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Fortsættes ...

DESCRIPTION

GOVERNMENTAL RIGHTS

[0001] This invention was made with government support under R01 AI073552 and HHSN272200700058C awarded by the NIH/NIAID and R01 HL113931 awarded by the NIH/HLBI. The government has certain rights in the invention.

CROSS REFERENCE TO RELATED APPLICATIONS

[0002] This application claims the benefit of U.S. Provisional Application number 62/243,829, filed October 20, 2015 and U.S. Provisional Application number 62/091,898, filed December 15, 2014.

FIELD OF THE INVENTION

[0003] The present disclosure encompasses compositions and methods for targeted cytokine delivery. Through specific delivery of cytokines, the compositions disclosed herein may improve immunotherapy by limiting side effects associated with immunotherapy.

BACKGROUND OF THE INVENTION

[0004] Systemic administration of high dose interleukin 2 (IL2) is one of the most potent forms of immunotherapy and is currently approved by the FDA for treatment of several malignancies. Efficacy of this treatment depends on activating cytotoxic lymphocytes (CTLs) such as natural killer cells (NK) and CD8⁺ T lymphocytes (CD8⁺ CTLs). Clinical trials have demonstrated approximately 15% partial or complete tumor responses, with up to 5% of patients having a durable long-lasting response resembling a cure. Despite these encouraging results in a minority of patients, most do not achieve a benefit or stop IL2 therapy prematurely due to complications such as blood pressure changes and pulmonary or systemic capillary leak. It is thought that the direct action of IL2 on vascular endothelium contributes to the majority of these side effects. The efficacy of IL2 is also limited by preferential activation of CD4⁺Foxp3⁺ regulatory T cells (T_{regs}), which decrease the tumor immune response. For these reasons treatment with high-dose IL2 has fallen out of favor clinically.

[0005] Side effects and decreased efficacy of IL2 therapy occur due to the high affinity trimeric $\alpha\beta\gamma$ IL2 receptor (IL2R), which is expressed by vascular endothelial cells and T_{regs} at baseline.

Thus CD4⁺Foxp3⁺T_{regs} and vascular endothelium are activated at much lower doses of IL2 than NK cells, which express the lower affinity βγ chains of the IL2R at rest. NK cells do express the high affinity α chain of IL2R after activation and depend on this trimeric receptor for peak cytolytic capacity. Mutant forms of IL2 with decreased affinity for IL2Rα have been described and offer a more favorable side effect profile. However, they also result in lower efficacy and decreased therapeutic potential due to decreased CTL activation. Therefore, there is a need in the art for a form of IL2 that could preferentially bind to and activate CTLs without activating T_{regs} and endothelial cells. Such an IL2 derivative might overcome such clinical barriers and result in more efficacious immunotherapy with fewer side effects.

SUMMARY OF THE INVENTION

[0006] In an aspect the disclosure provides, a composition comprising a cytokine linked to a ligand, wherein the ligand is not a corresponding binding partner to the cytokine.

[0007] In another aspect, the disclosure provides a method to deliver a cytokine to a target cell comprising contacting a target cell with a composition comprising a cytokine linked to a ligand. The ligand specifically binds to a receptor on the target cell and the ligand is not a corresponding binding partner to the cytokine.

[0008] In still another aspect, the disclosure provides a method to activate immune cells comprising contacting an immune cell with a composition comprising a proinflammatory cytokine linked to a ligand. The ligand specifically binds to a receptor on the immune cell thereby activating the cell and the ligand is not a corresponding binding partner to the cytokine.

[0009] In still yet another aspect, the disclosure provides a method to treat a tumor comprising identifying a subject with a tumor and administering to the subject a therapeutically effective amount of a composition comprising a proinflammatory cytokine linked to a ligand. The ligand specifically binds to a receptor on a target cell and the ligand is not a corresponding binding partner to the cytokine.

[0010] In a different aspect, the disclosure provides a method to treat a viral infection comprising administering to the subject a therapeutically effective amount of a composition comprising a proinflammatory cytokine linked to a ligand. The ligand specifically binds to a receptor on a target cell and the ligand is not a corresponding binding partner to the cytokine.

[0011] In other aspects, the disclosure provides a chimeric peptide comprising a cytokine peptide and a ligand peptide. The cytokine peptide is not a binding partner of the ligand peptide.

[0012] In certain aspects, the disclosure provides a chimeric peptide comprising a cytokine peptide and a ligand peptide. The ligand peptide binds to an NKG2D receptor.

[0013] In another different aspect, the disclosure provides a nucleic acid molecule comprising a sequence encoding a chimeric peptide of the disclosure.

[0014] In yet another different aspect, the disclosure provides a pharmaceutical composition comprising a chimeric peptide of the disclosure.

[0015] In still yet another different aspect, the disclosure provides a method of treating a subject diagnosed with cancer comprising administering to the subject a pharmaceutical composition of the disclosure.

BRIEF DESCRIPTION OF THE FIGURES

[0016] The application file contains at least one drawing executed in color. Copies of this patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

FIG. 1A, FIG. 1B, FIG. 1C, FIG. 1D, FIG. 1E and FIG. 1F depict a diagram, immunoblot and graphs showing the generation and *in vitro* evaluation of OMCP-mutIL-2. **(FIG. 1A)** Schematic structure of OMCP-mutIL-2. **(FIG. 1B)** Molecular weight of OMCP-mutIL-2 compared to mutIL-2 and wild-type IL-2. IL-2, mutIL-2, and OMCP-mutIL-2 were produced in mammalian cells and have higher molecular weights due to glycosylation. The lower migrating band for mutIL-2 corresponds to unglycosylated protein, likely due to lysis of the producing cells. Based on differences in molecular weight all cytokines and construct were administered on a molar basis with 1 μ l of 4.4 μ M solution defined as 1000 IU equivalents (IUe) herein. This effectively allows for equimolar comparison between IL-2, mutIL-2 and OMCP-mutIL-2 despite different molecular weights. **(FIG. 1C, FIG. 1D)** *In vitro* activation of A/J lymphocyte subsets after 36 hours of culture in 100 IUe of cytokines or OMCP-mutIL-2 construct. **(FIG. 1E, FIG. 1F)** Proliferation of B6 lymphocyte subsets after 5-day culture in 1000 IUe/ml of cytokines or OMCP-mutIL-2 construct. Graphs representative of 3-6 replicates per condition. black=saline; blue=wtIL-2, red=OMCP-mutIL-2, green=mutIL-2.

FIG. 2A, FIG. 2B, FIG. 2C, FIG. 2D, FIG. 2E, FIG. 2F, FIG. 2G, FIG. 2H, FIG. 2I, FIG. 2J, FIG. 2K, FIG. 2L, FIG. 2M, FIG. 2N and FIG. 2O depict graphs and images showing *in vivo* dosing of IL-2 and IL-2 constructs. Animal mortality **(FIG. 2A)** and morbidity assessed by weight loss **(FIG. 2B)** accumulation of ascites and pleural fluid (representative syringe-**FIG. 2C**; average from all mice in the group-**FIG. 2D**) and **(FIG. 2E)** organ inflammation after administration of wtIL-2. Animal mortality **(FIG. 2F, FIG. 2H, FIG. 2J)** and morbidity as assessed by weight loss **(FIG. 2G, FIG. 2I, FIG. 2K)** after administration of high dose wtIL-2 **(FIG. 2F, FIG. 2G)**, OMCP-mutIL-2 **(FIG. 2H, FIG. 2I)** and mutIL-2 **(FIG. 2J, FIG. 2K)** in anti-AsialoGM1 (solid line) or rabbit IgG-treated (dotted line) in A/J mice. Weight loss **(FIG. 2L)**, ascites (representative syringe-**FIG. 2M**; average from all mice in the group-**FIG. 2N**) and organ inflammation **(FIG. 2O)** in mice treated with 200,000 IUe of either wt IL-2, OMCP-mutIL-2 or mutIL-2. All graphs represent 46 animals per treatment condition. ns $p > .05$; * $p < .05$; **

p<.01; *** p<.001; black=saline; blue=wtIL-2, red=OMCP-mutIL-2, green=mutIL-2.

FIG. 3A, FIG. 3B, FIG. 3C, FIG. 3D, FIG. 3E, FIG. 3F, FIG. 3G, FIG. 3H, FIG. 3I and FIG. 3J depict graphs and images showing immunologic changes associated with IL-2 and IL-2 construct administration *in vivo*. (**FIG. 3A, FIG. 3B**) Total splenocyte counts after a five-day course of 200,000 IUe of IL-2 (blue), mutIL-2 (green) and OMCP-mutIL-2 (red). (**FIG. 3C**) NK cell expansion and activation after IL-2, mutIL-2, OMCP-mutIL-2, high dose IL-2, high dose mutIL-2 and IL-2/anti-IL-2 complexes measured by cell counts in the spleen (top) and KLRG1 upregulation (bottom). (**FIG. 3D**) CD4⁺Foxp3⁺T_{reg} expansion and activation as measured by cell counts in the spleen (top) and ICOS upregulation (bottom) as well as (**FIG. 3E**) NK/T_{reg} ratio in the spleen. Expansion of splenocytes (**FIG. 3F, FIG. 3G**) and NK cells (**FIG. 3H**) in B6 mice treated with 750,000 IUe of cytokine or construct. T_{reg} expansion and activation (**FIG. 3I**) as well as NK:T_{reg} ratio (**FIG. 3J**) in the spleen of B6 mice. All graphs represent an average cell count ± SEM from 5-10 mice per group. ns p>.05; * p<.05; ** p<.01; *** p<.001; black=saline; blue=wtIL-2, red=OMCP-mutIL-2, green=mutIL-2.

FIG. 4A, FIG. 4B, FIG. 4C, FIG. 4D and FIG. 4E depict graphs and images showing cytokine-mediated tumor immunotherapy. (**FIG. 4A**) *In vivo* cytotoxicity for YAC-1 lymphoma after intravenous injection. (**FIG. 4B, FIG. 4C**) LLC tumor growth after a five-day course of 750,000 IUe of cytokine treatment given as ten doses on days 5-10 post tumor injection. LLC tumor growth in mice depleted on NK cells (**FIG. 4D**) or mutant mice deficient in NKG2D (**FIG. 4E**). Data represents 5-6 mice per group. ns p>.05; * p<.05; ** p<.01; *** p<.001; black=saline; blue=wtIL-2, red=OMCP-mutIL-2, green=mutIL-2.

FIG. 5A, FIG. 5B, FIG. 5C, FIG. 5D, FIG. 5E, FIG. 5F, FIG. 5G, FIG. 5H, FIG. 5I, FIG. 5J and FIG. 5K depict graphs and a schematic showing IL-2 signaling in NK cells. (**FIG. 5A, FIG. 5B**) Serum levels after injection of 1x10⁶ IUe of fluorochromelabeled cytokine or construct i.v. (**FIG. 5C**) Degranulation of NK cells in the presence of cytokines and pentameric OMCP-mediated crosslinking of NKG2D as measured by surface CD107a expression at 1000 IUe/ml. STAT5 phosphorylation in isolated NK cells from A/J (**FIG. 5D**) or B6 mice (**FIG. 5E**) by increasing doses of cytokine. Decay in STAT5 phosphorylation after a 15 minute stimulation by 1000 IUe/ml (**FIG. 5F**) or 100 IUe/ml (**FIG. 5G**) of IL-2 or OMCP-mutIL-2. (**FIG. 5H**) Proposed model of competition between NK cells and stromal cells for IL-2. (**FIG. 5I**) STAT5 phosphorylation of B6 NK cells in the presence of other splenocytes by wtIL-2 and OMCP-mutIL-2. (**FIG. 5J**) STAT5 phosphorylation of wild-type or NKG2D^{-/-} NK cells by wtIL-2 and OMCP-mutIL-2 in the presence of competing splenocytes. (**FIG. 5K**) STAT5 phosphorylation, as measured by fold change over saline-treated controls, of wild-type NK cells in the presence of competing splenocytes treated with saturating concentrations of rat antimouse CD25 (clone 3C7) or rat IgG isotype control.

FIG. 6 depicts graphs showing B6 NK cells are preferentially activated by low dose OMCP-mutIL-2 but this selectivity disappears at the highest doses of cytokine or in the absence of NKG2D expression by NK cells. Left two graphs show B6 NK cells and right two graphs show BK NKG2D^{-/-} NK cells.

FIG. 7A, FIG. 7B and FIG. 7C depict imaging showing that inspection of the viscera demonstrates limited food consumption after a 5-day course of 200,000 or 750,000 IUe of wtIL-2. **FIG. 7D** depicts a graph showing that unlike the A/J strain, B6 mice are able to tolerate higher doses of wtIL-2 with only moderate weight loss after 750,000 IUe. Higher doses of 1,500,000 IUe IL-2 resulted in increased weight loss. Doses above this regimen led to animal death.

FIG. 8A depicts a graph showing that A/J mice treated with IL-2/anti-IL-2 antibodies or high dose mutIL-2 lost significant weight during treatment. The majority of IL-2/anti-IL-2 treated mice could not survive the full 200,000 IUe dosing and were sacrificed four days after starting treatment thus receiving 160,000-180,000 IUe. **FIG. 8B** depicts a graph and flow cytometric plot showing NK expansion with ULBP3-mutIL-2 and lower doses of OMCP-mutIL-2 in A/J spleen (top). NK activation, as measured by surface KLRG1 expression on NK cells treated with 200,000 IUe of mutIL-2 (green) or ULBP3-mutIL-2 (purple) in A/J spleen (bottom). **FIG. 8C** and **FIG. 8D** depict graphs showing that unlike the case for NK cells, little expansion of CD8⁺ or CD4⁺ Foxp3⁻ T cells was evident in either IL-2, OMCP-mut-IL-2, or mutIL-2 treated mice. **FIG. 8E** depicts a graph showing weight loss in B6 mice treated with high dose mutIL-2 or IL2/anti-IL-2 antibody complex. **FIG. 8F** and **FIG. 8G** depict graphs showing expansion of CD8⁺ or CD4⁺Foxp3⁻ T cells in cytokine treated B6 mice. Graphs represent 5-10 mice per group.

FIG. 9A and **FIG. 9B** depict graphs showing *in vitro* lysis of A/J tumors, such as LM2 lung adenocarcinoma (**FIG. 9A**) or YAC-1 lymphoma (**FIG. 9B**) by bulk splenocytes after a five day course of 200,000 IUe of cytokine given over ten doses. **FIG. 9C** shows *in vitro* lysis of LLC lung cancer by B6 splenocytes treated with 750,000 IUe of cytokines or constructs given over five days in ten doses.

FIG. 10A depicts flow cytometric plots showing that plate bound anti-NKG2D antibody (clone A10)-mediated augmentation of NK degranulation with cytokines added at 1000 IUe/ml. **FIG. 10B** depicts a flow cytometric plot showing CD69 levels on NK cells cultured at 100 IUe/ml of OMCP-mut-IL2 or mutIL-2 with pentameric OMCP.

FIG. 11A, FIG. 11B and **FIG. 11C** depict a schematic of the differential IL2 binding and activation *in vivo*. (**FIG. 11A**) Regular wild-type IL2 preferentially binds to cells such as CD4⁺Foxp3⁺T_{regs} and vascular endothelium, both of which express the high affinity α chain along with the signaling β and γ chains of the IL2 receptor. (**FIG. 11B**) The R38A and F42K mutations in IL2 decrease affinity for the α chain of the IL2 receptor. (**FIG. 11C**) By linking R38A/F42K IL2 to the high affinity NKG2D ligand OMCP delivery and binding of this cytokine to NKG2D-expressing CTLs such as NK cells and activated CD8⁺T cells is increased. Width of arrows indicates proposed strength of IL2 binding and/or signaling.

FIG. 12 depicts a schematic of the experimental design of immunotherapy experiments.

FIG. 13 depicts a schematic of the experimental design of vaccination experiments.

FIG. 14A and **FIG. 14B** depict graphs showing lung cancer susceptible and resistant strains of mice. (**FIG. 14A**) AJ and 129 mouse strains are susceptible to lung cancer as evidenced by tumor burden whereas B6 and C3H mouse strains are resistant to lung cancer as evidenced by tumor burden. (**FIG. 14B**) Upon incubation with freshly isolated NK cells from the various mouse strains, B6 and C3H NK cells result in significantly more LM2 lung carcinoma cell lysis than AJ and 129 NK cells.

FIG. 15 depicts a graph showing that in human men, a greater percentage of NK cells appear to produce TNF α in "resistant" patients versus "susceptible" patients.

FIG 16 depicts a graph showing that ex vivo cytokine activation can reverse natural killer cell dysfunction. Mouse NK Cells that did not show significant lysis of cancer cells (NK cells from 129 & AJ strains) were much more effective at lysis when treated with IL-2. NK cells from cancer-resistant strains also showed increase % of specific lysis.

FIG. 17A, FIG. 17B, FIG. 17C, FIG. 17D, FIG. 17E and **FIG. 17F** depict graphs showing binding of fluorescently labeled construct tested *in vitro* at 37 degrees in bulk splenocytes. The construct appears to only bind to NK cells (express NKG2D). Red line is OMCP-IL2 construct. (**FIG. 17A**) DX5+CD3- NK cell; (**FIG. 17B**) CD4+CD3+ T cells; (**FIG. 17C**) CD8+CD3+ T cells; (**FIG. 17D**) CD11C+CD11b- DCs; (**FIG. 17E**) CD11 c-CD11 b+ Macs; (**FIG. 17F**) CD19+CD3- B cells.

FIG. 18 depicts a schematic dosing regimen for IL2 or IL2 constructs.

FIG. 19 depicts a schematic dosing regimen for IL2 or IL2 constructs after irradiation.

FIG. 20A, FIG. 20B and **FIG. 20C** depict images and alignments of the OMCP structure. (**FIG. 20A**) Ribbon diagram of CPXV OMCP. Secondary structure elements are noted, S for beta strands and H for helix. The α 1/ α 2 portions of the platform domain are indicated in cyan and magenta, respectively. (**FIG. 20B**) Ribbon diagram of the α 1/ α 2 domain of MICA (PDB identifier 1HYR), with the α 3 domain removed for clarity. Residues that contact NKG2D are colored yellow. (**FIG. 20C**) Structure alignment of OMCP with NKG2DLs. The mature sequences of OMCP_{BR} (CPXV-BR-018; GenBank accession number NP_619807; PDB identifier 4FFE) and OMCP_{MPX} (MPXV-ZAR_1979_005-198; N3R; GenBank accession number AAY97396) are aligned with the ectodomain sequences of MICA (1HYR), MICB (1JE6), ULBP3 (1KCG), and RAE-1 β (1JFM). Known NKG2D contact residues for NKG2DLs are indicated in yellow. Asn residues likely to be glycosylated are noted by black boxes in panel C and as black side chains in panels A and B. OMCP_{br}=SEQ ID NO:13; OMCP_{mpx}=SEQ ID NO:14; MICA=SEQ ID NO:15; MICB=SEQ ID NO:16; ULBP3=SEQ ID NO:17; and RAE-1B=SEQ ID NO:18

FIG. 21 depicts a graph showing OMCP-targeted delivery of IL15. Higher levels of CD25 are evident when IL15 is delivered by OMCP vs naked cytokine alone in equimolar doses.

FIG. 22 depicts a graph showing that the D132R mutation in OMCP significantly decreases its NKG2D binding. NK expansion and activation in the presence of mutIL2, OMCP-mutIL2, and D132ROMCP-mutIL2 was tested. The D132R mutation ameliorated the superiority of natural

killer cell activation over cytokine alone.

FIG. 23 depicts various embodiments of the invention. 1. depicts OMCP helix 2 linked to cytokine. 2. depicts pegylation of the composition. 3. depicts a composition comprising engineered glycans. 4. depicts various linker lengths and compositions. 5. depicts an antibody linked to a cytokine. For example a Fab specific NKG2D antibody. 6. depicts a NKG2DL linked to a cytokine. For example, MIC or ULBP. 7 depicts an alternative OMCP linked to a cytokine. For example, OMCP_{mpx} could represent a preferred variant of OMCP, and mutant OMCP could represent either a gain or loss of function for NKG2D binding. 8. depicts re-targeting of the OMCP in a composition. For example, a mutant OMCP may be directed to NKG2A, NKG2C, NKG2E, etc. 9. depicts other viral protein linked to a cytokine. For example, the other viral protein may also bind to receptors on immune cells. 10. depicts OMCP linked to mutant cytokines. It is understood that the OMCP sequence could be from various sources such as cowpox or monkeypox. Also, Fc-chimeras of OMCP and IL2, and variants thereof may be used.

FIG. 24A and **FIG. 24B** depict the structure of OMCP in complex with NKG2D. (**FIG. 24A**) OMCP bound to NKG2D. OMCP is colored magenta and the protomers of NKG2D are colored cyan ("A") and yellow ("B"). NKG2D^A makes contacts primarily with the H2a helix and NKG2D^B with H2b. Mutations introduced to facilitate alternate crystal packing are shown in red. The S193-S194 bond is shown as a ball on each NKG2D protomer. The asparagines of putative hNKG2D glycosylation sites are shown in orange. The asparagine of the confirmed N-glycan site of OMCP is shown green (data not shown) (**FIG. 24B**) View of the interface between OMCP-NKG2D. The $\alpha 2$ domain of OMCP is shown in the front with the $\alpha 1$ domain behind. OMCP and NKG2D are shown with cartoon representations for the main chain, with the side chains of contact residues shown as sticks. Hydrogen bonds and salt bridges are indicated with green dotted lines.

FIG. 25A, **FIG. 25B** and **FIG. 25C** depicts the interface of OMCP and NKG2D. (**FIG. 25A**) The local environment of the OMCP-NKG2D binding interface surrounding the D132R residue. The D132R mutation ablates OMCP-NKG2D binding. (**FIG. 25B**) A representative experiment for binding of WT and (D132R) OMCP to NKG2D by SPR. 100 nM of OMCP or (D132R) OMCP were injected at 50 μ l/min over flowcells containing immobilized biotinylated murine NKG2D. (**FIG. 25C**) Ba/F3 cells transduced with NKG2D, FCRL5, or empty vector were stained with OMCP tetramers (solid line), D132R tetramers (dashed line), or WNV Dill tetramer control (gray histogram). Representative results from three independent experiments.

FIG. 26A, **FIG. 26B**, **FIG. 26C** and **FIG. 26D** depict the differences in the $\beta 5'$ - $\beta 5$ loop (L2) of human and murine NKG2D. (**FIG. 26A**, **FIG. 26B**) Superimposition of mNKG2D (grey) (PDB ID: 1HQ8) with the structure of OMCP-hNKG2D (yellow and cyan). Core binding residues Y152 (Y168) and Y199 (Y215) are positionally conserved, while core binding residue M184 (I200) is not. (**FIG. 26C**) Surface representation of OMCP (magenta) interacting with the $\beta 5'$ - $\beta 5$ loop. (**FIG. 26D**) Conservation of M184 and Q185. Only the NKG2D of mice, rats, guinea pigs, and flying foxes (not shown) differ. Conservation score is as computed by the ConSurf server. Human, orangutan, chimpanzee, gibbon, macaque-SEQ ID NO:19; Green monkey-SEQ ID

NO:20; Marmoset-SEQ ID NO:21; Mouse-SEQ ID NO:22; Rat-SEQ ID NO:23; Guinea pig-SEQ ID NO:24; Ground squirrel-SEQ ID NO:25; Deer mouse-SEQ ID NO:26; Naked mole rat-SEQ ID NO:27; Prairie vole-SEQ ID NO:28; European shrew-SEQ ID NO:29; Star-nosed mole-SEQ ID NO:30; Chinese hamster-SEQ ID NO:31; Cat-SEQ ID NO:32.

FIG. 27A, FIG. 27B, FIG. 27C, FIG. 27D, FIG. 27E, FIG. 27F, FIG. 27G, FIG. 27H and FIG. 27I depict a novel NKG2D binding adaptation. Surface representation of NKG2D and surface and cartoon representations of OMCP, MICA and ULBP3. Buried surface areas for NKG2D^A and NKG2D^B are indicated in cyan and yellow, respectively. Buried surface area by NKG2D is indicated for OMCP (magenta), MICA (green), and ULBP3 (orange). The core binding residues of NKG2D and NKG2D-binding elements of NKG2DLs are indicated. NKG2D (**FIG. 27A**) and OMCP (**FIG. 27B, FIG. 27C**) binding interactions. NKG2D (**FIG. 27D**) and MICA (**FIG. 27E, FIG. 27F**) binding interactions. NKG2D (**FIG. 27G**) and ULBP3 (**FIG. 27H, FIG. 27I**) binding interactions. (**FIG. 27J**) Alignment by secondary structure of NKG2DLs (PDB ID: OMCP (4FFE), MICA (1HYR), MICB (1JE6), ULBP3 (1KCG) and RAE-1 β (1JSK)). Contact residues are indicated for OMCP (magenta), MICA (green), ULBP3 (orange) and RAE-1 β (bold and italics). Secondary structure elements are noted above the sequence (arrow for beta sheets, cylinders for alpha helices). Predicted glycan sites are highlighted in black. OMCPbr=SEQ ID NO:13; OMCPmpx=SEQ ID NO:14; MICA=SEQ ID NO:15; MICB=SEQ ID NO:16; ULBP3=SEQ ID NO:17; and RAE-1B=SEQ ID NO:18

FIG. 28A, FIG. 28B, FIG. 28C, FIG. 28D and FIG. 28E depict activation of NK cells by cell-associated OMCP. Model depicting NKG2D interaction with (**FIG. 28A**) host, (**FIG. 28B**) cancer-induced, (**FIG. 28C**) viral, or (**FIG. 28D**) chimeric ligands. Binding interactions that lead to NKG2D-mediated signaling are indicated by DAP10 tyrosine phosphorylation (red filled circles). (**FIG. 28E**) IL-2-activated splenocytes were used as cytotoxic effectors against stably transduced Ba/F3 cell lines. Splenocytes were activated with 200 U/ml of IL-2 for 24 hours. Labeled target cells were co-incubated with activated splenocytes for 4 hours at effector:target ratios of 10:1, 20:1, and 40:1. Killing was measured by incorporation of 7AAD by CFSE-labeled target cells using flow cytometry. Representative data from five independent experiments is shown

FIG. 29A and FIG. 29B depict the electron density supporting a *cis* peptide conformation. Stereo view of the β 5- β 6 loop of hNKG2D. Residues 193-Ala-Ser-Ser-Phe-Lys-197 (SEQ ID NO:33) is displayed for the OMCP-hNKG2D structure (yellow) and the structure of hNKG2D alone (grey). The 2Fo-Fc map for OMCP- hNKG2D is displayed at 2σ .

FIG. 30A and FIG. 30B depicts graphs showing survival curves of C57Bl/6J mice following infection with West Nile Virus (WNV). Mice were treated with OMCP-IL2, OMCP(D132R)-IL2, IL2, IL(38R/42A) or PBS after infection with WNV. Infection with OMCP-IL2 and IL2(38R/42A) resulted in survival beyond 21 days in 40% of mice compared to 0 mice following treatment with PBS or OMCP(D132R)-IL2.

FIG. 31A, FIG. 31B, FIG. 31C and FIG. 31D depicts flow cytometry data showing that OMCP-Mutant IL2 activates NK and CD8⁺ T cells. **FIG. 31A** shows that a relatively higher proportion

of NK cells was evident in the OMCP-mutant IL2 group. **FIG. 31B** shows that perforin levels were higher in OMCP-mutant IL2 treated NK cells (red) compared to saline (black), IL2 (blue) or mutant IL2 (green) treated ones. **FIG. 31C** shows that similar to NK cells, higher intracellular levels of perforin were evident in CD8+ T cells treated with OMCP-mutant IL2 compared to other conditions. **FIG. 31 D** shows that when gating on CD4+Foxp3+CD45RA- T cells a relatively higher proportion of activated CD25+CD127- regulatory T cells was evident in IL2 treated peripheral blood lymphocyte cultures compared to other conditions.

FIG. 32 depicts a schematic of the various IL18-OMCP constructs. Three versions were made, each having OMCP attached to either WT human IL-18, WT murine IL-18, or mutant human IL-18 (which inhibits its interaction with IL-18BP).

FIG. 33 depicts a flow cytometry plot showing that IL18-OMCP activates NK cells. Peripheral blood lymphocytes were cultured for 48 hours in 4.4 μ M of either wild-type IL18 (blue), OMCP-IL18 (red) or saline (black). Activation of CD56+CD3-Natural killer cells, as measured by surface CD69 expression, was superior by OMCP-IL18 compared to wild-type IL18.

DETAILED DESCRIPTION OF THE INVENTION

[0017] The compositions and methods described herein provide for delivery of cytokines to a defined cell via a ligand. The fusion of a cytokine to a ligand which specifically binds to a protein on the target cell creates an "address" for delivery of the cytokine. Specifically, using the invention disclosed herein, IL2 is directly targeted to lymphocytes, such as natural killer (NK) cells and CD8+ cytotoxic T lymphocytes (CTLs), via the orthopoxvirus major histocompatibility complex class I-like protein (OMCP) ligand. However other NKG2D ligands, including but not limited to ULBP1, ULBP2, ULBP3, H60, Rae-1 α , Rae-1 β , Rae-1 δ , Rae-1 γ , MICA, MICB, h-HLA-A, could also be used instead of OMCP. Specific delivery of IL2 to lymphocytes will enhance the efficacy of IL2, which could lead to reduced dosages and a significant decrease in associated toxicity. This methodology may be used for other cytokines, including, but not limited to, IL15, IL18 and interferons.

[0018] Specific aspects of the invention are described in detail below.

I. COMPOSITION

[0019] In an aspect, the invention encompasses a composition comprising a cytokine linked to a ligand. The composition may further comprise a linker to connect the cytokine to the ligand. The cytokine, ligand and linker are described in greater detail below. It should be understood that any of the cytokines described in detail below can be linked to any of the ligands described in detail below in the absence or presence of any of the linkers described below. In another

aspect, the invention provides a nucleic acid molecule encoding a cytokine, a ligand, and optionally a linker.

(a) cytokine

[0020] As used herein, a "cytokine" is a small protein (~5-20 kDa) that is important in cell signaling. Cytokines are released by cells and affect the behavior of other cells and/or the cells that release the cytokine. Non-limiting examples of cytokines include chemokines, interferons, interleukins, lymphokines, tumor necrosis factor, monokines, and colony stimulating factors. Cytokines may be produced by a broad range of cells including, but not limited to, immune cells such as macrophages, B lymphocytes, T lymphocytes, mast cells and monocytes, endothelial cells, fibroblasts and stromal cells. A cytokine may be produced by more than one type of cell. Cytokines act through receptors and are especially important in the immune system, modulate the balance between humoral and cell-based immune responses, and regulate maturation, growth and responsiveness of cell populations. Cytokines are important in host responses to infection, immune responses, inflammation, trauma, sepsis, cancer and reproduction. A cytokine of the invention may be a naturally occurring cytokine or may be a mutated version of a naturally occurring cytokine. As used herein, "naturally occurring", which may also be referred to as wild-type, includes allelic variances. A mutated version or "mutant" of a naturally occurring cytokine refers to specific mutations that have been made to the naturally occurring sequence to alter the function, activity and/or specificity of the cytokine. In one embodiment, the mutations may enhance the function, activity and/or specificity of the cytokine. In another embodiment, the mutations may decrease the function, activity and/or specificity of the cytokine. The mutation may include deletions or additions of one or more amino acid residues of the cytokine.

[0021] Cytokines may be classified based on structure. For example, cytokines may be classified into four types: the four- α -helix bundle family, the IL1 family, the IL17 family and the cysteine-knot cytokines. Members of the four- α -helix bundle family have three-dimensional structures with four bundles of α -helices. This family is further divided into three sub-families: the IL2 subfamily, the interferon (IFN) subfamily and the IL10 subfamily. The IL2 subfamily is the largest and comprises several non-immunological cytokines including, but not limited to, erythropoietin (EPO) and thrombopoietin (TPO). In certain embodiments, a cytokine of the composition is a cytokine from the four- α -helix bundle family or a mutant thereof. A skilled artisan would be able to determine cytokines within the four- α -helix bundle family. In other embodiments, a cytokine of the composition is an IL2 subfamily cytokine or a mutant thereof. Non-limiting examples of members of the IL2 subfamily include IL2, IL4, IL7, IL9, IL15 and IL21. In a specific embodiment, a cytokine of the composition is IL2 or a mutant thereof. In certain embodiments, a cytokine of the composition is IL15 or a mutant thereof. The sequence information for the full length human IL15 amino acid sequence can be found using, for example, the GenBank accession number CAG46777.1, AAI00962.1 or AAI00963.1. The sequence information for the full length human IL15 mRNA sequence can be found using, for example, the GenBank accession number CR542007.1, KJ891469.1, NM_172175.2,

NM_000585.4 or CR541980.1. A skilled artisan will appreciate that IL15 may be found in a variety of species and methods of identifying analogs or homologs of IL15 are known in the art as described in detail below.

[0022] In another embodiment, a cytokine of the invention is an IL1 family cytokine or a mutant thereof. The IL1 family is a group of 11 cytokines, which plays a central role in the regulation of immune and inflammatory responses. Generally, the IL1 family of cytokines are proinflammatory cytokines that regulate and initiate inflammatory responses. Non-limiting examples of IL1 family cytokines include IL1 α , IL1 β , IL1Ra, IL18, IL36Ra, IL36 α , IL37, IL36 β , IL36 γ , IL38, and IL33. IL1 family members have a similar gene structure. A skilled artisan would be able to determine cytokines within the IL1 family. In certain embodiments, a cytokine of the composition is IL18 or a mutant thereof. The sequence information for the full length human IL18 amino acid sequence can be found using, for example, the GenBank accession number CAG46771.1. The sequence information for the full length human IL18 mRNA sequence can be found using, for example, the GenBank accession number KR710147.1, CR542001.1, CR541973.1 or KJ897054.1. A skilled artisan will appreciate that IL18 may be found in a variety of species and methods of identifying analogs or homologs of IL18 are known in the art as described in detail below.

[0023] In other embodiments, a cytokine of the composition is an interferon subfamily cytokine or a mutant thereof. Interferons are named for their ability to "interfere" with viral replication by protecting cells from virus infection. IFNs also have other functions: they activate immune cells, such as natural killer cells and macrophages; they increase host defenses by up-regulating antigen presentation by virtue of increasing the expression of major histocompatibility complex (MHC) antigens. Based on the type of receptor through which they signal, human interferons have been classified into three major types: Type I IFN, Type II IFN, and Type III IFN. Type I IFNs bind to a specific cell surface receptor complex known as the IFN- α/β receptor (IFNAR) that consists of IFNAR1 and IFNAR2 chains. Non-limiting examples of type I interferons present in humans are IFN- α , IFN- β , IFN- ϵ , IFN- κ and IFN- ω . Thus, in certain embodiments, a cytokine of the composition is a Type 1 IFN cytokine or a mutant thereof, including, but not limited to wild-type and mutant forms of IFN- α , IFN- β , IFN- ϵ , IFN- κ and IFN- ω . Type II IFNs bind to IFNGR that consists of IFNGR1 and IFNGR2 chains. Non-limiting examples of type II interferons present in humans is IFN- γ . Thus, in certain embodiments, a cytokine of the composition is a Type II IFN cytokine or a mutant thereof, including, but not limited to wild-type and mutant forms of IFN- γ . Type III IFNs signal through a receptor complex consisting of IL10R2 (also called CRF2-4) and IFNLR1 (also called CRF2-12). Non-limiting examples of type III interferons include IFN- λ 1, IFN- λ 2 and IFN- λ 3 (also called IL29, IL28A and IL28B respectively). Thus, in certain embodiments, a cytokine of the composition is a Type III IFN cytokine or a mutant thereof, including, but not limited to wild-type and mutant forms of IFN- λ 1, IFN- λ 2 and IFN- λ 3.

[0024] In certain embodiments, a cytokine of the invention is an interleukin or mutant thereof. The majority of interleukins are synthesized by helper CD4 T lymphocytes, as well as through monocytes, macrophages, and endothelial cells. Interleukins may promote the development

and differentiation of T and B lymphocytes and hematopoietic cells. Non-limiting examples of interleukins include IL1, IL2, IL3, IL4, IL5, IL6, IL7, IL8 (CXCL8), IL9, IL10, IL11, IL12, IL13, IL14, IL15, IL16, IL17, IL18, IL19, IL20, IL21, IL22, IL23, IL24, IL25, IL26, IL27, IL28, IL29, IL30, IL31, IL32, IL33, IL35, or IL36. Thus, in certain embodiments, a cytokine of the composition is an interleukin or a mutant thereof, including, but not limited to wild-type and mutant forms of IL1, IL2, IL3, IL4, IL5, IL6, IL7, IL8 (CXCL8), IL9, IL10, IL11, IL12, IL13, IL14, IL15, IL16, IL17, IL18, IL19, IL20, IL21, IL22, IL23, IL24, IL25, IL26, IL27, IL28, IL29, IL30, IL31, IL32, IL33, IL35, or IL36. In a specific embodiment, a cytokine of the composition is IL2 or a mutant thereof. IL2 is a lymphokine that induces the proliferation of responsive T cells. In addition, it acts on some B cells, via receptor-specific binding, as a growth factor and antibody production stimulant. The IL2 protein is secreted as a single glycosylated polypeptide, and cleavage of a signal sequence is required for its activity. The structure of IL2 comprises a bundle of 4 helices (termed A-D), flanked by 2 shorter helices and several poorly defined loops. Residues in helix A, and in the loop region between helices A and B, are important for receptor binding. Secondary structure analysis suggests similarity to IL4 and granulocyte-macrophage colony stimulating factor (GM-CSF). In a specific embodiment, a cytokine of the composition is IL2 or a variant thereof. A variant may be a truncated or mutated IL2. The sequence information for the full length human IL2 amino acid sequence can be found using, for example, the GenBank accession number AAA59140.1 or AAH70338.1. The sequence information for the full length human IL2 mRNA sequence can be found using, for example, the GenBank accession number BC070338.1 or M22005.1.

[0025] A skilled artisan will appreciate that IL2 may be found in a variety of species. Non-limiting examples include mouse (AAI16874.1), pig (NP_999026.1), cattle (AAQ10670.1), rat (EDM01295.1), rabbit (AAC23838.1), goat (AAQ10671.1), sheep (ABK41601.1), chicken (AAV35056.1), hamster (ERE88380.1), and dog (AAA68969.1). It is appreciated that the present invention is directed to analogs of IL2 in other organisms and is not limited to the human analog. Homologs can be found in other species by methods known in the art. For example, sequence similarity may be determined by conventional algorithms, which typically allow introduction of a small number of gaps in order to achieve the best fit. In particular, "percent identity" of two polypeptides or two nucleic acid sequences is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches may be performed with the BLASTN program to obtain nucleotide sequences homologous to a nucleic acid molecule of the invention. Equally, BLAST protein searches may be performed with the BLASTX program to obtain amino acid sequences that are homologous to a polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) are employed. See www.ncbi.nlm.nih.gov for more details. Generally a homolog will have a least 80, 81, 82, 83, 84, 85, 86, 87, 88, or 89% homology. In another embodiment, the sequence may be at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100% homologous to IL2.

[0026] In a specific embodiment, a cytokine of the composition is a wildtype sequence of IL2 such as the sequence set forth in SEQ ID NO:5 (APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCL EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNR WITFCQSIISTLT). In an alternative embodiment, a cytokine is a mutated version of IL2. In an embodiment, a mutation is a mutation that causes IL2 to preferentially bind the receptor IL2 β . In another embodiment, a mutation is a mutation that alters the function of IL2 such that IL2 has a decreased affinity for the IL2 receptor alpha (IL2R α). For example, a mutation may be one or more mutations selected from the group consisting of R38A, F42K and/or C125S relative to SEQ ID NO:5. The C125S mutation may be included to reduce protein aggregation. In a specific embodiment, a mutated version of IL2 comprises at least one mutation selected from the group consisting of R38A, F42K and C125S relative to SEQ ID NO:5. In another specific embodiment, a mutated version of IL2 comprises the mutations R38A, F42K and C125S relative to SEQ ID NO:5. In a specific embodiment, a cytokine of the composition is a mutated sequence of IL2 such as the sequence set forth in SEQ ID NO:6 (APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTKKFYMPKKATELKHLQCL EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNR WITFSQSIISTLT).

[0027] In an alternative aspect, a toxin is substituted for a cytokine. The term "toxin" means the toxic material or product of plants, animals, microorganisms (including, but not limited to, bacteria, viruses, fungi, rickettsiae or protozoa), or infectious substances, or a recombinant or synthesized molecule, whatever their origin and method of production. A toxin may be a small molecule, peptide, or protein that is capable of causing disease on contact with or absorption by body tissues interacting with biological macromolecules such as enzymes or cellular receptors. A toxin may be a "biotoxin" which is used to explicitly identify the toxin as from biological origin. Biotoxins may be further classified into fungal biotoxins, or short mycotoxins, microbial biotoxins, plant biotoxins, short phytotoxins and animal biotoxins. Non-limiting examples of biotoxins include: cyanotoxins, produced by cyanobacteria, such as microcystins, nodularins, anatoxin-a, cylindrospermopsins, lyngbyatoxin-a, saxitoxin, lipopolysaccharides, aplysiatoxins, BMAA; dinotoxins, produced by dinoflagellates, such as saxitoxins and gonyautoxins; necrotoxins produced by, for example, the brown recluse or "fiddle back" spider, most rattlesnakes and vipers, the puff adder, *Streptococcus pyogenes*; neurotoxins, produced by, for example, the black widow spider, most scorpions, the box jellyfish, elapid snakes, the cone snail, the Blue-ringed octopus, venomous fish, frogs, palythoa coral, various different types of algae, cyanobacteria and dinoflagellates, such as botulinum toxin (e.g. Botox), tetanus toxin, tetrodotoxin, chlorotoxin, conotoxin, anatoxin-a, bungarotoxin, caramboxin, curare; myotoxins, found in, for example, snake and lizard venoms; and cytotoxins such as ricin, from castor beans, apitoxin, from honey bees, and T-2 mycotoxin, from certain toxic mushrooms. In certain embodiments, a toxin is a cytotoxin. In an embodiment, a cytotoxin is selected from the group consisting of ricin, apitoxin, and T-2 mycotoxin. In a specific embodiment, a toxin is ricin.

[0028] In certain embodiments, a cytokine or toxin of the invention may be PEGylated for

improved systemic half-life and reduced dosage frequency. In an embodiment, PEG may be added to a cytokine or toxin. As such, a composition of the invention may comprise a cytokine or toxin comprising PEG. In an embodiment, PEG may be selected from the group consisting of PEG-10K, PEG-20K and PEG-40K. Methods of conjugating PEG to a protein are standard in the art. For example, see Kolate et al, Journal of Controlled Release 2014; 192(28): 67-81. Still further, a cytokine or toxin of the invention may be modified to remove T cell epitopes. T cell epitopes can be the cause of an immunogenicity issue upon administration of a composition to a subject. Through their presentation to T cells, they activate the process of anti-drug antibody development. Preclinical screening for T cell epitopes may be performed *in silico*, followed by *in vitro* and *in vivo* validation. T cell epitope-mapping tools such as EpiMatrix can be highly accurate predictors of immune response. Deliberate removal of T cell epitopes may reduce immunogenicity. Other means of improving the safety and efficacy of a composition of the invention by reducing their immunogenicity include humanization and PEGylation.

(b) ligand

[0029] As used herein, a "ligand" is a protein that specifically binds to a receptor on a target cell and is not the corresponding binding partner to the cytokine linked to the ligand. A ligand may be from a eukaryote, a prokaryote or a virus. In certain embodiments, a ligand may be from a virus. The phrase "specifically binds" herein means ligands bind to the target protein with an affinity (K_d) in the range of at least 0.1 mM to 1 pM, or in the range of at least 0.1 pM to 200 nM, or in the range of at least 0.1 pM to 10 nM. A dissociation constant (K_d) measures the propensity of a larger object to separate (dissociate) reversibly into smaller components. The dissociation constant is the inverse of the association constant. The dissociation constant may be used to describe the affinity between a ligand (L) and a target protein (P). As such, $K_d = ([P] \times [L]) / [C]$, wherein C is a ligand-target protein complex and wherein [P], [L] and [C] represent molar concentrations of the protein, ligand and complex, respectively. Methods of determining whether a ligand binds to a target protein are known in the art. For instance, see the Rossi and Taylor, Nature Protocols 2011; 6: 365-387.

[0030] A ligand may trigger a signal through its binding to a receptor on a target cell. A receptor is a protein molecule that may be embedded within the plasma membrane surface of a cell that receives chemical signals from outside the cell. When such chemical signals bind to a receptor, they cause some form of cellular/tissue response. In preferred embodiments, a target cell is an immune cell. Accordingly, a ligand of the composition binds to a receptor expressed on immune cells. Non-limiting example of immune cells include macrophages, B lymphocytes, T lymphocytes, mast cells, monocytes, dendritic cells, eosinophils, natural killer cells, basophils, neutrophils. Thus, in certain embodiments, immune cells include, but are not limited to, macrophages, B lymphocytes, T lymphocytes, mast cells, monocytes, dendritic cells, eosinophils, natural killer cells, basophils, neutrophils. In a specific embodiment, an immune cell is a natural killer cell or a T lymphocyte. Non-limiting examples of receptors expressed on immune cells include major histocompatibility complex (MHC; e.g. MHC I, MHC II, and MHC III),

toll-like receptors (TLRs; e.g. TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, TLR11, TLR12, and TLR13), CD94/NKG2 family receptor, endothelin receptors, signaling lymphocytic activation molecule (SLAM) family of receptors. Thus, in certain embodiments, a receptor on a target cell includes, but is not limited to, major histocompatibility complex (MHC; e.g. MHC I, MHC II, and MHC III), toll-like receptors (TLRs; e.g. TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10, TLR11, TLR12, and TLR13), CD94/NKG2 family receptor, endothelin receptors, signaling lymphocytic activation molecule (SLAM) family of receptors. In a specific embodiment, the receptor on a target cell is a CD94/NKG2 family receptor. In another specific embodiment, a ligand of the composition specifically binds to a receptor expressed on natural killer (NK) cells and CD8+ cytotoxic T lymphocytes (CTLs). In preferred embodiments, a ligand of the composition does not specifically bind to a receptor on vascular endothelial cells or regulatory T cells (T_{regs}).

[0031] A receptor expressed on NK cells and CTLs may be a CD94/NKG2 family receptor or KLRG1. KLRG1 (Killer cell lectin-like receptor subfamily G member 1) is a protein that in humans is encoded by the KLRG1 gene. CD94/NKG2 family receptors are a family of C-type lectin receptors which are expressed predominantly on the surface of NK cells and a subset of CD8+ T-lymphocyte. These receptors stimulate or inhibit cytotoxic activity of NK cells, therefore they are divided into activating and inhibitory receptors according to their function. CD94/NKG2 recognize MHC class I-related glycoproteins. CD94/NKG2 family includes seven members: NKG2A, NKG2B, NKG2C, NKG2D, NKG2E, NKG2F and NKG2H. Thus, in certain embodiments, a ligand of the invention specifically binds to a receptor selected from the group consisting of NKG2A, NKG2B, NKG2C, NKG2D, NKG2E, NKG2F and NKG2H. NKG2 receptors are transmembrane proteins type II which dimerize with CD94 molecule. CD94 contains a short cytoplasmic domain and it is responsible for signal transduction. Therefore NKG2 receptors form disulfide bonded heterodimers. NKG2D represents an exception, it is a homodimer. NKG2A and NKG2B receptors transmit inhibitory signal. NKG2C, NKG2E and NKG2H are activating receptors. NKG2D is activating receptor as well but it couples with adaptor protein DAP10 which carries signaling motif YINM (SEQ ID NO:34). Src or Jak kinases phosphorylate DAP10, which can then associate with p85 subunit of PI(3)K or adaptor molecule Grb2. This signaling triggers actin reorganization (cell polarization) and degranulation. NKG2F receptor function has not been clarified yet.

[0032] In a specific embodiment, a ligand of the composition specifically binds to the NKG2D receptor. NKG2D is an activating receptor found on NK cells and CD8+ T cells (both $\alpha\beta$ and $\gamma\delta$). The structure of NKG2D consists of two disulphide-linked type II transmembrane proteins with short intracellular domains incapable of transducing signals. The function of NKG2D on CD8+ T cells is to send co-stimulatory signals to activate them. In an embodiment, a ligand that binds to NKG2D may be an anti-NKG2D antibody. An "anti-NKG2D" includes all antibodies that specifically bind an epitope within NKG2D. The term "antibody" includes the term "monoclonal antibody". "Monoclonal antibody" refers to an antibody that is derived from a single copy or clone, including e.g., any eukaryotic, prokaryotic, or phage clone. Monoclonal antibodies can be produced using e.g., hybridoma techniques well known in the art, as well as recombinant technologies, phage display technologies, synthetic technologies or combinations of such

technologies and other technologies readily known in the art. Further by "antibody" is meant a functional monoclonal antibody, or an immunologically effective fragment thereof; such as an Fab, Fab', or F(ab')₂ fragment thereof. As long as the protein retains the ability specifically to bind its intended target, it is included within the term "antibody." Also included within the definition "antibody" for example are single chain forms, generally designated Fv, regions, of antibodies with this specificity. These scFvs are comprised of the heavy and light chain variable regions connected by a linker. Methods of making and using scFvs are known in the art. Additionally, included within the definition "antibody" are single-domain antibodies, generally designated sdAb, which is an antibody fragment consisting of a single monomeric variable antibody domain. A sdAb antibody may be derived from camelids (V_HH fragments) or cartilaginous fishes (V_{NAR} fragments). As used herein "humanized antibody" includes an anti-NKG2D antibody that is composed partially or fully of amino acid sequence sequences derived from a human antibody germline by altering the sequence of an antibody having non-human complementarity determining regions ("CDR"). The simplest such alteration may consist simply of substituting the constant region of a human antibody for the murine constant region, thus resulting in a human/murine chimera which may have sufficiently low immunogenicity to be acceptable for pharmaceutical use. Preferably, however, the variable region of the antibody and even the CDR is also humanized by techniques that are by now well known in the art. The framework regions of the variable regions are substituted by the corresponding human framework regions leaving the non-human CDR substantially intact, or even replacing the CDR with sequences derived from a human genome. CDRs may also be randomly mutated such that binding activity and affinity for NKG2D is maintained or enhanced in the context of fully human germline framework regions or framework regions that are substantially human. In certain embodiments, an anti-NKG2D antibody is a Fab, Fab', or F(ab')₂ fragment.

[0033] In another embodiment, ligands that bind to NKG2D share an MHC class I-related $\alpha 1\alpha 2$ superdomain that constitutes the common site for interaction with NKG2D. Non-limiting examples of ligands that bind to NKG2D include MHC class I-related glycoproteins such as MIC family proteins (i.e., MICA, MICB), UL16-binding family proteins (i.e., ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, ULBP6), retinoid acid early induce gene 1 (Rae1)-like proteins (i.e., Rae1 α , Rae1 β , Rae1 γ , Rae1 δ , Rae1 ϵ), members of the H60 protein family (i.e., H60a, H60b, H60c), h-HLA-A, as well as Mult1 in mice and orthopoxvirus major histocompatibility complex class I-like protein (OMCP). In certain embodiments, a ligand is a MHC class-I-related glycoprotein. In other embodiments, a ligand of the invention is selected from the group consisting of MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, ULBP6, Rae1 α , Rae1 β , Rae1 γ , Rae1 δ , Rae1 ϵ , H60a, H60b, H60c, h-HLA-A, Mult1 and OMCP. In an embodiment, a ligand is a UL16-binding family protein or a MIC family protein. In a specific embodiment, a ligand is selected from the group consisting of ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and ULBP6. In another specific embodiment, a ligand is ULBP3. In a specific embodiment, a ligand is orthopoxvirus major histocompatibility complex class I-like protein (OMCP) or a variant thereof. A variant may be a truncated or mutated OMCP that has about the same binding affinity of the full length OMCP. In an embodiment, a variant may be a truncated or mutated OMCP that has a slightly lower binding affinity relative to the binding affinity of the full length OMCP. In another embodiment, a variant is a truncated or mutated OMCP that has a slightly

higher binding affinity relative to the binding affinity of the full length OMCP. Methods to determine binding affinity of a ligand to target protein are known in the art and described above. OMCP specifically binds to NKG2D with a binding affinity of about 0.1 to about 5 nM. For example, OMCP specially binds to human NKG2D with a binding affinity of about 0.2 nM and mouse NKG2D with a binding affinity of about 3 nM. In a preferred embodiment, OMCP or a variant thereof binds to human NKG2D with a binding affinity of about 1000 nM to about 0.1 nM. In certain embodiments, OMCP or a variant thereof binds to human NKG2D with a binding affinity of about 100 nM to about 0.1 nM, about 10 nM to about 0.1 nM, or about 1 nM to about 0.1 nM. In other embodiments, OMCP or a variant thereof binds to human NKG2D with a binding affinity of about 1000 nM to about 1 nM, or about 1000 nM to about 10 nM, or about 1000 nM to about 100 nM. In still other embodiments, OMCP or a variant thereof binds to human NKG2D with a binding affinity of about 100 nM to about 1 nM, or about 100 nM to 10 nM. For example, OMCP or a variant thereof binds to human NKG2D with a binding affinity of about 1000 nM, about 500 nM, about 100 nM, about 50 nM, about 10 nM, about 9 nM, about 8 nM, about 7 nM, about 6 nM about 5 nM, about 4 nM, about 3 nM, about 2 nM, about 1 nM, about 0.9 nM, about 0.8 nM, about 0.7 nM, about 0.6 nM, about 0.5 nM, about 0.4 nM, about 0.3 nM, about 0.2 nM or about 0.1 nM. In another embodiment, a variant is a truncated or mutated OMCP that has binding affinity for one or more NKG2 family receptors other than NKG2D. For example, a variant is a truncated or mutated OMCP that has binding affinity for one or more NKG2 family receptors selected from the group consisting of NKG2A, NKG2B, NKG2C, NKG2E, NKG2F and NKG2H. Mutations to OMCP may be rationally selected via structure-based knowledge or mutations to OMCP may be identified via selection-based mutagenesis. In certain embodiments, mutations may be rationally selected to occur in the OMCP-NKG2D interface to either enhance or reduce binding affinity. Amino acids involved in binding at the OMCP-NKG2D interface are described in the Examples.

[0034] The structure of OMCP consists of an MHCI-like $\alpha 1/\alpha 2$ platform domain (**FIG. 20A**). The platform domain of OMCP has been trimmed to have only a six-stranded beta sheet with shorter flanking helices. The helix of the OMCP $\alpha 1$ domain (H1) is continuous, while the helix of the $\alpha 2$ domain is broken into two regions (H2a and H2b). The helices flank a six-stranded beta sheet and together form the characteristic platform that defines MHC proteins. Like other NKG2DLs (**FIG. 20B**), the alpha helices of OMCP are close together and thus have no groove for binding peptides or other ligands like antigen-presenting MHC platform domains. OMCP contains one disulfide bond between S5 and H2b, and this disulfide bond is conserved in most NKG2DLs (**FIG. 20C**). In certain embodiments, a ligand of the invention comprises one or more of the α helices of a MHC class I-related glycoprotein. In other embodiments, a ligand of the invention consists of one or more of the α helices of a MHC class I-related glycoprotein. More specifically, a ligand of the invention comprises the $\alpha 1$ domain (H1), $\alpha 2$ domain (H2), H2a, H2b, or combinations thereof of a MHC class I-related glycoprotein. Or, a ligand of the invention consists of the $\alpha 1$ domain (H1), $\alpha 2$ domain (H2), H2a, H2b, or combinations thereof of a MHC class I-related glycoprotein. In a specific embodiment, a ligand of the invention comprises the $\alpha 2$ domain (H2) of a MHC class I-related glycoprotein. In another specific embodiment, a ligand of the invention consists of the $\alpha 2$ domain (H2) of a MHC class I-related glycoprotein. A skilled artisan would be able to determine the location of the α helices in other

MHC class I-related glycoproteins, for example, using sequence alignment (see FIG. 20C, which is reproduced from Lazear et al. J Virol 2013; 87(2): 840-850, which is hereby incorporated by reference in its entirety). In an embodiment, a ligand of the invention comprises one or more of the α helices of OMCP. In another embodiment, a ligand of the invention comprises the $\alpha 1$ domain (H1), $\alpha 2$ domain (H2), H2a, H2b, or combinations thereof of OMCP. In still another embodiment, a ligand of the invention comprises the $\alpha 2$ domain (H2) of OMCP. In a specific embodiment, a ligand of the invention consists of one or more of the α helices of OMCP. In another specific embodiment, a ligand of the invention consists of the $\alpha 1$ domain (H1), $\alpha 2$ domain (H2), H2a, H2b, or combinations thereof of OMCP. In still another specific embodiment, a ligand of the invention consists of the $\alpha 2$ domain (H2) of OMCP.

[0035] The sequence information for the full length OMCP amino acid sequence can be found using, for example, the GenBank accession number 4FFE_Z, 4FFE_Y or 4FFE_X. A skilled artisan will appreciate that homologs of OMCP may be found in other species or viruses. For example, see Lefkowitz et al, Nucleic Acids Res 2005; 33: D311-316, which describes eighteen OMCP variants between cowpox and monkeypox virus strains. In an embodiment, OMCP is from an orthopoxvirus. In a specific embodiment, OMCP is from a cowpox virus or a monkeypox virus. In another specific embodiment, OMCP is from the Brighton Red strain of cowpoxvirus. Homologs can be found in other species by methods known in the art. For example, sequence similarity may be determined by conventional algorithms, which typically allow introduction of a small number of gaps in order to achieve the best fit. In particular, "percent identity" of two polypeptides or two nucleic acid sequences is determined using the algorithm of Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87:2264-2268, 1993). Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul et al. (J. Mol. Biol. 215:403-410, 1990). BLAST nucleotide searches may be performed with the BLASTN program to obtain nucleotide sequences homologous to a nucleic acid molecule of the invention. Equally, BLAST protein searches may be performed with the BLASTX program to obtain amino acid sequences that are homologous to a polypeptide of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST is utilized as described in Altschul et al. (Nucleic Acids Res. 25:3389-3402, 1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) are employed. See www.ncbi.nlm.nih.gov for more details. Generally a homolog will have a least 80, 81, 82, 83, 84, 85, 86, 87, 88, or 89% homology. In another embodiment, the sequence may be at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100% homologous to OMCP.

[0036] A skilled artisan will appreciate that structural homologs of OMCP may be found in other species or viruses. A structural homolog may be a protein that is structurally related but the sequence is a distal homolog. For example, OMCP has low sequence identity for endogenous NKG2D ligands however it was discovered that OMCP would bind to NKG2D based on structural homology. Structural homologs can be found in other species by methods known in the art. For example, protein structure prediction may be determined by various databases, such as Phyre and Phyre2. Such databases generate reliable protein models that may be used to determine structural homologs. The main results table in Phyre2 provides confidence

estimates, images and links to the three-dimensional predicted models and information derived from either Structural Classification of Proteins database (SCOP) or the Protein Data Bank (PDB) depending on the source of the detected template. For each match a link takes the user to a detailed view of the alignment between the user sequence and the sequence of known three-dimensional structure. See www.sbg.bio.ic.ac.uk/phyre2/ for more details. Generally, a structural homolog will have a least 50, 51, 52, 53, 54, 55, 56, 57, 58, or 59% confidence with OMCP. In an embodiment, a structural homolog will have a least 60, 61, 62, 63, 64, 65, 66, 67, 68, or 69% confidence with OMCP. In another embodiment, a structural homolog will have a least 70, 71, 72, 73, 74, 75, 76, 77, 78, or 79% confidence with OMCP. In still another embodiment, a structural homolog will have a least 80, 81, 82, 83, 84, 85, 86, 87, 88, or 89% confidence with OMCP. In still yet another embodiment, a structural homolog may have at least 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, or 100% confidence with OMCP. The structural information for OMCP-human NKG2D may be found using the PDB ID: 4PDC.

[0037] In a specific embodiment, a ligand of the composition is a sequence of OMCP such as the sequence set forth in SEQ ID NO:7 (HKLAFNFNLEINGSDTHSTVDVYLDDSQITFDGKDIRPTIPFMIGDEIFLPFYKNVFSEF FSLFRRVPTSTPYEDLTYFYECDYTDNKSTFDQFYLYNGEEYTVKTQEATNKNMWLTT SEFRLKKWFDGEDCIMHLRSLVRKMEDSKRNT). In an embodiment, a ligand of the composition is a sequence of OMCP comprising at least 80% identity to SEQ ID NO:7. For example, the ligand may have about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identity to SEQ ID NO:7.

[0038] In another specific embodiment, a ligand of the composition is a sequence of OMCP such as the sequence set forth in SEQ ID NO:13 (GHKLAFFNFNLEINGSDTHSTVDVYLDDSQITFDGKDIRPTIPFMIGDEIFLPFYKNVFSE FFSLFRRVPTSTPYEDLTYFYECDYTDNKSTFDQFYLYNGEEYTVKTQEATNKNMWLT TSEFRLKKWFDGEDCIMHLRSLVRKMEDSKR). In an embodiment, a ligand of the composition is a sequence of OMCP comprising at least 80% identity to SEQ ID NO:13. For example, the ligand may have about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identity to SEQ ID NO:13.

[0039] In still another specific embodiment, a ligand of the composition is a sequence of OMCP such as the sequence set forth in SEQ ID NO:14 (HKLHVHFNFKINGSKITNTADILLDNYPIMTFDGKDIYPSIAFMVGNKLFLLDLYKNIFVEF FRLFRVSVSSQYEELEYYSYCDYTNNRPTIKQHIFYNGEEYTEIDRSKKATNKNMWLIT SGFRLQKWFDSEDCIYLRSLVRRMEDSNK). In an embodiment, a ligand of the composition is a sequence of OMCP comprising at least 80% identity to SEQ ID NO:14. For example, the ligand may have about 80%, about 81%, about 82%, about 83%, about 84%, about 85%, about 86%, about 87%, about 88%, about 89%, about 90%, about 91%, about 92%, about 93%,

about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% identity to SEQ ID NO:14.

[0040] In an alternative aspect, a receptor expressed on immune cells may be PD1. PD1, also known as programmed cell death protein 1 and CD279 (cluster of differentiation 279), is a protein that in humans is encoded by the PDCD1 gene. PD1 is a cell surface receptor that belongs to the immunoglobulin superfamily and is expressed on T cells and pro-B cells. PD1 binds two ligands, PDL1 and PDL2. PD1, functioning as an immune checkpoint, plays an important role in down regulating the immune system by preventing the activation of T-cells. In certain embodiments, a ligand of the composition specifically binds to PD1. In an embodiment, a ligand that specifically binds to PD1 may be an anti-PD1 antibody. An "anti-PD1" includes all antibodies that specifically bind an epitope within PD1. The term "antibody" is described above. In another embodiment, a ligand that specifically binds to PD1 may be PDL1. PDL1 (programmed death-ligand 1 also known as cluster of differentiation 274 (CD274) or B7 homolog 1 (B7-H1), is a protein that in humans is encoded by the CD274 gene. PDL1 binds to its receptor, PD1, found on activated T cells, B cells, and myeloid cells, to modulate activation or inhibition. The affinity between PDL1 and PD1, as defined by the dissociation constant K_d , is 770nM.

[0041] In another aspect, a ligand of the composition may be Glucocorticoid-induced TNFR-related (GITR) ligand (GITRL). GITR activation by GITRL influences the activity of effector and regulatory T cells, thus participating in the development of immune response against tumors and infectious agents, as well as in autoimmune and inflammatory diseases. GITR triggering stimulates T effector activity and inhibits Treg activity. GITR inhibition may ameliorate autoimmune/inflammatory diseases whereas GITR activation may treat viral, bacterial and parasitic infections, as well as boost immune responses against tumors. GITRL is a type II transmembrane protein expressed at high levels on antigen presenting cells (APC) and endothelial cells.

[0042] In certain embodiments, a ligand of the invention is modified for improved systemic half-life and reduced dosage frequency. In an embodiment, N-glycans may be added to a ligand. While the biological function is typically determined by the protein component, carbohydrate can play a role in molecular stability, solubility, *in vivo* activity, serum half-life, and immunogenicity. The sialic acid component of carbohydrate in particular, can extend the serum half-life of protein therapeutics. Accordingly, new N-linked glycosylation consensus sequences may be introduced into desirable positions in the peptide backbone to generate proteins with increased sialic acid containing carbohydrate, thereby increasing *in vivo* activity due to a longer serum half-life. In another embodiment, PEG may be added to a ligand. Methods of conjugating PEG to a protein are standard in the art. For example, see Kolate et al, Journal of Controlled Release 2014; 192(28): 67-81. In an embodiment, a composition of the invention may comprise a ligand comprising PEG and/or one or more N-glycans. In an embodiment, PEG is selected from the group consisting of PEG-10K, PEG-20K and PEG-40K. Still further, a ligand of the invention may be modified to remove T cell epitopes. T cell epitopes can be the cause of an immunogenicity issue upon administration of a composition to a subject. Through

their presentation to T cells, they activate the process of anti-drug antibody development. Preclinical screening for T cell epitopes may be performed *in silico*, followed by *in vitro* and *in vivo* validation. T cell epitope-mapping tools such as EpiMatrix can be highly accurate predictors of immune response. Deliberate removal of T cell epitopes may reduce immunogenicity. Other means of improving the safety and efficacy of a composition of the invention by reducing their immunogenicity include humanization and PEGylation.

(c) linker

[0043] In an aspect, a composition of the invention further comprises a linker. The linker may be used to connect the cytokine to the ligand. It is to be understood that linking the cytokine to the ligand will not adversely affect the function of the cytokine or the ligand. Suitable linkers include amino acid chains and alkyl chains functionalized with reactive groups for coupling to both the cytokine and the ligand or combinations thereof.

[0044] In an embodiment, the linker may include amino acid side chains, referred to as a peptide linker. Amino acid residue linkers are usually at least one residue and can be 50 or more residues, but alone do not specifically bind to the target protein. In an embodiment, a linker may be about 1 to about 10 amino acids. In another embodiment, a linker may be about 10 to about 20 amino acids. In still another embodiment, a linker may be about 20 to about 30 amino acids. In still yet another embodiment, a linker may be about 30 to about 40 amino acids. In different embodiments, a linker may be about 40 to about 50 amino acids. In other embodiments, a linker may be more than 50 amino acids. For instance, a linker may be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 amino acids. In a specific embodiment, a linker is about 20 to about 30 amino acids. In another specific embodiment, a linker is about 26 amino acids.

[0045] Any amino acid residue may be used for the linker provided the linker does not specifically bind to the target protein. Typical amino acid residues used for linking are glycine, serine, alanine, leucine, tyrosine, cysteine, lysine, glutamic and aspartic acid, or the like. For example, a linker may be $(AAS)_n$, $(AAAL)_n$, $(G_nS)_n$ or $(G_2S)_n$, wherein A is alanine, S is serine, L is leucine, and G is glycine and wherein n is an integer from 1-20, or 1-10, or 3-10. Accordingly, n may be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20. Thus, in certain embodiments, a linker includes, but is not limited to, $(AAS)_n$, $(AAAL)_n$, $(G_nS)_n$ or $(G_2S)_n$, wherein A is alanine, S is serine, L is leucine, and G is glycine and wherein n is an integer from 1-20, or 1-10, or 3-10. A linker may comprise one or more epitope tags. For instance, a linker may comprise 1, 2, 3, 4, 5, 6, 7 or 8 epitope tags. In a specific embodiment, a linker comprises 2 epitope tags. Non-limiting examples of epitope tags include FLAG tag (DYKDDDK epitope (SEQ ID NO:9)), HA tag (YPYDVPDYA epitope (SEQ ID NO:10)), His tag (6x-His or 8x-His), Myc tag (EQKLISEEDL epitope (SEQ ID NO:11)) and V5 tag (GKPIPPLLGLDST epitope (SEQ ID NO:12)). In an embodiment, a linker may comprise at

least one tag selected from the group consisting of a FLAG tag and a His tag. In a specific embodiment, a linker comprises a FLAG tag and a His tag. In another specific embodiment, a linker comprises the sequence set forth in SEQ ID NO:8 (GSSGSSDYKDDDDKHHHHHHHHGSSGSS).

[0046] In another embodiment, an alkyl chain linking group may be coupled to the cytokine by reacting the terminal amino group or the terminal carboxyl group with a functional group on the alkyl chain, such as a carboxyl group or an activated ester. Subsequently the ligand is attached to the alkyl chain to complete the formation of the complex by reacting a second functional group on the alkyl chain with an appropriate group on the ligand. The second functional group on the alkyl chain is selected from substituents that are reactive with a functional group on the ligand while not being reactive with the cytokine. For example, when the ligand incorporates a functional group, such as a carboxyl group or an activated ester, the second functional group of the alkyl chain linking group can be an amino group or vice versa. It will be appreciated that formation of the conjugate may require protection and deprotection of the functional groups present in order to avoid formation of undesired products. Protection and deprotection are accomplished using protecting groups, reagents, and protocols common in the art of organic synthesis. Particularly, protection and deprotection techniques employed in solid phase peptide synthesis may be used. It will be appreciated that linking groups may alternatively be coupled first to the ligand and then to the cytokine.

[0047] An alternative chemical linking group to an alkyl chain is polyethylene glycol (PEG), which is functionalized in the same manner as the alkyl chain described above. Such a linker may be referred to as a heterobifunctional PEG linker or a homobifunctional PEG linker. Non-limiting examples of heterobifunctional PEG linkers include: O-(2-Aminoethyl)-O'-[2-(biotinylamino)ethyl]octaethylene glycol; O-(2-Aminoethyl)-O'-(2-carboxyethyl)polyethylene glycol hydrochloride M_p 3000; O-(2-Aminoethyl)-O'-(2-carboxyethyl)polyethylene glycol 5,000 hydrochloride M_p 5,000; O-(2-Aminoethyl)polyethylene glycol 3,000 M_p 3,000; O-(2-Aminoethyl)-O'-(2-(succinylamino)ethyl)polyethylene glycol hydrochloride M_p 10,000; O-(2-Azidoethyl)heptaethylene glycol; O-[2-(Biotinylamino)ethyl]-O'-(2-carboxyethyl)undecaethylene glycol; 21-[D(+)-Biotinylamino]-4,7,10,13,16,19-hexaoxaheneicosanoic acid; O-(2-Carboxyethyl)-O'-[2-(Fmoc-amino)-ethyl]heptacosaeethylene glycol; O-(2-Carboxyethyl)-O'-(2-mercaptoethyl)heptaethylene glycol; O-(3-Carboxypropyl)-O'-[2-(3-mercaptopropionylamino)ethyl]-polyethylene glycol M_w 3000; O-(3-Carboxypropyl)-O'-[2-(3-mercaptopropionylamino)ethyl]-polyethylene glycol M_w 5000; O-[N-(3-Maleimidopropionyl)aminoethyl]-O'-[3-(N-succinimidyl)-3-oxopropyl]heptacosaeethylene glycol; and O-[2-(3-Tritylthiopropionylamino)ethyl]polyethylene glycol M_p 3,000. Non-limiting examples of homobifunctional PEG linkers include: MAL-PEG-MAL (Bifunctional Maleimide PEG Maleimide); OPSS-PEG-OPSS (OPSS: orthopyridyl disulfide; PDP-PEG-PDP); HS-PEG-SH (Bifunctional Thiol PEG Thiol); SG-PEG-SG (Bifunctional PEG Succinimidyl Glutarate NHS ester); SS-PEG-SS (Bifunctional PEG Succinimidyl Succinate NHS ester); GAS-PEG-GAS (Bifunctional PEG Succinimidyl ester NHS-PEG-NHS); SAS-PEG-SAS (Bifunctional PEG Succinimidyl ester NHS-PEG-NHS); Amine-PEG-Amine (Bifunctional PEG Amine NH₂-PEG-

NH₂); AC-PEG-AC (Bifunctional Acrylate PEG Acrylate); ACA-PEG-ACA (Bifunctional Polymerizable PEG Acrylate Acrylamide); Epoxide-PEG-Epoxide (Bifunctional PEG Epoxide or EP); NPC-PEG-NPC (Bifunctional NPC PEG, Nitrophenyl Carbonate); Aldehyde-PEG-Aldehyde (ALD-PEG-ALD, bifunctional PEG propionaldehyde); AA-PEG-AA (Acid-PEG-Acid, AA - acetic acid or carboxyl methyl); GA-PEG-GA (Acid - PEG - Acid, GA: Glutaric acid); SA-PEG-SA (Bifunctional PEG carboxylic acid - Succinic Acid); GAA-PEG-GAA (Bifunctional PEG carboxylic acid, Glutaramide Acid); SAA-PEG-SAA (Bifunctional PEG carboxylic acid, Succinamide Acid); Azide-PEG-Azide (Bifunctional PEG azide, N₃-PEG-N₃); Alkyne-PEG-Alkyne (Bifunctional alkyne or acetylene PEG); Biotin-PEG-Biotin (Bifunctional biotin PEG linker); Silane-PEG-Silane (Bifunctional silane PEG); Hydrazide-PEG-Hydrazide (Bifunctional PEG Hydrazide); Tosylate-PEG-Tosylate (Bifunctional PEG Tosyl); and Chloride-PEG-Chloride (Bifunctional PEG Halide).

[0048] In certain embodiments, a linker of the invention may be modified for improved systemic half-life and reduced dosage frequency. In an embodiment, N-glycans are added to a linker. While the biological function is typically determined by the protein component, carbohydrates can play a role in molecular stability, solubility, *in vivo* activity, serum half-life, and immunogenicity. The sialic acid component of carbohydrate in particular, can extend the serum half-life of protein therapeutics. Accordingly, new N-linked glycosylation consensus sequences may be introduced into desirable positions in the peptide backbone to generate proteins with increased sialic acid containing carbohydrate, thereby increasing *in vivo* activity due to a longer serum half-life. In another embodiment, PEG is added to a linker. Methods of conjugating PEG to a protein are standard in the art. For example, see Kolate et al, Journal of Controlled Release 2014; 192(28): 67-81. In an embodiment, a composition of the invention comprises a ligand comprising PEG and/or one or more N-glycans. In an embodiment, PEG is selected from the group consisting of PEG-10K, PEG-20K and PEG-40K.

[0049] Another aspect of the invention involves cross-linking the peptides of the invention to improve their pharmacokinetic, immunogenic, diagnostic, and/or therapeutic attributes. Cross-linking involves joining two molecules by a covalent bond through a chemical reaction at suitable site(s) (e.g., primary amines, sulfhydryls) on the cytokine and ligand of the invention. In an embodiment, the cytokine and ligand may be crosslinked together. The cross-linking agents may form a cleavable or non-cleavable linker between the cytokine and the ligand. Cross-linking agents that form non-cleavable linkers between the cytokine and the ligand may comprise a maleimido- or haloacetyl-based moiety. According to the present invention, such non-cleavable linkers are said to be derived from maleimido- or haloacetyl-based moiety. Cross-linking agents comprising a maleimido-based moiety include N-succinimidyl 4-(maleimidomethyl)cyclohexanecarboxylate (SMCC), N-succinimidyl-4-(N-maleimidomethyl)-cyclohexane-1-carboxy-(6-amidocaproate), which is a "long chain" analog of SMCC (LC-SMCC), κ -maleimidoundecanoic acid N-succinimidyl ester (KMUA), γ -maleimidobutyric acid N-succinimidyl ester (GMBS), ϵ -maleimidocaproic acid N-hydroxysuccinimide ester (EMCS), m-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS), N-(α -maleimidoacetoxy)-succinimide ester [AMAS], succinimidyl-6-(β -maleimidopropionamido)hexanoate (SMPH), N-succinimidyl 4-(p-maleimidophenyl)-butyrate (SMPB), and N-(p-maleimidophenyl)isocyanate (PMPI). These cross-linking agents form non-cleavable linkers derived from maleimido-based moieties.

Crosslinking agents comprising a haloacetyl-based moiety include N-succinimidyl-4-(iodoacetyl)-aminobenzoate (SIAB), N-succinimidyl iodoacetate (SIA), N-succinimidyl bromoacetate (SBA) and N-succinimidyl 3-(bromoacetamido)propionate (SBAP). These cross-linking agents form non-cleavable linkers derived from haloacetyl-based moieties. Cross-linking agents that form non-cleavable linkers between the cytokine and the ligand may comprise N-succinimidyl 3-(2-pyridyldithio)propionate, 4-succinimidyl-oxycarbonyl- α -methyl- α -(2-pyridyldithio)-toluene (SMPT), N-succinimidyl-3-(2-pyridyldithio)-butyrate (SDPB), 2-iminothiolane, or acetylsuccinic anhydride.

(d) chimeric peptide

[0050] According to the present invention, there is provided a chimeric peptide comprising a cytokine peptide and a ligand peptide, wherein the cytokine peptide is not a binding partner of the ligand peptide and wherein the ligand peptide is a binding partner to a receptor expressed on natural killer (NK) cells or CD8+ cytotoxic T lymphocytes (CTLs), wherein the receptor is the NKG2D receptor, and wherein the cytokine peptide is selected from the group consisting of IL2, IL7, IL15, IL18, IL21, and mutants thereof. In still another aspect, the invention encompasses a chimeric peptide comprising a cytokine peptide and a ligand peptide, wherein the ligand peptide binds to an NKG2D receptor. It should be understood that "ligand peptide" is used interchangeably with "ligand" and "cytokine peptide" is used interchangeably with "cytokine" for purposes of descriptions herein of various cytokines and ligands that are suitable for use in the present compositions and methods.

[0051] In certain embodiments, the cytokine peptide is in the IL2 subfamily. More specifically, the cytokine peptide is selected from the group consisting of IL2, IL7, IL15 and IL21. In a specific embodiment, the cytokine peptide is IL15 or a mutant thereof. In another specific embodiment, the cytokine peptide is IL2 or a mutant thereof. In another embodiment, the cytokine peptide is mutant IL2 comprising at least one mutation selected from the group consisting of R38A, F42K and C125S. In a specific embodiment, the cytokine peptide comprises the amino acid sequence set forth in SEQ ID NO:5 or SEQ ID NO:6. In other embodiments, the cytokine peptide is in the IL1 family. More specifically, the cytokine peptide is selected from the group consisting of IL1 α , IL1 β , IL1Ra, IL18, IL36Ra, IL36 α , IL37, IL36 β , IL36 γ , IL38, and IL33. In a specific embodiment, the cytokine peptide is IL18 or a mutant thereof.

[0052] In certain embodiments, the ligand peptide is a MHC class-I-related glycoprotein. In another embodiment, the ligand peptide is OMCP, a portion thereof, or a mutant thereof. In an embodiment, the ligand peptide binds to a receptor expressed on NK cells and CD8+ CTLs. In a specific embodiment, the ligand peptide binds to an NKG2D receptor. In certain embodiments, the ligand peptide comprises the amino acid sequence set forth in SEQ ID NO:7 or a portion thereof that is capable of binding to the NKG2D receptor.

[0053] In other embodiments, a chimeric peptide further comprises a linker peptide. In certain

embodiments, a linker peptide comprises the amino acid sequence selected from the group consisting of $(AAS)_n$, $(AAAL)_n$, $(G_nS)_n$ or $(G_2S)_n$, wherein A is alanine, S is serine, L is leucine, and G is glycine and wherein n is an integer from 1-20, or 1-10, or 3-10. In a different embodiment, a linker peptide comprises at least one tag selected from the group consisting of a FLAG tag and a His tag. In an embodiment, a linker peptide is about 20 to about 30 amino acids. In a specific embodiment, a linker peptide comprises the amino acid sequence set forth in SEQ ID NO:8.

[0054] The invention also encompasses a nucleic acid molecule encoding a chimeric peptide as described herein. Additionally, the invention encompasses a pharmaceutical composition comprising a chimeric peptide as described herein. Pharmaceutical compositions are described in more detail in **Section I(f)**.

(e) preferred embodiments

[0055] By way of non-limiting example, several preferred compositions of the invention are depicted in **FIG. 23**. 1. depicts a composition comprising $\alpha 2$ domain (H2) of OMCP linked to a cytokine. 2. depicts a composition comprising OMCP linked to a cytokine, wherein the composition is pegylated. 3. depicts a composition comprising OMCP linked to a cytokine, wherein the composition comprises N-glycan. 4. depicts a composition comprising, OMCP linked to a cytokine, wherein the linker comprises various sequences and various lengths. 5. depicts a composition comprising a Fab specific antibody for NKG2D linked to a cytokine. 6. depicts a composition comprising various NKG2D ligands linked to a cytokine. 7. depicts a composition comprising a mutated version of OMCP linked to a cytokine, wherein the OMCP may be mutated to have improved binding affinity or weaker binding affinity. 8. depicts a composition comprising a mutated version of OMCP linked to a cytokine, wherein the OMCP may be mutated to have binding affinity for other NKG2 receptors. 9. depicts a composition comprising a viral protein linked to a cytokine. For example, OMCP binds to NKG2D. Additionally, CPXV203 binds to MHCI. 10. depicts a composition comprising OMCP linked to a mutated cytokine. It is understood that the OMCP sequence could be from various sources such as cowpox or monkeypox. Also, Fc-chimeras of OMCP and IL2, and variants thereof may be used.

[0056] In a preferred embodiment, the composition comprises IL2, IL15 or IL18 linked to OMCP. In another preferred embodiment, the composition comprises IL2, IL15 or IL18 linked to OMCP via a peptide linker. In still another preferred embodiment, the composition comprises IL2, IL15 or IL18 linked to OMCP via a peptide linker comprising about 20 to about 30 amino acids. In still yet another preferred embodiment, the composition comprises IL2, IL15 or IL18 linked to OMCP via a peptide linker comprising a FLAG tag and a His tag. In each of the foregoing embodiments, the IL2 may be a mutated version of IL2 comprising the mutations R38A and F42K.

[0057] In a different preferred embodiment, the composition comprises IL2 linked to OMCP. In

another preferred embodiment, the composition comprises IL2 linked to OMCP via a peptide linker. In still another preferred embodiment, the composition comprises IL2 linked to OMCP via a peptide linker comprising about 20 to about 30 amino acids. In still yet another preferred embodiment, the composition comprises IL2 linked to OMCP via a peptide linker comprising a FLAG tag and a His tag. In each of the foregoing embodiments, the IL2 may be a mutated version of IL2 comprising the mutations R38A and F42K.

[0058] In an exemplary embodiment, the composition comprises the DNA sequence set forth in SEQ ID NO:1

(CACAAACTCGCATTCAACTTCAATCTAGAAATAAATGGCAGTGATACACATTCTAC
 AGTAGATGTATATCTTGATGATTCTCAAATTATAACGTTTGATGGAAAAGATAT
 CCGTCCAACCATCCCGTTCATGATAGGTGATGAAATTTTCTTACCGTTTTATAAAA
 ATGTGTTTAGTGAGTTTTTCTCTCTGTTTAGAAGAGTTCCTACAAGTACTCCATATG
 AAGACTTGACATATTTTTATGAATGCGACTATACAGACAATAAATCTACATTTGATCA
 GTTTTATCTTTATAATGGCGAAGAATATACTGTCAAACACAGGAGGCCACTAATAA
 AAATATGTGGCTAACTACTTCCGAGTTTAGACTAAAAAATGGTTTCGATGGCGAAG
 ATTGTATAATGCATCTTAGATCGTTAGTTAGAAAAATGGAGGACAGTAAACGAAACA
 CTGGTGGTACCGGAAGTAGCGGTAGTAGTGATTACAAGGACGATGACGACAAGCA
 CCACCATCATCATCATCACCACGGTAGCAGCGGCAGCAGTGCCCCCACCTCTAGC
 AGCACAAAGAAGACCCAGCTGCAACTGGAACACCTCCTGCTGGACCTGCAGATGA
 TCCTGAACGGCATCAACA ACTACAAGAACCCCAAGCTGACCGCCATGCTGACCAA
 AAAGTTTTACATGCCCAAGAAGGCCACCGAGCTTAAACACCTGCAATGCCTTGAGG
 AGGAGCTGAAGCCCTGGAGGAGGTACTGAACCTGGCCCAGAGCAAGAACTTTCAT
 CTGAGGCCCAGGGACCTGATTAGCAACATCAACGTGATCGTGTTGGAGTTGAAGG
 GCAGCGAGACCACGTTTCATGTGCGAGTACGCCGACGAGACGGCCACCATAGTGG
 AGTTTCTTAACAGGTGGATCACCTTCTCACAGTCTATCATCAGCACCCCTGACC).

[0059] In another exemplary embodiment, the composition comprises the amino acid sequence set forth in SEQ ID NO:2

(HKLAFNFNLEINGS DTHSTVDVYLDDSQIITFDGKDIRPTIPFMIGDEIFLPFYKNVFSEF
 FSLFRRVPTSTPYEDLTYFYECDYTDNKSTFDQFYLYNGEEYTVKTQEATNKNMWLTT
 SEFRLKKWFDGEDCIMHLRSLVRKMEDSKRNTGGTGSSGSSDYKDDDDKHHHHHHH
 HGSSGSSAPTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTKKFYMPKKATE
 LKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETA
 TIVEFLNRWITFSQSIISTLT).

(f) pharmaceutical compositions

[0060] The present invention also provides pharmaceutical compositions. The pharmaceutical composition of the invention comprises the chimeric peptide of the invention, which is detailed above, as an active ingredient and at least one pharmaceutically acceptable excipient.

[0061] The pharmaceutically acceptable excipient may be a diluent, a binder, a filler, a buffering agent, a pH modifying agent, a disintegrant, a dispersant, a preservative, a lubricant, taste-masking agent, a flavoring agent, or a coloring agent. The amount and types of excipients utilized to form pharmaceutical compositions may be selected according to known principles of pharmaceutical science.

[0062] In one embodiment, the excipient may be a diluent. The diluent may be compressible (i.e., plastically deformable) or abrasively brittle. Non-limiting examples of suitable compressible diluents include microcrystalline cellulose (MCC), cellulose derivatives, cellulose powder, cellulose esters (i.e., acetate and butyrate mixed esters), ethyl cellulose, methyl cellulose, hydroxypropyl cellulose, hydroxypropyl methylcellulose, sodium carboxymethylcellulose, corn starch, phosphated corn starch, pregelatinized corn starch, rice starch, potato starch, tapioca starch, starch-lactose, starch-calcium carbonate, sodium starch glycolate, glucose, fructose, lactose, lactose monohydrate, sucrose, xylose, lactitol, mannitol, malitol, sorbitol, xylitol, maltodextrin, and trehalose. Non-limiting examples of suitable abrasively brittle diluents include dibasic calcium phosphate (anhydrous or dihydrate), calcium phosphate tribasic, calcium carbonate, and magnesium carbonate.

[0063] In another embodiment, the excipient may be a binder. Suitable binders include, but are not limited to, starches, pregelatinized starches, gelatin, polyvinylpyrrolidone, cellulose, methylcellulose, sodium carboxymethylcellulose, ethylcellulose, polyacrylamides, polyvinylloxazolidone, polyvinylalcohols, C₁₂-C₁₈ fatty acid alcohol, polyethylene glycol, polyols, saccharides, oligosaccharides, polypeptides, oligopeptides, and combinations thereof.

[0064] In another embodiment, the excipient may be a filler. Suitable fillers include, but are not limited to, carbohydrates, inorganic compounds, and polyvinylpyrrolidone. By way of non-limiting example, the filler may be calcium sulfate, both di- and tri-basic, starch, calcium carbonate, magnesium carbonate, microcrystalline cellulose, dibasic calcium phosphate, magnesium carbonate, magnesium oxide, calcium silicate, talc, modified starches, lactose, sucrose, mannitol, or sorbitol.

[0065] In still another embodiment, the excipient may be a buffering agent. Representative examples of suitable buffering agents include, but are not limited to, phosphates, carbonates, citrates, tris buffers, and buffered saline salts (e.g., Tris buffered saline or phosphate buffered saline).

[0066] In various embodiments, the excipient may be a pH modifier. By way of non-limiting example, the pH modifying agent may be sodium carbonate, sodium bicarbonate, sodium citrate, citric acid, or phosphoric acid.

[0067] In a further embodiment, the excipient may be a disintegrant. The disintegrant may be non-effervescent or effervescent. Suitable examples of non-effervescent disintegrants include, but are not limited to, starches such as corn starch, potato starch, pregelatinized and modified starches thereof, sweeteners, clays, such as bentonite, micro-crystalline cellulose, alginates, sodium starch glycolate, gums such as agar, guar, locust bean, karaya, pectin, and tragacanth. Non-limiting examples of suitable effervescent disintegrants include sodium bicarbonate in combination with citric acid and sodium bicarbonate in combination with tartaric acid.

[0068] In yet another embodiment, the excipient may be a dispersant or dispersing enhancing agent. Suitable dispersants may include, but are not limited to, starch, alginic acid, polyvinylpyrrolidones, guar gum, kaolin, bentonite, purified wood cellulose, sodium starch glycolate, isoamorphous silicate, and microcrystalline cellulose.

[0069] In another alternate embodiment, the excipient may be a preservative. Non-limiting examples of suitable preservatives include antioxidants, such as BHA, BHT, vitamin A, vitamin C, vitamin E, or retinyl palmitate, citric acid, sodium citrate; chelators such as EDTA or EGTA; and antimicrobials, such as parabens, chlorobutanol, or phenol.

[0070] In a further embodiment, the excipient may be a lubricant. Non-limiting examples of suitable lubricants include minerals such as talc or silica; and fats such as vegetable stearin, magnesium stearate or stearic acid.

[0071] In yet another embodiment, the excipient may be a taste-masking agent. Taste-masking materials include cellulose ethers; polyethylene glycols; polyvinyl alcohol; polyvinyl alcohol and polyethylene glycol copolymers; monoglycerides or triglycerides; acrylic polymers; mixtures of acrylic polymers with cellulose ethers; cellulose acetate phthalate; and combinations thereof.

[0072] In an alternate embodiment, the excipient may be a flavoring agent. Flavoring agents may be chosen from synthetic flavor oils and flavoring aromatics and/or natural oils, extracts from plants, leaves, flowers, fruits, and combinations thereof.

[0073] In still a further embodiment, the excipient may be a coloring agent. Suitable color additives include, but are not limited to, food, drug and cosmetic colors (FD&C), drug and cosmetic colors (D&C), or external drug and cosmetic colors (Ext. D&C).

[0074] The weight fraction of the excipient or combination of excipients in the composition may be about 99% or less, about 97% or less, about 95% or less, about 90% or less, about 85% or less, about 80% or less, about 75% or less, about 70% or less, about 65% or less, about 60% or less, about 55% or less, about 50% or less, about 45% or less, about 40% or less, about 35% or less, about 30% or less, about 25% or less, about 20% or less, about 15% or less, about 10% or less, about 5% or less, about 2%, or about 1% or less of the total weight of the composition.

[0075] The composition can be formulated into various dosage forms and administered by a number of different means that will deliver a therapeutically effective amount of the active ingredient. Such compositions can be administered orally, parenterally, or topically in dosage unit formulations containing conventional nontoxic pharmaceutically acceptable carriers, adjuvants, and vehicles as desired. Topical administration may also involve the use of transdermal administration such as transdermal patches or iontophoresis devices. The term parenteral as used herein includes subcutaneous, intravenous, intramuscular, or intrasternal injection, or infusion techniques. Formulation of drugs is discussed in, for example, Gennaro, A. R., Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton, Pa. (18th ed, 1995), and Liberman, H. A. and Lachman, L., Eds., Pharmaceutical Dosage Forms, Marcel Dekker Inc., New York, N.Y. (1980).

[0076] Solid dosage forms for oral administration include capsules, tablets, caplets, pills, powders, pellets, and granules. In such solid dosage forms, the active ingredient is ordinarily combined with one or more pharmaceutically acceptable excipients, examples of which are detailed above. Oral preparations may also be administered as aqueous suspensions, elixirs, or syrups. For these, the active ingredient may be combined with various sweetening or flavoring agents, coloring agents, and, if so desired, emulsifying and/or suspending agents, as well as diluents such as water, ethanol, glycerin, and combinations thereof.

[0077] For parenteral administration (including subcutaneous, intradermal, intravenous, intramuscular, and intraperitoneal), the preparation may be an aqueous or an oil-based solution. Aqueous solutions may include a sterile diluent such as water, saline solution, a pharmaceutically acceptable polyol such as glycerol, propylene glycol, or other synthetic solvents; an antibacterial and/or antifungal agent such as benzyl alcohol, methyl paraben, chlorobutanol, phenol, thimerosal, and the like; an antioxidant such as ascorbic acid or sodium bisulfite; a chelating agent such as ethylenediaminetetraacetic acid; a buffer such as acetate, citrate, or phosphate; and/or an agent for the adjustment of tonicity such as sodium chloride, dextrose, or a polyalcohol such as mannitol or sorbitol. The pH of the aqueous solution may be adjusted with acids or bases such as hydrochloric acid or sodium hydroxide. Oil-based solutions or suspensions may further comprise sesame, peanut, olive oil, or mineral oil.

[0078] For topical (e.g., transdermal or transmucosal) administration, penetrants appropriate to the barrier to be permeated are generally included in the preparation. Transmucosal administration may be accomplished through the use of nasal sprays, aerosol sprays, tablets, or suppositories, and transdermal administration may be via ointments, salves, gels, patches, or creams as generally known in the art.

[0079] In certain embodiments, a composition comprising a compound of the invention is encapsulated in a suitable vehicle to either aid in the delivery of the compound to target cells, to increase the stability of the composition, or to minimize potential toxicity of the composition. As will be appreciated by a skilled artisan, a variety of vehicles are suitable for delivering a composition of the present invention. Non-limiting examples of suitable structured fluid delivery

systems may include nanoparticles, liposomes, microemulsions, micelles, dendrimers and other phospholipid-containing systems. Methods of incorporating compositions into delivery vehicles are known in the art.

[0080] In one alternative embodiment, a liposome delivery vehicle may be utilized. Liposomes, depending upon the embodiment, are suitable for delivery of the compound of the invention in view of their structural and chemical properties. Generally speaking, liposomes are spherical vesicles with a phospholipid bilayer membrane. The lipid bilayer of a liposome may fuse with other bilayers (e.g., the cell membrane), thus delivering the contents of the liposome to cells. In this manner, the compound of the invention may be selectively delivered to a cell by encapsulation in a liposome that fuses with the targeted cell's membrane.

[0081] Liposomes may be comprised of a variety of different types of phospholipids having varying hydrocarbon chain lengths. Phospholipids generally comprise two fatty acids linked through glycerol phosphate to one of a variety of polar groups. Suitable phospholipids include phosphatidic acid (PA), phosphatidylserine (PS), phosphatidylinositol (PI), phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), phosphatidylcholine (PC), and phosphatidylethanolamine (PE). The fatty acid chains comprising the phospholipids may range from about 6 to about 26 carbon atoms in length, and the lipid chains may be saturated or unsaturated. Suitable fatty acid chains include (common name presented in parentheses) n-dodecanoate (laurate), n-tetradecanoate (myristate), n-hexadecanoate (palmitate), n-octadecanoate (stearate), n-eicosanoate (arachidate), n-docosanoate (behenate), n-tetracosanoate (lignocerate), cis-9-hexadecenoate (palmitoleate), cis-9-octadecanoate (oleate), cis,cis-9,12-octadecandienoate (linoleate), all cis-9, 12, 15-octadecatrienoate (linolenate), and all cis-5,8,11,14-eicosatetraenoate (arachidonate). The two fatty acid chains of a phospholipid may be identical or different. Acceptable phospholipids include dioleoyl PS, dioleoyl PC, distearoyl PS, distearoyl PC, dimyristoyl PS, dimyristoyl PC, dipalmitoyl PG, stearoyl, oleoyl PS, palmitoyl, linolenyl PS, and the like.

[0082] The phospholipids may come from any natural source, and, as such, may comprise a mixture of phospholipids. For example, egg yolk is rich in PC, PG, and PE, soy beans contains PC, PE, PI, and PA, and animal brain or spinal cord is enriched in PS. Phospholipids may come from synthetic sources too. Mixtures of phospholipids having a varied ratio of individual phospholipids may be used. Mixtures of different phospholipids may result in liposome compositions having advantageous activity or stability of activity properties. The above mentioned phospholipids may be mixed, in optimal ratios with cationic lipids, such as N-(1-(2,3-dioleolyoxy)propyl)-N,N,N-trimethyl ammonium chloride, 1,1'-dioctadecyl-3,3,3',3'-tetramethylindocarbocyanine perchlorate, 3,3'-deheptyloxacarbocyanine iodide, 1,1'-dedodecyl-3,3,3',3'-tetramethylindocarbocyanine perchlorate, 1,1'-dioleoyl-3,3,3',3'-tetramethylindocarbocyanine methanesulfonate, N-4-(delinoleylaminostyryl)-N-methylpyridinium iodide, or 1,1,-dilinoleyl-3,3,3',3'-tetramethylindocarbocyanine perchlorate.

[0083] Liposomes may optionally comprise sphingolipids, in which spingosine is the structural counterpart of glycerol and one of the one fatty acids of a phosphoglyceride, or cholesterol, a

major component of animal cell membranes. Liposomes may optionally, contain pegylated lipids, which are lipids covalently linked to polymers of polyethylene glycol (PEG). PEGs may range in size from about 500 to about 10,000 daltons.

[0084] Liposomes may further comprise a suitable solvent. The solvent may be an organic solvent or an inorganic solvent. Suitable solvents include, but are not limited to, dimethylsulfoxide (DMSO), methylpyrrolidone, N-methylpyrrolidone, acetonitrile, alcohols, dimethylformamide, tetrahydrofuran, or combinations thereof.

[0085] Liposomes carrying the compound of the invention (i.e., having at least one methionine compound) may be prepared by any known method of preparing liposomes for drug delivery, such as, for example, detailed in U.S. Pat. Nos. 4,241,046, 4,394,448, 4,529,561, 4,755,388, 4,828,837, 4,925,661, 4,954,345, 4,957,735, 5,043,164, 5,064,655, 5,077,211 and 5,264,618. For example, liposomes may be prepared by sonicating lipids in an aqueous solution, solvent injection, lipid hydration, reverse evaporation, or freeze drying by repeated freezing and thawing. In a preferred embodiment the liposomes are formed by sonication. The liposomes may be multilamellar, which have many layers like an onion, or unilamellar. The liposomes may be large or small. Continued high-shear sonication tends to form smaller unilamellar liposomes.

[0086] As would be apparent to one of ordinary skill, all of the parameters that govern liposome formation may be varied. These parameters include, but are not limited to, temperature, pH, concentration of methionine compound, concentration and composition of lipid, concentration of multivalent cations, rate of mixing, presence of and concentration of solvent.

[0087] In another embodiment, a composition of the invention may be delivered to a cell as a microemulsion. Microemulsions are generally clear, thermodynamically stable solutions comprising an aqueous solution, a surfactant, and "oil." The "oil" in this case, is the supercritical fluid phase. The surfactant rests at the oil-water interface. Any of a variety of surfactants are suitable for use in microemulsion formulations including those described herein or otherwise known in the art. The aqueous microdomains suitable for use in the invention generally will have characteristic structural dimensions from about 5 nm to about 100 nm. Aggregates of this size are poor scatterers of visible light and hence, these solutions are optically clear. As will be appreciated by a skilled artisan, microemulsions can and will have a multitude of different microscopic structures including sphere, rod, or disc shaped aggregates. In one embodiment, the structure may be micelles, which are the simplest microemulsion structures that are generally spherical or cylindrical objects. Micelles are like drops of oil in water, and reverse micelles are like drops of water in oil. In an alternative embodiment, the microemulsion structure is the lamellae. It comprises consecutive layers of water and oil separated by layers of surfactant. The "oil" of microemulsions optimally comprises phospholipids. Any of the phospholipids detailed above for liposomes are suitable for embodiments directed to microemulsions. The composition of the invention may be encapsulated in a microemulsion by any method generally known in the art.

[0088] In yet another embodiment, a composition of the invention may be delivered in a dendritic macromolecule, or a dendrimer. Generally speaking, a dendrimer is a branched tree-like molecule, in which each branch is an interlinked chain of molecules that divides into two new branches (molecules) after a certain length. This branching continues until the branches (molecules) become so densely packed that the canopy forms a globe. Generally, the properties of dendrimers are determined by the functional groups at their surface. For example, hydrophilic end groups, such as carboxyl groups, would typically make a water-soluble dendrimer. Alternatively, phospholipids may be incorporated in the surface of a dendrimer to facilitate absorption across the skin. Any of the phospholipids detailed for use in liposome embodiments are suitable for use in dendrimer embodiments. Any method generally known in the art may be utilized to make dendrimers and to encapsulate compositions of the invention therein. For example, dendrimers may be produced by an iterative sequence of reaction steps, in which each additional iteration leads to a higher order dendrimer. Consequently, they have a regular, highly branched 3D structure, with nearly uniform size and shape. Furthermore, the final size of a dendrimer is typically controlled by the number of iterative steps used during synthesis. A variety of dendrimer sizes are suitable for use in the invention. Generally, the size of dendrimers may range from about 1 nm to about 100 nm

II. METHODS

[0089] In an aspect, the invention encompasses a method to deliver a cytokine to a target cell. The method comprises contacting a target cell with a composition comprising a cytokine linked to a ligand, wherein the ligand specifically binds to a receptor on the target cell. Additionally, the method comprises contacting a target cell with a composition comprising a chimeric peptide as described in **Section I**. A target cell may be any cell comprising a target receptor for which the ligand specifically binds to. The ligand and specific binding are described in **Section I**. In certain embodiments, a target cell may be an immune cell. Non-limiting example of immune cells include macrophages, B lymphocytes, T lymphocytes, mast cells, monocytes, dendritic cells, eosinophils, natural killer cells, basophils, neutrophils. In certain embodiments, an immune cell is selected from the group consisting of a macrophage, B lymphocyte, T lymphocyte, mast cell, monocyte, dendritic cell, eosinophil, natural killer cell, basophil, and neutrophil. In a specific embodiment, a target cell is a natural killer (NK) cell and/or a CD8+ T cell. In other embodiments, a target cell is a NKG2D-expressing cell. Non-limiting examples of NKG2D-expressing cell include natural killer (NK) cells and CD8+ T cells (both $\alpha\beta$ and $\gamma\delta$). The chimeric peptide or the pharmaceutical composition of the invention may be used in a method to deliver a cytokine to a target cell, the method comprising contacting a target cell with composition comprising the chimeric peptide.

[0090] In another aspect, the invention encompasses a method to activate immune cells. The method comprises contacting an immune cell with a composition comprising a cytokine linked to a ligand, wherein the ligand specifically binds to a receptor on the immune cell thereby activating the cell. Additionally, the method comprises contacting an immune cell with a composition comprising a chimeric peptide as described in **Section I**. Non-limiting example of

immune cells include macrophages, B lymphocytes, T lymphocytes, mast cells, monocytes, dendritic cells, eosinophils, natural killer cells, basophils, neutrophils. In certain embodiments, an immune cell is selected from the group consisting of a macrophage, B lymphocyte, T lymphocyte, mast cell, monocyte, dendritic cell, eosinophil, natural killer cell, basophil, and neutrophil. In a specific embodiment, an immune cell is a natural killer (NK) cell and/or a CD8+ T cell. To facilitate activation of immune cells, a cytokine may be a proinflammatory cytokine. The term "proinflammatory cytokine" is a cytokine which promotes systemic inflammation. A skilled artisan would be able to determine those cytokines that are proinflammatory. In certain embodiments, a proinflammatory cytokine is IL1 α , IL1 β , IL2, IL3, IL6, IL7, IL9, IL12, IL15, IL17, IL18, IL21, IFN α , IFN γ , TNF α , MIF, G-CSF, GM-CSF or mutants thereof. In an embodiment, a proinflammatory cytokine is an IL1 family cytokine. In certain embodiments, an IL1 family cytokine is selected from the group consisting of IL1 α , IL1 β , IL1Ra, IL18, IL36Ra, IL36 α , IL37, IL36 β , IL36 γ , IL38, IL33 and mutants thereof. In a specific embodiment, a proinflammatory cytokine is selected from the group consisting of IL2, IL7, IL15, IL18, IL21 and mutants thereof. In another specific embodiment, a proinflammatory cytokine is selected from the group consisting of IL2, IL15, IL18, and mutants thereof. In an exemplary embodiment, a proinflammatory cytokine is IL2 or a mutant thereof. Activation of the immune cells may result in lysis of tumor cells. Accordingly, activation of immune cells may be measured by determining the amount of tumor cell lysis. In an embodiment, activation of the immune cells may result in about 10% to about 100% lysis of tumor cells. In another embodiment, activation of the immune cells may result in about 20% to about 80% lysis of tumor cells. In still another embodiment, activation of the immune cells may result in greater than 40% lysis of tumor cells. For example, activation of the immune cells may result in greater than 40%, greater than 45%, greater than 50%, greater than 55%, greater than 60%, greater than 65%, greater than 70%, greater than 75%, greater than 80%, greater than 85%, greater than 90%, greater than 95%, or greater than 99% lysis of tumor cells. The lysis of tumor cells may be measured using any standard assay (e.g., caspase assays, TUNEL and DNA fragmentation assays, cell permeability assays, and Annexin V assays).

[0091] The invention also provides the chimeric peptide or pharmaceutical composition of the invention for use in a method to treat a tumor. The method comprises identifying a subject with a tumor and administering to the subject a therapeutically effective amount of a composition comprising the chimeric peptide or pharmaceutical composition of the invention, wherein the chimeric peptide activates natural killer (NK) cells or CD8+ cytotoxic T lymphocytes (CTLs), thereby treating a tumor. Additionally, the method comprises administering to the subject a composition comprising a chimeric peptide as described in **Section I**. Specifically, the inventors have shown that delivering a cytokine to a target cell activates the cells bound by the composition, wherein the activated cells specifically lyse tumor cells thereby reducing the amount of cancer cells. In a specific embodiment, a cytokine is a proinflammatory cytokine as described in the preceding paragraph. Accordingly, a composition of the present invention, may be used in treating, stabilizing and preventing cancer and associated diseases in a subject. By "treating, stabilizing, or preventing cancer" is meant causing a reduction in the size of a tumor or in the number of cancer cells, slowing or preventing an increase in the size of a tumor or cancer cell proliferation, increasing the disease-free survival time between the

disappearance of a tumor or other cancer and its reappearance, preventing an initial or subsequent occurrence of a tumor or other cancer, or reducing an adverse symptom associated with a tumor or other cancer. The inventors have shown that a composition of the invention activates natural killer (NK) cells bound by the composition, wherein the activated NK cells specifically lyse tumor cells thereby reducing the amount of tumor cells. For example, as cancerous cells are "stressed", NKG2D ligands become upregulated, rendering the cell susceptible to NK cell-mediated lysis. In a desired embodiment, the percent of tumor or cancerous cells surviving the treatment is at least 20, 30, 40, 50, 60, 70, 80, 90 or 100% lower than the initial number of tumor or cancerous cells, as measured using any standard assay (e.g., caspase assays, TUNEL and DNA fragmentation assays, cell permeability assays, and Annexin V assays). Desirably, the decrease in the number of tumor or cancerous cells induced by administration of a composition of the invention is at least 2, 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50-fold greater than the decrease in the number of non-tumor or non-cancerous cells. Desirably, the methods of the present invention result in a decrease of 20, 30, 40, 50, 60, 50, 80, 90 or 100% in the size of a tumor or in the number of cancerous cells, as determined using standard methods. Desirably, at least 20, 30, 40, 50, 60, 70, 80, 90, or 95% of the treated subjects have a complete remission in which all evidence of the tumor or cancer disappears. Desirably, the tumor or cancer does not reappear or reappears after at least 1, 2, 3, 4, 5, 10, 15, or 20 years.

[0092] In another aspect, the invention encompasses a method to suppress immune cells. The method comprises contacting an immune cell with a composition comprising a cytokine linked to a ligand, wherein the ligand specifically binds to a receptor on the immune cell thereby suppressing the cell. Additionally, the method comprises contacting an immune cells with a composition comprising a chimeric peptide as described in **Section I**. Non-limiting example of immune cells include macrophages, B lymphocytes, T lymphocytes, mast cells, monocytes, dendritic cells, eosinophils, natural killer cells, basophils, neutrophils. In certain embodiments, an immune cell is selected from the group consisting of a macrophage, B lymphocyte, T lymphocyte, mast cell, monocyte, dendritic cell, eosinophil, natural killer cell, basophil, and neutrophil. In a specific embodiment, an immune cell is a natural killer (NK) cell and/or a CD8+ T cell. To facilitate suppression of immune cells, a cytokine may be an anti-inflammatory cytokine. The term "anti-inflammatory cytokine" is a cytokine that counteracts various aspects of inflammation, for example cell activation or the production of proinflammatory cytokines, and thus contributes to the control of the magnitude of the inflammatory response. A skilled artisan would be able to determine those cytokines that are anti-inflammatory. In certain embodiments, an anti-inflammatory cytokine is IL4, IL5, IL10, IL11, IL13, IL16, IL35, IFN α , TGF β , G-CSF or a mutant thereof. In a specific embodiment, an anti-inflammatory cytokine is IL10 or a mutant thereof. In another embodiment, the invention encompasses a method to kill immune cells. The method comprises contacting an immune cell with a composition comprising a toxin linked to a ligand, wherein the ligand specifically binds to a receptor on the immune cell thereby killing the cell. Suppression or killing of the immune cells may result in treatment, stabilization and prevention of autoimmune diseases caused by overactive immune cells. NKG2D-expressing cells and/or aberrant expression of host NKG2DLs have been implicated in diabetes, celiac disease and rheumatoid arthritis. For example, NK cells can recognize pancreatic beta cells

and destroy them. The destruction of pancreatic beta cells may lead to type 1 diabetes. By way of another example, overactive immune cells are involved in transplant/graft rejection. Accordingly, a composition of the present invention, may be used in treating, stabilizing and preventing an automimmune disease in a subject. In a specific embodiment, the autoimmune disease is type 1 diabetes. In another specific embodiment, the autoimmune disease is transplant or graft rejection. In still another specific embodiment, the autoimmune disease is rheumatoid arthritis.

[0093] In still yet another aspect, the invention encompasses a method to treat an infection comprising administering a composition comprising a cytokine linked to a ligand. For example, a composition comprising a cytokine linked to a ligand may specifically bind an immune cell that is then activated to target and lyse the infected host cell. Additionally, the method comprises administering to the subject a composition comprising a chimeric peptide as described in **Section I**. The term "infection" as used herein includes the presence of pathogens in or on a subject, which, if its growth were inhibited, would result in a benefit to the subject. As such, the term "infection" in addition to referring to the presence of pathogens also refers to normal flora which are not desirable. The term "pathogen" as used herein refers to an infectious agent that can produce disease. Non-limiting examples of an infectious agent include virus, bacterium, prion, fungus, viroid, or parasite that cause disease in a subject. In a specific embodiment, an infection is caused by pathogens such as bacteria or viruses. In certain embodiments, the infection is an intracellular infection. In an embodiment, the infection is a viral infection. In another embodiment, the viral infection is caused by a flavivirus. Flavivirus is a genus of viruses in the family Flaviviridae. Non-limiting examples of flaviviruses include Gadget's Gully virus, Kadam virus, Kyasanur Forrest disease virus, Langat virus, Omsk hemorrhagic fever virus, Tick-borne encephalitis virus, Louping ill virus, Aroa virus, Dengue viruses 1-4, Kedougou virus, Cacipacore virus, Koutango virus, Murray Valley encephalitis virus, St. Louis encephalitis virus, Usutu virus, West Nile virus, Yaounde virus, Kokobera virus group, Kokobera virus, Bagaza virus, Ilheus virus, Israel turkey meningoencephalomyelitis virus, Ntaya virus, Tembusu virus, Zika virus, Banzi virus, Bouboui virus, Edge Hill virus, Jugra virus, Saboya virus, Sepik virus, Uganda S virus, Wesselsbron virus, Yellow fever virus, Entebbe bat virus, Yokose virus, Apoi virus, Cowbone Ridge virus, Jutiapa virus, Modoc virus, Sal Vieja virus, San Perlita virus, Bukalasa bat virus, Carey Island virus, Dakar bat virus, Montana myotis leukoencephalitis virus, Phnom Penh bat virus, Rio Bravo virus, hepatitis C virus, e.g., hepatitis C virus genotypes 1-6, and GB virus A and B. In a certain embodiment, the flavivirus may be selected from the group consisting of West Nile virus, dengue virus, Japanese encephalitis virus, and yellow fever virus. In a specific embodiment, the viral infection is caused by West Nile virus. In certain embodiments, a pathogen, more specifically a virus, can induce the expression of proteins for which NKG2D binds. Accordingly, a composition comprising a cytokine linked to a ligand may specifically bind a NK cell that is then activated to target and lyse the infected host cell expressing NKG2D. In another embodiment, a composition comprising a cytokine linked to a ligand may activate cytotoxic T lymphocytes that recognize infected cells via other mechanisms for targeted killing.

[0094] In a different aspect, the invention encompasses a method to alleviate

immunosuppression related to radiation exposure or lymphotoxic substances comprising administering a composition comprising a cytokine linked to a ligand. Additionally, the method comprises administering a composition comprising a chimeric peptide as described in **Section I**. Additionally, a composition of the invention may be used to raise CD4 counts in HIV positive subjects. For example, a composition of the invention may be used to activate immune cells which can help restore the immune system of the subject.

[0095] In an alternative aspect, the invention encompasses a method of use as an adjuvant in a vaccine composition. For example, a composition of the invention may be used to expand CD8+ memory cells.

(a) administration

[0096] In certain aspects, a pharmacologically effective amount of a composition of the invention may be administered to a subject. Administration is performed using standard effective techniques, including peripherally (i.e. not by administration into the central nervous system) or locally to the central nervous system. Peripheral administration includes but is not limited to intravenous, intraperitoneal, subcutaneous, pulmonary, transdermal, intramuscular, intranasal, buccal, sublingual, or suppository administration. Local administration, including directly into the central nervous system (CNS) includes but is not limited to via a lumbar, intraventricular or intraparenchymal catheter or using a surgically implanted controlled release formulation. Pheresis may be used to deliver a composition of the invention. In certain embodiments, a composition of the invention may be administered via an infusion (continuous or bolus).

[0097] Pharmaceutical compositions for effective administration are deliberately designed to be appropriate for the selected mode of administration, and pharmaceutically acceptable excipients such as compatible dispersing agents, buffers, surfactants, preservatives, solubilizing agents, isotonicity agents, stabilizing agents and the like are used as appropriate. Remington's Pharmaceutical Sciences, Mack Publishing Co., Easton Pa., 16Ed ISBN: 0-912734-04-3, latest edition, provides a compendium of formulation techniques as are generally known to practitioners.

[0098] Effective peripheral systemic delivery by intravenous or intraperitoneal or subcutaneous injection is a preferred method of administration to a living patient. Suitable vehicles for such injections are straightforward. In addition, however, administration may also be effected through the mucosal membranes by means of nasal aerosols or suppositories. Suitable formulations for such modes of administration are well known and typically include surfactants that facilitate cross-membrane transfer. Such surfactants are often derived from steroids or are cationic lipids, such as N-[1-(2,3-dioleoyl)propyl]-N,N,N-trimethyl ammonium chloride (DOTMA) or various compounds such as cholesterol hemisuccinate, phosphatidyl glycerols and the like.

[0099] For therapeutic applications, a therapeutically effective amount of a composition of the

invention is administered to a subject. A "therapeutically effective amount" is an amount of the therapeutic composition sufficient to produce a measurable response (e.g., an immunostimulatory, an anti-angiogenic response, a cytotoxic response, tumor regression, immunoinhibitory, immunosuppression, infection reduction). Actual dosage levels of active ingredients in a therapeutic composition of the invention can be varied so as to administer an amount of the active compound(s) that is effective to achieve the desired therapeutic response for a particular subject. The selected dosage level will depend upon a variety of factors including the activity of the therapeutic composition, formulation, the route of administration, combination with other drugs or treatments, tumor size and longevity, the autoimmune disease, infection, and the physical condition and prior medical history of the subject being treated. In some embodiments, a minimal dose is administered, and dose is escalated in the absence of dose-limiting toxicity. Determination and adjustment of a therapeutically effective dose, as well as evaluation of when and how to make such adjustments, are known to those of ordinary skill in the art of medicine. In an aspect, a typical dose contains from about 10 IU/kg to about 1,000,000 IU/kg of a cytokine described herein. In an embodiment, a typical dose contains from about 10 IU/kg to about 100 IU/kg. In another embodiment, a typical dose contains about 100 IU/kg to about 1,000 IU/kg. In still another embodiment, a typical dose contains about 1,000 IU/kg to about 10,000 IU/kg. In yet still another embodiment, a typical dose contains about 10,000 IU/kg to about 100,000 IU/kg. In a different embodiment, a typical dose contains about 100,000 IU/kg to about 1,000,000 IU/kg. In certain embodiments, a typical dose contains about 500,000 IU/kg to about 1,000,000 IU/kg. In other embodiments, a typical dose contains about 100,000 IU/kg to about 500,000 IU/kg. Alternatively, a typical dose contains about 50,000 IU/kg to about 100,000 IU/kg. In another embodiment, a typical dose contains about 10,000 IU/kg to about 50,000 IU/kg. In still another embodiment, a typical dose contains about 5,000 IU/kg to about 10,000 IU/kg. In a specific embodiment, a typical dose contains about 5,000 IU/kg to about 200,000 IU/kg. In another specific embodiment, a typical dose contains about 5,000 IU/kg to about 500,000 IU/kg. In still another specific embodiment, a typical dose contains about 50,000 IU/kg to about 500,000 IU/kg. In still yet another specific embodiment, a typical dose contains about 250,000 IU/kg to about 750,000 IU/kg.

[0100] The frequency of dosing may be once, twice, three times or more daily or once, twice, three times or more per week or per month, as needed as to effectively treat the symptoms or disease. In certain embodiments, the frequency of dosing may be once, twice or three times daily. For example, a dose may be administered every 24 hours, every 12 hours, or every 8 hours. In a specific embodiment, the frequency of dosing may be twice daily.

[0101] Duration of treatment could range from a single dose administered on a one-time basis to a life-long course of therapeutic treatments. The duration of treatment can and will vary depending on the subject and the cancer or autoimmune disease or infection to be treated. For example, the duration of treatment may be for 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, or 7 days. Or, the duration of treatment may be for 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks or 6 weeks. Alternatively, the duration of treatment may be for 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, or 12 months. In still another embodiment, the duration of treatment may be for 1 year, 2 years, 3

years, 4 years, 5 years, or greater than 5 years. It is also contemplated that administration may be frequent for a period of time and then administration may be spaced out for a period of time. For example, duration of treatment may be 5 days, then no treatment for 9 days, then treatment for 5 days.

[0102] The timing of administration of the treatment relative to the disease itself and duration of treatment will be determined by the circumstances surrounding the case. Treatment could begin immediately, such as at the time of diagnosis, or treatment could begin following surgery. Treatment could begin in a hospital or clinic itself, or at a later time after discharge from the hospital or after being seen in an outpatient clinic.

[0103] Although the foregoing methods appear the most convenient and most appropriate and effective for administration of a composition of the invention, by suitable adaptation, other effective techniques for administration, such as intraventricular administration, transdermal administration and oral administration may be employed provided proper formulation is utilized herein.

[0104] In addition, it may be desirable to employ controlled release formulations using biodegradable films and matrices, or osmotic mini-pumps, or delivery systems based on dextran beads, alginate, or collagen.

(b) tumor

[0105] A composition of the invention may be used to treat or recognize a tumor derived from a neoplasm or a cancer. The neoplasm may be malignant or benign, the cancer may be primary or metastatic; the neoplasm or cancer may be early stage or late stage. Non-limiting examples of neoplasms or cancers that may be treated include acute lymphoblastic leukemia, acute myeloid leukemia, adrenocortical carcinoma, AIDS-related cancers, AIDS-related lymphoma, anal cancer, appendix cancer, astrocytomas (childhood cerebellar or cerebral), basal cell carcinoma, bile duct cancer, bladder cancer, bone cancer, brainstem glioma, brain tumors (cerebellar astrocytoma, cerebral astrocytoma/malignant glioma, ependymoma, medulloblastoma, supratentorial primitive neuroectodermal tumors, visual pathway and hypothalamic gliomas), breast cancer, bronchial adenomas/carcinoids, Burkitt lymphoma, carcinoid tumors (childhood, gastrointestinal), carcinoma of unknown primary, central nervous system lymphoma (primary), cerebellar astrocytoma, cerebral astrocytoma/malignant glioma, cervical cancer, childhood cancers, chronic lymphocytic leukemia, chronic myelogenous leukemia, chronic myeloproliferative disorders, colon cancer, cutaneous T-cell lymphoma, desmoplastic small round cell tumor, endometrial cancer, ependymoma, esophageal cancer, Ewing's sarcoma in the Ewing family of tumors, extracranial germ cell tumor (childhood), extragonadal germ cell tumor, extrahepatic bile duct cancer, eye cancers (intraocular melanoma, retinoblastoma), gallbladder cancer, gastric (stomach) cancer, gastrointestinal carcinoid tumor, gastrointestinal stromal tumor, germ cell tumors (childhood extracranial, extragonadal, ovarian), gestational trophoblastic tumor, gliomas (adult, childhood brain stem,

childhood cerebral astrocytoma, childhood visual pathway and hypothalamic), gastric carcinoid, hairy cell leukemia, head and neck cancer, hepatocellular (liver) cancer, Hodgkin lymphoma, hypopharyngeal cancer, hypothalamic and visual pathway glioma (childhood), intraocular melanoma, islet cell carcinoma, Kaposi sarcoma, kidney cancer (renal cell cancer), laryngeal cancer, leukemias (acute lymphoblastic, acute myeloid, chronic lymphocytic, chronic myelogenous, hairy cell), lip and oral cavity cancer, liver cancer (primary), lung cancers (non-small cell, small cell), lymphomas (AIDS-related, Burkitt, cutaneous T-cell, Hodgkin, non-Hodgkin, primary central nervous system), macroglobulinemia (Waldenstrom), malignant fibrous histiocytoma of bone/osteosarcoma, medulloblastoma (childhood), melanoma, intraocular melanoma, Merkel cell carcinoma, mesotheliomas (adult malignant, childhood), metastatic squamous neck cancer with occult primary, mouth cancer, multiple endocrine neoplasia syndrome (childhood), multiple myeloma/plasma cell neoplasm, mycosis fungoides, myelodysplastic syndromes, myelodysplastic/myeloproliferative diseases, myelogenous leukemia (chronic), myeloid leukemias (adult acute, childhood acute), multiple myeloma, myeloproliferative disorders (chronic), nasal cavity and paranasal sinus cancer, nasopharyngeal carcinoma, neuroblastoma, non-Hodgkin lymphoma, non-small cell lung cancer, oral cancer, oropharyngeal cancer, osteosarcoma/malignant fibrous histiocytoma of bone, ovarian cancer, ovarian epithelial cancer (surface epithelial-stromal tumor), ovarian germ cell tumor, ovarian low malignant potential tumor, pancreatic cancer, pancreatic cancer (islet cell), paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytoma, pineal astrocytoma, pineal germinoma, pineoblastoma and supratentorial primitive neuroectodermal tumors (childhood), pituitary adenoma, plasma cell neoplasia, pleuropulmonary blastoma, primary central nervous system lymphoma, prostate cancer, rectal cancer, renal cell carcinoma (kidney cancer), renal pelvis and ureter transitional cell cancer, retinoblastoma, rhabdomyosarcoma (childhood), salivary gland cancer, sarcoma (Ewing family of tumors, Kaposi, soft tissue, uterine), Sezary syndrome, skin cancers (nonmelanoma, melanoma), skin carcinoma (Merkel cell), small cell lung cancer, small intestine cancer, soft tissue sarcoma, squamous cell carcinoma, squamous neck cancer with occult primary (metastatic), stomach cancer, supratentorial primitive neuroectodermal tumor (childhood), T-Cell lymphoma (cutaneous), testicular cancer, throat cancer, thymoma (childhood), thymoma and thymic carcinoma, thyroid cancer, thyroid cancer (childhood), transitional cell cancer of the renal pelvis and ureter, trophoblastic tumor (gestational), unknown primary site (adult, childhood), ureter and renal pelvis transitional cell cancer, urethral cancer, uterine cancer (endometrial), uterine sarcoma, vaginal cancer, visual pathway and hypothalamic glioma (childhood), vulvar cancer, Waldenstrom macroglobulinemia, and Wilms tumor (childhood). In certain embodiments, the neoplasm or cancer may be selected from the group consisting of melanoma, renal cell carcinoma, lung cancer and blood cancer. As used herein, a "blood cancer" is a cancer that affects the blood, bone marrow and lymphatic system. There are three main groups of blood cancer: leukemia, lymphoma and myeloma. The four broad classification of leukemia are: acute lymphocytic leukemia (ALL), acute myelogenous leukemia (AML), chronic lymphocytic leukemia (CLL) and chronic myelogenous leukemia (CML). Lymphomas are divided into two categories: Hodgkin lymphoma and non-Hodgkin lymphoma. Most non-Hodgkin lymphomas are B-cell lymphomas, and either grow quickly (high-grade) or slowly (low-grade). There are 14 types of B-cell non-Hodgkin lymphomas. The

rest are T-cell lymphomas, named after a different cancerous white blood cell, or lymphocyte. Because myeloma frequently occurs at many sites in the bone marrow, it is often referred to as multiple myeloma.

(c) subject

[0106] A suitable subject includes a human, a livestock animal, a companion animal, a lab animal, or a zoological animal. In one embodiment, the subject may be a rodent, e.g. a mouse, a rat, a guinea pig, etc. In another embodiment, the subject may be a livestock animal. Non-limiting examples of suitable livestock animals may include pigs, cows, horses, goats, sheep, llamas and alpacas. In yet another embodiment, the subject may be a companion animal. Non-limiting examples of companion animals may include pets such as dogs, cats, rabbits, and birds. In yet another embodiment, the subject may be a zoological animal. As used herein, a "zoological animal" refers to an animal that may be found in a zoo. Such animals may include non-human primates, large cats, wolves, and bears. In a specific embodiment, the animal is a laboratory animal. Non-limiting examples of a laboratory animal may include rodents, canines, felines, and non-human primates. In certain embodiments, the animal is a rodent. Non-limiting examples of rodents may include mice, rats, guinea pigs, etc. In preferred embodiments, the subject is a human.

Table A. Sequences			
SEQ ID NO	Name	Sequence	Source
1	R38A, F42K, C125S IL2-OMCP construct	<p>CACAAACTCGCATTCAACTTCAATCTAGAAATAAATG GCAGTGATACACATTCTACAGTAGATGTATATCTTG ATGATTCTCAAATTATAACGTTTGATGGAAAAGAT ATCCGTCCAACCATCCCGTTCATGATAGGTGATGAA ATTTTCTTACCGTTTTATAAAAATGTGTTTAGTGAGTT TTTCTCTCTGTTTAGAAGAGTTCCTACAAGTACTCCAT ATGAAGACTTGACATATTTTTATGAATGCGACTATACA GACAATAAATCTACATTTGATCAGTTTTATCTTTATAA TGGCGAAGAATATACTGTCAAACACAGGAGGCCAC TAATAAAAATATGTGGCTAACTACTTCCGAGTTTAGA CTAAAAAATGGTTCGATGGCGAAGATTGTATAATGC ATCTTAGATCGTTAGTTAGAAAAATGGAGGACAGTAA ACGAAACACTGGTGGTACCGGAAGTAGCGGTAGTAG TGATTACAAGGACGATGACGACAAGCACCACCATCA TCATCATCACCACGGTAGCAGCGGCAGCAGTGCCCC CACCTCTAGCAGCACAAAGAAGACCCAGCTGCAACT</p> <p>GGAACACCTCCTGCTGGACCTGCAGATGATCCTGAA CGGCATCAACAACACTACAAGAACCCCAAGCTGACCGC CATGCTGACCAAAAAGTTTTACATGCCCAAGAAGGC CACCGAGCTTAAACACCTGCAATGCCTTGAGGAGGA GCTGAAGCCCTGGAGGAGGTAAGAACCTGGCCCA GAGCAAGAACTTTCATCTGAGGCCAGGGACCTGAT TAGCAACATCAACGTGATCGTGTTGGAGTTGAAGGG CAGCGAGACCACGTTTCATGTGCGAGTACGCCGACGA</p>	Synthesized

Table A. Sequences			
SEQ ID NO	Name	Sequence	Source
		GACGGCCACCATAGTGGAGTTTCTTAACAGGTGGAT CACCTTCTCACAGTCTATCATCAGCACCCCTGACC	
2	R38A, F42K, C125S IL2-OMCP construct	HKLAFNFNLEINGS DTHSTVDVYLDDSQITFDGKDIRPT IPFMIGDEIFLPFYKNVFSEFFSLFRRVPTSTPYEDLTYF YECDYTDNKSTFDQFYLYNGEEYTVKTQEATNKNMWL TTSEFRLKKWFDGEDCIMHLRSLVRKMEDSKRNTGGT GSSGSSDYKDDDDKHHHHHHHHGSSGSSAPTSSSTK KTQLQLEHLLLDLQMILNGINNYKNPKLTAMLTKKFYMP KKATELKHLCLEEEELKPLEEVLNLAQSKNFHLRPRDLI SNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFSQ SIISTLT	Synthesized
3	Melanoma tumor associate antigen tyrosinase- related protein 2 peptide	SVYDFFVWL	Homo sapiens
4	Highly immunoge nic peptide	SIINFEKL	Homo sapiens
5	WT IL2 (C125S)	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRM LTFKFYMPKKATELKHLCLEEEELKPLEEVLNLAQSKNF HLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFCQSIISTLT	Homo sapiens
6	R38A, F42K, C125S IL2	APTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTAM LTKKFYMPKKATELKHLCLEEEELKPLEEVLNLAQSKNF HLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFL NRWITFSQSIISTLT	Synthesized
7	OMCP	HKLAFNFNLEINGS DTHSTVDVYLDDSQITFDGKDIRPT IPFMIGDEIFLPFYKNVFSEFFSLFRRVPTSTPYEDLTYF YECDYTDNKSTFDQFYLYNGEEYTVKTQEATNKNMWL TTSEFRLKKWFDGEDCIMHLRSLVRKMEDSKRNT	Synthesized
8	Linker	GSSGSSDYKDDDDKHHHHHHHHGSSGSS	Synthesized
9	FLAG tag	DYKDDDK	Synthesized
10	HA tag	YPYDVPDYA	Synthesized

Table A. Sequences			
SEQ ID NO	Name	Sequence	Source
11	Myc tag	EQKLISEEDL	Synthesized
12	V5 tag	GKPIPPELLGLDST	Synthesized
13	OMCPbr	GHKLAFNFNLEINGS DTHSTVDVYLDDSQITFDGKDIRP TIPFMIGDEIFLPFYKNVFSEFFSLFRRVPTSTPYEDLTY	Cowpox virus
		FYECDYTDNKSTFDQFYLYNGEEYTVKTQEATNKNMW LTTSEFRLKKWFDGEDCIMHLRSLVRKMEDSKR	
14	OMCPmpx	HKLVHYFNKINGS DITNTADILLDNYPIMTFDGKDIYPSI AFMVGKFLDLYKNIFVEFFRLFRVSVSSQYEELEYYY SCDYTNNRPTIKQHYFYNGEEYTEIDRSKKATNKNSWLI TSGFRLQKWFDSEDCIYLRSLVRRMEDSNK	Monkeypox virus
15	MICA	MEPHSLRYNLTVLSWDGSGVQSGFLTEVHLDGQPFLRC RDRQKCRAPQGQWAEDVLGNKTWDRETRDLTGNG KDLRMTLAHIKDQKEGLHSLQEIRVCEIHEDNSTRSSQH FYYDGELFLSQNLETKEWTMPQSSRAQTLAMNVRNFL KEDAMKTKTHYHAMHADCLQELRRYLKSGVVLR	Homo sapiens
16	MICB	MEPHSLRYNLMVLSQDGSVQSGFLAEGHLDGQPFLRY DRQKRRAPQGQWAEDVLGAETWDTETEDLTENGQD LRRTLTHIKDQKGLHSLQEIRVCEIHEDSSTRGSRHFY YNGELFLSQNLETQESTVPQSSRAQTLAMNVTNFWKE DAMKTKTHYRAMQADCLQKLQRYLKSGVAIR	Homo sapiens
17	ULBP3	DAHSLWYNFTIIHLPRHGQQWCEVQSQVDQKNFLSYD CGSDKVLSMGHLEEQLYATDAWGKQLEMLREVGQRL RLELADTELEDFTPSGPLTLQVRMSCECEADGYIRGSW QFSFDGRKFLLFDSNNRKWTVVHAGARRMKEKWEKD SGLTTFFKMVSMRDCKSWLRDFLMHRKKRLE	Homo sapiens
18	RAE-1B	DAHSLRCNLTIKDPTPADPLWYEAKCFVGEILILHLSNIN KTMTSGDPGETANATEVKKCLTQPLKNLCQKLRNKVS NTKVDTHKTNGYPHLQVTMIYPQSQGRTPSATWEFNIS DSYFFTFYTENMSWRSANDESGVIMNKWKDDGEFVK QLKFLIHECSQKMDEFKQSKEK	Homo sapiens
19	NKG2D portion	LTIEMQKGDALYAS	Homo sapiens
20	NKG2D	LTIEMQKGEALYAS	Green

Table A. Sequences			
SEQ ID NO	Name	Sequence	Source
	portion		monkey
21	NKG2D portion	LTIEMQKGDCAVYAS	Marmoset
22	NKG2D portion	LTLVEIPKGSCAVYGS	Mouse
23	NKG2D portion	LTLVKTPSGTCAVYGS	Rat
24	NKG2D portion	LTLMDTQNGKCALYGS	Guinea pig
25	NKG2D portion	LTLVEMQNGTCIVYGS	Ground squirrel
26	NKG2D portion	LTWEMQSGSCAVYGS	Deer mouse
27	NKG2D portion	LSMVEMQNGTCAVYAS	Naked mole rat
28	NKG2D portion	LTLVEMQRGSCAVYGS	Prairie vole
29	NKG2D portion	VSIVEMQGGNCAVYGS	European shrew
30	NKG2D portion	VTVYEMQNGSCAVYGS	Star-nosed mole
31	NKG2D portion	LTLVEMQNGSCAVYGS	Chinese hamster
32	NKG2D portion	LTMVDMQNGTCAVYGS	Cat
33	OMCP portion	ASSFK	Cowpox virus
34	DAP10 signaling motif	YINM	Synthesized

EXAMPLES

[0107] The following examples are included to demonstrate preferred embodiments of the invention. It should be appreciated by those of skill in the art that the techniques disclosed in the examples that follow represent techniques discovered by the inventors to function well in

the practice of the invention, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

Introduction to Examples 1-6.

[0108] The IL-2R α chain serves to capture IL-2 at the cell surface to facilitate subsequent binding to the signaling part of the receptor, namely the IL-2R $\beta\gamma$ chains. Resting cytotoxic lymphocytes, such as natural killer (NK) and CD8⁺T cells, do not express appreciable IL-2R α at the cell surface and are thus not activated by low levels of IL-2¹. IL-2R α is expressed on this population after initial activation, however, and is required for maximum cytotoxic lymphocyte expansion². High dose IL-2 can induce the activation of all cytotoxic lymphocytes and is approved for treatment of several malignancies with an approximately 15% partial or complete tumor response³⁻⁵. Most patients do not benefit from such therapy due to activation of regulatory T cell (T_{regs}) and complications such as severe blood pressure alteration, generalized capillary leak, and end organ failure due to activation of vascular endothelium^{6,3,7}. Both vascular endothelium and T_{regs} express IL-2R α and are thus preferentially activated by IL-2 over cytotoxic lymphocytes⁸. Lowering the IL-2 dose can ameliorate side effects but also decreases efficacy. Mutant forms of IL-2, such as those with substitutions of alanine for arginine at the 38 position (R38A) and/or lysine for phenylalanine at the 42 position (F42K), decrease the affinity of IL-2 for IL-2R α and thus eliminate many side effects⁹. Such IL-2 α mutants may also decrease the efficacy of immunotherapy². A form of IL-2 that could preferentially activate cytotoxic lymphocytes in the absence of IL-2R α reactivity would be highly advantageous for clinical applications.

[0109] NKG2D recognizes MHC class-I-related stress ligands expressed by malignant or virally-transformed cells¹⁰. Of all the activating immunoreceptors NKG2D has the highest specificity for cytotoxic lymphocytes as it is constitutively expressed on both murine and human NK cells as well as activated CD8⁺T cells¹¹. Consequentially it has been argued that tumors and virally infected cells utilize shed NKG2D ligands as a mechanism of immune evasion^{12,13}. Orthopox major histocompatibility complex class I-like protein, or OMCP, is an NKG2D ligand decoy shed by monkeypox and cowpox virus infected cells. It is not expressed by small pox or vaccinia virus and thus not recognized by those immunized with small pox vaccine. As OMCP binds to both human and murine NKG2D with the highest affinity of any known ligand we thought it might function as an ideal targeting vector to optimally deliver IL-2 to cytotoxic lymphocytes^{14,15}. Here we describe the construction and function of a fusion protein designed to deliver an IL-2R α mutant to NKG2D-expressing lymphocytes¹⁵. We demonstrate that this construct overcomes decreased efficacy associated with mutations in the IL-2R α binding

region while retaining a favorable safety profile. Systemic administration of this fusion protein improves immunotherapy against both solid and liquid tumors. Targeted delivery of IL-2 can thus be safely used to maximally activate NKG2D-expressing lymphocytes, such as NK cells, to optimize immunotherapy without systemic side effects.

Example 1. NKG2D-targeted delivery of an IL-2 mutant preferentially activates cytotoxic lymphocytes *in vitro*.

[0110] To overcome the preferential activation of IL-2R α -expressing cells, we designed an IL-2 fusion protein that would target cytotoxic lymphocytes directly via the NKG2D receptor. This fusion protein combines the high affinity NKG2D ligand OMCP with an IL-2 mutated to reduce IL-2R α reactivity. Our construct, termed OMCP-mutIL-2, consists of the 152 residue OMCP protein fused to the N-terminus of the 133 amino acid R38A/F42K mutant form of human IL-2 (mutIL-2) via a flexible 30 residue linker (**FIG. 1A-B**). The construct was first assessed for its *in vitro* binding ability. Binding of fluorescently labeled construct was tested *in vitro* at 37°C in bulk splenocytes. **FIG. 17** shows that the construct appears to only bind to NK cells which express NKG2D. The construct does not show binding to CD4⁺CD3⁺ T cells, CD8⁺CD3⁺ T cells, CD11c⁺CD11b⁻ DCs, CD11c⁻CD11b⁺ Macs or CD19⁺CD3⁻ B cells.

[0111] We have previously demonstrated strain-specific differences in murine NK cell cytotoxicity and lung cancer immunosurveillance¹⁶ (and **Example 7**). Therefore, we set out to examine the efficacy of OMCP-mut-IL2 in activation of NK cells from two different strains of mice, namely A/J and B6 with poor and robust NK function, respectively. Compared to wild-type IL-2 (wtIL-2) or mutIL-2, OMCP-mutIL-2 strongly upregulated CD69 on NK cells of both strains after 36-hour co-culture with 100 IUe/ml of cytokine (**FIG. 1C**, left; **FIG. 6**, left two graphs)^{16,17}. At high concentrations a similar increase in CD69 expression was observed with OMCP-mut-IL-2, wtIL-2 or mutIL-2 (**FIG. 6**). Activation of CD4⁺Foxp3⁺T_{regs}, as measured by upregulation of ICOS, was evident with wtIL-2 only, but not with mutIL-2 nor OMCP-mutIL-2 (**FIG. 1C-D**). CD8⁺ and CD4⁺Foxp3⁻ effector T cells, on the other hand, demonstrated no upregulation of CD69 after 36 hours, even at highest doses of cytokines (**FIG. 1C-D** and data not shown). Longer exposure over a period of five days led to proliferation of both NK and CD8⁺ T cells exposed to wtIL-2 and OMCP-mutIL-2 (**FIG. 1E-F**). Importantly, OMCP-mutIL-2 activated CD8⁺ T cells and NK cells equivalently to mutIL-2 in NKG2D^{-/-} splenocytes, indicating that the increased activation was due to the effect of OMCP targeting upon NKG2D-bearing cells (**FIG. 1F**; **FIG. 6**, right two graphs). Only incubation with wtIL-2 led to CD4⁺Foxp3⁺T_{regs} and CD4⁺Foxp3⁻ effector cell proliferation (**FIG. 1E-F**). Thus exposure to OMCP-mutIL-2 results in preferential NK activation that is superior or equivalent to wtIL-2 in a dose-dependent manner. CD8⁺ T cells can also be activated but require prolonged exposure to higher doses of OMCP-mutIL-2.

Example 2. Low-dose cytokine therapy offers a favorable safety profile.

[0112] Dose-dependent toxicity can limit cytokine administration *in vivo*. To model human immunotherapy protocols we next treated A/J mice with wtIL-2 given as ten doses over a five day cycle¹⁸. While A/J mice tolerated 750,000 IUe of wtIL-2, significant mortality was evident at higher doses (**FIG. 2A-B**). Even after a 750,000 IUe dose mice demonstrated extreme distress, weight loss, decreased food consumption, ascites and hepatic inflammation (**FIG. 2A-E; FIG. 7A-C**). These side-effects mirror the capillary leak and distress associated with high dose IL-2 therapy in humans⁷. Treatment with anti-Asialo-GM1 ameliorated mortality, but not weight loss, induced by high dose wtIL-2 (1,500,000 IUe) in A/J mice, confirming that side effects of such therapy can occur independent of NK cells (**FIG. 2F-K**). Unlike the case for wtIL-2 no animal death was evident after 1,500,000 IUe of OMCP-mutIL-2 or mutIL-2 in the presence or absence of NK cells. Animal weight loss after 1,500,000 IUe of OMCP-mutIL-2 occurred only in NK-sufficient mice suggesting that toxicity of our construct was solely due to immunoactivation (**FIG. 2F-K**). A regimen of 200,000 IUe was well tolerated in A/J mice with minimal weight loss, distress, or organ inflammation for all cytokines (**FIG. 2L-O**). Capillary leak, however, was still evident by accumulation of pleural effusion and ascites after wtIL-2, but not OMCP-mutIL-2 or mutIL-2, at this dose. B6 mice were able to tolerate higher doses of wtIL-2 but still suffered significant morbidity over 750,000 IUe (**FIG. 7D**).

Example 3. OMCP-mutIL-2 preferentially expands and activates NK cells *in vivo* compared to wtIL-2 or mutIL-2.

[0113] To evaluate immunologic changes associated with cytokine treatment, A/J mice received 200,000 IUe of cytokine or construct given as ten equal doses over five days. Splenic lymphocytes were evaluated flow cytometrically on day six. Both wtIL-2 and OMCP-mutIL-2 increased lymphocyte content and splenic size over saline-treated controls (**FIG. 3A-B**). OMCP-mutIL-2 led to a substantial expansion and activation of NK cells measured by cellularity and surface KLRG1 levels (**FIG. 3C**). In OMCP-mutIL-2 treated mice NK cells comprised close to half of all splenic lymphocytes, paralleling or even surpassing the total lymphocyte counts of saline or mutIL-2-treated mice (**FIG. 3A vs. FIG. 3C**). NK expansion by 200,000 IUe of OMCP-mutIL-2 was superior to near toxic doses of wtIL-2 (750,000IU), high dose mutIL-2 (3,500,000 IUe), or wtIL-2 complexed to anti-IL-2 antibody (clone MAB602)¹⁹ (**FIG. 3C**). In fact, the majority of mice could not tolerate the full 200,000 IUe of wtIL-2/anti-IL-2 antibody and injections had to be terminated at 160,000 or 180,000 IUe with requisite animal sacrifice due to animal distress and rapid weight loss (**FIG. 8A**). WtIL-2 led to a significant expansion of CD4⁺Foxp3⁺T_{regs}, specifically the ICOS⁺ subset⁶ in A/J mice even when complexed to anti-IL-2 antibodies (**FIG. 3D**). Importantly the NK/T_{reg} ratio, which has been described as a predictive factor for success of immunotherapy²⁰, was dramatically increased in OMCP-mutIL-2 treated mice compared to all other treatment conditions (**FIG. 3E**). Superior expansion of NK cells by

OMCP-mutIL-2 was even possible at doses 2-fold lower than wtIL-2 (FIG. 8B). However, targeting NKG2D with a ~500-fold lower affinity NKG2D ligand, ULBP3, ameliorated efficacy of the fusion construct for expansion but still offered superior NK activation compared to mutIL-2 alone (FIG. 8B). No statistically significant increase in CD4⁺Foxp3⁻ or CD8⁺ T lymphocytes was evident after wtIL-2 or OMCP-mutIL-2 treatment, although a trend for CD8⁺ T cell expansion was evident (FIG. 8C-D). Such data is consistent with the prevalence of naïve T lymphocytes, expressing low levels of IL-2 receptors and NKG2D in specific pathogen-free mice.

[0114] Unlike the A/J strain little immunoactivation of lymphocytes was evident in B6 mice treated with 200,000 IUe of wtIL-2 (data not shown). At higher doses of 750,000 IUe OMCP-mutIL-2 expanded NK cells more robustly than wtIL-2 in this strain (FIG. 3F-H). IL-2/anti-IL-2 antibody complexes prevented T_{reg} expansion but, similar to the A/J strain, such treatment had toxicity and the majority of B6 mice could not tolerate the full 750,000 IUe dose (FIG. 3I). OMCP-mutIL-2, however, was well tolerated at this dose and led to a high NK/T_{reg} ratio (FIG. 3J). No expansion of NK cells was evident in OMCP-mutIL-2 treated B6 NKG2D^{-/-} mutants, confirming the requirement for NKG2D in the function of our construct (data not shown). No statistically significant expansion of B6 CD8⁺ or CD4⁺Foxp3⁻ T cells was evident in any treatment group although a trend for CD8⁺ T cell expansion was evident after wtIL-2 administration (FIG. 8F-G). Identical data was obtained for lung resident lymphocytes in both the A/J and B6 strains (data not shown).

Example 4. OMCP-mutIL-2 preferentially expands and activates NK cells in human peripheral blood lymphocytes compared to wtIL-2 or mutIL-2.

[0115] To demonstrate the effectiveness of OMCP-mutIL-2 in human lymphocytes, human peripheral blood lymphocytes were co-cultured for 36 hours in 100IUe of either wild-type IL2, R38A/F42K mutant form of IL-2 or OMCP-mutant IL-2.

NK cells: The cells were flow cytometrically analyzed and relative prevalence of CD56⁺CD3⁻ NK cells compared between conditions. A relatively higher proportion of NK cells was evident in the OMCP-mutant IL-2 group (FIG. 31A). Perforin levels were higher in OMCP-mutant IL-2 treated NK cells (red) compared to saline (black), IL-2 (blue) or mutant IL-2 (green) treated ones (FIG. 31B).

CD8⁺ T cells: Similar to NK cells, higher intracellular levels of perforin were evident in CD8⁺ T cells treated with OMCP-mutant IL-2 compared to other conditions (FIG. 31C).

Tregs: When gating on CD4⁺Foxp3⁺CD45RA⁻ T cells a relatively higher proportion of activated CD25⁺CD127⁻ regulatory T cells was evident in IL-2 treated peripheral blood lymphocyte cultures compared to other conditions (FIG. 31D). Taken together this data suggests that OMCP-mutIL-2 preferentially expands and activates NK cells and CD8⁺ cells in human peripheral blood lymphocytes compared to wtIL-2 or mutIL-2. Importantly, OMCP-mutIL-2 does

not activated regulatory T cells significantly relative to IL2.

Example 5. Treatment with OMCP-mutlL-2 offers superior immunologic control of malignancies *in vivo*.

[0116] Unlike T lymphocytes, which require prior antigen encounter for optimal antigen-specific tumor cytotoxicity, NK cells can mediate natural cytotoxicity without prior sensitization. NK cells also form the primary barrier for expansion of select malignancies, such as lymphoma and lung cancer^{16,17,21,22}. Treatment of A/J mice with OMCP-mutlL-2, compared to wtIL-2 or mutlL-2, led to enhanced *in vivo* clearance and *in vitro* lysis of YAC-1 cells by bulk splenocytes (**FIG. 4A, FIG. 9A-B**). Decreased growth of the highly aggressive Lewis Lung Carcinoma (LLC) cell line was evident in B6 mice after 750,000 IUe of OMCP-mutlL-2 compared to wtIL-2 or mutlL-2. Increased cytotoxicity was evident in OMCP-mutlL-2 treated splenocytes for the LLC cell line as well (**FIG. 4B-C; FIG. 9A-C**). Enhanced immunotherapy was lost in NKG2D^{-/-} mice or following NK depletion (**FIG. 4D-E**). In the absence of host NKG2D mutlL-2 actually increased the rate of LLC growth. Thus OMCP-mediated targeting of mutlL-2 offers a safer and more efficacious form of immunotherapy for both solid and liquid tumors in various strains of mice.

Example 6. Impact of NKG2D targeting on IL-2 signaling.

[0117] Antibody-IL-2 conjugates, or IL-2/anti-IL-2 antibody complexes demonstrate improved biologic activity over purified cytokine by extending the duration of serum half-life^{23,24}. To investigate whether linking IL-2 to OMCP increased serum half-life, we injected 500,000 IUe of fluorescently-labeled wtIL-2, mutlL-2 or OMCP-mutlL-2 into A/J and B6 mice and monitored serum clearance by serial blood draws. While OMCP-mutlL-2 had a slightly higher serum concentration at early time points, all constructs were undetectable in the blood one hour post-injection (**FIG. 5A-B**). This is significantly shorter than the described 11-14 hour serum half-life of antibody-IL-2 conjugates²³. Interestingly, despite the injection of identical amount of cytokine, lower cytokine levels were detected in B6 mice compared to A/J mice at all time points. Such data points to strain-specific differences in clearance of IL-2 and may explain why B6 mice are able to both tolerate and require higher doses of cytokine for NK expansion. Nevertheless, based on this data it is unlikely that prolonged circulation of construct was responsible for the increased activity of OMCP-mutlL-2 over wtIL-2.

[0118] We next considered the possibility that the superiority of OMCP-mutlL-2 was the result of signaling through NKG2D as antibody-mediated crosslinking of this receptor can activate NK cells (**FIG. 10A**)²⁵. While the addition of purified OMCP to mutlL-2 did not augment NK activation or expansion *in vitro* or *in vivo* (data not shown) we would not expect a monomeric ligand to crosslink NKG2D. We thus directly compared NK cell activation in the presence of

1000 IUe of OMCP-mutlL-2, mutlL-2 and mutlL-2 combined with equimolar concentration of pentamerized OMCP. No increase in NK activation, as measured by CD69 upregulation or degranulation, was evident in the presence of pentamerized OMCP (**FIG. 5C, FIG. 10B**). This suggests that NKG2D crosslinking is not responsible for augmented NK cell activation by OMCP-mutlL-2 at physiologic concentrations.

[0119] To evaluate IL-2 signaling we next quantitated STAT5 phosphorylation after a 15 minute cytokine stimulation of freshly isolated NK cells *in vitro*. Lower levels of STAT5 phosphorylation were evident in A/J compared to B6 NK cells at all concentrations tested (**FIG. 5D-E**) suggesting that lymphocyte dysfunction of A/J mice may at least partially be the result of inefficient IL-2 signal transduction. Surprisingly, for both B6 and A/J NK cells wtIL-2 and OMCP-mutlL-2 demonstrated an identical dose-dependent pattern of STAT5 phosphorylation (**FIG. 5D-E**). In the absence of NKG2D reactivity OMCP-mutlL-2 failed to increase STAT5 phosphorylation over mutlL-2 alone. Taken together these data suggested that IL-2 α reactivity is important for peak IL-2 signaling in resting NK cells, and that NKG2D-binding may effectively substitute for IL-2R α -binding in IL-2-mediated signal transduction. Such data, however, failed to explain the superior NK activation by OMCP-mutlL-2 *in vivo* or in bulk splenocyte cultures (**FIG. 1C-D, FIG. 3**).

[0120] IL-2 signaling results in the internalization of IL-2/IL-2R, with subsequent degradation of IL-2 and IL-2R $\beta\gamma$. The binding of OMCP-mutlL-2 to both the IL-2 receptor and NKG2D could thus lead to altered internalization and enhanced NK cell activation by prolonging IL-2 signaling. To test this we stimulated freshly isolated NK cells for 15 minutes, replaced the culture media with cytokine free media, and monitored STAT5 phosphorylation for four hours. Identical decay of phospho-STAT5 was evident for both wtIL-2 and OMCP-mutlL-2 (**FIG. 5F-G**). Thus altering duration of IL-2 signaling is not responsible for superior NK activation by OMCP-mutlL-2.

[0121] We next considered the possibility that superior NK activation by OMCP-mutlL-2 may be the result of altered cytokine interaction with competing stromal cells (**FIG. 5H**). Indeed, in the presence of other splenocytes OMCP-mutlL-2 demonstrated a dose-dependent enhancement in NK STAT5 phosphorylation over wtIL-2 (**FIG. 5I**). We next explored the interplay between IL-2R α expression by stromal cells and NKG2D expression by NK cells on IL-2 signal transduction. To accomplish this we isolated splenic NK cells from either wild-type or NKG2D^{-/-} B6 mice and combined them with wild-type splenocytes depleted of NK cells. Cultures were recombined in a 1:20 NK:splenocyte ratio, resembling the proportion normally present in resting wild-type B6 mice. For some cultures NK cell depleted splenocytes were treated with saturating concentrations of IL-2R α -blocking antibody (clone 3C7) prior to recombining with wild-type NK cells. The cultures were then stimulated with 1000 IUe of either wtIL-2 or OMCP-mutlL-2 for 15 minutes. STAT5 phosphorylation was identical in NKG2D^{-/-} or wild type NK cells in the presence of wtIL-2 (**FIG. 5J**, left two columns). Wild-type NK cells cultured with OMCP-mutlL-2 demonstrated superior STAT5 phosphorylation to cultures with wtIL-2. Little STAT5 phosphorylation was evident in NKG2D^{-/-} NK cells cultured with OMCP-

mutIL-2 (FIG. 5J, right two columns). In the presence of IL-2R α -blockade of competing splenocyte stromal cells, NK cell STAT5 phosphorylation by wtIL-2 increased to levels comparable to OMCP-mutIL-2 (FIG. 5K). Taken together these data demonstrate that IL-2-R α expression by "competing" stromal cells limits NK cell activation by wtIL-2 and this competition can be eliminated by the NKG2D-targeted, IL-2R α -binding impaired OMCP-mutIL-2 construct.

Discussion for Examples 1-6.

[0122] While IL-2 therapy initially showed great promise, it has been limited by activation of T_{regs} and toxic side effects associated with activation of vascular endothelium. Several strategies have been proposed to preferentially activate cytotoxic lymphocytes. One strategy has been to create mutants with increased affinity for IL-2R β to remove the preference for IL-2R α ^{26,27}. Importantly, these IL-2 mutants retain wild type binding for IL-2R α , and would therefore still be recognized by T_{reg} cells and vascular endothelium. Our results also suggest that competition with IL-2R α ⁺-expressing cells limits bioavailability of wtIL-2 to cytotoxic lymphocytes.

[0123] Another promising therapy involves anti-IL2 antibodies that sterically inhibit wtIL-2 binding to IL-2R α ^{1,28,29}. Such treatment can extend serum half-life²⁴ due to the Fc region of the antibody and potentially due to reduced competition for wtIL-2 from IL-2R α -expressing cells. Antibody-IL-2 fusion proteins have also been designed to target IL-2 to specific tumor antigens^{30,31}. While offering the potential for personalized therapy such antibody-mediated delivery of IL-2 to the tumor depends on the expression of a known tumor associated antigen, a situation that often does not exist. This approach could potentially be further limited by tumor-mediated alteration of the targeted antigen.

[0124] Finally, IL-2 mutants with reduced affinity for IL-2R α have been tested extensively. Compared to wtIL-2 these mutants can be administered in suprathreshold doses without IL-2R α -mediated capillary leak or systemic toxicity³². While these mutants have excellent safety profiles, they activate cytotoxic lymphocytes poorly (FIG. 5C-E)³³. Our approach combines several of the concepts above to target a safe form of IL-2 directly to cytotoxic lymphocytes, instead of tumors. This is accomplished by replacing the normal targeting of IL-2 to IL-2R α with NKG2D. The combination of an IL-2R α -deficient IL-2 fused to a high affinity NKG2D-ligand improves upon previous strategies by specifically expanding NK cells without any apparent activation of T_{regs} or capillary leak. These findings offer the promise of a potentially safe and highly efficacious form of IL-2.

[0125] One limitation in translating results from inbred lab animals to humans is the natural diversity in cytokine reactivity and environmentally dependent threshold for lymphocyte activation. Previous studies have demonstrated a correlation between *ex vivo* killing of tumor cells and enhanced long-term cancer immunity³⁴. Therefore, any potential therapy needs to

account for a population that has differential levels of cytotoxic lymphocyte activity. We have thus attempted to model this natural variation by using two strains of mice known to be highly resistant (B6) or susceptible (A/J) to carcinogenesis. For example, NK cells from B6 mice, are activated by wtIL-2 and extreme doses of mutIL-2. In contrast, IL-2/anti-IL-2 antibody complexes resulted in expansion of NK cells in A/J but not in B6 mice. Such variations highlight the limitations of translating results derived from a single strain of mice to immunologically diverse humans. Importantly, the OMCP-mutIL-2 construct was able to expand NK cells in both strains of mice, indicating that this therapy could be efficacious in populations with diverse NK function and cytokine reactivity.

[0126] Since OMCP has been described as an evolutionary antagonist of NKG2D³⁵ blockade of this immunoreceptor at the time of tumor therapy may be construed as counterproductive. Nevertheless, natural cytotoxicity and tumor clearance was augmented in OMCP-mutIL-2-treated mice even in the presence of established tumors. This suggests minimal or transient NKG2D receptor occupancy and preservation of function. Alternatively recent reports have demonstrated that shed NKG2D ligands may actually promote tumor immunity through reversal of NK desensitization imposed by chronic agonistic engagement³⁶. While we did not detect NK activation or expansion by monomeric or even pentameric OMCP, it is possible that within the tumor bed such competitive antagonism plays a paradoxical role in NK activation. In addition, IL-2 may upregulate receptors necessary for NK migration and tumor infiltration. It is thus possible that anti-tumor immunity mediated by OMCP-mutIL-2 may depend on NK cells located outside the tumor bed and not subject to local tumor-specific tolerance or anergy. Furthermore, OMCP maybe the ideal "targeting vector" due to its high affinity and long half-life of binding to human NKG2D.

[0127] While NK cells from two separate strains of mice were activated by OMCP-mutIL-2 we did not detect global expansion or activation of CD8⁺ T cells by our construct. This is most likely due to the fact that NKG2D is expressed only on select subsets of CD8⁺ T cells, namely memory or activated cytotoxic lymphocytes. Based on the paucity of this cell population in mice raised in specific pathogen-free environment, OMCP-mutIL-2-mediated activation was limited in our system to NK cells. To this end we focused on immunotherapy for lung cancer and lymphoma, whose growth is regulated primarily by NK cells^{16,17,22,37}. Nevertheless OMCP-mutIL-2 was able to expand CD8⁺ T cells when administered in high concentrations *in vitro* (**FIG. 1E-F**). Thus, it may be possible that NKG2D-targeted delivery of immunostimulatory cytokines may lead to the expansion and/or activation of antigen-specific CD8⁺ memory cells for long-term tumor immunity under normal immunologic conditions.

Methods for Examples 1-6.

[0128] Cytokine and Construct Generation: The sequences encoding human IL-2 (1-133; C125S) and mutant IL2 (1-133; R38A, F42K, C125S) were cloned into the pFM1.2R³⁸ with an

N-terminal FLAG/hexahistidine tag. The chimeric OMCP-mutIL-2 molecule comprises the full-length OMCP (1-152) coding sequence cloned in frame with a C-terminal FLAG/hexahistidine tag-mutant IL-2 (1-133; R38A, F42k, C125S) cloned into the pFM1.2R vector. Proteins were expressed by transient transfection into HEK293F (Life_Technologies). Supernatant was recovered at 72h and 144h post-transfection. Supernatants were supplemented with 5 mM imidazole and 0.02% sodium azide and purified by nickel-nitrilotriacetic acid (Ni-NTA) chromatography (Qiagen). Purified proteins were buffer exchanged into saline and flash frozen in liquid nitrogen. Equivalent *in vitro* and *in vivo* activity was documented for wild-type IL-2 generated in house and Teceleukin (Tecin™) available from the NCI repository (Frederick National Laboratory for Cancer Research). Thus for some experiments these two preparations of IL-2 were used interchangeably.

[0129] Wild-type IL-2 has a specific activity of 15×10^6 IU/mg³⁹. Thus, based on the molecular weight of 15.5kDa a 4.4 μ M solution is equivalent to 1000 IU/ μ l. Based on this calculation all cytokines and construct were administered on a molar basis with 1 μ l of 4.4 μ M solution defined as 1000IU equivalents (IUe from here on). Such a system allows for equimolar comparison between IL-2, mutIL-2 and OMCP-mutIL-2 despite difference in molecular weight.

[0130] Animals: A/J (8-12 weeks) and C57BL/6J (6-9 weeks) strains of mice were purchased from the Jackson Laboratory (Bar Harbor, Maine). NKG2D^{-/-} mice on the B6 background were kindly provided by Wayne Yokoyama and bred in house (Howard Hughes Institute of Medicine at Washington University in St. Louis). Animals were housed in a barrier facility in air-filtered cages and allowed free access to food and water. For some experiments A/J mice were treated with depleting concentrations of anti-Asialo-GM1 (50 μ l day -2; 25 μ l day -1) or control rabbit IgG (Wako Chemical Company). Animal procedures were approved by the animal studies committee of Washington University School of Medicine, St. Louis, MO.

[0131] Tissue harvest and in vitro cultures: Single cell suspension of splenocytes were obtained by crushing whole spleens through 70 μ m cell strainers prior to RBC lysis by ACK buffer (Lonza, Walkersville, MD) and re-filtration through a 40 μ m filter. Lungs were digested for 90 minutes at 37°C in 1 mg/ml collagenase II (Fisher Scientific), and 5 U/ml DNase I (Sigma-Aldridge) prior to processing in an identical fashion to spleens.

[0132] For *in vitro* cultures splenocytes from either A/J, B6, or NKG2D^{-/-} mice were extracted in a sterile fashion and seeded in 12-well plates in complete media (RPMI 1640 supplemented with 10% FBS, 100 U/ml Penicillin and Streptomycin, 2 mM L-glutamine and 50 μ M 2-Mercaptoethanol) at 5 million cells per ml per well. The cells were treated with increasing doses of human recombinant IL-2, mutIL-2, OMCP-mutIL-2, or OMCP for 36 hours as described in the manuscript. For some experiments bulk splenocytes were labeled with CFSE and cultured in 1000 IUe/ml of cytokine for 5 days prior to flow cytometric analysis. For NK isolation experiments bulk splenocytes were processed using either the NK cell isolation kit II or CD49b (DX5) positive magnetic bead selection (both from Miltenyi Biotech). For STAT5 phosphorylation experiments, isolated NK cells were stimulated in increasing concentrations of

IL-2 or construct at 100,000 cells/500 μ l for 15 minutes. For experiments evaluating the interaction of NK cells with splenic stroma, DX5 positively selected NK cells were labeled with CFSE (for identification after fixation and permeabilization) and recombined with NK depleted stromal cells. As described in the manuscript, for some studies NKG2D^{-/-} NK cells were combined with wild-type splenocyte stromal cells. For other experiments, NK-depleted splenocytes from wild-type B6 mice were treated with saturating concentrations of anti-IL-2 α blocking antibody (clone 3C7) or isotype control (both from Biolegend) prior to recombining with NK cells. For such competitive STAT5 phosphorylation experiments 100,000 cells were resuspended into 2 μ l complete media containing 1,000 IU/ml of either wtIL2, mutIL-2 or OMCP-mut-IL-2 (freshly prepared and pre-warmed). The cells were then incubated at 37 °C for 15 minutes

[0133] *Flow Cytometry:* All flow cytometric analysis was performed using saturating concentrations of fluorochrome-conjugated antibodies at 4°C in FACS buffer consisting of PBS with 2% FBS and 0.4% EDTA. All antibodies were anti-mouse and purchased from BD Bioscience or eBioscience and consisted of anti-CD4 (clones GK1.5 or RM4-5), anti-CD8 (clone 53-6.7), anti-CD278 (ICOS) (clone: 7E.17G9), anti-CD25 (clone PC61), anti-KLRG1 (clone 2F1), CD49b (Integrin alpha 2) (clone DX5), anti-CD3e (clone 1452C11), anti-CD45 (clone 30-F11), anti-CD69 PE (clone H1.2F3), anti-GITR (clone DTA-1), anti-Foxp3 (clone: FJK-16s) and Anti-Stat5 (clone 47/Stat5; pY694). Antibodies were conjugated to either FITC, PE, PerCP-CyTM5.5, PE-Cyanine7, APC, APC-eFluor® 780, eFluor® 450, or Alexa Fluor® 647.

[0134] Phospho-STAT5 evaluation was performed by paraformaldehyde fixation, methanol permeabilization and staining with AlexaFluor488-conjugated Anti-Stat5 (pY694) (BD Pharmingen; clone 612599). To accomplish this isolated NK cells or NK cells combined with NK-depleted splenocyte stromal cells were fixed in 2% paraformaldehyde (PFA) at 37 °C for 10 minutes after IL-2 stimulation for 15 minutes. The cells were then washed once with ice-cold PBS and permeabilized by adding 0.5 ml/tube of 90% Methanol on ice for 1 hour. The cells were washed once with ice-cold PBS (to remove methanol), and stained for 1 hour with anti-Stat5 (pY694) antibody at room temperature followed by one wash in PBS/0.5% fetal calf serum.

[0135] *In Vitro Cytotoxicity:* ⁵¹Chromium release was conducted by incubating the target cells with 100 mCi sodium ⁵¹chromate (PerkinElmer) for 1 hour. Bulk splenocytes were used as effector cells and incubated with targets at defined effector:target ratios for 4 hours at 37°C in round bottom 96 well plates. Specific lysis was expressed as (experimental release-spontaneous release)/(maximum release-spontaneous release) X100% with 0% specific lysis as lowest expressed value.

[0136] *In vivo cytokine injections:* For select experiment, the mice received intraperitoneal injections of cytokines in 200 μ l volume given as ten equal doses given twice a day over a period of five days. As described above all cytokines were normalized to IUe on a molar basis.

For select experiments, the mice were then sacrificed on day 6 and organs were fixed in 10% buffered formalin for histological analyses. For other experiments splenocyte and lung lymphocyte populations were analyzed flow cytometrically. For all the *in vivo* cytokine treatment experiments, animals were weighed (daily or every other day) and expressed as % change from start of cytokine therapy.

[0137] For evaluation of serum concentration wtIL-2, mutIL-2 or OMCP-mutIL-2 were labeled with Alexa Fluor® 647 (LifeTechnologies Inc.) according to manufacturer instructions. Serum was collected at times specified and concentration of cytokine determined fluoroscopically according to a standard curve.

[0138] *In vivo tumor studies:* Lewis lung carcinoma (LLC) cells were subcutaneously injected into B6 or B6 NKG20^{-/-} mice at 1×10^5 cells per mouse in 100 μ l of sterile saline. Once visible tumors were evident, day 5 post-injection, a five day course of cytokine treatment was started as described above. Measurement of cross sectional tumor diameter was performed using calipers and tumor volume estimated as $\frac{4}{3}\pi r^3$. The mice were sacrificed on day 24 post injection or once they reached a maximal tumor diameter of 20mm. For NK cell depletion, mice were treated with anti-NK1.1 antibody (clone PK136) or mouse IgG isotype control (both from BioXcell) at 500 μ g day -2, 250 μ g day -1 and 250 μ g weekly for the duration of the experiment. For lymphoma clearance experiments A/J mice were treated with ten doses of cytokine over a period of five days as described above and on day #6 injected intravenously with YAC-1 cells that were labeled with CFSE at 5×10^6 cells/mouse. Mice were sacrificed 4 hours later, lungs were digested and viability of YAC-1 determined by forward and side scatter analysis of CFSE⁺ cells.

[0139] *Statistics:* Comparison of splenic and lung-resident lymphocytes between various cytokine treatment conditions was performed by unpaired T-test with Welch's correction to account for unequal variance or unequal sample size. Tumor growth between different cytokine conditions was compared by multiple unpaired-T tests performed between various conditions at various time points using the Sidak-Bonferroni correction. Fold change in STAT5 phosphorylation was evaluated by unpaired T-test with Welch's correction in a similar fashion.

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Introduction to Examples 7-10.

[0141] Intracellular surveillance mediated by MHC class I (MHCI) is a critical host immune function and as such MHCI molecules are frequently targeted for destruction or intracellular retention by viruses [1]. Many herpesviruses encode at least one protein that prevents the cell surface expression of MHCI [1,2]. However, this immune evasion strategy renders the infected cell susceptible to NK cell-mediated lysis due to loss of inhibitory signals [3]. Viral infection also leads to cell surface display of NKG2D ligands (NKG2DLs) recognized by the activating receptor NKG2D, further predisposing the infected cell towards NK cell-mediated lysis. Therefore, viruses that target MHCI expression often also sabotage NKG2D-mediated cell responses by targeting NKG2DLs on the infected cell [4-7].

[0142] NKG2DLs are not normally expressed on the cell surface but can be induced by cellular stress [8]. The specific trigger for NKG2DL expression is not known but NKG2DLs are upregulated in response to several viral infections [9-12]. NKG2DLs comprise a large group of

proteins all recognized by NKG2D, despite having low sequence identity. NKG2DLs include the MIC (A and B) and ULBP (1-6) families in humans as well as MULT1 and the RAE-1 (α - ϵ) and H60 (a-c) families in mice [13]. The redundancy in NKG2DLs is likely due to a combination of tissue specific expression patterns of the ligands and the need to counter viral NKG2D evasion strategies [14]. Many viruses have evolved mechanisms to inhibit the cell surface expression of NKG2DLs as a means of interfering with NKG2D surveillance of viral infection. This strategy is most apparent among β - and γ -herpesviruses, in which four murine cytomegalovirus proteins (m138, m145, m152, m155) [15-18], two human cytomegalovirus proteins (UL16, UL142) [19,20] and one Kaposi's sarcoma-associated herpesvirus protein (K5) [21] have been demonstrated to block NKG2DL surface expression. This evasion strategy is also found in RNA viruses, as hepatitis C virus NS3/4a and human immunodeficiency virus Nef proteins also block the expression of a subset of NKG2DLs [22,23]. Additionally, human cytomegalovirus, herpes simplex virus type 1 and Epstein-Barr virus each also encode at least one miRNA that prevents translation of MICB [24,25]. Similarly, JCV and BKV polyoma viruses target ULBP3 with miRNAs [26]. However, blocking NKG2DL expression on the infected cell is an imperfect evasion strategy, since no single viral protein or miRNA has been shown to block the expression of all NKG2DLs.

[0143] Like several herpesviruses, cowpoxvirus (CPXV) also sabotages MHCI expression. CPXV expresses CPXV012 and CPXV203, two proteins that prevent TAP-mediated peptide transport and MHCI trafficking to the cell surface, respectively [27-34]. Ectromelia virus, a related orthopoxvirus, induces NKG2DL expression and NKG2D is critical for the control of ectromelia virus pathogenesis [35]. Infection with another orthopoxvirus, monkeypox virus, leads to dramatic expansion of NK cells but impaired NK cell function [36]. Together this suggests that CPXV infected cells would be sensitive to NK cell-mediated lysis.

[0144] Unlike herpesviruses, CPXV does not target NKG2DLs. Instead this virus targets NKG2D directly by encoding a competitive inhibitor of NKG2DLs, orthopoxvirus MHC class I-like protein (OMCP) [37,38]. OMCP is a 152 residue protein that is secreted from infected cells and antagonizes the NKG2D-mediated killing of NKG2DL-expressing target cells [37]. OMCP also plays an important role *in vivo*, with OMCP-null CPXV attenuated in mouse models of infection (M. Sun *et al*, personal communication). OMCP binds to murine NKG2D with an affinity equal or greater than all tested murine NKG2DLs, and to human NKG2D with an affinity \sim 5,000-fold higher than human NKG2DLs [37-40].

[0145] Despite their divergence in sequence identity, all known host NKG2DLs share common structural features [41,42]. NKG2DLs contain an MHCI-like platform domain composed of an eight-stranded beta sheet with two helices [43-47]. The platform domain is subdivided into α 1 and α 2 domains, with each domain containing four beta strands and an alpha helix. Unlike MHCI, the groove between the helices of the NKG2DL platform domain is closed and therefore NKG2DLs do not bind peptides.

[0146] Like host NKG2DLs, OMCP also adopts an MHCI-like platform domain [38]. However, the platform domain of OMCP has been trimmed to have only a six-stranded beta sheet with

shorter flanking helices. We termed the helix of the $\alpha 1$ domain H1 and the discontinuous helix of the $\alpha 2$ domain is termed H2a and H2b. The H2a and H2b helices of OMCP are also rearranged to be flatter against the beta sheet and to be splayed apart from each other. These differences in the OMCP structure were hypothesized to be important for the high affinity binding of OMCP to NKG2D. However, OMCP was still expected to bind to NKG2D in the same orientation as host NKG2DLs, i.e. with the alpha helices oriented diagonally within the symmetric NKG2D binding groove.

[0147] Here we report the 2.0 Å-resolution structure of human NKG2D bound to OMCP of the Brighton Red strain of cowpoxvirus. The structure reveals a significant reorientation of OMCP in the NKG2D binding groove relative to host NKG2DLs. The interface of OMCP with NKG2D is highly complementary, buries a significantly larger surface area than host NKG2DLs, and remains continuous across the entire NKG2D binding groove. This novel binding adaptation and high affinity allows OMCP to compete with the high local concentration of membrane-associated host NKG2DLs. We further show that the mechanism of NKG2D antagonism requires OMCP to be secreted, lest it lead to NKG2D signaling.

Example 7. Structure determination of OMCP-NKG2D.

[0148] We had previously solved the structure of OMCP alone and shown that, similar to host NKG2DLs, OMCP adopts an MHC-I-like platform domain [38]. Despite the overall similarity of the domain structure of OMCP to host NKG2DLs, OMCP had several notable deviations in the putative NKG2D-binding site that were hypothesized to be important for the high affinity binding of OMCP to NKG2D. To further understand the unusually high affinity of OMCP for NKG2D, we crystallized and solved the structure of OMCP bound to human NKG2D.

[0149] Initial crystallization trials with OMCP and NKG2D yielded ~30 different crystallization conditions. Subsequent data collection and molecular replacement of multiple low-resolution crystal forms all yielded similar partial solutions, with alternating sheets of OMCP-NKG2D complexes separated by undefined density. In the original structure of OMCP alone, the beta sheets packed to form a trimer with the alpha helices oriented away from the center [38]. An identical OMCP trimer formed in the OMCP-NKG2D partial solutions, with NKG2D now bound to the outward facing helices (data not shown). In an attempt to change the lattice packing, we introduced mutations into the beta sheet of OMCP that were designed to break the trimeric interface. These mutations were on the opposite face of OMCP from the NKG2D binding site to avoid disrupting OMCP-NKG2D binding. A mutant form of OMCP (Y23D, F95D) crystallized with NKG2D in a new space group and the crystals diffracted to 2.0 Å (**Table 1**)(**FIG. 24A**).

[0150] The electron density map was continuous and unambiguous throughout all chains of the structure, with the exception of Q108 in OMCP. This residue was situated in the center of the largest loop of OMCP and unambiguous density for this residue was also absent from the structure of OMCP alone [38]. The structure of OMCP bound to NKG2D showed no major differences from our previous structure of OMCP alone, with an RMSD for all atoms of 0.8 Å.

Likewise, NKG2D was also similar to previous NKG2D structures with RMSDs ranging from 0.5-0.9 Å. The β 3- β 4 loop of NKG2D is the only region of either OMCP or NKG2D that displayed above-average B factors. This loop is thought to be flexible and has had above average B factors in all previous NKG2D structures [48]. Interestingly, the peptide bond between S193-S194 in our NKG2D structure had a *cis* conformation not described in other NKG2D structures (FIG. 29).

Example 8. The interface between OMCP and NKG2D.

[0151] OMCP was hypothesized to bind to the same surface of NKG2D used by host NKG2DLs because (i) OMCP competed with host NKG2DLs for NKG2D and (ii) mutations within the NKG2DL-binding pocket of NKG2D altered OMCP binding affinity [38]. OMCP does bind NKG2D using the same concave binding pocket as host NKG2DLs (FIG. 24A). OMCP binds primarily using the discontinuous helices of its α 2 domain, H2a and H2b. The position of the H2a and H2b helices is such that every surface exposed side chain of both helices within the binding site directly contacts NKG2D (FIG. 24B). Only two contacts are found outside of H2a and H2b, Ile49 and Arg66. Both of these residues are within the α 1 domain but lie outside of the H1 helix.

[0152] Twelve OMCP residues contact eighteen NKG2D residues to form a mixture of bond types (Table 2). Three residues in each NKG2D half-site are known as core binding residues because they make contacts with all known host NKG2DLs. The core residues of NKG2D subunit A (NKG2D^A) (Tyr152, Tyr199, Met184) form two hydrogen bonds and make extensive hydrophobic contacts with OMCP residues. The core residues of NKG2D^A contact four OMCP residues and the most critical of these residues is Phe122. Phe122 makes multiple hydrophobic contacts with all three NKG2D^A core residues, including *pi*-stacking with Tyr152. Phe122 also forms a backbone-to-sidechain hydrogen bond with Tyr152. Interestingly, OMCP is the first NKG2D ligand not to utilize all six NKG2D core-binding residues, with only Met184 and Tyr152 of NKG2D subunit B (NKG2D^B) contacting OMCP. NKG2D^B Met184 and Tyr152 each make a single hydrogen bond and hydrophobic contacts with OMCP residues. Two OMCP residues, Trp127 and Asp132, make contacts with both NKG2D protomers. OMCP Trp127 forms a hydrogen bond to Lys150 of NKG2D^A and makes several hydrophobic contacts with Leu148 of NKG2D^B, Lys150 and Ser151 of NKG2D^A. OMCP Asp132 forms a hydrogen bond with Tyr152 of NKG2D^B and a salt bridge with Lys150 of NKG2D^A (FIG. 25A).

[0153] Due to the high affinity of the OMCP-NKG2D interaction we harnessed a high throughput *in vitro* selection approach to find NKG2D-binding null mutants (Table 3). The results of the screen identified D132 as an important residue for disrupting NKG2D binding. We then generated the mutation D132R in attempt to completely ablate NKG2D binding. Surprisingly, the D132R mutant alone was unable to bind to NKG2D at concentrations 35-fold above the K_D (FIG. 25B), but did not affect binding of OMCP to FcRL5-expressing cells (FIG.

25C). This mutation is likely to cause significant steric clashes, as well as disrupting both interactions made by Asp132 to NKG2D^A Lys150 and NKG2D^B Tyr152 (**FIG. 25A**).

[0154] Previously, the 14-fold higher affinity of OMCP for human vs murine NKG2D was mapped to three amino acid substitutions in the $\beta 5'$ - $\beta 5$ loop of NKG2D, abbreviated L2 [38]. In addition to the substitutions themselves (1182V, M184I and Q185P), the position of the loop between NKG2D orthologs differs. L2 in human NKG2D is bent towards the center of the concave binding cavity compared to L2 of murine NKG2D. Superimposition of murine NKG2D onto the human NKG2D-OMCP structure reveals that the contacts between OMCP and Met184 (mNKG2D residue 1200) in NKG2D^B and between Met184 (1200) and Glu185 (P201) in NKG2D^A would be altered due to the different position of the murine $\beta 5'$ - $\beta 5$ loop (**FIG. 26A-B**). This alteration would disrupt contacts with three residues in OMCP H2a, three residues in H2b and Arg66 within the $\alpha 1$ domain. Of the contact residues of L2, Met184 makes the most significant contacts in both NKG2Ds (**Table 2**)(**FIG. 26C**). Critically, of the 58 NKG2D sequences available in GenBank, 54 conserve the Met184 and Glu185 found in the high affinity human NKG2D (**FIG. 26D**).

[0155] Eighteen OMCP variants have been described between different CPXV and MPXV strains [51]. In this study we have crystallized OMCP from the Brighton Red strain of CPXV which has >60% sequence identity with the highly conserved sequence of the other 17 OMCP variants, collectively termed OMCP_{mpx}. Of the 12 OMCP contact residues observed, 9 are identical to OMCP_{mpx}. Of the remaining contacts, all three are conservative hydrophobic substitutions (I49L, T118I and M135I) (**FIG. 27**). OMCP_{mpx} binds to NKG2D and the substitutions in the NKG2D contact residues are unlikely to grossly affect the affinity of OMCP_{mpx} for NKG2D [37].

Example 9. A novel NKG2D-binding adaptation.

[0156] Host NKG2DLs have low sequence identity but overall similar structures, with MHCI-like platform domains binding diagonally across the symmetric binding groove created by the NKG2D homodimer [13,41,52]. Host ligands contact one NKG2D half site with H1 and the S1-S2 loop, and contact the second NKG2D half site with H2b. Despite the similar MHCI-like fold, OMCP binds the NKG2D binding groove in a novel orientation, rotating $\sim 45^\circ$ relative to host NKG2DLs (**FIG. 27**). Instead of using H1 and S1-S2 loop like host ligands, OMCP has replaced these contacts with H2a. This rotation leads to the helices of OMCP being perpendicular to the NKG2D binding groove, instead of lying diagonally across it.

[0157] Two unique rearrangements of H2a and H2b make the OMCP orientation possible. The $\alpha 2$ helices of OMCP and host NKG2DLs are discontinuous, with the two shorter helices hinged relative to each other. For host ligands, the angle between H2a and H2b is $\sim 90^\circ$, positioning H2a away from the NKG2D interface. In contrast, OMCP has increased the hinge angle

between the helices by $\sim 20^\circ$, leading to a $\alpha 2$ helix that is flatter relative to the beta sheet of OMCP. The flattening of the $\alpha 2$ helix allows H2a and H2b to closely complement the concave binding groove of the NKG2D homodimer (**FIG. 24B**). The tight fit of the $\alpha 2$ helix for NKG2D is reflected in the high shape complementarity (0.77) and buried surface area (2,612 \AA^2). In contrast, host NKG2DLs have shape complementarity ranging from 0.63-0.72 and buried surface areas ranging from 1,700-2,180 \AA^2 [43,44,46].

[0158] The second unique feature of the $\alpha 2$ helix is the separation of H2a and H2b relative to each other. This region also contains a translation that completely separates H2a and H2b into two distinct helices. This translation is critical for NKG2D binding because it allows each helix to be directly centered on the core binding sites of each NKG2D monomer (**FIG. 27**). This creates a symmetric binding site on OMCP that recognizes the symmetric binding groove created by the NKG2D dimer. The symmetry between OMCP and NKG2D binding is in stark contrast to the canonical binding of an asymmetric host ligand to the symmetric NKG2D binding groove [52]. However, one element of asymmetry remains in the OMCP-NKG2D interaction because each NKG2D half-site recognizes an OMCP helix in a different N- to C-terminal orientation, demonstrating again the flexibility of NKG2Ds rigid adaptation recognition [41,53].

[0159] The contact sites between NKG2D and host NKG2DLs are made up of two patches centered on the core binding sites of NKG2D and H1/S1-S2 loop and H2b of NKG2DLs [41]. As a result, the interface of NKG2D with NKG2DLs is discontinuous, particularly in the center of the NKG2D binding groove (**FIG. 27**). Due to the unique orientation of OMCP, H2a and H2b make continuous contacts along the entire NKG2D binding groove (**FIG. 27**). The sidechains of OMCP Lys126, Trp127, Glu131 and Asp132 make contacts with residues in the center of the NKG2D binding groove and bridge the core binding sites on each NKG2D monomer (**FIG. 24B**). In particular, OMCP Trp127 is directed towards the center of the NKG2D dimer and makes hydrophobic contacts with residues on both NKG2D monomers, effectively closing any gaps in the binding interface.

Example 10. Signaling of NKG2D upon ligand engagement.

[0160] CPXV and MPXV-infected cells secrete OMCP, which can act as an NKG2D-antagonist [37]. This immune evasion strategy is reminiscent of cancer induced-NKG2DL shedding. Some cancer cells proteolytically cleave NKG2DLs from the cell surface using matrix metalloproteinases (MMPs), simultaneously preventing NKG2D-bearing lymphocytes from targeting the cancer cell, as well as creating soluble NKG2DLs to inhibit NKG2D in *trans*. Cell-associated NKG2DLs trigger NKG2D effector functions (**FIG. 28A**), while cancer-induced, soluble NKG2DLs block NKG2D function (**FIG. 28B**). Like shed NKG2DLs, OMCP is soluble and blocks NKG2D function in *trans* [37] (**FIG. 28C**). Unlike host NKG2DLs, OMCP binds NKG2D with a novel orientation. We therefore asked whether OMCP could serve as a NKG2D agonist in the context of the cell membrane, analogously to host NKG2D ligands. Since OMCP is a secreted protein, an artificially cell-associated OMCP was constructed by using a

heterologous transmembrane domain from Thy1.1 [37] (FIG. 28D). To measure NKG2D-mediated cell killing, we stably transduced Ba/F3 cells with retroviral vectors expressing either the OMCP-Thy1.1 construct or host NKG2DLs. OMCP-Thy1.1 -expressing target cells were killed equivalently to host NKG2DL-transduced target cells, indicating that despite its altered binding orientation, cell-associated OMCP was able to activate NKG2D signaling (FIG. 28E). Thus, OMCP must be secreted lest it active NKG2D-effector functions itself, despite potential loss of efficacy due to diffusion.

Discussion for Examples 7-10.

[0161] While many viruses have adopted a general mechanism of NKG2D-sabotage by trying to retain multiple host-encoded NKG2D ligands within the infected cell, CPXV and MPXV take the very different approach of targeting NKG2D directly. Since NKG2D is monomorphic, this mechanism has the significant advantage of requiring a single protein to prevent NKG2D recognition of the infected cell. The large number of sequence-divergent host NKG2DLs and their associated polymorphisms are thought to be driven by selection from pathogen-encoded NKG2DL antagonists [14]. Likewise, viral NKG2L antagonists are under selective pressure from the diverse host NKG2DLs in a continual cycle of adaptation. Due to the need to recognize multiple NKG2DLs, NKG2D has a limited mutational space to adapt. The limited ability of NKG2D to mutate is yet another advantage of OMCP directly targeting NKG2D, instead of NKG2DLs.

[0162] Similarly to OMCP, some cancer cells shed host NKG2DLs to create their own soluble NKG2D antagonists. However, this strategy has the additional benefit of removing host NKG2DL from the surface of cancer cells. In contrast, CPXV and MPXV lack a known mechanism of blocking host NKG2DL surface expression. Secreted OMCP must then be able to compete efficiently against the high local concentration of multiple host NKG2DLs on the infected cell, as well as against diffusion away from the infected cell. One possible way to increase OMCP's ability to compete with host ligands would be to increase the avidity of OMCP by having multiple NKG2D-binding domains. However, a multimeric OMCP could crosslink NKG2D and potentially trigger NKG2D-mediated killing. Therefore, secreted OMCP must be monomeric to prevent aberrant NKG2D signaling. Thus to compensate for these deficiencies, OMCP must have the highest affinity possible to effectively compete against cell-associated host NKG2DLs [37,38]. The half-life of ligand-receptor interactions correlate well with physiological competitiveness [55]. OMCP binds human and murine NKG2D with half-lives of 348 and 54 seconds, respectively, compared to half-lives of 1.5-18 seconds for most NKG2DLs [38,44,56]. Indeed, the increased half-life for NKG2D allows OMCP to effectively antagonize NKG2D-mediated immunity in a murine infection model (M. Sun *et al*, personal communication).

[0163] To understand the molecular basis for the long half-life of OMCP for NKG2D, we previously determined the structure of OMCP alone, and here, we report the structure of OMCP bound to NKG2D. The structure of OMCP alone was grossly similar to that of host

NKG2D ligands, containing an atypical MHCI-like platform domain. Host NKG2D ligands bind with the helices of their platform domains oriented diagonally within the symmetric binding groove of NKG2D. Thus it was expected that OMCP was a viral mimic of host NKG2D ligands and would interact with NKG2D analogously.

[0164] The structure of OMCP-NKG2D instead revealed a novel orientation for an NKG2D ligand in the NKG2D binding groove. Alterations within the $\alpha 2$ domain helix allow OMCP to arrange its helices perpendicularly within the binding groove. This reorientation places the H2a and H2b helices directly in contact with the core binding sites of NKG2D and also forms the largest and most continuous binding interface with NKG2D. Because the forces (hydrogen bonds, van der Waals, hydrophobic interactions) that mediate protein-protein interactions are individually weak, a large, continuous interface with high shape complementary allows for a cumulatively strong interaction between proteins. This change in the binding orientation of OMCP reveals how the MHCI-like platform used by host ligands can be adapted by a pathogen to enhance NKG2D binding.

[0165] Since host NKG2DLs and OMCP have a similar MHCI-like platform, it is reasonable to wonder why no host ligand has evolved an analogous high-affinity interaction with NKG2D. One likely reason is that the host immune response must be carefully calibrated to balance the need for protection against the threat of autoimmunity. Since the expression of NKG2DLs on the cell surface signals for effector functions, even a small amount of high affinity host ligand on the cell surface could trigger an immune response, and the resulting tissue damage could be deleterious for the host. Indeed, NKG2D-expressing cells and/or aberrant expression of host NKG2DLs have been implicated in diabetes, celiac disease and rheumatoid arthritis [57-60]. Viruses are not constrained by autoimmune selective pressures. Therefore, CPXV and MPXV were free to evolve a viral NKG2DL with the highest possible affinity to maximize immune evasion potential.

[0166] Interestingly, OMCP triggers NKG2D signaling when attached to a target cell membrane, despite the novel orientation of OMCP relative to host NKG2DLs. The interaction of host NKG2DLs with the dimeric NKG2D bears broad structural similarity to the interaction between MHC molecules with their cognate T cell receptors (TCRs). In both cases, the NKG2DL/MHC lies diagonally across the surface created by the dimeric NKG2D/TCR. However, there are several examples of MHC-TCR complexes that, like OMCP-NKG2D, interact with unconventional orientations [61-65]. Several of these complexes involved autoimmune MHC-TCR complexes that were tilted or rotated outside of the normal range for MHC-TCR complexes [61,65]. While these receptors could induce TCR signaling at high MHC concentrations, they failed to assemble characteristic immunological synapses [66]. A striking example of unconventional binding was found when an *in vitro* peptide library-MHC-TCR (H2-L^d-42F3) screen produced a p3A1-H2-L^d-42F3 complex with an interface rotated $\sim 40^\circ$ relative to other H2-L^d-42F3 complexes. This rotation places the TCR nearly parallel with the MHC peptide-binding groove and shifted the interface center almost entirely on one of the MHC α helices - an orientation strikingly similar to the interface of OMCP-NKG2D [65]. Interestingly,

the p3A1-H2-L^d-42F3 complex failed to induce TCR signaling [65]. Thus, unlike OMCP/NKG2D, the orientation of MHC relative to TCR is an important factor for signaling.

[0167] OMCP-NKG2D and p3A1-H2-L^d-42F3 have opposite signaling outcomes, despite having very similar orientations. TCR signaling requires co-receptor binding to either the $\alpha 2/\beta 2$ or $\alpha 3$ domains of MHCII or MHCI, respectively. The failure of p3A1-H2-L^d-42F3 to signal, and of other unconventional MHC-TCR complexes to form true immunological synapses, is potentially due to the inability of co-receptors to form correct quaternary structures for signaling [64,65,67]. Signaling by NKG2D is not known to require co-receptor stimulation and the majority of NKG2DLs lack the co-receptor binding $\alpha 2/\beta 2$ or $\alpha 3$ domains of true MHC molecules. This difference in co-receptor dependency likely explains why OMCP (when attached via transmembrane) is still competent to stimulate NKG2D-signaling compared to MHC-TCR complexes with unconventional binding orientations. Further, it suggests that clustering of NKG2D on the cell surface is the major determinant of NKG2D-mediated activation.

Methods for Examples 7-10.

[0168] Identification of NKG2D-binding null mutant D132R. A high throughput *in vitro* selection approach based on combinatorial cell surface display was utilized to identify NKG2D-binding null mutants. The sequence of OMCP was globally mutagenized using error-prone PCR, and the mutated amplicons were spliced to a signal-less Thy1.1 cDNA via overlap extension PCR. This library of mutated OMCPs fused to unmutated Thy1.1 was cloned into the pMXs-IRES-EGFP retroviral transfer vector (kind gift of Toshio Kitamura, University of Tokyo) to generate a molecular library for transduction into Ba/F3 cells. The transductants were then sorted for green fluorescence and anti-Thy1.1 expression to yield a cellular library whose members all had surface expression of OMCP, filtering out mutations giving frameshifts, premature stop codons, and folding-incompetent OMCP. This OMCP library was sorted for NKG2D binding using NKG2D-tetramers. Sorted cells were cloned by limiting dilution and analyzed. The retroviral cassettes of cells lacking or having reduced NKG2D-binding activity were amplified and sequenced. Utilizing this approach, we identified Asp132 as a critical residue for NKG2D binding.

[0169] Protein expression and purification. OMCP_{BR} and human NKG2D expression constructs were previously described [38]. The (D132R) OMCP_{BR} protein was prepared identically to WT OMCP_{BR}. (23D/95D) OMCP-NKG2D complex was reconstituted by oxidative co-refolding from purified inclusion bodies, as described previously [38]. Refolded protein was slowly diluted 10-fold with water and captured on a 5 ml HiTrap Q HP column (GE Healthcare) using a Profinia instrument (Bio-Rad). The captured protein was washed with 50 mM Tris, pH 8.5, 20 mM NaCl and bulk eluted with 50 mM Tris, pH 8.5, 250 mM NaCl. The eluted protein was then concentrated and further purified by gel filtration chromatography on a Superdex S75 column (16/60; Amersham Biosciences). Fractions containing mono-dispersed OMCP-NKG2D complex (-50 kDa) were pooled and buffer exchanged into 25mM Ammonium acetate pH 7.4.

[0170] *Crystallization, data collection and processing.* Native protein crystals were grown by hanging drop vapor diffusion at 20°C by streak seeding into a well solution containing 15% PEG 3350, 0.2M MgCl₂, 0.1M Bis-Tris pH 6.75. Crystals were cryoprotected with well solution containing 15% glycerol before flash freezing directly in a liquid nitrogen bath. Diffraction data were collected at the Advanced Light Source synchrotron (beamline 4.2.2). Native (23D/95D) OMCP-hNKG2D crystal diffraction data were collected at 100 K and at a wavelength of 1.00004 Å. Additional diffraction data statistics are summarized in **Table 1**. Data processing with HKL2000 [68] showed the crystals belonged to the primitive monoclinic space group P2₁ (space group #4). The asymmetric unit of the crystal contained two copies of the (23D/95D) OMCP-hNKG2D complex.

[0171] *Model building and refinement.* The structures of human NKG2D (1MPU) [48] and OMCP (4FFE) [38] were used as search models for molecular replacement through Phenix [69]. Reiterative refinement and manual rebuilding were performed using Phenix and Coot [70], respectively. Both 2Fo-Fc and Fo-Fc maps were used for manual building and to place solvent molecules. The final model yielded an R_{work} of 16.6% and R_{free} of 21.4%, with 4% of all reflections set aside for free R factor cross-validation. Progress in refinement was also measured using the MOLPROBITY webserver [71]. The final Ramachandran statistics for the model were 98% favored and 0% outliers. Additional refinement statistics are summarized in **Table 1**. Images of structures were produced using the program PyMol [72].

[0172] *Structure analysis.* Analysis of the contact residues, buried surface area and shape complementarity of the OMCP-NKG2D interface were carried out using the programs Ligplot+ [73], PISA [74] and SC [75]. Structural programs as compiled by the SBGrid consortium [76]. Analysis of NKG2D conservation was performed using the ConSurf server [77-80]. GenBank numbers for species used in Consurf analysis are: Humans (30749494), Borean orangutan (21902299), Chimpanzee (57113989), Gibbon (332232684), Macaque (355785888), Green Monkey (635063485), Common marmoset (380848799), Mouse (148667521), Brown rat (149049263), Guinea Pig (348569092), Ground squirrel (532114387), Deer mouse (589967905), Naked mole rat (512868733), Prairie vole (532053033), European Shrew (505834608), Star-nosed mole (507978716), Chinese hamster (537136230), and Cat (410963826).

[0173] *Atomic coordinates.* The atomic coordinates (accession code 4PDC) have been deposited in the Protein Data Bank, Research Collaboratory for Structural Bioinformatics (Rutgers University, New Brunswick, NJ)

[0174] *In vitro NK cell killing assays.* Splenocytes from C57BL/6 mice were preactivated with 200 U/ml IL-2 for 24 hours and used as cytotoxic effectors against stably transduced Ba/F3 cell lines in standard killing assays. Target cells were carboxyfluorescein succinimidyl ester (CFSE) labeled and co-incubated with activated splenocytes at 37°C, 5% CO₂ for 4 hours at effector:target ratios of 10:1, 20:1, and 40:1. Killing percentage was determined by incorporation of the dead cell exclusion dye 7-amino-actinomycin D (7AAD) in the CFSE+

target population as assessed by flow cytometry. Percent specific lysis was calculated using the formula [(experimental dead % - background dead %) / (maximum release dead % - background dead %)] x 100. C57BL/6 mice were obtained from the National Cancer Institute (Charles River, MA). Mice were maintained under specific pathogen-free conditions and used between 8 and 12 weeks of age. Single cell suspensions of splenocytes used in killing assays were generated using standard protocols [81].

Table 1: Data collection and refinement statistics		
		<u>OMCP_{BR}-hNKG2D</u>
Data collection		
Space group	P2 ₁	
Cell dimensions		
a, b, c (Å)	43.3, 101.1, 91.4	
α, β, γ (°)	90.0, 91.6, 90.0	
Resolution (Å)	50-2.0 (2.07-2.00)	
R_{sym}	11.8 (48.5)	
I/σ	14.5 (3.8)	
Completeness (%)	93.5 (91.5)	
Redundancy	6.2 (5.3)	
Refinement		
Resolution (Å)	44-2.0	
Total reflections	309693	
Unique reflection	50139	
R_{work}	16.6% (21.0%)	
R_{free}	21.4% (29.5%)	
Wilson B-factor	21.62	
Protein residues	791	
Water molecules	524	
R.M.S. deviations		
Bond lengths (Å)	0.003	
Bond angles (°)	0.79	
^a As defined by PHENIX [69]		
Table 2: Interface contacts between NKG2D and OMCP		
NKG2D-A	OMCP	Bond type
Lys150	Asp132	Salt bridge
Lys150	Trp127	H bond
Lys150	Trp127	Φ(3)

Table 2: Interface contacts between NKG2D and OMCP		
NKG2D-A	OMCP	Bond type
Ser151	Lys126	H bond
Ser151	Trp127	Φ(1)
Tyr152	Phe122	H bond
Tyr152	Phe122	Φ(9)
Tyr152	Lys126	Φ(5)
Met184	Thr118	H bond
Met184	Thr119	Φ(1)
Met184	Phe122	Φ(5)
Gln185	Arg66	Φ(1)
Leu191	Phe122	Φ(1)
Tyr199	Phe122	Φ(4)
Glu201	Arg66	Salt bridge
Thr205	Arg66	H bond
NKG2D-B	OMCP	Bond type
Leu148	Trp127	Φ(1)
Ser151	Glu131	H bond
Tyr152	Asp132	H bond
Tyr152	Glu131	Φ(3)
Tyr152	Met135	Φ(5)
Ile182	Ile49	Φ(2)
Glu183	Arg142	Salt bridge
Met184	Met135	Φ(1)
Met184	Arg138	Φ(2)
Met184	Arg142	H bond
Lys186	Arg142	Φ(1)
Leu191	Met135	Φ(1)
Glu201	Arg138	Salt bridge

Hydrogen bonds (H bonds), salt bridges and carbon-to-carbon hydrophobic interactions (Φ) are shown for each contact residue. The number of hydrophobic interactions between contact residues is designated in parenthesis.

Table 3:NKG2D binding mutations identified through global			
Amino Acid	Frequency of Mutation	Associated Mutations	Solvent Accessible
D132	4	D132N D132N, T31S, V68A	++

K126	4	D132G, K126N, D76V D132G, K126N, D76V K126N K126N, S71G K126N, D132G, D76V K126N, D132G, D76V	++
K125	2	K125E, F65C	-
S120	2	K125E, F92V S120Y S120Y, E10A, N56K	-
D76	2	D76V, D132G, K126N D76V, D132G, K126N	++
W116	2	W116R W116R, K113Q	-
R123	2	R123G, D26G, F50L R123G, D21V, F128L	-
E75	1	E75D	-
S71	1	S71G, K126N	++
F92	1	F92V, K125E	+
F65	1	F65C, K125E	-
K113	1	K113Q, W116R	+
E10	1	E10A, N56K, S120Y	++
N56	1	E10A, N56K, S120Y	++
D21	1	D21V, R123G, F128L	++
F128	1	D21V, R123G, F128L	-
D26	1	D26G, F50L, R123G	++
F50	1	D26G, F50L, R123G	-
T31	1	T31S, V68A, D132N	++
V68	1	T31S, V68A, D132N	+
I30	1	I30L, L51F, L64P, M135T	-
L51	1	I30L, L51F, L64P, M135T	-
L64	1	I30L, L51F, L64P, M135T	++
M135	1	I30L, L51F, L64P, M135T	++
R67	1	R67S, L117P, T119N, F122L	+
L117	1	R67S, L117P, T119N, F122L	-
T119	1	R67S, L117P, T119N, F122L	++
F122	1	R67S, L117P, T119N, F122L	++

Mutations were sequenced from 17 clones expressing mutagenized OMCP-Thy1.1. Clones were selected for reduced binding to NKG2D tetramers. The selected clones showed variable deficits in NKG2D binding. Each clone had 1-4 mutations in the amino acid sequence of OMCP (5 clones with 1 mutation; 4 clones with 2 mutations; 6 clones with 3 mutations; 2 clones with 4 mutations). Silent mutations are not indicated. Mutations are listed in the order of frequency sequenced from the selected clones, and mutations that occurred together within individual clones are listed where applicable. Clones highlighted in grey have at least one mutation in a solvent inaccessible residue that may alter the overall stability of OMCP.

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[0175]

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Example 11. Individuals with poorly functioning natural killer cells are more susceptible to malignancies.

[0176] FIG. 14A shows that AJ and 129 are lung cancer susceptible strain of mice and B6 and C3H are lung cancer resistant strains of mice based on the larger tumor burden found in AJ and 129 mice. **FIG. 14B** shows that when NK cells from the various mouse strains were incubated with LM2 lung carcinoma cells at varying ratios, the NK cells freshly isolated from B6 and C3H mice (lung cancer resistant strains) resulted in significantly more lysis of LM2 lung carcinoma cells than the NK cells freshly isolated from AJ and 129 mice (lung cancer susceptible strains). Taken together these data show that strains of mice that are resistant to lung cancer have NK cells that more effectively lyse lung carcinoma cells. Further, susceptible

strains have poorly functioning NK cells.

[0177] That data also correlates with human data. **FIG. 15** shows that a greater percentage of NK cells appear to produce TNF α in "resistant" patients versus "susceptible" patients. Further, it has been shown that tumors downregulate the lytic capacity of NK cells, even if they were highly functional before.⁵³ Thus, even individuals with highly functioning NK cells may benefit from therapy to enhance NK cell function.

[0178] Notably, *ex vivo* cytokine activation can reverse natural killer cell dysfunction. **FIG. 16** shows that IL-2 activated NK cells from both resistant (B6 and C3H) and susceptible (AJ and 129) mouse strains can lyse LM2 lung cancer cells. Accordingly, mouse NK Cells that did not show significant lysis of cancer cells (NK cells from 129 & AJ strains) were much more effective at lysis when treated with IL-2. NK cells from cancer-resistant strains also showed increase % of specific lysis.

Example 12. OMCP-mutIL2 mediated immunotherapy *in vivo*.

[0179] Immunoregulation of malignancies involves an intricate interplay of multiple cellular components. CD4⁺Foxp3⁺ T_{regs} have been shown in multiple models to contribute to tumor-specific tolerance and facilitate tumor growth^{4,16,11}. NK cells and CD8⁺ CTLs contribute to immunoregulation of multiple tumors, such as melanoma^{12,18}. Other tumors, such as lung cancer, are controlled almost exclusively by NK cells with little contribution by the adaptive immune system^{19,20} (and unpublished data AS. Krupnick). In order to test OMCP-mutIL2 mediated immunotherapy we will rely on B16 melanoma expressing the model tumor antigen ovalbumin (MO5 tumor cell line)²¹. Multiple studies have demonstrated a role for both NK cells and CD8⁺ CTLs in controlling melanoma growth²²⁻²⁴. Thus the melanoma model offers an experimental advantage in studying OMCP-mutIL2, which can activate both types of cells (**FIG. 1E-F**). Reagents specific to this tumor, such as tetramers for the MHC Class I-restricted CD8⁺ T cell receptor specific for the melanoma tumor associated antigen tyrosinase-related protein 2 peptide SVYDFVWL (SEQ ID NO:3), can be readily purchased commercially (Proimmune, Sarasota, FL). The use of an ovalbumin-expressing cell line also offers the advantage of studying the immune response to a the highly immunogenic peptide SIINFEKL (SEQ ID NO:4) in addition to naturally occurring tumor associated antigens such as tyrosinase-related protein 2 which generally expands T cells with low avidity^{25,26}.

[0180] In order to perform the studies B6 mice will be injected subcutaneously with 1x10⁶ MO5 melanoma cells. One week after tumor injection mice will be divided into 4 groups (10 mice per group) and treated with ten twice a day injections of either: wild type IL2 (group #1); mutIL2 (group #2); OMCP-mutIL2 (group #3) or; saline (group #4) (**FIG. 12**). Tumor growth will be followed by daily measurements of diameter for 4 weeks, or until one of the groups develops

tumors > 2cm in diameter. At that point mice in all groups will be sacrificed for analysis. In addition to tumor growth, lymphocyte infiltration of both the tumor and draining inguinal lymph node will be evaluated by flow cytometry. We will quantitate the total number and activation status of CD4⁺Foxp3⁺ Tregs (evaluated by ICOS and GITR upregulation). We will also evaluate NK cell number and activation as measured by IFN- γ production and CD69 upregulation. Antigen-specific CTL generation will be evaluated by quantitating both CD8⁺ T cells and CD8⁺CD44^{hi}CD62L^{low} effector cells (ECs) that are primarily responsible for tumor clearance^{22,27,28}. Antigen specificity will be determined by identifying CD8⁺ CTLs with T cell receptor specific for either the ovalbumin peptide SIINFEKL (SEQ ID NO:4) or melanoma specific tyrosinase-related protein 2 peptide SVYDFVWL (SEQ ID NO:3) (both tetramers from Proimmune, Sarasota, Fl.). Tumor apoptosis will be quantitated by TUNEL staining.

[0181] Based on our *in vitro* tumor data and *in vivo* phenotypic analysis we suspect that the OMCP-mutIL2 group will demonstrate attenuation in tumor growth with high number of NK cells, antigen-specific CTLs, specifically CD8⁺ ECs, and fewer CD4⁺Foxp3⁺T_{regs}. If this turns out to be the case we would determine the relative role for CD8⁺ or NK CTLs by depletion experiments. Even if CTLs increase it is possible that MO5 growth will not be altered. If that turns out to be the case we would look in closer detail at the CD4⁺Foxp3⁺T_{regs} or in the presence and activation of myeloid-derived suppressor cells in **OMCP-mutIL2** treated mice. Based on melanoma data additional tumors will be tested using similar methods.

Example 13. CD8⁺ memory T cell generation after treatment with OMCP-mutIL2 fusion construct.

[0182] Once activation through their T cell receptor, naive CD8⁺ T cells primarily differentiate into short-lived CD44^{hi}CD62L^{low} effector cells (ECs) with cytolytic potential. A portion of activated cells, however, differentiate to long-lived CD44^{hi}CD62L^{hi} central memory T cells (CD8⁺ CMs)²⁹⁻³¹. CD8⁺ CMs act as an antigen specific reservoir for cellular protection and upon restimulation differentiate into CD8⁺ ECs with cytolytic function. The durability of CD8⁺ CMs makes them an ideal target for *ex vivo* generation and adoptive transfer for long-term protection³¹. The possibility of generating this cell population *in vivo* offers multiple advantages over an *ex vivo* system, including establishing a polyclonal population reactive to multiple tumor associated antigens and avoidance of costs associated with donor pheresis and *ex vivo* expansion. *In vivo* expansion of tumor antigen specific CD8⁺ CMs could also eliminate the need for frequent pheresis and cell readministration.

[0183] High dose IL2 therapy results in activation of both CD4⁺Foxp3⁺T_{regs} and CD8⁺ T cells but its effect on tumor associated antigen specific CD8⁺ CM generation is unknown. Some

have demonstrated, using antibody depletion, that CD4⁺Foxp3⁺T_{regs} interfere with tumor specific CD8⁺ CM generation^{17,32} while others, using different models, have demonstrated that CD4⁺Foxp3⁺T_{reg} depletion impairs CD8⁺ memory formation^{33,34}. OMCP-mutlL2 creates a unique immunologic environment where CD4⁺Foxp3⁺T_{regs} are maintained but not actively expanded (**FIG. 3**). While NKG2D is not expressed on resting CD8⁺ T cells, it is induced on this population upon activation³⁵. Thus, unlike mutlL2, OMCP-mutlL2 results in CD8⁺ T cell proliferation at levels comparable to wild-type IL2 in NKG2D-sufficient mice (**FIG. 1E-F**). The effect of OMCP-mutlL2 on CD8⁺ T cell memory formation, however, is unknown but is critical to decipher based on the long-term tumor specific immunity that this cell population can confer.

[0184] In order to test long-term memory formation after cytokine stimulation *in vivo* we will utilize a model of irradiated tumor cell vaccination and cytokine treatment. In order to accomplish this we will subcutaneously inject 1x10⁷ lethally irradiated (10Gy) MO5 melanoma cells into C57Bl/6 mice. The recipient mice will then be treated either regular IL2 (group #1), mutlL2 (group #2), OMCP-mutlL2 (group #3) or saline (group #4) in twice daily doses over a course of 5 days (**FIG. 13**). The mice will be sacrificed at various time points ranging from one to three months post infection (**FIG. 13**). Antigen-specific CD8⁺ CM formation will be assessed by phenotypic analysis of splenic, peripheral lymph node, lung, and liver-resident CD8⁺CD44^{hi}CD62L^{hi} CMs. Antigen specificity will be determined by MHC Class I staining for either the ovalbumin peptide, SIINFEKL (SEQ ID NO:4), or melanoma specific tyrosinase-related protein 2 peptide SVYDFVWL (SEQ ID NO:3) (both from Proimmune, Sarasota, FL.).

[0185] In order to test the functional protection of such vaccination protocols in a separate set of experiments mice from the four groups described above will not be sacrificed for phenotypic analysis and will be reinjected with live MO5 melanoma (1x10⁶ cells/mouse subcutaneously). Melanoma growth will be assessed by serial measurement of tumor diameter. Contribution of CD8⁺ T cells to any immunologic protection will be assessed by CD8-specific antibody depletion in a portion of mice (clone YTS 169.4, BioXcell Inc., West Lebanon, NH).

Example 14. Mechanism of CTL activation by OMCP-mutlL2 fusion construct.

[0186] A mechanistic understanding of the enhanced activation of effector cell function by the OMCP-mutlL2 chimera will be critical for optimizing this therapeutic agent. The interaction of the fusion protein with IL2R and NKG2D are likely to be dependent on several factors including the length of the linker peptide (**FIG. 1E-F**). Therefore, it is critical to understand the mechanism of OMCP-mutlL2 chimera mediated CTL activation in order to allow for optimization of the construct and design of future immunotherapy protocols. The two-domain chimeric protein could potentially increase the activation of NKG2D-expressing cells by three non-mutually exclusive mechanisms. First and foremost the OMCP-mutlL2 construct could increase the avidity of mutlL2 binding to targeted cells. This could lead to an increase in the

number of receptors occupied and increased signaling intensity compared to mutIL2. Additionally dual binding to both NKG2D and IL2R could decrease the rate of receptor internalization and increase the duration of signaling by IL2. It is also possible that the **OMCP-mutIL2** construct alters the signaling profile by the target cell by activating both the IL2 and NKG2D stimulatory pathways. These three non-mutually exclusive effects could explain the increase in activation of our construct of CTLs in an NKG2D-mediated fashion.

[0187] There are several methods for determining the avidity of a protein for a cell, either directly (radiolabeled, fluorescent) or indirectly (antigen exclusion)^{38,39}. We plan to determine the avidity of wild-type IL2, mutIL2, or OMCP-mutIL2 for CD4⁺Foxp3⁺ T_{regs}, NK cells, and CD8⁺ T lymphocytes using KinExA⁴⁰. To accomplish this we will isolate cells from splenocytes of either wild-type C57Bl/6 or NKG2D^{-/-} mice on a C57Bl/6 background using a magnetic bead isolation kit (Miltenyi Biotech, San Diego, Ca.). Target cells will be serially diluted by a factor of 2 in 11 falcon tubes in media containing 0.05% NaN₃. The 12th tube will contain just the media. OMCP-mutIL2 or mutIL2 alone will then be added to each tube of either wild-type or NKG2D^{-/-} cells and the cells with cytokine will be rotated at 4 °C for 36 h. At the end of 36 h, the cells were centrifuged at 2400 rpm for 4 min and the free construct present in the supernatant will be measured by an anti-IL2 ELISA. The equilibrium dissociation constant (K_d) will then be calculated⁴¹. This approach has the advantage of measuring the avidity of cell surface molecules at physiologic densities and obviates the need for labeling, which can artificially lower the affinity of antibodies for their antigens^{42,43}.

[0188] The two-domain structure of the fusion protein is likely to significantly increase the half-life of the protein on the surface of NKG2D⁺ and IL2R⁺ cells. Any increase in surface half-life likely affects both the internalization of the bound receptors and signaling intensity and duration. To address the internalization of receptors, we will incubate each construct with the above mentioned cell types over a range of times and monitor the change in cell surface expression of IL2Rβγ and NKG2D using flow cytometry as previously described⁴⁴. Of key interest will be the signaling profile of each construct. IL2-IL2R engagement signals through JAK-STAT pathways, while NKG2D signals through DAP10/12 pathways. While monomeric, soluble OMCP does not induce NKG2D signaling, OMCP can signal when concentrated locally on the cell surface⁴⁵. Therefore, it is critical to determine whether the chimera is capable of inducing dual signaling through IL2R and NKG2D. IL2-mediated signaling will be assessed by Western blot for phosphorylated JAK1 and JAK3 in freshly isolated CD4⁺Foxp3⁺ T_{regs}, NK cells or CD8⁺ T cells incubated in vitro with the construct^{46,47}. NKG2D-mediated signaling will be assessed by immunoprecipitation of DAP10 or DAP12 followed by Western blotting for phosphotyrosine as previously described^{48,49}.

[0189] Both IL2 and OMCP interact with their cognate receptors with high affinity; the fusion of the two proteins is anticipated to greatly enhance the avidity of the chimeric construct for cells expressing both IL2R and NKG2D. As a consequence, the tethering of the construct to two cell

surface receptors may lead to reduced internalization and increased duration of signaling. Combined these two phenomena represent the most likely mechanism for increased proliferation of NK cells *in vivo*. The signaling via NKG2D relies upon receptor clustering⁴⁵. Since the construct is soluble it is possible, though unlikely, that the chimera will cluster NKG2D and induce DAP10/12 signaling. However, should DAP10/12 signaling be detected, we will then investigate the importance of this signaling in the expansion of NK cells using cells derived from Vav1 knockout mice. Vav1 is a signal mediator downstream of DAP10⁵⁰. Using a Vav1 knockout has the advantage of leaving NKG2D expression intact, in contrast to DAP knockouts⁵⁰. This will remove the NKG2D signaling component while leaving the NKG2D-dependent targeting intact. A clearer understanding of the mechanism of action for OMCP-IL2 chimera dependent expansion will be crucial for further refinements of the therapeutic agent. Understanding these parameters will allow for testing of different construct designs, primarily in the length of the linker between OMCP and IL2, to calibrate the effects of the chimera.

Example 15. *In vivo* immunotherapy with IL-2, R38A/F42K IL2 or OMCP targeted IL2 constructs.

[0190] In order to determine if our construct plays a role in immunoregulation of malignancies as well as viral infections we will rely on *in vivo* models of B16 melanoma and mouse cytomegalovirus (MCMV). In one set of experiments B6 mice will be injected subcutaneously with 1×10^6 cells of the poorly immunogenic B16 melanoma cell line. One week after tumor injection mice will be divided into 13 groups (5 mice per group) and treated with five daily injections of IL2, R38A/F42K IL2, OMCP fusion constructs or saline as described in **FIG. 18** and **Table 4**. Tumor growth will be followed by daily measurements of diameter for 4 weeks or until one of the groups develops tumors > 2cm in diameter. At that point mice in all groups will be sacrificed for analysis. In addition to tumor growth lymphocyte infiltration of both the tumor and draining inguinal lymph node will be evaluated by flow cytometry. We will quantitate the total number and activation status of CD4⁺Foxp3⁺ Tregs (expressed as % of tumor infiltrating lymphocytes and % ICOS⁺). We will also evaluate NK cell number and activation as measured by IFN- γ production and CD69 upregulation. Tumor apoptosis will be evaluated by TUNEL staining.

Dose Cytokine	LOW DOSE	INTERMEDIATE DOSE	HIGH DOSE
IL2	Group 1	Group 2	Group 3
R38A/F42K IL2	Group 4	Group 5	Group 6
OMCP-wild-type IL2	Group 7	Group 8	Group 9
OMCP-R38A/F42K	Group 10	Group 11	Group 12

Dose Cytokine	LOW DOSE	INTERMEDIATE DOSE	HIGH DOSE
IL2			
Saline	Group 13		

[0191] In order to evaluate the therapeutic potential of IL2 in an infectious disease model, B6 mice will be infected with a sublethal dose of MCMV (5×10^4) particle forming units (PFUs) as previously described²⁹. Day 1 post infection the mice will be divided into 13 groups (5 mice per group) and treated with five daily injections of IL2, R38A/F42K IL2, OMCP fusion constructs or saline as described in FIG. 18 and Table 4. On post-infection day #6 the mice will be sacrificed and splenic and pulmonary viral load determined by standard plaque assay.

[0192] We expect that treatment with pure IL2 will have little effect on tumor growth or viral load as we expect to see preferential activation of T_{regs} over CTLs. We suspect that administration of the mutant R38A/F42K form of IL2 will result a lower tumor and viral burden compared to wild-type IL2 due to less activation of $CD4^+Foxp3^+$ Tregs. Nevertheless it is possible that despite lower levels of T_{reg} activation the tumor burden will be identical between IL2 and R38A/F42K IL2 due to decreased NK activation by the mutant form of IL2 as well. We expect OMCP IL2 construct-treated mice to have lower tumor burden compared to pure cytokine and predict that OMCP-R38A/F42K IL2 will demonstrate the best efficacy for immunotherapy with the most favorable side effect profile.

[0193] If we do not see an effect of OMCP expressing IL2 constructs we will closely evaluate our data for confounding factors such as excessive CTL death due to extreme stimulation as well as possible sequestration of CTLs in systemic organs such as the liver and lungs. If our hypothesis is supported and NK cells are activated and tumor growth ameliorated after OMCP-construct treatment we would repeat these experiments after NK depletion (using anti-NK1.1 clone PK136, mouse anti-mouse depleting antibody) and CD8 depletion (clone YTS169, rat anti-mouse $CD8^+$ T cell-depleting antibody) (both from BioXcell, West Lebanon, NH). Based on these results future work will focus on immunotherapy in primary carcinogenesis models.

Example 16. The effects of IL-2, R38A/F42K IL2 or OMCP targeted IL2 constructs on immunosuppression after radiation exposure.

[0194] Sublethal radiation exposure is a constant risk to those involved in combat duty. In addition to the direct carcinogenic effects of radiation-induced DNA damage, sublethal irradiation results in immunologic damage due to selective death of lymphocyte subsets. $CD8^+$

T cells and CD44^{lo} naïve T cells are specifically sensitive to radiation-induced death while NK cell function significantly declines after irradiation. CD4⁺25⁺ T cells as well as CD44^{hi} memory-like T cells, however, have a survival advantage after radiation. Both CD4⁺25⁺ T cells and CD8⁺CD44^{hi} T cells can downregulate immune responses, explaining why even limited exposure to radiation can result in significant immunosuppression. Pharmacologic interventions to restore the immune system can alleviate morbidity and mortality of radiation poisoning. Surprisingly the role of IL2 in alleviating radiation-induced changes has never been studied. The low affinity IL2 receptor is expressed on bone marrow-resident hematopoietic stem cells and committed NK progenitors. NK cells, in turn, can secrete granulocyte-macrophage colony-stimulating factor (GM-CSF) upon stimulation, a cytokine that can assist with hematopoietic recovery. Based on these data in this aim we plan to test the hypothesis that IL2 or OMCP-IL2 constructs can assist with hematopoietic recovery after sublethal and lethal irradiation.

[0195] Based on previously described models of radiation-induced hematopoietic damage and recovery we will irradiate B6 mice with either sublethal 4.5 or lethal 7.5Gy from a cesium source. Within one hour of exposure mice in both radiation doses will be randomly divided into 13 groups as described in **Table 4** and treated for five days with low, intermediate or high dose IL2, R38A/F42K IL2 or OMCP expressing IL2 constructs (**FIG. 18**). A portion of the mice will be injected with saline after irradiation (group 13) (**Table 4**) and unirradiated untreated B6 mice will be included as a control as well (group 14). On day 6 hematopoietic recovery will be monitored by flow cytometric analysis of peripheral blood obtained by superficial mandibular vein sampling. The sample will be analyzed for total number of NK cells, T cells, B cells, granulocytes, as well as monocytes and macrophages per ml of blood. Since 90% of untreated mice die 15-25 days after exposure to 7.5Gy, mice will be followed daily and survival curves in each treatment group will be compared by Kaplan-Meier analysis. Moribund mice in the 7.5Gy group will be carefully analyzed for cause of death evaluating the bone marrow, spleen and peripheral organs for both infection as well as hematopoietic failure by flow cytometry and tissue culture. Since mice in the sublethal 4.5Gy group are expected to survive long term, they will be sacrificed one month after exposure and peripheral lymphoid organs as well as bone marrow evaluated for hematopoietic recovery by flow cytometric analysis.

[0196] Radiation related DNA damage results in malignant transformation. Hematopoietic malignancies are especially prominent after radiation exposure. In order to evaluate the ability of IL2 or OMCP linked IL2 constructs to facilitate in clearing hematopoietic malignancies after radiation exposure we will treat B6 mice with sublethal exposure to 4.5Gy from a cesium source. Two days after irradiation the mice will be injected with 10³ RMA-S lymphoma cells i.p. and three days later treated for a five day course with low, intermediate or high dose IL2, R38A/F42K IL2 or OMCP expressing IL2 constructs (**Table 4, FIG. 19**). Unirradiated B6 mice will be included as a control (group 14) as well. The mice will be followed for survival.

[0197] We anticipate that wild-type IL2 alone will have a negligible effect on immunorestitution since it will most likely result in preferential expansion of CD4⁺Foxp3⁺ T_{regs}, which are already preserved after irradiation. We suspect, however, that R38A/F42K IL2 as well as OMCP

expressing IL2 constructs will expand the NK fraction in the peripheral blood and will contribute to broad hematopoietic recovery, albeit indirectly through secretion of homeostatic cytokines such as GM-CSF. If we detect no differences in hematopoietic recovery between IL2 and saline-treated groups, we will examine other confounding factors, such as homeostatic proliferation induced alteration of the immune system and the effect of IL2 or OMCP expressing IL2 constructs on such proliferation. While 200,000 IU of IL2 administered daily to B6 mice is not lethal, we realize that in the face of irradiation the mice might be weaker. It is thus possible that dosing might need to be adjusted. For the "functional" part of this experiment we plan to specifically utilize the well-established model of RMA-S lymphoma challenge due to the role of NK cells in controlling hematologic malignancies. This established assay will allow us to gain rapid experimental data to advance this aim. Based on this data we would extend this aim in the future utilizing a primary carcinogenesis model as well.

Example 17. OMCP-targeted delivery of IL15 enhances CD25 upregulation.

[0198] Interleukin 15 (IL15) is a cytokine with structural similarity to IL2. Like IL2, IL15 binds to and signals through a complex composed of IL2/IL15 receptor beta chain (CD122) and the common gamma chain (gamma-C, CD132). IL15 is secreted by mononuclear phagocytes (and some other cells) following infection by viruses. IL15 regulates T and natural killer (NK) cell activation and proliferation. Survival signals that maintain memory T cells in the absence of antigen are provided by IL15. This cytokine is also implicated in NK cell development. IL-15 belongs to the four α -helix bundle family of cytokine.

[0199] OMCP was linked to the cytokine IL15 and its ability to active NK cells compared to IL15 alone was examined. NK cell activation was measured by CD25 upregulation. As demonstrated in **FIG. 21**, higher levels of CD25 are evident when IL15 is delivered by OMCP vs naked cytokine alone in equimolar doses.

Example 18. OMCP-targeted delivery of IL18 enhances NK cell activation.

[0200] OMCP was linked to WT human IL18, WT murine IL18 or mutant human IL18 (which inhibits its interaction with IL18BP) and its ability to active NK cells was examined (**FIG. 32**). Peripheral blood lymphocytes were cultured for 48 hours in 4.4 μ M of either wild-type IL18 (blue), OMCP-IL18 (red) or saline (black). Activation of CD56⁺CD3⁻ natural killer cells, as measured by surface CD69 expression, was superior by OMCP-IL18 compared to wild-type IL18 (**FIG. 33**). This data demonstrates that linking OMCP to IL18 also enhances NK cell activation relative to IL18 without OMCP.

Example 19. The D132R mutation in OMCP significantly decreases its NKG2D binding.

[0201] To further test the necessity of NKG2D binding in targeted delivery of IL2, we tested NK expansion and activation in the presence of mutIL2, OMCP-mutIL2, and (D132R) OMCP-mutIL2. The D132R mutation ameliorated the superiority of natural killer cell activation over cytokine alone (**FIG. 22**). Thus high affinity NKG2D binding is critical for targeted delivery and lymphocyte activation by IL2.

Example 20. OMCP-IL2 effectively treats infection caused by West Nile Virus (WNV).

[0202] The ability of various constructs of the invention to treat infection caused by West Nile Virus (WNV) was evaluated. Mice were given OMCP-IL2, the binding null mutant of OMCP, OMCP(D132R)-IL2, IL2 alone, IL2(38R/42A) alone and PBS. Upon treatment with OMCP(D132R)-IL2 and PBS all mice succumbed to infection by about day 11. Following treatment with IL2 alone, approximately 20% of mice survived until day 21. However, treatment with IL2(38R/42A) and OMCP-IL2 resulted in about 40% of mice surviving beyond 21 days (**FIG. 30A**). These results were consistently repeatable as demonstrated in **FIG. 30B**.

References for Example 11-20.

[0203]

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HEADER  IMMUNE SYSTEM/VIRAL PROTEIN          17-APR-14  4PDC
TITLE   CRYSTAL STRUCTURE OF COWPOX VIRUS CPXV018 (OMCP) BOUND TO HUMAN NKG2D
COMPND  MOL_ID: 1;
COMPND  2 MOLECULE: NKG2-D TYPE II INTEGRAL MEMBRANE PROTEIN;
COMPND  3 CHAIN: A, B, C, D;
COMPND  4 FRAGMENT: UNP RESIDUES 93-215;
COMPND  5 SYNONYM: KILLER CELL LECTIN-LIKE RECEPTOR SUBFAMILY K MEMBER 1,NK
COMPND  6 CELL RECEPTOR D,NKG2-D-ACTIVATING NK RECEPTOR;
COMPND  7 ENGINEERED: YES;
COMPND  8 MOL_ID: 2;
COMPND  9 MOLECULE: CPXV018 PROTEIN;
COMPND  10 CHAIN: E, F;
COMPND  11 FRAGMENT: UNP RESIDUES 20-168;
COMPND  12 ENGINEERED: YES;
COMPND  13 MUTATION: YES
SOURCE  MOL_ID: 1;
SOURCE  2 ORGANISM_SCIENTIFIC: HOMO SAPIENS;
SOURCE  4 ORGANISM_TAXID: 9606;
SOURCE  5 GENE: KLRK1, D12S2489E, NKG2D;
SOURCE  6 EXPRESSION_SYSTEM: ESCHERICHIA COLI;
SOURCE  7 EXPRESSION_SYSTEM_TAXID: 469008;
SOURCE  8 EXPRESSION_SYSTEM_STRAIN: BL21(DE3)RIL;
SOURCE  9 EXPRESSION_SYSTEM_VECTOR_TYPE: PLASMID;
SOURCE  10 EXPRESSION_SYSTEM_PLASMID: PET21A(+);
SOURCE  11 MOL_ID: 2;
SOURCE  12 ORGANISM_SCIENTIFIC: COWPOX VIRUS;
SOURCE  13 ORGANISM_COMMON: CPV;
SOURCE  14 ORGANISM_TAXID: 10243;
SOURCE  15 GENE: CPXV018 CDS;
SOURCE  16 EXPRESSION_SYSTEM: ESCHERICHIA COLI;
SOURCE  17 EXPRESSION_SYSTEM_TAXID: 469008;
SOURCE  18 EXPRESSION_SYSTEM_STRAIN: BL21(DE3)RIL;
SOURCE  19 EXPRESSION_SYSTEM_VECTOR_TYPE: PLASMID;
SOURCE  20 EXPRESSION_SYSTEM_PLASMID: PET21A(+)
KEYWDS  SECRETED VIRAL PROTEIN, IMMUNE EVASION, ORTHOPOXVIRUS, MHC-LIKE FOLD,
KEYWDS  2 NK CELL RECEPTOR LIGAND, STRUCTURAL GENOMICS, CENTER FOR STRUCTURAL

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KEYWDS 3 GENOMICS OF INFECTIOUS DISEASES, CSGID, IMMUNE SYSTEM-VIRAL PROTEIN
 KEYWDS 4 COMPLEX

EXPDTA X-RAY DIFFRACTION
 AUTHOR E.LAZEAR,C.A.NELSON,D.H.FREMONT,CENTER FOR STRUCTURAL GENOMICS OF
 AUTHOR 2 INFECTIOUS DISEASES (CSGID)
 REVDAT 2 30-JUL-14 4PDC 1 JRNL
 REVDAT 1 21-MAY-14 4PDC 0
 JRNL AUTH E.LAZEAR,M.SUN,C.A.NELSON,J.A.CAMPBELL,L.N.CARAYANNOPOULOS,
 JRNL AUTH 2 A.R.FRENCH,D.H.FREMONT,
 JRNL AUTH 3 CENTER FOR STRUCTURAL GENOMICS OF INFECTIOUS DISEASES
 JRNL AUTH 4 (CSGID)
 JRNL TITL COWPOX VIRUS OMCP ANTAGONIZES NKG2D VIA AN UNEXPECTED
 JRNL TITL 2 BINDING ORIENTATION
 JRNL REF TO BE PUBLISHED
 REMARK 2 RESOLUTION: 1.99 ANGSTROMS.
 REMARK 3 REFINEMENT.
 REMARK 3 PROGRAM : PHENIX (PHENIX.REFINE: 1.8.4_1496)
 REMARK 3 AUTHORS : PAUL ADAMS,PAVEL AFONINE,VINCENT CHEN,IAN
 REMARK 3 REFINEMENT TARGET : ML
 REMARK 3 DATA USED IN REFINEMENT.
 REMARK 3 RESOLUTION RANGE HIGH (ANGSTROMS) : 1.99
 REMARK 3 RESOLUTION RANGE LOW (ANGSTROMS) : 45.67
 REMARK 3 MIN(FOBS/SIGMA_FOBS) : 1.380
 REMARK 3 COMPLETENESS FOR RANGE (%) : 92.9
 REMARK 3 NUMBER OF REFLECTIONS : 50042
 REMARK 3 FIT TO DATA USED IN REFINEMENT.
 REMARK 3 R VALUE (WORKING + TEST SET) : 0.168
 REMARK 3 R VALUE (WORKING SET) : 0.166
 REMARK 3 FREE R VALUE : 0.214
 REMARK 3 FREE R VALUE TEST SET SIZE (%) : 3.980
 REMARK 3 FREE R VALUE TEST SET COUNT : 1994
 REMARK 3 FIT TO DATA USED IN REFINEMENT (IN BINS).
 REMARK 3 BIN RESOLUTION RANGE COMPL. NWORK NFREE RWORK RFREE
 REMARK 3 1 45.6774 - 4.7969 1.00 3740 160 0.1646 0.1709
 REMARK 3 2 4.7969 - 3.8080 1.00 3733 155 0.1289 0.1960
 REMARK 3 3 3.8080 - 3.3268 1.00 3673 151 0.1493 0.1701
 REMARK 3 4 3.3268 - 3.0227 0.99 3700 158 0.1688 0.2284
 REMARK 3 5 3.0227 - 2.8061 0.95 3529 151 0.1864 0.2352
 REMARK 3 6 2.8061 - 2.6407 0.91 3353 142 0.1826 0.2189
 REMARK 3 7 2.6407 - 2.5084 0.90 3309 133 0.1790 0.2297
 REMARK 3 8 2.5084 - 2.3993 0.89 3281 134 0.1744 0.2545
 REMARK 3 9 2.3993 - 2.3069 0.89 3285 132 0.1778 0.2825
 REMARK 3 10 2.3069 - 2.2273 0.90 3327 131 0.1764 0.2197
 REMARK 3 11 2.2273 - 2.1577 0.90 3302 127 0.1777 0.2202
 REMARK 3 12 2.1577 - 2.0960 0.91 3328 152 0.1834 0.2460
 REMARK 3 13 2.0960 - 2.0408 0.91 3341 145 0.2098 0.2812
 REMARK 3 14 2.0408 - 1.9910 0.85 3147 123 0.2098 0.2951
 REMARK 3 BULK SOLVENT MODELLING.
 REMARK 3 METHOD USED : FLAT BULK SOLVENT MODEL
 REMARK 3 SOLVENT RADIUS : 1.11
 REMARK 3 SHRINKAGE RADIUS : 0.90
 REMARK 3 K_SOL : NULL
 REMARK 3 B_SOL : NULL
 REMARK 3 ERROR ESTIMATES.
 REMARK 3 COORDINATE ERROR (MAXIMUM-LIKELIHOOD
 BASED) : 0.230
 REMARK 3 PHASE ERROR (DEGREES, MAXIMUM-LIKELIHOOD
 BASED) : 20.990
 REMARK 3 B VALUES.
 REMARK 3 FROM WILSON PLOT (A**2) : 21.62
 REMARK 3 MEAN B VALUE (OVERALL, A**2) : NULL
 REMARK 3 OVERALL ANISOTROPIC B VALUE.
 REMARK 3 B11 (A**2) : NULL
 REMARK 3 B22 (A**2) : NULL
 REMARK 3 B33 (A**2) : NULL
 REMARK 3 B12 (A**2) : NULL
 REMARK 3 B13 (A**2) : NULL
 REMARK 3 B23 (A**2) : NULL
 REMARK 3 TWINNING INFORMATION.
 REMARK 3 FRACTION: NULL
 REMARK 3 OPERATOR: NULL
 REMARK 3 DEVIATIONS FROM IDEAL VALUES.
 REMARK 3 RMSD COUNT
 REMARK 3 BOND : 0.003 6687
 REMARK 3 ANGLE : 0.786 9030
 REMARK 3 CHIRALITY : 0.031 933
 REMARK 3 PLANARITY : 0.003 1150
 REMARK 3 DIHEDRAL : 13.423 2426
 REMARK 3 TLS DETAILS
 REMARK 3 NUMBER OF TLS GROUPS : NULL
 REMARK 3 NCS DETAILS
 REMARK 3 NUMBER OF NCS GROUPS : NULL
 REMARK 3 OTHER REFINEMENT REMARKS: NULL

REMARK 4 4PDC COMPLIES WITH FORMAT V. 3.30, 13-JUL-11
REMARK 100 THIS ENTRY HAS BEEN PROCESSED BY RCSB ON 21-APR-14.
REMARK 100 THE DEPOSITION ID IS D_1000201141.
REMARK 200 EXPERIMENTAL DETAILS
REMARK 200 EXPERIMENT TYPE : X-RAY DIFFRACTION
REMARK 200 DATE OF DATA COLLECTION : 19-OCT-10
REMARK 200 TEMPERATURE (KELVIN): 100
REMARK 200 PH : 6.75
REMARK 200 NUMBER OF CRYSTALS USED : 1
REMARK 200 SYNCHROTRON (Y/N): Y
REMARK 200 RADIATION SOURCE : ALS
REMARK 200 BEAMLINE : 4.2.2
REMARK 200 X-RAY GENERATOR MODEL : NULL
REMARK 200 MONOCHROMATIC OR LAUE (M/L): M
REMARK 200 WAVELENGTH OR RANGE (A): 1.00004
REMARK 200 MONOCHROMATOR : NULL
REMARK 200 OPTICS : NULL
REMARK 200 DETECTOR TYPE : CCD
REMARK 200 DETECTOR MANUFACTURER : NOIR-1
REMARK 200 INTENSITY-INTEGRATION SOFTWARE : HKL
REMARK 200 DATA SCALING SOFTWARE : HKL
REMARK 200 NUMBER OF UNIQUE REFLECTIONS : 50139
REMARK 200 RESOLUTION RANGE HIGH (A): 1.991
REMARK 200 RESOLUTION RANGE LOW (A): 50.000
REMARK 200 REJECTION CRITERIA (SIGMA(I)): NULL
REMARK 200 OVERALL
REMARK 200 COMPLETENESS FOR RANGE (%): 93.5
REMARK 200 DATA REDUNDANCY : 6.200
REMARK 200 R MERGE (I): 0.11800
REMARK 200 R SYM (I): NULL
REMARK 200 </SIGMA(I)> FOR THE DATA SET : 12.7000
REMARK 200 IN THE HIGHEST RESOLUTION SHELL.
REMARK 200 HIGHEST RESOLUTION SHELL, RANGE HIGH (A): 2.00
REMARK 200 HIGHEST RESOLUTION SHELL, RANGE LOW (A): 2.07
REMARK 200 COMPLETENESS FOR SHELL (%): 91.5
REMARK 200 DATA REDUNDANCY IN SHELL : 5.30
REMARK 200 R MERGE FOR SHELL (I): 0.48500
REMARK 200 R SYM FOR SHELL (I): NULL
REMARK 200 </SIGMA(I)> FOR SHELL : NULL
REMARK 200 DIFFRACTION PROTOCOL: SINGLE WAVELENGTH
REMARK 200 METHOD USED TO DETERMINE THE STRUCTURE: MOLECULAR
REPLACEMENT
REMARK 200 SOFTWARE USED: PHASER
REMARK 200 STARTING MODEL: 1MPU, 4FFE
REMARK 200 REMARK: NULL
REMARK 280 CRYSTAL
REMARK 280 SOLVENT CONTENT, VS (%): 42.94
REMARK 280 MATTHEWS COEFFICIENT, VM (ANGSTROMS**3/DA): 2.16
REMARK 280 CRYSTALLIZATION CONDITIONS: 15% PEG 3350, 0.2M MGCL2, 0.1M BIS
REMARK 280 -TRIS
REMARK 290 CRYSTALLOGRAPHIC SYMMETRY
REMARK 290 SYMMETRY OPERATORS FOR SPACE GROUP: P 1 21 1
REMARK 290 SYMOP SYMMETRY
REMARK 290 NNNMMM OPERATOR
REMARK 290 1555 X,Y,Z
REMARK 290 2555 -X,Y+1/2,-Z
REMARK 290 WHERE NNN -> OPERATOR NUMBER
REMARK 290 MMM -> TRANSLATION VECTOR
REMARK 290 CRYSTALLOGRAPHIC SYMMETRY TRANSFORMATIONS

REMARK 290 THE FOLLOWING TRANSFORMATIONS OPERATE ON THE ATOM/HETATM
REMARK 290 RECORDS IN THIS ENTRY TO PRODUCE CRYSTALLOGRAPHICALLY
REMARK 290 RELATED MOLECULES.
REMARK 290 SMTRY1 1 1.000000 0.000000 0.000000 0.000000
REMARK 290 SMTRY2 1 0.000000 1.000000 0.000000 0.000000
REMARK 290 SMTRY3 1 0.000000 0.000000 1.000000 0.000000
REMARK 290 SMTRY1 2 -1.000000 0.000000 0.000000 0.000000
REMARK 290 SMTRY2 2 0.000000 1.000000 0.000000 50.55500
REMARK 290 SMTRY3 2 0.000000 0.000000 -1.000000 0.000000
REMARK 290 REMARK: NULL
REMARK 300 BIOMOLECULE: 1, 2
REMARK 300 SEE REMARK 350 FOR THE AUTHOR PROVIDED AND/OR PROGRAM
GENERATED ASSEMBLY INFORMATION FOR THE STRUCTURE IN
REMARK 300 THIS ENTRY. THE REMARK MAY ALSO PROVIDE INFORMATION ON
REMARK 300 BURIED SURFACE AREA.
REMARK 300 REMARK: THE BIOLOGICAL UNIT OF HNKG2D IS A DIMER (CHAINS A & B AND
REMARK 300 CHAINS C & D
REMARK 350 COORDINATES FOR A COMPLETE MULTIMER REPRESENTING THE KNOWN
REMARK 350 BIOLOGICALLY SIGNIFICANT OLIGOMERIZATION STATE OF THE
REMARK 350 MOLECULE CAN BE GENERATED BY APPLYING BIOMT TRANSFORMATIONS
REMARK 350 GIVEN BELOW. BOTH NON-CRYSTALLOGRAPHIC AND
REMARK 350 CRYSTALLOGRAPHIC OPERATIONS ARE GIVEN.
REMARK 350 BIOMOLECULE: 1
REMARK 350 AUTHOR DETERMINED BIOLOGICAL UNIT: TRIMERIC
REMARK 350 APPLY THE FOLLOWING TO CHAINS: A, B, E
REMARK 350 BIOMT1 1 1.000000 0.000000 0.000000 0.000000
REMARK 350 BIOMT2 1 0.000000 1.000000 0.000000 0.000000

REMARK 350 BIOMT3 1 0.000000 0.000000 1.000000 0.000000
REMARK 350 BIOMOLECULE: 2
REMARK 350 AUTHOR DETERMINED BIOLOGICAL UNIT: TRIMERIC
REMARK 350 APPLY THE FOLLOWING TO CHAINS: C, D, F
REMARK 350 BIOMT1 1 1.000000 0.000000 0.000000 0.000000
REMARK 350 BIOMT2 1 0.000000 1.000000 0.000000 0.000000
REMARK 350 BIOMT3 1 0.000000 0.000000 1.000000 0.000000
REMARK 465 MISSING RESIDUES
REMARK 465 THE FOLLOWING RESIDUES WERE NOT LOCATED IN THE
REMARK 465 EXPERIMENT. (M=MODEL NUMBER; RES=RESIDUE NAME; C=CHAIN
REMARK 465 IDENTIFIER; SSSEQ=SEQUENCE NUMBER; I=INSERTION CODE.)
REMARK 465 M RES C SSSEQI
REMARK 465 GLU B 93
REMARK 500 GEOMETRY AND STEREOCHEMISTRY
REMARK 500 SUBTOPIC: CLOSE CONTACTS IN SAME ASYMMETRIC UNIT
REMARK 500 THE FOLLOWING ATOMS ARE IN CLOSE CONTACT.
REMARK 500 ATM1 RES C SSSEQI ATM2 RES C SSSEQI DISTANCE
REMARK 500 O HOH F 293 O HOH F 324 2.19
REMARK 500 REMARK: NULL
REMARK 500 GEOMETRY AND STEREOCHEMISTRY
REMARK 500 SUBTOPIC: CLOSE CONTACTS
REMARK 500 THE FOLLOWING ATOMS THAT ARE RELATED BY CRYSTALLOGRAPHIC
REMARK 500 SYMMETRY ARE IN CLOSE CONTACT. AN ATOM LOCATED WITHIN 0.15
REMARK 500 ANGSTROMS OF A SYMMETRY RELATED ATOM IS ASSUMED TO BE ON A
REMARK 500 SPECIAL POSITION AND IS, THEREFORE, LISTED IN REMARK 375
REMARK 500 INSTEAD OF REMARK 500. ATOMS WITH NON-BLANK ALTERNATE
REMARK 500 LOCATION INDICATORS ARE NOT INCLUDED IN THE CALCULATIONS.
REMARK 500 DISTANCE CUTOFF:
REMARK 500 2.2 ANGSTROMS FOR CONTACTS NOT INVOLVING HYDROGEN ATOMS
REMARK 500 1.6 ANGSTROMS FOR CONTACTS INVOLVING HYDROGEN ATOMS
REMARK 500 ATM1 RES C SSSEQI ATM2 RES C SSSEQI SSYMOP DISTANCE
REMARK 500 O HOH C 301 O HOH D 306 1655 2.15
REMARK 500 O HOH C 318 O HOH D 306 1655 2.19
REMARK 500 REMARK: NULL
REMARK 500 GEOMETRY AND STEREOCHEMISTRY
REMARK 500 SUBTOPIC: TORSION ANGLES
REMARK 500 TORSION ANGLES OUTSIDE THE EXPECTED RAMACHANDRAN REGIONS:
REMARK 500 (M=MODEL NUMBER; RES=RESIDUE NAME; C=CHAIN IDENTIFIER;
REMARK 500 SSSEQ=SEQUENCE NUMBER; I=INSERTION CODE).
REMARK 500 STANDARD TABLE:
REMARK 500 FORMAT:(10X,I3,1X,A3,1X,A1,I4,A1,4X,F7.2,3X,F7.2)
REMARK 500 EXPECTED VALUES: GJ KLEYWEGT AND TA JONES (1996). PHI/PSI-
REMARK 500 CHOLOGY: RAMACHANDRAN REVISITED. STRUCTURE 4, 1395 - 1400

REMARK 500 M RES CSSEQI	PSI	PHI
REMARK 500 SER A 151	-170.24	71.72
REMARK 500 THR A 162	-74.87	-58.64
REMARK 500 MET A 184	-75.63	-143.50
REMARK 500 TYR B 106	114.87	-162.70
REMARK 500 SER B 151	-171.27	67.58
REMARK 500 THR B 162	-35.85	164.34
REMARK 500 MET B 184	-59.05	-140.78
REMARK 500 SER C 151	-172.20	65.21
REMARK 500 MET C 184	-64.72	-143.36
REMARK 500 SER D 151	-170.57	74.89
REMARK 500 MET D 184	-66.96	-138.40
REMARK 500 ASN E 88	16.97	57.97
REMARK 500 THR E 104	-12.21	-141.68
REMARK 500 LYS F 35	-52.70	-131.11
REMARK 500 THR F 104	-6.09	-145.54

REMARK 500 REMARK: NULL
REMARK 525 SOLVENT
REMARK 525 THE SOLVENT MOLECULES HAVE CHAIN IDENTIFIERS THAT
REMARK 525 INDICATE THE POLYMER CHAIN WITH WHICH THEY ARE MOST
REMARK 525 CLOSELY ASSOCIATED. THE REMARK LISTS ALL THE SOLVENT
REMARK 525 MOLECULES WHICH ARE MORE THAN 5A AWAY FROM THE
REMARK 525 NEAREST POLYMER CHAIN (M = MODEL NUMBER;
REMARK 525 RES=RESIDUE NAME; C=CHAIN IDENTIFIER; SSSEQ=SEQUENCE
REMARK 525 NUMBER; I=INSERTION CODE):
REMARK 525 M RES CSSEQI
REMARK 525 HOH A 385 DISTANCE = 6.57 ANGSTROMS
REMARK 525 HOH A 387 DISTANCE = 6.32 ANGSTROMS
REMARK 525 HOH F 337 DISTANCE = 5.90 ANGSTROMS
REMARK 900 RELATED ENTRIES
REMARK 900 RELATED ID: 4FFE RELATED DB: PDB
REMARK 900 4FFE IS THE STRUCTURE OF FREE COWPOX VIRUS CPXV018 (OMCP)
REMARK 900 RELATED ID: 1MPU RELATED DB: PDB
REMARK 900 1MPU IS THE STRUCTURE OF FREE HUMAN NKG2D
IMMUNORECEPTOR.
REMARK 900 RELATED ID: 1HYR RELATED DB: PDB
REMARK 900 HUMAN NKG2D IN COMPLEX WITH MIC-A
REMARK 900 RELATED ID: 1JSK RELATED DB: PDB
REMARK 900 MOUSE NKG2D IN COMPLEX WITH RAE-1BETA
REMARK 900 RELATED ID: 1KCG RELATED DB: PDB
REMARK 900 HUMAN NKG2D IN COMPLEX WITH ULBP3
REMARK 900 RELATED ID: CSGID-IDP00259 RELATED DB: TARGETTRACK
DRRFF 4PDC A 93 215 IINP P26718 NKG2D HUMAN 93 215

DBREF 4PDC B 93 215 UNP P26718 NKG2D_HUMAN 93 215
 DBREF 4PDC C 93 215 UNP P26718 NKG2D_HUMAN 93 215
 DBREF 4PDC D 93 215 UNP P26718 NKG2D_HUMAN 93 215
 DBREF 4PDC E 1 149 UNP Q8QN43 Q8QN43_COWPX 20 168
 DBREF 4PDC F 1 149 UNP Q8QN43 Q8QN43_COWPX 20 168
 SEQADV 4PDC GLY E 0 UNP Q8QN43 EXPRESSION TAG
 SEQADV 4PDC ASP E 23 UNP Q8QN43 TYR 42 ENGINEERED MUTATION
 SEQADV 4PDC ASP E 95 UNP Q8QN43 PHE 114 ENGINEERED MUTATION
 SEQADV 4PDC GLY F 0 UNP Q8QN43 EXPRESSION TAG
 SEQADV 4PDC ASP F 23 UNP Q8QN43 TYR 42 ENGINEERED MUTATION
 SEQADV 4PDC ASP F 95 UNP Q8QN43 PHE 114 ENGINEERED MUTATION
 SEQRES 1 A 123 GLU SER TYR CYS GLY PRO CYS PRO LYS ASN TRP ILE CYS
 SEQRES 2 A 123 TYR LYS ASN ASN CYS TYR GLN PHE PHE ASP GLU SER LYS
 SEQRES 3 A 123 ASN TRP TYR GLU SER GLN ALA SER CYS MET SER GLN ASN
 SEQRES 4 A 123 ALA SER LEU LEU LYS VAL TYR SER LYS GLU ASP GLN ASP
 SEQRES 5 A 123 LEU LEU LYS LEU VAL LYS SER TYR HIS TRP MET GLY LEU
 SEQRES 6 A 123 VAL HIS ILE PRO THR ASN GLY SER TRP GLN TRP GLU ASP
 SEQRES 7 A 123 GLY SER ILE LEU SER PRO ASN LEU LEU THR ILE ILE GLU
 SEQRES 8 A 123 MET GLN LYS GLY ASP CYS ALA LEU TYR ALA SER SER PHE
 SEQRES 9 A 123 LYS GLY TYR ILE GLU ASN CYS SER THR PRO ASN THR TYR
 SEQRES 10 A 123 ILE CYS MET GLN ARG THR
 SEQRES 1 B 123 GLU SER TYR CYS GLY PRO CYS PRO LYS ASN TRP ILE CYS
 SEQRES 2 B 123 TYR LYS ASN ASN CYS TYR GLN PHE PHE ASP GLU SER LYS
 SEQRES 3 B 123 ASN TRP TYR GLU SER GLN ALA SER CYS MET SER GLN ASN
 SEQRES 4 B 123 ALA SER LEU LEU LYS VAL TYR SER LYS GLU ASP GLN ASP
 SEQRES 5 B 123 LEU LEU LYS LEU VAL LYS SER TYR HIS TRP MET GLY LEU
 SEQRES 6 B 123 VAL HIS ILE PRO THR ASN GLY SER TRP GLN TRP GLU ASP

SEQRES 7 B 123 GLY SER ILE LEU SER PRO ASN LEU LEU THR ILE ILE GLU
 SEQRES 8 B 123 MET GLN LYS GLY ASP CYS ALA LEU TYR ALA SER SER PHE
 SEQRES 9 B 123 LYS GLY TYR ILE GLU ASN CYS SER THR PRO ASN THR TYR
 SEQRES 10 B 123 ILE CYS MET GLN ARG THR
 SEQRES 1 C 123 GLU SER TYR CYS GLY PRO CYS PRO LYS ASN TRP ILE CYS
 SEQRES 2 C 123 TYR LYS ASN ASN CYS TYR GLN PHE PHE ASP GLU SER LYS
 SEQRES 3 C 123 ASN TRP TYR GLU SER GLN ALA SER CYS MET SER GLN ASN
 SEQRES 4 C 123 ALA SER LEU LEU LYS VAL TYR SER LYS GLU ASP GLN ASP
 SEQRES 5 C 123 LEU LEU LYS LEU VAL LYS SER TYR HIS TRP MET GLY LEU
 SEQRES 6 C 123 VAL HIS ILE PRO THR ASN GLY SER TRP GLN TRP GLU ASP
 SEQRES 7 C 123 GLY SER ILE LEU SER PRO ASN LEU LEU THR ILE ILE GLU
 SEQRES 8 C 123 MET GLN LYS GLY ASP CYS ALA LEU TYR ALA SER SER PHE
 SEQRES 9 C 123 LYS GLY TYR ILE GLU ASN CYS SER THR PRO ASN THR TYR
 SEQRES 10 C 123 ILE CYS MET GLN ARG THR
 SEQRES 1 D 123 GLU SER TYR CYS GLY PRO CYS PRO LYS ASN TRP ILE CYS
 SEQRES 2 D 123 TYR LYS ASN ASN CYS TYR GLN PHE PHE ASP GLU SER LYS
 SEQRES 3 D 123 ASN TRP TYR GLU SER GLN ALA SER CYS MET SER GLN ASN
 SEQRES 4 D 123 ALA SER LEU LEU LYS VAL TYR SER LYS GLU ASP GLN ASP
 SEQRES 5 D 123 LEU LEU LYS LEU VAL LYS SER TYR HIS TRP MET GLY LEU
 SEQRES 6 D 123 VAL HIS ILE PRO THR ASN GLY SER TRP GLN TRP GLU ASP
 SEQRES 7 D 123 GLY SER ILE LEU SER PRO ASN LEU LEU THR ILE ILE GLU
 SEQRES 8 D 123 MET GLN LYS GLY ASP CYS ALA LEU TYR ALA SER SER PHE
 SEQRES 9 D 123 LYS GLY TYR ILE GLU ASN CYS SER THR PRO ASN THR TYR
 SEQRES 10 D 123 ILE CYS MET GLN ARG THR
 SEQRES 1 E 150 GLY HIS LYS LEU ALA PHE ASN PHE ASN LEU GLU ILE ASN
 SEQRES 2 E 150 GLY SER ASP THR HIS SER THR VAL ASP VAL ASP LEU ASP
 SEQRES 3 E 150 ASP SER GLN ILE ILE THR PHE ASP GLY LYS ASP ILE ARG
 SEQRES 4 E 150 PRO THR ILE PRO PHE MET ILE GLY ASP GLU ILE PHE LEU
 SEQRES 5 E 150 PRO PHE TYR LYS ASN VAL PHE SER GLU PHE PHE SER LEU
 SEQRES 6 E 150 PHE ARG ARG VAL PRO THR SER THR PRO TYR GLU ASP LEU
 SEQRES 7 E 150 THR TYR PHE TYR GLU CYS ASP TYR THR ASP ASN LYS SER
 SEQRES 8 E 150 THR PHE ASP GLN ASP TYR LEU TYR ASN GLY GLU GLU TYR
 SEQRES 9 E 150 THR VAL LYS THR GLN GLU ALA THR ASN LYS ASN MET TRP
 SEQRES 10 E 150 LEU THR THR SER GLU PHE ARG LEU LYS LYS TRP PHE ASP
 SEQRES 11 E 150 GLY GLU ASP CYS ILE MET HIS LEU ARG SER LEU VAL ARG
 SEQRES 12 E 150 LYS MET GLU ASP SER LYS ARG
 SEQRES 1 F 150 GLY HIS LYS LEU ALA PHE ASN PHE ASN LEU GLU ILE ASN
 SEQRES 2 F 150 GLY SER ASP THR HIS SER THR VAL ASP VAL ASP LEU ASP
 SEQRES 3 F 150 ASP SER GLN ILE ILE THR PHE ASP GLY LYS ASP ILE ARG
 SEQRES 4 F 150 PRO THR ILE PRO PHE MET ILE GLY ASP GLU ILE PHE LEU
 SEQRES 5 F 150 PRO PHE TYR LYS ASN VAL PHE SER GLU PHE PHE SER LEU
 SEQRES 6 F 150 PHE ARG ARG VAL PRO THR SER THR PRO TYR GLU ASP LEU
 SEQRES 7 F 150 THR TYR PHE TYR GLU CYS ASP TYR THR ASP ASN LYS SER
 SEQRES 8 F 150 THR PHE ASP GLN ASP TYR LEU TYR ASN GLY GLU GLU TYR
 SEQRES 9 F 150 THR VAL LYS THR GLN GLU ALA THR ASN LYS ASN MET TRP
 SEQRES 10 F 150 LEU THR THR SER GLU PHE ARG LEU LYS LYS TRP PHE ASP
 SEQRES 11 F 150 GLY GLU ASP CYS ILE MET HIS LEU ARG SER LEU VAL ARG
 SEQRES 12 F 150 LYS MET GLU ASP SER LYS ARG

FORMUL 7 HOH *680(H2O)

HELIX 1 AA1 ASN A 119 SER A 129 1	11	HELIX 9 AA9 ILE E 41 ILE E 45 5	5
HELIX 2 AA2 GLN A 143 VAL A 149 5	7	HELIX 10 AB1 ILE E 49 LEU E 64 1	16
HELIX 3 AA3 ASN B 119 SER B 129 1	11	HELIX 11 AB2 THR E 111 LYS E 126 1	16
HELIX 4 AA4 GLN B 143 VAL B 149 5	7	HELIX 12 AB3 ASP E 129 ASP E 146 1	18
HELIX 5 AA5 ASN C 119 SER C 129 1	11	HELIX 13 AB4 ILE F 41 ILE F 45 5	5
HELIX 6 AA6 GLN C 143 VAL C 149 5	7	HELIX 14 AB5 ILE F 49 LEU F 64 1	16
HELIX 7 AA7 ASN D 119 GLN D 130 1	12	HELIX 15 AB6 THR F 111 LYS F 125 1	15
HELIX 8 AA8 GLN D 143 VAL D 149 5	7	HELIX 16 AB7 ASP F 129 ASP F 146 1	18
SHEET 1 AA1 2 SER A 94 CYS A 96 0		SHEET 5 AA8 8 ILE D 104 TYR D 106 -1 O CYS D 105 N CYS C 105	
SHEET 2 AA1 2 CYS B 96 CYS B 99 -1 O CYS B 99 N SER A 94		SHEET 6 AA8 8 ASN D 109 LYS D 118 -1 O TYR D 111 N ILE D 104	
SHEET 1 AA2 4 ILE A 104 TYR A 106 0		SHEET 7 AA8 8 ASN D 207 GLN D 213 -1 O ASN D 207 N LYS D 118	
SHEET 2 AA2 4 ASN A 109 LYS A 118 -1 O TYR A 111 N ILE A 104		SHEET 8 AA8 8 SER D 133 LEU D 134 -1 N SER D 133 O MET D 212	
SHEET 3 AA2 4 ASN A 207 GLN A 213 -1 O GLN A 213 N CYS A 118			

110
SHEET 4 AA2 4 SER A 133 LEU A 134-1 N SER A 133 O MET A
212

SHEET 1 AA3 4 HIS A 153 TRP A 154 O
SHEET 2 AA3 4 CYS A 189 ALA A 193-1 O TYR A 192 N HIS A
153
SHEET 3 AA3 4 LYS A 197 GLU A 201-1 O GLU A 201 N CYS A
189
SHEET 4 AA3 4 THR A 180 ILE A 182 1 N ILE A 182 O GLY A 198

SHEET 1 AA4 2 LEU A 157 HIS A 159 O
SHEET 2 AA4 2 TRP A 166 TRP A 168-1 O GLN A 167 N VAL A
158

SHEET 1 AA5 5 ILE B 104 TYR B 106 O
SHEET 2 AA5 5 ASN B 109 LYS B 118-1 O TYR B 111 N ILE B
104
SHEET 3 AA5 5 ASN B 207 ARG B 214-1 O ASN B 207 N LYS B
118
SHEET 4 AA5 5 HIS B 153 HIS B 159 1 N TRP B 154 O THR B
208
SHEET 5 AA5 5 TRP B 166 TRP B 168-1 O GLN B 167 N VAL B
158

SHEET 1 AA6 6 SER B 133 LEU B 134 O
SHEET 2 AA6 6 ASN B 207 ARG B 214-1 O MET B 212 N SER B
133
SHEET 3 AA6 6 HIS B 153 HIS B 159 1 N TRP B 154 O THR B
208
SHEET 4 AA6 6 CYS B 189 ALA B 193-1 O TYR B 192 N HIS B
153
SHEET 5 AA6 6 LYS B 197 GLU B 201-1 O LYS B 197 N ALA B
193

SHEET 6 AA6 6 THR B 180 ILE B 182 1 N ILE B 182 O GLY B 198
SHEET 1 AA7 2 CYS C 96 CYS C 99 O
SHEET 2 AA7 2 SER D 94 CYS D 96-1 O SER D 94 N CYS C
99
SHEET 1 AA8 8 SER C 133 LEU C 134 O
SHEET 2 AA8 8 ASN C 207 ARG C 214-1 O MET C 212 N SER C
133
SHEET 3 AA8 8 ASN C 109 LYS C 118-1 N CYS C 110 O GLN C
213
SHEET 4 AA8 8 ILE C 104 TYR C 106-1 N ILE C 104 O TYR C
111

SSBOND 1 CYS A 96 CYS A 105 1555 1555 2.05
SSBOND 2 CYS A 99 CYS A 110 1555 1555 2.03
SSBOND 3 CYS A 127 CYS A 211 1555 1555 2.04
SSBOND 4 CYS A 189 CYS A 203 1555 1555 2.03
SSBOND 5 CYS B 96 CYS B 105 1555 1555 2.03
SSBOND 6 CYS B 99 CYS B 110 1555 1555 2.03
SSBOND 7 CYS B 127 CYS B 211 1555 1555 2.04
SSBOND 8 CYS B 189 CYS B 203 1555 1555 2.04
SSBOND 9 CYS C 96 CYS C 105 1555 1555 2.03
SSBOND 10 CYS C 99 CYS C 110 1555 1555 2.03

CISPEP 1 GLY A 97 PRO A 98 0 1.20
CISPEP 2 SER A 194 SER A 195 0 -3.36
CISPEP 3 GLY B 97 PRO B 98 0 1.05
CISPEP 4 SER B 194 SER B 195 0 -1.59

CRYST1 43.315 101.110 91.368 90.00 91.63 90.00 P 1 21 1 8
ORIGX1 1.000000 0.000000 0.000000 0.000000
ORIGX2 0.000000 1.000000 0.000000 0.000000
ORIGX3 0.000000 0.000000 1.000000 0.000000
SCALE1 0.023087 0.000000 0.000659 0.000000
SCALE2 0.000000 0.009890 0.000000 0.000000
SCALE3 0.000000 0.000000 0.010949 0.000000

ATOM 1 N GLU A 93 -14.924 7.066 -22.137 1.00 59.38 N
ATOM 2 CA GLU A 93 -14.415 6.924 -23.496 1.00 58.81 C
ATOM 3 C GLU A 93 -15.440 6.231 -24.389 1.00 56.95 C
ATOM 4 O GLU A 93 -16.124 5.303 -23.956 1.00 61.11 O
ATOM 5 CB GLU A 93 -13.098 6.143 -23.497 1.00 60.00 C
ATOM 6 CG GLU A 93 -13.220 4.711 -22.966 1.00 72.71 C
ATOM 7 CD GLU A 93 -11.880 3.998 -22.928 1.00 80.57 C

ATOM 8 OE1 GLU A 93 -10.846 4.640 -23.211 1.00 79.10 O
ATOM 9 OE2 GLU A 93 -11.862 2.794 -22.593 1.00 85.72 O1
ATOM 10 HA GLU A 93 -14.242 7.805 -23.864 1.00 70.57 H
ATOM 11 HB2 GLU A 93 -12.756 6.110 -24.404 1.00 72.00 H
ATOM 12 HB3 GLU A 93 -12.464 6.603 -22.925 1.00 72.00 H
ATOM 13 HG2 GLU A 93 -13.801 4.719 -22.104 1.00 87.25 H
ATOM 14 HG3 GLU A 93 -13.794 4.213 -23.598 1.00 87.25 H
ATOM 15 N SER A 94 -15.537 6.687 -25.634 1.00 47.51 N
ATOM 16 CA SER A 94 -16.522 6.163 -26.571 1.00 43.60 C
ATOM 17 C SER A 94 -15.911 5.889 -27.937 1.00 40.17 C
ATOM 18 O SER A 94 -14.793 6.312 -28.231 1.00 42.40 O
ATOM 19 CB SER A 94 -17.684 7.143 -26.716 1.00 50.65 C
ATOM 20 OG SER A 94 -17.227 8.391 -27.207 1.00 53.61 O
ATOM 21 H SER A 94 -15.038 7.306 -25.963 1.00 57.02 H
ATOM 22 HA SER A 94 -16.874 5.320 -26.226 1.00 52.32 H
ATOM 23 HB2 SER A 94 -18.332 6.777 -27.339 1.00 60.78 H
ATOM 24 HB3 SER A 94 -18.096 7.276 -25.848 1.00 60.78 H
ATOM 25 HG SER A 94 -17.873 8.923 -27.284 1.00 64.33 H
ATOM 26 N TYR A 95 -16.862 5.174 -28.766 1.00 37.41 N
ATOM 27 CA TYR A 95 -16.245 4.875 -30.126 1.00 36.16 C
ATOM 28 C TYR A 95 -16.815 5.907 -31.089 1.00 32.15 C
ATOM 29 O TYR A 95 -17.812 6.566 -30.789 1.00 28.55 O
ATOM 30 CB TYR A 95 -16.696 3.473 -30.528 1.00 35.46 C
ATOM 31 CG TYR A 95 -15.877 2.361 -29.913 1.00 39.96 C
ATOM 32 CD TYR A 95 -16.224 4.767 -28.604 1.00 38.04 C

SHEET 1 AA9 5 SER C 166 TRP C 168 O
SHEET 2 AA9 5 HIS C 153 ILE C 160-1 N VAL C 158 O GLN C
167

SHEET 3 AA9 5 CYS C 189 ALA C 193-1 O TYR C 192 N HIS C
153
SHEET 4 AA9 5 LYS C 197 GLU C 201-1 O GLU C 201 N CYS C
189
SHEET 5 AA9 5 THR C 180 ILE C 182 1 N ILE C 182 O GLY C
198

SHEET 1 AB1 5 TRP D 166 TRP D 168 O
SHEET 2 AB1 5 HIS D 153 HIS D 159-1 N VAL D 158 O GLN D
167
SHEET 3 AB1 5 CYS D 189 ALA D 193-1 O TYR D 192 N HIS D
153
SHEET 4 AB1 5 LYS D 197 GLU D 201-1 O GLU D 201 N CYS D
189
SHEET 5 AB1 5 THR D 180 ILE D 182 1 N ILE D 182 O GLY D
198

SHEET 1 AB2 7 ILE E 37 PRO E 39 O
SHEET 2 AB2 7 GLN E 28 PHE E 32-1 N THR E 31 O ARG E
38

SHEET 3 AB2 7 ASP E 15 LEU E 24-1 N VAL E 22 O ILE E 29
SHEET 4 AB2 7 HIS E 1 ASN E 12-1 N ALA E 4 O ASP E 23

SHEET 5 AB2 7 TYR E 74 THR E 86-1 O GLU E 75 N ILE E 11
SHEET 6 AB2 7 LYS E 89 TYR E 98-1 O ASP E 93 N GLU E
82
SHEET 7 AB2 7 GLU E 101 TYR E 103-1 O GLU E 101 N TYR E
98

SHEET 1 AB3 7 ILE F 37 PRO F 39 O
SHEET 2 AB3 7 SER F 27 PHE F 32-1 N THR F 31 O ARG F
38
SHEET 3 AB3 7 ASP F 15 LEU F 24-1 N LEU F 24 O SER F 27

SHEET 4 AB3 7 HIS F 1 ASN F 12-1 N ASN F 12 O ASP F 15
SHEET 5 AB3 7 GLU F 75 THR F 86-1 O TYR F 81 N PHE F 5

SHEET 6 AB3 7 LYS F 89 TYR F 98-1 O THR F 91 N ASP F 84
SHEET 7 AB3 7 GLU F 101 TYR F 103-1 O GLU F 101 N TYR F
98

SSBOND 11 CYS C 127 CYS C 211 1555 1555 2.03
SSBOND 12 CYS C 189 CYS C 203 1555 1555 2.04
SSBOND 13 CYS D 96 CYS D 105 1555 1555 2.04
SSBOND 14 CYS D 99 CYS D 110 1555 1555 2.03
SSBOND 15 CYS D 127 CYS D 211 1555 1555 2.04
SSBOND 16 CYS D 189 CYS D 203 1555 1555 2.04
SSBOND 17 CYS E 83 CYS E 133 1555 1555 2.06
SSBOND 18 CYS F 83 CYS F 133 1555 1555 2.06

CISPEP 5 GLY C 97 PRO C 98 0 2.40
CISPEP 6 SER C 194 SER C 195 0 1.38
CISPEP 7 GLY D 97 PRO D 98 0 0.65
CISPEP 8 SER D 194 SER D 195 0 -3.12

ATOM 6301 HB2 ALA D 125 -19.830 59.309 14.613 1.00 31.59 H
ATOM 6302 HB3 ALA D 125 -18.315 59.403 14.144 1.00 31.59 H
ATOM 6303 N SER D 126 -17.562 59.727 11.351 1.00 25.39 N
ATOM 6304 CA SER D 126 -16.606 60.338 10.437 1.00 25.90 C
ATOM 6305 C SER D 126 -17.233 60.587 9.066 1.00 21.76 C
ATOM 6306 O SER D 126 -17.156 61.693 8.535 1.00 20.77 O
ATOM 6307 CB SER D 126 -15.363 59.460 10.298 1.00 24.59 C

ATOM 6308 OG SER D 126 -14.403 60.072 9.456 1.00 23.90 O
ATOM 6309 H SER D 126 -17.305 58.973 11.676 1.00 30.47 H
ATOM 6310 HA SER D 126 -16.328 61.195 10.798 1.00 31.08 H
ATOM 6311 HB2 SER D 126 -14.973 59.325 11.175 1.00 29.51 H
ATOM 6312 HB3 SER D 126 -15.621 58.607 9.915 1.00 29.51 H
ATOM 6313 HG SER D 126 -13.725 59.580 9.388 1.00 28.89 H
ATOM 6314 N CYS D 127 -17.866 59.564 8.501 1.00 22.12 N
ATOM 6315 CA CYS D 127 -18.500 59.692 7.192 1.00 22.37 C
ATOM 6316 C CYS D 127 -19.519 60.731 7.206 1.00 23.64 C
ATOM 6317 O CYS D 127 -19.765 61.513 6.260 1.00 23.85 O
ATOM 6318 CB CYS D 127 -19.053 58.341 6.731 1.00 23.71 C
ATOM 6319 SG CYS D 127 -17.786 57.091 6.427 1.00 20.25 S
ATOM 6320 H CYS D 127 -17.943 58.784 8.855 1.00 26.54 H
ATOM 6321 HA CYS D 127 -17.834 59.978 6.548 1.00 26.84 H
ATOM 6322 HB2 CYS D 127 -19.648 57.990 7.415 1.00 28.45 H
ATOM 6323 HB3 CYS D 127 -19.544 58.471 5.905 1.00 28.45 H
ATOM 6324 N MET D 128 -20.406 60.737 8.277 1.00 24.97 N
ATOM 6325 CA MET D 128 -21.524 61.666 8.398 1.00 26.23 C
ATOM 6326 C MET D 128 -21.036 63.111 8.394 1.00 26.46 C
ATOM 6327 O MET D 128 -21.642 63.975 7.764 1.00 29.60 O
ATOM 6328 CB MET D 128 -22.322 61.394 9.673 1.00 27.84 C

ATOM 6329 CG MET D 128 -23.246 60.187 9.582 1.00 42.42 C
ATOM 6330 SD MET D 128 -24.266 59.966 11.056 1.00 63.01 S
ATOM 6331 CE MET D 128 -25.311 61.419 10.970 1.00 61.60 C
ATOM 6332 H MET D 128 -26.244 60.200 9.950 1.00 38.00 H

ATOM	32	CD1 TYR A 95	-16.234	1.797	-26.694	1.00	39.91	C	ATOM	6332	H MET D 128	-20.314	60.209	6.950	1.00	29.96	H
ATOM	33	CD2 TYR A 95	-14.750	1.870	-30.557	1.00	39.04	C	ATOM	6333	HA MET D 128	-22.120	61.539	7.643	1.00	31.47	H
ATOM	34	CE1 TYR A 95	-15.488	0.775	-28.135	1.00	45.29	C	ATOM	6334	HB2 MET D 128	-21.701	61.237	10.401	1.00	33.41	H
ATOM	35	CE2 TYR A 95	-13.998	0.850	-30.006	1.00	44.91	C	ATOM	6335	HB3 MET D 128	-22.869	62.171	9.871	1.00	33.41	H
ATOM	36	CZ TYR A 95	-14.370	0.306	-28.795	1.00	46.64	C	ATOM	6336	HG2 MET D 128	-23.839	60.301	8.823	1.00	50.90	H
ATOM	37	OH TYR A 95	-13.617	-0.710	-28.249	1.00	43.67	O	ATOM	6337	HG3 MET D 128	-22.710	59.388	9.467	1.00	50.90	H
ATOM	38	H TYR A 95	-17.430	4.846	-28.559	1.00	44.89	H	ATOM	6338	HE1 MET D 128	-25.919	61.416	11.726	1.00	73.92	H
ATOM	39	HA TYR A 95	-15.278	4.910	-30.179	1.00	43.39	H	ATOM	6339	HE2 MET D 128	-24.752	62.212	10.998	1.00	73.92	H
ATOM	40	HB2 TYR A 95	-17.617	3.350	-30.250	1.00	42.56	H	ATOM	6340	HE3 MET D 128	-25.814	61.398	10.141	1.00	73.92	H
ATOM	41	HB3 TYR A 95	-16.630	3.389	-31.492	1.00	42.56	H	ATOM	6341	N SER D 129	-19.934	63.362	9.092	1.00	27.28	N
ATOM	42	HD1 TYR A 95	-16.988	2.111	-28.248	1.00	47.89	H	ATOM	6342	CA SER D 129	-19.385	64.711	9.196	1.00	30.17	C
ATOM	43	HD2 TYR A 95	-14.496	2.234	-31.374	1.00	46.85	H	ATOM	6343	C SER D 129	-18.834	65.196	7.859	1.00	28.90	C
ATOM	44	HE1 TYR A 95	-15.737	0.407	-27.318	1.00	54.35	H	ATOM	6344	O SER D 129	-18.574	66.386	7.686	1.00	28.22	O
ATOM	45	HE2 TYR A 95	-13.244	0.533	-30.449	1.00	53.90	H	ATOM	6345	CB SER D 129	-18.286	64.764	10.259	1.00	35.60	C
ATOM	46	HH TYR A 95	-13.948	-0.951	-27.516	1.00	52.40	H	ATOM	6346	OG SER D 129	-17.121	64.078	9.831	1.00	30.81	O
ATOM	47	N CYS A 96	-16.167	6.043	-32.241	1.00	28.25	N	ATOM	6347	H SER D 129	-19.482	62.766	9.517	1.00	32.74	H
ATOM	48	CA CYS A 96	-16.597	6.969	-33.278	1.00	23.26	C	ATOM	6348	HA SER D 129	-20.092	65.318	9.466	1.00	36.20	H
ATOM	49	C CYS A 96	-16.818	6.214	-34.584	1.00	27.35	C	ATOM	6349	HB2 SER D 129	-18.059	65.691	10.431	1.00	42.72	H
ATOM	50	O CYS A 96	-15.989	5.397	-34.985	1.00	25.95	O	ATOM	6350	HB3 SER D 129	-18.614	64.348	11.072	1.00	42.72	H
ATOM	51	CB CYS A 96	-15.561	8.079	-33.472	1.00	25.56	C	ATOM	6351	HG SER D 129	-17.301	63.272	9.680	1.00	36.97	H
ATOM	52	SG CYS A 96	-16.018	9.334	-34.695	1.00	27.08	S	ATOM	6352	N GLN D 130	-18.659	64.270	6.920	1.00	27.90	N
ATOM	53	H CYS A 96	-15.460	5.599	-32.448	1.00	33.90	H	ATOM	6353	CA GLN D 130	-18.164	64.603	5.589	1.00	25.08	C
ATOM	54	HA CYS A 96	-17.437	7.378	-33.016	1.00	27.92	H	ATOM	6354	C GLN D 130	-19.291	64.546	4.564	1.00	25.68	C
ATOM	55	HB2 CYS A 96	-15.428	8.530	-32.624	1.00	30.68	H	ATOM	6355	O GLN D 130	-19.051	64.318	3.379	1.00	25.29	O
ATOM	56	HB3 CYS A 96	-14.727	7.677	-33.761	1.00	30.68	H	ATOM	6356	CB GLN D 130	-17.035	63.654	5.189	1.00	27.46	C
ATOM	57	N GLY A 97	-17.937	6.497	-35.244	1.00	24.78	N	ATOM	6357	CG GLN D 130	-15.877	63.654	6.167	1.00	29.13	C
ATOM	58	CA GLY A 97	-18.277	5.840	-36.491	1.00	28.73	C	ATOM	6358	CD GLN D 130	-14.797	62.669	5.790	1.00	26.28	C
ATOM	59	C GLY A 97	-19.711	5.345	-36.494	1.00	30.42	C	ATOM	6359	OE1 GLN D 130	-14.110	62.843	4.786	1.00	25.42	O
ATOM	60	O GLY A 97	-20.560	5.912	-35.807	1.00	28.09	O	ATOM	6360	NE2 GLN D 130	-14.637	61.625	6.598	1.00	26.08	N
ATOM	61	H GLY A 97	-18.520	7.074	-34.984	1.00	29.73	H	ATOM	6361	H GLN D 130	-18.821	63.433	7.032	1.00	33.48	H
ATOM	62	HA2 GLY A 97	-18.162	6.460	-37.228	1.00	34.47	H	ATOM	6362	HA GLN D 130	-17.811	65.506	5.599	1.00	30.10	H
ATOM	63	HA3 GLY A 97	-17.688	5.082	-36.630	1.00	34.47	H	ATOM	6363	HB2 GLN D 130	-17.385	62.751	5.141	1.00	32.95	H
ATOM	64	N PRO A 98	-19.994	4.281	-37.266	1.00	30.69	N	ATOM	6364	HB3 GLN D 130	-16.692	63.922	4.322	1.00	32.95	H
ATOM	65	CA PRO A 98	-19.033	3.536	-38.091	1.00	29.74	C	ATOM	6365	HG2 GLN D 130	-15.482	64.539	6.190	1.00	34.95	H
ATOM	66	C PRO A 98	-18.509	4.341	-39.280	1.00	26.22	C	ATOM	6366	HG3 GLN D 130	-16.207	63.415	7.047	1.00	34.95	H
ATOM	67	O PRO A 98	-19.241	5.130	-39.878	1.00	28.36	O	ATOM	6367	HE21 GLN D 130	-14.034	61.036	6.425	1.00	31.30	H
ATOM	68	CB PRO A 98	-19.843	2.324	-38.566	1.00	27.73	C	ATOM	6368	HE22 GLN D 130	-15.136	61.539	7.293	1.00	31.30	H
ATOM	69	CG PRO A 98	-21.247	2.772	-38.528	1.00	29.99	C	ATOM	6369	N ASN D 131	-20.515	64.766	5.035	1.00	26.26	N
ATOM	70	CD PRO A 98	-21.353	3.723	-37.371	1.00	26.89	C	ATOM	6370	CA ASN D 131	-21.699	64.750	4.182	1.00	29.68	C
ATOM	71	HA PRO A 98	-18.286	3.234	-37.551	1.00	35.69	H	ATOM	6371	C ASN D 131	-21.772	63.462	3.370	1.00	28.66	C
ATOM	72	HB2 PRO A 98	-19.581	2.088	-39.469	1.00	33.28	H	ATOM	6372	O ASN D 131	-21.989	63.485	2.157	1.00	26.21	O
ATOM	73	HB3 PRO A 98	-19.703	1.579	-37.960	1.00	33.28	H	ATOM	6373	CB ASN D 131	-21.704	65.965	3.251	1.00	33.82	C
ATOM	74	HG2 PRO A 98	-21.466	3.222	-39.358	1.00	35.98	H	ATOM	6374	CG ASN D 131	-23.039	66.164	2.559	1.00	43.32	C
ATOM	75	HG3 PRO A 98	-21.827	2.006	-38.392	1.00	35.98	H	ATOM	6375	OD1 ASN D 131	-24.084	65.767	3.074	1.00	57.86	O
ATOM	76	HD2 PRO A 98	-21.993	4.424	-37.567	1.00	32.27	H	ATOM	6376	ND2 ASN D 131	-23.009	66.779	1.382	1.00	51.68	N
ATOM	77	HD3 PRO A 98	-21.585	3.244	-36.559	1.00	32.27	H	ATOM	6377	H ASN D 131	-20.689	64.929	5.861	1.00	31.51	H
ATOM	78	N CYS A 99	-17.232	4.142	-39.591	1.00	22.72	N	ATOM	6378	HA ASN D 131	-22.490	64.797	4.740	1.00	35.61	H
ATOM	79	CA CYS A 99	-16.582	4.768	-40.737	1.00	27.89	C	ATOM	6379	HB2 ASN D 131	-21.512	66.761	3.770	1.00	40.59	H
ATOM	80	C CYS A 99	-15.575	3.793	-41.326	1.00	21.11	C	ATOM	6380	HB3 ASN D 131	-21.026	65.842	2.568	1.00	40.59	H
ATOM	81	O CYS A 99	-15.165	2.848	-40.653	1.00	25.21	O	ATOM	6381	HD21 ASN D 131	-23.740	66.916	0.950	1.00	62.02	H
ATOM	82	CB CYS A 99	-15.865	6.062	-40.337	1.00	25.67	C	ATOM	6382	HD22 ASN D 131	-22.259	67.041	1.052	1.00	62.02	H
ATOM	83	SG CYS A 99	-16.919	7.351	-39.649	1.00	24.92	S	ATOM	6383	N ALA D 132	-21.587	62.341	4.058	1.00	29.65	N
ATOM	84	H CYS A 99	-16.707	3.634	-39.138	1.00	27.26	H	ATOM	6384	CA ALA D 132	-21.549	61.035	3.420	1.00	21.47	C
ATOM	85	HA CYS A 99	-17.245	4.977	-41.414	1.00	33.47	H	ATOM	6385	C ALA D 132	-22.010	59.962	4.394	1.00	21.23	C
ATOM	86	HB2 CYS A 99	-15.194	5.847	-39.670	1.00	30.81	H	ATOM	6386	O ALA D 132	-22.408	60.258	5.521	1.00	20.92	O
ATOM	87	HB3 CYS A 99	-15.433	6.429	-41.124	1.00	30.81	H	ATOM	6387	CB ALA D 132	-20.139	60.734	2.924	1.00	25.52	C
ATOM	88	N PRO A 100	-15.165	4.018	-42.583	1.00	24.66	N	ATOM	6388	H ALA D 132	-21.479	62.313	4.911	1.00	35.58	H
ATOM	89	CA PRO A 100	-14.053	3.244	-43.146	1.00	24.78	C	ATOM	6389	HA ALA D 132	-22.148	61.033	2.657	1.00	25.77	H
ATOM	90	C PRO A 100	-12.777	3.400	-42.312	1.00	27.64	C	ATOM	6390	HB1 ALA D 132	-20.133	59.860	2.502	1.00	30.63	H
ATOM	91	O PRO A 100	-12.552	4.460	-41.723	1.00	21.92	O	ATOM	6391	HB2 ALA D 132	-19.879	61.413	2.282	1.00	30.63	H
ATOM	92	CB PRO A 100	-13.882	3.841	-44.546	1.00	25.09	C	ATOM	6392	HB3 ALA D 132	-19.530	60.741	3.679	1.00	30.63	H
ATOM	93	CG PRO A 100	-15.217	4.427	-44.874	1.00	26.97	C	ATOM	6393	N SER D 133	-21.960	58.712	3.950	1.00	20.34	N
ATOM	94	CD PRO A 100	-15.757	4.935	-43.574	1.00	24.88	C	ATOM	6394	CA SER D 133	-22.241	57.581	4.818	1.00	23.44	C

C
 ATOM 144 CD1 TRP A 103 -11.883 6.664 -45.755 1.00 30.04
 C
 ATOM 145 CD2 TRP A 103 -13.663 8.023 -45.738 1.00 23.17
 C
 ATOM 146 NE1 TRP A 103 -12.351 6.759 -47.044 1.00 29.11
 N
 ATOM 147 CE2 TRP A 103 -13.442 7.588 -47.061 1.00 26.93
 C
 ATOM 148 CE3 TRP A 103 -14.731 8.887 -45.481 1.00 20.70
 C
 ATOM 149 CZ2 TRP A 103 -14.249 7.990 -48.123 1.00 28.53
 C
 ATOM 150 CZ3 TRP A 103 -15.530 9.286 -46.534 1.00 24.02
 C
 ATOM 151 CH2 TRP A 103 -15.285 8.837 -47.841 1.00 22.80
 C
 ATOM 152 H TRP A 103 -10.834 5.812 -42.486 1.00 27.37
 H
 ATOM 153 HA TRP A 103 -10.568 8.273 -43.616 1.00 27.52
 H
 ATOM 154 HB2 TRP A 103 -12.889 6.814 -43.011 1.00 25.59
 H
 ATOM 155 HB3 TRP A 103 -12.971 8.389 -43.183 1.00 25.59
 H
 ATOM 156 HD1 TRP A 103 -11.150 6.157 -45.490 1.00 36.05
 H
 ATOM 157 HE1 TRP A 103 -12.012 6.365 -47.729 1.00 34.93
 H
 ATOM 158 HE3 TRP A 103 -14.900 9.188 -44.818 1.00 24.84
 H
 ATOM 159 HZ2 TRP A 103 -14.088 7.695 -48.990 1.00 34.23
 H
 ATOM 160 HZ3 TRP A 103 -16.243 9.861 -46.374 1.00 28.82
 H
 ATOM 161 HH2 TRP A 103 -15.840 9.122 -48.531 1.00 27.37
 H
 ATOM 162 N ILE A 104 -11.122 9.737 -41.653 1.00 15.59
 N
 ATOM 163 CA ILE A 104 -11.210 10.546 -40.444 1.00 17.76
 C
 ATOM 164 C ILE A 104 -12.621 10.491 -39.868 1.00 21.68
 C
 ATOM 165 O ILE A 104 -13.587 10.764 -40.577 1.00 20.98
 O
 ATOM 166 CB ILE A 104 -10.853 12.022 -40.718 1.00 19.18
 C
 ATOM 167 CG1 ILE A 104 -9.470 12.139 -41.368 1.00 22.53
 C
 ATOM 168 CG2 ILE A 104 -10.910 12.835 -39.425 1.00 20.64
 C
 ATOM 169 CD1 ILE A 104 -9.156 13.530 -41.903 1.00 18.10
 C
 ATOM 170 H ILE A 104 -11.147 10.199 -42.378 1.00 18.71
 H

ATOM 171 HA ILE A 104 -10.594 10.201 -39.779 1.00 21.31
 H
 ATOM 172 HB ILE A 104 -11.510 12.384 -41.333 1.00 23.02
 H
 ATOM 173 HG12 ILE A 104 -8.795 11.917 -40.708 1.00 27.03
 H
 ATOM 174 HG13 ILE A 104 -9.421 11.518 -42.111 1.00 27.03
 H
 ATOM 175 HG21 ILE A 104 -10.683 13.757 -39.622 1.00 24.77
 H
 ATOM 176 HG22 ILE A 104 -11.803 12.785 -39.061 1.00 24.77
 H
 ATOM 177 HG23 ILE A 104 -10.275 12.465 -38.792 1.00 24.77
 H
 ATOM 178 HD11 ILE A 104 -8.270 13.523 -42.297 1.00 21.72
 H
 ATOM 179 HD12 ILE A 104 -9.815 13.765 -42.575 1.00 21.72
 H
 ATOM 180 HD13 ILE A 104 -9.189 14.164 -41.171 1.00 21.72
 H
 ATOM 181 N CYS A 105 -12.734 10.151 -38.587 1.00 19.34
 N
 ATOM 182 CA CYS A 105 -14.026 10.133 -37.909 1.00 18.07
 C
 ATOM 183 C CYS A 105 -14.117 11.285 -36.914 1.00 21.22
 C
 ATOM 184 O CYS A 105 -13.216 11.497 -36.102 1.00 21.20
 O
 ATOM 185 CB CYS A 105 -14.249 8.800 -37.196 1.00 23.12
 C
 ATOM 186 SG CYS A 105 -15.944 8.565 -36.591 1.00 26.35
 S
 ATOM 187 H CYS A 105 -12.073 9.926 -38.085 1.00 23.20
 H
 ATOM 188 HA CYS A 105 -14.731 10.246 -38.566 1.00 21.68
 H
 ATOM 189 HB2 CYS A 105 -14.053 8.079 -37.814 1.00 27.74
 H
 ATOM 190 HB3 CYS A 105 -13.653 8.750 -36.433 1.00 27.74
 H
 ATOM 191 N TYR A 106 -15.207 12.035 -37.000 1.00 17.94
 N
 ATOM 192 CA TYR A 106 -15.451 13.148 -36.097 1.00 18.87
 C
 ATOM 193 C TYR A 106 -16.943 13.284 -35.857 1.00 20.09
 C

C
 ATOM 6444 C LYS D 136 -23.326 50.350 -0.635 1.00 16.54 C
 ATOM 6445 O LYS D 136 -23.061 50.967 -1.664 1.00 16.88 O
 ATOM 6446 CB LYS D 136 -24.652 52.054 0.638 1.00 21.22
 C
 ATOM 6447 CG LYS D 136 -25.972 51.387 0.267 1.00 24.56
 C
 ATOM 6448 CD LYS D 136 -27.137 52.358 0.370 1.00 28.19
 C
 ATOM 6449 CE LYS D 136 -28.427 51.738 -0.151 1.00 28.08
 C
 ATOM 6450 NZ LYS D 136 -29.569 52.692 -0.091 1.00 28.58
 N1+
 ATOM 6451 H LYS D 136 -22.040 52.391 0.372 1.00 21.34 H
 ATOM 6452 HA LYS D 136 -23.633 50.432 1.385 1.00 25.82
 H
 ATOM 6453 HB2 LYS D 136 -24.759 52.480 1.512 1.00 25.47
 H
 ATOM 6454 HB3 LYS D 136 -24.468 52.739 -0.024 1.00 25.47
 H
 ATOM 6455 HG2 LYS D 136 -25.923 51.067 -0.648 1.00 29.47
 H
 ATOM 6456 HG3 LYS D 136 -26.138 50.648 0.872 1.00 29.47
 H
 ATOM 6457 HD2 LYS D 136 -27.270 52.601 1.300 1.00 33.82
 H
 ATOM 6458 HD3 LYS D 136 -26.944 53.148 -0.159 1.00 33.82
 H
 ATOM 6459 HE2 LYS D 136 -28.302 51.473 -1.076 1.00 33.70
 H
 ATOM 6460 HE3 LYS D 136 -28.650 50.965 0.391 1.00 33.70
 H
 ATOM 6461 HZ1 LYS D 136 -30.307 52.302 -0.401 1.00 34.29
 H
 ATOM 6462 HZ2 LYS D 136 -29.708 52.947 0.751 1.00 34.29
 H
 ATOM 6463 HZ3 LYS D 136 -29.391 53.410 -0.585 1.00 34.29
 H
 ATOM 6464 N VAL D 137 -23.490 49.032 -0.592 1.00 15.00 N
 ATOM 6465 CA VAL D 137 -23.377 48.194 -1.777 1.00 14.80
 C
 ATOM 6466 C VAL D 137 -24.767 47.914 -2.328 1.00 15.82 C
 ATOM 6467 O VAL D 137 -25.542 47.181 -1.714 1.00 17.01 O
 ATOM 6468 CB VAL D 137 -22.661 46.870 -1.462 1.00 18.73
 C
 ATOM 6469 CG1 VAL D 137 -22.505 46.037 -2.723 1.00 21.27
 C
 ATOM 6470 CG2 VAL D 137 -21.293 47.142 -0.828 1.00 19.01
 C
 ATOM 6471 H VAL D 137 -23.670 48.594 0.126 1.00 18.00 H
 ATOM 6472 HA VAL D 137 -22.867 48.663 -2.456 1.00 17.76
 H
 ATOM 6473 HB VAL D 137 -23.193 46.363 -0.829 1.00 22.47
 H
 ATOM 6474 HG11 VAL D 137 -22.052 45.209 -2.500 1.00 25.53
 H
 ATOM 6475 HG12 VAL D 137 -23.384 45.846 -3.086 1.00 25.53
 H
 ATOM 6476 HG13 VAL D 137 -21.981 46.537 -3.368 1.00 25.53
 H
 ATOM 6477 HG21 VAL D 137 -20.859 46.296 -0.638 1.00 22.82
 H
 ATOM 6478 HG22 VAL D 137 -20.755 47.658 -1.449 1.00 22.82
 H
 ATOM 6479 HG23 VAL D 137 -21.420 47.641 -0.006 1.00 22.82
 H
 ATOM 6480 N TYR D 138 -25.068 48.500 -3.485 1.00 15.98 N
 ATOM 6481 CA TYR D 138 -26.410 48.453 -4.061 1.00 20.40
 C
 ATOM 6482 C TYR D 138 -26.439 47.849 -5.467 1.00 19.25 C
 ATOM 6483 O TYR D 138 -27.512 47.551 -5.991 1.00 19.44
 O
 ATOM 6484 CB TYR D 138 -27.006 49.865 -4.106 1.00 16.40
 C
 ATOM 6485 CG TYR D 138 -26.405 50.758 -5.170 1.00 15.53
 C
 ATOM 6486 CD1 TYR D 138 -26.952 50.820 -6.446 1.00 18.12
 C
 ATOM 6487 CD2 TYR D 138 -25.293 51.544 -4.897 1.00 20.57
 C
 ATOM 6488 CE1 TYR D 138 -26.406 51.635 -7.419 1.00 18.07
 C
 ATOM 6489 CE2 TYR D 138 -24.742 52.366 -5.864 1.00 14.74
 C
 ATOM 6490 CZ TYR D 138 -25.298 52.407 -7.121 1.00 19.68
 C
 ATOM 6491 OH TYR D 138 -24.746 53.225 -8.080 1.00 18.98
 O
 ATOM 6492 H TYR D 138 -24.502 48.937 -3.963 1.00 19.18 H
 ATOM 6493 HA TYR D 138 -26.976 47.909 -3.492 1.00 24.48
 H

DK/EP 3233192 T3

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H
ATOM 542 HB3 CYS A 127 -17.842 11.374 -52.337 1.00 22.65
H
ATOM 543 N MET A 128 -18.765 9.315 -54.918 1.00 17.80
N
ATOM 544 CA MET A 128 -19.856 8.382 -55.179 1.00 25.06
C
ATOM 545 C MET A 128 -19.319 6.961 -55.283 1.00 22.86
C
ATOM 546 O MET A 128 -19.956 6.008 -54.835 1.00 25.41
O
ATOM 547 CB MET A 128 -20.593 8.754 -56.464 1.00 28.91
C
ATOM 548 CG MET A 128 -22.085 8.970 -56.280 1.00 40.17
C
ATOM 549 SD MET A 128 -22.957 9.136 -57.850 1.00 65.50
S
ATOM 550 CE MET A 128 -22.156 10.582 -58.544 1.00 43.48
C
ATOM 551 H MET A 128 -18.675 9.925 -55.518 1.00 21.37
H
ATOM 552 HA MET A 128 -20.490 8.426 -54.447 1.00 30.08
H
ATOM 553 HB2 MET A 128 -20.216 9.577 -56.812 1.00 34.70
H
ATOM 554 HB3 MET A 128 -20.474 8.040 -57.110 1.00 34.70
H
ATOM 555 HG2 MET A 128 -22.459 8.210 -55.808 1.00 48.20
H

ATOM 556 HG3 MET A 128 -22.227 9.782 -55.769 1.00 48.20
H
ATOM 557 HE1 MET A 128 -22.549 10.776 -59.410 1.00 52.17
H
ATOM 558 HE2 MET A 128 -22.288 11.334 -57.945 1.00 52.17
H
ATOM 559 HE3 MET A 128 -21.208 10.401 -58.644 1.00 52.17
H
ATOM 560 N SER A 129 -18.133 6.833 -55.865 1.00 22.61
N
ATOM 561 CA SER A 129 -17.491 5.535 -56.033 1.00 26.16
C
ATOM 562 C SER A 129 -17.085 4.913 -54.697 1.00 25.71
C
ATOM 563 O SER A 129 -16.695 3.745 -54.645 1.00 24.09
O
ATOM 564 CB SER A 129 -16.261 5.674 -56.935 1.00 25.52
C
ATOM 565 OG SER A 129 -15.546 4.455 -57.022 1.00 33.82
O
ATOM 566 H SER A 129 -17.673 7.491 -56.175 1.00 27.13
H
ATOM 567 HA SER A 129 -18.113 4.930 -56.467 1.00 31.39
H
ATOM 568 HB2 SER A 129 -16.551 5.932 -57.824 1.00 30.62
H
ATOM 569 HB3 SER A 129 -15.677 6.355 -56.567 1.00 30.62
H
ATOM 570 HG SER A 129 -16.039 3.855 -57.341 1.00 40.59
H
ATOM 571 N GLN A 130 -17.171 5.694 -58.628 1.00 20.18
N
ATOM 572 CA GLN A 130 -16.753 5.233 -52.303 1.00 22.43
C
ATOM 573 C GLN A 130 -17.916 5.241 -51.317 1.00 24.16
C
ATOM 574 O GLN A 130 -17.715 5.372 -50.111 1.00 27.76
O
ATOM 575 CB GLN A 130 -15.612 6.103 -51.779 1.00 23.18
C
ATOM 576 CG GLN A 130 -14.386 6.095 -52.674 1.00 25.86
C
ATOM 577 CD GLN A 130 -13.321 7.067 -52.215 1.00 22.81
C
ATOM 578 OE1 GLN A 130 -12.837 6.988 -51.087 1.00 19.87
O
ATOM 579 NE2 GLN A 130 -12.951 7.993 -53.091 1.00 20.58
N
ATOM 580 H GLN A 130 -17.470 6.500 -53.634 1.00 24.21
H
ATOM 581 HA GLN A 130 -16.427 4.322 -52.375 1.00 26.92
H
ATOM 582 HB2 GLN A 130 -15.923 7.019 -51.709 1.00 27.81
H
ATOM 583 HB3 GLN A 130 -15.345 5.778 -50.905 1.00 27.81
H
ATOM 584 HG2 GLN A 130 -14.001 5.205 -52.674 1.00 31.04
H
ATOM 585 HG3 GLN A 130 -14.650 6.342 -53.574 1.00 31.04
H
ATOM 586 HE21 GLN A 130 -12.349 8.589 -52.879 1.00 24.70
H
ATOM 587 HE22 GLN A 130 -13.313 8.016 -53.871 1.00 24.70
H
ATOM 588 N ASN A 131 -19.127 5.083 -51.839 1.00 23.03
N
ATOM 589 CA ASN A 131 -20.331 5.118 -51.016 1.00 28.97
C
ATOM 590 C ASN A 131 -20.870 6.396 -50.190 1.00 27.25
C

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C
ATOM 6842 C HIS D 159 -28.905 44.685 13.029 1.00 56.08 C
ATOM 6843 O HIS D 159 -28.829 45.584 13.867 1.00 51.08 O
ATOM 6844 CB HIS D 159 -26.785 43.370 12.962 1.00 48.52
C
ATOM 6845 CG HIS D 159 -27.304 41.969 13.065 1.00 50.74
C
ATOM 6846 ND1 HIS D 159 -26.815 41.062 13.981 1.00 52.54
N
ATOM 6847 CD2 HIS D 159 -28.266 41.318 12.869 1.00 56.93
C
ATOM 6848 CE1 HIS D 159 -27.454 39.914 13.845 1.00 63.50
C
ATOM 6849 NE2 HIS D 159 -28.340 40.043 12.874 1.00 64.61
N

ATOM 6850 H HIS D 159 -26.348 45.743 12.289 1.00 50.65 H
ATOM 6851 HA HIS D 159 -28.018 43.835 11.392 1.00 57.02
H
ATOM 6852 HB2 HIS D 159 -25.920 43.334 12.524 1.00 58.23
H
ATOM 6853 HB3 HIS D 159 -26.683 43.715 13.863 1.00 58.23
H
ATOM 6854 HD1 HIS D 159 -26.191 41.219 14.552 1.00 63.05
H
ATOM 6855 HD2 HIS D 159 -28.781 41.669 11.679 1.00 68.31
H

ATOM 6856 HE1 HIS D 159 -27.305 39.145 14.347 1.00 76.20
H
ATOM 6857 HE2 HIS D 159 -28.875 39.427 12.601 1.00 77.54
H

ATOM 6858 N ILE D 160 -30.011 43.984 12.807 1.00 60.19 N
ATOM 6859 CA ILE D 160 -31.243 44.209 13.553 1.00 72.28
C
ATOM 6860 C ILE D 160 -31.530 43.001 14.446 1.00 84.70 C
ATOM 6861 O ILE D 160 -31.991 41.970 13.955 1.00 84.61 O
ATOM 6862 CB ILE D 160 -32.433 44.447 12.609 1.00 73.35
C
ATOM 6863 CG1 ILE D 160 -32.142 45.623 11.674 1.00 59.74
C
ATOM 6864 CG2 ILE D 160 -33.694 44.725 13.407 1.00 85.05
C
ATOM 6865 CD1 ILE D 160 -33.047 45.674 10.476 1.00 64.40
C

ATOM 6866 H ILE D 160 -30.074 43.361 12.218 1.00 72.23 H
ATOM 6867 HA ILE D 160 -31.139 44.990 14.119 1.00 86.74
H
ATOM 6868 HB ILE D 160 -32.571 43.650 12.074 1.00 88.02
H
ATOM 6869 HG12 ILE D 160 -32.255 46.450 12.168 1.00 71.69
H
ATOM 6870 HG13 ILE D 160 -31.229 45.551 11.355 1.00 71.69
H
ATOM 6871 HG21 ILE D 160 -33.883 43.961 13.974 1.00 102.06
H
ATOM 6872 HG22 ILE D 160 -33.555 45.516 13.952 1.00 102.06
H
ATOM 6873 HG23 ILE D 160 -34.430 44.872 12.793 1.00 102.06
H
ATOM 6874 HD11 ILE D 160 -32.806 46.440 9.932 1.00 77.27
H
ATOM 6875 HD12 ILE D 160 -32.939 44.857 9.964 1.00 77.27
H
ATOM 6876 HD13 ILE D 160 -33.965 45.757 10.778 1.00 77.27
H
ATOM 6877 N PRO D 161 -31.256 43.117 15.758 1.00 91.91
N
ATOM 6878 CA PRO D 161 -31.459 41.971 16.655 1.00 100.89
C
ATOM 6879 C PRO D 161 -32.918 41.531 16.773 1.00 107.68
C
ATOM 6880 O PRO D 161 -33.184 40.448 17.295 1.00 110.28
O
ATOM 6881 CB PRO D 161 -30.946 42.484 18.008 1.00 104.17
C
ATOM 6882 CG PRO D 161 -30.073 43.643 17.685 1.00 92.23
C
ATOM 6883 CD PRO D 161 -30.672 44.267 16.470 1.00 90.01
C
ATOM 6884 HA PRO D 161 -30.917 41.218 16.370 1.00 121.07
H
ATOM 6885 HB2 PRO D 161 -31.696 42.763 18.557 1.00 125.00
H
ATOM 6886 HB3 PRO D 161 -30.439 41.786 18.451 1.00 125.00
H
ATOM 6887 HG2 PRO D 161 -30.073 44.268 18.426 1.00 110.68
H
ATOM 6888 HG3 PRO D 161 -29.173 43.331 17.500 1.00 110.68
H
ATOM 6889 HD2 PRO D 161 -31.365 44.898 16.720 1.00 108.01
H
ATOM 6890 HD3 PRO D 161 -29.984 44.687 15.930 1.00 108.01
H

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ATOM 591 O ASN A 131 -20.655 6.375 -48.992 1.00 24.85
O
ATOM 592 CB ASN A 131 -20.396 3.890 -50.104 1.00 30.97
C
ATOM 593 CG ASN A 131 -21.744 3.736 -49.429 1.00 34.40
C
ATOM 594 OD1 ASN A 131 -22.772 4.158 -49.962 1.00 38.37
O
ATOM 595 ND2 ASN A 131 -21.745 3.139 -48.241 1.00 40.30
N
ATOM 596 H ASN A 131 -19.280 4.953 -52.676 1.00 27.63
H
ATOM 597 HA ASN A 131 -21.111 5.107 -51.593 1.00 34.76
H
ATOM 598 HB2 ASN A 131 -20.232 3.093 -50.633 1.00 37.17
H
ATOM 599 HB3 ASN A 131 -19.721 3.973 -49.413 1.00 37.17
H
ATOM 600 HD21 ASN A 131 -22.485 3.028 -47.817 1.00 48.35
H
ATOM 601 HD22 ASN A 131 -21.006 2.864 -47.897 1.00 48.35
H
ATOM 602 N ALA A 132 -20.066 7.510 -50.846 1.00 25.64
N
ATOM 603 CA ALA A 132 -19.980 8.800 -50.181 1.00 21.88
C
ATOM 604 C ALA A 132 -20.378 9.915 -51.139 1.00 21.78
C
ATOM 605 O ALA A 132 -20.768 9.663 -52.277 1.00 22.40
O
ATOM 606 CB ALA A 132 -18.570 9.026 -49.656 1.00 20.15
C
ATOM 607 H ALA A 132 -19.903 7.543 -51.690 1.00 30.77
H
ATOM 608 HA ALA A 132 -20.591 8.813 -49.428 1.00 26.25
H
ATOM 609 HB1 ALA A 132 -18.531 9.890 -49.217 1.00 24.18
H
ATOM 610 HB2 ALA A 132 -18.352 8.323 -49.025 1.00 24.18
H
ATOM 611 HB3 ALA A 132 -17.949 9.006 -50.401 1.00 24.18
H
ATOM 612 N SER A 133 -20.270 11.151 -50.672 1.00 18.84
N
ATOM 613 CA SER A 133 -20.529 12.309 -51.509 1.00 21.81
C
ATOM 614 C SER A 133 -19.499 13.378 -51.190 1.00 19.07
C
ATOM 615 O SER A 133 -18.693 13.211 -50.276 1.00 17.95
O
ATOM 616 CB SER A 133 -21.945 12.833 -51.281 1.00 25.17
C
ATOM 617 OG SER A 133 -22.071 13.372 -49.979 1.00 30.73
O
ATOM 618 H SER A 133 -20.045 11.346 -49.865 1.00 22.61
H
ATOM 619 HA SER A 133 -20.438 12.061 -52.442 1.00 26.18
H
ATOM 620 HB2 SER A 133 -22.134 13.528 -51.931 1.00 30.20
H
ATOM 621 HB3 SER A 133 -22.574 12.102 -51.384 1.00 30.20
H
ATOM 622 HG SER A 133 -21.908 12.780 -49.406 1.00 36.88
H
ATOM 623 N LEU A 134 -19.516 14.469 -51.947 1.00 18.66
N
ATOM 624 CA LEU A 134 -18.644 15.594 -51.646 1.00 18.37
C
ATOM 625 C LEU A 134 -19.076 16.218 -50.327 1.00 17.90
C
ATOM 626 O LEU A 134 -20.216 16.046 -49.898 1.00 17.30
O
ATOM 627 CB LEU A 134 -18.675 16.627 -52.772 1.00 17.75
C
ATOM 628 CG LEU A 134 -17.977 16.210 -54.067 1.00 16.83
C
ATOM 629 CD1 LEU A 134 -18.320 17.168 -55.192 1.00 18.55
C
ATOM 630 CD2 LEU A 134 -16.469 16.142 -53.878 1.00 18.53
C
ATOM 631 H LEU A 134 -20.019 14.581 -52.635 1.00 22.40
H
ATOM 632 HA LEU A 134 -17.733 15.276 -51.549 1.00 22.05
H
ATOM 633 HB2 LEU A 134 -19.601 16.817 -52.988 1.00 21.31
H
ATOM 634 HB3 LEU A 134 -18.243 17.436 -52.457 1.00 21.31
H
ATOM 635 HG LEU A 134 -18.287 15.327 -54.322 1.00 20.20
H
ATOM 636 HD11 LEU A 134 -18.028 18.060 -54.946 1.00 22.26
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ATOM 637 HD12 LEU A 134 -17.866 16.882 -56.000 1.00 22.26
H
ATOM 638 HD13 LEU A 134 -19.280 17.161 -55.331 1.00 22.26
H
ATOM 639 HD21 LEU A 134 -16.266 15.491 -53.188 1.00 22.24

ATOM 6891 N THR D 162 -33.845 42.358 16.298 1.00 107.82
N
ATOM 6892 CA THR D 162 -35.265 42.042 16.398 1.00 113.32
C
ATOM 6893 C THR D 162 -35.606 40.838 15.526 1.00 113.82
C
ATOM 6894 O THR D 162 -36.327 39.935 15.953 1.00 117.27
O
ATOM 6895 CB THR D 162 -36.158 43.231 15.977 1.00 116.05
C
ATOM 6896 OG1 THR D 162 -36.171 43.348 14.549 1.00 118.64
O
ATOM 6897 CG2 THR D 162 -35.669 44.537 16.597 1.00 119.38
C
ATOM 6898 H THR D 162 -33.677 43.109 15.914 1.00 129.39
H
ATOM 6899 HA THR D 162 -35.476 41.818 17.318 1.00 135.98
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ATOM 6900 HB THR D 162 -37.063 43.072 16.288 1.00 139.27
H
ATOM 6901 HG1 THR D 162 -36.656 43.994 14.318 1.00 142.36
H
ATOM 6902 HG21 THR D 162 -36.242 45.270 16.321 1.00 143.26
H
ATOM 6903 HG22 THR D 162 -35.687 44.471 17.565 1.00 143.26
H
ATOM 6904 HG23 THR D 162 -34.761 44.721 16.310 1.00 143.26
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ATOM 6905 N ASN D 163 -35.079 40.834 14.305 1.00 109.79
N
ATOM 6906 CA ASN D 163 -35.341 39.764 13.348 1.00 106.91
C
ATOM 6907 C ASN D 163 -34.070 39.304 12.634 1.00 99.24
C
ATOM 6908 O ASN D 163 -34.132 38.638 11.599 1.00 96.09
O
ATOM 6909 CB ASN D 163 -36.389 40.223 12.329 1.00 110.79
C
ATOM 6910 CG ASN D 163 -36.099 41.606 11.774 1.00 109.36
C
ATOM 6911 OD1 ASN D 163 -34.944 41.980 11.575 1.00 98.35
O
ATOM 6912 ND2 ASN D 163 -37.154 42.377 11.533 1.00 116.08
N
ATOM 6913 H ASN D 163 -34.559 41.449 14.003 1.00 131.75
H
ATOM 6914 HA ASN D 163 -35.705 39.001 13.824 1.00 128.29
H
ATOM 6915 HB2 ASN D 163 -36.404 39.599 11.587 1.00 132.95
H
ATOM 6916 HB3 ASN D 163 -37.258 40.249 12.759 1.00 132.95
H
ATOM 6917 HD21 ASN D 163 -37.044 43.170 11.218 1.00 139.29
H
ATOM 6918 HD22 ASN D 163 -37.947 42.084 11.692 1.00 139.29
H
ATOM 6919 N GLY D 164 -32.918 39.661 13.195 1.00 96.98
N
ATOM 6920 CA GLY D 164 -31.634 39.227 12.670 1.00 87.96
C
ATOM 6921 C GLY D 164 -31.365 39.684 11.248 1.00 79.64
C
ATOM 6922 O GLY D 164 -30.536 39.102 10.548 1.00 69.70
O
ATOM 6923 H GLY D 164 -32.856 40.162 13.892 1.00 116.37
H
ATOM 6924 HA2 GLY D 164 -30.926 39.570 13.237 1.00 105.56
H
ATOM 6925 HA3 GLY D 164 -31.595 38.258 12.689 1.00 105.56
H
ATOM 6926 N SER D 165 -32.062 40.732 10.822 1.00 81.83
N
ATOM 6927 CA SER D 165 -31.935 41.238 9.460 1.00 71.12
C
ATOM 6928 C SER D 165 -30.735 42.170 9.313 1.00 57.71
C
ATOM 6929 O SER D 165 -30.340 42.844 10.265 1.00 55.24
O
ATOM 6930 CB SER D 165 -33.213 41.973 9.050 1.00 73.02
C
ATOM 6931 OG SER D 165 -33.077 42.556 7.766 1.00 71.30
O
ATOM 6932 H SER D 165 -32.820 41.171 11.307 1.00 98.19
H
ATOM 6933 HA SER D 165 -31.810 40.491 8.855 1.00 85.34
H
ATOM 6934 HB2 SER D 165 -33.948 41.341 9.033 1.00 87.63
H
ATOM 6935 HB3 SER D 165 -33.394 42.674 9.696 1.00 87.63
H
ATOM 6936 HG SER D 165 -33.785 42.955 7.555 1.00 85.56
H
ATOM 6937 N TRP D 166 -30.159 42.193 8.114 1.00 41.62
N
ATOM 6938 CA TRP D 166 -29.122 43.161 7.768 1.00 41.01
C

ATOM 1281 HG23 ILE A 173 -33.845 22.438 -49.079 1.00 74.42
H
ATOM 1282 HD11 ILE A 173 -33.826 23.276 -45.056 1.00 64.11
H
ATOM 1283 HD12 ILE A 173 -33.568 24.634 -45.840 1.00 64.11
H
ATOM 1284 HD13 ILE A 173 -34.596 23.568 -46.415 1.00 64.11
H
ATOM 1285 N LEU A 174 -29.284 24.363 -48.579 1.00 36.19
N
ATOM 1286 CA LEU A 174 -28.194 25.002 -47.854 1.00 33.01
C
ATOM 1287 C LEU A 174 -28.785 25.874 -46.762 1.00 25.23
C
ATOM 1288 O LEU A 174 -29.378 26.910 -47.051 1.00 35.07
O
ATOM 1289 CB LEU A 174 -27.317 25.839 -48.788 1.00 28.79
C
ATOM 1290 CG LEU A 174 -26.268 26.722 -48.096 1.00 30.47
C

ATOM 1291 CD1 LEU A 174 -25.235 25.873 -47.369 1.00 28.59
C
ATOM 1292 CD2 LEU A 174 -25.593 27.650 -49.086 1.00 23.68
C
ATOM 1293 H LEU A 174 -29.449 24.715 -49.346 1.00 43.42
H
ATOM 1294 HA LEU A 174 -27.640 24.322 -47.438 1.00 39.62
H
ATOM 1295 HB2 LEU A 174 -26.843 25.238 -49.385 1.00 34.54
H
ATOM 1296 HB3 LEU A 174 -27.892 26.422 -49.307 1.00 34.54
H
ATOM 1297 HG LEU A 174 -26.715 27.273 -47.434 1.00 36.57
H
ATOM 1298 HD11 LEU A 174 -24.589 26.458 -46.944 1.00 34.31
H
ATOM 1299 HD12 LEU A 174 -25.685 25.334 -46.699 1.00 34.31
H
ATOM 1300 HD13 LEU A 174 -24.790 25.299 -48.012 1.00 34.31
H
ATOM 1301 HD21 LEU A 174 -24.939 28.191 -48.616 1.00 28.42
H
ATOM 1302 HD22 LEU A 174 -25.154 27.119 -49.768 1.00 28.42
H
ATOM 1303 HD23 LEU A 174 -26.265 28.221 -49.492 1.00 28.42
H
ATOM 1304 N SER A 175 -28.630 25.450 -45.513 1.00 30.51
N
ATOM 1305 CA SER A 175 -29.152 26.205 -44.382 1.00 30.76
C
ATOM 1306 C SER A 175 -28.581 27.619 -44.380 1.00 30.60
C
ATOM 1307 O SER A 175 -27.416 27.820 -44.727 1.00 29.98
O
ATOM 1308 CB SER A 175 -28.819 25.511 -43.063 1.00 29.16
C
ATOM 1309 OG SER A 175 -29.013 24.111 -43.155 1.00 41.38
O
ATOM 1310 H SER A 175 -28.224 24.724 -45.293 1.00 36.61
H
ATOM 1311 HA SER A 175 -30.117 26.267 -44.458 1.00 36.91
H
ATOM 1312 HB2 SER A 175 -27.891 25.686 -42.842 1.00 35.00
H
ATOM 1313 HB3 SER A 175 -29.396 25.863 -42.368 1.00 35.00
H
ATOM 1314 HG SER A 175 -28.825 23.746 -42.422 1.00 49.66
H
ATOM 1315 N PRO A 176 -29.399 28.608 -43.989 1.00 27.59
N
ATOM 1316 CA PRO A 176 -28.904 29.986 -43.961 1.00 27.04
C
ATOM 1317 C PRO A 176 -27.802 30.194 -42.923 1.00 27.52
C
ATOM 1318 O PRO A 176 -27.783 29.514 -41.893 1.00 28.41
O
ATOM 1319 CB PRO A 176 -30.154 30.800 -43.603 1.00 27.57
C
ATOM 1320 CG PRO A 176 -31.030 29.849 -42.883 1.00 31.89
C
ATOM 1321 CD PRO A 176 -30.791 28.510 -43.515 1.00 24.67
C
ATOM 1322 HA PRO A 176 -28.583 30.252 -44.837 1.00 32.45
H
ATOM 1323 HB2 PRO A 176 -29.908 31.544 -43.030 1.00 33.08
H
ATOM 1324 HB3 PRO A 176 -30.583 31.117 -44.414 1.00 33.08
H
ATOM 1325 HG2 PRO A 176 -30.787 29.831 -41.944 1.00 38.27
H

ATOM 1326 HG3 PRO A 176 -31.957 30.116 -42.990 1.00 38.27
H
ATOM 1327 HD2 PRO A 176 -30.876 27.804 -42.856 1.00 29.60
H
ATOM 1328 HD3 PRO A 176 -31.394 28.376 -44.262 1.00 29.60
H
ATOM 1329 N ASN A 177 -26.890 31.117 -43.213 1.00 26.69
N

ATOM 7581 CB THR D 208 -9.287 50.797 7.138 1.00 18.70
C
ATOM 7582 OG1 THR D 208 -9.593 49.516 6.576 1.00 17.72
O
ATOM 7583 CG2 THR D 208 -7.842 50.802 7.622 1.00 23.48
C
ATOM 7584 H THR D 208 -9.652 49.398 9.132 1.00 26.07
H
ATOM 7585 HA THR D 208 -10.019 51.952 8.678 1.00 20.99
H
ATOM 7586 HB THR D 208 -9.386 51.482 6.458 1.00 22.43
H
ATOM 7587 HG1 THR D 208 -9.072 49.351 5.937 1.00 21.26
H
ATOM 7588 HG21 THR D 208 -7.244 50.618 6.881 1.00 28.17
H
ATOM 7589 HG22 THR D 208 -7.622 51.668 7.999 1.00 28.17
H
ATOM 7590 HG23 THR D 208 -7.719 50.121 8.303 1.00 28.17
H

ATOM 7591 N TYR D 209 -12.065 52.188 7.099 1.00 18.19
N
ATOM 7592 CA TYR D 209 -13.438 52.291 6.614 1.00 18.43
C
ATOM 7593 C TYR D 209 -13.528 53.013 5.280 1.00 18.76
C
ATOM 7594 O TYR D 209 -12.606 53.722 4.865 1.00 18.98
O
ATOM 7595 CB TYR D 209 -14.322 52.995 7.651 1.00 18.49
C
ATOM 7596 CG TYR D 209 -13.825 54.355 8.033 1.00 19.96
C
ATOM 7597 CD1 TYR D 209 -12.821 54.477 9.032 1.00 23.84
C
ATOM 7598 CD2 TYR D 209 -14.367 55.516 7.550 1.00 21.18
C
ATOM 7599 CE1 TYR D 209 -12.364 55.717 9.433 1.00 23.52
C
ATOM 7600 CE2 TYR D 209 -13.918 56.763 7.947 1.00 23.67
C
ATOM 7601 CZ TYR D 209 -12.914 56.856 8.887 1.00 25.34
C
ATOM 7602 OH TYR D 209 -12.459 58.091 9.288 1.00 25.68
O
ATOM 7603 H TYR D 209 -11.557 52.849 6.888 1.00 21.83
H
ATOM 7604 HA TYR D 209 -13.789 51.396 6.487 1.00 22.12
H
ATOM 7605 HB2 TYR D 209 -15.209 53.112 7.275 1.00 22.19
H
ATOM 7606 HB3 TYR D 209 -14.375 52.437 8.443 1.00 22.19
H
ATOM 7607 HD1 TYR D 209 -12.446 53.711 9.401 1.00 28.60
H
ATOM 7608 HD2 TYR D 209 -15.043 55.455 6.914 1.00 25.42
H
ATOM 7609 HE1 TYR D 209 -11.688 55.783 10.068 1.00 28.22
H
ATOM 7610 HE2 TYR D 209 -14.288 57.533 7.579 1.00 28.40
H
ATOM 7611 HH TYR D 209 -11.853 58.001 9.862 1.00 30.82
H

ATOM 7612 N ILE D 210 -14.657 52.805 4.615 1.00 17.13
N
ATOM 7613 CA ILE D 210 -14.930 53.405 3.322 1.00 15.89
C
ATOM 7614 C ILE D 210 -16.147 54.297 3.433 1.00 16.38
C
ATOM 7615 O ILE D 210 -17.221 53.836 3.825 1.00 16.32
O
ATOM 7616 CB ILE D 210 -15.183 52.337 2.244 1.00 15.95
C
ATOM 7617 CG1 ILE D 210 -13.990 51.379 2.155 1.00 22.22
C
ATOM 7618 CG2 ILE D 210 -15.457 52.997 0.902 1.00 16.76
C
ATOM 7619 CD1 ILE D 210 -14.247 50.150 1.290 1.00 22.46
C

ATOM 7620 H ILE D 210 -15.296 52.307 4.902 1.00 20.56
H
ATOM 7621 HA ILE D 210 -14.173 53.947 3.049 1.00 19.06
H
ATOM 7622 HB ILE D 210 -15.967 51.826 2.498 1.00 19.13
H
ATOM 7623 HG12 ILE D 210 -13.235 51.856 1.775 1.00 26.67
H
ATOM 7624 HG13 ILE D 210 -13.769 51.072 3.048 1.00 26.67
H
ATOM 7625 HG21 ILE D 210 -15.614 52.308 0.238 1.00 20.12
H

ATOM 7626 HG22 ILE D 210 -16.240 53.563 0.983 1.00 20.12
H
ATOM 7627 HG23 ILE D 210 -14.687 53.531 0.650 1.00 20.12
H
ATOM 7628 HD11 ILE D 210 -13.451 49.596 1.284 1.00 26.95
H
ATOM 7629 HD12 ILE D 210 -14.993 49.653 1.662 1.00 26.95
H

ATOM 1380 HD23 LEU A 179 -19.773 27.241 -44.820 1.00 24.97
 H
 ATOM 1381 N THR A 180 -20.347 31.443 -46.038 1.00 21.26
 N
 ATOM 1382 CA THR A 180 -20.231 32.721 -46.711 1.00 19.84
 C
 ATOM 1383 C THR A 180 -19.779 32.441 -48.136 1.00 21.52
 C
 ATOM 1384 O THR A 180 -18.640 32.036 -48.366 1.00 23.27
 O
 ATOM 1385 CB THR A 180 -19.238 33.651 -45.993 1.00 24.67
 C
 ATOM 1386 OG1 THR A 180 -19.714 33.921 -44.669 1.00 25.74
 O
 ATOM 1387 CG2 THR A 180 -19.074 34.963 -46.744 1.00 25.66
 C
 ATOM 1388 H THR A 180 -19.612 31.164 -45.691 1.00 25.51
 H
 ATOM 1389 HA THR A 180 -21.098 33.155 -46.740 1.00 23.81
 H
 ATOM 1390 HB THR A 180 -18.372 33.218 -45.942 1.00 29.61
 H
 ATOM 1391 HG1 THR A 180 -19.784 33.203 -44.237 1.00 30.89
 H
 ATOM 1392 HG21 THR A 180 -18.445 35.535 -46.276 1.00 30.80
 H
 ATOM 1393 HG22 THR A 180 -18.741 34.793 -47.639 1.00 30.80
 H
 ATOM 1394 HG23 THR A 180 -19.928 35.418 -46.806 1.00 30.80
 H
 ATOM 1395 N ILE A 181 -20.683 32.633 -49.039 1.00 22.03
 N

 ATOM 1396 CA ILE A 181 -20.372 32.385 -50.490 1.00 21.98
 C
 ATOM 1397 C ILE A 181 -19.733 33.621 -51.100 1.00 25.54
 C
 ATOM 1398 O ILE A 181 -20.283 34.720 -51.025 1.00 23.45
 O
 ATOM 1399 CB ILE A 181 -21.623 31.998 -51.297 1.00 25.31
 C
 ATOM 1400 CG1 ILE A 181 -22.295 30.767 -50.684 1.00 27.58
 C
 ATOM 1401 CG2 ILE A 181 -21.257 31.731 -52.759 1.00 29.37
 C
 ATOM 1402 CD1 ILE A 181 -21.409 29.523 -50.619 1.00 25.67
 C
 ATOM 1403 H ILE A 181 -21.487 32.906 -48.950 1.00 26.43
 H
 ATOM 1404 HA ILE A 181 -19.736 31.655 -50.550 1.00 26.37
 H
 ATOM 1405 HB ILE A 181 -22.249 32.738 -51.267 1.00 30.37
 H
 ATOM 1406 HG12 ILE A 181 -22.567 30.982 -49.778 1.00 33.09
 H
 ATOM 1407 HG13 ILE A 181 -23.076 30.544 -51.215 1.00 33.09
 H
 ATOM 1408 HG21 ILE A 181 -22.061 31.489 -53.246 1.00 35.24
 H
 ATOM 1409 HG22 ILE A 181 -20.869 32.534 -53.139 1.00 35.24
 H
 ATOM 1410 HG23 ILE A 181 -20.617 31.003 -52.796 1.00 35.24
 H
 ATOM 1411 HD11 ILE A 181 -21.913 28.797 -50.219 1.00 30.81
 H
 ATOM 1412 HD12 ILE A 181 -21.138 29.282 -51.519 1.00 30.81
 H
 ATOM 1413 HD13 ILE A 181 -20.628 29.720 -50.079 1.00 30.81
 H
 ATOM 1414 N ILE A 182 -18.567 33.418 -51.706 1.00 21.72
 N
 ATOM 1415 CA ILE A 182 -17.765 34.497 -52.261 1.00 20.53
 C
 ATOM 1416 C ILE A 182 -17.654 34.340 -53.767 1.00 23.40
 C
 ATOM 1417 O ILE A 182 -17.226 33.296 -54.256 1.00 22.37
 O
 ATOM 1418 CB ILE A 182 -16.346 34.515 -51.649 1.00 20.38
 C
 ATOM 1419 CG1 ILE A 182 -16.430 34.684 -50.132 1.00 20.79
 C
 ATOM 1420 CG2 ILE A 182 -15.494 35.626 -52.271 1.00 21.86
 C
 ATOM 1421 CD1 ILE A 182 -15.132 34.434 -49.414 1.00 22.03
 C
 ATOM 1422 H ILE A 182 -18.211 32.641 -51.808 1.00 26.06
 H
 ATOM 1423 HA ILE A 182 -18.192 35.347 -52.072 1.00 24.63
 H
 ATOM 1424 HB ILE A 182 -15.922 33.664 -51.838 1.00 24.45
 H
 ATOM 1425 HG12 ILE A 182 -16.708 35.593 -49.934 1.00 24.95
 H
 ATOM 1426 HG13 ILE A 182 -17.085 34.059 -49.784 1.00 24.95
 H
 ATOM 1427 HG21 ILE A 182 -14.613 35.611 -51.867 1.00 26.24
 H
 ATOM 1428 HG22 ILE A 182 -15.424 35.472 -53.226 1.00 26.24
 H
 ATOM 1429 HG23 ILE A 182 -15.921 36.481 -52.104 1.00 26.24
 H
 ATOM 1430 HD11 ILE A 182 -15.920 34.584 -49.489 1.00 26.43

ATOM 7680 CG ARG D 214 -26.467 57.167 -4.271 1.00 32.12
 C
 ATOM 7681 CD ARG D 214 -25.894 55.846 -4.775 1.00 28.20
 C
 ATOM 7682 NE ARG D 214 -26.798 55.208 -5.732 1.00 27.38
 N
 ATOM 7683 CZ ARG D 214 -26.767 55.390 -7.050 1.00 28.78
 C
 ATOM 7684 NH1 ARG D 214 -25.862 56.189 -7.606 1.00 27.43
 N1+
 ATOM 7685 NH2 ARG D 214 -27.649 54.766 -7.819 1.00 26.83
 N
 ATOM 7686 H ARG D 214 -24.019 58.961 -1.710 1.00 30.63
 H
 ATOM 7687 HA ARG D 214 -23.885 57.976 -4.183 1.00 39.04
 H
 ATOM 7688 HB2 ARG D 214 -25.349 57.025 -2.571 1.00 36.70
 H
 ATOM 7689 HB3 ARG D 214 -26.215 58.352 -2.630 1.00 36.70
 H
 ATOM 7690 HG2 ARG D 214 -27.369 57.004 -3.954 1.00 38.54
 H
 ATOM 7691 HG3 ARG D 214 -26.481 57.793 -5.012 1.00 38.54
 H
 ATOM 7692 HD2 ARG D 214 -25.047 56.011 -5.220 1.00 33.84
 H
 ATOM 7693 HD3 ARG D 214 -25.768 55.243 -4.026 1.00 33.84
 H
 ATOM 7694 HE ARG D 214 -27.395 54.674 -5.418 1.00 32.85
 H
 ATOM 7695 HH11 ARG D 214 -25.290 56.599 -7.113 1.00 32.91
 H

 ATOM 7696 HH12 ARG D 214 -25.851 56.297 -8.459 1.00 32.91
 H
 ATOM 7697 HH21 ARG D 214 -28.235 54.245 -7.466 1.00 32.19
 H
 ATOM 7698 HH22 ARG D 214 -27.629 54.875 -8.672 1.00 32.19
 H

 ATOM 7699 N THR D 215 -24.923 59.656 -5.672 1.00 49.40
 N
 ATOM 7700 CA THR D 215 -25.345 60.749 -6.538 1.00 47.09
 C

 ATOM 7701 C THR D 215 -26.665 61.379 -6.091 1.00 38.12
 C
 ATOM 7702 O THR D 215 -27.251 62.193 -6.808 1.00 43.45
 O
 ATOM 7703 CB THR D 215 -25.504 60.261 -7.984 1.00 43.89
 C
 ATOM 7704 OG1 THR D 215 -24.958 58.940 -8.113 1.00 51.06
 O
 ATOM 7705 CG2 THR D 215 -24.794 61.194 -8.917 1.00 44.94
 C

 ATOM 7706 H THR D 215 -24.753 58.927 -6.095 1.00 59.28
 H
 ATOM 7707 HA THR D 215 -24.664 61.440 -6.528 1.00 56.50
 H
 ATOM 7708 HB THR D 215 -26.445 60.247 -8.220 1.00 52.66
 H
 ATOM 7709 HG1 THR D 215 -25.043 58.670 -8.903 1.00 61.28
 H
 ATOM 7710 HG21 THR D 215 -25.168 62.086 -8.841 1.00 53.93
 H
 ATOM 7711 HG22 THR D 215 -23.850 61.228 -8.697 1.00 53.93
 H
 ATOM 7712 HG23 THR D 215 -24.893 60.887 -9.832 1.00 53.93
 H

 TER 7713 THR D 215

 ATOM 7714 N GLY E 0 -1.565 40.227 -65.921 1.00 24.87
 N
 ATOM 7715 CA GLY E 0 -1.695 39.502 -64.623 1.00 25.57
 C
 ATOM 7716 C GLY E 0 -2.109 40.445 -63.512 1.00 23.21
 C
 ATOM 7717 O GLY E 0 -2.318 41.635 -63.745 1.00 21.52
 O
 ATOM 7718 H1 GLY E 0 -2.226 39.984 -66.465 1.00 29.85
 H
 ATOM 7719 H2 GLY E 0 -1.608 41.105 -65.776 1.00 29.85
 H
 ATOM 7720 H3 GLY E 0 -0.783 40.027 -66.296 1.00 29.85
 H
 ATOM 7721 HA2 GLY E 0 -2.363 38.803 -64.704 1.00 30.68
 H
 ATOM 7722 HA3 GLY E 0 -0.846 39.096 -64.388 1.00 30.68
 H

 ATOM 7723 N HIS E 1 -2.229 39.916 -62.300 1.00 20.53
 N
 ATOM 7724 CA HIS E 1 -2.640 40.720 -61.155 1.00 19.68
 C
 ATOM 7725 C HIS E 1 -1.777 40.422 -59.946 1.00 18.24
 C
 ATOM 7726 O HIS E 1 -1.189 39.348 -59.847 1.00 15.98
 O
 ATOM 7727 CB HIS E 1 -4.111 40.469 -60.821 1.00 19.17
 C
 ATOM 7728 CG HIS E 1 -5.048 40.824 -61.931 1.00 22.06
 C
 ATOM 7729 ND1 HIS E 1 -5.356 42.128 -62.255 1.00 23.79
 N

ATOM 1430 HD11 ILE A 182 -13.269 34.981 -46.462 1.00 26.43
 H
 ATOM 1431 HD12 ILE A 182 -14.845 33.524 -49.589 1.00 26.43
 H
 ATOM 1432 HD13 ILE A 182 -14.466 35.060 -49.740 1.00 26.43
 H
 ATOM 1433 N GLU A 183 -18.035 35.379 -54.500 1.00 21.68
 N
 ATOM 1434 CA GLU A 183 -17.855 35.391 -55.943 1.00 27.56
 C
 ATOM 1435 C GLU A 183 -16.373 35.527 -56.271 1.00 29.48
 C
 ATOM 1436 O GLU A 183 -15.667 36.337 -55.670 1.00 31.01
 O
 ATOM 1437 CB GLU A 183 -18.648 36.533 -56.582 1.00 39.38
 C
 ATOM 1438 CG GLU A 183 -20.154 36.416 -56.407 1.00 45.85
 C
 ATOM 1439 CD GLU A 183 -20.911 37.550 -57.074 1.00 71.49
 C
 ATOM 1440 OE1 GLU A 183 -20.297 38.607 -57.336 1.00 65.31
 O
 ATOM 1441 OE2 GLU A 183 -22.120 37.382 -57.340 1.00 84.35
 O1-
 ATOM 1442 H GLU A 183 -18.402 36.090 -54.184 1.00 26.02
 H
 ATOM 1443 HA GLU A 183 -18.174 34.553 -56.314 1.00 33.07
 H
 ATOM 1444 HB2 GLU A 183 -18.368 37.370 -56.180 1.00 47.25
 H
 ATOM 1445 HB3 GLU A 183 -18.461 36.548 -57.534 1.00 47.25
 H
 ATOM 1446 HG2 GLU A 183 -20.454 35.582 -56.802 1.00 55.02
 H
 ATOM 1447 HG3 GLU A 183 -20.364 36.430 -55.461 1.00 55.02
 H
 ATOM 1448 N MET A 184 -15.908 34.723 -57.219 1.00 27.36
 N
 ATOM 1449 CA MET A 184 -14.520 34.765 -57.655 1.00 30.39
 C
 ATOM 1450 C MET A 184 -14.461 34.514 -59.154 1.00 36.58
 C
 ATOM 1451 O MET A 184 -14.269 35.441 -59.942 1.00 34.99
 O
 ATOM 1452 CB MET A 184 -13.684 33.732 -56.895 1.00 28.20
 C
 ATOM 1453 CG MET A 184 -12.200 33.780 -57.213 1.00 26.40
 C
 ATOM 1454 SD MET A 184 -11.300 32.412 -56.469 1.00 27.32
 S
 ATOM 1455 CE MET A 184 -11.827 31.057 -57.524 1.00 31.27
 C
 ATOM 1456 H MET A 184 -16.384 34.136 -57.631 1.00 32.83
 H
 ATOM 1457 HA MET A 184 -14.155 35.644 -57.468 1.00 36.47
 H
 ATOM 1458 HB2 MET A 184 -13.788 33.887 -55.943 1.00 33.85
 H
 ATOM 1459 HB3 MET A 184 -14.006 32.845 -57.120 1.00 33.85
 H
 ATOM 1460 HG2 MET A 184 -12.080 33.732 -58.175 1.00 31.68
 H
 ATOM 1461 HG3 MET A 184 -11.828 34.607 -56.871 1.00 31.68
 H
 ATOM 1462 HE1 MET A 184 -11.402 30.239 -57.223 1.00 37.53
 H
 ATOM 1463 HE2 MET A 184 -12.791 30.969 -57.468 1.00 37.53
 H
 ATOM 1464 HE3 MET A 184 -11.565 31.248 -58.439 1.00 37.53
 H
 ATOM 1465 N GLN A 185 -14.639 33.253 -59.535 1.00 34.02
 N
 ATOM 1466 CA GLN A 185 -14.708 32.865 -60.935 1.00 39.99
 C
 ATOM 1467 C GLN A 185 -16.136 32.439 -61.257 1.00 36.81
 C
 ATOM 1468 O GLN A 185 -16.749 31.687 -60.498 1.00 32.57
 O
 ATOM 1469 CB GLN A 185 -13.724 31.732 -61.230 1.00 31.78
 C
 ATOM 1470 CG GLN A 185 -13.525 31.454 -62.708 1.00 37.09
 C
 ATOM 1471 CD GLN A 185 -12.853 32.606 -63.427 1.00 49.35
 C
 ATOM 1472 OE1 GLN A 185 -11.834 33.129 -62.972 1.00 44.78
 O
 ATOM 1473 NE2 GLN A 185 -13.427 33.014 -64.554 1.00 50.69
 N
 ATOM 1474 H GLN A 185 -14.723 32.593 -58.990 1.00 40.83
 H
 ATOM 1475 HA GLN A 185 -14.480 33.624 -61.494 1.00 47.99
 H
 ATOM 1476 HB2 GLN A 185 -12.860 31.964 -60.855 1.00 38.14
 H
 ATOM 1477 HB3 GLN A 185 -14.053 30.918 -60.818 1.00 38.14
 H
 ATOM 1478 HG2 GLN A 185 -12.966 30.668 -62.810 1.00 44.51
 H
 ATOM 1479 HG3 GLN A 185 -14.390 31.304 -63.121 1.00 44.51

ATOM 7730 CD2 HIS E 1 -5.744 40.047 -62.794 1.00 22.57 C
 ATOM 7731 CE1 HIS E 1 -6.202 42.139 -63.270 1.00 22.50 C
 ATOM 7732 NE2 HIS E 1 -6.454 40.889 -63.614 1.00 22.56 N
 ATOM 7733 H HIS E 1 -2.078 39.090 -62.113 1.00 24.63 H
 ATOM 7734 HA HIS E 1 -2.537 41.660 -61.374 1.00 23.61 H
 ATOM 7735 HB2 HIS E 1 -4.231 39.528 -60.622 1.00 23.00 H
 ATOM 7736 HB3 HIS E 1 -4.352 41.003 -60.047 1.00 23.00 H
 ATOM 7737 HD1 HIS E 1 -5.045 42.826 -61.859 1.00 28.55 H
 ATOM 7738 HD2 HIS E 1 -5.743 39.118 -62.823 1.00 27.08 H
 ATOM 7739 HE1 HIS E 1 -6.559 42.897 -63.672 1.00 27.00 H
 ATOM 7740 HE2 HIS E 1 -6.977 40.642 -64.251 1.00 27.08 H
 ATOM 7741 N LYS E 2 -1.704 41.383 -59.031 1.00 18.21 N
 ATOM 7742 CA LYS E 2 -0.948 41.206 -57.804 1.00 17.86 C
 ATOM 7743 C LYS E 2 -1.636 41.890 -56.629 1.00 19.00 C
 ATOM 7744 O LYS E 2 -2.239 42.957 -56.769 1.00 19.28 O
 ATOM 7745 CB LYS E 2 0.478 41.736 -57.970 1.00 23.19 C
 ATOM 7746 CG LYS E 2 0.564 43.187 -58.389 1.00 27.11 C
 ATOM 7747 CD LYS E 2 1.980 43.554 -58.803 1.00 34.68 C
 ATOM 7748 CE LYS E 2 2.079 45.021 -59.188 1.00 38.27 C
 ATOM 7749 NZ LYS E 2 3.461 45.403 -59.589 1.00 38.97
 N1+
 ATOM 7750 H LYS E 2 -2.086 42.150 -59.100 1.00 21.85 H
 ATOM 7751 HA LYS E 2 -0.891 40.259 -57.605 1.00 21.44 H
 ATOM 7752 HB2 LYS E 2 0.943 41.647 -57.123 1.00 27.83 H
 ATOM 7753 HB3 LYS E 2 0.929 41.208 -58.647 1.00 27.83 H
 ATOM 7754 HG2 LYS E 2 -0.024 43.338 -59.145 1.00 32.53 H
 ATOM 7755 HG3 LYS E 2 0.307 43.752 -57.644 1.00 32.53 H
 ATOM 7756 HD2 LYS E 2 2.584 43.392 -58.061 1.00 41.61 H
 ATOM 7757 HD3 LYS E 2 2.239 43.020 -59.570 1.00 41.61 H
 ATOM 7758 HE2 LYS E 2 1.489 45.194 -59.937 1.00 45.93 H
 ATOM 7759 HE3 LYS E 2 1.824 45.567 -58.428 1.00 45.93 H
 ATOM 7760 HZ1 LYS E 2 4.024 45.259 -58.915 1.00 46.77 H
 ATOM 7761 HZ2 LYS E 2 3.719 44.919 -60.290 1.00 46.77 H
 ATOM 7762 HZ3 LYS E 2 3.487 46.265 -59.808 1.00 46.77 H
 ATOM 7763 N LEU E 3 -1.558 41.235 -55.477 1.00 15.59 N
 ATOM 7764 CA LEU E 3 -2.079 41.766 -54.229 1.00 13.41 C
 ATOM 7765 C LEU E 3 -0.905 41.903 -53.273 1.00 13.12 C
 ATOM 7766 O LEU E 3 -0.228 40.922 -52.981 1.00 12.97 O
 ATOM 7767 CB LEU E 3 -3.160 40.847 -53.681 1.00 14.06 C
 ATOM 7768 CG LEU E 3 -3.893 41.275 -52.390 1.00 12.36 C
 ATOM 7769 CD1 LEU E 3 -4.662 42.573 -52.590 1.00 15.83 C
 ATOM 7770 CD2 LEU E 3 -4.825 40.167 -51.968 1.00 11.74 C
 ATOM 7771 H LEU E 3 -1.197 40.458 -55.394 1.00 18.71 H
 ATOM 7772 HA LEU E 3 -2.463 42.644 -54.380 1.00 16.10 H
 ATOM 7773 HB2 LEU E 3 -3.835 40.727 -54.346 1.00 16.87 H
 ATOM 7774 HB3 LEU E 3 -2.748 39.990 -53.471 1.00 16.87 H
 ATOM 7775 HG LEU E 3 -3.246 41.413 -51.881 1.00 14.83 H
 ATOM 7776 HD11 LEU E 3 -5.110 42.805 -51.761 1.00 18.99
 H
 ATOM 7777 HD12 LEU E 3 -4.039 43.274 -52.837 1.00 18.99
 H
 ATOM 7778 HD13 LEU E 3 -5.315 42.447 -53.296 1.00 18.99
 H
 ATOM 7779 HD21 LEU E 3 -5.291 40.437 -51.162 1.00 14.08

ATOM 1479 HD3 GLN A 185 -14.930 31.307 50.121 1.00 47.91
 H
 ATOM 1480 HE21 GLN A 185 -13.084 33.665 -64.999 1.00 60.83
 H
 ATOM 1481 HE22 GLN A 185 -14.141 32.629 -64.837 1.00 60.83
 H
 ATOM 1482 N LYS A 186 -16.669 32.933 -62.370 1.00 41.91
 N
 ATOM 1483 CA LYS A 186 -18.026 32.585 -62.779 1.00 44.77
 C
 ATOM 1484 C LYS A 186 -18.149 31.085 -63.028 1.00 32.82
 C
 ATOM 1485 O LYS A 186 -17.492 30.537 -63.913 1.00 41.23
 O
 ATOM 1486 CB LYS A 186 -18.427 33.361 -64.033 1.00 55.29
 C
 ATOM 1487 CG LYS A 186 -18.429 34.868 -63.851 1.00 69.71
 C
 ATOM 1488 CD LYS A 186 -18.935 35.578 -65.096 1.00 87.98
 C
 ATOM 1489 CE LYS A 186 -18.822 37.087 -64.961 1.00 90.78
 C
 ATOM 1490 NZ LYS A 186 -17.407 37.529 -64.823 1.00 89.35
 N1+
 ATOM 1491 H LYS A 186 -16.266 33.470 -62.907 1.00 50.30
 H
 ATOM 1492 HA LYS A 186 -18.642 32.823 -62.088 1.00 53.72
 H
 ATOM 1493 HB2 LYS A 186 -17.802 33.150 -64.744 1.00 66.35
 H
 ATOM 1494 HB3 LYS A 186 -19.323 33.093 -64.293 1.00 66.35
 H
 ATOM 1495 HG2 LYS A 186 -19.012 35.100 -63.110 1.00 83.65
 H
 ATOM 1496 HG3 LYS A 186 -17.525 35.171 -63.674 1.00 83.65
 H
 ATOM 1497 HD2 LYS A 186 -18.406 35.301 -65.860 1.00 105.57
 H
 ATOM 1498 HD3 LYS A 186 -19.869 35.354 -65.235 1.00 105.57
 H
 ATOM 1499 HE2 LYS A 186 -19.194 37.507 -65.753 1.00 108.94
 H
 ATOM 1500 HE3 LYS A 186 -19.307 37.374 -64.172 1.00 108.94
 H

ATOM 1501 HZ1 LYS A 186 -16.940 37.281 -65.540 1.00 107.22
 H
 ATOM 1502 HZ2 LYS A 186 -17.371 38.415 -64.747 1.00 107.22
 H
 ATOM 1503 HZ3 LYS A 186 -17.043 37.160 -64.100 1.00 107.22
 H
 ATOM 1504 N GLY A 187 -18.991 30.427 -62.239 1.00 31.79
 N
 ATOM 1505 CA GLY A 187 -19.178 28.993 -62.350 1.00 33.62
 C
 ATOM 1506 C GLY A 187 -20.338 28.512 -61.506 1.00 28.83
 C
 ATOM 1507 O GLY A 187 -20.967 29.303 -60.803 1.00 31.67
 O
 ATOM 1508 H GLY A 187 -19.468 30.795 -61.626 1.00 38.15
 H
 ATOM 1509 HA2 GLY A 187 -19.350 28.758 -63.276 1.00 40.35
 H
 ATOM 1510 HA3 GLY A 187 -16.373 28.536 -62.060 1.00 40.35
 H
 ATOM 1511 N ASP A 188 -20.613 27.211 -61.571 1.00 26.78
 N
 ATOM 1512 CA ASP A 188 -21.741 26.613 -60.860 1.00 29.71
 C
 ATOM 1513 C ASP A 188 -21.302 25.691 -59.721 1.00 27.78
 C
 ATOM 1514 O ASP A 188 -22.110 24.929 -59.135 1.00 26.36
 O
 ATOM 1515 CB ASP A 188 -22.617 25.840 -61.843 1.00 34.87
 C
 ATOM 1516 CG ASP A 188 -23.227 26.735 -62.901 1.00 39.70
 C
 ATOM 1517 OD1 ASP A 188 -23.676 27.848 -62.551 1.00 38.40
 O
 ATOM 1518 OD2 ASP A 188 -23.248 26.332 -64.083 1.00 40.40
 O1-
 ATOM 1519 H ASP A 188 -20.154 26.645 -62.028 1.00 32.14
 H
 ATOM 1520 HA ASP A 188 -22.280 27.322 -60.476 1.00 35.65
 H
 ATOM 1521 HB2 ASP A 188 -22.077 25.170 -62.291 1.00 41.85
 H
 ATOM 1522 HB3 ASP A 188 -23.340 25.413 -61.357 1.00 41.85
 H
 ATOM 1523 N CYS A 189 -20.027 25.772 -59.349 1.00 25.17
 N
 ATOM 1524 CA CYS A 189 -19.485 24.978 -58.248 1.00 21.30
 C
 ATOM 1525 C CYS A 189 -18.739 25.877 -57.264 1.00 22.52
 C
 ATOM 1526 O CYS A 189 -18.363 27.001 -57.805 1.00 24.18
 O
 ATOM 1527 CB CYS A 189 -18.546 23.887 -58.776 1.00 24.76
 C
 ATOM 1528 SG CYS A 189 -19.310 22.735 -59.952 1.00 29.58
 S
 ATOM 1529 H CYS A 189 -19.448 26.286 -59.723 1.00 30.21

ATOM 7779 HD21 LEU E 3 -5.231 40.797 51.182 1.00 14.00
 H
 ATOM 7780 HD22 LEU E 3 -5.462 40.003 -52.680 1.00 14.08
 H
 ATOM 7781 HD23 LEU E 3 -4.305 39.366 -51.798 1.00 14.08
 H
 ATOM 7782 N ALA E 4 -0.654 43.124 -52.813 1.00 14.08 N
 ATOM 7783 CA ALA E 4 0.497 43.406 -51.961 1.00 13.44 C
 ATOM 7784 C ALA E 4 0.060 43.927 -50.597 1.00 17.16 C
 ATOM 7785 O ALA E 4 -0.878 44.720 -50.492 1.00 16.57 O
 ATOM 7786 CB ALA E 4 1.416 44.405 -52.632 1.00 18.34 C
 ATOM 7787 H ALA E 4 -1.140 43.813 -52.981 1.00 16.90 H
 ATOM 7788 HA ALA E 4 0.995 42.586 -51.822 1.00 16.13 H
 ATOM 7789 HB1 ALA E 4 2.172 44.578 -52.050 1.00 22.01 H
 ATOM 7790 HB2 ALA E 4 1.723 44.035 -53.474 1.00 22.01 H
 ATOM 7791 HB3 ALA E 4 0.925 45.227 -52.791 1.00 22.01 H
 ATOM 7792 N PHE E 5 0.753 43.463 -49.563 1.00 15.63 N
 ATOM 7793 CA PHE E 5 0.549 43.919 -48.195 1.00 13.64 C
 ATOM 7794 C PHE E 5 1.836 44.553 -47.690 1.00 14.46 C
 ATOM 7795 O PHE E 5 2.882 43.911 -47.705 1.00 13.48 O
 ATOM 7796 CB PHE E 5 0.153 42.757 -47.285 1.00 12.69 C
 ATOM 7797 CG PHE E 5 -1.145 42.107 -47.655 1.00 12.18 C
 ATOM 7798 CD1 PHE E 5 -1.202 41.174 -48.674 1.00 13.36 C
 ATOM 7799 CD2 PHE E 5 -2.305 42.415 -46.970 1.00 13.02 C
 ATOM 7800 CE1 PHE E 5 -2.394 40.571 -49.012 1.00 16.36 C
 ATOM 7801 CE2 PHE E 5 -3.500 41.813 -47.302 1.00 13.36 C
 ATOM 7802 CZ PHE E 5 -3.545 40.890 -48.324 1.00 16.42 C
 ATOM 7803 H PHE E 5 1.366 42.864 -49.633 1.00 18.75 H
 ATOM 7804 HA PHE E 5 -0.156 44.585 -48.174 1.00 16.37 H
 ATOM 7805 HB2 PHE E 5 0.845 42.079 -47.327 1.00 15.23 H
 ATOM 7806 HB3 PHE E 5 0.070 43.087 -46.377 1.00 15.23 H
 ATOM 7807 HD1 PHE E 5 -0.429 40.956 -49.142 1.00 16.03 H
 ATOM 7808 HD2 PHE E 5 -2.280 43.038 -46.280 1.00 15.63 H
 ATOM 7809 HE1 PHE E 5 -2.422 39.947 -49.701 1.00 19.63 H
 ATOM 7810 HE2 PHE E 5 -4.276 42.030 -46.837 1.00 16.03 H
 ATOM 7811 HZ PHE E 5 -4.350 40.483 -48.550 1.00 19.70 H
 ATOM 7812 N ASN E 6 1.761 45.806 -47.252 1.00 14.65 N
 ATOM 7813 CA ASN E 6 2.928 46.501 -46.714 1.00 15.88 C
 ATOM 7814 C ASN E 6 2.745 46.820 -45.232 1.00 16.33 C
 ATOM 7815 O ASN E 6 2.007 47.736 -44.871 1.00 15.03 O
 ATOM 7816 CB ASN E 6 3.201 47.786 -47.499 1.00 19.07 C
 ATOM 7817 CG ASN E 6 4.557 48.391 -47.170 1.00 26.15 C
 ATOM 7818 OD1 ASN E 6 4.646 49.449 -46.550 1.00 33.75 O
 ATOM 7819 ND2 ASN E 6 5.622 47.706 -47.572 1.00 23.45 N
 ATOM 7820 H ASN E 6 1.042 46.279 -47.255 1.00 17.58 H
 ATOM 7821 HA ASN E 6 3.704 45.926 -46.802 1.00 19.05 H
 ATOM 7822 HB2 ASN E 6 3.181 47.588 -48.448 1.00 22.89 H
 ATOM 7823 HB3 ASN E 6 2.519 48.441 -47.282 1.00 22.89 H
 ATOM 7824 HD21 ASN E 6 6.412 48.005 -47.411 1.00 28.14 H
 ATOM 7825 HD22 ASN E 6 5.522 46.963 -47.994 1.00 28.14 H
 ATOM 7826 N PHE E 7 3.411 46.041 -44.385 1.00 13.46 N
 ATOM 7827 CA PHE E 7 3.355 46.228 -42.942 1.00 16.36 C
 ATOM 7828 C PHE E 7 4.478 47.139 -42.488 1.00 15.66 C

DK/EP 3233192 T3

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H
ATOM 1530 HA CYS A 189 -20.214 24.548 -57.774 1.00 25.56
H
ATOM 1531 HB2 CYS A 189 -17.799 24.312 -59.224 1.00 29.72
H
ATOM 1532 HB3 CYS A 189 -18.222 23.367 -58.024 1.00 29.72
H
ATOM 1533 N ALA A 190 -18.520 25.374 -56.053 1.00 21.28
N
ATOM 1534 CA ALA A 190 -17.838 26.140 -55.015 1.00 21.57
C
ATOM 1535 C ALA A 190 -16.787 25.316 -54.311 1.00 18.66
C

ATOM 1536 O ALA A 190 -16.936 24.118 -54.073 1.00 17.27
O
ATOM 1537 CB ALA A 190 -18.838 26.661 -54.007 1.00 20.73
C
ATOM 1538 H ALA A 190 -18.759 24.585 -55.805 1.00 25.54
H
ATOM 1539 HA ALA A 190 -17.403 26.904 -55.425 1.00 25.89
H
ATOM 1540 HB1 ALA A 190 -18.366 27.166 -53.327 1.00 24.88
H
ATOM 1541 HB2 ALA A 190 -19.476 27.232 -54.462 1.00 24.88
H
ATOM 1542 HB3 ALA A 190 -19.298 25.909 -53.602 1.00 24.88
H
ATOM 1543 N LEU A 191 -15.664 25.981 -53.984 1.00 20.48
N
ATOM 1544 CA LEU A 191 -14.578 25.382 -53.216 1.00 18.02
C
ATOM 1545 C LEU A 191 -14.722 25.748 -51.745 1.00 17.63
C
ATOM 1546 O LEU A 191 -14.852 26.927 -51.421 1.00 16.65
O
ATOM 1547 CB LEU A 191 -13.226 25.869 -53.737 1.00 15.13
C
ATOM 1548 CG LEU A 191 -12.856 25.493 -55.171 1.00 21.15
C
ATOM 1549 CD1 LEU A 191 -11.760 26.409 -55.687 1.00 23.95
C
ATOM 1550 CD2 LEU A 191 -12.414 24.040 -55.236 1.00 19.16
C
ATOM 1551 H LEU A 191 -15.518 26.800 -54.200 1.00 24.57
H
ATOM 1552 HA LEU A 191 -14.613 24.416 -53.300 1.00 21.63
H
ATOM 1553 HB2 LEU A 191 -13.213 26.837 -53.683 1.00 18.15
H
ATOM 1554 HB3 LEU A 191 -12.533 25.509 -53.160 1.00 18.15
H
ATOM 1555 HG LEU A 191 -13.634 25.600 -55.741 1.00 25.38
H
ATOM 1556 HD11 LEU A 191 -11.540 26.155 -56.597 1.00 28.74
H
ATOM 1557 HD12 LEU A 191 -12.079 27.324 -55.667 1.00 28.74
H
ATOM 1558 HD13 LEU A 191 -10.979 26.317 -55.119 1.00 28.74
H
ATOM 1559 HD21 LEU A 191 -12.183 23.821 -56.153 1.00 22.99
H
ATOM 1560 HD22 LEU A 191 -11.641 23.919 -54.663 1.00 22.99
H
ATOM 1561 HD23 LEU A 191 -13.142 23.475 -54.934 1.00 22.99
H
ATOM 1562 N TYR A 192 -14.703 24.757 -50.855 1.00 15.23
N
ATOM 1563 CA TYR A 192 -14.718 25.056 -49.430 1.00 14.68
C
ATOM 1564 C TYR A 192 -13.365 25.597 -48.980 1.00 17.40
C
ATOM 1565 O TYR A 192 -12.324 25.129 -49.427 1.00 12.57
O
ATOM 1566 CB TYR A 192 -15.055 23.831 -48.568 1.00 16.60
C
ATOM 1567 CG TYR A 192 -14.916 24.199 -47.115 1.00 16.87
C
ATOM 1568 CD1 TYR A 192 -15.948 24.847 -46.450 1.00 14.23
C
ATOM 1569 CD2 TYR A 192 -13.724 23.981 -48.428 1.00 17.91
C
ATOM 1570 CE1 TYR A 192 -15.817 25.235 -45.140 1.00 15.45
C

ATOM 1571 CE2 TYR A 192 -13.584 24.368 -45.111 1.00 16.81
C
ATOM 1572 CZ TYR A 192 -14.637 24.997 -44.473 1.00 17.95
C
ATOM 1573 OH TYR A 192 -14.514 25.401 -43.164 1.00 18.94
O
ATOM 1574 H TYR A 192 -14.683 23.919 -51.048 1.00 18.28
H
ATOM 1575 HA TYR A 192 -15.386 25.737 -49.257 1.00 17.62
H
ATOM 1576 HB2 TYR A 192 -15.970 23.556 -48.734 1.00 19.92
H
ATOM 1577 HB3 TYR A 192 -14.437 23.110 -48.766 1.00 19.92
H
ATOM 1578 HD1 TYR A 192 -16.745 25.017 -46.898 1.00 17.07

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ATOM 7829 O PHE E 7 5.634 46.909 -42.829 1.00 14.02 O
ATOM 7830 CB PHE E 7 3.464 44.888 -42.217 1.00 14.45 C
ATOM 7831 CG PHE E 7 2.371 43.929 -42.549 1.00 13.89 C
ATOM 7832 CD1 PHE E 7 2.434 43.159 -43.700 1.00 13.75 C
C
ATOM 7833 CD2 PHE E 7 1.285 43.779 -41.705 1.00 13.24 C
C
ATOM 7834 CE1 PHE E 7 1.425 42.267 -44.007 1.00 13.98 C
ATOM 7835 CE2 PHE E 7 0.270 42.887 -42.009 1.00 16.30 C

ATOM 7836 CZ PHE E 7 0.342 42.131 -43.161 1.00 16.68 C
ATOM 7837 H PHE E 7 3.912 45.386 -44.628 1.00 16.16 H
ATOM 7838 HA PHE E 7 2.509 46.639 -42.702 1.00 19.63 H
ATOM 7839 HB2 PHE E 7 4.307 44.472 -42.456 1.00 17.33 H
ATOM 7840 HB3 PHE E 7 3.437 45.048 -41.260 1.00 17.33 H
ATOM 7841 HD1 PHE E 7 3.160 43.248 -44.274 1.00 16.50 H
ATOM 7842 HD2 PHE E 7 1.232 44.289 -40.928 1.00 15.89 H
ATOM 7843 HE1 PHE E 7 1.474 41.757 -44.784 1.00 16.77 H
ATOM 7844 HE2 PHE E 7 -0.457 42.796 -41.437 1.00 19.56 H
ATOM 7845 HZ PHE E 7 -0.337 41.530 -43.367 1.00 20.02 H
ATOM 7846 N ASN E 8 4.139 48.165 -41.715 1.00 16.72 N
ATOM 7847 CA ASN E 8 5.147 49.064 -41.166 1.00 17.71 C
ATOM 7848 C ASN E 8 4.955 49.290 -39.675 1.00 18.89 C
ATOM 7849 O ASN E 8 3.850 49.591 -39.218 1.00 16.16 O
ATOM 7850 CB ASN E 8 5.124 50.406 -41.893 1.00 17.97 C
ATOM 7851 CG ASN E 8 6.231 51.331 -41.433 1.00 21.21 C
ATOM 7852 OD1 ASN E 8 7.411 51.033 -41.604 1.00 24.65 O
ATOM 7853 ND2 ASN E 8 5.856 52.462 -40.850 1.00 23.34 N
ATOM 7854 H ASN E 8 3.332 48.362 -41.493 1.00 22.47 H
ATOM 7855 HA ASN E 8 6.023 48.669 -41.297 1.00 21.25 H
ATOM 7856 HB2 ASN E 8 5.236 50.253 -42.845 1.00 21.57 H
ATOM 7857 HB3 ASN E 8 4.275 50.844 -41.724 1.00 21.57 H
ATOM 7858 HD21 ASN E 8 6.449 53.019 -40.572 1.00 28.01 H
ATOM 7859 HD22 ASN E 8 5.020 52.638 -40.751 1.00 28.01 H
ATOM 7860 N LEU E 9 6.043 49.124 -38.928 1.00 15.50 N
ATOM 7861 CA LEU E 9 6.083 49.460 -37.513 1.00 16.76 C
ATOM 7862 C LEU E 9 7.182 50.492 -37.294 1.00 19.62 C
ATOM 7863 O LEU E 9 8.365 50.183 -37.428 1.00 18.29 O
ATOM 7864 CB LEU E 9 6.330 48.214 -36.656 1.00 17.53 C
ATOM 7865 CG LEU E 9 6.418 48.451 -35.145 1.00 16.67 C
ATOM 7866 CD1 LEU E 9 5.120 49.012 -34.599 1.00 22.09 C
ATOM 7867 CD2 LEU E 9 6.781 47.164 -34.417 1.00 17.22 C
ATOM 7868 H LEU E 9 6.786 48.811 -39.228 1.00 18.60 H
ATOM 7869 HA LEU E 9 5.236 49.851 -37.249 1.00 20.12 H
ATOM 7870 HB2 LEU E 9 5.605 47.589 -36.809 1.00 21.03 H
ATOM 7871 HB3 LEU E 9 7.167 47.812 -36.935 1.00 21.03 H
ATOM 7872 HG LEU E 9 7.119 49.099 -34.970 1.00 20.00 H
ATOM 7873 HD11 LEU E 9 5.213 49.149 -33.644 1.00 26.51 H
ATOM 7874 HD12 LEU E 9 4.933 49.857 -35.038 1.00 26.51 H
ATOM 7875 HD13 LEU E 9 4.405 48.381 -34.776 1.00 26.51 H
ATOM 7876 HD21 LEU E 9 6.830 47.343 -33.465 1.00 20.67 H
ATOM 7877 HD22 LEU E 9 6.098 46.498 -34.594 1.00 20.67 H
ATOM 7878 HD23 LEU E 9 7.641 46.851 -34.740 1.00 20.67 H

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H
 ATOM 1579 HD2 TYR A 192 -13.015 23.564 -46.861 1.00 21.49
 H
 ATOM 1580 HE1 TYR A 192 -16.521 25.660 -44.706 1.00 18.54
 H
 ATOM 1581 HE2 TYR A 192 -12.788 24.210 -44.657 1.00 20.17
 H
 ATOM 1582 HH TYR A 192 -13.753 25.200 -42.872 1.00 22.72
 H
 ATOM 1583 N ALA A 193 -13.392 28.573 -48.078 1.00 14.04
 N
 ATOM 1584 CA ALA A 193 -12.184 27.021 -47.395 1.00 14.46
 C
 ATOM 1585 C ALA A 193 -12.528 27.614 -46.037 1.00 14.85
 C
 ATOM 1586 O ALA A 193 -13.669 28.005 -45.784 1.00 16.32
 O
 ATOM 1587 CB ALA A 193 -11.440 28.029 -48.233 1.00 16.01
 C
 ATOM 1588 H ALA A 193 -14.103 28.995 -47.843 1.00 16.85
 H
 ATOM 1589 HA ALA A 193 -11.600 26.260 -47.251 1.00 17.35
 H
 ATOM 1590 HB1 ALA A 193 -10.644 28.309 -47.756 1.00 19.22
 H
 ATOM 1591 HB2 ALA A 193 -11.194 27.617 -49.076 1.00 19.22
 H
 ATOM 1592 HB3 ALA A 193 -12.017 28.792 -48.393 1.00 19.22
 H
 ATOM 1593 N SER A 194 -11.534 27.675 -45.162 1.00 13.15
 N
 ATOM 1594 CA SER A 194 -11.726 28.278 -43.857 1.00 12.99
 C
 ATOM 1595 C SER A 194 -11.964 29.777 -44.025 1.00 15.13
 C
 ATOM 1596 O SER A 194 -11.387 30.378 -44.930 1.00 16.35
 O
 ATOM 1597 CB SER A 194 -10.507 28.029 -42.963 1.00 15.47
 C
 ATOM 1598 OG SER A 194 -10.547 28.856 -41.815 1.00 15.91
 O
 ATOM 1599 H SER A 194 -10.741 27.374 -45.301 1.00 15.78
 H
 ATOM 1600 HA SER A 194 -12.505 27.888 -43.431 1.00 15.59
 H
 ATOM 1601 HB2 SER A 194 -10.506 27.100 -42.684 1.00 18.57
 H
 ATOM 1602 HB3 SER A 194 -9.701 28.226 -43.466 1.00 18.57
 H
 ATOM 1603 HG SER A 194 -9.875 28.710 -41.333 1.00 19.09
 H
 ATOM 1604 N SER A 195 -12.803 30.394 -43.191 1.00 13.88
 N
 ATOM 1605 CA SER A 195 -13.586 29.735 -42.148 1.00 14.38
 C
 ATOM 1606 C SER A 195 -15.056 29.686 -42.571 1.00 18.17
 C
 ATOM 1607 O SER A 195 -15.731 30.717 -42.606 1.00 15.70
 O
 ATOM 1608 CB SER A 195 -13.442 30.477 -40.821 1.00 15.67
 C
 ATOM 1609 OG SER A 195 -14.164 29.810 -39.798 1.00 20.71
 O
 ATOM 1610 H SER A 195 -12.941 31.242 -43.215 1.00 16.65
 H
 ATOM 1611 HA SER A 195 -13.268 28.826 -42.029 1.00 17.26
 H
 ATOM 1612 HB2 SER A 195 -12.503 30.510 -40.577 1.00 18.81
 H
 ATOM 1613 HB3 SER A 195 -13.791 31.376 -40.922 1.00 18.81
 H
 ATOM 1614 HG SER A 195 -14.080 30.224 -39.071 1.00 24.86
 H
 ATOM 1615 N PHE A 196 -15.542 28.492 -42.898 1.00 14.12
 N
 ATOM 1616 CA PHE A 196 -16.912 28.314 -43.376 1.00 16.50
 C
 ATOM 1617 C PHE A 196 -17.212 29.262 -44.530 1.00 16.82
 C
 ATOM 1618 O PHE A 196 -18.205 29.992 -44.522 1.00 15.43
 O
 ATOM 1619 CB PHE A 196 -17.909 28.514 -42.233 1.00 19.48
 C
 ATOM 1620 CG PHE A 196 -17.900 27.392 -41.233 1.00 20.88
 C
 ATOM 1621 CD1 PHE A 196 -17.045 27.420 -40.146 1.00 19.36
 C
 ATOM 1622 CD2 PHE A 196 -18.734 26.300 -41.395 1.00 21.00
 C
 ATOM 1623 CE1 PHE A 196 -17.028 26.381 -39.233 1.00 22.54
 C
 ATOM 1624 CE2 PHE A 196 -18.722 25.259 -40.489 1.00 24.48
 C
 ATOM 1625 CZ PHE A 196 -17.868 25.297 -39.409 1.00 23.71
 C
 ATOM 1626 H PHE A 196 -15.093 27.760 -42.851 1.00 16.94
 H
 ATOM 1627 HA PHE A 196 -17.014 27.407 -43.703 1.00 19.80
 H
 ATOM 1628 HB2 PHE A 196 -17.689 29.334 -41.763 1.00 23.38
 H

H
 ATOM 7879 N GLU E 10 6.781 51.720 -36.979 1.00 18.79 N
 ATOM 7880 CA GLU E 10 7.726 52.814 -36.766 1.00 25.42 C
 ATOM 7881 C GLU E 10 7.809 53.176 -35.290 1.00 25.51 C
 ATOM 7882 O GLU E 10 6.822 53.608 -34.700 1.00 24.74 O
 ATOM 7883 CB GLU E 10 7.320 54.046 -37.582 1.00 23.36 C
 ATOM 7884 CG GLU E 10 8.326 55.197 -37.512 1.00 31.78 C
 C
 ATOM 7885 CD GLU E 10 7.883 56.420 -38.300 1.00 32.30 C
 C
 ATOM 7886 OE1 GLU E 10 6.687 56.775 -38.234 1.00 36.09 O
 O
 ATOM 7887 OE2 GLU E 10 8.732 57.026 -38.988 1.00 36.34 O1-
 ATOM 7888 H GLU E 10 5.958 51.949 -36.880 1.00 22.55 H
 ATOM 7889 HA GLU E 10 8.608 52.534 -37.059 1.00 30.51 H
 ATOM 7890 HB2 GLU E 10 7.230 53.788 -38.512 1.00 28.04 H
 H
 ATOM 7891 HB3 GLU E 10 6.471 54.375 -37.248 1.00 28.04 H
 H
 ATOM 7892 HG2 GLU E 10 8.438 55.482 -36.588 1.00 38.14 H
 H
 ATOM 7893 HG3 GLU E 10 9.174 54.897 -37.876 1.00 38.14 H
 H
 ATOM 7894 N ILE E 11 8.988 52.981 -34.703 1.00 28.61 N
 ATOM 7895 CA ILE E 11 9.253 53.384 -33.326 1.00 25.78 C
 ATOM 7896 C ILE E 11 10.184 54.588 -33.321 1.00 24.72 C
 ATOM 7897 O ILE E 11 11.369 54.450 -33.528 1.00 24.06 O
 ATOM 7898 CB ILE E 11 9.891 52.248 -32.498 1.00 31.17 C
 ATOM 7899 CG1 ILE E 11 9.015 50.995 -32.536 1.00 30.05 C
 ATOM 7900 CG2 ILE E 11 10.114 52.692 -31.056 1.00 30.83 C
 C
 ATOM 7901 CD1 ILE E 11 9.421 50.004 -33.599 1.00 30.44 C
 ATOM 7902 H ILE E 11 9.662 52.612 -35.089 1.00 34.34 H
 ATOM 7903 HA ILE E 11 8.420 53.640 -32.900 1.00 30.94 H
 ATOM 7904 HB ILE E 11 10.752 52.031 -32.888 1.00 37.40 H
 ATOM 7905 HG12 ILE E 11 9.070 50.548 -31.677 1.00 36.06 H
 H
 ATOM 7906 HG13 ILE E 11 8.098 51.259 -32.712 1.00 36.06 H
 H
 ATOM 7907 HG21 ILE E 11 10.515 51.962 -30.560 1.00 37.00 H
 H
 ATOM 7908 HG22 ILE E 11 10.706 53.461 -31.051 1.00 37.00 H
 H
 ATOM 7909 HG23 ILE E 11 9.259 52.930 -30.664 1.00 37.00 H
 H
 ATOM 7910 HD11 ILE E 11 8.824 49.240 -33.563 1.00 36.53 H
 H
 ATOM 7911 HD12 ILE E 11 9.361 50.431 -34.468 1.00 36.53 H
 H
 ATOM 7912 HD13 ILE E 11 10.334 49.719 -33.432 1.00 36.53 H
 H
 ATOM 7913 N ASN E 12 9.610 55.765 -33.095 1.00 26.17 N
 ATOM 7914 CA ASN E 12 10.364 57.010 -33.023 1.00 30.19 C
 C
 ATOM 7915 C ASN E 12 10.274 57.565 -31.611 1.00 33.21 C
 ATOM 7916 O ASN E 12 9.309 58.238 -31.259 1.00 28.03 O
 ATOM 7917 CB ASN E 12 9.830 58.023 -34.042 1.00 28.09 C
 ATOM 7918 CG ASN E 12 10.710 59.256 -34.166 1.00 34.34 C
 C
 ATOM 7919 OD1 ASN E 12 11.388 59.657 -33.218 1.00 28.23 O
 O
 ATOM 7920 ND2 ASN E 12 10.701 59.869 -35.347 1.00 37.26 N
 N
 ATOM 7921 H ASN E 12 8.765 55.869 -32.977 1.00 31.41 H
 ATOM 7922 HA ASN E 12 11.297 56.834 -33.225 1.00 36.22 H
 H
 ATOM 7923 HB2 ASN E 12 9.784 57.599 -34.914 1.00 33.71 H
 H
 ATOM 7924 HB3 ASN E 12 8.947 58.312 -33.766 1.00 33.71 H
 H
 ATOM 7925 HD21 ASN E 12 11.181 60.571 -35.471 1.00 44.71 H
 H
 ATOM 7926 HD22 ASN E 12 10.214 59.562 -35.986 1.00 44.71 H
 H
 ATOM 7927 N GLY E 13 11.280 57.273 -30.797 1.00 33.39 N
 ATOM 7928 CA GLY E 13 11.269 57.704 -29.414 1.00 37.75 N
 N

H
 ATOM 1629 HB3 PHE A 196 -18.803 28.576 -42.603 1.00 23.38
 H
 ATOM 1630 HD1 PHE A 196 -16.476 28.146 -40.027 1.00 23.23
 H
 ATOM 1631 HD2 PHE A 196 -19.310 26.267 -42.125 1.00 25.20
 H
 ATOM 1632 HE1 PHE A 196 -16.451 26.410 -38.504 1.00 27.05
 H
 ATOM 1633 HE2 PHE A 196 -19.290 24.532 -40.608 1.00 29.38
 H
 ATOM 1634 HZ PHE A 196 -17.862 24.598 -38.795 1.00 28.45
 H
 ATOM 1635 N LYS A 197 -16.328 29.240 -45.519 1.00 12.88
 N
 ATOM 1636 CA LYS A 197 -16.488 30.028 -46.726 1.00 14.65
 C
 ATOM 1637 C LYS A 197 -16.602 29.102 -47.924 1.00 20.06
 C
 ATOM 1638 O LYS A 197 -16.201 27.937 -47.864 1.00 15.47
 O
 ATOM 1639 CB LYS A 197 -15.316 30.995 -46.902 1.00 17.78
 C
 ATOM 1640 CG LYS A 197 -15.280 32.100 -45.858 1.00 18.13
 C

 ATOM 1641 CD LYS A 197 -14.046 32.976 -45.998 1.00 21.25
 C
 ATOM 1642 CE LYS A 197 -14.128 34.170 -45.061 1.00 21.78
 C
 ATOM 1643 NZ LYS A 197 -12.877 34.972 -45.042 1.00 22.18
 N1+
 ATOM 1644 H LYS A 197 -15.612 28.764 -45.511 1.00 15.45
 H
 ATOM 1645 HA LYS A 197 -17.305 30.547 -46.664 1.00 17.58
 H
 ATOM 1646 HB2 LYS A 197 -14.486 30.497 -46.837 1.00 21.34
 H
 ATOM 1647 HB3 LYS A 197 -15.382 31.413 -47.775 1.00 21.34
 H
 ATOM 1648 HG2 LYS A 197 -16.063 32.662 -45.962 1.00 21.75
 H
 ATOM 1649 HG3 LYS A 197 -15.269 31.702 -44.973 1.00 21.75
 H
 ATOM 1650 HD2 LYS A 197 -13.257 32.461 -45.770 1.00 25.49
 H
 ATOM 1651 HD3 LYS A 197 -13.985 33.305 -46.908 1.00 25.49
 H
 ATOM 1652 HE2 LYS A 197 -14.851 34.749 -45.349 1.00 26.13
 H
 ATOM 1653 HE3 LYS A 197 -14.295 33.854 -44.159 1.00 26.13
 H
 ATOM 1654 HZ1 LYS A 197 -12.703 35.282 -45.858 1.00 26.61
 H
 ATOM 1655 HZ2 LYS A 197 -12.965 35.659 -44.484 1.00 26.61
 H
 ATOM 1656 HZ3 LYS A 197 -12.196 34.466 -44.774 1.00 26.61
 H
 ATOM 1657 N GLY A 198 -17.172 29.632 -49.001 1.00 21.19
 N
 ATOM 1658 CA GLY A 198 -17.291 28.916 -50.256 1.00 20.02
 C
 ATOM 1659 C GLY A 198 -16.977 29.862 -51.394 1.00 18.77
 C
 ATOM 1660 O GLY A 198 -17.644 30.880 -51.561 1.00 21.65
 O
 ATOM 1661 H GLY A 198 -17.505 30.424 -49.026 1.00 25.43
 H
 ATOM 1662 HA2 GLY A 198 -16.667 28.173 -50.278 1.00 24.02
 H
 ATOM 1663 HA3 GLY A 198 -18.193 28.577 -50.364 1.00 24.02
 H
 ATOM 1664 N TYR A 199 -15.942 29.535 -52.160 1.00 17.44
 N
 ATOM 1665 CA TYR A 199 -15.521 30.351 -53.289 1.00 16.54
 C
 ATOM 1666 C TYR A 199 -16.048 29.768 -54.591 1.00 23.54
 C
 ATOM 1667 O TYR A 199 -15.735 28.630 -54.944 1.00 19.00
 O
 ATOM 1668 CB TYR A 199 -13.997 30.446 -53.349 1.00 17.44
 C
 ATOM 1669 CG TYR A 199 -13.376 31.238 -52.222 1.00 14.05
 C
 ATOM 1670 CD1 TYR A 199 -13.236 30.889 -50.958 1.00 15.06
 C
 ATOM 1671 CD2 TYR A 199 -12.912 32.529 -52.432 1.00 17.40
 C
 ATOM 1672 CE1 TYR A 199 -12.663 31.410 -49.926 1.00 17.80
 C
 ATOM 1673 CE2 TYR A 199 -12.332 33.255 -51.409 1.00 15.39
 C
 ATOM 1674 CZ TYR A 199 -12.213 32.690 -50.156 1.00 15.83
 C
 ATOM 1675 OH TYR A 199 -11.637 33.406 -49.131 1.00 18.67
 O

 ATOM 1676 H TYR A 199 -15.461 28.832 -52.043 1.00 20.93
 H
 ATOM 1677 HA TYR A 199 -15.878 31.247 -53.189 1.00 19.84
 H

C
 ATOM 7929 C GLY E 13 10.163 57.015 -28.639 1.00 37.43 C
 ATOM 7930 O GLY E 13 10.112 55.786 -28.582 1.00 37.21 O
 ATOM 7931 H GLY E 13 11.979 56.827 -31.024 1.00 40.07 H
 ATOM 7932 HA2 GLY E 13 12.120 57.492 -28.998 1.00 45.30
 H
 ATOM 7933 HA3 GLY E 13 11.130 58.663 -29.371 1.00 45.30
 H
 ATOM 7934 N SER E 14 9.260 57.809 -28.068 1.00 44.23 N
 ATOM 7935 CA SER E 14 8.265 57.294 -27.129 1.00 48.10 C
 ATOM 7936 C SER E 14 6.947 56.870 -27.780 1.00 45.20 C
 ATOM 7937 O SER E 14 6.185 56.108 -27.185 1.00 44.70 O
 ATOM 7938 CB SER E 14 7.978 58.343 -26.052 1.00 44.32 C
 ATOM 7939 OG SER E 14 7.497 59.546 -26.627 1.00 49.63
 O
 ATOM 7940 H SER E 14 9.201 58.655 -28.209 1.00 53.08 H

 ATOM 7941 HA SER E 14 8.635 56.514 -26.686 1.00 57.72 H
 ATOM 7942 HB2 SER E 14 7.309 57.995 -25.444 1.00 53.18
 H
 ATOM 7943 HB3 SER E 14 8.799 58.531 -25.570 1.00 53.18
 H
 ATOM 7944 HG SER E 14 7.345 60.111 -26.024 1.00 59.56
 H
 ATOM 7945 N ASP E 15 6.670 57.358 -28.986 1.00 47.04 N
 ATOM 7946 CA ASP E 15 5.445 56.970 -29.683 1.00 51.32 C
 ATOM 7947 C ASP E 15 5.751 55.979 -30.804 1.00 46.88 C
 ATOM 7948 O ASP E 15 6.834 55.997 -31.394 1.00 42.45 O
 ATOM 7949 CB ASP E 15 4.707 58.201 -30.229 1.00 55.08 C
 ATOM 7950 CG ASP E 15 5.515 58.970 -31.250 1.00 56.39
 C
 ATOM 7951 OD1 ASP E 15 6.755 58.979 -31.140 1.00 57.41
 O
 ATOM 7952 OD2 ASP E 15 4.907 59.575 -32.160 1.00 64.51
 O1-
 ATOM 7953 H ASP E 15 7.168 57.909 -29.420 1.00 56.44 H
 ATOM 7954 HA ASP E 15 4.855 56.529 -29.052 1.00 61.58 H
 ATOM 7955 HB2 ASP E 15 3.884 57.913 -30.654 1.00 66.10
 H
 ATOM 7956 HB3 ASP E 15 4.507 58.801 -29.493 1.00 66.10
 H
 ATOM 7957 N THR E 16 4.790 55.100 -31.069 1.00 40.99 N
 ATOM 7958 CA THR E 16 4.933 54.071 -32.088 1.00 35.68 C
 ATOM 7959 C THR E 16 3.735 54.097 -33.026 1.00 38.72 C
 ATOM 7960 O THR E 16 2.618 54.422 -32.613 1.00 33.45 O
 ATOM 7961 CB THR E 16 5.068 52.671 -31.464 1.00 38.05 C
 ATOM 7962 OG1 THR E 16 3.910 52.381 -30.674 1.00 48.80
 O
 ATOM 7963 CG2 THR E 16 6.302 52.596 -30.585 1.00 39.99
 C
 ATOM 7964 H THR E 16 4.032 55.080 -30.662 1.00 49.19 H
 ATOM 7965 HA THR E 16 5.731 54.249 -32.611 1.00 42.82 H
 ATOM 7966 HB THR E 16 5.153 52.009 -32.168 1.00 45.66 H
 ATOM 7967 HG1 THR E 16 3.980 51.618 -30.331 1.00 58.56
 H
 ATOM 7968 HG21 THR E 16 6.378 51.711 -30.196 1.00 47.99
 H
 ATOM 7969 HG22 THR E 16 7.095 52.779 -31.112 1.00 47.99
 H
 ATOM 7970 HG23 THR E 16 6.240 53.250 -29.871 1.00 47.99
 H
 ATOM 7971 N HIS E 17 3.974 53.758 -34.290 1.00 31.94 N
 ATOM 7972 CA HIS E 17 2.917 53.737 -35.295 1.00 33.04 C
 ATOM 7973 C HIS E 17 2.903 52.408 -36.036 1.00 25.75 C
 ATOM 7974 O HIS E 17 3.919 51.976 -36.579 1.00 21.85 O
 ATOM 7975 CB HIS E 17 3.093 54.890 -36.284 1.00 33.14 C
 ATOM 7976 CG HIS E 17 3.093 56.242 -35.639 1.00 43.36 C
 ATOM 7977 ND1 HIS E 17 4.024 56.024 35.099 1.00 40.99 N


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ATOM 1728 HA ASN A 202  -16.234  27.180 -62.994  1.00 30.67
H
ATOM 1729 HB2 ASN A 202  -14.329  28.256 -63.910  1.00 35.55
H
ATOM 1730 HB3 ASN A 202  -13.464  26.980 -63.526  1.00 35.55
H
ATOM 1731 HD21 ASN A 202  -14.466  27.009 -66.985  1.00 46.15
H
ATOM 1732 HD22 ASN A 202  -13.873  28.067 -66.121  1.00 46.15
H
ATOM 1733 N CYS A 203  -16.440  24.785 -62.627  1.00 28.75
N
ATOM 1734 CA CYS A 203  -16.574  23.364 -62.325  1.00 25.56
C
ATOM 1735 C CYS A 203  -15.508  22.513 -63.014  1.00 26.17
C
ATOM 1736 O CYS A 203  -15.174  21.430 -62.539  1.00 23.90
O
ATOM 1737 CB CYS A 203  -17.967  22.874 -62.726  1.00 25.82
C
ATOM 1738 SG CYS A 203  -19.313  23.627 -61.778  1.00 33.04
S
ATOM 1739 H CYS A 203  -17.148  25.136 -62.966  1.00 34.50
H
ATOM 1740 HA CYS A 203  -16.479  23.238 -61.368  1.00 30.67
H
ATOM 1741 HB2 CYS A 203  -18.112  23.081 -63.663  1.00 30.99
H
ATOM 1742 HB3 CYS A 203  -18.011  21.914 -62.592  1.00 30.99
H
ATOM 1743 N SER A 204  -14.962  23.015 -64.118  1.00 26.58
N
ATOM 1744 CA SER A 204  -14.011  22.250 -64.918  1.00 28.83
C
ATOM 1745 C SER A 204  -12.568  22.426 -64.464  1.00 29.48
C

ATOM 1746 O SER A 204  -11.670  21.765 -64.980  1.00 30.84
O
ATOM 1747 CB SER A 204  -14.130  22.646 -66.391  1.00 34.76
C
ATOM 1748 OG SER A 204  -15.399  22.282 -66.905  1.00 36.78
O
ATOM 1749 H SER A 204  -15.127  23.801 -64.426  1.00 31.89
H
ATOM 1750 HA SER A 204  -14.230  21.308 -64.847  1.00 34.60
H
ATOM 1751 HB2 SER A 204  -14.020  23.607 -66.470  1.00 41.72
H
ATOM 1752 HB3 SER A 204  -13.440  22.190 -66.898  1.00 41.72
H
ATOM 1753 HG SER A 204  -15.456  22.503 -67.713  1.00 44.13
H
ATOM 1754 N THR A 205  -12.342  23.313 -63.501  1.00 30.18
N
ATOM 1755 CA THR A 205  -10.991  23.564 -63.010  1.00 31.93
C
ATOM 1756 C THR A 205  -10.595  22.490 -62.002  1.00 26.32
C
ATOM 1757 O THR A 205  -11.300  22.280 -61.017  1.00 27.11
O
ATOM 1758 CB THR A 205  -10.880  24.953 -62.354  1.00 30.33
C
ATOM 1759 OG1 THR A 205  -11.195  25.962 -63.322  1.00 32.74
O
ATOM 1760 CG2 THR A 205  -9.473  25.195 -61.822  1.00 28.31
C
ATOM 1761 H THR A 205  -12.951  23.783 -63.117  1.00 36.22
H
ATOM 1762 HA THR A 205  -10.369  23.528 -63.753  1.00 38.32
H
ATOM 1763 HB THR A 205  -11.503  25.011 -61.613  1.00 36.40
H
ATOM 1764 HG1 THR A 205  -10.660  25.917 -63.968  1.00 39.29
H
ATOM 1765 HG21 THR A 205  -9.420  26.073 -61.413  1.00 33.97
H
ATOM 1766 HG22 THR A 205  -9.250  24.524 -61.158  1.00 33.97
H
ATOM 1767 HG23 THR A 205  -8.831  25.146 -62.547  1.00 33.97
H
ATOM 1768 N PRO A 206  -9.462  21.808 -62.235  1.00 25.18
N
ATOM 1769 CA PRO A 206  -9.103  20.744 -61.290  1.00 27.92
C
ATOM 1770 C PRO A 206  -8.728  21.285 -59.913  1.00 27.31
C
ATOM 1771 O PRO A 206  -8.020  22.285 -59.806  1.00 24.19
O
ATOM 1772 CB PRO A 206  -7.918  20.051 -61.963  1.00 27.16
C
ATOM 1773 CG PRO A 206  -7.340  21.073 -62.876  1.00 35.92
C
ATOM 1774 CD PRO A 206  -8.479  21.937 -63.326  1.00 32.59
C
ATOM 1775 HA PRO A 206  -9.839  20.113 -61.199  1.00 33.50
H
ATOM 1776 HB2 PRO A 206  -7.271  19.786 -61.290  1.00 32.59
H
ATOM 1777 HB3 PRO A 206  -8.229  19.280 -62.463  1.00 32.59
H

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ATOM 8028 HG22 VAL E 20  0.075  46.311 -41.496  1.00 18.75
H
ATOM 8029 HG23 VAL E 20  -1.109  47.074 -40.761  1.00 18.75
H

ATOM 8030 N ASP E 21  -0.848  48.729 -45.518  1.00 15.97  N
ATOM 8031 CA ASP E 21  -1.440  49.125 -46.794  1.00 21.15  C
ATOM 8032 C ASP E 21  -1.657  47.896 -47.664  1.00 18.26  C
ATOM 8033 O ASP E 21  -0.754  47.072 -47.817  1.00 17.18  O
ATOM 8034 CB ASP E 21  -0.544  50.116 -47.543  1.00 22.93  C
ATOM 8035 CG ASP E 21  -0.289  51.386 -46.761  1.00 24.35  C
ATOM 8036 OD1 ASP E 21  -1.220  51.871 -46.088  1.00 25.88  O1-
ATOM 8037 OD2 ASP E 21  0.849  51.897 -46.822  1.00 27.99  O

ATOM 8038 H ASP E 21  -0.070  48.373 -45.604  1.00 19.17  H
ATOM 8039 HA ASP E 21  -2.300  49.546 -46.635  1.00 25.38  H
ATOM 8040 HB2 ASP E 21  0.312  49.696 -47.720  1.00 27.51  H
ATOM 8041 HB3 ASP E 21  -0.973  50.360 -48.378  1.00 27.51  H

ATOM 8042 N VAL E 22  -2.853  47.775 -48.230  1.00 15.73  N
ATOM 8043 CA VAL E 22  -3.147  46.699 -49.170  1.00 16.91  C
ATOM 8044 C VAL E 22  -3.314  47.289 -50.559  1.00 18.18  C
ATOM 8045 O VAL E 22  -4.196  48.120 -50.785  1.00 18.14  O

ATOM 8046 CB VAL E 22  -4.411  45.929 -48.787  1.00 13.15  C
ATOM 8047 CG1 VAL E 22  -4.570  44.701 -49.670  1.00 18.48  C
ATOM 8048 CG2 VAL E 22  -4.362  45.523 -47.319  1.00 14.73  C

ATOM 8049 H VAL E 22  -3.514  48.305 -48.086  1.00 18.86  H
ATOM 8050 HA VAL E 22  -2.403  46.077 -49.189  1.00 20.29  H

ATOM 8051 HB VAL E 22  -5.184  46.499 -48.919  1.00 15.79  H
ATOM 8052 HG11 VAL E 22  -5.376  44.228 -49.411  1.00 22.17  H
ATOM 8053 HG12 VAL E 22  -4.635  44.985 -50.595  1.00 22.17  H
ATOM 8054 HG13 VAL E 22  -3.797  44.127 -49.554  1.00 22.17  H
ATOM 8055 HG21 VAL E 22  -5.172  45.036 -47.099  1.00 17.68  H
ATOM 8056 HG22 VAL E 22  -3.587  44.958 -47.173  1.00 17.68  H
ATOM 8057 HG23 VAL E 22  -4.298  46.322 -46.773  1.00 17.68  H

ATOM 8058 N ASP E 23  -2.464  46.854 -51.482  1.00 15.34  N
ATOM 8059 CA ASP E 23  -2.482  47.357 -52.849  1.00 19.21  C
ATOM 8060 C ASP E 23  -2.905  46.259 -53.817  1.00 19.78  C
ATOM 8061 O ASP E 23  -2.353  45.158 -53.794  1.00 18.41  O

ATOM 8062 CB ASP E 23  -1.103  47.894 -53.253  1.00 21.71  C
ATOM 8063 CG ASP E 23  -0.614  49.015 -52.347  1.00 27.17  C
ATOM 8064 OD1 ASP E 23  -1.453  49.705 -51.735  1.00 25.29  O
ATOM 8065 OD2 ASP E 23  0.618  49.212 -52.256  1.00 37.02  O1-

ATOM 8066 H ASP E 23  -1.859  46.260 -51.339  1.00 18.40  H
ATOM 8067 HA ASP E 23  -3.122  48.083 -52.914  1.00 23.05  H
ATOM 8068 HB2 ASP E 23  -0.458  47.171 -53.209  1.00 26.06  H
ATOM 8069 HB3 ASP E 23  -1.152  48.240 -54.157  1.00 26.06  H

ATOM 8070 N LEU E 24  -3.888  46.567 -54.659  1.00 16.92  N
ATOM 8071 CA LEU E 24  -4.251  45.703 -55.777  1.00 17.78  C
ATOM 8072 C LEU E 24  -3.735  46.318 -57.072  1.00 20.26  C
ATOM 8073 O LEU E 24  -4.165  47.398 -57.462  1.00 21.27  O

ATOM 8074 CB LEU E 24  -5.768  45.506 -55.844  1.00 17.65  C
ATOM 8075 CG LEU E 24  -6.282  44.629 -56.988  1.00 20.38  C
ATOM 8076 GD1 LEU E 24  -5.743  43.211 -56.874  1.00 20.35  C
ATOM 8077 CD2 LEU E 24  -7.803  44.623 -57.009  1.00 21.16  C

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ATOM 1977 O GLY B 97 -10.551 2.054 -30.663 1.00 39.96 O	ATOM 8277 HG12 ILE E 37 -9.455 47.707 -43.344 1.00 20.70 H
ATOM 1978 H GLY B 97 -10.944 3.474 -32.680 1.00 39.71 H	ATOM 8278 HG13 ILE E 37 -8.002 47.999 -42.770 1.00 20.70 H
ATOM 1979 HA2 GLY B 97 -10.917 4.918 -30.800 1.00 37.46 H	ATOM 8279 HG21 ILE E 37 -10.905 46.411 -41.372 1.00 24.84 H
ATOM 1980 HA3 GLY B 97 -12.426 4.497 -30.648 1.00 37.46 H	ATOM 8280 HG22 ILE E 37 -11.209 47.550 -40.307 1.00 24.84 H
ATOM 1981 N PRO B 98 -11.429 3.019 -28.821 1.00 38.20 N	ATOM 8281 HG23 ILE E 37 -11.401 47.841 -41.858 1.00 24.84 H
ATOM 1982 CA PRO B 98 -12.139 4.096 -28.120 1.00 36.03 C	ATOM 8282 HD11 ILE E 37 -8.090 45.864 -43.663 1.00 20.64 H
ATOM 1983 C PRO B 98 -11.312 5.373 -27.973 1.00 35.11 C	ATOM 8283 HD12 ILE E 37 -7.823 45.784 -42.099 1.00 20.64 H
ATOM 1984 O PRO B 98 -10.086 5.318 -27.863 1.00 34.34 O	ATOM 8284 HD13 ILE E 37 -9.275 45.492 -42.673 1.00 20.64 H
ATOM 1985 CB PRO B 98 -12.439 3.480 -26.749 1.00 43.03 C	ATOM 8285 N ARG E 38 -10.007 50.450 -43.072 1.00 17.17 N
ATOM 1986 CG PRO B 98 -11.379 2.466 -26.551 1.00 44.90 C	ATOM 8286 CA ARG E 38 -10.945 51.180 -43.913 1.00 18.63 C
ATOM 1987 CD PRO B 98 -11.075 1.914 -27.912 1.00 43.35 C	ATOM 8287 C ARG E 38 -10.673 50.981 -45.400 1.00 15.53 C
ATOM 1988 HA PRO B 98 -12.973 4.301 -28.570 1.00 43.23 H	ATOM 8288 O ARG E 38 -9.529 50.822 -45.817 1.00 13.55 O
ATOM 1989 HB2 PRO B 98 -12.392 4.165 -26.065 1.00 51.64 H	ATOM 8289 CB ARG E 38 -10.905 52.672 -43.576 1.00 21.12 C
ATOM 1990 HB3 PRO B 98 -13.315 3.064 -26.761 1.00 51.64 H	ATOM 8290 CG ARG E 38 -9.612 53.367 -43.935 1.00 24.59 C
ATOM 1991 HG2 PRO B 98 -10.593 2.888 -26.172 1.00 53.88 H	ATOM 8291 CD ARG E 38 -9.832 54.826 -43.497 1.00 34.01 C
ATOM 1992 HG3 PRO B 98 -11.706 1.765 -25.965 1.00 53.88 H	ATOM 8292 NE ARG E 38 -8.473 55.561 -44.000 1.00 36.68 N
ATOM 1993 HD2 PRO B 98 -10.131 1.703 -27.988 1.00 52.02 H	ATOM 8293 CZ ARG E 38 -8.437 56.219 -45.156 1.00 39.43 C
ATOM 1994 HD3 PRO B 98 -11.628 1.138 -28.093 1.00 52.02 H	ATOM 8294 NH1 ARG E 38 -9.501 56.252 -45.953 1.00 38.87 N1+
ATOM 1995 N CYS B 99 -11.999 6.510 -27.991 1.00 28.31 N	ATOM 8295 NH2 ARG E 38 -7.330 56.851 -45.519 1.00 39.19 N
ATOM 1996 CA CYS B 99 -11.382 7.814 -27.782 1.00 31.04 C	ATOM 8296 H ARG E 38 -9.253 50.270 -43.444 1.00 20.60 H
ATOM 1997 C CYS B 99 -12.176 8.587 -26.750 1.00 29.57 C	ATOM 8297 HA ARG E 38 -11.842 50.859 -43.729 1.00 22.36 H
ATOM 1998 O CYS B 99 -13.297 8.207 -26.419 1.00 34.43 O	ATOM 8298 HB2 ARG E 38 -11.621 53.117 -44.056 1.00 25.34 H
ATOM 1999 CB CYS B 99 -11.330 8.620 -29.080 1.00 22.49 C	ATOM 8299 HB3 ARG E 38 -11.040 52.777 -42.621 1.00 25.34 H
ATOM 2000 SG CYS B 99 -10.222 7.973 -30.330 1.00 25.81 S	ATOM 8300 HG2 ARG E 38 -8.874 52.925 -43.487 1.00 29.50 H
ATOM 2001 H CYS B 99 -12.847 6.552 -28.127 1.00 33.97 H	ATOM 8301 HG3 ARG E 38 -9.488 53.339 -44.896 1.00 29.50 H
ATOM 2002 HA CYS B 99 -10.477 7.697 -27.453 1.00 37.25 H	ATOM 8302 HD2 ARG E 38 -10.433 55.252 -43.841 1.00 40.81 H
ATOM 2003 HB2 CYS B 99 -12.220 8.645 -29.464 1.00 26.99 H	ATOM 8303 HD3 ARG E 38 -9.621 54.869 -42.528 1.00 40.81 H
ATOM 2004 HB3 CYS B 99 -11.040 9.522 -28.872 1.00 26.99 H	ATOM 8304 HE ARG E 38 -7.764 55.568 -43.514 1.00 44.02 H
ATOM 2005 N PRO B 100 -11.599 9.682 -26.237 1.00 32.75 N	ATOM 8305 HH11 ARG E 38 -10.222 55.844 -45.724 1.00 46.64 H
ATOM 2006 CA PRO B 100 -12.421 10.607 -25.458 1.00 27.02 C	ATOM 8306 HH12 ARG E 38 -9.467 56.681 -46.698 1.00 46.64 H
ATOM 2007 C PRO B 100 -13.576 11.111 -26.303 1.00 29.55 C	ATOM 8307 HH21 ARG E 38 -6.639 56.834 -45.008 1.00 47.03 H
ATOM 2008 O PRO B 100 -13.455 11.152 -27.535 1.00 23.90 O	ATOM 8308 HH22 ARG E 38 -7.304 57.279 -46.264 1.00 47.03 H
ATOM 2009 CB PRO B 100 -11.450 11.733 -25.099 1.00 26.53 C	ATOM 8309 N PRO E 39 -11.746 50.991 -46.210 1.00 16.34 N
ATOM 2010 CG PRO B 100 -10.094 11.101 -25.168 1.00 24.03 C	ATOM 8310 CA PRO E 39 -11.558 50.928 -47.660 1.00 17.96 C
ATOM 2011 CD PRO B 100 -10.181 10.084 -26.262 1.00 29.20 C	ATOM 8311 C PRO E 39 -11.021 52.249 -48.203 1.00 17.79 C
ATOM 2012 HA PRO B 100 -12.756 10.184 -24.652 1.00 32.42 H	ATOM 8312 O PRO E 39 -11.322 53.300 -47.639 1.00 17.56 O
ATOM 2013 HB2 PRO B 100 -11.528 12.452 -25.745 1.00 31.83 H	ATOM 8313 CB PRO E 39 -12.968 50.636 -48.183 1.00 16.77 C
ATOM 2014 HB3 PRO B 100 -11.635 12.053 -24.202 1.00 31.83 H	ATOM 8314 CG PRO E 39 -13.872 51.230 -47.161 1.00 25.13 C
ATOM 2015 HG2 PRO B 100 -9.431 11.776 -25.381 1.00 28.84 H	ATOM 8315 CD PRO E 39 -13.172 51.069 -45.840 1.00 16.34 C
ATOM 2016 HG3 PRO B 100 -9.890 10.676 -24.321 1.00 28.84 H	ATOM 8316 HA PRO E 39 -10.961 50.203 -47.900 1.00 21.55 H
ATOM 2017 HD2 PRO B 100 -9.957 10.486 -27.116 1.00 35.04 H	ATOM 8317 HB2 PRO E 39 -13.095 51.063 -49.045 1.00 20.12 H
ATOM 2018 HD3 PRO B 100 -9.610 9.325 -26.064 1.00 35.04 H	ATOM 8318 HB3 PRO E 39 -13.103 49.678 -48.249 1.00 20.12 H
ATOM 2019 N LYS B 101 -14.678 11.479 -25.668 1.00 32.78 N	ATOM 8319 HG2 PRO E 39 -14.013 52.169 -47.360 1.00 30.16 H
ATOM 2020 CA LYS B 101 -15.875 11.896 -26.387 1.00 39.36 C	ATOM 8320 HG3 PRO E 39 -14.716 50.753 -47.159 1.00 30.16 H
ATOM 2021 C LYS B 101 -15.597 13.072 -27.325 1.00 32.37 C	ATOM 8321 HD2 PRO E 39 -13.332 51.842 -45.276 1.00 19.60 H
ATOM 2022 O LYS B 101 -14.877 14.005 -26.970 1.00 30.08 O	ATOM 8322 HD3 PRO E 39 -13.453 50.249 -45.406 1.00 19.60 H
ATOM 2023 CB LYS B 101 -16.984 12.266 -25.396 1.00 44.44 C	ATOM 8323 N THR E 40 -10.224 52.189 -49.267 1.00 16.36 N
ATOM 2024 CG LYS B 101 -18.332 12.570 -26.041 1.00 61.82 C	ATOM 8324 CA THR E 40 -9.672 53.389 -49.895 1.00 18.13 C
ATOM 2025 CD LYS B 101 -18.865 11.378 -26.824 1.00 74.76 C	ATOM 8325 C THR E 40 -9.954 53.377 -51.393 1.00 18.97 C

ATOM 2076 HZ2 TRP B 103 -6.761 13.373 -24.694 1.00 23.73
 H
 ATOM 2077 HZ3 TRP B 103 -6.578 12.953 -27.188 1.00 30.01
 H
 ATOM 2078 HH2 TRP B 103 -6.787 14.323 -25.336 1.00 21.37
 H
 ATOM 2079 N ILE B 104 -11.452 13.725 -32.566 1.00 17.20
 N
 ATOM 2080 CA ILE B 104 -11.198 13.133 -33.873 1.00 21.24
 C
 ATOM 2081 C ILE B 104 -10.616 11.753 -33.647 1.00 24.16
 C
 ATOM 2082 O ILE B 104 -9.835 11.559 -32.719 1.00 23.98
 O
 ATOM 2083 CB ILE B 104 -10.215 13.966 -34.726 1.00 21.34
 C
 ATOM 2084 CG1 ILE B 104 -10.796 15.348 -35.026 1.00 22.32
 C
 ATOM 2085 CG2 ILE B 104 -9.876 13.230 -36.033 1.00 24.29
 C
 ATOM 2086 CD1 ILE B 104 -9.849 16.253 -35.781 1.00 28.99
 C
 ATOM 2087 H ILE B 104 -10.949 14.396 -32.377 1.00 20.64
 H
 ATOM 2088 HA ILE B 104 -12.032 13.044 -34.359 1.00 25.48
 H
 ATOM 2089 HB ILE B 104 -9.395 14.083 -34.221 1.00 25.61
 H
 ATOM 2090 HG12 ILE B 104 -11.597 15.241 -35.564 1.00 26.78
 H
 ATOM 2091 HG13 ILE B 104 -11.018 15.783 -34.188 1.00 26.78
 H
 ATOM 2092 HG21 ILE B 104 -9.259 13.772 -36.550 1.00 29.15
 H
 ATOM 2093 HG22 ILE B 104 -9.467 12.377 -35.818 1.00 29.15
 H
 ATOM 2094 HG23 ILE B 104 -10.693 13.088 -36.536 1.00 29.15
 H
 ATOM 2095 HD11 ILE B 104 -10.283 17.107 -35.934 1.00 34.79
 H

ATOM 2096 HD12 ILE B 104 -9.046 16.381 -35.252 1.00 34.79
 H
 ATOM 2097 HD13 ILE B 104 -9.624 15.839 -36.628 1.00 34.79
 H
 ATOM 2098 N CYS B 105 -11.001 10.800 -34.489 1.00 22.22
 N
 ATOM 2099 CA CYS B 105 -10.421 9.462 -34.455 1.00 24.13
 C
 ATOM 2100 C CYS B 105 -9.930 9.120 -35.853 1.00 25.68
 C
 ATOM 2101 O CYS B 105 -10.660 9.288 -36.830 1.00 25.12
 O
 ATOM 2102 CB CYS B 105 -11.440 8.433 -33.962 1.00 25.61
 C
 ATOM 2103 SG CYS B 105 -10.702 6.857 -33.461 1.00 33.63
 S
 ATOM 2104 H CYS B 105 -11.602 10.904 -35.096 1.00 26.67
 H
 ATOM 2105 HA CYS B 105 -9.661 9.455 -33.852 1.00 28.95
 H
 ATOM 2106 HB2 CYS B 105 -11.908 8.799 -33.195 1.00 30.73
 H
 ATOM 2107 HB3 CYS B 105 -12.071 8.251 -34.676 1.00 30.73
 H
 ATOM 2108 N TYR B 106 -3.689 8.653 -35.949 1.00 22.66
 N
 ATOM 2109 CA TYR B 106 -8.061 8.421 -37.245 1.00 21.90
 C
 ATOM 2110 C TYR B 106 -6.840 7.512 -37.140 1.00 29.80
 C
 ATOM 2111 O TYR B 106 -5.832 7.876 -36.531 1.00 19.08
 O
 ATOM 2112 CB TYR B 106 -7.656 9.754 -37.874 1.00 22.79
 C
 ATOM 2113 CG TYR B 106 -7.090 9.639 -39.271 1.00 21.75
 C
 ATOM 2114 CD1 TYR B 106 -7.886 9.228 -40.333 1.00 23.00
 C
 ATOM 2115 CD2 TYR B 106 -5.766 9.961 -39.532 1.00 22.30
 C
 ATOM 2116 CE1 TYR B 106 -7.375 9.131 -41.614 1.00 22.33
 C
 ATOM 2117 CE2 TYR B 106 -5.247 9.871 -40.811 1.00 23.29
 C
 ATOM 2118 CZ TYR B 106 -6.056 9.455 -41.846 1.00 24.28
 C
 ATOM 2119 OH TYR B 106 -5.543 9.363 -43.116 1.00 28.23
 O
 ATOM 2120 H TYR B 106 -8.188 8.462 -35.277 1.00 27.19
 H
 ATOM 2121 HA TYR B 106 -8.703 7.995 -37.834 1.00 26.28
 H
 ATOM 2122 HB2 TYR B 106 -8.438 10.326 -37.919 1.00 27.35
 H
 ATOM 2123 HB3 TYR B 106 -6.980 10.168 -37.315 1.00 27.35
 H
 ATOM 2124 HD1 TYR B 106 -8.777 9.010 -40.179 1.00 27.60
 H
 ATOM 2125 HD2 TYR B 106 -5.218 10.244 -38.838 1.00 26.77
 H
 ATOM 2126 HE1 TYR B 106 -7.919 8.852 -42.315 1.00 26.80

ATOM 8376 CD1 PHE E 43 -13.203 46.434 -53.040 1.00 20.54
 C
 ATOM 8377 CD2 PHE E 43 -12.382 48.296 -56.303 1.00 22.45
 C
 ATOM 8378 CE1 PHE E 43 -11.912 45.996 -54.859 1.00 21.86
 C
 ATOM 8379 CE2 PHE E 43 -11.085 47.839 -56.127 1.00 25.06
 C
 ATOM 8380 CZ PHE E 43 -10.852 46.686 -55.403 1.00 20.17
 C
 ATOM 8381 H PHE E 43 -14.228 50.361 -55.133 1.00 26.57
 H
 ATOM 8382 HA PHE E 43 -16.434 48.922 -54.926 1.00 27.09
 H
 ATOM 8383 HB2 PHE E 43 -15.415 47.335 -56.156 1.00 27.54
 H
 ATOM 8384 HB3 PHE E 43 -14.854 48.702 -56.731 1.00 27.54
 H
 ATOM 8385 HD1 PHE E 43 -13.913 45.984 -54.667 1.00 24.65
 H
 ATOM 8386 HD2 PHE E 43 -12.532 49.074 -56.789 1.00 26.94
 H
 ATOM 8387 HE1 PHE E 43 -11.759 45.218 -54.372 1.00 26.23
 H
 ATOM 8388 HE2 PHE E 43 -10.372 48.309 -56.496 1.00 30.07
 H
 ATOM 8389 HZ PHE E 43 -9.983 46.378 -55.283 1.00 24.21
 H
 ATOM 8390 N MET E 44 -14.556 48.657 -52.513 1.00 23.05
 N
 ATOM 8391 CA MET E 44 -14.353 48.017 -51.212 1.00 21.06
 C
 ATOM 8392 C MET E 44 -15.333 48.520 -50.151 1.00 22.24
 C
 ATOM 8393 O MET E 44 -15.417 47.962 -49.059 1.00 19.63
 O
 ATOM 8394 CB MET E 44 -12.917 48.239 -50.730 1.00 19.76
 C
 ATOM 8395 CG MET E 44 -11.878 47.391 -51.456 1.00 21.55
 C
 ATOM 8396 SD MET E 44 -12.224 45.620 -51.414 1.00 21.18
 S
 ATOM 8397 CE MET E 44 -12.382 45.323 -49.660 1.00 17.95
 C
 ATOM 8398 H MET E 44 -14.167 49.420 -52.592 1.00 27.65
 H
 ATOM 8399 HA MET E 44 -14.480 47.061 -51.318 1.00 25.27
 H
 ATOM 8400 HB2 MET E 44 -12.685 49.171 -50.866 1.00 23.72
 H
 ATOM 8401 HB3 MET E 44 -12.869 48.023 -49.786 1.00 23.72
 H
 ATOM 8402 HG2 MET E 44 -11.846 47.665 -52.386 1.00 25.86
 H
 ATOM 8403 HG3 MET E 44 -11.013 47.534 -51.041 1.00 25.86
 H
 ATOM 8404 HE1 MET E 44 -12.572 44.383 -49.515 1.00 21.55
 H
 ATOM 8405 HE2 MET E 44 -11.550 45.564 -49.223 1.00 21.55
 H
 ATOM 8406 HE3 MET E 44 -13.107 45.865 -49.312 1.00 21.55
 H
 ATOM 8407 N ILE E 45 -16.073 49.575 -50.467 1.00 27.83
 N
 ATOM 8408 CA ILE E 45 -17.051 50.108 -49.527 1.00 22.95
 C
 ATOM 8409 C ILE E 45 -18.164 49.096 -49.288 1.00 21.71
 C
 ATOM 8410 O ILE E 45 -18.742 48.560 -50.231 1.00 21.43
 O
 ATOM 8411 CB ILE E 45 -17.634 51.442 -50.029 1.00 24.78
 C
 ATOM 8412 CG1 ILE E 45 -16.560 52.530 -49.916 1.00 25.65
 C
 ATOM 8413 CG2 ILE E 45 -18.877 51.838 -49.221 1.00 32.38
 C
 ATOM 8414 CD1 ILE E 45 -16.940 53.868 -50.511 1.00 38.64
 C
 ATOM 8415 H ILE E 45 -16.029 49.999 -51.214 1.00 33.40
 H
 ATOM 8416 HA ILE E 45 -16.612 50.275 -48.678 1.00 27.54
 H
 ATOM 8417 HB ILE E 45 -17.884 51.344 -50.961 1.00 29.73
 H
 ATOM 8418 HG12 ILE E 45 -16.363 52.572 -48.977 1.00 30.78
 H
 ATOM 8419 HG13 ILE E 45 -15.761 52.223 -50.372 1.00 30.78
 H
 ATOM 8420 HG21 ILE E 45 -19.219 52.680 -49.561 1.00 38.86
 H
 ATOM 8421 HG22 ILE E 45 -19.549 51.145 -49.316 1.00 38.86
 H
 ATOM 8422 HG23 ILE E 45 -18.630 51.934 -48.288 1.00 38.86
 H
 ATOM 8423 HD11 ILE E 45 -16.202 54.487 -50.392 1.00 46.36
 H
 ATOM 8424 HD12 ILE E 45 -17.125 53.752 -51.456 1.00 46.36
 H
 ATOM 8425 HD13 ILE E 45 -17.729 54.203 -50.057 1.00 46.36
 H

H
 ATOM 2176 HB3 ASN B 109 -3.825 9.328 -33.079 1.00 30.82
 H
 ATOM 2177 HD21 ASN B 109 -1.551 6.763 -32.448 1.00 34.32
 H
 ATOM 2178 HD22 ASN B 109 -2.728 7.355 -31.753 1.00 34.32
 H
 ATOM 2179 N CYS B 110 -6.355 9.262 -31.467 1.00 21.75
 N
 ATOM 2180 CA CYS B 110 -7.381 10.236 -31.115 1.00 19.96
 C
 ATOM 2181 C CYS B 110 -6.754 11.621 -31.065 1.00 20.85
 C
 ATOM 2182 O CYS B 110 -5.632 11.768 -30.591 1.00 18.06
 O
 ATOM 2183 CB CYS B 110 -8.015 9.899 -29.766 1.00 23.36
 C
 ATOM 2184 SG CYS B 110 -8.365 8.144 -29.523 1.00 28.07
 S
 ATOM 2185 H CYS B 110 -5.789 9.116 -30.836 1.00 26.10
 H
 ATOM 2186 HA CYS B 110 -8.076 10.235 -31.792 1.00 23.95
 H
 ATOM 2187 HB2 CYS B 110 -7.411 10.180 -29.061 1.00 28.03
 H
 ATOM 2188 HB3 CYS B 110 -8.854 10.380 -29.689 1.00 28.03
 H
 ATOM 2189 N TYR B 111 -7.475 12.626 -31.554 1.00 18.22
 N
 ATOM 2190 CA TYR B 111 -6.973 13.997 -31.572 1.00 16.26
 C
 ATOM 2191 C TYR B 111 -8.020 14.998 -31.110 1.00 18.87
 C
 ATOM 2192 O TYR B 111 -9.212 14.830 -31.370 1.00 17.84
 O
 ATOM 2193 CB TYR B 111 -6.517 14.392 -32.977 1.00 16.69
 C
 ATOM 2194 CG TYR B 111 -5.434 13.532 -33.571 1.00 17.24
 C
 ATOM 2195 CD1 TYR B 111 -4.095 13.773 -33.292 1.00 20.23
 C
 ATOM 2196 CD2 TYR B 111 -5.747 12.493 -34.436 1.00 19.87
 C
 ATOM 2197 CE1 TYR B 111 -3.102 12.992 -33.843 1.00 17.86
 C
 ATOM 2198 CE2 TYR B 111 -4.763 11.710 -34.994 1.00 19.29
 C
 ATOM 2199 CZ TYR B 111 -3.443 11.962 -34.696 1.00 19.83
 C
 ATOM 2200 OH TYR B 111 -2.463 11.177 -35.251 1.00 21.43
 O

H
 ATOM 8476 HD11 ILE E 49 -18.519 38.026 -48.983 1.00 36.14
 H
 ATOM 8477 HD12 ILE E 49 -17.400 39.047 -49.461 1.00 36.14
 H
 ATOM 8478 HD13 ILE E 49 -17.033 37.519 -49.224 1.00 36.14
 H
 ATOM 8479 N PHE E 50 -13.528 40.757 -46.443 1.00 14.54 N
 ATOM 8480 CA PHE E 50 -12.085 40.946 -46.383 1.00 17.11
 C
 ATOM 8481 C PHE E 50 -11.662 41.946 -45.309 1.00 16.26 C
 ATOM 8482 O PHE E 50 -10.690 41.706 -44.593 1.00 13.97
 O
 ATOM 8483 CB PHE E 50 -11.576 41.369 -47.758 1.00 15.93
 C
 ATOM 8484 CG PHE E 50 -11.833 40.337 -48.816 1.00 17.08
 C
 ATOM 8485 CD1 PHE E 50 -10.955 39.286 -49.001 1.00 17.90
 C
 ATOM 8486 CD2 PHE E 50 -12.980 40.391 -49.591 1.00 20.60
 C
 ATOM 8487 CE1 PHE E 50 -11.200 38.319 -49.958 1.00 19.37
 C
 ATOM 8488 CE2 PHE E 50 -13.230 39.428 -50.552 1.00 20.80
 C
 ATOM 8489 CZ PHE E 50 -12.342 38.391 -50.733 1.00 20.26
 C
 ATOM 8490 H PHE E 50 -13.927 41.248 -47.026 1.00 17.44 H
 ATOM 8491 HA PHE E 50 -11.672 40.095 -46.167 1.00 20.53
 H
 ATOM 8492 HB2 PHE E 50 -12.024 42.187 -48.023 1.00 19.11
 H
 ATOM 8493 HB3 PHE E 50 -10.618 41.515 -47.709 1.00 19.11
 H
 ATOM 8494 HD1 PHE E 50 -10.186 39.232 -48.480 1.00 21.48
 H
 ATOM 8495 HD2 PHE E 50 -13.584 41.088 -49.472 1.00 24.72
 H
 ATOM 8496 HE1 PHE E 50 -10.598 37.621 -50.081 1.00 23.24
 H
 ATOM 8497 HE2 PHE E 50 -13.999 39.479 -51.073 1.00 24.96
 H
 ATOM 8498 HZ PHE E 50 -12.507 37.744 -51.381 1.00 24.31
 H
 ATOM 8499 N LEU E 51 -12.392 43.050 -45.180 1.00 16.41 N
 ATOM 8500 CA LEU E 51 -12.055 44.057 -44.177 1.00 16.35
 C

ATOM 2201 H TYR B 111 -8.264 12.539 -31.884 1.00 21.87
 H
 ATOM 2202 HA TYR B 111 -6.209 14.064 -30.977 1.00 19.51
 H
 ATOM 2203 HB2 TYR B 111 -7.282 14.349 -33.571 1.00 20.03
 H
 ATOM 2204 HB3 TYR B 111 -6.181 15.302 -32.947 1.00 20.03
 H
 ATOM 2205 HD1 TYR B 111 -3.865 14.467 -32.717 1.00 24.28
 H
 ATOM 2206 HD2 TYR B 111 -6.638 12.321 -34.639 1.00 23.85
 H
 ATOM 2207 HE1 TYR B 111 -2.210 13.160 -33.644 1.00 21.44
 H
 ATOM 2208 HE2 TYR B 111 -4.988 11.013 -35.568 1.00 23.14
 H
 ATOM 2209 HH TYR B 111 -2.809 10.593 -35.746 1.00 25.72
 H
 ATOM 2210 N GLN B 112 -7.573 16.055 -30.444 1.00 16.37
 N
 ATOM 2211 CA GLN B 112 -8.440 17.199 -30.183 1.00 18.53
 C
 ATOM 2212 C GLN B 112 -7.660 18.496 -30.315 1.00 18.90
 C
 ATOM 2213 O GLN B 112 -6.506 18.591 -29.890 1.00 13.32
 O
 ATOM 2214 CB GLN B 112 -9.083 17.104 -28.798 1.00 18.31
 C
 ATOM 2215 CG GLN B 112 -10.016 18.266 -28.458 1.00 20.42
 C
 ATOM 2216 CD GLN B 112 -11.205 18.373 -29.402 1.00 22.22
 C
 ATOM 2217 OE1 GLN B 112 -11.057 18.710 -30.575 1.00 23.60
 O
 ATOM 2218 NE2 GLN B 112 -12.395 18.088 -28.886 1.00 27.09
 N
 ATOM 2219 H GLN B 112 -6.775 16.136 -30.133 1.00 19.65
 H
 ATOM 2220 HA GLN B 112 -9.152 17.210 -30.842 1.00 22.24
 H
 ATOM 2221 HB2 GLN B 112 -9.601 16.285 -28.751 1.00 21.98
 H
 ATOM 2222 HB3 GLN B 112 -8.380 17.085 -28.130 1.00 21.98
 H
 ATOM 2223 HG2 GLN B 112 -10.359 18.142 -27.559 1.00 24.51
 H
 ATOM 2224 HG3 GLN B 112 -9.517 19.096 -28.511 1.00 24.51
 H
 ATOM 2225 HE21 GLN B 112 -13.099 18.134 -29.378 1.00 32.51

ATOM 8501 C LEU E 51 -12.009 43.470 -42.757 1.00 15.68 C
 ATOM 8502 O LEU E 51 -11.023 43.865 -42.044 1.00 14.16 O
 ATOM 8503 CB LEU E 51 -13.045 45.228 -44.226 1.00 17.16
 C
 ATOM 8504 CG LEU E 51 -13.007 46.120 -45.473 1.00 18.54
 C
 ATOM 8505 CD1 LEU E 51 -14.064 47.212 -45.365 1.00 24.77
 C
 ATOM 8506 CD2 LEU E 51 -11.630 46.737 -45.699 1.00 22.00
 C
 ATOM 8507 H LEU E 51 -13.082 43.240 -45.657 1.00 19.69 H
 ATOM 8508 HA LEU E 51 -11.174 44.410 -44.377 1.00 19.62
 H
 ATOM 8509 HB2 LEU E 51 -13.943 44.866 -44.161 1.00 20.59
 H
 ATOM 8510 HB3 LEU E 51 -12.875 45.799 -43.461 1.00 20.59
 H
 ATOM 8511 HG LEU E 51 -13.219 45.579 -46.250 1.00 22.25
 H
 ATOM 8512 HD11 LEU E 51 -14.027 47.767 -46.160 1.00 29.72
 H
 ATOM 8513 HD12 LEU E 51 -14.938 46.799 -45.290 1.00 29.72
 H
 ATOM 8514 HD13 LEU E 51 -13.883 47.749 -44.578 1.00 29.72
 H
 ATOM 8515 HD21 LEU E 51 -11.659 47.289 -46.496 1.00 26.40
 H
 ATOM 8516 HD22 LEU E 51 -11.398 47.278 -44.929 1.00 26.40
 H
 ATOM 8517 HD23 LEU E 51 -10.981 46.025 -45.812 1.00 26.40
 H
 ATOM 8518 N PRO E 52 -13.065 42.750 -42.337 1.00 15.67
 N
 ATOM 8519 CA PRO E 52 -13.023 42.226 -40.962 1.00 16.66
 C
 ATOM 8520 C PRO E 52 -11.952 41.159 -40.777 1.00 15.48
 C
 ATOM 8521 O PRO E 52 -11.369 41.065 -39.700 1.00 15.44
 O
 ATOM 8522 CB PRO E 52 -14.425 41.638 -40.758 1.00 19.47
 C
 ATOM 8523 CG PRO E 52 -14.947 41.399 -42.123 1.00 23.22
 C
 ATOM 8524 CD PRO E 52 -14.344 42.450 -43.001 1.00 19.17
 C
 ATOM 8525 HA PRO E 52 -12.878 42.946 -40.328 1.00 19.99

''
ATOM 2325 HZ2 LYS B 118 -6.164 27.557 -20.680 1.00 42.23
H
ATOM 2326 HZ3 LYS B 118 -7.214 26.726 -20.129 1.00 42.23
H
ATOM 2327 N ASN B 119 0.236 28.473 -22.478 1.00 16.27
N
ATOM 2328 CA ASN B 119 1.659 28.241 -22.668 1.00 20.30
C
ATOM 2329 C ASN B 119 1.878 26.738 -22.763 1.00 16.48
C
ATOM 2330 O ASN B 119 0.946 25.951 -22.569 1.00 17.62
O
ATOM 2331 CB ASN B 119 2.499 28.869 -21.542 1.00 19.64
C
ATOM 2332 CG ASN B 119 2.262 28.228 -20.183 1.00 20.65
C
ATOM 2333 OD1 ASN B 119 2.498 27.035 -19.986 1.00 17.21
O
ATOM 2334 ND2 ASN B 119 1.823 29.036 -19.224 1.00 20.04
N
ATOM 2335 H ASN B 119 0.016 28.753 -21.695 1.00 19.52
H
ATOM 2336 HA ASN B 119 1.936 28.639 -23.508 1.00 24.36
H
ATOM 2337 HB2 ASN B 119 3.439 28.769 -21.759 1.00 23.57
H
ATOM 2338 HB3 ASN B 119 2.275 29.810 -21.471 1.00 23.57
H
ATOM 2339 HD21 ASN B 119 1.673 28.726 -18.436 1.00 24.05
H
ATOM 2340 HD22 ASN B 119 1.691 29.869 -19.391 1.00 24.05
H

ATOM 2341 N TRP B 120 3.102 26.333 -23.067 1.00 15.24
N
ATOM 2342 CA TRP B 120 3.362 24.930 -23.348 1.00 16.04
C
ATOM 2343 C TRP B 120 3.052 24.039 -22.148 1.00 19.13
C
ATOM 2344 O TRP B 120 2.588 22.909 -22.313 1.00 15.63
O
ATOM 2345 CB TRP B 120 4.813 24.733 -23.779 1.00 16.87
C
ATOM 2346 CG TRP B 120 5.085 23.340 -24.242 1.00 15.71
C
ATOM 2347 CD1 TRP B 120 5.006 22.874 -25.520 1.00 15.03
C
ATOM 2348 CD2 TRP B 120 5.465 22.226 -23.431 1.00 19.26
C
ATOM 2349 NE1 TRP B 120 5.318 21.540 -25.558 1.00 16.56
N
ATOM 2350 CE2 TRP B 120 5.604 21.116 -24.288 1.00 19.91
C
ATOM 2351 CE3 TRP B 120 5.703 22.059 -22.064 1.00 20.14
C
ATOM 2352 CZ2 TRP B 120 5.972 19.856 -23.823 1.00 20.45
C
ATOM 2353 CZ3 TRP B 120 6.068 20.807 -21.604 1.00 24.00
C
ATOM 2354 CH2 TRP B 120 6.199 19.721 -22.482 1.00 20.10
C
ATOM 2355 H TRP B 120 3.792 26.844 -23.117 1.00 18.29
H
ATOM 2356 HA TRP B 120 2.793 24.648 -24.082 1.00 19.25
H
ATOM 2357 HB2 TRP B 120 5.012 25.336 -24.510 1.00 20.25
H
ATOM 2358 HB3 TRP B 120 5.395 24.918 -23.025 1.00 20.25
H
ATOM 2359 HD1 TRP B 120 4.775 23.387 -26.261 1.00 18.03
H
ATOM 2360 HE1 TRP B 120 5.332 21.049 -26.264 1.00 19.88
H
ATOM 2361 HE3 TRP B 120 5.618 22.775 -21.476 1.00 24.16
H
ATOM 2362 HZ2 TRP B 120 6.060 19.134 -24.403 1.00 24.54
H
ATOM 2363 HZ3 TRP B 120 6.230 20.683 -20.697 1.00 28.80
H
ATOM 2364 HH2 TRP B 120 6.446 18.891 -22.144 1.00 24.12
H
ATOM 2365 N TYR B 121 3.297 24.553 -20.946 1.00 20.90
N
ATOM 2366 CA TYR B 121 3.179 23.750 -19.733 1.00 19.53
C
ATOM 2367 C TYR B 121 1.735 23.563 -19.268 1.00 17.33
C
ATOM 2368 O TYR B 121 1.386 22.498 -18.763 1.00 20.12
O
ATOM 2369 CB TYR B 121 4.006 24.375 -18.612 1.00 20.76
C
ATOM 2370 CG TYR B 121 5.478 24.438 -18.945 1.00 27.57
C
ATOM 2371 CD1 TYR B 121 6.266 23.294 -18.909 1.00 26.72
C
ATOM 2372 CD2 TYR B 121 6.077 25.635 -19.312 1.00 22.00
C
ATOM 2373 CE1 TYR B 121 7.607 23.343 -19.222 1.00 27.02
C
ATOM 2374 CE2 TYR B 121 7.418 25.893 -19.623 1.00 29.21
C

''
ATOM 8625 N PHE E 58 -4.216 41.746 -39.259 1.00 12.71 N
ATOM 8626 CA PHE E 58 -3.288 42.862 -39.119 1.00 12.91
C
ATOM 8627 C PHE E 58 -3.030 43.177 -37.645 1.00 15.14 C
ATOM 8628 O PHE E 58 -1.881 43.346 -37.236 1.00 12.36 O
ATOM 8629 CB PHE E 58 -3.814 44.103 -39.851 1.00 10.07
C
ATOM 8630 CG PHE E 58 -3.890 43.946 -41.352 1.00 13.18
C
ATOM 8631 CD1 PHE E 58 -3.394 42.810 -41.982 1.00 13.27
C
ATOM 8632 CD2 PHE E 58 -4.463 44.938 -42.135 1.00 15.09
C
ATOM 8633 CE1 PHE E 58 -3.470 42.667 -43.360 1.00 14.15
C
ATOM 8634 CE2 PHE E 58 -4.542 44.799 -43.518 1.00 14.94
C
ATOM 8635 CZ PHE E 58 -4.045 43.664 -44.127 1.00 15.54 C
ATOM 8636 H PHE E 58 -4.991 41.964 -39.561 1.00 15.25 H
ATOM 8637 HA PHE E 58 -2.441 42.616 -39.523 1.00 15.49
H
ATOM 8638 HB2 PHE E 58 -4.708 44.300 -39.529 1.00 12.09
H
ATOM 8639 HB3 PHE E 58 -3.226 44.850 -39.662 1.00 12.09
H
ATOM 8640 HD1 PHE E 58 -3.008 42.135 -41.471 1.00 15.93
H
ATOM 8641 HD2 PHE E 58 -4.801 45.703 -41.731 1.00 18.11
H
ATOM 8642 HE1 PHE E 58 -3.134 41.902 -43.768 1.00 16.98
H
ATOM 8643 HE2 PHE E 58 -4.928 45.471 -44.032 1.00 17.92
H
ATOM 8644 HZ PHE E 58 -4.095 43.571 -45.051 1.00 18.65 H
ATOM 8645 N SER E 59 -4.088 43.250 -36.844 1.00 12.44 N
ATOM 8646 CA SER E 59 -3.935 43.540 -35.418 1.00 15.47
C
ATOM 8647 C SER E 59 -3.058 42.488 -34.743 1.00 15.91 C
ATOM 8648 O SER E 59 -2.148 42.820 -33.978 1.00 14.84 O
ATOM 8649 CB SER E 59 -5.299 43.608 -34.727 1.00 19.05
C
ATOM 8650 OG SER E 59 -6.086 44.656 -35.260 1.00 26.66
O
ATOM 8651 H SER E 59 -4.902 43.137 -37.098 1.00 14.93 H
ATOM 8652 HA SER E 59 -3.503 44.402 -35.315 1.00 18.56
H
ATOM 8653 HB2 SER E 59 -5.763 42.766 -34.860 1.00 22.86
H
ATOM 8654 HB3 SER E 59 -5.165 43.766 -33.779 1.00 22.86
H
ATOM 8655 HG SER E 59 -6.211 44.532 -36.082 1.00 31.99
H
ATOM 8656 N GLU E 60 -3.325 41.221 -35.046 1.00 14.24 N
ATOM 8657 CA GLU E 60 -2.553 40.120 -34.483 1.00 16.03
C
ATOM 8658 C GLU E 60 -1.097 40.145 -34.956 1.00 14.22 C
ATOM 8659 O GLU E 60 -0.192 39.806 -34.197 1.00 18.48 O
ATOM 8660 CB GLU E 60 -3.198 38.780 -34.844 1.00 19.87
C
ATOM 8661 CG GLU E 60 -4.571 38.559 -34.219 1.00 27.96
C
ATOM 8662 CD GLU E 60 -4.514 38.305 -32.722 1.00 41.64
C
ATOM 8663 OE1 GLU E 60 -3.399 38.165 -32.175 1.00 41.26
O
ATOM 8664 OE2 GLU E 60 -5.592 38.243 -32.090 1.00 50.70
O1-
ATOM 8665 H GLU E 60 -3.952 40.972 -35.579 1.00 17.09 H
ATOM 8666 HA GLU E 60 -2.553 40.199 -33.517 1.00 19.30
H
ATOM 8667 HB2 GLU E 60 -3.302 38.734 -35.808 1.00 23.84
H
ATOM 8668 HB3 GLU E 60 -2.618 38.064 -34.543 1.00 23.84
H
ATOM 8669 HG2 GLU E 60 -5.114 39.348 -34.367 1.00 33.56
H
ATOM 8670 HG3 GLU E 60 -4.986 37.788 -34.637 1.00 33.56
H
ATOM 8671 N PHE E 61 -0.873 40.545 -36.208 1.00 15.60 N
ATOM 8672 CA PHE E 61 0.484 40.651 -36.745 1.00 14.83 C
ATOM 8673 C PHE E 61 1.364 41.506 -35.841 1.00 13.77 C
ATOM 8674 O PHE E 61 2.510 41.154 -35.556 1.00 15.86 O

DK/EP 3233192 T3

ATOM 2474 HE1 MET B 128 -0.994 13.260 -14.451 1.00 47.73
 H
 ATOM 2475 HE2 MET B 128 0.126 12.593 -15.359 1.00 47.73
 H
 ATOM 2476 HE3 MET B 128 0.540 13.426 -14.071 1.00 47.73
 H
 ATOM 2477 N SER B 129 -4.573 15.842 -18.029 1.00 29.26
 N
 ATOM 2478 CA SER B 129 -5.795 15.737 -17.233 1.00 32.80
 C
 ATOM 2479 C SER B 129 -6.901 14.984 -17.968 1.00 29.82
 C
 ATOM 2480 O SER B 129 -7.932 14.658 -17.381 1.00 30.42
 O

ATOM 2481 CB SER B 129 -6.296 17.127 -16.839 1.00 32.72
 C
 ATOM 2482 OG SER B 129 -6.872 17.799 -17.945 1.00 38.37
 O
 ATOM 2483 H SER B 129 -4.358 16.649 -18.235 1.00 35.11
 H
 ATOM 2484 HA SER B 129 -5.596 15.250 -16.418 1.00 39.36
 H
 ATOM 2485 HB2 SER B 129 -6.966 17.034 -16.144 1.00 39.26
 H
 ATOM 2486 HB3 SER B 129 -5.548 17.649 -16.509 1.00 39.26
 H
 ATOM 2487 HG SER B 129 -6.302 17.888 -18.556 1.00 46.05
 H
 ATOM 2488 N GLN B 130 -6.682 14.717 -19.251 1.00 32.61
 N
 ATOM 2489 CA GLN B 130 -7.630 13.962 -20.059 1.00 32.51
 C
 ATOM 2490 C GLN B 130 -7.007 12.648 -20.517 1.00 30.71
 C
 ATOM 2491 O GLN B 130 -7.402 12.083 -21.536 1.00 31.54
 O
 ATOM 2492 CB GLN B 130 -8.082 14.801 -21.255 1.00 34.47
 C
 ATOM 2493 CG GLN B 130 -8.648 16.155 -20.845 1.00 35.04
 C
 ATOM 2494 CD GLN B 130 -8.999 17.038 -22.023 1.00 35.73
 C
 ATOM 2495 OE1 GLN B 130 -9.762 16.647 -22.906 1.00 32.33
 O
 ATOM 2496 NE2 GLN B 130 -8.442 18.245 -22.040 1.00 42.10
 N
 ATOM 2497 H GLN B 130 -5.981 14.966 -19.681 1.00 39.14
 H
 ATOM 2498 HA GLN B 130 -8.411 13.755 -19.523 1.00 39.01
 H
 ATOM 2499 HB2 GLN B 130 -7.322 14.957 -21.837 1.00 41.37
 H
 ATOM 2500 HB3 GLN B 130 -8.774 14.319 -21.735 1.00 41.37
 H
 ATOM 2501 HG2 GLN B 130 -9.456 16.015 -20.327 1.00 42.05
 H
 ATOM 2502 HG3 GLN B 130 -7.988 16.822 -20.309 1.00 42.05
 H
 ATOM 2503 HE21 GLN B 130 -8.608 18.786 -22.687 1.00 50.53
 H
 ATOM 2504 HE22 GLN B 130 -7.915 18.484 -21.404 1.00 50.53
 H
 ATOM 2505 N ASN B 131 -6.032 12.168 -19.750 1.00 31.89
 N
 ATOM 2506 CA ASN B 131 -5.372 10.896 -20.028 1.00 35.86
 C
 ATOM 2507 C ASN B 131 -4.770 10.889 -21.431 1.00 35.32
 C
 ATOM 2508 O ASN B 131 -4.818 9.852 -22.125 1.00 31.56
 O
 ATOM 2509 CB ASN B 131 -6.358 9.740 -19.852 1.00 44.38
 C
 ATOM 2510 CG ASN B 131 -5.665 8.403 -19.679 1.00 65.46
 C
 ATOM 2511 OD1 ASN B 131 -5.153 8.093 -18.604 1.00 82.44
 O
 ATOM 2512 ND2 ASN B 131 -5.648 7.603 -20.737 1.00 73.37
 N
 ATOM 2513 H ASN B 131 -5.730 12.567 -19.050 1.00 38.26
 H
 ATOM 2514 HA ASN B 131 -4.650 10.772 -19.392 1.00 43.03
 H
 ATOM 2515 HB2 ASN B 131 -6.899 9.903 -19.063 1.00 53.26
 H

ATOM 2516 HB3 ASN B 131 -6.925 9.685 -20.638 1.00 53.26
 H
 ATOM 2517 HD21 ASN B 131 -5.267 6.833 -20.689 1.00 88.04
 H
 ATOM 2518 HD22 ASN B 131 -6.019 7.853 -21.472 1.00 88.04
 H
 ATOM 2519 N ALA B 132 -4.206 12.001 -21.838 1.00 25.52
 N
 ATOM 2520 CA ALA B 132 -3.593 12.132 -23.153 1.00 27.44
 C
 ATOM 2521 C ALA B 132 -2.264 12.868 -23.050 1.00 26.46
 C
 ATOM 2522 O ALA B 132 -1.802 13.178 -21.954 1.00 24.84
 O
 ATOM 2523 CB ALA B 132 -4.522 12.980 -24.100 1.00 34.38
 C

ATOM 8774 HB2 ARG E 66 8.743 39.094 -28.958 1.00 30.25
 H
 ATOM 8775 HB3 ARG E 66 8.190 39.588 -27.552 1.00 30.25
 H
 ATOM 8776 HG2 ARG E 66 6.013 38.803 -28.458 1.00 35.64
 H
 ATOM 8777 HG3 ARG E 66 6.939 37.901 -29.384 1.00 35.64
 H
 ATOM 8778 HD2 ARG E 66 7.142 37.828 -26.583 1.00 42.61
 H
 ATOM 8779 HD3 ARG E 66 6.195 36.831 -27.378 1.00 42.61
 H
 ATOM 8780 HE ARG E 66 8.901 36.691 -27.322 1.00 54.74
 H

ATOM 8781 HH11 ARG E 66 6.170 35.290 -28.581 1.00 58.11
 H
 ATOM 8782 HH12 ARG E 66 6.829 34.030 -29.025 1.00 58.11
 H
 ATOM 8783 HH21 ARG E 66 9.873 34.768 -27.999 1.00 60.99
 H
 ATOM 8784 HH22 ARG E 66 9.062 33.716 -28.674 1.00 60.99
 H

ATOM 8785 N ARG E 67 8.380 42.984 -29.513 1.00 18.67
 N
 ATOM 8786 CA ARG E 67 9.361 44.059 -29.578 1.00 20.20
 C
 ATOM 8787 C ARG E 67 10.020 44.281 -28.218 1.00 21.69
 C
 ATOM 8788 O ARG E 67 9.332 44.366 -27.204 1.00 17.08
 O
 ATOM 8789 CB ARG E 67 8.685 45.349 -30.057 1.00 21.97
 C
 ATOM 8790 CG ARG E 67 9.601 46.559 -30.135 1.00 27.90
 C
 ATOM 8791 CD ARG E 67 8.884 47.772 -30.720 1.00 40.95
 C
 ATOM 8792 NE ARG E 67 8.218 48.579 -29.698 1.00 59.70
 N
 ATOM 8793 CZ ARG E 67 6.960 48.412 -29.296 1.00 72.67
 C
 ATOM 8794 NH1 ARG E 67 6.199 47.460 -29.821 1.00 75.12
 N1+
 ATOM 8795 NH2 ARG E 67 6.457 49.206 -28.360 1.00 72.00
 N

ATOM 8796 H ARG E 67 7.587 43.230 -29.736 1.00 22.41
 H
 ATOM 8797 HA ARG E 67 10.053 43.823 -30.216 1.00 24.24
 H
 ATOM 8798 HB2 ARG E 67 8.323 45.197 -30.944 1.00 26.37
 H
 ATOM 8799 HB3 ARG E 67 7.964 45.566 -29.444 1.00 26.37
 H
 ATOM 8800 HG2 ARG E 67 9.906 45.787 -29.243 1.00 33.48
 H
 ATOM 8801 HG3 ARG E 67 10.358 46.350 -30.705 1.00 33.48
 H
 ATOM 8802 HD2 ARG E 67 9.532 48.335 -31.172 1.00 49.14
 H
 ATOM 8803 HD3 ARG E 67 8.211 47.468 -31.349 1.00 49.14
 H
 ATOM 8804 HE ARG E 67 8.673 49.208 -29.328 1.00 71.64
 H
 ATOM 8805 HH11 ARG E 67 6.518 46.941 -30.429 1.00 90.15
 H
 ATOM 8806 HH12 ARG E 67 5.388 47.361 -29.554 1.00 90.15
 H
 ATOM 8807 HH21 ARG E 67 6.944 49.825 -28.014 1.00 86.40
 H
 ATOM 8808 HH22 ARG E 67 5.645 49.101 -28.097 1.00 86.40
 H

ATOM 8809 N VAL E 68 11.348 44.362 -28.193 1.00 22.03
 N
 ATOM 8810 CA VAL E 68 12.059 44.659 -26.953 1.00 20.34
 C
 ATOM 8811 C VAL E 68 12.343 46.156 -26.894 1.00 22.74
 C
 ATOM 8812 O VAL E 68 12.682 46.762 -27.912 1.00 25.42
 O
 ATOM 8813 CB VAL E 68 13.384 43.867 -26.823 1.00 27.96
 C
 ATOM 8814 CG1 VAL E 68 13.108 42.374 -26.817 1.00 30.54
 C
 ATOM 8815 CG2 VAL E 68 14.361 44.220 -27.936 1.00 28.18
 C

ATOM 8816 H VAL E 68 11.858 44.250 -28.877 1.00 26.44
 H
 ATOM 8817 HA VAL E 68 11.494 44.428 -26.199 1.00 24.41
 H
 ATOM 8818 HB VAL E 68 13.803 44.095 -25.978 1.00 33.55
 H
 ATOM 8819 HG11 VAL E 68 13.950 41.899 -26.735 1.00 36.65
 H
 ATOM 8820 HG12 VAL E 68 12.534 42.163 -26.064 1.00 36.65
 H
 ATOM 8821 HG13 VAL E 68 12.670 42.131 -27.647 1.00 36.65
 H
 ATOM 8822 HG21 VAL E 68 15.174 43.705 -27.818 1.00 33.82
 H
 ATOM 8823 HG22 VAL E 68 13.051 44.009 -29.701 1.00 33.82
 H

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DK/EP 3233192 T3

ATOM 2523 CB ALA B 132 -4.533 12.880 -24.100 1.00 24.26
 C
 ATOM 2524 H ALA B 132 -4.166 12.717 -21.364 1.00 30.62
 H
 ATOM 2525 HA ALA B 132 -3.422 11.248 -23.515 1.00 32.93
 H
 ATOM 2526 HB1 ALA B 132 -4.107 12.937 -24.989 1.00 29.14
 H
 ATOM 2527 HB2 ALA B 132 -5.356 12.353 -24.179 1.00 29.14
 H
 ATOM 2528 HB3 ALA B 132 -4.719 13.742 -23.743 1.00 29.14
 H
 ATOM 2529 N SER B 133 -1.657 13.137 -24.201 1.00 21.19
 N
 ATOM 2530 CA SER B 133 -0.426 13.913 -24.270 1.00 20.84
 C
 ATOM 2531 C SER B 133 -0.540 14.942 -25.383 1.00 21.20
 C
 ATOM 2532 O SER B 133 -1.480 14.903 -26.177 1.00 19.82
 O
 ATOM 2533 CB SER B 133 0.776 13.001 -24.514 1.00 26.77
 C
 ATOM 2534 OG SER B 133 0.841 11.979 -23.535 1.00 32.82
 O
 ATOM 2535 H SER B 133 -1.844 12.875 -24.968 1.00 25.43
 H
 ATOM 2536 HA SER B 133 -0.292 14.381 -23.431 1.00 25.01
 H
 ATOM 2537 HB2 SER B 133 0.691 12.594 -25.390 1.00 32.13
 H
 ATOM 2538 HB3 SER B 133 1.588 13.530 -24.472 1.00 32.13
 H
 ATOM 2539 HG SER B 133 0.914 12.318 -22.770 1.00 39.39
 H
 ATOM 2540 N LEU B 134 0.404 15.873 -25.431 1.00 18.46
 N
 ATOM 2541 CA LEU B 134 0.479 16.796 -26.550 1.00 18.04
 C
 ATOM 2542 C LEU B 134 0.794 15.995 -27.806 1.00 21.00
 C
 ATOM 2543 O LEU B 134 1.303 14.877 -27.723 1.00 18.42
 O
 ATOM 2544 CB LEU B 134 1.540 17.869 -26.311 1.00 20.17
 C
 ATOM 2545 CG LEU B 134 1.167 18.973 -25.319 1.00 19.25
 C
 ATOM 2546 CD1 LEU B 134 2.400 19.780 -24.937 1.00 19.48
 C
 ATOM 2547 CD2 LEU B 134 0.096 19.889 -25.898 1.00 16.17
 C
 ATOM 2548 H LEU B 134 1.010 15.990 -24.831 1.00 22.15
 H
 ATOM 2549 HA LEU B 134 -0.379 17.231 -26.639 1.00 21.65
 H
 ATOM 2550 HB2 LEU B 134 2.341 17.437 -25.976 1.00 24.20
 H

ATOM 2551 HB3 LEU B 134 1.736 18.298 -27.159 1.00 24.20
 H
 ATOM 2552 HG LEU B 134 0.812 18.567 -24.513 1.00 23.10
 H
 ATOM 2553 HD11 LEU B 134 2.142 20.472 -24.308 1.00 23.37
 H
 ATOM 2554 HD12 LEU B 134 3.050 19.187 -24.528 1.00 23.37
 H
 ATOM 2555 HD13 LEU B 134 2.775 20.181 -25.736 1.00 23.37
 H
 ATOM 2556 HD21 LEU B 134 -0.117 20.576 -25.247 1.00 19.40
 H
 ATOM 2557 HD22 LEU B 134 0.435 20.297 -26.710 1.00 19.40
 H
 ATOM 2558 HD23 LEU B 134 -0.695 19.363 -26.097 1.00 19.40
 H
 ATOM 2559 N LEU B 135 0.486 16.570 -28.963 1.00 15.70
 N
 ATOM 2560 CA LEU B 135 0.693 15.894 -30.236 1.00 15.71
 C
 ATOM 2561 C LEU B 135 2.099 15.320 -30.370 1.00 18.68
 C
 ATOM 2562 O LEU B 135 3.084 16.020 -30.142 1.00 15.25
 O
 ATOM 2563 CB LEU B 135 0.430 16.862 -31.388 1.00 13.32
 C
 ATOM 2564 CG LEU B 135 0.715 16.342 -32.793 1.00 13.52
 C
 ATOM 2565 CD1 LEU B 135 -0.220 15.193 -33.142 1.00 16.61
 C
 ATOM 2566 CD2 LEU B 135 0.582 17.468 -33.796 1.00 13.74
 C
 ATOM 2567 H LEU B 135 0.152 17.359 -29.037 1.00 18.84
 H
 ATOM 2568 HA LEU B 135 0.062 15.161 -30.310 1.00 18.85
 H
 ATOM 2569 HB2 LEU B 135 -0.505 17.120 -31.360 1.00 15.99
 H
 ATOM 2570 HB3 LEU B 135 0.983 17.848 -31.255 1.00 15.99
 H
 ATOM 2571 HG LEU B 135 1.626 16.011 -32.831 1.00 16.22
 H
 ATOM 2572 HD11 LEU B 135 -0.017 14.882 -34.038 1.00 19.93
 H
 ATOM 2573 HD12 LEU B 135 -0.087 14.474 -32.504 1.00 19.93
 H

ATOM 8823 FB22 VAL E 68 13.804 44.006 -26.731 1.00 33.62
 H
 ATOM 8824 HG23 VAL E 68 14.560 45.169 -27.891 1.00 33.82
 H
 ATOM 8825 N PRO E 69 12.187 46.769 -25.710 1.00 21.06
 N
 ATOM 8826 CA PRO E 69 12.539 48.190 -25.618 1.00 24.69
 C
 ATOM 8827 C PRO E 69 14.021 48.401 -25.907 1.00 22.26
 C
 ATOM 8828 O PRO E 69 14.823 47.522 -25.593 1.00 19.66
 O
 ATOM 8829 CB PRO E 69 12.198 48.553 -24.168 1.00 20.34
 C
 ATOM 8830 CG PRO E 69 11.276 47.473 -23.698 1.00 22.90
 C
 ATOM 8831 CD PRO E 69 11.689 46.241 -24.428 1.00 24.19
 C
 ATOM 8832 HA PRO E 69 12.002 48.721 -26.227 1.00 29.63
 H
 ATOM 8833 HB2 PRO E 69 13.009 48.566 -23.636 1.00 24.40
 H
 ATOM 8834 HB3 PRO E 69 11.756 49.416 -24.142 1.00 24.40
 H
 ATOM 8835 HG2 PRO E 69 11.377 47.353 -22.741 1.00 27.48
 H
 ATOM 8836 HG3 PRO E 69 10.361 47.709 -23.918 1.00 27.48
 H
 ATOM 8837 HD2 PRO E 69 12.400 45.786 -23.949 1.00 29.03
 H
 ATOM 8838 HD3 PRO E 69 10.926 45.661 -24.573 1.00 29.03
 H
 ATOM 8839 N THR E 70 14.370 49.538 -26.499 1.00 24.37
 N
 ATOM 8840 CA THR E 70 15.756 49.821 -26.866 1.00 29.94
 C
 ATOM 8841 C THR E 70 16.152 51.237 -26.484 1.00 29.58
 C
 ATOM 8842 O THR E 70 15.305 52.123 -26.385 1.00 29.43
 O
 ATOM 8843 CB THR E 70 15.997 49.653 -28.383 1.00 31.13
 C
 ATOM 8844 OG1 THR E 70 15.358 50.722 -29.092 1.00 33.21
 O
 ATOM 8845 CG2 THR E 70 15.458 48.325 -28.879 1.00 33.64
 C
 ATOM 8846 H THR E 70 13.820 50.168 -26.701 1.00 29.24
 H
 ATOM 8847 HA THR E 70 16.341 49.205 -26.396 1.00 35.92
 H
 ATOM 8848 HB THR E 70 16.951 49.677 -28.560 1.00 37.36
 H
 ATOM 8849 HG1 THR E 70 15.485 50.636 -29.918 1.00 39.85
 H
 ATOM 8850 HG21 THR E 70 15.615 48.237 -29.832 1.00 40.36
 H
 ATOM 8851 HG22 THR E 70 15.895 47.594 -28.417 1.00 40.36
 H
 ATOM 8852 HG23 THR E 70 14.501 48.274 -28.713 1.00 40.36
 H
 ATOM 8853 N SER E 71 17.447 51.439 -26.274 1.00 28.05
 N
 ATOM 8854 CA SER E 71 17.991 52.775 -26.086 1.00 33.59
 C
 ATOM 8855 C SER E 71 18.133 53.456 -27.445 1.00 32.14
 C
 ATOM 8856 O SER E 71 18.290 54.673 -27.528 1.00 34.41
 O
 ATOM 8857 CB SER E 71 19.339 52.713 -25.369 1.00 30.01
 C
 ATOM 8858 OG SER E 71 20.249 51.897 -26.084 1.00 38.73
 O
 ATOM 8859 H SER E 71 18.036 50.813 -26.236 1.00 33.66
 H
 ATOM 8860 HA SER E 71 17.379 53.298 -25.543 1.00 40.31
 H
 ATOM 8861 HB2 SER E 71 19.703 53.610 -25.303 1.00 36.01
 H
 ATOM 8862 HB3 SER E 71 19.209 52.342 -24.483 1.00 36.01
 H
 ATOM 8863 HG SER E 71 20.986 51.869 -25.682 1.00 46.48
 H
 ATOM 8864 N THR E 72 18.084 52.655 -28.507 1.00 29.50
 N
 ATOM 8865 CA THR E 72 18.097 53.166 -29.873 1.00 29.84
 C
 ATOM 8866 C THR E 72 16.844 54.008 -30.118 1.00 28.11
 C
 ATOM 8867 O THR E 72 15.733 53.480 -30.080 1.00 28.11
 O
 ATOM 8868 CB THR E 72 18.157 52.014 -30.900 1.00 32.89
 C
 ATOM 8869 OG1 THR E 72 19.282 51.168 -30.614 1.00 37.51
 O
 ATOM 8870 CG2 THR E 72 18.275 52.554 -32.320 1.00 35.87
 C
 ATOM 8871 H THR E 72 18.043 51.797 -28.459 1.00 35.40
 H
 ATOM 8872 HA THR E 72 18.875 53.730 -30.000 1.00 35.81
 H
 ATOM 8873 HB THR E 72 17.342 51.491 -30.841 1.00 39.47
 H

C
ATOM 2673 O GLU B 141 -1.123 8.813 -42.942 1.00 27.37
O
ATOM 2674 CB GLU B 141 1.700 7.367 -44.078 1.00 34.11
C
ATOM 2675 CG GLU B 141 2.769 7.490 -45.160 1.00 36.43
C
ATOM 2676 CD GLU B 141 4.098 8.026 -44.638 1.00 46.40
C
ATOM 2677 OE1 GLU B 141 4.499 7.656 -43.512 1.00 42.36
O
ATOM 2678 OE2 GLU B 141 4.740 8.824 -45.356 1.00 49.27
O1-
ATOM 2679 H GLU B 141 2.886 8.919 -42.561 1.00 30.00
H
ATOM 2680 HA GLU B 141 0.883 9.233 -44.298 1.00 33.41
H
ATOM 2681 HB2 GLU B 141 2.082 6.864 -43.342 1.00 40.93
H
ATOM 2682 HB3 GLU B 141 0.952 6.879 -44.455 1.00 40.93
H
ATOM 2683 HG2 GLU B 141 2.932 6.613 -45.543 1.00 43.71
H
ATOM 2684 HG3 GLU B 141 2.452 8.097 -45.847 1.00 43.71
H
ATOM 2685 N ASP B 142 0.290 7.943 -41.429 1.00 28.26
N
ATOM 2686 CA ASP B 142 -0.758 7.684 -40.452 1.00 24.57
C
ATOM 2687 C ASP B 142 -1.332 8.975 -39.892 1.00 20.54
C
ATOM 2688 O ASP B 142 -2.446 8.987 -39.375 1.00 22.29
O
ATOM 2689 CB ASP B 142 -0.226 6.820 -39.310 1.00 25.59
C
ATOM 2690 CG ASP B 142 0.030 5.390 -39.737 1.00 31.43
C

ATOM 2691 OD1 ASP B 142 -0.408 5.011 -40.844 1.00 33.75
O
ATOM 2692 OD2 ASP B 142 0.658 4.641 -38.960 1.00 36.61
O1-
ATOM 2693 H ASP B 142 1.077 7.713 -41.171 1.00 33.91
H
ATOM 2694 HA ASP B 142 -1.479 7.199 -40.884 1.00 29.48
H
ATOM 2695 HB2 ASP B 142 0.612 7.194 -38.994 1.00 30.71
H
ATOM 2696 HB3 ASP B 142 -0.877 6.807 -38.592 1.00 30.71
H
ATOM 2697 N GLN B 143 -0.567 10.057 -39.996 1.00 21.57
N
ATOM 2698 CA GLN B 143 -1.007 11.352 -39.489 1.00 22.32
C
ATOM 2699 C GLN B 143 -1.076 12.372 -40.617 1.00 21.14
C
ATOM 2700 O GLN B 143 -0.821 13.555 -40.412 1.00 19.64
O
ATOM 2701 CB GLN B 143 -0.069 11.831 -38.383 1.00 16.49
C
ATOM 2702 CG GLN B 143 0.132 10.792 -37.295 1.00 21.19
C
ATOM 2703 CD GLN B 143 1.050 11.269 -36.196 1.00 21.57
C
ATOM 2704 OE1 GLN B 143 2.263 11.355 -36.384 1.00 19.08
O
ATOM 2705 NE2 GLN B 143 0.478 11.581 -35.039 1.00 19.58
N
ATOM 2706 H GLN B 143 0.213 10.068 -40.356 1.00 25.88
H
ATOM 2707 HA GLN B 143 -1.896 11.260 -39.112 1.00 26.78
H
ATOM 2708 HB2 GLN B 143 0.798 12.032 -38.769 1.00 19.78
H
ATOM 2709 HB3 GLN B 143 -0.443 12.626 -37.974 1.00 19.78
H
ATOM 2710 HG2 GLN B 143 -0.727 10.581 -36.897 1.00 25.43
H
ATOM 2711 HG3 GLN B 143 0.521 9.995 -37.686 1.00 25.43
H
ATOM 2712 HE21 GLN B 143 0.960 11.858 -34.382 1.00 23.50
H
ATOM 2713 HE22 GLN B 143 -0.374 11.507 -34.946 1.00 23.50
H
ATOM 2714 N ASP B 144 -1.441 11.906 -41.808 1.00 23.98
N
ATOM 2715 CA ASP B 144 -1.449 12.764 -42.986 1.00 24.23
C
ATOM 2716 C ASP B 144 -2.493 13.879 -42.881 1.00 22.36
C
ATOM 2717 O ASP B 144 -2.389 14.881 -43.582 1.00 21.23
O
ATOM 2718 CB ASP B 144 -1.678 11.933 -44.256 1.00 28.70
C
ATOM 2719 CG ASP B 144 -2.948 11.106 -44.203 1.00 27.60
C
ATOM 2720 OD1 ASP B 144 -3.543 10.979 -43.113 1.00 24.37
O
ATOM 2721 OD2 ASP B 144 -3.344 10.567 -45.258 1.00 40.47
O1-
ATOM 2722 H ASP B 144 -1.689 11.096 -41.960 1.00 28.78
H

H
ATOM 8973 N TYR E 79 7.670 45.095 -43.484 1.00 13.27 N
ATOM 8974 CA TYR E 79 7.514 43.775 -44.072 1.00 14.20 C
ATOM 8975 C TYR E 79 6.573 43.872 -45.256 1.00 14.36 C
ATOM 8976 O TYR E 79 5.421 44.279 -45.111 1.00 13.68 O
ATOM 8977 CB TYR E 79 6.982 42.777 -43.049 1.00 13.72 C
ATOM 8978 CG TYR E 79 6.699 41.404 -43.618 1.00 14.03 C
ATOM 8979 CD1 TYR E 79 7.700 40.665 -44.239 1.00 15.69 C
ATOM 8980 CD2 TYR E 79 5.438 40.835 -43.512 1.00 13.78 C
ATOM 8981 CE1 TYR E 79 7.447 39.401 -44.750 1.00 15.27 C
ATOM 8982 CE2 TYR E 79 5.177 39.579 -44.016 1.00 12.76 C
ATOM 8983 CZ TYR E 79 6.182 38.865 -44.635 1.00 15.58 C
ATOM 8984 OH TYR E 79 5.914 37.609 -45.136 1.00 14.38 O
ATOM 8985 H TYR E 79 6.924 45.484 -43.308 1.00 15.93 H
ATOM 8986 HA TYR E 79 8.375 43.460 -44.390 1.00 17.04 H
ATOM 8987 HB2 TYR E 79 7.638 42.675 -42.342 1.00 16.47 H
ATOM 8988 HB3 TYR E 79 6.153 43.120 -42.681 1.00 16.47 H
ATOM 8989 HD1 TYR E 79 8.553 41.027 -44.317 1.00 18.83 H
ATOM 8990 HD2 TYR E 79 4.756 41.311 -43.096 1.00 16.54 H
ATOM 8991 HE1 TYR E 79 8.124 38.920 -45.167 1.00 18.32 H
ATOM 8992 HE2 TYR E 79 4.325 39.215 -43.940 1.00 15.31 H
ATOM 8993 HH TYR E 79 6.606 37.285 -45.484 1.00 17.25 H
ATOM 8994 N PHE E 80 7.078 43.501 -46.426 1.00 13.15 N
ATOM 8995 CA PHE E 80 6.317 43.575 -47.664 1.00 14.24 C
ATOM 8996 C PHE E 80 6.024 42.162 -48.125 1.00 16.30 C
ATOM 8997 O PHE E 80 6.934 41.349 -48.213 1.00 15.43 O
ATOM 8998 CB PHE E 80 7.102 44.352 -48.722 1.00 17.01 C
ATOM 8999 CG PHE E 80 6.447 44.383 -50.071 1.00 19.40 C
ATOM 9000 CD1 PHE E 80 5.421 45.272 -50.337 1.00 18.32 C
ATOM 9001 CD2 PHE E 80 6.877 43.541 -51.084 1.00 19.37 C
ATOM 9002 CE1 PHE E 80 4.824 45.310 -51.585 1.00 23.34 C
ATOM 9003 CE2 PHE E 80 6.285 43.574 -52.334 1.00 18.06 C
ATOM 9004 CZ PHE E 80 5.259 44.459 -52.585 1.00 18.37 C
ATOM 9005 H PHE E 80 7.876 43.197 -46.529 1.00 15.78 H
ATOM 9006 HA PHE E 80 5.476 44.031 -47.504 1.00 17.09 H
ATOM 9007 HB2 PHE E 80 7.206 45.269 -48.422 1.00 20.41 H
ATOM 9008 HB3 PHE E 80 7.975 43.941 -48.827 1.00 20.41 H
ATOM 9009 HD1 PHE E 80 5.125 45.846 -49.668 1.00 21.98 H
ATOM 9010 HD2 PHE E 80 7.569 42.942 -50.920 1.00 23.25 H
ATOM 9011 HE1 PHE E 80 4.131 45.908 -51.751 1.00 28.00 H
ATOM 9012 HE2 PHE E 80 6.579 43.000 -53.004 1.00 21.67 H
ATOM 9013 HZ PHE E 80 4.858 44.482 -53.424 1.00 22.04 H
ATOM 9014 N TYR E 81 4.751 41.864 -48.376 1.00 13.87 N
ATOM 9015 CA TYR E 81 4.354 40.551 -48.870 1.00 15.55 C
ATOM 9016 C TYR E 81 3.404 40.698 -50.049 1.00 17.93 C
ATOM 9017 O TYR E 81 2.378 41.378 -49.952 1.00 14.45 O
ATOM 9018 CB TYR E 81 3.696 39.715 -47.768 1.00 13.17 C
ATOM 9019 CG TYR E 81 3.300 38.345 -48.261 1.00 15.78 C
ATOM 9020 CD1 TYR E 81 4.237 37.324 -48.352 1.00 19.61 C
ATOM 9021 CD2 TYR E 81 1.998 38.077 -48.663 1.00 18.88 C
ATOM 9022 CE1 TYR E 81 3.887 36.072 -48.816 1.00 19.41 C

P
 ATOM 2723 HA ASP B 144 -0.579 13.185 -43.065 1.00 29.08
 H
 ATOM 2724 HB2 ASP B 144 -1.742 12.532 -45.016 1.00 34.44
 H
 ATOM 2725 HB3 ASP B 144 -0.930 11.326 -44.374 1.00 34.44
 H

ATOM 2726 N LEU B 145 -3.477 13.728 -41.996 1.00 19.04
 N
 ATOM 2727 CA LEU B 145 -4.471 14.785 -41.804 1.00 22.41
 C
 ATOM 2728 C LEU B 145 -3.812 16.062 -41.284 1.00 23.21
 C
 ATOM 2729 O LEU B 145 -4.353 17.157 -41.440 1.00 16.02
 O
 ATOM 2730 CB LEU B 145 -5.590 14.338 -40.849 1.00 23.82
 C
 ATOM 2731 CG LEU B 145 -5.318 14.061 -39.362 1.00 27.11
 C
 ATOM 2732 CD1 LEU B 145 -5.111 15.321 -38.530 1.00 36.24
 C
 ATOM 2733 CD2 LEU B 145 -6.485 13.274 -38.783 1.00 28.90
 C
 ATOM 2734 H LEU B 145 -3.591 13.034 -41.501 1.00 22.85
 H
 ATOM 2735 HA LEU B 145 -4.878 14.990 -42.651 1.00 26.90
 H
 ATOM 2736 HB2 LEU B 145 -6.276 15.024 -40.873 1.00 28.59
 H
 ATOM 2737 HB3 LEU B 145 -5.962 13.519 -41.211 1.00 28.59
 H
 ATOM 2738 HG LEU B 145 -4.520 13.515 -39.283 1.00 32.54
 H
 ATOM 2739 HD11 LEU B 145 -4.946 15.068 -37.609 1.00 43.49
 H
 ATOM 2740 HD12 LEU B 145 -4.349 15.809 -38.881 1.00 43.49
 H
 ATOM 2741 HD13 LEU B 145 -5.909 15.870 -38.585 1.00 43.49
 H
 ATOM 2742 HD21 LEU B 145 -6.571 12.437 -39.266 1.00 32.28
 H
 ATOM 2743 HD22 LEU B 145 -6.313 13.100 -37.845 1.00 32.28
 H
 ATOM 2744 HD23 LEU B 145 -7.296 13.797 -38.880 1.00 32.28
 H
 ATOM 2745 N LEU B 146 -2.641 15.917 -40.669 1.00 18.69
 N
 ATOM 2746 CA LEU B 146 -1.906 17.067 -40.147 1.00 20.59
 C
 ATOM 2747 C LEU B 146 -1.461 18.011 -41.261 1.00 22.13
 C
 ATOM 2748 O LEU B 146 -1.050 19.139 -40.994 1.00 20.52
 O
 ATOM 2749 CB LEU B 146 -0.687 16.603 -39.346 1.00 17.78
 C
 ATOM 2750 CG LEU B 146 -0.968 15.902 -38.018 1.00 17.50
 C
 ATOM 2751 CD1 LEU B 146 0.325 15.414 -37.395 1.00 17.27
 C
 ATOM 2752 CD2 LEU B 146 -1.696 16.837 -37.055 1.00 20.64
 C
 ATOM 2753 H LEU B 146 -2.250 15.162 -40.542 1.00 22.42
 H
 ATOM 2754 HA LEU B 146 -2.485 17.564 -39.548 1.00 24.71
 H
 ATOM 2755 HB2 LEU B 146 -0.181 15.984 -39.896 1.00 21.34
 H
 ATOM 2756 HB3 LEU B 146 -0.140 17.380 -39.151 1.00 21.34
 H
 ATOM 2757 HG LEU B 146 -1.536 15.132 -38.178 1.00 21.00
 H
 ATOM 2758 HD11 LEU B 146 0.123 14.973 -36.555 1.00 20.72
 H
 ATOM 2759 HD12 LEU B 146 0.751 14.789 -38.003 1.00 20.72
 H
 ATOM 2760 HD13 LEU B 146 0.907 16.174 -37.239 1.00 20.72
 H

ATOM 2761 HD21 LEU B 146 -1.861 16.367 -36.223 1.00 24.77
 H
 ATOM 2762 HD22 LEU B 146 -1.142 17.615 -36.892 1.00 24.77
 H
 ATOM 2763 HD23 LEU B 146 -2.538 17.108 -37.455 1.00 24.77
 H
 ATOM 2764 N LYS B 147 -1.546 17.549 -42.505 1.00 18.08
 N
 ATOM 2765 CA LYS B 147 -1.162 18.363 -43.656 1.00 21.55
 C
 ATOM 2766 C LYS B 147 -2.100 19.543 -43.918 1.00 18.51
 C
 ATOM 2767 O LYS B 147 -1.884 20.547 -44.493 1.00 21.98
 O
 ATOM 2768 CB LYS B 147 -1.098 17.501 -44.915 1.00 21.16
 C
 ATOM 2769 CG LYS B 147 0.074 16.547 -44.957 1.00 30.69
 C
 ATOM 2770 CD LYS B 147 0.195 15.878 -46.321 1.00 36.31
 C
 ATOM 2771 CE LYS B 147 -0.442 14.498 -46.326 1.00 47.69
 C

U
 ATOM 9023 CE2 TYR E 81 1.640 36.827 -49.130 1.00 17.69
 C
 ATOM 9024 CZ TYR E 81 2.586 35.829 -49.203 1.00 17.85
 ATOM 9025 OH TYR E 81 2.237 34.580 -49.670 1.00 17.84
 O
 ATOM 9026 H TYR E 81 4.095 42.409 -48.267 1.00 16.64
 H
 ATOM 9027 HA TYR E 81 5.143 40.076 -49.177 1.00 18.66
 H
 ATOM 9028 HB2 TYR E 81 4.322 39.604 -47.036 1.00 15.81
 H
 ATOM 9029 HB3 TYR E 81 2.897 40.169 -47.459 1.00 15.81
 H
 ATOM 9030 HD1 TYR E 81 5.115 37.485 -48.092 1.00 23.54
 H
 ATOM 9031 HD2 TYR E 81 1.357 38.749 -48.615 1.00 22.66
 H
 ATOM 9032 HE1 TYR E 81 4.525 35.397 -48.868 1.00 23.29
 H
 ATOM 9033 HE2 TYR E 81 0.763 36.660 -49.392 1.00 21.22
 H
 ATOM 9034 HH TYR E 81 1.421 34.566 -49.870 1.00 21.41
 H
 ATOM 9035 N GLU E 82 3.755 40.055 -51.159 1.00 15.98
 N
 ATOM 9036 CA GLU E 82 3.003 40.184 -52.399 1.00 14.65
 C
 ATOM 9037 C GLU E 82 2.789 38.829 -53.047 1.00 14.84
 C
 ATOM 9038 O GLU E 82 3.732 38.055 -53.188 1.00 17.94
 O
 ATOM 9039 CB GLU E 82 3.737 41.109 -53.373 1.00 18.04
 ATOM 9040 CG GLU E 82 3.018 41.338 -54.689 1.00 16.30
 C
 ATOM 9041 CD GLU E 82 3.879 42.074 -55.695 1.00 22.72
 C
 ATOM 9042 OE1 GLU E 82 4.616 41.397 -56.440 1.00 20.02
 O
 ATOM 9043 OE2 GLU E 82 3.824 43.322 -55.736 1.00 20.27
 O1-
 ATOM 9044 H GLU E 82 4.434 39.531 -51.219 1.00 19.17
 H
 ATOM 9045 HA GLU E 82 2.134 40.571 -52.208 1.00 17.57
 H
 ATOM 9046 HB2 GLU E 82 3.857 41.974 -52.949 1.00 21.64
 H
 ATOM 9047 HB3 GLU E 82 4.604 40.722 -53.575 1.00 21.64
 H
 ATOM 9048 HG2 GLU E 82 2.774 40.481 -55.071 1.00 19.56
 H
 ATOM 9049 HG3 GLU E 82 2.223 41.870 -54.527 1.00 19.56
 H
 ATOM 9050 N CYS E 83 1.547 38.545 -53.433 1.00 15.34
 N
 ATOM 9051 CA CYS E 83 1.264 37.378 -54.257 1.00 12.96
 C
 ATOM 9052 C CYS E 83 0.843 37.867 -55.639 1.00 19.15
 C
 ATOM 9053 O CYS E 83 0.264 38.947 -55.785 1.00 15.77
 O
 ATOM 9054 CB CYS E 83 0.197 36.477 -53.621 1.00 16.84
 ATOM 9055 SG CYS E 83 -1.483 37.137 -53.496 1.00 23.13
 S
 ATOM 9056 H CYS E 83 0.854 39.012 -53.230 1.00 18.41
 H
 ATOM 9057 HA CYS E 83 2.076 36.857 -54.357 1.00 15.56
 H
 ATOM 9058 HB2 CYS E 83 0.144 35.661 -54.142 1.00 20.21
 H
 ATOM 9059 HB3 CYS E 83 0.486 36.260 -52.720 1.00 20.21
 H
 ATOM 9060 N ASP E 84 1.163 37.066 -56.648 1.00 17.04
 N
 ATOM 9061 CA ASP E 84 0.974 37.441 -58.041 1.00 17.78
 C
 ATOM 9062 C ASP E 84 0.295 36.299 -58.783 1.00 19.08
 C
 ATOM 9063 O ASP E 84 0.770 35.164 -58.744 1.00 16.97
 O
 ATOM 9064 CB ASP E 84 2.325 37.778 -58.678 1.00 20.88
 ATOM 9065 CG ASP E 84 2.208 38.205 -60.131 1.00 25.61
 C
 ATOM 9066 OD1 ASP E 84 1.845 37.363 -60.982 1.00 20.93
 O
 ATOM 9067 OD2 ASP E 84 2.505 39.382 -60.423 1.00 20.27
 O1-
 ATOM 9068 H ASP E 84 1.500 36.281 -56.547 1.00 20.45
 H
 ATOM 9069 HA ASP E 84 0.405 38.224 -58.092 1.00 21.34
 H
 ATOM 9070 HB2 ASP E 84 2.734 38.506 -58.184 1.00 25.05
 H
 ATOM 9071 HB3 ASP E 84 2.895 36.993 -58.642 1.00 25.05
 H

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 ATOM 2772 NZ LYS B 147 -0.373 13.845 -47.665 1.00 54.63
 N1+
 ATOM 2773 H LYS B 147 -1.824 16.762 -42.711 1.00 21.70
 H
 ATOM 2774 HA LYS B 147 -0.275 18.723 -43.499 1.00 25.85
 H
 ATOM 2775 HB2 LYS B 147 -1.910 16.973 -44.972 1.00 25.39
 H
 ATOM 2776 HB3 LYS B 147 -1.032 18.084 -45.688 1.00 25.39
 H
 ATOM 2777 HG2 LYS B 147 0.893 17.037 -44.784 1.00 36.83
 H
 ATOM 2778 HG3 LYS B 147 -0.052 15.855 -44.289 1.00 36.83
 H
 ATOM 2779 HD2 LYS B 147 -0.255 16.423 -46.986 1.00 43.57
 H
 ATOM 2780 HD3 LYS B 147 1.134 15.780 -46.547 1.00 43.57
 H
 ATOM 2781 HE2 LYS B 147 0.023 13.931 -45.691 1.00 57.23
 H
 ATOM 2782 HE3 LYS B 147 -1.376 14.579 -46.078 1.00 57.23
 H
 ATOM 2783 HZ1 LYS B 147 0.476 13.753 -47.915 1.00 65.55
 H
 ATOM 2784 HZ2 LYS B 147 -0.754 13.042 -47.632 1.00 65.55
 H
 ATOM 2785 HZ3 LYS B 147 -0.799 14.343 -48.268 1.00 65.55
 H
 ATOM 2786 N LEU B 148 -3.362 19.420 -43.518 1.00 18.78
 N
 ATOM 2787 CA LEU B 148 -4.353 20.450 -43.829 1.00 22.97
 C
 ATOM 2788 C LEU B 148 -4.868 21.167 -42.585 1.00 14.82
 C
 ATOM 2789 O LEU B 148 -6.011 21.617 -42.541 1.00 14.64
 O
 ATOM 2790 CB LEU B 148 -5.517 19.832 -44.607 1.00 26.00
 C
 ATOM 2791 CG LEU B 148 -5.160 19.380 -46.029 1.00 31.59
 C
 ATOM 2792 CD1 LEU B 148 -6.356 18.716 -46.679 1.00 33.85
 C
 ATOM 2793 CD2 LEU B 148 -4.670 20.547 -46.891 1.00 31.17
 C
 ATOM 2794 H LEU B 148 -3.870 18.755 -43.068 1.00 22.53
 H
 ATOM 2795 HA LEU B 148 -3.939 21.115 -44.401 1.00 27.56
 H

 ATOM 2796 HB2 LEU B 148 -5.837 19.055 -44.123 1.00 31.20
 H
 ATOM 2797 HB3 LEU B 148 -6.228 20.489 -44.677 1.00 31.20
 H
 ATOM 2798 HG LEU B 148 -4.446 18.725 -45.980 1.00 37.91
 H
 ATOM 2799 HD11 LEU B 148 -6.113 18.437 -47.575 1.00 40.61
 H
 ATOM 2800 HD12 LEU B 148 -6.614 17.944 -46.150 1.00 40.61
 H
 ATOM 2801 HD13 LEU B 148 -7.088 19.351 -46.716 1.00 40.61
 H
 ATOM 2802 HD21 LEU B 148 -3.878 20.931 -46.481 1.00 37.40
 H
 ATOM 2803 HD22 LEU B 148 -4.456 20.216 -47.778 1.00 37.40
 H
 ATOM 2804 HD23 LEU B 148 -5.371 21.215 -46.946 1.00 37.40
 H
 ATOM 2805 N VAL B 149 -4.000 21.295 -41.587 1.00 21.37
 N
 ATOM 2806 CA VAL B 149 -4.324 22.025 -40.365 1.00 16.00
 C
 ATOM 2807 C VAL B 149 -3.814 23.459 -40.465 1.00 15.16
 C
 ATOM 2808 O VAL B 149 -2.619 23.685 -40.651 1.00 17.77
 O
 ATOM 2809 CB VAL B 149 -3.708 21.343 -39.130 1.00 15.06
 C
 ATOM 2810 CG1 VAL B 149 -4.064 22.100 -37.853 1.00 19.91
 C
 ATOM 2811 CG2 VAL B 149 -4.179 19.899 -39.037 1.00 22.08
 C
 ATOM 2812 H VAL B 149 -3.206 20.964 -41.594 1.00 25.65
 H
 ATOM 2813 HA VAL B 149 -5.287 22.050 -40.252 1.00 19.19
 H
 ATOM 2814 HB VAL B 149 -2.742 21.340 -39.219 1.00 18.07
 H
 ATOM 2815 HG11 VAL B 149 -3.662 21.646 -37.096 1.00 23.89
 H
 ATOM 2816 HG12 VAL B 149 -3.721 23.005 -37.917 1.00 23.89
 H
 ATOM 2817 HG13 VAL B 149 -5.028 22.118 -37.755 1.00 23.89
 H
 ATOM 2818 HG21 VAL B 149 -3.781 19.488 -38.254 1.00 26.49
 H
 ATOM 2819 HG22 VAL B 149 -5.146 19.886 -38.963 1.00 26.49
 H
 ATOM 2820 HG23 VAL B 149 -3.902 19.425 -39.837 1.00 26.49
 H
 ATOM 2821 N LYS B 150 -4.723 24.422 -40.354 1.00 13.81
 N

''
 ATOM 9072 N TYR E 85 -0.824 36.598 -59.437 1.00 18.50 N
 ATOM 9073 CA TYR E 85 -1.525 35.609 -60.252 1.00 19.06 C
 ATOM 9074 C TYR E 85 -1.499 36.041 -61.713 1.00 20.41 C
 ATOM 9075 O TYR E 85 -2.219 36.955 -62.124 1.00 20.32 O
 ATOM 9076 CB TYR E 85 -2.960 35.422 -59.768 1.00 18.28 C
 ATOM 9077 CG TYR E 85 -3.596 34.138 -60.246 1.00 18.94 C
 ATOM 9078 CD1 TYR E 85 -3.038 32.910 -59.929 1.00 19.95 C
 ATOM 9079 CD2 TYR E 85 -4.760 34.154 -61.002 1.00 23.18 C
 ATOM 9080 CE1 TYR E 85 -3.813 31.733 -60.354 1.00 20.65 C
 ATOM 9081 CE2 TYR E 85 -5.345 32.979 -61.430 1.00 25.96 C
 ATOM 9082 CZ TYR E 85 -4.767 31.772 -61.099 1.00 23.05 C
 ATOM 9083 OH TYR E 85 -5.337 30.594 -61.524 1.00 26.20 O
 ATOM 9084 H TYR E 85 -1.201 37.371 -59.426 1.00 22.20 H
 ATOM 9085 HA TYR E 85 -1.068 34.757 -60.180 1.00 22.87 H
 ATOM 9086 HB2 TYR E 85 -2.965 35.412 -58.798 1.00 21.94 H
 ATOM 9087 HB3 TYR E 85 -3.499 36.160 -60.093 1.00 21.94 H
 ATOM 9088 HD1 TYR E 85 -2.259 32.880 -59.422 1.00 23.94 H
 ATOM 9089 HD2 TYR E 85 -5.152 34.968 -61.222 1.00 27.82 H
 ATOM 9090 HE1 TYR E 85 -3.226 30.917 -60.134 1.00 24.78 H
 ATOM 9091 HE2 TYR E 85 -6.124 33.002 -61.937 1.00 31.15 H
 ATOM 9092 HH TYR E 85 -6.033 30.755 -61.966 1.00 31.44 H
 ATOM 9093 N THR E 86 -0.648 35.368 -62.481 1.00 21.39 N
 ATOM 9094 CA THR E 86 -0.390 35.705 -63.874 1.00 20.93 C
 ATOM 9095 C THR E 86 -0.293 34.414 -64.674 1.00 21.34 C
 ATOM 9096 O THR E 86 0.496 33.532 -64.334 1.00 19.84 O
 ATOM 9097 CB THR E 86 0.921 36.515 -64.029 1.00 22.67 C
 ATOM 9098 OG1 THR E 86 0.862 37.696 -63.217 1.00 24.63 O
 ATOM 9099 CG2 THR E 86 1.149 36.917 -65.478 1.00 23.65 C
 ATOM 9100 H THR E 86 -0.196 34.690 -62.206 1.00 25.66 H
 ATOM 9101 HA THR E 86 -1.125 36.233 -64.223 1.00 25.12 H
 ATOM 9102 HB THR E 86 1.670 35.969 -63.744 1.00 27.20 H
 ATOM 9103 HG1 THR E 86 0.765 37.485 -62.410 1.00 29.56 H
 ATOM 9104 HG21 THR E 86 1.973 37.423 -65.555 1.00 28.38 H
 ATOM 9105 HG22 THR E 86 1.212 36.126 -66.035 1.00 28.38 H
 ATOM 9106 HG23 THR E 86 0.412 37.466 -65.790 1.00 28.38 H
 ATOM 9107 N ASP E 87 -1.096 34.300 -65.727 1.00 22.89 N
 ATOM 9108 CA ASP E 87 -1.097 33.101 -66.563 1.00 23.19 C
 ATOM 9109 C ASP E 87 -1.404 31.876 -65.703 1.00 26.71 C
 ATOM 9110 O ASP E 87 -0.771 30.830 -65.835 1.00 23.26 O
 ATOM 9111 CB ASP E 87 0.252 32.946 -67.275 1.00 25.03 C
 ATOM 9112 CG ASP E 87 0.247 31.838 -68.316 1.00 28.16 C
 ATOM 9113 OD1 ASP E 87 -0.798 31.626 -68.965 1.00 24.41 O
 ATOM 9114 OD2 ASP E 87 1.295 31.180 -68.478 1.00 26.54 O1-
 ATOM 9115 H ASP E 87 -1.653 34.904 -65.981 1.00 27.47 H
 ATOM 9116 HA ASP E 87 -1.789 33.181 -67.237 1.00 27.83 H
 ATOM 9117 HB2 ASP E 87 0.469 33.778 -67.725 1.00 30.03 H
 ATOM 9118 HB3 ASP E 87 0.934 32.737 -66.618 1.00 30.03 H
 ATOM 9119 N ASN E 88 -2.372 32.032 -64.803 1.00 29.28 N
 ATOM 9120 CA ASN E 88 -2.802 30.961 -63.906 1.00 25.51 C
 ATOM 9121 C ASN E 88 -1.681 30.405 -63.031 1.00 23.64 C

ATOM 2822 CA LYS B 150 -4.346 25.833 -40.340 1.00 15.89
 C
 ATOM 2823 C LYS B 150 -3.784 26.238 -38.987 1.00 14.81
 C
 ATOM 2824 O LYS B 150 -3.953 25.531 -37.996 1.00 17.84
 O
 ATOM 2825 CB LYS B 150 -5.542 26.729 -40.663 1.00 19.83
 C
 ATOM 2826 CG LYS B 150 -5.939 26.780 -42.121 1.00 18.05
 C
 ATOM 2827 CD LYS B 150 -6.947 27.893 -42.372 1.00 16.00
 C
 ATOM 2828 CE LYS B 150 -6.287 29.264 -42.452 1.00 20.31
 C
 ATOM 2829 NZ LYS B 150 -5.422 29.408 -43.661 1.00 20.83
 N1+
 ATOM 2830 H LYS B 150 -5.569 24.285 -40.285 1.00 16.58
 H

ATOM 2831 HA LYS B 150 -3.663 25.986 -41.011 1.00 19.07
 H
 ATOM 2832 HB2 LYS B 150 -6.310 26.409 -40.163 1.00 23.79
 H
 ATOM 2833 HB3 LYS B 150 -5.331 27.634 -40.386 1.00 23.79
 H
 ATOM 2834 HG2 LYS B 150 -5.153 26.952 -42.662 1.00 21.66
 H
 ATOM 2835 HG3 LYS B 150 -6.346 25.937 -42.373 1.00 21.66
 H
 ATOM 2836 HD2 LYS B 150 -7.400 27.728 -43.214 1.00 19.21
 H
 ATOM 2837 HD3 LYS B 150 -7.589 27.910 -41.645 1.00 19.21
 H
 ATOM 2838 HE2 LYS B 150 -6.976 29.946 -42.491 1.00 24.37
 H
 ATOM 2839 HE3 LYS B 150 -5.732 29.395 -41.667 1.00 24.37
 H
 ATOM 2840 HZ1 LYS B 150 -5.053 30.217 -43.676 1.00 25.00
 H
 ATOM 2841 HZ2 LYS B 150 -4.776 28.796 -43.647 1.00 25.00
 H
 ATOM 2842 HZ3 LYS B 150 -5.908 29.297 -44.398 1.00 25.00
 H
 ATOM 2843 N SER B 151 -3.129 27.394 -38.963 1.00 16.36
 N
 ATOM 2844 CA SER B 151 -2.654 28.008 -37.729 1.00 15.93
 C
 ATOM 2845 C SER B 151 -1.536 27.201 -37.075 1.00 14.66
 C
 ATOM 2846 O SER B 151 -1.004 26.253 -37.656 1.00 15.81
 O
 ATOM 2847 CB SER B 151 -3.817 28.195 -36.746 1.00 16.71
 C
 ATOM 2848 OG SER B 151 -3.442 29.042 -35.672 1.00 18.88
 O
 ATOM 2849 H SER B 151 -2.944 27.853 -39.666 1.00 19.63
 H
 ATOM 2850 HA SER B 151 -2.300 28.887 -37.937 1.00 19.12
 H
 ATOM 2851 HB2 SER B 151 -4.566 28.593 -37.215 1.00 20.05
 H
 ATOM 2852 HB3 SER B 151 -4.071 27.329 -36.390 1.00 20.05
 H
 ATOM 2853 HG SER B 151 -4.087 29.136 -35.142 1.00 22.86
 H
 ATOM 2854 N TYR B 152 -1.184 27.604 -35.862 1.00 13.42
 N
 ATOM 2855 CA TYR B 152 -0.041 27.051 -35.150 1.00 12.43
 C
 ATOM 2856 C TYR B 152 -0.498 26.485 -33.816 1.00 12.59
 C
 ATOM 2857 O TYR B 152 -1.349 27.075 -33.152 1.00 14.90
 O
 ATOM 2858 CB TYR B 152 1.015 28.128 -34.925 1.00 11.01
 C
 ATOM 2859 CG TYR B 152 1.401 28.904 -36.165 1.00 14.74
 C
 ATOM 2860 CD1 TYR B 152 1.697 28.254 -37.356 1.00 14.53
 C
 ATOM 2861 CD2 TYR B 152 1.476 30.291 -36.140 1.00 16.11
 C
 ATOM 2862 CE1 TYR B 152 2.063 28.964 -38.488 1.00 19.24
 C
 ATOM 2863 CE2 TYR B 152 1.837 31.011 -37.265 1.00 13.65
 C
 ATOM 2864 CZ TYR B 152 2.132 30.343 -38.436 1.00 18.79
 C
 ATOM 2865 OH TYR B 152 2.492 31.058 -39.558 1.00 16.60
 O

ATOM 2866 H TYR B 152 -1.602 28.212 -35.420 1.00 16.10
 H
 ATOM 2867 HA TYR B 152 0.353 26.334 -35.672 1.00 14.92
 H
 ATOM 2868 HB2 TYR B 152 0.676 28.764 -34.276 1.00 13.21
 H
 ATOM 2869 HB3 TYR B 152 1.818 27.708 -34.581 1.00 13.21
 H
 ATOM 2870 HD1 TYR B 152 1.656 27.325 -37.393 1.00 17.43
 H

ATOM 9122 O ASN E 88 -1.812 29.322 -62.465 1.00 24.76
 O
 ATOM 9123 CB ASN E 88 -3.430 29.821 -64.709 1.00 29.13
 C
 ATOM 9124 CG ASN E 88 -4.619 30.277 -65.532 1.00 35.20
 C
 ATOM 9125 OD1 ASN E 88 -4.620 30.161 -66.757 1.00 40.38
 O
 ATOM 9126 ND2 ASN E 88 -5.637 30.804 -64.860 1.00 37.30
 N

ATOM 9127 H ASN E 88 -2.804 32.767 -64.690 1.00 35.13
 H
 ATOM 9128 HA ASN E 88 -3.486 31.313 -63.314 1.00 30.61
 H
 ATOM 9129 HB2 ASN E 88 -2.766 29.457 -65.316 1.00 34.96
 H
 ATOM 9130 HB3 ASN E 88 -3.735 29.133 -64.097 1.00 34.96
 H
 ATOM 9131 HD21 ASN E 88 -6.335 31.078 -65.282 1.00 44.76
 H
 ATOM 9132 HD22 ASN E 88 -5.599 30.871 -64.004 1.00 44.76
 H
 ATOM 9133 N LYS E 89 -0.585 31.150 -62.920 1.00 20.99
 N
 ATOM 9134 CA LYS E 89 0.543 30.745 -62.087 1.00 22.61
 C
 ATOM 9135 C LYS E 89 0.681 31.653 -60.888 1.00 18.77
 C
 ATOM 9136 O LYS E 89 0.832 32.882 -60.978 1.00 17.15
 O
 ATOM 9137 CB LYS E 89 1.835 30.748 -62.902 1.00 24.56
 C
 ATOM 9138 CG LYS E 89 1.924 29.593 -63.887 1.00 35.41
 C
 ATOM 9139 CD LYS E 89 3.119 29.732 -64.818 1.00 45.55
 C
 ATOM 9140 CE LYS E 89 3.242 28.527 -65.737 1.00 46.80
 C
 ATOM 9141 NZ LYS E 89 1.975 28.255 -66.473 1.00 49.89
 N1+
 ATOM 9142 H LYS E 89 -0.469 31.902 -63.320 1.00 25.19
 H
 ATOM 9143 HA LYS E 89 0.391 29.841 -61.770 1.00 27.14
 H
 ATOM 9144 HB2 LYS E 89 1.888 31.575 -63.406 1.00 29.48
 H
 ATOM 9145 HB3 LYS E 89 2.590 30.682 -62.296 1.00 29.48
 H
 ATOM 9146 HG2 LYS E 89 2.018 28.762 -63.396 1.00 42.50
 H
 ATOM 9147 HG3 LYS E 89 1.120 29.573 -64.428 1.00 42.50
 H
 ATOM 9148 HD2 LYS E 89 3.008 30.524 -65.367 1.00 54.86
 H
 ATOM 9149 HD3 LYS E 89 3.930 29.799 -64.291 1.00 54.86
 H
 ATOM 9150 HE2 LYS E 89 3.941 28.695 -66.389 1.00 56.16
 H
 ATOM 9151 HE3 LYS E 89 3.459 27.744 -65.207 1.00 56.16
 H
 ATOM 9152 HZ1 LYS E 89 1.755 28.959 -66.971 1.00 59.87
 H
 ATOM 9153 HZ2 LYS E 89 2.077 27.548 -67.001 1.00 59.87
 H
 ATOM 9154 HZ3 LYS E 89 1.317 28.093 -65.895 1.00 59.87
 H
 ATOM 9155 N SER E 90 0.843 31.024 -59.709 1.00 16.33
 N
 ATOM 9156 CA SER E 90 0.971 31.729 -58.442 1.00 17.73
 C
 ATOM 9157 C SER E 90 2.439 31.908 -58.084 1.00 18.63
 C
 ATOM 9158 O SER E 90 3.171 30.928 -57.975 1.00 17.42
 O
 ATOM 9159 CB SER E 90 0.257 30.961 -57.328 1.00 17.54
 O
 ATOM 9160 OG SER E 90 -1.103 30.730 -57.645 1.00 20.05
 O
 ATOM 9161 H SER E 90 0.883 30.169 -59.631 1.00 19.60
 H
 ATOM 9162 HA SER E 90 0.565 32.607 -58.518 1.00 21.27
 H
 ATOM 9163 HB2 SER E 90 0.699 30.107 -57.203 1.00 21.05
 H
 ATOM 9164 HB3 SER E 90 0.305 31.479 -56.509 1.00 21.05
 H
 ATOM 9165 HG SER E 90 -1.501 31.461 -57.755 1.00 24.06
 H

ATOM 9166 N THR E 91 2.864 33.157 -57.912 1.00 17.55
 N
 ATOM 9167 CA THR E 91 4.222 33.455 -57.473 1.00 14.99
 C
 ATOM 9168 C THR E 91 4.178 34.462 -56.329 1.00 20.38
 C
 ATOM 9169 O THR E 91 3.207 35.208 -56.177 1.00 19.44
 O
 ATOM 9170 CB THR E 91 5.096 34.001 -58.621 1.00 18.36
 C

ATOM 2971 HG12 VAL B 158 8.995 21.041 -24.698 1.00 31.88
H
ATOM 2972 HG13 VAL B 158 8.524 19.567 -25.056 1.00 31.88
H
ATOM 2973 HG21 VAL B 158 10.602 18.117 -23.509 1.00 35.36
H
ATOM 2974 HG22 VAL B 158 10.249 17.689 -24.998 1.00 35.36
H
ATOM 2975 HG23 VAL B 158 11.747 18.046 -24.608 1.00 35.36
H
ATOM 2976 N HIS B 159 13.096 20.933 -26.357 1.00 22.33
N
ATOM 2977 CA HIS B 159 14.541 20.959 -26.523 1.00 29.47
C
ATOM 2978 C HIS B 159 15.215 20.956 -25.158 1.00 41.69
C
ATOM 2979 O HIS B 159 14.926 21.802 -24.315 1.00 37.55
O
ATOM 2980 CB HIS B 159 14.961 22.189 -27.327 1.00 33.99
C
ATOM 2981 CG HIS B 159 16.430 22.259 -27.601 1.00 41.87
C
ATOM 2982 ND1 HIS B 159 17.272 23.120 -26.929 1.00 45.71
N
ATOM 2983 CD2 HIS B 159 17.207 21.576 -28.474 1.00 42.10
C
ATOM 2984 CE1 HIS B 159 18.505 22.962 -27.377 1.00 52.16
C
ATOM 2985 NE2 HIS B 159 18.492 22.032 -28.314 1.00 50.26
N
ATOM 2986 H HIS B 159 12.757 21.698 -26.158 1.00 26.80
H
ATOM 2987 HA HIS B 159 14.824 20.167 -27.006 1.00 35.36
H
ATOM 2988 HB2 HIS B 159 14.501 22.177 -28.180 1.00 40.79
H
ATOM 2989 HB3 HIS B 159 14.714 22.985 -26.831 1.00 40.79
H
ATOM 2990 HD1 HIS B 159 17.033 23.672 -26.315 1.00 54.85
H
ATOM 2991 HD2 HIS B 159 16.923 20.920 -29.070 1.00 50.52
H
ATOM 2992 HE1 HIS B 159 19.255 23.428 -27.083 1.00 62.60
H
ATOM 2993 HE2 HIS B 159 19.178 21.757 -28.754 1.00 60.31
H
ATOM 2994 N ILE B 160 16.102 19.991 -24.944 1.00 47.95
N
ATOM 2995 CA ILE B 160 16.840 19.885 -23.692 1.00 58.27
C
ATOM 2996 C ILE B 160 18.248 20.455 -23.880 1.00 66.09
C
ATOM 2997 O ILE B 160 19.148 19.743 -24.324 1.00 70.94
O
ATOM 2998 CB ILE B 160 16.936 18.419 -23.208 1.00 63.95
C
ATOM 2999 CG1 ILE B 160 15.588 17.704 -23.348 1.00 56.29
C
ATOM 3000 CG2 ILE B 160 17.414 18.368 -21.768 1.00 67.71
C
ATOM 3001 CD1 ILE B 160 14.461 18.326 -22.545 1.00 48.29
C
ATOM 3002 H ILE B 160 16.295 19.377 -25.514 1.00 57.54
H
ATOM 3003 HA ILE B 160 16.389 20.404 -23.007 1.00 69.92
H
ATOM 3004 HB ILE B 160 17.585 17.958 -23.761 1.00 76.73
H
ATOM 3005 HG12 ILE B 160 15.326 17.717 -24.282 1.00 67.54
H

ATOM 3006 HG13 ILE B 160 15.690 16.787 -23.050 1.00 67.54
H
ATOM 3007 HG21 ILE B 160 17.467 17.442 -21.486 1.00 81.25
H
ATOM 3008 HG22 ILE B 160 18.290 18.782 -21.712 1.00 81.25
H
ATOM 3009 HG23 ILE B 160 16.784 18.849 -21.209 1.00 81.25
H
ATOM 3010 HD11 ILE B 160 13.650 17.815 -22.691 1.00 57.95
H
ATOM 3011 HD12 ILE B 160 14.698 18.311 -21.605 1.00 57.95
H
ATOM 3012 HD13 ILE B 160 14.332 19.242 -22.839 1.00 57.95
H
ATOM 3013 N PRO B 161 18.448 21.748 -23.558 1.00 69.70
N
ATOM 3014 CA PRO B 161 19.784 22.316 -23.778 1.00 73.07
C
ATOM 3015 C PRO B 161 20.833 21.764 -22.813 1.00 80.56
C
ATOM 3016 O PRO B 161 20.862 22.147 -21.644 1.00 84.37
O
ATOM 3017 CB PRO B 161 19.570 23.817 -23.556 1.00 69.03
C
ATOM 3018 CG PRO B 161 18.392 23.902 -22.659 1.00 63.55
C
ATOM 3019 CD PRO B 161 17.503 22.758 -23.048 1.00 60.94
C
ATOM 3020 HA PRO B 161 20.072 22.162 -24.692 1.00 87.68

ATOM 9271 HA LEU E 97 14.253 46.453 -44.811 1.00 24.85
H
ATOM 9272 HB2 LEU E 97 11.942 48.039 -44.617 1.00 22.48
H
ATOM 9273 HB3 LEU E 97 13.334 48.482 -45.212 1.00 22.48
H
ATOM 9274 HG LEU E 97 11.574 46.750 -46.559 1.00 29.80
H
ATOM 9275 HD11 LEU E 97 11.064 48.560 -47.938 1.00 37.30
H
ATOM 9276 HD12 LEU E 97 10.645 48.881 -46.440 1.00 37.30
H
ATOM 9277 HD13 LEU E 97 11.979 49.500 -47.043 1.00 37.30
H
ATOM 9278 HD21 LEU E 97 12.965 47.071 -48.388 1.00 29.70
H
ATOM 9279 HD22 LEU E 97 13.923 47.976 -47.500 1.00 29.70
H
ATOM 9280 HD23 LEU E 97 13.778 46.425 -47.186 1.00 29.70
H

ATOM 9281 N TYR E 98 14.840 47.417 -42.665 1.00 15.72
N
ATOM 9282 CA TYR E 98 15.182 48.046 -41.401 1.00 18.67
C

ATOM 9283 C TYR E 98 15.675 49.456 -41.704 1.00 22.10
C

ATOM 9284 O TYR E 98 16.701 49.630 -42.363 1.00 18.15
O
ATOM 9285 CB TYR E 98 16.247 47.242 -40.655 1.00 19.19
C
ATOM 9286 CG TYR E 98 16.571 47.797 -39.287 1.00 23.54
C
ATOM 9287 CD1 TYR E 98 17.573 48.742 -39.119 1.00 25.80
C
ATOM 9288 CD2 TYR E 98 15.864 47.387 -38.165 1.00 22.25
C
ATOM 9289 CE1 TYR E 98 17.866 49.257 -37.872 1.00 24.47
C
ATOM 9290 CE2 TYR E 98 16.153 47.895 -36.913 1.00 22.72
C
ATOM 9291 CZ TYR E 98 17.154 48.829 -36.774 1.00 26.85
C
ATOM 9292 OH TYR E 98 17.446 49.337 -35.533 1.00 29.33
O

ATOM 9293 H TYR E 98 15.511 47.325 -43.196 1.00 18.86
H
ATOM 9294 HA TYR E 98 14.392 48.107 -40.843 1.00 22.40
H
ATOM 9295 HB2 TYR E 98 15.930 46.333 -40.540 1.00 23.03
H
ATOM 9296 HB3 TYR E 98 17.064 47.243 -41.177 1.00 23.03
H
ATOM 9297 HD1 TYR E 98 18.056 49.032 -39.859 1.00 30.96
H
ATOM 9298 HD2 TYR E 98 15.187 46.755 -38.256 1.00 26.70
H
ATOM 9299 HE1 TYR E 98 18.543 49.887 -37.774 1.00 29.36
H
ATOM 9300 HE2 TYR E 98 15.674 47.609 -36.169 1.00 27.26
H
ATOM 9301 HH TYR E 98 16.941 48.995 -34.956 1.00 35.20
H

ATOM 9302 N ASN E 99 14.934 50.454 -41.232 1.00 19.00
N
ATOM 9303 CA ASN E 99 15.201 51.846 -41.579 1.00 17.34
C

ATOM 9304 C ASN E 99 15.317 52.027 -43.095 1.00 24.69
C

ATOM 9305 O ASN E 99 16.193 52.735 -43.589 1.00 20.15
O

ATOM 9306 CB ASN E 99 16.465 52.334 -40.868 1.00 18.40
C
ATOM 9307 CG ASN E 99 16.290 52.391 -39.355 1.00 18.42
C
ATOM 9308 OD1 ASN E 99 15.170 52.483 -38.856 1.00 19.63
O
ATOM 9309 ND2 ASN E 99 17.393 52.334 -38.623 1.00 23.08
N

ATOM 9310 H ASN E 99 14.263 50.350 -40.704 1.00 22.81
H
ATOM 9311 HA ASN E 99 14.460 52.391 -41.272 1.00 20.80
H
ATOM 9312 HB2 ASN E 99 17.195 51.726 -41.084 1.00 22.08
H
ATOM 9313 HB3 ASN E 99 16.681 53.226 -41.180 1.00 22.08
H
ATOM 9314 HD21 ASN E 99 17.342 52.363 -37.765 1.00 27.69
H
ATOM 9315 HD22 ASN E 99 18.161 52.269 -39.006 1.00 27.69
H
ATOM 9316 N GLY E 100 14.419 51.373 -43.825 1.00 19.11
N
ATOM 9317 CA GLY E 100 14.309 51.561 -45.260 1.00 22.08
C
ATOM 9318 C GLY E 100 15.283 50.739 -46.080 1.00 25.95
C
ATOM 9319 O GLY E 100 15.210 50.742 -47.308 1.00 24.82
O
ATOM 9320 H GLY E 100 13.856 50.807 -43.505 1.00 22.93

H
 ATOM 3021 HB2 PRO B 161 20.354 24.200 -23.132 1.00 82.83
 H
 ATOM 3022 HB3 PRO B 161 19.390 24.251 -24.404 1.00 82.83
 H
 ATOM 3023 HG2 PRO B 161 18.678 23.814 -21.737 1.00 76.25
 H
 ATOM 3024 HG3 PRO B 161 17.939 24.749 -22.798 1.00 76.25
 H
 ATOM 3025 HD2 PRO B 161 17.031 22.417 -22.272 1.00 73.12
 H
 ATOM 3026 HD3 PRO B 161 16.888 23.029 -23.748 1.00 73.12
 H
 ATOM 3027 N THR B 162 21.679 20.880 -23.334 1.00 82.80
 N
 ATOM 3028 CA THR B 162 22.732 20.185 -22.591 1.00 89.98
 C
 ATOM 3029 C THR B 162 23.165 19.019 -23.470 1.00 91.72
 C
 ATOM 3030 O THR B 162 24.340 18.653 -23.513 1.00 95.85
 O
 ATOM 3031 CB THR B 162 22.284 19.660 -21.201 1.00 95.35
 C
 ATOM 3032 OG1 THR B 162 23.364 18.945 -20.585 1.00 96.68
 O
 ATOM 3033 CG2 THR B 162 21.080 18.741 -21.324 1.00 98.91
 C
 ATOM 3034 H THR B 162 21.661 20.654 -24.164 1.00 99.36
 H
 ATOM 3035 HA THR B 162 23.490 20.778 -22.468 1.00 107.98
 H
 ATOM 3036 HB THR B 162 22.037 20.412 -20.640 1.00 114.42
 H
 ATOM 3037 HG1 THR B 162 23.588 18.294 -21.066 1.00 116.01
 H
 ATOM 3038 HG21 THR B 162 20.815 18.424 -20.446 1.00 118.69
 H
 ATOM 3039 HG22 THR B 162 20.337 19.220 -21.724 1.00 118.69
 H
 ATOM 3040 HG23 THR B 162 21.301 17.979 -21.881 1.00 118.69
 H

ATOM 3041 N ASN B 163 22.186 18.447 -24.166 1.00 91.10
 N
 ATOM 3042 CA ASN B 163 22.418 17.423 -25.177 1.00 91.71
 C
 ATOM 3043 C ASN B 163 22.143 17.982 -26.573 1.00 82.79
 C
 ATOM 3044 O ASN B 163 22.538 17.393 -27.580 1.00 78.88
 O
 ATOM 3045 CB ASN B 163 21.543 16.190 -24.907 1.00 94.16
 C
 ATOM 3046 CG ASN B 163 20.053 16.513 -24.865 1.00 93.87
 C
 ATOM 3047 OD1 ASN B 163 19.539 17.272 -25.687 1.00 91.61
 O
 ATOM 3048 ND2 ASN B 163 19.353 15.925 -23.900 1.00 94.10
 N
 ATOM 3049 H ASN B 163 21.354 18.643 -24.066 1.00 109.32
 H
 ATOM 3050 HA ASN B 163 23.347 17.147 -25.141 1.00 110.05
 H
 ATOM 3051 HB2 ASN B 163 21.688 15.540 -25.612 1.00 112.99
 H
 ATOM 3052 HB3 ASN B 163 21.791 15.810 -24.050 1.00 112.99
 H
 ATOM 3053 HD21 ASN B 163 18.509 16.073 -23.831 1.00 112.92
 H
 ATOM 3054 HD22 ASN B 163 19.744 15.398 -23.345 1.00 112.92
 H
 ATOM 3055 N GLY B 164 21.463 19.124 -26.622 1.00 81.60
 N
 ATOM 3056 CA GLY B 164 21.145 19.781 -27.877 1.00 76.23
 C
 ATOM 3057 C GLY B 164 20.312 18.905 -28.793 1.00 73.18
 C
 ATOM 3058 O GLY B 164 20.669 18.689 -29.951 1.00 76.11
 O
 ATOM 3059 H GLY B 164 21.172 19.542 -25.929 1.00 97.92
 H
 ATOM 3060 HA2 GLY B 164 20.652 20.597 -27.700 1.00 91.48
 H
 ATOM 3061 HA3 GLY B 164 21.967 20.012 -28.338 1.00 91.48
 H
 ATOM 3062 N SER B 165 19.200 18.399 -28.269 1.00 64.95
 N
 ATOM 3063 CA SER B 165 18.326 17.518 -29.031 1.00 57.43
 C
 ATOM 3064 C SER B 165 16.861 17.810 -28.744 1.00 45.57
 C
 ATOM 3065 O SER B 165 16.511 18.287 -27.663 1.00 44.26
 O
 ATOM 3066 CB SER B 165 18.635 16.056 -28.711 1.00 62.72
 C
 ATOM 3067 OG SER B 165 18.321 15.754 -27.362 1.00 67.74
 O
 ATOM 3068 H SER B 165 18.928 18.554 -27.468 1.00 77.94
 H
 ATOM 3069 HA SER B 165 18.481 17.659 -29.978 1.00 68.91

H
 ATOM 9321 HA2 GLY E 100 13.410 51.329 -45.541 1.00 26.49
 H
 ATOM 9322 HA3 GLY E 100 14.457 52.497 -45.467 1.00 26.49
 H
 ATOM 9323 N GLU E 101 16.189 50.032 -45.410 1.00 23.34
 N
 ATOM 9324 CA GLU E 101 17.208 49.242 -46.095 1.00 21.40
 C
 ATOM 9325 C GLU E 101 16.874 47.756 -46.068 1.00 25.31
 C
 ATOM 9326 O GLU E 101 16.667 47.178 -44.996 1.00 20.68
 O
 ATOM 9327 CB GLU E 101 18.576 49.483 -45.457 1.00 28.51
 C
 ATOM 9328 CG GLU E 101 19.701 48.678 -46.079 1.00 36.34
 C
 ATOM 9329 CD GLU E 101 21.060 49.064 -45.529 1.00 50.28
 C
 ATOM 9330 OE1 GLU E 101 21.512 50.198 -45.804 1.00 53.61
 O
 ATOM 9331 OE2 GLU E 101 21.673 48.237 -44.819 1.00 56.44
 O1-
 ATOM 9332 H GLU E 101 16.236 49.993 -44.552 1.00 28.01
 H
 ATOM 9333 HA GLU E 101 17.255 49.522 -47.022 1.00 25.68
 H
 ATOM 9334 HB2 GLU E 101 18.800 50.422 -45.548 1.00 34.21
 H
 ATOM 9335 HB3 GLU E 101 18.528 49.247 -44.518 1.00 34.21
 H
 ATOM 9336 HG2 GLU E 101 19.558 47.737 -45.893 1.00 43.61
 H
 ATOM 9337 HG3 GLU E 101 19.709 48.831 -47.037 1.00 43.61
 H
 ATOM 9338 N GLU E 102 16.828 47.141 -47.248 1.00 19.84
 N
 ATOM 9339 CA GLU E 102 16.530 45.717 -47.380 1.00 21.48
 C
 ATOM 9340 C GLU E 102 17.575 44.873 -46.653 1.00 22.97
 C
 ATOM 9341 O GLU E 102 18.764 45.180 -46.681 1.00 23.40
 O
 ATOM 9342 CB GLU E 102 16.447 45.279 -48.826 1.00 28.87
 C
 ATOM 9343 CG GLU E 102 15.053 45.320 -49.420 1.00 34.38
 C
 ATOM 9344 CD GLU E 102 14.891 44.382 -50.604 1.00 39.93
 C
 ATOM 9345 OE1 GLU E 102 14.841 43.150 -50.386 1.00 41.37
 O
 ATOM 9346 OE2 GLU E 102 14.807 44.875 -51.749 1.00 49.33
 O1-
 ATOM 9347 H GLU E 102 16.968 47.529 -48.003 1.00 23.81
 H
 ATOM 9348 HA GLU E 102 15.671 45.541 -46.945 1.00 25.78
 H
 ATOM 9349 HB2 GLU E 102 17.009 45.865 -49.357 1.00 34.65
 H
 ATOM 9350 HB3 GLU E 102 16.769 44.367 -48.896 1.00 34.65
 H
 ATOM 9351 HG2 GLU E 102 14.413 45.059 -48.740 1.00 41.25
 H
 ATOM 9352 HG3 GLU E 102 14.866 46.222 -49.724 1.00 41.25
 H
 ATOM 9353 N TYR E 103 17.121 43.797 -46.025 1.00 21.26
 N
 ATOM 9354 CA TYR E 103 18.031 42.827 -45.444 1.00 20.13
 C
 ATOM 9355 C TYR E 103 17.377 41.454 -45.470 1.00 20.08
 C
 ATOM 9356 O TYR E 103 16.155 41.338 -45.607 1.00 18.12
 O
 ATOM 9357 CB TYR E 103 18.430 43.236 -44.021 1.00 21.72
 C
 ATOM 9358 CG TYR E 103 17.330 43.173 -42.978 1.00 21.02
 C
 ATOM 9359 CD1 TYR E 103 16.273 44.078 -42.985 1.00 21.46
 C
 ATOM 9360 CD2 TYR E 103 17.374 42.232 -41.961 1.00 19.71
 C
 ATOM 9361 CE1 TYR E 103 15.279 44.024 -42.020 1.00 14.20
 C
 ATOM 9362 CE2 TYR E 103 16.388 42.171 -40.994 1.00 15.96
 C
 ATOM 9363 CZ TYR E 103 15.344 43.065 -41.029 1.00 14.97
 C
 ATOM 9364 OH TYR E 103 14.370 43.002 -40.059 1.00 13.45
 O
 ATOM 9365 H TYR E 103 16.289 43.607 -45.923 1.00 25.51
 H
 ATOM 9366 HA TYR E 103 18.837 42.786 -45.982 1.00 24.15
 H
 ATOM 9367 HB2 TYR E 103 19.144 42.651 -43.724 1.00 26.06
 H
 ATOM 9368 HB3 TYR E 103 18.752 44.151 -44.046 1.00 26.06
 H
 ATOM 9369 HD1 TYR E 103 16.226 44.722 -43.654 1.00 25.75

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H
ATOM 3070 HB2 SER B 165 18.106 15.488 -29.292 1.00 75.26
H
ATOM 3071 HB3 SER B 165 19.580 15.894 -28.859 1.00 75.26
H
ATOM 3072 HG SER B 165 17.505 15.890 -27.219 1.00 81.29
H
ATOM 3073 N TRP B 166 16.012 17.515 -29.723 1.00 40.98
N
ATOM 3074 CA TRP B 166 14.569 17.656 -29.572 1.00 34.55
C
ATOM 3075 C TRP B 166 13.945 16.298 -29.288 1.00 31.08
C

ATOM 3076 O TRP B 166 14.212 15.330 -29.999 1.00 34.34
O
ATOM 3077 CB TRP B 166 13.953 18.265 -30.830 1.00 30.13
C
ATOM 3078 CG TRP B 166 14.302 19.703 -31.041 1.00 30.81
C
ATOM 3079 CD1 TRP B 166 15.354 20.198 -31.756 1.00 36.26
C
ATOM 3080 CD2 TRP B 166 13.591 20.841 -30.538 1.00 28.21
C
ATOM 3081 NE1 TRP B 166 15.344 21.569 -31.726 1.00 34.03
N
ATOM 3082 CE2 TRP B 166 14.272 21.990 -30.984 1.00 27.63
C
ATOM 3083 CE3 TRP B 166 12.446 20.989 -29.751 1.00 23.82
C
ATOM 3084 CZ2 TRP B 166 13.846 23.280 -30.671 1.00 27.91
C
ATOM 3085 CZ3 TRP B 166 12.024 22.281 -29.440 1.00 24.12
C
ATOM 3086 CH2 TRP B 166 12.722 23.405 -29.901 1.00 25.08
C
ATOM 3087 H TRP B 166 16.252 17.226 -30.496 1.00 49.18
H
ATOM 3088 HA TRP B 166 14.379 18.243 -28.824 1.00 41.46
H
ATOM 3089 HB2 TRP B 166 14.265 17.769 -31.603 1.00 36.16
H
ATOM 3090 HB3 TRP B 166 12.987 18.201 -30.767 1.00 36.16
H
ATOM 3091 HD1 TRP B 166 15.987 19.677 -32.198 1.00 43.51
H
ATOM 3092 HE1 TRP B 166 15.918 22.081 -32.111 1.00 40.83
H
ATOM 3093 HE3 TRP B 166 11.977 20.257 -29.442 1.00 28.59
H
ATOM 3094 HZ2 TRP B 166 14.308 24.028 -30.975 1.00 33.49
H
ATOM 3095 HZ3 TRP B 166 11.263 22.398 -28.918 1.00 28.94
H
ATOM 3096 HH2 TRP B 166 12.416 24.254 -29.676 1.00 30.10
H
ATOM 3097 N GLN B 167 13.119 16.225 -28.250 1.00 27.39
N
ATOM 3098 CA GLN B 167 12.485 14.965 -27.879 1.00 30.85
C
ATOM 3099 C GLN B 167 11.020 15.147 -27.492 1.00 26.83
C
ATOM 3100 O GLN B 167 10.604 16.219 -27.048 1.00 24.25
O
ATOM 3101 CB GLN B 167 13.248 14.306 -26.729 1.00 31.47
C
ATOM 3102 CG GLN B 167 13.319 15.142 -25.462 1.00 39.54
C
ATOM 3103 CD GLN B 167 13.995 14.409 -24.315 1.00 47.76
C
ATOM 3104 OE1 GLN B 167 13.559 14.498 -23.168 1.00 47.44
O
ATOM 3105 NE2 GLN B 167 15.066 13.683 -24.618 1.00 48.92
N
ATOM 3106 H GLN B 167 12.910 16.889 -27.745 1.00 32.87
H
ATOM 3107 HA GLN B 167 12.517 14.364 -28.639 1.00 37.02
H
ATOM 3108 HB2 GLN B 167 12.811 13.469 -26.505 1.00 37.76
H
ATOM 3109 HB3 GLN B 167 14.157 14.132 -27.018 1.00 37.76
H
ATOM 3110 HG2 GLN B 167 13.827 15.949 -25.644 1.00 47.45
H

ATOM 3111 HG3 GLN B 167 12.419 15.371 -25.183 1.00 47.45
H
ATOM 3112 HE21 GLN B 167 15.482 13.251 -24.002 1.00 58.70
H
ATOM 3113 HE22 GLN B 167 15.344 13.645 -25.431 1.00 58.70
H
ATOM 3114 N TRP B 168 10.249 14.079 -27.868 1.00 23.01
N
ATOM 3115 CA TRP B 168 8.838 14.077 -27.318 1.00 26.18
C
ATOM 3116 C TRP B 168 8.659 13.855 -25.826 1.00 24.45
C
ATOM 3117 O TRP B 168 9.611 13.512 -25.128 1.00 28.38
O

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H
ATOM 9370 HD2 TYR E 103 18.076 41.623 -41.935 1.00 23.65
H
ATOM 9371 HE1 TYR E 103 14.573 44.630 -42.040 1.00 17.04
H
ATOM 9372 HE2 TYR E 103 16.430 41.528 -40.324 1.00 19.15
H
ATOM 9373 HH TYR E 103 14.536 42.375 -39.526 1.00 16.14
H
ATOM 9374 N THR E 104 18.199 40.415 -45.378 1.00 18.46
N
ATOM 9375 CA THR E 104 17.706 39.043 -45.423 1.00 21.91
C

ATOM 9376 C THR E 104 18.453 38.129 -44.461 1.00 20.34
C
ATOM 9377 O THR E 104 18.024 37.003 -44.211 1.00 22.09
O
ATOM 9378 CB THR E 104 17.830 38.452 -46.844 1.00 22.12
C
ATOM 9379 OG1 THR E 104 19.214 38.270 -47.169 1.00 23.24
O
ATOM 9380 CG2 THR E 104 17.185 39.369 -47.872 1.00 25.29
C
ATOM 9381 H THR E 104 19.052 40.478 -45.288 1.00 22.15
H
ATOM 9382 HA THR E 104 16.768 39.037 -45.176 1.00 26.30
H
ATOM 9383 HB THR E 104 17.377 37.595 -46.875 1.00 26.55
H
ATOM 9384 HG1 THR E 104 19.287 37.948 -47.941 1.00 27.89
H
ATOM 9385 HG21 THR E 104 17.271 38.985 -48.758 1.00 30.35
H
ATOM 9386 HG22 THR E 104 16.244 39.485 -47.668 1.00 30.35
H
ATOM 9387 HG23 THR E 104 17.620 40.236 -47.860 1.00 30.35
H

ATOM 9388 N VAL E 105 19.570 38.612 -43.925 1.00 23.32 N
ATOM 9389 CA VAL E 105 20.446 37.784 -43.105 1.00 21.10
C

ATOM 9390 C VAL E 105 20.199 37.994 -41.613 1.00 24.91 C
ATOM 9391 O VAL E 105 20.247 39.116 -41.110 1.00 23.61
O
ATOM 9392 CB VAL E 105 21.928 38.072 -43.414 1.00 26.35
C
ATOM 9393 CG1 VAL E 105 22.838 37.197 -42.560 1.00 25.25
C
ATOM 9394 CG2 VAL E 105 22.214 37.842 -44.892 1.00 28.02
C

ATOM 9395 H VAL E 105 19.844 39.421 -44.023 1.00 27.98 H
ATOM 9396 HA VAL E 105 20.275 36.850 -43.307 1.00 25.32
H
ATOM 9397 HB VAL E 105 22.121 39.000 -43.210 1.00 31.62
H
ATOM 9398 HG11 VAL E 105 23.762 37.400 -42.775 1.00 30.30
H
ATOM 9399 HG12 VAL E 105 22.667 37.385 -41.624 1.00 30.30
H
ATOM 9400 HG13 VAL E 105 22.649 36.265 -42.751 1.00 30.30
H
ATOM 9401 HG21 VAL E 105 23.150 38.028 -45.064 1.00 33.63
H
ATOM 9402 HG22 VAL E 105 22.014 36.918 -45.111 1.00 33.63
H
ATOM 9403 HG23 VAL E 105 21.655 38.435 -45.417 1.00 33.63
H

ATOM 9404 N LYS E 106 19.944 36.892 -40.916 1.00 28.46 N
ATOM 9405 CA LYS E 106 19.775 36.896 -39.469 1.00 32.57
C

ATOM 9406 C LYS E 106 21.133 36.835 -38.787 1.00 31.99 C
ATOM 9407 O LYS E 106 21.998 36.062 -39.198 1.00 30.22
O
ATOM 9408 CB LYS E 106 18.914 35.706 -39.033 1.00 33.52
C
ATOM 9409 CG LYS E 106 18.726 35.569 -37.528 1.00 37.03
C
ATOM 9410 CD LYS E 106 18.189 34.196 -37.165 1.00 45.30
C

ATOM 9411 CE LYS E 106 17.955 34.067 -35.665 1.00 57.12
C
ATOM 9412 NZ LYS E 106 19.210 34.241 -34.879 1.00 54.38
N1+

ATOM 9413 H LYS E 106 19.862 36.112 -41.269 1.00 34.15 H
ATOM 9414 HA LYS E 106 19.330 37.714 -39.198 1.00 39.08
H
ATOM 9415 HB2 LYS E 106 18.035 35.799 -39.431 1.00 40.22
H
ATOM 9416 HB3 LYS E 106 19.331 34.890 -39.351 1.00 40.22
H
ATOM 9417 HG2 LYS E 106 19.581 35.689 -37.086 1.00 44.43
H

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H
ATOM 3218 HD21 LEU B 174 12.283 17.151 -35.599 1.00 35.15
H
ATOM 3219 HD22 LEU B 174 12.004 17.303 -34.043 1.00 35.15
H
ATOM 3220 HD23 LEU B 174 13.474 16.992 -34.560 1.00 35.15
H
ATOM 3221 N SER B 175 12.242 11.686 -34.776 1.00 36.01
N
ATOM 3222 CA SER B 175 12.703 10.894 -35.911 1.00 38.08
C
ATOM 3223 C SER B 175 12.978 11.796 -37.114 1.00 39.53
C
ATOM 3224 O SER B 175 12.257 12.771 -37.345 1.00 35.10
O
ATOM 3225 CB SER B 175 11.679 9.818 -36.277 1.00 34.05
C
ATOM 3226 OG SER B 175 11.435 8.952 -35.181 1.00 46.41
O
ATOM 3227 H SER B 175 11.426 11.540 -34.548 1.00 43.22
H
ATOM 3228 HA SER B 175 13.532 10.451 -35.672 1.00 45.70
H
ATOM 3229 HB2 SER B 175 10.847 10.248 -36.530 1.00 40.86
H
ATOM 3230 HB3 SER B 175 12.022 9.297 -37.020 1.00 40.86
H
ATOM 3231 HG SER B 175 10.872 8.368 -35.397 1.00 55.69
H
ATOM 3232 N PRO B 176 14.024 11.475 -37.890 1.00 37.56
N
ATOM 3233 CA PRO B 176 14.394 12.331 -39.020 1.00 40.19
C
ATOM 3234 C PRO B 176 13.366 12.306 -40.148 1.00 39.31
C
ATOM 3235 O PRO B 176 12.536 11.398 -40.204 1.00 39.37
O
ATOM 3236 CB PRO B 176 15.725 11.738 -39.482 1.00 42.21
C
ATOM 3237 CG PRO B 176 15.663 10.317 -39.076 1.00 48.89
C
ATOM 3238 CD PRO B 176 14.882 10.281 -37.799 1.00 40.78
C
ATOM 3239 HA PRO B 176 14.530 13.245 -38.724 1.00 46.23
H
ATOM 3240 HB2 PRO B 176 15.803 11.818 -40.446 1.00 50.65
H
ATOM 3241 HB3 PRO B 176 16.459 12.192 -39.038 1.00 50.65
H
ATOM 3242 HG2 PRO B 176 15.212 9.803 -39.764 1.00 58.67
H
ATOM 3243 HG3 PRO B 176 16.562 9.981 -38.934 1.00 58.67
H
ATOM 3244 HD2 PRO B 176 14.341 9.477 -37.757 1.00 48.94
H
ATOM 3245 HD3 PRO B 176 15.478 10.350 -37.037 1.00 48.94
H
ATOM 3246 N ASN B 177 13.423 13.307 -41.022 1.00 32.05
N
ATOM 3247 CA ASN B 177 12.551 13.372 -42.192 1.00 37.49
C
ATOM 3248 C ASN B 177 11.058 13.384 -41.853 1.00 32.07
C
ATOM 3249 O ASN B 177 10.227 13.073 -42.704 1.00 32.22
O
ATOM 3250 CB ASN B 177 12.853 12.200 -43.134 1.00 43.25
C

ATOM 3251 CG ASN B 177 14.279 12.223 -43.656 1.00 42.46
C
ATOM 3252 OD1 ASN B 177 14.599 12.972 -44.579 1.00 48.73
O
ATOM 3253 ND2 ASN B 177 15.140 11.398 -43.072 1.00 42.22
N
ATOM 3254 H ASN B 177 13.967 13.970 -40.959 1.00 38.46
H
ATOM 3255 HA ASN B 177 12.746 14.191 -42.674 1.00 44.99
H
ATOM 3256 HB2 ASN B 177 12.722 11.367 -42.655 1.00 51.90
H
ATOM 3257 HB3 ASN B 177 12.253 12.243 -43.895 1.00 51.90
H
ATOM 3258 HD21 ASN B 177 15.959 11.376 -43.334 1.00 50.66
H
ATOM 3259 HD22 ASN B 177 14.879 10.886 -42.432 1.00 50.66
H
ATOM 3260 N LEU B 178 10.722 13.744 -40.615 1.00 29.94
N
ATOM 3261 CA LEU B 178 9.326 13.905 -40.208 1.00 27.52
C
ATOM 3262 C LEU B 178 8.926 15.373 -40.174 1.00 28.55
C
ATOM 3263 O LEU B 178 7.933 15.769 -40.785 1.00 28.18
O
ATOM 3264 CB LEU B 178 9.082 13.284 -38.831 1.00 25.65
C
ATOM 3265 CG LEU B 178 8.632 11.822 -38.770 1.00 29.25
C
ATOM 3266 CD1 LEU B 178 8.419 11.427 -37.326 1.00 30.04
C

C
ATOM 9518 NZ LYS E 113 20.513 45.300 -40.281 1.00 26.06
N1+
ATOM 9519 H LYS E 113 16.072 44.253 -34.623 1.00 19.69 H
ATOM 9520 HA LYS E 113 15.069 44.035 -37.002 1.00 18.78
H
ATOM 9521 HB2 LYS E 113 17.112 45.127 -36.544 1.00 24.65
H
ATOM 9522 HB3 LYS E 113 17.787 43.710 -36.317 1.00 24.65
H
ATOM 9523 HG2 LYS E 113 17.486 43.197 -38.557 1.00 24.58
H
ATOM 9524 HG3 LYS E 113 16.789 44.611 -38.789 1.00 24.56
H
ATOM 9525 HD2 LYS E 113 18.809 45.672 -38.228 1.00 27.28
H
ATOM 9526 HD3 LYS E 113 19.497 44.246 -38.071 1.00 27.28
H
ATOM 9527 HE2 LYS E 113 19.125 43.844 -40.352 1.00 29.38
H
ATOM 9528 HE3 LYS E 113 18.511 45.305 -40.492 1.00 29.38
H
ATOM 9529 HZ1 LYS E 113 20.565 46.139 -39.988 1.00 31.27
H
ATOM 9530 HZ2 LYS E 113 21.124 44.808 -39.861 1.00 31.27
H
ATOM 9531 HZ3 LYS E 113 20.682 45.288 -41.155 1.00 31.27
H
ATOM 9532 N ASN E 114 16.360 41.307 -35.924 1.00 14.24
N
ATOM 9533 CA ASN E 114 16.389 39.862 -36.127 1.00 15.14
C
ATOM 9534 C ASN E 114 15.036 39.200 -35.892 1.00 13.48
C
ATOM 9535 O ASN E 114 14.623 38.335 -36.663 1.00 14.71
O
ATOM 9536 CB ASN E 114 17.440 39.224 -35.217 1.00 20.17
C
ATOM 9537 CG ASN E 114 18.851 39.385 -35.758 1.00 27.46
C
ATOM 9538 OD1 ASN E 114 19.069 39.370 -36.971 1.00 22.82
O
ATOM 9539 ND2 ASN E 114 19.815 39.537 -34.858 1.00 24.63
N
ATOM 9540 H ASN E 114 16.790 41.576 -35.230 1.00 17.09
H
ATOM 9541 HA ASN E 114 16.648 39.884 -37.045 1.00 18.17
H
ATOM 9542 HB2 ASN E 114 17.402 39.647 -34.345 1.00 24.21
H
ATOM 9543 HB3 ASN E 114 17.255 38.276 -35.136 1.00 24.21
H
ATOM 9544 HD21 ASN E 114 20.631 39.631 -35.114 1.00 29.56
H
ATOM 9545 HD22 ASN E 114 19.624 39.540 -34.019 1.00 29.56
H
ATOM 9546 N MET E 115 14.350 39.596 -34.827 1.00 14.19
N
ATOM 9547 CA MET E 115 13.049 39.018 -34.518 1.00 15.83
C
ATOM 9548 C MET E 115 12.046 39.333 -35.625 1.00 15.36
C
ATOM 9549 O MET E 115 11.231 38.490 -36.006 1.00 14.90
O
ATOM 9550 CB MET E 115 12.536 39.543 -33.179 1.00 17.26
C

ATOM 9551 CG MET E 115 11.267 38.858 -32.708 1.00 23.77
C
ATOM 9552 SD MET E 115 10.596 39.578 -31.197 1.00 35.74
S
ATOM 9553 CE MET E 115 11.976 39.355 -30.071 1.00 45.72
C
ATOM 9554 H MET E 115 14.614 40.195 -34.270 1.00 17.03
H
ATOM 9555 HA MET E 115 13.142 38.056 -34.444 1.00 19.00
H
ATOM 9556 HB2 MET E 115 13.218 39.402 -32.505 1.00 20.71
H
ATOM 9557 HB3 MET E 115 12.348 40.491 -33.265 1.00 20.71
H
ATOM 9558 HG2 MET E 115 10.592 38.933 -33.400 1.00 28.52
H
ATOM 9559 HG3 MET E 115 11.460 37.923 -32.533 1.00 28.52
H
ATOM 9560 HE1 MET E 115 11.735 39.711 -29.202 1.00 54.87
H
ATOM 9561 HE2 MET E 115 12.173 38.408 -29.998 1.00 54.87
H
ATOM 9562 HE3 MET E 115 12.748 39.828 -30.420 1.00 54.87
H
ATOM 9563 N TRP E 116 12.109 40.558 -36.130 1.00 12.48
N
ATOM 9564 CA TRP E 116 11.240 40.990 -37.216 1.00 15.47
C
ATOM 9565 C TRP E 116 11.452 40.113 -38.447 1.00 14.04
C
ATOM 9566 O TRP E 116 10.498 39.712 -39.112 1.00 11.48
O

ATOM 3267 CD2 LEU B 178 7.356 11.576 -39.570 1.00 30.40
 C
 ATOM 3268 H LEU B 178 11.289 13.902 -39.987 1.00 35.93
 H
 ATOM 3269 HA LEU B 178 8.755 13.452 -40.848 1.00 33.02
 H
 ATOM 3270 HB2 LEU B 178 9.907 13.346 -38.326 1.00 30.78
 H
 ATOM 3271 HB3 LEU B 178 8.398 13.808 -38.385 1.00 30.78
 H
 ATOM 3272 HG LEU B 178 9.331 11.259 -39.137 1.00 35.10
 H
 ATOM 3273 HD11 LEU B 178 8.134 10.500 -37.292 1.00 36.05
 H
 ATOM 3274 HD12 LEU B 178 9.253 11.535 -36.844 1.00 36.05
 H
 ATOM 3275 HD13 LEU B 178 7.736 11.998 -36.940 1.00 36.05
 H
 ATOM 3276 HD21 LEU B 178 7.115 10.640 -39.499 1.00 36.49
 H
 ATOM 3277 HD22 LEU B 178 6.646 12.129 -39.209 1.00 36.49
 H
 ATOM 3278 HD23 LEU B 178 7.517 11.808 -40.498 1.00 36.49
 H
 ATOM 3279 N LEU B 179 9.706 16.171 -39.449 1.00 24.55
 N
 ATOM 3280 CA LEU B 179 9.420 17.591 -39.277 1.00 21.87
 C
 ATOM 3281 C LEU B 179 10.570 18.473 -39.737 1.00 24.32
 C
 ATOM 3282 O LEU B 179 11.735 18.189 -39.457 1.00 23.82
 O
 ATOM 3283 CB LEU B 179 9.114 17.896 -37.810 1.00 23.91
 C
 ATOM 3284 CG LEU B 179 7.814 17.348 -37.224 1.00 22.72
 C
 ATOM 3285 CD1 LEU B 179 7.760 17.633 -35.726 1.00 20.68
 C

ATOM 3286 CD2 LEU B 179 6.602 17.946 -37.927 1.00 23.32
 C
 ATOM 3287 H LEU B 179 10.416 15.909 -39.041 1.00 29.47
 H
 ATOM 3288 HA LEU B 179 8.637 17.821 -39.802 1.00 26.24
 H
 ATOM 3289 HB2 LEU B 179 9.839 17.539 -37.273 1.00 28.70
 H
 ATOM 3290 HB3 LEU B 179 9.088 18.860 -37.705 1.00 28.70
 H
 ATOM 3291 HG LEU B 179 7.791 16.387 -37.349 1.00 27.27
 H
 ATOM 3292 HD11 LEU B 179 6.931 17.280 -35.368 1.00 24.81
 H
 ATOM 3293 HD12 LEU B 179 8.516 17.203 -35.296 1.00 24.81
 H
 ATOM 3294 HD13 LEU B 179 7.800 18.592 -35.586 1.00 24.81
 H
 ATOM 3295 HD21 LEU B 179 5.795 17.579 -37.533 1.00 27.98
 H
 ATOM 3296 HD22 LEU B 179 6.616 18.910 -37.816 1.00 27.98
 H
 ATOM 3297 HD23 LEU B 179 6.642 17.721 -38.870 1.00 27.98
 H
 ATOM 3298 N THR B 180 10.228 19.547 -40.441 1.00 21.44
 N
 ATOM 3299 CA THR B 180 11.169 20.621 -40.726 1.00 24.48
 C
 ATOM 3300 C THR B 180 11.150 21.596 -39.556 1.00 24.18
 C
 ATOM 3301 O THR B 180 10.148 22.277 -39.330 1.00 20.49
 O
 ATOM 3302 CB THR B 180 10.814 21.367 -42.029 1.00 26.75
 C
 ATOM 3303 OG1 THR B 180 10.749 20.439 -43.119 1.00 26.99
 O
 ATOM 3304 CG2 THR B 180 11.848 22.444 -42.342 1.00 29.06
 C
 ATOM 3305 H THR B 180 9.444 19.678 -40.769 1.00 25.72
 H
 ATOM 3306 HA THR B 180 12.063 20.256 -40.812 1.00 29.38
 H
 ATOM 3307 HB THR B 180 9.951 21.798 -41.926 1.00 32.10
 H
 ATOM 3308 HG1 THR B 180 10.161 19.853 -42.966 1.00 32.39
 H
 ATOM 3309 HG21 THR B 180 11.611 22.903 -43.163 1.00 34.88
 H
 ATOM 3310 HG22 THR B 180 11.883 23.090 -41.619 1.00 34.88
 H
 ATOM 3311 HG23 THR B 180 12.724 22.041 -42.448 1.00 34.88
 H
 ATOM 3312 N ILE B 181 12.246 21.645 -38.804 1.00 23.05
 N
 ATOM 3313 CA ILE B 181 12.353 22.540 -37.656 1.00 22.09
 C
 ATOM 3314 C ILE B 181 12.910 23.895 -38.081 1.00 26.12
 C
 ATOM 3315 O ILE B 181 12.904 23.079 -38.711 1.00 22.50
 O

ATOM 9567 CB TRP E 116 11.515 42.458 -37.544 1.00 12.64
 C
 ATOM 9568 CG TRP E 116 10.633 43.043 -38.607 1.00 12.35
 C
 ATOM 9569 CD1 TRP E 116 10.933 43.189 -39.929 1.00 12.04
 C
 ATOM 9570 CD2 TRP E 116 9.312 43.572 -38.435 1.00 14.43
 C
 ATOM 9571 NE1 TRP E 116 9.883 43.779 -40.593 1.00 14.64
 N
 ATOM 9572 CE2 TRP E 116 8.874 44.021 -39.699 1.00 13.81
 C
 ATOM 9573 CE3 TRP E 116 8.459 43.711 -37.336 1.00 11.41
 C
 ATOM 9574 CZ2 TRP E 116 7.624 44.603 -39.892 1.00 14.26
 C
 ATOM 9575 CZ3 TRP E 116 7.216 44.288 -37.531 1.00 15.87
 C
 ATOM 9576 CH2 TRP E 116 6.811 44.726 -38.799 1.00 14.11
 C
 ATOM 9577 H TRP E 116 12.653 41.165 -35.857 1.00 14.98
 H
 ATOM 9578 HA TRP E 116 10.314 40.907 -36.938 1.00 18.56
 H
 ATOM 9579 HB2 TRP E 116 11.390 42.983 -36.738 1.00 15.17
 H
 ATOM 9580 HB3 TRP E 116 12.432 42.540 -37.847 1.00 15.17
 H
 ATOM 9581 HD1 TRP E 116 11.734 42.930 -40.324 1.00 14.44
 H
 ATOM 9582 HE1 TRP E 116 9.862 43.961 -41.433 1.00 17.57
 H
 ATOM 9583 HE3 TRP E 116 8.723 43.427 -36.491 1.00 13.69
 H
 ATOM 9584 HZ2 TRP E 116 7.351 44.891 -40.733 1.00 17.11
 H
 ATOM 9585 HZ3 TRP E 116 6.639 44.365 -36.808 1.00 19.05
 H

ATOM 9586 HH2 TRP E 116 5.967 45.105 -38.901 1.00 16.94
 H
 ATOM 9587 N LEU E 117 12.714 39.810 -38.725 1.00 13.03
 N
 ATOM 9588 CA LEU E 117 13.093 39.003 -39.878 1.00 13.36
 C
 ATOM 9589 C LEU E 117 12.619 37.564 -39.748 1.00 15.88
 C
 ATOM 9590 O LEU E 117 12.149 38.968 -40.719 1.00 15.15
 O
 ATOM 9591 CB LEU E 117 14.618 39.027 -40.063 1.00 13.94
 C
 ATOM 9592 CG LEU E 117 15.204 38.145 -41.175 1.00 15.98
 C
 ATOM 9593 CD1 LEU E 117 14.745 38.806 -42.552 1.00 16.70
 C
 ATOM 9594 CD2 LEU E 117 16.725 38.130 -41.103 1.00 24.05
 C
 ATOM 9595 H LEU E 117 13.384 40.067 -38.251 1.00 15.63
 H
 ATOM 9596 HA LEU E 117 12.688 39.381 -40.674 1.00 16.03
 H
 ATOM 9597 HB2 LEU E 117 14.884 39.940 -40.254 1.00 16.73
 H
 ATOM 9598 HB3 LEU E 117 15.027 38.744 -39.230 1.00 16.73
 H
 ATOM 9599 HG LEU E 117 14.892 37.235 -41.048 1.00 19.17
 H
 ATOM 9600 HD11 LEU E 117 15.135 38.026 -43.225 1.00 20.03
 H
 ATOM 9601 HD12 LEU E 117 13.777 38.559 -42.594 1.00 20.03
 H
 ATOM 9602 HD13 LEU E 117 15.039 39.520 -42.693 1.00 20.03
 H
 ATOM 9603 HD21 LEU E 117 17.069 37.567 -41.814 1.00 28.86
 H
 ATOM 9604 HD22 LEU E 117 17.055 39.036 -41.209 1.00 28.86
 H
 ATOM 9605 HD23 LEU E 117 16.997 37.777 -40.241 1.00 28.86
 H
 ATOM 9606 N THR E 118 12.748 37.002 -38.552 1.00 11.16
 N
 ATOM 9607 CA THR E 118 12.450 35.592 -38.362 1.00 15.63
 C
 ATOM 9608 C THR E 118 10.994 35.308 -37.997 1.00 15.23
 C
 ATOM 9609 O THR E 118 10.612 34.141 -37.919 1.00 16.44
 O
 ATOM 9610 CB THR E 118 13.340 34.974 -37.268 1.00 17.43
 C
 ATOM 9611 OG1 THR E 118 13.079 35.606 -36.008 1.00 19.94
 O
 ATOM 9612 CG2 THR E 118 14.807 35.139 -37.623 1.00 21.12
 C
 ATOM 9613 H THR E 118 13.004 37.412 -37.840 1.00 13.39
 H
 ATOM 9614 HA THR E 118 12.639 35.124 -39.190 1.00 18.76
 H
 ATOM 9615 HB THR E 118 12.140 34.000 -37.107 1.00 20.03
 H

DK/EP 3233192 T3

ATOM 3315 O ILE B 181 13.964 23.972 -36.711 1.00 23.50
 O
 ATOM 3316 CB ILE B 181 13.251 21.948 -36.557 1.00 23.97
 C
 ATOM 3317 CG1 ILE B 181 12.745 20.565 -36.131 1.00 23.66
 C
 ATOM 3318 CG2 ILE B 181 13.312 22.885 -35.356 1.00 22.95
 C
 ATOM 3319 CD1 ILE B 181 11.326 20.552 -35.592 1.00 28.66
 C
 ATOM 3320 H ILE B 181 12.947 21.167 -38.940 1.00 27.67
 H

ATOM 3321 HA ILE B 181 11.470 22.681 -37.281 1.00 26.51
 H
 ATOM 3322 HB ILE B 181 14.147 21.049 -36.914 1.00 20.77
 H
 ATOM 3323 HG12 ILE B 181 12.773 19.974 -36.899 1.00 28.39
 H
 ATOM 3324 HG13 ILE B 181 13.327 20.223 -35.434 1.00 28.39
 H
 ATOM 3325 HG21 ILE B 181 13.883 22.492 -34.677 1.00 27.55
 H
 ATOM 3326 HG22 ILE B 181 13.676 23.738 -35.640 1.00 27.55
 H
 ATOM 3327 HG23 ILE B 181 12.416 23.008 -35.005 1.00 27.55
 H
 ATOM 3328 HD11 ILE B 181 11.089 19.643 -35.348 1.00 34.39
 H
 ATOM 3329 HD12 ILE B 181 11.279 21.126 -34.812 1.00 34.39
 H
 ATOM 3330 HD13 ILE B 181 10.724 20.877 -36.279 1.00 34.39
 H
 ATOM 3331 N ILE B 182 12.203 24.958 -37.706 1.00 23.73
 N
 ATOM 3332 CA ILE B 182 12.514 26.304 -38.171 1.00 20.26
 C
 ATOM 3333 C ILE B 182 12.680 27.254 -36.992 1.00 23.35
 C
 ATOM 3334 O ILE B 182 11.782 27.378 -36.163 1.00 18.77
 O
 ATOM 3335 CB ILE B 182 11.400 26.838 -39.101 1.00 21.54
 C
 ATOM 3336 CG1 ILE B 182 11.154 25.858 -40.255 1.00 22.95
 C
 ATOM 3337 CG2 ILE B 182 11.751 28.230 -39.631 1.00 20.67
 C
 ATOM 3338 CD1 ILE B 182 9.889 26.137 -41.035 1.00 27.62
 C
 ATOM 3339 H ILE B 182 11.528 24.923 -37.174 1.00 28.48
 H
 ATOM 3340 HA ILE B 182 13.346 26.287 -38.669 1.00 24.31
 H
 ATOM 3341 HB ILE B 182 10.582 26.908 -38.585 1.00 25.85
 H
 ATOM 3342 HG12 ILE B 182 11.900 25.909 -40.873 1.00 27.54
 H
 ATOM 3343 HG13 ILE B 182 11.087 24.960 -39.894 1.00 27.54
 H
 ATOM 3344 HG21 ILE B 182 11.036 28.537 -40.210 1.00 24.80
 H
 ATOM 3345 HG22 ILE B 182 11.854 28.836 -38.881 1.00 24.80
 H
 ATOM 3346 HG23 ILE B 182 12.581 28.177 -40.130 1.00 24.80
 H
 ATOM 3347 HD11 ILE B 182 9.803 25.480 -41.743 1.00 33.14
 H
 ATOM 3348 HD12 ILE B 182 9.129 26.078 -40.435 1.00 33.14
 H
 ATOM 3349 HD13 ILE B 182 9.942 27.028 -41.415 1.00 33.14
 H
 ATOM 3350 N GLU B 183 13.821 27.934 -36.916 1.00 24.54
 N
 ATOM 3351 CA GLU B 183 14.022 28.911 -35.854 1.00 27.28
 C
 ATOM 3352 C GLU B 183 13.140 30.122 -36.128 1.00 29.16
 C
 ATOM 3353 O GLU B 183 13.045 30.599 -37.260 1.00 34.53
 O
 ATOM 3354 CB GLU B 183 15.494 29.314 -35.730 1.00 36.17
 C
 ATOM 3355 CG GLU B 183 16.063 30.065 -36.915 1.00 45.13
 C

ATOM 3356 CD GLU B 183 17.553 30.328 -36.767 1.00 52.61
 C
 ATOM 3357 OE1 GLU B 183 18.036 30.396 -35.616 1.00 55.37
 O
 ATOM 3358 OE2 GLU B 183 18.243 30.456 -37.800 1.00 57.38
 O1-
 ATOM 3359 H GLU B 183 14.482 27.851 -37.459 1.00 29.44
 H
 ATOM 3360 HA GLU B 183 13.745 28.522 -35.010 1.00 32.74
 H
 ATOM 3361 HB2 GLU B 183 15.592 29.062 -34.950 1.00 43.40
 H
 ATOM 3362 HB3 GLU B 183 16.024 28.510 -35.613 1.00 43.40
 H
 ATOM 3363 HG2 GLU B 183 15.927 29.540 -37.719 1.00 54.15
 H

ATOM 9615 HB THR E 118 13.149 34.026 -37.197 1.00 20.92
 H
 ATOM 9616 HG1 THR E 118 12.273 35.500 -35.795 1.00 23.93
 H
 ATOM 9617 HG21 THR E 118 15.362 34.748 -36.930 1.00 25.34
 H
 ATOM 9618 HG22 THR E 118 14.996 34.697 -38.465 1.00 25.34
 H
 ATOM 9619 HG23 THR E 118 15.024 36.081 -37.707 1.00 25.34
 H
 ATOM 9620 N THR E 119 10.183 36.346 -37.781 1.00 13.58
 N

ATOM 9621 CA THR E 119 8.800 36.131 -37.326 1.00 12.81
 C
 ATOM 9622 C THR E 119 7.709 36.798 -38.158 1.00 15.49 C
 ATOM 9623 O THR E 119 6.530 36.502 -37.968 1.00 14.16 O
 ATOM 9624 CB THR E 119 8.595 36.627 -35.875 1.00 12.82
 C
 ATOM 9625 OG1 THR E 119 8.665 38.059 -35.835 1.00 12.89
 O
 ATOM 9626 CG2 THR E 119 9.626 36.020 -34.943 1.00 17.46
 C
 ATOM 9627 H THR E 119 10.401 37.171 -37.886 1.00 16.30
 H
 ATOM 9628 HA THR E 119 8.524 35.177 -37.333 1.00 15.37
 H
 ATOM 9629 HB THR E 119 7.717 36.348 -35.570 1.00 15.38
 H
 ATOM 9630 HG1 THR E 119 9.416 38.318 -36.110 1.00 15.47
 H
 ATOM 9631 HG21 THR E 119 9.484 36.341 -34.038 1.00 20.95
 H
 ATOM 9632 HG22 THR E 119 9.551 35.053 -34.950 1.00 20.95
 H
 ATOM 9633 HG23 THR E 119 10.518 36.270 -35.229 1.00 20.95
 H
 ATOM 9634 N SER E 120 8.075 37.705 -39.056 1.00 11.68 N
 ATOM 9635 CA SER E 120 7.067 38.444 -39.814 1.00 15.43
 C
 ATOM 9636 C SER E 120 6.196 37.531 -40.684 1.00 12.04 C
 ATOM 9637 O SER E 120 4.966 37.593 -40.619 1.00 10.68 O
 ATOM 9638 CB SER E 120 7.737 39.510 -40.682 1.00 14.31
 C
 ATOM 9639 OG SER E 120 8.074 40.644 -39.901 1.00 13.97
 O
 ATOM 9640 H SER E 120 8.888 37.911 -39.244 1.00 14.01 H
 ATOM 9641 HA SER E 120 6.482 38.899 -39.189 1.00 18.51
 H
 ATOM 9642 HB2 SER E 120 8.546 39.140 -41.070 1.00 17.18
 H
 ATOM 9643 HB3 SER E 120 7.124 39.778 -41.384 1.00 17.18
 H
 ATOM 9644 HG SER E 120 8.604 40.424 -39.288 1.00 16.76
 H
 ATOM 9645 N GLU E 121 6.827 36.691 -41.502 1.00 13.53 N
 ATOM 9646 CA GLU E 121 6.080 35.770 -42.357 1.00 16.10
 C
 ATOM 9647 C GLU E 121 5.202 34.861 -41.501 1.00 14.09 C
 ATOM 9648 O GLU E 121 4.025 34.658 -41.788 1.00 14.66 O
 ATOM 9649 CB GLU E 121 7.030 34.933 -43.222 1.00 18.39
 C
 ATOM 9650 CG GLU E 121 6.315 34.029 -44.220 1.00 17.83
 C
 ATOM 9651 CD GLU E 121 7.270 33.236 -45.097 1.00 26.57
 C
 ATOM 9652 OE1 GLU E 121 8.499 33.395 -44.946 1.00 29.79
 O
 ATOM 9653 OE2 GLU E 121 6.786 32.450 -45.940 1.00 28.08
 O1-
 ATOM 9654 H GLU E 121 7.681 36.635 -41.580 1.00 16.24 H
 ATOM 9655 HA GLU E 121 5.503 36.279 -42.947 1.00 19.32
 H
 ATOM 9656 HB2 GLU E 121 7.606 35.532 -43.723 1.00 22.07
 H
 ATOM 9657 HB3 GLU E 121 7.566 34.370 -42.642 1.00 22.07
 H
 ATOM 9658 HG2 GLU E 121 5.761 33.399 -43.734 1.00 21.40
 H
 ATOM 9659 HG3 GLU E 121 5.762 34.576 -44.800 1.00 21.40
 H
 ATOM 9660 N PHE E 122 5.798 34.331 -40.439 1.00 13.77 N
 ATOM 9661 CA PHE E 122 5.101 33.510 -39.458 1.00 14.62
 C
 ATOM 9662 C PHE E 122 3.851 34.212 -38.924 1.00 14.41 C
 ATOM 9663 O PHE E 122 2.760 33.641 -38.928 1.00 13.91 O

ATOM 3364 HG3 GLU B 183 15.612 30.920 -36.995 1.00 54.15
 H
 ATOM 3365 N MET B 184 12.478 30.594 -35.030 1.00 29.01
 N
 ATOM 3366 CA MET B 184 11.478 31.648 -35.192 1.00 25.24
 C
 ATOM 3367 C MET B 184 11.643 32.571 -33.986 1.00 34.39
 C
 ATOM 3368 O MET B 184 11.916 33.764 -34.133 1.00 34.16
 O
 ATOM 3369 CB MET B 184 10.075 31.032 -35.263 1.00 25.23
 C
 ATOM 3370 CG MET B 184 8.947 31.974 -35.675 1.00 22.82
 C
 ATOM 3371 SD MET B 184 8.098 32.757 -34.293 1.00 34.48
 S
 ATOM 3372 CE MET B 184 7.450 31.341 -33.400 1.00 28.01
 C
 ATOM 3373 H MET B 184 12.592 30.314 -34.275 1.00 34.81
 H
 ATOM 3374 HA MET B 184 11.631 32.152 -38.006 1.00 30.28
 H
 ATOM 3375 HB2 MET B 184 10.093 30.305 -35.905 1.00 30.28
 H
 ATOM 3376 HB3 MET B 184 9.852 30.681 -34.386 1.00 30.28
 H
 ATOM 3377 HG2 MET B 184 9.317 32.877 -36.231 1.00 27.15
 H
 ATOM 3378 HG3 MET B 184 8.289 31.470 -36.179 1.00 27.15
 H
 ATOM 3379 HE1 MET B 184 6.964 31.655 -32.621 1.00 33.61
 H
 ATOM 3380 HE2 MET B 184 6.855 30.845 -33.984 1.00 33.61
 H
 ATOM 3381 HE3 MET B 184 8.189 30.777 -33.124 1.00 33.61
 H
 ATOM 3382 N GLN B 185 11.505 31.998 -32.794 1.00 32.90
 N
 ATOM 3383 CA GLN B 185 11.808 32.696 -31.549 1.00 32.39
 C
 ATOM 3384 C GLN B 185 12.769 31.850 -30.723 1.00 34.72
 C
 ATOM 3385 O GLN B 185 12.721 30.619 -30.759 1.00 28.22
 O
 ATOM 3386 CB GLN B 185 10.531 32.976 -30.754 1.00 29.62
 C
 ATOM 3387 CG GLN B 185 9.601 34.000 -31.390 1.00 33.22
 C
 ATOM 3388 CD GLN B 185 9.964 35.435 -31.046 1.00 40.19
 C
 ATOM 3389 OE1 GLN B 185 11.094 35.730 -30.652 1.00 41.44
 O
 ATOM 3390 NE2 GLN B 185 8.997 36.337 -31.186 1.00 34.22
 N

ATOM 3391 H GLN B 185 11.232 31.190 -32.679 1.00 39.48
 H
 ATOM 3392 HA GLN B 185 12.237 33.542 -31.749 1.00 38.87
 H
 ATOM 3393 HB2 GLN B 185 10.036 32.148 -30.659 1.00 35.55
 H
 ATOM 3394 HB3 GLN B 185 10.779 33.310 -29.877 1.00 35.55
 H
 ATOM 3395 HG2 GLN B 185 9.641 33.905 -32.355 1.00 39.87
 H
 ATOM 3396 HG3 GLN B 185 8.696 33.839 -31.080 1.00 39.87
 H
 ATOM 3397 HE21 GLN B 185 9.150 37.164 -31.007 1.00 41.06
 H
 ATOM 3398 HE22 GLN B 185 8.218 36.094 -31.461 1.00 41.06
 H
 ATOM 3399 N LYS B 186 13.654 32.506 -29.980 1.00 34.85
 N
 ATOM 3400 CA LYS B 186 14.542 31.796 -29.071 1.00 34.85
 C
 ATOM 3401 C LYS B 186 13.694 31.086 -28.016 1.00 28.04
 C
 ATOM 3402 O LYS B 186 12.924 31.726 -27.301 1.00 27.27
 O
 ATOM 3403 CB LYS B 186 15.533 32.763 -28.418 1.00 43.85
 C
 ATOM 3404 CG LYS B 186 16.859 32.136 -28.014 1.00 64.98
 C
 ATOM 3405 CD LYS B 186 17.666 31.694 -29.229 1.00 85.87
 C
 ATOM 3406 CE LYS B 186 19.083 31.299 -28.845 1.00 104.79
 C
 ATOM 3407 NZ LYS B 186 19.756 30.516 -29.918 1.00 110.38
 N1+
 ATOM 3408 H LYS B 186 13.758 33.359 -29.984 1.00 41.82
 H
 ATOM 3409 HA LYS B 186 15.043 31.127 -29.563 1.00 41.82
 H
 ATOM 3410 HB2 LYS B 186 15.725 33.478 -29.044 1.00 52.62
 H
 ATOM 3411 HB3 LYS B 186 15.125 33.130 -27.618 1.00 52.62
 H
 ATOM 3412 HG2 LYS B 186 17.383 32.788 -27.523 1.00 77.98
 H
 ATOM 3413 HG3 LYS B 186 16.690 31.357 -27.462 1.00 77.98
 H
 ATOM 3414 HD3 LYS B 186 17.220 32.025 -28.025 1.00 103.05
 H

ATOM 9664 CB PHE E 122 6.072 33.171 -38.319 1.00 16.68
 C
 ATOM 9665 CG PHE E 122 5.445 32.476 -37.144 1.00 16.24
 C
 ATOM 9666 CD1 PHE E 122 5.386 31.093 -37.091 1.00 19.07
 C
 ATOM 9667 CD2 PHE E 122 4.959 33.204 -38.070 1.00 17.52
 C
 ATOM 9668 CE1 PHE E 122 4.830 30.451 -36.003 1.00 20.81
 C
 ATOM 9669 CE2 PHE E 122 4.398 32.568 -34.980 1.00 21.23
 C
 ATOM 9670 CZ PHE E 122 4.337 31.189 -34.944 1.00 22.10
 C
 ATOM 9671 H PHE E 122 6.633 34.438 -40.261 1.00 16.53
 H
 ATOM 9672 HA PHE E 122 4.825 32.680 -39.877 1.00 17.54
 H
 ATOM 9673 HB2 PHE E 122 6.766 32.589 -38.667 1.00 20.02
 H
 ATOM 9674 HB3 PHE E 122 6.469 33.994 -37.995 1.00 20.02
 H
 ATOM 9675 HD1 PHE E 122 5.717 30.591 -37.801 1.00 22.89
 H
 ATOM 9676 HD2 PHE E 122 4.998 34.133 -36.089 1.00 21.02
 H
 ATOM 9677 HE1 PHE E 122 4.787 29.522 -35.983 1.00 24.98
 H
 ATOM 9678 HE2 PHE E 122 4.067 33.068 -34.268 1.00 25.48
 H
 ATOM 9679 HZ PHE E 122 3.959 30.758 -34.211 1.00 26.52
 H
 ATOM 9680 N ARG E 123 4.008 35.459 -38.491 1.00 9.96
 N
 ATOM 9681 CA ARG E 123 2.915 36.190 -37.862 1.00 12.21
 C
 ATOM 9682 C ARG E 123 1.821 36.555 -38.871 1.00 13.20
 C
 ATOM 9683 O ARG E 123 0.660 36.720 -38.501 1.00 16.26
 O
 ATOM 9684 CB ARG E 123 3.461 37.442 -37.164 1.00 13.63
 C
 ATOM 9685 CG ARG E 123 4.080 37.153 -35.797 1.00 14.82
 C
 ATOM 9686 CD ARG E 123 5.182 38.138 -35.440 1.00 19.31
 C
 ATOM 9687 NE ARG E 123 4.809 39.485 -35.833 1.00 25.00
 N
 ATOM 9688 CZ ARG E 123 5.551 40.304 -36.569 1.00 13.96
 C
 ATOM 9689 NH1 ARG E 123 6.763 39.963 -36.994 1.00 17.77
 N1+
 ATOM 9690 NH2 ARG E 123 5.076 41.500 -36.857 1.00 20.81
 N
 ATOM 9691 H ARG E 123 4.741 35.905 -38.551 1.00 11.95
 H
 ATOM 9692 HA ARG E 123 2.513 35.625 -37.183 1.00 14.65
 H
 ATOM 9693 HB2 ARG E 123 4.147 37.839 -37.724 1.00 16.36
 H
 ATOM 9694 HB3 ARG E 123 2.735 38.072 -37.035 1.00 16.36
 H
 ATOM 9695 HG2 ARG E 123 3.391 37.212 -35.117 1.00 17.78
 H
 ATOM 9696 HG3 ARG E 123 4.464 36.262 -35.805 1.00 17.78
 H
 ATOM 9697 HD2 ARG E 123 5.326 38.127 -34.481 1.00 23.17
 H
 ATOM 9698 HD3 ARG E 123 5.996 37.896 -35.908 1.00 23.17
 H
 ATOM 9699 HE ARG E 123 4.045 39.776 -35.567 1.00 30.00
 H
 ATOM 9700 HH11 ARG E 123 7.080 39.185 -36.811 1.00 21.33
 H
 ATOM 9701 HH12 ARG E 123 7.225 40.516 -37.464 1.00 21.33
 H
 ATOM 9702 HH21 ARG E 123 4.296 41.732 -36.579 1.00 24.98
 H
 ATOM 9703 HH22 ARG E 123 5.547 42.049 -37.323 1.00 24.98
 H
 ATOM 9704 N LEU E 124 2.184 36.657 -40.146 1.00 11.77
 N
 ATOM 9705 CA LEU E 124 1.207 36.917 -41.200 1.00 12.92
 C
 ATOM 9706 C LEU E 124 0.445 35.654 -41.598 1.00 14.87
 C
 ATOM 9707 O LEU E 124 -0.771 35.691 -41.805 1.00 14.46
 O
 ATOM 9708 CB LEU E 124 1.890 37.508 -42.437 1.00 14.80
 C
 ATOM 9709 CG LEU E 124 1.021 37.592 -43.700 1.00 11.83
 C
 ATOM 9710 CD1 LEU E 124 -0.216 38.439 -43.460 1.00 15.58
 C
 ATOM 9711 CD2 LEU E 124 1.822 38.135 -44.871 1.00 14.19
 C
 ATOM 9712 H LEU E 124 2.993 36.579 -40.429 1.00 14.12
 H
 ATOM 9713 HA LEU E 124 0.561 37.565 -40.877 1.00 15.50
 H
 ATOM 9714 HB3 LEU E 124 3.483 38.408 -43.985 1.00 17.70
 H

ATOM 3414 HD2 LYS B 186 17.236 30.923 -29.633 1.00103.05
H
ATOM 3415 HD3 LYS B 186 17.716 32.425 -29.864 1.00103.05
H
ATOM 3416 HE2 LYS B 186 19.604 32.101 -28.684 1.00125.75
H
ATOM 3417 HE3 LYS B 186 19.055 30.753 -28.044 1.00125.75
H
ATOM 3418 HZ1 LYS B 186 19.799 30.999 -30.664 1.00132.46
H
ATOM 3419 HZ2 LYS B 186 20.581 30.301 -29.664 1.00132.46
H
ATOM 3420 HZ3 LYS B 186 19.300 29.770 -30.081 1.00132.46
H
ATOM 3421 N GLY B 187 13.816 29.765 -27.932 1.00 25.29
N
ATOM 3422 CA GLY B 187 13.002 28.997 -27.007 1.00 25.76
C
ATOM 3423 C GLY B 187 13.264 27.506 -27.086 1.00 23.48
C
ATOM 3424 O GLY B 187 14.020 27.050 -27.944 1.00 19.67
O
ATOM 3425 H GLY B 187 14.362 29.294 -28.400 1.00 30.35
H

ATOM 3426 HA2 GLY B 187 13.181 29.291 -26.101 1.00 30.91
H
ATOM 3427 HA3 GLY B 187 12.064 29.152 -27.200 1.00 30.91
H
ATOM 3428 N ASP B 188 12.629 26.752 -26.190 1.00 17.61
N
ATOM 3429 CA ASP B 188 12.873 25.316 -26.064 1.00 20.10
C
ATOM 3430 C ASP B 188 11.623 24.472 -26.317 1.00 17.87
C
ATOM 3431 O ASP B 188 11.587 23.291 -25.973 1.00 18.91
O
ATOM 3432 CB ASP B 188 13.420 25.000 -24.673 1.00 22.84
C
ATOM 3433 CG ASP B 188 14.737 25.686 -24.393 1.00 27.00
C
ATOM 3434 OD1 ASP B 188 15.629 25.638 -25.265 1.00 28.51
O
ATOM 3435 OD2 ASP B 188 14.877 26.274 -23.300 1.00 29.60
O1-
ATOM 3436 H ASP B 188 12.044 27.053 -25.637 1.00 21.13
H
ATOM 3437 HA ASP B 188 13.544 25.055 -26.714 1.00 24.12
H
ATOM 3438 HB2 ASP B 188 12.780 25.296 -24.007 1.00 27.41
H
ATOM 3439 HB3 ASP B 188 13.559 24.043 -24.598 1.00 27.41
H
ATOM 3440 N CYS B 189 10.597 25.079 -26.901 1.00 15.55
N
ATOM 3441 CA CYS B 189 9.399 24.344 -27.293 1.00 18.29
C
ATOM 3442 C CYS B 189 9.129 24.575 -28.777 1.00 18.34
C
ATOM 3443 O CYS B 189 9.771 25.421 -29.403 1.00 16.24
O
ATOM 3444 CB CYS B 189 8.202 24.763 -26.437 1.00 21.42
C
ATOM 3445 SG CYS B 189 8.369 24.310 -24.685 1.00 19.88
S
ATOM 3446 H CYS B 189 10.568 25.919 -27.083 1.00 18.66
H
ATOM 3447 HA CYS B 189 9.549 23.395 -27.158 1.00 21.95
H
ATOM 3448 HB2 CYS B 189 8.103 25.726 -26.487 1.00 25.71
H
ATOM 3449 HB3 CYS B 189 7.404 24.331 -26.781 1.00 25.71
H
ATOM 3450 N ALA B 190 8.195 23.813 -29.337 1.00 17.84
N
ATOM 3451 CA ALA B 190 7.935 23.856 -30.773 1.00 16.98
C
ATOM 3452 C ALA B 190 6.443 23.850 -31.098 1.00 13.84
C
ATOM 3453 O ALA B 190 5.680 23.040 -30.566 1.00 13.74
O
ATOM 3454 CB ALA B 190 8.622 22.686 -31.461 1.00 18.20
C
ATOM 3455 H ALA B 190 7.697 23.260 -28.907 1.00 21.40
H
ATOM 3456 HA ALA B 190 8.312 24.674 -31.133 1.00 20.37
H
ATOM 3457 HB1 ALA B 190 8.440 22.729 -32.413 1.00 21.84
H
ATOM 3458 HB2 ALA B 190 9.577 22.744 -31.303 1.00 21.84
H
ATOM 3459 HB3 ALA B 190 8.275 21.858 -31.094 1.00 21.84
H
ATOM 3460 N LEU B 191 6.047 24.763 -31.982 1.00 11.45
N

ATOM 3461 CA LEU B 191 4.680 24.829 -32.492 1.00 14.13
C
ATOM 3462 C LEU B 191 4.554 23.994 -33.749 1.00 16.78
C
ATOM 3463 O LEU B 191 5.395 24.103 -34.642 1.00 15.44
O

ATOM 9714 HB2 LEU E 124 2.182 36.406 -42.223 1.00 17.76
H
ATOM 9715 HB3 LEU E 124 2.661 36.961 -42.652 1.00 17.76
H
ATOM 9716 HG LEU E 124 0.725 36.698 -43.934 1.00 14.19
H
ATOM 9717 HD11 LEU E 124 -0.740 38.470 -44.276 1.00 18.69
H
ATOM 9718 HD12 LEU E 124 -0.738 38.040 -42.746 1.00 18.69
H
ATOM 9719 HD13 LEU E 124 0.059 39.335 -43.209 1.00 18.69
H
ATOM 9720 HD21 LEU E 124 1.250 38.177 -45.652 1.00 17.03
H
ATOM 9721 HD22 LEU E 124 2.144 39.022 -44.648 1.00 17.03
H
ATOM 9722 HD23 LEU E 124 2.572 37.544 -45.041 1.00 17.03
H
ATOM 9723 N LYS E 125 1.158 34.538 -41.705 1.00 13.01
N
ATOM 9724 CA LYS E 125 0.593 33.347 -42.336 1.00 15.82
C
ATOM 9725 C LYS E 125 -0.148 32.421 -41.379 1.00 17.64
C

ATOM 9726 O LYS E 125 -0.543 31.320 -41.758 1.00 13.71
O
ATOM 9727 CB LYS E 125 1.698 32.572 -43.050 1.00 13.96
C
ATOM 9728 CG LYS E 125 2.202 33.285 -44.298 1.00 20.01
C
ATOM 9729 CD LYS E 125 3.130 32.408 -45.114 1.00 23.78
C
ATOM 9730 CE LYS E 125 3.436 33.035 -46.467 1.00 22.29
C
ATOM 9731 NZ LYS E 125 4.222 32.110 -47.321 1.00 26.85
N1+
ATOM 9732 H LYS E 125 1.965 34.443 -41.424 1.00 15.61
H
ATOM 9733 HA LYS E 125 -0.043 33.633 -43.010 1.00 18.98
H
ATOM 9734 HB2 LYS E 125 2.448 32.461 -42.444 1.00 16.76
H
ATOM 9735 HB3 LYS E 125 1.355 31.705 -43.317 1.00 16.76
H
ATOM 9736 HG2 LYS E 125 1.446 33.526 -44.855 1.00 24.01
H
ATOM 9737 HG3 LYS E 125 2.691 34.080 -44.035 1.00 24.01
H
ATOM 9738 HD2 LYS E 125 3.965 32.292 -44.635 1.00 28.53
H
ATOM 9739 HD3 LYS E 125 2.707 31.548 -45.265 1.00 28.53
H
ATOM 9740 HE2 LYS E 125 2.604 33.238 -46.922 1.00 26.74
H
ATOM 9741 HE3 LYS E 125 3.955 33.844 -46.335 1.00 26.74
H
ATOM 9742 HZ1 LYS E 125 4.392 32.492 -48.106 1.00 32.22
H
ATOM 9743 HZ2 LYS E 125 4.993 31.910 -46.923 1.00 32.22
H
ATOM 9744 HZ3 LYS E 125 3.764 31.359 -47.457 1.00 32.22
H

ATOM 9745 N LYS E 126 -0.352 32.867 -40.145 1.00 15.49
N
ATOM 9746 CA LYS E 126 -1.062 32.056 -39.168 1.00 14.17
C
ATOM 9747 C LYS E 126 -2.423 31.628 -39.718 1.00 14.30
C
ATOM 9748 O LYS E 126 -2.765 30.447 -39.682 1.00 14.19
O
ATOM 9749 CB LYS E 126 -1.230 32.826 -37.862 1.00 13.34
C
ATOM 9750 CG LYS E 126 -1.750 31.990 -36.705 1.00 16.84
C
ATOM 9751 CD LYS E 126 -1.636 32.761 -35.400 1.00 20.30
C
ATOM 9752 CE LYS E 126 -2.149 31.960 -34.218 1.00 23.97
C
ATOM 9753 NZ LYS E 126 -1.883 32.674 -32.933 1.00 26.21
N1+
ATOM 9754 H LYS E 126 -0.091 33.632 -39.851 1.00 18.59
H
ATOM 9755 HA LYS E 126 -0.546 31.257 -38.983 1.00 17.00
H
ATOM 9756 HB2 LYS E 126 -0.368 33.187 -37.601 1.00 16.00
H
ATOM 9757 HB3 LYS E 126 -1.858 33.551 -38.007 1.00 16.00
H
ATOM 9758 HG2 LYS E 126 -2.684 31.775 -36.855 1.00 20.21
H
ATOM 9759 HG3 LYS E 126 -1.223 31.179 -36.630 1.00 20.21
H
ATOM 9760 HD2 LYS E 126 -0.704 32.977 -35.238 1.00 24.36
H

ATOM 9761 HD3 LYS E 126 -2.161 33.575 -35.464 1.00 24.36
H
ATOM 9762 HE2 LYS E 126 -3.106 31.835 -34.305 1.00 28.76
H
ATOM 9763 HE3 LYS E 126 1.697 31.103 -34.190 1.00 28.76
H

ATOM 3463 O LEU B 191	3.593	24.103	-34.042	1.00	13.41
ATOM 3464 CB LEU B 191	4.288	26.269	-32.817	1.00	12.09
ATOM 3465 CG LEU B 191	4.165	27.255	-31.659	1.00	14.17
ATOM 3466 CD1 LEU B 191	4.052	28.666	-32.203	1.00	14.01
ATOM 3467 CD2 LEU B 191	2.958	26.915	-30.798	1.00	16.56
ATOM 3468 H LEU B 191	6.564	25.368	-32.309	1.00	13.74
ATOM 3469 HA LEU B 191	4.066	24.482	-31.825	1.00	16.96
ATOM 3470 HB2 LEU B 191	4.953	26.629	-33.424	1.00	14.51
ATOM 3471 HB3 LEU B 191	3.428	26.250	-33.264	1.00	14.51
ATOM 3472 HG LEU B 191	4.959	27.203	-31.105	1.00	17.01
ATOM 3473 HD11 LEU B 191	3.974	29.285	-31.461	1.00	16.81
ATOM 3474 HD12 LEU B 191	4.847	28.868	-32.721	1.00	16.81
ATOM 3475 HD13 LEU B 191	3.265	28.724	-32.768	1.00	16.81
ATOM 3476 HD21 LEU B 191	2.900	27.553	-30.070	1.00	19.87
ATOM 3477 HD22 LEU B 191	2.158	26.962	-31.345	1.00	19.87
ATOM 3478 HD23 LEU B 191	3.065	26.018	-30.445	1.00	19.87
ATOM 3479 N TYR B 192	3.513	23.172	-33.834	1.00	16.15
ATOM 3480 CA TYR B 192	3.244	22.485	-35.084	1.00	12.87
ATOM 3481 C TYR B 192	2.607	23.440	-36.076	1.00	18.63
ATOM 3482 O TYR B 192	1.704	24.209	-35.732	1.00	14.22
ATOM 3483 CB TYR B 192	2.322	21.279	-34.921	1.00	17.45
ATOM 3484 CG TYR B 192	2.041	20.673	-36.280	1.00	18.09
ATOM 3485 CD1 TYR B 192	2.958	19.818	-36.876	1.00	18.30
ATOM 3486 CD2 TYR B 192	0.901	21.013	-36.997	1.00	15.77
ATOM 3487 CE1 TYR B 192	2.731	19.287	-38.131	1.00	17.41
ATOM 3488 CE2 TYR B 192	0.666	20.487	-38.257	1.00	19.17
ATOM 3489 CZ TYR B 192	1.586	19.625	-38.819	1.00	19.87
ATOM 3490 OH TYR B 192	1.361	19.098	-40.072	1.00	20.58
ATOM 3491 H TYR B 192	2.962	22.999	-33.197	1.00	19.37
ATOM 3492 HA TYR B 192	4.082	22.174	-35.461	1.00	15.44
ATOM 3493 HB2 TYR B 192	2.753	20.611	-34.366	1.00	20.94
ATOM 3494 HB3 TYR B 192	1.482	21.561	-34.527	1.00	20.94
ATOM 3495 HD1 TYR B 192	3.734	19.589	-36.417	1.00	21.96
ATOM 3496 HD2 TYR B 192	0.281	21.595	-36.621	1.00	18.82
ATOM 3497 HE1 TYR B 192	3.351	18.706	-38.512	1.00	20.89
ATOM 3498 HE2 TYR B 192	-0.107	20.714	-38.722	1.00	23.00
ATOM 3499 HH TYR B 192	0.633	19.384	-40.377	1.00	24.69
ATOM 3500 N ALA B 193	3.077	23.360	-37.315	1.00	12.79
ATOM 3501 CA ALA B 193	2.483	24.079	-38.431	1.00	15.94
ATOM 3502 C ALA B 193	2.550	23.173	-39.650	1.00	18.77
ATOM 3503 O ALA B 193	3.498	22.402	-39.801	1.00	16.34
ATOM 3504 CB ALA B 193	3.211	25.385	-38.685	1.00	17.09
ATOM 3505 H ALA B 193	3.756	22.883	-37.538	1.00	15.35
ATOM 3506 HA ALA B 193	1.553	24.274	-38.238	1.00	19.13
ATOM 3507 HB1 ALA B 193	2.792	25.839	-39.433	1.00	20.50
ATOM 3508 HB2 ALA B 193	3.156	25.937	-37.890	1.00	20.50
ATOM 3509 HB3 ALA B 193	4.139	25.194	-38.892	1.00	20.50
ATOM 3510 N SER B 194	1.543	23.243	-40.509	1.00	15.79
ATOM 3511 CA SER B 194	1.535	22.414	-41.708	1.00	21.22
ATOM 3512 C SER B 194	2.354	23.092	-42.803	1.00	20.82
ATOM 3513 O SER B 194	2.449	24.317	-42.813	1.00	23.78

ATOM 9763 H3 LYS E 126	-1.097	31.103	-34.150	1.00	20.70
ATOM 9764 HZ1 LYS E 126	-1.008	32.800	-32.830	1.00	31.45
ATOM 9765 HZ2 LYS E 126	-2.290	33.466	-32.935	1.00	31.45
ATOM 9766 HZ3 LYS E 126	-2.188	32.193	-32.249	1.00	31.45
ATOM 9767 N TRP E 127	-3.177	32.587	-40.254	1.00	13.47
ATOM 9768 CA TRP E 127	-4.497	32.314	-40.828	1.00	13.36
ATOM 9769 C TRP E 127	-4.575	32.682	-42.311	1.00	14.64
ATOM 9770 O TRP E 127	-5.632	32.557	-42.929	1.00	13.48
ATOM 9771 CB TRP E 127	-5.573	33.078	-40.053	1.00	13.26
ATOM 9772 CG TRP E 127	-5.758	32.580	-38.653	1.00	16.00
ATOM 9773 CD1 TRP E 127	-5.306	33.163	-37.508	1.00	16.46
ATOM 9774 CD2 TRP E 127	-6.437	31.386	-38.256	1.00	14.01
ATOM 9775 NE1 TRP E 127	-5.666	32.408	-36.419	1.00	20.27
ATOM 9776 CE2 TRP E 127	-6.365	31.312	-36.851	1.00	19.93
ATOM 9777 CE3 TRP E 127	-7.108	30.374	-38.951	1.00	20.52
ATOM 9778 CZ2 TRP E 127	-6.931	30.266	-36.129	1.00	17.91
ATOM 9779 CZ3 TRP E 127	-7.672	29.339	-38.232	1.00	22.57
ATOM 9780 CH2 TRP E 127	-7.579	29.291	-36.835	1.00	25.03
ATOM 9781 H TRP E 127	-2.944	33.413	-40.298	1.00	16.16
ATOM 9782 HA TRP E 127	-4.886	31.367	-40.745	1.00	16.03
ATOM 9783 HB2 TRP E 127	-5.322	34.014	-40.006	1.00	15.92
ATOM 9784 HB3 TRP E 127	-6.420	32.986	-40.517	1.00	15.92
ATOM 9785 HD1 TRP E 127	-4.823	33.957	-37.470	1.00	19.75
ATOM 9786 HE1 TRP E 127	-5.484	32.594	-35.599	1.00	24.32
ATOM 9787 HE3 TRP E 127	-7.174	30.400	-39.878	1.00	24.62
ATOM 9788 HZ2 TRP E 127	-6.873	30.232	-35.201	1.00	21.50
ATOM 9789 HZ3 TRP E 127	-8.119	28.660	-38.684	1.00	27.09
ATOM 9790 HH2 TRP E 127	-7.969	28.581	-36.378	1.00	30.03
ATOM 9791 N PHE E 128	-3.452	33.118	-42.876	1.00	13.43
ATOM 9792 CA PHE E 128	-3.425	33.694	-44.221	1.00	12.84
ATOM 9793 C PHE E 128	-2.168	33.275	-44.986	1.00	14.69
ATOM 9794 O PHE E 128	-1.174	33.999	-44.999	1.00	14.50
ATOM 9795 CB PHE E 128	-3.509	35.223	-44.122	1.00	15.03
ATOM 9796 CG PHE E 128	-3.640	35.922	-45.446	1.00	15.62
ATOM 9797 CD1 PHE E 128	-4.757	35.729	-46.242	1.00	14.48
ATOM 9798 CD2 PHE E 128	-2.660	36.800	-45.879	1.00	17.09
ATOM 9799 CE1 PHE E 128	-4.884	36.381	-47.456	1.00	14.50
ATOM 9800 CE2 PHE E 128	-2.780	37.454	-47.092	1.00	18.86
ATOM 9801 CZ PHE E 128	-3.895	37.245	-47.881	1.00	19.29
ATOM 9802 H PHE E 128	-2.680	33.091	-42.497	1.00	16.11
ATOM 9803 HA PHE E 128	-4.198	33.381	-44.717	1.00	15.40
ATOM 9804 HB2 PHE E 128	-4.283	35.457	-43.587	1.00	18.04
ATOM 9805 HB3 PHE E 128	-2.703	35.551	-43.694	1.00	18.04
ATOM 9806 HD1 PHE E 128	-5.426	35.147	-45.961	1.00	17.38
ATOM 9807 HD2 PHE E 128	-1.906	36.942	-45.353	1.00	20.50
ATOM 9808 HE1 PHE E 128	-5.636	36.239	-47.985	1.00	17.40
ATOM 9809 HE2 PHE E 128	-2.112	38.036	-47.376	1.00	22.63
ATOM 9810 HZ PHE E 128	-3.979	37.684	-43.696	1.00	23.15
ATOM 9811 N ASP E 129	-2.214	32.108	-45.627	1.00	14.98
ATOM 9812 CA ASP E 129	-1.055	31.599	-46.357	1.00	14.76

H
 ATOM 3613 HG12 ILE B 200 12.753 25.116 -32.478 1.00 27.71
 H
 ATOM 3614 HG13 ILE B 200 12.486 25.794 -33.887 1.00 27.71
 H
 ATOM 3615 HG21 ILE B 200 13.816 27.306 -30.939 1.00 27.64
 H
 ATOM 3616 HG22 ILE B 200 12.476 28.029 -30.485 1.00 27.64
 H
 ATOM 3617 HG23 ILE B 200 12.594 26.447 -30.399 1.00 27.64
 H
 ATOM 3618 HD11 ILE B 200 14.709 25.194 -33.704 1.00 34.69
 H
 ATOM 3619 HD12 ILE B 200 14.587 26.775 -33.814 1.00 34.69
 H
 ATOM 3620 HD13 ILE B 200 14.854 26.095 -32.403 1.00 34.69
 H
 ATOM 3621 N GLU B 201 9.629 28.066 -30.445 1.00 18.17
 N
 ATOM 3622 CA GLU B 201 8.939 29.143 -29.751 1.00 18.13
 C
 ATOM 3623 C GLU B 201 9.234 29.096 -28.260 1.00 19.85
 C
 ATOM 3624 O GLU B 201 9.528 28.034 -27.703 1.00 17.15
 O
 ATOM 3625 CB GLU B 201 7.428 29.050 -30.006 1.00 16.42
 C
 ATOM 3626 CG GLU B 201 6.564 30.052 -29.239 1.00 24.81
 C
 ATOM 3627 CD GLU B 201 6.879 31.502 -29.577 1.00 29.39
 C
 ATOM 3628 OE1 GLU B 201 7.969 31.986 -29.202 1.00 28.55
 O
 ATOM 3629 OE2 GLU B 201 6.028 32.161 -30.213 1.00 33.83
 O1-
 ATOM 3630 H GLU B 201 9.663 27.329 -30.003 1.00 21.80
 H
 ATOM 3631 HA GLU B 201 9.251 29.994 -30.094 1.00 21.75
 H
 ATOM 3632 HB2 GLU B 201 7.268 29.193 -30.952 1.00 19.70
 H
 ATOM 3633 HB3 GLU B 201 7.130 28.161 -29.759 1.00 19.70
 H
 ATOM 3634 HG2 GLU B 201 5.632 29.892 -29.453 1.00 29.77
 H
 ATOM 3635 HG3 GLU B 201 6.710 29.929 -28.288 1.00 29.77
 H

 ATOM 3636 N ASN B 202 9.168 30.260 -27.625 1.00 21.76
 N
 ATOM 3637 CA ASN B 202 9.292 30.361 -26.179 1.00 22.40
 C
 ATOM 3638 C ASN B 202 8.163 29.592 -25.495 1.00 18.61
 C
 ATOM 3639 O ASN B 202 6.984 29.863 -25.726 1.00 17.60
 O
 ATOM 3640 CB ASN B 202 9.284 31.831 -25.750 1.00 25.89
 C
 ATOM 3641 CG ASN B 202 9.627 32.019 -24.284 1.00 30.35
 C
 ATOM 3642 OD1 ASN B 202 9.134 31.298 -23.417 1.00 28.07
 O
 ATOM 3643 ND2 ASN B 202 10.484 32.995 -24.002 1.00 32.66
 N
 ATOM 3644 H ASN B 202 9.049 31.017 -28.017 1.00 26.11
 H
 ATOM 3645 HA ASN B 202 10.135 29.969 -25.904 1.00 26.88
 H
 ATOM 3646 HB2 ASN B 202 9.938 32.317 -26.276 1.00 31.07
 H
 ATOM 3647 HB3 ASN B 202 8.399 32.199 -25.900 1.00 31.07
 H
 ATOM 3648 HD21 ASN B 202 10.713 33.144 -23.187 1.00 39.19
 H
 ATOM 3649 HD22 ASN B 202 10.810 33.477 -24.635 1.00 39.19
 H
 ATOM 3650 N CYS B 203 8.541 28.633 -24.654 1.00 15.24
 N
 ATOM 3651 CA CYS B 203 7.584 27.779 -23.962 1.00 18.87
 C
 ATOM 3652 C CYS B 203 6.517 28.573 -23.207 1.00 18.33
 C
 ATOM 3653 O CYS B 203 5.426 28.065 -22.954 1.00 20.66
 O
 ATOM 3654 CB CYS B 203 8.322 26.852 -22.989 1.00 18.37
 C
 ATOM 3655 SG CYS B 203 9.514 25.728 -23.774 1.00 24.48
 S
 ATOM 3656 H CYS B 203 9.361 28.456 -24.465 1.00 18.29
 H
 ATOM 3657 HA CYS B 203 7.132 27.223 -24.615 1.00 22.64
 H
 ATOM 3658 HB2 CYS B 203 8.809 27.397 -22.351 1.00 22.04
 H
 ATOM 3659 HB3 CYS B 203 7.668 26.309 -22.522 1.00 22.04
 H
 ATOM 3660 N SER B 204 6.830 29.819 -22.859 1.00 17.86
 N
 ATOM 3661 CA SER B 204 5.916 30.656 -22.087 1.00 22.50
 C

N
 ATOM 9913 H HIS E 136 -7.180 35.107 -51.939 1.00 13.89 H

 ATOM 9914 HA HIS E 136 -9.262 36.688 -51.948 1.00 16.87 H
 ATOM 9915 HB2 HIS E 136 -6.656 37.142 -50.979 1.00 14.40 H
 ATOM 9916 HB3 HIS E 136 -7.780 38.256 -50.865 1.00 14.40 H
 ATOM 9917 HD1 HIS E 136 -7.815 38.239 -48.334 1.00 17.48 H
 ATOM 9918 HD2 HIS E 136 -8.642 34.765 -49.890 1.00 16.93 H
 ATOM 9919 HE1 HIS E 136 -8.606 36.900 -46.556 1.00 23.37 H
 ATOM 9920 HE2 HIS E 136 -9.106 34.793 -47.509 1.00 19.86 H

 ATOM 9921 N LEU E 137 -6.903 37.539 -53.922 1.00 13.80 N
 ATOM 9922 CA LEU E 137 -6.548 38.344 -55.086 1.00 14.11 C
 C
 ATOM 9923 C LEU E 137 -7.567 38.163 -56.209 1.00 14.94 C

 ATOM 9924 O LEU E 137 -8.077 39.134 -56.758 1.00 16.40 O
 ATOM 9925 CB LEU E 137 -5.142 37.980 -55.573 1.00 13.09 C
 C
 ATOM 9926 CG LEU E 137 -4.711 38.506 -56.945 1.00 15.68 C
 C
 ATOM 9927 CD1 LEU E 137 -4.834 40.023 -57.025 1.00 19.57 C
 C
 ATOM 9928 CD2 LEU E 137 -3.285 38.070 -57.252 1.00 16.15 C
 C

 ATOM 9929 H LEU E 137 -6.280 37.003 -53.668 1.00 16.56 H
 ATOM 9930 HA LEU E 137 -6.545 39.281 -54.833 1.00 16.93 H
 H
 ATOM 9931 HB2 LEU E 137 -4.504 38.317 -54.925 1.00 15.71 H
 H
 ATOM 9932 HB3 LEU E 137 -5.079 37.012 -55.607 1.00 15.71 H
 H
 ATOM 9933 HG LEU E 137 -5.290 38.125 -57.623 1.00 18.82 H
 H
 ATOM 9934 HD11 LEU E 137 -4.553 40.316 -57.905 1.00 23.48 H
 H
 ATOM 9935 HD12 LEU E 137 -5.759 40.272 -56.873 1.00 23.48 H
 H

 ATOM 9936 HD13 LEU E 137 -4.267 40.422 -56.346 1.00 23.48 H
 H
 ATOM 9937 HD21 LEU E 137 -3.031 38.412 -56.123 1.00 19.37 H
 H
 ATOM 9938 HD22 LEU E 137 -2.693 38.425 -56.570 1.00 19.37 H
 H
 ATOM 9939 HD23 LEU E 137 -3.245 37.100 -57.252 1.00 19.37 H
 H
 ATOM 9940 N ARG E 138 -7.872 36.915 -56.536 1.00 15.03 N
 N
 ATOM 9941 CA ARG E 138 -8.821 36.624 -57.599 1.00 17.21 C
 C
 ATOM 9942 C ARG E 138 -10.223 37.129 -57.242 1.00 18.67 C
 C
 ATOM 9943 O ARG E 138 -10.941 37.654 -58.093 1.00 17.07 O
 O
 ATOM 9944 CB ARG E 138 -8.835 35.121 -57.883 1.00 17.26 C
 C
 ATOM 9945 CG ARG E 138 -7.536 34.621 -58.502 1.00 18.09 C
 C
 ATOM 9946 CD ARG E 138 -7.529 33.110 -58.664 1.00 22.76 C
 C
 ATOM 9947 NE ARG E 138 -8.525 32.659 -59.628 1.00 25.06 N
 N
 ATOM 9948 CZ ARG E 138 -8.955 31.407 -59.728 1.00 30.07 C
 C
 ATOM 9949 NH1 ARG E 138 -8.479 30.470 -58.918 1.00 28.66 N1+
 N
 ATOM 9950 NH2 ARG E 138 -9.870 31.092 -60.635 1.00 31.23 N
 N
 ATOM 9951 H ARG E 138 -7.542 36.217 -56.156 1.00 18.04 H
 H
 ATOM 9952 HA ARG E 138 -8.537 37.078 -58.408 1.00 20.66 H
 H
 ATOM 9953 HB2 ARG E 138 -8.973 34.644 -57.050 1.00 20.72 H
 H
 ATOM 9954 HB3 ARG E 138 -9.556 34.924 -58.501 1.00 20.72 H
 H
 ATOM 9955 HG2 ARG E 138 -7.426 35.020 -59.380 1.00 21.70 H
 H
 ATOM 9956 HG3 ARG E 138 -6.794 34.867 -57.928 1.00 21.70 H
 H
 ATOM 9957 HD2 ARG E 138 -6.655 32.828 -58.978 1.00 27.31 H
 H
 ATOM 9958 HD3 ARG E 138 -7.727 32.698 -57.809 1.00 27.31 H
 H
 ATOM 9959 HE ARG E 138 -8.856 33.242 -60.167 1.00 30.07 H
 H
 ATOM 9960 HH11 ARG E 138 -7.888 30.673 -58.328 1.00 34.40 H
 H
 ATOM 9961 HH12 ARG E 138 -8.761 29.661 -58.985 1.00 34.40 H
 H

ATOM 3662	C	SER B 204	4.864	31.354	-22.948	1.00	20.68
ATOM 3663	O	SER B 204	3.937	31.963	-22.420	1.00	22.63
ATOM 3664	GB	SER B 204	6.703	31.710	-21.302	1.00	20.13
ATOM 3665	OG	SER B 204	7.470	31.104	-20.279	1.00	22.97
ATOM 3666	H	SER B 204	7.571	30.206	-23.061	1.00	21.43
ATOM 3667	HA	SER B 204	5.449	30.098	-21.446	1.00	27.00
ATOM 3668	HB2	SER B 204	7.298	32.177	-21.909	1.00	24.15
ATOM 3669	HB3	SER B 204	6.080	32.335	-20.901	1.00	24.15
ATOM 3670	HG	SER B 204	7.898	31.690	-19.855	1.00	27.57
ATOM 3671	N	THR B 205	5.005	31.270	-24.267	1.00	18.95
ATOM 3672	CA	THR B 205	4.096	31.964	-25.178	1.00	19.15
ATOM 3673	C	THR B 205	2.756	31.236	-25.307	1.00	18.16
ATOM 3674	O	THR B 205	2.722	30.073	-25.709	1.00	16.01
ATOM 3675	CB	THR B 205	4.704	32.103	-26.585	1.00	25.38
ATOM 3676	OG1	THR B 205	6.060	32.554	-26.487	1.00	28.77
ATOM 3677	CG2	THR B 205	3.896	33.092	-27.420	1.00	24.93
ATOM 3678	H	THR B 205	5.621	30.817	-24.661	1.00	22.74
ATOM 3679	HA	THR B 205	3.924	32.855	-24.835	1.00	22.99
ATOM 3680	HB	THR B 205	4.684	31.241	-27.030	1.00	30.45
ATOM 3681	HG1	THR B 205	6.087	33.300	-26.103	1.00	34.52
ATOM 3682	HG21	THR B 205	4.286	33.174	-28.305	1.00	29.92
ATOM 3683	HG22	THR B 205	2.981	32.784	-27.506	1.00	29.92
ATOM 3684	HG23	THR B 205	3.897	33.964	-26.994	1.00	29.92
ATOM 3685	N	PRO B 206	1.645	31.917	-24.977	1.00	18.00
ATOM 3686	CA	PRO B 206	0.350	31.248	-25.140	1.00	17.87
ATOM 3687	C	PRO B 206	0.050	30.892	-26.593	1.00	20.20
ATOM 3688	O	PRO B 206	0.187	31.737	-27.477	1.00	14.53
ATOM 3689	CB	PRO B 206	-0.655	32.286	-24.621	1.00	22.87
ATOM 3690	CG	PRO B 206	0.134	33.198	-23.763	1.00	22.22
ATOM 3691	CD	PRO B 206	1.494	33.257	-24.382	1.00	21.86
ATOM 3692	HA	PRO B 206	0.306	30.450	-24.591	1.00	21.45
ATOM 3693	HB2	PRO B 206	-1.042	32.767	-25.369	1.00	27.45
ATOM 3694	HB3	PRO B 206	-1.345	31.841	-24.104	1.00	27.45
ATOM 3695	HG2	PRO B 206	-0.277	34.077	-23.758	1.00	26.66
ATOM 3696	HG3	PRO B 206	0.183	32.839	-22.864	1.00	26.66
ATOM 3697	HD2	PRO B 206	1.525	33.939	-25.071	1.00	26.23
ATOM 3698	HD3	PRO B 206	2.171	33.404	-23.703	1.00	26.23
ATOM 3699	N	ASN B 207	-0.342	29.644	-26.829	1.00	19.17
ATOM 3700	CA	ASN B 207	-0.792	29.207	-28.146	1.00	16.49
ATOM 3701	C	ASN B 207	-1.897	28.165	-28.010	1.00	19.54
ATOM 3702	O	ASN B 207	-2.061	27.557	-26.950	1.00	15.66
ATOM 3703	CB	ASN B 207	0.371	28.628	-28.961	1.00	19.53
ATOM 3704	CG	ASN B 207	1.225	29.702	-29.620	1.00	16.92
ATOM 3705	OD1	ASN B 207	0.877	30.221	-30.681	1.00	16.98
ATOM 3706	ND2	ASN B 207	2.356	30.023	-29.002	1.00	17.66
ATOM 3707	H	ASN B 207	-0.356	29.022	-26.235	1.00	23.00
ATOM 3708	HA	ASN B 207	-1.151	29.968	-28.629	1.00	19.79
ATOM 3709	HB2	ASN B 207	0.042	29.144	-29.272	1.00	22.42

ATOM 9962	HH21	ARG E 138	-10.180	31.697	-61.161	1.00	37.48
ATOM 9963	HH22	ARG E 138	-10.149	30.281	-60.700	1.00	37.48
ATOM 9964	N	SER E 139	-10.603	36.994	-55.978	1.00	16.32
ATOM 9965	CA	SER E 139	-11.907	37.474	-55.534	1.00	16.34
ATOM 9966	C	SER E 139	-11.968	39.002	-55.579	1.00	17.91
ATOM 9967	O	SER E 139	-13.011	39.582	-55.889	1.00	16.73
ATOM 9968	CB	SER E 139	-12.210	36.973	-54.121	1.00	15.40
ATOM 9969	OG	SER E 139	-12.117	35.559	-54.052	1.00	15.94
ATOM 9970	H	SER E 139	-10.129	36.630	-55.359	1.00	19.59
ATOM 9971	HA	SER E 139	-12.590	37.128	-56.129	1.00	19.61
ATOM 9972	HB2	SER E 139	-11.569	37.361	-53.504	1.00	18.47
ATOM 9973	HB3	SER E 139	-13.109	37.242	-53.877	1.00	18.47
ATOM 9974	HG	SER E 139	-12.668	35.209	-54.582	1.00	19.13
ATOM 9975	N	LEU E 140	-10.851	39.657	-55.274	1.00	16.92
ATOM 9976	CA	LEU E 140	-10.813	41.119	-55.262	1.00	16.54
ATOM 9977	C	LEU E 140	-10.772	41.679	-56.680	1.00	16.09
ATOM 9978	O	LEU E 140	-11.345	42.734	-56.953	1.00	20.02
ATOM 9979	CB	LEU E 140	-9.612	41.620	-54.459	1.00	14.74
ATOM 9980	CG	LEU E 140	-9.696	41.416	-52.944	1.00	13.44
ATOM 9981	CD1	LEU E 140	-8.341	41.666	-52.303	1.00	16.07
ATOM 9982	CD2	LEU E 140	-10.762	42.310	-52.316	1.00	17.46
ATOM 9983	H	LEU E 140	-10.105	39.281	-55.070	1.00	20.30
ATOM 9984	HA	LEU E 140	-11.617	41.450	-54.834	1.00	19.85
ATOM 9985	HB2	LEU E 140	-8.820	41.157	-54.771	1.00	17.68
ATOM 9986	HB3	LEU E 140	-9.514	42.572	-54.618	1.00	17.68
ATOM 9987	HG	LEU E 140	-9.941	40.494	-52.766	1.00	16.13
ATOM 9988	HD11	LEU E 140	-8.415	41.532	-51.346	1.00	19.28
ATOM 9989	HD12	LEU E 140	-7.696	41.045	-52.676	1.00	19.28
ATOM 9990	HD13	LEU E 140	-8.068	42.578	-52.490	1.00	19.28
ATOM 9991	HD21	LEU E 140	-10.784	42.151	-51.359	1.00	20.95
ATOM 9992	HD22	LEU E 140	-10.540	43.238	-52.493	1.00	20.95
ATOM 9993	HD23	LEU E 140	-11.624	42.096	-52.707	1.00	20.95
ATOM 9994	N	VAL E 141	-10.099	40.975	-57.583	1.00	19.49
ATOM 9995	CA	VAL E 141	-10.106	41.360	-58.987	1.00	19.08
ATOM 9996	C	VAL E 141	-11.545	41.319	-59.499	1.00	21.59
ATOM 9997	O	VAL E 141	-11.956	42.169	-60.284	1.00	25.99
ATOM 9998	CB	VAL E 141	-9.200	40.441	-59.836	1.00	19.66
ATOM 9999	CG1	VAL E 141	-9.450	40.649	-61.326	1.00	22.61
ATOM 10000	CG2	VAL E 141	-7.733	40.702	-59.517	1.00	18.87
ATOM 10001	H	VAL E 141	-9.633	40.274	-57.409	1.00	23.39
ATOM 10002	HA	VAL E 141	-9.779	42.270	-59.071	1.00	22.90
ATOM 10003	HB	VAL E 141	-9.396	39.515	-59.623	1.00	23.59
ATOM 10004	HG11	VAL E 141	-8.868	40.059	-61.829	1.00	27.13
ATOM 10005	HG12	VAL E 141	-10.378	40.445	-61.522	1.00	27.13
ATOM 10006	HG13	VAL E 141	-9.260	41.573	-61.551	1.00	27.13
ATOM 10007	HG21	VAL E 141	-7.183	40.116	-60.059	1.00	22.64
ATOM 10008	HG22	VAL E 141	-7.528	41.829	-59.717	1.00	22.64
ATOM 10009	HG23	VAL E 141	-7.570	40.525	-59.576	1.00	22.64


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..
ATOM 3758 HB ILE B 210 -1.857 19.127 -31.315 1.00 18.65
H
ATOM 3759 HG12 ILE B 210 -4.066 20.397 -32.538 1.00 18.99
H
ATOM 3760 HG13 ILE B 210 -2.814 21.208 -31.996 1.00 18.99
H
ATOM 3761 HG21 ILE B 210 -3.090 17.718 -32.716 1.00 17.13
H
ATOM 3762 HG22 ILE B 210 -3.207 17.237 -31.207 1.00 17.13
H
ATOM 3763 HG23 ILE B 210 -4.401 18.041 -31.879 1.00 17.13
H
ATOM 3764 HD11 ILE B 210 -2.655 20.938 -34.282 1.00 22.04
H
ATOM 3765 HD12 ILE B 210 -1.461 20.172 -33.565 1.00 22.04
H
ATOM 3766 HD13 ILE B 210 -2.714 19.360 -34.108 1.00 22.04
H
ATOM 3767 N CYS B 211 -4.031 17.845 -28.478 1.00 13.03
N
ATOM 3768 CA CYS B 211 -3.838 16.677 -27.628 1.00 16.24
C
ATOM 3769 C CYS B 211 -3.968 15.420 -28.469 1.00 20.33
C
ATOM 3770 O CYS B 211 -4.712 15.394 -29.452 1.00 17.44
O
ATOM 3771 CB CYS B 211 -4.848 16.651 -26.479 1.00 22.87
C
ATOM 3772 SG CYS B 211 -4.586 17.937 -25.240 1.00 32.56
S
ATOM 3773 H CYS B 211 -4.856 18.049 -28.607 1.00 15.64
H
ATOM 3774 HA CYS B 211 -2.945 16.699 -27.249 1.00 19.49
H
ATOM 3775 HB2 CYS B 211 -5.739 16.770 -26.844 1.00 27.44
H

ATOM 3776 HB3 CYS B 211 -4.789 15.793 -26.031 1.00 27.44
H
ATOM 3777 N MET B 212 -3.236 14.385 -28.075 1.00 20.62
N
ATOM 3778 CA MET B 212 -3.224 13.123 -28.796 1.00 19.04
C
ATOM 3779 C MET B 212 -3.266 11.958 -27.822 1.00 24.41
C
ATOM 3780 O MET B 212 -2.621 11.994 -26.773 1.00 20.80
O
ATOM 3781 CB MET B 212 -1.982 13.025 -29.676 1.00 22.84
C
ATOM 3782 CG MET B 212 -1.792 11.672 -30.333 1.00 22.92
C
ATOM 3783 SD MET B 212 -0.403 11.689 -31.475 1.00 24.54
S
ATOM 3784 CE MET B 212 -0.348 9.970 -31.974 1.00 31.53
C
ATOM 3785 H MET B 212 -2.729 14.391 -27.380 1.00 24.74
H
ATOM 3786 HA MET B 212 -4.003 13.081 -29.372 1.00 22.85
H
ATOM 3787 HB2 MET B 212 -2.047 13.688 -30.381 1.00 27.41
H
ATOM 3788 HB3 MET B 212 -1.199 13.201 -29.131 1.00 27.41
H
ATOM 3789 HG2 MET B 212 -1.616 11.006 -29.650 1.00 27.50
H
ATOM 3790 HG3 MET B 212 -2.592 11.441 -30.830 1.00 27.50
H
ATOM 3791 HE1 MET B 212 0.378 9.849 -32.605 1.00 37.83
H
ATOM 3792 HE2 MET B 212 -0.200 9.419 -31.189 1.00 37.83
H
ATOM 3793 HE3 MET B 212 -1.192 9.735 -32.390 1.00 37.83
H
ATOM 3794 N GLN B 213 -4.031 10.931 -28.178 1.00 22.35
N
ATOM 3795 CA GLN B 213 -4.116 9.713 -27.386 1.00 24.56
C
ATOM 3796 C GLN B 213 -4.148 8.501 -28.309 1.00 31.59
C
ATOM 3797 O GLN B 213 -5.071 8.346 -29.111 1.00 28.14
O
ATOM 3798 CB GLN B 213 -5.357 9.735 -26.493 1.00 27.78
C
ATOM 3799 CG GLN B 213 -5.480 8.534 -25.565 1.00 30.43
C
ATOM 3800 CD GLN B 213 -6.838 8.462 -24.893 1.00 33.92
C
ATOM 3801 OE1 GLN B 213 -7.736 7.766 -25.363 1.00 34.06
O
ATOM 3802 NE2 GLN B 213 -6.991 9.185 -23.788 1.00 30.76
N
ATOM 3803 H GLN B 213 -4.519 10.917 -28.886 1.00 26.82
H
ATOM 3804 HA GLN B 213 -3.333 9.644 -26.818 1.00 29.47
H
ATOM 3805 HB2 GLN B 213 -5.329 10.533 -25.941 1.00 33.34
H
ATOM 3806 HB3 GLN B 213 -5.445 9.755 -27.057 1.00 33.24

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ATOM 10058 C MET E 144 -13.406 45.645 -60.384 1.00 35.15
C
ATOM 10059 O MET E 144 -13.712 46.735 -60.871 1.00 34.51
O
ATOM 10060 CB MET E 144 -11.370 45.506 -58.919 1.00 25.24
C
ATOM 10061 CG MET E 144 -10.688 46.653 -59.650 1.00 29.40
C
ATOM 10062 SD MET E 144 -10.298 46.242 -61.360 1.00 42.62
S
ATOM 10063 CE MET E 144 -9.018 45.007 -61.143 1.00 35.57
C
ATOM 10064 H MET E 144 -12.835 43.813 -58.026 1.00 30.34
H
ATOM 10065 HA MET E 144 -13.182 46.340 -58.465 1.00 33.56
H
ATOM 10066 HB2 MET E 144 -11.078 45.533 -57.994 1.00 30.28
H
ATOM 10067 HB3 MET E 144 -11.076 44.679 -59.330 1.00 30.28
H
ATOM 10068 HG2 MET E 144 -11.278 47.423 -59.653 1.00 35.29
H
ATOM 10069 HG3 MET E 144 -9.859 46.870 -59.196 1.00 35.29
H
ATOM 10070 HE1 MET E 144 -8.721 44.703 -62.015 1.00 42.68
H
ATOM 10071 HE2 MET E 144 -8.276 45.403 -60.660 1.00 42.68
H
ATOM 10072 HE3 MET E 144 -9.381 44.262 -60.639 1.00 42.68
H
ATOM 10073 N GLU E 145 -13.501 44.505 -61.059 1.00 31.93
N
ATOM 10074 CA GLU E 145 -13.949 44.488 -62.446 1.00 31.71
C
ATOM 10075 C GLU E 145 -15.462 44.676 -62.551 1.00 30.25
C

ATOM 10076 O GLU E 145 -15.959 45.154 -63.568 1.00 33.30
O
ATOM 10077 CB GLU E 145 -13.522 43.186 -63.125 1.00 33.36
C
ATOM 10078 CG GLU E 145 -12.021 43.118 -63.401 1.00 35.77
C
ATOM 10079 CD GLU E 145 -11.606 41.844 -64.115 1.00 37.01
C
ATOM 10080 OE1 GLU E 145 -12.430 40.908 -64.196 1.00 36.72
O
ATOM 10081 OE2 GLU E 145 -10.454 41.782 -64.598 1.00 37.94
O1-
ATOM 10082 H GLU E 145 -13.313 43.729 -60.738 1.00 38.32
H
ATOM 10083 HA GLU E 145 -13.526 45.222 -62.919 1.00 38.05
H
ATOM 10084 HB2 GLU E 145 -13.754 42.440 -62.550 1.00 40.04
H
ATOM 10085 HB3 GLU E 145 -13.986 43.107 -63.973 1.00 40.04
H
ATOM 10086 HG2 GLU E 145 -11.769 43.869 -63.960 1.00 42.93
H
ATOM 10087 HG3 GLU E 145 -11.544 43.157 -62.558 1.00 42.93
H
ATOM 10088 N ASP E 146 -16.188 44.314 -61.498 1.00 33.13
N
ATOM 10089 CA ASP E 146 -17.638 44.488 -61.473 1.00 33.34
C
ATOM 10090 C ASP E 146 -18.047 45.808 -60.815 1.00 39.24
C
ATOM 10091 O ASP E 146 -19.225 46.021 -60.525 1.00 45.17
O
ATOM 10092 CB ASP E 146 -18.306 43.323 -60.738 1.00 33.65
C
ATOM 10093 CG ASP E 146 -18.110 41.998 -61.444 1.00 38.71
C
ATOM 10094 OD1 ASP E 146 -17.633 42.000 -62.600 1.00 44.37
O
ATOM 10095 OD2 ASP E 146 -18.444 40.953 -60.846 1.00 37.49
O1-
ATOM 10096 H ASP E 146 -15.864 43.964 -60.782 1.00 39.75
H
ATOM 10097 HA ASP E 146 -17.969 44.495 -62.385 1.00 40.00
H
ATOM 10098 HB2 ASP E 146 -17.924 43.249 -59.850 1.00 40.39
H
ATOM 10099 HB3 ASP E 146 -19.259 43.492 -60.677 1.00 40.39
H
ATOM 10100 N SER E 147 -17.081 46.693 -60.585 1.00 36.27
N
ATOM 10101 CA SER E 147 -17.357 47.964 -59.919 1.00 39.56
C
ATOM 10102 C SER E 147 -18.193 48.896 -60.799 1.00 40.84
C
ATOM 10103 O SER E 147 -17.812 49.204 -61.926 1.00 41.91
O
ATOM 10104 CB SER E 147 -16.049 48.657 -59.528 1.00 40.67
C
ATOM 10105 CG SER E 147 -16.299 49.901 -58.895 1.00 39.95
O
ATOM 10106 H SER E 147 -16.957 46.589 -60.805 1.00 43.50

```

ATOM 3806 HB3 GLN B 213 -6.143 9.753 -27.057 1.00 36.54
 H
 ATOM 3807 HG2 GLN B 213 -5.356 7.722 -26.080 1.00 36.51
 H
 ATOM 3808 HG3 GLN B 213 -4.803 8.597 -24.873 1.00 36.51
 H
 ATOM 3809 HE21 GLN B 213 -7.742 9.177 -23.371 1.00 36.91
 H
 ATOM 3810 HE22 GLN B 213 -6.339 9.661 -23.491 1.00 36.91
 H

ATOM 3811 N ARG B 214 -3.137 7.645 -28.192 1.00 26.52
 N
 ATOM 3812 CA ARG B 214 -3.047 6.450 -29.023 1.00 33.12
 C
 ATOM 3813 C ARG B 214 -4.103 5.415 -28.633 1.00 37.91
 C
 ATOM 3814 O ARG B 214 -4.624 5.431 -27.514 1.00 34.52
 O
 ATOM 3815 CB ARG B 214 -1.646 5.838 -28.929 1.00 42.25
 C
 ATOM 3816 CG ARG B 214 -0.556 6.668 -29.617 1.00 42.31
 C
 ATOM 3817 CD ARG B 214 0.652 5.824 -30.026 1.00 42.80
 C
 ATOM 3818 NE ARG B 214 0.268 4.633 -30.787 1.00 51.67
 N
 ATOM 3819 CZ ARG B 214 0.147 4.575 -32.112 1.00 45.75
 C
 ATOM 3820 NH1 ARG B 214 0.385 5.640 -32.865 1.00 40.29
 N
 ATOM 3821 NH2 ARG B 214 -0.212 3.438 -32.692 1.00 44.70
 N
 ATOM 3822 H ARG B 214 -2.488 7.735 -27.635 1.00 31.82
 H
 ATOM 3823 HA ARG B 214 -3.201 6.699 -29.947 1.00 39.74
 H
 ATOM 3824 HB2 ARG B 214 -1.405 5.751 -27.993 1.00 50.70
 H
 ATOM 3825 HB3 ARG B 214 -1.659 4.963 -29.347 1.00 50.70
 H
 ATOM 3826 HG2 ARG B 214 -0.924 7.074 -30.417 1.00 50.77
 H
 ATOM 3827 HG3 ARG B 214 -0.248 7.356 -29.006 1.00 50.77
 H
 ATOM 3828 HD2 ARG B 214 1.240 6.360 -30.582 1.00 51.36
 H
 ATOM 3829 HD3 ARG B 214 1.122 5.534 -29.228 1.00 51.36
 H
 ATOM 3830 HE ARG B 214 0.108 3.914 -30.343 1.00 62.00
 H
 ATOM 3831 HH11 ARG B 214 0.617 6.382 -32.498 1.00 48.35
 H
 ATOM 3832 HH12 ARG B 214 0.304 5.589 -33.719 1.00 48.35
 H
 ATOM 3833 HH21 ARG B 214 -0.367 2.741 -32.213 1.00 53.64
 H
 ATOM 3834 HH22 ARG B 214 -0.289 3.397 -33.548 1.00 53.64
 H
 ATOM 3835 N THR B 215 -4.411 4.526 -29.575 1.00 42.55
 N
 ATOM 3836 CA THR B 215 -5.441 3.504 -29.396 1.00 47.95
 C
 ATOM 3837 C THR B 215 -6.789 4.141 -29.072 1.00 47.59
 C
 ATOM 3838 O THR B 215 -7.890 4.169 -29.914 1.00 48.20
 O
 ATOM 3839 CB THR B 215 -5.061 2.502 -28.283 1.00 45.58
 C
 ATOM 3840 OG1 THR B 215 -3.858 1.816 -28.651 1.00 50.86
 O
 ATOM 3841 CG2 THR B 215 -6.166 1.475 -28.071 1.00 55.86
 C
 ATOM 3842 H THR B 215 -4.028 4.494 -30.344 1.00 51.06
 H
 ATOM 3843 HA THR B 215 -5.537 3.008 -30.223 1.00 57.54
 H
 ATOM 3844 HB THR B 215 -4.920 2.980 -27.451 1.00 54.70
 H
 ATOM 3845 HG1 THR B 215 -3.645 1.269 -28.050 1.00 61.03
 H

ATOM 3846 HG21 THR B 215 -5.911 0.855 -27.370 1.00 67.03
 H
 ATOM 3847 HG22 THR B 215 -6.988 1.922 -27.814 1.00 67.03
 H
 ATOM 3848 HG23 THR B 215 -6.320 0.980 -28.891 1.00 67.03
 H

TER 3849 THR B 215
 ATOM 3850 N GLU C 93 -21.096 71.394 -8.126 1.00 57.72
 N
 ATOM 3851 CA GLU C 93 -19.991 72.179 -7.586 1.00 64.40
 C
 ATOM 3852 C GLU C 93 -18.719 71.951 -8.396 1.00 60.46
 C
 ATOM 3853 O GLU C 93 -18.309 72.806 -9.183 1.00 62.51
 O

ATOM 10105 H SER E 147 -16.237 46.362 -60.605 1.00 43.52
 H
 ATOM 10107 HA SER E 147 -17.859 47.792 -59.107 1.00 47.47
 H
 ATOM 10108 HB2 SER E 147 -15.561 48.084 -58.916 1.00 48.80
 H
 ATOM 10109 HB3 SER E 147 -15.523 48.811 -60.329 1.00 48.80
 H
 ATOM 10110 HG SER E 147 -15.573 50.269 -58.687 1.00 47.94
 H

ATOM 10111 N LYS E 148 -19.326 49.349 -60.270 1.00 44.08
 N
 ATOM 10112 CA LYS E 148 -20.219 50.241 -61.006 1.00 49.92
 C
 ATOM 10113 C LYS E 148 -19.658 51.658 -61.121 1.00 48.76
 C
 ATOM 10114 O LYS E 148 -20.209 52.494 -61.838 1.00 51.47
 O
 ATOM 10115 CB LYS E 148 -21.595 50.281 -60.339 1.00 47.47
 C
 ATOM 10116 CG LYS E 148 -22.494 49.113 -60.710 1.00 50.15
 C
 ATOM 10117 CD LYS E 148 -23.784 49.125 -59.908 1.00 47.36
 C
 ATOM 10118 CE LYS E 148 -24.808 48.165 -60.488 1.00 50.24
 C
 ATOM 10119 NZ LYS E 148 -24.266 46.787 -60.642 1.00 51.53
 N1+
 ATOM 10120 H LYS E 148 -19.603 49.153 -59.479 1.00 52.90
 H
 ATOM 10121 HA LYS E 148 -20.335 49.894 -61.905 1.00 59.91
 H
 ATOM 10122 HB2 LYS E 148 -21.476 50.269 -59.376 1.00 56.96
 H
 ATOM 10123 HB3 LYS E 148 -22.047 51.098 -60.604 1.00 56.96
 H
 ATOM 10124 HG2 LYS E 148 -22.721 49.170 -61.651 1.00 60.18
 H
 ATOM 10125 HG3 LYS E 148 -22.029 48.282 -60.526 1.00 60.18
 H
 ATOM 10126 HD2 LYS E 148 -23.596 48.855 -58.995 1.00 56.83
 H
 ATOM 10127 HD3 LYS E 148 -24.162 50.018 -59.922 1.00 56.83
 H
 ATOM 10128 HE2 LYS E 148 -25.575 48.123 -59.896 1.00 60.29
 H
 ATOM 10129 HE3 LYS E 148 -25.079 48.481 -61.364 1.00 60.29
 H
 ATOM 10130 HZ1 LYS E 148 -24.890 46.252 -60.983 1.00 61.84
 H
 ATOM 10131 HZ2 LYS E 148 -23.562 46.796 -61.187 1.00 61.84
 H
 ATOM 10132 HZ3 LYS E 148 -24.014 46.470 -59.850 1.00 61.84
 H
 ATOM 10133 N ARG E 149 -18.566 51.925 -60.411 1.00 53.83
 N
 ATOM 10134 CA ARG E 149 -17.911 53.229 -60.464 1.00 58.71
 C
 ATOM 10135 C ARG E 149 -17.092 53.366 -61.747 1.00 57.83
 C
 ATOM 10136 O ARG E 149 -17.518 54.015 -62.704 1.00 57.91
 O
 ATOM 10137 CB ARG E 149 -17.015 53.422 -59.237 1.00 55.33
 C
 ATOM 10138 CG ARG E 149 -16.391 54.807 -59.099 1.00 52.08
 C
 ATOM 10139 CD ARG E 149 -17.379 55.834 -58.558 1.00 50.40
 C
 ATOM 10140 NE ARG E 149 -16.679 56.984 -57.985 1.00 49.43
 N
 ATOM 10141 CZ ARG E 149 -16.619 57.279 -56.687 1.00 45.97
 C
 ATOM 10142 NH1 ARG E 149 -17.237 56.531 -55.780 1.00 36.16
 N1+
 ATOM 10143 NH2 ARG E 149 -15.943 58.348 -56.292 1.00 50.80
 N
 ATOM 10144 H ARG E 149 -18.180 51.363 -59.887 1.00 64.60
 H
 ATOM 10145 HA ARG E 149 -18.586 53.925 -60.460 1.00 70.45
 H

ATOM 10146 HB2 ARG E 149 -17.545 53.260 -58.441 1.00 66.39
 H
 ATOM 10147 HB3 ARG E 149 -16.291 52.779 -59.281 1.00 66.39
 H
 ATOM 10148 HG2 ARG E 149 -15.641 54.757 -58.486 1.00 62.50
 H
 ATOM 10149 HG3 ARG E 149 -16.091 55.108 -59.971 1.00 62.50
 H
 ATOM 10150 HD2 ARG E 149 -17.944 56.150 -59.280 1.00 60.48
 H
 ATOM 10151 HD3 ARG E 149 -17.917 55.427 -57.861 1.00 60.48
 H
 ATOM 10152 HE ARG E 149 -16.273 57.511 -58.530 1.00 59.32
 H
 ATOM 10153 HH11 ARG E 149 -17.678 55.834 -56.025 1.00 43.39
 H

ATOM 3854 CB GLU C 93 -19.747 71.824 -6.115 1.00 58.36
C
ATOM 3855 CG GLU C 93 -18.795 72.760 -5.383 1.00 58.10
C
ATOM 3856 CD GLU C 93 -19.458 74.063 -4.971 1.00 61.87
C
ATOM 3857 OE1 GLU C 93 -20.558 74.362 -5.481 1.00 60.81
O
ATOM 3858 OE2 GLU C 93 -18.885 74.786 -4.129 1.00 60.23
O1-
ATOM 3859 HA GLU C 93 -20.216 73.122 -7.636 1.00 77.28
H
ATOM 3860 HB2 GLU C 93 -20.598 71.844 -5.647 1.00 70.03
H
ATOM 3861 HB3 GLU C 93 -19.371 70.930 -6.071 1.00 70.03
H
ATOM 3862 HG2 GLU C 93 -18.474 72.320 -4.580 1.00 69.72
H
ATOM 3863 HG3 GLU C 93 -18.050 72.973 -5.966 1.00 69.72
H
ATOM 3864 N SER C 94 -18.107 70.787 -8.197 1.00 55.28
N
ATOM 3865 CA SER C 94 -16.857 70.437 -8.856 1.00 48.47
C
ATOM 3866 C SER C 94 -16.938 69.038 -9.447 1.00 42.81
C
ATOM 3867 O SER C 94 -17.428 68.105 -8.805 1.00 35.00
O
ATOM 3868 CB SER C 94 -15.690 70.525 -7.872 1.00 51.57
C
ATOM 3869 OG SER C 94 -15.518 71.852 -7.409 1.00 59.31
O
ATOM 3870 H SER C 94 -18.404 70.172 -7.673 1.00 66.34
H
ATOM 3871 HA SER C 94 -16.691 71.062 -9.579 1.00 58.16
H
ATOM 3872 HB2 SER C 94 -15.872 69.947 -7.115 1.00 61.88
H
ATOM 3873 HB3 SER C 94 -14.878 70.239 -8.320 1.00 61.88
H
ATOM 3874 HG SER C 94 -14.875 71.887 -6.870 1.00 71.18
H
ATOM 3875 N TYR C 95 -16.457 68.908 -10.678 1.00 41.19
N
ATOM 3876 CA TYR C 95 -16.444 67.634 -11.379 1.00 38.72
C
ATOM 3877 C TYR C 95 -15.019 67.168 -11.629 1.00 38.41
C
ATOM 3878 O TYR C 95 -14.099 67.975 -11.764 1.00 32.89
O
ATOM 3879 CB TYR C 95 -17.190 67.743 -12.708 1.00 37.08
C
ATOM 3880 CG TYR C 95 -18.693 67.809 -12.573 1.00 37.60
C

ATOM 3881 CD1 TYR C 95 -19.338 69.017 -12.344 1.00 41.89
C
ATOM 3882 CD2 TYR C 95 -19.469 66.663 -12.685 1.00 34.68
C
ATOM 3883 CE1 TYR C 95 -20.712 69.080 -12.226 1.00 39.87
C
ATOM 3884 CE2 TYR C 95 -20.842 66.716 -12.569 1.00 36.52
C
ATOM 3885 CZ TYR C 95 -21.459 67.926 -12.340 1.00 40.73
C
ATOM 3886 OH TYR C 95 -22.829 67.980 -12.225 1.00 41.72
O
ATOM 3887 H TYR C 95 -16.127 69.557 -11.136 1.00 49.43
H
ATOM 3888 HA TYR C 95 -16.890 66.966 -10.835 1.00 46.47
H
ATOM 3889 HB2 TYR C 95 -16.899 68.549 -13.162 1.00 44.49
H
ATOM 3890 HB3 TYR C 95 -16.976 66.967 -13.249 1.00 44.49
H
ATOM 3891 HD1 TYR C 95 -18.837 69.797 -12.267 1.00 50.27
H
ATOM 3892 HD2 TYR C 95 -19.055 65.845 -12.840 1.00 41.62
H
ATOM 3893 HE1 TYR C 95 -21.132 69.895 -12.072 1.00 47.85
H
ATOM 3894 HE2 TYR C 95 -21.348 65.940 -12.645 1.00 43.82
H
ATOM 3895 HH TYR C 95 -23.074 68.771 -12.087 1.00 50.06
H
ATOM 3896 N CYS C 96 -14.853 65.853 -11.684 1.00 35.27
N
ATOM 3897 CA CYS C 96 -13.590 65.246 -12.064 1.00 33.31
C
ATOM 3898 C CYS C 96 -13.632 64.911 -13.550 1.00 27.94
C
ATOM 3899 O CYS C 96 -14.616 64.360 -14.036 1.00 24.96
O
ATOM 3900 CB CYS C 96 -13.329 63.990 -11.232 1.00 32.47
C
ATOM 3901 SG CYS C 96 -11.682 63.299 -11.433 1.00 36.22
S
ATOM 3902 H CYS C 96 -15.470 65.283 -11.503 1.00 42.33
H
ATOM 3903 HA CYS C 96 -12.867 65.874 -11.909 1.00 39.98
H

..
ATOM 10154 HH12 ARG E 149 -17.191 56.739 -54.947 1.00 43.39
H
ATOM 10155 HH21 ARG E 149 -15.543 58.842 -56.871 1.00 60.96
H
ATOM 10156 HH22 ARG E 149 -15.906 58.549 -55.457 1.00 60.96
H
TER 10157 ARG E 149
ATOM 10158 N GLY F 0 -3.228 29.760 20.619 1.00 29.41 N
ATOM 10159 CA GLY F 0 -3.768 30.515 19.453 1.00 26.44 C
ATOM 10160 C GLY F 0 -4.157 29.577 18.329 1.00 26.73 C
ATOM 10161 O GLY F 0 -4.379 28.388 18.561 1.00 25.80 O
ATOM 10162 H1 GLY F 0 -3.701 29.959 21.346 1.00 35.29 H
ATOM 10163 H2 GLY F 0 -3.283 28.886 20.459 1.00 35.29 H
ATOM 10164 H3 GLY F 0 -2.376 29.984 20.750 1.00 35.29 H
ATOM 10165 HA2 GLY F 0 -4.551 31.019 19.723 1.00 31.73 H
ATOM 10166 HA3 GLY F 0 -3.097 31.133 19.124 1.00 31.73 H
ATOM 10167 N HIS F 1 -4.237 30.106 17.110 1.00 21.94 N
ATOM 10168 CA HIS F 1 -4.640 29.302 15.960 1.00 20.81 C
ATOM 10169 C HIS F 1 -3.752 29.565 14.754 1.00 20.41 C
ATOM 10170 O HIS F 1 -3.175 30.643 14.618 1.00 18.02 O
ATOM 10171 CB HIS F 1 -6.099 29.577 15.600 1.00 19.93 C
ATOM 10172 CG HIS F 1 -7.065 29.227 16.687 1.00 24.76 C
ATOM 10173 ND1 HIS F 1 -7.406 27.926 16.989 1.00 25.09 N
ATOM 10174 CD2 HIS F 1 -7.762 30.008 17.546 1.00 26.11 C
ATOM 10175 CE1 HIS F 1 -8.273 27.921 17.986 1.00 27.35 C
ATOM 10176 NE2 HIS F 1 -8.505 29.171 18.343 1.00 27.19 N
ATOM 10177 H HIS F 1 -4.063 30.927 16.923 1.00 26.33 H
ATOM 10178 HA HIS F 1 -4.561 28.363 16.190 1.00 24.97 H
ATOM 10179 HB2 HIS F 1 -6.200 30.522 15.405 1.00 23.91 H
ATOM 10180 HB3 HIS F 1 -6.331 29.053 14.817 1.00 23.91 H

ATOM 10181 HD1 HIS F 1 -7.103 27.227 16.590 1.00 30.10 H
ATOM 10182 HD2 HIS F 1 -7.742 30.937 17.589 1.00 31.34 H
ATOM 10183 HE1 HIS F 1 -8.654 27.166 18.372 1.00 32.82 H
ATOM 10184 HE2 HIS F 1 -9.036 29.421 18.972 1.00 32.63 H
ATOM 10185 N LYS F 2 -3.635 28.568 13.884 1.00 17.59 N
ATOM 10186 CA LYS F 2 -2.874 28.734 12.658 1.00 18.28 C
ATOM 10187 C LYS F 2 -3.516 27.985 11.498 1.00 19.46 C
ATOM 10188 O LYS F 2 -4.114 26.920 11.668 1.00 15.97 O
ATOM 10189 CB LYS F 2 -1.424 28.284 12.858 1.00 21.88 C
ATOM 10190 CG LYS F 2 -1.243 26.852 13.311 1.00 29.22 C
ATOM 10191 GD LYS F 2 0.205 26.606 13.713 1.00 30.79 C
ATOM 10192 GE LYS F 2 0.429 25.175 14.167 1.00 40.64 C
ATOM 10193 NZ LYS F 2 1.839 24.947 14.592 1.00 46.99
N1+
ATOM 10194 H LYS F 2 -3.985 27.788 13.982 1.00 21.11 H
ATOM 10195 HA LYS F 2 -2.861 29.676 12.428 1.00 21.93 H
ATOM 10196 HB2 LYS F 2 -0.953 28.385 12.017 1.00 26.26
H
ATOM 10197 HB3 LYS F 2 -1.015 28.855 13.528 1.00 26.26
H
ATOM 10198 HG2 LYS F 2 -1.810 26.681 14.079 1.00 35.07
H
ATOM 10199 HG3 LYS F 2 -1.467 26.252 12.583 1.00 35.07
H
ATOM 10200 HD2 LYS F 2 0.781 26.775 12.951 1.00 36.94
H
ATOM 10201 HD3 LYS F 2 0.438 27.196 14.446 1.00 36.94
H
ATOM 10202 HE2 LYS F 2 -0.150 24.985 14.921 1.00 48.77
H
ATOM 10203 HE3 LYS F 2 0.233 24.573 13.433 1.00 48.77 H

ATOM 3904 HB2 CYS C 96 -13.445 64.208 -10.294 1.00 38.96 H
 H
 ATOM 3905 HB3 CYS C 96 -13.969 63.307 -11.490 1.00 38.96 H
 H
 ATOM 3906 N GLY C 97 -12.573 65.259 -14.272 1.00 28.67 N
 N
 ATOM 3907 CA GLY C 97 -12.490 64.946 -15.687 1.00 31.01 C
 C
 ATOM 3908 C GLY C 97 -12.065 66.130 -16.535 1.00 33.85 C
 C
 ATOM 3909 O GLY C 97 -11.450 67.067 -16.028 1.00 35.84 O
 O
 ATOM 3910 H GLY C 97 -11.888 65.677 -13.962 1.00 34.40 H
 H
 ATOM 3911 HA2 GLY C 97 -11.849 64.230 -15.820 1.00 37.22 H
 H
 ATOM 3912 HA3 GLY C 97 -13.357 64.643 -16.000 1.00 37.22 H
 H
 ATOM 3913 N PRO C 98 -12.391 66.097 -17.837 1.00 33.61 N
 N
 ATOM 3914 CA PRO C 98 -13.165 65.036 -18.492 1.00 34.25 C
 C
 ATOM 3915 C PRO C 98 -12.428 63.695 -18.552 1.00 32.91 C
 C

ATOM 3916 O PRO C 98 -11.200 63.661 -18.522 1.00 33.58 O
 O
 ATOM 3917 CB PRO C 98 -13.400 65.596 -19.897 1.00 43.48 C
 C
 ATOM 3918 CG PRO C 98 -12.285 66.542 -20.119 1.00 44.16 C
 C
 ATOM 3919 CD PRO C 98 -11.991 67.149 -18.785 1.00 39.32 C
 C
 ATOM 3920 HA PRO C 98 -14.019 64.916 -18.046 1.00 41.10 H
 H
 ATOM 3921 HB2 PRO C 98 -13.374 64.875 -20.546 1.00 52.18 H
 H
 ATOM 3922 HB3 PRO C 98 -14.253 66.056 -19.928 1.00 52.18 H
 H
 ATOM 3923 HG2 PRO C 98 -11.512 66.060 -20.452 1.00 52.99 H
 H
 ATOM 3924 HG3 PRO C 98 -12.560 67.225 -20.751 1.00 52.99 H
 H
 ATOM 3925 HD2 PRO C 98 -11.043 67.337 -18.701 1.00 47.19 H
 H
 ATOM 3926 HD3 PRO C 98 -12.526 67.946 -18.651 1.00 47.19 H
 H
 ATOM 3927 N CYS C 99 -13.195 62.610 -18.619 1.00 29.92 N
 N
 ATOM 3928 CA CYS C 99 -12.656 61.259 -18.747 1.00 30.84 C
 C
 ATOM 3929 C CYS C 99 -13.492 60.459 -19.732 1.00 33.78 C
 C
 ATOM 3930 O CYS C 99 -14.602 60.863 -20.076 1.00 29.20 O
 O
 ATOM 3931 CB CYS C 99 -12.646 60.535 -17.400 1.00 24.67 C
 C
 ATOM 3932 SG CYS C 99 -11.422 61.121 -16.229 1.00 27.04 S
 S
 ATOM 3933 H CYS C 99 -14.054 62.632 -18.593 1.00 35.90 H
 H
 ATOM 3934 HA CYS C 99 -11.746 61.303 -19.079 1.00 37.01 H
 H
 ATOM 3935 HB2 CYS C 99 -13.518 60.639 -16.987 1.00 29.60 H
 H
 ATOM 3936 HB3 CYS C 99 -12.473 59.593 -17.557 1.00 29.60 H
 H
 ATOM 3937 N PRO C 100 -12.963 59.314 -20.190 1.00 30.07 N
 N
 ATOM 3938 CA PRO C 100 -13.800 58.399 -20.968 1.00 29.87 C
 C
 ATOM 3939 C PRO C 100 -14.997 57.928 -20.148 1.00 33.56 C
 C
 ATOM 3940 O PRO C 100 -14.919 57.895 -18.917 1.00 26.53 O
 O
 ATOM 3941 CB PRO C 100 -12.852 57.239 -21.291 1.00 30.74 C
 C
 ATOM 3942 CG PRO C 100 -11.483 57.830 -21.199 1.00 29.98 C
 C
 ATOM 3943 CD PRO C 100 -11.566 58.853 -20.110 1.00 28.76 C
 C
 ATOM 3944 HA PRO C 100 -14.102 58.818 -21.789 1.00 35.84 H
 H
 ATOM 3945 HB2 PRO C 100 -12.965 56.531 -20.638 1.00 36.89 H
 H
 ATOM 3946 HB3 PRO C 100 -13.026 56.912 -22.188 1.00 36.89 H
 H
 ATOM 3947 HG2 PRO C 100 -10.843 57.138 -20.971 1.00 35.98 H
 H
 ATOM 3948 HG3 PRO C 100 -11.251 58.248 -22.043 1.00 35.98 H
 H
 ATOM 3949 HD2 PRO C 100 -11.393 58.444 -19.247 1.00 34.51 H
 H
 ATOM 3950 HD3 PRO C 100 -10.956 59.586 -20.286 1.00 34.51 H
 H

ATOM 3951 N LYS C 101 -16.086 57.579 -20.825 1.00 31.45 N
 N
 ATOM 3952 CA LYS C 101 -17.315 57.171 -20.154 1.00 38.12 C
 C

ATOM 10204 HZ1 LYS F 2 2.043 25.487 15.270 1.00 56.39 H
 H
 ATOM 10205 HZ2 LYS F 2 1.944 24.103 14.854 1.00 56.39 H
 H
 ATOM 10206 HZ3 LYS F 2 2.391 25.111 13.914 1.00 56.39 H
 H
 ATOM 10207 N LEU F 3 -3.404 28.589 10.321 1.00 18.68 N
 N
 ATOM 10208 CA LEU F 3 -3.925 28.030 9.086 1.00 17.42 C
 C
 ATOM 10209 C LEU F 3 -2.752 27.857 8.134 1.00 16.58 C
 C
 ATOM 10210 O LEU F 3 -2.066 28.828 7.807 1.00 15.05 O
 O
 ATOM 10211 CB LEU F 3 -4.995 28.945 8.485 1.00 15.28 C
 C
 ATOM 10212 CG LEU F 3 -5.747 28.440 7.256 1.00 18.11 C
 C
 ATOM 10213 CD1 LEU F 3 -6.670 27.286 7.622 1.00 17.93 C
 C
 ATOM 10214 CD2 LEU F 3 -6.527 29.581 6.615 1.00 15.66 C
 C
 ATOM 10215 H LEU F 3 -3.016 29.349 10.212 1.00 22.41 H
 H

ATOM 10216 HA LEU F 3 -4.319 27.160 9.258 1.00 20.90 H
 H
 ATOM 10217 HB2 LEU F 3 -5.657 29.121 9.171 1.00 18.34 H
 H
 ATOM 10218 HB3 LEU F 3 -4.568 29.779 8.234 1.00 18.34 H
 H
 ATOM 10219 HG LEU F 3 -5.105 28.115 6.606 1.00 21.73 H
 H
 ATOM 10220 HD11 LEU F 3 -7.134 26.987 6.824 1.00 21.52 H
 H
 ATOM 10221 HD12 LEU F 3 -6.139 26.561 7.987 1.00 21.52 H
 H
 ATOM 10222 HD13 LEU F 3 -7.312 27.592 8.282 1.00 21.52 H
 H
 ATOM 10223 HD21 LEU F 3 -6.998 29.243 5.837 1.00 18.80 H
 H
 ATOM 10224 HD22 LEU F 3 -7.162 29.931 7.260 1.00 18.80 H
 H
 ATOM 10225 HD23 LEU F 3 -5.906 30.278 6.349 1.00 18.80 H
 H

ATOM 10226 N ALA F 4 -2.520 26.620 7.706 1.00 17.17 N
 N
 ATOM 10227 CA ALA F 4 -1.347 26.278 6.911 1.00 13.80 C
 C
 ATOM 10228 C ALA F 4 -1.737 25.668 5.570 1.00 18.72 C
 C
 ATOM 10229 O ALA F 4 -2.616 24.807 5.492 1.00 15.41 O
 O
 ATOM 10230 CB ALA F 4 -0.455 25.321 7.681 1.00 16.99 C
 C
 ATOM 10231 H ALA F 4 -3.037 25.951 7.865 1.00 20.60 H
 H
 ATOM 10232 HA ALA F 4 -0.839 27.085 6.736 1.00 16.56 H
 H
 ATOM 10233 HB1 ALA F 4 0.319 25.105 7.138 1.00 20.38 H
 H
 ATOM 10234 HB2 ALA F 4 -0.172 25.747 8.506 1.00 20.38 H
 H
 ATOM 10235 HB3 ALA F 4 -0.955 24.514 7.880 1.00 20.38 H
 H
 ATOM 10236 N PHE F 5 -1.065 26.132 4.522 1.00 14.07 N
 N
 ATOM 10237 CA PHE F 5 -1.247 25.619 3.171 1.00 15.88 C
 C
 ATOM 10238 C PHE F 5 0.038 24.967 2.696 1.00 17.08 C
 C
 ATOM 10239 O PHE F 5 1.085 25.610 2.658 1.00 19.17 O
 O
 ATOM 10240 CB PHE F 5 -1.642 26.742 2.213 1.00 11.34 C
 C
 ATOM 10241 CG PHE F 5 -2.919 27.422 2.580 1.00 10.85 C
 C
 ATOM 10242 CD1 PHE F 5 -2.940 28.405 3.554 1.00 13.28 C
 C
 ATOM 10243 CD2 PHE F 5 -4.100 27.084 1.953 1.00 12.14 C
 C
 ATOM 10244 CE1 PHE F 5 -4.120 29.036 3.893 1.00 13.84 C
 C
 ATOM 10245 CE2 PHE F 5 -5.280 27.712 2.288 1.00 11.37 C
 C
 ATOM 10246 CZ PHE F 5 -5.291 28.686 3.258 1.00 14.78 C
 C
 ATOM 10247 H PHE F 5 -0.481 26.761 4.571 1.00 16.89 H
 H
 ATOM 10248 HA PHE F 5 -1.951 24.952 3.169 1.00 19.06 H
 H
 ATOM 10249 HB2 PHE F 5 -0.940 27.411 2.209 1.00 13.61 H
 H
 ATOM 10250 HB3 PHE F 5 -1.749 26.371 1.323 1.00 13.61 H
 H

ATOM 10251 HD1 PHE F 5 -2.151 28.643 3.984 1.00 15.93 H
 H
 ATOM 10252 HD2 PHE F 5 -4.100 26.425 1.296 1.00 14.56 H
 H

C
ATOM 4103 OD1 ASN C 109 -3.364 61.656 -14.015 1.00 30.85
O
ATOM 4104 ND2 ASN C 109 -3.434 61.653 -11.775 1.00 23.23
N
ATOM 4105 H ASN C 109 -7.173 62.292 -12.148 1.00 26.82
H
ATOM 4106 HA ASN C 109 -6.065 61.583 -14.526 1.00 25.60
H
ATOM 4107 HB2 ASN C 109 -5.452 60.336 -12.068 1.00 29.18
H
ATOM 4108 HB3 ASN C 109 -5.049 59.716 -13.475 1.00 29.18
H
ATOM 4109 HD21 ASN C 109 -2.705 62.105 -11.713 1.00 27.87
H
ATOM 4110 HD22 ASN C 109 -3.848 61.405 -11.062 1.00 27.87
H
ATOM 4111 N CYS C 110 -7.646 59.804 -15.053 1.00 16.78
N
ATOM 4112 CA CYS C 110 -8.675 58.825 -15.382 1.00 19.50
C
ATOM 4113 C CYS C 110 -8.083 57.420 -15.392 1.00 18.25
C
ATOM 4114 O CYS C 110 -6.991 57.210 -15.923 1.00 16.64
O
ATOM 4115 CB CYS C 110 -9.296 59.131 -16.745 1.00 22.08
C
ATOM 4116 SG CYS C 110 -9.588 60.882 -17.059 1.00 25.44
S
ATOM 4117 H CYS C 110 -7.122 59.987 -15.710 1.00 20.14
H
ATOM 4118 HA CYS C 110 -9.376 58.857 -14.712 1.00 23.40
H
ATOM 4119 HB2 CYS C 110 -8.700 58.804 -17.438 1.00 26.50
H
ATOM 4120 HB3 CYS C 110 -10.150 58.675 -16.807 1.00 26.50
H
ATOM 4121 N TYR C 111 -8.806 56.462 -14.823 1.00 16.40
N
ATOM 4122 CA TYR C 111 -8.350 55.074 -14.793 1.00 16.58
C
ATOM 4123 C TYR C 111 -9.442 54.103 -15.219 1.00 18.92
C
ATOM 4124 O TYR C 111 -10.626 54.362 -15.018 1.00 17.47
O
ATOM 4125 CB TYR C 111 -7.872 54.690 -13.391 1.00 15.45
C

ATOM 4126 CG TYR C 111 -6.797 55.583 -12.823 1.00 14.27
C
ATOM 4127 CD1 TYR C 111 -5.456 55.321 -13.059 1.00 17.54
C
ATOM 4128 CD2 TYR C 111 -7.124 56.680 -12.039 1.00 17.77
C
ATOM 4129 CE1 TYR C 111 -4.470 56.131 -12.535 1.00 19.61
C
ATOM 4130 CE2 TYR C 111 -6.148 57.495 -11.509 1.00 15.51
C
ATOM 4131 CZ TYR C 111 -4.822 57.216 -11.760 1.00 17.01
C
ATOM 4132 OH TYR C 111 -3.845 58.025 -11.239 1.00 17.34
O
ATOM 4133 H TYR C 111 -9.569 56.589 -14.446 1.00 19.67
H
ATOM 4134 HA TYR C 111 -7.603 54.973 -15.404 1.00 19.90
H
ATOM 4135 HB2 TYR C 111 -8.630 54.723 -12.786 1.00 18.53
H
ATOM 4136 HB3 TYR C 111 -7.516 53.788 -13.421 1.00 18.53
H
ATOM 4137 HD1 TYR C 111 -5.218 54.589 -13.580 1.00 21.04
H
ATOM 4138 HD2 TYR C 111 -8.019 56.868 -11.868 1.00 21.32
H
ATOM 4139 HE1 TYR C 111 -3.574 55.945 -12.703 1.00 23.53
H
ATOM 4140 HE2 TYR C 111 -6.382 58.229 -10.987 1.00 18.62
H
ATOM 4141 HH TYR C 111 -4.194 58.643 -10.790 1.00 20.81
H
ATOM 4142 N GLN C 112 -9.035 52.978 -15.797 1.00 18.21
N
ATOM 4143 CA GLN C 112 -9.954 51.869 -16.025 1.00 19.09
C
ATOM 4144 C GLN C 112 -9.246 50.536 -15.845 1.00 17.43
C
ATOM 4145 O GLN C 112 -8.135 50.330 -16.337 1.00 15.67
O
ATOM 4146 CB GLN C 112 -10.578 51.946 -17.416 1.00 21.52
C
ATOM 4147 CG GLN C 112 -11.604 50.841 -17.706 1.00 22.47
C
ATOM 4148 CD GLN C 112 -12.794 50.862 -16.753 1.00 23.56
C
ATOM 4149 OE1 GLN C 112 -12.685 50.483 -15.585 1.00 22.27
O
ATOM 4150 NE2 GLN C 112 -13.941 51.302 -17.256 1.00 30.82
N
ATOM 4151 H GLN C 112 -8.231 52.831 -16.067 1.00 21.85
H
ATOM 4152 HA GLN C 112 -10.671 51.917 -15.373 1.00 22.91

C
ATOM 10403 C THR F 16 1.993 15.543 -12.102 1.00 31.07 C
ATOM 10404 O THR F 16 0.939 15.126 -12.576 1.00 34.24 O
ATOM 10405 CB THR F 16 3.080 17.323 -13.451 1.00 27.23
C
ATOM 10406 OG1 THR F 16 1.821 17.538 -14.099 1.00 33.36
O
ATOM 10407 CG2 THR F 16 4.217 17.692 -14.394 1.00 29.69
C
ATOM 10408 H THR F 16 2.525 14.831 -14.556 1.00 35.11 H
ATOM 10409 HA THR F 16 3.993 15.762 -12.467 1.00 36.30
H
ATOM 10410 HB THR F 16 3.137 17.898 -12.672 1.00 32.67
H
ATOM 10411 HG1 THR F 16 1.758 18.338 -14.346 1.00 40.03
H
ATOM 10412 HG21 THR F 16 4.134 18.619 -14.667 1.00 35.62
H
ATOM 10413 HG22 THR F 16 5.070 17.570 -13.948 1.00 35.62
H
ATOM 10414 HG23 THR F 16 4.190 17.128 -15.183 1.00 35.62
H
ATOM 10415 N HIS F 17 2.176 15.746 -10.799 1.00 27.94 N
ATOM 10416 CA HIS F 17 1.086 15.654 -9.832 1.00 28.47 C
ATOM 10417 C HIS F 17 1.094 16.890 -8.941 1.00 23.00 C
ATOM 10418 O HIS F 17 2.112 17.220 -8.337 1.00 21.84 O
ATOM 10419 CB HIS F 17 1.207 14.388 -8.985 1.00 30.82 C
ATOM 10420 CG HIS F 17 1.084 13.122 -9.773 1.00 44.45 C
ATOM 10421 ND1 HIS F 17 2.129 12.592 -10.499 1.00 46.02
N
ATOM 10422 CD2 HIS F 17 0.037 12.283 -9.954 1.00 47.05 C
ATOM 10423 CE1 HIS F 17 1.733 11.479 -11.089 1.00 48.47
C
ATOM 10424 NE2 HIS F 17 0.467 11.269 -10.775 1.00 52.45
N
ATOM 10425 H HIS F 17 2.935 15.943 -10.446 1.00 33.53 H
ATOM 10426 HA HIS F 17 0.239 15.625 -10.304 1.00 34.16 H
ATOM 10427 HB2 HIS F 17 2.075 14.385 -8.551 1.00 36.99 H
ATOM 10428 HB3 HIS F 17 0.505 14.391 -8.316 1.00 36.99 H
ATOM 10429 HD1 HIS F 17 2.917 12.931 -10.557 1.00 55.22
H
ATOM 10430 HD2 HIS F 17 -0.813 12.374 -9.589 1.00 58.46 H
ATOM 10431 HE1 HIS F 17 2.255 10.936 -11.635 1.00 58.17
H
ATOM 10432 HE2 HIS F 17 -0.011 10.605 -11.042 1.00 62.94
H
ATOM 10433 N SER F 18 -0.044 17.573 -8.879 1.00 17.98 N
ATOM 10434 CA SER F 18 -0.177 18.794 -8.094 1.00 20.45 C
ATOM 10435 C SER F 18 -1.131 18.581 -8.932 1.00 21.00 C
ATOM 10436 O SER F 18 -2.266 18.124 -7.135 1.00 23.24 O
ATOM 10437 CB SER F 18 -0.679 19.942 -8.971 1.00 22.54 C
ATOM 10438 OG SER F 18 0.180 20.143 -10.082 1.00 30.00
O
ATOM 10439 H SER F 18 -0.765 17.345 -9.289 1.00 21.57 H
ATOM 10440 HA SER F 18 0.689 19.041 -7.734 1.00 24.54 H
ATOM 10441 HB2 SER F 18 -1.568 19.727 -9.294 1.00 27.05
H
ATOM 10442 HB3 SER F 18 -0.706 20.754 -8.442 1.00 27.05
H
ATOM 10443 HG SER F 18 -0.107 20.775 -10.555 1.00 36.00
H
ATOM 10444 N THR F 19 -0.665 18.867 -5.722 1.00 17.83 N
ATOM 10445 CA THR F 19 -1.425 18.615 -4.501 1.00 18.00 C
ATOM 10446 C THR F 19 -1.416 19.828 -3.570 1.00 16.45 C
ATOM 10447 O THR F 19 -0.451 20.592 -3.537 1.00 14.39 O
ATOM 10448 CB THR F 19 -0.853 17.389 -3.744 1.00 22.55 C
ATOM 10449 OG1 THR F 19 -0.964 16.223 -4.568 1.00 32.42
O
ATOM 10450 CG2 THR F 19 -1.601 17.142 -2.441 1.00 34.29
C
ATOM 10451 H THR F 19 0.103 19.228 -5.581 1.00 21.39 H

I
 ATOM 4252 HD2 LYS C 118 -6.561 43.428 -23.624 1.00 32.46
 H
 ATOM 4253 HD3 LYS C 118 -5.899 43.102 -24.921 1.00 32.46
 H
 ATOM 4254 HE2 LYS C 118 -7.910 43.596 -25.504 1.00 36.35
 H
 ATOM 4255 HE3 LYS C 118 -7.550 42.100 -25.910 1.00 36.35
 H
 ATOM 4256 HZ1 LYS C 118 -8.661 41.403 -24.053 1.00 50.14
 H
 ATOM 4257 HZ2 LYS C 118 -8.988 42.765 -23.682 1.00 50.14
 H
 ATOM 4258 HZ3 LYS C 118 -9.569 42.179 -24.873 1.00 50.14
 H
 ATOM 4259 N ASN C 119 -1.876 39.965 -23.186 1.00 16.38
 N
 ATOM 4260 CA ASN C 119 -0.438 40.141 -23.016 1.00 19.02
 C
 ATOM 4261 C ASN C 119 -0.135 41.640 -23.019 1.00 17.17
 C
 ATOM 4262 O ASN C 119 -1.030 42.453 -23.271 1.00 15.21
 O
 ATOM 4263 CB ASN C 119 0.354 39.374 -24.095 1.00 16.08
 C
 ATOM 4264 CG ASN C 119 0.249 39.985 -25.491 1.00 21.42
 C
 ATOM 4265 OD1 ASN C 119 0.176 41.202 -25.869 1.00 20.88
 O

J
 ATOM 10552 OD2 ASP F 26 0.328 22.403 14.526 1.00 47.17
 O1-
 ATOM 10553 H ASP F 26 -2.448 22.899 12.256 1.00 32.93 H
 ATOM 10554 HA ASP F 26 -1.511 21.095 11.662 1.00 43.49 H
 H
 ATOM 10555 HB2 ASP F 26 -1.421 20.710 14.453 1.00 48.76 H
 H
 ATOM 10556 HB3 ASP F 26 -0.663 19.743 13.445 1.00 48.76 H
 H
 ATOM 10557 N SER F 27 -4.227 20.173 11.955 1.00 32.09 N
 ATOM 10558 CA SER F 27 -5.231 19.180 11.597 1.00 34.04 C
 C
 ATOM 10559 C SER F 27 -5.743 19.470 10.195 1.00 27.53 C
 O
 ATOM 10560 O SER F 27 -6.229 20.565 9.922 1.00 25.46 O
 ATOM 10561 CB SER F 27 -6.386 19.183 12.596 1.00 35.84 C
 C
 ATOM 10562 OG SER F 27 -7.408 18.294 12.181 1.00 39.50 O
 O
 ATOM 10563 H SER F 27 -4.513 20.984 11.919 1.00 38.51 H
 ATOM 10564 HA SER F 27 -4.827 18.298 11.600 1.00 40.85 H
 H
 ATOM 10565 HB2 SER F 27 -6.055 18.903 13.463 1.00 43.01 H
 H

ATOM 4266 ND2 ASN C 119 0.267 39.119 -26.500 1.00 28.85 N
 N
 ATOM 4267 H ASN C 119 -2.115 39.664 -23.956 1.00 19.65 H
 H
 ATOM 4268 HA ASN C 119 -0.179 39.788 -22.151 1.00 22.82 H
 H
 ATOM 4269 HB2 ASN C 119 1.291 39.363 -23.846 1.00 19.30 H
 H
 ATOM 4270 HB3 ASN C 119 0.016 38.466 -24.144 1.00 19.30 H
 H
 ATOM 4271 HD21 ASN C 119 0.211 39.402 -27.311 1.00 34.62 H
 H
 ATOM 4272 HD22 ASN C 119 0.334 38.276 -26.343 1.00 34.62 H
 H
 ATOM 4273 N TRP C 120 1.108 42.013 -22.734 1.00 17.45 N
 N
 ATOM 4274 CA TRP C 120 1.443 43.427 -22.571 1.00 16.39 C
 C
 ATOM 4275 C TRP C 120 1.229 44.216 -23.861 1.00 19.16 C
 C
 ATOM 4276 O TRP C 120 0.768 45.360 -23.822 1.00 20.05 O
 O
 ATOM 4277 CB TRP C 120 2.888 43.592 -22.098 1.00 15.72 C
 C
 ATOM 4278 CG TRP C 120 3.216 45.005 -21.718 1.00 18.60 C
 C
 ATOM 4279 CD1 TRP C 120 3.152 45.554 -20.470 1.00 18.56 C
 C
 ATOM 4280 CD2 TRP C 120 3.652 46.053 -22.593 1.00 18.79 C
 C
 ATOM 4281 NE1 TRP C 120 3.518 46.876 -20.514 1.00 17.94 N
 N
 ATOM 4282 CE2 TRP C 120 3.830 47.208 -21.805 1.00 20.55 C
 C
 ATOM 4283 CE3 TRP C 120 3.903 46.128 -23.966 1.00 23.33 C
 C
 ATOM 4284 CZ2 TRP C 120 4.251 48.420 -22.342 1.00 21.40 C
 C
 ATOM 4285 CZ3 TRP C 120 4.321 47.334 -24.497 1.00 19.62 C
 C
 ATOM 4286 CH2 TRP C 120 4.492 48.463 -23.687 1.00 24.59 C
 C
 ATOM 4287 H TRP C 120 1.771 41.475 -22.631 1.00 20.94 H
 H
 ATOM 4288 HA TRP C 120 0.864 43.807 -21.892 1.00 19.67 H
 H
 ATOM 4289 HB2 TRP C 120 3.032 43.032 -21.319 1.00 18.86 H
 H
 ATOM 4290 HB3 TRP C 120 3.487 43.327 -22.813 1.00 18.86 H
 H
 ATOM 4291 HD1 TRP C 120 2.895 45.098 -19.701 1.00 22.28 H
 H
 ATOM 4292 HE1 TRP C 120 3.550 47.408 -19.839 1.00 21.53 H
 H
 ATOM 4293 HE3 TRP C 120 3.791 45.383 -24.511 1.00 28.00 H
 H
 ATOM 4294 HZ2 TRP C 120 4.366 49.172 -21.806 1.00 25.69 H
 H
 ATOM 4295 HZ3 TRP C 120 4.493 47.396 -25.409 1.00 23.55 H
 H
 ATOM 4296 HH2 TRP C 120 4.776 49.260 -24.072 1.00 29.50 H
 H
 ATOM 4297 N TYR C 121 1.555 43.605 -24.998 1.00 17.25 N
 N
 ATOM 4298 CA TYR C 121 1.432 44.280 -26.289 1.00 19.29 C
 C
 ATOM 4299 C TYR C 121 -0.035 44.502 -26.645 1.00 19.51 C
 C
 ATOM 4300 O TYR C 121 -0.406 45.554 -27.164 1.00 22.89 O
 O

ATOM 10566 HB3 SER F 27 -6.752 20.080 12.654 1.00 43.01 H
 H
 ATOM 10567 HG SER F 27 -8.039 18.302 12.736 1.00 47.40 H
 H
 ATOM 10568 N GLN F 28 -5.626 18.486 9.309 1.00 27.54 N
 N
 ATOM 10569 CA GLN F 28 -6.030 18.651 7.918 1.00 23.96 C
 C
 ATOM 10570 C GLN F 28 -7.541 18.819 7.811 1.00 23.35 C
 C
 ATOM 10571 O GLN F 28 -8.295 18.020 8.367 1.00 23.17 O
 O
 ATOM 10572 CB GLN F 28 -5.567 17.450 7.091 1.00 27.17 C
 C
 ATOM 10573 CG GLN F 28 -5.639 17.658 5.595 1.00 25.49 C
 C
 ATOM 10574 CD GLN F 28 -5.293 16.399 4.820 1.00 29.69 C
 C
 ATOM 10575 OE1 GLN F 28 -4.307 16.362 4.086 1.00 31.67 O
 O
 ATOM 10576 NE2 GLN F 28 -6.104 15.361 4.984 1.00 33.72 N
 N
 ATOM 10577 H GLN F 28 -5.312 17.706 9.491 1.00 33.05 H
 H
 ATOM 10578 HA GLN F 28 -5.810 19.447 7.556 1.00 28.76 H
 H
 ATOM 10579 HB2 GLN F 28 -4.644 17.254 7.317 1.00 32.60 H
 H
 ATOM 10580 HB3 GLN F 28 -6.126 16.688 7.310 1.00 32.60 H
 H
 ATOM 10581 HG2 GLN F 28 -6.540 17.922 5.355 1.00 30.58 H
 H
 ATOM 10582 HG3 GLN F 28 -5.009 18.351 5.341 1.00 30.58 H
 H
 ATOM 10583 HE21 GLN F 28 -5.950 14.625 4.566 1.00 40.46 H
 H
 ATOM 10584 HE22 GLN F 28 -6.783 15.424 5.508 1.00 40.46 H
 H
 ATOM 10585 N ILE F 29 -7.974 19.862 7.102 1.00 18.13 N
 N
 ATOM 10586 CA ILE F 29 -9.397 20.159 6.940 1.00 18.44 C
 C
 ATOM 10587 C ILE F 29 -9.830 20.136 5.472 1.00 17.32 C
 C
 ATOM 10588 O ILE F 29 -11.008 19.952 5.170 1.00 15.77 O
 O
 ATOM 10589 CB ILE F 29 -9.757 21.539 7.544 1.00 16.85 C
 C
 ATOM 10590 CG1 ILE F 29 -8.943 22.655 6.879 1.00 18.54 C
 C
 ATOM 10591 CG2 ILE F 29 -9.505 21.533 9.044 1.00 21.09 C
 C
 ATOM 10592 CD1 ILE F 29 -9.442 24.060 7.198 1.00 16.42 C
 C
 ATOM 10593 H ILE F 29 -7.456 20.418 6.700 1.00 21.76 H
 H
 ATOM 10594 HA ILE F 29 -9.912 19.486 7.411 1.00 22.13 H
 H
 ATOM 10595 HB ILE F 29 -10.699 21.708 7.389 1.00 20.22 H
 H
 ATOM 10596 HG12 ILE F 29 -8.024 22.592 7.181 1.00 22.25 H
 H
 ATOM 10597 HG13 ILE F 29 -8.982 22.538 5.917 1.00 22.25 H
 H
 ATOM 10598 HG21 ILE F 29 -9.735 22.404 9.405 1.00 25.31 H
 H
 ATOM 10599 HG22 ILE F 29 -10.056 20.848 9.454 1.00 25.31 H
 H
 ATOM 10600 HG23 ILE F 29 -8.568 21.345 9.206 1.00 25.31 H
 H

DK/EP 3233192 T3

ATOM 4401 HA MET C 128 -3.658 54.289 -26.810 1.00 34.46
 H
 ATOM 4402 HB2 MET C 128 -2.848 52.028 -28.251 1.00 35.71
 H
 ATOM 4403 HB3 MET C 128 -2.844 53.443 -28.966 1.00 35.71
 H
 ATOM 4404 HG2 MET C 128 -1.345 54.165 -27.220 1.00 49.47
 H
 ATOM 4405 HG3 MET C 128 -1.187 52.828 -26.854 1.00 49.47
 H

ATOM 10701 O ASP F 36 -9.384 18.462 -5.523 1.00 20.70 O
 ATOM 10702 CB ASP F 36 -11.679 17.146 -7.340 1.00 30.39
 C
 ATOM 10703 CG ASP F 36 -12.330 16.821 -8.671 1.00 38.61
 C
 ATOM 10704 OD1 ASP F 36 -12.968 17.723 -9.258 1.00 37.40
 O
 ATOM 10705 OD2 ASP F 36 -12.199 15.869 -9.134 1.00 42.12
 O1-

ATOM 4406 HE1 MET C 128 0.395 51.149 -29.952 1.00 95.30
 H
 ATOM 4407 HE2 MET C 128 -0.109 50.820 -28.481 1.00 95.30
 H
 ATOM 4408 HE3 MET C 128 -1.155 51.218 -29.609 1.00 95.30
 H
 ATOM 4409 N SER C 129 -5.945 52.601 -28.246 1.00 29.07
 N
 ATOM 4410 CA SER C 129 -7.157 52.672 -29.055 1.00 32.00
 C
 ATOM 4411 C SER C 129 -8.256 53.469 -28.358 1.00 36.56
 C
 ATOM 4412 O SER C 129 -9.307 53.735 -28.945 1.00 32.22
 O
 ATOM 4413 CB SER C 129 -7.669 51.267 -29.377 1.00 33.16
 C
 ATOM 4414 OG SER C 129 -8.267 50.670 -28.237 1.00 33.58
 O
 ATOM 4415 H SER C 129 -5.788 51.821 -27.920 1.00 34.88
 H
 ATOM 4416 HA SER C 129 -6.952 53.115 -29.893 1.00 38.40
 H
 ATOM 4417 HB2 SER C 129 -8.329 51.325 -30.085 1.00 39.79
 H
 ATOM 4418 HB3 SER C 129 -6.922 50.718 -29.664 1.00 39.79
 H
 ATOM 4419 HG SER C 129 -7.706 50.613 -27.615 1.00 40.30
 H
 ATOM 4420 N GLN C 130 -8.010 53.834 -27.102 1.00 33.51
 N
 ATOM 4421 CA GLN C 130 -8.946 54.642 -26.331 1.00 30.27
 C
 ATOM 4422 C GLN C 130 -8.314 55.976 -25.955 1.00 26.64
 C
 ATOM 4423 O GLN C 130 -8.730 56.622 -24.995 1.00 31.87
 O
 ATOM 4424 CB GLN C 130 -9.393 53.881 -25.082 1.00 30.65
 C
 ATOM 4425 CG GLN C 130 -10.037 52.545 -25.414 1.00 34.01
 C
 ATOM 4426 CD GLN C 130 -10.477 51.776 -24.191 1.00 33.95
 C
 ATOM 4427 OE1 GLN C 130 -11.212 52.290 -23.347 1.00 40.96
 O
 ATOM 4428 NE2 GLN C 130 -10.033 50.529 -24.089 1.00 34.20
 N
 ATOM 4429 H GLN C 130 -7.297 53.622 -26.670 1.00 40.22
 H
 ATOM 4430 HA GLN C 130 -9.731 54.822 -26.872 1.00 36.32
 H
 ATOM 4431 HB2 GLN C 130 -8.820 53.711 -24.521 1.00 36.78
 H
 ATOM 4432 HB3 GLN C 130 -10.043 54.416 -24.601 1.00 36.78
 H
 ATOM 4433 HG2 GLN C 130 -10.819 52.701 -25.966 1.00 40.81
 H
 ATOM 4434 HG3 GLN C 130 -9.396 51.998 -25.896 1.00 40.81
 H
 ATOM 4435 HE21 GLN C 130 -10.254 50.047 -23.411 1.00 41.04
 H
 ATOM 4436 HE22 GLN C 130 -9.523 50.203 -24.700 1.00 41.04
 H
 ATOM 4437 N ASN C 131 -7.312 56.382 -26.730 1.00 25.72
 N
 ATOM 4438 CA ASN C 131 -6.593 57.631 -26.495 1.00 31.52
 C
 ATOM 4439 C ASN C 131 -6.008 57.876 -25.091 1.00 30.51
 C
 ATOM 4440 O ASN C 131 -5.996 58.719 -24.433 1.00 30.75
 O

ATOM 10706 H ASP F 36 -9.314 17.699 -8.191 1.00 29.32 H
 ATOM 10707 HA ASP F 36 -11.541 19.162 -7.671 1.00 30.43 H
 H
 ATOM 10708 HB2 ASP F 36 -11.056 16.433 -7.128 1.00 36.46 H
 H
 ATOM 10709 HB3 ASP F 36 -12.376 17.189 -6.667 1.00 36.46 H
 H
 ATOM 10710 N ILE F 37 -11.317 19.592 -5.262 1.00 22.26 N
 ATOM 10711 CA ILE F 37 -11.081 19.940 -3.868 1.00 19.23 C
 ATOM 10712 C ILE F 37 -12.106 19.217 -3.019 1.00 20.45 C
 ATOM 10713 O ILE F 37 -13.226 18.982 -3.467 1.00 15.18 O
 ATOM 10714 CB ILE F 37 -11.176 21.460 -3.636 1.00 19.93 C
 ATOM 10715 CG1 ILE F 37 -10.676 21.821 -2.235 1.00 23.69 C
 C
 ATOM 10716 CG2 ILE F 37 -12.600 21.958 -3.851 1.00 19.45 C
 C
 ATOM 10717 CD1 ILE F 37 -10.392 23.301 -2.070 1.00 21.55 C
 C
 ATOM 10718 H ILE F 37 -12.046 19.918 -5.581 1.00 26.71 H
 ATOM 10719 HA ILE F 37 -10.197 19.642 -3.604 1.00 23.08 H
 ATOM 10720 HB ILE F 37 -10.602 21.899 -4.283 1.00 23.92 H
 ATOM 10721 HG12 ILE F 37 -11.351 21.572 -1.585 1.00 28.43 H
 H
 ATOM 10722 HG13 ILE F 37 -9.854 21.337 -2.050 1.00 28.43 H
 H
 ATOM 10723 HG21 ILE F 37 -12.625 22.916 -3.698 1.00 23.34 H
 H
 ATOM 10724 HG22 ILE F 37 -12.868 21.762 -4.762 1.00 23.34 H
 H
 ATOM 10725 HG23 ILE F 37 -13.190 21.507 -3.227 1.00 23.34 H
 H
 ATOM 10726 HD11 ILE F 37 -10.080 23.463 -1.166 1.00 25.86 H
 H
 ATOM 10727 HD12 ILE F 37 -9.710 23.564 -2.708 1.00 25.86 H
 H
 ATOM 10728 HD13 ILE F 37 -11.208 23.799 -2.233 1.00 25.86 H
 H
 ATOM 10729 N ARG F 38 -11.738 18.858 -1.797 1.00 17.84 N
 ATOM 10730 CA ARG F 38 -12.697 18.217 -0.916 1.00 20.68 C
 C
 ATOM 10731 C ARG F 38 -12.396 18.455 0.558 1.00 19.35 C
 ATOM 10732 O ARG F 38 -11.235 18.589 0.953 1.00 18.38 O
 O
 ATOM 10733 CB ARG F 38 -12.754 16.714 -1.198 1.00 22.95 C
 C
 ATOM 10734 CG ARG F 38 -11.423 16.000 -1.117 1.00 28.32 C
 C
 ATOM 10735 CD ARG F 38 -11.562 14.534 -1.510 1.00 33.42 C
 C
 ATOM 10736 NE ARG F 38 -10.260 13.892 -1.685 1.00 43.09 N
 N
 ATOM 10737 CZ ARG F 38 -9.592 13.252 -0.728 1.00 44.56 C
 C
 ATOM 10738 NH1 ARG F 38 -10.092 13.147 0.498 1.00 41.53 N1+
 ATOM 10739 NH2 ARG F 38 -8.414 12.710 -1.002 1.00 57.47 N
 N
 ATOM 10740 H ARG F 38 -10.954 18.971 -1.461 1.00 21.40 H
 ATOM 10741 HA ARG F 38 -13.576 18.584 -1.098 1.00 24.81 H
 H
 ATOM 10742 HB2 ARG F 38 -13.348 16.301 -0.551 1.00 27.54 H
 H
 ATOM 10743 HB3 ARG F 38 -13.104 16.580 -2.092 1.00 27.54 H
 H
 ATOM 10744 HG2 ARG F 38 -10.795 16.421 -1.725 1.00 33.98 H
 H
 ATOM 10745 HG3 ARG F 38 -11.091 16.041 -0.207 1.00 33.98 H
 H
 ATOM 10746 HD2 ARG F 38 -12.041 14.060 -0.812 1.00 40.11 H
 H
 ATOM 10747 HD3 ARG F 38 -12.045 14.473 -2.349 1.00 40.11 H
 H
 ATOM 10748 HE ARG F 38 -9.899 13.931 -2.465 1.00 51.71 H
 H
 ATOM 10749 HH11 ARG F 38 -10.856 13.497 0.682 1.00 49.84 H
 H
 ATOM 10750 HH12 ARG F 38 -9.651 13.790 1.467 1.00 49.84 H
 H

ATOM 4441 CB ASN C 131 -7.512 58.833 -26.721 1.00 40.00
 C
 ATOM 4442 CG ASN C 131 -6.739 60.121 -26.931 1.00 45.49
 C
 ATOM 4443 OD1 ASN C 131 -6.120 60.320 -27.975 1.00 53.22
 O
 ATOM 4444 ND2 ASN C 131 -6.769 61.001 -25.937 1.00 44.21
 N
 ATOM 4445 H ASN C 131 -7.025 55.944 -27.412 1.00 30.86
 H
 ATOM 4446 HA ASN C 131 -5.859 57.695 -27.126 1.00 37.83
 H
 ATOM 4447 HB2 ASN C 131 -8.053 58.675 -27.511 1.00 48.00
 H
 ATOM 4448 HB3 ASN C 131 -8.082 58.947 -25.945 1.00 48.00
 H
 ATOM 4449 HD21 ASN C 131 -6.346 61.746 -26.009 1.00 53.05
 H
 ATOM 4450 HD22 ASN C 131 7.044 60.898 25.220 1.00 53.05
 H

ATOM 4450 HD22 ASN C 131 -7.211 60.828 -25.220 1.00 53.05
 H
 ATOM 4451 N ALA C 132 -5.522 56.526 -24.641 1.00 27.31
 N
 ATOM 4452 CA ALA C 132 -4.952 56.397 -23.311 1.00 24.35
 C
 ATOM 4453 C ALA C 132 -3.654 55.604 -23.376 1.00 22.93
 C
 ATOM 4454 O ALA C 132 -3.175 55.264 -24.456 1.00 22.28
 O
 ATOM 4455 CB ALA C 132 -5.946 55.724 -22.377 1.00 24.10
 C
 ATOM 4456 H ALA C 132 -5.512 55.796 -25.096 1.00 32.77
 H
 ATOM 4457 HA ALA C 132 -4.753 57.279 -22.960 1.00 29.22
 H
 ATOM 4458 HB1 ALA C 132 -5.548 55.647 -21.496 1.00 28.92
 H
 ATOM 4459 HB2 ALA C 132 -6.750 56.264 -22.331 1.00 28.92
 H
 ATOM 4460 HB3 ALA C 132 -6.157 54.843 -22.724 1.00 28.92
 H
 ATOM 4461 N SER C 133 -3.086 55.317 -22.211 1.00 23.85
 N
 ATOM 4462 CA SER C 133 -1.908 54.470 -22.123 1.00 19.49
 C
 ATOM 4463 C SER C 133 -2.035 53.561 -20.913 1.00 19.76
 C
 ATOM 4464 O SER C 133 -2.954 53.714 -20.106 1.00 21.65
 O
 ATOM 4465 CB SER C 133 -0.637 55.315 -22.035 1.00 28.62
 C
 ATOM 4466 OG SER C 133 -0.593 56.041 -20.822 1.00 30.86
 O
 ATOM 4467 H SER C 133 -3.368 55.604 -21.451 1.00 28.62
 H
 ATOM 4468 HA SER C 133 -1.851 53.916 -22.917 1.00 23.39
 H
 ATOM 4469 HB2 SER C 133 0.135 54.730 -22.081 1.00 34.34
 H
 ATOM 4470 HB3 SER C 133 -0.622 55.940 -22.777 1.00 34.34
 H
 ATOM 4471 HG SER C 133 -1.256 56.554 -20.769 1.00 37.04
 H
 ATOM 4472 N LEU C 134 -1.131 52.597 -20.799 1.00 15.30
 N
 ATOM 4473 CA LEU C 134 -1.085 51.753 -19.618 1.00 16.31
 C
 ATOM 4474 C LEU C 134 -0.722 52.605 -18.413 1.00 18.61
 C
 ATOM 4475 O LEU C 134 -0.102 53.860 -18.558 1.00 17.38
 O

 ATOM 4476 CB LEU C 134 -0.082 50.615 -19.800 1.00 18.05
 C
 ATOM 4477 CG LEU C 134 -0.545 49.502 -20.739 1.00 18.46
 C
 ATOM 4478 CD1 LEU C 134 0.622 48.613 -21.151 1.00 18.54
 C
 ATOM 4479 CD2 LEU C 134 -1.633 48.677 -20.070 1.00 13.57
 C
 ATOM 4480 H LEU C 134 -0.535 52.413 -21.391 1.00 18.36
 H
 ATOM 4481 HA LEU C 134 -1.961 51.366 -19.465 1.00 19.57
 H
 ATOM 4482 HB2 LEU C 134 0.740 50.982 -20.162 1.00 21.66
 H
 ATOM 4483 HB3 LEU C 134 0.094 50.215 -18.934 1.00 21.66
 H
 ATOM 4484 HG LEU C 134 -0.919 49.899 -21.541 1.00 22.15
 H
 ATOM 4485 HD11 LEU C 134 0.296 47.919 -21.745 1.00 22.25
 H
 ATOM 4486 HD12 LEU C 134 1.285 49.154 -21.608 1.00 22.25
 H
 ATOM 4487 HD13 LEU C 134 1.011 48.214 -20.357 1.00 22.25
 H
 ATOM 4488 HD21 LEU C 134 -1.916 47.976 -20.678 1.00 16.29
 H
 ATOM 4489 HD22 LEU C 134 -1.278 48.287 -19.256 1.00 16.29
 H
 ATOM 4490 HD23 LEU C 134 -2.383 49.256 -19.859 1.00 16.29
 H
 ATOM 4491 N LEU C 135 -1.122 52.145 -17.232 1.00 17.61
 N
 ATOM 4492 CA LEU C 135 -0.861 52.863 -15.990 1.00 16.82
 C
 ATOM 4493 C LEU C 135 0.574 53.365 -15.907 1.00 17.04
 C
 ATOM 4494 O LEU C 135 1.521 52.614 -16.145 1.00 17.43
 O
 ATOM 4495 CB LEU C 135 -1.160 51.962 -14.792 1.00 13.74
 C
 ATOM 4496 CG LEU C 135 -0.816 52.517 -13.409 1.00 13.56
 C
 ATOM 4497 CD1 LEU C 135 -1.868 53.736 -13.089 1.00 14.51
 C
 ATOM 4498 CD2 LEU C 135 -0.994 51.438 -12.348 1.00 14.41
 C
 ATOM 4499 H LEU C 135 -1.553 51.409 -17.123 1.00 21.14
 H
 ATOM 4500 HA LEU C 135 -1.450 53.632 -15.941 1.00 20.18

ATOM 10750 HH12 ARG F 38 -9.551 12.730 1.107 1.00 49.64
 H
 ATOM 10751 HH21 ARG F 38 -8.085 12.773 -1.794 1.00 68.96
 H
 ATOM 10752 HH22 ARG F 38 -7.979 12.293 -0.388 1.00 68.96
 H

 ATOM 10753 N PRO F 39 -13.454 18.510 1.378 1.00 18.43 N
 ATOM 10754 CA PRO F 39 -13.287 18.624 2.828 1.00 18.67
 C

 ATOM 10755 C PRO F 39 -12.741 17.328 3.420 1.00 21.97 C
 ATOM 10756 O PRO F 39 -13.015 16.261 2.874 1.00 21.02
 O
 ATOM 10757 CB PRO F 39 -14.706 18.905 3.320 1.00 22.75
 C
 ATOM 10758 CG PRO F 39 -15.585 18.250 2.306 1.00 22.23
 C
 ATOM 10759 CD PRO F 39 -14.875 18.401 0.993 1.00 22.99
 C
 ATOM 10760 HA PRO F 39 -12.704 19.365 3.054 1.00 22.40
 H
 ATOM 10761 HB2 PRO F 39 -14.835 18.509 4.196 1.00 27.30
 H
 ATOM 10762 HB3 PRO F 39 -14.861 19.862 3.346 1.00 27.30
 H
 ATOM 10763 HG2 PRO F 39 -15.696 17.312 2.528 1.00 26.68
 H
 ATOM 10764 HG3 PRO F 39 -16.445 18.699 2.282 1.00 26.68
 H
 ATOM 10765 HD2 PRO F 39 -15.016 17.616 0.441 1.00 27.59
 H
 ATOM 10766 HD3 PRO F 39 -15.166 19.209 0.543 1.00 27.59
 H

 ATOM 10767 N THR F 40 -11.976 17.424 4.505 1.00 17.56 N
 ATOM 10768 CA THR F 40 -11.433 16.245 5.182 1.00 19.85
 C

 ATOM 10769 C THR F 40 -11.726 16.306 6.680 1.00 21.64 C

 ATOM 10770 O THR F 40 -11.068 15.646 7.482 1.00 25.05 O

 ATOM 10771 CB THR F 40 -9.914 16.121 4.970 1.00 22.38 C
 ATOM 10772 OG1 THR F 40 -9.253 17.246 5.562 1.00 22.26
 O
 ATOM 10773 CG2 THR F 40 -9.581 16.061 3.486 1.00 26.29
 C

 ATOM 10774 H THR F 40 -11.755 18.169 4.874 1.00 21.07 H
 ATOM 10775 HA THR F 40 -11.855 15.449 4.823 1.00 23.82
 H

 ATOM 10776 HB THR F 40 -9.596 15.305 5.387 1.00 26.85 H
 ATOM 10777 HG1 THR F 40 -8.423 17.183 5.449 1.00 26.71
 H
 ATOM 10778 HG21 THR F 40 -8.622 15.983 3.364 1.00 31.55
 H
 ATOM 10779 HG22 THR F 40 -10.014 15.294 3.080 1.00 31.55
 H
 ATOM 10780 HG23 THR F 40 -9.890 16.868 3.044 1.00 31.55
 H

 ATOM 10781 N ILE F 41 -12.714 17.115 7.042 1.00 20.01 N
 ATOM 10782 CA ILE F 41 -13.138 17.273 8.426 1.00 20.07
 C
 ATOM 10783 C ILE F 41 -14.638 17.573 8.393 1.00 21.37
 C
 ATOM 10784 O ILE F 41 -15.103 18.248 7.473 1.00 19.23
 O

 ATOM 10785 CB ILE F 41 -12.348 18.400 9.131 1.00 20.97 C
 ATOM 10786 CG1 ILE F 41 -12.551 18.369 10.647 1.00 25.82
 C
 ATOM 10787 CG2 ILE F 41 -12.723 19.766 8.564 1.00 19.25
 C
 ATOM 10788 CD1 ILE F 41 -11.871 17.205 11.329 1.00 28.28
 C

 ATOM 10789 H ILE F 41 -13.164 17.595 6.490 1.00 24.01 H
 ATOM 10790 HA ILE F 41 -12.997 16.444 8.909 1.00 24.09
 H

 ATOM 10791 HB ILE F 41 -11.405 18.256 8.956 1.00 25.16 H
 ATOM 10792 HG12 ILE F 41 -12.191 19.186 11.027 1.00 30.99
 H
 ATOM 10793 HG13 ILE F 41 -13.500 18.310 10.834 1.00 30.99
 H
 ATOM 10794 HG21 ILE F 41 -12.213 20.450 9.024 1.00 23.10
 H
 ATOM 10795 HG22 ILE F 41 -12.517 19.780 7.616 1.00 23.10
 H
 ATOM 10796 HG23 ILE F 41 -13.673 19.913 8.698 1.00 23.10
 H
 ATOM 10797 HD11 ILE F 41 -12.044 17.254 12.282 1.00 33.93
 H
 ATOM 10798 HD12 ILE F 41 -12.227 16.378 10.969 1.00 33.93
 H
 ATOM 10799 HD13 ILE F 41 -10.917 17.255 11.162 1.00 33.93
 H

H									
ATOM	4600	HZ2 LYS C 140	6.857	54.736	-0.926	1.00	59.85		
H									
ATOM	4601	HZ3 LYS C 140	5.676	53.957	-0.614	1.00	59.85		
H									
ATOM	4602	N GLU C 141	1.046	59.876	-3.593	1.00	24.55		
N									
ATOM	4603	CA GLU C 141	-0.002	60.674	-2.963	1.00	26.23		
C									
ATOM	4604	C GLU C 141	-1.169	60.917	-3.914	1.00	24.95		
C									
ATOM	4605	O GLU C 141	-2.327	60.758	-3.534	1.00	21.89		
O									
ATOM	4606	CB GLU C 141	0.559	62.010	-2.474	1.00	26.15		
C									
ATOM	4607	CG GLU C 141	1.543	61.885	-1.314	1.00	34.78		
C									
ATOM	4608	CD GLU C 141	2.855	61.219	-1.707	1.00	37.55		
C									
ATOM	4609	OE1 GLU C 141	3.227	61.278	-2.899	1.00	33.99		
O									
ATOM	4610	OE2 GLU C 141	3.514	60.634	-0.820	1.00	45.19		
O1-									
ATOM	4611	H GLU C 141	1.698	60.339	-3.910	1.00	29.46		
H									
ATOM	4612	HA GLU C 141	-0.342	60.193	-2.192	1.00	31.47		
H									
ATOM	4613	HB2 GLU C 141	1.022	62.442	-3.209	1.00	31.39		
H									
ATOM	4614	HB3 GLU C 141	-0.178	62.568	-2.178	1.00	31.39		
H									
ATOM	4615	HG2 GLU C 141	1.747	62.772	-0.978	1.00	41.74		
H									
ATOM	4616	HG3 GLU C 141	1.136	61.352	-0.613	1.00	41.74		
H									
ATOM	4617	N ASP C 142	-0.867	61.296	-5.152	1.00	22.41		
N									
ATOM	4618	CA ASP C 142	-1.915	61.567	-6.129	1.00	21.49		
C									
ATOM	4619	C ASP C 142	-2.560	60.282	-6.633	1.00	21.91		
C									
ATOM	4620	O ASP C 142	-3.686	60.300	-7.128	1.00	24.05		
O									
ATOM	4621	CB ASP C 142	-1.357	62.369	-7.307	1.00	24.21		
C									
ATOM	4622	CG ASP C 142	-0.908	63.760	-6.901	1.00	29.23		
C									
ATOM	4623	OD1 ASP C 142	-1.248	64.193	-5.776	1.00	30.52		
O									
ATOM	4624	OD2 ASP C 142	-0.223	64.424	-7.707	1.00	33.69		
O1-									
ATOM	4625	H ASP C 142	-0.067	61.403	-5.450	1.00	26.89		
H									
ATOM	4626	HA ASP C 142	-2.606	62.101	-5.707	1.00	25.79		
H									
ATOM	4627	HB2 ASP C 142	-0.590	61.901	-7.674	1.00	29.05		
H									
ATOM	4628	HB3 ASP C 142	-2.046	62.460	-7.983	1.00	29.05		
H									
ATOM	4629	N GLN C 143	-1.849	59.167	-6.501	1.00	17.21		
N									
ATOM	4630	CA GLN C 143	-2.357	57.882	-6.969	1.00	20.06		
C									
ATOM	4631	C GLN C 143	-2.424	56.880	-5.819	1.00	19.18		
C									
ATOM	4632	O GLN C 143	-2.183	55.696	-5.994	1.00	17.46		
O									
ATOM	4633	CB GLN C 143	-1.479	57.342	-8.097	1.00	18.97		
C									
ATOM	4634	CG GLN C 143	-1.248	58.349	-9.217	1.00	17.93		
C									
ATOM	4635	CD GLN C 143	-0.285	57.837	-10.270	1.00	21.93		
C									
ATOM	4636	OE1 GLN C 143	0.917	57.724	-10.024	1.00	19.88		
O									
ATOM	4637	NE2 GLN C 143	-0.808	57.520	-11.450	1.00	17.07		
N									
ATOM	4638	H GLN C 143	-1.069	59.128	-6.143	1.00	20.65		
H									
ATOM	4639	HA GLN C 143	-3.255	58.002	-7.317	1.00	24.08		
H									
ATOM	4640	HB2 GLN C 143	-0.614	57.098	-7.732	1.00	22.76		
H									
ATOM	4641	HB3 GLN C 143	-1.906	56.561	-8.482	1.00	22.76		
H									
ATOM	4642	HG2 GLN C 143	-2.094	58.540	-9.651	1.00	21.52		
H									
ATOM	4643	HG3 GLN C 143	-0.877	59.162	-8.840	1.00	21.52		
H									
ATOM	4644	HE21 GLN C 143	-0.302	57.225	-12.079	1.00	20.49		
H									
ATOM	4645	HE22 GLN C 143	-1.653	57.809	-11.584	1.00	20.49		
H									
ATOM	4646	N ASP C 144	-2.770	57.395	-4.639	1.00	22.78		
N									
ATOM	4647	CA ASP C 144	-2.791	56.572	-3.438	1.00	23.80		
C									
ATOM	4648	C ASP C 144	-3.893	55.512	-3.492	1.00	19.24		
C									
ATOM	4649	O ASP C 144	-3.854	54.538	-2.740	1.00	21.24		
O									

H									
ATOM	10900	HB2 GLU F 48	-21.420	27.614	-1.229	1.00	29.84		
H									
ATOM	10901	HB3 GLU F 48	-21.742	26.311	-0.384	1.00	29.84		
H									
ATOM	10902	HG2 GLU F 48	-21.930	27.643	1.536	1.00	31.18		
H									
ATOM	10903	HG3 GLU F 48	-21.702	28.932	0.635	1.00	31.18		
H									
ATOM	10904	N ILE F 49	-18.176	28.615	0.701	1.00	21.84	N	
ATOM	10905	CA ILE F 49	-17.393	29.848	0.657	1.00	19.58	C	
ATOM	10906	C ILE F 49	-15.911	29.570	0.422	1.00	21.99	C	
ATOM	10907	O ILE F 49	-15.314	30.091	-0.521	1.00	18.32	O	
ATOM	10908	CB ILE F 49	-17.560	30.650	1.958	1.00	22.04	C	
ATOM	10909	CG1 ILE F 49	-19.021	31.077	2.119	1.00	19.68	C	
C									
ATOM	10910	CG2 ILE F 49	-16.648	31.883	1.960	1.00	22.59	C	
C									
ATOM	10911	CD1 ILE F 49	-19.377	31.490	3.521	1.00	29.80	C	
ATOM	10912	H ILE F 49	-17.990	28.106	1.369	1.00	26.21	H	
ATOM	10913	HA ILE F 49	-17.714	30.397	-0.075	1.00	23.50	H	
ATOM	10914	HB ILE F 49	-17.317	30.082	2.707	1.00	26.45	H	
ATOM	10915	HG12 ILE F 49	-19.192	31.832	1.534	1.00	23.61	H	
H									
ATOM	10916	HG13 ILE F 49	-19.594	30.334	1.874	1.00	23.61	H	
H									
ATOM	10917	HG21 ILE F 49	-16.775	32.368	2.791	1.00	27.11	H	
ATOM	10918	HG22 ILE F 49	-15.726	31.594	1.883	1.00	27.11	H	
H									
ATOM	10919	HG23 ILE F 49	-16.882	32.449	1.208	1.00	27.11	H	
H									
ATOM	10920	HD11 ILE F 49	-20.312	31.747	3.546	1.00	35.76	H	
H									
ATOM	10921	HD12 ILE F 49	-19.222	30.743	4.119	1.00	35.76	H	
H									
ATOM	10922	HD13 ILE F 49	-18.820	32.242	3.779	1.00	35.76	H	
H									
ATOM	10923	N PHE F 50	-15.317	28.749	1.279	1.00	14.92	N	
ATOM	10924	CA PHE F 50	-13.876	28.544	1.238	1.00	18.72	C	
C									
ATOM	10925	C PHE F 50	-13.449	27.474	0.235	1.00	15.47	C	
ATOM	10926	O PHE F 50	-12.438	27.643	-0.442	1.00	15.17	O	
ATOM	10927	CB PHE F 50	-13.374	28.203	2.637	1.00	14.79	C	
ATOM	10928	CG PHE F 50	-13.688	29.267	3.644	1.00	20.85	C	
ATOM	10929	CD1 PHE F 50	-12.912	30.413	3.720	1.00	23.04	C	
C									
ATOM	10930	CD2 PHE F 50	-14.778	29.144	4.488	1.00	21.71	C	
C									
ATOM	10931	CE1 PHE F 50	-13.206	31.407	4.633	1.00	21.89	C	
ATOM	10932	CE2 PHE F 50	-15.074	30.134	5.408	1.00	21.18	C	
C									
ATOM	10933	CZ PHE F 50	-14.288	31.268	5.475	1.00	19.57	C	
C									
ATOM	10934	H PHE F 50	-15.724	28.301	1.890	1.00	17.90	H	
ATOM	10935	HA PHE F 50	-13.454	29.376	0.972	1.00	22.46	H	
H									
ATOM	10936	HB2 PHE F 50	-13.794	27.379	2.930	1.00	17.74	H	
H									
ATOM	10937	HB3 PHE F 50	-12.411	28.092	2.608	1.00	17.74	H	
H									
ATOM	10938	HD1 PHE F 50	-12.181	30.512	3.153	1.00	27.65	H	
H									
ATOM	10939	HD2 PHE F 50	-15.310	28.383	4.445	1.00	26.06	H	
H									
ATOM	10940	HE1 PHE F 50	-12.674	32.169	4.681	1.00	26.27	H	
H									
ATOM	10941	HE2 PHE F 50	-15.805	30.039	5.975	1.00	25.42	H	
H									
ATOM	10942	HZ PHE F 50	-14.486	31.934	6.094	1.00	23.49	H	
H									
ATOM	10943	N LEU F 51	-14.215	26.389	0.130	1.00	15.59	N	

U
ATOM 4650 CB ASP C 144 -2.949 57.449 -2.188 1.00 24.80
C

ATOM 4651 CG ASP C 144 -4.205 58.296 -2.215 1.00 24.61
C
ATOM 4652 OD1 ASP C 144 -4.881 58.345 -3.264 1.00 31.09
O
ATOM 4653 OD2 ASP C 144 -4.511 58.927 -1.183 1.00 34.04
O1-
ATOM 4654 H ASP C 144 -2.998 58.214 -4.509 1.00 27.33
H
ATOM 4655 HA ASP C 144 -1.942 56.108 -3.366 1.00 28.56
H
ATOM 4656 HB2 ASP C 144 -2.991 56.878 -1.405 1.00 29.76
H
ATOM 4657 HB3 ASP C 144 -2.188 58.046 -2.123 1.00 29.76
H
ATOM 4658 N LEU C 145 -4.864 55.678 -4.386 1.00 18.41
N
ATOM 4659 CA LEU C 145 -5.892 54.652 -4.544 1.00 19.62
C
ATOM 4660 C LEU C 145 -5.274 53.321 -4.976 1.00 20.78
C
ATOM 4661 O LEU C 145 -5.893 52.270 -4.826 1.00 14.96
O
ATOM 4662 CB LEU C 145 -6.968 55.078 -5.553 1.00 19.66
C
ATOM 4663 CG LEU C 145 -6.615 55.709 -6.908 1.00 27.10
C
ATOM 4664 CD1 LEU C 145 -5.336 55.184 -7.518 1.00 25.70
C
ATOM 4665 CD2 LEU C 145 -7.776 55.498 -7.879 1.00 21.56
C
ATOM 4666 H LEU C 145 -4.950 56.360 -4.903 1.00 22.09
H
ATOM 4667 HA LEU C 145 -6.328 54.513 -3.689 1.00 23.55
H
ATOM 4668 HB2 LEU C 145 -7.493 54.288 -5.756 1.00 23.59
H
ATOM 4669 HB3 LEU C 145 -7.540 55.718 -5.102 1.00 23.59
H
ATOM 4670 HG LEU C 145 -6.508 56.665 -6.784 1.00 32.52
H
ATOM 4671 HD11 LEU C 145 -5.185 55.630 -8.366 1.00 30.83
H
ATOM 4672 HD12 LEU C 145 -4.600 55.366 -6.913 1.00 30.83
H
ATOM 4673 HD13 LEU C 145 -5.422 54.228 -7.657 1.00 30.83
H
ATOM 4674 HD21 LEU C 145 -7.550 55.898 -8.734 1.00 25.87
H
ATOM 4675 HD22 LEU C 145 -7.927 54.547 -7.989 1.00 25.87
H
ATOM 4676 HD23 LEU C 145 -8.571 55.920 -7.517 1.00 25.87
H
ATOM 4677 N LEU C 146 -4.048 53.365 -5.494 1.00 16.14
N
ATOM 4678 CA LEU C 146 -3.384 52.158 -5.983 1.00 16.03
C
ATOM 4679 C LEU C 146 -2.981 51.231 -4.840 1.00 17.57
C
ATOM 4680 O LEU C 146 -2.655 50.065 -5.067 1.00 16.74
O
ATOM 4681 CB LEU C 146 -2.154 52.524 -6.821 1.00 17.95
C
ATOM 4682 CG LEU C 146 -2.410 53.275 -8.132 1.00 15.53
C
ATOM 4683 CD1 LEU C 146 -1.089 53.618 -8.817 1.00 16.96
C
ATOM 4684 CD2 LEU C 146 -3.292 52.460 -9.064 1.00 19.12
C
ATOM 4685 H LEU C 146 -3.579 54.081 -5.574 1.00 19.36
H

ATOM 4686 HA LEU C 146 -3.999 51.673 -6.555 1.00 19.23
H
ATOM 4687 HB2 LEU C 146 -1.575 53.083 -6.280 1.00 21.54
H
ATOM 4688 HB3 LEU C 146 -1.688 51.704 -7.048 1.00 21.54
H
ATOM 4689 HG LEU C 146 -2.870 54.106 -7.935 1.00 18.63
H
ATOM 4690 HD11 LEU C 146 -1.276 54.092 -9.642 1.00 20.36
H
ATOM 4691 HD12 LEU C 146 -0.564 54.179 -8.225 1.00 20.36
H
ATOM 4692 HD13 LEU C 146 -0.610 52.797 -9.007 1.00 20.36
H
ATOM 4693 HD21 LEU C 146 -3.435 52.962 -9.882 1.00 22.95
H
ATOM 4694 HD22 LEU C 146 -2.850 51.621 -9.264 1.00 22.95
H
ATOM 4695 HD23 LEU C 146 -4.142 52.291 -8.627 1.00 22.95
H
ATOM 4696 N LYS C 147 -3.014 51.744 -3.613 1.00 19.33
N
ATOM 4697 CA LYS C 147 -2.750 50.925 -2.433 1.00 19.87
C
ATOM 4698 C LYS C 147 -3.839 49.877 -2.192 1.00 17.73
C

U
ATOM 10950 CD2 LEU F 51 -13.442 22.452 0.490 1.00 18.07
C

ATOM 10951 H LEU F 51 -14.931 26.251 0.585 1.00 18.71
H
ATOM 10952 HA LEU F 51 -13.000 24.967 -0.573 1.00 20.21
H
ATOM 10953 HB2 LEU F 51 -15.772 24.533 -0.673 1.00 19.38
H
ATOM 10954 HB3 LEU F 51 -14.785 23.603 -1.485 1.00 19.38
H
ATOM 10955 HG LEU F 51 -14.751 23.775 1.327 1.00 28.27
H
ATOM 10956 HD11 LEU F 51 -15.826 21.705 1.367 1.00 30.46
H
ATOM 10957 HD12 LEU F 51 -16.748 22.794 0.667 1.00 30.46
H
ATOM 10958 HD13 LEU F 51 -15.950 21.742 -0.217 1.00 30.46
H
ATOM 10959 HD21 LEU F 51 -13.398 21.882 1.274 1.00 21.69
H
ATOM 10960 HD22 LEU F 51 -13.418 21.911 -0.314 1.00 21.69
H
ATOM 10961 HD23 LEU F 51 -12.700 23.076 0.492 1.00 21.69
H

ATOM 10962 N PRO F 52 -14.858 26.512 -2.718 1.00 15.74
N
ATOM 10963 CA PRO F 52 -14.770 27.012 -4.094 1.00 16.28
C

ATOM 10964 C PRO F 52 -13.685 28.072 -4.276 1.00 16.85
C
ATOM 10965 O PRO F 52 -13.036 28.106 -5.322 1.00 15.38
O
ATOM 10966 CB PRO F 52 -16.167 27.601 -4.350 1.00 19.09
C
ATOM 10967 CG PRO F 52 -16.760 27.811 -3.003 1.00 20.50
C
ATOM 10968 CD PRO F 52 -16.194 26.736 -2.139 1.00 20.80
C
ATOM 10969 HA PRO F 52 -14.611 26.279 -4.710 1.00 19.54
H
ATOM 10970 HB2 PRO F 52 -16.084 28.443 -4.822 1.00 22.91
H
ATOM 10971 HB3 PRO F 52 -16.697 26.971 -4.662 1.00 22.91
H
ATOM 10972 HG2 PRO F 52 -16.507 28.686 -2.669 1.00 24.59
H
ATOM 10973 HG3 PRO F 52 -17.725 27.732 -3.057 1.00 24.59
H
ATOM 10974 HD2 PRO F 52 -16.119 27.042 -1.222 1.00 24.96
H
ATOM 10975 HD3 PRO F 52 -16.731 25.930 -2.204 1.00 24.96
H

ATOM 10976 N PHE F 53 -13.485 28.921 -3.273 1.00 15.61
N
ATOM 10977 CA PHE F 53 -12.478 29.970 -3.374 1.00 15.34
C

ATOM 10978 C PHE F 53 -11.083 29.361 -3.477 1.00 14.81
C

ATOM 10979 O PHE F 53 -10.293 29.756 -4.334 1.00 15.50
O
ATOM 10980 CB PHE F 53 -12.555 30.922 -2.180 1.00 15.16
C
ATOM 10981 CG PHE F 53 -11.510 32.002 -2.204 1.00 15.82
C
ATOM 10982 CD1 PHE F 53 -11.679 33.131 -2.989 1.00 15.97
C
ATOM 10983 CD2 PHE F 53 -10.356 31.885 -1.448 1.00 15.98
C
ATOM 10984 CE1 PHE F 53 -10.719 34.123 -3.016 1.00 18.86
C
ATOM 10985 CE2 PHE F 53 -9.392 32.879 -1.470 1.00 13.90
C

ATOM 10986 CZ PHE F 53 -9.574 33.995 -2.256 1.00 13.75
C

ATOM 10987 H PHE F 53 -13.916 28.910 -2.528 1.00 18.73
H
ATOM 10988 HA PHE F 53 -12.640 30.486 -4.179 1.00 18.41
H
ATOM 10989 HB2 PHE F 53 -13.425 31.350 -2.176 1.00 18.19
H
ATOM 10990 HB3 PHE F 53 -12.436 30.411 -1.364 1.00 18.19
H
ATOM 10991 HD1 PHE F 53 -12.448 33.222 -3.504 1.00 19.16
H
ATOM 10992 HD2 PHE F 53 -10.229 31.133 -0.916 1.00 19.17
H
ATOM 10993 HE1 PHE F 53 -10.844 34.877 -3.546 1.00 22.64
H
ATOM 10994 HE2 PHE F 53 -8.620 32.791 -0.958 1.00 16.68
H

ATOM 10995 HZ PHE F 53 -8.927 34.664 -2.272 1.00 16.50
H
ATOM 10996 N TYR F 54 -10.790 28.389 -2.616 1.00 13.52
N
ATOM 10997 CA TYR F 54 -9.500 27.707 -2.649 1.00 13.81
C
ATOM 10998 C TYR F 54 -9.324 26.914 -3.935 1.00 13.72
C

O
 ATOM 4699 O LYS C 147 -3.603 48.867 -1.526 1.00 19.26
 O
 ATOM 4700 CB LYS C 147 -2.628 51.807 -1.188 1.00 23.96
 C
 ATOM 4701 CG LYS C 147 -1.400 52.698 -1.163 1.00 34.05
 C
 ATOM 4702 CD LYS C 147 -1.286 53.467 0.152 1.00 43.75
 C
 ATOM 4703 CE LYS C 147 -2.464 54.413 0.354 1.00 52.91
 C
 ATOM 4704 NZ LYS C 147 -2.213 55.423 1.423 1.00 63.31
 N1+
 ATOM 4705 H LYS C 147 -3.187 52.568 -3.436 1.00 23.19
 H
 ATOM 4706 HA LYS C 147 -1.908 50.459 -2.555 1.00 23.84
 H
 ATOM 4707 HB2 LYS C 147 -3.409 52.380 -1.136 1.00 28.75
 H
 ATOM 4708 HB3 LYS C 147 -2.592 51.234 -0.405 1.00 28.75
 H
 ATOM 4709 HG2 LYS C 147 -0.606 52.150 -1.263 1.00 40.86
 H
 ATOM 4710 HG3 LYS C 147 -1.458 53.341 -1.886 1.00 40.86
 H
 ATOM 4711 HD2 LYS C 147 -1.272 52.838 0.890 1.00 52.50
 H
 ATOM 4712 HD3 LYS C 147 -0.472 53.994 0.145 1.00 52.50
 H
 ATOM 4713 HE2 LYS C 147 -2.634 54.888 -0.474 1.00 63.49
 H
 ATOM 4714 HE3 LYS C 147 -3.245 53.896 0.607 1.00 63.49
 H
 ATOM 4715 HZ1 LYS C 147 -2.921 55.955 1.511 1.00 75.97
 H
 ATOM 4716 HZ2 LYS C 147 -2.060 55.014 2.198 1.00 75.97
 H
 ATOM 4717 HZ3 LYS C 147 -1.504 55.918 1.213 1.00 75.97
 H
 ATOM 4718 N LEU C 148 -5.028 50.122 -2.732 1.00 15.82
 N
 ATOM 4719 CA LEU C 148 -6.210 49.333 -2.387 1.00 18.04
 C
 ATOM 4720 C LEU C 148 -6.593 48.304 -3.450 1.00 18.60
 C

ATOM 4721 O LEU C 148 -7.686 47.744 -3.405 1.00 15.31
 O
 ATOM 4722 CB LEU C 148 -7.395 50.269 -2.151 1.00 23.06
 C
 ATOM 4723 CG LEU C 148 -7.130 51.452 -1.217 1.00 32.15
 C
 ATOM 4724 CD1 LEU C 148 -8.009 52.619 -1.612 1.00 32.37
 C
 ATOM 4725 CD2 LEU C 148 -7.363 51.056 0.236 1.00 30.03
 C
 ATOM 4726 H LEU C 148 -5.179 50.745 -3.306 1.00 18.98
 H
 ATOM 4727 HA LEU C 148 -6.038 48.856 -1.560 1.00 21.65
 H
 ATOM 4728 HB2 LEU C 148 -7.674 50.632 -3.007 1.00 27.68
 H
 ATOM 4729 HB3 LEU C 148 -8.122 49.753 -1.768 1.00 27.68
 H
 ATOM 4730 HG LEU C 148 -6.204 51.727 -1.308 1.00 38.58
 H
 ATOM 4731 HD11 LEU C 148 -7.833 53.363 -1.015 1.00 38.84
 H
 ATOM 4732 HD12 LEU C 148 -7.804 52.873 -2.526 1.00 38.84
 H
 ATOM 4733 HD13 LEU C 148 -8.939 52.351 -1.544 1.00 38.84
 H
 ATOM 4734 HD21 LEU C 148 -7.188 51.822 0.804 1.00 36.04
 H
 ATOM 4735 HD22 LEU C 148 -8.284 50.770 0.341 1.00 36.04
 H
 ATOM 4736 HD23 LEU C 148 -6.763 50.329 0.466 1.00 36.04
 H
 ATOM 4737 N VAL C 149 -5.897 48.054 -4.398 1.00 16.71
 N
 ATOM 4738 CA VAL C 149 -6.011 47.210 -5.548 1.00 14.87
 C
 ATOM 4739 C VAL C 149 -5.503 45.783 -5.380 1.00 14.53
 C
 ATOM 4740 O VAL C 149 -4.311 45.568 -5.166 1.00 16.23
 O
 ATOM 4741 CB VAL C 149 -5.409 47.803 -6.833 1.00 18.92
 C
 ATOM 4742 CG1 VAL C 149 -5.723 46.926 -8.036 1.00 20.42
 C
 ATOM 4743 CG2 VAL C 149 -5.930 49.222 -7.054 1.00 20.99
 C
 ATOM 4744 H VAL C 149 -4.894 48.363 -4.399 1.00 20.06
 H
 ATOM 4745 HA VAL C 149 -6.975 47.174 -5.658 1.00 17.84
 H
 ATOM 4746 HB VAL C 149 -4.445 47.849 -6.738 1.00 22.71
 H
 ATOM 4747 HG11 VAL C 149 -5.330 47.326 -8.828 1.00 24.51
 H
 ATOM 4748 HG12 VAL C 149 -5.347 46.044 -7.890 1.00 24.51
 H

ATOM 10999 O TYR F 54 -8.222 26.831 -4.473 1.00 12.92
 O
 ATOM 11000 CB TYR F 54 -9.338 26.783 -1.436 1.00 12.43
 C
 ATOM 11001 CG TYR F 54 -9.215 27.502 -0.107 1.00 13.97
 C
 ATOM 11002 CD1 TYR F 54 -8.682 28.785 -0.029 1.00 15.04
 C
 ATOM 11003 CD2 TYR F 54 -9.637 26.899 1.070 1.00 14.73
 C
 ATOM 11004 CE1 TYR F 54 -8.575 29.442 1.182 1.00 13.01
 C
 ATOM 11005 CE2 TYR F 54 -9.531 27.545 2.282 1.00 13.82
 C
 ATOM 11006 CZ TYR F 54 -9.002 28.814 2.333 1.00 14.13
 C
 ATOM 11007 OH TYR F 54 -8.901 29.461 3.537 1.00 13.26
 O
 ATOM 11008 H TYR F 54 -11.322 28.106 -2.003 1.00 16.22
 H
 ATOM 11009 HA TYR F 54 -8.793 28.371 -2.614 1.00 16.57
 H
 ATOM 11010 HB2 TYR F 54 -10.112 26.201 -1.384 1.00 14.92
 H
 ATOM 11011 HB3 TYR F 54 -8.536 26.250 -1.557 1.00 14.92
 H
 ATOM 11012 HD1 TYR F 54 -8.395 29.208 -0.805 1.00 18.05
 H
 ATOM 11013 HD2 TYR F 54 -9.996 26.041 1.039 1.00 17.67
 H
 ATOM 11014 HE1 TYR F 54 -8.217 30.299 1.221 1.00 15.61
 H
 ATOM 11015 HE2 TYR F 54 -9.820 27.127 3.061 1.00 16.58
 H
 ATOM 11016 HH TYR F 54 -9.194 28.970 -4.152 1.00 15.91
 H
 ATOM 11017 N LYS F 55 -10.403 26.303 -4.429 1.00 13.00
 N
 ATOM 11018 CA LYS F 55 -10.321 25.526 -5.661 1.00 15.12
 C
 ATOM 11019 C LYS F 55 -9.743 26.382 -6.786 1.00 14.25
 C
 ATOM 11020 O LYS F 55 -8.873 25.934 -7.535 1.00 15.64
 O
 ATOM 11021 CB LYS F 55 -11.695 24.982 -6.060 1.00 17.19
 C
 ATOM 11022 CG LYS F 55 -11.638 23.938 -7.159 1.00 18.78
 C
 ATOM 11023 CD LYS F 55 -13.025 23.546 -7.643 1.00 22.88
 C
 ATOM 11024 CE LYS F 55 -12.935 22.564 -8.795 1.00 27.95
 C
 ATOM 11025 NZ LYS F 55 -14.263 22.302 -9.406 1.00 35.34
 N1+
 ATOM 11026 H LYS F 55 -11.186 26.330 -4.075 1.00 15.60
 H
 ATOM 11027 HA LYS F 55 -9.727 24.772 -5.522 1.00 18.15
 H
 ATOM 11028 HB2 LYS F 55 -12.108 24.574 -5.283 1.00 20.62
 H
 ATOM 11029 HB3 LYS F 55 -12.243 25.717 -6.376 1.00 20.62
 H
 ATOM 11030 HG2 LYS F 55 -11.145 24.296 -7.913 1.00 22.53
 H
 ATOM 11031 HG3 LYS F 55 -11.200 23.142 -6.820 1.00 22.53
 H
 ATOM 11032 HD2 LYS F 55 -13.512 23.124 -6.918 1.00 27.45
 H
 ATOM 11033 HD3 LYS F 55 -13.495 24.337 -7.950 1.00 27.45
 H
 ATOM 11034 HE2 LYS F 55 -12.354 22.929 -9.480 1.00 33.53
 H
 ATOM 11035 HE3 LYS F 55 -12.581 21.722 -8.469 1.00 33.53
 H
 ATOM 11036 HZ1 LYS F 55 -14.180 21.724 -10.078 1.00 42.41
 H
 ATOM 11037 HZ2 LYS F 55 -14.816 21.961 -8.798 1.00 42.41
 H
 ATOM 11038 HZ3 LYS F 55 -14.609 23.060 -9.719 1.00 42.41
 H
 ATOM 11039 N ASN F 56 -10.210 27.622 -6.886 1.00 12.64
 N
 ATOM 11040 CA ASN F 56 -9.713 28.541 -7.906 1.00 15.26
 C
 ATOM 11041 C ASN F 56 -8.293 29.017 -7.618 1.00 16.59
 C
 ATOM 11042 O ASN F 56 -7.447 29.059 -8.511 1.00 15.03
 O
 ATOM 11043 CB ASN F 56 -10.640 29.751 -8.028 1.00 18.33
 C
 ATOM 11044 CG ASN F 56 -11.983 29.397 -8.634 1.00 28.04
 C
 ATOM 11045 OD1 ASN F 56 -12.091 28.463 -9.428 1.00 30.73
 O
 ATOM 11046 ND2 ASN F 56 -13.016 30.147 -8.264 1.00 32.03
 N
 ATOM 11047 H ASN F 56 -10.815 27.957 -6.376 1.00 15.17
 H
 ATOM 11048 HA ASN F 56 -9.706 28.085 -8.762 1.00 18.31
 H

ATOM 4749	HG13 VAL C 149	-6.685	46.864	-8.139	1.00	24.51
H						
ATOM 4750	HG21 VAL C 149	-5.539	49.577	-7.868	1.00	25.18
H						
ATOM 4751	HG22 VAL C 149	-6.896	49.194	-7.136	1.00	25.18
H						
ATOM 4752	HG23 VAL C 149	-5.677	49.772	-6.297	1.00	25.18
H						
ATOM 4753	N LYS C 150	-6.408	44.816	-5.500	1.00	13.93
N						
ATOM 4754	CA LYS C 150	-6.044	43.402	-5.450	1.00	18.06
C						
ATOM 4755	C LYS C 150	-5.531	42.912	-6.797	1.00	15.46
C						
ATOM 4756	O LYS C 150	-5.715	43.570	-7.819	1.00	15.34
O						
ATOM 4757	CB LYS C 150	-7.238	42.538	-5.030	1.00	16.72
C						
ATOM 4758	CG LYS C 150	-7.584	42.607	-3.553	1.00	17.69
C						
ATOM 4759	CD LYS C 150	-8.705	41.641	-3.194	1.00	15.55
C						
ATOM 4760	CE LYS C 150	-8.218	40.202	-3.082	1.00	17.69
C						
ATOM 4761	NZ LYS C 150	-7.374	39.972	-1.871	1.00	15.20
N1+						
ATOM 4762	H LYS C 150	-7.249	44.953	-5.613	1.00	16.72
H						
ATOM 4763	HA LYS C 150	-5.338	43.279	-4.796	1.00	21.68
H						
ATOM 4764	HB2 LYS C 150	-8.019	42.826	-5.528	1.00	20.06
H						
ATOM 4765	HB3 LYS C 150	-7.040	41.612	-5.241	1.00	20.06
H						
ATOM 4766	HG2 LYS C 150	-6.802	42.373	-3.030	1.00	21.22
H						
ATOM 4767	HG3 LYS C 150	-7.877	43.506	-3.335	1.00	21.22
H						
ATOM 4768	HD2 LYS C 150	-9.084	41.898	-2.339	1.00	18.65
H						
ATOM 4769	HD3 LYS C 150	-9.386	41.675	-3.884	1.00	18.65
H						
ATOM 4770	HE2 LYS C 150	-8.986	39.612	-3.029	1.00	21.23
H						
ATOM 4771	HE3 LYS C 150	-7.688	39.987	-3.884	1.00	21.23
H						
ATOM 4772	HZ1 LYS C 150	-6.656	40.498	-1.896	1.00	18.24
H						
ATOM 4773	HZ2 LYS C 150	-7.841	40.156	-1.136	1.00	18.24
H						
ATOM 4774	HZ3 LYS C 150	-7.110	39.123	-1.841	1.00	18.24
H						
ATOM 4775	N SER C 151	-4.903	41.742	-6.777	1.00	16.11
N						
ATOM 4776	CA SER C 151	-4.426	41.078	-7.985	1.00	17.40
C						
ATOM 4777	C SER C 151	-3.319	41.859	-8.690	1.00	14.09
C						
ATOM 4778	O SER C 151	-2.799	42.846	-8.160	1.00	16.03
O						
ATOM 4779	CB SER C 151	-5.585	40.834	-8.952	1.00	14.05
C						
ATOM 4780	OG SER C 151	-5.188	39.954	-9.988	1.00	14.91
O						
ATOM 4781	H SER C 151	-4.736	41.302	-6.057	1.00	19.33
H						
ATOM 4782	HA SER C 151	-4.063	40.213	-7.739	1.00	20.89
H						
ATOM 4783	HB2 SER C 151	-6.325	40.438	-8.467	1.00	16.86
H						
ATOM 4784	HB3 SER C 151	-5.856	41.679	-9.342	1.00	16.86
H						
ATOM 4785	HG SER C 151	-5.828	39.824	-10.515	1.00	17.89
H						
ATOM 4786	N TYR C 152	-2.961	41.385	-9.877	1.00	12.60
N						
ATOM 4787	CA TYR C 152	-1.828	41.905	-10.624	1.00	11.73
C						
ATOM 4788	C TYR C 152	-2.312	42.429	-11.968	1.00	17.09
C						
ATOM 4789	O TYR C 152	-3.220	41.852	-12.575	1.00	15.23
O						
ATOM 4790	CB TYR C 152	-0.770	40.814	-10.824	1.00	14.94
C						
ATOM 4791	CG TYR C 152	-0.394	40.065	-9.562	1.00	13.45
C						
ATOM 4792	CD1 TYR C 152	-0.119	40.743	-8.383	1.00	17.53
C						
ATOM 4793	CD2 TYR C 152	-0.317	38.678	-9.552	1.00	13.04
C						
ATOM 4794	CE1 TYR C 152	0.229	40.064	-7.232	1.00	15.99
C						
ATOM 4795	CE2 TYR C 152	0.031	37.989	-8.407	1.00	17.54
C						
ATOM 4796	CZ TYR C 152	0.303	38.688	-7.246	1.00	17.26
C						
ATOM 4797	OH TYR C 152	0.650	38.009	-6.097	1.00	14.46
O						

ATOM 11049	HB2 ASN F 56	-10.797	30.119	-7.144	1.00	22.00
H						
ATOM 11050	HB3 ASN F 56	-10.220	30.416	-8.595	1.00	22.00
H						
ATOM 11051	HD21 ASN F 56	-13.799	29.986	-8.581	1.00	38.43
H						
ATOM 11052	HD22 ASN F 56	-12.901	30.792	-7.708	1.00	38.43
H						
ATOM 11053	N VAL F 57	-8.039	29.391	-6.370	1.00	12.10
N						
ATOM 11054	CA VAL F 57	-8.714	29.855	-5.972	1.00	12.15
C						
ATOM 11055	C VAL F 57	-5.674	28.762	-6.181	1.00	12.63
C						
ATOM 11056	O VAL F 57	-4.603	29.015	-6.738	1.00	16.24
O						
ATOM 11057	CB VAL F 57	-6.708	30.312	-4.500	1.00	12.42
C						
ATOM 11058	CG1 VAL F 57	-5.284	30.566	-4.000	1.00	13.82
C						
ATOM 11059	CG2 VAL F 57	-7.555	31.571	-4.342	1.00	13.89
C						
ATOM 11060	H VAL F 57	-8.617	29.386	-5.733	1.00	14.52
H						
ATOM 11061	HA VAL F 57	-8.467	30.615	-6.522	1.00	14.57
H						
ATOM 11062	HB VAL F 57	-7.100	29.615	-3.951	1.00	14.90
H						
ATOM 11063	HG11 VAL F 57	-5.321	30.851	-3.074	1.00	16.59
H						
ATOM 11064	HG12 VAL F 57	-4.772	29.745	-4.074	1.00	16.59
H						
ATOM 11065	HG13 VAL F 57	-4.878	31.260	-4.544	1.00	16.59
H						
ATOM 11066	HG21 VAL F 57	-7.541	31.845	-3.412	1.00	16.67
H						
ATOM 11067	HG22 VAL F 57	-7.184	32.272	-4.900	1.00	16.67
H						
ATOM 11068	HG23 VAL F 57	-8.464	31.375	-4.617	1.00	16.67
H						
ATOM 11069	N PHE F 58	-5.994	27.548	-5.740	1.00	12.82
N						
ATOM 11070	CA PHE F 58	-5.062	26.430	-5.830	1.00	13.09
C						
ATOM 11071	C PHE F 58	-4.801	26.058	-7.285	1.00	14.82
C						
ATOM 11072	O PHE F 58	-3.660	25.848	-7.676	1.00	12.06
O						
ATOM 11073	CB PHE F 58	-5.588	25.207	-5.070	1.00	12.73
C						
ATOM 11074	CG PHE F 58	-5.695	25.402	-3.578	1.00	12.49
C						
ATOM 11075	CD1 PHE F 58	-5.281	26.581	-2.974	1.00	12.83
C						
ATOM 11076	CD2 PHE F 58	-6.213	24.396	-2.777	1.00	13.83
C						
ATOM 11077	CE1 PHE F 58	-5.388	26.751	-1.603	1.00	13.49
C						
ATOM 11078	CE2 PHE F 58	-6.322	24.566	-1.405	1.00	16.44
C						
ATOM 11079	CZ PHE F 58	-5.906	25.747	-0.821	1.00	11.02
C						
ATOM 11080	H PHE F 58	-6.749	27.346	-5.381	1.00	15.38
H						
ATOM 11081	HA PHE F 58	-4.217	26.690	-5.431	1.00	15.71
H						
ATOM 11082	HB2 PHE F 58	-6.473	24.991	-5.403	1.00	15.28
H						
ATOM 11083	HB3 PHE F 58	-4.988	24.461	-5.227	1.00	15.28
H						
ATOM 11084	HD1 PHE F 58	-4.931	27.287	-3.496	1.00	15.39
H						
ATOM 11085	HD2 PHE F 58	-6.497	23.600	-3.166	1.00	16.60
H						
ATOM 11086	HE1 PHE F 58	-5.107	27.546	-1.211	1.00	16.19
H						
ATOM 11087	HE2 PHE F 58	-6.672	23.884	-0.878	1.00	19.73
H						
ATOM 11088	HZ PHE F 58	-5.975	25.862	0.099	1.00	13.22
H						
ATOM 11089	N SER F 59	-5.853	25.970	-8.089	1.00	12.82
N						
ATOM 11090	CA SER F 59	-5.885	25.598	-9.486	1.00	18.28
C						
ATOM 11091	C SER F 59	-4.855	26.649	-10.229	1.00	18.53
C						
ATOM 11092	O SER F 59	-4.011	26.307	-11.056	1.00	15.62
O						
ATOM 11093	CB SER F 59	-7.046	25.406	-10.159	1.00	19.61
C						
ATOM 11094	OG SER F 59	-7.896	26.504	-9.896	1.00	29.67
O						
ATOM 11095	H SER F 59	-6.667	26.119	-7.853	1.00	15.39
H						
ATOM 11096	HA SER F 59	-5.208	24.754	-9.532	1.00	19.54
H						
ATOM 11097	HB2 SER F 59	-6.917	25.329	-11.118	1.00	23.54
H						

ATOM 4798 H TYR C 152	-3.371	40.745	-10.280	1.00	15.12	ATOM 11098 HB3 SER F 59	-7.458	24.598	-9.815	1.00	23.54	
H						H						
ATOM 4799 HA TYR C 152	-1.425	42.639	-10.134	1.00	14.07	ATOM 11099 HG SER F 59	-7.551	27.212	-10.189	1.00	35.60	
H						H						
ATOM 4800 HB2 TYR C 152	-1.110	40.166	-11.461	1.00	17.93	ATOM 11100 N GLU F 60	-5.070	27.925	-9.914	1.00	17.84	N
H						ATOM 11101 CA GLU F 60	-4.311	29.000	-10.554	1.00	15.88	
ATOM 4801 HB3 TYR C 152	0.036	41.224	-11.174	1.00	17.93	C						
H						ATOM 11102 C GLU F 60	-2.856	29.027	-10.090	1.00	14.19	C
ATOM 4802 HD1 TYR C 152	-0.165	41.672	-8.369	1.00	21.04	ATOM 11103 O GLU F 60	-1.958	29.374	-10.859	1.00	16.59	O
H						ATOM 11104 CB GLU F 60	-4.966	30.356	-10.286	1.00	19.52	
ATOM 4803 HD2 TYR C 152	-0.496	38.205	-10.333	1.00	15.65	C						
H						ATOM 11105 CG GLU F 60	-6.207	30.607	-11.124	1.00	26.68	
ATOM 4804 HE1 TYR C 152	0.412	40.533	-6.450	1.00	19.18	C						
H						ATOM 11106 CD GLU F 60	-5.906	30.696	-12.609	1.00	34.90	
ATOM 4805 HE2 TYR C 152	0.080	37.060	-8.416	1.00	21.05	C						
H						ATOM 11107 OE1 GLU F 60	-5.129	31.593	-13.010	1.00	37.82	
ATOM 4806 HH TYR C 152	0.657	37.182	-6.243	1.00	17.36	O						
H						ATOM 11108 OE2 GLU F 60	-6.442	29.886	-13.377	1.00	35.67	
ATOM 4807 N HIS C 153	-1.711	43.521	-12.428	1.00	11.85	O1-						
N						ATOM 11109 H GLU F 60	-5.646	28.194	-9.335	1.00	21.40	H
ATOM 4808 CA HIS C 153	-2.185	44.203	-13.628	1.00	13.69	ATOM 11110 HA GLU F 60	-4.313	28.855	-11.513	1.00	19.05	
C						H						
ATOM 4809 C HIS C 153	-1.038	44.802	-14.415	1.00	13.10	ATOM 11111 HB2 GLU F 60	-5.223	30.400	-9.352	1.00	23.42	
C						H						
ATOM 4810 O HIS C 153	-0.106	45.358	-13.836	1.00	13.18	ATOM 11112 HB3 GLU F 60	-4.326	31.058	-10.485	1.00	23.42	
O						H						
ATOM 4811 CB HIS C 153	-3.182	45.302	-13.254	1.00	12.79	ATOM 11113 HG2 GLU F 60	-6.833	29.877	-10.988	1.00	32.02	
C						H						
ATOM 4812 CG HIS C 153	-4.220	44.860	-12.274	1.00	15.44	ATOM 11114 HG3 GLU F 60	-6.610	31.445	-10.849	1.00	32.02	
C						H						
ATOM 4813 ND1 HIS C 153	-5.444	44.357	-12.661	1.00	13.49	ATOM 11115 N PHE F 61	-2.630	28.671	-8.829	1.00	16.80	N
N						ATOM 11116 CA PHE F 61	-1.278	28.576	-8.290	1.00	13.01	C
ATOM 4814 CD2 HIS C 153	-4.210	44.830	-10.920	1.00	15.97	ATOM 11117 C PHE F 61	-0.415	27.700	-9.188	1.00	15.28	C
C						ATOM 11118 O PHE F 61	0.721	28.048	-9.504	1.00	14.04	O
ATOM 4815 CE1 HIS C 153	-6.146	44.043	-11.587	1.00	16.56	ATOM 11119 CB PHE F 61	-1.302	28.013	-6.866	1.00	12.89	C
C						ATOM 11120 CG PHE F 61	0.067	27.780	-6.272	1.00	11.72	
ATOM 4816 NE2 HIS C 153	-5.419	44.317	-10.518	1.00	16.62	C						
N						ATOM 11121 CD1 PHE F 61	0.710	26.560	-6.430	1.00	12.06	
ATOM 4817 H HIS C 153	-1.025	43.888	-12.063	1.00	14.22	ATOM 11122 CD2 PHE F 61	0.698	28.775	-5.538	1.00	12.10	
H						C						
ATOM 4818 HA HIS C 153	-2.641	43.563	-14.198	1.00	16.43	ATOM 11123 CE1 PHE F 61	1.968	26.342	-5.878	1.00	14.29	
H						C						
ATOM 4819 HB2 HIS C 153	-2.697	46.043	-12.859	1.00	15.35	ATOM 11124 CE2 PHE F 61	1.954	28.563	-4.982	1.00	12.57	
H						C						
ATOM 4820 HB3 HIS C 153	-3.638	45.598	-14.057	1.00	15.35	ATOM 11125 CZ PHE F 61	2.589	27.347	-5.152	1.00	11.10	C
H						ATOM 11126 H PHE F 61	-3.247	28.479	-8.262	1.00	20.16	H
ATOM 4821 HD1 HIS C 153	-5.710	44.265	-13.474	1.00	16.19	ATOM 11127 HA PHE F 61	-0.883	29.462	-8.260	1.00	15.61	H
H						ATOM 11128 HB2 PHE F 61	-1.771	28.638	-6.292	1.00	15.46	
ATOM 4822 HD2 HIS C 153	-3.515	45.104	-10.366	1.00	19.16	H						
H						ATOM 11129 HB3 PHE F 61	-1.768	27.162	-6.876	1.00	15.46	
ATOM 4823 HE1 HIS C 153	-7.005	43.687	-11.584	1.00	19.87	H						
H						ATOM 11130 HD1 PHE F 61	0.299	25.884	-6.917	1.00	14.47	
ATOM 4824 HE2 HIS C 153	-5.665	44.199	-9.702	1.00	19.95	ATOM 11131 HD2 PHE F 61	0.277	29.596	-5.421	1.00	14.52	
H						H						
ATOM 4825 N TRP C 154	-1.104	44.682	-15.738	1.00	15.58	ATOM 11132 HE1 PHE F 61	2.391	25.522	-5.994	1.00	17.15	
N						ATOM 11133 HE2 PHE F 61	2.368	29.240	-4.496	1.00	15.08	
ATOM 4826 CA TRP C 154	-0.104	45.295	-16.598	1.00	15.13	H						
C						ATOM 11134 HZ PHE F 61	3.429	27.203	-4.781	1.00	13.32	H
ATOM 4827 C TRP C 154	-0.118	46.805	-16.411	1.00	15.13	ATOM 11135 N PHE F 62	-0.962	26.564	-9.605	1.00	15.38	N
C						ATOM 11136 CA PHE F 62	-0.203	25.622	-10.419	1.00	14.52	
ATOM 4828 O TRP C 154	-1.175	47.430	-16.468	1.00	13.30	C						
O						ATOM 11137 C PHE F 62	-0.191	26.018	-11.891	1.00	14.12	C
ATOM 4829 CB TRP C 154	-0.353	44.977	-18.078	1.00	15.45	ATOM 11138 O PHE F 62	0.847	25.938	-12.546	1.00	17.38	O
C						ATOM 11139 CB PHE F 62	-0.762	24.209	-10.254	1.00	17.80	
ATOM 4830 CG TRP C 154	0.036	43.598	-18.543	1.00	17.21	C						
C						ATOM 11140 CG PHE F 62	-0.503	23.620	-8.899	1.00	18.12	
ATOM 4831 CD1 TRP C 154	-0.751	42.717	-19.229	1.00	18.69	ATOM 11141 CD1 PHE F 62	0.767	23.192	-8.550	1.00	17.73	
C						C						
ATOM 4832 CD2 TRP C 154	1.310	42.957	-18.385	1.00	17.34	ATOM 11142 CD2 PHE F 62	-1.521	23.503	-7.972	1.00	13.87	
C						C						
ATOM 4833 NE1 TRP C 154	-0.049	41.567	-19.506	1.00	16.22	ATOM 11143 CE1 PHE F 62	1.015	22.857	-7.305	1.00	14.74	
N						C						
ATOM 4834 CE2 TRP C 154	1.217	41.687	-18.995	1.00	17.13	ATOM 11144 CE2 PHE F 62	-1.279	22.972	-6.723	1.00	16.22	
C						C						
ATOM 4835 CE3 TRP C 154	2.518	43.329	-17.783	1.00	15.92	ATOM 11145 CZ PHE F 62	-0.008	22.548	-6.389	1.00	16.45	C
C						ATOM 11146 H PHE F 62	-1.767	26.316	-9.432	1.00	18.46	H
ATOM 4836 CZ2 TRP C 154	2.283	40.790	-19.019	1.00	16.67	ATOM 11147 HA PHE F 62	0.715	25.614	-10.108	1.00	17.42	
C						H						
ATOM 4837 CZ3 TRP C 154	3.576	42.435	-17.809	1.00	13.50	ATOM 11148 HB2 PHE F 62	-1.768	27.162	-6.876	1.00	15.46	
C						ATOM 11149 HB3 PHE F 62	-1.768	27.162	-6.876	1.00	15.46	
ATOM 4838 CH2 TRP C 154	3.451	41.182	-18.422	1.00	14.99	ATOM 11150 HD1 PHE F 62	0.299	25.884	-6.917	1.00	14.47	
C						ATOM 11151 HD2 PHE F 62	0.277	29.596	-5.421	1.00	14.52	
ATOM 4839 H TRP C 154	-1.718	44.251	-16.159	1.00	18.70	H						
H						ATOM 11152 HE1 PHE F 62	2.391	25.522	-5.994	1.00	17.15	
ATOM 4840 HA TRP C 154	0.775	44.964	-16.357	1.00	18.16	ATOM 11153 HE2 PHE F 62	2.368	29.240	-4.496	1.00	15.08	
H						H						
ATOM 4841 HB2 TRP C 154	-1.301	45.083	-18.256	1.00	18.54	ATOM 11154 HZ PHE F 62	3.429	27.203	-4.781	1.00	13.32	H
H						ATOM 11155 N PHE F 62	-0.962	26.564	-9.605	1.00	15.38	N
ATOM 4842 HB3 TRP C 154	0.147	45.612	-18.613	1.00	18.54	ATOM 11156 CA PHE F 62	-0.203	25.622	-10.419	1.00	14.52	
H						C						
ATOM 4843 HD1 TRP C 154	-1.633	42.875	-19.480	1.00	22.43	ATOM 11157 C PHE F 62	-0.191	26.018	-11.891	1.00	14.12	C
H						ATOM 11158 O PHE F 62	0.847	25.938	-12.546	1.00	17.38	O
ATOM 4844 HE1 TRP C 154	-0.357	40.881	-19.924	1.00	19.46	ATOM 11159 CB PHE F 62	-0.762	24.209	-10.254	1.00	17.80	
H						C						
ATOM 4845 HE3 TRP C 154	2.608	44.160	-17.375	1.00	19.10	ATOM 11160 CG PHE F 62	-0.503	23.620	-8.899	1.00	18.12	
H						ATOM 11161 CD1 PHE F 62	0.767	23.192	-8.550	1.00	17.73	
ATOM 4846 HZ2 TRP C 154	2.203	39.957	-19.424	1.00	20.01	ATOM 11162 CD2 PHE F 62	-1.521					

ATOM	4887	CG1 VAL C 158	7.446	48.311	-21.402	1.00	16.67
C							
ATOM	4898	CG2 VAL C 158	9.398	49.897	-21.522	1.00	16.63
C							
ATOM	4899	H VAL C 158	8.768	50.049	-18.819	1.00	22.89
H							
ATOM	4900	HA VAL C 158	8.911	47.394	-19.369	1.00	21.65
H							
ATOM	4901	HB VAL C 158	9.433	47.857	-21.602	1.00	21.47
H							
ATOM	4902	HG11 VAL C 158	7.299	48.454	-22.350	1.00	22.40
H							
ATOM	4903	HG12 VAL C 158	7.194	47.405	-21.161	1.00	22.40
H							
ATOM	4904	HG13 VAL C 158	6.927	48.947	-20.887	1.00	22.40
H							
ATOM	4905	HG21 VAL C 158	9.218	50.011	-22.469	1.00	19.96
H							
ATOM	4906	HG22 VAL C 158	8.916	50.565	-21.010	1.00	19.96
H							
ATOM	4907	HG23 VAL C 158	10.350	49.975	-21.354	1.00	19.96
H							
ATOM	4908	N HIS C 159	11.405	47.314	-19.716	1.00	16.25
N							
ATOM	4909	CA HIS C 159	12.812	47.135	-19.375	1.00	21.00
C							
ATOM	4910	C HIS C 159	13.898	47.078	-20.618	1.00	21.62
C							
ATOM	4911	O HIS C 159	13.470	46.273	-21.516	1.00	19.38
O							
ATOM	4912	CB HIS C 159	12.968	45.855	-18.552	1.00	25.11
C							
ATOM	4913	CG HIS C 159	14.385	45.484	-18.249	1.00	23.93
C							
ATOM	4914	ND1 HIS C 159	15.041	44.462	-18.901	1.00	30.14
N							
ATOM	4915	CD2 HIS C 159	15.265	45.983	-17.348	1.00	28.59
C							
ATOM	4916	CE1 HIS C 159	16.269	44.354	-18.423	1.00	30.59
C							
ATOM	4917	NE2 HIS C 159	16.430	45.265	-17.479	1.00	31.14
N							
ATOM	4918	H HIS C 159	11.079	46.663	-20.174	1.00	19.50
H							
ATOM	4919	HA HIS C 159	13.104	47.882	-18.830	1.00	25.20
H							
ATOM	4920	HB2 HIS C 159	12.507	45.971	-17.706	1.00	30.13
H							
ATOM	4921	HB3 HIS C 159	12.570	45.119	-19.043	1.00	30.13
H							
ATOM	4922	HD1 HIS C 159	14.706	43.974	-19.525	1.00	36.16
H							
ATOM	4923	HD2 HIS C 159	15.112	46.683	-16.756	1.00	34.31
H							
ATOM	4924	HE1 HIS C 159	16.910	43.742	-18.703	1.00	36.71
H							
ATOM	4925	HE2 HIS C 159	17.147	45.390	-17.022	1.00	37.37
H							
ATOM	4926	N ILE C 160	14.703	47.947	-20.656	1.00	25.17
N							
ATOM	4927	CA ILE C 160	15.714	47.923	-21.708	1.00	25.24
C							
ATOM	4928	C ILE C 160	16.835	46.958	-21.317	1.00	32.27
C							
ATOM	4929	O ILE C 160	17.581	47.241	-20.379	1.00	31.75
O							
ATOM	4930	CB ILE C 160	16.310	49.328	-21.947	1.00	29.66
C							
ATOM	4931	CG1 ILE C 160	15.219	50.296	-22.407	1.00	26.24
C							
ATOM	4932	CG2 ILE C 160	17.433	49.264	-22.976	1.00	33.94
C							
ATOM	4933	CD1 ILE C 160	15.673	51.741	-22.507	1.00	35.20
C							
ATOM	4934	H ILE C 160	14.822	48.571	-20.076	1.00	30.21
H							
ATOM	4935	HA ILE C 160	15.314	47.613	-22.535	1.00	30.29
H							
ATOM	4936	HB ILE C 160	16.677	49.653	-21.110	1.00	35.59
H							
ATOM	4937	HG12 ILE C 160	14.910	50.022	-23.284	1.00	31.49
H							
ATOM	4938	HG13 ILE C 160	14.485	50.260	-21.774	1.00	31.49
H							
ATOM	4939	HG21 ILE C 160	17.790	50.156	-23.108	1.00	40.72
H							
ATOM	4940	HG22 ILE C 160	18.129	48.674	-22.646	1.00	40.72
H							
ATOM	4941	HG23 ILE C 160	17.077	48.923	-23.811	1.00	40.72
H							
ATOM	4942	HD11 ILE C 160	14.926	52.285	-22.803	1.00	42.25
H							
ATOM	4943	HD12 ILE C 160	15.974	52.038	-21.635	1.00	42.25
H							
ATOM	4944	HD13 ILE C 160	16.400	51.799	-23.147	1.00	42.25
H							
ATOM	4945	N PRO C 161	16.965	45.817	-22.025	1.00	32.29
N							
ATOM	4946	CA PRO C 161	18.018	44.864	-21.642	1.00	33.49
C							
ATOM	4947	C PRO C 161	19.426	45.439	-21.793	1.00	38.43
C							
ATOM	11197	HA PHE F 65	4.292	26.363	-12.373	1.00	16.60
H							
ATOM	11198	HB2 PHE F 65	3.619	27.419	-10.954	1.00	15.03
H							
ATOM	11199	HB3 PHE F 65	3.523	26.312	-12.087	1.00	15.03
H							
ATOM	11200	HD1 PHE F 65	6.108	28.619	-11.239	1.00	15.62
H							
ATOM	11201	HD2 PHE F 65	5.225	24.764	-11.803	1.00	15.71
H							
ATOM	11202	HE1 PHE F 65	8.316	28.061	-10.870	1.00	18.58
H							
ATOM	11203	HE2 PHE F 65	7.436	24.202	-11.434	1.00	18.74
H							
ATOM	11204	HZ PHE F 65	8.982	25.851	-10.969	1.00	19.69
H							
ATOM	11205	N ARG F 66	5.282	28.493	-14.731	1.00	15.25
N							
ATOM	11206	CA ARG F 66	5.986	28.096	-15.943	1.00	17.61
C							
ATOM	11207	C ARG F 66	7.345	27.528	-15.594	1.00	25.02
C							
ATOM	11208	O ARG F 66	8.085	28.103	-14.797	1.00	25.04
O							
ATOM	11209	CB ARG F 66	6.142	29.273	-16.894	1.00	18.04
C							
ATOM	11210	CG ARG F 66	4.896	29.554	-17.694	1.00	22.17
C							
ATOM	11211	CD ARG F 66	4.516	30.995	-17.574	1.00	24.66
C							
ATOM	11212	NE ARG F 66	5.588	31.875	-18.023	1.00	26.85
N							
ATOM	11213	CZ ARG F 66	5.720	33.140	-17.643	1.00	26.45
C							
ATOM	11214	NH1 ARG F 66	4.850	33.681	-16.797	1.00	25.82
N1+							
ATOM	11215	NH2 ARG F 66	6.724	33.865	-18.107	1.00	29.31
N							
ATOM	11216	H ARG F 66	5.544	29.245	-14.407	1.00	18.30
H							
ATOM	11217	HA ARG F 66	5.476	27.406	-16.396	1.00	21.13
H							
ATOM	11218	HB2 ARG F 66	6.352	30.068	-16.379	1.00	21.65
H							
ATOM	11219	HB3 ARG F 66	6.860	29.082	-17.517	1.00	21.65
H							
ATOM	11220	HG2 ARG F 66	5.060	29.356	-18.629	1.00	26.60
H							
ATOM	11221	HG3 ARG F 66	4.165	29.014	-17.356	1.00	26.60
H							
ATOM	11222	HD2 ARG F 66	3.734	31.165	-18.123	1.00	29.59
H							
ATOM	11223	HD3 ARG F 66	4.325	31.199	-16.646	1.00	29.59
H							
ATOM	11224	HE ARG F 66	6.139	31.571	-18.609	1.00	32.21
H							
ATOM	11225	HH11 ARG F 66	4.195	33.211	-16.495	1.00	30.99
H							
ATOM	11226	HH12 ARG F 66	4.940	34.500	-16.552	1.00	30.99
H							
ATOM	11227	HH21 ARG F 66	7.289	33.516	-18.654	1.00	35.18
H							
ATOM	11228	HH22 ARG F 66	6.814	34.684	-17.861	1.00	35.18
H							
ATOM	11229	N ARG F 67	7.660	26.395	-16.206	1.00	21.33
N							
ATOM	11230	CA ARG F 67	8.865	25.653	-15.896	1.00	25.35
C							
ATOM	11231	C ARG F 67	9.889	25.840	-17.006	1.00	30.18
C							
ATOM	11232	O ARG F 67	9.701	26.664	-17.904	1.00	29.69
O							
ATOM	11233	CB ARG F 67	8.526	24.172	-15.705	1.00	22.56
C							
ATOM	11234	CG ARG F 67	7.327	23.950	-14.797	1.00	21.84
C							
ATOM	11235	CD ARG F 67	7.287	22.543	-14.225	1.00	23.91
C							
ATOM	11236	NE ARG F 67	7.381	21.509	-15.253	1.00	27.20
N							
ATOM	11237	CZ ARG F 67	6.343	20.966	-15.883	1.00	31.04
C							
ATOM	11238	NH1 ARG F 67	5.103	21.355	-15.813	1.00	27.45
N1+							
ATOM	11239	NH2 ARG F 67	6.548	20.027	-16.798	1.00	29.30
N							
ATOM	11240	H ARG F 67	7.178	26.030	-16.818	1.00	25.59
H							
ATOM	11241	HA ARG F 67	9.246	25.989	-15.069	1.00	30.42
H							
ATOM	11242	HB2 ARG F 67	8.324	23.781	-16.570	1.00	27.07
H							
ATOM	11243	HB3 ARG F 67	9.289	23.723	-15.309	1.00	27.07
H							
ATOM	11244	HG2 ARG F 67	7.370	24.575	-14.056	1.00	26.21
H							
ATOM	11245	HG3 ARG F 67	6.513	24.092	-15.306	1.00	26.21
H							
ATOM	11246	HD2 ARG F 67	8.034	22.429	-13.617	1.00	28.69

C
 ATOM 4948 O PRO C 161 20.344 45.006 -21.093 1.00 39.19
 O
 ATOM 4949 CB PRO C 161 17.810 43.692 -22.612 1.00 34.26
 C
 ATOM 4950 CG PRO C 161 16.429 43.848 -23.134 1.00 31.11
 C
 ATOM 4951 CD PRO C 161 16.174 45.321 -23.164 1.00 27.41
 C
 ATOM 4952 HA PRO C 161 17.887 44.559 -20.731 1.00 40.18
 H
 ATOM 4953 HB2 PRO C 161 18.456 43.747 -23.333 1.00 41.12
 H
 ATOM 4954 HB3 PRO C 161 17.902 42.853 -22.134 1.00 41.12
 H
 ATOM 4955 HG2 PRO C 161 16.374 43.474 -24.028 1.00 37.33
 H
 ATOM 4956 HG3 PRO C 161 15.804 43.405 -22.539 1.00 37.33
 H
 ATOM 4957 HD2 PRO C 161 16.497 45.705 -23.994 1.00 32.89
 H
 ATOM 4958 HD3 PRO C 161 15.231 45.505 -23.028 1.00 32.89
 H
 ATOM 4959 N THR C 162 19.577 46.399 -22.701 1.00 41.08
 N
 ATOM 4960 CA THR C 162 20.863 47.035 -22.974 1.00 43.65
 C
 ATOM 4961 C THR C 162 21.495 47.605 -21.709 1.00 48.57
 C
 ATOM 4962 O THR C 162 22.589 47.196 -21.318 1.00 52.38
 O
 ATOM 4963 CB THR C 162 20.704 48.164 -24.030 1.00 41.19
 C
 ATOM 4964 OG1 THR C 162 20.643 47.588 -25.339 1.00 51.79
 O
 ATOM 4965 CG2 THR C 162 21.861 49.168 -23.983 1.00 50.32
 C

 ATOM 4966 H THR C 162 18.934 46.707 -23.182 1.00 49.29
 H
 ATOM 4967 HA THR C 162 21.470 46.371 -23.337 1.00 52.38
 H
 ATOM 4968 HB THR C 162 19.880 48.646 -23.857 1.00 49.42
 H
 ATOM 4969 HG1 THR C 162 19.988 47.065 -25.393 1.00 62.14
 H
 ATOM 4970 HG21 THR C 162 21.730 49.857 -24.653 1.00 60.38
 H
 ATOM 4971 HG22 THR C 162 21.904 49.584 -23.107 1.00 60.38
 H
 ATOM 4972 HG23 THR C 162 22.701 48.714 -24.157 1.00 60.38
 H
 ATOM 4973 N ASN C 163 20.799 48.544 -21.075 1.00 46.77
 N
 ATOM 4974 CA ASN C 163 21.340 49.264 -19.928 1.00 44.73
 C
 ATOM 4975 C ASN C 163 20.590 48.965 -18.630 1.00 46.38
 C
 ATOM 4976 O ASN C 163 20.716 49.698 -17.648 1.00 47.39
 O
 ATOM 4977 CB ASN C 163 21.324 50.768 -20.213 1.00 48.30
 C
 ATOM 4978 CG ASN C 163 19.972 51.258 -20.685 1.00 47.25
 C
 ATOM 4979 OD1 ASN C 163 18.934 50.711 -20.313 1.00 46.02
 O
 ATOM 4980 ND2 ASN C 163 19.978 52.292 -21.520 1.00 46.65
 N
 ATOM 4981 H ASN C 163 20.003 48.784 -21.292 1.00 56.13
 H
 ATOM 4982 HA ASN C 163 22.264 48.998 -19.802 1.00 53.68
 H
 ATOM 4983 HB2 ASN C 163 21.550 51.246 -19.399 1.00 57.96
 H
 ATOM 4984 HB3 ASN C 163 21.974 50.965 -20.905 1.00 57.96
 H
 ATOM 4985 HD21 ASN C 163 19.236 52.608 -21.817 1.00 55.98
 H
 ATOM 4986 HD22 ASN C 163 20.724 52.645 -21.762 1.00 55.98
 H
 ATOM 4987 N GLY C 164 19.813 47.885 -18.633 1.00 43.17
 N
 ATOM 4988 CA GLY C 164 19.118 47.429 -17.441 1.00 38.67
 C
 ATOM 4989 C GLY C 164 18.202 48.466 -16.815 1.00 39.65
 C
 ATOM 4990 O GLY C 164 17.958 48.435 -15.609 1.00 42.49
 O
 ATOM 4991 H GLY C 164 19.673 47.394 -19.326 1.00 51.80
 H
 ATOM 4992 HA2 GLY C 164 18.584 46.651 -17.664 1.00 46.40
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 ATOM 4993 HA3 GLY C 164 19.772 47.165 -16.775 1.00 46.40
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 ATOM 4994 N SER C 165 17.686 49.376 -17.636 1.00 34.82
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 ATOM 4995 CA SER C 165 16.856 50.474 -17.153 1.00 32.20
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 ATOM 4996 C SER C 165 15.364 50.169 -17.287 1.00 27.87

H
 ATOM 11248 HE ARG F 67 8.166 21.230 -15.466 1.00 32.65
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 ATOM 11249 HH11 ARG F 67 4.962 21.962 -15.021 1.00 32.94
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 ATOM 11250 HH12 ARG F 67 4.440 20.998 -16.028 1.00 32.94
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 ATOM 11251 HH21 ARG F 67 7.349 19.771 -16.980 1.00 35.16
 H
 ATOM 11252 HH22 ARG F 67 5.880 19.676 -17.211 1.00 35.16
 H
 ATOM 11253 N VAL F 68 10.975 25.085 -16.925 1.00 32.53 N
 ATOM 11254 CA VAL F 68 11.968 25.069 -17.970 1.00 34.51
 C
 ATOM 11255 C VAL F 68 12.281 23.609 -18.307 1.00 38.41 C
 ATOM 11256 O VAL F 68 12.207 22.750 -17.429 1.00 36.57
 O
 ATOM 11257 CB VAL F 68 13.276 25.800 -17.529 1.00 41.03
 C
 ATOM 11258 CG1 VAL F 68 13.813 25.221 -16.223 1.00 39.01
 C
 ATOM 11259 CG2 VAL F 68 14.334 25.745 -18.624 1.00 43.43
 C
 ATOM 11260 H VAL F 68 11.152 24.564 -16.264 1.00 39.04 H
 ATOM 11261 HA VAL F 68 11.642 25.505 -18.763 1.00 41.42
 H
 ATOM 11262 HB VAL F 68 13.063 26.733 -17.371 1.00 49.24
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 ATOM 11263 HG11 VAL F 68 14.619 25.699 -15.974 1.00 46.81
 H
 ATOM 11264 HG12 VAL F 68 13.140 25.323 -15.532 1.00 46.81
 H
 ATOM 11265 HG13 VAL F 68 14.014 24.280 -16.354 1.00 46.81
 H

 ATOM 11266 HG21 VAL F 68 15.128 26.213 -18.318 1.00 52.11
 H
 ATOM 11267 HG22 VAL F 68 14.547 24.819 -18.811 1.00 52.11
 H
 ATOM 11268 HG23 VAL F 68 13.985 26.174 -19.421 1.00 52.11
 H
 ATOM 11269 N PRO F 69 12.585 23.312 -19.583 1.00 40.10
 N
 ATOM 11270 CA PRO F 69 12.933 21.923 -19.904 1.00 43.70
 C
 ATOM 11271 C PRO F 69 14.276 21.526 -19.307 1.00 46.21
 C
 ATOM 11272 O PRO F 69 15.248 22.268 -19.453 1.00 49.34
 O
 ATOM 11273 CB PRO F 69 12.994 21.915 -21.437 1.00 42.03
 C
 ATOM 11274 CG PRO F 69 12.269 23.147 -21.865 1.00 44.28
 C
 ATOM 11275 CD PRO F 69 12.538 24.147 -20.794 1.00 37.27
 C
 ATOM 11276 HA PRO F 69 12.243 21.314 -19.599 1.00 52.45
 H
 ATOM 11277 HB2 PRO F 69 13.919 21.944 -21.728 1.00 50.44
 H
 ATOM 11278 HB3 PRO F 69 12.552 21.122 -21.777 1.00 50.44
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 ATOM 11279 HG2 PRO F 69 12.619 23.453 -22.716 1.00 53.14
 H
 ATOM 11280 HG3 PRO F 69 11.319 22.961 -21.930 1.00 53.14
 H
 ATOM 11281 HD2 PRO F 69 13.392 24.582 -20.941 1.00 44.72
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 ATOM 11282 HD3 PRO F 69 11.813 24.789 -20.737 1.00 44.72
 H
 ATOM 11283 N THR F 70 14.325 20.373 -18.647 1.00 48.67
 N
 ATOM 11284 CA THR F 70 15.550 19.908 -18.009 1.00 60.44
 C
 ATOM 11285 C THR F 70 15.727 18.407 -18.178 1.00 59.62
 C
 ATOM 11286 O THR F 70 14.758 17.671 -18.367 1.00 55.15
 O
 ATOM 11287 CB THR F 70 15.565 20.240 -16.507 1.00 59.77
 C
 ATOM 11288 OG1 THR F 70 14.479 19.568 -15.855 1.00 58.31
 O
 ATOM 11289 CG2 THR F 70 15.441 21.742 -16.286 1.00 62.29
 C
 ATOM 11290 H THR F 70 13.657 19.840 -18.554 1.00 58.41
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 ATOM 11291 HA THR F 70 16.309 20.349 -18.422 1.00 72.53
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 ATOM 11292 HB THR F 70 16.404 19.943 -16.121 1.00 71.73
 H
 ATOM 11293 HG1 THR F 70 14.482 19.746 -15.034 1.00 69.97
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 ATOM 11294 HG21 THR F 70 15.451 21.939 -15.336 1.00 74.75
 H
 ATOM 11295 HG22 THR F 70 16.182 22.201 -16.711 1.00 74.75
 H
 ATOM 11296 HG23 THR F 70 14.809 22.065 -16.666 1.00 74.75

ATOM 4996 O SER C 165	15.324	50.109	-17.207	1.00	27.07	ATOM 11296 N THR F 70	17.009	22.000	-10.000	1.00	74.70
ATOM 4997 O SER C 165	14.943	49.486	-18.223	1.00	25.68	ATOM 11297 N SER F 71	16.978	17.966	-18.107	1.00	61.53
ATOM 4998 CB SER C 165	17.193	51.756	-17.917	1.00	38.18	ATOM 11298 CA SER F 71	17.303	16.549	-18.178	1.00	66.52
ATOM 4999 OG SER C 165	16.391	52.837	-17.475	1.00	43.62	ATOM 11299 C SER F 71	16.917	15.841	-16.883	1.00	61.49
ATOM 5000 H SER C 165	17.803	49.378	-18.488	1.00	41.79	ATOM 11300 O SER F 71	16.835	14.613	-16.840	1.00	59.94
ATOM 5001 HA SER C 165	17.048	50.625	-16.214	1.00	38.64	ATOM 11301 CB SER F 71	18.795	16.361	-18.457	1.00	70.57
ATOM 5002 HB2 SER C 165	18.126	51.976	-17.769	1.00	45.81	ATOM 11302 OG SER F 71	19.580	17.021	-17.479	1.00	74.17
ATOM 5003 HB3 SER C 165	17.032	51.611	-18.863	1.00	45.81	ATOM 11303 H SER F 71	17.665	18.476	-18.016	1.00	73.84
ATOM 5004 HG SER C 165	16.586	53.533	-17.903	1.00	52.34	ATOM 11304 HA SER F 71	16.805	16.144	-18.905	1.00	79.82
ATOM 5005 N TRP C 166	14.579	50.679	-16.340	1.00	31.94	ATOM 11305 HB2 SER F 71	19.002	15.414	-18.441	1.00	84.68
ATOM 5006 CA TRP C 166	13.119	50.583	-16.387	1.00	23.07	ATOM 11306 HB3 SER F 71	19.002	16.731	-19.330	1.00	84.68
ATOM 5007 C TRP C 166	12.515	51.944	-16.699	1.00	27.85	ATOM 11307 HG SER F 71	20.396	16.911	-17.642	1.00	89.01
ATOM 5008 O TRP C 166	12.805	52.927	-16.018	1.00	29.97	ATOM 11308 N THR F 72	16.682	16.626	-15.833	1.00	62.01
ATOM 5009 CB TRP C 166	12.561	50.059	-15.063	1.00	22.45	ATOM 11309 CA THR F 72	16.339	16.091	-14.517	1.00	54.74
ATOM 5010 CG TRP C 166	12.817	48.608	-14.846	1.00	20.87	ATOM 11310 C THR F 72	15.134	15.150	-14.598	1.00	49.84
ATOM 5011 CD1 TRP C 166	13.887	48.054	-14.214	1.00	28.32	ATOM 11311 O THR F 72	14.027	15.588	-14.906	1.00	53.35
ATOM 5012 CD2 TRP C 166	11.989	47.519	-15.267	1.00	20.19	ATOM 11312 CB THR F 72	16.026	17.225	-13.522	1.00	57.21
ATOM 5013 NE1 TRP C 166	13.779	46.685	-14.212	1.00	29.81	ATOM 11313 OG1 THR F 72	17.057	18.220	-13.583	1.00	59.71
ATOM 5014 CE2 TRP C 166	12.622	46.331	-14.853	1.00	21.03	ATOM 11314 CG2 THR F 72	15.929	16.683	-12.103	1.00	49.20
ATOM 5015 CE3 TRP C 166	10.773	47.434	-15.951	1.00	18.26	ATOM 11315 H THR F 72	16.715	17.485	-15.859	1.00	74.41
ATOM 5016 CZ2 TRP C 166	12.082	45.074	-15.100	1.00	20.42	ATOM 11316 HA THR F 72	17.093	15.587	-14.173	1.00	65.69
ATOM 5017 CZ3 TRP C 166	10.238	46.186	-16.198	1.00	19.14	ATOM 11317 HB THR F 72	15.176	17.629	-13.753	1.00	68.66
ATOM 5018 CH2 TRP C 166	10.890	45.020	-15.772	1.00	22.75	ATOM 11318 HG1 THR F 72	16.890	18.840	-13.042	1.00	71.65
ATOM 5019 H TRP C 166	14.873	51.093	-15.646	1.00	38.33	ATOM 11319 HG21 THR F 72	15.732	17.405	-11.485	1.00	59.04
ATOM 5020 HA TRP C 166	12.861	49.968	-17.091	1.00	27.68	ATOM 11320 HG22 THR F 72	15.223	16.021	-12.049	1.00	59.04
ATOM 5021 HB2 TRP C 166	12.974	50.547	-14.334	1.00	26.94	ATOM 11321 HG23 THR F 72	16.769	16.270	-11.848	1.00	59.04
ATOM 5022 HB3 TRP C 166	11.601	50.197	-15.051	1.00	26.94	ATOM 11322 N PRO F 73	15.345	13.851	-14.327	1.00	47.67
ATOM 5023 HD1 TRP C 166	14.591	48.532	-13.838	1.00	33.98	ATOM 11323 CA PRO F 73	14.252	12.884	-14.470	1.00	42.23
ATOM 5024 HE1 TRP C 166	14.345	46.139	-13.865	1.00	35.77	ATOM 11324 C PRO F 73	13.246	12.910	-13.323	1.00	44.81
ATOM 5025 HE3 TRP C 166	10.335	48.203	-16.237	1.00	21.91	ATOM 11325 O PRO F 73	12.230	12.217	-13.393	1.00	43.07
ATOM 5026 HZ2 TRP C 166	12.513	44.299	-14.818	1.00	24.50	ATOM 11326 CB PRO F 73	14.984	11.543	-14.503	1.00	43.10
ATOM 5027 HZ3 TRP C 166	9.429	46.117	-16.653	1.00	22.96	ATOM 11327 CG PRO F 73	16.189	11.769	-13.668	1.00	42.60
ATOM 5028 HH2 TRP C 166	10.506	44.192	-15.952	1.00	27.30	ATOM 11328 CD PRO F 73	16.597	13.199	-13.901	1.00	44.19
ATOM 5029 N GLN C 167	11.676	52.003	-17.727	1.00	22.33	ATOM 11329 HA PRO F 73	13.788	13.019	-15.311	1.00	50.67
ATOM 5030 CA GLN C 167	11.066	53.265	-18.126	1.00	24.92	ATOM 11330 HB2 PRO F 73	14.422	10.851	-14.121	1.00	51.72
ATOM 5031 C GLN C 167	9.614	53.084	-18.554	1.00	20.54	ATOM 11331 HB3 PRO F 73	15.231	11.325	-15.416	1.00	51.72
ATOM 5032 O GLN C 167	9.185	51.964	-18.912	1.00	18.82	ATOM 11332 HG2 PRO F 73	15.967	11.627	-12.734	1.00	51.12
ATOM 5033 CB GLN C 167	11.872	53.904	-19.257	1.00	26.21	ATOM 11333 HG3 PRO F 73	16.894	11.164	-13.946	1.00	51.12
ATOM 5034 CG GLN C 167	11.910	53.089	-20.540	1.00	31.52	ATOM 11334 HD2 PRO F 73	16.923	13.596	-13.078	1.00	53.02
ATOM 5035 CD GLN C 167	12.781	53.730	-21.610	1.00	33.46	ATOM 11335 HD3 PRO F 73	17.261	13.249	-14.607	1.00	53.02
ATOM 5036 OE1 GLN C 167	13.768	54.399	-21.306	1.00	35.78	ATOM 11336 N TYR F 74	13.524	13.683	-12.280	1.00	43.68
ATOM 5037 NE2 GLN C 167	12.412	53.532	-22.870	1.00	34.85	ATOM 11337 CA TYR F 74	12.612	13.764	-11.146	1.00	36.00
ATOM 5038 H GLN C 167	11.444	51.330	-18.209	1.00	26.80	ATOM 11338 C TYR F 74	12.852	15.007	-10.302	1.00	34.98
ATOM 5039 HA GLN C 167	11.080	53.873	-17.370	1.00	29.90	ATOM 11339 O TYR F 74	13.985	15.312	-9.931	1.00	37.75
ATOM 5040 HB2 GLN C 167	11.482	54.767	-19.467	1.00	31.45	ATOM 11340 CB TYR F 74	12.740	12.518	-10.271	1.00	34.00
ATOM 5041 HB3 GLN C 167	12.787	54.024	-18.958	1.00	31.45	ATOM 11341 CG TYR F 74	11.779	12.501	-9.107	1.00	33.28
ATOM 5042 HG2 GLN C 167	12.289	52.209	-20.347	1.00	37.82	ATOM 11342 CD1 TYR F 74	10.522	11.926	-9.231	1.00	37.86
ATOM 5043 HG3 GLN C 167	11.009	53.011	-20.892	1.00	37.82	ATOM 11343 CD2 TYR F 74	12.124	13.064	-7.884	1.00	31.82

P
 ATOM 5044 HE21 GLN C 167 12.872 53.873 -23.511 1.00 41.82
 H
 ATOM 5045 HE22 GLN C 167 11.713 53.062 -23.044 1.00 41.82
 H
 ATOM 5046 N TRP C 168 8.865 54.180 -18.504 1.00 19.48
 N
 ATOM 5047 CA TRP C 168 7.471 54.186 -18.926 1.00 24.91
 C
 ATOM 5048 C TRP C 168 7.401 54.322 -20.439 1.00 28.19
 C
 ATOM 5049 O TRP C 168 8.390 54.684 -21.077 1.00 29.68
 O
 ATOM 5050 CB TRP C 168 6.715 55.320 -18.236 1.00 22.90
 C
 ATOM 5051 CG TRP C 168 6.806 55.241 -16.746 1.00 18.59
 C
 ATOM 5052 CD1 TRP C 168 7.589 56.003 -15.932 1.00 20.28
 C
 ATOM 5053 CD2 TRP C 168 6.101 54.331 -15.890 1.00 18.57
 C
 ATOM 5054 NE1 TRP C 168 7.410 55.631 -14.620 1.00 19.79
 N
 ATOM 5055 CE2 TRP C 168 6.501 54.607 -14.568 1.00 18.17
 C
 ATOM 5056 CE3 TRP C 168 5.168 53.313 -16.114 1.00 19.34
 C
 ATOM 5057 CZ2 TRP C 168 6.000 53.903 -13.474 1.00 19.51
 C
 ATOM 5058 CZ3 TRP C 168 4.672 52.614 -15.028 1.00 18.19
 C
 ATOM 5059 CH2 TRP C 168 5.090 52.912 -13.724 1.00 17.53
 C
 ATOM 5060 H TRP C 168 9.146 54.943 -18.225 1.00 23.37
 H
 ATOM 5061 HA TRP C 168 7.056 53.346 -18.676 1.00 29.89
 H
 ATOM 5062 HB2 TRP C 168 7.091 56.169 -18.516 1.00 27.48
 H
 ATOM 5063 HB3 TRP C 168 5.778 55.272 -18.483 1.00 27.40
 H
 ATOM 5064 HD1 TRP C 168 8.158 56.679 -16.222 1.00 24.34
 H
 ATOM 5065 HE1 TRP C 168 7.804 55.985 -13.942 1.00 23.74
 H
 ATOM 5066 HE3 TRP C 168 4.886 53.110 -16.977 1.00 23.20
 H
 ATOM 5067 HZ2 TRP C 168 6.276 54.098 -12.607 1.00 23.42
 H
 ATOM 5068 HZ3 TRP C 168 4.051 51.936 -15.166 1.00 21.83
 H
 ATOM 5069 HH2 TRP C 168 4.739 52.427 -13.013 1.00 21.04
 H
 ATOM 5070 N GLU C 169 6.242 54.030 -21.020 1.00 30.70
 N

 ATOM 5071 CA GLU C 169 6.122 54.022 -22.474 1.00 35.60
 C
 ATOM 5072 C GLU C 169 6.155 55.434 -23.049 1.00 36.18
 C
 ATOM 5073 O GLU C 169 6.337 55.608 -24.254 1.00 37.85
 O
 ATOM 5074 CB GLU C 169 4.844 53.301 -22.910 1.00 39.61
 C
 ATOM 5075 CG GLU C 169 3.559 53.974 -22.490 1.00 33.74
 C
 ATOM 5076 CD GLU C 169 2.372 53.021 -22.532 1.00 38.01
 C
 ATOM 5077 OE1 GLU C 169 2.228 52.285 -23.532 1.00 37.73
 O
 ATOM 5078 OE2 GLU C 169 1.587 53.002 -21.562 1.00 35.40
 O1-
 ATOM 5079 H GLU C 169 5.517 53.835 -20.600 1.00 36.84
 H
 ATOM 5080 HA GLU C 169 6.876 53.536 -22.844 1.00 42.72
 H
 ATOM 5081 HB2 GLU C 169 4.840 53.240 -23.878 1.00 47.53
 H
 ATOM 5082 HB3 GLU C 169 4.847 52.410 -22.528 1.00 47.53
 H
 ATOM 5083 HG2 GLU C 169 3.653 54.299 -21.581 1.00 40.49
 H
 ATOM 5084 HG3 GLU C 169 3.375 54.712 -23.092 1.00 40.49
 H
 ATOM 5085 N ASP C 170 5.994 56.440 -22.192 1.00 34.47
 N
 ATOM 5086 CA ASP C 170 6.132 57.827 -22.629 1.00 33.57
 C
 ATOM 5087 C ASP C 170 7.609 58.221 -22.703 1.00 33.88
 C
 ATOM 5088 O ASP C 170 7.943 59.327 -23.127 1.00 37.21
 O
 ATOM 5089 CB ASP C 170 5.363 58.777 -21.699 1.00 36.54
 C
 ATOM 5090 CG ASP C 170 6.038 58.968 -20.348 1.00 37.03
 C
 ATOM 5091 OD1 ASP C 170 6.943 58.181 -19.995 1.00 34.20
 O
 ATOM 5092 OD2 ASP C 170 5.647 59.913 -19.628 1.00 37.14
 O1-
 ATOM 5093 H ASP C 170 5.805 56.348 -21.358 1.00 41.35
 H

C
 ATOM 11344 CE1 TYR F 74 9.637 11.908 -8.173 1.00 40.32
 C
 ATOM 11345 CE2 TYR F 74 11.245 13.051 -6.819 1.00 28.53
 C
 ATOM 11346 CZ TYR F 74 10.003 12.472 -6.969 1.00 35.36
 C
 ATOM 11347 OH TYR F 74 9.120 12.456 -5.915 1.00 37.99
 O
 ATOM 11348 H TYR F 74 14.230 14.169 -12.204 1.00 52.42
 H
 ATOM 11349 HA TYR F 74 11.702 13.801 -11.479 1.00 43.20
 H
 ATOM 11350 HB2 TYR F 74 12.565 11.734 -10.814 1.00 40.80
 H
 ATOM 11351 HB3 TYR F 74 13.641 12.477 -9.913 1.00 40.80
 H
 ATOM 11352 HD1 TYR F 74 10.273 11.545 -10.042 1.00 45.43
 H
 ATOM 11353 HD2 TYR F 74 12.961 13.455 -7.781 1.00 38.18
 H
 ATOM 11354 HE1 TYR F 74 8.799 11.519 -8.272 1.00 48.39
 H
 ATOM 11355 HE2 TYR F 74 11.489 13.431 -6.006 1.00 34.24
 H

 ATOM 11356 HH TYR F 74 9.464 12.829 -5.246 1.00 45.59
 H
 ATOM 11357 N GLU F 75 11.767 15.712 -9.998 1.00 32.78
 N
 ATOM 11358 CA GLU F 75 11.816 16.888 -9.141 1.00 25.81
 C

 ATOM 11359 C GLU F 75 10.590 16.935 -8.235 1.00 29.12
 C
 ATOM 11360 O GLU F 75 9.484 16.581 -8.649 1.00 30.51
 O
 ATOM 11361 CB GLU F 75 11.892 18.167 -9.974 1.00 35.92
 C
 ATOM 11362 CG GLU F 75 13.193 18.358 -10.729 1.00 38.70
 C
 ATOM 11363 CD GLU F 75 13.265 19.711 -11.411 1.00 41.84
 C
 ATOM 11364 OE1 GLU F 75 12.460 19.955 -12.333 1.00 39.49
 O
 ATOM 11365 OE2 GLU F 75 14.120 20.535 -11.018 1.00 43.44
 O1-
 ATOM 11366 H GLU F 75 10.977 15.524 -10.282 1.00 39.33
 H
 ATOM 11367 HA GLU F 75 12.607 16.643 -8.581 1.00 30.97
 H
 ATOM 11368 HB2 GLU F 75 11.174 18.154 -10.626 1.00 43.10
 H
 ATOM 11369 HB3 GLU F 75 11.781 18.928 -9.383 1.00 43.10
 H
 ATOM 11370 HG2 GLU F 75 13.934 18.294 -10.107 1.00 46.44
 H

 ATOM 11371 HG3 GLU F 75 13.269 17.672 -11.411 1.00 46.44
 H
 ATOM 11372 N ASP F 76 10.798 17.370 -6.998 1.00 27.11
 N
 ATOM 11373 CA ASP F 76 9.716 17.527 -6.037 1.00 25.30
 C
 ATOM 11374 C ASP F 76 9.802 18.922 -5.426 1.00 18.73
 C
 ATOM 11375 O ASP F 76 10.778 19.253 -4.754 1.00 19.05
 O
 ATOM 11376 CB ASP F 76 9.793 16.447 -4.956 1.00 25.98
 C
 ATOM 11377 CG ASP F 76 8.511 16.323 -4.158 1.00 33.41
 C
 ATOM 11378 OD1 ASP F 76 7.419 16.365 -4.766 1.00 28.50
 O
 ATOM 11379 OD2 ASP F 76 8.596 16.176 -2.919 1.00 44.45
 O1-

 ATOM 11380 H ASP F 76 11.571 17.585 -6.687 1.00 32.53
 H
 ATOM 11381 HA ASP F 76 8.864 17.444 -6.493 1.00 30.36
 H
 ATOM 11382 HB2 ASP F 76 9.969 15.591 -5.377 1.00 31.18
 H
 ATOM 11383 HB3 ASP F 76 10.509 16.667 -4.340 1.00 31.18
 H

 ATOM 11384 N LEU F 77 8.786 19.738 -5.689 1.00 15.80
 N
 ATOM 11385 CA LEU F 77 8.767 21.135 -5.256 1.00 15.34
 C
 ATOM 11386 C LEU F 77 7.693 21.357 -4.206 1.00 19.57
 C
 ATOM 11387 O LEU F 77 6.536 20.990 -4.414 1.00 16.25
 O
 ATOM 11388 CB LEU F 77 8.520 22.055 -6.447 1.00 13.25
 C
 ATOM 11389 CG LEU F 77 9.510 21.914 -7.604 1.00 18.29
 C
 ATOM 11390 CD1 LEU F 77 8.906 22.436 -8.889 1.00 24.51
 C
 ATOM 11391 CD2 LEU F 77 10.790 22.653 -7.281 1.00 21.55
 C

 ATOM 11392 H LEU F 77 8.083 19.504 -6.125 1.00 18.96
 H
 ATOM 11393 HA LEU F 77 9.626 21.362 -4.868 1.00 18.41
 H

ATOM 5143 HA LEU C 174 9.967 55.593 -13.366 1.00 28.33
 H
 ATOM 5144 HB2 LEU C 174 10.575 53.402 -13.548 1.00 25.65
 H
 ATOM 5145 HB3 LEU C 174 12.027 53.708 -12.998 1.00 25.65
 H
 ATOM 5146 HG LEU C 174 11.061 54.109 -10.865 1.00 21.92
 H
 ATOM 5147 HD11 LEU C 174 8.875 53.398 -10.470 1.00 23.64
 H
 ATOM 5148 HD12 LEU C 174 8.886 54.590 -11.521 1.00 23.64
 H
 ATOM 5149 HD13 LEU C 174 8.697 53.093 -12.019 1.00 23.64
 H
 ATOM 5150 HD21 LEU C 174 10.794 51.860 -10.320 1.00 25.97
 H
 ATOM 5151 HD22 LEU C 174 10.687 51.501 -11.864 1.00 25.97
 H
 ATOM 5152 HD23 LEU C 174 12.053 52.054 -11.269 1.00 25.97
 H
 ATOM 5153 N SER C 175 10.689 57.209 -11.661 1.00 26.24
 N
 ATOM 5154 CA SER C 175 11.166 58.084 -10.595 1.00 23.83
 C
 ATOM 5155 C SER C 175 11.378 57.288 -9.308 1.00 25.15
 C
 ATOM 5156 O SER C 175 10.734 56.258 -9.099 1.00 21.90
 O
 ATOM 5157 CB SER C 175 10.187 59.234 -10.365 1.00 27.90
 C
 ATOM 5158 OG SER C 175 10.203 60.135 -11.461 1.00 34.12
 O
 ATOM 5159 H SER C 175 9.875 57.348 -11.901 1.00 31.49
 H
 ATOM 5160 HA SER C 175 12.019 58.464 -10.856 1.00 28.60
 H
 ATOM 5161 HB2 SER C 175 9.293 58.873 -10.266 1.00 33.49
 H
 ATOM 5162 HB3 SER C 175 10.444 59.711 -9.560 1.00 33.49
 H
 ATOM 5163 HG SER C 175 9.662 60.763 -11.324 1.00 40.94
 H
 ATOM 5164 N PRO C 176 12.209 57.760 -8.440 1.00 23.75
 N
 ATOM 5165 CA PRO C 176 12.646 57.005 -7.232 1.00 23.82
 C
 ATOM 5166 C PRO C 176 11.560 57.003 -6.157 1.00 26.93
 C
 ATOM 5167 O PRO C 176 10.702 57.885 -6.138 1.00 25.00
 O
 ATOM 5168 CB PRO C 176 13.901 57.729 -6.726 1.00 30.63
 C
 ATOM 5169 CG PRO C 176 13.790 59.110 -7.259 1.00 34.23
 C
 ATOM 5170 CD PRO C 176 13.094 58.987 -8.584 1.00 32.51
 C
 ATOM 5171 HA PRO C 176 12.873 56.091 -7.461 1.00 28.59
 H
 ATOM 5172 HB2 PRO C 176 13.907 57.735 -5.756 1.00 36.75
 H
 ATOM 5173 HB3 PRO C 176 14.694 57.290 -7.073 1.00 36.75
 H
 ATOM 5174 HG2 PRO C 176 13.266 59.652 -6.648 1.00 41.08
 H
 ATOM 5175 HG3 PRO C 176 14.676 59.488 -7.374 1.00 41.08
 H

 ATOM 5176 HD2 PRO C 176 12.518 59.753 -8.734 1.00 39.01
 H
 ATOM 5177 HD3 PRO C 176 13.742 58.884 -9.298 1.00 39.01
 H
 ATOM 5178 N ASN C 177 11.611 56.003 -5.280 1.00 20.91
 N
 ATOM 5179 CA ASN C 177 10.723 55.914 -4.124 1.00 26.58
 C
 ATOM 5180 C ASN C 177 9.249 55.841 -4.507 1.00 27.22
 C
 ATOM 5181 O ASN C 177 8.392 56.360 -3.795 1.00 27.05
 O
 ATOM 5182 CB ASN C 177 10.957 57.102 -3.188 1.00 28.67
 C
 ATOM 5183 CG ASN C 177 12.372 57.143 -2.644 1.00 32.73
 C
 ATOM 5184 OD1 ASN C 177 12.886 56.139 -2.152 1.00 39.20
 O
 ATOM 5185 ND2 ASN C 177 13.013 58.302 -2.739 1.00 33.01
 N
 ATOM 5186 H ASN C 177 12.166 55.348 -5.335 1.00 25.10
 H
 ATOM 5187 HA ASN C 177 10.937 55.106 -3.632 1.00 31.90
 H
 ATOM 5188 HB2 ASN C 177 10.799 57.926 -3.676 1.00 34.41
 H
 ATOM 5189 HB3 ASN C 177 10.348 57.039 -2.436 1.00 34.41
 H
 ATOM 5190 HD21 ASN C 177 13.818 58.374 -2.444 1.00 39.62
 H
 ATOM 5191 HD22 ASN C 177 12.623 58.981 -3.095 1.00 39.62
 H
 ATOM 5192 N LEU C 178 8.961 55.193 -5.631 1.00 22.55
 N

ATOM 11443 CG PHE F 80 4.626 25.256 5.097 1.00 22.06
 C
 ATOM 11444 CD1 PHE F 80 3.607 24.372 5.411 1.00 22.52
 C
 ATOM 11445 CD2 PHE F 80 -5.030 26.173 6.052 1.00 19.44
 C
 ATOM 11446 CE1 PHE F 80 -3.000 24.406 6.653 1.00 24.51
 C
 ATOM 11447 CE2 PHE F 80 4.426 26.211 7.295 1.00 20.54
 C

 ATOM 11448 CZ PHE F 80 3.412 25.328 7.596 1.00 20.28
 C
 ATOM 11449 H PHE F 80 6.075 26.269 1.522 1.00 17.96
 H
 ATOM 11450 HA PHE F 80 3.671 25.487 2.516 1.00 19.00
 H
 ATOM 11451 HB2 PHE F 80 5.381 24.282 3.500 1.00 25.17
 H
 ATOM 11452 HB3 PHE F 80 6.163 25.619 3.842 1.00 25.17
 H
 ATOM 11453 HD1 PHE F 80 3.327 23.749 4.780 1.00 27.02
 H
 ATOM 11454 HD2 PHE F 80 5.714 26.771 5.855 1.00 23.33
 H
 ATOM 11455 HE1 PHE F 80 2.316 23.809 6.854 1.00 29.42
 H
 ATOM 11456 HE2 PHE F 80 4.704 26.833 7.929 1.00 24.65
 H

 ATOM 11457 HZ PHE F 80 3.005 25.353 8.432 1.00 24.33
 H
 ATOM 11458 N TYR F 81 2.952 27.686 3.295 1.00 13.47
 N
 ATOM 11459 CA TYR F 81 2.553 29.014 3.746 1.00 15.11
 C
 ATOM 11460 C TYR F 81 1.595 28.918 4.926 1.00 17.28
 C
 ATOM 11461 O TYR F 81 0.586 28.208 4.869 1.00 14.65
 O
 ATOM 11462 CB TYR F 81 1.905 29.803 2.614 1.00 12.73
 C
 ATOM 11463 CG TYR F 81 1.506 31.189 3.044 1.00 17.49
 C
 ATOM 11464 CD1 TYR F 81 2.430 32.225 3.046 1.00 16.62
 C
 ATOM 11465 CD2 TYR F 81 0.213 31.459 3.469 1.00 14.65
 C
 ATOM 11466 CE1 TYR F 81 2.073 33.496 3.451 1.00 19.10
 C
 ATOM 11467 CE2 TYR F 81 -0.152 32.725 3.879 1.00 18.37
 C

 ATOM 11468 CZ TYR F 81 0.781 33.739 3.866 1.00 19.41
 C
 ATOM 11469 OH TYR F 81 0.420 35.004 4.267 1.00 20.36
 O
 ATOM 11470 H TYR F 81 2.295 27.140 3.193 1.00 16.17
 H
 ATOM 11471 HA TYR F 81 3.341 29.499 4.038 1.00 18.13
 H
 ATOM 11472 HB2 TYR F 81 2.535 29.884 1.861 1.00 15.28
 H
 ATOM 11473 HB3 TYR F 81 1.107 29.337 2.318 1.00 15.28
 H
 ATOM 11474 HD1 TYR F 81 3.302 32.061 2.768 1.00 19.95
 H
 ATOM 11475 HD2 TYR F 81 -0.418 30.776 3.480 1.00 17.58
 H

 ATOM 11476 HE1 TYR F 81 2.700 34.182 3.444 1.00 22.92
 H
 ATOM 11477 HE2 TYR F 81 -1.023 32.894 4.157 1.00 22.05
 H
 ATOM 11478 HH TYR F 81 -0.389 35.014 4.493 1.00 24.43
 H
 ATOM 11479 N GLU F 82 1.910 29.648 5.991 1.00 15.52
 N
 ATOM 11480 CA GLU F 82 1.145 29.563 7.224 1.00 15.50
 C
 ATOM 11481 C GLU F 82 0.925 30.935 7.832 1.00 19.21
 C
 ATOM 11482 O GLU F 82 1.858 31.731 7.929 1.00 16.31
 O
 ATOM 11483 CB GLU F 82 1.865 28.661 8.228 1.00 18.78
 C
 ATOM 11484 CG GLU F 82 1.115 28.456 9.537 1.00 21.18
 C
 ATOM 11485 CD GLU F 82 1.954 27.739 10.577 1.00 28.40
 C
 ATOM 11486 OE1 GLU F 82 2.678 28.425 11.330 1.00 28.83
 O
 ATOM 11487 OE2 GLU F 82 1.893 26.492 10.637 1.00 29.39
 O1-

 ATOM 11488 H GLU F 82 2.567 30.202 6.022 1.00 18.63
 H
 ATOM 11489 HA GLU F 82 0.278 29.173 7.034 1.00 18.59
 H
 ATOM 11490 HB2 GLU F 82 1.996 27.789 7.824 1.00 22.54
 H
 ATOM 11491 HB3 GLU F 82 2.725 29.056 8.440 1.00 22.54
 H
 ATOM 11492 HG2 GLU F 82 0.864 29.321 9.897 1.00 25.42
 H

ATOM 5193 CA LEU C 178 7.586 55.018 -6.087 1.00 22.76
 C
 ATOM 5194 C LEU C 178 7.205 53.547 -6.144 1.00 24.97
 C
 ATOM 5195 O LEU C 178 6.143 53.162 -5.657 1.00 27.82
 O
 ATOM 5196 CB LEU C 178 7.390 55.657 -7.461 1.00 21.51
 C
 ATOM 5197 CG LEU C 178 7.366 57.186 -7.511 1.00 24.49
 C
 ATOM 5198 CD1 LEU C 178 7.248 57.640 -8.953 1.00 24.38
 C
 ATOM 5199 CD2 LEU C 178 6.224 57.756 -6.679 1.00 22.93
 C
 ATOM 5200 H LEU C 178 9.549 54.842 -6.152 1.00 27.06
 H
 ATOM 5201 HA LEU C 178 6.989 55.459 -5.463 1.00 27.31
 H
 ATOM 5202 HB2 LEU C 178 8.113 55.363 -8.037 1.00 25.81
 H
 ATOM 5203 HB3 LEU C 178 6.546 55.345 -7.822 1.00 25.81
 H
 ATOM 5204 HG LEU C 178 8.200 57.528 -7.154 1.00 29.39
 H
 ATOM 5205 HD11 LEU C 178 7.233 58.609 -8.978 1.00 29.25
 H
 ATOM 5206 HD12 LEU C 178 8.011 57.307 -9.451 1.00 29.25
 H
 ATOM 5207 HD13 LEU C 178 6.427 57.286 -9.329 1.00 29.25
 H
 ATOM 5208 HD21 LEU C 178 6.245 58.724 -6.738 1.00 27.52
 H
 ATOM 5209 HD22 LEU C 178 5.383 57.421 -7.027 1.00 27.52
 H
 ATOM 5210 HD23 LEU C 178 6.336 57.478 -5.757 1.00 27.52
 H

ATOM 5211 N LEU C 179 8.075 52.732 -6.735 1.00 19.58
 N
 ATOM 5212 CA LEU C 179 7.821 51.303 -6.896 1.00 17.86
 C
 ATOM 5213 C LEU C 179 8.977 50.444 -6.402 1.00 21.63
 C
 ATOM 5214 O LEU C 179 10.147 50.751 -6.648 1.00 22.35
 O
 ATOM 5215 CB LEU C 179 7.558 50.971 -8.367 1.00 21.35
 C
 ATOM 5216 CG LEU C 179 6.290 51.513 -9.021 1.00 19.98
 C
 ATOM 5217 CD1 LEU C 179 6.291 51.174 -10.502 1.00 19.74
 C
 ATOM 5218 CD2 LEU C 179 5.044 50.954 -8.349 1.00 21.35
 C
 ATOM 5219 H LEU C 179 8.831 52.987 -7.057 1.00 23.50
 H
 ATOM 5220 HA LEU C 179 7.030 51.064 -6.388 1.00 21.44
 H
 ATOM 5221 HB2 LEU C 179 8.306 51.307 -8.885 1.00 25.62
 H
 ATOM 5222 HB3 LEU C 179 7.526 50.005 -8.451 1.00 25.62
 H
 ATOM 5223 HG LEU C 179 6.274 52.479 -8.932 1.00 23.97
 H
 ATOM 5224 HD11 LEU C 179 5.482 51.524 -10.906 1.00 23.68
 H
 ATOM 5225 HD12 LEU C 179 7.070 51.578 -10.917 1.00 23.68
 H
 ATOM 5226 HD13 LEU C 179 6.324 50.210 -10.605 1.00 23.68
 H
 ATOM 5227 HD21 LEU C 179 4.259 51.318 -8.788 1.00 25.62
 H
 ATOM 5228 HD22 LEU C 179 5.050 49.987 -8.429 1.00 25.62
 H
 ATOM 5229 HD23 LEU C 179 5.049 51.209 -7.414 1.00 25.62
 H
 ATOM 5230 N THR C 180 8.639 49.362 -5.708 1.00 18.15
 N
 ATOM 5231 CA THR C 180 9.600 48.313 -5.406 1.00 22.56
 C
 ATOM 5232 C THR C 180 9.556 47.299 -6.548 1.00 20.55
 C
 ATOM 5233 O THR C 180 8.552 46.807 -6.729 1.00 17.30
 O
 ATOM 5234 CB THR C 180 9.293 47.614 -4.066 1.00 21.01
 C
 ATOM 5235 OG1 THR C 180 9.224 48.585 -3.015 1.00 25.27
 O
 ATOM 5236 CG2 THR C 180 10.368 46.594 -3.730 1.00 28.16
 C
 ATOM 5237 H THR C 180 7.851 49.213 -5.399 1.00 21.78
 H
 ATOM 5238 HA THR C 180 10.492 48.691 -5.362 1.00 27.08
 H
 ATOM 5239 HB THR C 180 8.443 47.151 -4.132 1.00 25.22
 H
 ATOM 5240 HG1 THR C 180 8.616 49.142 -3.178 1.00 30.32
 H
 ATOM 5241 HG21 THR C 180 10.163 45.163 -2.886 1.00 33.79
 H
 ATOM 5242 HG22 THR C 180 10.413 45.920 -4.426 1.00 33.79
 H
 ATOM 5243 HD23 THR C 180 11.220 47.022 2.650 1.00 22.70

ATOM 11493 HG3 GLU F 82 0.323 27.922 9.369 1.00 25.42
 H
 ATOM 11494 N CYS F 83 -0.314 31.205 8.236 1.00 16.05 N
 ATOM 11495 CA CYS F 83 -0.618 32.408 8.996 1.00 14.60 C
 ATOM 11496 C CYS F 83 -1.077 31.989 10.386 1.00 17.53 C
 ATOM 11497 O CYS F 83 -1.688 30.932 10.562 1.00 19.01 O
 ATOM 11498 CB CYS F 83 -1.672 33.270 8.287 1.00 21.05 C
 ATOM 11499 SG CYS F 83 -3.338 32.591 8.159 1.00 20.77 S
 ATOM 11500 H CYS F 83 -0.996 30.705 8.082 1.00 19.26 H
 ATOM 11501 HA CYS F 83 0.189 32.937 9.092 1.00 17.52 H
 ATOM 11502 HB2 CYS F 83 -1.742 34.112 8.763 1.00 25.26
 H
 ATOM 11503 HB3 CYS F 83 -1.363 33.440 7.383 1.00 25.26
 H
 ATOM 11504 N ASP F 84 -0.746 32.815 11.370 1.00 13.89 N
 ATOM 11505 CA ASP F 84 -1.007 32.510 12.768 1.00 17.39
 C
 ATOM 11506 C ASP F 84 -1.702 33.696 13.425 1.00 21.87 C
 ATOM 11507 O ASP F 84 -1.286 34.844 13.257 1.00 19.44 O
 ATOM 11508 CB ASP F 84 0.302 32.175 13.492 1.00 19.88
 C
 ATOM 11509 CG ASP F 84 0.095 31.813 14.952 1.00 29.70
 C
 ATOM 11510 OD1 ASP F 84 -0.328 32.693 15.737 1.00 23.11
 O
 ATOM 11511 OD2 ASP F 84 0.378 30.651 15.318 1.00 31.40
 O1-
 ATOM 11512 H ASP F 84 -0.361 33.574 11.250 1.00 16.67 H
 ATOM 11513 HA ASP F 84 -1.595 31.740 12.826 1.00 20.87
 H
 ATOM 11514 HB2 ASP F 84 0.721 31.418 13.053 1.00 23.86
 H
 ATOM 11515 HB3 ASP F 84 0.889 32.946 13.456 1.00 23.86
 H
 ATOM 11516 N TYR F 85 -2.766 33.406 14.165 1.00 17.83 N
 ATOM 11517 CA TYR F 85 -3.500 34.426 14.897 1.00 20.90
 C
 ATOM 11518 C TYR F 85 -3.523 34.050 15.370 1.00 21.48 C
 ATOM 11519 O TYR F 85 -4.217 33.118 16.776 1.00 22.77 O
 ATOM 11520 CB TYR F 85 -4.918 34.575 14.344 1.00 20.94
 C
 ATOM 11521 CG TYR F 85 -5.590 35.873 14.726 1.00 19.46
 C
 ATOM 11522 CD1 TYR F 85 -5.044 37.093 14.351 1.00 23.95
 C
 ATOM 11523 CD2 TYR F 85 -6.781 35.880 15.443 1.00 24.58
 C
 ATOM 11524 CE1 TYR F 85 -5.652 38.284 14.690 1.00 21.09
 C
 ATOM 11525 CE2 TYR F 85 -7.401 37.068 15.784 1.00 25.21
 C
 ATOM 11526 CZ TYR F 85 -6.831 38.266 15.402 1.00 24.37
 C
 ATOM 11527 OH TYR F 85 -7.436 39.454 15.734 1.00 24.90
 O
 ATOM 11528 H TYR F 85 -3.086 32.614 14.260 1.00 21.40 H
 ATOM 11529 HA TYR F 85 -3.045 35.278 14.806 1.00 25.08
 H
 ATOM 11530 HB2 TYR F 85 -4.881 34.535 13.375 1.00 25.13
 H
 ATOM 11531 HB3 TYR F 85 -5.463 33.848 14.683 1.00 25.13
 H
 ATOM 11532 HD1 TYR F 85 -4.248 37.108 13.870 1.00 28.73
 H
 ATOM 11533 HD2 TYR F 85 -7.165 35.073 15.699 1.00 29.50
 H
 ATOM 11534 HE1 TYR F 85 -5.272 39.093 14.434 1.00 25.31
 H
 ATOM 11535 HE2 TYR F 85 -8.196 37.059 16.266 1.00 30.25
 H
 ATOM 11536 HH TYR F 85 -8.142 39.306 16.164 1.00 29.88
 H
 ATOM 11537 N THR F 86 -2.739 34.777 17.158 1.00 20.16 N
 ATOM 11538 CA THR F 86 -2.580 34.497 18.577 1.00 23.51
 C
 ATOM 11539 C THR F 86 -2.558 35.808 19.355 1.00 22.77 C
 ATOM 11540 O THR F 86 -1.775 36.704 19.040 1.00 22.32 O
 ATOM 11541 CB THR F 86 -1.280 33.708 18.847 1.00 27.41
 C
 ATOM 11542 OG1 THR F 86 -1.277 32.503 18.069 1.00 22.82
 O
 ATOM 11543 CG2 THR F 86 1.152 32.252 20.220 1.00 24.65

DK/EP 3233192 T3

ATOM 5243 PG23 THR C 180 11.230 47.055 -5.855 1.00 33.78
 H
 ATOM 5244 N ILE C 181 10.633 47.229 -7.325 1.00 19.65
 N
 ATOM 5245 CA ILE C 181 10.726 46.266 -8.420 1.00 19.28
 C

 ATOM 5246 C ILE C 181 11.226 44.924 -7.902 1.00 16.96
 C
 ATOM 5247 O ILE C 181 12.275 44.842 -7.261 1.00 13.49
 O
 ATOM 5248 CB ILE C 181 11.659 46.760 -9.540 1.00 21.11
 C
 ATOM 5249 CG1 ILE C 181 11.236 48.150 -10.022 1.00 18.12
 C
 ATOM 5250 CG2 ILE C 181 11.664 45.776 -10.704 1.00 19.77
 C
 ATOM 5251 CD1 ILE C 181 9.805 48.234 -10.525 1.00 25.78
 C
 ATOM 5252 H ILE C 181 11.327 47.730 -7.240 1.00 23.58
 H
 ATOM 5253 HA ILE C 181 9.843 46.133 -8.800 1.00 23.13
 H
 ATOM 5254 HB ILE C 181 12.560 46.819 -9.185 1.00 25.33
 H
 ATOM 5255 HG12 ILE C 181 11.326 48.775 -9.295 1.00 21.74
 H
 ATOM 5256 HG13 ILE C 181 11.820 48.417 -10.749 1.00 21.74
 H
 ATOM 5257 HG21 ILE C 181 12.258 46.107 -11.395 1.00 23.73
 H
 ATOM 5258 HG22 ILE C 181 11.974 44.913 -10.386 1.00 23.73
 H
 ATOM 5259 HG23 ILE C 181 10.762 45.695 -11.053 1.00 23.73
 H
 ATOM 5260 HD11 ILE C 181 9.623 49.144 -10.808 1.00 30.93
 H
 ATOM 5261 HD12 ILE C 181 9.698 47.627 -11.274 1.00 30.93
 H
 ATOM 5262 HD13 ILE C 181 9.203 47.984 -9.807 1.00 30.93
 H
 ATOM 5263 N ILE C 182 10.471 43.873 -8.193 1.00 15.47
 N
 ATOM 5264 CA ILE C 182 10.754 42.552 -7.654 1.00 15.31
 C
 ATOM 5265 C ILE C 182 10.921 41.530 -8.770 1.00 20.29
 C
 ATOM 5266 O ILE C 182 10.081 41.426 -9.662 1.00 15.60
 O
 ATOM 5267 CB ILE C 182 9.631 42.095 -8.703 1.00 19.87
 C
 ATOM 5268 CG1 ILE C 182 9.419 43.135 -5.596 1.00 18.35
 C
 ATOM 5269 CG2 ILE C 182 9.959 40.735 -6.096 1.00 17.54
 C
 ATOM 5270 CD1 ILE C 182 8.174 42.899 -4.758 1.00 19.47
 C
 ATOM 5271 H ILE C 182 9.782 43.900 -8.707 1.00 18.56
 H
 ATOM 5272 HA ILE C 182 11.582 42.586 -7.149 1.00 18.37
 H
 ATOM 5273 HB ILE C 182 8.810 42.015 -7.212 1.00 23.85
 H
 ATOM 5274 HG12 ILE C 182 10.135 43.117 -5.001 1.00 22.02
 H
 ATOM 5275 HG13 ILE C 182 9.340 44.012 -6.003 1.00 22.02
 H
 ATOM 5276 HG21 ILE C 182 9.237 40.472 -5.504 1.00 21.04
 H
 ATOM 5277 HG22 ILE C 182 10.054 40.085 -6.811 1.00 21.04
 H
 ATOM 5278 HG23 ILE C 182 10.788 40.803 -5.598 1.00 21.04
 H
 ATOM 5279 HD11 ILE C 182 8.111 43.594 -4.084 1.00 23.36
 H
 ATOM 5280 HD12 ILE C 182 7.395 42.926 -5.335 1.00 23.36
 H

 ATOM 5281 HD13 ILE C 182 8.241 42.030 -4.331 1.00 23.36
 H
 ATOM 5282 N GLU C 183 12.013 40.776 -8.717 1.00 17.61
 N
 ATOM 5283 CA GLU C 183 12.211 39.676 -9.648 1.00 20.35
 C
 ATOM 5284 C GLU C 183 11.144 38.620 -9.401 1.00 20.70
 C
 ATOM 5285 O GLU C 183 10.829 38.289 -8.258 1.00 21.07
 O
 ATOM 5286 CB GLU C 183 13.610 39.075 -9.500 1.00 26.30
 C
 ATOM 5287 CG GLU C 183 14.730 40.031 -9.891 1.00 27.61
 C
 ATOM 5288 CD GLU C 183 16.108 39.407 -9.763 1.00 38.86
 C
 ATOM 5289 OE1 GLU C 183 16.214 38.165 -9.858 1.00 36.41
 O
 ATOM 5290 OE2 GLU C 183 17.086 40.160 -9.564 1.00 42.70
 O1-
 ATOM 5291 H GLU C 183 12.653 40.881 -8.152 1.00 21.14
 H
 ATOM 5292 HA GLU C 183 12.114 40.002 -10.556 1.00 24.42

ATOM 11543 CG2 THR F 86 -1.155 33.333 20.520 1.00 24.66
 C
 ATOM 11544 H THR F 86 -2.280 35.452 16.887 1.00 24.20
 H
 ATOM 11545 HA THR F 86 -3.331 33.967 18.889 1.00 28.22
 H

 ATOM 11546 HB THR F 86 -0.517 34.252 18.598 1.00 32.89
 H
 ATOM 11547 HG1 THR F 86 -1.322 32.690 17.251 1.00 27.36
 H
 ATOM 11548 HG21 THR F 86 -0.333 32.858 20.472 1.00 29.58
 H
 ATOM 11549 HG22 THR F 86 -1.138 34.161 20.856 1.00 29.58
 H
 ATOM 11550 HG23 THR F 86 -1.906 32.806 20.596 1.00 29.58
 H
 ATOM 11551 N ASP F 87 -3.415 35.920 20.367 1.00 21.80
 N
 ATOM 11552 CA ASP F 87 -3.493 37.140 21.166 1.00 21.76
 C
 ATOM 11553 C ASP F 87 -3.709 38.351 20.255 1.00 25.94
 C
 ATOM 11554 O ASP F 87 -3.058 39.382 20.404 1.00 24.45
 O
 ATOM 11555 CB ASP F 87 -2.221 37.313 22.002 1.00 24.06
 C
 ATOM 11556 CG ASP F 87 -2.336 38.433 23.021 1.00 25.87
 C
 ATOM 11557 OD1 ASP F 87 -3.451 38.663 23.533 1.00 26.46
 O
 ATOM 11558 OD2 ASP F 87 -1.309 39.082 23.305 1.00 27.96
 O1-
 ATOM 11559 H ASP F 87 -3.962 35.304 20.612 1.00 26.15
 H
 ATOM 11560 HA ASP F 87 -4.248 37.077 21.772 1.00 26.11
 H
 ATOM 11561 HB2 ASP F 87 -2.043 36.489 22.480 1.00 28.88
 H
 ATOM 11562 HB3 ASP F 87 -1.480 37.521 21.411 1.00 28.88
 H
 ATOM 11563 N ASN F 88 -4.611 38.192 19.291 1.00 22.91
 N
 ATOM 11564 CA ASN F 88 -4.971 39.255 18.351 1.00 24.97
 C
 ATOM 11565 C ASN F 88 -3.803 39.741 17.489 1.00 23.23
 C
 ATOM 11566 O ASN F 88 -3.880 40.805 16.877 1.00 24.47
 O
 ATOM 11567 CB ASN F 88 -5.580 40.433 19.112 1.00 25.84
 C
 ATOM 11568 CG ASN F 88 -6.788 40.027 19.930 1.00 36.58
 C
 ATOM 11569 OD1 ASN F 88 -6.720 39.928 21.155 1.00 44.27
 O
 ATOM 11570 ND2 ASN F 88 -7.905 39.783 19.253 1.00 40.67
 N
 ATOM 11571 H ASN F 88 -5.040 37.459 19.157 1.00 27.49
 H
 ATOM 11572 HA ASN F 88 -5.651 38.913 17.750 1.00 29.96
 H
 ATOM 11573 HB2 ASN F 88 -4.916 40.798 19.717 1.00 31.01
 H
 ATOM 11574 HB3 ASN F 88 -5.861 41.110 18.477 1.00 31.01
 H
 ATOM 11575 HD21 ASN F 88 -8.619 39.549 19.671 1.00 48.81
 H
 ATOM 11576 HD22 ASN F 88 -7.914 39.859 18.396 1.00 48.81
 H
 ATOM 11577 N LYS F 89 -2.736 38.952 17.429 1.00 19.11
 N
 ATOM 11578 CA LYS F 89 -1.563 39.305 16.639 1.00 23.78
 C
 ATOM 11579 C LYS F 89 -1.421 38.394 15.422 1.00 22.87
 C
 ATOM 11580 O LYS F 89 -1.475 37.167 15.537 1.00 22.29
 O

 ATOM 11581 CB LYS F 89 -0.303 39.240 17.503 1.00 26.55
 C
 ATOM 11582 CG LYS F 89 -0.226 40.350 18.549 1.00 32.53
 C
 ATOM 11583 CD LYS F 89 0.900 40.113 19.546 1.00 46.00
 C
 ATOM 11584 CE LYS F 89 1.075 41.298 20.484 1.00 56.99
 C
 ATOM 11585 NZ LYS F 89 -0.193 41.656 21.180 1.00 56.00
 N1+
 ATOM 11586 H LYS F 89 -2.667 38.200 17.840 1.00 22.93
 H
 ATOM 11587 HA LYS F 89 -1.661 40.216 16.321 1.00 28.53
 H
 ATOM 11588 HB2 LYS F 89 -0.286 38.390 17.970 1.00 31.86
 H
 ATOM 11589 HB3 LYS F 89 0.475 39.318 16.930 1.00 31.86
 H
 ATOM 11590 HG2 LYS F 89 -0.064 41.197 18.104 1.00 39.04
 H
 ATOM 11591 HG3 LYS F 89 -1.062 40.384 19.040 1.00 39.04
 H
 ATOM 11592 HD2 LYS F 89 0.695 39.320 20.080 1.00 55.20

DK/EP 3233192 T3

H
 ATOM 5343 HB3 LYS C 186 13.778 36.056 -18.044 1.00 53.27
 H
 ATOM 5344 HG2 LYS C 186 14.050 34.732 -15.564 1.00 74.83
 H
 ATOM 5345 HG3 LYS C 186 15.075 34.622 -16.771 1.00 74.83
 H
 ATOM 5346 HD2 LYS C 186 14.653 36.961 -15.237 1.00 84.87
 H
 ATOM 5347 HD3 LYS C 186 15.949 36.044 -15.154 1.00 84.87
 H
 ATOM 5348 HE2 LYS C 186 16.519 36.660 -17.334 1.00 102.60
 H
 ATOM 5349 HE3 LYS C 186 15.228 37.586 -17.407 1.00 102.60
 H
 ATOM 5350 HZ1 LYS C 186 17.069 38.826 -16.922 1.00 111.43
 H

ATOM 5351 HZ2 LYS C 186 16.161 38.893 -15.795 1.00 111.43
 H
 ATOM 5352 HZ3 LYS C 186 17.337 38.050 -15.729 1.00 111.43
 H
 ATOM 5353 N GLY C 187 11.707 38.550 -17.977 1.00 22.70
 N
 ATOM 5354 CA GLY C 187 10.938 39.312 -18.943 1.00 24.36
 C
 ATOM 5355 C GLY C 187 11.284 40.784 -18.913 1.00 21.56
 C
 ATOM 5356 O GLY C 187 12.096 41.226 -18.094 1.00 17.20
 O
 ATOM 5357 H GLY C 187 12.298 39.013 -17.555 1.00 27.25
 H
 ATOM 5358 HA2 GLY C 187 11.111 38.972 -19.835 1.00 29.23
 H
 ATOM 5359 HA3 GLY C 187 9.991 39.213 -18.754 1.00 29.23
 H
 ATOM 5360 N ASP C 188 10.659 41.544 -19.808 1.00 18.15
 N
 ATOM 5361 CA ASP C 188 10.960 42.961 -19.960 1.00 17.36
 C
 ATOM 5362 C ASP C 188 9.738 43.846 -19.697 1.00 19.08
 C
 ATOM 5363 O ASP C 188 9.709 45.001 -20.117 1.00 15.87
 O
 ATOM 5364 CB ASP C 188 11.509 43.226 -21.365 1.00 19.74
 C
 ATOM 5365 CG ASP C 188 12.824 42.513 -21.618 1.00 23.22
 C
 ATOM 5366 OD1 ASP C 188 13.720 42.596 -20.754 1.00 19.57
 O
 ATOM 5367 OD2 ASP C 188 12.958 41.864 -22.675 1.00 26.62
 O1-
 ATOM 5368 H ASP C 188 10.050 41.258 -20.344 1.00 21.78
 H
 ATOM 5369 HA ASP C 188 11.648 43.206 -19.321 1.00 20.83
 H
 ATOM 5370 HB2 ASP C 188 10.866 42.914 -22.020 1.00 23.69
 H
 ATOM 5371 HB3 ASP C 188 11.657 44.179 -21.472 1.00 23.69
 H
 ATOM 5372 N CYS C 189 8.739 43.299 -19.008 1.00 16.64
 N
 ATOM 5373 CA CYS C 189 7.539 44.052 -18.630 1.00 17.86
 C
 ATOM 5374 C CYS C 189 7.259 43.887 -17.138 1.00 16.95
 C
 ATOM 5375 O CYS C 189 7.791 42.980 -16.504 1.00 15.25
 O
 ATOM 5376 CB CYS C 189 6.326 43.596 -19.447 1.00 16.46
 C
 ATOM 5377 SG CYS C 189 6.412 43.997 -21.213 1.00 19.92
 S
 ATOM 5378 H CYS C 189 8.730 42.481 -18.739 1.00 19.97
 H
 ATOM 5379 HA CYS C 189 7.686 44.995 -18.808 1.00 21.43
 H
 ATOM 5380 HB2 CYS C 189 6.245 42.632 -19.368 1.00 19.75
 H
 ATOM 5381 HB3 CYS C 189 5.532 44.021 -19.088 1.00 19.75
 H
 ATOM 5382 N ALA C 190 6.424 44.763 -16.584 1.00 14.88
 N
 ATOM 5383 CA ALA C 190 6.146 44.757 -15.149 1.00 15.16
 C
 ATOM 5384 C ALA C 190 4.655 44.804 -14.854 1.00 12.33
 C
 ATOM 5385 O ALA C 190 3.901 45.546 -15.487 1.00 12.28
 O

ATOM 5386 CB ALA C 190 6.845 45.927 -14.478 1.00 18.64
 C
 ATOM 5387 H ALA C 190 6.003 45.373 -17.020 1.00 17.85
 H
 ATOM 5388 HA ALA C 190 6.500 43.940 -14.766 1.00 18.19
 H
 ATOM 5389 HB1 ALA C 190 6.651 45.907 -13.528 1.00 22.37
 H
 ATOM 5390 HB2 ALA C 190 7.801 45.847 -14.622 1.00 22.37
 H
 ATOM 5391 HB3 ALA C 190 6.520 46.754 -14.866 1.00 22.37

H
 ATOM 11643 HZ PHE F 92 -1.134 38.506 8.092 1.00 22.43 H
 ATOM 11644 N ASP F 98 4.528 32.693 8.151 1.00 18.85 N
 ATOM 11645 CA ASP F 93 5.714 31.893 7.904 1.00 19.59 C
 ATOM 11646 C ASP F 93 5.583 31.237 6.539 1.00 21.25 C
 ATOM 11647 O ASP F 93 4.484 30.852 6.130 1.00 15.85 O
 ATOM 11648 CB ASP F 93 5.887 30.841 9.000 1.00 23.31 C
 ATOM 11649 CG ASP F 93 7.131 29.997 8.810 1.00 31.07 C
 ATOM 11650 OD1 ASP F 93 8.143 30.533 8.309 1.00 32.52
 O1-
 ATOM 11651 OD2 ASP F 93 7.093 28.797 9.164 1.00 33.33
 O
 ATOM 11652 H ASP F 98 3.817 32.386 7.778 1.00 22.62 H
 ATOM 11653 HA ASP F 93 6.497 32.466 7.898 1.00 23.51 H
 ATOM 11654 HB2 ASP F 93 5.955 31.288 9.859 1.00 27.98
 H
 ATOM 11655 HB3 ASP F 93 5.119 30.249 8.994 1.00 27.98
 H
 ATOM 11656 N GLN F 94 6.695 31.128 5.825 1.00 16.48 N
 ATOM 11657 CA GLN F 94 6.698 30.390 4.575 1.00 21.95 C
 ATOM 11658 C GLN F 94 8.029 29.686 4.368 1.00 20.37 C
 ATOM 11659 O GLN F 94 9.078 30.195 4.754 1.00 17.80 O
 ATOM 11660 GB GLN F 94 6.378 31.314 3.394 1.00 16.26 C
 ATOM 11661 CG GLN F 94 7.372 32.427 3.149 1.00 21.74 C
 ATOM 11662 CD GLN F 94 7.010 33.272 1.933 1.00 28.61 C
 ATOM 11663 OE1 GLN F 94 5.878 33.231 1.442 1.00 23.71
 O
 ATOM 11664 NE2 GLN F 94 7.976 34.041 1.440 1.00 34.71
 N
 ATOM 11665 H GLN F 94 7.454 31.469 6.042 1.00 19.77 H
 ATOM 11666 HA GLN F 94 6.007 29.709 4.613 1.00 26.34 H
 ATOM 11667 HB2 GLN F 94 6.337 30.777 2.587 1.00 19.52
 H
 ATOM 11668 HB3 GLN F 94 5.513 31.725 3.553 1.00 19.52
 H
 ATOM 11669 HG2 GLN F 94 7.393 33.009 3.925 1.00 26.09
 H
 ATOM 11670 HG3 GLN F 94 8.249 32.042 2.998 1.00 26.09
 H
 ATOM 11671 HE21 GLN F 94 7.823 34.537 0.754 1.00 41.66
 H
 ATOM 11672 HE22 GLN F 94 8.754 34.042 1.806 1.00 41.66
 H
 ATOM 11673 N ASP F 95 7.961 28.494 3.780 1.00 19.52 N
 ATOM 11674 CA ASP F 95 9.139 27.680 3.502 1.00 19.57 C
 ATOM 11675 C ASP F 95 9.090 27.193 2.064 1.00 21.52 C
 ATOM 11676 O ASP F 95 8.010 27.017 1.496 1.00 17.71 O
 ATOM 11677 CB ASP F 95 9.219 26.471 4.443 1.00 24.75 C
 ATOM 11678 CG ASP F 95 9.408 28.861 5.898 1.00 36.23 C
 ATOM 11679 OD1 ASP F 95 10.173 27.809 6.181 1.00 35.86
 O
 ATOM 11680 OD2 ASP F 95 8.792 26.202 6.762 1.00 36.50
 O1-
 ATOM 11681 H ASP F 95 7.225 28.128 3.527 1.00 23.42 H
 ATOM 11682 HA ASP F 95 9.939 28.216 3.619 1.00 23.48 H
 ATOM 11683 HB2 ASP F 95 8.395 25.964 4.375 1.00 29.70
 H
 ATOM 11684 HB3 ASP F 95 9.971 25.918 4.182 1.00 29.70
 H
 ATOM 11685 N TYR F 96 10.266 26.978 1.488 1.00 17.67 N
 ATOM 11686 CA TYR F 96 10.397 26.363 0.173 1.00 17.08
 C
 ATOM 11687 C TYR F 96 11.265 25.123 0.294 1.00 20.00 C
 ATOM 11688 O TYR F 96 12.344 25.188 0.880 1.00 20.02 O
 ATOM 11689 CB TYR F 96 11.028 27.329 -0.828 1.00 18.79
 C
 ATOM 11690 CG TYR F 96 10.392 28.694 -0.885 1.00 16.85
 C
 ATOM 11691 CD1 TYR F 96 10.737 29.681 0.029 1.00 18.78

O
 ATOM 5771 CB THR C 215 -7.992 65.528 -16.697 1.00 37.58
 C
 ATOM 5772 OG1 THR C 215 -7.256 66.123 -15.621 1.00 31.78
 O
 ATOM 5773 CG2 THR C 215 -8.750 64.313 -16.184 1.00 39.25
 C
 ATOM 5774 H THR C 215 -5.945 64.125 -16.517 1.00 44.09
 H
 ATOM 5775 HA THR C 215 -7.551 64.721 -18.540 1.00 49.88
 H
 ATOM 5776 HB THR C 215 -8.637 66.169 -17.036 1.00 45.09
 H
 ATOM 5777 HG1 THR C 215 -6.693 65.577 -15.322 1.00 38.13
 H
 ATOM 5778 HG21 THR C 215 -9.354 64.576 -15.471 1.00 47.10
 H
 ATOM 5779 HG22 THR C 215 -9.266 63.916 -16.903 1.00 47.10
 H
 ATOM 5780 HG23 THR C 215 -8.126 63.654 -15.841 1.00 47.10
 H
 TER 5781 THR C 215
 ATOM 5782 N GLU D 93 -18.518 60.935 -24.144 1.00 50.72
 N
 ATOM 5783 CA GLU D 93 -15.948 61.865 -23.176 1.00 55.05
 C
 ATOM 5784 C GLU D 93 -17.021 62.338 -22.200 1.00 56.26
 C
 ATOM 5785 O GLU D 93 -18.143 62.642 -22.604 1.00 53.30
 O
 ATOM 5786 CB GLU D 93 -15.318 63.062 -23.888 1.00 63.84
 C
 ATOM 5787 CG GLU D 93 -14.372 63.872 -23.016 1.00 63.90
 C
 ATOM 5788 CD GLU D 93 -13.844 65.113 -23.716 1.00 77.81
 C
 ATOM 5789 OE1 GLU D 93 -14.545 65.642 -24.605 1.00 77.09
 O
 ATOM 5790 OE2 GLU D 93 -12.725 65.558 -23.379 1.00 78.31
 O1-
 ATOM 5791 HA GLU D 93 -15.255 61.413 -22.669 1.00 66.06
 H
 ATOM 5792 HB2 GLU D 93 -14.813 62.740 -24.651 1.00 76.60
 H
 ATOM 5793 HB3 GLU D 93 -16.025 63.654 -24.188 1.00 76.60
 H
 ATOM 5794 HG2 GLU D 93 -14.844 64.157 -22.217 1.00 76.68
 H
 ATOM 5795 HG3 GLU D 93 -13.613 63.319 -22.773 1.00 76.68
 H
 ATOM 5796 N SER D 94 -16.675 62.405 -20.918 1.00 45.44
 N
 ATOM 5797 CA SER D 94 -17.646 62.768 -19.894 1.00 42.83
 C
 ATOM 5798 C SER D 94 -16.982 63.218 -18.597 1.00 36.20
 C
 ATOM 5799 O SER D 94 -15.871 62.800 -18.274 1.00 34.62
 O
 ATOM 5800 CB SER D 94 -18.576 61.582 -19.613 1.00 47.30
 C
 ATOM 5801 OG SER D 94 -19.526 61.895 -18.609 1.00 57.24
 O
 ATOM 5802 H SER D 94 -15.886 62.245 -20.616 1.00 54.53
 H
 ATOM 5803 HA SER D 94 -18.189 63.502 -20.221 1.00 51.40
 H
 ATOM 5804 HB2 SER D 94 -19.046 61.353 -20.430 1.00 56.75
 H
 ATOM 5805 HB3 SER D 94 -18.042 60.828 -19.317 1.00 56.75
 H
 ATOM 5806 HG SER D 94 -20.025 61.234 -18.470 1.00 68.69
 H
 ATOM 5807 N TYR D 95 -17.673 64.086 -17.866 1.00 33.40
 N
 ATOM 5808 CA TYR D 95 -17.266 64.466 -16.520 1.00 33.91
 C
 ATOM 5809 C TYR D 95 -17.891 63.519 -15.505 1.00 30.98
 C
 ATOM 5810 O TYR D 95 -18.999 63.025 -15.711 1.00 31.07
 O
 ATOM 5811 CB TYR D 95 -17.675 65.905 -16.213 1.00 39.04
 C
 ATOM 5812 CG TYR D 95 -16.785 66.949 -16.840 1.00 41.85
 C
 ATOM 5813 CD1 TYR D 95 -15.603 67.336 -16.227 1.00 42.03
 C
 ATOM 5814 CD2 TYR D 95 -17.130 67.557 -18.040 1.00 50.41
 C
 ATOM 5815 CE1 TYR D 95 -14.785 68.293 -16.790 1.00 48.64
 C
 ATOM 5816 CE2 TYR D 95 -16.319 68.517 -18.613 1.00 52.83
 C
 ATOM 5817 CZ TYR D 95 -15.147 68.881 -17.983 1.00 57.25
 C
 ATOM 5818 OH TYR D 95 -14.331 69.837 -18.545 1.00 60.24
 O
 ATOM 5819 H TYR D 95 -18.394 64.473 -18.132 1.00 40.08
 H
 ATOM 5820 HA TYR D 95 -16.301 64.400 -16.446 1.00 40.69
 H
 ATOM 5821 HB2 TYR D 95 -18.576 66.050 -16.542 1.00 46.85

C
 ATOM 12071 H THR F 119 8.712 31.883 -7.419 1.00 19.57 H
 ATOM 12072 HA THR F 119 6.924 33.825 -8.102 1.00 16.72
 H
 ATOM 12073 HB THR F 119 6.029 32.495 -9.760 1.00 18.46
 H
 ATOM 12074 HG1 THR F 119 7.746 30.596 -9.056 1.00 18.65
 H
 ATOM 12075 HG21 THR F 119 7.806 32.396 -11.281 1.00 27.16
 H
 ATOM 12076 HG22 THR F 119 7.850 33.757 -10.482 1.00 27.16
 H
 ATOM 12077 HG23 THR F 119 8.833 32.582 -10.096 1.00 27.16
 H
 ATOM 12078 N SER F 120 6.372 31.435 -6.184 1.00 14.66 N
 ATOM 12079 CA SER F 120 5.353 30.736 -5.405 1.00 13.72
 C
 ATOM 12080 C SER F 120 4.494 31.689 -4.583 1.00 15.42 C
 ATOM 12081 O SER F 120 3.267 31.564 -4.561 1.00 14.45 O
 ATOM 12082 CB SER F 120 6.000 29.701 -4.490 1.00 13.00
 C
 ATOM 12083 OG SER F 120 6.308 28.529 -5.215 1.00 13.36
 O
 ATOM 12084 H SER F 120 7.183 31.245 -5.972 1.00 17.59 H
 ATOM 12085 HA SER F 120 4.766 30.264 -6.016 1.00 16.46
 H
 ATOM 12086 HB2 SER F 120 6.817 30.070 -4.121 1.00 15.60
 H
 ATOM 12087 HB3 SER F 120 5.382 29.479 -3.776 1.00 15.60
 H
 ATOM 12088 HG SER F 120 6.841 28.709 -5.839 1.00 16.03
 H
 ATOM 12089 N GLU F 121 5.127 32.640 -3.906 1.00 12.33 N
 ATOM 12090 CA GLU F 121 4.374 33.607 -3.114 1.00 15.40
 C
 ATOM 12091 C GLU F 121 3.490 34.461 -4.020 1.00 15.41 C
 ATOM 12092 O GLU F 121 2.297 34.645 -3.758 1.00 13.55 O
 ATOM 12093 CB GLU F 121 5.317 34.491 -2.307 1.00 17.29
 C
 ATOM 12094 CG GLU F 121 4.607 35.381 -1.317 1.00 19.47
 C
 ATOM 12095 CD GLU F 121 5.568 36.252 -0.541 1.00 26.69
 C
 ATOM 12096 OE1 GLU F 121 6.760 35.884 -0.447 1.00 27.63
 O
 ATOM 12097 OE2 GLU F 121 5.132 37.303 -0.028 1.00 31.22
 O1-
 ATOM 12098 H GLU F 121 5.980 32.748 -3.888 1.00 14.80 H
 ATOM 12099 HA GLU F 121 3.801 33.131 -2.493 1.00 18.48
 H
 ATOM 12100 HB2 GLU F 121 5.931 33.926 -1.813 1.00 20.74
 H
 ATOM 12101 HB3 GLU F 121 5.811 35.061 -2.918 1.00 20.74
 H
 ATOM 12102 HG2 GLU F 121 3.992 35.960 -1.794 1.00 23.37
 H
 ATOM 12103 HG3 GLU F 121 4.122 34.828 -0.684 1.00 23.37
 H
 ATOM 12104 N PHE F 122 4.095 34.977 -5.083 1.00 13.83 N
 ATOM 12105 CA PHE F 122 3.375 35.708 -6.123 1.00 14.10
 C
 ATOM 12106 C PHE F 122 2.122 34.964 -6.588 1.00 15.86 C
 ATOM 12107 O PHE F 122 1.038 35.545 -6.674 1.00 14.66 O
 ATOM 12108 CB PHE F 122 4.314 35.954 -7.308 1.00 15.83
 C
 ATOM 12109 CG PHE F 122 3.651 36.569 -8.505 1.00 17.67
 C
 ATOM 12110 CD1 PHE F 122 3.586 37.944 -8.644 1.00 16.84
 C
 ATOM 12111 CD2 PHE F 122 3.124 35.770 -9.510 1.00 15.73
 C
 ATOM 12112 CE1 PHE F 122 2.991 38.512 -9.751 1.00 19.00
 C
 ATOM 12113 CE2 PHE F 122 2.525 36.331 -10.617 1.00 21.26
 C
 ATOM 12114 CZ PHE F 122 2.461 37.707 -10.740 1.00 21.83
 C
 ATOM 12115 H PHE F 122 4.940 34.915 -5.230 1.00 16.59 H
 ATOM 12116 HA PHE F 122 3.101 36.570 -5.772 1.00 16.92
 H
 ATOM 12117 HB2 PHE F 122 5.023 36.552 -7.024 1.00 19.00
 H
 ATOM 12118 HB3 PHE F 122 4.694 35.105 -7.585 1.00 19.00
 H
 ATOM 12119 HD1 PHE F 122 3.942 38.490 -7.982 1.00 20.21
 H
 ATOM 12120 HD2 PHE F 122 3.166 34.845 -9.430 1.00 18.87
 H
 ATOM 12121 HE1 PHE F 122 2.946 39.438 -9.831 1.00 22.80

ATOM 5821 HE1 TYR D 95 -15.375 66.000 -15.375 1.00 15.375
H
ATOM 5822 HB3 TYR D 95 -17.653 66.037 -15.252 1.00 46.85
H
ATOM 5823 HD1 TYR D 95 -15.356 66.941 -15.421 1.00 50.44
H
ATOM 5824 HD2 TYR D 95 -17.920 67.312 -18.465 1.00 60.50
H
ATOM 5825 HE1 TYR D 95 -13.994 68.541 -16.368 1.00 58.37
H
ATOM 5826 HE2 TYR D 95 -16.561 68.915 -19.418 1.00 63.40
H
ATOM 5827 HH TYR D 95 -14.664 70.113 -19.265 1.00 72.28
H
ATOM 5828 N CYS D 96 -17.171 63.269 -14.415 1.00 25.95
N
ATOM 5829 CA CYS D 96 -17.651 62.404 -13.343 1.00 25.00
C
ATOM 5830 C CYS D 96 -17.873 63.227 -12.080 1.00 26.60
C
ATOM 5831 O CYS D 96 -17.011 64.017 -11.687 1.00 24.78
O
ATOM 5832 CB CYS D 96 -16.654 61.274 -13.078 1.00 24.34
C
ATOM 5833 SG CYS D 96 -17.220 60.018 -11.906 1.00 25.98
S
ATOM 5834 H CYS D 96 -16.388 63.595 -14.272 1.00 31.14
H
ATOM 5835 HA CYS D 96 -18.498 62.010 -13.603 1.00 30.00
H
ATOM 5836 HB2 CYS D 96 -16.465 60.826 -13.918 1.00 29.21
H
ATOM 5837 HB3 CYS D 96 -15.838 61.659 -12.724 1.00 29.21
H
ATOM 5838 N GLY D 97 -19.032 63.042 -11.454 1.00 23.68
N
ATOM 5839 CA GLY D 97 -19.358 63.738 -10.223 1.00 26.95
C

ATOM 5840 C GLY D 97 -20.783 64.263 -10.206 1.00 29.72
C
ATOM 5841 O GLY D 97 -21.654 63.711 -10.880 1.00 30.29
O
ATOM 5842 H GLY D 97 -19.651 62.512 -11.730 1.00 28.42
H
ATOM 5843 HA2 GLY D 97 -19.245 63.135 -9.472 1.00 32.33
H
ATOM 5844 HA3 GLY D 97 -18.755 64.489 -10.108 1.00 32.33
H
ATOM 5845 N PRO D 98 -21.033 65.333 -9.432 1.00 27.73
N
ATOM 5846 CA PRO D 98 -20.059 66.060 -8.605 1.00 26.88
C
ATOM 5847 C PRO D 98 -19.526 65.247 -7.425 1.00 25.52
C
ATOM 5848 O PRO D 98 -20.262 64.465 -6.822 1.00 24.79
O
ATOM 5849 CB PRO D 98 -20.855 67.272 -8.110 1.00 31.02
C
ATOM 5850 CG PRO D 98 -22.272 66.852 -8.178 1.00 32.89
C
ATOM 5851 CD PRO D 98 -22.370 65.945 -9.363 1.00 31.01
C
ATOM 5852 HA PRO D 98 -19.315 66.363 -9.148 1.00 32.02
H
ATOM 5853 HB2 PRO D 98 -20.601 67.480 -7.197 1.00 37.23
H
ATOM 5854 HB3 PRO D 98 -20.692 68.030 -8.693 1.00 37.23
H
ATOM 5855 HG2 PRO D 98 -22.510 66.380 -7.366 1.00 39.46
H
ATOM 5856 HG3 PRO D 98 -22.837 67.632 -8.298 1.00 39.46
H
ATOM 5857 HD2 PRO D 98 -23.046 65.266 -9.214 1.00 37.21
H
ATOM 5858 HD3 PRO D 98 -22.550 66.455 -10.167 1.00 37.21
H
ATOM 5859 N CYS D 99 -18.247 65.439 -7.115 1.00 22.53
N
ATOM 5860 CA CYS D 99 -17.605 64.787 -5.978 1.00 24.42
C
ATOM 5861 C CYS D 99 -16.595 65.739 -5.345 1.00 27.19
C
ATOM 5862 O CYS D 99 -16.094 66.638 -6.017 1.00 26.74
O
ATOM 5863 CB CYS D 99 -16.895 63.496 -6.407 1.00 28.73
C
ATOM 5864 SG CYS D 99 -17.971 62.187 -7.066 1.00 27.37
S
ATOM 5865 H CYS D 99 -17.719 65.952 -7.559 1.00 27.03
H
ATOM 5866 HA CYS D 99 -18.275 64.563 -5.313 1.00 29.30
H
ATOM 5867 HB2 CYS D 99 -16.250 63.716 -7.097 1.00 34.48
H
ATOM 5868 HB3 CYS D 99 -16.432 63.131 -5.637 1.00 34.48
H
ATOM 5869 N PRO D 100 -16.293 65.547 -4.051 1.00 23.29
N
ATOM 5870 CA PRO D 100 -15.166 66.276 -3.458 1.00 27.44
C
ATOM 5871 C PRO D 100 -13.882 66.019 -4.245 1.00 28.68

ATOM 12121 HE1 PHE F 122 2.170 35.786 -11.281 1.00 25.51
H
ATOM 12122 HE2 PHE F 122 2.170 35.786 -11.281 1.00 25.51
H
ATOM 12123 HZ PHE F 122 2.057 38.089 -11.485 1.00 26.20
H
ATOM 12124 N ARG F 123 2.271 33.671 -6.857 1.00 14.87 N
ATOM 12125 CA ARG F 123 1.135 32.875 -7.423 1.00 15.14
C
ATOM 12126 C ARG F 123 0.102 32.529 -6.394 1.00 16.12 C
ATOM 12127 O ARG F 123 -1.047 32.276 -8.759 1.00 15.25
O
ATOM 12128 CB ARG F 123 1.752 31.596 -8.055 1.00 17.25
C
ATOM 12129 CG ARG F 123 2.417 31.851 -9.407 1.00 15.66
C
ATOM 12130 CD ARG F 123 2.949 30.582 -10.069 1.00 16.20
C
ATOM 12131 NE ARG F 123 4.170 30.101 -9.428 1.00 17.22
N
ATOM 12132 CZ ARG F 123 4.237 29.081 -8.574 1.00 13.04
C
ATOM 12133 NH1 ARG F 123 3.150 28.391 -8.242 1.00 11.59
N1+
ATOM 12134 NH2 ARG F 123 5.408 28.743 -8.054 1.00 13.48
N
ATOM 12135 H ARG F 123 2.996 33.228 -6.721 1.00 17.85 H
ATOM 12136 HA ARG F 123 0.763 33.388 -8.129 1.00 18.17
H
ATOM 12137 HB2 ARG F 123 2.418 31.220 -7.460 1.00 20.70
H
ATOM 12138 HB3 ARG F 123 1.030 30.965 -8.191 1.00 20.70
H
ATOM 12139 HG2 ARG F 123 1.767 32.250 -10.006 1.00 18.79
H
ATOM 12140 HG3 ARG F 123 3.164 32.456 -9.280 1.00 18.79
H
ATOM 12141 HD2 ARG F 123 2.278 29.884 -10.005 1.00 19.44
H
ATOM 12142 HD3 ARG F 123 3.149 30.769 -11.000 1.00 19.44
H
ATOM 12143 HE ARG F 123 4.904 30.508 -9.617 1.00 20.67
H
ATOM 12144 HH11 ARG F 123 2.387 28.605 -8.575 1.00 13.91
H
ATOM 12145 HH12 ARG F 123 3.210 27.734 -7.691 1.00 13.91
H
ATOM 12146 HH21 ARG F 123 6.116 29.182 -8.266 1.00 16.17
H
ATOM 12147 HH22 ARG F 123 5.480 28.083 -7.505 1.00 16.17
H
ATOM 12148 N LEU F 124 0.455 32.535 -5.113 1.00 15.08 N
ATOM 12149 CA LEU F 124 -0.532 32.315 -4.062 1.00 16.64
C
ATOM 12150 C LEU F 124 -1.329 33.584 -3.789 1.00 17.66 C
ATOM 12151 O LEU F 124 -2.555 33.542 -3.651 1.00 14.64 O
ATOM 12152 CB LEU F 124 0.137 31.848 -2.766 1.00 12.40
C
ATOM 12153 CG LEU F 124 -0.767 31.818 -1.525 1.00 15.66
C
ATOM 12154 CD1 LEU F 124 -1.960 30.901 -1.736 1.00 18.94
C
ATOM 12155 CD2 LEU F 124 0.001 31.410 -0.273 1.00 12.65
C
ATOM 12156 H LEU F 124 1.256 32.662 -4.827 1.00 18.10 H
ATOM 12157 HA LEU F 124 -1.151 31.626 -4.347 1.00 19.97
H
ATOM 12158 HB2 LEU F 124 0.473 30.948 -2.903 1.00 14.88
H
ATOM 12159 HB3 LEU F 124 0.877 32.443 -2.572 1.00 14.88
H
ATOM 12160 HG LEU F 124 -1.112 32.712 -1.376 1.00 18.80
H
ATOM 12161 HD11 LEU F 124 -2.507 30.907 -0.935 1.00 22.72
H
ATOM 12162 HD12 LEU F 124 -2.475 31.223 -2.492 1.00 22.72
H
ATOM 12163 HD13 LEU F 124 -1.639 30.003 -1.912 1.00 22.72
H
ATOM 12164 HD21 LEU F 124 -0.607 31.405 0.482 1.00 15.18
H
ATOM 12165 HD22 LEU F 124 0.373 30.524 -0.406 1.00 15.18
H
ATOM 12166 HD23 LEU F 124 0.715 32.049 -0.120 1.00 15.18
H
ATOM 12167 N LYS F 125 -0.628 34.711 -3.714 1.00 16.52 N
ATOM 12168 CA LYS F 125 -1.208 35.923 -3.146 1.00 13.85
C
ATOM 12169 C LYS F 125 -1.934 36.817 -4.144 1.00 18.09 C
ATOM 12170 O LYS F 125 -2.316 37.935 -3.802 1.00 17.06 O
ATOM 12171 CB LYS F 125 -0.117 36.732 -2.443 1.00 16.06

C
 ATOM 5872 O PRO D 100 -13.681 64.904 -4.730 1.00 26.75
 O
 ATOM 5873 CB PRO D 100 -15.073 65.703 -2.043 1.00 29.15
 C
 ATOM 5874 CG PRO D 100 -16.420 65.125 -1.767 1.00 25.98
 C

 ATOM 5875 CD PRO D 100 -16.950 64.656 -3.079 1.00 24.13
 C
 ATOM 5876 HA PRO D 100 -15.349 67.228 -3.420 1.00 32.93
 H
 ATOM 5877 HB2 PRO D 100 -14.392 65.013 -2.014 1.00 34.98
 H
 ATOM 5878 HB3 PRO D 100 -14.869 66.414 -1.415 1.00 34.98
 H
 ATOM 5879 HG2 PRO D 100 -16.333 64.382 -1.150 1.00 31.17
 H
 ATOM 5880 HG3 PRO D 100 -16.996 65.811 -1.394 1.00 31.17
 H
 ATOM 5881 HD2 PRO D 100 -16.693 63.734 -3.238 1.00 28.95
 H
 ATOM 5882 HD3 PRO D 100 -17.913 64.769 -3.115 1.00 28.95
 H
 ATOM 5883 N LYS D 101 -13.027 67.031 -4.357 1.00 31.41
 N
 ATOM 5884 CA LYS D 101 -11.915 66.997 -5.306 1.00 34.02
 C
 ATOM 5885 C LYS D 101 -10.851 65.943 -4.997 1.00 34.04
 C
 ATOM 5886 O LYS D 101 -10.078 65.570 -5.884 1.00 40.88
 O
 ATOM 5887 CB LYS D 101 -11.254 68.377 -5.379 1.00 40.64
 C
 ATOM 5888 CG LYS D 101 -12.150 69.458 -5.975 1.00 44.15
 C
 ATOM 5889 CD LYS D 101 -11.383 70.749 -6.223 1.00 55.25
 C
 ATOM 5890 CE LYS D 101 -12.306 71.866 -6.691 1.00 57.18
 C
 ATOM 5891 NZ LYS D 101 -11.566 73.132 -6.955 1.00 56.55
 N1+
 ATOM 5892 H LYS D 101 -13.069 67.753 -3.892 1.00 37.69
 H
 ATOM 5893 HA LYS D 101 -12.271 66.799 -6.186 1.00 40.82
 H
 ATOM 5894 HB2 LYS D 101 -11.011 68.655 -4.482 1.00 48.77
 H
 ATOM 5895 HB3 LYS D 101 -10.459 68.314 -5.931 1.00 48.77
 H
 ATOM 5896 HG2 LYS D 101 -12.505 69.147 -6.823 1.00 52.98
 H
 ATOM 5897 HG3 LYS D 101 -12.874 69.649 -5.358 1.00 52.98
 H
 ATOM 5898 HD2 LYS D 101 -10.957 71.032 -5.399 1.00 66.30
 H
 ATOM 5899 HD3 LYS D 101 -10.716 70.598 -6.911 1.00 66.30
 H
 ATOM 5900 HE2 LYS D 101 -12.743 71.594 -7.513 1.00 68.62
 H
 ATOM 5901 HE3 LYS D 101 -12.967 72.040 -6.003 1.00 68.62
 H
 ATOM 5902 HZ1 LYS D 101 -12.132 73.763 -7.226 1.00 67.86
 H
 ATOM 5903 HZ2 LYS D 101 -11.160 73.407 -6.213 1.00 67.86
 H
 ATOM 5904 HZ3 LYS D 101 -10.955 73.000 -7.588 1.00 67.86
 H
 ATOM 5905 N ASN D 102 -10.804 65.470 -3.755 1.00 27.12
 N
 ATOM 5906 CA ASN D 102 -9.836 64.445 -3.366 1.00 27.98
 C
 ATOM 5907 C ASN D 102 -10.503 63.098 -3.072 1.00 26.71
 C
 ATOM 5908 O ASN D 102 -9.946 62.283 -2.360 1.00 25.40
 O
 ATOM 5909 CB ASN D 102 -9.026 64.914 -2.150 1.00 30.15
 C

 ATOM 5910 CG ASN D 102 -9.898 65.481 -1.045 1.00 36.72
 C
 ATOM 5911 OD1 ASN D 102 -11.120 65.332 -1.062 1.00 37.16
 O
 ATOM 5912 ND2 ASN D 102 -9.271 66.145 -0.078 1.00 41.06
 N
 ATOM 5913 H ASN D 102 -11.322 65.725 -3.118 1.00 32.55
 H
 ATOM 5914 HA ASN D 102 -9.215 64.311 -4.099 1.00 33.58
 H
 ATOM 5915 HB2 ASN D 102 -8.535 64.160 -1.787 1.00 36.19
 H
 ATOM 5916 HB3 ASN D 102 -8.409 65.608 -2.430 1.00 36.19
 H
 ATOM 5917 HD21 ASN D 102 -9.720 66.485 0.571 1.00 49.28
 H
 ATOM 5918 HD22 ASN D 102 -8.416 66.238 -0.102 1.00 49.28
 H
 ATOM 5919 N TRP D 103 -11.696 62.897 -3.630 1.00 25.27
 N
 ATOM 5920 CA TRP D 103 -12.400 61.619 -3.534 1.00 19.72

C
 ATOM 12172 CG LYS F 125 0.491 36.018 -1.252 1.00 20.08
 C
 ATOM 12173 CD LYS F 125 1.351 36.960 -0.420 1.00 22.60
 C
 ATOM 12174 CE LYS F 125 1.664 36.362 0.940 1.00 23.37
 C

 ATOM 12175 NZ LYS F 125 2.510 37.267 1.764 1.00 23.92
 N1+
 ATOM 12176 H LYS F 125 0.183 34.801 -3.985 1.00 19.83
 H
 ATOM 12177 HA LYS F 125 -1.854 35.662 -2.471 1.00 16.62
 H
 ATOM 12178 HB2 LYS F 125 0.595 36.915 -3.076 1.00 19.28
 H
 ATOM 12179 HB3 LYS F 125 -0.499 37.566 -2.127 1.00 19.28
 H
 ATOM 12180 HG2 LYS F 125 -0.219 35.674 -0.688 1.00 24.10
 H
 ATOM 12181 HG3 LYS F 125 1.052 35.291 -1.567 1.00 24.10
 H
 ATOM 12182 HD2 LYS F 125 2.188 37.123 -0.881 1.00 27.13
 H
 ATOM 12183 HD3 LYS F 125 0.874 37.794 -0.283 1.00 27.13
 H
 ATOM 12184 HE2 LYS F 125 0.834 36.205 1.417 1.00 28.04
 H
 ATOM 12185 HE3 LYS F 125 2.142 35.527 0.818 1.00 28.04
 H
 ATOM 12186 HZ1 LYS F 125 3.282 37.423 1.348 1.00 28.71
 H
 ATOM 12187 HZ2 LYS F 125 2.090 38.041 1.894 1.00 28.71
 H
 ATOM 12188 HZ3 LYS F 125 2.678 36.891 2.553 1.00 28.71
 H

 ATOM 12189 N LYS F 126 -2.143 36.328 -5.363 1.00 14.39
 N
 ATOM 12190 CA LYS F 126 -2.855 37.102 -6.371 1.00 15.04
 C
 ATOM 12191 C LYS F 126 -4.200 37.597 -5.829 1.00 15.14
 C
 ATOM 12192 O LYS F 126 -4.500 38.788 -5.906 1.00 13.71
 O
 ATOM 12193 CB LYS F 126 -3.057 36.270 -7.637 1.00 15.31
 C
 ATOM 12194 CG LYS F 126 -3.569 37.060 -8.822 1.00 14.58
 C
 ATOM 12195 CD LYS F 126 -3.293 36.319 -10.120 1.00 18.23
 C
 ATOM 12196 CE LYS F 126 -3.981 36.970 -11.302 1.00 24.64
 C
 ATOM 12197 NZ LYS F 126 -3.627 36.281 -12.575 1.00 24.00
 N1+
 ATOM 12198 H LYS F 126 -1.883 35.553 -5.630 1.00 17.27
 H
 ATOM 12199 HA LYS F 126 -2.323 37.879 -6.605 1.00 18.05
 H
 ATOM 12200 HB2 LYS F 126 -2.207 35.876 -7.889 1.00 18.37
 H
 ATOM 12201 HB3 LYS F 126 -3.700 35.569 -7.449 1.00 18.37
 H
 ATOM 12202 HG2 LYS F 126 -4.528 37.183 -8.738 1.00 17.49
 H
 ATOM 12203 HG3 LYS F 126 -3.119 37.918 -8.857 1.00 17.49
 H
 ATOM 12204 HD2 LYS F 126 -2.338 36.318 -10.289 1.00 21.87
 H
 ATOM 12205 HD3 LYS F 126 -3.620 35.409 -10.043 1.00 21.87
 H
 ATOM 12206 HE2 LYS F 126 -4.943 36.917 -11.183 1.00 29.56
 H
 ATOM 12207 HE3 LYS F 126 -3.700 37.896 -11.367 1.00 29.56
 H
 ATOM 12208 HZ1 LYS F 126 -4.039 36.675 -13.258 1.00 28.80
 H
 ATOM 12209 HZ2 LYS F 126 -2.748 36.318 -12.706 1.00 28.80
 H

 ATOM 12210 HZ3 LYS F 126 -3.878 35.427 -12.538 1.00 28.80
 H
 ATOM 12211 N TRP F 127 -4.983 36.690 -5.245 1.00 15.14
 N
 ATOM 12212 CA TRP F 127 -6.284 37.040 -4.663 1.00 15.40
 C
 ATOM 12213 C TRP F 127 -6.357 36.731 -3.163 1.00 15.55
 C
 ATOM 12214 O TRP F 127 -7.408 36.886 -2.532 1.00 13.20
 O
 ATOM 12215 CB TRP F 127 -7.397 36.293 -5.400 1.00 11.59
 C
 ATOM 12216 CG TRP F 127 -7.543 36.706 -6.833 1.00 15.11
 C
 ATOM 12217 CD1 TRP F 127 -7.053 36.059 -7.931 1.00 17.05
 C
 ATOM 12218 CD2 TRP F 127 -8.229 37.863 -7.323 1.00 15.18
 C
 ATOM 12219 NE1 TRP F 127 -7.390 36.744 -9.075 1.00 17.58
 N
 ATOM 12220 CE2 TRP F 127 -8.114 37.854 -8.729 1.00 18.89

C
 ATOM 5921 C TRP D 103 -12.378 60.891 -4.872 1.00 20.07
 C
 ATOM 5922 O TRP D 103 -12.240 61.516 -5.927 1.00 20.39
 O
 ATOM 5923 CB TRP D 103 -13.853 61.822 -3.094 1.00 22.50
 C
 ATOM 5924 CG TRP D 103 -14.018 62.103 -1.636 1.00 21.05
 C
 ATOM 5925 CD1 TRP D 103 -13.247 62.919 -0.865 1.00 26.32
 C
 ATOM 5926 CD2 TRP D 103 -15.014 61.552 -0.768 1.00 22.01
 C
 ATOM 5927 NE1 TRP D 103 -13.708 62.920 0.430 1.00 31.25
 N
 ATOM 5928 CE2 TRP D 103 -14.792 62.088 0.516 1.00 23.75
 C
 ATOM 5929 CE3 TRP D 103 -16.075 60.660 -0.952 1.00 21.83
 C
 ATOM 5930 CZ2 TRP D 103 -15.589 61.759 1.611 1.00 26.02
 C
 ATOM 5931 CZ3 TRP D 103 -16.868 60.336 0.136 1.00 24.01
 C
 ATOM 5932 CH2 TRP D 103 -16.620 60.884 1.401 1.00 22.41
 C
 ATOM 5933 H TRP D 103 -12.124 63.494 -4.077 1.00 30.33
 H
 ATOM 5934 HA TRP D 103 -11.959 61.060 -2.876 1.00 23.66
 H
 ATOM 5935 HB2 TRP D 103 -14.225 62.572 -3.583 1.00 27.00
 H
 ATOM 5936 HB3 TRP D 103 -14.355 61.017 -3.298 1.00 27.00
 H
 ATOM 5937 HD1 TRP D 103 -12.520 63.412 -1.172 1.00 31.59
 H
 ATOM 5938 HE1 TRP D 103 -13.369 63.369 1.081 1.00 37.50
 H
 ATOM 5939 HE3 TRP D 103 -16.245 60.292 -1.789 1.00 26.20
 H
 ATOM 5940 HZ2 TRP D 103 -15.427 62.122 2.452 1.00 31.22
 H
 ATOM 5941 HZ3 TRP D 103 -17.577 59.744 0.025 1.00 28.82
 H
 ATOM 5942 HH2 TRP D 103 -17.169 60.649 2.114 1.00 26.90
 H
 ATOM 5943 N ILE D 104 -12.524 59.571 -4.821 1.00 16.86
 N
 ATOM 5944 CA ILE D 104 -12.597 58.755 -6.027 1.00 17.78
 C

ATOM 5945 C ILE D 104 -13.993 58.831 -6.627 1.00 18.20
 C
 ATOM 5946 O ILE D 104 -14.975 58.549 -5.944 1.00 18.57
 O
 ATOM 5947 CB ILE D 104 -12.255 57.281 -5.735 1.00 20.02
 C
 ATOM 5948 CG1 ILE D 104 -10.857 57.168 -5.119 1.00 20.67
 C
 ATOM 5949 CG2 ILE D 104 -12.338 56.446 -7.015 1.00 19.79
 C
 ATOM 5950 CD1 ILE D 104 -10.571 55.825 -4.403 1.00 17.10
 C
 ATOM 5951 H ILE D 104 -12.585 59.120 -4.092 1.00 20.23
 H
 ATOM 5952 HA ILE D 104 -11.965 59.091 -6.681 1.00 21.34
 H
 ATOM 5953 HB ILE D 104 -12.901 56.935 -5.099 1.00 24.02
 H
 ATOM 5954 HG12 ILE D 104 -10.197 57.313 -5.815 1.00 24.80
 H
 ATOM 5955 HG13 ILE D 104 -10.783 57.847 -4.432 1.00 24.80
 H
 ATOM 5956 HG21 ILE D 104 -12.120 55.525 -6.805 1.00 23.75
 H
 ATOM 5957 HG22 ILE D 104 -13.240 56.500 -7.368 1.00 23.75
 H
 ATOM 5958 HG23 ILE D 104 -11.707 56.798 -7.662 1.00 23.75
 H
 ATOM 5959 HD11 ILE D 104 -9.673 55.834 -4.118 1.00 20.52
 H
 ATOM 5960 HD12 ILE D 104 -11.215 55.668 -3.774 1.00 20.52
 H
 ATOM 5961 HD13 ILE D 104 -10.648 55.134 -5.159 1.00 20.52
 H
 ATOM 5962 N CYS D 105 -14.076 59.199 -7.902 1.00 17.45
 N
 ATOM 5963 CA CYS D 105 -15.354 59.239 -8.602 1.00 17.74
 C
 ATOM 5964 C CYS D 105 -15.465 58.067 -9.573 1.00 21.30
 C
 ATOM 5965 O CYS D 105 -14.560 57.821 -10.371 1.00 19.85
 O
 ATOM 5966 CB CYS D 105 -15.524 60.563 -9.345 1.00 20.49
 C
 ATOM 5967 SG CYS D 105 -17.186 60.797 -10.022 1.00 29.47
 S
 ATOM 5968 H CYS D 105 -13.404 59.431 -8.385 1.00 20.94
 H
 ATOM 5969 HA CYS D 105 -16.073 59.163 -7.955 1.00 21.29
 H
 ATOM 5970 HB2 CYS D 105 -15.347 61.293 -8.731 1.00 24.59
 H

C
 ATOM 12221 CE3 TRP F 127 -8.930 38.906 -6.710 1.00 19.66
 C
 ATOM 12222 CZ2 TRP F 127 -8.675 38.847 -9.531 1.00 19.66
 C
 ATOM 12223 CZ3 TRP F 127 -9.486 39.891 -7.507 1.00 17.24
 C
 ATOM 12224 CH2 TRP F 127 -9.353 39.854 -8.904 1.00 23.08
 C
 ATOM 12225 H TRP F 127 -4.783 35.856 -5.172 1.00 18.17
 H
 ATOM 12226 HA TRP F 127 -6.434 37.991 -4.779 1.00 18.48
 H
 ATOM 12227 HB2 TRP F 127 -7.202 35.343 -5.382 1.00 13.91
 H
 ATOM 12228 HB3 TRP F 127 -8.240 36.468 -4.953 1.00 13.91
 H
 ATOM 12229 HD1 TRP F 127 -6.560 35.270 -7.908 1.00 20.46
 H
 ATOM 12230 HE1 TRP F 127 -7.183 36.511 -9.877 1.00 21.10
 H
 ATOM 12231 HE3 TRP F 127 -9.022 38.937 -5.785 1.00 23.59
 H
 ATOM 12232 HZ2 TRP F 127 -8.589 38.826 -10.457 1.00 23.59
 H
 ATOM 12233 HZ3 TRP F 127 -9.954 40.589 -7.111 1.00 20.69
 H
 ATOM 12234 HH2 TRP F 127 -9.737 40.530 -9.415 1.00 27.70
 H
 ATOM 12235 N PHE F 128 -5.230 36.311 -2.599 1.00 13.38
 N
 ATOM 12236 CA PHE F 128 -5.188 35.772 -1.243 1.00 17.23
 C
 ATOM 12237 C PHE F 128 -3.938 36.245 -0.498 1.00 16.62
 C
 ATOM 12238 O PHE F 128 -2.925 35.552 -0.476 1.00 14.98
 O
 ATOM 12239 CB PHE F 128 -5.234 34.241 -1.310 1.00 12.61
 C
 ATOM 12240 CG PHE F 128 -5.412 33.567 0.020 1.00 15.81
 C
 ATOM 12241 CD1 PHE F 128 -6.504 33.855 0.818 1.00 17.23
 C
 ATOM 12242 CD2 PHE F 128 -4.503 32.619 0.454 1.00 13.57
 C
 ATOM 12243 CE1 PHE F 128 -6.674 33.226 2.031 1.00 14.89
 C
 ATOM 12244 CE2 PHE F 128 -4.668 31.985 1.669 1.00 16.18
 C
 ATOM 12245 CZ PHE F 128 -5.756 32.288 2.459 1.00 14.81
 C
 ATOM 12246 H PHE F 128 -4.483 36.329 -2.987 1.00 16.05
 H
 ATOM 12247 HA PHE F 128 -5.967 36.079 -0.753 1.00 20.67
 H
 ATOM 12248 HB2 PHE F 128 -5.976 33.977 -1.876 1.00 15.13
 H
 ATOM 12249 HB3 PHE F 128 -4.402 33.922 -1.693 1.00 15.13
 H
 ATOM 12250 HD1 PHE F 128 -7.126 34.486 0.536 1.00 20.67
 H
 ATOM 12251 HD2 PHE F 128 -3.767 32.412 -0.075 1.00 16.29
 H
 ATOM 12252 HE1 PHE F 128 -7.409 33.432 2.563 1.00 17.87
 H
 ATOM 12253 HE2 PHE F 128 -4.047 31.355 1.954 1.00 19.41
 H
 ATOM 12254 HZ PHE F 128 -5.870 31.864 3.278 1.00 17.78
 H
 ATOM 12255 N ASP F 129 -4.011 37.426 0.108 1.00 16.80
 N
 ATOM 12256 CA ASP F 129 -2.863 37.972 0.828 1.00 17.78
 C
 ATOM 12257 C ASP F 129 -2.895 37.537 2.290 1.00 19.18
 C
 ATOM 12258 O ASP F 129 -3.800 36.814 2.714 1.00 16.91
 O
 ATOM 12259 CB ASP F 129 -2.819 39.504 0.714 1.00 18.37
 C
 ATOM 12260 CG ASP F 129 -4.066 40.185 1.263 1.00 16.63
 C
 ATOM 12261 OD1 ASP F 129 -4.707 39.642 2.181 1.00 16.14
 O
 ATOM 12262 OD2 ASP F 129 -4.394 41.289 0.779 1.00 16.62
 O1-
 ATOM 12263 H ASP F 129 -4.708 37.928 0.119 1.00 20.16
 H
 ATOM 12264 HA ASP F 129 -2.050 37.621 0.432 1.00 21.34
 H
 ATOM 12265 HB2 ASP F 129 -2.055 39.834 1.212 1.00 22.04
 H
 ATOM 12266 HB3 ASP F 129 -2.734 39.747 -0.221 1.00 22.04
 H
 ATOM 12267 N GLY F 130 -1.900 37.976 3.052 1.00 15.15
 N
 ATOM 12268 CA GLY F 130 -1.783 37.608 4.450 1.00 17.82
 C
 ATOM 12269 C GLY F 130 -2.997 37.984 5.277 1.00 16.60
 C

H
 ATOM 5971 HB3 CYS D 105 -14.895 60.592 -10.083 1.00 24.59
 H
 ATOM 5972 N TYR D 106 -16.577 57.343 -9.481 1.00 17.44
 N
 ATOM 5973 CA TYR D 106 -16.858 56.216 -10.365 1.00 18.50
 C
 ATOM 5974 C TYR D 106 -18.354 56.134 -10.632 1.00 19.85
 C
 ATOM 5975 O TYR D 106 -19.139 55.879 -9.718 1.00 18.05
 O
 ATOM 5976 CB TYR D 106 -16.362 54.902 -9.755 1.00 15.27
 C
 ATOM 5977 CG TYR D 106 -16.488 53.707 -10.675 1.00 17.55
 C
 ATOM 5978 CD1 TYR D 106 -15.878 53.702 -11.922 1.00 20.29
 C
 ATOM 5979 CD2 TYR D 106 -17.202 52.577 -10.293 1.00 20.08
 C

 ATOM 5980 CE1 TYR D 106 -15.981 52.613 -12.768 1.00 20.50
 C
 ATOM 5981 CE2 TYR D 106 -17.309 51.476 -11.136 1.00 18.23
 C
 ATOM 5982 CZ TYR D 106 -16.692 51.502 -12.373 1.00 22.08
 C
 ATOM 5983 OH TYR D 106 -16.785 50.418 -13.224 1.00 18.81
 O
 ATOM 5984 H TYR D 106 -17.198 57.488 -8.902 1.00 20.92
 H
 ATOM 5985 HA TYR D 106 -16.403 56.351 -11.211 1.00 22.20
 H
 ATOM 5986 HB2 TYR D 106 -15.425 55.000 -9.524 1.00 18.33
 H
 ATOM 5987 HB3 TYR D 106 -16.879 54.715 -8.956 1.00 18.33
 H
 ATOM 5988 HD1 TYR D 106 -15.394 54.448 -12.195 1.00 24.35
 H
 ATOM 5989 HD2 TYR D 106 -17.616 52.557 -9.460 1.00 24.10
 H
 ATOM 5990 HE1 TYR D 106 -15.565 52.629 -13.600 1.00 24.60
 H
 ATOM 5991 HE2 TYR D 106 -17.790 50.727 -10.869 1.00 21.87
 H
 ATOM 5992 HH TYR D 106 -17.243 49.811 -12.867 1.00 22.58
 H
 ATOM 5993 N LYS D 107 -18.732 56.351 -11.888 1.00 16.29
 N
 ATOM 5994 CA LYS D 107 -20.132 56.364 -12.294 1.00 20.57
 C
 ATOM 5995 C LYS D 107 -20.916 57.330 -11.404 1.00 24.05
 C
 ATOM 5996 O LYS D 107 -21.998 57.015 -10.907 1.00 17.53
 O
 ATOM 5997 CB LYS D 107 -20.708 54.947 -12.249 1.00 20.83
 C
 ATOM 5998 CG LYS D 107 -19.963 53.987 -13.184 1.00 20.22
 C
 ATOM 5999 CD LYS D 107 -20.505 52.566 -13.145 1.00 20.35
 C
 ATOM 6000 CE LYS D 107 -19.817 51.694 -14.198 1.00 23.07
 C
 ATOM 6001 NZ LYS D 107 -20.217 50.259 -14.138 1.00 21.00
 N1+
 ATOM 6002 H LYS D 107 -18.185 56.495 -12.536 1.00 19.55
 H
 ATOM 6003 HA LYS D 107 -20.193 56.682 -13.208 1.00 24.68
 H
 ATOM 6004 HB2 LYS D 107 -20.637 54.604 -11.344 1.00 24.99
 H
 ATOM 6005 HB3 LYS D 107 -21.638 54.974 -12.523 1.00 24.99
 H
 ATOM 6006 HG2 LYS D 107 -20.041 54.311 -14.094 1.00 24.26
 H
 ATOM 6007 HG3 LYS D 107 -19.029 53.957 -12.923 1.00 24.26
 H
 ATOM 6008 HD2 LYS D 107 -20.338 52.180 -12.271 1.00 24.42
 H
 ATOM 6009 HD3 LYS D 107 -21.457 52.579 -13.332 1.00 24.42
 H
 ATOM 6010 HE2 LYS D 107 -20.045 52.029 -15.080 1.00 27.69
 H
 ATOM 6011 HE3 LYS D 107 -18.857 51.741 -14.065 1.00 27.69
 H
 ATOM 6012 HZ1 LYS D 107 -21.095 50.182 -14.267 1.00 25.20
 H
 ATOM 6013 HZ2 LYS D 107 -19.791 49.797 -14.768 1.00 25.20
 H
 ATOM 6014 HZ3 LYS D 107 -20.011 49.919 -13.341 1.00 25.20
 H

 ATOM 6015 N ASN D 108 -20.318 58.503 -11.205 1.00 23.09
 N
 ATOM 6016 CA ASN D 108 -20.912 59.622 -10.473 1.00 24.38
 C
 ATOM 6017 C ASN D 108 -21.096 59.378 -8.976 1.00 22.29
 C
 ATOM 6018 O ASN D 108 -21.565 60.261 -8.262 1.00 28.01
 O
 ATOM 6019 CB ASN D 108 -22.253 60.012 -11.103 1.00 25.10
 C

ATOM 12270 O GLY F 130 -3.425 37.224 6.147 1.00 14.67 O
 ATOM 12271 H GLY F 130 -1.273 38.496 2.775 1.00 18.18 H
 ATOM 12272 HA2 GLY F 130 -1.654 36.649 4.518 1.00 21.38 H
 ATOM 12273 HA3 GLY F 130 -1.007 38.048 4.832 1.00 21.38 H
 H
 ATOM 12274 N GLU F 131 -3.560 39.156 5.010 1.00 13.72 N
 ATOM 12275 CA GLU F 131 -4.732 39.598 5.751 1.00 18.76 C
 C
 ATOM 12276 C GLU F 131 -5.928 38.710 5.433 1.00 16.47 C
 ATOM 12277 O GLU F 131 -6.715 38.380 6.322 1.00 13.63 O
 ATOM 12278 CB GLU F 131 -5.052 41.056 5.440 1.00 19.73 C
 C
 ATOM 12279 CG GLU F 131 -6.078 41.653 6.382 1.00 26.43 C
 C

 ATOM 12280 CD GLU F 131 -6.202 43.154 6.229 1.00 27.13 C
 C
 ATOM 12281 OE1 GLU F 131 -5.568 43.715 5.309 1.00 19.31 O
 ATOM 12282 OE2 GLU F 131 -6.931 43.773 7.034 1.00 31.50 O1-
 O1-
 ATOM 12283 H GLU F 131 -3.285 39.709 4.412 1.00 16.47 H
 ATOM 12284 HA GLU F 131 -4.550 39.527 6.702 1.00 22.52 H
 ATOM 12285 HB2 GLU F 131 -4.239 41.579 5.514 1.00 23.68 H
 ATOM 12286 HB3 GLU F 131 -5.404 41.115 4.538 1.00 23.68 H
 ATOM 12287 HG2 GLU F 131 -6.945 41.260 6.196 1.00 31.71 H
 ATOM 12288 HG3 GLU F 131 -5.816 41.465 7.296 1.00 31.71 H
 H
 ATOM 12289 N ASP F 132 -6.067 38.318 4.169 1.00 15.33 N
 ATOM 12290 CA ASP F 132 -7.115 37.374 3.801 1.00 13.35 C
 C
 ATOM 12291 C ASP F 132 -6.949 36.086 4.596 1.00 14.58 C
 ATOM 12292 O ASP F 132 -7.918 35.557 5.137 1.00 15.18 O
 ATOM 12293 CB ASP F 132 -7.094 37.063 2.305 1.00 15.90 C
 C
 ATOM 12294 CG ASP F 132 -7.322 38.286 1.444 1.00 17.33 C
 C
 ATOM 12295 OD1 ASP F 132 -8.013 39.232 1.887 1.00 16.63 O
 ATOM 12296 OD2 ASP F 132 -6.809 38.292 0.308 1.00 18.06 O1-
 O1-
 ATOM 12297 H ASP F 132 -5.575 38.581 3.515 1.00 18.40 H
 ATOM 12298 HA ASP F 132 -7.980 37.756 4.018 1.00 16.02 H
 ATOM 12299 HB2 ASP F 132 -6.229 36.690 2.073 1.00 19.08 H
 ATOM 12300 HB3 ASP F 132 -7.794 36.422 2.107 1.00 19.08 H
 H
 ATOM 12301 N CYS F 133 -5.716 35.591 4.680 1.00 14.32 N
 ATOM 12302 CA CYS F 133 -5.449 34.328 5.364 1.00 14.59 C
 C
 ATOM 12303 C CYS F 133 -5.892 34.382 6.825 1.00 15.41 C
 ATOM 12304 O CYS F 133 -6.499 33.441 7.328 1.00 14.68 O
 ATOM 12305 CB CYS F 133 -3.964 33.968 5.286 1.00 18.53 C
 C
 ATOM 12306 SG CYS F 133 -3.547 32.418 6.119 1.00 24.44 S
 S
 ATOM 12307 H CYS F 133 -5.017 35.968 4.350 1.00 17.18 H
 ATOM 12308 HA CYS F 133 -5.951 33.622 4.927 1.00 17.51 H
 ATOM 12309 HB2 CYS F 133 -3.712 33.881 4.353 1.00 22.24 H
 ATOM 12310 HB3 CYS F 133 -3.448 34.677 5.702 1.00 22.24 H
 H
 ATOM 12311 N ILE F 134 -5.593 35.489 7.496 1.00 14.80 N
 ATOM 12312 CA ILE F 134 -5.980 35.661 8.890 1.00 12.54 C
 ATOM 12313 C ILE F 134 -7.507 35.701 9.031 1.00 14.20 C
 ATOM 12314 O ILE F 134 -8.068 35.120 9.957 1.00 14.69 O
 O

 ATOM 12315 CB ILE F 134 -5.370 36.952 9.483 1.00 14.54 C
 ATOM 12316 CG1 ILE F 134 -3.842 36.854 9.542 1.00 15.52 C
 C
 ATOM 12317 CG2 ILE F 134 -5.935 37.240 10.873 1.00 13.23 C
 C
 ATOM 12318 CD1 ILE F 134 -3.302 35.789 10.488 1.00 20.56 C
 C
 ATOM 12319 H ILE F 134 5.165 32.157 7.165 1.00 17.76 H

ATOM 6070 HD2 TYR D 111 -17.440 54.089 -2.162 1.00 24.91
H
ATOM 6071 HE1 TYR D 111 -18.064 54.885 -6.664 1.00 22.30
H
ATOM 6072 HE2 TYR D 111 -19.212 53.110 -3.267 1.00 21.42
H
ATOM 6073 HH TYR D 111 -19.863 53.553 -6.540 1.00 23.82
H
ATOM 6074 N GLN D 112 -14.190 57.329 -0.673 1.00 17.91
N
ATOM 6075 CA GLN D 112 -12.866 57.552 -0.119 1.00 20.98
C
ATOM 6076 C GLN D 112 -12.549 56.483 0.914 1.00 18.40
C
ATOM 6077 O GLN D 112 -13.417 56.045 1.668 1.00 17.57
O
ATOM 6078 CB GLN D 112 -12.750 58.949 0.496 1.00 23.03
C
ATOM 6079 CG GLN D 112 -11.326 59.331 0.905 1.00 24.86
C
ATOM 6080 CD GLN D 112 -10.317 59.175 -0.225 1.00 29.43
C
ATOM 6081 OE1 GLN D 112 -9.797 58.083 -0.469 1.00 32.59
O
ATOM 6082 NE2 GLN D 112 -10.033 60.270 -0.920 1.00 35.19
N
ATOM 6083 H GLN D 112 -14.747 56.965 -0.128 1.00 21.49
H
ATOM 6084 HA GLN D 112 -12.211 57.483 -0.831 1.00 25.18
H

ATOM 6085 HB2 GLN D 112 -13.057 59.602 -0.152 1.00 27.63
H
ATOM 6086 HB3 GLN D 112 -13.306 58.987 1.290 1.00 27.63
H
ATOM 6087 HG2 GLN D 112 -11.318 60.259 1.187 1.00 29.83
H
ATOM 6088 HG3 GLN D 112 -11.045 58.760 1.637 1.00 29.83
H
ATOM 6089 HE21 GLN D 112 -9.469 60.234 -1.568 1.00 42.23
H
ATOM 6090 HE22 GLN D 112 -10.414 61.015 -0.721 1.00 42.23
H
ATOM 6091 N PHE D 113 -11.293 56.059 0.921 1.00 15.24
N
ATOM 6092 CA PHE D 113 -10.808 55.082 1.878 1.00 19.47
C
ATOM 6093 C PHE D 113 -10.013 55.796 2.963 1.00 22.57
C
ATOM 6094 O PHE D 113 -9.202 56.673 2.676 1.00 23.44
O
ATOM 6095 CB PHE D 113 -9.955 54.026 1.172 1.00 25.43
C
ATOM 6096 CG PHE D 113 -10.730 53.179 0.198 1.00 22.13
C
ATOM 6097 CD1 PHE D 113 -11.227 53.727 -0.976 1.00 29.41
C
ATOM 6098 CD2 PHE D 113 -10.953 51.836 0.450 1.00 23.89
C
ATOM 6099 CE1 PHE D 113 -11.940 52.951 -1.877 1.00 30.31
C
ATOM 6100 CE2 PHE D 113 -11.666 51.054 -0.447 1.00 21.37
C
ATOM 6101 CZ PHE D 113 -12.160 51.613 -1.610 1.00 23.83
C
ATOM 6102 H PHE D 113 -10.692 56.330 0.369 1.00 18.29
H
ATOM 6103 HA PHE D 113 -11.562 54.637 2.294 1.00 23.37
H
ATOM 6104 HB2 PHE D 113 -9.247 54.472 0.681 1.00 30.51
H
ATOM 6105 HB3 PHE D 113 -9.571 53.436 1.839 1.00 30.51
H
ATOM 6106 HD1 PHE D 113 -11.084 54.627 -1.159 1.00 35.29
H
ATOM 6107 HD2 PHE D 113 -10.625 51.455 1.232 1.00 28.66
H
ATOM 6108 HE1 PHE D 113 -12.270 53.330 -2.659 1.00 36.37
H
ATOM 6109 HE2 PHE D 113 -11.812 50.154 -0.265 1.00 25.65
H
ATOM 6110 HZ PHE D 113 -12.637 51.089 -2.213 1.00 28.60
H
ATOM 6111 N PHE D 114 -10.275 55.420 4.209 1.00 21.22
N
ATOM 6112 CA PHE D 114 -9.633 56.027 5.368 1.00 22.84
C
ATOM 6113 C PHE D 114 -8.840 54.967 6.111 1.00 25.57
C
ATOM 6114 O PHE D 114 -9.409 53.987 6.590 1.00 20.97
O
ATOM 6115 CB PHE D 114 -10.682 56.665 6.280 1.00 25.74
C
ATOM 6116 CG PHE D 114 -11.434 57.787 5.629 1.00 22.57
C
ATOM 6117 CD1 PHE D 114 -12.523 57.530 4.817 1.00 23.79
C
ATOM 6118 CD2 PHE D 114 -11.041 59.102 5.819 1.00 30.88
C
ATOM 6119 CE1 PHE D 114 -13.208 58.562 4.209 1.00 26.61
C

ATOM 12370 CG LEU F 137 -6.696 31.348 11.597 1.00 17.25
C
ATOM 12371 CD1 LEU F 137 -6.909 29.855 11.775 1.00 21.45
C
ATOM 12372 CD2 LEU F 137 -5.239 31.707 11.858 1.00 16.99
C
ATOM 12373 H LEU F 137 -8.195 32.769 8.263 1.00 17.06
H
ATOM 12374 HA LEU F 137 -8.542 30.538 9.499 1.00 19.75
H
ATOM 12375 HB2 LEU F 137 -6.472 31.425 9.572 1.00 20.18
H
ATOM 12376 HB3 LEU F 137 -7.000 32.784 10.182 1.00 20.18
H
ATOM 12377 HG LEU F 137 -7.240 31.808 12.254 1.00 20.69
H
ATOM 12378 HD11 LEU F 137 -6.640 29.603 12.672 1.00 25.74
H
ATOM 12379 HD12 LEU F 137 -7.848 29.653 11.641 1.00 25.74
H
ATOM 12380 HD13 LEU F 137 -6.372 29.380 11.122 1.00 25.74
H
ATOM 12381 HD21 LEU F 137 -4.994 31.404 12.747 1.00 20.39
H
ATOM 12382 HD22 LEU F 137 -4.682 31.271 11.195 1.00 20.39
H
ATOM 12383 HD23 LEU F 137 -5.136 32.670 11.797 1.00 20.39
H
ATOM 12384 N ARG F 138 -9.817 33.006 11.100 1.00 15.78
N
ATOM 12385 CA ARG F 138 -10.767 33.360 12.147 1.00 21.48
C
ATOM 12386 C ARG F 138 -12.162 32.844 11.802 1.00 20.46
C
ATOM 12387 O ARG F 138 -12.903 32.389 12.676 1.00 17.61
O
ATOM 12388 CB ARG F 138 -10.791 34.875 12.353 1.00 20.11
C
ATOM 12389 CG ARG F 138 -9.496 35.437 12.926 1.00 22.32
C
ATOM 12390 CD ARG F 138 -9.536 36.954 13.003 1.00 22.66
C
ATOM 12391 NE ARG F 138 -10.564 37.424 13.925 1.00 25.37
N
ATOM 12392 CZ ARG F 138 -10.969 38.686 14.016 1.00 33.49
C
ATOM 12393 NH1 ARG F 138 -10.435 39.618 13.241 1.00 30.85
N1+
ATOM 12394 NH2 ARG F 138 -11.917 39.018 14.882 1.00 35.00
N
ATOM 12395 H ARG F 138 -9.477 33.681 10.690 1.00 18.94
H
ATOM 12396 HA ARG F 138 -10.490 32.948 12.979 1.00 25.77
H
ATOM 12397 HB2 ARG F 138 -10.948 35.305 11.498 1.00 24.13
H
ATOM 12398 HB3 ARG F 138 -11.507 35.096 12.969 1.00 24.13
H
ATOM 12399 HG2 ARG F 138 -9.364 35.090 13.822 1.00 26.78
H
ATOM 12400 HG3 ARG F 138 -8.755 35.181 12.354 1.00 26.78
H
ATOM 12401 HD2 ARG F 138 -8.678 37.281 13.315 1.00 27.20
H
ATOM 12402 HD3 ARG F 138 -9.731 37.313 12.123 1.00 27.20
H
ATOM 12403 HE ARG F 138 -10.932 36.845 14.443 1.00 30.44
H
ATOM 12404 HH11 ARG F 138 -9.821 39.407 12.676 1.00 37.02
H
ATOM 12405 HH12 ARG F 138 -10.700 40.433 13.303 1.00 37.02
H
ATOM 12406 HH21 ARG F 138 -12.267 38.417 15.388 1.00 42.00
H
ATOM 12407 HH22 ARG F 138 -12.178 39.836 14.942 1.00 42.00
H
ATOM 12408 N SER F 139 -12.505 32.898 10.520 1.00 17.64
N
ATOM 12409 CA SER F 139 -13.798 32.413 10.056 1.00 19.10
C
ATOM 12410 C SER F 139 -13.890 30.893 10.165 1.00 20.53
C
ATOM 12411 O SER F 139 -14.945 30.348 10.492 1.00 20.71
O
ATOM 12412 CB SER F 139 -14.042 32.855 8.613 1.00 21.03
C
ATOM 12413 OG SER F 139 -14.120 34.266 8.526 1.00 16.92
O
ATOM 12414 H SER F 139 -12.003 33.212 9.896 1.00 21.17
H
ATOM 12415 HA SER F 139 -14.496 32.797 10.609 1.00 22.92
H
ATOM 12416 HB2 SER F 139 -13.308 32.545 8.059 1.00 25.24
H
ATOM 12417 HB3 SER F 139 -14.877 32.473 8.302 1.00 25.24
H
ATOM 12418 HG SER F 139 -13.402 34.611 8.793 1.00 20.30
H
ATOM 12419 N LEU F 140 -12.783 30.210 9.897 1.00 17.28
N

ATOM 6120 CE2 PHE D 114 -11.723 60.139 5.214 1.00 23.44
 C
 ATOM 6121 CZ PHE D 114 -12.809 59.869 4.409 1.00 28.06
 C
 ATOM 6122 H PHE D 114 -10.835 54.801 4.413 1.00 25.46
 H
 ATOM 6123 HA PHE D 114 -9.020 56.719 5.073 1.00 27.40
 H
 ATOM 6124 HB2 PHE D 114 -11.325 55.987 6.540 1.00 30.89
 H
 ATOM 6125 HB3 PHE D 114 -10.240 57.019 7.067 1.00 30.89
 H
 ATOM 6126 HD1 PHE D 114 -12.796 56.652 4.678 1.00 28.55
 H
 ATOM 6127 HD2 PHE D 114 -10.308 59.288 6.361 1.00 37.05
 H
 ATOM 6128 HE1 PHE D 114 -13.941 58.378 3.667 1.00 31.94
 H
 ATOM 6129 HE2 PHE D 114 -11.451 61.018 5.351 1.00 28.13
 H
 ATOM 6130 HZ PHE D 114 -13.271 60.565 4.001 1.00 33.67
 H
 ATOM 6131 N ASP D 115 -7.526 55.161 6.199 1.00 23.12
 N
 ATOM 6132 CA ASP D 115 -6.645 54.131 6.737 1.00 26.22
 C
 ATOM 6133 C ASP D 115 -6.365 54.317 8.228 1.00 30.31
 C
 ATOM 6134 O ASP D 115 -5.656 53.516 8.831 1.00 25.41
 O
 ATOM 6135 CB ASP D 115 -5.328 54.096 5.957 1.00 27.72
 C
 ATOM 6136 CG ASP D 115 -4.615 55.436 5.940 1.00 34.76
 C
 ATOM 6137 OD1 ASP D 115 -5.100 56.389 6.587 1.00 33.82
 O
 ATOM 6138 OD2 ASP D 115 -3.558 55.530 5.282 1.00 32.71
 O1-
 ATOM 6139 H ASP D 115 -7.122 55.879 5.954 1.00 27.74
 H
 ATOM 6140 HA ASP D 115 -7.075 53.269 6.626 1.00 31.46
 H
 ATOM 6141 HB2 ASP D 115 -4.735 53.447 6.367 1.00 33.26
 H
 ATOM 6142 HB3 ASP D 115 -5.512 53.843 5.039 1.00 33.26
 H
 ATOM 6143 N GLU D 116 -6.920 55.373 8.817 1.00 29.51
 N
 ATOM 6144 CA GLU D 116 -6.821 55.578 10.259 1.00 35.02
 C
 ATOM 6145 C GLU D 116 -7.960 54.814 10.921 1.00 33.34
 C
 ATOM 6146 O GLU D 116 -9.096 55.282 10.940 1.00 33.54
 O
 ATOM 6147 CB GLU D 116 -6.860 57.067 10.624 1.00 38.38
 C
 ATOM 6148 CG GLU D 116 -5.921 57.960 9.836 1.00 42.91
 C
 ATOM 6149 CD GLU D 116 -8.444 58.351 8.458 1.00 44.87
 C
 ATOM 6150 OE1 GLU D 116 -7.627 58.078 8.155 1.00 38.52
 O
 ATOM 6151 OE2 GLU D 116 -5.664 58.934 7.673 1.00 52.44
 O1-
 ATOM 6152 H GLU D 116 -7.360 55.986 8.404 1.00 35.41
 H
 ATOM 6153 HA GLU D 116 -5.980 55.216 10.580 1.00 42.03
 H
 ATOM 6154 HB2 GLU D 116 -7.781 57.389 10.462 1.00 46.06
 H

ATOM 6155 HB3 GLU D 116 -6.665 57.163 11.565 1.00 46.06
 H
 ATOM 6156 HG2 GLU D 116 -5.768 58.775 10.338 1.00 51.49
 H
 ATOM 6157 HG3 GLU D 116 -5.083 57.487 9.712 1.00 51.49
 H
 ATOM 6158 N SER D 117 -7.650 53.636 11.457 1.00 30.25
 N
 ATOM 6159 CA SER D 117 -8.674 52.697 11.907 1.00 27.86
 C
 ATOM 6160 C SER D 117 -9.509 53.219 13.077 1.00 33.38
 C
 ATOM 6161 O SER D 117 -8.988 53.810 14.022 1.00 30.47
 O
 ATOM 6162 CB SER D 117 -8.028 51.365 12.297 1.00 31.01
 C
 ATOM 6163 OG SER D 117 -7.150 51.529 13.392 1.00 34.10
 O
 ATOM 6164 H SER D 117 -6.845 53.355 11.571 1.00 36.30
 H
 ATOM 6165 HA SER D 117 -9.279 52.525 11.169 1.00 33.44
 H
 ATOM 6166 HB2 SER D 117 -8.725 50.737 12.543 1.00 37.21
 H
 ATOM 6167 HB3 SER D 117 -7.527 51.024 11.539 1.00 37.21
 H
 ATOM 6168 HG SER D 117 -6.803 50.792 13.595 1.00 40.92
 H

ATOM 12420 CA LEU F 140 -12.766 28.753 9.949 1.00 20.30
 C
 ATOM 12421 C LEU F 140 -12.769 28.260 11.394 1.00 21.22
 C
 ATOM 12422 O LEU F 140 -13.346 27.216 11.695 1.00 23.85
 O
 ATOM 12423 CB LEU F 140 -11.554 28.201 9.195 1.00 21.20
 C
 ATOM 12424 CG LEU F 140 -11.611 28.339 7.669 1.00 20.22
 C
 ATOM 12425 CD1 LEU F 140 -10.258 28.037 7.052 1.00 19.97
 C
 ATOM 12426 CD2 LEU F 140 -12.680 27.431 7.075 1.00 21.22
 C
 ATOM 12427 H LEU F 140 -12.030 30.565 9.682 1.00 20.74
 H
 ATOM 12428 HA LEU F 140 -13.566 28.415 9.517 1.00 24.37
 H
 ATOM 12429 HB2 LEU F 140 -10.762 28.671 9.500 1.00 25.44
 H
 ATOM 12430 HB3 LEU F 140 -11.469 27.257 9.399 1.00 25.44
 H
 ATOM 12431 HG LEU F 140 -11.841 29.254 7.446 1.00 24.27
 H
 ATOM 12432 HD11 LEU F 140 -10.323 28.132 6.086 1.00 23.96
 H
 ATOM 12433 HD12 LEU F 140 -9.605 28.662 7.402 1.00 23.96
 H
 ATOM 12434 HD13 LEU F 140 -10.003 27.129 7.279 1.00 23.96
 H
 ATOM 12435 HD21 LEU F 140 -12.689 27.542 6.112 1.00 25.46
 H
 ATOM 12436 HD22 LEU F 140 -12.473 26.510 7.300 1.00 25.46
 H
 ATOM 12437 HD23 LEU F 140 -13.543 27.676 7.445 1.00 25.46
 H
 ATOM 12438 N VAL F 141 -12.132 29.008 12.288 1.00 19.00
 N
 ATOM 12439 CA VAL F 141 -12.164 28.668 13.704 1.00 23.28
 C
 ATOM 12440 C VAL F 141 -13.590 28.802 14.237 1.00 25.21
 C
 ATOM 12441 O VAL F 141 -14.020 28.017 15.081 1.00 24.34
 O
 ATOM 12442 CB VAL F 141 -11.210 29.556 14.528 1.00 19.95
 C
 ATOM 12443 CG1 VAL F 141 -11.452 29.377 16.024 1.00 26.02
 C
 ATOM 12444 CG2 VAL F 141 -9.758 29.225 14.198 1.00 24.20
 C
 ATOM 12445 H VAL F 141 -11.678 29.714 12.101 1.00 22.80
 H
 ATOM 12446 HA VAL F 141 -11.886 27.745 13.814 1.00 27.94
 H
 ATOM 12447 HB VAL F 141 -11.367 30.487 14.305 1.00 23.94
 H
 ATOM 12448 HG11 VAL F 141 -10.838 29.947 16.514 1.00 31.23
 H
 ATOM 12449 HG12 VAL F 141 -12.368 29.624 16.227 1.00 31.23
 H
 ATOM 12450 HG13 VAL F 141 -11.300 28.448 16.259 1.00 31.23
 H
 ATOM 12451 HG21 VAL F 141 -9.177 29.794 14.727 1.00 29.04
 H
 ATOM 12452 HG22 VAL F 141 -9.591 28.293 14.410 1.00 29.04
 H
 ATOM 12453 HG23 VAL F 141 -9.605 29.382 13.253 1.00 29.04
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 ATOM 12454 N ARG F 142 -14.315 29.802 13.745 1.00 21.37
 N

ATOM 12455 CA ARG F 142 -15.718 29.978 14.107 1.00 23.25
 C
 ATOM 12456 C ARG F 142 -16.534 28.742 13.722 1.00 30.62
 C
 ATOM 12457 O ARG F 142 -17.319 28.235 14.525 1.00 27.61
 O
 ATOM 12458 CB ARG F 142 -16.286 31.230 13.436 1.00 28.79
 C
 ATOM 12459 CG ARG F 142 -17.776 31.456 13.656 1.00 34.59
 C
 ATOM 12460 CD ARG F 142 -18.109 31.669 15.122 1.00 36.74
 C
 ATOM 12461 NE ARG F 142 -19.526 31.963 15.311 1.00 43.29
 N
 ATOM 12462 CZ ARG F 142 -20.073 33.164 15.149 1.00 47.11
 C
 ATOM 12463 NH1 ARG F 142 -19.325 34.201 14.794 1.00 40.67
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 ATOM 12464 NH2 ARG F 142 -21.373 33.330 15.342 1.00 53.09
 N
 ATOM 12465 H ARG F 142 -14.017 30.395 13.197 1.00 25.65
 H
 ATOM 12466 HA ARG F 142 -15.785 30.095 15.068 1.00 27.90
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 ATOM 12467 HB2 ARG F 142 -15.818 32.006 13.782 1.00 34.55
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 ATOM 12468 HB3 ARG F 142 -16.138 31.161 12.479 1.00 34.55
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DK/EP 3233192 T3

H
ATOM 6265 N SER D 123 -16.486 55.436 12.848 1.00 21.52
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ATOM 6266 CA SER D 123 -16.412 55.419 11.391 1.00 23.20
C
ATOM 6267 C SER D 123 -17.680 56.030 10.804 1.00 23.42
C
ATOM 6268 O SER D 123 -17.620 56.862 9.898 1.00 20.31
O
ATOM 6269 CB SER D 123 -16.216 53.993 10.871 1.00 21.62
C
ATOM 6270 OG SER D 123 -14.982 53.454 11.306 1.00 19.63
O
ATOM 6271 H SER D 123 -16.512 54.655 13.208 1.00 25.82
H
ATOM 6272 HA SER D 123 -15.856 55.954 11.103 1.00 27.84
H
ATOM 6273 HB2 SER D 123 -16.938 53.435 11.202 1.00 25.94
H
ATOM 6274 HB3 SER D 123 -16.229 54.007 9.901 1.00 25.94
H
ATOM 6275 HG SER D 123 -14.957 53.434 12.146 1.00 23.55
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ATOM 6276 N GLN D 124 -18.827 55.611 11.331 1.00 20.37
N
ATOM 6277 CA GLN D 124 -20.107 56.170 10.922 1.00 24.01
C
ATOM 6278 C GLN D 124 -20.123 57.683 11.103 1.00 25.04
C
ATOM 6279 O GLN D 124 -20.549 58.420 10.214 1.00 21.92
O
ATOM 6280 CB GLN D 124 -21.238 55.534 11.725 1.00 28.29
C
ATOM 6281 CG GLN D 124 -22.605 56.135 11.471 1.00 32.29
C
ATOM 6282 CD GLN D 124 -23.667 55.497 12.338 1.00 34.18
C
ATOM 6283 OE1 GLN D 124 -23.490 55.356 13.549 1.00 37.41
O
ATOM 6284 NE2 GLN D 124 -24.773 55.089 11.722 1.00 37.93
N
ATOM 6285 H GLN D 124 -18.888 55.000 11.933 1.00 24.45
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ATOM 6286 HA GLN D 124 -20.255 55.975 9.983 1.00 28.81
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ATOM 6287 HB2 GLN D 124 -21.284 54.591 11.501 1.00 33.95
H
ATOM 6288 HB3 GLN D 124 -21.042 55.636 12.669 1.00 33.95
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ATOM 6289 HG2 GLN D 124 -22.579 57.033 11.672 1.00 38.75
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ATOM 6290 HG3 GLN D 124 -22.848 55.995 10.543 1.00 38.75
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ATOM 6291 HE21 GLN D 124 -25.405 54.720 12.174 1.00 45.51
H
ATOM 6292 HE22 GLN D 124 -24.855 55.194 10.873 1.00 45.51
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ATOM 6293 N ALA D 125 -19.652 58.135 12.260 1.00 25.98
N
ATOM 6294 CA ALA D 125 -19.640 59.555 12.584 1.00 27.07
C

ATOM 6295 C ALA D 125 -18.721 60.311 11.636 1.00 24.27
C
ATOM 6296 O ALA D 125 -19.057 61.397 11.168 1.00 27.08
O
ATOM 6297 CB ALA D 125 -19.207 59.766 14.027 1.00 26.32
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ATOM 6298 H ALA D 125 -19.331 57.633 12.880 1.00 31.18
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ATOM 6299 HA ALA D 125 -20.537 59.912 12.483 1.00 32.48
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ATOM 6300 HB1 ALA D 125 -19.206 60.716 14.221 1.00 31.59
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HETATM12604 O HOH A 303 -26.938 32.739 -45.146 1.00 27.98
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HETATM12605 O HOH A 304 -26.382 16.536 -35.436 1.00 35.92
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HETATM12606 O HOH A 305 -19.043 4.283 -27.862 1.00 40.38
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HETATM12608 O HOH A 307 -13.369 10.269 -60.520 1.00 31.03
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HETATM12609 O HOH A 308 -19.209 3.822 -43.074 1.00 38.43
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HETATM12610 O HOH A 309 -23.006 34.055 -48.572 1.00 21.85
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HETATM12611 O HOH A 310 -13.086 4.848 -49.321 1.00 25.83
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HETATM12612 O HOH A 311 -26.139 21.686 -35.299 1.00 30.33
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HETATM12613 O HOH A 312 -28.024 21.488 -43.474 1.00 27.79

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ATOM 12565 HA LYS F 148 -21.964 20.071 17.211 1.00 72.30
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ATOM 12566 HB2 LYS F 148 -23.268 18.980 14.962 1.00 67.50
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ATOM 12567 HB3 LYS F 148 -23.866 19.091 16.426 1.00 67.50
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ATOM 12568 HG2 LYS F 148 -23.325 21.542 15.336 1.00 77.61
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ATOM 12569 HG3 LYS F 148 -24.431 20.736 14.525 1.00 77.61
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ATOM 12570 HD2 LYS F 148 -25.788 20.632 16.361 1.00 85.44
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ATOM 12571 HD3 LYS F 148 -24.645 21.234 17.292 1.00 85.44
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ATOM 12572 HE2 LYS F 148 -25.877 22.701 15.219 1.00 92.19
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ATOM 12573 HE3 LYS F 148 -26.277 22.850 16.752 1.00 92.19
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ATOM 12574 HZ1 LYS F 148 -23.822 23.524 15.749 1.00 90.72
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ATOM 12575 HZ2 LYS F 148 -24.826 24.491 16.145 1.00 90.72
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ATOM 12576 HZ3 LYS F 148 -24.187 23.660 17.145 1.00 90.72
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ATOM 12577 N ARG F 149 -19.938 18.236 16.295 1.00 62.51
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ATOM 12578 CA ARG F 149 -19.219 16.968 16.305 1.00 65.70
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ATOM 12579 C ARG F 149 -17.746 17.180 16.640 1.00 70.51
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ATOM 12580 O ARG F 149 -17.410 17.671 17.718 1.00 79.82
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ATOM 12581 CB ARG F 149 -19.361 16.277 14.948 1.00 59.09
C
ATOM 12582 CG ARG F 149 -18.637 14.951 14.834 1.00 53.79
C
ATOM 12583 CD ARG F 149 -18.960 14.289 13.514 1.00 43.18
C
ATOM 12584 NE ARG F 149 -18.021 13.226 13.181 1.00 43.60
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ATOM 12585 CZ ARG F 149 -18.019 12.580 12.021 1.00 40.65
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ATOM 12586 NH1 ARG F 149 -18.915 12.894 11.095 1.00 30.30
N1+
ATOM 12587 NH2 ARG F 149 -17.125 11.627 11.791 1.00 40.71
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ATOM 12588 H ARG F 149 -19.434 18.921 16.169 1.00 75.01
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ATOM 12589 HA ARG F 149 -19.603 16.389 16.982 1.00 78.85
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ATOM 12590 HB2 ARG F 149 -20.303 16.112 14.782 1.00 70.91
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ATOM 12591 HB3 ARG F 149 -19.007 16.865 14.263 1.00 70.91
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ATOM 12592 HG2 ARG F 149 -17.679 15.101 14.877 1.00 64.55
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ATOM 12593 HG3 ARG F 149 -18.921 14.363 15.551 1.00 64.55
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ATOM 12594 HD2 ARG F 149 -19.848 13.902 13.562 1.00 51.81
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ATOM 12595 HD3 ARG F 149 -18.925 14.954 12.808 1.00 51.81
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ATOM 12596 HE ARG F 149 -17.372 13.078 13.725 1.00 52.32
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ATOM 12597 HH11 ARG F 149 -19.492 13.514 11.246 1.00 36.36
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ATOM 12598 HH12 ARG F 149 -18.919 12.478 10.342 1.00 36.36
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ATOM 12599 HH21 ARG F 149 -16.546 11.425 12.394 1.00 48.86
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ATOM 12600 HH22 ARG F 149 -17.127 11.207 11.040 1.00 48.86
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HETATM12933 O HOH D 370 -13.314 41.381 16.992 1.00 38.82
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HETATM12934 O HOH D 371 -12.620 44.975 19.857 1.00 38.87
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HETATM12935 O HOH D 372 -34.361 45.041 6.117 1.00 40.66
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HETATM12936 O HOH D 373 -19.902 30.159 10.064 1.00 39.21
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HETATM12937 O HOH D 374 -19.665 42.831 -10.863 1.00 37.18
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HETATM12938 O HOH D 375 -26.348 36.818 9.412 1.00 40.39
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HETATM12939 O HOH D 376 -4.888 48.505 8.181 1.00 40.81
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HETATM12940 O HOH D 377 -38.516 50.575 6.009 1.00 40.44
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HETATM12941 O HOH D 378 -20.538 43.117 -13.094 1.00 39.95
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HETATM12942 O HOH D 379 -19.702 45.502 -14.659 1.00 39.92
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HETATM12943 O HOH D 380 -5.678 50.415 4.198 1.00 39.75
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HETATM12944 O HOH D 381 -30.979 39.861 1.528 1.00 41.67

DK/EP 3233192 T3

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 HETATM12615 O HOH A 314 -24.877 25.289 -37.453 1.00 23.03
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 HETATM12616 O HOH A 315 -23.432 2.197 -46.149 1.00 45.83
 O
 HETATM12617 O HOH A 316 -15.724 4.062 -48.517 1.00 31.61
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 HETATM12618 O HOH A 317 -2.800 10.432 -52.680 1.00 44.34
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 HETATM12619 O HOH A 318 -6.188 13.669 -60.812 1.00 40.71
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 HETATM12620 O HOH A 319 -17.985 34.899 -42.506 1.00 31.50
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 HETATM12621 O HOH A 320 -28.621 20.922 -40.469 1.00 33.98
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 HETATM12622 O HOH A 321 -18.645 2.611 -46.685 1.00 37.54
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 HETATM12623 O HOH A 322 -16.885 31.002 -38.916 1.00 34.95
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 HETATM12626 O HOH A 325 -25.288 14.441 -48.620 1.00 43.09
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 HETATM12636 O HOH A 335 -12.122 33.154 -42.888 1.00 16.62
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 HETATM12646 O HOH A 345 -26.536 23.160 -45.165 1.00 23.77
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 HETATM12647 O HOH A 346 -19.582 22.927 -55.390 1.00 23.00
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 HETATM12648 O HOH A 347 -16.406 39.317 -52.362 1.00 24.48
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 HETATM12649 O HOH A 348 -19.870 13.559 -61.687 1.00 25.43
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 HETATM12651 O HOH A 350 -25.211 15.985 -50.444 1.00 26.75
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 HETATM12661 O HOH A 360 -19.674 31.626 -42.674 1.00 30.26
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 HETATM12978 O HOH E 219 12.831 35.059 -42.689 1.00 35.03
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 HETATM12979 O HOH E 220 24.777 35.876 -39.786 1.00 29.06
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 HETATM12980 O HOH E 221 6.701 51.104 -45.448 1.00 33.91
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 HETATM12981 O HOH E 222 12.353 56.858 -41.891 1.00 27.59
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 HETATM12984 O HOH E 225 7.373 32.445 -56.036 1.00 21.09
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 HETATM12985 O HOH E 226 20.215 35.480 -46.604 1.00 39.99
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 HETATM12986 O HOH E 227 0.274 42.725 -65.832 1.00 45.95
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 HETATM12987 O HOH E 228 20.314 50.527 -35.492 1.00 41.02
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 HETATM12988 O HOH E 229 -13.880 51.341 -57.551 1.00 16.07
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 HETATM12989 O HOH E 230 -9.877 56.257 -54.396 1.00 38.99
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 HETATM12990 O HOH E 231 19.372 46.521 -43.375 1.00 36.47
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 HETATM12991 O HOH E 232 10.082 46.364 -50.427 1.00 33.92
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 HETATM12992 O HOH E 233 -4.763 40.408 -66.546 1.00 29.64
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 HETATM12665 O HOH A 364 -11.637 19.556 -66.569 1.00 33.87
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 HETATM12669 O HOH A 368 -10.425 25.413 -65.962 1.00 35.77
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 HETATM12670 O HOH A 369 -9.161 5.879 -39.249 1.00 34.25
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 HETATM12671 O HOH A 370 -18.300 10.506 -31.994 1.00 36.35
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 HETATM12680 O HOH A 379 -16.419 2.684 -23.261 1.00 44.81
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 HETATM12698 O HOH B 307 8.535 29.943 -42.456 1.00 25.29
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 HETATM12699 O HOH B 308 17.183 22.927 -33.325 1.00 30.12
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 HETATM13012 O HOH E 253 4.438 36.255 -30.141 1.00 19.18
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 HETATM13023 O HOH E 264 20.395 43.071 -35.226 1.00 22.50
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 HETATM13025 O HOH E 266 5.948 37.514 -57.958 1.00 22.22
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HETATM12710	O	HOH B 319	-5.064	28.662	-33.402	1.00	14.84
HETATM12711	O	HOH B 320	-0.641	25.295	-40.104	1.00	16.14
HETATM12712	O	HOH B 321	-11.520	28.571	-23.818	1.00	16.31
HETATM12713	O	HOH B 322	-3.374	9.071	-36.835	1.00	18.45
HETATM12714	O	HOH B 323	-0.055	32.309	-17.018	1.00	18.39
HETATM12715	O	HOH B 324	3.189	33.018	-20.171	1.00	18.28
HETATM12716	O	HOH B 325	-5.716	23.544	-31.680	1.00	17.51
HETATM12717	O	HOH B 326	-7.778	25.335	-32.190	1.00	20.77
HETATM12718	O	HOH B 327	5.182	11.904	-26.234	1.00	22.76
HETATM12719	O	HOH B 328	0.569	16.085	-21.723	1.00	23.02
HETATM12720	O	HOH B 329	0.937	31.798	-19.549	1.00	24.18
HETATM12721	O	HOH B 330	-13.021	20.020	-31.614	1.00	24.50
HETATM12722	O	HOH B 331	3.995	14.352	-26.698	1.00	23.37
HETATM12723	O	HOH B 332	14.224	30.035	-32.640	1.00	25.70
HETATM12724	O	HOH B 333	-7.490	27.848	-33.238	1.00	25.54
HETATM12725	O	HOH B 334	-5.169	21.656	-16.578	1.00	30.03
HETATM12726	O	HOH B 335	16.448	28.602	-29.252	1.00	32.34
HETATM12727	O	HOH B 336	-9.952	24.998	-25.300	1.00	30.97
HETATM12728	O	HOH B 337	9.267	11.535	-33.926	1.00	30.70
HETATM12729	O	HOH B 338	8.054	17.921	-19.843	1.00	30.34
HETATM12730	O	HOH B 339	7.164	34.418	-24.473	1.00	30.85
HETATM12731	O	HOH B 340	11.232	14.303	-23.072	1.00	32.23
HETATM12732	O	HOH B 341	8.410	19.631	-43.642	1.00	31.16
HETATM12733	O	HOH B 342	4.481	10.919	-23.082	1.00	32.72
HETATM12734	O	HOH B 343	-7.870	31.981	-24.993	1.00	31.40

HETATM12735	O	HOH B 344	-3.840	23.475	-17.848	1.00	31.75
HETATM12736	O	HOH B 345	2.532	18.248	-47.620	1.00	33.84
HETATM12737	O	HOH B 346	13.735	7.524	-29.443	1.00	34.06
HETATM12738	O	HOH B 347	-14.962	17.976	-30.150	1.00	32.26
HETATM12739	O	HOH B 348	4.136	23.700	-46.211	1.00	32.83
HETATM12740	O	HOH B 349	-2.426	11.269	-17.697	1.00	35.49
HETATM12741	O	HOH B 350	-13.944	14.462	-24.392	1.00	33.38
HETATM12742	O	HOH B 351	-3.090	28.155	-43.632	1.00	30.23
HETATM12743	O	HOH B 352	-1.055	8.052	-26.335	1.00	34.44
HETATM12744	O	HOH B 353	8.522	8.421	-33.424	1.00	35.00
HETATM12745	O	HOH B 354	-17.059	10.653	-29.833	1.00	35.53
HETATM12746	O	HOH B 355	11.635	34.307	-26.685	1.00	35.41
HETATM12747	O	HOH B 356	6.262	34.779	-33.537	1.00	33.96
HETATM12748	O	HOH B 357	-8.415	3.584	-36.360	1.00	36.83
HETATM12749	O	HOH B 358	-9.995	6.919	-24.630	1.00	37.21
HETATM12750	O	HOH B 359	-14.513	11.209	-22.723	1.00	36.93
HETATM12751	O	HOH B 360	-8.537	24.316	-23.199	1.00	36.37
HETATM12752	O	HOH B 361	-1.440	31.437	-20.936	1.00	34.91
HETATM12753	O	HOH B 362	8.698	7.570	-35.879	1.00	36.82
HETATM12754	O	HOH B 363	2.994	20.628	-17.252	1.00	34.26
HETATM12755	O	HOH B 364	3.214	9.908	-26.806	1.00	37.49
HETATM12756	O	HOH B 365	12.116	14.910	-38.546	1.00	35.59
HETATM12757	O	HOH B 366	4.147	6.848	-30.946	1.00	37.66

HETATM13040	O	HOH E 281	9.133	43.203	-24.913	1.00	23.31
HETATM13041	O	HOH E 282	-0.022	28.496	-54.254	1.00	26.47
HETATM13042	O	HOH E 283	-10.823	36.928	-60.637	1.00	26.82
HETATM13043	O	HOH E 284	-2.121	28.455	-41.577	1.00	24.93
HETATM13044	O	HOH E 285	-5.464	33.520	-33.616	1.00	27.31
HETATM13045	O	HOH E 286	-17.829	45.581	-57.484	1.00	28.74
HETATM13046	O	HOH E 287	-4.493	36.679	-63.305	1.00	27.08
HETATM13047	O	HOH E 288	1.016	28.462	-51.948	1.00	27.71
HETATM13048	O	HOH E 289	-3.511	35.823	-36.227	1.00	28.06
HETATM13049	O	HOH E 290	-16.812	41.433	-50.490	1.00	28.24
HETATM13050	O	HOH E 291	0.187	46.054	-31.298	1.00	28.00
HETATM13051	O	HOH E 292	-5.426	31.215	-32.437	1.00	28.84
HETATM13052	O	HOH E 293	0.502	29.144	-42.913	1.00	27.70
HETATM13053	O	HOH E 294	-4.808	29.865	-54.597	1.00	27.78
HETATM13054	O	HOH E 295	22.421	43.427	-39.132	1.00	30.32
HETATM13055	O	HOH E 296	11.179	42.696	-53.972	1.00	30.80
HETATM13056	O	HOH E 297	-2.214	45.207	-32.541	1.00	28.97
HETATM13057	O	HOH E 298	-1.764	28.823	-59.641	1.00	29.72
HETATM13058	O	HOH E 299	-3.429	31.385	-31.382	1.00	29.67
HETATM13059	O	HOH E 300	11.117	49.531	-28.997	1.00	31.74
HETATM13060	O	HOH E 301	-4.127	34.263	-64.552	1.00	30.14
HETATM13061	O	HOH E 302	-0.485	44.239	-61.488	1.00	31.15
HETATM13062	O	HOH E 303	-14.393	43.942	-38.116	1.00	31.07
HETATM13063	O	HOH E 304	2.566	47.641	-53.345	1.00	30.24
HETATM13064	O	HOH E 305	4.512	40.888	-59.410	1.00	32.48
HETATM13065	O	HOH E 306	-11.173	37.034	-38.891	1.00	31.40

HETATM13066	O	HOH E 307	12.095	51.302	-27.196	1.00	31.96
HETATM13067	O	HOH E 308	19.773	49.195	-41.917	1.00	32.90
HETATM13068	O	HOH E 309	11.250	37.355	-52.662	1.00	33.58
HETATM13069	O	HOH E 310	2.614	47.673	-32.320	1.00	32.65
HETATM13070	O	HOH E 311	-6.447	53.782	-54.513	1.00	33.00
HETATM13071	O	HOH E 312	3.910	32.129	-67.637	1.00	34.32
HETATM13072	O	HOH E 313	-14.244	45.353	-35.552	1.00	33.15
HETATM13073	O	HOH E 314	-18.235	33.767	-59.082	1.00	36.30
HETATM13074	O	HOH E 315	-9.409	34.823	-61.574	1.00	32.98
HETATM13075	O	HOH E 316	-7.834	46.259	-34.483	1.00	33.62
HETATM13076	O	HOH E 317	-6.143	54.995	-42.264	1.00	35.37
HETATM13077	O	HOH E 318	21.026	47.280	-36.350	1.00	34.72
HETATM13078	O	HOH E 319	15.659	38.724	-31.069	1.00	34.44
HETATM13079	O	HOH E 320	-5.651	56.934	-39.702	1.00	35.54
HETATM13080	O	HOH E 321	15.208	36.049	-33.692	1.00	33.34
HETATM13081	O	HOH E 322	13.888	41.711	-52.696	1.00	36.49
HETATM13082	O	HOH E 323	12.233	50.136	-31.246	1.00	35.94
HETATM13083	O	HOH E 324	-4.570	44.952	-31.061	1.00	36.45
HETATM13084	O	HOH E 325	15.080	38.473	-51.092	1.00	38.07
HETATM13085	O	HOH E 326	3.345	29.845	-50.391	1.00	36.20
HETATM13086	O	HOH E 327	-6.582	36.254	-37.028	1.00	34.54
HETATM13087	O	HOH E 328	-6.625	47.890	-58.536	1.00	35.70
HETATM13088	O	HOH E 329	21.296	41.812	-37.662	1.00	36.82

DK/EP 3233192 T3

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KRUPNICK, Alexander S.

LAZEAR, Eric R.

FREMONT, Daved H.

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Asn Pro Lys Leu Thr Ala Met Leu Thr Lys Lys Phe Tyr Met Pro Lys
35 40 45

Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu Glu Glu Leu Lys
50 55 60

Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu
65 70 75 80

Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile Val Leu Glu Leu
85 90 95

Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala Asp Glu Thr Ala
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Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Ser Gln Ser Ile
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Ile Ser Thr Leu Thr
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<211> 151

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<213> Artificial Sequence

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His Ser Thr Val Asp Val Tyr Leu Asp Asp Ser Gln Ile Ile Thr Phe
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Asp Gly Lys Asp Ile Arg Pro Thr Ile Pro Phe Met Ile Gly Asp Glu
35 40 45

Ile Phe Leu Pro Phe Tyr Lys Asn Val Phe Ser Glu Phe Phe Ser Leu
50 55 60

Phe Arg Arg Val Pro Thr Ser Thr Pro Tyr Glu Asp Leu Thr Tyr Phe
65 70 75 80

Tyr Glu Cys Asp Tyr Thr Asp Asn Lys Ser Thr Phe Asp Gln Phe Tyr
85 90 95

Leu Tyr Asn Gly Glu Glu Tyr Thr Val Lys Thr Gln Glu Ala Thr Asn
100 105 110

Lys Asn Met Trp Leu Thr Thr Ser Glu Phe Arg Leu Lys Lys Trp Phe
 115 120 125

Asp Gly Glu Asp Cys Ile Met His Leu Arg Ser Leu Val Arg Lys Met
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Glu Asp Ser Lys Arg Asn Thr
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<211> 28

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<213> Artificial Sequence

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<213> Cowpox virus

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			20					25					30		

Phe	Asp	Gly	Lys	Asp	Ile	Arg	Pro	Thr	Ile	Pro	Phe	Met	Ile	Gly	Asp
		35					40					45			

Glu	Ile	Phe	Leu	Pro	Phe	Tyr	Lys	Asn	Val	Phe	Ser	Glu	Phe	Phe	Ser
	50					55					60				

Leu	Phe	Arg	Arg	Val	Pro	Thr	Ser	Thr	Pro	Tyr	Glu	Asp	Leu	Thr	Tyr
65					70					75					80

Phe	Tyr	Glu	Cys	Asp	Tyr	Thr	Asp	Asn	Lys	Ser	Thr	Phe	Asp	Gln	Phe
				85					90					95	

Tyr	Leu	Tyr	Asn	Gly	Glu	Glu	Tyr	Thr	Val	Lys	Thr	Gln	Glu	Ala	Thr
			100					105					110		

Asn	Lys	Asn	Met	Trp	Leu	Thr	Thr	Ser	Glu	Phe	Arg	Leu	Lys	Lys	Trp
		115					120					125			

Phe	Asp	Gly	Glu	Asp	Cys	Ile	Met	His	Leu	Arg	Ser	Leu	Val	Arg	Lys
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Met	Glu	Asp	Ser	Lys	Arg
145					150

<210> 14

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Thr Asn Thr Ala Asp Ile Leu Leu Asp Asn Tyr Pro Ile Met Thr Phe
 20 25 30

Asp Gly Lys Asp Ile Tyr Pro Ser Ile Ala Phe Met Val Gly Asn Lys
 35 40 45

Leu Phe Leu Asp Leu Tyr Lys Asn Ile Phe Val Glu Phe Phe Arg Leu
 50 55 60

Phe Arg Val Ser Val Ser Ser Gln Tyr Glu Glu Leu Glu Tyr Tyr Tyr
 65 70 75 80

Ser Cys Asp Tyr Thr Asn Asn Arg Pro Thr Ile Lys Gln His Tyr Phe
 85 90 95

Tyr Asn Gly Glu Glu Tyr Thr Glu Ile Asp Arg Ser Lys Lys Ala Thr
 100 105 110

Asn Lys Asn Ser Trp Leu Ile Thr Ser Gly Phe Arg Leu Gln Lys Trp
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 130 135 140

Met Glu Asp Ser Asn Lys
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<210> 15

<211> 181

<212> PRT

<213> Homo sapiens

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Gly Ser Val Gln Ser Gly Phe Leu Thr Glu Val His Leu Asp Gly Gln
 20 25 30

Pro Phe Leu Arg Cys Arg Asp Arg Gln Lys Cys Arg Ala Lys Pro Gln
 35 40 45

Gly Gln Trp Ala Glu Asp Val Leu Gly Asn Lys Thr Trp Asp Arg Glu
 50 55 60

Thr Arg Asp Leu Thr Gly Asn Gly Lys Asp Leu Arg Met Thr Leu Ala
65 70 75 80

His Ile Lys Asp Gln Lys Glu Gly Leu His Ser Leu Gln Glu Ile Arg
85 90 95

Val Cys Glu Ile His Glu Asp Asn Ser Thr Arg Ser Ser Gln His Phe
100 105 110

Tyr Tyr Asp Gly Glu Leu Phe Leu Ser Gln Asn Leu Glu Thr Lys Glu
115 120 125

Trp Thr Met Pro Gln Ser Ser Arg Ala Gln Thr Leu Ala Met Asn Val
130 135 140

Arg Asn Phe Leu Lys Glu Asp Ala Met Lys Thr Lys Thr His Tyr His
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Ala Met His Ala Asp Cys Leu Gln Glu Leu Arg Arg Tyr Leu Lys Ser
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Gly Val Val Leu Arg
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<212> PRT

<213> Homo sapiens

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20 25 30

Pro Phe Leu Arg Tyr Asp Arg Gln Lys Arg Arg Ala Lys Pro Gln Gly
35 40 45

Gln Trp Ala Glu Asp Val Leu Gly Ala Glu Thr Trp Asp Thr Glu Thr
50 55 60

Glu Asp Leu Thr Glu Asn Gly Gln Asp Leu Arg Arg Thr Leu Thr His
65 70 75 80

Ile Lys Asp Gln Lys Gly Gly Leu His Ser Leu Gln Glu Ile Arg Val
85 90 95

Cys Glu Ile His Glu Asp Ser Ser Thr Arg Gly Ser Arg His Phe Tyr
100 105 110

Tyr Asn Gly Glu Leu Phe Leu Ser Gln Asn Leu Glu Thr Gln Glu Ser
115 120 125

Thr Val Pro Gln Ser Ser Arg Ala Gln Thr Leu Ala Met Asn Val Thr

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Asn Phe Trp Lys Glu Asp Ala Met Lys Thr Lys Thr His Tyr Arg Ala
145                150                155                160

Met Gln Ala Asp Cys Leu Gln Lys Leu Gln Arg Tyr Leu Lys Ser Gly
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Val Ala Ile Arg
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<211> 178
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Asp Ala His Ser Leu Trp Tyr Asn Phe Thr Ile Ile His Leu Pro Arg
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His Gly Gln Gln Trp Cys Glu Val Gln Ser Gln Val Asp Gln Lys Asn
20                25                30

Phe Leu Ser Tyr Asp Cys Gly Ser Asp Lys Val Leu Ser Met Gly His
35                40                45

Leu Glu Glu Gln Leu Tyr Ala Thr Asp Ala Trp Gly Lys Gln Leu Glu
50                55                60

Met Leu Arg Glu Val Gly Gln Arg Leu Arg Leu Glu Leu Ala Asp Thr
65                70                75                80

Glu Leu Glu Asp Phe Thr Pro Ser Gly Pro Leu Thr Leu Gln Val Arg
85                90                95

Met Ser Cys Glu Cys Glu Ala Asp Gly Tyr Ile Arg Gly Ser Trp Gln
100                105                110

Phe Ser Phe Asp Gly Arg Lys Phe Leu Leu Phe Asp Ser Asn Asn Arg
115                120                125

Lys Trp Thr Val Val His Ala Gly Ala Arg Arg Met Lys Glu Lys Trp
130                135                140

Glu Lys Asp Ser Gly Leu Thr Thr Phe Phe Lys Met Val Ser Met Arg
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Asp Cys Lys Ser Trp Leu Arg Asp Phe Leu Met His Arg Lys Lys Arg
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Leu Glu

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<211> 174

<212> PRT

<213> Homo sapiens

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 20 25 30

Ile Leu His Leu Ser Asn Ile Asn Lys Thr Met Thr Ser Gly Asp Pro
 35 40 45

Gly Glu Thr Ala Asn Ala Thr Glu Val Lys Lys Cys Leu Thr Gln Pro
 50 55 60

Leu Lys Asn Leu Cys Gln Lys Leu Arg Asn Lys Val Ser Asn Thr Lys
 65 70 75 80

Val Asp Thr His Lys Thr Asn Gly Tyr Pro His Leu Gln Val Thr Met
 85 90 95

Ile Tyr Pro Gln Ser Gln Gly Arg Thr Pro Ser Ala Thr Trp Glu Phe
 100 105 110

Asn Ile Ser Asp Ser Tyr Phe Phe Thr Phe Tyr Thr Glu Asn Met Ser
 115 120 125

Trp Arg Ser Ala Asn Asp Glu Ser Gly Val Ile Met Asn Lys Trp Lys
 130 135 140

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 145 150 155 160

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<211> 16

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<211> 16

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<211> 16

<212> PRT

<213> *Callithrix jacchus*

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<210> 22

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<213> *Mus musculus*

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<210> 23

<211> 16

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<213> *Rattus norvegicus*

<400> 23

Leu	Thr	Leu	Val	Lys	Thr	Pro	Ser	Gly	Thr	Cys	Ala	Val	Tyr	Gly	Ser
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<210> 24

<211> 16

<212> PRT

<213> *Cavia porcellus*

<400> 24

Leu	Thr	Leu	Met	Asp	Thr	Gln	Asn	Gly	Lys	Cys	Ala	Leu	Tyr	Gly	Ser
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<210> 25

<211> 16

<212> PRT

<213> *Spermophilus sensu stricto*

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<210> 26

<211> 16

<212> PRT

<213> *Peromyscus maniculatus*

<400> 26

Leu	Thr	Val	Val	Glu	Met	Gln	Ser	Gly	Ser	Cys	Ala	Val	Tyr	Gly	Ser
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 1 5 10 15 -----

<210> 27

<211> 16

<212> PRT

<213> *Heterocephalus glaber*

<400> 27

Leu Ser Met Val Glu Met Gln Asn Gly Thr Cys Ala Val Tyr Ala Ser
 1 5 10 15

<210> 28

<211> 16

<212> PRT

<213> *Microtus ochrogaster*

<400> 28

Leu Thr Leu Val Glu Met Gln Arg Gly Ser Cys Ala Val Tyr Gly Ser
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<210> 29

<211> 16

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<213> *Sorex araneus*

<400> 29

Val Ser Ile Val Glu Met Gln Gly Gly Asn Cys Ala Val Tyr Gly Ser
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<210> 30

<211> 16

<212> PRT

<213> *Condylura cristata*

<400> 30

Val Thr Val Tyr Glu Met Gln Asn Gly Ser Cys Ala Val Tyr Gly Ser
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<210> 31

<211> 16

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<213> *Cricetulus griseus*

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<210> 32

<211> 16

<212> PRT

<213> *Felis catus*

<400> 32

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<212> PRT

<213> Cowpox virus

<400> 33

Ala Ser Ser Phe Lys
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<210> 34

<211> 4

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<213> Artificial Sequence

<220>

<223> SYNTHESIZED

<400> 34

Tyr Ile Asn Met
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REFERENCES CITED IN THE DESCRIPTION

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PATENTKRAV

1. Kimærisk peptid, der omfatter et cytokinpeptid og et ligandpeptid, hvor cytokinpeptidet ikke er en bindingspartner for ligandpeptidet, og hvor ligandpeptidet er en bindingspartner for
5 en receptor, der udtrykkes på naturlige dræber (NK)-celler eller cytotoxiske CD8+-T-lymfocytter (CTL), hvor receptoren er NKG2D-receptoren, og hvor cytokinpeptidet er valgt fra gruppen bestående af IL2, IL7, IL15, IL18, IL21 og mutanter deraf.
2. Kimærisk peptid ifølge krav 1, hvor cytokinpeptidet er et muteret interleukin-2 (IL2).
10
3. Kimærisk peptid ifølge krav 2, hvor det muterede interleukin-2 omfatter mindst én mutation valgt fra gruppen bestående af R38A, F42K og C125S.
4. Kimærisk peptid ifølge et hvilket som helst af kravene 1-3, hvor cytokinpeptidet omfatter
15 aminosyresekvensen ifølge SEQ ID NO: 6.
5. Kimærisk peptid ifølge et hvilket som helst af kravene 1-4, hvor ligandpeptidet er klasse-I-lignende protein af orthopoxvirus fra det større histokompatibilitetskompleks (OMCP) eller en del deraf, eller et muteret OMCP.
20
6. Kimærisk peptid ifølge et hvilket som helst af kravene 1-5, der endvidere omfatter et linker-peptid på ca. 20 til ca. 30 aminosyrer.
7. Kimærisk peptid ifølge et hvilket som helst foregående krav, hvor ligandpeptidet binder
25 sig til receptoren med større affinitet end cytokinpeptidet binder sig til dets målcytokinreceptor.
8. Farmaceutisk sammensætning, der omfatter det kimæriske peptid ifølge et hvilket som helst af kravene 1-7 og en farmaceutisk acceptabel excipients, der er virksom til systemisk indgivelse af det kimæriske peptid.
30
9. Kimærisk peptid ifølge et hvilket som helst af kravene 1-7 eller en farmaceutisk sammensætning ifølge krav 8 til anvendelse i en fremgangsmåde til indgivelse af et cytokin i en målcelle, hvilken fremgangsmåde omfatter at bringe en målcelle i kontakt med en sammensætning, der omfatter det kimæriske peptid.

10. Kimærisk peptid eller farmaceutisk sammensætning til anvendelse ifølge krav 9, hvor målcellen er en NK-celle eller en CD8+-CTL.
- 5 11. Kimærisk peptid eller farmaceutisk sammensætning ifølge et hvilket som helst af kravene 1-10 til anvendelse i en fremgangsmåde til at behandle en tumor, hvilken fremgangsmåde omfatter:
- a) identificering af en person med en tumor og
- b) indgivelse til personen af en terapeutisk virksom mængde af en sammensætning, der
- 10 omfatter det kimæriske peptid, hvor det kimæriske peptid aktiverer naturlige dræber (NK)-celler eller cytotoksiske CD8+-T-lymfocytter (CTL), hvorved tumoren behandles.
12. Kimærisk peptid eller farmaceutisk sammensætning ifølge et hvilket som helst af kravene 1-10 til anvendelse i en fremgangsmåde til at behandle en virusinfektion, hvilken
- 15 fremgangsmåde omfatter indgivelse til en person af en terapeutisk virksom mængde af en sammensætning, der omfatter det kimæriske peptid.

DRAWINGS

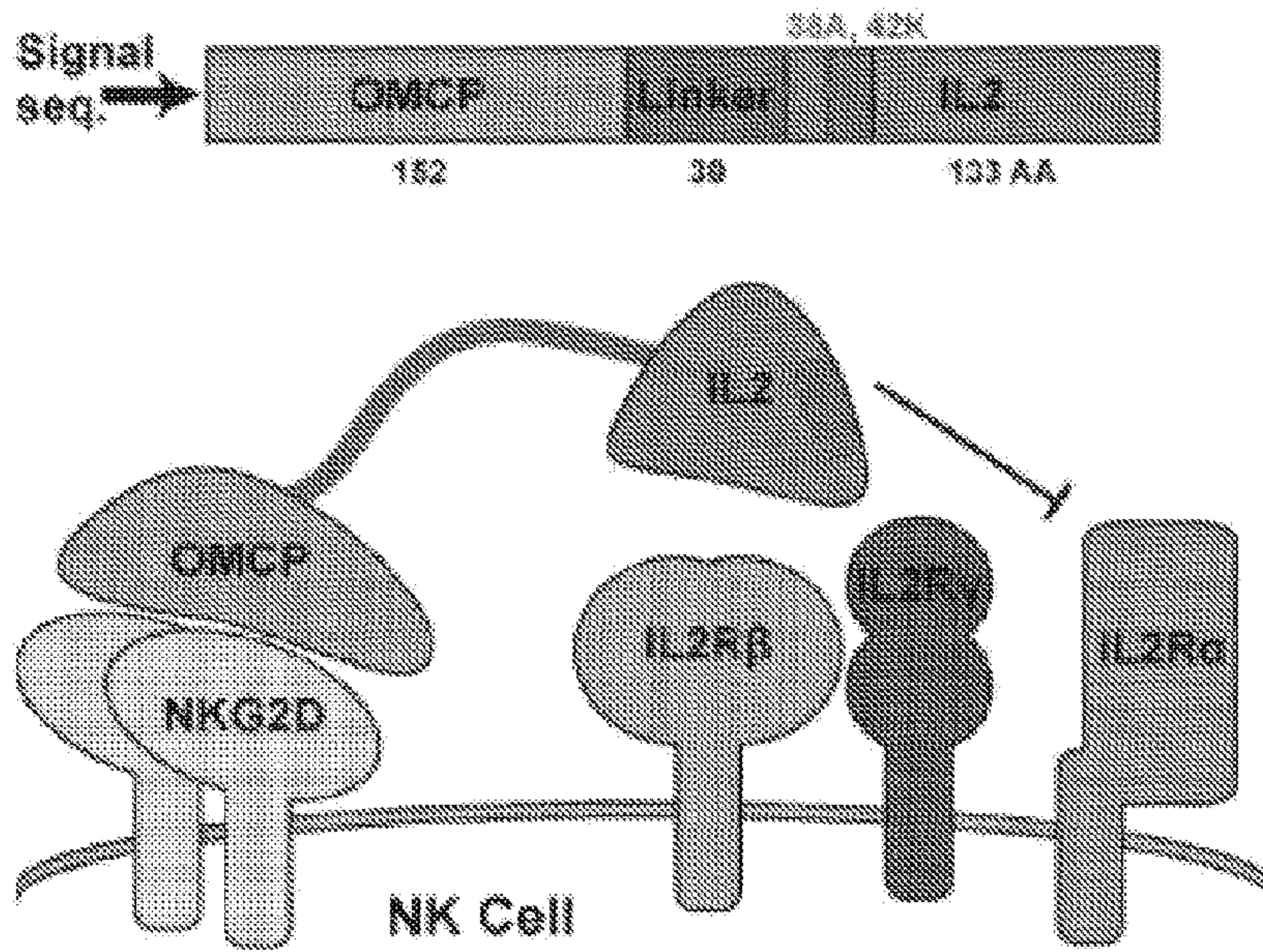


FIG. 1A

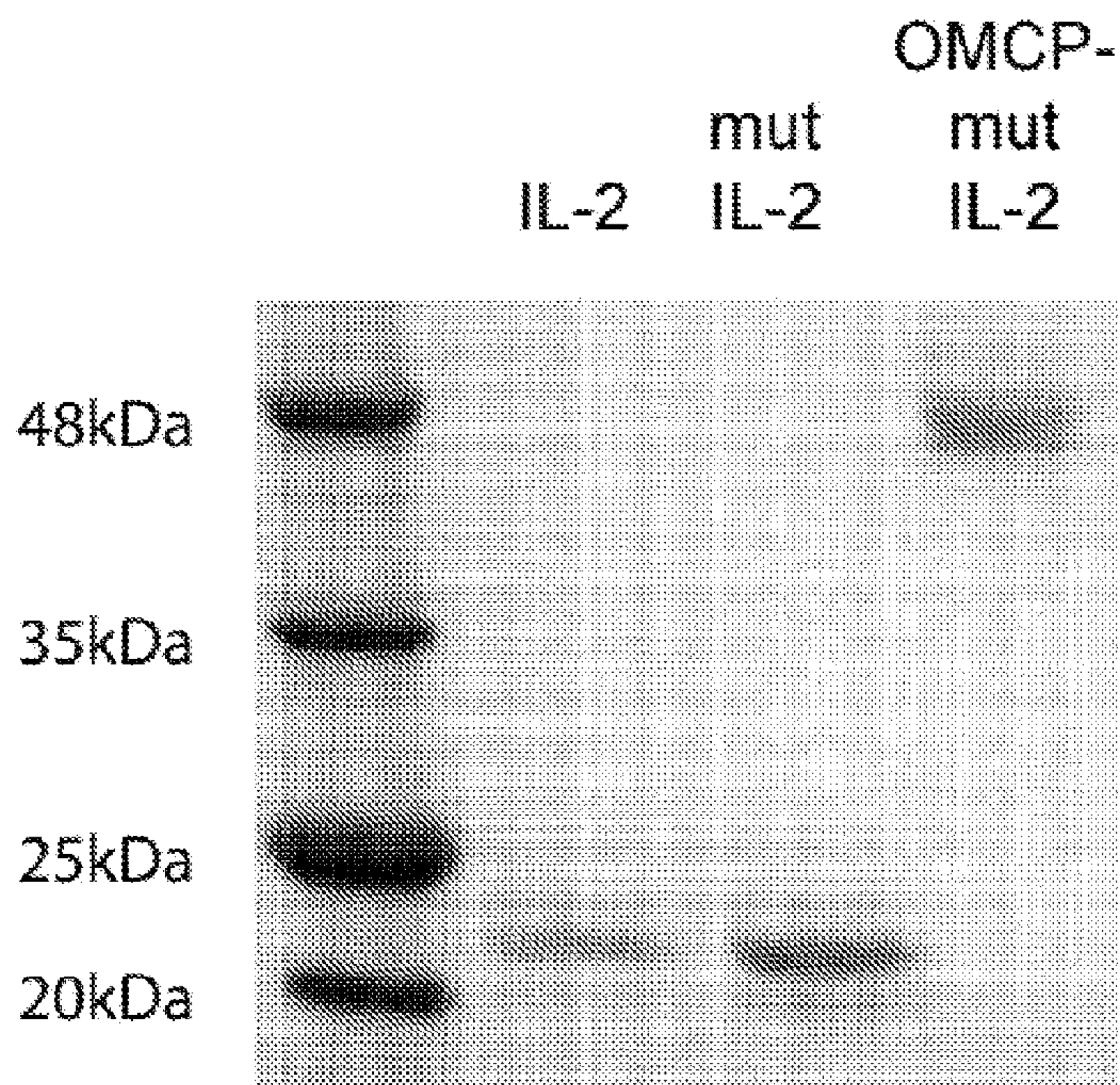


FIG. 1B

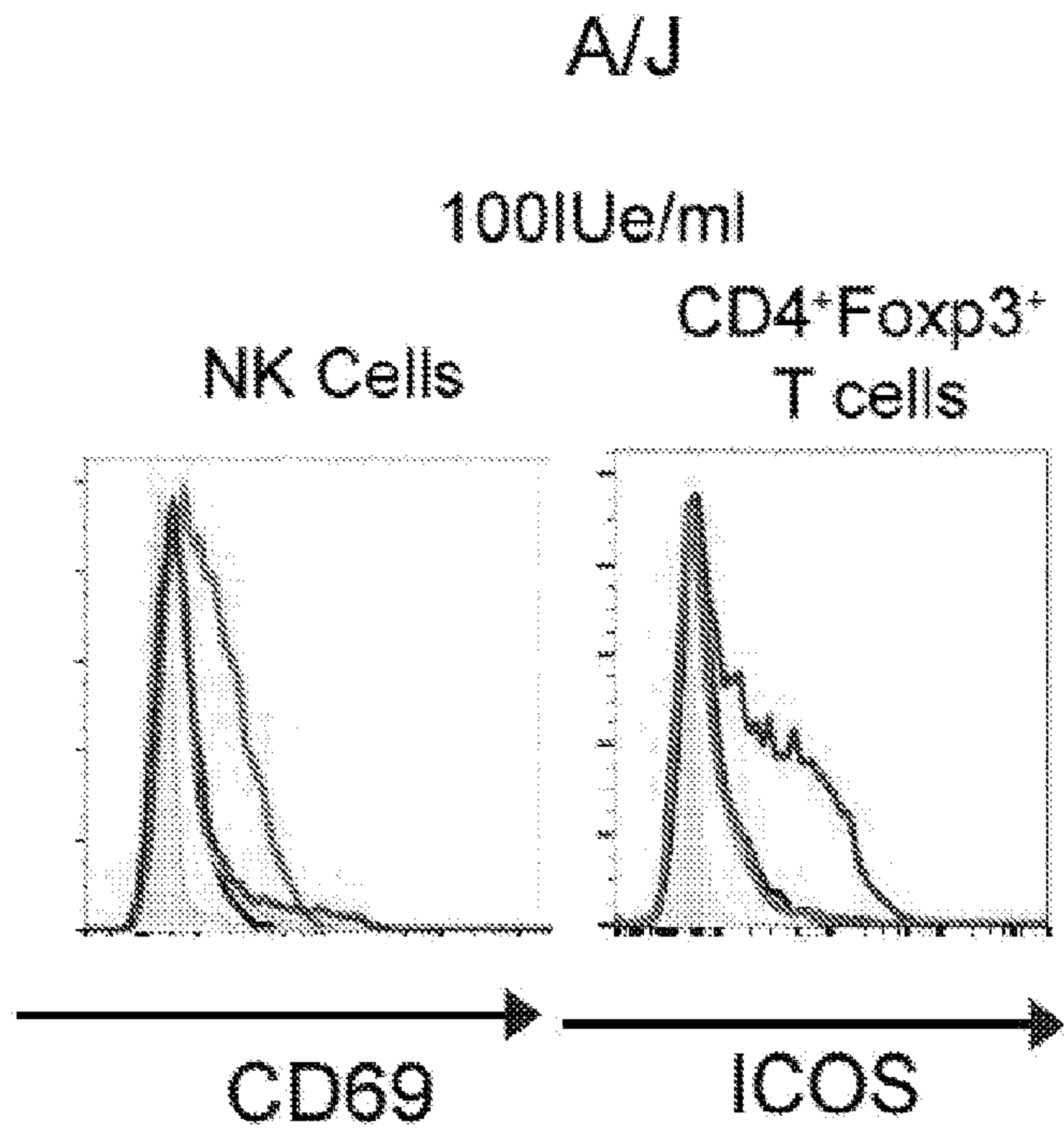


FIG. 1C

OMCP-mutIL-2, wild-type IL-2, mutIL-2, Saline

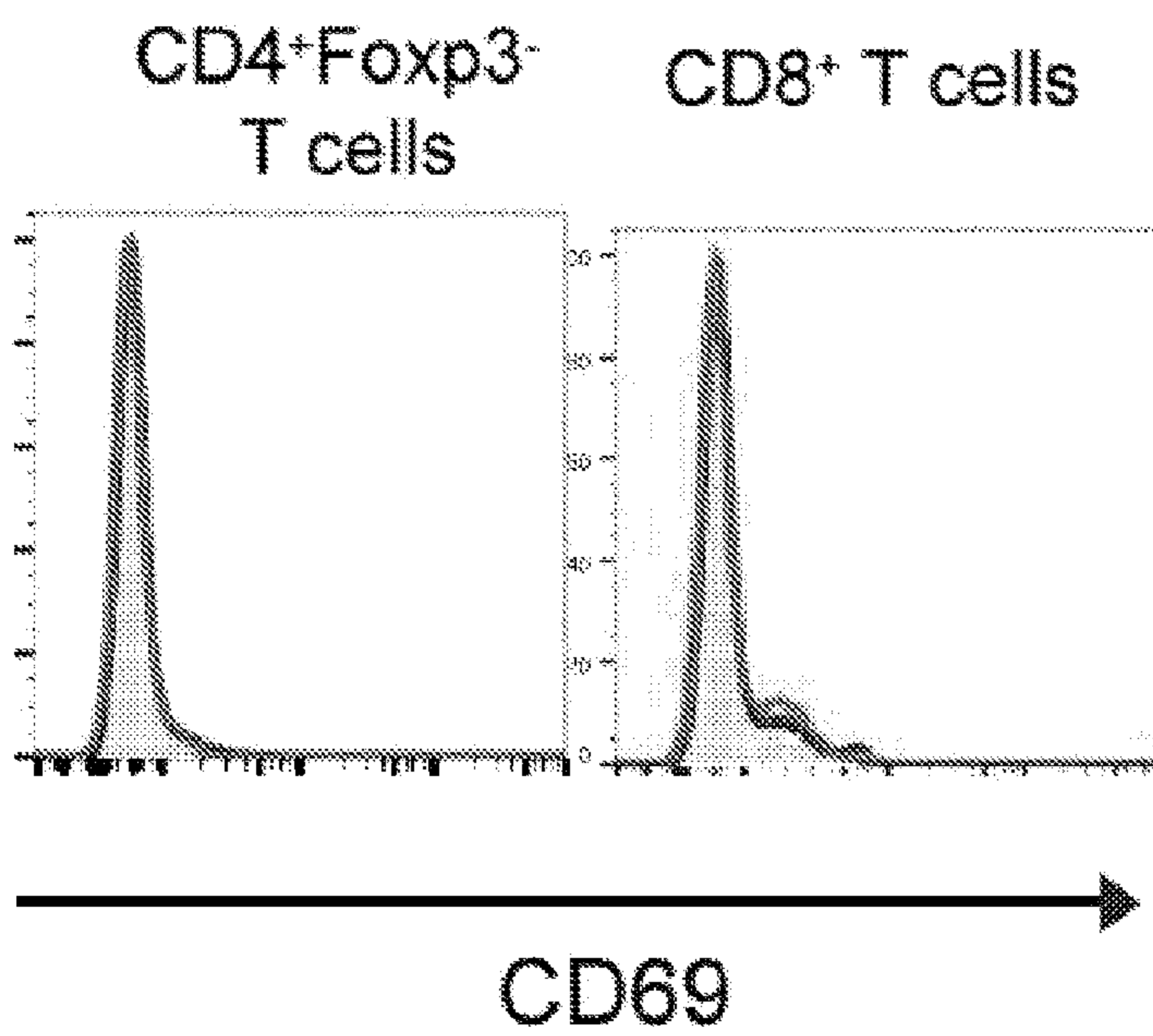


FIG. 1D

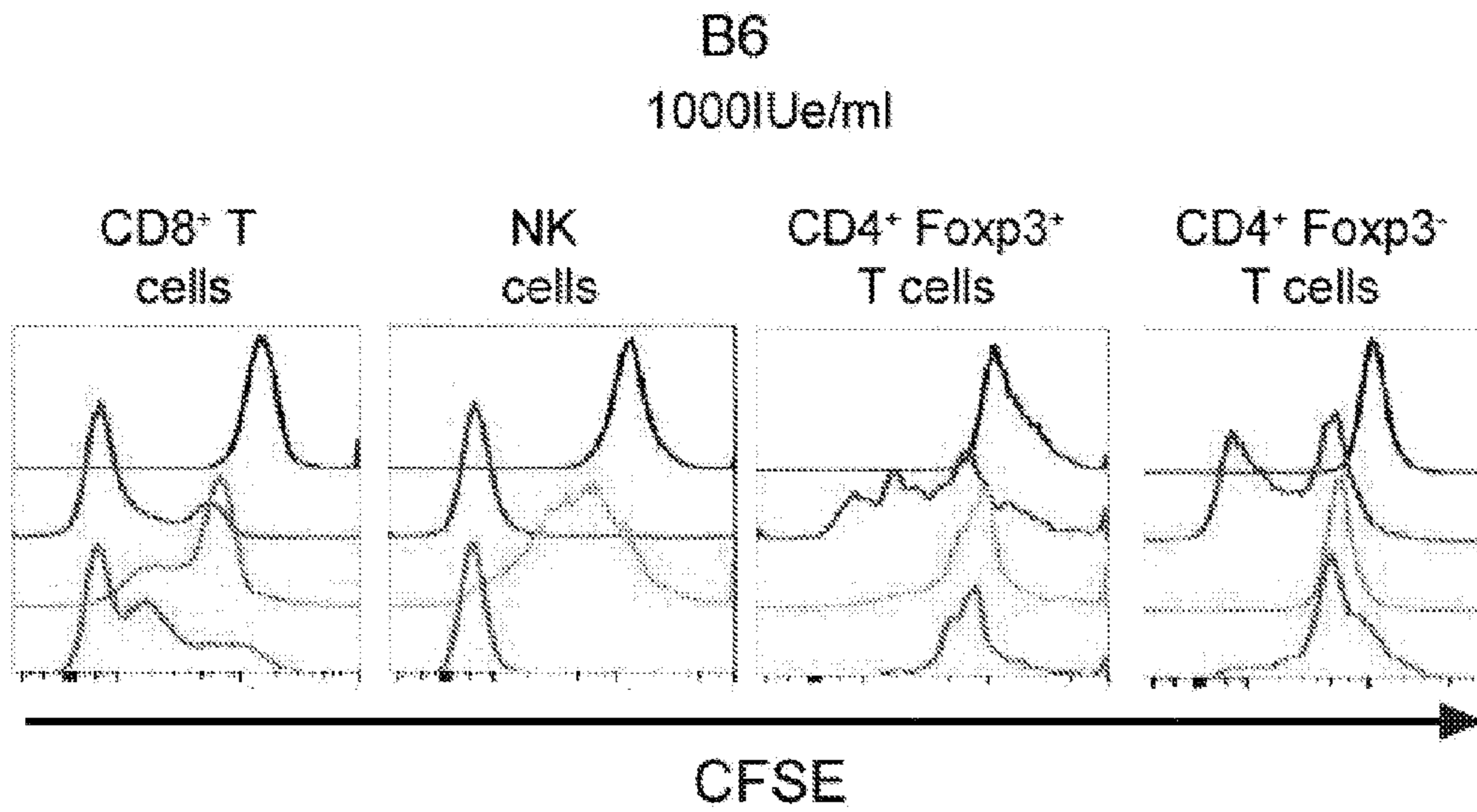


FIG. 1E

OMCP-mutIL-2, wild-type IL-2, mutIL-2, Saline

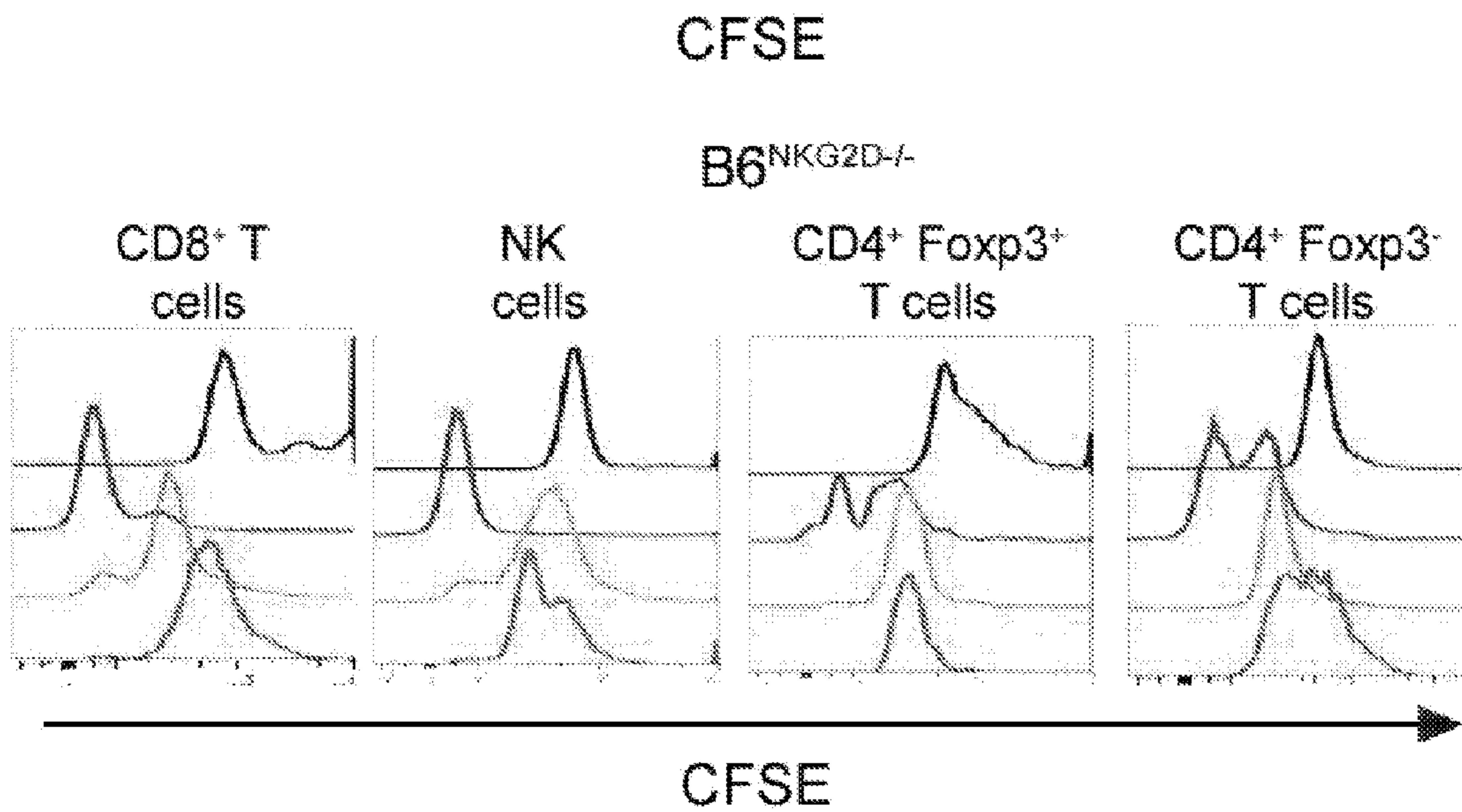


FIG. 1F

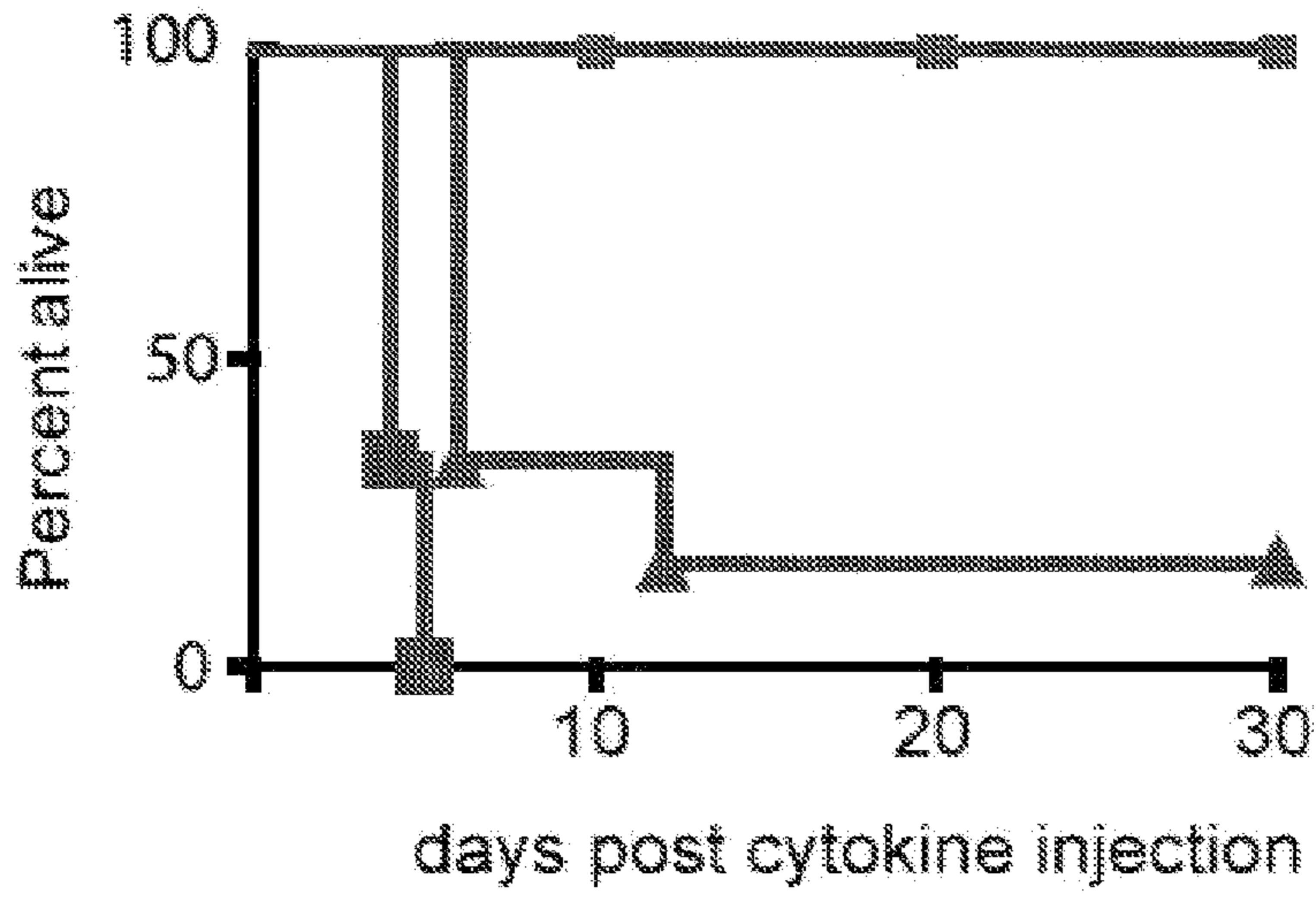


FIG. 2A

- 750,000IUe wtIL-2
- 1,500,000IUe wtIL-2
- 3,500,000IUe wtIL-2

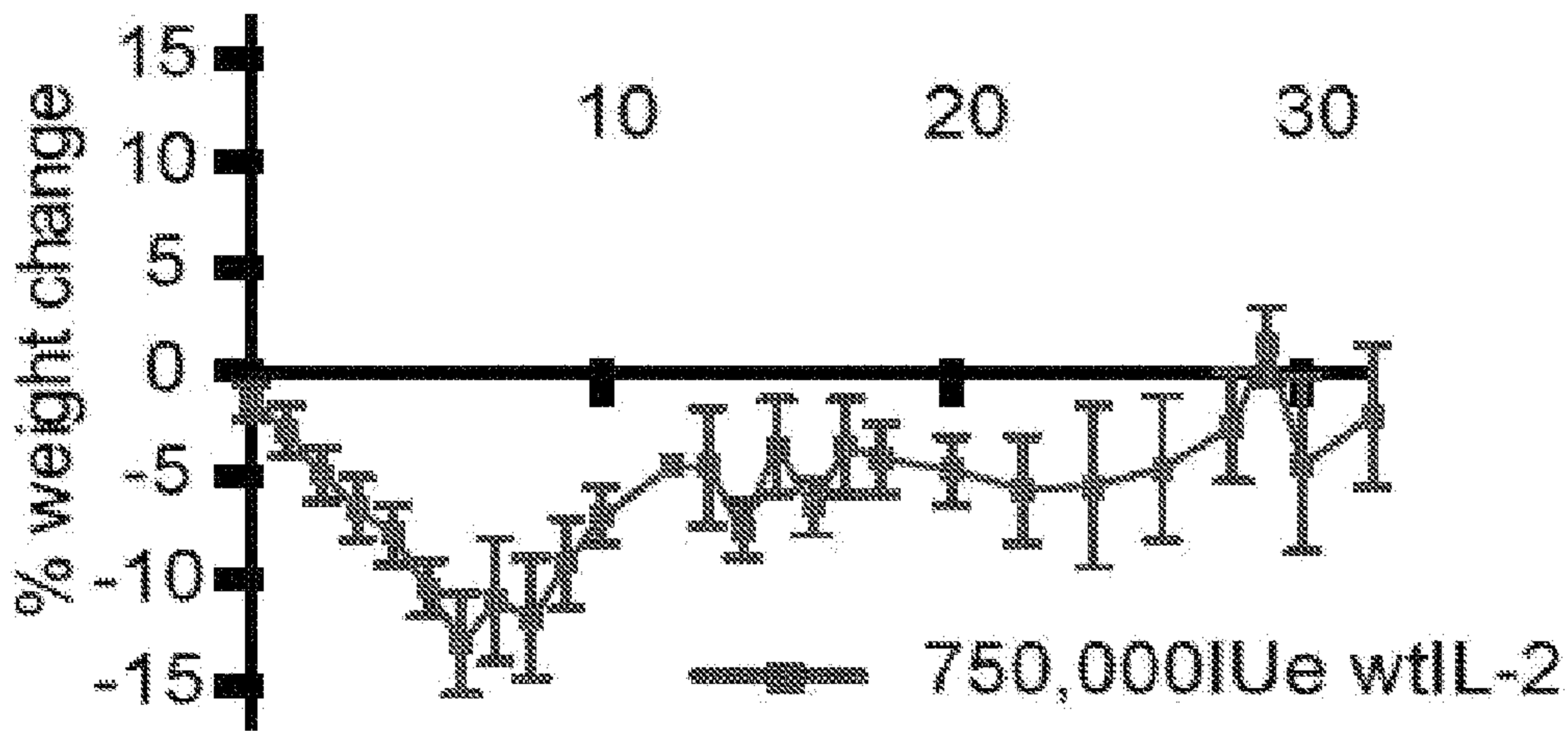


FIG. 2B

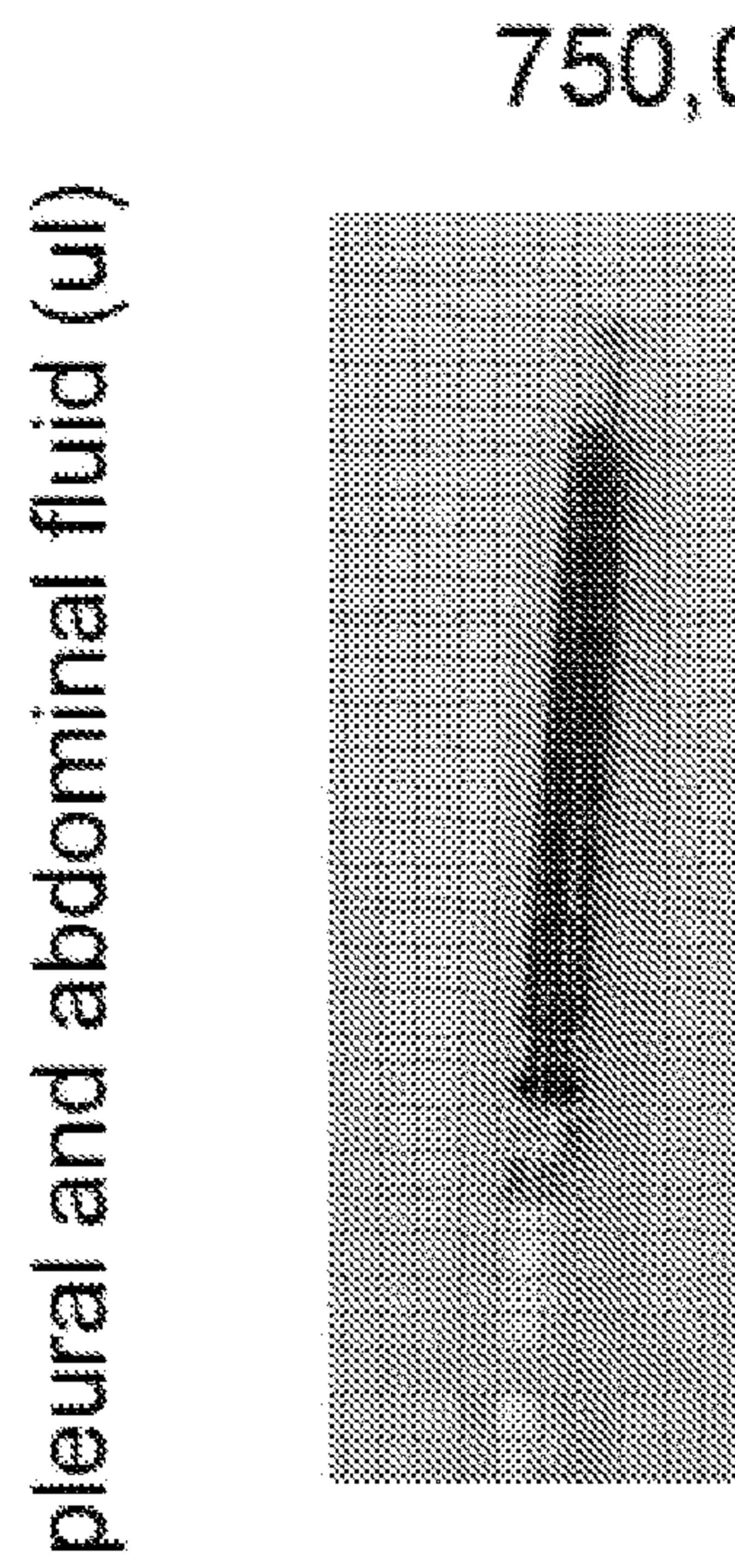


FIG. 2C

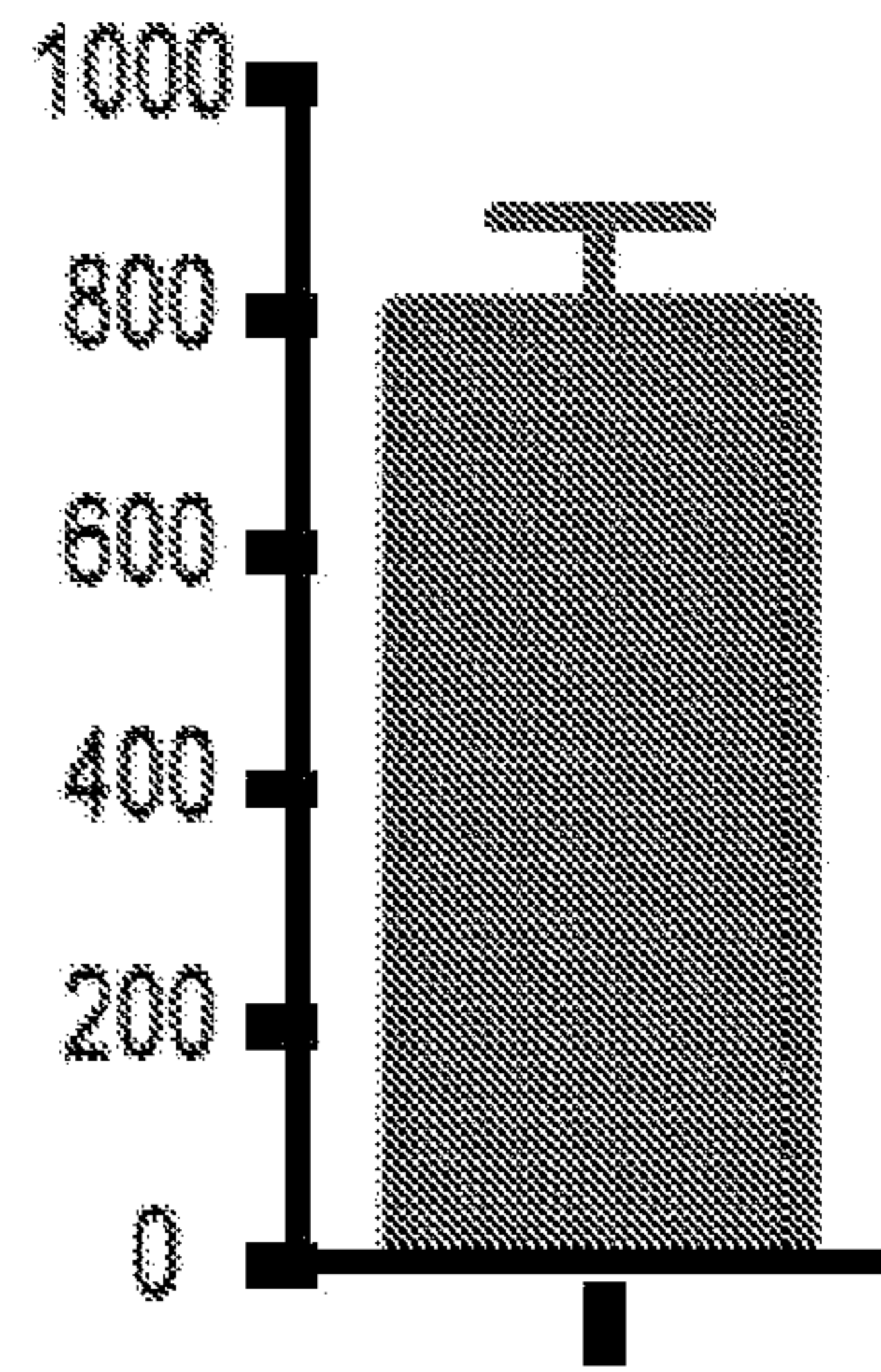


FIG. 2D

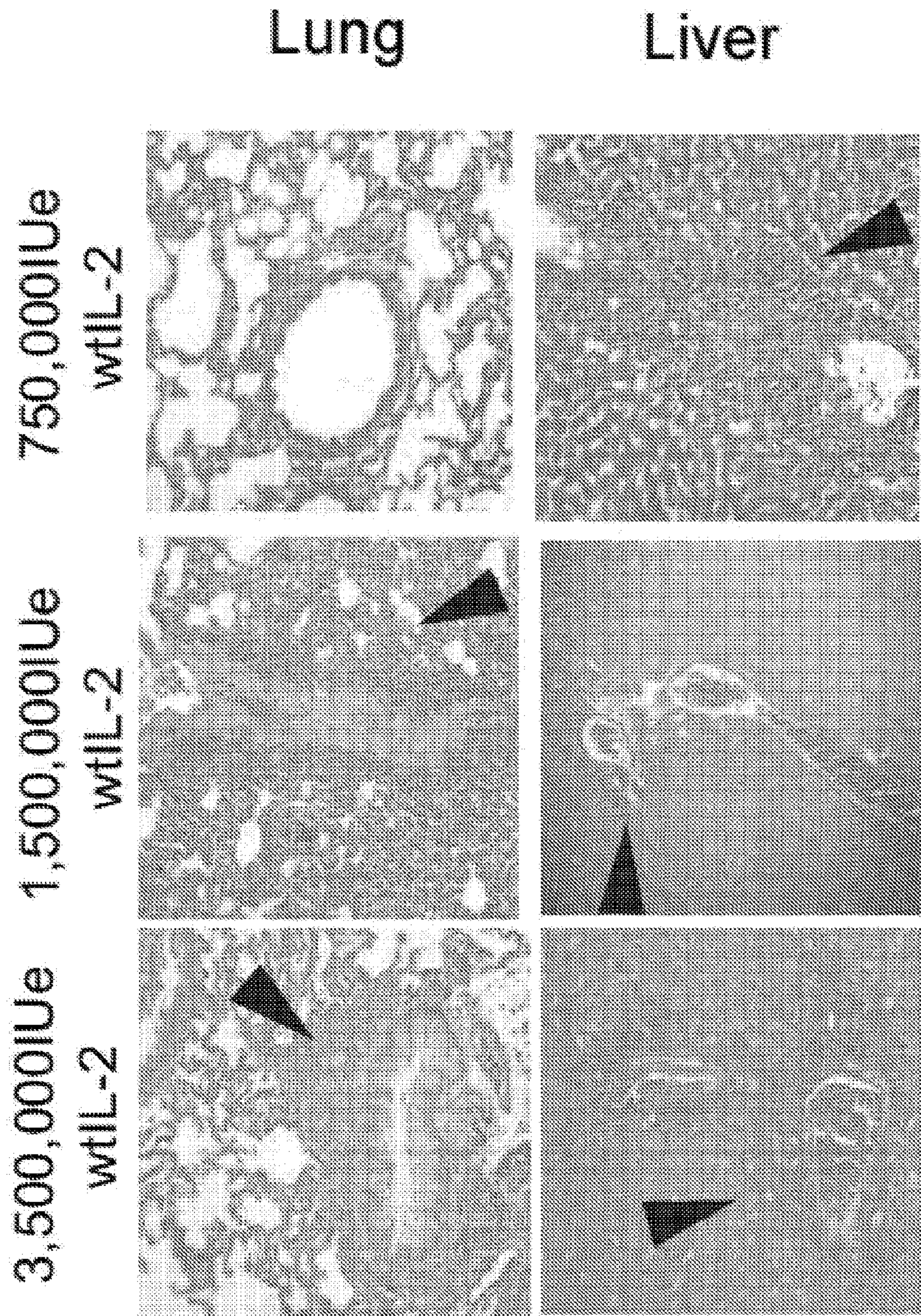


FIG. 2E

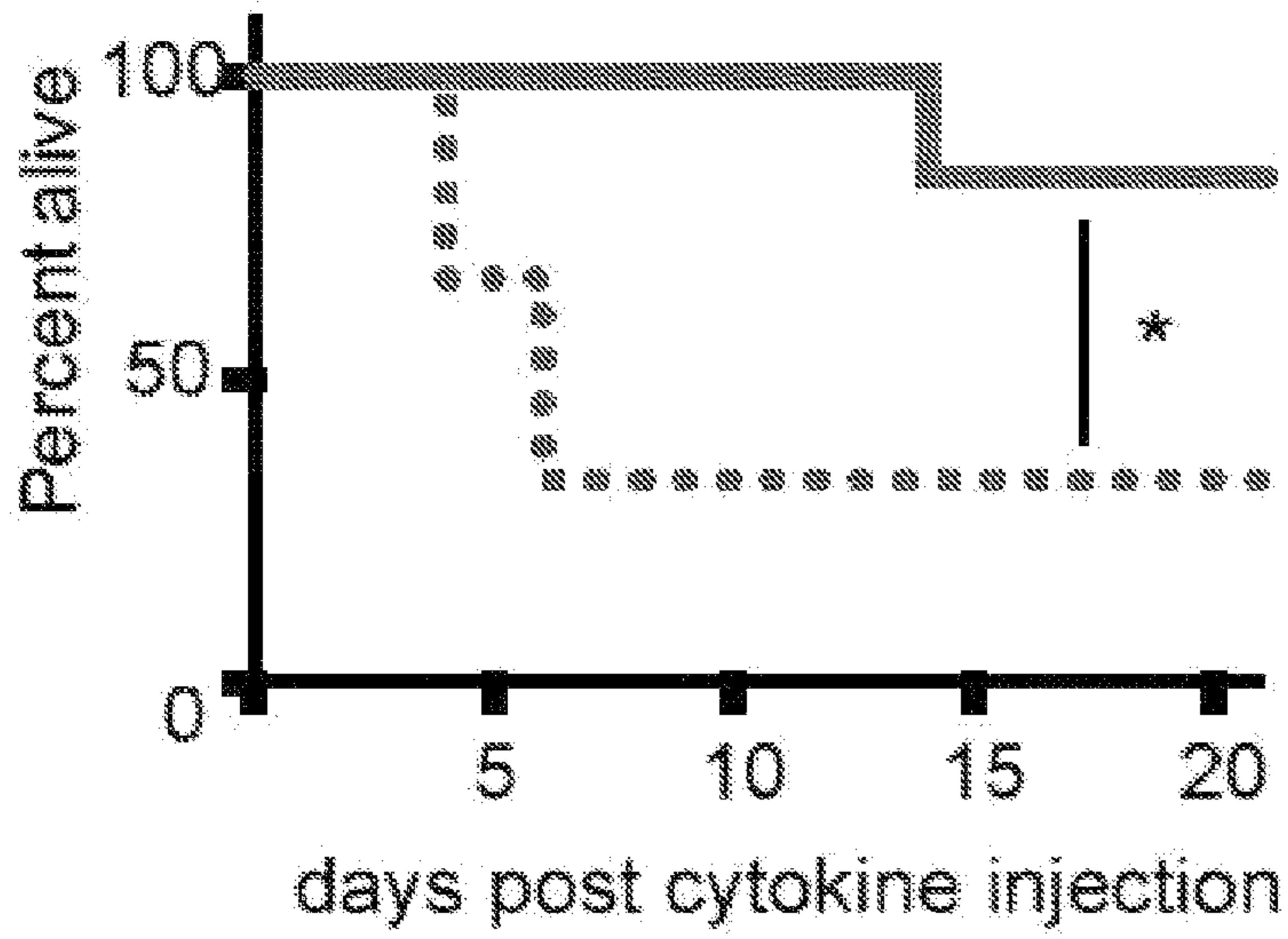


FIG. 2F

--- +rabbit IgG
 ——— +anti-asialoGM

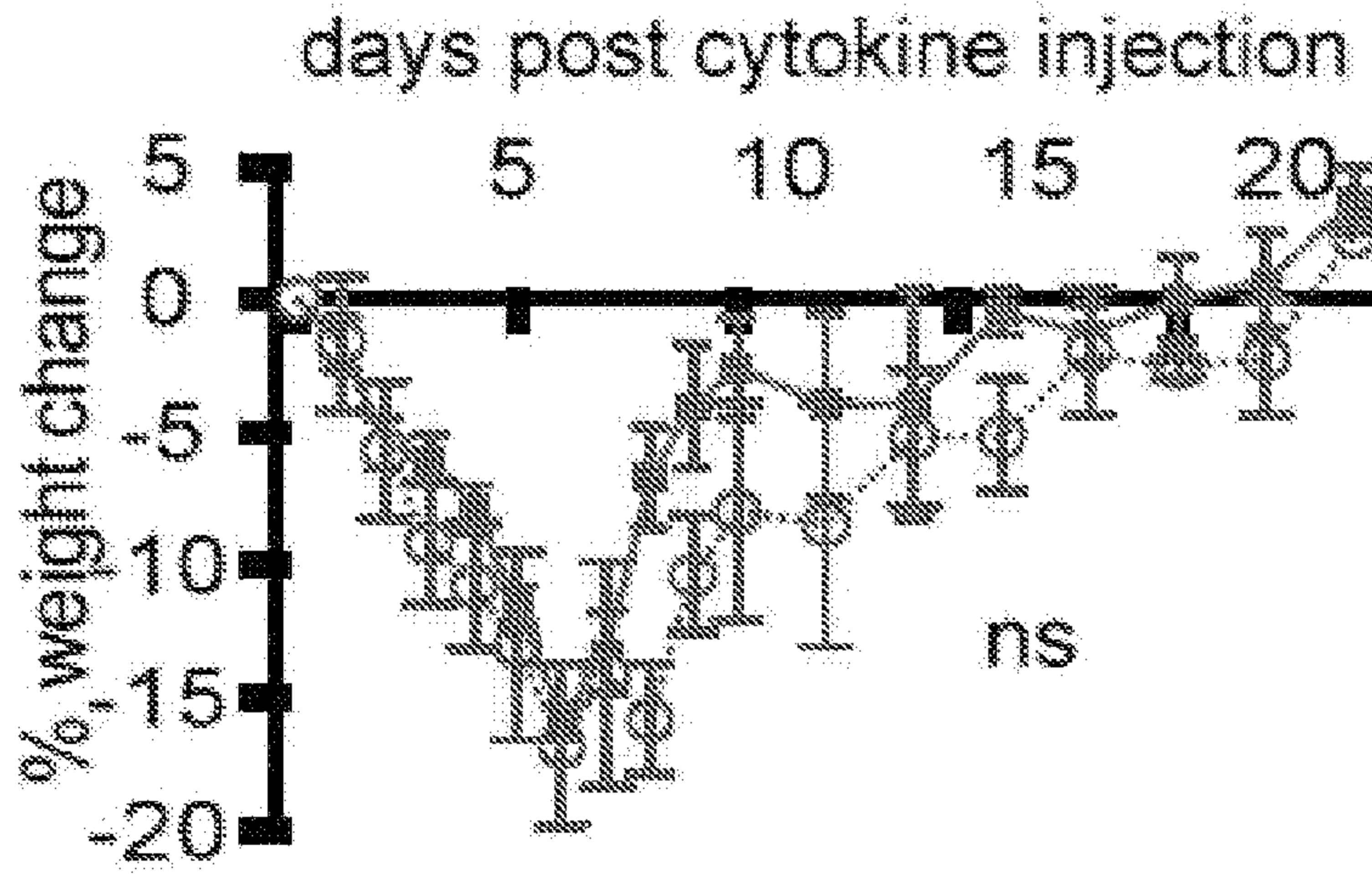


FIG. 2G

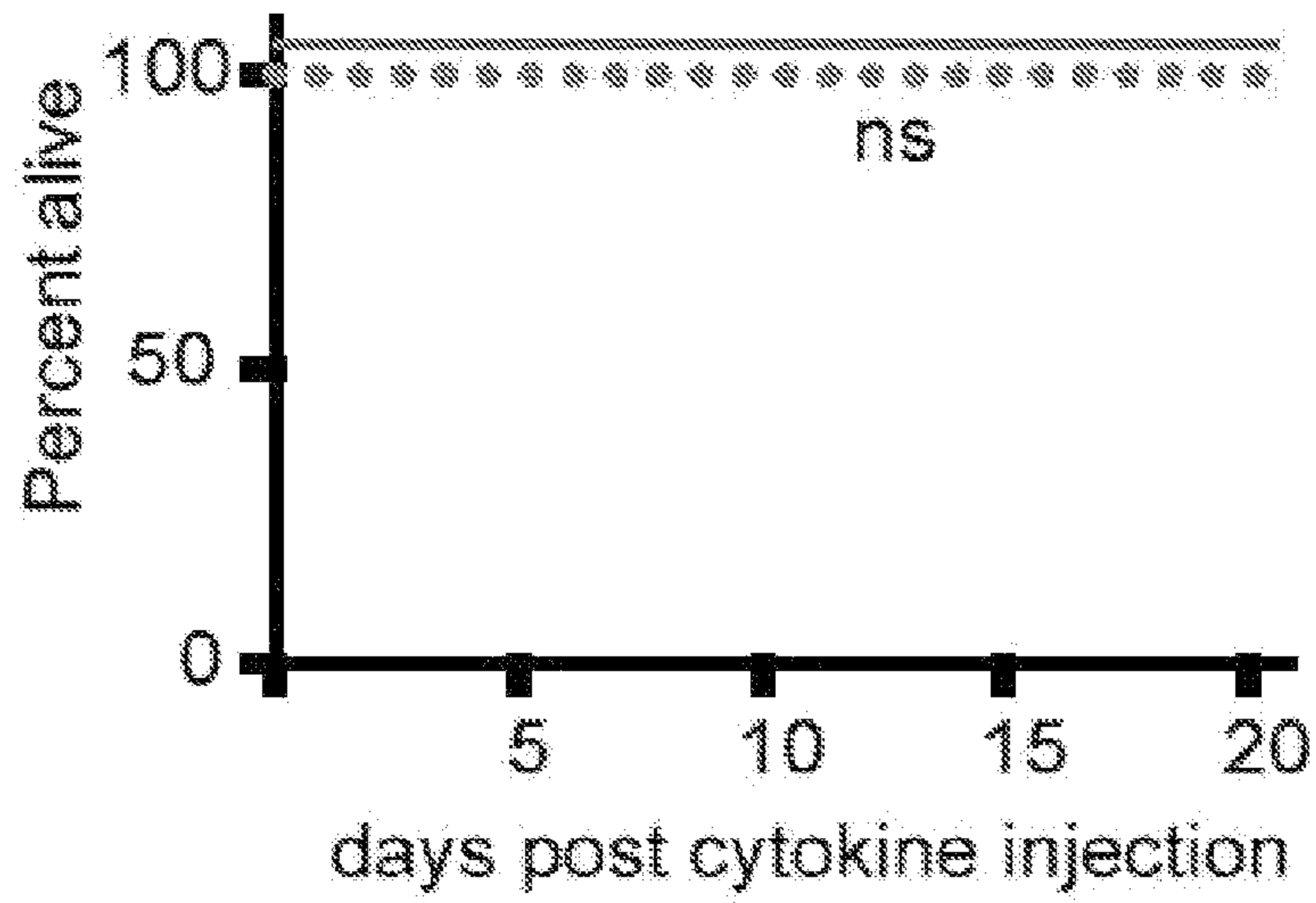


FIG. 2H

..... +rabbit IgG
 ----- +anti-asialoGM

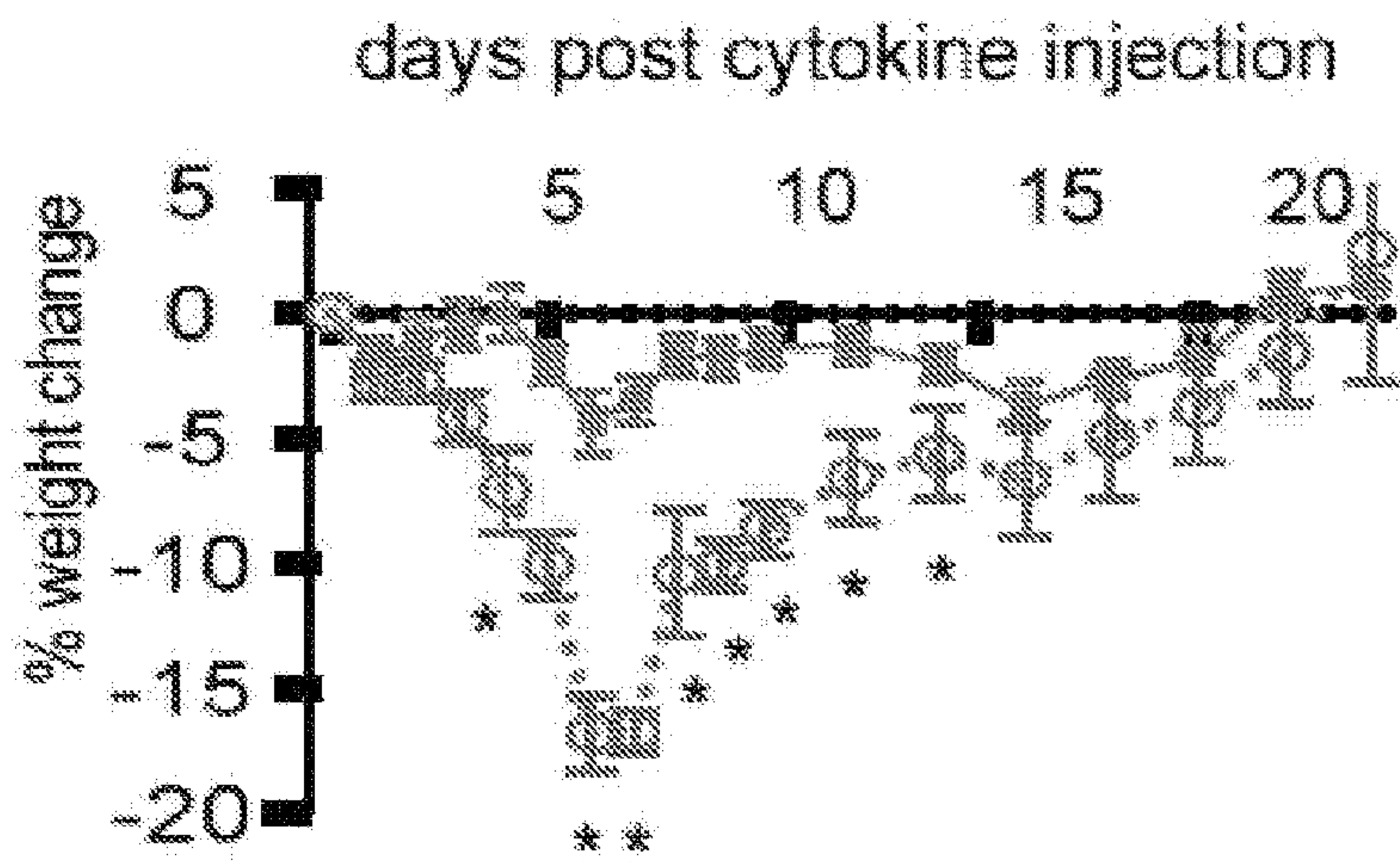


FIG. 2I

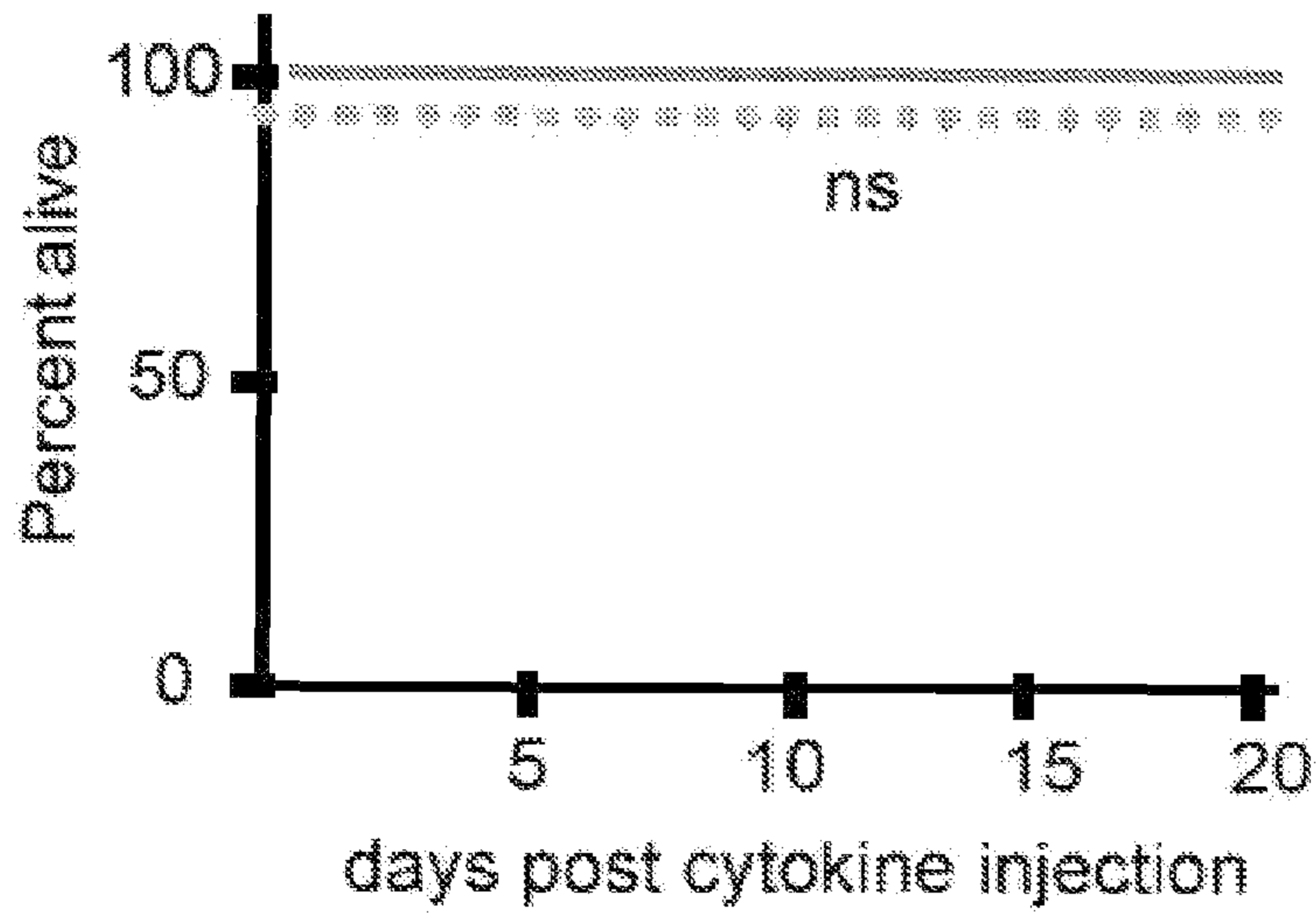


FIG. 2J

--- +rabbit IgG
 ----- +anti-asialoGM

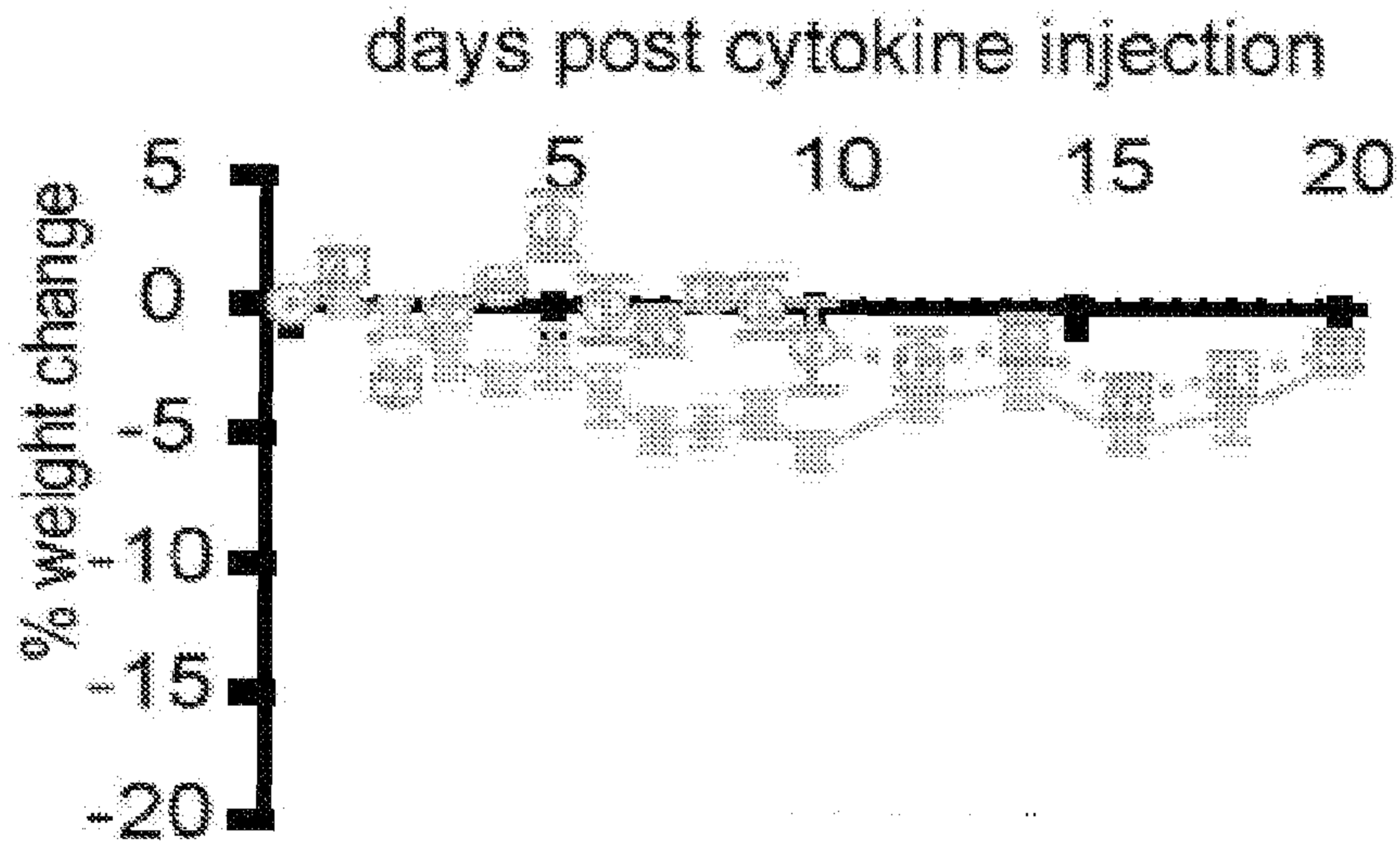
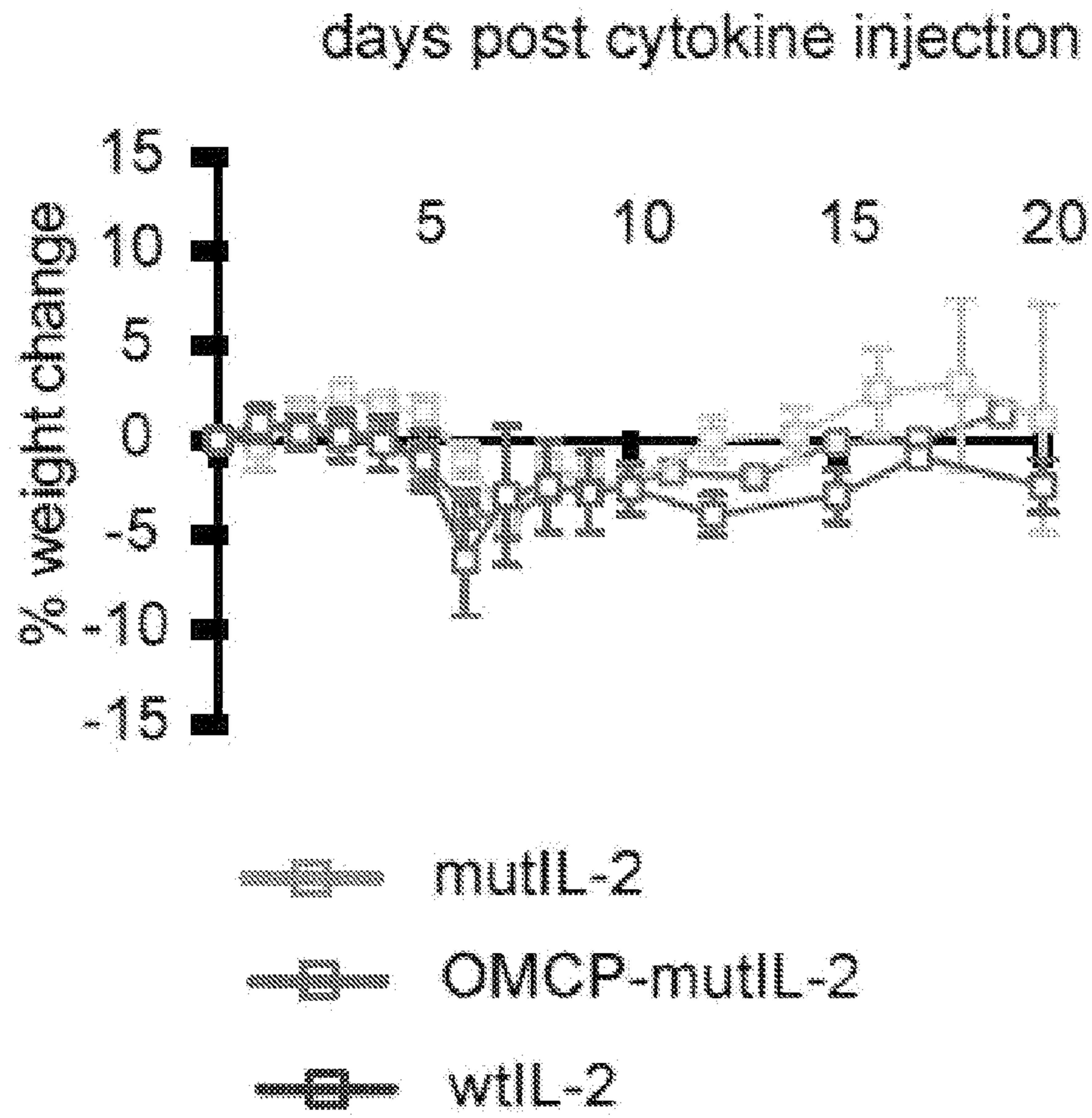


FIG. 2K

**FIG. 2L**

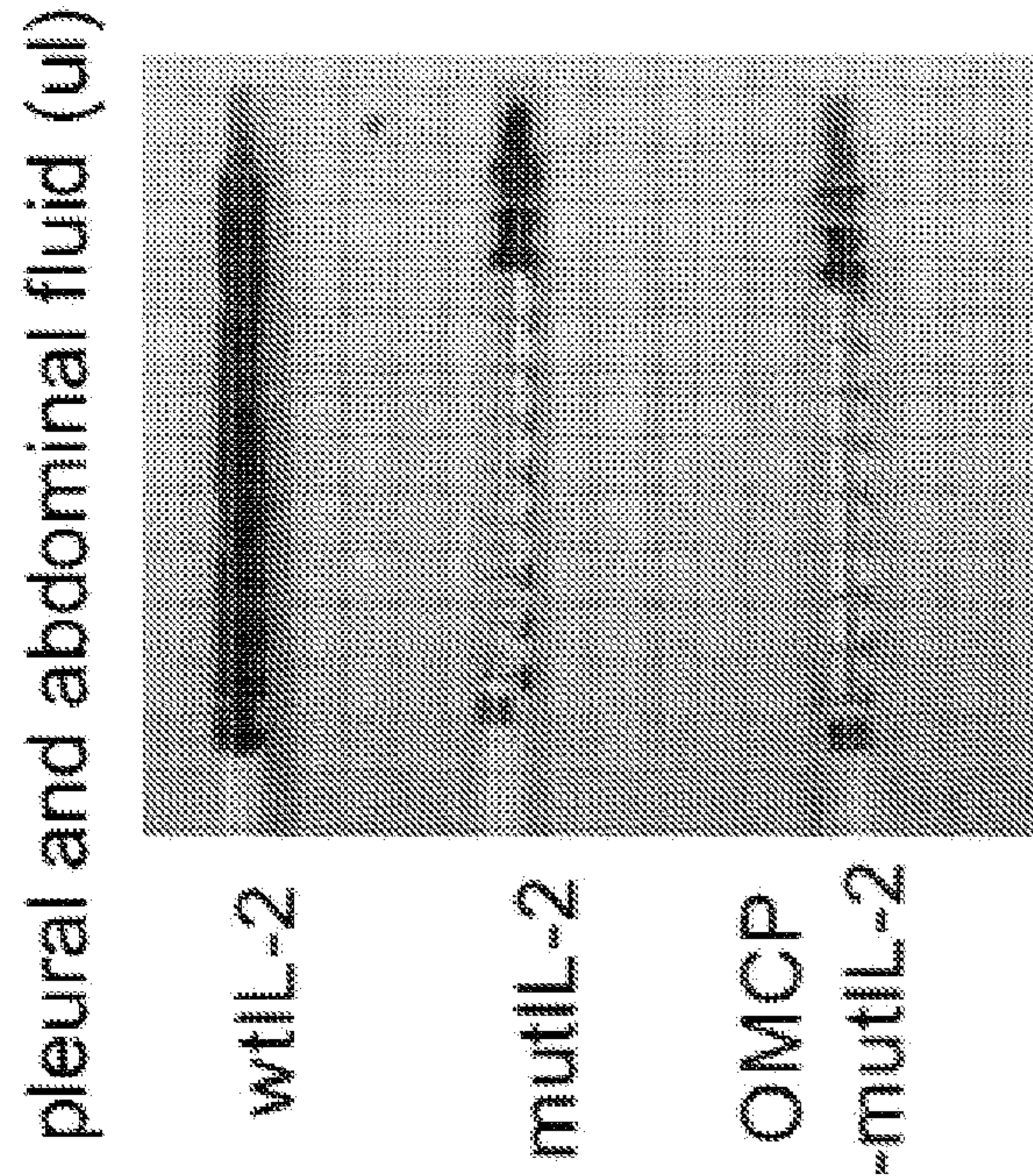


FIG. 2M

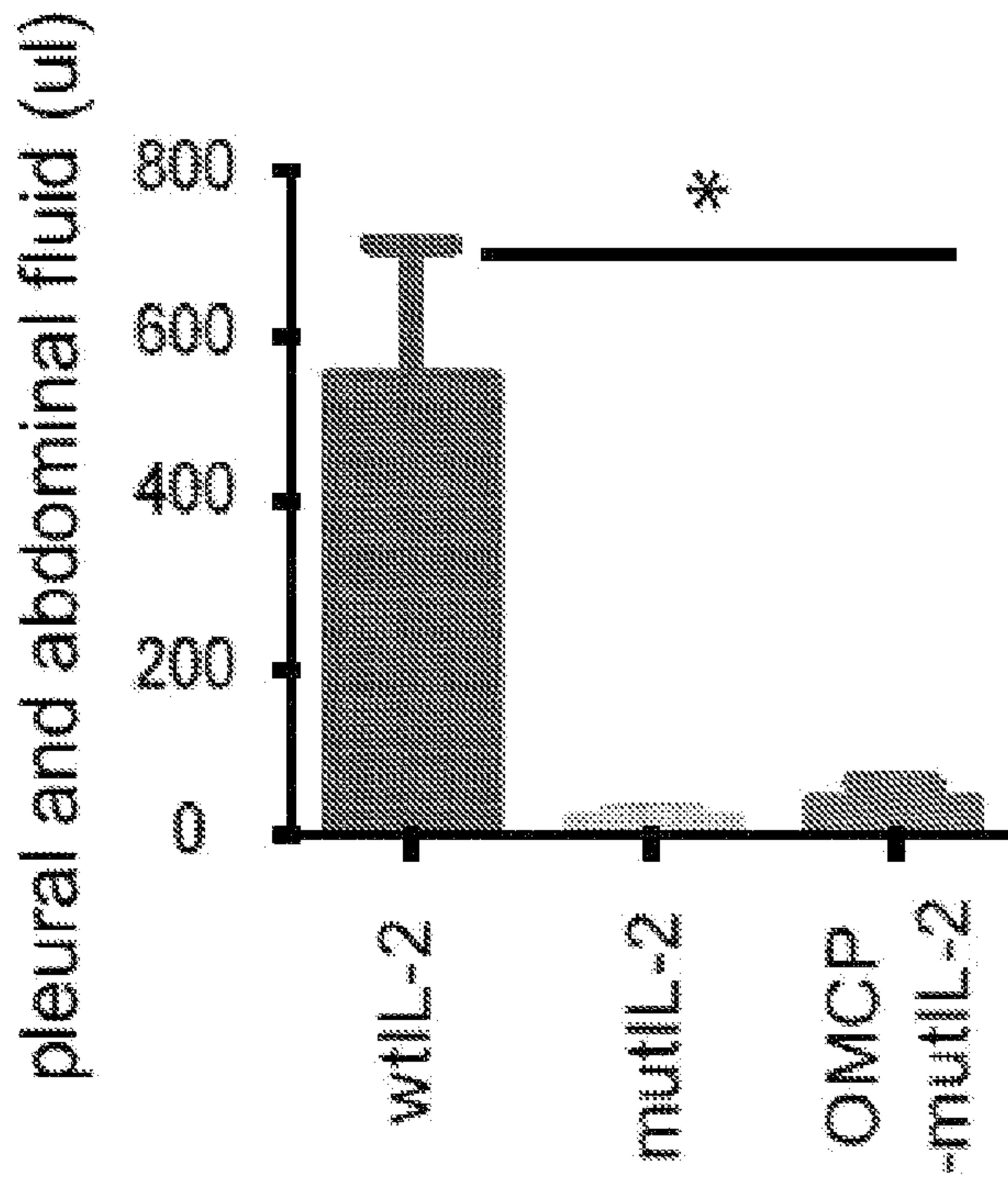


FIG. 2N

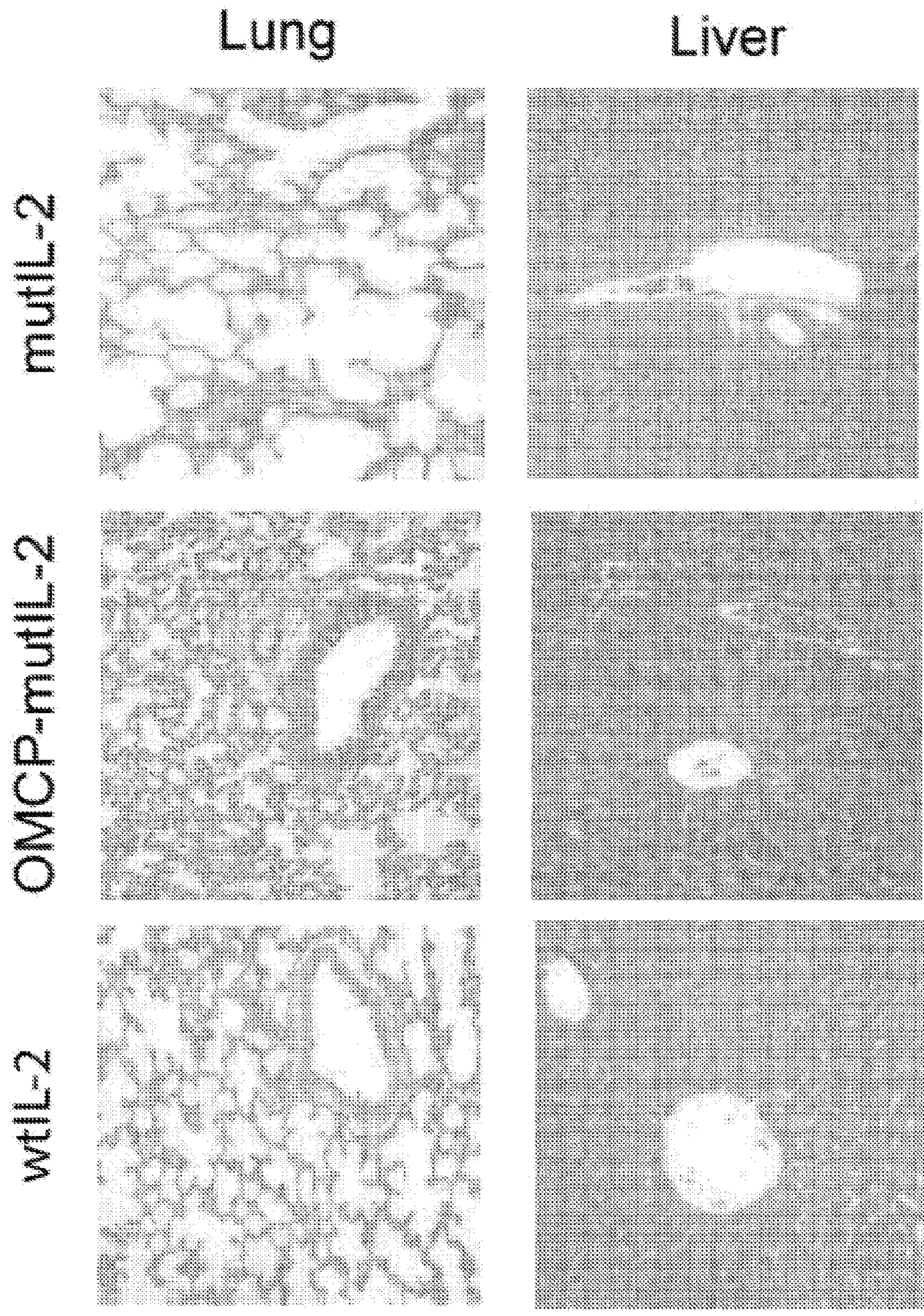


FIG. 20

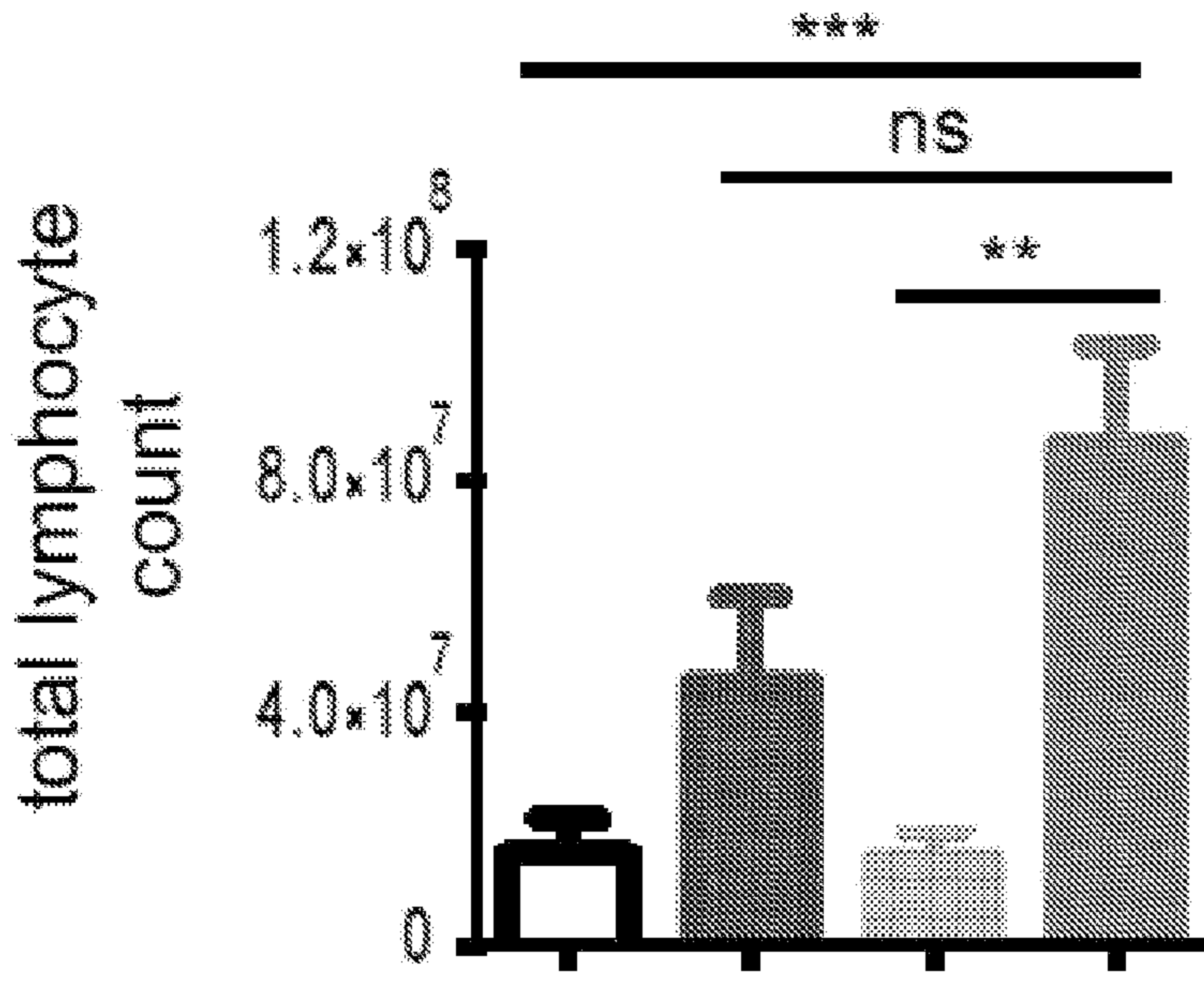


FIG. 3A

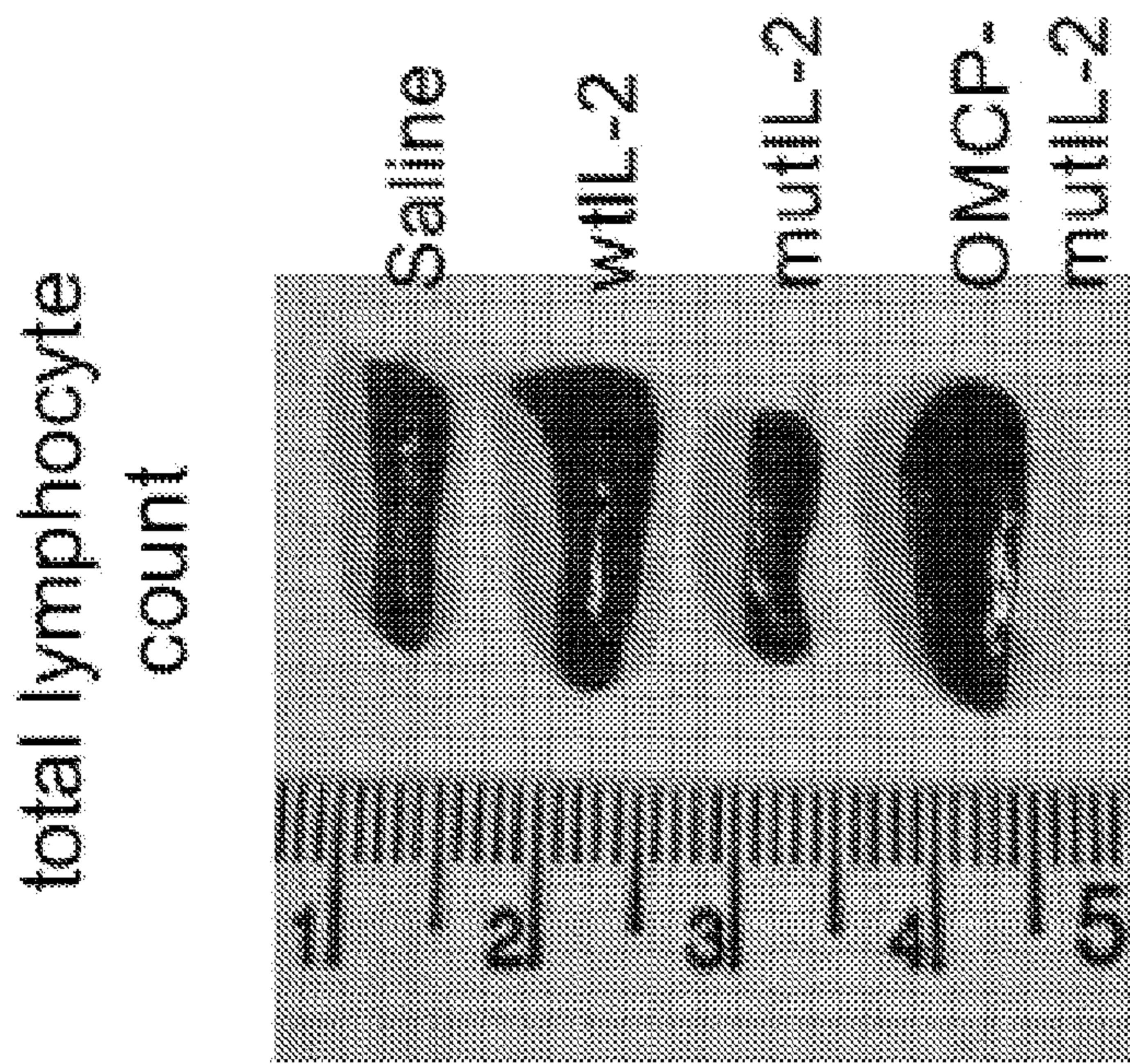


FIG. 3B

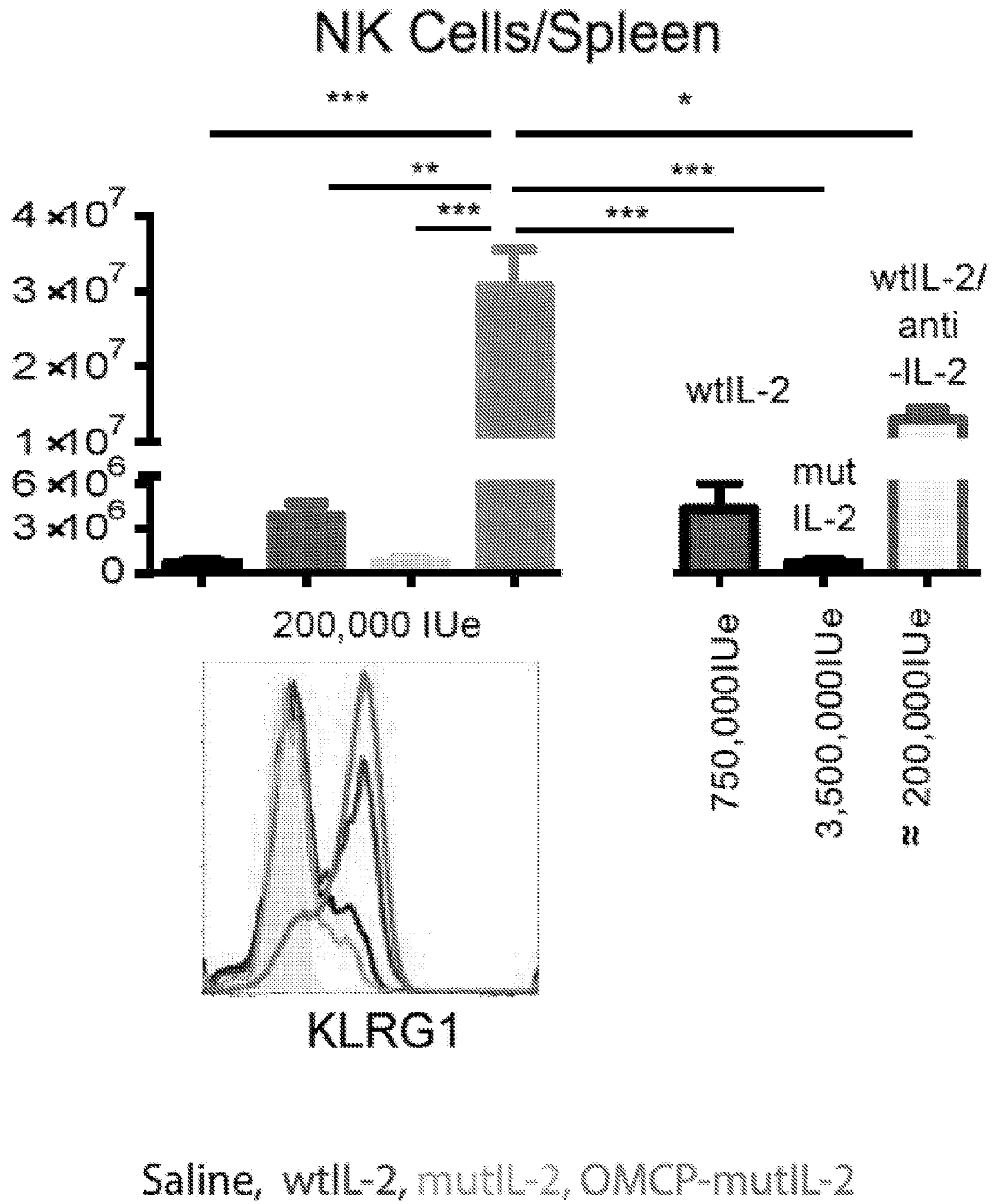
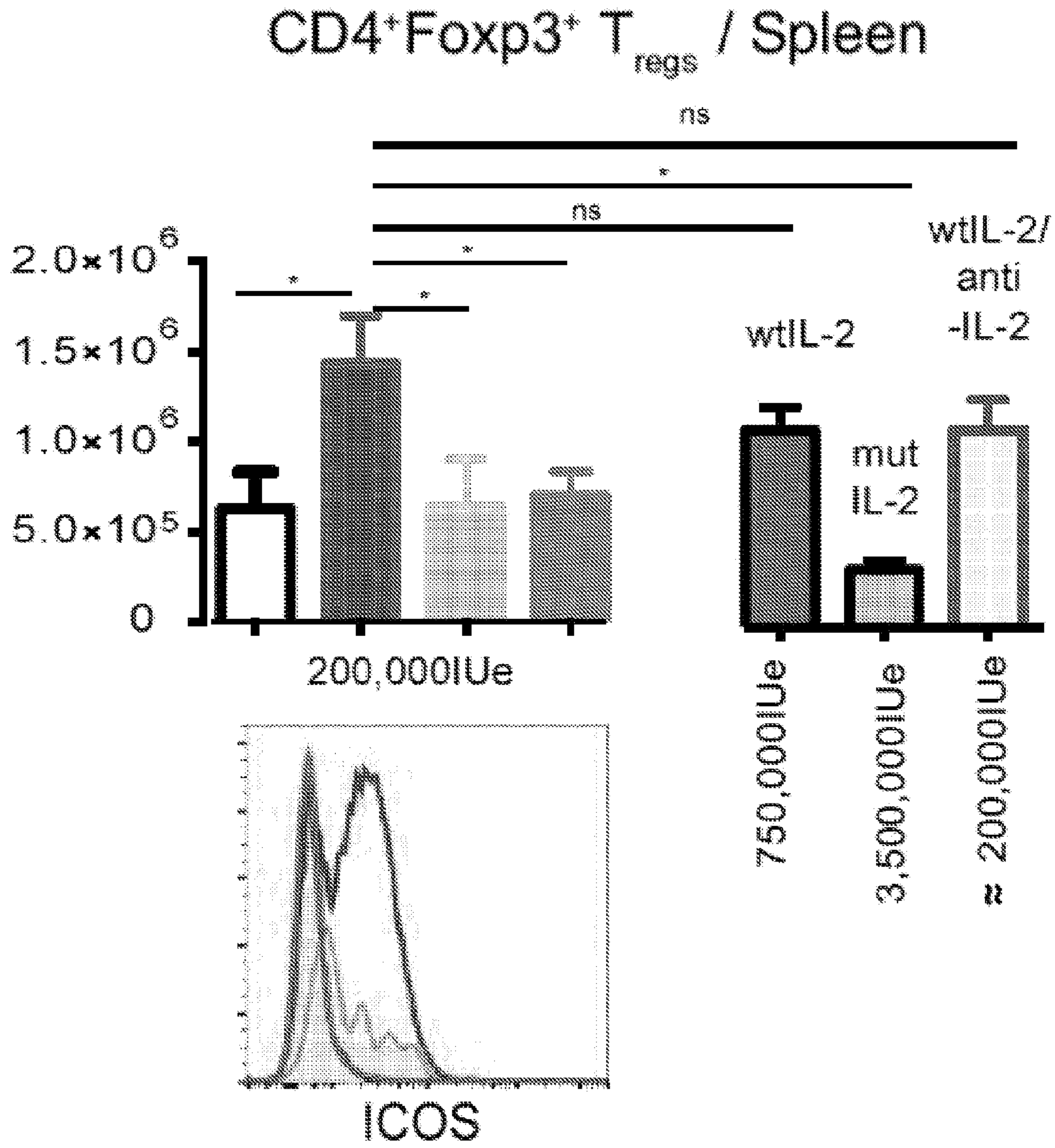
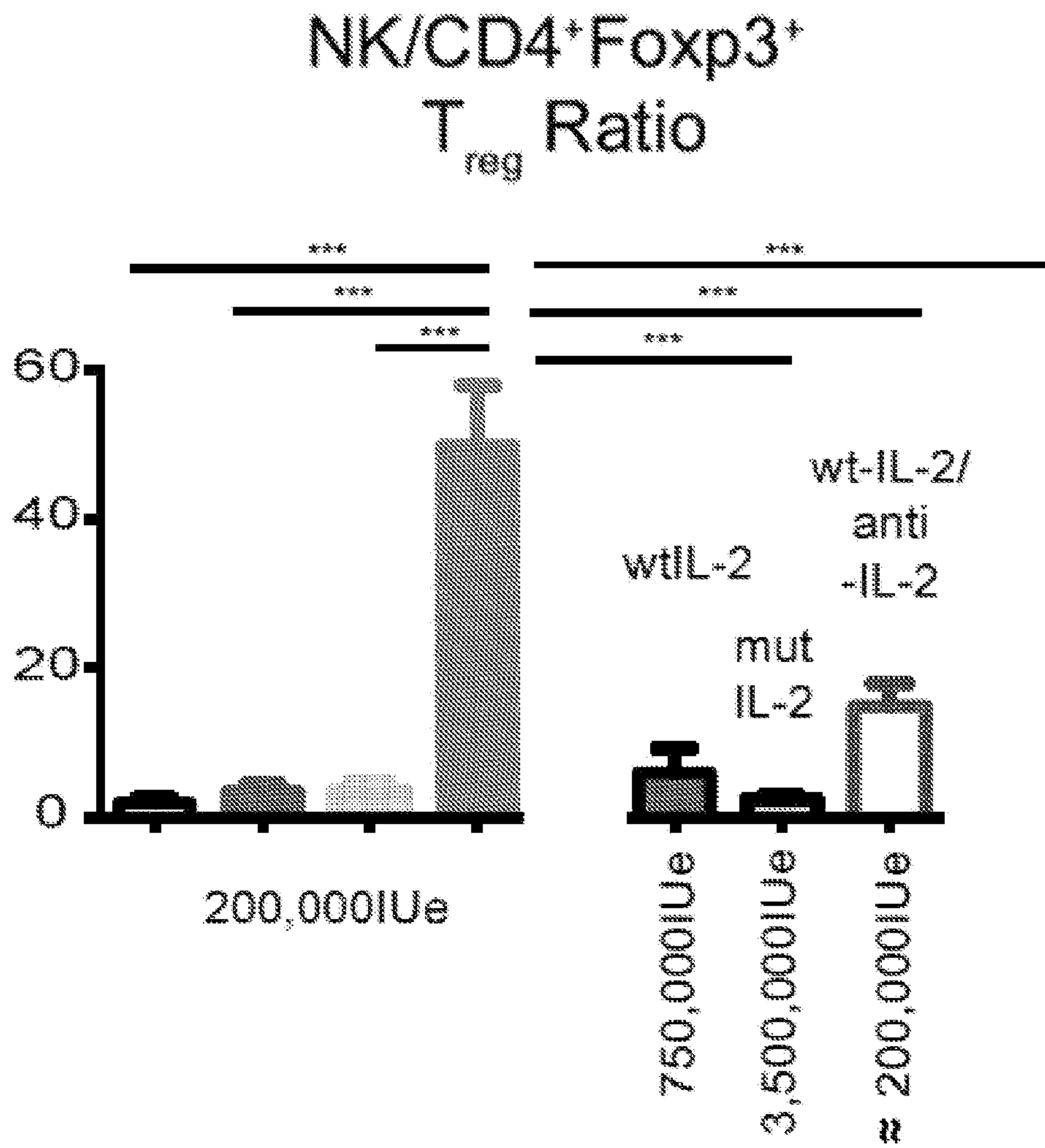


FIG. 3C



Saline, wtlIL-2, mutIL-2, OMCP-mutIL-2

FIG. 3D



Saline, wtlIL-2, mutIL-2, OMCP-mutIL-2

FIG. 3E

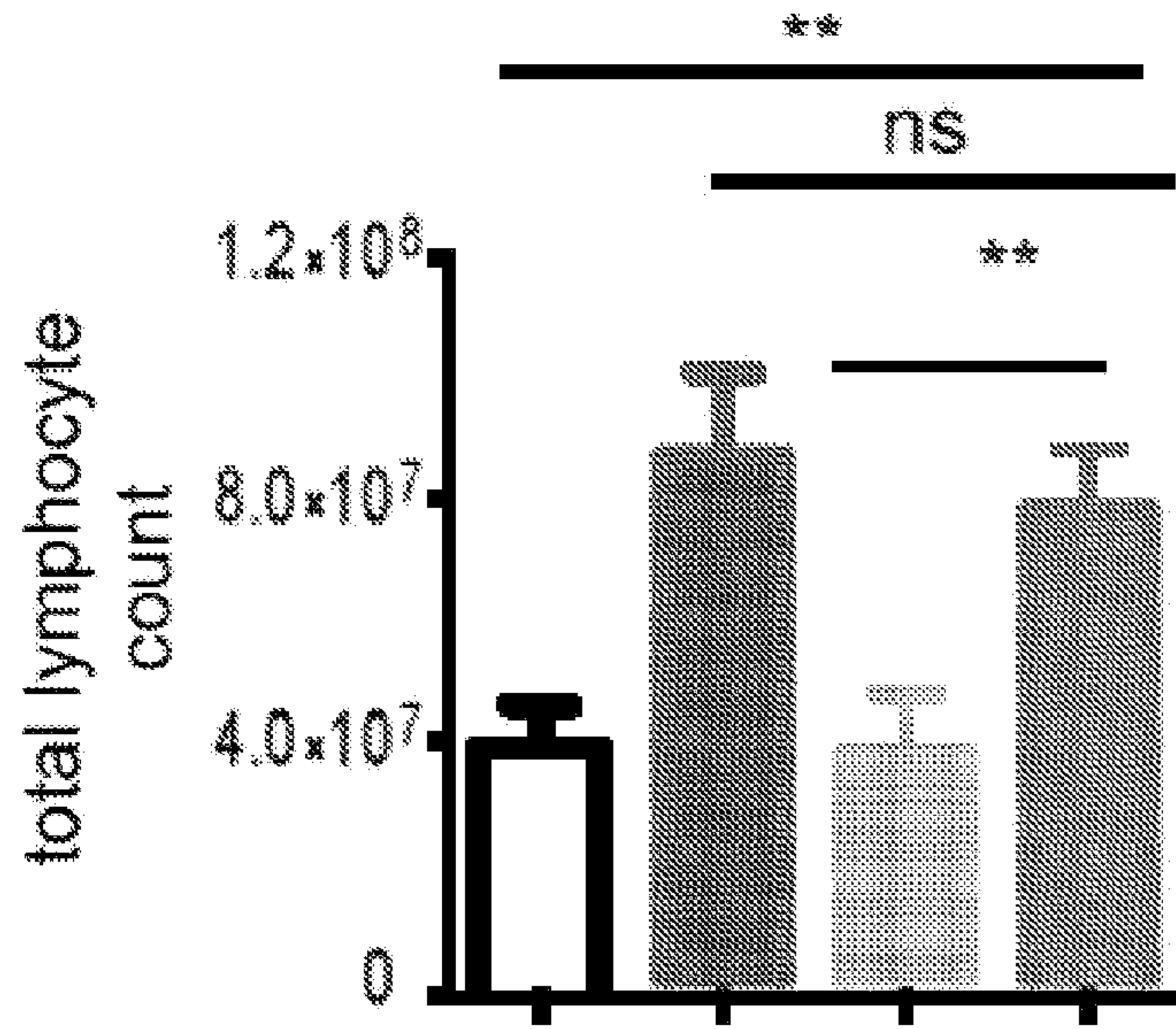


FIG. 3F

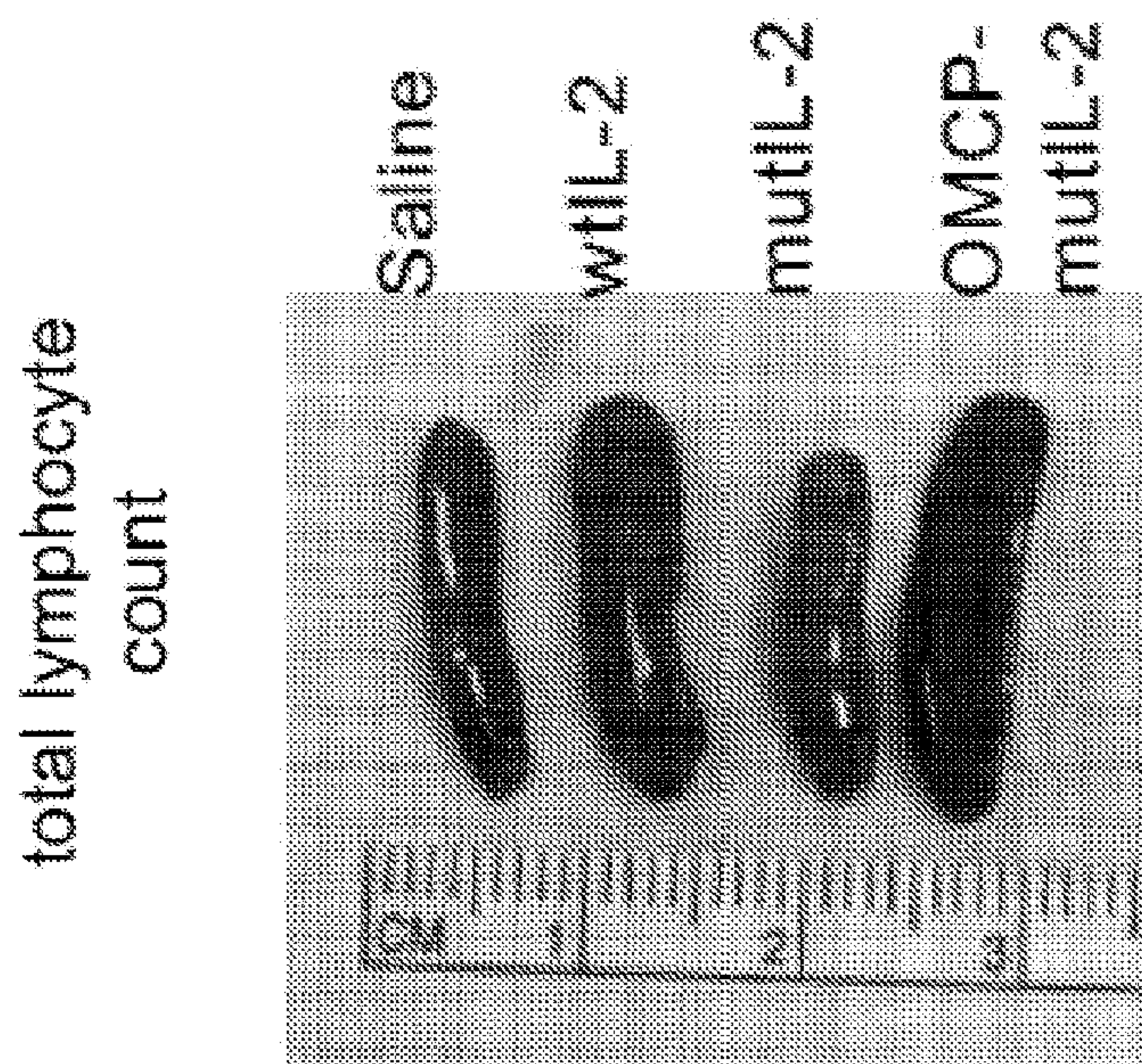


FIG. 3G

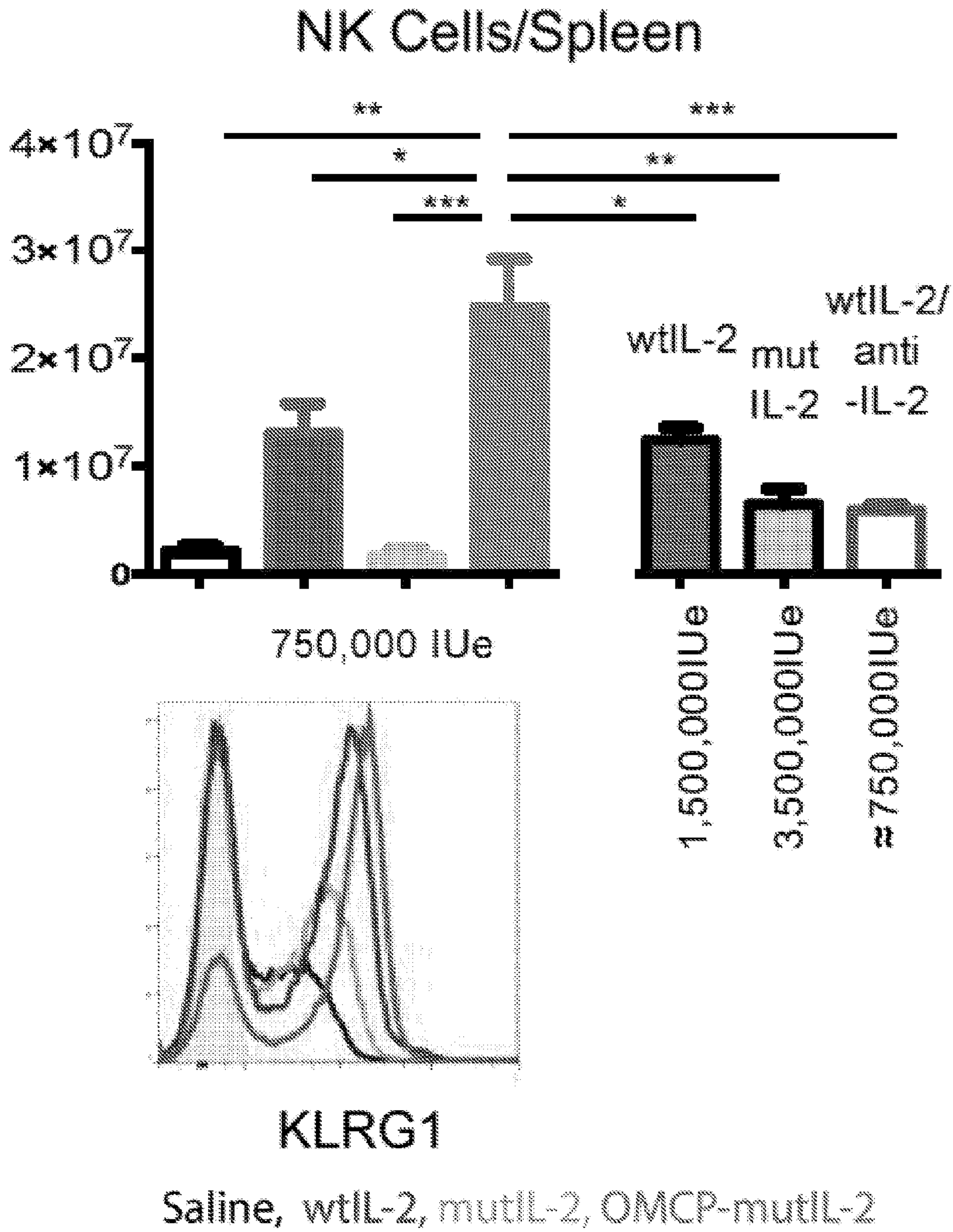
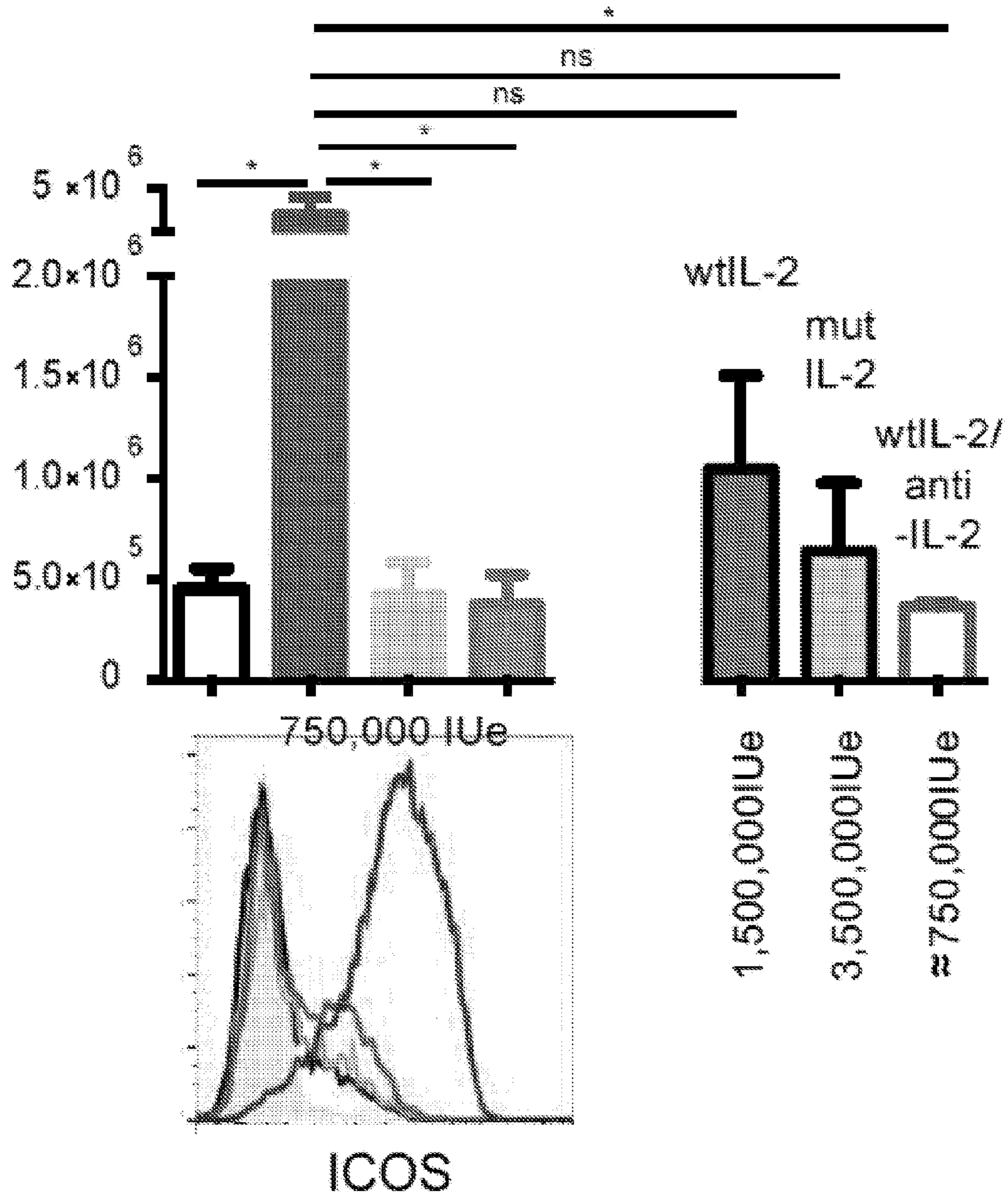
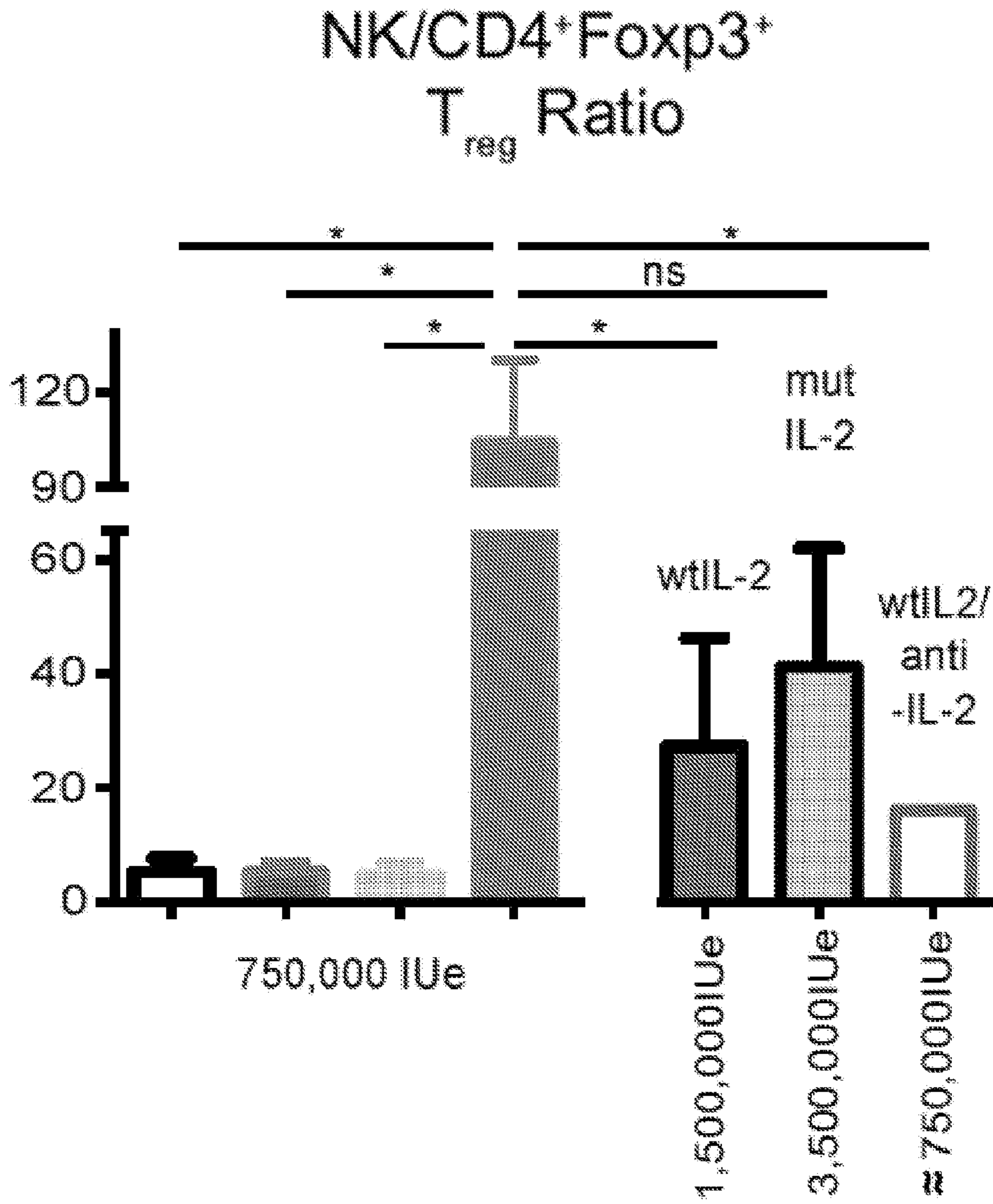


FIG. 3H

CD4⁺Foxp3⁺ T_{regs} / Spleen

Saline, wtIL-2, mutIL-2, OMCP-mutIL-2

FIG. 3I



Saline, wtlIL-2, mutIL-2, OMCP-mutIL-2

FIG. 3J

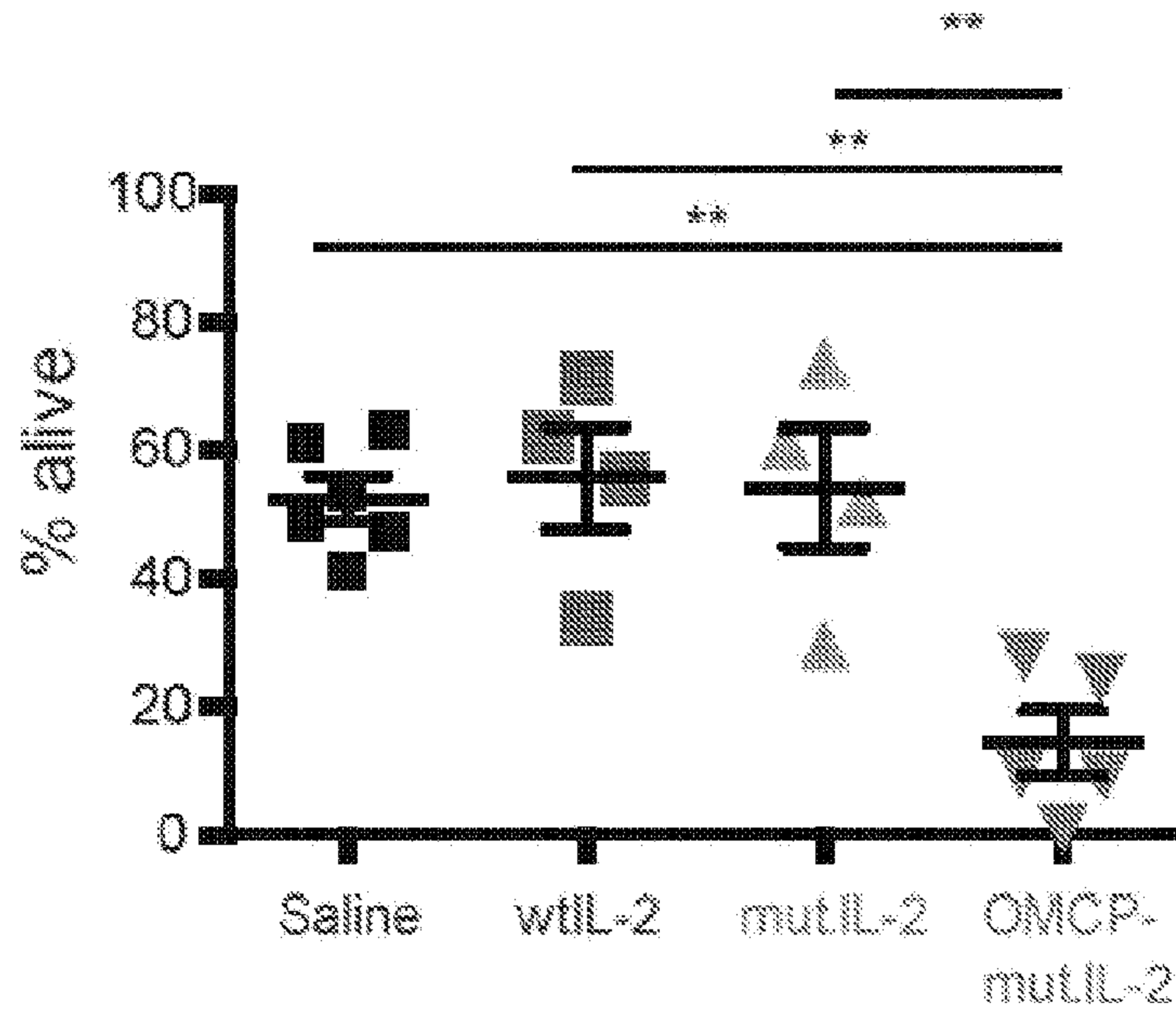


FIG. 4A

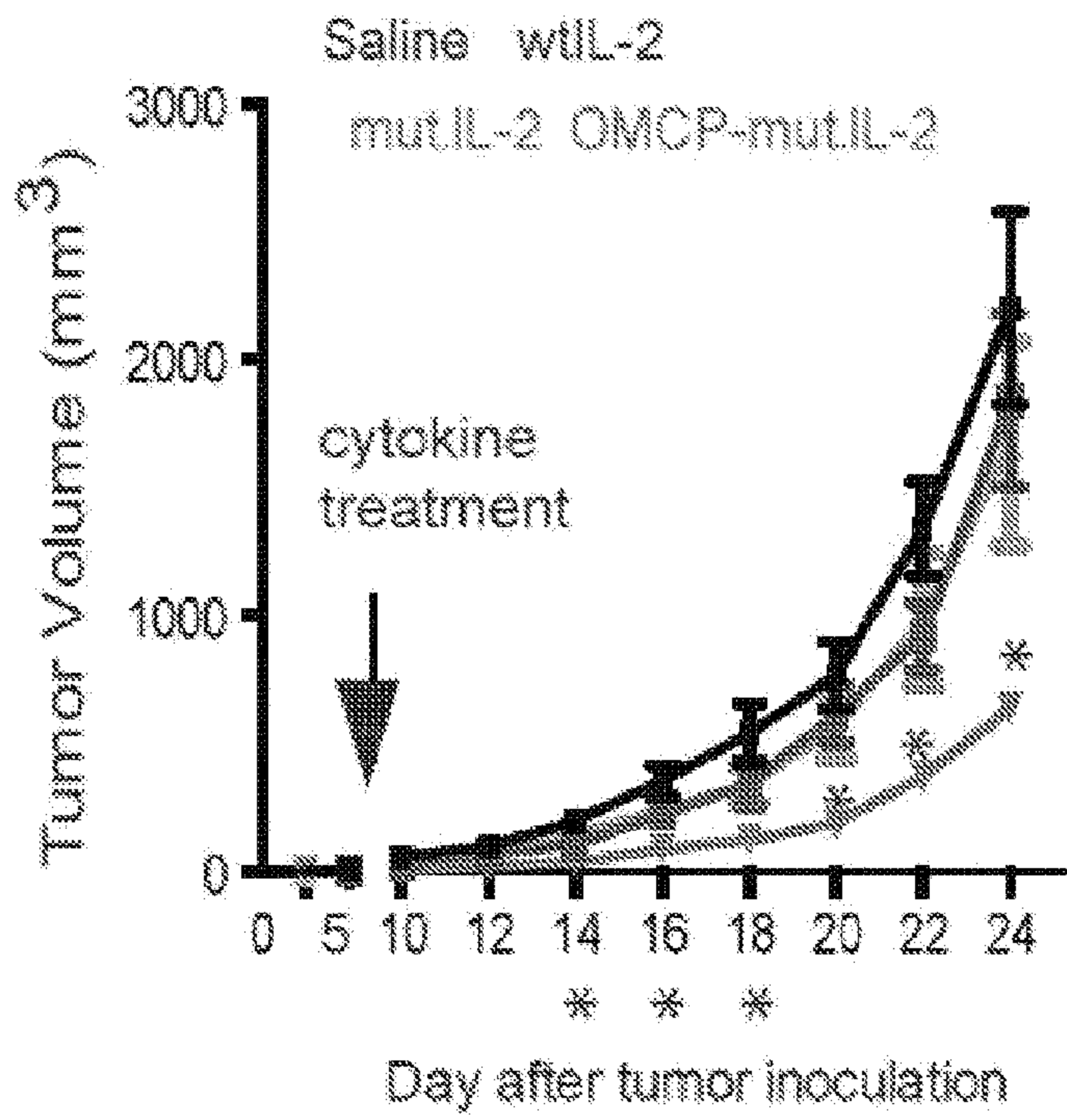


FIG. 4B

Saline wtIL-2 mult-2 OMCP-mult-2



FIG. 4C

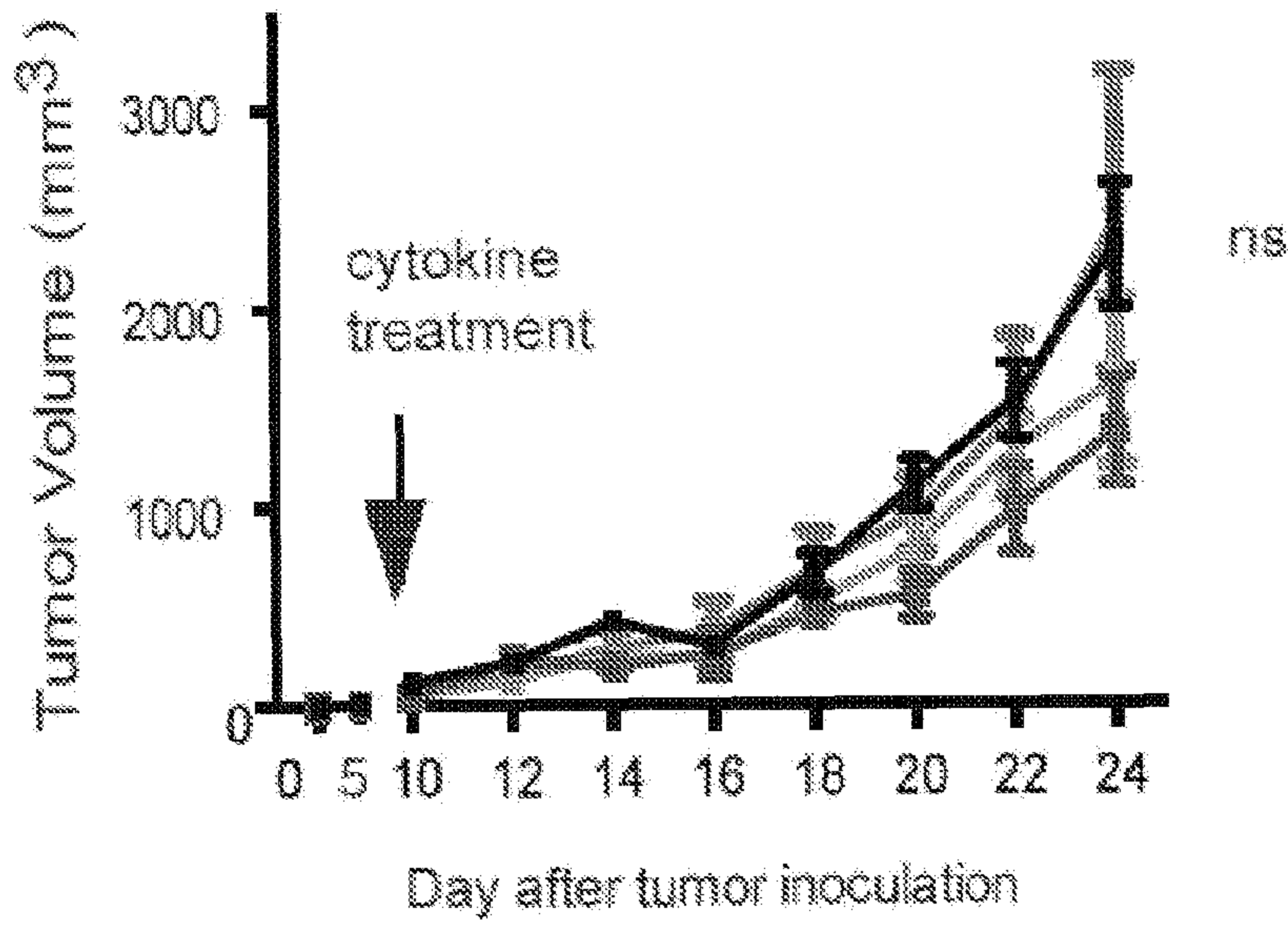


FIG. 4D

Saline wtIL-2 mutIL-2 OMCP-mutIL-2

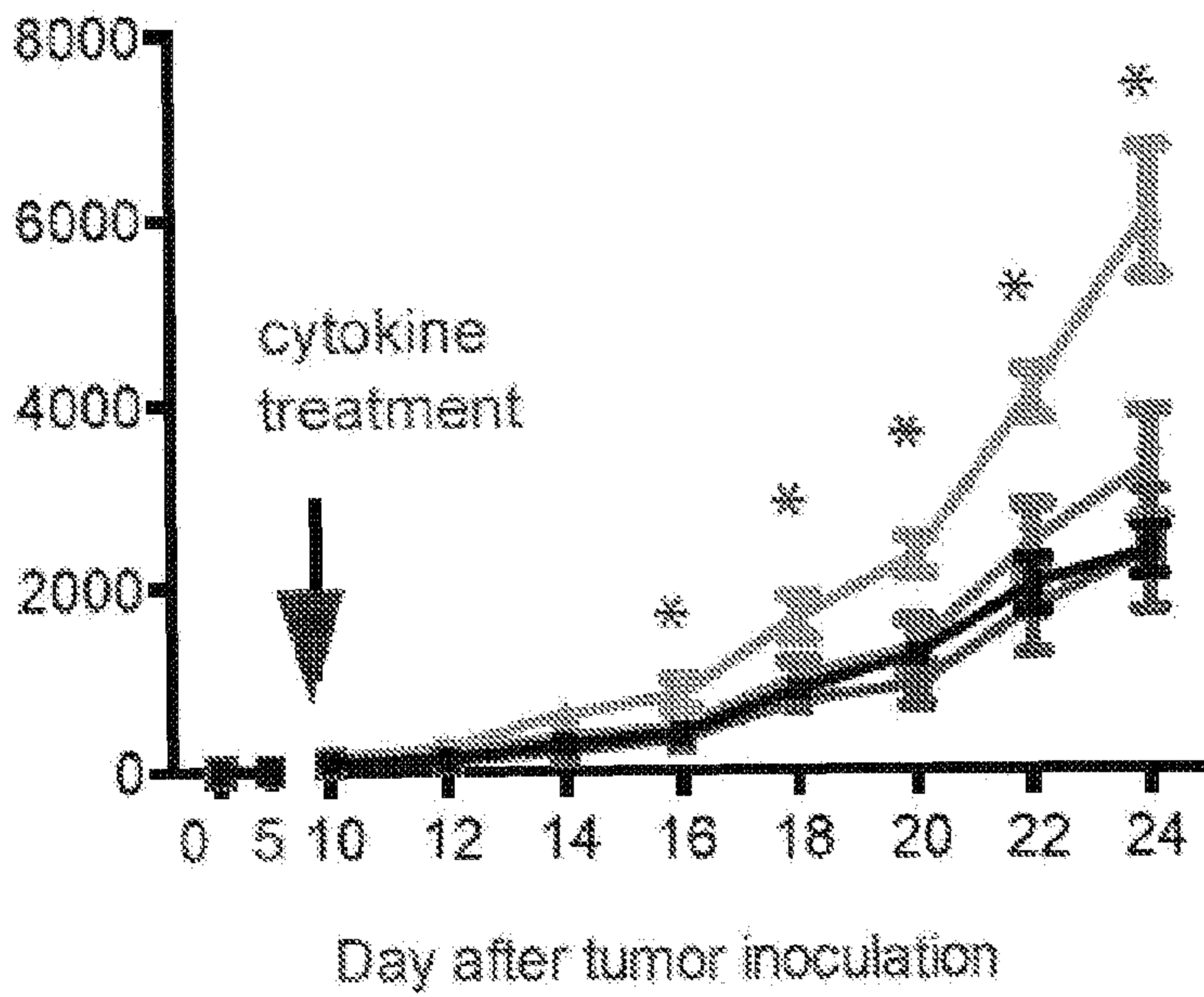


FIG. 4E

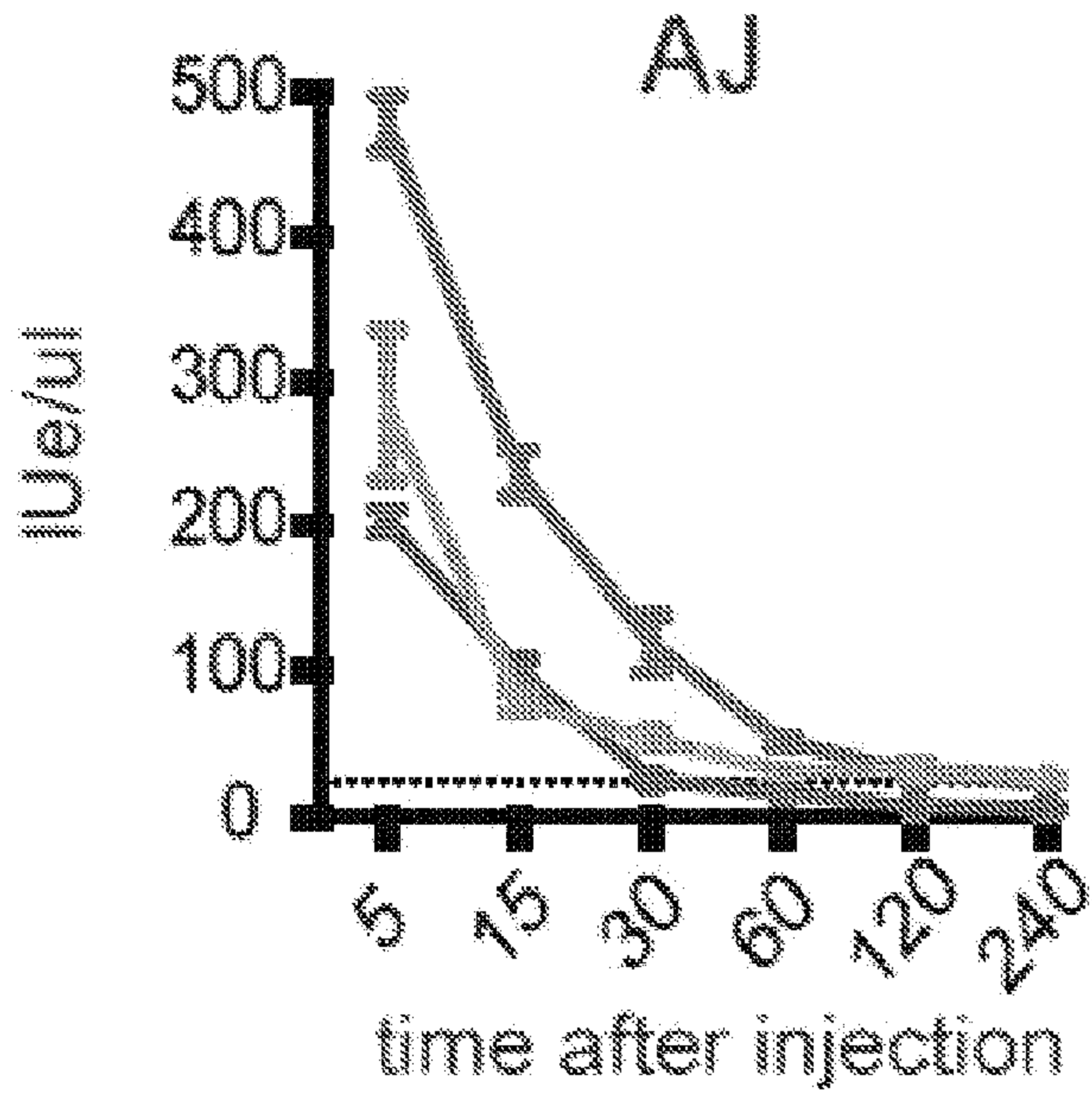


FIG. 5A

OMCP-mutIL-2, wtIL-2, mutIL-2

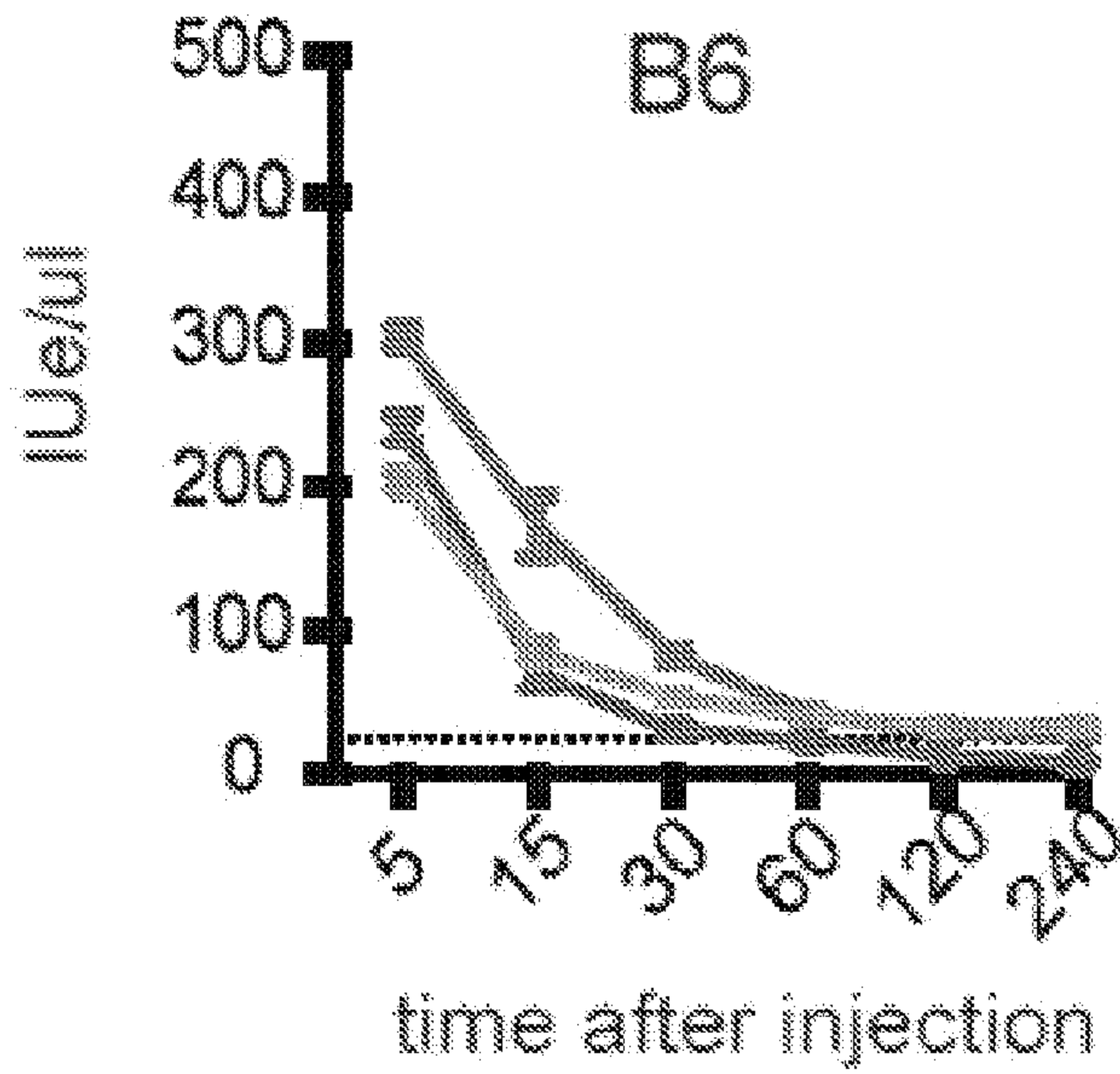
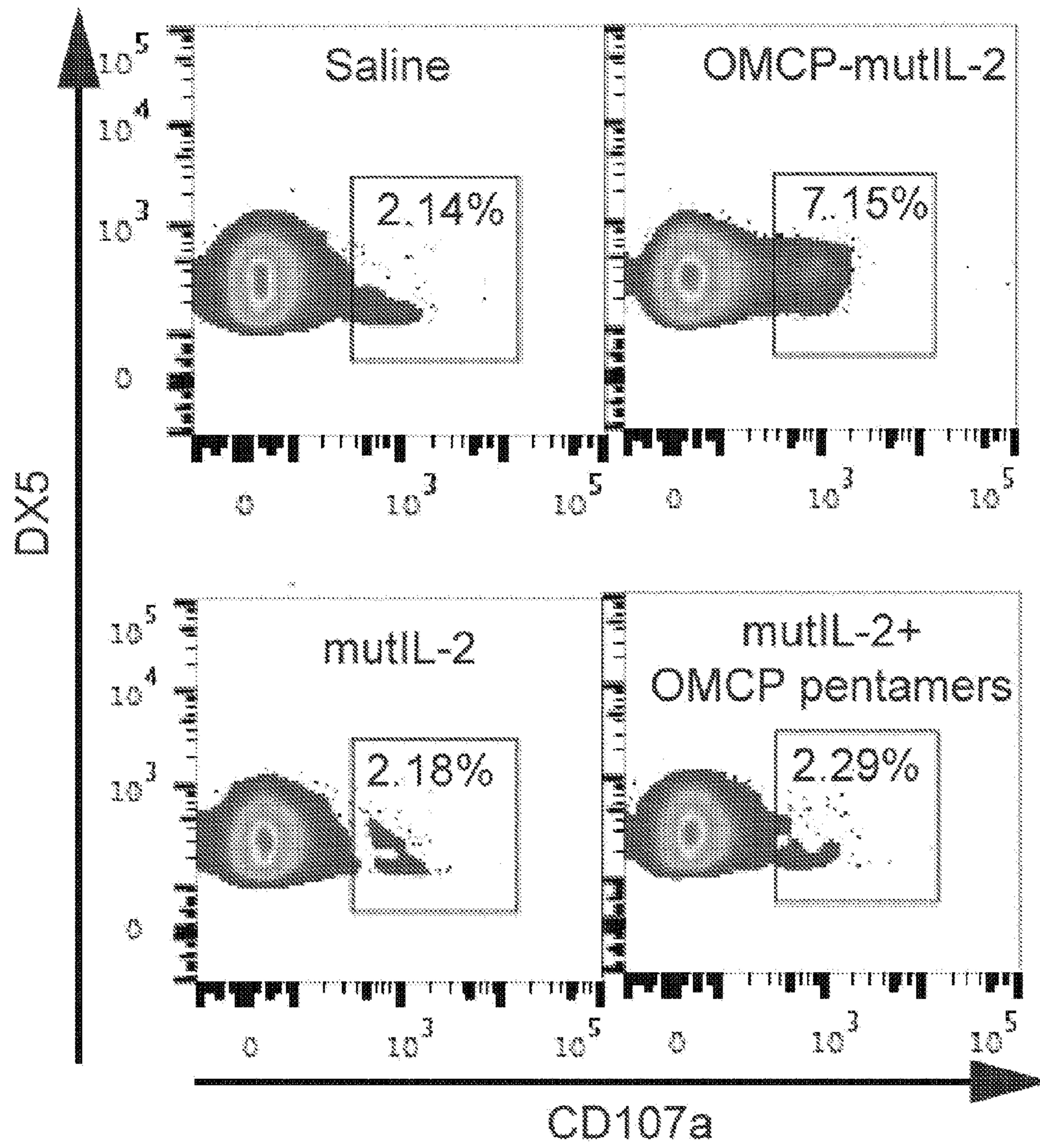


FIG. 5B

**FIG. 5C**

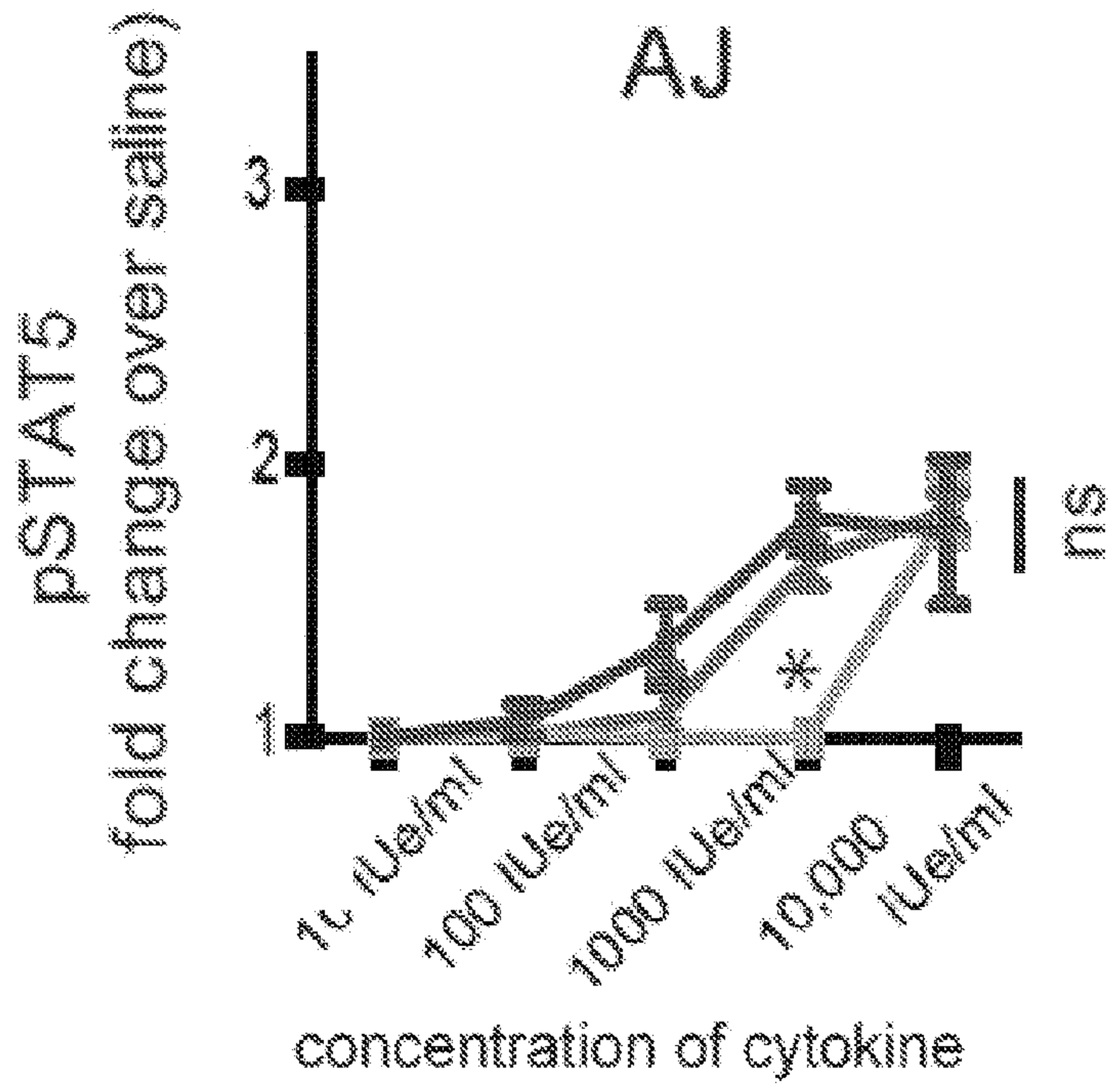


FIG. 5D

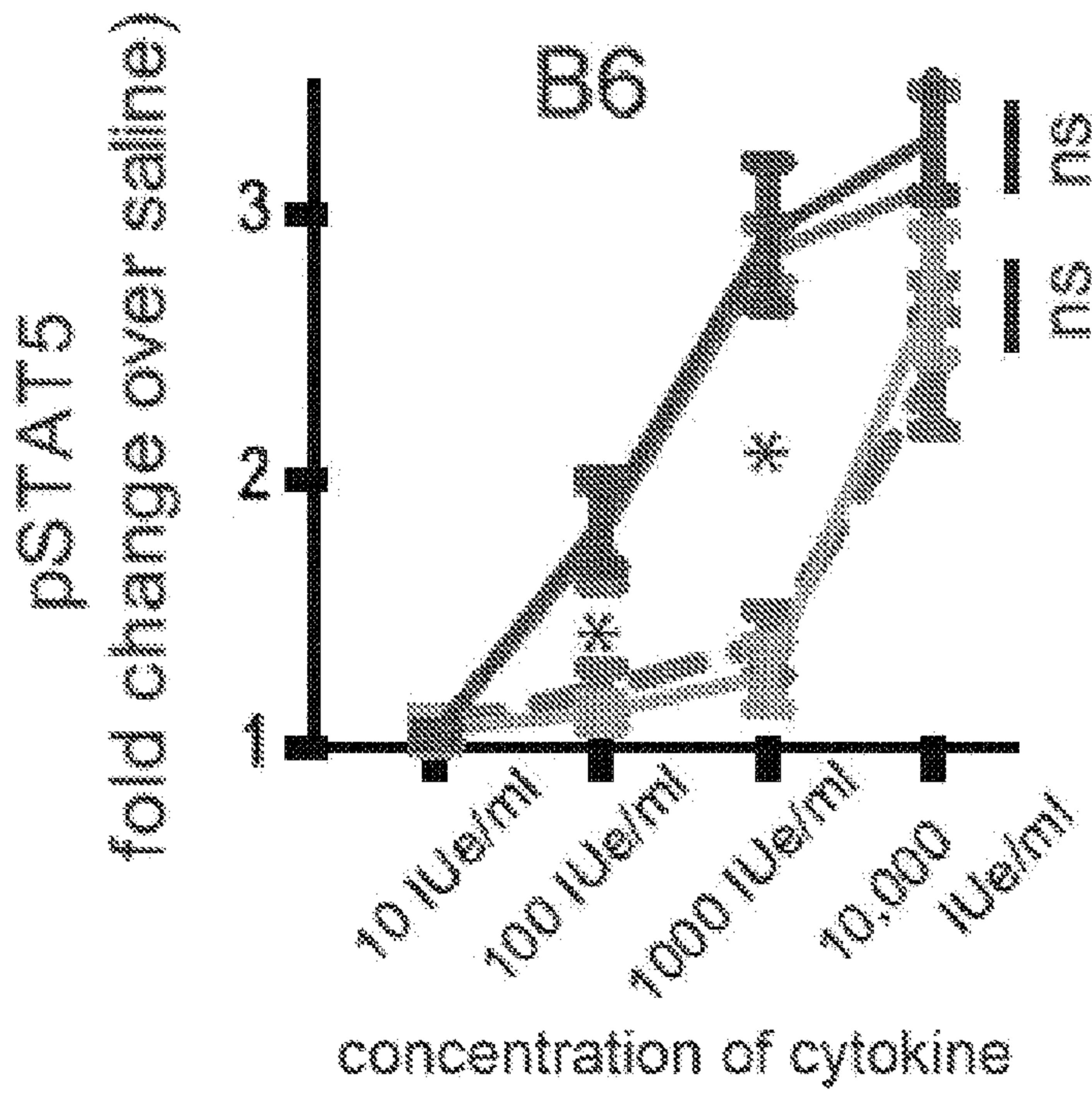
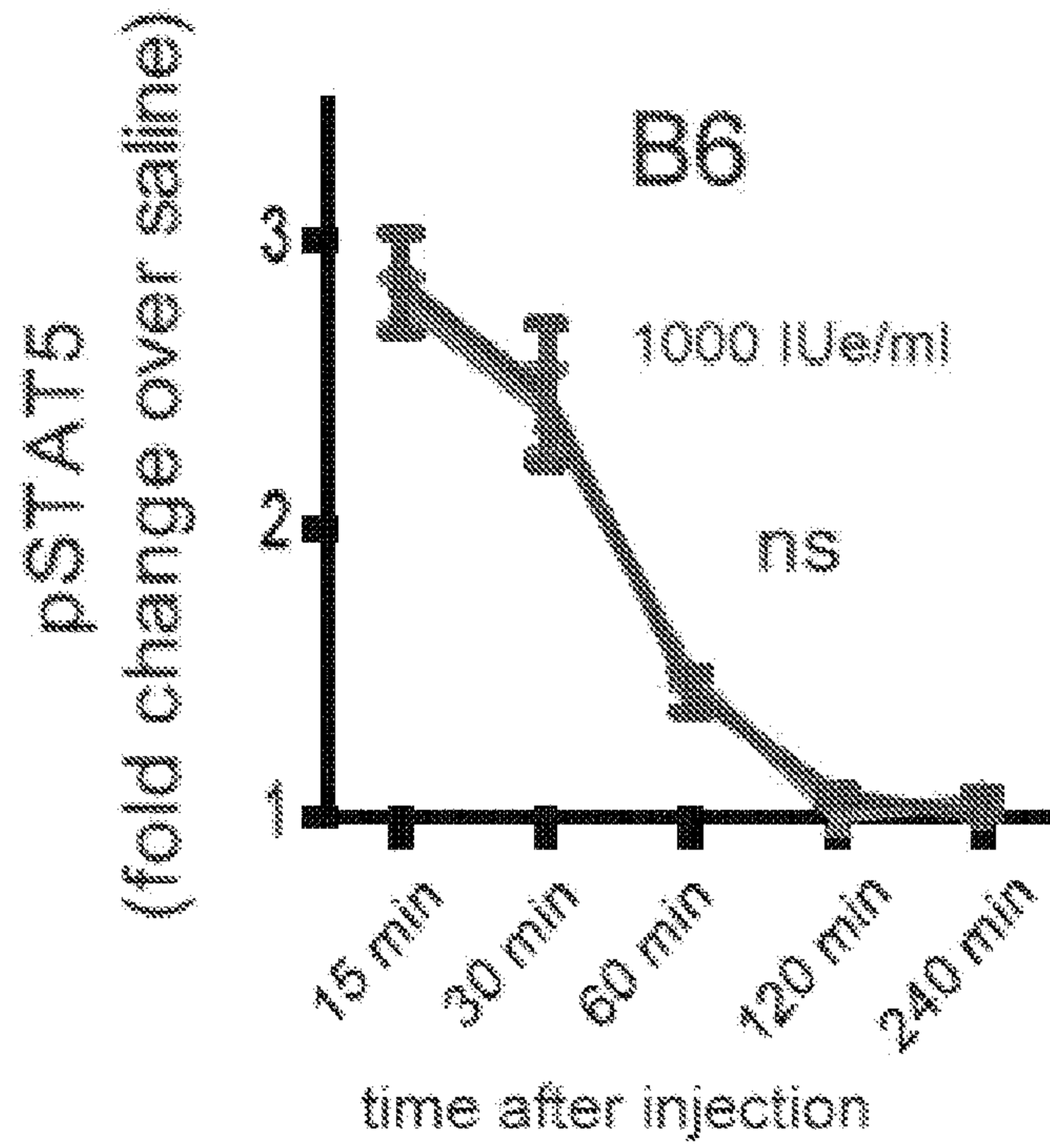
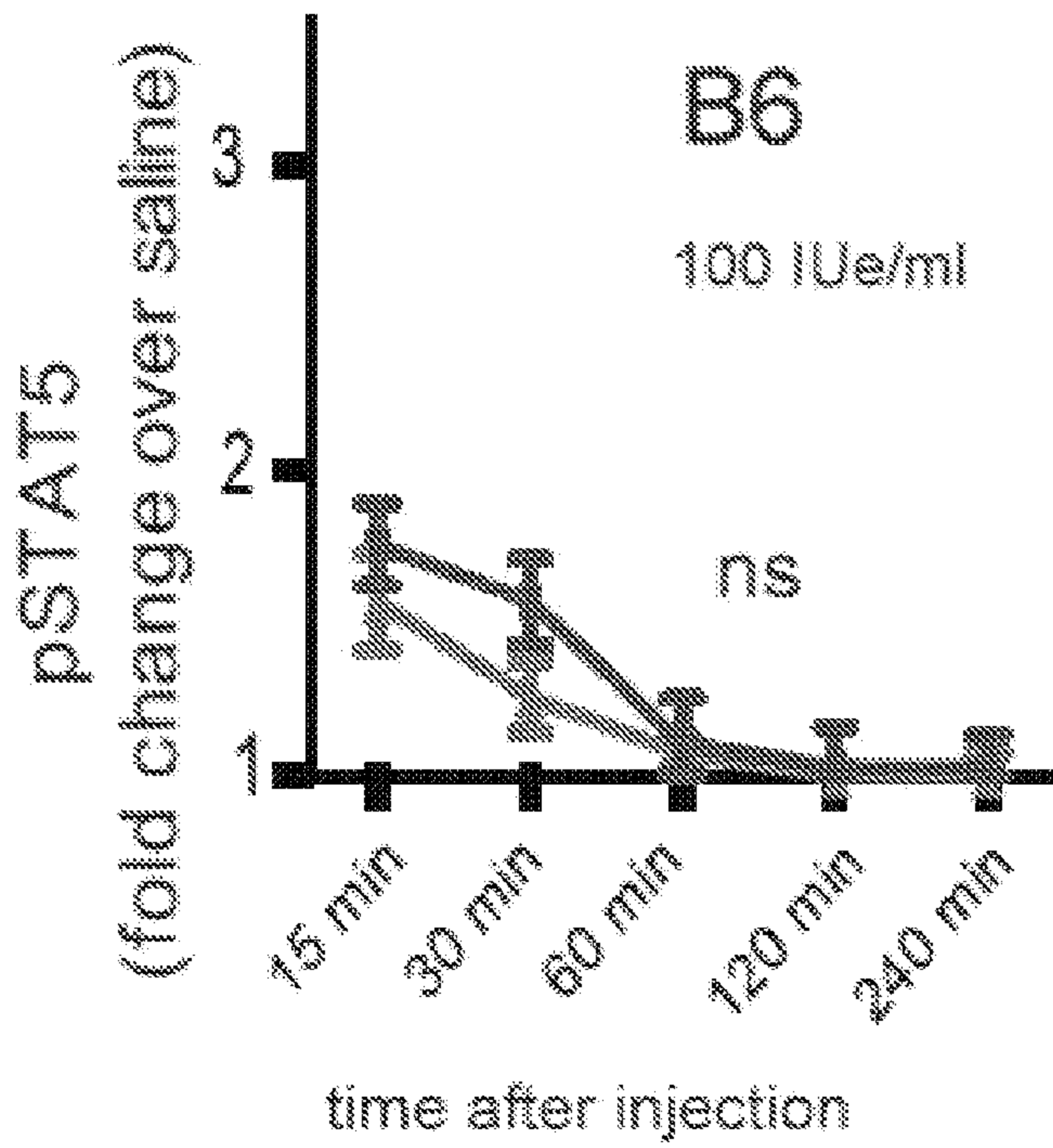


FIG. 5E

**FIG. 5F****FIG. 5G**

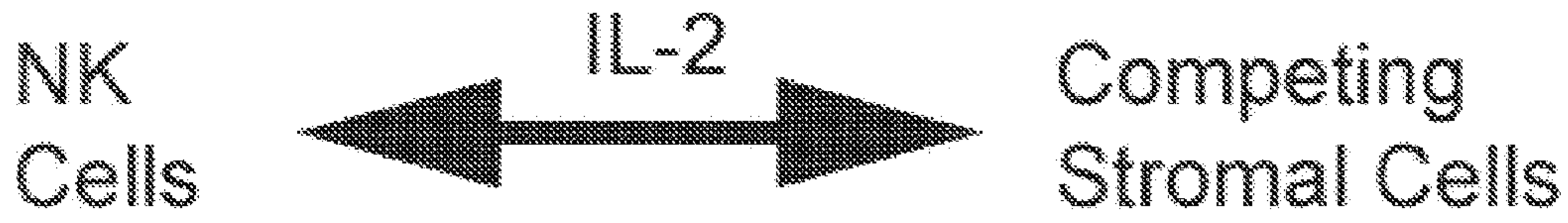


FIG. 5H

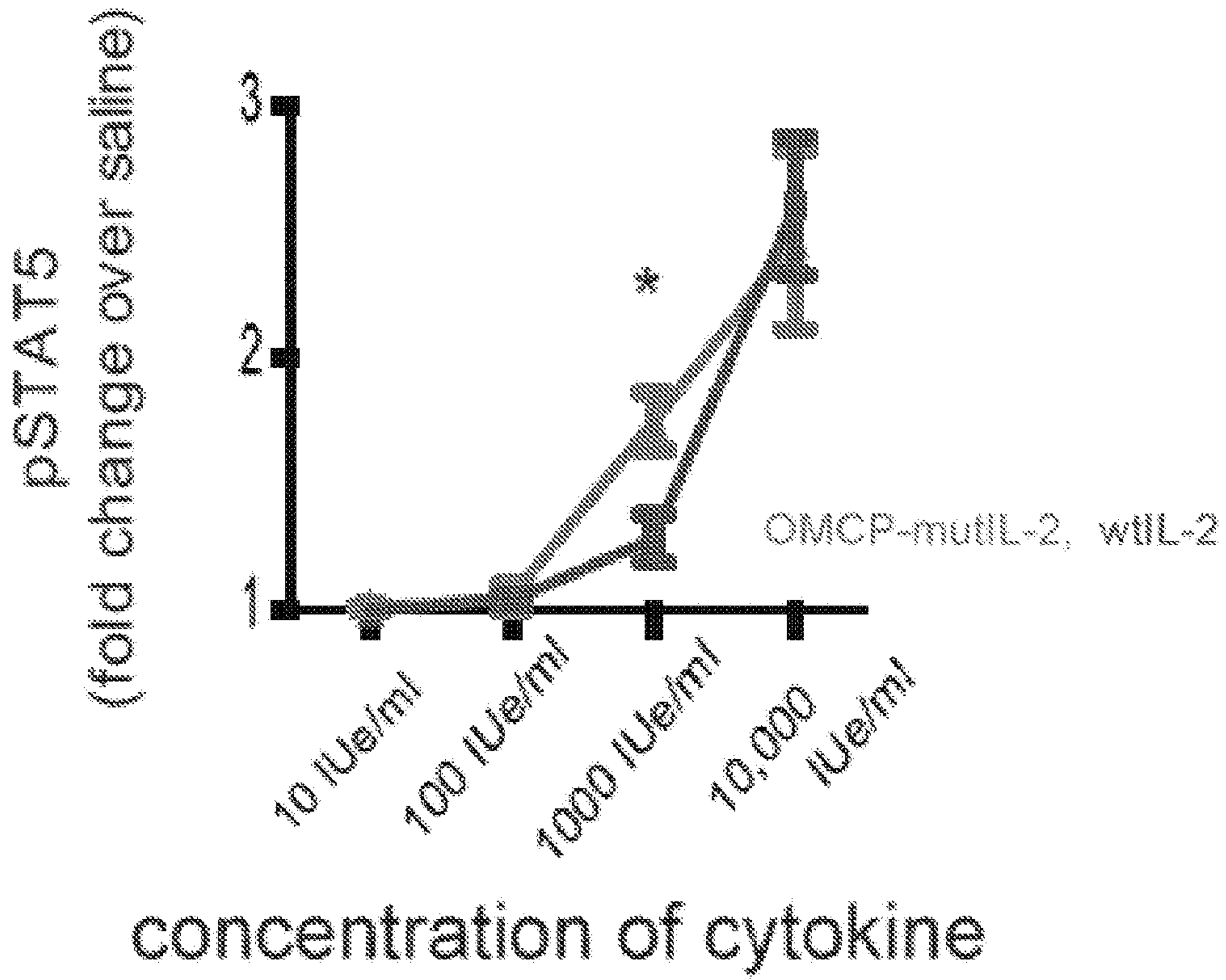
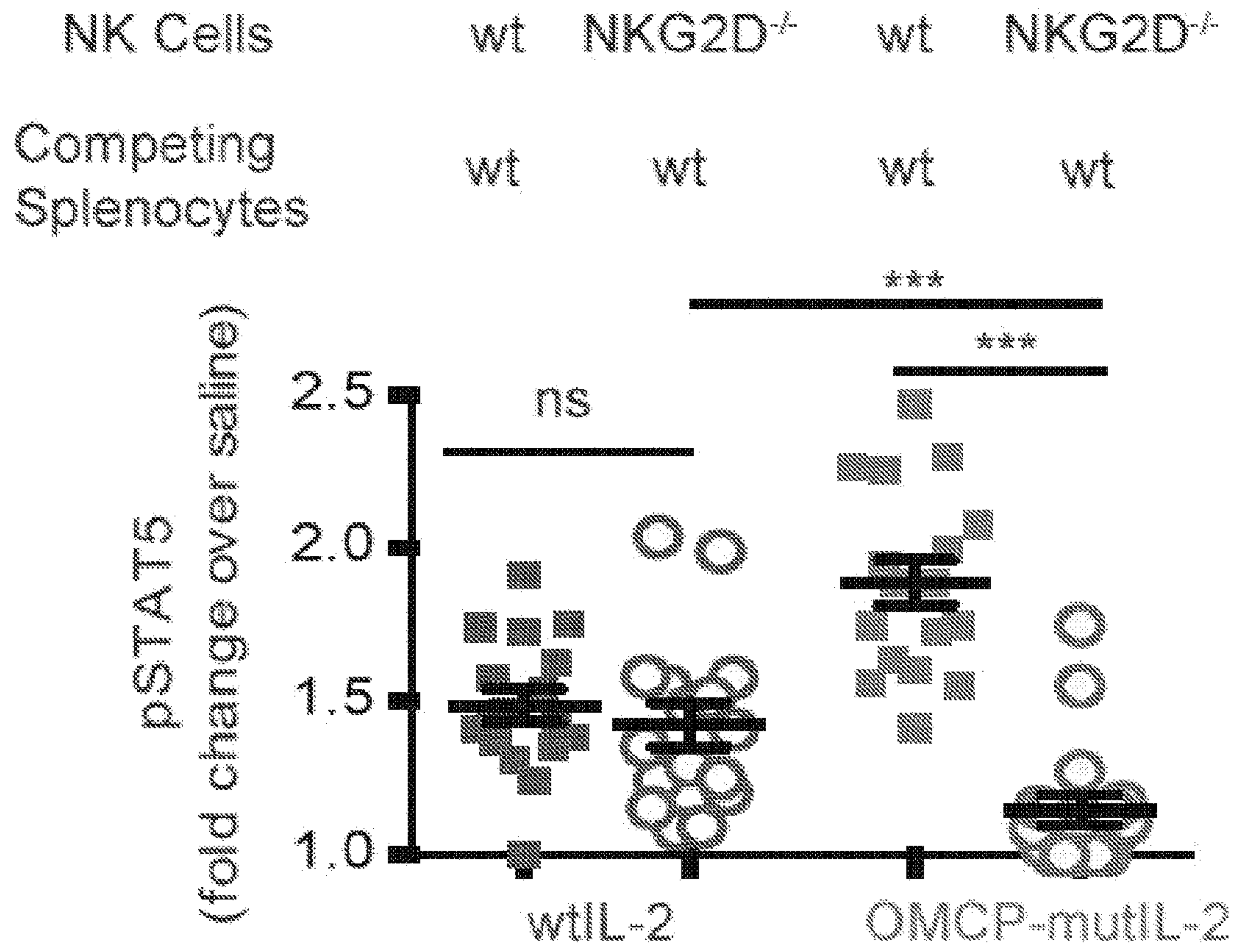
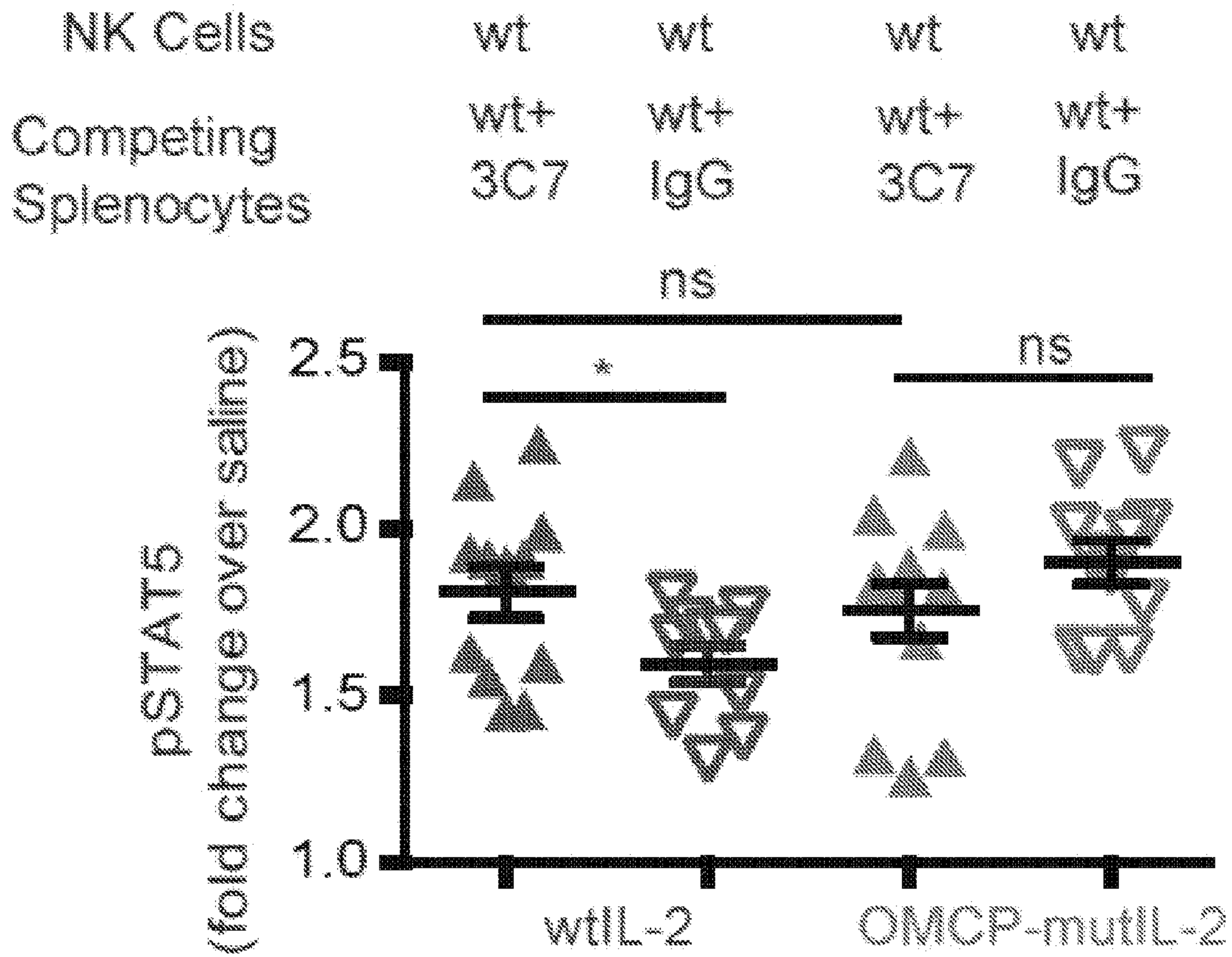
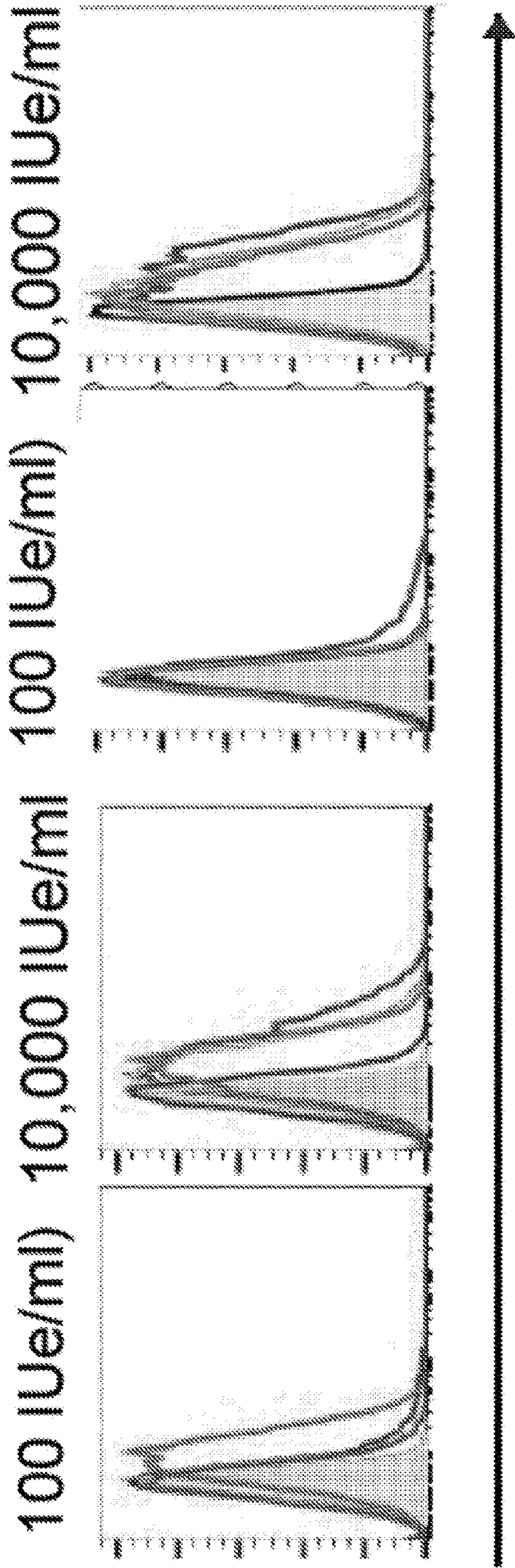


FIG. 5I

**FIG. 5J**

NK cells + splenocytes

**FIG. 5K**



Saline, OMCP-mutL-2,
wild-type IL-2, mutL-2, isotype

FIG. 6

Saline

200,000IUe

750,000IUe



FIG. 7A

FIG. 7B

FIG. 7C

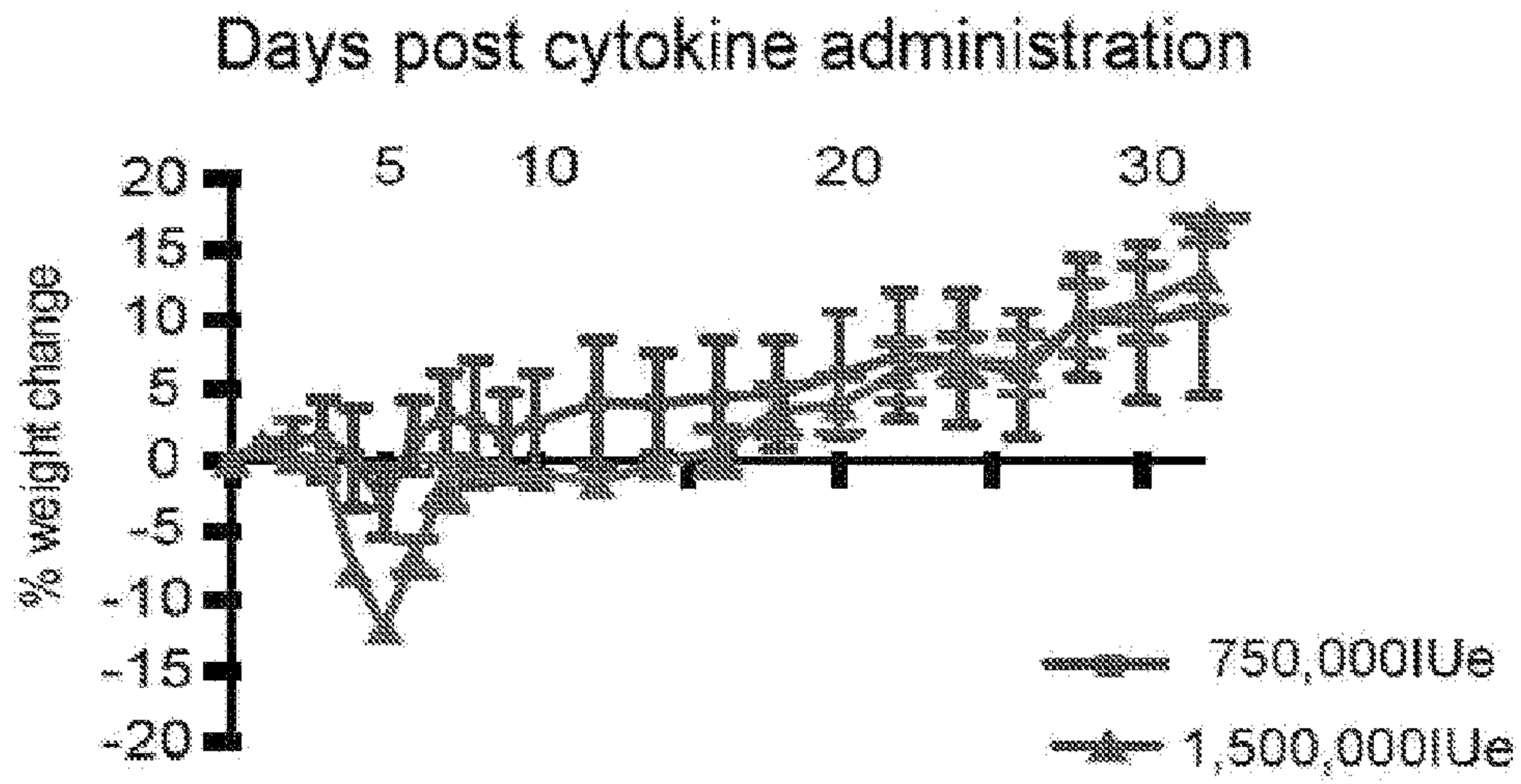
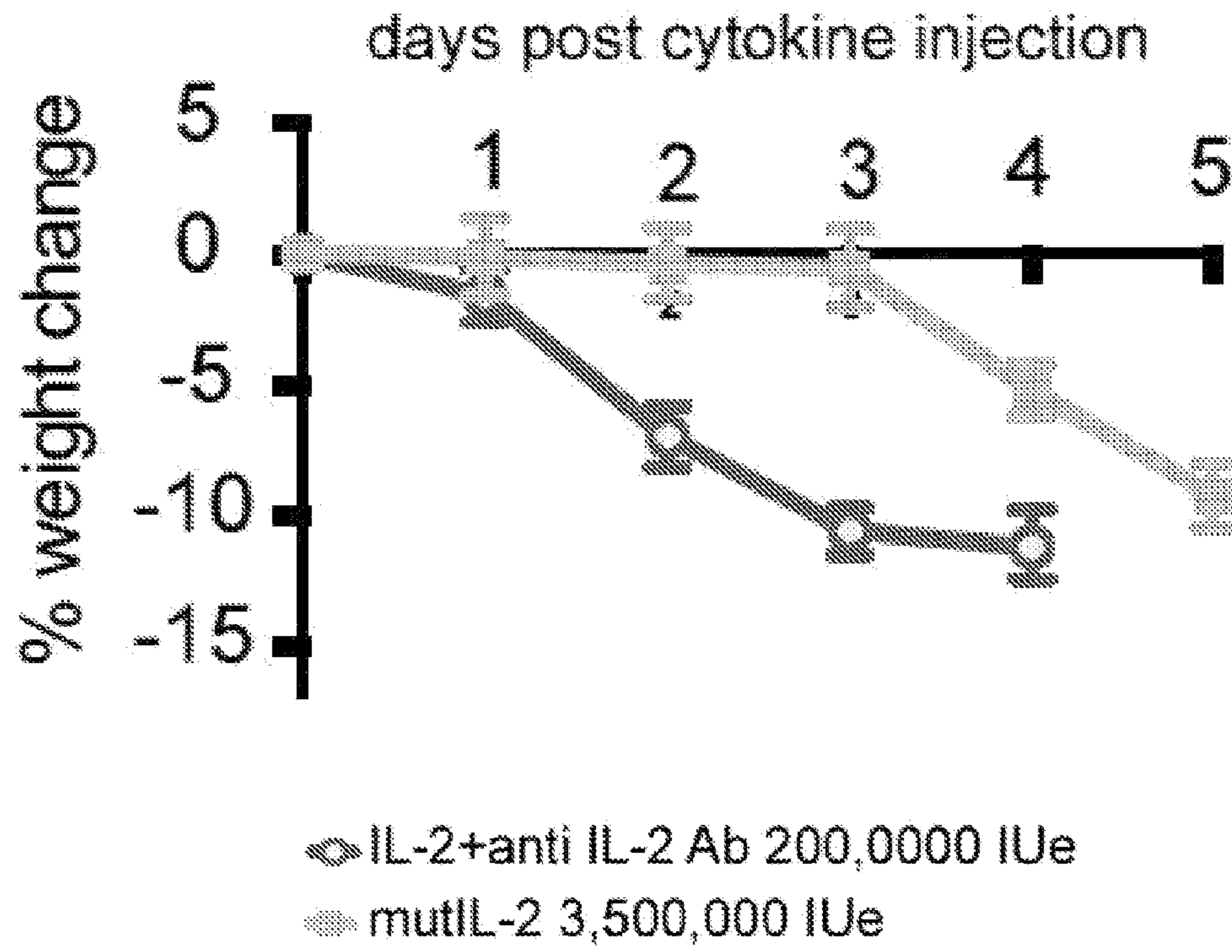


FIG. 7D

**FIG. 8A**

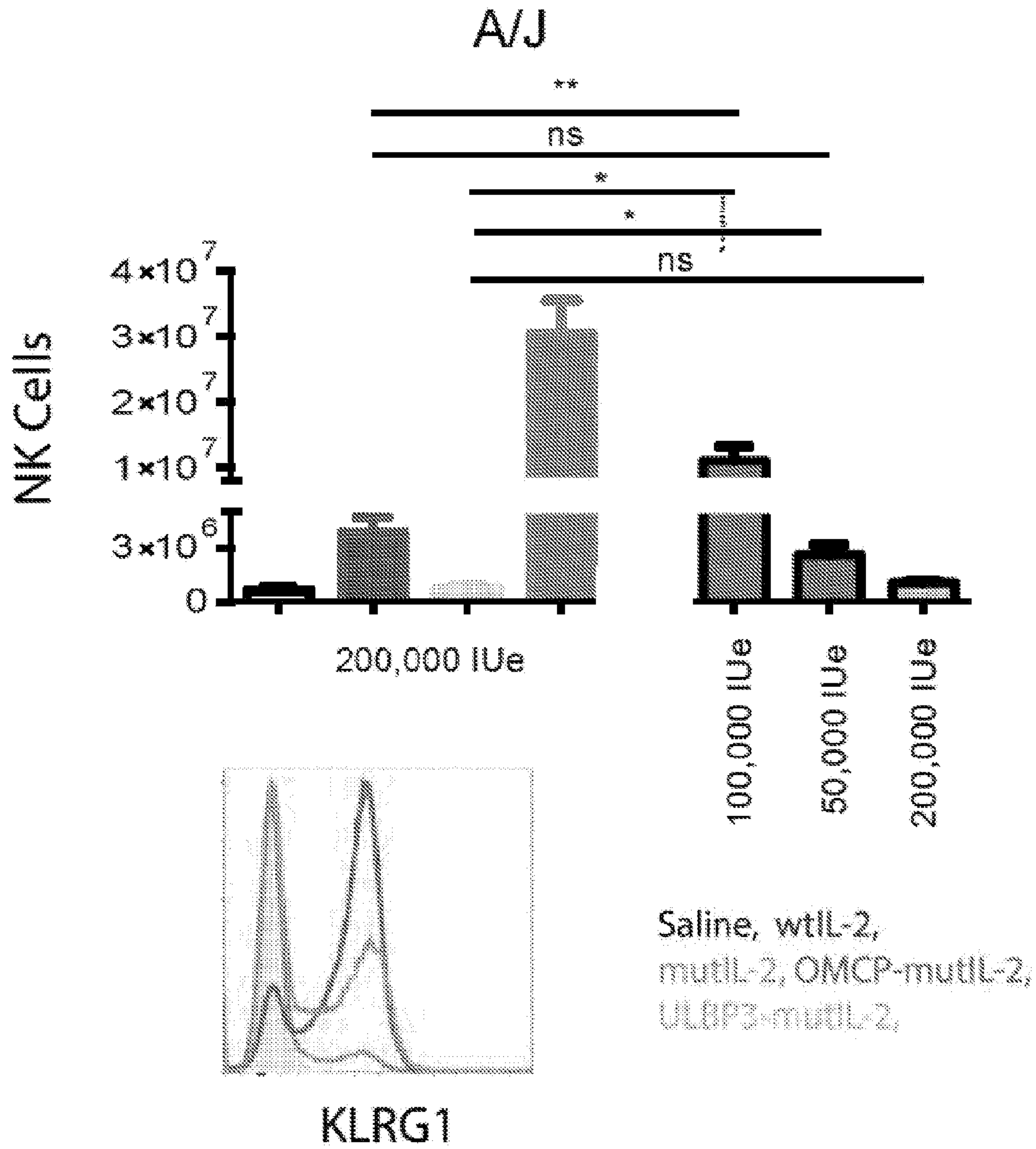
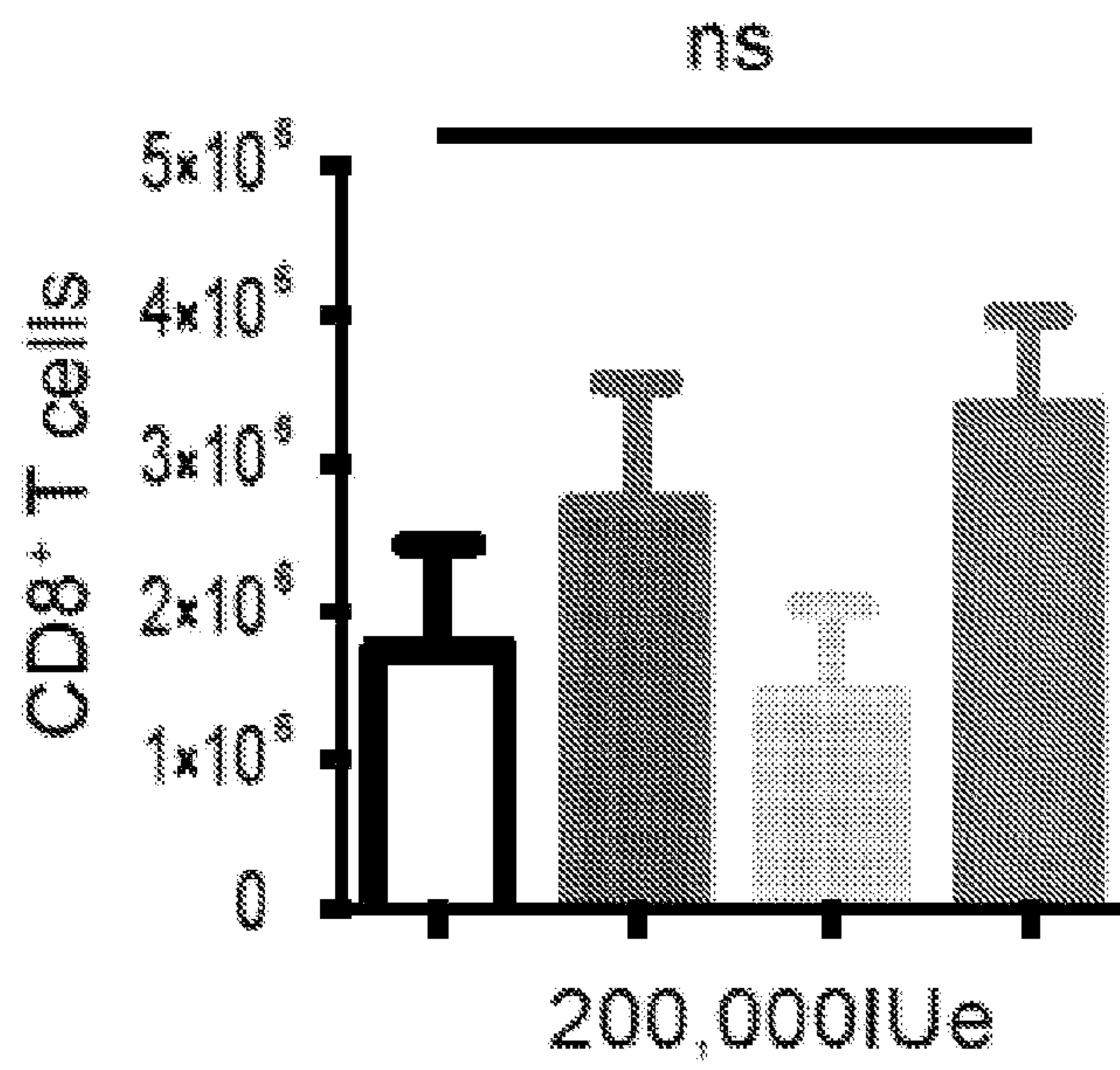
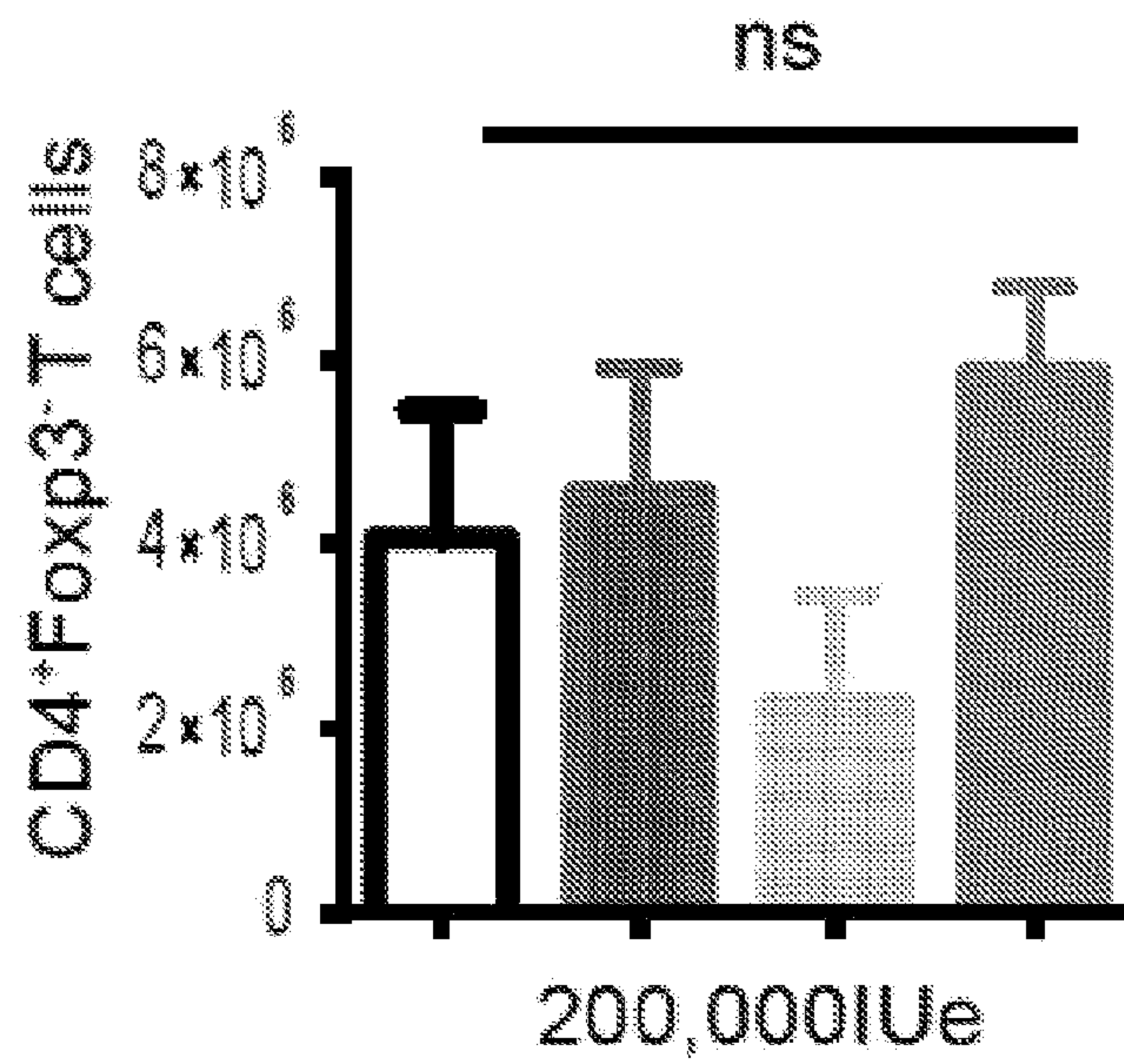
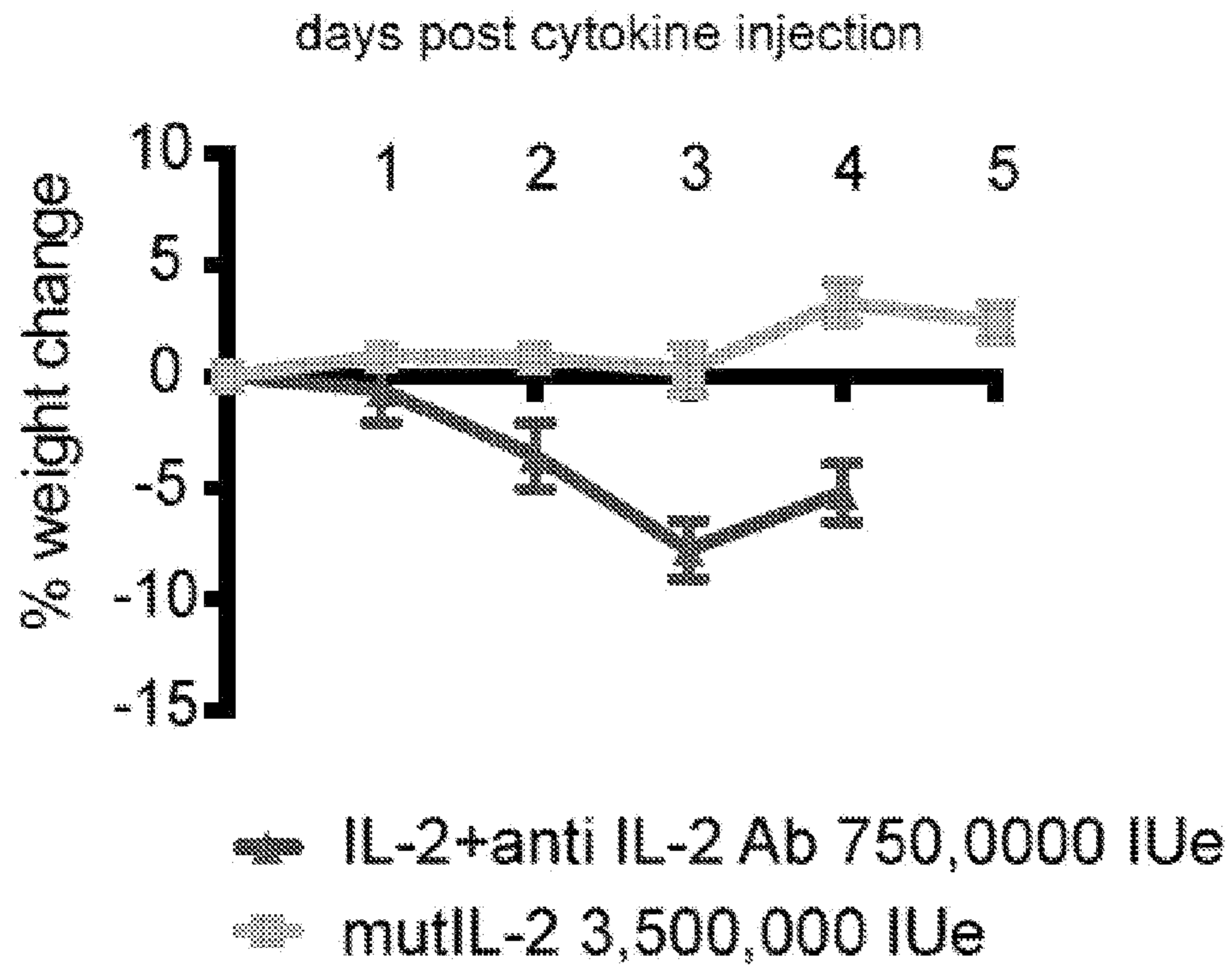


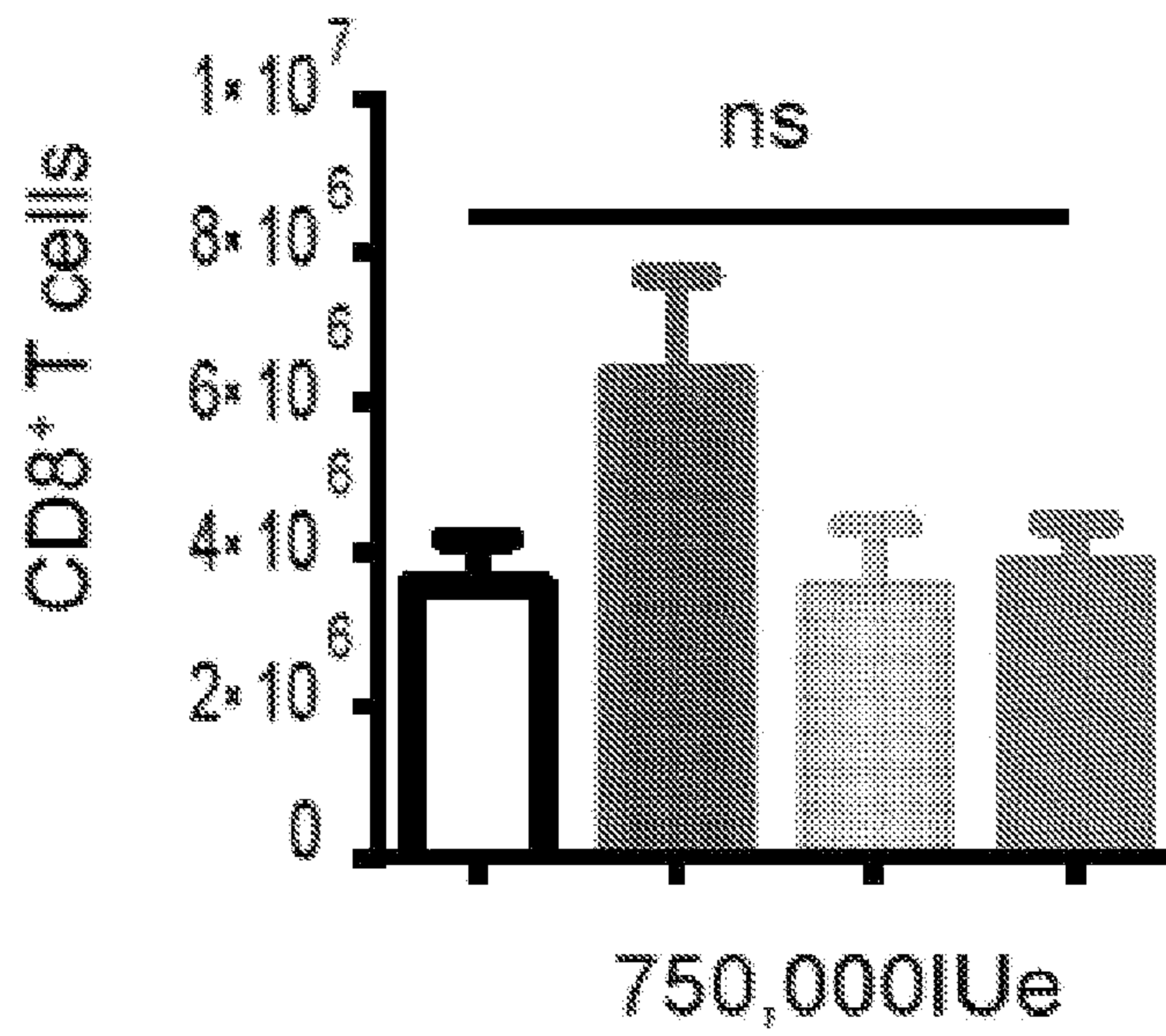
FIG. 8B

**FIG. 8C**

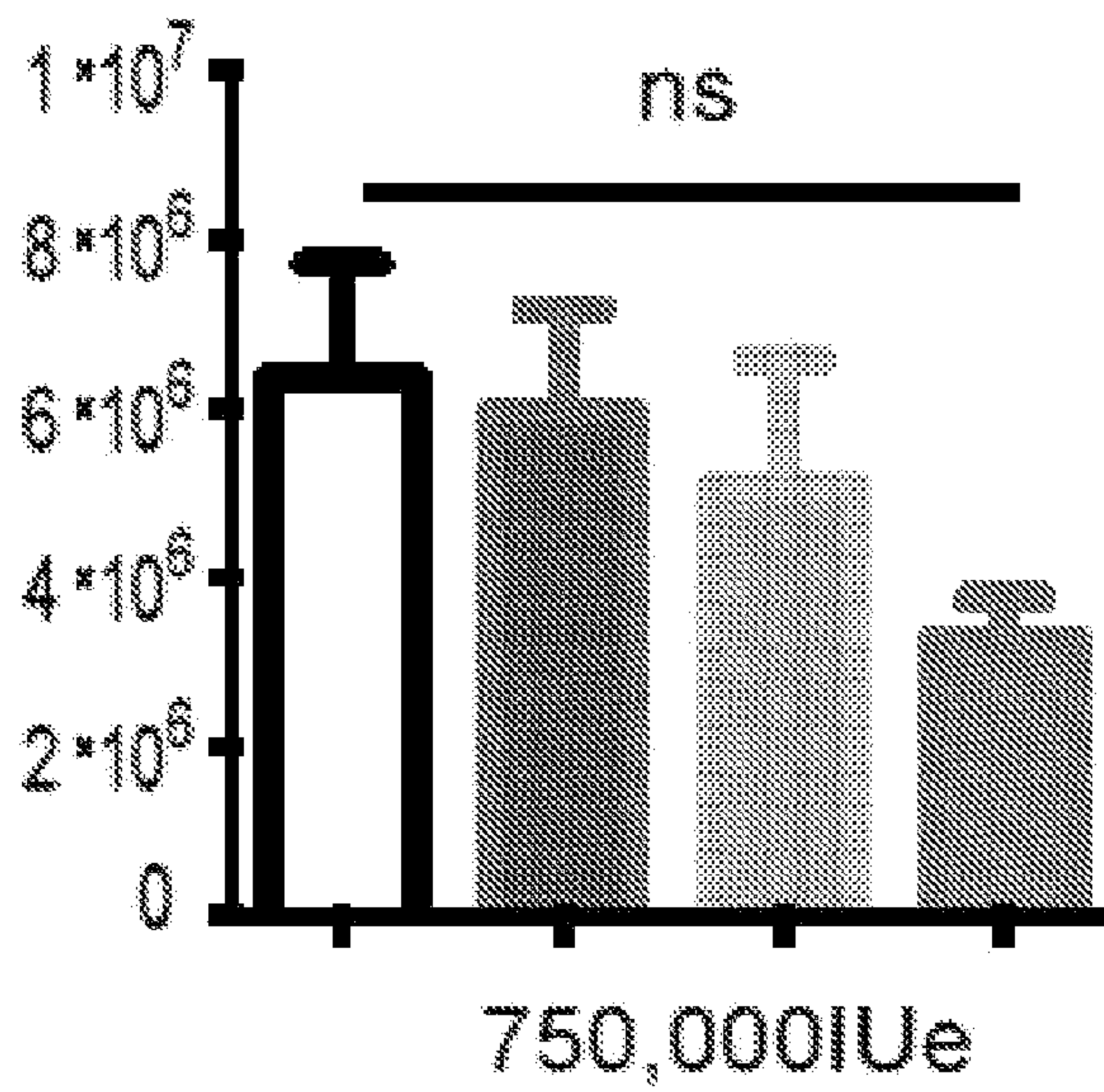
Saline, wtlL-2, mutIL-2, OMCP-mutIL-2,

**FIG. 8D**

**FIG. 8E**

**FIG. 8F**

Saline, wtIL-2, mutIL-2, OMCP-mutIL-2,

**FIG. 8G**

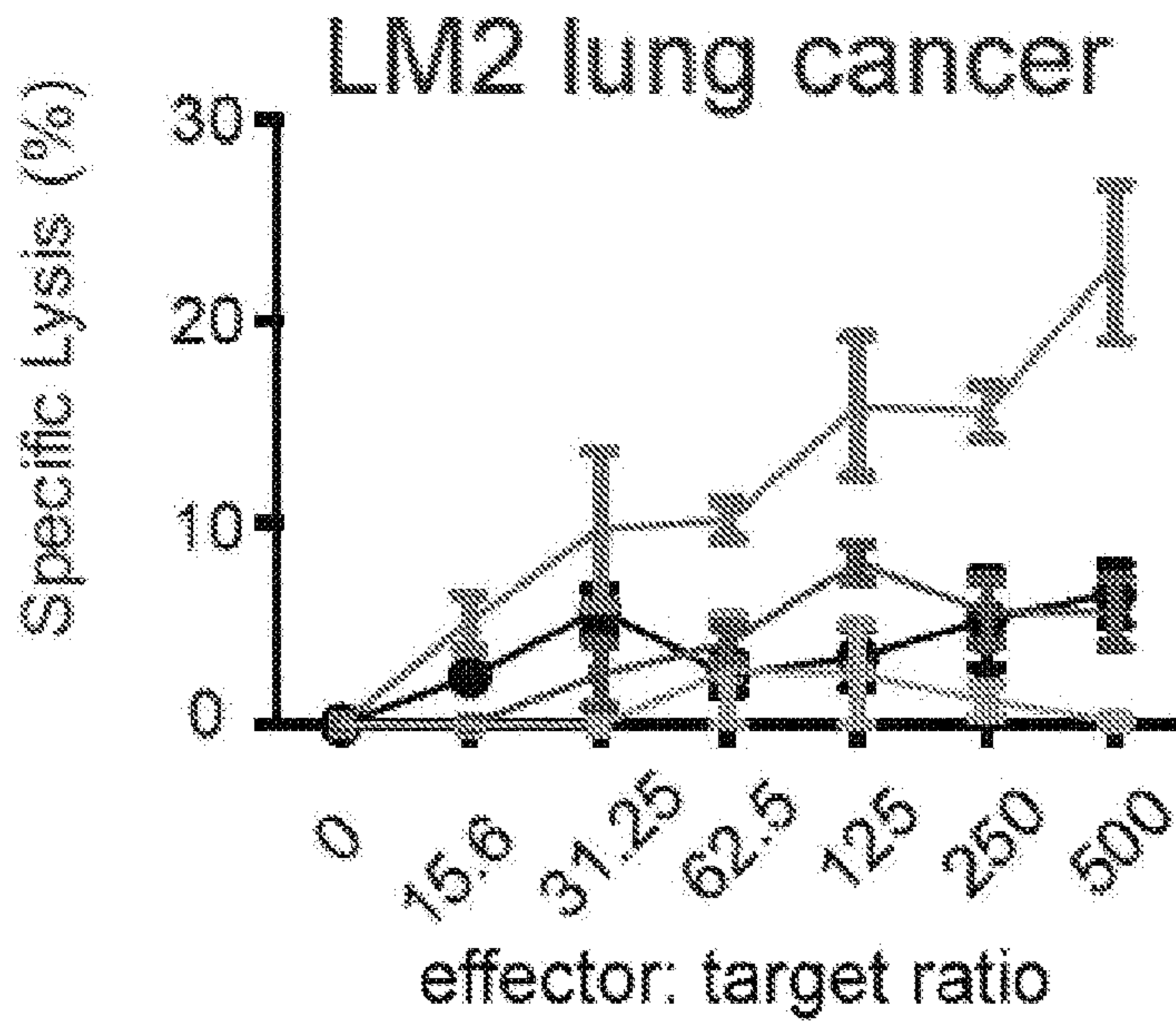


FIG. 9A

saline, wtIL-2, mutIL-2, OMCP-mutIL-2

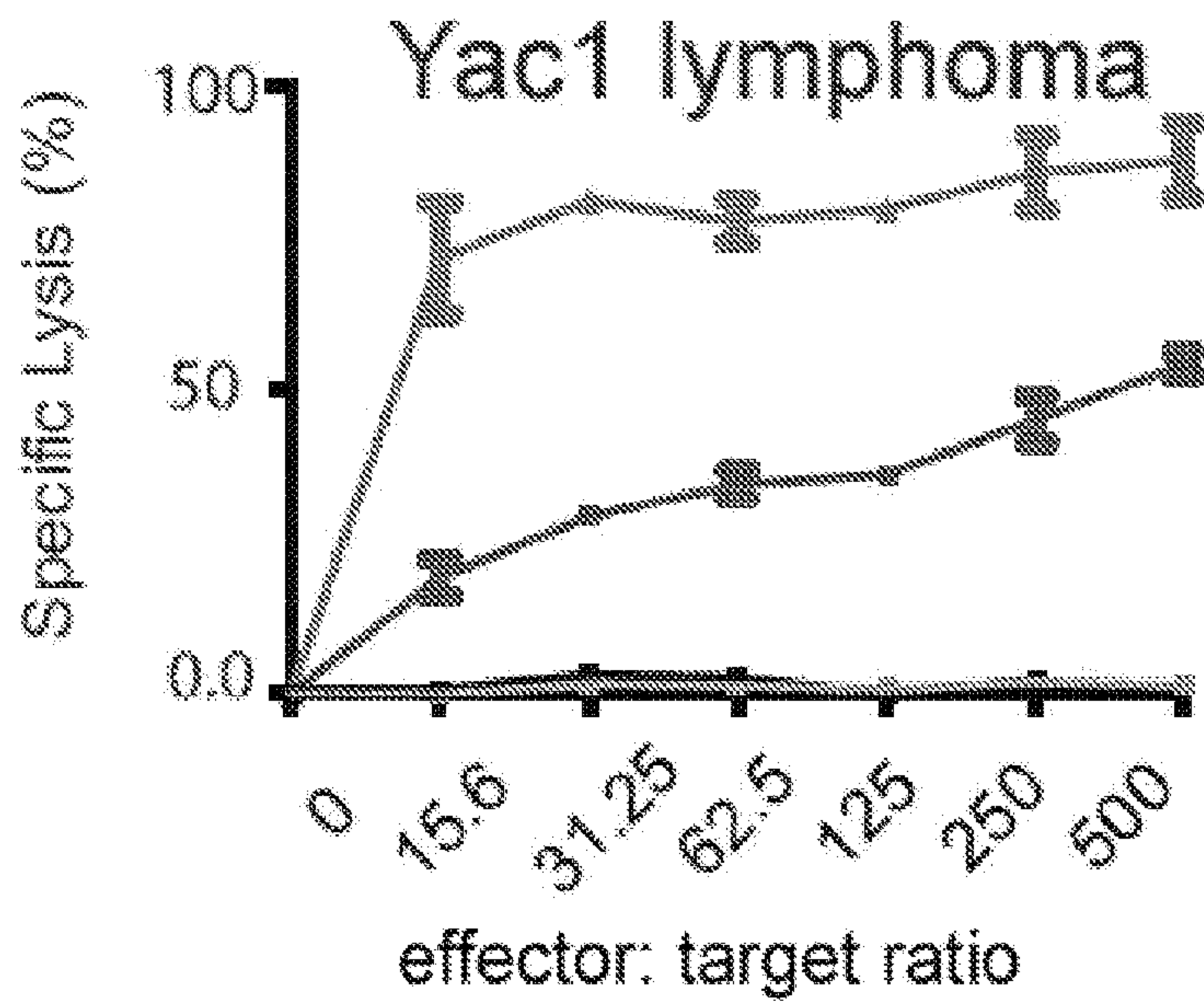
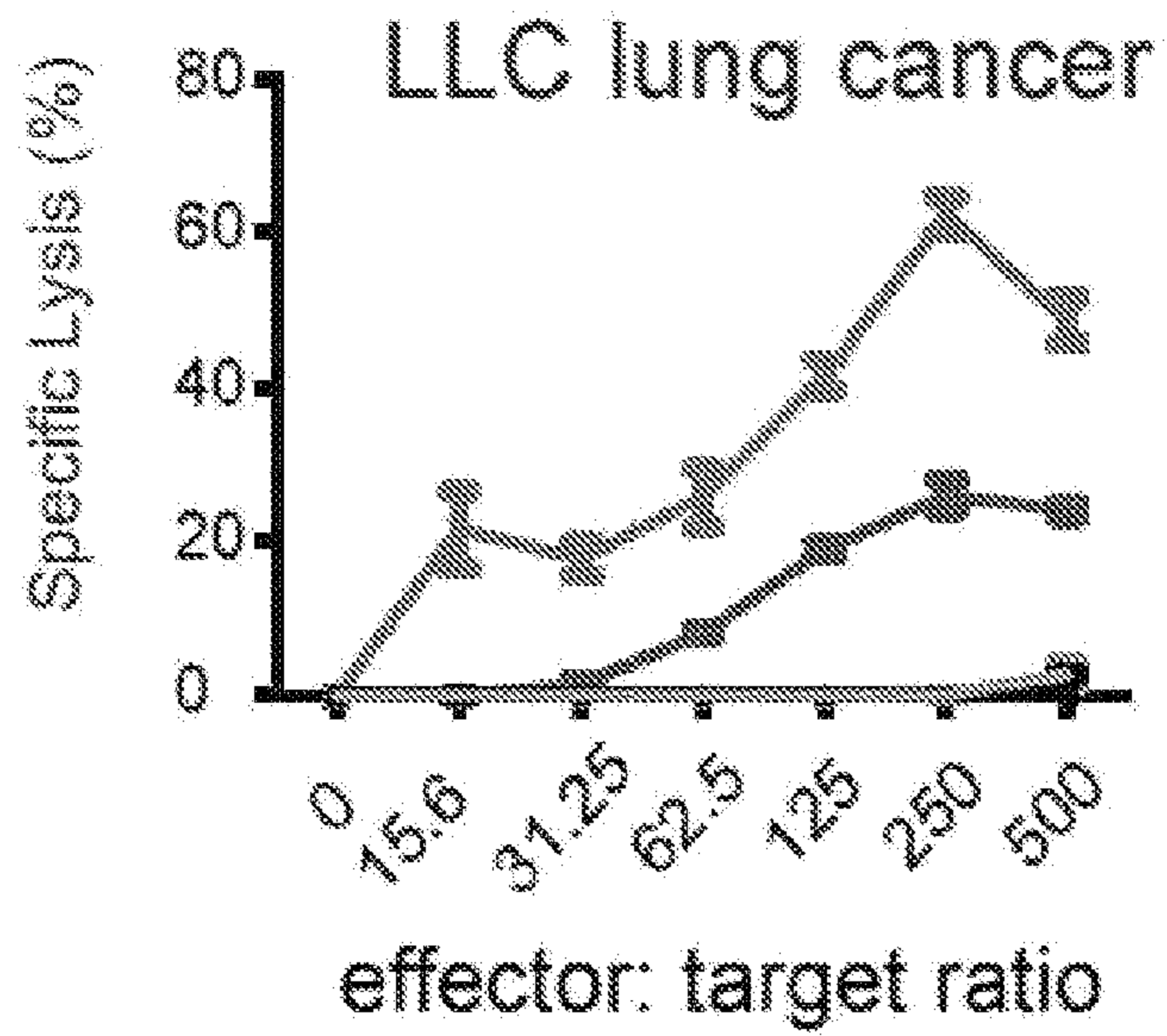


FIG. 9B



saline, wtIL-2, mutIL-2, OMCP-mutIL-2

FIG. 9C

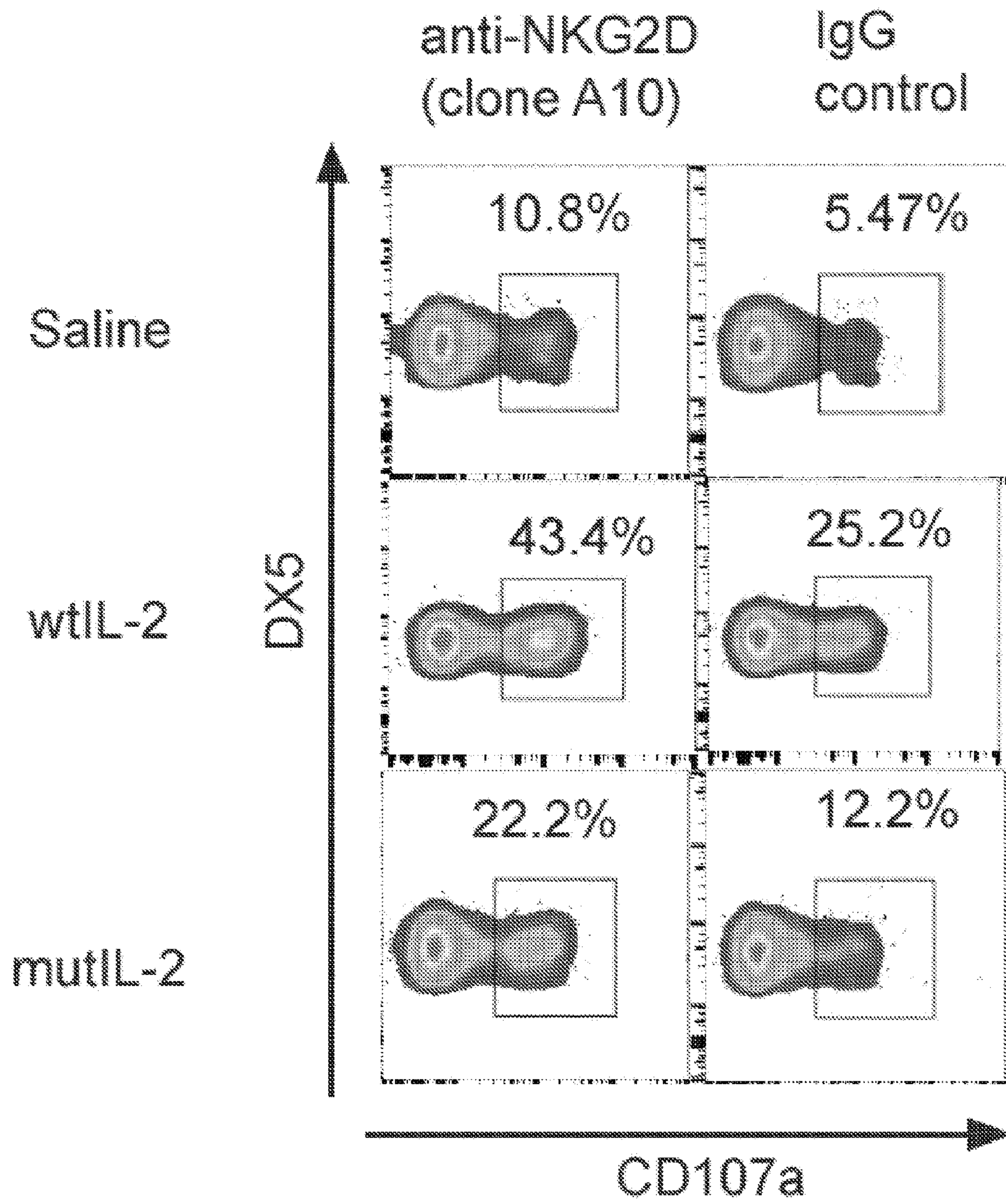
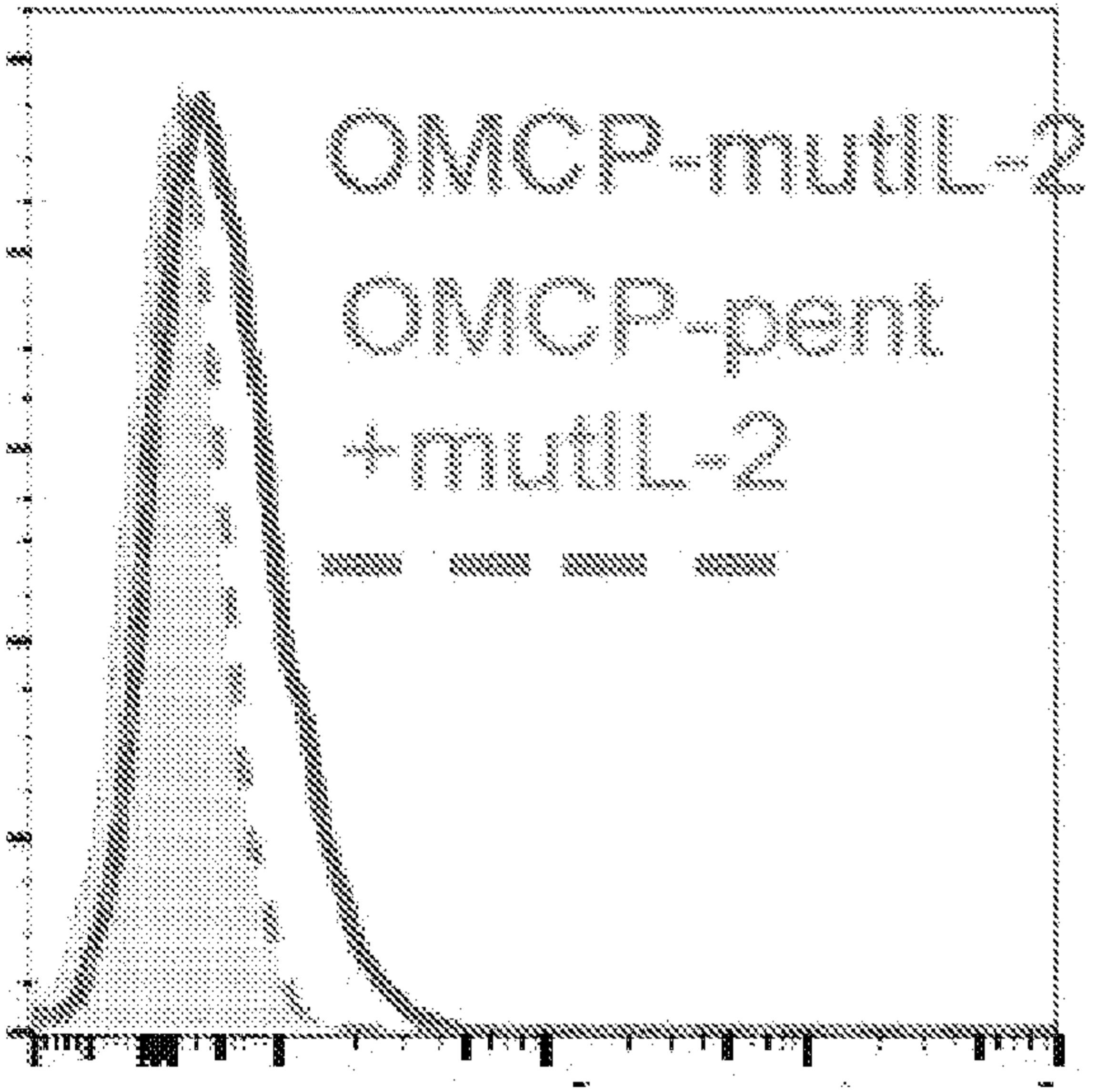
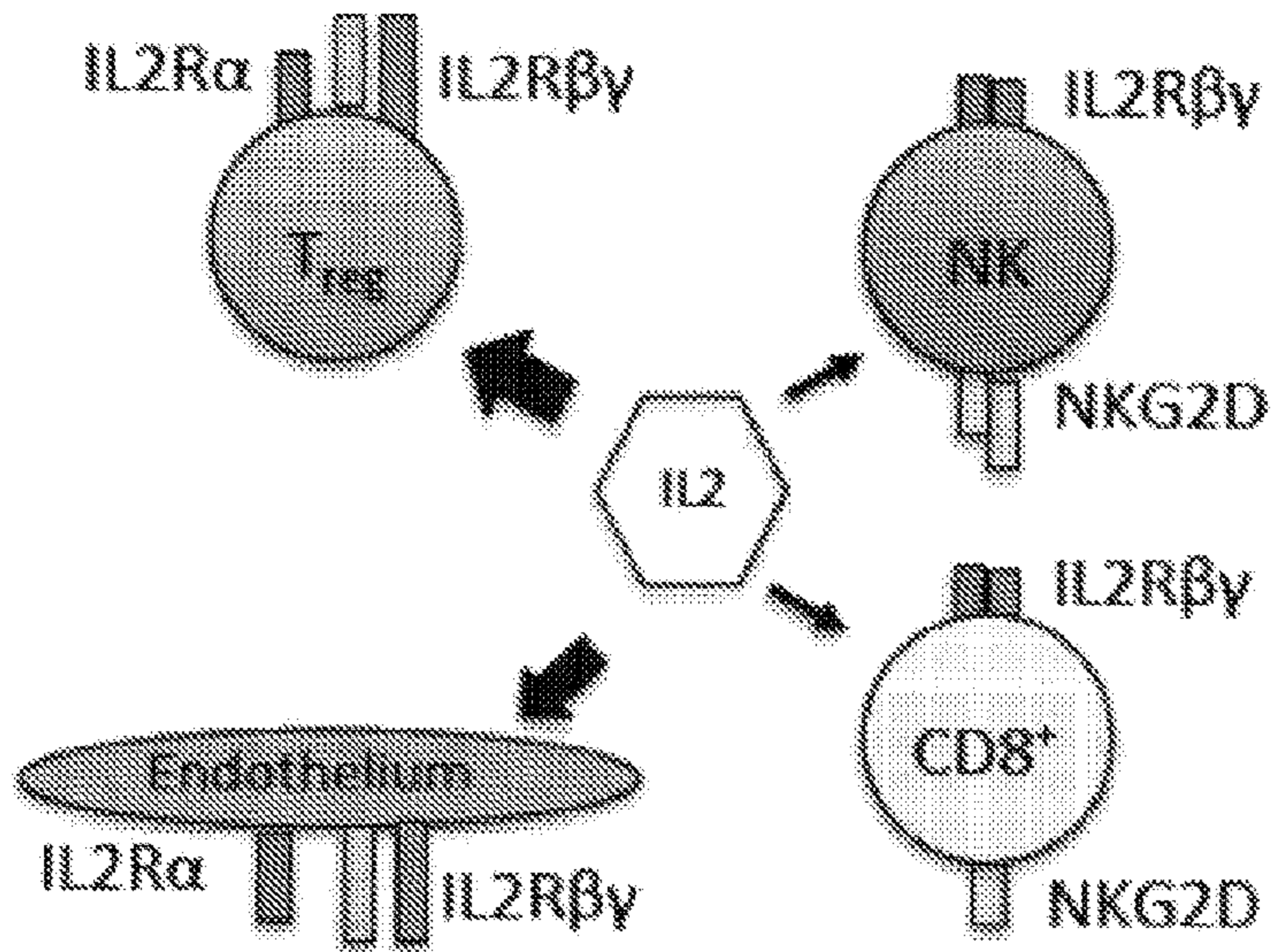
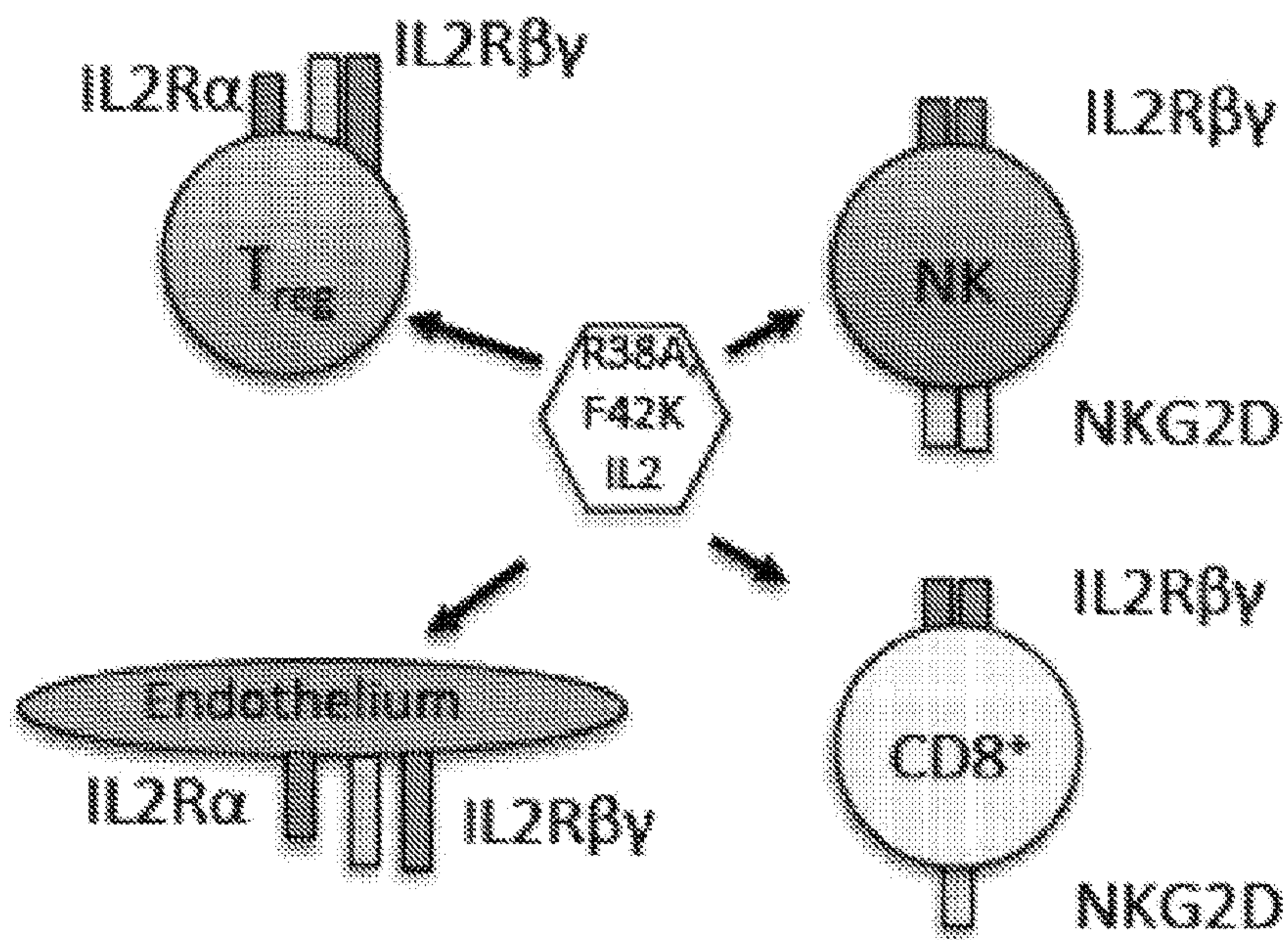


FIG. 10A



CD69

FIG. 10B

**FIG. 11A****FIG. 11B**

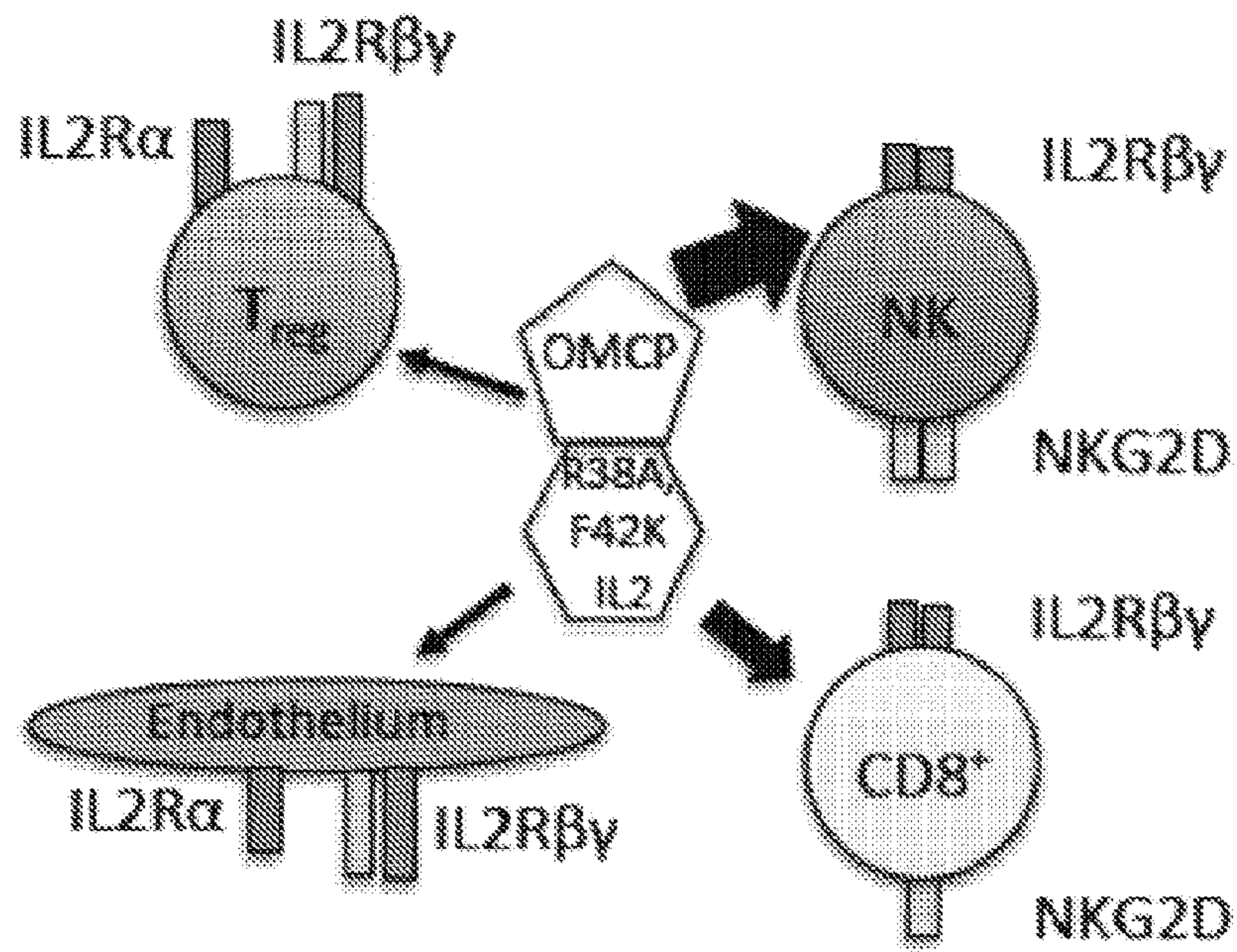
**FIG. 11C**



FIG. 12

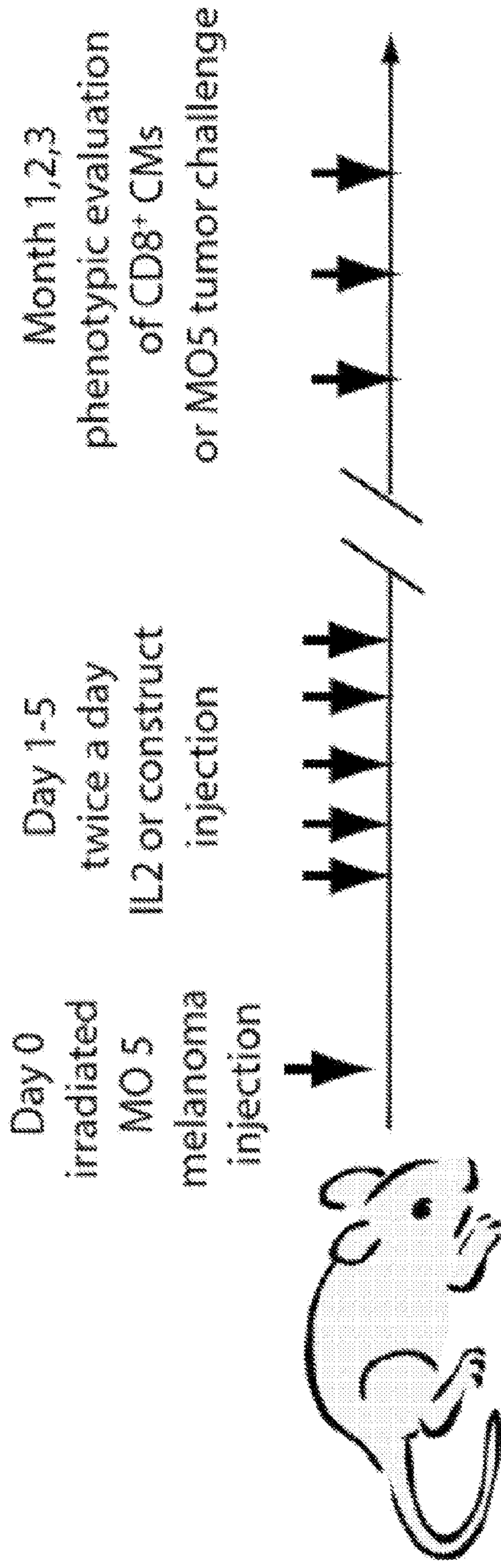


FIG. 13

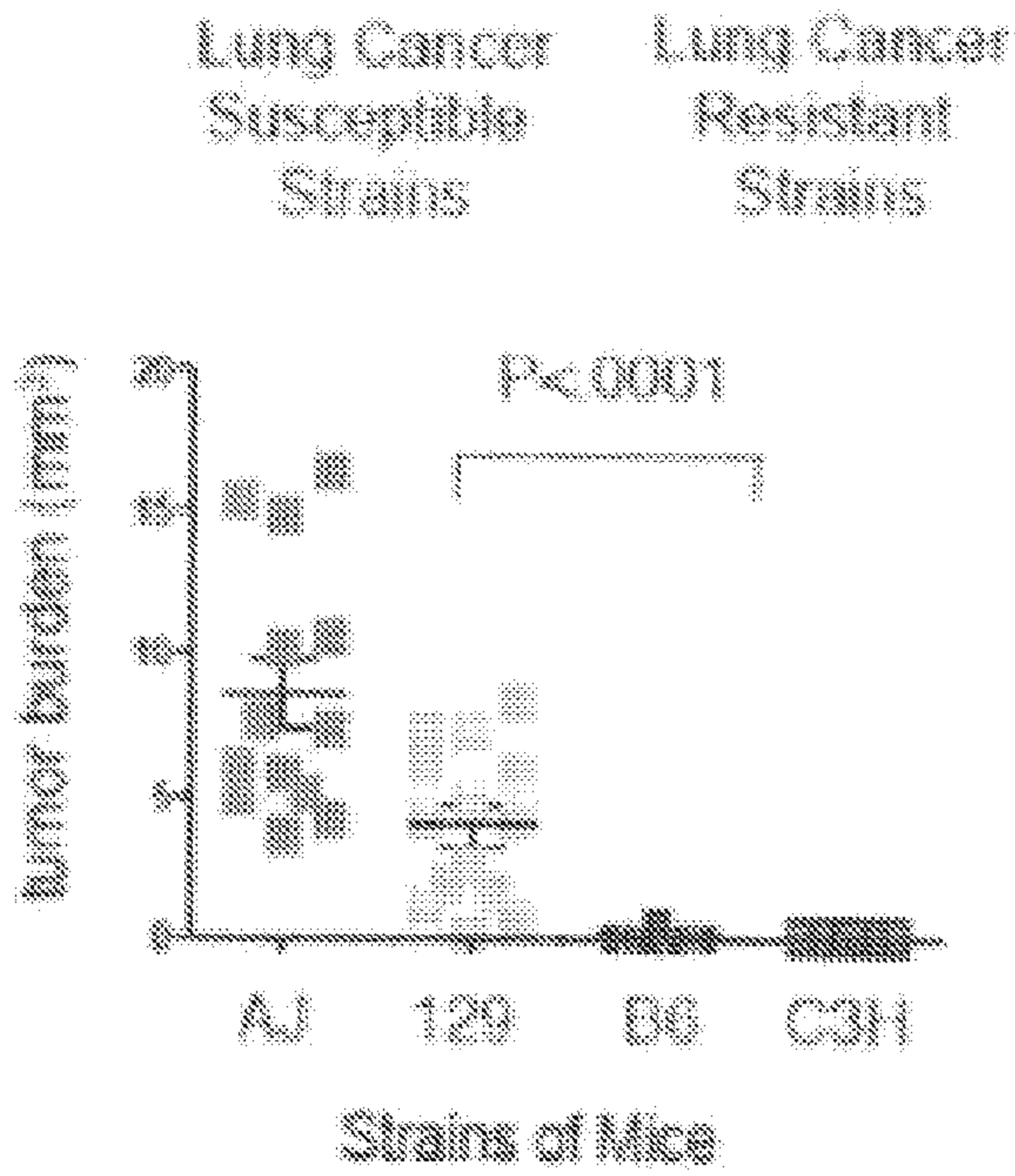


FIG. 14A

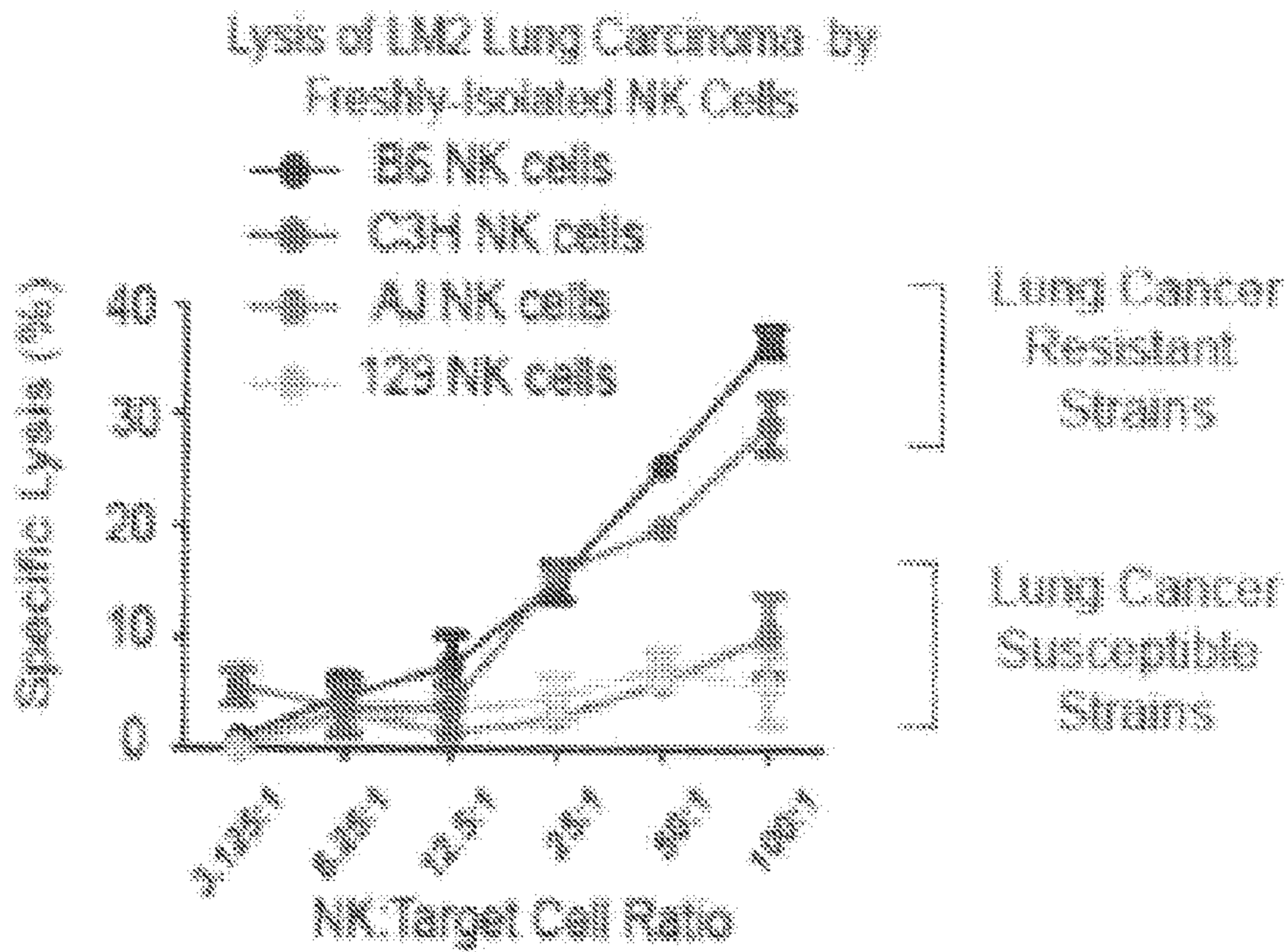


FIG. 14B

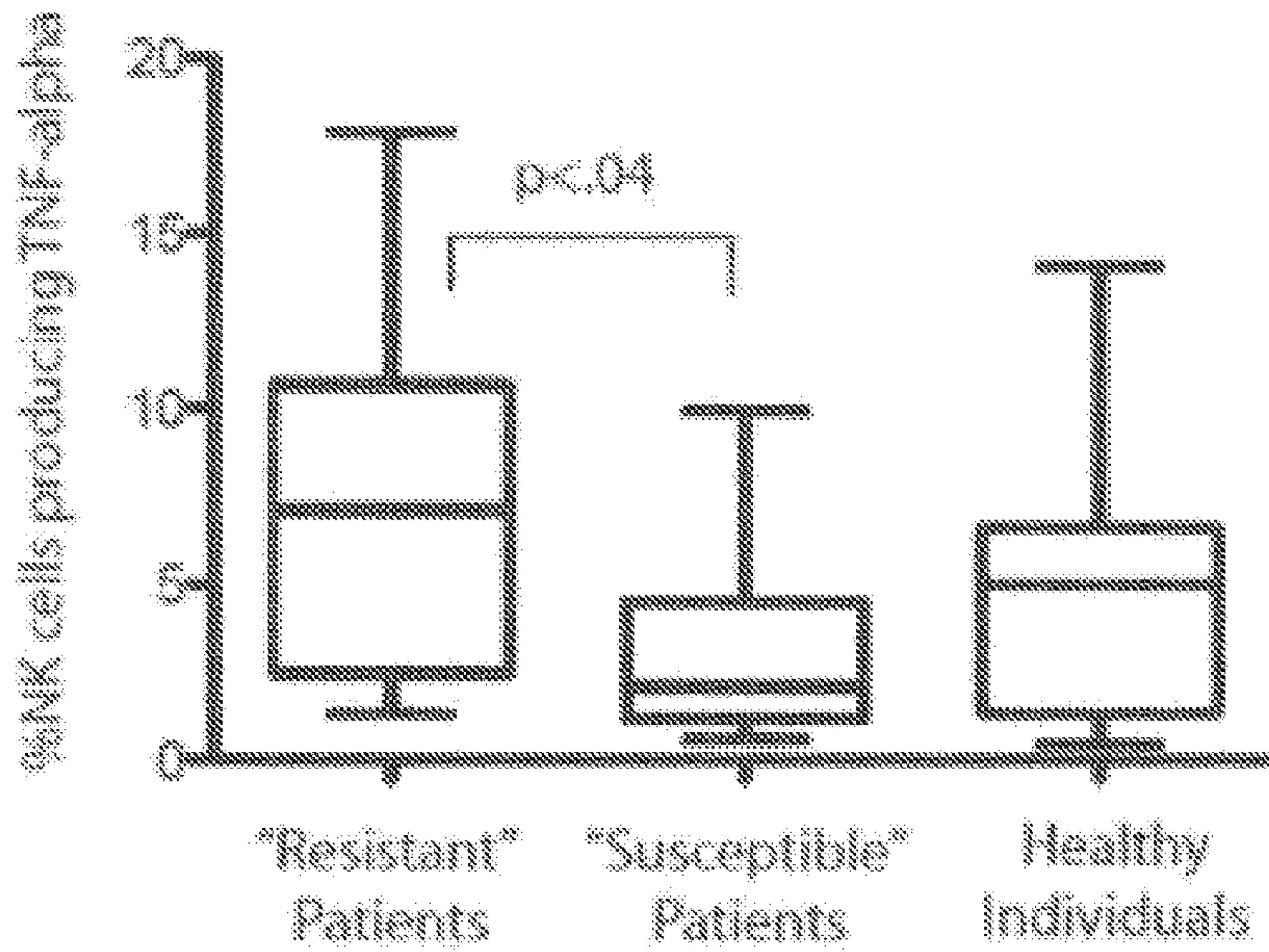


FIG. 15

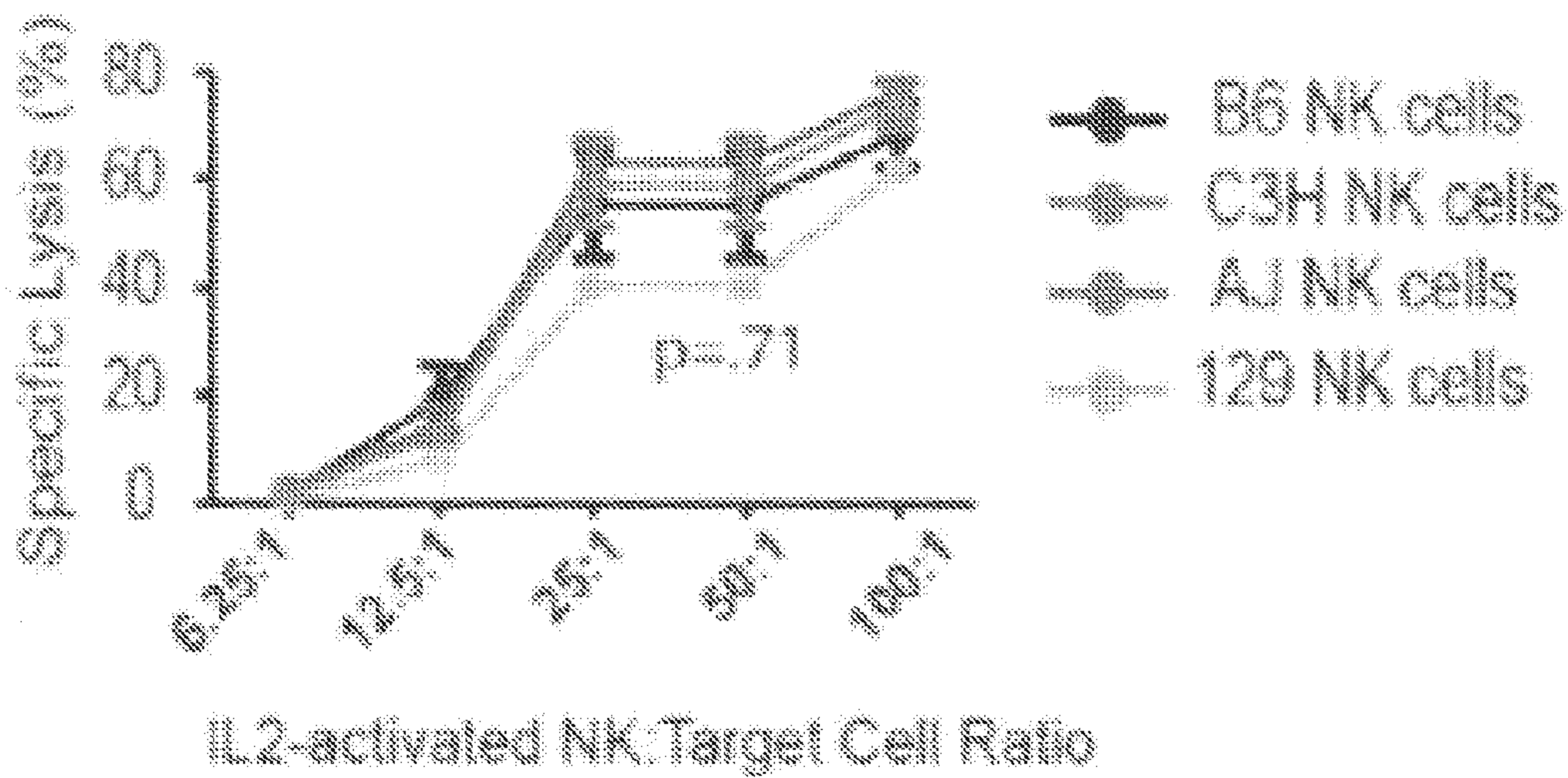


FIG. 16

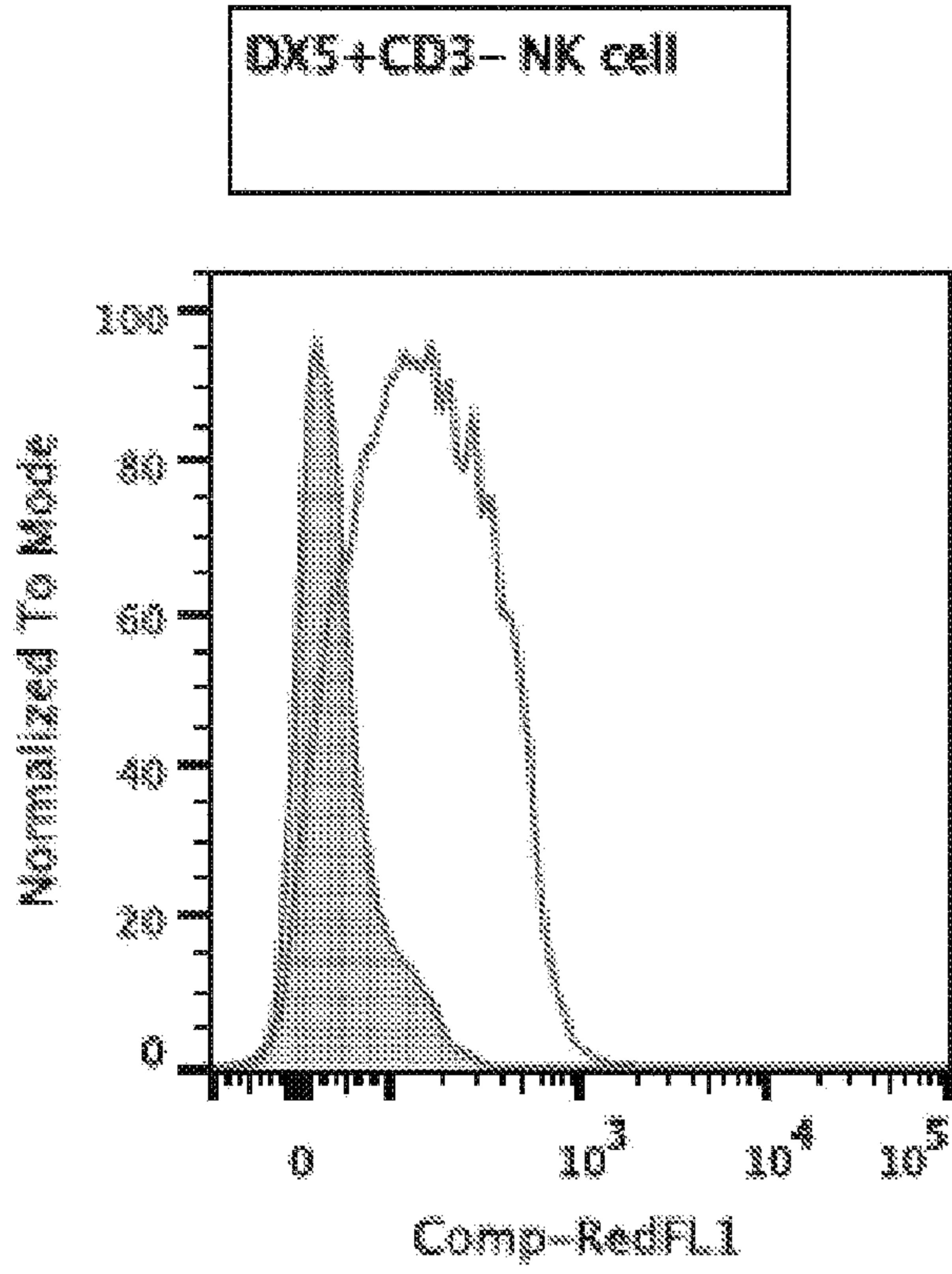


FIG. 17A

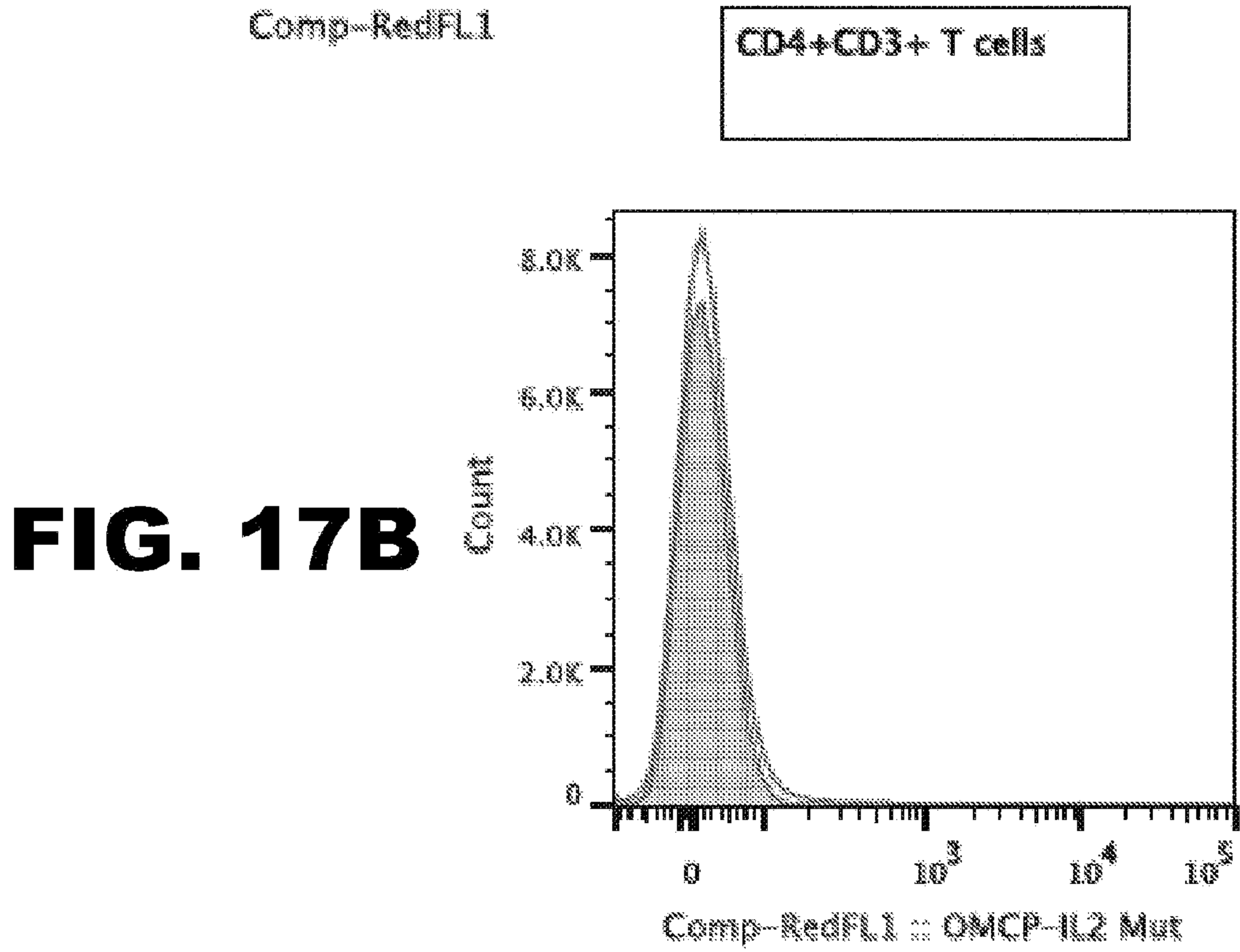


FIG. 17B

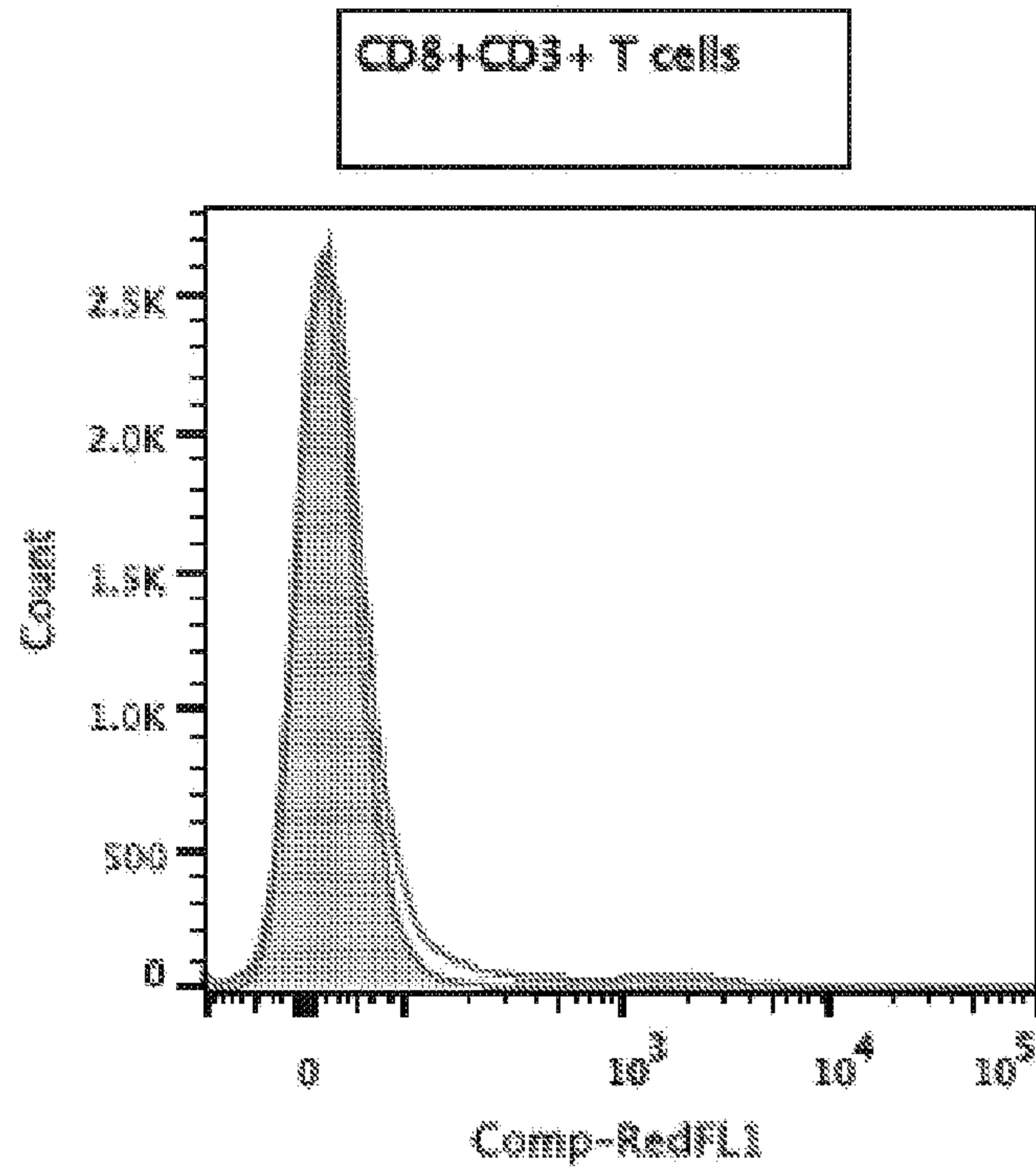
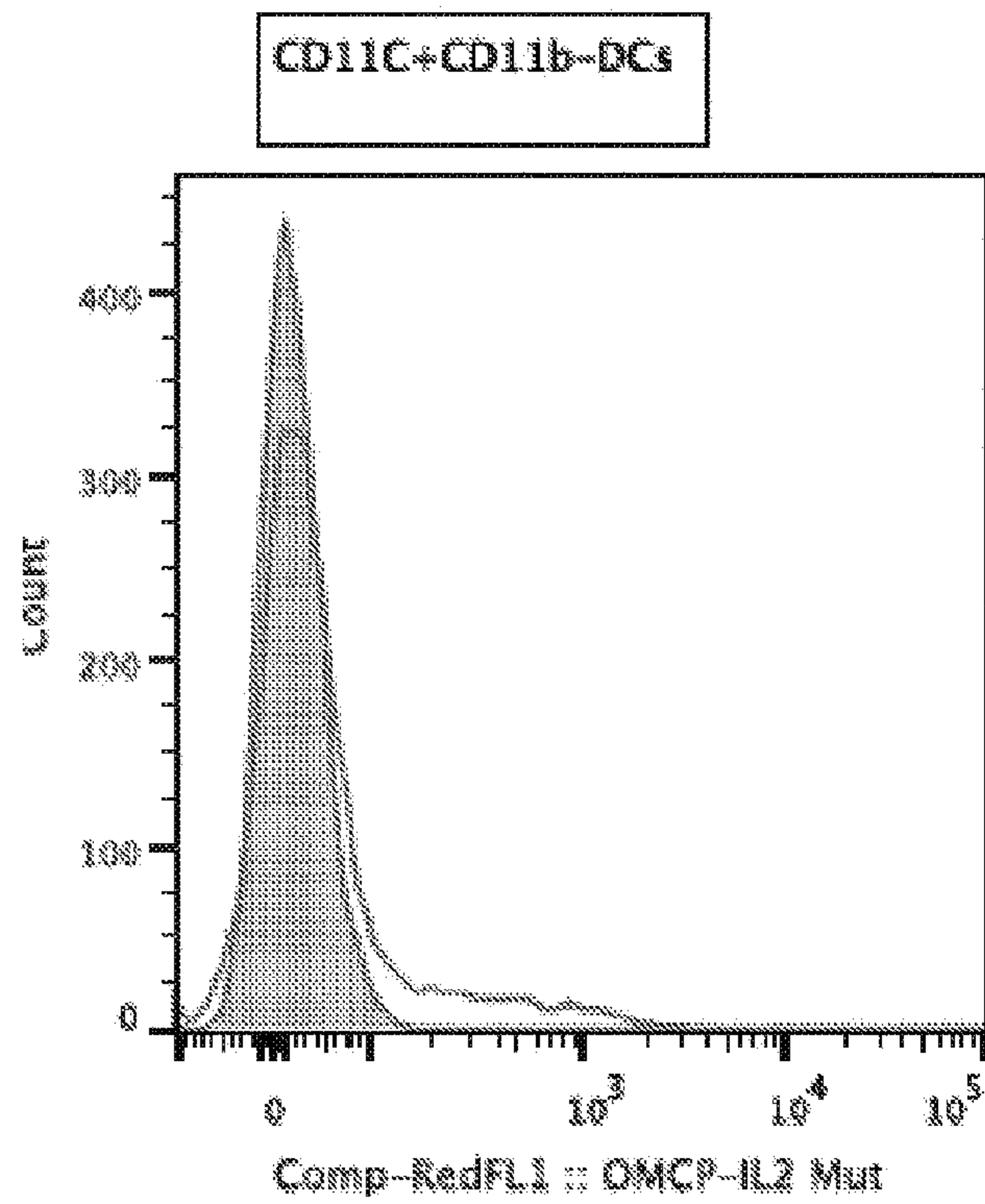


FIG. 17C

FIG. 17D



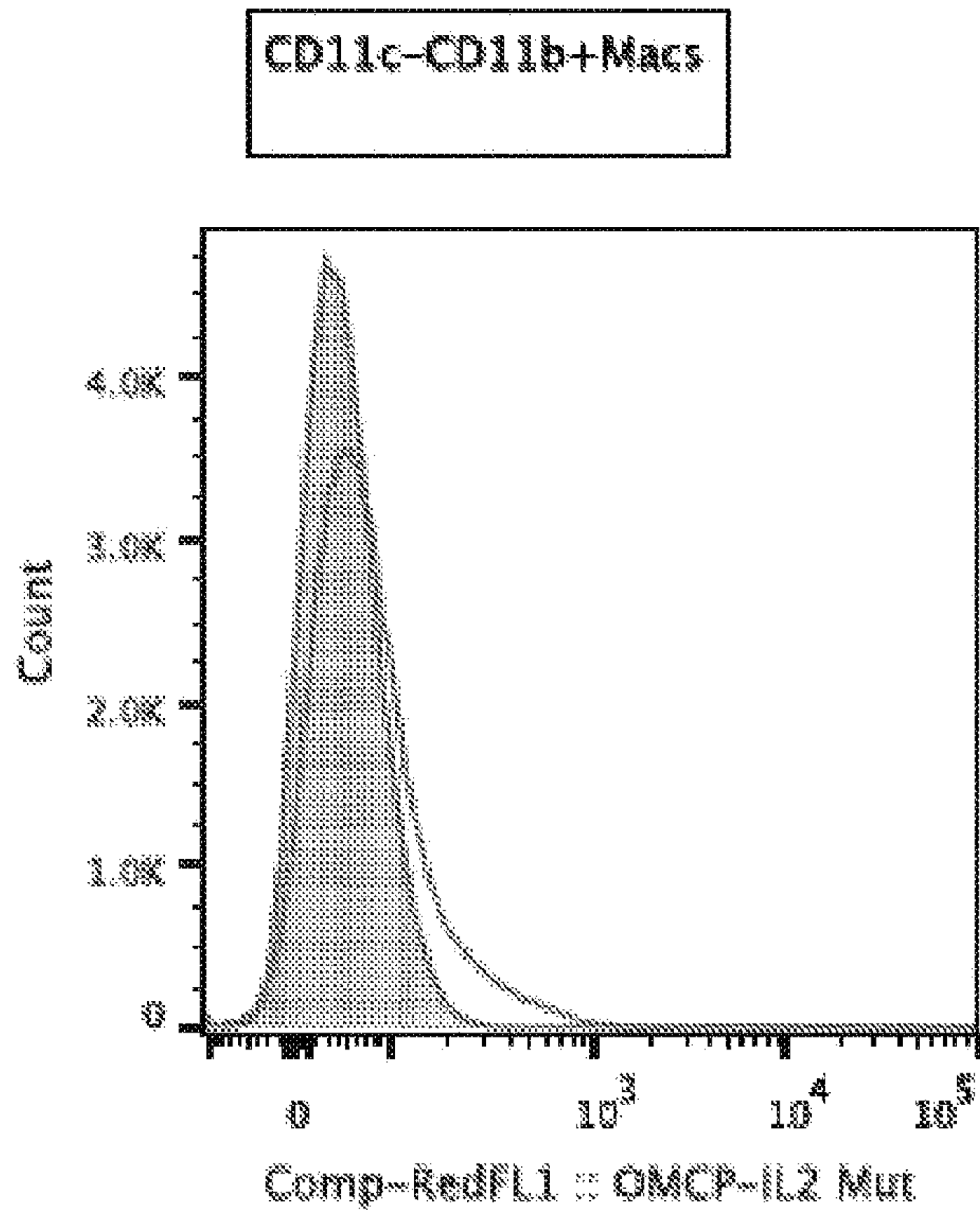
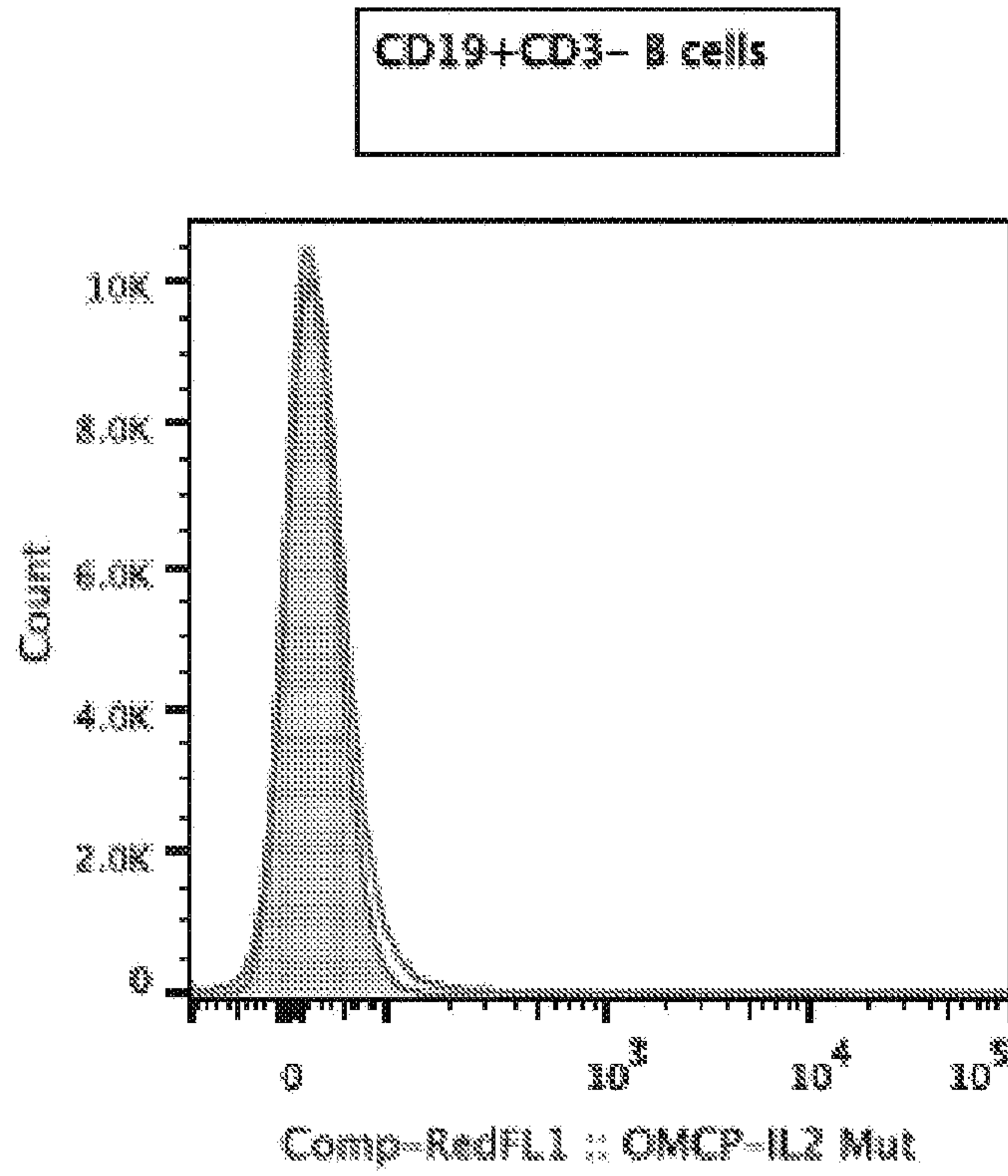


FIG. 17E

FIG. 17F



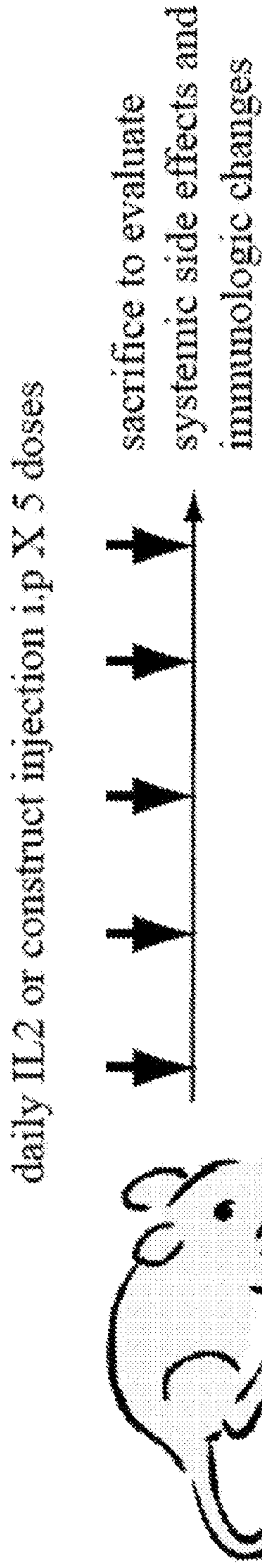


FIG. 18

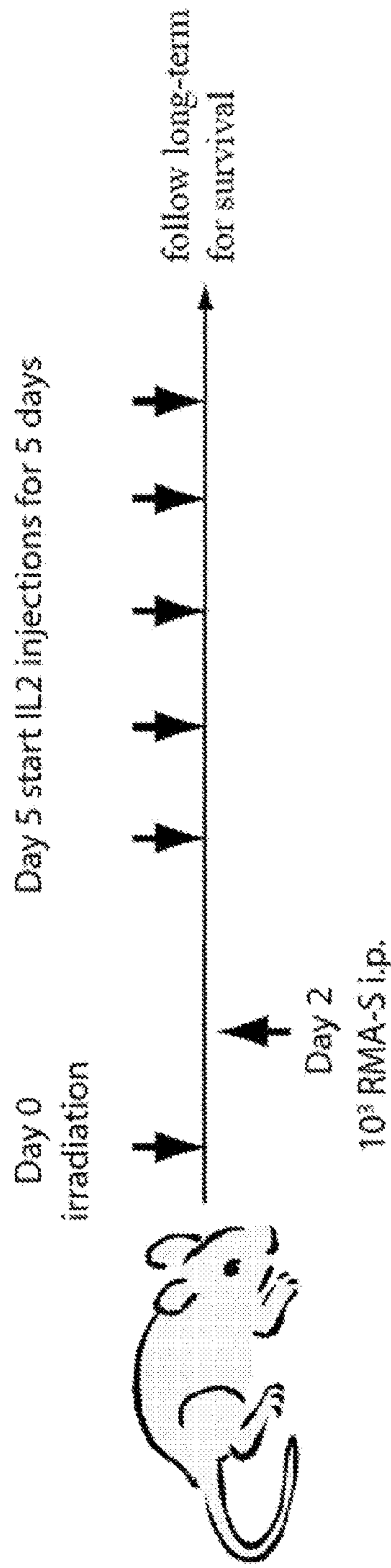


FIG. 19

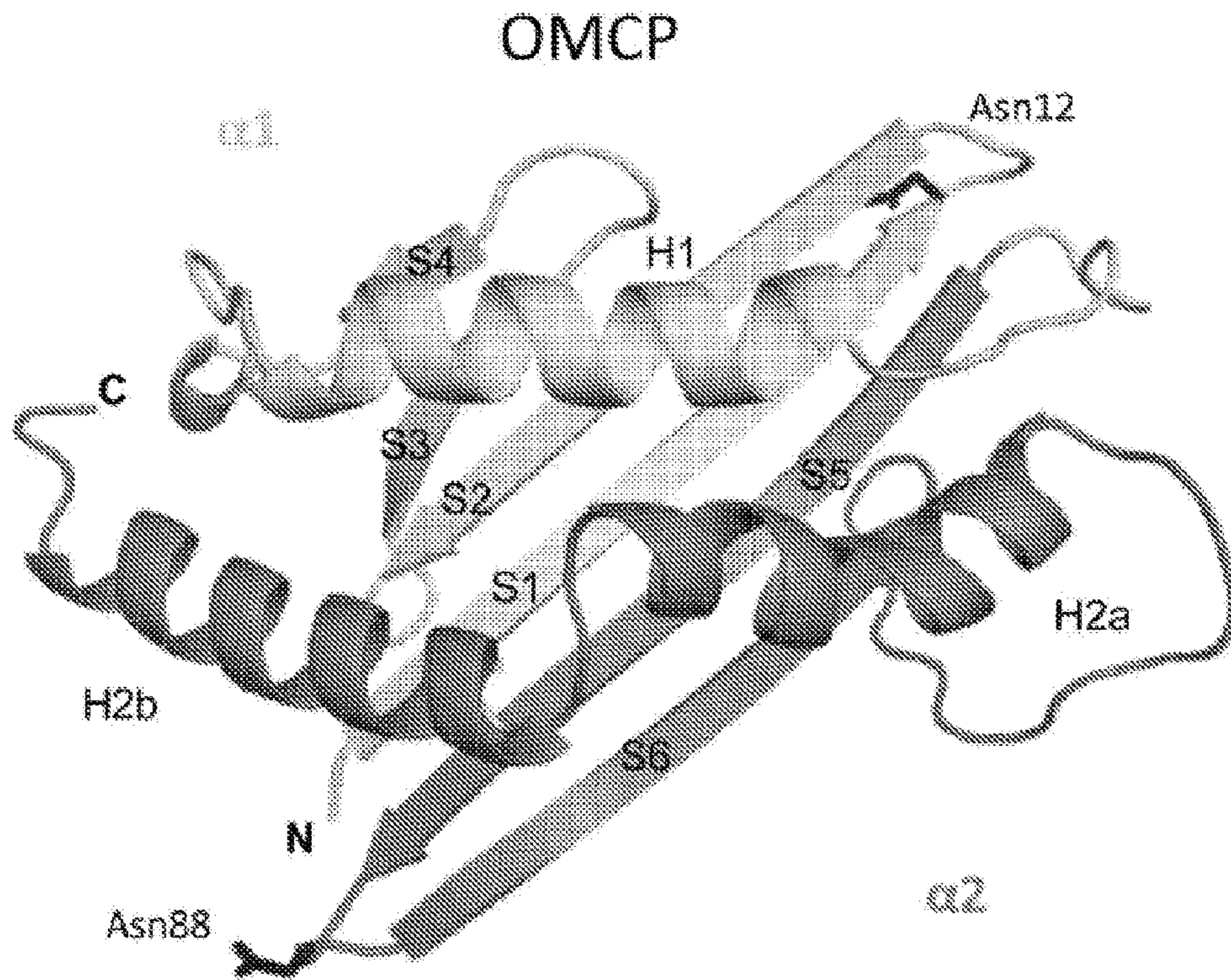


FIG. 20A

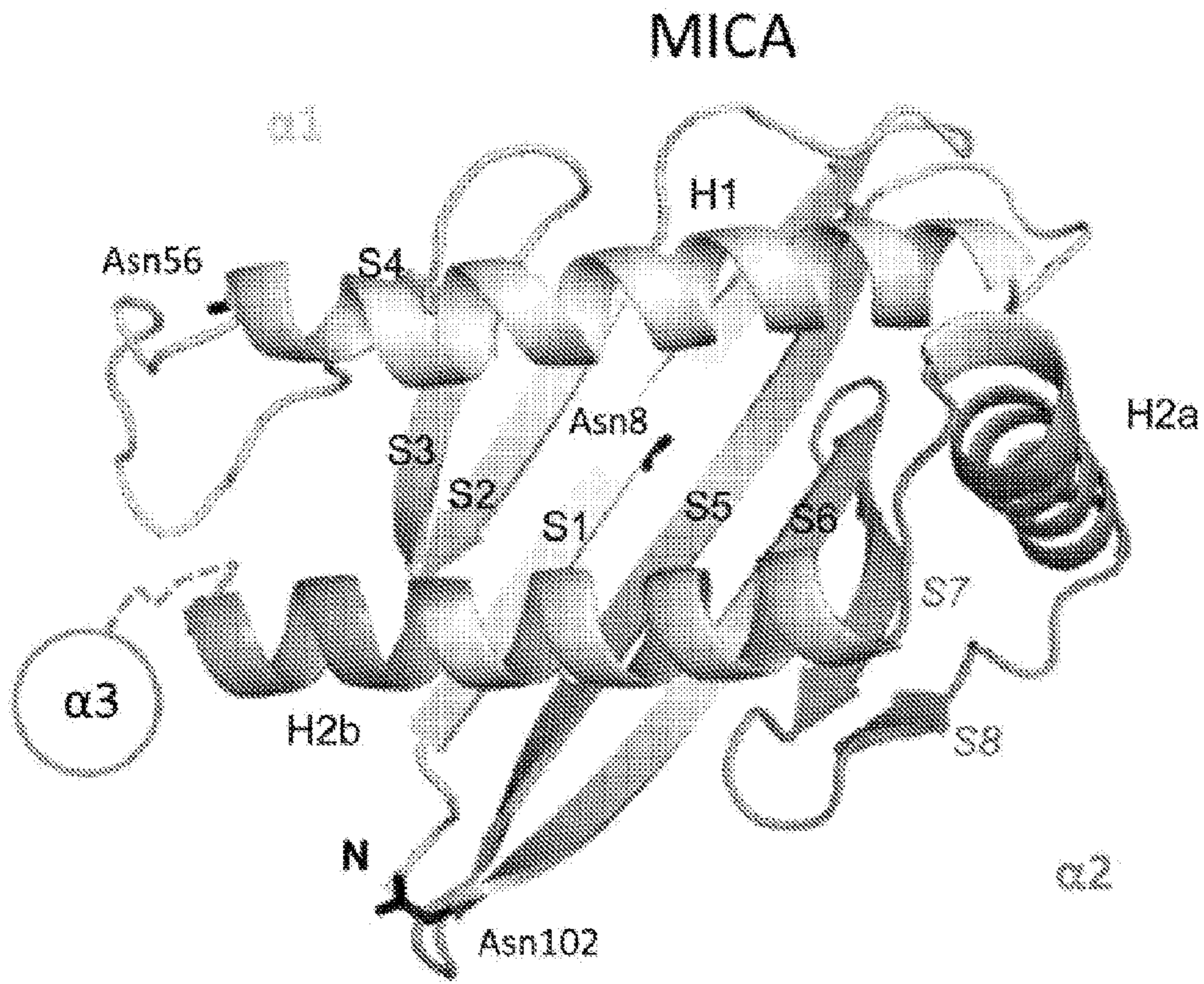


FIG. 20B

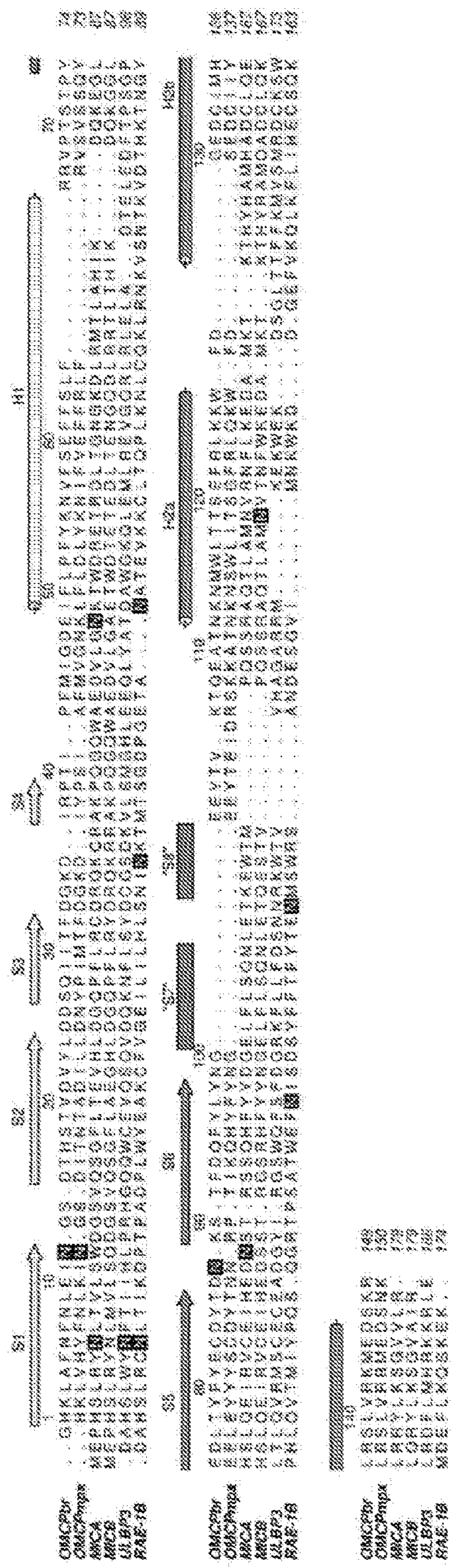


FIG. 20C

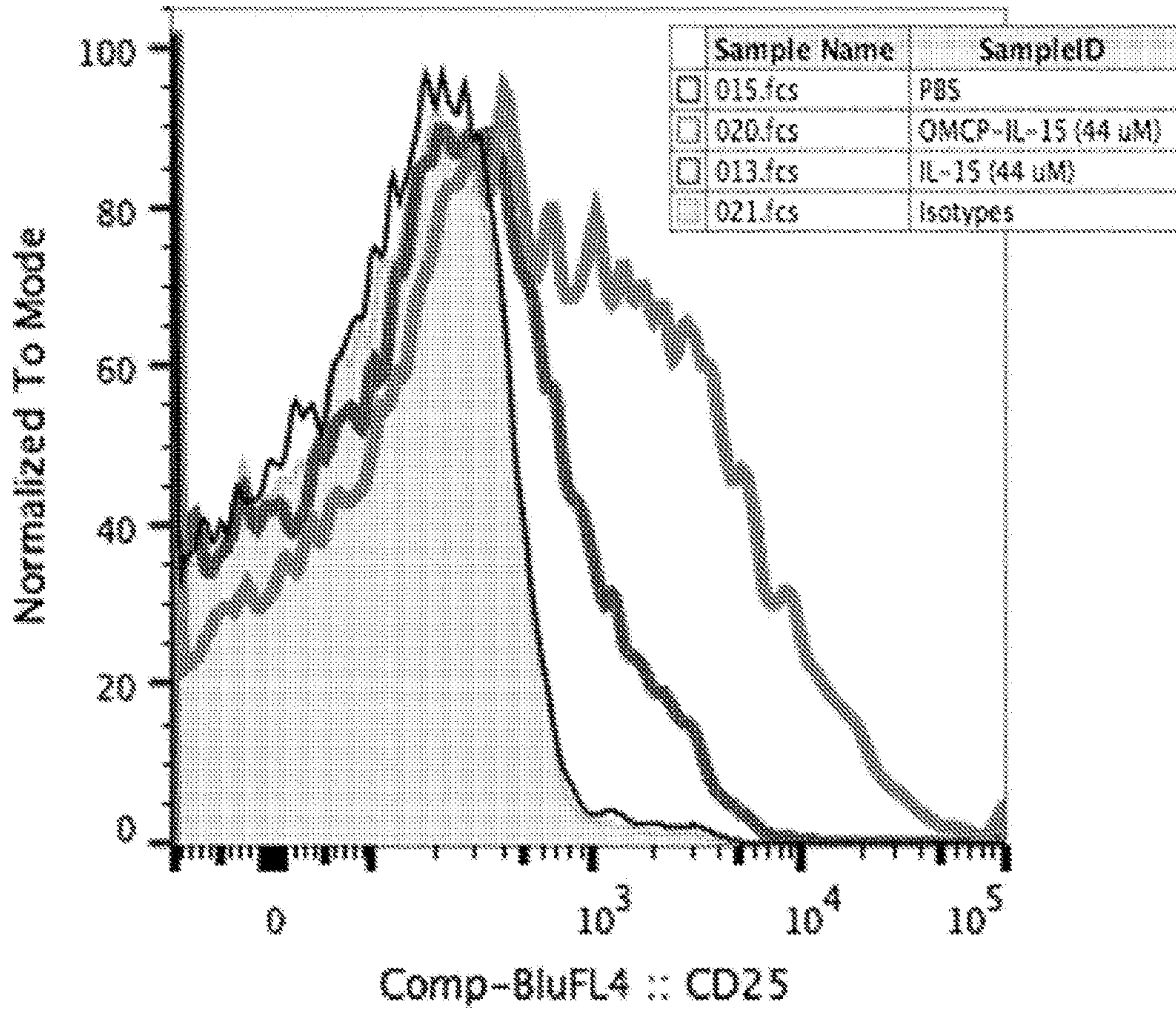
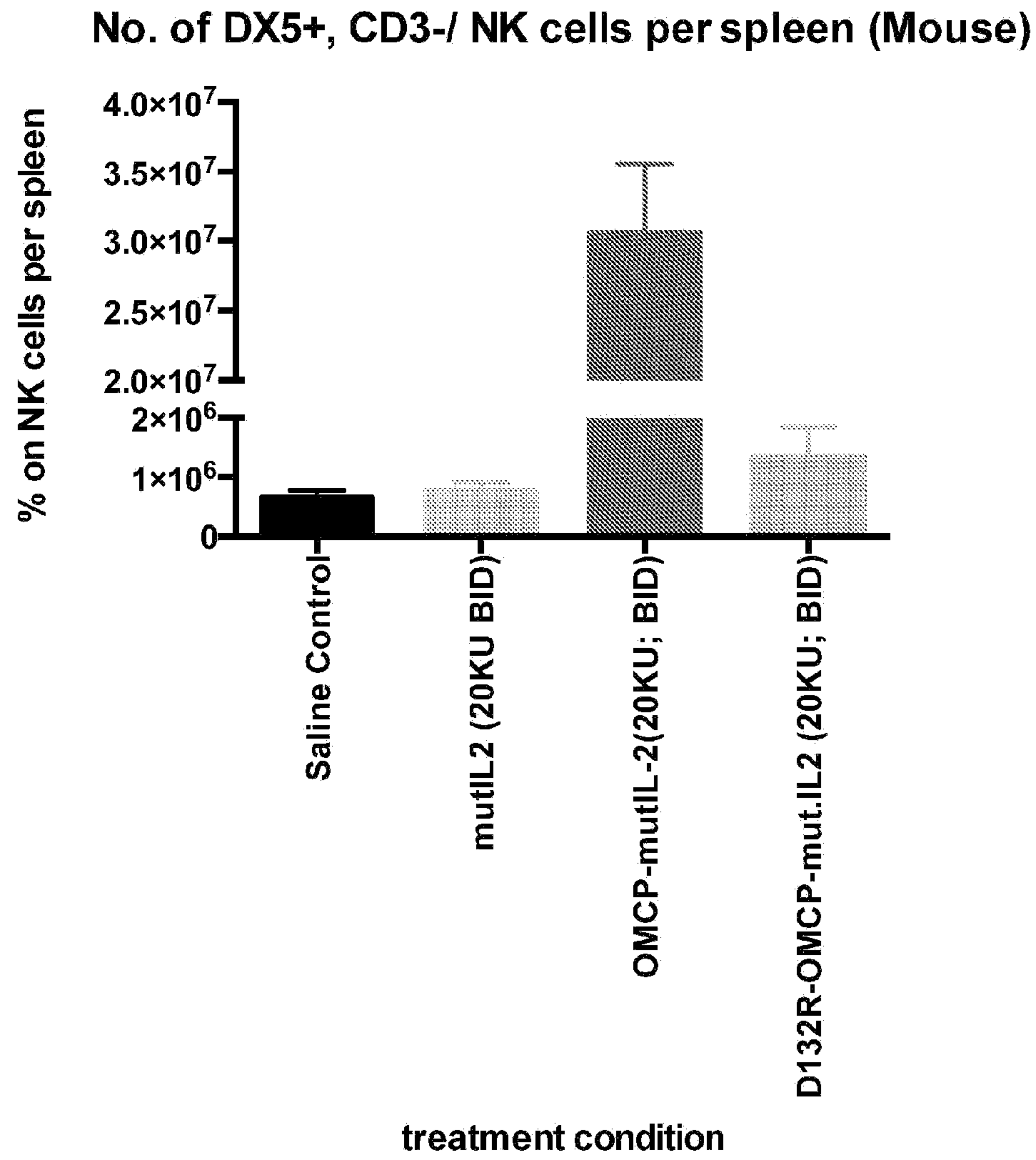


FIG. 21

**FIG. 22**

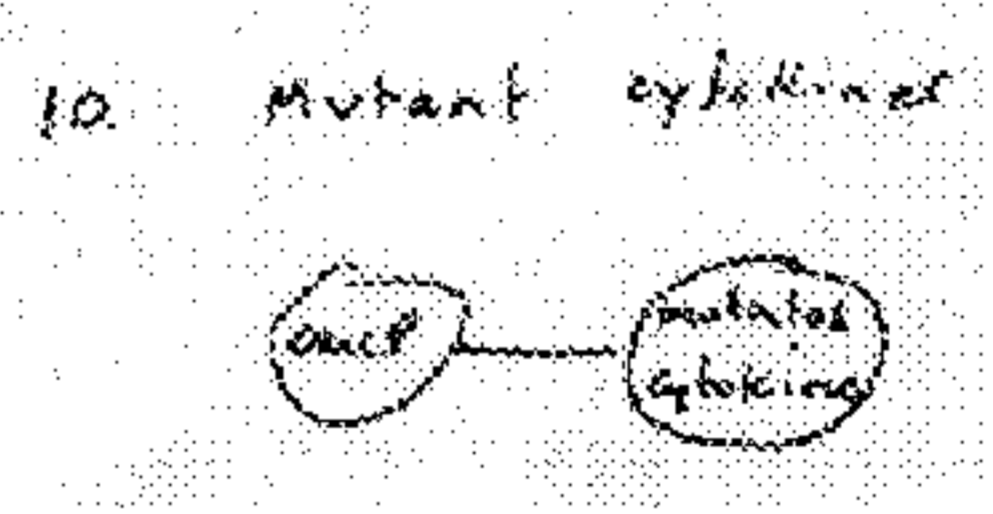
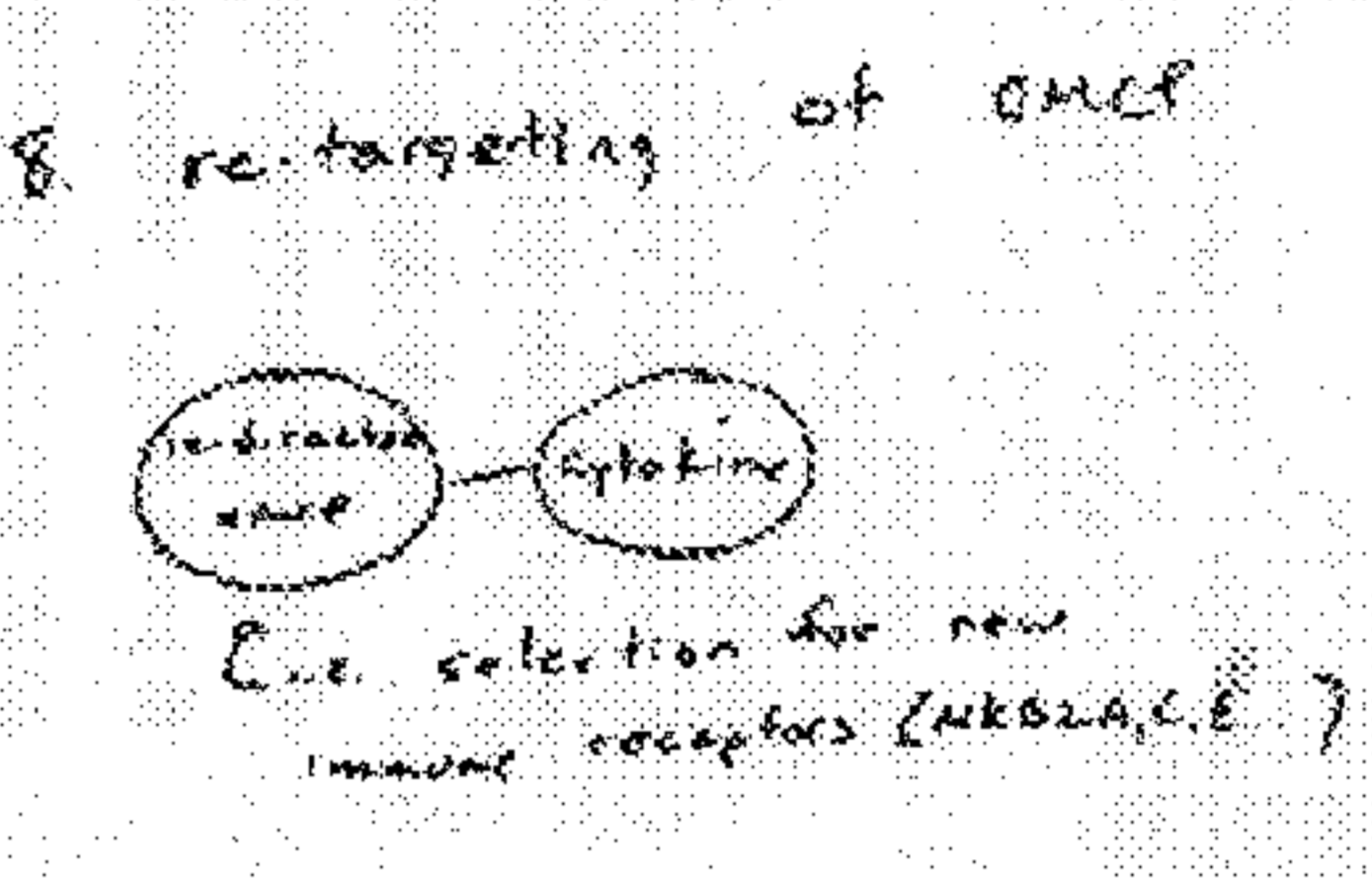
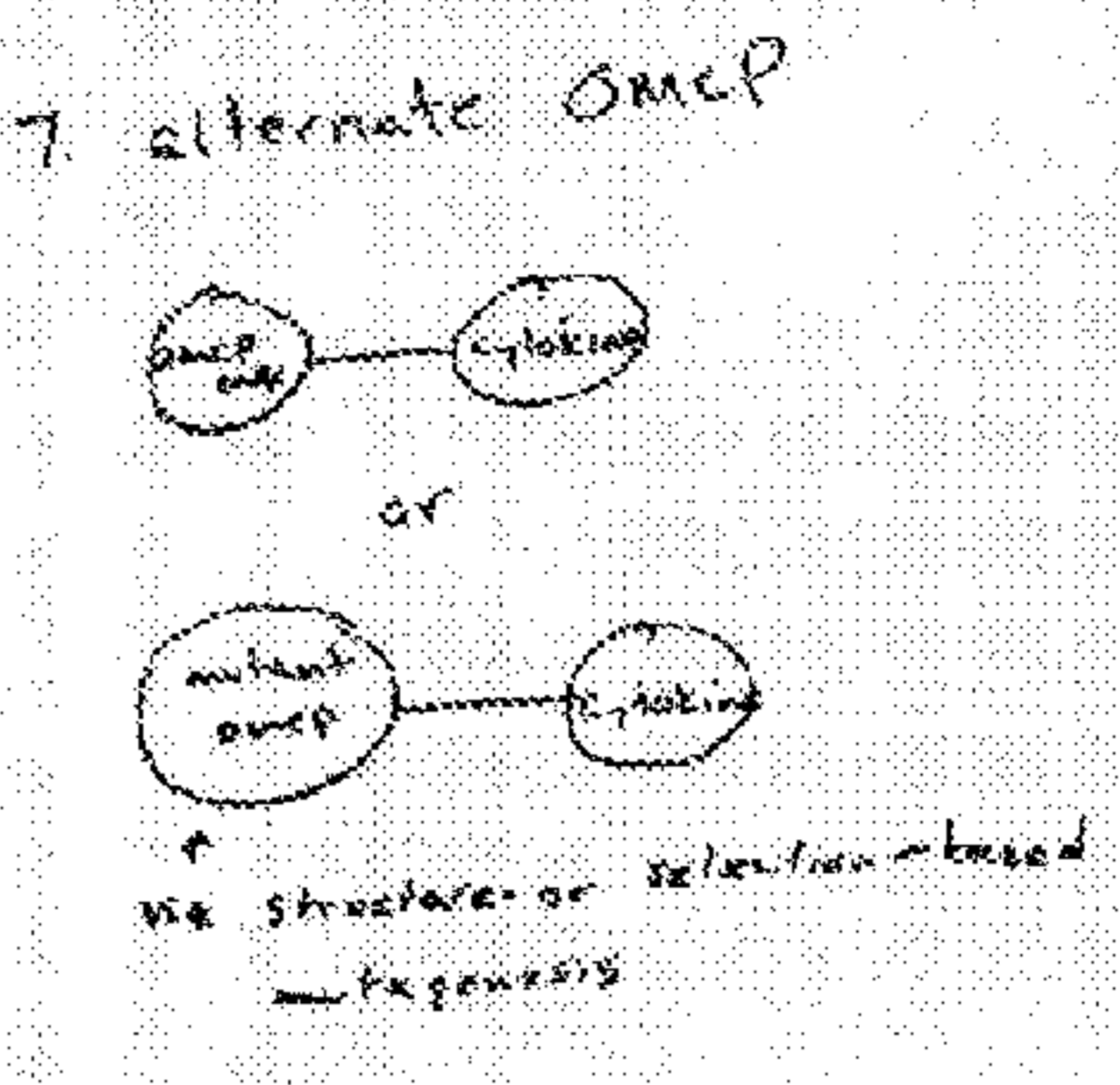
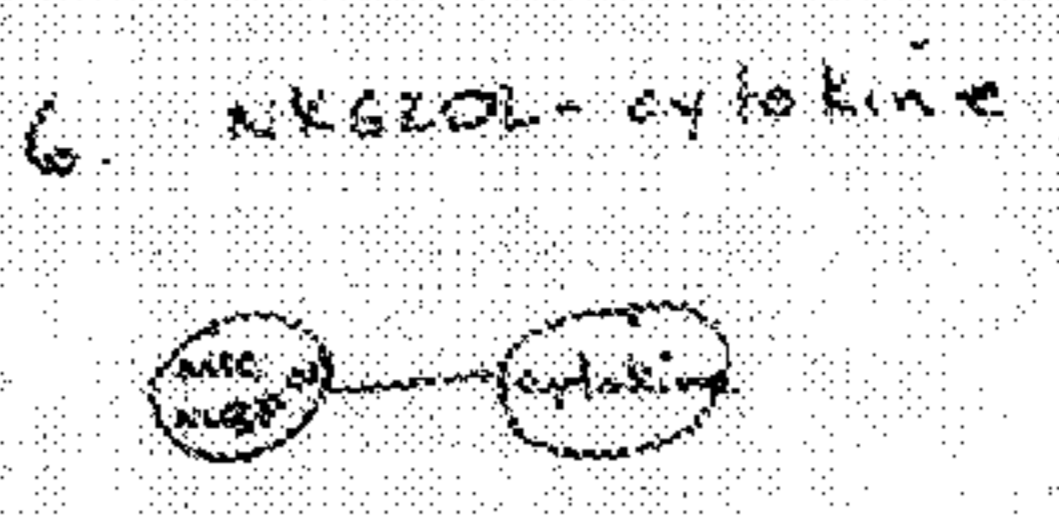
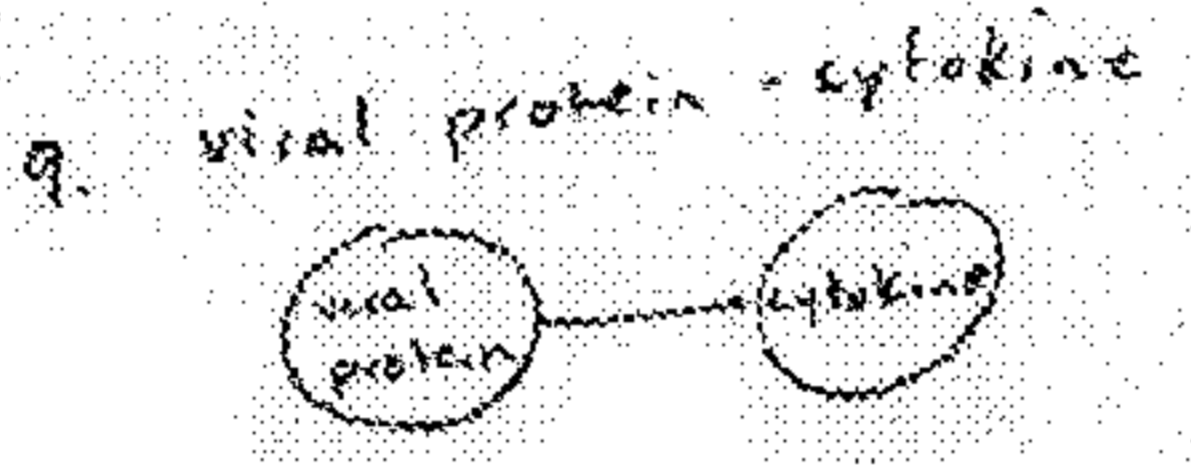
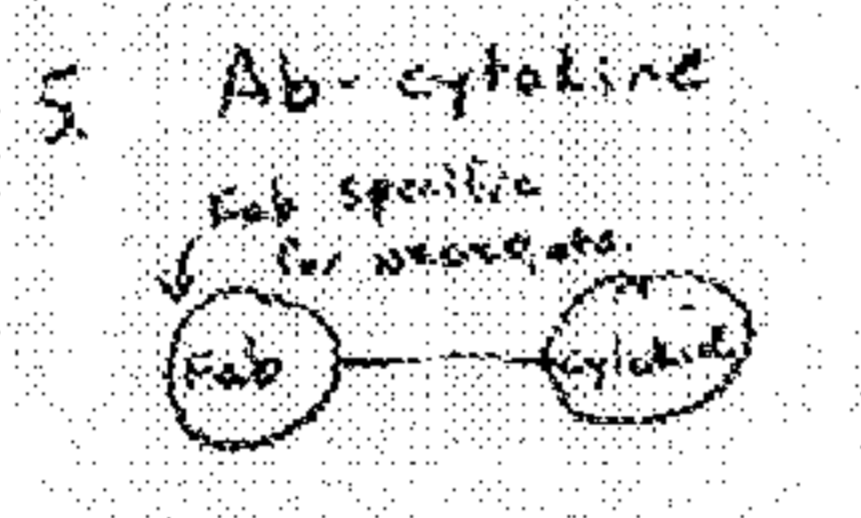
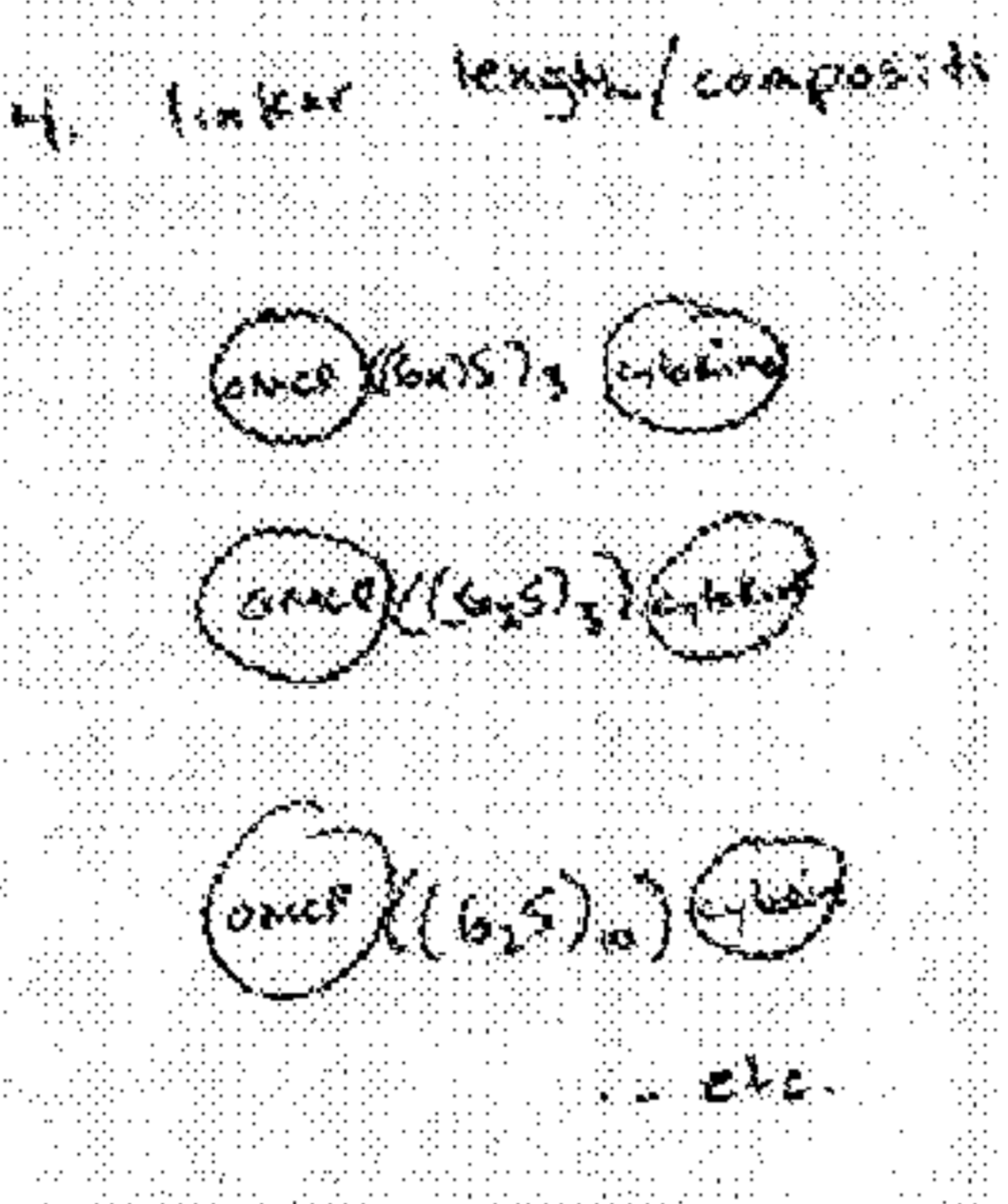
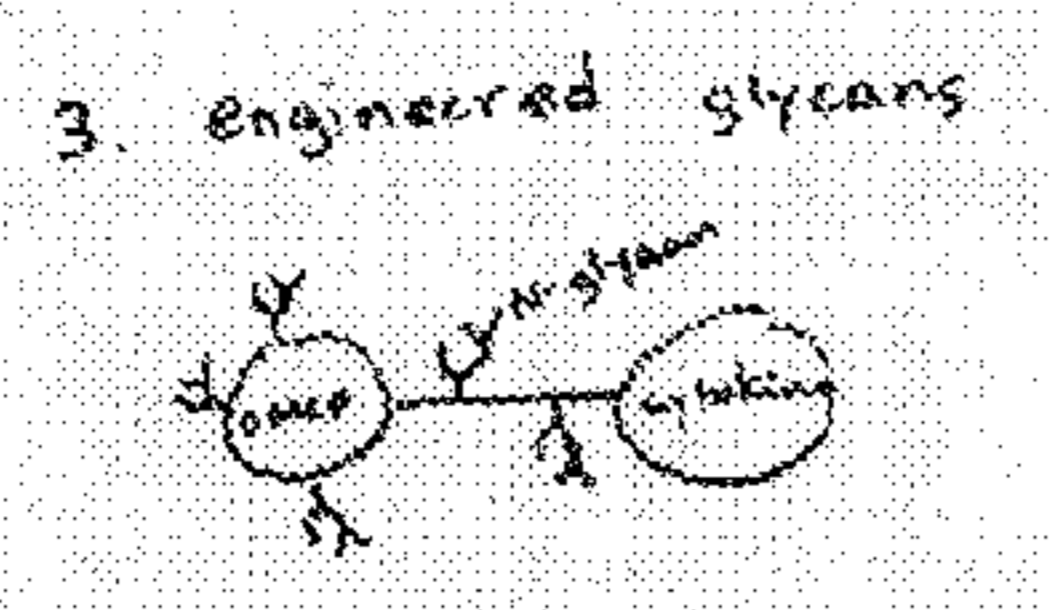
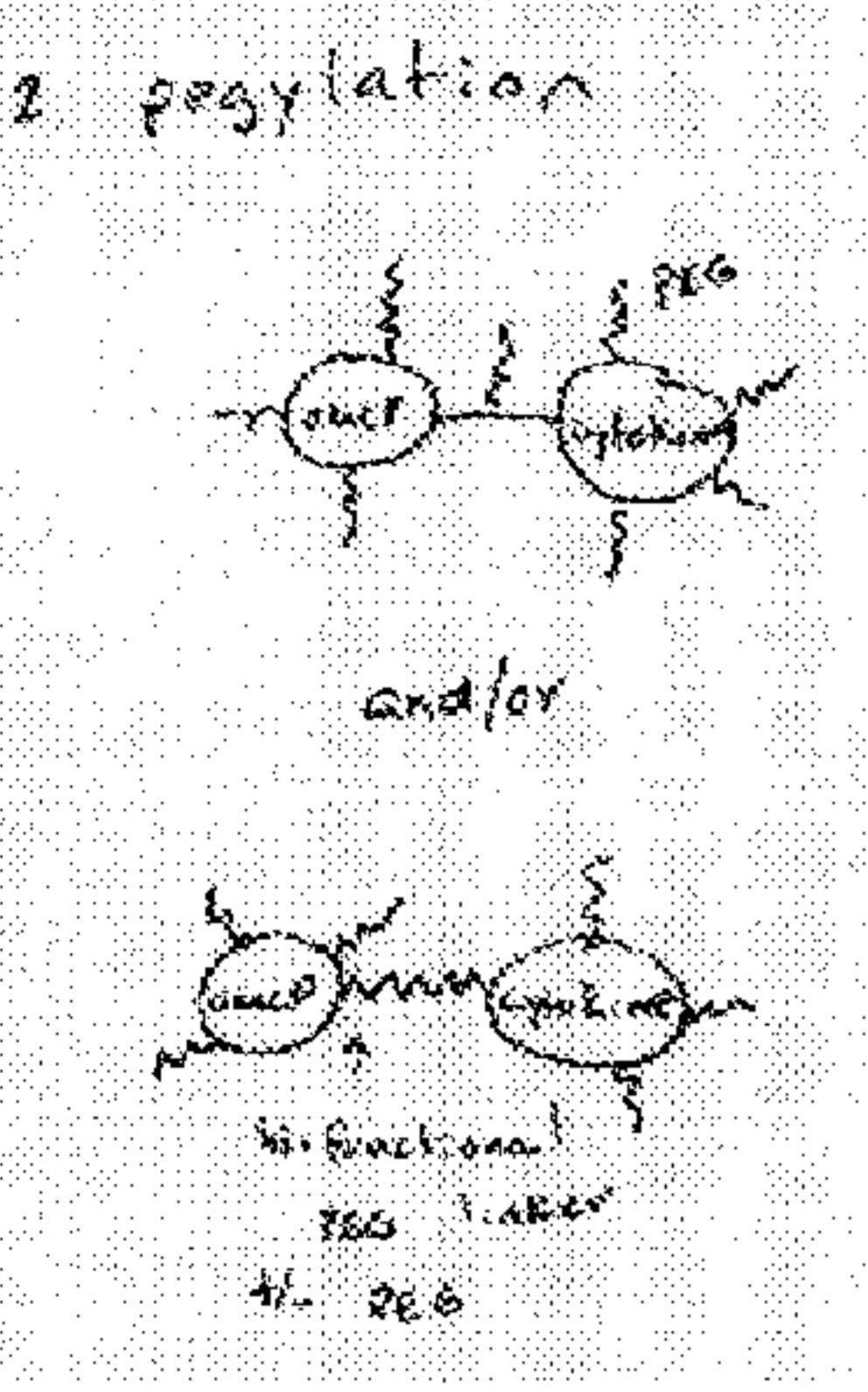
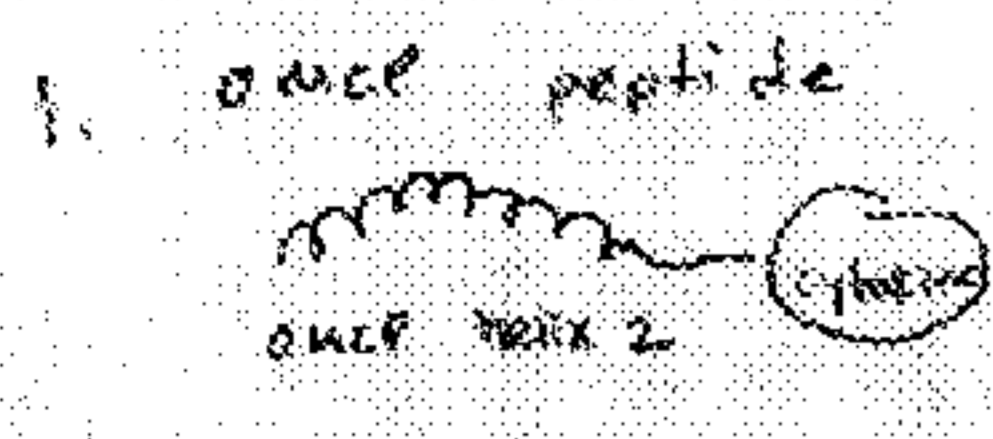


FIG. 23

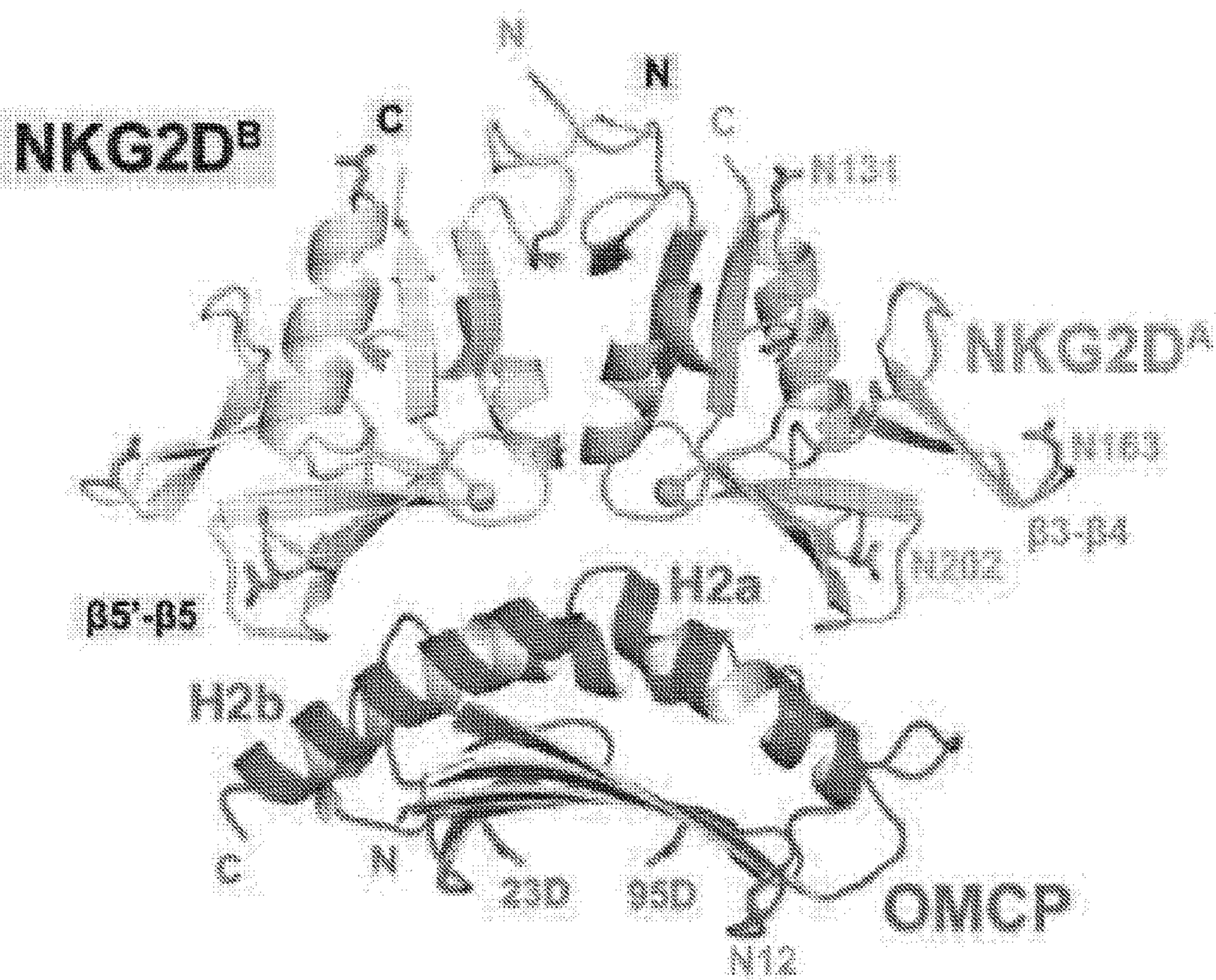


FIG. 24A

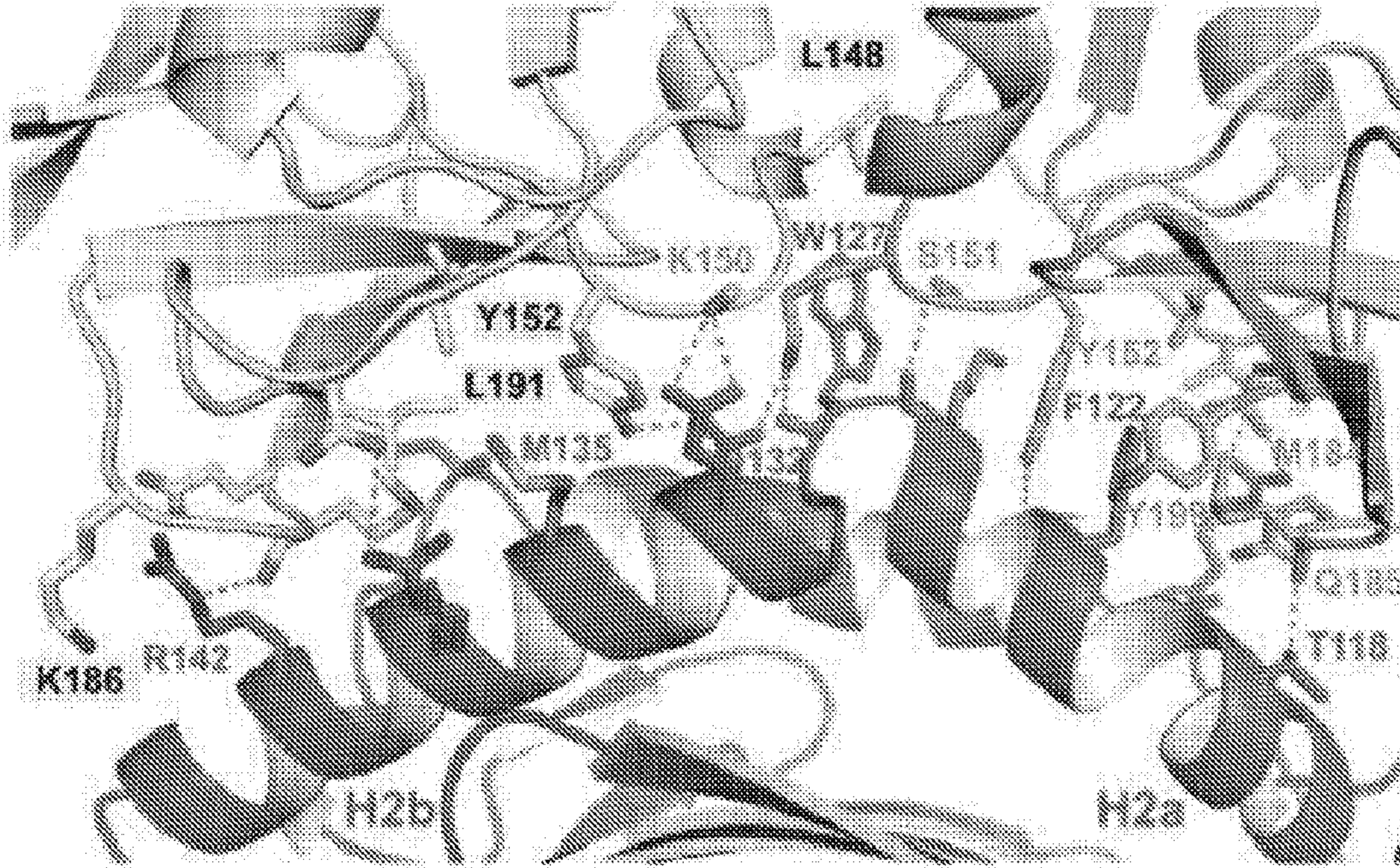


FIG. 24B

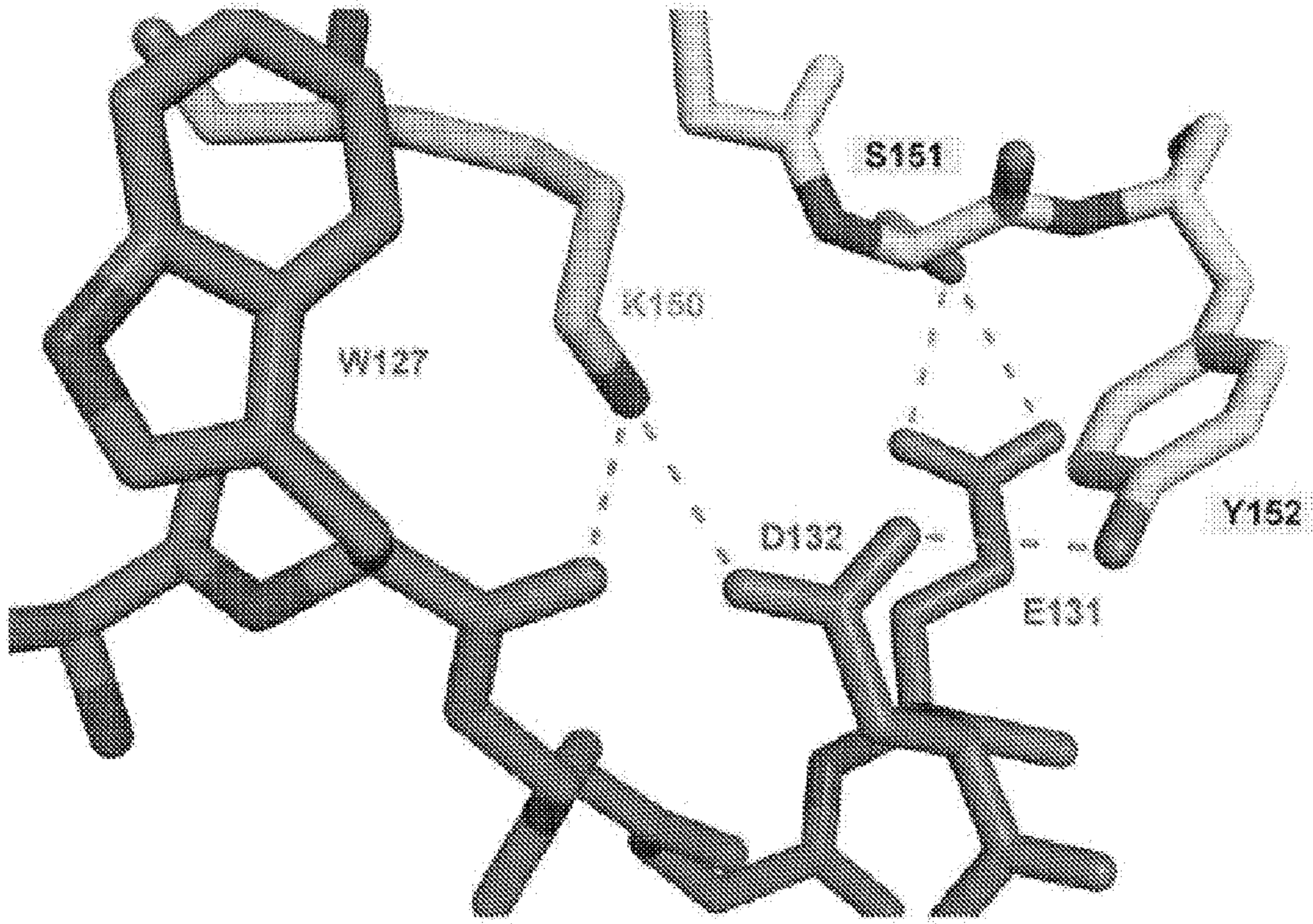


FIG. 25A

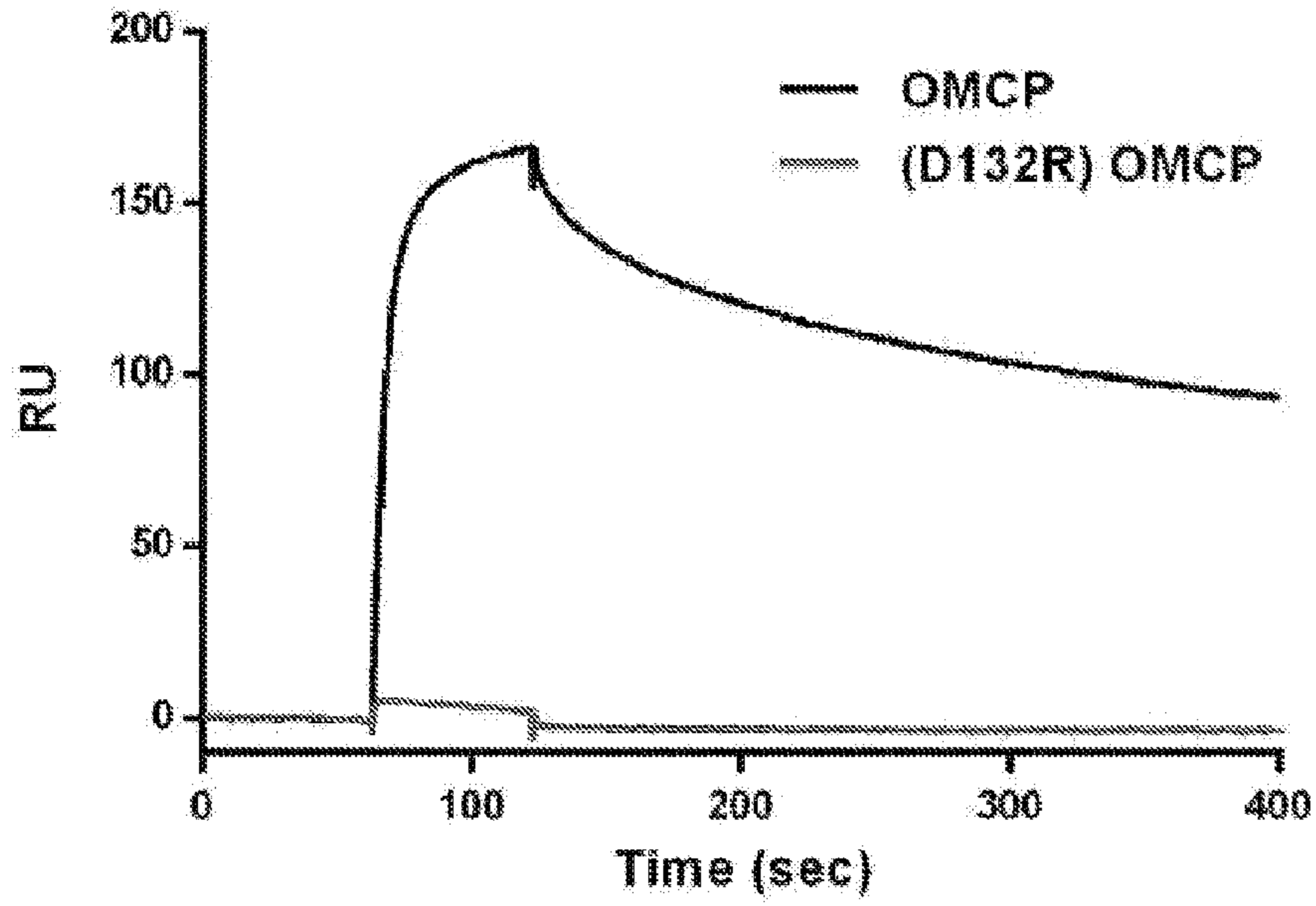


FIG. 25B

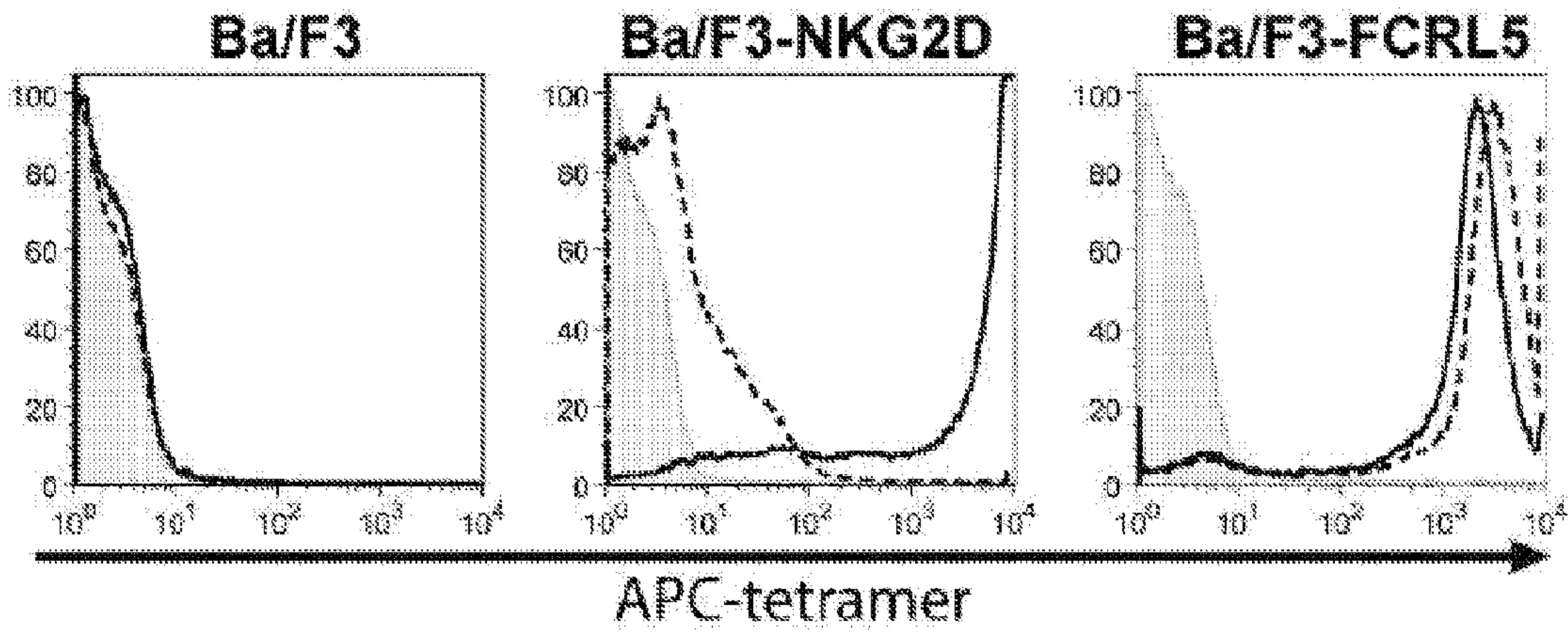


FIG. 25C

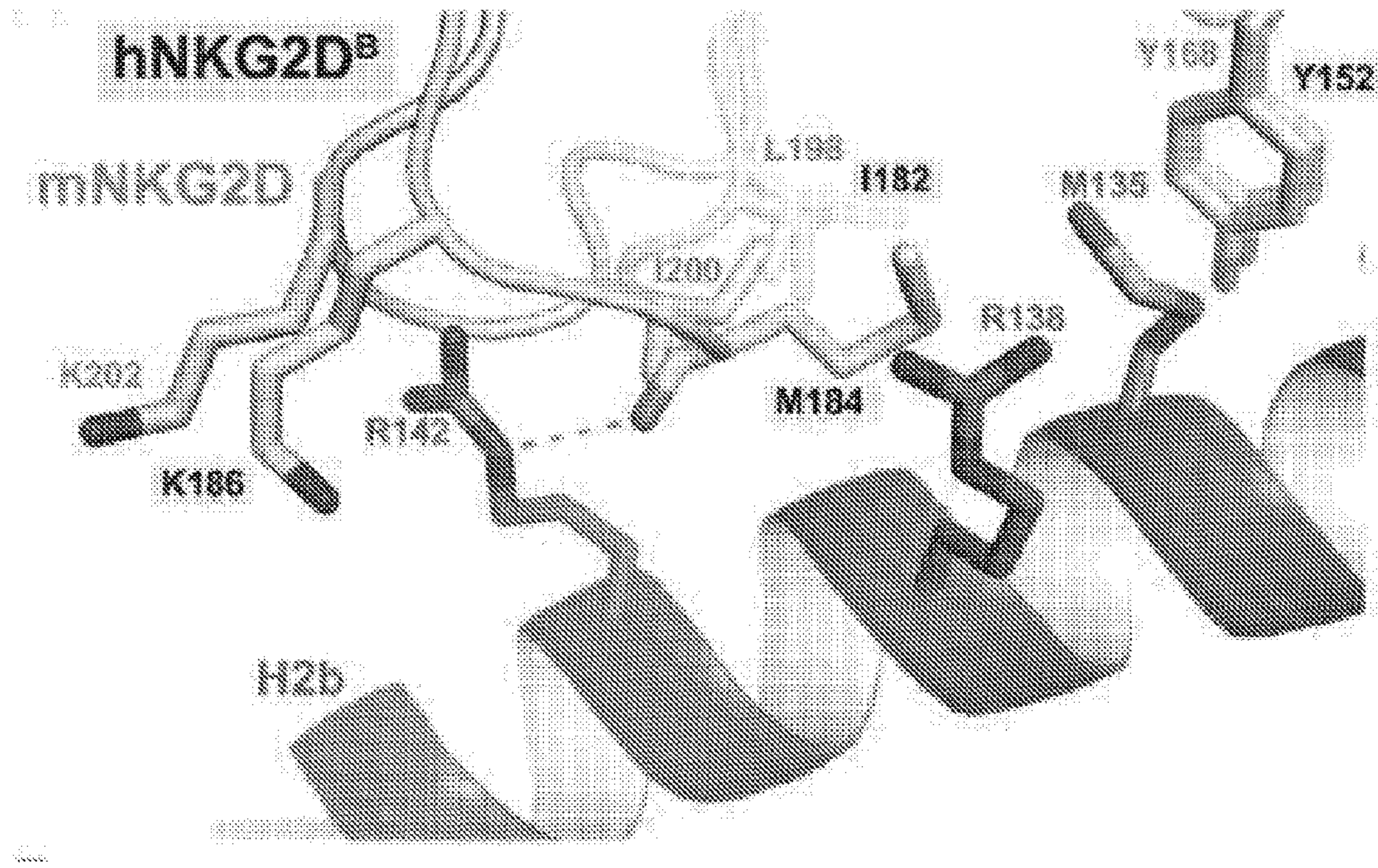


FIG. 26A

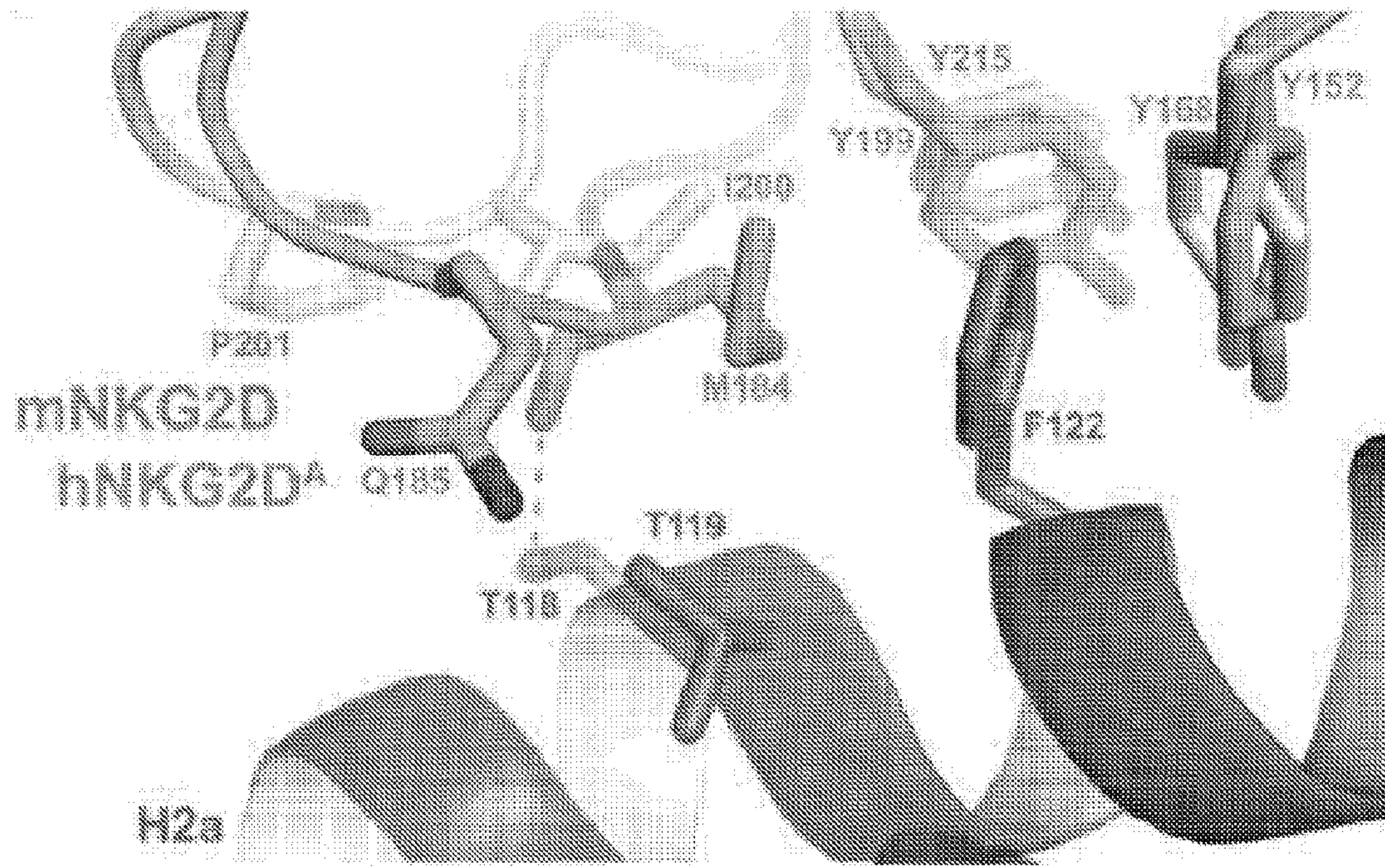


FIG. 26B

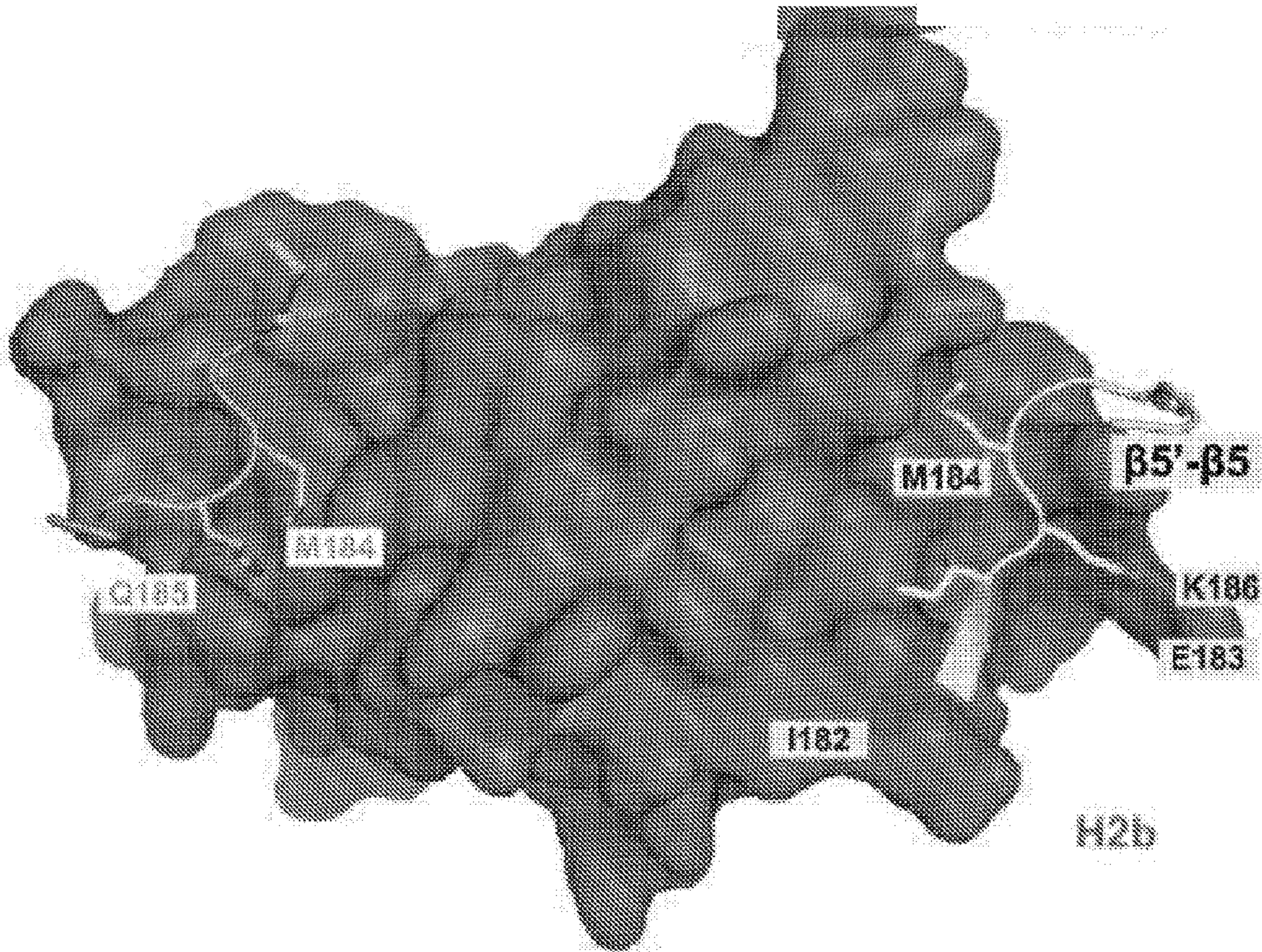


FIG. 26C

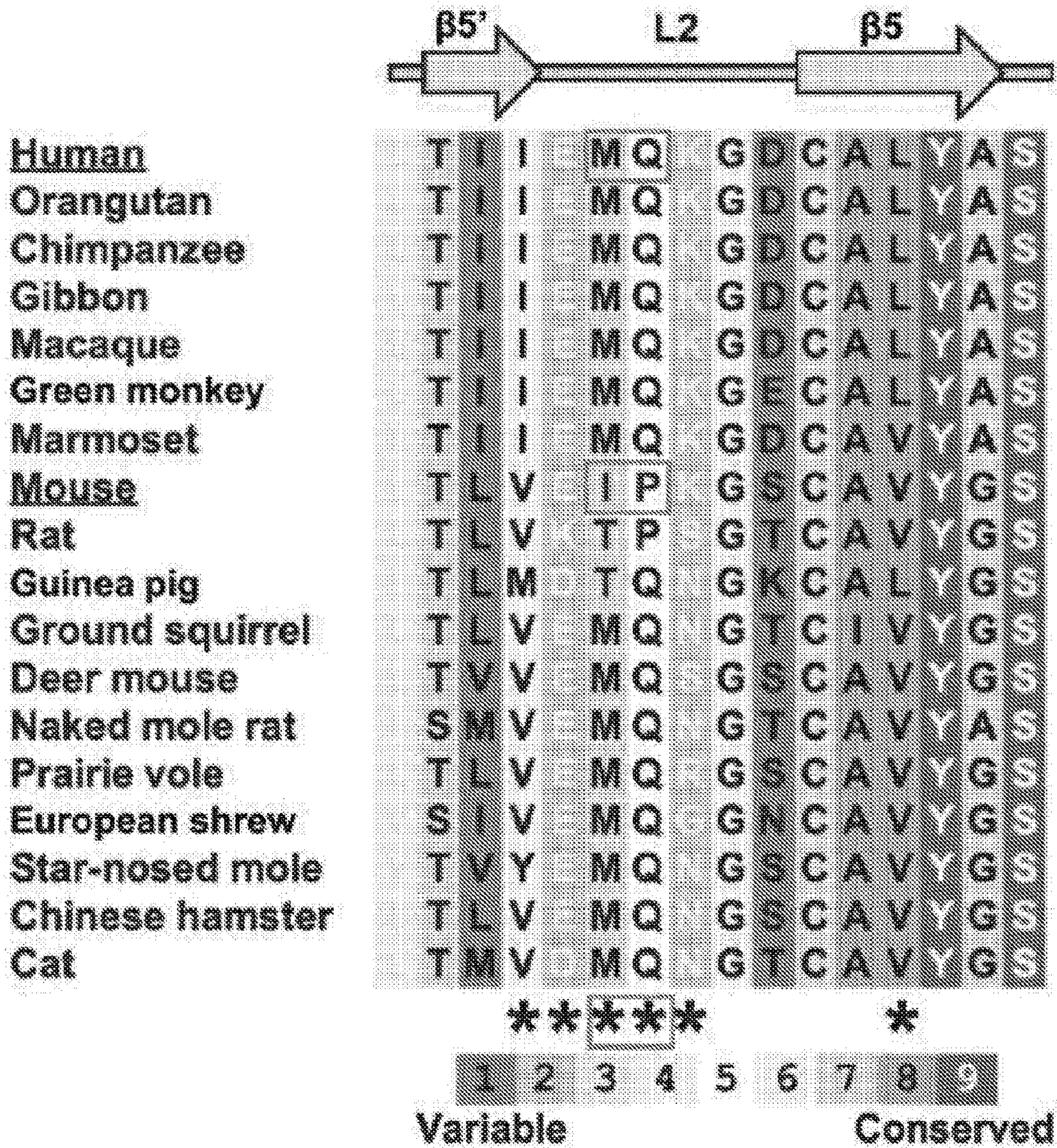


FIG. 26D

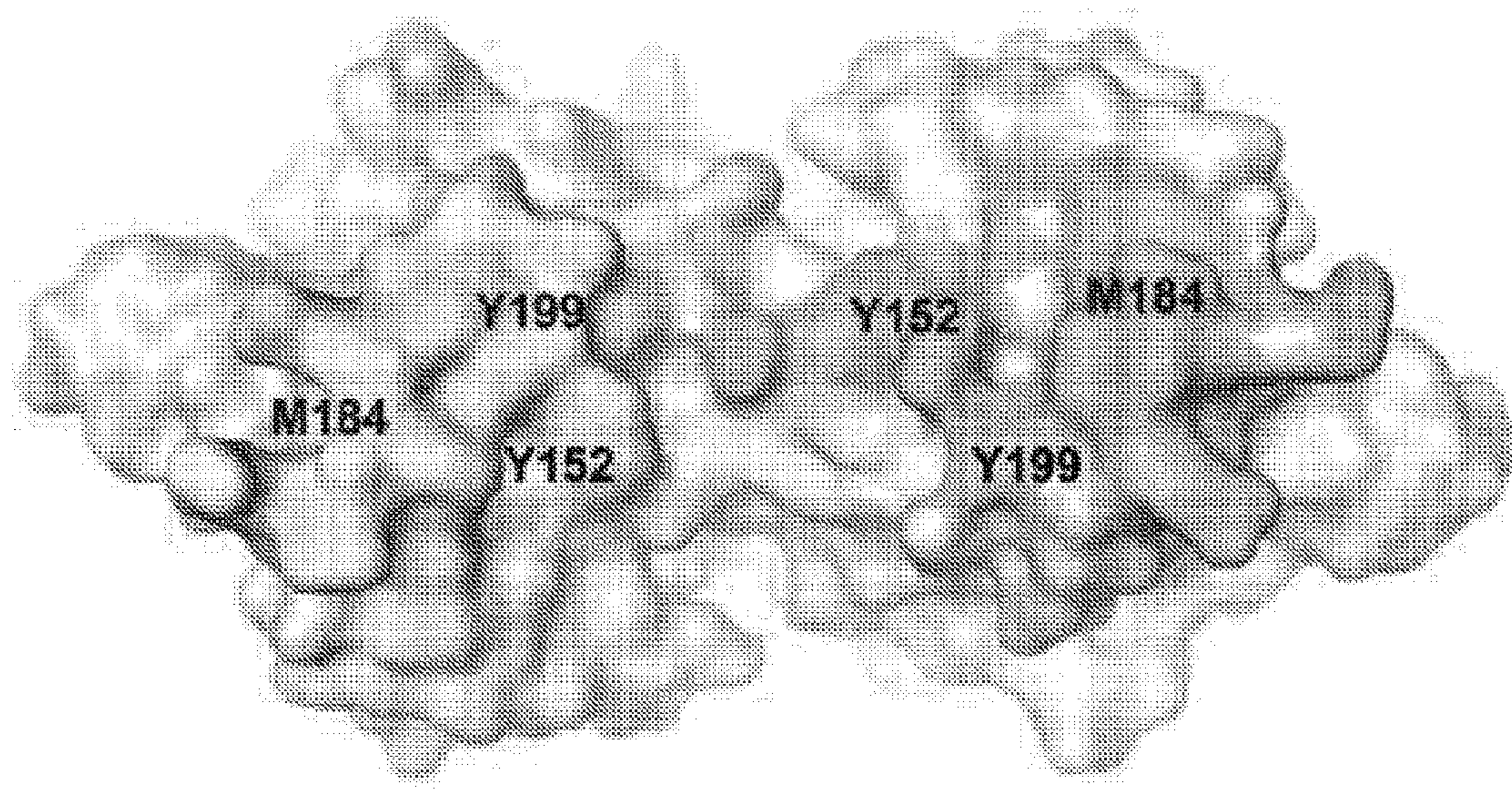


FIG. 27A

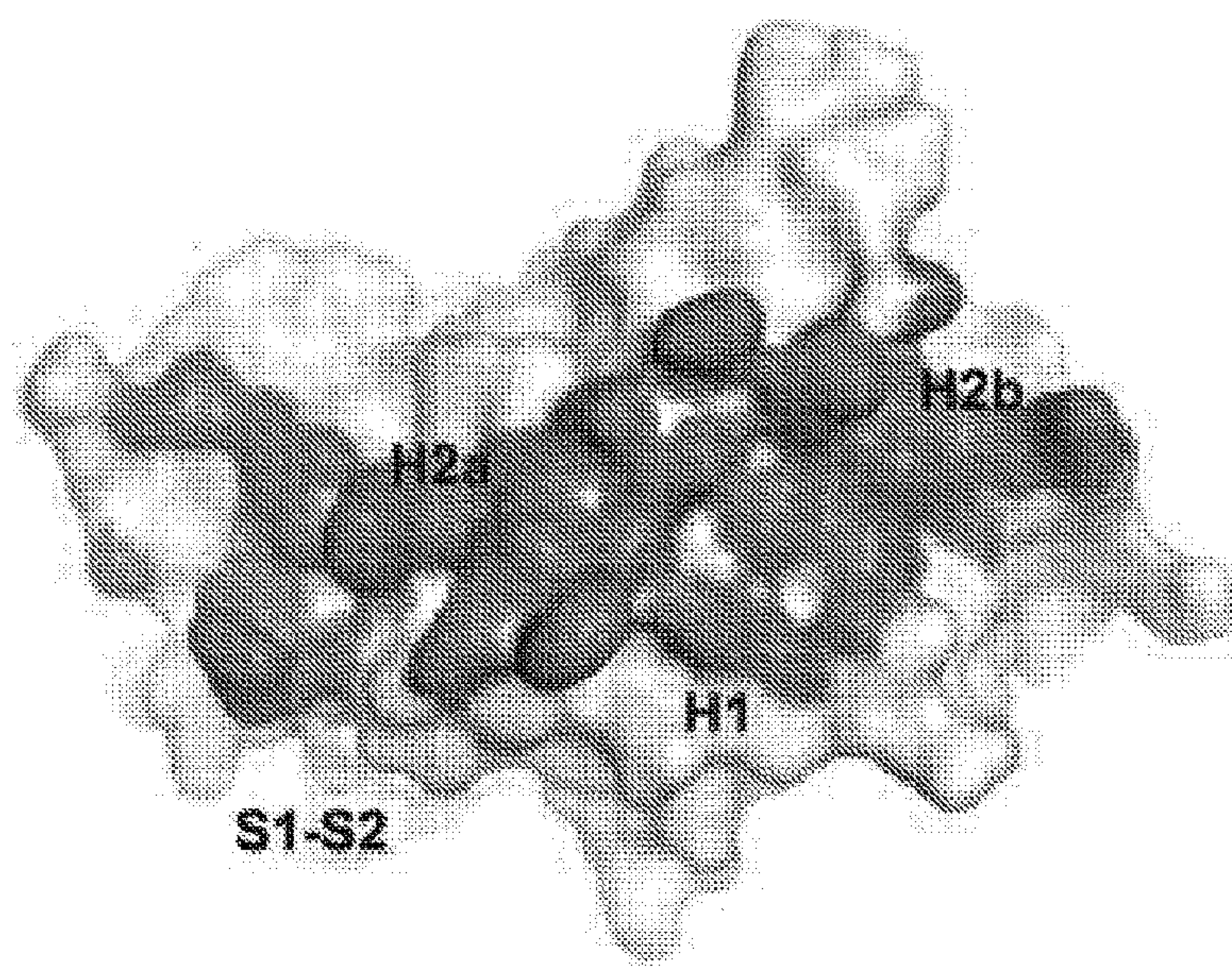


FIG. 27B

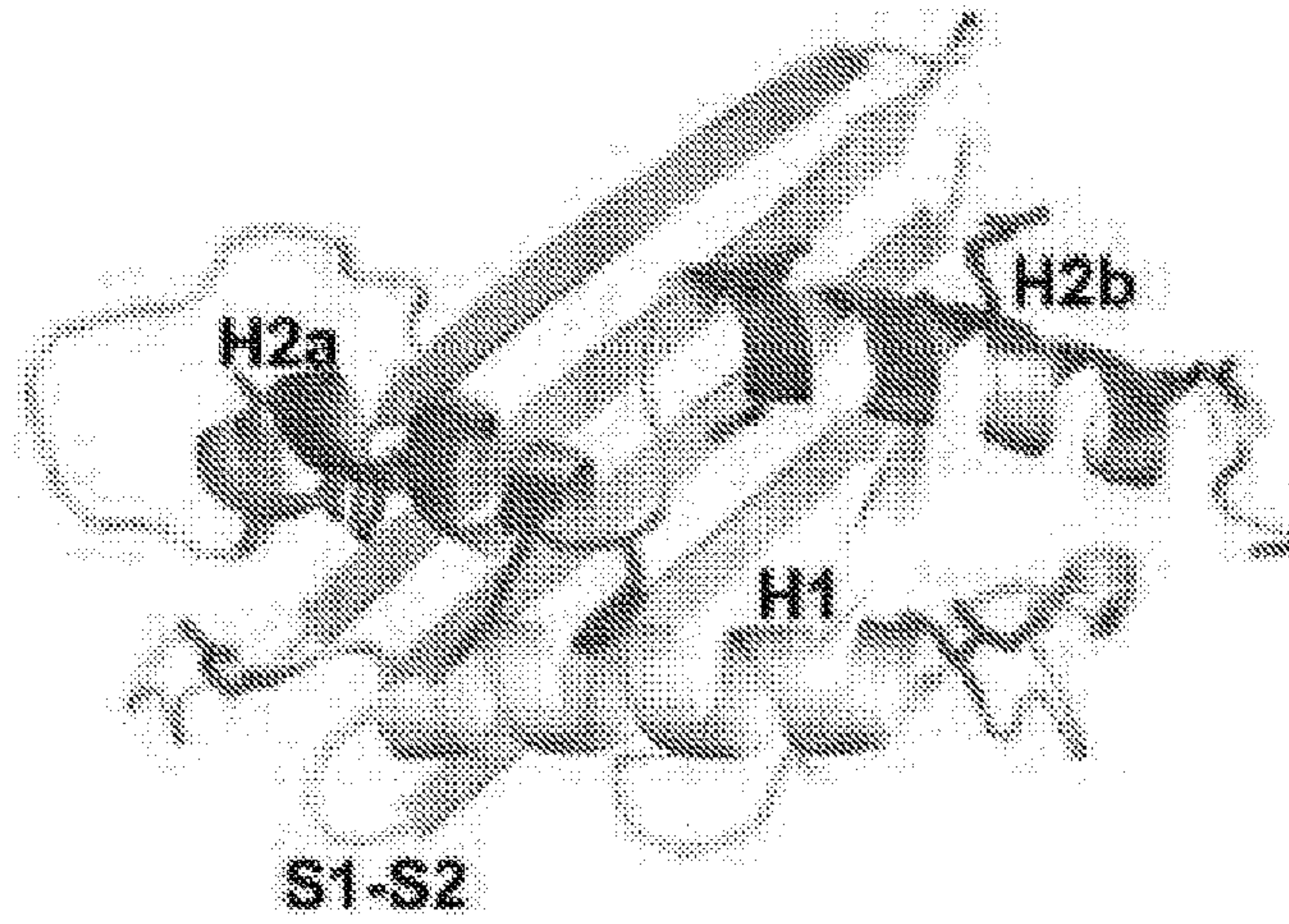


FIG. 27C

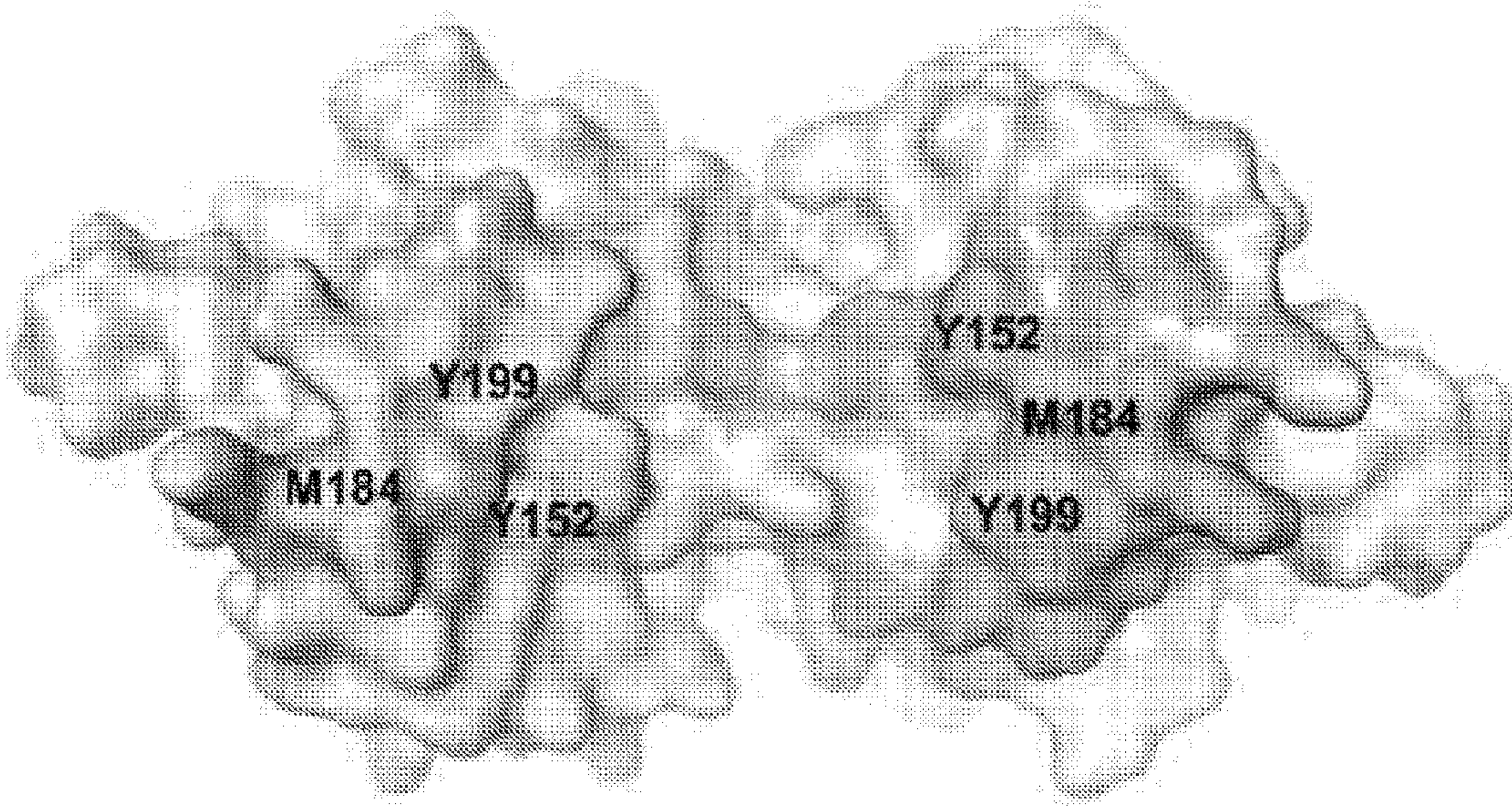


FIG. 27D

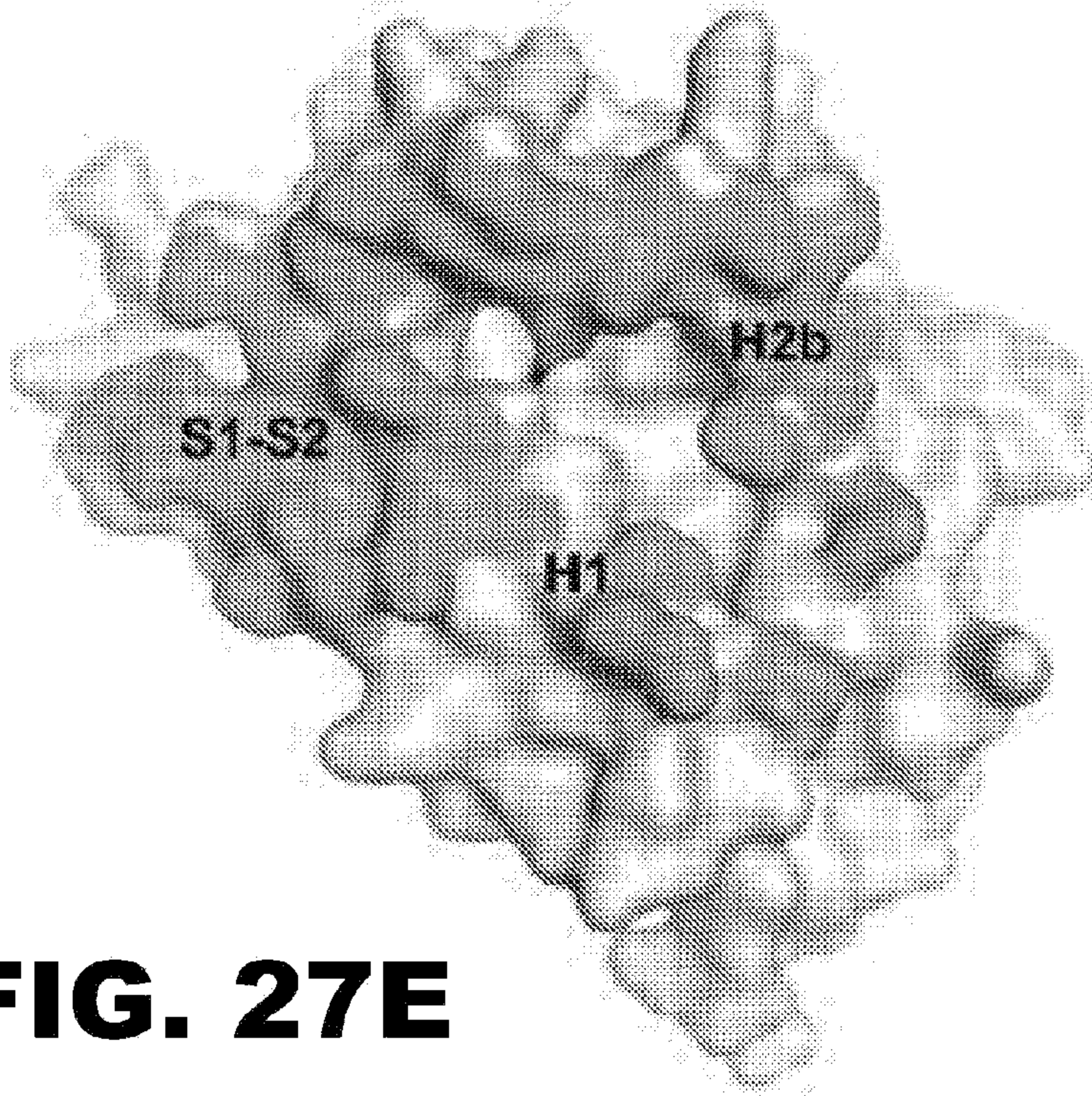


FIG. 27E

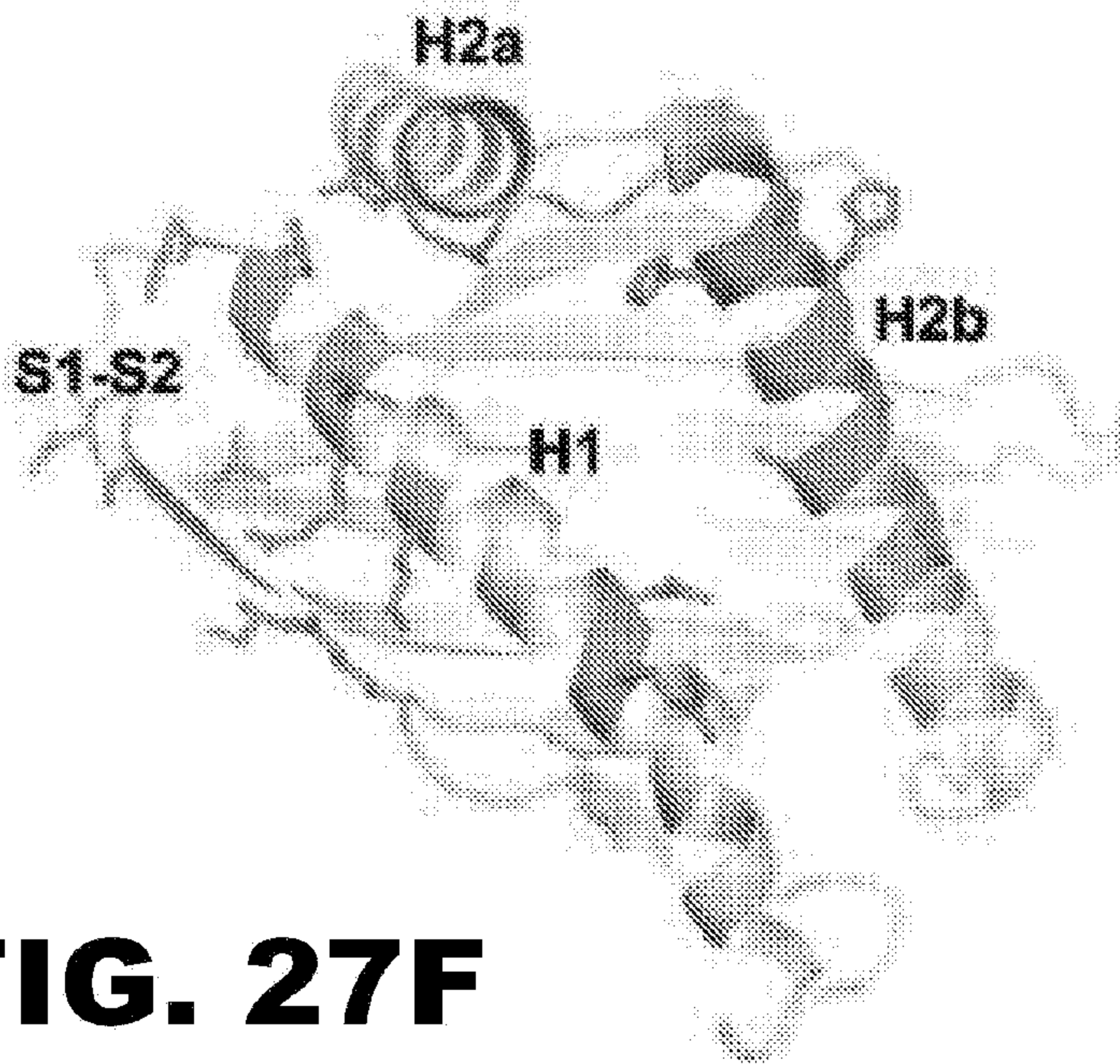


FIG. 27F

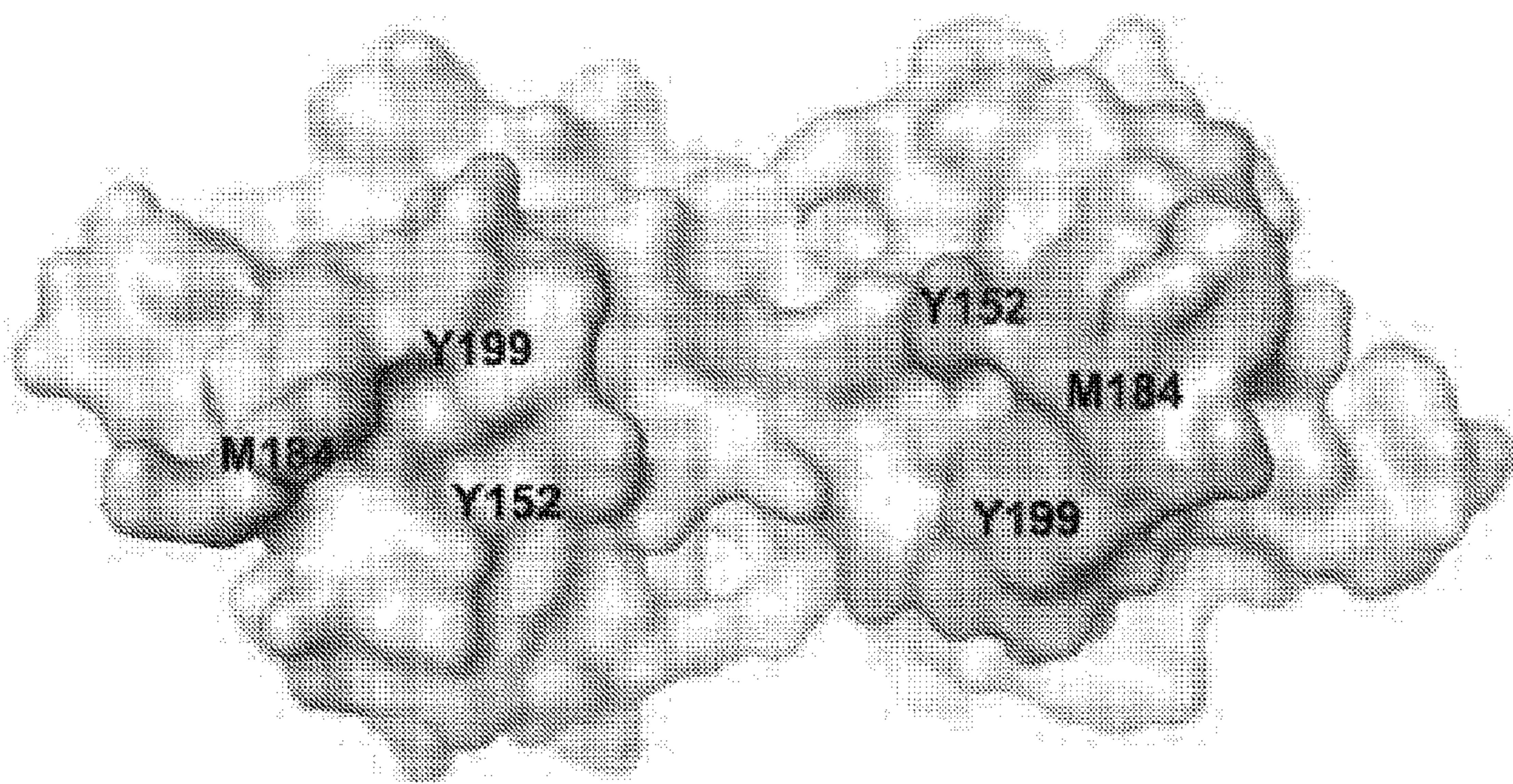


FIG. 27G

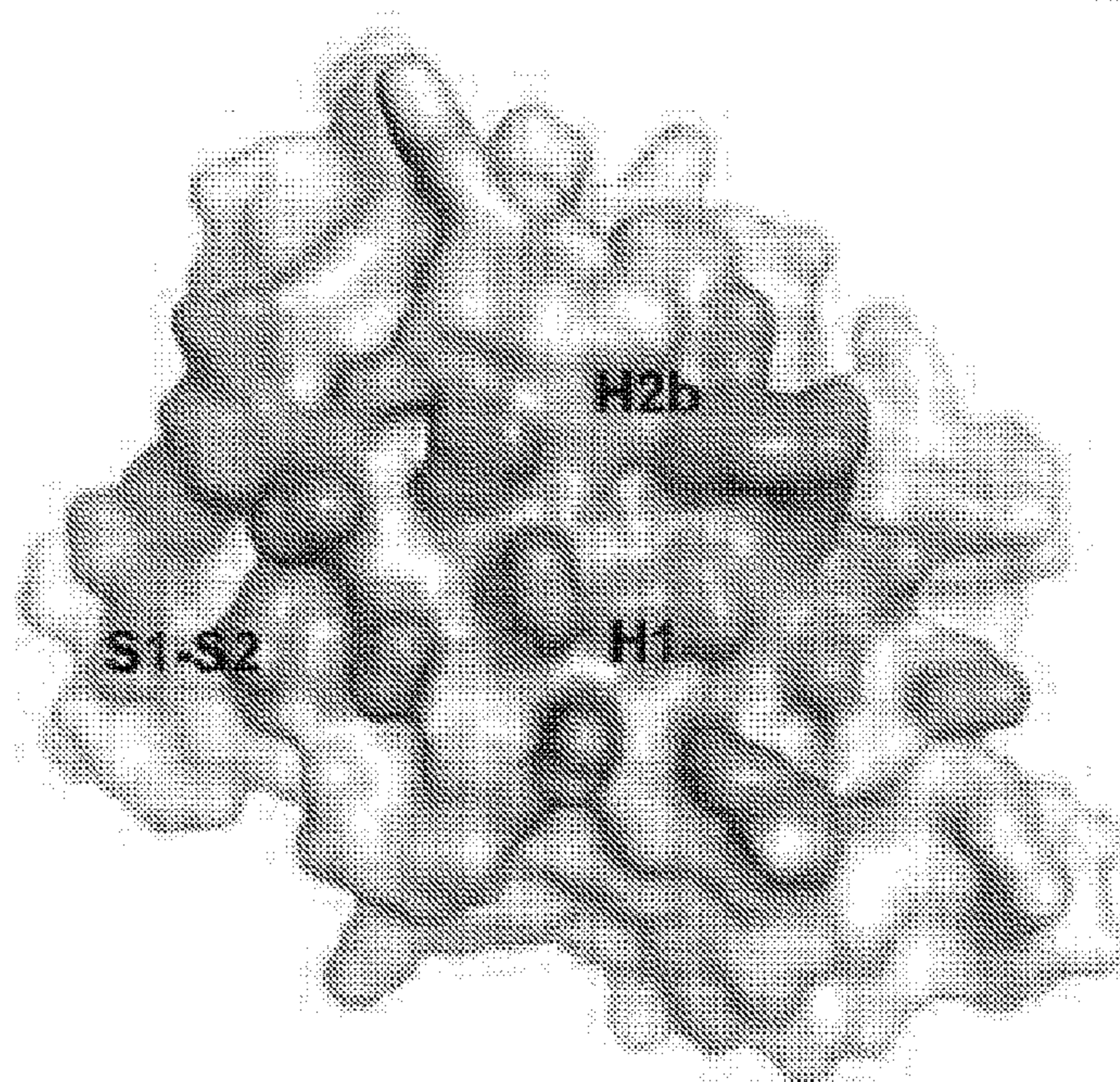


FIG. 27H

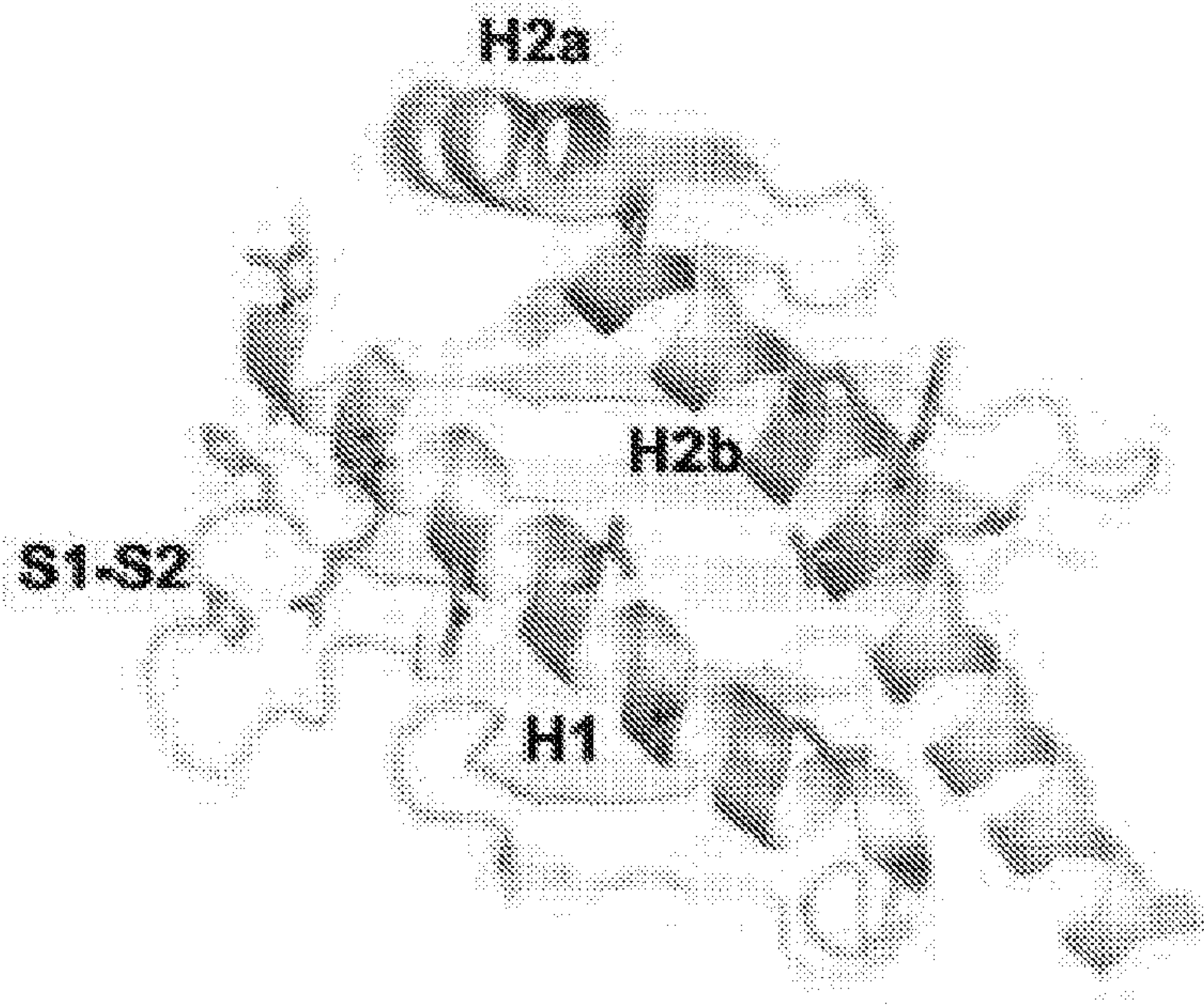


FIG. 271

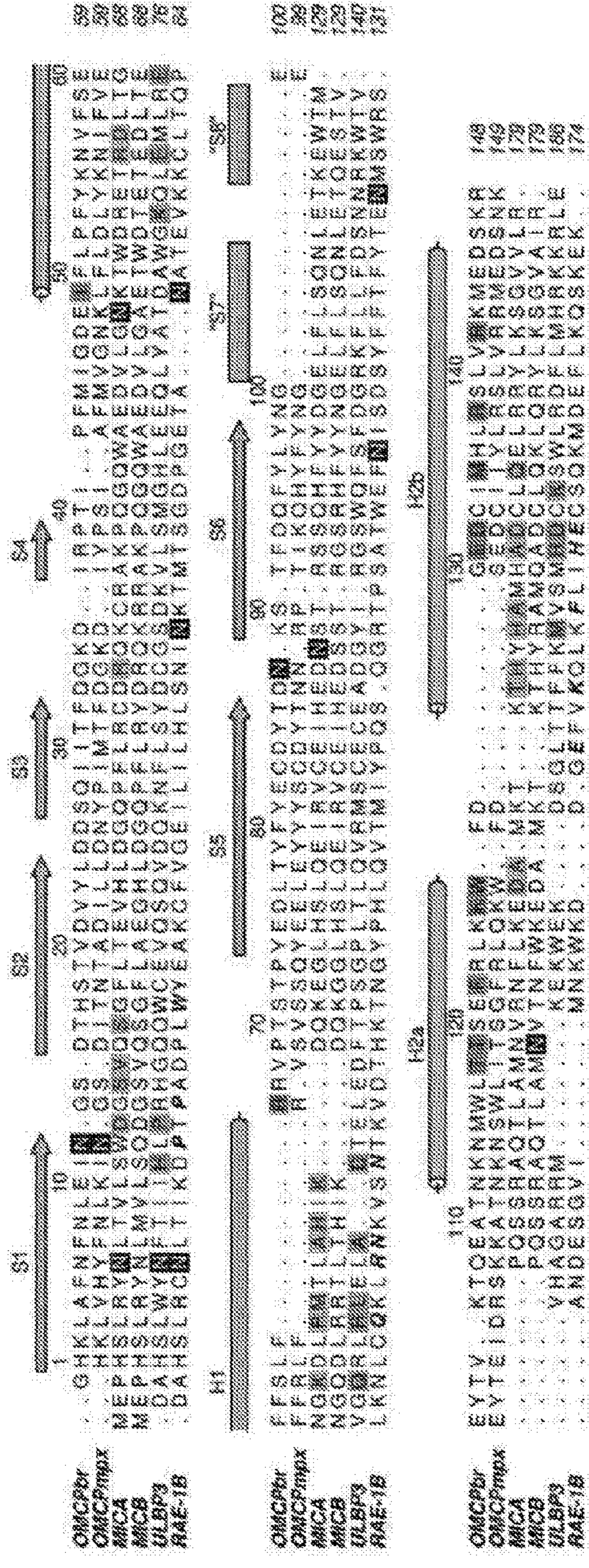


FIG. 27J

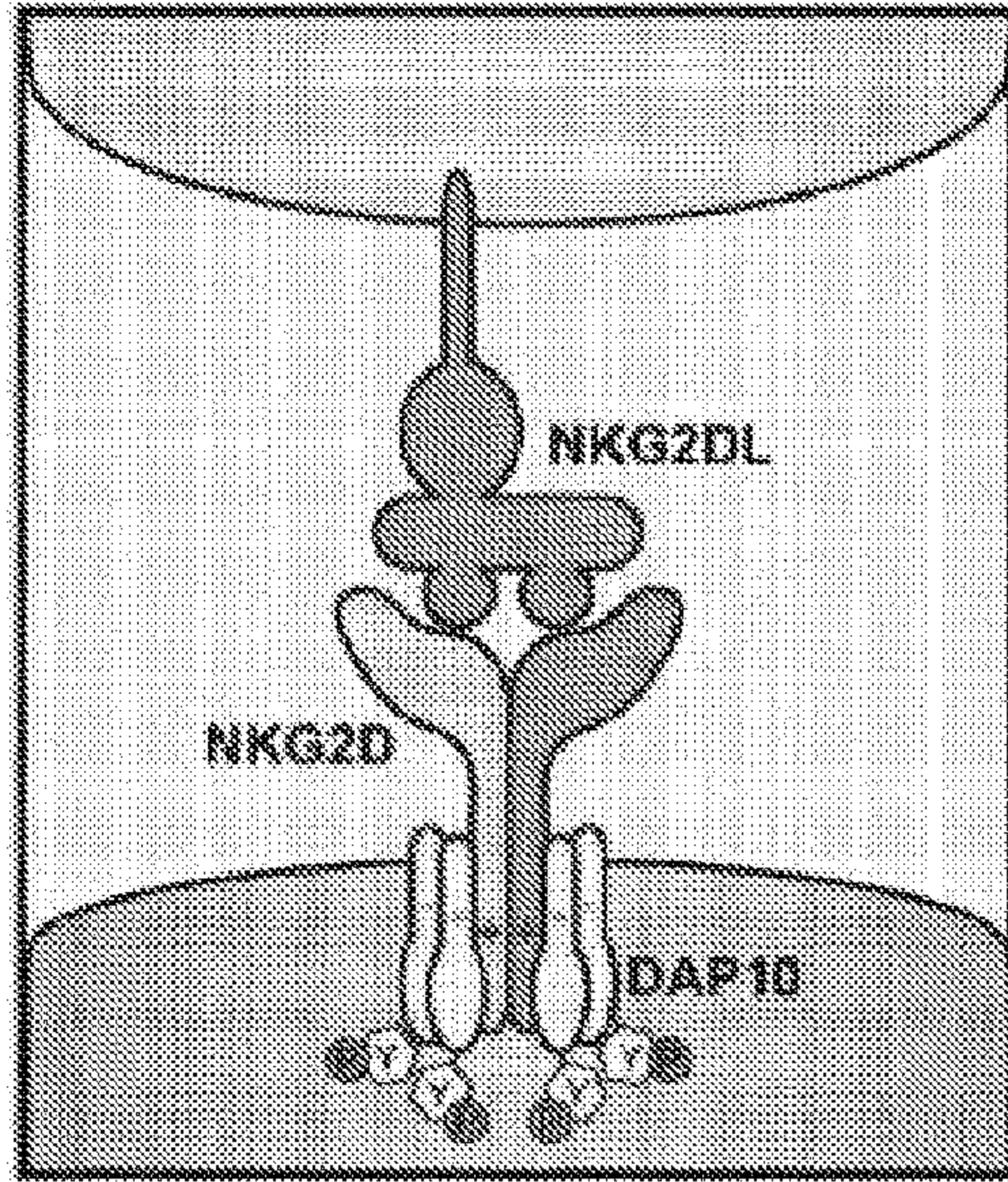


FIG. 28A

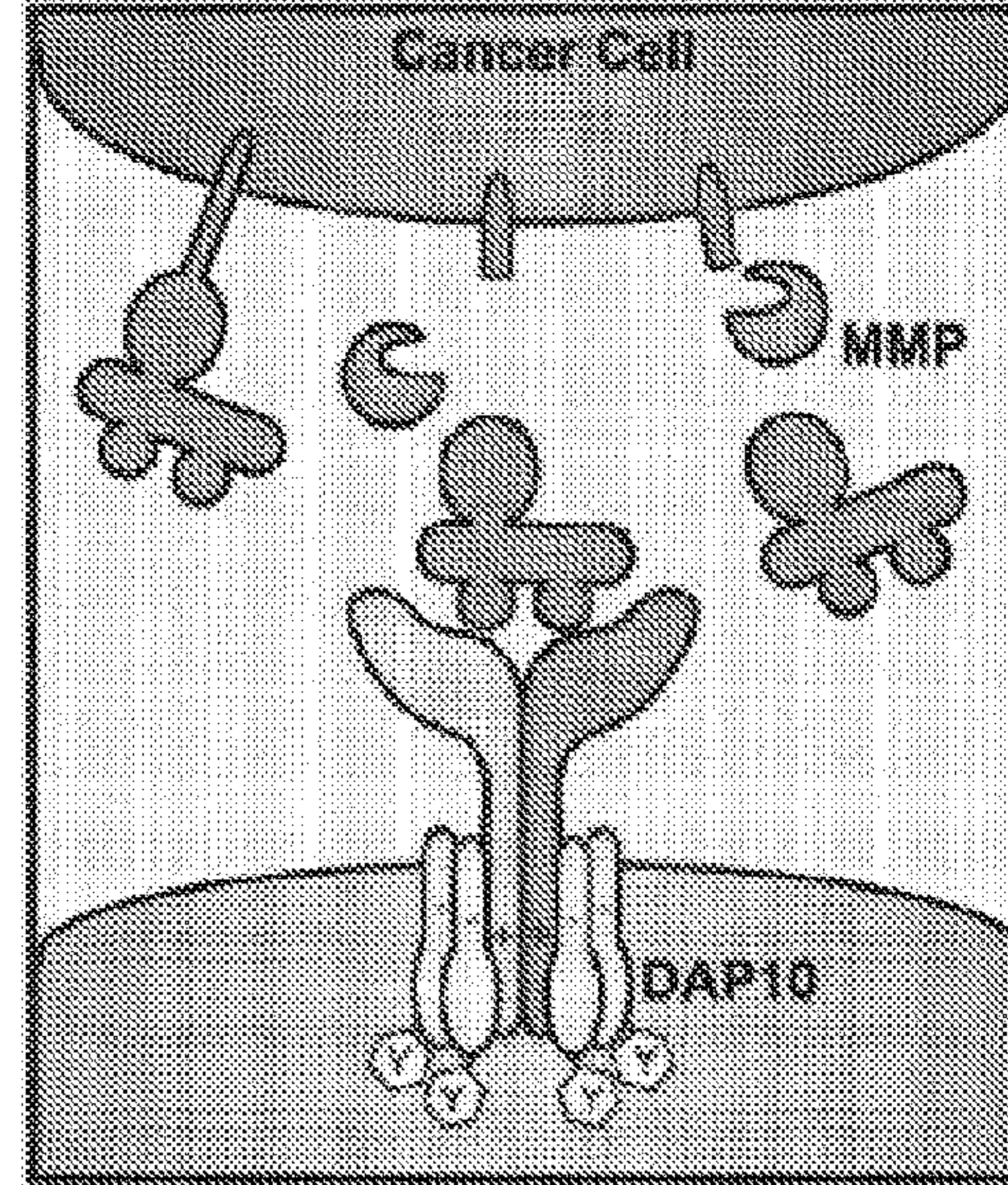


FIG. 28B

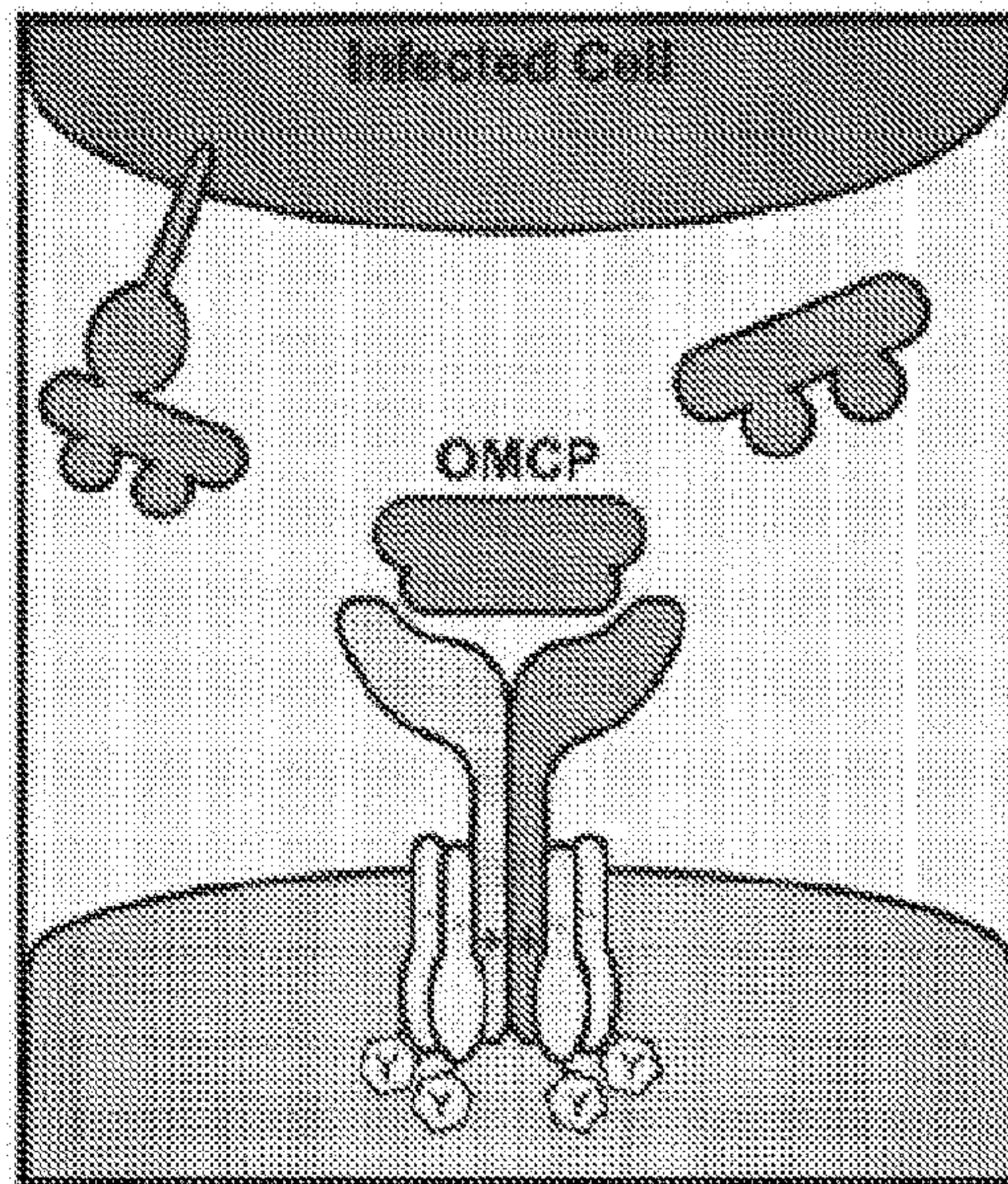


FIG. 28C

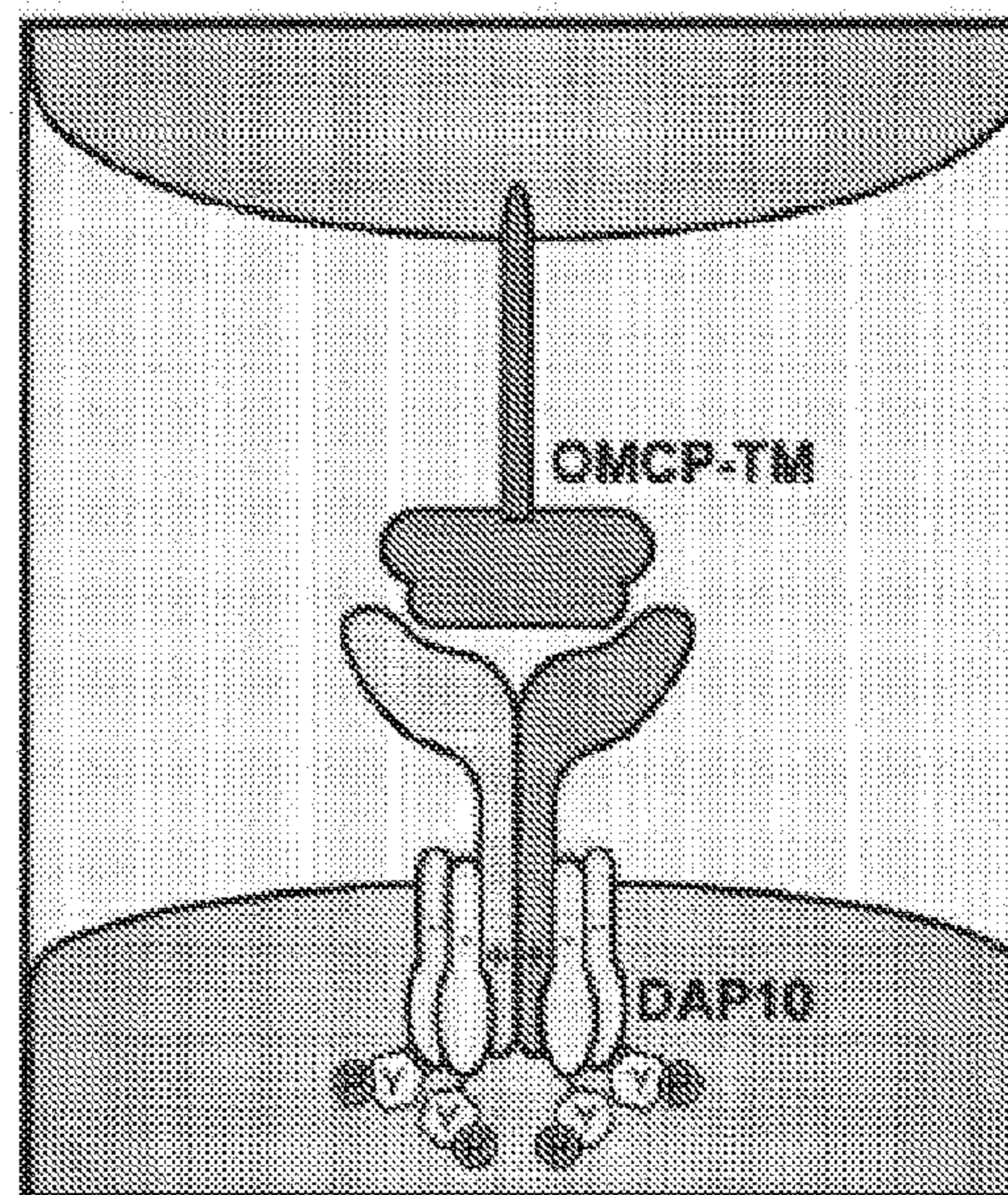


FIG. 28D

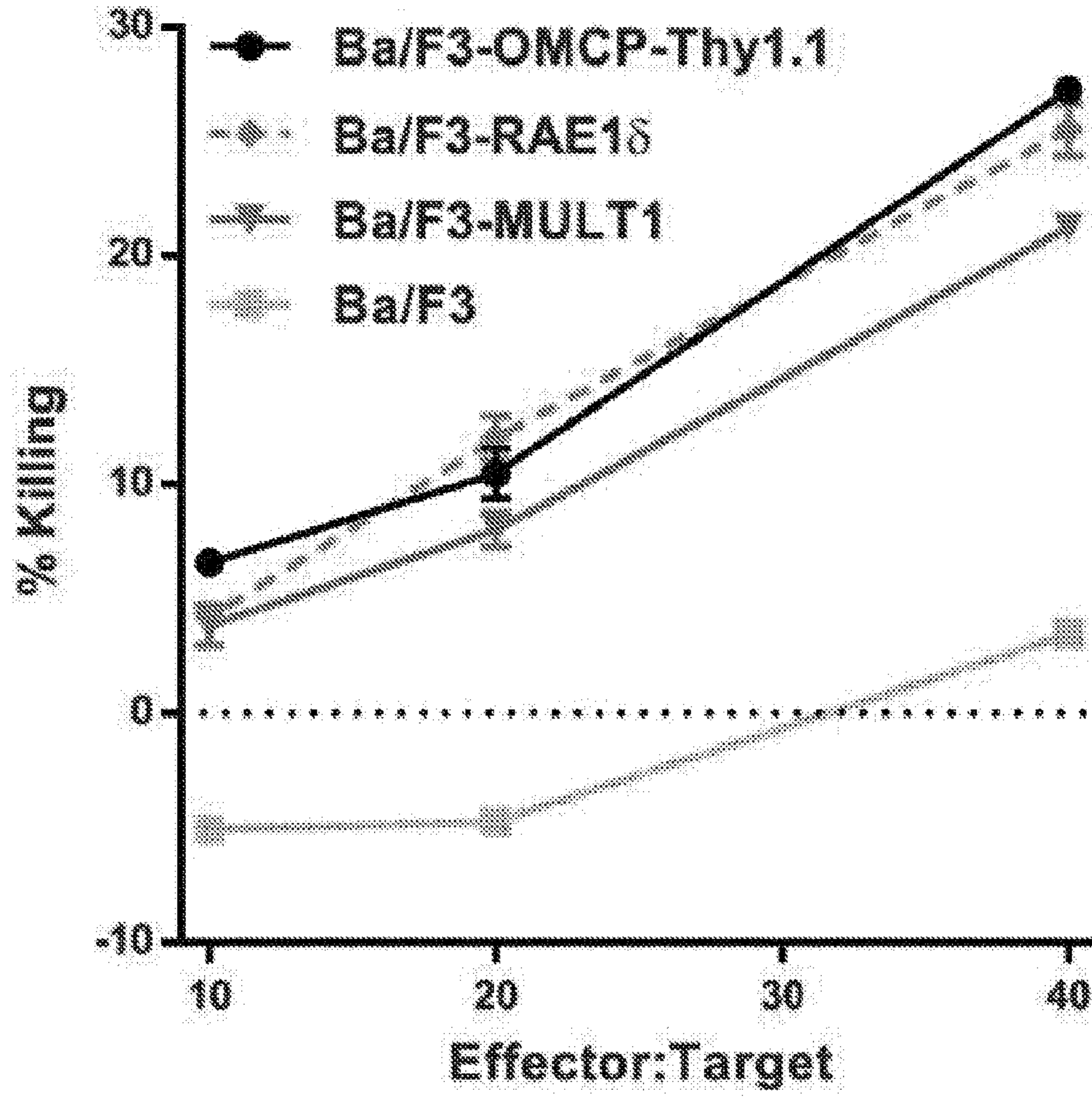


FIG. 28E

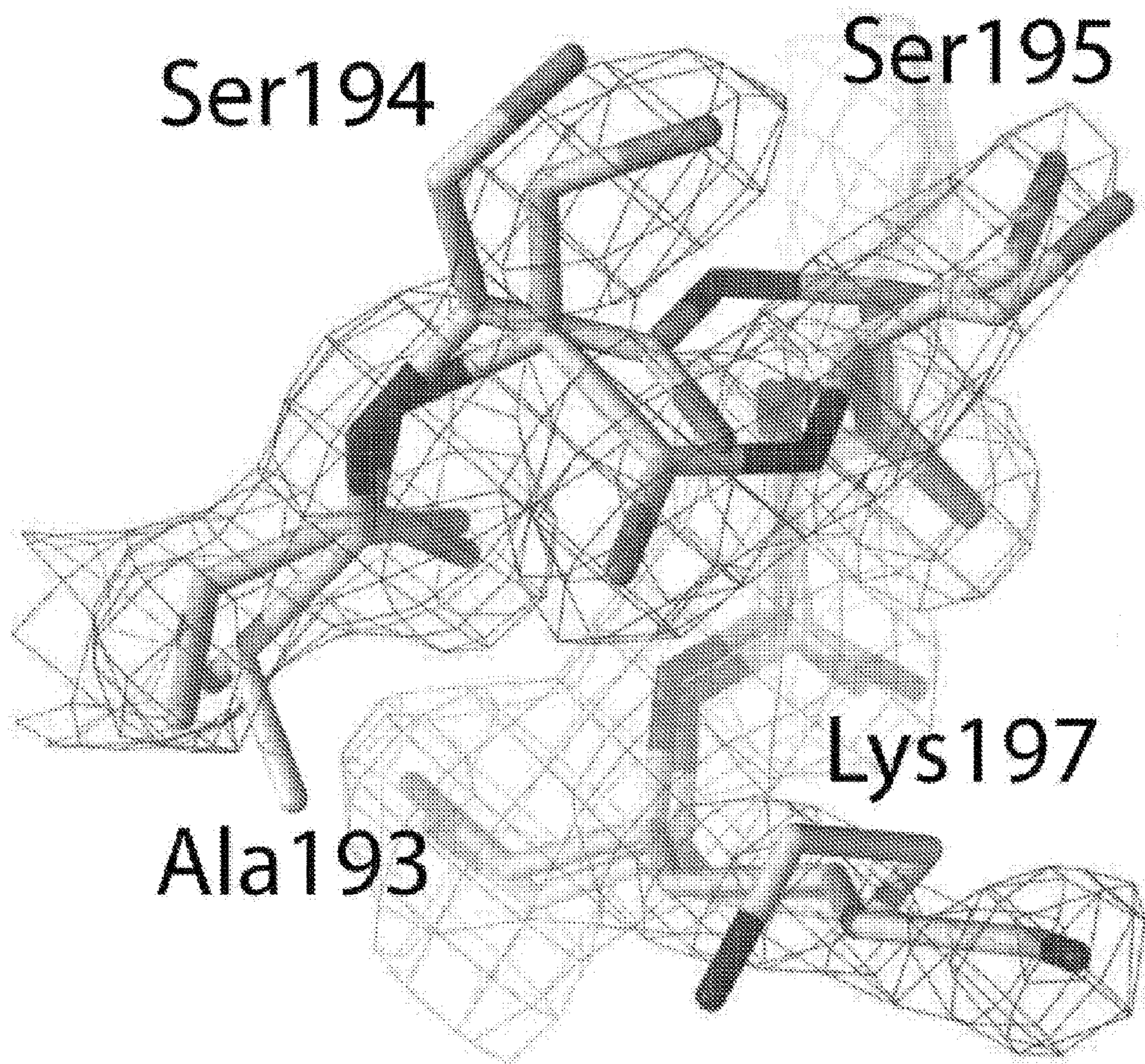


FIG. 29A

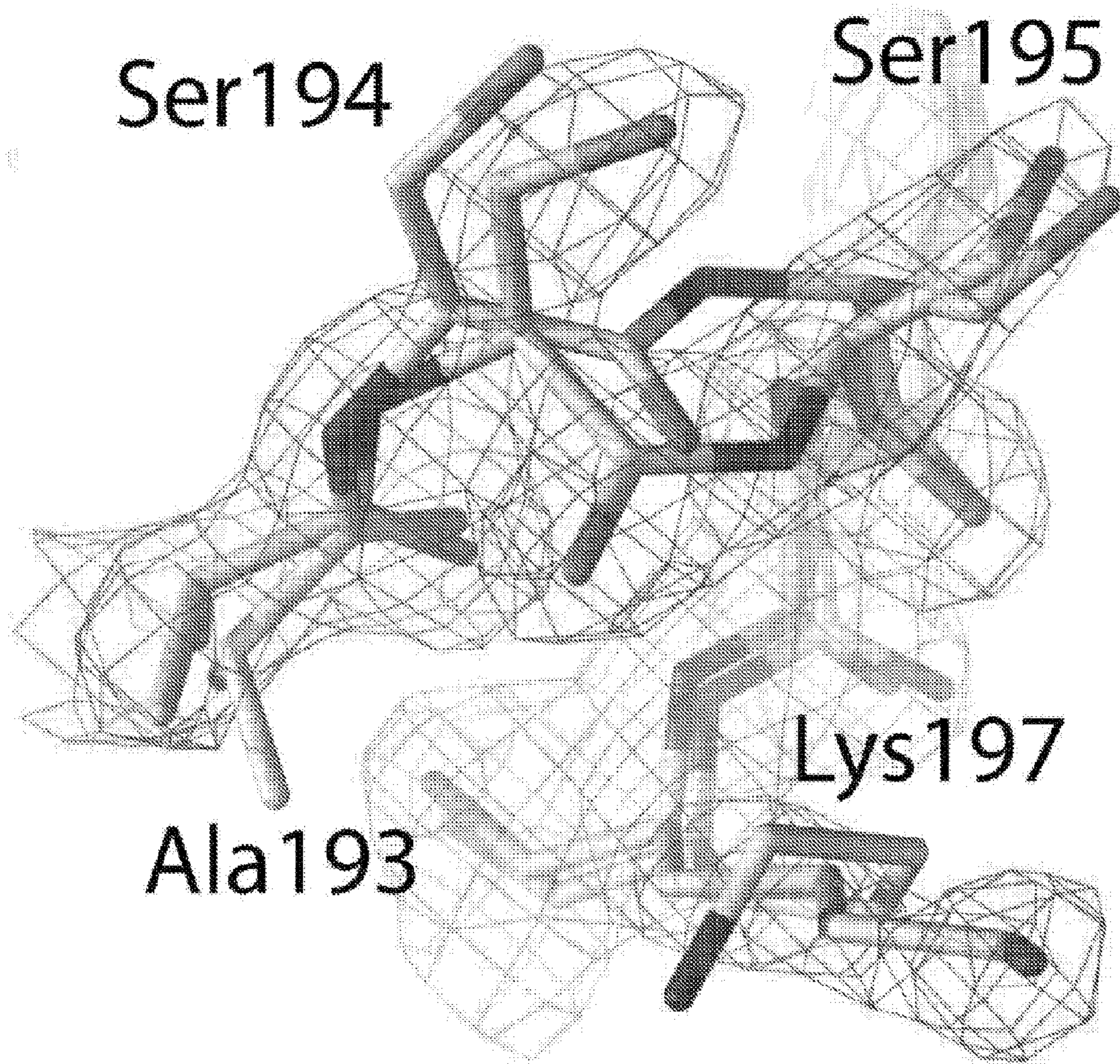


FIG. 29B

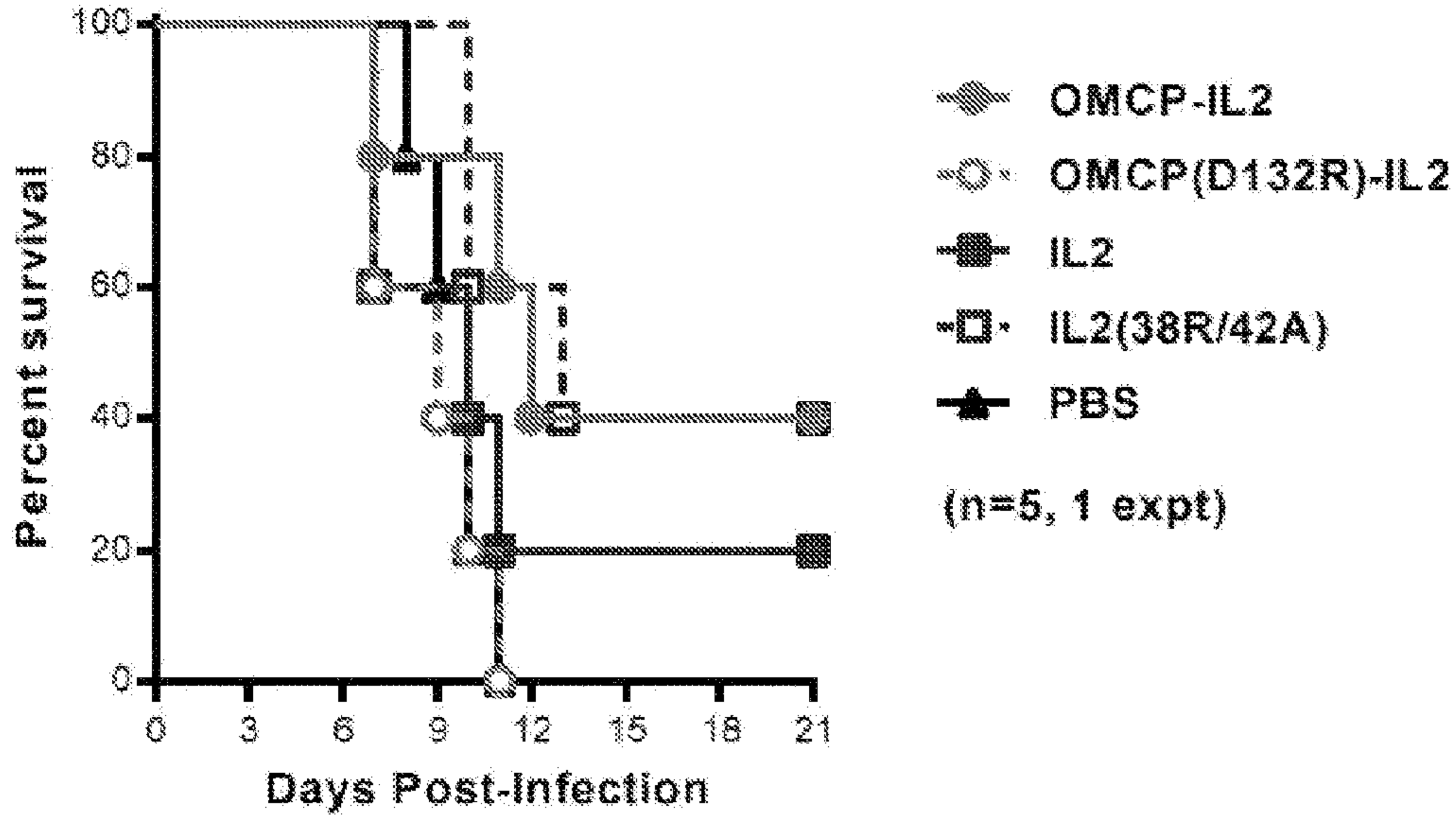


FIG. 30A

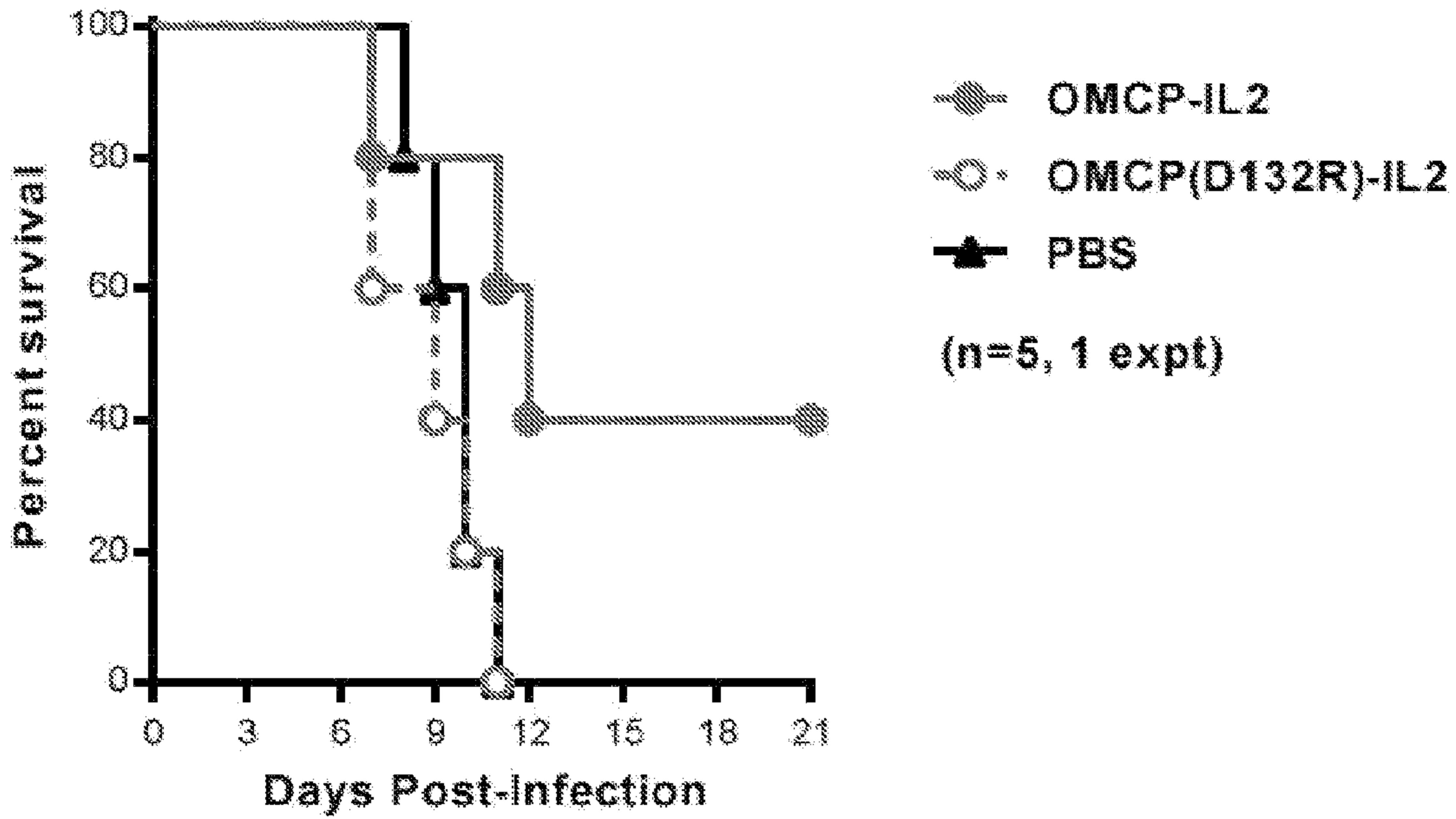


FIG. 30B

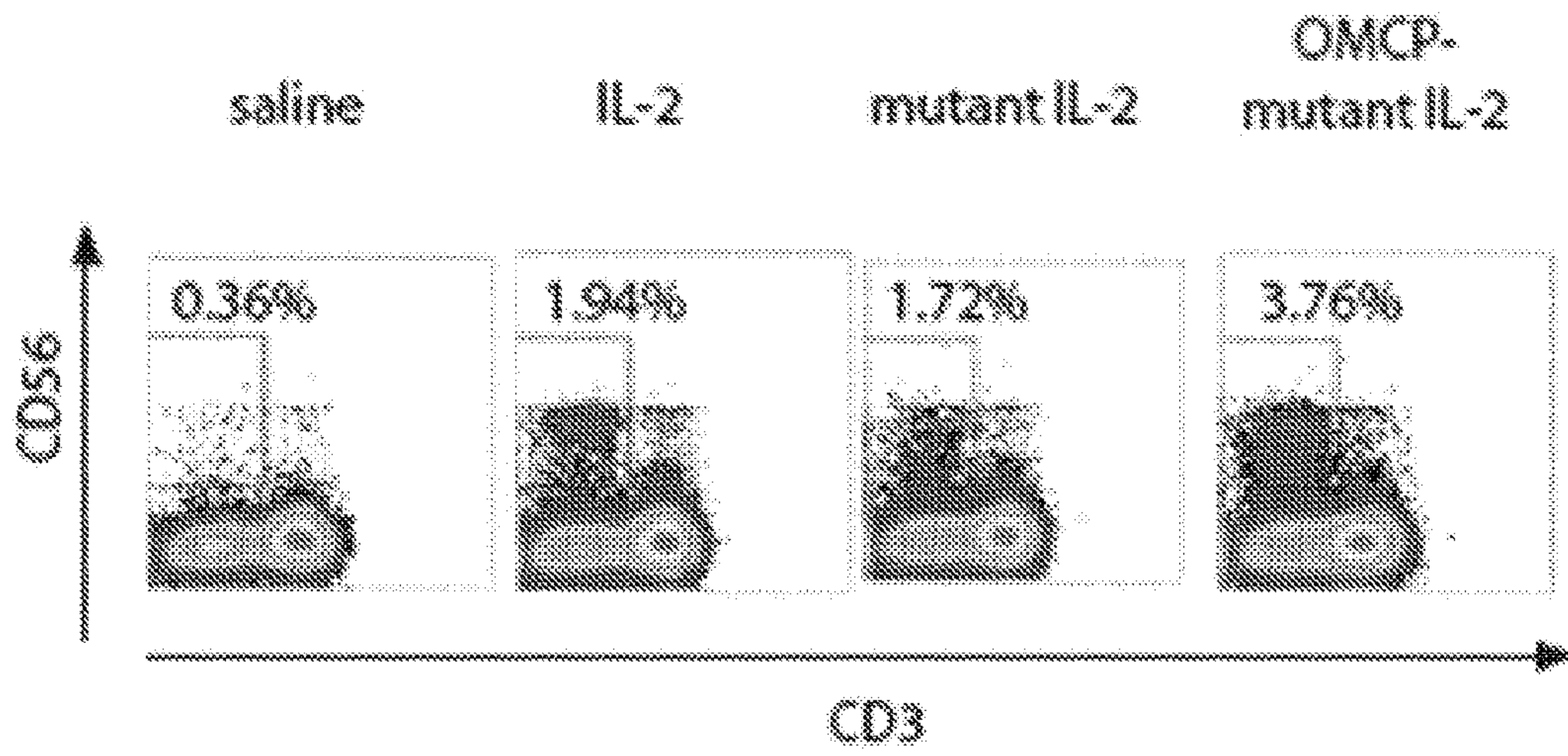


FIG. 31A

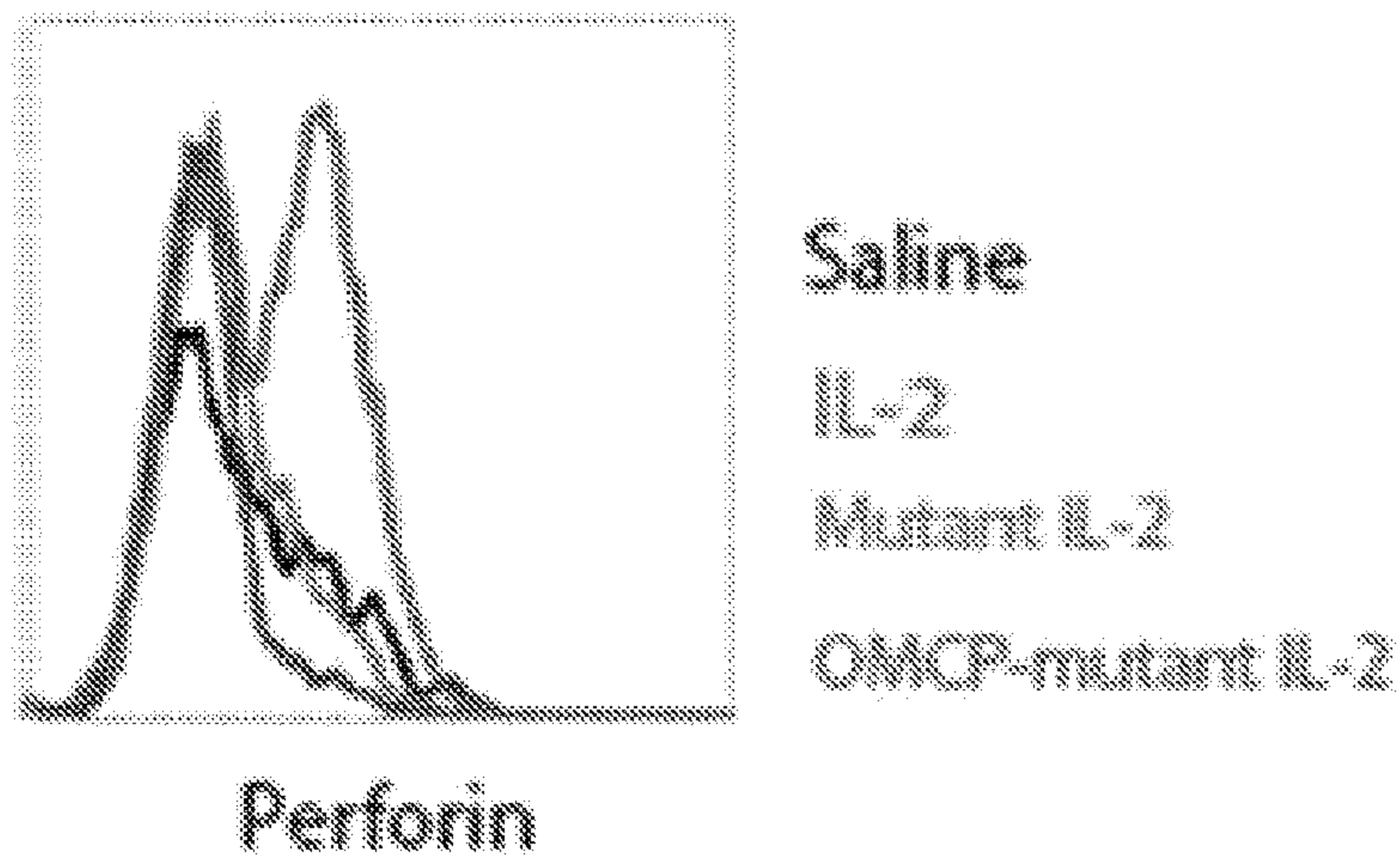


FIG. 31B

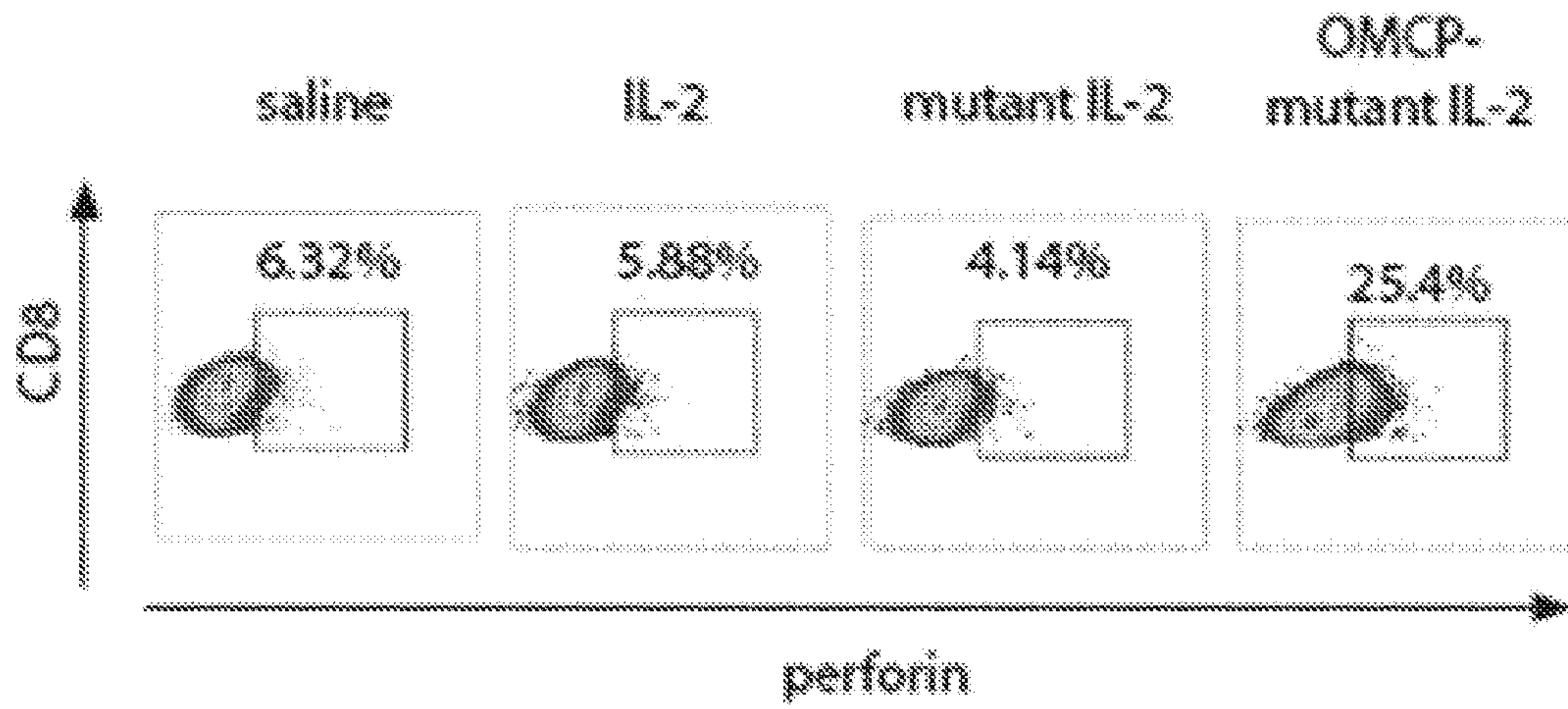


FIG. 31C

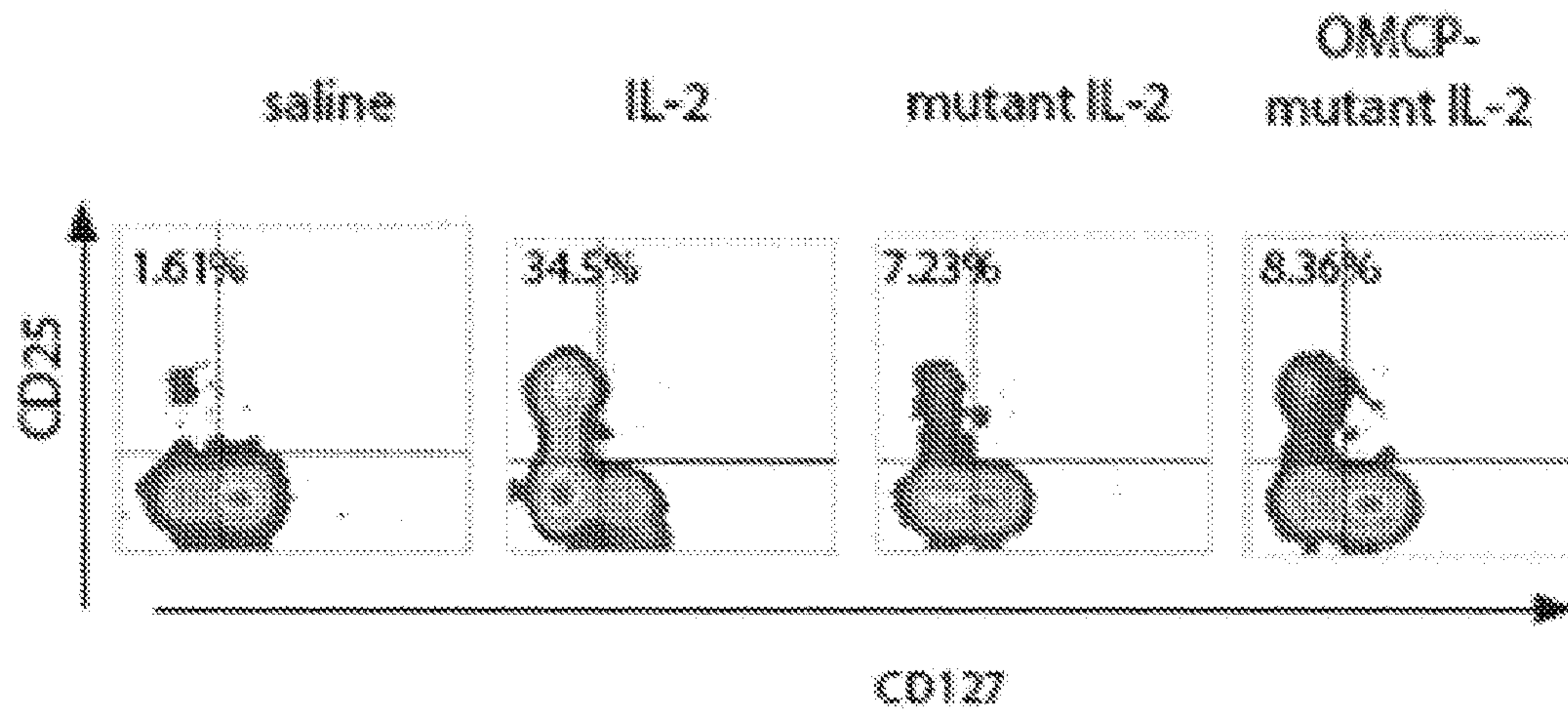


FIG. 31D

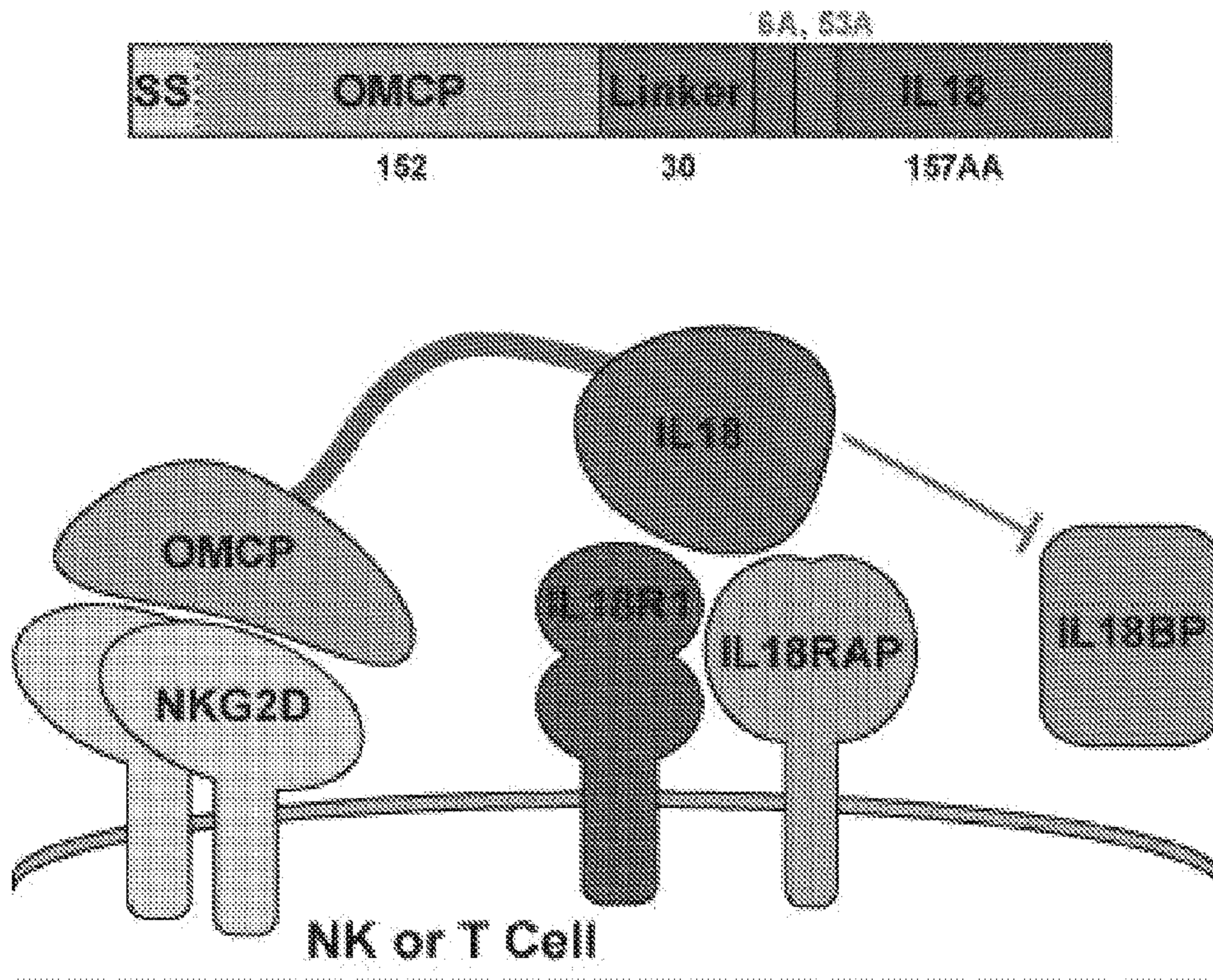
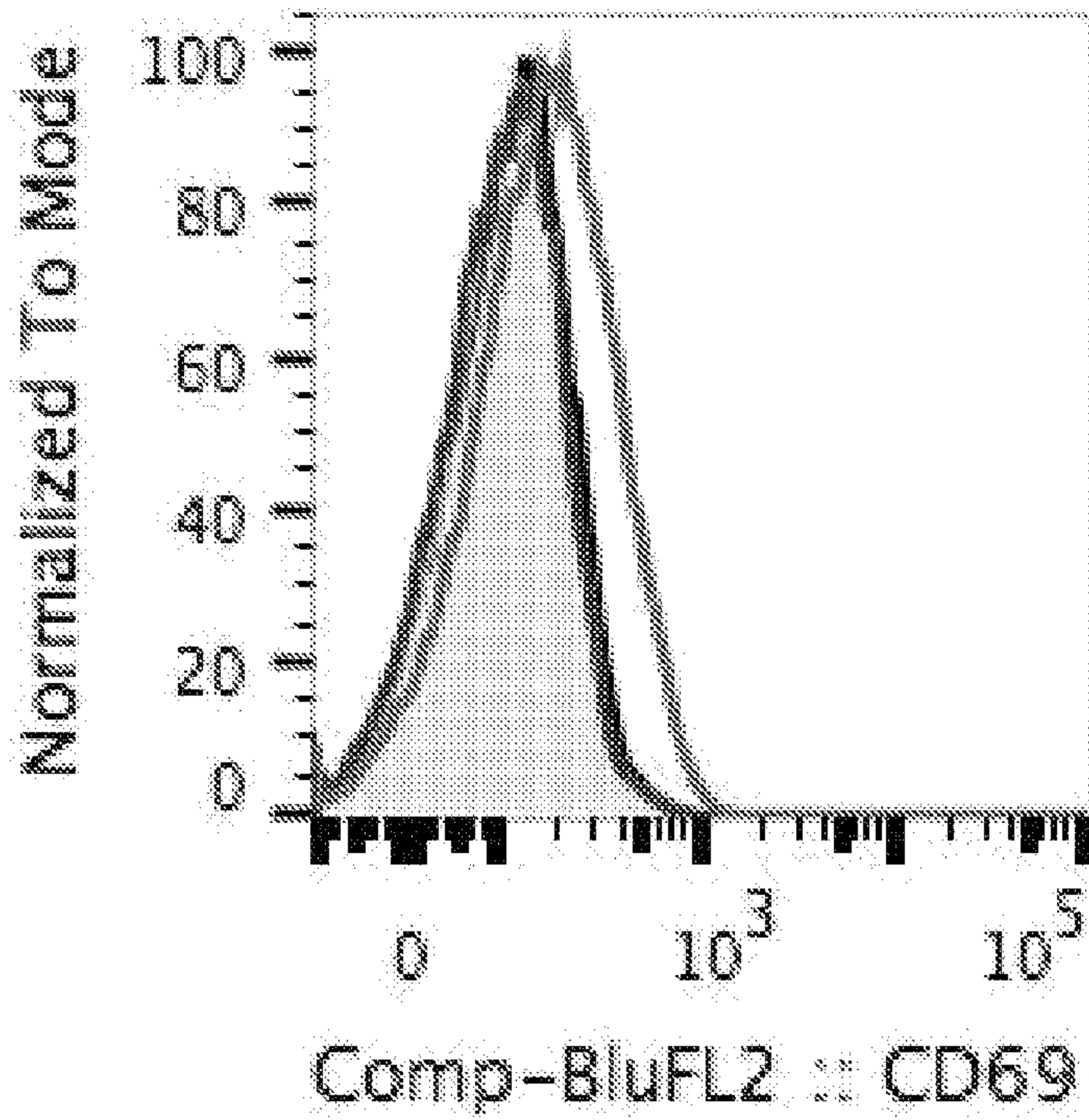


FIG. 32



	Sample Name	SampleID
<input type="checkbox"/>	021.fcs	OMCP-hIL-18 (4.4)
<input type="checkbox"/>	015.fcs	hIL-18 (4.4)
<input type="checkbox"/>	030.fcs	PBS (Isotype)
<input type="checkbox"/>	009.fcs	PBS#1

FIG. 33