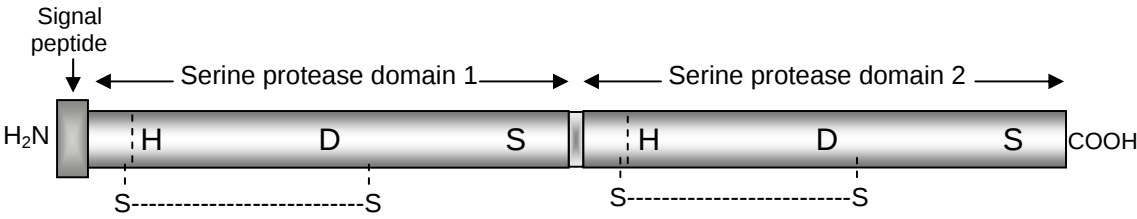


A

1	ATGAAGTGGTGCTGGGGCCCAAGTGTCTCATCGCGGGTGCCACAGTCCCTCATGGAGGGT	841	AGCCAGAGACCCCGGAGATGAGTGATGAGGACAGCTGTGTAGCCTGTGGATCCTTGAGG
1	M K W C W G P V L L I A G A T V L M E G	281	S P E T P E M S D E D S C V A C G S L R
61	CTTCAAGCCGCTCAGCGTGCCTGTGGACAGCGTGGCCCGGCCCCCAAGCCTCAGGAG	901	ACAGCAGGTGCCCCAGGCAGGAGCACCTCCCATGGCCCTGGGAGGCCAGGCTGATGCAC
21	L Q A A Q R A C G Q R G P G P P K P Q E	301	T A G P Q A G A P S P W P W E A R L M H
121	GGCAACACAGTCCCTGGCGAGTGGCCCTGGCAGGCCAGTGTGAGGAGGCAAGGACCCAC	961	CAGGGACAGCTGGCCTGTGGCGGAGCCCTGGTGTGACAGGAGGCGGTGCTAACTGCTGCC
41	G N T V P G E W P W Q A S V R R Q G A H	321	Q G Q L A C G G A L V S E E A V L T A A
181	ATCTGCAGCGGCTCCCTGGTGGCAGACACCTGGGTCTCTACTGCTGCCACTGCTTTGAA	1021	CACTGCTTCATTGGCGGCCAGGCCCCAGAGGAATGGAGCGTAGGGCTGGGACAGACCG
61	I C S G S L V A D T W V L T A A H C F E	341	H C F I G R Q A P E E W S V G L G T R P
241	AAGGCAGCAGCAACAGAAGTGAATTCCTGGTCAAGTGGTCTGGGTTCTCTGCAGCGTGAG	1081	GAGGAGTGGGCGCTGAAGCAGCTCATCTGCATGGAGCCTACACCCACCTGAGGGGGGC
81	K A A A T E L N S W S V V L G S L Q R E	361	E E W G L K Q L I L H G A Y T H P E G G
301	GGACTCAGCCCTGGGGCCGAAGAGGTGGGGGTGGCTGCCCTGCAGTTGCCAGGGCCTAT	1141	TACGACATGGCCCTCCTGTCTGTGGCCAGCCTGTGACACTGGGAGCCAGCCTGCGGCC
101	G L S P G A E E V G V A A L Q L P R A Y	381	Y D M A L L L L A Q P V T L G A S L R P
361	AACCACTACAGCCAGGGCTCAGACCTGGCCCTGCTGCAGCTCGCCACCCACGACCCAC	1201	CTCTGCCTGCCCTATCCTGACCACCACCTGCCTGATGGGAGCGTGGCTGGGTTCTGGGA
121	N H Y S Q G S D L A L L Q L A H P T T H	401	L C L P Y P D H H L P D G E R G W V L G
421	ACACCCCTCTGCCTGCCCCAGCCGCCCATCGCTTCCCTTTGGAGCCTCTGCTGGGCC	1261	CGGGCCCGCCAGGAGCAGGCATCAGCTCCCTCCAGACAGTGGCCGTGACCTCTCTGGGG
141	T P L C L P Q P A H R F P F G A S C W A	421	R A R P G A G I S S L Q T V P V T L L G
481	ACTGGCTGGGATCAGGACACAGTGATGCTCTGGGACCTACGCAATCTGCGCTGCGT	1321	CCTAGGGCTGCAGCGGCTGCATGCAGCTCCTGGGGGTGATGGCAGCCCTATTCTGCCG
161	T G W D Q D T S D A P G T L R N L R L R	441	P R A C S R L H A A P G G D G S P I L P
541	CTCATCAGTCGCCCCACATGTAACTGTATCTACAACAGCTGCACCAAGCAGACCTGTCC	1381	GGGATGGTGTGTACCAAGTGTGTGGGTGAGCTGCCAGCTGTGAGGGCCTGTCTGGGGCA
181	L I S R P T C N C I Y N Q L H Q R H L S	461	G M V C T S A V G E L P S C E G L S G A
601	AACCCGGCCCGCCTGGGATGCTATGTGGGGGCCCGCAGCTGGGGTGCAAGGGCCCTGT	1441	CCACTGGTGCATGAGGTGAGGGGCACATGGTTCCTGGCCGGGTGCACAGCTTCGAGAGT
201	N P A R P G M L C G G P Q P G V Q G P C	481	P L V H E V R G T W F L A G L H S F G D
661	CAGGGAGATTCCGGGGCCCTGTGCTGTGCCTCGAGCTGACGGACACTGGGTTTCAGGCT	1501	GCTTGCCAAGGCCCCGCGAGGCCGCGGCTTCCACCGCTCCCTGCCTATGAGGACTGG
221	Q G D S G G P V L C L E P D G H W V Q A	501	A C Q G P A R P A V F T A L P A Y E D W
721	GGCATCATCAGCTTTGCATCAAGCTGTGCCAGGAGGACGCTCCTGTGCTGCTGACCAAC	1561	GTCAGCAGTTTGGACTGGCAGGTCTACTTCGCCGAGGAACAGAGCCCGAGGCTGAGCCT
241	G I I S F A S S C A Q E D A P V L L T N	521	V S S L D W Q V Y F A E E P E P E A E P
781	ACAGCTGCTCACAGTTCTGGTGCAGGCTCGAGTTCAAGGGGCGAGCTTCTGGCCAG	1621	GGAAGCTGCCTGGCCAACATAAGCCAACCAACAGCTGCTGA
261	T A A H S S W L Q A R V Q G A A F L A Q	541	G S C L A N I S Q P T S C *

B



C

<i>Hs</i>	GVQGPCQGDSSGGPVLCLEPD.....GELPSCEGLSGAPLVHEVR
<i>Pt</i>	GVQGPCQGDSSGGPVLCLEPD.....GELPSCEGLSGAPLVHEVR
<i>Mm</i>	GEQGPCQGDSSGGPVMCREPD.....GEPHCEGLSGAPLVHEIR
<i>Rt</i>	GVQGPCQGDSSGGPVMCREPD.....GEPHCEGLSGAPLVHEVR
<i>Bt</i>	GMQGPCQGDSSGGPVLCREPD.....GEPHCEGLSGAPLVHEVR
<i>Cf</i>	GVQGPCQGDSSGGPVLCREPD.....GEPHCEGLSGTPLVHEVR
	Spd1 Spd2