

gi	62955291	ref	NP_001017661.1	-----MMFGSLLF-----AVCCSAALAHF-----NKNLDQHWELWKKHKVLLSCEDEEVEGRRR--LWERNLQITVHNLEASMGMSYDLAINHMDMTTBEILOQLAVTRVPP-----GFKRPTAEVSSFA	113
gi	66912207	ref	NP_001019580.1	-----MMFGSLLF-----AVCCSAALAHF-----NKNLDQHWELWKKTKYKLIYVTEVEEVEGRRQ--LWERNLQITVHNLEASMGMSYDLAINHMDMTTBEILOQLALTHVPS-----GFKRQIANIVGSSGD	113
gi	10946582	ref	NP_067256.1	-----MRAPGHAAIRWLFWMPLVCSVAMEQLQR-----DPTLDYHWDLWKKTHEKEYDKNEEVEVRRLL--IWEKNLKFVIMLHNLEHSMGMHSYVGMNMGDMTNEEISCRMGALRISR-----QBPK--TIVTFRYSNR	121
gi	8393221	ref	NP_059016.1	-----MAVLGAGPV-----LCDNGATAER-----PTLDHHWDLWKKTRMRRNTDQNEEDVRRLL--IWEKNLKFVIMLHNLEHSMGMHSYVGMNMGDMTPEEVIYGMGSLRIPR-----PWNRR--SGTLKSSNQ	111
gi	23110962	ref	NP_004070.3	-----MKRLVCVLL-----VCS SAVAQLHK-----DPTLDHHWDLWKKTKYKQYKKEKNEEAVRRLL--IWEKNLKFVIMLHNLEHSMGMHSYDLGMNHLGDMTSEEVMSLMSLVRVPS-----QWQR--NITYKSNPNR	113
gi	114559418	ref	XP_001171268.1	-----MKRLVCVLL-----VCS SAVAQLHK-----DPTLDHHWDLWKKTKYKQYKKEKNEEAVRRLL--IWEKNLKFVIMLHNLEHSMGMHSYDLGMNHLGDMTSEEVMSLMSLVRVPS-----QWQR--NITYKSNPNR	113
gi	50950139	ref	NP_001002938.1	-----MKNLVGLLP-----LCS YAVAQVHK-----DPTLDHHWDLWKKTKYKQYKKEEVEAVRRLL--IWEKNLKFVIMLHNLEHSMGMHSYDLGMNHLGDMTSEEVMSLMSLVRVPS-----QWQR--NITYKSNPNR	113
gi	75812934	ref	NP_001028787.1	-----MNWLWALL-----LCS SAMAHVHR-----DPTLDHHWDLWKKTKYKQYKKEEVEAVRRLL--IWEKNLKFVIMLHNLEHSMGMHSYDLGMNHLGDMTSEEVMSLMSLVRVPS-----QWQR--NITYKSNPNR	113
gi	71897043	ref	NP_001026516.1	-----MELLRCMAV-----LVT LVAVMGHP-----DPTLDQHWLWKKAHGKEYRHOAEEGQRRRA--IWEKNLRLVIMLHNLEHSLGLHSYQLGMNMGDMTSEEVAALLTGLRVPPY-----GHNQ--TSTVRRRGG	112
gi	18413505	ref	NP_567376.1	MGSAK--SAMLILLVAVMVIASCATAIDMSVVSYDDNN-----RLHSVFDAEASLIEESVMVHKGVYV--SVAEKERRLITFEDNLRFTINRRAEN-----LSYRLGLTGFADLRLHEYKVEVCHGADPRPPRNHVMTSSDRYKTSADD	135
gi	18413507	ref	NP_567377.1	MGYAK--SAMLIFLLALVVIASCATAIDMSVVSYDDNNHVVITAGPGRRGGLFDAAEATLMEFESVMVHKGVYV--SVAEKERRLITFEDNLRFTINRRAEN-----LSYRLGLRFDLRLHEYGEICHGADPRPPRNHVMTSSDRYKTSADD	142
gi	42567068	ref	NP_567686.2	MGFVRFVCMITLFLVLLVFLVASAPSSAMDLPATSGGHNRR-----SNEEVFIFIFOMMMSKRGTYTNAIGEKERRFQNFKDNLRFDIQHNKAKN-----LSYQLGLTRFDLRLVQEYRDLFPGS--PKP--KQRNLKTSRRYVPLAGD	131



gi	62955291	ref	NP_001017661.1	VVPDITLDWRDKGVVTSVKNGCAGCSWAFSSVAGALEGQLMKTIGKLVDSLSPONLVDCCS--KYGNLGCNG--GYMSQAFQYVIDNGGIDSESYPPYCGQSGCRVYDPS--QRAANCISYKVFVSQGDQALKBALANIGFVSVVAID--ATRPO	257
gi	66912207	ref	NP_001019580.1	AVPDSLDWREKGVVSSVKMGACGCSWAFSSVAGALEGQLMKTIGKLVDSLSPONLVDCCS--KYGNKGCNG--GFMSDAFQYVIDNGGIDSDSAMPYRGVQQQCSVSSS--QRAANCKYYFVRQGDENALKQAVASVGFISVAID--ATRPO	257
gi	10946582	ref	NP_067256.1	TLPDITVDWREKGCVTVEVKYCGSCAGCWAFSAVAGALEGQLKLTIGKLLISL SAONLVDCCSNEEYGNKGGCGG--GYMTEAFQYIIDNGGIEADASYPKAMDEKCHNSK--NRAATCSRYIQLPFGDEEDALKEAVATKGFVSVGID--ASHS	267
gi	8393221	ref	NP_059016.1	TLPDSVDWREKGCVTINVKYCGSCGCSWAFSAEGALEGQLKLTIGKLVSL SAONLVDCCSIEEYGNKGGCGG--GFMTTEAFQYIIDNITS--IDSSEASYPKAMDEKCLYDPK--NRAATCSRYIELPFGDEEALKEAVATKGFVSVGID--ASHS	257
gi	23110962	ref	NP_004070.3	ILPDSVDWREKGCVTVEVKYCGSCGACWAFSAVAGALEAQQLKLTIGKLVSL SAONLVDCCST--EYGNKGCNG--GFMTTEAFQYIIDNKGIDSDASYPKAMDKQCVYDPSK--YRAATCSKYTELPGREDVLKEAVANKGFVSVGVD--ARHP	258
gi	114559418	ref	XP_001171268.1	ILPDSVDWREKGCVTVEVKYCGSCGACWAFSAVAGALEAQQLKLTIGKLVSL SAONLVDCCST--EYGNKGCNG--GFMTTEAFQYIIDNKGIDSDASYPKAMDKQCVYDPSK--YRAATCSKYTELPGREDVLKEAVANKGFVSVGVD--ALHP	258
gi	50950139	ref	NP_001002938.1	KLPDSVDWREKGCVTVEVKYCGSCGACWAFSAVAGALEAQQLKLTIGKLVSL SAONLVDCCST--EYGNKGCNG--GFMTTEAFQYIIDNNGIDSEASYPKAMNGKCRVYDPSK--KRAATCSKYTELPGSEEDALKEAVANKGFVSVVAID--ASHYS	258
gi	75812934	ref	NP_001028787.1	KLPDSMDWREKGCVTVEVKYCGSCGACWAFSAVAGALEAQVLLKLTIGKLVSL SAONLVDCCSM--AKYGNKGGCGG--GFMTTEAFQYIIDNNGIDSEASYPKAMDKQCVYDVK--NRAATCSRYIELPFGDEEALKEAVANKGFVSVGID--ASHS	258
gi	71897043	ref	NP_001026516.1	--APDAMDWREKGCVTVEKNGCAGCAGCWAFSAVAGALEAQVLLKLTIGKLVSL SAONLVDCCSM--MYGNKGGCGG--GFMTTEAFQYIIDNNGIDSEESYPPYMAQNGTCCQNVVS--TRAATCSKYVELPVADEAALKDAVANVGFVSVVAID--ATQPT	255
gi	18413505	ref	NP_567376.1	VLPKESVDWRNEGAVTEVKDQGLCRS WAFSTVGAVEGLNKIVTIGELVTLSEODLINCNK---ENNGCGG--GKLETAAYEFIMKNGGLGIDNDYVYKAVNGVCDGRLKENNKNVMIDGYENLPANDESALMKAVAHQ--FVTAVID--SSRE	278
gi	18413507	ref	NP_567377.1	VLPKESVDWRNEGAVTEVKDQGLCRS WAFSTVGAVEGLNKIVTIGELVTLSEODLINCNK---ENNGCGG--GKLETAAYEFIMKNGGLGIDNDYVYKAVNGVCDGRLKENNKNVMIDGYENLPANDESALMKAVAHQ--FVTAVID--SSRE	285
gi	42567068	ref	NP_567686.2	QLPESVDWRNEGAVTEVKDQGLCRS WAFSTVAAVEGLNKIVTIGELVTLSEODLINCNL---VNGYCGGLMDTAFQFLINNGLDSEKDYVYKAVNGVCDGRLKENNKNVMIDGYENLPANDESALMKAVAHQ--FVTAVID--KKSQE	275



gi	62955291	ref	NP_001017661.1	FIFYRSGVYDDPSCTQKVNHGVLAVGYGILSGDYLWLVKNSWGAAGFDGGYIIRIARNKNN-----MCGIASIASEACPVI-----	330
gi	66912207	ref	NP_001019580.1	FVLMHSGVYNDPTCSKRVNHAVLVVGYGILSGDHWLVKNSWGRFRFDGGYIRMARNNKNN-----MCGIASIAYACYVPM-----	330
gi	10946582	ref	NP_067256.1	FFLYRSGVYDDPSCTGNVNHGVLVVGYGILDKGDKYWLKNSWGLNFGDQGYIRMARNNKNN-----HCGIASIYCSYPEI-----	340
gi	8393221	ref	NP_059016.1	FFLYRSGVYDDPSCTENMNHGVLVVGYGILDKGDKYWLKNSWGLHFGDQGYIRMARNNKNN-----HCGIASIYCSYPEI-----	330
gi	23110962	ref	NP_004070.3	FFLYRSGVYVYEPSCTQNVNHGVLVVGYGDLNKGKEYWLKNSWGNHFGEEGYIRMARNNKNN-----HCGIASIFPSYPEI-----	331
gi	114559418	ref	XP_001171268.1	FFLYRSGVYVYEPSCTQNVNHGVLVVGYGDLNKGKEYWLKNSWGNHFGEEGYIRMARNNKNN-----HCGIASIFPSYPEI-----	331
gi	50950139	ref	NP_001002938.1	FFLYRSGVYVYEPSCTQNVNHGVLVVGYGDLNKGKEYWLKNSWGNHFGDQGYIRMARNSGN-----HCGIASIYPSYPEI-----	331
gi	75812934	ref	NP_001028787.1	FFLYRSGVYVYEPSCTQNVNHGVLVVGYGDLNKGKEYWLKNSWGLHFGDQGYIRMARNSGN-----HCGIASIYPSYPEI-----	331
gi	71897043	ref	NP_001026516.1	FFLYRSGVYDDPRCTQEVNHGVLVVGYGILNEKDFWLKNSWGERFDDGGYIRMSRNHAN-----HCGIASIYASYPQI-----	328
gi	18413505	ref	NP_567376.1	FQLVRESGVFDGSG--CGTILNHGVLVVGYGILNEGRDYLWLVKNSRGTITWGEAGYMKMARNIANPRGLCGIAMRASYPKLSNFSFDKSSIA	364
gi	18413507	ref	NP_567377.1	FQLVRESGVFDGSG--CGTILNHGVLVVGYGILNEGRDYLWLVKNSRGTITWGEAGYMKMARNIANPRGLCGIAMRASYPKLSNFSFDKVSVA	371
gi	42567068	ref	NP_567686.2	FMLYRSCTIYNGP--CGTILNHALVIVVYGILNEGRDYWIIVKNSWGTITWGDAGYIKIARNFDPKGLCGIAMLASYPKLSANNA-----	356

