

gi	29540531	ref	NP_001046.2	-----MELIQDTRRPPLEVVKGVPLIKVFAEALGPLQSFQARPDLLISTYPKSGITWVSGILDMMIYQGG-DLEKCHRAPIFRMVFPFLEFKAPGIP--SGMELTKDTP-APRLKTHLPLALLP	150
gi	73958421	ref	XP_855578.1	-----MEDIPDTRRPLKLVKGIPLIKVFAEALSLQDFQAQDDLLISTYPKSGITWVSEILDMIVQGG-DVEKCRRAVPIRVPFLEFKAPGIP--TGLEVLKDTF-APRLKTHLPLALLP	150
gi	29135333	ref	NP_803487.1	-----MELIQDTRRPPAKVYKGIPLIKVFAEALGPLESFEAWDDLLISTYPKSGITWVSEILDMIVQGG-DLEKQRAVPIRVPFLEFKAPGIP--TGLEVLKDTF-APRLKTHLPLALLP	150
gi	19526822	ref	NP_598431.1	-----MAQNPSPNMEPLRKLPLVVKGIPLIKVFAETMEQLQNFATAWDDLLISTYPKSGITWVSEIMDMIVQGG-KLDKCGRAPVYARIPFLEFKAPGIP--PGLLETLETF-APRIKTHLPLSLLP	150
gi	13929194	ref	NP_114022.1	-----MEFRRPPLVHVKGIPLIKVFAETIGPLQNFATAWDDLLISTYPKSGITWVSEIMDMIVQGG-KLEKCGRAPVYARIPFLEFKAPGIP--SGLLETLETF-APRLKTHLPLSLLP	150
gi	292617156	ref	XP_002663266.1	-----MEISDFSSMKLNSRPELIDFEGISMIHYFTDNWEKVKNFQARDDILLIATYPKAGITWVSYILLDLLYFGNESPERQTSQPIYMRVFPFLEACFEGIP--FGTELADNLPSPRLIKTHLPLVQLVP	150
gi	56118730	ref	NP_899191.2	-----MEISDFSSMKLNSRPELIDFEGISMIHYFTDNWEKVKNFQARDDILLIATYPKAGITWVSYILLDLLYFGNESPERQTSQPIYMRVFPFLEACFEGIP--FGTELADNLPSPRLIKTHLPLVQLVP	150
gi	47271425	ref	NP_899190.2	-----MEIPDFSSMKLNSRPELIDFEGISMIHYFTDNWEKVKNFQARDDILLIATYPKAGITWVSYILLDLLYFGNESPERQTSQPIYMRVFPFLEACFEGIP--LGTTELADNLPSPRFIKTHLPLVQLVP	150
gi	33636713	ref	NP_891986.1	-----MDMPDFSSIS--SRPTIFEFEGISMINHFTENWEKVKNFQARDDILLIATYPKAGITWVSYILLDLLYFGENAPEHTSQPIYMRVFPFLESCFKVIA--SGTELADNLPSPRLIKTHLPLVQLVP	150
gi	213385247	ref	NP_001132953.1	-----MDLSDISIKPLSRPKIFEFEGISMIHYFTDNWEKVKNFQARDDILLIATYPKAGITWVSYILLDLLYFGVEPENGQSSLPYMRVFPFLESCFKVIA--SGTELADNLPSPRLIKTHLPLVQLVP	150
gi	45387665	ref	NP_991183.1	-----MTDKKFPDVASMKQCRPDMDFEYVPLTRFFTDNWENVNFQARDDILLIATYPKAGITWVSYILLDLLYFGVEPENGQSSLPYMRVFPFLESCFKVIA--SGTELADNLPSPRLIKTHLPLVQLVP	150
gi	158288256	ref	XP_001688267.1	MAFEYIETIDPLFVQNLGKCEDDYLMVRAKQYSHVPIKIPNWVPAHCFEVDVFKNHEKDLLEAEVYVDDVWVSYPKSGITWVQEMVWVICNDL-NFEAARANSLOSRFPFLEASSFAPVSENT-YEVARNTPRRFIKTHLPLVSMPLP	150
gi	118776884	ref	XP_001230449.1	-----MARFKR-----HEKELLEAEVYVDDVWVSYPKSGITWVQEMVWVICNDL-NFEAARATKISARFPFLEIGLQSAALHFS-FKDVKDMPRPRFIKSHLPLVSMPLP	150
gi	158288258	ref	XP_559691.3	MSFEYIETIDPLFVQNLGKCEDDYLMVRAKQYSHVPIKIPNWVPAHCFEVDVFKNHEKDLLEAEVYVDDVWVSYPKSGITWVQEMVWVICNDL-NFEAARATKISARFPFLEIGLQSAALHFS-FKDVKDMPRPRFIKSHLPLVSMPLP	150
gi	158284423	ref	XP_306965.4	MAFEYIETIDPLFVQNLGKCEDDYLMVRAKQYSHVPIKIPNWVPAHCFEVDVFKNHEKDLLEAEVYVDDVWVSYPKSGITWVQEMVWVICNDL-NFEAARANSLOSRFPFLEASSFAPVSENT-YEVARNTPRRFIKTHLPLVSMPLP	150
gi	158288260	ref	XP_310136.4	MAFEYIETIDPLFVQNLGKCEDDYLMVRAKQYSHVPIKIPNWVPAHCFEVDVFKNHEKDLLEAEVYVDDVWVSYPKSGITWVQEMVWVICNDL-NFEAARANSLOSRFPFLEASSFAPVSENT-YEVARNTPRRFIKTHLPLVSMPLP	150
gi	158284634	ref	XP_307608.4	MAFEYIETIDPLFVQNLGKCEDDYLMVRAKQYSHVPIKIPNWVPAHCFEVDVFKNHEKDLLEAEVYVDDVWVSYPKSGITWVQEMVWVICNDL-NFEAARANSLOSRFPFLEASSFAPVSENT-YEVARNTPRRFIKTHLPLVSMPLP	150



gi	29540531	ref	NP_001046.2	TLLDQKVVVYVARNADKDVAVSYHFFYHMAKVHPDPGTDWDFLEKFMVGEVSYGSWYQHVQEWELSRTHP-VLYLIFYEDMKENPKREIQKILEFVGRSLPEETVDFVVOHLSFKEMKKNPMTNY-----TIVPQEFMDHSISPPFM	300
gi	73958421	ref	XP_855578.1	TLLDQKVVVYVARNADKDVAVSYHFFYRMAKVHPDPDWDWDFLEKFMVGEVSYGSWYQHVQEWELSRTHP-VLYLIFYEDMKENPKREIQKILEFVGRSLPEETVDFVVOHLSFKEMKKNMANY-----TIVPQEFMDHSISAPFM	300
gi	29135333	ref	NP_803487.1	TLLDQKVVVYVARNADKDVAVSYHFFYRMAKVHPDPGTDWDFLEKFMVGEVSYGSWYQHVQEWELSRTHP-VLYLIFYEDMKENPKREIQKILEFVGRSLPEETVDFVVOHLSFKEMKKNMANY-----TIVPQEFMDHSISAPFM	300
gi	19526822	ref	NP_598431.1	SLLDQKIKVIYIARNADKDVAVSYHFFYMAKLVHPDPGTDWDFLEKFMVGEVSYGSWYQHVQEWELSRTHP-VLYLIFYEDMKENPKREIQKILEFVGRSLPEETVDFVVOHLSFKEMKKNMANY-----TIVPQEFMDHSISAPFM	300
gi	13929194	ref	NP_114022.1	SLLDQKIKVIYIARNADKDVAVSYHFFYMAKLVHPDPGTDWDFLEKFMVGEVSYGSWYQHVQEWELSRTHP-VLYLIFYEDMKENPKREIQKILEFVGRSLPEETVDFVVOHLSFKEMKKNMANY-----TIVPQEFMDHSISAPFM	300
gi	292617156	ref	XP_002663266.1	SFWEQNSKVVYVARNADKDVAVSYHFFDRNMNMGQPEPGDWNIFLQKFMVGEVSYGSWYQHVQEWELSRTHP-VLYLIFYEDMKENPKREIQKILEFVGRSLPEETVDFVVOHLSFKEMKKNMANY-----TIVPQEFMDHSISAPFM	300
gi	56118730	ref	NP_899191.2	SFWEQNSKVVYVARNADKDVAVSYHFFDRNMNMGQPEPGDWNIFLQKFMVGEVSYGSWYQHVQEWELSRTHP-VLYLIFYEDMKENPKREIQKILEFVGRSLPEETVDFVVOHLSFKEMKKNMANY-----TIVPQEFMDHSISAPFM	300
gi	47271425	ref	NP_899190.2	SFWEQNSKVVYVARNADKDVAVSYHFFDRNMNMGQPEPGDWNIFLQKFMVGEVSYGSWYQHVQEWELSRTHP-VLYLIFYEDMKENPKREIQKILEFVGRSLPEETVDFVVOHLSFKEMKKNMANY-----TIVPQEFMDHSISAPFM	300
gi	33636713	ref	NP_891986.1	SFWEQNSKVVYVARNADKDVAVSYHFFDRNMNMGQPEPGDWNIFLQKFMVGEVSYGSWYQHVQEWELSRTHP-VLYLIFYEDMKENPKREIQKILEFVGRSLPEETVDFVVOHLSFKEMKKNMANY-----TIVPQEFMDHSISAPFM	300
gi	213385247	ref	NP_001132953.1	SFWEQNSKVVYVARNADKDVAVSYHFFDRNMNMGQPEPGDWNIFLQKFMVGEVSYGSWYQHVQEWELSRTHP-VLYLIFYEDMKENPKREIQKILEFVGRSLPEETVDFVVOHLSFKEMKKNMANY-----TIVPQEFMDHSISAPFM	300
gi	45387665	ref	NP_991183.1	SFWEQNSKVVYVARNADKDVAVSYHFFDRNMNMGQPEPGDWNIFLQKFMVGEVSYGSWYQHVQEWELSRTHP-VLYLIFYEDMKENPKREIQKILEFVGRSLPEETVDFVVOHLSFKEMKKNMANY-----TIVPQEFMDHSISAPFM	300
gi	158288256	ref	XP_001688267.1	RWWEVKKPIIHIRRNPKSVAVSYFFHSERFF---YKCSMDIFLRSFVREHQFFSPYAHAVIEYHELQDCDN-ILHLTYEEMKRYLPAVVRKVCFFGKSYSKPELELLYQHLSEFKSIRDNPILNR--EKPNDPKITT---PFI	300
gi	118776884	ref	XP_001230449.1	RWWEVKKPIIHIRRNPKSVAVSYFFHSERFF---YKCSMDIFLRSFVREHQFFSPYAHAVIEYHELQDCDN-ILHLTYEEMKRYLPAVVRKVCFFGKSYSKPELELLYQHLSEFKSIRDNPILNR--EKPNDPKITT---PFI	300
gi	158288258	ref	XP_559691.3	RWWEVKKPIIHIRRNPKSVAVSYFFHSQGIH---YRGSMDIFLRSFVREHQFFSPYAHAVIEYHELQDCDN-ILHLTYEEMKRYLPAVVRKVCFFGKSYSKPELELLYQHLSEFKSIRDNPILNR--EKPNDPKITT---PFI	300
gi	158284423	ref	XP_306965.4	RWWEVKKPIIHIRRNPKSVAVSYFFHSQGIH---YRGSMDIFLRSFVREHQFFSPYAHAVIEYHELQDCDN-ILHLTYEEMKRYLPAVVRKVCFFGKSYSKPELELLYQHLSEFKSIRDNPILNR--EKPNDPKITT---PFI	300
gi	158288260	ref	XP_310136.4	RWWEVKKPIIHIRRNPKSVAVSYFFHSQGIH---YRGSMDIFLRSFVREHQFFSPYAHAVIEYHELQDCDN-ILHLTYEEMKRYLPAVVRKVCFFGKSYSKPELELLYQHLSEFKSIRDNPILNR--EKPNDPKITT---PFI	300
gi	158284634	ref	XP_307608.4	AFWTVRPKLVVRRNPKSVAVSYHHSVSLHC--YRGSMDIFLRSFVREHQFFSPYAHAVIEYHELQDCDN-ILHLTYEEMKRYLPAVVRKVCFFGKSYSKPELELLYQHLSEFKSIRDNPILNR--EKPNDPKITT---PFI	300



gi	29540531	ref	NP_001046.2	RKGMAGDWKTTFTVAQNERFDADYAEKMGAGCSLSFRSEL	339
gi	73958421	ref	XP_855578.1	RKGISGDWKTFTVAQNERFDADYAKMEGCGLSFRITQL	339
gi	29135333	ref	NP_803487.1	RKGIAGDWKSTFTVAQNELFEAHYAKKMR-AAATPLRWEL	339
gi	19526822	ref	NP_598431.1	RKGG	339
gi	13929194	ref	NP_114022.1	RKGTAGDWKNTFTVAQNERFDAHYAKTMTDCDFKRCLEL	339
gi	292617156	ref	XP_002663266.1	RKGVGDWRNHTVAQNEQFDEYVYKQMKNTTVKFRTEV	339
gi	56118730	ref	NP_899191.2	RKGVGDWRNHTVAQNEQFDEYVYKQMKNTTVKFRTEV	339
gi	47271425	ref	NP_899190.2	RKGVGDWRNHTVAQNEQFDEYVYKQMKNTTVKFRTEI	339
gi	33636713	ref	NP_891986.1	RKGVGDWRNHTVAQNEQFDEYVYKQMKNTTVKFRTEI	339
gi	213385247	ref	NP_001132953.1	RKGVGDWRNHTVAQNEQFDEYVYKQMKNTTVKFRTEI	339
gi	45387665	ref	NP_991183.1	RKGVGDWRNHTVAQNEQFDEYVYKQMKNSGVTFRTEI	339
gi	158288256	ref	XP_001688267.1	RKGEADGWKHELTPQIHMLEDWTKERV-NPEHRKLF	339
gi	118776884	ref	XP_001230449.1	RKGEADGWKHELTPQIHMLEDWTKERV-NPEHRKLF	339
gi	158288258	ref	XP_559691.3	RKGEADGWKHELTPQIHMLEDWTKERV-NPEHRKLF	339
gi	158284423	ref	XP_306965.4	RKGEADGWKHELTPQIHMLEDWTKERV-NPEHRKLF	339
gi	158288260	ref	XP_310136.4	RKGEADGWKHELTPQIHMLEDWTKERV-NPEHRKLF	339
gi	158284634	ref	XP_307608.4	RKGEADGWKRELTPQELIHALDRVPLDRVSKDSKYATLQ	339

