

gi	4551509	ref	NP_728832.2	-----MTMDAALPSELLVTPQPLVGFSGCLDTRVRSV	32
gi	158295977	ref	XP_316549.4	-----MSLDASALPSELLTAAAPLVGLSGLDVQRSV	32
gi	62241019	ref	NP_796214.2	-----MSPTQWDFPVELCCRPMAFVTLGLDDVYNAV	32
gi	62662652	ref	XP_224848.3	MEHLFNKKPRRIPGLVCGTIVTQAQVLPVPTFAGKRKRLLLPGLGLGLSVVGGVRPRRPSLILLALSGPTETRRCCSGSRAWFPSSGFLRPSYALPKRLLKQLCKLMLVFCVILN	150
gi	39995076	ref	NP_068761.4	-----MSPTQWDFPVELCCRPMAFVTLGLDDVYNAV	32
gi	114597093	ref	XP_526747.2	-----MSPTQWDFPVELCCRPMAFVTLGLDDVYNAV	104
gi	73979590	ref	XP_540029.2	-----MSPTQWDFPVELCCRPMAFVTLGLDDVYNAV	32
gi	156121041	ref	NP_001095667.1	-----MSPTQWDFPVELCCRPMAFVTLGLDDVYNAV	32
gi	71895863	ref	NP_001026707.1	-----MTPSQWDLPELCCRPMAFVTLGLDDVYNAV	32
gi	50233897	ref	NP_955920.2	-----MSPAGWDLPELCCRPMAFVTLGLDDVYNAV	32
gi	186532794	ref	NP_201396.4	-----MEEYPEELRTPPVSLVLFQVLAELHAST	28
gi	115448281	ref	NP_001047920.1	-----MEDYPEELRTPPLSLVTVGCPQLHPAI	28
gi	17551872	ref	NP_497264.1	MDPEVAGDWIAGRPLQLVFLVSLGNLNPVNPKA	30



gi	4551509	ref	NP_728832.2	HKAVWEAFSGSLQRKAADRAAVQYK	175
gi	158295977	ref	XP_316549.4	HKIVWDAFN--NAKKPDTESIQYK	172
gi	62241019	ref	NP_796214.2	HRAVWDAFCAN--RRADRVPISFK	172
gi	62662652	ref	XP_224848.3	HRAVWDAFCAN--RRADRVPISFK	290
gi	39995076	ref	NP_068761.4	HRAVWDAFCAN--RRADRVPISFK	172
gi	114597093	ref	XP_526747.2	HRAVWDAFCAN--RRADRVPISFK	244
gi	73979590	ref	XP_540029.2	HRAVWDAFCAN--RRADRVPISFK	172
gi	156121041	ref	NP_001095667.1	HRAVWDAFCAN--RRADRVPISFK	172
gi	71895863	ref	NP_001026707.1	HRAVWDAFCAN--RRADRVPISFK	172
gi	50233897	ref	NP_955920.2	HRAVWDAFCAN--RRADRVPISFK	172
gi	186532794	ref	NP_201396.4	KYLSHQQPPINALAFPDFSQISLLLAHDDQISRTSSFRDPLSVDSSASPISRCGGILKRDWLLKRTKVPALVAAFPSSHIF-GDPTQWLQVCSDDLDSLKSIVRPNKIKLVVVVSSP----	172
gi	115448281	ref	NP_001047920.1	SAALSRSQPPMNLALPDFSKASIL-----ARTAKARDPLAPPAP-----AGILKKDWLLKRTKVPALVAAMFRADQVS-GDPAQWLQVCSDDLNLKSVIGRNTKLVVLLVSSA-----	158
gi	17551872	ref	NP_497264.1	NSIVNVFERNR--TADKPLPILIR--VVSGLDIPPKRETGG--KGILRREWPQKYLKDPKVALIVVFIDLEWHPWEEKTEAESKVASIRGSLR-HGKIALVLIQKES--TSISDNLAAADRAHELCCQCSLSKOL	160



gi	4551509	ref	NP_728832.2	FILPHT--EHLGVALRLES AFLDMAQSYVALMSKRIRNRDQLT-AAHTSLKIRHOFKLGFAEMRODFTSGOKYVLYKFS CFPNYSYLVRRHFQAVANLDEIRINDG-----	300
gi	158295977	ref	XP_316549.4	FVLPHT--DHLMGHIFRLOS AFL ELAQSYYTQMMKQIRLHRDQLT-DAHTLLKIRHOFKLGFTSELKLDQSN-----ALRHYRQTYFLDDVRIVDI-----	279
gi	62241019	ref	NP_796214.2	FVLPHT--DHLVGYIIRLENAFYEHAQTYYYTEIRRVS SHKEFLNKTTHOLLFVRHQFKIAFFSELKODTON-----ALKNYRTAYNLVHELRAHET-----	280
gi	62662652	ref	XP_224848.3	FVLPHT--DHLVGYIIRLENAFYEHAQTYYYTEIRRVS SHKEFLNKTTHOLLFVRHQFKIAFFSELKODTON-----ALKNYRTAYNLVHELRAHET-----	398
gi	39995076	ref	NP_068761.4	FVLPHT--DHLVGYIIRLENAFYEHAQTYYYTEIRRVS SHKEFLNKTTHOLLFVRHQFKIAFFSELKODTON-----ALKNYRTAYNLVHELRAHET-----	280
gi	114597093	ref	XP_526747.2	FVLPHT--DHLVGYIIRLENAFYEHAQTYYYTEIRRVS SHKEFLNKTTHOLLFVRHQFKIAFFSELKODTON-----ALKNYRTAYNLVHELRAHET-----	352
gi	73979590	ref	XP_540029.2	FVLPHT--DHLVGYIIRLENAFYEHAQTYYYTEIRRVS SHKEFLNKTTHOLLFVRHQFKIAFFSELKODTON-----ALKNYRTAYNLVHELRAHET-----	280
gi	156121041	ref	NP_001095667.1	FVLPHT--DHLVGYIIRLENAFYEHAQTYYYTEIRRVS SHKEFLNKTTHOLLFVRHQFKIAFFSELKODTON-----ALKNYRTAYNLVHELRAHET-----	280
gi	71895863	ref	NP_001026707.1	FVLPHT--DHLVGYIIRLENAFYEHAQTYYYTEIRRVS SHKEFLNKTTHOLLFVRHQFKIAFFSELKODTON-----ALKNYRTAYNLVHELRAHET-----	280
gi	50233897	ref	NP_955920.2	FVLPHT--DHLVGYIIRLENAFYEHAQTYYYTEIRRVS SHKEFLNKTTHOLLFVRHQFKIAFFSELKODTON-----ALKNYRTAYNLVHELRAHET-----	280
gi	186532794	ref	NP_201396.4	LFFNSSI--VSELNLSLSRLASAFALSYREGRRIKSRIEKRS--SNSLDLNVRYCFKVAVYAEFRRDWGE-----ALKFYEDAVHSLHEMIGSTRRLPATQRLVETKITAELQHFPIST	287
gi	115448281	ref	NP_001047920.1	VVLVERD--EMEWIKSLNKLTTVFAELCTIYKDEGRVVKARIEKRN--FSSVELSIRYCFKVAVYAEFRRDWGE-----ALKFVEEGIRVLHEMIGSTRLPPTQRLVLEKAVAEQHFPIKST	273
gi	17551872	ref	NP_497264.1	FILPADNLLAPNTTNLQNFALKLELAFHELCAFYQQRLLKTIIRSN--IPNNSPALVVRQCFKLAFLSELRODHT-----ALRNYRLAYDQQRDVEQWDG-----	285



gi	4551509	ref	NP_728832.2	-----LMFKLKPRLDAINQFIILHVEKHRSRV-----GFKDLAFEHAWLSTQHSVFAELFCEAIKNGLPALQIQ-----HPGIYVYHKAAEFVMKRRDAAMEAVAAQASSEATPTPIQNPGLSYTEFFGIR-----	419
gi	158295977	ref	XP_316549.4	-----LFFRLNAPKDSISQFNKHIKGYRQR-----GFKELLFEBYAWLSVQYSFAELFCDVAKNGLAPLQIQ-----HPGIYFHKAAEYVIGLRKEAFLQCTALGTAGTGEQFTISN-SALYSDFFGIRG-----	398
gi	62241019	ref	NP_796214.2	-----LCFQHTPLDAIAQFRKHIDLCKKKI-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----	405
gi	62662652	ref	XP_224848.3	-----LCFQHTPLDAIAQFRKHIDLCKKKI-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----	523
gi	39995076	ref	NP_068761.4	-----LCFQHTPLDAIAQFRKHIDLCKKKI-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----	405
gi	114597093	ref	XP_526747.2	-----LCFQHTPLDAIAQFRKHIDLCKKKI-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----	477
gi	73979590	ref	XP_540029.2	-----LCFQHTPLDAIAQFRKHIDLCKKKI-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----	405
gi	156121041	ref	NP_001095667.1	-----LCFQHTPLDAIAQFRKHIDLCKKKI-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----	405
gi	71895863	ref	NP_001026707.1	-----LCFQHTPLDAIAQFRKHIDLCKKKI-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----	405
gi	50233897	ref	NP_955920.2	-----LCFQHTPLDAIAQFRKHIDLCKKKI-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----GSAELAFEHAAMWAKQFAFGDLFDEAIKLGTAIQIQ-----	405
gi	186532794	ref	NP_201396.4	-----LLLHGGLLEAVWFHGHKTSYEVKVV-----GSTFIFLHWDMMSRQFLVFAGLELTSATQVPLS NQGTAEI SLTEFFYPAYYQLAAHYLKDKKSALELLELLMSETAQEI DSSASVTSVY-----	423
gi	115448281	ref	NP_001047920.1	-----LLLHGGLLVGAVIWRKHRSYERVV-----GSPVAFVLEWFWRSQFLVFAGLELTSATQVPLS NQGTAEI SLTEFFYPAYYQLAAHYLKDKKSALELLELLMSETAQEI DSSASVTSVY-----	409
gi	17551872	ref	NP_497264.1	RGMCCLCFLHSTALEAINMRRHITVVFSSSPGIYPTLHLLWWSKQCYQFAHLFERSVAGGLSALALN-----PGTHLDAAASITYAAANTEALAKRNAPQNVYPPSPDPLANSVSY--FFGQFWR-----	417



gi|45551509|ref|NP_728832.2|
gi|158295977|ref|XP_316549.4|
gi|62241019|ref|NP_796214.2|
gi|62662652|ref|XP_224848.3|
gi|39995076|ref|NP_068761.4|
gi|114597093|ref|XP_526747.2|
gi|73979590|ref|XP_540029.2|
gi|156121041|ref|NP_001095667.1|
gi|71895863|ref|NP_001026707.1|
gi|50233897|ref|NP_955920.2|
gi|186532794|ref|NP_201396.4|
gi|115448281|ref|NP_001047920.1|
gi|17551872|ref|NP_497264.1|

...610...620...630...640...650...660...670...680...690...700...710...720...730...740...750



gi|45551509|ref|NP_728832.2|
gi|158295977|ref|XP_316549.4|
gi|62241019|ref|NP_796214.2|
gi|62662652|ref|XP_224848.3|
gi|39995076|ref|NP_068761.4|
gi|114597093|ref|XP_526747.2|
gi|73979590|ref|XP_540029.2|
gi|156121041|ref|NP_001095667.1|
gi|71895863|ref|NP_001026707.1|
gi|50233897|ref|NP_955920.2|
gi|186532794|ref|NP_201396.4|
gi|115448281|ref|NP_001047920.1|
gi|17551872|ref|NP_497264.1|

...760...770...780...790...800...810...820...830...840...850...860...870...880...890...900



gi|45551509|ref|NP_728832.2|
gi|158295977|ref|XP_316549.4|
gi|62241019|ref|NP_796214.2|
gi|62662652|ref|XP_224848.3|
gi|39995076|ref|NP_068761.4|
gi|114597093|ref|XP_526747.2|
gi|73979590|ref|XP_540029.2|
gi|156121041|ref|NP_001095667.1|
gi|71895863|ref|NP_001026707.1|
gi|50233897|ref|NP_955920.2|
gi|186532794|ref|NP_201396.4|
gi|115448281|ref|NP_001047920.1|
gi|17551872|ref|NP_497264.1|

...910...920...930...940...950...960...970...980...990...1000...1010...1020...1030...1040...1050



gi|45551509|ref|NP_728832.2|
gi|158295977|ref|XP_316549.4|
gi|62241019|ref|NP_796214.2|
gi|62662652|ref|XP_224848.3|
gi|39995076|ref|NP_068761.4|
gi|114597093|ref|XP_526747.2|
gi|73979590|ref|XP_540029.2|
gi|156121041|ref|NP_001095667.1|
gi|71895863|ref|NP_001026707.1|
gi|50233897|ref|NP_955920.2|
gi|186532794|ref|NP_201396.4|
gi|115448281|ref|NP_001047920.1|
gi|17551872|ref|NP_497264.1|

...1060...1070...1080...1090...1100...1110...1120...1130...1140...1150...1160...1170...1180...1190...1200



