

Supplementary Table S1Genetic features of open reading frames in the *Serratia liquefaciens* phage vB_Slq_MQ-4 genome and their homology to other proteins.

ORF name	Start	Stop	Strand	Gene length	Function	Best hit NCBI accession and species	Query Coverage (%)	E-value	Identity (%)
ORF1	78	605	+	528	putative small terminase subunit	YP_009284265.1 putative small terminase subunit [Enterobacter phage Arya]	100%	1e-73	72.57%
ORF2	589	2634	+	2046	terminase large subunit family protein	YP_009168912.1 terminase large subunit family protein [Escherichia phage vB_EcoM_ECO1230-10]	100%	0.0	80.65%
ORF3	2641	3180	+	540	hypothetical protein	YP_009600727.1 hypothetical protein FDH43_gp54 [Escherichia phage vB_EcoM_ECOO78]	100%	1e-64	59.78%
ORF4	3180	4736	+	1557	phage portal protein	EFJ2475500.1 phage portal protein [Escherichia coli]	99%	0.0	67.31%
ORF5	4813	6783	+	1971	major capsid protein	YP_009600725.1 major capsid protein [Escherichia phage vB_EcoM_ECOO78]	99%	0.0	74.31%
ORF6	6845	7135	+	291	hypothetical protein	EFJ2475502.1 hypothetical protein [Escherichia coli]	97%	5e-40	75.53%

ORF7	7135	7488	+	354	hypothetical protein	YP_009600723.1 hypothetical protein FDH43_gp50 [Escherichia phage vB_EcoM_ECOO78]	100%	2e-61	80.34%
ORF8	7491	7823	+	333	hypothetical protein	YP_009600722.1 hypothetical protein FDH43_gp49 [Escherichia phage vB_EcoM_ECOO78]	100%	1e-48	71.82%
ORF9	7810	8367	+	558	hypothetical protein	YP_009100027.1 hypothetical protein ep3_0035 [Escherichia phage vB_EcoM-ep3]	100%	3e-94	73.51%
ORF10	8370	8951	+	582	hypothetical protein	YP_009600720.1 hypothetical protein FDH43_gp47 [Escherichia phage vB_EcoM_ECOO78]	99%	7e-90	67.19%
ORF11	8948	9598	+	651	phage baseplate assembly protein	WP_108322376.1 phage baseplate assembly protein [Limnohabitans sp. MMS-10A-192]	98%	6e-77	62.62%
ORF12	9646	9984	+	339	phage baseplate protein GpW	EFJ2475508.1 phage baseplate protein [Escherichia coli]	100%	2e-56	76.79%
ORF13	9985	10899	+	915	Phage baseplate assembly protein GpJ	YP_009284277.1 putative baseplate J-like protein [Enterobacter phage Arya]	100%	2e-143	72.70%
ORF14	10892	11485	+	594	tail protein	YP_009100032.1 tail protein	99%	1e-72	54.08%

						[Escherichia phage vB_EcoM-ep3]			
ORF15	11487	13889	+	2403	prophage tail fiber N-terminal domain-containing protein	WP_084710302.1 prophage tail fiber N-terminal domain-containing protein [Serratia]	89%	0.0	76.54%
ORF16	13892	14698	+	807	hypothetical protein	MBN5380434.1 hypothetical protein [Serratia marcescens]	100%	5e-159	83.21%
ORF17	14765	16270	+	1506	phage tail protein	EFJ2475512.1 phage tail protein [Escherichia coli]	100%	0.0	64.07%
ORF18	16279	16584	+	306	hypothetical protein	YP_009100035.1 hypothetical protein ep3_0043 [Escherichia phage vB_EcoM-ep3]	100%	3e-41	66.34%
ORF19	16581	17246	+	666	tail fiber protein	QKN87915.1 putative tail fiber protein [Acinetobacter phage vB_AbaP_Alexa]	100%	4e-83	72.85%
ORF20	17372	18796	+	1425	putative phage tail protein	YP_009168895.1 putative phage tail protein [Escherichia phage vB_EcoM_ECO1230-10]	99%	0.0	78.44%
ORF21	18796	19305	+	510	phage major tail tube protein	WP_208776240.1 phage major tail tube protein [Roseomonas marmotae]	99%	2e-77	73.21%

ORF22	19364	19660	+	297	phage tail assembly protein	WP_201964259.1 phage tail assembly protein [Aeromonas caviae]	95%	5e-35	61.70%
ORF23	20120	22141	+	2022	phage tail tape measure protein	WP_201964260.1 phage tail tape measure protein [Aeromonas caviae]	87%	2e-180	71.47%
ORF24	22138	22545	+	408	phage tail protein	WP_018006782.1 phage tail protein [Cupriavidus neocaledonicus]	100%	3e-50	60.00%
ORF25	22545	22754	+	210	putative tail protein X	YP_009284289.1 putative tail protein X [Enterobacter phage Arya]	95%	8e-31	80.30%
ORF26	22751	23794	+	1044	Phage transcriptional regulator	YP_009100043.1 transcriptional regulator [Escherichia phage vB_EcoM-ep3]	99%	0.0	69.65%
ORF27	23904	24785	+	882	putative transcriptional regulator	YP_009168887.1 putative transcriptional regulator [Escherichia phage vB_EcoM_ECO1230-10]	98%	1e-69	50.34%
ORF28	24782	25099	+	318	hypothetical protein	WP_246896048.1 hypothetical protein [Enterobacter hormaechei]	93%	3e-18	44.44%
ORF29	25115	25357	+	243	ogr/Delta-like zinc finger family protein	WP_080750241.1 ogr/Delta-like zinc finger family protein [Enterobacter]	82%	6e-16	51.52%

ORF30	25367	25576	+	210	hypothetical protein	No hit	No hit	No hit	No hit
ORF31	25608	25689	-	82	tRNA-Arg-TCT				
ORF32	25994	27205	+	1212	tyrosine-type recombinase/integrase	EFJ2475470.1 tyrosine-type recombinase/integrase [Escherichia coli]	100%	0.0	83.13%
ORF33	27556	28236	-	681	hypothetical protein	YP_009100047.1 hypothetical protein ep3_0060 [Escherichia phage vB_EcoM-ep3]	99%	1e-126	84.00%
ORF34	28334	28837	-	504	single-stranded DNA-binding protein	EFJ2475472.1 single-stranded DNA-binding protein [Escherichia coli]	100%	3e-68	73.65%
ORF35	28853	29062	-	210	hypothetical protein	EFJ2475473.1 hypothetical protein [Escherichia coli]	100%	4e-12	44.93%
ORF36	29065	29463	-	399	hypothetical protein	YP_009600697.1 hypothetical protein FDH43_gp24 [Escherichia phage vB_EcoM_ECOO78]	93%	3e-55	76.61%
ORF37	29450	29662	-	213	hypothetical protein	YP_009168936.1 hypothetical protein ECOPH_gp54 [Escherichia phage vB_EcoM_ECO1230-10]	94%	7e-29	77.27%
ORF38	29676	30662	-	987	putative replicative DNA helicase	YP_009168935.1 putative replicative DNA helicase	99%	2e-146	63.02%

ORF39	30662	32005	-	1344	Exodeoxyribonuclease VIII	[Escherichia phage vB_EcoM_ECO1230-10] SAL03255.1 exonuclease VIII [Caballeronia fortuita]	97%	9e-119	44.29%
ORF40	32083	32637	-	555	putative DNA binding helix-turn helix protein	YP_009284306.1 putative DNA binding helix-turn helix protein [Enterobacter phage Arya]	95%	8e-48	45.86%
ORF41	32784	34208	+	1425	putative DNA helicase	YP_009284307.1 putative DNA helicase [Enterobacter phage Arya]	97%	0.0	72.83%
ORF42	34471	34662	+	192	hypothetical protein	No hit	No hit	No hit	No hit
ORF43	34662	35072	+	411	hypothetical protein	YP_009600690.1 hypothetical protein FDH43_gp17 [Escherichia phage vB_EcoM_ECOO78]	99%	2e-55	66.91%
ORF44	35074	35238	+	165	hypothetical protein	YP_009284313.1 hypothetical protein BI096_gp48 [Enterobacter phage Arya]	85%	4e-04	46.81%
ORF45	35235	35474	+	240	hypothetical protein	YP_009284314.1 hypothetical protein BI096_gp47 [Enterobacter phage Arya]	81%	1e-10	48.44%
ORF46	35471	35716	+	246	hypothetical protein	No hit	No hit	No hit	No hit

ORF47	35709	36086	+	378	hypothetical protein	QPI13715.1 hypothetical protein SIPHO4S_00019 [Serratia phage Tsm2]	69%	1e-22	56.32%
ORF48	36071	36310	+	240	hypothetical protein	DAM52166.1 TPA: MAG TPA: hypothetical protein [Siphoviridae sp.]	96%	1e-10	42.17%
ORF49	36307	36549	+	243	hypothetical protein	YP_009168927.1 hypothetical protein ECOPH_gp45 [Escherichia phage vB_EcoM_ECO1230-10]	88%	2e-22	73.24%
ORF50	36631	36816	+	186	hypothetical protein	YP_009168926.1 hypothetical protein ECOPH_gp44 [Escherichia phage vB_EcoM_ECO1230-10]	75%	9e-10	58.70%
ORF51	36813	37037	+	225	hypothetical protein	YP_009168924.1 hypothetical protein ECOPH_gp42 [Escherichia phage vB_EcoM_ECO1230-10]	97%	3e-29	73.61%
ORF52	37050	39743	+	2694	toprim domain-containing protein	WP_222182770.1 toprim domain-containing protein [Geminicoccus sp. CPCC 101083]	88%	0.0	46.07%
ORF53	39872	40306	+	435	hypothetical protein	WP_238969447.1 hypothetical protein [Serratia marcescens]	97%	4e-57	66.43%

ORF54	40352	40600	+	249	hypothetical protein	No hit	No hit	No hit	No hit
ORF55	40654	40980	+	327	hypothetical protein	WP_163604316.1 hypothetical protein [Leclercia adecarboxylata]	98%	1e-22	43.40%
ORF56	41035	41328	+	294	hypothetical protein	No hit	No hit	No hit	No hit
ORF57	41719	42183	+	465	hypothetical protein	YP_009100015.1 hypothetical protein ep3_0022 [Escherichia phage vB_EcoM-ep3]	88%	2e-56	61.76%
ORF58	42180	42386	+	207	hypothetical protein	RQO38606.1 hypothetical protein DBR37_01545 [Herminiimonas sp. KBW02]	100%	1e-11	43.42%
ORF59	42376	42882	+	507	lysozyme	WP_060056565.1 lysozyme [Burkholderia ubonensis]	100%	2e-60	56.14%
