

CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT

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Rat ----MPSSPLR---VAVVCSNNQNRSM EAHNILSKRG-FS-VRSFGTGTTHVKLPGPAPDKPNVYDFK-TTYDQMYNDLLRKK-KELYTQNGILHMLDRNKRIKPRPERFON-----CKDLFDLILTCEERVYDQV 119
Mouse ----MPSSPLR---VAVVCSNNQNRSM EAHNILSKRG-FS-VRSFGTGTTHVKLPGPAPDKPNVYDFK-TTYDQMYNDLLRKK-KELYTQNGILHMLDRNKRIKPRPERFON-----CTDLFDLILTCEERVYDQV 119
Human ----MPSSPLR---VAVVCSNNQNRSM EAHNILSKRG-FS-VRSFGTGTTHVKLPGPAPDKPNVYDFK-TTYDQMYNDLLRKK-KELYTQNGILHMLDRNKRIKPRPERFON-----CKDLFDLILTCEERVYDQV 119
Bovin ----MPSSPLR---VAVVCSNNQNRSM EAHNILSKRG-FS-VRSFGTGTTHVKLPGPAPDKPNVYDFK-TTYDQMYNDLLRKK-KELYTQNGILHMLDRNKRIKPRPERFON-----CKDLFDLILTCEERVYDQV 119
Chick ----MPSSPLR---VAVVCSNNQNRSM EAHNILSKRG-FS-VRSFGTGTTHVKLPGPAPDKPNVYDFK-TTYDQMYNDLLRKK-KELYTQNGILHMLDRNKRIKPRPERFON-----CKDVFDLILTCEERVYDQV 119
Xenla ----MPTAPLR---VAVVCSNNQNRSM EAHNILSKRS-FN-VRSFGTGTTHVKLPGPAPDKPNVYDFK-TTYEQMVSDDLKDK-KELYTQNGILHMLDRNRRIKPRPERFON-----CKDYFDLVIITCEERVYDQV 119
Danre ----MPHPHLR---VAVVCSNNQNRSM EAHNILSKRG-FD-VRSFGTGTTHVKLPGPAPDKPNVYDFK-TTYEQMYNDLVRKK-KELYTQNGILHMLDRNKRIKSRPERFOS-----CRDQFDLVIITCEERVYDQV 119
Drosophila ----XIDPSKLA---VAVVCSNNQNRSM EAHNFLAKKG-FN-VRSYGTGERVRLPGXAFDKPNVYDFG-ITKYEDIYRDLLESKD-KEYFTQNGLLHMLDRNRRIKCKPERFOD-----TKEQFDIIVITCEERVYDQV 120
Dicdi_cut ---------KR---IAMVCASNQNRSM EAHHLFVKNG-FKNIRSFGTSAHCKLPGPFIHQNPISFSG-IPTVQEIYTSLNKQD-QELYTRNGLLMLERNISVKLAPKEKWQE-----QSKPFEIVYTFDQRVYDAV 116
CryneHomologue VDKDVPQGRRRPLFCVVCASNQNRSM EAHYVLNKNKS-FR-VVSAAGTGSAVRPLPGPAIDKPNVYRFG-IPTVDIVRDLSESQD-POLYTRNGILPMLDRNRKKVKAPEKWQEL-----KSVLADVVITCEERCYDAV 126
Ashgo_cut -----LR---LCTVCASNQNRSMESHVRLKEAG--YDVSSYGTGSAVRPLPGLSIDKPNVYDFG-IPTVNDIYNDLLAQS-AERYKSNGLLEMLDRNRRIKKAPEKWHD-----SQKVFDFVITCEERCDFSV 114
Klula_cut -----LK---FCTVCASNQNRSMESHVRLKEAG--YDVSSYGTGSAVRPLPGLSIDKPNVYDFG-IPTVDIYNDLISQS-EDRYKQNGVLEMLDRNRRLKKAPEKWHD-----GRKVFDFVITCEERCDFSV 114
Canga ----MDQKQALK---FCTVCASNQNRSMESHVRLKEAG--YEVSSYGTGSAVRPLPGLSFDKPNVYDFG-IPTVNDIYNDLISQS-AERYKANGLLQMLDRNRRLKKAPEKWQI-----GTKTFDFVITCEERCDFSV 120
Yeast ----MPSHRNLSLK---FCTVCASNQNRSMESHVRLKEAG--YVSSYGTGSAVRPLPGLSIDKPNVYDFG-IPTVNDIYNDLISQS-ADRYKSNGLLOMLDRNRRLKKAPEKWQE-----STKVFDFVITCEERCDFSV 122
Debha ----MVSDSLK---ICTVCAANNRSMESHVRLKADAG--YVNSRFGTGSAVRPLPGPVVDKPNVYDFG-IPTVDDIYRDLTSQEVHKMVESNGLIRMINRNHRHIKRAPEKWHNNA-----SAGKFDLVIITCEERCDFLV 122
Yarli ----MTELK---MCTVCASNQNRSM EAHVRLKEAG--FDVSSYGTGSAVRPLPGPAIDKPNVYDFG-IPTVDDIYNELSAQD-ERLYTANGLLTMMLDRNRRIKTAPEKWWI-----HKNVDFVITCEERCDFEAV 117
Schpo ----MAPKTNLQ---ISVVCASNQNRSM EAHVRLNKNAG--YQVDSYGTGSAVRPLPGLSIDKPNVYDFG-IPTVDEIYKLELAQD-SRLYTANGLLTMMLDRNRRIKRAPEKRWOD-----QDSIYNIVITCEERCDAI 120
Neucr_cut -----LK---FCTVCASNQNRSMEGHLRRLSLAN--YVPVISFGTGSLVRLPGPPIITQPNVYKFNEITSYDSIVYRELEAKD-PRLYVRANGLLNMLGRNRVVKWGPERWDVVGMPRVKHKD-----DKGADGMGEGVADVITCEERCWDAV 134
Chagb_cut -----LK---FCTVCASNQNRSMEGHLRRLAQAN--YVPVISFGTGSLVRLPGPPIITQPNVYKFNEITSYDSIVYRELEAKD-PRLYVRANGLLNMLGRNRVVKWGPERWDVVGMPRVKHKD-----DQGSIGMEAGVDPDVITCEERCWDAV 134
Gibze_cut -----LK---FCTVCASNQNRSM EAHLRLSLQAD--YVPVISFGTGSLVRLPGPPIITQPNVYHFNKISYDSMFRLEESKD-ARLVKNNGLLNMLNRNRGVKWPGRWDVVGMPRQLQHAKE-----DRGSEGTEGGLVDIVITCEERCWDAV 134
Aspor_cut -----LR---FCTVCASNQNRSM EAHLRLSLTAPFPFFVISFGTGSLVRLPGPPIITQPNVYNFNTISYSIMYEELYSKD-ERLYVRANGLLNMLERNRNLKWGPERFDVWVPGMPRVVDHVAKGDKGALGTEGGVVVDVIITCEERCWDAV 138
Aspfor_cut -----LK---FCTVCASNQNRSM EAHLRLSLTAPFPFFVISFGTGSLVRLPGPPIITQPNVYNFNTISYSIMYDELLAKD-ERLYVRANGLLNMLDRNRNLKWGPERFDVWVPGMPRVVDHVSKGDKGALGTEGGVDVVIITCEERCWDAV 138
ruler 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150
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..*::* * * * : :
Rat ----VEDLNSR---EQET---CQPVHVNVVDIQDNHEEATLGAFLICELCQCQIHTED-----MENEIDELLOEFEEKSGRA-FLHTVCFY 194
Mouse ----VEDLNSR---EQET---CQPVHVNVVDIQDNHEEATLGAFLICELCQCQIHTED-----MENEIDELLOEFEEKSGRA-FLHTVCFY 194
Human ----VEDLNSR---EQET---CQPVHVNVVDIQDNHEEATLGAFLICELCQCQIHTED-----MENEIDELLOEFEEKSGRT-FLHTVCFY 194
Bovin ----VEDLNSR---EQET---CQPVHVNVVDIQDNHEEATLGAFLICELCQCQIHTED-----MENEIDELLOEFEEKSGRT-FLHTVCFY 194
Chick ----VEDLNSR---EQET---CQPVHVNVVDIQDNHEEATLGAFLICELCQCQIHTED-----MENEIDELLOEFEEKSGRT-FLHTVCFY 194
Xenla ----VEELNSR---EQET---CQPVHVNVVDIQDNHEEATLGAFLICELCQCQIHTED-----MENEIDELLOEFEDKSGRT-FLHTICFY 194
Danre ----LEDLNSR---EQES---FQPVHVNVVDIQDNHEEATLGAFLICELCQCQIHTED-----MENEMDELLOEFEEKSHRP-FLHSVCFY 194
Drosophila VXXHSEX---ESVD---NRFPVHVLNVDVVDNADALXGAFVIIDIXINXAKSTD-----LDNDIDELLOEFEEKRRKV-ILHSVLFY 195
Dicdi_cut IEDLLQR---DVS---SLLQPVHINLVQDKTHEEAVGCAQHAEIITIEIKLNLN-----WEKLDIILEDFYKTSRQ-FLHTLMFY 193
CryneHomologue CDDLLTR---SGEY---NRPIIHIINIEIKDNPEEABHIAQOSILELARAIEASDD-----LSDSIDAILNAHGDKHPHT-LLHTVGFY 201
Ashgo_cut CEDLMNR---GGQLNKIVHVINLDIRDDNENAKIGGRAMLRELVKALNSKMQDCEQ-----QQVFPEDTIMDVVADVQOAHQPPLLYSPAYY 198
Klula_cut CEDLMNR---GGQLNLIAHINIDIKDDNENAKIGGTRAILRLADMLRDKVFBCEK-----NGTQFEDFIMDVFTWQEKYPKLPLTYSAAYY 198
Canga ----CEDLMNR---GGRLNKIVHVINIDIRDDNENAKIGGRAILELANMLNEKVSCEQ-----NDTIFEDCILDLTKWQEAPHPQLPCLYAPSY 204
Yeast ----CEDLMNR---GGKLNKIVHVINVDIKDDENAKIGSKAILLADMLNDKIEGCEK-----DDTIFEDCIMDILTETWSHSSQLPSLYAPSY 206
Debha LDDLNVRLVKKDQADTEIKQAVHINIDIKDDYENAVIIGKGILKLVNIEHEFRNTNKQRRLDHDFDD-----ESDITILEDQMMKLAKWQEHTHLPLTYSVAYY 223
Yarli CDDLMRD---GEKLRPVHVNVVDIRDNEHDSVIGAQGILKLARSLADSKD-----LDAQIMGIMDSQWQHPKPLPMHAGYF 193
Schpo CEDLYRR---GETLNRPVYLLNVVDIKDNHEEASVGGKAILLDLVNKLTEAQQK-----LEBLFPSIMADFQSNHPKPLVLYTIHFF 197
Neucr_cut IEDLLNR---GSPLNRPVHVINIDIKDNHEEASVGGRAIVDLADSLNKAIAEEREKVGASAFDSCSGVARSGFDERVVDVLAETWERWPNLPATWTLAWF 231
Chagb_cut VDDLNR---GSPLNRPVHVINIDIKDNHQSASIGGGAMVDLADSLNRAAEMEERDKVGAAVFDAGGAASRASFDERVPVVLGEWQERWPGLPSTWTLSWF 231
Gibze_cut VDDLNR---GSPLNRPVHVINVEIKDNHEEAAVGGQILDLANSLNAAAREERDAVGASAFDNSSASSRATFDERVPDILASQERWPNLPATWTVAWF 231
Aspor_cut VDDLNR---GSLNRPVHVNVVDIKDNHEEALVGGKAILLARNLNAAAVQERKANNSSEGWNGTGEARRSFDERKPVPEILAAWQEKWPNLPAWTLAWL 235
Aspfor_cut VDDLNR---GAALNRPVHVNVVDIRDNEEALVGGKAILLARTLNDAATQERKIHGAEGWENGNGEARRSFDERVPPEILASQEKWPNLPAWTLAWL 235
ruler .....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....
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