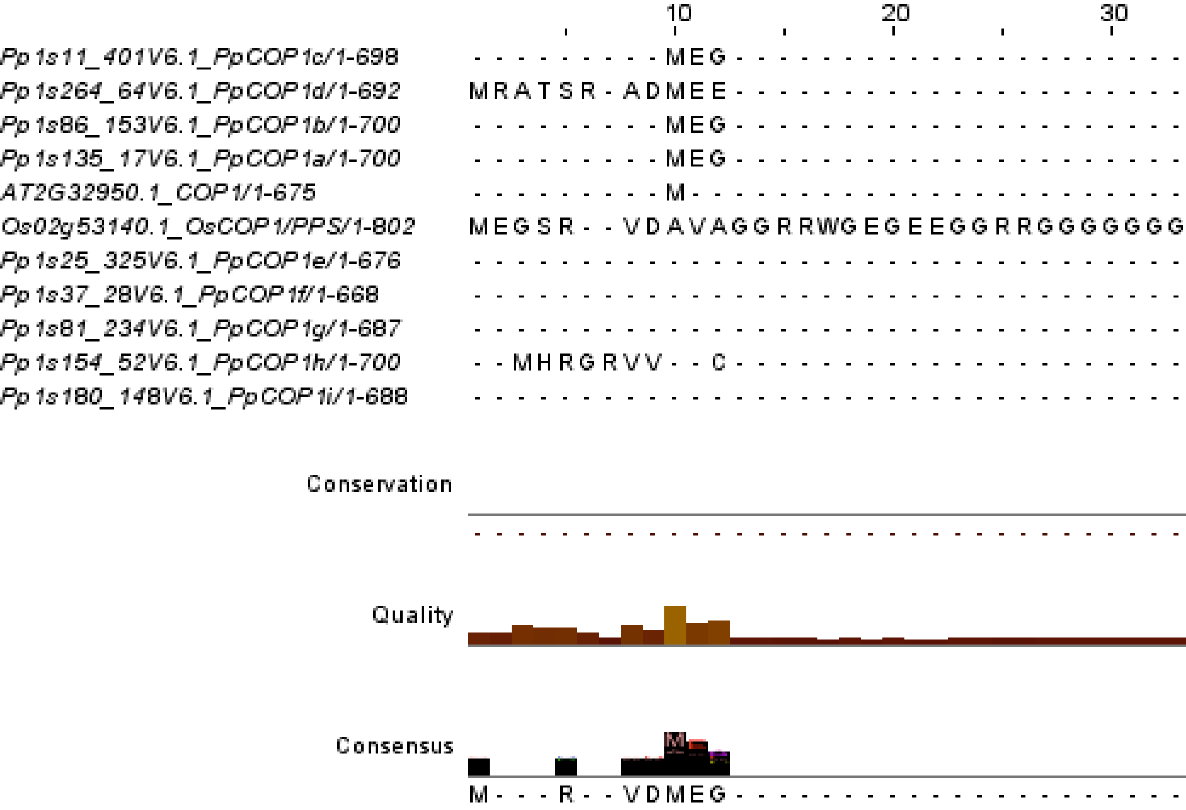

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Pp1s86_153V6.1_PpCOP1b/1-700      ---------MEG---------------------
Pp1s135_17V6.1_PpCOP1a/1-700      ---------MEG---------------------
AT2G32950.1_COP1/1-675            ---------M-----------------------
Os02g53140.1_OsCOP1/PPS/1-802     MEGSR--VDAVAGGRRWGEGEEGGRRGGGGGGG
Pp1s25_325V6.1_PpCOP1e/1-676      ---------------------------------
Pp1s37_28V6.1_PpCOP1f/1-668       ---------------------------------
Pp1s81_234V6.1_PpCOP1g/1-687      ---------------------------------
Pp1s154_52V6.1_PpCOP1h/1-700      --MHRGRVV--C---------------------
Pp1s180_148V6.1_PpCOP1i/1-688     ---------------------------------

Conservation                      ---------------------------------

Quality

Consensus                         M---R--VDMEG---------------------
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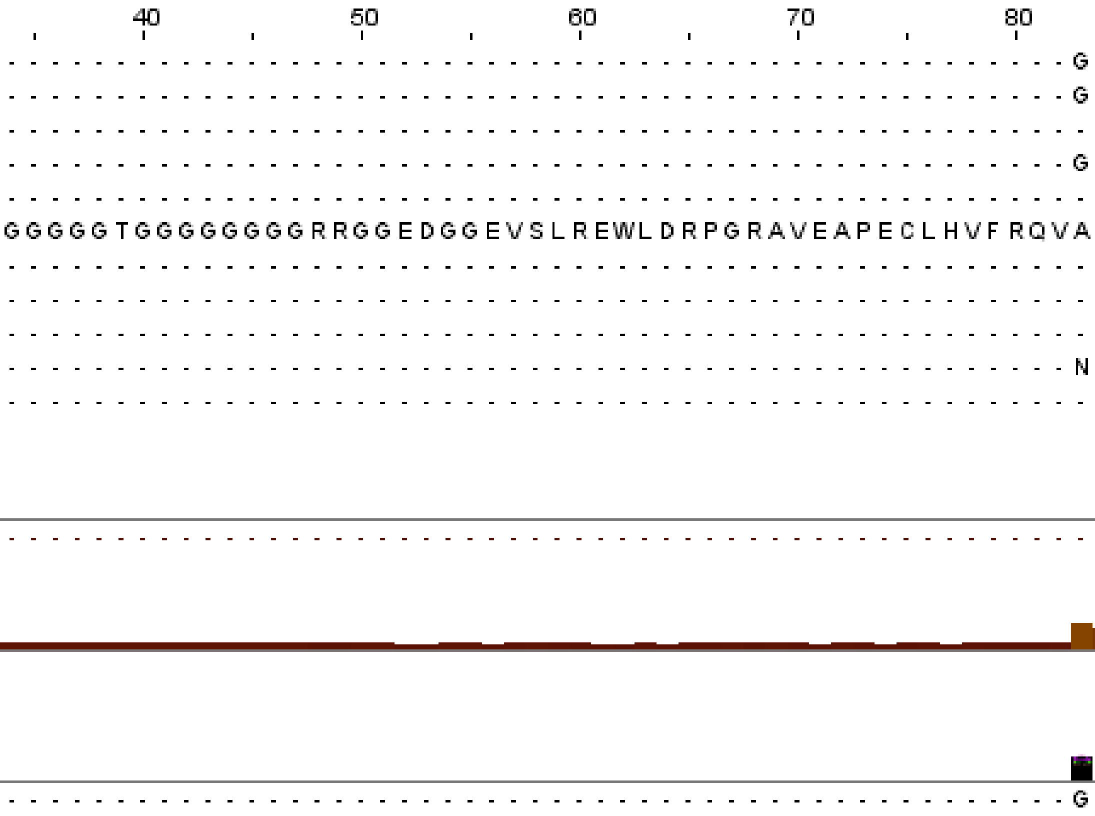

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-------------------------------------------------G
-------------------------------------------------G
--------------------------------------------------
-------------------------------------------------G
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--------------------------------------------------
--------------------------------------------------
-------------------------------------------------N
--------------------------------------------------
--------------------------------------------------
-------------------------------------------------G
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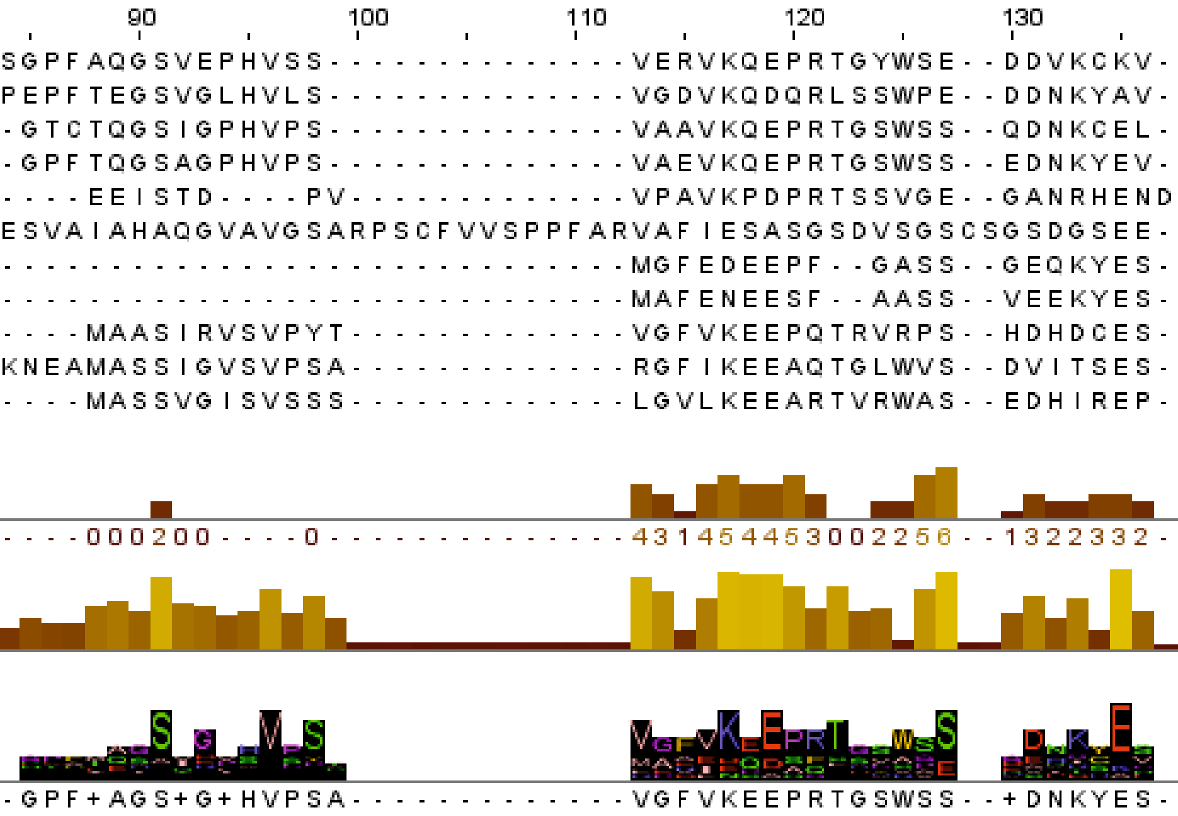
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PEPFTEGSVGLHVLS--------------VGDVKQDQRLSSWPE--DDNKYAV-
-GTCTQGSIGPHVPS--------------VAAVKQEPRTGSWSS--QDNKCEL-
-GPFTQGSAGPHVPS--------------VAEVKQEPRTGSWSS--EDNKYEV-
----EEISTD----PV-------------VPAVKPDPRTSSVGE--GANRHEND
ESVAIAHAQGVAVGSARPSCFVVSPPFARVAFIESASGSDVSGSCSGSDGSEE-
-----------------------------MGFEDEEPF--GASS--GEQKYES-
-----------------------------MAFENEESF--AASS--VEEKYES-
----MAASIRVSVPYT-------------VGFVKEEPQTRVRPS--HDHDCES-
KNEAMASSIGVSVPSA-------------RGFIKEEAQTGLWVS--DVITSES-
----MASSVGISVSSS-------------LGVLKEEARTVRWAS--EDHIREP-

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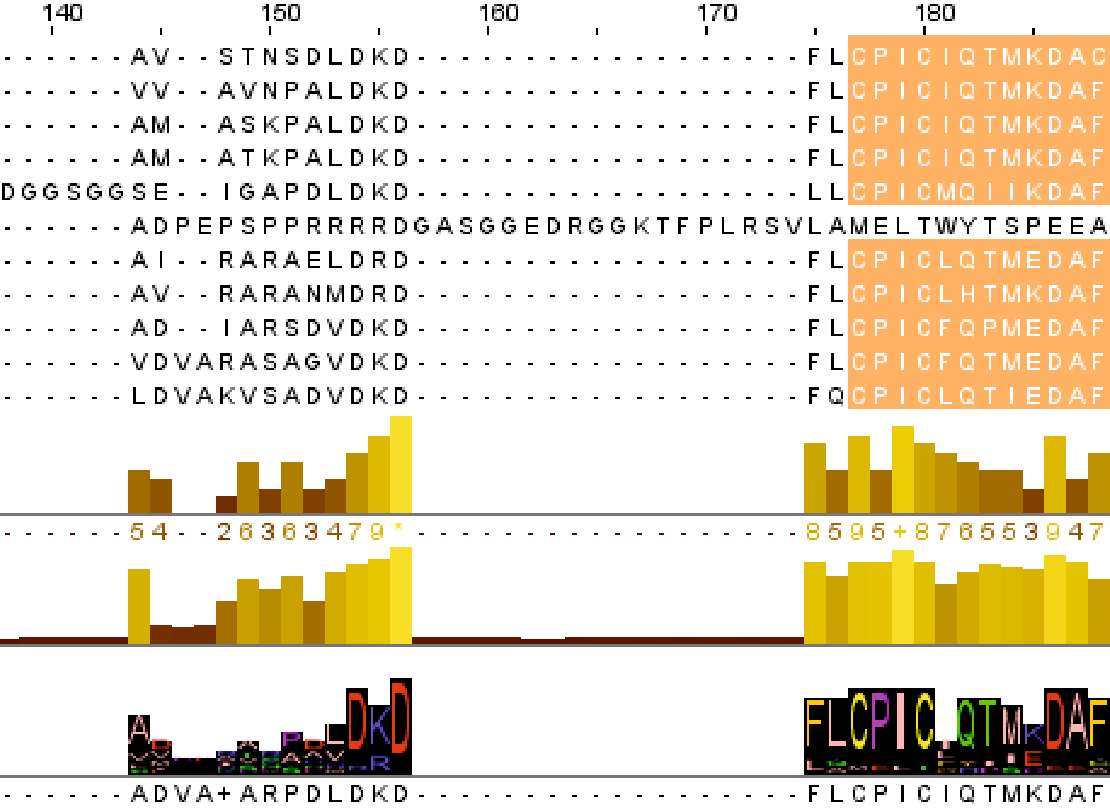
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-------VV--AVNPALDKD------------------FLCPICIQTMKDAF
-------AM--ASKPALDKD------------------FLCPICIQTMKDAF
-------AM--ATKPALDKD------------------FLCPICIQTMKDAF
DGGSGGSE--IGAPDLDKD------------------LLCPICMQIIKDAF
-------ADPEPSPPRRRRDGASGGEDRGGKTFPLRSVLAMELTWYTSPEEA
-------AI--RARAELDRD------------------FLCPICLQTMEDAF
-------AV--RARANMDRD------------------FLCPICLHTMKDAF
-------AD--IARSDVDKD------------------FLCPICFQPMEDAF
-------VDVARASAGVDKD------------------FLCPICFQTMEDAF
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-------ADVA+ARPDLDKD------------------FLCPICIQTMKDAF
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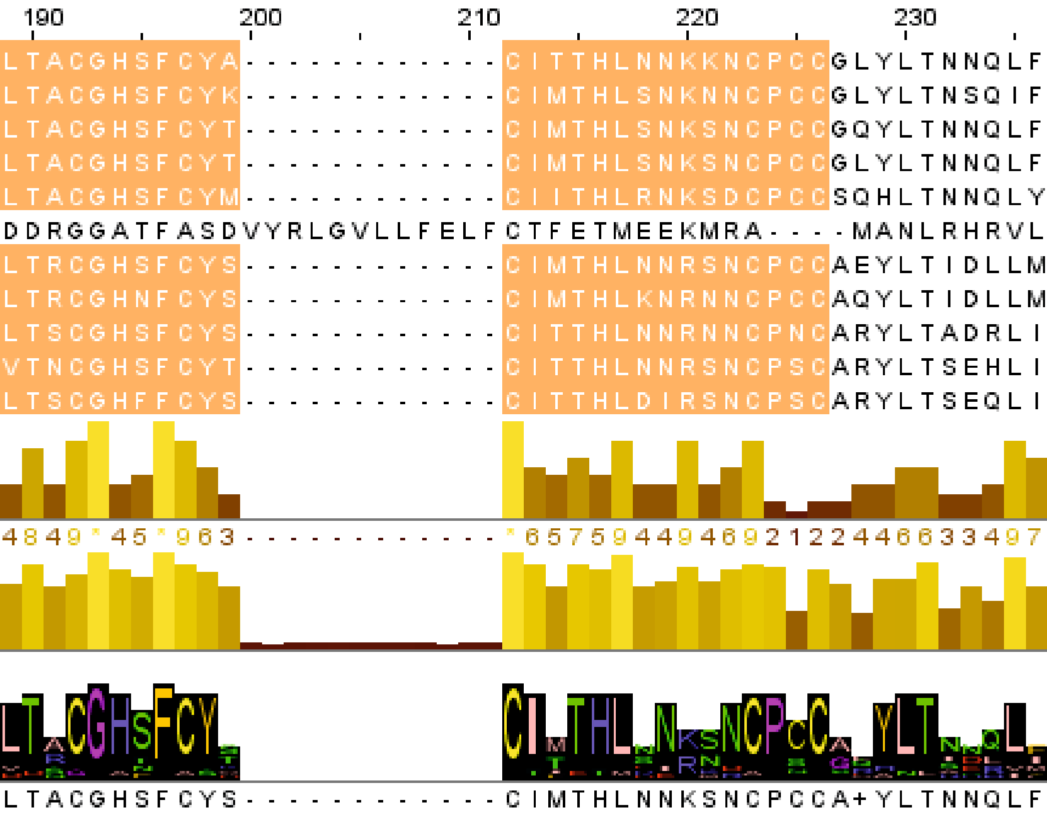
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LTACGHSFCYM------------CIITHLRNKSDCPCCSQHLTNNQLY
DDRGGATFASDVYRLGVLLFELFCTFETMEEKMRA----MANLRHRVL
LTRCGHSFCYS------------CIMTHLNNRSNCPCCAEYLTIDLLM
LTRCGHNFCYS------------CIMTHLKNRNNCPCCAQYLTIDLLM
LTSCGHSFCYS------------CITTHLNNRNNCPNCARYLTADRLI
VTNCGHSFCYT------------CITTHLNNRSNCPSCARYLTSEHLI
LTSCGHFFCYS------------CITTHLDIRSNCPSCARYLTSEQLI
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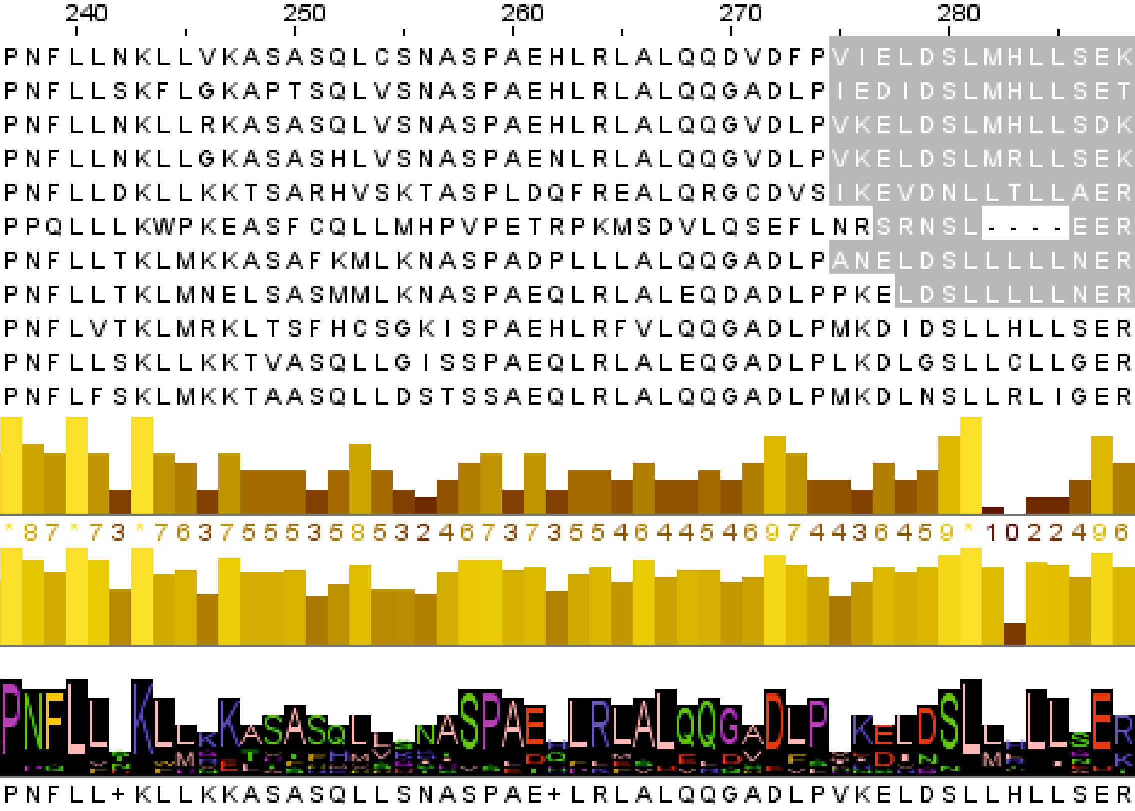
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PNFLLDKLLKKTSARHVSKTASPLDQFREALQRGCDVSIKEVDNLLTLLAER
PPQLLLKWPKEASFCQLLMHPVPETRPKMSDVLQSEFLNRSRNSL----EER
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PNFLLTKLMNELSASMMLKNASPAEQLRLALEQDADLPPKELDSLLLLLNER
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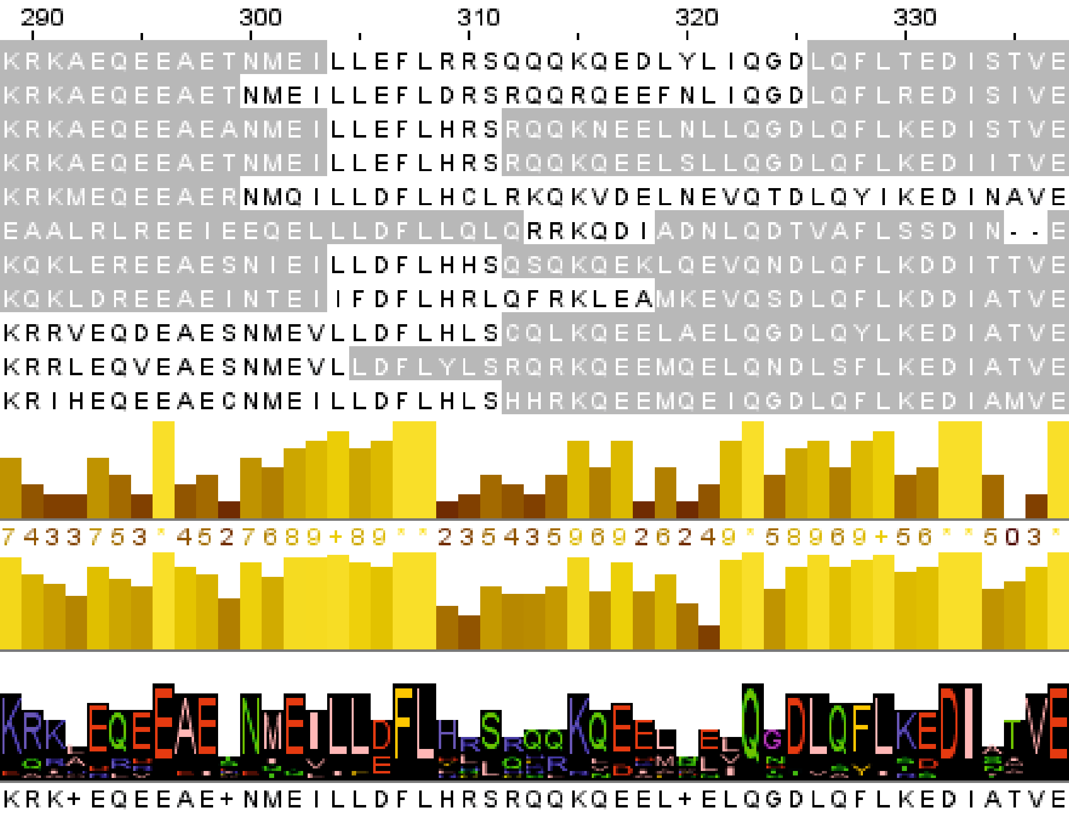
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KRKMEQEEAERNMQILLDFLHCLRKQKVDELNEVQTDLQYIKEDINAVE
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KQKLEREEAESNIEILLDFLHHSQSQKQEKLQEVQNDLQFLKDDITTVE
KQKLDREEAEINTEIIFDFLHRLQFRKLEAMKEVQSDLQFLKDDIATVE
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7433753*4527689+89**23543596926249*58969+56**503*

KRK+EQEEAE+NMEILLDFLHRSRQQKQEEL+ELQGDLQFLKEDIATVE
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KQRQDLLHITEKNALKIRMIAGGPSSSRPDTLATNENTSKGEAT
KQRQDLLRAKEKYALKIRMIGDGPSTSMPDTLAACEKTSKSGVT
RHRIDLYRARDRYSVKLRMLGDDPSTRNAWPHEKNQIGFNSNSL
AHQQSALGQCGNFSFEL-----------------DKEVCSETVE
RRLRWLLLSKDRHSKRVR--EESPFSDL-DTHTRSDDASTGGAV
RRLRCLLASNKSHSKRVC--EESPLSDL-DIHTEYGSTSTGGAV
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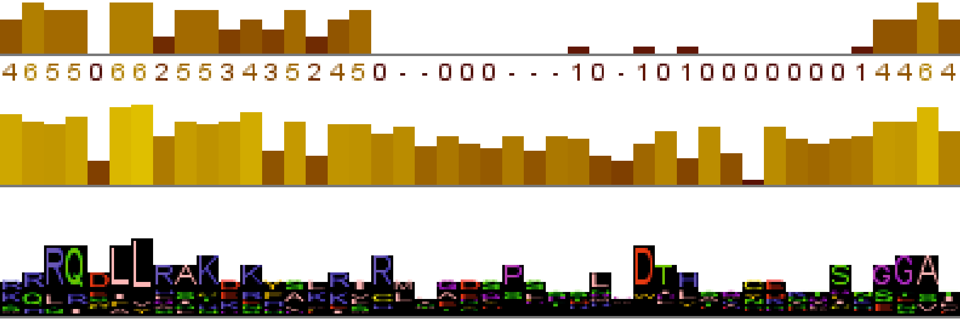

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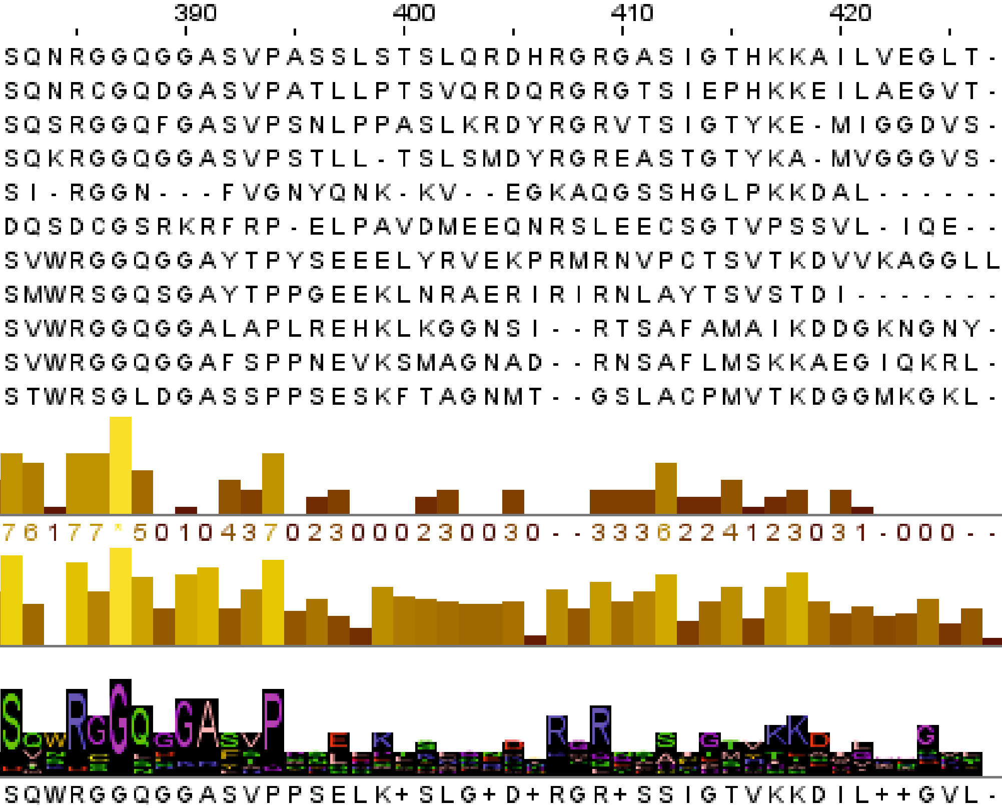
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SQKRGGQGGASVPSTLL-TSLSMDYRGREASTGTYKA-MVGGGVS-
SI-RGGN---FVGNYQNK-KV--EGKAQGSSHGLPKKDAL------
DQSDCGSRKRFRP-ELPAVDMEEQNRSLEECSGTVPSSVL-IQE--
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SMWRSGQSGAYTPPGEEKLNRAERIRIRNLAYTSVSTDI-------
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SVWRGGQGGAFSPPNEVKSMAGNAD--RNSAFLMSKKAEGIQKRL-
STWRSGLDGASSPPSESKFTAGNMT--GSLACPMVTKDGGMKGKL-
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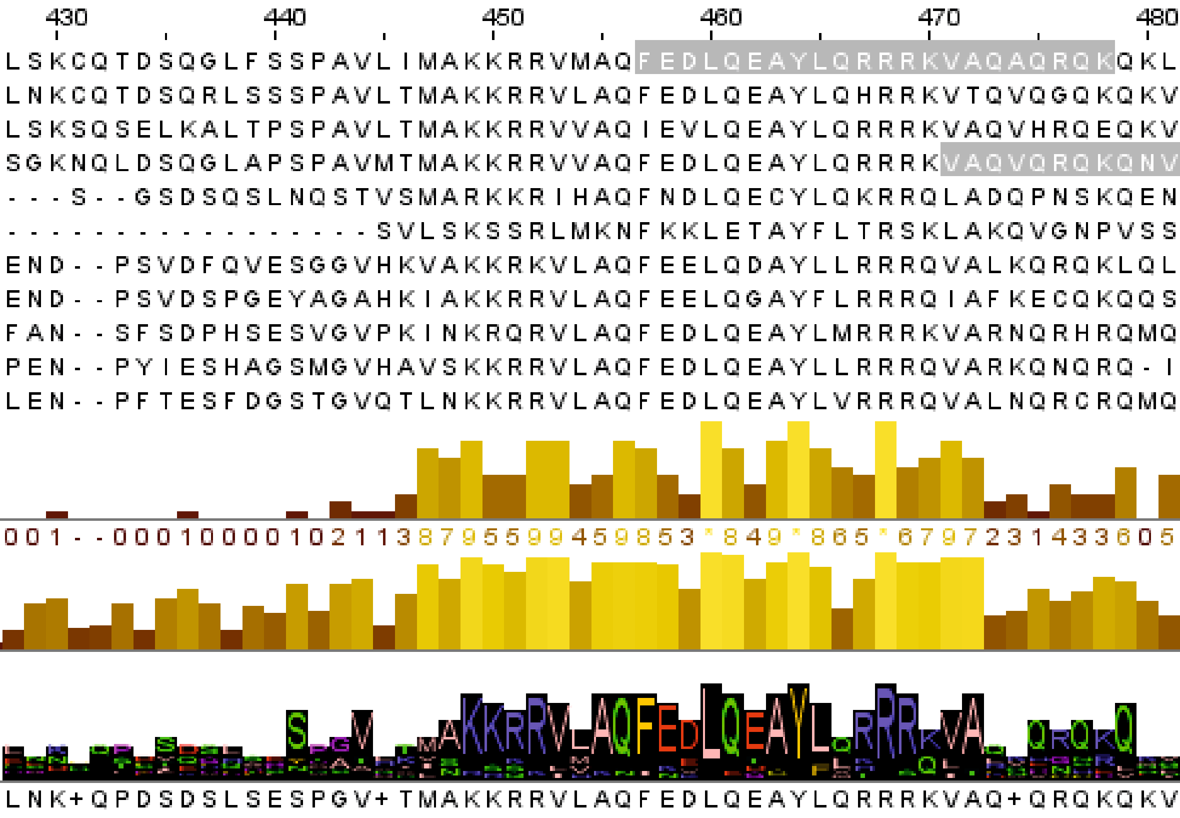
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---S--GSDSQSLNQSTVSMARKKRIHAQFNDLQECYLQKRRQLADQPNSKQEN
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END--PSVDFQVESGGVHKVAKKRKVLAQFEELQDAYLLRRRQVALKQRQKLQL
END--PSVDSPGEYAGAHKIAKKRRVLAQFEELQGAYFLRRRQIAFKECQKQQS
FAN--SFSDPHSESVGVPKINKRQRVLAQFEDLQEAYLMRRRKVARNQRHRQMQ
PEN--PYIESHAGSMGVHAVSKKRRVLAQFEDLQEAYLLRRRQVARKQNQRQ-I
LEN--PFTESFDGSTGVQTLNKKRRVLAQFEDLQEAYLVRRRQVALNQRCRQMQ

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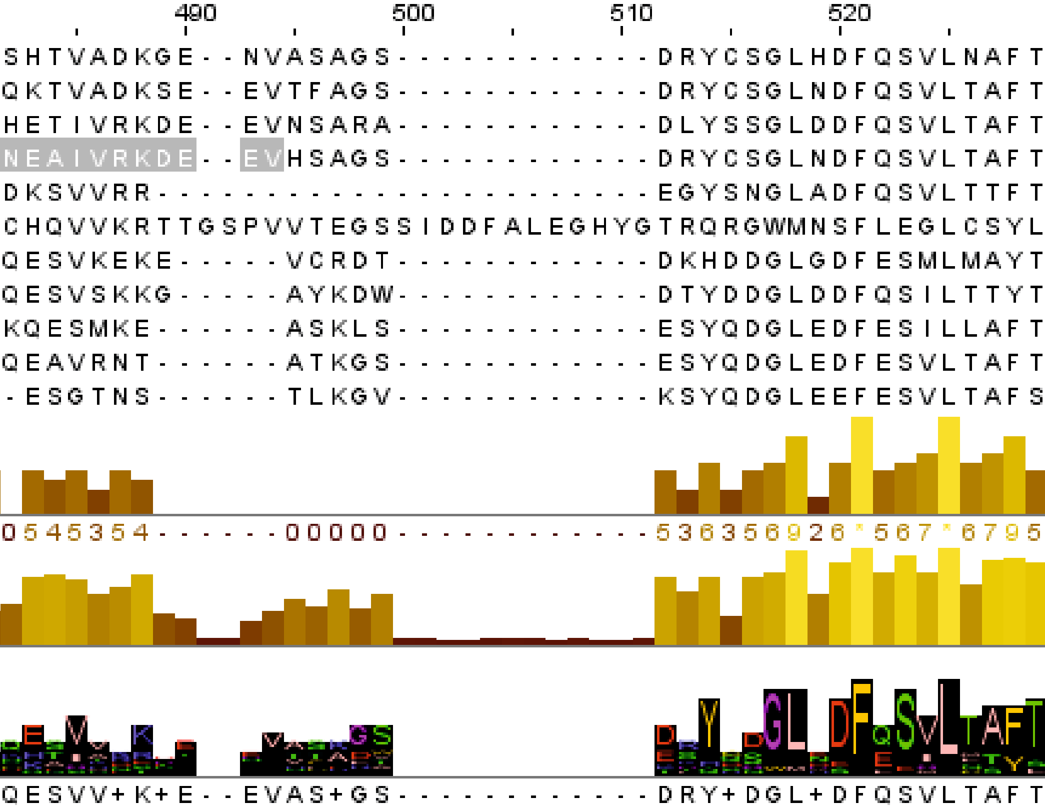

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HETIVRKDE--EVNSARA------------DLYSSGLDDFQSVLTAFT
NEAIVRKDE--EVHSAGS------------DRYCSGLNDFQSVLTAFT
DKSVVRR-----------------------EGYSNGLADFQSVLTTFT
CHQVVKRTTGSPVVTEGSSIDDFALEGHYGTRQRGWMNSFLEGLCSYL
QESVKEKE-----VCRDT------------DKHDDGLGDFESMLMAYT
QESVSKKG-----AYKDW------------DTYDDGLDDFQSILTTYT
KQESMKE------ASKLS------------ESYQDGLEDFESILLAFT
QEAVRNT------ATKGS------------ESYQDGLEDFESVLTAFT
-ESGTNS------TLKGV------------KSYQDGLEEFESVLTAFS
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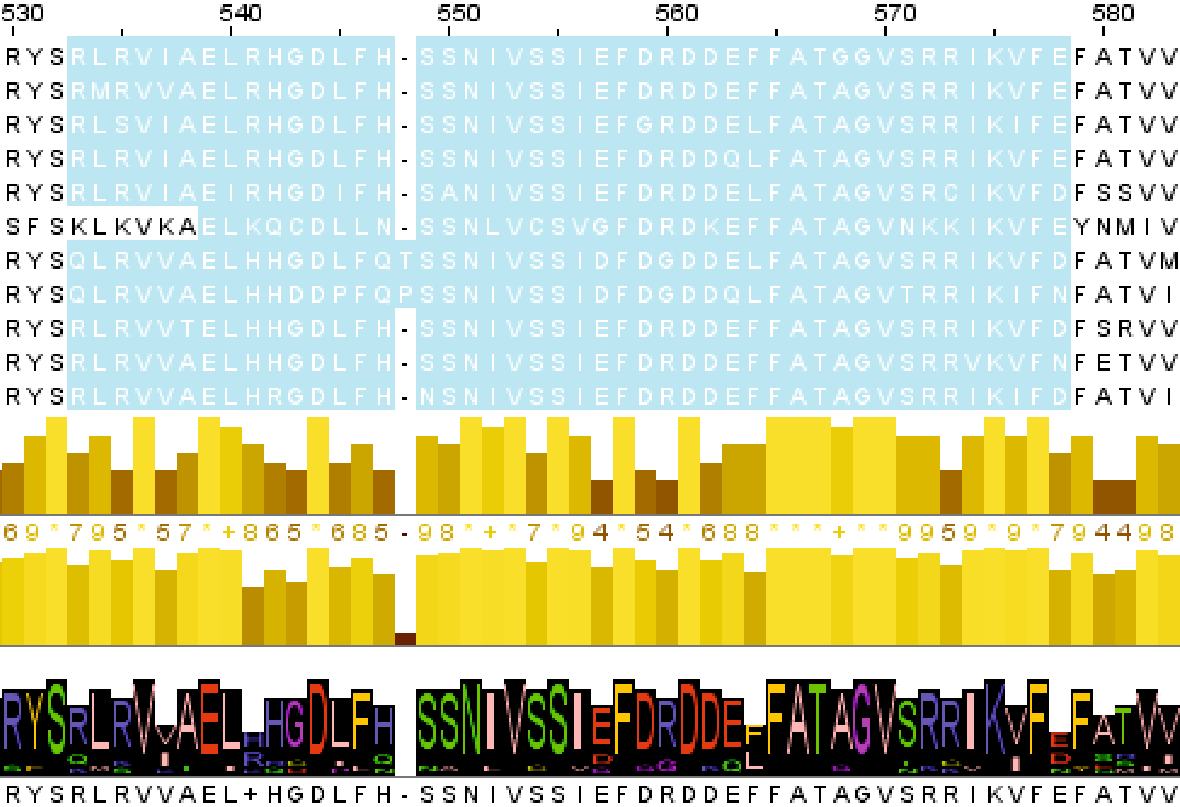
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69*795*57*+865*685-98*+*7*94*54*688***+**9959*9*794498
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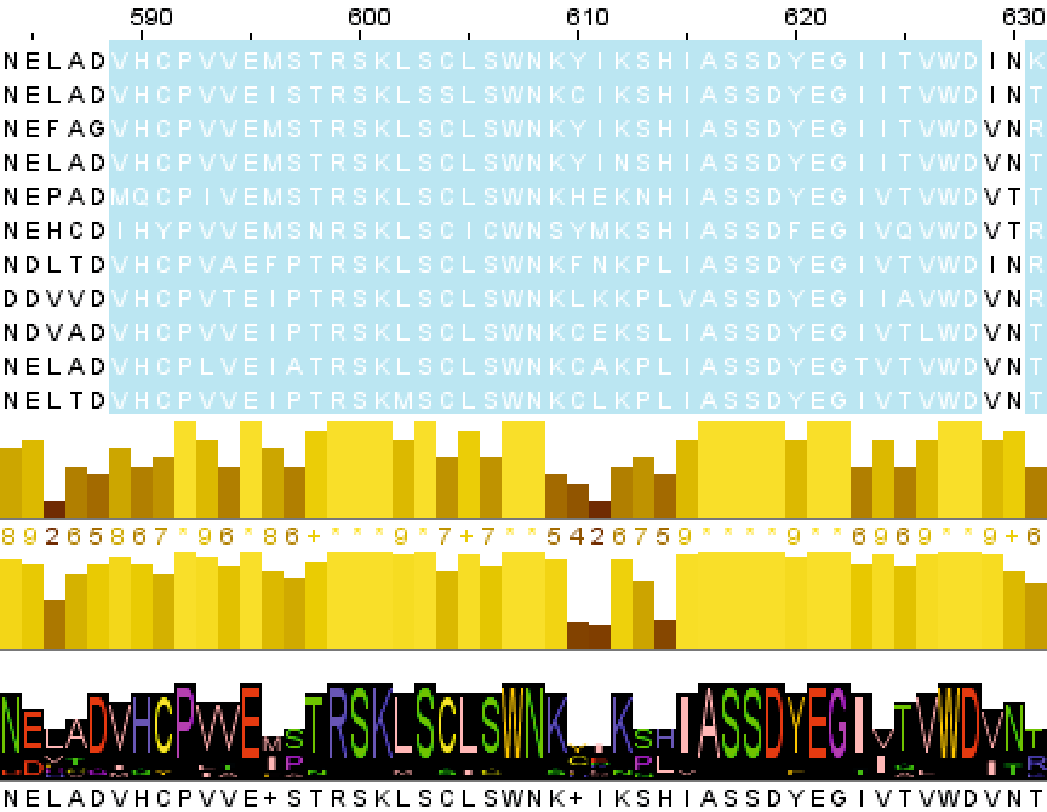
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N E F A G V H C P V V E M S T R S K L S C L S W N K Y I K S H I A S S D Y E G I I T V W D V N R
N E L A D V H C P V V E M S T R S K L S C L S W N K Y I N S H I A S S D Y E G I I T V W D V N T
N E P A D M Q C P I V E M S T R S K L S C L S W N K H E K N H I A S S D Y E G I V T V W D V T T
N E H C D I H Y P V V E M S N R S K L S C I C W N S Y M K S H I A S S D F E G I V Q V W D V T R
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8 9 2 6 5 8 6 7 * 9 6 * 8 6 + * * * 9 * 7 + 7 * * 5 4 2 6 7 5 9 * * * * 9 * * 6 9 6 9 * * 9 + 6
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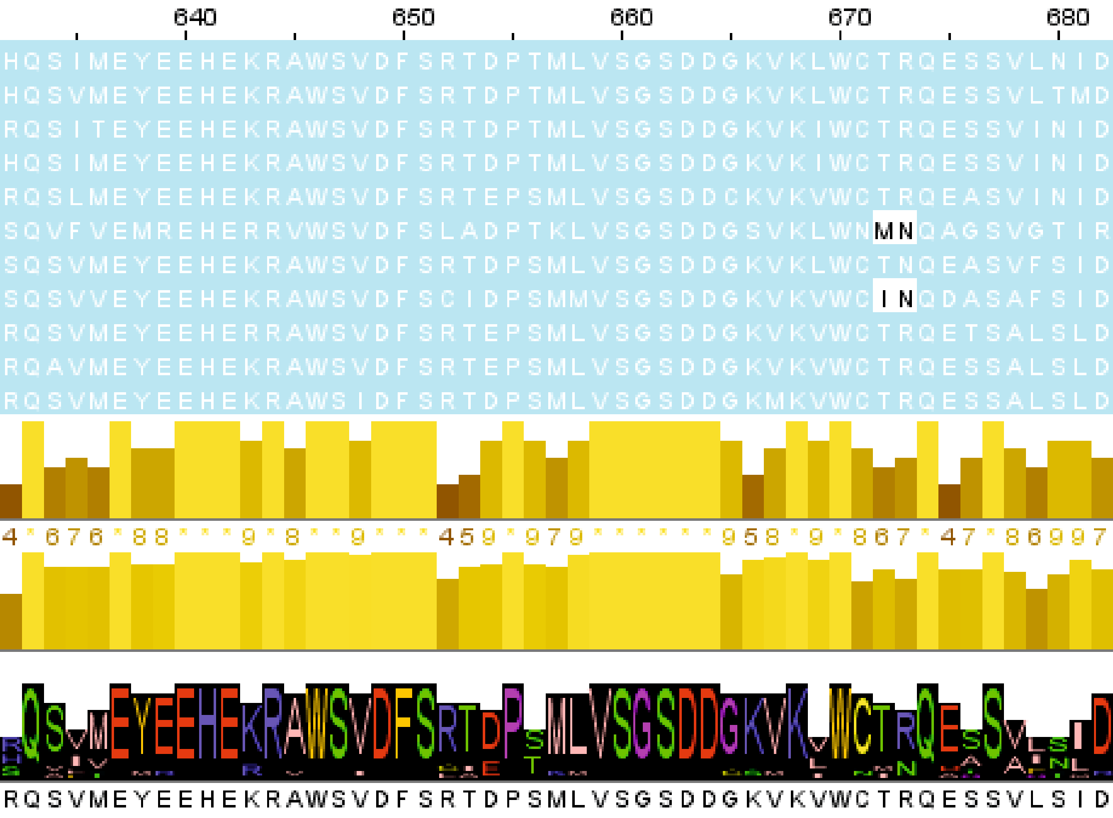
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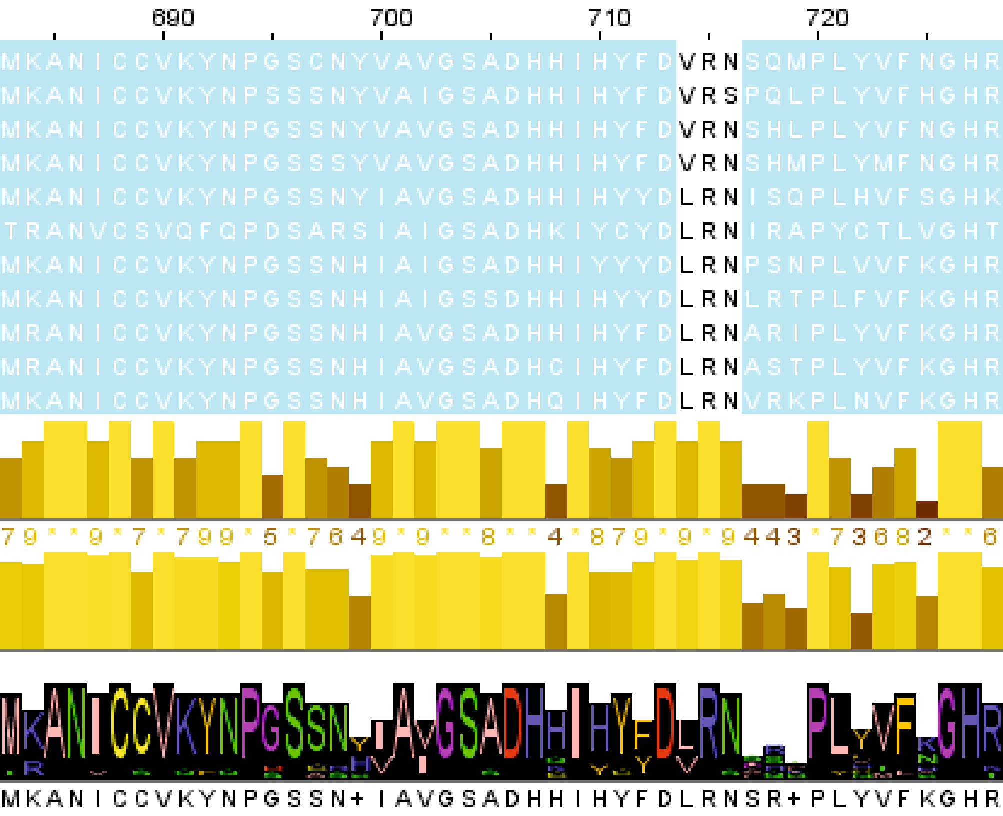
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79**9*7*799*5*7649*9**8**4*879*9*9443*73682**6
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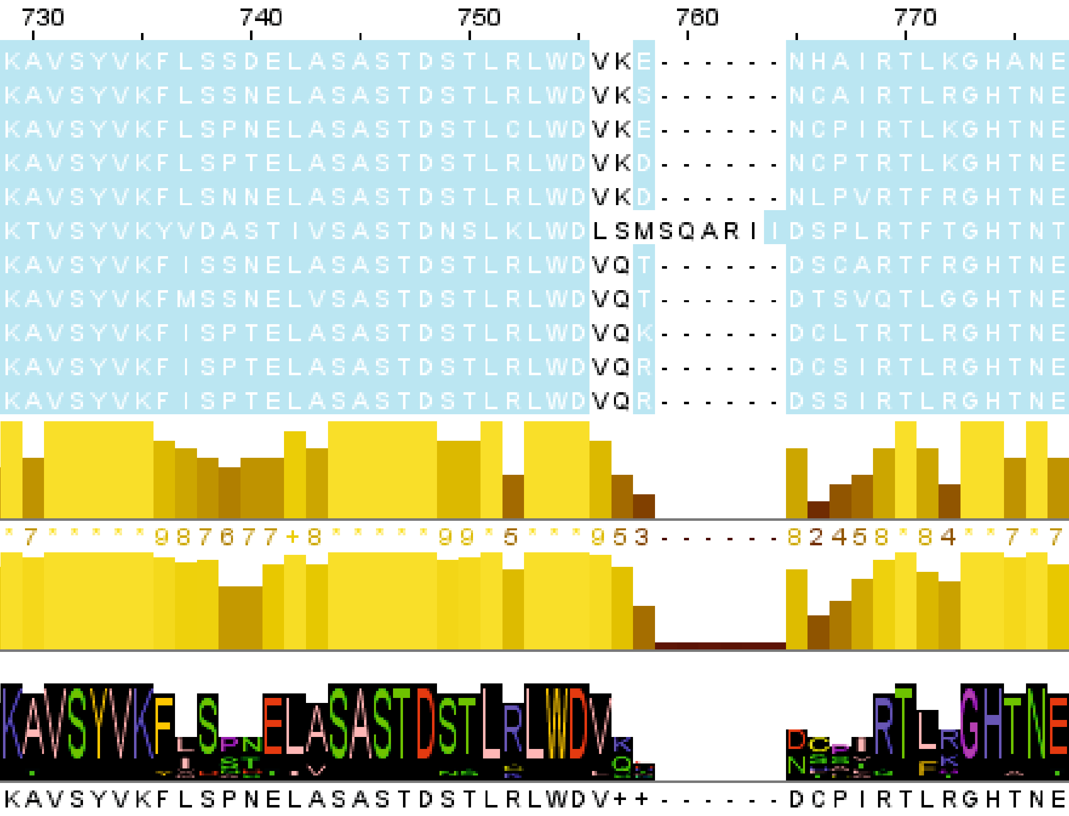
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KAVSYVKFISPTELASASTDSTLRLWDVQR------DCSIRTLRGHTNE
KAVSYVKFISPTELASASTDSTLRLWDVQR------DSSIRTLRGHTNE

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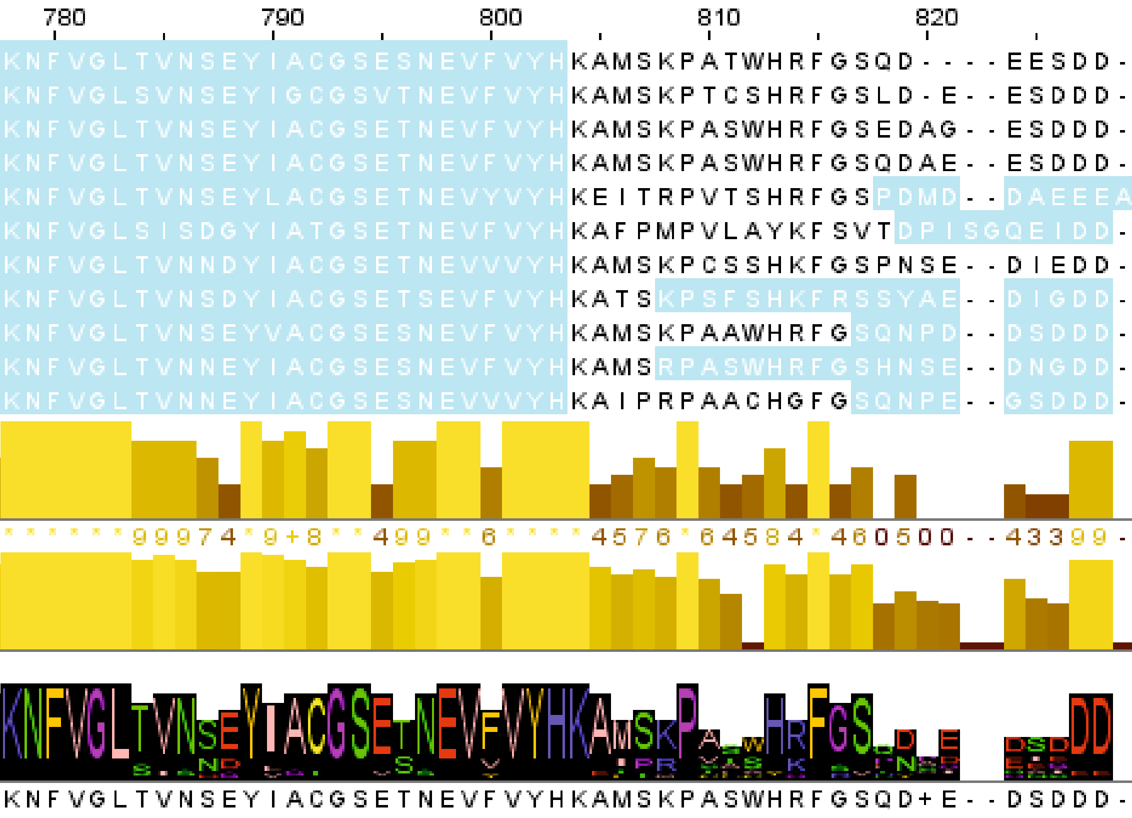
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KNFVGLTVNNDYIACGSETNEVVVYHKAMSKPCSSHKFGSPNSE--DIEDD-
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******99974*9+8**499**6****4576*64584*460500--43399-
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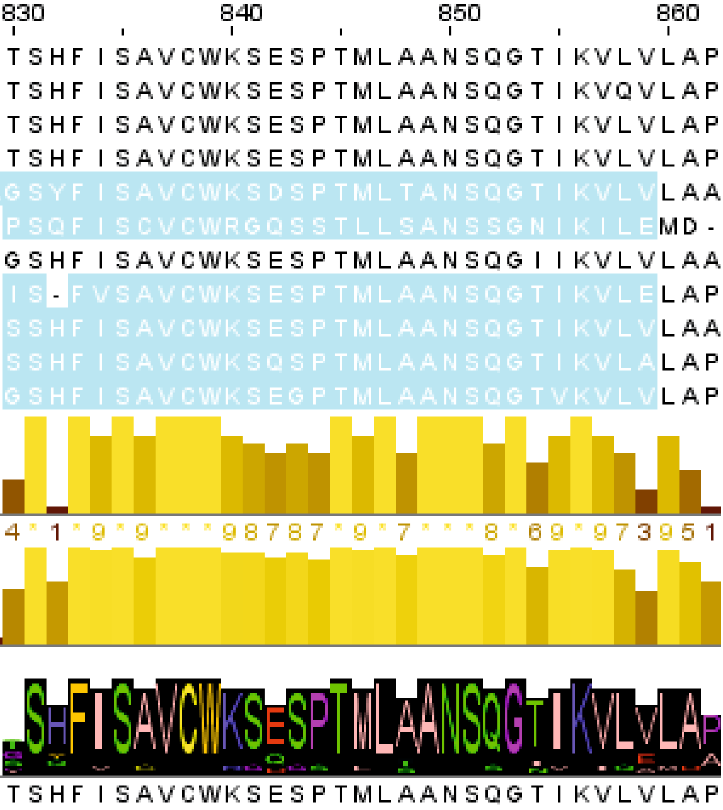

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