Annotation

ORF	Annotation
1	SSC: 38-370, CP: Yes, SCS Glimmer, ST: NI, Blast-Start: Avani, gene 1, NCBI, 1: 1, 100%, 6e-74, Gap: 0, LO Yes, RBS: Kibler 6, Karlin Marlin, 1.742, -5.269, No, F: HNH endonuclease, SIF-BLAST HNH endonuclease, NCBI, Avani, gene 1,YP_009013096.1, 99%, 6e-74, SIF-HHPred: HNH endonuclease, PDB, Geobacillus virus E2, 5H0M_A, 68/111 (61% alignment), 97.89, SIF-Syn: endonuclease, downstream is terminase small subunit like in Soul22
2	SSC: 437-691, CP: yes, SCS: both, ST: SS, Blast-Start: Avani, gene 2, BioProject, 1: 1, 99%, 2e-51, Gap: 66, LO: yes, RBS: Kibler 6, Karlin Medium, 2.838, -2.985, yes, F: terminase, small subunit, SIF-BLAST: terminase small subunit, NCBI, Avani, gene 2, YP_009013097.1, 99%, 2e-51, SIF-HHPred: NKF, Interpro, PF04102.17, 49%, 100%, SIF-Syn: terminase small subunit, upstream is endonuclease, downstream is terminase like in Soul22
3	SSC: 663-2183, CP: yes, SCS: both, ST: NI, Blast-Start: Avani, gene 3, BioProject, 1: 1, 100%, 0.0, Gap: -29, LO: no, RBS: Kibler 6, Karlin Medium, 2.314, -4.629, no, F: terminase, large subunit, SIF-BLAST: hypothetical protein CL78_gp003, NCBI, Avani, gene 3, YP_009013098.1, 100%, 0.0, SIF-HHPred: Terminase large subunit, PDB, Byrnievirus HK97, 6Z6D_A, 88%, 100%, SIF-Syn: terminase small subunit, upstream is endonuclease, downstream is terminase large subunit like in Soul22
4	SSC: 2180-3604, CP: yes, SCS: both, ST: NI, Blast-Start: Avani, gene 4, BioProject, 1: 1, 100.00%, 0.0, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.446, -3.764, no, F: portal protein, SIF-BLAST: portal protein, NCBI, Avani, gene 4, YP_009013099.1, 100.00%, 0.0, SIF-HHPred: portal protein, PDB, Mycobacterium phage Bxb1, 9D94_Fd, 94%, 100%, SIF-Syn: portal protein, upstream is terminase large subunit, downstream is capsid maturation protein
5	SSC: 3585-4229, CP: yes, SCS: both-GM, ST: NI, Blast-Start: Avani, gene 5, BioProject, 1 : 1, 100.00%, 8e-155, Gap: -20, LO: no, RBS: Kibler 6, Karlin Medium, 1.736, -5.261, no, F: capsid maturation protease, SIF-BLAST: head maturation protease, NCBI, Avani, gene 5, YP_009013100.1, 100.00%, 8e-155, SIF-HHPred: Phage minor capsid protein 2, InterPro, Lactococcus phage, PF06152.16, 35%, 98%, SIF-Syn: capsid maturation protease, upstream is portal protein, downstream is scaffolding protein like in Soul22
6	SSC: 4307-4855, CP: yes, SCS: both, ST: NI, Blast-Start: Jabbawokkie, gene 7, BioProject, 1 : 1, 99%, 7e-124, Gap: 77, LO: no, RBS: Kibler 6, Karlin Medium, 2.974, -2.601, yes, F: scaffolding protein, SIF-BLAST: head

	scaffolding protein, NCBI, Jabbawokkie, gene 7, YP_008410678.1, 99%, 7e-124, SIF-HHPred: Scaffold protein, PDB, Dubowvirus dv80alpha, 6B0X_g, 64%, 99%, SIF-Syn: scaffolding protein, upstream is capsid maturation protease, downstream is major capsid protein, like in Soul22
7	SSC: 4878-5813, CP: yes, SCS: both, ST: NI, Blast-Start: Che9d, gene 7, BioProject, 1 : 1, 100%, 0.0, Gap: 22, LO: yes, RBS: Kibler 6, Karlin Medium, 3.187, -2.507, yes, F: major capsid protein, SIF-BLAST: major capsid protein, NCBI, Che9d, gene 7, NP_817980.1, 100%, 0.0, SIF-HHPred: major capsid protein, PDB, Mycobacterium phage Ogopogo, 8ECN_D, 100%, 100%, SIF-Syn: major capsid protein, upstream is scaffolding protein, downstream is hypothetical protein
8	SSC: 5825-5968, CP: yes, SCS: both, ST: NI, Blast-Start: Jabbawokkie, gene 9, BioProject, 1 : 1, 98%, 1e-23, Gap: 11, LO: yes, RBS: Kibler 6, Karlin Medium, 1.967, -4.780, yes, F: NKF, SIF-BLAST: hypothetical protein N850_gp009, NCBI, Jabbawokkie, gene 9, YP_008410680.1, 98%, 1e-23, SIF-HHPred: NKF, InterPro, PF20942.2, 30%, 82%, SIF-Syn: hypothetical protein, upstream is major capsid protein, downstream is head to tail stopper, like in Demsculpinboyz
9	SSC: 5986-6441, CP: yes, SCS: both, ST: NI, Blast-Start: Jabbawokkie, gene 10, BioProject, 1 : 1, 99%, 8e-107, Gap: 17, LO: yes, RBS: Kibler 6, Karlin Medium, 2.907, -3.393, yes, F: head-to-tail adaptor, SIF-BLAST: head-tail adaptor, NCBI, Jabbawokkie, gene 10, YP_008410681.1, 99%, 8e-107, SIF-HHPred: Head-to-tail adaptor, PDB, Mycobacterium phage Bxb1, 9D94_Ga, 78%, 100%, SIF-Syn: head to tail adaptor, upstream is hypothetical protein, downstream is head to tail stopper, like in Demsculpinboyz
10	SSC: 6438-6791, CP: yes, SCS: both, ST: NI, Blast-Start: Che9d, gene 10, BioProject, 1 : 1, 99%, 2e-77, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 2.974, -3.651, yes, F: head-to-tail stopper, SIF-BLAST: head-tail adaptor, NCBI, Che9d, gene 10, NP_817983.1, 99%, 2e-77, SIF-HHPred: Head-to-tail stopper, NCBI, Mycobacterium phage Bxb1, 9D94_Hc, 91%, 100%, SIF-Syn: head to tail stopper, upstream is head to tail adaptor, downstream is hypothetical protein like in Demsculpinboyz
11	SSC: 6788-6964, CP: yes, SCS: both, ST: SS, Blast-Start: Che9d, gene 11, BioProject, 1 : 1, 98%, 7e-34, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.189, -4.257, no, F: NKF, SIF-BLAST: hypothetical protein PBI_CHE9D_11, NCBI, Che9d, gene 11, NP_817984.1, 98%, 7e-34, SIF-HHPred: NKF, InterPro, PF21828.1, 48%, 87%, SIF-Syn: hypothetical protein, upstream is head to tail stopper, downstream is hypothetical protein, like in Demsculpinboyz

12	SSC: 6948-7220, CP: yes, SCS: both, ST: NI, Blast-Start: Che9d, gene 12, BioProject, 1 : 1, 99%, 2e-56, Gap: -17, LO: yes, RBS: Kibler 6, Karlin Medium, 2.271, -4.129, yes, F: NKF, SIF-BLAST: neck protein, NCBI, Che9d, gene 12, NP_817985.1, 99%, 2e-56, SIF-HHPred: NKF, InterPro, Actinobacteria, PF17395.7, 86%, 97%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein like in Avani
13	SSC: 7213-7617, CP: yes, SCS: both, ST: NI, Blast-Start: Che9d, gene 13, BioProject, 1 : 1, 99%, 1e-92, Gap: -8, LO: yes, RBS: Kibler 6, Karlin Medium, 2.321, -4.041, yes, F: tail terminator, SIF-BLAST: hypothetical protein PBI_CHE9D_13, NCBI, Che9d, gene 13, NP_817986.1, 99%, 1e-92, SIF-HHPred: Tail terminator, PDB, Mycobacterium phage Bxb1, 9D94_Ic, 97%, 100%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is minor tail protein like in Avani
14	SSC: 7679-8272, CP: yes, SCS: both, ST: NI, Blast-Start: Jabbawokkie, gene 15, BioProject, 1 : 1, 99%, 1e-142, Gap: 61, LO: yes, RBS: Kibler 6, Karlin Medium, 2.87, -3.724, no, F: major tail protein, SIF-BLAST: major tail protein, NCBI, Jabbawokkie, gene 15, YP_008410686.1, 99%, 1e-142, SIF-HHPred: Major tail protein, PDB, Mycobacterium phage Bxb1, 9D9L_J, 97%, 100%, SIF-Syn: minor tail protein, upstream is hypothetical protein, downstream is tail assembly chaperone like in Avani
15	SSC: 8371-8982, CP: yes, SCS: both, ST: SS, Blast-Start: Jabbawokkie, gene 16, BioProject, 1 : 1, 100%, 8e-143, Gap: 98, LO: yes, RBS: Kibler 6, Karlin Medium, 2.131, -4.498, no, F: tail assembly chaperone, SIF-BLAST: tail assembly chaperone, NCBI, Jabbawokkie, gene 16, YP_008410688.1, 100%, 8e-143, SIF-HHPred: Phage tail assembly chaperone, InterPro, T1 Gp40, PF08748.16, 79%, 90%, SIF-Syn: tail assembly chaperone, upstream is minor tail protein, downstream is tail assembly chaperone, like Avani
16	SSC: 9027-9272, CP: yes, SCS: both-GM, ST: NI, Blast-Start: Jabbawokkie, gene 17, BioProject, 1 : 220, 99%, 8e-49, Gap: 44, LO: no, RBS: Kibler 6, Karlin Medium, 1.736, -6.486, no, F: tail assembly chaperone, SIF-BLAST: tail assembly chaperone, NCBI, Jabbawokkie, gene 17, YP_008410687.1, 98%, 4e-35, SIF-HHPred: NKF, InterPro, PF17318.7, 40%, 99%, SIF-Syn: tail assembly chaperone, upstream is tail assembly chaperone, downstream is tape measure protein, like in Avani
17	SSC: 9625-12816, CP: yes, SCS: both, ST: SS, Blast-Start: Jabbawokkie, gene 19, BioProject, 1 : 1, 100%, 0.0, Gap: -8, LO: no, RBS: Kibler 6, Karlin Medium, 2.46, -4.198, no, F: tape measure protein, SIF-BLAST: tail length tape measure protein, NCBI, Jabbawokkie, gene 19, YP_008410690.1, 100%, 0.0, SIF-HHPred: Tape measure, PDB, Chivirus chi, 8VJH_Q, 30%, 98%, SIF-Syn:

	tape measure protein, upstream is tail assembly chaperone, downstream is minor tail protein, like Avani
18	SSC: 12813-13742, CP: yes, SCS: both, ST: NI , Blast-Start: Che9d, gene 18, BioProject, 1 : 1, 100%, 0.0, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.805, -3.033, yes, F: minor tail protein, SIF-BLAST: minor tail protein, NCBI, Che9d, gene 18, NP_817991.1, 100%, 0.0, SIF-HHPred: hypothetical protein, PDB, Bacillus phage SPP1, 2X8K_A, 87%, 100%, SIF-Syn: minor tail protein, upstream is tape measure protein, downstream is minor tail protein, like Avani
19	SSC: 13744-15408, CP: yes, SCS: both, ST: NI , Blast-Start: Che9d, gene 19, BioProject, 1 : 1, 100%, 0.0, Gap: 1, LO: yes, RBS: Kibler 6, Karlin Medium, 1.989, -4.793, no, F: minor tail protein, SIF-BLAST: minor tail protein, NCBI, Che9d, gene 19, NP_817992.1, 100%, 0.0, SIF-HHPred: Minor tail protein, PDB, Mycobacterium phage Bxb1, 9D93_Oa, 99%, 100%, SIF-Syn: minor tail protein, upstream is minor tail protein, downstream is minor tail protein, like Avani
20	SSC: 15408-15773, CP: yes, SCS: both, ST: SS, Blast-Start: Che9d, gene 20, BioProject, 1 : 1, 99%, 6e-82, Gap: -1, LO: no, RBS: Kibler 6, Karlin Medium, 1.251, -6.331, no, F: minor tail protein, SIF-BLAST: minor tail protein, NCBI, Che9d, gene 20, NP_817993.1, 99%, 6e-82, SIF-HHPred: NKF, InterPro, Mycobacterium phage D29 and L5 gene 29, PF10910.13, 94%, 100%, SIF-Syn: minor tail protein, upstream is minor tail protein, downstream is minor tail protein, like Avani
21	SSC: 15770-16093, CP: yes, SCS: both, ST: NI , Blast-Start: Che9d, gene 21, BioProject, 1 : 1, 99%, 9e-72, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 3.139, -2.417, yes, F: minor tail protein, SIF-BLAST: minor tail protein, NCBI, Che9d, gene 21, NP_817994.1, 99%, 9e-72, SIF-HHPred: Head-to-tail joining protein, PDB, Dinoroseobacter phage vB_DshS-R4C, 8GTD_O, 91%, 98%, SIF-Syn: - SIF-Syn: minor tail protein, upstream is minor tail protein, downstream is minor tail protein, like Avani
22	SSC: 16090-16398, CP: yes, SCS: both, ST: SS , Blast-Start: Che9d, gene 22, BioProject, 1 : 1, 99%, 3e-67, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 2.798, -3.319, yes, F: minor tail protein, SIF-BLAST: minor tail protein, NCBI, Che9d, gene 22, NP_817995.1, 99%, 3e-67, SIF-HHPred: Virion-associated phage protein, PDB, Ralstonia phage GP4, 8JOU_i, 87%, 99%, SIF-Syn: minor tail protein, upstream is minor tail protein, downstream is minor tail protein, like Avani
23	SSC: 16395-17096, CP: yes, SCS: both, ST: SS , Blast-Start: Jabbawokkie, gene 25, BioProject, 1 : 1, 100%, 6e-168, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 1.769, -6.018, no, F: minor tail protein, SIF-BLAST: minor tail

	protein, NCBI, Jabbawokkie, gene 25, YP_008410696.1, 100%, 6e-168, SIF-HHPred: Levanase, PDB, Bacillus subtilis, 4B1M_C, 68%, 95%, SIF-Syn: minor tail protein, upstream is minor tail protein, downstream is minor tail protein, like Avani
24	SSC: 17093-19555, CP: yes, SCS: both, ST: NI, Blast-Start: Saroj, gene 19, NCBI, 53 : 29, 94%, 0.0, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 1.577, -5.653, no, F: minor tail protein, SIF-BLAST: minor tail subunit, NCBI, Saroj, gene 19, UCR74395.1, 94%, 0.0, SIF-HHPred: Minor tail protein, PDB, Mycobacterium phage Bxb1, 9D93_Pb, 75%, 100%, SIF-Syn: minor tail protein, upstream is minor tail protein, downstream is minor tail protein, like Avani
25	SSC: 19552-21453, CP: yes, SCS: both, ST: SS , Blast-Start: Juniper1, gene 19, NCBI, 1 : 1, 100%, 0.0, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.011, -5.656, no, F: minor tail protein, SIF-BLAST: minor tail protein, NCBI, Juniper1, gene 19, XJP08484.1, 100%, 0.0, SIF-HHPred: Minor tail protein, PDB, Mycobacterium phage Bxb1, 9D93_Sa, 67%, 100%, SIF-Syn: minor tail protein, upstream is minor tail protein, downstream is minor tail protein, like Avani
26	SSC: 21453-22616, CP: yes, SCS: both, ST: NI, Blast-Start: Royals2015, gene 20, BioProject, 1 : 1, 99%, 3e-135, Gap: -1, LO: yes, RBS: Kibler 6, Karlin Medium, 1.412, -5.917, no, F: minor tail protein, SIF-BLAST: minor tail protein, NCBI, Royals2015, gene 20, YP_009961951.1, 99%, 3e-135, SIF-HHPred: NKF, 17%, SIF-Syn: minor tail protein, upstream is minor tail protein like in Avani, downstream is not similar in other F2 phages
27	SSC: 22681-23022, CP: yes, SCS: both, ST: NI, Blast-Start: Gandalph, gene 21, BioProject, 1 : 1, 99%, 2e-68, Gap: 64, LO: yes, RBS: Kibler 6, Karlin Medium, 3.187, -2.808, yes, F: NKF, SIF-BLAST: head protein, NCBI, Gandalph, gene 21, YP_009957533.1, 99%, 2e-68, SIF-HHPred: Virion-associated phage protein, PDB, Ralstonia phage GP4, 8JOU_i, 97%, 100%, SIF-Syn: not similar to F2 phages
28	SSC: 23061-23315, CP: yes, SCS: both, ST: SS, Blast-Start: Minerva, gene 43, BioProject, 1 : 1, 99%, 3e-54, Gap: 38, LO: no, RBS: Kibler 6, Karlin Medium, 2.87, -2.897, yes, F: minor tail protein, SIF-BLAST: minor tail protein, NCBI, Minerva, gene 43, YP_009123996.1, 99%, 3e-54, SIF-HHPred: NKF, PDB, Rhodopseudomonas palustris CGA009, 5JN6_A, 48%, 94%, SIF-Syn: not similar to F2 phages
29	SSC: 23330-23968, CP: yes, SCS: both-GM, ST: NI, Blast-Start: DonkeyKong, gene 23, BioProject, 1 : 1, 100%, 9e-138, Gap: 8, LO: no, RBS: Kibler 6, Karlin Medium, 2.87, -4.122, yes, F: minor tail protein, SIF-BLAST: minor tail protein,

	NCBI, DonkeyKong, gene 23, YP_009956052.1, 99%, 4e-138, SIF-HHPred: Minor tail protein, PDB, Mycobacterium phage Bxb1, 9D93_Lb, 96%, 99%, SIF-Syn: not similar to F2 phages, downstream is minor tail protein like in Avani, upstream not in other F2 phages
30	SSC: 24074-24949, CP: yes , SCS: both-GL, ST: NI, Blast-Start: SG4, gene 24, BioProject, 1 : 36, 100%, 6e-172, Gap: 105, LO: no, RBS: Kibler 6, Karlin Medium, 2.219, -4.174, no, F: minor tail protein, SIF-BLAST: minor tail protein, NCBI, SG4, gene 24, YP_009013226.1, 100%, 6e-172, SIF-HHPred: Minor tail protein, PDB, Mycobacterium phage Bxb1, 9D93_Qa, 99%, 97%, SIF-Syn: minor tail protein, upstream not in other F2 phages, downstream is helix turn helix DNA binding protein
31	SSC: 24955-25152, CP: yes, SCS: both-GL, ST: SS , Blast-Start: SG4, gene 25, BioProject, 1 : 1, 98%, 1e-38, Gap: 2, LO: yes, RBS: Kibler 6, Karlin Medium, 1.461, -6.661, no, F: helix-turn-helix DNA binding domain, SIF-BLAST: HTH DNA binding protein, NCBI, SG4, gene 25, YP_009013227.1, 98%, 1e-38, SIF-HHPred: Hepatocyte nuclear factor 1-beta, PDB, Homo sapiens, 2H8R_A, 86%, 96%, SIF-Syn: helix turn helix DNA binding protein, upstream is minor tail protein like in Avani, downstream is hypothetical protein, not in other F2 phages
32	SSC: 25155-25298, CP: yes, SCS: Genemark, ST: NI , Blast-Start: Fastidio, gene 26, NCBI, 1 : 2, 96%, 3e-23, Gap: 2, LO: no, RBS: Kibler 6, Karlin Medium, 2.036, -5.207, no, F: NKF, SIF-BLAST: hypothetical protein SEA_FASTIDIO_26, NCBI, Fastidio, gene 26, XKC18184, 93.75%, 3e-23, SIF-HHPred: NKF, 50%, SIF-Syn: hypothetical protein, downstream is helix turn helix DNA binding protein, upstream is hypothetical protein like in Avani
33	SSC: 25301-25585, CP: yes, SCS: both, ST: SS , Blast-Start: Bobi, gene 28, BioProject, 1 : 1, 99%, 2e-59, Gap: 2, LO: yes, RBS: Kibler 6, Karlin Medium, 3.208, -2.253, yes, F: NKF, SIF-BLAST: hypothetical protein PBI_BOBI_28, NCBI, Bobi, gene 28, YP_008408985.1, 99%, 2e-59, SIF-HHPred: NKF, 80%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein like in Avani
34	SSC: 25592-25738, CP: no, SCS: Glimmer, ST: SS, Blast-Start: Rocky Horror, gene 28, BioProject, 1 : 1, 98%, 2e-25, Gap: 6, LO: yes, RBS: Kibler 6, Karlin Medium, 2.115, -4.454, yes, F: NKF, SIF-BLAST: hypothetical protein FGG57_gp028, NCBI, Rocky Horror, gene 28, YP_009636092.1, 98%, 2e-25, SIF-HHPred: NKF, 88%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein like in Avani
35	SSC: 25735-25902, CP: yes, SCS: both-GM, ST: NI , Blast-Start: Klebsiella pneumoniae, N/A, NCBI, 1 : 1, 98%, 5e-31, Gap: -4, LO: yes, RBS: Kibler 6,

	Karlin Medium, 3.295, -1.931, yes, F: NKF, SIF-BLAST: hypothetical protein, NCBI, Klebsiella pneumoniae, WP_016032723.1, 98%, 5e-31, SIF-HHPred: NKF, 78%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein like in Avani
36	SSC: 26023-26256, CP: yes, SCS: both, ST: SS, Blast-Start: Inventum, gene 29, BioProject, 1 : 1, 99%, 3e-42, Gap: 120, LO: yes, RBS: Kibler 6, Karlin Medium, 3.187, -2.219, yes, F: NKF, SIF-BLAST: hypothetical protein VC69_gp029, NCBI, Inventum, gene 29, YP_009125310.1, 99%, 3e-42, SIF-HHPred: NKF, 60%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is lysin A, like in Avani,
37	SSC: 26253-27422, CP: yes, SCS: both, ST: NI , Blast-Start: KristaRAM, gene 31, BioProject, 1 : 1, 100%, 0.0, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.192, -4.229, no, F: lysin A, SIF-BLAST: endolysin, NCBI, KristaRAM, gene 31, YP_009958984.1, 100%, 0.0, SIF-HHPred: Bifunctional autolysin, PDB, Staphylococcus aureus subsp. aureus NCTC 8325, 4KNK_A, 42%, 99%, SIF-Syn: lysin A, upstream is hypothetical protein, downstream is lysin B, like in Avani
38	SSC: 27422-28423, CP: yes, SCS: both-GM, ST: NI , Blast-Start: ShroomBoi, gene 28, NCBI, 1 : 1, 100%, 0.0, Gap: -1, LO: no, RBS: Kibler 6, Karlin Medium, 1.201, -6.436, no, F: lysin B, SIF-BLAST: lysin B, NCBI, ShroomBoi, gene 28, WKW86414.1, 100%, 0.0, SIF-HHPred: Gene 12 protein, PDB, Fromanvirus D29, 3HC7_A, 72%, 100%, SIF-Syn: lysin B, upstream is lysin A like in Avani, downstream is not in other FS phages
39	SSC: 28408-28956, CP: yes, SCS: Glimmer, ST: NI, Blast-Start: ShroomBoi, gene 28, NCBI, 1: 157, 90%, 3e-29, Gap: 9, LO: yes, RBS: Kibler 6, Karlin Medium, 1.082, -6.622, no, F: holin, SIF-BLAST: lysin B, NCBI, ShroomBoi, gene 28, WKW86414.1, 100%, 0.0, SIF-HHPred: Holin, r1t-type, InterPro, lactococcus, PF16945.10, 90%, 100%, SIF-Syn: not in other F2 phages, upstream is holin, downstream is Lysin B like in Soul 22
40	SSC: 28433-28666, CP: yes, SCS: both, ST: SS, Blast-Start: Fruitloop, gene 31, BioProject, 1: 1, 99%, 6e-44, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.381, -3.837, no, F: holin, SIF-BLAST: holin, NCBI, Fruitloop, gene 31, YP_002241716.1, 99%, 6e-44, SIF-HHPred: NKF, InterPro, PF10874.13, 90%, 100%, SIF-Syn: holin, upstream is not in other F2 phages, downstream is hypothetical protein like in Soul22
41	SSC: 28663-29037, CP: yes, SCS: both, ST: NI, Blast-Start: MilleniumForce, gene 34, BioProject, 1: 1, 99%, 3e-80, Gap: 105, LO: yes, RBS: Kibler 6, Karlin Medium, 1.657, -5.486, no, F: minor tail protein, SIF-BLAST: minor tail protein, NCBI, MilleniumForce, gene 34, YP_009959700.1, 99%, 3e-80, SIF-HHPred:

	NKF, 38%, SIF-Syn: hypothetical protein, upstream is holin, downstream is hypothetical protein like in Soul22
42	SSC: 29062-29295, CP: yes, SCS: both-GM, ST: SS , Blast-Start: Boomer, gene 36, BioProject, 1: 1, 99%, 3e-50, Gap: 105, LO: yes, RBS: Kibler 6, Karlin Medium, 2.151, -4.315, no, F: NKF, SIF-BLAST: hypothetical protein BOOMER_36, NCBI, Boomer, gene 36, YP_002014252.1, 99%, 3e-50, SIF-HHPred: NKF, InterPro, Proteobacteria, PF17273.7, 57%, 97%, SIF-Syn: not in other F2 phages, upstream is hypothetical protein, downstream is DNA-Q like DNA polymerase III subunit, like in Soul22
43	SSC: 29282-30103, CP: yes, SCS: both, ST: SS , Blast-Start: Shauna1, gene 32, BioProject, 1: 1, 100%, 0.0, Gap: -14, LO: yes, RBS: Kibler 6, Karlin Medium, 2.798, -3.048, yes, F: DnaQ-like (DNA polymerase III subunit), SIF-BLAST: DnaQ-like exonuclease, NCBI, Shauna1, gene 32, YP_009608214.1, 100%, 0.0, SIF-HHPred: Exonuclease MrfB, PDB, Bacillus subtilis, 8UN9_A, 71%, 100%, SIF-Syn: DNAQ-like DNA polymerase III subunit, upstream is hypothetical protein, downstream is hypothetical protein, not like other F2 phages
44	SSC: 30187-30408, CP: yes, SCS: both-GL, ST: SS, Blast-Start: Cabrinians, gene 36, BioProject, 1: 1, 99%, 6e-44, Gap: 83, LO: yes, RBS: Kibler 6, Karlin Medium, 2.033, -5.282, no, F: NKF, SIF-BLAST: hypothetical protein AU088_gp036, NCBI, Cabrinians, gene 36, WKW86414.1, 100%, 0.0, SIF-HHPred: NKF, 57%, SIF-Syn: hypothetical protein, upstream is DNAQ like DNA polymerase III subunit, downstream is hypothetical protein, like in Soul22
45	SSC: 30401-30493, CP: yes, SCS: both, ST: SS , Blast-Start: Fruitloop, gene 36, BioProject, 1:1, 97%, 5e-10, Gap: -8, LO: no, RBS: Kibler 6, Karlin Medium, 1.747, -5.22, no, F: NKF, SIF-BLAST: gp36, NCBI, Fruitloop, gene 36, YP_002241721, 100%, 4e-10, SIF-HHPred: NKF, 89%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein like in Soul22
46	SSC: 30562-30753, CP: yes, SCS: both, ST: SS , Blast-Start: Frankie, gene 43, NCBI, 1: 1, 98%, 2e-35, Gap: 27, LO: no, RBS: Kibler 6, Karlin Medium, 2.411, -3.915, no, F: NKF, SIF-BLAST: hypothetical protein SEA_FRANKIE_43, NCBI, Frankie, gene 43, AUX81969, 98%, 2e-35, SIF-HHPred: NKF, 84%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein, like in Soul22
47	SSC: 30781-31179 **,** CP: yes, SCS: Neither, ST: NI, Blast-Start: Babsiella, gene 69, BioProject, 1: 1, 99%, 4e-94, Gap: 211, LO: yes, RBS: Kibler 6, Karlin Medium, 1.164, -7.421, no, F: mycobacteriophage mobile element 1 (MPME 1), SIF-BLAST: mobile element MPME, NCBI, Babsiella, gene 69,

	YP_009013086, 99%, 4e-94, SIF-HHPred: NKF, 57%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein, like in Soul22
48	SSC: 31391-31627, CP: yes, SCS: both, ST: SS, Blast-Start: Avani, gene 45, BioProject, 1: 1, 99%, 2e-48, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 2.748, -3.071, yes, F: NKF, SIF-BLAST: hypothetical protein CL78_gp045, NCBI, Avani, gene 45, YP_009013140, 99%, 2e-48, SIF-HHPred: NKF, 43%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein, not like other F2 phages
49	SSC: 31624-31815, CP: yes, SCS: both-GM, ST: NI , Blast-Start: Plumbus, gene 42, BioProject, 1: 6, 98%, 5e-39, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 3.05, -3.493, yes, F: NKF, SIF-BLAST: hypothetical protein KNV67_gp042, NCBI, Plumbus, gene 42, YP_010113825, 98%, 5e-39, SIF-HHPred: NKF, 76%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein, not like other F2 phages
50	SSC: 31809-32009, CP: yes, SCS: both, ST: SS , Blast-Start: Sparkdehlily, gene 43, BioProject, 1: 1, 98%, 9e-37, Gap: -1, LO: no, RBS: Kibler 6, Karlin Medium, 1.804, -5.945, no, F: helix-turn-helix DNA binding domain, SIF-BLAST: HTH DNA binding protein, NCBI, Sparkdehlily, gene 43, YP_009187199, 98%, 9e-37, SIF-HHPred: NKF, InterPro, PF11242.13, 52%, 96%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein, not like other F2 phages
51	SSC: 32009-32329, CP: yes, SCS: both, ST: SS , Blast-Start: ShroomBoi, gene 41, BioProject, 1: 1, 98%, 3e-71, Gap: 65, LO: yes, RBS: Kibler 6, Karlin Medium, 1.625, -6.513, no, F: NKF, SIF-BLAST: hypothetical protein SEA_SHROOMBOI_41, NCBI, ShroomBoi, gene 41, WKW86427, 98%, 3e-71, SIF-HHPred: NKF, 64%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein, like in Soul22
52	SSC: 32395-32613, CP: yes, SCS: both, ST: NA, Blast-Start: Henu3 PeY-2017, gene 41, NCBI, 1: 1, 89%, 8e-33, Gap: 243, LO: yes, RBS: Kibler 6, Karlin Medium, 0.787, -7.508, no, F: NKF, SIF-BLAST: hypothetical protein Henu3_gp41, NCBI, Henu3 PeY-2017, gene 41, QBJ00870, 89%, 8e-33, SIF-HHPred: NKF, 78%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is integrase, like in Soul22
53	SSC: 32857-33975, CP: yes, SCS: both, ST: SS, Blast-Start: CaptainTrips, gene 41, BioProject, 1: 1, 100%, 0.0, Gap: 243, LO: yes, RBS: Kibler 6, Karlin Medium, 2.429, -4.644, no, F: integrase, SIF-BLAST: integrase, NCBI, CaptainTrips, gene 41, YP_009202321, 100%, 0.0, SIF-HHPred: Int protein,

	PDB, Enterococcus faecalis, Clostridioides difficile, 6EMY_B, 79%, 100%, SIF-Syn: integrase, upstream is hypothetical protein, downstream is hypothetical protein, like in Soul22
54	SSC: 34040-34492, CP: yes , SCS: both, ST: SS, Blast-Start: MoonBeam, gene 42, BioProject, 1: 12, 99%, 6e-104, Gap: 265, LO: no, RBS: Kibler 6, Karlin Medium, 1.728, -6.298, no, F: lipoprotein, SIF-BLAST: hypothetical protein I5H67_gp042, NCBI, MoonBeam, gene 42, YP_009960108.1, 99%, 6e-104, SIF-HHPred: Uncharacterized lipoprotein YifL, PDB, Pseudomonas aeruginosa PAO1, Escherichia coli K-12, 8H1R_F, 34%, 91%, SIF-Syn: hypothetical protein, upstream is integrase, downstream is immunity repressor like in Soul22
55	SSC: 34758-35426, CP: yes, SCS: Glimmer, ST: NI, Blast-Start: EleanorGeorge, gene 43, BioProject, 1: 1, 100%, 3e-159, Gap: 67, LO: yes, RBS: Kibler 6, Karlin Medium, 0.58, -8.116, no, F: immunity repressor, SIF-BLAST: transcriptional repressor, NCBI, EleanorGeorge, gene 43, YP_009956494, 100%, 3e-159, SIF-HHPred: P22 C2 repressor, DNA-binding domain, SCOPe, Salmonella bacteriophage P22, SCOP_d3jxbc_, 36%, 98%, SIF-Syn: immunity repressor, upstream is not in F2 phages, downstream is hypothetical protein like in Avani
56	SSC: 35494-35727, CP: yes, SCS: both, ST: SS , Blast-Start: Ardmore, gene 39, BioProject, 1: 43, 99%, 1e-47, Gap: 67, LO: no, RBS: Kibler 6, Karlin Medium, 1.625, -5.49, no, F: NKF, SIF-BLAST: gp39, NCBI, Ardmore, gene 39, YP_003495180.1, 99%, 1e-47, SIF-HHPred: ComR, PDB, Streptococcus suis 05ZYH33, 5FD4_B, 84%, 99%, SIF-Syn: hypothetical protein not in F2 phages, downstream is hypothetical protein like in Soul22, upstream is hypothetical protein like in Soul 22
57	SSC: 35783-36070, CP: yes, SCS: both, ST: NI, Blast-Start: StAnnes, gene 47, NCBI, 1 : 1, 99%, 7e-63, Gap: 55, LO: yes, RBS: Kibler 6, Karlin Medium, 2.895, -2.906, yes, F: NKF, SIF-BLAST: hypothetical protein PBI_STANNES_47, NCBI, StAnnes, gene 47, QGJ88217.1, 99%, 6e-63, SIF-HHPred: NKF, 73%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is excise like in Soul22
58	SSC: 36158-36418, CP: yes , SCS: both, ST: SS , Blast-Start: Filuzino, gene 48, BioProject, 1 : 1, 99%, 8e-55, Gap: 87, LO: no, RBS: Kibler 6, Karlin Medium, 2.87, -2.817, no, F: excise, SIF-BLAST: excisionase, NCBI, Filuzino, gene 48, YP_009957037.1, 99%, 8e-55, SIF-HHPred: Recombination Directionality Factor RdfS, PDB, Mesorhizobium japonicum R7A, 8DGL_C, 66%, 98%, SIF-Syn: - SIF-Syn: excise, upstream is hypothetical protein like in Soul 22, downstream is hypothetical protein not in other F2 phages

59	SSC: 36550-36966, CP: no, SCS: Glimmer, ST: NI, Blast-Start: Mova, gene 51, NCBI, 1 : 1, 99%, 2e-95, Gap: 131, LO: no, RBS: Kibler 6, Karlin Medium, 2.17, -5.326, no, F: HNH endonuclease, SIF-BLAST: HNH endonuclease, NCBI, Mova, gene 51, QNN98886, 99%, 2e-95, SIF-HHPred: Zinc-binding loop region of homing endonuclease, InterPro, organism, PF05551.16, 82%, 100%, SIF-Syn: hypothetical protein not in other F2 phages, downstream is hypothetical protein, upstream is excise like in Soul22
60	SSC: 37014-37154, CP: yes, SCS: both-GL, ST: NI, Blast-Start: Bobi, gene 54, BioProject, 1 : 18, 98%, 8e-22, Gap: 47, LO: no, RBS: Kibler 6, Karlin Medium, 1.758, -6.185, no, F: NKF, SIF-BLAST: hypothetical protein PBI_BOBI_54, NCBI, Bobi, gene 54, YP_008409011.1, 98%, 8e-22, SIF-HHPred: Initiation-control protein YabA, PDB, Bacillus subtilis subsp. subtilis str. 168, 5DOL_B, 89%, 97%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein like in Soul22
61	SSC: 37195-37371, CP: yes, SCS: Glimmer, ST: SS , Blast-Start: Fruitloop, gene 50, BioProject, 1 : 1, 100%, 1e-33, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 2.37, -4.001, no, F: NKF, SIF-BLAST: gp50, NCBI, Fruitloop, gene 50, YP_002241735, 100%, 1e-33, SIF-HHPred: NKF, 82%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein like in Soul22
62	SSC: 37324-37746, CP: yes, SCS: both-GL, ST: SS , Blast-Start: Filuzino, gene 51, BioProject, 1 : 1, 99%, 3e-92, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 1.956, -4.721, no, F: NKF, SIF-BLAST: hypothetical protein I5H37_gp051, NCBI, Filuzino, gene 51, YP_009957040.1, 99%, 3e-92, SIF-HHPred: NKF, 48%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein like in Soul22
63	SSC: 37866-38510, CP: yes, SCS: both, ST: SS , Blast-Start: Moonbeam, gene 50, BioProject, 1 : 29, 100%, 1e-144, Gap: 494, LO: no, RBS: Kibler 6, Karlin Medium, 2.033, -4.702, yes, F: NKF, SIF-BLAST: hypothetical protein I5H67_gp050, NCBI, Moonbeam, gene 50, YP_009960116.1, 100%, 1e-144, SIF-HHPred: NKF, 67%, SIF-Syn: hypothetical protein, upstream is not in F2 phages, downstream is hypothetical protein like in Soul22
64	SSC: 38507-38659, CP: yes (gene mark predicts start 38820), SCS: both, ST: NI , Blast-Start: Bobi, gene 58, BioProject, 1 : 1, 98%, 4e-27, Gap: 494, LO: no, RBS: Kibler 6, Karlin Medium, 1.966, -4.781, no, F: membrane protein, SIF-BLAST: membrane protein, NCBI, Bobi, gene 58, YP_008409015.1, 98%, 4e-27, SIF-HHPred: NKF, 64%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is hypothetical protein not in F2 phages

65	SSC: 38656-38787, CP: no, SCS: both, ST: SS , Blast-Start: Moonbeam, gene 52, BioProject, 1 : 1, 98%, 1e-21, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 3.05, -2.584, yes, F: NKF, SIF-BLAST: hypothetical protein I5H67_gp052, NCBI, Moonbeam, gene 52, YP_009960118.1, 98%, 1e-21, SIF-HHPred: NKF, 74%, SIF-Syn: hypothetical protein not in other F2 phages, upstream is hypothetical protein, downstream is hypothetical protein like in Soul22
66	SSC: 38825-39106, CP: yes, SCS: both, ST: SS , Blast-Start: Inventum, gene 50, BioProject, 1 : 1, 99%, 2e-59, Gap: 165, LO: no, RBS: Kibler 6, Karlin Medium, 2.8, -3.025, yes, F: NKF, SIF-BLAST: hypothetical protein VC69_gp050, NCBI, Inventum, gene 50, YP_009125331.1, 99%, 2e-59, SIF-HHPred: NKF, 49%, SIF-Syn: hypothetical protein, upstream hypothetical protein not in other F2 phages, downstream is hypothetical protein like in Soul22
67	SSC: 39103-39450, CP: yes, SCS: both, ST: SS , Blast-Start: Hades, gene 57, BioProject, 1 : 1, 99%, 1e-78, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.384, -3.972, no, F: NKF, SIF-BLAST: hypothetical protein PBI_HADES_57, NCBI, Hades, gene 57, YP_009125236.1, 99%, 1e-78, SIF-HHPred: NKF, InterPro, Mycobacterium tuberculosis, PF05305.19, 60%, 100%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is WhiB family transcription factor like in Avani
68	SSC: 39450-39851, CP: yes, SCS: both, ST: SS , Blast-Start: Ardmore, gene 50, BioProject, 1 : 1, 99%, 5e-94, Gap: -1, LO: no, RBS: Kibler 6, Karlin Medium, 2.081, -4.602, no, F: WhiB family transcription factor, SIF-BLAST: gp50, NCBI, Ardmore, gene 50, YP_003495191.1, 99%, 5e-94, SIF-HHPred: Redox- and pH-responsive transcriptional regulator, PDB, Mycobacterium tuberculosis H37Rv, 8CWT_A, 61%, 100%, SIF-Syn: WhiB family transcription factor, upstream is hypothetical protein, downstream is WhiB family transcription factor like in Avani
69	SSC: 39848-40348, CP: yes, SCS: both, ST: SS , Blast-Start: Fruitloop, gene 56, BioProject, 1 : 1, 99%, 3e-117, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 2.113, -4.395, no, F: WhiB family transcription factor, SIF-BLAST: hypothetical protein FRUITLOOP_56, NCBI, Fruitloop, gene 56, YP_002241741.1, 99%, 3e-117, SIF-HHPred: NKF, InterPro, PF11242.13, 26%, 97%, SIF-Syn: WhiB family transcription factor, upstream is WhiB family transcription factor, downstream is helix turn helix protein like in Avani
70	SSC: 40345-40710, CP: yes, SCS: both, ST: SS , Blast-Start: Ardmore, gene 52, BioProject, 1 : 1, 99%, 3e-83, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.705, -3.302, no, F: helix-turn-helix DNA binding domain, SIF-BLAST: DNA binding protein, NCBI, Ardmore, gene 52, YP_003495193.1,

	99%, 3e-83, SIF-HHPred: Putative uncharacterized protein, PDB, Hyperthermus butylicus DSM 5456, 2LVS_A, 78%, 99%, SIF-Syn: helix turn helix DNA binding protein, upstream is WhiB family transcription factor, downstream is hypothetical protein like in Avani
71	SSC: 40710-40865, CP: yes, SCS: both, ST: SS , Blast-Start: Beakin, gene 62, NCBI, 1 : 2, 98%, 3e-30, Gap: -1, LO: no, RBS: Kibler 6, Karlin Medium, 2.549, -3.627, yes, F: NKF, SIF-BLAST: hypothetical protein SEA_BEAKIN_62, NCBI, Beakin, gene 62, UVK63048.1, 98%, 3e-30, SIF-HHPred: NKF, 61%, SIF-Syn: hypothetical protein, upstream is helix turn helix DNA binding protein, downstream is not in other F2 phages
72	SSC: 40862-41284, CP: yes, SCS: both, ST: SS , Blast-Start: Squirty, gene 64, BioProject, 1 : 1, 99%, 1e-94, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.566, -3.531, yes, F: NKF, SIF-BLAST: hypothetical protein PBI_SQUIRTY_64, NCBI, Squirty, gene 64, YP_009124616.1, 99%, 1e-94, SIF-HHPred: NKF, 67%, SIF-Syn: not in other F2 phages, upstream is hypothetical protein, downstream is hypothetical protein like in Avani
73	SSC: 41281-41523, CP: yes, SCS: both, ST: SS , Blast-Start: Blexus, gene 61, BioProject, 1 : 1, 99%, 2e-49, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 2.774, -3.018, no, F: NKF, SIF-BLAST: hypothetical protein I5H15_gp061, NCBI, Blexus, gene 61, YP_009954748.1, 99%, 2e-49, SIF-HHPred: NKF, 86%, SIF-Syn: hypothetical protein, upstream is not in other F2 phages, downstream is hypothetical protein like in Avani
74	SSC: 41537-42115, CP: yes, SCS: both, ST: SS, Blast-Start: WIVSmall, gene 21, BioProject, 1 : 1, 99%, 1e-135, Gap: 13, LO: yes, RBS: Kibler 6, Karlin Medium, 3.043, -2.807, no, F: NKF, SIF-BLAST: single strand annealing protein, NCBI, WIVSmall, gene 21, YP_008059922.1, 99%, 1e-135, SIF-HHPred: NKF, InterPro, PF06378.16, 63%, 100%, SIF-Syn: hypothetical protein, upstream is hypothetical protein, downstream is HNH endonuclease like in Avani
75	SSC: 42112-42474, CP: yes, SCS: Glimmer, ST: SS, Blast-Start: Dorothy, gene 64, BioProject, 1 : 1, 99%, 4e-8, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.296, -4.076, no, F: HNH endonuclease, SIF-BLAST: HNH endonuclease, NCBI, Dorothy, gene 64, YP_009592039.1, 99%, 4e-82, SIF-HHPred: Recombination endonuclease VII, SCOPe, Bacteriophage T4, SCOP_d1e7la2, 58%, 98%, SIF-Syn: HNH endonuclease like in Avani, upstream is hypothetical protein, downstream is not in other F2 phages
76	SSC: 42471-43148, CP: yes, SCS: both, ST: NI, Blast-Start: Drago, gene 63, BioProject, 1 : 1, 100%, 3e-162, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.716, -3.279, yes, F: NKF, SIF-BLAST: hypothetical protein

	CL68_gp063, NCBI, Drago, gene 63, YP_009016141.1, 100%, 3e-162, SIF-HHPred: NKF, InterPro, Gammaproteobacteria, PF17457.7, 85%, 100%, SIF-Syn: not in other F2 phages, upstream is hypothetical protein like in Avani, downstream is not in other F2 phages
77	SSC: 43145-43252, CP: yes, SCS: both, ST: SS, Blast-Start: Spartacus, gene 69, BioProject, 1 : 1, 97%, 3e-16, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 3.141, -2.394, yes, F: NKF, SIF-BLAST: hypothetical protein FDI13_gp069, NCBI, Spartacus, gene 69, YP_009607889.1, 97%, 3e-16, SIF-HHPred: NKF, 63%, SIF-Syn: not in other F2 phages, upstream not in other F2 phages, downstream not in other F2 phages
78	SSC: 43249-43491, CP: yes, SCS: both, ST: SS , Blast-Start: Phayonce, gene 69, BioProject, 1 : 1, 99%, 3e-49, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 1.592, -5.543, no, F: NKF, SIF-BLAST: hypothetical protein SEA_PHAYONCE_55, NCBI, Phayonce, gene 69, YP_009198399.1, 99%, 3e-49, SIF-HHPred: NKF, 25%, SIF-Syn: not in other F2 phages, upstream not in other F2 phages, downstream not in other F2 phages
79	SSC: 43476-46010, CP: yes, SCS: both-GL, ST: NI, Blast-Start: goodii, NA, NCBI, 1 : 98, 100%, 0.0, Gap: -16, LO: yes, RBS: Kibler 6, Karlin Medium, 0.917, -7.716, no, F: DNA methyltransferase, SIF-BLAST: DNA methyltransferase, NCBI, goodii, NA, WP_235717009.1, 100%, 0.0, SIF-HHPred: SWI/SNF-related matrix-associated actin-dependent regulator of chromatin, PDB, Xenopus laevis, synthetic construct, Homo sapiens, 8V6V_X, 48%, 100%, SIF-Syn: not in other F2 phages, upstream not in other F2 phages, downstream not in other F2 phages
80	SSC: 45993-46139, CP: yes, SCS: both, ST: SS, Blast-Start: no significant blast alignments, Gap: 109, LO: no, RBS: Kibler 6, Karlin Medium, 2.974, -2.681, yes, F: NKF, SIF-HHPred: NKF, InterPro, PF07505.16, 50%, 98%, SIF-Syn: not in other F2 phages, upstream not in other F2 phages, downstream not in other F2 phages
81	SSC: 46018-46278, CP: yes, SCS: both-GM, ST: NI, Blast-Start: Eradicator, gene 60, NCBI, 1 : 1, 99%, 8e-55, Gap: 116, LO: no, RBS: Kibler 6, Karlin Medium, 1.454, -6.87, no, F: NKF, SIF-BLAST: hypothetical protein SEA_ERADICATOR_60, NCBI, Eradicator, gene 60, QYW01425.1, 99%, 8e-55, SIF-HHPred: NKF, 26%, SIF-Syn: not in other F2 phages, upstream not in other F2 phages, downstream is hypothetical protein like in Avani
82	SSC: 46256-46399, CP: no, SCS: Glimmer, ST: SS, Blast-Start: ShroomBoi, gene 73, NCBI, 1 : 1, 98%, 7e-26, Gap: 116, LO: no, RBS: Kibler 6, Karlin Medium, 1.981, -4.731, no, F: NKF, SIF-BLAST: hypothetical protein SEA_SHROOMBOI_73, NCBI, ShroomBoi, gene 73, WKW86457.1, 98%,

	7e-26, SIF-HHPred: NKF, 55%, SIF-Syn: hypothetical protein like in Avani, upstream not in other F2 phages, downstream not in other F2 phages
83	SSC: 46399-46746, CP: yes , SCS: both, ST: NI, Blast-Start: ShroomBoi, gene 74, NCBI, 1 : 1, 99%, 1e-77, Gap: -1, LO: no, RBS: Kibler 6, Karlin Medium, 3.13, -2.356, yes, F: NKF, SIF-BLAST: hypothetical protein SEA_SHROOMBOI_74, NCBI, ShroomBoi, gene 74, WKW86458.1, 99%, 1e-77, SIF-HHPred: NKF, InterPro, PF14216.11, 88%, 100%, SIF-Syn: not in other F2 phages, upstream is hypothetical like in Avani, downstream not in other F2 phages
84	SSC: 46746-47558, CP: yes (gene mark predicts 48130-48550), SCS: both, ST: SS , Blast-Start: ShroomBoi, gene 75, NCBI, 1 : 1, 100%, 0, Gap: -1, LO: no, RBS: Kibler 6, Karlin Medium, 2.219, -4.236, no, F: RepA-like replication initiator, SIF-BLAST: RepA-like replication initiator, NCBI, ShroomBoi, gene 75, WKW86459.1, 100%, 0.0, SIF-HHPred: N-terminal phage replisome organiser, InterPro, PF09681.15, 35%, 99%, SIF-Syn: not in other F2 phages, upstream not in other F2 phages, downstream is hypothetical like in Avani
85	SSC: 47600-47818, CP: yes, SCS: Glimmer, ST: NI, Blast-Start: Flathead, gene 75, NCBI, 1 : 16, 99%, 8e-43, Gap: 41, LO: no, RBS: Kibler 6, Karlin Medium, 2.716, -3.489, yes, F: NKF, SIF-BLAST: hypothetical protein SEA_FLATHEAD_75, NCBI, Flathead, gene 75, QGH79206.1, 99%, 8e-43, SIF-HHPred: NKF, 66.6%, SIF-Syn: hypothetical protein like in Avani, upstream not in other F2 phages, downstream not in other F2 phages
86	SSC: 47815-48138, CP: yes, SCS: Glimmer, ST: SS , Blast-Start: Estave1, gene 83, NCBI, 1 : 1, 99%, 3e-73, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.974, -2.664, yes, F: NKF, SIF-BLAST: hypothetical protein PBI_ESTAVE1_83, NCBI, Estave1, gene 83, YP_009124274.1, 99%, 3e-73, SIF-HHPred: NKF, 87%, SIF-Syn: not in other F2 phages, upstream hypothetical protein like in Avani, downstream hypothetical protein like in Avani
87	SSC: 48135-48329, CP: yes, SCS: Glimmer, ST: SS, Blast-Start: Flathead, gene 77, NCBI, 1 : 1, 98%, 6e-38, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 2.615, -3.489, yes, F: NKF, SIF-BLAST: hypothetical protein SEA_FLATHEAD_77, NCBI, Flathead, gene 77, QGH79208.1, 98%, 6e-38, SIF-HHPred: NKF, 73%, SIF-Syn: hypothetical protein like in Avani, upstream not in F2 phages, downstream not in F2 phages
88	SSC: 48455-48766, CP: yes, SCS: both-GM, ST: NA, Blast-Start: QuickMath, gene 78, BioProject, 1 : 1, 91%, 4e-49, Gap: 125, LO: no, RBS: Kibler 6, Karlin Medium, 2.625, -4.378, yes, F: NKF, SIF-BLAST: hypothetical protein I5H83_gp078, NCBI, QuickMath, gene 78, YP_009961801.1, 91%, 4e-49,

	SIF-HHPred: NKF, 45%, SIF-Syn: not in F2 phages, upstream hypothetical protein like Avani, downstream not in F2 phages
89	SSC: 48763-49149, CP: yes, SCS: both, ST: SS , Blast-Start: Mahavrat, gene 79, BioProject, 1 : 1, 99%, 2e-88, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 1.981, -5.196, no, F: NKF, SIF-BLAST: hypothetical protein I5H59_gp79, NCBI, Mahavrat, gene 79, YP_009959344.1, 99%, 2e-88, SIF-HHPred: NKF, 89%, SIF-Syn: not in other F2 phages, upstream not in F2 phages, downstream not in F2 phages, like in Demsculpinboyz
90	SSC: 49456-49710, CP: yes, SCS: Glimmer, ST: SS , Blast-Start: Nitzel, gene 77, BioProject, 1 : 24, 99%, 1e-52, Gap: 306, LO: no, RBS: Kibler 6, Karlin Medium, 2.895, -2.845, yes, F: NKF, SIF-BLAST: hypothetical protein I5H70_gp77, NCBI, Nitzel, gene 77, YP_009960452.1, 99%, 1e-52, SIF-HHPred: NKF, 69%, SIF-Syn: not in other F2 phages, upstream not in F2 phages, downstream is hypothetical protein like in Demsculpinboyz
91	SSC: 49686-50078, CP: yes, SCS: both-GL, ST: NI, Blast-Start: Ramsey, gene 86, BioProject, 8 : 1, 94%, 9e-82, Gap: -25, LO: no, RBS: Kibler 6, Karlin Medium, 2.095, -4.573, no, F: NKF, SIF-BLAST: gp86, NCBI, Ramsey, gene 86, YP_002241873.1, 94%, 9e-82, SIF-HHPred: NKF, 49%, SIF-Syn: hypothetical protein like in Demsculpinsboyz, upstream not in F2 phages, downstream is hypothetical protein like in Demsculpinboyz
92	SSC: 50075-50290, CP: yes, SCS: both, ST: SS , Blast-Start: ShiLan, gene 86, BioProject, 1 : 1, 99%, 3e-43, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 2.625, -3.328, no, F: NKF, SIF-BLAST: hypothetical protein FDI15_gp086, NCBI, ShiLan, gene 86, YP_009608161.1, 99%, 3e-43, SIF-HHPred: NKF, 84%, SIF-Syn: hypothetical protein like in Demsculpinboyz, upstream is hypothetical protein like in Demsculpinboyz, downstream is not in other F2 phages
93	SSC: 50283-50471, CP: yes, SCS: both, ST: SS , Blast-Start: Inventum, gene 81, BioProject, 1 : 1, 98%, 1e-36, Gap: -8, LO: no, RBS: Kibler 6, Karlin Medium, 2.46, -4.198, no, F: NKF, SIF-BLAST: hypothetical protein VC69_gp081, NCBI, Inventum, gene 81, YP_009125362.1, 98%, 1e-36, SIF-HHPred: NKF, 82%, SIF-Syn: not in other F2 phages, upstream hypothetical protein in Demsculpinsboyz, downstream hypothetical protein like in Demsculpinsboyz
94	SSC: 50468-50659, CP: yes, SCS: Glimmer, ST: SS , Blast-Start: SG4, gene 88, BioProject, 1 : 1, 98%, 1e-38, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.075, -4.823, yes, F: NKF, SIF-BLAST: hypothetical protein CL94_gp088, NCBI, SG4, gene 88, YP_009013290.1, 98%, 1e-38, SIF-HHPred: NKF, 87%, SIF-Syn: hypothetical protein like in

	Demsculpinsboyz, upstream is not in other F2 phages, downstream is hypothetical protein like in Demsculpinsboyz
95	SSC: 50656-50835, CP: yes, SCS: both, ST: SS , Blast-Start: Plumbus, gene 88, BioProject, 1 : 1, 98%, 1e-33, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 3.187, -2.684, yes, F: NKF, SIF-BLAST: hypothetical protein KNV67_gp088, NCBI, Plumbus, gene 88, YP_010113871.1, 98%, 1e-33, SIF-HHPred: NKF, 83%, SIF-Syn: hypothetical protein like in Avani, upstream hypothetical protein like in Demsculpinsboyz, downstream not in other F2 phages
96	SSC: 50852-51304, CP: yes, SCS: both, ST: SS, Blast-Start: Mahavrat, gene 85, BioProject, 1 : 1, 99%, 5e-108, Gap: 16, LO: yes, RBS: Kibler 6, Karlin Medium, 2.633, -3.452, yes, F: NKF, SIF-BLAST: hypothetical protein I5H59_gp85, NCBI, Mahavrat, gene 85, YP_009959350.1, 99%, 5e-108, SIF-HHPred: NKF, 79%, SIF-Syn: not in other F2 phages, upstream hypothetical protein like in Avani, downstream is hypothetical protein like in Avani
97	SSC: 51301-51420, CP: no, SCS: Glimmer, ST: NI, Blast-Start: Gandalph, gene 90, BioProject, 1 : 1, 98%, 3e-19, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.706, -3.239, yes, F: NKF, SIF-BLAST: hypothetical protein I5H42_gp090, NCBI, Gandalph, gene 90, YP_009957602.1, 98%, 3e-19, SIF-HHPred: DNA double-strand break repair rad50 ATPase, PDB, Pyrococcus furiosus, 1L8D_B, 69.2%, 91%, SIF-Syn: hypothetical protein like in Avani, upstream not in other F2 phages, downstream not in other F2 phages
98	SSC: 51417-51743, CP: yes, SCS: both, ST: SS , Blast-Start: Hamulus, gene 92, BioProject, 1 : 1, 100%, 3e-72, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 2.8, -3.025, yes, F: NKF, SIF-BLAST: hypothetical protein HAMULUS_92, NCBI, Hamulus, gene 92, YP_008409156.1, 100%, 3e-72, SIF-HHPred: RNA polymerase Rpb1, domain 1, InterPro, PF04997.17, 24%, 95%, SIF-Syn: not in other F2 phages, upstream is hypothetical protein like in Avani, downstream is hypothetical protein like in Demsculpinsboyz
99	SSC: 51866-52024, CP: yes (gene mark predicts start at 53420), SCS: both, ST: SS , Blast-Start: Phanphagia, gene 94, NCBI, 1 : 38, 98%, 4e-30, Gap: 122, LO: no, RBS: Kibler 6, Karlin Medium, 2.136, -5.254, no, F: NKF, SIF-BLAST: hypothetical protein SEA_PHANPHAGIA_94, NCBI, Phanphagia, gene 94, QIQ63783.1, 98%, 4e-30, SIF-HHPred: NKF, InterPro, PF06348.16, 62%, 99%, SIF-Syn: not in other F2 phages, upstream is not in other F2 phages, downstream is hypothetical protein like in Demsculpinsboyz
100	SSC: 52024-52302, CP: yes, SCS: both, ST: NI, Blast-Start: Bobi, gene 95, BioProject, 1 : 1, 99%, 5e-57, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium,

	2.741, -3.166, F: NKF, SIF-BLAST: hypothetical protein PBI_BOBI_95, NCBI, Bobi, gene 95, YP_008409052.1, 99%, 5e-57, SIF-HHPred: NKF, 66%, SIF-Syn: hypothetical protein like in Demsculpinsboyz, upstream is not in other F2 phages, downstream is
101	SSC: 52299-52985, CP: yes, SCS: both-GL, ST: SS, Blast-Start: Bobi, gene 96, BioProject, 1 : 1, 100%, 3e-164, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 3.122, -3.393, yes, F: NKF, SIF-BLAST: hypothetical protein PBI_BOBI_96, NCBI, Bobi, gene 96, YP_008409053.1, 100%, 3e-164, SIF-HHPred: Terminase gpNU1 subunit domain, SCOPe, Escherichia phage, Hit, 29%, 97%, SIF-Syn: hypothetical protein like in Avani, upstream is hypothetical protein like in Avani, downstream is hypothetical protein like in Avani
102	SSC: 52982-53584, CP: yes, SCS: both-GL, ST: SS , Blast-Start: Bobi, gene 97, BioProject, 1 : 1, 100%, 9e-147, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.677, -4.128, yes, F: NKF, SIF-BLAST: hypothetical protein PBI_BOBI_97, NCBI, Bobi, gene 97, YP_008409054, 100%, 9e-147, SIF-HHPred: T5orf172 domain, InterPro, PF10544.14, 34%, 99%, SIF-Syn: hypothetical protein like in Avani, upstream is hypothetical protein like in Avani, downstream is hypothetical protein like in Avani
103	SSC: 53771-53935, CP: yes, SCS: both, ST: NI, Blast-Start: FancyPants, gene 101, BioProject, 1 : 1, 100%, 5e-30, Gap: 186, LO: yes, RBS: Kibler 6, Karlin Medium, 1.778, -5.155, no, F: NKF, SIF-BLAST: hypothetical protein I5H36_gp101, NCBI, FancyPants, gene 101, YP_009956980.1, 100%, 5e-30, SIF-HHPred: FYVE-finger-containing Rab5 effector protein rabenosyn-5, PDB, Mus musculus, Homo sapiens, 1Z0J_B, 70%, 95%, SIF-Syn: hypothetical protein like in Avani, upstream is hypothetical protein like in Avani, downstream is hypothetical protein like in Avani
104	SSC: 53941-54099, CP: no, SCS: Glimmer, ST: SS , Blast-Start: Jabbawokkie, gene 103, BioProject, 1 : 1, 98%, 3e-30, Gap: 5, LO: yes, RBS: Kibler 6, Karlin Medium, 2.974, -2.742, yes, F: NKF, SIF-BLAST: hypothetical protein N850_gp101, NCBI, Jabbawokkie, gene 103, YP_008410774.1, 98%, 3e-30, SIF-HHPred: NKF, 63%, SIF-Syn: hypothetical protein like in Avani, upstream is hypothetical protein like in Avani, downstream is hypothetical protein like in Avani
105	SSC: 54096-54353, CP: yes, SCS: both, ST: SS, Blast-Start: Yoshi, gene 112, BioProject, 1 : 1, 99%, 2e-51, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 1.86, -5.750, no, F: NKF, SIF-BLAST: AlpA-like transcriptional regulator, NCBI, Yoshi, gene 112, YP_009614016.1, 99%, 2e-51, SIF-HHPred: NKF, 84%, SIF-Syn: hypothetical protein like in Avani, upstream is hypothetical protein like in Avani, downstream is hypothetical protein like in Avani

106	SSC: 54350-54820, CP: yes, SCS: both, ST: SS, Blast-Start: Jabbawokkie, gene 105, BioProject, 1 : 1, 99%, 3e-103, Gap: 51, LO: no, RBS: Kibler 6, Karlin Medium, 0.674, -7.455, no, F: NKF, SIF-BLAST: hypothetical protein N850_gp103, NCBI, Jabbawokkie, gene 105, YP_008410776.1, 99%, 3e-103, SIF-HHPred: NKF, 86%, SIF-Syn: hypothetical protein like in Avani, upstream is hypothetical protein like in Avani, downstream is glycosyltransferase like in Avani
107	SSC: 54872-56038, CP: yes, SCS: both, ST: NI, Blast-Start: Yoshi, gene 114, BioProject, 1 : 1, 100%, 0.0, Gap: 51, LO: no, RBS: Kibler 6, Karlin Medium, 2.141, -4.477, no, F: glycosyltransferase, SIF-BLAST: glycosyltransferase, NCBI, Yoshi, gene 114, YP_009614018.1, 100%, 0.0, SIF-HHPred: Putative glycosyltransferase, PDB, Streptococcus parasanguinis FW213, 5HEA_A, 48%, 99%, SIF-Syn: glycosyltransferase like in Avani, upstream is hypothetical protein like in Avani, downstream is glycosyltransferase
108	SSC: 56035-56730, CP: yes, SCS: both, ST: NI, Blast-Start: Soul22, gene 101, BioProject, 1 : 1, 100%, 1e-168, Gap: -4, LO: no, RBS: Kibler 6, Karlin Medium, 2.705, -4.262, yes, F: glycosyltransferase, SIF-BLAST: galactosyl transferase, NCBI, Soul22, gene 101, YP_009963916.1, 100%, 1e-168, SIF-HHPred: CESA_CelA_like, NCBI, cd06421, 90%, 99%, SIF-Syn: glycosyltransferase like in Avani, upstream is glycosyltransferase like in Avani, downstream is glycosyltransferase like in Avani
109	SSC: 56727-57329, CP: yes, SCS: both, ST: NI, Blast-Start: Yoshi, gene 116, BioProject, 1 : 1, 100%, 2e-142, Gap: -4, LO: yes, RBS: Kibler 6, Karlin Medium, 2.095, -5.339, yes, F: glycosyltransferase, SIF-BLAST: glucosyltransferase, NCBI, Yoshi, gene 116, YP_009614020.1, 100%, 2e-142, SIF-HHPred: Glycosyltransferase family 25 protein, PDB, Aggregatibacter actinomycetemcomitans NUM4039, 8XKD_A, 87%, 100%, SIF-Syn: glycosyltransferase like Avani, upstream is glycosyltransferase like in Avani