

NP_001375421.1	MATLEKLMKAFESLKSFOQQQQQQQQQQQQQQQQQPPPPPPPPPPQLPQPPQAQP	60
XP_030865871.1	MATLEKLMKAFESLKSFOQQQQQQ-----QQQQQPPPPPPPLPQLPQPPQAQP	50
XP_016806693.2	MATLEKLMKAFESLKSFOQQQQQ-----QQQQQPPPPPPPLPQLPQPPQAQP	50
XP_003813027.3	MATLEKLMKAFESLKSFOQQQQ-----QQQQQPPPPPPPLPQLPQPPQAQP	48

NP_001375421.1	LLPQFQ--PPPPPPPPPGFAVAEEPLHRPKKELSATKKDRVNHCLTTCENIVAQSVRNS	118
XP_030865871.1	LLPQFQPQPPPPPPPPPGFAVAEEPLHRPKKELSATKKDRVNHCLTTCENIVAQSVRNS	110
XP_016806693.2	LLPQFQ--PPPPPPPPPGFAVAEEPLHRPKKELSATKKDRVNHCLTTCENIVAQSVRNS	108
XP_003813027.3	LLPQFQ--PPPPPPPPPGFAVAEEPLHRPKKELSATKKDRVNHCLTTCENIVAQSVRNS	106

NP_001375421.1	PEFQKLLGIAMELFLLCSDDAESDVRMVADECLNKVIRKALMDSNLPRLQLELYEIKKNG	178
XP_030865871.1	PEFQKLLGIAMELFLLCSDDAESDVRMVADECLNKVIRKALMDSNLPRLQLELYEIKKNG	170
XP_016806693.2	PEFQKLLGIAMELFLLCSDDAESDVRMVADECLNKVIRKALMDSNLPRLQLELYEIKKNG	168
XP_003813027.3	PEFQKLLGIAMELFLLCSDDAESDVRMVADECLNKVIRKALMDSNLPRLQLELYEIKKNG	166

NP_001375421.1	APRSLRAALWRFAELAHLVRPQKCRPYLVNLLPCLTRTSKRPEESVQETLAAAVPKIMAS	238
XP_030865871.1	APRSLRAALWRFAELAHLVRPQKCRPYLVNLLPCLTRTSKRPEESVQETLAAAVPKIMAS	230
XP_016806693.2	APRSLRAALWRFAELAHLVRPQKCRPYLVNLLPCLTRTSKRPEESVQETLAAAVPKIMAS	228
XP_003813027.3	APRSLRAALWRFAELAHLVRPQKCRPYLVNLLPCLTRTSKRPEESVQETLAAAVPKIMAS	226

NP_001375421.1	PGMFANDNEIKVLLKAFIANKLSSSPTIRRTAAGSAVSIQHSRRTQYFYSWLLNVLLGL	298
XP_030865871.1	PGMFANDNEIKVLLKAFIANKLSSSPTIRRTAAGSAVSIQHSRRTQYFYSWLLNVLLGL	290
XP_016806693.2	PGMFANDNEIKVLLKAFIANKLSSSPTIRRTAAGSAVSIQHSRRTQYFYSWLLNVLLGL	288
XP_003813027.3	PGMFANDNEIKVLLKAFIANKLSSSPTIRRTAAGSAVSIQHSRRTQYFYSWLLNVLLGL	286

NP_001375421.1	LVPVEDEHSTLLILGVLLTLRylvLPLQQQVKDTSLKGSFGVTRKEMEVSPSABQLVQVY	358
XP_030865871.1	LVPVEDEHSTLLILGVLLTLRylvLPLQQQVKDTSLKGSFGVTRKEMEVSPSABQLVQVY	350
XP_016806693.2	LVPVEDEHSTLLILGVLLTLRylvLPLQQQVKDTSLKGSFGVTRKEMEVSPSABQLVQVY	348
XP_003813027.3	LVPVEDEHSTLLILGVLLTLRylvLPLQQQVKDTSLKGSFGVTRKEMEVSPSABQLVQVY	346

NP_001375421.1	ELTLHHTQHQDHNVTGALELLQQLFRTPPPELLQTLTAVGGIGQLTAAKEESGGGRSRSG	418
XP_030865871.1	ELTLHHTQHQDHNVTGALELLQQLFRTPPPELLQTLTAVGGIGQLTAAKEESGGGRSRSG	410
XP_016806693.2	ELTLHHTQHQDHNVTGALELLQQLFRTPPPELLQTLTAVGGIGQLTAAKEESGGGRSRSG	408
XP_003813027.3	ELTLHHTQHQDHNVTGALELLQQLFRTPPPELLQTLTAVGGIGQLTAAKEESGGGRSRSG	406

NP_001375421.1	SIVELIAGGSSCSPVLSRKQKGVLGEEEALEDDESRSDDVSSALTASVKDEISGEL	478
XP_030865871.1	SIVELIAGGSSCSPVLSRKQKGVLGEEEALEDDESRSDDVSSALTASVKDEISGEL	470
XP_016806693.2	SIVELIAGGSSCSPVLSRKQKGVLGEEEALEDDESRSDDVSSALTASVKDEISGEL	468
XP_003813027.3	SIVELIAGGSSCSPVLSRKQKGVLGEEEALEDDESRSDDVSSALTASVKDEISGEL	466

NP_001375421.1	AASSGVSTPGSAGHDIIITEQPRSQHTLQADSVDLASCDLTSSATDGDDEEDILSHSSSQVS	538
XP_030865871.1	AASSGVSTPGSAGHDIIITEQPRSQHTLQADSVDLASCDLTSSATDGDDEEDILSHSSSQVS	530
XP_016806693.2	AASSGVSTPGSAGHDIIITEQPRSQHTLQADSVDLASCDLTSSATDGDDEEDILSHSSSQVS	528
XP_003813027.3	AASSGVSTPGSAGHDIIITEQPRSQHTLQADSVDLASCDLTSSATDGDDEEDILSHSSSQVS	526

NP_001375421.1	AVPSDPAMDINDGTQASSPISDSSQTTTEGPDSAVTPSDSSEIVLDGTDNQYLGQIGQP	598
XP_030865871.1	AVPSDPAMDINDGTQASSPISDSSQTTTEGPDSAVTPSDSSEIVLDGTDNQYLGQIGQP	590
XP_016806693.2	AVPSDPAMDINDGTQASSPISDSSQTTTEGPDSAVTPSDSSEIVLDGTDNQYLGQIGQS	588
XP_003813027.3	AVPSDPAMDINDGTQASSPISDSSQTTTEGPDSAVTPSDSSEIVLDGTDNQYLGQIGQS	586

NP_001375421.1	QDEDEATGILPDEASEAFRNSMALQAAHLKNMHSRQPSDSSVDKFFVLREATEPGD	658
XP_030865871.1	QDEDEATGILPDEASEAFRNSMALQAAHLKNMHSRQPSDSSVDKFFVLREATEPGD	650
XP_016806693.2	QDEDEATGILPEEASEAFRNSMALQAAHLKNMHSRQPSDSSVDKFFVLREATEPGD	648
XP_003813027.3	QDEDEATGILPEEASEAFRNSMALQAAHLKNMHSRQPSDSSVDKFFVLREATEPGD	646

NP_001375421.1	QENKPCRIKIGD1IGQSTDDDSAPLVHCVRLLSASFLLTGKKNVLPVDRDVRVSVKALALSC	718
XP_030865871.1	QENKPCRIKIGD1IGQSTDDDSAPLVHCVRLLSASFLLTGKKNVLPVDRDVRVSVKALALSC	710
XP_016806693.2	QENKPCRIKIGD1IGQSTDDDSAPLVHCVRLLSASFLLTGKKNVLPVDRDVRVSVKALALSC	708
XP_003813027.3	QENKPCRIKIGD1IGQSTDDDSAPLVHCVRLLSASFLLTGKKNVLPVDRDVRVSVKALALSC	706

NP_001375421.1	VGAVALHPESFFSKLYKVPDLTTEYPEEQVSDILN1YDHGDPQVRGATAILCGTLICS	778
XP_030865871.1	VGAVALHPESFFSKLYKVPDLTTEYPEEQVSDILN1YDHGDPQVRGATAILCGTLICS	770
XP_016806693.2	VGAVALHPESFFSKLYKVPDLTTEYPEEQVSDILN1YDHGDPQVRGATAILCGTLICS	768
XP_003813027.3	VGAVALHPESFFSKLYKVPDLTTEYPEEQVSDILN1YDHGDPQVRGATAILCGTLICS	766

NP_001375421.1	ILSRSRFHVGDNMGITIRLTGNFTSLADCIPLLRKTLDDESVTKCLACTAVRHCVMSLC	838
XP_030865871.1	ILSRSRFHVGDNMGITIRLTGNFTSLADCIPLLRKTLDDESVTKCLACTAVRHCVMSLC	830
XP_016806693.2	ILSRSRFHVGDNMGITIRLTGNFTSLADCIPLLRKTLDDESVTKCLACTAVRHCVMSLC	828
XP_003813027.3	ILSRSRFHVGDNMGITIRLTGNFTSLADCIPLLRKTLDDESVTKCLACTAVRHCVMSLC	826

NP_001375421.1	SSSYSSELGLQLIIDVLTLRNSSYWLVRTELLETLAEIDFRLVSFLEAKAENLHRGAHHYT	898
XP_030865871.1	SSSYSSELGLQLIIDVLTLRNSSYWLVRTELLETLAEIDFRLVSFLEAKAENLHRGAHHYT	890
XP_016806693.2	SSSYSSELGLQLIIDVLTLRNSSYWLVRTELLETLAEIDFRLVSFLEAKAENLHRGAHHYT	888
XP_003813027.3	SSSYSSELGLQLIIDVLTLRNSSYWLVRTELLETLAEIDFRLVSFLEAKAENLHRGAHHYT	886

NP_001375421.1	GLLKLQERVLNNVVIHLLGDEDPVRVHVAASLIRLVPKLFYKCDQGQADPVVAVARDOQ	958
XP_030865871.1	GLLKLQERVLNNVVIHLLGDEDPVRVHVAASLIRLVPKLFYKCDQGQADPVVAVARDOQ	950
XP_016806693.2	GLLKLQERVLNNVVIHLLGDEDPVRVHVAASLIRLVPKLFYKCDQGQADPVVAVARDOQ	948
XP_003813027.3	GLLKLQERVLNNVVIHLLGDEDPVRVHVAASLIRLVPKLFYKCDQGQADPVVAVARDOQ	946

NP_001375421.1	SVYKLLMHETQPPSHFSVSTTTRIYRGYNLLPSITDVTMENNLSRVIAAVSHELITSTT	1018
XP_030865871.1	SVYKLLMHETQPPSHFSVSTTTRIYRGYNLLPSITDVTMENNLSRVIAAVSHELITSTT	1010
XP_016806693.2	SVYKLLMHETQPPSHFSVSTTTRIYRGYNLLPSITDVTMENNLSRVIAAVSHELITSTT	1008
XP_003813027.3	SVYKLLMHETQPPSHFSVSTTTRIYRGYNLLPSITDVTMENNLSRVIAAVSHELITSTT	1006

NP_001375421.1	RALTFCGCCALCLLSTAFPVC1WSLGHWCQVPLSASDESRSKSTVGMATMILTLLSSAW	1078
XP_030865871.1	RALTFCGCCALCLLSTAFPVC1WSLGHWCQVPLSASDESRSKSTVGMATMILTLLSSAW	1070
XP_016806693.2	RALTFCGCCALCLLSTAFPVC1WSLGHWCQVPLSASDESRSKSTVGMATMILTLLSSAW	1068
XP_003813027.3	RALTFCGCCALCLLSTAFPVC1WSLGHWCQVPLSASDESRSKSTVGMATMILTLLSSAW	1066

NP_001375421.1	FPILDLSAHQDALILAGNLLAASAPKSLRSSWASEEANPAATKQEEVWPALGDRALVPMV	1138
XP_030865871.1	FPILDLSAHQDALILAGNLLAASAPKSLRSSWASEEANPAATKQEEVWPALGDRALVPMV	1130
XP_016806693.2	FPILDLSAHQDALILAGNLLAASAPKSLRSSWASEEANPAATKQEEVWPALGDRALVPMV	1128
XP_003813027.3	FPILDLSAHQDALILAGNLLAASAPKSLRSSWASEEANPAATKQEEVWPALGDRALVPMV	1126

NP_001375421.1	EQLFSHLLKVINICAHVLDDVAPGPAIKAAPSLTNPPSLSP1RRKKEKEPEGEQASVPL	1198
XP_030865871.1	EQLFSHLLKVINICAHVLDDVAPGPAIKAAPSLTNPPSLSP1RRKKEKEPEGEQASVPL	1190
XP_016806693.2	EQLFSHLLKVINICAHVLDDVAPGPAIKAAPSLTNPPSLSP1RRKKEKEPEGEQASVPL	1188
XP_003813027.3	EQLFSHLLKVINICAHVLDDVAPGPAIKAAPSLTNPPSLSP1RRKKEKEPEGEQASVPL	1186

NP_001375421.1	SPKGSSEASASASQSDTSGPVTTSKSSSLGFSYHLPSYKLHDVLKATHANYKVTLDLQN	1258
XP_030865871.1	SPKGSSEASASASQSDTSGPVTTSKSSSLGFSYHLPSYKLHDVLKATHANYKVTLDLQN	1250
XP_016806693.2	SPKGSSEASASASQSDTSGPVTTSKSSSLGFSYHLPSYKLHDVLKATHANYKVTLDLQN	1248
XP_003813027.3	SPKGSSEASASASQSDTSGPVTTSKSSSLGFSYHLPSYKLHDVLKATHANYKVTLDLQN	1246

NP_001375421.1	STEKFGGFLRSALDVLSQLLELATLQDIGKCVEEILGYLKSDFSREPMMATVCVQQLKT	1318
XP_030865871.1	STEKFGGFLRSALDVLSQLLELATLQDIGKCVEEILGYLKSDFSREPMMATVCVQQLKT	1310
XP_016806693.2	STEKFGGFLRSALDVLSQLLELATLQDIGKCVEEILGYLKSDFSREPMMATVCVQQLKT	1308
XP_003813027.3	STEKFGGFLRSALDVLSQLLELATLQDIGKCVEEILGYLKSDFSREPMMATVCVQQLKT	1306

NP_001375421.1	LFCTNLASQFDGLSSNPSKSGRAQRLGSSSVRPLGYHCFMAYPTHFTQALADASLRNM	1378
XP_030865871.1	LFCTNLASQFDGLSSNPSKSGRAQRLGSSSVRPLGYHCFMAYPTHFTQALADASLRNM	1370
XP_016806693.2	LFCTNLASQFDGLSSNPSKSGRAQRLGSSSVRPLGYHCFMAYPTHFTQALADASLRNM	1368
XP_003813027.3	LFCTNLASQFDGLSSNPSKSGRAQRLGSSSVRPLGYHCFMAYPTHFTQALADASLRNM	1366

NP_001375421.1	VQAQEQNDTSGWFDVLQKVSTQLKTNLTSTVTKNRADKNAIHNHRLFEPLV1KALKQYTT	1438
XP_030865871.1	VQAQEQNDTSGWFDVLQKVSTQLKTNLTSTVTKNRADKNAIHNHRLFEPLV1KALKQYTT	1430
XP_016806693.2	VQAQEQNDTSGWFDVLQKVSTQLKTNLTSTVTKNRADKNAIHNHRLFEPLV1KALKQYTT	1428
XP_003813027.3	VQAQEQNDTSGWFDVLQKVSTQLKTNLTSTVTKNRADKNAIHNHRLFEPLV1KALKQYTT	1426

NP_001375421.1	TTCVQLQKVQLDLLAQLVQLRVNYCLLDSQDQVFIGFVLKQFEYIEVGQFRESEAIIPNIF	1498
XP_030865871.1	TTCVQLQKVQLDLLAQLVQLRVNYCLLDSQDQVFIGFVLKQFEYIEVGQFRESEAIIPNIF	1490
XP_016806693.2	TTTSVQLQKVQLDLLAQLVQLRVNYCLLDSQDQVFIGFVLKQFEYIEVGQFRESEAIIPNIF	1488
XP_003813027.3	TTTSVQLQKVQLDLLAQLVQLRVNYCLLDSQDQVFIGFVLKQFEYIEVGQFRESEAIIPNIF	1486

NP_001375421.1	FFVLVLLSYERYHSKOIIGIPK1IQLCDGIMASGRKAVTHAIPALQPIVHDLFVLRGTNKA	1558
XP_030865871.1	FFVLVLLSYERYHSKOIIGIPK1IQLCDGIMASGRKAVTHAIPALQPIVHDLFVLRGTNKA	1550
XP_016806693.2	FFVLVLLSYERYHSKOIIGIPK1IQLCDGIMASGRKAVTHAIPALQPIVHDLFVLRGTNKA	1548
XP_003813027.3	FFVLVLLSYERYHSKOIIGIPK1IQLCDGIMASGRKAVTHAIPALQPIVHDLFVLRGTNKA	1546

NP_001375421.1	DAGKELETQKEVVVSMMLRLIQYHQVLEMFILVLQQCHKENEDKWRLSRQIADIILPML	1618
XP_030865871.1	DAGKELETQKEVVVSMMLRLIQYHQVLEMFILVLQQCHKENEDKWRLSRQIADIILPML	1610
XP_016806693.2	DAGKELETQKEVVVSMMLRLIQYHQVLEMFILVLQQCHKENEDKWRLSRQIADIILPML	1608
XP_003813027.3	DAGKELETQKEVVVSMMLRLIQYHQVLEMFILVLQQCHKENEDKWRLSRQIADIILPML	1606

NP_001375421.1	AKQQMHDISHAELGVLNLTPEILAPSSLRPVDMLLSMFVTPNTMASVSTVOLWISGILA	1678
XP_030865871.1	AKQQMHDISHAELGVLNLTPEILAPSSLRPVDMLLSMFVTPNTMASVSTVOLWISGILA	1670
XP_016806693.2	AKQQMHDISHAELGVLNLTPEILAPSSLRPVDMLLSMFVTPNTMASVSTVOLWISGILA	1668
XP_003813027.3	AKQQMHDISHAELGVLNLTPEILAPSSLRPVDMLLSMFVTPNTMASVSTVOLWISGILA	1666

NP_001375421.1	ILRVLISQSTEDIVLSRIQELSFSPLYISCTVINRLRGDSNSTLEEHSBGKQIKNLPPE	1738
XP_030865871.1	ILRVLISQSTEDIVLSRIQELSFSPLYISCTVINRLRGDSNSTLEEHSBGKQIKNLPPE	1730
XP_016806693.2	ILRVLISQSTEDIVLSRIQELSFSPLYISCTVINRLRGDSNSTLEEHSBGKQIKNLPPE	1728
XP_003813027.3	ILRVLISQSTEDIVLSRIQELSFSPLYISCTVINRLRGDSNSTLEEHSBGKQIKNLPPE	1726

NP_001375421.1	TFSRFLQLQVGILLEDIVTKQLKVMSEQQHTFYCQELGTLMLCLIHFKSGMFRRITAA	1798
XP_030865871.1	TFSRFLQLQVGILLEDIVTKQLKVMSEQQHTFYCQELGTLMLCLIHFKSGMFRRITAA	1790
XP_016806693.2	TFSRFLQLQVGILLEDIVTKQLKVMSEQQHTFYCQELGTLMLCLIHFKSGMFRRITAA	1788
XP_003813027.3	TFSRFLQLQVGILLEDIVTKQLKVMSEQQHTFYCQELGTLMLCLIHFKSGMFRRITAA	1786

NP_001375421.1	ATRLFRSDGCGGSFYTLDSNLNRARSMITTHPALVLLWCQIILLVNHNTDYRWAEVQQT	1858
XP_030865871.1	ATRLFRSDGCGGSFYTLDSNLNRARSMITTHPALVLLWCQIILLVNHNTDYRWAEVQQT	1850
XP_016806693.2	ATRLFRSDGCGGSFYTLDSNLNRARSMITTHPALVLLWCQIILLVNHNTDYRWAEVQQT	1848
XP_003813027.3	ATRLFRSDGCGGSFYTLDSNLNRARSMITTHPALVLLWCQIILLVNHNTDYRWAEVQQT	1846

NP_001375421.1	KRHSLSSTKLLSPQMSGEEDSDLAALKGMCNREIVRGALLFCFDYVQNLHDESHLTW	1918
XP_030865871.1	KRHSLSSTKLLSPQMSGEEDSDLAALKGMCNREIVRGALLFCFDYVQNLHDESHLTW	1910
XP_016806693.2	KRHSLSSTKLLSPQMSGEEDSDLAALKGMCNREIVRGALLFCFDYVQNLHDESHLTW	1908
XP_003813027.3	KRHSLSSTKLLSPQMSGEEDSDLAALKGMCNREIVRGALLFCFDYVQNLHDESHLTW	1906

NP_001375421.1	LIVNHIQDLISLSHEPPVQDPTSAVHRNSAASGLF1QAIQSRCENLSTPTTLKKTLOCLE	1978
XP_030865871.1	LIVNHIQDLISLSHEPPVQDPTSAVHRNSAASGLF1QAIQSRCENLSTPTTLKKTLOCLE	1970
XP_016806693.2	LIVNHIQDLISLSHEPPVQDPTSAVHRNSAASGLF1QAIQSRCENLSTPTTLKKTLOCLE	1968
XP_003813027.3	LIVNHIQDLISLSHEPPVQDPTSAVHRNSAASGLF1QAIQSRCENLSTPTTLKKTLOCLE	1966

NP_001375421.1	GIHLSQSGAVLTLYVDRLLCTPFRVLARMVDILACRVEMLLAANLQSSMAQLPMEELNR	2038
XP_030865871.1	GIHLSQSGAVLTLYVDRLLCTPFRVLARMVDILACRVEMLLAANLQSSMAQLPMEELNR	2030
XP_016806693.2	GIHLSQSGAVLTLYVDRLLCTPFRVLARMVDILACRVEMLLAANLQSSMAQLPMEELNR	2028
XP_003813027.3	GIHLSQSGAVLTLYVDRLLCTPFRVLARMVDILACRVEMLLAANLQSSMAQLPMEELNR	2026

NP_001375421.1	IQEYILQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPSPVSSHPLDGDGHVSLTVSPDKD	2098
XP_030865871.1	IQEYILQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPSPVSSHPLDGDGHVSLTVSPDKD	2090
XP_016806693.2	IQEYILQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPSPVSSHPLDGDGHVSLTVSPDKD	2088
XP_003813027.3	IQEYILQSSGLAQRHQRLYSLLDRFRLSTMQDSLSPSPVSSHPLDGDGHVSLTVSPDKD	2086

NP_001375421.1	WYVHLVKSQCWTRSDSALLEGAELVNR1PAEDMSAFMNSSEFNLSLLAPCISLGMSEISG	2158
XP_030865871.1	WYVHLVKSQCWTRSDSALLEGAELVNR1PAEDMSAFMNSSEFNLSLLAPCISLGMSEISG	2150
XP_016806693.2	WYVHLVKSQCWTRSDSALLEGAELVNR1PAEDMSAFMNSAFNLSLLAPCISLGMSEISG	2148
XP_003813027.3	WYVHLVKSQCWTRSDSALLEGAELVNR1PAEDMSAFMNSAFNLSLLAPCISLGMSEISG	2146

NP_001375421.1	GQKSALFEAAREVTLARVSGTVQQLPAVHHVFQPELPAEPAAYNSKLNLD1FGDAALYQSL	2218
XP_030865871.1	GQKSALFEAAREVTLARVSGTVQQLPAVHHVFQPELPAEPAAYNSKLNLD1FGDAALYQSL	2210
XP_016806693.2	GQKSALFEAAREVTLARVSGTVQQLPAVHHVFQPELPAEPAAYNSKLNLD1FGDAALYQSL	2208
XP_003813027.3	GQKSALFEAAREVTLARVSGTVQQLPAVHHVFQPELPAEPAAYNSKLNLD1FGDAALYQSL	2206

NP_001375421.1	PTLARALAQYLVVYVSKLPSHLHLPPEKEKD1VKFVVAATLEALSNH1IHEQIPLSLDLQAG	2278
XP_030865871.1	PTLARALAQYLVVYVSKLPSHLHLPPEKEKD1VKFVVAATLEALSNH1IHEQIPLSLDLQAG	2270
XP_016806693.2	PTLARALAQYLVVYVSKLPSHLHLPPEKEKD1VKFVVAATLEALSNH1IHEQIPLSLDLQAG	2268
XP_003813027.3	PTLARALAQYLVVYVSKLPSHLHLPPEKEKD1VKFVVAATLEALSNH1IHEQIPLSLDLQAG	2266

NP_001375421.1	LDCCCLALQLPGLWSVVSSTFVTHACSLIYCVHF1LEAIVAQPEGQLLSPERRTNTPKA	2338
XP_030865871.1	LDCCCLALQLPGLWSVVSSTFVTHACSLIYCVHF1LEAIVAQPEGQLLSPERRTNTPKA	233