CLUSTAL X (1.83) MULTIPLE SEQUENCE ALIGNMENT


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1Human_similar ---MLSSPLRVAVVCVSNVNRSMEAHSILRRKGLS----VRSFGTESHVRLPGPRPNRPVVYDFA-TTYKQMYNDLLRKD-RERYTRNGILHILGRNERIKPGPERFQE---------------------CTDSFDVIFTCEESVYDTVV   120
2Human_similar ---MLSSTLRVAVVCVSNVNRSMEAHSILRKKGLS----VRSFGTESHVRLPGPRPNRPVVYDFA-TTYKEMYNDLLRKD-RECYTRNGILHILGRNERIKPGPERFQE---------------------CTDFFDVIFTCEESVYDTVV   120
3Human_similar ---MLSSPLRVAVVCVSNINRSMEAHSILRRKGLS----VRSFGTESHVRLPGRRPNHPVVYDFA-TTYKEMYNDLLRKD-RECYTHNGILHILGRNERIKPGPERFQE---------------------CTEFFDVIFTCEERVYDTVV   120
           Rat ---MPSSPLRVAVVCSSNQNRSMEAHNILSKRGFS----VRSFGTGTHVKLPGPAPDKPNVYDFK-TTYDQMYNDLLRKD-KELYTQNGILHMLDRNKRIKPRPERFQN---------------------CKDLFDLILTCEERVYDQVV   120
         Mouse ---MPSSPLRVAVVCSSNQNRSMEAHNILSKRGFS----VRSFGTGTHVKLPGPAPDKPNVYDFK-TTYDQMYNDLLRKD-KELYTQNGILHMLDRNKRIKPRPERFQN---------------------CTDLFDLILTCEERVYDQVV   120
         Human ---MPSSPLRVAVVCSSNQNRSMEAHNILSKRGFS----VRSFGTGTHVKLPGPAPDKPNVYDFK-TTYDQMYNDLLRKD-KELYTQNGILHMLDRNKRIKPRPERFQN---------------------CKDLFDLILTCEERVYDQVV   120
         Bovin ---MPSSPLRVAVVCSSNQNRSMEAHNILSKRGFS----VRSFGTGTHVKLPGPAPDKPNVYDFK-TTYDQMYNDLLRKD-KELYTQNGILHMLDRNKRIKPRPERFQN---------------------CKDLFDLILTCEERVYDQVV   120
         Chick ---MPSSPLRVAVVCSSNQNRSMEAHNILSKRGFS----VRSFGTGTHVKLPGPAPDKPNVYDFK-TTYDQMYNDLLRKD-KELYTQNGILHMLDRNKRIKPRPERFQN---------------------CKDVFDLILTCEERVYDQVV   120
         Xenla ---MPTAPLRVAVVCSSNQNRSMEAHNILSKRSFN----VRSFGTGTHVKLPGPAPDKPNVYDFK-TTYEQMYSDLLKKD-KELYTQNGILHMLDRNRRIKPRPERFQN---------------------CKDYFDLVITCEERVYDQVV   120
         Danre ---MPPHPLRVAVVCSSNQNRSMEAHNILSKRGFD----VRSFGTGTHVKLPGPAPDKPNIYDFK-TTYEQMYNDLVRKD-KELYTQNGILHMLDRNKRIKSRPERFQS---------------------CRDQFDLVITCEERVYDQVL   120
     Dicdi_cut --------KRIAMVCASNQNRSLEAHHLFVKNGFKN---IRSFGTSAHCKLPGPSIHQPNIFSFG-TPYQEIYTSLKNQD-QELYIRNGLLNMLERNISVKLAPEKWQEE--------------------QQSKFEIVYTFDQRVYDAVI   117
     Ashgo_cut --------LRLCTVCASNNNRSMESHRVLKEAG----YDVSSYGTGSAVRLPGLSIDKPNVYPFG-TPYNDIYNDLLAQS-AERYKSNGLLEMLDRNRRIKKAPEKWHD--------------------SQKVFDFVFTCEERCFDSVC   115
     Klula_cut --------LKFCTVCASNNNRSMESHRVLEEAG----YDVSSYGTGSAVRLPGLSIDKPNVYSFG-TPYDDIYNDLISQS-EDRYKQNGVLEMLDRNRKLKKAPEKWHD--------------------GRKVFDFVFTCEERCFDSVC   115
         Canga --MDQKQALKFCTVCASNNNRSMESHRILQEAG----YEVSSYGTGSAVRLPGLSFDKPNVYPFG-TPYNDIYNDLLSQS-AERYKANGLLQMLDRNRRLKKAPEKWQE--------------------GTKTFDFVFTCEERCFDAVC   121
         Yeast MPSHRNSNLKFCTVCASNNNRSMESHKVLQEAG----YNVSSYGTGSAVRLPGLSIDKPNVYSFG-TPYNDIYNDLLSQS-ADRYKSNGLLQMLDRNRRLKKAPEKWQE--------------------STKVFDFVFTCEERCFDAVC   123
         Debha ---MVSDSLKICTVCAANNNRSMESHKQLKDAG----YNVRSFGTGSAVRLPGPSVDKPNVYEFG-TPYDDIYRDLTSQEYHKMYESNGLIRMINRNRHIKRAPEKWHNNA------------------SAGKFDLVITCEERCFDLVL   123
         Yarli -----MTELKMCTVCASNQNRSMEAHKVLKEAG----FDVESYGTGSAVRLPGPAYDKPNIYAFG-TPYDDIYNELSAQD-ERLYTANGLLTMLDRNRKIKTAPERWVE--------------------HKNVFDVVFTCEERCFEAVC   118
         Schpo --MAPKTNLQISVICASNQNRSMEAHNVLKNAG----YQVDSFGTGSAVRLPGPSIDKPNIYQFG-YPYDEIYKELEAQD-SRLYTANGLLKMLDRNRRIKRAPCRWQD--------------------QDSIYNIVITCEERCYDAIC   121
     Neucr_cut --------LKFCTVCASNQNRSMEGHLRLSLAN----YPVISFGTGSLVRLPGPSITQPNVYKFNETSYDSIYRELEAKD-PRLYRANGLLNMLGRNRQVKWGPERWQDWQIGMPRTKHKD--DKGADGMEGGVADVVITCEERCWDAVI   135
     Chagb_cut --------LKFCTVCASNQNRSMEGHLRLAQAN----YPVISFGTGSLVRLPGPTITQPNVYKFNETSYDSIYRELEAKD-PRLYRANGLLNMLGRNRVIKWGPERWQDWQVGMPRVKHEK--DQGSIGMEAGVPDIVITCEERCWDAVV   135
     Gibze_cut --------LKFCTVCASNNNRSMEAHLRLSQAD----YPVISFGTGSLVRLPGPTITQPNVYHFNKTSYDSMFKELESKD-ARLYKNNGILNMLNRNRGVKWGPERWQDWQVGVPRLQHAK--DRGSEGTEGGLVDIVITCEERCWDAVV   135
     Aspor_cut --------LRFCTVCASNQNRSMEAHLRLSTAPS--PFPVISFGTGSLVRLPGPSITQPNVYNFNTTSYSQMYEELYSKD-ERLYRNNGLLNMLERNRNLKWGPERFQDWVPGMPRVDHVAKGDKGALGTEGGVVDVIITCEERCWDAVV   139
     Aspfu_cut --------LKFCTVCASNQNRSMEAHLRLSTAPS--PFPVISFGTGSLVRLPGPSITQPNVYNFNTTSYSQMYDELLAKD-ERLYRNNGLLNMLDRNRNLKWGPERFQDWVPGMPRVDHVSKGDKGALGTEGGTVDVIITCEERCWDAVV   139
         Cryne ----------MCHKVEEDRYFVWFVRAITKNSFR-----VVSAGTGSAVRLPGPAIDKPNVYRFG-TPYDDIYRDLESQD-PQLYTRNGILPMLDRNRKVKKAPEKWQEL--------------------KSVLADVVITCEERCYDAVC   113
         ruler 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150
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1Human_similar EDLCSR-------EQQT--FQPVHVINMDIQDTLEDATLGAFLICEICQCLQQSDD---------------------IEDNLEELLLQMEEKAG-KSFLHTVCFY   194
2Human_similar EDLCSR-------EQQT--FQPVHVINMEIQDTLEDATLGAFLICEICQCLQQSDD---------------------MEDNLEELLLQMEEKAG-KSFLHTVCFY   194
3Human_similar EDLCSR-------EQQT--FQPVHVINMDIKDTLEGAILGAFLICEICQCLQQSDD---------------------MEDSLEELLLQMEEKAG-KSFLHTVCFY   194
           Rat EDLNSR-------EQET--CQPVHVVNVDIQDNHEEATLGAFLICELCQCIQHTED---------------------MENEIDELLQEFEEKSG-RAFLHTVCFY   194
         Mouse EDLNSR-------EQET--CQPVHVVNVDIQDNHEEATLGAFLICELCQCIQHTED---------------------MENEIDELLQEFEEKSG-RAFLHTVCFY   194
         Human EDLNSR-------EQET--CQPVHVVNVDIQDNHEEATLGAFLICELCQCIQHTED---------------------MENEIDELLQEFEEKSG-RTFLHTVCFY   194
         Bovin EDLNSR-------EQET--CQPVHVINVDIQDNHEEATLGAFLICELCQCIQHTED---------------------MENEIDELLQEFEEKSG-RTFLHTVCFY   194
         Chick EDLNSR-------EQET--CQPVHVINVDIQDNHEEATLGAFLICELCQCIQHTED---------------------MENEIDELLQEFEEKSG-RTFLHTVCFY   194
         Xenla EELNSR-------EQET--CQPVHVINVDIQDNHEEATLGAFLICELCQCIQHTED---------------------MENEIDELLQEFEDKSG-RTFLHTICFY   194
         Danre EDLNSR-------EQES--FQPVHVINVDIQDNHEEATLGAFLICELCQCIQHTDD---------------------MENEMDELLQEFEEKSH-RPFLHSVCFY   194
     Dicdi_cut EDLLQR-------DVSSSLLQPVHIINLQVKDTHEEAVGGAQHALEITSIIEKTLN---------------------WEEKLDQILEDFYKQTS-RQFLHTLMFY   193
     Ashgo_cut EDLMNR-------GGQLN--KIVHVINLDIRDDNENAKIGGRAMLELVKALNSKMQECDQ-------------QGVPFEDTIMDVVADWQQAHPQLPLLYSPAYY   198
     Klula_cut EDLMNR-------GGQLN--LIAHIINIDIKDDNENAKIGGRAILRLADMLRDKVFECEK-------------NGTQFEDFIMDVFTEWQEKYPKLPLTYSAAYY   198
         Canga EDLMNR-------GGRLN--KIVHVINIDIRDDNENAKIGGRAILELANMLNEKVSECEQ-------------NDTLFEDCILDILTKWQEAHPQLPCLYAPSYY   204
         Yeast EDLMNR-------GGKLN--KIVHVINVDIKDDDENAKIGSKAILELADMLNDKIEQCEK-------------DDIPFEDCIMDILTEWQSSHSQLPSLYAPSYY   206
         Debha DDLMVRLVNKDQADTEIK--QAVHIINIDIKDDYENAVIGGKGILKLVNMIHEFRNTNKQRRLDHDFDD---ESDTILEDQMMKLLAKWQQEHTHLPTLYSVAYY   223
         Yarli DDLMDR-------GEKLQ--RPVHVINVDIRDNHEDSVIGAQGILKLARSLADSKD---------------------LDAQIMGIMDSWQEQHPKLPLMHAVGYF   193
         Schpo EDLYRR-------GETLN--RPVYLINVDIKDNHEEASVGGKAILDLVNKLTEAQDK---------------------LEELFPSIMADFQSNHPKLPVLYTIHFF   197
     Neucr_cut EDLLNR-------GSPLN--RPVHVINIDIKDNHEEASVGGRAIVDLADSLNKIAAEEREKVGASAFDSGSVGARSGFDERVPDVLAEWQERWPNLPATWTLAWF   231
     Chagb_cut DDLLNR-------GSPLN--RPVHVINIDIKDNHQDASIGGGAMVDLADSLNRAAMEERDKVGAAVFDAGGAASRASFDERVPEVLGEWQERWPGLPSTWTLSWF   231
     Gibze_cut DDLMNR-------GSPLN--RPVHVINVEIKDNHEEAAVGGQGILDLANSLNAAAREERDAVGASAFDNGSASSRATFDERVPDILASWQERWPNLPATWTVAWF   231
     Aspor_cut DDLMNK-------GSLLN--RPVHVFNVDIKDNHEEALVGGKAILELANRLNEAAVQERKANNSEGWENGTGEARRSFDEKVPEILAAWQEKWPNLPALWTLAWL   235
     Aspfu_cut DDLMNK-------GAALN--RPVHVFNVDIRDNHEEALVGGKAILELATRLNDAATQERKIHGAEGWENGNGEARRSFDERVPEILASWQEKWPNLPALWTLAWL   235
         Cryne DDLLTR-------SGEYN--RPIHIINIEIKDNPEEAHIAGQSILELARAIEASDD---------------------LDSDIDAILNAHGDKHP-HTLLHTVGFY   187
         ruler .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.....
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