

**Table S1: Mass spectrometry identification of proteins forming particles of phage 48 propagated on *S. epidermidis* strain SE48.**

<b>Protein</b>	<b>Source</b>	<b>Gene</b>	<b>MW (kDa)</b>	<b>calc. pI</b>	<b>SAF</b>	<b>NSAF (%)</b>	<b>Sum (Coverage)</b>	<b>Sum (# Peptides)</b>	<b>Sum (# Unique Peptides)</b>
major capsid protein	phage 48	<i>gp7</i>	30	5,4	0,67	43,48	67%	18	18
capsid scaffolding protein	phage 48	<i>gp6</i>	22	4,7	0,38	24,83	57%	12	12
portal protein	phage 48	<i>gp3</i>	56	4,8	0,14	9,14	61%	25	25
capsid morphogenesis protein	SeCl <sub>SE48</sub>	<i>gp14</i>	28	5,1	0,12	7,74	66%	12	12
receptor-binding protein	phage 48	<i>gp19</i>	97	7,1	0,02	1,40	23%	14	14
lower tail fiber	phage 48	<i>gp20</i>	58	5,1	0,03	1,92	24%	10	10
YopX-like protein	phage 48	<i>gp58</i>	16	4,5	0,07	4,35	39%	4	4
minor capsid protein	phage 48	<i>gp4</i>	37	8,6	0,02	1,44	18%	5	5
tail-associated lysin	phage 48	<i>gp18</i>	70	8,7	0,01	0,53	10%	5	5
Gam-like nuclease inhibitor	phage 48	<i>gp40</i>	18	5,5	0,02	1,62	42%	4	4
adaptor protein	phage 48	<i>gp9</i>	12	6,0	0,03	1,88	44%	3	3
ssDNA binding protein	phage 48	<i>gp42</i>	21	6,8	0,02	1,05	23%	3	3
ERF-like single-strand annealing protein	phage 48	<i>gp41</i>	24	5,5	0,01	0,63	14%	2	2

Structural proteins of phage and phage-derived small-headed particles purified in CsCl gradient were determined by LC-MS/MS analysis. (N)SAF - (normalized) spectral abundance factor; Sum (Coverage) - percentage of protein sequence covered by identified peptides; Sum (#Peptides) - number of peptides assigned to protein group, including peptides that are shared with other protein groups; Sum (#Unique peptides) - number of peptides that are unique to the specific protein group.