

>Tb_CAP5.5 (XP_844545)
WEEVDDEELLKLCSDSLVRYADINFLPSNSMFSRLDGDGRFIQPVEVRRPSEFAQCGEEN
IDAVRGVVLSSCVEAGTLGDSWVVSALSLLATDEERVKAMFASTTPAEKQMGAYRVLLNK
DGWWKNILVDDFLPTVGGVPCYARCIDDSGELWPSLLQKAYAKLYGSYASITGGDTLLAL
QNFTGAPVYRFDKAWRDAATDEEKKNALIQKITGYVEAHNPVILSVPTGRKAATAVANGL
REGYSYALLSVHNFPEENITLLKMFNPWEPAMPWSGQWREGSDKWTEHSEIQSSCEPCFE
AHDGIFFIEWSEAVEVFNGCGVLYLDEKPVYD

>Tb_CALP1.2 (XP_001218911)
GENSSPDDTLAACIAKKTkFVDLIFPPGQESLQIGTPHKLKVIPOWERPSMYLSDENALHA
RLFRNNIHPGNIDEGELGDSWFTGALACMAEFPDRVRDMFRHRSIEEGKNEREIGAYRV
TFNKDGWWTNVIIDDYLPSCGGHPMFARSYGDPMELWVSLAQKAYAKLHGGYGFLVVGDP
LRALQDLTGFPSCSSFNATFENAKMNGGEELFVHLLQYQTSYQITILTVPTRGALKLQAS
VEAYEATGLLPGHVYTVLSVMPFPEYNLRLLLLRNSWANHSHKRWNGAWKRGSEKWKQYP
GVAAACAGACDADGVLCVEWSEALALFAGCGVCFVQDTPYDYRI

>Tb_CALP11.3 (XP_828540)
ALPIWDDLKEGYGRENVMPCEGHWNDTFTPELSSVQKSAGARYVCIGEARRGVEFCII
RAADPLNIKQTVVGDSCMVCSLICALYQQRFPKAKIISNVIFPQSDGVPVVPKPKGYC
VKMLVNGITRLITVDDRFPANPQTGEMLCYTSRDKSELWVSIMEKAFVKVCGGSYDFPGS
SSSSDLYKLSGWLPDSVDFTVKDFDRNLQWSRFNRYADGSLITVSTPPLSEAEERLL
LASEHAYAVLDMREMSGVRLVQLMNPWSRRAWSGKFSLNDKRPEVVKVLTQLQYGSPOAD
QGIFWITWDDLCTNFSRCSLSWNPYMLFKTP

>HsCAPN1 (NP_005177)
YLGQDYEQLRVRCLQSGTLFRDEAFPPVPQSLGYKDLGPNSSKTYGIKWKRPTELLSNPQ
FIVDGATRTDICQALGDCWLLAAIASLTLNDTLLHRVPHGQSFQNGYAGIFHFQLWQF
GEWVDVVVDDLPIKDGKLVFVHSAEGNEFWALLEKAYAKVNGSYEALSGGSTSEGFED
FTGGVTEWYELRKAPSDLYQIILKALERGSLLGCSIDISSVLDMEAITFKKLVKGHAYSV
TGAKQVNYRGQVSLIRMRNPWGEVEWTGAWSDSSEWNNVDPYERDQLRVKMEDGEFWM
SFRDFMREFTRLEICNLTPDALKSRT

>Pgin (P25806)
AAPKAKKAAQKLDIDDLREQALSSTTITKEISKIILPTKNLRDDNNTVHQYREVGFGQNG
AHNLWDTVVQGIAGDCYMLAALSIAWVWPALLNMDVDIMSNQDEWRLYRYFIGRSKQTY
ANRPSGSGTSTNEILOEGYKVPIFARSRYWFNGEYWPALFEQAYANWKFPNDSKYNAIL
QIGGGWPEEALCELSGDSWFTSSGKMLLSSFTDLSLLNFMKSMCYSWKTIKPMVIVTPCW
EPLPPMMPGIAAYHAYTVLGYTVSNGAYYLIIRNPWGVTEPTGDGVLKSRDWVIHFDMK
WFNLSKDDGIFALRLDKVRENFWYIAYMY

>Dm_CalpA (Q_11002)
SEVQDYETILNSCLASGSLFEDPLFPASNESLQFSRRPDRHIEWLRPHEIAENPQFFVEG
YSRFDVQOGELGDCWLLAATANLTQESNLFFRVIPAEQSFEENYAGIFHFRFWQYQKWVD
VIIDRLPTYNGELMYMHSTEFNEFWALLEKAYAKLHGSYEALKGGSTCEAMEDFTGGV
SEWYDLKEAPGNLFTILQKAAERNMMSGCSIEPDPNVTEAETPQGLIRGHAYSITKVCLI
DIVTPNRQKIPMIRMRNPWGNEAEWNGPWSDSSEWRYIPEEQKAEIGLTFDRDGEFWM
SFQDFLNHFDRVEICNLSPDSLTEDQ

>Dm_SOL (P_27398)
EALTKWQNI IQYCRDNSELFVDDSFPPAPKSLYYPASGAGEGNPVVQWRRPHEINCDGG
AYPPWAVFRTPLPDSDICQVGLGNCWLLSALAVLAEREDLVKEVLVTKEICGQAYQVRLC
KDGKWTTLVDDLLPCDKRGHLVYSQAKRKQLWVPLIEKAVAKIHGCYEALVSGRAIEGL
ATLTGAPCESIPLQASSLPMPSEDELDKDLIWAQLLSSRCVRFLMGASCAGGGMKVDEEE
YQOKGLRPRHAYSVLDVKDIQGHRLKLRNPWGHYSWRGDWSDDSSLWTDDLRLDALMPHG
ASEGVFWISFEDVLNYFDCIDICKVRSWNEVRL

>Sm (P_27730)
VASKQYETLVKRLKTERTLWEDPDFPANDKAIIGNLPDFRERIEWKRPHEINPNKFFAGG
ASRFDIEQALGDCWLLAVVASISGYPQLFDQVVPKDQELKGPEYVGVVRFWRFRFGHW

EVLIDDRLPVROGRNTLVFMHSNDPTEFWSALLEKAYAKLNGCYAHLSSGGSQSEAMEDLT
GGICLSLELNQKERPSDLIDQLKIYAQRCCLMGCSIDSSVMEQKMDNGLIGSHAYSLTGV
YPVNYRGRTOQLMRLRNPWGDSHEWKGAWC DGSPQWREISEQEKKNINLSFTADGEFWMS
YEDFVTCFSRVEVCHLGLESLEYNQ

>Ce_tra-3 (Q_22036)

FGNQNYEKLKIKKQPFVDTLFPPTNQSLFLEQRQSSDIVWKRPGELHPDPHLFVEG
ASPNDVTOGILGNCWFVSACSALTHNFKLLAQVIPDADDQEWSTKHAYAGIFRFRFWRFG
KWVEVVIDDLLPTRDGLKLLFARSKTPNEFWSALLEKAFKLYGCYENLVGGHLSDALQDV
SGGVAETLHVRKFLKDDPNDTELKLFNDLKTAFDKGALVVAIAARTKEEIEESLDCGLV
KGHAYAVSAVCTIDVTNPNSRFTSFIGSKRKQNLIRLQNPWGEKEWNGAWSDDSPWQ
NVSASQLSTMGVQPANSDDDGDFWMPWESFVHYFTDISLCQLFNSTSVFSFS

>At_dek1 (Q8RVL2)

ELAVKEALSARGDKQFTDQEFPPNDRSLFVDTQNPSPKLQVVSEWMRPDSIVKENGSDS
RPCLFSGDANPSDVCQGRLGDCWFLSAVAVLTEVSRRISEVIITPEYNEEGIYTVRFCIQG
EWVPVVIDDWIPCESPGKPAFATSRKLNELWVSMVEKAYAKLHGSYEAELEGGLVQDALVD
LTGGAGEEIDLRSQAQIDLASGRLWSQLLRFKQEGFLLGAGSPSGSDVHVSSSGIVQGH
AYSVLQVREVDGHRVQIRNPWANEVEWNGPWSDDSPPEWTD RMRKHKLKHVPQSKEGIFWM
SWQDFQIHFRSIYVCRVYPREMRYSV

>Ehis (Q51GC6)

MFTDDEFPALERSIGKIDSILPSSLTFLRPNEYMEHPQLYENGLIEPLDIQOGCLGDCYFL
AALASLSEFPERIKTKIKSCGNGKYEITLFYMGKERHIVIDDLIPCNGQPFFSHNNGDE
LWVMLLEKAYAKVVGSYGEIEGGIPFLALSDLTGMPVKRISTRETQVNRFLFKKIADYDKK
KYCMVANVPDTPGIDIEKEYGLVENHAYTLIGAYEVDGIKLLKIRNPWGCCEWKGKWRDD
DPAWTESMKKLEVVVNDGIYFMEIGDFVKFFDELTVVIFYKDWDCFNS

>Cpar (Q5CW80)

FQENIINQSINICLKEQYILIVEQMVRSLMLSCKKQKMMVVKWKLNSNVELFPISNFVNI
TSSNIIOGFIDCSFIVVLSLLEHEKKFDSNLLSNLISPIKFSIKNQNHQONQNTNGYQ
KIHNENNNNNINELDDVLCLYKCKLLINGIWRNIFVDSLIPIDSGNNCLLSHFDCNKYY
GITLIEKAYLKVMANRYDSVESNPSIDLYYLTGWIPETISIKSHYEKKSIFYLNLWNRK
KPIQNGYCLMALGTNEINSNIDNHARLSPSNYRSSRDKPLNRFNEIDNNQLEYKFISKE
DICKKTGLVTKHAYQVLRIVELVNQENDSIRRLILLRNPWGKISWKGKFSKYDKEIWTNE
LVELLGNHFNYKVNQDNGIFWIEWNDILKWFSHIYLAWDPEKVS KHL

>PfalC (Q8ID83)

CKKCDKKRCIFHYVNGFKLYGWLNYKWTDPDGFLELSIRQKRKFD SWKRLSELYENPIVM
SPYLYNNCIRQGFVADCSFLSSLTVLIEYEKHKIPVISSIIITPCSWNYLCINKTWP IFN
PCGMYICRLHCNGIQRKIIIDDYVPVKNNNSLLVAYSNNQKELWVTLLLEKAFVKLMGGSY
SMFGSNPGSDLYLTGWIPVTISLKS KISSPPSFDKHSTHSLIRDERIDELVYETNEVM
INKKHGYVNSVEFVEDTKYNHNNNNNNNNKNTDHDQYMCDDNICFN NYNFCYKDDYEVN
KLQKQFLKEELATMDFAKYMNGSVDNYSDLIKRGGHKT LGINCEEGKYEPYEQYEQYEEY
DEKWDSVWNNIYDGIKKGCVVCLGTLELKDAAPSGLDYPEGVSI STGIVTRHAYSILNI
ENYNGDKLLYIKNPWGCIRWKGRYSHNDYETWTKELQKKNYSLEKAISKDDGCFWIPWK
DVIKYFSHIYICWNSVIFPYQF

>Ca_palB (Q5AK25)

ESLDKPRITISDKLEWISSKLTQETFFPPVIOFNENFTSHNELFVDTISPIQDNDNKIFEK
LPNKLAKFEYIEISNWDNDITHLKNLYQDILPNC SFVSSFLAII DANIPIIDTITPQKSS
QKYKVSRLRFNGALRNVI VDSKFPIMPNSRNLI IKSYSDELTYWPALIEKAYLTIMNGYN
FSGSNMANDAYVLSGWLPOI IKLSNGQLPSNIDDLWRLRTOGKVTMGIGTGTLSKQLSSQ
LHLVSGHDYVIDNIKDGVITVKNPWLPKDRVVEIKNFNF KYLYVNWKPDHKPYQH

>An_palB (Z_54244)

FIFPPWKAEPSTEFETGTNGDVLFTDKPDLHLSNLQORDIFAGWKRPHLLSGQVDDAGM
PLNPVMTVSGNTDLVQDVLTDCSVASLCATTSR SERGLDDTLLPIVYPCIHNSMKSDIS
PSGKYIFRFYFNGCFRKVVIDDRLPSSKTSRSLY MIDRNHRNFMWPALVEKAYLKL RGGY

EFPGSNSGTDLWVLTGWIPQVFLHSDEVTADQIWSDLFKSFHSGDVLLTIGTGKLTRE
QKELGLVSEHDYAILDMKELKGRRQFLIKNPWAGTDAVYPALFADPGFPNSPFLSPGTF
WMDCEMVLQNFENLYLNWNPGIFAYQE

>Hs_CAPN7 (AAH_56202)

INGIEYVPMNVDLRRERFAYPMPFCDRWGKLPSPKQKTTFSKWVRPEDLTNNPTMIYTV
SSFSIKQTIIVSDCSFVASLAISAAYERRFNKKLITGIIYPQNKDGEPEYNPCGKYMVKLH
LNGVPRKVIIDDQLPVDHKGELLCSYSNNKSELVWVSLIEKAYMKVMGGYDFPGSNSNIDL
HALTGWIPERIAMHSDSQTFSKDNSFRMLYQRFHKGDVLITASTGMMTEAEGEKWGLVPT
HAYAVLDIREFKGLRFIQLKNPWSHLRWKGRYSENDVENWTPPELQKYLNFDPRTAQKIDN
GIFWISWDDLCQYYDVIYLSWNPGLFKEST

>Sc_Rim13 (Q_03792)

TINSRFYPPPIPISEASPVSWNKTEYCAPGTEELQRRYPGRAKLQNEEDYSGGIEQCRDVP
DCSLVASLINLRSKNLNLPLIKQISSTKYHVNLFSNGSNKRLVTVDISQIPTSVDGKQLS
LKSNDISDKIGELALLLVSKGTYSTDGSNISIDTYRLSGFLPEITQVNSYPFEKLWKFHK
SNLCLMGAGTGNRSNDMIKPLVENHDYSIIDITYDSRLVKLDRPRNSALNVEISYEQYLK
NFKQLYLNWNQEKLFKRS

>Tt_21TM (EAR_94203)

DTPMKYLRIIEEFKKSQKTYKDETYVASNDILNEEMANEVKEWKRPPTATLTKDSISPM
DIRQGYIGDCYLSAMSVMGEKRTESLLLYDCPEFDKEAREKCGAYILKFWINSNWMYVI
VDNLPFAPDGKLLLGQAEDPNELWPSIIKAYSKLYGGYNQIEGGKVSALQELTGGLP
EEITLDFKQDNVDGYILGAGSPAHERGDKAVSPQGIYVGHAYALLDVQDVGKLVCLRN
PHGNHGTEWSGDWSDKSPKWNPRRLRKLVGDTFEDDGKFWMSVHDFVVEYRALYVCRLFD
QIWIWF

>Tt_3TM (EAR_84910)

EDTTEYQMRKKHLDQNPGSIFIDEQFPDRESLCNNWDDITDQATLKSWSQITWLRPKDF
LKLAPGEQIKLFDTIENDIKQIGLDCYFLSSLSSLAEREMLIKRLFETKTYQENGLYA
IWLNIEGEWRCIVVDDHIPCKNKQPAFTRSNGNELWVLLLEKAYAKAYGSYYKIEGGNPA
VALRDLTGAPYVNFDEKEPDSMFNLFHDKSGRGDILTCYTPSTEIREAQDLVGLYSGH
AYSILDVQIKIKTQDGKEHRILQIRNPWGKGEWKGDWADNDEKLWNKYTMSQVPSFKREED
GSFWMSIQDFCKYFEGVGACQIQESAKYNS

>Hs_CAPN15 (O_75808)

EAKALWENIVAFCRENNVSFVDDSFPPGPESVGFPAAGDSVQQRVQRWLRPQEIINCSVFRD
HRATWSVFHTLRPSDILQGLLGNCFWLSALAVLAERPDLVERVMVTRSLCAEGAYQVRLC
KDGTWTTVLVDDMLPCDEAGCLLFSQAQRKQLWVALIEKALAKLHGSYFALQAGRAIEGL
ATLTGAPCESLALQLSSTNPREEPVDTDLIWKMLSSKEAGFLMGASCGGGNMKVDDSA
ESLGLRPRHAYSILDVRDVQGTRLLRLRNPWGRFSWNGSWSDEWPHWPGHLRGELMPHGS
SEGVFWMMEYGFVRYFDSVDICKVHSDWQEARV

>Tt_EF5 (EAS_05791)

ENPIDFDKQYQDLDNKPYEDSEFPKLESITKDVKTFEKAKNMIWKRASDIYNDLKVFFD
RVEPDDIKQGLGDCYFLSSLVLAERENLITRFLITKNSNPCKVYSVWICKDSEWVQVI
LDDYLPCKEDGMPAFSSANGDELWVLIKCYAKIYGAYDKIEAGLTVEAIKDLTGAPG
KTIKNDDAELVWDFIYTNEQKKHLLTCGSQSDNRGIETKKESGIVSSHAYGILDAQEVKT
KKGLARLIKIRNPWGSMEWKGDWSDNSKLWTEEIRKQLNYYDSKDDGIFWMDVKDFVKEF
AETSVNYINDDYYY

>Tt_D2 (EAS_07113)

IQVQDEEEISSDEQIETEEIFTDKEFPPLIESISYDQVAYINQLEKQTPLVFKRVNEVI
KDGVNLFNDTTSIYDVKQGLLDCYFIVCMIVLSQYPNVIKSLFRNQSYNEKGKYILN
LIKNGKSVKVVVDDYLPCYQDSRGFAFAQSPNNVAIWPSLLEKAMAKLHKNYLNIEGNE
NKLGPSTSAVLMHLVGCPSQQTYFGKEKTNSFKDIEEAWAKILESFNKGYLQTTGVSKSE
FTGEKALDNGLVANHAYSIIEVRFQDKLKLKLNPNWAKTEWKLDWSESTCWTEELKQO
VNLEVKDDGIFWMSFQDFYQNFYSVNVAFFNPSYQYS

>Shis (AAO_61486)

KEDGDYQKIIAAKKQYTDSDFPAAAFASLVNEKKSQLPANQLAEWKNLHWARAKDIFGTDK
FTVFDQNITPNDILQGDGNGCYFLSALSIAIEFPKRIRDIFETEENPVGCVAVKVCING
EFRTILVDDQFPCTQGDGFGSGKIPAFSKTQNKELWVLILEKIWAKLNHNYENTITGFAS
EAFRCLTGAPVEFYNHDIYVDNIWDQIVEADKRNIIICTSAGRTNLTSEDYSKIGLVSDHA
YAVISVFDIDSKEHGRLQLLKLRLNPWGHKEWMDWSDKSDKWNDLRLKQVNFVDADDGVF
FISYRDYMNYYRSTTICKVHDDYKHKSIK
>Hs_CAPN5 (NP_004046)
YEDQNYALSRRDCRRRKVLFEDPLFPATDDSLYYKGTGPAVRWKRPKGICEDPRLFVDG
ISSHDLHQGVGNCWFVAACSSLASRESLWQKVIPDWKEQEWDPEKPNAYAGIFHFHFWR
FGEWVDVVIDDRLPTVNNQLIYCHSRSRNEFWCALVEKAYAKLAGCYQALDGGNTADALV
DFTGGVSEPIDLTEGDFANDETKRNQLFERMLKVHSRGGLISASIKAVTAADMEARLACG
LVKGHAYAVTDVRKVRLGHGLLAFFKSEKLDMIRLRNPWGEREWNGPWSDTSEEWQKVSK
SEREKMGTVTQDDGEFWMTFEDVCRYFTDIKCRVINTSHLSIH