A

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     1                                                                               126
Mco  MKLFICILALAATAMA-EESNVD-LLKSSNEVFTANMFQEVVKAKPGENVVLSAFSVISPLAQLSLASVGESHDEILKAIGLPNDNVTKEVETDVSKQLRSVKGVELRLANKVYVRQGAVINDEFAAV  126
Bmo  MKTIICLFTIAIAAMA-GETDLQKIIRESNDQFTAQMFSEVVKNNPGKSVVMSAFSVLPPLAQLALASVGESHDEELLKAIGFPDDDAIRTEBASKSRDLRSIKGVELKMANKVYVHDGGKLDENFAVV  127
Mse  MKIIMCIFGIAALAMA-GETDLQKIIRESNDQFTAQMFSEVVKANPGQNVVLSAFSVIPPIGQLALASVGESHDELLRAILALPNDNVTKDVBADINRGVRAVKGVDLKMASIKYVAKGLEINDDFAAV  127
Pxy  MKLLICVLSVVVATAMADEIEDFKQQLNNGNDLFTANMFSEVLKQQNGKNVVMSAFSVLTPVAQLSLASSGETHDLLLLKTLGLPSDEAIKSVBPLVNAKLRDIKGVTLKQASIRIYLPLTAELADDFAAA  128
Cpo  MNTLIFFTAVVAMASATGEE---KIILNDGNNVFTANMFSEVVKEQACKSVVMSAFSVLQPLAQLALASVGESHDELLRAIGLPNDNVTKAVEPKVTAQLRAVQGVKINMANKIYIPTNAQVKEDFAAL  125
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Mco  SKDVENSDVKNVDFTKNVEAAKEINEWVEENTNHKIKDLVSSESIDASTAAVLVNAIYFKGKWKKPFDESAIRDLDBFVTKDQPIKKPTMHKSGDFKYAESKELDAKLLELPYEGDQSSLLIVLPNEI  254
Bmo  SRDVENSDVQNVDFSKNTVAAKSINDVNVDFTKNVEAAKEINEWVEENTNHKIKDLVSSESIDASTAAVLVNAIYFKGKWKKPFDESAIRDLDBFVTKDQPIKKPTMHKSGDFKYAESKELDAKLLELPYEGDQSSLLIVLPNEI  255
Mse  SRDVEGSEVQNVDFVKNVEAAGAINKWVEDQTNNRIKNLVDPDAIDETIRSVLVNAIYFKGSWKDFVKERIMDRDEHVSKDKTIKVPTMIGKKDVRYADVPELDAKMIEMSYEGDQASMIIILPNQV  255
Pxy  SRDVEGSEAKNLDFTKNVESSKEINDVWEEQTNNRIQDLVDPDSIKPDTASLLVNAIYFKGTWKSKFDNASSTERDEHVSKDKTVKVPTMYQKASFKYGESAELDAKLLEMPYEGEKASFLIILPNDI  256
Cpo  SKSVEGSEFKNIDFTKNVPAAQEINSWVEDHTNHKIKDLVDPNSIGADTRAVLVNALYFKGSWEKFNDKAITDSDEHVTKDKTVKVPTMYKDDFKYAESKELDAKLLELPYEGKEASFLIVLPNEI  253
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Mco  DGIGSLVEKLKDPTALSKAVENMFYNEVNVDLPKFKIETTTDLKAVIKKMNIVKLFTGGEARINNLIKGESDLFITDAIQKAFIDVNEEGAEAAAAN  351
Bmo  DGITQLQEALKDPKTIETAQQSMYSTEVDLYLPKFKIETETNLKDVISNMNVNKIENN-DAQITRLLKGES-ISVSEAIQKAFIEINEEGAEAAAAN  350
Mse  DGITALEQKLKDPKALSRAEERLYNTEVEIYLPKFKIETTTDLKEVMSNMGSSLFEPGKATIDKLLKSKAPLYIGDAIQKAFIEVNEEGSEAAAAN  352
Pxy  EGLPALTEKLKEPQHINKALSEMYKGEIQVYIPKFKIETETDLKEVMSNMGSSLFEPGKATIDKLLKSKAPLYIGDAKQKAFIEVNEEGSEAAAAN  353
Cpo  DGLPALQEKLKNPTALDKAVAEMREVEVNVYLPKFKIETTIDLKKVLQKIGITSLFDAAKARIDNLLKNESGLYVSDAIQKAFIEVNEEGAEAAAAN  350
                                                                            *********
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B

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CpSPN1C  ---VFTIDRTMIIPETYLMADRPFLFYLNVGSSILENGSEQS   40
CpSPN1D  ---DLGIYVMMLKPEIW-EKADRPFLFFLNAGSTTLENCSYQS   39
CpSPN1B  AFQVVSRSGKFYYVEPKEFNADHPFLFFINSHSNELENCAYIH   43
CpSPN1E  --AFLVEESLALVEELYEDADHPFIFHLRQGARTLENCVVNF   41
CpSPN1A  -DFGVTYLSAYVKPET-YENADHPFIFILKSGESALFGCVEYN   41
CpSPN1F  -VFPVPMAASWPPPRVREFIADHAFIFLLKACDSALFGCVEAN   42
Consensus ────────────────                    PF
         Reactive Centre Loop
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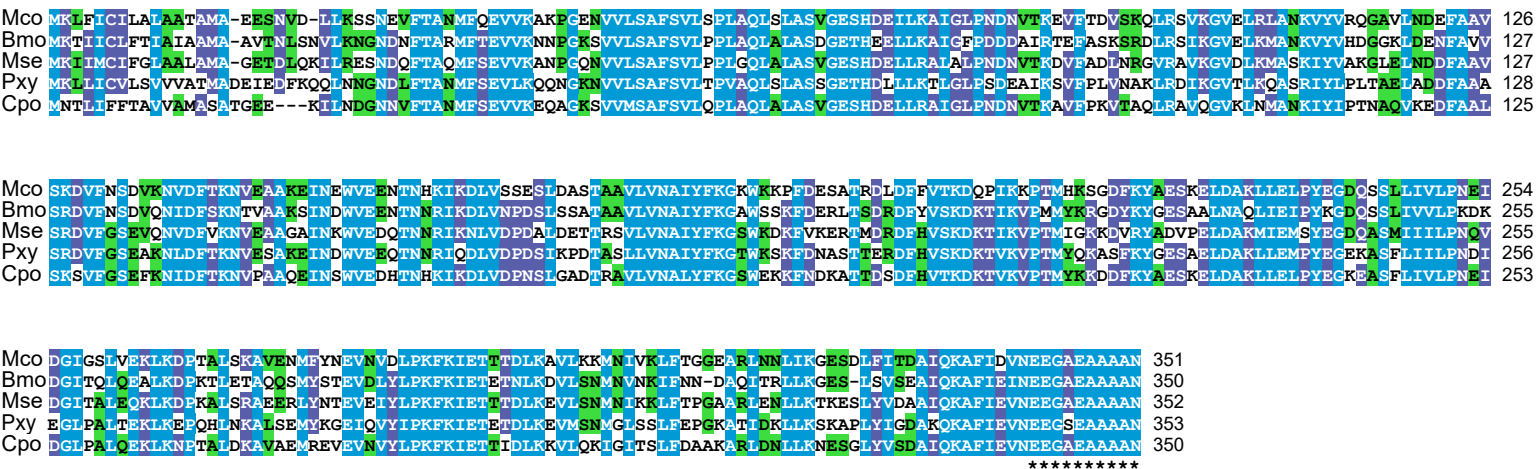
Figure S3 Comparison of protein sequences encoded by *serpin1* in several lepidopteran insects. **(A)** Sequence alignment of conserved region of serpin1 proteins in *Mamestra configurata*, *Bombyx mori*, *Manduca sexta*, *Plutella xylostella*, and *Cydia pomonella*. The hinge region preceding the reactive center loop (RCL) showed almost identical residues (in blue background) and similar residues (in green or purple background) were also indicated. **(B)** Alignment of *C. pomonella* serpin1 carboxyl-terminal inhibitor domain variants following the hinge region with the RCL and P1 positions are highlighted in red.