

Annotation

Metadata

- G&C content:
- Genome length:
- Morphology: Siphoviridae
- Naming:
- Source of isolation:
- Host range: M Smegmatis
- Temperate/lysogenic: Lytic/temperate
- Nucleotide bias:
- Taxonomy: Caudoviricetes

Template

SSC: [coordinate numbers], CP: [yes/no] , SCS:, ST: [SS, NA(not applicable, NI(not informative), Blast-Start: [phage name, gene number, NCBI, Q : S, coverage, e value/no significant, Blast alignments], GAP: [number of bp], LO [yes/no/NA], RBS: [kibler6, Karlin medium, Z score, Final score, yes/no], F: [Gene Function/NKF] , SIF : SIF-BLAST [NKF / function, NCBI, phage name and gene number, NCBI gene accession number, %alignment, evalule], SIF-HHPred [NKF / function, NCBI, phage name and gene number (if applicable, Hit, %alignment*, probability], SIF-Syn: [NKF / function, flanking genes and phages used to infer]

Links

HHPred: <https://toolkit.tuebingen.mpg.de/jobs/5411092>

Phamerator: <https://phamerator.org/phages>

NCBI: <https://blast.ncbi.nlm.nih.gov/Blast.cgi>

, STarterator N/A - if there is no file

N/I - no informat doesnt help at all if it doesnt call it or doesnt have it as most anotated

Ss - most anotated

ORF	Annotation
1	SSC: [136, 564], CP: (coding potential [yes] , SCS [Glimmer], ST: starterator [SS], Blast-Start: [Kenuha5,1, NCBI, 1 : 1, 99%, 2e-97], GAP (or overlap: [0], LO (Longest ORF [no], RBS: [kibler6, Karlin medium, 1.872, -4.952, no], F: [Terminase small subunit] , SIF : SIF-BLAST [terminase small subunit, NCBI, Kenuha5 and gene 1, MN369739.1 ,99%, 2e-97], SIF-HHPred [terminase small subunit, PDB, 6Z6E_A , 56.6%, 97.83], SIF-Syn: [terminis subunit, terminase large subunit and phages used were Sisi, Totinger, and Kenuha5]
2	SSC: [587,2224], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [sparkdehlily, 2, NCBI, 1 :1, coverage, 0.0, GAP (or overlap: [158], LO (Longest ORF [yes], RBS: [kibler6, Karlin medium,1.807,-5.086, no], F: [Terminase large subunit] , SIF : SIF-BLAST [Terminase large subunit, NCBI, spardelihly 2, YP_009187158.1, 100%, 0.0], SIF-HHPred [terminase large subunit, PDB, HK97 (if applicable, 6Z6D_A , 83.15%, 100], SIF-Syn: [Terminase large subunit, Terminase small subunit, and portal protein are the flanking genes. and phages used to infer were totinger, mantra, and sparkdelihly]
3	SSC: [2255, 3625], CP: [yes] , SCS: Glimmer, ST: [Ni], Blast-Start: [MadMen, 3, NCBI, 1 :1, 100%, 0.0], GAP: [31], LO [yes], RBS: [kibler6, Karlin medium,

	2.749, -3.280, yes], F: [Portal protein] , SIF : SIF-BLAST [portal protein, Genmark, MadMen 3, UAW08481.1 , 100%, 0.0], SIF-HHPred [portal protein, PDB, Bxb1 (if applicable, 9D94_Fd , 90.37, 100], SIF-Syn: [Portal Protein, Major tail protein and capsid maturate protease and phages used to infer were madmen and mantra]
4	SSC: [3612, 4367], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [gUmbie 4r, NCBI, 1 : 1, 100%, 0.0], GAP: [-13], LO [yes], RBS: [kibler6, Karlin medium, 2.912, -4.109, yes], F: [Capsid maturation protease] , SIF : SIF-BLAST [head maturation protease, gUmbie 4, NCBI YP_009018880.1 , 100%, 0.0], SIF-HHPred [phage minor capsid protein, Pfam, PF06152.16 , 28.85%, 98.88], SIF-Syn: [capsid maturation protease, flanking genes are portal protein and scaffolding protein and phages used to infer were mantra and Madmen]
5	SSC: [4452, 5045], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Saal, 5, NCBI, Q1 : 1, 99%, 3e-137], GAP: [85], LO [yes], RBS: [kibler6, Karlin medium, 3.225, -2.808, yes], F: [scaffolding protein] , SIF : SIF-BLAST [head scaffolding protein, NCBI, saal 5, NCBI, YP_009007472.1 , 99%, 3e-137], SIF-HHPred [scaffold protein, PDB, 80Alpha, 6BOX_g , 88.89%, 97.68], SIF-Syn: [scaffolding protein, capsid maturation protease - major capsid protein and phages used to infer were madmen and mantra]
6	SSC: [5064, 5885], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Saal, 6 NCBI, 1 : 1, 100%,0.0], GAP: [19], LO [yes], RBS: [kibler6, Karlin medium, 2.571, -3.571, yes], F: [Major capsid protein] , SIF : SIF-BLAST [major capsid protein, NCBI, Saal and 6, YP_009007473.1 100%, 0.0], SIF-HHPred [major capsid protein, PDB, micobacterium virus Che8 and (if applicable, 8E16_C , 99.23%, 99.98], SIF-Syn: [major capsid protein,scaffolding protein, head to tail addaptor and phages used to infer were Saal, Madmen]
7	SSC: [5894, 6463], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Saal, 7, NCBI, 1:1, 99%,4e-130], GAP: [9], LO [yes], RBS: [kibler6, Karlin medium, 1.315, -6.453, no], F: [Head to-tail adaptor] , SIF : SIF-BLAST [head to tail adaptor, NCBI, Saal and 7, YP_009007474.1 , 99%, 4e-130], SIF-HHPred [head completion protein, NCBI, phage name DT57C, 8HQO_Q , 84.74%, 99.93], SIF-Syn: [head to tail adaptor, flanking genes are major capsid protein and head to tail stopper and phages used to infer totinger and mantra]
8	SSC: [6460-6789] CP:[yes] SCS: [Glimmer] ST: starterator [SS], Blast-Start: [Rialto, 9, NCBI, 1:1, Coverage 99%, e value 3e-71] Gap: [-3], LO: [yes] RBS: [Kibler6, Karlin medium, 1.795, -5.462, No] F : [head-to-tail stopper] SIF : - SIF-BLAST [Head-to-tail-stopper, NCBI, Rialto GP 9, NCBI gene 9, WNM65575.1 , 99%, 3e-71] - SIF-HHPred [head-to-tail stopper, PDB, phage name is mycobacterium Bxb 1 9D94_Hc , %alignment* is 88.18%, probability is 99.61%] - SIF-Syn: [Head-to-tail stopper, downstream head-to-tail stop terminator, upstream head-to-tail adapter with rialto, totinger, and Gigioioui. Little to no differences in these areas of each of their genomes. I used totinger as the phage most similar to mine because mine is not yet in phamerator]

9	SSC: [6826, 7122] CP: [yes] SCS (Glimmer ST: starterator [SS, NA(not applicable, NI(not informative] Blast-Start: [Pacc40, 9, NCBI, 1 : 1, 99%,1e-65, Blast alignments] Gap: [37] LO (Longest ORF [no] RBS: [kibler6, karlin medium, 2.832, -3.030, yes] and F : [Minor capsid protein] SIF function as below: - SIF-BLAST [haid-to-tail connector, NCBI, Pacc40 and 9,YP_002241593.1, 99%,1e-65] - SIF-HHPred [Minor capsid protein, Pfam, N/A, PF11114.13 , 68.69%, 99.31] - SIF-Syn: [Hypothetical Protein, head to tail stop, tail terminator, Pacc40 and Mantra]
10	SSC: [7112, 7516] CP: (coding potential [yes] SCS: [Genemark] ST: [SS], Blast-Start: [Boomer, 11, NCBI, 1 : 1, 99%,3.0e-89] Gap: [-10] LO (Longest ORF [yes] RBS: [kibler6, Karlin medium, Z1.248, -6.241, no] F : [Head-to-tail] (NCBI and phamerator, SIF function as below: - SIF-BLAST [Head-to-tail adapter], NCBI, Boomer and 11,YP_002014227, 99%, 3.0e-89], SIF-HHPred [Tail terminator, Protein Data Bank, Bxb 1, 9D94_Ic ,91.85%, 99.81%], SIF-Syn: [Head-to-tail adapter, head to tail stopper, major capsid protein and Boomer and sparkdelily]
11	SSC: start/stop coordinates. [7626, 8435], CP: (coding potential [yes] , SCS: [glimmer], ST: [SS], Blast-Start: [Empress, 11, NCBI, 1 : 26, 100%, 0.0], GAP : [110], LO (Longest ORF [yes], RBS: [kibler6, Karlin medium, 3.167,-2.339, yes], F: [Major Tail Protein] , SIF : SIF-BLAST [Major tail protein, NCBI, emress and 11,YP_009956679,100%, 0.0], SIF-HHPred [Major Tail protein, PDB, Bxb 1, 9D9L_J ,63.70%, 99.82%], SIF-Syn: [major tail subunit, tail terminator and tail assembly chaperone and Empress, totinger, boomer]
12	SSC: [8549, 9100], CP: [yes] , SCS [Glimmer], ST: [SS], Blast-Start: [Pacc4p, 12, NCBI, 1 : 1, 99%,8e-130], GAP : [114], LO (Longest ORF [yes], RBS: [kibler6, Karlin medium, 2.988, -2.708, yes], F: [Tail assembly chaperone] , SIF : SIF-BLAST [Tail assembly chaperone, NCBI, Pacc40 and 12, YP_002241597, 99%,8e-130], SIF-HHPred [Tail assembly protein, Pfam, PF17388.7 , 28.80%, 95.85], SIF-Syn: [Tail assembly chaperone, Major tail subunit, tail assembly chaperone, and Pacc40, Gigioiuoi]
13	SSC: [9051, 9485], CP: [yes] , SCS [Glimmer], ST: starterator [NI], Blast-Start: [Byougenkin, 13, NCBI, 1 : 168, 99%, 1e-96], GAP (or overlap: [-49], LO (Longest ORF [no], RBS: [kibler6, Karlin medium, 2.988, -2.708, yes], F: [Tail Assembly chaperone] , SIF : SIF-BLAST [Tail assembly chaperone, NCBI, Byougenkin and 13, YP_009955319, 99%, 12-96], SIF-HHPred [NKF], SIF-Syn: [tail assembly protein, tail assembly chaperone, tape measure protein, byougenkin, pacc4p, empress]
14	SSC: start/stop coordinates. [9504, 12992], CP: [yes] , SCS [Glimmer], ST: [SS], Blast-Start: [starceovich, 15, NCBI, 1 : 1,100%, 0.0], GAP: [19], LO (Longest ORF [yes], RBS: [kibler6, Karlin medium, 2.492, -3.812, no], F: [Tape Measure protein] , SIF : SIF-BLAST [Tap measure protein, NCBI, starceovich and 15,WNM68406.1,100%, 0.0], SIF-HHPred [tap measure protein, pdb, Chi, 8VJH_Q , 34.56%,97.57], SIF-Syn: [Tape measure protein, tail assembly chaperone, minor tail protein Starceovich, Pacc40]
15	SSC: start/stop coordinates. [12993,14702], CP: (coding potential [yes] , SCS [Glimmer], ST: starterator [SS], Blast-Start: [starceovich, 16, NCBI, 1 : 1, 100%, 0.0], GAP (or overlap: [1], LO (Longest ORF [yes], RBS: [kibler6, Karlin medium, 1.974, -4.821, no], F: [Minor Tail Protein] , SIF : SIF-BLAST [Minor

	Tail protein, NCBI, starceвич and 16, WNM68407.1 , 100%, 0.0], SIF-HHPred [minor tail protein, pdb, bxb, 9D93_Mf , 26.84%, 99.66%], SIF-Syn: Minor Tail Protein, Tape measure protein and Starceвич, totinger, pacc40]
16	SSC: start/stop coordinates. [14759, 16468], CP: (coding potential [yes] , SCS [Glimmer], ST: starterator [SS], Blast-Start: [Pacc 40, 16, NCBI, 1 : 1, 100%, 0.0], GAP (or overlap: [57], LO (Longest ORF [yes], RBS: [kibler6, Karlin medium, 3.323, -2.606, yes], F: [Minor tail protein] , SIF : SIF-BLAST [Minor tail protein, NCBI, Pacc40 and 16, YP_002241600.1 , 100%, 0.0], SIF-HHPred [Minor tail protein, PDB, Bxb1, 9D93_Oa , 91.20%, 100], SIF-Syn: [Minor tail protein, minor tail protein and minor tail protein, starceвич, pacc40, gigioioui]
17	SSC: [16525, 17355], CP: (coding potential [yes] , SCS [Glimmer], ST: starterator [NI], Blast-Start: [Saal, 17, NCBI, 1 : 6, 100%, 0.0], GAP (or overlap: [57], LO (Longest ORF [no], RBS: [kibler6, Karlin medium, 2.895, -3.190, yes], F: [Minor tail protein] , SIF : SIF-BLAST [minor tailprotein, NCBI, Saal 17, YP_009007484.1 , 100%, 0.0], SIF-HHPred [sucrose polymerase, Pfam, PF09244.15 , 11.55%, 36.16], SIF-Syn: [minor tail protein, flanking genes are minor tail protein and minor tail protein and phages used, pacc40 starceвич, saal]
18	SSC: start/stop coordinates. [17352, 19889], CP: (coding potential [yes] , SCS: [Glimmer], ST: starterator [SS], Blast-Start: [Mantra, 18, NCBI, 1 : 1, 100%, 0.0], GAP (or overlap: [-3], LO (Longest ORF [yes], RBS: [kibler6, Karlin medium, 2.436, -4.695, no], F: [Minor tail protein] , SIF : SIF-BLAST [minor tail protein, NCBI, mantra, 18, YP_009959382.1 , 100%, 0.0], SIF-HHPred [minor tail protein, PDB, Bxb 1, 9D93_Pb , 72.92% 100], SIF-Syn: [minor tail protein, minor tail protein, minor tail protein and phages used starceвич, mantra, pacc40]
19	SSC: start/stop coordinates. [19886, 21772], CP: (coding potential [yes] , SCS [Glimmer], ST: starterator [SS, NA(not applicable, NI(not informative], Blast-Start: [Rialto, 21, NCBI, 1 : 1, 100%, 0.0], GAP (or overlap: [-3], LO (Longest ORF [yes], RBS: [kibler6, Karlin medium, 2.829, 3.626, no], F: [minor tail protein] , SIF : SIF-BLAST [minor tail protein, NCBI, Rialto, 21, WNM65587.1 , 100%, 0.0], SIF-HHPred [minor tail protein, PDB, bxb1 (if applicable, 9D93_Sa , 78.86%, 100], SIF-Syn: [minor tail protein, minor tail protein and minor tail protein, rialto, pacc40]
20	SSC: start/stop coordinates. [21769, 22935], CP: (coding potential [yes] , SCS [Genemark], ST: starterator [SS], Blast-Start: [rialto, 22, NCBI, 1 : 1, 100%, 0.0], GAP (or overlap: [], LO (Longest ORF [no], RBS: [kibler6, Karlin medium, 1.626, -5.539, no], F: [minor tail protein] , SIF : SIF-BLAST [minor tail protein, NCBI, rialto, 22, WNM65588.1 , 100%, 0.0], SIF-HHPred [NA], SIF-Syn: [minor tail protein, hypothetical protein, minor tail protein and rialto, pacc40, starceвич]
21	SSC: start/stop coordinates. [22953, 23294], CP: (coding potential [yes] , SCS [Glimmer], ST: starterator [NI], Blast-Start: [Pacc40, 21, NCBI, 1 : 1, 99%, 5e-69], GAP (or overlap: [18], LO (Longest ORF [no], RBS: [kibler6, Karlin medium, 3.225, -2.156, yes], F: [hypothetical protein] , SIF : SIF-BLAST [Gp 21, NCBI, Pacc40 and 21, NCBI, YP_002241605.1 , 99%, 5e-69], SIF-HHPred

	[virion associated phage protein, NCBI, 8JOU_i , 94.73%, 99.92], SIF-Syn: [Hypothetical protein, minor tail protein, hypothetical protein and Saal, pacc40]
22	SSC: start/stop coordinates. [23317, 23571], CP: (coding potential [yes] , SCS start choice source, ST: starterator [SS], Blast-Start: [pacc40, 22, NCBI, 1 : 1, 99%,2e-54], GAP (or overlap: [23], LO (Longest ORF [yes], RBS: [kibler6, Karlin medium, 2.033, -4.699, yes], F: [hypothetical protein] , SIF : SIF-BLAST [minor tail protein, NCBI, Pacc40 and 22, YP_002241606.1 , 99%, 2e-54], SIF-HHPred [uncharacterized protein, PDB, 5JN6_A , 48.2%, 94.26], SIF-Syn: [Hypothetical protien, hypothetical protiens and rialto, pacc40, totinger]
23	SSC: start/stop coordinates. [23584, 24222], CP: (coding potential [yes] , SCS [Glimmer], ST: starterator [SS, NA(not applicable, NI(not informative], Blast-Start: [sisi, 23, NCBI, 1 : 1,100%, 3e-147], GAP (or overlap: [13], LO (Longest ORF [yes], RBS: [kibler6, Karlin medium, 2.513, -3.628, yes], F: [minor tail protien] , SIF : SIF-BLAST [minor tail protein NCBI, SiSi and 23, YP_008051149.1 , 100%, 3e-147], SIF-HHPred [minor tail protein, NCBI, 9D93_Lb , 51.17%, 99.04], SIF-Syn: [minor tail protein, flanked by minor tail proteins, and totinger and sisi were used]
24	SSC: [24219, 25160], CP: [yes] , SCS: Glimmer, ST: [SS, NA(not applicable, NI(not informative], Blast-Start: [rialto, gene number 26, Genbank, 1 : 1, 100%,0.0], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 2.064, -4.635, yes], F: [minor tail protein] , SIF : SIF-BLAST [hypothetical protein, Genbank, rialto and gene number 26, WNM65592.1 100%, 0.0], SIF-HHPred [minor tail protein, PDB, phage Bxb1 9D93_Qa , 36.62%, 98.86], SIF-Syn: [hypothetical protein, flanking genes were hypothetical proteins and minor tail proteins and phages used to infer were totinger, rialto, starcovich]
25	SSC: [25362, 25165], CP: [yes] , SCS: [Glimmer], ST: [SS], Blast-Start: [pacc40, 25, NCBI, 1 : 1, 98%, 2e-38], GAP: [5], LO [yes], RBS: [kibler6, Karlin medium, 1.484, -6.661, no], F: [Helix-turn-Helix DNA binding domain protein] , SIF : SIF-BLAST [HTH DNA binding protein, NCBI,Pacc40 gene 25, YP_002241609.1 , 98%, 2e-38], SIF-HHPred [Transcritpion factor, PDB, , 2H8R_A , 87.88%, 97.05], SIF-Syn: [DNA binding protein, flanking genes are hypothetical protein and phages used to infer were pacc40 and totinger]
26	SSC: [25511, 25807], CP: [yes] , SCS: [Glimmer], ST: [SS], Blast-Start: [Boomer 27, NCBI, 1 : 1, 99%, 3e-64], GAP: [149], LO [yes], RBS: [kibler6, Karlin medium, 3.427, -2.253, yes], F: [Hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, NCBI, boomer 27, YP_002014243.1 , 99%, 3e-64], SIF-HHPred [aligate lyase, PDB, 7W13_A , 27.23%, 80.65], SIF-Syn: [hypothetical protein, flanking genes were HTH DNA BINDING DOMAIN PROTEIN hypothetical proten and phages used to infer were phlipplop and boomer]
27	SSC: [25814,25963], CP: [yes] , SCS:, ST: [SS], Blast-Start: [Boomer, 28, NCBI, 1 : 1, 100%,5e-26], GAP: [7], LO [yes], RBS: [kibler6, Karlin medium, 2.143, -4.454, yes], F: [hypothetical protein] , SIF : SIF-BLAST [hypothetical protien, NCBI, boomer 28, YP_002014244.1 , 100%, 5e-26], SIF-HHPred

	[NKF], SIF-Syn: [hypothetical protein, flanking genes were both hypothetical proteins and phages used to infer were boomer, phlipphlop and totinger]
28	SSC: [25960, 26097], CP: [yes] , SCS: Glimmer, ST: [NI], Blast-Start: [Rialto 30, NCBI, 1 : 1, 98%, 1e-21], GAP: [6], LO [yes], RBS: [kibler6, Karlin medium, 3.258, -2.090, yes], F: [hypothetical] , SIF : SIF-BLAST [membrane protein, Genbank, rialto 30, OR475257.1 , 98%, 1e-21], SIF-HHPred [Mitoregulin, Pfam, PF22002.1 , 53.33%,81.58], SIF-Syn: [hypothetical protein, flanking genes were both hypothetical proteins and phages used to infer were phlipphlop totinger and boomer]
29	SSC: [26231, 27477], CP: [yes] , SCS:, ST: [SS], Blast-Start: [rialto, 31, NCBI, 1 : 1, 100%, 0.0], GAP: [133], LO [yes], RBS: [kibler6, Karlin medium, 1.655, -5.480, no], F: [transposase] , SIF : SIF-BLAST [transposase, Genbank, Rialto 31, WNM65597.1 , 100%, 0.0], SIF-HHPred [Transposon-associated protein, PDB, 8H1J_A , 81.3%*, 100%], SIF-Syn: [transposase, flanking genes were both hypothetical proteins and phages used to infer phlipphlop and rialto]
30	SSC: [27612, 27863], CP: [yes] , SCS: GeneMark, ST: [SS], Blast-Start: [Ogopogo, 29, Genbank, 1 : 1, 99%, 6e-46], GAP: [105], LO [yes], RBS: [kibler6, Karlin medium, 1.954, -4.845, no], F: [hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, Genbank, ogopogo 29, AVJ50668.1 , 99%, 6e-46], SIF-HHPred [Histone chaperone, Pfam, PF18215.6 , 23.8, 59.37], SIF-Syn: [hypothetical protiens, flanking genes were hypothetical protein and transposase and phages used to infer rialto and phlipphlop]
31	SSC: [27860, 29131], CP: [yes] , SCS:, ST: [NI], Blast-Start: [Saal, 30, NCBI, 1 : 1, 100%, 0.0], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 2.222, -4.229, yes], F: [Lysin A] , SIF : SIF-BLAST [Endolysin, NCBI, Saal, 30, YP_009007497.1 ,100%, 0.0], SIF-HHPred [Peptidoglycan Recognizing Protein, PDB, phage K12 (if applicable, 3D2Y_A , 43.87, 99.5], SIF-Syn: [Lysin A, flanking genes hypothetical protein and Lysin B and phages used to infer rialto boomer pacc40]
32	SSC: [29131, 30132], CP: [yes] , SCS: Glimmer, ST: [NI(not informative)], Blast-Start: [Saal, 31, NCBI, 1 : 1, 100%, 0.0], GAP: [0], LO [yes], RBS: [kibler6, Karlin medium, 2.598, -3.593, yes], F: [Lysin B] , SIF : SIF-BLAST [endolysin, NCBI, Saal 31, YP_009007498.1 , 100%, 0.0], SIF-HHPred [Lysin B , NCBI, D29, 12(if applicable, 3HC7_A , 72.16%, 100], SIF-Syn: [Lysin B, flanking genes were lysin A and Holin and phages used to infer rialto, totinger, boomer]
33	SSC: [30146, 30379], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Hamulus, 33, NCBI, 1 : 1, 99%, 3e-43], GAP: [14], LO [no], RBS: [kibler6, Karlin medium, 2.917, -3.145, yes], F: [Holin] , SIF : SIF-BLAST [Holin, NCBI, Hamulus 33, YP_008409097.1 , 99%, 3e-43], SIF-HHPred [Holin, Pfam, PF16945.10 , 89.74%, 99.89], SIF-Syn: [Holin, flanking genes were Lysin B and hypothetical protein and phages used to infer rialto, totinger]
34	SSC: [30376, 30750], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Saal, 33, NCBI, 1 : 1, 99%, 3e-80], GAP: [-3], LO [yes], RBS: [kibler6, Karlin

	medium, 1.682, -5.486, no], F: [Minor tail protein] , SIF : SIF-BLAST [minor tail protein, NCBI, Saal 33, YP_009007500.1, 99%, 3e-80], SIF-HHPred [NKF], SIF-Syn: [hypothetical protein, flanking genes are holin and hypothetical proteins and phages used to infer saal, rialto] When in did a blast of rialtos gene 37 it said minor tail protein
35	SSC: [30775, 31008], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Leperchaun, 34, GenBank, 1 : 1, 99%, 3e-49], GAP: [-5], LO [yes], RBS: [kibler6, Karlin medium, 2.807, -3.082, yes], F: [Hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, Genbank, Leprechaun 34, QYC53856.1, 99%, 3e-49], SIF-HHPred [NKF], SIF-Syn: [Hypothetical protein, flanking genes are hypothetical proteins and DNAA-like DNA polymerase III and phages used to infer rialto, saal]
36	SSC: [30995, 31816], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Che8 , 37 NCBI, 1 : 1, 100%, 0.0], GAP: [-13], LO [yes], RBS: [kibler6, Karlin medium, 2.832, -3.048, yes], F: [DnaQ-like polymerase III subunit] , SIF : SIF-BLAST [DNAQ-like DNA polymerase III subunit, NCBI, Che8 37, NP_817375.1, 100%, 0.0], SIF-HHPred [Exonuclease, PDB, Hit, 62.77, 99.48], SIF-Syn: [DnaQ-like DNA polymerase III subunit, flanking genes are hypothetical proteins and phages used to infer rialto, saal]
37	SSC: [31891, 32124], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [Hamulus, 37, NCBI, 1 : 1, 99%, 4e-47], GAP: [75], LO [no], RBS: [kibler6, Karlin medium, 2.234, -5.305, no], F: [Hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, NCBI, Haumulus, 37, YP_008409101.1, 99%, 4e-47], SIF-HHPred [Hypothetical protein, Scop. Berkeley, SCOP_d2ns0a1, 32.05%, 38.11], SIF-Syn: [Hypothetical protein, flanking genes are DNAQ-like DNA polymerase III subunit and hypothetical proteins and phages used to infer were saal pacc40]
38	SSC: [32362, 32493], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [Krakatau 39, NCBI, 1 : 1, 100%, 1e-22], GAP: [238], LO [no], RBS: [kibler6, Karlin medium, 1.806, -5.227, no], F: [Hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, NCBI, Krakatau 39, NCBI gene YP_009958895.1, 100%, 1.3e-22], SIF-HHPred [C-terminal domain Scope, SCOP_d3p0ya2, 36.36%, 48 probability], SIF-Syn: [hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer were pacc40 totinger and saal]
39	SSC: [32657, 32457], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [Totinger 41, Genbank, 1 : 1, 100%, 2e-39], GAP: [36], LO [yes], RBS: [kibler6, Karlin medium, 2.782, -3.900, yes], F: [Hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, Genbank, totinger 41, XIJ70788.1, 100%, 2e-39], SIF-HHPred [Structural protein, PDB, its from a type of archea, 7WHG_G, 98.5%, probability is 80.3], SIF-Syn: [hypothetical protein, flanking genes are hypothetical protein and endonuclease and phages used to infer were saal and pacc40]
40	SSC: [33053, 34342], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [GUmbe, gene 41, NCBI, 1 : 1, 100%, 0.0], GAP: [396], LO [yes], RBS: [kibler6, Karlin medium, 2.425, -3.911, no], F: [tyrosine integrase] , SIF : SIF-BLAST [endonuclease, NCBI, GUmbe gene 41, NCBI gene

	YP_009018917.1, 100%, 0.0] some similar proteins were called as tyrosine integrase and endonuclease is not a function that sea phages accepts., SIF-HHPred [Integrase protein-DNA complex, NCBI, protein from a virus, Hit, 76%, 100 probability], SIF-Syn: [tyrosine integrase, flanking genes are both hypothetical proteins and phages used to infer saal, pacc40 gigiouiu]
41	SSC: [34871, 34425], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [cornie, 36, NCBI, 1 : S, 99%, 4e-98], GAP: [83], LO [yes], RBS: [kibler6, Karlin medium, 1.990, -5.809, no], F: [hypothetical protein] , SIF : SIF-BLAST [hypothetical protien NCBI, Cornie 36, YP_009856222.1, 99%, 4e-98], SIF-HHPred [uncharacterized lipoprotein, PDB, from ecoli, 8H1R_F, %alignment* was 35.57%, 90.93], SIF-Syn: [hypothetical protein, flanking genes are hypothetical protein and tyrosine integrase and phages used to infer were pacc40]
42	SSC: [35637, 35134], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [Karhdo, 44, genbank, 1 : 1, 99%, 3e-115], GAP: [number of bp], LO [no], RBS: [kibler6, Karlin medium, 1.179, -6.464, no], F: [Immunity repressor] , SIF : SIF-BLAST [immunity repressor, gene bank, Karhdo 44, WKW86670.1, 99%, 3e-115], SIF-HHPred [DNA-binding domain, Scop, alsmonella bacteriophage p22, SCOP_d3jxbc_, 36.90%, 98], SIF-Syn: [immunity repressor, flanking genes are hypothetical protiens and phages used to infer pacc40 karhdo]
43	SSC: [35821, 36126], CP: [yes] , SCS: gene mark, ST: [SS], Blast-Start: [Slsi, 46, NCBI, 1 : 1, 99%, 13-67], GAP: [184], LO [no], RBS: [kibler6, Karlin medium, 2.208, -5.307, no], F: [Cro] , SIF : SIF-BLAST [transcriptional repressor, PDB, Sisi, 46, YP_008051172.1, 99%, 1e-67], SIF-HHPred [Transcription regulator, NCBI, Streptococcus suis, 5FD4_B, 60.9%, 98.73, SIF-Syn: [NKF] , STarcevich phage shows Cro on the gene 46, it is most similar to the location of phlipphop gene 43 with an antirepressor flanking the gene down stream
44	SSC: [36187, 37053], CP: [yes] , SCS: glimmer, ST: [NA], Blast-Start: [Gandalph, 47, NCBI, 1 : 1, 100%, 0.0], GAP: [61], LO [yes], RBS: [kibler6, Karlin medium, 3.069, -2.620, yes], F: [antirepressor] , SIF : SIF-BLAST [antirepressor, NCBI, Gadalph 47, YP_009957559.1, 100%,0.0], SIF-HHPred [antirepressor, Pfam, PF03374.19, 34.60%, probability is 97.93], SIF-Syn: [antirepressor, flanking genes are cro and hypothetical proteins and phages used to infer was starcevish]
45	SSC: [37050, 37349], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Che8, 50, NCBI, 1 : 1, 99%, 5e-66], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 1.933, -4.888, yes], F: [hypothetical protein] , SIF : SIF-BLAST [hhpothetical protein, NCBI, Che8 50, NP_817388.1, 99%, 5e-66], SIF-HHPred [uncharacterized protein, PDB,6TCB_A, %alignment* is 29%, 69.08], SIF-Syn: [hypothetical protien, flanking genes were antirepressor and hypothetical proteinsand phages used to infer starcovich]

46	SSC: [37346, 37464], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [gandalph, 49, NCBI, 1 : 1,99%, 3e-44], GAP: [-3], LO [no], RBS: [kibler6, Karlin medium, 1.236, -6.265, no], F: [hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, NCBI, gandalph 49, YP_009957561.1, 99%, 3e-44], SIF-HHPred [BssS protein family, Pfam, PF13991.11 , 36.99%, 90.18], SIF-Syn: [Hypothetical protein, flanking genes were hypothetical proteins and phages used to infer pacc40 and totinger]
47	SSC: [37650, 37847], CP: [yes] , SCS: Gene mark - had a lower e value, ST: [SS], Blast-Start: [Inventum, 45, NCBI, 1 : 31, 98%, 3e-39], GAP: [186] no coding potential in between, LO [yes], RBS: [kibler6, Karlin medium, 3.030, -2.640, yes], F: [hypothetical protein] , SIF : SIF-BLAST [Hypothetical proteien, NCBI, Inventum and 45, YP_009125326.1, 98%, 3e-39], SIF-HHPred [terminase subunit domain, Scob, escherichia phage(if applicable, scop_d6hn7b1,78%, scob is 99.12], SIF-Syn: [hypothetical protein, flanking genes were both hypothetical proteinsand phages used to infer were saal, inventum]
48	SSC: [37891, 38274], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [boomer, 53, NCBI, 1 : 1, 99%, 4e-84], GAP: [44], LO [yes], RBS: [kibler6, Karlin medium, 1.506, -5.848, no], F: [hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, NCBI, Boomer 53, YP_002014269.1, 99%, 4e-84], SIF-HHPred [Sensory box protein signaling protein, PDB, 2YON_A , 14%, 22.54], SIF-Syn: [hypothetical protein, flanking genes are hypothetical proteins and phages used to infer mantra and saal]
49	SSC: [38301, 38459], CP: [yes] , SCS: Glimmer , ST: [NA], Blast-Start: [Blexus 50, NCBI, 1 : 11, 98%, 2e-25], GAP: [25], LO [no], RBS: [kibler6, Karlin medium, 1.872, -4.952, no], F: [hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, NCBI, Plexus, 50, YP_009954737.1, 98%, 2e-25], SIF-HHPred [Mitotic spindle assembly checkpoint protein, PDB, 1GO4_F , 60%, 95.43], SIF-Syn: [Hypothetical protein, flanking genes are bothe hypothetical proteins and phages used to infer were saal and sparkdehlily]
50	SSC: [38676, 38500], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [no hits on NCBI], GAP: [41], LO [no], RBS: [kibler6, Karlin medium, 2.550, -3.690, yes], F: [Hypothetical protein] , SIF : SIF-BLAST [No hits on NCBI], SIF-HHPred [osmolarity sensor protein, PDB, 5XGA_A , %alignment is 25.4%, 67.22%], SIF-Syn: [NKF]

51	SSC: [38629, 39168], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [ogopogo, 58, GenBank, 1 : 1, 99%, 2e-97], GAP: [129] might be some coding potential between these genes, LO [no], RBS: [kibler6, Karlin medium, 1.621, -5.610, no], F: [hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, NCBI,Ogopogo 58, AVJ50697.1, 99%, 2e-97], SIF-HHPred [Peptidase, Pfam, PF03574.20 , %lignmetn was 33.89%, 69.38%], SIF-Syn: [Hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer pacc40 and mantra]
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52	SSC: [39203, 39964], CP: [yes] , SCS: Glimmer smaller e value, ST: [SS], Blast-Start: [Estave1, 57, NCBI, 1 : 1, 100%, 1e-175], GAP: [35], LO [yes], RBS: [kibler6, Karlin medium, 2.807, -3.019, yes], F: [hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, NCBI, Estave1 57, YP_009124248.1, 100%, evalue 1e-175], SIF-HHPred [uncharacterized protein, PDB, 2KPQ_A, %alignment is 29.9%, 22.74, SIF-Syn: [hypothetical proteins, flanking genes are both hypothetical proteins and phages used to infer estave1 and saal]
53	SSC: [40044, 40325], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Mova, 56, Genbank, 1 : 1, 99%, 8e-59], GAP: [120] no coding potential between the genes, LO [yes], RBS: [kibler6, Karlin medium, 2.200,-4.275, no], F: [hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, Genbank, Mova 56 QNN98891.1, 99%, 8e-59], SIF-HHPred [Interleukin, PDB, 8QY4_D, %alignment 59.6% , 52.05], SIF-Syn: [Hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer estave1 and saal]
54	SSC: [40322, 40669], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Hades, 57, NCBI, 1 : 1, 99%, 1e-78], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 2.415, -3.972, no], F: [Hypothetical proteins] , SIF : SIF-BLAST [hypothetical protein, NCBI, Hades 57, YP_009125236.1, 99%, 1e-78], SIF-HHPred [protein of unknown funtion, pFam, PF05305.19, %alignment* 59%, 99.55], SIF-Syn: [Hypothetical protens flanking genes are both hypothetical protein and whib family transcription factor and phages used to infer Estave1 adn saal]
55	SSC: [40660, 41163], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [BobaPhett, 61, NCBI, 1 : 1, 99%, 4e-119], GAP: [-9], LO [yes], RBS: [kibler6, Karlin medium, 2.510, -4.161, yes], F: [Whib Family transcription factor] , SIF : SIF-BLAST [Whib family transcription facotor, NCBI, BobaPhett, 61, YP_009954849.1,99%, 4e-119], SIF-HHPred [Transcriptional regulator, PDB, 8CYF_A, %alignment 49%, 99.81], SIF-Syn: [Whib, flanking genes are HTH DNA binding protein and hypothetical protein and phages used to infer Estave1 gigioiuoi]
56	SSC: [41160, 41645], CP: [yes] , SCS: Genemark - lower e value from blast, ST: [NA], Blast-Start: [Sisi, 56, NCBI, 1 : 1, 99%, 1e-111], GAP: [-3], LO [No]], RBS: [kibler6, Karlin medium, 2.729, -3.182, yes], F: [Helix turn Helix DNA binding protien] , SIF : SIF-BLAST [hypothetical protein, NCBI, Sisi, 56, YP_008051182.1, 99%, 1e-111], SIF-HHPred [Helix - turn-Helix complex, PDB, Hit, %alignment is 34.57%, 95.67], SIF-Syn: [Helix turn Helix DNA binding domain, flanking genes Whib and phages used to infer Sparkdehlily and totinger] There were several different possibilities for the call which is either hypothetical protein or HTH DNA binding domain.
57	SSC: [41642, 41926], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Eish, 63, NCBI, 1 : 1, 99%, 2e-61], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 2.818, -3.138, yes], F: [Whib family transcription factor] , SIF : SIF-BLAST [Helix hum helix DNA binding domain protein, NCBI, Eish, 63, YP_009956405.1, 99%, 2e-61], SIF-HHPred [Transcription Regulator Whib, PDB, 8DY7_H, %alignment 76.84%, 99.88], SIF-Syn: [Whib, flanking

	genes were HTH DNA binding protein and Hypothetical proteins and phages used to infer Inventum]
58	SSC: [41923, 42288], CP: [yes/no] , SCS: Glimmer, ST: [SS], Blast-Start: [Kimberlium, 63, NCBI, 1 : 1, 99%, 5e-84], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 2.874, -3.023, yes], F: [DNA binding protein] , SIF : SIF-BLAST [DNA binding protein, NCBI, Kimberliumm, 63, YP_009198167.1 99%, 5e-84], SIF-HHPred [DNA BINDING PROTEIN, PDB, 2LVS_A , %alignment 77.87%, 99.41%], SIF-Syn: [Helix-turn-helix DNA binding protein, flanking genes were whib and DNA binding domain and phages used to infer totinger , kenuha5]
59	SSC: [42288, 42443], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Buzzlyseyear, 67, NCBI, 1 : 2, 98%, 2e-29], GAP: [0], LO [no], RBS: [kibler6, Karlin medium, 1.747, -5.351, no], F: [hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, NCBI, BuzzLyseyear, 67, YP_009125060.1, 98%, 2e-29], SIF-HHPred [Protein FAM221A/B, NCBI, PF14753.11 , 88.46%, 66.64], SIF-Syn: [Hypothetical protein, flanking genes wer DNA binding protein and hypothetical proteins and phages used to infer totinger and saal]
60	SSC: [42443, 42676] CP: [yes] SCS: GlimmerST: [SS] Blast-Start: [Whouxphf, 59, NCBI, 1 : 1, 99%, 4e-45] Gap: [0] LO [yes] RBS: [kibler6, Karlin medium, 2.598, -3.593, yes] F : [Hypothetical protein] , SIF - SIF-BLAST [hypothetical protein, NCBI, Whouxphf, 59, YP_009963344.1, 99%, 4e-45] - SIF-HHPred [Secretion system needle protein co-chaperone, PDB, 7Y6C_A , %alignment 53.6%, 73.02] - SIF-Syn: [Hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer saal, sparkdehlily]
61	SSC: [42673, 43137] CP: [yes] SCS: Glimmerc ST: [SS] Blast-Start: [Bobaphett, 67, NCBI, 1 : 1, 99%, 4e-104] Gap: [-3] LO [no] RBS: [kibler6, Karlin medium, 2.808, -3.369, yes] F : [hypothetical protien] , SIF function as: - SIF-BLAST [Hypothetical protein, NCBI, Bobaphett 67, YP_009954855.1, 99%, 4e-104] - SIF-HHPred [Gam like Protein, NCBI, PF07352.17, %alignment 51.6%, 98.91] - SIF-Syn: [hypothetical protein, flanking genes are RecA-like DNA recombinase and hypothetical proteins and phages used to infer were bobaphett]
62	SSC: [43134, 44111] CP: [yes] SCS: Glimmer ST: [SS] Blast-Start: [Job42 gene 67, NCBI, 1 : 1, 100%, 0.0] Gap: [-3] LO [yes] RBS: [kibler6, Karlin medium, 3.087, -2.584, yes] F : [RecA-like DNA recombinase] SIF: - SIF-BLAST [RecA-like DNA recombinase, Job42 67, YP_008126657.1, 100%, 0.0], SIF-HHPred [Protein recA; Alpha and beta proteins, Pfaml, PF13479.11 , %alignment 55.8%, 99.32] - SIF-Syn: [RecA-like DNA recombinase, flanking genes are hypothetical protine and HNH endouclease and phages used to infer inventum and Bobaphett]
63	SSC: [44267, 44470] CP: [not on gene mark] SCS: Glimmer ST: [NA] Blast-Start: [Eish, gene number 68, NCBI, 1 : 54, 99%, 9e-41] Gap: [156], LO [no] RBS: [kibler6, Karlin medium, 1.284, -6.167, no] F : [HNH endonuclease] , SIF supporting information for function - SIF-BLAST [HNH endonuclease, NCBI, Eish 68, YP_009956410.1, 99%, 9e-41] - SIF-HHPred [RNA-guided DNA endonuclease, PDB , from selenomonas sp, synthetic construct

	8W1P_G, %alignment 41.17%, 86,93] - SIF-Syn: [HNH endonuclease, flanking genes are both hypothetical proteins and phages used to infer inventum and Bobaphett]
64	SSC: [44467, 46986], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [superGrey, gene number 70, NCBI, 1 : 1, 100%, 0.0], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 2.750, -3.279, yes], F: [DNA methyltransferase] , SIF : SIF-BLAST [DNA methylase N-4, NCBI, SuperGrey 70, YP_009962840.1, 100%, 0.0], SIF-HHPred [DNA binding protein (Nucleosome complex, PDB, 8V6V_X, %alignment 47%, probability 100%), SIF-Syn: [DNA methylase, flanking genes were HDHendonuclease and hypothetical proteins and phages used to infer saal]
65	SSC: [46983, 47132], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [Ramsey, 68, NCBI, 1 : 1, 98%, 1e-27], GAP: [-6], LO [yes]], RBS: [kibler6, Karlin medium, 2.442, -3.854, yes], F: [hypothetical protein] , SIF : SIF-BLAST [Hypothetical protien, NCBI, Ramsey 68, YP_002241855.1, 98%, 1e-27], SIF-HHPred [NKF / function, Scope, SCOP_d4eh1a1, %alignment 86%, probability 70.72%], SIF-Syn: [hypothetical protein, flanking genes DNA methylase and hypothetical protien phages used to infer ramsey and inventum]
66	SSC: [47129, 47779], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [FreddyB 73 genbank, 1 : 1, 97%, 5e-136], GAP: [-3], LO [no], RBS: [kibler6, Karlin medium, 1.695, -5.318, no], F: [DNA methyltransferase] , SIF : SIF-BLAST [DNA methyltransferase, Genbank, FreddyB 73, XAO35142.1 97%, 5e-136], SIF-HHPred [DNA cytosine-5 mehtyltranseferase, Scope, SCOP_d3ubta_, %alignment 76.5%, 99.93], SIF-Syn: [DNA methyltransferase, flanking genes were both hypothetical proteins and phages used to infer FreddyB]
67	SSC: [47844, 48557], CP: [yes] , SCS: Glimmer (it had the best e value, ST: [SS, NA(not applicable, NI(not informative], Blast-Start: [Akhila, 60, Genbank, 1 : 247, 100%, 4e-162], GAP: [65], LO [no], RBS: [kibler6, Karlin medium, 1.782, -5.280, no], F: [DNA methyltransferase] , SIF : SIF-BLAST [DNA methylase, Genbank,Akhila, 60, QUE26246.1 100%, 4e-162], SIF-HHPred [DNA methylase, NCBI, cd00315, %alignment 22.69%, 96.44], SIF-Syn: [DNA methylase, flanking genes were both hypothetical proteins and phages used to infer ovechkin and Akhila]
68	SSC: [48687, 48526], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [shauna1, 68, NCBI, 1 : 1, 98%, 7e-28], GAP: [-31], LO [yes], RBS: [kibler6, Karlin medium, 1.445, -5.896, yes], F: [Hypothetcial protien] , SIF : SIF-BLAST [Ark-like repressor, NCBI,Shauna1, 68, YP_009608250.1, 98%, 7e-28], SIF-HHPred [Domain, PFAM, PF22180.1, %alignment 85.2%, 98.79], SIF-Syn: [hypothetica protein, flanking genes were all hypothetical proteins and phages used to infer shauna and pacc40]
69 Very few phages	SSC: [49057, 48680], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Quico, gene number, 79 NCBI, 1 : 1, 99%, 3e-81], GAP: [3], LO [yes], RBS: [kibler6, Karlin medium, 2.571, -4.416, yes], F: [Hypothetical protein] , SIF : SIF-BLAST [hypothetical protien, NCBI, Quico 79, YP_009194603.1, 99%, 3e-81], SIF-HHPred [uncharacterized small protien, Pfam, PF10055.14, %alignment

have this protein	15.1%, probability 82.71%], SIF-Syn: [hypothetical protein, flanking genes are both hypothetical protein and phages used to infer were ovechkin and Quico]
70	SSC: [49393, 49064], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Ramsey 72, NCBI, 1 : 7, 99%, 4e-74], GAP: [7], LO [no], RBS: [kibler6, Karlin medium, 1.287, -6.811, no] and], F: [hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, NCBI, Ramsey 72, YP_002241859.1, 99%, 4e-74], SIF-HHPred [Hypothetical protein, PDB, ZUR8_A , %alignment 22.73%, probability 83.3], SIF-Syn: [hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer ovechkind and Ramsey]

71 No blast alignments	SSC: [49697, 49467], CP: [no] , SCS: glimmer, ST: [NI(not informative)], Blast-Start: [no significant, Blast alignments], GAP: [74], LO [no], RBS: [kibler6, Karlin medium, 1.334, -6.063, no], F: [hypothetical protein] , SIF : SIF-BLAST [No blast alignments], SIF-HHPred [Hypothetical protein, PDB, 2G1U_A , %alignment 40.3%, probability 27.92], SIF-Syn: [NKF- there were no similar alignments to compare this gene with
72	SSC: [49897, 50019], CP: [yes/no] , SCS: glimmer, ST: [SS], Blast-Start: [OwlsT2W, gene number 74, NCBI, 1 : 2, 98%, 9e-20], GAP: [200] no other coding potential here, LO [no], RBS: [kibler6, Karlin medium, 2.930,-2.845, yes], F: [hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, PDB, OwlsT2W gene 74 YP_009960968.1, 98%, 9e-20], SIF-HHPred [Regulator of rDNA transcription factor, NCBI, 7SUK_SV , %alignment 17.1%, probability 36.87], SIF-Syn: [hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer were fancypants and owl2w]
73	SSC: [50058, 50234], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [rialto, 80, NCBI, 1 : 15, 98%, 3e-34], GAP: [39], LO [no], RBS: [kibler6, Karlin medium, 1.912, -5.396, no], F: [Hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, Genbank, Rialto, 80, WNM65644.1 , 98%,3e-34], SIF-HHPred [Hypothetical protein, Pfam, PF14354.11 , %alignment 15.5%, 77.56], SIF-Syn: [hypothetical protein, flanking genes are upstream RepA-like replication initiator and phages used to infer rialto and pacc40]
74	SSC: [50231, 51136], CP: [yes] , SCS: glimmer, ST: [SS], Blast-Start: [RockyHorror, 74, NCBI, 1 : 1, 100, 0.0], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 1.933, -4.888, no], F: [RepA-like replication initiator] , SIF : SIF-BLAST [replication initiation protein, NCBI, Rockyhorror, 74, YP_009636138.1,100%, 0.0], SIF-HHPred [N-terminal phage replisome organiser, Pfam, PF09681.15 , %alignment 28.8%, probability 92.44], SIF-Syn: [replication initiator, flanking genes are both hypothetical protein and phages used to infer ovechkin, rialto, rocky horror]

75	SSC: [51133, 51495], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Che8, gene number 79, NCBI, 1 : 1, 99%, 1e-80], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 2.200, -4.416, yes], F: [Helicase loader] , SIF : SIF-BLAST [helicase loader, NCBI, che8, 79, NP_817417.1 99%, 1e-80], SIF-HHPred [Replisome organizer, PDB, phage G39P 1NO1_B , %alignment 57.02%, 99.38], SIF-Syn: [helicase loader, flanking genes are both hypothetical protein and RepA-ike initiator and phages used to infer Che8, Ovechkin]
76	SSC: [51488, 51712], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [RockyHorror, 76, NCBI, 1 : 1, 99%, 1e-44], GAP: [-7], LO [no], RBS: [kibler6, Karlin medium, 1.911, -5.779, no], F: [Hypothetical Protein] , SIF : SIF-BLAST [hypothetical protein, NCBI, RokyHorror, 76, YP_009636140.1, 99%, 1e-44], SIF-HHPred [Werner Helicase, Pfam, PF18279.6, %alignment 13.33%, probability 55.05], SIF-Syn: [Hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer were rockyHorror and Fancypants]
77	SSC: [51792, 51992], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Doug, gene 77, NCBI, 1 : 1, 99%, 3e-39], GAP: [80], LO [no], RBS: [kibler6, Karlin medium, 3.247, -2.175, no], F: [Hypothetical proteins] , SIF : SIF-BLAST [Hypothetical protein, NCBI, Doug, 77, YP_009956216.1, 99%, 3e-39], SIF-HHPred [Hypothetical protein, SCOPe, SCOP_d1wi9a1 , %alignment 38.8%, probability 68.8], SIF-Syn: [hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer were spartacus and Doug]
78	SSC: [51977, 52183], CP: [yes] , SCS:Glimmer, ST: [NA], Blast-Start: [Alexphander,78, GenBank, 1 : 63, 99%, 1e-40], GAP: [15], LO [yes], RBS: [kibler6, Karlin medium, 2.220, -4.313, yes], F: [Hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, GenBank, Alexphander, 78, AVO24524.1 , 99%, 1e-40], SIF-HHPred [AutoPhagy receptor zinc finger Pfam, PF18112.6, %alignment 10.14%, probability 71.41], SIF-Syn: [Hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer were alexphander and Rocky Horror]
79	SSC: [52180, 52536], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Fatidio, 79, Genbank, 1 : 1, 99%, 1e-79], GAP: [3], LO [no], RBS: [kibler6, Karlin medium, 2.298, -4.600, yes], F: [Hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, Genbank, Fastidio, 79, XKC18156.1 , 99%, 1e-79], SIF-HHPred [uncharacterized protein, SCOPe, from a Bacillus bacteria SCOP_d2heqa1 , %alignment 27.73%, probability 93.92], SIF-Syn: [Hypothetical proteins, flanking genes and are both hypothetical proteins, phages used to infer were gigioiui and fastidio]
80	SSC: [52533, 52862], CP: [yes] , SCS: glimmer, ST: [SS], Blast-Start: [Gigioiui, 74, Genbank, 1 : 1, 99%, 2e-73], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 2.582, -4.393, yes], F: [Hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, Genbank, Gigioiui, 74, UXE03047.1 , 99%, 2e-73], SIF-HHPred [Microneme protein, Pfam, PF21496.2 , %alignment 17.27%, probability 47.79], SIF-Syn: [Hypothetical protein, flanking genes are Hypothetical proteins and phages used to infer were gigioiui and fastidio]

81	SSC: [52859, 53179], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Argie, 64, Genbank, 1 : 1, 50%, 1e-30], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 2.513, -3.769, yes], F: [hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, NCBI, Argie, 64, QBP31181.1 50%, 1e-30], SIF-HHPred [Hydrolase, PDB, 5LB7_B, %alignment 34.58%, probability 83.91], SIF-Syn: [hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer were Linstu] Potential fusion protein
82	SSC: [53459, 54103], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [CaptainTrips, 95 , NCBI, 1 : 1, 100%, 2e-156], GAP: [142], LO [yes], RBS: [kibler6, Karlin medium, 2.175, -4.677, no], F: [Hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, NCBI, CaptainTrips, 95, YP_009202375.1, 100%, 2e-156], SIF-HHPred [Metal binding protein, PDB, 8Q5B_A, %alignment 14.88%, probability 96.89], SIF-Syn: [hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer CatpainTrips]
83	SSC: [54212, 54436], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Boomer, 97 NCBI, 1 : 1, 99%, 1e-44], GAP: [109], LO [yes], RBS: [kibler6, Karlin medium, 2.571, -4.161, yes], F: [Helix-turn-helix DNA binding domain, MerR-Like] , SIF : SIF-BLAST [MerR-like transcriptional regulator, NCBI, Boomer, 97 , YP_002014313.1, 99%, 1e-44], SIF-HHPred [Recombination directionality factor, PDB, 8DGL_C, %alignment 77.33%, probability 98.99], SIF-Syn: [Hypothetical protein, flanking genes were both hypothetical protein and phages used to infer Boomer]
84	SSC: [54433, 54600], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Mutaforma13, 96, NCBI, 1 : 1, 100%, 5e-29], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 1.984, -4.720, yes], F: [Hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, NCBI, Mutaforma13, 96, YP_009591403.1, 100%, 5e-29], SIF-HHPred [Rab GTPase, PDB, 1Z0J_B, %alignment 69.64%, probability 94.48], SIF-Syn: [Hypothetical protein, flanking genes were both hypothetical protein and phages used to infer were mutaforma13]
85	SSC: [54609, 54827], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [Galactic, 97, NCBI, 1 : 1, 99%, 4e-42], GAP: [9], LO [yes], RBS: [kibler6, Karlin medium, 3.010, -4.208, yes], F: [hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, NCBI, Galactic, 97, YP_009957500.1, 99%, 4e-42], SIF-HHPred [NKF, Pfam, PF12644.12, %alignment 41.10%, probability 73.21], SIF-Syn: [Hypothetical protein, flanking genes are both hypothetical proteins and phages used to infer Galactic]
86	SSC: [54831, 55031], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Bubbles123, 91, NCBI, 1 : 1, 99%, 2e-39], GAP: [4], LO [yes], RBS: [kibler6, Karlin medium, 1.895, -5.046, no], F: [Hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, NCBI, Bubbles123, 91, YP_009955103.1, 99%, 2e-39], SIF-HHPred [Iron-Sulfur Cluster-binding, NCBI, cd21117,

	%alignment 53.73%, probability 66.39], SIF-Syn: [Hypothetical protein, flanking genes were both hypothetical proteins and phages used to infer is Bubbles123]
87	SSC: [55028, 55441], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [ovechkin, 101, NCBI, 1 : 1, 99%, 6e-93], GAP: [3], LO [yes], RBS: [kibler6, Karlin medium, 1.984, -5.372, yes], F: [Hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, NCBI, Ovechkin, 101, YP_009211265.1, 99%, 6e-93], SIF-HHPred [Coiled-coil domain-containing protein, PDB, 6H9M_B , %alignment 43.48%, probability 69.54], SIF-Syn: [Hypothetical protein, flanking genes were both hypothetical proteins and phages used to infer were ovechkin]
88	SSC: [55438, 55680], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [SiSi, 95, NCBI, 1 : 1, 99%, 5e-51], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 2.165, -4.409, no], F: [Hypothetical protein] , SIF : SIF-BLAST [Hypothetical protein, NCBI, Sisi, 95, YP_008051221.1 99%, 5e-51], SIF-HHPred [Family of unknown function, PDB, PF19844.4 , %alignment 22.22%, probability 64.56], SIF-Syn: [Hypothetical protein, flanking genes were upstream hypothetical and downstream, polypeptide N-acetylgalactosamine and phages used to infer Sisi]
89	SSC: [55677, 57287], CP: [yes] , SCS: Glimmer, ST: [NA], Blast-Start: [LEOZINHO, 97, Genbank, 1 : 1, 100%, 0.0], GAP: [-3], LO [yes], RBS: [kibler6, Karlin medium, 2.093, -5.402, no], F: [Glycosyltransferase] , SIF : SIF-BLAST [Glycosyltransferase, Genbank, leozinho, 97, UVK58936.1 , 100%, 0.0], SIF-HHPred [Polypeptide alpha-N-acetylgl, NCBI, cd02510 , %alignment 39.29%, probability 99.72], SIF-Syn: [Glycosyltransferase, flanking genes are hypothetical proteins and phages used to infer Leoxinho]
90	SSC: [57290, 57496], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [Daenerys, 100, NCBI, 1 : 1, 99%, 3e-42], GAP: [3], LO [no], RBS: [kibler6, Karlin medium, 2.502, -4.751, no], F: [Hypothetical protein] , SIF : SIF-BLAST [hypothetical protein, NCBI, Daenerys, 100, YP_008410669.1, 99%, 3e-42], SIF-HHPred [second Tudor Domain, NCBI, cd21181 , %alignment 72.46%, probability 97.71], SIF-Syn: [hypothetical protein, flanking genes are hypstream galactosyltransferase and downstream glycosyltransferase and phages used to infer Daenerys]
91	SSC: [57493, 58116], CP: [yes] , SCS: Glimmer, ST: [SS], Blast-Start: [StAnnes, 109, Genbank, 1 : 1, 100%, 4e-148], GAP: [-3], LO [no], RBS: [kibler6, Karlin medium, 1.821, -5.886, no], F: [Glycosyltransferase] , SIF : SIF-BLAST [Glycosyltransferase, Genbank, StAnnes, 109, QGJ88273.1 , %alignment, evalule], SIF-HHPred [Glycosyltransferase, PDB, 8XKD_A , %alignment 25.10%, probability 99.88], SIF-Syn: [Glycosyltransferase, flanking genes were upstream hypothetical proteins and downstream HNH endoculease and phages used to infer were StAnnes and spoonbyl]

Phage general info

Size and pircuter

4,5,8 and use 6 to show how many are in the sample about...

Tail width - 11.539 nm

Tail length - 186.118 nm

Capsid - 59.406 nm

Orpham - 81 - or a potential fusion protein

- 71