

gi | 7363433 | ref | NP_034561.1 | LGLSFTMPQIQDPASPSDGSTROSSPERLLDENVNTNFSQPNSPSEYCFDVS DMVN VFKLELVEKLF AEDTEAKNPFSTQD TDLDL-----EMLAPYIPMDDDFQLRSFDQLSPLENSPSPPSMS--TVI 900
 gi | 13242249 | ref | NP_077335.1 | LGLSFTMPQIQDPASPSDGSTROSSPE-----PNSPSEYCFDVS DMVN VFKLELVEKLF AEDTEAKNPFSAQD TDLDL-----EMLAPYIPMDDDFQLRSFDQLSPLENSPSPPSVVS--TVI 900
 gi | 4504385 | ref | NP_001521.1 | LELSF TMPQIQDQTPSPSDGSTROSSP-----EPNSPSEYCFYVDS DMVNEFKLELVEKLF AEDTEAKNPFSTQD TDLDL-----EMLAPYIPMDDDFQLRSFDQLSPLESSASPEASPPQSTVTI 900
 gi | 114653409 | ref | XP_001168785.1 | LELSF TMPQIQDQTPSPSDGSTROSSP-----EPNSPSEYCFYVDS DMVNEFKLELVEKLF AEDTEAKNPFSTQD TDLDL-----EMLAPYIPMDDDFQLRSFDQLSPLESSASPEASPPQSTVTI 900
 gi | 73963131 | ref | XP_537471.2 | LELSF TMPQIQDQTPSPSDGSTROSSPEVSSGKSKHIEFLLPNSPSEYCFDVS DMVNEFKLELVEKLF AEDTEAKNPFSTQD TDLDL-----EMLAPYIPMDDDFQLRSFDQLSPLENSSTSPQSA--TII 900
 gi | 117935055 | ref | NP_776764.2 | LELSF TMPQIQDQTPSPSDGSTROSSP-----EPNSPSEYCFDVS DMVNEFKLELVEKLF AEDTEAKNPFSTQD TDLDL-----EMLAPYIPMDDDFQLRSFDQLSPLENSSTSPQSA--TNI 900
 gi | 45383550 | ref | NP_989628.1 | LELSF TMPQIQDQTPSPSDASTSSSP-----EPSNPNDYCFDVDNDMANEFKLELVEKLF AIDTEAKNPFSTQD TDLDL-----EMLAPYIPMDDDFQLRSFDQLSPLESSSGS--NAA--TII 900
 gi | 41053885 | ref | NP_956527.1 | -----LLPCRRRHFG-----
 gi | 24651293 | ref | NP_524584.2 | VANSPLSPLPNSTATASNPESHQQQQHINQQQQQQOQHHPQHNSNSSSNIDPLFNYSNDTSCSGLHSPSITKSPEDSSLPSCSPNSLIQEDDFEFAFAMRAPYIPIDDDMPLLETETDLMWCPPDLQTMVPEKIDAIQ 900
760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900



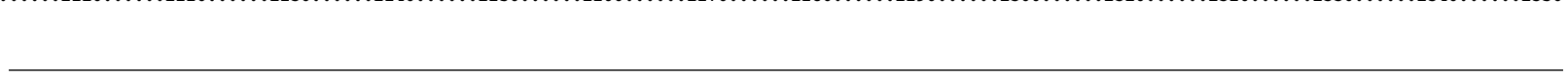
gi | 7363433 | ref | NP_034561.1 | GFOOTQLQKPIITATAITL-----TATTDESKIEIKDNKEDIKILIASPSTQVPEITAKASAYS-GTHSR TASPRDRAGKRVIEQDKAHPRSLK-LSVTLNORNIVPEEELNPKTIASONAQRKRKMEHDGSLFQAAGIGTLLQOPG 1050
 gi | 13242249 | ref | NP_077335.1 | GFOOTQLQKPIITVTAIA-----TATTDESKAVTKDNIEDIKILIASPSTQVPEITAKASAYS-GTHSR TASPRDRAGKRVIEKDKAHPRSLN-LSVTLNORNIVPEEELNPKTIALONAQRKRKMEHDGSLFQAAGIGTLLQOPG 1050
 gi | 4504385 | ref | NP_001521.1 | VFQQTQIQEPTANATITL-----TATTDELKTVTKDRMEDIKILIASPSPTHIHKEITTSATSSPYR-DTQSR TASPNRAGKGVIEQTEKSHPRSPNVLSVALSORTTVPEEELNPKILALONAQRKRKMEHDGSLFQAAGIGTLLQOPD 1050
 gi | 114653409 | ref | XP_001168785.1 | VFQQTQIQEPTANATITL-----TATTDELKTVTKDRMEDIKILIASPSPTHIHKEITTSATSSPYR-DTQSR TASPNRAGKGVIEQTEKSHPRSPNVLSVALSORTTVPEEELNPKILALONAQRKRKMEHDGSLFQAAGIGTLLQOPD 1050
 gi | 73963131 | ref | XP_537471.2 | VFQPTPMQEPPLTITSTL-----TATTDELKTVTKDGIEDIKILIAAPSPTHVVKVITTSATSSPYR-DTQSR TASPNRAGKGVIEQTEKSHPRSPNVLSVALSORTTVPEEELNPKILALONAQRKRKMEHDGSLFQAAGIGTLLQOPD 1050
 gi | 117935055 | ref | NP_776764.2 | VFQPTPMQEPPIAVITL-----TATSDELKTVTKDGMEDIKILIAFSPPHVVKPPCATSSPYR-DTQSR TASPNRAGKGVIEQTEKSHPRSPNVLSVALSORTTVPEEELNPKILALONAQRKRKMEHDGSLFQAAGIGTLLQOPD 1050
 gi | 45383550 | ref | NP_989628.1 | ILQQTQIP-----STAADEIKPVAER-VDDVKALIVPSPPVHVINDTSSAPSPYS-GNRSR TASPIRAGKGVIEQTEKSCFGAPSLITVTLNKRSTAMDEELNPKMLALHNAQRKRKMEHDGSLFQAAGIGSLFQGTG 1050
 gi | 41053885 | ref | NP_956527.1 | -----PLHPTT-----CAVHLERS-----VAVGMPLHDPAP 1050
 gi | 24651293 | ref | NP_524584.2 | QQLLQLQDQHQQVAGNIGYQQQQQQPQLLQVHFNSLCSSPAETVSSLSPPVQQHQQQQAAVFTSDSELAALLCSGNGTLLSILAGSGVTVVAEECNERLQHQHQQQDCTSGNEFRITFQLQQLGLLEEQQRQQQQQQQQQQ 1050
910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050



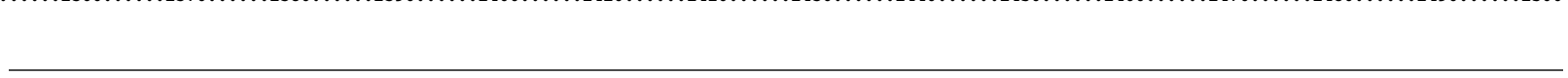
gi | 7363433 | ref | NP_034561.1 | DCAPTMSLSWKR-----VKGFISSEQNGTEOKIILIPSDLACRLLGQSMDESGLPQLTSDYDCEVNAPE-----IQGSRNLLQGEELLRALDQVN----- 1200
 gi | 13242249 | ref | NP_077335.1 | DRAPMMSLSWKR-----VKGYISSEQDGMEOKTIIFLIPSDLACRLLGQSMDESGLPQLTSDYDCEVNAPE-----IQGSRNLLQGEELLRALDQVN----- 1200
 gi | 4504385 | ref | NP_001521.1 | DHAATMSLSWKR-----VKGCKSSEQNGMEOKTIILIPSDLACRLLGQSMDESGLPQLTSDYDCEVNAPE-----IQGSRNLLQGEELLRALDQVN----- 1200
 gi | 114653409 | ref | XP_001168785.1 | DHAATMSLSWKR-----VKGCKSSEQNGMEOKTIILIPSDLACRLLGQSMDESGLPQLTSDYDCEVNAPE-----IQGSRNLLQGEELLRALDQVN----- 1200
 gi | 73963131 | ref | XP_537471.2 | DRATMSLSWKR-----VKGCKSSEQNGMEOKTIILIPSDLACRLLGQSMDESGLPQLTSDYDCEVNAPE-----IQGSRNLLQGEELLRALDQVN----- 1200
 gi | 117935055 | ref | NP_776764.2 | DRATMSLSWKR-----VKGCKSSEQNGMEOKTIILIPSDLACRLLGQSMDESGLPQLTSDYDCEVNAPE-----IQGSRNLLQGEELLRALDQVN----- 1200
 gi | 45383550 | ref | NP_989628.1 | DRGGNASLWKR-----VKACKTNGHNGVEOKIILISLDIASKLLGQSMDESGLPQLTSDYDCEVNAPE-----IQGSRNLLQGEELLRALDQVN----- 1200
 gi | 41053885 | ref | NP_956527.1 | HRAAVSSTTERC-----LRC----- 1200
 gi | 24651293 | ref | NP_524584.2 | QQLLNLNIECKKKEKYDVMGGSLCHPMEDAFENDYSKDSANLDCWDLIQMVVDTEPVSPNAASPPCKVSAIQLLQQQLQQQLQQQQIILNAVPLIITQNNKELMQQQQQQQLQEQQLQEQPAIKLLNGASIAPIVTKAIIRLVE 1200
1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200



gi | 7363433 | ref | NP_034561.1 | -----
 gi | 13242249 | ref | NP_077335.1 | -----
 gi | 4504385 | ref | NP_001521.1 | -----
 gi | 114653409 | ref | XP_001168785.1 | -----
 gi | 73963131 | ref | XP_537471.2 | -----
 gi | 117935055 | ref | NP_776764.2 | -----
 gi | 45383550 | ref | NP_989628.1 | -----
 gi | 41053885 | ref | NP_956527.1 | -----
 gi | 24651293 | ref | NP_524584.2 | SKPPTTQSRMAKVNLPQQQHGKRRHLNSATGAGNPVESKRLKSGTLCLDVQSPOLLOGLIGKDPAQOQTAAKRAGSERWQLHAEKQKQKQQQQNSV LKNLLVSGRDDDDSEAMIIDEDNSLVQPIPLGKYGLPLHCHTSTSSVI 1350
1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350



gi | 7363433 | ref | NP_034561.1 | -----
 gi | 13242249 | ref | NP_077335.1 | -----
 gi | 4504385 | ref | NP_001521.1 | -----
 gi | 114653409 | ref | XP_001168785.1 | -----
 gi | 73963131 | ref | XP_537471.2 | -----
 gi | 117935055 | ref | NP_776764.2 | -----
 gi | 45383550 | ref | NP_989628.1 | -----
 gi | 41053885 | ref | NP_956527.1 | -----
 gi | 24651293 | ref | NP_524584.2 | RDYHNNPLISGTFNQLSPVPGGSDSSGGDGETGVSVSLDDVPPGLIACDIDASSDGIENSLMDGASGSPRKRLLSSTNSSTNQAESAPPALDVEIPVTKSVEEVEFGGSGSNAPSRKRTSIFLDSSNPLLHPTAMMDLVNDDYIMG 1500
1360.....1370.....1380.....1390.....1400.....1410.....1420.....1430.....1440.....1450.....1460.....1470.....1480.....1490.....1500



gi		7363433		ref		NP_034561.1		-----	1521
gi		13242249		ref		NP_077335.1		-----	1521
gi		4504385		ref		NP_001521.1		-----	1521
gi		114653409		ref		XP_001168785.1		-----	1521
gi		73963131		ref		XP_537471.2		-----	1521
gi		117935055		ref		NP_776764.2		-----	1521
gi		45383550		ref		NP_989628.1		-----	1521
gi		41053885		ref		NP_956527.1		-----	1521
gi		24651293		ref		NP_524584.2		E G G F E F S D N Q L E Q V L G W P E I A	1521
							1510.....1520.	
