

Table S1. Features of the ORFs of phage SH6, predicted functions and best matches with databases

ORF	Strand	Start (pb)	Stop (pb)	Size(aa)	MW(kDa)	pI	SD sequence(GAGAA) a	Predicted function	Blast (extent, size aligned protein (aa)) b	% aa identity	E Value	Accession number
1	+	6	581	191	17.6	5.7	<u>GACAAATG</u>		pSf2_069 [Shigella phage pSf-2] (44/171; 171)	26%	5,00E-06	YP_009113007.1
2	+	584	823	79	9.2	9.3	<u>AAGTAttATG</u>		B508_00060 [Escherichia phage ADB-2] (79/79; 79)	100%	5,00E-50	YP_007112677.1
3	+	895	1089	64	7.3	5.1	<u>ACGAAgATG</u>		Shf1p02 [Shigella phage Shf1] (64/64; 64)	100%	1,00E-38	YP_004414821.1
4	+	1092	1559	155	18.0	5.7	<u>GGCAAtcATG</u>		Shf1p03 [Shigella phage Shf1] (143/155; 155)	92%	2,00E-101	YP_004414822.1
5	+	1638	1868	76	8.7	4.8	<u>GAGGAttcaccATG</u>		Shf1p05 [Shigella phage Shf1] (75/76; 76)	99%	2,00E-47	YP_004414824.1
6	+	1875	2102	75	8.6	9.7	<u>AATAAtcATG</u>		pSf2_064 [Shigella phage pSf-2] (74/75; 75)	99%	2,00E-48	YP_009113002.1
7	+	2099	2209	36	4.0	5.2	<u>GAGGTACTAAAATG</u>		pSf2_063 [Shigella phage pSf-2] (31/36; 36)	86%	2,00E-13	YP_009113001.1
8	+	2122	2379	85	9.4	8.7	<u>TAGCGctATG</u>		pSf2_062 [Shigella phage pSf-2] (53/57; 57)	93%	2,00E-27	YP_009113000.1
9	+	2389	2580	63	7.2	4.1	<u>GATTTtaacaATG</u>		pSf2_061 [Shigella phage pSf-2] (60/63; 63)	95%	4,00E-36	YP_009112999.1
10	+	2652	3140	162	18.1	5.0	<u>GAGGAtataATG</u>		B508_00095 [Escherichia phage ADB-2] (147/162; 172)	91%	2,00E-104	YP_007112684.1
11	+	3212	3718	168	19.0	6.5	<u>GAAAGcattcATG</u>		B508_00100 [Escherichia phage ADB-2] (141/168; 168)	84%	5,00E-101	YP_007112685.1
12	+	3718	3867	49	5.6	7.8	<u>GAGAAataATG</u>		pSf2_058 [Shigella phage pSf-2] (49/49; 49)	100%	1,00E-26	YP_009112996.1
13	+	3948	4154	68	8.0	6.3	<u>GAGGAatcagctATG</u>		Shf1p14 [Shigella phage Shf1] (65/68; 68)	96%	2,00E-41	YP_004414831.1
14	+	4138	4425	95	11.2	6.3	<u>AAGAAagATG</u>		pSf2_056 [Shigella phage pSf-2] (91/95; 95)	96%	1,00E-60	YP_009112994.1
15	+	4425	5060	212	24.0	9.5	<u>TAGACcATG</u>		pSf2_055 [Shigella phage pSf-2] (189/212; 212)	89%	5,00E-137	YP_009112993.1
16	+	5209	5427	72	8.0	7.7	<u>AAGGGtggttttATG</u>		T1p66 [Enterobacteria phage T1] (71/72; 72)	98.0%	1,00E-44	YP_003878.1
17	+	5485	5931	148	17.3	8.3	<u>GGGAAcactcATG</u>		T1p65 [Enterobacteria phage T1] (141/148; 148)	95%	3,00E-101	YP_003879.1
18	+	6015	6548	177	20.1	5.6	<u>GAATAaatcATG</u>		morphogenetic protein [Escherichia phage ADB-2] (176/177; 203)	99%	3,00E-126	YP_007112690.1
19	+	6657	7229	190	21.7	5.3	<u>GATACtgcacATG</u>	Kinase	T1p62 [Enterobacteria phage T1] (189/190; 190)	99%	4,00E-138	YP_003883.1
20	+	7302	7511	69	7.9	4.0	<u>TCGAAATG</u>		T1p61 [Enterobacteria phage T1] (67/69; 69)	97%	8,00E-41	YP_003884.1
21	+	7508	7852	114	13.1	9.3	<u>AAGAAgcATG</u>		Shf1p23 [Shigella phage Shf1] (103/114; 114)	90%	2,00E-69	YP_004414839.1
22	+	7852	8082	76	8.8	9.2	<u>GGTAAgtaATG</u>		T1p59 [Enterobacteria phage T1] (76/76; 76)	100%	9,00E-47	YP_003886.1
23	+	8082	8285	67	7.4	5.1	<u>AAtAAtggATG</u>		T1p58 [Enterobacteria phage T1] (63/67; 67)	94%	9,00E-39	YP_003887.1
24	+	8450	8611	53	6.0	9.2	<u>GAGAAAttgcataATG</u>		Shf1p26 [Shigella phage Shf1] (52/53; 53)	99%	9,00E-28	YP_004414842.1
25	+	8592	8777	61	7.0	9.7	<u>AGGAAgATG</u>		B508_00155 [Escherichia phage ADB-2] (60/61; 61)	99%	9,00E-34	YP_007112696.1
26	+	8779	9006	75	8.4	9.7	<u>GAGATtttaacATG</u>		Shf1p28 [Shigella phage Shf1] (65/75; 75)	87%	1,00E-39	YP_004414844.1
27	+	9091	9615	174	20.2	4.8	<u>ACTAAATG</u>	Terminase small subunit	T1p54 terS [Enterobacteria phage T1] (173/174; 174)	99%	2,00E-121	YP_003891.1
28	+	9640	11223	527	60.8	6.0	<u>GCGCCcacATG</u>	Terminase large subunit	T1p53 terL [Enterobacteria phage T1] (525/527; 527)	99%	0.0	YP_003892.1
29	+	11227	12561	444	50.0	4.9	<u>GGTAAtaaATG</u>	Portal protein	T1p52 [Enterobacteria phage T1] (425/427; 427)	99%	0.0	YP_003893.1
30	+	12551	13312	253	29.0	9.5	<u>TAGAAgATG</u>	Minor capsid protein	JMPW1_027 [Escherichia phage JMPW1] (252/253; 253)	99%	0.0	ALT58231.1
31	+	13315	14427	370	40.1	5.1	<u>GAGATtaaaaATG</u>	Major capsid protein	pSf2_039 [Shigella phage pSf-2] (369/370; 370)	99%	0.0	YP_009112977.1
32	+	14439	14915	158	17.0	5.0	<u>GGGAAaatatcATG</u>		T1p49 [Enterobacteria phage T1] (156/158; 158)	99%	1,00E-109	YP_003896.1
33	+	14978	15745	255	26.5	4.4	<u>GAGAAatcattATG</u>		B508_00205 [Escherichia phage ADB-2] (250/255; 255)	98%	1,00E-180	YP_007112706.1
34	+	15838	16797	319	35.2	5.6	<u>GAGAAgtaatcATG</u>		B508_00210 [Escherichia phage ADB-2] (319/319; 319)	100%	0.0	YP_007112707.1
35	+	16847	17134	95	10.6	4.8	<u>GAGAAatcaaaATG</u>		T1p46 [Enterobacteria phage T1] (92/95; 95)	97%	6,00E-58	YP_003899.1
36	+	17179	17589	136	15.5	8.6	<u>GTAAttATG</u>		B508_00220 [Escherichia phage ADB-2] (134/136; 136)	99%	6,00E-95	YP_007112709.1
37	+	17580	17960	126	14.2	5.0	<u>GTGGAggATG</u>		T1p44 [Enterobacteria phage T1] (123/123; 123)	100%	3,00E-82	YP_003901.1
38	+	17860	18396	178	20.1	9.7	<u>GAGATtgATG</u>		B508_00225 [Escherichia phage ADB-2] (157/178; 268)	88%	3,00E-110	YP_007112710.1
39	+	18386	18784	132	15.2	8.7	<u>GCAAAATG</u>		T1p42 [Enterobacteria phage T1] (132/132; 132)	100%	3,00E-93	YP_003903.1
40	+	18787	19455	240	26.1	4.5	<u>GAAAGcggATG</u>	Major tail protein	T1p41 [Enterobacteria phage T1] (221/222; 222)	99%	6,00E-161	YP_003904.1
41	+	19569	19886	105	12.0	5.6	<u>GAGAAacatcATG</u>		Shf1p43 [Shigella phage Shf1] (104/105; 105)	99.0%	2,00E-71	YP_004414859.1
42	+	20006	20203	65	7.5	5.2	<u>CTGAAATG</u>	Tape measure chaperone	B508_00250 [Escherichia phage ADB-2] (65/65; 65)	100%	3,00E-39	YP_007112715.1
43	+	20242	23115	957	103.8	5.7	<u>GTTATATG</u>	Tail tape measure protein	tail tape measure protein [Escherichia phage ADB-2] (931/957; 957)	97%	0.0	YP_007112716.1
44	+	23118	23471	117	13.0	5.0	<u>GTTAAAtATG</u>	Minor tail protein	putative phage minor tail protein [Escherichia phage ADB-2] (116/117; 117)	99%	4,00E-81	YP_007112717.1
45	+	23521	24333	270	30.2	6.2	<u>GTAGAATG</u>	Minor tail protein	T1p36 [Enterobacteria phage T1] (259/260; 260)	99%	0.0	YP_003909.1
46	+	24330	25064	244	28.3	5.7	<u>AGGAAaaatcaATG</u>	Minor tail protein	T1p35 [Enterobacteria phage T1] (244/244; 244)	100%	0.0	YP_003910.1
47	+	25061	25660	199	20.9	9.0	<u>TTAAAttATG</u>	Tail assembly protein	T1p34 [Enterobacteria phage T1] (199/199; 199)	100%	4,00E-140	YP_003911.1
48	+	25738	29187	1149	127.3	4.8	<u>GTAACatcATG</u>	Tail fiber protein	Shf1p50 [Shigella phage Shf1] (1133/1149; 1149)	99%	0.0	YP_004414866.1
49	-	29215	30171	318	34.2	6.6	<u>GGTAAttATG</u>		Shf1p51 [Shigella phage Shf1] (314/318; 318)	99%	0.0	YP_004414867.1
50	-	30174	30404	76	8.3	8.9	<u>GAGGAcatacaaATG</u>	Lipoprotein	pSf2_020 [Shigella phage pSf-2] (75/76; 76)	99%	3,00E-47	YP_009112958.1
51	+	30930	31994	354	40.1	5.1	<u>GATAAacgcaATG</u>	exodeoxyribonuclease VIII	pSf2_019 [Shigella phage pSf-2] (353/354; 354)	99%	0.0	YP_009112957.1
52	+	32069	32716	226	55.6	5.1	<u>GTTATaATG</u>	Recombination	T1p28 erf [Enterobacteria phage T1] (224/226; 226)	99%	3,00E-165	YP_003917.1
53	+	32763	33188	141	16.2	6.1	<u>GAGAAaaacATG</u>	Single stranded DNA binding	Shf1p55 [Shigella phage Shf1] (126/137; 137)	91%	2,00E-77	YP_004414871.1
54	-	33222	34901	559	60.1	4.6	<u>GAGTTtatctATG</u>	Tail fiber	AV954_gp28 [Enterobacteria phage SSL2009a] (268/538; 538)	50%	4,00E-169	YP_002720067.2
55	-	35002	35922	306	34.6	5.9	<u>AAGAAttATG</u>	Putative DNA primase	T1p24 priA [Enterobacteria phage T1] (303/306; 306)	99%	0.0	YP_003921.1
56	-	35999	36451	150	17.2	10.2	<u>GAGAAAtcaagATG</u>		pSf2_014 [Shigella phage pSf-2] (150/150; 150)	100%	5,00E-106	YP_009112952.1
57	+	36551	38563	670	75.8	6.8	<u>GTGAcATG</u>	ATP-dependent helicase	T1p22 helA [Enterobacteria phage T1] (663/670; 672)	99%	0.0	YP_003923.1
58	+	38560	38976	138	15.9	8.6	<u>CCGGGATG</u>		Shf1p60 [Shigella phage Shf1] (132/138; 138)	96%	3,00E-94	YP_004414876.1
59	+	39044	39757	237	27.0	6.0	<u>GACTAaagATG</u>	DNA methylase	T1p 20 Dam [Enterobacteria phage T1] (234/237; 237)	99%	6,00E-165	YP_003925.1
60	+	39853	40005	83	6.6	4.0	<u>GAGATATG</u>		T1p19 [Enterobacteria phage T1] (50/83; 83)	60%	2,00E-23	YP_003926.1
61	+	40057	40281	74	8.6	9.3	<u>GAAACaaaATG</u>		B508_00360 [Escherichia phage ADB-2] (69/69; 69)	100%	9,00E-43	YP_007112737.1

62	+	40362	40763	133	15.5	8.4	<u>TATAA</u> aggATG		Shfl1p66 [<i>Shigella</i> phage Shfl1] (88/95; 95)	93%	2,00E-59	YP_004414880.1
63	+	40842	41993	383	43.0	6.5	<u>TAAAA</u> tATG		Shfl1p67 [<i>Shigella</i> phage Shfl1] (377/383; 383)	98%	0.0	YP_004414881.1
64	+	42057	42233	58	6.5	6.0	<u>TATATc</u> ATG		T1p14 [<i>Enterobacteria</i> phage T1] (55/58; 58)	95%	6,00E-32	YP_003931.1
65	+	42352	42567	71	7.6	9.3	<u>GAGAT</u> tATG	Holin	T1p13 hol [<i>Enterobacteria</i> phage T1] (71/71; 71)	100%	4,00E-42	YP_003932.1
66	+	42567	43055	162	18.3	9.5	<u>GAGATa</u> ATG	Endolysin	B508_00380 [<i>Escherichia</i> phage ADB-2] (161/162; 162)	99%	2,00E-114	YP_007112741.1
67	+	43055	43456	133	14.3	8.4	<u>AGGA</u> AttATG	Spanin	Shfl1p71 [<i>Shigella</i> phage Shfl1] (125/133; 133)	94%	4,00E-77	YP_004414885.1
68	-	43469	43684	71	8.1	4.7	<u>GAAAGcatc</u> ATG		B508_00390 [<i>Escherichia</i> phage ADB-2] (67/71; 71)	94%	1,00E-41	YP_007112743.1
69	-	43874	44281	135	16.3	9.2	<u>GTTA</u> AtgatATG		T1p10 [<i>Enterobacteria</i> phage T1] (130/135; 135)	96%	6,00E-92	YP_003935.1
70	-	44286	45854	522	58.1	6.3	<u>GTTT</u> AttgtgATG		Shfl1p74 [<i>Shigella</i> phage Shfl1] (521/522; 522)	99%	0.0	YP_004414887.1
71	-	45931	46347	138	15.8	9.2	<u>GTGA</u> AtgcaATG		T1p07 [<i>Enterobacteria</i> phage T1] (136/138; 138)	99%	3,00E-93	YP_003938.1
72	-	46428	46637	69	8.1	3.5	<u>GCTA</u> AtttaATG		T1p06 [<i>Enterobacteria</i> phage T1] (62/69; 69)	90%	4,00E-37	YP_003939.1
73	-	46641	46865	74	8.0	9.9	<u>TAAAA</u> ATG		T1p05 [<i>Enterobacteria</i> phage T1] (71/74; 74)	96%	2,00E-41	YP_003940.1
74	-	46943	47086	47	5.1	9.5	<u>AAAAA</u> ATG		Shfl1p78 [<i>Shigella</i> phage Shfl1] (47/47; 47)	100%	3,00E-25	YP_004414891.1
75	-	47083	47403	106	12.0	9.8	<u>GAGGA</u> ATAATG		pSf2_078 [<i>Shigella</i> phage pSf-2] (102/106; 106)	96%	4,00E-69	YP_009113016.1
76	-	47419	47619	66	7.5	9.2	<u>GAGGCattg</u> tATG		T1p02 [<i>Enterobacteria</i> phage T1] (64/66; 66)	97%	7,00E-38	YP_003943.1
77	-	47612	47983	123	13.7	5.1	<u>GTA</u> AATTATATG		Shfl1p81 [<i>Shigella</i> phage Shfl1] (115/123; 123)	93%	6,00E-79	YP_004414894.1
78	-	47988	48218	76	8.8	6.2	<u>GAGAA</u> tcaccatATG		pSf2_075 [<i>Shigella</i> phage pSf-2] (75/76; 76)	99%	3,00E-47	YP_009113013.1
79	-	48294	48629	111	13.2	7.7	<u>GGGAA</u> ATG		Shfl1p85 [<i>Shigella</i> phage Shfl1] (102/111; 111)	93%	6,00E-69	YP_004414897.1
80	-	48712	48897	61	6.9	7.9	<u>AGCA</u> AAATG		pSf2_073 [<i>Shigella</i> phage pSf-2] (57/61; 61)	93%	5,00E-32	YP_009113011.1
81	-	48913	49098	61	6.8	8.8	<u>AACAA</u> aATG		B508_00040 [<i>Escherichia</i> phage ADB-2] (59/61; 61)	99%	4,00E-33	YP_007112675.1
82	-	49159	49863	234	26.1	7.7	<u>GAGT</u> CacgATG	DNA methylase	putative site specific DNA methylase [<i>Shigella</i> phage Shfl1] (228/234; 234)	99%	4,00E-170	YP_004414898.1

a start codon is indicated in boldface, Match to SD sequence is indicated by underlining, SD sequence is indicated in uppercase

b The number of identical amino acids/ The total number of amino acids

Table S2. Features of the ORFs of phage SH7, predicted functions of proteins and best matches with databases

ORF	Start (pb)	Stop (pb)	Strand	Size (aa)	MW (kDa)	pI	SD sequence (GAGAA) a	Predicted function	Blast (extent; Size (aa)) b	% aa identity	E Value	Accession number
1	2178	1	-	725	82.8	5.6	<u>GAGGA</u> aattATG	Membrane-associated protein ; affects host membrane ATPase	RB32ORF001c [Enterobacteria phage RB32](732/725; 725)	99%	0.0	YP_802943.1
2	2392	2189	-	67	8.1	6.6	TTGAAATG		RB32ORF002c [Enterobacteria phage RB32](67/67; 67)	100%	3,00E-39	YP_802944.1
3	4264	2447	-	605	68.3	7.2	<u>GATAA</u> agtATG	DNA topoisomerase subunit DNA-dependent ATPase	60plus39 [Enterobacteria phage RB32](605/605; 605)	100%	0.0	YP_802945.1
4	4594	4334	-	86	9.3	7.7	GTGAATtATG		39.1 [Enterobacteria phage RB14] (86/86; 86)	100%	1,00E-55	YP_002854340.1
5	4773	4597	-	59	6.7	8.4	<u>GAA</u> TaattATG	FmdB family transcriptional regulator	RB32ORF006c [Enterobacteria phage RB32](58/58; 58)	100%	4,00E-34	YP_802948.1
6	5195	4776	-	139	16.4	4.7	AAATTTATTaATG		F413_gp229 [Enterobacteria phage ime09](134/139; 139)	96%	2,00E-93	YP_007004389.1
7	5410	5195	-	71	8.4	5.0	<u>GAA</u> ATtgtaATG	Modifier of suppressor tRNAs	RB14ORF8 [Enterobacteria phage RB14](69/71; 71)	97%	1,00E-41	YP_002854344.1
8	5693	5424	-	89	10.2	5.3	<u>GAGAA</u> ataaATG		e112_011 [Escherichia phage e11/2](89/89; 93)	100%	4,00E-58	YP_009030895.1
9	6288	5791	-	165	18.7	9.1	<u>GAGAG</u> ataactATG	MotB/modifier of transcription	RB32ORF009c [Enterobacteria phage RB32](165/165; 165)	100%	9,00E-116	YP_802951.1
10	6904	6365	-	179	20.2	5.0	<u>GAGAT</u> aattATG		motB [Enterobacteria phage ime09](176/179;179)	98%	2,00E-124	YP_007004394.1
11	7407	6907	-	166	19.9	5.7	<u>GATA</u> AataaATG	Adenylyribosylating enzyme	ACG-C40_0011 [Enterobacteria phage v8_EcoM_ACG-C40](162/166; 166)	98%	9,00E-117	YP_006986562.1
12	8154	7471	-	227	26.0	4.9	AGGAAaatttaATG		dexA [Enterobacteria phage T4] (227/227; 227)	100%	4.27225E-117	NP_049629.1
13	8411	8154	-	85	10.1	7.9	TAGCTATCTTTATG	Exonuclease A	AR1_015 [Enterobacteria phage AR1](82/85; 85)	96%	8,00E-52	YP_009167826.1
14	8523	8389	-	44	5.1	3.8	AGTAAGttgATG		DexA.2 [Enterobacteria phage T4] (44/44; 81)	100%	2,00E-21	NP_049631.1
15	8881	8621	-	86	9.9	8.8	<u>GAGG</u> CtatATG	DNA helicase	ACQ28_gp015[Yersinia phage PST](86/86;86)	100%	2,00E-53	YP_009153618.1
16	10207	8888	-	439	50.0	7.6	<u>GGG</u> CActtccgATG		D862_gp259 [Enterobacteria phage v8_EcoM_ACG-C40](439/439; 439)	100%	0.0	YP_006986566.1
17	10515	10204	-	103	12.1	9.5	<u>GATA</u> AATATG	RNA polymerase ADP-ribosylase (anti-sigma factor)	dda.1 [Enterobacteria phage RB51] (103/103; 103)	100%	1,00E-67	YP_002853974.1
18	11263	10517	-	248	29.0	9.9	<u>GAGAA</u> aatATG		[Escherichia phage slur04](247/248; 248)	99%	4,00E-176	CUL02133.1
19	11988	11386	-	249	23.4	5.9	TGAGGTAGTTGAATG	Adenylyribosylating enzyme	RB27_021 [Enterobacteria phage RB27](199/200; 200)	99%	2,00E-145	YP_009102226.1
20	12608	11985	-	208	24.3	5.3	<u>GAGG</u> CtatcATG		AS348_gp118 [Escherichia phage slur14](206/207; 207)	99%	2,00E-149	YP_009180793.1
21	12858	12676	-	60	7.0	4.3	AGGAAttaatATG	Adenylyribosylating enzyme	[Enterobacteria phage RB51](60/60; 60)	100%	8.9476E-146	YP_002853978.1
22	13337	12867	-	157	18.3	6.1	<u>GAAA</u> TcacATG	Transcription modulator	ACG-C40_0021 [Enterobacteria phage v8_EcoM_ACG-C40](151/156; 156)	97%	1,00E-106	YP_006986572.1
23	13494	13330	-	55	6.2	5.8	<u>GATA</u> AatcATG		ModA.4 [Shigella phage Shf12](52/54; 54)	96%	2,00E-28	YP_004414923.1
24	13694	13491	-	67	8.1	6.3	<u>AA</u> CAaATG	Transcription modulator under heat shock	Srh [Enterobacteria phage T4] (66/67; 67)	99%	3,00E-38	NP_049640.1
25	14154	13669	-	161	18.5	4.5	<u>GAGG</u> AaatATG		F413_gp214 [Enterobacteria phage ime09](161/161; 161)	100%	3,00E-110	YP_007004408.1
26	14504	14163	-	113	12.6	3.9	<u>GAGG</u> CttttgtaATG	Affects phosphorylation of host	slur07_00238 [Escherichia phage slur07](112/113; 113)	99%	5,00E-75	CUL02483.1
27	14710	14504	-	69	8.2	5.6	<u>GAGAG</u> ccatATG		RB14ORF27 [Enterobacteria phage RB14](68/68; 68)	100%	2,00E-42	YP_002854363.1
28	15051	14806	-	81	9.2	5.6	<u>GAGA</u> AttacATG	Small outer capsid protein	RB3_030 [Enterobacteria phage RB3] (81/81; 81)	98.6%	3,00E-52	YP_009098416.1
29	15653	15135	-	172	20.2	5.2	<u>GAGA</u> AttacATG	dCTP pyrophosphatase	AS348_gp107 [Escherichia phage slur14] (171/172; 172)	99%	3,00E-124	YP_009180804.1
30	16950	15922	-	342	39.8	9.3	<u>GAGT</u> AaaaATG	DNA primase DNA helicase	F413_gp207 [Enterobacteria phage ime09](341/342; 342)	99%	0.0	YP_007004416.1
31	17117	16953	-	54	5.9	5.4	<u>GAGG</u> TtaatATG		61.1 [Enterobacteria phage RB51](54/54; 54)	100%	5,00E-28	YP_002853989.1
32	17475	17119	-	118	13.8	4.8	<u>GAGG</u> TtagtATG	Spackle periplasmic protein	48 [Shigella phage pS5-1](117/118; 118)	99%	1,00E-78	YP_009110855.1
33	17781	17488	-	97	11.0	4.6	<u>GAGA</u> TtatcATG		BN81_039 [Yersinia phage phiD1](96/97; 97)	99%	2,00E-64	YP_009149278.1
34	18091	17837	-	84	9.7	5.8	<u>GAAA</u> AgaatATG	RNA metabolism moderator	Shf12p041 [Shigella phage Shf12](84/84; 84)	100%	2,00E-52	YP_004414938.1
35	18397	18155	-	80	9.6	10.3	<u>GATA</u> AtATG		RB3_037 [Enterobacteria phage RB3](79/80; 80)	99%	9,00E-50	YP_009098423.1
36	18581	18399	-	60	7.0	5.2	<u>GAGA</u> TtggTATG	Discriminator of mRNA degradation	dmd [Enterobacteria phage T4](60/60; 60)	100%	5.82742E-35	NP_049653.1
37	20067	18640	-	475	53.5	5.5	<u>GAGT</u> AagtGTG		ACQ54_gp036 [Escherichia phage HY01](473/475; 475)	99%	0.0	YP_009148487.1
38	20421	20077	-	114	13.3	4.9	<u>AAGA</u> AatttaATG	Head vertex assembly chaperone	40 [Enterobacteria phage T4](114/114; 114)	100%	5,00E-75	NP_049655.1
39	21595	20414	-	393	44.1	5.4	<u>GAAA</u> AaatgaATG	RecA-like recombination protein	F412_gp232 [Escherichia phage wV7](392/393; 393)	99%	0.0	YP_007004784.1
40	22515	21673	-	281	32.4	7.1	<u>GAGT</u> GgaaATG	Beta-glucosyltransferase	RB14ORF41 [Enterobacteria phage RB14](280/280; 280)	100%	0.0	YP_002854377.1
41	23252	22512	-	247	28.6	5.4	<u>GAGG</u> TttaaATG	DCMP hydroxymethylase	ACQ28_gp041 [Yersinia phage PST](246/246; 246)	100%	0.0	YP_009153644.1
42	23657	23406	-	83	9.4	9.4	<u>GAAA</u> AgATG	Immunity to superinfection membrane protein	RB32ORF044c [Enterobacteria phage RB32](82/83; 83)	99%	1,00E-48	YP_802986.1
43	24045	23665	-	126	14.2	7.5	<u>GAGAA</u> TgaaATG	Membrane protein	RB51ORF047 [Enterobacteria phage RB51](126/126; 126)	100%	1,00E-86	YP_002854002.1
44	26924	24228	-	898	103.6	5.9	<u>GAAT</u> AtctATG		gp43 [Enterobacteria phage T4](897/898; 898)	99%	0.0	NP_049662.1
45	27371	27003	-	122	14.6	8.9	<u>GTAAA</u> ATG	Translational repressor protein	regA [Enterobacteria phage T4](122/122; 122)	100%	6,00E-84	NP_049663.1
46	27936	27373	-	187	21.4	7.7	<u>AAGA</u> GatATG	Clamp-loader small subunit	slur04_00026 [Escherichia phage slur04](187/187; 187)	100%	2,00E-133	CUL01898.1
47	28897	27938	-	319	35.8	7.0	<u>GGA</u> AAttATG		HY01_0048 [Escherichia phage HY01](319/319; 319)	100%	0.0	YP_009148499.1
48	29635	28949	-	228	24.9	4.9	<u>GAAA</u> TtacATG	Sliding clamp of DNA polymerase	45 [Enterobacteria phage RB32](228/228; 228)	100%	6,00E-164	YP_802993.1
49	30080	29691	-	129	14.7	6.8	<u>GTG</u> TAttATG	RNA polymerase binding protein	rpba [Enterobacteria phage T4](129/129; 129)	100%	3,00E-90	NP_049667.1
50	30290	30090	-	66	7.9	5.0	<u>TATA</u> AtcttATG	Recombination endonuclease subunit	45.2 [Enterobacteria phage T4](62/62; 62)	100%	2,00E-37	NP_049668.1
51	31973	30333	-	546	61.8	7.1	<u>CAAAA</u> tataATG		46 [Escherichia phage e11/2](546/546; 560)	100%	0.0	YP_009030664.1
52	32275	32012	-	87	10.6	4.9	<u>TAGA</u> TaATG	Recombination endonuclease subunit	46.1 [Enterobacteria phage AR1](85/87; 87)	98%	4,00E-55	YP_009167869.1
53	32462	32199	-	88	10.2	4.2	<u>GGCAA</u> cactATG		46.2 [Enterobacteria phage ime09](87/87; 87)	100%	1,00E-55	YP_007004441.1
54	33478	32459	-	339	39.2	4.9	<u>GAT</u> ATATG	Recombination endonuclease subunit	slur04_00034 [Escherichia phage slur04](338/339; 339)	99%	0.0	CUL01906.1
55	33615	33475	-	46	5.4	4.2	<u>GAT</u> ATATG		47.1 [Enterobacteria phage T4] (45/46; 46)	98%	4,00E-21	NP_813808.1
56	34857	33655	-	400	46.9	6.1	<u>GAGGA</u> tattaaATG	α -glucosyltransferase	RB51ORF065 [Enterobacteria phage RB51](399/400; 400)	99%	0.0	YP_002854018.1
57	35097	34924	-	57	6.7	9.7	<u>GAA</u> AGATG	Membrane protein	RB32ORF061c [Enterobacteria phage RB32] (55/57; 57)	96%	2,00E-31	YP_803003.1
58	35304	35101	-	67	7.9	9.4	<u>GAT</u> ATtgattgATG		RB32ORF062c [Enterobacteria phage RB32] (67/67; 67)	100%	1,00E-41	YP_803004.1
59	35590	35273	-	105	12.4	8.8	<u>GAGAA</u> ataatATG	Sigma factor for late transcription	α -gt.4 [Enterobacteria phage T4](105/105; 105)	100%	3,00E-67	NP_049677.1
60	35810	35592	-	72	8.5	4.2	<u>GATT</u> TtttatATG		α -gt.5 [Enterobacteria phage T4](72/72; 72)	100%	7,00E-43	NP_049678.1
61	36351	35794	-	185	21.5	5.4	<u>GTG</u> AAaATG	Sigma factor for late transcription	55 [Escherichia phage e11/2](185/185; 187)	100%	2,00E-134	YP_009030673.1
62	36699	36430	-	89	10.8	5.6	<u>GATG</u> atgATG		RB14ORF65 [Enterobacteria phage RB14](89/89; 89)	100%	3,00E-58	YP_002854401.1
63	36917	36696	-	73	8.3	3.7	<u>GCT</u> AAggtATG	Sigma factor for late transcription	55.1 [Enterobacteria phage AR1](73/73; 73)	100%	3,00E-43	YP_009167879.1
64	37240	36914	-	108	12.7	9.7	<u>GATA</u> AagtATG		ECML134_067 [Escherichia phage ECML-134](108/108; 108)	100%	7,00E-71	YP_009102542.1
65	37494	37294	-	66	7.7	7.9	<u>GGGAA</u> atttaaATG	Sigma factor for late transcription	55.3 [Enterobacteria phage RB32](66/66; 66)	100%	1,00E-40	YP_803010.1
66	37626	37495	-	43	5.1	8.1	<u>GAGG</u> AAaatATG		55.4 [Enterobacteria phage T4](43/43; 43)	100%	5,00E-22	NP_049683.1
67	37927	37634	-	98	11.8	9.7	<u>TTAA</u> AtctcATG	Sigma factor for late transcription	55.5 [Enterobacteria phage T4](96/97; 97)	99%	6,00E-61	NP_049684.1
68	38096	37920	-	58	6.8	7.9	<u>GAGGA</u> tttgatATG		55.6 [Enterobacteria phage ime09](58/58; 58)	100%	3,00E-33	YP_007004455.1
69	38563	38255	-	102	11.7	9.2	<u>AGGAA</u> tagttGTG	Glutaredoxin	nrhH [Enterobacteria phage T4](101/102; 102)	99%	6,00E-67	NP_049686.1
70	38778	38566	-	70	7.9	9.2	<u>GTA</u> AAATG		55.8 [Enterobacteria phage T4](70/70; 70)	100%	5,00E-40	NP_049687.1

71	38900	38787	-	75	4.5	4.5	<u>GTA</u> AAATG	Anaerobic nucleotide reductase subunit	RB32ORF074c [Enterobacteria phage RB32] (37/37; 37)	100%	2,00E-17	YP_803016.1
72	39363	38893	-	156	18.2	5.9	<u>GTTAA</u> accacATG	Ribonucleotide reductase of class III activating protein	F413_gp170 [Enterobacteria phage ime09] (156/156; 156)	100%	1,00E-110	YP_007004459.1
73	41177	39360	-	605	68.0	6.6	<u>GAGT</u> TtaaaATG	Anaerobic NTP reductase large subunit	ShfI2p080 [Shigella phage ShfI2] (604/605; 605)	99%	0.0	YP_004414977.1
74	41647	41174	-	158	18.1	8.8	<u>GGG</u> TTttatATG	Packaging and recombination endonuclease VII	49 [Enterobacteria phage T4] (157/157; 157)	100%	4,00E-111	NP_049692.1
75	42175	41690	-	161	18.8	4.5	<u>GAGA</u> TgggaCATG	Inhibitor of host Lon protease	pin [Enterobacteria phage RB3] (159/161; 161)	99%	2,00E-112	YP_009098466.1
76	42314	42159	-	51	6.2	3.9	<u>ACG</u> AGaATG		49.1 [Enterobacteria phage T4] (51/51; 51)	100%	8,00E-28	NP_049695.1
77	42619	42299	-	162	12.6	4.5	<u>GTG</u> AAAAaATG	Nucleotide reductase subunit C	49.2 [Enterobacteria phage T4] (105/106; 106)	99%	8,00E-71	NP_049696.1
78	43020	42631	-	129	14.9	4.8	<u>GAGAA</u> tatttttaaATG		RB32ORF082c [Enterobacteria phage RB51] (71/71; 71)	100%	2,00E-42	YP_002854042.1
79	43280	43017	-	87	10.0	6.7	<u>GAAT</u> AatATG	Thioredoxin, glutaredoxin	nrdC [Enterobacteria phage T4] (87/87; 87)	100%	3,00E-57	NP_049698.1
80	43524	43282	-	80	9.4	7.9	<u>GAGAA</u> gaaaATG		NrdC.1 [Enterobacteria phage T4] (80/80; 80)	100%	2,00E-50	NP_049699.1
81	43825	43511	-	104	12.1	6.1	<u>TTGAA</u> ATG		RB32ORF085c [Enterobacteria phage RB32] (104/104; 104)	100%	3,00E-71	YP_803027.1
82	44751	43822	-	310	35.9	9.3	<u>GAGAA</u> gaacATG	Thioredoxin	HY01_0081 [Escherichia phage HY01] (302/309; 309)	98%	0.0	YP_009148532.1
83	45835	44804	-	343	40.2	6.2	<u>GTGG</u> TataATG		slur03_00199 [Escherichia phage slur03] (337/343; 343)	98%	0.0	CUL01789.1
84	46885	45863	-	340	39.5	9.2	<u>AGGAA</u> acactATG		ECML134_087 [Escherichia phage ECML-134] (321/340; 340)	94%	0.0	YP_009102562.1
85	47784	46894	-	296	33.9	9.2	<u>GAGG</u> AAAAatATG		nrdC.6 [Enterobacteria phage T4T] (292/296; 296)	99%	0.0	ADJ39810.1
86	48200	47796	-	134	15.3	5.7	<u>GAGA</u> TtattATG		ACG-C40_0088 [Enterobacteria phage vB_EcoM_ACG-C40] (131/134; 134)	98%	2,00E-90	YP_006986641.1
87	48783	48256	-	176	20.8	6.7	<u>GAACA</u> gaaaATG		nrdC.8 [Enterobacteria phage RB14] (175/175; 175)	100%	3,00E-121	YP_002854428.1
88	49158	48844	-	104	12.4	9.6	<u>GGTAA</u> ATG		nrdC.9 [Enterobacteria phage RB32] (102/104; 104)	98%	5,00E-69	YP_803034.1
89	50216	49248	-	322	36.4	5.0	<u>GAGAA</u> TaaaATG	Thioredoxin	F412_gp179 [Escherichia phage wV7] (322/322; 322)	100%	0.0	YP_007004837.1
90	50474	50274	-	67	7.7	6.6	<u>GAGT</u> AacaaaATG		g099/BN81_099 [Yersinia phage phiD1] (66/66; 66)	100%	1,00E-40	YP_009149338.1
91	51606	50593	-	337	39.0	6.3	<u>TATA</u> AggctgaATG		nrdC.11 [Enterobacteria phage RB32] (334/337; 337)	99%	0.0	YP_803037.1
92	52064	51603	-	153	17.9	9.4	<u>GATA</u> AttATG		RB51ORF103/RB32ORF096c [Enterobacteria phage RB51] (152/153; 153)	99%	4,00E-105	YP_002854056.1
93	52588	52067	-	173	19.3	4.9	<u>GAGG</u> AAaatATG		AR1_101 [Enterobacteria phage AR1] (173/173; 173)	100%	2,00E-122	YP_009167912.1
94	53140	52595	-	181	21.0	5.2	<u>GAGT</u> AtgtaATG		slur07_00168 [Escherichia phage slur07] (179/181; 181)	99%	1,00E-128	CUL02413.1
95	53244	53140	-	34	4.2	8.1	<u>GAGAA</u> agagaATG		F412_gp172 [Escherichia phage wV7] (34/34; 34)	100%	2,00E-13	YP_007004844.1
96	53478	53305	-	58	6.7	5.3	<u>TGGA</u> AtaATG		mobD.2a [Enterobacteria phage RB14] (57/57; 57)	100%	8,00E-33	YP_002854439.1
97	53662	53468	-	65	7.6	5.0	<u>GAGT</u> TtaagtATG		mobD.3 [Enterobacteria phage RB51] (64/64; 64)	100%	6,00E-38	YP_002854061.1
98	53868	53665	-	67	7.6	4.3	<u>TGGA</u> AtaATG		MobD.4 [Yersinia phage PST] (67/67; 67)	100%	1,00E-37	YP_009153706.1
99	54056	53868	-	62	7.2	4.2	<u>GAGAA</u> catcATG		g110/BN81_110 [Yersinia phage phiD1] (62/62; 62)	100%	3,00E-36	YP_009149349.1
100	54538	54152	-	128	14.6	5.5	<u>GAGAC</u> tgaATG		slur04_00078 [Escherichia phage slur04] (128/128; 128)	100%	2,00E-86	CUL01950.1
101	54828	54535	-	97	11.1	4.9	<u>GAGG</u> CctttATG	Membrane protein	ri [Enterobacteria phage T4] (97/97; 97)	100%	8,00E-65	NP_049717.1
102	55053	54841	-	71	8.3	10.2	<u>GGGT</u> AtatATG		g113/BN81_113 [Yersinia phage phiD1] (70/70; 70)	100%	8,00E-42	YP_009149352.1
103	55677	55096	-	194	21.6	6.2	<u>GACT</u> agATG	Thymidine kinase	tk [Enterobacteria phage RB32] (193/193; 193)	100%	2,00E-140	YP_803049.1
104	55867	55679	-	62	7.3	4.1	<u>TATA</u> AattccttATG		slur07_00159 [Escherichia phage slur07] (62/62; 62)	100%	2,00E-33	CUL02404.1
105	56049	55864	-	61	7.2	4.5	<u>GAAA</u> TtaataATG		tk.2 [Enterobacteria phage RB32] (61/61; 61)	100%	8,00E-34	YP_803051.1
106	56219	56046	-	57	6.6	5.2	<u>GTA</u> AAccgaaATG		RB14ORF113/RB32ORF110c [Enterobacteria phage RB14] (57/57; 57)	97.6%	1,00E-30	YP_002854449.1
107	57095	56628	-	156	17.5	6.3	<u>GAGT</u> ActagtATG		tk.4 [Enterobacteria phage RB51] (154/155; 155)	99%	9,00E-110	YP_002854072.1
108	57439	57092	-	115	13.1	9.0	<u>AGTAA</u> ATG	valyl-tRNA synthetase modifier	vs [Enterobacteria phage T4] (115/115; 115)	100%	6,00E-77	NP_049724.1
109	57977	57432	-	181	20.7	9.7	<u>GGTA</u> AgcATG		vs.1 [Enterobacteria phage T4] (181/181; 181)	100%	1,00E-128	NP_049725.1
110	58446	57985	-	153	18.0	8.9	<u>GAGAA</u> ataacATG	Site-specific RNA endonuclease	regB [Enterobacteria phage T4] (152/153; 153)	99%	8,00E-108	NP_049726.1
111	58784	58506	-	93	10.9	5.4	<u>GAAA</u> AatactaATG		RB27_120 [Enterobacteria phage RB27] (92/92; 92)	100%	6,00E-60	YP_009102325.1
112	59080	58784	-	98	11.4	4.9	<u>TTGAA</u> tATG		vs.4 [Enterobacteria phage AR1] (95/98; 98)	97%	2,00E-61	YP_009167932.1
113	59264	59043	-	73	8.2	4.1	<u>GAGT</u> CtctaATG		vs.5 [Enterobacteria phage RB27] (73/73)	100%	6,00E-46	YP_009102327.1
114	59626	59264	-	120	13.8	5.8	<u>GAGG</u> TttatATG	Pyruvate formate-lyase	vs.6 [Enterobacteria phage RB51] (120/120; 120)	100%	2,00E-81	YP_002854079.1
115	60014	59634	-	126	15.0	9.3	<u>GTTAA</u> ATG		vs.7 [Enterobacteria phage T4] (124/126; 126)	98%	1,00E-86	CAA28221.1
116	60499	59960	-	179	20.2	8.8	<u>GAGAA</u> gaaaATG		slur14_00014 [Escherichia phage slur14] (178/179; 179)	99%	3,00E-129	YP_009180624.1
117	61113	60640	-	157	17.8	8.9	<u>AGGAA</u> acacATG	Internal head protein II	ipli [Enterobacteria phage RB32] (157/157; 157)	100%	2,00E-109	YP_803065.1
118	61447	61130	-	105	12.1	9.4	<u>AGGAA</u> acacATG	Internal head protein III	slur04_00097 [Escherichia phage slur04] (105/105; 105)	100%	2,00E-70	CUL01969.1
119	62030	61536	-	164	18.6	9.6	<u>GAGG</u> TattATG	Endolysin	e [Enterobacteria phage RB32] (164/164; 164)	100%	5,00E-117	YP_803066.1
120	62523	62068	-	151	17.6	5.2	<u>TATCA</u> ctgaATG	Nudix hydrolase	e112_129 [Escherichia phage e11] (2/147/151; 151)	97%	9,00E-107	YP_009030734.1
121	62993	62505	-	162	19.4	8.4	<u>GAAA</u> AtttaaATG	Membrane protein	e.2 [Enterobacteria phage RB51] (162/162; 162)	97.8%	9,00E-114	YP_002854086.1
122	63352	62990	-	120	14.1	7.7	<u>AGGAA</u> tcacgATG	Membrane protein	e.3 [Enterobacteria phage RB3] (119/120; 120)	99%	1,00E-80	YP_009098516.1
123	63726	63334	-	130	15.2	9.6	<u>GAGAA</u> tATG		e.4 [Enterobacteria phage RB32] (127/130; 130)	98%	3,00E-85	YP_803069.1
124	64309	63695	-	204	24.1	5.4	<u>GTTAA</u> AtaggaATG		gp146/RM00_gp144 [Shigella phage pSs-1] (201/204; 204)	99%	3,00E-145	YP_009110952.1
125	64944	64351	-	197	22.1	6.1	<u>AGGAA</u> atactATG		gp147/RM00_gp145 [Shigella phage pSs-1] (197/197; 197)	100%	9,00E-134	YP_009110953.1
126	65337	65002	-	111	13.0	4.3	<u>GAAA</u> AacattATG		slur04_00106 [Escherichia phage slur04] (110/111; 111)	99%	7,00E-73	CUL01978.1
127	65546	65382	-	54	6.1	4.0	<u>GAGAA</u> ataaaATG		RB69p145/RB69ORF145c [Enterobacteria phage RB69] (53/54; 54)	98%	4,00E-30	NP_861835.1
128	65878	65615	-	87	10.2	4.5	<u>GAGAA</u> cgaaATG		e.8 [Enterobacteria phage ime09] (87/87; 109)	100%	4,00E-57	YP_007004513.1
129	66583	66110	-	157	17.2	9.5	<u>AGGAA</u> ataagATG		ACQ54_gp126 [Escherichia phage HY01] (156/157; 157)	99%	1,00E-106	YP_009148577.1
130	67319	66969	-	116	14.2	6.5	<u>AGGAA</u> aatATG		F413_gp248 [Enterobacteria phage ime09] (114/116; 116)	98%	9,00E-79	YP_0070044516.1
131	68742	68455	-	95	11.3	4.9	<u>GTTG</u> AtaATG		ACQ54_gp129 [Escherichia phage HY01] (94/95; 95)	99%	2,00E-61	YP_009148580.1
132	69125	68745	-	126	14.3	4.6	<u>GTGAA</u> TagaATG		F413_gp246 [Enterobacteria phage ime09] (126/127; 127)	99%	1,00E-85	YP_0070044518.1
133	69312	69127	-	61	6.6	7.8	<u>GAGAA</u> ataaaATG		tRNA.4 [Enterobacteria phage T4] (61/61; 61)	100%	9,00E-33	NP_049748.1
134	69676	69389	-	95	10.2	8.9	<u>AAAA</u> ATG	internal head protein	ACQ54_gp132 [Escherichia phage HY01] (95/95; 95)	100%	3,00E-59	YP_009148583.1
135	70206	69751	-	151	17.1	5.1	<u>AAAGA</u> AtaATG		gp57B [Enterobacteria phage T4] (151/151; 152)	100%	2,00E-106	NP_049750.1
136	70448	70206	-	80	8.7	4.4	<u>AGGT</u> ActataATG	Chaperone for long and short tail fiber formation	ShfI2p143 [Shigella phage ShfI2] (80/80; 80)	100%	3,00E-45	YP_004415038.1
137	71161	70448	-	237	26.9	5.3	<u>GAGAA</u> acataATG	Deoxynucleotide monophosphate kinase	slur14_00046 [Escherichia phage slur14] (234/237; 237)	99%	5,00E-172	YP_009180646.1
138	71741	71211	-	176	19.7	4.4	<u>GAGGA</u> atatATG	Tail completion and sheath stabilizer protein	3 [Enterobacteria phage T4] (176/176; 184)	100%	2,00E-125	AAA50419.1
139	72672	71848	-	274	31.6	10.1	<u>GGCA</u> TaATG	DNA end protector protein	2 [Enterobacteria phage T4] (273/274; 274)	99%	0.0	NP_049754.1
140	73124	72672	-	150	17.6	9.6	<u>GAGAA</u> ttccaATG	Head completion protein	4 [Enterobacteria phage RB32] (150/150; 150)	100%	3,00E-105	YP_803090.1
141	73172	73762	+	196	23.0	5.9	<u>GAGG</u> GcccccATG	Baseplate wedge subunit	ShfI2p149 [Shigella phage ShfI2] (19			

143	73905	73768	-	45	5.5	4.9	<u>GACATcc</u> ATG	Replication initiation protein	RepEB oriE [Enterobacteria phage T4] (43/45; 45)	96%	7,00E-21	NP_049758.1
144	75006	74872	-	44	5.4	5.3	CTCATATG	Replication initiation protein	RepEA oriE [Enterobacteria phage T4] (35/43; 50)	81%	4,00E-13	NP_049759.1
145	75448	76002	+	184	20.6	4.5	<u>CACCAattg</u> ATG		e112_162 [Escherichia phage e11/2] (182/184; 184)	99%	6,00E-129	YP_009030759.1
146	76003	76296	+	97	10.2	8.6	<u>CATAAA</u> ATG		5.4 [Enterobacteria phage T4] (97/97; 97)	100%	2,00E-63	NP_049763.1
147	76305	78287	+	660	74.3	4.6	<u>GATTTaaa</u> ATG	Baseplate wedge component	6 [Yersinia phage PST] (659/660; 660)	99%	0.0	YP_009153751.1
148	78284	81382	+	1033	118.9	5.0	<u>TATATcaca</u> ATG	Baseplate wedge component	gp7 [Enterobacteria phage AR1] (1025/1032; 1032)	99%	0.0	YP_009167970.1
149	81375	82379	+	334	38.0	4.6	<u>TAAAA</u> tagATG	Baseplate wedge component	ECML134_151 [Escherichia phage ECML-134] (333/334; 334)	99%	0.0	YP_009102626.1
150	82443	83309	+	288	31.0	5.0	<u>GAAACcgct</u> ATG	Baseplate wedge tail fiber connector	9 [Enterobacteria phage T4] (285/288; 288)	99%	0.0	NP_049767.1
151	83309	85114	+	601	66.3	4.5	<u>CTCAAta</u> ATG	Baseplate wedge subunit and tail pin	10 [Escherichia phage e11/2] (601/601; 601)	100%	0.0	YP_009030765.1
152	85114	85773	+	219	24.1	5.2	<u>TTGCATA</u> ATG	Baseplate wedge subunit and tail pin	11 [Escherichia phage e11/2] (219/219; 219)	100%	8,00E-159	YP_009030766.1
153	85770	87320	+	516	55.4	5.8	<u>GAGAA</u> tagcATG	Short tail fibers	12 [Escherichia phage e11/2] (514/516; 516)	99%	0.0	YP_009030767.1
154	87330	88787	+	486	52.6	4.8	<u>TACAA</u> ATG	Fibrin neck whiskers	wac [Enterobacteria phage RB27] (475/485; 485)	98%	0.0	YP_009102364.1
155	88819	89748	+	309	34.7	4.9	<u>AAGGA</u> ttttaaATG	Neck protein	Shf12p161 [Shigella phage Shf12] (308/309; 309)	99%	0.0	YP_004415055.1
156	89750	90520	+	256	29.6	4.6	<u>GTTAA</u> tATG	Neck protein	14 [Enterobacteria phage RB3] (256/256; 256)	100%	0.0	YP_009098546.1
157	90562	91380	+	272	31.6	4.9	<u>GAGAA</u> atcATG	Tail sheath stabilizer and completion	15 [Enterobacteria phage T4] (272/272; 272)	100%	0.0	NP_049774.1
158	91389	91883	+	164	18.4	4.6	<u>GAGGT</u> ttattATG	Terminase DNA packaging enzyme small subunit	16 [Enterobacteria phage T4] (164/164; 164)	100%	4,00E-116	NP_049775.1
159	91867	93699	+	610	69.8	5.6	<u>GATAA</u> ATG	Terminase large subunit nuclease and ATPase	17 [Enterobacteria phage RB32] (610/610; 610)	100%	0.0	YP_803107.1
160	93731	95710	+	659	71.3	4.8	<u>GATTAAa</u> aATG	Tail sheath monomer	g171 [Yersinia phage phiD1] (656/659; 659)	99%	0.0	CC189062.1
161	95827	96318	+	163	18.5	4.7	<u>GCTAA</u> ATG	Tail tube monomer	19 [Enterobacteria phage T4] (163/163; 163)	100%	4,00E-116	NP_049781.1
162	96402	97976	+	524	61.0	5.4	<u>GAGAA</u> taacaATG	Portal vertex protein of the head	20 [Enterobacteria phage RB3] (524/524; 524)	100%	0.0	YP_009098553.1
163	97976	98233	+	85	9.7	3.8	<u>GAGGA</u> tttttaATG	Prohead core	gp67 /F413_gp094 [Enterobacteria phage ime09] (85/85; 85)	100%	9,00E-45	YP_007004547.1
164	98233	98658	+	141	15.9	10.1	<u>GATGA</u> ataATG	Prohead core	68 [Enterobacteria phage T4] (141/141; 141)	100%	7,00E-95	NP_049784.1
165	98658	99296	+	212	23.3	5.0	<u>GATTAA</u> gctaATG	Prohead core scaffold protein and protease	21 [Enterobacteria phage RB51] (212/212; 212)	100%	2,00E-151	YP_002854128.1
166	99327	100136	+	269	29.8	4.6	<u>TACAA</u> aATG	Prohead core scaffold protein	22 [Escherichia phage ECML-134] (268/269; 269)	99%	0.0	YP_009102644.1
167	100155	101720	+	521	56.1	5.3	<u>CACAA</u> ATG	Precursor of major head subunit	gp187 /RM00_gp185 [Shigella phage pss-1] (521/521; 521)	100%	0.0	YP_009110993.1
168	101804	103087	+	427	47.0	4.7	<u>GCGCA</u> ATG	Precursor of head vertex subunit	ACQ54_gp165 [Escherichia phage HY01] (427/427; 427)	100%	0.0	AHK11022.1
169	104124	103120	-	334	37.6	5.4	<u>GATTAA</u> ttATG	RNA ligase	Shf12p177 [Shigella phage Shf12] (328/334; 334)	98%	0.0	YP_004415069.1
170	104412	104134	-	92	11.0	5.0	<u>GTGAA</u> aaaATG		24.2 [Enterobacteria phage T4] (92/92; 92)	100%	9,00E-60	NP_049791.1
171	104614	104399	-	71	8.3	10.5	<u>GATAA</u> cATG		24.3 [Enterobacteria phage RB32] (71/71; 71)	100%	1,00E-41	YP_803119.1
172	105833	104703	-	377	40.5	4.6	<u>GATAA</u> cttATG	Large capsid outer capsid	hoc [Enterobacteria phage RB32] (339/376; 376)	90%	0.0	YP_803120.1
173	106523	105843	-	226	25.6	4.5	<u>GAGGA</u> aatatATG	Minor capsid protein inhibitor of prohead protease	inh [Enterobacteria phage RB27] (225/226; 226)	99%	2,00E-159	YP_009102383.1
174	106574	108085	+	503	57.9	9.3	<u>TAGAC</u> ATG	RNA-DNA and DNA- helicase; DNA dependent ATPase	uvsW [Enterobacteria phage RB51] (503/503; 503)	100%	0.0	YP_002854137.1
175	108111	108341	+	76	8.8	4.2	<u>GAGAA</u> aaagATG	RNA-DNA and DNA- helicase; DNA dependent ATPase	uvsW [Escherichia phage e11/2] (76/76; 80)	100%	4,00E-44	YP_009030789.1
176	108564	108397	-	55	6.1	4.4	<u>GACAA</u> tcATG		uvsY_-2 [Enterobacteria phage T4] (55/55; 100)	100%	1,00E-30	NP_049797.1
177	108915	108688	-	75	9.1	4.9	<u>GAAAA</u> ataATG		uvsY_-1 [Escherichia phage e11/2] (75/75; 75)	100%	6,00E-47	YP_009030792.1
178	109328	108915	-	137	15.8	7.8	<u>GAGAA</u> caatATG	Repair and ssDNA binding	uvsY [Enterobacteria phage RB32] (137/137; 137)	100%	9,00E-93	YP_803126.1
179	109793	109395	-	132	15.1	4.6	<u>GAGT</u> TactataATG	Baseplate wedge subunit	slur04_00168 [Escherichia phage slur04] (132/132; 132)	100%	5,00E-89	CUL02029.1
180	110419	109793	-	208	23.9	5.6	<u>GAGC</u> TaaatATG	Baseplate hub subunit	26 [Enterobacteria phage T4] (208/208; 208)	100%	2,00E-149	NP_049801.1
181	110470	111219	+	249	29.3	5.8	<u>GAGC</u> AtcttATG	Baseplate hub assembly catalyst	51 [Enterobacteria phage ime09] (247/249; 249)	99%	8,00E-180	YP_007004565.1
182	111219	112394	+	391	44.4	5.2	<u>AACAA</u> taATG	Baseplate hub subunit	27 [Enterobacteria phage RB32] (390/391; 391)	99%	0.0	YP_803130.1
183	112414	112872	+	153	17.3	5.0	<u>CTAAA</u> ATG	Baseplate hub distal subunit	28 [Enterobacteria phage RB32] (152/152; 177)	100%	5,00E-106	YP_803131.1
184	112869	114641	+	590	64.3	5.1	<u>GATTAA</u> tttgaATG	Baseplate hub subunit and tail length determinator	Shf12p194 [Shigella phage Shf12] (581/590; 590)	98%	0.0	YP_004415085.1
185	114650	115744	+	364	39.7	8.9	<u>GAATA</u> aATG	Tail-tube assembly	slur14_00092 [Escherichia phage slur14] (361/364; 364)	99%	0.0	YP_009180692.1
186	115744	116709	+	321	34.9	5.1	<u>GACTT</u> tttaATG	baseplate tail tube initiator	D862_gp081 [Enterobacteria phage v8_EcoM_ACC-C40] (319/321; 321)	99%	0.0	YP_006986749.1
187	117028	116738	-	96	10.7	4.7	<u>CACAA</u> aATG		alt_-3 [Enterobacteria phage RB51] (96/96; 96)	100%	3,00E-59	YP_002854150.1
188	119146	117089	-	685	75.9	5.8	<u>GATAA</u> atcATG	RNA polymerase ADP-ribosylase	F412_gp080 [Escherichia phage wV7] (679/685; 685)	99%	0.0	YP_007004936.1
189	121210	119150	-	686	76.4	5.7	<u>GAGGA</u> AtATG	RNA polymerase ADP-ribosylase	alt [Enterobacteria phage AR1] (681/685; 685)	99%	0.0	YP_009168013.1
190	121448	121260	-	62	7.1	4.5	<u>GGTAA</u> aggtttATG		Shf12p200 [Shigella phage Shf12] (62/62; 62)	100%	6,00E-36	YP_004415091.1
191	122908	121445	-	487	55.3	6.1	<u>GATGA</u> acaaATG	DNA ligase	30 [Yersinia phage PST] (485/487; 487)	99%	0.0	YP_009153798.1
192	123174	122905	-	89	10.8	7.8	<u>GAGC</u> AttctaATG		30.1 [Enterobacteria phage LZ9] (89/89; 89)	100%	7,00E-60	CAJ32735.1
193	124013	123174	-	279	32.4	5.9	<u>GAGAC</u> TctctATG		30.2 [Enterobacteria phage RB32] (275/279; 279)	99%	0.0	YP_803141.1
194	124468	124010	-	152	17.2	9.0	<u>TTGAA</u> aATG		30.3 [Enterobacteria phage T6] (150/152; 152)	99%	3,00E-106	CAD30031.1
195	124667	124461	-	68	8.0	5.0	<u>AGGAA</u> tttagtATG		30.4 [Enterobacteria phage AR1] (67/68; 68)	99%	3,00E-40	YP_009168019.1
196	124861	124664	-	65	7.2	5.2	<u>GAGGT</u> TctgtATG		30.5 [Enterobacteria phage RB51] (65/65; 65)	100%	3,00E-37	YP_002854159.1
197	125148	124861	-	95	10.8	6.7	<u>GAAAA</u> taactATG		30.6 [Enterobacteria phage RB14] (95/95; 95)	100%	1,00E-63	YP_002854539.1
198	125554	125189	-	121	14.2	6.1	<u>GAGAA</u> taaaaATG		Shf12p208 [Shigella phage Shf12] (121/121; 121)	100%	5,00E-85	YP_004415099.1
199	125955	125623	-	110	12.9	6.7	<u>GAGAA</u> taaaaATG		30.8 [Enterobacteria phage RB51] (109/110; 110)	99%	3,00E-72	YP_002854162.1
200	126284	126066	-	72	8.2	11.3	<u>AGGCA</u> ATG		30.9 [Yersinia phage PST] (72/72; 72)	100%	7,00E-42	YP_009153807.1
201	126737	126489	-	82	9.3	8.1	<u>GAGAA</u> tttttaaATG	Lysis inhibition accessory protein, rapid lysis phenotype	rliII [Enterobacteria phage T4] (82/82; 82)	100%	5,00E-51	NP_049824.1
202	127220	126885	-	111	12.1	5.3	<u>GAAAA</u> cgATG	Head assembly cochaperone with GroEL	31 [Enterobacteria phage T4] (111/111; 111)	100%	4,00E-72	NP_049825.1
203	127585	127277	-	102	11.5	8.0	<u>GTA</u> AtaaATG		31.1 [Enterobacteria phage T4] (101/102; 102)	99%	2,00E-65	NP_049826.1
204	127822	127586	-	78	9.3	9.6	<u>GTGAA</u> taATG	Tail fiber	RB27_209 [Enterobacteria phage RB27] (77/78; 78)	99%	5,00E-48	YP_009102414.1
205	128403	127822	-	193	21.2	8.0	<u>ATGAA</u> ATG	dCMP deaminase	cd [Enterobacteria phage RB32] (193/193; 193)	100%	8,00E-140	YP_803153.1
206	128735	128400	-	112	12.7	7.9	<u>TACTA</u> tatATG		RB27_211 [Enterobacteria phage RB27] (111/111; 112)	100%	4,00E-74	YP_009102416.1
207	128974	128735	-	80	89.3	5.3	<u>GA</u> TCaacaATG		cd.2 [Enterobacteria phage RB51] (79/79; 79)	100%	6,00E-48	YP_002854170.1
208	129138	128965	-	57	6.5	4.6	<u>GGTA</u> TtactgtTTG		AR1_225 [Enterobacteria phage AR1] (57/57; 176)	100%	3,00E-30	YP_009168036.1
209	129495	129217	-	92	10.8	4.9	<u>GAGGA</u> AaattgttATG		ACQ54_gp205 [Escherichia phage HY01] (92/92; 175)	100%	3,00E-59	YP_009148656.1
210	129833	129558	-	92	10.1	4.9	<u>GAGGT</u> aaatATG		cd.3 [Enterobacteria phage T4] (91/91; 91)	100%	3,00E-58	NP_049831.1
211	130036	129836	-	66	7.9	4.4	<u>GAAAA</u> cttATG		cd.4 [Enterobacteria phage AR1] (66/66; 66)	100%	4,00E-39	YP_009168038.1
212	130256	130029	-	75	8.6	8.7	<u>TTGAA</u> ATG		cd.5 [Enterobacteria phage AR1] (74/75; 75)	99%	2,00E-46	YP_009168039.1
213	131131	130226	-	301	35.2	8.4	<u>AGGA</u> AttaaATG	Deoxyribonucleotide 3' phosphatase; 5' Polynucleotide kinase	pseT [Enterobacteria phage RB27] (286/301; 301)	95%	0.0	YP_009102420.1
214	131430	131128	-	100	11.5	8.5	<u>GAGAA</u> AaataaATG		F412_gp055 [Escherichia phage wV7] (98/100; 100)	98%	2,00E-63	YP_007004961.1

215	131657	131427	-	76	8.9	7.9	<u>GATAA</u> atgtaa ATG	pseT.1 [Enterobacteria phage RB32] (75/76; 76)	99%	3,00E-47	YP_803160.1
216	131953	131654	-	99	11.6	8.8	<u>GACCTT</u> tctaa ATG	pseT.2 [Enterobacteria phage RB32] (98/99; 99)	99%	2,00E-65	YP_803161.1
217	132303	131950	-	117	13.0	8.9	<u>TAAAC</u> ttt ATG	slur07_00036 [Escherichia phage slur07] (114/117; 117)	97%	5,00E-75	CUL02290.1
218	132800	132294	-	168	19.1	6.4	<u>GAGGA</u> cttt ATG	slur04_00206 [Escherichia phage slur04] (167/168; 168)	99%	2,00E-120	CUL02067.1
219	133986	132862	-	374	43.5	4.9	<u>GAGGA</u> Atacaca ATG	rnlA [Enterobacteria phage AR1] (372/374; 374)	99%	0.0	YP_009168046.1
220	134449	134039	-	136	15.8	9.2	<u>GCCAT</u> ttttat ATG	denA [Enterobacteria phage RB51] (136/136; 136)	100%	5,00E-94	YP_002854181.1
221	135655	134477	-	392	46.0	5.0	<u>GAAAA</u> att ATG	F412_gp048 [Escherichia phage wV7] (376/392; 392)	96%	0.0	YP_007004968.1
222	136386	135655	-	243	28.0	9.6	<u>GTAAAT</u> gta ATG	mobE [Enterobacteria phage RB3] (235/243; 243)	97%	1,00E-175	YP_009098612.1
223	138650	136386	-	754	86.0	5.9	<u>GAGGA</u> ctt ATG	nrda [Enterobacteria phage T6] (752/754; 754)	99%	0.0	AB148936.1
224	138967	138641	-	108	12.4	9.2	<u>AACAA</u> t ATG	Shf12p233 [Shigella phage Shf12] (108/108; 108)	100%	3,00E-74	YP_004415123.1
225	139184	138921	-	87	10.0	5.2	<u>GAGGA</u> tat ATG	ECML134_228 [Escherichia phage ECML-134] (86/87; 87)	99%	1,00E-55	YP_009102703.1
226	140068	139208	-	286	33.2	6.3	<u>ATGAA</u> cta ATG	RM00_gp240 [Shigella phage pSs-1] (284/286; 286)	99%	0.0	YP_009111048.1
227	140856	140272	-	194	21.9	5.3	<u>GAGGA</u> Attgtgca ATG	RM00_gp242 [Shigella phage pSs-1] (189/194; 194)	97%	2,00E-137	YP_009111050.1
228	141113	140853	-	86	10.3	3.9	<u>GACCT</u> tttca ATG	D862_gp039 [Enterobacteria phage vB_EcoM_ACG-C40] (79/81; 81)	98%	5,00E-49	YP_006986792.1
229	141457	141098	-	119	13.3	4.9	<u>GAGAA</u> aaatatt ATG	ACQ54_gp227 [Escherichia phage HY01] (109/119; 119)	92%	5,00E-75	YP_009148676.1
230	141710	141468	-	80	9.5	5.0	<u>GAGAA</u> ttaa ATG	frd.1 [Enterobacteria phage ime09] (80/80; 80)	100%	2,00E-50	YP_007004611.1
231	142130	141765	-	121	14.3	5.8	<u>GAAAA</u> cgta ATG	frd2 [Enterobacteria phage LZ7] (114/121; 121)	94%	2,00E-77	AAA74684.1
232	142423	142175	-	82	9.7	3.8	<u>GCCAA</u> tactctg ATG	e112_255 [Escherichia phage e11/2] (76/82; 82)	93%	2,00E-46	YP_009030850.1
233	143456	142548	-	302	33.5	4.8	<u>GAAAT</u> aaaa ATG	32 [Enterobacteria phage ime09] (301/302; 302)	99%	0.0	YP_007004614.1
234	144209	143556	-	217	26.0	9.4	<u>GATTT</u> tctact ATG	59 [Enterobacteria phage RB14] (217/217; 217)	100%	2,00E-154	YP_002854574.1
235	144544	144206	-	112	12.8	4.5	<u>TTGAA</u> cttt ATG	33 [Enterobacteria phage T4] (112/112; 112)	100%	1,00E-72	NP_049857.1
236	144791	144522	-	89	10.4	5.0	<u>GTGAA</u> ta ATG	dsbA [Enterobacteria phage T4] (89/89; 89)	100%	7,00E-55	NP_049858.1
237	145705	144800	-	306	35.1	8.9	<u>TAGAA</u> ATG	rnh [Enterobacteria phage T4] (299/301; 305)	99%	0.0	NP_049859.1
238	145822	149694	+	1290	140.4	5.3	<u>GGGA</u> Ga ATG	slur04_00227 [Escherichia phage slur04] (1256/1290; 1290)	97%	0.0	CUL02088.1
239	149703	150818	+	371	40.2	5.3	<u>GAGGT</u> att ATG	pSs1_00253 [Shigella phage pSs-1] (364/371; 371)	98%	0.0	YP_009111061.1
240	150881	151537	+	218	23.3	6.1	<u>GGGC</u> Ataca ATG	36 [Enterobacteria phage RB51] (217/218; 218)	99%	2,00E-154	YP_002854202.1
241	151546	154857	+	1104	118.8	5.8	<u>GAGGA</u> ctt ATG	37 [Enterobacteria phage AR1] (1050/1103; 1103)	95%	0.0	YP_009168069.1
242	154889	155683	+	264	26.7	7.8	<u>GAGGT</u> ttat ATG	ECP7_01126 [Escherichia coli O157 typing phage 7] (252/264; 264)	95%	7,00E-125	AKE45993.1
243	155714	156370	+	218	25.2	7.7	<u>GAGGT</u> cta ATG	t [Enterobacteria phage ime09] (218/218; 218)	100%	3,00E-159	YP_007004625.1
244	156643	156371	-	90	10.6	5.4	<u>TATAG</u> ttta ATG	asiA [Enterobacteria phage T4] (90/90; 90)	100%	4,00E-56	NP_049866.1
245	156808	156656	-	50	5.9	4.6	<u>GATTAT</u> tttga ATG	asiA.1 [Enterobacteria phage RB51] (50/50; 50)	100%	1,00E-25	YP_002854207.1
246	157083	156805	-	92	10.8	4.5	<u>GGGAA</u> ggtct ATG	arn [Enterobacteria phage RB51] (92/92; 92)	100%	4,00E-57	YP_002854208.1
247	157298	157167	-	43	5.2	8.6	<u>TTGAG</u> ATG	arn.1 [Enterobacteria phage RB14] (43/43; 43)	100%	1,00E-22	YP_002854588.1
248	157665	157369	-	98	11.4	8.6	<u>GAGGA</u> cttttacta ATG	ECML134_254 [Escherichia phage ECML-134] (96/98; 98)	98%	2,00E-63	YP_009102729.1
249	158126	157665	-	153	17.9	5.3	<u>TTTTA</u> a ATG	arn.3 [Yersinia phage PST] (152/153; 153)	99%	1,00E-109	YP_009153859.1
250	158452	158123	-	109	12.7	9.2	<u>GAGGA</u> ataaata ATG	arn.4 [Enterobacteria phage ime09] (109/109; 109)	100%	2,00E-74	YP_007004633.1
251	159098	158463	-	211	23.6	7.8	<u>TAGAA</u> a ATG	ECML134_257 [Escherichia phage ECML-134] (210/211; 211)	99%	3,00E-148	YP_009102732.1
252	159374	159225	-	49	4.9	9.5	<u>AGGAA</u> atcaa ATG	MotA.1 [Enterobacteria phage T4] (48/49; 49)	99%	3,00E-21	NP_049874.1
253	160699	159371	-	442	50.5	7.7	<u>GTAAAT</u> t ATG	52 [Enterobacteria phage RB51] (441/442; 442)	99%	0.0	YP_002854215.1
254	160844	160704	-	46	5.1	8.2	<u>TACTA</u> ATG	52.1 [Enterobacteria phage RB14] (46/46; 46)	100%	5,00E-21	YP_002854596.1
255	160995	160837	-	52	5.6	4.2	<u>GAAAA</u> ATG	ac [Enterobacteria phage RB14] (52/52; 52)	100%	6,00E-27	YP_002854597.1
256	161589	161083	-	168	18.8	9.6	<u>ATTAAT</u> ctatcgccgt ATG	e112_280 [Escherichia phage e11/2] (166/168; 168)	99%	1,00E-119	YP_009030875.1
257	161817	161602	-	71	8.2	4.2	<u>GTGAA</u> t ATG	slur04_00246 [Escherichia phage slur04] (71/71; 71)	100%	2,00E-43	CUL02107.1
258	161933	161826	-	35	4.2	5.3	<u>GTAA</u> Aata ATG	ndd.2 [Enterobacteria phage AR1] (32/35; 36)	91%	2,00E-13	YP_009168086.1
259	162130	161933	-	65	7.5	9.4	<u>GAAAA</u> t ATG	ndd.2a [Enterobacteria phage ime09] (65/65; 65)	100%	5,00E-38	YP_007004641.1
260	162251	162138	-	37	43	9.5	<u>CACAA</u> a ATG	AR1_277 [Enterobacteria phage AR1] (36/37; 80)	97%	2,00E-14	YP_009168088.1
261	162857	162495	-	120	14.2	5.4	<u>TACAA</u> cg ATG	Shf12p275 [Shigella phage Shf12] (117/120; 120)	98%	1,00E-80	YP_004415161.1
262	163396	162839	-	185	21.2	7.7	<u>GAAAG</u> tctcaa ATG	denB [Enterobacteria phage RB14] (184/185; 185)	99%	2,00E-135	YP_002854607.1
263	163727	163329	-	132	15.3	4.8	<u>GCGTA</u> ATG	RB14ORF272 [Enterobacteria phage RB14] (106/109; 109)	97%	1,00E-70	YP_002854608.1
264	163888	163694	-	64	7.5	7.8	<u>GAAAA</u> tt ATG	denB.1 [Enterobacteria phage RB51] (64/64; 64)	100%	9,00E-36	YP_002854227.1
265	164859	163921	-	312	35.5	5.5	<u>GAAAA</u> tt ATG	rliB [Enterobacteria phage ime09] (310; 312; 312)	99%	0.0	YP_007004650.1
a Start codon is indicated in boldface; Mach to SD sequence is indicated by underlining; SD position is indicated in uppercase											
b The number of identical amino acids/ The total number of amino acids											