

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      MATTPTSLPIPEDPRDLKFNAGKFDEVMTSDAHYYVDRFGVKRWTIAGFQYTAEEAIRA 60

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

pdb|2VFN|A      MDPDQYSIEADKKFKYSAKLSDYPTLQDAASAADVGLLIDRDYNYFYGGETVDFGGKVLTI 60
Tailspike      VGDAAFRQEANKKFKYSVKLSDYSTLQEAAATAAVDGVLLIDRDYTFDNETVDFGGKVLTI 180
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pdb|2VFN|A      ECKAKFIGDGNLIFTKLGKGSRIAGVFMESSTTPWVIKPWTDDNQWLTDAAAVVATLKQS 120
Tailspike      DCKAKFIGDGNLFTNLGAGSLVNSPYMESATTPWVIKPWTDDNQWITDPAVVATLKQS 240
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pdb|2VFN|A      KTDGYQPTVSDYVKFPGIETLLPPNAKQNI TSTLEIRECI GVEVHRASGLMAGFLFRGC 180
Tailspike      KTDGYQPTVNDYAKFPGIESLLPPEAKDQNI SSVLEIRECT GVEVHRASGLMACFLFRRC 300
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pdb|2VFN|A      HFCKMVDANNPSGGKDGIIITFENLSGDWKGKGYVIGGRTSYGSVSSAQFLRNNGGFERDG 240
Tailspike      HFCKMIDADNPIGGKDGVIITFENLSGDWKGKGYVIGGRTSYGSVSSAQFLRNNGGFARDG 360
***** :** :** ***** :***** :***** :***** :***** ***** *

pdb|2VFN|A      GVIGFTSYRAGESGVKTWQGTVGSTTSRNYNLQFRDSVVIYPVWDGFDLADTDMNPELD 300
Tailspike      GVIGFTSYRAGESGVKTWQGSVGSSTARNYNLQFRDSVVIYPVWEGFDLADTDMNPEDD 420
***** :** :** :***** :***** :***** :***** :***** :***** *

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

pdb|2VFN|A      HESVFTNIAI IDTNTKDFQANQIYISGACRVNGLRLIGIRSTDQSLTIDAPNSTVSGIT 420
Tailspike      HETVFTNIAI IDTNTKNFPANQIYISGACRVNGLRLVIGIRSTNEQSLTIDAPNSTVSGIT 540
** :***** :* ***** :***** :***** :* *****

pdb|2VFN|A      GMVDPSRINVANLA E E L G N I R A N S F G Y S A A I K L R I H K L S K T L D S G A L Y S H I N G G A G S G 480
Tailspike      G L V D P S R I N V A N L A D E G L G N T R I N S F N N D S A A L Q L R I H K L T K T L D S G A V Y S H I N G G P G S G 600
* :***** :***** * * * . * * * :***** :***** :***** :***** *

pdb|2VFN|A      SAYTQLTAISGSTPDAVSLKVNHKDCRGA E I P F V P D I A S D D F I K D S S C F L P Y W E N N S T S L 540
Tailspike      S A W T E I T A I S G S L P D A V S L K I N R G D Y R A V E I P V A M S P L P E N A V R D I G S I S M Y L E G - - D S L 658
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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	<a href="#">pfam09251</a>	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															
<a href="#">Query_16388</a>	6	FKYSVKLS	SDYSTLQ	EAAATA	AVDGLI	DRDYTF	TDNETV	DFGGKVL	TIDCKAK	FIGDGNL	TFTNLG	AGSLV	NSPYMES	ATT	85									
<a href="#">Cdd:pfam09251</a>	7	FKYSVKLS	SDYPTLQ	DAASA	AVDGLL	IDRDY	TFYGG	ETVDF	GGKVL	TECKAK	FIGDGNL	IFTKL	GKSR	IAGVFM	ESTTT	86								
		90	100	110	120	130	140	150	160															
<a href="#">Query_16388</a>	86	PWVIKP	WTDNQW	ITDPA	AAVVAT	LKQSK	TDGYQ	PTVND	YAKF	PGIES	LLPPE	AKDQ	NISS	VLEIR	ECTG	VEVHR	ASGLMA	165						
<a href="#">Cdd:pfam09251</a>	87	PWVIKP	WTDNQW	LTDAA	AVVATL	LKQSK	TDGYQ	PTVSD	YVKFP	GIETL	LLPNA	KQNI	STLE	IREC	IGVEV	HRASGL	MA	166						
		170	180	190	200	210	220	230	240															
<a href="#">Query_16388</a>	166	CFLFRR	CHFC	KMID	ADNPI	GGKDV	ITFEN	LSGD	WGKGN	YVIG	GR	TSYGS	VSSAQ	FLRN	NGGF	ARDG	GVIG	FTSYR	AGES	245				
<a href="#">Cdd:pfam09251</a>	167	GFLFRG	CHFC	KMVD	ANNP	SGGDG	IITFEN	LSGD	WGKGN	YVIG	GR	TSYGS	VSSAQ	FLRN	NGGF	ERD	GGVI	GFTSYR	AGES	246				
		250	260	270	280	290	300	310	320															
<a href="#">Query_16388</a>	246	GVKTW	QGS	VGSS	TARN	YNLQ	FRDS	VVLY	PVWE	GFDL	GADT	DMNP	EDDR	PGD	FPFS	QYPV	HMLP	LNHL	IDNLL	VRG	SLG	VG	325	
<a href="#">Cdd:pfam09251</a>	247	GVKTW	QGT	VGST	TSRN	YNLQ	FRDS	VVLY	PVWD	GFDL	GADT	DMNP	ELDR	PGD	YPIT	QYPL	QLPL	NHLI	DNLL	VRG	ALG	VG	326	
		330	340	350	360	370	380	390	400															
<a href="#">Query_16388</a>	326	FGMDG	KGLY	VSNIT	VEDC	AGS	GAYIL	AHET	VFTN	IAI	IDT	NTKN	FPAN	QIY	ISG	ACRV	NGLR	LVG	IRST	NEQ	GLT	ID	APN	405
<a href="#">Cdd:pfam09251</a>	327	FGMDG	KGM	YVSN	ITVED	CAGS	GAYLL	THES	VFTN	IAI	IDT	NTK	DFQ	ANQ	IYIS	GACR	VNGL	RLLI	GIRST	DGQ	GLT	ID	APN	406
		410	420	430	440	450	460																	
<a href="#">Query_16388</a>	406	STVSG	ITGL	VDP	SRIN	VANL	ADE	GLGN	TRIN	SFN	NSA	ALQL	RIH	KLTK	LD	SGA	VYSH	INGG	PGSG					472
<a href="#">Cdd:pfam09251</a>	407	STVSG	ITGM	VDP	SRIN	VANL	ADE	GLGN	TRIN	SFG	YD	SAAI	KLR	IHK	LSK	TL	D	SGA	LYSH	INGG	AGSG			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.