

gi | 161077812 | ref | NP_001096977.1 | MEVESENKRA... 150
gi | 158288915 | ref | XP_310731.4 | MKKPA... 62
gi | 110625656 | ref | NP_035180.2 | MDIEN... 120
gi | 21914829 | ref | NP_071601.2 | MDVNE... 120
gi | 21735596 | ref | NP_055271.2 | MDVNE... 120
gi | 114632793 | ref | XP_001143474.1 | MDVNE... 120
gi | 57107291 | ref | XP_535012.1 | MDVNE... 120
gi | 139948333 | ref | NP_001077116.1 | MDVNE... 120
gi | 45383532 | ref | NP_989635.1 | MEIEK... 118
gi | 39752647 | ref | NP_945329.1 | MATD... 120
gi | 79325245 | ref | NP_001031708.1 | ME... 73
gi | 18424679 | ref | NP_568968.1 | MAS... 77
gi | 115474565 | ref | NP_001060879.1 | MAS... 93



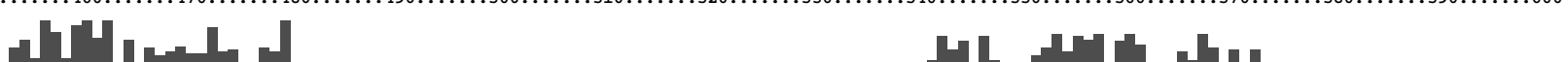
gi | 161077812 | ref | NP_001096977.1 | KGVWGL... 297
gi | 158288915 | ref | XP_310731.4 | KGVWGP... 212
gi | 110625656 | ref | NP_035180.2 | KGVWG... 264
gi | 21914829 | ref | NP_071601.2 | KGVWG... 264
gi | 21735596 | ref | NP_055271.2 | KGVWG... 264
gi | 114632793 | ref | XP_001143474.1 | KGVWG... 264
gi | 57107291 | ref | XP_535012.1 | KGVWG... 264
gi | 139948333 | ref | NP_001077116.1 | KGVWG... 264
gi | 45383532 | ref | NP_989635.1 | KGVWG... 262
gi | 39752647 | ref | NP_945329.1 | KGVWG... 264
gi | 79325245 | ref | NP_001031708.1 | KGVWG... 217
gi | 18424679 | ref | NP_568968.1 | KGVWG... 223
gi | 115474565 | ref | NP_001060879.1 | KGVWG... 237



gi | 161077812 | ref | NP_001096977.1 | MARAV... 445
gi | 158288915 | ref | XP_310731.4 | IARAV... 357
gi | 110625656 | ref | NP_035180.2 | IARAV... 409
gi | 21914829 | ref | NP_071601.2 | IARAV... 409
gi | 21735596 | ref | NP_055271.2 | IARAV... 409
gi | 114632793 | ref | XP_001143474.1 | IARAV... 409
gi | 57107291 | ref | XP_535012.1 | IARAV... 409
gi | 139948333 | ref | NP_001077116.1 | IARAV... 409
gi | 45383532 | ref | NP_989635.1 | IARAV... 407
gi | 39752647 | ref | NP_945329.1 | IARAV... 410
gi | 79325245 | ref | NP_001031708.1 | IARAV... 361
gi | 18424679 | ref | NP_568968.1 | IARAV... 367
gi | 115474565 | ref | NP_001060879.1 | IARAV... 381



gi | 161077812 | ref | NP_001096977.1 | DDMAD... 509
gi | 158288915 | ref | XP_310731.4 | EDMTD... 422
gi | 110625656 | ref | NP_035180.2 | NEIPD... 469
gi | 21914829 | ref | NP_071601.2 | NEIPD... 469
gi | 21735596 | ref | NP_055271.2 | NEIPD... 469
gi | 114632793 | ref | XP_001143474.1 | NEIPD... 469
gi | 57107291 | ref | XP_535012.1 | NEIPD... 469
gi | 139948333 | ref | NP_001077116.1 | NEIPD... 469
gi | 45383532 | ref | NP_989635.1 | CEIPD... 467
gi | 39752647 | ref | NP_945329.1 | LDMPD... 470
gi | 79325245 | ref | NP_001031708.1 | ESLDD... 511
gi | 18424679 | ref | NP_568968.1 | ESLDD... 517
gi | 115474565 | ref | NP_001060879.1 | DSLDD... 531



gi	161077812	ref	NP_001096977.1	-----	509
gi	158288915	ref	XP_310731.4	-----	422
gi	110625656	ref	NP_035180.2	-----	469
gi	21914829	ref	NP_071601.2	-----	469
gi	21735596	ref	NP_055271.2	-----	469
gi	114632793	ref	XP_001143474.1	-----	469
gi	57107291	ref	XP_535012.1	-----	469
gi	139948333	ref	NP_001077116.1	-----	469
gi	45383532	ref	NP_989635.1	-----	467
gi	39752647	ref	NP_945329.1	-----	470
gi	79325245	ref	NP_001031708.1	LALFLARAVIDDVLPAPFNLEIISSKLRPNSSCTETVVKMARSLIFARHAGERLLRCWGGSGWAVEDAKDKISNLLLEYES SGLVSEACKCIHELGMPPFNHEVVKKALVMGMEKKKDKMMLDLEESFSEGLITITNQMTKGFTRVKDGLE	661
gi	18424679	ref	NP_568968.1	LALFLARAVIDDVLPAPLNLEIDISTKLPKSTCTETVRSARSLISARHAGERLLRSWGGGTGWIVEDAKDKISKLLLEEYETGGVTSEACQCIRDLMGPPFNHEVVKKALVMAMEKOND-RLLNLLLEECFGEGLITITNQMTKGFGRVNDSLD	666
gi	115474565	ref	NP_001060879.1	LGLFLARAVIDDVLPAPLNLEIISGKLPNCSGAETLNMARSLATARHAGERLLRCWGGGTGWVVEDTKDKIAKLLLEYESGGDVGEACNCIRELHMPFNHEVVKKALVMAMEKKNDRILGLLEECFGEGLITITNQMTKGFRRVDGLD	680
			610.....620.....630.....640.....650.....660.....670.....680.....690.....700.....710.....720.....730.....740.....750	

gi	161077812	ref	NP_001096977.1	-----	509
gi	158288915	ref	XP_310731.4	-----	422
gi	110625656	ref	NP_035180.2	-----	469
gi	21914829	ref	NP_071601.2	-----	469
gi	21735596	ref	NP_055271.2	-----	469
gi	114632793	ref	XP_001143474.1	-----	469
gi	57107291	ref	XP_535012.1	-----	469
gi	139948333	ref	NP_001077116.1	-----	469
gi	45383532	ref	NP_989635.1	-----	467
gi	39752647	ref	NP_945329.1	-----	470
gi	79325245	ref	NP_001031708.1	DLALDIPNAKEKFNDYVVEYGKKNQWVSSSFLTSLTEDANVCG	702
gi	18424679	ref	NP_568968.1	DLSLDIPNAKEKFELYASHAMDNGWLLPEFGISATG	702
gi	115474565	ref	NP_001060879.1	DLALDIPDAREKFLSYVEHAKKSGWLLPEFGVATSA	716
			760.....770.....780.....790	