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                        *        20         *        40         *        60         *        80
CAH11_Rnor : MGGAARLSAPQALVLWAALGAAAHIGPAPDPEDWWSYKENLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Mmus : MGGAARLSAPQALVLWAALGAAAHIGPAPDPEDWWSYKENLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Fcat : MGVAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Ecab : MGGAAPLSAPQALVLWAALGAAAYIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Sscr : MGGAARLSAPRALVLWAVLGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Btau : MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Cfam : MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Hsap : MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Ptro : MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Pabe : MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Ppyg : MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Mmul : MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Cjac : MGAAARLSAPRALVLWAALGAAAHIGPAPDPEDWWSYKDNLHGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Ttru : MGGAARLNAPRALLLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVELKRVLYDPFLP :  85
CAH11_Oari : MGAAPRLSAPRVLVLWAALGAAAHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVDLKRVLYDPFLP :  85
CAH11_Cpor : ----------------------AHIGPAPDPEDWWSYKDNLQGNFVPGPPFWGLVNAAWSLCAVGKRQSPVDVDLKRVLYDPFLP :  63
CAH11_Mdom : MGGPMRLSPPRALLLGAALGAAAHIGPAPAPEDWWTYKDNLQGSFVPGPPFWGLVNAAWSLCAVGKRQSPVDIELRRVLYDPFLP :  85
CAH11_Acar : -------------------------------EDWWAYKETLHGSFVPGPPFWGLVNSAWSLCAIGKRQSPVDVNTSQMVYDPFLP :  54
CAH11_Xtro : ----RRVIYP---------GESAQFSPAKTYEEWWAYKEAVQGSFVPGPAFWGLVNSAWNLCTIGKRQSPININTSQIIFDPFLP :  72
                    *        100        *        120        *        140        *        160        *
CAH11_Rnor : PLRLSTGGEKLRGTLYNTGRHVSFLPASRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Mmus : PLRLSTGGEKLRGTLYNTGRHVSFLPASRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHEGFSAEV-QLIHFNQELYG : 169
CAH11_Fcat : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Ecab : PLRLSTGGEKLRGTLYNTGRHVSFLPAARPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Sscr : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELLLLFGAHDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Btau : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Cfam : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Hsap : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Ptro : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Pabe : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Ppyg : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Mmul : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Cjac : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEVVQLIHFNQELYG : 170
CAH11_Ttru : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Oari : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 169
CAH11_Cpor : PLRLSTGGEKLRGTLYNTGRHVSFLPASRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHQGFSAEV-QLIHFNQELYG : 147
CAH11_Mdom : PLRLSTGGEKLRGTLYNTGRHVSFLPAPRPVVNVSGGPLLYSHRLSELRLLFGARDGAGSEHQINHESFSAEV-QLIHFNQELYG : 169
CAH11_Acar : PLRLSTGGKKISGTMYNTGRHVSFRPDPLQLVNVSGGPLLYSHRLQEIRLHFGSEDGFGSEHQIDGETYSAEV-QLIHYNQELYP : 138
CAH11_Xtro : PLRLSMTGTTVSGTMHNTGRHVSFRLDKEQPVNISGGPLLYNHRLEEVMLHFGSENSIGSEHLMNKETSAGEV-QLIHYNQDLYS : 156
                        180        *        200        *        220        *        240        *
CAH11_Rnor : NLSAASRGPNGLAILSLFVN------VAGSSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Mmus : NLSAASRGPNGLAILSLFVN------VAGSSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Fcat : NLSAASRGPNGLAILSLFVN------VAGSSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Ecab : NLSAASRGPNGLAILSLFVN------VAGSSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Sscr : NLSAASRGPNGLAILSLFVNV---SQVAGNSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 251
CAH11_Btau : NLSAATRGPNGLAILSLFVN------VAGSSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Cfam : NLSAASRGPNGLAILSLFVN------VAGSSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Hsap : NFSAASRGPNGLAILSLFVN------VASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Ptro : NFSAASRGPNGLAILSLFVN------VASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Pabe : NFSAASRGPNGLAILSLFVN------VASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Ppyg : NFSAASRGPNGLAILSLFVN------VASTSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Mmul : NFSAASRSPNGLAILSLFVN------VAGSSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Cjac : NFSAASRGPNGLAILSLFVN------VAGSSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 249
CAH11_Ttru : NLSAASRGPNGLAILSLFVN------VAGSSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Oari : NLSAATRGPNGLAILSLFVN------VAGSSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 248
CAH11_Cpor : NLSTASRGPNGLAILSLFVN------VAGSSNPFLSRLLNRDTITRISYKNDAYFLQDLSLELLFPESFGFITYQGSLSTPPCSE : 226
CAH11_Mdom : NLSAASRGPNGLAVLALFVNQPSPTQVAANSNPFLSRLLNRDTITRISYKNDAYFVQDLSLEQLFPESFGFITYQGSMSTPPCSE : 254
CAH11_Acar : NISEASRNPNGLAVISIFAN------IGPSPNPFLTRLLNRETITRISYKNDAYLLHDLSLEDLYPETFGFITYQGSMTTPPCYE : 217
CAH11_Xtro : NVTEASRNPNGLAVISLFLN------VADNSNSFLNRMLNRETITRISFRNEATYIQDLSIEDLYPDTFGFLTYQGSMTIPPCYE : 235
                    260        *        280        *        300        *        320        *
CAH11_Rnor : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNGRPLQPLAHRALRGNRDPRHPERRCRGPNYRLHVDGGPHGR--- : 328
CAH11_Mmus : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNGRPLQPLAHRALRGNRDPRHPERRCRGPNYRLHVDGGPHGR--- : 328
CAH11_Fcat : TVTWILIDRALNITSLQ------------------------------------------------------------------ : 265
CAH11_Ecab : TVTWILIDRALNITSLQVILCLHHLSALPP----------------------------------------------------- : 278
CAH11_Sscr : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNGRPLQPLAHRALRGNRDPRHPERRCRGPNYRLHVDGAPHGR--- : 331
CAH11_Btau : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNGRPLQPLAHRALRGNRDPRHPERRCRGPNYRLHVDGAPHGR--- : 328
CAH11_Cfam : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNGRPLQPLAHRALRGNRDPRHPERRCRGPNYRLHVDGAPHGR--- : 328
CAH11_Hsap : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGPNYRLHVDGVPHGR--- : 328
CAH11_Ptro : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGPNYRLHVDGVPHGR--- : 328
CAH11_Pabe : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGPNYRLHVDGAPHGR--- : 328
CAH11_Ppyg : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNSRPLQPLAHRALRGNRDPRHPERRCRGPNYRLHVDGAPHGR--- : 328
CAH11_Mmul : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNGRPLQPLAHRALRGNRDPRHPERRCRGPNYRLHVDGAPHGR--- : 328
CAH11_Cjac : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNGRPLQPLAHRALRGNRDPRHPERRCRGPNYRLH----------- : 321
CAH11_Ttru : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNGRPLQPLTHRALRGNRDPRHPERRCRGPNYRLH----------- : 320
CAH11_Oari : TVTWILIDRALNITSLQ-MHSLRLLSQNPPSQIFQSLSGNGRPLQPLAHRALRGNRDPRHPERRCRGPNYRLHVDDVPHGL--- : 328
CAH11_Cpor : TVTWILIDRPLNITSLQ-MHSLRLLSQNPPSQIFQSLSGNGRPLQPLAHRALRGNRDPRHPERRCRGPNYRLH----------- : 298
CAH11_Mdom : TVTWILIDRALNVTSLQ-MHSLRLLSQNPPSQIFQSLSGNGRPLQPLAHRALRGNRDSRHPERRCRGPNYRLHG--MPWSL--- : 332
CAH11_Acar : TATWILIDRPINITSVQ-IHSLRLLSQNLPSQIFRSMSDNSRPLQPLLHRSLRGNRDPRRPTRRCKGGNFRLH----------- : 289
CAH11_Xtro : TVTWIVIDRPLNITSMQ-MHSLRLLSQNQPSQIFQSMSDNFRPVQPLFHRGLRGNLDFRKPGRKCKGANYKLHIDRPTSSKNAN : 318
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