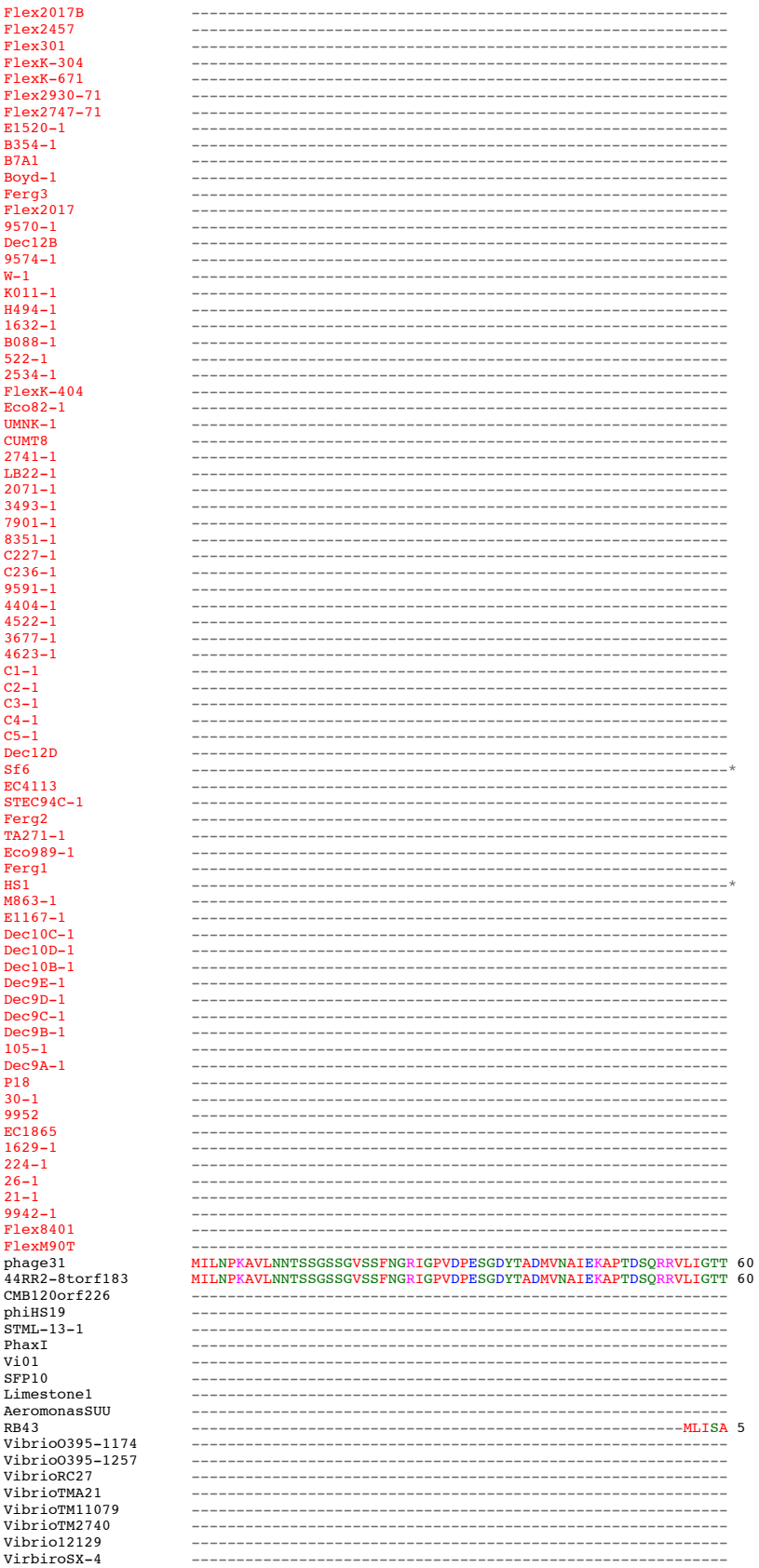
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FlexK-671
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Boyd-1
Ferg3
Flex2017
9570-1
Dec12B
9574-1
W-1
K011-1
H494-1
1632-1
B088-1
522-1
2534-1
FlexK-404
Eco82-1
UMNK-1
CUMT8
2741-1
LB22-1
2071-1
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7901-1
8351-1
C227-1
C236-1
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C1-1
C2-1
C3-1
C4-1
C5-1
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Ferg1
HS1
M863-1
E1167-1
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9942-1
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FlexM90T
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PhaxI
Vi01
SFP10
Limestone1
AeromonasSUU
RB43
MLISA 5
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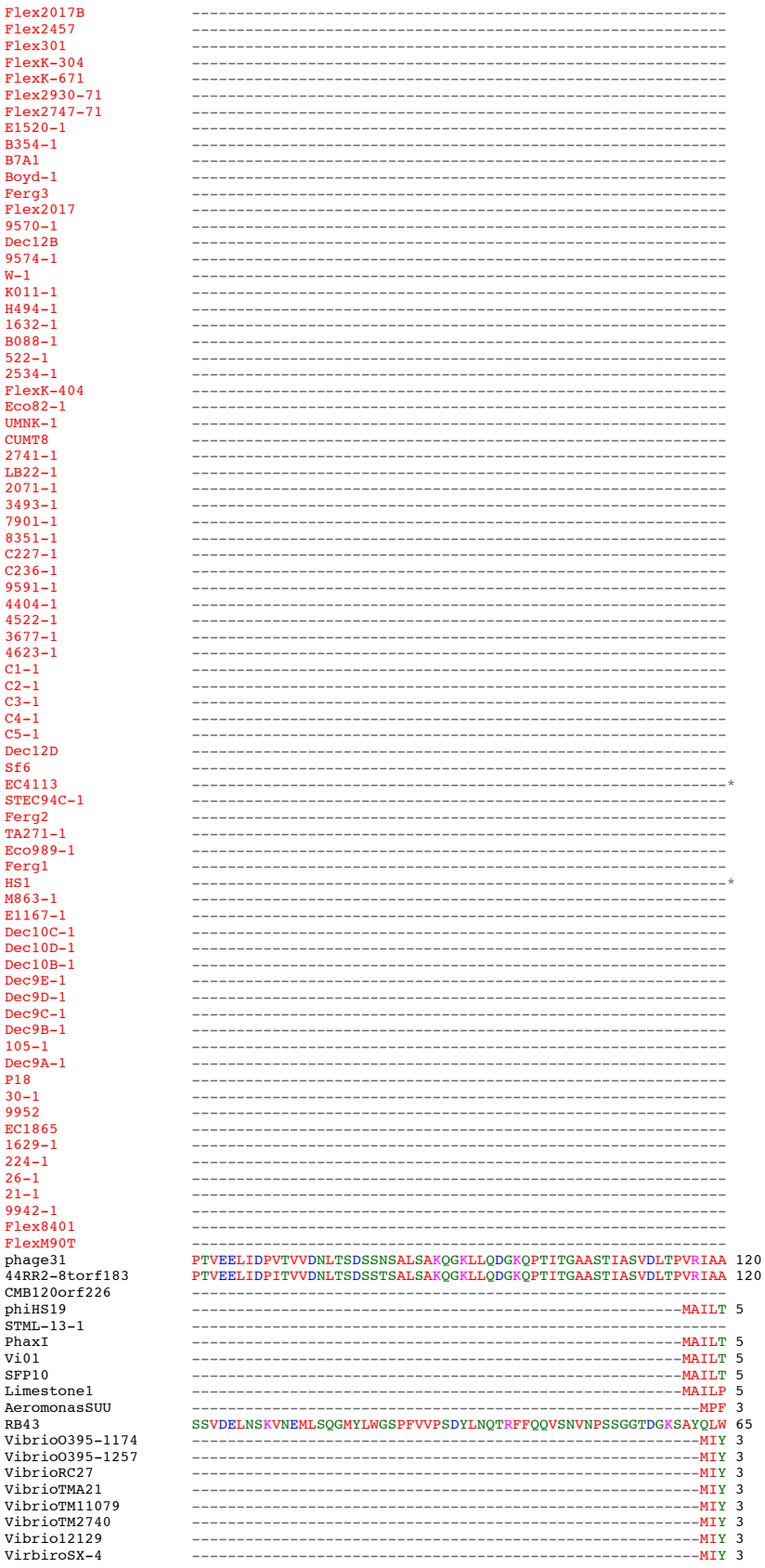
Vibrio12129
VirbiroSX-4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8351-1
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C1-1
C2-1
C3-1
C4-1
C5-1
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Sf6
EC4113
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Ferg2
TA271-1
Eco989-1
Ferg1
HS1
M863-1
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Dec10D-1
Dec10B-1
Dec9E-1
Dec9D-1
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Dec9B-1
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Dec9A-1
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26-1
21-1
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FlexM90T
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CMB120orf226
phiHS19
STML-13-1
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SFP10
Limestone1
AeromonasSUU
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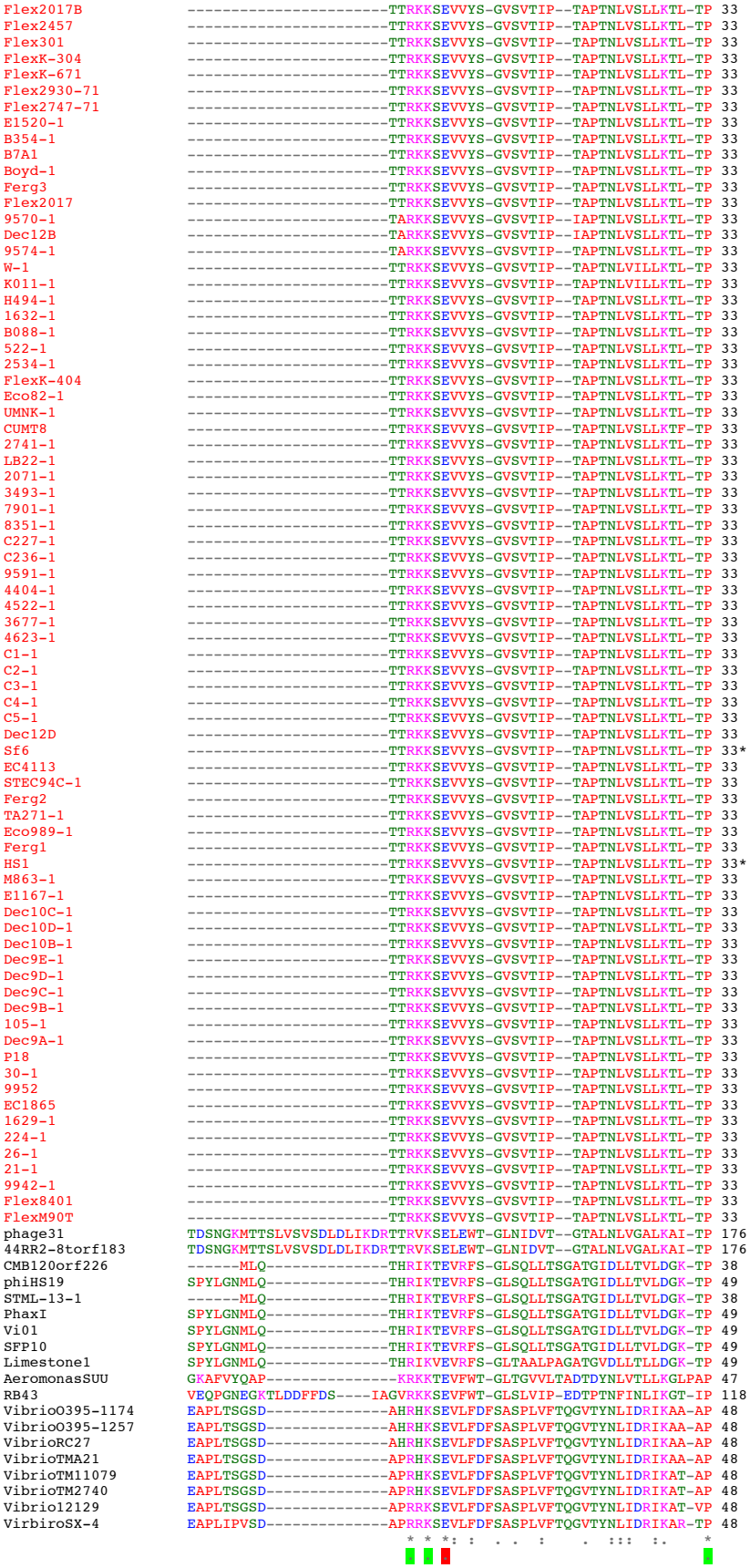
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B354-1 ----------TTRKKSEVVYS-GVSVTIP--TAPTNLVSLLKTL-TP 33
B7A1 ----------TTRKKSEVVYS-GVSVTIP--TAPTNLVSLLKTL-TP 33
Boyd-1 ----------TTRKKSEVVYS-GVSVTIP--TAPTNLVSLLKTL-TP 33
Ferg3 ----------TTRKKSEVVYS-GVSVTIP--TAPTNLVSLLKTL-TP 33
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2534-1 ----------TTRKKSEVVYS-GVSVTIP--TAPTNLVSLLKTL-TP 33
FlexK-404 ----------TTRKKSEVVYS-GVSVTIP--TAPTNLVSLLKTL-TP 33
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UMNK-1 ----------TTRKKSEVVYS-GVSVTIP--TAPTNLVSLLKTL-TP 33
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Ferg2 ----------TTRKKSEVVYS-GVSVTIP--TAPTNLVSLLKTL-TP 33
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Ferg1 ----------TTRKKSEVVYS-GVSVTIP--TAPTNLVSLLKTL-TP 33
HS1 ----------TTRKKSEVVYS-GVSVTIP--TAPTNLVSLLKTL-TP 33*
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phiHS19 SPYLGNMLQ----------THRIKTEVRFS-GLSQLLTSGATGIDLLTVLDGK-TP 49
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Limestone1 SPYLGNMLQ----------THRIKVEVRFS-GLTAALPAGATGVDLLTLLDGK-TP 49
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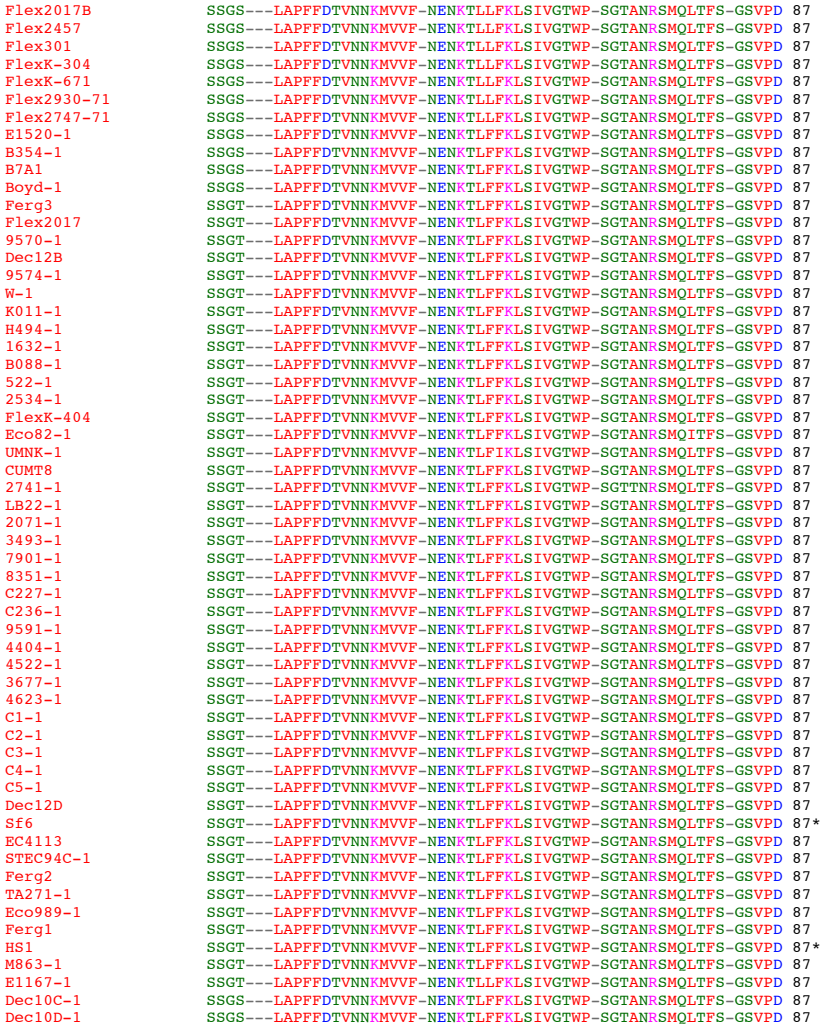
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K011-1 SSGT---LAPFFDTVNNKMVVF-NENKTLFFKLSIVGTWP-SGTANRSMQLTFS-GSVPD 87
H494-1 SSGT---LAPFFDTVNNKMVVF-NENKTLFFKLSIVGTWP-SGTANRSMQLTFS-GSVPD 87
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C236-1 SSGT---LAPFFDTVNNKMVVF-NENKTLFFKLSIVGTWP-SGTANRSMQLTFS-GSVPD 87
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Sf6 SSGT---LAPFFDTVNNKMVVF-NENKTLFFKLSIVGTWP-SGTANRSMQLTFS-GSVPD 87*
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Ferg2 SSGT---LAPFFDTVNNKMVVF-NENKTLFFKLSIVGTWP-SGTANRSMQLTFS-GSVPD 87
TA271-1 SSGT---LAPFFDTVNNKMVVF-NENKTLFFKLSIVGTWP-SGTANRSMQLTFS-GSVPD 87
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HS1 SSGT---LAPFFDTVNNKMVVF-NENKTLFFKLSIVGTWP-SGTANRSMQLTFS-GSVPD 87*
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SFP10 NPSSPTGLAPFFKLSDHKFHAF-PYDSILPVKVNIVGSWS-GSTSNRTMILDFV-GSVGN 106
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VibrioTMA21 IFGS---LLPFFDTVANLLRSF-NDDASLHFKANFIGSFP-GSAATRSLELDFL-GTEGN 102
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VibrioTM2740 VFGS---LLPFFDTAANLLRSF-NDDASLHFKANFIGSFP-GSAATRSLELDFL-GTEGN 102
Vibrio12129 VFGN---LLPFFDTAANLLRSF-NDDASLHFKANFIGSFP-GSAATRSLELDFL-GTEGN 102
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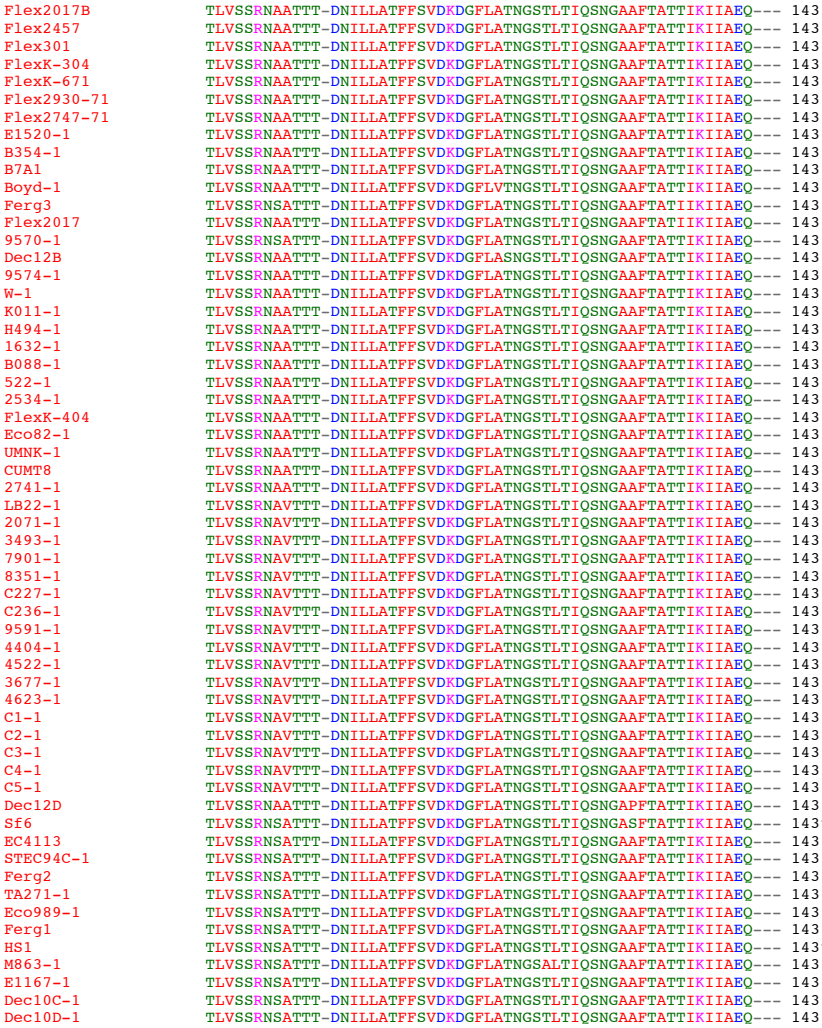
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phiHS19 QLSRSRDASVPPPDTLSFITFFSVDKDGNLATNGAQMKLYSYGGDFTITEVVLIAEQVVP 166
STML-13-1 QLSRSRDASVPPPDTLSFITFFSVDKDGNLATNGAQMKLYSYGGDFTITEVVLIAEQVVP 155
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Vi01 QLSRSRDASVPPPDTLSFITFFSVDKDGNLATNGAQIKLYSYGGDFTITEVVLIAEQVVP 166
SFP10 QLSRSRDASVPPPDTLSFITFFSVDKDGNLATNGAQMKLYSYGGDFTITEVVLIAEQVVP 166
Limestone1 QLSKSRDSSLPPPDVLSFITFFSVDKAGNLVTNGAQMKLNSYGGDFTINEIILIAEQVVP 166
AeromonasSUU RLVASRDAAVTT-DVITLATFFSIDRDGGIVTSGTSPIIRSNGGSYTLNSVLLIAEQATR 160
RB43 TLTLNRSQSVTT-STLSFVTFFSVDKNGNMVTNGTAFNIFANGSPFTVSEVLLVAEQRTT 232
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VibrioTM2740 RLVQNRSLEVDE-DVMTFSTFFSVDKNGNIATNGTAIQIRANGRDFTCTKLLLIAEQETY 161
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W-1                 ---------
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C2-1                ---------
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C4-1                ---------
C5-1                ---------
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VibrioTM11079       STEMLGGGA 170
VibrioTM2740        STEMLGGGA 170
Vibrio12129         STEILGGGA 170
VirbiroSX-4         STEMLGGGA 170
```

Figure S3. Conserved residues in Sf6 tail needle knob-like proteins.

The proteins shown in the figure S1 tree were aligned by Clustal W at the web site http://www.ebi.ac.uk/Tools/msa/clustalw2/ [Larkin *et al.* (2007) Clustal W and Clustal X version 2.0. Bioinformatics 23: 2947-2948; asjens SR, Thuman-Commike PA (2011) Evolution of mosaically related tailed bacteriophage genomes seen through the lens of phage P22 virion assembly. Virology 411: 393-415]. The tail needle knob sequences containing only residues homologous to Sf6 amino acids 140 to 282 from P22-like phages are shown above with labels on the left in red text (Sf6 and HS1 are noted with an asterisk (*) at the right end of those lines. The complete sequences of the extant homologues of this domain from outside the P22-like phage group are aligned below with labels in black text of the left. The consensus sequence is shown below with asterisks (*) marking universally conserved amino acids, colons (:) marking amino acids with strongly similar properties - scoring > 0.5 in the Gonnet PAM 250 matrix, and periods (.) marking amino acids with weakly similar properties - scoring ≤ 0.5 in the Gonnet PAM 250 matrix. In the bottom line red boxes indicate the universal conservation of the residues that contact the bound glutamate, green boxes indicate other universally conserved amino acids, and "P" marks amino acids that contact the phosphate ion on the 3-fold axis in Sf6.