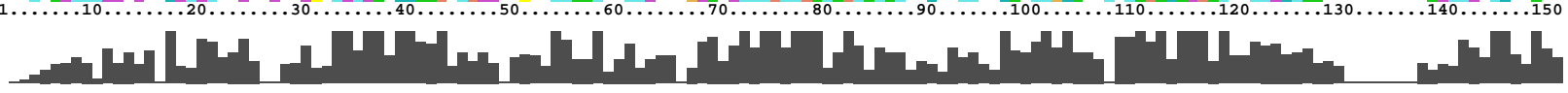


gi | 17647149 | ref | NP_523517.1 | MSNDNDDDFMCDDEED -VDLEYS EDS -NSEPNVDLENQYNSKALKKEE -EPKAALASFOKVLLEN -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----NMALLONFYETITLD 138
gi | 31211457 | ref | XP_314698.1 | MSNDNDDDFMCDDEED -VDLEYS EDS -NSEPNVDLENQYNSKALKKEE -APQDALRSFOKVLLEN -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----NMELLONFYETITLD 139
gi | 194671647 | ref | XP_001250692.2 | MSNDNDDDFMCDDEED -VDLEYS EDS -NSEPNVDLENQYNSKALKKEE -DPKAALSSFOKVLLELE -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----NMDFLCOVMDLLOEFYETITLD 144
gi | 71896195 | ref | NP_001026767.1 | MSNDNDDDFMCDDEED -VDLEYS EDS -NSEPNVDLENQYNSKALKKEE -DPKAALSSFOKVLLELE -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 137
gi | 23463271 | ref | NP_695209.1 | MSNDNDDDFMCDDEED -VDLEYS EDS -NSEPNVDLENQYNSKALKKEE -DPKAALSSFOKVLLELE -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 137
gi | 114656917 | ref | XP_510388.2 | MSNDNDDDFMCDDEED -VDLEYS EDS -NSEPNVDLENQYNSKALKKEE -DPKAALSSFOKVLLELE -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 137
gi | 70909327 | ref | NP_034069.2 | MSNDNDDDFMCDDEED -VDLEYS EDS -NSEPNVDLENQYNSKALKKEE -DPKAALSSFOKVLLELE -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 137
gi | 4759264 | ref | NP_004227.1 | MSNDNDDDFMCDDEED -VDLEYS EDS -NSEPNVDLENQYNSKALKKEE -DPKAALSSFOKVLLELE -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 137
gi | 74000051 | ref | XP_862009.1 | MSNDNDDDFMCDDEED -VDLEYS EDS -NSEPNVDLENQYNSKALKKEE -DPKAALSSFOKVLLELE -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 137
gi | 50344764 | ref | NP_001002055.1 | MSNDNDDDFMCDDEED -VDLEYS EDS -NSEPNVDLENQYNSKALKKEE -DPKAALSSFOKVLLELE -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 137
gi | 17505264 | ref | NP_491740.1 | ---MGDEYV -DDD EED -YGFYEYEDDS -GSEPNVDLENQYNSKALKKEE -DPKAALSSFOKVLLELE -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 134
gi | 18401293 | ref | NP_565632.1 | -----MASDADMEDYVGFYEYEDDE -QEEQVDLENQYNSKGMVET -EPEALSGFAEVVQME -PEKADWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 133
gi | 115435976 | ref | NP_001042746.1 | -----MGSDADMEDYVGFYEYEDDE -PEEQVDLENQYNSKGMVET -EPEALSGFAEVVQME -PEKADWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 133
gi | 39969429 | ref | XP_366105.1 | ---MSDDDFMQASDDEEYDFYEDDD -NNDGAVDIENKYYNAKQLQS -DPEALDEFLEIPLE -ESKGDWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 143
gi | 85074731 | ref | XP_965733.1 | ---MSDDDFMQASDDEEYDFYEDDD -EEDTGDVDIENKYYNAKQLQS -DPEALDEFLEIPLE -ESKGDWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 140
gi | 67992726 | ref | NP_001018220.1 | ---MSNDNDDDFMCDDEED -VDLEYS EDS -NSEPNVDLENQYNSKALKKEE -EPKAALASFOKVLLEN -GEGKEWGFKALKOMIKINFLCNLNFPEMMNRYKQLLTYIKS -AVTRNHSSEKINSILDYISTSK -----MDLLOEFYETITLD 138



gi | 17647149 | ref | NP_523517.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 284
gi | 31211457 | ref | XP_314698.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 285
gi | 194671647 | ref | XP_001250692.2 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 290
gi | 71896195 | ref | NP_001026767.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 283
gi | 23463271 | ref | NP_695209.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 283
gi | 114656917 | ref | XP_510388.2 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 283
gi | 70909327 | ref | NP_034069.2 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 283
gi | 4759264 | ref | NP_004227.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 283
gi | 74000051 | ref | XP_862009.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 283
gi | 50344764 | ref | NP_001002055.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 283
gi | 17505264 | ref | NP_491740.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 283
gi | 18401293 | ref | NP_565632.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 283
gi | 115435976 | ref | NP_001042746.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 279
gi | 39969429 | ref | XP_366105.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 289
gi | 85074731 | ref | XP_965733.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 286
gi | 67992726 | ref | NP_001018220.1 | ALRDAKNDRLWFKINTKLGKLYLFRSDFTKLQKILKQLHQSCTDD -GEDDLKKGQOLLEIYALEIOMYTAQNNKLLKALYEOS ---LHKISAIPHPPLIMGVIRECGGKMHLEGEFEKAHTDFFFAFKNYDESGSPRRITCLKYLIVLA 285



gi | 17647149 | ref | NP_523517.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 421
gi | 31211457 | ref | XP_314698.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 422
gi | 194671647 | ref | XP_001250692.2 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 427
gi | 71896195 | ref | NP_001026767.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 420
gi | 23463271 | ref | NP_695209.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 420
gi | 114656917 | ref | XP_510388.2 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 420
gi | 70909327 | ref | NP_034069.2 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 420
gi | 4759264 | ref | NP_004227.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 420
gi | 74000051 | ref | XP_862009.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 421
gi | 50344764 | ref | NP_001002055.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 420
gi | 17505264 | ref | NP_491740.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 432
gi | 18401293 | ref | NP_565632.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 415
gi | 115435976 | ref | NP_001042746.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 415
gi | 39969429 | ref | XP_366105.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 425
gi | 85074731 | ref | XP_965733.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 422
gi | 67992726 | ref | NP_001018220.1 | NMLMKSGINPFDSQEAQPKYKNDPEILAMTNLVS -AYQNNDI TEF EKILKTNHNSIMDDPFIREHIEBELLNRIRTOVLKIKLIPYTRIHIPFISKELNIDVADVESLLVOCILDNTIHGRIDQVNLLELDHQR -----SASR 418



gi		17647149		ref		NP_523517.1		-----YNALEKWSNQIQSLQFAVVQKMA-----	444
gi		31211457		ref		XP_314698.1		-----DIALEKLATQINSVQAAIINKMA-----	445
gi		194671647		ref		XP_001250692.2		-----YTALDKWTNQLNSLNQAVVSKLA-----	450
gi		71896195		ref		NP_001026767.1		-----YTALDKWTNQLNSLNQAVVSKLA-----	443
gi		23463271		ref		NP_695209.1		-----YTALDKWTNQLNSLNQAVVSKLA-----	443
gi		114656917		ref		XP_510388.2		-----YTALDKWTNQLNSLNQAVVSKLA-----	443
gi		70909327		ref		NP_034069.2		-----YTALDKWTNQLNSLNQAVVSKLA-----	443
gi		4759264		ref		NP_004227.1		-----YTALDKWTNQLNSLNQAVVSKLA-----	443
gi		74000051		ref		XP_862009.1		-----YTALDKWTNQLNSLNQAVVSKLA-----	444
gi		50344764		ref		NP_001002055.1		-----YTALDKWTNQLNSLNQAVVSKLA-----	443
gi		17505264		ref		NP_491740.1		-----TKKSDSKPGTSSEFSTTTSVLISSILQPPATSSCHQLSMDGLRVWAERLDSIQSNIGTRIKF-----	495
gi		18401293		ref		NP_565632.1		-----LHKAVDKWNSOLKSLSSNITSRVC-----	439
gi		115435976		ref		NP_001042746.1		-----KYQAIDKWTNQLKNIYQIVSNRVG-----	439
gi		39969429		ref		XP_366105.1		-----VAIKSLADALPLYFGQLFSSEGLSTGEASAGFFGGAEEGDFFMGFDEPLGGLGHAVRRSIRAGKGNAGLAWGRGSSSGAGSVSVLNASAVHSTF-----	522
gi		85074731		ref		XP_965733.1		-----QAIVLSEAVGNLENAVEKSTDGFPQPG-----GDFMNSMADQSADIGSLDDIMRSMGSGK-----RGRRVGLTQRAY-----	490
gi		67992726		ref		NP_001018220.1		-----IHNQLVEDVQKLWNIAIK-----	437

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