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Bacteriophage-encoded depolymerases: their diversity and biotechnological applications

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Table S1 – Characteristics of all depolymerases identified in completely sequenced dsDNA phages

<i>Bacillus</i> phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
NST1	HM214492	790	yes	185-419	233	Pectate_lyase_3	PF12708	99,4	1,2E-12	Unclassified
Bobb	YP_009056510	222	yes	5-202	196	DUF867	PF05908	100,0	4,0E-79	M
BigBertha	AGY46593	816	yes	98-466	368	Pectate_lyase_3	PF12708	99,8	6,9E-17	M
Blastoid	AGY46829	561	yes	56-330	274	Pectate_lyase_3	PF12708	99,9	1,3E-21	S
CampHawk	AGY46940	497	yes	366-440	74	Peptidase_S74	PF13884	99,6	6,6E-16	M
	AGY46975	1059	yes	131-492	361	Pectate_lyase_3	PF12708	98,5	8,2E-06	
	AGY46977	720	yes	212-489	277	Pectate_lyase_3	PF12708	99,9	2,8E-21	
	AGY46980	621	yes	15-270	255	Pectate_lyase_3	PF12708	99,9	1,3E-20	
Glittering	AGY47215	573	yes	45-328	283	Pectate_lyase_3	PF12708	99,9	4,0E-21	S
Grass	AGY47298	607	no	9-270	261	Pectate_lyase_3	PF12708	99,8	5,0E-20	Unclassified
Page	AGY47935	581	yes	123-360	237	Pectate_lyase_3	PF12708	99,8	2,0E-19	Unclassified
phiAGATE	AGB62649	610	no	9-287	278	Pectate_lyase_3	PF12708	99,9	9,0E-20	M
	YP_007349243	224	no	5-200	194	DUF867	PF05908	100,0	8.3E-80	
Pony	AGY48254	581	yes	123-388	265	Pectate_lyase_3	PF12708	99,8	4,0E-19	Unclassified
poppyseed	AGY48030	581	yes	123-360	237	Pectate_lyase_3	PF12708	99,8	2,0E-19	Unclassified
Riggi	AGY48191	561	yes	45-330	285	Pectate_lyase_3	PF12708	99,9	1,5E-20	S
Spock	AGY48483	741	yes	17-220	203	Pectate_lyase_3	PF12708	99,9	3,2E-20	M
Staley	AGY48730	892	yes	183-448	265	Pectate_lyase_3	PF12708	99,7	3,4E-15	S
Andromeda	YP_007517493	556	yes	43-318	275	Pectate_lyase_3	PF12708	99,9	4,0E-21	S
B103	Q37893	860	yes	103-332	230	Pectate_lyase_3	PF12708	99,9	4,4E-21	P
				642-860	219	Peptidase_G2	PF11962	100,0	5,6E-84	
Bastille	YP_006907302	278	unknown	2-208	206	Pectate_lyase_3	PF12708	99,7	7,3E-16	M

Bcp1	YP_009031349	279	yes	2-208	206	Pectate_lyase_3	PF12708	99,7	2,4E-01	M
BPS10C	YP_009003154	278	yes	9-208	199	Pectate_lyase_3	PF12708	99,4	6,7E-12	M
BPS13	YP_006907824	278	yes	9-208	199	Pectate_lyase_3	PF12708	99,4	6,6E-12	M
CAM003	YP_009036975	315	yes	39-245	206	Pectate_lyase_3	PF12708	99,7	1,6E-15	M
Curly	YP_007517572	557	yes	43-317	274	Pectate_lyase_3	PF12708	99,9	1,3E-21	S
Eoghan	YP_007517417	557	yes	43-317	274	Pectate_lyase_3	PF12708	99,9	1,3E-20	S
				343-557	214	Pectin lyase-like	SUPFAM0048925	98,2	7,1E-05	
Finn	YP_007517647	543	yes	52-320	268	Pectate_lyase_3	PF12708	99,9	1,9E-20	S
GA_1	NP_073695.1	740	unknown	559-619	60	End_tail_spike	PF12219	98,2	2,3E-06	P
				620-675	55	Peptidase_S74	PF13884	99,0	6,3E-10	
Gemini	AGE60867	556	yes	43-318	275	Pectate_lyase_3	PF12708	99,9	3,1E-21	S
Hakuna	YP_009036526	278	yes	9-208	199	Pectate_lyase_3	PF12708	99,4	1,8E-11	M
Hoody T	YP_009035268	278	yes	2-208	206	Pectate_lyase_3	PF12708	99,7	9,5E-16	M
Megatron	YP_009036150	278	yes	9-208	199	Pectate_lyase_3	PF12708	99,4	1,9E-11	M
MG-B1	YP_008060120	703	yes	121-378	258	Pectate_lyase_3	PF12708	99,8	1,7E-19	S
Nf	ACH57080	861	yes	103-332	216	Pectate_lyase_3	PF12708	99,9	1,5E-21	P
				642-861	217	Peptidase_G2	PF11962	100,0	2,0E-84	
phi105	NP_690774	853	yes	119-350	213	Pectate_lyase_3	PF12708	99,9	6,6E-22	S
				630-850	218	Peptidase_G2	PF11962	100,0	9,3E-86	
	ADF59152	856	yes	122-353	213	Pectate_lyase_3	PF12708	99,9	3,7E-22	
				633-853	218	Peptidase_G2	PF11962	100,0	1,2E-85	
phi29	ACE96035	854	yes	104-333	230	Pectate_lyase_3	PF12708	99,9	5,2E-22	P
				643-854	212	Peptidase_G2	PF11962	100,0	2,4E-80	
PM1	YP_007678034	589	no	12-283	271	Pectate_lyase_3	PF12708	99,8	2,5E-18	S
PZA	AAA88489	854	yes	104-333	230	Pectate_lyase_3	PF12708	99,9	2,8E-21	P
				643-854	212	Peptidase_G2	PF11962	100,0	2,0E-80	
SP10	YP_007003341	596	no	4-277	273	Pectate_lyase_3	PF12708	99,9	2,4E-20	M
	YP_007003328	481	no	9-321	312	Glyco_hydro_32N:	PF00251	100,0	1,9E-70	
				358-440	82	Glyco_hydro_32C:	PF08244	99,5	7,4E-13	

SPO1	YP_002300374	696	yes	206-473	267	Pectate_lyase_3	PF12708	99,9	3,8E-21	M
SPP1	NP_690719	599	unknown	22-293	271	Pectate_lyase_3	PF12708	99,8	2,1E-18	S
	NP_690860	197	no	5-190	184	DUF867	PF05908	100,0	3.4E-78	
taylor	AGE60945	557	yes	43-317	274	Pectate_lyase_3	PF12708	99,9	8,3E-20	S
Troll	YP_008430873	814	yes	120-499	379	Pectate_lyase_3	PF12708	99,8	6,2E-17	M
phiNIT1	YP_008318429	477	no	9-321	312	Glyco_hydro_32N:	PF00251	100,0	1,4E-70	Unclassified
				360-441	81	Glyco_hydro_32C:	PF08244	99,5	1,7E-13	
	YP_008318292	208	Yes	7-199	193	DUF867	PF05908	100.0	1.3E-80	
vB_BceM_Bc431v3	YP_007677121	777	yes	83-462	379	Pectate_lyase_3	PF12708	99,8	8,3E-18	M
Brucella phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
Fz	AHB81145	526	yes	52-133	81	Pectate_lyase_3	PF12708	97,6	9,1E-05	P
Tb a	AEY69698	526	yes	52-133	81	Pectate_lyase_3	PF12708	97,6	9,1E-05	P
Burkholderia phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
BcepMigl	YP_007236804	712	yes	198-453	255	Pectate_lyase_3	PF12708	99,8	1,3E-18	P
Bcep22	NP_944291	688	yes	197-453	256	Pectate_lyase_3	PF12708	99,8	7,1E-19	P
Caulobacter phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
Cr30	AGS80957	394	no	33-353	320	Glyco_hydro_39	PF01229	100,0	1,3E-29	M
Cellulophaga phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size	Class	Database*	Prob	E-value	

					(aa)					
phi10:1	YP_008242013	496	yes	90-305	215	Pec_lyase_C	PF00544	100,0	1,0E-43	S
phi13:1	AGO49035	1245	yes	433-612	179	Lipase_GDSL_3	PF14606	99,5	1,7E-13	S
				851-1060	209	Pec_lyase_C	PF00544	100,0	5,6E-40	
phi13:2	AGO49697	658	yes	265-473	208	Pec_lyase_c	PF00544	100,0	7,3E-43	P
	AGO49696	777	yes	147-324	177	Pectate_lyase_3	PF12708	97,8	4,5E-05	
phi19:2	AGO48665	1248	yes	436-615	179	Lipase_GDSL_3	PF14606	99,5	1,4E-13	S
				854-1063	209	Pec_lyase_C	PF00544	100,0	3,1E-37	
phi19:3	YP_008240873	777	yes	147-385	238	Pectate_lyase_3	PF12708	97,7	7,9E-05	P
phi3:1	AGO49328	1094	yes	701-909	350	Pec_lyase_C	PF00544	100,0	1,6E-37	M
				285-464	179	Lipase_GDSL_3	PF14606	99,9	3,9E-23	
phi38:2	AGO49248	1094	yes	285-464	179	Lipase_GDSL_3	PF14606	99,8	4,8E-18	M
				701-909	208	Pec_lyase_C	PF00544	100,0	8,2E-38	
phi39:1	YP_008242178	677	yes	284-492	208	Pec_lyase_c	PF00544	100,0	1,6E-42	S
phi3ST:2	AGO47740	1130	yes	285-464	179	Lipase_GDSL_3	PF14606	99,8	1,9E-20	M
				701-909	208	Pec_lyase_c	PF00544	100,0	1,2E-37	
phi46:3	YP_008241124	744	yes	114-352	238	Pectate_lyase_3	PF12708	97,9	3,6E-05	P
phi47:1	AGO49746	1130	yes	285-464	179	Lipase_GDSL_3	PF14606	99,8	5,6E-19	M
				701-909	208	Pec_lyase_c	PF00544	100,0	1,2E-37	
phiSM	YP_007675684	1094	no	285-464	179	Lipase_GDSL_3	PF14606	99,8	7,1E-19	M
				701-909	208	Pec_lyase_C	PF00544	100,0	1,1E-37	
phiST	YP_007673458	1248	no	436-615	179	Lipase_GDSL_3	PF14606	99,6	1,1E-14	S
				854-1063	209	Pec_lyase_C	PF00544	100,0	6,3E-40	
Clostridium phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size	Class	Database*	Prob	E-value	

					(aa)					
CpV1	ADR30483	667	unknown	178-402	224	Pectate_lyase_3	PF12708	99,8	7,8E-19	P
phi24R	AEW47853	629	yes	119-348	229	Pectate_lyase_3	PF12708	99,5	5,2E-14	P
phiCP7R	YP_006383591	624	yes	134-358	225	Pectate_lyase_3	PF12708	99,8	5,9E-18	P
phiCPV4	YP_006488624	624	yes	134-358	225	Pectate_lyase_3	PF12708	99,8	3,8E-18	P
phiZP2	YP_006488654	631	yes	141-363	223	Pectate_lyase_3	PF12708	99,8	8,4E-19	P
Cronobacter phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
vB_CsaM_GAP31	YP_006987059	712	yes	136-365	229	Pectate_lyase_3	PF12708	98,9	7,2E-08	M
vB_CsaM_GAP32	YP_006987233	673	no	107-357	250	Pectate_lyase_3	PF12708	98,1	1,0E-05	M
vB_CskP_GAP227	YP_007348361	858	yes	289-537	248	Pectate_lyase_3	PF12708	99,8	2,6E-17	P
Enterobacter phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
CUS-3 provirus	ABQ88383	1013	yes	146-212	67	End_N_terminal	PF12218	99,8	9,3E-21	P
				213-662	449	End_beta_propel	PF12217	100,0	1,3E-172	
				663-817	154	End_tail_spike	PF12219	100,0	8,3E-73	
				818-874	56	Peptidase_S74	PF13884	98,6	5,0E-08	
K1-5	YP_654148	811	yes	30-102	73	End_N_terminal	PF12218	99,4	3,0E-13	P
				103-544	442	End_beta_propel	PF12217	99,7	2,0E-17	
				546-705	159	End_tail_spike	PF12219	100,0	1,4E-52	
				706-761	55	Peptidase_S74	PF13884	99,4	9,7E-14	
	YP_654147	632	yes	27-302	275	Pectate_lyase_3	PF12708	98,2	1,8E-05	
				429-504	76	End_tail_spike	PF12218	99,2	8,5E-11	
				505-563	58	Peptidase_S74	PF13884	99,4	6,6E-14	

K1E	CAJ29458	837	yes	39-102	63	End_N_terminal	PF12218	100,0	4,1E-17	P
				109-563	454	End_beta_propel	PF12217	100,0	2,0E-151	
				564-729	165	End_tail_spike	PF12219	100,0	2,0E-65	
				730-787	57	Peptidase_S74	PF13884	99,2	1,4E-11	
K1F	YP_338127	1064	yes	246-312	67	End_N_terminal	PF12218	99,8	3,5E-18	P
				313-754	442	End_beta_propel	PF12217	100,0	3,0E-135	
				756-910	154	End_tail_spike	PF12219	100,0	2,6E-75	
				911-966	55	Peptidase_S74	PF13884	97,8	2,7E-05	
	CAJ29390	1100	yes	246-312	67	End_N_terminal	PF12218	99,8	3,5E-19	
				313-755	442	End_beta_propel	PF12217	100,0	3,0E-135	
				756-910	154	End_tail_spike	PF12219	100,0	2,1E-75	
				911-966	55	Peptidase_S74	PF13884	97,8	2,2E-05	
phi92	CBY99572	918	yes	76-142	66	End_N_terminal	PF12218	100,0	9,0E-32	M
				143-598	455	End_beta_propel	PF12217	100,0	6,0E-197	
				599-756	157	End_tail_spike	PF12219	100,0	7,9E-62	
				757-814	57	Peptidase_S74	PF13884	99,0	1,9E-10	
	CBY99579	804	yes	231-475	244	Pectate_lyase_3	PF12708	99,8	9,6E-19	
vB_KleM-RaK2	YP_007007685	779	yes	574-652	79	End_tail_spike	PF12219	97,8	3,1E-05	M
				653-711	58	Peptidase_S74	PF13884	99,3	6,7E-13	
Erwinia phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
Ea35-70	YP_009004869	640	unknown	135-375	240	Pectate_lyase_3	PF12708	99,8	2,6E-17	M
Ea9-2	YP_009007463	869	unknown	297-535	238	Pectate_lyase_3	PF12708	99,7	7,1E-16	P

Era103	YP_001039683	657	no	82-316	234	Pectate_lyase_3	PF12708	99,7	8,4E-17	P
PEp14	YP_005098420	928	no	343-583	240	Pectate_lyase_3	PF12708	99,7	2,7E-16	P
phiEa100	CBX45113	657	no	82-317	235	Pectate_lyase_3	PF12708	99,7	1,6E-17	P
phiEa1H	CBX44510	657	no	82-316	234	Pectate_lyase_3	PF12708	99,7	1,6E-16	P
PhiEaH1	YP_009010167	634	no	139-377	238	Pectate_lyase_3	PF12708	99,8	8,6E-18	S
phiEaH2	AFQ96603	605	yes	83-328	245	Pectate_lyase_3	PF12708	99,8	1,2E-17	S
phiEt88	YP_004327331	658	yes	171-522	351	Pectate_lyase_3	PF12708	99,5	6,8E-13	M
vB_EamP-L1	AEJ81510	823	unknown	248-486	238	Pectate_lyase_3	PF12708	99,6	4,3E-15	P
Escherichia phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
ECML-4	AFO10349	1057	yes	529-720	192	Pectate_lyase_3	PF12708	98,2	4,5E-06	Unclassified
K1G	ADA82273	984	yes	167-233	67	End_N_terminal	PF12218	99,9	2,9E-26	S
				234-693	459	End_beta_propel	PF12217	100,0	1,0E-185	
				694-851	157	End_tail_spike	PF12219	100,0	1,9E-59	
				852-909	57	Peptidase_S74	PF13884	99,3	2,9E-12	
K1-ind1	ADA82374	721	yes	162-428	266	Pectate_lyase_3	PF12708	99,6	2,2E-14	S
K1H	ADA82322	984	yes	167-233	67	End_N_terminal	PF12218	99,9	8,4E-26	S
				234-693	459	End_beta_propel	PF12217	100,0	8,0E-187	
				694-851	157	End_tail_spike	PF12219	100,0	2,7E-64	
				852-909	57	Peptidase_S74	PF13884	99,1	8,0E-11	
K1ind3	ADA82474	721	yes	162-428	266	Pectate_lyase_3	PF12708	99,6	1,3E-14	S
PBECO 4	AGC35227	713	no	137-385	248	Pectate_lyase_3	PF12708	99,7	2,1E-16	M
phAPEC8	YP_007348539	921	yes	76-142	67	End_N_terminal	PF12218	96,5	1,1E-31	M
				143-601	458	End_beta_propel	PF12217	100,0	2,0E-196	

				602-759	157	End_tail_spike	PF12219	100,0	1,5E-60	
				760-817	57	Peptidase_S74	PF13884	99,1	8,9E-11	
phAPEC8	YP_007348546	1017	yes	381-632	251	Pectate_lyase_3	PF12708	99,4	2,3E-12	M
vB_EcoP_ACG-C91	YP_006987816	811	unknown	39-102	64	End_N_terminal	PF12218	99,2	1,4 E-17	P
				103-545	442	End_beta_propel	PF12217	100,0	8,0E-169	
				546-705	159	End_tail_spike	PF12219	100,0	2,2E-59	
				706-761	55	Peptidase_S74	PF13884	99,3	5,8E-12	
Klebsiella phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
KP32	YP_003347555	869	yes	296-495	177	Pectate_lyase_3	PF12708	99,9	7,4E-21	P
				770-825	55	Peptidase_S74	PF13884	98,0	6,1E-06	
Lactobacillus phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
phiPYB5	ADA79896	597	yes	303-596	294	Glyco_hydro_66	PF13199	100,0	2,0E-87	S
	ADA79897	271	yes	3-268	266	Glyco_hydro_66	PF13199	100,0	2,3E-88	
Leuconostoc phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
phiLNTR3	YP_009044242	503	no	32-254	222	Pectate_lyase_3	PF12708	99,8	2,0E-18	S
Pantoea phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size	Class	Database*	Prob	E-value	

					(aa)					
LIMElight	YP_007002901	854	yes	282-518	236	Pectate_lyase_3	PF12708	99,6	1,6E-14	P
Prochlorococcus phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
P-SSM2	YP_214529	1094	yes	971-1037	66	Peptidase_S74	PF13884	99,4	1,2E-13	M
P-SSM5	AGN12301	463	no	340-408	68	Peptidase_S74	PF13884	99,6	7,2E-17	M
Pseudomonas phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
Lu11	AFH14728	268	yes	170-220	50	Peptidase_S74	PF13884	99,6	1,1E-16	M
tf	CCE60816	883	yes	384-562	179	Lipase_GDSL_3	PF14606	99,8	9,3E-19	P
phi15	YP_004286222	727	yes	194-496	303	Pectate_lyase_3	PF12708	99,2	6,9E-11	P
Af	YP_007237194	741	yes	207-296	90	Pectate_lyase_3	PF12708	98,1	3,0E-06	P
Rhodococcus phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
ReqiPepy6	ADD80892	542	yes	66-321	255	Pectate_lyase_3	PF12708	99,3	8,6E-12	S
ReqiPoco6	ADD80999	541	yes	64-321	258	Pectate_lyase_3	PF12708	98,1	3,5E-05	S
Salmonella phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
epsilon34	ABA54611	606	yes	151-426	276	Pectate_lyase_3	PF12708	99,7	1,7E-16	P
HK620	NP_112090	710	yes	150-417	267	Pectate_lyase_3	PF12708	99,8	7,5E-18	P

Marshall	AGY47555	1057	yes	529-720	192	Pectate_lyase_3	PF12708	98,2	5,3E-06	M
	AGY47556	698	yes	158-698	541	Pectin lyase-like	SUPFAM	100,0	6,0E-143	
Maynard	AGY47760	1057	yes	529-720	192	Pectate_lyase_3	PF12708	98,2	5,3E-06	M
PVP-SE1	YP_004893855	712	yes	136-379	243	Pectate_lyase_3	PF12708	98,5	3,2E-06	M
SSE-121	AFU63680	712	yes	136-379	243	Pectate_lyase_3	PF12708	98,5	3,2E-06	M
Vi01	YP_004327544	1057	yes	529-720	192	Pectate_lyase_3	PF12708	98,3	4,5E-06	M
PhiSH19	YP_007008117	724	yes	286-520	235	Pectate_lyase_3	PF12708	99,7	1,2E-16	M
Serratia phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
Eta	YP_008130362	724	yes	139-387	214	Pectate_lyase_3	PF12708	99,8	1,5E-17	S
phiMAM1	AFX93502	707	yes	90-341	252	Pectate_lyase_3	PF12708	99,7	5,1E-17	M
	AFX93505	799	yes	162-422	261	Pectate_lyase_3	PF12708	99,6	1,7E-14	
	AFX93507	248	yes	10-159	150	End_tail_spike	PF12219	99,8	8,8E-21	
				160-212	53	Peptidase_S74	PF13884	99,7	5,9E-18	
Shigella phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
Sf6	AAQ12204	623	unknown	160-408	249	Pectate_lyase_3	PF12708	99,9	6,2E-21	P
Staphylococcus phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
37	YP_240092	887	yes	137-368	231	Pectate_lyase_3	PF12708	99,9	1,7E-22	S
				648-877	229	Peptidase_G2	PF11962	100,0	1,8E-87	
6ec	AIA64067	890	yes	133-365	233	Pectate_lyase_3	PF12708	99,9	7,2E-22	S

				645-877	233	Peptidase_G2	PF11962	100,0	1,6E-87	
CNPH82	YP_950618	888	yes	138-369	231	Pectate_lyase_3	PF12708	99,9	9,5E-22	S
				658-886	228	Peptidase_G2	PF11962	100,0	8,9E-88	
PH15	YP_950681	888	yes	138-369	231	Pectate_lyase_3	PF12708	99,9	9,0E-23	S
				658-886	228	Peptidase_G2	PF11962	100,0	5,9E-88	
vB_SepiS-phiIPLA5	AFM73722	888	yes	138-369	232	Pectate_lyase_3	PF12708	99,9	8,4E-23	S
				658-886	229	Peptidase_G2	PF11962	100,0	3,7E-88	
vB_SepiS-phiIPLA7	AFM73788	888	yes	138-368	231	Pectate_lyase_3	PF12708	99,9	1,2E-21	S
				647-879	233	Peptidase_G2	PF11962	100,0	8,2E-88	
vB_SepS_SEP9	AHG23941	892	yes	135-367	233	Pectate_lyase_3	PF12708	99,9	5,7E-22	S
				658-886	229	Peptidase_G2	PF11962	100,0	1,9E-87	
Streptococcus phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
2167	CBW39235	1469	yes	1375-1426	52	Peptidase_S74	PF13884	99,1	2,7E-11	Unclassified
8140	CBW39181	1179	yes	1085-1136	52	Peptidase_S74	PF13884	99,2	7,6E-12	Unclassified
34117	CBW39031	1633	yes	1539-1590	52	Peptidase_S74	PF13884	99,1	3,2E-11	Unclassified
40922	CBW38974	2102	yes	2008-2059	52	Peptidase_S74	PF13884	99,1	7,4E-11	Unclassified
DCC1738	YP_009043178	2130	yes	2036-2087	52	Peptidase_S74	PF13884	99,2	1,3E-11	Unclassified
IC1	YP_009043945	2417	yes	2323-2374	52	Peptidase_S74	PF13884	99,0	1,3E-10	Unclassified
K13	YP_009042723	2107	yes	2013-2064	52	Peptidase_S74	PF13884	99,2	1,1E-11	Unclassified
P9	ABL61072	366	yes	90-366	277	Hyaluronidase_1	PF07212	100,0	8,7E-76	S

phiNIH1	AAL15086	337	yes	65-337	273	Hyaluronidase_1	PF07212	100,0	9,0E-146	S
Spn1	AHN84645	1550	yes	1456-1507	52	Peptidase_S74	PF13884	99,2	8,9E-12	Unclassified
V22	CBW38917	1468	yes	1374-1425	52	Peptidase_S74	PF13884	99,2	1,0E-11	Unclassified
Streptomyces phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
Lika	YP_008050881	448	unknown	337-396	60	Peptidase_S74	PF13884	99,6	5,3E-16	S
phiCAM	AFV51346	370	unknown	271-326	56	Peptidase_S74	PF13884	99,5	1,6E-15	S
phiELB20	AFO10889	425	yes	317-377	61	Peptidase_S74	PF13884	99,5	5,4E-15	S
phiHau3	YP_006906201	439	unknown	334-393	60	Peptidase_S74	PF13884	99,6	6,5E-16	S
phiSASD1	YP_003714746	528	yes	16-283	267	Pectate_lyase_3	PF12708	99,8	9,6E-20	S
				340-525	185	Pectin lyase-like	SUPFAM0047350	98,3	2,9E-05	
R4	YP_006990138	425	unknown	317-377	61	Peptidase_S74	PF13884	99,5	3,2E-15	S
Sujidade	YP_008051427	448	unknown	337-396	60	Peptidase_S74	PF13884	99,6	3,1E-16	S
Zemlya	YP_008060258	448	yes	337-396	60	Peptidase_S74	PF13884	99,5	2,3E-15	S
Xanthomonas phages										
Phage name	Protein ID	Size (aa)	Structural?	HHpred analysis						Phage family
				Query	Size (aa)	Class	Database*	Prob	E-value	
vB_XveM_DIBBI	AEX65697	852	yes	159-402	244	Pectate_lyase_3	PF12708	99,8	7,6E-18	M

*Protein family (Pfam)

Methods

Depolymerase search, activity and database

To identify putative depolymerases, a query of all genes with polymer-degrading activity from dsDNA phages with complete genome sequences deposited in NCBI (<http://www.ncbi.nlm.nih.gov/pubmed>) was first performed. Afterwards, BLASTP searches were conducted to identify other genes from phage origin with high homology, indicating new probable depolymerases. The BLASTP was executed using all standard parameters with an E-value cut-off of 1×10^{-5} .

To confirm depolymerase-related activity, all genes were screened through HHpred webserver (<http://toolkit.tuebingen.mpg.de/hhpred>) using Pfam, InterProScan and COG with an E-value cut-off of 1×10^{-5} and at least 80% of query coverage. The depolymerases activity class was determined according to the best hits given. A database was created, sorting the depolymerases according to their catalytic class, and linking this information with the phage family and host genus, from which the gene was found.