

gi | 22507337 | ref | NP\_683734.1 | MS PAAAAADGGERRRPPPLGGREGRSARARGYGGPAGAAALGLALLGLALYLVPAAAAALAVLAVGA AAWWGLSREPRGPRALS FVDRARHPRPALTASPPPAKSPVNGS --- LCEPRSP - LGGPDPAEILLMGSYLKPKGPPPEPALR 144  
gi | 16758424 | ref | NP\_446074.1 | MS PAAAAADGGERRRPPPLGVREGRGRTGCGGPAGAAALGLALLGLALYLVPAAAAALAVLAVGA AAWWGLSREPRGPRGLS FVRESRRHPRPALTASPLPAKSPVNGS --- LCEPRSP - LGGPDPAEILLMGSYLKPKGPPPEPALR 144  
gi | 73957770 | ref | XP\_546930.2 | MS PAAATAAGGNRRRPTAS VREGRG -- WCGRPAGAAALLGLSLLGLVLYLVPAAAAALAVLAVGA AAWWGLSREPRGSRALS LVLVWARRQRT -- LLASP - PAKSAANGN --- LLEPRSP - LEGPDPAEILLMGSYLKPKGPPPEPAPA 139  
gi | 150378545 | ref | NP\_001092885.1 | MS PAAAAAGAGERRRPIAS VRDGRG -- RCGGGPAGAAALLGLSLVGLLLYLVPAAAAALAVLAVGT TAAWGLSREPRGSRPLSS FVRKARHRT -- LFASP - PAKSTANGN --- LLEPRIL - LEGPDPAEILLMGSYMGKPGPPPEPAPA 139  
gi | 26051278 | ref | NP\_742017.1 | MS PAAAAAGAGERRRPIAS VRDGRG -- RCGGGPAGAAALLGLSLVGLLLYLVPAAAAALAVLAVGT TAAWGLSREPRGSRPLSS FVQKARHRT -- LFASP - PAKSTANGN --- LLEPRIL - LEGPDPAEILLMGSYLKPKGPPPEPAPA 139  
gi | 114613887 | ref | XP\_001144107.1 | MS PAAAAAGAGERRRPIAS VRDGRG -- RCGGGPAGAAALLGLSLVGLLLYLVPAAAAALAVLAVGT TAAWGLSREPRGSRPLSS FVQKARHRT -- LFASP - PAKSTANGN --- LLEPRIL - LEGPDPAEILLMGSYMGKPGPPPEPAPA 139  
gi | 114614075 | ref | XP\_001154568.1 | MS PAAAAAGAGERRRPIAS VRDGRG -- RCGGGPAGAAALLGLSLVGLLLYLVPAAAAALAVLAVGT TAAWGLSREPRGSRPLSS FVQKARHRT -- LFASP - PAKSTANGN --- LLEPRIL - LEGPDPAEILLMGSYLKPKGPPPEPAPA 139  
gi | 118100010 | ref | XP\_415711.2 | MS PAAAAAGAGERRRPIAS VRDGRG -- RCGGGPAGAAALLGLSLVGLLLYLVPAAAAALAVLAVGT TAAWGLSREPRGSRPLSS FVQKARHRT -- LFASP - PAKSTANGN --- LLEPRIL - LEGPDPAEILLMGSYMGKPGPPPEPAPA 139  
gi | 189524475 | ref | XP\_696713.3 | MS PAAAAAGAGERRRPIAS VRDGRG -- RCGGGPAGAAALLGLSLVGLLLYLVPAAAAALAVLAVGT TAAWGLSREPRGSRPLSS FVQKARHRT -- LFASP - PAKSTANGN --- LLEPRIL - LEGPDPAEILLMGSYMGKPGPPPEPAPA 139  
gi | 21356627 | ref | NP\_650096.1 | MS PAAAAAGAGERRRPIAS VRDGRG -- RCGGGPAGAAALLGLSLVGLLLYLVPAAAAALAVLAVGT TAAWGLSREPRGSRPLSS FVQKARHRT -- LFASP - PAKSTANGN --- LLEPRIL - LEGPDPAEILLMGSYMGKPGPPPEPAPA 139  
gi | 158298249 | ref | XP\_554380.3 | MS PAAAAAGAGERRRPIAS VRDGRG -- RCGGGPAGAAALLGLSLVGLLLYLVPAAAAALAVLAVGT TAAWGLSREPRGSRPLSS FVQKARHRT -- LFASP - PAKSTANGN --- LLEPRIL - LEGPDPAEILLMGSYMGKPGPPPEPAPA 139



gi | 22507337 | ref | NP\_683734.1 | --- QDPRERPGR --- RPPAR --- SPPASAVRVHHVYPALPTPLLRPSRRPDRHCGPLSSRFVITPRRRYPIQQAQYSLLGALPTVCWNGGHKAVLSPRNSRMVCSPTVTRIAAPPD SKLFRSSMSEQILD TLSSPSSNAPDPC 282  
gi | 16758424 | ref | NP\_446074.1 | --- QDPRDRPGR --- RPPSR --- SPPSSSARVHHVYPALPTPLLRPSRRPDRHCGPLSSRFVITPRRRYPIQQAQYSLLGALPTVCWNGGHKAVLSARNRSMVCSPTVTRIAAPPD SKLFRSPMPPEQILS TLSSPSSNAPDPC 282  
gi | 73957770 | ref | XP\_546930.2 | --- PEARLDRERGR --- RPPVRTAS PAPS AHQVQVH --- PSLPTSLLRPSRRPDRHCGPLSSRFVITPRRRYPIQQAQYSLLGALPTVCWNGGHKAVLSPRNSRMVCSPTVTRIAAPPD SKLFRSPMPPEQILS TLSSPSSNAPDPC 42  
gi | 150378545 | ref | NP\_001092885.1 | --- PEARLDRERGR --- RPPVRTAS PAPS AHQVQVH --- PSLPTSLLRPSRRPDRHCGPLSSRFVITPRRRYPIQQAQYSLLGALPTVCWNGGHKAVLSPRNSRMVCSPTVTRIAAPPD SKLFRSPMPPEQILS TLSSPSSNAPDPC 281  
gi | 150378545 | ref | XP\_596969.4 | --- PEARLDRERGR --- RPPVRTAS PAPS AHQVQVH --- PSLPTSLLRPSRRPDRHCGPLSSRFVITPRRRYPIQQAQYSLLGALPTVCWNGGHKAVLSPRNSRMVCSPTVTRIAAPPD SKLFRSPMPPEQILS TLSSPSSNAPDPC 42  
gi | 26051278 | ref | NP\_742017.1 | --- PEARLDRERGR --- RPPVRTAS PAPS AHQVQVH --- PSLPTSLLRPSRRPDRHCGPLSSRFVITPRRRYPIQQAQYSLLGALPTVCWNGGHKAVLSPRNSRMVCSPTVTRIAAPPD SKLFRSPMPPEQILS TLSSPSSNAPDPC 42  
gi | 114613887 | ref | XP\_001144107.1 | --- PEGDLRNRPGR --- RPPARAPRSPPPSPPAHRVHHVYPSLPTPLLRPSRRPDRHCGPLSSRFVITPRRRYPIQQAQYSLLGALPTVCWNGGHKAVLSPRNSRMVCSPTVTRIAAPPD SKLFRSPMPPEQILS TLSSPSSNAPDPC 284  
gi | 114614075 | ref | XP\_001154568.1 | --- PEGDLRNRPGR --- RPPARAPRSPPPSPPAHRVHHVYPSLPTPLLRPSRRPDRHCGPLSSRFVITPRRRYPIQQAQYSLLGALPTVCWNGGHKAVLSPRNSRMVCSPTVTRIAAPPD SKLFRSPMPPEQILS TLSSPSSNAPDPC 284  
gi | 118100010 | ref | XP\_415711.2 | --- PEGDLRNRPGR --- RPPARAPRSPPPSPPAHRVHHVYPSLPTPLLRPSRRPDRHCGPLSSRFVITPRRRYPIQQAQYSLLGALPTVCWNGGHKAVLSPRNSRMVCSPTVTRIAAPPD SKLFRSPMPPEQILS TLSSPSSNAPDPC 12  
gi | 189524475 | ref | XP\_696713.3 | PRDILMGSYLAKPEESPSAAVRPAGSGSMHPRQLRERLARPNHAVHTPNRRLSFGDPAGNASRFITPORHYPLQQTGTSPIGVMPAKWDGGRKKNILTORNSPTVHSPVTVKIRAPDSTRSSFFNHLNSPGAVTSPGIGADPC 276  
gi | 21356627 | ref | NP\_650096.1 | ERSFYSNTLSLRLSNLSLVGLVPKITEQEQLSRNRPDILPPHPPQESPTRSVLEELKEISRKRINEDTQQAQDYTKRSCQONVDVDFVAHHRQQKRLNLOQNCQFKRQELTVSVPRLHSLSAASALQHMNNGTISF 295  
gi | 158298249 | ref | XP\_554380.3 | TRSVLDALKEISRKRINSEELDADRIKQCQLSLELDAAAGGPPS TAAVAIGTHGLATKRREQAMES PASPSELGPGGLGGVGRAPSGEGEQTKRKLCKVKNLISLSSSLVAMNTPKRNVPVRNDRRLYMHNSISMSPAI 281



gi | 22507337 | ref | NP\_683734.1 | AKETVLNALKE-KKKRTVAEEDQLHLDGQENKRRRHDSGGSGHSAFEPLVANG--VPAAFVVKPGSLKRRSLASQSSDDHLNK---RSRTSSVSSLAS-ACITGIPSSRNATISSYSTRGISQLWKRSGPTSSPSSPASSRSQTPER 424  
gi | 16758424 | ref | NP\_446074.1 | AKETVLNALKE-KKKRTVAEEDQLHLDGQENKRRRHDSGGSGHSAFEPLVANG--VPAAFVVKPGSLKRRSLASQSSDDHLNK---RSRTSSVSSLAS-CTGIPSSRNATISSYSTRGISQLWKRSGPTSSPSSPASSRSQTPER 424  
gi | 73957770 | ref | XP\_546930.2 | AKETVLSALKE-RKKRTVEEEDQIFSDSQENKRRRHDSGGSGHSAFEPLVANG--VPAAFVVKPGSLKRRSLASQSSDDHLNK---RSRTSSVSSLAS-TYTGIPSSRNATISSYSTRGISQLWKRSGPTSSPSSPASSRSQTPER 184  
gi | 150378545 | ref | NP\_001092885.1 | AKETVLNALKE-RKKRTVEEEDQMSADGQENKRRRHDSGGSGHSAFEPLVANG--VPAAFVVKPGSLKRRSLASQSSDDHLNK---RSRTSSVSSLAS-CTGIPSSRNATISSYSTRGISQLWKRSGPTSSPSSPASSRSQTPER 424  
gi | 150378545 | ref | XP\_596969.4 | AKETVLSALKE-RKKRTVEEEDQIFSDSQENKRRRHDSGGSGHSAFEPLVANG--VPAAFVVKPGSLKRRSLASQSSDDHLNK---RSRTSSVSSLAS-TYTGIPSSRNATISSYSTRGISQLWKRSGPTSSPSSPASSRSQTPER 185  
gi | 26051278 | ref | NP\_742017.1 | AKETVLSALKE-RKKRTVEEEDQIFSDSQENKRRRHDSGGSGHSAFEPLVANG--VPAAFVVKPGSLKRRSLASQSSDDHLNK---RSRTSSVSSLAS-TYTGIPSSRNATISSYSTRGISQLWKRSGPTSSPSSPASSRSQTPER 185  
gi | 114613887 | ref | XP\_001144107.1 | AKETVLSALKE-RKKRTVEEEDQIFSDSQENKRRRHDSGGSGHSAFEPLVANG--VPAAFVVKPGSLKRRSLASQSSDDHLNK---RSRTSSVSSLAS-TYTGIPSSRNATISSYSTRGISQLWKRSGPTSSPSSPASSRSQTPER 426  
gi | 114614075 | ref | XP\_001154568.1 | AKETVLSALKE-RKKRTVEEEDQIFSDSQENKRRRHDSGGSGHSAFEPLVANG--VPAAFVVKPGSLKRRSLASQSSDDHLNK---RSRTSSVSSLAS-TYTGIPSSRNATISSYSTRGISQLWKRSGPTSSPSSPASSRSQTPER 427  
gi | 118100010 | ref | XP\_415711.2 | AAG---RHDSSGGQSAFEPLVANG--APASLIPKPGSLKRRSLASQSSDDHLNK---RSRTSSVSSLAS-TYTGIPSSRNATISSYSTRGISQLWKRSGPTSSPSSPASSRSQTPER 115  
gi | 189524475 | ref | XP\_696713.3 | SREAVLSVLR-SRKRVEEEDKSAASGGQSKRRRHDSGGSGHSAFEPLVANG--APASLIPKPGSLKRRSLASQSSDDHLNK---RSRTSSVSSLAS-TYTGIPSSRNATISSYSTRGISQLWKRSGPTSSPSSPASSRSQTPER 419  
gi | 21356627 | ref | NP\_650096.1 | TQSPPEQVAKRPNCSYNDITSSLS SCRHSNKRKLLDRERFQHSKNDTLASGGSSPENSPENVAKIQRKVDAAVSKAMSPVVVAAPVAPASRAISAPAKQVAPVTEKPKLILFNARQSLTAEQPRPDLSPPEVDAGEYAGQVFK 445  
gi | 158298249 | ref | XP\_554380.3 | IPTSSSLVGLATPENASKPEMQLPLPHRAPPKITLFLNRYEAAAMTVGADRSGSPSARGTSRHSASRLSSDGEDDEHGE--GSGKVQVFK--KERKPNVDVTLGLGEGGSSSRDILKPKPAPSKLIVMLKCLSDPDLDDYEE 422



gi | 22507337 | ref | NP\_683734.1 | PAKKIREEEPQQSSSPLVTDKESGPEKVIDITGKQSSW---TSPPTPGSSGQRKKIOLLPSRRGD---QLTLPPLP-ELGYSITAEDDLMEKASLQWFKVLEDKPDASASATDGPSPSPPTFTLPAVGAASFP 560  
gi | 16758424 | ref | NP\_446074.1 | PAKKIREEEPCHQSSSAPLVTDKESGPEKVIDITGKQSSW---TSPPTPGSSGQRKKIOLLPSRRGD---QLTLPPLP-ELGYSITAEDDLMEKASLQWFKVLEDKPDASASATDGPSPSPPTFTLPAVGAASFP 561  
gi | 73957770 | ref | XP\_546930.2 | PAKKIREDELSHHSSSTPLAADKESQGEKAADITTSKAQNSW---SSPPTPGSSGQRKKIOLLPSRRGD---RLTLPPLP-ELGYSITAEDDLMEKASLQWFKVLEDKPDASASATDGPSPSPPTFTLPAVGAASFP 321  
gi | 150378545 | ref | NP\_001092885.1 | PAKKIREDELCHHSSSTPLAADKESQGEKAADITPRKKQNSW---NSQSTPGSSGQRKKIOLLPSRRGD---QLTLPPLP-ELGYSITAEDDLMEKASLQWFKVLEDKPDASASATDGPSPSPPTFTLPAVGAASFP 561  
gi | 150378545 | ref | NP\_001092885.1 | PAKKIREDELCHHSSSTPLAADKESQGEKAADITPRKKQNSW---NSQSTPGSSGQRKKIOLLPSRRGD---QLTLPPLP-ELGYSITAEDDLMEKASLQWFKVLEDKPDASASATDGPSPSPPTFTLPAVGAASFP 321  
gi | 26051278 | ref | NP\_742017.1 | PAKKIREDELCHHSSSTPLAADKESQGEKAADITPRKKQNSW---NSQSTPGSSGQRKKIOLLPSRRGD---QLTLPPLP-ELGYSITAEDDLMEKASLQWFKVLEDKPDASASATDGPSPSPPTFTLPAVGAASFP 321  
gi | 114613887 | ref | XP\_001144107.1 | PAKKIREDELCHHSSSTPLAADKESQGEKAADITPRKKQNSW---NSQSTPGSSGQRKKIOLLPSRRGD---QLTLPPLP-ELGYSITAEDDLMEKASLQWFKVLEDKPDASASATDGPSPSPPTFTLPAVGAASFP 562  
gi | 114614075 | ref | XP\_001154568.1 | PAKKIREDELCHHSSSTPLAADKESQGEKAADITPRKKQNSW---NSQSTPGSSGQRKKIOLLPSRRGD---QLTLPPLP-ELGYSITAEDDLMEKASLQWFKVLEDKPDASASATDGPSPSPPTFTLPAVGAASFP 563  
gi | 118100010 | ref | XP\_415711.2 | PAKKIREDELCHHSSSTPLAADKESQGEKAADITPRKKQNSW---NSQSTPGSSGQRKKIOLLPSRRGD---QLTLPPLP-ELGYSITAEDDLMEKASLQWFKVLEDKPDASASATDGPSPSPPTFTLPAVGAASFP 221  
gi | 189524475 | ref | XP\_696713.3 | AAKKAREEDATSPSSSTFAKIDKVAADPPSPNTIKLTPKSEAPVATSDSGSSGQRKKIOLLPSRRGD---QLTLPPLP-ELGYSITAEDDLMEKASLQWFKVLEDKPDASASATDGPSPSPPTFTLPAVGAASFP 560  
gi | 21356627 | ref | NP\_650096.1 | PKQNSMLAANKPVERTHKHLALMISGLGELYLGEDELDAAPKSAAPAVTLPTVVKPIIAPVTTSTLVTSTALISTAPSKPIILSNQVVKPADVPTNTSTGVPKLVLEDPAPPAPKTEQTPKFKIDKVPAAQADIPPKFELS 595  
gi | 158298249 | ref | XP\_554380.3 | EQEEQSRPSPRAIAPQSRNGFSFGSNAPAKDVIDGPKELPAGSPKQPATTLKDSAASTPVAASSTP---ETVVAVPAACSAANEAKTASAPSEAKTLTFSFGNSGTTTVEPPPVAITTTSTGFSLSAKPLATS 565



gi | 22507337 | ref | NP\_683734.1 | A... 688  
gi | 16758424 | ref | NP\_446074.1 | A... 688  
gi | 73957770 | ref | XP\_546930.2 | A... 452  
gi | 194678652 | ref | XP\_596969.4 | T... 692  
gi | 150378545 | ref | NP\_001092885.1 | T... 451  
gi | 26051278 | ref | NP\_742017.1 | T... 451  
gi | 114613887 | ref | XP\_001144107.1 | T... 701  
gi | 114614075 | ref | XP\_001154568.1 | T... 693  
gi | 118100010 | ref | XP\_415711.2 | S... 355  
gi | 189524475 | ref | XP\_696713.3 | S... 700  
gi | 21356627 | ref | NP\_650096.1 | K... 745  
gi | 158298249 | ref | XP\_554380.3 | K... 704



gi | 22507337 | ref | NP\_683734.1 | A... 823  
gi | 16758424 | ref | NP\_446074.1 | A... 823  
gi | 73957770 | ref | XP\_546930.2 | A... 507  
gi | 194678652 | ref | XP\_596969.4 | V... 834  
gi | 150378545 | ref | NP\_001092885.1 | V... 595  
gi | 26051278 | ref | NP\_742017.1 | A... 595  
gi | 114613887 | ref | XP\_001144107.1 | A... 845  
gi | 114614075 | ref | XP\_001154568.1 | A... 837  
gi | 118100010 | ref | XP\_415711.2 | A... 442  
gi | 189524475 | ref | XP\_696713.3 | F... 809  
gi | 21356627 | ref | NP\_650096.1 | N... 869  
gi | 158298249 | ref | XP\_554380.3 | F... 812



gi | 22507337 | ref | NP\_683734.1 | S... 955  
gi | 16758424 | ref | NP\_446074.1 | S... 957  
gi | 73957770 | ref | XP\_546930.2 | P... 649  
gi | 194678652 | ref | XP\_596969.4 | H... 972  
gi | 150378545 | ref | NP\_001092885.1 | P... 730  
gi | 26051278 | ref | NP\_742017.1 | P... 730  
gi | 114613887 | ref | XP\_001144107.1 | P... 973  
gi | 114614075 | ref | XP\_001154568.1 | P... 972  
gi | 118100010 | ref | XP\_415711.2 | P... 581  
gi | 189524475 | ref | XP\_696713.3 | K... 950  
gi | 21356627 | ref | NP\_650096.1 | K... 1012  
gi | 158298249 | ref | XP\_554380.3 | T... 960



gi | 22507337 | ref | NP\_683734.1 | T... 1081  
gi | 16758424 | ref | NP\_446074.1 | T... 1080  
gi | 73957770 | ref | XP\_546930.2 | T... 1071  
gi | 194678652 | ref | XP\_596969.4 | T... 1097  
gi | 150378545 | ref | NP\_001092885.1 | T... 868  
gi | 26051278 | ref | NP\_742017.1 | T... 865  
gi | 114613887 | ref | XP\_001144107.1 | T... 1109  
gi | 114614075 | ref | XP\_001154568.1 | T... 1110  
gi | 118100010 | ref | XP\_415711.2 | T... 689  
gi | 189524475 | ref | XP\_696713.3 | P... 1075  
gi | 21356627 | ref | NP\_650096.1 | K... 1142  
gi | 158298249 | ref | XP\_554380.3 | A... 1083



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gi | 22507337 | ref | NP_683734.1 |
gi | 16758424 | ref | NP_446074.1 |
gi | 73957770 | ref | XP_546930.2 |
gi | 194678652 | ref | XP_596969.4 |
gi | 150378545 | ref | NP_001092885.1 |
gi | 26051278 | ref | NP_742017.1 |
gi | 114613887 | ref | XP_001144107.1 |
gi | 114614075 | ref | XP_001154568.1 |
gi | 118100010 | ref | XP_415711.2 |
gi | 189524475 | ref | XP_696713.3 |
gi | 21356627 | ref | NP_650096.1 |
gi | 158298249 | ref | XP_554380.3 |

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 SGQSG---TPGTTTTFSG-SLSQNTLG--APSQSSPFAFVSGSTPESKPVFVG---TSTPTFGQSAPAPG-VGTTGSSLSFGASSTPAQGFVG--VGP-FGSAAPSFIFIGAGSKTPGARQRLQARRQHTRKK- 1199  
 SGQSG---TIGTTTTFGGSLSONTLG--APSQSSPFAFVSGSTPESKPVFVG---TSTPTFGQSAPAPG-VGTTGSSLSFGASSTPAQGFVG--VGP-FGSGAPSFIFIGAGSKTPGARQRLQARRQHTRKK- 1199  
 TGQSG---AAASTTTFGGGLSSTLG--APSQSTPFAFNVASTPESKPVFVG---TSTPTFGQNTTAPG-VGVEGSSLSFGASSTPAQGFVG--VGP-FGSAAPSFIFIGAGSKTPGARQRLQARRQHTRKK- 890  
 AGQSG---ATGSTTAPFGGGLSONSLG--TFSQTTTSAFVSVTSTPDSKPVFVG---TSTPTFGQNTTAPG-VGAAGSSLSFGASSTPAQGFVG--VGP-FGSTAPSFIFIGAGSKTPGARQRLQARRQHTRKK- 1216  
 AGQSG---STATSTPFAGGLGQNALG--TTGQSTPFAFNVGSTTESKPVFVG---TATPTFGQNTTAPG-VGTSGSSLSFGASSAPAQGFVG--VGP-FGSAAPSFIFIGAGSKTPGARQRLQARRQHTRKK- 987  
 AGQSG---STATSTPFAGGLGQNALG--TTGQSTPFAFNVGSTTESKPVFVG---TATPTFGLNTTAPG-VGTSGSSLSFGASSAPAQGFVG--VAP-FGSAALSFIFIGAGSKTPGARQRLQARRQHTRKK- 984  
 AGQSG---STATSTPFAGGLGQNALG--TTGQSTPFAFNVGSTTESKPVFVG---TATPTFGLNTTAPG-VGTSGSSLSFGASSAPAQGFVG--VAP-FGSAALSFIFIGAGSKTPGARQRLQARRQHTRKK- 1228  
 AGQSG---STATSTPFAGGLGQNSLG--TTSQSTPFAFNVGSTTESKPVFVG---TATPTFGQNTTAPG-VGTSGSSLSFGASSAPAQGFVG--VAP-FGSAAPSFIFIGAGSKTPGARQRLQARRQHTRKK- 1229  
 AGQSG---AAAAATPFGSSLTFCITLG--APSQSTPFAFTVPSSTDAKPVFVG---TPAPTFGQSTPVPVAVGSGGGLSFGTPTSPASAFPG--VGTSTFGPSTPFAFIFIGAGSKT-GARQRLQARRQHTRKK- 809  
 GAPLANS-NTAPSTPAPPAFSGGFNFG--ASLSSTPFGTPAPAAQPGFSPGANNTDSKPAFGTSIPAFG-QASPGMEMPFSPGTPGFGAMGGLGASPFGASPAFIFIGTGTITSGARR-LQARRQHTRKK- 1201  
 NAVSATONQKPSGVFSFGAAKSTAG--TTAGNAPFSFGASAGGIASPPSNQGLNIAKPFSEFGG-AGG--TPAPNVFSGPAPAPPASNPTG---GFNFGGVSPAQQANAGNMFAPTPESRPIRKAIRRLQK 1266  
 NAGSGSTFGGFNAITPAAGTMSNGIGGNTTAPANKPFTFGASSAGPMVQNNAG---QQQQQQQQAAAPSGGAFNFNLSNAAPKPFN-FTG---GLGNANANVASPPMFGSPVATARPAAAFRRLQV-- 1205  
 .....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330..

