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gi | 24649832 | ref | NP_651305.1 | -----MSSSKIALLVSDKTLGLLDLGRKSLVALGFDLVAASGGTATSLRAGLKVDRVSEITGAPEMLGRRVKTLHPAVHAGIL 150
gi | 158302073 | ref | XP_321707.3 | -----FLHPSLPAALVSVSDKSLGVEFARGLNELGKLVASGGTAKAIRDLGLFPVRDVSITIGAPEMLGRRVKTLHPAVHAGIL 150
gi | 27229048 | ref | NP_080471.1 | -----MAPSQALALFVSDKTLGLVEFARSLASLGLSLVAASGGTAKAIRDAGLAVRDVSELGFPPEMLGRRVKTLHPAVHAGIL 150
gi | 48675845 | ref | NP_112276.2 | -----MASSQLALFVSDKTLGLVEFARNLASHLGLSLVAASGGTAKAIRDAGLAVRDVSELGFPPEMLGRRVKTLHPAVHAGIL 150
gi | 20127454 | ref | NP_004035.2 | -----MAPQQLALFVSDKTLGLVEFARNLTALGLNLVAASGGTAKALRDAGLAVRDVSELGFPPEMLGRRVKTLHPAVHAGIL 150
gi | 114583143 | ref | XP_001150375.1 | -----MAPQQLALFVSDKTLGLVEFARNLTALGLNLVAASGGTAKALRDAGLAVRDVSELGFPPEMLGRRVKTLHPAVHAGIL 150
gi | 115497442 | ref | NP_001068722.1 | -----MAPQQLALFVSDKTLGLVEFARNLASHLGLNLVAASGGTAKALRDAGLAVRDVSELGFPPEMLGRRVKTLHPAVHAGIL 150
gi | 74005447 | ref | XP_863050.1 | -----MAPQQLALFVSDKTLGLVEFARSLTAVGLSLLASGGTATALRDAGLAVRDVSELGFPPEMLGRRVKTLHPAVHAGIL 150
gi | 45384004 | ref | NP_990509.1 | -----MAARQQLALLVSEKAGLVEFARSLNALGLGLIASGGTATALRDAGLAVRDVSELGFPPEMLGRRVKTLHPAVHAGIL 150
gi | 130507931 | ref | NP_001076265.1 | -----MASEIALLVSDKTLGLVEFARLLVSVGLSLVAASGGTAKALRDAGLAVRDVSELGFPPEMLGRRVKTLHPAVHAGIL 150
gi | 6323768 | ref | NP_013839.1 | -----MANYTKTALLSVYDKTGLLDLARGLLEKNVRIIASGGTARMIRDAGFPIDVSAITHPAPEMLGRRVKTLHPAVHAGIL 150
gi | 50311693 | ref | XP_455873.1 | -----MP-HTKTAALLSVYDKTGLLDLARGLLEKNVRIIASGGTAKMVRREAGFPVDDVSAITHPAPEMLGRRVKTLHPAVHAGIL 150
gi | 45198731 | ref | NP_985760.1 | -----MVYSKTAALLSVYDKTGLLDLARGLLEKNVRIIASGGTAKMVRREAGFPVDDVSAITHPAPEMLGRRVKTLHPAVHAGIL 150
gi | 19075527 | ref | NP_588027.1 | -----MYALLSVYDKTGLLELAKALTSKGVKLLSGGGTAKMIRESGMEVDVSAITHPAPEMLGRRVKTLHPAVHAGIL 150
gi | 39944906 | ref | XP_361990.1 | -----MASSQRIATVSVYDKTGLLDLARGLLEKNVRIIASGGTAKMIRESGFPVEDVSAITHPAPEMLGRRVKTLHPAVHAGIL 150
gi | 32422769 | ref | XP_331828.1 | -----MAANQRIATVSVYDKTGLLDLARGLLEKNVRIIASGGTAKMIRESGFPVEDVSAITHPAPEMLGRRVKTLHPAVHAGIL 150
gi | 71985564 | ref | NP_741452.2 | -----MMDGKSLAIIISVSDKTLGLTFLAHGLVSAGLTLIASGGTAKAIRDQGLIVHDVAIVKFPPEMLGRRVKTLHPAVHAGIL 150
gi | 30686280 | ref | NP_850240.1 | -----MLSS--AAATATVSARSGDILCGLFRKRSVAPFRFTQPPVYRTSLCPFSFVAVRAMAESOTARNPQSSSGEKQALISLSDKRLDASLGNGLQELGYTIVSTGGASLLENAGVSVTKVEKLRHFPPEMLDGRVKTLHPAVHAGIL 150
gi | 115475287 | ref | NP_001061240.1 | -----MPLNLASSPAAAAAARKVCAQVRAVSPRHLLPRALDHQSRVLSLSSSSSAGRAAGVRAMAAABAGASTATAQAK--SSGVKQALISLSDKTLGLTFLAHGLVSAGLTLIASGGTAKAIRDQGLIVHDVAIVKFPPEMLDGRVKTLHPAVHAGIL 150
1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150

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gi | 24649832 | ref | NP_651305.1 | SR-TIDSFLADMRKQGFDDLTLVVCNLYFPFASVAVK-PDVITLADAVENIDIGGVTLLRAAAKNHRVTVVCEAVDYDRVLSLKAAG--NITVTRQALAKAFTHHTATYDDAISDYFRKOYV-SGVSQLPLRYGMNPHOKPAQLYTLQ-L 300
gi | 158302073 | ref | XP_321707.3 | AR-MTESDQRDISQQKVELAQLVVCNLYFPGLTIISK-PDVIITADAVENIDIGGVTLLRAAAKNHRVTVLCCPKDYPKVLLEEIRQHG--DTTPATRQLLAKAFTHHTAEYDAISDYFRKOYS-AGVSQLNLRYGMNPHOKPAQLYTL-L 300
gi | 27229048 | ref | NP_080471.1 | AR-NIPEDAADMARLDENLRVVCNLYFPFKVTAS-PDVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYGAVAEMHGSDDKDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGISQMPRLRYGMNPHOTPAQLYTL-K 300
gi | 48675845 | ref | NP_112276.2 | AR-NIPEDAADMARLDENLRVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYGAVAEMHGSDDKDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGISQMPRLRYGMNPHOTPAQLYTL-K 300
gi | 20127454 | ref | NP_004035.2 | AR-NIPEDNADMARLDENLRVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVVVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-Q 300
gi | 114583143 | ref | XP_001150375.1 | AR-NIPEDNADMARLDENLRVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVVVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-Q 300
gi | 115497442 | ref | NP_001068722.1 | AR-NIPEDNADMARLDENLRVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-K 300
gi | 74005447 | ref | XP_863050.1 | AR-NIPEDNADMARLDENLRVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-K 300
gi | 45384004 | ref | NP_990509.1 | AR-NIPEDNADMARLDENLRVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-K 300
gi | 130507931 | ref | NP_001076265.1 | AR-QTPSDNADMEKLFGLRVVAVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-T-R 300
gi | 6323768 | ref | NP_013839.1 | AR-DIDSDEKDLKEQHLKQVDFVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-T-R 300
gi | 50311693 | ref | XP_455873.1 | AR-NLESDEKDLKEQHLKQVDFVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-T-R 300
gi | 45198731 | ref | NP_985760.1 | AR-NLESDEKDLKEQHLKQVDFVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-T-R 300
gi | 19075527 | ref | NP_588027.1 | AR-DIPSDEKDLVLEQSLKIDIVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-Q 300
gi | 39944906 | ref | XP_361990.1 | AR-NLESDEKDLAQSIDKVDVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-Q 300
gi | 32422769 | ref | XP_331828.1 | AR-ELASDEKDLAQSIDKVDVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-Q 300
gi | 71985564 | ref | NP_741452.2 | AR-DTESDRKDLKHNHSFVSVVCNLYFPFKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-Q 300
gi | 30686280 | ref | NP_850240.1 | ARRDVEHMEALNEHGIGTFDDVVVNLVFPYKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-Q 300
gi | 115475287 | ref | NP_001061240.1 | ARRDVEHMEALNEHGIGTFDDVVVNLVFPYKVTAS-PGVITVEAVEEIDIGGVTLLRAAAKNHRVTVVCEPEDEYVAVSTEMQSSKSDTSLERRRHLAKAFTHHTAQYDEAISDYFRKOYS-KGVSQMPLRYGMNPHOTPAQLYTL-Q 300
.....160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300

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gi | 24649832 | ref | NP_651305.1 | AKLPLTIVLNASPGFINLCDALNAGWLV-RELKRALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 158302073 | ref | XP_321707.3 | ERLPLKVVNASPGFINLCDALNAGWLV-RELKRALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 27229048 | ref | NP_080471.1 | PKLPLTIVLNGAPGFINLCDALNAGWLV-TELKRALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 48675845 | ref | NP_112276.2 | PKLPLTIVLNGAPGFINLCDALNAGWLV-TELKRALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 20127454 | ref | NP_004035.2 | PKLPLTIVLNGAPGFINLCDALNAGWLV-TELKRALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 114583143 | ref | XP_001150375.1 | PKLPLTIVLNGAPGFINLCDALNAGWLV-TELKRALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 115497442 | ref | NP_001068722.1 | PKLPLTIVLNGAPGFINLCDALNAGWLV-TELKRALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 74005447 | ref | XP_863050.1 | PKLPLTIVLNGAPGFINLCDALNAGWLV-TELKRALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 45384004 | ref | NP_990509.1 | PKLPLTIVLNGAPGFINLCDALNAGWLV-TELKRALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 130507931 | ref | NP_001076265.1 | PALPLTIVLNGAPGFINLCDALNAGWLV-RELKRALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 6323768 | ref | NP_013839.1 | DELPFFKVLCSGSPGINLLDALNSWPLV-KELSASLNLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 50311693 | ref | XP_455873.1 | EELPFFKVLCSGSPGINLLDALNSWPLV-KELSASLNLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 45198731 | ref | NP_985760.1 | DELPFFKVLCSGSPGINLLDALNSWPLV-KELSASLNLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 19075527 | ref | NP_588027.1 | GELPFFKVLCSGSPGINLLDALNSWPLV-KELRENTGI PAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 39944906 | ref | XP_361990.1 | GKL PFFKVLCSGSPGINLLDALNSWPLV-KELKALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 32422769 | ref | XP_331828.1 | GKL PFFKVLCSGSPGINLLDALNSWPLV-KELKALGLPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 71985564 | ref | NP_741452.2 | DEMP LKVLCSGSPGINLLDALNSWPLV-KELSDALKMPAASFKHVS-PAGAAVGVPLNPAQAKLQCMVDDLYEQLTLP-LATAYARARGADRMSFFGDFVALSDVCDVVTAKIISREVS-----DGIIPAGYEEPALEILLKKKKG 450
gi | 30686280 | ref | NP_850240.1 | HQKAAFVYDKSLAEVNAAGLATAIQHHGKEMSYNNYLDADAANNCVFEFESPICVVKHTNPE-----CGVASRDQILEAVRLAVKADPVSAFGGIVAFNTILDEDLAKEIREFRSPIDGQTRMFYIIVVAPGYTEKGLLEILLKKG--S 450
gi | 115475287 | ref | NP_001061240.1 | HQKAAFVYDKSLAEVNAAGLATAIQHHGKEMSYNNYLDADAANNCVFEFESPICVVKHTNPE-----CGVASRDQILEAVRLAVKADPVSAFGGIVAFNTILDEDLAKEIREFRSPIDGQTRMFYIIVVAPGYTEKGLLEILLKKG--S 450
.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450

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gi |24649832|ref|NP_651305.1|      GYCVLQMDPNVEPSAVERKIFGLTLEQRNRDAVIDALFSLNVVSRKRGPF---LPEAVRDLIVATIALKYTOSNSVVCYAKDGOVIGIGAGQOSRIHCTRLAGDKADNWLRQHPVSVAGMKFKAGVKRAEISNAIDNYVNGTIVGKDM-F 600
gi |158302073|ref|XP_321707.3|    SYCVLQIDPNVEPFPVERKTLFGLQLEQRNRDADINKALFNIIVTKNKT---LPEGALRDLIVATIALKYTOSNSVVCYAKDGOVIGIGAGQOSRIHCTRLAGDKADNWLRQHPRVAGMQFRKGVKRAEISNAIDNYVNGTIVGKDM-F 600
gi |27229048|ref|NP_080471.1|    NYCVLQMDQSQCKPDENEVRLFLGLRLSQRKRNNGVVDKSLFSNIVTKNKD---LPEALRDLIVATIAVKYTOSENVCYAKDGOVIGIGAGQOSRIHCTRLAGDKANSWWLRHHPVLSMKFKAGVKRAEISNAIDQYVVTGTIGEGE-D 600
gi |48675845|ref|NP_112276.2|    SYCVLQMDQSQKPDENEVRLFLGLRLSQRKRNNGVVDKSLFSNIVTKNKD---LPEALRDLIVATIAVKYTOSENVCYAKDGOVIGIGAGQOSRIHCTRLAGDKANSWWLRHHPVLSMKFKAGVKRAEISNAIDQYVVTGTIGEGE-D 600
gi |20127454|ref|NP_004035.2|    NYCVLQMDQSQKPDENEVRLFLGLHLSSQRKRNNGVVDKSLFSNVVTKNKD---LPEALRDLIVATIAVKYTOSENVCYAKNGOVIGIGAGQOSRIHCTRLAGDKANYWLRHHPVLSMKFKGTGVKRAEISNAIDQYVVTGTIGEGE-D 600
gi |114583143|ref|XP_001150375.1| NYCVLQMDQSQKPDENEVRLFLGLHLSSQRKRNNGVVDKSLFSNVVTKNKD---LPEALRDLIVATIAVKYTOSENVCYAKNGOVIGIGAGQOSRIHCTRLAGDKANCWWLRHHPVLSMKFKGTGVKRAEISNAIDQYVVTGTIGEGE-D 600
gi |115497442|ref|NP_001068722.1| NYCVLQMDQSQKPDENEVRLFLGLRLSQRKRNNGVVDKSLFSNIVTKNKD---LPEALRDLIVATIAVKYTOSENVCYAKNGOVIGIGAGQOSRIHCTRLAGDKANCWWLRHHPVLSMKFKGTGVKRAEISNAIDQYVVTGTIGEGE-D 600
gi |74005447|ref|XP_863050.1|    NYCVLQMDQSNPDENEVRLFLGLRLSQRKRNNGVVDKSLFSNIVTKNKD---LPEALRDLIVATIAVKYTOSENVCYAKNGOVIGIGAGQOSRIHCTRLAGDKANCWWLRHHPVLSMKFKGTGVKRAEISNAIDQYVVTGTIGESVY 600
gi |45384004|ref|NP_990509.1|    GYCVLQMDPNVEPDDNEIRILYGLQLMQKRNNAVIDRLEFKNIVTKNKT---LPEAVRDLIVASIAVKYTOSENVCYAKDGOVIGIGAGQOSRIHCTRLAGDKANSWWLRHHPVLSMKFKAGVKRAEISNAIDQYVVTGTIGEGE-D 600
gi |130507931|ref|NP_001076265.1| NYCVLQMDPEVEPDEEVRVLFGLHLKQRKNGAVIDKELFSLNIVSRGKGL---SEALRDLIVASIAVKYTOSENVCYAKDGOVIGIGAGQOSRIHCTRLAGDKADNWLRHHPVLSMKFRGGVKRAEMANAILDYVSGTIVGEGP-D 600
gi |6323768|ref|NP_013839.1|    KYCILLQIDPNVPEAVERRQVYGVTLQQRNDAINQSTFKFIVSQNKN---LPEQAIIDLIVATIAIKYTOSENVCYAKNGMVVGLGAGQOSRIHCTRLAGDKADNWLRHHPVLSMKFRGGVKRAEMANAILDYVSGTIVGEGP-D 600
gi |50311693|ref|XP_455873.1|    KYCILLQIDPNVPEAVERRQVYGVTLQQRNDAINQSTFKFIVSQNKN---LPEQAIIDLIVATIAIKYTOSENVCYAKNGMVVGLGAGQOSRIHCTRLAGDKADNWLRHHPVLSMKFRGGVKRAEMANAILDYVSGTIVGEGP-D 600
gi |45198731|ref|NP_985760.1|    KYCILLQIDPNVPEAVERRQVYGVTLQQRNDAINQSTFKFIVSQNKN---LPEQAIIDLIVATIAIKYTOSENVCYAKNGMVVGLGAGQOSRIHCTRLAGDKADNWLRHHPVLSMKFRGGVKRAEMANAILDYVSGTIVGEGP-D 600
gi |19075527|ref|NP_588027.1|    KYCIVLQMDPKVPAEITRQVYGISIQQRHNHAKIDFLFEKVVSKNKD---LPEKALIDLIVATIAIKYTOSENVCYAKNGMVVGLGAGQOSRIHCTRLAGDKADNWLRHHPVLSMKFRGGVKRAEMANAILDYVSGTIVGEGP-D 600
gi |39944906|ref|XP_361990.1|    RYLVLQMDADVPSQQLRLRIVYGVSLAQHRNDVEVSPASFTVLVPKDGP---ALPEALRDLIVATIAIKYTOSENVCYAKNGOVIGIGAGQOSRIHCTRLAGDKADNWLRHHPVLSMKFRGGVKRAEMANAILDYVSGTIVGEGP-D 600
gi |32422769|ref|XP_331828.1|    RYLVLQMDVPEPEPSKSETRIVFGITLQGRNDVEVSPASFTVLVPKDGP---ALPEALRDLIVATIAIKYTOSENVCYAKNGOVIGIGAGQOSRIHCTRLAGDKADNWLRHHPVLSMKFRGGVKRAEMANAILDYVSGTIVGEGP-D 600
gi |71985564|ref|NP_741452.2|    NYCVLKINPNVLPSETEERIVFGLRLRQRKRNNAVINAEIFNIVVGSANE---LNKQAIIDLIVATIAIKYTOSENVCYAKNGOVIGIGAGQOSRIHCTRLAGDKADNWLRHHPVLSMKFRGGVKRAEMANAILDYVSGTIVGEGP-D 600
gi |30686280|ref|NP_850240.1|    KTLRLILEAKNDQKGLSLRQVGGWLDQSDLDLTPEDISFNVSVDKTP---SEELADAKFAWLCVKHVKSNIAIVAKNCLMGMGSGPNRLESRLIAFRKAG----- 600
gi |115475287|ref|NP_001061240.1| KTLRLILEAKRSGKGMLSLRQVGGWLDQSDLDLTPEDILFTVTERAPO---DEELSDAKFAWLCVKHVKSNIAIVAKNCLMGMGSGPNRLESRLIAFRKAG----- 600
.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi |24649832|ref|NP_651305.1|      LSQFEGMFDKAPAQLTSEKVEWLKQLSGLVALGSDAFFPFR--DNIDRASLSGVSVIASPAGSTNDAGVIAACDEHGIIAHT-----NLRLFHH 708
gi |158302073|ref|XP_321707.3|    VAQFQFAMLEKVPAPLTGEDKEQWTRDLTGVSLSGSDAFFPFR--DNVDRAKLSGVSVIASPAGSTNDAGVIDACNEHDIVMVT-----NLRLFHH 708
gi |27229048|ref|NP_080471.1|    LVKWEALFEEVPELLTEAEKKEWVDKLSGVSVSSDAFFPFR--DNVDRAKRSGVAVIVAPSGSTADKVVIEACDELGIVLAHT----DLRFLHH 708
gi |48675845|ref|NP_112276.2|    LVKWKALFEEVPELLTEAEKKEWVDKLSGVSVSSDAFFPFR--DNVDRAKRSGVAVIVAPSGSTADKVVIEACDELGIVLAHT----DLRFLHH 708
gi |20127454|ref|NP_004035.2|    LLIKWKALFEEVPELLTEAEKKEWVDKLEVSISSSDAFFPFR--DNVDRAKRSGVAVIAAPSGSAADKVVIEACDELGIIAHT----NLRLFHH 708
gi |114583143|ref|XP_001150375.1| LLIKWKALFEEVPELLTEAEKKEWVDKLEVSISSSDAFFPFR--DNVDRAKRSGVAVIAAPSGSAADKVVIEACDELGIIAHT----NLRLFHH 708
gi |115497442|ref|NP_001068722.1| LLIKWKALFEEVPELLTEAEKKEWVDKLEVSISSSDAFFPFR--DNVDRAKRSGVAVIAAPSGSAADKVVIEACDELGIIAHT----NLRLFHH 708
gi |74005447|ref|XP_863050.1|    NHKWKALFEEVPELLTEAEKKEWVDKLEVSISSSDAFFPFR--DNVDRAKRSGVAVIAAPSGSAADKVVIEACDELGIIAHT----NLRLFHH 708
gi |45384004|ref|NP_990509.1|    LVKWQAMFEEVPAQLTEAEKKEWVDKLEVSISSSDAFFPFR--DNVDRAKRIGVQFIVAPSGSAADKVVIEACDELGIIAHT----NLRLFHH 708
gi |130507931|ref|NP_001076265.1| KEVWKGLFEEVPEPLSEVEKKNWISSLQVALSSDAFFPFR--DNVDRAKRSQVAVIAAPSGSTADEVVVAKNELGIIIVHT----NIRLFHH 708
gi |6323768|ref|NP_013839.1|    LSEYQSKFEEIPKPFTEPEEKWELSKLNVLSLSSDAFFPFR--DNVYRAVKSQVAVIAAPSGSVMDKVVVFAADSFQVLYVEN----PIRLFHH 708
gi |50311693|ref|XP_455873.1|    KSEYESKFPETIPEPLTEAEKKEWVDKLEVSISSSDAFFPFR--DNVYRAVKSQVAVIAAPSGSVMDKVVVFAADSFQVLYVEN----PIRLFHH 708
gi |45198731|ref|NP_985760.1|    KSEYESKFPETIPEPLTEAEKKEWVDKLEVSISSSDAFFPFR--DNVYRAVKSQVAVIAAPSGSVMDKVVVFAADSFQVLYVEN----PIRLFHH 708
gi |19075527|ref|NP_588027.1|    REQWESAFETIPEPLTEAEKKEWVDKLEVSISSSDAFFPFR--DNVYRAVKSQVAVIAAPSGSVMDKVVVFAADSFQVLYVEN----PIRLFHH 708
gi |39944906|ref|XP_361990.1|    RESFEALFEEVPAAFGAEAREEWLGLNVAISSDAFFPFR--DNVYRAARSQVAVIAAPSGSQNDQVFDIADKLGITFVEQ----SVRLFHH 708
gi |32422769|ref|XP_331828.1|    RESFEALFEEVPAAFTEQEKNEWLSKLDVCSISSDAFFPFR--DNVYRAARSQVAVIAAPSGSQNDQVFDIADKLGITFVEQ----SVRLFHH 708
gi |71985564|ref|NP_741452.2|    IDQWQVFNPEVPEPLAEDDRKQWLSQTGVVMSDAFLPFR--DNVDCARQFQVSVVAHPGGSVRDDIKIACDEHGIIAHT----GLRLFHH 708
gi |30686280|ref|NP_850240.1|    -----EEAKGAALASDAFFPFAWKDAVEEAQOMGIGVIAEPGGSIRDQDAIDCCCKYGVSLLLF-----NVRHFRH 708
gi |115475287|ref|NP_001061240.1|    -----EEAKGAALASDAFFPFAWNAVEEAQONGIGVIAEFGSMRDQDAVDCCKYGVSLLLF-----GVRHFRH 708
.....610.....620.....630.....640.....650.....660.....670.....680.....690.....700

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