

LYP264						
Start	End	Strand	aa Length	Locus Tag	Annotation	Closest P2 Homolog
1	231	-	77	LYP264_phanotate_1	tape measure protein; tail protein	
265	402	+	45	LYP264_phanotate_2	phage protein of unknown function	
539	991	+	150	LYP264_phanotate_3	hypothetical protein	
1059	1295	-	78	LYP264_phanotate_4	hypothetical protein	
1297	1767	-	156	LYP264_phanotate_5	homology to phage exonuclease	orf91; unknown, conserved ASCH superfamily domain - possible RNA binding protein
1764	4058	-	764	LYP264_phanotate_6	putative phage replication initiation protein	A; DNA replication; site-specific nice at ori
4048	4407	-	119	LYP264_phanotate_7	conserved hypothetical protein	orf83; unknown, highly conserved
4474	4563	-	29	LYP264_phanotate_8	homology to phage integrase	
4658	4990	-	110	LYP264_phanotate_9	hypothetical protein	
5054	5554	-	166	LYP264_phanotate_10	DNA replication protein	B; DNA replication; lagging strand synthesis
5551	5721	-	56	LYP264_phanotate_11	hypothetical protein	orf78; unknown; highly conserved
5724	5996	-	90	LYP264_phanotate_12	cox regulatory protein	cox; repressor of C expression; directionality factor required for excision
6000	6149	-	49	LYP264_phanotate_13	homology to various	
6150	6443	+	97	LYP264_phanotate_14	putative C protein immunity repressor	C; immunity repressor
6513	7493	+	326	LYP264_phanotate_15	integrase	int; integrase
7497	7805	-	102	LYP264_phanotate_16	hypothetical protein; homology to various	
7812	7934	-	40	LYP264_phanotate_17	putative tail sheath protein	
7939	8079	-	46	LYP264_phanotate_18	hypothetical protein; homology to various	
8192	8287	-	31	LYP264_phanotate_19	hypothetical protein	
8292	8387	-	31	LYP264_phanotate_20	hypothetical protein; homology to DNA-binding transcriptional regulator domain	
8419	8640	-	73	LYP264_phanotate_21	putative positive regulator of late gene transcription	ogr; activator of late transcription; C4 Zn-finger protein
8702	9895	-	397	LYP264_phanotate_22	putative baseplate hub protein	D; baseplate hub
9898	10362	-	154	LYP264_phanotate_23	putative tape measure protein; tail protein	U; tail-tube initiator?
10374	12803	-	809	LYP264_phanotate_24	putative phage tail tape measure protein	T; tail tape measure
12796	12915	-	39	LYP264_phanotate_25	putative gpE+E' phage tail protein	E+E'; tail assembly chaperone; -1 frameshift extension of gpE
12948	13229	-	93	LYP264_phanotate_26	putative phage tail fiber protein; assembly protein	E; tail assembly chaperone
13293	13811	-	172	LYP264_phanotate_27	putative major tail tube protein	F II; tail tube
13824	15011	-	395	LYP264_phanotate_28	putative major tail sheath protein	F I; tail sheath
15076	15654	-	192	LYP264_phanotate_29	putative DNA invertase	P2_phanotate_25

15665	15820	-	51	LYP264_phanotate_30	homology to lysin and NA binding proteins	
15836	15955	-	39	LYP264_phanotate_31	putative minor tail protein	I; baseplate
15978	16115	-	45	LYP264_phanotate_32	hypothetical protein; homology to various	P2_phanotate_22
16213	16320	-	35	LYP264_phanotate_33	hypothetical protein; homology to rhamogalacturonate lyase B	
16290	16736	-	148	LYP264_phanotate_34	putative tail fiber assembly protein	G; tail fiber
16733	17698	-	321	LYP264_phanotate_35	putative tail fiber protein	H; tail fiber
17695	18306	-	203	LYP264_phanotate_36	putative tail fiber protein	I; baseplate
18299	19207	-	302	LYP264_phanotate_37	putative baseplate assembly protein J	J; baseplate
19212	19559	-	115	LYP264_phanotate_38	putative baseplate assembly protein W	W; baseplate.
19556	20197	-	213	LYP264_phanotate_39	putative phage baseplate assembly protein V	V; tail spike
20266	20715	-	149	LYP264_phanotate_40	putative phage virion morphogenesis protein; tail completion protein S	S; tail completion - tube terminator?
20712	21128	-	138	LYP264_phanotate_41	putative tail completion protein	R; tail completion - sheath terminator?
21091	21249	-	52	LYP264_phanotate_42	putative outer membrane lipoprotein Rz1	lysC; lysis control, Rz1-like spanin component
21236	21649	-	137	LYP264_phanotate_43	putative lysis regulatory protein LysB	lysB; lysis control, Rz-like spanin component
21646	22098	-	150	LYP264_phanotate_44	putative lysozyme; endolysin	orf81; unknown; highly conserved
22139	22360	-	73	LYP264_phanotate_45	putative primosomal protein [E. coli]; homology to class II holin	orf30; unknown; highly conserved
22351	22554	-	67	LYP264_phanotate_46	putative tail protein; baseplate protein X	X; baseplate
22554	23054	-	166	LYP264_phanotate_47	putative head completion/stabilization protein	L; capsid completion protein
23152	23913	-	253	LYP264_phanotate_48	putative terminase	M; terminase small subunit
23917	25071	-	384	LYP264_phanotate_49	putative major capsid protein N	N; major capsid precursor
25103	25966	-	287	LYP264_phanotate_50	putative capsid-scaffolding protein	O; capsid scaffold; proved protease
25967	26074	+	35	LYP264_phanotate_51	conserved hypothetical protein	
26131	27900	+	589	LYP264_phanotate_52	putative terminase, ATPase subunit	P; terminase large subunit; DNA-dependent ATPase
27900	28931	+	343	LYP264_phanotate_53	putative capsid portal protein Q	Q; portal
28956	29078	+	40	LYP264_phanotate_54	unknown hypothetical; homology to capsid protein, peptidase, various	

Table 1

LYP215						
Start	End	Strand	Length	Locus Tag	Annotation	Closest P2 Homolog
552	1586	+	344	LYP215_phanotate_1	capsid portal protein Q; capsid packaging protein	Q; portal
1734	1841	-	35	LYP215_phanotate_2	similarity to phage tail length tape measure protein	
1940	3544	-	534	LYP215_phanotate_3	hypothetical protein	fun(Z); FudR sensitivity; blocks phage T5
3594	4145	-	183	LYP215_phanotate_4	putative exonuclease	
4218	4337	-	39	LYP215_phanotate_5	hypothetical protein	
4324	6600	-	758	LYP215_phanotate_6	DNA replication protein	A; DNA replication; site-specific nice at ori
6590	6865	-	91	LYP215_phanotate_7	replication initiation protein	orf83; unknown, highly conserved
6862	7086	-	74	LYP215_phanotate_8	zinc finger domain containing protein	orf82; unknown C4-type zinc finger protein, DksA/TraR family
7086	7388	-	100	LYP215_phanotate_9	conserved hypothetical phage protein	ofr81; unknown; highly conserved
7388	7612	-	74	LYP215_phanotate_10	conserved hypothetical phage protein	orf80; unknown; highly conserved, DUF2732
7676	8176	-	166	LYP215_phanotate_11	DNA replication protein	B; DNA replication; lagging strand synthesis
8173	8343	-	56	LYP215_phanotate_12	conserved hypothetical phage protein; possible peptide chain release factor 3 domain containing protein	orf78; unknown; highly conserved
8346	8618	-	90	LYP215_phanotate_13	cox regulatory protein	cox; repressor of C expression; directionality factor required for excisuiou
8688	8780	-	30	LYP215_phanotate_14	hypothetical protein	
8771	9064	+	97	LYP215_phanotate_15	immunity repressor	C; immunity repressor
9104	10114	+	336	LYP215_phanotate_16	integrase	Int; integrase
10190	10288	-	32	LYP215_phanotate_17	hypothetical protein	
10289	10390	-	38	LYP215_phanotate_18	hypothetical protein	
10387	10605	-	72	LYP215_phanotate_19	putative positive regulator of late gene transcription; Ogr	ogr; activtor of late transcription; C4 Zn-finger protein
10687	11850	-	387	LYP215_phanotate_20	putative tail fiber; late control protein D	D; baseplate hub
11850	12326	-	158	LYP215_phanotate_21	tape measure; tail protein	U; tail -tube initiator?
12344	14791	-	815	LYP215_phanotate_22	phage tail length tape measure protein	T; tail tape measure
14784	14903	-	39	LYP215_phanotate_23	gpE+E'; putative tail protein; phage tail fiber	E+E'; tail assembly chaperone; -1 framsehift extension of gpE
14936	15211	-	91	LYP215_phanotate_24	gpE; tail protein; phage tail fiber	E; tail assembly chaperone
15268	15780	-	170	LYP215_phanotate_25	major tail tube protein; gpFII	F _{II} ; tail tube
15799	16989	-	396	LYP215_phanotate_26	major tail sheath protein; gpFI	F _I ; tail sheath
17211	17399	-	42	LYP215_phanotate_27	hypothetical protein	
17471	18517	-	348	LYP215_phanotate_28	hypothetical protein	
18514	18630	-	38	LYP215_phanotate_29	hypothetical protein	
18627	18794	-	55	LYP215_phanotate_30	conserved hypothetical phage protein	
18797	20182	-	461	LYP215_phanotate_31	hypothetical protein; putative head domain containing protein	
20319	20450	-	43	LYP215_phanotate_32	hypothetical protein	
20455	20979	-	174	LYP215_phanotate_33	phage tail fiber assembly protein; G	G; tail fiber assembly
20983	23712	-	909	LYP215_phanotate_34	phage tail fiber protein; H	H; tail fiber;; or, old; nuclease; blocks growth of phage
23723	24253	-	176	LYP215_phanotate_35	baseplate assembly protein; I	I; baseplate
24246	25154	-	302	LYP215_phanotate_36	baseplate assembly protein; J	orf30; unknown; highly conserved;; or J; baseplate
25159	25506	-	115	LYP215_phanotate_37	baseplate assembly protein; W	W; baseplate
25503	26144	-	213	LYP215_phanotate_38	baseplate assembly protein; V	V; tail spike
25211	26663	-	150	LYP215_phanotate_39	tail completion protein; S	S; tail completion - tube terminator?
26656	27132	-	158	LYP215_phanotate_40	tail completion protein; R	R; tail completion - sheath terminator?
27086	27244	-	52	LYP215_phanotate_41	outer membrane lipoprotein Rz1; lysC	lysC; lysis control, Rz1-like spanin component

27231	27656	-	141	LYP215_phanotate_42	lysin; phage spanin Rz; lysB	lysB; lysis control, Rz-like spanin component
27644	28069	-	141	LYP215_phanotate_43	holin; putative antiholin; lysA	lysA; antiholin
28084	28581	-	165	LYP215_phanotate_44	lysin; lysozyme EC 3.2.1.17; K	K; endolysin
28581	28862	-	93	LYP215_phanotate_45	holin, possibly family II; gpY	holin
28866	29069	-	67	LYP215_phanotate_46	tail fiber; tail completion protein; X	X; baseplate
29069	29578	-	169	LYP215_phanotate_47	capsid completion-stabilization protein; L	L; capsid completion protein
29678	30421	-	247	LYP215_phanotate_48	terminase, small unit	M; terminase small subunit
30425	31498	-	357	LYP215_phanotate_49	major capsid protein precursor	N; major capsid precursor
31557	32477	-	306	LYP215_phanotate_50	capsid scaffolding protein; O	O; capsid scaffold; proved protease
32585	33805	+	407	LYP215_phanotate_51	large terminase subunit; P	P; terminase large subunit; DNA-dependent ATPase