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 TECHNIQUES D'UTILISATION  
 (54) Title: TISSUE TYPE PLASMINOGEN ACTIVATOR (t-PA) VARIANTS: COMPOSITIONS AND METHODS OF USE

(57) **Abrégé/Abstract:**

Variants of tissue plasminogen factor exhibit significantly enhanced fibrin stimulation, dramatically increased discrimination among fibrin co-factors, marked resistance to inhibition by PAI-1, and substantially increased zymogenicity, a combination of properties that enhance the therapeutic utility of the enzyme.

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<p>(54) Title: <b>TISSUE TYPE PLASMINOGEN ACTIVATOR (t-PA) VARIANTS: COMPOSITIONS AND METHODS OF USE</b></p> <p>(57) Abstract</p> <p>Variants of tissue plasminogen factor exhibit significantly enhanced fibrin stimulation, dramatically increased discrimination among fibrin co-factors, marked resistance to inhibition by PAI-1, and substantially increased zymogenicity, a combination of properties that enhance the therapeutic utility of the enzyme.</p>		

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## TISSUE TYPE PLASMINOGEN ACTIVATOR (t-PA) VARIANTS: COMPOSITIONS AND METHODS OF USE

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10 Governmental Rights

This invention was made with governmental support from the United States Government, National Institutes of Health, Grants HL52475 and HL31950; the United States Government has certain rights in the invention.

15 The invention comprises protein single chain variants of tissue type plasminogen activator, also referred to as t-PA as well as nucleic acids encoding such protein single chain variants of tissue type plasminogen activator. The t-PA protein variants have higher zymogenicity than the wild-type single chain t-PA form. Methods of making and using the t-PA variant compositions are also described.

20 Background

Tissue-type plasminogen activator (t-PA) is a serine protease that plays a critical role in the process of fibrinolysis, the dissolution of clots, by activating plasminogen to the protease plasmin. t-PA has been fully identified and characterized by underlying DNA sequence and deduced amino acid sequence. See Pennica et al., *Nature*, 301: 214 (1983) and U.S. Pat. No. 25 4,853,330, issued Aug. 1, 1989, the teachings of both of which are incorporated by reference. The nucleotide sequence and deduced primary amino acid sequence of human t-PA is depicted in Fig. 1A, Fig. 1B and Fig. 1C.

30 The group of amino acid residues from -35 to -1 preceding the sequence of the mature t-PA is the "pro" sequence. The mature t-PA molecule (amino acid residues 1-527) contains five domains that have been defined with reference to homologous or otherwise similar structures identified in various other proteins such as trypsin, chymotrypsin, plasminogen, prothrombin, fibronectin, and epidermal growth factor (EGF). These domains have been

designated, starting at the N-terminus of the amino acid sequence of mature t-PA, as 1) the finger region (F) that has variously been defined as including amino acid residues 1 to about 44, 2) the growth factor region (G) that has been variously defined as stretching from about amino acid residues 45 to 91 (based upon its homology with EGF), 3) kringle one (K1) that has been defined as stretching from about amino acid residue 92 to about amino acid residue 173, 4) kringle two (K2) that has been defined as stretching from about amino acid residue 180 to about amino acid residue 261, and 5) the so-called serine protease domain (P) that generally has been defined as stretching from about amino acid residue 264 to the C-terminal end of the molecule at amino acid residue 527. These domains, which are situated generally adjacent to one another, or are separated by short "linker" regions, account for the entire amino acid sequence of from 1 to 527 amino acid residues of the mature form of t-PA.

Each domain has been described variously as contributing certain specific biologically significant properties. The finger domain has been characterized as containing a sequence of at least major importance for high binding affinity to fibrin. (This activity is thought important for the high specificity that t-PA displays with respect to clot lysis at the locus of a fibrin-rich thrombus.) The growth factor-like region likewise has been associated with cell surface binding activity. The kringle 2 region also has been strongly associated with fibrin binding and with the ability of fibrin to stimulate the activity of t-PA. The serine protease domain is responsible for the enzymatic cleavage of plasminogen to produce plasmin.

t-PA is unusual among proteases in the level of the enzymatic activity of its precursor. In general, proteases are synthesized as zymogens, inactive precursors that must either be proteolytically processed or bind to a specific co-factor to develop substantial catalytic activity. The increase in catalytic efficiency after zymogen activation, or zymogenicity, is dramatic in almost all cases, although varying widely among individual members of the chymotrypsin family. For example, strong zymogens, i.e., those having high zymogenicity, such as trypsinogen, chymotrypsinogen, or plasminogen are almost completely inactive, with measured zymogenicities of  $10^4$  to  $10^6$  (Robinson, N. C., Neurath, H., and Walsh, K. A. (1973) *Biochemistry* 12, 420-426; Gertler, A., Walsh, K. A., and Neurath, H. (1974) *Biochemistry* 13, 1302-1310). Other serine proteases exhibit intermediate zymogenicity. For example, the enzymatic activity of Factor XIIa is 4000-fold greater than that of its corresponding zymogen, Factor XII (Silverberg, M., and Kaplan, A. P. (1982) *Blood* 60, 64), and the catalytic efficiency of urokinase is 250-fold greater than that of pro-urokinase (Lijnen, H. R., Van Hoef,

B., Nelles, L., and Collen, D. (1990) *J. Biol. Chem.* **265**, 5232-5236). By contrast, the catalytic activities of single and two chain t-PA vary by a factor of only 5-10.

5 The zymogenicity, expressed as the ratio of the activity of the mature cleaved two-chain enzyme to that of the single chain precursor form, is only 5-10 for wild-type t-PA, in contrast to other precursors of other proteases that have little or no catalytic activity. Thus, the single chain form of wild-type t-PA is not a true zymogen.

10 There have been many attempts to improve the usefulness of t-PA by genetic engineering. These efforts have been only partially successful. The state of the art has been reviewed by Krause, J., & Tanswell, P. *Arzneim.-Forsch.* **39**: 632-637 (1989) and in U.S. patent No. 5,616,486.

15 Despite the profound advantages associated with natural t-PA as a clot-dissolving agent, it is not believed that the natural protein necessarily represents the optimal t-PA agent under all circumstances. Therefore, several variants have been proposed or devised to enhance specific properties of t-PA. Certain of those variants address disadvantages associated with the use of natural t-PA in situations where an agent with a longer half-life or slower clearance rate would be preferred, e.g., in the treatment of deep-vein thrombosis and following reperfusion of an infarct victim, or where a single-chain agent is preferred.

20 For example, removal of a substantial portion or all of the finger domain results in a molecule with substantially diminished fibrin binding characteristics, albeit in return there is a decrease in the overall rate of clearance of the resultant entity—See WO 89/00197 published Jan. 12, 1989.

25 Variants are described in EPO Pat. Publ. No. 199,574 that have amino acid substitutions at the proteolytic cleavage sites at positions 275, 276, and 277. These variants, characterized preferentially as t-PA variants having an amino acid other than arginine at position 275, are referred to as protease-resistant one-chain t-PA variants in that, unlike natural t-PA, which can exist in either a one-chain or two-chain form, they are resistant to protease cleavage at position 275 and are therefore not converted metabolically in vivo into a two-chain form. This form is thought to have certain advantages biologically and commercially, in that it is more stable while the fibrin binding and fibrin stimulation are increased relative to two-chain t-PA. Furthermore, plasminogen activators are described that comprise one domain capable of interacting with fibrin and the protease domain of urokinase, with one embodiment

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being urokinase altered to make it less susceptible to forming two-chain urokinase. See WO 88/05081 published Jul. 14, 1988.

For further patent literature regarding modification of the protease cleavage site of t-PA, see, for example, EPO Pat.Nos. 241,209; EP 201,153 published Nov. 12, 1986; EP 233,013 published Aug. 19, 1987; EP 292,009 published Nov. 23, 1988; EP 293,936 published Dec. 7, 1988; and EP 293,934 published Dec. 7, 1988; and WO 88/10119.

Glycosylation mutants at positions 117-119, 184-186, and 448-450 exhibited higher specific activity as the mole percent carbohydrate was reduced. See EPO Pub. No. 227,462 published Jul. 1, 1987. This patent application additionally discloses using an assay of fibrin/fibrin degradation products and teaches that one may also modify the t-PA molecule at positions 272-280 or delete up to 25 amino acids from the C-terminus. Further, the t-PA mutants with Asn 119, Ala 186 and Asn 450, which have the N-glycosylation sites selectively removed by DNA modification but contain residual O-linked carbohydrate, were found to be about two-fold as potent as melanoma t-PA in an in vitro lysis assay. See EPO Publ. No. 225,286 published Jun. 10, 1987.

Replacement of the amino acid at position 449 of t-PA with any amino acid except arginine to modify the glycosylation site, as well as modification of Arg 275 or deletion of the - 3 to 91 region, is also taught. See WO 87/04722 published Aug. 13, 1987. An amino acid substitution at position 448 of t-PA is disclosed as desirable to remove glycosylation. See EPO Pub. No. 297,066 published Dec. 28, 1988. The combination of modifications at positions 448-450 and deletion of the N-terminal 1-82 amino acids is disclosed by WO 89/00191 published Jan. 12, 1989. Additionally, urokinase has been modified in the region of Asp 302 -Ser 303 -Thr 304 to prevent glycosylation. See EPO Pub. No. 299,706 published Jan. 18, 1989.

However, alteration of the glycosylation sites, and in particular that at amino acid 117, seems invariably to result in a molecule having affected solubility characteristics that may result additionally in an altered circulating half-life pattern and/or fibrin binding characteristics. See EPO Pat. Publ. No. 238,304, published Sep. 23, 1987.

When the growth factor domain of t-PA is deleted, the resultant variant is still active and binds to fibrin, as reported by A. J. van Zonneveld et al., *Thrombos. Haemostas.* **54** (1): 4 (1985). Various deletions in the growth factor domain have also been reported in the patent literature. See EPO Publ. No. 241,209 (del-51-87), EPO Publ. No. 241,208 (del-51-87 and

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del-51-173), PCT 87/04722 (deletion of all or part of the N-terminal 1 - 91), EPO Publ. No. 231,624 (all of growth factor domain deleted), and EPO Publ. No. 242,836 and Jap. Pat. Appl. Kokai No. 62 - 269688 (some or all of the growth factor domain deleted).

5 It has further been shown that t-PA can be modified both in the region of the first kringle domain and in the growth factor domain, resulting in increased circulatory half-life. See EPO Pat. Publ. No. 241,208 published Oct. 14, 1987. The region between amino acids 51 and 87, inclusive, can be deleted from t-PA to result in a variant having slower clearance from plasma. Browne et al., *J. Biol. Chem.*, 263: 1599-1602 (1988). Also, t-PA can be modified, without adverse biological effects, in the region of amino acids 67 to 69 of the  
10 mature, native t-PA, by deletion of certain amino acid residues or replacement of one or more amino acids with different amino acids. See EPO Pat. Publ. No. 240,334 published Oct. 7, 1987.

A hybrid of t-PA/urokinase using the region of t-PA encompassing amino acids 273 - 527 is also disclosed. See EPO 290,118 published Nov. 9, 1988. Serpin-resistant mutants of  
15 human t-PA with alterations in the protease domain, including del296-302 t-PA, R304S t-PA, and R304E t-PA, are disclosed in Madison et al., *Nature*, 339: 721-724 (1989). The above list is not an exhaustive review of the numerous variants of t-PA that have been described.

As a result of the catalytic activity of precursor t-PA, despite effective clot lysis at targeted sites, nondesirable proteolysis occurs systemically resulting in the deleterious  
20 depletion of circulating fibrinogen,  $\alpha$ 2-anti-plasmin and plasminogen. What is needed are more zymogenic t-PA variant proteins that provide effective local clot lysis with diminished systemic proteolytic effects.

### Summary of the Invention

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The present invention provides single chain variant t-PA proteins having at least two substitutions of basic amino acid residues by neutral or acidic amino acid residues, compared to the wild-type human t-PA, as well as polynucleotides encoding such single chain variant t-PA proteins. The single chain variant t-PA proteins of the present invention have the R275  
30 amino acid residue substituted by an amino acid residue chosen from the group consisting of glycine, serine, threonine, asparagine, tyrosine, glutamine, aspartic acid, and glutamic acid. Preferably the single chain variant t-PA proteins of the present invention have the R275 amino

acid residue substituted by an amino acid residue chosen from the group consisting of an aspartic acid residue and a glutamic acid residue, and most preferably by a glutamic acid residue.

5 The single chain variant t-PA proteins of the present invention have additionally at least one other basic amino acid residue in the serine protease region residue substituted by a non-basic amino acid such that the salt bridge interaction normally found in wildtype single chain t-PA between aspartate 477 and lysine 429 is disrupted. Preferably, basic amino acids are replaced with polar or acidic amino acids, and more preferably, amino acid residues chosen from the group consisting of glycine, serine, threonine, asparagine, tyrosine, glutamine,  
10 aspartic acid and glutamic acid.

The salt bridge interaction between aspartate 477 and lysine 429 can be disrupted by a substitution at position 477 or 429, or by an appropriate substitution at a position within the serine protease region that provides an alternative salt bridge interaction partner for at least one of aspartate 477 and lysine 429. In one preferred embodiment, the H417 amino acid residue is  
15 substituted by an amino acid residue chosen from the group consisting of glycine, serine, threonine, asparagine, tyrosine, glutamine, aspartic acid, and glutamic acid. More preferably the single chain variant t-PA proteins of the present invention have both the R275 amino acid residue and the H417 amino acid residue substituted by an amino acid residue chosen from the group consisting of an aspartic acid residue and a glutamic acid residue. Two exemplary  
20 preferred single chain variant t-PA proteins are the t-PA variants designated as R275E,H417E and R275E,H417D.

In another preferred embodiment, the K429 amino acid residue is substituted by an amino acid residue chosen from the group consisting of glycine, serine, threonine, asparagine, tyrosine, glutamine, aspartic acid, and glutamic acid. More preferably the single chain variant  
25 t-PA proteins of the present invention have both the R275 amino acid residue and the K429 amino acid residue substituted by an amino acid residue chosen from the group consisting of glycine, serine, threonine, asparagine, tyrosine, glutamine, aspartic acid, and glutamic acid. One preferred single chain variant t-PA protein is the t-PA variant designated as R275E,K429Y.

30 The single chain variant t-PA proteins of the present invention exhibit greater zymogenicity, expressed as the ratio of the activity of the mature cleaved two-chain enzyme to that of the single chain precursor form, than that of the wild type single chain t-PA protein.



The single chain variant t-PA proteins of the present invention have zymogenicity of at least 10, preferably about 50 to about 200.

5 The single chain variant t-PA proteins of the present invention exhibit a greater fibrin stimulation factor, expressed as the ratio of the catalytic efficiencies in the presence and absence of fibrin, compared to the wild type single chain t-PA protein. The single chain variant t-PA proteins of the present invention have a fibrin stimulation factor of at least 7,000, preferably about 20,000 to about 50,000.

10 The single chain variant t-PA proteins of the present invention exhibit a reduced inhibition by plasminogen activator inhibitor 1 (PAI-1) to the wild type single chain t-PA protein. The single chain variant t-PA proteins of the present invention are at least a factor of 5, preferably at least a factor of about 9, most preferably at least a factor of about 200 less inhibited by PAI-1 compared to the wild type single chain t-PA protein.

15 The single chain variant t-PA proteins of the present invention exhibit a greater fibrin selectivity factor, expressed as the ratio of the catalytic efficiencies in the presence fibrin to that in the presence of fibrinogen, compared to the wild type single chain t-PA protein. Preferred embodiments of the single chain variant t-PA proteins of the present invention have a fibrin selectivity factor of at least 10, preferably at least 50, more preferably at least 100.

#### Brief Description of the Drawings

20 In the drawings,

Figs. 1A, 1B and 1C show the nucleotide sequence and deduced amino acid sequence of the full-length human t-PA cDNA; and

25 Fig. 2 is a graphical representation of the results of standard chromogenic assays of plasminogen activation in the presence of buffer (open squares), DESAFIB (open diamonds), fibrinogen (open circles), cyanogen bromide fragments of fibrinogen (open triangles) or the stimulatory peptide P368 (hatched squares).

#### Detailed Description of the Preferred Embodiments

30 As used herein, "wild-type t-PA" refers to the t-PA protein naturally occurring in humans. While this human t-PA is exemplified by the amino acid sequence depicted in Figs. 1A, 1B and 1C, the term wild-type t-PA should be understood to encompass naturally occurring allelic variations.

### t-PA Variant Compositions

The t-PA variant cDNAs and the corresponding expressed recombinant proteins of this invention are useful compounds that function in the serine protease-mediated control of fibrinolysis as described herein.

5           The t-PA variant cDNAs of the present invention contain at least one nucleotide substitution to generate a t-PA cDNA that encodes a noncleavable single chain t-PA variant, i.e., not cleavable by plasmin under normal conditions. The nucleotide substitution results in a substitution of a glutamic acid (E) for an arginine (R) at amino acid residue 275 (or position 15 using the chymotrypsin numbering system) in the t-PA precursor that is responsible for  
10           creating a noncleavable variant. Positions 15, 144, 156, and 194 of the chymotrypsin numbering system correspond to positions 275, 417, 429, and 477, respectively, in the t-PA numbering system as depicted in Fig. 1.

          The variants, which are substitution mutants, are designated by the single letter code of the wild type human t-PA amino acid residue, the position of the residue relative to the amino  
15           terminus of the mature human t-PA as depicted in Fig. 1, followed by the single letter code of the amino acid residue substituted for the amino acid residue in mature human t-PA. The substitution of glutamic acid for arginine at position 275 is designated as R275E. Equivalent substitutions generating noncleavable single chain t-PA are known in the art (Higgins, D.L., et al., (1990) *Thrombosis Res.* 57: 527-539).

20           In addition to the R275E substitution, the variant cDNAs of the present invention further comprise at least one other nucleotide substitution at a separate site to create a t-PA variant having at least two amino acid substitutions. Preferred cDNA variants include at least one nucleotide substitution that results in an amino acid substitution of an amino acid residue chosen from the group consisting of glycine, serine, threonine, asparagine, tyrosine, glutamine,  
25           aspartic acid, and glutamic acid for a histidine at amino acid residue position 417. Preferred embodiments are designated R275E,H417D and R275E,H417E. A further cDNA variant comprises at least one nucleotide substitution resulting in the substitution of an amino acid residue chosen from the group consisting of glycine, serine, threonine, asparagine, tyrosine, glutamine, aspartic acid, and glutamic acid for the lysine (K) at amino acid residue position  
30           429. One such preferred embodiment is designated R275E,K429Y.

The variant t-PA cDNAs of the present invention are useful for generating the recombinant expressed variant t-PAs described above. In a further embodiment, the variant t-PA cDNAs have therapeutic uses in gene therapy as described below.

5 The invention includes embodiments such as expression vectors or plasmids in which the cDNAs for encoding variant t-PAs are operably linked to provide for the expression of recombinant variant t-PAs for use in the methods as described below. One preferred embodiment is the expression of a variant t-PA protein by COS 1 cells comprising pSVT7 expression vector operably linked to a polynucleotide encoding the variant protein. Constitutive and inducible expression vectors are disclosed. In a further embodiment,  
10 transiently and stably transfected cells contain cDNA encoding variant t-PAs.

The resultant recombinant expressed t-PA variants described herein are characterized as having one or more of the following structural and functional properties: 1) The t-PA variant is in the form of a noncleavable single chain protein containing an R275E amino acid substitution or equivalents thereof that prevent cleavage by t-PA activating enzymes; 2) The t-PA variant exhibits increased resistance to inhibition by the serpin plasminogen activator inhibitor, type I (PAI-1); 3) The t-PA variants has diminished catalytic activity on substrates, such as plasminogen, in the absence of co-factors, such as fibrin; 4) The t-PA variants exhibit enhanced stimulation by fibrin; 5) The t-PA variants exhibit comparable catalytic activity to substrates, such as plasminogen, in the presence of co-factors, such as fibrin; and 6) In view of  
15 the proceeding properties, the t-PA variants thus are effective at local fibrinolysis function without extensive systemic proteolysis thereby negating the depletion of circulating fibrinogen,  $\alpha$ 2-anti-plasmin and plasminogen, as is seen with wild type human single chain t-PA precursor.  
20

Preferred recombinant expressed t-PA variants thus include R275E,H417D,  
25 R275E,H417E and R275E,K429Y, and conservative substitutions thereof. In general, examples of conservative substitutions include the substitution of one non-polar (hydrophobic) residue such as isoleucine, valine, leucine or methionine for another, the substitution of one polar (hydrophilic) residue for another such as between arginine and lysine, between glutamine and asparagine, between glycine and serine, the substitution of one basic residue such as  
30 lysine, arginine or histidine for another, or the substitution of one acidic residue, such as aspartic acid or glutamic acid for another. For further discussion of the classifications of

amino acids see Lehninger, A.L., Biochemistry, 2<sup>nd</sup> Edition, Worth Publishers, New York, 1975, pp.71-94.

The phrase "conservative substitution" also includes the use of a chemically derivatized residue in place of a non-derivatized residue provided that such protein displays the requisite binding activity. "Chemical derivative" refers to a subject protein having one or more residues chemically derivatized by reaction of a functional side group. Such derivatized molecules include for example, those molecules in which free amino groups have been derivatized to form amine hydrochlorides, p-toluene sulfonyl groups, carbobenzoxy groups, t-butylloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups may be derivatized to form salts, methyl and ethyl esters or other types of esters or hydrazides. Free hydroxyl groups may be derivatized to form O-acyl or O-alkyl derivatives. The imidazole nitrogen of histidine may be derivatized to form N-im-benzylhistidine. Also included as chemical derivatives are those peptides which contain one or more naturally occurring amino acid derivatives of the twenty standard amino acids. For example, 4-hydroxyproline may be substituted for proline; 5-hydroxylysine may be substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine; and ornithine may be substituted for lysine. D-amino acids may also be included in place of one or more L-amino acids.

In the specific case of the present invention, basic amino acids, i.e., arginine, lysine and histidine are replaced with non-basic amino acids. Preferably basic amino acids are replaced with polar or acidic amino acids, i.e. amino acid residues chosen from the group consisting of glycine, serine, threonine, asparagine, tyrosine, glutamine, aspartic acid and glutamic acid. Conservative substitutions are thus defined, for the purpose of the present invention, as meaning that non-basic amino acids replacing particular basic amino acids in mature wild type human t-PA may be chosen from the group of non-basic amino acids generally, preferably from the group consisting of glycine, serine, threonine, asparagine, tyrosine, glutamine, aspartic acid and glutamic acid, and more preferably from the group consisting of tyrosine, aspartic acid and glutamic acid, For example, the use of aspartic acid instead of glutamic acid to replace an histidine residue is a conservative substitution. Preferred variants are R275E,H417D and R275E,H417E, described in Example 1 and the R275E,K429Y variant, described in Example 2.

The expressed recombinant t-PA variants having at least two amino acid substitutions, e.g., R275E,H417D, R275E,H417E and R275E,K429Y, further exhibit unique properties. R275E and R275E,H417E are activated by both fibrinogen and fibrin while R275E,K429Y is activated primarily by fibrin and is not sensitive to fibrinogen. The latter is also more resistant than the R275E,H417D and R275E,H417E variants to inhibition by PAI-1. These characteristics provide additional advantages in administering the compounds as therapeutic thrombolytic compositions as further described below. In addition, the t-PA variants described herein are useful in diagnostic applications as described below.

## 10 Methods of making and Using t-PA Variant Compositions

### Methods of Making

The t-PA variant cDNA and recombinant expressed variant proteins described above are useful in a number of methodological aspects as described in Examples 1 and 2. In particular, the isolated cDNA clones are useful in an expression vector system to produce encoded t-PA variant proteins of this invention. Thus, expression vector systems having a t-PA variant cDNA operably linked therein, including cells containing the expression vectors, are contemplated for generating the recombinant expressed variant proteins of this invention.

### Diagnostic Applications

Preferred diagnostic methodological aspects are described herein. In particular, the recombinant expressed t-PA variants of the present invention are useful in diagnostic assays to detect fibrin and fibrin degradation products that have altered activities. The assays are thus indicated in thrombotic conditions. Other diagnostic applications, including kits comprising antibodies against the t-PA variants are familiar to one of ordinary skill in the art.

### Therapeutic Applications

The t-PA variant cDNAs of the present invention are useful in genetic therapeutic applications for use in ameliorating thrombotic disorders including both acute and chronic conditions. Acute conditions include among others both heart attack and stroke while chronic situations include those of arterial and deep vein thrombosis and restenosis. Preferred

therapeutic compositions thus include the cDNA compounds themselves as naked DNA, presented as part of a viral vector delivery system or other vector-based gene expression delivery system, presented in a liposome delivery system and the like.

5 The recombinant expressed t-PA variant proteins of the present invention are contemplated as thrombolytic therapeutic agents for ameliorating the same conditions outlined above. Based on the individual structural and functional properties of various t-PA variant proteins described above, the selection of the particular t-PA variant is determined by the desired therapeutic outcome. For example, the fibrinogen-mediated activation of endogenous human t-PA is activated by bleeding which then results in a widespread undesired systemic response. Thus, to mediate fibrinolytic processes locally in either an acute or chronic thrombotic condition while simultaneously preventing proteolytic activation systemically, one would therefore use the t-PA variant, namely R275E,K429Y, that is primarily activated by fibrin and not fibrinogen. A composition for use as thrombolytic therapeutic agents generally consists of a physiologically effective amount of the t-PA variant protein in a pharmaceutically suitable excipient. Depending on the mode of administration and the condition to be treated, 15 the thrombolytic therapeutic agents are administered in single or multiple doses. If "bolus" doses are administered, doses of about 0.01 to about 0.6 mg/kg will typically be administered, preferably doses of about 0.05 to about 0.2 mg/kg, with subsequent administrations of about 0.1 to about 0.2 mg/kg to maintain a t-PA blood level of about 3 microgram/ml. One skilled in the art will appreciate that variations in dosage depend on the condition to be treated. In other applications, a composition of variant t-PA in a gel composition is useful in preventing the formation of adhesions.

Other variations and uses of the present invention will be apparent to one skilled in the art.

25

### Example 1

#### **Site Directed Mutagenesis And Construction Of Expression Vectors Encoding Variants Of T-PA**

Oligonucleotide directed site specific mutagenesis was performed by the method of Zoller and Smith (Zoller, M. I., and Smith, M. (1984) DNA 3, 479-488) as modified by Kunkel (Kunkel, T. A. (1985) Proc. Natl. Acad. Sci. U.S.A 82, 488-492). Mutations were introduced into the 290 bp *SacI* - *SmaI* fragment of cDNA encoding t-PA that had been 30

previously subcloned into bacteriophage M13mp18. The mutagenic primers had the following nucleotide sequences:

H417D: 5' – CTACGGCAAGGACGAGGCCTTGT – 3' (SEQ ID NO: 8)

H417E: 5' – CTACGGCAAGGAGGAGGCCTTGT – 3' (SEQ ID NO: 9)

5 Following mutagenesis, ssDNA corresponding to the entire 290 bp *SacI* – *SmaI* fragment was fully sequenced to assure the presence of the desired mutation and the absence of any additional mutations. The sequence corresponding to the 290 bp *SacI* – *SmaI* fragment of the H417D mutation is shown in SEQ ID NO: 5; the corresponding sequence of the H417E mutation is shown in SEQ ID NO: 6. Replicative form (RF) DNA was prepared for  
10 appropriate phage, and the mutated 290 bp *SacI* – *SmaI* fragments were recovered after digestion of RF DNA with *SacI* and *SmaI* and electrophoresis of the digestion products on an agarose gel. The isolated, mutated *SacI* – *SmaI* fragments were used to replace the corresponding fragment in full length cDNAs encoding wild type human t-PA or t-PA/R275E to yield new, full length cDNAs encoding t-PA/H417D; t-PA/H417E; t-PA/R275E,H417D  
15 (SEQ ID NO: 1); and t-PA/R275E,H417E (SEQ ID NO: 2).

#### **Expression of enzymes by transient transfection of COS cells.**

cDNAs encoding t-PA; t-PA/R275E; t-PA/H417D; t-PA/H417E; t-PA/R275E,H417D; and t-PA/R275E were ligated into the transient expression vector pSVT7 which is described in  
20 Madison, E. L., et al. (1989) *Nature* 339, 721-724; Bird, P.M., et al., (1987) *J. Cell Biol.* 105: 2905-2914; and Sambrook, J., et al., (1986) *Mol. Biol. Med.* 3: 459-481. See also U.S. Pat. No. 5,550,042, which describes the construction and use of pSVT7 as well as the deposit with American Type Culture Collection, 12301 Parklawn Dr., Rockville, MD 20852 of cultures comprising other pSVT7 t-PA constructs. Vectors with  
25 ligated cDNA inserts were then introduced into COS 1 cells by electroporation using a Bio Rad Gene Pulser.<sup>TM</sup> An aliquot containing 20 µg of cDNA, 100 µg of carrier DNA and approximately 10<sup>7</sup> COS cells were placed into a 0.4 cm cuvette, and electroporation was performed at 320 V, 960 µFD, and  $\Omega = \infty$ . Following electroporation, cells were incubated overnight at 37 degrees Celsius in DMEM containing 10% fetal calf serum and 5 mM sodium  
30 butyrate. Cells were then washed with serum free medium and incubated in DMEM for 48 hours at 37 degrees Celsius. After the incubation with serum free media, conditioned media

were collected. Enzyme concentrations in aliquots of the the collected conditioned media were determined by ELISA.

#### **Kinetic analysis of plasminogen activation using indirect chromogenic assays.**

5 Indirect chromogenic assays of t-PA utilized the substrates lys-plasminogen (American Diagnostica, Greenwich, CT) and Spectrozyme<sup>TM</sup> PL (American Diagnostica) and were performed as previously described (Madison, E. L., Goldsmith, E. J., Gerard, R. D., Gething, M.-J., and Sambrook, J. F. (1989) *Nature* **339**, 721-724; Madison, E. L., Goldsmith, E. J., Gerard, R. D., Gething, M. J., Sambrook, J. F., and Bassel-Duby, R. S. (1990) *Proc. Natl. Acad. Sci. U.S.A.* **87**, 3530-3533; Madison, E. L., Goldsmith, E. J., Gething, M. J., Sambrook, J. F., and Gerard, R. D. (1990) *J. Biol. Chem.* **265**, 21423-21426.). Assays were performed both in the presence and absence of the co-factor DESAFIB (American Diagnostica). The concentration of lys-plasminogen was varied from 0.0125 – 0.2  $\mu$ M in the presence of DESAFIB and from 0.9 – 15  $\mu$ M in the absence of the co-factor.

15

#### **Kinetic analysis of t-PA activity using a small, synthetic substrate**

The direct chromogenic assay utilized the substrate methylsulfonyl-D-cyclohexyltyrosyl-glycyl-arginine-p-nitroaniline (Spectrozyme t-PA, American Diagnostica) and was performed as previously described (Strandberg, L., and Madison, E. L. (1995) *J. Biol. Chem.* **270**, 23444-23449; Smith, J. W., Tachias, K., and Madison, E. L. (1995) *J. Biol. Chem.* **270**, 30486-30490).

20

#### **Measurement of second order rate constants for inhibition by PAI-1**

25 Second order rate constants for the inhibition of wild type human t-PA and variant t-PA were measured under pseudo-first order conditions as previously described. Briefly, enzyme and inhibitor were preincubated at 23 degrees Celsius for periods of time varying from 0 – 30 minutes. Following preincubation, the mixtures were diluted, and the residual enzymatic activity was measured in a standard indirect chromogenic assay. For each enzyme, the concentrations of enzyme and inhibitor and the times of preincubation were chosen to yield several data points for which the residual enzymatic activity varied between 20% and 80% of

30



the initial activity. Data were analyzed by plotting the natural logarithm of the ratio (residual activity/initial activity) versus time of preincubation and measuring the resulting slopes. Division of this slope by  $-[I]$  yielded the second order rate constants shown.

5 It was found that replacement of histidine 417 of t-PA with an acidic residue selectively suppresses the catalytic activity of single chain t-PA. Histidine 417 was replaced by either an aspartate or glutamate residue to yield two variants: t-PA/H417D and t-PA/H417E. Accurate measurement of the enzymatic activity toward plasminogen of the single chain form of these two variants proved difficult, however, because the plasmin produced in this assay rapidly converted the single chain enzymes into their mature, two-chain form by  
10 cleaving the R275-I276 peptide bond. Consequently, to overcome this technical difficulty, we also constructed noncleavable forms of the two mutated enzymes by introducing the additional mutation R275E into the existing mutants.

Wild type human t-PA, t-PA/R275E, and all four variants containing mutations at position 417 were expressed by transient expression of COS-1 cells. Since this procedure  
15 yielded predominantly single chain enzymes, two-chain t-PAs were generated by treating the enzyme preparations with plasmin-Sepharose<sup>TM</sup> (Strandberg, L., and Madison, E. L. (1995) *J. Biol. Chem.* **270**, 23444-23449). Quantitative conversion of the enzymes into their mature, two-chain form was confirmed by SDS-PAGE. As expected, variants containing the mutation R275E were synthesized and secreted exclusively as single chain enzymes and were not  
20 cleaved by plasmin-Sepharose.

The enzymatic activity of the single and two-chain forms of wild type human t-PA and each variant toward a small synthetic substrate is listed in Table I below. Mutation of histidine 417 had only very modest effects on the activity of the two-chain enzymes. Two-chain t-PA/H417D and t-PA/H417E displayed 67% or 80%, respectively, the activity of the two-  
25 chain, wild type human t-PA enzyme in this assay. The H417D and H417E mutations, however, had more significant effects on the activities of the single chain enzymes. Compared to single chain t-PA/R275E, single chain t-PA/R275E,H417D (SEQ ID NO: 1) and t-PA/R275E,H417E (SEQ ID NO: 2) exhibited approximately 16% or 25%, respectively, the activity of single chain t-PA/R275E.

30

Table 1

*Kinetic constants for cleavage of the chromogenic substrate  
Spectrozyme t-PA by single- and two-chain t-PA variants*

Enzyme	$K_{cat}$ ( $s^{-1}$ )	$K_m$ (mM)	$K_{cat}/K_m$ ( $M^{-1}s^{-1}$ )
<b>Two-chain form</b>			
t-PA	59	0.4	$1.5 \times 10^5$
t-PA/H417D	41	0.4	$1.0 \times 10^5$
t-PA/H417E	58	0.5	$1.2 \times 10^5$
<b>Single-chain form</b>			
t-PA/R275E	26	0.7	$3.7 \times 10^4$
t-PA/R275E,H417D	5.9	1.0	$5.9 \times 10^3$
t-PA/R275E,H417E	12	1.3	$9.2 \times 10^3$

All of the variants analyzed maintained high enzymatic activity towards the natural substrate, plasminogen, in the presence of the co-factor fibrin (Table II below). The catalytic activity of the two-chain form of wild type human t-PA, t-PA/H417D, and t-PA/H417E varied by a factor of only 1.4. Similarly, the activities of single chain t-PA/R275E, t-PA/R275E,H417D, and t-PA/R275E,H417E differed by a factor of less than 1.8.

Table II

*Kinetic constants for activation of plasminogen by single- and two-chain t-PA variants in the presence of fibrin*

Enzyme	$K_{cat}$ ( $s^{-1}$ )	$K_m$ ( $\mu M$ )	$K_{cat}/K_m$ ( $M^{-1}s^{-1}$ )
<b>Two-chain form</b>			
t-PA	0.11	0.017	$6.5 \times 10^6$
t-PA/H417D	0.11	0.024	$4.6 \times 10^6$
t-PA/H417E	0.10	0.022	$4.5 \times 10^6$
<b>Single-chain form</b>			
t-PA/R275E	0.16	0.017	$9.4 \times 10^6$
t-PA/R275E,H417D	0.23	0.043	$5.3 \times 10^6$
t-PA/R275E,H417E	0.17	0.028	$6.1 \times 10^6$

In the absence of a co-factor, the mutations at position 417 had little effect on the activity of two-chain t-PA toward plasminogen; however, these mutations significantly reduced the catalytic efficiency of single chain t-PA (Table III below). Compared to that of single chain t-PA/R275E, the activity of t-PA/R275E,H417D and t-PA/R275E,H417E was reduced by a factor of approximately 14 or 6, respectively. In this assay, the "zymogenicity", or ratio of the activities of the two-chain and single chain form of a particular enzyme, were approximately 9 for wild type t-PA. By contrast, for variants containing the H417D or H417E mutation, this ratio increased to approximately 150 or 50, respectively (Table III).

Table III

*Kinetic constants for activation of plasminogen by single- and two-chain variants of t-PA in the absence of a cofactor*

Enzyme	$K_{cat}(s^{-1})$	$K_m(\mu M)$	$K_{cat}/K_m(M^{-1}s^{-1})$
<b>Two-chain form</b>			
t-PA	0.093	6.7	$1.4 \times 10^4$
t-PA/H417D	0.110	6.8	$1.6 \times 10^4$
t-PA/H417E	0.099	8.7	$1.1 \times 10^4$
<b>Single-chain form</b>			
t-PA/R275E	0.014	9.5	$1.5 \times 10^3$
t-PA/R275E,H417D	0.001	9.4	$1.1 \times 10^2$
t-PA/R275E,H417E	0.002	8.5	$2.4 \times 10^2$

Molecular details of the stimulation of t-PA by fibrin, a complex process that almost certainly involves multiple points of contact between the two proteins, remain unclear. While fibrin stimulation of two-chain t-PA may occur through a single mechanism; stimulation of single chain t-PA by fibrin co-factors, however, appears to utilize at least two distinct mechanisms. First, fibrin apparently stimulates both single- and two-chain t-PA through a templating mechanism resulting in formation of a ternary complex which greatly augments the local concentration of enzyme and substrate. Second, because single- and two-chain t-PA have equivalent activity in the presence but not the absence of fibrin, it seems likely that binding to fibrin induces a conformational change in the activation domain of single chain t-PA. Similar activation of plasminogen upon binding to streptokinase as well as activation of prothrombin

by binding to staphylocoagulase have been described previously. Although the mechanism of this nonclassical, nonproteolytic activation of serine protease zymogens remains completely unclear, the behavior of single chain t-PA/R275E,H417D and t-PA/R275E,H417E indicates that His 417 does not play an essential role in this process. In addition, the properties of two-  
5 chain t-PA/H417D and t-PA/H417E indicate that His 417 does not play an essential role during zymogen activation of t-PA through the classical, proteolytic mechanism.

The primary effect of the H417D and H417E mutations was a selective reduction of the activity of single chain t-PA in the absence of fibrin and, consequently, an increase in the zymogenicity of the enzyme. At the molecular level this effect could be mediated either by  
10 stabilizing a less active, new conformation of single chain t-PA or by shifting the equilibrium between one or more existing conformations, with distinct activities, towards the less active conformation. Without being held to a single hypothesis, based on structural studies of trypsinogen, trypsin, chymotrypsinogen, and chymotrypsin, that the existence of an equilibrium among multiple conformations of the activation domain is likely to be a general  
15 feature of chymotrypsinogen family zymogens.

It is believed that the effect produced by converting His 417 to an acidic residue is mediated by disrupting the important salt bridge between Asp 477 and Lys 429 by providing an alternative, electrostatic interaction for Lys 429. The observation of an electrostatic interaction between K429 and E417 in the recently reported structure of the protease domain  
20 of two-chain u-PA, although the distance and geometry of this interaction vary somewhat in the two members of the unit cell in this study, lends credence to this hypothesis. Moreover, as observed in this study, formation of a new salt bridge between Lys 429 and Asp/Glu 417 would be expected to selectively suppress the activity of single chain t-PA because Lys 429 does not interact with Asp 477 in the two-chain enzyme. Instead, in two-chain t-PA, as in  
25 other mature chymotrypsin like enzymes, the mature amino terminus inserts into the activation pocket and plays this role. Consequently, as observed, two-chain t-PA/H417D and t-PA/H417E are expected to maintain high catalytic activity. Variants of t-PA containing an acidic residue at position 417, therefore, exhibit significantly enhanced zymogenicity.

**Table IV****Stimulatory effect of fibrin on the catalytic efficiencies for variants of t-PA**

<b>Enzyme</b>	<b>Fold stimulation of <math>k_{cat}/K_m</math></b>
<b>Two-Chain form</b>	
t-PA	460
t-PA/H417D	290
t-PA/H417E	410
<b>Single-chain form</b>	
t-PA/R275E	6300
t-PA/R275E,H417D	48,200
t-PA/R275E,H417E	25,400

5 The extent of fibrin stimulation displayed by the single chain form of the mutated enzymes examined in this study is significantly greater than that displayed by wild type t-PA. Wild type, two-chain t-PA possesses a fibrin stimulation factor, defined as the ratio of the catalytic efficiencies in the presence and absence of fibrin, of approximately 460 (Table IV above). The two-chain variants display similar stimulation factors of 290 (t-PA/H417D) and 410 (t-PA/H417E). Single chain wild type t-PA, with a fibrin stimulation factor of 6300, is
 10 stimulated to a substantially greater degree than the two-chain enzymes, presumable reflecting the ability of fibrin to stimulate the single chain enzymes not only through a templating mechanism but also by inducing nonproteolytic zymogen activation. Stimulation of single chain t-PA is further enhanced by the H417D or H417E mutations. The fibrin stimulation factors for single chain t-PA/R275E,H417D and t-PA/H417E are 48,200 and 25,400,
 15 respectively (Table IV above). Enhanced fibrin stimulation of the variants did not result from increased activity in the presence of fibrin but rather from decreased activity in the absence of a stimulator, an observation consistent with the belief that the effects of these mutations are mediated by disruption of a salt bridge between Lys 429 and Asp 477 in single chain t-PA.

20 The single chain form of a zymogen-like variant of t-PA is expected to exhibit reduced activity not only towards substrates (Tables I and III, above) but also towards specific inhibitors. To demonstrate this, we measured the second order rate constant for inhibition of

single chain t-PA/R275E, t-PA/R275E,H417D, and t-PA/R275E,H417E by the serpin plasminogen activator inhibitor, type 1 (PAI-1) (Table V below). As expected, both variants containing mutations at position 417 exhibited resistance to inhibition by PAI-1. The second order rate constant for inhibition by PAI-1 of t-PA/R275E,H417D or t-PA/R275E,H417E was reduced by factors of approximately 12 or 9, respectively, compared with t-PA/R275E.

Table V

*Inhibition of wild type and variants of t-PA by PAI-1*

Enzyme	Second Order Rate Constant ( $M^{-1}s^{-1}$ )
t-PA/R275E	$1.8 \times 10^6$
t-PA/R275E,H417D	$1.5 \times 10^5$
t-PA/R275E,H417E	$2.1 \times 10^5$

t-PA exhibits unusually high catalytic activity as a single chain enzyme and consequently very low zymogenicity. By contrast, a closely related enzyme urokinase (u-PA) exhibits much lower catalytic activity as a single chain enzyme and substantially higher zymogenicity. An important finding of this study is that the presence or absence of a favorable electrostatic interaction between residues at positions 417 and 429 appears to be the major determinant of this key functional distinction between the two human plasminogen activators. The zymogenicity of wild type t-PA, u-PA, and t-PA containing an aspartate at position 417 are approximately 9, 250, and 150, respectively.

These studies demonstrated structure/function relationships within the activation domain of t-PA, and elucidated the molecular basis of important functional distinctions between t-PA and u-PA. These results can also aid the design of improved thrombolytic agents. For example t-PA/R275E,H417D, exhibits substantially enhanced fibrin stimulation, resistance to inhibition by PAI-1, and significantly increased zymogenicity, a useful combination of properties that enhances the therapeutic utility of the enzyme.

## Example 2

### **Site Directed Mutagenesis And Construction Of Expression Vectors Encoding Variants Of T-PA.**

5 Oligonucleotide directed site specific mutagenesis was performed as described in Example 1. The K429Y mutation was introduced into the 290 bp *SacI* – *SmaI* fragment of cDNA encoding t-PA that had been previously subcloned into bacteriophage M13mp18. The mutagenic primer had the following nucleotide sequence:

5' – CGGAGCGGCTGTATGAGGCTCATGT – 3' (SEQ ID NO: 10).

10 Following mutagenesis, ssDNA corresponding to the entire 290 bp *SacI* – *SmaI* fragment was fully sequenced to assure the presence of the desired mutation and the absence of any additional mutations. The sequence corresponding to the 290 bp *SacI* – *SmaI* fragment of the K429Y mutation is shown in SEQ ID NO: 7. Replicative form (RF) DNA was prepared for appropriate phage, and the mutated 290 bp *SacI* – *SmaI* fragment was recovered  
15 after digestion of RF DNA with *SacI* and *SmaI* and electrophoresis of the digestion products on an agarose gel. The isolated, mutated *SacI* – *SmaI* fragment was used to replace the corresponding fragment in full length cDNAs encoding wild type t-PA or t-PA/R275E to yield new, full length cDNAs encoding t-PA/K429Y and t-PA/R275E,K429Y.

20 **Expression of enzymes by transient transfection of COS cells.**

cDNAs encoding t-PA, t-PA/R275E, t-PA/K429Y, and t-PA/R275E,K429Y were ligated into the transient expression vector pSVT7 and then introduced into COS cells by electroporation using a Bio Rad Gene pulser as described in Example 1. Following electroporation, cells were incubated overnight at 37 degrees Celsius in DMEM containing  
25 10% fetal calf serum and 5mM sodium butyrate. Cells were then washed with serum free medium and incubated in DMEM for 48 hours at 37 degrees Celsius. After the incubation with serum free media, conditioned media were collected and enzyme concentrations were determined by ELISA.

30 **Purification of wild type and mutated variants of t-PA.**

Wild type and mutated variants of t-PA were purified using an FPLC system and a 1 ml HISTRAP™ chelating column (Pharmacia Biotech). The column was charged with 0.1 M

CuSO<sub>4</sub> solution, washed with 5 – 10 ml distilled water, and equilibrated with start buffer (0.02 M NaHPO<sub>4</sub>, pH 7.2, 1 M NaCl and 1 mM Imidazole). Conditioned medium containing wild type or variants of t-PA was adjusted to 1 M NaCl and injected into the column with a 50 ml superloop (Pharmacia Biotech). The column was then washed with 10 column volumes of start buffer and eluted using a 0 – 0.32 M linear gradient of imidazole in the same buffer. Peak fractions were collected and pooled. Purified t-PA samples were concentrated, and buffer was exchanged to 25 mM Tris (pH = 7.5), 50 mM NaCl, 1 mM EDTA, using a Centriplus<sup>TM</sup> 30 concentrator (Amicon).

10 **Kinetic analysis of t-PA activity using a small, synthetic substrate.**

The direct chromogenic assay utilized the substrate methylsulfonyl-D-cyclohexyltyrosyl-glycyl-arginine-p-nitroaniline (Spectrozyme t-PA, American Diagnostica) and was performed as described in Example 1.

15 **Kinetic analysis of plasminogen activation using indirect chromogenic assays.**

Indirect chromogenic assays of t-PA utilized the substrates lys-plasminogen (American Diagnostica) and Spectrozyme PL (American Diagnostica) and were performed as previously described in Example 1. Assays were performed both in the presence and absence of the co-factor DESAFIB (American Diagnostica).

20

**Indirect Chromogenic Assays in the presence of Various Fibrin Co-factors.**

Standard indirect chromogenic assays were performed. Briefly, 0.25 – 1ng of enzyme, 0.2 μM lys-plasminogen and 0.62 mM Spectrozyme PL were present in a total volume of 100 μl. Assays were performed either in the presence of buffer, 25 μg/ml DESAFIB, 100 μg/ml fibrinogen, 100 μg/ml cyanogen bromide fragments of fibrinogen (American Diagnostica), or 100 μg/ml of the stimulatory, thirteen amino acid peptide P368. P368 was kindly provided by Marshall Runge (University of Texas Medical Center, Galveston, TX.). Assays were performed in microtiter plates, and the optical density at 405 nm was measured every 30 seconds for one hour in a Molecular Devices Thermomax. Reactions were performed at 37 degrees Celsius.

30



**Measurement of second order rate constants for inhibition by PAI-1.**

Second order rate constants for the inhibition of wild type and mutated t-PA were measured under pseudo-first order conditions as described in Example 1.

5 Oligonucleotide directed site specific mutagenesis was used to produce a mutation of Lys 429 of t-PA that selectively suppressed the catalytic activity of single chain t-PA. Lysine 429 was replaced by a tyrosine residue to yield t-PA/K429Y. In addition, to permit accurate measurement of the enzymatic activity toward plasminogen of the single chain form of this variant, a noncleavable form of the mutated enzyme was constructed by introducing the  
10 additional mutation R275E into the existing mutant to yield the R275E,K429Y variant.

Wild type t-PA, t-PA/R275E, t-PA/K429Y, and t-PA/R275E,K429Y were expressed by transient expression in COS 1 cells as described in Example 1. Since this procedure yielded predominantly single chain enzymes, two-chain t-PAs were generated by treating the enzyme preparations with plasmin-Sepharose. Quantitative conversion of the enzymes into  
15 their mature, two-chain form was confirmed by SDS-PAGE. As previously demonstrated, variants containing the mutation R275E were synthesized and secreted exclusively as single chain enzymes and were not cleaved by plasmin-Sepharose.

**Table VI**

*Kinetic constants for cleavage of the chromogenic substrate  
Spectrozyme t-PA by single- and two-chain t-PA variants*

<b>Enzyme</b>	<b><math>K_{cat}(s^{-1})</math></b>	<b><math>K_m(mM)</math></b>	<b><math>K_{cat}/K_m(M^{-1}s^{-1})</math></b>
<b>Two-chain form</b>			
t-PA	40	0.5	$8.0 \times 10^4$
t-PA/K429Y	35	0.5	$7.0 \times 10^4$
<b>Single-chain form</b>			
t-PA/R275E	24	0.7	$3.4 \times 10^4$
t-PA/R275E,K429Y	0.3	0.5	$6.0 \times 10^2$

20 The enzymatic activity of the single and two-chain forms of wild type and t-PAs toward a small synthetic substrate is listed in Table VI above. Mutation of lysine 429 had little effect on the activity of two-chain t-PA. Two-chain t-PA/K429Y displayed approximately

90% of the activity of the two-chain, wild type enzyme in this assay. By contrast, the K429Y mutation had a very substantial effect on the activity of single chain t-PA. Single chain t-PA/R275E,K429Y exhibited approximately 2% of the activity of single chain t-PA/R275E. In this assay, the zymogenicity, defined as the ratio of the activities of the two-chain to that of the single chain form of a particular enzyme, was approximately 2.5 for wild type t-PA. By contrast, for variants containing the K429Y mutation, this ratio increased to approximately 117 (Table VI).

In the absence of a co-factor, the K429Y mutation had little effect on the activity of two-chain t-PA toward plasminogen; however, this mutation significantly reduced the catalytic efficiency of single chain t-PA (Table VII below). Compared with that of single chain t-PA/R275E, the activity of single chain t-PA/R275E,K429Y was reduced by a factor of 17. By contrast, the activities of two-chain t-PA and t-PA/K429Y differed by a factor of only 1.2.

**Table VII**

*Kinetic constants for activation of plasminogen by single- and two-chain variants of t-PA in the absence of a cofactor*

Enzyme	$K_{cat}(s^{-1})$	$K_m(\mu M)$	$K_{cat}/K_m(M^{-1}s^{-1})$
<b>Two-chain form</b>			
t-PA	0.16	10	$1.6 \times 10^4$
t-PA/K429Y	0.18	14	$1.3 \times 10^4$
<b>Single-chain form</b>			
t-PA/R275E	[0.038]	[30]	$1.3 \times 10^3$
t-PA/R275E,K429Y	0.00046	5.9	$7.8 \times 10^1$

All of the variants analyzed in this study maintained reasonably high enzymatic activity towards the natural substrate plasminogen in the presence of the co-factor fibrin (Table VIII below). The single chain form of variants containing the K429Y mutation were, however, affected to a slightly greater extent than the corresponding mature, two-chain enzymes. Two-chain t-PA/K429Y possessed approximately 75% of the activity of two-chain t-PA while single chain t-PA/R275E,K429Y exhibited approximately 40% of the activity of single chain t-PA/R275E.

**Table VIII**  
*Kinetic constants for activation of plasminogen by single- and two-chain t-PA variants in the presence of fibrin*

Enzyme	$K_{cat}(s^{-1})$	$K_m(\mu M)$	$K_{cat}/K_m(M^{-1}s^{-1})$
<b>Two-chain form</b>			
t-PA	0.08	0.02	$4.0 \times 10^6$
t-PA/K429Y	0.08	0.03	$3.0 \times 10^6$
<b>Single-chain form</b>			
t-PA/R275E	0.10	0.02	$5.0 \times 10^6$
t-PA/R275E,K429Y	0.10	0.07	$2.0 \times 10^6$

The extent of fibrin stimulation displayed by the single chain form of t-PA/R275E,K429Y is significantly greater than that displayed by wild type t-PA. Wild type, two-chain t-PA possesses a fibrin stimulation factor, defined as the ratio of the catalytic efficiencies in the presence and absence of fibrin, of approximately 250 (Table IX below). The two-chain t-PA/K429Y variant displays a similar stimulation factor of 230. Single chain wild type t-PA, with a fibrin stimulation factor of 3800, is stimulated to a substantially greater degree than the two-chain enzymes, presumable reflecting the ability of fibrin to stimulate the single chain enzymes not only through a templating mechanism but also by inducing nonproteolytic zymogen activation. Stimulation of single chain t-Pa is further enhanced by the K429Y mutation. The fibrin stimulation factor for single chain t-PA/R275E,K429Y is approximately 26,000. Enhanced fibrin stimulation of the variant did not result from increased activity in the presence of fibrin but rather from decreased activity in the absence of a stimulator, an observation consistent with our proposal that the effects of these mutations are mediated by disruption of a salt bridge between Lys 429 and Asp 477 in single chain t-PA.

Table IX

*Stimulatory effect of fibrin on the catalytic efficiencies for variants of t-PA*

Enzyme	Fold stimulation of $k_{cat}/K_m$
<b>Two-chain form</b>	
t-PA	250
t-PA/K429Y	230
<b>Single-chain form</b>	
t-PA/R275E	3800
t-PA/R275E,K429Y	26,000

The mutated enzyme t-PA/R275E,K429Y is not only stimulated to a significantly greater extent by soluble fibrin than t-PA (Table IX above), but it is also substantially more discriminating among fibrin co-factors than the wild type enzyme (Fig. 2). The two-chain form of both wild type t-PA and t-PA/K429Y are strongly stimulated by soluble fibrin monomers (DESAFIB), fibrinogen, CNBr fragments of fibrinogen, and a 13 amino acid peptide (P368). Single chain t-PA/R275E, on the other hand, is stimulated strongly by soluble fibrin and fibrinogen and moderately by the CNBr fragments and peptide P368. In striking contrast to these enzymes, single chain t-PA/R275E,K429Y, although dramatically stimulated by fibrin monomers, is virtually nonresponsive to fibrinogen, CNBr fragments of fibrinogen, peptide P368.

The ratio of the specific activity of a plasminogen activator in the presence of fibrin to that in the presence of fibrinogen, or "fibrin selectivity factor", is one indication of the "clot selectivity" an enzyme will demonstrate in vivo. An enzyme with enhanced fibrin selectivity can accomplish efficient thrombolysis while displaying decreased systemic activity. Under the conditions of the assays reported here, the fibrin selectivity is 1.5 for two-chain t-PA, 1.5 for two-chain t-PA/K429Y, and 1.0 for single chain t-PA/R275E. The fibrin selectivity factor for single chain t-PA/R275E,K429Y, however, is 146. This double mutant, therefore, is approximately two orders of magnitude more discriminating between fibrin and fibrinogen than either single or two-chain wild type t-PA.

The single chain form of a zymogen-like variant of t-PA is expected to exhibit reduced activity not only towards substrates (Tables VI and VIII above) but also towards specific

inhibitors. The second order rate constant for inhibition of the single chain form of both t-PA/R275E and t-PA/R275E,K429Y by the serpin plasminogen activator inhibitor, type 1 (PAI-1), the primary physiological inhibitor of t-PA is shown in Table X below. As expected, t-PA/R275E,K429Y exhibited resistance to inhibition by PAI-1. The second order compared with t-PA/R275E.

**Table X***Inhibition of wild type and variants of t-PA by PAI-1*

Enzyme	Second order rate constant ( $M^{-1}s^{-1}$ )
t-PA/R275E	$1.8 \times 10^6$
t-PA/R275E,K429Y	$7.7 \times 10^3$

An important finding of this study is that conversion of lysine 429 to tyrosine residue selectively suppresses the activity of single chain t-PA and thereby substantially enhances the zymogenicity of the enzyme. We have demonstrated, in addition, that single chain t-PA/R275E,K429Y is significantly more fibrin stimulated and substantially more fibrin selective than either single or two-chain, wild type t-PA. Single chain t-PA/R275E,K429Y also exhibits marked resistance to inhibition by PAI-1. It is believed that the effects of this mutation are mediated by disruption of a critical salt bridge formed by Lys 429 and Asp 477 that has been predicted to be present in single- but not two-chain t-PA. The primary role of this putative salt bridge is believed to be stabilization of the active conformation of single chain t-PA. Two-chain t-PA/K429Y, therefor, as demonstrated in this study, is expected to maintain high enzymatic activity.

These results aid in the design of improved thrombolytic agents. For Example t-PA/R275E,K429Y, exhibits significantly enhanced fibrin stimulation, dramatically increased discrimination among fibrin co-factors, marked resistance to inhibition by PAI-1, and substantially increased zymogenicity, a combination of properties that enhance the therapeutic utility of the enzyme.

The foregoing is intended to be illustrative of the present invention, but not limiting. Numerous variations and modifications of the present invention may be effected without departing from the true spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
- (ii) TITLE OF INVENTION: Tissue Type Plasminogen Activator (T-Pa)  
Variants Having Zymogen Characteristics:  
Compositions and Methods of Use
- (iii) NUMBER OF SEQUENCES: 11
- (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<sup>TM</sup> PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS<sup>TM</sup>
  - (D) SOFTWARE: Patent In Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 2,271,697
  - (B) FILING DATE: 12-November-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 60/030,655
  - (B) FILING DATE: 12-November-1996
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: SWAIN, Margaret
  - (B) REGISTRATION NUMBER: 10926
  - (C) REFERENCE/DOCKET NUMBER: 1247-103
- (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: 527 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

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

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				20					25					30		
10	Tyr	Cys	Trp	Cys	Asn	Ser	Gly	Arg	Ala	Gln	Cys	His	Ser	Val	Pro	Val
			35					40					45			
	Lys	Ser	Cys	Ser	Glu	Pro	Arg	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Gln	Gln
15		50					55					60				
	Ala	Leu	Tyr	Phe	Ser	Asp	Phe	Val	Cys	Gln	Cys	Pro	Glu	Gly	Phe	Ala
	65					70					75					80
20	Gly	Lys	Cys	Cys	Glu	Ile	Asp	Thr	Arg	Ala	Thr	Cys	Tyr	Glu	Asp	Gln
					85					90					95	
	Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser	Gly	Ala	Glu
				100					105					110		
25	Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro	Tyr	Ser	Gly
			115					120					125			
	Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His	Asn	Tyr	Cys
30		130					135					140				
	Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val	Phe	Lys	Ala
	145					150					155					160
35	Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys	Ser	Glu	Gly
					165					170					175	
	Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg	Gly	Thr	His
				180					185					190		
40	Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	Ser	Met	Ile
			195					200					205			
	Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala	Gln	Ala	Leu
45		210					215					220				
	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ala	Lys
	225					230					235					240
50	Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp	Glu	Tyr	Cys
					245					250					255	
	Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr	Ser	Gln	Pro
				260					265					270		
55	Gln	Phe	Glu	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala	Ser	His	Pro
			275					280					285			
	Trp	Gln	Ala	Ala	Ile	Phe	Ala	Lys	His	Arg	Arg	Ser	Pro	Gly	Glu	Arg

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	290		295		300														
	Phe	Leu	Cys	Gly	Gly	Ile	Leu	Ile	Ser	Ser	Cys	Trp	Ile	Leu	Ser	Ala			
	305					310					315					320			
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	Leu	Gly	Arg	Thr	Tyr	Arg	Val	Val	Pro	Gly	Glu	Glu	Glu	Gln	Lys	Phe			
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	Glu	Val	Glu	Lys	Tyr	Ile	Val	His	Lys	Glu	Phe	Asp	Asp	Asp	Thr	Tyr			
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15	Asp	Asn	Asp	Ile	Ala	Leu	Leu	Gln	Leu	Lys	Ser	Asp	Ser	Ser	Arg	Cys			
	370						375					380							
	Ala	Gln	Glu	Ser	Ser	Val	Val	Arg	Thr	Val	Cys	Leu	Pro	Pro	Ala	Asp			
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	Leu	Gln	Leu	Pro	Asp	Trp	Thr	Glu	Cys	Glu	Leu	Ser	Gly	Tyr	Gly	Lys			
					405					410					415				
	Asp	Glu	Ala	Leu	Ser	Pro	Phe	Tyr	Ser	Glu	Arg	Leu	Lys	Glu	Ala	His			
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	Val	Arg	Leu	Tyr	Pro	Ser	Ser	Arg	Cys	Thr	Ser	Gln	His	Leu	Leu	Asn			
			435					440					445						
30	Arg	Thr	Val	Thr	Asp	Asn	Met	Leu	Cys	Ala	Gly	Asp	Thr	Arg	Ser	Gly			
	450						455					460							
	Gly	Pro	Gln	Ala	Asn	Leu	His	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly			
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	Pro	Leu	Val	Cys	Leu	Asn	Asp	Gly	Arg	Met	Thr	Leu	Val	Gly	Ile	Ile			
					485					490					495				
	Ser	Trp	Gly	Leu	Gly	Cys	Gly	Gln	Lys	Asp	Val	Pro	Gly	Val	Tyr	Thr			
40				500					505					510					
	Lys	Val	Thr	Asn	Tyr	Leu	Asp	Trp	Ile	Arg	Asp	Asn	Met	Arg	Pro				
			515					520					525						

45 2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 527 amino acids

(B) TYPE: amino acid

50 (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

55 (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:



(A) ORGANISM: Homo sapiens

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

1	Ser	Tyr	Gln	Val	Ile	Cys	Arg	Asp	Glu	Lys	Thr	Gln	Met	Ile	Tyr	Gln
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10	Gln	His	Gln	Ser	Trp	Leu	Arg	Pro	Val	Leu	Arg	Ser	Asn	Arg	Val	Glu
				20					25					30		
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			35				40						45			
15	Lys	Ser	Cys	Ser	Glu	Pro	Arg	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Gln	Gln
		50					55					60				
20	Ala	Leu	Tyr	Phe	Ser	Asp	Phe	Val	Cys	Gln	Cys	Pro	Glu	Gly	Phe	Ala
	65					70					75					80
	Gly	Lys	Cys	Cys	Glu	Ile	Asp	Thr	Arg	Ala	Thr	Cys	Tyr	Glu	Asp	Gln
				85						90					95	
25	Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser	Gly	Ala	Glu
				100					105					110		
	Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro	Tyr	Ser	Gly
			115					120					125			
30	Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His	Asn	Tyr	Cys
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	Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val	Phe	Lys	Ala
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	Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys	Ser	Glu	Gly
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40	Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg	Gly	Thr	His
				180					185					190		
	Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	Ser	Met	Ile
			195					200					205			
45	Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala	Gln	Ala	Leu
			210				215					220				
	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ala	Lys
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	Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp	Glu	Tyr	Cys
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55	Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr	Ser	Gln	Pro
				260					265					270		
	Gln	Phe	Glu	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala	Ser	His	Pro
			275					280					285			

	Trp	Gln	Ala	Ala	Ile	Phe	Ala	Lys	His	Arg	Arg	Ser	Pro	Gly	Glu	Arg
	290						295					300				
5	Phe	Leu	Cys	Gly	Gly	Ile	Leu	Ile	Ser	Ser	Cys	Trp	Ile	Leu	Ser	Ala
	305					310					315					320
	Ala	His	Cys	Phe	Gln	Glu	Arg	Phe	Pro	Pro	His	His	Leu	Thr	Val	Ile
					325					330					335	
10	Leu	Gly	Arg	Thr	Tyr	Arg	Val	Val	Pro	Gly	Glu	Glu	Glu	Gln	Lys	Phe
				340					345					350		
	Glu	Val	Glu	Lys	Tyr	Ile	Val	His	Lys	Glu	Phe	Asp	Asp	Asp	Thr	Tyr
15			355					360					365			
	Asp	Asn	Asp	Ile	Ala	Leu	Leu	Gln	Leu	Lys	Ser	Asp	Ser	Ser	Arg	Cys
	370						375					380				
20	Ala	Gln	Glu	Ser	Ser	Val	Val	Arg	Thr	Val	Cys	Leu	Pro	Pro	Ala	Asp
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	Leu	Gln	Leu	Pro	Asp	Trp	Thr	Glu	Cys	Glu	Leu	Ser	Gly	Tyr	Gly	Lys
					405					410					415	
25	Glu	Glu	Ala	Leu	Ser	Pro	Phe	Tyr	Ser	Glu	Arg	Leu	Lys	Glu	Ala	His
				420					425					430		
	Val	Arg	Leu	Tyr	Pro	Ser	Ser	Arg	Cys	Thr	Ser	Gln	His	Leu	Leu	Asn
30			435					440					445			
	Arg	Thr	Val	Thr	Asp	Asn	Met	Leu	Cys	Ala	Gly	Asp	Thr	Arg	Ser	Gly
	450						455					460				
35	Gly	Pro	Gln	Ala	Asn	Leu	His	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
	465				470						475					480
	Pro	Leu	Val	Cys	Leu	Asn	Asp	Gly	Arg	Met	Thr	Leu	Val	Gly	Ile	Ile
					485					490					495	
40	Ser	Trp	Gly	Leu	Gly	Cys	Gly	Gln	Lys	Asp	Val	Pro	Gly	Val	Tyr	Thr
				500					505					510		
	Lys	Val	Thr	Asn	Tyr	Leu	Asp	Trp	Ile	Arg	Asp	Asn	Met	Arg	Pro	
45			515					520					525			

## 2) INFORMATION FOR SEQ ID NO:3:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 527 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: not relevant
- 55 (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

5

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

10	Ser	Tyr	Gln	Val	Ile	Cys	Arg	Asp	Glu	Lys	Thr	Gln	Met	Ile	Tyr	Gln
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	Gln	His	Gln	Ser	Trp	Leu	Arg	Pro	Val	Leu	Arg	Ser	Asn	Arg	Val	Glu
				20					25					30		
15	Tyr	Cys	Trp	Cys	Asn	Ser	Gly	Arg	Ala	Gln	Cys	His	Ser	Val	Pro	Val
			35					40					45			
	Lys	Ser	Cys	Ser	Glu	Pro	Arg	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Gln	Gln
20		50					55					60				
	Ala	Leu	Tyr	Phe	Ser	Asp	Phe	Val	Cys	Gln	Cys	Pro	Glu	Gly	Phe	Ala
	65					70					75					80
25	Gly	Lys	Cys	Cys	Glu	Ile	Asp	Thr	Arg	Ala	Thr	Cys	Tyr	Glu	Asp	Gln
					85					90					95	
	Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser	Gly	Ala	Glu
				100					105					110		
30	Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro	Tyr	Ser	Gly
			115					120					125			
	Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His	Asn	Tyr	Cys
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	Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val	Phe	Lys	Ala
	145					150					155					160
40	Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys	Ser	Glu	Gly
					165					170					175	
	Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg	Gly	Thr	His
				180					185					190		
45	Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	Ser	Met	Ile
			195					200					205			
	Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala	Gln	Ala	Leu
50		210					215					220				
	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ala	Lys
	225					230					235					240
55	Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp	Glu	Tyr	Cys
					245					250					255	
	Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr	Ser	Gln	Pro
				260					265					270		



(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

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

5	CTACGGCAAG CATGAGGCCT TGTCTCCTTT CTATTCGGAG CGGCTGAAGG AGGCTCATGT	60
15	CAGACTGTAC CCATCCAGCC GCTGCACATC ACAACATTTA CTTAACAGAA CAGTCACCGA	120
	CAACATGCTG TGTGCTGGAG ACACTCGGAG CGGCGGGCCC CAGGCAAAC TGCACGACGC	180
20	CTGCCAGGGC GATTCGGGAG GCCCCCTGGT GTGTCTGAAC GATGGCCGCA TGACTTTGGT	240
	GGGCATCATC AGCTGGGGCC TGGGCTGTGG ACAGAAGGAT GTCCCGGGTG	290

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: not relevant

(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

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

45	CTACGGCAAG GACGAGGCCT TGTCTCCTTT CTATTCGGAG CGGCTGAAGG AGGCTCATGT	60
	CAGACTGTAC CCATCCAGCC GCTGCACATC ACAACATTTA CTTAACAGAA CAGTCACCGA	120
50	CAACATGCTG TGTGCTGGAG ACACTCGGAG CGGCGGGCCC CAGGCAAAC TGCACGACGC	180
	CTGCCAGGGC GATTCGGGAG GCCCCCTGGT GTGTCTGAAC GATGGCCGCA TGACTTTGGT	240
55	GGGCATCATC AGCTGGGGCC TGGGCTGTGG ACAGAAGGAT GTCCCGGGTG	290

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 base pairs

- 36 -

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

5 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

10

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

15

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

CTACGGCAAG	GAGGAGGCCT	TGTCTCCTTT	CTATTCGGAG	CGGCTGAAGG	AGGCTCATGT	60
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CAACATGCTG	TGTGCTGGAG	AACTCGGAG	CGGCGGGCCC	CAGGCAAAC	TGCACGACGC	180
25 CTGCCAGGGC	GATTCGGGAG	GCCCCCTGGT	GTGTCTGAAC	GATGGCCGCA	TGACTTTGGT	240
GGGCATCATC	AGCTGGGGCC	TGGGCTGTGG	ACAGAAGGAT	GTCCCGGGTG		290

(2) INFORMATION FOR SEQ ID NO:7:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: not relevant

35

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

40

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

45

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

50 CTACGGCAAG	CATGAGGCCT	TGTCTCCTTT	CTATTCGGAG	CGGCTGTATG	AGGCTCATGT	60
CAGACTGTAC	CCATCCAGCC	GCTGCACATC	ACAACATTTA	CTTAACAGAA	CAGTCACCGA	120
CAACATGCTG	TGTGCTGGAG	AACTCGGAG	CGGCGGGCCC	CAGGCAAAC	TGCACGACGC	180
55 CTGCCAGGGC	GATTCGGGAG	GCCCCCTGGT	GTGTCTGAAC	GATGGCCGCA	TGACTTTGGT	240
GGGCATCATC	AGCTGGGGCC	TGGGCTGTGG	ACAGAAGGAT	GTCCCGGGTG		290

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

10 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

15 (iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

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

CTACGGCAAG GACGAGGCCT TGT

23

25 (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

35 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

40 (vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

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

CTACGGCAAG GAGGAGGCCT TGT

23

50 (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: not relevant  
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

5 (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

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

CGGAGCGGCT GTATGAGGCT MCATGT

25



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## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(IV) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

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

CGGAGCGGCT GTATGAGGCT MCATGT

25

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 527 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(IV) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

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

Ser	Tyr	Gln	Val	Ile	Cys	Arg	Asp	Glu	Lys	Thr	Gln	Met	Ile	Tyr	Gln
1				5				10						15	
Gln	His	Gln	Ser	Trp	Leu	Arg	Pro	Val	Leu	Arg	Ser	Asn	Arg	Val	Glu
			20					25					30		
Tyr	Cys	Trp	Cys	Asn	Ser	Gly	Arg	Ala	Gln	Cys	His	Ser	Val	Pro	Val
		35				40						45			
Lys	Ser	Cys	Ser	Glu	Pro	Arg	Cys	Phe	Asn	Gly	Gly	Thr	Cys	Gln	Gln
		50				55					60				
Ala	Leu	Tyr	Phe	Ser	Asp	Phe	Val	Cys	Gln	Cys	Pro	Glu	Gly	Phe	Ala
65					70					75					80
Gly	Lys	Cys	Cys	Glu	Ile	Asp	Thr	Arg	Ala	Thr	Cys	Tyr	Glu	Asp	Gln
				85						90				95	
Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser	Gly	Ala	Glu
			100					105						110	
Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro	Tyr	Ser	Gly
		115					120					125			

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Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His	Asn	Tyr	Cys
	130					135					140				
Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val	Phe	Lys	Ala
145					150					155					160
Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys	Ser	Glu	Gly
				165					170					175	
Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg	Gly	Thr	His
			180					185					190		
Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	Ser	Met	Ile
		195					200					205			
Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala	Gln	Ala	Leu
	210					215					220				
Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	Asp	Ala	Lys
225					230					235					240
Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp	Glu	Tyr	Cys
				245					250					255	
Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr	Ser	Gln	Pro
			260					265					270		
Gln	Phe	Arg	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala	Ser	His	Pro
	275						280					285			
Trp	Gln	Ala	Ala	Ile	Phe	Ala	Lys	His	Arg	Arg	Ser	Pro	Gly	Glu	Arg
	290					295					300				
Phe	Leu	Cys	Gly	Gly	Ile	Leu	Ile	Ser	Ser	Cys	Trp	Ile	Leu	Ser	Ala
305					310					315					320
Ala	His	Cys	Phe	Gln	Glu	Arg	Phe	Pro	Pro	His	His	Leu	Thr	Val	Ile
				325					330					335	
Leu	Gly	Arg	Thr	Tyr	Arg	Val	Val	Pro	Gly	Glu	Glu	Glu	Gln	Lys	Phe
			340						345				350		
Glu	Val	Glu	Lys	Tyr	Ile	Val	His	Lys	Glu	Phe	Asp	Asp	Asp	Thr	Tyr
		355					360					365			
Asp	Asn	Asp	Ile	Ala	Leu	Leu	Gln	Leu	Lys	Ser	Asp	Ser	Ser	Arg	Cys
	370					375					380				
Ala	Gln	Glu	Ser	Ser	Val	Val	Arg	Thr	Val	Cys	Leu	Pro	Pro	Ala	Asp
385					390					395					400
Leu	Gln	Leu	Pro	Asp	Trp	Thr	Glu	Cys	Glu	Leu	Ser	Gly	Tyr	Gly	Lys
				405					410					415	
His	Glu	Ala	Leu	Ser	Pro	Phe	Tyr	Ser	Glu	Arg	Leu	Lys	Glu	Ala	His
			420						425				430		
Val	Arg	Leu	Tyr	Pro	Ser	Ser	Arg	Cys	Thr	Ser	Gln	His	Leu	Leu	Asn
		435						440				445			
Arg	Thr	Val	Thr	Asp	Asn	Met	Leu	Cys	Ala	Gly	Asp	Thr	Arg	Ser	Gly
	450					455					460				
Gly	Pro	Gln	Ala	Asn	Leu	His	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
465					470					475					480
Pro	Leu	Val	Cys	Leu	Asn	Asp	Gly	Arg	Met	Thr	Leu	Val	Gly	Ile	Ile
				485					490					495	
Ser	Trp	Gly	Leu	Gly	Cys	Gly	Gln	Lys	Asp	Val	Pro	Gly	Val	Tyr	Thr
			500						505				510		
Lys	Val	Thr	Asn	Tyr	Leu	Asp	Trp	Ile	Arg	Asp	Asn	Met	Arg	Pro	
		515					520					525			

**THE EMBODIMENTS OF THE INVENTION IN WHICH AN EXCLUSIVE PROPERTY OR PRIVILEGE IS CLAIMED ARE DEFINED AS FOLLOWS:**

1. A protein variant of a single chain human tissue-type plasminogen activator protein as set forth in SEQ ID NO:11, said variant having R275 and at least one other basic amino acid residue in the serine protease region substituted by a non-basic amino acid residue thereby disrupting the salt bridge interaction between aspartate 477 and lysine 429.
2. The protein variant of claim 1 wherein the non-basic amino acid residue is chosen from the group consisting of glycine, serine, threonine, asparagine, tyrosine, glutamine, aspartic acid, and glutamic acid and having a zymogenicity of at least 10.
3. The protein variant of claim 1 having a zymogenicity of at least 75.
4. The protein variant of claim 1 having a zymogenicity of at least 100.
5. The protein variant of claim 1 having a fibrin stimulation factor of at least 10,000.
6. The protein variant of claim 1 having a fibrin stimulation factor of at least 20,000.
7. The protein variant of claim 2 having a fibrin stimulation factor of at least 10,000.
8. The protein variant of claim 2 having a fibrin stimulation factor of at least 20,000.
9. The protein variant of claim 3 having a fibrin stimulation factor of at least 20,000.
10. The protein variant of claim 1 wherein the protein variant is at least a factor of 5 less inhibited by PAI-1 compared to wild type single chain human tissue-type plasminogen activator protein.

11. The protein variant of claim 1 wherein the protein variant is at least a factor of 9 less inhibited by PAI-1 compared to wild type single chain human tissue-type plasminogen activator protein.
12. The protein variant of claim 1 wherein the protein variant is at least a factor of 200 less inhibited by PAI-1 compared to wild type single chain human tissue-type plasminogen activator protein.
13. The protein variant of claim 8 wherein the protein variant is at least a factor of 9 less inhibited by PAI-1 compared to wild type single chain human tissue-type plasminogen activator protein.
14. The protein variant of claim 8 wherein the protein variant is at least a factor of 200 less inhibited by PAI-1 compared to wild type single chain human tissue-type plasminogen activator protein.
15. The protein variant of claim 1 wherein the protein variant has a fibrin selectivity factor of at least 100.
16. The protein variant of claim 8 wherein the protein variant has a fibrin selectivity factor of at least 100.
17. The protein variant of claim 14 wherein the protein variant has a fibrin selectivity factor of at least 100.
18. A polynucleotide encoding the protein variant of claim 1.
19. An expression vector comprising the polynucleotide of claim 18.
20. A cell comprising the expression vector of claim 19.

21. A protein variant of a single chain human tissue-type plasminogen activator protein as set forth in SEQ ID NO:11, said protein variant having amino acid substitutions selected from the group consisting of:
  - (i) R275E,H417D,
  - (ii) R275E,H417E, and
  - (iii) R275E,K429Y.
22. A polynucleotide encoding the protein variant of claim 21.
23. An expression vector comprising the polynucleotide of claim 22.
24. A cell comprising the expression vector of claim 23.
25. A composition for the treatment of a thrombotic condition comprising a physiologically effective amount of the protein variant of claim 1 in a pharmaceutically suitable excipient.
26. The composition of claim 25 wherein the dose of the protein variant is from about 0.05 milligram per kilogram body weight to about 0.2 milligram per kilogram body weight.
27. A diagnostic kit comprising the protein variant of claim 1 and instructions for use, wherein said diagnostic kit is for diagnosing a thrombotic condition.
28. A diagnostic kit comprising polynucleotides that specifically hybridize to the polynucleotide of claim 18 and instructions for use, wherein said diagnostic kit is for diagnosing a thrombotic condition.
29. A method of making the protein variant of a single chain human tissue-type plasminogen activator protein comprising the steps of culturing the cell of claim 24.

30. The method of claim 29 further comprising the additional step of purifying the protein variant.
31. A protein variant of a single chain human tissue-type plasminogen activator protein as set forth in SEQ ID NO:11, said protein variant having R275E and K429Y amino acid substitutions.
32. Use of a therapeutically effective amount of the protein variant according to any one of claims 1-17 in the treatment of a thrombotic condition in a patient in need of such therapy.
33. Use of the protein variant according to any one of claims 1-17 in the manufacture of a medicament for the treatment of a thrombotic condition.
34. A protein variant of a single chain human tissue-type plasminogen activator protein having the amino acid sequence as set forth in SEQ ID No:1, 2 or 3.

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GTTCTGAGCACAGGGCTGGAGAGAAAACCTCTGCGAGGAAAGGGAAGGAGCAAGCCGTGA

							-35						-30			
							met	asp	ala	met	lys	arg	gly	leu		
							ATG	GAT	GCA	ATG	AAG	AGA	GGG	CTC		
												-20				
cys	cys	val	leu	leu	leu	cys	gly	ala	val	phe	val	ser	pro	ser		
TGC	TGT	GTG	CTG	CTG	CTG	TGT	GGA	GCA	GTC	TTC	GTT	TCG	CCC	AGC		
													-10			
gln	glu	ile	his	ala	arg	phe	arg	arg	gly	ala	arg	SER	TYR	GLN		
CAG	GAA	ATC	CAT	GCC	CGA	TTC	AGA	AGA	GGA	GCC	AGA	TCT	TAC	CAA		
												10				
VAL	ILE	CYS	ARG	ASP	GLU	LYS	THR	GLN	MET	ILE	TYR	GLN	GLN	HIS		
GTG	ATC	TGC	AGA	GAT	GAA	AAA	ACG	CAG	ATG	ATA	TAC	CAG	CAA	CAT		
													20			
GLN	SER	TRP	LEU	ARG	PRO	VAL	LEU	ARG	SER	ASN	ARG	VAL	GLU	TYR		
CAG	TCA	TGG	CTG	CGC	CCT	GTG	CTC	AGA	AGC	AAC	CGG	GTG	GAA	TAT		
												30				
CYS	TRP	CYS	ASN	SER	GLY	ARG	ALA	GLN	CYS	HIS	SER	VAL	PRO	VAL		
TGC	TGG	TGC	AAC	AGT	GGC	AGG	GCA	CAG	TGC	CAC	TCA	GTG	CCT	GTC		
													40			
LYS	SER	CYS	SER	GLU	PRO	ARG	CYS	PHE	ASN	GLY	GLY	THR	CYS	GLN		
AAA	AGT	TGC	AGC	GAG	CCA	AGG	TGT	TTC	AAC	GGG	GGC	ACC	TGC	CAG		
												50				
GLN	ALA	LEU	TYR	PHE	SER	ASP	PHE	VAL	CYS	GLN	CYS	PRO	GLU	GLY		
CAG	GCC	CTG	TAC	TTC	TCA	GAT	TTC	GTG	TGC	CAG	TGC	CCC	GAA	GGA		
													60			
PHE	ALA	GLY	LYS	CYS	CYS	GLU	ILE	ASP	THR	ARG	ALA	THR	CYS	TYR		
TTT	GCT	GGG	AAG	TGC	TGT	GAA	ATA	GAT	ACC	AGG	GCC	ACG	TGC	TAC		
												70				
GLU	ASP	GLN	GLY	ILE	SER	TYR	ARG	GLY	THR	TRP	SER	THR	ALA	GLU		
GAG	GAC	CAG	GGC	ATC	AGC	TAC	AGG	GGC	ACG	TGG	AGC	ACA	GCG	GAG		
													80			
SER	GLY	ALA	GLU	CYS	THR	ASN	TRP	ASN	SER	SER	ALA	LEU	ALA	GLN		
AGT	GGC	GCC	GAG	TGC	ACC	AAC	TGG	AAC	AGC	AGC	GCG	TTG	GCC	CAG		
												90				
LYS	PRO	TYR	SER	GLY	ARG	ARG	PRO	ASP	ALA	ILE	ARG	LEU	GLY	LEU		
AAG	CCC	TAC	AGC	GGG	CGG	AGG	CCA	GAC	GCC	ATC	AGG	CTG	GGC	CTG		
													100			
GLY	ASN	HIS	ASN	TYR	CYS	ARG	ASN	PRO	ASP	ARG	ASP	SER	LYS	PRO		
GGG	AAC	CAC	AAC	TAC	TGC	AGA	AAC	CCA	GAT	CGA	GAC	TCA	AAG	CCC		
													110			
													120			
													130			
													140			
													150			

FIG. 1A

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TRP	CYS	TYR	VAL	PHE	LYS	160	ALA	GLY	LYS	TYR	SER	SER	GLU	PHE	CYS
TGG	TGC	TAC	GTC	TTT	AAG	GCG	GCG	GGG	AAG	TAC	AGC	TCA	GAG	TTC	TGC
SER	170	PRO	ALA	CYS	SER	GLU	GLY	ASN	SER	ASP	180	CYS	TYR	PHE	GLY
AGC	THR	CCT	GCC	TGC	TCT	GAG	GGA	AAC	AGT	GAC	TGC	TAC	TTT	GGG	
ASN	GLY	SER	ALA	TYR	ARG	190	GLY	THR	HIS	SER	LEU	THR	GLU	SER	GLY
AAT	GGG	TCA	GCC	TAC	CGT	GGC	ACG	CAC	AGC	CTC	ACC	GAG	TCG	GGT	
ALA	200	CYS	LEU	PRO	TRP	ASN	SER	MET	ILE	LEU	210	ILE	GLY	LYS	VAL
GCC	SER	TGC	CTC	CCG	TGG	AAT	TCC	ATG	ATC	CTG	ATA	GGC	AAG	GTT	
TYR	THR	ALA	GLN	ASN	PRO	220	SER	ALA	GLN	ALA	LEU	GLY	LEU	GLY	LYS
TAC	ACA	GCA	CAG	AAC	CCC	AGT	GCC	CAG	GCA	CTG	GGC	CTG	GGC	AAA	
HIS	230	TYR	CYS	ARG	ASN	PRO	ASP	GLY	ASP	ALA	240	LYS	PRO	TRP	CYS
CAT	ASN	TAC	TGC	CGG	AAT	CCT	GAT	GGG	GAT	GCC	AAG	CCC	TGG	TGC	
HIS	VAL	LEU	LYS	ASN	ARG	250	ARG	LEU	THR	TRP	GLU	TYR	CYS	ASP	VAL
CAC	GTG	CTG	AAG	AAC	CGC	AGG	CTG	ACG	TGG	GAG	TAC	TGT	GAT	GTG	
PRO	260	CYS	SER	THR	CYS	GLY	LEU	ARG	GLN	TYR	270	SER	GLN	PRO	GLN
CCC	SER	TGC	TCC	ACC	TGC	GGC	CTG	AGA	CAG	TAC	AGC	CAG	CCT	CAG	
PHE	ARG	ILE	LYS	GLY	GLY	280	LEU	PHE	ALA	ASP	ILE	ALA	SER	HIS	PRO
TTT	CGC	ATC	AAA	GGA	GGG	CTC	TTC	GCC	GAC	ATC	GCC	TCC	CAC	CCC	
TRP	290	ALA	ALA	ILE	PHE	ALA	LYS	HIS	ARG	ARG	300	SER	PRO	GLY	GLU
TGG	GLN	GCT	GCC	ATC	TTT	GCC	AAG	CAC	AGG	AGG	TCG	CCC	GGA	GAG	
ARG	PHE	LEU	CYS	GLY	GLY	310	ILE	LEU	ILE	SER	SER	CYS	TRP	ILE	LEU
CGG	TTC	CTG	TGC	GGG	GGC	ATA	CTC	ATC	AGC	TCC	TGC	TGG	ATT	CTC	
SER	320	ALA	HIS	CYS	PHE	GLN	GLU	ARG	PHE	PRO	330	PRO	HIS	HIS	LEU
TCT	ALA	GCC	CAC	TGC	TTC	CAG	GAG	AGG	TTT	CCG	CCC	CAC	CAC	CTG	
THR	VAL	ILE	LEU	GLY	ARG	340	THR	TYR	ARG	VAL	VAL	PRO	GLY	GLU	GLU
ACG	GTG	ATC	TTG	GGC	AGA	ACA	TAC	CGG	GTG	GTC	CCT	GGC	GAG	GAG	

FIG. 1B



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GLU	GLN	LYS	PHE	GLU	VAL	GLU	LYS	TYR	ILE	VAL	HIS	LYS	GLU	PHE
GAG	CAG	AAA	TTT	GAA	GTC	GAA	AAA	TAC	ATT	GTC	CAT	AAG	GAA	TTC
ASP	ASP	ASP	THR	TYR	ASP	ASN	ASP	ILE	ALA	LEU	LEU	GLN	LEU	LYS
GAT	GAT	GAC	ACT	TAC	GAC	AAT	GAC	ATT	GCG	CTG	CTG	CAG	CTG	AAA
SER	ASP	SER	SER	ARG	CYS	ALA	GLN	GLU	SER	SER	VAL	VAL	ARG	THR
TCG	GAT	TCG	TCC	CGC	TGT	GCC	CAG	GAG	AGC	AGC	GTG	GTC	CGC	ACT
VAL	CYS	LEU	PRO	PRO	ALA	ASP	LEU	GLN	LEU	PRO	ASP	TRP	THR	GLU
GTG	TGC	CTT	CCC	CCG	GCG	GAC	CTG	CAG	CTG	CCG	GAC	TGG	ACG	GAG
CYS	GLU	LEU	SER	GLY	TYR	GLY	LYS	HIS	GLU	ALA	LEU	SER	PRO	PHE
TGT	GAG	CTC	TCC	GGC	TAC	GGC	AAG	CAT	GAG	GCC	TTG	TCT	CCT	TTC
TYR	SER	GLU	ARG	LEU	LYS	GLU	ALA	HIS	VAL	ARG	LEU	TYR	PRO	SER
TAT	TCG	GAG	CGG	CTG	AAG	GAG	GCT	CAT	GTC	AGA	CTG	TAC	CCA	TCC
SER	ARG	CYS	THR	SER	GLN	HIS	LEU	LEU	ASN	ARG	THR	VAL	THR	ASP
AGC	CGC	TGC	ACA	TCA	CAA	CAT	TTA	CTT	AAC	AGA	ACA	GTC	ACC	GAC
ASN	MET	LEU	CYS	ALA	GLY	ASP	THR	ARG	SER	GLY	GLY	PRO	GLN	ALA
AAC	ATG	CTG	TGT	GCT	GGA	GAC	ACT	CGG	AGC	GGC	GGG	CCC	CAG	GCA
ASN	LEU	HIS	ASP	ALA	CYS	GLN	GLY	ASP	SER	GLY	GLY	PRO	LEU	VAL
AAC	TTG	CAC	GAC	GCC	TGC	CAG	GGC	GAT	TCG	GGA	GGC	CCC	CTG	GTG
CYS	LEU	ASN	ASP	GLY	ARG	MET	THR	LEU	VAL	GLY	ILE	ILE	SER	TRP
TGT	CTG	AAC	GAT	GGC	CGC	ATG	ACT	TTG	GTG	GGC	ATC	ATC	AGC	TGG
GLY	LEU	GLY	CYS	GLY	GLN	LYS	ASP	VAL	PRO	GLY	VAL	TYR	THR	LYS
GGC	CTG	GGC	TGT	GGA	CAG	AAG	GAT	GTC	CCG	GGT	GTG	TAC	ACC	AAG
VAL	THR	ASN	TYR	LEU	ASP	TRP	ILE	ARG	ASP	ASN	MET	ARG	PRO	OP
GTT	ACC	AAC	TAC	CTA	GAC	TGG	ATT	CGT	GAC	AAC	ATG	CGA	CCG	TGA

FIG. 1C

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CCAGGAACACCCGACTCCTCAAAAGCAAATGAGATCCCGCCTCTTCTTCTTCAGAAGACA  
CTGCAAAGGCGCAGTGCTTCTCTACAGACTTCTCCAGACCCACCACACCGCAGAAGCGGG  
ACGAGACCCTACAGGAGAGGGAAGAGTGCATTTTCCCAGATACTTCCCATTTTGGGAAGT  
TTTCAGGACTTGGTCTGATTTTCAGGATACTCTGTCAGATGGGAAGACATGAATGCACACT  
AGCCTCTCCAGGAATGCCTCCTCCCTGGGCAGAAAGTGGCCATGCCACCCTGTTTTTCAGCTA  
AAGCCCAACCTCCTGACCTGTCACCGTGAGCAGCTTTGGAAACAGGACCACAAAAATGAA  
AGCATGTCTCAATAGTAAAAGATAACAAGATCTTTCAGGAAAGACGGATTGCATTAGAA  
ATAGACAGTATATTTATAGTCACAAGAGCCCAGCAGGGCCTCAAAGTTGGGGCAGGCTGGC  
TGGCCCGTCATGTTCCCTCAAAAGCACCCCTTGACGTCAAGTCTCCTTCCCCTTTCCCCTACT  
CCCTGGCTCTCAGAAGGTATTCCTTTTGTGTACAGTGTGTAAAGTGTAAATCCTTTTTCT  
TTATAAACTTTAGAGTAGCATGAGAGAATTGTATCATTGAACTAGGCTTCAGCATA  
TTTATAGCAATCCATGTTAGTTTTTACTTTCTGTTGCCACAACCCTGTTTTATACTGTA  
CTTAATAAATTCAGATATATTTTTTCCAAAAA

**FIG. 1D**

FIG. 2A

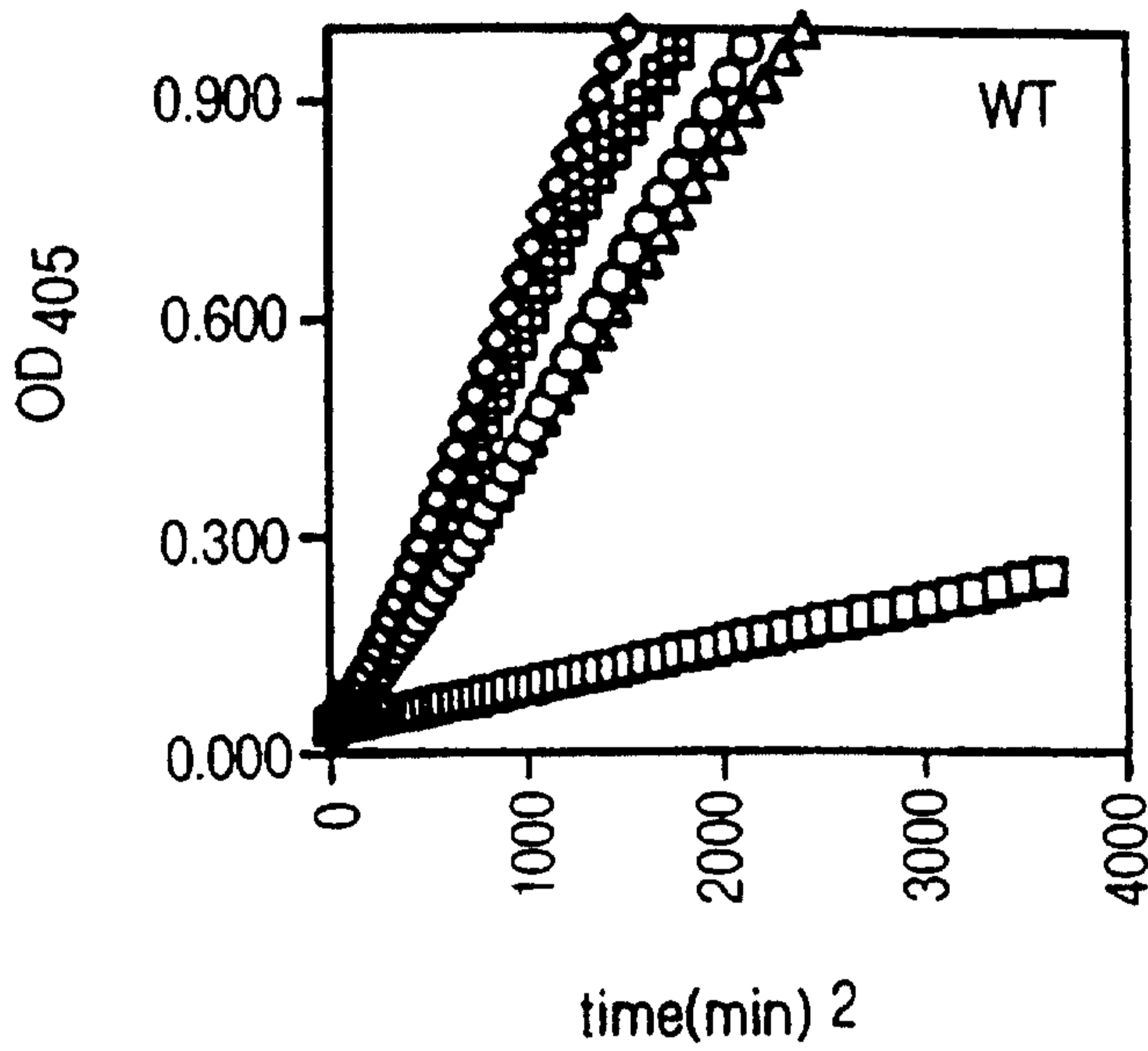


FIG. 2B

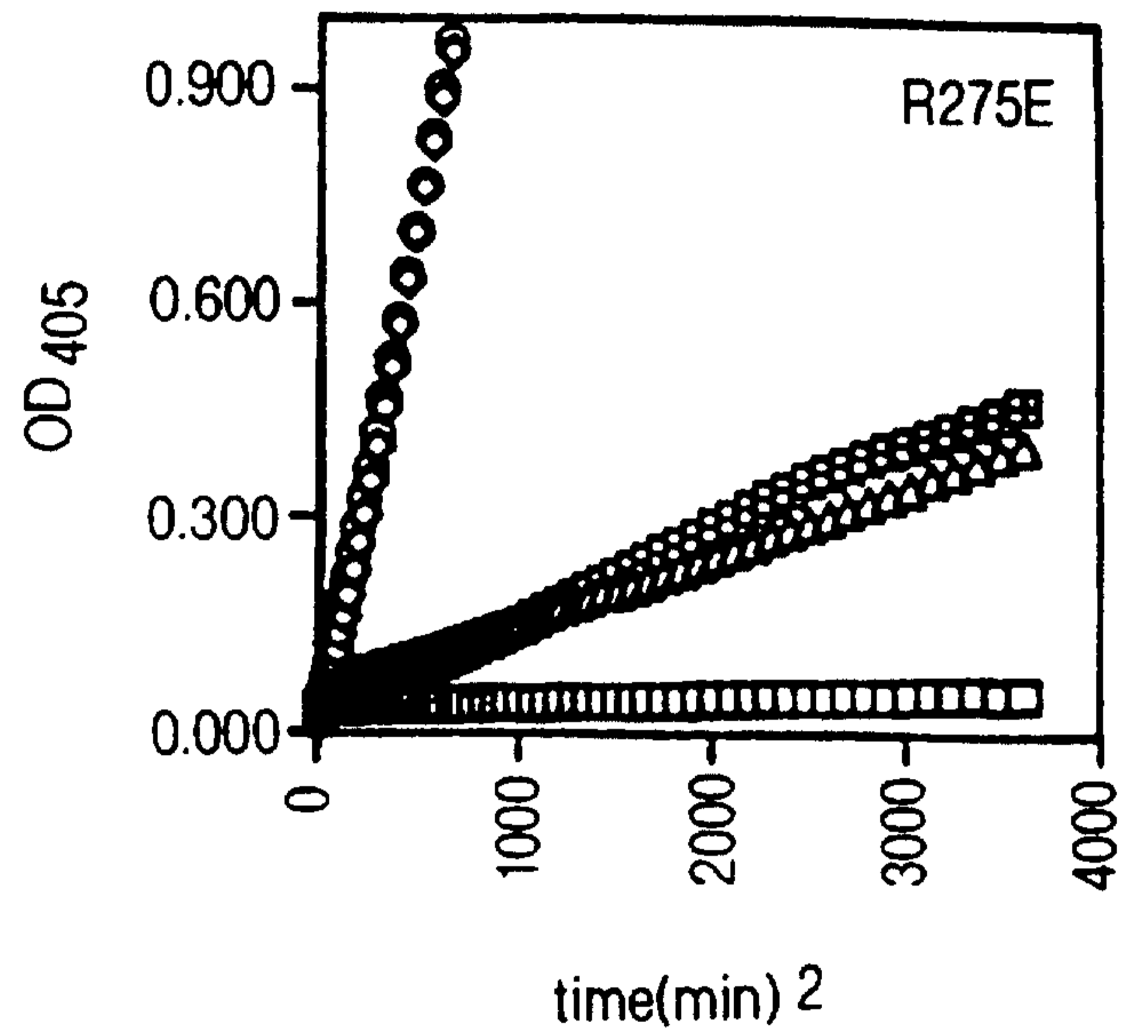


FIG. 2C

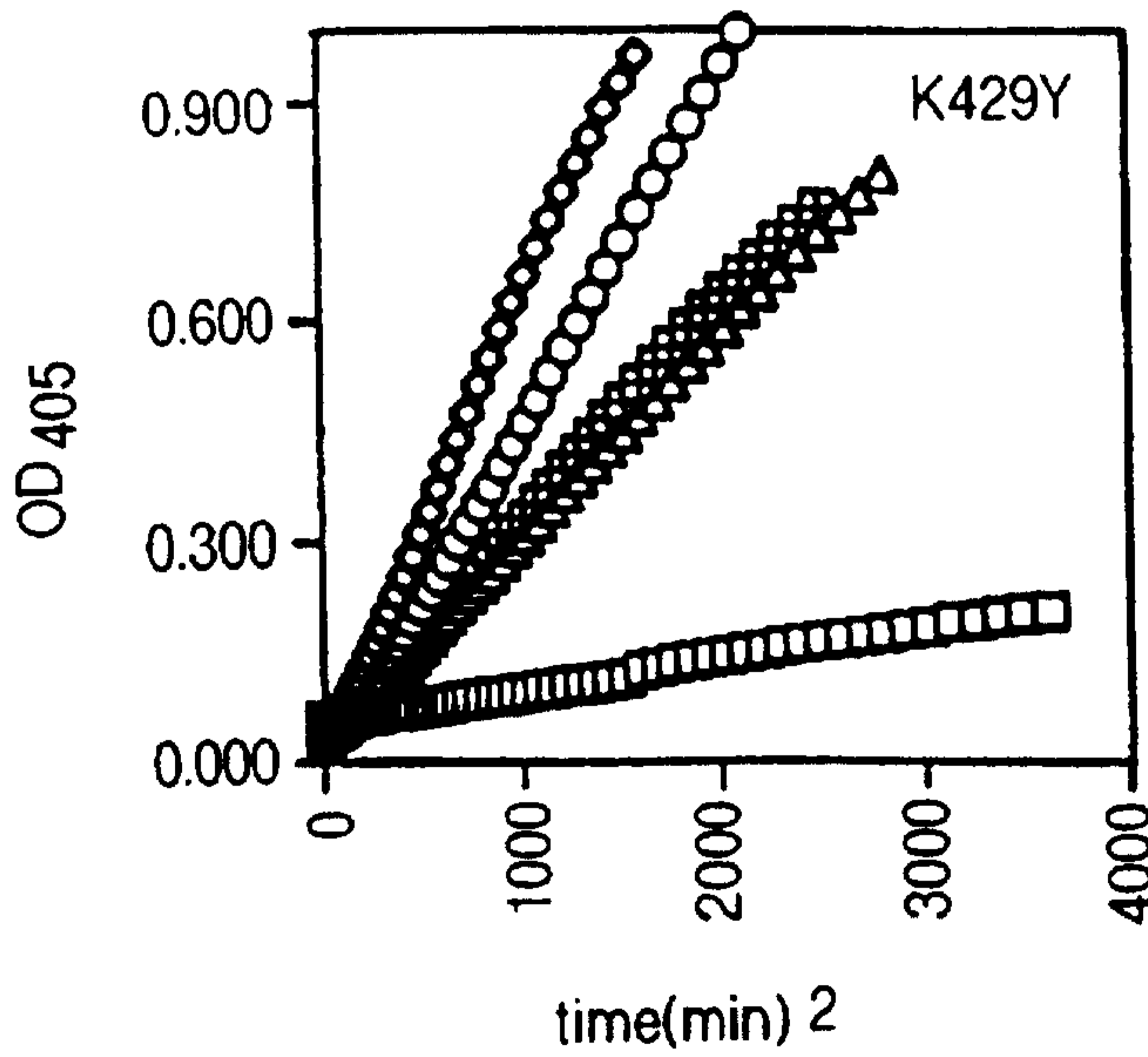


FIG. 2D

