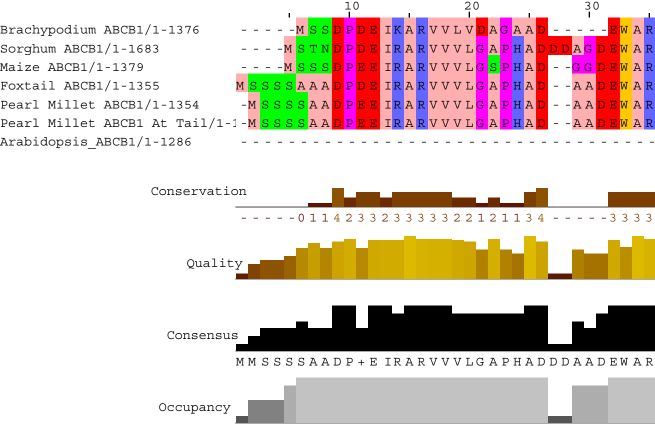
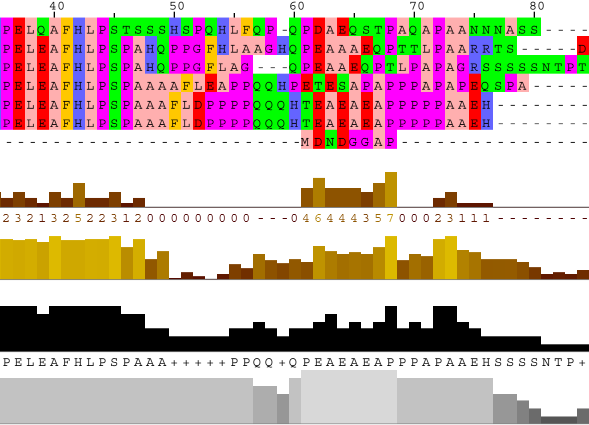

10
20
30
Brachypodium ABCB1/1-1376 -----MSSDPDEIKARVVLVDAGAAD-----EWAR
Sorghum ABCB1/1-1683 ----MSTNDPDEIRARVVVLGAPHADDDAGDEWAR
Maize ABCB1/1-1379 ----MSSSDPEEIRARVVVLGSPHAD--GGDEWAR
Foxtail ABCB1/1-1355 MSSSSAAADPDEIRARVVVLGAPHAD--AADEWAR
Pearl Millet ABCB1/1-1354 -MSSSSAADPEEIRARVVVLGAPHAD--AADEWAR
Pearl Millet ABCB1 At Tail/1-1 -MSSSSAADPEEIRARVVVLGAPHAD--AADEWAR
Arabidopsis_ABCB1/1-1286 -----------------------------------
Conservation
-----011423323333322121134-----3333
Quality
Consensus
MMSSSSAADP+EIRARVVVLGAPHADDDAADEWAR
Occupancy

Figure S7: Protein alignment of ABCB1 in sorghum, maize, pearl millet, foxtail millet, rice,


40
50
60
70
80

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PELEAFHLPSPAHQPPGFHLAAGHQPEAAAEQPTTLPAARRTS-----D
PELEAFHLPSPAHQPPGFLAG---QPEAAEQPTLPAPAGRSSSSSNTPT
PELEAFHLPSPAAAAFLEAPPQQHPETESAPAPPPAPAPEQSPA-----
PELEAFHLPSPAAAFLDPPPPQQQHTEAEAEAPPPPPAAEH--------
PELEAFHLPSPAAAFLDPPPPQQQHTEAEAEAPPPPPAAEH--------
-------------------------MDNDGGAP----------------
```

```
2321325223120000000000---046444357000231111--------
```

```
PELEAFHLPSPAAA+++++PPQQ+QPEAEAEAPPPAPAAEHSSSSNTP+
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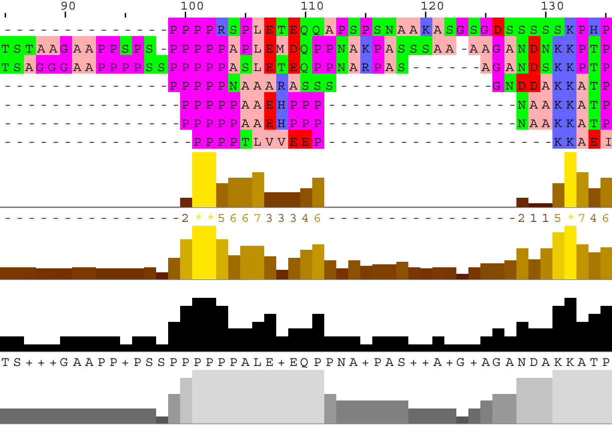
Brachypodium distachyon and Arabidopsis. The D2_AtTail protein is indicated with



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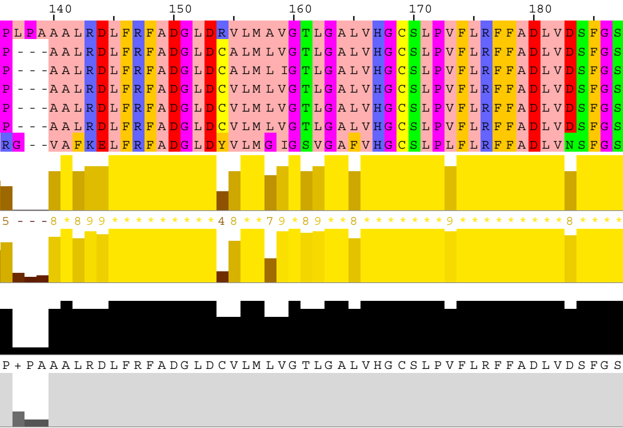
        90                  100                 110                 120                 130
--------------PPPPRSPLETEQQAPSPSNAAKASGSGDSSSSSKPHP
TSTAAGAAPPSPS-PPPPPAPLEMDQPPNAKPASSSAA-AAGANDNKKPTP
TSAGGGAAPPPPSSPPPPPASLETEQPPNARPAS------AGANDSKKPTP
--------------PPPPPNAAARASSS-------------GNDDAKKATP
---------------PPPPPAAEHPPP----------------NAAKKATP
---------------PPPPPAAEHPPP----------------NAAKKATP
----------------PPPPTLVVEEP-------------------KKAEI
---------------2**566733346----------------2115*746
TS+++GAAPP+PSSPPPPPPALE+EQPPNA+PAS++A+G+AGANDAKKATP
```

‘Pearl millet ABCB1 At Tail’. The four white boxes in the COOH-region indicate, from


140
150
160
170
180
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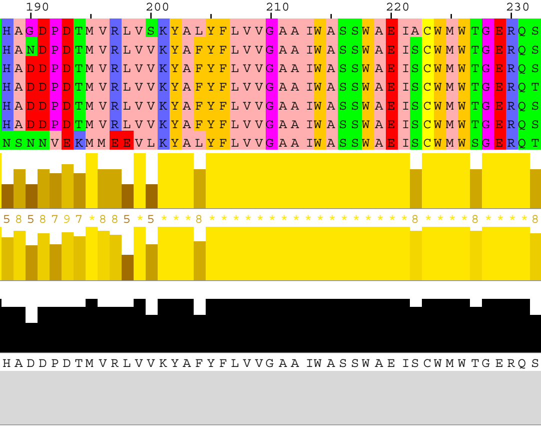
P---AALRDLFRFADGLDCALMLVGTLGALVHGCSLPVFLRFFADLVDSFGS
P---AALRDLFRFADGLDCALMLIGTLGALVHGCSLPVFLRFFADLVDSFGS
P---AALRDLFRFADGLDCVLMLVGTLGALVHGCSLPVFLRFFADLVDSFGS
P---AALRDLFRFADGLDCVLMLVGTLGALVHGCSLPVFLRFFADLVDSFGS
P---AALRDLFRFADGLDCVLMLVGTLGALVHGCSLPVFLRFFADLVDSFGS
RG--VAFKELFRFADGLDYVLMGIGSVGAFVHGCSLPLFLRFFADLVNSFGS
5---8*899*********48**79*89**8*******9*********8****
P+PAAALRDLFRFADGLDCVLMLVGTLGALVHGCSLPVFLRFFADLVDSFGS

eft to right, two β-sheets and two α-helices.


190
200
210
220
230

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HADDPDTMVRLVVKYAFYFLVVGAAIWASSWAEISCWMWTGERQT
HADDPDTMVRLVVKYAFYFLVVGAAIWASSWAEISCWMWTGERQS
HADDPDTMVRLVVKYAFYFLVVGAAIWASSWAEISCWMWTGERQS
NSNNVEKMMEEVLKYALYFLVVGAAIWASSWAEISCWMWSGERQT

5 8 5 8 7 9 7 * 8 8 5 * 5 * * * 8 * * * * * * * * * * * * * * * * * 8 * * * * 8 * * * * 8

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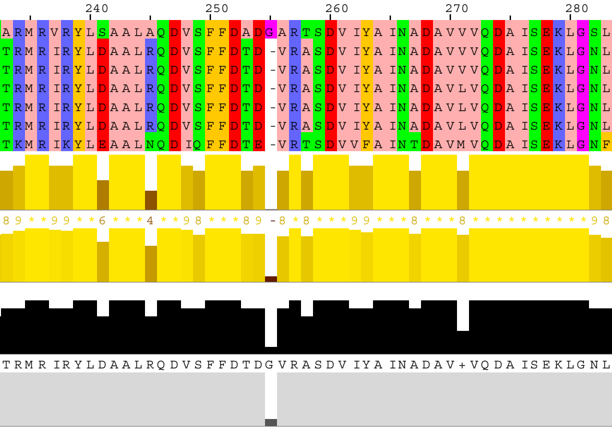

240
250
260
270
280

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TRMRIRYLDAALRQDVSFFDTD-VRASDVIYAINADAVVVQDAISEKLGNL
TRMRIRYLDAALRQDVSFFDTD-VRASDVIYAINADAVLVQDAISEKLGNL
TRMRIRYLDAALRQDVSFFDTD-VRASDVIYAINADAVLVQDAISEKLGNL
TRMRIRYLDAALRQDVSFFDTD-VRASDVIYAINADAVLVQDAISEKLGNL
TKMRIKYLEAALNQDIQFFDTE-VRTSDVVFAINTDAVMVQDAISEKLGNF
89**99**6***4**98***89-8*8***99***8***8**********98
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```

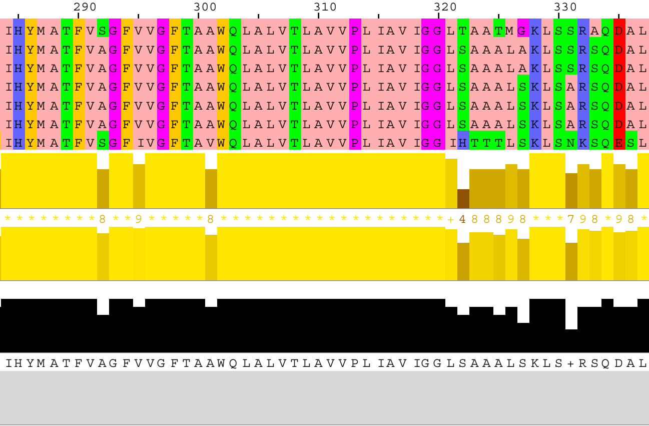

290
300
310
320
330

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IHYMATFVAGFVVGFTAAWQLALVTLAVVPLIAVIGGLSAAALSKLSARSQDAL
IHYMATFVAGFVVGFTAAWQLALVTLAVVPLIAVIGGLSAAALSKLSARSQDAL
IHYMATFVAGFVVGFTAAWQLALVTLAVVPLIAVIGGLSAAALSKLSARSQDAL
IHYMATFVSGFIVGFTAVWQLALVTLAVVPLIAVIGGIHTTTLSKLSNKSQESL
********8**9*****8*******************+488898***798*98*
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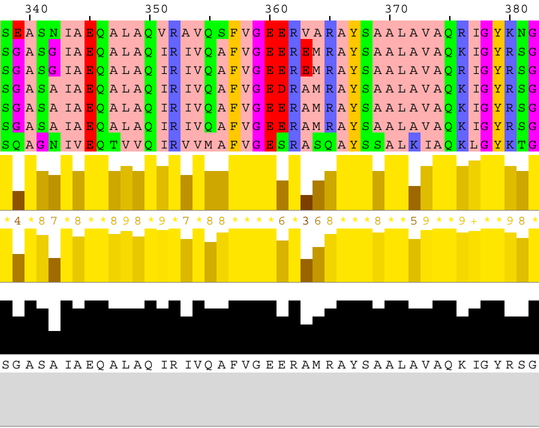
340
350
360
370
380

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SGASAIAEQALAQIRIVQAFVGEDRAMRAYSAALAVAQKIGYRSG
SGASAIAEQALAQIRIVQAFVGEERAMRAYSAALAVAQKIGYRSG
SGASAIAEQALAQIRIVQAFVGEERAMRAYSAALAVAQKIGYRSG
SQAGNIVEQTVVQIRVVMAFVGESRASQAYSSALKIAQKLGYKTG
*4*87*8**898*9*7*88****6*368***8**59**9+**98*
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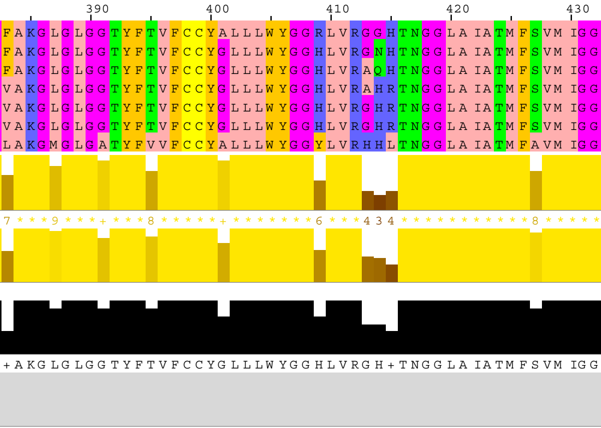
390
400
410
420
430

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FAKGLGLGGTYFTVFCCYGLLLWYGGHLVRAQHTNGGLAIATMFSVMIGG
VAKGLGLGGTYFTVFCCYGLLLWYGGHLVRAHRTNGGLAIATMFSVMIGG
VAKGLGLGGTYFTVFCCYGLLLWYGGHLVRGHRTNGGLAIATMFSVMIGG
VAKGLGLGGTYFTVFCCYGLLLWYGGHLVRGHRTNGGLAIATMFSVMIGG
LAKGMGLGATYFVVFCCYALLLWYGGYLVRHHLTNGGLAIATMFAVMIGG

7***9***+***8*****+*******6***434***********8*****

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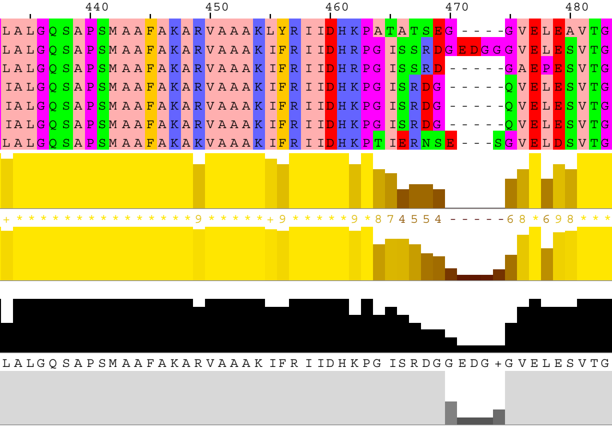
```


440
450
460
470
480

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LALGQSAPSMAAFAKARVAAAKIFRIIDHRPGISSRD-----GAEPESVTG
IALGQSAPSMAAFAKARVAAAKIFRIIDHKPGISRDG-----QVELESVTG
IALGQSAPSMAAFAKARVAAAKIFRIIDHKPGISRDG-----QVELESVTG
IALGQSAPSMAAFAKARVAAAKIFRIIDHKPGISRDG-----QVELESVTG
LALGQSAPSMAAFAKAKVAAAKIFRIIDHKPTIERNSE---SGVELDSVTG
+***************9*****+9*****9*874554-----68*698***
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```

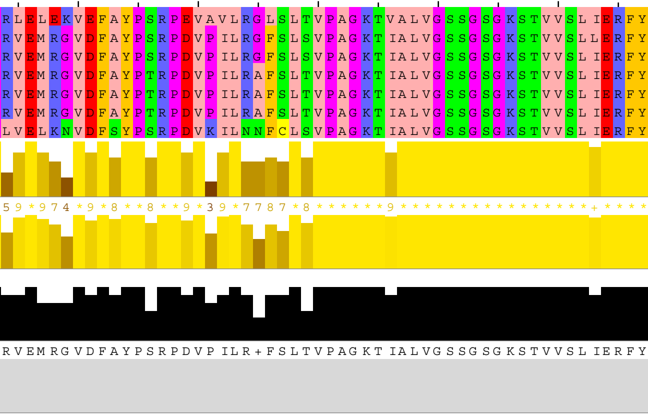
490
500
510
520
530

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RVEMRGVDFAYPSRPDVPILRGFSLSVPAGKTIALVGSSGSGKSTVVSLIERFY
RVEMRGVDFAYPTRPDVPILRAFSLTVPAGKTIALVGSSGSGKSTVVSLIERFY
RVEMRGVDFAYPTRPDVPILRAFSLTVPAGKTIALVGSSGSGKSTVVSLIERFY
RVEMRGVDFAYPTRPDVPILRAFSLTVPAGKTIALVGSSGSGKSTVVSLIERFY
LVELKNVDFSYPSRPDVKILNNFCLSVPAGKTIALVGSSGSGKSTVVSLIERFY
59*974*9*8**8**9*39*7787*8******9****************+****
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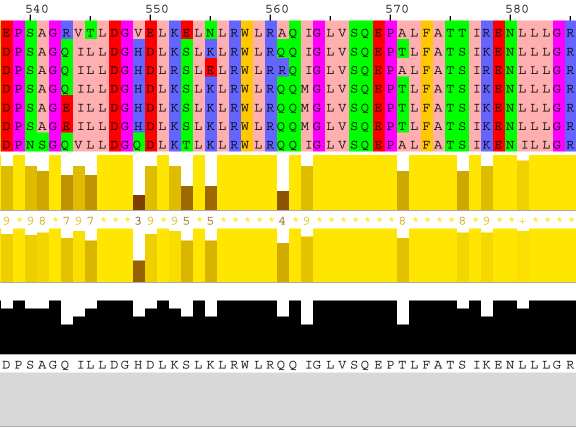
540
550
560
570
580

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DPSAGQILLDGHDLKSLKLRWLRQQMGLVSQEPTLFATSIKENLLLGR
DPSAGEILLDGHDLKSLKLRWLRQQMGLVSQEPTLFATSIKENLLLGR
DPSAGEILLDGHDLKSLKLRWLRQQMGLVSQEPTLFATSIKENLLLGR
DPNSGQVLLDGQDLKTLKLRWLRQQIGLVSQEPALFATSIKENILLGR
9*98*797***39*95*5*****4*9*******8****8*9**+****
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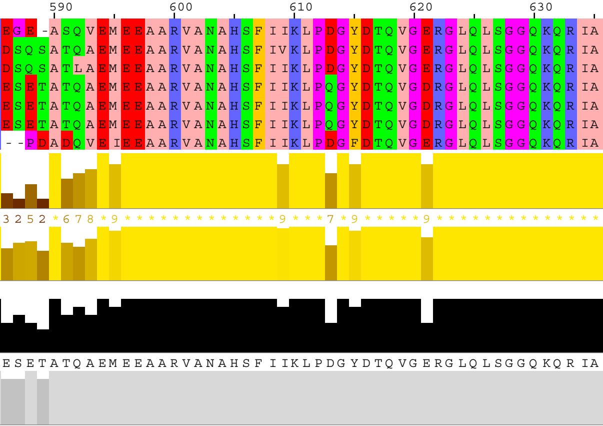

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DSQSATQAEMEEAARVANAHSFIVKLPDGYDTQVGERGLQLSGGQKQRIA
DSQSATLAEMEEAARVANAHSFIIKLPDGYDTQVGERGLQLSGGQKQRIA
ESETATQAEMEEAARVANAHSFIIKLPQGYDTQVGDRGLQLSGGQKQRIA
ESETATQAEMEEAARVANAHSFIIKLPQGYDTQVGDRGLQLSGGQKQRIA
ESETATQAEMEEAARVANAHSFIIKLPQGYDTQVGDRGLQLSGGQKQRIA
--PDADQVEIEEAARVANAHSFIIKLPDGFDTQVGERGLQLSGGQKQRIA
3252*678*9*************9***7*9*****9**************
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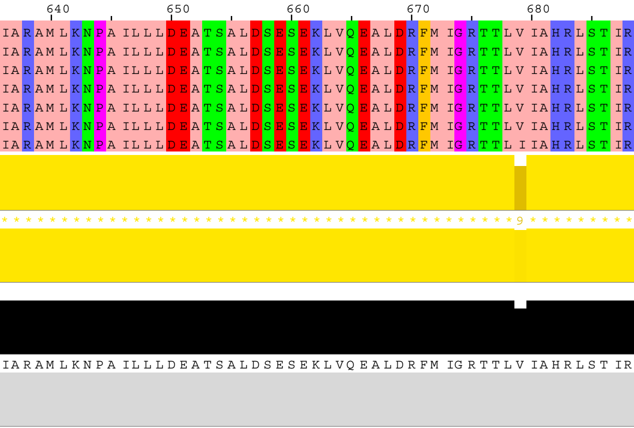

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IARAMLKNPAILLLDEATSALDSESEKLVQEALDRFMIGRTTLVIAHRLSTIR
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IARAMLKNPAILLLDEATSALDSESEKLVQEALDRFMIGRTTLIIAHRLSTIR
*******************************************9*********
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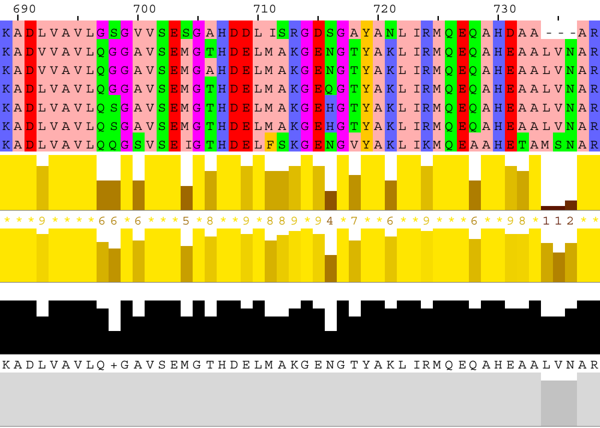
690
700
710
720
730

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KADVVAVLQGGAVSEMGAHDELMAKGENGTYAKLIRMQEQAHEAALVNAR
KADLVAVLQGGAVSEMGTHDELMAKGEQGTYAKLIRMQEQAHEAALVNAR
KADLVAVLQSGAVSEMGTHDELMAKGEHGTYAKLIRMQEQAHEAALVNAR
KADLVAVLQSGAVSEMGTHDELMAKGEHGTYAKLIRMQEQAHEAALVNAR
KADLVAVLQQGSVSEIGTHDELFSKGENGVYAKLIKMQEAAHETAMSNAR
***9****66*6***5*8**9*889*94*7**6**9***6**98*112**
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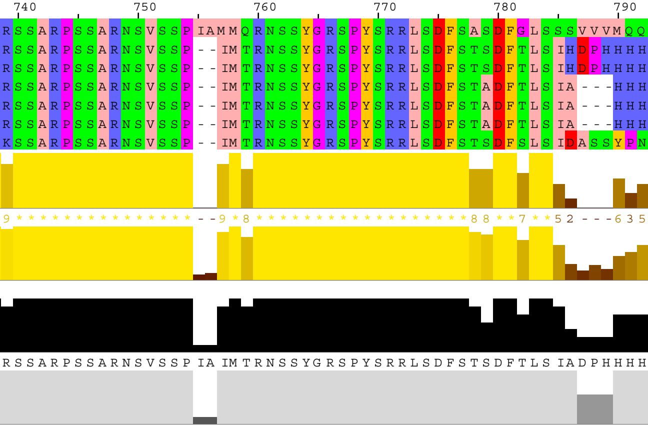
740
750
760
770
780
790

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RSSARPSSARNSVSSP--IMTRNSSYGRSPYSRRLSDFSTSDFTLSIHDPHHHH
RSSARPSSARNSVSSP--IMTRNSSYGRSPYSRRLSDFSTSDFTLSIHDPHHHH
RSSARPSSARNSVSSP--IMTRNSSYGRSPYSRRLSDFSTADFTLSIA---HHH
RSSARPSSARNSVSSP--IMTRNSSYGRSPYSRRLSDFSTADFTLSIA---HHH
RSSARPSSARNSVSSP--IMTRNSSYGRSPYSRRLSDFSTADFTLSIA---HHH
KSSARPSSARNSVSSP--IMTRNSSYGRSPYSRRLSDFSTSDFSLSIDASSYPN
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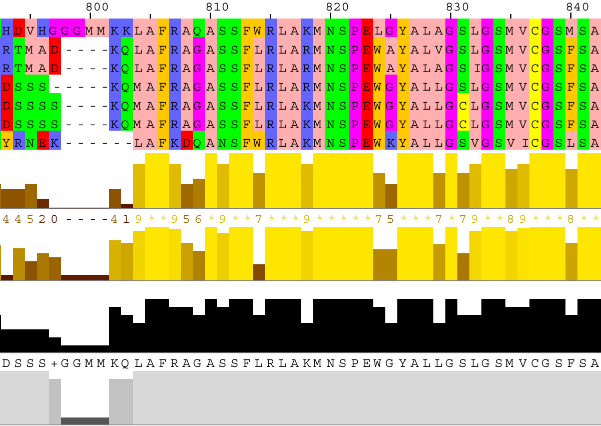
800
810
820
830
840

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DSSS-----KQMAFRAGASSFLRLARMNSPEWGYALLGSLGSMVCGSFSA
DSSSS----KQMAFRAGASSFLRLAKMNSPEWGYALLGCLGSMVCGSFSA
DSSSS----KQMAFRAGASSFLRLAKMNSPEWGYALLGCLGSMVCGSFSA
YRNEK------LAFKDQANSFWRLAKMNSPEWKYALLGSVGSVICGSLSA
44520----419**956*9**7***9*****75***7*79**89***8**
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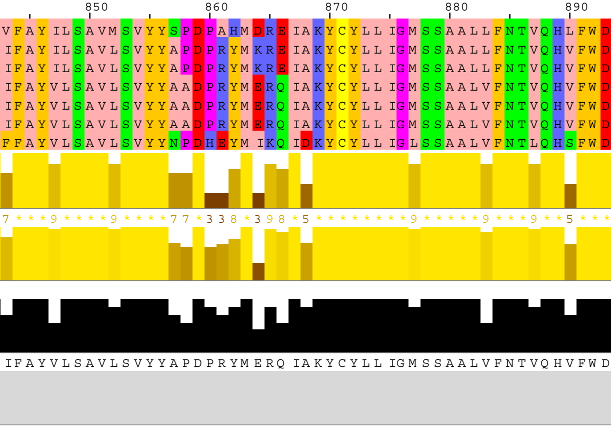
850
860
870
880
890
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IFAYVLSAVLSVYYAADPRYMERQIAKYCYLLIGMSSAALVFNTVQHVFWD
IFAYVLSAVLSVYYAADPRYMERQIAKYCYLLIGMSSAALVFNTVQHVFWD
FFAYVLSAVLSVYYNPDHEYMIKQIDKYCYLLIGLSSAALVFNTLQHSFWD
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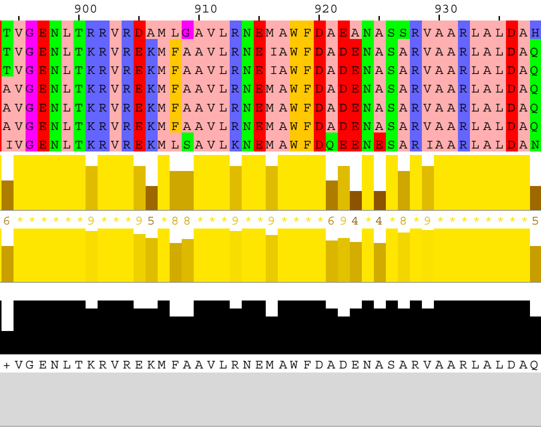
900
910
920
930

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TVGENLTKRVREKMFAAVLRNEIAWFDADENASARVAARLALDAQ
AVGENLTKRVREKMFAAVLRNEMAWFDADENASARVAARLALDAQ
AVGENLTKRVREKMFAAVLRNEMAWFDADENASARVAARLALDAQ
AVGENLTKRVREKMFAAVLRNEMAWFDADENASARVAARLALDAQ
IVGENLTKRVREKMLSAVLKNEMAWFDQEENESARIAARLALDAN
6******9***95*88***9**9****694*4*8*9********5
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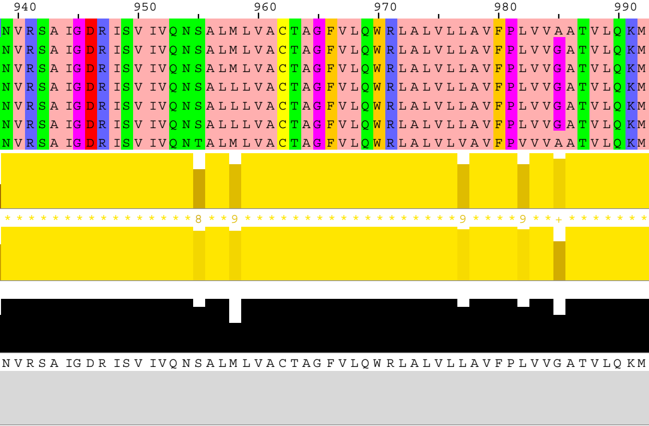

940
950
960
970
980
990

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NVRSAIGDRISVIVQNSALLLVACTAGFVLQWRLALVLLAVFPLVVGATVLQKM
NVRSAIGDRISVIVQNSALLLVACTAGFVLQWRLALVLLAVFPLVVGATVLQKM
NVRSAIGDRISVIVQNSALLLVACTAGFVLQWRLALVLLAVFPLVVGATVLQKM
NVRSAIGDRISVIVQNTALMLVACTAGFVLQWRLALVLVAVFPVVVAATVLQKM
****************8**9******************9****9**+*******
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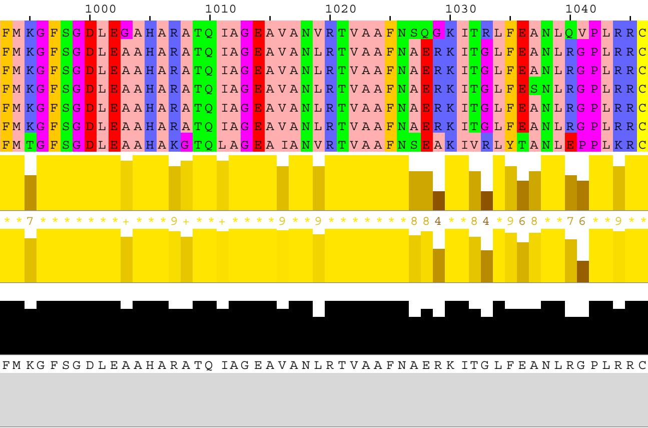

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FMKGFSGDLEAAHARATQIAGEAVANLRTVAAFNAERKITGLFEANLRGPLRRC
FMKGFSGDLEAAHARATQIAGEAVANLRTVAAFNAERKITGLFESNLRGPLRRC
FMKGFSGDLEAAHARATQIAGEAVANLRTVAAFNAERKITGLFEANLRGPLRRC
FMKGFSGDLEAAHARATQIAGEAVANLRTVAAFNAERKITGLFEANLRGPLRRC
FMTGFSGDLEAAHAKGTQLAGEAIANVRTVAAFNSEAKIVRLYTANLEPPLKRC

**7*******+***9+**+****9**9*******884**84*968**76**9**

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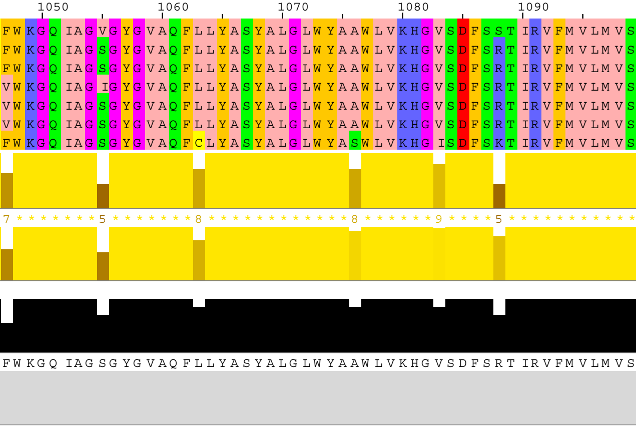
1050
1060
1070
1080
1090

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VWKGQ IAGSGYGVAQFLLYASYALGLWYAAWLVKHGVSDFSRT IRVFMVLMVS
FWKGQ IAGSGYGVAQFCLYASYALGLWYASWLVKHGISDFSKT IRVFMVLMVS
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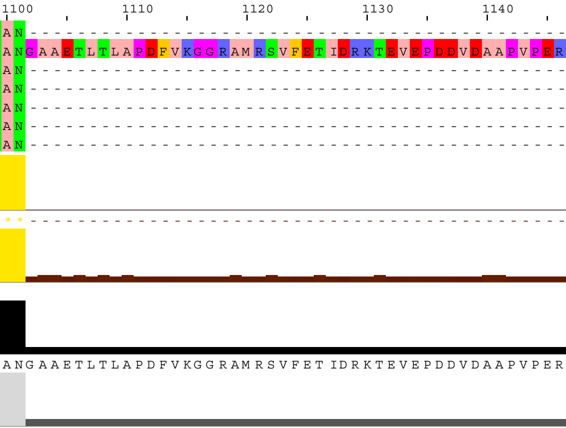
1100
1110
1120
1130
1140

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AN---------------------------------------------
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AN---------------------------------------------
AN---------------------------------------------
AN---------------------------------------------
AN---------------------------------------------
AN---------------------------------------------

**---------------------------------------------

ANGAAETLTLAPDFVKGGRAMRSVFETIDRKTEVEPDDVDAAPVPER
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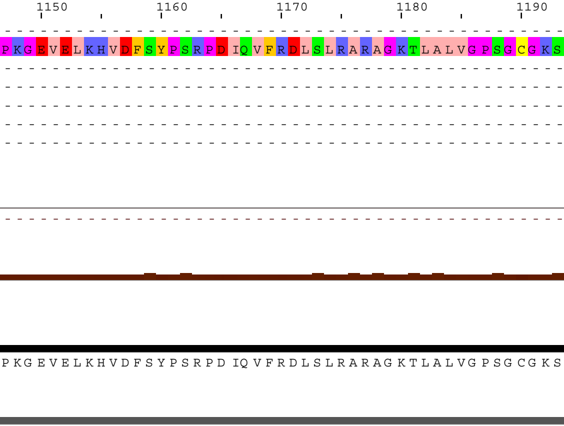
1150
1160
1170
1180
1190

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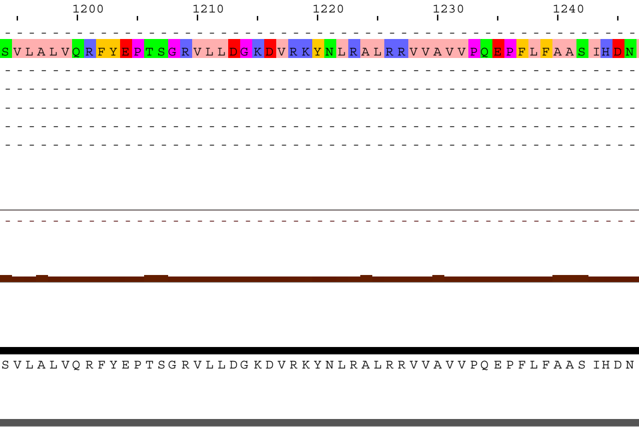
1200
1210
1220
1230
1240

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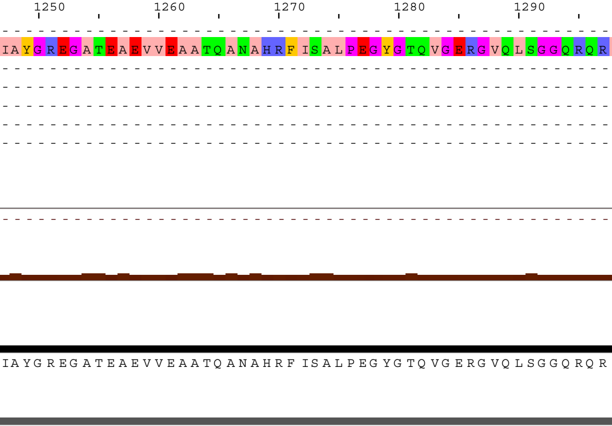
1250
1260
1270
1280
1290

```
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IAYGREGATEAEVVEAATQANAHRFISALPEGYGTQVGERGVQLSGGQRQR
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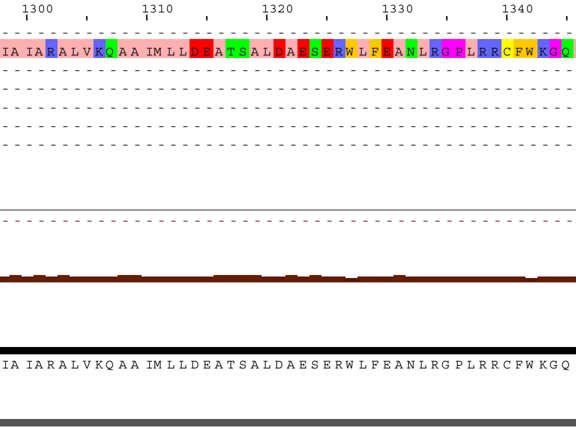

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  1300      1310      1320      1330      1340
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IAIARALVKQAAIMLLDEATSALDAESERWLFEANLRGPLRRCFWKGQ
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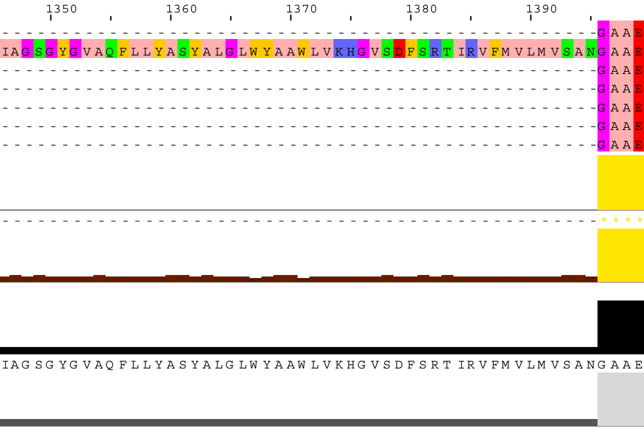
1350
1360
1370
1380
1390

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--------------------------------------------------GAAE
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--------------------------------------------------GAAE
--------------------------------------------------GAAE
--------------------------------------------------GAAE
--------------------------------------------------GAAE
--------------------------------------------------GAAE

--------------------------------------------------****

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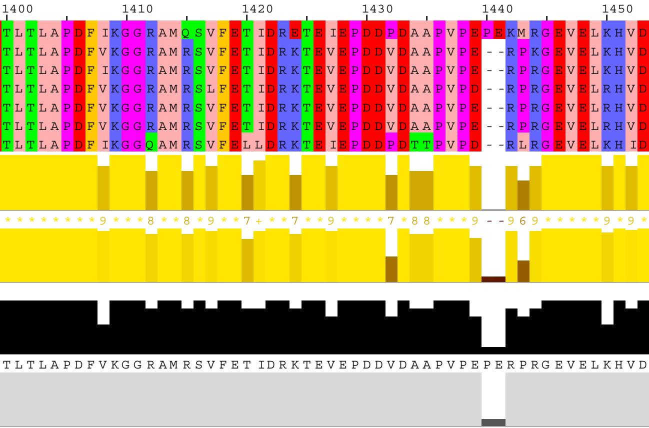
1400
1410
1420
1430
1440
1450

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TLTLAPDFIKGGRAMRSVFETIDRKTEVEPDDVDAAPVPE--RPRGEVELKHVD
TLTLAPDFVKGGRAMRSLFETIDRKTEVEPDDVDAAPVPD--RPRGEVELRHVD
TLTLAPDFVKGGRAMRSVFETIDRKTEVEPDDVDAAPVPE--RPRGEVELRHVD
TLTLAPDFVKGGRAMRSVFETIDRKTEVEPDDVDAAPVPE--RPRGEVELRHVD
TLTLAPDFIKGGQAMRSVFELLDRKTEIEPDDPDTTPVPD--RLRGEVELKHID
********9***8**8*9**7+**7**9****7*88***9--969*****9*9*
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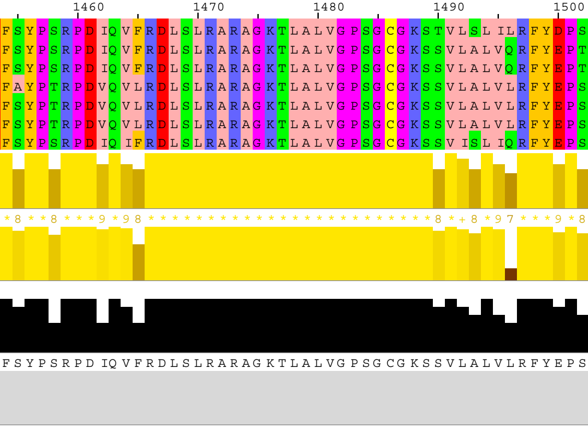
1460
1470
1480
1490
1500
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FSYPSRPDIQIFRDLSLRARAGKTLALVGPSGCGKSSVISLIQRFYEPS
*8**8***9*98************************8*+8*97***9*8
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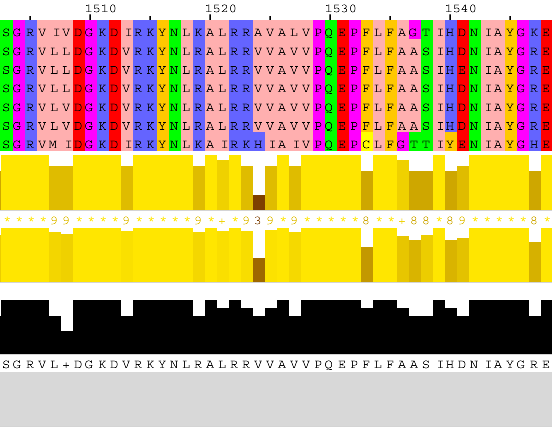
1510
1520
1530
1540

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SGRVLLDGKDVRKYNLRALRRVVAVVPQEPFLFAASIHDNIAYGRE
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SGRVLVDGKDVRKYNLRALRRVVAVVPQEPFLFAASIHDNIAYGRE
SGRVMIDGKDIRKYNLKAIRKHIAIVPQEPCLFGTTIYENIAYGHE
****99****9*****9*+*939*9*****8**+88*89*****8*
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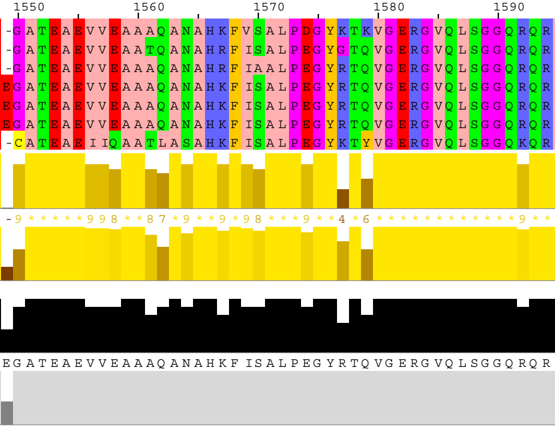
1550
1560
1570
1580
1590

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-GATEAEVVEAATQANAHRFISALPEGYGTQVGERGVQLSGGQRQR
-GATEAEVVEAAAQANAHRFIAALPEGYRTQVGERGVQLSGGQRQR
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EGATEAEVVEAAAQANAHKFISALPEGYRTQVGERGVQLSGGQRQR
EGATEAEVVEAAAQANAHKFISALPEGYRTQVGERGVQLSGGQRQR
-CATEAEIIQAATLASAHKFISALPEGYKTYVGERGVQLSGGQKQR

-9*****998**87*9**9*98***9**4*6*************9**

EGATEAEVVEAAAQANAHKFISALPEGYRTQVGERGVQLSGGQRQR
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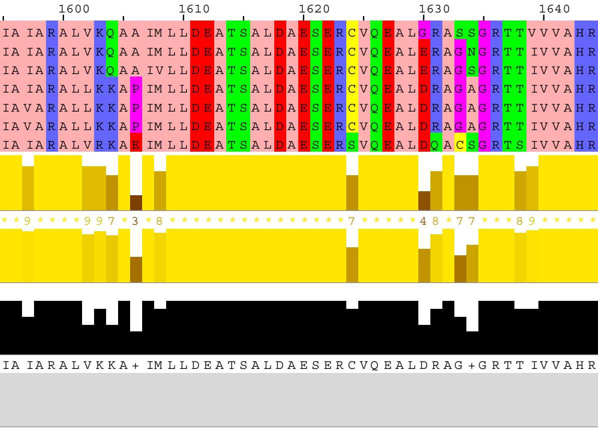
1600
1610
1620
1630
1640

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IAVARALLKKAPIMLLDEATSALDAESERCVQEALDRAGAGRTTIVVAHR
IAIARALVRKAEIMLLDEATSALDAESERSVQEALDQACSGRTSIVVAHR
**9****997*3*8***************7*****48*77***89*****
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```

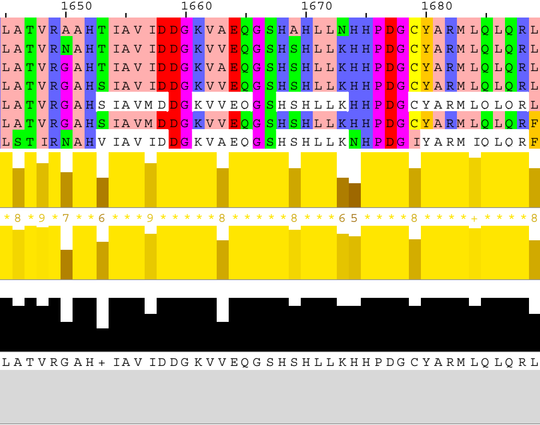
1650
1660
1670
1680

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LSTIRNAHVIAVIDDGKVAEQGSHSHLLKNHPDGIYARMIQLQRF
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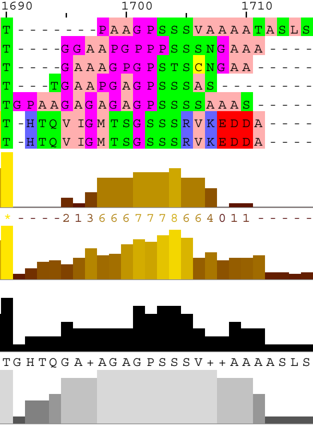

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T----GAAAGPGPSTSCNGAA-----
T---TGAAPGAGPSSSAS--------
TGPAAGAGAGAGPSSSSAAAS-----
T-HTQVIGMTSGSSSRVKEDDA----
T-HTQVIGMTSGSSSRVKEDDA----
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1690
1700
1710
*----213667778664011------
TGHTQGA+AGAGPSSSV++AAAASLS