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594197 1 M-----WPEKVWGLFLLVL-----SFS-----QAC-GQVCR-HIGVEVEKFPQL--SKEGDVILGGIFYFHNRWKTRENAYTAKPLPTECR-SL
744222 1 M-----PQVIAELFFIGLLLKL-----TSA-----QVR-ASSCQ-ILGSPFEPLL--SREGDVVIGGAFSVHSKVTPQPSLSHQEKPAQTSQCS-SV
594233 1 M-----QLAVGVLFVTL-----DLVCO--TYGTKELSQF--MAV-----RGG-DLVCO--TYGTKELSQF--SMEGDINIGGIFSFHQNPVITDPALHFNPEMIQCE-GL
Ca12 1 M-----PVCVCMMLLFALPHG-----AFG-----AED-NLKC-K-MLGRPEFPELL--SQEGDITIGGAFTLHSQMSKPSLSFEETPEDLTCS-RI
Ca02.1 1 M-----EISVIFLCFISLFDLNSAGDLKAPENSLKQVGPREDTTGA-----AAP-SDICR-LQGSARLPAP--SKDGFVIGGVFVSIHRYTVTVNHNYYTTMPEPFRCR-VI
581784 1 M-----EISVFLFCFISLFDLNSAGDLKAPENSLKQQLGPREDDTTGA-----TAP-SVKCR-LQGSARLPAP--SKDGFVIGGVFVSIHRYTVTVNHNYYTTMPEPFRCR-VI
584633 1 M-----EISVFLFCFISLFDLNSAGDLKAPENSLKQQLGPREDDTTGA-----TAP-SVICR-LQGFARLPAP--SKNDFLIGGVFVSIHRYTVTVNHNYYTTMPEPFRGRSI
Ca09 1 M-----ADITGTLGLFFTLITLTVS-----SST-----SFN-APTCK-LWRKFQLNEM--HEPQVLLGGLFQVHYSSVFPPEWTFPTSEPHQVPT-RF
589261 1 M-----GARA-----GLD-----VAG-AMLCV-HWQORSDRNL--SADGDVMTGGFLNLYYIPSAVQOYPTQLPHYRCR-SL
716738 1 M-----VLO-----VVQ-ALTCV-QWSTPTEQGL--FQDGHVVVGGFLNLYYIPSAVQOYPTQLPHYRCR-SL
Ca15.1 1 M-----SLSRIFTLIVGFGGRELGLG-----VLO-----VVQ-ALTCV-QWSTPTEQGL--FQDGHVVVGGFLNLYYIPSAVQOYPTQLPHYRCR-SL
571614 1 M-----GARA-----GLD-----VAG-AMLCV-HWQORSDRNL--SADGDVMTGGFLNLYYIPSAVQOYPTQLPHYRCR-SL
744432 1 M-----ARTTVVLFYICLL-----MRT-----MSK-TQCT-CT-VTGTGFMEF--LKEGDLIIGGVFVSMSTRVLVDNDYMAIP-SAYCT-RW
Ca13 1 MSWMGWIPSRQGVQLLCLCCMIPV-----IAL-----LDQ-SQHCVRVPGSMLFVL--EKRGDIIIGGLFSLHDMVVEPNLFFTSTPPPTQCT-RF
611619 1 M-----S-----SVT-----SPS-SSLCR-LQNSFQ-PGF--EANGDFITGGMFLHFNQEMPDNLNNTTTPPEPFRGR-SL
611624 1 MDRSFLSCWGFLLLWAISSIFFPVFS-----GLQHIAKEKNDTHGLEAGDNDASPS-LPRCV-KTVDTORPAL--HSRQVMTGGIFPLHYSASVSSQKYINKPELITCS-GF
611613 1 M-----GDPENPQL--SKDGDIIIGGIFSFHSSWINRRDNTYMHKPLPLQCI-SL
735220 1 M-----DIGPFLLAFLFPL-----HVSADSTCK-LKAKFNLSGYKNVKKVVTGGMFPVHMRVSSGGNTSRLPVPVSSGCE-GF
179742 1 A-----PDIIGGIFPIHEDVDKE--TESFEPHIRPC-IRF

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594197 73 NFRGFQFAQAMLETFINEINKSDTLLE-DVIVGYKIYDSCANIVNSIKLVLAITNRQDKES-----ASD-EESCT--KP-AQVQAIMGESSSSPCTATASVIGPFIHPVISHFATCAC
744222 76 NLREFRFAQSMIFAEEINKSDFLLE-NVSIQYRIYDTCSTLSSVRAAMALMNGE-----STA-GKNCS--YR-SSVHAIIGESSEFSTIVLSRLTGPFEIPVISHSATCEC
594233 71 DPGELOVAFMFAINEINSSDLEL-GLILGYRIFDSCPSVPLSIRASLNLNRY-----ESG-GDSCS--KL-SNVHAVIGETTSTSTIGIARTMGPNFLIPVISHSATCAC
Ca12 75 NLREFRFAQSMIFAEEINSSDLEL-NISIGYKVFDTGCLTLPSTRAVMALMNGKT-----RTP-EGGCS--SR-TSVHAIIGASESSSTIVMLQISGIFQIPVISHFATCAC
Ca02.1 98 DHHELQLSHAMVFAEEINNSTELLE-GIKLGYQIHDSCAAVPIAVNVAFQLLNTLDPV-----FVT-GDNCS--QS-GMVMVAVGEGSGTSPSISISRVIGSFDIPLVSHFATCAC
581784 98 NHRELRLSHAMVFAEEINNSTELLE-GIKLGYQIHDSCAAVPIAVNVAFQLLNTLDPV-----FVT-GDNCS--QS-GMVMVAVGEGSGTSPSISISRVIGSFDIPLVSHFATCAC
584633 99 DHHELRLSHAMVFAEEINNSTELLE-GINLGYQIHDSCAAVPIAVNVAFQLLNTLDPV-----FVT-GDNCS--QS-GMVMVAVVAESGSGTSPSISISRVIGSFDIPLVSHFATCAC
Ca09 79 DILGRHAMTMAFAVQIEINKNPDLLE-NLTLGYRLYDNCALVVGFGSALASQEEA-----FAL-QGGCA--GS-PPVLGIVGDSLSTFTIASASVGLGKIPMVSFYATCSC
589261 2 -----TMAFAVEEINRNSDLEL-GVRLGYGIRDSCFRYPWALDGAISLVTGDSNSCNVAASAG-GNT-GAVEA--GE-KVPLIIGAASSTGTGLMLSSILQSL--SISYFASCPC
716738 39 DLAGFRHAMTMAFAVEEINRNSDLEL-NVTLGYSLYDNCALVIGFSAALSMVSGQEQ-----FLO-QEKCL--GT-PPVLGIVGDSLSTFTIASASVGLGKIPMVSFYATCSC
Ca15.1 82 ENLPLQYIYAMVFAVEEINNSAALLE-GVKLGYHIRDSCALHPWTTQAALALVAQDSASCELATPADYSAE-TSEK--GA-ASVPLIIGGASSNAKILLGLTISPL--SISYFASCPC
571614 64 DIESLKYMYFMFAVEEINRNSDLEL-GVRLGYGIRDSCFRYPWALDGAISLVTGDSNSCNVAASAG-GNT-GAVEA--GE-KVPLIIGAASSTGTGLMLSSILQSL--SISYFASCPC
744432 73 NDRELKFRFAFVEEINRDGKLEL-GVTLGYRLYNGCSEN-IRAFAVEAVTGE-----GCS-----SQVQALLGHSSSGVSEINLILSPESIFQVSHLSTCAC
Ca13 87 SFRTFRWMTMAFAVEEINRNSAALLE-NITLGYKIYDSCSTPHQSLKAALDLMGSEKDSQFEG-----KLQ-REGCD-----GNVPAVIGDGGSTQSLVVARFLGVFHPVQVSYFSSCAC
611619 60 DPRAFRWAQFMKLAVEEINRNSDLEL-DHVLGYKLFDSQGYPLTQORAALSLLNCP-----TDG-SSTCT--GA-APLLAVIGESSSSSVMLSLWGLVQPFKIPVISHSATCAC
611624 106 DHRAFRRWMTMAFAVNEINNSDLEL-GVKLGYRILDGC DHVPTSLOALLSLMTWKQV-----EEM-IPACL--AD-SPVAAVIGLASSSPTGAAHILGSEFNIPVSYFATCCTC
611613 47 NFRGFQFAQAMLETFINEINKSDTLLE-GITLGCCKLYDSCRSIARGVRASLALINGET-----TFKLSDECT--KP-AQVQAIMGETSSSNMVAATVIGPFIHPVISHFATCAC
735220 74 NLRTRFRWTRFMFAVEEINKREDLEL-DTDLGYVITYDSCFTISKAVEGTLTYLTQDE-----AVP-NYRCG--NG-PPLAALVAGAGSDLSATARILGLYHFPVQVSYFSSCAC
179742 35 QQSGFVLALAMINAIEDMNKSPPLADANITLGYRILDSCSDVSTALRATNDLMOQ-----GNC-NSSGSSSSCGQPIMAVVGASYSSETSIAIARQLTLPMPQISYSSSAVL

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594197 180 LSDKNKYPSPFLRTIPSDHYQSRALAQLVKHYFGWTWVGAVRSDNDYGNNG-----MATFLETAEELG-ICVEYSVAVF-RTDPM----IKLQI-----
744222 179 LSDRKEHPSFFERTIASDLYQSRALAQLVKHYFGWTWVGAVNSDSDYGNNG-----MATFLTAAQEEG-VCVEYTEKFKH-RAEP-----EKLLKV-----
594233 174 LGNRRDYPAFFERTIPSDIYQSOALAKLVKHYFGWTWVGAVRTNSDYGNNG-----MTAEFLKAAEKEG-VCVEYSVAIY-RTDPR----KWFLEV-----
Ca12 179 LSNRKEYPSFFERTIPSDFYQSRALAKLVKHYFGWTWVGAVKSDNDYGNNG-----LATFIMAAEQEG-VCVEYSEGFSS-WTDPS----EQIARV-----
Ca02.1 204 LSDKQKYPSPFFERTIPSDQFQADALVKLKHFGWTWVGAVCSDSYGNNG-----MAEFLHAAQKEG-ICVEYSESFY-RTHPH--SRIKRV-----
581784 204 LSDKQKYPSPFFERTIPSDQFQADALAKLVKHYFGWTWVGAVCSDSYGNNG-----MAEFLHAAQKEG-ICVEYSESFY-RTHPH--SRIKRV-----
584633 205 LSDKQKYPSPFFERTIPSDQFQADALAKLVKHYFGWTWVGAVCSDSYGNNG-----MAEFLHAAQKEG-ICVEYSESFY-RTHPH--SRIKRV-----
Ca09 185 LTNRQRFPSPFFERTIPSDDFQVRAMIQILKHFGWTWVGLVSDDDYGLHV-----ARSEQSDLVQSGGQGLAYLEVLP-WDNYL--SENRI-----
589261 99 LSDHQRFPSFFERTIPSDAFQVRAMIQILKHFGWTWVGLVSDDDYGLHV-----ARSEQSDLVQSGGQGLAYLEVLP-WDNYL--SENRI-----
716738 145 LSDRQRFPSPFFERTIPSDAFQVRAMIQILKHFRWSWVGLVSDDDYGLHV-----ARSEQSDLTRSGGQGLAYLEILP-WGYNP--GELTOV-----
Ca15.1 194 LSDRHRYPSPFFERTIPSDIYQAOALAQVLRFNWTWVGAVVANNYGHVA-----VKVFEQQTQGGK-VCLAFVETLQ-RETIV--ADAVRA-----
571614 175 LSDRAKYPSPFFERTIPNDQHOVKAIAQLLVHFNWTWVGLLCCERDYGRFA-----IQIEQEEIRGKE-MCMFEIETVN-RETLT--TDARRI-----
744432 168 LSDKKKYPTFFERTIPSDHFOISGLVQLLKFEDWRWVGIVYATGSYSDDG-----TAHEVKEAEKEG-ICVEYRLCFS-IASG----EKSTAI-----
Ca13 195 LSDKTQFPFRTIPSDLFQVQALVQLVHYFGWTWVGAVTADGDAYGRGG-----AATFANEVRRLE-ACTALYEMIP-KTQSQ--AATSSI-----
611619 164 LSDKRKYPTFFERTIPNDQHOVKAIAQLLVHFNWTWVGLLCCERDYGRFA-----AEGLLRELKSTK-VCVAVQEIIP-LVYNQ--LRVQAI-----
611624 212 LSDKSTYPSFFERTIPSDLFQVRGLVQVMTFMSWLVWGTIGTDDYSHYC-----IQAFSHQLRQCG-VCVEFQLTIP-KSPTA--AELKEM-----
611613 152 KCPPGTRKVLQKQKPVCCYDCLRCAGEEISNSTDSISCVRCHSDFWSNERRDTCIKKKEEFLSYEEMGALLTAASLLG-TCLTAVVMFIFFRYR--TPTVIRANNSLSFLLLSLT
735220 179 LKSKFQFPFFERTIPNDQHOVKAIAQLLVHFNWTWVGTISADDDYGYKGE-----IKDKEQVEEAG-VCSFSETLIP-KVNSP--ENTORI-----
179742 141 LSDKTHFPFRTIPNDKYOTTAMITLSHYGNWVGIITTDGSYGLSA-----LDQFVSOASAKG-ICVAFKSIIP-QSVSSQDTSATTKT-----

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594197 262 ----- IDIT - KSS ----- TSKVITVTELSPGDLNVLLQEFSSQHNLIT ----- GYQWVGSESWIDSDSHIAA-MDVHHIIPDCAVGLSTPKAHVTGMKEEIMDVK-QL---SSSS-K
744222 260 ----- VEVI - RRG ----- TARVIVGFLAYVEMNNLLOQDLSLHNVIT ----- GLOFVGVEAWITANSIVT-PTSFGVLGCSLGFAVEKAATSDLDDEFL-----
594233 256 ----- VDTI - KKS ----- TSKVIVAFVDGTDLDLIVKELHAQSVT ----- GLOWVGSEGWITYRFIAS-PENYAVVQCAVGFAALNTHLPGIQEFLADSR-PS---TPG-N
Ca12 261 ----- VTVI - KSG ----- SARVIVGAFAQSEMSALBEFAVKQNLIT ----- GLOWVGSESWITAGHIAL-KKYSALITGSLGFTTRKTKITGLOEFLLOVN-PS---QNPQ-N
Ca02.1 286 ----- ADVI - RRS ----- TAVVIVAFVASTEMMILLEELISHEPSP ----- PROWIGSESWITDPDLR---FSFCAITGFAIQRSVIPGLRDFLLDLS-PS---KVAS-S
581784 286 ----- ADVI - RRS ----- TAVVIVAFVASTSSGDLRILEELISREPS ----- PROWIGSESWITDLDLRL---FSFCAITGFAIQRSVIPGLRDFLLDLS-PS---KVAS-S
584633 287 ----- ADVI - RRS ----- TAVVIVAFVASTSSGDLRILEELISREPS ----- PROWIGSESWITDSEILR---FSFCAITGFAIQRSVIPGLRDFLLDLS-PS---KVAS-S
Ca09 268 ----- VHVI - KES ----- TARVLMVFAHQSHMIHLMEEVVRQKVT ----- GLOWLASEAWTGTTFLOT-PDFMPYVNGTIGTAIRRGEITGLRDFLLRIR-PGQSSNNTS-Y
589261 182 ----- VHVI - KES ----- TARVLMVFAHEIHMIOQMDPEVVQGNVT ----- GROWVASEALSTAAVLQV-PHFMPYVIRGMLGIAIRRGEIPGRDFLRQVR-PDRHSRDE-T
716738 228 ----- VEVM - KKS ----- TARVIVVFAEQSHMIQMLEEIVVQNLIT ----- GLOWIASEAWTAAAVLQV-TELMPYVIRGMLGIAIRRGEIPGRDFLLGLH-PDLHEISNR-N
Ca15.1 276 ----- ARTI - QAS ----- TARVILVFSWYTDVGHFRQIQKINVT ----- DROFLASEAWSTSEVLLKDPDTSTVASGVVGVAIASQHIPGDFRFLRGLN-PS---LRPS-D
571614 257 ----- ALTI - QAA ----- TARVILVFCWYIDAKEILLELAKRINIT ----- GROFLASEALSTSEELLQELAIAEVANGVLGVAVQSSITPGEHFHLRSLN-PV---QRPD-D
744432 249 ----- VKAL - QES ----- SARVVLLEMSFKKAFNLMEVEMNNIT ----- DKOWLSESWITQADLAS-SKRQHITQCATGFALPQMPIGLGDFLLSLK-PS---DEPQ-S
Ca13 277 ----- ISNI - RSS ----- GARVVLVFAVEQDVARLFDFAVRQKLT ----- GIOWLASEAWSTAALSTPKRYHHILQCSMGFAIRRADIPGLQDFLLRLH-PSSA-EADD-D
611619 246 ----- MQVM - RTS ----- SARVIVVFAEVEIMPLFRDYMKNIT ----- GIOWIASEAWTASVFTG-SKYYPVIGTIGLGRKGIHPRSDYLLTVN-PQ---VYPN-N
611624 294 ----- ADRL - QSS ----- TARVIVVFAEATGQLLEFLFLIYRNMT ----- GIOWVASEAWTASLTT-PRFHALBGLTGFSPGAEIPGLKEBELLNIC-PS---PKPG-M
611613 267 LCFLCSSLFGRPSGWSCMLRHAFFGITFVLCISIKLQAELYSONIT ----- GLOWVGSDAWITDHSITD-SSGHSILGSLGFTVSKAKILGLEEHLRGLH-PA---QFPT-S
735220 261 ----- IQTL - VKS ----- TAKIIVVFSDDVLSPLTELLRHINIT ----- NRTWIASEAWTASALMLK-PGASLLGCTLGFVAVKRASIPGLQHYLLDLD-PY---G-D
179742 227 ----- ARTI - YKNP ----- KVQVILISEAKPSQMKFLFHKIKSMMLKPGETNGEGRMRVVASDSWSISRYIYG-NLTLEDIGYVVLGFTFKSGNVSFREYLEQLGAPE---ENKIN

594197 352 ELFRFEWLEALDCKFEDSVST----TTEQRECSGHEDLAGVKNIEFDMSLMPLIFNYNLYKGVYAVAHALHEDILSC-----NNTCNKTAQLDPEFTILOHIRSTHFKTK-EGDEYVENE
744222 339 --IGDFWETEPECKETIED-----GMAGPATCOENGDLAFAFKGYADVAELRYSGNLYKAVYAVAHSLHSTLQCSI-----SGVCDKTVKVTHQOILQHIKRIRFKTK-EGDEYVENE
594233 346 NGLVELWEVTEKCTLSPPRA-----QSPLAACGKESLRDASTREFTDVSASLLNNVYKATYAIHAHALHLLTCKEKEGPFENNTCADRHNVQPWVHYLTLVNFSTTK-IGDNVHDE
Ca12 351 NLLKEFWETEPCSFQSDV-----HGATQCSGVEKLRDIQNPFDTDVSLELRISNNVYKAVYAVAHAMHSMMLKCGQ-SGEAVNGSCTTKKDFELKQVVEHLQSNVFTLQ-SGERVYEDD
Ca02.1 373 PVLTEFWEDSEFCRLG-----KGERMCDGSEDMITLQSPYTDTSSELRTNMVYKAVYAIHAHAENAV-CQDTNA---TTRCSKFTTINPKKVLTLQKTVNFSSQ--NGYAVSEDA
581784 373 PVLTEFWEDSEFCRLG-----KGERMCDGSEDMITLQSPYTDTSSELRTNMVYKAVYAIHAHAENAV-CQDTNA---TTRCSKFTTINPKKVLTLQKTVNFSSQ--NGYAVSEDA
584633 374 PVLTEFWEDSEFCRLG-----KGERMCDGSEDMITLQSPYTDTSSELRTNMVYKAVYAIHAHAENAV-CQDTNA---TTRCSKFTTINPKKVLTLQKTVNFSSQ--NGYAVSEDA
Ca09 361 DMVQQFWEYSEFOCKFGAS-----GSAEACTGDENIQQVDAEFLDVSNLRPEYNYKAVYALAYALDDMTQCEPGRGPFSGGSCADIHKLEPWFVHYLQHVNFSTT-FGDQVSEDE
589261 275 SMVRQFWEYTEFOCKFDPPGL-----VEAGEVLCTGQEAIEDADTEFLDLSNLRPEYNYKAVYALAYALDDALCEPGRGPFSAHSCAENQRLQPWLVYSLEKVNFTTS-FGDQVSEDE
716738 321 SLVRQFWEYTEFOCRFAPPTGW---VEGGGLLCTGEEELGRVQTEFLDVSNLRPEYNYKAVYALAYALHEDMLHCVPGRGPFDEHSCATLESKPPWVLEHILQSNVFTTA-FGDQVSEDE
Ca15.1 367 KFLQEFWEWEEFGCSPSPSSSETSGDLNASLPPSCGAESLEGVQHPFTDTSHLRVTYNYVYLAAYAAHALHSLSCPIHNSPSGTSHTSPKGIKTELOHLQSKVNFSTP-QGKHYE-R
571614 348 EFLKDFWEMEEKCSPLVQLLHSC--LFASLPPSCGAESEVEMEHFPTDTSKLRVAHNVYLAAYAAHALHSLSCPGQDPPGKSNSSPNHIRPDLVQHLNRVNFSTP-RGFTFYF-Q
744432 339 DIVKAMWDFEFCNSFS--PSTSAACTGTEDETRTVINDYTEVTHFRANNVYKAVYALAYALHSLLQCEGNSNPTTKGBCVNKKEVQPKVLEHILQSNVNFSTTK-YGSKVFEKQ
Ca13 370 PFLIPFWEVEVFOCSLDPHG-----HSEAKRPCSGTEELRSVKNIYSDVSQLRISYNYKAVYALAYAIKAMRSCCEKSGSPFSQACPDLDNIHPWOLHHYIKQVNYTNR-FGDEIKFDE
611619 336 PLVKELEWETLYGCRSSLSS-----SSHVPLCTGQEPLEQHSAFMNTSSPRVTYNYKAVYAIHAHSLHNLFCPPGPGPFKNNTCAQRNNVQPWLVQHSILQEVAFKIS--GEVWYEDQ
611624 384 EFNMFWEDELGCKLNSDTK-----SADESVCTGSEDELRYSQSYTDVSVQVRIYNYKAVYAIHAHALHSLLNCSESPGNS--VGTCKKREPFTSKQLQHLQKSNVNFSTP-FKEKVFEDQ
611613 371 AFMTEFWEDREAGSLNITG-----STGRRPCSGSESQNDTSPFTDVTLEFRTNVYKSVYVVAHALDNLMKCEKGEFSEGSADPKHIQFQVWLVHYINTVRENTS-EGETVYFER
735220 348 TLSEEFWEVTHG-----LCTGLETVAQLKNTYSDVSQLRITYSVYKAVYAVAHALHNLHCEQGRGPFNGRDCNTNISSFEPWOLMYYIKVNYRVTVPHTGEEIYFD-
179742 330 PFLQEFYMHMNA-----VSGGEDKHVPEALRSLWEHVHADLIFSVEMAVSAITQAVATICR-----RTDCKTLGVSQVQVWVLAALWMOEFL-KL-RQKSYKEDS

594197 459 NGDPPAKYELINWQPTENGWVFPVGLYDASLPAD-RQLTLNTR-TLVWAQKKSLO-VPVSVCSSEKCPGTRKVLQKQKPVCCYDCLRCADGEISNS TDSISCVRCHSE-FWSNERRDA
744222 444 NGDPPAKYELINWQPTENGWVFPVGLYDASLPAD-RQLTLNTR-TLVWAQN-SEQ-VPVSVCSSEKCPGTRKVLQKQKPVCCYDCLRCADGEISNS TDSISCVRCHSE-FWSNERRDA
594233 458 MGDPPVRYALVNWQMDAEGYVLFETIGDYDASRPEG-HQFMNDGVKALWAGE-NLE-VPRSVCSSECLPGTRRAVFKGRPICCFDCAICADGKFSNS TNAVCKDCPPE-YKSNERRNN
Ca12 461 YGDPAATYELVNWQMSPEGNTVFGNYDASQPNG-RQFTMNNI-NITWAAR-LQK-RPLSVCSOSCEPGERQAVIKGKPICCFTCAVACAAGEISNSNSAECLQCPLE-FWSNEDHSQ
Ca02.1 476 NGDPVASYELVNWKKS GSGSIEVVPVGYDASLPEG-QEFRIFR--DITWVDG-RKQ-VPVSVCS DSCPGTRKVLQKQKPICCYDCVQCPGEISNV TDSPECIPCLDD-FWPNPERNA
581784 476 NGDPVASYELVNWKKS GSGSIEVVPVGYDASLPEG-QEFRIFR--DITWVDG-RKQ-VPVSVCS DSCPGTRKVLQKQKPICCYDCVQCPGEISNV TDSPECIPCLDD-FWPNPERNA
584633 477 NGDPVASYELVNWKKS GSGSIEVVPVGYDASLPEG-QEFRIFR--DITWVDG-RKQ-VPVSVCS DSCPGTRKVLQKQKPICCYDCVQCPGEISNV TDSPECIPCLDD-FWPNPERNA
Ca09 471 NGDVLPIYDILNWQWLPDQRTQVQNVGEVKRSPSRG-EELQIHED-KIFWNFE-SNK-PPHSVCSSECPGTRMRSRKKQPVCFFDCLLCESEGI SNT TDSMECTSCPED-FWSSPQRDH
589261 389 NGDVLPIYDILNWQWLPDQRTQVQNVGEVKRSPSRG-EELTYED-KIFWNFE-SNK-PPSVCSSECPGTRMRSRKKQPVCFFDCLLCESEGEISNT TDSMECTSCPED-FWSSPQRDH
716738 437 NGDALPIYDILNWQWLPDQRTQVQNVGEVKRSPSRG-EELTYED-KIFWNFE-SNK-PPSLSA-----ALTVFLGSEGEISNT TDSMECTSCPED-FWSSPQRDH
Ca15.1 485 GADIPAMYDILNWQSGTDCITLQLVLLGAVAG-----FDLQNLNES-ELIWSAK-YNQ-VPVSVCSSECPGTRKANRKGEPICCFDCLPCADGEISNTSGSLQCDRCPPE-FWSNDGRTA
571614 464 GSDMTARYDILNWQKTPNGPLKLVVGRVDC-----FDLILNES-AIQWSTG-LNQVVPVSVCSSECPGTRKANRKGEPICCFDCLPCADGEISNTSGSLQCDRCPPE-FWSNDGRTA
744432 449 NENSVAQYDILNWQMSREDGSDIVTIGQYDTSFKGE-ELKVAADDA-KIVWGGK-YKQ-VPRSVCREPPTGRKAINKLPVCCFDCECPDGTFSNDGFCDFSCFPQE-LWPNQKNL
Ca13 483 NGDPAAMYDILNWQWLPDQRTQVQNVGEVKRSPSRG-EELQIHED-KIFWNFE-SNK-PPHSVCSSECPGTRMRSRKKQPVCFFDCLLCESEGI SNT TDSMECTSCPED-FWSSPQRDH
611619 447 RGDSPYPIYDILNWQWLPDQRTQVQNVGEVKRSPSRG-EELQIHED-KIFWNFE-SNK-PPHSVCSSECPGTRMRSRKKQPVCFFDCLLCESEGI SNT TDSMECTSCPED-FWSSPQRDH
611624 496 KGEPPVLYDILNWQKDSVSNIRFKVGSYDGSAPLK-QQLQMDQN-AIVWTGG-KSK-VPVSLCAAPCPGSRQARRKQVPHCCFDCLPCADGQISNTGSTECORCPPE-YWPDKDKVK
611613 483 SGDSPARYELVNWQWLPDQRTQVQNVGEVKRSPSRG-EELQIHED-KIFWNFE-SNK-PPHSVCSSECPGTRMRSRKKQPVCFFDCLLCESEGI SNT TDSMECTSCPED-FWSSPQRDH
735220 448 DGDVEGFYDILNWQWLPDQRTQVQNVGEVKRSPSRG-EELQIHED-KIFWNFE-SNK-PPHSVCSSECPGTRMRSRKKQPVCFFDCLLCESEGI SNT TDSMECTSCPED-FWSSPQRDH
179742 423 SGDINMGYELVNWQWLPDQRTQVQNVGEVKRSPSRG-EELQIHED-KIFWNFE-SNK-PPHSVCSSECPGTRMRSRKKQPVCFFDCLLCESEGI SNT TDSMECTSCPED-FWSSPQRDH

TM1 TM2 TM3
594197 575 CIKKKEEFLSYEEMMGALLTAASLLGCTCLTAVVMFIFFRYRQTPPIVRANNSLSFLLLSLTLCLFLCSLTFIGRPSGWSCLMRHTAFGITFVLCI SCVLGKTMVVLMFAFRATLP - GSNVM
744222 559 CIKKKEEFLSYEEMMGALLTAASLLGCTCLTAVVMFIFFRYRRTPIVRANNSLSFLLLSLTLCLFLCSLTFIGRPSGWSCLMRHTAFGITFVLCI SCVLGKTMVVLMFAFRATLP - GSNVM
594233 574 CNLKAIEFLTEFRELMLGILLVAFSFGACLSSTTIALIFFRQTPPIVRANNSLSFLLLSLTLCLFLCSLTFIGRPSGWSCLMRHTAFGITFVLCI SCVLGKTMVVLMFAFRATLP - GSNMM
Ca12 576 CVPKVI EFLSFEETMGALLAASLFGAALTSLVFCVFFFRHTPLVVKASNSLSFLLLSLTLCLFLCSLTFIGRPSRWSCVLRHTAFGITFALCM SCVLAKTVAVLFAFTAKRP - GNTVF
Ca02.1 590 CFPKPV EFLSFEVGLIILAVFSVGCACLAVIDAAVFFHRTSPPIVRANNSLSFLLLSLTLCLFLCSLTFIGAPSHLSCLMRHTAFGITFVLCI SCVLGKTMVVLMFAFRATLP - GSNVM
581784 590 CFLKPV EFLSFEVGLIILAVFSVGCACLAVIDAAVFFHRTSPPIVRANNSLSFLLLSLTLCLFLCSLTFIGAPSHLSCLMRHTAFGITFVLCI SCVLGKTMVVLMFAFRATLP - GSNVM
584633 591 CFLKPV EFLSFEVGLIILAVFSVGCACLAVIDAAVFFHRTSPPIVRANNSLSFLLLSLTLCLFLCSLTFIGAPSHLSCLMRHTAFGITFVLCI SCVLGKTMVVLMFAFRATLP - GSNVM
Ca09 586 CVPKKE EFLSYHEPLGICLTAASLLGCTVISVVLGFIHHRSTPPIVRANNSLSFLLLSLTLCLFLCSLTFIGRPLWTCOLRHAFAFGISFVLCV SCILVKTMMVVLAVFRASKPGGGATL
589261 504 CVPKKE EFLSYHEPLGICLTAASLLGCTVISAVVLGFIHHRSTPPIVRANNSLSFLLLSLTLCLFLCSLTFIGRPLWTCOLRHAFAFGISFVLCV SCILVKTMMVVLAVFRASKPGGGATL
716738 517 CVPKKE EFLSYHEPLGICLTAASLLGCTVISAVVLGFIHHRSTPPIVRANNSLSFLLLSLTLCLFLCSLTFIGRPLWTCOLRHAFAFGISFVLCV SCILVKTMMVVLAVFRASKPGGGATL
Ca15.1 595 CVPRQL DFLSNETLGLVALTAVAVS GAVVTTAVFVFLHYRHTPMVRANNSLSFLLLSLTLCLFLCSLTFIGRPSVWSCRFQQAFAFGISFVLCV SCLOVKTMMVVLAVFRASARPGAGALM
571614 575 CVPRQL DFLSNETLGLVALTAVAVS GAVVTTAVFVFLHYRHTPMVRANNSLSFLLLSLTLCLFLCSLTFIGRPSVWSCRFQQAFAFGISFVLCV SCILVKTMMVVLAVFRASARPGAGALM
744432 564 CLPKPSE EFLSFEITGALLSGFCGAVFLSLLTLLIFLHRTSPPIVRANNSLSFLLLSLTLCLFLCSLTFIGRPSVWSCRFQQAFAFGISFVLCV SCILVKTMMVVLAVFRASARPGAGALM
Ca13 599 CVPKQVE EFLSFGDTIGIALLVVSLSGFLTCAVALVFFYHRTSPPIVRANNSLSFLLLSLTLCLFLCSLTFISPPSQWSCLMRHTAFGITFVLCI SCILGKTMVVLMFAFRATLP - GSDVM
611619 562 CIPKVE EFLSAY - DSLGIALMVTSSVVGACATIAATFAVFFYHRTSPPIVRANNSLSFLLLSLTLCLFLCSLTFIGEPTTWSCLMRHTAFGITFVLCV SCILGKTMVVLMFAFRATLP - GHNIM
611624 611 CLPGIE EFLSFESETMGIIILVILTLVGLVLLTFLAPPHPKNTAHA - NYKIIYECVVGSPIGFVLMGYIGLLAVLSFQLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
611613 598 CIPKSI EFLSAHKELLGTLVLFSLGVLFTTFMFLIFYCHKETPIVRANNSLSFLLLSLTLCLFLCSLTFIGRPSGWSCLMRHTAFGITFVLCI SCVLGKTMVVLMFAFRATLP - GSNML
735220 563 CVPKIIE EFLSAGEPLGITLIVISAFGALVTIAVGVVFIYVNGTPLVEANDAVLSLSLFLSVVTFCLSEVFLGEPONWSCMTSQVALALGFAFLCLV SCITMSDLF - - - - - QPFR - - - - - HNEKC
179742 539 CISKEQL EFLSFWNDIFAVVLLAFSAGIILLCLLTSALFLYQRDTPVVKAAAGGLSQAFLSFLVVSYSIAMLEVGEPSSLOCKARQVLEGISFTLVCV SCILVKTMMVVLAVFRASARPGAGALM

TM4 TM5 TM6
594197 694 KWFGPA QORLQCVLGETLIQ - - - - - VITICLLWLSISPPSPNKFNVA - - - - - KDRITILECALGSAVGFVAVLGYIGLLAMFCFILAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
744222 678 KWFGPA QORLQCVLGETLIQ - - - - - AFICLLWLTISPPSPFNKIKDF - - - - - KDRITILECALGSAVGFVAVLGYIGLLAMFCFILAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
594233 693 KWFGAA QORLQCVLGETLIQ - - - - - VITICLLWLTINPPFPKNTKHY - - - - - KDKIILECALGSAVGFVAVLGYIGLLAMFCFILAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
Ca12 695 YCSVPL - QRFVSFACITLQ - - - - - VITICLLWLTISPPSPFNKNTAHA - - - - - KDKIILECALGSAVGFVAVLGYIGLLAMFCFILAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
Ca02.1 709 KWFGPP QORMTVVTFETSIQ - - - - - VITICLVWLVVNPFPVRNLTYY - - - - - KERIILECALGSSVGFVAVLGYIGLLAAVCLVLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
581784 709 KWFGPP QORMTVVTFETSIQ - - - - - VITICLVWLVVNPFPVRNLTYY - - - - - KERIILECALGSSVGFVAVLGYIGLLAAVCLVLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
584633 710 KWFGPP QORMTVVTFETSIQ - - - - - VITICLVWLVVNPFPVRNLTYY - - - - - KERIILECALGSSVGFVAVLGYIGLLAAVCLVLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
Ca09 706 KWFGAV QORGTVLGLTISIQ - - - - - AATCFAWLLSSSPKPKHNIQYH - - - - - KDKIVFECVVGSTVGFVAVLSYIGLLAAILSEFLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
589261 624 KWFGAV QORMTVVILTISIQ - - - - - AATCISWILLASPPPKHNTQYS - - - - - NERIIYECVVGSTVGFVAVLSYIGLLAAILSEFLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
716738 637 KWFGAV QORGTVLGLTISIQ - - - - - AATCISWILLASPPPKHNTQYS - - - - - NERIIYECVVGSTVGFVAVLSYIGLLAAILSEFLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
Ca15.1 715 KWFGPS QORGSVCIETCQARVITICLVWLVVNPFPVRNLTYY - - - - - GLOVTECAMASVGFVAVLSYIGLLAAILSEFLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
571614 695 KWFGPS QORGSVGLTISIQ - - - - - IVICIGIWLVSPPKPERDLGFQ - - - - - GSKVTECAMASVGFVAVLSYIGLLAAILSEFLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
744432 683 KWFGPK QORLQCVLGETLIQ - - - - - VITICLLWLTINPPFPKNTAHA - - - - - KDKIILECALGSAVGFVAVLGYIGLLAMFCFILAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
Ca13 718 KWFGPK QORLQCVLGETLIQ - - - - - VITICLVWLVVNPFPVRNLTYY - - - - - KERIILECALGSSVGFVAVLGYIGLLAAVCLVLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
611619 680 KWLGPQ QORLQCVLGETLIQ - - - - - VITICLVWLVVNPFPVRNLTYY - - - - - KERIILECALGSSVGFVAVLGYIGLLAAVCLVLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
611624 731 KLFGPS QORLQCVLGETLIQ - - - - - VITICLVWLVVNPFPVRNLTYY - - - - - KERIILECALGSSVGFVAVLGYIGLLAAVCLVLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
611613 717 KWFGPA QORLQCVLGETLIQ - - - - - VITICLVWLVVNPFPVRNLTYY - - - - - KERIILECALGSSVGFVAVLGYIGLLAAVCLVLAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
735220 676 NFNLC LHCRC SFVL - - - - - Q - - - - - AVACTVWLVVNPFPVRNLTYY - - - - - NDKIILECALGSAVGFVAVLGYIGLLAMFCFILAFLARLNPDPNFNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY
179742 658 R - - - - - KIYOPYAITITICVALQ - - - - - TATCICWLVVLSYAHIK - - - - - Q - - - - - PTTLLQYCHEGYSVVAEFGVMLGYIATLAFVCFICAFKGRKLEPOYNEAKLITFSMLIFCAVWVAFVPAVYVSSPGKY

TM7 clip
594197 810 SVAVEIFAILSSSFGLLICIFIPKCYIILLKPERNTKKNLMGKEGPTH - - - - -
744222 794 SVAVEIFAILSSSFGLLICIFIPKCYIILLKPERNTKKNLMGKEGPTH - - - - -
594233 809 TVAVEIFAILASSVGLLFCIFAPKCFIILLKPEKNSKKHLMNKK - - - - -
Ca12 810 TVAVEIFAILASSVGLLFCIFAPKCFIILLKPEKNSKKHLMNKK - - - - -
Ca02.1 825 TVAVEIFAILASSVGLLFCIFAPKCFIILLKPEKNSKKHLMNKK - - - - -
581784 825 TVAVEIFAILASSVGLLFCIFAPKCFIILLKPEKNSKKHLMNKK - - - - -
584633 826 TVAVEIFAILASSVGLLFCIFAPKCFIILLKPEKNSKKHLMNKK - - - - -
Ca09 822 ADAVEVFAILSSSFGLLVAFGPKCYIILLRPERNTKRAIMAR - - - - -
589261 740 ADAVEVFAILASSVGLLAFGPKCYIILLRPERNTKRAIMGRVK - - - - -
716738 753 ADAVEVFAILASSVGLLAFGPKCYIILLRPERNTKRAIMDRD - - - - -
Ca15.1 833 SVAVEIFAILASSVGLLFCIFAPKCFIILLRPEKNTKKNLMNKK - - - - -
571614 811 VVAVEIFAILASSVGLLFCIFAPKCFIILLRPEKNTKKNLMNKK - - - - -
744432 799 TVAVEIFAILASSVGLLFCIFAPKCFIILLRPEKNTKKNLMNKK - - - - -
Ca13 834 STLTEIFAILASSVGLLFCIFAPKCFIILLRPEKNTKKNLMNKK - - - - -
611619 796 SDAVEVFAILASSVGLLFCIFAPKCFIILLKPERNTKKNLMGKE - - - - -
611624 849 TVAVEVFAILASSVGLLFCIFAPKCFIILLRPERNTKKNLMGKE - - - - -
611613 833 LVAVEIFAILASSVGLLFCIFAPKCFIILLRPELNTKKNLMGKE - - - - -
735220 788 MVAVQIFAILASSVGLLFCIFAPKCYIILLKPERNTKKNLMGKE - - - - -
179742 770 LPAVEMVVVILTSNYGILSCHFEPKCYIILLKPERNTKKNLMGKE - - - - -