

draft phage Superstar (BD2)

gene at the coordinates 31,549 to 31,764 (gene 47 on Phamerator)

Nr	Hit	Name	Probability	E-value	Score	SS	Aligned cols	Target Length
<input type="checkbox"/> 1	PF11985.12	; Phage_Mu_Gp27 ; Bacteriophage Mu, Gp27	99.14	3.8e-10	74.45	6.2	50	197
<input type="checkbox"/> 2	Q9T1W7	TERS_BPMU Probable terminase, small subunit gp27 OS=Escherichia phage Mu OX=10677 GN=Mup27 PE=1 SV=1	99	5.2e-9	68.47	7	54	191
<input type="checkbox"/> 3	7PC1_A	StbA; Plasmid conjugation, Plasmid partition, Helix-Turn-Helix, DNA BINDING PROTEIN; HET: MSE; 1.9A {Escherichia coli K-	98.74	2.9e-7	51.6	7.5	44	72
<input type="checkbox"/> 4	PF17273.6	; DUF5338 ; Family of unknown function (DUF5338)	98.21	0.000014	43.83	5.3	43	68
<input type="checkbox"/> 5	5FD5_B	Ferric uptake regulation protein; fur, ferric uptake regulator, apo, mur, transcription; HET: SO4, EDO; 1.91A {Rhizobium	97.95	0.00023	43.6	7.6	56	141

Template alignment | [CDD](#)

1. **PF11985.12 ; Phage_Mu_Gp27 ; Bacteriophage Mu, Gp27**

Probability: 99.14%, E-value: 3.8e-10, Score: 74.45, Aligned cols: 50, Identities: 12%, Similarity: 0.064, Template Neff: 7.3

Q ss_pred		HHhCCHHHHHHHHHHHHhCC-CCHHHHHHHHHH-----HCCCC-----CCHHHHHHHHHHHHHH	
Q Q_6715591	19	YAAMNEDEQGALAPHILGE-TSADWLSSTLR-----RHGHD-----VSATTIRTYRRSLRQ	68 (71)
Q Consensus	19	~L~r~l~l~g~s~i~L~-----~G~-----iS~stv~R~l~	68 (71)
		++. ++. ++ +.+ .++ + +++ .+ + ++ +.	
T Consensus	1	Id~LP~eire~l~L~t~e~i~L~-----G~-----iSrSav~Ry~	71 (197)
T PF11985.12	1	ADRLPPPLREALANLWFEQKYSLDQILAHNLALARGERSMLPPELAAAPAIPPEAVPGRSGLHAHLKGVSK	71 (197)
T ss_pred		CccCCHHHHHHHHHHHHhCCCCHHHHHHHHHHHHhhccCCChHHhCCCCCCCCCChHHHHHHHHHHHHH	