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gi |18425101|ref|NP_569038.1|          -----MNVLSRSVALISVFLLPFLFSSVDN--PDRRVLVLLDDLS--LKSSSHIFFNILKSRGFDFLDKFLAEDSKLALQRVGYQYLVGLIIFAPST--ERFGGSLDQKSIADFDVSGRDLILSADLAASDLIN 150
gi |115471133|ref|NP_001059165.1|     -----MAAPRHHLALAVALLVVTAADADEGGPRGRRVVLVVDLDA--VRSSSHAFASLQGRGFDDFLRLADDPKLSLHRYGYQYLVGLVLFAPST--PRFGGSVDQNSILEFIDAGHDMILAADSASDLIN 150
gi |24640745|ref|NP_511096.2|         -----MMWKALLIIVLAVIAIACQAVLEIDANILVLLDNLNLA--IRETHSIFFKSLQDRGFKLYKLLADDSLLLSKYGLEYLVKQVLIIFAPSV--BEFGGDSVSRRLAQFVDGQGNLIVAGSEKSGDALR 150
gi |158295782|ref|XP_316417.4|        -----MSNRSVLGFTGILLALLAHTPAAVVAEPGEILLVLLDNLNLA--IRETHSIFFKSLQERGKYLTKFLADDAGLVLKSYGFLYVQHLILFAPSV--BEFGGSLSEBAIIEFDINGGNLIVAGSASGDPLR 150
gi |20070197|ref|NP_005207.2|         -----MGYFRKAGAGSFGRRRKMFPSTAAARAWA--LFWLLLPGLAVCASGPRLLVLLDNLN--VRETHSLFFRSKLDGRGFLFRTKATDDPSLSLKIYGEFLYDNLIIIFSPSV--EDFGGNINVEITFAFIDGGGSVLVAASDIDGDLR 150
gi |114554462|ref|XP_001161661.1|     -----MGYFRKAGAGSFGRRRKMFPSTAAARAWA--LFWLLLPGLAVCASGPRLLVLLDNLN--VRETHSLFFRSKLDGRGFLFRTKATDDPSLSLKIYGEFLYDNLIIIFSPSV--EDFGGNINVEITFAFIDGGGSVLVAASDIDGDLR 150
gi |46195798|ref|NP_031864.2|        -----MKMDFRLAVRANP--LCGLLLAVLGCVCASGPRLLVLLDNLN--VRETHSLFFRSKLDGRGFLFRTKATDDPSLSLKIYGEFLYDNLIIIFSPSV--EDFGGNINVEITFAFIDGGGSVLVAASDIDGDLR 150
gi |58865778|ref|NP_001012104.1|     -----MKMDFRLAVRANP--LCGLLLAVLGCVCASGPRLLVLLDNLN--VRETHSLFFRSKLDGRGFLFRTKATDDPSLSLKIYGEFLYDNLIIIFSPSV--EDFGGNINVEITFAFIDGGGSVLVAASDIDGDLR 150
gi |50979164|ref|NP_001003321.1|     -----MRRRRKMEAGAAARAWA--LLWLLLPGLGVCASGPRLLVLLDNLN--LRETHSLFFRSKLDRAFELFTKATDDPSLSLKIYGEFLYDNLIIIFSPSV--EDFGGNINVEITFAFIDGGGSVLVAASDIDGDLR 150
gi |155371877|ref|NP_001094543.1|     -----MATRAARVMSGWMLLLPGLGAGASGPRLLVLLDNLN--LRETHSLFFRSKLDGRGFLFRTKATDDPSLSLKIYGEFLYDNLIIIFSPSV--EDFGGNINVEITFAFIDGGGSVLVAASDIDGDLR 150
gi |118101269|ref|XP_423294.2|        -----MPRADEKMAAAEVR--LWLLAAVAAGA--GPRSLVLLDNLN--LRDTHSLFFRSKLDGRGFLFRTKATDDPSLSLKIYGEFLYDNLIIIFSPSI--EDFGGNINVEITFAFIDGGGSVLVAASDIDGDLR 150
gi |47085831|ref|NP_998258.1|        -----MATALSGGFSKNAFLSALMLQAVLGDKLVLLDNLN--LRETHSIFFRSKLDGRGFLFRTKATDDPSLSLKIYGEFLYDNLIIIFSPSV--EDFGGNINVEITFAFIDGGGSVLVAASDIDGDLR 150
gi |17536165|ref|NP_495655.1|        -----MRWLPG-----LLLLIASIGFQSLADRVLVLGETAA--VKDTHSVFLNRSVGRHELVRAADDSQLALFKHGQFLDHLFIPLAPGV--VFGGSLSPSEIKKFDVDAAGGNLVAASDIDGDLR 150
gi |124506940|ref|XP_001352067.1|     MKIKIKNPLVCFLLFLFLLSFRYSCEKKKLTQVYKPKSIIGRIKKNIKQYKPKLILITDITINERYSSFLHILNTEGNYISKIINILSPDDIHKINVCLYDGLIILDLINDKTIVEILKASYLKLFDKKKHIFSLNNVIGKNAV 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi |18425101|ref|NP_569038.1|          GIATKCGVDDED SAMVIDHISFVSVDVDGDHLLIAA--DDLVK-----SDVILGKI---KIEAPVLFKRVGVAHSLNPTNNLVVLVLEA--SPAYSANPKSLLSPPQLIGSSISLVSMOARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |115471133|ref|NP_001059165.1|     GIATKCGVDDED PEAMVIDHINYAATADEAGDHTLIAG--DDLK-----SDVILGSK---KIEAPVLFKRVGVAHSLNPTNNLVVLVLEA--SPAYSANPKSLLSPPQLIGSSISLVSMOARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |24640745|ref|NP_511096.2|         EFASKEGFLDEE--NAVIDDHLHYDVS--DAGDHTILIVASAKNLIQ---ADIVVKGKARQADAPLRLYRGTLIADAKENPRLVLLKLLAETAASYNPEASV--DIPHAVGRGILLIAALQARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |158295782|ref|XP_316417.4|        ELASKEGFEVDEE--KAVIDDHLHYDVS--DAGDHTILIVASAKNLIQ---ADIVVKGKARQADAPLRLYRGTLIADAKENPRLVLLKLLAETAASYNPEASV--DIPHAVGRGILLIAALQARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |20070197|ref|NP_005207.2|         ELGSECGIEFDEE--KTAVIDHHNYDIS--DLGQHTLIVADTENLLK---APTIVGKS-----SLNPILFRGVGMVADPDPNPLVDILIGSSTSYSFPPDKPIITQYPHVGKNTLLIAGLQARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |114554462|ref|XP_001161661.1|     ELGSECGIEFDEE--KTAVIDHHNYDIS--DLGQHTLIVADTENLLK---APTIVGKS-----SLNPILFRGVGMVADPDPNPLVDILIGSSTSYSFPPDKPIITQYPHVGKNTLLIAGLQARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |46195798|ref|NP_031864.2|        ELGSECGIEFDEE--KTAVIDHHNYDIS--DLGQHTLIVADTENLLK---APTIVGKS-----SLNPILFRGVGMVADPDPNPLVDILIGSSTSYSFPPDKPIITQYPHVGKNTLLIAGLQARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |58865778|ref|NP_001012104.1|     ELGSECGIEFDEE--KTAVIDHHNYDIS--DLGQHTLIVADTENLLK---APTIVGKS-----SLNPILFRGVGMVADPDPNPLVDILIGSSTSYSFPPDKPIITQYPHVGKNTLLIAGLQARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |50979164|ref|NP_001003321.1|     ELGSECGIEFDEE--KTAVIDHHNYDIS--DLGQHTLIVADTENLLK---APTIVGKS-----SLNPILFRGVGMVADPDPNPLVDILIGSSTSYSFPPDKPIITQYPHVGKNTLLIAGLQARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |155371877|ref|NP_001094543.1|     ELGSECGIEFDEE--KTAVIDHHNYDIS--DLGQHTLIVADTENLLK---APTIVGKS-----SLNPILFRGVGMVADPDPNPLVDILIGSSTSYSFPPDKPIITQYPHVGKNTLLIAGLQARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |118101269|ref|XP_423294.2|        ELGSECGIEFDEE--KTAVIDHHNYDIS--DLGQHTLIVADTENLLK---APTIVGKS-----SLNPILFRGVGMVADPDPNPLVDILIGSSTSYSFPPDKPIITQYPHVGKNTLLIAGLQARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |47085831|ref|NP_998258.1|        ELGSECGIEFDEE--KTAVIDHHNYDIS--DLGQHTLIVADTENLLK---APTIVGKS-----SLNPILFRGVGMVADPDPNPLVDILIGSSTSYSFPPDKPIITQYPHVGKNTLLIAGLQARNRNVVSGSVQLFSDRLIRGVKAGS-- 300
gi |17536165|ref|NP_495655.1|        ETAAEHGFEEEA--GTSVIDHHNYDQHLSDGHTLIVVKGDLIS-----AELVGNB-----AKLHPVLKGLVAGTKNALLSIVRASGTAAYSYPKAVRATNPSIAGSRHLVGGQSRNNRVVSGSSELFSTNTFFSAKTNVNSP-- 300
gi |124506940|ref|XP_001352067.1|     HYLNENINISVHGN--SSVNDYFNNIVIKNDKKEKEINIKKRKKEEFTINQIISNPIPIKIRNNILFKGTAKHSVLLKKEKFLVLELCTRICLLYDKNDQVTK--RQKQGTDLILSALOLENNSRIVVSGSSIEIFSDYFFN----- 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi |18425101|ref|NP_569038.1|          NYEYKSGNEQFVTELSKWFPHRGHLKAGNLVHHRVGETDEPA--IYRIKDDLEFSVEIYEW--SGKSWEPIYVANDVOQVFMMSPVVLKILS---TDKKGLEHTSFKVYVDVYGVGFQFKVEYKGLGYTTLSEKQIIPVRPVRHN--EYERFIT 450
gi |115471133|ref|NP_001059165.1|     IRHEKAGNEQFVTELSKWFPHRGHLKAVNVKHNKVGTEINPEG--MYRINDDLEYSVEIYEW--SGTSWEPYVADVOQVFMMSPVVLKILS---TDKKGLEHTSFKVYVDVYGVGFQFKVEYKGLGYTTLSEKQIIPVRPVRHN--EYERFIT 450
gi |24640745|ref|NP_511096.2|         VFKLAGNRDVAESISKWFVFGTGRRLRVAASVQHHKEGELLPPDAQAYIITDPVVYITIGIEEL--VOGEWARAFKASDIOLEFRIDPFVFTFLK---QTNTGAAQAKFKIPDVYGVGFQFKVDYNRVGYTHLYSSTQVSVRPLEHT--QYERFIT 450
gi |158295782|ref|XP_316417.4|        KHFARSGNQDVAMALSKWFVFGNGVIRARSVSHSKEGEGQPPS--SYVTVDPVYITIEITRSGDGKWKAFKASDIOLEFRIDPFVFTFLK---FVGGGRYEARFLIPDVYGVGFQFKVDYNRVGYTHLYSSTQVSVRPLEHT--QYERFIT 450
gi |20070197|ref|NP_005207.2|         QRYSGTGNYLELAVALSRWVFKEEGVLRVGPVSHHRVGETAPPN--AYVTVDLVEYSIIVIQQL--SNGKWWPFDGDDIOLFEFRIDPFVFTFLK---RKG--GKYSVGFQKLPDVYGVGFQFKVDYNRVGYTHLYSSTQVSVRPLEHT--QYERFIT 450
gi |114554462|ref|XP_001161661.1|     QRYSGTGNYLELAVALSRWVFKEEGVLRVGPVSHHRVGETAPPN--AYVTVDLVEYSIIVIQQL--SNGKWWPFDGDDIOLFEFRIDPFVFTFLK---RKG--GKYSVGFQKLPDVYGVGFQFKVDYNRVGYTHLYSSTQVSVRPLEHT--QYERFIT 450
gi |46195798|ref|NP_031864.2|        QRYSGTGNYLELAVALSRWVFKEEGVLRVGPVSHHRVGETAPPN--AYVTVDLVEYSIIVIQQL--SNGKWWPFDGDDIOLFEFRIDPFVFTFLK---RKG--GKYSVGFQKLPDVYGVGFQFKVDYNRVGYTHLYSSTQVSVRPLEHT--QYERFIT 450
gi |58865778|ref|NP_001012104.1|     QRYSGTGNYLELAVALSRWVFKEEGVLRVGPVSHHRVGETAPPN--AYVTVDLVEYSIIVIQQL--SNGKWWPFDGDDIOLFEFRIDPFVFTFLK---RKG--GKYSVGFQKLPDVYGVGFQFKVDYNRVGYTHLYSSTQVSVRPLEHT--QYERFIT 450
gi |50979164|ref|NP_001003321.1|     QRYSGTGNYLELAVALSRWVFKEEGVLRVGPVSHHRVGETAPPN--AYVTVDLVEYSIIVIQQL--SNGKWWPFDGDDIOLFEFRIDPFVFTFLK---RKG--GKYSVGFQKLPDVYGVGFQFKVDYNRVGYTHLYSSTQVSVRPLEHT--QYERFIT 450
gi |155371877|ref|NP_001094543.1|     QRYSGTGNYLELAVALSRWVFKEEGVLRVGPVSHHRVGETAPPN--AYVTVDLVEYSIIVIQQL--SDGKWVPPFDGDDIOLFEFRIDPFVFTFLK---RKG--GKYSVGFQKLPDVYGVGFQFKVDYNRVGYTHLYSSTQVSVRPLEHT--QYERFIT 450
gi |118101269|ref|XP_423294.2|        KRYSGTGNYLELAVALSRWVFKEEGVLRVGPVSHHRVGETAPPN--AYVTVDLVEYSIIVIEKL--SDGKWVPPFDGDDIOLFEFRIDPFVFTFLK---RKG--GKYSVGFQKLPDVYGVGFQFKVDYNRVGYTHLYSSTQVSVRPLEHT--QYERFIT 450
gi |47085831|ref|NP_998258.1|        KRYEQTGNQDLAEALSRAWVFKEAGVLRVGDVTHHPVGEVTEPPA--AYVTVDLVEYSIIVIEML--SGGKWVPPFDGDDIOLFEFRIDPFVFTFLK---RKG--GKYSVGFQKLPDVYGVGFQFKVDYNRVGYTHLYSSTQVSVRPLEHT--QYERFIT 450
gi |17536165|ref|NP_495655.1|        VQAGDQSGNADFAITARWVKKSGVLRVKTNNHKKKGTIVPPVEGYFITLDVVYITIEIEEL--KNGKWVPPFDGDDIOLFEFRIDPFVFTFLK---NSN--GRISVAFKLPDVLGVFKLQVYVRRVGYTHLYDYVQVSVRPLEHT--QYERFIT 450
gi |124506940|ref|XP_001352067.1|     ---IHNAKQFTYELIKWNLKKSQIIRNVNFKFYDINQDKSINFFNIDFVNMSIDLYHL--KSNFPIVKNNTIQIICKIHLISRFLNPKYSINNPVYINFLPKKEGIVYKLDIYLKNGKYNILNLEYSIPRITLLHWYDNKKVKVF 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi |18425101|ref|NP_569038.1|  TAYPYYGACFTTMAGFFVFSFVLYHK----- 497
gi |115471133|ref|NP_001059165.1| SAYPYYAASFSTMGAFVFSFVLYHK----- 497
gi |24640745|ref|NP_511096.2|  SAFPYYTSAFSMMIGVFVFSFVLFHFKDE----FVGRAAKEDKKSQ 497
gi |158295782|ref|XP_316417.4|  SAYPYYASAFSMVVGMFVFSFVLFHFKDDGSKPARITTAASAKKAQ 497
gi |20070197|ref|NP_005207.2|  SAYPYYASAFSMMGLGFVFSIVFLHMKEK-----EKSD 497
gi |114554462|ref|XP_001161661.1| SAYPYYASAFSMMGLGFVFSIVFLHMKEK-----EKSD 497
gi |46195798|ref|NP_031864.2|  SAYPYYASAFSMMAGLVFVFSIVFLHMKEK-----EKSD 497
gi |58865778|ref|NP_001012104.1| SAYPYYASAFSMMAGLVVFSIVFLHMKEK-----EKSD 497
gi |50979164|ref|NP_001003321.1| SAYPYYASAFSMMGLGFVFSIVFLHMKEK-----EKSD 497
gi |155371877|ref|NP_001094543.1| SAYPYYASAFSMMGLGFVFSIVFLHMKEK-----EKSD 497
gi |118101269|ref|XP_423294.2|  SAYPYYAGAFSMMVGLFVFSIVFLHMKEK-----EKSD 497
gi |47085831|ref|NP_998258.1|  SAFPYYASAFSMMAGLVVFSIVFLHMREK-----EKSD 497
gi |17536165|ref|NP_495655.1|  SAYPYYASSFSMMAGLVVFSIVVLYHKDTPVKG---AKVLDSEKKKN 497
gi |124506940|ref|XP_001352067.1| KNYPFYFYIMLSLIYFILLILLFDNSYLGSN---KEQHPKPKLQ 497
      .....460.....470.....480.....490.....

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