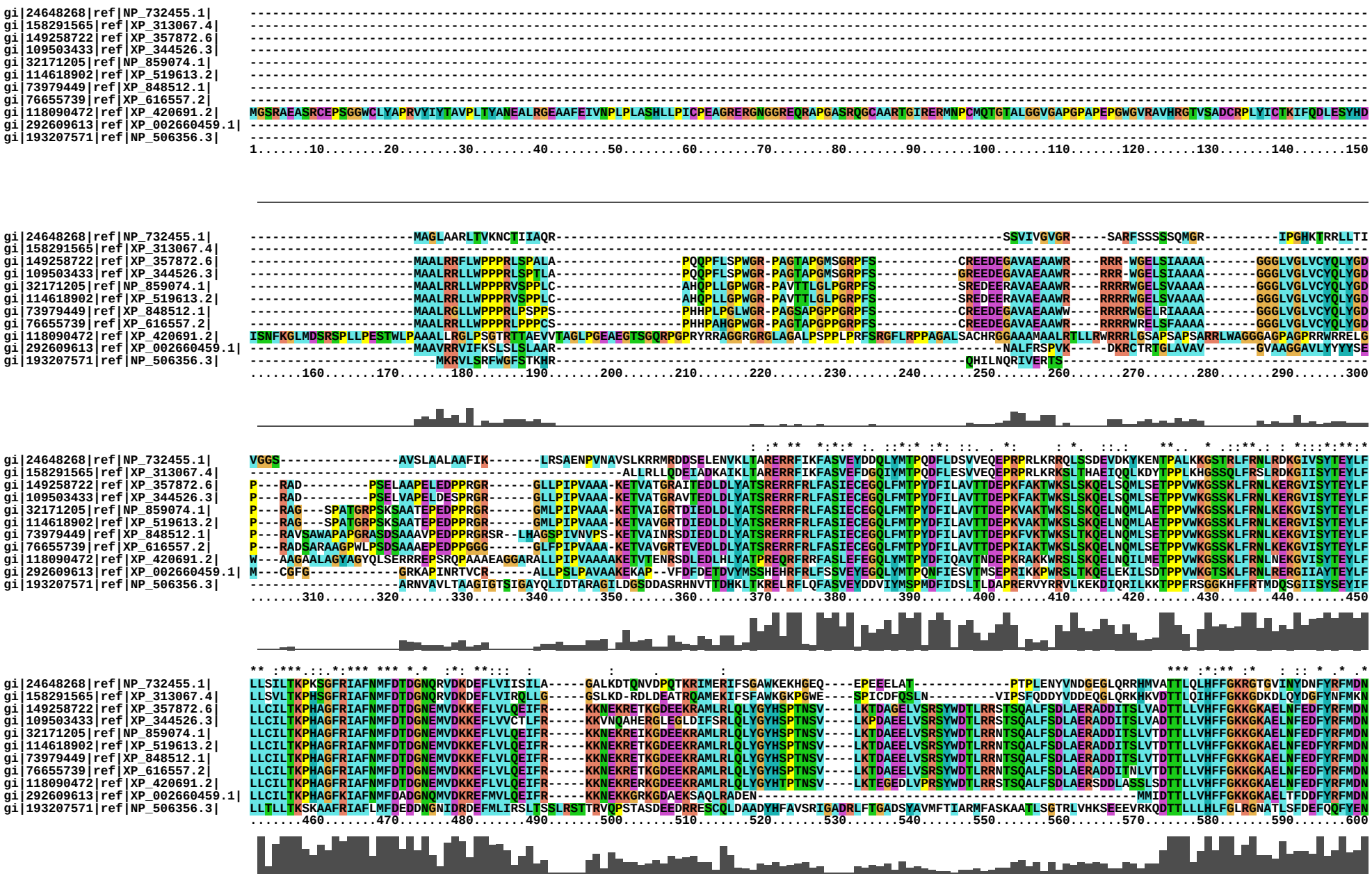
gi|24648268|ref|NP_732455.1|
gi|158291565|ref|XP_313067.4|
gi|149258722|ref|XP_357872.6|
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gi|32171205|ref|NP_859074.1|
gi|114618902|ref|XP_519613.2|
gi|73979449|ref|XP_848512.1|
gi|76655739|ref|XP_616557.2|
gi|118090472|ref|XP_420691.2|
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1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130.....140.....150
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PQQPFLSPWGR-PAGTAPGMSGRPFS
CREEDEGAVAEAAWR
RRR-WGELSIAAAA
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PQQPFLSPWGR-PAGTAPGMSGRPFS
GREEDEGAVAEAAWR
RRR-WGELSIAAAA
GGGLVGLVCYQLYGD
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ALLRLLQDEIADKAIKLTARERRFIKFASVEFDGQIYMTPQDFLESVVEQEPRPRLKRKSLTHAEIQQLKDYTPPLKHGSSQLFRSLRDKGIISYTEYLF
P---RAD
PSELAAPELEDPPRGR
GLLPIPVAAA-KETVATGRAITEDLDLYATSRERRFRLFASIECEGQLFMTPYDFILAVTTDEPKFAKTWKSLSKQELSQMLSETPPVWKGSSKLFRNLKERGVISYTEYLF
P---RAD
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P---RAG---SPATGRPSKSAATEPEDPPRGR
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P---RAVSAWAPAPGRASDSAAAVPEDPPRGRSR--LHAGSPIVNVPS-KETVAINRSDIEDLDLYATSRERRFRLFASIECEGQLFMTPYDFILAVTTDEPKFVKTWKSLTKQELNQMLSETPPVWKGSSKLFRNLKEKGVISYTEYLF
P---RADSARAAGPWLPSDSAAAEPEDPPGGG
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W---AAGAALAGYAGYQLSERRREPSRQPAAAEAGGARALLPIPVAAAAKETVTENRSDLEDLHLYATPREQRFRRFASLEFEGQLYMTPYDFIQAVTNDEPKRAKKWRSLSKQELNQILMETPPVWKGSSKLFRNLNEKGVISYTEYLF
M---CGFG
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ALLPSLPAVAAKEKAP--VFDFDETDVYMSSHEHRFRLFSSVEYEGQLYMTPQNFIESVTMSEPRIKKPWRSLTKQELEKILSDTPPVWKGTSKLFRNLRERGIIAYTEYLF
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.....310.....320.....330.....340.....350.....360.....370.....380.....390.....400.....410.....420.....430.....440.....450
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.....460.....470.....480.....490.....500.....510.....520.....530.....540.....550.....560.....570.....580.....590.....600

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gi|24648268|ref|NP_732455.1|     LQTEVLELEFHEFSKGNSVISELDFAKILLRYTYLATDEYDVFLERLLERVKD-EKGISFHDFRDFCHFLNNLDDFTIAMRMYTLADRAISKDEFSRAVKICTGYKLSPHLIDTVFAIFDADGDGLLSYKEFIAIMKDRLHRGFKS----   750
gi|158291565|ref|XP_313067.4|    LQTEVLELEFCEFSKGHERISEVDFAKILLRYTYLDTDEYDNYLDRLLDREAK-EKGVSFDEFRQFCQFLNNLDDFSIAMRMYTLADQPISKDEFSRAVKICTGSELNSHLIDTVFAIFDEDGDGLLSYKEFIAIMKDRVHRGFKVSHYE   750
gi|149258722|ref|XP_357872.6|    LQTEVLEIEFLSYSNGMNTISEEDFAHILLRYT--NVENTSVFLENVRYSISE-EKGITFDEFRSFFQFLNNLEDFAIALNMYNFASRSIGQDEFKRAVYVATGLKLSPHLVNTVFKIFDVDKDDQLSYKEFIGIMKDRLHRGFRG----   750
gi|109503433|ref|XP_344526.3|    LQTEVLEIEFLSYSNGMNTISEEDFAHILLRYT--NVENTSVFLENVRYSIPE-EKGITFDEFRSFFQFLNNLEDFAIALNMYNFASRSIGQDEFKRAVYVATGLKLSPHLVNTVFKIFDVDKDDQLSYKEFIGIMKDRLHRGFRG----   750
gi|32171205|ref|NP_859074.1|     LQTEVLEIEFLSYSNGMNTISEEDFAHILLRYT--NVENTSVFLENVRYSIPE-EKGITFDEFRSFFQFLNNLEDFAIALNMYNFASRSIGQDEFKRAVYVATGLKFSPHLVNTVFKIFDVDKDDQLSYKEFIGIMKDRLHRGFRG----   750
gi|114618902|ref|XP_519613.2|    LQTEVLEIEFLSYSNGMNTISEEDFAHILLRYT--NVENTSVFLENVRYSIPE-EKGITFDEFRSFFQFLNNLEDFAIALNMYNFASRSIGQDEFKRAVYVATGLKFSPHLVNTVFKIFDVDKDDQLSYKEFIGIMKDRLHRGFRG----   750
gi|73979449|ref|XP_848512.1|     LQTEVLEIEFLSYSNGMNTISEEDFAHILLRYT--NVENTSVFLENVRYSIPE-EKGITFDEFRSFFQFLNNLEDFAIALNMYNFASRSIGQDEFKRAVYVATGLKLSPHLVNTVFKIFDVDKDDQLSYKEFIGIMKDRLHRGFRG----   750
gi|76655739|ref|XP_616557.2|     LQTEVLEIEFLSYSNGMNTISEEDFAHILLRYT--NVENTSVFLENVRYSIPE-EKGITFDEFRSFFQFLNNLEDFAIALNMYNFASRSIGQDEFKRAVYVATGLKLSPHLVNTVFKIFDVDKDDQLSYKEFIGIMKDRLHRGFRG----   750
gi|118090472|ref|XP_420691.2|    LQTEVLEIEFLSYSNGMNTISEEDFAHILLRYT--NVENTSSYLENMRCRIPE-EKGITFDEFRSFFQFLNNLEDFTIAMQMYNFASRSIGQDEFKRAVYVATGVKLSPHLVNTVFKIFDVDRDDQLSYKEFIGIMKDRLNRGFRG----   750
gi|292609613|ref|XP_002660459.1| LQTEMLEIEFLTYSKGMTTISEEDFARILLRYT--NVEDIRSYLENVRHAYLT-RRGSP----------------DVVFSMPDCSLLALSQSHLR---------------------------------DLFVLRVSGLWAPFEQ----   750
gi|193207571|ref|NP_506356.3|    LQEELMEIEFYEFARGKTAISPVDFARLILRYSIVNFDDYHKYLQRVQEKSDDDEPGISLSQWATFSRFLNNLAEFQSAVRLYVNSNVPVSEPEFARAVGCTIGKELDPVVVSMIFRIFDENNDGTLSYPEFLAVMSDRLHRGLRG----   750
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gi|158291565|ref|XP_313067.4|    HIVEDYLDDIEKGTVYADNFRQLLKMRSRACRRLRRYLLYFYYH   794
gi|149258722|ref|XP_357872.6|    ------YKTVQKYPTFKSCLKKELHSR-----------------   794
gi|109503433|ref|XP_344526.3|    ------YKTVQKYPTFKSCLKKELHSR-----------------   794
gi|32171205|ref|NP_859074.1|     ------YKTVQKYPTFKSCLKKELHSR-----------------   794
gi|114618902|ref|XP_519613.2|    ------YKTVQKYPTFKSCLKKELHSR-----------------   794
gi|73979449|ref|XP_848512.1|     ------YKTVQKYPTFKSCLKKELHSR-----------------   794
gi|76655739|ref|XP_616557.2|     ------YKTVQKYPTFKSCLKKELHSR-----------------   794
gi|118090472|ref|XP_420691.2|    ------YKPIQRYTTFKSCVRKELYSR-----------------   794
gi|292609613|ref|XP_002660459.1| ------FVHLARMTSPSSPIPTE---------------------   794
gi|193207571|ref|NP_506356.3|    -----RLEKPWGWKPFKNCVISEVSRA-----------------   794
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