

gi	24581770	ref	NP_525100.2	-----MEDRDT-----EPVLLSKHAKNLLRFLNLLPAMASHDNTRSTIVFFAVCGLDVNLN--LH-LVPPDLRODIIIDWIYGLVLPDRD--NEKNCG--GFMC-CRAMVPKTEAEILECMRNVQWGLAMT	116
gi	158296694	ref	XP_317045.4	-----MDNNEEG-----EEVEFRKHAKYFIRFLHLPGRLLASHDSTRVTIAFFAVSGLDVLDS--LH-MLTDTFQDDICNWIYKLVVVKP--GERGYG--GIQGSSTFDVIGTPDSCGLQLYR---WGLLAIH	114
gi	27369904	ref	NP_766215.1	-----MATTEDDRLAGSGE-----GERLDFLRDRHVRFFORCLOVLPERYSSLETSLRTIAFFALSGLDMLDS--LD-VVN--KDDIIEWIYSLQVLPTD--DRSNLNRCCGFRGSSYLGIPIFNP--SKNPGAAHPYDSGHIAMT	125
gi	13592025	ref	NP_112344.1	-----MAATEDDRLAGSGE-----GERLDFLRDRHVRFFORCLOVLPERYSSLETSLRTIAFFALSGLDMLDS--LD-VVN--KDDIIEWIYSLQVLPTD--DRSNLNRCCGFRGSSYLGIPIFNP--SKNPGTAHPYDSGHIAMT	125
gi	167860116	ref	NP_005014.2	-----MAATEDERLAGSGE-----GERLDFLRDRHVRFFORCLOVLPERYSSLETSLRTIAFFALSGLDMLDS--LD-VVN--KDDIIEWIYSLQVLPTD--DRSNLNRCCGFRGSSYLGIPIFNP--SKAPGTAHPYDSGHIAMT	125
gi	114601194	ref	XP_526978.2	-----MAATEDERLAGSGE-----GERLDFLRDRHVRFFORCLOVLPERYSSLETSLRTIAFFALSGLDMLDS--LD-VVN--KDDIIEWIYSLQVLPTD--DRSNLNRCCGFRGSSYLGIPIFNP--SKAPGTAHPYDSGHIAMT	125
gi	73970468	ref	XP_538560.2	-----MAATEDERLAGSGE-----GERLDFLRDRHVRFFORCLOVLPERYSSLETSLRTIAFFALSGLDMLDS--LD-VVN--KDDIIEWIYSLQVLPTD--DRSNLNRCCGFRGSSYLGIPIFNP--SKNPGTAHPYDSGHIAMT	125
gi	62751976	ref	NP_001015560.1	-----MAATEDERPTGSGE-----GERLDFLRDRHVRFFORCLOVLPERYSSLETSLRTIAFFALSGLDMLDS--LD-VVN--KDDIIEWIYSLQVLPTD--DRSNLNRCCGFRGSSYLGIPIFNP--SKNPGTAHPYDSGHIAMT	125
gi	71834640	ref	NP_001025426.1	-----MADFES-----VDFLRERHVRFFORCLYVLPERYAPYETSRLTIAFFALSGLDVLGA--LD-VVD--RHSLEIWIYSLQVLPTA--DQSNLQRCGFRGSSHIGVPISS--SKGPGAPHPYDSGHVMT	114
gi	17532631	ref	NP_496848.1	-----MCDISTEDQLLEFARKAAESGDDTQTTEFKKHITGFLIRHLNVFPQPNYNTLETSSRNTIFLFAISLDDLGE--LDNLLTPTERRQAYIDWYGLQFT--NGNVCGFRGSSHCEN--SGYDEANLAQI	119
gi	15225494	ref	NP_181487.1	MSETAVSIDSDRSKSEEDDEEYSPFVQSPSANPEKDRHMLYEMMYELLPHYVQSEINRLLAHFIIISGLHFLGARDVD--KDVVAKWVLSFQAPFTNRYSLKDGFEYGFGRSHPPTDE--NGDLKHNGSHLAST	138
gi	115434546	ref	NP_001042031.1	-----	



gi	24581770	ref	NP_525100.2	YTSLAVLVTLGDDLSRLDRKSLVGVAAVOKPEGSFSAACIDGSEDDMRFYVCAATICYMLD--YWGVDVNETMFQFITRSLRVDYGFSELEGEAEHGGTTPCALAALHLSGQL--HRLDATT-----VERMKRWLIFRQMD--GFQGRF	254
gi	158296694	ref	XP_317045.4	YTGIAVLVALGDDLSRLNRRRAIEGVAAVQREDGFSATIEGSEQDMRFYVCAAAICAMLN--DWGRVDRKKMADYILKSIKSYDYGISOHYEMESHGGTTPCATAALELSGQL--HLLSADT-----RDKIIRWLVFRQD--GFQGRF	252
gi	27369904	ref	NP_766215.1	YTGSLCLLILGDDLSRVVDEKACLALGRLALQLEDGFSFCAVPEGSENDMRFYVCAACICYMLN--NWSGMDMKKAIYIRRSMSYDNGLAAGAGLESHGGSTPCGIAASLCLMGKL--EEVFSSEKE--LNRKRWLIMRQON--GVHGRP	264
gi	13592025	ref	NP_112344.1	YTGSLCLLILGDDLSRVVDEKACLALGRLALQLEDGFSFCAVPEGSENDMRFYVCAACICYMLN--NWSGMDMKKAIYIRRSMSYDNGLAAGAGLESHGGSTPCGIAASLCLMGKL--EEVFSSEKE--LNRKRWLIMRQON--GVHGRP	264
gi	167860116	ref	NP_005014.2	YTGSLCLVILGDDLSRVNKEACLALGRLALQLEDGFSFCAVPEGSENDMRFYVCAACICYMLN--NWSGMDMKKAIYIRRSMSYDNGLAAGAGLESHGGSTPCGIAASLCLMGKL--EEVFSSEKE--LNRKRWLIMRQON--GVHGRP	264
gi	114601194	ref	XP_526978.2	YTGSLCLVILGDDLSRVNKEACLALGRLALQLEDGFSFCAVPEGSENDMRFYVCAACICYMLN--NWSGMDMKKAIYIRRSMSYDNGLAAGAGLESHGGSTPCGIAASLCLMGKL--EEVFSSEKE--LNRKRWLIMRQON--GVHGRP	264
gi	73970468	ref	XP_538560.2	YTGSLCLVILGDDLSRVNKEACLALGRLALQLEDGFSFCAVPEGSENDMRFYVCAACICYMLN--NWSGMDMKKAIYIRRSMSYDNGLAAGAGLESHGGSTPCGIAASLCLMGKL--EEVFSSEKE--LNRKRWLIMRQON--GVHGRP	264
gi	62751976	ref	NP_001015560.1	YTGSLCLVILGDDLSRVNKEACLALGRLALQLEDGFSFCAVPEGSENDMRFYVCAACICYMLN--NWSGMDMKKAIYIRRSMSYDNGLAAGAGLESHGGSTPCGIAASLCLMGKL--EEVFSSEKE--LNRKRWLIMRQON--GVHGRP	264
gi	71834640	ref	NP_001025426.1	YTGSLCLVILGDDLSRVNKEACLALGRLALQLEDGFSFCAVPEGSENDMRFYVCAACICYMLN--NWSGMDMKKAIYIRRSMSYDNGLAAGAGLESHGGSTPCGIAASLCLMGKL--EEVFSSEKE--LNRKRWLIMRQON--GVHGRP	264
gi	17532631	ref	NP_496848.1	YTSALLSLAILGDDLSRVNKEACLALGRLALQLEDGFSFCAVPEGSENDMRFYVCAACICYMLD--DWSGMDRQKTIIDYIRRSSTPFDGIGGAGLESHGGSTPCAVASLCLMGKL--REVFSEKE--LGRKRWLIMRQON--GFQGRF	253
gi	15225494	ref	NP_181487.1	YTSALLSLAILGDDLSRVNKEACLALGRLALQLEDGFSFCAVPEGSENDMRFYVCAACICYMLD--DWSGMDRQKTIIDYIRRSSTPFDGIGGAGLESHGGSTPCAVASLCLMGKL--REVFSEKE--LGRKRWLIMRQON--GFQGRF	262
gi	115434546	ref	NP_001042031.1	YCALAILKVIQHDLSLIDSKLLISMINIQDDGSEFMPHIGGTEIDRFVYCAAAICYMLD--SWSGMDKESAKNYLLNCQSYDGGFGLIPGSESHGGGTPCATAASLRLMGYIGVDLNSDSS--IIDPSLLNWLQIQANDGGFQGR	286
				-----HTCVVFSAAICSLMK--DWTGMKKEKAKQYLLNCQSYDGGFGLIPGSESHGGGTPCATAASLRLMGYIGVDLNSLDEPSSIDVRLLEWCLIQIQANDGGFQGR	102



gi	24581770	ref	NP_525100.2	NKPVDTCYFVWIGATLKLILKIFQYTNFEKRNRYILSTQDRLVGGFAKWPDS--HPDPFHITLGLCGLAFTGEPGLSPVNPVSLNMSMAAYAHLOHLHEQWR--ADGRGDEDI--SVSSAFKQQLHL--SKGVVETS--TTTTSN--PLISAG	395
gi	158296694	ref	XP_317045.4	NKPVDTCYFVWIAATLKLILKIFQYTNFEKRNRYILSTQDRLVGGFAKWPDS--YTPDFHISYFGLCGLAFTGEPGLSPVNPVSLNMSMAAYAHLOHLHEQWR--ADGRGDEDI--SVSSAFKQQLHL--SKGVVETS--TTTTSN--PLISAG	368
gi	27369904	ref	NP_766215.1	NKPVDTCYFVWIGATLKLILKIFQYTNFEKRNRYILSTQDRLVGGFAKWPDS--HPDPFHITLGLCGLAFTGEPGLSPVNPVSLNMSMAAYAHLOHLHEQWR--ADGRGDEDI--SVSSAFKQQLHL--SKGVVETS--TTTTSN--PLISAG	377
gi	13592025	ref	NP_112344.1	NKPVDTCYFVWIGATLKLILKIFQYTNFEKRNRYILSTQDRLVGGFAKWPDS--HPDPFHITLGLCGLAFTGEPGLSPVNPVSLNMSMAAYAHLOHLHEQWR--ADGRGDEDI--SVSSAFKQQLHL--SKGVVETS--TTTTSN--PLISAG	377
gi	167860116	ref	NP_005014.2	NKPVDTCYFVWIGATLKLILKIFQYTNFEKRNRYILSTQDRLVGGFAKWPDS--HPDPFHITLGLCGLAFTGEPGLSPVNPVSLNMSMAAYAHLOHLHEQWR--ADGRGDEDI--SVSSAFKQQLHL--SKGVVETS--TTTTSN--PLISAG	377
gi	114601194	ref	XP_526978.2	NKPVDTCYFVWIGATLKLILKIFQYTNFEKRNRYILSTQDRLVGGFAKWPDS--HPDPFHITLGLCGLAFTGEPGLSPVNPVSLNMSMAAYAHLOHLHEQWR--ADGRGDEDI--SVSSAFKQQLHL--SKGVVETS--TTTTSN--PLISAG	377
gi	73970468	ref	XP_538560.2	NKPVDTCYFVWIGATLKLILKIFQYTNFEKRNRYILSTQDRLVGGFAKWPDS--HPDPFHITLGLCGLAFTGEPGLSPVNPVSLNMSMAAYAHLOHLHEQWR--ADGRGDEDI--SVSSAFKQQLHL--SKGVVETS--TTTTSN--PLISAG	377
gi	62751976	ref	NP_001015560.1	NKPVDTCYFVWIGATLKLILKIFQYTNFEKRNRYILSTQDRLVGGFAKWPDS--HPDPFHITLGLCGLAFTGEPGLSPVNPVSLNMSMAAYAHLOHLHEQWR--ADGRGDEDI--SVSSAFKQQLHL--SKGVVETS--TTTTSN--PLISAG	377
gi	71834640	ref	NP_001025426.1	NKPVDTCYFVWIGATLKLILKIFQYTNFEKRNRYILSTQDRLVGGFAKWPDS--HPDPFHITLGLCGLAFTGEPGLSPVNPVSLNMSMAAYAHLOHLHEQWR--ADGRGDEDI--SVSSAFKQQLHL--SKGVVETS--TTTTSN--PLISAG	377
gi	17532631	ref	NP_496848.1	NKPVDTCYFVWIGATLKLILKIFQYTNFEKRNRYILSTQDRLVGGFAKWPDS--HPDPFHITLGLCGLAFTGEPGLSPVNPVSLNMSMAAYAHLOHLHEQWR--ADGRGDEDI--SVSSAFKQQLHL--SKGVVETS--TTTTSN--PLISAG	377
gi	15225494	ref	NP_181487.1	NKPVDTCYFVWIGATLKLILKIFQYTNFEKRNRYILSTQDRLVGGFAKWPDS--HPDPFHITLGLCGLAFTGEPGLSPVNPVSLNMSMAAYAHLOHLHEQWR--ADGRGDEDI--SVSSAFKQQLHL--SKGVVETS--TTTTSN--PLISAG	375
gi	115434546	ref	NP_001042031.1	NKSSDTCYAFWIGGVLKIIIGAYRFIDHGALRSFLLYCS--PYGGFTKFLYD--AFPDIHYSYGLAALSLEEGLEPLCTELGILSAAL--	189

