

gi|73956677|ref|XP_546740.2| MRITLAARSRAPARFALTSPTAILTQCHAGPCTAVRRRIITGPASTGRQRAAGAAEGLSLRVGRVGFSGRGPAPRGSNTRLDALPGHDPFVAADTPTVLRERRKESGAGACRRRPPCGAGCGSPVTPGGRCPTOPPPWKSAGWDPGASPRAS 150
gi|119927960|ref|XP_593064.3| ----- 150
gi|30794514|ref|NP_035772.1| ----- 150
gi|109475899|ref|XP_342993.3| ----- 150
gi|4885645|ref|NP_005418.1| ----- 150
gi|118100986|ref|XP_417545.2| ----- 150
gi|34330176|ref|NP_899183.1| ----- 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

gi|73956677|ref|XP_546740.2| PPIRTAGRGLEAAPPSPSLPRDASAOATAAPNPWTWGRDPHPGAQRGALPADSDGLLELDLIEBELLVNMKDPEGLQTPWRFMSKDWTLTEFPCSRLLALLPWFQCHRLGDDAAATDSLPSHEPWASRRPPLHTDLHLRAPAPRTEGV 300
gi|119927960|ref|XP_593064.3| ----- 300
gi|30794514|ref|NP_035772.1| ----- 300
gi|109475899|ref|XP_342993.3| ----- 300
gi|4885645|ref|NP_005418.1| ----- 300
gi|118100986|ref|XP_417545.2| ----- 300
gi|34330176|ref|NP_899183.1| ----- 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

gi|73956677|ref|XP_546740.2| SPALALPVLRPKVCISLSONPASSGDDQALAGAPGAYGHRVCSLSDSGSRGPGFSATSSGECPRDIGNRGCQGLVLRPQGLILDRWPCTWRPQESAQTSNARLPGDRVTDGSQSEEP LLPRALPPNWGLEPGPPLCKSKPPSGPGAGKMS 450
gi|119927960|ref|XP_593064.3| ----- 450
gi|30794514|ref|NP_035772.1| -----M 450
gi|109475899|ref|XP_342993.3| ----- 450
gi|4885645|ref|NP_005418.1| -----MAQS 450
gi|118100986|ref|XP_417545.2| -----MSSMEEGVVYP-----LSDPSPVKMS 450
gi|34330176|ref|NP_899183.1| -----MS 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

gi|73956677|ref|XP_546740.2| OSTANDEGATFEHLWSSLEPDSTYFDLPPQNSSEVVG---AAGMDFVHLCGM---TTPVMSQFNLLSSTMDQ-MSSRAASAPYTPPEHAASVPTHSPIYAPSSSTFDTMSAPAIPSNTDYPGPHHFDVTFQSSSTAKSAITWYS 600
gi|119927960|ref|XP_593064.3| ESAAR-----ASALGA---APTG-----SSLQSQFNLLSSTMDQ-MSSRAASAPYTPPEHAASVPTHSPIYAPSSSTFDTMSAPVIPSNTDYPGPHHFEVTFQSSSTAKSAITWYS 600
gi|30794514|ref|NP_035772.1| AQSSTSSSTFEHLWSSLEPDSTYFDLPPSQSTSEASGS---EESNMDVFHLQ-----GMAFNLLSSTMDQ-MSSRAASAPYTPPEHAASVPTHSPIYAPSSSTFDTMSAPVIPSNTDYPGPHHFEVTFQSSSTAKSAITWYS 600
gi|109475899|ref|XP_342993.3| -MFG-----OV-QHAGASAAVAKA---TPEFGRDCDK-----KQAFNLLSSTMDQ-MSSRAASAPYTPPEHAASVPTHSPIYAPSSSTFDTMSAPVIPSNTDYPGPHHFEVTFQSSSTAKSAITWYS 600
gi|4885645|ref|NP_005418.1| TANSDDGGTTFEHLWSSLEPDSTYFDLPPSSRGNNEVVG---TDSMDVFHLCGM---TTSVMAQFNLLSSTMDQ-MSSRAASAPYTPPEHAASVPTHSPIYAPSSSTFDTMSAPVIPSNTDYPGPHHFEVTFQSSSTAKSAITWYS 600
gi|118100986|ref|XP_417545.2| QSSPADESTFEHLWSTLAPDSTYFDLPPSSHTCSNEVSNR---TEVTMDVFQMRGM---NDSVMSQFNLLSSTMDQSIGSRAASTSPYSSEHTSNVPTHSPIYAPSSSTFDAMSAPVIPSNTDYPGPHHFEVTFQSSSTAKSAITWYS 600
gi|34330176|ref|NP_899183.1| QSSPADEGPTFEHLWSTLAPDSTYFDLPPQAGHSQDRASLSPGNRAVCMQVYHMRDMNDNVMSQYLLSSTMDQGLGNRAASTSPYSSEHTSNVPTHSPIYAPSSSTFDAMSAPVIPSNTDYPGPHHFEVTFQSSSTAKSAITWYS 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600



gi|73956677|ref|XP_546740.2| PLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHEVTEVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLSQVYDDPVTGRQSVMPVYEPPOVGEFTTILYNFMCNSSCVGGMNRRLPILIIITLETDRDQVLRGRSFEGRIC 750
gi|119927960|ref|XP_593064.3| PLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHEVTEVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLSQVYDDPVTGRQSVMPVYEPPOVGEFTTILYNFMCNSSCVGGMNRRLPILIIITLETDRDQVLRGRSFEGRIC 750
gi|30794514|ref|NP_035772.1| PLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHEVTEVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLSQVYDDPVTGRQSVMPVYEPPOVGEFTTILYNFMCNSSCVGGMNRRLPILIIITLETDRDQVLRGRSFEGRIC 750
gi|109475899|ref|XP_342993.3| PLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHEVTEVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLSQVYDDPVTGRQSVMPVYEPPOVGEFTTILYNFMCNSSCVGGMNRRLPILIIITLETDRDQVLRGRSFEGRIC 750
gi|4885645|ref|NP_005418.1| PLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHEVTEVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLSQVYDDPVTGRQSVMPVYEPPOVGEFTTILYNFMCNSSCVGGMNRRLPILIIITLETDRDQVLRGRSFEGRIC 750
gi|118100986|ref|XP_417545.2| PLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHEVTEVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLSQVYDDPVTGRQSVMPVYEPPOVGEFTTILYNFMCNSSCVGGMNRRLPILIIITLETDRDQVLRGRSFEGRIC 750
gi|34330176|ref|NP_899183.1| PLLKKLYCQIAKTCPIQIKVSTPPPPGTAIRAMPVYKKAHEVTEVVKRCPNHELGRDFNEGOSAPASHLIRVEGNLSQVYDDPVTGRQSVMPVYEPPOVGEFTTILYNFMCNSSCVGGMNRRLPILIIITLETDRDQVLRGRSFEGRIC 750
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750



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gi | 73956677 | ref | XP_546740.2 | ACPGRDRKADEHDHYREQQALSESAANKGAASKRAFQSPPAVPALGANVKKRRHGDEDVYVMHVRGRENFEVLMKVKESLELMELVPOQLVDYRQOQQOQLLQRP-SHLQPSYGPVLSPMNKAHG-GVNKLPVSNQLVGPQPPHGSAA 900
gi | 119927960 | ref | XP_593064.3 | ACPGRDRKADEHDHYREQQALNESAAKSGAASKRAFQSPPTAPALGTNVKRRHGDDVYVIHVRGRENFEILMKVKESLELMELVPOQLVDYRQOQQOQLLQRP-SHLQPPSYGPVLSPMNKAHG-AVNKLPVSNQLVGPQPPHGSAA 900
gi | 30794514 | ref | NP_035772.1 | ACPGRDRKADEHDHYREQQALNESTIKNGAASKRAFQSPPAIPALGTNVKRRHGDEDMFYMHVRGRENFEILMKVKESLELMELVPOQLVDYRQOQQOQLLQRP-SHLQPPSYGPVLSPMNKAHG-GVNKLPVSNQLVGPQPPHGSAA 900
gi | 109475899 | ref | XP_342993.3 | ACPGRDRKADEHDHYREQQALNESTIKNGAASKRAFQSPPAIPALGTNVKRRHGDEDMFYMHVRGRENFEILMKVKESLELMELVPOQLVDYRQOQQOQLLQRP-SHLQPPSYGPVLSPMNKAHG-GVNKLPVSNQLVGPQPPHGSAA 900
gi | 4885645 | ref | NP_005418.1 | ACPGRDRKADEHDHYREQQALNESAAKNGAASKRAFQSPPAVPALGAGVKKRRHGDEDYVYLQVRGRENFEILMKVKESLELMELVPOQLVDYRQOQLLQRP-SHLQPPSYGPVLSPMNKAHG-GVNKLPVSNQLVGPQPPHGSAA 900
gi | 118100986 | ref | XP_417545.2 | ACPGRDRKADEHDHYREQQALNENAAKNGANKRIFKQSPQALPALGPGVKKRRHGDEEMYYVIVRGRNFEILMKIKESLELVLPVPOQLVDYRQOQQOQLLQRP-SHLQPPSYGPVLSPMNKAHGGINKLPVSNQLVGPQAQHSSES 900
gi | 34330176 | ref | NP_899183.1 | ACPGRDRKADEHDHFREQQALNESVAKNGANKRNFKQPTNTIGPSINIKRRHGDEEMYYVIVRGRNFEILMKIKESLELVLPVPOQLVDYRQOQQOQLLQRP-SHLQPPSYGPVLSPMNKAHGGINKLPVSNQLVGPQAQHSSES 900
.....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900

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gi | 73956677 | ref | XP_546740.2 | GPNLGPMPGILNHHGHALPASSEMNGSHSAQSMVSGSHCTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQNIYHLQNLTIEDLGALKIPDQYRMTIWRGLQDLKQSHDYG-AQQLIRSSSNASTIIGSGGELQQRVMEAVHFRV 1050
gi | 119927960 | ref | XP_593064.3 | GPNLGPMPGILNHHGHTLPANGEMNGGSSQSMVSGSHCTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQNIYHLQNLTIEDLGALKIPDQYRMTIWRGLQDLKQSHDYS-AQQLIRSSSNASTIIGSGGELQQRVMEAVHFRV 1050
gi | 30794514 | ref | NP_035772.1 | GPNLGPMPGMLNHHGHGSMANGEMNGGSSQSMVSGSHCTPPPPYHADPSLVSFLTGLGCPNCIECFYFTSQGLQSIYHLQNLTIEDLGALKIPDQYRMTIWRGLQDLKQSHDCG--QQLLRSSSNAATIIGSGGELQQRVMEAVHFRV 1050
gi | 109475899 | ref | XP_342993.3 | GPNLGSMPG-----DHSMPANGEMNGGSSQSMVSGSHCTPPPPYHADPSLVSFLTGLGCPNCIECFYFTSQGLQSIYHLQNLTIEDLGALKIPDQYRMTIWRGLQDLKQSHDCG--QQLLRSSSNAATIIGSGGELQQRVMEAVHFRV 1050
gi | 4885645 | ref | NP_005418.1 | TPNLGPVGPMLNHHGHAVPANGEMSSSHSAQSMVSGSHCTPPPPYHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPDQYRMTIWRGLQDLKQSHDYS-AQQLLRSSSNAATIIGSGGELQQRVMEAVHFRV 1050
gi | 118100986 | ref | XP_417545.2 | APSLGPMPGMLN--SHPMQPNGEMNGGSSQSMVSGSHCTPPPPYHADPSLVSFLTGLGCPNCIDYFTSQGLQNIYHLQNLTIEDLGALKIPDQYRMTIWRGLQDLKQSHDYG-AQQLIRSSSNASTIIGSGGELQQRVMEAVHFRV 1050
gi | 34330176 | ref | NP_899183.1 | SASLSHMGANMLG--GHMQSNGDVNGAHOQSIVSTSHCTPPPPYHADPSLVSFLTGLGCPNCIDYFTSQGLQSIYHLQNLTIEDLGALKIPDQYRMTIWRGLQDLKQSHDYG--QQLLRSSSNASTIIGSGGELQQRVMEAVHFRV 1050
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050

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gi | 73956677 | ref | XP_546740.2 | RHTIITIPNRGGPGGSGPDEWADFGFDLPDCKSRKQSIKEEFTESIN 1098
gi | 119927960 | ref | XP_593064.3 | RHTIITIPNRGGPAGGAGPDEWADFGFDLPDCKSRKQSIKEEFTESAN 1098
gi | 30794514 | ref | NP_035772.1 | RHTIITIPNRGGAGAVTPDEWADFGFDLPDCKSRKQSIKEEFTESH 1098
gi | 109475899 | ref | XP_342993.3 | RHTIITIPNRGGAGGVTPDEWADFGFDLPDCKSRKQSIKEEFTESH 1098
gi | 4885645 | ref | NP_005418.1 | RHTIITIPNRGGPGG--GPDEWADFGFDLPDCKARKQSIKEEFTESH 1098
gi | 118100986 | ref | XP_417545.2 | RHTIITIPNRG----AADEWADFGFDLPDCKSRKQSIKEEFTESIN 1098
gi | 34330176 | ref | NP_899183.1 | RHTIITIPNRGPAN--GPEWDFGFDMPDCKRLHKKSIKEEFAEGDVH 1098
.....1060.....1070.....1080.....1090.....

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