

gi	19913406	ref	NP_001058.2	MEVSP-LQPVNENMQVNIKKNEEA	-----	KKRLSVERIYOKKTOLEHI	43
gi	73966009	ref	XP_537646.2	MEVSP-LQPVNENMQISKIKKNEEA	-----	KKRLSVERIYOKKTOLEHI	43
gi	194676107	ref	XP_001254458.2	MEVSP-LQVQ-----LAGGARRGASA	-----	RPQISAA-----ARERGVVW	35
gi	6755849	ref	NP_035753.1	MELSP-LQPVNENMLMNK-KKNEDG	-----	KKRLSVERIYOKKTOLEHI	42
gi	38259192	ref	NP_071519.2	MEVSP-LQPVNENMLLNK-KKNEDG	-----	KKRLSVERIYOKKTOLEHI	42
gi	45382161	ref	NP_990122.1	MELLDSPAPLRPLHDNRLPKADGA	-----	CKRLSVERIYOKKTOLEHI	44
gi	51467892	ref	NP_001003834.1	-----MAGTEGPKLSLFENKALSKPKKD	-----	EKRLSVERIYOKKTOLEHI	42
gi	17535065	ref	NP_496536.1	-----MSDSDSEPSIEDSPKKKTAPEKKEKASPKKKKDANE	-----	SMVMEEDRNVTSLDKKGGGSKQMAIEDIYOKKSOLEHI	76
gi	124809097	ref	XP_001348490.1	-----	-----	MAKNKTIERYOKKSOIEHI	20
gi	15229538	ref	NP_189031.1	-----MATKLPQNSNAANVAKAPAKSR	-----	AAAGGKTIIEMYOKKSOLEHI	44
gi	115448107	ref	NP_001047833.1	-----MAAAAARLPLQSSSGHNAAG	-----	GGGKTIIEMYOKKTOLEHI	41
gi	6324241	ref	NP_014311.1	-----	-----	VSASDKYOKISOLEHI	21
gi	50305715	ref	XP_452818.1	-----	-----	MTQS	20
gi	45191011	ref	NP_985265.1	-----	-----	MTAIMTKE	24
gi	19112597	ref	NP_595805.1	-----	-----	KNASEYOKITOLEHI	24
gi	39975823	ref	XP_369302.1	-----	-----	SNVSTQVRLTPREHV	87
gi	32411425	ref	XP_326193.1	MDLSDMDDSMNDFLDNSESQYSPKPKAKPAKPAKAAKAAKPAAPKPKLQTKLT	-----	EGMDGGTFDDTPPSSSEKQKAPAPKKSANKLITIEIENDLMLDDVADTKPQTKKATATEYOKKTOLEHI	141
gi	32411425	ref	XP_326193.1	MSDSDVESMPEGESDAYSPVKKPAK-----KPAAKKAAAPKAPAA-KLTLQTLTGAKAAGKRRPKDSEDEDGSPGDKDDGMLDTPPNAKKOKKAPV-KKAAGKPLAETIENDSMQIDSVAPAKKTGAAKTATEMYOKKTOLEHI	-----	-----	140



gi	19913406	ref	NP_001058.2	LLRPDTYIGSVELVTLQ-MWVYDEDVG-INYREVIFVPLGPKIFDEILVNAADNKORDPK	-----	MSCIRVTIDPENNLISIWNGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETASREY	186
gi	73966009	ref	XP_537646.2	LLRPDTYIGSVELVTLQ-MWVYDEDVG-MNYREVIFVPLGPKIFDEILVNAADNKORDPK	-----	MSCIRVTIDPENNLISIWNGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETASREY	186
gi	194676107	ref	XP_001254458.2	VVRPPRAGRGFSASTRV-PWARRD-----REEETFPWCQIQSSFLR	-----	ENNLISIWNGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETASREY	151
gi	6755849	ref	NP_035753.1	LLRPDTYIGSVELVTLQ-MWVYDEDVG-INYREVIFVPLGPKIFDEILVNAADNKORDPK	-----	MSCIRVTIDPENNLISIWNGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETASREY	185
gi	38259192	ref	NP_071519.2	LLRPDTYIGSVELVTLQ-MWVYDEDVG-INYREVIFVPLGPKIFDEILVNAADNKORDPK	-----	MSCIRVTIMMR-NNLISIWNGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETASREY	184
gi	45382161	ref	NP_990122.1	LLRPDTYIGSVELVTLQ-MWVYDEDVG-LNCRDIFVPLGPKIFDEILVNAADNKORDPK	-----	MSCIKVTIDPENNLISIWNGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETASREY	187
gi	51467892	ref	NP_001003834.1	LLRPDTYIGSVELVTLQ-MWVYDEDVG-MNCRDIFVPLGPKIFDEILVNAADNKORDPK	-----	MNCIKVNIDPENNLISIWNGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETASREY	185
gi	17535065	ref	NP_496536.1	LLRPDTYIGSVELVTEKTPMVMVYVMESEKLEQRDIFVPLGPKIFDEILVNAADNKORDPK	-----	MNTIKVTIDPENNLISIWNGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETASREY	221
gi	124809097	ref	XP_001348490.1	LLRPDTYIGSVEMHTQL-LWVWVWKEKNNRVMQKNIYVPLGPKIFDEILVNAADNKAREKESSENPM	-----	CIKTEINKENKRIISVNGGEGIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETASREY	169
gi	15229538	ref	NP_189031.1	LLRPDTYIGSVELVTEKHTQL-LWVYEDGVA-MVQRPVYVIVPLGPKIFDEILVNAADNKORDPK	-----	MDSVQVVIDVEQNLISVNCNSGAGVPEIHOEGEGLYVPEMIFGHLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETADGKR	186
gi	115448107	ref	NP_001047833.1	LLRPDTYIGSVELVTEKHTQL-LWVYEDGVA-MVRSVYVIVPLGPKIFDEILVNAADNKORDPK	-----	MDSLRVEIDADEGRISVYVNGDGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETADGKR	183
gi	6324241	ref	NP_014311.1	LKRDPDYIGSVELVTEKHTQL-QWIVYDEETDCMIEKNNRVMQKNIYVPLGPKIFDEILVNAADNKVRDPS	-----	MKRIDVNIHAEHTIEVKNNDGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETADGKR	165
gi	50305715	ref	XP_452818.1	LKRDPDYIGSVELVTEKHTQL-QWIVYDEETDCMIEKNNRVMQKNIYVPLGPKIFDEILVNAADNKVRDPS	-----	MKKIDVNIHAEHTIEVKNNDGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETADGKR	164
gi	45191011	ref	NP_985265.1	LKRDPDYIGSVEMQDFH-MWVHDAEMDCMVEKQVNIYVPLGPKIFDEILVNAADNKVRDPS	-----	MKKIEVNIHAEHTIEVKNNDGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETADGKR	168
gi	19112597	ref	NP_595805.1	LKRDPDYIGSVELVTEKHTQL-QWIVYDEETDCMIEKNNRVMQKNIYVPLGPKIFDEILVNAADNKVRDPS	-----	MNTLKVTLDEPEANVNIHAEHTIEVKNNDGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETADGKR	231
gi	39975823	ref	XP_369302.1	LKRDPDYIGSVERTETK-MWTFNKQTLVFNIRVAFVPLGPKIFDEILVNAADNKVRDPS	-----	MNTLKVTLDEPEANVNIHAEHTIEVKNNDGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETADGKR	285
gi	32411425	ref	XP_326193.1	LKRDPDYIGSVELVTEKHTQL-QWIVYDEETDCMIEKNNRVMQKNIYVPLGPKIFDEILVNAADNKVRDPS	-----	MNTLKVTLDEPEANVNIHAEHTIEVKNNDGKGIIPVVEHKVEKMYVPALIFGQLLTSSNYDDDEKVTGGRRNGYGAKLNCIFSTKFTVETADGKR	284



gi	19913406	ref	NP_001058.2	KKMFQKQWMDNMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	294
gi	73966009	ref	XP_537646.2	KKMFQKQWMDNMGKAGEMELRPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	294
gi	194676107	ref	XP_001254458.2	KKMFQKQWMDNMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	259
gi	6755849	ref	NP_035753.1	KKMFQKQWMDNMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	293
gi	38259192	ref	NP_071519.2	KKMFQKQWMDNMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	292
gi	45382161	ref	NP_990122.1	KKLFQKQWMDNMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	295
gi	51467892	ref	NP_001003834.1	KRCFKQKQWMDNMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	293
gi	17535065	ref	NP_496536.1	KSAFKQKQWMDNMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	298
gi	124809097	ref	XP_001348490.1	KKEFKQKQWMDNMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	315
gi	15229538	ref	NP_189031.1	LKKYKQVFNENMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	297
gi	115448107	ref	NP_001047833.1	QKKYKQVFNENMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	295
gi	6324241	ref	NP_014311.1	GQKVVQKVENNMSICHPKPKITSYKKGPSYTKVIFKPDITRFGMKE-LDNDILGVMRRRVYDINGSVRD	-----	INVYLNKGLKIRNFKNYVELYLKLSLEKKRQ	286
gi	50305715	ref	XP_452818.1	GQKVVQKVENNMSICHPKPKITSYKKGPSYTKVIFKPDITRFGMKE-LDNDILGVMRRRVYDINGSVRD	-----	INVYLNKGLKIRNFKNYVELYLKLSLEKKRQ	291
gi	45191011	ref	NP_985265.1	GQKVVQKVENNMSICHPKPKITSYKKGPSYTKVIFKPDITRFGMKE-LDNDILGVMRRRVYDINGSVRD	-----	INVYLNKGLKIRNFKNYVELYLKLSLEKKRQ	292
gi	19112597	ref	NP_595805.1	MKKYKQKQWMDNMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	341
gi	39975823	ref	XP_369302.1	GKRYKQKQWMDNMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	403
gi	32411425	ref	XP_326193.1	GKRYKQKQWMDNMGKAGEMELKPFN-GEDYTCITFPDLSKFKMQS-LDKDIVALMVRRAVDIAGS	-----	TKDVKVFLNGNKLKPKVGFRRSYVDMYLLKDKLDEP	401




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** ** ** ** **
gi | 19913406 | ref | NP_001058.2 | VDGLKPGQRKVLVFCFKRN--DKREVKVAQLAGSVAEMS SYHHGEMSLMMI IINLAONFVGSNNLNLLOPIGQFQTRILHGGKDSASPRYIFTMLSPARLLFPKDDHTLKFLYDDNORVEPEWYIPIIPMVLINGAEGIGTGWSCKIPNF 867
gi | 73966009 | ref | XP_537646.2 | VDGLKPGQRKVLVFCFKRN--DKREVKVAQLAGSVAEMS SYHHGEMSLMMI IINLAONFVGSNNLNLLOPIGQFQTRILHGGKDSASPRYIFTMLSPARLLFPKDDHTLKFLYDDNORVEPEWYIPIIPMVLINGAEGIGTGWSCKIPNF 867
gi | 194676107 | ref | XP_001254458.2 | VDGLKPGQRKVLVFCFKRN--DKREVKVAQLAGSVAEMS SYHHGEMSLMMI IINLAONFVGSNNLNLLOPIGQFQTRILHGGKDSASPRYIFTMLSPARLLFPKDDHTLKFLYDDNORVEPEWYIPIIPMVLINGAEGIGTGWSCKIPNF 832
gi | 6755849 | ref | NP_035753.1 | VDGLKPGQRKVLVFCFKRN--DKREVKVAQLAGSVAEMS SYHHGEMSLMMI IINLAONFVGSNNLNLLOPIGQFQTRILHGGKDSASPRYIFTMLSPARLLFPKDDHTLKFLYDDNORVEPEWYIPIIPMVLINGAEGIGTGWSCKIPNF 866
gi | 38259192 | ref | NP_071519.2 | VDGLKPGQRKVLVFCFKRN--DKREVKVAQLAGSVAEMS SYHHGEMSLMMI IINLAONFVGSNNLNLLOPIGQFQTRILHGGKDSASPRYIFTMLSPARLLFPKDDHTLKFLYDDNORVEPEWYIPIIPMVLINGAEGIGTGWSCKIPNF 865
gi | 45382161 | ref | NP_990122.1 | VDGLKPGQRKVLVFCFKRN--DKREVKVAQLAGSVAEMS SYHHGEMSLMMI IINLAONFVGSNNLNLLOPIGQFQTRILHGGKDSASPRYIFTMLSPARLLFPKDDHTLKFLYDDNORVEPEWYIPIIPMVLINGAEGIGTGWSCKIPNF 868
gi | 51467892 | ref | NP_001003834.1 | VDGLKPGQRKVLVFCFKRN--DKREVKVAQLAGSVAEMS SYHHGEMSLMMI IINLAONFVGSNNLNLLOPIGQFQTRILHGGKDSASPRYIFTMLSPARLLFPKDDHTLKFLYDDNORVEPEWYIPIIPMVLINGAEGIGTGWSCKIPNF 866
gi | 17535065 | ref | NP_496536.1 | VDGLKPGQRKVLVFCFKRN--DKREVKVAQLAGSVAEMS SYHHGEMSLMMI IINLAONFVGSNNLNLLOPIGQFQTRILHGGKDSASPRYIFTMLSPARLLFPKDDHTLKFLYDDNORVEPEWYIPIIPMVLINGAEGIGTGWSCKIPNF 902
gi | 124809097 | ref | XP_001348490.1 | MDGWKPGQRKVLVFCFKRN--LRNECKVAQLVGYIAEHSAYHHGESSLQOI IINMAQTFVGSNNINFLPECGQFGRSRKEGGKDAASARYIFTKLASSTRSIFNEYDDPILKMLNEEGKIEPQYIYFVIFILVNGCEGIGTGYSSFIPNY 891
gi | 15229538 | ref | NP_189031.1 | VDGLKPGQRKVLVFCFKRN--ARKEIKVAQLVGYVSLLSAYHHGESSLQOI IINMAQTFVGSNNINFLPECGQFGRSRKEGGKDAASARYIFTKLASSTRSIFNEYDDPILKMLNEEGKIEPQYIYFVIFILVNGCEGIGTGYSSFIPNY 856
gi | 115448107 | ref | NP_001047833.1 | VDGLKPGQRKVLVFCFKRN--LVKEIKVAQLVGYVSEHSAYHHGESSLQOI IINMAQTFVGSNNINFLPECGQFGRSRKEGGKDAASARYIFTKLASSTRSIFNEYDDPILKMLNEEGKIEPQYIYFVIFILVNGCEGIGTGYSSFIPNY 856
gi | 6324241 | ref | NP_014311.1 | LDGFKPGQRKVLVFCFKRN--LKSSELKVAQLVGYVSEHSAYHHGESSLQOI IINMAQTFVGSNNINFLPECGQFGRSRKEGGKDAASARYIFTKLASSTRSIFNEYDDPILKMLNEEGKIEPQYIYFVIFILVNGCEGIGTGYSSFIPNY 844
gi | 50305715 | ref | XP_452818.1 | LDGLKPGQRKVLVFCFKRN--LKSSELKVAQLVGYVSEHSAYHHGESSLQOI IINMAQTFVGSNNINFLPECGQFGRSRKEGGKDAASARYIFTKLASSTRSIFNEYDDPILKMLNEEGKIEPQYIYFVIFILVNGCEGIGTGYSSFIPNY 848
gi | 45191011 | ref | NP_985265.1 | LDGLKPSQRKVLVFCFKRN--LKSSELKVAQLVGYVSEHSAYHHGESSLQOI IINMAQTFVGSNNINFLPECGQFGRSRKEGGKDAASARYIFTKLASSTRSIFNEYDDPILKMLNEEGKIEPQYIYFVIFILVNGCEGIGTGYSSFIPNY 852
gi | 19112597 | ref | NP_595805.1 | VDGLKPGQRKVLVFCFKRN--LVHEIKVAQLVGYVSEHSAYHHGESSLQOI IINMAQTFVGSNNINFLPECGQFGRSRKEGGKDAASARYIFTKLASSTRSIFNEYDDPILKMLNEEGKIEPQYIYFVIFILVNGCEGIGTGYSSFIPNY 897
gi | 39975823 | ref | XP_369302.1 | IDGLKPGQRKVLVFCFKRN--LVKDKKVAQLVGYVSEHSAYHHGESSLQOI IINMAQTFVGSNNINFLPECGQFGRSRKEGGKDAASARYIFTKLASSTRSIFNEYDDPILKMLNEEGKIEPQYIYFVIFILVNGCEGIGTGYSSFIPNY 967
gi | 32411425 | ref | XP_326193.1 | VDGLKPGQRKVLVFCFKRN--LIHQKVAQLVGYVSEHSAYHHGESSLQOI IINMAQTFVGSNNINFLPECGQFGRSRKEGGKDAASARYIFTKLASSTRSIFNEYDDPILKMLNEEGKIEPQYIYFVIFILVNGCEGIGTGYSSFIPNY 967
.....910.....920.....930.....940.....950.....960.....970.....980.....990.....1000.....1010.....1020.....1030.....1040.....1050

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gi | 19913406 | ref | NP_001058.2 | DVREIVNNIRRLMD-----GEEPLPML--PSYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 996
gi | 73966009 | ref | XP_537646.2 | DVREIVNNIRRLMD-----GEEPLPML--PSYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 996
gi | 194676107 | ref | XP_001254458.2 | DVREIVNNIRRLMD-----GEEPLPML--PSYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 961
gi | 6755849 | ref | NP_035753.1 | DVREIVNNIRRLMD-----GEEPLPML--PSYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 995
gi | 38259192 | ref | NP_071519.2 | DVREIVNNIRRLMD-----GEEPLPML--PSYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 994
gi | 45382161 | ref | NP_990122.1 | DVREIVNNIRRLMD-----GEEPLPML--PSYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 997
gi | 51467892 | ref | NP_001003834.1 | DVREIVNNIRRLMD-----GEEPLPML--PSYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 999
gi | 17535065 | ref | NP_496536.1 | NPRELVKNIKRLIA-----GEPQKALA--PWYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 1032
gi | 124809097 | ref | XP_001348490.1 | NPKDIIDNIKRYLN-----KEPLIPMV--PWYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 1017
gi | 15229538 | ref | NP_189031.1 | NPRIIVANVRRLLN-----GESVPMVD--PWYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 986
gi | 115448107 | ref | NP_001047833.1 | NPRIIVANVRRLLN-----DEPVEPMD--PWYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 951
gi | 6324241 | ref | NP_014311.1 | NPLEIIRLHMLN-----DEELEQMH--PWYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 971
gi | 50305715 | ref | XP_452818.1 | NPMDIVNNVRRLLM-----GEEMEQMA--PWYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 975
gi | 45191011 | ref | NP_985265.1 | NPMDIVNNVRRLLM-----GDEPDDMA--PWYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 979
gi | 19112597 | ref | NP_595805.1 | NPMDIVNNVRRLLM-----GEPLEIMT--PWYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 1025
gi | 39975823 | ref | XP_369302.1 | HPEIIVRNLIKRRMGRDSDGEGEKPPEPMT--PWYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 1106
gi | 32411425 | ref | XP_326193.1 | HPLDIVEINLKRMRGRDSDGEGEKPPEPMT--PWYKFKGIIIEELAPNC---YVISGEVAILNST--TIEISELPVIRTWC--TYKEQVLEPMLNGTEKTPPLITDYREYHDTTVKVFVKMTEKLAEEAVRG---LHKVFKLQTSLT 1104
.....1060.....1070.....1080.....1090.....1100.....1110.....1120.....1130.....1140.....1150.....1160.....1170.....1180.....1190.....1200

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gi | 19913406 | ref | NP_001058.2 | CNSMVLFDHVGCLKKYDITVDILDRDFELRLKYYGLRKEWLLGMLGAEAKLNNQARFILEKIDGKIIENKPKKELIKVLIORGYSDDPVKAWKEAG---QKVPDEEENEESDNEKETEKSVDSDSGP---TFNYLLD 1130
gi | 73966009 | ref | XP_537646.2 | CNSMVLFDHVGCLKKYDITVDILDRDFELRLKYYGLRKEWLLGMLGAEAKLNNQARFILEKIDGKIIENKPKKELIKVLIORGYSDDPVKAWKEAG---QKVPDEEENEESDNEKETEKSVDSDSGP---TFNYLLD 1130
gi | 194676107 | ref | XP_001254458.2 | CNSMVLFDHVGCLKKYDITVDILDRDFELRLKYYGLRKEWLLGMLGAEAKLNNQARFILEKIDGKIIENKPKKELIKVLIORGYSDDPVKAWKEAG---QKVPDEEENEESDNEKETEKSVDSDSGP---TFNYLLD 1095
gi | 6755849 | ref | NP_035753.1 | CNSMVLFDHVGCLKKYDITVDILDRDFELRLKYYGLRKEWLLGMLGAEAKLNNQARFILEKIDGKIIENKPKKELIKVLIORGYSDDPVKAWKEAG---QKVPDEEENEESDNEKETEKSVDSDSGP---TFNYLLD 1127
gi | 38259192 | ref | NP_071519.2 | CNSMVLFDHVGCLKKYDITVDILDRDFELRLKYYGLRKEWLLGMLGAEAKLNNQARFILEKIDGKIIENKPKKELIKVLIORGYSDDPVKAWKEAG---QKVPDEEENEESDNEKETEKSVDSDSGP---TFNYLLD 1127
gi | 45382161 | ref | NP_990122.1 | CNSMVLFDHVGCLKKYDITVDILDRDFELRLKYYGLRKEWLLGMLGAEAKLNNQARFILEKIDGKIIENKPKKELIKVLIORGYSDDPVKAWKEAG---QKVPDEEENEESDNEKETEKSVDSDSGP---TFNYLLD 1122
gi | 51467892 | ref | NP_001003834.1 | CNSMVLFDHVGCLKKYDITVDILDRDFELRLKYYGLRKEWLLGMLGAEAKLNNQARFILEKIDGKIIENKPKKELIKVLIORGYSDDPVKAWKEAG---QKVPDEEENEESDNEKETEKSVDSDSGP---TFNYLLD 1126
gi | 17535065 | ref | NP_496536.1 | TFCMVLFDAAAGCLRTYTPPEAITQKPEYRQEKYVLRKDYLLGVLQAQSKRLNQRARFILAKINQIVLENKPKKELIKVLIORGYSDDPVKAWKEAG---QKVPDEEENEESDNEKETEKSVDSDSGP---TFNYLLD 1178
gi | 124809097 | ref | XP_001348490.1 | TTNMVLFDPNLKLQRVSTELDILKFCYQRLKAVENRKSIVLISKLEKRIISNKKFILAIVNNELVNKKKKKVLVEELRYKGV---DPYDKINKIR---KEETPEGLLELDAADNPDEEETIAGIIVK---DYDYLLS 1149
gi | 15229538 | ref | NP_189031.1 | TSNMHLFDKKGVIKVVYTPQILLEEFDLRFYVYKREKREIVVKNMETELIKLEKARFILAVLSGEIIVNKRKADIVEDLRKGFPPFRKAESVEAA--IAGAVDDAABEPEELVDPESSSSYIPGS---EYDYLLA 1122
gi | 115448107 | ref | NP_001047833.1 | ---GKGVK---
gi | 6324241 | ref | NP_014311.1 | LNMVAFDPHGKIKKYNVNEILSEFYVYVRLVYVYQKRKDHMSERLQWVEKYSFQVYKFKMIIIEKELIVTINKPRNAIQIIOLENLGFPRFNKGGKPYVYGSNDPE--IABQINDVKGATSDSE--DEESSHEDTENVINGPEELGYVEWLLG 1118
gi | 50305715 | ref | XP_452818.1 | LSNMVAFDPOGKIKKYYDDVRLIDSDFYVRLTYVYQKRKDIYGERLKWVEKLSYQVFKMIMIVEKLLSVNKKPRVLFEEELMSLGFPRINKEGKPTVYKGVVEQAQIBALNDEDDDDDDKSEAEADNAESEDVVNGPEEKFNGYVYLLG 1125
gi | 45191011 | ref | NP_985265.1 | LSNMVAFDPAHNKIKKYYDDVRLIDSDFYVRLTYVYQKRKDIYGERLKWVEKLSYQVFKFKMIIIEBELRVTKKASVLMKESLGLFPRVDAEGKPHFVEDL--LEEMDASDPEFAEAL--DEGGEVADENVVVGLEKFGYVEWLLG 1126
gi | 19112597 | ref | NP_595805.1 | TSNMIAFDASGRIKKYYNDVEIITPEYVYVRLTYVYQKRKDHMSERLQWVEKYSFQVYKFKMIIIEKELIVTINKPRNAIQIIOLENLGFPRFNKGGKPYVYGSNDPE--IABQINDVKGATSDSE--DEESSHEDTENVINGPEELGYVEWLLG 1154
gi | 39975823 | ref | XP_369302.1 | IITNLVAFDTNGQIRKYDKVEDILEEYHYVRLNVYARKAHWLRVFDADYRKLINOVYRFSIIEIDGKLVVSKKKKSVLVOELRQKVPFPGQETGKKAQDEEBEF---EDEEDE---RQETNKQ 1226
gi | 32411425 | ref | XP_326193.1 | TITNLVAFDTNGQIRKYDKVEDILEEYHYVRLNVYARKAHWLRVFDADYRKLINOVYRFSIIEIDGKLVVSKKKKSVLVOELRQKVPFPGQETGKKAQDEEBEF---EDEEDE---RQETNKQ 1232
.....1210.....1220.....1230.....1240.....1250.....1260.....1270.....1280.....1290.....1300.....1310.....1320.....1330.....1340.....1350

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gi	19913406	ref	NP_001058.2	MPLWYLTKKKKDELCKLRNEKEQELDTLKRKSPDLWKEDLATFIELEAVEAKEKODEQVGLPGKGGKAKGKKTQMA-----EVLVSPRGQRVIPRITIEMKABAEKKNKKIKNENT-----	1244
gi	73966009	ref	XP_537646.2	MPLWYLTKKKKDELCKLRNEKEQELDTLKRKSPDLWKEDLATFVELEAVEETKKEQEEQIGLPGKGGKGGKKTQMA-----EVLVSPCGKRVIPRVTIEMKABAEKKNKKIKNENT-----	1244
gi	194676107	ref	XP_001254458.2	MPLWYLTKKKKDELCKLRNEKEQELDTLKRKSPDLWKEDLAAVFVELE-----SENV-----	1148
gi	6755849	ref	NP_035753.1	MPLWYLTKKKKDELCKORNEKEQELNLTQKQSPDLWKEDLAVFIELEVEEAKKEKODEQVGLPGKAGKAKGKKAQMCADVLVSPRGKRVIPQVTVMKABAEKKNIRKKIKSENV-----	1242
gi	38259192	ref	NP_071519.2	MPLWYLTKKKKDELCKORNEKEQELNLTQKQSPDLWKEDLAAVFVELEVEEAKKEKODEQVGLPGKAGKAKGKKAQIS-----EVLVSPVGKRVIPQVTMEMRABAEKKNIRKKIKSENV-----	1241
gi	45382161	ref	NP_990122.1	MPLWYLTKKKKDELCKORNEKEQELNLTQKQSPDLWKEDLAAVFVELEDAVEAKQODEMAGITGKPLKVKGGKQGGKQVTKAQLAEVMPSPHGIRVVRVTAEMKABAEKKNIRKKIKSEKN-----	1245
gi	51467892	ref	NP_001003834.1	MPMWYLTKKKKDELCKORDAKMTLNTLKMKAAPDLWKEDLAAVFIELEERVEQKEKBAQNAMPLVKGVKPKVVKVKN-----ETMPVPGRRVIPRITSTMKVAVKKEKGGKSKKGA-----	1242
gi	17535065	ref	NP_496536.1	MALIKLSKEEKNKLIKSEKEMAEVRIEKKKIQWQDLWHDLDNFVSELDLQEAEREKADQASIKNAAKKLAADAKTGRGP-KKNVCEVLVSPKDGRIEPMLEDAATKAKVEKMSQPKKERVKK-----	1300
gi	124809097	ref	XP_001348490.1	MPFSLLEKVEDLLTTLKKEKRELEILRNIVETMMLKDIKVEEAIERQNVLSNREESNFKVARKQGPSMCK-----KTKKLLSDEE-----	1239
gi	15229538	ref	NP_189031.1	MAIASLTIKVEELLDLRDKMIIVADMKKTTPKSLWLDLSDLESDDKLEKLDLKDAAVQQAIEAAQKIRAKSGAAVK-----VKRQAPKKPAPKKTAKKA-----	1218
gi	115448107	ref	NP_001047833.1	-----	956
gi	6324241	ref	NP_014311.1	MRIWSLTKERYQKLLKQKQEKTELENLTKLAKDIWNTDLKAFVGVY-----QEFQRDAEARGGNVFNKGSKTK-----GKGRKLVDDDEDVPSKKNKSTARKGKIK-----	1220
gi	50305715	ref	XP_452818.1	MKIWALTKERYEKLKMQQEKQTELERLLKLAKDLWEIDLDDFVEHY-----BKFIQYDEEVRNSIVPDAATTCK-----GK-RRRKGKNDND-SKQPKK--RARKSVK-----	1222
gi	45191011	ref	NP_985265.1	MKIWSLTKERYERLLREKQNKAEQLQELGKAKDLWNADLDMFVREY-----EFIKYDTEVRDGTIRAVGSKVK-----GK-KRAKDDDDVNSKPKKPK--SSVKKLK-----	1225
gi	19112597	ref	NP_595805.1	MPLWSLTYERYVELLKKKDEVMAEALDALIKKPKELWLHDLDAFEHAWNKVMDDIQREMLEEEQSSRD-FVNRTKKPR-----GKSTGTRKPRALAGSSSSAVKKEASSEPK-----	1263
gi	39975823	ref	XP_369302.1	MAIWSLTERLERLKKLEAKKAEFDLNSKSEKDLWCKDLDDFVMEWENQLKLDABITNIRRMGRRVSRKIGAGK-----GGRKAKADDYAPTKAKAPAKKPKAEAKK-----	1334
gi	32411425	ref	XP_326193.1	MPIWSLTFERLDKLLQIAAKKAEHDELDALEKDLWCRDLDAFAEWEQQLRLEDEVRKEIRQGRVRSYKCGAVSRL-----KKSRAKDDDEDVPGAKKAKAKAPKAEIKTKQORFLEKFSGMKPKPKSTAFIDGADD-----	1370



gi	19913406	ref	NP_001058.2	-----	1244
gi	73966009	ref	XP_537646.2	-----	1244
gi	194676107	ref	XP_001254458.2	-----	1148
gi	6755849	ref	NP_035753.1	-----	1242
gi	38259192	ref	NP_071519.2	-----	1241
gi	45382161	ref	NP_990122.1	-----	1245
gi	51467892	ref	NP_001003834.1	-----	1242
gi	17535065	ref	NP_496536.1	-----	1300
gi	124809097	ref	XP_001348490.1	-----	1239
gi	15229538	ref	NP_189031.1	-----	1218
gi	115448107	ref	NP_001047833.1	-----	956
gi	6324241	ref	NP_014311.1	-----	1220
gi	50305715	ref	XP_452818.1	-----	1222
gi	45191011	ref	NP_985265.1	-----	1225
gi	19112597	ref	NP_595805.1	-----	1263
gi	39975823	ref	XP_369302.1	-----	1386
gi	32411425	ref	XP_326193.1	-----VPEKTKHERWD-----AALKAE--EKPPVKAAPKSG-----LDGVDDFSDDDFAALSKPKTKIK-----	1520
				LSDDDFDLLNKAAPAAAKKDEDAEPTTIAEVRKRAKRAVAKPKTVALSDESDDEFLDIAKVTITSEKTTTSASAVSAEEOSEQPVAKPARAAGAKKPIVDEDESPLDDFDDESEEVIPKPTTKRAIAAKKPALEDESDFVFG-----	



gi	19913406	ref	NP_001058.2	-----EGSPQEDG-----VELEG	1257
gi	73966009	ref	XP_537646.2	-----EGSPOEES-----IEIEG	1257
gi	194676107	ref	XP_001254458.2	-----EGSPQEDG-----MEMES	1161
gi	6755849	ref	NP_035753.1	-----EGTPAEDG-----AEPGS	1255
gi	38259192	ref	NP_071519.2	-----EGTPAEDG-----AEPG-	1253
gi	45382161	ref	NP_990122.1	-----ESDEKQEGNE-----SGDKFPSS	1263
gi	51467892	ref	NP_001003834.1	-----LVMKMEFDDEADAADG-----LGVGLAR	1267
gi	17535065	ref	NP_496536.1	-----EPKEPKEP-----KKVKK	1313
gi	124809097	ref	XP_001348490.1	-----SEGGDISPS-----SEFLV	1253
gi	15229538	ref	NP_189031.1	-----SESEITIAS-----YSAMD	1232
gi	115448107	ref	NP_001047833.1	-----	956
gi	6324241	ref	NP_014311.1	-----	1225
gi	50305715	ref	XP_452818.1	-----	1227
gi	45191011	ref	NP_985265.1	-----	1229
gi	19112597	ref	NP_595805.1	-----	1268
gi	39975823	ref	XP_369302.1	-----KESPVEEVD-----ESLAPITARAKRAATKK-----KQWIVD--DDESDF	1429
gi	32411425	ref	XP_326193.1	DAPSEPIPPPKPKAKKAKKPKIVVEDDEDMLSEAEKPAHAAPKPKRAAAVKKSPVLEDDDFESDADDKILSEAKPAPAKATAKRAAAKSPVLEDDDESDDGDKMVSEAKPAPANPRKRAAAKAKSFFIDEDESSEASD-----	1670



