

CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT

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```
Mge -----  
Mpn -----  
Mga -----  
Mpe -----  
Uur -----  
Mpu -----  
Fnu_N -----  
Fnu2_C -----  
Tde -----  
Tpa -----  
Lint -----  
Gme -----  
Bce -----  
Bsu -----  
Bha -----  
Oih1 -----  
Lmo -----  
Sau -----  
Sep -----  
Sxy -----  
Smu -----  
Sbo -----  
Sag -----  
Spy -----  
Ssl -----  
Spn -----  
Lla -----  
Lga -----  
Lde -----  
Lbr -----  
Lpl -----  
Lca -----  
Efa -----  
Efam -----  
Lme -----  
Ooe -----  
Tte -----  
Eac -----  
Cth -----  
Cac -----  
Ctet -----  
Cpel -----  
Oih2 -----  
Rso -----  
Rme -----  
Bfu -----  
Bpe -----  
Cvi -----  
Nme -----  
Neu -----  
Xca1 -----  
Xax1 -----  
Xfa -----  
Cbu -----  
Ctep -----  
Mma -----  
Rru1 -----  
Ccr -----  
Nar1 -----  
Bme -----  
Mlo1 -----  
Sme -----  
Atu -----  
Rsp1 -----  
Bja -----  
Mlo2 -----  
Rsp2 MAAGAPSGAGGADGPRPARAGGGRRRAQAGGHRRHPPACGDDPRPALSDHARSARPRSHALRDRAALSVPRAAADRTL RGP  
Rru3 -----  
Rru4 -----  
Rru7 -----  
Rru2 -----  
Xax3 -----  
Xca2 -----  
Xax2 -----  
Mka -----  
Rru5 -----  
Sav -----  
Rru6 -----  
Nar2 -----  
Cpe2 -----  
ruler 1.....10.....20.....30.....40.....50.....60.....70.....80
```

80

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Mge	-----	MK	2
Mpn	-----	MK	2
Mga	-----	MVIRGFIL	8
Mpe	-----	-----	-----
Uur	-----	MEIRG	5
Mpu	-----	MKK	3
Fnu_N	-----	MYT	3
Fnu2_C	-----	NMDKN	5
Tde	-----	MANISFVL	9
Tpa	-----	-----	-----
Lint	-----	MSMPG	5
Gme	-----	MEGDQQLNTISL	12
Bce	-----	MP	2
Bsu	-----	MA	2
Bha	-----	MA	2
Oih1	-----	MVA	3
Lmo	-----	MTK	3
Sau	-----	-----	-----
Sep	-----	-----	-----
Sxy	-----	-----	-----
Smu	-----	M	1
Sbo	-----	M	1
Sag	-----	M	1
Spy	-----	MSICKGLTVDLVNIKGEIM	21
Ssl	-----	M	1
Spn	-----	MM	2
Lla	-----	M	1
Lga	-----	MVEA	4
Lde	-----	MINT	4
Lbr	-----	MIES	4
Lpl	-----	MAGS	4
Lca	-----	MADS	4
Efa	-----	MIEV	4
Efam	-----	MSEV	4
Lme	-----	MAQN	4
Ooe	-----	MDEQQ	5
Tte	-----	ME	2
Eac	-----	MTEDK	5
Cth	-----	MSSDAAY	7
Cac	-----	M	1
Ctet	-----	M	1
Cpel	-----	M	1
Oih2	-----	MK	2
Rso	-----	MELT	4
Rme	-----	MELT	4
Bfu	-----	MDTS	4
Bpe	-----	-----	-----
Cvi	-----	-----	-----
Nme	-----	MP	2
Neu	-----	MS	2
Xca1	-----	MNT	3
Xax1	-----	MNT	3
Xfa	-----	MNT	3
Cbu	-----	-----	-----
Ctep	-----	MNFDQKGLKRSITV	15
Mma	-----	-----	-----
Rru1	-----	-----	-----
Ccr	-----	-----	-----
Nar1	-----	-----	-----
Bme	-----	-----	-----
Mlo1	-----	-----	-----
Sme	-----	-----	-----
Atu	-----	-----	-----
Rsp1	-----	-----	-----
Bja	-----	-----	-----
Mlo2	-----	MMPPN	5
Rsp2	ARRGEVPRWHDTRPPARCGAGASARRGAAAHQDDQFHPORPRAHADELGRSQPDRRLQSRPDRRLCRSGRHPRGHPAAA	160	
Rru3	-----	MPV	3
Rru4	-----	MTRSRRCALA	10
Rru7	-----	-----	-----
Rru2	-----	-----	-----
Xax3	-----	-----	-----
Xca2	-----	MPOSAAVAELAFISALRAERAHAAMP	26
Xax2	-----	MPOSAAWVEDTFLSDGSAAIATCAAV	26
Mka	-----	-----	-----
Rru5	-----	MTRKT	5
Sav	-----	MST	3
Rru6	-----	MRC	4
Nar2	-----	-----	-----
Cpe2	-----	-----	-----
ruler90.....100.....110.....120.....130.....140.....150.....160	-----	-----

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Table with 3 columns: Sequence identifier (e.g., Mge, Mpn, Mga), aligned amino acid sequence (with gaps), and position number (e.g., 55, 56, 57). The table shows a multiple sequence alignment of various proteins, with gaps represented by dashes and specific residues highlighted in color.

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Mge LGKREFIFLNQKPVVEQKKKIIANLLKLPKPAVILKSFLD--CGVLLAVNQTYQVPILKINLFSSTELSFVETVINEQFA 133
Mpn LGKREFGLSOKTLVEQQQLHLLNLLKLNPPAAILKSFSD--PTVLLQVNQTYQVPILKIDFFSSTELSFVETVINEQFA 133
Mga LGNREYSYLSLSPERKKEKTKRLLLEIQPPVLILKSFLD--FVFLKECNKEYKVPILCTDMYSNELNISIQLYISKQLA 140
Mpe WGNDEYLVLKQFDEKLVLKKEIKELIQLTTPPLVLVLSRSFPA--KGIILELAKKYDISILSTKESADLNYINTFLTEKLS 128
Uur FGSKSNVFNKFSFETIISKKLGILLDNPLLIIFGKNFKH--AGILLKLAERYKIPIVEVKVSYFELNFTINSYISQKLS 135
Mpu WGTNBSKFFFKI GSEKAKSSIEEIFSRIKIMLVLSKGFDPKNYSTIIETIANKHKTPVIFYKASLSEINTLGLVLLQYFA 138
Fnu_N CSLKESRFIATPSKERKESVISKVMISLDFPALIFTKDAII--AEFVYVYAKKYNKNILFSNEKASVTIRKLFKFFLSKTL 135
Fnu2_C FSKIEFKLENLPIIERVNNLKKFLNVDIPMIVLVVDANPP--EYFFDLVKKSCHILALAPYKKAQIVANFNNDLSDSFFS 140
Tde FGRGEYALATLATEKLDLSTIEKMFSPKIPCCFLSNDLKP--FKPLEISDKHNCPIILSTLSNELALRLLRLSNTFA 141
Tpa FGRGEHAYLLALLEOGRYGAIEKMFITDLPCCIFSHGITP--PEKFLHLAEPSSCPILVTRLTSSELRLMRVLSNIFA 131
Lint FKGEMAWITSTRPMEDEKIAAEFFGPHLNCIIFHGNMP--PIIFMENCEKLGIPLMISEVSTHKFTILSGLDRSLA 137
Gme LGNTEISYLRQLHEELATIFVDFKCEYFISCIIVKGLDP--PQFLKDAEAEREAPLLVTPLOSTFISLITKFLERELL 144
Bce LGKTELFDFDITLSEQKQERMKALCTEETPCIIIVARNQDV--PELLQASRESGMPLLRSSQTTLRLSSRLTNVLEKLA 132
Bsu LGKTELSFFEQLPPEEKKQRMDSLCTDVTFAIILSRDMP--PQELIDASEKNGVPLRSPLKTRLSSRLTNFLESRLA 132
Bha LGRTLSFYKQLSPVDKEERMSKLCITDTPGIIISRGLEV--PPPELLKASEKVGVPVLRSNITLRLSSMLTNFLESQLA 132
Oih1 ICKTEMAVLTQMTSHNRYSVLKEMFKDDTPAVVSRNLAI--PEELKEASEKSGVPLQSPRKTTRVIRLRLSGLDASLA 133
Lmo FGMTETISFSEGMPEERLKRKYKQMCRTKTPAFVISRNLV--PKELVAAAKEADIPVLRSLKTRLSSVYITNLESRLA 133
Sau LGTTELSFYNNLDPKDRACRMRKLCRPEPAIIVTRGLQP--PEELVEAAKELNPLIVAKDATSLMSRLTTFLEHALA 130
Sep LGTTELSFYNNLPEDEKGRMRKLCRPEPAIIVTRGLEP--PEELIQASQETHPIIVAKDATSLMSRLTTFLEHELA 130
Sxy LGTTELSFYNNLPEDEKGRMRKLCRPEPAIIVTRGLEP--PEELIEAAKEHEPPLITISKIATQLMSRLTTFLEHELA 130
Smu LGMKEWYLTQMTSHNRYSVLKEMFQETPAIIVARDLTI--PEEMLLAAKEEGIAVLQSHVPTSRLSGEMSWYLDSCLA 132
Sbo LGMKEWYLTQMTSHNRYSVLKEMFQETPAIIVARNLAI--PEEMISAAKEGIAIILQSHVPTSRLSGEMSWYLDSCLA 132
Sag VGMKEWYVLMAMTGNHRYQVLRMFQKETPAIIVARDLEI--PEEMVEAAKDTGIAIILQSKAPTSLRSGEVSWYLDSCLA 132
Spy FGMKEWYLTQMTSHNRYSVLKEMFKDDTPAVVSRNLAI--PKEMVQAAKEEGISLSSRVSTRLAGEMSWYLDASLA 152
Ssl VGMKEWYVLTQMTSHNRYSVLKEMFQETPAIIVARGLDI--PEEMVRAAKENGVAVLQGRNGTSSLSGEMSWYLDSCLA 132
Spn LGMKEWYVLTQMTSHNRYSVLKEMFQETPAIIVARGLVV--PEEMKAAKEGIAIILQSHVPTSRLSGELSSYLDSCLA 133
Lla FGMKEWYVMTVVGDNRYDLLKVMMAKETPVVIVARNLEI--PSEMVAAKKSDIVLQSRATSRLSGELSSYLDSCLA 132
Lga LGRTETISYARLDHDLRERVFNKMATPETPCFIVSRGLEP--PSEMLEAAKEKIPVFSNMMATLHSSVITQFLDEKLA 135
Lde LGRTETISYARLDHDLRERVFNKMATPETPCFIVSRGLEP--PSEMLEAAKEKIPVFSNMMATLHSSVITQFLDEKLA 135
Lbr LGITETISFAKMSHKEKLLNVMRMCQETPAFVISTQLDP--PEELIQSAAEAGIPILGTKLTTRVLSNMTNFLEKLA 133
Lpl LGKTEIAYSKNMSHDERLMIFRKMQLTTPAFVISTGLPV--PEELVQAGEENGVPILGKMTSSRLLSNMTNFLEKLA 134
Lca FGRTEISYFARNMSDEERLLIKRMATEDTPAFVSRGLEA--PAEMITAAATAHIPVLSRILPTLRLSSLTVEYLDSCLA 134
Efa FGSKEITFAERMMPERLLVMRRLCAKDTPAFVSRGLEI--PEELITAAKENGVSVLRSPITSRLLGELSSYLDGRLA 134
Efam FGSKEISFAERMPEERLLIMRRLCSEDMPAFVSRGLEA--PEEMIQAAENGGIAVLRSPITSRLLGELSSYLDGRLA 134
Lme LGITETISFSEMSHDELLVFRMADEKTPAFVISTGLPI--SDELNQAADAEAHIPILSSTLTSRLLSNMTYVYLGELA 134
Ooe YGVNETEYAKTMTHEHKTIVFKMASSETPAFVISTNLKI--PEELIEAAKADAGIPVLTSSLTSRLLSNMTYVYLAQLS 135
Tte MKKVETTFVEQLPDEVLAERADKFFAPIPCLIVTRDLNI--RQETIEAAKHDYRLLRTEKASTKFINRLINVLDEKLA 132
Eac IKGGEHDYFGTLDRAATRLRRLKLEKLSYEIPVLVARGLDF--SSDINMAKKYNRIRIIRSQMSTKFKINKASVYLSKLA 135
Cth IGVETISYLAQLTSEERYSLDEFFKCFPCMVVARGLEV--FPEMLVESRKYGIPFRTKETTTRVLSALISLVNLELA 140
Cac IGAKEWYVFLNAMPPEIREKRIRKYFQFETPCIVLARGLKP--QKELLDCSKEYNRWLLRSKQTRFINKIMNVLDKLA 130
Ctet IKGTEWYVFLDVMSPERLKRKRVKFFQFETPCVITRNKLP--HKEVLENSRKYNRWLLRNTSNISRTFISKLMNVLDKLA 130
Cpe1 IGAKEWYVFLDVMSPERLKRKRVKFFQFETPCVITRNKLP--HKEVLENSRKYNRWLLRNTSNISRTFISKLMNVLDKLA 130
Oih2 LGKKEIYVYQRLSEENRKRQMGELILLEPPFLVVDGVPD--PPDLRLCTRSTPLFTSPVSSAAVIDHLRLVLSRISA 140
Rso LGKPEILYVYQRLDDEPRKRGKMGELILLEPPFLVVDGMEP--PPDLRLCTRSTPLFTSPVSSAAVIDHLRLVLSRISA 140
Bfu LCDGAEIAYYKQRTDEDRSRHMAELIGLEPPFLVVDGVPD--PPDLRLCTRSTPLFTSPVSSAAVIDHLRLVLSRISA 140
Bpe FQGEFLAYYTRFDLRRRHHMDELLIGGVPAILLADGLTP--PQDLIDQCAHQHVPVLRVAAAQLIDLRLVYLGKLA 132
Cvi LGLAEVDYLNKLEQSAAKTALDQLFHKSMSVVMVANGQPV--PRLLRDYCHSHNVPLMCSTLESPLYLMDVLRVYLRALA 105
Nme VGLAESEYLNRLSESGETGQYQGLDFDLSMSLVIVANGLPV--SPGLRDYCHKNIDPLLTSKLESPLYLMDVLRVYLRQRTLA 135
Neu LNQTSVNYLDQDDVSLKRLNQLAKSQAACLIVADDAP--PNAIRQFVNEQSVPLIQSAAVASELIIWRLQSVLARMLA 136
Xca1 LGTEELAWLDSLDARQWETIEKIIQVQPLALAIKNSQSC--PEDLRAAADESNPLWISPKRGHELLNHLSYHLARTLA 137
Xax1 LGTEELAWLDSLDARQWETIEKIIQVQPLALAIKNSQSC--PEDLRAAADESNPLWISPKRGHELLNHLSYHLARTLA 137
Xfa LGTEELTWLDSLEPNKRKETIEKIIQVQPLALAIKNSQSC--PEDMRTAADNSQIPLWVSPKRGHELLNHLSYHLARILA 137
Cbu -----MSLHQSPGETPGP 13
Ctep LGNTEIRYLNHLSDERKTAFAFNVSRMPCCIIILSNKLD--QELVDMATGAGIPVFIIRCSSTKIIYITDFLDEEFS 147
Mma ----- 130
Rru1 QGGRGGGRQPPRPKKTAKKTPAEQTPAKQSDHHSRSLRRCRRDLSLPQYSPGIFSKSRPLTPGLPSSILGDMDK 130
Ccr -----
Nar1 -----
Bme -----MTPEE 5
Mlo1 -----MPDPVA 6
Sme -----MNA 3
Atu -----MNA 3
Rsp1 -----MTGA 4
Bja -----MSD 3
Mlo2 IAIGTIDMPKPS---EAAIIFRFEPDROYLAWHAVGAFILSDADRIDIEPAPG--VDDALLAFPLLGPVMAALLHQRG 129
Rsp2 TVR-RCALPELPG---EGGFRTRFAPERAELEWQTVGTRFVPG-IVTASPHAG--VSEDLVAYPLLGSVLALALEQLG 310
Rru3 ILIRVAVSPLDGQVFSR-RIRFIEATLCDFDVEDVARYRVDGGLHVTIEAARGIAADAPEIRLFFFTVLAFLCFRRG 126
Rru4 VTIAFGRYVFSVASPGMN--WHVVGGRFRFTVASVGSYRISRGVITIDFQAGVVASA--VQYLLCTAFVVLCHQRG 130
Rru7 ITIRHAASFPPSPPLLFESPLVGVFAEGAIVLRINPGLGFLIEGGARIVDATA--QGEAIEAIFLFGQCLGFLALQRR 110
Rru2 ITLRGPPVPPPVLRLDRDGIQVADGHTVIDPNCVRIGLTGGRDIMVDPAPG--ASWPEIQWLLGPGGLGVICHQRG 111
Xax3 VVIEEGEVPDRDLDPVSVLWVSGRDSVLLQVQVRIHVHAGRAMRVQRNL--RHDESWRFLFGSALGYLCLQRS 116
Xca2 LDVVVARAPRLVPAEPPVVRTHAAAGLLCGVMDECNVLMVSVAEARRAMVSSDMLMHAYHLRYELIEFAVFLAARGMS 164
Xax2 LDLLPRAPGRDAEPPVVRTHAGGGLLCGIMDANCYMLMSVQRRAMLVSEDMLAHAYHVRYELIEFAVFLAARGMS 163
Mka -----M 1
Rru5 LTLRRCWVPRDLPDVAVWSPFVEITAADGAVLIRIPGILAFIRDGRHVTLDQDSD--AATGVIEEFLFSVAGAVLHQRG 141
Sav DLAALLASVPTAVAKARLLLRDSTGTTIYAVSPDEQLAYRSEQLGHTVITISGHAPQFVALAASRIAREMIRAALLRD 143
Rru6 DGADDADIVTLLGPPAAAPETGPGHVPVRRADERTLLSLPGIGRFHIEGCDRVGIEAAEGADPVLLGLLGGFVLAAL 142
Nar2 ERERMVTFGPVPEAIENSVNEEDIFVISDEEFLFTSLDHRVHYRRGAGLTVQLPPAGLDSYELFLWGTVFGAVAWLN 108
Cpe2 ENKVDIKIKKDIIPKDVIEKIPSVSWFKYDVSMTVFTVKNISFYIYDGNIVVQPSNENADNQIKTFLGTGTFGMILLQ 108
ruler250.....260.....270.....280.....290.....300.....310.....320



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Mge	T-VQKLHG-VLLEIFG	--GVVFLEGRSGIGKSEALDLINKN	----	HLIGDDAIEIYRLGNRLF	----	RAQAL	196
Mpn	T-VAQIHG-VLLEVFG	--GVVLLTGRSGIGKSEALDLINKN	----	HLFVGDDAIEIYRLGNRLF	----	RAQEV	196
Mga	K-YTIHHG-VLIEVYG	--EGVLLIGESGIGKSEVAMELRKN	----	FLFVADDAISIAIRIDRLIG	----	RPTET	203
Mpe	K-KEYLHG-NLLELFG	--LGVLLMGESGLGKSEISIELIKHG	----	BMFIADDAIVCSNVFNKIIG	----	RAPKR	191
Uhr	H-QSLVHG-TLLSVFG	--IGVILMGESGVGKSELAIELVKKG	----	HIFVGDAILVNRIIGNLYG	----	RAEDS	198
Mpu	K-KVQVHG-TLVSVFG	--MGILLVGSGLGKSEAAELVQKG	----	HVLISSDAVLVSHYGNKYFG	----	KAPYI	201
Fnu2_C	I-EEVEYDYSLMEIHG	--GVGLMTGYSNARKG-VMIELIERG	----	HRMVTDKNLIIRRVGENDLVGVNAQKKEKL	----		203
Fnu2_C	E-TISVHG-VLVELFG	--FGVLLTGRSGIGKSEALELIHRG	----	HRLIADDMVKFYRDYQGDVVG	----	KSAAE	203
Tde	F-RISLHG-VWVEVFG	--LGILIMGS SGV GKSEALELIERG	----	HRLVADDVVEISCSINGNTLVGR	----	GANKI	206
Tpa	F-TIALHG-VLVEVYG	--VGILISGDSGVGKSEALELIERG	----	HRLVADDLVEISCVNGNSLIGR	----	GVHKS	196
Lint	F-RTMRHG-VLIEVFG	--IGILLISGDSGVGKSEALELIERG	----	HRLVADDMVEIRRLSESYLIG	----	TCSDL	201
Gme	F-TTHIHG-VLVDVVG	--VGVLLLGKSGIGKSEALDLVIRG	----	HRLVADDVVFVKKKMPAALVG	----	QAAEA	208
Bce	F-TTAVHG-VLVDIYG	--GVGLITGDSGVGKSEALELVKRG	----	HRLVADDSVEIRQEDEDMLVG	----	SSFDL	196
Bsu	F-TTAVHG-VLVDIYG	--GVGLITGDSGVGKSEALELVKRG	----	HRLVADDVVEIRQEDQDTLVG	----	NAPEL	196
Bha	F-TTAVHG-VLVDIYG	--IGVLLITGDSGVGKSEALDLVRRG	----	HRLVADDSVEIRREHEDTLVG	----	RSPEL	196
Oih1	F-FTAIHG-VLVDIYG	--GVGLITGDSGVGKSEALELVKRG	----	HRLVADDNVEIRQEDYDSLIG	----	NAPPL	197
Lmo	F-VISMHG-VLVDIYG	--LGVLITGDSGVGKSEALELVKRG	----	HRLVADDNVEIRQEDMTLIG	----	SSPAI	197
Sau	K-TTSLHG-VLVDVYG	--GVGLITGDSGIGKSEALELVKRG	----	HRLVADDNVEIRQINKDELIG	----	KPPKL	194
Sep	K-TTSLHG-VLVDVYG	--GVGLITGDSGIGKSEALELVKRG	----	HRLVADDNVEIKETFKDELVG	----	KPPKL	194
Sxy	R-TTSLHG-VLVDVYG	--GVGLITGDSGIGKSEALELIKRG	----	HRLVADDNVEIREISKDELIG	----	RAPKL	194
Smu	E-RTSVHG-VLMDIYG	--MGVLIQGDSGIGKSETGLELVKRG	----	HRLVADDRVDVFAKDEETLWG	----	EPAEI	196
Sbo	E-RTSVHG-VLMDIYG	--MGVLIQGDSGIGKSETGLELVKRG	----	HRLVADDRVDVFAKDEETLWG	----	EPAEI	196
Sag	E-RTSVHG-VLMDIYG	--MGVLIQGDSGIGKSETGLELVKRG	----	HRLVADDRVDVYAKDEETLWG	----	EPAEI	196
Spy	E-RTSVHG-VLMDIYG	--MGVLIQGDSGIGKSETGLELVKRG	----	HRLVADDRVDVYAKDEETLWG	----	EPAEI	216
Ssl	E-RTSVHG-VLMDIYG	--MGVLIQGDSGIGKSETGLELVKRG	----	HRLVADDRVDVYAKDEETLWG	----	EPAEI	196
Spn	E-RTSVHG-VLMDIYG	--MGVLIQGDSGIGKSETGLELVKRG	----	HRLVADDRVDIFAKDEITLWG	----	EPAEI	197
Lla	E-RTTVHG-VLMDIFG	--GVGLIQGASGIGKSETGLELVKRG	----	HRLVADDRVDVFORDAFTLSG	----	EPAEI	196
Lga	F-RKSIHG-VLVEIYG	--MGVLIIGNSGVGKSEALDLVRRG	----	HRLIADDRVDVYQKDDKTIVG	----	EAPKI	199
Lde	E-RSSVHG-VLVEVFG	--MGVLLIQGDSGVGKSEALALVQHG	----	HRLIADDRVDVYQRDHETVVG	----	EAPRI	199
Lbr	E-RQSVHG-VLVDIYG	--GVGLITGDSGVGKSEALELVKRG	----	HRLIADDRVDVYQDEQTLVG	----	AAPAI	197
Lpl	E-RQSVHG-VLVDIYG	--GVGLITGDSGVGKSEALELVKRG	----	HRLIADDRVDVYQDEQTLVG	----	EAPAI	198
Lca	E-RRSMHG-VLVDIYG	--LGVLITGDSGVGKSEALELVQKG	----	HRLIADDRVDVYQDEQTLVG	----	AAPPI	198
Efa	V-RTSVHG-VLVDVYG	--LGVLITGDSGIGKSEALELIKRG	----	HRLIADDRVDVYQDELTIVG	----	EPPKI	198
Efam	F-RTSVHG-VLVDVYG	--LGVLITGDSGIGKSEALELIKRG	----	HRLIADDRVDVYQDELTIVG	----	EPPKI	198
Lme	F-RKNVHG-VLIDVHG	--LGVLITGDAGIGKTESALELIQCGK	----	ARLVADDRVDIYQDEERLIG	----	EPNGV	199
Ooe	E-RKSVHG-VLIDVHG	--IGVLLITGDPGIGKTEAAELIQCGK	----	ARLVADDRVDIYAEDEQRLVG	----	APPEV	200
Tte	F-QTIHG-VLVDVYG	--IGVLLIGESGIGKSEALELVKRG	----	HRLVADDAVEIRKIGEDKIQG	----	SAPET	196
Eac	F-SKTIVHG-VLVDIYG	--IGVLLMGESGVGKSEALELVKRG	----	HRLVADDAVEIRRIEDDMLVG	----	EAPDI	199
Cth	E-RTREHG-VLVEVFG	--EGVLLIGESGVGKSEALELVKRG	----	HRLVADDVVEIRRVSEKTLFG	----	TAPDE	204
Cac	F-ETRIHG-VLVDIYG	--LGILITGDSGIGKSEALELIKRG	----	HRLVADDAVDIKEIES-VLVG	----	KSPYI	193
Ctet	F-ETRLHG-VLVDVYG	--IGVLLITGDSGIGKSEALELIKRG	----	HRLVADDAVDIKEIEG-KLIG	----	SSPYV	193
Cpel	F-ETRLHG-VLVDVYG	--IGVLLITGDSGIGKSEALELIKRG	----	HRLVADDAVDIKEIDG-DLIG	----	RSPEI	193
Oih2	F-EIAVHG-VCMNVLG	--IGVLLIRGDSGVGKSELAAITLLGRG	----	HRLVADDVIVLKRRLSHKTLIG	----	THNDK	196
Rso	F-RVTMHG-VFLDILG	--MGVLLMGDSGLGKSELGLLEISRG	----	HGLVADDAVDFVRLGPDFIEG	----	RCPPPL	204
Rme	F-RVTMHG-VFLDILG	--MGVLLMGDSGLGKSELGLLEISRG	----	HGLVADDAVDFVRLGPDFIEG	----	RCPPPL	204
Bfu	F-RATLHG-VFLDILG	--MGVLLITGDSGLGKSELGLLEISRG	----	HGLVADDAVDFVRLGPDFIEG	----	RCPPPL	204
Bpe	F-TTIVHG-VFLDVLG	--LGVLLITGDSGLGKSELALQLISRG	----	HGLVADDAVELSRTAPGVIEG	----	HCPQL	196
Cvi	V-STVLHG-VFLDVFE	--IGVLLMGDSAMGKSELALQLISRG	----	HGMVADDAVELYRIGPDTLEG	----	RCPPPL	169
Nme	A-SSVHG-VFLDVFE	--IGVLLITGDSGLGKSELALQLISRG	----	HSLIADDAVELFRIQPETLEG	----	RCSPM	199
Neu	F-AITRHG-VLLDVVG	--MGVLLITGDSGVGKSELALQLISRG	----	HGLVADDDVVELHRIQPETLEG	----	QCPPPL	200
Xca1	F-RVTLHG-VFMEIYS	--IGVLLITGAGSGKSELALQLISRG	----	HRLVADDAPEFTQIAPDVLDG	----	TCPEL	201
Xax1	F-RVTLHG-VFMEIYS	--IGVLLITGAGSGKSELALQLISRG	----	HRLVADDAPEFTQIAPDVLDG	----	TCPEL	201
Xfa	F-RATLHG-VFMEIYS	--IGVLLITGAGSGKSELALQLISRG	----	HRLVADDAPEFTQIAPDVLDG	----	TCPEI	201
Cbu	L-KQTWHA-NFLVIDK	--MGVLLITGAGNIGKSELALQLIDRG	----	HQLVCDVDVLDLQEN-NQLIG	----	SCPSV	76
Ctep	L-YQQYHG-NFLDVVG	--GVGLITGDSGLGKSEVALDLIERG	----	HGLVADDDVVKRKGKTKLVAS	----	RNNII	212
Mma	--MTLVHGTCVAIDGR	--GVLLRGPSSGGKSDLALRLIDGG	----	AVLVADDQTHLREGNALIAE	----	PPAET	62
Rru1	F-PPTVHGTAIARDGW	--AVLLRGPSSGKSDLALRLMIDRG	----	AVLVGDDQLIVLAGPAGPALA	----	PPDP	193
Ccr	--MIRHGGLIALRHQGLWRG	--ALFMDKDGAGKSTTASALIRAG	----	FRLVADDRVVFPAAGRLVGR	----	APET	65
Nar1	M-SVVRQAGCVAIGGR	--GLLIEGAPGTGKSELALALIDRG	----	ATLVGDDGVLRVQGGRLIAA	----	PHPH	63
Bme	E-RSGLHATTLQLLGR	--GVMMIGRSGAGKTEALALTLIERAASRREE	----	AVLVADDRVTLHREGDRLIAE	----	VPTA	74
Mlo1	Q-PENIHGTAILIGER	--GVLLITGDSGAGKTEALALTLIDHCRARGLF	----	SRLIGDDRLAAARAGRLVCR	----	VPAP	75
Sme	F-FVNVHGTAIVLGT	--GILLITGDSGKSELALALSCLSEVHRHRGF	----	AALVADDRVDTLENGRIVAR	----	CPAA	72
Atu	E-RFNLHATAIVVDGT	--GLLITGDSGKSELAFSLTEAERCGLP	----	AALVADDDQIFVYRDGETITAE	----	RPEA	72
Rsp1	D-RTILHASCVALDGR	--GLLILGDSGKSELALALMALG	----	ADLVADDRVTEIEGQGDVAR	----	CPAA	67
Bja	G-GPSVHASAVKVCNL	--AVLIRGDSGKSKRLAFDLIMAGRAGVVER	----	AVLVGDDRVHLATVQDEIEVR	----	PAPP	73
Mlo2	L-LVLHASAIAAAGKG	--AIFMDKDGAGKSTTASALIRAG	----	HELLTDDVVALDLARPDPAPMIVAGFPQIKL	----		196
Rsp2	L-FTIHASAVSVGGHG	--VMMGDKGAGKSTTATAMIRAG	----	HPLIADDDIVAVDEG	----	FRLRPGFPQVKL	373
Rru3	L-IFLHASAVALDGRA	--LLLSGDSGKSTLAAALLARG	----	YPLLSDDLCALDVSCDPEMILPCTAHLKL	----		193
Rru4	L-LPLHASCVAINGRA	--VAIAGASGAGKSTLAAALVRLG	----	YPLLGDVVCVIDASEINAPHVLPAIPRLKL	----		197
Rru7	Q-PALRAASVVRDGRA	--VVLAGAAGVGSSTLAAALMAKG	----	WGLLADEVTLIDP	----	RTLLIPPAPGRIKL	174
Rru2	V-LPLHACAIRTGKGG	--LAIVGNSGAGKSTTATALVQKG	----	HRLIGDDVVLVDPDTG	----	LAQPCFPMVKL	175
Xax3	L-FPLHACALRTGTQT	--VAFAGHSAGKSTLAAALLLRG	----	HGLLSDDLVIRLDSAGAMVLPAPFRLKL	----		183
Xca2	L-VPLHGACVGCWGHG	--ALLLGSAGKSTLALHSLLRG	----	LQFVAEDGVFVEPHSLVAGVANFLHLRPA	----		231
Xax2	L-VPLHGACVGRGRS	--VLLLGSAGKSTLALHSLLRG	----	LDFVAEDGVFVAPNSLLTGVANFLHLRAE	----		230
Mka	E-RVVVHG-TLMDVFG	--GVGLITGDSGVGKSEALELIKRG	----	HRLVDDDAVIECDDSYEYVFG	----	RPPEN	66
Rru5	V-LPLHASCVMIGDVA	--VAMAGVSRGKSTLALGLSMRG	----	HEVTVDDVCPVVFHETKALVVPGP	----	PRLRL	207
Sav	G-WTLLHASAVVRDGR	--ALLAFDGKAGKSTLALVLRG	----	AQLLADRVRVFKRIGADLRVLPWF	----	SAAAI	210
Rru6	L-RQRGLPLDCAALGVEGGALLIVGASGLGKSLAATLARG	----	WPLVADGVLVAFTAPQARLLR	----	GAPRI	211	
Nar2	G-LVPLHASAVDVGGR	--IVAFTADSGGKSTLAAAGLAGLG	----	LPHVCDLTLVSVDPDGIHALPAKPLKLV	----		176
Cpe2	RNKVAIHGGAILIGEN	--AIIITGDSGAGKSTLAINAFRQYK	----	YQFMADDVCSLIELQDEIFIEP	----	AVPQQKI	176
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CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT

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Mga NKHFIEVRGLGILNVTKMGYIEIKKSSAHISIVVEL---INIQNN---QPYNFERLQKQTRYKVIENIKVPHVVLPIIS 275
Mpe FFGFLEVRGLGILINASRVFGEIKVKESQINVIIEI---VEFD---KVHTFERLGKDLQYKEILGVKIPYVLIPIIT 262
Uur IKDFIEIRGLGIMNFSRSFGIERMIESTKIEIVIEL---IKPAKH---EKIKFERFGREIQHKEFLEKIAHYIPIVI 270
Mpu TKNLLIEVRGLGILIDLSVGLKSVLPCEINPVVEL---KDYEQ---NKSNDRLGNKVLKYQIGEWKIPKIEIPIR 272
Fnu_N GHFYLEIDIKDGVVDVTDHFGVKAIRIEKKNILNLIY---EENWE---KKFVDRGLDVEYQDFVGEKIQKVIIPVR 273
Fnu2_C LFFMEIRGLGVIDIKTLVGLSARLSKRLDMIIEI---QAVDN---SDYMSAPSTHLYEDVLGKPIKRIEIVS 272
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Lint LRHMEIRGLGILINIKDFIGISVRSKRSKISLVNINL---EENWE---GKD-FDRGTLENTEELLGVPILRIPVVR 271
Gme IQYHIEIRGLGVLNINKNLFGVSSIREKKIEMVIEL---VEWD---QQE-YDRGLDDEVYITLDELEPYIKIPVR 278
Bce IEHLLIEIRGLGIINVTMLFGAGAVRNKRIITLVINL---EIWDQ---KKN-YDRGLDDEEKMIIDDELTKITLIPVR 266
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Sau IEHLLIEIRGLGIINVTMLFGAGSILTEKRIRLNINL---ENWNK---QKL-YDRVGLNEETLSILDDELTKITLIPVR 264
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Cth IRHFIEIRGVGIIIDVMSLYGAGAVKPFENINLVLIQL---EYWDQ---KKD-YERLGLVDDYKAVELINIPCLTIPVR 274
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Ctet TSGMLEVRGLGIIIDVPSLYGLSSVLDTKTIQVVIHL---EQWKK---DQD-YDRLGIDEINRDLINVPVKITLIPR 263
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Bfu LQNLLEVRGLGLLDIKTIFGETAVRRMKIKLIVQL---VRR---PDGEFQRLPLESQTVDVGLGLPIKSVMTIQVA 273
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Rru1 LRGLIEVRGLGLVEMPAADVPVPLALVVDLVPPGPI---ERLPPPA---QADIGGASVALVRLDPFEASAVKLDLALA 266
Ccr LAGLIEVRGLGVVTAANVFAETALVIRCVDPGRV---ERLPEPR---FERIAGVDVVPFDLWPPPEAAPAKIRMMQ 138
Nar1 IAGKLEVRNVGIVDLP-VSAPVPSLLVRLVDVAPR---FVG-TPD---VMEICGIALPLVRLWPESVPLHLRAEMALS 134
Bme LAGGVEIRGAGLFRIP-YRVATPLDLVVLLVNGDEA---ERYPGKE---RWIFEEVS--LPRLLPALSANQDSNALS 144
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Sme IRGLIEIRGSGIAEVD-TVSGCVLDWAIMVRAFPD---PRLPPE---EELQLEIQRNPLRLPLVEGPLSPVDALAA 143
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Rsp1 IAGLIEARGLGILRAIPALIEARVVI-----LAVEL---GRSET-----ERLP--HFHEIQVLRPLDLVLGQEG 125
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Rru3 WCDAAARLGIAIDGM-TPVRRHLDKFRIPVRSASDA---PLGP---GTIIRLKRVMTRAEQVTRPPLGAE--ALCYD 261
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Rru7 WKDSATHLGLAAL-PAVRPGWNGHAPYGGHLAP---APVP---LAAIILIEQAYTAKTAGIDKIAPREALAAALND 245
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Nar2 DDALVLEALEARPVSPMGKKNASAVKALLALPLTDLVFIEKG---ERIEIPVPGAAKFLLPALYRGFVHVAR 251
Cpe2 CRDAMEKMGVIMDDFELIDEDRKYVIFTHESFVKERKQLQAVFEIQPYDGEVVKIEEVSQGEKMKIILRNIVRIEIIIS 256
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Mpn	PGRNSEIIESA	---	VIDFKLK-HSGYNSALDFIENQKAILKRRKDES	---	312	
Mga	SGRRSSEIIESA	---	VIDLKLKRDWQYNSGDDFVERYYKMTKEE	---	317	
Mpe	PGKISDMIEVI	---	VAKLKLK-LSGYNSFKEMEEKSMEDDDE	---	301	
Uur	EGRSISDIIEA	---	ITDYKLLK-TSGYNSAEFFLQINKKGI	---	308	
Mpu	QGRSVASLIEAS	---	ANMFLSK-LNGHDVLAMIQERSLNDE	---	309	
Fnu_N	KGRNLAVIIEA	---	ALTFRLR-RMGHNTPLEFLTQSQETIEKKKKERE	---	319	
Fnu2_C	SGRNAAMVEVM	---	VMDYMSGLLGQK	---	296	
Tde	PGRNVPILIEA	---	AKNERLK-SMGYFSAREFSRNVLRIETDSARAFYYTDDDTY	---	329	
Tpa	PGRNIPILIEA	---	AMNERLK-RMGYFSAKEFNQSVLKLMEQNAHAAPYYRPDDTY	---	319	
Lint	PGRNIPILIEA	---	AMNQLRK-KLGKNAAQEFNQKLSQYLQQKVERNPTQNG	---	321	
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Efam	TGRNVAVIIEVA	---	AMNFRAR-TMGFDATKTFEERLSRLIEENSQND	---	312	
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Ooe	SGRN TASVIDAA	---	ALKYRTE-RMGFDALSTLEQRQTKLTKENEIHDQANT	---	319	
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Cac	PGRN VAVIIEAA	---	AANYRYN-LSSKISPVDTINKRIEESTNYD	---	304	
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Xfa	PGRN LAVLTEAA	---	TRLHILR-TKGIDPATMFIARHSNLLERRPP	---	316	
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Mma	ASTRDIMPL	---	---	---	143	
Rru1	VARGDSKLAC	---	---	---	276	
Ccr	SLGVQS	---	---	---	144	
Nar1	VHGLTTC	---	---	---	141	
Bme	AIEAFLFFERWF	---	SAE	---	159	
Mlo1	RLSITPFL	---	---	---	153	
Sme	LLPOI	---	---	---	148	
Atu	LAONLFKINVK	---	---	---	154	
Rsp1	RHFPSALLRLR	---	SGRVA	---	142	
Bja	YSPLPLVVAAL	---	TKSSSSVNPSCDCLKNGNHNMPILATE	---	174	
Mlo2	FSYVTRFGRAALSGDFAAHLRQC	SAIANHVGVFRLVPTGLDRIGEAVALVESDLAAGDLAAGR	RRR	---	333	
Rsp2	FAYVTRFGAEALNCAAGARHLRQ	AAATAASGVLRHVIVPHALDRLEPVVALIERDAGAAA	---	---	505	
Rru3	LIHRFRLGIALG	---	YQSMLTALAPLVRSAPIIQLNRRDDL	GALPDLADHVIRLARDERRD	---	320
Rru4	AVYRRKMGAMG	---	LLPQIFATMTVIGALVFGHRLLR	CGDLSGLDALARSVA--ARQEGRC	---	330
Rru7	QLHGGTFAGALA	---	ARPACFDLLITLVGGVVPVQLSRPHWGMLTAPLVELLTAEMAR	---	300	
Rru2	MTYRVYLADALH	---	GRRHVLSAATRLAAHVVPVWELVRTADFADLAEMLDMLEGLAGA	---	301	
Xax3	YLARPQAAVRMG	---	LHAATFAHAAAIARQVVPVWRLRPRRFDALDITVDLIEAHVGA	---	306	
Xca2	ADQPYAAGQPGW	---	SHFIAQVQQRGVYRMQRGAHPDAAVDALLQLLHRAASSLPGA	---	362	
Xax2	QDQPYAAGQPGW	---	ORFVEVQVRIGMFTLHRGTHPQASVDALLQLLQ	---	352	
Mka	PHHPDSMRPDEPV	STPSEEEKVVKWKERDGRVPHLDVVPGRDTATLIETVALQESLRRR	---	---	208	
Rru5	LCRRLLDRRVGLRQDLVRLAALVPLYQMSR	PDGFPVPSLLADLIAS	TVVAKGRDAADD	---	340	
Sav	FPRIDPAAVPALVDGERTLGEDDFMSGAT	EDRYDHFGLAHGIDGGSDLARATVAEHLAALPHHVVVLGHDVGANADFL	---	---	370	
Rru6	GDRAGAALMADLAGLASLTPCWLLP	GETLDTLAATADVLNRSRAAPLQTRTPAE	---	---	347	
Nar2	GDRAVHEQFILR	---	FCSKVRFWLRRRPFPLRFGADLQSKAMLLDDMKCK	---	300	
Cpe2	HGIPPAVYFKKVINIAKNTLVFR	IKRPRGQFVDRQIELTEKELMLKCNV	---	---	305	
ruler490.....500.....510.....520.....530.....540.....550.....560	---	---	---	---	



CLUSTAL X (1.81) MULTIPLE SEQUENCE ALIGNMENT

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Mge ----- 311
Mpn ----- 312
Mga ----- 317
Mpe ----- 301
Uur ----- 308
Mpu ----- 309
Fnu_N ----- 319
Fnu2_C ----- 296
Tde ----- 329
Tpa ----- 319
Lint ----- 321
Gme ----- 325
Bce ----- 309
Bsu ----- 310
Bha ----- 310
Oih1 ----- 310
Lmo ----- 312
Sau ----- 310
Sep ----- 310
Sxy ----- 314
Smu ----- 311
Sbo ----- 310
Sag ----- 311
Spy ----- 330
Ssl ----- 309
Spn ----- 312
Lla ----- 309
Lga ----- 319
Lde ----- 316
Lbr ----- 311
Lpl ----- 315
Lca ----- 319
Efa ----- 311
Efam ----- 312
Lme ----- 321
Ooe ----- 319
Tte ----- 305
Eac ----- 308
Cth ----- 318
Cac ----- 304
Ctet ----- 305
Cpel ----- 307
Oih2 ----- 306
Rso ----- 324
Rme ----- 323
Bfu ----- 322
Bpe ----- 308
Cvi ----- 288
Nme ----- 320
Neu ----- 323
Xca1 ----- 316
Xax1 ----- 316
Xfa ----- 316
Cbu ----- 192
Ctep ----- 342
Mma ----- 143
Rru1 ----- 276
Ccr ----- 144
Nar1 ----- 141
Bme ----- 159
Mlo1 ----- 153
Sme ----- 148
Atu ----- 154
Rsp1 ----- 142
Bja ----- 174
Mlo2 ----- 333
Rsp2 ----- 505
Rru3 ----- 320
Rru4 ----- 330
Rru7 ----- 300
Rru2 ----- 301
Xax3 ----- 306
Xca2 ----- 362
Xax2 ----- 352
Mka ----- 208
Rru5 ----- 340
Sav AKLS DSP 377
Rru6 ----- 347
Nar2 ----- 300
Cpe2 ----- 305
ruler .....
    
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