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1 **Table 1 | Sequence analysis of FLiP genome and open reading frames.**

ORF or gene	D r.	Nucleotide coordinates (start–stop)	GC %	Length (aa)	Calc. MW (kDa)	Calc. pI	Protein	Function	TM-helix predictions	Blast (E- value)	HHpred (prob. %)
1	F	155–445	31.96	97	11.2	9.70					
2	F	540–782	32.51	81	9.6	4.33					
3	F	836–1138	33.66	101	11.8	6.22			1		
4	F	1138–1557	34.52	140	15.8	4.57					helix-turn-helix motif (98.6)
5	F	1799–2008	39.52	70	7.1	10.5					
6	F	2011–2229	31.05	73	9.0	9.80					
7	F	2703–2957	33.73	85	10.3	12.92	gp7	S	1		
8	F	3036–3971	37.07	312	34.6	5.07	gp8	S, MCP		<i>Cellulophaga</i> phage φ48:2 (0.020)	
9	F	3992–4363	43.01	124	12.9	10.77	gp9	S	1	<i>Cellulophaga</i> phage φ12a:1 (5e-04)	
10	F	4385–4861	35.01	159	18.5	6.83			1		
11	F	4845–5321	37.32	159	17.9	9.42	gp11	S	1		
12	F	5324–5770	33.56	149	17.0	4.63					
13	F	5770–6780	35.61	337	38.4	4.31					
14	F	6780–7445	37.39	222	25.2	9.61	gp14	S, lytic enzyme	1	lytic enzyme (4e-28)	lytic enzyme (99.8)
15	F	7510–8853	31.99	448	53.5	9.06				<i>Cellulophaga</i> phage φ48:2 (3e-12)	replication initiation protein (97.0)
16	F	8865–9110	28.86	82	9.3	8.46					coiled-coiled protein (92.1)

ORF or gene as in Fig. 1; Direction (Dir.) F, forward; R, reverse; Nucleotide coordinates refer to FLiP genome; gp, confirmed by proteomics (see Supplementary Table S2); S, structural protein; MCP, major capsid protein; Number of predicted transmembrane (TM) helices. Gene functions as predicted by BlastP, Psi-Blast and HHpred programs. E-value of the most relevant Blast match indicated. Most relevant HHpred predictions are listed.

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1	F	155–445	31,96	97	11,2	9,7					
2	F	540–782	32,51	81	9,6	4,33					
3	F	836–1138	33,66	101	11,8	6,22			1		
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