

gi	45383582	ref	NP_989609.1	-----MF	2
gi	118089754	ref	XP_001232193.1	-----	
gi	31981333	ref	NP_036035.2	-----	
gi	38454274	ref	NP_942064.1	-----	
gi	19718734	ref	NP_003255.2	-----	
gi	114596429	ref	XP_001155239.1	-----	
gi	52546732	ref	NP_001005264.1	-----	
gi	27806379	ref	NP_776622.1	-----	
gi	47086413	ref	NP_997977.1	-----	
gi	24664561	ref	NP_524757.1	-----	
gi	118792131	ref	XP_551799.2	MLATTHMLYVLIATCVIPFGAALSRTVLYQAPDECRVSSGGGEHDIILVCHLRTINSELENTNFVSIQPPONTVRLRLLECNDALFFOSSLSPPSFRSLVLELRDLTIYCKLGLNLTIDGSRGLQELRNLTIRTHNGDWMSTMLEMASNFV- MRPSPALLTLVFGH-IFGVFGAALSLSKLSVQAPDECRWDGYTEDDLALLRLRTINSELENTNFVLEPENTVRLRLQCCDGLFFOSSLSPPSFGKQLKHALTIYCKIANLSEGSFGLQELVNLIRTHNDWSISLDTAPVFTFS 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150	149 149

gi	45383582	ref	NP_989609.1	NQSKQKPTMKLMWQAWLIYTALAAHLPEEQALRQACLSCDATQSCNCSFMGLDFIPPGLTGKITVNLNAHNRKLRIRTHDLQKAVNLRILLQSNQISSIDEDSFGSQGKLELLDLSNNSLAHLSPVWFGPPLFSLQHLRIQGNSSYSDLGE	152
gi	118089754	ref	XP_001232193.1	-----MHTWKMWAICTALAAVLPPEQALRQACLSCDATQSCNCSFMGLDFIPPGLTGKITVNLNAHNRKLRIRTHDLQKAVNLRILLQSNQISSIDEDSFGSQGKLELLDLSNNSLAHLSPVWFGPPLFSLQHLRIQGNSSYSDLGE	141
gi	31981333	ref	NP_036035.2	-----MLRALWLFWILLV-AIVLFSKRCSAQ-ESSLCDASGVCDCGRSRFSSTIPSGLTAAKMLDLSFNKIITYIGHGDLRACANLQVILKSSRINTIEGDAFYSLGSLLEHLDLSDNHLSSLSSWFGPPLSLLKYLNLGMGNPYQLGV	141
gi	38454274	ref	NP_942064.1	-----MLQALWLFWILLV-AVIGLSREGHSAQ-ASLSCDAAGVCDGSSRSFSTIPSGLTAAKMLDLSFNKIITYIGHGDLRACANLQVILKSSRINTIEGDAFYSLGSLLEHLDLSDNHLSSLSSWFGPPLSLLKYLNLGMGNPYQLGV	141
gi	19718734	ref	NP_003255.2	-----MPHLLMVMVVLG-VIISLSKEESSNQ-ASLSCDRNGICKGSSGSLNSIPSGLTAAVKELDLSNRIITYISNSDLQRCVNLQALVLTSSNGINTIEEDSFFSLGSLLEHLDLSYNYLSNLSSSWFKPLSLLTFLNLLGNPYKILGE	141
gi	114596429	ref	XP_001155239.1	-----MPHLLMVMVVLG-VIISLSKEESSNQ-ASLSCDRNGICKGSSGSLNSIPSGLTAAVKELDLSNRIITYISNSDLQRCVNLQALVLTSSNGINTIEEDSFFSLGSLLEHLDLSYNYLSNLSSSWFKPLSLLTFLNLLGNPYKILGE	141
gi	52546732	ref	NP_001005264.1	-----MSRVLWTLWVLG-AVNLKSKEEADPSSSLSCDPTGVCDCGRSRSLNSMPSGLTAAVRELDLSNNEITYIGNSDLRDCVNLKALRLESNGINTIEEESFLDLWLEHLDLSYNYLSNLSSSWFRPLSLLKFLNLLGNPYKSLGE	142
gi	27806379	ref	NP_776622.1	-----MPRALWTAWWA-VII-LSTEGASDOASSLSCDPTGVCDCGHSRSLNSIPSGLTAGVKSLELDLSNNDITYVGNRDLQRCVNLKLRIGANEIHFVEEDSFFHLRNLVLDLSYNYLSNLSSSWFRSLYLVKFLNLLGNLYKILGE	141
gi	47086413	ref	NP_997977.1	-----MRLVGTMTAAILLIMFILAQGLECSQ--TCKCDQMYFCNCSNNLHQVPT-VPSDVVLGLDLSFNQIESINMTDLSYNELIILNLHKKLRHHRDAFKQHNLEVLDSLANNLNLSPSWFHLKLLQQLNLVGNPYSLVGF	139
gi	24664561	ref	NP_524757.1	EPFQLELRLDLSNINWLPDGMVCPILKSLQHLNASYNKIQDISNFYFSASLSRKARVCGSTLQSLDLSANKMVSLEPTAMLSALGRITLHNAKMSMSFLADRAFEGLLSLRVVDSLNRRLSLPPELFAETKQLQETYLRRNSINVLAP	299
gi	118792131	ref	XP_551799.2	ELAKLQRLDLSQNNMWSVDPGFICPLARLSYINLQNRRLDLSVHFHSASLSTRLSKCKGSSIVLDDSHNTIDNLPFAIFSGLGLTDLRLQSNGLYIADRAFEGVLVSRLELSLNRRLNLPPELFAEAKHKEITYLQNSLNLVLP	299
			160.....170.....180.....190.....200.....210.....220.....230.....240.....250.....260.....270.....280.....290.....300	



gi	45383582	ref	NP_989609.1	SSPFSSLRNLSLHLGN-----PQFSIIHQGNFEGIVFLNLTLRIDGDNLSQYEPGSLKSRKINHMITSIR	218
gi	118089754	ref	XP_001232193.1	-----SSPFSSLRNLSLHLGN-----PQFSIIHQGNFEGIVFLNLTLRIDGDNLSQYEPGSLKSRKINHMITSIR	207
gi	31981333	ref	NP_036035.2	TSLEFNLTNLQHLRIGNV-----EFSFEIRRIDFAGLTSNLELEIKALSRLNYQSGLKSRIRDTHLTLHLS	208
gi	38454274	ref	NP_942064.1	TSLEFNLTNLQHLRIGNV-----DFFSEIRRIDFAGLTSNLELEIQVLSIQVYSRSLQIRDIYHLTLHLS	208
gi	19718734	ref	NP_003255.2	TSLEFSLTKLQILRVGNM-----DFFFKIQKDFAGLTFLELEIDASDLQSYESKSLKSIQNVSHLILHMK	208
gi	114596429	ref	XP_001155239.1	TSLEFSLTKLQILRVGNM-----DFFFKIQKDFAGLTFLELEIDASDLQSYESKSLKSIQNVSHLILHMK	208
gi	52546732	ref	NP_001005264.1	YPLFSQLTNLRILKVGNI-----YFSEIQKDFAGLTFLELEIDASNLRQYEPKSLKSIQNSYLALRMK	209
gi	27806379	ref	NP_776622.1	TSLEFSLTKLQILRVGNM-----NSFSEIHEKDFGLTFLELEISAQNLQIVVPEKSLKSIQNSIHLILHLK	208
gi	47086413	ref	NP_997977.1	APIFSSLVNLRILHLGNS-----PSLRELHKNGLDVLTHLDEMTFFGNSNLSRYSNGSLKAAREPIGSVSLSQNLFES	210
gi	24664561	ref	NP_524757.1	G-IFGELAEALLVLDLASNELNSQWNAAFVGLKRLMMLDLSANKIRLEAHIFRPLASLQILKLEDNYIDLPGGIFADLTNLHLILSRNRIYVTEQRTLQGLKKNLVLSLDFNRISRMDQRSLVNCSQLQDLHLNDNKLQAVPEALA	448
gi	118792131	ref	XP_551799.2	G-IFSDLKQLLVLDLSNNELTSEWINPAIFGVVCAHPFRSEFKQNNEARAHDLPSSDRAGVALRKTSEKAAKAPLGLGALHVLISNRLCTVDHFTFSGLSNLSLSDYNRISRIRDRQALRNHSALQELHNLGNKLLQVDPALY	446
			310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450	



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gi	118089754	ref	XP_001232193.1	-----RIDVFSAVIRDLLHSAIWLVRKIKLAFVPEKIIILLRIMSSFAKIKSLKQCLFDALIVPEIVSILEGPKLMEVEMKDCITLLGFKWYKQIHANQSQS--LRLITLLEN-LSIEEYFLYFDL	325
gi	31981333	ref	NP_036035.2	ESAFLEIFADILSSVRLVLRDLNLARFQFSLPVDVEVSSPMKKLAFRGSVLDLDFNELLKLLRYILELSEVEFDDCTLNGLGDFNPSSESVVSELGKVEVTVIIR-LHIPQFYLYFDL	328
gi	38454274	ref	NP_942064.1	ESAFLEIFADILSSVRYLELRDLNLARFQFSELSVDEINSPMKKLAFRNDLDDKSNELLKLLRYILELMEVEFDDCTLNGLGDFNPSSESVVSELGKVEVTVIIR-LHIPQFYLYFDL	328
gi	19718734	ref	NP_003255.2	CHILLLEIFVDVTSVVECLELRDLDLDTFHFSELSTGETNSLIKKFTFRNVKIIDESLFOVMKLLNQISGLLELEFDDCTLNGLGDFNPSSESVVSELGKVEVTVIIR-LHIPRFYLYFDL	328
gi	114596429	ref	XP_001155239.1	CHILLLEIFVDVTSVVECLELRDLDLDTFHFSELSTGETNSLIKKFTFRNVKIIDESLFOVMKLLNQISGLLELEFDDCTLNGLGDFNPSSESVVSELGKVEVTVIIR-LHIPRFYLYFDL	328
gi	52546732	ref	NP_001005264.1	QPVLVVEIFVDLSSSLKHLERLDHLDTFHFSEASINETHLVKKWIFRNVKIVDRFTGVVRLNLYVSGVLEVEFDDCTLYGLGDFDIPDVKIKINQIETLVRR-LHIPHFYSFYDM	329
gi	27806379	ref	NP_776622.1	CPVLLVDILVDIVSSLDLDFELRDLNLTTFHFSEASISEMSTSVKKLIFRNVQFDESDFVEVVKLFNYSVGLLEVEFDDCTHDGIGDFRALSLDRIRHLGNVETLIR-LHIPQFFLFHDL	328
gi	47086413	ref	NP_997977.1	-----DPELVSKVLQDVSHPETLLIKDVTMKTNTSTPFFKMKVKEGGTKSLTFQNSSTLDOALTSFLEFMDGSP-LSFIGLEDIQFVIGGEWQK---AKYTHHDSLRAYLRN-IEEGPFGFSSM	326
gi	24664561	ref	NP_524757.1	HVQLLKTLDVGENMISGIENTSITQLESYGLRMTENLTHIRRGVFRMSSQLILNLSQNKLSIEAGSLQRNSQLQAIRLDGNQLKSIAGLFTLPLNVLNLSGNRLEKFDYSHIPIGLQWLDVRANRITQLGNVFEIESELSLSTF	598
gi	118792131	ref	XP_551799.2	DVPLLRLLDGENHISNIDNASFRHMAHYGLRLTENNIEIIRGTFRAMKSLHILNLSQNKLRKVQASFDNNKIQAIRLDGNVLTIDAGLFTKPLNLLWNLISDNHLEVEDYALIPITGLQWLDIHANKITLGNVFEIESELSLSTF	596
			460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600	



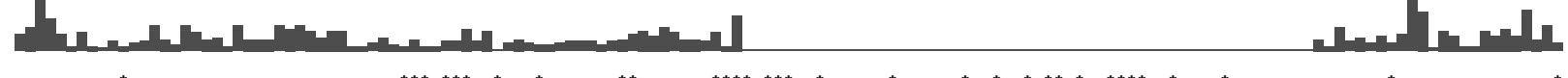
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gi	118089754	ref	XP_001232193.1	QSVLDLLSLFRKVIIVEN	TKVFLVPCKLSQHLLSLEYLDLSEANLIG	DQSLHESACGG	AWPDLQTLNLNLSNLSLSDLKMKGKSLFHLRN		411
gi	31981333	ref	NP_036035.2	STVYSLLLEKVKRIITVEN	SKVFLVPCFSFQHLKSLSEFLDLSENLMV	BEYLKNSACKG	AWPDLQTLNLNLSNHLRSRQKTAETILLTLKN		414
gi	38454274	ref	NP_942064.1	STVYSLLLEKVKRIITVEN	SKVFLVPCFSFQHLKSLSEFLDLSENLMV	BEYLKNSACKG	AWPDLQTLNLNLSNHLRSRQKTAETILLTLKN		414
gi	19718734	ref	NP_003255.2	STLYSLTERVKRIITVEN	SKVFLVPCLLSQHLKSLSEYLDLSENLMV	BEYLKNSACED	AWPDLQTLNLNLSNHLRSRQKTAETILLTLKN		414
gi	114596429	ref	XP_001155239.1	STLYSLTERVKRIITVEN	SKVFLVPCLLSQHLKSLSEYLDLSENLMV	BEYLKNSACED	AWPDLQTLNLNLSNHLRSRQKTAETILLTLKN		414
gi	52546732	ref	NP_001005264.1	SSIIYSLTERVKRIITVEN	SKVFLVPCLLSQHLKSLSEYLDLSENLMV	BEYLKNSACED	AWPDLQTLNLNLSNHLRSRQKTAETILLTLKN		415
gi	27806379	ref	NP_776622.1	SSIIYPLTERVKRIITVEN	SKVFLVPCLLSQHLKSLSEYLDLSENLMV	BEYLKNSACKD	AWPDLQTLNLNLSNHLRSRQKTAETILLTLKN		414
gi	47086413	ref	NP_997977.1	TELGFLLKHFHNVSVII	ATVFVVPKETTFLKNLEYMDLSONLIT	DLTIQPLTYTGSGAYQNLNMLNVSQVLSKSLGLMSRLVTNLKK		414	
gi	24664561	ref	NP_524757.1	DASVNLLETITASSIPNSVEVLYLDNQISKIQPYTFPKPNLTRVLDVNRITLLEPNALRLSPVADREIPBEFYIGHNAYECCDNLDWLQKVNRESRTPQLMDLDDIHCRLAYARGSSSHVSLTEAKSDDFLCKVASHCFALCHCCDF					748
gi	118792131	ref	XP_551799.2	DASVNLLETITASSIPNSVEVLYLDNQISKIQPYTFPKPNLTRVLDVNRITLLEPNALRLSPVADREIPBEFYIGHNAYECCDNLDWLQKVNRESRTPQLMDLDDIHCRLAYARGSSSHVSLTEAKSDDFLCKVASHCFALCHCCDF					746



gi	45383582	ref	NP_989609.1	LNLNDISENPFGEIPDMCEWP	ENLKYLNLSSTQIPKLT	CIPSLTEVLVDVSNLQDFG	LQLPFLKELYLTKNHLKTLF	BATDIPNLVAMTSIRNK	519
gi	118089754	ref	XP_001232193.1	LNLNDISENPFGEIPDMCEWP	ENLKYLNLSSTQIPKLT	CIPSLTEVLVDVSNLQDFG	LQLPFLKELYLTKNHLKTLF	BATDIPNLVAMTSIRNK	507
gi	31981333	ref	NP_036035.2	LNSLDISRNTHFMPDSCQWP	EKMRFNLSSTGIRVVKT	CIPQTEVLVDVSNLQDFG	LFLPRLQELYISRNLKTLF	DASLFPVLLVMKIRENA	510
gi	38454274	ref	NP_942064.1	LNSLDISRNTHFMPDSCQWP	EKMRFNLSSTGIRVVKT	CIPQTEVLVDVSNLQDFG	LFLPRLQELYISRNLKTLF	DASLFPVLLVMKIRENA	510
gi	19718734	ref	NP_003255.2	LTVNIDISKNSFHSMPETCQWP	EKMRYLNLSSTRIHSVVG	CIPKLEILVDVSNLQDFG	LNLPLKELYISRNLKTLF	DASLFPVLLVMKIRENA	510
gi	114596429	ref	XP_001155239.1	LTVNIDISKNSFHSMPETCQWP	EKMRYLNLSSTRIHSVVG	CIPKLEILVDVSNLQDFG	LNLPLKELYISRNLKTLF	DASLFPVLLVMKIRENA	510
gi	52546732	ref	NP_001005264.1	LTVNIDISKNSFHSMPETCQWP	EKMRYLNLSSTRIHSVVG	CIPKLEILVDVSNLQDFG	LNLPLKELYISRNLKTLF	DASLFPVLLVMKIRENA	511
gi	27806379	ref	NP_776622.1	LTVNIDISKNSFHSMPETCQWP	EKMRYLNLSSTRIHSVVG	CIPKLEILVDVSNLQDFG	LNLPLKELYISRNLKTLF	DASLFPVLLVMKIRENA	510
gi	47086413	ref	NP_997977.1	LTVNIDISKNSFHSMPETCQWP	EKMRYLNLSSTRIHSVVG	CIPKLEILVDVSNLQDFG	LNLPLKELYISRNLKTLF	DASLFPVLLVMKIRENA	510
gi	24664561	ref	NP_524757.1	LTVNIDISKNSFHSMPETCQWP	EKMRYLNLSSTRIHSVVG	CIPKLEILVDVSNLQDFG	LNLPLKELYISRNLKTLF	DASLFPVLLVMKIRENA	510
gi	118792131	ref	XP_551799.2	LTVNIDISKNSFHSMPETCQWP	EKMRYLNLSSTRIHSVVG	CIPKLEILVDVSNLQDFG	LNLPLKELYISRNLKTLF	DASLFPVLLVMKIRENA	510



gi	45383582	ref	NP_989609.1	LNSFSKEEFESFKQEMLLDASANNFICS	CEFLSFIHHEAGIAQVLVGPESVICDS	SPLTVRGAQVGSVQLS		LMECHRSLLVSLICHLVFLFILLL	614
gi	118089754	ref	XP_001232193.1	LNSFSKEEFESFKQEMLLDASANNFICS	CEFLSFIHHEAGIAQVLVGPESVICDS	SPLTVRGAQVGSVQLS		LMECHRSLLVSLICHLVFLFILLL	553
gi	31981333	ref	NP_036035.2	VSTFSKDLGSLFKLELEAGDNHFVICS	CELLSFTMETPALAQILVDWDPDLYLCS	SPRLHGHRLQDARPS		VLECHQAAVLSGVCALLLILLV	605
gi	38454274	ref	NP_942064.1	VSTFSKDLGSLFKLELEAGDNHFVICS	CELLSFTMETPALAQILVDWDPDLYLCS	SPRLHGHRLQDARPS		VLECHQAAVLSGVCALLLILLV	605
gi	19718734	ref	NP_003255.2	ITTFKSKEQLDSFHTLKLLEAGGNFVICS	CEFLSFTQEQALAKVLIDWPANLYLCS	SPSHVHVGQVODVRLS		VSECHRTALVSGMCCALLLILLT	605
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gi	27806379	ref	NP_776622.1	ITTFKSKEQLDSFHTLKLLEAGGNFVICS	CEFLSFTQEQALAKVLIDWPANLYLCS	SPSHVHVGQVODVRLS		VSECHRTALVSGMCCALLLILLT	605
gi	47086413	ref	NP_997977.1	ITTFKSKEQLDSFHTLKLLEAGGNFVICS	CEFLSFTQEQALAKVLIDWPANLYLCS	SPSHVHVGQVODVRLS		VSECHRTALVSGMCCALLLILLT	605
gi	24664561	ref	NP_524757.1	ITTFKSKEQLDSFHTLKLLEAGGNFVICS	CEFLSFTQEQALAKVLIDWPANLYLCS	SPSHVHVGQVODVRLS		VSECHRTALVSGMCCALLLILLT	605
gi	118792131	ref	XP_551799.2	ITTFKSKEQLDSFHTLKLLEAGGNFVICS	CEFLSFTQEQALAKVLIDWPANLYLCS	SPSHVHVGQVODVRLS		VSECHRTALVSGMCCALLLILLT	605



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gi	118089754	ref	XP_001232193.1	VVVGKYYHA-VWYMRMVAWLQAKRKP	APTCDICVDAFVSYSESDSNWVENIMVQLE	QACPPFRLCLHKRDFVPGKWI	VDNIIDISIEKSHKTLFVLS	EHFVQSEWCKYELDFSHFR	LDENNDAVAILLLEPIQSQAIPKRFCKLR	701
gi	31981333	ref	NP_036035.2	GALCHRFHG-LWYLRMMVAWLQAKRKP	APCRDVCYDAFVSYSESDSNWVENIMVQLE	QACPPFRLCLHKRDFVPGKWI	VDNIIDISIEKSHKTLFVLS	EHFVQSEWCKYELDFSHFR	LDENNDAVAILLLEPIQSQAIPKRFCKLR	753
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gi	27806379	ref	NP_776622.1	GVLCHRFHG-LWYLRMMVAWLQAKRKP	APSRNICVDAFVSYSESDSNWVENIMVQLE	QACPPFRLCLHKRDFVPGKWI	VDNIIDISIEKSHKTLFVLS	EHFVQSEWCKYELDFSHFR	LDENNDAVAILLLEPIQSQAIPKRFCKLR	753
gi	47086413	ref	NP_997977.1	GVLCHRFHG-LWYLRMMVAWLQAKRKP	APSRNICVDAFVSYSESDSNWVENIMVQLE	QACPPFRLCLHKRDFVPGKWI	VDNIIDISIEKSHKTLFVLS	EHFVQSEWCKYELDFSHFR	LDENNDAVAILLLEPIQSQAIPKRFCKLR	753
gi	24664561	ref	NP_524757.1	VLTCHKLVH-TWYLRMMVAWLQAKRKP	APSRNICVDAFVSYSESDSNWVENIMVQLE	QACPPFRLCLHKRDFVPGKWI	VDNIIDISIEKSHKTLFVLS	EHFVQSEWCKYELDFSHFR	LDENNDAVAILLLEPIQSQAIPKRFCKLR	754
gi	118792131	ref	XP_551799.2	VLTCHKLVH-TWYLRMMVAWLQAKRKP	APSRNICVDAFVSYSESDSNWVENIMVQLE	QACPPFRLCLHKRDFVPGKWI	VDNIIDISIEKSHKTLFVLS	EHFVQSEWCKYELDFSHFR	LDENNDAVAILLLEPIQSQAIPKRFCKLR	754



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gi|52546732|ref|NP_001005264.1|KIMNTKTYLEWPPDDAQREGFWLNLRTAIKS-----785
gi|27806379|ref|NP_776622.1|KIMNTKTYLEWPFVDETQREGFWLNLRAAIRS-----784
gi|47086413|ref|NP_997977.1|KIMNSRTYLEWPEDEDKRDEFWSNLRRAALQRDEC-----788
gi|24664561|ref|NP_524757.1|LVLKINTYLOWG---DKLFWQKLRFALPDVSSSOR-----SNVAG---QSCHVPIINHASVHHHHVHQAMPLPHSVHHHQQFMLPPPQPPGFRFRPSLHQQQQQQQQQIRGNNTTQQQQQQQAALLMGGGVGGPAPQ1316
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gi|19718734|ref|NP_003255.2|-----784
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gi|52546732|ref|NP_001005264.1|-----785
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