

P1LT[Vc] 1 -----MD---- IAELELFVSVKHNASDLHLHLSAGVPFPMVRIDGVEVRKLG-VYFA42
P1LT[Pa] 1 -----MD---- ITELLEFSAKQGSADLHLHLSAGLPPMIRVDGDVRRIN-LPPL42
P1LT[Ps] 1 -----MD---- ITELLEFSAKQGSADLHLHLSAGLPPMIRVDGDVRRIN-LPPL42
P1LT[Nm] 1 -----MQ---- ITDLLAFGAKNKASDLHLHLSGGISPMIRVHGDVRRIN-LPEM42
P1LT[Ng] 1 -----MQ---- ITDLLAFGAKNKASDLHLHLSGGISPMIRVHGDVRRIN-LPEM42
P1LT[Dn] 1 -----MTDESLESEKELK---- LDDLFRFAQKQGSADLHLHLSGVPFPMIRIDGDVRRIN-LPPL54
P1LT[Ab] 1 -----MD---- ITELLEFSAQVNRASDLHLHLSAGIPPMIRVDGVEVRKIN-LPAM42
P1LT[Aa] 1 -----MFEKQVEVEQKELK---- ILEIIEKAIELGASDLHLHLSAGAPPAVIRIDGYIKFLKDFPRL55
P1LT[Mx] 1 -----MAN---- LHOLLKAMVEKGSADLHVTVTGSPPRLRVLDGELVLPKTA-L43
P1LU[Vc] 1 -----MELNQY---- LDGM LTHKASDLYITVGVAPILYRVLDGELVLAQG-BA-L41
P1LU[Pa] 1 -----MEFEKL---- LRLMVEKGGSDLFITAGVPPSMKVNGRVM PVT-KTFL42
P1LU[Ps] 1 -----MEFEKL---- LRLMVEKGGSDLFITAGVPPSMKVNGRVM PVT-KTFL42
P1LU[Nm] 1MNTDN LHD ILDEMVQVYSQKKQSRSETPAEIGAHFPLDLRRCETAEBAQNASDILISKGFPPSLKINSALTPQP-QKAL78
P1LU[Ng] 1MNTDN LHD ILDETVQVYSQKKQSRSETPAEIGTHFPLDLRRCETAEBAQNASDILISKGFPPSLKINSALTPQP-QKAL78
P1LU[Dn] 1 -----MNLDPK---- TLRQWFDNVLVFAHQREASDIFINSQNVAVKTNGLHFLQ-EAF151
P1LU[Ab] 1 -----MDFNDL---- LNLMAKHKASDLFITAGVPPSLKINSEITPVS-KTKL42
P1LU[Aa] 1 -----M---- LDQLLRKALEKASDILHLVKGSKVEVIRTPDGLDTEEFPI42
P1LT[Vc] 43 THSDVHRLIFEIMND--AQRSEYEELKLEVDPSFELPN-VGRFRVNAFHQARGCSAVFRTIPTV IPTLEQLDAE--EIFS116
P1LT[Pa] 43 BHKQVHALIYDIMND--KQRKDFEEFLELTDPSFEVPG-VARFRVNAFNRNGAGAVFRTIPSKVLTMEELGGM--EVFK116
P1LT[Ps] 43 DHKQVHALIYDIMND--KQRKDFEEFLELTDPSFEVPG-VARFRVNAFNRNGAGAVFRTIPSKVLTMEELGGM--EVFR116
P1LT[Nm] 43 SAEVEGNMVTSMVND--HORKIYQOINLVDPSFELPN-VARFRVNAFNIIGRGPAAVFRTPSTVLSLEELKAP--SIFQ116
P1LT[Ng] 43 SAEVEGNMVTSMVND--HORKIYQOINLVDPSFELPN-VARFRVNAFNIIGRGPAAVFRTPSTVLSLEELKAP--SIFQ116
P1LT[Dn] 55 QNQMRDMIFGITMD--AOMKSFEEKWADPSTFELIRG-VSRFRVNVFQNRGMGIVFRTIPSKVLSLEELKAB--AKFV128
P1LT[Ab] 43 DHEVHNLIYDIMND--KQRDYEEKLELTDPSFEVPN-LARFRVNVFNQRNGAGAVFRTIPSOVLTEELGLG--KIFR116
P1LT[Aa] 46 TPEDTOKLAYSVMSE--KHROKLEENGQVDFSEFVGRG-VGRFRANVFYQSGVAALLSLPAEIPFEFKLGLP--DKVL129
P1LT[Mx] 44 SPVETKQLCYSILTD--AQKHKEEDNLDLSEFGVKG-LSRFRANIPMORGAVAAAFRTIPFKLTFQELGLP--PVVA117
P1LU[Vc] 42 SVADVTALLHAMDD--ARQAEFKQTFREANFAVVRD--SGRFRVSAFYQRLNLAGMVLRRITETNIPTEPEELKLP--EVLQ114
P1LU[Pa] 43 SPEQTRTEVHGVMNE--QQRDFFAENHCENFAISARG-IGRFRVSAFYQRLNLAGMVLRRITETNIPTEPEELKLP--EVLK116
P1LU[Ps] 43 SPEQTRTEVHGVMNE--QQRDFTEENHCENFAISARG-IGRFRVSAFYQRLNLAGMVLRRITETNIPTEPEELKLP--DVLK116
P1LU[Nm] 79 TGEETAIAAASSTMA--EOSEIFRRDGEINYSVQSRSGTRYRANAYHSQGSAGLVLRRINHVIPMQEELGLP--EKLK152
P1LU[Ng] 79 TGEETAIAAASSTMA--EOSEIFRRDGEINYSVQSRSGTRYRANAYHSQGSAGLVLRRINHVIPMQEELGLP--EKLK152
P1LU[Dn] 52 DEEDVM IAKAISRP--EAFEFELKTYECNIMVEVFN-VTYLRANAYYQKMGPIVMRLIPAKIPAIEEINLQPHILK127
P1LU[Ab] 43 DGM IIAQLIDITQO--KORQEFIEETHCENAILNREKNERFRVSAFOQRDPMGMVTRITETKIPSPDDHLPL--PLLK117
P1LU[Aa] 43 DIDLFEVFKLELIEHHPKKEKLEEQGVLDLSYAIK-VSRFRVNLKQORGTAMALYRIFPDIPFEFKLNLPL--PVM118
Walker A Asp box
P1LT[Vc] 117 K I-ANYEKGLVLTGPTGSGKSTTLAAMVNVVYAHNKHHLITIEDPIEFVHSNNKCLINQREVHRDTHSFKNALRSALR194
P1LT[Pa] 117 K I-SDVPRGLVLVTGPTGSGKSTTLAAMDLYLNNTKYHHLITIEDPIEFVHESKCKLVNQRVHRDTHLGFSEALRSALR194
P1LT[Ps] 117 K I-TDVPRLGLVLVTGPTGSGKSTTLAAMDLYLNNTKYHHLITIEDPIEFVHESKCKLVNQRVHRDTHLGFSEALRSALR194
P1LT[Nm] 117 K I-AESPRGMVLVTGPTGSGKSTTLAAMINYNETOPAHHLITIEDPIEFVHQSKKSLINQRELHQHTLSFANALRSALR194
P1LT[Ng] 117 K I-AESPRGMVLVTGPTGSGKSTTLAAMINYNETOPAHHLITIEDPIEFVHQSKKSLINQRELHQHTLSFANALRSALR194
P1LT[Dn] 129 D I-IDVPRGLVLVTGPTGSGKSTTLAAMIDHINNHRHEHLITIEDPIEFVHESKCKLVNQRVHRDTHSFKNALRSALR206
P1LT[Ab] 117 D I-CDYPRGLVLVTGPTGSGKSTTLAAMDLYNNHRYHHLITIEDPIEFVHEPKKCLINQREVHRDTHLGFSEALRSALR194
P1LT[Aa] 130 EL-CHRMKGLILVTGPTGSGKSTTLAAMIDYINNTKSYHHLITIEDPIEFVFKHKMSLVNQRVGDGTRNFYALKNSLR194
P1LT[Mx] 118 EL-VKPRGLILVTGPTGSGKSTTLAAMIDKINTEHREHHLITIEDPIEFVHPKKNCLVNRVGDGTRNFYALKNSLR194
P1LU[Vc] 115 NL-IAAKRGLVLVVGAPGTGKSTSLAAMIGYRNKNSGHLISIEDPIEFIHQHGQIVTQREVGIDTDSFEVALKNTLR194
P1LU[Pa] 117 KL-ALTKRGLVIFVVGAPGTGKSTSLAAMIGYRNKNSGHLISIEDPIEFIHQHGQIVTQREVGIDTDSFEVALKNTLR194
P1LU[Ps] 117 KL-ALTKRGLVIFVVGAPGTGKSTSLAAMIGYRNKNSGHLISIEDPIEFIHQHGQIVTQREVGIDTDSFEVALKNTLR194
P1LU[Nm] 153 DL-AVAPRGLLIIVGPTGSGKSTTMATMLEHRNKTLPSHIVITIEDPIEFIYKPRRCIFTQREIGVDTINWQAVQNAAR230
P1LU[Ng] 153 DL-AVAPRGLLIIVGPTGSGKSTTMATMLEHRNKTLPSHIVITIEDPIEFIYKPRRCIFTQREIGVDTINWQAVQNAAR230
P1LU[Dn] 128 EL-LVKRGLVITIGATGNGKSTTLASMDVFRNERTKNHLITIEDPIEFMFKSKSVQIQREVGIDTKTYGAAKSSLR205
P1LU[Ab] 118 EL-AMSKRGIITVIGATGNGKSTSLASMIQHRNKSHKHLITIEDPIEFIEHAGCIITQREVGIDTDSFEVALKNTLR195
P1LU[Aa] 119 Q TALKHSAGMLVTVGPTGSGKSTTISASLINEIKRSLRVHLITIEDPIEFYFKIQSFIQREVGIDTDSFEFLGLRALR197
Walker B His box
P1LT[Vc] 195 EDDPDIILVGEMLRDLPETIRLALTAAEFGHLVFGTLRTSSAAKTIDRVIDVFPQSDKDMVRSMLSESIRAVIAQGLLKR-V272
P1LT[Pa] 195 EDDPDIILVGEMLRDLPETIRLALTAAEFGHLVFGTLRTSSAAKTIDRVVDVFAAEKAMVRSMLSESQVISOVITLKK-I272
P1LT[Ps] 195 EDDPDIILVGEMLRDLPETIRLALTAAEFGHLVFGTLRTSSAAKTIDRVVDVFAAEKAMVRSMLSESQVISOVITLKK-V272
P1LT[Nm] 195 EDDPDIILVGEMLRDLPETIGLALTAAEFGHLVFGTLRTGAAKTVDRIVDVFAAEKEMVRSMLSESITAVISOVITLKKTHD273
P1LT[Ng] 195 EDDPDIILVGEMLRDLPETIGLALTAAEFGHLVFGTLRTGAAKTVDRIVDVFAAEKEMVRSMLSESITAVISOVITLKKTHD273
P1LT[Dn] 207 EDDPDIILVGEMLRDLPETIRLALTAAEFGHLVFGTLRTSSAAKTIDRVIDVFPABEKDMVRSMLSESQVISOVITLKK-I284
P1LT[Ab] 195 EDDPDIILVGEMLRDLPETIRLALTAAEFGHLVFGTLRTSSAAKTIDRVIDVFPABEKDMVRSMLSESQVISOVITLKK-E272
P1LT[Aa] 208 EDDPDIILVGEMLRDLPETIRLALTAAEFGHLVFGTLRTNATIDTIRIVDFIPFLNQEQVIRVLSFIQOIIISOVITLKKIG286
P1LT[Mx] 196 QDDPDIILVGEMLRDLTEAATLTAETGHCYATLRTNSAVOTINRVLDVFPYQVQVRAAMSVLEGVMSQALVAKAG274
P1LU[Vc] 193 QAPDVLIGEVHRSRETMHYATFAETGHLCLATLRANNANQALERIHFFPADRHQVWMDLSNLKAIYAQGLVPTPD273
P1LU[Pa] 195 QAPDVLIGEVHRSRETMHYATFAETGHLCLATLRANNANQALERIHFFPADRHQVWMDLSNLKAIYAQGLVPTPD273
P1LU[Ps] 195 QAPDVLIGEVHRSRETMHYATFAETGHLCLATLRANNANQALDRIHFFPADRHQVWMDLSNLKAIYAQGLVPTPD273
P1LU[Nm] 231 QSPDVCIGEVHRSREMYAMQLAQFGHLCLIFTLRANTAPQSLERILNFPYKQHNQILIDIALNLGICORLALKKD309
P1LU[Ng] 231 QSPDVCIGEVHRSREMYAMQLAQFGHLCLIFTLRANTAPQSLERILNFPYKQHNQILIDIALNLGICORLALKKD309
P1LU[Dn] 206 EAPDVLIGEVHRSREMYAMQFAETGHLCLATLRATNSVALERLYNFFLDQREKQLDLSENRCLITQRLIPK-I283
P1LU[Ab] 196 QAPDVLIGEVHRSREMYAALFAETGHLVFATLRANNANQALERIHFFPADRHQVIFMDLSNLKAVISQGLVPTPD274
P1LU[Aa] 198 EDDPDIILVGEMLRDLPETIRLALTAAEFGHLVFGTLRTNDAVETINRIGMFDLRRHQIRQMLASTLAVYISOVITLKK276
AIRNLIRE motif
P1LT[Vc] 273 GGRVAAHEIMLTPAIRNLIREDKVAQMYSIQTGAA-HGMQTMELQNAKOLIAREVVDQAEVQSKIELDLKAFA----345
P1LT[Pa] 273 GGRVAAHEIMIGTPAIRNLIREDKVAQMYSIQTGGS-LGMQTLDMCKLGLVAKGLISRENAAREKAKIPNF----344
P1LT[Ps] 273 GGRVAAHEIMIGTPAIRNLIREDKVAQMYSIQTGGS-LGMQTLSCCLKGLVAKGLISRDSAKEYAKIPNF----344
P1LT[Nm] 274 GGRVASHIELIANPAVNRNLIRENKITQINSVLTQTA-SGMQTMQSLQSHVROGLIAPEARRRAQNSSEMSF----347
P1LT[Ng] 274 GGRVASHIELIANPAVNRNLIRENKITQINSVLTQTA-SGMQTMQSLQSHVROGLIAPEARRRAQNSSEMSF----347
P1LT[Dn] 285 GGRVAAHEVVLVGTSAVKNLIREDKVAQIYSTIQTGSG-YGMQTLDQALSALVKEGKVDRLMASKAHDKDNFM----357
P1LT[Ab] 273 GGRVAAHEIMIGTPAIRNLIREDKVAQMYSIQTGAT-HGMQTLDSQKYLKGLAKGILNLPTRAVAKSPESF----344
P1LT[Aa] 287 E-GRVLAYELLIPNTPAIRNLIRENKLOQVYSSIQGSEQAETGSMQTMNQTLQYKGLKGLITLEDAM EASPDPKELERMIRG364
P1LT[Mx] 275 EGRILALFVNVVNPNAIRNLIREDKVHQIYSSMQVQAKFMQTFNOALALLLRRLLITQEDA FGRSSDAEELRNILAT353
P1LU[Vc] 272 EGRHGVLEVLNLSRITADLIRRGELHLEKATMARS-QEVMQTFDQALYLVVDDKIQSDALHSAADNLRMLK349
P1LU[Pa] 274 EGRRAVIEVLLNTPLAADLIRKGEVHLEKGLMKRS-TEQGMQTFDQALYLYTQGEITYEDALLHADNLRMLK351
P1LU[Ps] 274 EGRRAVIEVLLNTPLAADLIRKGEVHLEKGLMKRS-TDLGMQTFDQALYLYTQGEITYEDALLHADNLRMLK351
P1LU[Nm] 310 KTRTAVVDDLNTTPAQDFILKGLDLMNISKIMETA-KTDMQTMQNLFLFYRHGIIISYEBALROSVANNLRLLQL387
P1LU[Ng] 310 KTRTAVVDDLNTTPAQDFILKGLDLMNISKIMETA-KTDMQTMQNLFLFYRHGIIISYEBALROSVANNLRLLQL387
P1LU[Dn] 284 GGRVAAHEMMNTPYIQQLHDCQVDKIHEVLERGDATRCVFSFDRCIFDLYEGLIEYDTALQFVQSANNFRVVRN362
P1LU[Ab] 275 GGRRAVIEVLLNTPLELSDYIRQGEIYKIKELMARS-GELEMQTFDQALFLFYRHGIIISYADALHADNLRMLK352
P1LU[Aa] 277 GSKVPPVIEIMTQITREAILENRPODKPELIEKRLVYSGOTFDQALFLFYRKLILIDETALLYARRPADLRLK355
P1LT[Vc] -----
P1LT[Pa] -----
P1LT[Ps] -----
P1LT[Nm] -----
P1LT[Ng] -----
P1LT[Dn] -----
P1LT[Ab] -----
P1LT[Aa] 365 GR-----ALPGMQRPGGGAG-----R-----366
P1LT[Mx] 354 GGGG-----ALPGMQRPGGGAG-----R-----372
P1LU[Vc] 350 KRGGDY--GSGS-----L-----QNVKIDME-----368
P1LU[Pa] 352 GSESDA--DHL-----SSLT-----QGLSEITDDDPAGRRFR-----382
P1LU[Ps] 352 GSETDG--EHL-----T SVS-----QGLTEMSDDDPG-RSFR-----381
P1LU[Nm] 388 HKEGKT--PELLYDRVGNL-----LIS-----408
P1LU[Ng] 388 HKEGKT--PELLYDRVGNL-----LIS-----408
P1LU[Dn] 363 ESKRRL--PDLGTAAGDSYTVLSDDRLERELIRKAKEEMRSKEFGR-----406
P1LU[Ab] 353 SEEANK--PEDNRAGMSEME-----RKM TFDGQ-----RRNLK-----383
P1LU[Aa] 356 ISTDEN IIEGDN YLT-----408