

gi	208022641	ref	NP_003189.2	MHGGRCGPRTRRPESSGEEAAPVTAMAAES-----ALQVVEKLOAR-----	LAANPPPKK-----LLKYLKLLSLTLPITVD	67
gi	114554661	ref	XP_513196.2	-----MSSSLC-----LLKYLKLLSLTLPITVD	-----MSSSLC-----LLKYLKLLSLTLPITVD	22
gi	31543847	ref	NP_038764.2	-----MAAES-----ALQVVEKLOAR-----	-----LAANPPPKK-----LLKYLKLLSLTLPITVD	41
gi	8394425	ref	NP_058799.1	-----MAAES-----ALQVVEKLOAR-----	-----LAANPPPKK-----LLKYLKLLSLTLPITVD	41
gi	73950625	ref	XP_535361.2	--MAQDGEKENPMRELRIRKLCIINICVSGEGDRLEAARAAVKLEQITGQTPVFSKARYIVRSFGIRRNEKIAVHCIVRGAKABELEKGLKVREYELRKNNFSDTGNGFGIQEHLIDLGIKYDPSIGIYGLDFVLLKYLKLLSLTLPITVD	-----LAANPPPKK-----LLKYLKLLSLTLPITVD	148
gi	71896861	ref	NP_001026076.1	-----MAES-----VLEVVGRLOR-----	-----LAGSADPKK-----LLKSLKRLSELPIITVD	40
gi	47087443	ref	NP_998620.1	-----MAEE-----LLEAVEKLOLR-----	-----LGDQEPKK-----LLKYLKLLSLTLPITVD	40
gi	24649262	ref	NP_732846.1	-----MASTSN-----LLDVVRHYORS-----	-----TEKHGEDEQR-----LLHCTTLLFNLPKIFE	43



gi	208022641	ref	NP_003189.2	ILAEYGVGKTVNSLRKH-EHVGSFARDLVAQWKLVVVERNAE-----PDEFDFEKSNSRKRPRDALQKEEEMEGDYQETWKATGSRYSYPDHRQKHKRKLSELERPHKVSHGHERRDERKRCRMSPTYSSDPESSDYGHVSPSPCTSS	211
gi	114554661	ref	XP_513196.2	ILAEYGVGKTVNSLRKH-EHVGSFARDLVAQWKLVVVERNAE-----PDEFDFEKSNSRKRPRDALQKEEEMEGDYQETWKATGSRYSYPDHRQKHKRKLSELERPHKVSHGHERRDERKRCRMSPTYSSDPESSDYGHVSPSPCTSS	166
gi	31543847	ref	NP_038764.2	ILVETGVGKTVNSFRKHEQVGNFARDLVAQWKLVVVERNSE-----AEDDFEKNNSRKRPRDALQREBELEGNYQESWKPSSGSRYSYSPDHRQKHKRKLSEPERPHKVAHSHHEKRDERRKCRMSPTYSSDPESSDYGHVSPSPCTSS	184
gi	8394425	ref	NP_058799.1	ILVETGVGKTVNSFRKHEQVGNFARDLVAQWKLVVVERNSE-----AEDDFEKNNSRKRPRDALQREBELEGNYQESWKPSSGSRYSYSPDHRQKHKRKLSEPERPHKVAHSHHEKRDERRKCRMSPTYSSDPESSDYGHVSPSPCTSS	184
gi	73950625	ref	XP_535361.2	ILAEYGVGKTVNSLRKH-EHVGSFARDLVAQWKLVVVERNEP-----PDEFDFEKSNSRKRPRDAVQREBELEGNYQESWKPSSGSRYSYSPDHRQKHKRKLSEPERTHKVSHVQRERDERKRCRMSPTYSSDPESSDYGHVSPSPCTSS	292
gi	71896861	ref	NP_001026076.1	ILVETGVGKTVNSLRKH-ELVGDFAKNLVARWKKLVVPSLEADRNLDSEDCDVERSGSRKQQAQSFQEDBEHDQDYSSPFPQSSQOLYSPDHRQKHKRKLSEPERPHKVAHSHHEKRDERRKCRMSPTYSSDPESSDYGHVSPSPCTSS	187
gi	47087443	ref	NP_998620.1	ILVETGVGKTVNSLRKH-EYAGEAANLVAQWKLVV-----EKSDRPSVKGDE-----RSHSRIEACRHRVRESRSPVEPP-----LMEEECHHEMGOYCHQSSPFPQYRHS-----A	140
gi	24649262	ref	NP_732846.1	HLQETGIGKTVNALRKISGEGVGAAKTLVTKWAKMAVAK-----DPSIASPTAIHNEEDSGKTKSSDEDPPQENKGNSSSGEDLNTSKHSHKASAKHRSRSHKSRSD	155



gi	208022641	ref	NP_003189.2	PHOMYVDHYRSLEEDQEPVSHQKPGKGHSNAPQDRLGASQERHLGEPHGKGVVSNKEHKSSHDKRPFVDAKSDEKASVVSREKSHKALSKEENR-RPPSGDNAREKPPSSGVKKEKDRREGSSLLKKCLPPS--EAASDNHLK-KPKK	356
gi	114554661	ref	XP_513196.2	PHOMYVDHYRSLEEDQEPVSHQKPGKGHSNAPQDRLGASQERHLGEPHGKGVVSNKEHKSSHDKRPFVDAKSDEKASVVSREKSHKALSKEENR-RPPSGDNAREKPPSSGVKKEKDRREGSSLLKKCLPPS--EAASDNHLK-KPKK	311
gi	31543847	ref	NP_038764.2	PHOMYDLSRSPEEDQEPVSHQKPGKGVHNTFODRLGVSS-----HLGEQGGAVSHKQRRSSHKEKHPADAREDEKISAVSREKSHKALSKEENR-RLLSGDSAKEKLPSSVVKKDKDRREGSSLLKKCLPPS--EAASDNHLK-KPKK	325
gi	8394425	ref	NP_058799.1	PHOMYDLSRSPEEDQEPVSHQKPGKGVHNTFODRLGVSS-----HLGEQGGAVSHKQRRSSHKEKHPADAREDEKISAVSREKSHKALSKEENR-RLLSGDSAKEKLPSSVVKKDKDRREGSSLLKKCLPPS--EAASDNHLK-KPKK	326
gi	73950625	ref	XP_535361.2	PHOMYVDHYRSLEEDQEPVSHQKPGKGVHNTFODRLGASQERHLGEPHGKGVVSNKEHKSSHDKRPFVDAKSDEKASVVSREKSHKALSKEENR-RPPSGDNAREKPPSSGVKKEKDRREGSSLLKKCLPPS--EAASDNHLK-KPKK	435
gi	71896861	ref	NP_001026076.1	PQDLYVDPVYAS-DEQEPEVPHRVKMGHG--FOEKLGEIWRNPGDLHDHNRASRSKSHKKEKRFDRGENKKAFAFPEKLLKTSFKKHLQSSPVVVGASKEKQRMLDGLKKEKNRENSSSRKEKLVQPLVEEVDNHLK-KRKH	333
gi	47087443	ref	NP_998620.1	PQYQSDPEYSPPEDEPESPPFNN-----IRHRSKPKPEVRRHNSQDRLDQER-----RKQPPGGERTN-----RADREOCGISHRSKHDRHLS	229
gi	24649262	ref	NP_732846.1	DKKHKSRDKKDRDREKQKE-----AKEHKEKKSNGEHSKSDSSKSSSSSHKSSKESHKSEHLKSKHEKD-----KSHSELKEVKDKSSKSHKSSSSKSKRSF-----PRREE-ESQK	264



gi	208022641	ref	NP_003189.2	RDPEKAKLDKSKOGLDSFDI-----GKGAGDLLPKVKEKGSN-NLKTPEGKVKTNLDRKSLGSL-PKVEETDMEDEFEPMTSFEYSLSYDQPRKKKKKIVKTSALG-DKGLKKNDSKSTGKNLDSVQKLPKVNKIKSE--KPGADL	496
gi	114554661	ref	XP_513196.2	RDPEKAKLDKSKOGLDSFDI-----GKGAGDLLPKVKEKGSN-NLKTPEGKVKTNLDRKSLGSL-PKVEETDMEDEFEPMTSFEYSLSYDQPRKKKKKIVKTSALG-DKGLKKNDSKSTGKNLDSVQKLPKVNKIKSE--KPGADL	451
gi	31543847	ref	NP_038764.2	KDSEKAKSDKNKOSVDGVDI-----GRCTGDPLPKAKEKVPN-HLKAQEGKVRTNADGKSAGPLHPRKAEIDVDDDEFERPTMSTFEYSLSYDQPRKKKKKIVKTSALG-DKGLKKNDSKSTGKNLDSVQKLPKVNKIKSE--KPGADL	468
gi	8394425	ref	NP_058799.1	KDSEKAKSDKNKOSVDGVDI-----GRCTGDPLPKAKEKVPN-HLKAQEGKVRTNADGKSAGPLHPRKAEIDVDDDEFERPTMSTFEYSLSYDQPRKKKKKIVKTSALG-DKGLKKNDSKSTGKNLDSVQKLPKVNKIKSE--KPGADL	468
gi	73950625	ref	XP_535361.2	KDPEKAKSDKNKOSLSDADI-----GKGT-----RDRVSN-NLKTSEG-----KPAMSSSDISYDQPRKKKKKIVKTSATLGE-EKGLKKNDSKSTGKNLDSVQKLPKVNKIKSE--KPGADL	543
gi	71896861	ref	NP_001026076.1	QNSEKSKLGKSKPSLETSNTEREKQKAESDSSRIKKEKTSGLKTSSEKHKASELDKKTDLSSSFQDGEVEDEFEPMTSFEYSLSYDQPRKKKKKIVKTSALG-DKGLKKNDSKSTGKNLDSVQKLPKVNKIKSE--KPGADL	483
gi	47087443	ref	NP_998620.1	KGGSDGKSRERKEVPPGVD-----DEEPP-----EAPTMSFEYSLSYDAPTPTKPKKQPPPPPP--APLPSASSSKSKANGTSSKR-SKSSSSSVTTFVPEK	325
gi	24649262	ref	NP_732846.1	AKIPKVKSKSESDADGFD-----SMGANFDDVLLGLNITPSSKSSSNKPKFVAKPTAAPSSSALAPATTAGSKSEALS--SRETSKPKPELLAS	357



gi	208022641	ref	NP_003189.2	AKLRKVP-DVLPVLPDLP-LPAIQANRYRPLPSLELISFPQPKRKAFFSSPOEEEEAGFTGRRMNSKMOVYSGSKCAYLPKMMTLHQCCIRVLKNNIDSIFEVGGVPSVLEPVLERCIPDQLYRIEEYNHVLIEEDQLWVKVCHRDFKEE	644
gi	114554661	ref	XP_513196.2	AKLRKVP-DVLPVLPDLP-LPAIQANRYRPLPSLELISFPQPKRKAFFSSPOEEEEAGFTGRRMNSKMOVYSGSKCAYLPKMMTLHQCCIRVLKNNIDSIFEVGGVPSVLEPVLERCIPDQLYRIEEYNHVLIEEDQLWVKVCHRDFKEE	599
gi	31543847	ref	NP_038764.2	TRPRKVPDVLPALEPDP-LPAIQANRYRPLPSLELISFPQPKRKAFFSSPOEEEEAGFTGRRMNSKMOVYSGSKCAYLPKMMTLHQCCIRVLKNNIDSIFEVGGVPSVLEPVLERCIPDQLYRIEEYNHVLIEEDQLWVKVCHRDFKEE	617
gi	8394425	ref	NP_058799.1	TRPRKVPDVLPALEPDP-LPAIQANRYRPLPSLELISFPQPKRKAFFSSPOEEEEAGFTGRRMNSKMOVYSGSKCAYLPKMMTLHQCCIRVLKNNIDSIFEVGGVPSVLEPVLERCIPDQLYRIEEYNHVLIEEDQLWVKVCHRDFKEE	617
gi	73950625	ref	XP_535361.2	AKLRKVPADALPVLDPDLP-LPMIQANRYRPLPSLELISFPQPKRKAFFSSPOEEEEAGFTGRRMNSKMOVYSGSKCAYLPKMMTLHQCCIRVLKNNIDSIFEVGGVPSVLEPVLERCIPDQLYRIEEYNHVLIEEDQLWVKVCHRDFKEE	692
gi	71896861	ref	NP_001026076.1	PKPNNMLIDVVPDLPDLP-LPMIQANRYRPLPSLELISFPQPKRKAFFSSPOEEEEAGFTGRRMNSKMOVYSGSKCAYLPKMMTLHQCCIRVLKNNIDSIFEVGGVPSVLEPVLERCIPDQLYRIEEYNHVLIEEDQLWVKVCHRDFKEE	632
gi	47087443	ref	NP_998620.1	---RKKVVDVVPDLPDLP-LPAIQANRYRPLPSLELISFPQPKRKAFFSSPOEEEEAGFTGRRMNSKMOVYSGSKCAYLPKMMTLHQCCIRVLKNNIDSIFEVGGVPSVLEPVLERCIPDQLYRIEEYNHVLIEEDQLWVKVCHRDFKEE	470
gi	24649262	ref	NP_732846.1	AKLEPLDNLALQLELTISSNKKPMLNQLVMDVVFNQGGSHKAAASRYFNESEALAQISSKTMRTKIYSGVRTQQLVSLFDLRTVLCQNDALRYTGGVFPFVLERAPQLLNFEVNPQLMDDSDVLWQVQVQRHCRS	507



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gi | 208022641 | ref | NP_003189.2 | RPEEYESWREMYLRLQDAREQRLRVLTKNIQFAHAN-KPKGROAKMAFVNSVAKPPRDVRRROEKFGTGG-----AAVPEKIKIKPAPYPMGSSHASA---SISFNPSPEEPAYDGPSTSSAHLAP-VVSSTVSYDPR-KPTVKKIAPM 783
gi | 114554661 | ref | XP_513196.2 | RPEEYESWREMYLRLQDAREQRLRVLTKNIQFAHAN-KPKGROAKMAFVNSVAKPPRDVRRROEKFGTGG-----AAIPEKIKIKPAPYPTGSSHASSE---SNFNPSPPEEPAYDGPSTSSAHLAP-VVSSTVSYDPR-KPTVKKIAPM 738
gi | 31543847 | ref | NP_038764.2 | RPEEYESWREMYLRLQDAREQRLRLLTNNIRSAHAN-KPKGROAKMAFVNSVAKPPRDVRRROEKFGTGG-----AAVPEKIRIKPAPYTTGSSHPASN---SSNFHSPPEELAYDGPSTSSAHLAP-VASSSVSYDPR-KPAVKKIAPM 758
gi | 8394425 | ref | NP_058799.1 | RPEEYESWREMYLRLQDAREQRLRLLTNNIRSAHAN-KPKGROAKMAFVNSVAKPPRDVRRROEKFGTGG-----AAVPEKIRIKPAPYTTGSSHPASN---SSNFHSPPEELAYDGPSTSSAHLAP-VASSSVSYDPR-KPAVKKIAPM 758
gi | 73950625 | ref | XP_535361.2 | RPEEYESWREMYLRLQDAREQRLRVLTKNIRSAHAN-KPKGROAKMAFVNSVAKPPRDVRRROEKFGTGG-----AAVPEKIRIKPAPYPTGNSHAPSGSGSSNEFSAPPEEPAYDGPSTSSAHLAP-VLS-IVSYDPR-KPTVKKIAPM 833
gi | 71896861 | ref | NP_001026076.1 | KPEEFESWREMYLRLHDAREQRLMLLARNIGSAHAN-KPKGRVAKMAFVNSIVKPPRDVRRROEKFGTGG-----ALVPERIKIKPVLVTSQKSHARVSE-----EERSVDGPSTSSAHSVPSGSTFSSYDPR-KPPVKKIAPM 764
gi | 47087443 | ref | NP_998620.1 | APQEEYSWRELYLRLHHERERLEKLTNIRSAHAN-KPKLRQVAKMAFVNSAVKPPRDVRRROEKFGTKDGEFSISAAPPSAKIRPATNYSIQKPSDGG-----QSSFSPPAPESSSRSAF---SSAAGHSARDKPVVKKIAPM 607
gi | 24649262 | ref | NP_732846.1 | RREEMETWREMYLRCQEKDRKLSITLAESIKASQKISEAPVVKIQLAFVDSMVKPPRSVQRKQEQYGTGK-----KLIATPAARVAALSVPIN-----AAKVGDAIRLRLVLAARDIAQVAG--PARSKKAPL 629
      .....760.....770.....780.....790.....800.....810.....820.....830.....840.....850.....860.....870.....880.....890.....900

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gi | 208022641 | ref | NP_003189.2 | MAKTIKAFKNRFSRR 798
gi | 114554661 | ref | XP_513196.2 | MAKTIKAFKNRFSRR 753
gi | 31543847 | ref | NP_038764.2 | MAKTIKAFKNRFSRR 773
gi | 8394425 | ref | NP_058799.1 | MAKTIKAFKNRFSRR 773
gi | 73950625 | ref | XP_535361.2 | MAKTIKAFKNRFSRR 848
gi | 71896861 | ref | NP_001026076.1 | MAKTIKAFKNRFSRR 779
gi | 47087443 | ref | NP_998620.1 | MAKTIKAFKNRFSRR 622
gi | 24649262 | ref | NP_732846.1 | MAKTLQFMRGRLLKR- 643
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