

CLUSTAL X (1.83) multiple sequence alignment

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gi|3548805      MKFGKDFS---SEWQQAYVDYKYLKTLVKDINRFKRRKTLHG----- 39
gi|3548806      MKFGKEFSSQMPVEWHEAYMDYDLSQLKEIIFKRRKTNPHGPHHHHHLLHRKMTLHR 60
gi|7487574      MRFGKEFVSQMPIEWQEQAYIDYAYLKTILQDIQASRRNSDSNNQ----- 44
gi|4324975      MKFAEHLSAHITPEWRKQYIQYEAFKDMLYSAQDQAPSVEVTDEDT----- 46
gi|4176766      MKFAEHLSAHITPEWRKQYIQYEAFKDMLYSAQDQAPSVEVTDEDT----- 46
gi|6093320      MKFAEHLSAHITPEWRKQYIQYEAFKDMLYSAQDQAPSVEVTDEDT----- 46
gi|22832470     MKFAEHLSAHITPEWRKQYINYEEMKAMLYLAVEEAPSVEVEDDV----- 46
gi|3880858      MKFGEQLASHLTPWEWRKQYIDYERLKNLLYDDMMEVP----ADDDR----- 42
gi|22946878     MKFGKTLDNLMVPEWRQYMYNLYELKQIRNAVEKAPSGSRPSNDV----- 46
gi|7290442      MKFGKTYESHLTIEWRQYMYRQYDGLKELIKQGVENAPSPLTSSDYE----- 46
gi|5832411      MKFGKVEGQSVAEWASAYFDYKGGKIIAGIAKNPSEGLY----- 42
gi|28922701     MKFAKELEQEAPEWRVKYLNKLGKLIKSVTRAIQRASTPNLARRPDSLHAAPAALF 60
gi|731805       MKFADHLTESAIPWRDKYIDYKVGKKLRRYKEKLDAAEEQSSSYR----- 47
gi|731951       MRFSHFLKYNAVPEWQNHMYDSEKLNLIYTLQTDLEQVGDNEEGFG----- 47
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gi|3548805      ---GQISLSS----- 46
gi|3548806      AFSGLISTSPKKKHHGGGGHGGHGIH----- 90
gi|7487574      --SSTPSFARNLTRYIN----- 59
gi|4324975      -----
gi|4176766      -----
gi|6093320      -----
gi|22832470     -----
gi|3880858      -----
gi|22946878     -----
gi|7290442      -----
gi|5832411      -----
gi|28922701     HHLHKKRTPQHRWSDTTPGSHGSPGADQLQSGGPELDRTPTKNNRNSKGSIEARGERS 120
gi|731805       -----
gi|731951       -----

gi|3548805      -----
gi|3548806      -----
gi|7487574      -----
gi|4324975      -----
gi|4176766      -----
gi|6093320      -----
gi|22832470     -----
gi|3880858      -----
gi|22946878     -----
gi|7290442      -----
gi|5832411      -----
gi|28922701     GLTTLPDNEVQYGSILPPSRSSDRTEFELPAPAMKIASRTGRRRDSIVASPTSPVSNRFG 180
gi|731805       -----
gi|731951       -----

gi|3548805      -----TVLEIEDGITTATIQQVSS-TASQRYETTF 75
gi|3548806      -----FSDSDDIIEGKIHVTAPILINSASHGYETTF 123
gi|7487574      -----RDALVSENHDIVVNTVTRLEEGLETAAYETTF 92
gi|4324975      -----
gi|4176766      -----
gi|6093320      -----
gi|22832470     -----
gi|3880858      -----
gi|22946878     -----
gi|7290442      -----
gi|5832411      -----TSGILGETPEEAT 55
gi|28922701     PRRTKSMAGADGQSTATSSVELPPSATIAQRSPHRLSRVLSNSHLRRTMSNRDSTAL 240
gi|731805       -----SWMPVSVYQTFQQRREPGRSDDGYRSGPAFFKDY 84
gi|731951       -----AGKSSNITDRFKNKFVFNKAKEDTSSGMNKDAGIVEET 85

gi|3548805      MTAKEGGYELVFFRRLDEFNKVEKRYREKVEVKEAAVLNKQMDALIAFRLKMK--- 132
gi|3548806      MASEEGGEYETVFFRRLDEFNKVEKRYREKVEVKEAAVLNKQMDALIAFRVKEHPD 183
gi|7487574      KAGEAGDDEFVTFRTLDREFNKVNFFYRLKVTARTEALALNKQMDALIAFRHKVMD-- 150
gi|4324975      -VKRYFAKFEKFFQTCCEKELAKINTFYSEKLEAQRFFATLQNELQSSLDAQKESTG-- 103
gi|4176766      -VKRYFAKFEKFFQTCCEKELAKINTFYSEKLEAQRFFATLQNELQSSLDAQKESTG-- 103
gi|6093320      -VKRYFAKFEKFFQTCCEKELAKINTFYSEKLEAQRFFATLQNELQSSLDVQKSSA-- 103
gi|22832470     -LKRHFANFDENFFHYCDKELKINTFYSEKLEATRKFATLNAELKTSIEESERSAK-- 103
gi|3880858      -REEHISRLDEKFNEDQDELTKINLFFSQIAEGQKHHLELQTELQVFKDVLGSRSD-- 99
gi|22946878     -AIGYYRNFEEELFFNSCRVELTKVNYFFAHKQAEHRKLATLNYQLDRRAQDPRGS-- 103
gi|7290442      -VQAYYKAFEETFLTECQSELTKVNYFFAHKQAEHRKLATLNYQLDRRAQDPRGS-- 103
gi|5832411      VKRGOIHRFHPLQFELDQANKVEEFFENLVSDARERMDLISDQVDIYKELRAFKKG-- 113
gi|28922701     QNLESVRTAETEFFFLDNELDKIETFYKQKEDQATKRLAALREQLHEMRRRTTEIA-- 298
gi|731805       SALQREPVADFIEDWLSIFQLSKCNEFWLLKEDDKFEVLQSLHYSLQKNYERDNL 144
gi|731951       IELRELPTAQTVAAKPSFRMKEKIFVYKRRSSSASSVSTANENLQDLDYTFVGDLT 145
.          .          : * :          :

gi|3548805      ----EESTVEMARFALHGVSPAELAKNP-----SMKVHMEAIIEGGSSRAGRSD 179
gi|3548806      GWPWEERTVEMTQLASDVANAAVAASTPAGARSMKVGAQAAMEAIIEGGSSKAGKSSD 243
gi|7487574      -----QNKNPVDFVDSVE 164
gi|4324975      -----VTTL----- 107
gi|4176766      -----VTTL----- 107
gi|6093320      -----VTAL----- 107
gi|22832470     -----KSKG----- 107
gi|3880858      -----TTGI----- 103
gi|22946878     -----TASR----- 107

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gi7290442 -----DSSL----- 107
gi5832411 -----TLES----- 117
gi28922701 -----DAKQKEMER 308
gi731805 NRSSSNVDMSTSLYAAG-----LAGRSDSRVNSIDSDS 177
gi731951 E-----KQKVDDFYKRTEAKFY 162

gi3548805 E-DDYYTDEEDHNDVFFTPANNLSKMKSSSAFIEVLDSIKINNKAL-QSNTKSVLKV 237
gi3548806 EEDDDDAEKEEDNGVSGEVSQVGRKMKAGRPPPIEVLDRVKNHTKETP-RSTIKSVLQA 302
gi7487574 DINGSASEVGSCKTEHNVADLMRNETSNESLERIRMNKREITPLSAIKTILKV 224
gi4324975 -----RQRR 111
gi4176766 -----RQRR 111
gi6093320 -----RQRR 111
gi22832470 -----HKR- 110
gi3880858 -----RRRF 107
gi22946878 -----GSAS 111
gi7290442 -----SQRA 111
gi5832411 -----GSVLIQKQHSKLRQLDSILNFSRLQPAYHIPARK 153
gi28922701 GSGSKSHPGDGGSGNGKDSGTWIGPLRTKFMKPGPNKALQKMETETPMAPQKPEEGD 368
gi731805 RSMYGSMPCTKEAKKPRLLSLLAYCQKVLKDNRLPSWPKRGFSLQLDQRDASRRGRET 237
gi731951 DKFDALVKDLKKIGVIEYDIDDDTLFNEPIASTNDEVPPLD.DDEDDDEFYDDQSNIED 222

gi3548805 SNHTELFKSRDNLKIEEKLICAFVEFHRKLWYLSYRLV-----FISENVFYQIT-SRD 291
gi3548806 SNLTELKFSRENLRKVEAKLRRAFVEFYQKRLRLKSY----- 339
gi7487574 HKQDELKFRDNLKEVEKRLQVAFIEFYQKRLKKNYSFLNASAVSKIMKKYDKIA-KRN 283
gi4324975 KPVFHL SHEERVQHRNIKDLKLAFFSEFYL.SL.LLQNYQLNFTGFRKILKHKHDKILETSR 171
gi4176766 KPVFHL SHEERVQHRNIKDLKLAFFSEFYL.SL.LLQNYQLNFTGFRKILKHKHDKILETSR 171
gi6093320 KPVFHL SHEERVQHRNIKDLKLAFFSEFYL.SL.LLQNYQLNFTGFRKILKHKHDKILETSR 171
gi22832470 -----HAALPDRKARELKLAFSEFYL.SL.LLQNYQLNFTGFRKILKHKHDKILRVDT 162
gi3880858 G---GKDFHKETTRNEQQLKLAFFSEFYL.SL.LVQNFQQLNATGFRKILKHKHDKITGNER 164
gi22946878 SWSRQPEGKRKFPF--IKKRLAMSEFYL.SL.LLQNYQLNFTGFRKILKHKHDKILETSR 169
gi7290442 ERS-----QKKLMT--TRQLRYAIEFYLSL.LLQNYQLNETGFRKILKHKHDKIMRSLVA 164
gi5832411 SVPTDAYTPMYSYRKLKSKLKTLLDFYDYLKLSYQYQLNQAFRKLKVKYDKTLHTLD 213
gi28922701 YVRRPNKDDVSYRVAKRKLKALQEYRGLLELLKSYALLNRTAFRKLKVKYDKAVNARP 428
gi731805 FAFGASLEMTTTQARNL.SNAIEEYLYLQLVKSFRDINVTGFRMVKFKDKTCHTRE 297
gi731951 NTALLHHSQYNIKSKKSLKKSIVNLIDLCQLKSFIELNRI.GFAKITKSKDKVHLNLT 282
* : : : * : : :

gi3548805 AAKSYMVMVDSKLSGSSEVMKLMENVEATFIKQFT----- 327
gi3548806 -----SSDEVTRLVERVEATFIKHFS----- 360
gi7487574 AAKLYMEMVDSKLSSESEVHKL.LLKVSEFIEHFS----- 319
gi4324975 GADWRVAHVEVAPPYTCCKINQLISETAEAVTNELE----- 207
gi4176766 GADWRVAHVEVAPPYTCCKINQLISETAEAVTNELE----- 207
gi6093320 GADWRVIAHVEVAPPYTCCKINQLISETAEAVTNELE----- 207
gi22832470 GAKWRQYEAESHFTNKIDININETETVTGELE----- 198
gi3880858 GLDWRINKVEKSSFFLNREIETLITNVEVTSVINDLE----- 200
gi22946878 GFAWYKYLKSTLAIITLQLDRMISTTENMYTDYLA----- 205
gi7290442 AGRWVFNVDLAPFDVRLQRMITIEVEDLYTHLA----- 200
gi5832411 QG-FWVDYMSRYTTFDFTITNQHLHVEDIYARLFT----- 248
gi28922701 TYRYMNEKVNKTWFVNSDVVDGHIRTVEDLYARYFE----- 464
gi731805 LTTFMSYARTHYTLFKHADANVQLVAQMQUITSSQPTPTSELSSAQRDKEPITWLETQI 357
gi731951 RTELTIESEQFKDYAFQAEITELLNSKISQLVTFYARITDRPHN-----IS 329
:

gi3548805 -----NGNRTKGMNLRPKPKRERHRTFS-----TVALVAIVRT 362
gi3548806 -----NANRSKGMNLRPKAKRERHRTFST-----VVALFAIIRT 396
gi7487574 -----NSNRRGEMSHLRPKINKERHLITFSTGFFGGCISLIVALGLIIHA 365
gi4324975 -----DGRQKAMKRLRVPP.LGAAQAPAWTTFRVGLFCGIFIVLNLITLV 253
gi4176766 -----DGRQKAMKRLRVPP.LGAAQAPAWTTFRVGLFCGIFIVLNLITLV 253
gi6093320 -----DGRQKAMKRLRVPP.LGAAQAPAWTTFRVGLFCGIFIVLNLITLV 253
gi22832470 -----GGDRQAMKRLRVPP.LGEOQSP--WTFKVLG.FSGSIVLVIVVVV 242
gi3880858 -----AGNRQAMKRLRVPP.LSEKQKPP--LTFSLGL.FIGASII.LLAILL 244
gi22946878 -----NGDRSEAMKRLRVPP.LGHPTPP--VHVSAGL.FLGLFVLSAICFI 249
gi7290442 -----NGDRSLAMEKRLRVPP.LGEPTPP--SMVFRAGIAL.GMLTMLVATAI 244
gi5832411 -----NHNKLALEHLKS--FROKE-HFSANSRFG.LL.FGAGLPLAIEAAC 291
gi28922701 -----KGNHKVAAGKLRN--ILRRPGDASGSAFRSGLLIGF.GAVFAVQGLI 508
gi731805 TEWFTTAL.TNSPKDRKHNTHLKKLTIQYSISEQVHRNRSIVQMLVGLGIGVSMTLI 417
gi731951 HSKQELKSYLHDHIVWERSNTWKDML.GLLSQADELTPKETEYNANKLVGLDLEYRWPL 389
:

gi3548805 RNILQDDGQ---KQYMNMTFPLYSLFGFIMLHMTYAAANIYWRQYRVNYSFIFGFKQG 418
gi3548806 RNILQEEGQ---KQYMNMTFPLYSLFGFVVLHILMAGNIYWRQYRVNYSFIFGFKQG 452
gi7487574 RNIMGTPGQ---RTYMETMFLYRF.FGVVLMHDVYAANIYWRQYRVNYSFIFGFKQG 421
gi4324975 AAVFKLET----DRSIWPLIRIYRGGFLLIEFL.LLGINTYGWRQAGVNHVIFELNPR 308
gi4176766 AAVFKLET----DRSIWPLIRIYRGGFLLIEFL.LLGINTYGWRQAGVNHVIFELNPR 308
gi6093320 AAVFKLET----DRTWPLIRIYRGGFLLIEFL.LLGINTYGWRQAGVNHVIFELNPR 308
gi22832470 SAIFHEIS----GENLKVTFRLYRGLLIEFIFLIGVNIYGNRSVGNVHVLIFELDPR 297
gi3880858 TWIASPARP---QEPKWAVRLFRG.LL.LL.FLIFLGVNMAGWAAAGVNHVIFEVDP 300
gi22946878 SYFVAVDTS----PEFRYTFVSLFRG.PISGVTGFC.LAINIKVYETVGNQVLI.FEVERR 304
gi7290442 SYWKRAPL----EDHTPGLMRLFRGPFTWVIFNFYMAANVAGWQAGVNHVIFELDPR 299
gi5832411 Y-----YNATEQSSYLLQI.WGGFLLVIFAFVLDLDCYWEKTRVNMVIFEFNRQ 342
gi28922701 YGSELLFQDDHTLKENTSYLLQYGGF.LMILLFAL.FLACRIWTLNKINYPFIFELDTR 568
gi731805 TYTYLIGISSEETSFTHKILFPLGWGVNMLIAFLV.LVNCFIWHRGGINYR.FMLG.EIQ 477
gi731951 PRPILNKF.TSINWALPKLFFTKAKYIYF.IILVTGLLGIKTFDAAQHRCMALVEVCA 449
:

gi3548805 T-----ELGYKQVLFVGF.SIGALALLCVLANLDMETDPKTKDYQALTELLPLFLLIAM 471
gi3548806 T-----ELGYRQVLFVGLSIGV.FALLCLANLDMEDVPEKTDYQALTELLPLFLLTGM 505
gi7487574 T-----ELGYRHVLLLSFGL.GTSLCAVLLNLDMEMDAQTKDYRLVTELPLFLLV-- 472
gi4324975 S-----NL.SHQHLFEIAGFLG.LWCL.SLLACFFAPISVIP--TYVYPLALYGF.MVFFLI 360
gi4176766 S-----NL.SHQHLFEIAGFLG.LWCL.SLLACFFAPISVIP--TYVYPLALYGF.MVFFLI 360

gi6093320 N-----NLHQHLEIAGLGLWCLSLACFFAPISIIIP--IYVPLALYGFVWFLLI 360
gi22832470 N-----HLSQHLMEAAIFGVIWTL SMLSFLYSASLAIP-AFINPLTLTLMVFLA 349
gi3880858 N-----HLSYQTLMQIASFMIMLWSFAVLAYLAHMLHIP-PFAPPLAMVVLILL 352
gi22946878 N-----AIGAMRALEISSFFGYMCTLSLILYLLHKEFFIEDPIYIPLVQAVFVWVFL 357
gi17290442 S-----HLQPATFLEIACFTGILWALSMLGFLYNDLIGVSDPYVPLGLLIMVGLLV 352
gi5832411 K-----SLNWRQHLEIVGAVFFIFSLFFFLCMR--NFFPGFTIYFPALLGLVGVGFTLI 393
gi28922701 H-----NLDWQVAEFSPFFALLGVFLWLNFSRFHWEEMYL YYPALLIGLSLLILF 621
gi731805 SKNGTQFNDFATSKIPKLYLFTFFIVPCAVCSMLSFALEKLTPLGLYIGIVSFLF 537
gi731951 FLWASEAIPLHITAFVLVPLVLFKVLKTS DGAIMS AASASSELAAMSSITMILLAGF 509

gi3548805 FVVLVVPFNIFYRSSRFFLTLFHMLAAPLYKVTLPDFLADQLCSQAQLRSIEFYIC 531
gi3548806 FVVLVLPFNIFYRSSRFFLTLFHLAAPLYKVTLPDFLADQLTSQVQALRSIEFYIC 565
gi7487574 -----VHLPDFLGDQLTSQVQALRSIEFYIC 499
gi4324975 N-----PTKTFYKSRFWLLKLLFRVFTAPFHKVGADFADWADQLNSL SVILMDLEYMIC 415
gi4176766 N-----PTKTFYKSRFWLLKLLFRVFTAPFHKVGADFADWADQLNSL SVILMDLEYMIC 415
gi6093320 N-----PTKTFYKSRFWLLKLLFRVFTAPFHKVGADFADWADQLNSL SVILMDLEYMIC 415
gi22832470 N-----PFHVL YHDARFWLWRITGRVCSAPFHFVGFADFWLGDQNSLATAILDFEYLIC 404
gi3880858 NPI-AKPDSVFRHNSRFLWKHCYKCTSPHFVFTDFWLGDQNSLTTAFLDFQYFVC 411
gi22946878 N-----PFRILFYSGRWLLVMGRILLSPFFVFNADFVADWADQNTSLVVTIVDHYLYVR 412
gi7290442 V-----PLPIMNWPARWITIKLVGRVITAPLHYVGFADFWMDQNSLVSIVDHYLYVR 407
gi5832411 AP-----VIVPYWRMRYLIQIRVFLSGLSTVHFQDFADQNSLTYACGNISLFFC 448
gi28922701 FP-----APIFYHRARRWFLYSHYRLLLAGLYPVEFRDFLGDWICSLTYSAANIPMFFC 676
gi731805 CPSGLIPYWDKVVHTRKWLVTIRLMSGFFPVEFGDFLGDII CSLTYASIDIAMFFC 597
gi731951 TLGEVLAQYNIKVLASWLLAFAGCKPRNVLLMAMCVVFLSMWISNVAAPVLTYSLLSP 569

gi3548805 YYGWDFKQRK-----NTCKDSQVNTFLFIVSAFPFFSRFLQ 569
gi3548806 HYGWGDYKRI-----NTCTESDAYNAFLIVAVIPVSRLLQ 603
gi7487574 YYGWDFYRFR-----NTCTSNIGFRFTFYIVAVIPYWRLLQ 538
gi4324975 FYSLELKWID-----ESKGLLPNNSEESGICHKYTYGVRVAVQCPAWLRFIQ 462
gi4176766 FYSLELKWID-----ESKGLLPNNSEESGICHKYTYGVRVAVQCPAWLRFIQ 462
gi6093320 FYSFELKWID-----ESKGLLPNDPQEPFCHKYTYGVRVAVQCPAWLRFIQ 462
gi22832470 FYFTNGWIT-----EAR-----DASICMEKDFIIRP VCNCLPAWFRFAQ 443
gi3880858 FYATEVDYSNGWIEVKGINSTTGSVPWGSVELSNGKQDCASAAGLRSLMSIIPAMIRFLQ 471
gi22946878 FYVRYFLDRS-----VNNCFEPDVMVPIITMCLPGWFRFAQ 443
gi7290442 FYAISWLRDR-----VNNCFEPDVMVPIITMCLPGWFRFAQ 443
gi5832411 LYKRLWRPQ-----LCNSSHSPLLGFFTLPLGLRVFQ 482
gi28922701 LYANEDWQP-----MCNSSHRLQGFNALLPPIWRALQ 710
gi731805 VYSHTPNLLCG-----SSHSRAMGLVSLCSPYWRFMQ 629
gi731951 LLDAMDADSPFAQALVLG-----VALAANIIGMSSPISSPQNIISM 611

gi3548805 CMRRMLEE--KNIEQGYNGFKYIVIVVAVCLGMAYEVDD--KDRQIWRLLGGITSAM 624
gi3548806 CLRRLEFEE--KNPEQGYNGLYKYLTIIVAVCLRTYSVDE--DNQFIWRILAGIFSAT 656
gi7487574 CIRRMVED--RDL SHGNGIKYLLTIVAASLRATYTLNR-----GSNWNITAWVFSGV 589
gi4324975 CLRRYRDT-KRAFPHLVNAGYSTTFMVFALYSTHKE-RGHSOTMVFYLVIVFYII 520
gi4176766 CLRRYRDT-KRAFPHLVNAGYSTTFMVFALYSTHKE-RGHSOTMVFYLVIVFYII 520
gi6093320 CLRRYRDT-KRAFPHLVNAGYSTTFMVFALYSTHKE-QNHSOTVVFYLVWVFCII 520
gi22832470 CLRRYRDS-REAFPHLVNAGYSTTFMVFIFATLKSFSHPNYASTFDNPTWLVIIASIV 502
gi3880858 CLRRYRDT-KRVPHLVNAGYSTTFVAVACGALNKYYEA-TDPNTTSIFFYIWLISYIM 529
gi22946878 -----
gi7290442 CLRRFRDSGSKSMSYLINAGKYSTTFLVVLFLRRNSEGGYANTFSPNYTWLFLSSCVV 503
gi5832411 CFRRYSDS-LKSFPHLVNAGKYSTTFLVVLFLRRNSEGGYANTFSPNYTWLFLSSCVV 534
gi28922701 CLRRYHDT-KNVFPHLVNAGKYSTTFLVVLFLRRNSEGGYANTFSPNYTWLFLSSCVV 762
gi731805 CLRRFADS-GDWPHLVNAGKYSTTFLVVLFLRRNSEGGYANTFSPNYTWLFLSSCVV 682
gi731951 YLKPYGIWGWQFAVALLPSGILAMLLWILLFTTFKMKIKLEKFKPKTKFTKYQYII 671

gi3548805 AVVFCTYWDLVYDWGLLNRTSK-----NPWLRDNLIPHKVYVVLAMILNV 670
gi3548806 AAIFCTYWDLVYDWGLLNRTSK-----NPWLRDNLIPHKVYVVLAMILNV 702
gi7487574 ATFYGYWDLVYDWGLLQGRCK-----NSFLRDKLLVPHKTYVYAAVMLNV 635
gi4324975 SSCYTLIWDLKMWDGLFDKNAG-----ENTFLREEIVYPQKAYYCAIIEVD 567
gi4176766 SSCYTLIWDLKMWDGLFDKNAG-----ENTFLREEIVYPQKAYYCAIIEVD 567
gi6093320 SSCYTLIWDLKMWDGLFDKNAG-----ENTFLREEIVYPQKAYYCAIIEVD 567
gi22832470 SSCYATYWDIKMWDGLFDKNAG-----ENTFLREEVYSSSTGFYFFAILDEL 549
gi3880858 SFYTYFLWDIFMDWGLIDPRAPK-----EARFLREEMIGSKWYVYMAIAQDF 577
gi22946878 -----DAFEFEPDYAVAWVYFVIVENT 445
gi7290442 ATIYCYLWDVIRDFGLFRIMRG-----ERIFLRKQLVYVYQAFYFVIVENL 549
gi5832411 NSLFSYTWDLMDWNLVLRKDG-----RWQFREHRLKQLWYVYIAMIENL 580
gi28922701 NACYTTIWDLMDWNLVLRKDG-----RWQFREHRLKQLWYVYIAMIENL 808
gi731805 NSILTSAMDWMDWSFAHNTSYNWLRRDDL YLAKKNWENGYSFSRKL VYFAMIWIDI 742
gi731951 TVYVATILLWCVESQIEGAFSSGQIAIPIVLFVFGTGLLSTQDLNAPFWSIVILAMGGI 731

gi3548805 VLRFAWMQTVLDFK--FESIHTQTVAVVASLEIIRRGWVFRLLLRTHI----- 719
gi3548806 LLRFQWLVQVDFN--FSFMHRQTMVAVVSLLEIIRRGWVFRLENEHNLNVGKYRAF 760
gi7487574 LLRLVWLQTVLDFK--FSLHRETMWALMACLEIIRRGWVFRLENEHNLNVGKYRAF 693
gi4324975 ILRFQWLVQVDFN--FESIHTQTVAVVASLEIIRRGWVFRLLLRTHI----- 719
gi4176766 ILRFQWLVQVDFN--FESIHTQTVAVVASLEIIRRGWVFRLLLRTHI----- 719
gi6093320 ILRFQWLVQVDFN--FESIHTQTVAVVASLEIIRRGWVFRLLLRTHI----- 719
gi22832470 ALRFQWLVQVDFN--FESIHTQTVAVVASLEIIRRGWVFRLLLRTHI----- 719
gi3880858 VLRFAWMQTVLDFK--FESIHTQTVAVVASLEIIRRGWVFRLLLRTHI----- 719
gi22946878 LLRCVWILEFALVH--QELIAPYNGKSLICFSEIARRFFWVFLRLENEHNLNVGKYRAF 503
gi7290442 VLRLFWAVEFTILY--HNLMTYPMRTISSILEIIRRGWVFRLLLRTHI----- 719
gi5832411 IYRSSIFYCIFPN--HIQHSSTISFFVTLAEIMRRCMNLVREHEEYIYRNLRAAR 637
gi28922701 LLRFQWLVQVDFN--FESIHTQTVAVVASLEIIRRGWVFRLLLRTHI----- 719
gi731805 LRFQWLVQVDFN--FESIHTQTVAVVASLEIIRRGWVFRLLLRTHI----- 719
gi731951 ALGKAVSSGLLSTIAKALQKIEENDGVFALLCIFGILMLVGVGTVSHVSAIIIPLVQ 791

gi3548805 -----

gi3548806 TVPLPFNYDEDDDKGN----- 776
gi7487574 TVPLPFNYEEDGDHNN----- 710
gi4324975 DISVAPLNADDQTLLEQMMDDQDGVRRNQKNRSWKYNQSI SLRRPRLASQSKARDTKVLI 687
gi4176766 DISVAPLNADDQTLLEQMMDDQDGVRRNQKNRSWKYNQSI SLRRPRLASQSKARDTKVLI 687
gi6093320 DISVAPLNADDQTLLEQMMDDQDGVRRNQKNRSWKYNQSI SLRRPRLASQSKARDTKVLI 682
gi22832470 DISIAPLDS SDQALILRLMDEADGVINRYTKANRPKPKVKDPEKRSLLQTRGSLPDLRI 667
gi3880858 DISVKPIRKGDLSSLKMDQMDGVTHRGQDLMERVKKKKSAKASRQLLRKNRFRMIA 695
gi22946878 DIFITRLDPQEEFLESVMDNTEDLG-----REKLNKKYF----- 538
gi7290442 DIHLAALNPRQERMLESMDSDGVSNNRKSNERIRLKGKEYF----- 649
gi5832411 ELKPLDFVKPHSDVFSHQISSDKNYTDEEDSMDQTDVDEAQFS----- 682
gi28922701 DTPLPYQLDQFVERPSQETSAGELEAETGTTGAVQEQERRGTISSMAASIRERIRGVSVA 925
gi731805 DAPLPYPIAQVGDSDMSDDLGSKAFSSLNDIPITPSHDNNPHSFAEPMPAYRGTFRRRS 859
gi731951 EVGDKLGNPKAAPILVFGCALLSSCGMLASSGFPNVTASIKVDRKGDYLSVMTFLTRG 851

gi3548805 -----
gi3548806 -----
gi7487574 -----
gi4324975 EDTDDEANT----- 696
gi4176766 EDTDDEANT----- 696
gi6093320 EDTDDEANT----- 691
gi22832470 DMDSKKL----- 674
gi3880858 AAPVVTTFIDTTNT----- 710
gi22946878 -----
gi7290442 -----
gi5832411 -----
gi28922701 GATSPWAASPSPATGAHPPEEGAI SPHAESGATSGEGATGTGFSLSGGGFRRRHVE 985
gi731805 SVFENISRSIPWAHATDFQRPTVNTVDDRSPE TDESEVESIM----- 902
gi731951 VPASILAFLCVITLGYIMASVVKGNATSA----- 881

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gi5832411 -----
gi28922701 EDDDEDDSDRRSVQDRMEAREAEMLVKRARGEPPDSDVSE 1087
gi731805 -----
gi731951 -----