

	10	20	30	40	50	60
dmel						
dsim	maskvsilllltvhllaaqtfaqeliawqr-----					
dsec	maskvsilllltvhllatqtfaqeltawqr-----					
dere	maskvsiflllltvhllaaqtfaqeltawqr-----					
dyak	maskttlllltisllaahsfaqefsaawqr-----					
dana	maskatilllatty--ghllaaqeyhgwsr-----					
dpse	maskcmillallvpllnaqtfnqpgypgfg-----					
dper	maskci1lll-dgplp----rgcsiplpgd-----					
dwil	maskci1lllmgpyl----vaqsyyrgt-----					
dmoj	mtckysilllvasvsagrqnrrpqqqpavp-----					
dvir	mpnkys1lllggs-clslclfltpatngngqri-----					
dgri	m1lllssy1lisl1clci--gpavsssifagv-----					
Consensus	MasK s1LLL1 1					
Prim.cons.	MASK3S1LLLT2LLAAQTFAQELSAWQRA2VNNVVYTNNI33SR2P2SIRSR22222V					
	70	80	90	100	110	120
dmel	--qqqqqqqqqlqlqqq111qqqqhqrnprpelglrs-----					
dsim	--qqqlqlqqqqrqqqq----qqqlnprpelglrsrm-----					
dsec	--qqqlqlqqqqrqqqq----qq--lnprpelglrs-----					
dere	--hqqplqqqqqqqlpr-----nprpelglrs-----					
dyak	--ppqqqqpr-----ssrpelglra-----					
dana	--lgarfgggg-----vvppqndlqa-----					
dpse	--ggqvlpqpqgpppdnq----rpleevqppgnsqerq-----pq					
dper	--rgksrrprarqtn----ghwrrssrretarrds-----pk					
dwil	--aapsvpaaaakgandlqrpigwdqqwnnnnvqtnq-----qy					
dmoj	--sfdnqiqsrsrvaapaqnristvsaaasppniqqq----ypaqpla---pve					
dvir	-pd1hd1lqrpqgevmlaqetwsdqriaashtgqqtwnvqrnvaevptaqqqqhqpiip					
dgri	kpteqdqqnpqqdpqltaqqswnsqrrsaqrpetssagtvn1-----vpktqlqq---pns					
Consensus	q q rpe					
Prim.cons.	KPQQQ4QQQ2QQRQQQQAQ552QQQR2NPRPELGLRSQN2QRNVAEVP33QLQQQHQPP6					
	130	140	150	160	170	180
dmel	lpgnpwt-qnnqeaisdvvavdltkrepvtpppntrPP--PVFSYMDRFSSELFKEIIKSQ					
dsim	ypenrwnnnqnneaisdvvavdltksepvtppptrPP--PVFSYMDRFSSELFKEIIKSQ					
dsec	lpgnrwi-qnnqeaisdvvavdlskrepvtppptrPP--PVFSYMDRFSSELFKEIIKSQ					
dere	----qtnqytkeptsdvvvmvdltkhepanppptrPP--PVFSYMDRFSGQLFDQIIKSQ					
dyak	-qntnprtqdnqhpidsvvavadlskpeptnapptrPP--PAYSYMMDRFSAELFKQIMKSQ					
dana	----qedirvpsapqrqrnggqsrnaptaptrAPVIPKTSFMDRFSSKLYAKIAPAQ					
dpse	nppsqippqrqpanvgane--vplptvsnsxptrPP--AKQSFKDRFSSKLFQPIASRS					
dper	iptaryrprdsrpscwmpr--crcpr-sptvptrPP--AKQSFKDRFSSKLFQPIASRS					
dwil	gptandsprvqgvdesgsgs--glsqpppvstsptrPP--AQKNYMEQFSSKLFQQIATRA					
dmoj	apdasrtspstvtvlgidgsadqsaaggqsrgpsgpirPP--AQFNRYRERFSSTLFQPISRNN					
dvir	asatasapaaspeivngfnq-aagrpassagptrPP--AQYNYRERFSSVLFQPISRSN					
dgri	apalatapatavtv-lgvdrpnq-asvqpssssptrPP--AHYNYRERFSSKLFQPIARNN					
Consensus	p p p PTRPP a s%m#RFSS LFq I					
Prim.cons.	AP42RWTPQ3NQE2ISDVVAVDL2KREP24PPPTRPPVI2VFSYMDRFSKLFQPIAKSQ					

	190	200	210	220	230	240
dmel						
dsim	SQQNVVFSPFSVHALLALIYGASDGKTFRELQKAGEFSKNAMAVAQDFESVIKYKKHLEG					
dsec	SQQNVVFSPFSVHALMALVYGASDGKTYRELKKKAGEFSKNAMAVAQDFESVIKYKMHLEG					
dere	SQQNVVFSPFSVHALLALVYGASDGKTYRELKKKAGEFSKNAMAVAQDFESVIKYKMHLEG					
dyak	GQQNVVLSPFSVHALLALIYGASDGKTFRELQKAGEFSKNAMAVAQDFESVIKYRMHLEG					
dana	SQQNVVFSPFSVQALLALIYGASSGKTFRELQKAGEFSKNAMAVAHDFENVIVIKYKMHLEG					
dpse	AGSNFVYSPVSVHSILALIYGTSGKTRRELKSAGEFVDDQIDVAMIFEKLIFRSDLGN					
dper	QRQNLVFSPPSVHALLGMIYGASEGRTAQELQQAGEFGPDPQAVGQDFRQLIKQRRQLQS					
dwil	QRQNLVFSPPSVHALLGMIYGASEGRTAQELQQAGEFGPDPQAVGQDFRQLIKQRRQLQS					
dmoj	QQKNIVYSPAMVHSQALMLYIVSHGQTFEELQQAGIFSVDTTKVSDQLSLLSLQ-QLQN					
dvir	ANRNVVYSPSSVHAMLAMLYGVSAGETATELRSAGQFDQNLTAMDFQRVRKLERELQN					
dgri	GQQNVVYSPATMHAMLGLLYGVSSNETAAELQRVGQFGNKQLDVAIEFEQVRRTESQLPN					
Consensus	ARKNVVFSPASMHSMLLYSVSSGQTSDELQRAGNFDIGKIEVAMDFKNVDQQHKKLVN					
Prim. cons.	qqNvV%SP SVHa\$La\$ YGaS G T Elq AG#F # aVaqDFe vik L SQQNVVFSPFSVHALLALIYGASDGKT2RELQKAGEFSKNAMAVAQDFESVIKY2MHLE2					
	250	260	270	280	290	300
dmel	ADLTLATKVYYNRELGGVNHSYDEYAKFYFSAGTEAVDMQNAKDAAKINAWVMDTTRNK					
dsim	ADLTLATKYYNRELGGVXPSPYDEYAKFYFSAGTEAVDMQNGKDTAARINAWVMDQTRNK					
dsec	ADLTLATKVYYNRELGGVNPSPYDEYAKFYFSAGTEAVDMQNGKDTAARINAWVMDQTRNK					
dere	ADLTLATKVYYNQELGGVNPSPYDAYAKFYFSAGTEAVDMQNGKDT SARINAWVMDQTRSK					
dyak	TDLTLATKVYYNQELGGVNHHSYDAYAKFYFSAGTEAVDMQNGKDT SARINAWVMDKTRSK					
dana	VELKMATKLYHNQLKGAYPGPEFSQFYNTADEAVDMTRAKDTSEKINFVWSDSTDGK					
dpse	AELTMASRMFYNKNMGGGINHDYPEYAEYYYSSGIEPVDMGRSRETAGWINAWVSDKTRNK					
dper	AELTMASRMFYNKNMGGGINHDYPEYAEYYYSSGIEPVDMGRSRETAGWINAWVSDKTRNK					
dwil	AEIIIVASKVLYNPAQGPNERFPKYALTYFNTIEITFPNPQDPRTNTANAINGWVRDRTKNT					
dmoj	AQLIVANKLFYNHELAMVNPDYAHLYFNSEIEGVNMKRSANTASRINA AWADATRNI					
dvir	AQLIVANKLYYNREIDELNPRYLAFASQYYGSETEAVNMRKSRDTAAKINAWASDATRG					
dgri	TRLIVANKLYYNRELSAPNDRYEAFALEYYNSEIEAVDMKKPRNTAAEINQWVS RATNKI					
Consensus	a#Lt A K %YN #\$gg N Y %A Y%ss Eav#M #TAa INaWV D Trnk					
Prim. cons.	ADLTLATKVYYNRELGGVNPSPYDEYAKFYFSSGTEAVDMQN2KDTAARINAWV2D3TRNK					
	310	320	330	340	350	360
dmel	IRDLVTPTDVPQTQALLVNavyFQGRWEHEFATMDTSPYDFQHTNGRISKVAMMFNDDV					
dsim	IRELVTPADVPQTQALFVNavyFKGRWEHEFATMDTSPSDFQHSNGRISKVAMMFNDDV					
dsec	IRELVTPADVPQTQALLVNavyFKGRWEHEFATMDTSPSDFQHSNGRISKVAMMFNDDV					
dere	IRELVTSGIDPQTQALLVNavyFKSRWEHEFAIMDTAPSDFHHSNGKTSQVAMMFNDDV					
dyak	IRELVTPGMDPQTQALLVNavyFQGRWEHEFAIMDTSPYDFHHSNGRTSKVAMMFNDDV					
dana	IRNLAAPSDITEQTEALLVNAYFKGRWENEFAIMDTQPSNFKHSDGRISVAMMFNDDV					
dpse	IRELVTPSDIDGQTEAMLVNAYFKARWATEFSATDTISGKFRRGSGAPS NVAMMFNDDV					
dper	IRELVTPSDIDGQTEAMLVNAYFKARWATEFSATDTISGKFRRGSGAPS NVAMMFNDDV					
dwil	IKQLITQSEIDDQTQAILLNAYFKARWANEFSTRDTMPAKFRMGNGAAINVAMMFNDDV					
dmoj	IRDLVSPNDIDDETQALLVNAYFKARWANEFSAMDTTPDKFRVNSNKAVTVAMMFNDDV					
dvir	IRDLVQPSDIDEQTQALLVTAYFKARWANEFSEMDTTAEKFRMGNNAAITVPMMFNDDL					
dgri	IRELVSPSDIDEQTEAMMVDAIYFKARWANEFSAMDTTPAKFRLNGVTPITVPMMFNDDI					
Consensus	IR#LVTPSD!D QT#A\$LVNA!YFKaRWa EFs mDT p kFr ng s VAMM%NDDV					
Prim. cons.	IRELVTPSDIDPQTQALLVNAYFKARW22EF2TMDTSPSKFRHSNGRISKVAMMFNDDV					
	370	380	390	400	410	420
dmel	YGLAELPELGATALELAYKDSATSMLILLPNETTGLKMLQQLSRPEFDLNRVAHRLRRQ					
dsim	YGLAELPELGATALELAYKDSATSMLILLPNQTTGLAKMLQQLSRPEFDLNRVAHRLRRQ					
dsec	YGLAELPELGATALELAYKDSATSMLILLPNQTTGLAKMLQQLSRPEFDLNRVAHRLRRQ					
dere	YGLAELPELGATALELAYKDSATSMLILLPNQTTGLAKMMQQLSRPEFDLNRVAHRLRRQ					
dyak	YGLAELPELGATALELAYKDSATSMLILLPNQTTGLAKMMQQLSRPEFDLNRVAHRLRRQ					
dana	YSLADIPELGASALGLNYRDSNISMLILLPKQVNGLRALEAQLADPQFDLNRIAARLRQ					
dpse	FGYADLPDLGATALEMPYADSEVSMLILLPYQVDGLAQLEQQLARPQNDLNRIAARLRQ					
dper	FGYADLPDLGATALEMPYADSEVSMLILLPYQVDGLAQLEQQLARPQNDLNRIAARLRQ					
dwil	FDYAEELPDLHATALEMPYAGTQISMLIILPNQVNGLTQLERQLARPEYDLNIAARLRRE					
dmoj	YAYAELPDLDAVALELPYAGTEVSMLFVLPNQVDGLPQLERQLE--RTDLNQIAARLRRE					
dvir	FDIAELPELDATALELPYAGTPISMLIILPNQVNGLAQLERQLE--RHDLNQIAARLHRD					
dgri	FAYAQLPELDATALELPYVDNDASMLLILPNQPNGLAQLERNLASTNHDLNIAARLRRE					
Consensus	%g A#LP#LgATALE\$pY ds SMLILLPnQvnGlaq\$eqQL rp# DLN !AaRLRR#					
Prim. cons.	YGLAELPELGATALELPY2DSATSMLILLPNQVNGLAQLEQQL2RPEFDLNRIAARLRQ					

	430	440	450	460	470	480	
dmel	SVAVRLPKFQFEQE QDMTEPLKNLGVHQMF TPNSQVTKLMQPVRSKILQKAYINVGEAGTEASAAS						
dsim	PVAVRLPKFQFEQE QDMTQPLKDLGVHQMF TPNSQVTKLLDHPVRSKILQKAYINVGEAGTEASAAS						
dsec	PVAVRLPKFQFEQE QDMTQPLKDLGVHQMF TPNSQVTKLLDHPVRSKILQKAYINVGEAGTEATAAS						
dere	SVAVLPKFQFEQE QDMTQPLKDLGVQQMF TPNSQVTKLLDQPVRSKILQKAYINVGEAGTEASAAS						
dyak	SVAVLPKFQFEQE QDMTQPLKDLGIHQMF TPNSQVNKLLDHPVRSKILQKAYINVGEAGTEASAAS						
dana	NVLVRLPKFRIEFQDQMTQPLKQMDVQEMFGPKSQIKTMLNDRVKEKILQKAFIDVN EAGTEAAAAS						
dpse	TVTIRIPKFRIQFEQDMTEPLQLGVREMFTRSSQVTKMLDRPVRSKILQKAFLNVN EAGSEAAAAS						
dper	TVTIRIPKFRIQFEQDMTEPLQLGVREMFTRSSQVTKMLDRPVRSKILQKAFLNVN EAGSEAAAAS						
dwil	TVTVRIPRFRIEFQDMTEPLQRLGVKEMFTSRQVDAMLDKPAMVSKIQQQKAFIDVN EAGSEASASS						
dmoj	MVAVRLPKFRIEFQDMTLPQELGVRRMFTANSQVNTILMRPVVKSKILQKAFIDVN EAGSEAAAAT						
dvir	MVTVRIPKFRIEFELDMTGPLQLGVRRMFTPKSQVDAMLLQPVRSKILQKAFIDVN EAGSEAAAAS						
dgri	MVTVRVPKFRIEFQDMMSGPLQELGVRRMFTKQSEVDAMLMQPVRSKVLQKAFIDVN EAGSEAAAAS						
Consensus	V VR1PKFriEFQDMT PLq#LGV MFTp SQV k\$Ld PVRVSKILQKA%I#VnEAGsEAaAAS						
Prim. cons.	3VAVRLPKFRIEFQDMTQPL22LGVRQMFTPNSQVTKMLDQPVRSKILQKAFINVNEAG2EAAAAS						
	490	500	510	520	530	540	550
dmel	YAKFVP L SLPPKPTEFVANRPFVFAVRTPASVLFIGHVEYPTPMSV-----						
dsim	YAKFVP L SLPPKPTEFVANHPFVFAVRTPTSVLFIGHVEYPTPVSV-----						
dsec	YAKFVP L SLPPKPTEFVANRPFVFAVRTPTSVLFIGHVEYPTPVSV-----						
dere	YAKFVP L SLPPKPTEFIANRPFVFAIRTPTSVLFIGHVEYPTPMSVKN-KPNFDFYRN-----						
dyak	YAKFVP L SLPPKPTQFVANRPFVFAIRTPAVLFIGHVENPTPMSVKNPEPYSDIYRN-----						
dana	YAKFVP L SLPAKSPEFTADHPFVFAIRTPDSVLFIGHVLQPTAMA-----						
dpse	YAKFVP L SLPVKSREFNADHPFVFALRTPDSVLFIGHVLQPTAMA-----						
dper	YAKFVP L SLPVKSREFNADHPFVFALRTPDSVLFIGHVLQPTAMA-----						
dwil	YAKFVP L SLPVKSHEFTADHPFIFAIRSPNAVLFIGHVVQPTQVA-----						
dmoj	FAKFVP L LP MKSREFIADHPFLFAIRTPESVLFIGHVVQPPQINARQ-----						
dvir	YAKFVP L SLPVKSREFVADHPFVFAIRTPDSVLFIGHVVQPPQVSGRQ-----						
dgri	YAKFVP L SLPVQSLEFTADHPFLFAIRTPETVLFIGHVVQPLQATRSQ-----						
Consensus	YAKFVPLSLP Ks EF A#hPF!FA!RTP SVLFIGHV qPt						
Prim. cons.	YAKFVPLSLP2KS2EFVADHPFVFAIRTPTSVLFIGHVEQPTPMSV3Q23P33D3YRN FSSRQ						

Alignment annotation:

Residues conserved for 80 % or more (upper-case letters) : 195 is 35.39 %

Residues conserved for 50 % and less than 80 % (lower-case letters) : 87 is 15.79 %

Residues conserved less than 50 % (white space) : 233 is 42.29 %

IV conserved positions (!) : 5 is 0.91 %

LM conserved positions (\$) : 7 is 1.27 %

FY conserved positions (%) : 8 is 1.45 %

NDQEBZ conserved positions (#): 16 is 2.90 %

Residues of the N-terminal extension are printed in lower case, with serpin core residues in UPPER CASE. The putative scissile bond marked in bold (**rP**). The consensus flexible hinge region residues of inhibitory serpins and the PF residues at the C-terminal RCL “shutter region” are marked in RED. The putative protease cleavage site in the RCL, P1/P1’, is marked in green.