

Serp

Multiple Alignments of R C L Sequences

		P17-----P8-----P1/P1'-----P14'PF
<i>Spn27A</i> (CG11331)	mel sim sec yak ere ana pse per wil moj vir gri	EKGTEAYAATVVEIENKFGGSTAIEEFNVNRPF EKGTEAYAATVVEIENKFGGSTAIEEFNVNRPF EKGTEAYAATVVEIENKFGGSTAIEEFNVNRPF EKGTEAYAATVVEIENKFGGSTTIEEFNVNRPF EKGTEAYAATVVEIENKFGGSTLIEEFNVNRPF EKGTEAYAATVVEIENKFGGSTIIEEFNVNRPF EKGTEAYAATVVEIENKFGGSTTIEEFNVNRPF EKGTEAYAATVVEIENKFGGSTTIEEFNVNRPF EKGTEAYAATVVEIENKFGGSIVIEEFNVNRPF EQGTEAYAATVVEIENKFGGSQTIVEFNVNRPF EQGTEAYAATVVEIENKFGGSQTIVEFNVNRPF EQGTEAYAATVVEIENKFGGPTKIEEFNVNRPF *.:*****: * * * * *
<i>Spn28B</i> (CG6717)	mel sim sec yak ere	EKGGEASAATGVLTRRKKSIDNLIQPPMEFIADHPF EKGGEASAATGILTRRKKSIDNLRLLPMEFIVDHPF EKGGEASAATGVLTRRKKSIDNLRLLPMEFIVDHPF ERGTKASAATGVLIRRKKSIDNLKPPPMEFVADHPF ERGAKASAATGVLIRPKKSIDNMKLPPMEFIADHPF *: * :*****: * * * * *: * * * * *
<i>Spn28Da</i> (CG31902)	mel sim sec yak ere	EEGGSAGSASASPIRGLSDYATSVVTFVNSPF EEGGSAGSASANPIRGLSDYAASLVTFVNSPF EEGGSAGSASANPIQGLSDYAASVVTFVNSPF EEGASAGSASASLFRGLSDYPASVASFTVNSPF EEGASAGSASASLLRGWSDYPANVASVRVDRPF ***:*****: : * * * * : : : * : **
<i>Spn28Db</i> (CG33121)	mel sim sec yak ere	HNKKVYVRMMSHVGRFRIADHSYGQIIEMPF HNRKAYVRMMSHVGRFRIADHSYGQIIELPF HNREAYVRMMSHVGRFRIADHSYGQIIELPF HNKKVYVRMMSHVGRFRMADQSYGQIIELPF HNKAVHVRMMSQVGRFRMAKQSYGQIIELPF **: : : * * * * : * * * * : * * * * : *
<i>Spn28Dc</i> (CG7219)	mel sim sec yak ere ana pse per wil moj vir gri	EQGTEAAASSVTYLKKS GPDVLFRGDTPF EQGTEAAASSVTYLKKS GPDVLFRGDTPF EQGTEAAASSVTYLKKS GPDVLFRGDTPF EQGTEAAASSVTYLKKS GPDVVFGRDTPF EQGTEAAASSVTYLKKS GPDVVFGRDTPF EQGTEAAAATVTYLKKS GPDVLFRGDTPF EQGTEAAAATVTYVKKSGPDVLFRGDTPF EQGTEAAAATVTYVKKSGPDVLFRGDTPF EQGTEAAAATIAYLKKS GPDILFRVDTPF EQGTEAAAATAAILKKSGPEVLFRAETPF EQGTEAAAASAAILKKSGPEVVFRAETPF EQGTEAAAASA AVLKKSGPDVVFRAETPF *****: : : * * * * : : * * : ***
<i>Spn28F</i> (CG8137)	mel sim yak ere ana (16627) ana (21984)	EEGAEEAAATALLFVRY SMP-MPSSQMVFNADHPF EEGAEEAAATALLTVRY SKP-RPSSQMVFNADHPF EEGAEEAAATKIVVYPLS ---AHPIWMDFNVDHPF EEGAEEAAITKIDMVFKSASRPQPI - -DFIADHPF EEGAEEAAVTAVVAVHICANCATPSRMSFIANHPF EEGAEEASAASAVSIVFYE - - - - -MDFHADHPF *****: * : : * * * * : * : * * *

<i>Spn42De</i> (CG9460)	mel sim sec yak ere ana pse per wil	EKGTTASGATFIKVSVESLTIGEEVFEFIADHPPF EKGTTASGATFVKVSVESLLIGEEVFEFIADHPPF EKGTTASGATFVKVSVESLLIGEEVFEFIAYHPPF EKGTTASGATYVNAAVESLLIGEEVFETADHPPF EKGTTASGATFVQVAVESLLIGEEVFESADHPPF EKGTTASGATFVKAELES LVIGEQTVEFVADHPPF ENGTTASAATAVKFSLES AFMG-EVQQFTADHPPF ENGTTASAATAVKFSLES AFMG-EVQQFTADHPPF EKGTTATGASFSKVLELEVIGEVTYNFTVDHPPF *:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:
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<i>Spn43Aa</i> (CG12172)	mel sim sec yak ere ana pse per wil moj vir gri	EIGCEAAGASYAAGVPMSLPLDPKTFVADHPPF EIGCEAAGASYAAGVPMSLPLDPKTFVADHPPF EIGCEAAGASYAAGVPMSLPLDPKTFVADHPPF EIGCEAAGASYAAGVPMSLPLDPKTFVADHPPF EIGCEAAGASYAAGVPMSLPLDPKTFVADHPPF EIGCEAAGVSYAAGVPMSLPLDPKTFVADHPPF EIGCEAAGVSYAAGVPMSLPLDPKTFVADHPPF EIGCEAAGVSYAAGVPMSLPLDPKTFVADHPPF EIGCEAAGISYAAGVPMSLPLDPKTFVADHPPF EIGCEAAGVSYAAGVPMSLPLDPKTFVADHPPF EIGCEAAGISYAAGVPMSLPLDPKTFVADHPPF EIGCEAAGVSYAAGVPMSLPLEPKTFVADHPPF *****
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<i>Spn43Ab</i> (1865)	mel sim sec yak ere ana pse per wil moj vir gri	EAGVDQPLETGLLKGLFSRSKKFEADHPPF EAGVEQPLETGLLKGLFSRSKKFEADHPPF EAGVEQPLETGFLKGLFSRSKKFEADHPPF EAGLEQPLETGLLKGLFSRSKKFEADHPPF EAGLEQPLETGLLKGLFSRSKKFEADHPPF EAGVEQPLETGVLKGLFSRSKKFEADHPPF EAGVEQPLESGVLKGLFSRSKKFEADHPPF EAGVEQPLESGVLKGLFSRSKKFEADHPPF EAGVEPSLEQGVKGLFSRSKKFEADHPPF EAGVEQPLETGVLKGLFSRSKKFEADHPPF EAGVEQPLESGVLKSFRTKKFEADHPPF EAGVEQPLESGLLKGLFSRNKKFEADHPPF ***:***:***:***:***:***:***:***:***:***:
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<i>Spn43Ac</i> (CG1857)	mel sim sec yak ere ana pse per wil moj vir gri	EAGTEASAASYAKFVPLSLPPKPTEFVANRPPF EAGTEASAASYAKFVPLSLPPKPTEFVANRPPF EAGTEATAASYAKFVPLSLPPKPTEFVANRPPF EAGTEASAASYAKFVPLSLPPKPTEFVANRPPF EAGTEASAASYAKFVPLSLPPKPTEFVANRPPF EAGTEAAAASYAKFVPLSLPAKSPEFTADHPPF EAGSEAAAASYAKFVPLSLPVKSREFNADHPPF EAGSEAAAASYAKFVPLSLPVKSREFNADHPPF EAGSEASASSYAKFVPLSLPVKSHEFTADHPPF EAGSEAAAATFAKFVPLSLPMKSREFIADHPPF EAGSEAAAASYAKFVPLSLPVKSREFVADHPPF EAGSEAAAASYAKFVPLSLPVQSLEFTADHPPF ***:***:***:***:***:***:***:***:***:***:
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<i>Spn43Ad</i> (CG1859)	mel sim sec yak ere ana pse per moj vir gri	EDGGNADDSFS--FGDLFRRALPLVINHPF EEGGNADDSFY--FGDLFRRALPLVINHPF EEGGNADDSFS--FGDLFRRALPLVINHPF EEGGNAEDSFS--FGDLFRRALPLVINHPF EEGGHADDSFS--FGDLFRRALPLVINHPF EKGGTDGDSFS--FGDLFRRALPLVINHPF EEGGSAGDSFS--FGDLFRRALPLVINHPF EEGGSAGDSFS--FGDLFRRALPLVINHPF EAGGEAEQTFVAAFTDLFRSTLSLVINHPF EAGGEAEQTFVAAFTDLFRSTLSLVINHPF EQGAEAEQTFATFTDLFRSTLSVVINHPF * * . : * * * * * : * : * * * * *
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<i>Spn47C</i> (CG7722)	mel sim sec yak ere ana pse per wil moj vir gri	EFGCEVAPEAEVQPEVLKK-NPDRKFFKADRPF EFGCEVAPEAEVQPEVLKK-NPDRKFFKADRPF EFGCEVAPEAEVQPEVLKK-NPDRKFFKADRPF EFGCEVAPESDVQPEVLKK-NPDRKVFKADRPF EFGCEVAPESDVQPEVPKK-NPDRKVFKADRPF EAGCETAPEPDTHIHKTKN-NPDRKIFRADRPF ESGCETDPDKPARAAAFVQ-NPDRKLFMANRPF ESGCETDPDTPSRAAAAFVQ-NPDRKLFMTNRPF ENGCEVDIENKPGPTVPIVPDAERKIFRANRPF EAGCTTNIDESTKNRFVKA-NPERKVFVADHPF EAGCEIDANTPAETSTETS-NPERKVFADHPF ESGCGTADHTQGRVAAAKV-NPERKVFKANQPF * * * . : : * . * : : *
<i>Spn53F</i> (CG10956)	mel sim sec yak ere ana	EATYPREFRVNATKSVMIPMMHEDSKFAFGILGNLKATAVLVPF EATYPREFRVNAAKSVMIPMMHEDRRSP-----N EATYPREFRVNAAKSVMIPMMHEDSKFAFGILGNLKATAILVPF EATYPREFRVSAARKVMIPMMHEDSKFAFGNLATLKASAVLVPF EATYPRQFRVSAAKEVLIPMMHEDSKFAFGTLGHLKATAVLVPF GATYDREFRVSSQRTINVPMMHEDSKFAFGDLEKLQATALLPF * * * . * * * . * * * . : : : * * * * : .
<i>Spn55B</i> (CG10913)	mel sim sec yak ere ana pse per wil moj vir gri	EEGTEAAAATGMIMMTRMMTFPLQFQADRPF EEGTEAAAATGMIMMTRMMTFPLQFQADRPF EEGTEAAAATGMIMMTRMMTFPLQFQADRPF EEGTEAAAATGMIMMTRMMTFPLQFQADRPF EEGTEAAAATGMIMMTRMMTFPLQFQADRPF EEGTEAAAATGMIMMTRMMTFPIQFQADRPF EEGTEAAAATGMIMMTRMMTFPLQFQADRPF EEGTEAAAATGMIMMTRMMTFPIQFQADRPF EEGTEAAAATGMIMMTRMMLPLQFQADRPF EEGTEAAAATGIIMMTRMMLPLQFQADRPF EEGTEAAAATGMIMMTRMMLPLQFQADRPF * * * * * . * * * * * . * . * * * * * *
<i>Spn75F</i> (CG32203)	mel sim sec yak ere	ETALTNRTFTLLRQNKPKFVYTTQMMYTEAPMDFFNNDQVRGVMVPF EKALTNRTFTLLRQNRKPFVYTVEMMYTEAPMEFFNNDQVRGVVVPF EKALTNRTFTLLRQNRKPFVYTVEMMYTEAPMQFFNNDQVRGVVVPF EKAMTNRLFSYIRPNRKPFFVYKVEMIYTEAPMEFFNEDQVRGVMVPF EKAMTNRTFRWIRPNRRTFVYRVQMIYIEAPMEFFSGDQCRGVMVPF * : * * * * * : * * : : * * * : * : * * * * * * * * * * * *
<i>Spn76A</i> (CG3801)	mel sim sec yak	FKDSAFKSKAKIKINNFRVNHGIRFQPILRLEVDDIDTGKTETFEVNRPF FKDSAFKSKAKIKINDFRVNHGIRFQPILRLDVDDIDTGKTEKFEVNRPF FKDSAFKSKAKIKINDFRVNHGIRFQPILRLDLVDDIDTEKTEKFEVNRPF FKDSGFSSKPNIKINDFRVNHGVQFEPTQRLNVVEDIDTQNAQTFEVNRPF * * * * . * : * . * * * * * * * . * : * * * * * : * * * * *
<i>Spn77Ba</i> (CG6680)	mel sim sec yak ere ana pse per wil moj vir gri	EQGTTAGAVTEAALANKATPPKFLLNRPF EQGTTAGAVTEAALANKATPPKFLLNRPF EQGTTAGAVTEAALANKATPPKFLLNRPF EQGTTAGAVTEAALSNAKATPPKFQLNRPF EQGTTAGAVTEAALANKATPPKFQLNRPF EQGTTAGAVTAAALINKATPPKFLLNKP EQGTTAGAVTAAVLANKATPPKFQLNKP EQGTTAGAVTAAVLANKATPPKFQLNKP EKGTAAAVTSASLVNKATPPKFVLNKP EKGTAAAVTSAVLSNKSPPKFYLNRPF EKGTAAAVTASVLSNKSPPKFQLNRPF EQGTTAAGVTVSSLSNKSPPKFHLNRPF * : * * * * . * * : * * : : * * * * * * * * * *
<i>Spn77Bb</i> (CG6663)	mel sim wil	VDEEGLPNAVPQKSSGKN--NIKFHVNRPF VDEEGLPDAVPQKSSGTN--NIKFMTRPF VDEKGTAAAFSAATLSNKAAPPKFMINKPF * * * . * . * . : : . * * : : * *

characterised by a consensus sequence of small side-chain residues: E[EKR]G[TSG][ET][AGS][YAGS][AGS][VAGS][TS]. These residues form a flexible hinge region, 17-8 residues N-terminal to the putative protease cleavage site residues, P1/P1', marked in green. Both inhibitory serpins and non-inhibitory serpin folds have conserved PF residues at the C-terminal "shutter region" of the RCL. Note that the *Spn42Da* orthologues contain a mixture of several splice variants and the putative P1/P1' sites are unmarked. *Spn100A* represents a novel protein fold of unknown function, with two stretches of homology to the serpin-fold, one of which contains a putative RCL with partial conservation of the inhibitory serpin flexible hinge-region residues.