

A. Alignment of amino acid sequences present on Tailspike (gp65) STGO 35-1 phage and Salmonella phage P22 tail-spike 2FNA/A, was analysis by using CLUSTAL O version 1.2.4 (Sievers and Higgins, 2014).

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pdb|2VFN|A      ----- 0
Tailspike      MATTPTSLSPISEDPRDLKFNAGKFDEVMTSDAHYYVDRFGVKRWTIAGFQYTAEEAIRA 60

pdb|2VFN|A      ----- 0
Tailspike      YGYITMDSFEDGATLTLPNQVLRYEATGEYYRWDGAFPKAVAAGSTPASTGGVGLGAWIS 120

pdb|2VFN|A      MDPDQYSIEADKKFKYSAKLSDYPTLQDAASAADVGLLIDRDYNYFYGGETVDFGGKVLTII 60
Tailspike      VGDAAFRQEANKKFKYSVKLSDYSTLQEAATAAVDGVLLIDRDYTFDTNETVDFGGKVLTII 180
                :.      :   **:*****.*****   **:**:*****:*****.*   ..*****

pdb|2VFN|A      ECKAKFIGDGNLIFTKLKGKSRIAGVFMESTTTPWVIKPWTDNQNWLTDAAAVVATLKQS 120
Tailspike      DCKAKFIGDGNLFTNLGAGSLVNSPYMESATTPWVIKPWTDNQNWITDPAAVVATLKQS 240
                :*****   **:**   :   .   :***:*****:*****:.* *****

pdb|2VFN|A      KTDGYQPTVSDYVKFPGIETLLPPNAKQNIITSTLEIRECIGVEVHRASGLMAGFLFRGC 180
Tailspike      KTDGYQPTVNDYAKFPGIESLLPPEAKDQNISSVLEIRECTGVEVHRASGLMACFLFRRC 300
                *****.*.*****:****:*.***:*.***** ***** *****

pdb|2VFN|A      HFCKMVDANNPSGGKDGIIITFENLSGDWKGNYVIGGRTSYGSVSSAQFLRNNGGFERDG 240
Tailspike      HFCKMIDADNPITGGKDGVIITFENLSGDWKGNYVIGGRTSYGSVSSAQFLRNNGGFARDG 360
                *****:*.** *****:*****:*****:***** *****

pdb|2VFN|A      GVIGFTSYRAGESGVKTWQGTVGSTTSRNYNLQFRDSVVIYPVWDGFDLGADTDMNPELD 300
Tailspike      GVIGFTSYRAGESGVKTWQGSVGSSTARNYNLQFRDSVVIYPVWEGFDLGADTDMNPEDD 420
                *****:*****:*.***:*.*****:*****:*****:*****

pdb|2VFN|A      RPGDYPIITQYPLHQLPLNHLIDNLLVRGALGVGFGMDGKGMVYSNITVEDCAGSGAYLLT 360
Tailspike      RPGDFPFSQYPVHMLPLNHLIDNLLVRGSLGVGFGMDGKGLYVSNITVEDCAGSGAYILA 480
                ***:*.***:*. *****:*****:*****:*****:*****:*.

pdb|2VFN|A      HESVFTNIAIIDTNTKDFQANQIYISGACRVNGLRLIGIRSTDGQSLTIDAPNSTVSGIT 420
Tailspike      HETVFTNIAIIDTNTKNFPANQIYISGACRVNGLRLVGIRSTNEQGLTIDAPNSTVSGIT 540
                **:*****:*. *****:*****:*****:*. *****

pdb|2VFN|A      GMVDPSRINVANLAEEGLGNIRANSFGYDSAAIKLRIHKLSKTLD SGALYSHINGGAGSG 480
Tailspike      GLVDPSRINVANLADEGLGNTRINSFNDSAAQLRIHKLTKTLD SGAVYSHINGGPGSG 600
                *:*****:***** * ** . ***:*****:*****:***** ***

pdb|2VFN|A      SAYTQLTAISGSTPDAVSLKVNHKDCRGAIEIPFVPDIASDDFIKDSSCFLLPYWENNSTSL 540
Tailspike      SAWTEITAISSLTPDAVSLKINRGDYRAVEIPVAMSPLPENAVRDIGSISMYLEG--DSL 658
                **:***:***** *****:*. * *.***. . . :. :.* ..: * * . **

pdb|2VFN|A      KALVKKPNGELVRLTLATLL 560
Tailspike      KALVRRADGSYTRLTLA--- 675
                *****:*. .*****

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Match sequence (*) marked in red and in blue different sequence.

B. Conserved domains on PhageP22-tail [lcl|Query_16388] (Marchler-Bauer et al., 2015).

Name	Accession	Description	Interval	E-value
PhageP22-tail	pfam09251	Salmonella phage P22 tail-spike	79-274	0e+00

Pssm-ID: 312676 Cd Length: 550 Bit Score: 632.91 E-value: 0e+00

			10	20	30	40	50	60	70	80			
Query_16388	6	FKYSVKLSDYSTLQ	EAATAAVDGV	LIDRDYTF	TDNETVD	FGGKVLTI	DC	KA	FIGDGNLT	FTNLGAGSLVNSPYMESATT	85		
Cdd:pfam09251	7	FKYSVKLSDYPTLQ	DAASAADVGL	LIDRDYNY	FGGETVD	FGGKVLTI	E	C	KAFIGDGNLT	IFTKLKGSR	IAGVFMES	TTT	86
		90	100	110	120	130	140	150	160				
Query_16388	86	PWVIKPWTDN	QWITDPA	AVVATLKQSKT	DGYQPTV	NDYAKFPGIES	LLPPEAKDQNI	SSVLEIRECT	GVEVHRASGLMA	165			
Cdd:pfam09251	87	PWVIKPWTDN	QWLTDA	AVVATLKQSKT	DGYQPTVSDVY	KFPGIETLLP	PNAGQNI	TS	LEIRECT	GVEVHRASGLMA	166		
		170	180	190	200	210	220	230	240				
Query_16388	166	CFLFRRCHFC	KMIDAN	PIGGK	DGVI	TFENLSGD	WGKGNV	VIGGR	TSYGSVSSAQFLRN	NGGFARDG	GVIGFTSYRAGES	245	
Cdd:pfam09251	167	GFLFRGCHFC	KMVDAN	NP	SGGKDGI	I	TFENLSGD	WGKGNV	VIGGR	TSYGSVSSAQFLRN	NGGFERD	GVIGFTSYRAGES	246
		250	260	270	280	290	300	310	320				
Query_16388	246	GVKTWQGS	VGSTARNYNL	QFRDSV	LYPVW	EGFDL	GADTDMNP	EDDRPGDF	PFSSQYYP	HMLPLNHLIDNLLVRGSLGVG	325		
Cdd:pfam09251	247	GVKTWQGT	VGSTTSRNYNL	QFRDSV	IYPVW	DGFDL	GADTDMNP	ELDRPGDY	PITQYPLHQLPLNHLIDNLLVRGALGVG	326			
		330	340	350	360	370	380	390	400				
Query_16388	326	FGMDGKGLYVSN	ITVEDCAGSGAYIL	AHETVFTN	IAI	IDTNTKNF	PANQIYISGACRVNGLRLVGIR	STNEQGLTIDAPN	405				
Cdd:pfam09251	327	FGMDGKGMVYSN	ITVEDCAGSGAYLL	THESVFTN	IAI	IDTNTKDFQANQIYISGACRVNGLRLIGIR	STDGQGLTIDAPN	406					
		410	420	430	440	450	460						
Query_16388	406	STVSGITGLVDPS	RINVANLADEGLGN	TRIN	SFNNDSAA	LQLRIHKLTK	TLDSGAVYSHINGGPGSG	472					
Cdd:pfam09251	407	STVSGITGMVDPS	RINVANLAEEGLGN	IRANS	FGYDSAAIKLRIHKL	SKTLDSGALYSHINGGAGSG	473						

Figure S1. Alignment of amino acid sequences of the tailspike (gp65), STGO 35-1 phage, and super families and putative conserved domains of P22 tail (pfam09251);

Match sequence (*) marked in red and in blue different sequence.