

gi	51100966	ref	NP_766012.2	-----MTAAANWVANGASLEDCHSNLFS-----LAELTGIKWRRYNFGGHGDGCGPIISAPAD	150
gi	109496031	ref	XP_341091.3	-----MASHRQRNQLGDAFGLDHWITTCQGM-----VQKCEGQNPGAHHPVLAEVSLASSNNAQK-----VLESQAVKQKIQKTCIPCTCALCSAQAAPPASCTHAHRRRLWTLVLMPTSHLVFCA	150
gi	44771211	ref	NP_056150.1	-----MTAAANWVANGASLEDCHSNLFS-----LAELTGIKWRRYNFGGHGDGCGPIISAPAD	150
gi	73995266	ref	XP_534693.2	-----MTAAANWVANGASLEDCHSNLFS-----LAELTGIKWRRYNFGGHGDGCGPIISAPAD	150
gi	119909346	ref	XP_595505.3	-----MTAAANWVANGASLEDCHSNLFS-----LAELTGIKWRRYNFGGHGDGCGPIISAPAD	150
gi	118098868	ref	XP_415317.2	-----MTAAANWVANGASLEDCHSNLFS-----LAELTGIKWRRYNFGGHGDGCGPIISAPAD	150
gi	161085371	ref	NP_730591.2	-----MTHONHQINGASLEDCHTNFVA-----LTDLCGKWRKRVNGERPNAASDPLA-----D	150



gi	51100966	ref	NP_766012.2	-----DPILLSFIRCLQAN-----LLCVWR-----RDVKPD-----CKELWIFWNGDEPNLVGVIIHHELVVEEGLWEN-----GLSYECRLLLFKAIHN	300
gi	109496031	ref	XP_341091.3	-----LCSRLILHLPAPLLHPQAPWTHHITLAGEPRRMRTDKAPSOESGRLRIFTDRYTGKNVNDP-----ARGIKMLGWKPSWCIKRCAPHPDPACAIQPHGATFPVVEGTVRKGGRRIKSVNTFFTFHP	300
gi	44771211	ref	NP_056150.1	-----DPILLSFIRCLQAN-----LLCVWR-----RDVKPD-----CKELWIFWNGDEPNLVGVIIHHELVVEEGLWEN-----GLSYECRLLLFKAIHN	300
gi	73995266	ref	XP_534693.2	-----DPILLSFIRCLQAN-----LLCVWR-----RDVKPD-----CKELWIFWNGDEPNLVGVIIHHELVVEEGLWEN-----GLSYECRLLLFKAIHN	300
gi	119909346	ref	XP_595505.3	-----DPILLSFIRCLQAN-----LLCVWR-----RDVKPD-----CKELWIFWNGDEPNLVGVIIHHELVVEEGLWEN-----GLSYECRLLLFKAIHN	300
gi	118098868	ref	XP_415317.2	-----DPILLSFIRCLQAN-----LLCVWR-----RDVKPD-----CKELWIFWNGDEPNLVGVIIHHELVVEEGLWEN-----GLSYECRLLLFKAIHN	300
gi	161085371	ref	NP_730591.2	-----PILRSYSRCIQAD-----MLCVWRVOSTKTDHAPPNALTPEMTSTKVVHPPLSLAAAKELWIFWYGEEDLSELVDAELLRVAANQALWNG-----HWKCALTYECRSLLFKAIHN	300



gi	51100966	ref	NP_766012.2	-----LLER-----CLMDK-----NFVRIGKWFVRPYDKDEKPVNKSSEHLS-----CAFTFFLHGESNVCTS	450
gi	109496031	ref	XP_341091.3	-----PSVGGLANVALVESPQCT-----DRLMVKGWRLRGGHRRELEDPLKATWQTGAPIWNTFKCGGPFMSSGSSKEPGGNPASIMDGLGLRTSIHPSLRKEGSCSCSCLVSGCSEIMHCGRSRGLAKGISDWYRTPLLPQFGTLNHSCKWCPOSGS	450
gi	44771211	ref	NP_056150.1	-----LLER-----CLMDK-----NFVRIGKWFVRPYDKDEKPVNKSSEHLS-----CAFTFFLHGESNVCTS	450
gi	73995266	ref	XP_534693.2	-----LLER-----CLMDK-----NFVRIGKWFVRPYDKDEKPVNKSSEHLS-----CAFTFFLHGESNVCTS	450
gi	119909346	ref	XP_595505.3	-----LLER-----CLMDK-----NFVRIGKWFVRPYDKDEKPVNKSSEHLS-----CAFTFFLHGESNVCTS	450
gi	118098868	ref	XP_415317.2	-----LLER-----CLMDK-----NFVRIGKWFVRPYDKDEKPVNKSSEHLS-----CAFTFFLHGESNVCTS	450
gi	161085371	ref	NP_730591.2	-----LMERFVLEK-----DIVRFGKWFVQPCSTSSDRLFGRSOSHL-----FSPTFFVHGDIVCAS	450



gi	51100966	ref	NP_766012.2	-----VEIAQHQP-----IYLINEEHLHMA-----OSSPAP-----FQVLVSPYGLNGTLTGAYKMS	600
gi	109496031	ref	XP_341091.3	-----YRAAVQACCVHTYKAGWTPSACEESHRLNMPPLSGAVLSATPLWDLLEVFMLSDHQTHFASKVILKLPGLRMPTRQFGPAPDFKAVGKIDWLTSLDQTLGMGNRLARONRELAGEPPGLPSAHLPPQLPSHVLVSPYGLNGTLTGAYKMS	600
gi	44771211	ref	NP_056150.1	-----VEIAQHQP-----IYLINEEHLHMA-----OSSPAP-----FQVLVSPYGLNGTLTGAYKMS	600
gi	73995266	ref	XP_534693.2	-----VEIAQHQP-----IYLINEEHLHMA-----OSSPAP-----FQVLVSPYGLNGTLTGAYKMS	600
gi	119909346	ref	XP_595505.3	-----VEIAQHQP-----IYLINEEHLHMA-----OSSPAP-----FQVLVSPYGLNGTLTGAYKMS	600
gi	118098868	ref	XP_415317.2	-----VEIAQHQP-----IYLINEEHLHMA-----OSSPAP-----FQVLVSPYGLNGTLTGAYKMS	600
gi	161085371	ref	NP_730591.2	-----IDLREHPAVR-----PLTKEHLTEAAAFAAAESPSPGNSGSAASAGGAVPNFGQDPNGASMDG-----LDGGEAAKAAAPPHARKVMLAPFGIAGILTGNVYKAS	600



gi	51100966	ref	NP_766012.2	-----DPAARKLIEEWHCFYPMVLRKKEEPRAEALGYDDDFPVAVEVIVGGVVRMVYPSAFVLVSOND-----IPVPS-----GHGTVACQGLGSKVDP-----NCGMPLTPPTSPPEQVIGESGGVOSAASHLGSODGGMSTMHSPKRSRKTTPK	750
gi	109496031	ref	XP_341091.3	-----DPAARKLIEEWHCFYPMVLRKKEEPRAEALGYDDDFPVAVEVIVGGVVRMVYPSAFVLVSOND-----IPVPSGTSAGGHVITACQGLGSKVDP-----IPVPSGTSAGGHVITACQGLGSKVDP-----NCGMPLTPPTSPPEQVIGESGGVOSAASHLGSODGGMSTMHSPKRSKIPPK	750
gi	44771211	ref	NP_056150.1	-----DPAARKLIEEWHCFYPMVLRKKEEPRAEALGYDDDFPVAVEVIVGGVVRMVYPSAFVLVSOND-----IPVPS-----GHGTVACQGLGSKVDP-----NCGMPLTPPTSPPEQVIGESGGVOSAASHLGSODGGMSTMHSPKRSKIPPK	750
gi	73995266	ref	XP_534693.2	-----DPAARKLIEEWHCFYPMVLRKKEEPRAEALGYDDDFPVAVEVIVGGVVRMVYPSAFVLVSOND-----IPVPS-----GHGTVACQGLGSKVDP-----NCGMPLTPPTSPPEQVIGESGGVOSAASHLGSODGGMSTMHSPKRSKIPPK	750
gi	119909346	ref	XP_595505.3	-----DPAARKLIEEWHCFYPMVLRKKEEPRAEALGYDDDFPVAVEVIVGGVVRMVYPSAFVLVSOND-----IPVPS-----GHGTVACQGLGSKVDP-----NCGMPLTPPTSPPEQVIGESGGVOSAASHLGSODGGMSTMHSPKRSKIPPK	750
gi	118098868	ref	XP_415317.2	-----DPAARKLIEEWHCFYPMVLRKKEEPRAEALGYDDDFPVAVEVIVGGVVRMVYPSAFVLVSOND-----IPVPS-----GHGTVACQGLGSKVDP-----NCGMPLTPPTSPPEQVIGESGGVOSAASHLGSODGGMSTMHSPKRSKIPPK	750
gi	161085371	ref	NP_730591.2	-----DPAARKLIEEWHCFYPMVLRKKEEPRAEALGYDDDFPVAVEVIVGGVVRMVYPSAFVLVSOND-----IPVPS-----GHGTVACQGLGSKVDP-----NCGMPLTPPTSPPEQVIGESGGVOSAASHLGSODGGMSTMHSPKRSKIPPK	750



gi	51100966	ref	NP_766012.2	HMVRRVWREICILSRASQKRSQMSPTTREEEAHSF	AAWDFVDPQTVVSCSCSRHK	LLKRC	900
gi	109496031	ref	XP_341091.3	HMVRRVWKECILNRAQSKRSQMSAPAGEEPAHSF	AAWDFVDPQTVVSCSCSRHK	LLKRC	900
gi	44771211	ref	NP_056150.1	HMVHRVWKECILNRTQSKRSQMSPTLEEEPAHSF	AAWDFVDPQTVVSCSCSRHK	LLKRC	900
gi	73995266	ref	XP_534693.2	HMVHRVWKECILNRAQSKRSQMSPTLEEEPAHSF	AAWDFVDPQTVVSCSCSRHK	LLKRC	900
gi	119909346	ref	XP_595505.3	HMVHRVWKECILNRTQSKRSQMSPTLEEEPAHSF	AAWDFVDPQTVVSCSCSRHK	LLKRC-T	900
gi	118098868	ref	XP_415317.2	HMVHRVWKECILNRSQSKRTIITANLEEEVPNT	AAWDFVDPQTVVSCSCSRHK	FKORCA	900
gi	161085371	ref	NP_730591.2	AVSALERLAFQPPYDQRPISGFTFNNTNTHIPASAAVEMPERTWDCVNMNTHLVDAAAAAVAASSTPASGTSLSADGDENEONKPPQDSKLVVOCITQQQQQKLVNFVDMOKAPCICTNAQCNSSSISNIISNKRKPQPPLGSPA	AVWDFVDPQTVVSCSCSRHK	LLKRC	900



gi	51100966	ref	NP_766012.2	VGPSRPATISQPGFSAGLPSSSSSLPPASSKHKTTERQKDGKLRKP	LVPFHHRPVSVAELCVCEDAPGQK	LGLAGIDASLEVSNTRKYDKQMAVPSRNTSKQMNLL	1050
gi	109496031	ref	XP_341091.3	VGPSRPPTLSQPGFSAGPPPSLPPASSKHKTTERQKDGKLRKP	LVPFHHRPVSVAELCVCEDAPGQK	LGLAGIDSSLEVSSSRKYDKQMAVPSRNTSKQMDLL	1050
gi	44771211	ref	NP_056150.1	VGNRPPTVPSQPGFSAGPSSSSSLPPASSKHKTTERQKDGKLRKP	LVPFHHRPVSVAELCVCEDAPGQK	LGLAGIDSSLEVSSSRKYDKQMAVPSRNTSKQMNLL	1050
gi	73995266	ref	XP_534693.2	VGNRPPTVPSQPGFSAGPSSSSSLPPASSKHKTTERQKDGKLRKP	LVPFHHRPVSVAELCVCEDAPGQK	LGLAGIDSSLEVSSSRKYDKQMAVPSRNTSKQMNLL	1050
gi	119909346	ref	XP_595505.3	VGPSRPPATISQPGFSAGPSSSSSLPPASSKHKTTERQKDGKLRKP	LVPFHHRPVSVAELCVCEDAPGQK	LGLAGIDSSLEVSSSRKYDKQMAVPSRNTSKQMNLL	1050
gi	118098868	ref	XP_415317.2	AGSRPPMINSQPGFSAGPSSSSSLPPASSKHKTTERQKDGKLRKP	LVPFHHRPVSVAELCVCEDAPGQK	LGLAGIDSSLEVSSSRKYDKQMAVPSRNTSKQMNLL	1050
gi	161085371	ref	NP_730591.2	LRAAVTGGSGNKSSSSSSSSSSSSSYQQHYHQHLLQQOQRPGTVPVLPATAAASHSSLSNLTASNSSAATPRRHNVPHKRLHLSLASTASTATFRKHNHSNTITDTNIPKQRHLGNTPHGTPHGGASTYSRNSLGGDS	LVPFHHRPVSVAELCVCEDAPGQK	LGLAGIDSSLEVSSSRKYDKQMAVPSRNTSKQMNLL	1050



gi	51100966	ref	NP_766012.2	PMDSPHSPIPLPPTLSPPRGQ	EAESLDPPSVVNPALYNGLDLQQLSTIEDRTVLVQORLPPLMAEAS	ETALYSGLRPSYTESSDRWVQSFRLPSS	1200
gi	109496031	ref	XP_341091.3	PMDSPHSPIPLPPTLSPPRGQ	ETESLDPPSVVNPALYNGLDLQQLSLEDRTVLVQORLPPLMAEAS	ETALYSGLRPSYTESSDRWVQSFRLPSS	1200
gi	44771211	ref	NP_056150.1	PMDSPHSPIPLPPTLSPPRGQ	ETESLDPPSVVNPALYNGLDLQQLSLEDRTVLVQORLPPLMAEAS	ETALYCGIRPSPNPESSEKWHWSYRLPSS	1200
gi	73995266	ref	XP_534693.2	PMDSPHSPIPLPPTLSPPRGQ	ETESLDPPSVVNPALYNGLDLQQLSLEDRTVLVQORLPPLMAEAS	ETALYCGIRPSPNPESSEKWHWSYRLPSS	1200
gi	119909346	ref	XP_595505.3	PMDSPHSPIPLPPTLSPPRGQ	EAESLDPPSVVNPALYNGLDLQQLSLEDRTVLVQORLPPLMAEAS	ETALYCGIRPSPNPESSEKWHWSYRLPSS	1200
gi	118098868	ref	XP_415317.2	PMDSPHSPIPLPPTLSPPRGQ	EAESLDPPSVVNPALYNGLDLQQLSLEDRTVLVQORLPPLMAEAS	ETALYCGIRPSPNPESSEKWHWSYRLPSS	1200
gi	161085371	ref	NP_730591.2	SMPVAISVEEAPAPSPHPNSAHSPTSIVPPAEGQLLMSPHAPTISVSNLQPPPTIDHLLDKRTAPPTPQDHSKSTIVGASPVVHQIPSEVPPSYTDHAAAGGGPAGGGLGTPGPSVPAOQAPATPATATAGGAGSGGGSNATGANAAGT	EAESLDPPSVVNPALYNGLDLQQLSLEDRTVLVQORLPPLMAEAS	ETALYCGIRPSPNPESSEKWHWSYRLPSS	1200



gi	51100966	ref	NP_766012.2	AEFRPPELQGERFDALDINPESTALORLLAOPNKRFKIWOQEPVQVLPFLDPSPLSQQPGDILGEVNDPVTFFED	GDIKYIFITANKKCKGTTEKDSLKKNKSEDF	1350
gi	109496031	ref	XP_341091.3	AEFRPPELQGEGFHVLVDVSPESTALORLLAOPNKRFKIWOQEPVQVLPFLDPSPLSQQPGDILGEVNDPVTFFED	GDIKYIFITANKKCKGTTEKDSLKKNKSEDF	1350
gi	44771211	ref	NP_056150.1	AEFRPPELQGERCDAKMEVNSESTALORLLAOPNKRFKIWOQEPVQVLPFLDPSPLSQQPGDILGEVNDPVTFFED	GDIKYIFITANKKCKGTTEKDSLKKNKSEDF	1350
gi	73995266	ref	XP_534693.2	AEFRPPELQGERCDAKMEVNSESTALORLLAOPNKRFKIWOQEPVQVLPFLDPSPLSQQPGDILGEVNDPVTFFED	GDIKYIFITANKKCKGTTEKDSLKKNKSEDF	1350
gi	119909346	ref	XP_595505.3	AEFRPPELQGERCDAKMEVNSESTALORLLAOPNKRFKIWOQEPVQVLPFLDPSPLSQQPGDILGEVNDPVTFFED	GDIKYIFITANKKCKGTTEKDSLKKNKSEDF	1350
gi	118098868	ref	XP_415317.2	AEFRPPALPCERDDAKMEVNDPSALTKRLLAOPNKRFKIWOQEPVQVLPFLDPSPLSQQPGDILGEVNDPVTFFED	GDIKYIFITANKKCKGTTEKDSLKKNKSEDF	1350
gi	161085371	ref	NP_730591.2	ISVKKLEMQQTPSAAMAIAKQEPGAQGRGVGGVTSSTTEALNNFKRLNPKLTLKDDPSEYDEENLKEVIYDFQYQEWYDYSIVKRPKMEQRRRPRYAKNLYEGQNHVKPVMPSPGS VYGSQQLSLDESASQAGGGGQAAGS	GDIKYIFITANKKCKGTTEKDSLKKNKSEDF	1350



gi	51100966	ref	NP_766012.2	GTKDVTTPGHSTPVDPDGNAMS	IFSSATKTDVRODSSAAGRAGSGLTQVTDLAPSLHLDLNIIFDSSDDELGAVSPALRSS	KMPAVGTEDRPLGKDGRAAVYPPTVADLQRMFPT	1500
gi	109496031	ref	XP_341091.3	GTKDVTTPGHSTPVDPDGNAMS	IFSSATKTDVRODSSAAGRAGSGLTQVTDLAPSLHLDLNIIFDSSDDELGAVSPALRSS	KMPAVGTEDRPLGKDGRAAVYPPTVADLQRMFPT	1500
gi	44771211	ref	NP_056150.1	GTKDVTTPGHSTPVDPDGNAMS	IFSSATKTDVRODSSAAGRAGSGLTQVTDLAPSLHLDLNIIFDSSDDELGAVSPALRSS	KMPAVGTEDRPLGKDGRAAVYPPTVADLQRMFPT	1500
gi	73995266	ref	XP_534693.2	GTKDVTTPGHSTPVDPDGNAMS	IFSSATKTDVRODSSAAGRAGSGLTQVTDLAPSLHLDLNIIFDSSDDELGAVSPALRSS	KMPAVGTEDRPLGKDGRAAVYPPTVADLQRMFPT	1500
gi	119909346	ref	XP_595505.3	GTKDVTTPGHSTPVDPDGNAMS	IFSSATKTDVRODSSAAGRAGSGLTQVTDLAPSLHLDLNIIFDSSDDELGAVSPALRSS	KMPAVGTEDRPLGKDGRAAVYPPTVADLQRMFPT	1500
gi	118098868	ref	XP_415317.2	GTKDVTTPGHSTPVDPDGNAMS	IFSSATKTDVRODSSAAGRAGSGLTQVTDLAPSLHLDLNIIFDSSDDELGAVSPALRSS	KMPAVGTEDRPLGKDGRAAVYPPTVADLQRMFPT	1500
gi	161085371	ref	NP_730591.2	VGIANSTASGSDVEADGSSFFQGLNLIKTEPLGLHSPSCKESKSGSGNSGGSGSGGNLFTAEGLNPLNLDLQLEFETSNDGESSVQIHTPPDSNNPSNGGCSAVTINIIBDLKRSTAVAAVAASAAAAAASGAGNIQAEDLTQMFPT	IFSSATKTDVRODSSAAGRAGSGLTQVTDLAPSLHLDLNIIFDSSDDELGAVSPALRSS	KMPAVGTEDRPLGKDGRAAVYPPTVADLQRMFPT	1500



gi|51100966|ref|NP\_766012.2| PSLEQHPAFSP-----VMNYKDGVSSEVTALGMMESEPVVSMVPTHLTEFRMEVEDGLGSPKPEIKDFSYVHKVVPQFPFVGGSSMFAPLKLTPSHCLLPLKIPDACLFRPSSWAVPP 1650  
gi|109496031|ref|XP\_341091.3| PSLEQHPAFSP-----VMNYKDGVSSEVTALGMMESEPVVSMVPTHLTEFRMEVEDGLGSPKPEIKDFSYVHKVVPQFPFVGGSSMFAPLKLTPSHCLLPLKIPDACLFRPSSWAVPP 1650  
gi|44771211|ref|NP\_056150.1| PSLEQHPAFSP-----VMNYKDGVSSEVTALGMMESEPVVSMVSTQLTEFKMEVEDGLGSPKPEIKDFSYVHKVVPQFPFVGGSSMFAPLKLMLPSQCLLPLKIPDACLFRPSSWAVPP 1650  
gi|73995266|ref|XP\_534693.2| PSLEQHPAFSP-----VMNYKDGVSSEVTALGMMESEPVVSMVSTQLTEFKMEVEDGLGSPKPEIKDFSYVHKVVPQFPFVGGSSMFAPLKLMLPSQCLLPLKIPDACLFRPSSWAVPP 1650  
gi|119909346|ref|XP\_595505.3| PSLEQHPAFSP-----VMNYKDGVSSEVTALGMMESEPVVSMVSTQLTEFKMEVEDGLGSPKPEIKDFSYVHKVVPQFPFVGGSSMFAPLKLMLPSQCLLPLKIPDACLFRPSSWAVPP 1650  
gi|118098868|ref|XP\_415317.2| PSLEQHPAFSP-----VMSYKDGISSEVTTLGMMESEPVVSMVPTQLAEFKMEVEDGLGSPKPEIKDFSYVHKVVPQFPFVGGSSVFAPLKLMLPSQCLLPLKIPDACLFRPSSWAVPP 1650  
gi|161085371|ref|NP\_730591.2| PSHEQHPFNSPCQTDVVMVLDLSDVTTTTIIITSSITTTCTNTTITSSINTTTTACSNPNSIMLAAAQAPVTVVAIQVSKMVKQEVNLELGSPEEIPNDWVYVYRPPQEKFGVSTRYAPLTLNLSQTOPPLTLPDGCFTPTWSSHKS 1650  
.....1510.....1520.....1530.....1540.....1550.....1560.....1570.....1580.....1590.....1600.....1610.....1620.....1630.....1640.....1650



gi|51100966|ref|NP\_766012.2| KMEQLPMPAAASIRDGYNNVPSVGLADDPDYV--NTPQMNTPVTLNSAAPASNSGAGVLPSPATPRFSVPTPRTPRTPRTPRGGGTASGGSVKYDSDOGSPASTP 1800  
gi|109496031|ref|XP\_341091.3| KMEQLPMPAAASIRDGYNNVPSVGLADADYL--NTPQMNTPVTLNSAAPASNSGAGVLPSPATPRFSVPTPRTPRTPRTPRGGGTASGGSVKYDSDOGSPASTP 1800  
gi|44771211|ref|NP\_056150.1| KIEQLPMPAAAFIRDGYNNVPSVGLADDPDYL--NTPQMNTPVTLNSAAPASNSGAGVLPSPATPRFSVPTPRTPRTPRTPRGGGTASGGSVKYDSDOGSPASTP 1800  
gi|73995266|ref|XP\_534693.2| KIEQLPMPAAAFIRDGYNNVPSVGLADDPDYL--NTPQMNTPVTLNSAAPASNSGAGVLPSPATPRFSVPTPRTPRTPRTPRGGGTASGGSVKYDSDOGSPASTP 1800  
gi|119909346|ref|XP\_595505.3| KIEQLPMPAAAFIRDGYNNVPSVGLADDPDYL--NTPQMNTPVTLNSAAPASNSGAGVLPSPATPRFSVPTPRTPRTPRTPRGGGTASGGSVKYDSDOGSPASTP 1800  
gi|118098868|ref|XP\_415317.2| KIEQLPMPAAAFIRDGYNNVPSVGLADDPDYL--NTPQMNTPVTLNSAAPASNSGAGVLPSPATPRFSVPTPRTPRTPRTPRGGGTASGGSVKYDSDOGSPASTP 1800  
gi|161085371|ref|NP\_730591.2| RAATLAKAAAAQQQDHQKHQALQORIQHLQOKLQQLQLNQQQQAAAAAAGGGVGHQKHQHLHDLLSAPRTPLPSTVQPLSSGGSOYLLNQLNCPQAPPGASMOOLMHRAGMSPISPGPGMGPYAARSSPMSRATPHTHP 1800  
.....1660.....1670.....1680.....1690.....1700.....1710.....1720.....1730.....1740.....1750.....1760.....1770.....1780.....1790.....1800



gi|51100966|ref|NP\_766012.2| -----STTRPLNSVEP-----ATMOPPEAHSLYVLLILSDSVMNVFKDRNFDSCCIACACNMN-----IKGADVGLYLPDS 1950  
gi|109496031|ref|XP\_341091.3| -----STTRPLNSVEP-----ATMOPPEAHSLYVLLILSDSVMNVFKDRNFDSCCIACACNMN-----VKGADVGLYLPDS 1950  
gi|44771211|ref|NP\_056150.1| -----STTRPLNSVEP-----ATMOPPEAHSLYVLLILSDSVMNIFKDRNFDSCCIACACNMN-----IKGADVGLYLPDS 1950  
gi|73995266|ref|XP\_534693.2| -----STTRPLNSVEP-----ATMOPPEAHSLYVLLILSDSVMNIFKDRNFDSCCIACACNMN-----IKGADVGLYLPDS 1950  
gi|119909346|ref|XP\_595505.3| -----STTRPLNSVEP-----ATMOPPEAHSLYVLLILSDSVMNIFKDRNFDSCCIACACNMN-----IKGADVGLYLPDS 1950  
gi|118098868|ref|XP\_415317.2| -----STTRPLNSVEP-----ATVQPIPEAHSLYVLLILSDSVMLNIFKDRNFDSCCIACACNMN-----IKGADVGLYLPDS 1950  
gi|161085371|ref|NP\_730591.2| PYPYDLAVASPATSSYLNRPLHSQEPHMHGLGGGAGVGVGHGCGGGHGMVAVYTGADAGIVSGGTAMAAGSSSLLQELPEVNSVLVNILLYDIALNVFRDHFDSVVCVQADPQKIGNIRGADSGVYVLPVGVFNPFPSSGAGGA 1950  
.....1810.....1820.....1830.....1840.....1850.....1860.....1870.....1880.....1890.....1900.....1910.....1920.....1930.....1940.....1950



gi|51100966|ref|NP\_766012.2| -----SKEDQYRCTCGFSAIVNRKLGYNGLFLEDELDFGKNSDIGAAERLLMCCQSSGOSTLLPOV--EGARKAPEPPVSLLLLLLQNG 2100  
gi|109496031|ref|XP\_341091.3| -----SKEDQYRCTCGFSAIVNRRLGYNGLFLEDELDFGKNSDIGAAERLLMCCQTSQOSTLLPOV--EGARKAPEPPVSLLLLLLQNG 2100  
gi|44771211|ref|NP\_056150.1| -----SNEDQYRCTCGFSAIMNRKLGYNGLFLEDELDFGKNSDIGAAERLLMCCQSS---HFLPQV--EGTKKPEPPVSLLLLLLQNG 2100  
gi|73995266|ref|XP\_534693.2| -----SNEDQYRCTCGFSAIMNRKLGYNGLFLEDELDFGKNSDIGAAERLLMCCQ---HFLPQV--EGARKSPEPPVSLLLLLLQNG 2100  
gi|119909346|ref|XP\_595505.3| -----SNEDQYRCTCGFSAIMNRKLGYNGLFLEDELDFGKNSDIGAAERLLMCCQ---HFLPQV--EGARKSPEPPVSLLLLLLQNG 2100  
gi|118098868|ref|XP\_415317.2| -----SNEDQYRCTCGFSAIMNRKLGYNGLFLEDELDFGKNSDIGAAERLLMCCQ---HFLPQV--EGARKSPEPPVSLLLLLLQNG 2100  
gi|161085371|ref|NP\_730591.2| LAGQRMNLGPFSSAGFGGMRMISAFGGSPASASMPGAGSGHGHGPNGGSSNSSCTPPSSNPHITGVVDDDPVECCGFSAVVNRRLSHRAGLFVEDEVEITGIADDPGRNKQPTLLSITQSLSRKNQNKQGPGETSSALDKIGAGGLPNGQ 2100  
.....1960.....1970.....1980.....1990.....2000.....2010.....2020.....2030.....2040.....2050.....2060.....2070.....2080.....2090.....2100



gi|51100966|ref|NP\_766012.2| HTQP-----FASLSFLDYISSANRHALPCVSWTYDR-----VQADNNDYWTFCFNALQCGQYVDNPTGKGVDEALVRSATVHCWPHSNVLDTSMLSSQDVVRM 2250  
gi|109496031|ref|XP\_341091.3| HTQP-----FASLSFLDYISSSRHALPCVSWTYDR-----VQADNNDYWTFCFNALQCGQYVDNPTGKGVDEALVRSATVHCWPHSNVLDTSMLSSQDVVRM 2250  
gi|44771211|ref|NP\_056150.1| HTQP-----FASLSFLDYISSNRRQTLPCVSWTYDR-----VQADNNDYWTFCFNALQCGQYVDNPTGKGVDEALVRSATVHWSPHSNVLDISMLSSQDVVRM 2250  
gi|73995266|ref|XP\_534693.2| HTQP-----FASLSFLDYISSNSRQTLPCVSWTYDR-----VQADNNDYWTFCFNALQCGQYVDNPTGKGVDEALVRSATVHWSPHSNVLDISMLSSQDVVRM 2250  
gi|119909346|ref|XP\_595505.3| HTQP-----FASLSFLDYISSRQTLPCVSWTYDR-----VQADNNDYWTFCFNALQCGQYVDNPTGKGVDEALVRSATVHWSPHSNVLDISMLSSQDVVRM 2250  
gi|118098868|ref|XP\_415317.2| HTQP-----FTLSCLDVMSSNRRQTLPCVSWTYDR-----LQADSNDSWIFCFNALQCGQYVDNPTGKGVDEALVRSATVHWSPHSNVLDISMLSSQDVVRM 2250  
gi|161085371|ref|NP\_730591.2| LEQLGHAVFDLLLDQCSIIQTSSSVHRALQSHRRRMSRRRIFGNNGAPLASLAIANVLEFMDAHDVLSLALESRLAFENORMNMMDFHNGSSSSHQOQLTAFHAPPALRHKLKLAGIGARLTVHKVYLPVGFTRNKEIVR 2250  
.....2110.....2120.....2130.....2140.....2150.....2160.....2170.....2180.....2190.....2200.....2210.....2220.....2230.....2240.....2250



gi|51100966|ref|NP\_766012.2| LLSLQPFLLQDAIQKRRTG---RTWENIQHVQGPLTWOQPHKMAGRGTYSSESPPELPIPIILLVGVYDKDFLTIISPFSLPFWERLLLEPYGGHRDVAYIVVCPENEALLEGAKTFFRDLSAVYEMCRLGQHKPICKVLRDGMIRVGTVA 2400  
gi|109496031|ref|XP\_341091.3| LLSLQPFLLQDAIQKRRTG---RTWENIQHVQGPLTWOQPHKMAGRGTYSSESPPELPIPIILLVGVYDKDFLTIISPFSLPFWERLLLEPYGGHRDVAYIVVCPENEALLEGAKTFFRDLSAVYEMCRLGQHKPICKVLRDGMIRVGTVA 2400  
gi|44771211|ref|NP\_056150.1| LLSLQPFLLQDAIQKRRTG---RTWENIQHVQGPLTWOQPHKMAGRGTYSSESPPELPIPIILLVGVYDKDFLTIISPFSLPFWERLLLEPYGGHRDVAYIVVCPENEALLEGAKTFFRDLSAVYEMCRLGQHKPICKVLRDGMIRVGTVA 2400  
gi|73995266|ref|XP\_534693.2| LLSLQPFLLQDAIQKRRTG---RTWENIQHVQGPLTWOQPHKMAGRGTYSSESPPELPIPIILLVGVYDKDFLTIISPFSLPFWERLLLEPYGGHRDVAYIVVCPENEALLEGAKTFFRDLSAVYEMCRLGQHKPICKVLRDGMIRVGTVA 2400  
gi|119909346|ref|XP\_595505.3| LLSLQPFLLQDAIQKRRTG---RTWENIQHVQGPLTWOQPHKMAGRGTYSSESPPELPIPIILLVGVYDKDFLTIISPFSLPFWERLLLEPYGGHRDVAYIVVCPENEALLEGAKTFFRDLSAVYEMCRLGQHKPICKVLRDGMIRVGTVA 2400  
gi|118998868|ref|XP\_415317.2| LLSLQPFLLQDAIQKRRTG---RTWENIQHVQGPLTWOQPHKMAGRGTYSSESPPELPIPIILLVGVYDKDFLTIISPFSLPFWERLLLEPYGGHRDVAYIVVCPENEALLEGAKTFFRDLSAVYEMCRLGQHKPICKVLRDGMIRVGTVA 2400  
gi|161085371|ref|NP\_730591.2| MNAIQPMLQNAFHCKSRGGSGSKDASSVNTVSGPLTWQPHRLLAGR---ASQCCEPQPIPEVVVGVYKDWISVAPHSIHWKDFLEPYSYARDVAYIVVCPDNEHVNCTRYSYFRELSTYEMCKLGKHTPIR--GWDGFLQVGAARN 2400  
.....2260.....2270.....2280.....2290.....2300.....2310.....2320.....2330.....2340.....2350.....2360.....2370.....2380.....2390.....2400



gi|51100966|ref|NP\_766012.2| QKLTDELVESEWPNPWSSESDNHSRLKLYAQVCRHHLAPYLATLQDLSGLLMPKHOQPPAEAQGOATPGNAGSLPNSG---SGAPPAGSAFNPSTSS--SSANTPSSSSAS--SGPPGSSAASAPGITOMNTSSSGFGGGVG-GGN 2550  
gi|109496031|ref|XP\_341091.3| QKLTDELVESEWPNPWSSESDNHSRLKLYAQVCRHHLAPYLATLQDLSGLLMPKHOQPPAEAQGOATPGNAG--SSSG---SGAPPAGSAFNPSTSS--SSA--ASSSSC--SGPPGSSAASAPGITOMNTSSSGFGGGVG-GGN 2550  
gi|44771211|ref|NP\_056150.1| QKLTDELVESEWPNPWSSESDNHSRLKLYAQVCRHHLAPYLATLQDLSGLLMPKHOQPPAAAQGOATPGNAGPLANG---SAAPPAGSAFNPSTN--SSNTNPAASSASGSSVPPVSSASAPGISQITSSSGFGSGVG-GGN 2550  
gi|73995266|ref|XP\_534693.2| QKLTDELVESEWPNPWSSESDNHSRLKLYAQVCRHHLAPYLATLQDLSGLLMPKHOQPPAAAQGOATPGNAGPLASNAG---TVSSAGSAFNPSTN--SSSGNPAASSASGSSVPPVSSASAPVINQITSSSGFGASVVG-GGN 2550  
gi|119909346|ref|XP\_595505.3| QKLTDELVESEWPNPWSSESDNHSRLKLYAQVCRHHLAPYLATLQDLSGLLMPKHOQPPAAAQVPPGSAAGPLASNAG---SAAPSAFNPSTN--GSSNPAASSASGSSVPPVSTASAPINQITSSSGFGSGVG-GGN 2550  
gi|118998868|ref|XP\_415317.2| QKLTDELVESEWPNPWSSESDNHSRLKLYAQVCRHHLAPYLATLQDLSGLLMPKHOQPPAPASTQIPGNTGPVPSNCLSTSGAPPFGSSFNSTPNGGTTSLPAGSSSSGSSVPLQASAPVGNVMSATLPGFSGNIGSGGN 2550  
gi|161085371|ref|NP\_730591.2| NVPADRETPLDDWLRLEHAALAEQIRRYAVAFIQQLAPLRSRVPNDKILLNPPDGSNSHSGKGGSSSSSSVSLPG---GDLPTDNIKLEPGTEFQVQPMENIKQEPG-G 2550  
.....2410.....2420.....2430.....2440.....2450.....2460.....2470.....2480.....2490.....2500.....2510.....2520.....2530.....2540.....2550



gi|51100966|ref|NP\_766012.2| PSAGGSSDRTPGNVACG-DTEPGQSCFCSODGQDQSVTERERIGIPTPEPSADSHAYPPAVVIYVMDPFFTYTAEDSSSGNFWLLSLMRCYTEMIDHLEPHMRSFFILOIVPCQYMLQTMKD-EHVFIYIQLKSMFAFVYCCRRPLPT 2700  
gi|109496031|ref|XP\_341091.3| PSAGGSSDRTPGNVACG-DAEHAQSCACPSODGQDQSVTERERIGIPTPEPSADSHAYPPAVVIYVMDPFFTYTAEDSSSGNFWLLSLMRCYTEMIDHLEPHMRSFFILOIVPCQYMLQTMKD-EHVFIYIQLKSMFAFVYCCRRPLPT 2700  
gi|44771211|ref|NP\_056150.1| PSTGGISADRTQGNIGCGGDIPGQSSQPSODGQDQSVTERERIGIPTPEPSADSHAYPPAVVIYVMDPFFTYAEDSSSGNFWLLSLMRCYTEMIDHLEPHMRSFFILOIVPCQYMLQTMKD-EQVFIYIQLKSMFAFVYCCRRPLPT 2700  
gi|73995266|ref|XP\_534693.2| PGIGASSADRTQGNIGCGVDPEPGQSSQSLDQDQSVTERERIGIPTPEPSADSHAYPPAVVIYVMDPFFTYTAEDSSSGNFWLLSLMRCYTEMIDHLEPHMRSFFILOIVPCQYMLQTMKD-EQVFIYIQLKSMFAFVYCCRRPLPT 2700  
gi|119909346|ref|XP\_595505.3| PSTGASTAERTQGLGCGADTEPGQSSQPSODGQDQSVTERERIGIPTPEPSADSHAYPPAVVIYVMDPFFTYTAEDSSSGNFWLLSLMRCYTEMIDHLEPHMRSFFILOIVPCQYMLQTMKD-EQVFIYIQLKSMFAFVYCCRRPLPT 2700  
gi|118998868|ref|XP\_415317.2| TSTGQNAADRSQGSFPGGDTTEAGQNLSCQDEQGVTERERIGIPTPEPSADSHAYPPAVVIYVMDPFFTYTAEDSSSGNFWLLSLMRCYTEMIDHLEPHMRSFFILOIVPCQYMLQTMKD-EQVFIYIQLKSMFAFVYCCRRPLPT 2700  
gi|161085371|ref|NP\_730591.2| VGRGGTAAGETKPTLILGDPLGMEETLEDIN---PSAIVLVVNPFFAFASDS-CELERLALIALRCYAEILKAVPDSVRSQMIQIISLESVMELGPKCENRRKRFSDERCLALNIFSSGRHHLVH 2700  
.....2560.....2570.....2580.....2590.....2600.....2610.....2620.....2630.....2640.....2650.....2660.....2670.....2680.....2690.....2700



gi|51100966|ref|NP\_766012.2| QIHKSLTGFQPAASIEMLKNERPSP--PIQLYSPFFILAPIKDKQ---TEPGEFGEASQKYNVLFVGVYCLSHDQRWLLASCTDLHGELLETCVNNIALPNSRRSKSVSARKVGLQKLNEWCLGIVOMTSLPWRVVIQRLGRLGH 2850  
gi|109496031|ref|XP\_341091.3| QIHKSLTGFQPAASIEMLKNERPSP--PIQLYSPFFILAPIKDKQ---TEPGEAFGEASQKYNVLFVGVYCLSHDQRWLLASCTDLHGELLETCVNNIALPNSRRSKSVSARKVGLQKLNEWCLGIVOMTSLPWRVVIQRLGRLGH 2850  
gi|44771211|ref|NP\_056150.1| QIHKSLTGFQPAASIEMLKNERPSP--PIQLYSPFFILAPIKDKQ---TEPGEFGEASQKYNVLFVGVYCLSHDQRWLLASCTDLHGELLETCVNNIALPNSRRSKSVSARKVGLQKLNEWCLGIVOMTSLPWRVVIQRLGRLGH 2850  
gi|73995266|ref|XP\_534693.2| QIHKSLTGFQPAASIEMLKNERPSP--PIQLYSPFFILAPIKDKQ---TEPGEFGEASQKYNVLFVGVYCLSHDQRWLLASCTDLHGELLETCVNNIALPNSRRSKSVSARKVGLQKLNEWCLGIVOMTSLPWRVVIQRLGRLGH 2850  
gi|119909346|ref|XP\_595505.3| QIHKSLTGFQPAASIEMLKNERPSP--PIQLYSPFFILAPIKDKQ---TEPGEFGEASQKYNVLFVGVYCLSHDQRWLLASCTDLHGELLETCVNNIALPNSRRSKSVSARKVGLQKLNEWCLGIVOMTSLPWRVVIQRLGRLGH 2850  
gi|118998868|ref|XP\_415317.2| QIHKSLTGFQPAASIEMLKNERPSP--PIQLYSPFFILAPIKDKQ---TEPGEFGEASQKYNVLFVGVYCLSHDQRWLLASCTDLHGELLETCVNNIALPNSRRSKSVSARKVGLQKLNEWCLGIVOMTSLPWRVVIQRLGRLGH 2850  
gi|161085371|ref|NP\_730591.2| AQSVMKSLTGFQTAANMEAFLETKDEPNRRAYKMTAPFVLAPMHERNDKIDFSRSAGSMHGQNEHRYVSMVCNLYCLEEDQAWLLAATDERGEMLEKICINDVPPNRRRRKAPARYVALKLLMDFIMGIISOQMWRLVIGRIGRI 2850  
.....2710.....2720.....2730.....2740.....2750.....2760.....2770.....2780.....2790.....2800.....2810.....2820.....2830.....2840.....2850



gi|51100966|ref|NP\_766012.2| GELKDWISILLGECSLQTIISKRLKDVCRMCGISAADSPSILSACLVAPEPQGSFVVMQDAVMTGVSFGRSTALNMQSSQLNTPQDASCTHILLVFPSTSTIQVAPANYPNEDGFSPNNDMDFVDFLFPDDMDNDIGILMTGNLHSSPNSSPV 3000  
gi|109496031|ref|XP\_341091.3| GELKDWISILLGECSLQTIISKRLKDVCRMCGISAADSPSILSACLVAPEPQGSFVVMQDAVMTGVSFGRSTALNMQSSQLNTPQDASCTHILLVFPSTSTIQVAPANYPNEDGFSPNNDMDFVDFLFPDDMDNDIGILMTGNLHSSPNSSPV 3000  
gi|44771211|ref|NP\_056150.1| GELKDWISILLGECSLQTIISKRLKDVCRMCGISAADSPSILSACLVAPEPQGSFVVMQDAVMTGVSFGRSTALNMQSSQLNTPQDASCTHILLVFPSTSTIQVAPANYPNEDGFSPNNDMDFVDFLFPDDMDNDIGILMTGNLHSSPNSSPV 3000  
gi|73995266|ref|XP\_534693.2| GELKDWISILLGECSLQTIISKRLKDVCRMCGISAADSPSILSACLVAPEPQGSFVVMQDAVMTGVSFGRSTALNMQSSQLNTPQDASCTHILLVFPSTSTIQVAPANYPNEDGFSPNNDMDFVDFLFPDDMDNDIGILMTGNLHSSPNSSPV 3000  
gi|119909346|ref|XP\_595505.3| GELKDWISILLGECSLQTIISKRLKDVCRMCGISAADSPSILSACLVAPEPQGSFVVMQDAVMTGVSFGRSTALNMQSSQLNTPQDASCTHILLVFPSTSTIQVAPANYPNEDGFSPNNDMDFVDFLFPDDMDNDIGILMTGNLHSSPNSSPV 3000  
gi|118998868|ref|XP\_415317.2| GELKDWISILLGECSLQTIISKRLKDVCRMCGISAADSPSILSACLVAPEPQGSFVVMQDAVMTGVSFGRSTALNMQSSQLNTPQDASCTHILLVFPSTSTIQVAPANYPNEDGFSPNNDMDFVDFLFPDDMDNDIGILMTGNLHSSPNSSPV 3000  
gi|161085371|ref|NP\_730591.2| SELKWSFLLSKQQLQKASKQFKMCKQCTLMVY--PHLSACLVTLEPDAKLRVMPDAVTFDERFSIISQNP---LAPQDVICTHILLVFPSTSAVCAPIETROFQNEPQVDDI---FLTFEEGNEDESDADIGDLFDWTHMDRV 3000  
.....2860.....2870.....2880.....2890.....2900.....2910.....2920.....2930.....2940.....2950.....2960.....2970.....2980.....2990.....3000



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.. *** :. . :* : .: . : ** : ***:***:*** : .* *****: .: **:*:*:* * : .:***: . : . . : :**
gi | 51100966 | ref | NP_766012.2 | PSPGSPSGIGVGSFHQHSRSQGERLLSREAPEELK---OOLALGYFVSTAKAENLPWFWSSCPOARNOCPLFLKASLHHHS--VAQTDPELLPARTSORAP--HPLDSKTTSDVLRFCWSTTPY---PGSRAIQPPRTALPAFPTSW 3150
gi | 109496031 | ref | XP_341091.3 | PSPGSPSGIGVGSFHQHSRSQGERLLSREAPEELK---OOLALGYFVSTAKAENLPWFWSSCPOARNOCPLFLKASLHHHS--VAQTDPELLPVRSORAP--HPLDSKTTSDVLRFRVLEQYNALSWLTCNPATQDRSCLPVHFVVLT 3150
gi | 44771211 | ref | NP_056150.1 | PSPGSPSGIGVGSFHQHSRSQGERLLSREAPEELK---OOLALGYFVSTAKAENLPWFWSSCPOARNOCPLFLKASLHHHS--VAQTDPELLPARNSORVP--HPLDSKTTSDVLRFRVLEQYNALSWLTCNPATQDRSCLPVHFVVLT 3150
gi | 73995266 | ref | XP_534693.2 | PSPGSPSGIGVGSFHQHSRSQGERLLSREAPEELK---OOLALGYFVSTAKAENLPWFWSSCPOARNOCPLFLKASLHHHS--VAQTDPELLPARNSORVP--HPLDSKTTSDVLRFRVLEQYNALSWLTCNPATQDRSCLPVHFVVLT 3150
gi | 119909346 | ref | XP_595505.3 | PSPGSPSGIGVGSFHQHSRSQGERLLSREAPEELK---OOLALGYFVSTAKAENLPWFWSSCPOARNOCPLFLKASLHHHS--VAQTDPELLPARNSORVP--HPLDSKTTSDVLRFRVLEQYNALSWLTCNPATQDRSCLPVHFVVLT 3150
gi | 118098868 | ref | XP_415317.2 | PSPGSPSGIGVGSFHQHSRSQGERLLSREAPEELK---OOLALGYFVSTAKAENLPWFWSSCPOARNOCPLFLKASLHHHS--IAQTDPELLPARNSORVP--HPLDSKTTSDVLRFRVLEQYNALSWLTCNPATQDRSCLPVHFVVLT 3150
gi | 161085371 | ref | NP_730591.2 | SNHSGSPGRMDDNRSWQAGGNFKCTPPQEVVEVGLNOOPISVGYMVSITAPTGRMPAFWWSACPHELDVCPVFLKTAALHLVPSIQSADDILNSINAHQSGNDHPLDNLADVLRFRVLEQYNALSWLALDSNTHDRLSCLPINVQILM 3150
.....3010.....3020.....3030.....3040.....3050.....3060.....3070.....3080.....3090.....3100.....3110.....3120.....3130.....3140.....3150

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gi | 51100966 | ref | NP_766012.2 | CSRSCMP- 3160
gi | 109496031 | ref | XP_341091.3 | OLYNAIMNML 3160
gi | 44771211 | ref | NP_056150.1 | OLYNAIMNII 3160
gi | 73995266 | ref | XP_534693.2 | OLYNAIMNII 3160
gi | 119909346 | ref | XP_595505.3 | OLYNAIMNII 3160
gi | 118098868 | ref | XP_415317.2 | OLYNAIMNII 3160
gi | 161085371 | ref | NP_730591.2 | DLYYLAATA 3160
.....3160

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