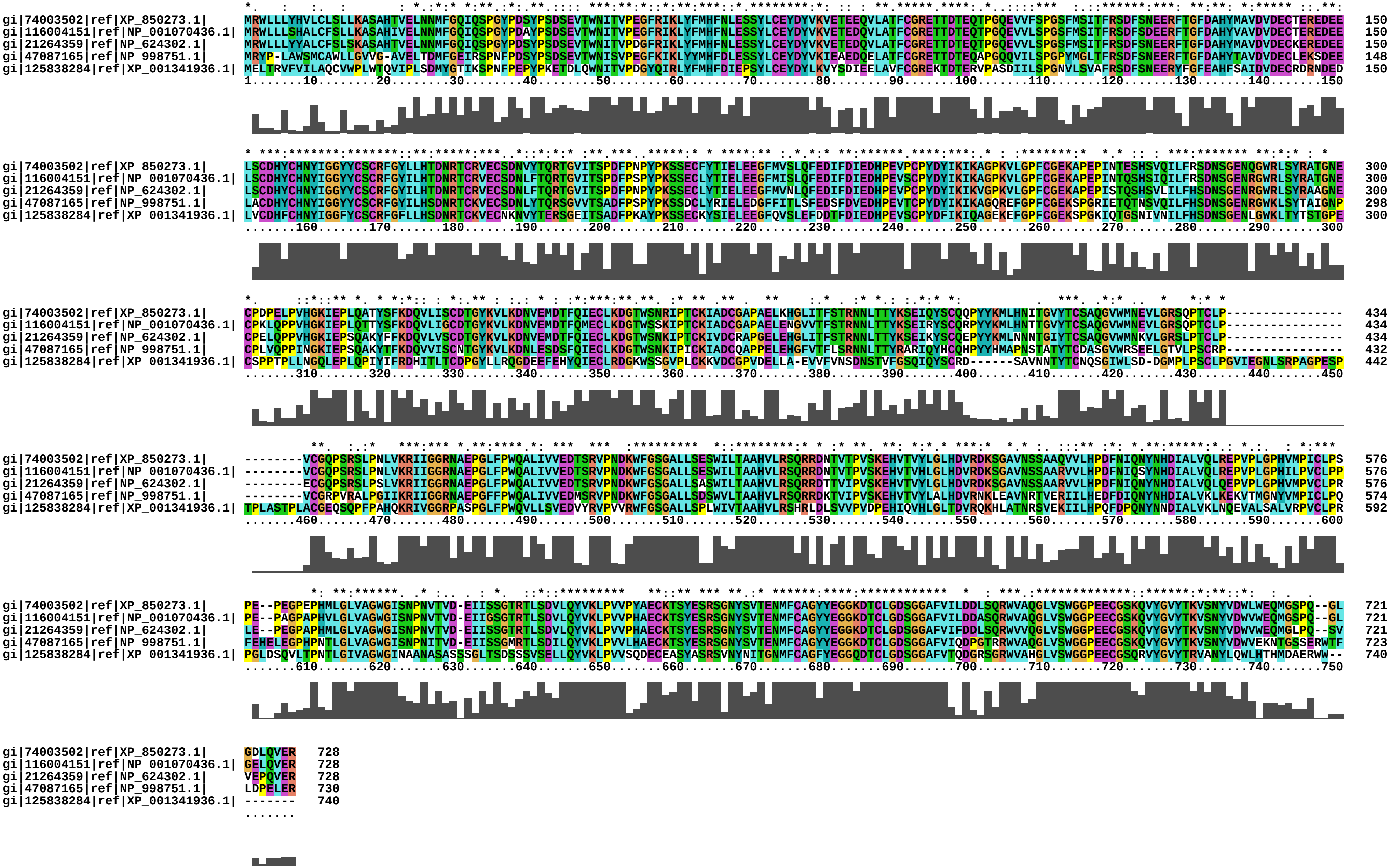

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gi|74003502|ref|XP_850273.1|       MRWLLLYHVLCLSLLKASAHTVELNNMFGQIQSPGYPDSYPSDSEVTWNITVPEGFRIKLYFMHFNLESSYLCEYDYVKVETEEQVLATFCGRETTDTEQTPGQEVVFSPGSFMSITFRSDFSNEERFTGFDAHYMAVDVDECTEREDEE   150
gi|116004151|ref|NP_001070436.1|   MRWLLLSHALCFSLLKASAHIVELNNMFGQIQSPGYPDAYPSDSEVTWNITVPEGFRIKLYFMHFNLESSYLCEYDYVKVETEDQVLATFCGRETTDTEQTPGQEVVLSPGSFMSITFRSDFSDEERFTGFDAHYVAVDVDECTEREDEE   150
gi|21264359|ref|NP_624302.1|       MRWLLLYYALCFSLSKASAHTVELNNMFGQIQSPGYPDSYPSDSEVTWNITVPDGFRIKLYFMHFNLESSYLCEYDYVKVETEDQVLATFCGRETTDTEQTPGQEVVLSPGSFMSITFRSDFSNEERFTGFDAHYMAVDVDECKEREDEE   150
gi|47087165|ref|NP_998751.1|       MRYP-LAWSMCAWLLGVVG-AVELTDMFGEIRSPNFPDSYPSDSEVTWNISVPEGFKIKLYYMHFDLESSYLCEYDYVKIEAEDQELATFCGRETTDTEQAPGQQVILSPGPYMGLTFRSDFSNEERFTGFDAHYTAVDVDECLEKSDEE   148
gi|125838284|ref|XP_001341936.1|   MELTRVFVILAQCVWPLWTQVIPLSDMYGTIKSPNFPEPYPKETDLQWNITVPDGYQIRLYFMHFDIEPSYLCEYDYLKVYSDIEELAVFCGREKTDTERVPASDIILSPGNVLSVAFRSDFSNEERYFGFEAHFSAIDVDECRDRNDED   150
                                   1.......10........20........30........40........50........60........70........80........90........100.......110.......120.......130.......140.......150

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gi|74003502|ref|XP_850273.1|       LSCDHYCHNYIGGYYCSCRFGYLLHTDNRTCRVECSDNVYTQRTGVITSPDFPNPYPKSSECFYTIELEEGFMVSLQFEDIFDIEDHPEVPCPYDYIKIKAGPKVLGPFCGEKAPEPINTESHSVQILFRSDNSGENQGWRLSYRATGNE   300
gi|116004151|ref|NP_001070436.1|   LSCDHYCHNYIGGYYCSCRFGYILHTDNRTCRVECSDNLFTQRTGVITSPDFPSPYPKSSECLYTIELEEGFMISLQFEDIFDIEDHPEVSCPYDYIKIKAGPKVLGPFCGEKAPEPINTQSHSIQILFRSDNSGENRGWRLSYRATGNE   300
gi|21264359|ref|NP_624302.1|       LSCDHYCHNYIGGYYCSCRFGYILHTDNRTCRVECSDNLFTQRTGVITSPDFPNPYPKSSECLYTIELEEGFMVNLQFEDIFDIEDHPEVPCPYDYIKIKVGPKVLGPFCGEKAPEPISTQSHSVLILFHSDNSGENRGWRLSYRAAGNE   300
gi|47087165|ref|NP_998751.1|       LACDHYCHNYIGGYYCSCRFGYILHSDNRTCKVECSDNLYTQRSGVVTSADFPSPYPKSSDCLYRIELEDGFFITLSFEDSFDVEDHPEVTCPYDYIKIKAGQREFGPFCGEKSPGRIETQTNSVQILFHSDNSGENRGWKLSYTAIGNP   298
gi|125838284|ref|XP_001341936.1|   LVCDHFCHNYIGGFYCSCRFGFLLHSDNRTCKVECNKNVYTERSGEITSADFPKAYPKSSECKYSIELEEGFQVSLEFDDTFDIEDHPEVSCPYDFIKIQAGEKEFGPFCGEKSPGKIQTGSNIVNILFHSDNSGENLGWKLTYTSTGPE   300
                                   .......160.......170.......180.......190.......200.......210.......220.......230.......240.......250.......260.......270.......280.......290.......300

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gi|74003502|ref|XP_850273.1|       CPDPELPVHGKIEPLQATYSFKDQVLISCDTGYKVLKDNVEMDTFQIECLKDGTWSNRIPTCKIADCGAPAELKHGLITFSTRNNLTTYKSEIQYSCQQPYYKMLHNITGVYTCSAQGVWMNEVLGRSQPTCLP----------------   434
gi|116004151|ref|NP_001070436.1|   CPKLQPPVHGKIEPLQTTYSFKDQVLIGCDTGYKVLKDNVEMDTFQMECLKDGTWSSKIPTCKIADCGAPAELENGVVTFSTRNNLTTYKSEIRYSCQRPYYKMLHNTTGVYTCSAQGVWMNEVLGRSQPTCLP----------------   434
gi|21264359|ref|NP_624302.1|       CPELQPPVHGKIEPSQAKYFFKDQVLVSCDTGYKVLKDNVEMDTFQIECLKDGTWSNKIPTCKIVDCRAPGELEHGLITFSTRNNLTTYKSEIKYSCQEPYYKMLNNNTGIYTCSAQGVWMNKVLGRSLPTCLP----------------   434
gi|47087165|ref|NP_998751.1|       CPLVQPPINGKIEPSQAKYTFKDQVVISCNTGYKVLKDNLESDSFQIECLKDGTWSNKIPICKIADCQAPPELEHGFVTFLSRNNLTTYRARIQYHCQHPYYHMAPNSTATYTCDASGVWRSEELGTVLPSCRP----------------   432
gi|125838284|ref|XP_001341936.1|   CSPPTPLLNGQLEPLQPIYIFRDHITLTCDPGYLLRQGDEEFEHYQIECLRDGKWSSGVPLCKKVDCGPVDELLA-EVVFVNSDNSTVFGSQIQYSCRD------SAVNNTYTCNQSGIWLSD-DGMPLPSCLPGVIEGNLSRPAGPESP   442
                                   .......310.......320.......330.......340.......350.......360.......370.......380.......390.......400.......410.......420.......430.......440.......450

                                           **.  :.:*    ***:*** *.**:****.*: ***  ***   :*********   *::*********:* *  :* **. **: *:*.* ***:*   *.* :.  :::** :*: *.**:*****:*.: *.:.   : *:***
gi|74003502|ref|XP_850273.1|       --------VCGQPSRSLPNLVKRIIGGRNAEPGLFPWQALIVVEDTSRVPNDKWFGSGALLSESWILTAAHVLRSQRRDNTVTPVSKEHVTVYLGLHDVRDKSGAVNSSAAQVVLHPDFNIQNYNHDIALVQLREPVPLGPHVMPICLPS   576
gi|116004151|ref|NP_001070436.1|   --------VCGQPSRSLPNLVKRIIGGRNAEPGLFPWQALIVVEDTSRVPNDKWFGSGALLSESWILTAAHVLRSQRRDNTVTPVSKEHVTVHLGLHDVRDKSGAVNSSAARVVLHPDFNIQSYNHDIALVQLREPVPLGPHILPVCLPP   576
gi|21264359|ref|NP_624302.1|       --------ECGQPSRSLPSLVKRIIGGRNAEPGLFPWQALIVVEDTSRVPNDKWFGSGALLSASWILTAAHVLRSQRRDTTVIPVSKEHVTVYLGLHDVRDKSGAVNSSAARVVLHPDFNIQNYNHDIALVQLQEPVPLGPHVMPVCLPR   576
gi|47087165|ref|NP_998751.1|       --------VCGRPVRALPGIIKRIIGGRNAEPGFFPWQALIVVEDMSRVPNDKWFGSGALLSDSWVLTAAHVLRSQRRDKTVIPVSKEHVTVYLALHDVRNKLEAVNRTVERIILHEDFDIQNYNHDIALVKLKEKVTMGNYVMPICLPQ   574
gi|125838284|ref|XP_001341936.1|   TPLASTPLACGEQSQPFPAHQKRIVGGRPASPGLFPWQVLLSVEDVYRVPVVRWFGSGALLSPLWIVTAAHVLRSHRLDLSVVPVDPEHIQVHLGLTDVRQKHLATNRSVEKIILHPQFDPQNYNNDIALVKLNQEVALSALVRPVCLPR   592
                                   .......460.......470.......480.......490.......500.......510.......520.......530.......540.......550.......560.......570.......580.......590.......600

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gi|74003502|ref|XP_850273.1|       PE--PEGPEPHMLGLVAGWGISNPNVTVD-EIISSGTRTLSDVLQYVKLPVVPYAECKTSYESRSGNYSVTENMFCAGYYEGGKDTCLGDSGGAFVILDDLSQRWVAQGLVSWGGPEECGSKQVYGVYTKVSNYVDWLWEQMGSPQ--GL   721
gi|116004151|ref|NP_001070436.1|   PE--PAGPAPHVLGLVAGWGISNPNVTVD-EIIGSGTRTLSDVLQYVKLPVVPHAECKTSYESRSGNYSVTENMFCAGYYEGGKDTCLGDSGGAFVILDDASQRWVAQGLVSWGGPEECGSKQVYGVYTKVSNYVDWVWEQMGSPQ--GL   721
gi|21264359|ref|NP_624302.1|       LE--PEGPAPHMLGLVAGWGISNPNVTVD-EIISSGTRTLSDVLQYVKLPVVPHAECKTSYESRSGNYSVTENMFCAGYYEGGKDTCLGDSGGAFVIFDDLSQRWVVQGLVSWGGPEECGSKQVYGVYTKVSNYVDWVWEQMGLPQ--SV   721
gi|47087165|ref|NP_998751.1|       FEHELEGPHPNTLGLVAGWGISNPNITVD-EIISSGMRTLSDILQYVKLPVVLHAECKTSYESRSGNYSVTENMFCAGYYEGGKDTCLGDSGGAFVIQDPGTRRWVAQGLVSWGGPEECGSKQVYGVYTKVSNYVDWVEKNTGSSERWTF   723
gi|125838284|ref|XP_001341936.1|   PGLDSQVLTPNTLGIVAGWGINAANASASSSGLTSDSSSVSELLQYVKLPVVSQDECEASYASRSVNYNITGNMFCAGFYEGGQDTCLGDSGGAFVTQDGRSGRWVAHGLVSWGGPEECGSQRVYGVYTRVANYLQWLHTHMDAERWW--   740
                                   .......610.......620.......630.......640.......650.......660.......670.......680.......690.......700.......710.......720.......730.......740.......750

gi|74003502|ref|XP_850273.1|       GDLQVER   728
gi|116004151|ref|NP_001070436.1|   GELQVER   728
gi|21264359|ref|NP_624302.1|       VEPQVER   728
gi|47087165|ref|NP_998751.1|       LDPELER   730
gi|125838284|ref|XP_001341936.1|   -------   740
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