

gi	56550035	ref	NP_057290.2	-----MSCAEVMYHPQPYGASOYLPNPMAATTCPTAYYQPAPQPGOOKLAVFSKMODSLEVTLPKQEEDEEEE--EEE-KD--QPAEMEY	83
gi	114587993	ref	XP_001134745.1	-----MSCAEVMYHPQPYGASOYLPNPMAATTCPTAYYQPAPQPGOOKLAVFSKMODSLEVTLPKQEEDEEEE--EEEKID--QPAEMEY	84
gi	149268091	ref	XP_283372.5	-----MSCAEVMYHPQPYGASOYLPNPVAAAATCPTACVHPAPQPGOOKLAVFSKMODSLEVTLPKQEEEEEEEEDEEEKID--QPAEMEY	86
gi	109492746	ref	XP_573239.2	MKVPAHGPPLIANPSRARSRRITARGRRGSALAAVAAGSATRTAAAAAASGGDSSGAAAQPAAMS SCAEVMYHPQPYGASOYLPNPVAAAATCPTACVHPAPQPGOOKLAVFSKMODSLEVTLPKQEEEEEEEEDEEEKID--QPAEMEY	148
gi	194663888	ref	XP_001249735.2	-----MSCAEVMYHPQPYGASOYLPNPVAAAATCPTACVHPAPQPGOOK--LAVFSKMODSLEVTLPKQEEEEEEEEDEEEKID--QPAEMEY	85
gi	74001064	ref	XP_848630.1	-----MPKKLAVYSKMODSLEVTLPKQEEEEEEEEDEEEKID--QPAEMEY	46
gi	118083728	ref	XP_416671.2	-----MDSPLCSLGRMIATMKESVLSDS--PVNFSLEKELAAAKNKMQLSRSEFELLPSEE--SSGEEDRCKDILQADAEY	67
gi	292617571	ref	XP_002663398.1	-----MTAFTISELWSSSLALDIEGGGGVQSGQKXKFSVFSRMRDSEFFPSHCQONKQFGALKSRSEFELLPSEE--SSGEEDRCKDILQADAEY	89



gi	56550035	ref	NP_057290.2	LNSRCVLFITYFGDIGSVVDEHFSRALGQAIILHPESAISKSKMGLTPLWRDSSALS--SQRNSFPFISFWTSSYQPPAPCLGGVHPDFQVTPGPGTFEADPSPWPGHNLHOTGPAPPPAVESWYPLTISQVSPSYSHMHDVYMRHHHP	232
gi	114587993	ref	XP_001134745.1	LNSRCVLFITYFGDIGSVVDEHFSRALGQAIILHPESAISKSKMGLTPLWRDSSALS--SQRNSFPFISFWTSSYQPPAPCLGGVHPDFQVTPGPGTFEADPSPWPGHNLHOTGPAPPPAVESWYPLTISQVSPSYSHMHDVYMRHHHP	233
gi	149268091	ref	XP_283372.5	LNSRCVLFITYFGDIGSVVDEHFSRALGQANILHPESAISKSKMGLTPLWRDSSALS--SQRNSFPFISFWTSSYQPPAPCLGGVHPDFQVTPAGHFTTADPNVWPGHGLHOTGPAPPPAVESWYPLTISQVSPSYSHMHDVYMRHHHP	235
gi	109492746	ref	XP_573239.2	LNSRCVLFITYFGDIGSVVDEHFSRALGQANILHPESAISKSKMGLTPLWRDSSALS--SQRNSFPFISFWTSSYQPPAPCLGGVHPDFQVTPAGHFTTADPNVWPGHGLHOTGPAPPPAVESWYPLTISQVSPSYSHMHDVYMRHHHP	297
gi	194663888	ref	XP_001249735.2	LNSRCVLFITYFGDIGSVVDEHFSRALGQASTLHQESAISKSKMGLTPLWRDSSALS--SQRNSFPFISFWTSSYQPPAPCLGGVHPDFQVTPAGHFTTADPNVWPGHGLHOTGPAPPPAVESWYPLTISQVSPSYSHMHDVYMRHHHP	234
gi	74001064	ref	XP_848630.1	LNSRCVLFITYFGDIGSVVDEHFSRALGQASTLHQESAISKSKMGLTPLWRDSSALS--NQRNSFPFISFWTSSYQPPAPCLGGVHPDFQVTPAGHFTTADPNVWPGHGLHOTGPAPPPAVESWYPLTISQVSPSYSHMHDVYMRHHHP	195
gi	118083728	ref	XP_416671.2	LNSRCVLFITYFGDIGSVVDEHFSRALGQASTLHQESAISKSKMGLTPLWRDSSALS--SQRNSFPFISFWTSSYQPPAPCLGGVHPDFQVTPAGHFTTADPNVWPGHGLHOTGPAPPPAVESWYPLTISQVSPSYSHMHDVYMRHHHP	215
gi	292617571	ref	XP_002663398.1	LSARCVFITYFRDIGDVIDEHFSRALGQASTLHQESAISKSKMGLTPLWRDSSALS--NQRNSFPFISFWTSSYQPPAPCLGGVHPDFQVTPAGHFTTADPNVWPGHGLHOTGPAPPPAVESWYPLTISQVSPSYSHMHDVYMRHHHP	230



gi	56550035	ref	NP_057290.2	HAHMHRHRRHHHHHHPPAGSALDPSYGPLLMPVSHAARIAPAPCDITKTEPTTVTATSANAWAGAFHGTVDIVPSVG---FDITG---LQHQDK---SKESPWY	326
gi	114587993	ref	XP_001134745.1	HAHMHRHRRHHHHHHPPAGSALDPSYGPLLMPVSHAARIAPAPCDITKTEPTTVTATSANAWAGAFHGTVDIVPSVG---FDITG---LQHQDK---SKESPWY	327
gi	149268091	ref	XP_283372.5	HAHVHRH---HHHHHPTAGSALDPAVGHLLMPVSHAARIAPAPCDITKTEPTTVTATSANAWAGAFHGTVDIVPSVG---FDITG---LQHQDK---SKESPWY	326
gi	109492746	ref	XP_573239.2	HAHMHRH---HHHHHPTAGSALDPAVGHLLMPVSHAARIAPAPCDITKTEPTTVTATSANAWAGAFHGTVDIVPSVG---FETG---LQHQDK---SKESTWY	389
gi	194663888	ref	XP_001249735.2	HVHHRHRRHHHHHHPPAGSALDPSYGPLLMPVSHAARIAPAPCDITKTEPTTVTATSANAWAGAFHGTVDIVPSVG---FDAGEPGDFLLSIEERR---KMPETNH	334
gi	74001064	ref	XP_848630.1	HAHMHRHRRHHHHHHPPAGSALDPSYGPLLMPVSHAARIAPAPCDITKTEPTTVTATSANAWAGAFHGTVDIVPSVG---FETG---ITVD---	280
gi	118083728	ref	XP_416671.2	HP-----HMHHRH---SSHRDPRYGLLMPVSHAARIAPAPCDITKTEPTTVTATSANAWAGAFHGTVDIVPSVG---FDAG---LQHQDK---SKDTSWF	299
gi	292617571	ref	XP_002663398.1	HPHPH---AHVVLHHAHSPALDPRFNPLLLPGVRAVSCSPTCTDIKTELEPSSIPVPSWPAFVHGSVDIYDAAAPQALLLQETISAGDTEPLLQKSKPALHIRMPLERFFQDSWREVVYKKEGPREIAQLKDRVNGGECALLCIRGQY	375



gi	56550035	ref	NP_057290.2	-----	326
gi	114587993	ref	XP_001134745.1	-----	327
gi	149268091	ref	XP_283372.5	-----	326
gi	109492746	ref	XP_573239.2	-----	389
gi	194663888	ref	XP_001249735.2	-----	334
gi	74001064	ref	XP_848630.1	-----	280
gi	118083728	ref	XP_416671.2	-----	299
gi	292617571	ref	XP_002663398.1	ERNAGVIKTLGGLVVFDSCHNGVFD	401

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