

[Walker A]

AF0814	1	-----	MKVAVTGRPGVGKTTCLKVHESLKDK--MTVGGF
MK0827	1	-----	MPHNVLTGRPGTKTTVCLKVRNVLEEEG-YTVGGI
MA3402	1	-----	MRIEGKEKTMRLIAVTGSPGVGKSTVVAKTAEKLAEPGFKIGGI
MTH1068	1	-----	MKILITGRPGSGKSTMVGRRLRDYLEGMG-FSVGGI
APE0781	1	MFSRGASTMQSRELREQLLGCVKSRKSLHVTGPPGSGKSTFVSRIAEALRVKG-CRLGGF	
PH0792	1	-----	MRFFVSGMPGVGKTTLAKRTADEVRREG-FKVGGI
PAB1537	1	-----	MRFFVSGMPGVGKTTLAKRIADEIRREG-YKVGGI
MJ1559	1	-----	MIYNFKHYIHQFKGCGETMRIFITGMPGVGKTTLALKIAEKLKELG-YKVGGF
PAE3292	1	-----	MTWRER-----AELRIGISGMPGVGKTTLVLKIAELARSR--VKVCGF
SSO2171	1	-----	MLEESKNALRVFITGNPGVGKTTILLFLINKLSENN-YKVAGF
aq_1292	1	-----	MKIIITGEPGVGKTTLVKKIVERLKGRA---IGF
TM0036	1	-----	MKILITGRPGVGKTTLIKKLKLS-RLLQNA---GGF
Ta0998	1	-----	MIPLAIKIGITGPVGSIKSEALQKIIDMLKNDN-LNVQGV
TVN0737	1	-----	MIEMAIKIGITGPVGSIKAEALQKIIGMLQNDG-LNVQGV

AF0814	34	ITKEVR--RDGVRVGFKLVDLSSGNEEWLARVGE--GKA-----RVGKYAVNVEGLEEFL
MK0827	37	YCPEIR--EGGRRIGFEIVDLTEGDRYLLAREGA--SGP-----RVGRYGVFVDNLERAA
MA3402	46	RTAEIR--KEGHREGFSIRDLATGKTGILSHVKG--SGP-----RLGKYHVNLDLDERIG
MTH1068	35	ITPEVR--VGGSRWGFEVVDIASGRRGLLASVET--EGP-----RIGRYGVNVGVMDELA
APE0781	60	MAPEVR--RGGRRVAFKIVDIASGEEGYLAVADESLAAPGGRRARHGRLVLVDEAWRVM
PH0792	35	ITEEIR--EGGKRTGFRVIALDTGEIGRLAYVGY--GYP-----RLGKYVIDVEGFERVA
PAB1537	35	ITQEIR--TGPKRSGFRVIALDTGEIGRLAYVGY--GYP-----RVGRYVDIEGFDRVA
MJ1559	53	ITKEIR--DGGKRVGFKIITLDTNEETILAYVGD--GKI-----KVGKYAVFIENIDNVG
PAE3292	42	VTVEVR--EGGTRIGFEDVDLANGRMALARVGR--GEP-----SVGKYVNLEACN---
SSO2171	43	YCPEVR--ENGRRIGFRITVDITTNEGDWLAKENAP-GRV-----KIGKYTVLEDSAKRIT
aq_1292	32	WTEEVRDPETKKRTGFRITTE-GKKKIFSSKFFTSKKL-----VGSYGVNVQYFEELA
TM0036	31	YTEEMR--EGEKRIGFKIITLD-GEIGILARTDLPSPYR-----VGKYVYNLKDLEEIG
Ta0998	40	LVSQVT--NNGKLTGYTTIEDIESKRKAQFCDFNFVSRVK-----IDKLGVDTKILEEIL
TVN0737	40	LISKVS--DDGKLTGYTTIEDILTKKKVQFCDEKFVSRVK-----IDKLGVDTRLLEEIL

[Walker B]

AF0814	85	-DSVR---T---DADLVIIIDEVGPMELKSRKFVRFVENLMGRER-LLFTIHL--KSRH
MK0827	88	-ESIER-AVK---RTDVVIVDEVGPMELKSNAFVDAVRAADAHTPAIFVVHE--RSRH
MA3402	97	-ANAVR-NAL---ACDLVVIDEIGPMELISQSFSVAVEEVLES DKPVLAVLHH--SSRH
MTH1068	86	-VPAIRRAML---EDDCIIIDEIGPMELKSREFRRTVDEVLSDDVLLIAAVHR--KTLQ
APE0781	118	-SHAIRNAFE---HADIIIVDEIGPMELAVPGFREALTEILDGKPLVTVFHRRLRLTD
PH0792	86	IPALSRLALR---GADLIVIDEIGPMEFKSNEFLKALGLVLKSEKHLLATVHR--RLV
PAB1537	86	IPAISRLALR---DADIIIVDEIGPMEFKSNEFLKALGLVLKSEKPLLATVHR--KLV
MJ1559	104	VEAIKRALK---DADIIIDEIGAMEFKSRKFSEVVDDEVIKSDKPLLATLHR--NWV
PAE3292	90	--VISEALRR---ECDLKIIDEIGAMEFKCKNFGEDELQTAHTSPRVIATVHR--NYI
SSO2171	95	--EITLSNIN---KADVLAIDEIGPMELKIPTIKKLIETILNNQKPLIATVLRH-----
aq_1292	85	IPILERAYREAKKDRRKVIIDEIGKMELFSKKFRDLVRQIMHDPNVNVVATIPI-RDVH
TM0036	82	VRSLERAFQE--KD--LIIVDEIGKMELLSRKFRREVVEKIF-DSEKDVIAITIK--KSSD
Ta0998	92	IPSLQKARET----ADVIVIDEIGKLENTTKKVHAEIETTLKCGKPLIVTLHK--RSRN
TVN0737	92	IPSLQKARES----ADVIIIDEVGKLENTTKKIHSEIETTLKCGKPLIVTLHK--RSRN

AF0814	133	RLLDRIIR---EFKVVVIDESNRN---RTAAEITRILEG-----
MK0827	140	PVVVDLREERPDVVRFRVTLNSNRDELSDRILHEHVLEWLEER-----
MA3402	149	PLAQRFRK---GFEVLTVDKGNRDELPEKITNRFLRKLKLG-----
MTH1068	139	S--IKKRE---DIRFVVDPEKRD---RVYLRITIDLLG-DYHGMR--
APE0781	173	PGLYKLE---RGCIVWLDERNRGP LI-RLVSEIASALSNEACGNS--
PH0792	138	DRYRPLG-----EYWLTPENRNAVFSEILGRIKGLLKEK-----
PAB1537	138	DRYRPLG-----RYWLTPENRNEVFAEILMEIRKVLGRNENAGNKA
MJ1559	156	NKFKDKG-----ELYTLTIENREKLFEEILNKILAGLK-----
PAE3292	141	DIKKKGL---EIIWLTRENWGLVFRQLLIQLGLTQ-----
SSO2171	143	-TQKPMGG---RIYVITVENRDSIKYEILNYILSSLD-----
aq_1292	144	PLVKEIRR-LPGAVLIELTPENRDVILEDLISLLER-----
TM0036	134	PFVEKIKN-RNDVVFELNEKNRNSLLNEILSVLKFNKGKQ-----
Ta0998	145	PVLQEIKS-LEGVRVFDITPINKNILPFKVMHVLKGEE-----
TVN0737	145	PVLQEIKS-LEGVRVFDITPINKNILPFKVMHVLKGEE-----