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(54) **Title**: KINASE AND PHOSPHATASE ASSAYS

(57) **Abrégé/Abstract**:
Compositions, methods, and kits for detecting and monitoring kinase or phosphatase activity are described. The compositions typically include a peptide, a detectable moiety, and a protease cleavage site. Modification of a peptide by a kinase or phosphatase alters the proteolytic sensitivity of the peptide, resulting in a change of a detectable property of the composition. Panel assays for determining substrates or modulators of kinase or phosphatase activity are also described.

ABSTRACT

Compositions, methods, and kits for detecting and monitoring kinase or phosphatase activity are described. The compositions typically include a peptide, a detectable moiety, and a protease cleavage site. Modification of a peptide by a kinase or phosphatase alters the proteolytic sensitivity of the peptide, resulting in a change of a detectable property of the composition. Panel assays for determining substrates or modulators of kinase or phosphatase activity are also described.

KINASE AND PHOSPHATASE ASSAYS

TECHNICAL FIELD

This invention relates to kinase and phosphatase assays, and more particularly to compositions, methods, and kits useful for monitoring kinase and phosphatase activity.

BACKGROUND

One of the most important classes of intracellular activities is post-translational modification of proteins. Post-translational modification activities modify proteins within living cells to effect changes in their biological activity and/or function. Major types of protein post-translational modification include protein phosphorylation, methylation, prenylation, glycosylation, ubiquitination, sulfation, and proteolysis.

Protein modification by kinases and phosphatases is generally recognized as an important mechanism for regulating protein function. Protein kinases modify proteins by the addition of phosphate groups (phosphorylation), primarily on the amino acids tyrosine, serine, or threonine. Protein phosphatases, in contrast, act to remove these phosphate groups. Changes in the phosphorylation state of proteins can affect enzymatic activity, protein localization, and protein-protein interactions. Such changes can subsequently modulate cellular metabolism, regulation, growth, and differentiation.

Researchers have found more than 400 human diseases and disorders arising from genetic defects in protein kinases. Thus, the over 600 kinases and phosphatases encoded by the human genome represent potentially powerful targets for drugs. Current methods of measuring protein kinase activity, however, have many disadvantages, hampering the ability to rapidly screen kinases for drugs. For example, many current methods for measuring kinase activity rely on the incorporation and measurement of ^{32}P into the protein substrates of interest. In whole cells, this necessitates the use of high levels of radioactivity to efficiently label the cellular ATP pool and to ensure that the target protein is efficiently labeled with radioactivity. After incubation with one or more test drugs, the cells must be lysed and the protein of interest purified to determine its relative degree of phosphorylation. This method requires large numbers of cells, long preincubation times, and careful manipulation and washing steps to avoid artifactual phosphorylation or dephosphorylation. Alternative kinase assay methods, such as those based on phosphorylation-specific antibodies using ELISA-type approaches, involve the difficulty of producing antibodies that distinguish between phosphorylated and non-phosphorylated proteins.

There is thus a need for assays to monitor kinase and phosphatase enzymatic activities that are sensitive, simple to use, and adaptable to high-throughput screening methods.

SUMMARY

The invention is based on compositions of matter comprising a peptide having a motif, such as a recognition motif for a post-translational modification activity, and a detectable moiety. The compositions are surprisingly useful as sensors of post-translational modification activities, including kinase and phosphatase activities. The compositions can also be used to determine modulators of such activities. The invention also relates to methods of determining substrates and modulators of post-translational modification activities.

In one aspect, the invention provides compositions of matter. The compositions can include a peptide having a length from five to fifty amino acids. For example, the peptides can have a length from 8 to 50 amino acids, a length from 8 to 25 amino acids, or a length from 8 to 15 amino acids. Compositions can include a first detectable moiety, where the first detectable moiety is associated with the peptide, e.g., either covalently (optionally through a linker (L)) or non-covalently. Suitable linkers include GABA, diaminopentanyl, and aminohexanoyl groups.

In some embodiments, the compositions can include a second detectable moiety. Accordingly, in some compositions described herein, a first detectable moiety and a second detectable probe moiety can form a dark quenching RET pair. In other embodiments, a first detectable moiety and a second detectable moiety can form a FRET pair. In some embodiments, a first detectable moiety is 7-hydroxycoumarin-3-carboxamide and a second detectable moiety is 5-FAM.

In one aspect, a peptide can contain a motif selected from AIYAA (SEQ ID NO: 1); QDYLS (SEQ ID NO: 4); EIYGV (SEQ ID NO: 7); TX$_1$YVA, where X$_1$ can be G, A, or E (SEQ ID NO: 110); EEYIQ (SEQ ID NO: 17); or DYSQV (SEQ ID NO: 20). A motif can be a recognition motif for a tyrosine kinase and can be selected from EAIYAAP (SEQ ID NO: 2); DQDYLSL (SEQ ID NO: 5); EEEYIQI (SEQ ID NO: 18); EEIYGVI (SEQ ID NO: 8); LTGYVAR (SEQ ID NO: 11); ITAYVAT (SEQ ID NO: 12); ITEYVAT (SEQ ID NO: 13); or GDYSQVL (SEQ ID NO: 21). Peptides having such recognition motifs include the following: EAEAIYAAPGDK (SEQ ID NO: 3); GDQDYLSLDK (SEQ ID NO: 6); EEEEYIQIVK (SEQ ID NO: 19); EEEIYGVIEK (SEQ ID NO: 9); GVLTGYVARRK (SEQ ID NO: 14); DDEITAYVATRK (SEQ ID NO: 15); TGIITEYVATRK (SEQ ID NO: 16); and EGDYSQVLEK (SEQ ID NO: 22).

In some embodiments, when a recognition motif for a tyrosine kinase is EAIYAAP (SEQ ID NO: 2), the tyrosine kinase can be selected from the group Abl1, Abl2, BMX, CSF1R, Csk, EPHB4, Fes/Fps, FGFR1, FGFR4, Fgr, FLT3, Fyn, Hck, IGF1R, IRKβ, ITK, Jak3, KDR, c-KIT, Lck, Lyn A, Lyn B, c-MET, Src, Src N1, Src N2, SYK, TIE2, TRKa, and YES. Alternatively, if the recognition motif for a tyrosine kinase is DQDYLSL (SEQ ID NO: 5), the tyrosine kinase can be selected from CaMKII, CDK7/CycH, CK1δ, IKKα, and IKKβ. In another embodiment, if a recognition motif for a tyrosine kinase is EEIYGVI (SEQ ID NO: 8), the tyrosine kinase can be Abl1, Abl2, BMX, CSF1R, Csk, EPHB4, Fes/Fps, FGFR1, Fgr, FLT3, Fyn, Hck, IGF1R, IRKβ, IRTK, ITK, Jak3, KDR, c-KIT, Lck, Lyn A, Lyn B, c-MET, Src, Src N1, Src N2, SYK, TIE2, TRKa, or YES. In yet another embodiment, if a recognition motif for a tyrosine kinase is LTGYVAR (SEQ ID NO: 11), the tyrosine kinase can be CSF1R, FLT3, or c-KIT. In an additional embodiment, if a recognition motif for a tyrosine kinase is EEEYIQI (SEQ ID NO: 18), the tyrosine kinase can be EGFR, Zap-70, PDGFR, FGFR4, Abl 1, or Lyn B.

In another aspect, a peptide can have a motif selected from RR(S/T)L (SEQ ID NO: 145); L(S/T)TT (SEQ ID NO: 146); L(S/T)LD (SEQ ID NO: 147); RX$_1$(S/T)X$_2$, where X$_1$ can be V, A, or Q and X$_2$ can be V or L (SEQ ID NO: 148); TS(S/T)L (SEQ ID NO: 149); X$_1$(S/T)PX$_2$ where X$_1$ can be P or I and X$_2$ can be G, K, or D (SEQ ID NO: 150); (S/T)X$_1$X$_2$VA, where X$_1$ can be A, E, or Q and X$_2$ can be Y or H (SEQ ID NO: 151); I(S/T)IAN (SEQ ID NO: 152); SIA(S/T)I (SEQ ID NO: 153); (S/T)VPPS*P, where

S* is a phosphorylated serine (SEQ ID NO: 154); $DX_1(S/T)X_2$, where X_1 can be A or E and X_2 can be I or Q (SEQ ID NO: 155); and D(S/T)QV (SEQ ID NO: 156).

In another aspect, a peptide can include a motif selected from $RRX_1(S/T)L$, where X_1 can be F, W, or Y (SEQ ID NO: 45); $LX_1(S/T)TT$, where X_1 can be F, W, or Y (SEQ ID NO: 48); $X_1L(S/T)LD$, where X_1 can be F, W, or Y (SEQ ID NO: 51); $RX_1X_2(S/T)X_3$, where X_1 can be V, A, or Q, X_2 can be F, W, or Y, and X_3 can be V or L (SEQ ID NO: 54); $TX_1S(S/T)L$, where X_1 can be F, W, or Y (SEQ ID NO: 61); $X_1X_2(S/T)PX_3$ where X_1 can be P or I, X_2 can be F, W, or Y, and X_3 can be G, K, or D (SEQ ID NO: 64); $X_1(S/T)X_2X_3VA$, where X_1 can be F, W, or Y, X_2 can be A, E, or Q, and X_3 can be Y or H (SEQ ID NO: 71); $IX_1(S/T)IAN$, where X_1 can be F, W, or Y (SEQ ID NO: 78); $SIAX_1(S/T)I$, where X_1 can be F, W, or Y (SEQ ID NO: 81); (S/T)VPPS*P, where S* is a phosphorylated serine (SEQ ID NO: 84); $DX_1X_2(S/T)X_3$, where X_1 can be A or E, X_2 can be F, W, or Y, and X_3 can be I or Q (SEQ ID NO: 87); and $DX_1(S/T)QV$, where X_1 can be F, W, or Y (SEQ ID NO: 92).

In certain embodiments, a motif can be selected from RRF(S/T)L (SEQ ID NO: 157); LF(S/T)TT (SEQ ID NO: 158); YL(S/T)LD (SEQ ID NO: 159); $RX_1F(S/T)X_2$, where X_1 can be V, A, or Q and X_2 can be V or L (SEQ ID NO: 160); TFS(S/T)L (SEQ ID NO: 161); $X_1F(S/T)PX_2$ where X_1 can be P or I and X_2 can be G, K, or D (SEQ ID NO: 162); $F(S/T)X_1X_2VA$, where X_1 can be A, E, or Q and X_2 can be Y or H (SEQ ID NO: 163); IF(S/T)IAN (SEQ ID NO: 164); SIAF(S/T)I (SEQ ID NO: 165); $DX_1F(S/T)X_2$, where X_1 can be A or E and X_2 can be I or Q (SEQ ID NO: 166); and DY(S/T)QV (SEQ ID NO: 167).

In another aspect, the invention provides peptides containing motifs that can be recognition motifs for serine/threonine kinases. Examples of recognition motifs for serine/threonine kinase include LRRFSLG (SEQ ID NO: 46); GLFSTTP (SEQ ID NO: 49); DYLSLDK (SEQ ID NO: 52); NRVFSVA (SEQ ID NO: 55); PRAFSVG (SEQ ID NO: 56); RRQFSLR (SEQ ID NO: 57); RTFSSLA (SEQ ID NO: 62); APFSPGG (SEQ ID NO: 65); HPFSPKK (SEQ ID NO: 66); KIFSPDV (SEQ ID NO: 67); EFTAYVA (SEQ ID NO: 72); IFTEYVA (SEQ ID NO: 73); VFTQHVA (SEQ ID NO: 74); RIFSIANS (SEQ ID NO: 79); DSIAFSIV (SEQ ID NO: 82); FSVPPS*PD, where S* is a phosphorylated serine (SEQ ID NO: 85); EDAFSII (SEQ ID NO: 88); EDEFSQN (SEQ

ID NO: 89); or EGDYSQV (SEQ ID NO: 93). Peptides having such recognition motifs include the following: ALRRFSLGEK (SEQ ID NO: 47); VAPFSPGGRAK (SEQ ID NO: 68); RGGLFSTTPGGTK (SEQ ID NO: 50); KLNRVFSVAC (SEQ ID NO: 58); GDQDYLSLDK (SEQ ID NO: 53); ARPRAFSVGK (SEQ ID NO: 59); RRRQFSLRRKAK (SEQ ID NO: 60); RPRTFSSLAEGK (SEQ ID NO: 63); AKHPFSPKKAK (SEQ ID NO: 69); DDEFTAYVATRK (SEQ ID NO: 75);TGIFTEYVATRK (SEQ ID NO: 76); TGVFTQHVATRK (SEQ ID NO: 77); QRIFSIANSIVK (SEQ ID NO: 80); RIDSIAFSIVGK (SEQ ID NO: 83); PRPFSVPPS*PDK, where S* is a phosphorylated Serine (SEQ ID NO: 86); EEDAFSIIGK (SEQ ID NO: 90); REDEFSQNEEK (SEQ ID NO: 91); IIKIFSPDVEK (SEQ ID NO: 70); and EGDYSQVLEK (SEQ ID NO: 22).

When a recognition motif for a serine/threonine kinase is LRRFSLG (SEQ ID NO: 46), the serine/threonine kinase can be selected from the group consisting of Akt1, Akt2, Akt3, Aurora A, CaMKII, CDK2/CycA, CDK3/CycE, CDK7/CycH, MAPKAP-K1α, MAPKAP-K1β, MAPKAP-K1γ, MSK1, PAK2, PKA, PKG, and ROCK. In other embodiments, when a recognition motif for a serine/threonine kinase is GLFSTTP (SEQ ID NO: 49), the serine/threonine kinase can be selected from p38γ, p38δ, and REDK. Alternatively, if a recognition motif for a serine/threonine kinase is NRVFSVA (SEQ ID NO: 55), the serine/threonine kinase can be Akt3, AMPK, CaMKII, CDK7/CycH, CHK2, IKKα, MAPKAP-K1α, MAPKAP-K2, MAPKAP-K3, MAPKAP-K5, PAK2, PKA, PKCβII, REDK, ROCK, ROCK2, or SGK1. In another embodiment, if a recognition motif for a serine/threonine kinase is PRAFSVG (SEQ ID NO: 56), the serine/threonine kinase can be selected from the group consisting of Akt1, Akt2, Akt3, CaMKII, CDK7/CycH, IKKβ, MAPKAP-K1α/RSK1, MAPKAP-K1β/RSK2, MAPKAP-K1γ/RSK3, MSK1, PAK2, PIM1, PKA, PKG, REDK, and SGK1. A recognition motif for a serine/threonine kinase can be RRQFSLR (SEQ ID NO: 57), where the serine/threonine kinase can be Akt1, Akt2, Akt3, CaMKII, CHK1, CHK2, MAPKAP-K1α, MAPKAP-K1β, MAPKAP-K1γ, MSK1, p70 S6 Kinase, PAK2, PIM1, PKA, PKCα, PKCβI, PKCβII, PKCγ, PKCδ, PKCε, PKCζ, PKCη, PKCθ, PKCι, PKG, ROCK, ROCK2, or SGK1. In another embodiment, a recognition motif for a serine/threonine kinase is RTFSSLA (SEQ ID NO: 62), and the serine/threonine kinase is selected from the group consisting of Akt1, CDK2/CycA, CDK6, IKKβ, MAPKAP-K1α, MAPKAP-K1β, MAPKAP-K1γ, p70 S6 Kinase, PAK2, and PKA. A recognition motif for a serine/threonine kinase can be APFSPGG (SEQ ID NO: 65), and the serine/threonine kinase can be selected from the group consisting of CDK2/CycA, CDK3/CycE, ERK1, ERK2, IKKα, p38β, p38γ, and p38δ.

Any of the compositions described herein can include a protease cleavage site, such as a chymotrypsin protease cleavage site, a caspase 3 protease cleavage site, a cathepsin G protease cleavage site, a trypsin protease cleavage site, an elastase protease cleavage site, an endoproteinase Asp-N protease cleavage site, or an endoproteinase Glu-N protease cleavage site. In certain embodiments, the protease cleavage site can include a sequence FS, FT, or Y.

The compositions can exhibit a detectable property, such as an optical property, a magnetic property, or a radioactive property. For example, an optical property can be a molar extinction coefficient at an excitation wavelength, a quantum efficiency, an excitation spectrum, an emission spectrum, an excitation wavelength maximum, an emission wavelength maximum, a ratio of excitation amplitudes at two wavelengths, a ratio of emission amplitudes at two wavelengths, an excited state lifetime, an anisotropy, a polarization of emitted light, a resonance energy transfer, or a quenching of emission at a wavelength. The optical property can be a fluorescent property, e.g., a fluorescence excitation spectrum, a fluorescence emission spectrum, a fluorescence excitation wavelength maximum, a fluorescence emission wavelength maximum, a ratio of fluorescence excitation amplitudes at two wavelengths, a ratio of fluorescence emission amplitudes at two wavelengths, a fluorescence excited state lifetime, a fluorescence anisotropy, or a quenching of fluorescence emission at a wavelength. In certain embodiments, a composition can exhibit a fluorescence excitation maximum in the range from 250 to 750 nm and a fluorescence emission maximum in the range from 450 to 800 nm.

A detectable moiety can be, for example, a fluorescent molecule such as 5-FAM, 6-FAM, 7-hydroxycoumarin-3-carboxamide, 6-chloro-7-hydroxycoumarin-3-carboxamide, fluorescein-5-isothiocyanate, dichlorotriazinylaminofluorescein, tetramethylrhodamine-5-isothiocyanate, tetramethylrhodamine-6-isothiocyanate, succinimidyl ester of 5-carboxyfluorescein, succinimidyl ester of 6-carboxyfluorescein, 5-carboxytetramethylrhodamine, 6-carboxymethylrhodamine, and 7-amino-4-methylcoumarin-3-acetic acid. In other embodiments, a detectable moiety is a binding pair member, e.g., an epitope for an antibody or biotin.

In another aspect, the invention provides a method for characterizing a kinase. The method includes the steps of contacting a composition described previously with a protein kinase under conditions effective for the protein kinase to phosphorylate the composition, and measuring the ability of the protein kinase to phosphorylate the composition.

In yet another aspect, the invention features a method for identifying a substrate of a kinase. The method includes contacting a composition described above with a protein kinase; contacting the composition and the protein kinase with a protease to form a protease mixture; and comparing a measurable property in the protease mixture with the measurable property in a control protease mixture lacking the protein kinase. The composition is identified as a substrate of the protein kinase if the measurable property in the protease mixture is different from the measurable property in the control protease mixture. ATP can be present during the contacting step with the kinase. In some embodiments, a measurable property in the protease mixture is compared with a measurable property in a control protease mixture lacking ATP, where the composition is identified as a substrate of the kinase if the measurable property in the protease mixture is different from the measurable property in the control protease mixture.

In some embodiments of the method, two or more different compositions are contacted independently with the protein kinase and ATP during the contacting step to form two or more kinase mixtures. Each of the kinase mixtures is contacted independently with a protease during the contacting step with the protease to form two or more protease mixtures. A measurable property in each of the protease mixtures is compared with the measurable property in a corresponding control mixture. In other embodiments, two or more different protein kinases are contacted independently with the composition and the ATP during the contacting step to form two or more kinase mixtures. Each of the kinase mixtures is then contacted independently with a protease to form two or more protease mixtures, and a measurable property in each of the protease mixtures is compared with the measurable property in a corresponding control mixture.

The comparison of measurable properties can occur concurrently with the protease contacting step or after the protease contacting step. The contacting step can be completed by inhibiting a proteolytic activity of the protease, e.g., by adding a reagent to the protease mixtures or by heating the protease mixtures. The reagent can be aprotinin, PMSF, TPCK, AEBSF, chymotrypsin inhibitor 1, and chymotrypsin inhibitor 2.

The invention also provides a method for identifying a modulator of activity of a kinase. In the method, a mixture of a protein kinase, a substrate for the protein kinase, and a test compound are mixed; the mixture is contacted with a protease to form a protease mixture; and

a measurable property in the protease mixture is compared to the measurable property in a control mixture of the substrate, the protein kinase, and the protease in the absence of the test compound. The test compound is identified as a modulator of activity of the kinase if the measurable property in the protease mixture is different from the measurable property in the control mixture. ATP can be present during the kinase contacting step.

In some embodiments, two or more different test compounds can be contacted independently with the protein kinase, ATP, and the substrate in the contacting step to form two or more kinase mixtures. Each of the kinase mixtures is contacted independently with a protease to form two or more protease mixtures, and a measurable property in each of the protease mixtures is compared with the measurable property in a corresponding control mixture. In other embodiments, two or more different protein kinases are contacted independently with ATP, the test compound, and the substrate to form two or more kinase mixtures; each of the kinase mixtures is contacted independently with a protease to form two or more protease mixtures; and a measurable property in each of the protease mixtures is compared with the measurable property in a corresponding control mixture. The comparison step can occur during or after the protease contacting step. The protease contacting step may be completed as described previously.

In another aspect, the invention provides phosphorylated compositions of matter. Such compositions of matter can be useful as substrates for phosphatases. For example, a

Y or an S/T in a motif described above may be phosphorylated, e.g., chemically or enzymatically. In other embodiments, a Y or an S/T in a recognition motif for a tyrosine kinase or a S/T kinase, respectively, may be phosphorylated to result in a recognition motif for a protein phosphatase. Examples of a protein phosphatase recognition motif include LRRFS*LG (SEQ ID NO: 96); GLFS*TTP (SEQ ID NO: 99); DYLS*LDK (SEQ ID NO: 102); NRVFS*VA (SEQ ID NO: 105); PRAFS*VG (SEQ ID NO: 106); RRQFS*LR (SEQ ID NO: 107); RTFSS*LA (SEQ ID NO: 112); APFS*PGG (SEQ ID NO: 115); HPFS*PKK (SEQ ID NO: 116); KIFS*PDV (SEQ ID NO: 117); EFT*AYVA (SEQ ID NO: 122); IFT*EYVA (SEQ ID NO: 123); VFT*QHVA (SEQ ID NO: 124); RIFS*IANS (SEQ ID NO: 129); DSIAFS*IV (SEQ ID NO: 132); FS*VPPS*PD (SEQ ID NO: 135); EDAFS*II (SEQ ID NO: 138); EDEFS*QN (SEQ ID NO: 139), and EGDYS*QV (SEQ ID NO: 143), where S* represents a phosphorylated serine and T* represents a phosphorylated threonine.

Examples of peptides comprising phosphatase recognition motifs include EAEAIY*AAPGDK (SEQ ID NO: 25); GDQDY*LSLDK (SEQ ID NO: 28); EEEEY*IQIVK (SEQ ID NO: 41); EEEIY*GVIEK (SEQ ID NO: 31); GVLTGY*VARRK (SEQ ID NO: 36); DDEITAY*VATRK (SEQ ID NO: 37); TGIITEY*VATRK (SEQ ID NO: 38), and EGDY*SQVLEK (SEQ ID NO: 44), where Y* represents a phosphorylated tyrosine. In other embodiments, a peptide comprising a phosphatase recognition motif has a sequence selected from ALRRFS*LGEK (SEQ ID NO: 97); VAPFS*PGGRAK (SEQ ID NO: 118); RGGLFS*TTPGGTK (SEQ ID NO: 100); KLNRVFS*VAC (SEQ ID NO: 108); GDQDYLS*LDK (SEQ ID NO: 103); ARPRAFS*VGK (SEQ ID NO: 109); RRRQFS*LRRKAK (SEQ ID NO: 110); RPRTFSS*LAEGK (SEQ ID NO: 113); AKHPFS*PKKAK (SEQ ID NO: 119); DDEFT*AYVATRK (SEQ ID NO: 125); TGIFT*EYVATRK (SEQ ID NO: 126); TGVFT*QHVATRK (SEQ ID NO: 127); QRIFS*IANSIVK (SEQ ID NO: 130); RIDSIAFS*IVGK (SEQ ID NO: 133); PRPFS*VPPS*PDK (SEQ ID NO: 136); EEDAFS*IIGK (SEQ ID NO: 140); REDEFS*QNEEK (SEQ ID NO: 141); IIKIFS*PDVEK (SEQ ID NO: 120), and EGDYS*QVLEK (SEQ ID NO: 144).

In certain embodiments, a phosphatase recognition motif is EAIY*AAP (SEQ ID NO:24), and the phosphatase is selected from the group consisting of PTP1B, LAR, and

LCA. Alternatively, a phosphatase recognition motif can be DQDYLS*L (SEQ ID NO: 27), and the phosphatase can be PP1α, PP2A, PP2B, or PP2C. In other embodiments, a phosphatase recognition motif is LRRFS*LG (SEQ ID NO: 96), and the phosphatase is selected from the group consisting of PP1α, PP2A, and PP2C. In yet other embodiments, a phosphatase recognition motif is GLFS*TTP (SEQ ID NO: 99), and the phosphatase is selected from PP1α, PP2A, PP2B, or PP2C. Additionally, a phosphatase recognition motif can be NRVFS*VA (SEQ ID NO: 105), and the phosphatase can be PP1α, PP2A, PP2B, or PP2C; a phosphatase recognition motif can be PRAFS*VG (SEQ ID NO: 106), with the phosphatase selected from the group consisting of PP1α, PP2A, and PP2B; the phosphatase recognition motif can be RRQFS*LR, (SEQ ID NO: 107) and the phosphatase can be PP1α, PP2A, or PP2B; a phosphatase recognition motif can be RTFSS*LA (SEQ ID NO: 112), and the phosphatase can be PP1α, PP2A, or PP2B; a phosphatase recognition motif can be APFS*PGG (SEQ ID NO: 115), and the phosphatase can be PP1α or PP2A; a phosphatase recognition motif can be EEIY*GVI (SEQ ID NO: 30), and the phosphatase can be PTP1B, LAR, or LCA; or the phosphatase recognition motif can be LTGY*VAR (SEQ ID NO: 33), and the phosphatase can be PTP1B, LAR, or LCA.

In an additional aspect, the invention provides a method for characterizing a phosphatase. The method includes contacting a composition described above (e.g., a phosphorylated composition) with a protein phosphatase under conditions effective for the protein phosphatase to dephosphorylate the composition, and measuring the ability of the protein phosphatase to dephosphorylate the composition.

The invention also provides a method for identifying a substrate of a phosphatase, which includes contacting a composition described above with a protein phosphatase; contacting the composition and the protein phosphatase with a protease to form a protease mixture; and comparing a measurable property in the protease mixture with a measurable property in a control protease mixture lacking phosphatase, where the composition is identified as a substrate of the phosphatase if the measurable property in the protease mixture is different from the measurable property in the control protease mixture.

In certain embodiments, two or more different compositions are contacted independently with the phosphatase to form two or more phosphatase mixture; each of the phosphatase mixtures is contacted independently with a protease to form two or more protease mixtures; and a measurable property in each of the protease mixtures is compared with the measurable property in a corresponding control mixture. In other embodiments, two or more different phosphatases are contacted independently with the composition; each of the phosphatase mixtures is contacted independently with a protease to form two or more protease mixtures; and a measurable property in each of the protease mixtures is compared with the measurable property in a corresponding control mixture.

The invention also provides a method for identifying a modulator of activity of a phosphatase, including contacting a mixture of a protein phosphatase, a substrate for the protein phosphatase, and a test compound to form a phosphatase mixture; contacting the phosphatase mixture with a protease to form a protease mixture; and comparing a measurable property in the protease mixture to the measurable property in a control protease mixture lacking the test compound, where the test compound is identified as a modulator of activity of the phosphatase if the measurable property in the protease mixture is different from the measurable property in the control mixture. In certain embodiments, two or more different test compounds may be contacted independently with the phosphatase and the substrate to form two or more phosphatase mixtures; each of the phosphatase mixtures may be contacted independently with a protease to form two or more protease mixtures; and a measurable property in each of the protease mixtures may be compared with the measurable property in a corresponding control mixture. In other embodiments, two or more different phosphatases are contacted independently with the test compound and the substrate to form two or more phosphatase mixtures; each of the phosphatase mixtures is contacted independently with a protease to form two or more protease mixtures; and a measurable property in each of the protease mixtures is compared with the measurable property in a corresponding control mixture.

In an additional aspect, the invention provides articles of manufacture. An article of manufacture can include packaging matter and a composition of matter described herein associated with the packaging material. The article can further comprise a protein kinase or a protein phosphatase; a protease; ATP; and/or buffers.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control.

The details of one or more embodiments of the invention are set forth in the accompanying drawings and the description below. Other features, objects, and advantages of the invention will be apparent from the description and drawings, and from the claims.

DESCRIPTION OF DRAWINGS

FIG. 1 is a schematic indicating the effect on a fluorescence signal of differential sensitivity of a composition to a protease. In the Kinase Reaction, a substrate for a kinase (e.g., a composition of matter according to the present invention) is phosphorylated by the kinase. As is shown, the substrate in both the unphosphorylated and phosphorylated states exhibits FRET between the donor and acceptor fluorophores on the N- and C-termini of the substrate. In the Development (Protease) Reaction, the phosphorylated and unphosphorylated substrates are exposed to a protease, which differentially cleaves the unphosphorylated substrate relative to the phosphorylated substrate. As shown in the Detection panel, cleavage of the unphosphorylated substrate disrupts FRET between the donor and acceptor fluorophores, and results in a measurable change in the ratio of the donor fluorescence emission value relative to the acceptor fluorescence emission value.

FIG. 2 is a flow chart for identifying modulators of the activity of a Tyrosine (FIG. 2A) or Serine/Threonine (FIG. 2B) kinase.

FIG. 3 illustrates the derivation of kinetic parameters for Abl 1 kinase.

FIG. 4 demonstrates the dependence of % phosphorylation on Akt 1 kinase concentration.

FIG. 5 demonstrates the dependence of % phosphorylation on Abl 1 kinase concentration.

FIG. 6 demonstrates dose-dependent inhibition of Abl 1 kinase.

FIG. 7 demonstrates dose-dependent inhibition of Akt 1 kinase.

FIG. 8 demonstrates % phosphorylation data with varying concentrations of PKA kinase.

FIG. 9 demonstrates % phosphorylation data with varying concentrations of PKCα.

DETAILED DESCRIPTION

The present invention is based in part on the finding that compositions of matter that include peptides and detectable moieties can be designed to act as sensors of post-translational modification activities, including kinase or phosphatase activity. Post-translational modification of a composition containing a peptide results in a modulation of the rate and efficiency of cleavage of the modified peptide by a protease as compared to the non-modified peptide. The attachment of at least one detectable moiety to the peptide in the composition couples the cleavage of the peptide in the composition to a change in a detectable property of the composition that can be used to monitor post-translational activity in a sample and to assay for modulators of a post-translational activity. See FIG. 1.

Compositions of the present invention can be used in assay methods, particularly methods for high-throughput and miniaturized screening systems for drug discovery and profiling. In addition, methods and kits described herein typically exhibit a large dynamic range, high Z'-factor values, and increased sensitivity by employing a ratiometric analysis to eliminate well-to-well variations. Finally, methods of the present invention can be performed under near initial velocity conditions and produce accurate IC_{50} data for kinase and phosphatase inhibitors.

Definitions

Generally, the nomenclature used herein and many of the fluorescence, computer, detection, chemistry, and laboratory procedures described herein are commonly employed in the art.

Abbreviations: t-Boc, tert-butyloxycarbonyl; Bzl, benzyl; CaMK, calmodulin dependent kinase; CKI, casein kinase 1; PDGF, platelet derived growth factor; Fmoc, fluorenylmethyloxycarbonyl; EGF, epidermal growth factor; ELISA, enzyme-linked immuno absorbant assay; FGF, fibroblast growth factor; HF, hydrogen fluoride; HOBT, N-Hydroxybenzotriazole; PyBop, Benzotriazole- I -yl-oxy-tris-pyyrolidino-phosphonium hexafluorophosphate; TFA, trifluoroacteic acid; FITC, fluorescein isothiocyanate; RET, resonance energy transfer; FRET, fluorescence resonance energy transfer; FAM, carboxyfluorescein.

As employed throughout the disclosure, the following terms, unless otherwise indicated, shall be understood to have the following meanings:

The term "RET" means resonance energy transfer, and refers to the radiationless transmission of an energy quantum from its site of absorption to the site of its utilization in a molecule, or system of molecules, by resonance interaction between chromophores, over distances considerably greater than interatomic, without substantial conversion to thermal energy, and without the donor and acceptor coming into kinetic collision. A donor is a moiety that initially absorbs energy (e.g., optical energy), and an acceptor is the moiety to which the energy is subsequently transferred. Fluorescence resonance energy transfer (FRET) and time-resolved fluorescence resonance energy transfer (TR-FRET) are types of RET.

The term "acceptor" refers to a chemical or biological moiety that operates via resonance energy transfer, e.g., a quencher. In RET applications, acceptors may re-emit energy transferred from a donor fluorescent moiety as fluorescence (e.g., FRET) and are "acceptor fluorescent moieties." As used herein, such a donor fluorescent moiety and an acceptor fluorescent moiety are referred to as a "FRET pair." Examples of acceptors include coumarins and related fluorophores; xanthenes such as fluoresceins; fluorescent proteins; rhodols, and rhodamines; resorufins; cyanines; difluoroboradiazaindacenes; and phthalocyanines. In other RET applications, acceptors generally do not re-emit the transferred energy and are sometimes referred to as “dark quenchers.” A fluorescent donor moiety and a dark quenching acceptor moiety may be referred to herein as a “dark quenching RET pair.” Examples of dark quenchers include indigos; benzoquinones; anthraquinones; azo compounds; nitro compounds; indoanilines; and di- and triphenylmethanes.

The term “quencher” refers to a molecule or part of a compound that is capable of reducing light emission (e.g. fluorescence emission) from a detectable moiety. Such reduction includes reducing the emission of light after the time when a photon is normally emitted from a fluorescent moiety. Quenching may occur by any of several mechanisms, including resonance energy transfer (RET), fluorescence resonance energy transfer (FRET), photo-induced electron transfer, paramagnetic enhancement of intersystem crossing, Dexter exchange coupling, dark quenching, and excitation coupling (e.g., the formation of dark complexes). Preferred quenchers include those that operate by RET, particularly FRET.

The term “bead” refers to a substantially spherical particle such as a sphere or microsphere. Beads may be used within a wide size range. Preferred beads are typically within the range of 0.01 to 100 μm in diameter. Beads may be composed of any material and may comprise fluorescent, luminescent, electro-luminescent, chemo-luminescent, magnetic, or paramagnetic probes. Such beads are commercially available from a variety of sources including Molecular Probes, Sigma, and Polysciences.

The terms “cleavage site,” “protease cleavage site,” and “protease site” are used interchangeably and refer to an amide bond that can be cleaved by a protease and one or more amino acids on either side of the bond. The designations "P_1", "P_2", "P_3" etc. refer to the amino acid positions 1 amino acid, 2 amino acids and 3 amino acids N-terminal to the bond. The designations "P'_1", "P'_2", "P'_3" etc. refer to the amino acids positions 1 amino acid, 2 amino acids and 3 amino acids C-terminal to the bond, as shown below:

Protease cleavage site

$$\begin{array}{c} \downarrow \\ P_3\,P_2\,P_1 - P'_1\;P'_2\,P'_3 \end{array}$$

The term "detectable moiety" refers to a chemical moiety useful as a marker, indicator, or contrast agent. A detectable moiety may be capable of being detected by absorption spectroscopy, luminescence spectroscopy, fluorescence spectroscopy, magnetic resonance spectroscopy (e.g., MRI), or radioisotope detection. The term "fluorescent moiety" refers to a detectable moiety that can absorb electromagnetic energy and is capable of at least partially re-emitting some fraction of that energy as electromagnetic radiation. Suitable fluorescent moieties include, but are not limited to, coumarins and related dyes, xanthene dyes such as fluoresceins, rhodols, and rhodamines, resorufins, cyanine dyes, bimanes, acridines, isoindoles, dansyl dyes, aminophthalic hydrazides such as luminol, and isoluminol derivatives, aminophthalimides, aminonaphthalimides, aminobenzofurans, aminoquinolines, dicyanohydroquinones, semiconductor fluorescent nanocrystals, fluorescent proteins, and fluorescent europium and terbium complexes and related compounds. In some embodiments, a detectable moiety can be a member of a specific binding pair, or can be associated (e.g., covalently) with a member of a specific binding pair. Specific binding pairs are pairs of molecules that are capable of specific interaction with one another, e.g., have an affinity for one another. For example, a specific binding pair can be ligand-protein binding pairs, e.g., enzyme-substrate, biotin-streptavidin, or epitope-antibody binding pairs. A binding pair that includes a detectable moiety has a larger apparent size than a corresponding binding pair that does not include a detectable moiety, and a larger apparent size than either member of the binding pair alone. Complexes of binding pairs can be detected by a method described herein or by other methods known to those of skill in the art, e.g., in an immunoassay format, a gel shift assay, or a chromatographic assay.

The term "motif" refers to an amino acid sequence at least five amino acids in length. In some embodiments, a motif can be a "recognition motif" for a phosphatase or a kinase, i.e., an amino acid sequence that is effective as a substrate for a protein phosphatase or protein kinase. In some embodiments, a recognition motif may be modified from a naturally existing sequence by at least one amino acid substitution. In some embodiments, the affinity (apparent K_d) of a kinase or phosphatase for a recognition motif is about 1 mM or less, or about 10 μM or less, or about1 μM or less, or about 0.1 μM or less. A recognition motif need not be an optimal or preferred recognition motif, but encompasses sequences whose phosphorylation by a kinase can be detected or whose de-phosphorylation by a phosphatase can be detected. In some embodiments, a recognition motif overlaps with or encompasses a protease cleavage site. In other embodiments, a protease cleavage site does not overlap or encompass a recognition motif.

The term "modulates" refers to partial or complete enhancement or inhibition of an activity or process (e.g., by attenuation of rate or efficiency).

The term "modulator" refers to a chemical compound (naturally occurring or non-naturally occurring), such as a biological macromolecule (e.g., nucleic acid, protein, peptide, hormone, polysaccharide, lipid), an organic molecule, or an extract made from biological materials such as bacteria, plants, fungi, or animal (particularly mammalian, including human) cells or tissues. Modulators may be evaluated for potential activity as inhibitors or enhancers (directly or indirectly) of a biological process or processes (e.g., agonist, partial antagonist, partial agonist, inverse agonist, antagonist, antineoplastic agents, cytotoxic agents, inhibitors of neoplastic transformation or cell proliferation, cell proliferation-promoting agents, and the like) by inclusion in screening assays described herein. The activity of a modulator may be known, unknown, or partially known.

The term "non-naturally occurring" refers to the fact that an object, compound, or chemical cannot be found in nature. For example, a peptide or polynucleotide that is present in an organism (including viruses) that can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory is naturally-occurring, while such a peptide or polynucleotide that has been intentionally modified by man is non-naturally occurring.

The term "optical property" refers to a property of a composition, compound, or moiety and can be any one of the following: a molar extinction coefficient at an appropriate excitation wavelength, a fluorescent or luminescent quantum efficiency, a shape of an excitation spectrum or emission spectrum, an excitation wavelength maximum or emission wavelength maximum, a ratio of excitation amplitudes at two different wavelengths, a ratio of emission amplitudes at two different wavelengths, an excited state lifetime, a fluorescent anisotropy, or any other measurable optical property derived from the composition, compound, or moiety, either spontaneously or in response to electromagnetic, electrical, or chemical stimulation or reaction. One type of optical property is a fluorescent property, which refers to an optical property that can be detected using fluorescence-based techniques. The fluorescent property can be any one of the following: a molar extinction coefficient at an appropriate excitation wavelength, a fluorescent quantum efficiency, a shape of an excitation or emission spectrum, an excitation wavelength maximum, an emission magnitude at any wavelength during or at one or more times after excitation of a fluorescent moiety, a ratio of excitation amplitudes at two different wavelengths, a ratio of emission amplitudes at two different wavelengths, an excited state lifetime, a fluorescent anisotropy, or any other measurable property of a fluorescent moiety. In some embodiments, a fluorescent property refers to fluorescence emission or the fluorescence emission ratio at two or more wavelengths.

The term "peptide" refers to a polymer of two or more amino acids joined together through amide bonds. Amino acids may be natural or unnatural amino acids, including, for example, beta-alanine, phenylglycine, and homoarginine. For a review, see Spatola, A.F., in *Chemistry and Biochemistry of Amino Acids, Peptides and Proteins*, B. Weinstein, eds., Marcel Dekker, New York, p. 267 (1983). All of the amino acids used in the present invention may be either the D- or L-isomer. Chemically modified or substituted amino acids including phosphorylated (e.g., phospho-serine (phosphorylated at the hydroxyl of the side chain), phospho-tyrosine (phosphorylated at the OH of the side-chain phenyl ring), and phospho-threonine (phosphorylated at the hydroxyl of the size chain)), sulfated, methylated, or prenylated amino acids can also be used to create peptides for specific applications.

The terms "post-translational modification" and "post-translational type modification" are used interchangeably and refer to enzymatic or non-enzymatic modification of one or more amino acid residues in a peptide. Typical modifications include phosphorylation, dephosphorylation, glycosylation, methylation, sulfation, ubiquitination, prenylation, and ADP-ribsoylation. Preferred post-translational type modifications include phosphorylation and dephosphorylation. The term post-translational modification includes non-covalent type modifications that may affect protein activity, structure, or function, such as protein-protein interactions or the binding of allosteric modulators, other modulators, or second messengers such as calcium, cAMP, or inositol phosphates to the motif, recognition motif, or peptide.

The term "test compound" refers to a compound to be tested by one or more screening method(s) of the invention, e.g., to determine if it is a putative modulator of a kinase or phosphatase. A test compound can be any chemical, such as an inorganic chemical, an organic chemical, a protein, a peptide, a carbohydrate, a lipid, or a combination thereof. Typically, various predetermined concentrations (e.g., various dilutions) of test compounds are used for screening, such as 0.01 micromolar, 1 micromolar, and 10 micromolar. Test compound controls can include the measurement of a signal in the absence of the test compound or a comparison to a compound known to modulate the target activity.

Compositions

Compositions of the present invention include a peptide. Peptides of the invention can have a length from five to fifty amino acids and can include one or more motifs. Typically, a motif is five amino acids or longer in length. A motif can be a recognition motif, e.g., for a tyrosine kinase, a serine/threonine kinase, or a phosphatase. Compositions of the present invention can include a first detectable moiety, and in some embodiments, a second detectable moiety. Compositions of the present invention can include a protease cleavage site.

Kinases and Phosphatases

In general, protein kinases act on peptides by adding a phosphate group to a free hydroxyl group on an amino acid (a process known as phosphorylation), primarily on the amino acids tyrosine, serine, or threonine. The protein kinases that enzymatically catalyze these reactions may be classified into a number of distinct families based on structural and functional properties. Kinases within a family may have a similar overall topology, similar modes of regulation, and/or similar substrate specificities (e.g., see Table 1 of U.S. Pat. No. 6,410,255). For example, members of the AGC (protein kinase A, G or C) families of kinases may prefer phosphorylation recognition motifs with basic amino acids (e.g., R or K), while those in the CMGC group may prefer proline containing motifs.

Another family of kinases are the Serine/Threonine kinases, which phosphorylate serine or threonine amino acids, and Tyrosine kinases, which phosphorylate tyrosine amino acids.

Serine/Threonine (S/T) kinases suitable for use in the present invention include, without limitation, the following: Akt1, Akt2, Akt3, Aurora A, BARK/GRK2, CaMKII, CaMKIIa, CDK1/Cyc B, CDK2/CycA, CDK4/CAK, CDK3/CycE, CDK6/CAK, CDK7/CycH, CK1δ, CKIIα, MAPKAP-K1α, MAPKAP-K1β, MAPKAP-K1γ, MSK1, PAK2, PKA, PKG, ROCK, ROCK2, ERK1, ERK2, ERK5, GSK-3α, MLCK, mTOR, NEK2, IKKα, IKKβ, p38β, p38γ, p38δ, REDK, AMPK, MAPKAP-K2, MAPKAP-K3, MAPKAP-K5, SGK1, PIM1, CHK1, CHK2, PKCα, PKCβI, PKCβII, PKCγ, PKCδ, PKCε, PKCζ, PKCη, PKCθ, PKCι, Raf-1, and p70 S6 Kinase.

Tyrosine kinases suitable for use in the present invention include, without limitation, the following: Abl1, Abl2, BMX, Brk, CSF1R, Csk, Erb-B2, EGFR, EphB4, Fes/Fps, FGFR1, FGFR3, FGFR4, Fgr, FLT3, Fyn, FynT, HCK, Hyl, IGF1R, IRKβ, ITK, Jak3, KDR, c-KIT, Lck, Lyn A, Lyn B, c-MET, Src, Src N1, Src N2, SYK, Tec, TIE2, TRKA, VEGFR-1/Flt, YES, and IRTK. Tyrosine kinases characterized as receptor tyrosine kinases, and that are also suitable, include EGFR, EphB4, Erb-B2, FGFR1, FGFR3, FGFR4, FLT3/FLT2, FMS/CSFR1, IGF1R, KDR, c-KIT, c-MET, TIE2, TRKA, and VEGFR-1/Flt. Tyrosine protein kinases characterized as soluble tyrosine protein kinases are also suitable, and include Abl1, Abl2, Brk, BMX, Csk, Fes/Fps, Fgr, Fyn, FynT, Hck, Hyl, ITK, Jak3, Lck, LynA, LynB, Src, Src, N1, SYK, Tec, and YES. CLK1 is a dual protein kinase and may also be used in the present invention.

Eukaryotic protein phosphatases are structurally and functionally diverse enzymes that have been classified into three distinct gene families. Two of these families dephosphorylate phosphoserine and phosphothreonine amino acids, whereas the protein tyrosine phosphatase family (PTPs) dephosphorylates phosphotyrosine amino acids. A subfamily of the PTPs, the dual specificity phosphatases, dephosphorylates all three phosphoamino acids. Within each family, catalytic domains are reported to be highly conserved, with functional diversity endowed by regulatory domains and subunits.

The protein serine or threonine phosphatases type 1 and 2A reportedly account for as much as 95% of the phosphatase activity in cell extracts (Brautigan and Shriner, Methods. Enzymol. 159: 339-346 (1988)). These enzymes have broad substrate specificities and may be regulated *in vivo* through targeting of the enzymes to discrete sub-cellular localizations. The total number of protein tyrosine phosphatases encoded in the mammalian genome has been estimated at between 500 and approximately 2000.

Phosphatases for use in the present invention include, without limitation, the following: PTEN, PTP-meg 1, T-cell-PTP N2, PTP1B, LAR, LCA, PP1α, PP2A, PP2B, and PP2C.

Motifs and Peptides for measuring protein phosphorylation and dephosphorylation

Motifs suitable for detecting or measuring kinase or phosphatase activity generally include an amino acid residue which, when modified, modulates the rate of cleavage of a composition by a protease as compared to the unmodified composition. Typically, peptides of the invention include a motif having a single protease cleavage site (although more may be useful in some applications) and are soluble (e.g. 0.1 mg/ml or greater) in aqueous solution. As one of skill in the art will recognize, the design and size of peptides for specific compositions and the choice of a particular protease is dependent upon the application for which the composition is to be used. For example, for resonance energy transfer type applications, a peptide will typically be in the range of 5 to 50 amino acids in length, or 8 to 50 amino acids in length, or 8 to 25 amino acids in length, or 8 to 15 amino acids in length. For polarization-based applications, these and larger large peptides (e.g., for example 50 to 100 amino acids in length, and up to and including entire protein domains) may be desirable.

Peptides suitable for the invention may include basic amino acids, particularly at the termini, to enhance solubility. In addition, in some embodiments, a peptide can include a C-terminal K in order to provide a locus for conjugation to a detectable moiety (e.g., a fluorescein derivative). A protease cleavage site can be located at any position in a peptide, including within a motif or recognition motif. A motif, recognition motif, or protease cleavage site may be located at any position within a peptide with respect to a first or second detectable moiety.

Tyrosine phosphorylation or dephosphorylation

Compositions for detecting and monitoring tyrosine kinase activity incorporate a motif (e.g., a recognition motif for a tyrosine kinase) into a peptide, and typically have a single Tyr (Y) as the only aromatic amino acid in the composition. It may also be preferable in certain cases to eliminate or reduce the number of negatively charged amino acids in the P'_1, P'_2 or P'_3 positions. Phosphorylation of a tyrosine amino acid by a tyrosine-directed protein kinase activity modulates the rate of hydrolysis of the composition by a protease (e.g., chymotrypsin) as compared to the non-phosphorylated composition. Illustrative examples of recognition motifs and peptide substrates for tyrosine kinases are shown in Table 2 of U.S. Pat. No. 6,410,255 for use with the protease chymotrypsin. Other illustrative motifs, recognition motifs, and peptides for tyrosine kinases are shown in Table 1, below.

Table 1

Motif	**Illustrative Recognition Motif**	**Illustrative Peptide Sequence**
AIYAA (SEQ ID NO: 1)	EAIYAAP (SEQ ID NO: 2)	EAEAIYAAPGDK (SEQ ID NO: 3)
QDYLS (SEQ ID NO: 4)	DQDYLSL (SEQ ID NO: 5)	GDQDYLSLDK (SEQ ID NO: 6)
EIYGV (SEQ ID NO:7)	EEIYGVI (SEQ ID NO:8)	EEEIYGVIEK (SEQ ID NO:9)
TX$_1$YVA, where X$_1$ can be G, A, or E (SEQ ID NO: 10)	LTGYVAR (SEQ ID NO: 11); ITAYVAT (SEQ ID NO: 12); ITEYVAT (SEQ ID NO: 13)	GVLTGYVARRK (SEQ ID NO: 14); DDEITAYVATRK (SEQ ID NO: 15); TGIITEYVATRK (SEQ ID NO: 16)
EEYIQ (SEQ ID NO: 17)	EEEYIQI (SEQ ID NO: 18)	EEEEYIQIVK (SEQ ID NO: 19)
DYSQV (SEQ ID NO: 20)	GDYSQVL (SEQ ID NO:	EGDYSQVLEK (SEQ ID

	21)	NO: 22)

Compositions for detecting protein tyrosine phosphatase activity incorporate a motif (e.g., a recognition motif for a tyrosine kinase) into a peptide, where one or more tyrosine amino acids in the motif are phosphorylated. Dephosphorylation of a tyrosine amino acid in such compositions by a tyrosine-directed protein phosphatase activity modulates the rate of hydrolysis by a protease (e.g., chymotrypsin) as compared to the phosphorylated composition. Illustrative phosphatase motifs, recognition motifs, and peptides are shown in Table 2, below, where Y* indicates a phosphorylated tyrosine.

Table 2

Motif	**Illustrative Recognition Motif**	**Illustrative Peptide Sequence**
AIY*AA (SEQ ID NO: 23)	EAIY*AAP (SEQ ID NO: 24)	EAEAIY*AAPGDK (SEQ ID NO: 25)
QDY*LS (SEQ ID NO: 26)	DQDY*LSL (SEQ ID NO: 27)	GDQDY*LSLDK (SEQ ID NO: 28)
EIY*GV (SEQ ID NO: 29)	EEIY*GVI (SEQ ID NO: 30)	EEEIY*GVIEK (SEQ ID NO: 31)
TX_1Y*VA, where X_1 can be G, A, or E (SEQ ID NO: 32)	LTGY*VAR (SEQ ID NO: 33); ITAY*VAT (SEQ ID NO: 34); ITEY*VAT (SEQ ID NO: 35)	GVLTGY*VARRK (SEQ ID NO: 36); DDEITAY*VATRK (SEQ ID NO: 37); TGIITEY*VATRK (SEQ ID NO: 38)
EEY*IQ (SEQ ID NO: 39)	EEEY*IQI (SEQ ID NO: 40)	EEEEY*IQIVK (SEQ ID NO: 41)
DY*SQV (SEQ ID NO: 42)	GDY*SQVL (SEQ ID NO: 43)	EGDY*SQVLEK (SEQ ID NO: 44)

Serine/Threonine (S/T) phosphorylation or dephosphorylation

Compositions for measuring serine or threonine kinase activities incorporate a motif (e.g., a recognition motif for a S/T kinase) typically containing a single aromatic amino acid (Tyr, Trp or Phe) generally within about three amino acids of a serine or threonine amino acid. A serine or threonine amino acid is phosphorylated by an appropriate serine or threonine specific kinase. It may be preferable in certain cases (depending on the protease selected) to eliminate or reduce the number of negatively charged amino acids (e.g. Asp or Glu amino acids) in the P'_1, P'_2 or P'_3 positions to ensure that serine or threonine phosphorylation provides a large modulation in proteolytic sensitivity of the composition upon phosphorylation. Examples of illustrative recognition motifs and peptides are provided in Table 3 of U.S. 6,410,255 for use with chymotrypsin. Illustrative motifs, recognition motifs, and peptides for S/T kinases are also shown in Table 3, below.

Table 3

Motif	**Illustrative Recognition Motif**	**Illustrative Peptide Sequence**
RRX$_1$(S/T)L, where X$_1$ can be F, W, or Y (SEQ ID NO: 45)	LRRFSLG (SEQ ID NO: 46)	ALRRFSLGEK (SEQ ID NO: 47)
LX$_1$(S/T)TT, where X$_1$ can be F, W, or Y (SEQ ID NO: 48)	GLFSTTP (SEQ ID NO: 49)	RGGLFSTTPGGTK (SEQ ID NO: 50)
X$_1$L(S/T)LD, where X$_1$ can be F, W, or Y (SEQ ID NO: 51)	DYLSLDK (SEQ ID NO: 52)	GDQDYLSLDK (SEQ ID NO: 53)
RX$_1$X$_2$(S/T)X$_3$, where X$_1$ can be V, A, or Q, X$_2$ can be F, W, or Y, and X$_3$ can be V or L (SEQ ID NO: 54)	NRVFSVA (SEQ ID NO: 55), PRAFSVG (SEQ ID NO: 56), RRQFSLR (SEQ ID NO: 57)	KLNRVFSVAC (SEQ ID NO: 58), ARPRAFSVGK (SEQ ID NO: 59), RRRQFSLRRKAK (SEQ ID NO: 60)
TX$_1$S(S/T)L, where X$_1$ can be F, W, or Y (SEQ ID NO: 61)	RTFSSLA (SEQ ID NO: 62)	RPRTFSSLAEGK (SEQ ID NO: 63)
X$_1$X$_2$(S/T)PX$_3$ where X$_1$ can be P or I, X$_3$ can be F, W, or Y, and X$_2$ can be G, K, or D (SEQ ID NO: 64)	APFSPGG (SEQ ID NO: 65), HPFSPKK (SEQ ID NO: 66), KIFSPDV (SEQ ID NO: 67)	VAPFSPGGRAK (SEQ ID NO: 68), AKHPFSPKKAK (SEQ ID NO: 69), IIKIFSPDVEK (SEQ ID NO: 70),
X$_1$(S/T)X$_2$X$_3$VA, where X$_1$ can be F, W, or Y, X$_2$ can be A, E, or Q,	EFTAYVA (SEQ ID NO: 72), IFTEYVA (SEQ ID NO: 73),	DDEFTAYVATRK (SEQ ID NO: 75),

and X_3 can be Y or H (SEQ ID NO: 71)	VFTQHVA (SEQ ID NO: 74)	TGIFTEYVATRK (SEQ ID NO: 76), TGVFTQHVATRK (SEQ ID NO: 77)
IX_1(S/T)IAN, where X_1 can be F, W, or Y (SEQ ID NO: 78)	RIFSIANS (SEQ ID NO: 79)	QRIFSIANSIVK (SEQ ID NO: 80)
SIAX_1(S/T)I, where X_1 can be F, W, or Y (SEQ ID NO: 81)	DSIAFSIV (SEQ ID NO: 82)	RIDSIAFSIVGK (SEQ ID NO: 83)
(S/T)VPPS*P, where S* is a phosphorylated serine (SEQ ID NO: 84)	FSVPPS*PD, where S* is a phosphorylated serine (SEQ ID NO: 85),	PRPFSVPPS*PDK, where S* is a phosphorylated Serine (SEQ ID NO: 86)
DX_1X_2(S/T)X_3, where X_1 can be A or E, X_2 can be F, W, or Y, and X_3 can be I or Q (SEQ ID NO: 87)	EDAFSII (SEQ ID NO: 88), EDEFSQN (SEQ ID NO: 89)	EEDAFSIIGK (SEQ ID NO: 90), REDEFSQNEEK (SEQ ID NO: 91)
DX_1(S/T)QV, where X_1 can be F, W, or Y (SEQ ID NO: 92)	EGDYSQV (SEQ ID NO: 93)	EGDYSQVLEK (SEQ ID NO: 22)

Compositions for detecting protein serine or threonine phosphatase activity incorporate a motif (e.g., a recognition motif for a S/T kinase) into a peptide, where one or more serine or threonine amino acids in the motif are phosphorylated. Dephosphorylation of a serine or threonine amino acid in the composition by a serine- or threonine- directed protein phosphatase activity modulates the rate of hydrolysis by a protease (e.g., chymotrypsin) as compared to the phosphorylated composition. Illustrative phosphatase motifs, recognition motifs, and peptides are set forth in Table 4, below, where (S/T)* indicates a phosphorylated serine or threonine, S* indicates a phosphorylated serine, and T* indicates a phosphorylated threonine.

Table 4

Motif	**Illustrative Recognition Motif**	**Illustrative Peptide Sequence**
RRX$_1$(S/T)*L, where X$_1$ can be F, W, or Y (SEQ ID NO: 95)	LRRFS*LG (SEQ ID NO: 96)	ALRRFS*LGEK (SEQ ID NO: 97)
LX$_{1(}$S/T)*TT, where X$_1$ can be F, W, or Y (SEQ ID NO: 98)	GLFS*TTP (SEQ ID NO: 99)	RGGLFS*TTPGGTK (SEQ ID NO: 100)
X$_1$L(S/T)*LD, where X$_1$ can be F, W, or Y (SEQ ID NO: 101)	DYLS*LDK (SEQ ID NO: 102)	GDQDYLS*LDK (SEQ ID NO: 103)
RX$_1$X$_2$(S/T)*X$_3$, where X$_1$ can be V, A, or Q, X$_2$ can be F, W, or Y, and X$_3$ can be V or L (SEQ ID NO: 104)	NRVFS*VA (SEQ ID NO: 105), PRAFS*VG (SEQ ID NO: 106), RRQFS*LR (SEQ ID NO: 107)	KLNRVFS*VAC (SEQ ID NO: 108), ARPRAFS*VGK (SEQ ID NO: 109), RRRQFS*LRRKAK (SEQ ID NO: 110)
TX$_1$S(S/T)*L, where X$_1$ can be F, W, or Y (SEQ ID NO: 111)	RTFSS*LA (SEQ ID NO: 112)	RPRTFSS*LAEGK (SEQ ID NO: 113)
X$_1$X$_2$(S/T)*PX$_3$ where X$_1$ can be P or I, X$_3$ can be F, W, or Y, and X$_2$ can be G, K, or D (SEQ ID NO: 114)	APFS*PGG (SEQ ID NO:115), HPFS*PKK (SEQ ID NO: 116), KIFS*PDV (SEQ ID NO: 117)	VAPFS*PGGRAK (SEQ ID NO: 118), AKHPFS*PKKAK (SEQ ID NO: 119), IIKIFS*PDVEK (SEQ ID NO: 120),
X$_1$(S/T)*X$_2$X$_3$VA, where X$_1$ can be F, W, or Y, X$_2$ can be A, E, or Q, and X$_3$ can be Y or H (SEQ ID NO: 121)	EFT*AYVA (SEQ ID NO: 122), IFT*EYVA (SEQ ID NO: 123), VFT*QHVA (SEQ ID NO: 124)	DDEFT*AYVATRK (SEQ ID NO: 125), TGIFT*EYVATRK (SEQ ID NO: 126), TGVFT*QHVATRK (SEQ ID NO: 127)

IX_1(S/T)*IAN, where X_1 can be F, W, or Y (SEQ ID NO: 128)	RIFS*IANS (SEQ ID NO: 129)	QRIFS*IANSIVK (SEQ ID NO: 130)
SIAX_1(S/T)*I, where X_1 can be F, W, or Y (SEQ ID NO: 131)	DSIAFS*IV (SEQ ID NO: 132)	RIDSIAFS*IVGK (SEQ ID NO: 133)
(S/T)*VPPS*P (SEQ ID NO: 134)	FS*VPPS*PD (SEQ ID NO: 135)	PRPFS*VPPS*PDK (SEQ ID NO: 136)
DX_1X_2(S/T)*X_3, where X_1 can be A or E, X_2 can be F, W, or Y, and X_3 can be I or Q (SEQ ID NO: 137)	EDAFS*II (SEQ ID NO: 138), EDEFS*QN (SEQ ID NO: 139)	EEDAFS*IIGK (SEQ ID NO: 140), REDEFS*QNEEK (SEQ ID NO: 141)
DX_1(S/T)*QV, where X_1 can be F, W, or Y (SEQ ID NO: 142)	EGDYS*QV (SEQ ID NO: 143)	EGDYS*QVLEK (SEQ ID NO: 144)

Protease

Many proteases for use in the present invention are commonly available at high purity. Typically, the proteolytic activity of a protease for a composition is modulated by the presence or absence of a post-translationally modified (e.g., phosphorylated) amino acid in a motif. Preferred compositions exhibit a significant modulation, e.g. at least 1.5, 2, 3, 4, 5, 7, 10, 15, 20, 25, 30, 35, 40, 50 or 100 fold modulation, of proteolytic reactivity when modified as compared to when non-modified. See Table 5 below for illustrative proteases.

TABLE 5

Name	**EC**	**Type**	**Peptide**	**Primary Specificity**
Caspase 3		Cysteine	DXXD -P'_1	P_1=Asp, P'_1 = neutral preferred
Cathepsin G	EC 3.4.21.20	Serine	P_1-P'_1	P_1 = aromatic preferred, W, Y, F
Chymotrypsin	EC 3.4.21.1	Serine	P_1-P'_1	P_1 = aromatic preferred, W, Y, F

Elastase	EC 3.4.21.36	Serine	P_1-P'_1	P_1 = uncharged, non aromatic, e.g. A, V, L, 1, G, S, T
Endoproteinase Asp-N		Unknown	P_1-Asp	P'_1=Asp or P'_1=Cysteic acid P_1 = non-specific
Endoproteinase Glu-N	EC 3.4.21.9	Serine	Glu- P'_1	P_1 = Glu or Asp P'_1 = non-specific
Streptomyces griseus	EC 3.4.21.82	Serine	Glu- P'_1	P_1 = Glu or Asp P'_1 = non-specific
Staphylococcus aureus V8	EC 3.4.21.19	Serine	Glu- P'_1	P_1 = Glu or Asp P'_1 = non-specific

Proteases that may be used to measure peptide phosphorylation or dephosphorylation include those that recognize a composition that includes at least one motif position in which the presence or absence of a phosphorylated amino acid modulates the activity of the protease towards that composition. The flexibility in choice of motifs containing or lacking phosphorylated amino acids (e.g., tyrosine, serine or threonine) combined with the flexibility in choice of the protease enables many protein kinase or phosphatase activities to be measured using the present invention.

In a cell-based application of the present method, the expression of a protease within a cell is regulated (e.g., using inducible nucleic acid constructs that encode the protease). Suitable nucleic acid constructs can be designed and used as a matter of routine by those skilled in the art. In such cell-based assays, an appropriate measurable (e.g., optical) property of a composition that includes at least one motif position in which the presence or absence of a phosphorylated residue modulates the activity of the protease towards that composition can be monitored at one or more time intervals after the onset of increased expression of the protease.

Detectable Moieties

The choice of a detectable moiety is governed by a number of factors including the mode of detection, the availability of specific instrumentation, and the ease of coupling of the detectable moiety to a peptide. Other factors that may be relevant to a particular use include the effect of a detectable moiety on the solubility of a composition, the kinetics of the post-translational activity or protease activity with respect to a composition, and the desired detection sensitivity of an assay.

Numerous detectable moieties are commercially available or can be readily made. In general, a detectable moiety can exhibit an optical property, a magnetic property, or a radioactive property. Thus, once associated with a peptide, a detectable moiety allows a resulting composition to exhibit an optical property, a magnetic property, or a radioactive property that is similar to or the same as that of the detectable moiety alone. In some embodiments, the association of a detectable moiety with a peptide may alter a detectable property of the detectable moiety to a greater or lesser extent. For example, conjugation of a fluorophore to a peptide may result in a composition having an emission maximum that is different from that of the fluorophore alone in solution. In other embodiments, a detectable moiety can be a member of a specific binding pair. For example, a detectable moiety can be the ligand member of a ligand-protein binding pair, e.g., the biotin member of the biotin-streptavidin binding pair.

For fluorescent detectable moieties, preferred fluorophores typically exhibit good quantum yields, long excited state lifetimes, and large extinction coefficients; are resistant to collisional quenching and bleaching; and should be easily conjugated to a peptide. Fluorophores that show absorbance and emission in the red and near-infrared range are useful in whole animal studies because of reduced scattering background fluorescence and greater transmission through tissues. Examples of illustrative fluorophores include cyanines, oxazines, thiazines, porphyrins, phthalocyanines, fluorescent infrared-emitting polynuclear aromatic hydrocarbons such as violanthrones, fluorescent proteins, near IR squaraine dyes. (for example, as shown in Dyes and Pigments 17:19-27 (1991), U.S. Patent No. 5,631,169 to Lakowicz et al., issued May 20, 1997, and organo-metallic complexes such as ruthenium and lanthanide complexes of U.S. Patent Nos. 4,745,076 and 4,670,572, the disclosures of which are incorporated herein by reference).

Suitable fluorophores and dark quenchers for use in the present invention are commercially available, e.g., from Molecular Probes (Eugene, OR), Attotec (Germany), Amersham, and Biosearch Technologies (Novato, CA). Specific fluorophores include, without limitation, fluorescein isothiocyanate (especially fluorescein-5-isothiocyanate), 5-FAM (5-carboxyfluorescein), 6-FAM (6-carboxyfluorescein), 5,6-FAM, 7-

hydroxycoumarin-3-carboxamide, 6-chloro-7-hydroxycoumarin-3-carboxamide, dichlorotriazinylaminofluorescein, tetramethylrhodamine-5 (and -6)-isothiocyanate, 1,3-bis- (2-dialkylamino-5-thienyl)-substituted squarines, the succinimidyl esters of 5 (and 6) carboxyfluoroscein, 5 (and 6)-carboxytetramethylrhodamine, and 7-amino-4-methylcoumarin-3-acetic acid. Semiconductor fluorescent nanocrystals are available with a range of emission spectra, are highly fluorescent and are also useful (see Bruchez et al., Science 281: 2013-2016).

Lanthanide complexes (e.g., metal chelates of Eu or Tb) are also useful and have the advantage of not being quenched by oxygen. Their long lifetimes (on the order of ms as compared to ns for other fluorophores) may allow easy suppression of the auto-fluorescence of biological samples, as fluorescent signals may be measured after background signals have decayed. Accordingly, lanthanide complexes, such as Eu or Tb metal chelates, may be particularly useful, e.g., in time-resolved FRET (TR-FRET) applications. See, for example, U.S. Pat. Nos. 5,639,615, 5,622,821, and 5,656,433.

Illustrative luminescent moieties include chemiluminescent, electroluminescent, and bioluminescent compounds. Preferred bioluminescent compounds include bioluminescent proteins such as firefly, bacterial, or click beetle luciferases, aequorins, and other photoproteins (for example as described in U.S. Patents 5,221,623, issued June 22, 1989 to Thompson et al., 5,683,888 issued November 4, 1997 to Campbell; 5,674,713 issued September 7, 1997 to DeLuca et al.; 5,650,289 issued July 22, 1997 to Wood; and 5,843,746 issued December 1, 1998 to Tatsumi et al.). Preferred electroluminescent moieties include ruthenium complexes, as for example described in U.S; Patent 5,597,910 issued to Jan 28, 1997 to Gudibande. Preferred chemiluminescent moieties include those based on 1,2-dioxetanes, as for example described in U.S. Patents 4,372,745 issued February 8, 1983 to Mandle et al., 5,656,207 issued August 12, 1997 to Woodhead et al., and 5,800,999 issued September 1, 1998 issued to Bronstein et al.

Magnetic detectable moieties include MR contrast agents, e.g., chelates of paramagnetic, ferromagnetic, or diamagnetic metal ions, or magnetic particles (e.g., USPIOs, MIONs; see U.S. Pat. No. 5,262,176). In some embodiments, a chelate may comprise a lipophilic group as described in U.S. patents 5,628,982, issued May 13, 1997 to Lauffer et al., and U.S. patent 5,242,681, issued September 7, 1993 to Elgavish et al.

For reviews of metal chelates useful in MR imaging, see Lauffer, "Paramagnetic Metal Complexes as Water Proton Relaxation Agents for NMR Imaging: Theory and Design," Chem. Rev. 87(5):901-927 (1987); and Caravan et al., "Gadolinium (III) Chelates as MRI Contrast Agents: Structure, Dynamics, and Applications," Chem. Rev. 99(9):2293-2352 (1999).

In some applications it may be desirable to derivatize a detectable moiety to render it more hydrophobic and permeable to cell membranes. The derivatizing groups may undergo hydrolysis inside cells to regenerate the compositions, thus trapping them within cells. For this purpose, it is preferred that phenolic hydroxyls or free amines in the structures are acylated with C_1-C_4 acyl groups (e.g. formyl, acetyl, n-butyl) or converted to, e.g., esters and carbonates, as described in Bundgaard, H., Design of Prodrugs, Elsevier Science Publishers (1985), Chapter 1, page 3 *et seq*. Further modification of fluorescent moieties may also be accomplished e.g., as described in U.S. Patent No. 5,741,657 issued 4/21/98 to Tsien et al.

A detectable moiety may be attached to a peptide by a linker (L) that provides a spacer between the detectable moiety and the peptide, thereby preventing steric or charge interference of the detectable moiety on the interaction between, e.g., the recognition motif of the peptide and a kinase or phosphatase. Preferred linkers are substantially stable under cellular conditions and easily coupled to a peptide and detectable moiety. Examples include flexible aliphatic linkers such as γ-amino-n-butyric acid (GABA), diaminopentane, and aminohexanoyl, as well as rigid aromatic linkers. Such linkers are known in the art and described for example in the Handbook of Fluorescent Probes and Research Chemicals, by Richard Haugland, published by Molecular Probes.

Non-covalent methods of attachment may also be used to associate a peptide with a detectable moiety. For example, a peptide may be designed to encompass a specific binding site for a fluorescent moiety, as described in pending U.S. Patents 6,054,271; 6,008,378, and 5,932,474. Labeling may then be achieved by incubation of a peptide with a membrane-permeable fluorescent binding partner, which has the advantages of enabling the expression of peptides within intact living cells, and the subsequent labeling of these peptides *in situ* to create compositions of the present invention within intact living cells.

Fluorescent proteins

For some cell-based applications, fluorescent detectable moieties include endogenously fluorescent proteins, functional engineered fluorescent proteins, and variants thereof. Use of such proteins allows the fluorophore and peptide to be expressed within living cells without the addition of other co-factors or fluorophores. Such compositions provide the ability to monitor post-translational activities within defined cell populations, tissues, or a transgenic organism, for example, by the use of inducible controlling nucleotide sequences to produce a sudden increase in the expression of a composition and protease.

Endogenously fluorescent proteins have been isolated and cloned from a number of marine species including the sea pansies *Renilla reniformis*, *R. kollikeri* and *R. mullerei* and from the sea pens Ptilosarcus, Stylatula and Acanthoptilum, as well as from the Pacific Northwest jellyfish, *Aequorea victoria* (Szent-Gyorgyi et al. (SPIE conference 1999), D.C. Prasher et al., Gene, 111:229-233 (1992)). These proteins are capable of forming a highly fluorescent, intrinsic chromophore through the cyclization and oxidation of internal amino acids within the protein that can be spectrally resolved from weakly fluorescent amino acids such as tryptophan and tyrosine.

Fluorescent proteins have also been observed in other organisms. For example, the cloning and expression of yellow fluorescent protein from *Vibrio fischeri* strain Y-1 has been described by T.O. Baldwin et al., Biochemistry (1990) 29:5509-15. This protein requires flavins as fluorescent co-factors. The cloning of Peridinin-chlorophyll a binding protein from the dinoflagellate Symbiodinium sp. was described by B.J. Moms et al., Plant Molecular Biology, (1994) 24:673:77. One useful aspect of this protein is that it fluoresces in red. The cloning of phycobiliproteins from marine cyanobacteria such as Synechococcus, e.g., phycoerythrin and phycocyanin, is described in S.M. Wilbanks et al., J. Biol. Chem. (1993) 268:1226-35. These proteins require phycobilins as fluorescent co-factors, whose insertion into the proteins involves auxiliary enzymes. The proteins fluoresce at yellow to red wavelengths. See also PCT US 01/04625.

A variety of mutants of the GFP from *Aequorea victoria* have been created that have distinct spectral properties, improved brightness, and enhanced expression and folding in mammalian cells compared to the native GFP (e.g., see Table 7 of U.S. 6,410,255 and also Green Fluorescent Proteins, Chapter 2, pages 19 to 47, edited by Sullivan and Kay, Academic Press; U.S. patent Nos: 5,625,048 to Tsien et al., issued April 29, 1997; 5,777,079 to Tsien et al., issued July 7, 1998; and U.S. Patent No. 5,804,387 to Cormack et al., issued September 8, 1998). In many cases these functional engineered fluorescent proteins have superior spectral properties to wild-type *Aequorea* GFP and are preferred for use in the compositions of the invention.

Cell-based Assays

The methods of the present invention can also be employed in cell-based assays. Recombinant production of the compositions within living cells involves, in one embodiment, expressing nucleic acids having sequences that encode a fluorescent protein (e.g., as a detectable moiety) and a peptide of interest as a fusion protein. In one embodiment, a composition comprises a first fluorescent protein (e.g., as the first detectable moiety), a peptide containing a motif, such as a recognition motif for a Y or S/T kinase, a protease site, and a second fluorescent protein (as a second detectable moiety) fused together as a single polypeptide chain. Nucleic acids encoding fluorescent proteins can be obtained by methods known in the art. For example, a nucleic acid encoding the protein can be isolated by polymerase chain reaction of cDNA from a suitable organism using primers based on the DNA sequence of the fluorescent protein. PCR methods are described in, for example, U.S. Pat. No. 4,683,195; Mullis et al. (1987); Cold Spring Harbor Symp. Quant. Biol. 51:263; and Erlich, ed., PCR Technology, (Stockton Press, NY, 1989). Suitable clones may then be identified, isolated and characterized by fluorescence activated cell sorting (FACS), typically enabling the analysis of a few thousand cells per second. The construction of expression vectors and the expression of genes in transfected cells involve the use of molecular cloning techniques also well known in the art; see, e.g., Sambrook et al., Molecular Cloning -- A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, (1989) and Current Protocols in Molecular Biology, F.M. Ausubel et al., eds. Nucleic acids used to transfect cells with sequences coding for expression of the polypeptide of interest generally will be in the form of an expression vector including expression control sequences operatively linked to a nucleotide sequence coding for expression of the composition comprising the peptide and fluorescent proteins.

In an alternative embodiment, a composition can include a reporter protein (e.g., as a first detectable moiety), a peptide containing a motif described herein, such as a recognition motif for a Y or S/T kinase, a protease site, and a multimerized ubiquitin fusion protein together as a single polypeptide chain. In these embodiments, the motif-containing peptide functions as a linker between the reporter protein and the multimerized ubiquitin fusion protein. Such a polypeptide can be used to carry out an assay for a kinase (or a phosphatase) in a cell. For example, if a suitable kinase is present and active in a cell, the peptide will be phosphorylated and not subject to degradation by a protease, thereby allowing the ubiquitin fusion protein to destabilize (e.g., promote degradation of) the reporter protein. If kinase activity is not present or is inhibited, the motif-containing peptide will be subject to degradation by the protease, thereby preventing the multimerized ubiquitin fusion protein from destabilizing the reporter protein and preserving reporter protein activity. Suitable reporter proteins, multimerized ubiquitin fusion proteins, and constructs for use in such an embodiment are described in WO 01/57242.

Methods of measurement and detection

Methods of measurement and detection include, without limitation, fluorescence spectroscopy, luminescence spectroscopy, absorption spectroscopy, and magnetic resonance spectroscopy (e.g., NMR, MRI). Fluorescent methods include continuous or time resolved fluorescence spectroscopy, fluorescence correlation spectroscopy, fluorescence polarization spectroscopy, and resonance energy based fluorescence spectroscopy. Methods of performing such assays on fluorescent materials are well known in the art and are described in, e.g., Lakowicz, J.R., Topics in Fluorescence Spectroscopy, volumes 1 to 3, New York: Plenum Press (1991); Herman, B., Resonance energy transfer microscopy, in Fluorescence Microscopy of Living Cells in Culture, Part B, Methods in Cell Biology, vol. 30, ed. Taylor, D.L. & Wang, Y.-L., San Diego: Academic Press (1989), pp. 219-243; Turro, N.J., Modern Molecular Photochemistry, Menlo Park: Benjamin/Cummings Publishing Col, Inc. (1978), pp. 296-361; and Bernard Valeur, "Molecular Fluorescence: Principles and Applications" Wiley VCH, 2002.

The selection and use of specific detectable moieties (e.g., specific fluorophores or quenchers) for particular applications is generally known in the art; for example, see Berlman, I.B., Energy transfer parameters of aromatic compounds, Academic Press, New York and London (1973), which contains tables of spectral overlap integrals for the selection of resonance energy transfer partners. Additional information sources include the Molecular Probes Catalog (2003) and website; and Tsien et al., 1990 Handbook of Biological Confocal Microscopy, pp. 169-178.

Methods and Assays

Compositions of the present invention can be used in a variety of methods. Standard techniques are usually used for chemical synthesis, fluorescence monitoring and detection, optics, molecular biology, and computer software and integration. Chemical reactions, cell assays, and enzymatic reactions are typically performed according to the manufacturer's specifications where appropriate. See, generally, Lakowicz, J.R. *Topics in Fluorescence Spectroscopy*, (3 volumes) New York: Plenum Press (1991), and Lakowicz, J. R. *Emerging applications of florescence spectroscopy to cellular imaging: lifetime imaging, metal-ligand probes, multi photon excitation and light quenching,* Scanning Microsc. Suppl. Vol. 10 (1996) pages 213-24, for fluorescence techniques; Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2ed. (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., for molecular biology methods; *Cells: A Laboratory Manual,* 1st edition (1998) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., for cell biology methods; and *Optics Guide 5* Melles Griot® Irvine CA, and *Optical Waveguide Theory,* Snyder & Love (published by Chapman & Hall) for general optical methods, all of which are incorporated herein by reference.

Compositions of the present invention can be used to prepare phosphorylated compositions. Methods of the present invention can also be used to characterize a kinase or a phosphatase, e.g., to measure kinetic or thermodynamic parameters. In one method, a composition of matter is used in a reaction with a kinase or phosphatase. The composition is contacted with a kinase or phosphatase under conditions effection for the kinase or phosphatase to phosphorylate or dephosphorylate the composition, respectively, and the ability of the kinase to phosphorylate (or the phosphatase to dephosphorylate) the composition is measured. Ability to phosphorylate a composition may be measured in a number of ways, e.g., in terms of % phosphorylation of the composition in a given time period, at a particular concentration of kinase, or at a particular temperature; or in terms of kinetic parameters (e.g., V_{max}, K_m). See Examples 1 and 2 and FIGs. 3-5 and 8-9. Methods for using a composition are described in, for example, U.S. Pat. Nos. 6,410,255, 5,917,012, and in Rodems et al., "A FRET-based Assay Platform for Ultra-High Density Drug Screening of Protein Kinases and Phosphatases," ASSAY and Drug Development Technologies, Vol. 1 (1-1), Nov. 2002.

Methods of the present invention can be used to determine whether or not a composition of matter is a substrate for a kinase or phosphatase. In one method, a composition of matter is contacted with an enzyme, e.g., a protein kinase or protein phosphatase; the composition and enzyme are then contacted with a protease; and a measurable property in the protease mixture is monitored. A measurable property can be a detectable property of a composition, a detectable property of a cleavage product of a composition (e.g., a detectable property of a donor fluorescent moiety or a detectable property of an acceptor fluorescent moiety), a detectable property of an enzyme, buffer, or reagent, or any combination thereof. For example, a measurable property may be the net fluorescence emission at a wavelength (or a ratio of the net fluorescence emission at two wavelengths) after a composition has been partially cleaved (e.g., 70% cleavage). In this situation, the measurable property reflects the contribution of the intact composition and the mixture of cleavage products to the fluorescence emission of the mixture at the particular wavelength under consideration.

For kinase reactions, ATP is generally included when a composition is contacted with kinase (e.g., during an incubation with the kinase enzyme). As one of skill in the art will recognize, in those methods employing phosphatase enzymes, a phosphorylated composition of matter as described above is contacted with a phosphatase enzyme. Incubation conditions for a contacting step can vary, e.g., in enzyme concentration, substrate concentration, temperature, and length of time. Incubation temperature conditions typically can be from about 15 to about 40 °C; in some embodiments, the temperature may be about room temperature, e.g., about 20-25 °C.

A measurable property in a protease mixture may be compared to a measurable property in a control mixture. A control mixture can include the composition of matter and the protease and is typically prepared without the addition of enzyme and/or without the addition of ATP (e.g., for kinase reactions). Other control samples can comprise a phosphorylated version of the composition incubated with the protease in order to correct for any cleavage of the phosphorylated composition by the protease. One of skill in the art can typically design appropriate control mixtures for reference.

A measurable property can be monitored during an incubation with a kinase or phosphatase or when a kinase or phosphatase incubation is complete. Similarly, a measurable property can be monitored during a protease incubation or when a protease incubation is complete. Typically, a measurable property is measured after a predetermined time period of a kinase, phosphatase, or protease incubation. For example, a measurable property may be measured within 12 hours of the initiation of a kinase (phosphatase) or protease incubation. In some embodiments, a measurable property is measured within 30 minutes, 1 hour, 2 hours, or 4 hours of initiation. A protease incubation can be stopped by a number of known methods, including the addition of a reagent to inhibit proteolytic activity (e.g., aprotinin, PMSF, TPCK, AEBSF, chymotrypsin inhibitor 1, chymotrypsin inhibitor 2), by heating and/or denaturing the protease sample, and by altering pH or metal concentration (e.g., by chelating an active site metal).

A composition is identified as a substrate of a kinase (or phosphatase) if a measurable property in the protease mixture is different from the measurable property in the appropriate control mixture. Generally, the measurable property should be statistically significantly different from the measurable property in the control mixture. As one of skill in the art will recognize, whether or not a difference is statistically significant will depend on the type of measurable property, the type of measurement, and the experimental conditions. It is understood that when comparing measurable properties, a statistically significant difference indicates that that substrate may warrant further study. Typically, a difference in measurable properties is considered statistically significant at p

<0.05 with an appropriate parametric or non-parametric statistic, e.g., Chi-square test, Student's t-test, Mann-Whitney test, or F-test. In some embodiments, a difference is statistically significant at $p < 0.01$, $p < 0.005$, or $p < 0.001$.

Typically, a detectable property will be an optical property, such as a fluorescence property. In one aspect, the method may be based on a difference in a fluorescence anisotropy measurement of a composition before and after cleavage with a protease. In this case, a composition typically comprises a peptide moiety which contains a motif, e.g., a recognition motif for a kinase or phosphatase, a protease site, and a fluorescent detectable moiety. Modification of the peptide by the kinase (or phosphatase) activity results in a modulation of the rate at which a protease cleaves the peptide, which is sensed by a measurable (e.g., statistically different) change in fluorescence polarization of the composition upon cleavage.

Polarization measurements are based on the relative rotational movement of a fluorophore compared to the excited state life-time of that fluorophore. For globular molecules in dilute solution, the relationship between polarization (p) and the degree of rotational movement can be readily derived (see Weber, Polarization of the fluorescence of solutions, in Fluorescence and Phosphorescence Analysis, Don Hercules (ed.), Interscience Publishers, New York, Chapter 8, pages 217-240 (1966)). Rotational movement can be related to the rotational diffusion constant of the molecule, and hence to the molecular volume. In practice there is a close correlation between molecular size and relative polarization of emitted light from a fluorophore. As a consequence, a significant change in fluorescence polarization can occur when compositions of the present invention are acted upon by a protease. Polarization-based assays are relatively easy to set up and can be obtained over a wide concentration, temperature, and ionic strength range.

In another embodiment of the method, fluorescence anisotropy measurements can be enhanced by attaching one end of a peptide of a composition to a solid matrix or a bead. In either case, cleavage of the composition results in a large drop in fluorescence polarization because of the increased rotational flexibility of the cleavage product of the composition once separated from the solid matrix or bead.

In another aspect, the present invention takes advantage of resonance energy transfer either between two fluorescent moieties (FRET), or a bioluminescent moiety and fluorescent moiety (bioluminescent resonance energy transfer, BRET), or a fluorescent moiety and a quencher (e.g., RET dark quenching) to provide a fluorescent readout.

In FRET applications, a composition typically comprises a first fluorescent detectable moiety and a second fluorescent detectable moiety coupled to a peptide such that a motif (e.g., a recognition motif) and a protease cleavage site are located between the two detectable moieties. In this case, cleavage of the peptide by a protease results in an alteration in energy transfer between the first fluorescent moiety and the second fluorescent moiety that may be used to monitor and measure kinase or phosphatase activity.

In FRET cases, fluorescent moieties are typically chosen such that the excitation spectrum of one of the moieties (the acceptor fluorescent moiety) overlaps with the emission spectrum of the donor fluorescent moiety. The donor fluorescent moiety is excited by light of appropriate wavelength and intensity within the donor fluorescent moiety's excitation spectrum and under conditions in which direct excitation of the acceptor fluorophore is minimized. The donor fluorescent moiety then transfers the absorbed energy by non-radiative means to the acceptor, which subsequently re-emits some of the absorbed energy as fluorescence emission at a characteristic wavelength. FRET applications can include TR-FRET applications. In these embodiments, a Ln complex, such as a Eu or Tb metal chelate, is used as a fluorescent donor moiety, as described above. Typically, the Ln complex is chosen so that one of its emission bands overlaps with an excitation band of the acceptor fluorescent moiety.

FRET can be manifested as a reduction in the intensity of the fluorescent signal from the donor, reduction in the lifetime of its excited state, and/or an increase in emission of fluorescence from the acceptor fluorescent moiety. When a peptide having a donor fluorescent moiety and acceptor fluorescent moiety is cleaved, the donor fluorescent moiety and the acceptor fluorescent moiety physically separate, and FRET is diminished or eliminated. Under these circumstances, fluorescence emission from the donor increases and fluorescence emission from the acceptor decreases. Accordingly, a ratio of emission amplitudes at wavelengths characteristic (e.g., the emission maximum) of the donor relative to the acceptor should increase as compared to the same ratio under

FRET conditions (e.g., when emission of the donor is quenched (e.g., reduced) by the acceptor).

The efficiency of FRET is dependent on the separation distance and the orientation of the donor fluorescent moiety and acceptor fluorescent moiety, the fluorescent quantum yield of the donor moiety, and the spectral overlap with the acceptor moiety. Forster derived the relationship:

$$E = (F^\circ - F)/F^\circ = Ro^6/(R^6 + Ro^6)$$

where E is the efficiency of FRET, F and F° are the fluorescence intensities of the donor in the presence and absence of the acceptor, respectively, and R is the distance between the donor and the acceptor. Ro, the distance at which the energy transfer efficiency is 50% of maximum is given (in Å) by:

$$Ro = 9.79 \times 10^3(K^2QJn^{-4})^{1/6}$$

where K^2 is an orientation factor having an average value close to 0.67 for freely mobile donors and acceptors, Q is the quantum yield of the unquenched fluorescent donor, n is the refractive index of the intervening medium, and J is the overlap integral, which expresses in quantitative terms the degree of spectral overlap. The characteristic distance Ro at which FRET is 50% efficient depends on the quantum yield of the donor, the extinction coefficient of the acceptor, the overlap between the donor's emission spectrum and the acceptor's excitation spectrum, and the orientation factor between the two fluorophores.

Changes in the degree of FRET can be determined as a function of a change in a ratio of the amount of fluorescence from the donor and acceptor moieties, a process referred to as "ratioing." By calculating a ratio, the assay is less sensitive to, for example, well-to-well fluctuations in substrate concentration, photobleaching and excitation intensity, thus making the assay more robust. This is of particular importance in automated screening applications where the quality of the data produced is important for its subsequent analysis and interpretation.

For example, in some embodiments of the method, a ratiometric analysis is performed, wherein a ratio of fluorescence emission at two different wavelengths is compared between a protease mixture and a control mixture. In a typical FRET-based assay, the two wavelengths can correspond to the emissions maxima for two detectable (e.g., fluorescent) moieties of the composition. Thus, if a composition is a substrate for a kinase, the phosphorylated composition will be less susceptible to cleavage by a protease. Accordingly, the phosphorylated composition will maintain FRET between the donor and acceptor moieties (e.g., the FRET pair), resulting in a low emissions ratio of the donor to the acceptor moiety. A control sample in such a case, however, will be subject to cleavage by the protease. Cleavage disrupts FRET between the donor and acceptor moieties, leading to a larger emissions ratio of the donor to the acceptor moiety. In some embodiments, the emissions ratio of the control mixture will be more than 1.5, 2, 3, 4, 5, 7, 10, 15, 20, 25, 30, 40, 50, or 100 times larger than the emissions ratio of a protease mixture.

The present invention can also be used to determine whether a sample (e.g., a cell, an extract, a purified protein, a tissue, an organism) has general kinase or phosphatase activity or a specific kinase or specific phosphatase activity, e.g., abl-1 kinase activity. The method typically involves contacting a sample with a composition of matter (e.g., under appropriate conditions to enable phosphorylation (or dephosphorylation) of the composition), and then contacting the sample and composition mixture with a protease, e.g., a protease known to cleave the composition in the absence of the post-translational modification. The degree of post-translational modification activity in the sample is assessed, e.g., as described above, such as by monitoring a measurable property of the sample-composition mixture and comparing it to the measurable property of a control mixture.

In some cases, a composition and a protease may be added to a sample at the same time. Alternatively, in the case where a sample contains cells, the method would typically involve stimulation of the cells and then either lysing the cells in the presence of the composition or, in the case where the composition is expressed within the cells, lysing the cells in the presence of a protease to measure composition modification.

One application of the assay is to either introduce or express the composition in living eukaryotic or prokaryotic cells to enable the measurement of intracellular post-translational activities. In one aspect, the method would involve a composition comprising a first fluorescent protein, a peptide containing a motif (e.g., a recognition motif) and a protease site, and a second fluorescent protein fused together as a single polypeptide chain. In this case the first fluorescent protein and the second fluorescent protein would be selected to enable FRET to occur as described above. A pair of functional engineered fluorescent proteins for example would be, Topaz (S65G, S72A, K79R, T203Y) and W1B (F64L, S65T, Y66W, N1461, M153T,V163A), as shown in Table 7 of U.S. Pat. No. 6,410,255.

In another aspect, a method can involve a composition comprising a peptide containing one or more binding sites for a fluorescent moiety, a motif (e.g., a recognition motif), and a protease cleavage site. For example, a binding site could comprise a sequence that recognizes a fluorescent moiety, as described in pending U.S. Patent Appls. Ser. No. 08/955,050, filed October 21, 1997, entitled Methods of Using Synthetic Molecules and Target Sequences; Ser. No. 08/955,859, filed October 21, 1997, entitled Synthetic Molecules that Specifically React with Target Sequences; and Ser. No. 08/955,206, filed October 21, 1997, entitled Target Sequences for Synthetic Molecules. In this case, expression of a peptide comprising a recognition motif, protease cleavage site, and binding site could be accomplished using genetic means as described above. The addition of a membrane-permeable fluorescent moiety capable of binding to the binding site would enable the creation *in situ* of composition according to the present invention.

Another application of the method is to use inducible controlling nucleotide sequences to produce a sudden increase in the expression of either a composition, a kinase or phosphatase, or a protease, e.g., by inducing expression of a construct. A suitable protease could be expressed within a cell, or induced, or introduced using a membrane-translocating sequence (see U.S. patent No. 5,807,746, issued Sept. 15 1998 to Lin et al.) The efficiency of FRET may be typically monitored at one or more time intervals after the onset of increased expression of a protease.

In BRET applications, a composition typically comprises a luminescent moiety and a fluorescent moiety coupled to a peptide such that a motif and protease site are located between them. In this case, cleavage of the peptide by a protease results in an alteration in energy transfer between the luminescent moiety and the fluorescent moiety that may be used to determine kinase or phosphatase activity, as described above. In this case, the luminescent and fluorescent moieties are typically chosen such that the emission spectrum of the luminescent moiety overlaps with the excitation spectrum of the fluorescent moiety. Because a luminescent moiety provides light through a chemiluminescent, electroluminescent, or bioluminescent reaction, there is no requirement for direct light excitation to create the excited state in the luminescent moiety. Instead, appropriate substrates or a voltage must be provided to (or applied to) the luminescent moiety to create an excited state luminescent moiety. In the case of bioluminescent proteins, such substrates are generically referred to as luciferins (for example, see U.S. patent 5,650,289 issued July 22, 1997 to Wood). If BRET occurs, the energy from the excited state of a luminescent moiety is transferred to a fluorescent moiety by non-radiative means, rather than being emitted as light from the luminescent moiety. Because luminescent and fluorescent moieties typically are chosen to emit light at characteristic wavelengths, an emission ratio of the two can also provide a ratiometric readout as described for the FRET based applications above. BRET can be manifested as a reduction in the intensity of a fluorescent signal from the luminescent moiety, a reduction in the lifetime of its excited state, and/or an increase in emission of fluorescence from the fluorescent moiety. When a peptide substrate that connects a luminescent moiety and a fluorescent moiety is cleaved, the luminescent moiety and the fluorescent moiety physically separate, and BRET is diminished or eliminated. Under these circumstances, light emission from the luminescent moiety increases and fluorescence emission from the fluorescent moiety decreases. The efficiency of BRET is typically dependent on the same separation and orientation factors as described above for FRET.

In dark quenching RET applications, a composition typically comprises a first fluorescent moiety (e.g., a donor) and a dark quencher moiety (e.g., acceptor) coupled to the peptide such that a motif and protease site are located between them. In this case, cleavage of the peptide by a protease results in an alteration in energy transfer between the first fluorescent moiety and the dark quencher moiety that may be used to monitor post-translational activity. A fluorescent moiety and dark quencher moiety are typically chosen such that the absorption spectrum of the dark quencher (the acceptor moiety) overlaps with the emission spectrum of the donor fluorescent moiety. The donor fluorescent moiety is excited by light of appropriate intensity within the donor fluorescent moiety's excitation spectrum. The donor fluorescent moiety then transfers the absorbed energy by non-radiative means to the dark quencher, which in this case does not re-emit a substantial amount of the absorbed energy as light (e.g., forming a dark quenching RET pair). Dark quenching RET can be manifested as a reduction in the intensity of a fluorescent signal from a donor or a reduction in the lifetime of its excited state. When a peptide that connects a donor fluorescent moiety and a dark quencher moiety is cleaved, the donor fluorescent moiety and the dark quencher moiety physically separate, and dark quenching RET is diminished or eliminated. Under these circumstances, fluorescence emission from the donor fluorescent moiety increases.

Another mechanism of quenching contemplated in the present invention involves the formation and detection of an excitonic dimer (e.g., static quenching) between a fluorophore and a quencher. Typically, static quenching results when the interaction of a fluorophore with a quencher forms a stable non-fluorescent or weakly fluorescent ground state complex. Since this complex typically has a different absorption spectrum from the fluorophore, the presence of an absorption change is diagnostic of this type of quenching (in contrast, collisional quenching is a transient excited state interaction and therefore does not affect the absorption spectrum). Pure static quenching can reduce the intensity of fluorescence but does not necessarily decrease the measured lifetime of emission.

In magnetic detection-based assays, a composition typically comprises a metal chelate or metal particle, as described above, coupled to a peptide having a motif (e.g., a recognition motif) and a protease site. In these cases, the metal chelate or particle should be chosen to have a characteristic magnetic signal, e.g., T_1, T_2, or R_1, that will change when it is bound or associated with the intact peptide as compared to the cleaved peptide. Cleavage of the peptide by a protease results in an alteration in the magnetic signal that may be used to monitor post-translational activity.

In radio-isotope detection-based assays, a composition typically comprises a radioisotope (e.g., a radiolabel such as ^{32}P, ^{35}S, ^{3}H, ^{14}C or others known to those of skill in the art) coupled to a peptide having a motif (e.g., a recognition motif) and a protease site. In these cases, monitoring of a location of a radiolabel (e.g., in a gel) or monitoring of a size of a cleavage product (e.g., in a gel) before and after proteolytic cleavage provides a method for monitoring post-translational activity.

The assays of the present invention can be used in drug screening assays to identify compounds that alter or modulate a kinase or phosphatase activity. In one embodiment, an assay is performed on a sample *in vitro* (e.g. in a sample isolated from a cell, or a cell lysate, or a purified or partially-purified enzyme) containing an activity for which a drug screen is desired. A sample containing a known amount of activity is contacted with a composition of the invention and with a test compound. The activity of the sample is monitored after addition of a protease, as described above, for example, by monitoring a measurable property of the composition. A measurable property of the sample in the presence of the test compound can be compared with the measurable property of a sample similarly treated in the absence of the test compound (e.g., the control reaction). A difference indicates that the test compound alters the activity. In preferred embodiments, the method is used to evaluate putative inhibitors of a kinase or phosphatase activity.

In another embodiment, an ability of a test compound to alter or to modulate a kinase or phosphatase activity in a cell-based assay may be determined. In these assays, cells transfected with an expression vector encoding a composition of the invention, as described above, are exposed to different amounts of the test compound, and the effect on a measurable property (e.g., an optical property such as FRET or fluorescence polarization) in each cell can be determined after induction or introduction of a suitable protease. Typically, as with any method of the present invention, the change in the measurable property is compared to that of untreated controls.

Any of the methods of the present invention can be modified to be performed in a high-throughput or ultra-high-throughput manner. For example, a method to identify a substrate of a particular kinase or phosphatase may be modified to contact a plurality of compositions (e.g., two or more different compositions), independently, with a particular kinase or phosphatase enzyme, to form a plurality of enzyme mixtures. Each enzyme mixture is treated with a protease, and a measurable property of each protease mixture is monitored and compared to an appropriate control sample. Similarly, a particular composition can be evaluated for its suitability as a substrate of a plurality of kinases or phosphatases (e.g., two or more different kinases or phosphatases). Thus, a particular composition of matter may be contacted, independently, with a plurality of enzymes to form a plurality of enzyme mixtures. Each mixture is treated with a protease and a measurable property of each protease mixture is monitored and compared to an appropriate control sample. As one of skill in the art will appreciate, such high-throughput methods are particularly amenable to multi-well plate or 2-D array panel formats, wherein a plurality of compositions are screened for suitability as substrates for a plurality of different enzymes. See Example 4, below. Devices for incubating and monitoring multi-well plates are known in the art. Similar panel assays may be envisioned for methods to identify modulators of a kinase or phosphatase activity. See Example 3, below.

In another embodiment, a plurality of different compositions of matter may be contacted simultaneously with a single kinase or phosphatase; the reaction mixture may then be contacted with a protease; and a plurality of measurable properties may be monitored and compared to the measurable properties of an appropriate control sample. Typically, each of the compositions of matter comprises a FRET pair having a characteristic excitation wavelength of the donor and emissions ratio of the donor to the acceptor, so that each FRET pair can be tracked independently of the others. An appropriate control sample would include the plurality of compositions of matter treated with the protease in the absence of the kinase, phosphatase, and/or ATP. As one of skill in the art will recognize, other measurable properties can be similarly monitored to facilitate the use of such a method with detectable moieties for dark quenching RET and magnetic detection applications.

Alternatively, arrays of compositions having known recognition motifs may be created in order to create an activity profile of kinase or phosphatase activities in a sample. In this case, screening of the array is used to characterize the activities within a sample by incubating the array with a sample containing the activities, adding an appropriate protease, and then monitoring a measurable property from each member of the array. Those array members that are more efficiently modified after exposure to the sample may be identified by the degree to which the measurable property of that array member is altered as compared to the appropriate control samples.

The dynamic range, quality, and robustness of the methods of the present invention can be evaluated statistically. For example, the Z′-Factor is a statistic designed to reflect both assay signal dynamic range and the variation associated with signal measurements. Signal-to-noise (S/N) or signal-to-background (S/B) ratios alone are unsatisfactory in this regard because they do not take into account the variability in sample and background measurements and signal dynamic range. The Z′-Factor takes into account these factors, and because it is dimensionless, it can be used to compare similar assays. The relationship of Z'-factor values to assay quality are summarized in Table 6, below. Typically, assays of the present invention yield Z'-factors of greater than or equal to 0.5.

A Z'-factor may be determined by evaluating the dynamic range of a method. In some embodiments, the dynamic range may be defined by 0% inhibition and 100% inhibition controls. A 0% inhibition control is performed by contacting a composition of the present invention with a kinase and ATP to form a kinase mixture, contacting the kinase mixture with a protease to form a protease mixture, and monitoring a measurable property of the protease mixture. A measurable property can be an emissions ratio, such as the ratio of coumarin emission at 445 nm to fluorescein emission at 520 nm. Typically, the reaction conditions of the kinase reaction are chosen to phosphorylate about 10-40% of the composition in a predetermined time period (e.g., 30 mins., 1 hr., 2 hr., or 4 hr.). The % phosphorylation of a sample can be calculated by using the following equation:

$$\textbf{\% Phosphorylation} = \mathbf{1 - [((\text{Emission Ratio} \times Fc) - Fa) / ((Fb - Fa) + (\text{Emission Ratio} \times (Fc - Fd)))]}$$

where Emission Ratio is the ratio of donor emission signal to acceptor emission signal, as indicated above; Fa is the average donor emission signal of the 100% phosphorylation control; Fb is the average donor emission signal of the 0% phosphorylation control; Fc is the average acceptor emission signal of the 100% phosphorylation control; and Fd is the average acceptor emission signal of the 0% phosphorylation control.

The 100% inhibition control is performed similarly, but in the absence of ATP (100% inhibition of the kinase), to yield 0% phosphorylated composition. A 100% phosphorylated composition can also be included as a control. Both 0% and 100% inhibition controls can be performed in duplicate. The Z'-factor is then calculated as follows:

$$\textbf{Z'-factor} = (1 - (3 \times \sigma 0\%\ \text{inhibition}) + (3 \times \sigma 100\%\ \text{inhibition})) / (\mu\ \text{of}\ 100\%\ \text{inhibition} - \mu\ \text{of}\ 0\%\ \text{inhibition})$$

Table 6

Z'-factor value	**Relation to Assay Quality**
1	Excellent Assay
$1 > Z' \geq 0.5$	An excellent assay
$0.5 > Z' > 0$	A double assay
0	A "yes/no" type assay
< 0	Assay unreliable

The methods of the present invention can be used with various systems for spectroscopic measurement. In one embodiment, the system comprises 1) a reagent for an assay and 2) a device comprising at least one plate (e.g., a multi-well plate) or container and a platform, such as a multi-well plate platform, e.g., for incubating and/or detecting a signal from the plate or container. The system can further comprise a detector, such as a detector appropriate for detecting a signal from a sample or a plate. The system can comprise multiple plates or containers or multi-well platforms. In this context, a reagent for an assay includes any reagent useful to perform biochemical or biological *in vitro* or *in vivo* testing procedures, such as, for example, buffers, co-factors, proteins such as enzymes or proteases, carbohydrates, lipids, nucleic acids, active fragments thereof, organic solvents such as DMSO, chemicals (e.g., ATP), analytes, therapeutics, compositions, cells, antibodies, ligands, and the like. In this context, an active fragment is a portion of a reagent that has substantially the activity of the parent reagent.

The compositions of the present invention are suited for use with systems and methods that utilize automated and integratable workstations for identifying substrates and modulators of kinase or phosphatase activity. Such systems are described generally in the art (see U.S. Patent Nos. 4,000,976 to Kramer et al. (issued January 4, 1977), 5,104,621 to Host et al. (issued April 14, 1992), 5,125,748 to Bjornson et al. (issued June 30, 1992), 5,139,744 to Kowalski (issued August 18, 1992), 5,206,568 to Bjornson et al. (issued April 27, 1993), 5,350,564 to Mazza et al. (September 27, 1994), 5,589,351 to Harootunian (issued December 31, 1996), and PCT Application Nos. WO 93/20612 to Baxter Deutschland GMBH (published October 14, 1993), WO 96/05488 to McNeil et al. (published February 22, 1996), WO 93/13423 to Agong et al. (published July 8, 1993) and PCT/US98/09526 to Stylli et al., filed May 14, 1998).

For some embodiments of the invention, particularly for plates with 96, 192, 384 ,864 and 3456 wells per plate, detectors are available for integration into the system. Such detectors are described in U.S. Patent 5,589,351 (Harootunian), U.S. Patent 5,355,215 (Schroeder), and PCT patent application WO 93/13423 (Akong). Alternatively, an entire plate may be "read" using an imager, such as a Molecular Dynamics FluorImager 595 (Sunnyvale, CA). Multi-well platforms having greater than 864 wells, including 3,456 wells, can also be used in the present invention (see, for example, PCT Application PCT/US98/11061, filed 6/2/98).

In another embodiment, the system may comprise a two dimensional array of compositions dispersed on a substratum (e.g., a multi-well plate), for example as described in U.S. patents Nos. 4,216,245 issued August 5, 1980 to Johnson, 5,721,435 issued February 24, 1998 to Troll, and 5,601,980 issued February 11, 1997 issued to Gordon et al. Such a system provides the ability to rapidly profile large numbers of compositions and or large numbers of samples in a simple, miniaturized high throughput format.

The present invention also provides articles of manufacture, such as kits. Typically, a kit includes a container and a composition of matter of the present invention. In some embodiments, a kit can include one or more of the following: a multi-well plate, a protease, one or more enzymes (kinase or phosphatase enzymes), buffers, a source of ATP, and directions for use of the kit. A kit can be useful for determining substrates of kinase or phosphatase activity or for identifying a modulator of a kinase or phosphatase activity.

EXAMPLES

Example 1 – Determination of Kinase Kinetic Parameters with Kinase Substrates

a. Determination of kinetic parameters for Akt 1 kinase, a serine/threonine kinase

ATP was serially diluted in a Corning 384-well round bottom non-binding surface plate. A substrate for Akt 1, SEQ ID NO: 59 modified by having a 7-hydroxycoumarin moiety conjugated to the ε-NH2 of the C-terminal lysine and a 5-FAM moiety conjugated to an N-terminal GABA linker, prepared as described in U.S. Pat. No. 6,410,255, was mixed with Akt 1 kinase and added to the ATP dilutions. The final concentration of SEQ ID NO: 59 was 2 μM in each well; the final concentration of Akt1 was 16 nM. The plates were allowed to incubate at room temperature for 1 hour. Chymotrypsin was then added to each well (final concentration 100 ng/ml) and the plates allowed to incubate for 1 hour at room temperature. The plate was read using a TECAN SAFIRE™ monochromator-based fluorescence plate reader (Excitation at 400 nm (12 nm bandwidth); Emission at 445 nm (12 nm bandwidth); and Emission at 520 nm (12 nm bandwidth). Curve fitting and data presentation were performed using Prism™ software from GraphPad Software, Inc. The apparent Km was 15 μM.

b. Determination of kinetic parameters for Abl 1 kinase, a tyrosine kinase

ATP was serially diluted (0.8 μM to 100 μM) in a Corning 384-well round bottom non-binding surface plate. A substrate for Abl 1, SEQ ID NO: 3 modified by having a 7-hydroxycoumarin moiety conjugated to the ε-NH2 of the C-terminal lysine and a 5-FAM moiety conjugated to an N-terminal GABA linker, prepared as described in U.S. Pat. No. 6,410,255, was mixed with Abl 1 kinase and added to the ATP dilutions. The final concentration of SEQ ID NO: 3 was 2 μM in each well; the final concentration of Abl-1 was 16 nM. The plates were allowed to incubate at room temperature for 1 hour. Chymotrypsin was then added to each well (final concentration 1.25 ng/ml) and the plates allowed to incubate for 1 hour at room temperature. The plate was read using a TECAN SAFIRE™ monochromator-based fluorescence plate reader (Excitation at 400 nm (12 nm bandwidth); Emission at 445 nm (12 nm bandwidth); and Emission at 520 nm (12 nm bandwidth). Curve fitting and data presentation were performed using Prism™ software from GraphPad Software, Inc. As can be seen from FIG. 3, the Vmax of Abl 1 kinase with SEQ ID NO: 3 is 7%, corresponding to 0.02 pmol/min, and the apparent Km is 7 μM. See FIG. 3.

Example 2 – Dependence of Percent Phosphorylation on Kinase Concentration and Evaluation of Z'-Factor Values

a. Akt 1

Akt 1 kinase was serially diluted in a 384 well plate (final concentration ranging from 156 ng/ml to 20,000 ng/ml). Kinase reactions were initiated by the addition of a solution of Akt 1 substrate, SEQ ID NO: 59 (modified as described in Example 1a above; 2 μM final concentration), and ATP (15 μM final concentration). The plates were allowed to incubate at room temperature for 1 hour. Chymotrypsin was then added to each well (final concentration 100 ng/ml) and the plates allowed to incubate for 1 hour at room temperature. The plate was read using a TECAN SAFIRE™ monochromator-based fluorescence plate reader (Excitation at 400 nm (12 nm bandwidth); Emission at 445 nm (12 nm bandwidth); and Emission at 520 nm (12 nm bandwidth). Curve fitting and data presentation were performed using Prism™ software from GraphPad Software, Inc.

% phosphorylation data are set forth in FIG. 4. Z'-factor values for varying kinase concentrations and % phosphorylation of the substrate are demonstrated in Table 7 below. High Z'-factor values are seen when even as little as 10% of the substrate is phosphorylated.

Table 7: Z'-Factor Values for Akt 1

ng Akt 1 kinase per well	% Phosphorylation	Z'-factor value
5.0	8	0.78
10.0	12	0.88
25.0	20	0.91
37.5	28	0.92
42.0	30	0.92
50.0	33	0.93
75.0	38	0.93
100.0	43	0.92
150.0	50	0.90

b. Abl 1

Abl 1 kinase was serially diluted in a 384 well plate (final concentration ranging from 4.9 ng/ml to 10,000 ng/ml). Kinase reactions were initiated by the addition of a solution of Abl 1 substrate, SEQ ID NO: 3 (modified as described in Example 1b above; 2 μM final concentration), and ATP (7 μM final concentration). The plates were allowed to incubate at room temperature for 1 hour. Chymotrypsin was then added to each well and the plates allowed to incubate for 1 hour at room temperature. The plate was read using a TECAN SAFIRE™ monochromator-based fluorescence plate reader (Excitation at 400 nm (12 nm bandwidth); Emission at 445 nm (12 nm bandwidth); and Emission at 520 nm (12 nm bandwidth). Curve fitting and data presentation were performed using Prism™ software from GraphPad Software, Inc.

% phosphorylation data are set forth in FIG. 5. Z'-factor values for varying kinase concentrations and % phosphorylation of the substrate are demonstrated in Table 8 below. High Z'-factor values are seen when even as little as 10% of the substrate is phosphorylated.

Table 8: Z'-Factor Values for Abl 1 Assay

ng Abl 1 kinase per well	% Phosphorylation	Z'-factor value
0.50	10	0.72
0.75	15	0.79
1.00	23	0.84
1.30	30	0.85
1.50	35	0.86
2.00	46	0.93
2.50	53	0.94
3.00	61	0.94
3.50	79	0.95

c. PKA and PKCα Kinases

Experiments similar to those outlined above were performed for 8 compositions of matter (SEQ ID NOs: 47, 50, 43, 58, 59, 60, 63, and 68) against PKA and PKCα. FIG. 8 demonstrates the % phosphorylation by the serine/threonine kinase PKA of the 8 compositions against which it was screened. As shown, SEQ ID NO: 47 modified as described, is the best substrate for the kinase because it yielded maximal phosphorylation even at low kinase concentrations.

FIG. 9 demonstrates the % phosphorylation by PKCα of the 8 compositions against which it was screened. As shown, only SEQ ID NO: 60 modified as described, is phosphorylated by this S/T kinase.

Example 3 – Identifying Modulators of Kinase Activity

a. Abl 1 (Tyrosine kinase) Inhibitors

Two test compounds (Staurosporine and Genistein, available from Calbiochem) were evaluated for their ability to inhibit phosphorylation of an Abl 1 substrate (SEQ ID NO: 3, modified as described in Example 1b above) by Abl 1. Serial dilutions of the respective test compound (final concentration ranging from 0.3 to 500,000 nM) were dispensed in 384 well plates. 5 μL of an Abl 1 kinase/Abl 1 substrate solution (final concentration of 1.5 ng Abl 1/well and 2 μM of Abl 1 substrate/well) were added to each well, along with 2.5 μL of ATP (final concentration of 10 μM). The plate was mixed and incubated for 1 hour at room temperature. 5 μL of chymotrypsin were added to each well (final concentration of 1 μg/mL), and the plate mixed and allowed to incubate at room temperature for 1 hour. The plate was read using a TECAN SAFIRE™ monochromator-based fluorescence plate reader (Excitation at 400 nm (12 nm bandwidth); Emission at 445 nm (12 nm bandwidth); and Emission at 520 nm (12 nm bandwidth). Curve fitting and data presentation were performed using Prism™ software from GraphPad Software, Inc.

The dynamic range of the Abl 1 assay was defined by performing 0% and 100% inhibition controls. The 0% inhibition control phosphorylated 30% of the Abl 1 substrate, while the 100% inhibition control was a kinase reaction done in the absence of ATP, resulting in nonphosphorylated Abl 1 substrate. As a nonphosphorylated Abl1 substrate is cleaved completely by chymotrypsin, it will exhibit a loss of FRET and a concomitant increase in the Emissions ratio at 445 nm (coumarin)/520 nm (fluorescein).

FIG. 6 demonstrates the inhibition curves by Staurosporine and Genistein for phosphorylation of the Abl 1 substrate by Abl 1. An IC_{50} value is defined as the inhibitor concentration that produces a half-maximal shift in the same Emissions ratio. Error bars on FIG. 6 represent one standard deviation from the mean of three replicates. As can be seen from FIG. 6, the IC_{50} is 33 nM for Staurosporine and 4.1 μM for Genistein.

b. Akt 1 (Serine/Threonine kinase) Inhibitors

Two test compounds (Staurosporine and Ro-31-8220 (available from Calbiochem) were evaluated for their ability to inhibit phosphorylation of an Akt 1 substrate (SEQ ID NO: 59, modified as described in Example 1a above) by Akt 1. Serial dilutions of the respective test compound (final concentration ranging from 0.019 to 50,000 nM) were dispensed in 384 well plates. 5 μL of an Akt 1 kinase/Akt 1 substrate solution (final concentration of 42 ng Akt 1/well and 2 μM of Akt 1 substrate/well were added to each well, along with 2.5 μL of ATP (final concentration of 10.5μM). The plate was mixed and incubated for 1 hour at room temperature. 5 μL of chymotrypsin were added to each well (final concentration of 100 ng/mL), and the plate mixed and allowed to incubate at room temperature for 1 hour. The plate was read using a TECAN SAFIRE™ monochromator-based fluorescence plate reader (Excitation at 400 nm (12 nm bandwidth); Emission at 445 nm (12 nm bandwidth); and Emission at 520 nm (12 nm bandwidth). Curve fitting and data presentation were performed using Prism™ software from GraphPad Software, Inc.

The dynamic range of the Akt 1 assay was defined by performing 0% and 100% inhibition controls. The 0% inhibition control phosphorylated 30% of the Akt 1 substrate, while the 100% inhibition control was a kinase reaction done in the absence of ATP, resulting in nonphosphorylated Akt 1 substrate. As a nonphosphorylated Akt 1 substrate is cleaved completely by chymotrypsin, it will exhibit a loss of FRET and a concomitant increase in the Emissions ratio at 445 nm (coumarin)/520 nm (fluorescein).

FIG. 7 demonstrates the inhibition curves by Staurosporine and Ro-31-8220 for phosphorylation of the Akt 1 substrate by Akt 1. An IC_{50} value is defined as the inhibitor concentration that produces a half-maximal shift in the same Emissions ratio. Error bars on FIG. 7 represent one standard deviation from the mean of three replicates. As can be seen from FIG. 7, the IC_{50} is 17.2 nM for Staurosporine and 408 nM for Ro-31-8220.

The experiment was repeated using 15 μM ATP and 3 ng/well Akt 1 and was also successful.

Example 4 – Panel Assays for Evaluating Substrates for Kinases

Compositions are screened against S/T and Y kinases in a series of multi-well (96 or 384 well) plate formats to evaluate their suitability as substrates for serine/threonine kinases and/or tyrosine kinases. Each composition has a 7-hydroxycoumarin moiety conjugated to the ε-NH2 of the C-terminal lysine and a 5-FAM moiety conjugated to an N-terminal GABA linker.

The following kinases are screened: Akt1, Akt2, Akt3, Aurora A, CaMKII, CDK2/CycA, CDK3/CycE, CDK7/CycH, MAPKAP-K1α, MAPKAP-K1β, MAPKAP-K1γ, MSK1, PAK2, PKA, PKG, ROCK, ROCK2, CDK2/CycA, CDK3/CycE, ERK1, ERK2, IKKα, IKKβ, p38β, p38γ, p38δ, REDK, AMPK, CDK6, MAPKAP-K2, MAPKAP-K3, MAPKAP-K5, SGK1, PIM1, CHK1, CHK2, PKCα, PKCβI, PKCβII, PKCγ, PKCδ, PKCε, PKCζ, PKCη, PKCθ, PKCι, and p70 S6 Kinase, Abl1, Abl2, BMX, CSF1R, Csk, EphB4, Fes/Fps, FGFR1, FGFR4, Fgr, FLT3, Fyn, Hck, IGF1R, IRKβ, ITK, Jak3, KDR, c-KIT, Lck, Lyn A, Lyn B, c-MET, Src, Src N1, Src N2, SYK, TIE2, TRKa, YES, CK1δ, IKKα, IKKβ, IRTK, CDK1, CDK5/p35, MEK1, MEK5, MEK2, MKK3, MKK4, MKK7, RAF1, GSK3α, GSK3β, MEKK1, CK1δ, CK-1α, CKIIα, JNK1, JNK2, JNK3, and EGFR.

A 384 multiwell plate defines a matrix as follows: each of columns 1-20 of the plate correspond to a particular kinase, while rows 1-16 in each kinase column correspond to duplicate samples of 8 different compositions of matter that are potential kinase substrates. Columns 21-24 correspond to control columns, representing 0% phosphorylated controls (100% inhibition of kinase, no ATP), and 100% phosphorylated control (e.g., synthetic phosphorylated composition). For a set of 20 kinases, 5 μl of 2x final concentration of each kinase are dispensed to each row of the respective kinase column of the plate. 5 μL of kinase buffer are added to control columns 21-24. Each of the compositions of matter and ATP are then added to the appropriate rows of each kinase column to result in a final concentration of 2 μM composition/0.8 μM ATP per well; these samples are prepared in duplicate. The compositions of matter are also added to the appropriate rows of control columns 23 and 24 to result in a final concentration of 2 μM unphosphorylated composition. Phosphorylated compositions of matter are added to the appropriate rows of columns 21 and 22 to result in a final concentration of 2 μM phosphorylated composition. The plate is then mixed on a shaker and incubated for 1 hour at room temperature to allow kinase reactions to proceed. 5 μL of chymotrypsin are then added to each well. The plate is mixed on a plate shaker and incubated for 1 hour at room temperature. The plate is read using a TECAN SAFIRE™ monochromator-based fluorescence plate reader (Excitation at 400 nm (12 nm bandwidth); Emission at 445 nm (12 nm bandwidth); and Emission at 520 nm (12 nm bandwidth). Similar assays with varying kinase concentrations are also performed.

Example 5 – Phosphatase Assays

8 compositions of matter were screened against 6 phosphatases to evaluate their suitability as substrates for phosphatases. The compositions corresponded to SEQ ID NOs: 31, 97, 100, 103, 109, 110, 113, and 118, with each peptide having a 7-hydroxycoumarin moiety conjugated to the ε-NH2 of the C-terminal lysine and a 5-FAM

moiety conjugated to an N-terminal GABA linker. The following phosphatases were used PP1α, PP2A, PP2B, PP2C, PTP1B, and LAR.

Each composition was diluted to 4 μM using the appropriate phosphatase buffer for each of the phosphatases. Each of the phosphatases was diluted by serially titrating (each dilution a 2-fold reduction in phosphatase concentration) using the appropriate phosphatase buffer (as recommended by the vendor). The volume of each phosphatase dilution was 5 μl. 5 μl of each 4 μM composition was added to each serial dilution of each phosphatase. The samples were mixed on a plate shaker for 60 seconds and incubated at room temperature for one hour. Reactions were performed in duplicate. After the one hour phosphatase reaction, 5 μl of chymotrypsin was added to each reaction. The plate was mixed on a plate shaker and incubated for 1 hour at room temperature. The plate was then read using a TECAN SAFIRE™ monochromator-based fluorescence plate reader (Excitation at 400 nm (12 nm bandwidth); Emission at 445 nm (12 nm bandwidth); and Emission at 520 nm (12 nm bandwidth) to evaluate whether any of the compositions were substrates of any of the phosphatases. Appropriate controls for each composition and phosphatase were prepared, corresponding to: the nonphosphorylated version of the composition (untreated); the nonphosphorylated version of the composition treated with phosphatase only; the nonphosphorylated version of the composition treated with chymotrypsin only; the nonphosphorylated composition treated with both phosphatase and chymotrypsin; the phosphorylated composition (untreated); the phosphorylated composition treated with phosphatase alone; and the phosphorylated composition treated with chymotrypsin only.

The results indicated that SEQ ID NOs: 100, 109, and 110 were substrates of PP1α. Similarly, SEQ ID NOs: 103, 109, 110, and 113 were substrates of PP2A; SEQ ID NOs: 100 and 110 were substrates of PP2B; SEQ ID NOs: 100, 109, and 110 were substrates of PP2C; and SEQ ID NO: 31 was a substrate for both PTP1B and LAR.

A number of embodiments of the invention have been described. Nevertheless, it will be understood that various modifications may be made without departing from the spirit and scope of the invention. Accordingly, other embodiments are within the scope of the following claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i)APPLICANT: Invitrogen Corporation

(ii) TITLE OF INVENTION: Kinase and Phosphatase Assays

(iii) NUMBER OF SEQUENCES: 167

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MBM & CO.
(B) STREET: P.O. BOX 809, STATION B
(C) CITY: OTTAWA
(D) PROVINCE: ONTARIO
(E) COUNTRY: CANADA
(F) POSTAL CODE: K1P 5P9

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: Windows NT Ver. 4.0
(D) SOFTWARE: MSWord 97

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 2,445,420
(B) FILING DATE: 2003-10-31
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/490,771
(B) FILING DATE: 2003-07-29
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: SWAIN, Margaret
(B) REGISTRATION NUMBER: 10926
(C) REFERENCE/DOCKET NUMBER: 198d-107

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 613/567-0762
(B) TELEFAX: 613/563-7671

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid

```
            (C) STRANDEDNESS:
            (D) TOPOLOGY:

     (ii) MOLECULE TYPE: protein

     (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Artificial Sequence
             (F) TISSUE TYPE:

     (ix) FEATURE:
            (A) NAME/KEY:
            (B) LOCATION:
            (C) IDENTIFICATION METHOD:
            (D) OTHER INFORMATION: Exemplary motif

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Ile Tyr Ala Ala
 1              5

(2) INFORMATION FOR SEQ ID NO:2:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 7 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY:

     (ii) MOLECULE TYPE: protein

     (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Artificial Sequence
             (F) TISSUE TYPE:

     (ix) FEATURE:
            (A) NAME/KEY:
            (B) LOCATION:
            (C) IDENTIFICATION METHOD:
            (D) OTHER INFORMATION: Exemplary motif

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Ala Ile Tyr Ala Ala Pro
 1              5

(2) INFORMATION FOR SEQ ID NO:3:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 12 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY:
```

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Glu Ala Glu Ala Ile Tyr Ala Ala Pro Gly Asp Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Gln Asp Tyr Leu Ser
 1               5
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Asp Gln Asp Tyr Leu Ser Leu
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Asp Gln Asp Tyr Leu Ser Leu Asp Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Glu Ile Tyr Gly Val
 1              5
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Glu Glu Ile Tyr Gly Val Ile
 1              5
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:

(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu Glu Glu Ile Tyr Gly Val Ile Glu Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: Variant
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Gly, Ala, or Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Thr Xaa Tyr Val Ala
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```
Leu Thr Gly Tyr Val Ala Arg
 1               5
```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```
Ile Thr Ala Tyr Val Ala Thr
 1               5
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

```
     (ix) FEATURE:
           (A) NAME/KEY:
           (B) LOCATION:
           (C) IDENTIFICATION METHOD:
           (D) OTHER INFORMATION: Exemplary motif

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ile Thr Glu Tyr Val Ala Thr
 1               5

(2) INFORMATION FOR SEQ ID NO:14:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 11 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY:

     (ii) MOLECULE TYPE: protein

     (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Artificial Sequence
            (F) TISSUE TYPE:

     (ix) FEATURE:
           (A) NAME/KEY:
           (B) LOCATION:
           (C) IDENTIFICATION METHOD:
           (D) OTHER INFORMATION: Exemplary motif

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Gly Val Leu Thr Gly Tyr Val Ala Arg Arg Lys
 1               5                  10

(2) INFORMATION FOR SEQ ID NO:15:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 12 amino acids
           (B) TYPE: amino acid
           (C) STRANDEDNESS:
           (D) TOPOLOGY:

     (ii) MOLECULE TYPE: protein

     (vi) ORIGINAL SOURCE:
            (A) ORGANISM: Artificial Sequence
            (F) TISSUE TYPE:

     (ix) FEATURE:
           (A) NAME/KEY:
           (B) LOCATION:
```

(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Asp Asp Glu Ile Thr Ala Tyr Val Ala Thr Arg Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
Thr Gly Ile Ile Thr Glu Tyr Val Ala Thr Arg Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Glu Glu Tyr Ile Gln
 1              5
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Glu Glu Glu Tyr Ile Gln Ile
 1              5
```

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

```
Glu Glu Glu Glu Tyr Ile Gln Ile Val Lys
```

1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```
Asp Tyr Ser Gln Val
 1               5
```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```
Gly Asp Tyr Ser Gln Val Leu
 1               5
```

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```
Glu Gly Asp Tyr Ser Gln Val Leu Glu Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ala Ile Tyr Ala Ala

1 5

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```
Glu Ala Ile Tyr Ala Ala Pro
 1               5
```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Glu Ala Glu Ala Ile Tyr Ala Ala Pro Gly Asp Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```
Gln Asp Tyr Leu Ser
 1               5
```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Asp Gln Asp Tyr Leu Ser Leu
 1               5
```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Gly Asp Gln Asp Tyr Leu Ser Leu Asp Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:29:

```
     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 5 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

    (ii) MOLECULE TYPE: protein

    (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

    (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif

    (ix) FEATURE:
          (A) NAME/KEY: MOD_RES
          (B) LOCATION: 3
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: phosphorylated Tyr

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Glu Ile Tyr Gly Val
 1               5

(2) INFORMATION FOR SEQ ID NO:30:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 7 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

    (ii) MOLECULE TYPE: protein

    (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

    (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif

    (ix) FEATURE:
          (A) NAME/KEY: MOD_RES
          (B) LOCATION: 4
          (C) IDENTIFICATION METHOD:
```

(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```
Glu Glu Ile Tyr Gly Val Ile
 1               5
```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
Glu Glu Glu Ile Tyr Gly Val Ile Glu Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:

(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Gly, Ala, or Glu

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Thr Xaa Tyr Val Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
Leu Thr Gly Tyr Val Ala Arg
 1               5
```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```
Ile Thr Ala Tyr Val Ala Thr
 1               5
```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES

(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```
Ile Thr Glu Tyr Val Ala Thr
 1              5
```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```
Gly Val Leu Thr Gly Tyr Val Ala Arg Arg Lys
 1              5                   10
```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 7
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```
Asp Asp Glu Ile Thr Ala Tyr Val Ala Thr Arg Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 7
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```
Thr Gly Ile Ile Thr Glu Tyr Val Ala Thr Arg Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```
Glu Glu Tyr Ile Gln
 1               5
```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

```
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Glu Glu Glu Tyr Ile Gln Ile
 1               5

(2) INFORMATION FOR SEQ ID NO:41:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 10 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

    (ii) MOLECULE TYPE: protein

    (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

    (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif

    (ix) FEATURE:
          (A) NAME/KEY: MOD_RES
          (B) LOCATION: 5
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: phosphorylated Tyr

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Glu Glu Glu Glu Tyr Ile Gln Ile Val Lys
 1               5                   10

(2) INFORMATION FOR SEQ ID NO:42:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 5 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

    (ii) MOLECULE TYPE: protein

    (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

    (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
```

(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
Asp Tyr Ser Gln Val
 1              5
```

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
Gly Asp Tyr Ser Gln Val Leu
 1              5
```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
Glu Gly Asp Tyr Ser Gln Val Leu Glu Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```
Arg Arg Xaa Xaa Leu
 1               5
```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```
Leu Arg Arg Phe Ser Leu Gly
 1               5
```

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```
Ala Leu Arg Arg Phe Ser Leu Gly Glu Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```
Leu Xaa Xaa Thr Thr
 1               5
```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence

(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```
Gly Leu Phe Ser Thr Thr Pro
 1               5
```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```
Arg Gly Gly Leu Phe Ser Thr Thr Pro Gly Gly Thr Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:

(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```
Xaa Leu Xaa Leu Asp
 1               5
```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```
Asp Tyr Leu Ser Leu Asp Lys
 1               5
```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```
Gly Asp Gln Asp Tyr Leu Ser Leu Asp Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Val, Ala, or Gln

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3, 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: VARIANT

(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 6, 7, 8
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Val or Leu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```
Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5
```

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

```
Asn Arg Val Phe Ser Val Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
  (A) NAME/KEY:
  (B) LOCATION:
  (C) IDENTIFICATION METHOD:
  (D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

```
Pro Arg Ala Phe Ser Val Gly
 1               5
```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 7 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS:
  (D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: Artificial Sequence
  (F) TISSUE TYPE:

(ix) FEATURE:
  (A) NAME/KEY:
  (B) LOCATION:
  (C) IDENTIFICATION METHOD:
  (D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
Arg Arg Gln Phe Ser Leu Arg
 1               5
```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 10 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS:
  (D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: Artificial Sequence
  (F) TISSUE TYPE:

(ix) FEATURE:
  (A) NAME/KEY:

(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
Lys Leu Asn Arg Val Phe Ser Val Ala Cys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```
Ala Arg Pro Arg Ala Phe Ser Val Gly Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
Arg Arg Arg Gln Phe Ser Leu Arg Arg Lys Ala Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
Thr Xaa Ser Xaa Leu
 1               5
```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
Arg Thr Phe Ser Ser Leu Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
Arg Pro Arg Thr Phe Ser Ser Leu Ala Glu Gly Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Pro or Ile

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2, 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Gly, Lys, or Asp

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 6, 7, 8
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa
 1               5
```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:

(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```
Ala Pro Phe Ser Pro Gly Gly
 1               5
```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
His Pro Phe Ser Pro Lys Lys
 1               5
```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
Lys Ile Phe Ser Pro Asp Val
 1               5
```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```
Val Ala Pro Phe Ser Pro Gly Gly Arg Ala Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```
Ala Lys His Pro Phe Ser Pro Lys Lys Ala Lys
```

1 5 10

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Ile Ile Lys Ile Phe Ser Pro Asp Val Glu Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Pro or Ile

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3, 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ala, Glu, or Gln

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 5, 6, 7
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Tyr or His

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```
Glu Phe Thr Ala Tyr Val Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
Ile Phe Thr Glu Tyr Val Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
Val Phe Thr Gln His Val Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
Asp Asp Glu Phe Thr Ala Tyr Val Ala Thr Arg Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```
Thr Gly Ile Phe Thr Glu Tyr Val Ala Thr Arg Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Thr Gly Val Phe Thr Gln His Val Ala Thr Arg Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ile Xaa Xaa Ile Ala Asn
1 5

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```
Arg Ile Phe Ser Ile Ala Asn Ser
 1               5
```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
Gln Arg Ile Phe Ser Ile Ala Asn Ser Ile Val Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
Ser Ile Ala Xaa Xaa Ile
 1               5
```

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
Asp Ser Ile Ala Phe Ser Ile Val
 1               5

(2) INFORMATION FOR SEQ ID NO:83:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 12 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

    (ii) MOLECULE TYPE: protein

    (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

    (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Arg Ile Asp Ser Ile Ala Phe Ser Ile Val Gly Lys
 1               5                  10

(2) INFORMATION FOR SEQ ID NO:84:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 6 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

    (ii) MOLECULE TYPE: protein

    (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

    (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif

    (ix) FEATURE:
          (A) NAME/KEY: VARIANT
          (B) LOCATION: 1
          (C) IDENTIFICATION METHOD:
```

(D) OTHER INFORMATION: Xaa = Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
Xaa Val Pro Pro Ser Pro
 1              5
```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
Phe Ser Val Pro Pro Ser Pro Asp
 1              5
```

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Artificial Sequence
    (F) TISSUE TYPE:

(ix) FEATURE:
    (A) NAME/KEY:
    (B) LOCATION:
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
    (A) NAME/KEY: MOD_RES
    (B) LOCATION: 9
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```
Pro Arg Pro Phe Ser Val Pro Pro Ser Pro Asp Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 8 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Artificial Sequence
    (F) TISSUE TYPE:

(ix) FEATURE:
    (A) NAME/KEY:
    (B) LOCATION:
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
    (A) NAME/KEY: VARIANT
    (B) LOCATION: 2
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Xaa = Ala or Glu

(ix) FEATURE:
    (A) NAME/KEY: VARIANT
    (B) LOCATION: 3, 4
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
    (A) NAME/KEY: VARIANT
    (B) LOCATION: 5
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: phosphorylated Ser

(ix) FEATURE:
    (A) NAME/KEY: VARIANT
    (B) LOCATION: 6, 7, 8
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Xaa = Ile or Gln

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```
Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5
```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 7 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Artificial Sequence
    (F) TISSUE TYPE:

(ix) FEATURE:
    (A) NAME/KEY:
    (B) LOCATION:
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```
Glu Asp Ala Phe Ser Ile Ile
 1               5
```

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 7 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```
Glu Asp Glu Phe Ser Gln Asn
 1               5
```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```
Glu Glu Asp Ala Phe Ser Ile Ile Gly Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```
Arg Glu Asp Glu Phe Ser Gln Asn Glu Glu Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, Tyr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```
Asp Xaa Xaa Gln Val
 1               5
```

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```
Glu Gly Asp Tyr Ser Gln Val
 1               5
```

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

```
Glu Gly Asp Tyr Ser Gln Val Leu Glu Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = phosphorylated Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

```
Arg Arg Xaa Xaa Leu
 1              5
```

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5

(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

```
Leu Arg Arg Phe Ser Leu Gly
 1              5
```

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

```
Ala Leu Arg Arg Phe Ser Leu Gly Glu Lys
 1              5                   10
```

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
    (A) NAME/KEY:
    (B) LOCATION:
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
    (A) NAME/KEY: VARIANT
    (B) LOCATION: 2
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
    (A) NAME/KEY: MOD_RES
    (B) LOCATION: 3
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Xaa = phosphorylated Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```
Leu Xaa Xaa Thr Thr
 1               5
```

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 7 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Artificial Sequence
    (F) TISSUE TYPE:

(ix) FEATURE:
    (A) NAME/KEY:
    (B) LOCATION:
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
    (A) NAME/KEY: MOD_RES
    (B) LOCATION: 4
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```
Gly Leu Phe Ser Thr Thr Pro
 1               5
```

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```
Arg Gly Gly Leu Phe Ser Thr Thr Pro Gly Gly Thr Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = phosphorylated Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```
Xaa Leu Xaa Leu Asp
 1               5
```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```
Asp Tyr Leu Ser Leu Asp Lys
 1               5
```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 7
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```
Gly Asp Gln Asp Tyr Leu Ser Leu Asp Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Val, Ala, or Gln

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3, 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 6, 7, 8
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Val or Leu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```
Arg Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5
```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Asn Arg Val Phe Ser Val Ala

1 5

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

```
Pro Arg Ala Phe Ser Val Gly
 1               5
```

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

```
Arg Arg Gln Phe Ser Leu Arg
 1               5
```

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 7
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

```
Lys Leu Asn Arg Val Phe Ser Val Ala Cys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 7
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

```
Ala Arg Pro Arg Ala Phe Ser Val Gly Lys
 1              5                   10
```

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

```
Arg Arg Arg Gln Phe Ser Leu Arg Arg Lys Ala Lys
 1              5                   10
```

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 5 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Artificial Sequence
    (F) TISSUE TYPE:

(ix) FEATURE:
    (A) NAME/KEY:
    (B) LOCATION:
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
    (A) NAME/KEY: VARIANT
    (B) LOCATION: 2
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
    (A) NAME/KEY: MOD_RES
    (B) LOCATION: 4
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Xaa = phosphorylated Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

```
Thr Xaa Ser Xaa Leu
 1               5
```

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 7 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Artificial Sequence
    (F) TISSUE TYPE:

(ix) FEATURE:
    (A) NAME/KEY:
    (B) LOCATION:

(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

```
Arg Thr Phe Ser Ser Leu Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 7
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

```
Arg Pro Arg Thr Phe Ser Ser Leu Ala Glu Gly Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: Artificial Sequence
  (F) TISSUE TYPE:

(ix) FEATURE:
  (A) NAME/KEY:
  (B) LOCATION:
  (C) IDENTIFICATION METHOD:
  (D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
  (A) NAME/KEY: VARIANT
  (B) LOCATION: 1
  (C) IDENTIFICATION METHOD:
  (D) OTHER INFORMATION: Xaa = Pro or Ile

(ix) FEATURE:
  (A) NAME/KEY: VARIANT
  (B) LOCATION: 2, 3
  (C) IDENTIFICATION METHOD:
  (D) OTHER INFORMATION: Xaa = Gly, Lys, or Asp

(ix) FEATURE:
  (A) NAME/KEY: MOD_RES
  (B) LOCATION: 4
  (C) IDENTIFICATION METHOD:
  (D) OTHER INFORMATION: Xaa = phosphorylated Ser or Thr

(ix) FEATURE:
  (A) NAME/KEY: VARIANT
  (B) LOCATION: 6, 7, 8
  (C) IDENTIFICATION METHOD:
  (D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

```
Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa
 1               5
```

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 7 amino acids
  (B) TYPE: amino acid
  (C) STRANDEDNESS:
  (D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
  (A) ORGANISM: Artificial Sequence

(F) TISSUE TYPE:

(ix) FEATURE:
    (A) NAME/KEY:
    (B) LOCATION:
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
    (A) NAME/KEY: MOD_RES
    (B) LOCATION: 4
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

```
Ala Pro Phe Ser Pro Gly Gly
 1               5
```

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 7 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
    (A) ORGANISM: Artificial Sequence
    (F) TISSUE TYPE:

(ix) FEATURE:
    (A) NAME/KEY:
    (B) LOCATION:
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
    (A) NAME/KEY: MOD_RES
    (B) LOCATION: 4
    (C) IDENTIFICATION METHOD:
    (D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

```
His Pro Phe Ser Pro Lys Lys
 1               5
```

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

```
Lys Ile Phe Ser Pro Asp Val
 1               5
```

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

```
Val Ala Pro Phe Ser Pro Gly Gly Arg Ala Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

```
Ala Lys His Pro Phe Ser Pro Lys Lys Ala Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:

```
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif

     (ix) FEATURE:
          (A) NAME/KEY: MOD_RES
          (B) LOCATION: 6
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: phosphorylated Ser

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Ile Ile Lys Ile Phe Ser Pro Asp Val Glu Lys
 1               5                  10

(2) INFORMATION FOR SEQ ID NO:121:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 9 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

     (ii) MOLECULE TYPE: protein

     (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

     (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif

     (ix) FEATURE:
          (A) NAME/KEY: VARIANT
          (B) LOCATION: 1
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

     (ix) FEATURE:
          (A) NAME/KEY: MOD_RES
          (B) LOCATION: 2
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Xaa = phosphorylated Ser or Thr

     (ix) FEATURE:
          (A) NAME/KEY: VARIANT
          (B) LOCATION: 3, 4
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Xaa = Ala, Glu, or Gln
```

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 5, 6, 7
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Tyr or His

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

```
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Val Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

```
Glu Phe Thr Ala Tyr Val Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

```
Ile Phe Thr Glu Tyr Val Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

```
Val Phe Thr Gln His Val Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

```
Asp Asp Glu Phe Thr Ala Tyr Val Ala Thr Arg Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5

(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

```
Thr Gly Ile Phe Thr Glu Tyr Val Ala Thr Arg Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

```
Thr Gly Val Phe Thr Gln His Val Ala Thr Arg Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = phosphorylated Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

```
Ile Xaa Xaa Ile Ala Asn
 1              5
```

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

```
Arg Ile Phe Ser Ile Ala Asn Ser
```

```
 1               5

(2) INFORMATION FOR SEQ ID NO:130:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 12 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

    (ii) MOLECULE TYPE: protein

    (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

    (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif

    (ix) FEATURE:
          (A) NAME/KEY: MOD_RES
          (B) LOCATION: 5
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: phosphorylated Ser

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Gln Arg Ile Phe Ser Ile Ala Asn Ser Ile Val Lys
 1               5                  10

(2) INFORMATION FOR SEQ ID NO:131:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 6 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

    (ii) MOLECULE TYPE: protein

    (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

    (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif
```

```
     (ix) FEATURE:
            (A) NAME/KEY: VARIANT
            (B) LOCATION: 4
            (C) IDENTIFICATION METHOD:
            (D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

     (ix) FEATURE:
            (A) NAME/KEY: MOD_RES
            (B) LOCATION: 5
            (C) IDENTIFICATION METHOD:
            (D) OTHER INFORMATION: Xaa = phosphorylated Ser or Thr

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Ser Ile Ala Xaa Xaa Ile
 1               5

(2) INFORMATION FOR SEQ ID NO:132:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 8 amino acids
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY:

     (ii) MOLECULE TYPE: protein

     (vi) ORIGINAL SOURCE:
             (A) ORGANISM: Artificial Sequence
             (F) TISSUE TYPE:

     (ix) FEATURE:
            (A) NAME/KEY:
            (B) LOCATION:
            (C) IDENTIFICATION METHOD:
            (D) OTHER INFORMATION: Exemplary motif

     (ix) FEATURE:
            (A) NAME/KEY: MOD_RES
            (B) LOCATION: 6
            (C) IDENTIFICATION METHOD:
            (D) OTHER INFORMATION: phosphorylated Ser

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Asp Ser Ile Ala Phe Ser Ile Val
 1               5

(2) INFORMATION FOR SEQ ID NO:133:

      (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 12 amino acids
            (B) TYPE: amino acid
```

(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 8
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

```
Arg Ile Asp Ser Ile Ala Phe Ser Ile Val Gly Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = phosphorylated Ser or Thr

(ix) FEATURE:

(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

```
Xaa Val Pro Pro Ser Pro
 1               5
```

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3, 7
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```
Phe Ser Val Pro Pro Ser Pro Asp
 1               5
```

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 12 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence

(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5, 9
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

```
Pro Arg Pro Phe Ser Val Pro Pro Ser Pro Asp Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ala or Glu

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3, 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: MOD_RES

(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = phosphorylated Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 6, 7, 8
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ile or Gln

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

```
Asp Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5
```

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

```
Glu Asp Ala Phe Ser Ile Ile
 1               5
```

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

```
Glu Asp Glu Phe Ser Gln Asn
 1               5
```

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

```
Glu Glu Asp Ala Phe Ser Ile Ile Gly Lys
```

1 5 10

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

```
Arg Glu Asp Glu Phe Ser Gln Asn Glu Glu Lys
 1               5                  10
```

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Phe, Trp, or Tyr

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = phosphorylated Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

```
Asp Xaa Xaa Gln Val
 1               5
```

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```
Glu Gly Asp Tyr Ser Gln Val
 1               5
```

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

```
Glu Gly Asp Tyr Ser Gln Val Leu Glu Lys
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Arg Xaa Leu
1

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Leu Xaa Thr Thr
1

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:

(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

```
Leu Xaa Leu Asp
 1
```

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Val, Ala, or Gln

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4, 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Val or Leu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Arg Xaa Xaa Xaa Xaa
 1   5

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

Thr Ser Xaa Leu
 1

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Pro or Ile

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr
(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Gly, Lys, or Asp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

```
Xaa Xaa Pro Xaa Xaa
 1               5
```

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2

(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ala, Glu, or Gln

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3, 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Tyr or His

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

```
Xaa Xaa Xaa Xaa Val Ala
 1               5
```

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

```
Ile Xaa Ile Ala Asn
 1               5
```

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: (1)...(5)
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Any Amino Acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```
Ser Ile Ala Xaa Ile
 1               5
```

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 1
(C) IDENTIFICATION METHOD:

(D) OTHER INFORMATION: Xaa = Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: MOD_RES
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: phosphorylated Ser

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

```
Xaa Val Pro Pro Ser Pro
 1               5
```

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ala or Glu

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4, 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ile or Gln

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```
Asp Xaa Xaa Xaa Xaa
 1              5

(2) INFORMATION FOR SEQ ID NO:156:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 4 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

    (ii) MOLECULE TYPE: protein

    (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

    (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif

    (ix) FEATURE:
          (A) NAME/KEY: VARIANT
          (B) LOCATION: 2
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Xaa = Ser or Thr

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

Asp Xaa Gln Val
 1

(2) INFORMATION FOR SEQ ID NO:157:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 5 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

    (ii) MOLECULE TYPE: protein

    (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

    (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif
```

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

```
Arg Arg Phe Xaa Leu
 1               5
```

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

```
Leu Phe Xaa Thr Thr
 1               5
```

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

```
Tyr Leu Xaa Leu Asp
 1               5
```

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Val, Ala, or Gln

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 5, 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Val or Ile

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```
Arg Xaa Phe Xaa Xaa Xaa
 1               5
```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```
Thr Phe Ser Xaa Leu
 1               5
```

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 1
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Pro or Ile

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 5, 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Gly, Lys, or Asp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

```
Xaa Phe Xaa Pro Xaa Xaa
 1               5
```

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:

```
          (A) NAME/KEY: VARIANT
          (B) LOCATION: 2
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Xaa = Ser or Thr

     (ix) FEATURE:
          (A) NAME/KEY: VARIANT
          (B) LOCATION: 3
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Xaa = Ale, Glu, or Gln

     (ix) FEATURE:
          (A) NAME/KEY: VARIANT
          (B) LOCATION: 4, 5
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Xaa = Tyr or His
                                 Xaa = Any Amino Acid

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Phe Xaa Xaa Xaa Xaa Val Ala
 1               5

(2) INFORMATION FOR SEQ ID NO:164:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 6 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY:

     (ii) MOLECULE TYPE: protein

     (vi) ORIGINAL SOURCE:
           (A) ORGANISM: Artificial Sequence
           (F) TISSUE TYPE:

     (ix) FEATURE:
          (A) NAME/KEY:
          (B) LOCATION:
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Exemplary motif

     (ix) FEATURE:
          (A) NAME/KEY: VARIANT
          (B) LOCATION: 3
          (C) IDENTIFICATION METHOD:
          (D) OTHER INFORMATION: Xaa = Ser or Thr

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Ile Phe Xaa Ile Ala Asn
 1               5
```

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 5
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

```
Ser Ile Ala Phe Xaa Ile
 1               5
```

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 2
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ala or Glu

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 4
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 5, 6
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ile or Gln

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

```
Asp Xaa Phe Xaa Xaa Xaa
 1               5
```

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Artificial Sequence
(F) TISSUE TYPE:

(ix) FEATURE:
(A) NAME/KEY:
(B) LOCATION:
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Exemplary motif

(ix) FEATURE:
(A) NAME/KEY: VARIANT
(B) LOCATION: 3
(C) IDENTIFICATION METHOD:
(D) OTHER INFORMATION: Xaa = Ser or Thr

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

```
Asp Tyr Xaa Gln Val
 1               5
```

WHAT IS CLAIMED IS

1. A composition of matter comprising:

a) a peptide having a length from five to fifty amino acids, said peptide comprising a motif selected from the group consisting of:

AIYAA (SEQ ID NO: 1),
QDYLS (SEQ ID NO: 4),
EIYGV (SEQ ID NO: 7),
TX$_1$YVA, where X$_1$ can be G, A, or E (SEQ ID NO: 110),
EEYIQ (SEQ ID NO: 17), and
DYSQV (SEQ ID NO: 20); and

b) a first detectable moiety, wherein said first detectable moiety is associated with said peptide.

2. A composition of matter comprising:

a) a peptide having a length from five to fifty amino acids, said peptide comprising a motif selected from the group consisting of:

RR(S/T)L (SEQ ID NO: 145),
L(S/T)TT (SEQ ID NO: 146),
L(S/T)LD (SEQ ID NO: 147),
RX$_1$(S/T)X$_2$, where X$_1$ can be V, A, or Q and X$_2$ can be V or L (SEQ ID NO: 148),
TS(S/T)L (SEQ ID NO: 149),
X$_1$(S/T)PX$_2$ where X$_1$ can be P or I and X$_2$ can be G, K, or D (SEQ ID NO: 150),
(S/T)X$_1$X$_2$VA, where X$_1$ can be A, E, or Q and X$_2$ can be Y or H (SEQ ID NO: 151),
I(S/T)IAN (SEQ ID NO: 152),
SIA(S/T)I (SEQ ID NO: 153),

(S/T)VPPS*P, where S* is a phosphorylated serine (SEQ ID NO: 154),

$DX_1(S/T)X_2$, where X_1 can be A or E and X_2 can be I or Q (SEQ ID NO: 155), and

D(S/T)QV (SEQ ID NO: 156); and

b) a first detectable moiety, wherein said first detectable moiety is associated with said peptide.

3. A composition of matter comprising:

a) a peptide having a length from five to fifty amino acids, said peptide comprising a motif selected from the group consisting of:

$RRX_1(S/T)L$, where X_1 can be F, W, or Y (SEQ ID NO: 45),

$LX_1(S/T)TT$, where X_1 can be F, W, or Y (SEQ ID NO: 48),

$X_1L(S/T)LD$, where X_1 can be F, W, or Y (SEQ ID NO: 51),

$RX_1X_2(S/T)X_3$, where X_1 can be V, A, or Q, X_2 can be F, W, or Y, and X_3 can be V or L (SEQ ID NO: 54),

$TX_1S(S/T)L$, where X_1 can be F, W, or Y (SEQ ID NO: 61),

$X_1X_2(S/T)PX_3$ where X_1 can be P or I, X_2 can be F, W, or Y, and X_3 can be G, K, or D (SEQ ID NO: 64),

$X_1(S/T)X_2X_3VA$, where X_1 can be F, W, or Y, X_2 can be A, E, or Q, and X_3 can be Y or H (SEQ ID NO: 71),

$IX_1(S/T)IAN$, where X_1 can be F, W, or Y (SEQ ID NO: 78),

$SIAX_1(S/T)I$, where X_1 can be F, W, or Y (SEQ ID NO: 81),

(S/T)VPPS*P, where S* is a phosphorylated serine (SEQ ID NO: 84),

$DX_1X_2(S/T)X_3$, where X_1 can be A or E, X_2 can be F, W, or Y, and X_3 can be I or Q (SEQ ID NO: 87), and

$DX_1(S/T)QV$, where X_1 can be F, W, or Y (SEQ ID NO: 92).

4. The composition of claim 3, further comprising a first detectable moiety, wherein said first detectable moiety is associated with said peptide.

5. The composition of claim 3, wherein said peptide comprises a motif selected from the group consisting of:

RRF(S/T)L (SEQ ID NO: 157),
LF(S/T)TT (SEQ ID NO: 158),
YL(S/T)LD (SEQ ID NO: 159),
$RX_1F(S/T)X_2$, where X_1 can be V, A, or Q and X_2 can be V or L (SEQ ID NO: 160),
TFS(S/T)L (SEQ ID NO: 161),
$X_1F(S/T)PX_2$ where X_1 can be P or I and X_2 can be G, K, or D (SEQ ID NO: 162),
$F(S/T)X_1X_2VA$, where X_1 can be A, E, or Q and X_2 can be Y or H (SEQ ID NO: 163),
IF(S/T)IAN (SEQ ID NO: 164),
SIAF(S/T)I (SEQ ID NO: 165),
$DX_1F(S/T)X_2$, where X_1 can be A or E and X_2 can be I or Q (SEQ ID NO: 166), and
DY(S/T)QV (SEQ ID NO: 167).

6. The composition of claim 1, 2, 4, or 5, wherein said first detectable moiety is covalently linked to said peptide.

7. The composition of any of claims 1-5, wherein said peptide comprises a protease cleavage site.

8. The composition of claim 7, wherein said protease cleavage site is selected from the group consisting of a chymotrypsin protease cleavage site, a caspase 3 protease cleavage site, a cathepsin G protease cleavage site, a trypsin protease cleavage site, an elastase protease cleavage site, an endoproteinase Asp-N protease cleavage site, and an endoproteinase Glu-N protease cleavage site.

9. The composition of claim 1, 2, 4, or 5, further comprising a second detectable moiety.

10. The composition of any of claims 1-5, wherein said peptide has a length from 8 to 50 amino acids.

11. The composition of claim 10, wherein said peptide has a length from 8 to 25 amino acids.

12. The composition of claim 11, wherein said peptide has a length from 8 to 15 amino acids.

13. The composition of claim 1, 2, 4, or 5, wherein said composition exhibits an optical property, a magnetic property, or a radioactive property.

14. The composition of claim 13, wherein said composition exhibits an optical property selected from the group consisting of a molar extinction coefficient at an excitation wavelength, a quantum efficiency, an excitation spectrum, an emission spectrum, an excitation wavelength maximum, an emission wavelength maximum, a ratio of excitation amplitudes at two wavelengths, a ratio of emission amplitudes at two wavelengths, an excited state lifetime, an anisotropy, a polarization of emitted light, a resonance energy transfer, and a quenching of emission at a wavelength.

15. The composition of claim 14, wherein said optical property is selected from the group consisting of a fluorescence excitation spectrum, a fluorescence emission spectrum, a fluorescence excitation wavelength maximum, a fluorescence emission wavelength maximum, a ratio of fluorescence excitation amplitudes at two wavelengths, a ratio of fluorescence emission amplitudes at two wavelengths, a fluorescence excited state lifetime, a fluorescence anisotropy, and a quenching of fluorescence emission at a wavelength.

16. The composition of claim 13 or 15, wherein said composition exhibits a fluorescence excitation maximum in the range from 250 to 750 nm and a fluorescence emission maximum in the range from 450 to 800 nm.

17. The composition of claim 16, wherein said detectable moiety is selected from the group consisting of 5-FAM, 6-FAM, 7-hydroxycoumarin-3-carboxamide, 6-chloro-7-hydroxycoumarin-3-carboxamide, fluorescein-5-isothiocyanate, dichlorotriazinylaminofluorescein, tetramethylrhodamine-5-isothiocyanate, tetramethylrhodamine-6-isothiocyanate, succinimidyl ester of 5-carboxyfluorescein, succinimidyl ester of 6-carboxyfluorescein, 5-carboxytetramethylrhodamine, 6-carboxymethylrhodamine, and 7-amino-4-methylcoumarin-3-acetic acid.

18. The composition of claim 1, 2, 4, or 5, wherein said first detectable moiety is a member of a specific binding pair.

19. The composition of claim 9, wherein said first detectable moiety and said second detectable probe moiety form a dark quenching RET pair.

20. The composition of claim 9, wherein said first detectable moiety and said second detectable moiety form a FRET pair.

21. The composition of claim 20, wherein said first detectable moiety is 7-hydroxycoumarin-3-carboxamide and said second detectable moiety is 5-FAM.

22. The composition of claim 1, 2, 4, or 5, wherein said detectable probe moiety is covalently linked to said peptide via a linker (L).

23. The composition of claim 19, wherein said L is selected from the group consisting of GABA, diaminopentanyl, and aminohexanoyl.

24. The composition of claim 1, wherein said motif is a recognition motif for a tyrosine kinase, said recognition motif selected from the group consisting of:

EAIYAAP (SEQ ID NO: 2),
DQDYLSL (SEQ ID NO: 5),
EEEYIQI (SEQ ID NO: 18),
EEIYGVI (SEQ ID NO: 8),
LTGYVAR (SEQ ID NO: 11),
ITAYVAT (SEQ ID NO: 12),
ITEYVAT (SEQ ID NO: 13), and
GDYSQVL (SEQ ID NO: 21).

25. The composition of claim 3 or 5, wherein said motif is a recognition motif for a serine/threonine kinase, said recognition motif selected from the group consisting of:

LRRFSLG (SEQ ID NO: 46),
GLFSTTP (SEQ ID NO: 49),
DYLSLDK (SEQ ID NO: 52),
NRVFSVA (SEQ ID NO: 55),
PRAFSVG (SEQ ID NO: 56),
RRQFSLR (SEQ ID NO: 57),
RTFSSLA (SEQ ID NO: 62),
APFSPGG (SEQ ID NO: 65),
HPFSPKK (SEQ ID NO: 66),
KIFSPDV (SEQ ID NO: 67),
EFTAYVA (SEQ ID NO: 72),
IFTEYVA (SEQ ID NO: 73),
VFTQHVA (SEQ ID NO: 74),
RIFSIANS (SEQ ID NO: 79),
DSIAFSIV (SEQ ID NO: 82),
FSVPPS*PD, where S* is a phosphorylated serine (SEQ ID NO: 85),
EDAFSII (SEQ ID NO: 88),
EDEFSQN (SEQ ID NO: 89), and

EGDYSQV (SEQ ID NO: 93).

26. The composition of claim 24, wherein said recognition motif for a tyrosine kinase is EAIYAAP (SEQ ID NO: 2), and wherein said tyrosine kinase is selected from the group consisting of Abl1, Abl2, BMX, CSF1R, Csk, EPHB4, Fes/Fps, FGFR1, FGFR4, Fgr, FLT3, Fyn, Hck, IGF1R, IRKβ, ITK, Jak3, KDR, c-KIT, Lck, Lyn A, Lyn B, c-MET, Src, Src N1, Src N2, SYK, TIE2, TRKa, and YES.

27. The composition of claim 24, wherein said recognition motif for a tyrosine kinase is DQDYLSL (SEQ ID NO: 5), and wherein said tyrosine kinase is selected from the group consisting of CaMKII, CDK7/CycH, CK1δ, IKKα, and IKKβ.

28. The composition of claim 25, wherein said recognition motif for a serine/threonine kinase is LRRFSLG (SEQ ID NO: 46), and wherein said serine/threonine kinase is selected from the group consisting of Akt1, Akt2, Akt3, Aurora A, CaMKII, CDK2/CycA, CDK3/CycE, CDK7/CycH, MAPKAP-K1α, MAPKAP-K1β, MAPKAP-K1γ, MSK1, PAK2, PKA, PKG, and ROCK.

29. The composition of claim 25, wherein said recognition motif for a serine/threonine kinase is GLFSTTP (SEQ ID NO: 49), and wherein said serine/threonine kinase is selected from the group consisting of p38γ, p38δ, and REDK.

30. The composition of claim 25, wherein said recognition motif for a serine/threonine kinase is NRVFSVA (SEQ ID NO: 55), and wherein said serine/threonine kinase is selected from the group consisting of Akt3, AMPK, CaMKII, CDK7/CycH, CHK2, IKKα, MAPKAP-K1α, MAPKAP-K2, MAPKAP-K3, MAPKAP-K5, PAK2, PKA, PKCβII, REDK, ROCK, ROCK2, and SGK1.

31. The composition of claim 25, wherein said recognition motif for a serine/threonine kinase is PRAFSVG (SEQ ID NO: 56), and wherein said serine/threonine kinase is selected from the group consisting of Akt1, Akt2, Akt3,

CaMKII, CDK7/CycH, IKKβ, MAPKAP-K1α/RSK1, MAPKAP-K1β/RSK2, MAPKAP-K1γ/RSK3, MSK1, PAK2, PIM1, PKA, PKG, REDK, and SGK1.

32. The composition of claim 25, wherein said recognition motif for a serine/threonine kinase is RRQFSLR (SEQ ID NO: 57), and wherein said serine/threonine kinase is selected from the group consisting of Akt1, Akt2, Akt3, CaMKII, CHK1, CHK2, MAPKAP-K1α, MAPKAP-K1β, MAPKAP-K1γ, MSK1, p70 S6 Kinase, PAK2, PIM1, PKA, PKCα, PKCβI, PKCβII, PKCγ, PKCδ, PKCε, PKCζ, PKCη, PKCθ, PKCι, PKG, ROCK, ROCK2, and SGK1.

33. The composition of claim 25, wherein said recognition motif for a serine/threonine kinase is RTFSSLA (SEQ ID NO: 62), and wherein said serine/threonine kinase is selected from the group consisting of Akt1, CDK2/CycA, CDK6, IKKβ, MAPKAP-K1α, MAPKAP-K1β, MAPKAP-K1γ, p70 S6 Kinase, PAK2, and PKA.

34. The composition of claim 25, wherein said recognition motif for a serine/threonine kinase is APFSPGG (SEQ ID NO: 65), and wherein said serine/threonine kinase is selected from the group consisting of CDK2/CycA, CDK3/CycE, ERK1, ERK2, IKKα, p38β, p38γ, and p38δ.

35. The composition of claim 24, wherein said recognition motif for a tyrosine kinase is EEIYGVI (SEQ ID NO: 8), and wherein said tyrosine kinase is selected from the group consisting of Abl1, Abl2, BMX, CSF1R, Csk, EPHB4, Fes/Fps, FGFR1, Fgr, FLT3, Fyn, Hck, IGF1R, IRKβ, IRTK, ITK, Jak3, KDR, c-KIT, Lck, Lyn A, Lyn B, c-MET, Src, Src N1, Src N2, SYK, TIE2, TRKa, and YES.

36. The composition of claim 24, wherein said recognition motif for a tyrosine kinase is LTGYVAR (SEQ ID NO: 11), and wherein said tyrosine kinase is selected from the group consisting of CSF1R, FLT3, and c-KIT.

37. The composition of claim 24, wherein said recognition motif for a tyrosine kinase is EEEYIQI (SEQ ID NO: 18), and wherein said tyrosine kinase is selected from the group consisting of EGFR, Zap-70, PDGFR, FGFR4, Abl 1, and Lyn B.

38. The composition of claim 1, wherein said peptide is selected from the group consisting of:

EAEAIYAAPGDK (SEQ ID NO: 3),
GDQDYLSLDK (SEQ ID NO: 6),
EEEEYIQIVK (SEQ ID NO: 19),
EEEIYGVIEK (SEQ ID NO: 9),
GVLTGYVARRK (SEQ ID NO: 14),
DDEITAYVATRK (SEQ ID NO: 15),
TGIITEYVATRK (SEQ ID NO: 16), and
EGDYSQVLEK (SEQ ID NO: 22).

39. The composition of claim 3, wherein said peptide is selected from the group consisting of:

ALRRFSLGEK (SEQ ID NO: 47),
VAPFSPGGRAK (SEQ ID NO: 68),
RGGLFSTTPGGTK (SEQ ID NO: 50),
KLNRVFSVAC (SEQ ID NO: 58),
GDQDYLSLDK (SEQ ID NO: 53),
ARPRAFSVGK (SEQ ID NO: 59),
RRRQFSLRRKAK (SEQ ID NO: 60),
RPRTFSSLAEGK (SEQ ID NO: 63),
AKHPFSPKKAK (SEQ ID NO: 69),
DDEFTAYVATRK (SEQ ID NO: 75),
TGIFTEYVATRK (SEQ ID NO: 76),
TGVFTQHVATRK (SEQ ID NO: 77),
QRIFSIANSIVK (SEQ ID NO: 80),
RIDSIAFSIVGK (SEQ ID NO: 83),

PRPFSVPPS*PDK, where S* is a phosphorylated Serine (SEQ ID NO: 86),

EEDAFSIIGK (SEQ ID NO: 90),
REDEFSQNEEK (SEQ ID NO: 91),
IIKIFSPDVEK (SEQ ID NO: 70), and
EGDYSQVLEK (SEQ ID NO: 22).

40. The composition of claim 7, wherein said protease cleavage site is FS, FT, or Y.

41. A method for characterizing a kinase, said method comprising:

a) contacting a composition of claims 1, 2, or 4 with a protein kinase under conditions effective for said protein kinase to phosphorylate said composition; and

b) measuring the ability of said protein kinase to phosphorylate said composition.

42. A method for identifying a substrate of a kinase, comprising:

a) contacting a composition of claims 1, 2, or 4 with a protein kinase;

b) contacting said composition and said protein kinase with a protease to form a protease mixture; and

c) comparing a measurable property in said protease mixture with the measurable property in a control protease mixture lacking said protein kinase, wherein said composition is identified as a substrate of said protein kinase if said measurable property in said protease mixture is different from said measurable property in said control protease mixture.

43. The method of claim 42, wherein ATP is present during said contacting step a).

44. A method for identifying a substrate of a kinase, comprising:

a) contacting a composition of claims 1, 2, or 4 with a protein kinase and ATP;

b) contacting said composition, said protein kinase, and said ATP with a protease to form a protease mixture;

c) comparing a measurable property in said protease mixture with a measurable property in a control protease mixture lacking said ATP, wherein said composition is identified as a substrate of said kinase if said measurable property in said protease mixture is different from said measurable property in said control protease mixture.

45. The method of claim 44, wherein two or more different compositions of claims 1, 2, or 4 are contacted independently with said protein kinase and said ATP during said contacting step a) to form two or more kinase mixtures, wherein each of said kinase mixtures is contacted independently with a protease during said contacting step b) to form two or more protease mixtures, and wherein a measurable property in each of said protease mixtures is compared with the measurable property in a corresponding control mixture.

46. The method of claim 44, wherein two or more different protein kinases are contacted independently with said composition and said ATP during said contacting step a) to form two or more kinase mixtures, wherein each of said kinase mixtures is contacted independently with a protease during said contacting step b) to form two or more protease mixtures, and wherein a measurable property in each of said protease mixtures is compared with the measurable property in a corresponding control mixture.

47. The method of claim 44, wherein said comparing step c) occurs concurrently with said contacting step b).

48. The method of claim 44, wherein said comparing step c) occurs after said contacting step b).

49. The method of claim 48, wherein said contacting step b) is completed by inhibiting a proteolytic activity of said protease.

50. The method of claim 49, wherein said proteolytic activity is inhibited by adding a reagent to said protease mixtures or by heating said protease mixtures.

51. The method of claim 50, wherein said reagent is aprotinin, PMSF, TPCK, AEBSF, chymotrypsin inhibitor 1, and chymotrypsin inhibitor 2.

52. A method for identifying a modulator of activity of a kinase, comprising:

a) forming a mixture of a protein kinase, a substrate for said protein kinase, and a test compound;

b) contacting said mixture with a protease to form a protease mixture; and

c) comparing a measurable property in said protease mixture to the measurable property in a control mixture of said substrate, said protein kinase, and said protease in the absence of said test compound, wherein said test compound is identified as a modulator of activity of said kinase if said measurable property in said protease mixture is different from said measurable property in said control mixture.

53. The method of claim 52, wherein ATP is present during said contacting step a).

54. A method for identifying a modulator of activity of a kinase, comprising:

a) contacting a protein kinase, a substrate for said protein kinase, ATP, and a test compound to form a kinase mixture;

b) contacting said kinase mixture with a protease to form a protease mixture;

c) comparing a measurable property in said protease mixture with the measurable property in a control mixture comprising said composition, said protein kinase, and said protease in the absence of said test compound, wherein said composition is identified as a modulator of activity of said kinase if said measurable property in said protease mixture is different from said measurable property in said control mixture.

55. The method of claim 54, wherein two or more different test compounds are contacted independently with said protein kinase, said ATP, and said substrate in said contacting step a) to form two or more kinase mixtures, wherein each of said kinase mixtures is contacted independently with a protease in said contacting step b) to form two

or more protease mixtures, and wherein a measurable property in each of said protease mixtures is compared with the measurable property in a corresponding control mixture.

56. The method of claim 54, wherein two or more different protein kinases are contacted independently with said ATP, said test compound, and said substrate in said contacting step a) to form two or more kinase mixtures, wherein each of said kinase mixtures is contacted independently with a protease in said contacting step b) to form two or more protease mixtures, and wherein a measurable property in each of said protease mixtures is compared with the measurable property in a corresponding control mixture.

57. The method of claim 54, wherein said comparing step c) occurs during said contacting step b).

58. The method of claim 54, wherein said comparing step c) occurs after said contacting step b).

59. The method of claim 58, wherein said contacting step b) is completed by inhibiting a proteolytic activity of said protease.

60. The method of claim 59, wherein said proteolytic activity is inhibited by adding a reagent to said protease mixtures or by heating said protease mixtures.

61. The method of claim 60, wherein said reagent is aprotinin, PMSF, TPCK, AEBSF, chymotrypsin inhibitor 1, and chymotrypsin inhibitor 2.

62. The composition of claim 1, wherein said Y in said motif is phosphorylated.

63. The composition of claim 2, 3, 4, or 5, wherein said S/T in said motif is phosphorylated.

64. The composition of claim 24, wherein said recognition motif for a tyrosine kinase is phosphorylated at the Y, and wherein said phosphorylated recognition motif is a recognition motif for a protein phosphatase.

65. The composition of claim 5, wherein said peptide comprises a protein phosphatase recognition motif selected from the group consisting of:

LRRFS*LG (SEQ ID NO: 96),
GLFS*TTP (SEQ ID NO: 99),
DYLS*LDK (SEQ ID NO: 102),
NRVFS*VA (SEQ ID NO: 105),
PRAFS*VG (SEQ ID NO: 106),
RRQFS*LR (SEQ ID NO: 107)
RTFSS*LA (SEQ ID NO: 112),
APFS*PGG (SEQ ID NO: 115),
HPFS*PKK (SEQ ID NO: 116),
KIFS*PDV (SEQ ID NO: 117),
EFT*AYVA (SEQ ID NO: 122),
IFT*EYVA (SEQ ID NO: 123),
VFT*QHVA (SEQ ID NO: 124),
RIFS*IANS (SEQ ID NO: 129),
DSIAFS*IV (SEQ ID NO: 132),
FS*VPPS*PD (SEQ ID NO: 135),
EDAFS*II (SEQ ID NO: 138),
EDEFS*QN (SEQ ID NO: 139), and
EGDYS*QV (SEQ ID NO: 143),

wherein S* represents a phosphorylated serine and T* represents a phosphorylated threonine.

66. The composition of claim 1, wherein said peptide comprises a protein phosphatase recognition motif, and wherein said peptide is selected from the group consisting of:

EAEAIY*AAPGDK (SEQ ID NO: 25),
GDQDY*LSLDK (SEQ ID NO: 28),
EEEEY*IQIVK (SEQ ID NO: 41),
EEEIY*GVIEK (SEQ ID NO: 31),
GVLTGY*VARRK (SEQ ID NO: 36),
DDEITAY*VATRK (SEQ ID NO: 37),
TGIITEY*VATRK (SEQ ID NO: 38), and
EGDY*SQVLEK (SEQ ID NO: 44),

wherein Y* represents a phosphorylated tyrosine.

67. The composition of claim 3, wherein said peptide has a sequence selected from the group consisting of:

ALRRFS*LGEK (SEQ ID NO: 97),
VAPFS*PGGRAK (SEQ ID NO: 118),
RGGLFS*TTPGGTK (SEQ ID NO: 100),
KLNRVFS*VAC (SEQ ID NO: 108),
GDQDYLS*LDK (SEQ ID NO: 103),
ARPRAFS*VGK (SEQ ID NO: 109),
RRRQFS*LRRKAK (SEQ ID NO: 110),
RPRTFSS*LAEGK (SEQ ID NO: 113),
AKHPFS*PKKAK (SEQ ID NO: 119),
DDEFT*AYVATRK (SEQ ID NO: 125),
TGIFT*EYVATRK (SEQ ID NO: 126),
TGVFT*QHVATRK (SEQ ID NO: 127),
QRIFS*IANSIVK (SEQ ID NO: 130),
RIDSIAFS*IVGK (SEQ ID NO: 133),
PRPFS*VPPS*PDK (SEQ ID NO: 136)
EEDAFS*IIGK (SEQ ID NO: 140),
REDEFS*QNEEK (SEQ ID NO: 141),
IIKIFS*PDVEK (SEQ ID NO: 120), and

EGDYS*QVLEK (SEQ ID NO: 144),

wherein S* represents a phosphorylated serine and T* represents a phosphorylated threonine.

68. The composition of claim 64, wherein said phosphatase recognition motif is EAIY*AAP, wherein Y* is a phosphorylated tyrosine (SEQ ID NO: 24), and wherein said phosphatase is selected from the group consisting of PTP1B, LAR, and LCA.

69. The composition of claim 65, wherein said phosphatase recognition motif is DQDYLS*L, wherein S* is a phosphorylated serine (SEQ ID NO: 27), and wherein said phosphatase is selected from the group consisting of PP1α, PP2A, PP2B, and PP2C.

70. The composition of claim 65, wherein said phosphatase recognition motif is LRRFS*LG, wherein S* is a phosphorylated serine (SEQ ID NO: 96), and wherein said phosphatase is selected from the group consisting of PP1α, PP2A, and PP2C.

71. The composition of claim 65, wherein said phosphatase recognition motif is GLFS*TTP, wherein S* is a phosphorylated serine (SEQ ID NO: 99), and wherein said phosphatase is selected from the group consisting of PP1α, PP2A, PP2B, and PP2C.

72. The composition of claim 65, wherein said phosphatase recognition motif is NRVFS*VA, wherein S* is a phosphorylated serine (SEQ ID NO: 105), and wherein said phosphatase is selected from the group consisting of PP1α, PP2A, PP2B, and PP2C.

73. The composition of claim 65, wherein said phosphatase recognition motif is PRAFS*VG, wherein S* is a phosphorylated serine (SEQ ID NO: 106), and wherein said phosphatase is selected from the group consisting of PP1α, PP2A, and PP2B.

74. The composition of claim 65, wherein said phosphatase recognition motif is RRQFS*LR, wherein S* is a phosphorylated serine (SEQ ID NO: 107), and wherein said phosphatase is selected from the group consisting of PP1α, PP2A, and PP2B.

75. The composition of claim 65, wherein said phosphatase recognition motif is RTFSS*LA, wherein S* is a phosphorylated serine (SEQ ID NO: 112), and wherein said phosphatase is selected from the group consisting of PP1α, PP2A, and PP2B.

76. The composition of claim 65, wherein said phosphatase recognition motif is APFS*PGG, wherein S* is a phosphorylated serine (SEQ ID NO: 115), and wherein said phosphatase is selected from the group consisting of PP1α and PP2A.

77. The composition of claim 64, wherein said phosphatase recognition motif is EEIY*GVI, wherein Y* is a phosphorylated tyrosine (SEQ ID NO: 30), and wherein said phosphatase is selected from the group consisting of PTP1B, LAR, and LCA.

78. The composition of claim 64, wherein said phosphatase recognition motif is LTGY*VAR, wherein Y* is a phosphorylated tyrosine (SEQ ID NO: 33), and wherein said phosphatase is selected from the group consisting of PTP1B, LAR, and LCA.

79. A method for characterizing a phosphatase, said method comprising:

a) contacting a composition of claim 62 or claim 63 with a protein phosphatase under conditions effective for said protein phosphatase to dephosphorylate said composition; and

b) measuring the ability of said protein phosphatase to dephosphorylate said composition.

80. A method for identifying a substrate of a phosphatase, comprising:

a) contacting a composition of claim 62 or claim 63 with a protein phosphatase;

b) contacting said composition and said protein phosphatase with a protease to form a protease mixture; and

c) comparing a measurable property in said protease mixture with a measurable property in a control protease mixture lacking said phosphatase, wherein said composition is identified as a substrate of said phosphatase if said measurable property in said protease mixture is different from said measurable property in said control protease mixture.

81. The method of claim 80, wherein two or more different compositions of claim 62 or claim 63 are contacted independently with said phosphatase during said contacting step a) to form two or more phosphatase mixtures, wherein each of said phosphatase mixtures is contacted independently with a protease during said contacting step b) to form two or more protease mixtures, and wherein a measurable property in each of said protease mixtures is compared with the measurable property in a corresponding control mixture.

82. The method of claim 80, wherein two or more different phosphatases are contacted independently with said composition during said contacting step a), wherein each of said phosphatase mixtures is contacted independently with a protease during said contacting step b) to form two or more protease mixtures, and wherein a measurable property in each of said protease mixtures is compared with the measurable property in a corresponding control mixture.

83. A method for identifying a modulator of activity of a phosphatase, comprising:

a) contacting a mixture of a protein phosphatase, a substrate for said protein phosphatase, and a test compound to form a phosphatase mixture;

b) contacting said phosphatase mixture with a protease to form a protease mixture; and

c) comparing a measurable property in said protease mixture to the measurable property in a control protease mixture lacking said test compound, wherein said test compound is identified as a modulator of activity of said phosphatase if said measurable property in said protease mixture is different from said measurable property in said control mixture.

84. The method of claim 83, wherein two or more different test compounds are contacted independently with said phosphatase and said substrate during said contacting step a) to form two or more phosphatase mixtures, wherein each of said phosphatase mixtures is contacted independently with a protease during said contacting step b) to form two or more protease mixtures, and wherein a measurable property in each of said protease mixtures is compared with the measurable property in a corresponding control mixture.

85. The method of claim 83, wherein two or more different phosphatases are contacted independently with said test compound and said substrate during said contacting step a) to form two or more phosphatase mixtures, wherein each of said phosphatase mixtures is contacted independently with a protease during said contacting step b) to form two or more protease mixtures, and wherein a measurable property in each of said protease mixtures is compared with the measurable property in a corresponding control mixture.

86. An article of manufacture comprising:

a) packaging matter; and

b) a composition of matter according to claim 1, 2, 4, 5, 62, or 63 associated with said packaging material.

87. The article of claim 86, further comprising a protein kinase or a protein phosphatase.

88. The article of claim 86, further comprising a protease.

89. The article of claim 87, further comprising ATP.

90. The composition of claim 18, wherein said member of a specific binding pair is an epitope.

91. The composition of claim 18, wherein said member of a specific binding pair is biotin.

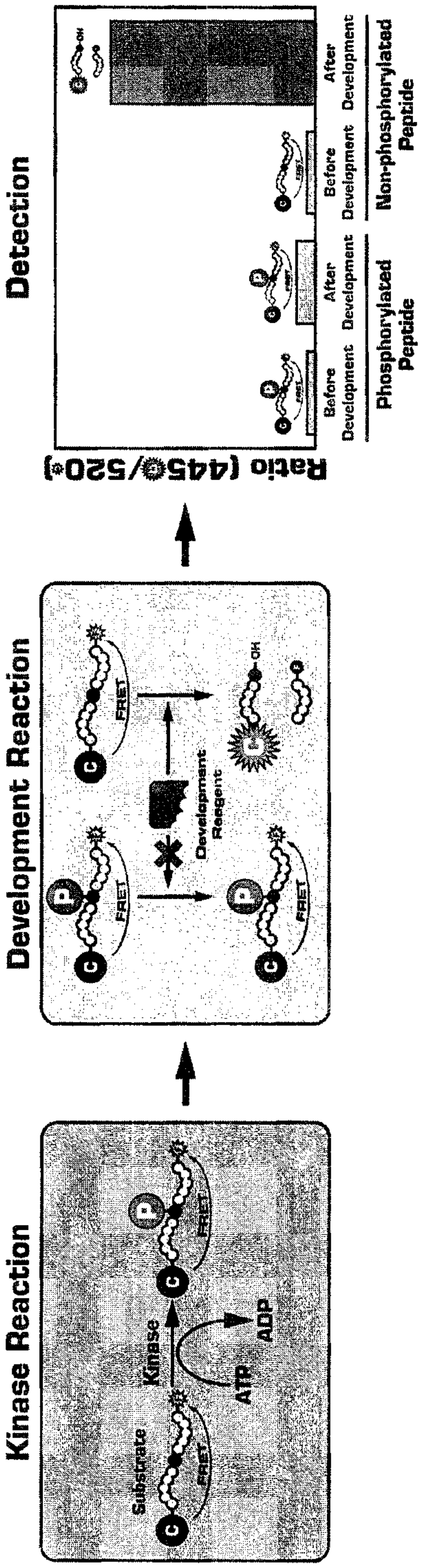
Kinase Reaction
Substrate
FRET
Kinase
ATP
ADP
C
P
Development Reaction
Development Reagent
OH
Detection
Ratio (445/520)
Before Development
After Development
Phosphorylated Peptide
Non-phosphorylated Peptide

FIG. 1

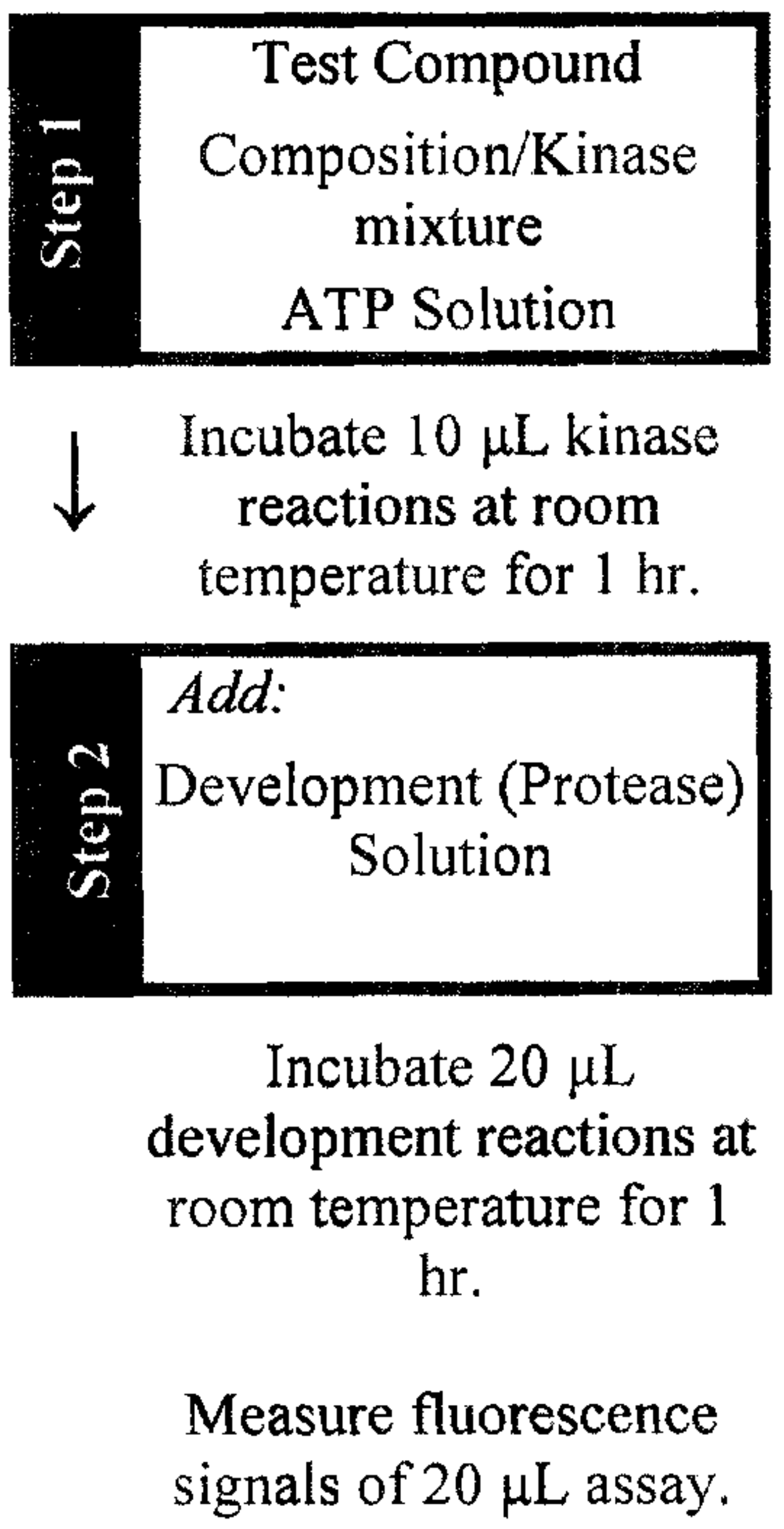
Step 1
Test Compound
Composition/Kinase mixture
ATP Solution
Incubate 10 µL kinase reactions at room temperature for 1 hr.
Step 2
Add:
Development (Protease) Solution
Incubate 20 µL development reactions at room temperature for 1 hr.
Measure fluorescence signals of 20 µL assay.

FIG. 2A

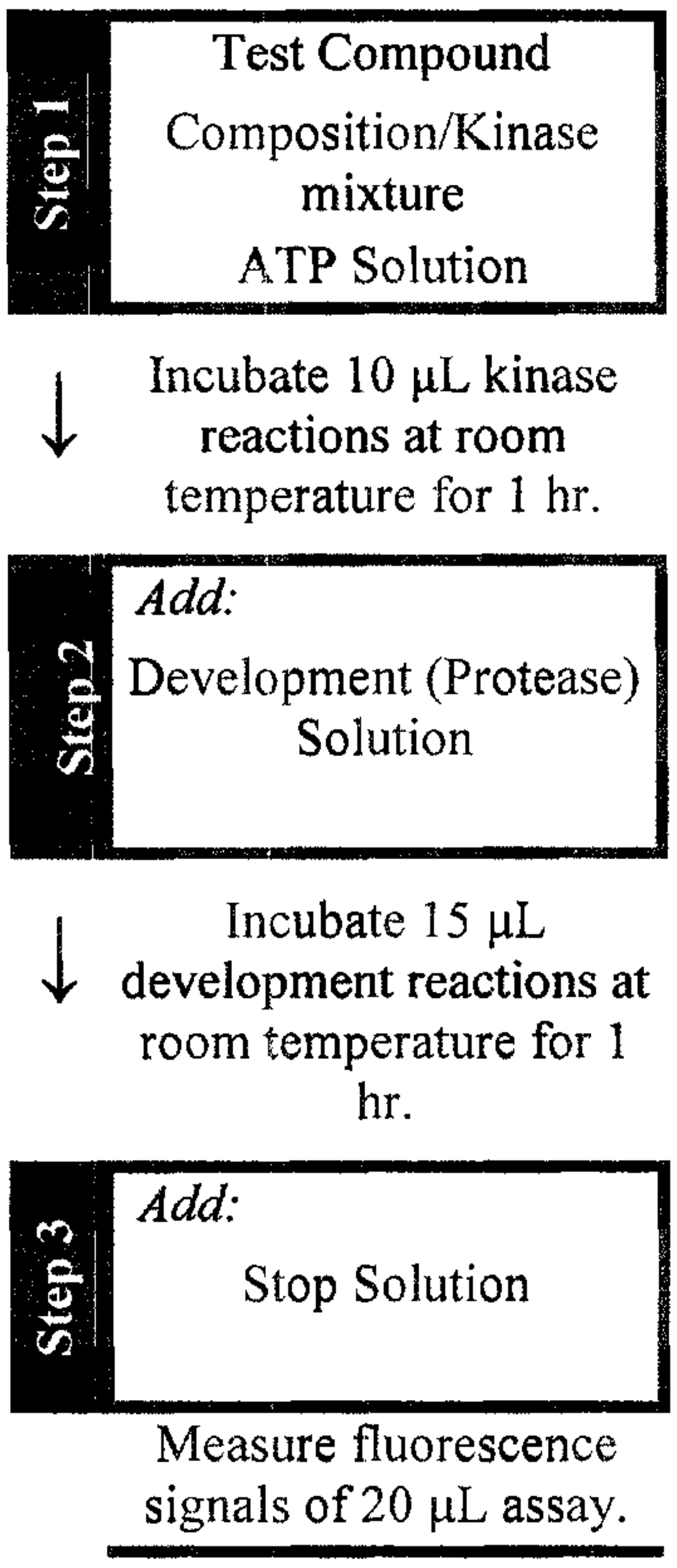
Step 1
Test Compound
Composition/Kinase mixture
ATP Solution
Incubate 10 µL kinase reactions at room temperature for 1 hr.
Step 2
Add:
Development (Protease) Solution
Incubate 15 µL development reactions at room temperature for 1 hr.
Step 3
Add:
Stop Solution
Measure fluorescence signals of 20 µL assay.

FIG. 2B

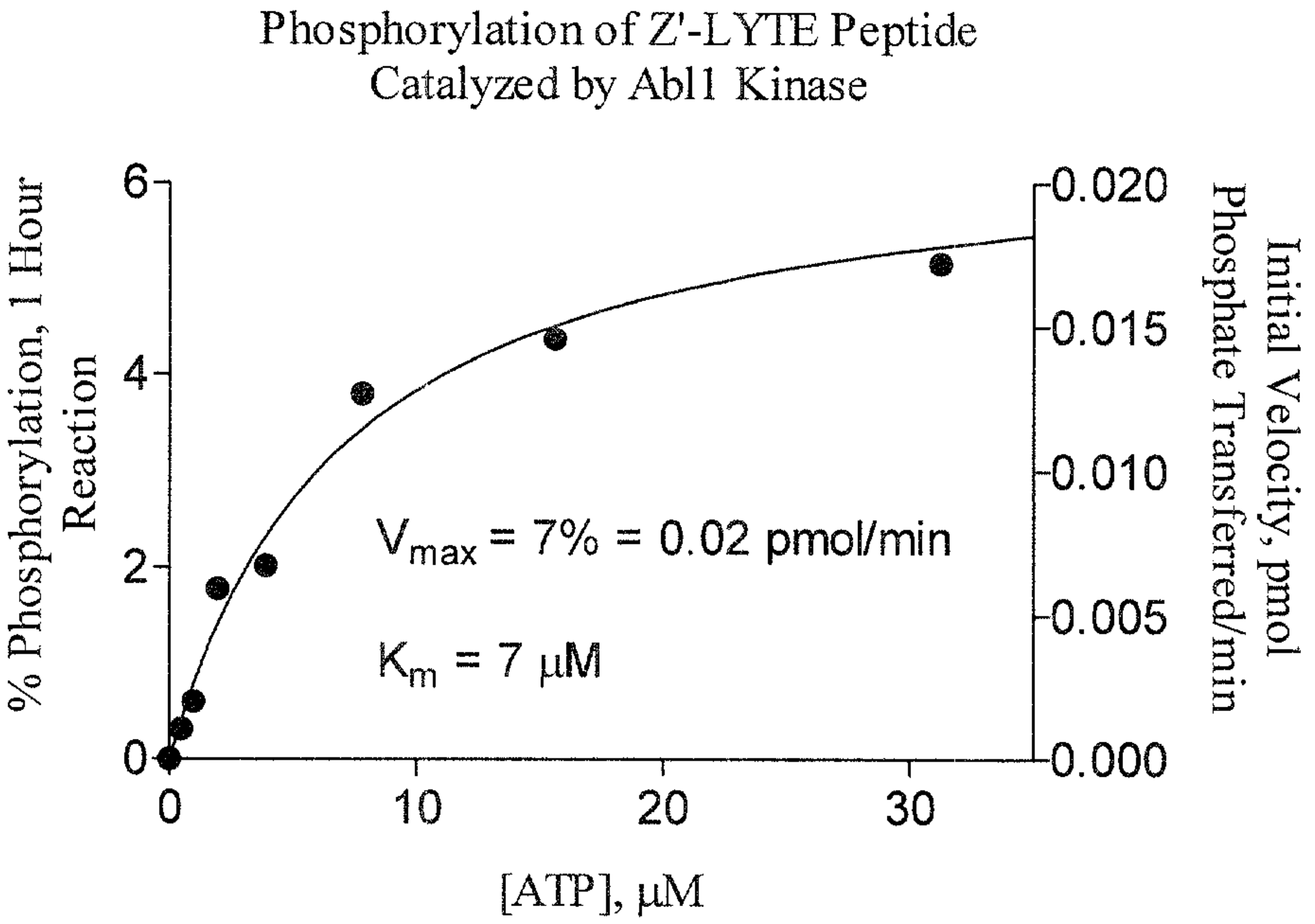
Phosphorylation of Z'-LYTE Peptide
Catalyzed by Abl1 Kinase
% Phosphorylation, 1 Hour Reaction
0
2
4
6
0
10
20
30
[ATP], μM
Initial Velocity, pmol Phosphate Transferred/min
0.000
0.005
0.010
0.015
0.020
V_max = 7% = 0.02 pmol/min
K_m = 7 μM

FIG. 3

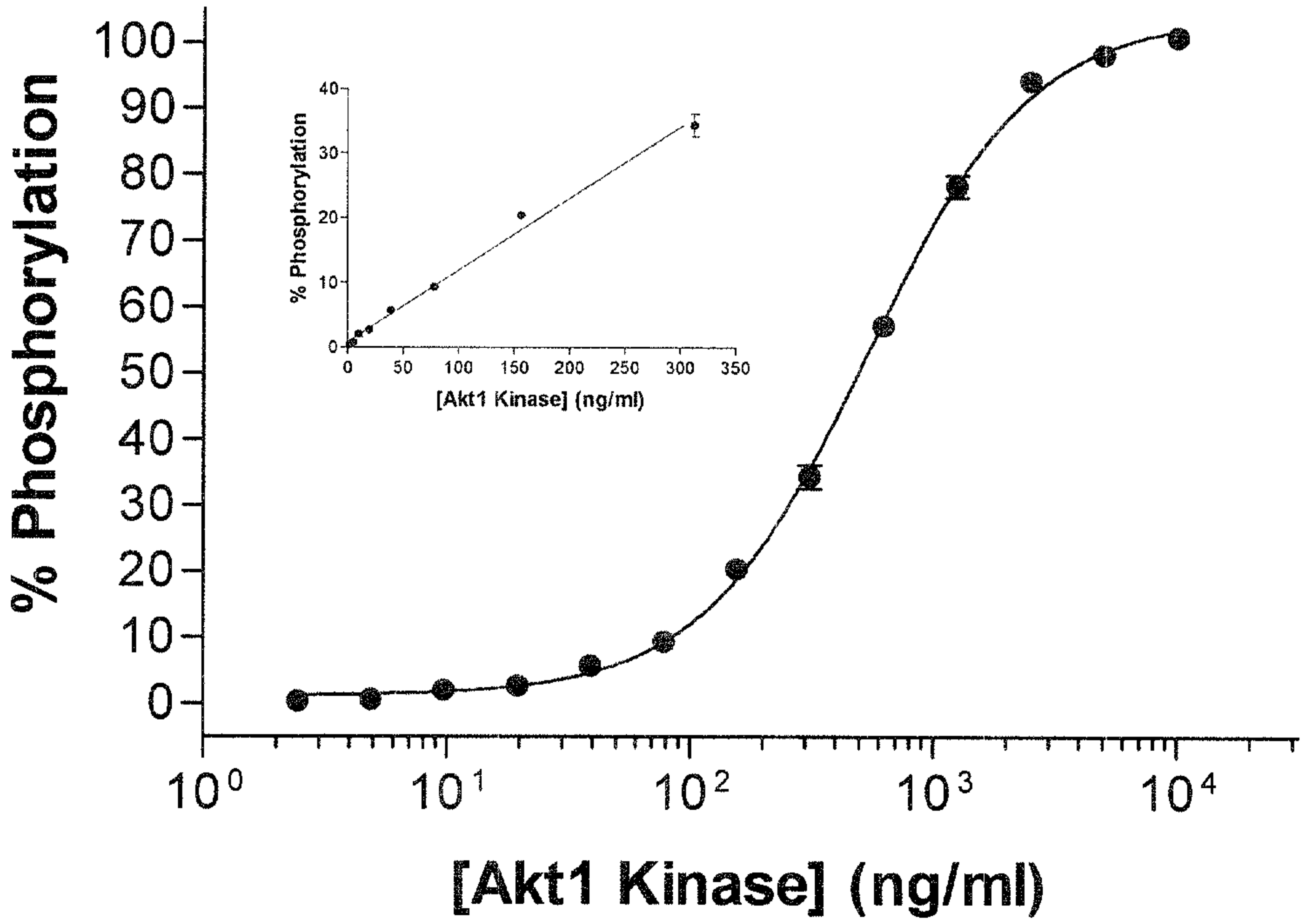
% Phosphorylation
100
90
80
70
60
50
40
30
20
10
0
10^0
10^1
10^2
10^3
10^4
[Akt1 Kinase] (ng/ml)
% Phosphorylation
40
30
20
10
0
0
50
100
150
200
250
300
350
[Akt1 Kinase] (ng/ml)

FIG. 4

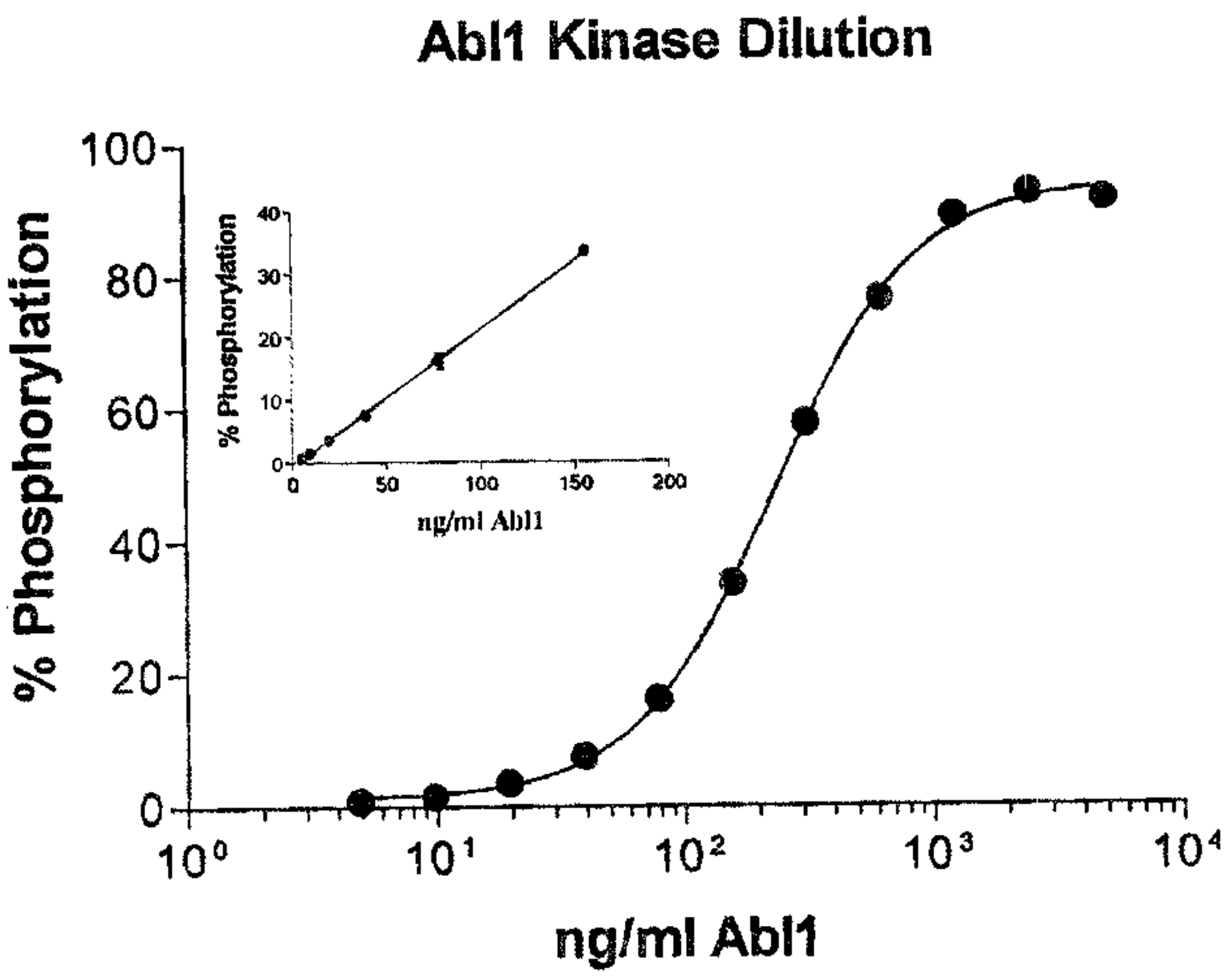
Abl1 Kinase Dilution
% Phosphorylation
100
80
60
40
20
0
10⁰
10¹
10²
10³
10⁴
ng/ml Abl1
% Phosphorylation
40
30
20
10
0
0
50
100
150
200
ng/ml Abl1

FIG. 5

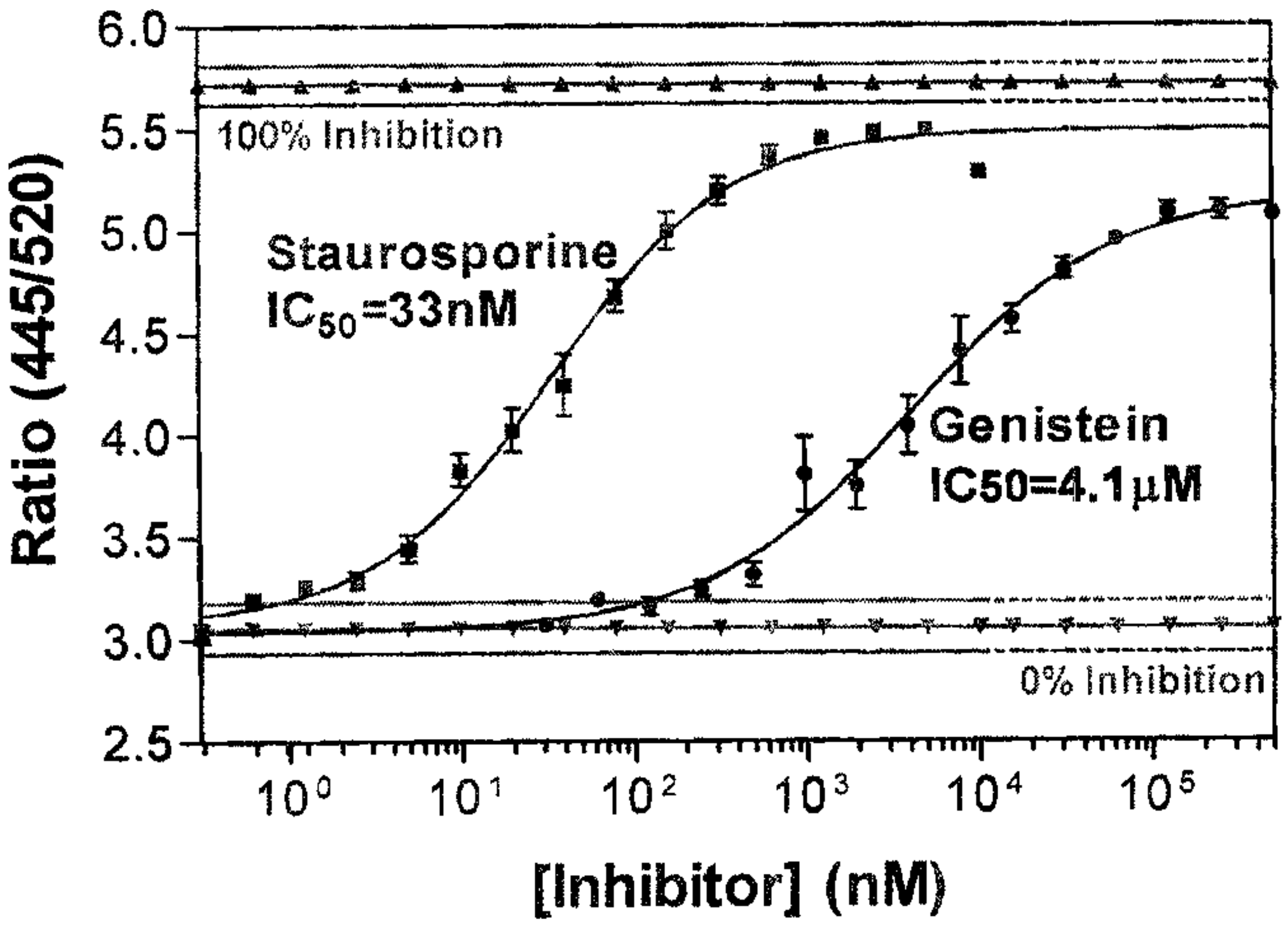
6.0
5.5
5.0
4.5
4.0
3.5
3.0
2.5
Ratio (445/520)
100% Inhibition
Staurosporine
IC_{50}=33nM
Genistein
IC50=4.1μM
0% Inhibition
10^0
10^1
10^2
10^3
10^4
10^5
[Inhibitor] (nM)

FIG. 6

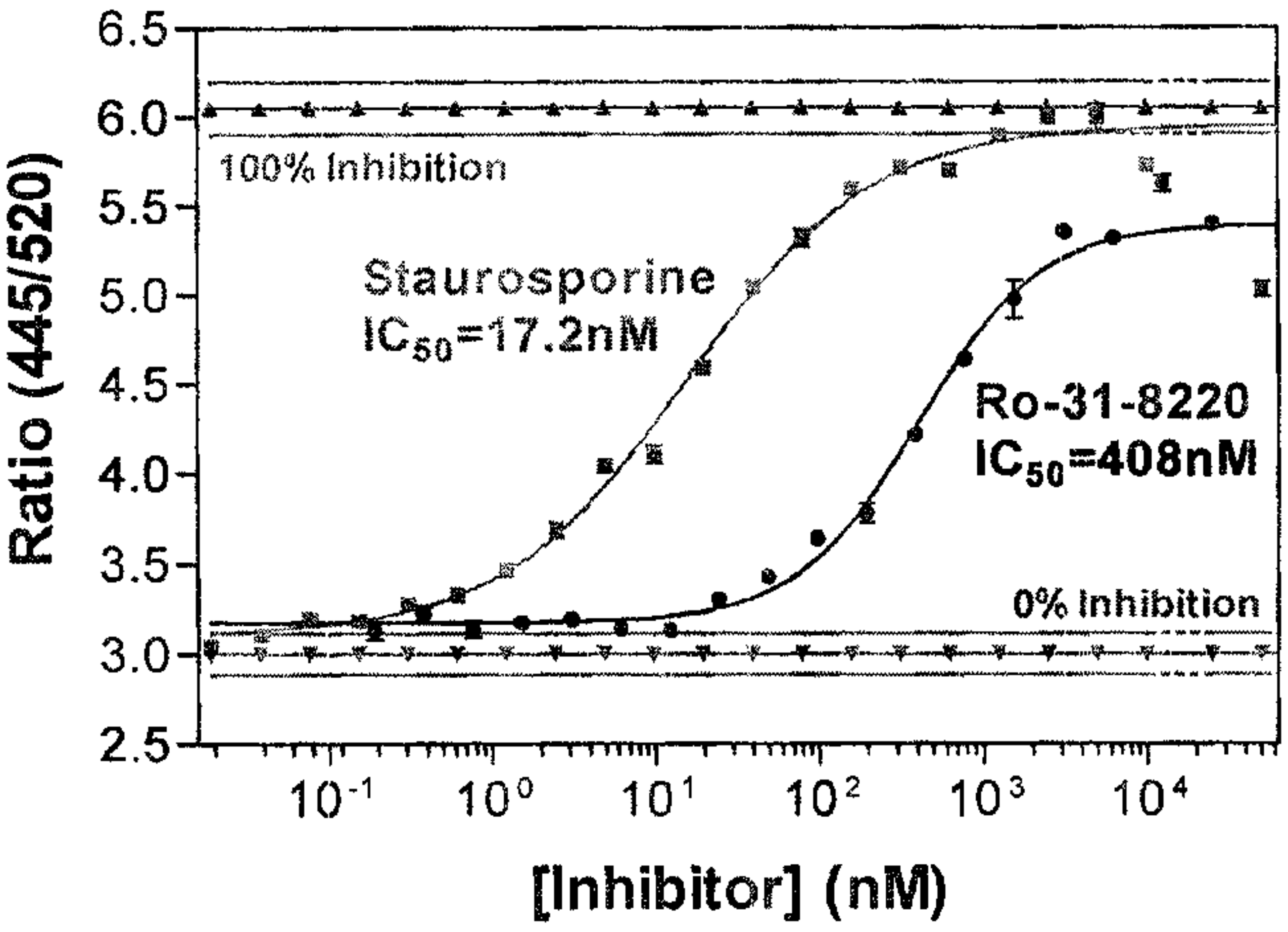
6.5
6.0
5.5
5.0
4.5
4.0
3.5
3.0
2.5
Ratio (445/520)
100% Inhibition
Staurosporine
IC$_{50}$=17.2nM
Ro-31-8220
IC$_{50}$=408nM
0% Inhibition
10^{-1}
10^{0}
10^{1}
10^{2}
10^{3}
10^{4}
[Inhibitor] (nM)

FIG. 7

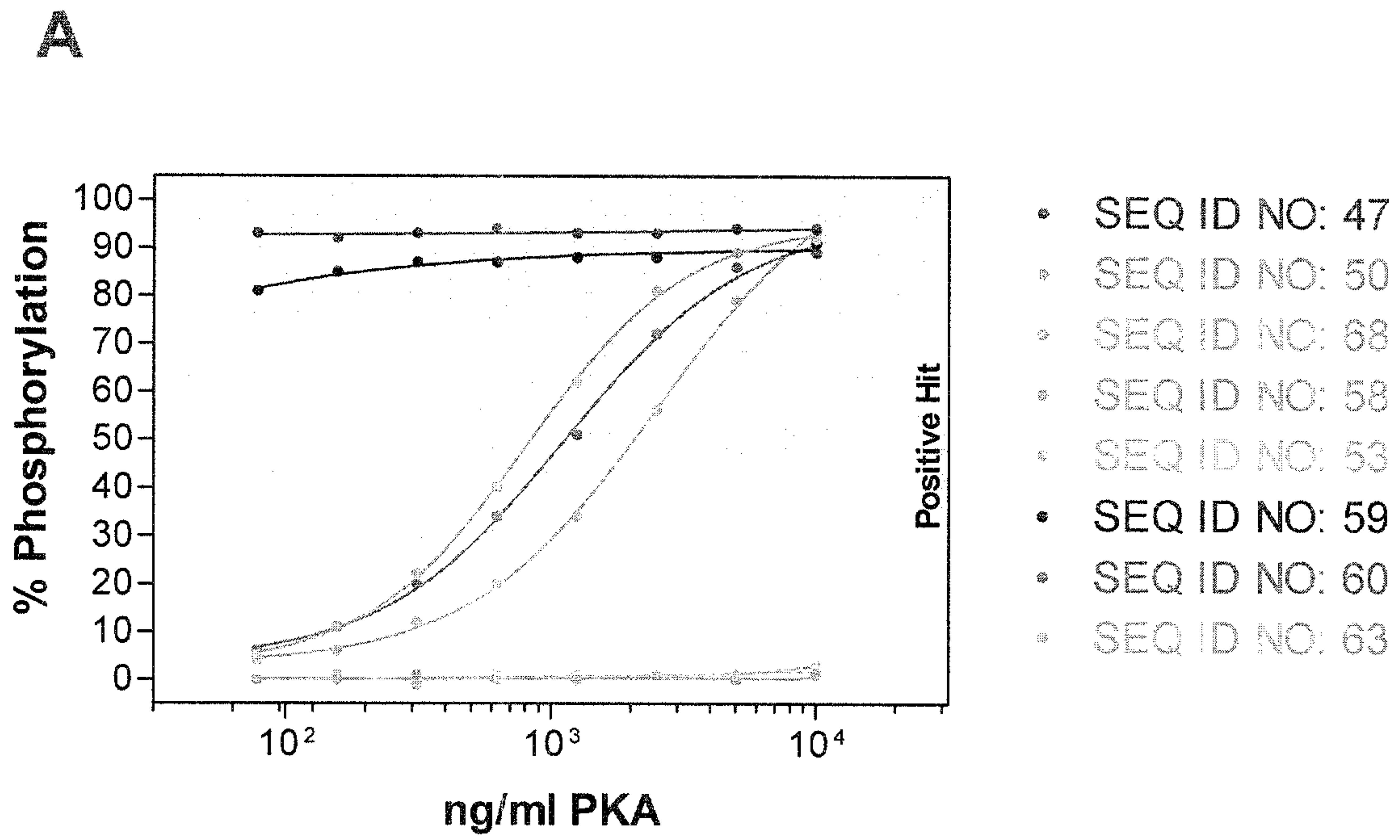
A
% Phosphorylation
100
90
80
70
60
50
40
30
20
10
0
10^2
10^3
10^4
ng/ml PKA
Positive Hit
● SEQ ID NO: 47
● SEQ ID NO: 50
● SEQ ID NO: 68
● SEQ ID NO: 58
● SEQ ID NO: 53
● SEQ ID NO: 59
● SEQ ID NO: 60
● SEQ ID NO: 63

FIG. 8

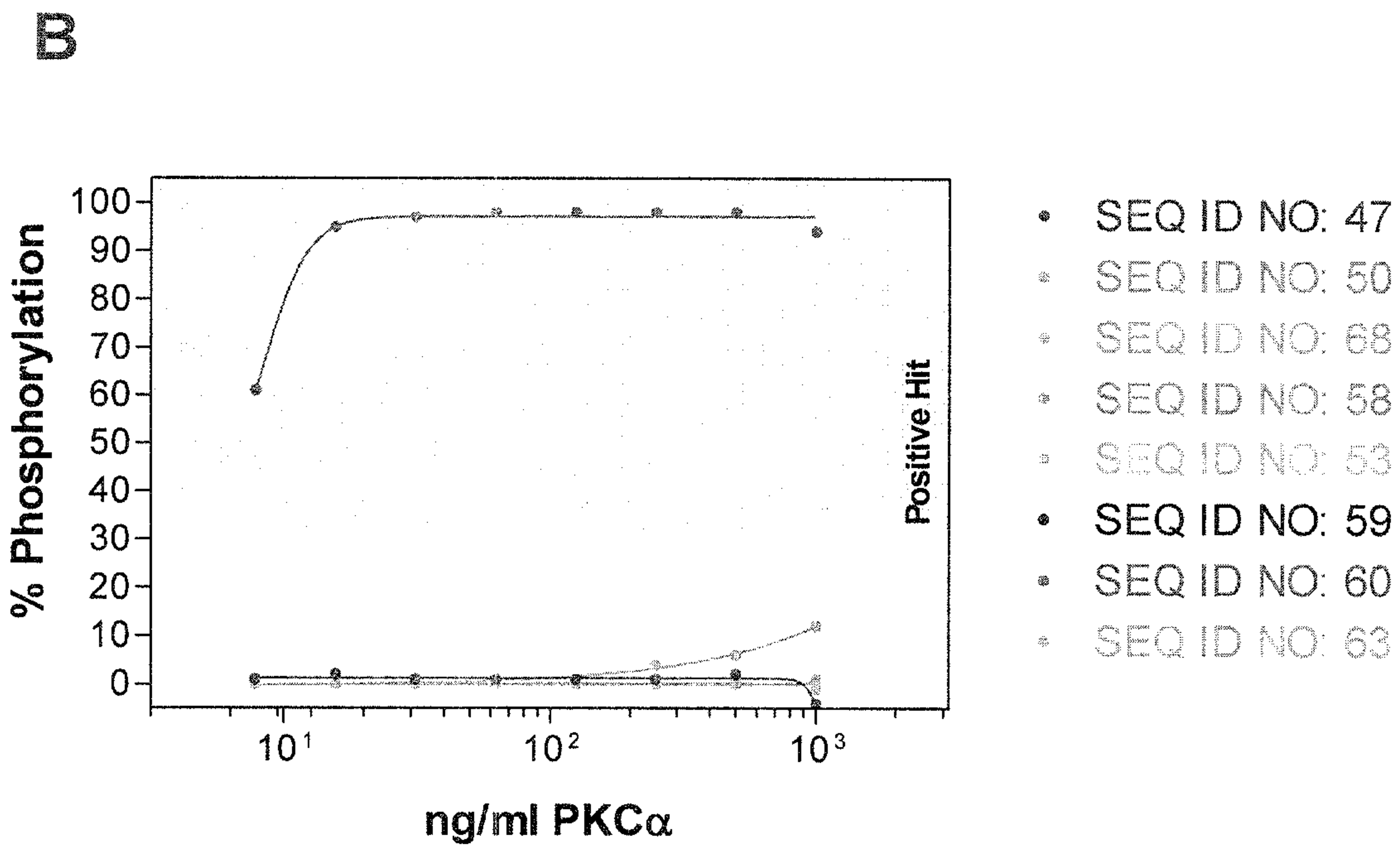
B
% Phosphorylation
100
90
80
70
60
50
40
30
20
10
0
10^1
10^2
10^3
ng/ml PKCα
Positive Hit
SEQ ID NO: 47
SEQ ID NO: 50
SEQ ID NO: 68
SEQ ID NO: 58
SEQ ID NO: 53
SEQ ID NO: 59
SEQ ID NO: 60
SEQ ID NO: 63

FIG. 9