

ID	Phages	Sensitive bacteria*	Sources*	References
NC_015250.1	Acinetobacter phage 133	<i>A. johnsonii</i> (HER 1423)	raw sewage, Quebec, Canada	1,2, 3
NC_014660.1	Acinetobacter phage Ac42	<i>Acinetobacter</i> sp.	therapeutic phage library, Eliava Institute of Bacteriophage, Georgia	3
NC_014661.1	Acinetobacter phage Acj61	<i>A. johnsonii</i>	sewage, New Orlean, USA	3
NC_014663.1	Acinetobacter phage Acj9	<i>A. johnsonii</i>	sewage, New Orlean, USA	3
MH165274.1	Acinetobacter phage AM101	<i>A. baumannii</i> LUH 3712	water, river Moscow, Russia	-
MH713599.1	Acinetobacter phage KARL-1	<i>A. baumannii</i>	pond water, Germany	4
MH460829.1	Acinetobacter phage vB_ApiM_fHyAci03	<i>A. pittii</i>	municipal sewage, Hyvinkää, Finland	5
NC_018087.3	Acinetobacter phage ZZ1	<i>A.baumannii</i>	sewage, fishpond along the Yellow River, China	6,7
NC_015251.1	Aeromonas phage 65	<i>A. salmonicida</i>	water, river “La Petite Mouge”, France	1, 3, 8, 9
KY290955.1	Aeromonas phage 65.2	<i>A. salmonicida</i>	water, river “La Petite Mouge”, France	1, 3, 8, 9, 10
NC_005260.1	Aeromonas phage Aeh1	<i>A. hydrophila</i>	sewage, Oshkosh, USA	3, 11, 12, 13
MG250483.1	Aeromonas phage Ah1	<i>A. hydrophila</i>	wastewater, Russia	-
MF498773.1	Aeromonas phage AS-szw	<i>A. salmonicida</i>	water from river, Guangdong Province, China	14
MF448340.1	Aeromonas phage AS-zj	<i>A. salmonicida</i>	water from river, Guangdong Province, China	14
MH791401.1	Aeromonas phage AsFcp_2	<i>A. salmonicida</i>	sewage	-
MH791398.1	Aeromonas phage Asswx_1	<i>A. salmonicida</i>	sewage	-
MH791414.1	Aeromonas phage Aswh_1	<i>A. salmonicida</i>	freshwater	-
NC_019538.1	Aeromonas phage CC2	<i>A.hydrophila</i>	sewage, China	15
NC_014636.1	Aeromonas phage phiAS5	<i>A. salmonicida</i>	water, Han-river, Korea	16
NC_023688.1	Aeromonas phage PX29	<i>A. salmonicida</i>	sewage, New Orlean, USA	3
NC_008515.1	Bacteriophage RB32	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
NC_029013.1	Citrobacter phage IME-CF2	<i>C. freundii</i>	hospital sewage, China	-
NC_028755.1	Citrobacter phage Margaery	<i>C. freundii</i>	-	-
MH823906.1	Citrobacter phage Maroon	<i>C. freundii</i>	wastewater, Brazos County, USA	18
NC_028857.1	Citrobacter phage Merlin	<i>C. freundii</i>	water, College Station, USA	19
NC_025414.1	Citrobacter phage Miller	<i>C. freundii</i>	sewage, Bryan, USA	20
NC_027331.1	Citrobacter phage Moon	<i>C. freundii</i>	sewage, College Station, USA	21
NC_031057.1	Citrobacter phage vB_CfrM_CfP1	<i>C. freundii</i>	wastewater treatment plant, Frossos, Portugal	22
LT614807.1	Cronobacter phage Pet-CM3-4	<i>Cr. malonaticus</i>	wastewater treatment plant, Petržalka, Slovakia	23

NC_019398.1	Cronobacter phage vB_CsaM_GAP161	<i>Cr. sakazakii</i>	sewage, Guelph, Canada	24
KX431559.1	Cronobacter phage vB_CsaM_leB	<i>Cr. sakazakii</i>	slurry, cattle farmer in Clonakilty, Ireland	25
KX431560.1	Cronobacter phage vB_CsaM_leN	<i>Cr. sakazakii</i>	slurry, cattle farmer in Clonakilty, Ireland	25
MG999954.1	Enterobacter phage myPSH1140	<i>E. cloacae</i>	sewage water treatment plants, India	26
NC_023561.1	Enterobacter phage PG7	<i>E. cloacae</i>	fishpond water, China	-
NC_041980.1	Enterobacter phage phiEap-3	<i>E. aerogenes</i>	sewage wastewater sample, Navy General Hospital, China	27
KT184308.1	Enterobacteria phage Aplg8	<i>E. coli</i> O121:H19	sewage, USA	-
NC_027983.1	Enterobacteria phage AR1 DNA	<i>E. coli</i> O157:H7	fresh manure, Dairy farms in St. Croix County , USA	28
KT184309.1	Enterobacteria phage ATK47	<i>E. coli</i> O26:H11	sewage, USA	-
KT184310.1	Enterobacteria phage ATK48	<i>E. coli</i> O26:H12	sewage, USA	-
NC_019500.1	Enterobacteria phage Bp7	<i>E. coli</i> O78.A	chicken feces, Shandong Province, China	29
NC_014662.1	Enterobacteria phage CC31	<i>E. coli</i> B strain S/6/4	sewage, New Orlean, USA	3
NC_025425.1	Enterobacteria phage GEC-3S	<i>E. coli</i> O104:H4	therapeutic phage library, Eliava Institute of Bacteriophage, Georgia	30
KT184311.1	Enterobacteria phage GiZh	<i>E. coli</i> O111:NM 96-3166	sewage, USA	-
NC_018855.1	Enterobacteria phage HX01	<i>E. coli</i> DM01	duck feces, duck factory, China	31
NC_014260.1	Enterobacteria phage IME08	<i>E. coli</i> strain 8099	hospital sewage, China	32
NC_012741.1	Enterobacteria phage JS10	<i>E. coli</i> K12	feces, diarrhea patient, Bangladesh	33
NC_010105.1	Enterobacteria phage JS98	<i>E. coli</i>	feces, diarrhea patient, Bangladesh	33
NC_012740.1	Enterobacteria phage JSE	<i>E.coli</i> K12	sewage, sewage station, Switzerland	33
KT184312.1	Enterobacteria phage Kha5h	<i>E. coli</i> O103:H2 90-3128	sewage, USA	-
NC_009821.1	Enterobacteria phage Phi1	<i>E. coli</i> K-12 (F+)	therapeutic phage library, Eliava Institute of Bacteriophage, Georgia	34
NC_028847.1	Enterobacteria phage QL01	<i>E. coli</i> DE205B	duck feces, poultry market in Nanjing, China	67
KM606999.1	Enterobacteria phage RB10	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
NC_012638.1	Enterobacteria phage RB14	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
NC_014467.1	Enterobacteria phage RB16	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
MH553563.1	Enterobacteria phage RB18	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
NC_025448.1	Enterobacteria phage RB27	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
NC_025419.1	Enterobacteria phage RB3	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
KM607001.1	Enterobacteria phage RB33	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
NC_007023.1	Enterobacteria phage RB43	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
NC_005066.1	Enterobacteria phage RB49	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
KM606995.1	Enterobacteria phage RB5	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17

NC_012635.1	Enterobacteria phage RB51	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
KM607002.1	Enterobacteria phage RB55	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
KM607003.1	Enterobacteria phage RB59	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
KM606996.1	Enterobacteria phage RB6	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
NC_027979.1	Enterobacteria phage RB68	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
NC_004928.1	Enterobacteria phage RB69	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
KM606997.1	Enterobacteria phage RB7	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
KM606998.1	Enterobacteria phage RB9	<i>E.coli</i>	sewage treatment plants, Long Island, USA	17
NC_000866.4	Enterobacteria phage T4	<i>E.coli</i>	sewage/ fecal material	36,37
KJ477684.1	Enterobacteria phage T4 strain wild	<i>E.coli</i>	sewage/ fecal material	36, 37, 38
HM137666.1	Enterobacteria phage T4T	<i>E.coli</i>	sewage/ fecal material	36,37
MH550421.1	Enterobacteria phage T6	<i>E.coli</i>	sewage/ fecal material	36,37
NC_019399.1	Enterobacteria phage vB_EcoM_ACG-C40	<i>E.coli</i>	sewage, Guelph water treatment plant, Canada	39
MH051915.1	Enterobacteria phage vB_EcoM_IME339	<i>E. coli</i> BL21(DE3)	sewage, State Key Laboratory of Pathogens and Biosecurity, China	40
MH051916.1	Enterobacteria phage vB_EcoM_IME340	<i>E. coli</i> BL21(DE3)	sewage, State Key Laboratory of Pathogens and Biosecurity, China	40
NC_028894.1	Enterobacteria phage vB_EcoM_VR20	<i>E.coli</i> Be	municipal wastewater, Lithuania	41
NC_028925.1	Enterobacteria phage vB_EcoM_VR25	<i>E. coli</i> MH1	municipal wastewater, Lithuania	42
NC_028957.1	Enterobacteria phage vB_EcoM_VR26	<i>E. coli</i> MH1	municipal wastewater, Lithuania	42
NC_028881.1	Enterobacteria phage vB_EcoM_VR5	<i>E.coli</i> Be	sewage, Lithuania	41
NC_014792.1	Enterobacteria phage vB_EcoM-VR7	<i>E.coli</i> Be	sewage, Lithuania	41
MH059636.2	Erwinia phage Cronus	<i>Er. amylovora</i> DSM17948	organic waste, Denmark	-
NC_041863.1	Escherichia coli O157 typing phage 3	<i>E. coli</i> O157:H7	National Microbiology Laboratory, Winnipeg	43
NC_041864.1	Escherichia coli O157 typing phage 6	<i>E. coli</i> O157:H7	National Microbiology Laboratory, Winnipeg	43
MK234886.1	Escherichia phage AnYang	<i>E. coli</i> O157	soil, China	-
NC_029091.1	Escherichia phage APCEc01	<i>E. coli</i> DPC6051	human faecal, Ireland	44

NC_041919.1	Escherichia phage CF2	<i>E. coli</i> CP9	chicken feces, Texas private farm, USA	45
MK327929.1	Escherichia phage D5505	<i>E. coli</i> DSM101114	surface water, Braunschweig, Germany	46
NC_024125.2	Escherichia phage e11/2	<i>E.coli</i> O157:H7	bovine fecal, bovine fecal, Ireland	47,48
NC_041936.1	Escherichia phage ECD7	<i>E. coli</i> O104:H4	chicken excrements, Moscow region, Russia	50,49
NC_025449.1	Escherichia phage ECML-134	<i>E. coli</i> O157:H7	fresh and salt water, water estuary, Georgia	51
MH791409.1	Escherichia phage EcWhh-1	<i>E.coli</i>	freshwater	-
NC_041920.1	Escherichia phage HP3	<i>E. coli</i> CP9	duck/geese feces, Houston parks, USA	45
NC_027349.1	Escherichia phage HY01	<i>E. coli</i> O157:H7	swine fecal, farm at Seoul National University in Suwon, South Korea	52
NC_031047.1	Escherichia phage HY03	<i>Escherichia coli</i> O157:H7	-	-
AP018932.1	Escherichia phage KIT03	<i>Escherichia coli</i> O157:H7	soil, Kyoto poultry farm, Japan	53
NC_021344.2	Escherichia phage Lw1	<i>Escherichia coli</i> BL21(DE3)	contaminant of lysed cells	54
NC_031934.1	Escherichia phage MX01	<i>Escherichia coli</i> DE217	duck feces	-
MH992122.1	Escherichia phage OLB35	<i>Escherichia coli</i>	wastewater treatment facility	-
MK047717.1	Escherichia phage p000v	<i>Escherichia coli</i> O157:H7	wastewater, San Francisco, California	55
MK047718.1	Escherichia phage p000y	<i>Escherichia coli</i> O157:H7	wastewater, San Francisco, California	55
KU925172.1	Escherichia phage PE37	<i>Escherichia coli</i> O157:H7	bovine intestine, retail stores in Fukuoka, Japan	100
LC348379.1	Escherichia phage PP01	<i>Escherichia coli</i> O157:H7	swine stool, Japan	56
MH359124.1	Escherichia phage SF	<i>Escherichia coli</i> O157:H7	sewage facility, Universiti Sains Malaysia campus in Penang, Malaysia	57
NC_028927.1	Escherichia phage slur02	<i>Escherichia coli</i> MG1655	slurry, dairy farm slurry tank in the East Midlands, UK	58
NC_042129.1	Escherichia phage slur03	<i>Escherichia coli</i> MG1655	slurry, dairy farm slurry tank in the East Midlands, UK	58
NC_042130.1	Escherichia phage slur04	<i>Escherichia coli</i> MG1655	slurry, dairy farm slurry tank in the East Midlands, UK	58
NC_028780.1	Escherichia phage slur07	<i>Escherichia coli</i> MG1655	slurry, dairy farm slurry tank in the East Midlands, UK	58
LN881733.1	Escherichia phage slur08	<i>Escherichia coli</i> MG1655	slurry, dairy farm slurry tank in the East Midlands, UK	58
LN881734.1	Escherichia phage slur11	<i>Escherichia coli</i> MG1655	slurry, dairy farm slurry tank in the East Midlands, UK	58
LN881737.1	Escherichia phage slur13	<i>Escherichia coli</i> MG1655	slurry, dairy farm slurry tank in the East Midlands, UK	58
NC_028448.1	Escherichia phage slur14	<i>Escherichia coli</i> MG1655	slurry, dairy farm slurry tank in the East Midlands, UK	58
NC_041990.1	Escherichia phage ST0	<i>Escherichia coli</i> H8	wastewater, Beijing sewage treatment plant, China	59
LC348380.1	Escherichia phage T2	<i>E.coli</i>	sewage/ fecal	36,37
NC_031030.1	Escherichia phage UFV-AREG1	<i>Escherichia coli</i> O157	cowshed wastewater, Brazil	60
MH992510.1	Escherichia phage vB_EcoM_DalCa	<i>E.coli</i>	raw sewage, Frossos wastewater treatment plant, Portugal	-
MK327937.1	Escherichia phage vB_EcoM_G10400	<i>E.coli</i> DSM 103266	pig manure, Hameln, Germany	46

MK327932.1	Escherichia phage vB_EcoM_G2248	<i>E.coli</i> DSM 103255	pig manure, Hameln, Germany	46
MK327933.1	Escherichia phage vB_EcoM_G2285	<i>E.coli</i> DSM 103256	pig manure, Hameln, Germany	46
MK327934.1	Escherichia phage vB_EcoM_G2469	<i>E.coli</i> DSM 103258	pig manure, Hameln, Germany	46
MK327935.1	Escherichia phage vB_EcoM_G2494	<i>E.coli</i> DSM 103259	pig manure, Hameln, Germany	46
MK327936.1	Escherichia phage vB_EcoM_G2540	<i>E.coli</i> DSM 103260	pig manure, Hameln, Germany	46
MK327944.1	Escherichia phage vB_EcoM_G2540-3	<i>E.coli</i> DSM 103260	pig manure, Hameln, Germany	46
MK327940.1	Escherichia phage vB_EcoM_G29	<i>E.coli</i> DSM 103247	pig manure, Hameln, Germany	46
MK327941.1	Escherichia phage vB_EcoM_G37-3	<i>E.coli</i> DSM 103248	pig manure, Hameln, Germany	46
MK327939.1	Escherichia phage vB_EcoM_G4498	<i>E.coli</i> DSM 103261	pig manure, Hameln, Germany	46
MK327945.1	Escherichia phage vB_EcoM_G4500	<i>E.coli</i> DSM 103262	pig manure, Hameln, Germany	46
MK327946.1	Escherichia phage vB_EcoM_G4507	<i>E.coli</i> DSM 103263	pig manure, Hameln, Germany	46
MK327942.1	Escherichia phage vB_EcoM_G50	<i>E.coli</i> DSM 103250	pig manure, Hameln, Germany	46
MK327947.1	Escherichia phage vB_EcoM_G5211	<i>E.coli</i> DSM 103264	pig manure, Hameln, Germany	46
MK327943.1	Escherichia phage vB_EcoM_G53	<i>E.coli</i> DSM 103251	pig manure, Hameln, Germany	46
MK373787.1	Escherichia phage vB_EcoM_G8	<i>E.coli</i> DSM 103243	pig manure, Hameln, Germany	46
MK373779.1	Escherichia phage vB_EcoM_G9062	<i>E.coli</i> DSM 103265	pig manure, Hameln, Germany	46
MH355584.1	Escherichia phage vB_EcoM_JB75	<i>E.coli</i>	raw sewage, Frossos wastewater treatment plant, Portugal	61
NC_024124.2	Escherichia phage vB_EcoM_JS09	<i>Escherichia coli</i> (APEC)	sewage, swine farm in Jiangsu Province, China	62
MK373781.1	Escherichia phage vB_EcoM_KAW1E185	<i>E.coli</i> DSM 103253	clinical wastewater, Braunschweig, Germany	46
MK373782.1	Escherichia phage vB_EcoM_KAW3E185	<i>E.coli</i> DSM 103253	clinical wastewater, Braunschweig, Germany	46
MK373784.1	Escherichia phage vB_EcoM_MM02	<i>E.coli</i> DSM 498	duck feces, Braunschweig, Germany	46

MK373785.1	Escherichia phage vB_EcoM_OE5505	<i>E.coli</i> DSM 101114	surface water, Braunschweig, Germany	46
NC_024794.1	Escherichia phage vB_EcoM_PhAPEC2	<i>Escherichia coli</i> (APEC)	water, rivers and brooks in and around Brussels in the vicinity of poultry houses, Belgium	63
MK373786.1	Escherichia phage vB_EcoM_R5505	<i>E.coli</i> DSM 101114	surface water, Braunschweig, Germany	46
MK373778.1	Escherichia phage vB_EcoM_WFbE185	<i>E.coli</i> DSM 103253	sewage, Wolfenbüttel, Germany	46
MK373775.1	Escherichia phage vB_EcoM_WFK	<i>E.coli</i> DSM 101124	sewage, Wolfenbüttel, Germany	46
MK373774.1	Escherichia phage vB_EcoM_WFL6982	<i>E.coli</i> DSM 101124	sewage, Wolfenbüttel, Germany	46
MG781190.1	Escherichia phage vB_EcoM- fFiEco06	<i>Escherichia coli</i> 123738	municipal wastewater, Finland	64
MG781191.1	Escherichia phage vB_EcoM- fHoEco02	<i>Escherichia coli</i> 123738	hospital wastewater, Helsinki, Finland	64
MG867727.1	Escherichia phage vB_EcoM-G28	<i>E.coli</i>	manure, Germany	-
MK977694.1	Escherichia phage vB_EcoM- Sa45lw	<i>Escherichia coli</i> ATCC 13706	surface water, Salinas produce-growing area, USA	65
NC_031103.1	Escherichia phage vB_EcoM- UFV13	<i>Escherichia coli</i> UFV30	sewage, Viçosa sewerage system, Brasil	66, 101
NC_031928.1	Escherichia phage WG01	<i>Escherichia coli</i> DE017	duck feces, poultry market in Nanjing, China	67
NC_019505.1	Escherichia phage wV7	<i>Escherichia coli</i> O157:H7	human feces/hamburger meat	68,69
MH560358.1	Escherichia virus KFS-EC	<i>Escherichia coli</i> O157:H7	wastewater, South Korea	-
LR027390.1	Escherichia virus vB_Eco_mar005P1	<i>E.coli</i> MG1655	sea water, Great Yarmouth, UK	70
LR027387.1	Escherichia virus vB_Eco_mar005P1 strain vB_Eco_mar006P2	<i>E.coli</i> MG1655	sea water, Great Yarmouth, UK	70
LR027383.1	Escherichia virus vB_Eco_mar005P1 strain vB_Eco_mar007P3	<i>E.coli</i> MG1655	sea water, Great Yarmouth, UK	70
LR027386.1	Escherichia virus vB_Eco_mar005P1 strain vB_Eco_mar008P4	<i>E.coli</i> MG1655	sea water, Great Yarmouth, UK	70

LR027391.1	Escherichia virus vB_Eco_mar005P1 strain vB_Eco_mar009P5	<i>E.coli</i> MG1655	sea water, Great Yarmouth, UK	70
MN022785.1	Escherichia virus VEc20	<i>Escherichia coli</i>	feces and sewage, poultry farm, Russia	-
MG751100.1	Klebsiella phage KP1	<i>Klebsiella pneumoniae</i>	sewage, Chungcheongbuk-do, South Korea	71
KY000080.1	Klebsiella phage KPV15	<i>Klebsiella pneumoniae</i>	clinical material, Russia	-
MN044033.1	Klebsiella phage Marfa	<i>K. pneumoniae</i> 1776c	swine fecal, Texas and Michigan, USA	72
NC_028750.1	Klebsiella phage Matisse	<i>Klebsiella pneumoniae</i>	sewage, College Station, USA	73
MH333064.1	Klebsiella phage Mineola	<i>K. pneumoniae</i>	activated sludge, Bryan municipal wastewater, USA	74
NC_041981.1	Klebsiella phage Miro	<i>K. pneumoniae</i> A1	sewage, College Station, USA	75
NC_031095.1	Klebsiella phage PKO111	<i>Klebsiella oxytoca</i> ATCC 43863	sewage, Suwon sewage treatment facility, South Korea	76
MG746602.1	Klebsiella phage vB_Kpn_F48	<i>K. pneumoniae</i> 12C47	sewage, Florence Careggi University hospital, Italy	77
NC_031087.1	Klebsiella phage vB_KpnM_KpV477	<i>Klebsiella pneumoniae</i> KPB463	clinical sample, Burdenko Neurosurgery Institute, Russia	78
KX078569.1	Morganella phage vB_MmoM_MP1	<i>M. morganii</i>	sewage, Braga wastewater treatment plant, Portugal	79
NC_028940.1	Pectobacterium bacteriophage PM2	<i>P. carotovorum</i> subsp. <i>carotovorum</i>	soil, Chinese cabbage fields in Pyeongchang, South Korea	80
MK310184.1	Phage NC-G	<i>Escherichia coli</i> NC101	human fecal, individuals diagnosed with Crohn's disease, USA	81
MG696114.1	Proteus phage phiP4-3	<i>Proteus penneri</i>	fish, China	-
NC_028762.1	Proteus phage vB_PmiM_Pm5461	<i>Proteus mirabilis</i> 417	wastewater plant raw effluent, Portugal	-
KY971610.1	Pseudomonas phage PspYZU05	<i>Pseudomonas sp.</i>	sewage	-
NC_042044.1	Salmonella phage Melville	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Newport	wastewater, Austin, USA	82
NC_020416.1	Salmonella phage S16	<i>S. enterica</i>	sewage, Gelderland municipal sewage plant, Netherlands	83
NC_027344.1	Salmonella phage STML-198	<i>Salmonella</i>	surface water, Maryland, USA	84
NC_026607.2	Salmonella phage STP4-a	<i>Salmonella Typhimurium</i> ATCC 14028	sewage, Qingdao, China	85
NC_031065.1	Salmonella phage vB_SnwM_CGG4-1	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar Newport	sewage, Guelph Wastewater Treatment Plant, Canada	86
NC_024121.1	Serratia phage PS2	<i>S. marcescens</i> S2	fishpond water	87
NC_025829.1	Shigella phage pSs-1	<i>Shigella sonnei</i> ATCC 25931	water, Hongjecheon stream, South Korea	88

MF327006.1	Shigella phage Sf20	<i>Shigella boydii</i> ; <i>Shigella flexneri</i>	water, Red Cedar River, USA	89
NC_042077.1	Shigella phage Sf21	<i>Shigella flexneri</i> ; <i>Shigella sonnei</i> ; <i>E.coli</i> K12	water, Red Cedar River, USA	89
NC_042039.1	Shigella phage Sf22	<i>Shigella flexneri</i> , <i>Shigella boydii</i> , <i>Shigella dysenteriae</i> , <i>Shigella sonnei</i>	biofilm, buoy in the middle of the Grand River, USA	89
MF158046.1	Shigella phage Sf23	<i>Shigella flexneri</i> , <i>Shigella boydii</i> , <i>Shigella dysenteriae</i>	biofilm, buoy in the middle of the Grand River, USA	89
NC_042078.1	Shigella phage Sf24	<i>Shigella flexneri</i> ; <i>Shigella sonnei</i> ; <i>E.coli</i> K12	water, Red Cedar River, USA	89
MF327009.1	Shigella phage Sf25	<i>Shigella flexneri</i> ; <i>Shigella sonnei</i> ; <i>E.coli</i> K12, <i>Shigella dysenteriae</i>	water, Red Cedar River, USA	89
KX828711.1	Shigella phage SH7	<i>Shigella flexneri</i>	water, wadi of Chotrana, Tunisia	90
NC_031085.1	Shigella phage SHBML-50-1	<i>Shigella sonnei</i>	surface water, Maryland park, USA	102
NC_015457.1	Shigella phage Shfl2	<i>Shigella flexneri</i> 37	sewage water, Brazil	102
NC_030953.1	Shigella phage SHFML-11	<i>Shigella sonnei</i>	therapeutic phage library, Eliava Institute of Bacteriophage, Georgia	102
NC_031011.1	Shigella phage SHFML-26	<i>Shigella sonnei</i>	therapeutic phage library, Eliava Institute of Bacteriophage, Georgia	102
NC_031090.1	Shigella phage SHSML-52-1	<i>Shigella sonnei</i>	surface water, Maryland park, USA	102
NC_014595.1	Shigella phage SP18	<i>Shigella sonnei</i>	water, Gap River, South Korea	91
NC_005083.2	Vibrio phage KVP40	<i>Vibrio parahaemolyticus</i>	polluted sea water, Urado Bay, Japan	92,93
NC_021529.2	Vibrio phage nt-1	<i>Vibrio natriegens</i>	saltmarsh mud, Gloucester County, USA	99
KT919972.1	Vibrio phage phi-Grn1	<i>Vibrio alginolyticus</i>	coastal seawater, Crete, Greece	94
KT919973.1	Vibrio phage phi-ST2	<i>Vibrio alginolyticus</i>	coastal seawater, Crete, Greece	94
MK568540.1	Vibrio phage ValB1_HC	<i>Vibrio alginolyticus</i>	-	-
NC_028829.1	Vibrio phage ValKK3	<i>Vibrio alginolyticus</i>	marine sediment, Kota Kinabalu, Malaysia	103
KU160494.1	Vibrio phage vB_VmeM-32	<i>Vibrio metschnikovii</i> DSM 29715	sediment sample, lake Elmenteita, Kenya	95
NC_023568.1	Vibrio phage VH7D	<i>Vibrio harveyi</i>	seawater, Xiamen abalone farm, China	96
JN849462.1	Vibriophage phi-pp2	<i>Vibrio parahaemolyticus</i>	water, aquaculture waterways around southern Taiwan, Taiwan	97
LR215722.1	Yersinia phage fPS-2	<i>Y. pseudotuberculosis</i> O:1a	pig stools, pig farms Finland	98

NC_027353.1	Yersinia phage phiD1	<i>Yersinia pestis</i>	-	-
NC_027404.1	Yersinia phage PST	<i>Yersinia pseudotuberculosis</i>	-	-

"-" - no data was found

"*" - data were obtained from literature and genome annotation, BioSample database

References

1. Petrov, V. M., Nolan, J. M., Bertrand, C., Levy, D., Desplats, C., Krisch, H. M., and Karam, J. D. (2006). Plasticity of the gene functions for DNA replication in the T4-like phages. *Journal of molecular biology* 361, 46–68. doi: 10.1016/j.jmb.2006.05.071
2. Coffi, H. (1995). *Lysotypie des Acinetobacter*. Master's Thesis. Laval University, Quebec, Canada
3. Petrov, V. M., Ratnayaka, S., Nolan, J. M., Miller, E. S., and Karam, J. D. (2010). Genomes of the T4-related bacteriophages as windows on microbial genome evolution. *Virology journal* 7:292. doi: 10.1186/1743-422X-7-292
4. Jansen, M., Wahida, A., Latz, S., Krüttgen, A., Häfner, H., Buhl, E. M., Ritter, K., and Horz, H. P. (2018). Enhanced antibacterial effect of the novel T4-like bacteriophage KARL-1 in combination with antibiotics against multi-drug resistant *Acinetobacter baumannii*. *Scientific reports* 8:14140. doi: 10.1038/s41598-018-32344-y
5. Pulkkinen, E., Wicklund, A., Oduor, J., Skurnik, M., and Kiljunen, S. (2019). Characterization of vB_ApiM_fHyAci03, a novel lytic bacteriophage that infects clinical *Acinetobacter* strains. *Archives of virology* 164, 2197–2199. doi: 10.1007/s00705-019-04284-z
6. Jin, J., Li, Z. J., Wang, S. W., Wang, S. M., Chen, S. J., Huang, D. H., Zhang, G., Li, Y. H., Wang, X. T., Wang, J., and Zhao, G. Q. (2014). Genome organisation of the *Acinetobacter* lytic phage ZZ1 and comparison with other T4-like *Acinetobacter* phages. *BMC genomics* 15:793. doi: 10.1186/1471-2164-15-793
7. Jin, J., Li, Z. J., Wang, S. W., Wang, S. M., Huang, D. H., Li, Y. H., Ma, Y. Y., Wang, J., Liu, F., Chen, X. D., Li, G. X., Wang, X. T., Wang, Z. Q., and Zhao, G. Q. (2012). Isolation and characterization of ZZ1, a novel lytic phage that infects *Acinetobacter baumannii* clinical isolates. *BMC microbiology* 12:156. doi: 10.1186/1471-2180-12-156
8. Popoff, M. 1971. Étude sur les *Aeromonas salmonicida*, II. Caractérisation des bactériophages actifs sur les «*Aeromonas salmonicida*» et lysotypie. *Annales de Recherche Vétérinaires* 2, 33–45
9. Ackermann, H. W., Dauguet, C., Paterson, W. D., et al. (1985). *Aeromonas* bacteriophages: reexamination and classification. *Ann Inst Pasteur Vir.*136, 175–199
10. Vincent, A. T., Paquet, V. E., Bernatchez, A., Tremblay, D. M., Moineau, S., and Charette, S. J. (2017). Characterization and diversity of phages infecting *Aeromonas salmonicida* subsp. *salmonicida*. *Scientific reports* 7:7054. doi: 10.1038/s41598-017-07401-7

11. Chow, M. S., and Rouf, M. A. (1983). Isolation and Partial Characterization of Two *Aeromonas hydrophila* Bacteriophages. *Applied and environmental microbiology* 45, 1670–1676. doi: 10.1128/AEM.45.5.1670-1676.1983
12. Ackermann, H. W., and Krisch, H. M. (1997). A catalogue of T4-type bacteriophages. *Archives of virology* 142, 2329–2345. doi: 10.1007/s007050050246
13. Tétart, F., Desplats, C., Kutateladze, M., Monod, C., Ackermann, H. W., and Krisch, H. M. (2001). Phylogeny of the major head and tail genes of the wide-ranging T4-type bacteriophages. *Journal of bacteriology* 183, 358–366. doi: 10.1128/JB.183.1.358-366.2001
14. Chen, L., Yuan, S., Liu, Q., Mai, G., Yang, J., Deng, D., Zhang, B., Liu, C., and Ma, Y. (2018). In Vitro Design and Evaluation of Phage Cocktails Against *Aeromonas salmonicida*. *Frontiers in microbiology* 9:1476. doi:10.3389/fmicb.2018.01476
15. Shen, C. J., Liu, Y. J., and Lu, C. P. (2012). Complete Genome Sequence of *Aeromonas hydrophila* Phage CC2. *Journal of virology* 86:10900. doi: 10.1128/JVI.01882-12
16. Kim, J. H., Son, J. S., Choi, Y. J., Choresca, C. H., Jr, Shin, S. P., Han, J. E., Jun, J. W., and Park, S. C. (2012). Complete genome sequence and characterization of a broad-host range T4-like bacteriophage phiAS5 infecting *Aeromonas salmonicida* subsp. *salmonicida*. *Veterinary microbiology* 157, 164–171. doi: 10.1016/j.vetmic.2011.12.016
17. Russell, R. L. (1967). *Speciation among the T-even bacteriophages*. Ph.D. thesis, California Institute of Technology, Pasadena, CA.
18. McDermott, J. R., Shao, Q., O'Leary, C., Kongari, R., and Liu, M. (2019). Complete Genome Sequence of *Citrobacter freundii* Myophage Maroon. *Microbiology resource announcements* 8:e01145-19. doi: 10.1128/MRA.01145-19
19. LeSage, K. C., Hargrove, E. C., Cahill, J. L., Rasche, E. S., and Kutty Everett, G. F. (2015). Complete Genome Sequence of *Citrobacter freundii* Myophage Merlin. *Genome announcements* 3:e01133-15. doi: 10.1128/genomeA.01133-15
20. Hwang, K., Luna, A. J., Hernandez, A. C., and Kutty Everett, G. F. (2015). Complete Genome Sequence of *Citrobacter freundii* Myophage Miller. *Genome announcements* 3:e01425-14. doi: 10.1128/genomeA.01425-14
21. Edwards, G. B., Luna, A. J., Hernandez, A. C., and Kutty Everett, G. F. (2015). Complete Genome Sequence of *Citrobacter freundii* Myophage Moon. *Genome announcements* 3:e01427-14. doi: 10.1128/genomeA.01427-14

- 22.Oliveira, H., Pinto, G., Oliveira, A., Oliveira, C., Faustino, M. A., Briers, Y., Domingues, L., and Azeredo, J. (2016). Characterization and genome sequencing of a *Citrobacter freundii* phage CfP1 harboring a lysin active against multidrug-resistant isolates. *Applied microbiology and biotechnology* 100, 10543–10553. doi: 10.1007/s00253-016-7858-0
- 23.Madurkay, M., Kadličeková, V., Turňa, J., and Drahovska, H. (2019). Bacteriophage application for control of *Cronobacter* in liquid media and in biofilms. *Journal of Food & Nutrition Research* 58, 85-91
- 24.Abbasifar, R., Kropinski, A. M., Sabour, P. M., Ackermann, H. W., Lingohr, E. J., and Griffiths, M. W. (2012). Complete genome sequence of *Cronobacter sakazakii* bacteriophage vB_CsaM_GAP161. *Journal of virology*, 86, 13806–13807. doi: 10.1128/JVI.02546-12
- 25.Endersen, L., Buttmer, C., Nevin, E., Coffey, A., Neve, H., Oliveira, H., Lavigne, R., and O'Mahony, J. (2017). Investigating the biocontrol and anti-biofilm potential of a three phage cocktail against *Cronobacter sakazakii* in different brands of infant formula. *International journal of food microbiology* 253, 1–11. doi: 10.1016/j.ijfoodmicro.2017.04.009
- 26.Manohar, P., Tamhankar, A. J., Lundborg, C. S., and Nachimuthu, R. (2019). Therapeutic Characterization and Efficacy of Bacteriophage Cocktails Infecting *Escherichia coli*, *Klebsiella pneumoniae*, and *Enterobacter* Species. *Frontiers in microbiology* 10:574. doi: 10.3389/fmicb.2019.00574
- 27.Zhao, J., Zhang, Z., Tian, C., Chen, X., Hu, L., Wei, X., Li, H., Lin, W., Jiang, A., Feng, R., Yuan, J., Yin, Z., and Zhao, X. (2019). Characterizing the Biology of Lytic Bacteriophage vB_EaeM_φEap-3 Infecting Multidrug-Resistant *Enterobacter aerogenes*. *Frontiers in microbiology* 10:420. doi: 10.3389/fmicb.2019.00420
- 28.Ronner, A. B., and Cliver, D. O. (1990). Isolation and Characterization of a Coliphage Specific for *Escherichia coli* 0157:H7. *Journal of food protection* 53, 944–947. doi: 10.4315/0362-028X-53.11.944
- 29.Zhang, C., Li, W., Liu, W., Zou, L., Yan, C., Lu, K., and Ren, H. (2013). T4-like phage Bp7, a potential antimicrobial agent for controlling drug-resistant *Escherichia coli* in chickens. *Applied and environmental microbiology*, 79, 5559–5565. doi: 10.1128/AEM.01505-13
- 30.Merabishvili, M., De Vos, D., Verbeken, G., Kropinski, A. M., Vandenheuveld, D., Lavigne, R., Wattiau, P., Mast, J., Ragimbeau, C., Mossong, J., Scheres, J., Chanishvili, N., Vanechoutte, M., and Pirnay, J. P. (2012). Selection and characterization of a candidate therapeutic bacteriophage that lyses the *Escherichia coli* O104:H4 strain from the 2011 outbreak in Germany. *PloS one* 7:e52709. doi: 10.1371/journal.pone.0052709

31. Tang, F., Li, Y., Zhang, W., and Lu, C. (2012). Complete genome sequence of T4-Like *Escherichia coli* bacteriophage HX01. *Journal of virology* 86:13871. doi: 10.1128/JVI.02698-12
32. Jiang, X., Jiang, H., Li, C., Wang, S., Mi, Z., An, X., Chen, J., and Tong, Y. (2011). Sequence characteristics of T4-like bacteriophage IME08 benome termini revealed by high throughput sequencing. *Virology journal* 8:194. doi: 10.1186/1743-422X-8-194
33. Denou, E., Bruttin, A., Barretto, C., Ngom-Bru, C., Brüssow, H., and Zuber, S. (2009). T4 phages against *Escherichia coli* diarrhea: potential and problems. *Virology* 388, 21–30. doi: 10.1016/j.virol.2009.03.009
34. Arbiol, C., Comeau, A. M., Kutateladze, M., Adamia, R., and Krisch, H. M. (2010). Mobile regulatory cassettes mediate modular shuffling in T4-type phage genomes. *Genome biology and evolution* 2, 140–152. doi: 10.1093/gbe/evq006
35. Xu, J., Chen, M., He, L., Zhang, S., Ding, T., Yao, H., Lu, C., and Zhang, W. (2016). Isolation and characterization of a T4-like phage with a relatively wide host range within *Escherichia coli*. *Journal of basic microbiology* 56, 405–421. doi: 10.1002/jobm.201500440
36. Abedon, S. T. (2000). The murky origin of Snow White and her T-even dwarfs. *Genetics*, 155, 481–486
37. Anderson, T. F. (1944). Virus reactions inside of bacterial host cells. *J. Bact*, 47:113
38. Bryson, A. L., Hwang, Y., Sherrill-Mix, S., Wu, G. D., Lewis, J. D., Black, L., Clark, T. A., and Bushman, F. D. (2015). Covalent Modification of Bacteriophage T4 DNA Inhibits CRISPR-Cas9. *mBio* 6:e00648. doi: 10.1128/mBio.00648-15
39. Chibeu, A., Lingohr, E. J., Masson, L., Manges, A., Harel, J., Ackermann, H. W., Kropinski, A. M., and Boerlin, P. (2012). Bacteriophages with the ability to degrade uropathogenic *Escherichia coli* biofilms. *Viruses* 4, 471–487. doi: 10.3390/v4040471
40. Li, P., Lin, H., Mi, Z., Xing, S., Tong, Y., and Wang, J. (2019). Screening of Polyvalent Phage-Resistant *Escherichia coli* Strains Based on Phage Receptor Analysis. *Frontiers in microbiology* 10:850. doi: 10.3389/fmicb.2019.00850
41. Kaliniene, L., Klaus, V., and Truncaite, L. (2010). Low-temperature T4-like coliphages vB_EcoM-VR5, vB_EcoM-VR7 and vB_EcoM-VR20. *Archives of virology* 155, 871–880. doi: 10.1007/s00705-010-0656-6
42. Kaliniene, L., Zajančauskaitė, A., Šimoliūnas, E., Truncaitė, L., and Meškys, R. (2015). Low-temperature bacterial viruses VR - a small but diverse group of *E. coli* phages. *Archives of virology* 160, 1367–1370. doi: 10.1007/s00705-015-2388-0

43. Cowley, L. A., Beckett, S. J., Chase-Topping, M., Perry, N., Dallman, T. J., Gally, D. L., and Jenkins, C. (2015). Analysis of whole genome sequencing for the *Escherichia coli* O157:H7 typing phages. *BMC genomics* 16:271. doi: 10.1186/s12864-015-1470-z
44. Dalmasso, M., Strain, R., Neve, H., Franz, C. M., Cousin, F. J., Ross, R. P., and Hill, C. (2016). Three New *Escherichia coli* Phages from the Human Gut Show Promising Potential for Phage Therapy. *PloS one* 11:e0156773. doi: 10.1371/journal.pone.0156773
45. Green, S. I., Kaelber, J. T., Ma, L., Trautner, B. W., Ramig, R. F., and Maresso, A. W. (2017). Bacteriophages from ExPEC Reservoirs Kill Pandemic Multidrug-Resistant Strains of Clonal Group ST131 in Animal Models of Bacteremia. *Scientific reports* 7:46151. doi: 10.1038/srep46151
46. Korf, I., Meier-Kolthoff, J. P., Adriaenssens, E. M., Kropinski, A. M., Nimtz, M., Rohde, M., van Raaij, M. J., and Wittmann, J. (2019). Still Something to Discover: Novel Insights into *Escherichia coli* Phage Diversity and Taxonomy. *Viruses* 11:454. doi: 10.3390/v11050454
47. Coffey, B., Ross, R. P., O'Flynn, G., O'Sullivan, O., Casey, A., Callanan, M., Coffey, A., and McAuliffe, O. (2014). Complete Genome Sequence of vB_EcoM_112, a T-Even-Type Bacteriophage Specific for *Escherichia coli* O157:H7. *Genome announcements* 2:e00393-14. doi: 10.1128/genomeA.00393-14
48. O'Flynn, G., Ross, R. P., Fitzgerald, G. F., and Coffey, A. (2004). Evaluation of a cocktail of three bacteriophages for biocontrol of *Escherichia coli* O157:H7. *Applied and environmental microbiology* 70, 3417–3424. doi: 10.1128/AEM.70.6.3417-3424.2004
49. Aleshkin, A. V., Rubalskii, E. O., Volozhantsev, N. V., Verevkin, V. V., Svetoch, E. A., Kiseleva, I. A., Bochkareva, S. S., Borisova, O. Y., Popova, A. V., Bogun, A. G., and Afanas'ev, S. S. (2015). A small-scale experiment of using phage-based probiotic dietary supplement for prevention of *E. coli* traveler's diarrhea. *Bacteriophage* 5:e1074329. doi: 10.1080/21597081.2015.1074329
50. Aleshkin, A. V., Volozhantsev, N. V., Svetoch, E. A., Kiseleva, I. A., Rubal'sky, E. O., Afanas'ev, S. S., et al. (2016). Bacteriophages as probiotics: phage-based probiotic dietary supplement in prophylaxis against foodborne infections. *Infekc. Bolezni* 14, 31-40
51. Carter, C. D., Parks, A., Abuladze, T., Li, M., Woolston, J., Magnone, J., Senecal, A., Kropinski, A. M., and Sulakvelidze, A. (2012). Bacteriophage cocktail significantly reduces *Escherichia coli* O157: H7 contamination of lettuce and beef, but does not protect against recontamination. *Bacteriophage* 2, 178–185. doi: 10.4161/bact.22825

52. Lee, H., Ku, H. J., Lee, D. H., Kim, Y. T., Shin, H., Ryu, S., and Lee, J. H. (2016). Characterization and Genomic Study of the Novel Bacteriophage HY01 Infecting Both *Escherichia coli* O157:H7 and *Shigella flexneri*: Potential as a Biocontrol Agent in Food. *PloS one*, 11:e0168985. doi: 10.1371/journal.pone.0168985
53. Pham-Khanh, N. H., Sunahara, H., Yamadeya, H., Sakai, M., Nakayama, T., Yamamoto, H., Truong Thi Bich, V., Miyanaga, K., and Kamei, K. (2019). Isolation, Characterisation and Complete Genome Sequence of a *Tequatrovirus* Phage, *Escherichia* phage KIT03, Which Simultaneously Infects *Escherichia coli* O157:H7 and *Salmonella enterica*. *Current microbiology* 76, 1130–1137. doi: 10.1007/s00284-019-01738-0
54. Kushkina, A. I., Tovkach, F. I., Comeau, A. M., Kostetskii, I. E., Lisovski, I., Ostapchuk, A. M., Voychuk, S. I., Gorb, T. I., and Romaniuk, L. V. (2013). Complete Genome Sequence of *Escherichia* Phage Lw1, a New Member of the RB43 Group of Pseudo T-Even Bacteriophages. *Genome announcements* 1:e00743-13. doi: 10.1128/genomeA.00743-13
55. Howard-Varona, C., Vik, D. R., Solonenko, N. E., Gazitua, M. C., Hobbs, Z., Honaker, R. W., Kinkhabwala, A. A., and Sullivan, M. B. (2018). Whole-Genome Sequences of Phages p000v and p000y, Which Infect the Bacterial Pathogen Shiga-Toxigenic *Escherichia coli*. *Microbiology resource announcements* 7:e01400-18. doi:10.1128/MRA.01400-18
56. Morita, M., Tanji, Y., Mizoguchi, K., Akitsu, T., Kijima, N., and Unno, H. (2002). Characterization of a virulent bacteriophage specific for *Escherichia coli* O157:H7 and analysis of its cellular receptor and two tail fiber genes. *FEMS microbiology letters* 211, 77–83. doi: 10.1111/j.1574-6968.2002.tb11206.x
57. Zaman, S. F. J. (2014). *Isolation and Characterization of Bacteriophage from Raw Sewage Specific for Escherichia Coli O157: H7*. Ph.D. thesis, Universiti Sains Malaysia, Penang, Malaysia
58. Smith, R., O'Hara, M., Hobman, J. L., and Millard, A. D. (2015). Draft Genome Sequences of 14 *Escherichia coli* Phages Isolated from Cattle Slurry. *Genome announcements* 3:e01364-15. doi: 10.1128/genomeA.01364-15
59. Liu, H., Liu, X., and Li, J. (2017). Complete genome of a novel virulent phage ST0 lysing *Escherichia coli* H8. *Standards in genomic sciences* 12:85. doi: 10.1186/s40793-017-0304-9
60. Lopez, M. E., Batalha, L. S., Vidigal, P. M., Albino, L. A., Boggione, D. M., Gontijo, M. T., Bazzolli, D. M., and Mendonca, R. C. (2016). Genome Sequence of the Enterohemorrhagic *Escherichia coli* Bacteriophage UFV-AREG1. *Genome announcements*, 4:e00412-16. doi: 10.1128/genomeA.00412-16

61. Barros, J., Melo, L., Poeta, P., Igrejas, G., Ferraz, M. P., Azeredo, J., and Monteiro, F. J. (2019). Lytic bacteriophages against multidrug-resistant *Staphylococcus aureus*, *Enterococcus faecalis* and *Escherichia coli* isolates from orthopaedic implant-associated infections. *International journal of antimicrobial agents* 54, 329–337. doi: 10.1016/j.ijantimicag.2019.06.007
62. Zhou, Y., Bao, H., Zhang, H., and Wang, R. (2015). Isolation and Characterization of Lytic Phage vB_EcoM_JS09 against Clinically Isolated Antibiotic-Resistant Avian Pathogenic *Escherichia coli* and Enterotoxigenic *Escherichia coli*. *Intervirology* 58, 218–231. doi: 10.1159/000437426
63. Tsonos, J., Oosterik, L. H., Tuntufye, H. N., Klumpp, J., Butaye, P., De Greve, H., Hernalsteens, J. P., Lavigne, R., and Goddeeris, B. M. (2014). A cocktail of in vitro efficient phages is not a guarantee for in vivo therapeutic results against avian colibacillosis. *Veterinary microbiology* 171, 470–479. doi: 10.1016/j.vetmic.2013.10.021
64. Kiljunen, S., Wicklund, A., and Skurnik, M. (2018). Complete Genome Sequences of Two *Escherichia* Phages Isolated from Wastewater in Finland. *Genome announcements* 6:e00401-18. doi: 10.1128/genomeA.00401-18
65. Liao, Y. T., Zhang, Y., Salvador, A., and Wu, V. (2019). Genome Sequence of a T4-like Phage, *Escherichia* Phage vB_EcoM-Sa45lw, Infecting Shiga Toxin-Producing *Escherichia coli* Strains. *Microbiology resource announcements* 8:e00804-19. doi: 10.1128/MRA.00804-19
66. Duarte, V. S., Dias, R. S., Kropinski, A. M., Vidigal, P. M., Sousa, F. O., Xavier, A. S., Silva, C. C., and de Paula, S. O. (2016). Complete Genome Sequence of vB_EcoM-UFV13, a New Bacteriophage Able To Disrupt *Trueperella pyogenes* Biofilm. *Genome announcements*, 4:e01292-16. doi: 10.1128/genomeA.01292-16
67. Chen, M., Zhang, L., Abdelgader, S. A., Yu, L., Xu, J., Yao, H., Lu, C., and Zhang, W. (2017). Alterations in gp37 Expand the Host Range of a T4-Like Phage. *Applied and environmental microbiology*, 83:e01576-17. doi: 10.1128/AEM.01576-17
68. Ahmed, R., Bopp, C., Borczyk, A., and Kasatiya, S. (1987). Phage-typing scheme for *Escherichia coli* O157:H7. *The Journal of infectious diseases* 155, 806–809. doi: 10.1093/infdis/155.4.806
69. Kropinski, A. M., Lingohr, E. J., Moyles, D. M., Chibeu, A., Mazzocco, A., Franklin, K., Villegas, A., Ahmed, R., She, Y. M., & Johnson, R. P. (2012). *Escherichia coli* O157:H7 typing phage V7 is a T4-like virus. *Journal of virology*, 86:10246. doi: 10.1128/JVI.01642-12
70. Michniewski, S., Redgwell, T., Grigonyte, A., Rihtman, B., Aguilo-Ferretjans, M., Christie-Oleza, J., Jameson, E., Scanlan, D. J., and Millard, A. D. (2019).

Riding the wave of genomics to investigate aquatic coliphage diversity and activity. *Environmental microbiology* 21, 2112–2128. doi: 10.1111/1462-2920.14590

71. Kim, Y., Bang, I., Yeon, Y. E., Park, J. Y., Han, B. K., Kim, H., and Kim, D. (2018). Draft genome sequence of lytic bacteriophage KP1 infecting bacterial pathogen *Klebsiella pneumoniae*. *The Microbiological Society of Korea* 54, 152–154.
72. Harb, L., Boeckman, J., Newkirk, H., Liu, M., Gill, J. J., and Ramsey, J. (2019). Complete Genome Sequence of the Novel *Klebsiella pneumoniae* Phage Marfa. *Microbiology resource announcements* 8:e00748-19. doi: 10.1128/MRA.00748-19
73. Provasek, V. E., Lessor, L. E., Cahill, J. L., Rasche, E. S., and Kutty Everett, G. F. (2015). Complete Genome Sequence of Carbapenemase-Producing *Klebsiella pneumoniae* Myophage Matisse. *Genome announcements* 3:e01136-15. doi: 10.1128/genomeA.01136-15
74. Boeckman, J. X., Lessor, L., Gill, J. J., and Liu, M. (2019). Complete Genome Sequence of *Klebsiella pneumoniae* Myophage Mineola. *Microbiology resource announcements*, 8:e00257-19. doi: 10.1128/MRA.00257-19
75. Mijalis, E. M., Lessor, L. E., Cahill, J. L., Rasche, E. S., and Kutty Everett, G. F. (2015). Complete Genome Sequence of *Klebsiella pneumoniae* Carbapenemase-Producing *K. pneumoniae* Myophage Miro. *Genome announcements*, 3:e01137-15. doi: 10.1128/genomeA.01137-15
76. Park, E. A., Kim, Y. T., Cho, J. H., Ryu, S., and Lee, J. H. (2017). Characterization and genome analysis of novel bacteriophages infecting the opportunistic human pathogens *Klebsiella oxytoca* and *K. pneumoniae*. *Archives of virology*, 162, 1129–1139. doi: 10.1007/s00705-016-3202-3
77. Ciacci, N., D'Andrea, M. M., Marmo, P., Demattè, E., Amisano, F., Di Pilato, V., Fraziano, M., Lupetti, P., Rossolini, G. M., and Thaller, M. C. (2018). Characterization of vB_Kpn_F48, a Newly Discovered Lytic Bacteriophage for *Klebsiella pneumoniae* of Sequence Type 101. *Viruses* 10:482. doi: 10.3390/v10090482
78. Komisarova, E. V., Kislichkina, A. A., Krasilnikova, V. M., Bogun, A. G., Fursova, N. K., and Volozhantsev, N. V. (2017). Complete Nucleotide Sequence of *Klebsiella pneumoniae* Bacteriophage vB_KpnM_KpV477. *Genome announcements*, 5:e00694-17. doi: 10.1128/genomeA.00694-17
79. Oliveira, H., Pinto, G., Oliveira, A., Noben, J. P., Hendrix, H., Lavigne, R., Łobocka, M., Kropinski, A. M., and Azeredo, J. (2017). Characterization and genomic analyses of two newly isolated *Morganella* phages define distant

- members among *Tevenvirinae* and *Autographivirinae* subfamilies. *Scientific reports* 7:46157. doi: 10.1038/srep46157
- 80.Lim, J. A., Lee, D. H., and Heu, S. (2015). Isolation and Genomic Characterization of the T4-Like Bacteriophage PM2 Infecting *Pectobacterium carotovorum* subsp. *carotovorum*. *The plant pathology journal* 31, 83–89. doi: 10.5423/PPJ.NT.09.2014.0099
 - 81.Gogokhia, L., Buhrke, K., Bell, R., Hoffman, B., Brown, D. G., Hanke-Gogokhia, C., Ajami, N. J., Wong, M. C., Ghazaryan, A., Valentine, J. F., Porter, N., Martens, E., O'Connell, R., Jacob, V., Scherl, E., Crawford, C., Stephens, W. Z., Casjens, S. R., Longman, R. S., and Round, J. L. (2019). Expansion of Bacteriophages Is Linked to Aggravated Intestinal Inflammation and Colitis. *Cell host & microbe* 25, 285.e8–299.e8. doi: 10.1016/j.chom.2019.01.008
 - 82.Zhang, K., Xie, Y., O'Leary, C. J., Liu, M., and Gill, J. J. (2019). Complete Genome Sequence of *Salmonella enterica* Serovar Newport Myophage Melville. *Microbiology resource announcements* 8:e00255-19. doi: 10.1128/MRA.00255-19
 - 83.Marti, R., Zurfluh, K., Hagens, S., Pianezzi, J., Klumpp, J., and Loessner, M. J. (2013). Long tail fibres of the novel broad-host-range T-even bacteriophage S16 specifically recognize *Salmonella* OmpC. *Molecular microbiology* 87, 818–834. doi: 10.1111/mmi.12134
 - 84.Woolston, J., Parks, A. R., Abuladze, T., Anderson, B., Li, M., Carter, C., Hanna, L. F., Heyse, S., Charbonneau, D., and Sulakvelidze, A. (2013). Bacteriophages lytic for *Salmonella* rapidly reduce *Salmonella* contamination on glass and stainless steel surfaces. *Bacteriophage* 3:e25697. doi: 10.4161/bact.25697
 - 85.Li, M., Li, M., Lin, H., Wang, J., Jin, Y., and Han, F. (2016). Characterization of the novel T4-like *Salmonella enterica* bacteriophage STP4-a and its endolysin. *Archives of virology*, 161, 377–384. doi: 10.1007/s00705-015-2647-0
 - 86.El-DougDoug, N. K., Cucic, S., Abdelhamid, A. G., Brovko, L., Kropinski, A. M., Griffiths, M. W., and Anany, H. (2019). Control of *Salmonella* Newport on cherry tomato using a cocktail of lytic bacteriophages. *International journal of food microbiology* 293, 60–71. doi: 10.1016/j.ijfoodmicro.2019.01.003
 - 87.Teng, T., Zhang, G., Fan, X., Zhang, Z., Zhang, L., Wu, D., Chen, S., Li, Y., and Jin, J. (2018). Complete genome sequence analysis of PS2, a novel T4-like bacteriophage that infects *Serratia marcescens* clinical isolates. *Archives of virology* 163, 1997–2000. doi: 10.1007/s00705-018-3803-0
 - 88.Jun, J. W., Giri, S. S., Kim, H. J., Yun, S. K., Chi, C., Chai, J. Y., Lee, B. C., and Park, S. C. (2016). Bacteriophage application to control the contaminated water with *Shigella*. *Scientific reports* 6:22636. doi: 10.1038/srep22636

89. Doore, S. M., Schrad, J. R., Dean, W. F., Dover, J. A., and Parent, K. N. (2018). *Shigella* Phages Isolated during a Dysentery Outbreak Reveal Uncommon Structures and Broad Species Diversity. *Journal of virology* 92:e02117-17. doi: 10.1128/JVI.02117-17
90. Hamdi, S., Rousseau, G. M., Labrie, S. J., Tremblay, D. M., Kourda, R. S., Ben Slama, K., and Moineau, S. (2017). Characterization of two polyvalent phages infecting *Enterobacteriaceae*. *Scientific reports*, 7:40349. doi: 10.1038/srep40349
91. Kim, K. H., Chang, H. W., Nam, Y. D., Roh, S. W., and Bae, J. W. (2010). Phenotypic characterization and genomic analysis of the *Shigella sonnei* bacteriophage SP18. *Journal of microbiology (Seoul, Korea)* 48, 213–222. doi: 10.1007/s12275-010-0055-4
92. Matsuzaki, S., Tanaka, S., Koga, T., and Kawata, T. (1992). A broad-host-range vibriophage, KVP40, isolated from sea water. *Microbiology and immunology* 36, 93–97. doi: 10.1111/j.1348-0421.1992.tb01645.x
93. Miller, E. S., Heidelberg, J. F., Eisen, J. A., Nelson, W. C., Durkin, A. S., Ciecko, A., Feldblyum, T. V., White, O., Paulsen, I. T., Nierman, W. C., Lee, J., Szczypinski, B., and Fraser, C. M. (2003). Complete genome sequence of the broad-host-range vibriophage KVP40: comparative genomics of a T4-related bacteriophage. *Journal of bacteriology* 185, 5220–5233. doi: 10.1128/jb.185.17.5220-5233.2003
94. Skliros, D., Kalatzis, P. G., Katharios, P., & Flemetakis, E. (2016). Comparative Functional Genomic Analysis of Two *Vibrio* Phages Reveals Complex Metabolic Interactions with the Host Cell. *Frontiers in microbiology* 7:1807. doi: 10.3389/fmicb.2016.01807
95. Akhwale, J. K., Rohde, M., Rohde, C., Bunk, B., Spröer, C., Boga, H. I., Klenk, H. P., and Wittmann, J. (2019). Isolation, characterization and analysis of bacteriophages from the haloalkaline lake Elmenteita, Kenya. *PloS one* 14:e0215734. doi: 10.1371/journal.pone.0215734
96. Luo, Z. H., Yu, Y. P., Jost, G., Xu, W., and Huang, X. L. (2015). Complete genome sequence of a giant *Vibrio* bacteriophage VH7D. *Marine genomics* 24, 293–295. doi: 10.1016/j.margen.2015.10.005
97. Lin, Y. R., and Lin, C. S. (2012). Genome-wide characterization of *Vibrio* phage ϕ pp2 with unique arrangements of the mob-like genes. *BMC genomics* 13:224. doi: 10.1186/1471-2164-13-224
98. Salem, M., Virtanen, S., Korkeala, H., and Skurnik, M. (2015). Isolation and characterization of *Yersinia*-specific bacteriophages from pig stools in Finland. *Journal of applied microbiology* 118, 599–608. doi: 10.1111/jam.12722

99. Comeau, A. M., Arbiol, C., and Krisch, H. M. (2014). Composite conserved promoter-terminator motifs (PeSLs) that mediate modular shuffling in the diverse T4-like myoviruses. *Genome biology and evolution* 6, 1611–1619. doi: 10.1093/gbe/evu129
100. Son, H. M., Duc, H. M., Masuda, Y., Honjoh, K. I., and Miyamoto, T. (2018). Application of bacteriophages in simultaneously controlling *Escherichia coli* O157:H7 and extended-spectrum beta-lactamase producing *Escherichia coli*. *Applied microbiology and biotechnology* 102, 10259–10271. doi: 10.1007/s00253-018-9399-1
101. da Silva Duarte, V., Dias, R. S., Kropinski, A. M., Campanaro, S., Treu, L., Siqueira, C., Vieira, M. S., da Silva Paes, I., Santana, G. R., Martins, F., Crispim, J. S., da Silva Xavier, A., Ferro, C. G., Vidigal, P., da Silva, C. C., and de Paula, S. O. (2018). Genomic analysis and immune response in a murine mastitis model of vB_EcoM-UFV13, a potential biocontrol agent for use in dairy cows. *Scientific reports* 8:6845. doi: 10.1038/s41598-018-24896-w
102. Subramanian, S., Parent, K. N., and Doore, S. M. (2020). Ecology, Structure, and Evolution of *Shigella* Phages. *Annual Review of Virology* 7:1. doi:10.1146/annurev-virology-010320-052547
103. Lal, T. M., Sano, M., Hatai, K., & Ransangan, J. (2016). Complete genome sequence of a giant *Vibrio* phage ValKK3 infecting *Vibrio alginolyticus*. *Genomics data* 8, 37–38. doi: 10.1016/j.gdata.2016.03.002