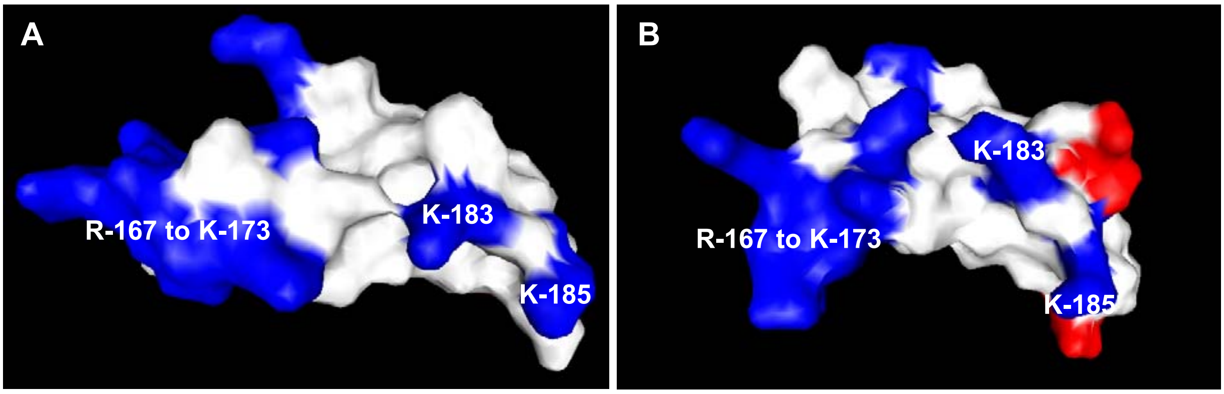
Supplementary table 1: Results of amino-terminal sequence analysis of hydrolysed human FSAP.

Multiple sequences were detected in parallel in nearly equimolar amounts. *, cysteine residues; +, signal intensity of peak was to weak to identify corresponding amino acid.

Peptide	Cleavage after residue	Amino acid identified in the following cycle numbers:									
		1	2	3	4	5	6	7	8	9	10
F1	Gly-23	F	S	L	M	S	L	L			
F2	Gly-23	F	S	L	M	S	L	L	E	S	L
F3 and F4	Lys-169	R	R	S	K	F	T	*	A	*	P
	Arg-171	S	K	F	T	*	A	*	P	D	Q
	Lys-173	F	T	*	A	*	P	D	Q	F	K
	Lys-185	G	K	F	*	E	I	G	S	D	D
F5	Lys-169	R	R	S	+	F	T	+	A		
F6	Lys-319	S	T	A	G	K	H	P	W	Q	A
	Arg-480	Q	L	Y	D	H	M	I	D	D	S
F7	Lys-110	V	Q	N	T	*	K	D	N	P	*
F8	Lys-110	V	Q	N	T	*	K	D	N	P	*
	Lys-517	D	G	T	Y	Y	V	Y	G	I	V
F9	Lys-319	S	T	A	G	K	H	P	W	Q	A
F10	Gly-23	F	+	+	M	+	L	+	E		
	Lys-319	S	T	A	G	+	H	P			
	Lys-470	L	I	A	N	T	L	*	N		
	Arg-480	Q	L	Y	D	H	M	I	D	D	
F11 and F12	Gly-23	F	S	L	M	S	L	L	E	S	L
	Lys-432	T	V	*	L	P	D	G	S		
	Lys-470	L	I	A	N	T	L	*	N	S	
	Arg-480	Q	L	Y	D	H	M	I	D	D	S
	Lys-517	D	G	T	Y	Y	V	Y	G	I	V
F13	Lys-110	V	Q	N							
	Lys-319	S	T	A							
	Lys-470	L	I	A	N	T	L				
	Arg-480	Q	L	Y	D						
F14	Gly-23	F	+	L	M	+	L	L	E	S	L
	Lys-169	R	R	+	+	F	T	+	A		
F15	Lys-110	V	+	N	T	*	+	D	N	P	
	Lys-432	T	+	*	L	P	+	G			
	Lys-470	L	I	A	N	+	L	*			
	Arg-480	Q	+	Y	+	+	+	I			
F16	Lys-110	V	+	N	T	*	+	D	N	P	
	Lys-432	T	+	*	L	P	D	G	+	F	
	Lys-470	L	I	A	N	+	L	*	N	S	
	Arg-480	Q	+	Y	D	H	M	I	+	D	
F17	Lys-110	V	Q	N	T	*	K	D	N	P	
	Lys-173	F	T	*	A	*	P	G	Q	F	
	Lys-185	G	K	F	*	E	I	G	S	+	
F18	Lys-294	L	P	G	F	D	S	*	G	K	T
	Lys-432	T	V	*	L	P	D	G	S	F	P
	Lys-470	L	I	A	N	T	L	*	N	S	R
	Arg-480	Q	L	Y	D	H	M	I	D	D	S
	Lys-517	D	G	T	Y	Y	V	Y	G	I	V
F19	Lys-319	S	T	A	G	K	H	P	W	Q	A
	Lys-416	L	K	P	V	D	G	H	*	A	L

Supplementary Figure 1



```
Alignment with HUMAN TPA  P00750

TPA    PVKSCSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKCCE
FSAP   VVPVCRPNPCQNGATCSRHKRRSKFTCACPDQFKGKFCE
```

```
Alignment with HUMAN Factor IX  P00740

FIX    DGDQCESNPCLNGGSCKDDI--NSYECWCPFGFEGKNCE
FSAP   VVPVCRPNPCQNGATCSRHKRRSKFTCACPDQFKGKFCE
```

Model of the three-dimensional structure of EGF3 of human FSAP: A) The available solution structure of the closely related EGF domain of human tissue-type plasminogen activator (TPA) (Protein Data Bank code 1tpg) was used to model the EGF3 domain of FSAP using SWISS-MODEL. Basic residues are drawn in blue, acidic residues in red and neutral residues in white. Residues Arg-167 to Lys-173, Lys-183, and Lys-185 are indicated. B) Similar results were obtained when the modelling was performed with the EGF1 domain of human Factor IX (Protein Data Bank code 1 ixa). Alignment between the EGF3 domain of FSAP and the EGF domain of tPA as well as the EGF1 domain of Factor IX is shown.