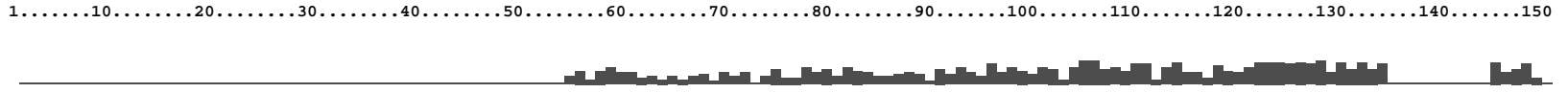
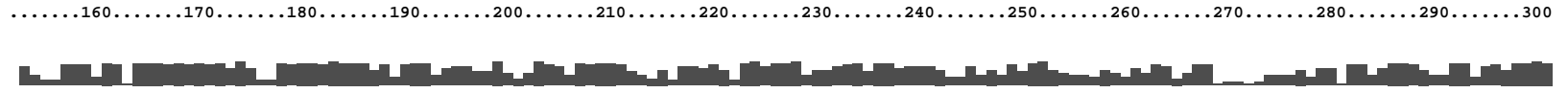


gi | 188219762 | ref | NP\_057532.2 | -----MLFNSVLRQPLGVLNRGWSQVPLQSLLLTGYQCNDDEHTSYGETVGPVPPFGCTFSSAPNMEHLAVANEEGFVRLYN-----TESQSF 86  
gi | 73960856 | ref | XP\_547399.2 | -----MLFNSVLRQPLGVLNRGWSQVPLQSLLLTGYQCNDDEHTSYGETVGPVPPFGCTFSSAPNMEHLAVANEEGFVRLYN-----TESQAY 86  
gi | 31982955 | ref | NP\_084042.1 | -----MLFNSVLRQPLGVLNRGWSHYPLOSLLSGYQCNDDEHTSYGETVGPVPPFGCTFCTAPSMHEHLAVANEEGFVRLYN-----TESQSF 86  
gi | 62659969 | ref | XP\_223074.3 | MTSVWRGVWRPGLAVAGVGKKVYSRCGGRKRLRNLGAISSAFSSAESSPQDEMLFNSVLRQPLGVLNRGWSHYPLOSLLSGYRCNDDEHTSYGETVGPVPPFGCTFCTAPSMHEHLAVANEEGFVRLYN-----TESQTS 140  
gi | 114572393 | ref | XP\_525058.2 | -----MLFNSVLRQPLGVLNRGWSQVPLQSLLLTGYQCNDDEHTSYGETVGPVPPFGCTFSSAPNMEHLAVANEEGFVRLYN-----TESQSF 86  
gi | 71895517 | ref | NP\_001026219.1 | -----MLCRALLLR---AAGHRQSSLLPLQHLLDGYRCREDDHLSYGETIGMFPVPPFGCTFSSAPNMEHLAVANEEGFVRLYD-----TEAQN 82  
gi | 27545239 | ref | NP\_775348.1 | -----MLLFHHVVDRCAGKRRGRNGEORLPLSLLDLDCYECARRDEHSYGAASAAVPPFGCTFSSAHGQNLAVANEEGFVTLFN-----TQSK-- 85  
gi | 18405469 | ref | NP\_566822.1 | -----MRDHTAQKIYYPAGFRDSEPMESRERSRVFNVIQLRELNGFRVRRKRFADSELCREIAGVAVEHDIWITPLAVFCKTSTRNSQLFAVSDDEDGHVSLFNSSSKKFASATHQEN 116  
gi | 115454769 | ref | NP\_001050985.1 | -----



gi | 188219762 | ref | NP\_057532.2 | RKKCFKEMAHWNVAVFDLAWVPGELKLVTAAGDQAKFWDVKAGELIGTCKGHQCSLKSVAFSKFEKAVFCTGGRDGNIMVWDRTRCNKKDGFYRQVNOISGAHNISDKOTPSKPKKK--QNSKGLAPSVDFQOSVTVVLFQDENTLVSAGA 235  
gi | 73960856 | ref | XP\_547399.2 | RKKCVKEMAHWNVAVFDLAWVPGELKLVTAAGDQAKFWDVKAGELIGTCKGHQCSLKSVAFSKFEKAVFCTGGRDGNIMVWDRTRCNKKDGFYRQVNOISGAHNISDKOTPSKPKKK--QNSKGLAPSVDFQOSVTVVLFQDENTLVSAGA 235  
gi | 31982955 | ref | NP\_084042.1 | KKTCTFKEMAHWNVAVFDLAWVPGELKLVTAAGDQAKFWDVRAGELMGTCKGHQCSLKSVAFSKFEKAVFCTGGRDGNIMIWDTRCNKKDGFYRQVNOISGAHNISDKOTPSKPKKK--QNSKGLAPSVDSQOSVTVVLFQDENTLVSAGA 235  
gi | 62659969 | ref | XP\_223074.3 | KKTCTFKEMAHWNVAVFDLAWVPGELKLVTAAGDQAKFWDVKAGELMGTCKGHQCSLKSVAFSKFEKAVFCTGGRDGNIMIWDTRCNKKDGFYRQVNOISGAHNISDKOTPSKPKKK--QNSKGLAPSVDSQOSVTVVLFQDENTLVSAGA 289  
gi | 114572393 | ref | XP\_525058.2 | RKKCFKEMAHWNVAVFDLAWVPGELKLVTAAGDQAKFWDVKAGELIGTCKGHQCSLKSVAFSKFEKAVFCTGGRDGNIMVWDRTRCNKKDGFYRQVNOISGAHNISDKOTPSKPKKK--QNSKGLAPSVDFQOSVTVVLFQDENTLVSAGA 235  
gi | 71895517 | ref | NP\_001026219.1 | TKLISKEWQAHNSAVFDLAWVPGELKLVTAAGDQAKFWDVKAGELIGTCKGHQCSLKSVAFSKFEKAVFCTGGRDGNIMVWDRTRCNKKDGFYRQVNOISGAHNISDKOTPSKPKKK--QNSKGLAPSVDFQOSVTVVLFQDENTLVSAGA 232  
gi | 27545239 | ref | NP\_775348.1 | GSSVLKQWQAHNDAVFDIAWVPGTNCVIVASGDQAKFWDVVIIGDLLGTFKGHQCSLKSVAFSKFEKAVFCTGGRDGNIMIWDTRCNKKDGFYRQVNOISGAHNISDKOTPSKPKKK--GMAPFVDSQOSVTVVLFQDENTLVSAGA 230  
gi | 18405469 | ref | NP\_566822.1 | EKARFRDWIAHYNAIFDISWIKGDSCLLTAAGDQAKFWDVVEENKCGVLLIGHTGTVKSMCSHPNNSDLLVSGSRDGFALWDLRCKSSSHKEEFCINSGVMVKAHLSPLSKRIRR-----RKAASSTITVLYVKDEIATATAGA 258  
gi | 115454769 | ref | NP\_001050985.1 | -----



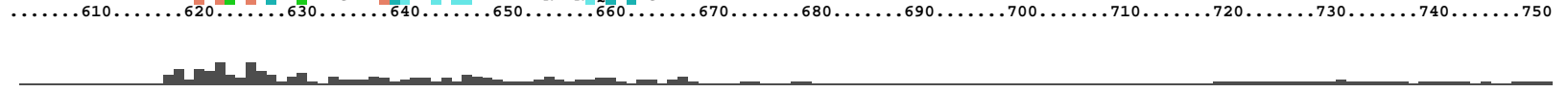
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gi | 73960856 | ref | XP\_547399.2 | VDGVIKIVWDLRKNYTAAYRQEPPIASKSFLYPGSSSTRKRLGYSSLILDSTGSLTFANCTDDNIYMFNMTGLKTSPLVAIFNGHONSTFYVKSLSLSPDDQFLVSGSSDEAAIYIKVSTPWOPPTVLLGHSQEVTISVCWCPSDFTKIATPCSDNTL 385  
gi | 31982955 | ref | NP\_084042.1 | VDGIIKVVWDLRKNYTAAYRQEPPIASKSFLYPGSSSTRKRLGYSSLILDSTGSLTFANCTDDNIYMFNMTGLKTSPLVAIFNGHONSTFYVKSLSLSPDDQFLVSGSSDEAAIYIKVSTPWOPPTVLLGHSQEVTISVCWCPSDFTKIATPCSDNTL 385  
gi | 62659969 | ref | XP\_223074.3 | VDGIIKVVWDLRKNYTAAYRQEPPIASKSFLYPGSSSTRKRLGYSSLILDSTGSLTFANCTDDNIYMFNMTGLKTSPLVAIFNGHONSTFYVKSLSLSPDDQFLVSGSSDEAAIYIKVSTPWOPPTVLLGHSQEVTISVCWCPSDFTKIATPCSDNTL 389  
gi | 114572393 | ref | XP\_525058.2 | VDGIIKVVWDLRKNYTAAYRQEPPIASKSFLYPGSSSTRKRLGYSSLILDSTGSLTFANCTDDNIYMFNMTGLKTSPLVAIFNGHONSTFYVKSLSLSPDDQFLVSGSSDEAAIYIKVSTPWOPPTVLLGHSQEVTISVCWCPSDFTKIATPCSDNTL 384  
gi | 71895517 | ref | NP\_001026219.1 | VDGVIKVVWDLRKNYTAAYRQEPPIASKSFLYPGSSSTRKRLGYSSLILDSTGANLFANCTDDNIYMFNMTGLKTSPLVAIFNGHONSTFYVKSLSLSPDDQFLVSGSSDEAAIYIKVSTPWOPPTVLLGHSQEVTISVCWCPSDFTKIATPCSDNTL 382  
gi | 27545239 | ref | NP\_775348.1 | VDGIIKVVWDLRKNYTAAYRQEPPIASKSFLYPGSSSTRKRLGYSSLILDSTGSLTFANCTDDNIYMFNMTGLKTSPLVAIFNGHONSTFYVKSLSLSPDDQFLVSGSSDEAAIYIKVSTPWOPPTVLLGHSQEVTISVCWCPSDFTKIATPCSDNTL 380  
gi | 18405469 | ref | NP\_566822.1 | PDSALKFWDIRKLRKAPFAC--ASPPQSDPTNTKEKRSRSHGIVLSQDSGGTYLTASCDNRIRIYLYNLRMDKGPVIRKAVTGSKIEFFVKSASIPDGTTHLGGSSDGNMVIWVQVNDPQVDFPIILKGDHDFEAVDVAHASDDFTV 406  
gi | 115454769 | ref | NP\_001050985.1 | -----HMDKGPVIRKAVTGSKIEFFVKSASIPDGTTHLGGSSDGNMVIWVQVNDPQVDFPIILKGDHDFEAVDVAHASDDFTV 84



gi | 188219762 | ref | NP\_057532.2 | KIWRLLNRG--LEEKPGGDKLSIVGWAQOKKKEARADLVVITNSQSTPAKAPRAKCNPSNPSPPSSAACAPSCAGDLPLPSNTPTFSIKTSPAKARSPINRRGVSFVSPKPPSSFKMSIRNWWTRTPSSPPVTPPASETKISSPRKALIPV 534  
gi | 73960856 | ref | XP\_547399.2 | KIWRLLNRG--LEEKGGDKLSIVGWAQOKKKEARADLVVITNSQSTPAKAPRAKCNPSNPSPPSSAACAPSCAGDLPLPSNTPTFSIKTSPAKARSPINRRGVSFVSPKPPSSFKMSIRNWWTRTPSSPPVTPPASETKISSPRKALIPV 534  
gi | 31982955 | ref | NP\_084042.1 | KIWRLLNRG--LEEK--GDKHSIVGWTQOKKKEVKAQCVTVVPSQSTPAKAPRAKCNPSNPSPPSSAACAPSCAGDLPLPSNTPTFSIKTTPATIRSSVRRGVSFVSPKPPSSFKMSIRNWWTRTPSSPPVTPPASETKISSPRKALIPV 533  
gi | 62659969 | ref | XP\_223074.3 | KIWRLLNRG--LEEKPEGDKHSIVGWTQOKKKEVKAQCVTVVPSQSTPAKAPRAKCNPSNPSPPSSAACAPSCAGDLPLPSNTPTFSIKTTPVTRSPVRRGVSFVSPKPPSSFKMSIRNWWTRTPSSPPVTPPASETKISSPRKALIPV 587  
gi | 114572393 | ref | XP\_525058.2 | KIWRLLNRG--LEEKPEGDKHSIVGWTQOKKKEVKAQCVTVVPSQSTPAKAPRAKCNPSNPSPPSSAACAPSCAGDLPLPSNTPTFSIKTTPVTRSPVRRGVSFVSPKPPSSFKMSIRNWWTRTPSSPPVTPPASETKISSPRKALIPV 384  
gi | 71895517 | ref | NP\_001026219.1 | RIWRLQHYPEBEKVSNAKAKLVGWVTKKKPEQRGAGRSASPOSTPAKAFVSVG--SPCASSPRPAACAPSVSGDLPPLSNTPTVSLKIQMAIACCTPAKLSGASPRTPSKPLVPSKMSIKHWIARTPCSSPEVG-----KKTIPSPRKALAEV 526  
gi | 27545239 | ref | NP\_775348.1 | RIWRLNRKPEGENSTIQDGNLVGWIRKQVSNRTPGHHSEVELTSSKNPQSVRSVLSLAPQATCAPTGA--ALPLPSNTPTFSIKTTPVTRSPVRRGVSFVSPKPPSSFKMSIRNWWTRTPSSPPVTPPASETKISSPRKALIPV 495  
gi | 18405469 | ref | NP\_566822.1 | RLWNIENN-----ICTNANATASVSRVRRRVVLSNTEAKERLEMNRETEPKQKSSLSDDDDYNDQSMPIIRTPESQKKTSSSSLSSEEDICERTPETTFNPPSVLNP 519  
gi | 115454769 | ref | NP\_001050985.1 | RVWNERR-----VFFN-----TSSPTVIRKRIIAPNTGSRSSASHELARTSLRDVGAAC--SADGELPTGRSPVLRVLEFPTESAKKRAFRLFQDSLDIRKSPEAQNMPPSVLPP 194



gi | 188219762 | ref | NP\_057532.2 | SQ-----KSSQAEACSESRNRVRRRLDSSCLESVKQKCVKCCNVTLELDQVENLHLDLCLLAGNVEDLKDLSLGPTKSS--KIEGAGTISEPPEPPIPYASESCGTLPLPLR--PCGEGSEVMVGKENSPPENKNWLLAMAARK--AENP 675  
gi | 73960856 | ref | XP\_547399.2 | SL-----KSSQAVACSESRNRVRRRLDSSCLESVKQKCVKCCNVTLELDQVENLHLDLCLLAGNVEDLKDLSLVPKPS--KIEGASITSEPPSPASPYASESCGTLPLPLR--PCGEGSEVMVGKENSPPENKNWLLAMAARK--AENS 675  
gi | 31982955 | ref | NP\_084042.1 | SQ-----KSSQADACSESRNRVRRRLDSSCLESVKQKCVKCCNVTLELDQVQESLRLDLCLLCSGTQEVLSQDSEGGTKSS--KIEGAGTISEPPEPVPVSECGPLPLPLR--PCGEGSEVMVGKENSPPENKNWLLAMAARK--AENS 678  
gi | 62659969 | ref | XP\_223074.3 | SQ-----KSSQADACSESRNRVRRRLDSSCLESVKQKCVKCCNVTLELDQVQESLRLDLCLLCSGTQEVLSQDSEGGTKSS--KIEGAGTISEPPEPVPVSECGPLPLPLR--PCGEGSEVMVGKENSPPENKNWLLAMAARK--AENS 724  
gi | 114572393 | ref | XP\_525058.2 | SQ-----KSSQADACSESRNRVRRRLDSSCLESVKQKCVKCCNVTLELDQVQESLRLDLCLLCSGTQEVLSQDSEGGTKSS--KIEGAGTISEPPEPVPVSECGPLPLPLR--PCGEGSEVMVGKENSPPENKNWLLAMAARK--AENS 384  
gi | 71895517 | ref | NP\_001026219.1 | TQSLLEISSTPKAHSQAERKRRRLDC--KEDEAGOKLQDCSCTVELDQVAKKSLNLCVLAAGQACRACDEGLSLADLLEHEDSTHSPKELSPFGSLVNSGTLQPPVPLQ--SPERDSDVVDKENSPPERKNWLSALGKLR--HGKA 674  
gi | 27545239 | ref | NP\_775348.1 | LQG-----LSFERRVRRRLTEG--DSASSGLGEEIDGVSLEYLVNPKRSRVSSTLTK--KEBDFGLESEKROGS-----DGAESGKENSPPRRTDWSLVISQKFKGSAQPK 592  
gi | 18405469 | ref | NP\_566822.1 | -----SVKRRITRDVFLVTP-----HSLKRRITRDVFA-----SSSCEHTKHVHDLALLAHSSTVKNLKNQAQVYRCLKK 535  
gi | 115454769 | ref | NP\_001050985.1 | -----



gi		188219762		ref		NP_057532.2		SPRSPSSQTPNSRRQSG---KKLPSPVVITTP-----SMRKICTYFHRKQEDFCGPEHSTEL	730
gi		73960856		ref		XP_547399.2		SPRSPSSQTPNSRRQSG---KTSPPGPVITTP-----SMRKICTYFHRKSQDDYCSPEQSTEL	730
gi		31982955		ref		NP_084042.1		SPRSPSSQTPNSRRQSG---KTSPPGPVITTP-----SMRKICTYFRRKTODDFCSPEHSTEL	729
gi		62659969		ref		XP_223074.3		SPRSPSSQTPNSRRQSR---KTSPPGPVITTPN-----SMRKICTYFRRKTODDFCSPEHSTEL	783
gi		114572393		ref		XP_525058.2		-----	384
gi		71895517		ref		NP_001026219.1		GS-PPSSYISAKRCEAAVVITSPKTAVNLSV-----SMRKICTYFHRKPON-----	720
gi		27545239		ref		NP_775348.1		SPSSGSSQDTRTLESPPAAVSPRPKVFSPPIINKKASPSKPMKKISSYFMKRTQD-----	647
gi		18405469		ref		NP_566822.1		-----	535
gi		115454769		ref		NP_001050985.1		-----	245

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