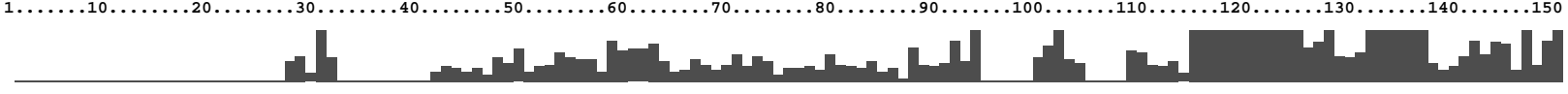


gi | 111607496 | ref | NP_666257.2 | ...MOYLN-----IKEDCNAMAFCAKMRSSFKKTEVKQVVPPEPQVEVIFVLLDREPLRLGSGEYTAE---ELCIR---AAQECSTISPLCHNLFALYDESTKLWYAPNRIITVDDKMSLR | 150
gi | 109475184 | ref | XP_342873.3 | MGAWREGGGGAGRCVQERRPPPPSRQLLRSQVRAQRCSPPCLSLAAGVHAGPRKASRVASQTPDPRHCAKPRGPAHEVISSEWALEGKEENPVCFSGTLDNRINAGISPLCHNLFALYDESTKLWYAPNRIITVDDKMSLR | 150
gi | 102469034 | ref | NP_002218.2 | ...MOYLN-----IKEDCNAMAFCAKMRSSKKTENVLEAPEPQVEVIFVLLDREPLRLGSGEYTAE---ELCIR---AAQACRISPLCHNLFALYDESTKLWYAPNRIITVDDKMSLR | 150
gi | 114556987 | ref | XP_001161295.1 | ...MOYLN-----IKEDCNAMAFCAKMRSSKKTENVLEAPEPQVEVIFVLLDREPLRLGSGEYTAE---ELCIR---AAQACRISPLCHNLFALYDESTKLWYAPNRIITVDDKMSLR | 150
gi | 73956132 | ref | XP_865150.1 | ...MOYLN-----IKEDCNAMAFCAKMRSSKKTENVLEAPEPQVEVIFVLLDREPLRLGSGEYTAE---ELCIR---AAQECSTISPLCHNLFALYDESTKLWYAPNRIITVDDKMSLR | 150
gi | 45382379 | ref | NP_990201.1 | ...MOYLN-----VKEDCKAMAFCAKMRSTKSEVNLEAQHGQLELVFLQDQSPICMTSGEFTSE---ELCIE---AAQKCSISPLCHNLFALYDESTKLWYAPNRIITVDDKMSLR | 150
gi | 56790256 | ref | NP_571148.1 | ...MPELA-----VMDLGRGLCVKMKKQKRAEMTPTAMKGLETHFVLAHTHOLEFFKACYTAE---DLCVE---AAKRCRISPLCHNLFALYDESTKLWYAPNRIITVDDKMSLR | 150



gi | 111607496 | ref | NP_666257.2 | ...HYRMRFYFTNWHGINDNEQSVWRHSPPKQKNGYEKKRVPEATPLLDASSLEYLFAQGOYDLIKCLAPIRDPKTEQDGHDIENECLGMAVLAISHYAMMKMQLPELPKDISYKRYIPETLNKSIQRNLLTRMRINNPFKDFLKEFNK | 300
gi | 109475184 | ref | XP_342873.3 | ...HYRMRFYFTNWHGINDNEQSVWRHSPPKQKNGYEKKRVPEATPLLDASSLEYLFAQGOYDLIKCLAPIRDPKTEQDGHDIENECLGMAVLAISHYAMMKMQLPELPKDISYKRYIPETLNKSIQRNLLTRMRINNPFKDFLKEFNK | 300
gi | 102469034 | ref | NP_002218.2 | ...HYRMRFYFTNWHGINDNEQSVWRHSPPKQKNGYEKKIPDATPLLDASSLEYLFAQGOYDLVKCLAPIRDPKTEQDGHDIENECLGMAVLAISHYAMMKMQLPELPKDISYKRYIPETLNKSIQRNLLTRMRINNPFKDFLKEFNK | 300
gi | 114556987 | ref | XP_001161295.1 | ...HYRMRFYFTNWHGINDNEQSVWRHSPPKQKNGYEKKIPDATPLLDASSLEYLFAQGOYDLVKCLAPIRDPKTEQDGHDIENECLGMAVLAISHYAMMKMQLPELPKDISYKRYIPETLNKSIQRNLLTRMRINNPFKDFLKEFNK | 300
gi | 73956132 | ref | XP_865150.1 | ...HYRMRFYFTNWHGINDNEQSVWRHSPPKQKNGYEKKIPDATPLLDASSLEYLFAQGOYDLVKCLAPIRDPKTEQDGHDIENECLGMAVLAISHYAMMKMQLPELPKDISYKRYIPETLNKSIQRNLLTRMRINNPFKDFLKEFNK | 300
gi | 45382379 | ref | NP_990201.1 | ...YRMRFYFTNWHGINDNEQSVWRHSPPKSKNSYDKLAPGPTPLLDANSLEYLFAQGOYDLVRELAPIRDPKNDQEVHETIENECLGMAVLAISHYAIKKNVKLPPELPKDISYKRYIPETLNKSIQRNLLTRMRINNPFKDFLKEFNK | 300
gi | 56790256 | ref | NP_571148.1 | ...HYRMRFYFTNWHGINDNEQSVWRHSPPKSKNSYDKLAPGPTPLLDANSLEYLFAQGOYDLVRELAPIRDPKNDQEVHETIENECLGMAVLAISHYAIKKNVKLPPELPKDISYKRYIPETLNKSIQRNLLTRMRINNPFKDFLKEFNK | 300



gi | 111607496 | ref | NP_666257.2 | ...ICDSSVSTHDLKVKYLATLETLKHYGAEIFETSMLLISSENELSRCHSNDSC-NVLYE-EVMVTGNLGIQWRQKPNVVEKEKNKLRKKLEYNKHKDDERNKLRREWNFSYFPEITHIVIKESVVSINKQDNKMKELKSSHEEAL | 450
gi | 109475184 | ref | XP_342873.3 | ...ICDSSVSTHDLKVKYLATLETLKHYGAEIFETSMLLISSENELSRCHSNDSC-NVLYE-EVMVTGNLGIQWRQKPNVVEKEKNKLRKKLEYNKHKDDERNKLRREWNFSYFPEITHIVIKESVVSINKQDNKMKELKSSHEEAL | 450
gi | 102469034 | ref | NP_002218.2 | ...ICDSSVSTHDLKVKYLATLETLKHYGAEIFETSMLLISSENEMNWFPHSNDSC-NVLYE-EVMVTGNLGIQWRQKPNVVEKEKNKLRKKLEYNKHKDDERNKLRREWNFSYFPEITHIVIKESVVSINKQDNKMKELKSSHEEAL | 450
gi | 114556987 | ref | XP_001161295.1 | ...ICDSSVSTHDLKVKYLATLETLKHYGAEIFETSMLLISSENEMNWFPHSNDSC-NVLYE-EVMVTGNLGIQWRQKPNVVEKEKNKLRKKLEYNKHKDDERNKLRREWNFSYFPEITHIVIKESVVSINKQDNKMKELKSSHEEAL | 450
gi | 73956132 | ref | XP_865150.1 | ...ICDSSVSTHDLKVKYLATLETLKHYGAEIFETSMLLISSENEMNWFPHSNDSC-NVLYE-EVMVTGNLGIQWRQKPNVVEKEKNKLRKKLEYNKHKDDERNKLRREWNFSYFPEITHIVIKESVVSINKQDNKMKELKSSHEEAL | 450
gi | 45382379 | ref | NP_990201.1 | ...ICDSSVSPRDLKVKYLSMETLTKHYGAEIFETSMLLISSSEINRFKNCDDGE-IIPLYEVVITGNNGIQWRKPSVQVEK-----KKKSDGKIKKDEDRYKTRDLWNNFSYFPEITHIVIKESVVSINKQDNKMKELKSSHEEAL | 450
gi | 56790256 | ref | NP_571148.1 | ...IQDSNIGLYDLKVKYLSMETLTKHYGAEIFETSMLLISSSEINRFKNCDDGE-IIPLYEVVITGNNGIQWRKPSVQVEK-----SGWTLFSDPHETITHIVIKDCCVTIYRQDNKTMELDLDFYRDAAL | 450



gi | 111607496 | ref | NP_666257.2 | ...SFVSLVDGYFRLTADAHHYLCTDVAAPPLIVHNIONGCHGPICTEYAINKLRQEGSEEGMYVLRWSCTDFDNILMTVTCFEKSEVLGG---QKQFNQIEVOKGRYSLHGSMDHFPPLRDLNMLHKKQILRTDNISFVLRKCCOPKPRE | 600
gi | 109475184 | ref | XP_342873.3 | ...SFVSLVDGYFRLTADAHHYLCTDVAAPPLIVHNIONGCHGPICTEYAINKLRQEGSEEGMYVLRWSCTDFDNILMTVTCFEKSEVLGN---QKQFNQIEVOKGRYSLHGSVDHFPPLRDLNMLHKKQILRTDNISFVLRKCCOPKPRE | 600
gi | 102469034 | ref | NP_002218.2 | ...SFVSLVDGYFRLTADAHHYLCTDVAAPPLIVHNIONGCHGPICTEYAINKLRQEGSEEGMYVLRWSCTDFDNILMTVTCFEKSEQVQV---AQKQFNQIEVOKGRYSLHGSDRSFPPLGDLMSHLKKQILRTDNISFVLRKCCOPKPRE | 600
gi | 114556987 | ref | XP_001161295.1 | ...SFVSLVDGYFRLTADAHHYLCTDVAAPPLIVHNIONGCHGPICTEYAINKLRQEGSEEGMYVLRWSCTDFDNILMTVTCFEKSEQVQV---AQKQFNQIEVOKGRYSLHGSDRSFPPLGDLMSHLKKQILRTDNISFVLRKCCOPKPRE | 600
gi | 73956132 | ref | XP_865150.1 | ...SFVSLVDGYFRLTADAHHYLCTDVAAPPLIVHNIONGCHGPICTEYAINKLRQEGSEEGMYVLRWSCTDFDNILMTVTCFEKSEQVQV---AQKQFNQIEVOKGRYSLHGSDRSFPPLGDLMSHLKKQILRTDNISFVLRKCCOPKPRE | 600
gi | 45382379 | ref | NP_990201.1 | ...SFASLIDGYFRLTADAHHYLCTDVAAPPLIENIKGCHGPICTEYAINKLRQEGSEAGMYVLRWSCTNFNLLMTVTCLEGPENIN---SVQYKFNQIEVOKGGVFLHGSNRSFASLKEMLMDLHKGILRTDNISFVLRKCCOPKPRE | 600
gi | 56790256 | ref | NP_571148.1 | ...SFAALVDGYFRLTADAHHYLCTDVAAPSSVVOLENGCHGPICTEYAINKLRQEGSEEGTYVLRWSCTEYFNFTIMTVTCLELDLDCESR---PVPQKFNQIEVOKGRYSLHGSDRSFPPLGDLMSHLKKQILRTDNISFVLRKCCOPKPRE | 600



gi | 111607496 | ref | NP_666257.2 | ...ISNLLVATK-KAQEQPVVYMSQSLSDRILKDDIIOGHEHLGRGTRTHIYSGTLLDYKDEE--GIAEKKIKVILKVLDPDSHRDI SLAFFEAASMMROVSHKHIVLYLGVQVDRVENIMVEEFVGGPDLDFMHRKSDALTPWKFKVAKQ | 750
gi | 109475184 | ref | XP_342873.3 | ...ISNLLVATK-KAQEQPVVYMSQSLSDRILKDDIIOGHEHLGRGTRTHIYSGTLLDYKDEE--GIAEKKIKVILKVLDPDSHRDI SLAFFEAASMMROVSHKHIVLYLGVQVDRVENIMVEEFVGGPDLDFMHRKSDALTPWKFKVAKQ | 750
gi | 102469034 | ref | NP_002218.2 | ...ISNLLVATK-KAQEQPVVYMSQSLSDRILKDDIIOGHEHLGRGTRTHIYSGTLLDYKDEE--GTSEKKIKVILKVLDPDSHRDI SLAFFEAASMMROVSHKHIVLYLGVQVDRVENIMVEEFVGGPDLDFMHRKSDVLTTPWKFKVAKQ | 750
gi | 114556987 | ref | XP_001161295.1 | ...ISNLLVATK-KAQEQPVVYMSQSLSDRILKDDIIOGHEHLGRGTRTHIYSGTLLDYKDEE--GTSEKKIKVILKVLDPDSHRDI SLAFFEAASMMROVSHKHIVLYLGVQVDRVENIMVEEFVGGPDLDFMHRKSDVLTTPWKFKVAKQ | 750
gi | 73956132 | ref | XP_865150.1 | ...ISNLLVATK-KAQEQPVVYMSQSLSDRILKDDIIOGHEHLGRGTRTHIYSGTLLDYKDEE--GTSEKKIKVILKVLDPDSHRDI SLAFFEAASMMROVSHKHIVLYLGVQVDRVENIMVEEFVGGPDLDFMHRKSDVLTTPWKFKVAKQ | 750
gi | 45382379 | ref | NP_990201.1 | ...ISNLLVATK-KAQEQPVAHGLGSLFHRIRKEEIMQEGHEHLGRGTRTHIYSGTLLDYKDEE--NGYQNEKEIKVILKVLDPDSHRDI SLAFFEAASMMROVSHKHIVLYLGVQVDRVENIMVEEFVGGPDLDFMHRKSELLTPWKFKVAKQ | 750
gi | 56790256 | ref | NP_571148.1 | ...ISNLLVMTDREPVVQKKTQVSLSDRILKKEIIVGHEHLGRGTRTHIYAGILKPKSDDEDLGGYSYEVKVVLLKVLGSGHRDI SLAFFEAASMMROVSHKHIALLYLGVQVDRVENIMVEEFVGGPDLDFMRRQTPLSLTAWKFOVAKQ | 750



gi	111607496	ref	NP_666257.2	LASALSYLEDKDLVHGNVCTKNLLAREGIDSDIGPFIKLSDPGIPVSLTRQECIERIPWIAPECVEDSKNLSVAADKWSFGITLWEICYNGEIPDKKTLIEK-ERFVESRCRPVTPSCKELADLMTRCMNYDPNORPFFRAIMRDIN	900
gi	109475184	ref	XP_342873.3	LASALSYLEDKDLVHGNVCTKNLLAREGIDSDIGPFIKLSDPGIPVSLTRQECIERIPWIAPECVEDSKNLSVAADKWSFGITLWEICYNGEIPDKKTLIEK-ERFVESRCRPVTPSCKELADLMTRCMNYDPNORPFFRAIMRDIN	900
gi	102469034	ref	NP_002218.2	LASALSYLEDKDLVHGNVCTKNLLAREGIDSECGPFIKLSDPGIPITVLSRQECIERIPWIAPECVEDSKNLSVAADKWSFGITLWEICYNGEIPDKKTLIEK-ERFVESRCRPVTPSCKELADLMTRCMNYDPNORPFFRAIMRDIN	900
gi	114556987	ref	XP_001161295.1	LASALSYLEDKDLVHGNVCTKNLLAREGIDSECGPFIKLSDPGIPITVLSRQECIERIPWIAPECVEDSKNLSVAADKWSFGITLWEICYNGEIPDKKTLIEK-ERFVESRCRPVTPSCKELADLMTRCMNYDPNORPFFRAIMRDIN	900
gi	73956132	ref	XP_865150.1	LASALSYLEDKDLVHGNVCTKNLLAREGIDSECGPFIKLSDPGIPITVLSRQECIERIPWIAPECVEDSKNLSVAADKWSFGITLWEICYNGEIPDKKTLIEK-ERFVESRCRPVTPSCKELADLMTRCMNYDPNORPFFRAIMRDIN	900
gi	45382379	ref	NP_990201.1	LASALSYLEDKDLVHGNVCTKNLLAREGIDTEYGPFIKLSDPGIPITVLSRQECVERIPWIAPECVEDSKNLSVAADKWSFGITLWEICYNGEIPDKKTLIEK-ERFVGHFMFLITPSCKELADLMTRCMNYDPNORPFFRAIMRDIN	900
gi	56790256	ref	NP_571148.1	LASALSYLEDKKMHVGVCTKNLLVARDGLDEGGPFIKLSDPGIPITVLSRQECVDRIPWIAPECVVDLTLNLSVAADKWSFGITLWEICYNGEIPDKKTLIEK-ERFYAAQCOLATPDCDELAKLMLHMTYDPRRLEFFRAIVRDIV	900



gi	111607496	ref	NP_666257.2	KLEEONPDIVSEKQPTTEVDPTHFVKRFLKRIKRDLDGEGHFGKVELCRYDPEGDNTGEQVAVKSLKPEGGNHADLKKETIILRNLYHENIVKYKGIEMEDGGNGIKLIMEFLPSGSLKEYLPKNNKINLKOOLKYAVQICKGMDVYLS	1050
gi	109475184	ref	XP_342873.3	KLEEONPDIVSEKQPTTEVDPTHFVKRFLKRIKRDLDGEGHFGKVELCRYDPEGDNTGEQVAVKSLKPEGGNHADLKKETIILRNLYHENIVKYKGIEMEDGGNGIKLIMEFLPSGSLKEYLPKNNKINLKOOLKYAVQICKGMDVYLS	1050
gi	102469034	ref	NP_002218.2	KLEEONPDIVSEKQPTTEVDPTHFVKRFLKRIKRDLDGEGHFGKVELCRYDPEGDNTGEQVAVKSLKPEGGNHADLKKETIILRNLYHENIVKYKGIEMEDGGNGIKLIMEFLPSGSLKEYLPKNNKINLKOOLKYAVQICKGMDVYLS	1050
gi	114556987	ref	XP_001161295.1	KLEEONPDIVSEKQPTTEVDPTHFVKRFLKRIKRDLDGEGHFGKVELCRYDPEGDNTGEQVAVKSLKPEGGNHADLKKETIILRNLYHENIVKYKGIEMEDGGNGIKLIMEFLPSGSLKEYLPKNNKINLKOOLKYAVQICKGMDVYLS	1050
gi	73956132	ref	XP_865150.1	KLEEONPDIVSEKQPTTEVDPTHFVKRFLKRIKRDLDGEGHFGKVELCRYDPEGDNTGEQVAVKSLKPEGGNHADLKKETIILRNLYHENIVKYKGIEMEDGGNGIKLIMEFLPSGSLKEYLPKNNKINLKOOLKYAVQICKGMDVYLS	1050
gi	45382379	ref	NP_990201.1	KLEEONPDIVSEKQPTTEVDPTHFVKRFLKRIKRDLDGEGHFGKVELCRYDPEGDNTGEQVAVKSLKPEGGNHADLKKETIILRNLYHENIVKYKGIEMEDGGNGIKLIMEFLPSGSLKEYLPKNNKINLKOOLKYAVQICKGMDVYLS	1050
gi	56790256	ref	NP_571148.1	MVEKONPSIQP--VPMLEVDPTVFVKRFLKRIKRDLDGEGHFGKVELCRYDPEGDNTGELVAVKSLKPEENREEQSNLWRETHILRELYHENIVKYKGIENEEGGRSIKLIMEFLPAGSLKEYLPKNNKINLKTLLNYSVQICKGMDVYLS	1050



gi	111607496	ref	NP_666257.2	ROYVHRDLAARNVLVESEHQVIGDFGLTKAETDKEYYTVKDDRDSPVFWYAPECLIQCKFYIASDVWSFGVTLHELLTYCDSDFSPMALFLKMGIPTHGQMTVTRLVNLTKEGKRLPCPPNCPDEVYQLMRKCWCFOPSNRITFQNLTI	1200
gi	109475184	ref	XP_342873.3	ROYVHRDLAARNVLVESEHQVIGDFGLTKAETDKEYYTVKDDRDSPVFWYAPECLIQCKFYIASDVWSFGVTLHELLTYCDSDFSPMALFLKMGIPTHGQMTVTRLVNLTKEGKRLPCPPNCPDEVYQLMRKCWCFOPSNRITFQNLTI	1200
gi	102469034	ref	NP_002218.2	ROYVHRDLAARNVLVESEHQVIGDFGLTKAETDKEYYTVKDDRDSPVFWYAPECLIQCKFYIASDVWSFGVTLHELLTYCDSDFSPMALFLKMGIPTHGQMTVTRLVNLTKEGKRLPCPPNCPDEVYQLMRKCWCFOPSNRITFQNLTI	1200
gi	114556987	ref	XP_001161295.1	ROYVHRDLAARNVLVESEHQVIGDFGLTKAETDKEYYTVKDDRDSPVFWYAPECLIQCKFYIASDVWSFGVTLHELLTYCDSDFSPMALFLKMGIPTHGQMTVTRLVNLTKEGKRLPCPPNCPDEVYQLMRKCWCFOPSNRITFQNLTI	1200
gi	73956132	ref	XP_865150.1	ROYVHRDLAARNVLVESEHQVIGDFGLTKAETDKEYYTVKDDRDSPVFWYAPECLIQCKFYIASDVWSFGVTLHELLTYCDSDFSPMALFLKMGIPTHGQMTVTRLVNLTKEGKRLPCPPNCPDEVYQLMRKCWCFOPSNRITFQNLTI	1200
gi	45382379	ref	NP_990201.1	ROYVHRDLAARNVLVESEHQVIGDFGLTKAETDKEYYTVKDDRDSPVFWYAPECLIQCKFYIASDVWSFGVTLHELLTYCDSDFSPMALFLKMGIPTHGQMTVTRLVNLTKEGKRLPCPPNCPDEVYQLMRKCWCFOPSNRITFQNLTI	1200
gi	56790256	ref	NP_571148.1	RNYIHRDLAARNVLVENEGTVKIGDFGLTKSIKDNEGYYTVKDDLDSPVFWYAPECLIHCKFYIASDVWSFGVTLHELLTYCDSDFSPMALFLKMGIPTHGQMTVTRLVNLTKEGKRLPCPPNCPDEVYQLMRKCWCFOPSNRITFQNLTI	1200



gi	111607496	ref	NP_666257.2	EGFEALLK--	1210
gi	109475184	ref	XP_342873.3	EGFEALLK--	1210
gi	102469034	ref	NP_002218.2	EGFEALLK--	1210
gi	114556987	ref	XP_001161295.1	EGFEALLK--	1210
gi	73956132	ref	XP_865150.1	EGFEALLK--	1210
gi	45382379	ref	NP_990201.1	EGFEIMSKM	1210
gi	56790256	ref	NP_571148.1	ANFQMLDNG	1210

