

CLUSTAL X (1.81.1-alpha) MULTIPLE SEQUENCE ALIGNMENT

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Mba1	-----FGAQQGSKP-----SGGLLVVAFISDPDD	24
Psp2	-----LSTGVITNEV-----TGSVLVVKPISDPDS	24
Ybe1	WLNNTGTARLQANVDDRG-----DLDGSQLDMLMPFYDTPS	36
Ype5	WLNQFGSAKQVNLDEKL-----SLKGSQLDVLLPLTDSPD	36
Eco14	WLNQFGTAKTQLSVVSDF-----SLKGSSLDVLLPFYNTPK	36
Sen3	WLNQFGTAKVNLGLDKD-----SLDNASLDLPLLYDDKK	36
Ymo1	WLGHTGKAQVKLQVDDKN-----DFSGSELHLFVPLYNQPE	36
Yen2	WLGHTGQAQVKLQTDKKN-----DFSGSEIDLFIPLYDQPE	36
Pas1	-----NDDVMQGSDFSKSGIADMGFAALQPETEKSAAGEVRANLPLSDGKLTSGSIDLFIPLYDGDG	61
Yfr1	WLGQYGNARVQLNSNS-----IGNADVLIPLTETQ-	30
Yfr5	WLSQFGHARVQLNSSG-----TGNADILLPLVESQ-	30
Yps7	WLSQFGTARVQLNINDDF-----HLDGSAADVLIPLYDNE-	35
Yfr2	WLSQFGTARVQMNVDNDF-----KLDGSAADVLIPLYDNO-	35
Yfr3	WLSQFGTARVQLNDNNL-----SLKGSADFMLLPLYDDQ-	35
Yps4	WLNQFGTARVQLNVSDDF-----KLDNSALDVLVPLKDS-	35
Yps2	WLNRFGTAAQVNLNFDKNF-----SLKESLDDWLPWYDSA-	35
Esa2	WLSHFGTAAQVTLDDVNG-----NWDNSAFDLFAPLYDNK-	35
Plu1	WLSQFGTAKINLVNDRHG-----RLDESSVDLVPFYDDKD	36
Eco1	WLOHYGTAEVNLQSGNN-----FDGSSLDLPLPFYDSE-	33
Pru1	WLNRFGSSQIHLEADKKF-----SLKNSQIDLLMPWYETE-	35
Pal3	WLNRFGSSQIKLEADKKF-----SLKNSQIDLLPLIYETE-	35
Eta1	WLNQFGTARVQLDADEHF-----SFKNSQFDLAPLYEQK-	35
Sg11	WLNQFGTARQLQDLDNKF-----SLKNSQLDILLIPLYEQP-	35
Eco26	WFENFGTAHIQLQVDKNE-----SLKNSQLELFPVFEED-	35
Pmi1	WLNQFGHARVLSADKNL-----TLKNSSAELLIPLYEQK-	35
Efe5	WLNQYGNARIKLVDDSF-----SLKDAEFDLIPWMDTK-	35
Eco20	WLGKYGTARVKNLVDDKF-----SLKDSLEMLYPIYDTP-	35
Eco25	WLSRFGTARITLGVDEDF-----SLKNSQFDLHPWYETP-	35
Eco15	WLNNTGTAXISLGVDEDF-----SLKNSQFDLHPWYDTP-	35
Eco6	WLSRFGTARVSLGVDEDF-----SLKSSSFEFLHPWYETP-	35
Efe2	WLSQFGTARVTLSADEHF-----TLKGSALDILLIPLYDTP-	35
Efe3	WLSQNGTVRVTLGLDEDF-----TLKGSADFLLIPWHDTP-	35
Pal2	WLSKAGNVKLNIDFDKKF-----SIKNSQFDLIPWYDQE-	35
Csu1	-----LRDFFPFGDRE-----YPFERTAIDWLPFYDSE-	29
Eco3	WLSPWGNASVDVKVDNEG-----HFTGSRGSWFVPLQDND-	35
Cko1	WLSPWGNASVLDLRIDNEG-----SFTGSRGGWFIPWQDNT-	35
Sen1	WLSANGSASVDVKVDNEG-----HFNRSRGSWFVPLQDKQ-	35
Eca1	WLSPWGNASVNRVDDNG-----TFNGSSGSWFIPWQDNN-	35
Esp2	WLSPWGNASVDLLVDEEG-----KFNSSGRWFIPWQDNN-	35
Esa3	LLSPWGNATVDLLVDEEG-----NFNSSGSLFIPWQDNN-	35
Kpn1	WLSPWGNANVDLLVDEEG-----KFTGSKGSWFVPLQDND-	35
Pan1	LLSPYGNAEFNLNVDMAG-----NFDGTGGNLFSPHADEN-	35
Eta2	LLSPYGRASVSLALSDDG-----SFNGTSAQLLTPWQDNY-	35
Spr1	LLSPYGNAKLSLVMSDQG-----DFSGSSGQLFSPLYDYN-	35
Yin1	LLGKFGKAQVNLAVDDKG-----SLKSSFSLFSWYEND-	35
Yin2	LLGKFGKAQVNLAVDDNG-----SLKSAFSLFSPWYEND-	35
Yfr4	LLGKFGQAQVSLAVDDHG-----DFSKSTFSLFIPWYEND-	35
Ymo2	LLGRFGQAQVNLVSMNKG-----NLNRSTASLFTPWYDSE-	35
Eco10	TLSPYGVKVRSNLSIGQGG-----DLDGSSIDYFVFWYDNO-	35
Eal1	ALSPYGVKVRSNLSIGQGG-----DLEGSSIDYFIPWYDQ-	35
Sty4	MSPYVKIRTSLSVGEQG-----DLDGSSLDYFVFWYDNE-	34
Eco16	VLSPYGSVRTLSLIGEGG-----DLDGSTFDYFVFWYDNO-	35
Ahy1	SASRYGSEQEVOYWRQQLATQFEENEANAFAASLLGAMGTARTRVTLDDDF-----NMVTAEADLLIPLAEEQ	67
Sen2	-----LIFRGGVNLDEGA-----KYRSSEFDMFIPVQETT	30
Efe4	-----AQFRGGITLEDAS-----KYRSAEADLLIPLYQST	30
Bpe1	GLPFLRNLOGGLSHDFES-----GRTSLQNLNTIDEVYRAG	35
Bav2	GLRFLRNLOGDLRHDNDN-----GRTSLELRTIDQVYRKG	35
Bbr1	ELPFLRRLQGGVNYDFSN-----KDLSLDLRTIDEVHRGE	35
Bpa2	GLPWLRRLLEGVNSYDFSG-----RDVAVDVRTIDALHLDQ	35
Bav1	GLPWLRRLDGGRLRYDLDP-----GRLSFLRITIDDLMVSE	35
Pma1	-----AQTSVNISGGTESDTSF-----SINSLMKLGEIAKDDQGD	35
Pma3	-----AQTNFINISGGESDTSF-----SINSLMKLGEIAKDEEGD	35
Pma5	-----AQTSLNIGGGTESDTSF-----SLNSLMKLGEIAKDDQGD	35
Pma4	-----AQTTVSINGTSNSETS-----SLDSLMKLREMATDDEGD	35
Ssp1	-----AQTTLGLDAATSSDLTG-----YLDSEFMRKTLIDGDDNEGD	35
Ssp2	-----SOTEFGVGFESDADMTY-----YLNSLISLAQLGSDDNGY	35
Plu2	-----TNAPS-----WVTSWDTVTPCPVYVSEN	23
Clal	-----SKSKEELVKNMASSVINTSANEIAKEFIDSLNTSNTDLSFN-----VNERSGFSGNAKALLIPVSEDN	64
Rba1	-----LSVGSDDTMGLDKNKSD-----TKTEAMTVYRLKETG	31
ruler	1.....10.....20.....30.....40.....50.....60.....70.....80	



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Table of sequence alignment with columns for sequence identifiers (e.g., Mba1, Psp2), amino acid sequences, and residue numbers (90-160). Includes a ruler at the bottom.



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	* *		* *							
Mba1	NANKYWATTKKTKG	----	NGLE	-----	ERALDGDIEAGVPLPYMNVATVFKNFQNDSEIS	145				
Psp2	LRANQYYGLSGWKSGL	----	NNIN	-----	EKALNGSDVELGMPPLPYLPNTNLYRSENWEG-AS	145				
Ybe1	LAANGYLRLSDWRDS	----	PDFS-SYS	-----	ERPATGFDLRAEALPSLPOLGGKLMVEQYFGNDV	155				
Ype5	LAANGYFVSGWKN	----	PDDL-KYD	-----	EKVANGFDLRSEAYLPTLPOLGGKLIYEQYFGDEV	155				
Eco14	LSANGYKRLSDWFQS	----	PTVT-DVD	-----	ERPADGWDIRAEGWLPAYPOLGGKLVYEQYFGNEV	156				
Sen3	LSANGYKRLSGWKDS	----	SEYE-DIQ	-----	ERVANGYDIRAEGYLPAPPOLGAQLVWEQYFGDDV	157				
Ymo1	LSANSYFRLTDWHQNS	----	TRLE-DVD	-----	ERAASGYDIRTEAYLPYPOLGGKLMVEQYFGNEV	156				
Yen2	LSANSYHRLGGWKN	----	TRLE-DVD	-----	ERAANGYDIRTEAYLPHYPOLGGKLMVEQYFGDEV	156				
Pas1	LSANGYFGLTDWYSS	----	SALD-GYA	-----	ERAANGYDIRAQWFPVYPOLSGKLFPEQYFGDDI	181				
Yfr1	FSANGYFRLTDWHQS	----	VLADME-DYN	-----	ERPANGFDVRAEALPSYPOLGGRLMVEKYFGKGV	152				
Yfr5	FSANGYFRLTDWHQS	----	VLSDME-DYN	-----	ERPANGFDVRAAYLPAYPOLGGSLMVEKYFGKGV	152				
Yps7	LSANNYFGLTDWHQS	----	RDFI-DYN	-----	ERPANGYDLRAEALPSYPOLGGKAMVEKYRGDDV	155				
Yfr2	LSANSYIGTSDWHQS	----	RDFA-DYN	-----	ERPANGYDVRAEALPSHPOLGGKLMVEKYRGEEV	155				
Yfr3	LSANSYLRLTDWHQS	----	RDFA-DYN	-----	ERPANGYDLRVEAYLPAYPOLGTNLKVEQYFGNEV	155				
Yps4	FSANTYFGLTGWHQS	----	RDFS-SYD	-----	ERPADGFDIRTEAYLPAYPOLGGKLMVEKYRGDEV	155				
Yps2	LAANGYFRLNGWHSS	----	RDFS-DYK	-----	ERPATGGDLRANAYLPALPOLGGKLMVEQYTGERV	155				
Esa2	LSANTYIGTSDWHNS	----	GDFD-NYN	-----	EKPADGFDVRAEGLPSFPOLGAKLMVEQYFGDNV	156				
Plu1	MSANAYFRLSDWHNA	----	RDLV-NYY	-----	ERPANGYDLIADMYLPSMPSLGAKIKVEQYFGDNV	156				
Eco1	SSVNGYFRMSGWHES	----	YNKK-DYD	-----	ERPANGFDIRENGYLPSPALGARLMVEQYFGDNV	153				
Pru1	LSANSYHRLSGWRSS	----	RDLA-DHS	-----	ARPSNGWDVRAEGLPSYPHIGGKLTVEQYFGDSV	155				
Pal3	LSANSYHRLSGWRNS	----	RDLA-DYS	-----	TRPANGYDLRAEGLPIYPHIGGKLTVEQYFGEEA	155				
Eta1	LSANGYLRLSDWNNS	----	SDFK-DIQ	-----	ERPANGYDIRAQWLPSPOLGGKLTVEQYFGGV	155				
Sgl1	IGANNYLRLTNWRDS	----	KDFA-DYQ	-----	ERPANGYDMSLEGVVPALPOLGGNLYVEQYFGKEV	155				
Eco26	LGANSYLRLSNWRNS	----	SNIV-DYE	-----	ERPANGYDLNFKSWLPSYPOLGGDIKVEKYFGDDV	155				
Pmi1	LSSNHYHRLSSWRAS	----	NNIL-DYS	-----	ERPANGYDIRTEGYFPAYPOLGTKLIPEQYFGKEV	155				
Efe5	FGANTYFGLSDWKN	----	RDLA-DYL	-----	ERPANGYDVSAGWLPAYPOLGASVQPEKYFGKNV	156				
Eco20	LSANGYIRASGWKKS	----	PDIE-DYQ	-----	ERPANGYDIRAEGYLPAPPOLGASLMVEQYFGDEV	156				
Eco15	LSSNGYLRLSNWRSA	----	PELDNDYE	-----	ARPANGYDVRAEGLPAWPHLGGKLVYEQYFGDEV	156				
Eco15	LSSNAYIGLTGWRSA	----	PELDNDFE	-----	ARPANGYDLRAEGLPAWPOLGGKLVYEQYFGDEV	156				
Eco6	LSGNGYLRLSNWRSA	----	PELDNDYE	-----	ARPANGYDLRAEGLPAWPOLGGKLVYEQYFGDEV	156				
Efe2	LGANGYLRLTGWRDA	----	PELDNDFE	-----	ARPANGYDVRAEGLPAYPOLGAKLMVEQYFGDEV	156				
Efe3	LGANGYLRLSGWRDA	----	PELDNDFE	-----	ARPANGYDVRAEGLPAYPOLGATLMVEQYFGDEV	156				
Pal2	LNANSYFGLTSWKS	----	SELNDFN	-----	AKPAHGWDIQVEGLPNYPHGGNLRVEQYFGDSV	156				
Csu1	FSMNGYGLSSPRHS	----	SLQPNYQ	-----	ESPAAGLDLFRLHYWLPFFPRLGGKIFVEQYFGKQV	150				
Eco3	LSANFYQPPAAWHEQ	----	TATQE	-----	QRMARGYDLTARMRPFYQHLNTSVSVEQYFGDRV	153				
Cko1	LSANYYQPPASWHEQ	----	TTATE	-----	QRMARGYDVTQAQMRPFYQHLNTSVSVEQYFGERV	153				
Sen1	LSANYYQPPADWQTH	----	TATLE	-----	QRMARGYDINAQMRPFYQHLNTSVSVEQYFGDSV	153				
Eca1	LSANYYQPPAGWRDD	----	SDVQE	-----	QRMARGYDVTAKAWLPWFHHLNTSVSVEQYFGDSV	153				
Esp2	LSANYYQPPASWRDS	----	SDVQE	-----	QRMARGYDVTAKAWLPWFHHLNTSVSVEQYFGDNV	153				
Esa3	LSANYYQPLGGWQHR	----	AGLLE	-----	QRMARGYDVTQAQALPFYQHLNTSVSVEQYFGDQV	153				
Kpn1	LSANYYHPLGDWQLRD	----	NQOQE	-----	QRMAAGYDVTQAQARLPFYQHLNTSVSVEQYFGDSV	154				
Pan1	FSANYYHPLSGWRNRG	----	SDSQ	-----	SRMARGYDITTSQYLPFYQHLNTSVSVEQYFGDEV	153				
Eta2	LSANYYHPLSGWRNR	----	NSSQ	-----	SRMARGYDITTRGYLPFYHQLGVTLSVEQYLGDR	153				
Spr1	FSANYYPLSALAQR	----	DNAQFL	-----	SRPASGYDITTSQYLPFYQHLNTSVSVEQYFGDEV	155				
Yin1	LATNYYHPLSGWKDSK	----	DFDDYL	-----	ERPARGYDVRAQGYLPAYPOLGASVVEQYFGDEV	155				
Yin2	LASNYYHPLSGWKDSK	----	DFDDYL	-----	ERPARGYDVHAQGYLPAYPOLGASVVEQYFGDEV	155				
Yfr4	LATNYYHPLSGWKDSK	----	DFDDYL	-----	ERPARGYDVRLQGYLPAYPOLGASVVEQYFGDEV	155				
Ymo2	FSANYYHPLSHWKDSE	----	DFDDYL	-----	ERPARGYDLRSQGYLPAYPOLGVSAVVEHYFGDEV	157				
Eco10	FSGNYHPLSDWKDSE	----	DFDFYE	-----	ERPARGYDIRAEALPAYPOLGGKLVFEQYFGNEV	155				
Eal1	FSGNYHPLSGWKNSE	----	DFDFYE	-----	ERPARGYDIRAEALPAYPOLGGKLVFEQYFGDEV	155				
Sty4	FSGNYHPLSDWKDSE	----	DFDFYE	-----	ERPARGYDIRMESWLPFYPOLGAKLVFEQYFGDEV	154				
Eco16	FSGNYHPLSDWKDSE	----	DFDFYE	-----	ERPARGYDVRAEGLPAWPOLGAKLVFEQYFGDEV	155				
Ahy1	LGANFYTPLSSWRDSP	----	RFEGME	-----	ERAARGYDVRLEAYLPAYPOLNSASLTAQYVGERV	188				
Sen2	FSGNYFPLTGWRTS	----	AAHFHD	-----	ERPARGYDLRTKGLPDPFWSGELTVEQYFGDKV	155				
Efe4	LGNWYFPLSDWKAS	----	KVQPLHD	-----	ERPATGYDVRLEKALPSLPNFGAELAPEQYFGDKV	155				
Bpe1	LYGNVYAPLSDWKGAK	----	RNNRRE	-----	EKPASGMDVGVYRPAFAPGLSLSATFRWNGAEV	156				
Bav2	FYGNVYAPMSGWTGAK	----	RDNRRE	-----	ERPASGMDLGMKSPGFAPGLSLKANYFRWNGAAV	156				
Bbr1	LYGNVYAPMSGWKA	----	RAERRE	-----	ERPASGMDVGVRLQPEALPLAIKQGYFRWNGAAV	156				
Bpa2	LYGNVYAPLSDWKA	----	RAERRE	-----	ERPAAGYDVGFTARPEAVQGLALNAQYFRWNGA	156				
Bav1	LYANVYAPLSDWKGAR	----	RDSRRE	-----	ERPAAGYDLGGQLS--SDAGLSLQAAVFRWNGAGI	154				
Pma1	FRNNWYMAITNEKDVIKGV	----	YQ	-----	ERVVPGWDLEVGYRLPNNPELAFFYIRGFNWDYK	163				
Pma3	FRNNWYISITDEKDVITKGV	----	SYK	-----	ERVVPGWDVLELGYRLPNNPELAFFVRGFNWDYKHT	163				
Pma5	LRNNWYMSITNEKDVITKGV	----	SYK	-----	ERVVPGWDVLELGYRLPNNPELAFFVRGFNWDYKNT	163				
Pma4	LRNNWYMSITEQKNVTVNGT	----	VYT	-----	ERVVPGWDVEAGYRFPNHPEMAVFKGFNWDYKNT	163				
Ssp1	LRNNWYINGADKNTINNID	----	YV	-----	ERVVPGWDVEVGYRIPSYPOLAIFVRGFNWDYQDH	162				
Ssp2	LRNNWYIAGTGIKRITTSGR	----	YDTTSLAAGTYDETTL	----	LERVVPGWDVALNRYLPSYPOLSLGIRGFRWDMRK	184				
Plu2	LNSNYHRLTDWKL	----	TG	----	VDNNE	-----	EKARGYDVELALAVPYVPSAHRVVKHCWNGIAS	145		
Cla1	NANVYQRLSSWIDS	----	YV	----	DFDK	----	YVQ	-----	ERPANGYDAKIKYAFPSLINVSFAKMGQNYGNKV	196
Rba1	FRANAYQAVSKTL	----	TYN	----	GIQ	-----	ETALDGYDAKLTANLPYFYSS	-----	NLYGKLS	143
ruler170.....180.....190.....200.....210.....220.....230.....240									



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Table with 4 columns: Sequence ID (e.g., Mba1, Psp2, Ybe1), Sequence Alignment (e.g., GSKD-----IKGNDLQLRAVPGITGLEIQAGRTFFSDSSGTD--ENYINIFVNTQLFADKPRV-----N), and Position (e.g., 204, 195, 223). The alignment shows conserved regions across various species, with gaps represented by dashes.



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Mba1	HQNIISKDAYKLES	EDRRYKVRRTN	-----	-----	NIVKQIKSLGVKVSGL	246			
Psp2	ETGISDTSANLTSVSDQKFAKVR	RQN	-----	-----	LIVKQ-KEMDLTVIGF	236			
Ybe1	RRTLQGSNDLVERNNQIVLE	YKKQD	VINLYV	SNNVSGRAA	-----	ET	-----	KQLVSVV-TSKYGLRNIQ	283
Ype5	KRSLMGSRYNLVDNRNNQIVMKYR	RQN	RVTLLEL	PARVSGAAR	-----	QT	-----	MPLVANA-TAQQIDRLE	283
Eco14	QRSLAANRLLELVNRNNDVVLE	YRKQT	LITLQL	PPDVYGAEL	-----	TT	-----	VTLTFQV-NAKYGLSRIE	284
Sen3	RRTLGGSRDLINRNNNIVLE	YRKQD	LISLKV	QNKVGTGES	-----	ET	-----	LPVSVNV-KSKYPLDHIS	287
Ymo1	TRTLAGSRMDLVDNRNNNIVLE	YRKQD	VVTLNL	PAKVSQKEK	-----	QV	-----	LPINVTN-NARHGLDRIE	284
Yen2	TRTLAGSRMDLVDNRNNNIVLE	YRKQD	VVTLNL	PEKVSQKEK	-----	QV	-----	VPINVTN-NARHGLDRIE	284
Pas1	KRTLADNRVHLVERNNNIVLKH	RERA	QLSLYL	PTGLSGFGG	-----	ER	-----	KLINVSF-NGKYRLKHTQ	309
Yfr1	MRSLMGSRVDIVDRNNIVM	QVEKQD	LIKLTL	PETLAAYAI	-----	TN	-----	LSLTGNL-TAKYGAERME	284
Yfr5	MRSLAGSRVDLVDNRNNIVM	QVEKQD	LINLTL	PETISAHAL	-----	EN	-----	VTLTGTN-ASKYGTERTIE	284
Yps7	SRTLAGSRVDLVERNNHIVLD	YQKQD	LVRLSL	PDSLADGPF	-----	SO	-----	LSVTAQV-TATHGLERID	283
Yfr2	TRTLAGSRVDLVERNNNIVLD	YQKQD	LIRLSL	PERVEGKAG	-----	DI	-----	ATVNAQV-TSKYGLERID	283
Yfr3	SRTLAGSRVDLVERNNNIVLE	YQKQD	LIQVLV	PNQMTGSAP	-----	ET	-----	IKVEAQN-TAKYGLKRID	283
Yps4	NRTLAGSRVDLVERNNNIVLD	YQKQD	LIHLVL	PDRISGSGG	-----	GA	-----	ITLTAQV-FAKYGFSRIE	283
Yps2	TRLLAESRYNLVDNRNNNIVLE	YQKQD	VVRLTSLPATISGL	PLG	-----	QV	-----	YQVNAQV-QGASAVREIV	284
Esa2	RRSLAGSRVDLVDNRNNEI	ILQYKKK	-----	-----	-----	-----	-----	-----	249
Plu1	LRSLAGSRVDLVERNNNII	LNVLKQD	QHPRL	VPVIEISSY	-----	GG	-----	EVKPIQI-QSDTFPKNVT	284
Eco1	LRTLGSGRVDLVDNRNNNII	LEKQD	LISLNI	PHDINGTER	-----	ST	-----	OKIQIIV-KSKYGLDRIV	281
Pru1	FRSLMGSRVDLVERNNHIVLE	YKKND	VIQLNI	ANSTIGYAG	-----	EK	-----	IPLSFTV-ASKYGLSHLK	283
Pal3	FRSLMGSRVDLVERNNHILLD	YKND	TIYLN	NASITGISG	-----	EK	-----	IPLKVTI-NSQVGFNRIN	283
Eta1	MRSLAGSRVDLVERNNHIL	QYRKE	VIRLHT	VGRVTGYAG	-----	ER	-----	KSLGVSU-NSSYGLERID	283
Sgl1	MRTLAGSRVDLVDNRNNNIVLE	YRKE	VIHLYT	ADHLAGYAG	-----	EQ	-----	KSLNVSI-NTKYGLERID	283
Eco26	MRKLAGQRVDLVERNNNII	LDYRKE	IIKIDG	VDVTSGFSG	-----	EK	-----	KRLDIRV-NSKYPLDRID	283
Pmi1	IRTLAGSRVDLVDNRNNNII	LDYRKE	LVFLSM	VDSINGYAK	-----	EE	-----	RDLOQVQ-KTKYPLANIE	283
Efe5	MREVQNRVDLVERNNNIVLE	YKKS	TLRISL	PDAIEGESG	-----	AT	-----	IPVTLNVSHASNGIQSVQ	285
Eco20	RRVLAGSRVDLVERNNNIVLE	YRKE	VIRIAL	PERTEGKGG	-----	QT	-----	LSLGLVSKATHGLKNVQ	285
Eco25	RRSLAGSRVDLVDNRNNNIVLE	YRKE	LVRLTL	TDPVTGKSG	-----	EV	-----	KSLVSSL-QTKYALKGN	284
Eco15	RRSLAGSRVDLVDNRNNNIVLE	YRKE	LIRLSL	LDPVKGKSG	-----	ET	-----	KPLVSSL-QTKYALKGN	284
Eco6	RRSLVGRVDLVDNRNNNIVLE	YRKE	LVRLTL	TDPVKGKSG	-----	EV	-----	KSLVSSL-QTKYALKGN	284
Efe2	RRSLGSRHDLVDNRNNNIVLE	YRKE	LVKLQL	NDPVTGKGG	-----	EQ	-----	KPLVASL-QSKYALKTIQ	284
Efe3	RRSLAGSRHDLVDNRNNNIVLE	YRKE	LVKLQL	HDPVTGKGG	-----	EQ	-----	KPLVASL-QSKYALKTLR	284
Pal2	TRRLSGNRVDLVERNNNII	LNQKKT	VLHLSL	PSKIQGITG	-----	QS	-----	VPLVKSF-TSKYPLKHIE	284
Csu1	MRFLNENRYNDFVSRNHN	IVFNSEY	YDIFVS	PASISAIEF	-----	AS	-----	STVSLKCPNTKT-LAHFE	278
Eco3	SQSLRGSRYDNPQRNNLPT	LEYRQK	TLTVFLATPP	DLKPG	-----	ET	-----	VPLKQI-RSRHGIRQLI	282
Cko1	SQSLRGSRYDNPQRNNLPT	MEYRQK	TLTVFLATPP	DLQPG	-----	ET	-----	VPLKQI-RSRHGIRHVT	282
Sen1	SQSLRGSRYDMPQRNALPT	MEYRQK	TLTVFLATPP	DLTPG	-----	ET	-----	VTLKQV-RSVHGIRHLS	282
Eca1	TRSLRGSRYDPAERNSLP	VMFRQK	TLVSVLATPP	DLKGG	-----	ET	-----	VMLKQI-RSTHGIRQLH	282
Esp2	TRSLRGSRYDVPDRISLP	VMFRQK	TLVSVLATPP	DLTPG	-----	ET	-----	VVLKQV-RSTHGIRQLH	282
Esa3	SRSLRGSRYDRVERTNVP	VMFRQK	TLVSVLATPP	DLQSG	-----	ET	-----	VALKQV-RSRHGIRQLS	282
Kpn1	SNSLRGSRYDPERDNL	PVVEYRQK	NLTVVFLATPP	DLQSG	-----	ET	-----	VQLKQI-HSLHGKALH	283
Pan1	ARSLRGSRYDVTTRSQNP	VMAFRQK	TLVSVFLATPP	QLNPG	-----	ES	-----	VPLKQI-RASHGKALS	282
Eta2	ARSLGSRVDSVNRDNSP	VMAFRQK	TLVSVFLATPP	QLOPG	-----	ET	-----	LRLKQI-ANKNTIKAVS	282
Spr1	AKSLRGSRYDNIERKNVP	VMAFRQK	TLQVFLATPP	QRLQPG	-----	ET	-----	LPLVLEI-KTNKITRVS	284
Yin1	MRSLKGSRYDLVDNRND	IVLEYKEA	SLALDLAAV	PMTLLEG	-----	DI	-----	YLMQPLV-RSKYKIVGVT	284
Yin2	MRSLKGSRYDLVDNRND	IVLEYKEA	VLSIDLAAV	PMTLLEG	-----	DV	-----	YMMQPLV-RSKYKIVGVT	284
Yfr4	MRSLMGSRVDLVDNRND	IVLEYKEA	GLMLDLAAV	PATLLEG	-----	DV	-----	YLMQPLV-NGKYPIASVS	285
Ymo2	LRSLKGSRYDLVDNRND	IVLEYKEQ	VLEADLAAV	PDSLMEG	-----	ES	-----	YILRPLV-KSKYPIIDL	286
Eco10	AHSLMGSRHDFVERNNF	IVLEYREK	PLDVTLWLKADATNE	HPECVTKDTP	EEAIGLEK	CKWTN	NALI	NHNYKIVAAS	301
Eal1	AHSLMGSRHDFVERNNF	IVLEYREK	HLDVTLWLKADATNE	HPECVTKDTP	EEAVGLEK	CKWTN	NALI	NHNYKIVAAS	301
Sty4	QHSLMGSRHDFVDRNNF	IILEYREK	PLDVTLWLKADATNE	HPECVIEDT	PEAAVGLEK	CKWTN	NALI	NHNYKIVSAS	300
Eco16	KHSLMGSRHDFVERNNF	IVLEYREOD	PLDVTLWLKADATNE	HPECVTKDTP	ELAVGLEK	CKWTN	NALI	NHNYKIVAAS	301
Ahy1	-KSLAGMRHDLIERNNDM	VLEYRDKV	LLKASL	NDQVSAVEG	-----	QA	-----	LTLTINI-QHSRQIASIQ	314
Sen2	PSNTTN-RTAFVDRND	IVMAYREQA	-SKIRITAMP	VSGLSG	-----	-----	-----	TLVTLMATIDSRVPIEKVE	282
Efe4	ASNTTN-RTAFVDRND	IVMAYREQA	-SRIRVYASP	VNGSQS	-----	-----	-----	DTVTLSATINSRVPVERIE	282
Bpe1	AFSPDARRHALVERENR	IVLNTRRKEI	ILPLVSVK	VTLOADG	-----	-----	-----	RVTVIGATOPFATVTVR	285
Bav2	VFNLDAAHRNALVERENR	IVLNTRRKEI	ILPLVSVK	VTLOADG	-----	-----	-----	RITLVGOTQQAQATVNT	284
Bbr1	AFDLQARMGEFVERENR	IVLQTRRKHVV	PLTIARV	TDPATG	-----	-----	-----	RITVTGVTEPGAQVSLG	283
Bpa2	PFDRGARLQDFVRRER	IVLQTRRKHVV	PLTIARV	TDPATG	-----	-----	-----	RITVTGVTEPLADVQSL	286
Bav1	PNLTSRRHQVVERESR	IVLNTRRKAITL	PLSIAQL	RGDPTNG	-----	-----	-----	AIEVSGQTEAGARIMLT	280
Pma1	KKNMVTQMTQPVKRRK	VDLLERSAG	-----	-----	GVQNR	-----	-----	AKGV	263
Pma3	KKNITQMTQPVKRVND	VLLERAAINSS	-----	GAATFTVR	VS	-----	-----	AQGT	270
Pma5	KKNMITQMTQPVKRE	NVLLERYGAN	-----	-----	STFN	-----	-----	AKGS	264
Pma4	KQNLVTQMTQPVRRR	EVLLERSTGG	-----	-----	QNR	-----	-----	ARGI	262
Ssp1	KQNLVTQMTQPVRRR	EVLLERVKEPTK	-----	-----	NGSITS	I	-----	AQGI	268
Ssp2	RENLLQMRQPVORRND	VLLERWPKPKK	TTGGNGS	FINQ	-----	-----	-----	AAGI	296
Plu2	KPRFSNTPVEFERMD	DRRFEKIRE	EQKVISAH	NNEQPPA	-----	-----	-----	-----	251
Clal	SNTIEGTRTQFIDRD	SMVLEYRATPNKY	HISVCGD	LGNDKHC	ILLKN	-----	-----	GFDEVVKNTPMRVTPHSCVV	338
Rba1	FEPIREKLYRPVOREN	RIMKKAIKLG	-----	-----	VTVSGV	-----	-----	-----	245
ruler330.....340.....350.....360.....370.....380.....390.....400								



CLUSTAL X (1.81.1-alpha) MULTIPLE SEQUENCE ALIGNMENT

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Mba1	-----	-----	-----	-----	246	
Psp2	-----	-----	-----	-----	236	
Ybe1	DDQGA	AAAGGKIIF	OGPSQFALQLPPO	-----	311	
Ype5	WEASA	LTLAGGKITG	SGNNWQITLPSY	-----	310	
Eco14	DDDAE	LKQAGGKIIS	NTGNQITLQIPAW	-----	312	
Sen3	WEDDN	LVKNGGKISE	NNGSWSVTLPHY	-----	314	
Ymo1	WDAAD	VINAGGNISD	OGNLAYHITPPY	-----	312	
Yen2	WDAAD	VIKAGGOVIN	OGNLAYVIAMPY	-----	312	
Pas1	WMDGA	LKARGGRIIA	LSNNSYVVQPPNY	-----	337	
Yfr1	WSAPA	LMAAGGSIIIP	LTMSASVTLPPY	-----	312	
Yfr5	WSAPV	LVTGGAITP	LAMESAVVTLPAY	-----	312	
Yps7	WQSAE	LMAAGGVLKQ	TSKNGLETLPEY	-----	311	
Yfr2	WDSAA	LIAAGGTLSK	GSSNSISITLPPY	-----	311	
Yfr3	WDIYV	LVAAGGVVTE	TSSQNISIKLPPY	-----	311	
Yps4	WDATP	LENAGGSTSP	LTQSSLSVTLPFY	-----	311	
Yps2	WSDAE	LTAAGGTLTP	LSTTQFNVLVPPY	-----	312	
Esa2	-----	-----	-----	-----	249	
Plu1	WDIPE	LKQKNGGMIN	IESTHGYITQLPEY	-----	313	
Eco1	WDDSS	LRSQGGQIQHSGS	QSAQDYQAILPAY	-----	312	
Pru1	WNAET	LVAAGGHVQE	NGKYSLVLPAY	-----	310	
Pal3	WHDAS	LVAAGGVIDEK	NGAYSIILPTY	-----	311	
Eta1	WSASS	LIAAGGKLVREN	EGSWSVILPEH	-----	311	
Sg11	WSAPE	LIAAGGKIQVES	IDNYSIVLPDY	-----	311	
Eco26	WLANI	FLANGKINNEG	LHNYSIILPDY	-----	311	
Pmi1	WSASK	LNAQGGQIKHHG	GTHYTVILPQY	-----	311	
Efe5	WSDSA	LAAAGGKITGS	GTSWQITLPAY	-----	312	
Eco20	WEAPS	LIAEGGKITGO	GSQWQITLPAY	-----	312	
Eco25	WEATA	LEAAGGKVTT	GKDILVLPAY	-----	311	
Eco15	TEAAA	LEAAGGKVSTS	GKDIVTLPGY	-----	311	
Eco6	TEAAS	LQSAAGKVAVS	GKDIQVTPPY	-----	311	
Efe2	TDAAT	LTAAGGVISTA	DNQVTVLPAY	-----	311	
Efe3	AEAAE	LQSAAGVVNTE	ANQVTVLPAY	-----	311	
Pal2	WQAPE	FLAVGGSISD	DQATLTLPSY	-----	311	
Csu1	WEAQN	LIEAGGELITV	SAGKSNAEYTVKLP	-----	310	
Eco3	WQGDT	QILSLTPGAQANS	AEGWTLIMPDI	-----	311	
Cko1	WQGDT	QALSLTAGAKADS	AEGWTLIMPDI	-----	311	
Sen1	WQGDT	QALSLTAGTDTR	NTEGWTLIMPDI	-----	311	
Eca1	WQGDT	QALSLTSPANSTSS	DGWSIIPAW	-----	311	
Esp2	WQGDT	HALSLTSPANANS	DEGWSVIMPAW	-----	311	
Esa3	WQGDT	QALSLTPPLDSTS	ADGWSVIMPAW	-----	311	
Kpn1	WQGDT	QALSLTPPVDA	SSPDGWSIIMPVW	-----	312	
Pan1	WQGDT	QALSLTSPPNNA	IDGWSVIVPPW	-----	311	
Eta2	WQGDT	QALSLTPPPDN	SDFDQWSIIPAW	-----	311	
Spr1	WQGDT	QALSLTPSONS	NDPHGWSLIVPQW	-----	313	
Yin1	WNGDT	VPLSLLATAGATN	POGWQITLPAW	-----	313	
Yin2	WBGDA	VPLLLVPTAGANN	POGWQITLPAW	-----	313	
Yfr4	WQGDT	VPLALLATAGVDN	HPOGWQITLPAW	-----	314	
Ymo2	WLGDL	LPLQLLATAGSH	NPOGWQITLPAW	-----	315	
Eco10	WQAKNNAAS	WQAKNNAARTL	VMPVIKENTL	TEGNNNHNNLVP	-----	346
Eal1	WQAKN	NAARTL	VMPVIKENTL	TEGNNNRNIVL	-----	337
Sty4	WQAKN	NAARTL	VMPVVKADAL	TEGNNSWNLVP	-----	336
Eco16	WQAKN	NANRTL	VMPVVKANAL	TEGNNNRNVL	-----	337
Ahy1	WLGDLG	LPGDGL	LGLSPADTAG	QDKRALTLPSL	-----	343
Sen2	WBGDA	ELIAGLQIQGS	-----	LGSGLILPQL	-----	308
Efe4	WBGDA	ELIGGLQOQGN	-----	VNSGLRPLDL	-----	308
Bpe1	WPDGM	TGTATADASGR	FVTSAGDQPS	GVVLLARR	-----	320
Bav2	WPDGS	SGQSRADAS	GVYRIESR	KDQPSGPIRLKAV	-----	319
Bbr1	WPNGE	VVVQAQD	SGTYRATSARD	VMVGGPVRRAT	-----	318
Bpa2	WPDGT	ATSVRANAAG	GFREASSAGDM	TSGLIRARAT	-----	321
Bav1	WPDGS	GNWVRADASGR	YRARS	GDMPSGTVRAQAR	-----	315
Pma1	-----	-----	-----	-----	263	
Pma3	-----	-----	-----	-----	270	
Pma5	-----	-----	-----	-----	264	
Pma4	-----	-----	-----	-----	262	
Ssp1	-----	-----	-----	-----	268	
Ssp2	-----	-----	-----	-----	296	
Plu2	-----	-----	-----	-----	251	
Cla1	WEKGF	YITDMSGKV	VQIIR	SCTPKTDLNAVAG	-----	372
Rba1	-----	-----	-----	-----	245	
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