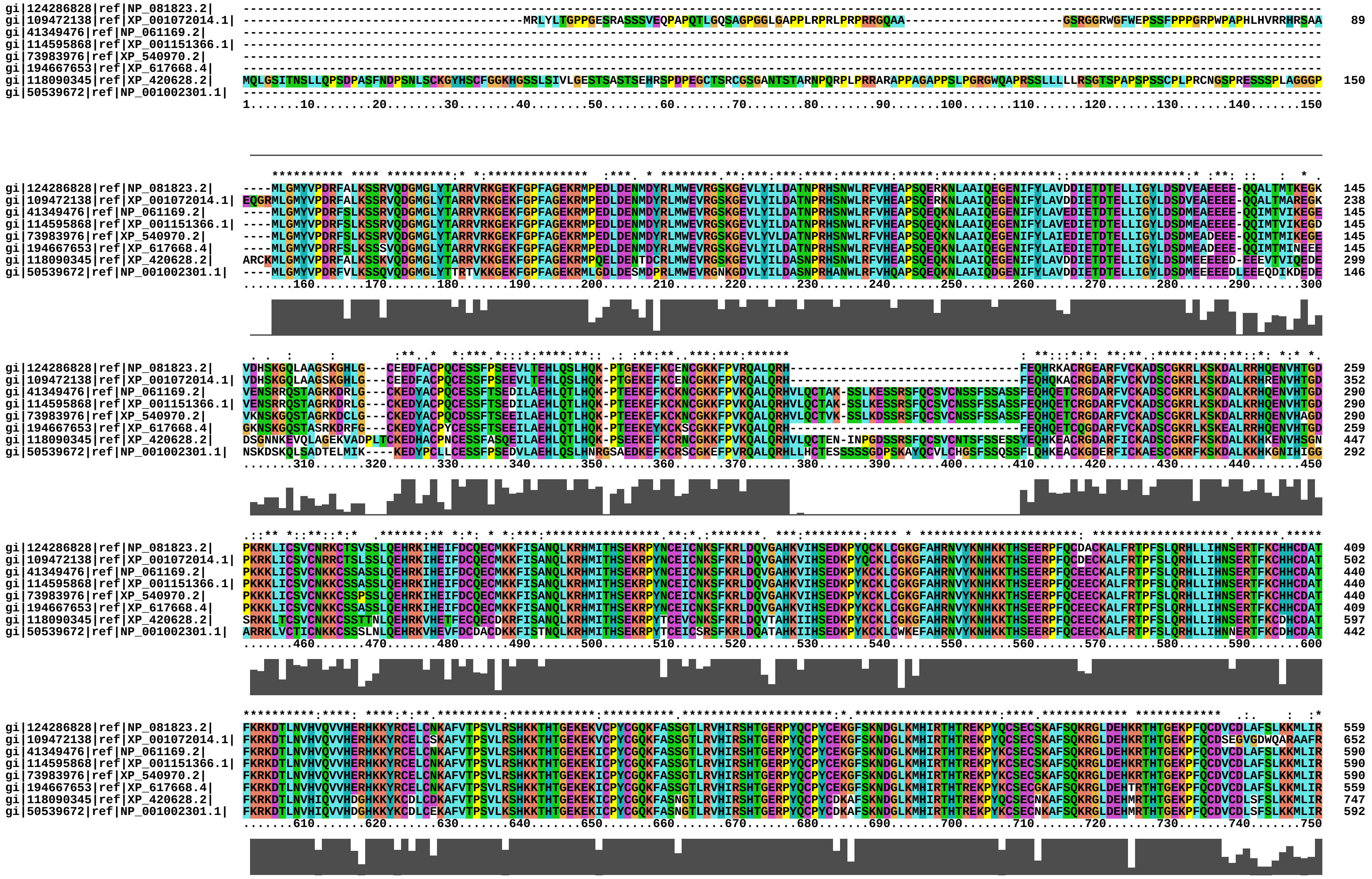

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gi|41349476|ref|NP_061169.2|     ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|114595868|ref|XP_001151366.1| ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|73983976|ref|XP_540970.2|     ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|194667653|ref|XP_617668.4|    ------------------------------------------------------------------------------------------------------------------------------------------------------
gi|118090345|ref|XP_420628.2|    MQLGSITNSLLQPSDPASFNDPSNLSCKGYHSCFGGKHGSSLSIVLGESTSASTSEHRSPDPEGCTSRCGSGANTSTARNPQRPLPRRARAPPAGAPPSLPGRGWQAPRSSLLLLLRSGTSPAPSPSSCPLPRCNGSPRESSSPLAGGGP   150
gi|50539672|ref|NP_001002301.1|  ------------------------------------------------------------------------------------------------------------------------------------------------------
                                 1.......10........20........30........40........50........60........70........80........90.......100.......110.......120.......130.......140.......150

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gi|41349476|ref|NP_061169.2|     ----MLGMYVPDRFSLKSSRVQDGMGLYTARRVRKGEKFGPFAGEKRMPEDLDENMDYRLMWEVRGSKGEVLYILDATNPRHSNWLRFVHEAPSQEQKNLAAIQEGENIFYLAVEDIETDTELLIGYLDSDMEAEEEE-QQIMTVIKEGE   145
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gi|73983976|ref|XP_540970.2|     ----MLGMYVPDRFSLKSSRVQDGMGLYTARRVRKGEKFGPFAGEKRMPEDLDENMDYRLMWEVRGSKGEVLYVLDATNPRHSNWLRFVHEAPSQEQKNLAAIQEGENIFYLAIEDIETDTELLIGYLDSDMEADEEE-QQIMTMIKEGE   145
gi|194667653|ref|XP_617668.4|    ----MLGMYVPDRFSLKSSSVQDGMGLYTARRVRKGEKFGPFAGEKRMPEDLDENMDYRLMWEVRGSKGEVLYILDATNPRHSNWLRFVHEAPSQEQKNLAAIQEGENIFYLAIEDIETDTELLIGYLDSDMEADEEE-QQIMTMINEEE   145
gi|118090345|ref|XP_420628.2|    ARCKMLGMYVPDRFALKSSKVQDGMGLYTARRVKKGEKFGPFAGEKRMPQELDENTDCRLMWEVRGSKGEVLYILDASNPRHSNWLRFVHEAPSQEQKNLAAIQEGENIFYLAVDDIETDTELLIGYLDSDMEEEEED-EEEVTVIQEDE   299
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gi|124286828|ref|NP_081823.2|    VDHSKGQLAAGSKGHLG---CEEDFACPQCESSFPSEEVLTEHLQSLHQK-PTGEKEFKCENCGKKFPVRQALQRH--------------------------------FEQHRKACRGEARFVCKADSCGKRLKSKDALRRHQENVHTGD   259
gi|109472138|ref|XP_001072014.1| VDHSKGQLAAGSKGHLG---CEEDFACPQCESSFPSEEVLTEHLQSLHQK-PTGEKEFKCENCGKKFPVRQALQRH--------------------------------FEQHQKACRGDARFVCKVDSCGKRLKSKDALKRHRENVHTGD   352
gi|41349476|ref|NP_061169.2|     VENSRRQSTAGRKDRLG---CKEDYACPQCESSFTSEDILAEHLQTLHQK-PTEEKEFKCKNCGKKFPVKQALQRHVLQCTAK-SSLKESSRSFQCSVCNSSFSSASSFEQHQETCRGDARFVCKADSCGKRLKSKDALKRHQENVHTGD   290
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gi|73983976|ref|XP_540970.2|     VKNSKGQSTAGRKDCLG---CKEDYACPQCDSSFTSEEILAEHLQTLHQK-PTEEKEFKCKNCGKKFPVKQALQRHVLQCTVK-SSLKDSSRSFQCSVCNSSFSSASSFEQHQETCRGDARFVCKADSCGKRLKSKDALRRHQENVHAGD   290
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gi|118090345|ref|XP_420628.2|    DSGNNKEVQLAGEKVADPLTCKEDHACPNCESSFASQEILAEHLQTLHQK-PSEEKEFKCRNCGKKFPVKQALQRHVLQCTEN-INPGDSSRSFQCSVCNTSFSSESSYEQHKEACRGDARFICKADSCGKRFKSKDALKKHKENVHSGN   447
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gi|109472138|ref|XP_001072014.1| PKRKLICSVCNRRCTSLSSLQEHRKIHEIFDCQECMKKFISANQLKRHMITHSEKRPYNCEICNKSFKRLDQVGAHKVIHSEDKPYQCKLCGKGFAHRNVYKNHKKTHSEERPFQCDECKALFRTPFSLQRHLLIHNSERTFKCHHCDAT   502
gi|41349476|ref|NP_061169.2|     PKKKLICSVCNKKCSSASSLQEHRKIHEIFDCQECMKKFISANQLKRHMITHSEKRPYNCEICNKSFKRLDQVGAHKVIHSEDKPYKCKLCGKGFAHRNVYKNHKKTHSEERPFQCEECKALFRTPFSLQRHLLIHNSERTFKCHHCDAT   440
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gi|73983976|ref|XP_540970.2|     PKKKLICSVCNKKCSSPSSLQEHRKIHEIFDCQECMKKFISANQLKRHMITHSEKRPYNCEICNKSFKRLDQVGAHKVIHSEDKPYKCKLCGKGFAHRNVYKNHKKTHSEERPFQCEECKALFRTPFSLQRHLLIHNSERTFKCHHCDAT   440
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gi|50539672|ref|NP_001002301.1|  ARRKLVCTICNKKCSSSLNLQEHRKVHEVFDCDACDKKFISTNQLKRHMITHSEKRPYTCEICSRSFKRLDQATAHKIIHSEDKPYKCKLCWKEFAHRNVYKNHKKTHSEERPFQCEECKALFRTPFSLQRHLLIHNNERTFKCDHCDAT   442
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gi|109472138|ref|XP_001072014.1| FKRKDTLNVHVQVVHERHKKYRCELCSKAFVTPSVLRSHKKTHTGEKEKVCPYCGQKFASSGTLRVHIRSHTGERPYQCPYCEKGFSKNDGLKMHIRTHTREKPYQCSECSKAFSQKRGLDEHKRTHTGEKPFQCDSEGVGDWQARAAFR   652
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gi|114595868|ref|XP_001151366.1| FKRKDTLNVHVQVVHERHKKYRCELCNKAFVTPSVLRSHKKTHTGEKEKICPYCGQKFASSGTLRVHIRSHTGERPYQCPYCEKGFSKNDGLKMHIRTHTREKPYKCSECSKAFSQKRGLDEHKRTHTGEKPFQCDVCDLAFSLKKMLIR   590
gi|73983976|ref|XP_540970.2|     FKRKDTLNVHVQVVHERHKKYRCELCNKAFVTPSVLRSHKKTHTGEKEKICPYCGQKFASSGTLRVHIRSHTGERPYQCPYCEKGFSKNDGLKMHIRTHTREKPYKCSECSKAFSQKRGLDEHKRTHTGEKPFQCDVCDLAFSLKKMLIR   590
gi|194667653|ref|XP_617668.4|    FKRKDTLNVHVQVVHERHKKYRCELCNKAFVTPSVLRSHKKTHTGEKEKICPYCGQKFASSGTLRVHIRSHTGERPYQCPYCEKGFSKNDGLKMHIRTHTREKPYKCSECGKAFSQKRGLDEHTRTHTGEKPFQCDVCDLAFSLKKMLIR   559
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gi|50539672|ref|NP_001002301.1|  FKRKDTLNVHIQVVHDGHKKYKCDLCEKAFVTPSVLKSHKKTHTGEKEKICPYCGQKFASNGTLRVHIRSHTGERPYQCPYCDKAFSKNDGLKMHIRTHTREKPYKCSECNKAFSQKRGLDEHMRTHTGEKPFQCDVCDLSFSLKKMLIR   592
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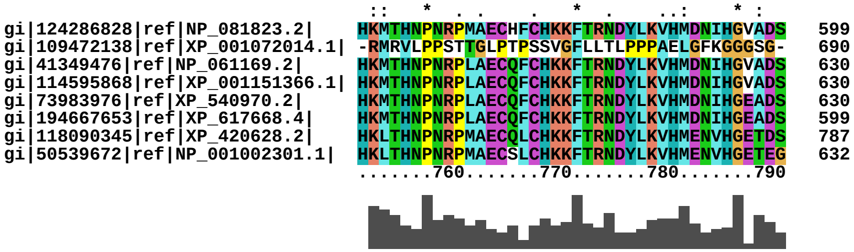

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gi|73983976|ref|XP_540970.2|         HKMTHNPNRPLAECQFCHKKFTRNDYLKVHMDNIHGEADS   630
gi|194667653|ref|XP_617668.4|        HKMTHNPNRPLAECQFCHKKFTRNDYLKVHMDNIHGEADS   599
gi|118090345|ref|XP_420628.2|        HKLTHNPNRPMAECQLCHKKFTRNDYLKVHMENVHGETDS   787
gi|50539672|ref|NP_001002301.1|      HKLTHNPNRPMAECSLCHKKFTRNDYLKVHMENVHGETEG   632
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