Figure S1. Amino acid alignment of Lep-Caspase-1 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 cleavage sites.

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                    10        20        30        40        50        60        70        80        90       100
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Aa-Caspase-1        MA-DEVAQNNG----GDREQRP--NGSG--DEGDAWG--SHESSHVRRHARMPVDRNSPYYNMNHKNRGIAFIFNHEHFDIHSLKSRTGTNVDSDNLHKV
Ba-Caspase-1        MS-EVQDNGFSEPSSIEPEQRP--NGGGDCDEGDAWGGGSHESSSARRYARMTVDRNAAYYNMNHKNRGMAIIFNHEHFDIHSLKSRTGTNVDSDNLARV
Bm-Caspase-1        MA-DEEKKTNG----SGTDQRK--NGNE--DEGDAWG--SHGSSQGRRYAKMPVERYAHYYNMNHNNRGMAIIFNHEHFEIHNLKSRTGTNVDSDSLSKV
Ep-Caspase-1        MS-EAQPENNGSGGE---EQRP--NGGG--DEGDAWG--SSDPSFSRIVGRMPVDRNAAYYNMKHKHRGFAVIFNHEHFDVHSLKSRTGTNVDSDSLNKV
Gm-Caspase-1        MSQEANQSNNG-----NDEQRA--NGG-D-DEGDAWG--SHGSVNKPRYAKMPVNRNSPYYKMDHKRRGVAVIFNHEFFDVHSLKPRTGTNVDSDNLARV
Ha-Caspase-1        ML-DGDVQDNG---SVETEQRP--NGGG--DEGDAQG--SHDSSHARRFARMPVDRNAPYYNMNHKYRGMAIIFNHEHFDIHSLKSRTGTNVDSDNLAKV
He-Caspase-1        MS-EVNEQDNG-----ETEQRP--NGGG--DEGDAWG--SHESSSIRHYAKMPVERNAPYYNMNHKNRGIAVIFNHEHFDIHNLKSRTGTNVDCDNLSKV
Hm-Caspase-1        MS-EVNEQDNG-----ETEQRP--NGGG--DEGDAWG--SHESSSIRHYAKMPVERNAPYYNMNHKNRGIAVIFNHEHFDIHNLKSRTGTNVDCDNLSKV
Hn-Caspase-1        MS-EVNEQDNG-----ETEQRP--NGGG--DEGDAWG--SHESSSIRHYAKMPVDRNAPYYNMNHKNXXXAVIFNHEHFDIHNLKSRTGTNVDCDNLSKV
Hs-Caspase-1        ML-DGDVQDNG---SVETEQRT--NGGG--DEGDAQG--SHDSSHSRRLARMPVDRNAPYYNMNHKYRGMAVIFNHEHFDIHSLKSRTGTNVDSDNLSKV
Hv-Caspase-1        ML-DGDVQDNG---SVEAEQRA--NGGG--DEGDAQG--SHNSSHSRRIARMPVDRNAPYYNMNHKYRGIALIFNHEHFDIHSLKSRTGTNVDSDNLFKV
Lm-Caspase-1        ME-D-ESLNNG---VEETEQRPN-GGGG--DEGDASG--SRDSSQGARYARMPVERNDPYYNMKHKYRGMAIIFNHEHFNIHSLKSRTGTNVDCDNLSKV
Mb-Caspase-1        ML-DGEPQDNG---SVDTEQRPNANGGG--DEGDALG--SHESSNARRYARMPVDRNAPYYNMNHKYRGMAIIFNHEHFDIHSLKSRTGTNVDSDNLAKV
Ms-Caspase-1        MS-DEEPQNNG----AQEEQRP--NGGG--DEGDAWG--SHESSRVRRYAKMPVDRNAPYYNMGHKHRGMAIIFNHEHFDIHSLKSRTGTNVDGDNLAKV
Se-Caspase-1        ML-DGK-QDNGNVDSVDTKQRT--NGGG--DEGDALG--SHNSSQPTRYARMPVDRNAPYYNMNHKYRGMAIIFNHEHFDIHSLKSRTGTNVDSDNLSKV
Sf-Caspase-1        ML-DGK-QDNGNVDSVDIKQRT--NGGG--DEGDALG--SNSSSQPNRVARMPVDRNAPYYNMNHKHRGMAIIFNHEHFDIHSLKSRTGTNVDSDNLSKV
Sl-Caspase-1        ML-DGK-QDNGNVDSVDTKQRT--NGGG--DEGDALG--SHNSSQPSRIARMPVDRNAPYYNMNHKHRGMAIIFNHEHFDIHSLKSRTGTNVDSDNLSKV
Tn-Caspase-1        ML-DGESQDNG---FVETEQRP--NGGG--DEGDALG--SHESSQSRRYAKMPVDKNAPYYNMNHKYRGMAIIFNHEHFDIHSLKSRTGTNVDSDNLAKV

                   110       120       130       140       150       160       170       180       190       200
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Aa-Caspase-1        LKGLGFLVTVRHNCKAEEVNHYIQQIADLDHSDHDCLLVAVLTHGELGMLYAK-------------------------------------------
Ba-Caspase-1        LKGLGFRVTVLVDRKADDVNKYPQQISEMDHTDNDCLLIAVLSHGELGMLYAKGTHYKPDNLFYHFTADRCQTLA------------------------
Bm-Caspase-1        LRGLGFSVTVLHNLRAEDINRYIQQISEMDHTDNDCLLVAVLSHGELGMLYAKDTHYKPDNLWYYFTADKCPTLAGKPKLFFIQACQGDKLDGGITLS-N
Ep-Caspase-1        LRTLGFRVTVLNNLKFEDVNKYIQDLAAMDHSDSDCLLIAVLSHGELGMLYAKDTHYKPDNLWDYFTADKCPTL--------------------------
Gm-Caspase-1        LKNLGFRVTIFNNLRFHELNARVQEIAEMDYSDDDCLLMAVLTHGEMGILYARDTHYKAENLWYHFTADRCPTLAGKPKLFFIQACQGDRLDGGITLT-T
Ha-Caspase-1        LKGLGFRVTALNNLKSEEVIRYVQETAEMNHSDFDCLLIAVLTHGELGMLYAKDTHYKPENLWYYFTGDKCPTLAGKPKLFFIQACQGDKLDGGITLS-R
He-Caspase-1        LKTLGFRVTILNNLKFEDVNRYLQQVAEMDHTENDCLLMAVLSHGEMGMLYAKDTHYKPDTLWYYFTADKCPTLAGKPKLFFIQACQGDKLDGGITLSSX
Hm-Caspase-1        LKSLGFRVTILNNLKFEDVNRYLQQVAEMDHTENDCLLMAVLSHGEMGMLYAKDTHYKPDTLWYYFTADKCPTLAGKPKLFFIQACQGDKLDGGITLSSR
Hn-Caspase-1        LKSLGFRVTILNNLKFEDVNRYLQQVAEMDHTENDCLLMAVLSHGEMGMLYAKDTHYKPDTLWYYFTADKCPTLAGKPKLFFIQACQGDKLDGGITLSSR
Hs-Caspase-1        LKGLGFRVTVLSNLKSEEVIKYIQTTADMDHSDFDCLLIAVLTHGELGMLYAKDTHYKPENLWYYFTGDKCPTLAGKPKLFFIQACQGDKLDGGITLS-R
Hv-Caspase-1        LKGLGFRVTVLTNSKSEEVMKYIQEVADMDHTDFDCLVIAVLTHGELGMLYAKDTHYKPENLWYYFTGDKCPTLAGKPKLFFIQACQGDKLDGGITLS-R
Lm-Caspase-1        LKGLGFRVTVLNNLTSGEILTYIYQTAEMDHSDFDCLLIATLTHGEMGMLYAKDTHYKPETLWSHFTADKCPTLAGKPKLFFIQACQGDKLDAGITLN-R
Mb-Caspase-1        LKGLGFRVTVLSNLKSEEVIKYVQQTADMDHTEFDCLLIAVLTHGELGMLYAKDTHYKPDNLWYYFTGDKCPTLAGKPKLFFIQACQGDKLDGGVNLVSY
Ms-Caspase-1        LKGLGFRVTMLHNSKAEEINKYIQEIADMDHSENDCLLVAVLTHGELGMLYAKDTHYKPDNLWYYFTADKCPTLAGKPNYFFIQACQGDKLDGGITLTNR
Se-Caspase-1        LKGLGFRVTVLNNLKSDDINKYVQQTADMDHSDADCLLVAVLTHGELGMLYAKDTHYKPENLWYYFTADKCPSLAGKPKLFFIQACQGDKLDGGITLS-R
Sf-Caspase-1        LKTLGFKVTVFPNLKSEEINKFIQQTAEMDHSDADCLLVAVLTHGELGMLYAKDTHYKPDNLWYYFTADKCPTLAGKPKLFFIQACQGDRLDGGITLS-R
Sl-Caspase-1        LKGLGFKVTVFTNLKSEEINKYVQQTADMDHSDADCLLVAVLTHGELGMLYAKDTHYKPENLWYYFTADKCPTLAGKPKLFFIQACQGDKLDGGVTLS-R
Tn-Caspase-1        LKGSGFRVTVLTNLKSEEILKYVQQTADMDHSDSDCLLIAVLTHGELGMLYAKDTHYKPENLWYYFTGDKCPTLAGKPKLFFIQACQGDKSDGGVTLS-R

                   210       220       230       240       250       260       270       280       290       300
                        |....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
Aa-Caspase-1        ----------------------------------------------------------------------------------------------
Ba-Caspase-1        ----------------------------------------------------------------------------------------------
Bm-Caspase-1        TETDGSSSSSYRIPIHADFLIVFSTVPGYYSWRNTTRGSWFMQSLCEELRNYGTQRDILTLLTFVCQRVALDFESNTPDITPMH-QQKQVPCINSMLTRL
Ep-Caspase-1        ----------------------------------------------------------------------------------------------
Gm-Caspase-1        TETDGSSSTQYRIPVHADFLIAFSTVPGYFSWRNTTRGSWFMQALCEELRFYGTERDILQLLTFVNQKVALDYESNTPDVPSMH-QQKQVPCITSMLTRL
Ha-Caspase-1        TETDGSSSASYKIPVHADFLIVFSTVPGYYSWRNTTRGSWFMQALCEELRYAGTERDILTLLTFVCQRVALDYESNTPDLMPMH-QQKQVPCITSMLTRL
He-Caspase-1        TETDGSSS-SYRIPFT---LIS----------------------------------------------------------------------
Hm-Caspase-1        TETDGSSS-SYRIPIHADFLIVFSTVPGYYSWRNTTRGSWFMQALCEELRYSGTERDILTLLTFVTQKVALDYESNTPDMLTMH-QQKQVPCTNTMLTRL
Hn-Caspase-1        TETDGSSS-SYRIPIQHXFLIVFSTVPGYYSWRNTTRGSWFMQALCEELRYSGTRKRYPDLVNFVTQKVALDYESNTPDMLTMH-QQKQAPCTNTMLTRL
Hs-Caspase-1        TETDGSSSASYKIPVHADFLIVFSTVPGYYSWRNTTRGSWFMQALCDELRYAGTERDILTLLTFVCQRVALDYESNTPDLMPMH-QQKQVPCITSMLTRL
Hv-Caspase-1        TETDGSSSASYKIPVHADFLIVFSTVPGYYSWRNTTRGSWFMQALCDELRYNGTERDILTLLTFVCQRVALDYESNTPDLMPMH-QQKQVPCITSMLTRL
Lm-Caspase-1        TETDGSTSVPYKIPVYADFLIVFSTVPGYYSWRNTTRGSWFMQALCEELRYSGTERDILTLLTFVWQRVALDFESNTPDFLTMHEQQKQVPCIT-MLTRL
Mb-Caspase-1        TETDGSPSASYKIPVHADFLIVFSTVPGYYSWRNTTRGSWFMQALCEELRYAGTERDILTLLTFVCQRVALDFESNTPDLMPMH-QQKQVPCITSMLTRL
Ms-Caspase-1        TETDGLSSASYRIPIHADFLIVFSTVPGYYSWRNTTRGSWFMQALCEELRYTGTERDILTLLTFVCQKVALDFESNTPDLLPMH-QQKQVPCITSMLTRL
Se-Caspase-1        TETDGSPSASYRIPVHADFLIAFSTVPGYFSWRNTTRGSWFMQALCEELRYAGTERDILTLLTFVCQRVALDFESNSPDSMIMH-QQKQVPCITSMLTRL
Sf-Caspase-1        TETDGSPSTSYRIPVHADFLIAFSTVPGYFSWRNTTRGSWFMQALCEELRYAGTERDILTLLTFVCQKVALDFESNAPDSAMMH-QQKQVPCITSMLTRL
Sl-Caspase-1        TETDGSPSASYRIPVHADFLIAFSTVPGYFSWRNTTRGSWFMQALCEELRYAGTERDILTLLTFVCQKVALDFESNAPDSAMMH-QQKQVPCITSMLTRL
Tn-Caspase-1        TETDGSPSTSYKIPVHADFLIVFSTVPGYYSWRNTTRGSWFMQALCEELRYAGTERDILTLLTFVCQRVALDFESNTPDLMPMH-QQKQVPCITSMLTRL

                    ....|....
Aa-Caspase-1        ---------
Ba-Caspase-1        ---------
Bm-Caspase-1        LLFGKK---
Ep-Caspase-1        ---------
Gm-Caspase-1        LIFGKK---
Ha-Caspase-1        LVFGRK---
He-Caspase-1        ---------
Hm-Caspase-1        LIFNKKQ--
Hn-Caspase-1        LIFNKK---
Hs-Caspase-1        LVFGRK---
Hv-Caspase-1        LVFGRK---
Lm-Caspase-1        LVFGK----
Mb-Caspase-1        LVFGKK---
Ms-Caspase-1        LVFGKK---
Se-Caspase-1        LVFGKK---
Sf-Caspase-1        LVFGKKQSH
Sl-Caspase-1        LVFGKKQSH
Tn-Caspase-1        LVFGKK---
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