

Figure S7. Amino acid alignment of noctuid-derived caspase-1 and caspase-2 sequences. Identical residues are shaded in dark grey and conserved residues in lighter grey. Blue frames indicate putative cleavage sites. Note the apparent lack of cleavage site between the prodomain and the large subunit in caspase-2 sequences.

<i>Sf-C1</i>	1	-----ALGNSSSQPNRVARMPVDRNAPYYNMNHKYGMAIIFNHEHFDIHS-LKSRGTGNVDSNLSKVLKTLGKRVTVFFNLK	79
<i>Se-C1</i>	1	MLDGK-QDNGNVDSVDTKQR--TNGGDEGDALGSHNSQPTRYARMPVDRNAPYYNMNHKYGMAIIFNHEHFDIHS-LKSRGTGNVDSNLSKVLKTLGKRVTVFFNLK	107
<i>Mb-C1</i>	1	MLDGEQDNG---SVDTQRPNANGGDEGDALGSHNSNARRYARMPVDRNAPYYNMNHKYGMAIIFNHEHFDIHS-LKSRGTGNVDSNLSKVLKTLGKRVTVFFNLK	107
<i>Ha-C1</i>	1	MLDGDVQDNG---SVETEQR--PNGGDEGDAQGSHDSHARRFARMPVDRNAPYYNMNHKYGMAIIFNHEHFDIHS-LKSRGTGNVDSNLSKVLKTLGKRVTVFFNLK	105
<i>Hv-C1</i>	1	MLDGDVQDNG---SVEAEQR--ANGGDEGDAQGSHNSHSRRIARMPVDRNAPYYNMNHKYGMAIIFNHEHFDIHS-LKSRGTGNVDSNLSKVLKTLGKRVTVFFNLK	105
<i>Hs-C1</i>	1	MLDGDVQDNG---SVETEQR--TNGGDEGDAQGSHDSHSRRIARMPVDRNAPYYNMNHKYGMAIIFNHEHFDIHS-LKSRGTGNVDSNLSKVLKTLGKRVTVFFNLK	105
<i>Se-C2</i>	1	-----MAH-----SSTNGSQVSCAESFNSYKN-EFYDMNHKYRGKALIFNHDREDID--IPPRAGSLKCCDNIEECITAGLSVDIFHNFK	78
<i>Mb-C2</i>	1	-----MAERNEET-----APH-PGPCNAYRN-EFYNNMYKYRGKALIFNHHYATALEIRFRGTTNRCCESLVECKQLASVDIFCDLK	78
<i>Ha-C2</i>	1	-----MSEGNVTEQ-KLENTNGTRPKCLPESNSYRN-EFYNNMHKYRGKALICNHEHFEID--LRPRPGTGKCCENLEKCLNYLGESVDATSNPK	87
<i>Hv-C2</i>	1	-----MSEGNVTEQ-KLKSSNGTRPKCSTTFNSYRN-EFYNNMHKYRGKALIFNHEYBEID--LNPRPGTGKCCENLEKCLKDLGESVDVLCDDPK	87
<i>Hs-C2</i>	1	-----MSEGNVTEQKKLKSSNGTSPKCLTTSNSYRN-EFYNNMHKYRGKALIFNHEFEID--LNPRPGTGKCCENLEKCLKDLGESVDVLCDDPK	88
<i>Sf-C1</i>	80	SEEVNKFIOQTABMDHSDADCLLVAVLTHGELGMLYAKDTHYKFDNLWYYFTADKCPFLAGPKLFFIQACQGERLDGGITLS-----KSETDSSPSTSYRIPVHADFLI	184
<i>Se-C1</i>	108	SDDINRYVQQTADMDHSDADCLLVAVLTHGELGMLYAKDTHYKFDNLWYYFTADKCPFLAGPKLFFIQACQGERLDGGITLS-----KSETDSSPSTSYRIPVHADFLI	212
<i>Mb-C1</i>	108	SEEVIRYVQQTADMDHSDADCLLVAVLTHGELGMLYAKDTHYKFDNLWYYFTADKCPFLAGPKLFFIQACQGERLDGGVNVVS-----KSETDSSPSTSYRIPVHADFLI	213
<i>Ha-C1</i>	106	SEEVIRYVQQTABMDHSDADCLLVAVLTHGELGMLYAKDTHYKFDNLWYYFTADKCPFLAGPKLFFIQACQGERLDGGITLS-----KSETDSSPSTSYRIPVHADFLI	210
<i>Hv-C1</i>	106	SEEVIRYVQQTADMDHSDADCLLVAVLTHGELGMLYAKDTHYKFDNLWYYFTADKCPFLAGPKLFFIQACQGERLDGGITLS-----KSETDSSPSTSYRIPVHADFLI	210
<i>Hs-C1</i>	106	SEEVIRYVQQTADMDHSDADCLLVAVLTHGELGMLYAKDTHYKFDNLWYYFTADKCPFLAGPKLFFIQACQGERLDGGITLS-----KSETDSSPSTSYRIPVHADFLI	210
<i>Se-C2</i>	79	YTDIMKQIEQTABMDHSDADCLLVAVLTHGELGMLYAKDTHYKFDNLWYYFTADKCPFLAGPKLFFIQACQGERLDGGITLS-----KSETDSSPSTSYRIPVHADFLI	183
<i>Mb-C2</i>	79	YAEIMMHIKKTAKINSHNDCLLVVLIHGEPCKLYAYDTHYRSNLWLFTEENCPTLAGPKLFFVFOACQGEDYDGTITIT-----KSETDSSPSTSYRIPVHADFLI	188
<i>Ha-C2</i>	88	YGEIMYHIKKTAKINSHNDCLLVVLIHGEPCKLYAYDTHYRSNLWLFTEENCPTLAGPKLFFVFOACQGEDYDGTITIT-----KSETDSSPSTSYRIPVHADFLI	192
<i>Hv-C2</i>	88	YAEIMMHIKKTAKINSHNDCLLVVLIHGEPCKLYAYDTHYRSNLWLFTEENCPTLAGPKLFFVFOACQGEDYDGTITIT-----KSETDSSPSTSYRIPVHADFLI	192
<i>Hs-C2</i>	89	YAEIMMHIKKTAKINSHNDCLLVVLIHGEPCKLYAYDTHYRSNLWLFTEENCPTLAGPKLFFVFOACQGEDYDGTITIT-----KSETDSSPSTSYRIPVHADFLI	193
<i>Sf-C1</i>	185	AFSTVPGYFSWRNTTRGSWFMOALCEELRYAGTE-RDILTLLTFVCCRVALDFESNAPDSAMHQQKOVPCITSMLTRLLVFGKQSHL-----	272
<i>Se-C1</i>	213	AFSTVPGYFSWRNTTRGSWFMOALCEELRYAGTE-RDILTLLTFVCCRVALDFESNAPDSAMHQQKOVPCITSMLTRLLVFGKQSHL-----	296
<i>Mb-C1</i>	214	VFSTVPGYFSWRNTTRGSWFMOALCEELRYAGTE-RDILTLLTFVCCRVALDFESNAPDLMPMHQQKOVPCITSMLTRLLVFGKQSHL-----	297
<i>Ha-C1</i>	211	VFSTVPGYFSWRNTTRGSWFMOALCEELRYAGTE-RDILTLLTFVCCRVALDFESNAPDLMPMHQQKOVPCITSMLTRLLVFGKQSHL-----	294
<i>Hv-C1</i>	211	VFSTVPGYFSWRNTTRGSWFMOALCEELRYAGTE-RDILTLLTFVCCRVALDFESNAPDLMPMHQQKOVPCITSMLTRLLVFGKQSHL-----	294
<i>Hs-C1</i>	211	VFSTVPGYFSWRNTTRGSWFMOALCEELRYAGTE-RDILTLLTFVCCRVALDFESNAPDLMPMHQQKOVPCITSMLTRLLVFGKQSHL-----	294
<i>Se-C2</i>	184	VLSTVPGYFAWRNRDRGSWFMOALCEELRYAGTE-RDILTLLTFVCCRVALDFESNAPDLMPMHQQKOVPCITSMLTRLLVFGKQSHL-----	290
<i>Mb-C2</i>	189	ARSTVPGYFSWRNTTRGSWFMOALCEELRYAGTE-RDILTLLTFVCCRVALDFESNAPDLMPMHQQKOVPCITSMLTRLLVFGKQSHL-----	294
<i>Ha-C2</i>	193	AKSTVPGYFSWRNTTRGSWFMOALCEELRYAGTE-RDILTLLTFVCCRVALDFESNAPDLMPMHQQKOVPCITSMLTRLLVFGKQSHL-----	295
<i>Hv-C2</i>	193	AKSTVPGYFSWRNTTRGSWFMOALCEELRYAGTE-RDILTLLTFVCCRVALDFESNAPDLMPMHQQKOVPCITSMLTRLLVFGKQSHL-----	294
<i>Hs-C2</i>	194	AKSTVPGYFSWRNTTRGSWFMOALCEELRYAGTE-RDILTLLTFVCCRVALDFESNAPDLMPMHQQKOVPCITSMLTRLLVFGKQSHL-----	295