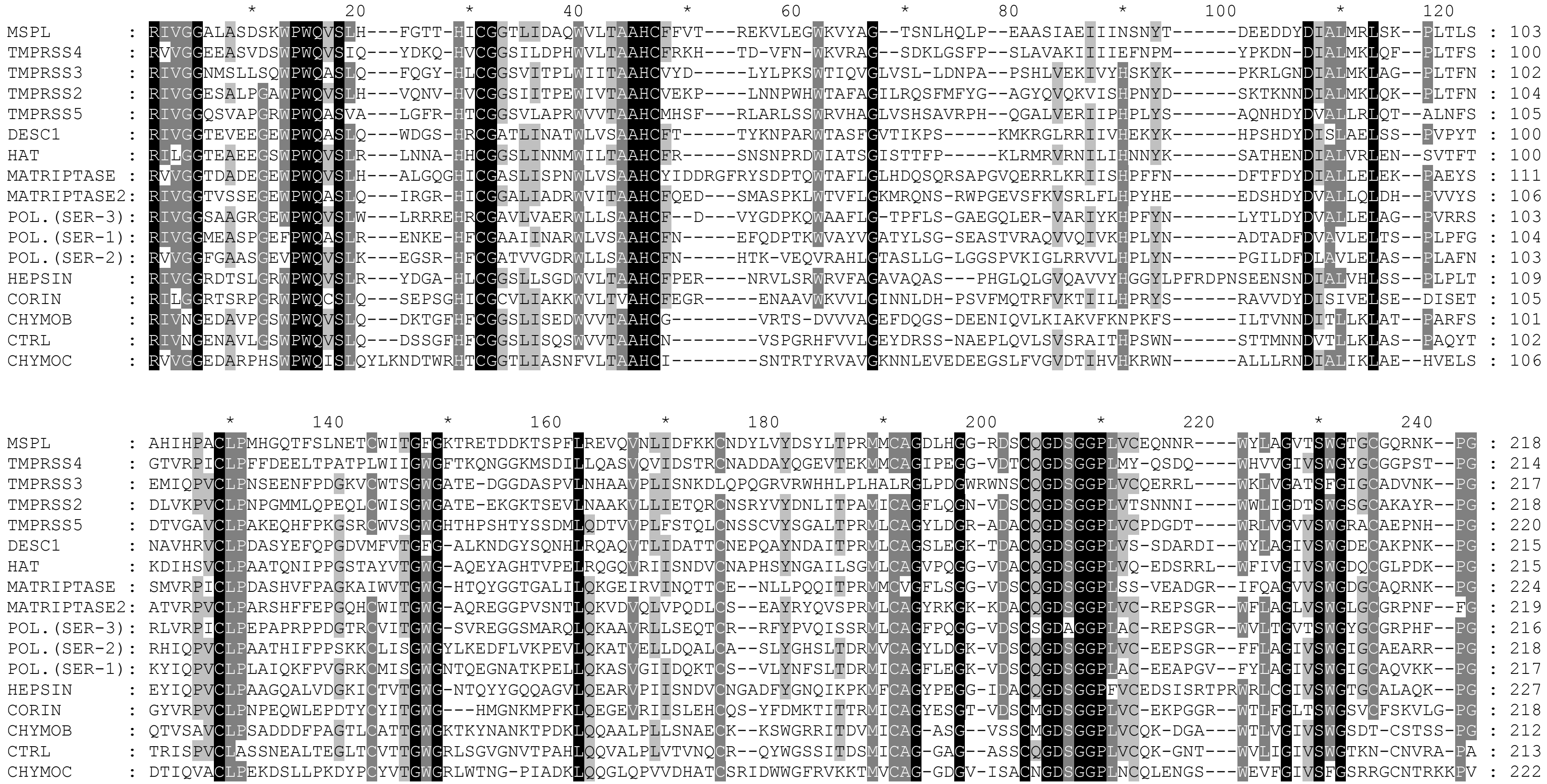

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                      *        20         *        40         *        60         *        80         *       100         *       120
MSPL       : RIVGGALASDSKWPWQVSLH---FGTT-HICGGTLIDAQWVLTAAHCFFVT---REKVLEGWKVYAG--TSNLHQLP--EAASIAEIIINSNYT------DEEDDYDIALMRLSK--PLTLS : 103
TMPRSS4    : RVVGGEEASVDSWPWQVSIQ---YDKQ-HVCGGSILDPHWVLTAAHCFRKH---TD-VFN-WKVRAG--SDKLGSFP--SLAVAKIIIIEFNPM------YPKDN-DIALMKLQF--PLTFS : 100
TMPRSS3    : RIVGGNMSLLSQWPWQASLQ---FQGY-HLCGGSVITPLWIITAAHCVYD-----LYLPKSWTIQVGLVSL-LDNPA--PSHLVEKIVYHSKYK------PKRLGNDIALMKLAG--PLTFN : 102
TMPRSS2    : RIVGGESALPGAWPWQVSLH---VQNV-HVCGGSIITPEWIVTAAHCVEKP----LNNPWHWTAFAGILRQSFMFYG--AGYQVQKVISHPNYD------SKTKNNDIALMKLQK--PLTFN : 104
TMPRSS5    : RIVGGQSVAPGRWPWQASVA---LGFR-HTCGGSVLAPRWVVTAAHCMHSF---RLARLSSWRVHAGLVSHSAVRPH--QGALVERIIPHPLYS------AQNHDYDVALLRLQT--ALNFS : 105
DESC1      : RIVGGTEVEEGEWPWQASLQ---WDGS-HRCGATLINATWLVSAAHCFT-----TYKNPARWTASFGVTIKPS-----KMKRGLRRIIVHEKYK------HPSHDYDISLAELSS--PVPYT : 100
HAT        : RILGGTEAEEGSWPWQVSLR---LNNA-HHCGGSLINNMWILTAAHCFR-----SNSNPRDWIATSGISTTFP-----KLRMRVRNILIHNNYK------SATHENDIALVRLEN--SVTFT : 100
MATRIPTASE : RVVGGTDADEGEWPWQVSLH---ALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFN------DFTFDYDIALLELEK--PAEYS : 111
MATRIPTASE2: RIVGGTVSSEGEWPWQASLQ---IRGR-HICGGALIADRWVITAAHCFQED---SMASPKLWTVFLGKMRQNS-RWPGEVSFKVSRLFLHPYHE------EDSHDYDVALLQLDH--PVVYS : 106
POL.(SER-3): RIVGGSAAGRGEWPWQVSLW---LRRREHRCGAVLVAERWLLSAAHCF--D---VYGDPKQWAAFLG-TPFLS-GAEGQLER-VARIYKHPFYN------LYTLDYDVALLELAG--PVRRS : 103
POL.(SER-1): RIVGGMEASPGEFPWQASLR---ENKE-HFCGAAIINARWLVSAAHCFN-----EFQDPTKWVAYVGATYLSG-SEASTVRAQVVQIVKHPLYN------ADTADFDVAVLELTS--PLPFG : 104
POL.(SER-2): RVVGGFGAASGEVPWQVSLK---EGSR-HFCGATVVGDRWLLSAAHCFN-----HTK-VEQVRAHLGTASLLG-LGGSPVKIGLRRVVLHPLYN------PGILDFDLAVLELAS--PLAFN : 103
HEPSIN     : RIVGGRDTSLGRWPWQVSLR---YDGA-HLCGGSLLSGDWVLTAAHCFPER----NRVLSRWRVFAGAVAQAS---PHGLQLGVQAVVYHGGYLPFRDPNSEENSNDIALVHLSS--PLPLT : 109
CORIN      : RILGGRTSRPGRWPWQCSLQ---SEPSGHICGCVLIAKKWVLTVAHCFEGR-----ENAAVWKVVLGINNLDH-PSVFMQTRFVKTIILHPRYS------RAVVDYDISIVELSE--DISET : 105
CHYMOB     : RIVNGEDAVPGSWPWQVSLQ---DKTGFHFCGGSLISEDWVVTAAHCG--------VRTS-DVVVAGEFDQGS-DEENIQVLKIAKVFKNPKFS------ILTVNNDITLLKLAT--PARFS : 101
CTRL       : RIVNGENAVLGSWPWQVSLQ---DSSGFHFCGGSLISQSWVVTAAHCN--------VSPGRHFVVLGEYDRSS-NAEPLQVLSVSRAITHPSWN------STTMNNDVTLLKLAS--PAQYT : 102
CHYMOC     : RVVGGEDARPHSWPWQISLQYLKNDTWRHTCGGTLIASNFVLTAAHCI--------SNTRTYRVAVGKNNLEVEDEEGSLFVGVDTIHVHKRWN------ALLLRNDIALIKLAE--HVELS : 106

                      *       140         *       160         *       180         *       200         *       220         *       240
MSPL       : AHIHPACLPMHGQTFSLNETCWITGFGKTRETDDKTSPFLREVQVNLIDFKKCNDYLVYDSYLTPRMMCAGDLHGG-RDSCQGDSGGPLVCEQNNR----WYLAGVTSWGTGCGQRNK--PG : 218
TMPRSS4    : GTVRPICLPFFDEELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPEGG-VDTCQGDSGGPLMY-QSDQ----WHVVGIVSWGYGCGGPST--PG : 214
TMPRSS3    : EMIQPVCLPNSEENFPDGKVCWTSGWGATE-DGGDASPVLNHAAVPLISNKDLQPQGRVRWHHLPLHALRGLPDGWRWNSCQGDSGGPLVCQERRL----WKLVGATSFGIGCADVNK--PG : 217
TMPRSS2    : DLVKPVCLPNPGMMLQPEQLCWISGWGATE-EKGKTSEVLNAAKVLLIETQRCNSRYVYDNLITPAMICAGFLQGN-VDSCQGDSGGPLVTSNNNI----WWLIGDTSWGSGCAKAYR--PG : 218
TMPRSS5    : DTVGAVCLPAKEQHFPKGSRCWVSGWGHTHPSHTYSSDMLQDTVVPLFSTQLCNSSCVYSGALTPRMLCAGYLDGR-ADACQGDSGGPLVCPDGDT----WRLVGVVSWGRACAEPNH--PG : 220
DESC1      : NAVHRVCLPDASYEFQPGDVMFVTGFG-ALKNDGYSQNHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGK-TDACQGDSGGPLVS-SDARDI--WYLAGIVSWGDECAKPNK--PG : 215
HAT        : KDIHSVCLPAATQNIPPGSTAYVTGWG-AQEYAGHTVPELRQGQVRIISNDVCNAPHSYNGAILSGMLCAGVPQGG-VDACQGDSGGPLVQ-EDSRRL--WFIVGIVSWGDQCGLPDK--PG : 215
MATRIPTASE : SMVRPICLPDASHVFPAGKAIWVTGWG-HTQYGGTGALILQKGEIRVINQTTCE--NLLPQQITPRMMCVGFLSGG-VDSCQGDSGGPLSS-VEADGR--IFQAGVVSWGDGCAQRNK--PG : 224
MATRIPTASE2: ATVRPVCLPARSHFFEPGQHCWITGWG-AQREGGPVSNTLQKVDVQLVPQDLCS--EAYRYQVSPRMLCAGYRKGK-KDACQGDSGGPLVC-REPSGR--WFLAGLVSWGLGCGRPNF--FG : 219
POL.(SER-3): RLVRPICLPEPAPRPPDGTRCVITGWG-SVREGGSMARQLQKAAVRLLSEQTCR--RFYPVQISSRMLCAGFPQGG-VDSCSGDAGGPLAC-REPSGR--WVLTGVTSWGYGCGRPHF--PG : 216
POL.(SER-2): RHIQPVCLPAATHIFPPSKKCLISGWGYLKEDFLVKPEVLQKATVELLDQALCA--SLYGHSLTDRMVCAGYLDGK-VDSCQGDSGGPLVC-EEPSGR--FFLAGIVSWGIGCAEARR--PG : 218
POL.(SER-1): KYIQPVCLPLAIQKFPVGRKCMISGWGNTQEGNATKPELLQKASVGIIDQKTCS--VLYNFSLTDRMICAGFLEGK-VDSCQGDSGGPLAC-EEAPGV--FYLAGIVSWGIGCAQVKK--PG : 217
HEPSIN     : EYIQPVCLPAAGQALVDGKICTVTGWG-NTQYYGQQAGVLQEARVPIISNDVCNGADFYGNQIKPKMFCAGYPEGG-IDACQGDSGGPFVCEDSISRTPRWRLCGIVSWGTGCALAQK--PG : 227
CORIN      : GYVRPVCLPNPEQWLEPDTYCYITGWG---HMGNKMPFKLQEGEVRIISLEHCQS-YFDMKTITTRMICAGYESGT-VDSCMGDSGGPLVC-EKPGGR--WTLFGLTSWGSVCFSKVLG-PG : 218
CHYMOB     : QTVSAVCLPSADDDFPAGTLCATTGWGKTKYNANKTPDKLQQAALPLLSNAECK--KSWGRRITDVMICAG-ASG--VSSCMGDSGGPLVCQK-DGA---WTLVGIVSWGSDT-CSTSS-PG : 212
CTRL       : TRISPVCLASSNEALTEGLTCVTTGWGRLSGVGNVTPAHLQQVALPLVTVNQCR--QYWGSSITDSMICAG-GAG--ASSCQGDSGGPLVCQK-GNT---WVLIGIVSWGTKN-CNVRA-PA : 213
CHYMOC     : DTIQVACLPEKDSLLPKDYPCYVTGWGRLWTNG-PIADKLQQGLQPVVDHATCSRIDWWGFRVKKTMVCAG-GDGV-ISACNGDSGGPLNCQLENGS---WEVFGIVSFGSRRGCNTRKKPV : 222
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