Figure S2. Amino acid alignment of Lep-Caspase-2 sequences. Identical residues are boxed in grey. Critical amino acids involved in substrate-binding are boxed in purple. Critical amino acids involved in the active site, including the catalytic cysteine residue, are boxed in red. Blue frames indicate putative cleavage sites.

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                        10        20        30        40        50        60        70        80        90       100
                ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Ha-Caspase-2    MSEGNGVTEQK-LENTNGTRPKCLPESNSYRNEFYNMNHKYRGKAIICNHEHFEIDLKPRP--GTGKDCENLEKCLNYLGFSVDALSNPKYGEIMYHIKK
Hs-Caspase-2    MSEGNGVTEQKKLKSSNGTSPKCLTTSNSYRNEYYNMNHKYRGKAIIFNHEFFEIDLNPRP--GTGKDCENLEKCLKELGFSVDVLSNPKYAEIMNHVKK
Hv-Caspase-2    MSEGNGVTEQK-LKSSNGTRPKCSTTFNSYRNEYYNMNHKYRGKAIIFNHEYFEIDLNPRP--GTGKDCENLEKCLKDLGFSVDVLCDPKYAEIMNHVKK
Mb-Caspase-2    MAERN-----------EETAPHPGP-CNAYRNEFYNMNYKYRGKALIFNHHHYATALELRPRGGTNKDCESLVECLKQLAFSVDVFCDLKYAEIMKHIKK
Se-Caspase-2    MAHSS----------TNGSQVSCAESFNSYKNEFYDMNHKYRGKAIIFNHDRFDIDIPPRA--GSLKDCDNLEECLTALGFSVDIFHNFKYTDIMKQIEQ

                       110       120       130       140       150       160       170       180       190       200
                ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Ha-Caspase-2    TASMNHSKNDCLLIVVLTHGTNGMLYAKDTNYRPEKLWNLFTEENCPTLAGKPKLFVFQACQGEEYDDGITLT-----KNIETDGWFEPNRNPTHPDFLV
Hs-Caspase-2    IASMNHSKNDCLLIVVLTHGMNGKLFAKDTDYRPEKLWGPFTEENCPTLAGKPKLFVFQACQGEDYDDGITLT-----KHSETDGWFEPDRNPTHPDFLV
Hv-Caspase-2    IASMNHSKNDCLLIVVLTHGMNGRLFAKDTDYRPEKLWNPFTAENCPTLAGKPKLFVFQACQGEDYDDGITLT-----KLSETDGWFEPDRNPTHPDFLV
Mb-Caspase-2    TAKINHSNHDCLLIVVLIHGEPGKLYAYDTHYRSENLWLRFTEENCPTLAGKPKLFIFQACQGEDYDDGVTLTSSDYIKHIETDGWFEPDKIPVYPDFLL
Se-Caspase-2    TAEMNHSKNDCLLIMVLSHGESGLLYARDTHYRAENLWSPFTDAKCPTLAGKPKLFMFQACQGDKYDDGITLK-----RETETDGWYEPHKNPVHPDFLL

                       210       220       230       240       250       260       270       280       290       300
                ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Ha-Caspase-2    AKSTVPGYYSWRNSTRGSYFITALCEELNYSGKT-TDILTLLTFVCQKVALNFESSTDEDISNEKKQVPCISSTLTRRLVFSEKPD-RSKDMNSFVKCFE
Hs-Caspase-2    AKSSVPGYYSWRNSSRGTWFISSLCEELYYSGKT-TDILTLLTFVCQKVALNFESSTLEDVSNEKKQVPCISSMLTRRLVFNEKPE-SSQDMNSLVKCFE
Hv-Caspase-2    AKSSVPGYYSWRNSSRGSWFISALCEELYYSAKT-TDILTLLTFVCQKVALNFESSTLEDDSNEKKQVPCISSMLTRRLVFSEKPE-SSEDINSLVKCFE
Mb-Caspase-2    ARSTVPGYFSWRNIDCGSWFIQALCQELNYSATE-MDILTLLTFVNQKVALNYESSTLNAISNRKKEVPCFSSMLTRRLVFTEKPD-NLSSTKSLLDYFK
Se-Caspase-2    VLSTVPGYFAWRNRDRGSWFIQALYEELTYTGEDPIDILTLLTYVCQKVALNFQSETSNDVTNYKKQVPCISSMLTRRLVLAKKPNGKSSSMDSFLNSFK

                ....|...
Ha-Caspase-2    DNCLC---
Hs-Caspase-2    DNCL----
Hv-Caspase-2    DNCL----
Mb-Caspase-2    ECTTKNKN
Se-Caspase-2    NCSFNFE-
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