

Isolation and Characterization of Two Novel Siphoviruses Novomoskovsk And Bolokhovo Encoding Polysaccharide Depolymerases Active Against *Bacillus pumilus*

Anna V. Skorynina^{1*}, Olga N. Koposova¹, Olesya A. Kazantseva¹, Emma G. Pilgrimova¹, Natalya A. Ryabova² and Andrey M. Shadrin^{1*}

¹ G.K. Skryabin Institute of Biochemistry and Physiology of Microorganisms, Pushchino Scientific Center for Biological Research of the Russian Academy of Sciences, Federal Research Center, Pushchino, Prospect Nauki, 5, Russia

² Institute of Protein Research RAS, Pushchino, Institutskaya st., 4, Russia

* Correspondence: Anna V. Skorynina, Phone: +7(953)967-44-37. E-mail: s_an.net@mail.ru; Andrey M Shadrin, E-mail: andrey2010s@gmail.com.

Supplementary Information:

Table S1. Annotation of the *Bacillus* phage Bolokhovo

| ORF№ | Start codon | Stop codon | Strand | Blast results | | Conserved domains, Blast | | Hhpred results | Annotation |
|------|-------------|------------|--------|---|-------------------|--------------------------|-------|---|--------------------------------------|
| | | | | Name | E-val | Name, (region) | E-val | (Prob./E-val) | |
| 1 | 65 | 739 | + | putative terminase small subunit [<i>Bacillus</i> phage 056SW001B] | 1e ⁻⁷⁷ | | | sm_term_P27; phage terminase, small subunit, putative, P27 family (89,28/3,6) | putative terminase small subunit |
| | | | | putative terminase small subunit [<i>Bacillus</i> phage 019DV002] | 6e ⁻⁷⁶ | | | | |
| | | | | putative terminase small subunit [<i>Bacillus</i> phage 276BB001] | 6e ⁻⁷⁶ | | | Terminase_4; Phage terminase, small subunit (88,04/5,6) | |
| | | | | exopolyphosphatase domain protein [<i>Geobacillus</i> phage GBK1] | 3e ⁻⁶⁴ | | | COG3747; Phage terminase, small subunit [Mobilome: prophages, transposons], (86,89/9,2) | |
| 2 | 858 | 1187 | + | hp | | | | | hp |
| 3 | 1533 | 1252 | - | hp | | | | P2_Phage_GpR; P2 phage tail completion protein R (GpR) (90,17/1,7) | hp |
| 4 | 1802 | 2083 | + | hp | | | | hp | hp |
| 5 | 2412 | 2134 | - | hp | | | | hp | hp |
| 6 | 2554 | 2399 | - | hp | | | | PMP1_2; ATPase proteolipid family (97,25/0,002) | Predicted lipoprotein signal peptide |
| | | | | | | | | Mucin15; Cell-membrane associated Mucin15 (97,22/0,00073) | |

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|----|------|------|---|---|-----|-------------------------|----------------------|--|-------------------------|
| | | | | | | | | PRIMA1; Proline-rich membrane anchor (1 96,09/0,015) | |
| | | | | | | | | STEVOR; variant surface antigen, stevor family, (95,68/0,058) | |
| 7 | 2968 | 2633 | - | hp | | | | hp | hp |
| 8 | 3304 | 3047 | - | hp | | | | hp | hp |
| 9 | 3408 | 5093 | + | terminase large subunit [<i>Bacillus</i> virus Glittering] | 0.0 | Terminase_GpA (52-314) | 6.85e ⁻⁰⁶ | Terminase_GpA; Phage terminase large subunit (GpA) (100/6,4e ⁻³²) | Terminase large subunit |
| | | | | terminase large subunit [<i>Bacillus</i> virus Riggi] | 0.0 | | | Terminase_1; Phage Terminase (100/1,2e ⁻³⁰) | |
| | | | | terminase large subunit [<i>Bacillus</i> virus Blastoid] | 0.0 | | | YbcX; Phage terminase, large subunit GpA (99,98/4,1e ⁻²⁸) | |
| 10 | 5175 | 6494 | + | portal protein [<i>Bacillus</i> virus Curly] | 0.0 | DUF935 (57-394) | 7.58e ⁻²¹ | gp29; Mu-like prophage protein gp29 (100/6,1e ⁻³⁰) | portal protein |
| | | | | portal protein [<i>Bacillus</i> virus Glittering] | 0.0 | gp29 (92-413) | 4.39e ⁻⁰⁹ | portal_HK97; phage portal protein, HK97 family (99,97/2,5e ⁻²⁸) | |
| | | | | portal protein [<i>Bacillus</i> phage Leo2] | 0.0 | | | BeeE; Phage portal protein BeeE (99,97/1,1e ⁻²⁸) | |
| 11 | 6548 | 7450 | + | phage head morphogenesis protein [<i>Bacillus</i> virus Curly] | 0.0 | phageSPP1_gp7 (150-261) | 9.02e ⁻¹⁶ | COG2369; Uncharacterized conserved protein, contains phage Mu gpF-like domain (99,87/2e ⁻¹⁹) | Minor head protein |
| | | | | minor head protein [<i>Bacillus</i> virus Glittering] | 0.0 | Phage_Mu_F (144-254) | 9.57e ⁻¹⁵ | phageSPP1_gp7; phage putative head morphogenesis protein, SPP1_gp7 family (99,83/1,2e ⁻¹⁹) | |
| | | | | minor head protein [<i>Bacillus</i> phage Leo2] | 0.0 | COG2369 (150-261) | 1.50e ⁻⁰⁴ | COG5585; NAD ⁺ --asparagine ADP-ribosyltransferase (99,72/1,3e ⁻¹⁵) | |
| 12 | 7953 | 7483 | - | hp | | | | YifL; Predicted small periplasmic lipoprotein YifL (98,6/2,8e ⁻⁷) | hp |

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|----|------|-------|---|--|--------------------|--|--|--|---|
| | | | | | | | | Lysis_col; Lysis protein (97,41/0,00023) | |
| | | | | | | | | Slp; Starvation-inducible outer membrane lipoprotein, 97,11/0,00057 | |
| | | | | | | | | COG5510; Predicted small secreted protein, (96,95/0,0014) | |
| 13 | 8075 | 7950 | - | ribonuclease [<i>Bacillus</i> phage Leo2] | 3e ⁻¹⁷ | | | hp | hp |
| 14 | 8461 | 9303 | + | scaffold protein [<i>Bacillus</i> virus Curly] | 0.0 | | | Mu-like_Pro; Mu-like prophage I protein (99,88/6,4e ⁻²¹) | prohead protease |
| | | | | scaffold protein [<i>Bacillus</i> virus Andromeda] | 0.0 | | | Phage_GPO; Phage capsid scaffolding protein (GPO) serine peptidase (99,57/4,1e ⁻¹³) | |
| | | | | scaffold protein [<i>Bacillus</i> virus Riggi] | 3e ⁻¹⁷⁰ | | | proheadase_HK97; phage prohead protease, HK97 family (99,3/7,8e ⁻¹¹) | |
| | | | | | | | | Peptidase_S78; <i>Caudovirus</i> prohead serine protease (99,14/1,2e ⁻⁹) | |
| 15 | 9325 | 9747 | + | hp | | | | COG5471; Predicted phage recombinase, RecA/RadA family (99,67/5,7e ⁻¹⁵) | DUF2190 domain- containing protein |
| | | | | | | | | COG5471; Predicted phage recombinase, RecA/RadA family (86,05/7,4) | |
| 16 | 9767 | 10657 | + | major capsid protein [<i>Bacillus</i> virus Glittering] | 0.0 | | | d,183,1,1 (A:104-383) Major capsid protein gp5 {Bacteriophage HK97 [TaxId: 37554]} (99,95/4,6e ⁻²⁷) | Major capsid protein |
| | | | | major capsid protein [<i>Bacillus</i> phage Leo2] | 0.0 | | | major_cap_HK97; phage major capsid protein, HK97 family | |

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|----|-------|-------|---|--|-------------------|----------------------|----------------------|---|-------------------------|
| | | | | | | | | (99,93/1,5e ⁻²⁴) | |
| | | | | major capsid protein [<i>Bacillus</i> virus Riggi] | 0.0 | | | COG4653; Predicted phage phi-C31 gp36 major capsid-like protein (99,93/8,4e ⁻²⁵) | |
| 17 | 10732 | 10953 | + | hp | | | | Ribosomal_L9_N; Ribosomal protein L9, N-terminal domain (95,15/0,039) | hp |
| | | | | | | | | d,100,1,1 (A:1-52) Ribosomal protein L9 N-domain { <i>Bacillus stearothermophilus</i> [TaxId: 1422]} (93,69/0,15) | |
| | | | | | | | | d,100,1,1 (I:1-55) Ribosomal protein L9 N-domain { <i>Thermus thermophilus</i> [TaxId: 274]} (91,77/0,35) | |
| | | | | | | | | Packaging_FI; DNA packaging protein FI (90,85/0,42) | |
| 18 | 10967 | 11359 | + | head-to-tail adaptor [<i>Bacillus</i> phage 056SW001B] | 4e ⁻²⁶ | DUF1320 (2-65) | 2.42e ⁻⁰⁶ | gp436; Mu-like prophage protein gp36 (99,88/5e ⁻²¹) | head completion protein |
| | | | | head-to-tail adaptor [<i>Bacillus</i> phage 276BB001] | 6e ⁻²⁶ | gp436 (2-122) | 7.41e ⁻⁰³ | Phage_connect_1; Phage gp6-like head-tail connector protein (98,76/1,3e ⁻⁷) | |
| | | | | head-to-tail adaptor [<i>Bacillus</i> phage 019DV002] | 1e ⁻²⁵ | | | | |
| 19 | 11364 | 11807 | + | tail completion and head joining protein [<i>Bacillus</i> virus Riggi] | 6e ⁻⁷² | COG5005 (4-147) | 9.42e ⁻¹³ | Phage_tail_S; Phage virion morphogenesis family (99,85/5,7e ⁻²¹) | tail completion protein |
| | | | | tail completion and head joining protein [<i>Bacillus</i> virus Riggi] | 6e ⁻⁷² | Phage_tail_S (6-141) | 4.59e ⁻⁰⁸ | COG5005; Mu-like prophage protein gpG, (99,8/2,6e ⁻¹⁸) | |
| | | | | head-to-tail stopper [<i>Bacillus</i> phage 276BB001] | 2e ⁻⁵² | | | tail_comp_S; phage virion morphogenesis (putative tail completion) protein, (99,79/2,7e ⁻ | |

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|----|-------|-------|---|--|--------------------|--|--|--|----------------------------|
| | | | | | | | | ¹⁸⁾ | |
| 20 | 11804 | 12232 | + | tail terminator [<i>Bacillus</i> phage 019DV002] | 4e ⁻³⁷ | | | Phage_tail_U; Phage minor tail protein U (99,66/2,6e ⁻¹⁴) | tail terminator protein |
| | | | | | | | | Gp37; Gp37 protein (97,15/0,016) | |
| 21 | 12244 | 12420 | + | hp | | | | hp | hp |
| 22 | 12420 | 13358 | + | major tail protein [<i>Bacillus</i> phage 019DV002] | 9e ⁻¹⁰⁶ | | | DUF2001; Phage tail tube protein 98,49/b,106,1,3 (A:5-143) Phage-like element PBSX protein XkdM { <i>Bacillus subtilis</i> [TaxId: 1423]} (98,24/0,000014) | tail tube protein |
| | | | | | | | | Phage_tail_2; Phage tail tube protein (93,86/2,2) | |
| | | | | | | | | | |
| 23 | 13383 | 13724 | + | tail assembly chaperone [<i>Bacillus</i> phage 019DV002] | 7e ⁻¹⁹ | | | Phage_TAC_4; Phage tail assembly chaperone (98,68/5,9e ⁻⁷) | tail assembly chaperone |
| | | | | tail assembly chaperone [<i>Bacillus</i> phage 019DV002] | 6e ⁻¹⁸ | | | Phage_TAC_1; Phage tail assembly chaperone (98,51/0,0000046) | |
| | | | | tail assembly chaperone [<i>Bacillus</i> phage 276BB001] | 7e ⁻¹⁴ | | | Phage_TAC_14; Phage tail assembly chaperone protein, TAC (97,93/0,00022) | |
| 24 | 13769 | 13966 | + | aldolase/citrate lyase family protein [<i>Bacillus</i> virus Blastoid] | 1e ⁻¹¹ | | | Phage_P2_GpE; Phage P2 GpE (98,53/3,9e ⁻⁸) | tail assembly chaperone |
| | | | | tail assembly chaperone [<i>Bacillus</i> phage 276BB001] | 1e ⁻¹⁰ | | | Phage_TAC_6; Phage tail assembly chaperone protein, TAC (96,41/0,013) | |

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|----|-------|-------|---|---|------------|---------------------------|---------------|---|-----------------------------------|
| | | | | tail assembly chaperone [<i>Bacillus</i> phage 019DV002] | $4e^{-10}$ | | | phage_TIGR02216; phage conserved hypothetical protein (95,51/0,055) | |
| 25 | 13978 | 16296 | + | tape measure protein [<i>Bacillus</i> virus Taylor] | 0.0 | HI1514 (62-292) | $2.10e^{-23}$ | COG5283; Phage-related tail protein (99,26/0,000022) | tape measure protein |
| | | | | tail length tape measure protein [<i>Bacillus</i> phage Carmen17] | $7e^{-21}$ | tape_meas_nterm (129-203) | $2.58e^{-16}$ | HI1514; Phage tail tape-measure protein, controls tail length (99,2/0,0000013) | |
| | | | | tail length tape measure protein [<i>Bacillus</i> phage Wes44] | $7e^{-21}$ | COG5412 (153-651) | $1.10e^{-11}$ | YqbO; Phage-related minor tail protein (98,9/0,00031) | |
| 26 | 16310 | 18805 | + | tail fiber [<i>Bacillus</i> phage Leo2] | 0.0 | | | FN3; Fibronectin type 3 domain (99,74/2,1e ⁻¹⁴) | putative tail fiber protein |
| | | | | tail fiber [<i>Bacillus</i> virus Blastoid] | 0.0 | | | Receptor mediating netrin-dependent axon guidance (99,7/4,4e ⁻¹³) | |
| | | | | minor tail protein [<i>Bacillus</i> phage 276BB001] | 0.0 | | | Neural cell adhesion molecule L1 (99,5/1,7e ⁻¹⁰) | |
| 27 | 18810 | 19109 | + | minor tail protein [<i>Bacillus</i> phage 019DV002] | $1e^{-29}$ | | | hp | hp |
| | | | | minor tail protein [<i>Bacillus</i> phage 276BB001] | $3e^{-29}$ | | | | |
| 28 | 19110 | 20777 | + | putative tailspike, beta-helical glycoside hydrolase [<i>Bacillus</i> virus Andromeda] | 0.0 | Pectate_lyase_3 (44-183) | $6.75e^{-06}$ | RR_plus_rpt_1; twin-arg-translocated uncharacterized repeat protein (99,94/5,9e ⁻²²) | Pectate lyase superfamily protein |
| | | | | putative tailspike, beta-helical glycoside [<i>Bacillus</i> phage Gemini] | 0.0 | NosD (355-553) | $5.33e^{-05}$ | b,80,1,3 (A:) Rhamnogalacturonase A {Fungus (<i>Aspergillusaculeatus</i>) [TaxId: 5053]} (99,86/5,4e ⁻¹⁹) | |

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|----|-------|-------|---|---|--------------------|-------------------|----------------------|--|-----------------------|
| | | | | tailspike [<i>Bacillus</i> virus Curly] | 0.0 | | | b,80,1,3 (A:) Rhamnogalacturonase A {Fungus (<i>Aspergillus aculeatus</i>) [TaxId: 5053]} (99,86/5,4e ⁻¹⁹) | |
| | | | | | | | | b,80,1,3 (A:) Polygalacturonase { <i>Erwinia carotovora</i> , subsp, carotovora [TaxId: 554]} (99,82/1,5e ⁻¹⁶) | |
| 29 | 20790 | 21740 | + | minor tail protein [<i>Bacillus</i> phage 019DV002] | 8e ⁻¹⁴⁴ | | | Phage_GPD; Phage late control gene D protein (GPD) (99,95/1,7e ⁻²⁴) | Baseplate hub protein |
| | | | | minor tail protein [<i>Bacillus</i> phage 276BB001] | 3e ⁻¹⁴³ | | | COG4379; Mu-like prophage tail protein gpP (99,94/7e ⁻²³) | |
| | | | | minor tail protein [<i>Microbacterium</i> phage Alakazam] | 8e ⁻²¹ | | | VI_Rhs_Vgr; type VI secretion system Vgr family protein, (99,9/8,4e ⁻²¹) | |
| | | | | | | | | Prophage_tail; Prophage endopeptidase tail (99,84/1,9e ⁻¹⁸) | |
| 30 | 21737 | 21988 | + | collagen triple helix repeat containing protein [<i>Bacillus</i> phage vB_BpsS-36] | 3e ⁻¹⁸ | | | gp45; Mu-like prophage protein gp45 (98,24/0,000022) | Tail spike protein |
| | | | | | | | | Phage_base_V; Type VI secretion system, phage-baseplate injector (98/0,0001) | |
| | | | | | | | | b,40,8,1 (A:6-129) Tail-associated lysozyme gp5, N-terminal domain {Bacteriophage T4 [TaxId: 10665]} (97,84/0,00033) | |
| 31 | 22004 | 22420 | + | phosphodiesterase [<i>Bacillus</i> virus Blastoid] | 6e ⁻⁸⁹ | PRK12704 (13-134) | 2.49e ⁻⁰⁴ | GvpP; Gas vesicle protein (98,44/0,000079) | putative holin |
| | | | | phosphodiesterase [<i>Bacillus</i> virus Riggi] | 3e ⁻⁸⁶ | | | RNase_Y; ribonuclease Y (98,29/0,00023) | |
| | | | | transposase [<i>Bacillus</i> phage Leo2] | 2e ⁻⁸⁵ | IATP (37-74) | 2.53e ⁻⁰³ | EnvC; Septal ring factor EnvC, activator of murein hydrolases | |

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|----|-------|-------|---|--|-------------------|----------------------|----------------------|---|-------------------------------------|
| | | | | | | | | AmiA and AmiB (97,960,0044) | |
| | | | | holin [<i>Bacillus</i> phage 019DV002] | 2e ⁻²³ | RNase_Y (15-131) | 5.13e ⁻⁰³ | Holin_BhlA; BhlA holin family (97,78/0,0014) | |
| 32 | 22432 | 23331 | + | cell wall hydrolase/autolysin [<i>Bacillus</i> virus Andromeda] | 0.0 | MurNAc-LAA (3-180) | 3.35e ⁻⁶² | c,56,5,6 (A:) N-acetylmuramoyl-L-alanine amidase CwlV { <i>Paenibacillus polymyxa</i> [TaxId: 1406]} (99,97/2,7e ⁻²⁸) | N-acetylmuramoyl-L-alanine amidase |
| | | | | | | Amidase_3 (4-179) | 4.30e ⁻⁵⁵ | | |
| | | | | cell wall hydrolase/autolysin [<i>Bacillus</i> virus Andromeda] | 0.0 | Ami_3 (64-179) | 3.29e ⁻³⁰ | spore_cwlD; N-acetylmuramoyl-L-alanine amidase CwlD (99,95/3e ⁻²⁶) | |
| | | | | | | spore_cwlD (2-179) | 9.79e ⁻²⁹ | | |
| | | | | endolysin [<i>Bacillus</i> virus Glittering] | 0.0 | mltD (208-299) | 5.02e ⁻²³ | c,56,5,6 (A:1-180) Endolysin Ply, catalytic domain {Bacteriophage Psa [TaxId: 171618]} (99,95/1,4e ⁻²⁵) | |
| | | | | | | LysM (209-251) | 7.49e ⁻¹⁶ | | |
| | | | | | | spore_safA (211-250) | 2.03e ⁻⁰⁴ | | |
| 33 | 23416 | 23625 | + | holin [<i>Bacillus</i> virus Glittering] | 7e ⁻⁴² | | | Phage_holin_1; Bacteriophage holing (99,04/1,1e ⁻⁹) | holin |
| | | | | | | | | holin_phiLC3; holin, phage phi LC3 family (98,97/1,7e ⁻⁹) | |
| 34 | 23800 | 24165 | + | hp | | | | hp | hp |
| 35 | 24338 | 25231 | + | ssDNA binding protein [<i>Bacillus</i> phage 019DV002] | 2e ⁻⁹⁶ | | | gp32; gp32 DNA binding protein like (99,88/1,8e ⁻²¹) | Single-stranded DNA-binding protein |
| | | | | phosphoesterase [<i>Geobacillus</i> phage GBK1] | 4e ⁻⁵⁷ | | | | |
| 36 | 25237 | 25590 | + | hp | | | | hp | hp |
| 37 | 25637 | 26860 | + | helicase [<i>Bacillus</i> virus Curly] | 0.0 | DnaB (17-429) | 1.47e ⁻⁴⁸ | DnaB; Replicative DNA helicase (100/1,6e ⁻³⁵) | DnaB-like replicative helicase |
| | | | | helicase [<i>Bacillus</i> virus Curly] | 0.0 | PRK08840 (49-376) | 6.93e ⁻²⁴ | DnaB; replicative DNA helicase, This model describes the helicase DnaB, a homohexameric protein | |

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|----|-------|-------|---|---|-------------------|---------------------------|----------------------|---|----------------------------------|
| | | | | | | | | required for DNA replication (100/1,3e ⁻³⁴) | |
| | | | | DNA helicase [Bacillus virus Glittering] | 0.0 | DnaB_C (201-376) | 4.40e ⁻²⁰ | phage_DnaB; phage replicative helicase, DnaB family, HK022 subfamily, (100/5,1e ⁻³³) | |
| 38 | 26853 | 27863 | + | primase [Bacillus virus Andromeda] | 0.0 | dnaG (7-313) | 7.97e ⁻³² | dnaG; DNA primase, catalytic core, (100/1e ⁻³⁸) | DnaG-like primase |
| | | | | primase [Bacillus virus Curly] | 0.0 | Toprim_2 (226-308) | 3.07e ⁻¹⁴ | DnaG; DNA primase (bacterial type), (100/1,9e ⁻³⁵) | |
| | | | | primase [Bacillus virus Curly] | 0.0 | 3.07e-14 (36-87) | 4.89e ⁻⁰⁶ | TraI_TIGR; conjugative transfer relaxase protein TraI (99,94/8e ⁻²⁵) | |
| 39 | 27860 | 28213 | + | hp | | | | hp | hp |
| 40 | 28215 | 28553 | + | transcriptional repressor [Bacillus virus Glittering] | 8e ⁻⁷⁰ | DeoR (60-91) | 7.98e ⁻⁰⁵ | Sig70_famx3; RNA polymerase sigma-70 factor, TIGR02954 family, (98,54/3,5e ⁻⁷) | RNA polymerase sigma-70 factor |
| | | | | transcriptional regulator [Bacillus virus Riggi] | 1e ⁻⁶² | Fis (57-94) | 5.43e ⁻⁰³ | SigE-fam_strep; RNA polymerase sigma-70 factor, sigma-E family, (98,47/0,0000013) | |
| | | | | hp | | sigma70-ECF (63-96) | 5.71e-03 | Sig-70_gvs1; RNA polymerase sigma-70 factor, Rhodopirellula/Verrucomicrobium family (98,39/8,8e ⁻⁷) | |
| 41 | 28566 | 31655 | + | DNA polymerase III alpha subunit [Bacillus virus Curly] | 0.0 | dnaE (6-1029) | 0.0 | DnaE; DNA polymerase III, alpha subunit (100/6,3e ⁻¹⁷¹) | DNA polymerase III alpha subunit |
| | | | | | | Polc (6-992) | 0.0 | | |
| | | | | DNA polymerase III alpha subunit [Bacillus virus Andromeda] | 0.0 | PHP_PolIIIA_DnaE3 (6-285) | 1.37e ⁻⁹⁶ | polc; DNA-directed DNA polymerase III (polc) (00/6,3e ⁻¹⁵⁸) | |
| | | | | | | DNA_pol3_alpha (299-559) | 2.00e ⁻⁹¹ | | |

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| | | | | DNA polymerase III alpha subunit [<i>Bacillus virus</i> Andromeda] | 0.0 | POLIIIAc (9-71) | $4.76e^{-16}$ | polC_Gram_pos; DNA polymerase III, alpha chain, Gram-positive type (100/4,6e ⁻¹²⁴) | |
| 42 | 31658 | 32503 | + | UvrD/REP helicase [<i>Bacillus virus</i> Curly] | 0.0 | PDDEXK_1 (10- 262) | $1.94e^{-17}$ | COG2887; RecB family exonuclease (99,96/2,6e ⁻²⁶) | RecB family exonuclease |
| | | | | PD-(D/E)XK nuclease [<i>Bacillus virus</i> Glittering] | 0.0 | | | cas_AF1879; CRISPR-associated protein Cas4/Csa1, subtype I- A/APERN (99,91/9,5e ⁻²²) | |
| | | | | RecB-like protein [<i>Bacillus</i> phage Leo2] | 0.0 | COG2887 (12-178) | $1.56e^{-05}$ | AddB; ATP-dependent helicase/DNAse subunit B (99,9/4,1e ⁻²¹) | |
| | | | | CRISPR/Cas system associated protein [<i>Bacillus virus</i> Finn] | 0.0 | | | rexB_recomb; ATP-dependent nuclease subunit B (99,89/1,1e ⁻²⁰) | |
| 43 | 32500 | 33006 | + | endonuclease [<i>Bacillus</i> phage Leo2] | $6e^{-103}$ | DUF1064 (11-110) | $5.12e^{-28}$ | c,52,1,16 (A:7-168) TnsA endonuclease, N-terminal domain { <i>Escherichia coli</i> [TaxId: 562]} (99,47/1,2e ⁻¹³) | Endonuclease |
| | | | | Holliday junction resolvase [<i>Bacillus</i> virus Blastoid] | $1e^{-102}$ | | | Phage_endo_I; Phage endonuclease I (99,09/5,8e ⁻¹⁰) | |
| | | | | restriction endonuclease-like protein [<i>Bacillus</i> phage Anath] | $4e^{-31}$ | | | Tn7_Tnp_TnsA_N; TnsA endonuclease N terminal (98,23/0,0000016) | |
| 44 | 33053 | 33733 | + | RNA polymerase sigma-70 factor [<i>Bacillus virus</i> Curly] | $7e^{-168}$ | sigma70-ECF (80- 220) | $5.01e^{-15}$ | spore_sigmaE; RNA polymerase sigma-E factor (99,95/9,5e ⁻²⁶) | RNA polymerase sigma-E factor |
| | | | | RNA polymerase sigma-70 factor [<i>Bacillus virus</i> Andromeda] | $1e^{-163}$ | RpoE (77-225) | $8.44e^{-08}$ | SigW_bacill; RNA polymerase sigma-W factor, This sigma factor is restricted to certain lineages of the order Bacillales (99,94/1,8e ⁻²⁵) | |

| | | | | | | | | | |
|----|-------|-------|---|---|-------------|------------------------|---------------|---|---------------------------------------|
| | | | | RNA polymerase sigma-70 factor [<i>Bacillus virus Eoghan</i>] | $6e^{-136}$ | Sigma70_r4 (169-218) | $8.72e^{-07}$ | RpoE_Sigma70; RNA polymerase sigma factor RpoE (99,94/2,5 e^{-25}) | |
| 45 | 33730 | 33981 | + | hp | | | | hp | hp |
| 46 | 33974 | 34255 | + | hp | | | | hp | hp |
| 47 | 34248 | 34481 | + | hp | | | | hp | hp |
| 48 | 34481 | 35191 | + | thymidylate synthase [<i>Bacillus</i> phage Leo2] | $1e^{-169}$ | Thy1 (21-225) | $1.59e^{-41}$ | d,207,1,1 (A:1-216) Thy1 homologue { <i>Thermotoga maritima</i> [TaxId: 2336]} (100/6 e^{-36}) | thymidylate synthase |
| | | | | thymidylate synthase [<i>Bacillus</i> virus Glittering] | $2e^{-158}$ | thyX (9-232) | $2.25e^{-38}$ | thyX; thymidylate synthase, flavin-dependent (100/6,1 e^{-34}) | |
| | | | | ThyX-like thymidylate synthase [<i>Streptomyces</i> phage Blueeyedbeauty] | $3e^{-82}$ | ThyX (6-230) | $1.36e^{-30}$ | Thy1; Thymidylate synthase complementing protein (100/3,4 e^{-33}) | |
| 49 | 35293 | 35439 | + | hp | | | | POTRA_TamA_1; POTRA domain TamA domain 1 (62,95/7,3) | hp |
| 50 | 35453 | 35806 | + | cysteine-rich domain containing protein [<i>Bacillus</i> virus Glittering] | $2e^{-81}$ | PRK14276 (84-113) | $2.33e^{-04}$ | DnaJ_C; DnaJ C terminal domain (97,47/0,00098) | DnaJ domain-containing protein |
| | | | | cysteine-rich zinc finger protein [<i>Bacillus</i> virus Riggi] | $4e^{-75}$ | COG1107 (80-113) | $1.23e^{-03}$ | Molecular chaperone (DnaJ superfamily) (97,31/0,0015) | |
| | | | | | | DnaJ_CXXCXGXG (83-113) | $8.83e^{-03}$ | DnaJ; DnaJ-class molecular chaperone with C-terminal Zn finger domain (97,19/0,0029) | |
| 51 | 35971 | 36153 | + | hp | | | | FeoB; Fe ²⁺ transport system protein B (80,91/20) | Prediction lipoprotein signal peptide |
| 52 | 36150 | 36314 | + | hp | | | | hp | hp |
| 53 | 36527 | 36841 | + | hp | | | | hp | hp |

| | | | | | | | | | |
|----|-------|-------|---|---|-------------|--------------------|---------------|--|----------------|
| 54 | 36838 | 37425 | + | deoxynucleoside monophosphate kinase [<i>Bacillus virus</i> Curly] | $2e^{-131}$ | | | Pmev_kin_anim; phosphomevalonate kinase, animal type (99,78/9,5e ⁻¹⁷) | kinase |
| | | | | phosphate mevalonate kinase [<i>Bacillus</i> phage Leo2] | $9e^{-118}$ | | | c,37,1,17 (A:) Gluconate kinase { <i>Escherichia coli</i> [TaxId: 562]} (99,72/1,5e ⁻¹⁵) | |
| | | | | nucleoside kinase [<i>Bacillus</i> phage Anath] | $3e^{-34}$ | | | c,37,1,1 (A:3-127,A:159-222) Adenylate kinase {Maize (<i>Zea mays</i>) [TaxId: 4577]} (99,7/1e ⁻¹⁵) | |
| | | | | P-loop containing nucleoside triphosphate hydrolase [<i>Listeria</i> phage LP-026] | $5e^{-29}$ | | | c,37,1,1 (A:) Deoxynucleoside monophosphate kinase {Bacteriophage T4 [TaxId: 10665]} (99,7/1,2e ⁻¹⁴) | |
| 55 | 37425 | 37769 | + | hp | | | | Syntaphilin; Golgi-localised syntaxin-1-binding clamp (94,04/0,41) | hp |
| | | | | | | | | Golgin_A5; Golgin subfamily A member (5 93,85/2,4) | |
| | | | | | | | | Synaptic vesicle protein EHS-1 and related EH domain proteins (92,19/3,8) | |
| 56 | 37916 | 38725 | + | serine-threonine kinase [<i>Bacillus virus</i> Andromeda] | 0.0 | STKc_CDK9 (60-187) | $2.32e^{-04}$ | d,144,1,7 (A:) Protein kinase C, theta type {Human (<i>Homo sapiens</i>) [TaxId: 9606]} (100/1,9e ⁻³³) | protein kinase |
| | | | | serine-threonine kinase [<i>Bacillus virus</i> Curly] | $1e^{-162}$ | Pkinase (59-187) | $5.29e^{-03}$ | d,144,1,7 (A:) cAMP-dependent PK, catalytic subunit {Baker's yeast (<i>Saccharomyces cerevisiae</i>) [TaxId: 4932]} (100/2,6e ⁻³³) | |
| | | | | serine-threonine protein kinase [<i>Bacillus</i> phage Leo2] | $2e^{-155}$ | | | d,144,1,7 (E:) cAMP-dependent PK, catalytic subunit {Mouse (<i>Mus musculus</i>) [TaxId: 10090]} (100/3,4e ⁻³²) | |
| 57 | 38716 | 39147 | + | hp | | | | hp | hp |

| | | | | | | | | | |
|----|-------|-------|---|----|--|--|--|---|--|
| 58 | 39119 | 39535 | + | | | | | zf-C2HCIX2C; Zinc-finger (96,99/0,0014) | hp |
| | | | | | | | | phage_arpU; phage transcriptional regulator, ArpU family (63,71/6,1) | |
| 59 | 39532 | 39648 | + | hp | | | | hp | hp |
| 60 | 39650 | 39997 | + | hp | | | | hp | hp |
| 61 | 39997 | 40230 | + | hp | | | | hp | hp |
| 62 | 40232 | 40540 | + | hp | | | | hp | hp |
| 63 | 40540 | 40971 | + | | | | | CopC; Copper-binding protein CopC (methionine-rich) (98,26/0,00011) | hp |
| | | | | | | | | YifL; Predicted small periplasmic lipoprotein YifL (97,75/0,000078) | |
| | | | | | | | | YifL; Predicted small periplasmic lipoprotein YifL (97,75/0,000078) | |
| | | | | | | | | LPAM_1; Prokaryotic membrane lipoprotein lipid attachment site (97,56/0,00015) | |
| 64 | 40988 | 41125 | + | hp | | | | hp | hp |
| 65 | 41227 | 41610 | + | hp | | | | DUF2582; Winged helix-turn- helix domain (DUF2582) (98,65/8,9e ⁻⁷) | putative transcriptional regulator |
| | | | | | | | | COG2865; Predicted transcriptional regulator, contains HTH domain (98,55/0,0000018) | |
| | | | | | | | | a,4,5,60 (A:86-162) Segregation and condensation protein B, ScpB { <i>Chlorobium tepidum</i> [TaxId: 1097]} (98,41/0,000015) | |

| | | | | | | | | | |
|----|-------|-------|---|--|------------|----------------------------|---------------|--|--|
| | | | | | | | | PaaX; PaaX-like protein (98,17/0,000048) | |
| | | | | | | | | a,4,5,2 (A:2-72) LexA repressor, N-terminal DNA-binding domain { <i>Escherichia coli</i> [TaxId: 562]} (98,15/0,000088) | |
| | | | | | | | | a,4,5,39 (A:) Penicillinase repressor BlaI { <i>Bacillus licheniformis</i> [TaxId: 1402]} (98,14/0,00011) | |
| 66 | 41612 | 42037 | + | hp | | | | hp | hp |
| 67 | 42255 | 43544 | + | FtsK/SpoIIIE ATPase [<i>Bacillus virus</i> Curly] | 0.0 | FtsK (190-388) | $2.23e^{-22}$ | T7SS_EccC_a; type VII secretion protein EccCa (99,86/9e ⁻²⁰) | FtsK/SpoIIIE family protein |
| | | | | FtsK/SpoIIIE family protein [<i>Bacillus virus</i> Riggi] | 0.0 | PRK10263 (182- 379) | $4.25e^{-13}$ | FtsK; DNA segregation ATPase FtsK/SpoIIIE and related proteins (99,76/1,8e ⁻¹⁶) | |
| | | | | FtsK-like DNA translocase [<i>Bacillus</i> phage 019DV002] | 0.0 | T7_EssCb_Firm (163-389) | $8.33e^{-10}$ | PvdE; ABC-type siderophore export system, fused ATPase and permease components (98,69/6,4e ⁻⁹) | |
| 68 | 43807 | 44082 | + | replication/relaxation protein [<i>Bacillus virus</i> Curly] | $5e^{-63}$ | | | Replic_Relax; Replication- relaxation (98,96/3,8e ⁻⁹) | Replic_Relax superfamily protein |
| | | | | plasmid replication- relaxation protein [<i>Bacillus virus</i> Riggi] | $1e^{-60}$ | | | DpnII; DpnII restriction endonuclease (93,27/1,1) | |
| | | | | plasmid replication- relaxation protein [<i>Bacillus virus</i> Blastoid] | $1e^{-60}$ | | | capSnatchArena; RNA endonuclease, cap-snatching, arenavirus family (92,65/0,69) | |

| | | | | | | | | | |
|----|-------|-------|---|--|--|---|----------------------|---|----------------------------|
| 69 | 44095 | 44508 | + | hp | | | | TrbC; TrbC/VIRB2 family (98,95/1,6e ⁻⁸) | TrbC/VIRB2 family protein |
| | | | | | | | | VirB2; Type IV secretory pathway (98,47/0,0000064) | |
| | | | | | | | | conj_TIGR03745; integrating conjugative element membrane protein, PFL_4702 family (98,17/0,00014) | |
| | | | | | | | | Maff2; Maff2 family (97,51/0,0036) | |
| 70 | 44579 | 44782 | + | DNA binding domain protein [<i>Bacillus</i> phage 019DV002] | 6e ⁻²⁵ | gatA (22-43) | 6.87e ⁻⁰³ | Arc; Arc-like DNA binding domain (96,23/0,033) | DNA binding domain protein |
| | | | | hp | antidote_CC2985; putative addiction module antidote protein, CC2985 family (95,93/0,045) | | | | |
| | | | | | COG4710; Predicted DNA-binding protein with an HTH domain 95,88/0,12 | | | | |
| | | | | | a,43,1,1 (A:) Arc repressor { <i>Salmonella</i> bacteriophage P22 [TaxId: 10754]} (94,95/0,16) | | | | |
| 71 | 45289 | 44801 | - | hp | | | | hp | hp |
| 72 | 46030 | 45437 | - | DNA polymerase III epsilon subunit [<i>Bacillus</i> virus Curly] | 8e ⁻¹⁴² | DEDDh (4-157) | 3.95e ⁻³⁷ | PolC; DNA polymerase III, alpha subunit (gram-positive type) (99,87/6,4e ⁻²⁰) | DEDDh exonuclease |
| | | | | EXOIII (1-162) | 8.53e ⁻²⁶ | | | | |
| | | | | DNA polymerase III epsilon subunit [<i>Bacillus</i> virus Glittering] | 2e ⁻¹³⁷ | DnaQ (1-162) | 9.01e ⁻²⁶ | dnaQ_proteo; DNA polymerase III, epsilon subunit, Proteobacterial (99,85/7,1e ⁻¹⁹) | |
| | | | | DEDDh 3'-5' exonuclease [<i>Paenibacillus</i> phage Scottie] | 3e ⁻³⁵ | RNase_T (4-156) | 5.32e ⁻²⁵ | | |
| | | | | polC_Gram_pos (2-167) | 3.02e ⁻²⁴ | dinG_rel; DnaQ family exonuclease/DinG family helicase, putative (99,82/7,1e ⁻¹⁸) | | | |
| 73 | 46767 | 46030 | - | peptidase [<i>Bacillus</i> | 2e ⁻⁵⁰ | | | ImmA; Zn-dependent peptidase | peptidase |

| | | | | | | | | | |
|----|-------|-------|---|--|--------------------|-----------------------|----------------------|--|-----------------------------|
| | | | | phage Leo2] | | | | ImmA, M78 family (98,82/7,8e ⁻⁸) | |
| | | | | | | | | Peptidase_M78; IrrE N-terminal-like domain (98,69/2,3e ⁻⁷) | |
| | | | | zinc-dependent metalloprotease [<i>Bacillus</i> virus Blastoid] | 9e ⁻⁴⁹ | | | COG3800; Predicted transcriptional regulator (98,39/0,0000038) | |
| | | | | | | | | MPTase-PolyVal; Metallopeptidase superfamily domain (98,05/0,000016) | |
| 74 | 46995 | 46768 | - | | | | | SlyX; SlyX (92,79/1,4) | hp |
| | | | | | | | | GTPase-activating protein 92,01/2,1 | |
| | | | | | | | | SlyX; Uncharacterized coiled-coil protein SlyX (sensitive to lysis X) (89,6/3,7) | |
| 75 | 47355 | 47837 | + | Holliday junction resolvase [<i>Bacillus</i> virus Glittering] | 5e ⁻¹¹¹ | PHA00159 (58-129) | 4.46e ⁻⁰⁶ | c,52,1,17 (A:) Endonuclease I (Holliday junction resolvase) {Bacteriophage T7 [TaxId: 10760]} (99,43/1,8e ⁻¹²) | holliday junction resolvase |
| | | | | T7-like endonuclease [<i>Bacillus</i> virus Curly] | 2e ⁻¹¹⁰ | Phage_endo_I (58-129) | 8.84e ⁻⁰⁴ | Phage_endo_I; Phage endonuclease I (98,73/1,4e ⁻⁷) | |
| | | | | endonuclease [<i>Bacillus</i> phage Leo2] | 7e ⁻¹⁰⁹ | | | Vsr; DNA mismatch endonuclease Vsr (98,08/0,000012) | |
| 76 | 47884 | 48045 | + | hp | | | | hp | hp |
| 77 | 48046 | 48210 | + | hp | | | | FlaG; Uncharacterized conserved protein, FlaG/YvyC family (99,76/4,3e ⁻¹⁸) | FlaG/YvyC family protein |
| | | | | | | | | d,352,1,1 (A:2-109) Hypothetical protein YvyC { <i>Bacillus subtilis</i> [TaxId: 1423]} (99,76/3,7e ⁻¹⁸) | |
| | | | | | | | | FlaG; FlaG protein 99,74/7,6e ⁻¹⁸ | |
| 78 | 48210 | 48377 | + | hp | | nifE (5-42) | 9.38e ⁻⁰³ | e,3,1,1 (A:328-668) Penicillin binding protein 2a (PBP2A), C-terminal domain { <i>Staphylococcus</i> | hp |

| | | | | | | | | | |
|----|-------|-------|---|--|------------|--|--|--|--|
| | | | | | | | | <i>aureus</i> [TaxId: 1280]} (90,99/0,53) | |
| | | | | | | | | Activator-TraM; Transcriptional activator TraM (89,76/0,3) | |
| | | | | | | | | XisI; XisI protein (88,95/1,5) | |
| | | | | | | | | bioW; 6-carboxyhexanoate--CoA ligase, Alternate name: pimeloyl- CoA synthase, [Biosynthesis of cofactors, prosthetic groups, and carriers, Biotin] (87,93/1,2) | |
| 79 | 48402 | 48554 | + | hp | | | | Transcription factor (contains Zn finger) (97,82/0,0000046) | putative transcription factor |
| | | | | | | | | CpXC; CpXC protein (97,57/0,00023) | |
| | | | | | | | | Transcription factor BLIMP- 1/PRDI-BF1, contains C2H2-type Zn-finger and SET domains (97,45/0,000092) | |
| | | | | | | | | Transcriptional repressor SALM (97,4/0,0000058) | |
| 80 | 48556 | 48702 | + | hp | | | | hp | hp |
| 81 | 48896 | 49570 | + | putative terminase small subunit [<i>Bacillus</i> phage 056SW001B] | $1e^{-77}$ | | | sm_term_P27; phage terminase, small subunit, putative, P27 family (89,28/3,6) | putative terminase small subunit |
| | | | | putative terminase small subunit [<i>Bacillus</i> phage 019DV002] | $6e^{-76}$ | | | Terminase_4; Phage terminase, small subunit (88,04/5,6) | |
| | | | | putative terminase small subunit [<i>Bacillus</i> phage 276BB001] | $6e^{-76}$ | | | COG3747; Phage terminase, small (86,89/9,2) | |
| | | | | exopolyphosphatase domain protein | $3e^{-64}$ | | | | |

| | | | | | | | | | |
|--|--|--|--|-------------------------------------|--|--|--|--|--|
| | | | | [<i>Geobacillus</i> phage GBK1] | | | | | |
|--|--|--|--|-------------------------------------|--|--|--|--|--|

Table S2. Annotation of the Bacillus phage Novomoskovsk

| ORF№ | Start codon | Stop codon | Strand | Blast results | | Conserved domains, Blast | | Hhpred results | Annotation |
|------|-------------|------------|--------|---|-------------------|--------------------------|-------|--|--------------------------|
| | | | | Name | E-val | Name, (region) | E-val | (Prob./E-val) | |
| 1 | 65 | 739 | + | Putative terminase small subunit [<i>Bacillus phage</i> 056SW001B] | 1e ⁻⁷³ | | | sm_term_P27; phage terminase, small subunit, putative, P27 family, 92,77/0,94 | Terminase, small subunit |
| | | | | | | | | Terminase_4; Phage terminase, small subunit (91,46/2) | |
| | | | | | | | | COG3747; Phage terminase, small subunit (90,62/2,5) | |
| 2 | 1292 | 1074 | - | hp | | | | | hp |
| 3 | 1756 | 1457 | - | hp | | | | g,37,1,1 (A:67-101) Zinc finger protein 295, ZNF295 (95,4/0,0066) | hp |
| 4 | 2006 | 1749 | - | hp | | | | | hp |
| 5 | 2189 | 2031 | - | hp | | | | FixS; Cytochrome oxidase maturation protein cbb3-type (77,84/8,2) | hp |
| | | | | | | | | ccoS; cytochrome oxidase maturation protein, cbb3-type, CcoS from Rhodobacter capsulatus has been shown essential for incorporation of redox-active prosthetic groups (heme, Cu) into cytochrome cbb (3) oxidase, (76,32/10) | |
| | | | | | | | | CD225; Interferon-induced transmembrane protein | |

| | | | | | | | | | |
|----|------|------|---|---|-----|------------------------|-----------------------|---|--------------------------|
| | | | | | | | | (72,77/6,3) | |
| | | | | | | | | FixS; Cytochrome oxidase maturation protein, CcoS/FixS family [Posttranslational modification, protein turnover, chaperones] (75,87/11) | |
| 6 | 2407 | 2195 | - | hp | | | | | hp |
| 7 | 2700 | 2404 | - | hp | | | | | hp |
| 8 | 3089 | 2832 | - | hp | | | | | hp |
| 9 | 3318 | 3091 | - | hp | | | | | hp |
| 10 | 3419 | 5104 | + | Terminase [<i>Bacillus virus Finn</i>] | 0.0 | Terminase_GpA (52-314) | $1.14 \cdot 10^{-5}$ | Terminase_GpA; Phage terminase large subunit (GpA) (100/1,5e ⁻³¹) | Terminase, large subunit |
| | | | | | | | | Terminase_1; Phage Terminase (100/1,2e ⁻³¹) | |
| | | | | | | | | COG5323; Large terminase phage packaging protein (100/3e ⁻³⁰) | |
| 11 | 5187 | 6506 | + | Portal [<i>Bacillus virus Riggi</i>] | 0.0 | DUF935 (90-394) | $4.54 \cdot 10^{-21}$ | gp29; Mu-like prophage protein gp29 100/4e ⁻³¹ | Portal protein |
| | | | | Portal protein [<i>Bacillus virus Glittering</i>] | 0.0 | | | portal_HK97; phage portal protein, HK97 family, (99,97/6,6e ⁻²⁸) | |
| | | | | Portal protein [<i>Bacillus virus Curly</i>] | 0.0 | gp29 (93-397) | $4.56 \cdot 10^{-8}$ | BeeE; Phage portal protein BeeE (99,96/4,1e ⁻²⁸) | |
| | | | | Portal protein [<i>Bacillus virus Blastoid</i>] | 0.0 | | | Phage_portal; Phage portal protein (99,96/1,5e ⁻²⁷) | |
| 12 | 6560 | 7462 | + | Phage head morphogenesis protein [<i>Bacillus virus Finn</i>] | 0.0 | Phage_Mu_F (144-254) | $8.39 \cdot 10^{-15}$ | phageSPP1_gp7; phage putative head morphogenesis protein, SPP1 gp7 family, (99,85/2,3e ⁻²⁰) | Minor head protein |
| | | | | Minor head protein | 0.0 | PhageSPP1_gp7 | $3.60 \cdot 10^{-14}$ | Phage_min_cap2; Phage minor | |

| | | | | | | | | | |
|----|------|------|---|--|--------------------|------------------|-----------------------|---|--|
| | | | | [<i>Bacillus</i> virus Riggi] | | (151-261) | | capsid protein 2 (99,84/4,3e ⁻¹⁹) | |
| | | | | Minor head protein [<i>Bacillus</i> phage Leo2] | 0.0 | COG2369 (19-264) | 2.12·10 ⁻³ | Phage_Mu_F; Phage Mu protein F like protein (99,81/1e ⁻¹⁸) | |
| 13 | 7977 | 7495 | - | hp | | | | YifL; Predicted small periplasmic lipoprotein YifL (98,17/9,2e ⁻⁶) | Putative signal peptide-containing protein |
| | | | | | | | | COG5510; Predicted small secreted protein (97,12/0,001) | |
| 14 | 8096 | 7977 | - | Ribonuclease [<i>Bacillus</i> phage Leo2] | 3e ⁻¹³ | | | | |
| | | | | Hypothetical protein Riggi_14 [<i>Bacillus</i> virus Riggi] | 6e ⁻¹⁵ | | | | hp |
| 15 | 8516 | 9352 | + | Scaffold protein [<i>Bacillus</i> virus Finn] | 2e ⁻¹⁷⁵ | | | Mu-like_Pro; Mu-like prophage I protein (99,9/1,4e ⁻²¹) | |
| | | | | Scaffold protein [<i>Bacillus</i> virus Riggi] | 1e ⁻¹⁷² | | | COG4388; Mu-like prophage I protein [Mobilome: prophages, transposons], (99,87/1,8e ⁻²⁰) | |
| | | | | Scaffold protein [<i>Bacillus</i> virus Curly] | 8e ⁻¹⁷⁰ | | | Phage_GPO; Phage capsid scaffolding protein (GPO) serine peptidase (99,52/1,6e ⁻¹³) | |
| | | | | Putative protease I [Prokaryotic dsDNA virus sp.] | 2e ⁻⁴ | | | proheadase_HK97; phage prohead protease, HK97 family, This model describes the prohead protease of HK97 and related phage, (99,32/8,4e ⁻¹¹) | Prohead protease |
| | | | | | | | | COG3740; Phage head maturation protease [Mobilome: prophages, transposons], (99,15/2,6e ⁻⁹) | |

| | | | | | | | | | |
|----|-------|-------|---|--|-----|----------------|-----------------------|---|-----------------------------------|
| 16 | 9373 | 9795 | + | hp | | | | COG5471; Predicted phage recombinase, RecA/RadA family (99,75/1,1e ⁻¹⁶) | DUF2190 domain-containing protein |
| | | | | | | | | DUF2190 (99,49/2,8·10 ⁻¹²) | |
| 17 | 9814 | 10707 | + | Major capsid protein [<i>Bacillus</i> phage Leo2] | 0.0 | | | Major capsid protein gp5 {Bacteriophage} HK97 (99,95/3,3e ⁻²⁶) | Major capsid protein |
| | | | | Major capsid protein [<i>Bacillus</i> virus Glittering] | 0.0 | | | major_cap_HK97; phage major capsid protein, HK97 family, (99,93/3e ⁻²³) | |
| | | | | Major capsid protein [<i>Bacillus</i> virus Riggi] | 0.0 | | | Phage_capsid; Phage capsid family (99,9/5,3e ⁻²³) | |
| 18 | 10726 | 10995 | + | hp | | | | Rep-A_N; Replication factor-A protein 1, N-terminal domain (47,48/25) | hp |
| 19 | 11070 | 11291 | + | hp | | | | Ribosomal_L9_N; Ribosomal protein L9, N-terminal domain (94,28/0,068) | hp |
| | | | | | | | | d,100,1,1 (A:1-52) Ribosomal protein L9 N-domain { <i>Bacillus stearothermophilus</i> } (94,03/0,095) | |
| | | | | | | | | Packaging_FI; DNA packaging protein FI (92,83/0,29) | |
| 20 | 11305 | 11697 | + | hp | | DUF1320 (2-65) | 2.18·10 ⁻⁵ | gp436; Mu-like prophage protein gp36 (99,83/4,3e ⁻¹⁹) | head completion protein |
| | | | | | | gp436 (2-74) | 2.98·10 ⁻³ | Phage_connect_1; Phage gp6-like head-tail connector protein (98,58/0,0000011 ¹) | |

| | | | | | | | | | |
|----|-------|-------|---|---|------------|--|--|--|-------------------------|
| 21 | 11886 | 11767 | - | hp | | | | | hp |
| 22 | 12029 | 12145 | + | Virion morphogenesis protein [<i>Bacillus phage</i> Leo2] | $3e^{-20}$ | | | COG5005; Mu-like prophage protein gpG [Mobilome: prophages, transposons], (98,95/3,8e ⁻⁹) | tail completion protein |
| | | | | Tail completion and head joining protein [<i>Bacillus virus</i> Riggi] | $9e^{-9}$ | | | Phage_tail_S; Phage virion morphogenesis family (98,91/9e ⁻¹⁰) | |
| | | | | Head-to-tail stopper [<i>Bacillus phage</i> 276BB001] | $3e^{-6}$ | | | Tail_comp_S; phage virion morphogenesis (putative tail completion) protein, This model describes protein S of phage P2, suggested experimentally to act in tail completion and stable head joining, and related proteins from a number of phage, (98,65/3,7e ⁻⁸) | |
| | | | | Tail completion protein [<i>Bacillus virus</i> Blastoid] | $5e^{-8}$ | | | Phge_HK97_gp10; phage protein, HK97 gp10 family, This model represents an uncharacterized, highly divergent bacteriophage family (98,63/7,2e ⁻⁸) | |
| 23 | 12142 | 12576 | + | hp | | | | Phage_tail_U; Phage minor tail protein U (99,57/1,3e ⁻¹³) | tail terminator protein |
| 24 | 12588 | 12764 | + | hp | | | | Predicted translation initiation factor related to eIF-1A [Translation, ribosomal structure and biogenesis] (72,07/13) | hp |
| | | | | | | | | eIF-1A; eukaryotic/archaeal initiation factor 1A, Recommended nomenclature: eIF-1A for eukaryotes, aIF-1A for Archaea (70,11/20) | |

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|----|-------|-------|---|---|--------------------|---------------------------|----------------------|---|-------------------------|
| | | | | | | | | b,40,4,5 (A:) Archaeal initiation factor-1a, aIF1a { <i>Methanococcus jannaschii</i> [TaxId: 2190]} (67,47/21) | |
| 25 | 12764 | 13702 | + | Major tail protein [<i>Bacillus</i> phage 019DV002] | 3e ⁻¹⁰⁴ | | | Phage tail tube protein 98,54/0,000012 | Tail tube protein |
| | | | | Major tail protein [<i>Bacillus</i> phage 276BB001] | 4e ⁻¹⁰⁴ | | | Phage-like element PBSX protein XkdM { <i>Bacillus subtilis</i> 98,35/0,000046 | |
| | | | | | | | | Phage_tail_2; Phage tail tube protein 9(5,08/1,1) | |
| 26 | 13727 | 14068 | + | hp | | | | Phage_TAC_4; Phage tail assembly chaperone (98,52/0,0000022) | Tail assembly chaperone |
| | | | | | | | | Phage_TAC_1; Phage tail assembly chaperone 98,37/0,000009 | |
| | | | | | | | | Phage_TAC_5; Phage XkdN-like tail assembly chaperone protein, TAC (87,48/4,1) | |
| 27 | 14113 | 14319 | + | hp | | | | | hp |
| 28 | 14323 | 16641 | + | Tape measure protein [<i>Bacillus</i> virus Eoghan] | 0.0 | HI1514 (62-292) | 6.47e ⁻²⁶ | COG5412; Phage-related protein (99,78/2,3e ⁻¹²) | Tape measure protein |
| | | | | Tape measure protein [<i>Bacillus</i> virus Taylor] | 0.0 | tape_meas_nterm (129-203) | 1.29e ⁻¹⁶ | HI1514; Phage tail tape-measure protein, controls tail length (99,11/0,0000036) | |
| | | | | Tape measure protein [<i>Bacillus</i> phage Leo2] | 0.0 | COG5412 (153-666) | 4.42e ⁻¹² | | |
| | | | | Tape measure protein [<i>Bacillus</i> virus Curly] | 0.0 | PHA01351 (462-596) | 2.73e ⁻⁴ | | |
| 29 | 16655 | 19150 | + | Tail fiber [<i>Bacillus</i> virus Blastoid] | 0.0 | | | Receptor mediating netrin-dependent axon guidance (99,94/7,3e ⁻²³) | Putative tail protein |
| | | | | Tail fiber [<i>Bacillus</i> | 0.0 | | | FN3; Fibronectin type 3 domain | |

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|----|-------|-------|---|--|--------------------|-------------------------------|----------------------|--|--|
| | | | | phage Leo2] | | | | (99,8/6,1e ⁻¹⁶) | |
| | | | | Minor tail protein [<i>Bacillus</i> phage 276BB001] | 0.0 | | | Neural cell adhesion molecule L1 (99,74/1,6e ⁻¹⁵) | |
| | | | | | | | | Peripheral benzodiazepine receptor PRAX-1 99,68/(1,6e ⁻³) | |
| | | | | | | | | Adhesion-type protein (99,61/2,1e ⁻¹³) | |
| 30 | 19155 | 19454 | + | Minor tail protein [<i>Bacillus</i> phage 019DV002] | 4e ⁻²⁸ | | | | hp |
| 31 | 19454 | 21085 | + | Putative tailspike, beta-helical glycoside [<i>Bacillus</i> virus Finn] | 0.0 | Beta_helix (370- 524) | 3.48e ⁻¹² | phage_tailspike_middle; N- terminal and middle domains of tailspike protein in <i>Acinrtobacter</i> bacteriophages (99,23/3e ⁻⁸) | Putative tailspike |
| | | | | Tailspike [<i>Bacillus</i> virus Riggi] | 0.0 | NosD_copper_f am (252-497) | 5.79e ⁻⁷ | | |
| | | | | Tailspike [<i>Bacillus</i> virus Blastoid] | 0.0 | NosD (264-425) | 6.25e ⁻³ | | |
| 32 | 21100 | 22050 | + | Minor tail protein [<i>Bacillus</i> phage 019DV002] | 6e ⁻¹⁴⁸ | | | COG4379 Mu-like prophage tail protein gpP (99,96/5,7e ⁻²⁵) | Baseplate hub protein and central tail fiber |
| | | | | Minor tail protein [<i>Bacillus</i> phage 276BB001] | 3e ⁻¹⁴⁷ | | | COG3501 VgrG 99,93/1,3e ⁻²² | |
| | | | | Minor tail protein [<i>Streptomyces</i> phage Zuko] | 7e ⁻⁴⁵ | | | Prophage_tail; Prophage endopeptidase tail (99,84/6,4e ⁻¹⁹) | |

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| 33 | 22047 | 22640 | + | Collagen triple helix repeat containing protein [<i>Bacillus</i> phage vB_BpsS-36] | $7e^{-110}$ | | | b,21,1,3 (A:162-264) receptor binding protein, rbp, C-terminal domain { <i>Lactococcus lactis</i> } phage p2 (96,75/0,031) | Receptor-binding protein |
| | | | | | | | | Caudo_bapla_RBP; Receptor-binding protein of phage tail base-plate <i>Siphoviridae</i> , head (87,3/12) | |
| 34 | 22657 | 23073 | + | Phosphodiesterase [<i>Bacillus</i> virus Riggi] | $1e^{-90}$ | PRK12704 (13-136) | $4.23e^{-5}$ | RNase_Y; ribonuclease Y (98,98 \, 1,3e ⁻⁷) | putative holin |
| | | | | Transposase [<i>Bacillus</i> phage Leo2] | $1e^{-87}$ | RNase_Y (15-136) | $3.32e^{-3}$ | Holin_BhlA; BhlA holin family (98,94/3,8e ⁻⁸) | |
| | | | | Phosphodiesterase [<i>Bacillus</i> virus Blastoid] | $8e^{-81}$ | IATP (37-80) | $5.87e^{-3}$ | AtpF; FoF1-type ATP synthase, membrane subunit b or b' (97,38/0,024) | |
| 35 | 23087 | 23986 | + | Cell wall hydrolase/autolysin [<i>Bacillus</i> virus Eoghan] | 0.0 | MurNAc-LAA (3-180) | $1.88e^{-65}$ | c,56,5,6 (A:) N-acetylmuramoyl-L-alanine amidase CwlV { <i>Paenibacillus polymyxa</i> } (99,97/2,2e ⁻²⁸) | N-acetylmuramoyl-L-alanine amidase |
| | | | | | | Amidase_3 (4-179) | $2.17e^{-57}$ | | |
| | | | | | | mltD (200-296) | $1.94e^{-21}$ | | |
| | | | | | | LysM (209-251) | $1.68e^{-15}$ | | |
| | | | | | | spore_safA (211-250) | $5.15e^{-4}$ | | |
| 36 | 24072 | 24281 | + | hp | | | | Phage_holin_1; Bacteriophage holin (99,59/9,6e ⁻¹⁵) | Holin |
| | | | | | | | | Holin_phiLC3; holin, phage phi LC3 family, Phage proteins for bacterial lysis typically include a membrane-disrupting protein, or holin, and one or more cell wall | |

| | | | | | | | | | |
|----|-------|-------|---|--|-------------------|--------------------|----------------------|--|-------------------------------------|
| | | | | | | | | degrading enzymes that reach the cell wall because of holin action, (99,56/1,4e ⁻¹⁴) | |
| | | | | | | | | Holin_SPP1; holin, SPP1 family, This model represents one of more than 30 families of phage proteins, all lacking detectable homology with each other, known or believed to act as holins, (90,01/2,1) | |
| 37 | 24458 | 24823 | + | Holin [<i>Bacillus</i> virus Andromeda] | 3e ⁻⁶⁶ | | | DUF5105; Domain of unknown function (90,98/2,9) | hp |
| | | | | Holin [<i>Bacillus</i> virus Blastoid] | 6e ⁻⁶² | | | | |
| | | | | Holin [<i>Bacillus</i> virus Curly] | 2e ⁻⁶¹ | | | | |
| | | | | Holin [<i>Bacillus</i> virus Finn] | 2e ⁻⁵⁷ | | | | |
| 38 | 24987 | 25880 | + | ssDNA binding protein [<i>Bacillus</i> phage 019DV002] | 2e ⁻⁹⁶ | | | gp32; gp32 DNA binding protein like (99,86/8,5e ⁻²¹) | Single-stranded DNA-binding protein |
| | | | | ssDNA binding protein [<i>Bacillus</i> phage 056SW001B] | 5e ⁻⁹⁶ | | | | |
| 39 | 25886 | 26239 | + | hp | | | | | hp |
| 40 | 26268 | 27509 | + | Helicase [<i>Bacillus</i> virus Finn] | 0.0 | DnaB (21-433) | 3.53e ⁻⁵⁰ | DnaB; Replicative DNA helicase (100/9,2e ⁻³⁶) | DnaB-like replicative helicase |
| | | | | | | PRK07773 (21-379) | 4.66e ⁻²² | | |
| | | | | | | DnaB_C (205-380) | 3.58e ⁻²⁰ | | |
| 41 | 27502 | 28512 | + | DNA primase [<i>Bacillus</i> virus Riggi] | 0.0 | dnaG (3-314) | 5.05e ⁻³² | dnaG; DNA primase, catalytic core (100/2,7e ⁻³⁹) | DnaG-like primase |
| | | | | | | Toprim_2 (212-294) | 7.14e ⁻¹⁴ | | |

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| | | | | | | TOPRIM_DnaG _primases (212- 285) | 2.15e ⁻¹² | | |
| | | | | | | ZnF_CHCC (22-73) | 2.60e ⁻⁶ | | |
| 42 | 28509 | 28871 | + | Putative 60 kDa chaperonin [Prokaryotic dsDNA virus sp.] | 1.2 | | | | hp |
| 43 | 28879 | 29199 | + | Transcriptional regulator [<i>Bacillus</i> virus Riggi] | 2e ⁻⁷⁵ | DeoR (57-88) | 1.66e ⁻³ | COG5606; Predicted DNA- binding protein, XRE-type HTH domain (97,56/0,00094) | Putative transcriptional regulator |
| 44 | 29212 | 32292 | + | DNA polymerase III [<i>Bacillus</i> virus Riggi] | 0.0 | dnaE (6-1026) | 0 | | DNA polymerase III alpha subunit |
| | | | | polc (6-989) | | 0 | | | |
| | | | | PHP_PolIIIA_D naE3 (6-285) | | 3.49e ⁻⁹⁵ | | | |
| | | | | DNA_pol3_alph a (297-559) | | 4.86e ⁻⁹² | | | |
| | | | | POLIIIAc (9- 71) | | 2.31e ⁻¹⁶ | | | |
| 45 | 32295 | 33140 | + | PD-(D/E)XK nuclease [<i>Bacillus</i> virus Riggi] | 0.0 | PDDEXK_1 (10-196) | 5.16e ⁻¹⁷ | COG2887; RecB family exonuclease (99,96/2,3e ⁻²⁶) | RecB family exonuclease |
| | | | | | | COG2887 (12- 178) | 1.38e ⁻⁴ | | |
| 46 | 33137 | 33646 | + | Endonuclease [<i>Bacillus</i> phage Leo2] | 5e ⁻¹⁰⁹ | DUF1064 (11- 110) | 1.04e ⁻²⁸ | DUF1064 (99,67/2e ⁻¹⁴) | Endonuclease |
| | | | | | | | | TnsA endonuclease, N-terminal domain (99,47/2,1e ⁻¹³) | |
| | | | | | | | | Phage_endo_I (99,08/1,2e ⁻⁹) | |
| 47 | 33643 | 33915 | + | hp | | TM1586_NiRda se (7-77) | 3.15e ⁻³ | TA0956 ; <i>Thermoplasma acidophilum</i> protein TA0956 | hp |

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|----|-------|-------|---|---|--------------------|----------------------|----------------------|--|--------------------------------|
| | | | | | | Frm2-like (7-66) | 6.52e ⁻³ | (92,18/0,55) tRNA-Thr_ED ; Archaea-specific editing domain of threonyl-tRNA synthetase (91,98/2) | |
| 48 | 33971 | 34651 | + | RNA polymerase sigma 70 factor [<i>Bacillus virus Riggi</i>] | 8e ⁻¹⁶⁴ | sigma70-ECF (80-220) | 6.35e ⁻¹⁶ | spore_sigmaE; RNA polymerase sigma-E factor, Members of this family comprise the Firmicutes lineage endospore formation-specific sigma factor SigE, also called SpoIIGB and sigma (29, 99,95/4,1e ⁻²⁶) | RNA polymerase sigma factor |
| | | | | | | Sigma70_r4 (169-218) | 8.79e ⁻⁸ | | |
| | | | | | | RpoE (79-224) | 1.94e ⁻⁷ | | |
| | | | | | | PRK09647 (79-221) | 1.75e ⁻⁴ | | |
| 49 | 34648 | 34899 | + | hp | | | | | hp |
| 50 | 34899 | 35609 | + | Thymidylate synthase [<i>Bacillus virus Blastoid</i>] | 5e ⁻¹⁶⁸ | thyX (9-232) | 3.98e ⁻⁴¹ | thyX; thymidylate synthase, flavin-dependent (100/1,4e ⁻³³) | Thymidylate synthase |
| | | | | | | Thy1 (21-225) | 2.57e ⁻⁴⁰ | Thy1; Thymidylate synthase complementing protein (100/3,7e ⁻³³) | |
| 51 | 35712 | 36065 | + | Cysteine-rich zinc finger protein [<i>Bacillus virus Riggi</i>] | 5e ⁻⁸² | | | g,54,1,1 (A:) Cysteine-rich domain of the chaperone protein DnaJ (98,13/0,000026) | DnaJ domain-containing protein |
| 52 | 36062 | 36229 | + | Protease [Human immunodeficiency virus 1] | 0.72 | | | PepSY_TM; PepSY-associated TM region 75,89/20 | hp |
| | | | | | | | | PiuB; Uncharacterized iron-regulated membrane protein [Function unknown] (68,96/35) | |
| | | | | | | | | Predicted membrane protein, contains DoH and Cytochrome b-561/ferric reductase transmembrane domains [Signal transduction mechanisms] | |

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| | | | | | | | | (63,6/45) | |
| 53 | 36230 | 36412 | + | hp | | | | Secretory carrier membrane protein [Intracellular trafficking, secretion, and vesicular transport] (75,88/19) | hp |
| | | | | | | | | Phage_holin_3_5; Bacteriophage holin Hol, superfamily III (61,84/41) | |
| | | | | | | | | FeoB; Fe2+ transport system protein B [Inorganic ion transport and metabolism] (61,62/68) | |
| 54 | 36409 | 36585 | + | DNA binding protein [<i>Bacillus</i> virus Blastoid] | 4e ⁻²⁶ | | | | hp |
| 55 | 36798 | 37112 | + | hp | | | | | hp |
| 56 | 37113 | 37697 | + | Deoxynucleoside monophosphate kinase [<i>Bacillus</i> virus Finn] | 4e ⁻¹⁴³ | PRK01184 (15-193) | 1.95e ⁻⁶ | Deoxynucleoside monophosphate kinase Bacteriophage T4 (99,85/2,3e ⁻¹⁹) | Kinase |
| | | | | Phosphate mevalonate kinase [<i>Bacillus</i> phage Leo2] | 3e ⁻¹²⁴ | P-mevalo_kinase (17-122) | 2.43e ⁻⁶ | Pmev_kin_anim; phosphomevalonate kinase, animal type, (99,85/5e ⁻¹⁹) | |
| 57 | 37697 | 38017 | + | hp | | | | | hp |
| 58 | 38080 | 38973 | + | Serine/threonine kinase [<i>Bacillus</i> virus Rigg] | 0.0 | STKc_CK1 (88-149) | 5.59e ⁻³ | d,144,1,7 (A:) Protein kinase C, theta type {Human (<i>Homo sapiens</i>) [TaxId: 9606]} (99,97/2,3e ⁻²⁹) | Serine/threonine kinase |
| 59 | 38970 | 39401 | + | hp | | | | BrnT_toxin; Ribonuclease toxin, BrnT, of type II toxin-antitoxin system (98,54,0,0000021) | hp |

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|----|-------|-------|---|---------------------|-----|----------------|----------------------|--|---|
| | | | | | | | | flg_new; flagellar operon protein (97,96,0,000096) | |
| 60 | 39373 | 39789 | + | hp | | | | zf-C2HClx2C; Zinc-finger 97,1,0,0015 | hp |
| 61 | 39786 | 39917 | + | hp | | | | YycI; Two-component signal transduction system YycFG, regulatory protein YycI [Signal transduction mechanisms], (69,16/3,9) | hp |
| | | | | | | | | Uncharacterized conserved protein, contains TBC domain [Signal transduction mechanisms, General function prediction only] (57,65/26) | |
| 62 | 39904 | 40248 | + | hp | | | | | hp |
| 63 | 40245 | 40478 | + | hp | | | | | hp |
| 64 | 40480 | 40791 | + | hp | | N2227 (26-70) | 7.92e ⁻⁰³ | | hp |
| 65 | 40791 | 41222 | + | hp | | | | YifL; Predicted small periplasmic lipoprotein YifL (98,07/0,0000075) | Predicted signal peptide- containing protein |
| 66 | 41224 | 41376 | + | hp | | | | SPC12; Microsomal signal peptidase 12 kDa subunit (SPC12) (71,08/18) | hp |
| | | | | | | | | Polytopic membrane protein Prominin [General function prediction only] (68,55/17) | |
| 67 | 41470 | 41901 | + | hp | | | | | hp |
| 68 | 42119 | 43402 | + | FtsK/SpoIIIE family | 0.0 | FtsK (190-436) | 1.55e ⁻²² | T7SS_EccC_a; type VII | FtsK/SpoIIIE- |

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|----|-------|-------|---|--|-------------------|-------------------------|----------------------|---|----------------------------------|
| | | | | protein [<i>Bacillus</i> virus Riggi] | | | | secretion protein EccCa (99,87/2,8e ⁻²⁰) | family protein |
| | | | | | | FtsK_SpoIIIE (191-338) | 3.25e ⁻¹² | FtsK; DNA segregation ATPase FtsK/SpoIIIE and related proteins (99,76/1,5e ⁻¹⁶) | |
| | | | | | | PRK10263 (189-379) | 7.78e ⁻¹² | | |
| | | | | | | T7_EssCb_Firm (163-389) | 2.42e ⁻⁹ | | |
| 69 | 43665 | 43940 | + | Replication/relaxation protein [<i>Bacillus</i> phage Leo2] | 9e ⁻⁶³ | | | Replic_Relax; Replication-relaxation (98,97/3,5e ⁻⁹) | Replic_Relax superfamily protein |
| 70 | 43953 | 44366 | + | hp | | | | TrbC; TrbC/VIRB2 family (99,02/5e ⁻⁹) | TrbC/VIRB2 family protein |
| | | | | | | | | VirB2; Type IV secretory pathway, VirB2 components (pilins) (98,21/0,000039) | |
| 71 | 44441 | 44644 | + | Hypothetical protein Riggi_69 [<i>Bacillus</i> virus Riggi] | 2e ⁻⁴² | | | Arc; Arc-like DNA binding domain (97,97/0,000057) | Putative ParG-like protein |
| | | | | Hypothetical protein ANDROMEDA_70 [<i>Bacillus</i> virus Andromeda] | 2e ⁻⁴² | | | a,43,1,1 (A:) Arc repressor { <i>Salmonella bacteriophage</i> P22 [TaxId: 10754]} (97,84/0,00011) | |
| | | | | DNA binding domain protein [<i>Bacillus phage</i> 019DV002] | 4e ⁻²⁵ | gatA (22-43) | 2.83e ⁻⁰³ | a,43,1,1 (A:) Mnt repressor { <i>Salmonella bacteriophage</i> P22 [TaxId: 10754]} (97,75/0,00039) | |
| | | | | DNA binding protein [<i>Bacillus phage</i> 035JT001] | 2e ⁻⁵ | | | RHH_7; Transcriptional regulator, RHH-like, CopG (97,69/0,0002) | |

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|----|-------|-------|---|---|--------------------|-----------------------|----------------------|--|-----------------------------------|
| | | | | DNA binding protein [<i>Bacillus phage</i> 022DV001] | 3e ⁻⁵ | | | a,43,1,3 (A:) Plasmid partition protein ParG { <i>Salmonella</i> <i>enterica</i> [TaxId: 28901]} (97,27/0,0021) | |
| 72 | 45155 | 44664 | - | hp | | | | | hp |
| 73 | 45914 | 45318 | - | DNA polymerase III [<i>Bacillus phage</i> Leo2] | 3e ⁻¹²⁰ | DEDDh (5-158) | 1.94e ⁻³⁸ | PolC; DNA polymerase III, alpha subunit (gram-positive type) (99,86/1,4e ⁻¹⁹) | DEDDh exonuclease |
| | | | | | | EXOIII (2-163) | 2.45e ⁻²⁸ | Predicted exonuclease (99,82/4,5e ⁻¹⁷) | |
| | | | | | | PolC (3-168) | 2.08e ⁻²⁶ | | |
| | | | | | | RNase_T (5- 157) | 3.22e ⁻²⁶ | | |
| 74 | 46624 | 45911 | - | Zinc-dependent metalloprotease [<i>Bacillus virus</i> Blastoid] | 1e ⁻⁴⁷ | | | ArdC; Antirestriction protein ArdC (99,03/3,3e ⁻⁹) | Putative metallopeptidase |
| | | | | Peptidase [<i>Bacillus</i> phage Leo2] | 2e ⁻³⁵ | | | MPTase-PolyVal; Metallopeptidase superfamily domain (99,02/4,3e ⁻⁹) | |
| | | | | | | | | ImmA; Zn-dependent peptidase ImmA, M78 family (98,71/6,1e ⁻⁸) | |
| 75 | 46906 | 46625 | - | hp | | | | | hp |
| 76 | 47212 | 47694 | + | Holliday junction resolvase [<i>Bacillus</i> virus Riggi] | 3e ⁻¹¹² | PHA00159 (59- 129) | 2.03e ⁻⁰⁵ | Endonuclease I (Holliday junction resolvase) (99,12/1,2e ⁻⁹) | Holliday junction resolvase |

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| | | | | T7-like endonuclease [<i>Bacillus</i> virus Finn] | $7e^{-112}$ | Phage_endo_I (59-129) | $2.59e^{-03}$ | Very short patch repair (VSR) endonuclease (98,98/3,3e ⁻⁹) | |
| 77 | 47698 | 47844 | + | hp | | | | b,34,1,1 (A:189-235) Biotin-- [acetyl-CoA-carboxylase] ligase C-terminal domain { <i>Pyrococcus horikoshii</i> [TaxId: 53953]} (75,62/7,5) | hp |
| 78 | 47834 | 47989 | + | hp | | | | e,3,1,1 (A:328-668) Penicillin binding protein 2a (PBP2A), C- terminal domain { <i>Staphylococcus aureus</i> [TaxId: 1280]} (92,85,0,3) | hp |
| | | | | | | | | CheD; Chemotaxis receptor (MCP) glutamine deamidase CheD [Cell motility, Signal transduction mechanisms], (86,32/1,9) | |
| | | | | | | | | CheD ; CheD chemotactic sensory transduction (85,49/3) | |
| | | | | | | | | e,3,1,1 (A:293-692) Penicillin- binding protein 2, PBP2 { <i>Staphylococcus aureus</i> [TaxId: 1280]} (85,24/2,5) | |
| 79 | 48019 | 48171 | + | hp | | | | Transcription factor (contains Zn finger) [Transcription] (97,87/0,0000064) | Putative DNA- binding protein |
| | | | | | | | | CpXC; CpXC protein (97,66/0,000054) | |
| | | | | | | | | Transcription factor BLIMP- 1/PRDI-BF1, contains C2H2- type Zn-finger and SET domains [Transcription] (97,34/0,00009) | |

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| | | | | | | | | Transcriptional repressor SALM [Transcription] (97,3/0,0000097) | |
| 80 | 48173 | 48319 | + | hp | | | | | hp |
| 81 | 48492 | 49166 | + | Putative terminase small subunit [<i>Bacillus</i> phage 056SW001B] | 1e ⁻⁷³ | | | sm_term_P27; phage terminase, small subunit, (92,77/0,94) | Terminase, small subunit |
| | | | | | | | | Terminase_4; Phage terminase, small subunit (91,46/2) | |
| | | | | | | | | COG3747; Phage terminase, small subunit (90,62/2,5) | |

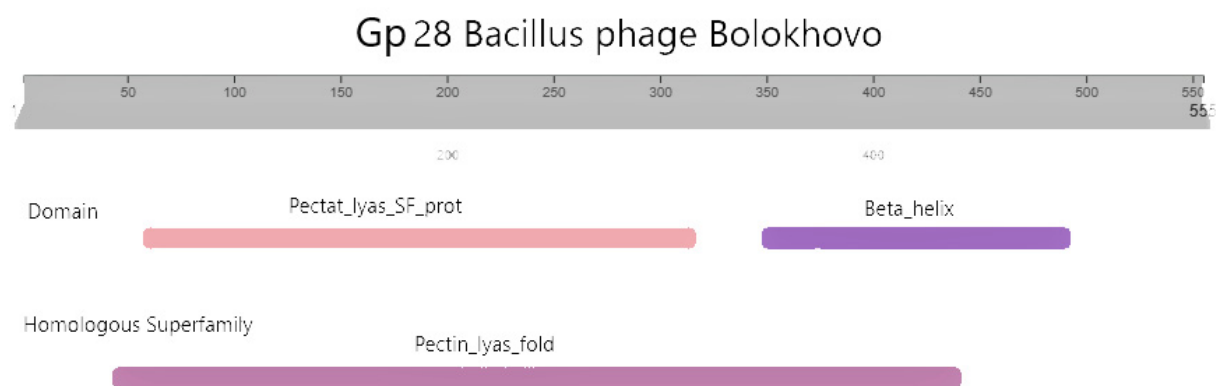


Figure S1. Domain organization of the depolymerase Gp28 of Bolokhovo

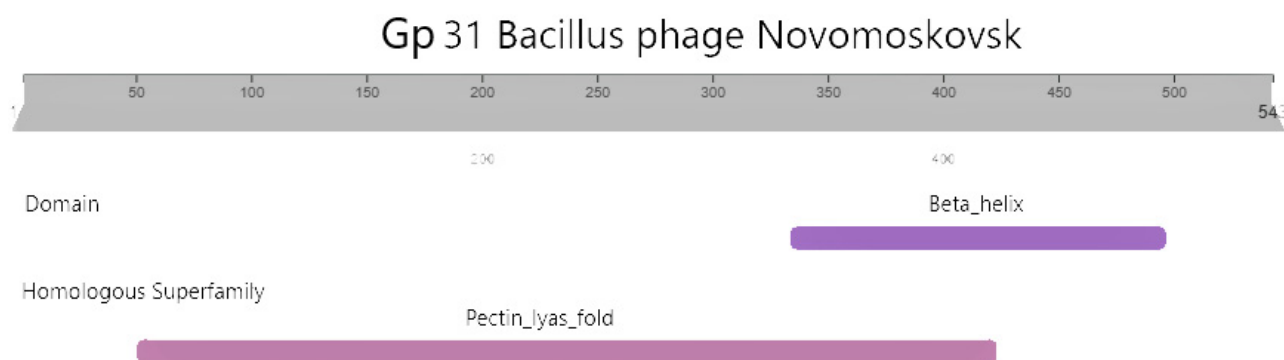


Figure S2. Domain organization of the depolymerase Gp31 of Novomoskovsk