

10 20 30 40 50 60 70 80 90 100 110 120 130 140

W1

ATP-1_CB -----MKSDFTDYSIQNYYSKRNNNPLLPSSL-RACITCKSCCGKTNLIMNLLDDEYCEDYDYDNLIFYF-----STTLFPCY---QALINGFANGDSSKKEIRECF 94
 ATP-1_CC -----MKNLRAQLPVINFDQIQVQGTGVKLRHGALLPNSIHAIVFCPSNCGKTNALSLIIVHP-----NCRUFENI---LYL-----SKSLNPKY---QFLET-LLKQIDGEGFFTF 98
 ATP-2_TC MCKVFLFVFKSMLKLVQKDLIKISNHDYSVCVPYQHFPKHNFLFNNSVGRGLVVRSCGKTNVILSLIHLHP-----NRURFT--DIYLE-----SKTLQPKY---QFLKS-VLAPDKVGYEYE 113
 ATP-2_NV -----MDIPNYSNTGANKKYQLCKFMPSDNF-RLLISCPSPGSGKTNCLIHMLVTP-----LHFDKIYLY-----AKNLESKY---QDLIHTFSDISHEVGYSVIE 90
 ATP-1_CI -----MDVSVFKHPF-TMLITCPTGSGKSVFVKELIANA-----NVMLNQPPEKIIV-----AYGVWQFY---DTIT-----NVTFVE----- 64
 ATP-1_SP -----MTVVFVHPF-TCMVAQPTGSGKTVFVRKLLKYN-----QDLIEKPPQKILW-----CYGVYKAY---TEMM---AEVPTIEFIE----- 68
 ATP-1_TC -----MDLRFKSPF-TAIVACPTACGKTHFIRFKHL-----SLICDTEFEFVRLW-----FYDEWFLY---QNMNDINNLQRFEFQ----- 70
 ATP-1_XT -----MDTRLQHPF-SCILACPSNCKSYFVKQLIVNA-----DMLLSHKPDNIIVW-----FYACWOKLY---DELSS---SFPHFIE----- 68
 ATP-2_DR -----MGFDNVFGHGQVQDAGVDFRFQHPF-TCHISCPSSGKTFVVKMLLQNC-----EPLMFSKNVENVIR-----VYNSWFLY---DDL-----KMYDKFKIK----- 84
 ATP-1_NV -----MEDRRFRPCPC-AIMVVCPSGKTTWVQSLLRQA-----PKAFDKRFHKILC-----CYGQWPKY---DWMQKKL-----GVEFHQ----- 68
 ATP-3_CR -----MVKLSWQS-TLLIVCPSGKSTLARQIVEQR-----NTLFDVDSKICF-----WYDTEFSV-----PDSMKNRPDMLR----- 65
 ATP-1_CR -----MFDQKTKMTPQFRFPS-QTTVICATCSGKTSIVRKILENL-----DSSFSTNIDNIF-----WFGVD-----NDGIPKHIPQITCIE----- 73
 AAL73466 -----MESQFDKTIQVENLNKQDS-SILIAQRRSGKTVLCINLLLY-----ITEKYSYQSII-----LSDTGGIETNSAFDIDKNFIFESR 80
 AAL69857 -----MNRFKKEHFFRSLNKSFP-RALVCGSGGKTMVLSLFSST-----LIDKYKHIFLE-----PVYNEAYDSIWPDHVNVKVTSEDEYSLVTTKQ 87
 CAE52735 -----MDIVREKFNRLNLDYF-RMVLICGSGGKTTFLSLFKT-----FITKYKHIFLE-----PILNPSYNYWVPDHIYKITTAELEYSLSKMKQ 87
 YP_031593 -----MEQVPIKEMRLSDLRPNKSIDTDLGGT-KLVVILCKPSSGKSTLTKALDS-----KRHFIPCAVVI-----SGSEANFYKGVVPDFL 79
 NP_078656 -----MDSVNIQLDLDLRPNKSEMETDIGGM-KLTIICRPSGKSVIKSLIAS-----KRYDIPAAVVI-----SGSEANHFYKTIIPSCF 79
 AAP74205 -----MILKELSLTELRFKPPDEMGGKLLVILCKPQKGVKSLKSLIAA-----KRHFIPAAVVI-----SGSEANHFYKSLLENPCF 74
 NP_048749 -----MSYSITQSPRSIKDGA-IVGVVCRSGKSVIKSLIYY-----KRNALPIGLMI-----SGTEAGNGY-----FSSYVPEIFVVDFF 72
 NP_077388 -----VNDIYNTAIKYQKTVNFAHAMLTNGCMKSLNYGIQPF-IVIVYVCPGSGKSOFTRNLISSR-----LIEPSPETIEFITPEKGTVPLEEKVAEHAHCAEAGNDAQGNPLTTKLNPTFILPFKDAV 120

W2

ATP-1_CB RTQNFVVDKKNKEISLHISEN---CDDIPDPSSIDPN-RKTLIIFDDLMLEK---QNK---TEQYIT-RGRNNDQCFYISNYIKLKP---NTIREANFIVFSQDK-MNL---EYTYRD-HCGEVDR-PTFLEWVT 214
 ATP-1_CC EHEAVI---KP-----EDAKPNSLMIFFDVACEK---QDH---IKAFPC-MGRKVDSEFYLCITYTRIPK---HLIRDNANFVLVFERODEMNLKHYD---DHNVTDMYNSFRDICS 196
 ATP-2_TC DGAEI---EP-----PKEIKPYSIIFDDVVIC---NQNI---IRDYFC-FGRNNDQCFYISNYIKLKP---OLIRDNANFVLVFERODEMNLKHYD---DHNVTDMYNSFRDICS 211
 ATP-2_NV CSSDDV---TPV-----GELDDETQKIIIFDDVEYCEK---NQAP---HIDYFI-RGRNNDQCFYISNYIKLKP---DVRNCSHFVYDFPSTNERGIT---RELGVSKEQYS 185
 ATP-1_CI -----GVPEVBS-----FDGK-QRVLIVDDLMGD---SNSK---LTDFTFSSHILNLSVIFIVNLFYKN---QTHISLNAHYITAFKNPR-CATQATLAQWYPGK--T-NFLKAAFA 162
 ATP-1_SP -----GPPSSFD-----GVIDPN-LRNLIIIVDDLMAECT---KDNM---MTEFTFSGSHRNLSVIFIVNLFHAGRETRTISLNAQYLVIVYKNPR-DKSOITHLGROYPGQ--T-KYVQEAYN 172
 ATP-1_TC -----GVPDINE-----FDG-V-KATLIIIDDLRE---ANGS---VDFEFTGSHRNLSVFNITNLFYQCKGORDISLNAQYLVIVYKNPR-DKAOINFLARQEPEN--I-KFVQESYK 170
 ATP-1_XT -----GLPQTFM-----DDDLFPPGKVMIIIVDDLMESAS---ENVE---EKAFTKYVHARNLSIMVIVNVEFCQKKSRTINLNTKYMVLKFNPR-DKLOITLISROMYPGK--T-RFFLEAF 174
 ATP-2_DR -----GLPESFD-----DDHLFPP-E-KTNLIIIDDLMECS---NNLE---VSRVFTQYSHKNNSKKIVNLFYQCKKSRTISLNAQYLVIVYKNPR-DSGQNVVIAQWYFAGN--T-KFFMECYH 190
 ATP-1_NV -----GLPDSVT-----ELFGKHDTPGLIIIDDLMDQID---R---ALKFTQESHHDITTFISLTPFPGGR-SRTASINSHFFVMEFDRPR-NKLGRTLAQWYFAGN--LDYVMDAYD 169
 ATP-3_CR -----EGLPNIEE-----LKKYKQDQAMVVIDDLMKID---QMSG---MERIVSVLAHYDMVIFLHTIFY-SKVIINLQOASYIILPKNNA-DKSSVRCIGSMPG---ACNTFLAAYN 169
 ATP-1_CR -----GLPDEVF-----LKQHRFKNNIIVDDLMNIFA---RDKKSLHLNDFLFCVYAHYVCAIFNLSAFALPPT---TNNSTYLLMLNLS-DASQKNLLOQFGEK---WRGALKAYQ 178
 AAL73466 -----QLDEI---IPKLMKY---EKEKKKRNQKYMIIIVDDINLKN---RSKL---LDDLYS-KSRNINMVIIVVYSKIV---ITNIRSNIDILEMSQNNSGLESMEYCIN---TELDKREFYRIFRE 189
 AAL69857 -----KIEKYI---ESKGTKNADMFLIIIDDMGDQKT---RSSC---LDDLLN-HGRNLSIITLCCITYKHVAVNG---RTSITHFCCCNVSDSDIENMLRSM---IVGSKDLLKSIISM 190
 CAE52735 -----DLVNL-----GKRSINHKFVLIIDDLGDMQL---KSKI---LSDLVN-TGRIRMSIVMLCCITYRHVPS---NCRSSITHCCCNVSDADIENTRSM---LVATKQIKALSV 186
 YP_031593 -----IYHQF-----SPSIEDRERROVKAKAEMGSKSWLLVVIDDCMNAKMFENDE---VRALEK-NGRNINLVVIVIANQYVMDL---TPDLRASSVDGVELEFENNVTYRDKTYANF---ASVVEPKKIYPTM 195
 NP_078656 -----IYNKF-----NDSIEKLEKROITAKNIGL-KTSWLLIIDDCCMDSKLFCEKT---VMDLEK-NGRNINLVVIVIANQYVMDL---KPVIRATIDGVELEFENNVTYRDKTYANF---FASIPKKEFFILM 194
 AAP74205 -----VYNKF-----DADIITRVKORQALAKNV-DPEHSMLLIEDDCMNAKMFENHEA---VMDLEK-NGRNINLVVIVIANQYVMDLNA---SLRCCIDGVELEFTE---TSQTCVDKIYKQ-FGGNIPKQTFILM 189
 NP_048749 -----NKD-----GLEKLEROK---KAACKGMSKVFVVIDDLAFDTSIMKQPV---MRYLFM-NGRNINLVVIVIANQYVADLG---PPAIFANIDILLVCEAIQANRWLYN---MFFGCFESFEDFNKVL 183
 NP_077388 -----SDINL-----NDNPNENI---FCKAASNGPICVMDCCMFLGSCHS---ISSEF---HALPSKI---SDFPKCSGYTVIVVILHNMNPRHNRGNIKDLKIKOSKCHVISPOLLEISOV 223

290 300 310 320 330 340 350 360 370 380 390 400

ATP-1_CB -----EIKWCKNFFTIIDKTSDS-----DNGKFKK-----MLKYFFVL----- 247
 ATP-1_CC -----ACWKKYGFVVIDKDSLE-----KSGRMKRG-----FYCFISIN----- 229
 ATP-2_TC -----QCWQKPYGFVVIDKDAEQ-----DNGRYRNG-----FDQFIKI----- 244
 ATP-2_NV -----KVSQKPYGFVIVKSPDKKI-----AFN-----FYGRV----- 212
 ATP-1_CI -----DATKRAYGYLLIDFRQATD-----ERLRIRTR-----FPGEIQ-DVYLPVY----- 203
 ATP-1_SP -----DATKNPYGYLLIDLKANTL-----ESHRLRTH-----LFPNEFT-TVVVPK----- 213
 ATP-1_TC -----DATMRPYGYLLIDLKQNTPE-----DDFRIRTN-----LDPDEPCYVYIPKKNYKYSK----- 219
 ATP-1_XT -----DATSOPYGYLLIDLRSNTP-----BELRRTG-----LPPPSLP-AVYVVKKCSK----- 220
 ATP-2_DR -----DATSIPYGYLLIDYKAHTP-----DQYRRTA-----VLSDRPYYVILQKR----- 231
 ATP-1_NV -----QATKRPYSCLLIDFHQKTP-----DNLRLRSD-----LDPDEFMYAFFPNRSGEAYIEGEEGGNTSVNDAQRKRKRSGGWVDDPYTTHGKRKARSRVHPRQVCG 268
 ATP-3_CR -----DATSOPYGYLLIDLHKNPC-----DEIRYRDN-----LPLGKIT-HVFIPK----- 209
 ATP-1_CR -----SVMSKPYNAMMINNDPNAD-----PCFRIMEN-----FLHEFFIIVYK----- 215
 AAL73466 -----NTINNOYVYVILHDNVNKL-----KIVKADFFQLENKGGKQKIKL----- 230
 AAL69857 -----SSIAGRRRVLIIDDSVFSF-----GEQRICFD-----SADEHVINNDVNPILLKQFHMKNLPLKILLSYE----- 252
 CAE52735 -----RAASRGKVVYIENNTVFAN-----KDRIICYD-----TADGKSVIEQKPDATLLSDFSHMCKQLHTLSDDNKDTYFDLSNLSINDDRDKKDCIYSPEREASSNMALKYSKQESLOEL 299
 YP_031593 -----ETVCOROMFIDNTKATDMHDSVFWYKAPYSKSAVAPFGARSYWKYACSKTGEEMPAVEDDNVWIKLGDLLKELPAGALVITYGKDGPSDDDEGLSDGVSVEYQSD 319
 NP_078656 -----EKIITODTALYIDNTI-----INPAHWSDCVKYYIASLENIDELFGCEEYKAYCV----- 244
 AAP74205 -----EKVTODTFCLYIDNTTTRQWEDVYV---RYYKAPLLTDADV-----GEGFKDYAGVA----- 239
 NP_048749 -----NACTENYGVVLDNTK-----LSNDPQDCVHFHAKMRDNFMKMGHRAFWKFSKRRKDDSDDEADNGVRLIKSKDSKR----- 258
 NP_077388 -----IKNYSFGFPSSALIEVVKDIL-----NHARLNSKYSWLYINVVP---SESFWSYSPSDQVPMFNLQTLFYNSCLIRVFRKRSOTQMQYIKKINAIIFYFE----- 321