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Title	Things are getting hairy: Enterobacteria bacteriophage vB_PcaM_CBB
Authors	Buttimer, Colin;Hendrix, Hanne;Oliveira, Hugo;Casey, Aidan;Neve, Horst;McAuliffe, Olivia;Ross, R. Paul;Hill, Colin;Noben, Jean-Paul;O'Mahony, Jim;Lavigne, Rob;Coffey, Aidan
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Supplementary S3

Table S1 - Annotation of Enterobacteria phage vB_PcaM_CBB

ORF	Predicted product	start	Stop	Length (aa)	Strand	Start Codon
CBB_1	Hypothetical protein	20	197	55	+	ATG
CBB_2	Hypothetical protein	1427	1615	62	+	ATG
CBB_3	Conserved hypothetical protein	1800	2477	225	+	ATG
CBB_4	Conserved hypothetical protein	2627	2896	89	+	ATG
CBB_5	Conserved hypothetical protein	3032	3316	94	+	ATG
CBB_6	Conserved hypothetical protein	3352	3741	129	+	ATG
CBB_7	Hypothetical protein	3906	3793	57	-	ATG
CBB_8	Hypothetical protein	3965	4117	50	+	ATG
CBB_9	Conserved hypothetical protein	4165	4437	90	+	ATG
CBB_10	Conserved hypothetical protein	4501	4947	148	+	ATG
CBB_11	Conserved hypothetical protein	5024	5479	151	+	ATG
CBB_12	Hypothetical protein	5560	5685	41	+	ATG
CBB_13	Hypothetical protein	5758	5985	75	+	ATG
CBB_14	Conserved hypothetical protein	6059	6481	140	+	ATG
CBB_15	Conserved hypothetical protein	6663	6998	111	+	ATG
CBB_16	Conserved hypothetical protein	7068	7235	55	+	ATG
CBB_17	Conserved hypothetical protein	7319	7498	59	+	ATG
CBB_18	Conserved hypothetical protein	7989	8243	123	+	ATG
CBB_19	Conserved hypothetical protein	7989	8243	84	+	ATG
CBB_20	Hypothetical protein	8248	8406	52	+	ATG
CBB_21	Conserved hypothetical protein	8696	8929	77	+	ATG
CBB_22	Putative membrane protein	8953	9111	52	+	ATG
CBB_23	Conserved hypothetical protein	9123	9326	67	+	ATG
CBB_24	Conserved hypothetical protein	9326	9502	58	+	ATG
CBB_25	Conserved hypothetical protein	9581	9784	67	+	ATG

CBB_26	Conserved hypothetical protein	9814	10164	116	+	ATG
CBB_27	Putative membrane protein	10391	10642	83	+	ATG
CBB_28	Hypothetical protein	10674	10832	52	+	ATG
CBB_29	Structural protein	10841	11716	291	+	ATG
CBB_30	Conserved hypothetical protein	11856	12053	65	+	ATG
CBB_31	Conserved hypothetical protein	12017	12142	41	+	ATG
CBB_32	Hypothetical protein	12132	12326	64	+	ATG
CBB_33	Putative membrane protein	12370	12723	117	+	ATG
CBB_34	Hypothetical protein	12720	13109	129	+	ATG
CBB_35	Conserved hypothetical protein	13181	13372	63	+	ATG
CBB_36	Conserved hypothetical protein	13435	13821	128	+	ATG
CBB_37	Conserved hypothetical protein	13941	14183	80	+	ATG
CBB_38	Structural protein	14240	14758	172	+	ATG
CBB_39	Conserved hypothetical protein	14822	15160	112	+	ATG
CBB_40	Hypothetical protein	15403	15750	115	+	ATG
CBB_41	Conserved hypothetical protein	15841	16059	72	+	ATG
CBB_42	Conserved hypothetical protein	16235	16837	200	+	ATG
CBB_43	Conserved hypothetical protein	17042	17374	110	+	ATG
CBB_44	Conserved hypothetical protein	17584	17826	80	+	ATG
CBB_45	Conserved hypothetical protein	17906	18793	295	+	ATG
CBB_46	Conserved hypothetical protein	18869	19207	112	+	ATG
CBB_47	Conserved hypothetical protein	19411	19641	76	+	ATG
CBB_48	Conserved hypothetical protein	19725	20072	115	+	ATG

CBB_49	Hypothetical protein	20272	20463	63	+	ATG
CBB_50	Conserved hypothetical protein	20533	20709	58	+	ATG
CBB_51	Conserved hypothetical protein	21113	21382	89	+	ATG
CBB_52	Hypothetical protein	21452	22009	185	+	ATG
CBB_53	Conserved hypothetical protein	22520	23107	195	+	ATG
CBB_54	Conserved hypothetical protein	23110	23721	203	+	ATG
CBB_55	Conserved hypothetical protein	23696	24328	210	+	ATG
CBB_56	Conserved hypothetical protein	24459	25058	199	+	ATG
CBB_57	Conserved hypothetical protein	25055	25576	173	+	ATG
CBB_58	Conserved hypothetical protein	25537	26139	200	+	ATG
CBB_59	Conserved hypothetical protein	26146	26559	137	+	ATG
CBB_60	Conserved hypothetical protein	26573	27016	147	+	ATG
CBB_61	Conserved hypothetical protein	27096	27572	158	+	ATG
CBB_62	Conserved hypothetical protein	27576	27746	56	+	ATG
CBB_63	Conserved hypothetical protein	27751	28359	202	+	ATG
CBB_64	Conserved hypothetical protein	28360	29247	295	+	ATG
CBB_65	Conserved hypothetical protein	29231	29551	105	+	ATG
CBB_66	Conserved hypothetical protein	29595	29993	132	+	ATG
CBB_67	Conserved hypothetical protein	30018	30368	116	+	ATG
CBB_68	Putative membrane protein	30409	30729	106	+	ATG
CBB_69	Conserved hypothetical protein	30733	31506	257	+	TTG
CBB_70	Conserved hypothetical protein	31506	32300	264	+	ATG
CBB_71	Conserved hypothetical protein	32990	33514	174	+	ATG

CBB_72	DNA N-6-adenine-methyltransferase	33527	34069	180	+	ATG
CBB_73	cytitidyltransferase	34091	34630	179	+	ATG
CBB_74	Conserved hypothetical protein	34614	34895	93	+	ATG
CBB_75	Conserved hypothetical protein	34942	35490	182	+	ATG
CBB_76	Conserved hypothetical protein	35528	35686	52	+	ATG
CBB_77	Conserved hypothetical protein	35673	36374	233	+	ATG
CBB_78	Putative membrane protein	36371	36574	67	+	ATG
CBB_79	Conserved hypothetical protein	36555	37667	370	+	TTG
CBB_80	Conserved hypothetical protein	37709	38440	243	+	ATG

CBB_81	Conserved hypothetical protein	38485	38784	99	+	ATG
CBB_82	Conserved hypothetical protein	38781	39077	98	+	ATG
CBB_83	RNA ligase 1 and tail fiber attachment catalyst	39142	40290	382	+	ATG
CBB_84	Conserved hypothetical protein	40325	40561	78	+	ATG
CBB_85	Conserved hypothetical protein	40554	40774	74	+	GTG
CBB_86	Conserved hypothetical protein	40791	41015	74	+	ATG
CBB_87	polynucleotide 5'-kinase and 3'-phosphatase	41003	41935	310	+	ATG
CBB_88	Conserved hypothetical protein	41991	42200	69	+	ATG
CBB_89	Putative membrane protein	42213	42380	55	+	ATG
CBB_90	Conserved hypothetical protein	42370	42642	90	+	ATG
CBB_91	Conserved hypothetical protein	42639	42977	112	+	ATG
CBB_92	Putative membrane protein	42979	43206	75	+	ATG
CBB_93	Conserved hypothetical protein	43187	43435	82	+	ATG
CBB_94	Conserved hypothetical protein	43432	43788	118	+	ATG
CBB_95	Conserved hypothetical protein	43788	44033	81	+	ATG
CBB_96	Conserved hypothetical protein	44077	44715	212	+	ATG

CBB_97	putative serine/threonine protein phosphatase	44715	45494	259	+	ATG
CBB_98	Conserved hypothetical protein	45494	45952	152	+	ATG
CBB_99	Conserved hypothetical protein	45963	47201	412	+	ATG
CBB_100	DNA ligase	47228	48643	471	+	ATG
CBB_101	Conserved hypothetical protein	48640	49065	141	+	ATG
CBB_102	metallophosphoesterase	49043	49834	263	+	ATG
CBB_103	Conserved hypothetical protein	49836	50264	142	+	ATG

CBB_104	ATP-dependent Clp protease proteolytic subunit	50278	50970	230	+	ATG
CBB_105	Conserved hypothetical protein	50987	51274	95	+	ATG
CBB_106	Conserved hypothetical protein	51280	51735	151	+	ATG
CBB_107	Conserved hypothetical protein	51781	52335	184	+	ATG
CBB_108	Conserved hypothetical protein	52320	52847	175	+	ATG
CBB_109	Conserved hypothetical protein	52837	53319	160	+	ATG
CBB_110	CMP/dCMP deaminase	53306	53761	151	+	ATG
CBB_111	Putative membrane protein	53763	54032	89	+	ATG
CBB_112	Major tail protein	54740	54084	218	+	ATG
CBB_113	bifunctional nicotinamide mononucleotide adenylyltransferase/ADP-ribose pyrophosphatase	54982	56079	365	+	ATG
CBB_114	Conserved hypothetical protein	56123	56641	172	+	ATG

CBB_115	nicotinamide phosphoribosyltransferase	56702	58189	495	+	ATG
CBB_116	Putative membrane protein	58232	58453	73	+	ATG
CBB_117	Conserved hypothetical protein	58455	59402	315	+	ATG
CBB_118	Structural protein	59615	60061	148	+	ATG
CBB_119	Conserved hypothetical protein	60073	60315	80	+	ATG
CBB_120	putative Sir2-like protein	60328	61119	263	+	ATG
CBB_121	Conserved hypothetical protein	61135	62034	299	+	ATG
CBB_122	Putative membrane protein	62034	62336	100	+	ATG
CBB_123	PhoH family protein	62407	63846	479	+	ATG
CBB_124	Conserved hypothetical protein	63894	64076	60	+	ATG
CBB_125	Conserved hypothetical protein	64251	64943	230	+	ATG
CBB_126	Putative membrane protein	64940	65146	68	+	ATG
CBB_127	Putative membrane protein	65153	65302	49	+	ATG
CBB_128	Conserved hypothetical protein	65377	65922	181	+	ATG

CBB_129	Conserved hypothetical protein	65949	66791	200	+	ATG
CBB_130	Conserved hypothetical protein	66793	67407	204	+	ATG
CBB_131	co-chaperonin GroES	67407	67688	93	+	ATG
CBB_132	tyrosyl-tRNA synthetase	67698	6893	421	+	ATG
CBB_133	Putative lipoprotein	68985	69171	68	+	ATG
CBB_134	Conserved hypothetical protein	69317	69958	213	+	ATG
CBB_135	dCMP deaminase	69948	70313	121	+	ATG
CBB_136	Hypothetical protein	70300	70620	106	+	TTG
CBB_137	Hypothetical protein	70613	71239	208	+	ATG
CBB_138	Conserved hypothetical protein	71229	71486	85	+	ATG
CBB_139	Hypothetical protein	71483	71683	66	+	ATG
CBB_140	Conserved hypothetical protein	71696	72247	183	+	ATG

CBB_141	anaerobic NTP reductase large subunit	72380	74217	611	+	ATG
CBB_142	Hypothetical protein	74304	74621	105	+	ATG
CBB_143	Conserved hypothetical protein	74628	75074	148	+	ATG
CBB_144	Structural protein	75120	75884	254	+	ATG
CBB_145	anaerobic ribonucleoside-triphosphate reductase activating protein	75881	76354	157	+	ATG
CBB_146	Conserved hypothetical protein	76347	76523	58	+	ATG
CBB_147	Conserved hypothetical protein	76602	79310	902	+	ATG
CBB_148	Structural protein	79320	82070	916	+	ATG
CBB_149	Structural protein	82083	84833	916	+	ATG
CBB_150	Conserved hypothetical protein	84966	85526	186	+	ATG
CBB_151	Hypothetical protein	85483	85752	89	+	ATG

CBB_152	putative tRNA-His guanylyltransferase	85749	86528	259	+	ATG
CBB_153	Conserved hypothetical protein	87000	87302	154	+	ATG
CBB_154	Conserved hypothetical protein	87000	87302	100	+	ATG
CBB_155	Conserved hypothetical protein	87310	87789	159	+	ATG
CBB_156	Conserved hypothetical protein	87786	88418	210	+	ATG
CBB_157	putative N-4 cytosine-specific methyltransferase	88427	89287	286	+	ATG
CBB_158	Conserved hypothetical protein	89284	89619	111	+	ATG
CBB_159	nucleotidyltransferase	89628	90878	416	+	ATG
CBB_160	Conserved hypothetical protein	90878	91294	138	+	ATG
CBB_161	Conserved hypothetical protein	91298	91801	167	+	ATG
CBB_162	Conserved hypothetical protein	91791	92360	189	+	GTG

CBB_163	acyl carrier protein	92332	92748	138	+	ATG
CBB_164	Structural protein	92821	93189	122	+	ATG
CBB_165	Structural protein	93186	93500	104	+	ATG
CBB_166	Conserved hypothetical protein	93574	93963	129	+	ATG
CBB_167	Conserved hypothetical protein	93974	94228	84	+	ATG
CBB_168	Conserved hypothetical protein	94890	95255	121	+	ATG
CBB_169	Structural protein	95287	95727	146	+	ATG
CBB_170	Conserved hypothetical protein	95771	96202	143	+	ATG
CBB_171	GTP cyclohydrolase	96192	96695	167	+	GTG
CBB_172	Conserved hypothetical protein	96676	96963	95	+	ATG
CBB_173	thymidine kinase	96976	97545	189	+	ATG
CBB_174	Putative membrane protein	97599	98108	169	+	ATG
CBB_175	Putative membrane protein	98105	98713	202	+	ATG
CBB_176	Conserved hypothetical protein	98710	99069	119	+	ATG
CBB_177	Putative membrane protein	99071	99205	44	+	ATG
CBB_178	Hypothetical protein	99207	99806	199	+	ATG
CBB_179	Hypothetical protein	99808	100128	106	+	ATG
CBB_180	Conserved hypothetical protein	100131	100678	182	+	ATG
CBB_181	RNA ligase	100759	101995	418	+	ATG

CBB_182	Conserved hypothetical protein	101998	102606	202	+	ATG
CBB_183	Structural protein	102737	104251	504	+	ATG
CBB_184	Putative membrane protein	104304	104444	46	+	ATG
CBB_185	Conserved hypothetical protein	104498	104920	140	+	GTG
CBB_186	Conserved hypothetical protein	104913	105488	191	+	ATG
CBB_187	lysozyme	105603	106538	311	+	TTG
CBB_188	sigma 54 modulation protein/ribosomal protein S30EA	106561	106899	112	+	ATG
CBB_189	Conserved hypothetical protein	106983	107384	133	+	ATG
CBB_190	Hypothetical protein	107371	107514	47	+	ATG
CBB_191	Conserved hypothetical protein	107501	107716	71	+	ATG

CBB_192	multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase/ phosphatase	107713	108828	371	+	ATG
CBB_193	nudix hydrolase	108894	109316	140	+	ATG
CBB_194	glutaredoxin	109342	109578	140	+	ATG
CBB_195	Conserved hypothetical protein	109580	109993	137	+	ATG
CBB_196	Conserved hypothetical protein	109996	110340	114	+	ATG
CBB_197	Conserved hypothetical protein	110388	110630	80	+	ATG
CBB_198	Conserved hypothetical protein	110675	111175	166	+	ATG
CBB_199	Conserved hypothetical protein	111202	111531	109	+	ATG
CBB_200	Conserved hypothetical protein	111541	111903	120	+	ATG
CBB_201	Neck protein	111951	112736	261	+	ATG
CBB_202	Conserved hypothetical protein	112774	113028	84	+	ATG

CBB_203	putative deoxynucleoside monophosphate kinase	113067	113708	213	+	ATG
CBB_204	tail sheath monomer	113797	116451	884	+	ATG
CBB_205	Structural protein	116558	117247	229	+	ATG
CBB_206	Structural protein	117331	118107	258	+	ATG
CBB_207	Structural protein	118118	119212	364	+	ATG
CBB_208	head completion protein	119212	119670	152	+	ATG
CBB_209	Conserved hypothetical protein	119672	120235	187	+	ATG
CBB_210	Structural protein	120263	120808	181	+	ATG
CBB_211	Structural protein	120811	121371	186	+	ATG
CBB_212	Structural protein	121384	122820	478	+	ATG
CBB_213	Structural protein	122838	123767	309	+	ATG
CBB_214	Structural protein	123767	124177	136	+	ATG
CBB_215	Conserved hypothetical protein	124181	124555	124	+	ATG
CBB_216	ATPase	124693	126036	447	+	ATG
CBB_217	Putative membrane protein	126078	127430	450	+	ATG

CBB_218	Conserved hypothetical protein	127539	127775	218	+	ATG
CBB_219	Conserved hypothetical protein	127777	128469	230	+	ATG
CBB_220	Conserved hypothetical protein	128469	128777	102	+	ATG
CBB_221	Conserved hypothetical protein	128764	129351	195	+	ATG
CBB_222	Conserved hypothetical protein	129358	129687	109	+	ATG
CBB_223	thymidylate synthase	129650	130579	309	+	ATG
CBB_224	Structural protein	132533	130611	640	-	ATG
CBB_225	Structural protein	133259	132621	212	-	ATG
CBB_226	Long tail fiber proximal subunit	138084	137934	1553	-	ATG
CBB_227	Structural protein	138944	138084	286	-	ATG
CBB_228	Structural protein	140166	139024	380	-	ATG
CBB_229	Structural protein	140272	140769	165	+	ATG
CBB_230	Structural protein	140780	141388	202	+	ATG
CBB_231	Structural protein	141399	142505	368	+	ATG
CBB_232	MutT/NUDIX hydrolase family protein	142976	142509	148	-	ATG
CBB_233	Tail sheath stabilizer and completion protein	144323	142986	445	-	ATG
CBB_234	Structural protein	145816	144320	498	-	ATG

CBB_235	ATP-dependent Clp protease ATP-binding subunit clpA	144320	145816	765	+	ATG
CBB_236	Structural protein	158274	148252	3340	-	ATG
CBB_237	Baseplate wedge	161820	158356	1154	-	ATG
CBB_238	base plate protein	162285	161896	129	-	ATG
CBB_239	baseplate hub subunit and tail lysozyme	162784	162296	162	-	ATG
CBB_240	Baseplate hub subunit and tail lysozyme	165504	162820	894	-	ATG
CBB_241	Structural protein	167891	165504	795	-	ATG
CBB_242	Baseplate wedge protein	168217	167903	104	-	ATG

CBB_243	Structural protein	169931	169071	245	-	ATG
CBB_244	sigma factor for late transcription	169071	169931	286	+	ATG
CBB_245	recombination endonuclease subunit	169918	170949	343	+	ATG
CBB_246	recombination endonuclease subunit	170962	173103	713	+	ATG
CBB_247	Structural protein	173132	173866	244	+	ATG
CBB_248	DNA endonuclease VII	174344	173868	158	-	ATG
CBB_249	Conserved hypothetical protein	175307	175131	58	-	ATG
CBB_250	Structural protein	176185	175328	285	-	ATG
CBB_251	Structural protein	176250	178418	722	+	ATG
CBB_252	portal vertex protein of head	178435	180171	578	+	ATG
CBB_253	Conserved hypothetical protein	180229	180459	76	+	ATG
CBB_254	Structural protein	181414	182043	274	+	ATG
CBB_255	prohead core scaffold and protease	181414	182043	209	+	ATG
CBB_256	Structural protein	182112	183236	274	+	ATG

CBB_257	Precursor of major head subunit	183315	184490	391	+	ATG
CBB_258	Conserved hypothetical protein	184644	185060	138	+	ATG
CBB_259	Conserved hypothetical protein	185089	185400	103	+	ATG
CBB_260	Putative tail fiber protein	185445	187064	539	+	ATG
CBB_261	Tail fiber assembly protein	187057	187470	137	+	ATG
CBB_262	Conserved hypothetical protein	187916	190948	100	+	ATG
CBB_263	DNA polymerase	187916	190948	1010	+	ATG
CBB_264	Conserved hypothetical protein	190964	191476	170	+	ATG
CBB_265	Conserved hypothetical protein	191541	192272	243	+	ATG
CBB_266	putative phosphoesterase or phosphohydrolase	192319	192933	204	+	ATG

CBB_267	Conserved hypothetical protein	192945	193154	69	+	ATG
CBB_268	co-chaperonin GroES	193160	193459	90	+	ATG
CBB_269	Structural protein	193452	194171	239	+	ATG
CBB_270	Structural protein	194219	194875	218	-	ATG
CBB_271	Structural protein	194891	195451	186	-	ATG
CBB_272	RNaseH ribonuclease	195646	196632	328	+	ATG
CBB_273	Conserved hypothetical protein	196632	197132	166	+	ATG
CBB_274	terminase DNA packaging enzyme large subunit	197176	197883	235	+	ATG
CBB_275	DNA terminase packaging enzyme large subunit	197870	199519	549	+	ATG
CBB_276	Structural protein	199556	200845	429	+	ATG
CBB_277	ssDNA binding protein	201073	202116	347	+	ATG
CBB_278	RecA-like protein	202175	203305	376	+	ATG

CBB_279	Conserved hypothetical protein	203307	203771	154	+	ATG
CBB_280	putative DNA polymerase III epsilon subunit	203817	204662	281	+	ATG
CBB_281	NA-DNA + DNA-DNA helicase	204685	206169	494	+	ATG
CBB_282	Conserved hypothetical protein	204685	206169	145	+	ATG
CBB_283	Conserved hypothetical protein	206670	207173	167	+	ATG
CBB_284	Conserved hypothetical protein	207173	208018	281	+	ATG
CBB_285	Conserved hypothetical protein	208005	208724	239	+	ATG
CBB_286	Structural protein	208721	209068	115	+	ATG
CBB_287	Putative membrane protein	209034	209684	216	+	ATG
CBB_288	Conserved hypothetical protein	209668	210021	117	-	ATG
CBB_289	Structural protein	210079	211050	323	+	ATG
CBB_290	putative DNA primase	211113	212159	348	+	ATG
CBB_291	DNA primase-helicase	212167	213663	498	+	ATG
CBB_292	Structural protein	213666	213935	89	+	ATG

CBB_293	Conserved hypothetical protein	213937	214095	52	+	ATG
CBB_294	Structural protein	214097	214495	132	+	ATG
CBB_295	Conserved hypothetical protein	214541	215485	314	+	ATG
CBB_296	Conserved hypothetical protein	215485	215703	72	+	ATG
CBB_297	Conserved hypothetical protein	215700	216503	267	+	ATG
CBB_298	Structural protein	216536	217180	214	+	ATG
CBB_299	Structural protein	217193	217528	111	+	ATG
CBB_300	Restriction endonuclease type II-like	217568	218269	233	+	ATG
CBB_301	Conserved hypothetical protein	218274	218825	183	+	ATG
CBB_302	Structural protein	218854	219432	192	+	ATG
CBB_303	ribonucleotide-diphosphate reductase alpha subunit	219508	221838	776	+	ATG
CBB_304	Conserved hypothetical protein	221881	222054	257	+	ATG
CBB_305	ribonucleotide-diphosphate reductase subunit beta	222664	223785	373	+	ATG
CBB_306	Putative membrane protein	223824	224012	62	+	ATG
CBB_307	Conserved hypothetical protein	224073	224306	77	+	ATG
CBB_308	Structural protein	224318	224698	126	+	ATG

CBB_309	Conserved hypothetical protein	224698	225414	238	+	ATG
CBB_310	Structural protein	225436	226089	217	-	ATG
CBB_311	Putative membrane protein	226101	226811	236	-	ATG
CBB_312	Putative membrane protein	226944	227318	124	+	ATG
CBB_313	dihydrofolate reductase	227315	227833	172	+	ATG
CBB_314	ribonuclease H	227833	228267	144	+	ATG
CBB_315	DNA helicase Dda	228264	229604	446	+	ATG
CBB_316	Structural protein	229672	230217	181	+	ATG
CBB_317	Conserved hypothetical protein	230236	230430	64	+	ATG

CBB_318	translation initiation factor IF-3	230504	231010	168	+	ATG
CBB_319	ATP-dependent Clp protease	231071	231604	177	+	ATG
CBB_320	Structural protein	231666	232199	177	+	ATG
CBB_321	Structural protein	231189	233799	536	+	ATG
CBB_322	Structural protein	233799	236342	847	+	ATG
CBB_323	Putative membrane protein	236433	236717	94	+	ATG
CBB_324	DNA gyrase subunit B	236813	238786	657	+	ATG

CBB_325	DNA topoisomerase II	238837	240243	468	+	ATG
CBB_326	Structural protein	240331	243014	789	+	ATG
CBB_327	Conserved hypothetical protein	242709	243014	101	+	ATG
CBB_328	DNA polymerase III alpha subunit	242974	243492	172	+	ATG
CBB_329	Conserved hypothetical protein	243539	243913	124	+	ATG
CBB_330	Conserved hypothetical protein	243924	244244	106	+	ATG
CBB_331	Conserved hypothetical protein	244288	244578	96	+	ATG
CBB_332	sliding clamp loader subunit	244581	245534	317	+	ATG
CBB_333	Conserved hypothetical protein	245543	246163	206	+	ATG
CBB_334	Structural protein	246221	246790	189	+	ATG
CBB_335	Structural protein	246790	247473	227	+	ATG
CBB_336	Conserved hypothetical protein	247473	248267	264	+	ATG
CBB_337	Conserved hypothetical protein	248404	248943	179	+	ATG
CBB_338	Conserved hypothetical protein	248977	249177	66	+	ATG
CBB_339	Conserved hypothetical protein	249236	250432	398	+	ATG

CBB_340	toxic ion resistance protein	250525	251667	380	+	ATG
CBB_341	Conserved hypothetical protein	251734	252066	110	+	ATG
CBB_342	putative metallopeptidase	252066	252740	224	+	ATG
CBB_343	Putative membrane protein	252797	253894	365	+	ATG
CBB_344	Structural protein	253891	254445	184	+	ATG
CBB_345	Conserved hypothetical protein	254558	254737	59	+	ATG
CBB_346	Putative membrane protein	254749	255096	115	+	ATG
CBB_347	Conserved hypothetical protein	255145	255777	210	+	ATG
CBB_348	Conserved hypothetical protein	255777	256262	161	+	ATG
CBB_349	Conserved hypothetical protein	256322	256046	574	+	ATG
CBB_350	Hypothetical protein	258785	259024	79	+	ATG
CBB_351	Conserved hypothetical protein	259027	259467	146	+	ATG
CBB_352	Conserved hypothetical protein	259469	259672	67	+	ATG
CBB_353	Conserved hypothetical protein	259672	260019	115	+	ATG
CBB_354	Conserved hypothetical protein	260021	260335	104	+	ATG
CBB_355	Hypothetical protein	260322	260672	116	+	ATG
CBB_356	Conserved hypothetical protein	260659	261378	239	+	ATG
CBB_357	Conserved hypothetical protein	361368	261616	82	+	ATG
CBB_358	Conserved hypothetical protein	361621	261815	64	+	ATG
CBB_359	Conserved hypothetical protein	261832	262851	339	+	ATG
CBB_360	Conserved hypothetical protein	262861	263232	123	+	ATG

CBB_361	nicotinamide-nucleotide adenylyltransferase	263250	264299	349	+	ATG
CBB_362	nicotinamide mononucleotide transporter PnuC	264296	265099	267	+	ATG
CBB_363	Hypothetical protein	365101	265212	103	+	ATG
CBB_364	Conserved hypothetical protein	265432	265674	80	+	ATG
CBB_365	Conserved hypothetical protein	265721	265924	67	+	ATG
CBB_366	Conserved hypothetical protein	265921	266358	145	+	ATG
CBB_367	Hypothetical protein	266355	266660	101	+	ATG
CBB_368	Conserved hypothetical protein	266657	266968	103	+	ATG
CBB_369	Conserved hypothetical protein	266977	267321	114	+	ATG
CBB_370	Structural protein	267305	267658	117	+	ATG
CBB_371	Conserved hypothetical protein	267658	268017	119	+	ATG
CBB_372	Conserved hypothetical protein	268028	268333	101	+	ATG
CBB_373	Conserved hypothetical protein	268330	268779	149	+	ATG
CBB_374	Conserved hypothetical protein	268895	269311	138	+	ATG

CBB_375	Conserved hypothetical protein	269337	270125	275	+	ATG
CBB_376	Conserved hypothetical protein	270125	271390	421	+	ATG
CBB_377	Conserved hypothetical protein	271430	272620	396	+	ATG
CBB_378	Conserved hypothetical protein	272817	273290	157	+	ATG
CBB_379	Conserved hypothetical protein	273314	273646	110	+	ATG
CBB_380	putative 5'3'-deoxyribonucleotidase	273650	274237	195	+	ATG
CBB_381	Conserved hypothetical protein	274231	274755	184	+	ATG
CBB_382	Conserved hypothetical protein	274908	275486	192	+	ATG
CBB_383	Conserved hypothetical protein	276036	276362	108	+	ATG
CBB_384	Conserved hypothetical protein	276721	276870	49	+	ATG
CBB_385	Conserved hypothetical protein	276870	277124	84	+	ATG

CBB_386	Conserved hypothetical protein	277124	277815	263	+	ATG
CBB_387	Conserved hypothetical protein	277908	278285	125	+	GTG
CBB_388	Conserved hypothetical protein	278242	278703	153	+	ATG
CBB_389	Conserved hypothetical protein	278703	278972	89	+	ATG
CBB_390	Conserved hypothetical protein	278969	279484	171	+	ATG
CBB_391	Hypothetical protein	279438	279893	151	+	GTG
CBB_392	peptidyl-tRNA hydrolase	279874	280302	142	+	ATG
CBB_393	Putative membrane protein	280575	280934	119	+	ATG
CBB_394	Conserved hypothetical protein	280924	281157	77	+	ATG
CBB_395	Hypothetical protein	281139	281300	53	+	ATG
CBB_396	Conserved hypothetical protein	281303	281557	84	+	ATG
CBB_397	Conserved hypothetical protein	281564	281926	120	+	ATG
CBB_398	Conserved hypothetical protein	281910	282374	154	+	ATG

CBB_399	DNA-cytosine methyltransferase	282396	283256	286	+	ATG
CBB_400	Conserved hypothetical protein	283249	283560	103	+	ATG
CBB_401	Conserved hypothetical protein	283563	283904	113	+	ATG
CBB_402	Conserved hypothetical protein	283901	284605	234	+	ATG
CBB_403	Conserved hypothetical protein	284616	284972	118	+	ATG
CBB_404	Hypothetical protein	284976	285500	174	+	ATG
CBB_405	Conserved hypothetical protein	285502	285699	65	+	ATG
CBB_406	Conserved hypothetical protein	286108	286341	77	+	TTG
CBB_407	Conserved hypothetical protein	286338	286478	46	+	ATG
CBB_408	Conserved hypothetical protein	286581	286904	107	+	TTG
CBB_409	Conserved hypothetical protein	286950	287381	143	+	ATG
CBB_410	Conserved hypothetical protein	287391	287585	64	+	ATG
CBB_411	Conserved hypothetical protein	287587	287937	116	+	ATG
CBB_412	Conserved hypothetical protein	287948	288283	111	+	ATG
CBB_413	Hypothetical protein	288587	288790	67	+	ATG
CBB_414	Hypothetical protein	288793	288909	38	+	ATG
CBB_415	Putative membrane protein	288912	289204	97	+	ATG
CBB_416	Hypothetical protein	289202	289468	88	+	ATG
CBB_417	Conserved hypothetical protein	289425	289715	96	+	ATG
CBB_418	Conserved hypothetical protein	289786	289986	66	+	ATG
CBB_419	Conserved hypothetical protein	290507	290740	77	+	ATG

CBB_420	HNH	290851	291255	134	+	ATG
CBB_421	Putative membrane protein	291456	291608	50	+	ATG
CBB_422	Conserved hypothetical protein	291615	291815	66	+	ATG
CBB_423	Putative membrane protein	291815	292030	71	+	ATG
CBB_424	Putative membrane protein	292027	292224	65	+	ATG
CBB_425	Conserved hypothetical protein	292224	292664	146	+	ATG
CBB_426	Hypothetical protein	292771	292983	70	+	ATG
CBB_427	Hypothetical protein	292983	293228	81	+	ATG
CBB_428	Hypothetical protein	293231	293458	75	+	ATG
CBB_429	Hypothetical protein	293458	293718	86	+	ATG
CBB_430	Hypothetical protein	293781	293984	67	+	ATG
CBB_431	Conserved hypothetical protein	293985	294785	266	+	ATG
CBB_432	Hypothetical protein	294787	295089	100	+	ATG
CBB_433	Conserved hypothetical protein	295082	295489	135	+	ATG
CBB_434	Hypothetical protein	295486	295713	75	+	ATG
CBB_435	Conserved hypothetical protein	295860	296153	97	+	ATG
CBB_436	Conserved hypothetical protein	296228	296510	93	+	ATG
CBB_437	Conserved hypothetical protein	296513	296710	65	+	ATG
CBB_438	Conserved hypothetical protein	296694	297059	121	+	ATG
CBB_439	Conserved hypothetical protein	297059	297415	118	+	ATG
CBB_440	Conserved hypothetical protein	297566	297799	77	+	ATG
CBB_441	Hypothetical protein	287796	298419	207	+	ATG
CBB_442	Putative membrane protein	298580	298416	54	-	ATG
CBB_443	Putative membrane protein	298638	299012	124	+	ATG
CBB_444	Conserved hypothetical protein	299204	299788	194	+	ATG

CBB_445	Conserved hypothetical protein	299807	300313	168	+	ATG
CBB_446	Conserved hypothetical protein	300462	300677	71	+	ATG
CBB_447	Conserved hypothetical protein	300741	300983	80	+	ATG
CBB_448	Putative membrane protein	300996	301466	156	+	ATG
CBB_449	Hypothetical protein	301822	301499	107	-	TTG
CBB_450	Conserved hypothetical protein	301908	302054	48	+	ATG
CBB_451	Conserved hypothetical protein	302871	303272	133	+	TTG
CBB_452	Conserved hypothetical protein	303296	303505	69	+	ATG
CBB_453	Conserved hypothetical protein	303601	303825	74	+	ATG
CBB_454	Conserved hypothetical protein	303825	304223	132	+	ATG
CBB_455	Conserved hypothetical protein	304960	305559	199	+	ATG
CBB_456	Conserved hypothetical protein	305594	305947	117	+	GTG
CBB_457	Conserved hypothetical protein	306246	306680	144	+	GTG
CBB_458	Conserved hypothetical protein	306761	307072	103	+	ATG
CBB_459	Conserved hypothetical protein	307418	307648	76	+	ATG
CBB_460	Hypothetical protein	307810	308058	82	+	ATG
CBB_461	Conserved hypothetical protein	308384	308710	108	+	ATG
CBB_462	Conserved hypothetical protein	308798	309034	78	+	ATG
CBB_463	Conserved hypothetical protein	309027	309512	161	+	ATG
CBB_464	Conserved hypothetical protein	309514	309717	67	+	ATG
CBB_465	Hypothetical protein	309819	310202	127	+	ATG
CBB_466	Conserved hypothetical protein	310195	310458	87	+	ATG
CBB_467	Conserved hypothetical protein	310740	310958	72	+	ATG

CBB_468	Conserved hypothetical protein	310951	311301	116	+	ATG
CBB_469	Conserved hypothetical protein	311332	311727	131	+	ATG
CBB_470	Conserved hypothetical protein	311949	312266	105	+	ATG
CBB_471	Conserved hypothetical protein	312370	312621	83	+	GTG
CBB_472	Conserved hypothetical protein	312784	313227	147	+	ATG
CBB_473	Conserved hypothetical protein	313316	313441	41	+	ATG
CBB_474	Conserved hypothetical protein	313431	313574	47	+	ATG
CBB_475	Conserved hypothetical protein	313561	313809	82	+	ATG
CBB_476	PrlF antitoxin like protein	313917	314393	158	+	ATG
CBB_477	Conserved hypothetical protein	314383	314901	172	+	ATG
CBB_478	Conserved hypothetical protein	314891	315019	42	+	ATG
CBB_479	Putative membrane protein	315019	315333	104	+	ATG
CBB_480	Putative membrane protein	315333	315671	112	+	ATG
CBB_481	Putative lipoprotein	315671	315988	105	+	ATG
CBB_482	Putative membrane protein	315998	316297	99	+	ATG
CBB_483	Conserved hypothetical protein	316356	316493	45	+	AAG
CBB_484	Conserved hypothetical protein	316468	316671	67	+	ATG
CBB_485	Conserved hypothetical protein	316707	317192	161	+	ATG
CBB_486	Hypothetical protein	317245	317511	88	+	ATG
CBB_487	Putative lipoprotein	317511	317957	148	+	ATG
CBB_488	Conserved hypothetical protein	318005	318136	43	+	ATG
CBB_489	Conserved hypothetical protein	318191	318814	207	+	GTG
CBB_490	Conserved hypothetical protein	318898	319257	119	+	ATG
CBB_491	Conserved hypothetical protein	319369	319557	62	+	ATG
CBB_492	Conserved hypothetical protein	319565	319762	65	+	ATG
CBB_493	Hypothetical protein	319847	320068	73	+	ATG

CBB_494	Structural protein	320745	321431	228	+	ATG
CBB_495	S-adenosyl-L-methionine-dependent methyltransferase	321487	322026	179	+	ATG
CBB_496	Structural protein	323175	322042	377	+	ATG
CBB_497	Conserved hypothetical protein	323350	323925	191	+	ATG
CBB_498	Putative membrane protein	323937	324242	101	+	ATG
CBB_499	Putative membrane protein	324246	324728	160	+	ATG
CBB_500	Conserved hypothetical protein	324788	325309	173	+	ATG
CBB_501	Putative membrane protein	325354	325824	156	+	ATG
CBB_502	Putative membrane protein	325834	326283	149	+	ATG
CBB_503	Conserved hypothetical protein	326355	326600	81	+	ATG
CBB_504	Putative membrane protein	326593	327318	241	+	GTG
CBB_505	Conserved hypothetical protein	327311	327430	39	+	ATG
CBB_506	Putative membrane protein	327433	327867	144	+	ATG
CBB_507	Conserved hypothetical protein	327921	328448	175	+	ATG
CBB_508	Conserved hypothetical protein	328450	328773	107	+	ATG
CBB_509	Conserved hypothetical protein	328773	329156	125	+	ATG
CBB_510	Conserved hypothetical protein	329214	329405	63	+	ATG
CBB_511	transcriptional regulator	330631	330861	76	+	ATG
CBB_512	Conserved hypothetical protein	330858	331007	49	+	ATG

CBB_513	subfamily RNA polymerase sigma-70 subunit	331103	332091	330	+	GTG
CBB_514	Conserved hypothetical protein	332108	312818	236	+	ATG
CBB_515	Conserved hypothetical protein	332827	333018	63	+	ATG
CBB_516	Conserved hypothetical protein	333073	334047	324	+	ATG
CBB_517	Hypothetical protein	334461	334634	98	+	ATG
CBB_518	Hypothetical protein	334461	334634	57	+	ATG
CBB_519	endonuclease V N-glycosylase UV repair enzyme	334700	335134	144	+	ATG
CBB_520	Conserved hypothetical protein	335198	335383	61	+	ATG
CBB_521	Conserved hypothetical protein	335458	335853	131	+	ATG
CBB_522	Putative membrane protein	335850	336044	64	+	ATG
CBB_523	Conserved hypothetical protein	336041	336274	77	+	ATG
CBB_524	Conserved hypothetical protein	336949	337752	267	+	ATG
CBB_525	Conserved hypothetical protein	337822	338832	336	+	ATG
CBB_526	Conserved hypothetical protein	338899	339423	174	+	ATG
CBB_527	Conserved hypothetical protein	339433	340227	264	+	ATG

CBB_528	HNH	340294	340860	188	+	ATG
CBB_529	Putative membrane protein	340862	341182	106	+	ATG
CBB_530	Conserved hypothetical protein	341299	342369	356	+	ATG
CBB_531	Conserved hypothetical protein	342424	342612	62	+	ATG
CBB_532	Conserved hypothetical protein	342609	342866	85	+	ATG
CBB_533	Conserved hypothetical protein	342863	342030	55	+	ATG
CBB_534	Structural protein	343063	343335	90	+	ATG
CBB_535	Conserved hypothetical protein	343417	344337	306	+	ATG
CBB_536	Structural protein	344368	345027	219	+	ATG
CBB_537	Structural protein	345042	345689	215	+	ATG
CBB_538	Conserved hypothetical protein	345789	346571	260	+	ATG
CBB_539	Putative membrane protein	345789	346571	107	+	ATG
CBB_540	Putative membrane protein	346911	347099	62	+	ATG
CBB_541	Putative membrane protein	347102	347263	53	+	TTG
CBB_542	Conserved hypothetical protein	347277	348047	256	+	ATG
CBB_543	Putative membrane protein	348094	348444	116	+	ATG

CBB_544	Putative membrane protein	348444	348782	112	+	ATG
CBB_545	Putative membrane protein	348782	349132	116	+	ATG
CBB_546	Putative membrane protein	349199	349495	98	+	ATG
CBB_547	Putative lipoprotein	349547	350170	207	+	ATG
CBB_548	Structural protein	350849	350196	217	-	ATG
CBB_549	Structural protein	351530	350859	223	-	ATG
CBB_550	Kelch-like protein	352396	351539	285	-	ATG
CBB_551	Structural protein	353100	352396	234	-	ATG
CBB_552	Structural protein	353952	353119	280	-	ATG
CBB_553	Structural protein	354701	354030	223	-	ATG

CBB_554	Kelch-like protein	355464	354667	265	-	ATG
CBB_555	Hypothetical protein	357350	357538	62	+	ATG
CBB_556	Conserved hypothetical protein	357723	358400	225	+	ATG
CBB_557	Conserved hypothetical protein	358550	358819	89	+	ATG
CBB_558	Conserved hypothetical protein	358955	359239	94	+	ATG
CBB_559	Conserved hypothetical protein	359275	359664	129	+	ATG
CBB_560	Hypothetical protein	359889	359716	57	-	ATG
CBB_561	Hypothetical protein	359888	360040	50	+	ATG
CBB_562	Conserved hypothetical protein	360088	360360	90	+	ATG
CBB_563	Conserved hypothetical protein	360424	360870	148	+	ATG
CBB_564	Conserved hypothetical protein	360947	361402	151	+	ATG
CBB_565	Hypothetical protein	361483	361608	41	+	ATG
CBB_566	Hypothetical protein	361681	361908	75	+	ATG
CBB_567	Conserved hypothetical protein	361982	362404	140	+	ATG
CBB_568	Conserved hypothetical protein	362586	362921	111	+	ATG
CBB_569	Conserved hypothetical protein	362991	363158	55	+	ATG
CBB_570	Conserved hypothetical protein	363242	363421	59	+	ATG
CBB_571	Conserved hypothetical protein	363494	363865	123	+	ATG
CBB_572	Conserved hypothetical protein	363912	364166	84	+	ATG
CBB_573	Hypothetical protein	365171	365329	52	+	ATG
CBB_574	Conserved hypothetical protein	364619	364852	77	+	ATG
CBB_575	Putative membrane protein	364876	365034	52	+	ATG
CBB_576	Conserved hypothetical protein	365046	365249	67	+	ATG
CBB_577	Conserved hypothetical protein	365282	365425	47	+	ATG
CBB_578	Conserved hypothetical protein	365504	365707	67	+	ATG

CBB_579	Conserved hypothetical protein	365737	366087	116	+	ATG
CBB_580	Putative membrane protein	366314	366565	83	+	ATG
CBB_581	Hypothetical protein	366597	366755	52	+	ATG
CBB_582	Structural protein	366764	367639	291	+	ATG
CBB_583	Conserved hypothetical protein	367779	367976	65	+	ATG
CBB_584	Conserved hypothetical protein	367940	368065	41	+	ATG
CBB_585	Hypothetical protein	368055	368249	64	+	ATG
CBB_586	Putative membrane protein	368293	368646	117	+	ATG
CBB_587	Hypothetical protein	368643	369032	129	+	ATG
CBB_588	Conserved hypothetical protein	369104	369295	63	+	ATG
CBB_589	Conserved hypothetical protein	369358	369744	128	+	ATG
CBB_590	Conserved hypothetical protein	369864	370106	80	+	ATG
CBB_591	Conserved hypothetical protein	370163	370681	172	+	ATG
CBB_592	Conserved hypothetical protein	370745	371083	112	+	ATG
CBB_593	Hypothetical protein	371326	371673	115	+	ATG
CBB_594	Conserved hypothetical protein	371764	371982	72	+	ATG
CBB_595	Conserved hypothetical protein	372158	372760	200	+	ATG
CBB_596	Conserved hypothetical protein	372965	373297	110	+	ATG
CBB_597	Conserved hypothetical protein	373507	373749	80	+	ATG
CBB_598	Conserved hypothetical protein	373829	374716	295	+	ATG
CBB_599	Conserved hypothetical protein	374792	375130	112	+	ATG
CBB_600	Conserved hypothetical protein	375334	375564	76	+	ATG
CBB_601	Conserved hypothetical protein	375648	375995	115	+	ATG

CBB_602	Hypothetical protein	376195	376386	63	+	ATG
CBB_603	Conserved hypothetical protein	376456	376632	58	+	ATG
CBB_604	Conserved hypothetical protein	377036	377305	89	+	ATG
CBB_605	Hypothetical protein	377375	377932	185	+	ATG

Stop codon	Molecular weigth (KDa)	Blastp result
TAG	6.65	_
TAA	7.00	_
TAA	25.17	hypothetical protein GAP32_005 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.13	hypothetical protein GAP32_006 [Cronobacter phage vB_CsaM_GAP32]
TAG	10.83	hypothetical protein GAP32_008 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.96	hypothetical protein GAP32_007 [Cronobacter phage vB_CsaM_GAP32]
TAA	6.30	_
TGA	5.58	_
TGA	10.08	hypothetical protein GAP32_009 [Cronobacter phage vB_CsaM_GAP32]
TAA	16.80	hypothetical protein GAP32_010 [Cronobacter phage vB_CsaM_GAP32]
TAA	17.13	hypothetical protein GAP32_011 [Cronobacter phage vB_CsaM_GAP32]
TAA	4.54	_
TAA	8.43	_
TAA	16.39	hypothetical protein GAP32_012 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.23	hypothetical protein [Citrobacter amalonaticus]
TAA	6.68	hypothetical protein N748_03710 [Legionella pneumophila str. 121004]
TAA	6.51	hypothetical protein VPBG_00116 [Vibrio phage helene 12B3]
TAA	14.45	hypothetical protein GAP32_014 [Cronobacter phage vB_CsaM_GAP32]
TGA	9.99	hypothetical protein GAP32_015 [Cronobacter phage vB_CsaM_GAP32]
TAA	5.88	_
TAA	8.56	hypothetical protein GAP32_017 [Cronobacter phage vB_CsaM_GAP32]
TGA	6.06	hypothetical protein GAP32_018A [Cronobacter phage vB_CsaM_GAP32]
TAA	7.51	hypothetical protein GAP32_019 [Cronobacter phage vB_CsaM_GAP32]
TAA	6.86	hypothetical protein GAP32_020 [Cronobacter phage vB_CsaM_GAP32]
TAA	7.56	hypothetical protein GAP32_021 [Cronobacter phage vB_CsaM_GAP32]

TAA	13.40	hypothetical protein GAP32_022 [Cronobacter phage vB_CsaM_GAP32]
TGA	9.44	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TGA	5.87	_
TAA	31.54	hypothetical protein GAP32_025 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.04	hypothetical protein GAP32_026 [Cronobacter phage vB_CsaM_GAP32]
TGA	4.86	hypothetical protein GAP32_027 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.12	_
TGA	13.52	_
TAA	14.27	_
TAA	7.27	hypothetical protein GAP32_029 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.27	hypothetical protein GAP32_030 [Cronobacter phage vB_CsaM_GAP32]
TGA	9.53	hypothetical protein GAP32_031 [Cronobacter phage vB_CsaM_GAP32]
TAA	18.82	hypothetical protein GAP32_032 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.64	hypothetical protein GAP32_033 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.92	_
TAA	8.27	hypothetical protein GAP32_034 [Cronobacter phage vB_CsaM_GAP32]
TGA	23.42	hypothetical protein GAP32_035 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.84	hypothetical protein GAP32_036 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.16	hypothetical protein GAP32_037 [Cronobacter phage vB_CsaM_GAP32]
TAA	33.78	hypothetical protein GAP32_039 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.26	hypothetical protein GAP32_040 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.64	hypothetical protein GAP32_041 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.49	hypothetical protein GAP32_042 [Cronobacter phage vB_CsaM_GAP32]

TAA	7.18	_
TAA	6.43	hypothetical protein GAP32_044 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.35	hypothetical protein GAP32_046 [Cronobacter phage vB_CsaM_GAP32]
TAA	20.69	_
TAA	23.35	hypothetical protein GAP32_048 [Cronobacter phage vB_CsaM_GAP32]
TGA	23.78	hypothetical protein GAP32_050 [Cronobacter phage vB_CsaM_GAP32]
TAA	25.13	hypothetical protein GAP32_051 [Cronobacter phage vB_CsaM_GAP32]
TGA	23.04	hypothetical protein GAP32_052 [Cronobacter phage vB_CsaM_GAP32]
TAG	20.85	hypothetical protein GAP32_053 [Cronobacter phage vB_CsaM_GAP32]
TAA	23.71	hypothetical protein GAP32_054 [Cronobacter phage vB_CsaM_GAP32]
TGA	15.94	hypothetical protein GAP32_055 [Cronobacter phage vB_CsaM_GAP32]
TAA	17.35	hypothetical protein GAP32_057 [Cronobacter phage vB_CsaM_GAP32]
TAA	18.37	hypothetical protein GAP32_058 [Cronobacter phage vB_CsaM_GAP32]
TGA	6.48	hypothetical protein GAP32_059 [Cronobacter phage vB_CsaM_GAP32]
TAA	23.72	hypothetical protein [Aeromonas allosaccharophila]
TAA	35.49	hypothetical protein GAP32_060 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.91	hypothetical protein GAP32_061 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.79	hypothetical protein GAP32_062 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.41	hypothetical protein GAP32_063 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.54	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	29.85	hypothetical protein GAP32_065 [Cronobacter phage vB_CsaM_GAP32]
TAA	30.72	hypothetical protein GAP32_066 [Cronobacter phage vB_CsaM_GAP32]
TAA	21.26	hypothetical protein GAP32_067 [Cronobacter phage vB_CsaM_GAP32]

TAA	20.59	DNA N-6-adenine-methyltransferase [Cronobacter phage vB_CsaM_GAP32]
TAA	20.43	cytitidyltransferase [Cronobacter phage vB_CsaM_GAP32]
TAA	10.90	hypothetical protein GAP32_070 [Cronobacter phage vB_CsaM_GAP32]
TAA	21.01	hypothetical protein GAP32_071 [Cronobacter phage vB_CsaM_GAP32]
TGA	6.20	hypothetical protein GAP32_073 [Cronobacter phage vB_CsaM_GAP32]
TGA	27.34	hypothetical protein GAP32_074 [Cronobacter phage vB_CsaM_GAP32]
TGA	7.65	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TGA	42.67	hypothetical protein GAP32_076 [Cronobacter phage vB_CsaM_GAP32]
TGA	28.09	hypothetical protein GAP32_077 [Cronobacter phage vB_CsaM_GAP32]

TGA	11.32	hypothetical protein GAP32_078 [Cronobacter phage vB_CsaM_GAP32]
TGA	11.45	hypothetical protein GAP32_079 [Cronobacter phage vB_CsaM_GAP32]
TAA	44.10	RNA ligase 1 and tail fiber attachment catalyst [Cronobacter phage vB_CsaM_GAP32]
TAA	9.27	hypothetical protein GAP32_081 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.71	hypothetical protein GAP32_082 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.52	hypothetical protein GAP32_083 [Cronobacter phage vB_CsaM_GAP32]
TAA	35.99	polynucleotide 5'-kinase and 3'-phosphatase [Cronobacter phage vB_CsaM_GAP32]
TAA	7.71	GAP32_085 [Cronobacter phage vB_CsaM_GAP32]
TAA	6.47	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TGA	10.90	hypothetical protein GAP32_088 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.94	hypothetical protein GAP32_089 [Cronobacter phage vB_CsaM_GAP32]
TGA	8.47	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TGA	9.58	hypothetical protein GAP32_091 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.06	hypothetical protein GAP32_092 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.78	hypothetical protein GAP32_093 [Cronobacter phage vB_CsaM_GAP32]
TAA	24.93	hypothetical protein GAP32_094 [Cronobacter phage vB_CsaM_GAP32]

TAA	30.02	putative serine/threonine protein phosphatase [Cronobacter phage vB_CsaM_GAP32]
TAA	17.25	hypothetical protein GAP32_097 [Cronobacter phage vB_CsaM_GAP32]
TAA	47.48	hypothetical protein GAP32_098 [Cronobacter phage vB_CsaM_GAP32]
TGA	53.23	DNA ligase [Cronobacter phage vB_CsaM_GAP32]
TGA	16.67	hypothetical protein GAP32_100 [Cronobacter phage vB_CsaM_GAP32]
TAA	30.56	metallophosphoesterase [Cronobacter phage vB_CsaM_GAP32]
TAA	14.64	hypothetical protein GAP32_102 [Cronobacter phage vB_CsaM_GAP32]

TAA	25.46	ATP-dependent Clp protease proteolytic subunit [Cronobacter phage vB_CsaM_GAP32]
TGA	10.46	hypothetical protein GAP32_104 [Cronobacter phage vB_CsaM_GAP32]
TAA	17.75	hypothetical protein GAP32_105 [Cronobacter phage vB_CsaM_GAP32]
TAA	22.46	hypothetical protein GAP32_106 [Cronobacter phage vB_CsaM_GAP32]
TGA	20.60	hypothetical protein GAP32_107 [Cronobacter phage vB_CsaM_GAP32]
TAA	19.09	hypothetical protein GAP32_108 [Cronobacter phage vB_CsaM_GAP32]
TAA	16.85	CMP/dCMP deaminase [Cronobacter phage vB_CsaM_GAP32]
TAA	10.40	hypothetical protein GAP32_110 [Cronobacter phage vB_CsaM_GAP32]
TAA	21.75	Ig domain-containing protein [Cronobacter phage vB_CsaM_GAP32]
TAA	42.17	bifunctional nicotinamide mononucleotide adenylyltransferase/ADP-ribose pyrophosphatase [Cronobacter phage vB_CsaM_GAP32]
TAA	20.20	hypothetical protein GAP32_113 [Cronobacter phage vB_CsaM_GAP32]

TAA	55.68	nicotinamide phosphoribosyltransferase [Cronobacter phage vB_CsaM_GAP32]
TAA	8.39	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	37.08	hypothetical protein GAP32_116 [Cronobacter phage vB_CsaM_GAP32]
TAA	16.64	hypothetical protein GAP32_118 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.60	hypothetical protein GAP32_118A [Cronobacter phage vB_CsaM_GAP32]
TAA	29.72	putative Sir2-like protein [Cronobacter phage vB_CsaM_GAP32]
TAA	34.45	hypothetical protein GAP32_120 [Cronobacter phage vB_CsaM_GAP32]
TAG	11.13	hypothetical protein GAP32_121 [Cronobacter phage vB_CsaM_GAP32]
TAA	53.57	PhoH family protein [Cronobacter phage vB_CsaM_GAP32]
TAA	7.03	hypothetical protein GAP32_123 [Cronobacter phage vB_CsaM_GAP32]
TGA	27.02	hypothetical protein GAP32_124 [Cronobacter phage vB_CsaM_GAP32]
TGA	7.26	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	5.62	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	22.37	hypothetical protein GAP32_126 [Cronobacter phage vB_CsaM_GAP32]

TAA	31.87	hypothetical protein GAP32_127 [Cronobacter phage vB_CsaM_GAP32]
TAA	22.68	hypothetical protein GAP32_129 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.26	co-chaperonin GroES [Cronobacter phage vB_CsaM_GAP32]
TAA	47.60	tyrosyl-tRNA synthetase [Cronobacter phage vB_CsaM_GAP32]
TAA	7.80	hypothetical protein GAP32_132 [Cronobacter phage vB_CsaM_GAP32]
TGA	25.45	hypothetical protein GAP32_133 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.72	dCMP deaminase [Cronobacter phage vB_CsaM_GAP32]
TAA	12.88	_
TAA	24.62	_
TGA	10.21	hypothetical protein GAP32_135 [Cronobacter phage vB_CsaM_GAP32]
TAA	7.74	_
TAA	21.16	hypothetical protein GAP32_136 [Cronobacter phage vB_CsaM_GAP32]

TGA	69.42	anaerobic NTP reductase large subunit [Cronobacter phage vB_CsaM_GAP32]
TAA	12.19	_
TAA	18.00	hypothetical protein GAP32_139 [Cronobacter phage vB_CsaM_GAP32]
TGA	25.22	_
TGA	17.91	anaerobic ribonucleoside-triphosphate reductase activating protein [Cronobacter phage vB_CsaM_GAP32]
TAA	6.57	hypothetical protein GAP32_142 [Cronobacter phage vB_CsaM_GAP32]
TAA	98.07	hypothetical protein GAP32_143 [Cronobacter phage vB_CsaM_GAP32]
TAA	98.70	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	100.67	hypothetical protein GAP32_145 [Cronobacter phage vB_CsaM_GAP32]
TAA	22.00	hypothetical protein GAP32_146 [Cronobacter phage vB_CsaM_GAP32]
TGA	10.61	_

TGA	29.85	putative tRNA-His guanylyltransferase [Cronobacter phage vB_CsaM_GAP32]
TAA	19.59	hypothetical protein GAP32_148 [Cronobacter phage vB_CsaM_GAP32]
TGA	11.23	hypothetical protein GAP32_149 [Cronobacter phage vB_CsaM_GAP32]
TGA	18.38	hypothetical protein GAP32_150 [Cronobacter phage vB_CsaM_GAP32]
TAA	25.22	hypothetical protein GAP32_151 [Cronobacter phage vB_CsaM_GAP32]
TGA	33.21	putative N-4 cytosine-specific methyltransferase [Cronobacter phage vB_CsaM_GAP32]
TAA	12.97	hypothetical protein GAP32_153 [Cronobacter phage vB_CsaM_GAP32]
TAA	48.92	hypothetical protein GAP32_154 [Cronobacter phage vB_CsaM_GAP32]
TAA	16.13	hypothetical protein GAP32_155 [Cronobacter phage vB_CsaM_GAP32]
TAA	19.46	hypothetical protein GAP32_156 [Cronobacter phage vB_CsaM_GAP32]
TGA	21.48	hypothetical protein GAP32_158 [Cronobacter phage vB_CsaM_GAP32]

TAA	15.80	acyl carrier protein [Cronobacter phage vB_CsaM_GAP32]
TGA	14.09	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAG	11.90	hypothetical protein GAP32_161 [Cronobacter phage vB_CsaM_GAP32]
TAA	15.24	hypothetical protein GAP32_162 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.36	hypothetical protein GAP32_163 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.61	hypothetical protein GAP32_164 [Cronobacter phage vB_CsaM_GAP32]
TAA	17.18	hypothetical protein GAP32_165 [Cronobacter phage vB_CsaM_GAP32]
TAA	16.86	hypothetical protein GAP32_167 [Cronobacter phage vB_CsaM_GAP32]
TAA	19.77	GTP cyclohydrolase [Terasakiella pusilla]
TAA	11.16	hypothetical protein GAP32_168 [Cronobacter phage vB_CsaM_GAP32]
TGA	21.41	thymidine kinase [Cronobacter phage vB_CsaM_GAP32]
TGA	19.78	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TGA	23.04	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	13.58	hypothetical protein GAP32_173 [Cronobacter phage vB_CsaM_GAP32]
TAA	4.71	_
TAA	23.57	_
TAA	12.32	_
TTG	21.27	hypothetical protein GAP32_174 [Cronobacter phage vB_CsaM_GAP32]
TAA	47.45	RNA ligase [Cronobacter phage vB_CsaM_GAP32]

TAA	24.17	hypothetical protein GAP32_355 [Cronobacter phage vB_CsaM_GAP32]
TAA	55.82	hypothetical protein GAP32_176 [Cronobacter phage vB_CsaM_GAP32]
TAA	5.03	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TGA	17.28	hypothetical protein GAP32_178 [Cronobacter phage vB_CsaM_GAP32]
TAG	21.94	hypothetical protein GAP32_179 [Cronobacter phage vB_CsaM_GAP32]
TGA	35.38	lysozyme [Cronobacter phage vB_CsaM_GAP32]
TAA	12.88	sigma 54 modulation protein/ribosomal protein S30EA [Cronobacter phage vB_CsaM_GAP32]
TGA	16.15	hypothetical protein GAP32_184 [Cronobacter phage vB_CsaM_GAP32]
TGA	5.63	_
TGA	8.66	hypothetical protein GAP32_185 [Cronobacter phage vB_CsaM_GAP32]

TAA	42.75	multifunctional tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase/phosphatase [Cronobacter phage vB_CsaM_GAP32]
TAA	16.50	nudix hydrolase [Cronobacter phage vB_CsaM_GAP32]
TAA	8.70	glutaredoxin [Cronobacter phage vB_CsaM_GAP32]
TAA	15.18	hypothetical protein GAP32_189 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.50	hypothetical protein GAP32_190 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.39	hypothetical protein GAP32_191 [Cronobacter phage vB_CsaM_GAP32]
TAA	18.85	hypothetical protein GAP32_192 [Cronobacter phage vB_CsaM_GAP32]
TAA	11.97	hypothetical protein GAP32_193 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.48	hypothetical protein GAP32_194 [Cronobacter phage vB_CsaM_GAP32]
TAA	29.62	neck protein [Cronobacter phage vB_CsaM_GAP32]
TAA	9.77	hypothetical protein GAP32_196 [Cronobacter phage vB_CsaM_GAP32]

TGA	24.82	putative deoxynucleoside monophosphate kinase [Cronobacter phage vB_CsaM_GAP32]
TAA	95.91	tail sheath monomer [Cronobacter phage vB_CsaM_GAP32]
TAA	25.39	hypothetical protein GAP32_199 [Cronobacter phage vB_CsaM_GAP32]
TAA	29.03	hypothetical protein GAP32_200 [Cronobacter phage vB_CsaM_GAP32]
TAA	39.83	hypothetical protein GAP32_201 [Cronobacter phage vB_CsaM_GAP32]
TAA	17.69	head completion protein [Cronobacter phage vB_CsaM_GAP32]
TAA	21.53	hypothetical protein GAP32_203 [Cronobacter phage vB_CsaM_GAP32]
TAA	20.95	hypothetical protein GAP32_204 [Cronobacter phage vB_CsaM_GAP32]
TAA	20.24	hypothetical protein GAP32_205 [Cronobacter phage vB_CsaM_GAP32]
TAA	53.17	hypothetical protein GAP32_206 [Cronobacter phage vB_CsaM_GAP32]
TAA	33.36	hypothetical protein GAP32_207 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.86	hypothetical protein GAP32_208 [Cronobacter phage vB_CsaM_GAP32]
TGA	14.33	hypothetical protein GAP32_209 [Cronobacter phage vB_CsaM_GAP32]
TGA	50.67	ATPase [Cronobacter phage vB_CsaM_GAP32]
TAG	51.29	hypothetical protein GAP32_211 [Cronobacter phage vB_CsaM_GAP32]

TAA	8.64	hypothetical protein GAP32_212 [Cronobacter phage vB_CsaM_GAP32]
TAA	26.15	hypothetical protein GAP32_213 [Cronobacter phage vB_CsaM_GAP32]
TGA	11.58	hypothetical protein GAP32_214 [Cronobacter phage vB_CsaM_GAP32]
TAA	22.36	hypothetical protein GAP32_215 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.86	hypothetical protein GAP32_216 [Cronobacter phage vB_CsaM_GAP32]
TAA	35.33	thymidylate synthase [Cronobacter phage vB_CsaM_GAP32]
TAA	68.10	hypothetical protein GAP32_218 [Cronobacter phage vB_CsaM_GAP32]
TAA	24.19	hypothetical protein GAP32_219 [Cronobacter phage vB_CsaM_GAP32]
TAA	153.27	long tail fiber proximal subunit [Cronobacter phage vB_CsaM_GAP32]
TAA	30.02	hypothetical protein GAP32_221 [Cronobacter phage vB_CsaM_GAP32]
TAA	41.68	hypothetical protein GAP32_222 [Cronobacter phage vB_CsaM_GAP32]
TAA	19.05	hypothetical protein GAP32_223 [Cronobacter phage vB_CsaM_GAP32]
TAA	21.80	hypothetical protein GAP32_224 [Cronobacter phage vB_CsaM_GAP32]
TAA	40.39	hypothetical protein GAP32_225 [Cronobacter phage vB_CsaM_GAP32]
TAA	17.72	MutT/NUDIX hydrolase family protein [Cronobacter phage vB_CsaM_GAP32]
TAA	51.35	tail sheath stabilizer and completion protein [Cronobacter phage vB_CsaM_GAP32]
TGA	57.00	hypothetical protein GAP32_228 [Cronobacter phage vB_CsaM_GAP32]

TAA	84.34	ATP-dependent Clp protease ATP-binding subunit clpA [Cronobacter phage vB_CsaM_GAP32]
TAA	379.94	hypothetical protein GAP32_230 [Cronobacter phage vB_CsaM_GAP32]
TAA	131.71	baseplate wedge [Cronobacter phage vB_CsaM_GAP32]
TAA	14.83	base plate protein [Cronobacter phage vB_CsaM_GAP32]
TAA	18.49	baseplate hub subunit and tail lysozyme [Cronobacter phage vB_CsaM_GAP32]
TAA	97.09	baseplate hub subunit and tail lysozyme [Cronobacter phage vB_CsaM_GAP32]
TAA	88.83	hypothetical protein GAP32_235 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.23	hypothetical protein GAP32_236 [Cronobacter phage vB_CsaM_GAP32]

TAA	27.69	hypothetical protein GAP32_237 [Cronobacter phage vB_CsaM_GAP32]
TGA	33.56	sigma factor for late transcription [Cronobacter phage vB_CsaM_GAP32]
TAA	39.92	recombination endonuclease subunit [Cronobacter phage vB_CsaM_GAP32]
TAA	82.05	recombination endonuclease subunit [Cronobacter phage vB_CsaM_GAP32]
TAA	27.28	hypothetical protein [Erwinia phage PhiEaH1]
TAA	18.15	DNA endonuclease VII [Escherichia phage 121Q]
TAA	6.93	hypothetical protein GAP32_242 [Cronobacter phage vB_CsaM_GAP32]
TAA	32.55	hypothetical protein GAP32_243 [Cronobacter phage vB_CsaM_GAP32]
TAA	78.41	hypothetical protein GAP32_244 [Cronobacter phage vB_CsaM_GAP32]
TAA	65.18	portal vertex protein of head [Cronobacter phage vB_CsaM_GAP32]
TAA	8.63	hypothetical protein GAP32_246 [Cronobacter phage vB_CsaM_GAP32]
TAA	30.25	hypothetical protein GAP32_247 [Cronobacter phage vB_CsaM_GAP32]
TAA	23.24	prohead core scaffold and protease [Cronobacter phage vB_CsaM_GAP32]
TAA	42.55	hypothetical protein GAP32_249 [Cronobacter phage vB_CsaM_GAP32]

TAA	42.11	precursor of major head subunit [Cronobacter phage vB_CsaM_GAP32]
TAA	15.98	hypothetical protein GAP32_252 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.02	hypothetical protein GAP32_253 [Cronobacter phage vB_CsaM_GAP32]
TAA	56.65	putative tail fiber protein [Cronobacter phage vB_CsaM_GAP32]
TAA	16.06	tail fiber assembly protein [Cronobacter phage vB_CsaM_GAP32]
TAA	11.31	hypothetical protein GAP32_256 [Cronobacter phage vB_CsaM_GAP32]
TAA	115.94	DNA polymerase [Cronobacter phage vB_CsaM_GAP32]
TAA	19.32	hypothetical protein GAP32_258 [Cronobacter phage vB_CsaM_GAP32]
TAA	26.74	hypothetical protein GAP32_259 [Cronobacter phage vB_CsaM_GAP32]
TAA	23.92	putative phosphoesterase or phosphohydrolase [Cronobacter phage vB_CsaM_GAP32]

TAA	8.22	hypothetical protein GAP32_261 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.74	co-chaperonin GroES [Cronobacter phage vB_CsaM_GAP32]
TAA	28.50	hypothetical protein GAP32_263 [Cronobacter phage vB_CsaM_GAP32]
TAA	22.43	hypothetical protein GAP32_264 [Cronobacter phage vB_CsaM_GAP32]
TAA	19.23	hypothetical protein GAP32_265 [Cronobacter phage vB_CsaM_GAP32]
TAA	38.17	RNaseH ribonuclease [Cronobacter phage vB_CsaM_GAP32]
TAA	19.04	hypothetical protein GAP32_267 [Cronobacter phage vB_CsaM_GAP32]
TAA	27.52	terminase DNA packaging enzyme large subunit [Cronobacter phage vB_CsaM_GAP32]
TAA	62.89	DNA terminase packaging enzyme large subunit [Cronobacter phage vB_CsaM_GAP32]
TAA	48.67	hypothetical protein GAP32_270 [Cronobacter phage vB_CsaM_GAP32]
TAA	38.62	ssDNA binding protein [Cronobacter phage vB_CsaM_GAP32]
TAA	41.44	RecA-like protein [Cronobacter phage vB_CsaM_GAP32]

TAA	17.96	hypothetical protein GAP32_273 [Cronobacter phage vB_CsaM_GAP32]
TAA	32.53	putative DNA polymerase III epsilon subunit [Cronobacter phage vB_CsaM_GAP32]
TGA	56.09	RNA-DNA + DNA-DNA helicase [Cronobacter phage vB_CsaM_GAP32]
TAA	17.16	hypothetical protein GAP32_277 [Cronobacter phage vB_CsaM_GAP32]
TAA	19.15	hypothetical protein GAP32_278 [Cronobacter phage vB_CsaM_GAP32]
TAA	32.25	hypothetical protein GAP32_279 [Cronobacter phage vB_CsaM_GAP32]
TGA	28.82	hypothetical protein GAP32_280 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.30	hypothetical protein GAP32_281 [Cronobacter phage vB_CsaM_GAP32]
TGA	25.11	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	14.23	hypothetical protein GAP32_283 [Cronobacter phage vB_CsaM_GAP32]
TAA	36.68	hypothetical protein GAP32_284 [Cronobacter phage vB_CsaM_GAP32]
TGA	40.38	putative DNA primase [Cronobacter phage vB_CsaM_GAP32]
TAA	55.75	DNA primase-helicase [Cronobacter phage vB_CsaM_GAP32]
TGA	10.37	hypothetical protein GAP32_287 [Cronobacter phage vB_CsaM_GAP32]

TAA	5.60	hypothetical protein GAP32_288 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.70	hypothetical protein GAP32_289 [Cronobacter phage vB_CsaM_GAP32]
TAA	34.25	hypothetical protein GAP32_290 [Cronobacter phage vB_CsaM_GAP32]
TGA	8.36	hypothetical protein GAP32_291 [Cronobacter phage vB_CsaM_GAP32]
TAA	30.22	hypothetical protein GAP32_292 [Cronobacter phage vB_CsaM_GAP32]
TAA	23.65	hypothetical protein GAP32_293 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.15	hypothetical protein GAP32_294 [Cronobacter phage vB_CsaM_GAP32]
TGA	26.64	hypothetical protein GAP32_295 [Cronobacter phage vB_CsaM_GAP32]
TAA	20.26	hypothetical protein GAP32_296 [Cronobacter phage vB_CsaM_GAP32]
TAA	20.83	hypothetical protein GAP32_297 [Cronobacter phage vB_CsaM_GAP32]
TAA	87.79	ribonucleotide-diphosphate reductase alpha subunit [Cronobacter phage vB_CsaM_GAP32]
TAA	30.80	gp559 [Bacillus phage G]
TAA	43.37	ribonucleotide-diphosphate reductase subunit beta [Cronobacter phage vB_CsaM_GAP32]
TAA	7.09	hypothetical protein GAP32_301 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.14	hypothetical protein GAP32_302 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.78	hypothetical protein GAP32_303 [Cronobacter phage vB_CsaM_GAP32]

TAA	26.30	hypothetical protein GAP32_304 [Cronobacter phage vB_CsaM_GAP32]
TAA	24.21	hypothetical protein GAP32_305 [Cronobacter phage vB_CsaM_GAP32]
TAA	26.33	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	13.97	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	19.68	dihydrofolate reductase [Cronobacter phage vB_CsaM_GAP32]
TGA	16.20	ribonuclease H [Cronobacter phage vB_CsaM_GAP32]
TAA	51.65	DNA helicase Dda [Cronobacter phage vB_CsaM_GAP32]
TAA	19.94	hypothetical protein GAP32_311 [Cronobacter phage vB_CsaM_GAP32]
TAA	7.30	hypothetical protein GAP32_312 [Cronobacter phage vB_CsaM_GAP32]

TAA	18.74	translation initiation factor IF-3 [Cronobacter phage vB_CsaM_GAP32]
TAA	20.09	ATP-dependent Clp protease [Cronobacter phage vB_CsaM_GAP32]
TAA	20.64	hypothetical protein GAP32_315 [Cronobacter phage vB_CsaM_GAP32]
TAA	61.65	hypothetical protein GAP32_316 [Cronobacter phage vB_CsaM_GAP32]
TAA	96.34	hypothetical protein GAP32_317 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.58	hypothetical membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	74.42	DNA gyrase subunit B [Cronobacter phage vB_CsaM_GAP32]

TAA	53.17	DNA topoisomerase II [Cronobacter phage vB_CsaM_GAP32]
TAG	87.98	hypothetical protein GAP32_321 [Cronobacter phage vB_CsaM_GAP32]
TGA	11.84	hypothetical protein GAP32_322 [Cronobacter phage vB_CsaM_GAP32]
TAA	20.57	DNA polymerase III alpha subunit [Cronobacter phage vB_CsaM_GAP32]
TAA	13.94	hypothetical protein GAP32_324 [Cronobacter phage vB_CsaM_GAP32]
TAA	11.70	hypothetical protein GAP32_325 [Cronobacter phage vB_CsaM_GAP32]
TGA	11.15	hypothetical protein GAP32_326 [Cronobacter phage vB_CsaM_GAP32]
TAA	36.15	sliding clamp loader subunit [Cronobacter phage vB_CsaM_GAP32]
TAA	24.06	hypothetical protein GAP32_328 [Cronobacter phage vB_CsaM_GAP32]
TAA	21.94	hypothetical protein GAP32_329 [Cronobacter phage vB_CsaM_GAP32]
TAA	25.70	hypothetical protein GAP32_330 [Cronobacter phage vB_CsaM_GAP32]
TAA	30.76	hypothetical protein GAP32_331 [Cronobacter phage vB_CsaM_GAP32]
TAA	19.20	hypothetical protein GAP32_332 [Cronobacter phage vB_CsaM_GAP32]
TAA	7.02	hypothetical protein GAP32_333 [Cronobacter phage vB_CsaM_GAP32]
TAA	45.96	hypothetical protein GAP32_334 [Cronobacter phage vB_CsaM_GAP32]

TAA	42.63	toxic ion resistance protein [Cronobacter phage vB_CsaM_GAP32]
TAA	13.01	hypothetical protein GAP32_336 [Cronobacter phage vB_CsaM_GAP32]
TGA	25.57	putative metallopeptidase [Cronobacter phage vB_CsaM_GAP32]
TGA	42.11	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	20.71	hypothetical protein GAP32_339 [Cronobacter phage vB_CsaM_GAP32]
TGA	6.44	hypothetical protein GAP32_340 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.26	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	25.48	hypothetical protein VPBG_00153 [Vibrio phage helene 12B3]
TGA	18.99	hypothetical protein GAP32_342 [Cronobacter phage vB_CsaM_GAP32]
TAA	64.97	hypothetical protein GAP32_343 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.26	_
TAA	17.29	hypothetical protein GAP32_344 [Cronobacter phage vB_CsaM_GAP32]
TAA	7.74	hypothetical protein GAP32_345 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.81	hypothetical protein GAP32_346 [Cronobacter phage vB_CsaM_GAP32]
TGA	12.35	hypothetical protein GAP32_347 [Cronobacter phage vB_CsaM_GAP32]
TGA	13.29	_
TGA	27.60	hypothetical protein GAP32_348 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.91	hypothetical protein GAP32_349 [Cronobacter phage vB_CsaM_GAP32]
TAA	7.65	hypothetical protein GAP32_350 [Cronobacter phage vB_CsaM_GAP32]
TAA	39.69	hypothetical protein GAP32_351 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.27	hypothetical protein GAP32_352 [Cronobacter phage vB_CsaM_GAP32]

TGA	40.33	nicotinamide-nucleotide adenylyltransferase [Cronobacter phage vB_CsaM_GAP32]
TAA	30.12	nicotinamide mononucleotide transporter PnuC [Cronobacter phage vB_CsaM_GAP32]
TAA	11.83	_
TAA	9.22	hypothetical protein GAP32_356 [Cronobacter phage vB_CsaM_GAP32]
TGA	8.38	hypothetical protein JS09_0194 [Escherichia phage vB_EcoM_JS09]
TGA	17.42	hypothetical protein GAP32_357 [Cronobacter phage vB_CsaM_GAP32]
TGA	11.61	_
TAA	11.70	hypothetical protein GAP32_358 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.01	hypothetical protein GAP32_359 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.82	hypothetical protein RaK2_00182 [Enterobacteria phage vB_KleM-RaK2]
TAG	13.97	hypothetical protein GAP32_360 [Cronobacter phage vB_CsaM_GAP32]
TGA	11.83	hypothetical protein GAP32_361 [Cronobacter phage vB_CsaM_GAP32]
TAA	17.30	hypothetical protein GAP32_362 [Cronobacter phage vB_CsaM_GAP32]
TAA	15.96	hypothetical protein GAP32_364 [Cronobacter phage vB_CsaM_GAP32]

TAA	29.73	hypothetical protein GAP32_365 [Cronobacter phage vB_CsaM_GAP32]
TAA	49.56	hypothetical protein GAP32_366 [Cronobacter phage vB_CsaM_GAP32]
TAA	45.37	hypothetical protein GAP32_367 [Cronobacter phage vB_CsaM_GAP32]
TAG	18.24	hypothetical protein GAP32_368 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.84	hypothetical protein GAP32_369 [Cronobacter phage vB_CsaM_GAP32]
TAA	21.98	putative 5'3'-deoxyribonucleotidase [Cronobacter phage vB_CsaM_GAP32]
TAA	21.05	hypothetical protein GAP32_371 [Cronobacter phage vB_CsaM_GAP32]
TAA	21.86	hypothetical protein GAP32_372 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.90	hypothetical protein GAP32_374 [Cronobacter phage vB_CsaM_GAP32]
TGA	5.31	hypothetical protein GAP32_374A [Cronobacter phage vB_CsaM_GAP32]
TGA	9.80	hypothetical protein GAP32_375 [Cronobacter phage vB_CsaM_GAP32]

TAA	30.18	hypothetical protein GAP32_376 [Cronobacter phage vB_CsaM_GAP32]
TGA	15.24	hypothetical protein GAP32_377 [Cronobacter phage vB_CsaM_GAP32]
TGA	17.78	hypothetical protein GAP32_378 [Cronobacter phage vB_CsaM_GAP32]
TGA	10.60	hypothetical protein GAP32_379 [Cronobacter phage vB_CsaM_GAP32]
TAA	20.33	hypothetical protein GAP32_380 [Cronobacter phage vB_CsaM_GAP32]
TGA	17.79	_
TAA	16.92	peptidyl-tRNA hydrolase [Cronobacter phage vB_CsaM_GAP32]
TAA	13.85	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	8.75	hypothetical protein GAP32_385 [Cronobacter phage vB_CsaM_GAP32]
TAA	6.27	_
TGA	10.07	hypothetical protein GAP32_387 [Cronobacter phage vB_CsaM_GAP32]
TGA	13.63	hypothetical protein GAP32_388 [Cronobacter phage vB_CsaM_GAP32]
TAA	18.72	hypothetical protein GAP32_389 [Cronobacter phage vB_CsaM_GAP32]

TAA	32.94	DNA-cytosine methyltransferase [Cronobacter phage vB_CsaM_GAP32]
TAA	11.73	hypothetical protein GAP32_391 [Cronobacter phage vB_CsaM_GAP32]
TGA	13.37	hypothetical protein GAP32_392 [Cronobacter phage vB_CsaM_GAP32]
TAA	27.62	hypothetical protein GAP32_393 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.28	hypothetical protein GAP32_394 [Cronobacter phage vB_CsaM_GAP32]
TAA	20.74	_
TAA	7.88	hypothetical protein GAP32_395 [Cronobacter phage vB_CsaM_GAP32]
TGA	8.78	hypothetical protein GAP32_397 [Cronobacter phage vB_CsaM_GAP32]
TAG	5.33	hypothetical protein GAP32_398 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.32	hypothetical protein GAP32_399 [Cronobacter phage vB_CsaM_GAP32]
TAA	16.39	hypothetical protein GAP32_400 [Cronobacter phage vB_CsaM_GAP32]
TAA	7.45	hypothetical protein GAP32_401 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.34	hypothetical protein GAP32_402 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.02	hypothetical protein [Paenibacillus elgii]
TGA	7.68	_
TAA	4.50	_
TGA	11.07	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	10.43	_
TAA	11.02	hypothetical protein GAP32_404 [Cronobacter phage vB_CsaM_GAP32]
TAA	7.38	hypothetical protein AE04_00280 [Enterobacter aerogenes MGH 78]
TAA	8.78	hypothetical protein GAP32_405 [Cronobacter phage vB_CsaM_GAP32]

TAA	15.88	hypothetical protein RaK2_00219 [Enterobacteria phage vB_KleM-RaK2]
TGA	5.85	hypothetical protein GAP32_408 [Cronobacter phage vB_CsaM_GAP32]
TAA	7.92	hypothetical protein GAP32_409 [Cronobacter phage vB_CsaM_GAP32]
TGA	7.79	_
TAA	7.46	hypothetical protein GAP32_411 [Cronobacter phage vB_CsaM_GAP32]
TAA	16.95	hypothetical protein GAP32_412 [Cronobacter phage vB_CsaM_GAP32]
TGA	7.96	_
TAA	9.06	_
TAA	8.91	_
TAA	9.76	_
TAA	7.37	_
TAA	31.18	hypothetical protein GAP32_415 [Cronobacter phage vB_CsaM_GAP32]
TGA	11.17	_
TGA	16.01	hypothetical protein GAP32_416 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.65	_
TAA	11.65	hypothetical protein GAP32_417 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.10	hypothetical protein GAP32_418 [Cronobacter phage vB_CsaM_GAP32]
TGA	7.77	hypothetical protein GAP32_419 [Cronobacter phage vB_CsaM_GAP32]
TGA	14.35	hypothetical protein GAP32_420 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.86	hypothetical protein GAP32_421 [Cronobacter phage vB_CsaM_GAP32]
TGA	8.77	hypothetical protein GAP32_422 [Cronobacter phage vB_CsaM_GAP32]
TAA	22.95	_
TAG	6.21	_
TAA	13.92	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	22.99	hypothetical protein [Clostridiaceae bacterium mt10]

TAA	19.31	hypothetical protein GAP32_425 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.28	hypothetical protein GAP32_426 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.42	hypothetical protein GAP32_427 [Cronobacter phage vB_CsaM_GAP32]
TAA	17.67	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TGA	12.97	_
TAA	5.50	hypothetical protein GAP32_431 [Cronobacter phage vB_CsaM_GAP32]
TGA	15.96	hypothetical protein GAP32_432 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.15	hypothetical protein GAP32_433 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.40	hypothetical protein GAP32_434 [Cronobacter phage vB_CsaM_GAP32]
TAA	15.67	hypothetical protein GAP32_435 [Cronobacter phage vB_CsaM_GAP32]
TAA	22.79	hypothetical protein GAP32_436 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.68	hypothetical protein GAP32_437 [Cronobacter phage vB_CsaM_GAP32]
TAA	16.17	hypothetical protein [Clostridium sp. GD3]
TAA	12.15	hypothetical protein [Escherichia phage vB_EcoS_FFH1]
TAA	9.02	hypothetical protein GAP32_439 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.86	_
TAA	12.71	hypothetical protein GAP32_440 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.29	hypothetical protein GAP32_441 [Cronobacter phage vB_CsaM_GAP32]
TAA	19.18	hypothetical protein GAP32_442 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.19	hypothetical protein GAP32_443 [Cronobacter phage vB_CsaM_GAP32]
TAA	15.22	_
TAG	10.19	hypothetical protein GAP32_445 [Cronobacter phage vB_CsaM_GAP32]
TGA	8.66	hypothetical protein GAP32_446 [Cronobacter phage vB_CsaM_GAP32]

TAA	14.25	hypothetical protein GAP32_447 [Cronobacter phage vB_CsaM_GAP32]
TAA	15.68	hypothetical protein GAP32_448 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.42	hypothetical protein GAP32_451 [Cronobacter phage vB_CsaM_GAP32]
TGA	9.83	hypothetical protein GAP32_453A [Cronobacter phage vB_CsaM_GAP32]
TAA	17.05	hypothetical protein GAP32_454 [Cronobacter phage vB_CsaM_GAP32]
TAA	4.56	hypothetical protein GAP32_455 [Cronobacter phage vB_CsaM_GAP32]
TAA	5.31	hypothetical protein [Yersinia kristensenii]
TAG	9.26	hypothetical protein GAP32_456 [Cronobacter phage vB_CsaM_GAP32]
TGA	18.14	hypothetical protein GAP32_457 [Cronobacter phage vB_CsaM_GAP32]
TGA	19.72	hypothetical protein VPFG_00288 [Vibrio phage nt-1]
TAA	5.11	hypothetical protein GAP32_458 [Cronobacter phage vB_CsaM_GAP32]
TAA	11.86	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	12.40	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	11.60	hypothetical protein GAP32_461 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.85	hypothetical protein GAP32_462 [Cronobacter phage vB_CsaM_GAP32]
TGA	5.33	hypothetical protein GAP32_462A [Cronobacter phage vB_CsaM_GAP32]
TAA	7.91	hypothetical protein GAP32_463 [Cronobacter phage vB_CsaM_GAP32]
TAA	18.55	hypothetical protein GAP32_464 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.26	_
TAA	16.31	hypothetical protein GAP32_465 [Cronobacter phage vB_CsaM_GAP32]
TAA	4.84	hypothetical protein GAP32_466 [Cronobacter phage vB_CsaM_GAP32]
TGA	24.12	hypothetical protein GAP32_468 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.22	hypothetical protein GAP32_469 [Cronobacter phage vB_CsaM_GAP32]
TGA	7.20	hypothetical protein GAP32_470 [Cronobacter phage vB_CsaM_GAP32]
TAG	7.44	hypothetical protein GAP32_471 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.43	_

TAA	24.72	hypothetical protein GAP32_473 [Cronobacter phage vB_CsaM_GAP32]
TAA	20.99	hypothetical protein GAP32_474 [Cronobacter phage vB_CsaM_GAP32]
TAA	40.94	hypothetical protein GAP32_475 [Cronobacter phage vB_CsaM_GAP32]
TAA	21.62	hypothetical protein GAP32_476 [Cronobacter phage vB_CsaM_GAP32]
TAA	11.57	hypothetical protein GAP32_477 [Cronobacter phage vB_CsaM_GAP32]
TAA	18.21	hypothetical protein GAP32_478 [Cronobacter phage vB_CsaM_GAP32]
TAA	19.65	hypothetical protein GAP32_479 [Cronobacter phage vB_CsaM_GAP32]
TAA	18.63	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	16.81	_
TAA	9.24	hypothetical protein GAP32_481 [Cronobacter phage vB_CsaM_GAP32]
TAA	28.55	hypothetical protein GAP32_482 [Cronobacter phage vB_CsaM_GAP32]
TAA	3.96	hypothetical protein GAP32_483 [Cronobacter phage vB_CsaM_GAP32]
TAA	16.72	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	20.65	hypothetical protein GAP32_485 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.01	hypothetical protein GAP32_486 [Cronobacter phage vB_CsaM_GAP32]
TGA	14.78	hypothetical protein GAP32_487 [Cronobacter phage vB_CsaM_GAP32]
TGA	6.99	hypothetical protein [Salmonella phage SKML-39]
TGA	8.77	transcriptional regulator [Cronobacter phage vB_CsaM_GAP32]
TAA	5.55	hypothetical protein GAP32_489 [Cronobacter phage vB_CsaM_GAP32]

TAA	37.92	subfamily RNA polymerase sigma-70 subunit [Cronobacter phage vB_CsaM_GAP32]
TAA	26.63	hypothetical protein GAP32_492 [Cronobacter phage vB_CsaM_GAP32]
TAA	7.20	hypothetical protein GAP32_493 [Cronobacter phage vB_CsaM_GAP32]
TGA	37.22	hypothetical protein GAP32_494 [Cronobacter phage vB_CsaM_GAP32]
TAA	11.47	_
TGA	6.57	_
TAA	16.95	endonuclease V N-glycosylase UV repair enzyme [Cronobacter phage vB_CsaM_GAP32]
TAA	6.99	hypothetical protein GAP32_499 [Cronobacter phage vB_CsaM_GAP32]
TGA	15.54	hypothetical protein GAP32_500 [Cronobacter phage vB_CsaM_GAP32]
TGA	7.15	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	8.82	hypothetical protein GAP32_502 [Cronobacter phage vB_CsaM_GAP32]
TAA	31.25	hypothetical protein GAP32_504 [Cronobacter phage vB_CsaM_GAP32]
TAA	39.56	hypothetical protein GAP32_505 [Cronobacter phage vB_CsaM_GAP32]
TAA	19.85	hypothetical protein GAP32_506 [Cronobacter phage vB_CsaM_GAP32]
TAA	30.74	hypothetical protein GAP32_507 [Cronobacter phage vB_CsaM_GAP32]

TAA	21.78	HNH endonuclease [Cronobacter phage vB_CsaM_GAP32]
TAA	12.48	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	40.50	hypothetical protein GAP32_510 [Cronobacter phage vB_CsaM_GAP32]
TGA	7.21	hypothetical protein GAP32_511 [Cronobacter phage vB_CsaM_GAP32]
TGA	10.40	hypothetical protein GAP32_512 [Cronobacter phage vB_CsaM_GAP32]
TAA	6.23	hypothetical protein GAP32_514 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.45	hypothetical protein GAP32_515 [Cronobacter phage vB_CsaM_GAP32]
TAA	35.70	hypothetical protein GAP32_520 [Cronobacter phage vB_CsaM_GAP32]
TAA	24.75	hypothetical protein SP19_190 [Salmonella phage 19]
TAA	24.14	hypothetical protein SP19_190 [Salmonella phage 19]
TAG	29.12	hypothetical protein GAP32_521 [Cronobacter phage vB_CsaM_GAP32]
TAG	12.12	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	7.10	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	5.89	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	29.98	hypothetical protein GAP32_524 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.14	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]

TAA	13.12	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	13.29	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TAA	10.86	_
TAA	22.41	hypothetical protein GAP32_529 [Cronobacter phage vB_CsaM_GAP32]
TAA	23.81	hypothetical protein GAP32_530 [Cronobacter phage vB_CsaM_GAP32]
TAA	24.84	hypothetical protein GAP32_531 [Cronobacter phage vB_CsaM_GAP32]
TAG	31.83	kelch-like protein 17 [Chrysochromulina sp. CCMP291]
TAA	25.38	_
TAG	31.25	_
TAA	25.40	hypothetical protein GAP32_002 [Cronobacter phage vB_CsaM_GAP32]

TAA	29.91	_
TAA	7.00	_
TAA	25.17	hypothetical protein GAP32_005 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.13	hypothetical protein GAP32_006 [Cronobacter phage vB_CsaM_GAP32]
TAG	10.83	hypothetical protein GAP32_008 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.96	hypothetical protein GAP32_007 [Cronobacter phage vB_CsaM_GAP32]
TAA	6.30	_
TGA	5.58	_
TAA	10.08	hypothetical protein GAP32_009 [Cronobacter phage vB_CsaM_GAP32]
TAA	16.80	hypothetical protein GAP32_010 [Cronobacter phage vB_CsaM_GAP32]
TAA	17.13	hypothetical protein GAP32_011 [Cronobacter phage vB_CsaM_GAP32]
TAA	4.54	_
TAA	8.43	_
TAA	16.39	hypothetical protein GAP32_012 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.23	hypothetical protein [Citrobacter amalonaticus]
TAA	6.68	hypothetical protein Lste_0119 [Legionella steelei]
TAA	6.51	hypothetical protein VPBG_00116 [Vibrio phage helene 12B3]
TAA	14.45	hypothetical protein GAP32_014 [Cronobacter phage vB_CsaM_GAP32]
TGA	9.99	hypothetical protein GAP32_015 [Cronobacter phage vB_CsaM_GAP32]
TAA	5.88	_
TAA	8.56	hypothetical protein GAP32_017 [Cronobacter phage vB_CsaM_GAP32]
TGA	6.06	hypothetical protein GAP32_018A [Cronobacter phage vB_CsaM_GAP32]
TAA	7.51	hypothetical protein GAP32_019 [Cronobacter phage vB_CsaM_GAP32]
TAA	6.86	hypothetical protein GAP32_020 [Cronobacter phage vB_CsaM_GAP32]
TAA	7.56	hypothetical protein GAP32_021 [Cronobacter phage vB_CsaM_GAP32]

TAA	13.40	hypothetical protein GAP32_022 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.44	Putative membrane protein [Cronobacter phage vB_CsaM_GAP32]
TGA	5.87	_
TAA	31.54	hypothetical protein GAP32_025 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.04	hypothetical protein GAP32_026 [Cronobacter phage vB_CsaM_GAP32]
TGA	4.86	hypothetical protein GAP32_027 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.12	_
TGA	13.52	_
TAA	14.27	_
TAG	7.27	hypothetical protein GAP32_029 [Cronobacter phage vB_CsaM_GAP32]
TAA	14.27	hypothetical protein GAP32_030 [Cronobacter phage vB_CsaM_GAP32]
TGA	9.53	hypothetical protein GAP32_031 [Cronobacter phage vB_CsaM_GAP32]
TAA	18.82	hypothetical protein GAP32_032 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.64	hypothetical protein GAP32_033 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.92	_
TAA	8.27	hypothetical protein GAP32_034 [Cronobacter phage vB_CsaM_GAP32]
TGA	23.42	hypothetical protein GAP32_035 [Cronobacter phage vB_CsaM_GAP32]
TAA	12.84	hypothetical protein GAP32_036 [Cronobacter phage vB_CsaM_GAP32]
TAA	9.16	hypothetical protein GAP32_037 [Cronobacter phage vB_CsaM_GAP32]
TAA	33.78	hypothetical protein GAP32_039 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.26	hypothetical protein GAP32_040 [Cronobacter phage vB_CsaM_GAP32]
TAA	8.64	hypothetical protein GAP32_041 [Cronobacter phage vB_CsaM_GAP32]
TAA	13.49	hypothetical protein GAP32_042 [Cronobacter phage vB_CsaM_GAP32]

TAA	7.18	_
TAA	6.43	hypothetical protein GAP32_044 [Cronobacter phage vB_CsaM_GAP32]
TAA	10.35	hypothetical protein GAP32_046 [Cronobacter phage vB_CsaM_GAP32]
TAA	20.69	_

Acession number	E value	MS identification of structural proteins of CBB capsid	Shared Structural proteins of GAP32	Structural proteins shared with Rak2	pfam domain hit	E-value
YP_006987	2.00E-88					
YP_006987	6.00E-56					
YP_006987	1.00E-38					
YP_006987	1.00E-83					
YP_006987	8.00E-56					
YP_006987	5.00E-100					
YP_006987	3.00E-102					
YP_006987	1.00E-60					
WP_04649	5.00E-09					
CAH17234.	1.00E-10					
YP_007877	9.00E-06					
YP_006987	8.00E-51					
YP_006987	2.00E-52					
YP_006987	4.00E-48					
YP_006987	2.00E-15					
YP_006987	7.00E-37					
YP_006987	8.00E-24					
YP_00698 7124.1	4.00E-39					

YP_006987	2.00E-60					
YP_006987	2.00E-29					
YP_006987	1.00E-83	Yes	Yes		PF01145.22 Band_7	1.00E-27
YP_006987	1.00E-29					
YP_006987	8.00E-03					
YP_006987	1.00E-18					
YP_006987	7.00E-23					
YP_006987	3.00E-41					
YP_006987	1.00E-96	Yes	Yes	Yes		
YP_006987	1.00E-60					
YP_006987	7.00E-16					
YP_006987	5.00E-88					
YP_006987	5.00E-58					
YP_006987	7.00E-46					
YP_006987	0.00E+00				PF06067.8 DUF932	5.10E-37
YP_006987	2.00E-63					
YP_006987	2.00E-28					
YP_006987	1.00E-64					

YP_006987	9.00E-28					
YP_006987	2.00E-37					
YP_006987	4.00E-108					
YP_006987	3.00E-19					
YP_006987	1.00E-33					
YP_006987	2.00E-88					
YP_006987	1.00E-53					
YP_006987	5.00E-72					
YP_006987	1.00E-59					
YP_006987	1.00E-81					
YP_006987	1.00E-107					
YP_006987	2.00E-19					
WP_04206	4.00E-30					
YP_006987	0.E+00					
YP_006987	1.00E-54					
YP_006987	3.00E-79					
YP_006987	2.00E-74					
YP_006987	5.00E-25					
YP_006987	1.00E-92					
YP_006987	9.00E-99					
YP_006987	2.00E-87					

YP_006987	3.00E-125				PF05869.8 Dam	2.00E-27
YP_006987	2.00E-86				PF01467.23 CTP_transf_like	8.90E-06
YP_006987	2.00E-46					
YP_006987	9.00E-75					
YP_006987	2.00E-04					
YP_006987	6.00E-129				PF01966.19 HD	2.30E-04
YP_006987	3.00E-20					
YP_006987	0.00E+00					
YP_006987	4.00E-169					

YP_006987	1.00E-46					
YP_006987	6.00E-50					
YP_006987	0.00E+00				PF09511.7 RNA_lig_T4_1	8.40E-15
YP_006987	2.00E-34					
YP_006987	6.00E-29					
YP_006987	2.00E-41					
YP_006987	0.00E+00				PF13671.3 AAA_33	1.70E-16
YP_006987	5.00E-29					
YP_006987	8.00E-15					
YP_006987	6.00E-45					
YP_006987	1.00E-69					
YP_006987	6.00E-19					
YP_006987	8.00E-45					
YP_006987	4.00E-65					
YP_006987	3.00E-42					
YP_006987	1.00E-125					

YP_006987	0.00E+00				PF00149.25 Metallophos	1.70E-15
YP_006987	4.00E-92					
YP_006987	0.00E+00					
YP_006987	0.00E+00				PF01068.18 DNA_ligase_A_M	6.20E-20
YP_006987	3.00E-72					
YP_006987	1.00E-163				PF00149.25 Metallophos	4.20E-11
YP_006987	1.00E-67					

YP_006987	2.00E-153	Yes			PF00574.20 CLP_protease	4.20E-40
YP_006987	2.00E-56					
YP_006987	4.00E-90					
YP_006987	9.00E-41					
YP_006987	6.00E-98					
YP_006987	4.00E-60					
YP_006987	5.00E-106				PF00383.20 dCMP_cyt_deam_1	7.00E-24
YP_006987	7.00E-37					
YP_006987	2.00E-98	Yes	Yes	Yes	PF02368.15 Big_2	1.90E-20
YP_006987	0				PF00293.25CTP_transf_like, PF00293.25 NUDIX	4.7E-6, 5.6E-1
YP_006987	3.00E-72					

YP_006987	0.00E+00				PF04095.13 NAPRTase	2.40E-36
YP_006987	3.00E-07					
YP_006987	1.00E-74					
YP_006987	7.00E-99	Yes	Yes			
YP_006987	1.00E-11					
YP_006987	1.00E-158				PF02146.14 SIR2	5.90E-26
YP_006987	0.00E+00					
YP_006987	8.00E-56					
YP_006987	0			?	PF13638.3 PIN_4, PF02562.13 PhoH	2.1E-23, 1.2E-
YP_006987	4.00E-16					
YP_006987	5.00E-137					
YP_006987	9.00E-17					
YP_006987	3.00E-21					
YP_006987	1.00E-107					

YP_006987	7.00E-54					
YP_006987	7.00E-135					
YP_006987	1.00E-55				PF00166.18 Cpn10	1.60E-12
YP_006987	0.00E+00				PF00579.22 tRNA-synt_1b, PF01479.22 S4	1.4E-64, 2.60E
YP_006987	4.00E-40					
YP_006987	5.00E-129					
YP_006987	4.00E-75				PF00383.20 dCMP_cyt_deam_1	2.40E-06
YP_006987	1.00E-16					
YP_006987	7.00E-115				PF13521.3 AAA_28	5.20E-20

YP_006987	0				PF13597.3 NRDD	2.50E-160
YP_006987	1.00E-61					
		Yes				
YP_006987	1.00E-98				PF13353.3 Fer4_12	2.10E-50
YP_006987	3.00E-24					
YP_006987	0.00E+00					
YP_006987	0.00E+00		Yes			
YP_006987	0.00E+00		Yes			
YP_006987	1.00E-99					

YP_006987	6.00E-175				PF04446.9 Thg1	1.60E-31
YP_006987	2.00E-77					
YP_006987	8.00E-63				PF14216.3 DUF4326	6.80E-18
YP_006987	1.00E-71					
YP_006987	2.00E-51					
YP_006987	0.00E+00				PF01555.15 N6_N4_Mtase	1.90E-34
YP_006987	2.00E-40					
YP_006987	0.00E+00				PF10127.6 Nuc-transf	3.80E-18
YP_006987	2.00E-71					
YP_006987	3.00E-65					
YP_006987	8.00E-120					

YP_006987	3.00E-12				PF00550.22 PP-binding	4.40E-09
YP_006987	7.00E-63			Yes		
YP_006987	2.00E-52			Yes		
YP_006987	1.00E-73					
YP_006987	5.00E-32					
YP_006987	2.00E-32					
YP_006987	2.00E-95	Yes				
YP_006987	1.00E-57					
WP_02887	1.00E-47				PF08719.8 DUF1768	8.40E-52
YP_006987	8.00E-08					
YP_006987	3.00E-120				PF00265.15 TK	1.70E-52
YP_006987	2.00E-93					
YP_006987	1.00E-103					
YP_006987	3.00E-80					
YP_006987	2.00E-73					
YP_006987	0				PF09414.7 RNA_ligase	1.60E-15

YP_006987	7.00E-44					
YP_006987	0	Yes			PF11443.5 DUF2828, PF11443.5 DUF2828	6.7E-10, 9.9E-
YP_006987	8.00E-17					
YP_006987	2.00E-89					
YP_006987	9.00E-76					
YP_006987	0.00E+00					
YP_006987	8.00E-64				PF02482.16 Ribosomal_S30AE	3.10E-13
YP_006987	2.00E-52					
YP_006987	2.00E-26					

YP_006987	0.00E+00				PF01743.17 PolyA_pol, PF12627.4 PolyA_pol_RNAbd	2.60E-17, 3.5(
YP_006987	2.00E-93				PF00293.25 NUDIX	7.60E-15
YP_006987	1.00E-45				PF00462.21 Glutaredoxin	7.70E-11
YP_006987	7.00E-84				PF09424.7 YqeY	4.50E-06
YP_006987	2.00E-66					
YP_006987	1.00E-48					
YP_006987	4.00E-95				PF01661.18 Macro	8.90E-08
YP_006987	6.00E-59					
YP_006987	4.00E-70					
YP_006987	0.00E+00	Yes		Yes		
YP_006987	4.00E-24					

YP_006987	2.00E-113					
YP_006987	0.00E+00		Yes	Yes	PF04984.11 Phage_sheath_1	1.40E-27
YP_006987	3.00E-167	Yes	Yes	Yes		
YP_006987	0.00E+00		Yes	Yes		
YP_006987	0	Yes				
YP_006987	2.00E-103				PF08722.8 Tn7_Tnp_TnsA_N	6.40E-07
YP_006987	1.00E-103					
YP_006987	1.00E-126	Yes	Yes	Yes		
YP_006987	1.00E-83		Yes	Yes		
YP_006987	0.00E+00		Yes	Yes		
YP_006987	6.00E-177	Yes		Yes		
YP_006987	1.00E-65	Yes		Yes		
YP_006987	6.00E-76					
YP_006987	0.00E+00					
YP_006987	0.00E+00				PF13203.3 DUF2201_N, PF13203.3 DUF2201_N, PF09967.6 DUF2201	2.4E-5, 1.9E-2

YP_006987	8.00E-38					
YP_006987	1.00E-146					
YP_006987	2.00E-61					
YP_006987	9.00E-131					
YP_006987	4.00E-45					
YP_006987	0.00E+00				PF00303.16 Thymidylat_synt	5.50E-104
YP_006987	0.00E+00	Yes	Yes	Yes		
YP_006987	1.00E-133	Yes	Yes		PF14301.3 DUF4376	7.20E-12
YP_006987	0.00E+00	Yes	Yes			
YP_006987	5.00E-163	Yes	Yes	Yes		
YP_006987	0.00E+00	Yes	Yes			
YP_006987	5.00E-98		Yes	Yes		
YP_006987	6.00E-141	Yes	Yes			
YP_006987	0.00E+00	Yes	Yes	Yes		
YP_006987	2.00E-107				PF00293.25 NUDIX	4.50E-14
YP_006987	0.00E+00	Yes	Yes		PF16724.2 T4-gp15_tss	2.40E-07
YP_006987	0.00E+00	Yes	Yes	Yes		

YP_006987	0.00E+00				PF00004.26 AAA, PF07724.11 AAA_2, PF10431.6 ClpB_D2-small, PF02861.17 Clp_N	3.30E-15, 2E-3
YP_006987	0.00E+00	Yes	Yes	Yes		
YP_006987	0.00E+00	Yes	Yes	Yes		
YP_006987	3.00E-83		Yes	Yes	PF04965.11 GPW_gp25	3.60E-10
YP_006987	8.00E-100				PF00959.16 Phage_lysozyme	3.40E-08
YP_006987	0.00E+00	Yes	Yes		PF00959.16 Phage_lysozyme	9.30E-09
YP_006987	0.00E+00	Yes		Yes		
YP_006987	7.00E-62	Yes			PF11246.5 Phage_gp53	7.50E-05

YP_006987	6.00E-174	Yes	Yes	Yes		
YP_006987	0.00E+00					
YP_006987	0.00E+00				PF00149.25 Metallophos	1.70E-04
YP_006987	0.00E+00				PF13476.3 AAA_23	1.10E-11
YP_009010	4.00E-23	Yes				
YP_009102	3.00E-64					
YP_006987	2.00E-24					
YP_006987	1.00E-178			Yes		
YP_006987	0.00E+00	Yes	Yes			
YP_006987	0.00E+00		Yes	Yes	PF07230.8 Peptidase_S80	2.00E-36
YP_006987	2.00E-33					
YP_006987	7.00E-120	Yes		Yes		
YP_006987	4.00E-142		Yes	Yes	PF03420.10 Peptidase_S77	4.00E-21
YP_006987	0.00E+00	Yes				

YP_006987	0.00E+00	Yes	Yes	Yes	PF07068.8 Gp23, PF07068.8 Gp23	9.60E-11, 7.6E
YP_006987	2.00E-92					
YP_006987	3.00E-70				PF10544.6 T5orf172	1.50E-09
YP_006987	0.00E+00	Yes	Yes	Yes		
YP_006987	4.00E-72					
YP_006987	8.00E-63					
YP_006987	0.00E+00				PF03104.16 DNA_pol_B_exo1, PF00136.18 DNA_pol_B, PF00136.18 DNA_pol_B	9.60E-20, 1.90
YP_006987	3.00E-31					
YP_006987	4.00E-175					
YP_006987	7.00E-139				PF00149.25 Metallophos	1.70E-04

YP_006987	1.00E-25					
YP_006987	3.00E-58				PF00166.18 Cpn10	4.70E-17
YP_006987	2.00E-141			Yes		
YP_006987	1.00E-121	Yes	Yes	Yes		
YP_006987	3.00E-124	Yes	Yes	Yes		
YP_006987	0.00E+00				PF02739.13 5_3_exonuc_N	7.50E-17
YP_006987	1.00E-99					
YP_006987	6.00E-93					
YP_006987	0.00E+00				PF03237.12 Terminase_6	3.50E-23
YP_006987	0.00E+00	Yes				
YP_006987	0.00E+00			?		
YP_006987	0.00E+00				PF00154.18 RecA	9.90E-15

YP_006987	9.00E-98					
YP_006987	0.00E+00				PF00929.21RNase_T, PF12843.4 QSregVF_b	1.10E-19, 1.50
YP_006987	0.00E+00				PF00271.28 Helicase_C, PF04851.12 ResIII	6.30E-7, 7.10E
YP_006987	8.00E-79					
YP_006987	5.00E-116					
YP_006987	0.00E+00					
YP_006987	9.00E-170					
YP_006987	1.00E-63	Yes				
YP_006987	1.00E-154					
YP_006987	5.00E-78					
YP_006987	0.00E+00		Yes			
YP_006987	0.00E+00					
YP_006987	0.00E+00				PF03796.12 DnaB_C	2.80E-15
YP_006987	4.00E-51	Yes				

YP_006987	1.00E-18					
YP_006987	2.00E-85	Yes				
YP_006987	0.00E+00					
YP_006987	4.00E-38					
YP_006987	5.00E-169					
YP_006987	5.00E-137	Yes	Yes	Yes		
YP_006987	1.00E-68	Yes				
YP_006987	2.00E-165				PF12705.4 PDDEXK_1	2.10E-04
YP_006987	6.00E-112					
YP_006987	3.00E-123		Yes	Yes		
YP_006987	0.00E+00				PF03477.13 ATP-cone, PF00317.18 Ribonuc_red_lgN, PF02867.12 Ribonuc_red_lgC	8.50E-13, 2.40
YP_009015	4.00E-07					
YP_006987	0.00E+00				PF00268.18 Ribonuc_red_sm	1.10E-48
YP_006987	1.00E-17					
YP_006987	4.00E-41					
YP_006987	5.00E-85			Yes		

YP_006987	2.00E-133				PF01503.14 PRA-PH	5.60E-09
YP_006987	2.00E-136			Yes		
YP_006987	5.00E-158					
YP_006987	4.00E-46					
YP_006987	2.00E-94				PF00186.16 DHFR_1	5.60E-38
YP_006987	9.00E-93				PF00075.21 RNase_H	1.20E-37
YP_006987	0				PF13604.3 AAA_30, PF13538.3 UvrD_C_2	1.40E-21, 1.70
YP_006987	2.00E-100		Yes	Yes		
YP_006987	1.00E-34					

YP_006987	2.00E-105				PF05198.13 IF3_N, PF00707.19 IF3_C	3.80E-19, 5.8(
YP_006987	9.00E-98				PF02617.14 ClpS	1.10E-13
YP_006987	1.00E-122	Yes	Yes		PF13619.3 KTSC	1.60E-14
YP_006987	0.00E+00		Yes			
YP_006987	0.00E+00	Yes	Yes	Yes		
YP_006987	5.00E-52					
YP_006987	0.00E+00				PF02518.23 HATPase_c, PF00204.22 PF01751.19 DNA_gyraseB, Toprim	3.10E-10, 2.5(

YP_006987	0.00E+00				PF00521.17 DNA_topoisoIV	1.90E-65
YP_006987	0.00E+00		Yes	Yes		
YP_006987	6.00E-60					
YP_006987	2.00E-114				PF07733.9 DNA_pol3_alpha	5.70E-08
YP_006987	2.00E-83					
YP_006987	4.00E-66					
YP_006987	2.00E-50					
YP_006987	0.00E+00				PF13177.3 DNA_pol3_delta2	6.80E-14
YP_006987	6.00E-140					
YP_006987	2.00E-124	Yes				
YP_006987	1.00E-151		Yes			
YP_006987	1.00E-180					
YP_006987	2.00E-54					
YP_006987	3.00E-33					
YP_006987	0.00E+00					

YP_006987	0.00E+00				PF05816.8 TelA	5.30E-52
YP_006987	5.00E-48					
YP_006987	2.00E-118					
YP_006987	0.00E+00					
YP_006987	6.00E-107		Yes	Yes		
YP_006987	2.00E-16					
YP_006987	1.00E-61					
YP_007877	2.00E-48					
YP_006987	3.00E-102					
YP_006987	5.00E-132					
YP_006987	2.00E-28					
YP_006987	6.00E-35					
YP_006987	5.00E-63					
YP_006987	5.00E-63					
YP_006987	2.00E-133					
YP_006987	1.00E-41					
YP_006987	3.00E-23					
YP_006987	0.00E+00					
YP_006987	1.00E-78					

YP_006987	0.00E+00				PF01467.23 CTP_transf_like, PF13521.3 AAA_28	0.00014, 2.6E-
YP_006987	0.00E+00				PF04973.9 NMN_transporter	7.50E-38
YP_006987	2.00E-43					
YP_009037	6.00E-03					
YP_006987	2.00E-81					
YP_006987	4.00E-66					
YP_006987	7.00E-60					
YP_007007	9.00E-30			Yes		
YP_006987	4.00E-59					
YP_006987	8.00E-33					
YP_006987	7.00E-92					
YP_006987	3.00E-43					

YP_006987	0.00E+00				PF14243.3 DUF4343	1.80E-23
YP_006987	0.00E+00					
YP_006987	0.00E+00				PF00004.26 AAA	4.20E-06
YP_006987	4.00E-98					
YP_006987	1.00E-46					
YP_006987	3.00E-128				PF06941.9 NT5C	7.70E-13
YP_006987	1.00E-104					
YP_006987	5.00E-118					
YP_006987	5.00E-59					
YP_006987	7.00E-26					
YP_006987	1.00E-48					

YP_006987	2.00E-124				PF14243.3 DUF4343	4.50E-26
YP_006987	1.00E-46					
YP_006987	9.00E-95					
YP_006987	7.00E-44					
YP_006987	6.00E-59					
YP_006987	1.00E-85				PF01981.13 PTH2	1.50E-11
YP_006987	5.00E-64					
YP_006987	9.00E-39					
YP_006987	2.00E-46					
YP_006987	1.00E-40					
YP_006987	2.00E-72					

YP_006987	0.00E+00				PF00145.14 DNA_methylase, PF00145.14 DNA_methylase	5.3E-25, 1.30E
YP_006987	2.00E-49					
YP_006987	8.00E-60					
YP_006987	1.00E-110					
YP_006987	7.00E-71					
YP_006987	4.00E-38					
YP_006987	2.00E-48					
YP_006987	4.00E-24					
YP_006987	7.00E-67					
YP_006987	3.00E-61					
YP_006987	2.00E-25					
YP_006987	1.00E-70					
WP_01049	6.00E-21					
YP_006987	1.00E-39					
YP_006987	3.00E-38					
KDF37778.1	2.00E-09					
YP_006987	4.00E-35					

YP_007007	2.00E-49				PF13392.3 HNH_3, PF10955.5 DUF2757	5.1E-7, 3.0E-5
YP_006987	1.00E-22					
YP_006987	2.00E-26					
YP_006987	8.00E-04					
YP_006987	3.00E-56					
YP_006987	1.00E-179					
YP_006987	4.00E-89					
YP_006987	2.00E-60					
YP_006987	2.00E-33					
YP_006987	4.00E-37					
YP_006987	2.00E-82					
YP_006987	2.00E-78					
YP_006987	1.00E-38					
YP_006987	5.00E-22					
WP_05566	1.00E-04					

YP_006987	7.00E-69					
YP_006987	2.00E-44					
YP_006987	2.00E-34					
YP_006987	6.00E-77					
YP_006987	5.00E-20					
YP_006987	2.00E-69					
YP_006987	9.00E-34					
YP_006987	6.00E-43					
YP_006987	6.00E-56					
YP_006987	2.00E-107					
YP_006987	2.00E-75				PF07087.8 DUF1353	6.60E-26
WP_05062	5.00E-04					
YP_009031	3.00E-12					
YP_006987	3.00E-22					
YP_006987	3.00E-70					
YP_006987	9.00E-39					
YP_006987	2.00E-112					
YP_006987	1.00E-38					
YP_006987	5.00E-50					
YP_006987	2.00E-38					

YP_006987	7.00E-31					
YP_006987	3.00E-59					
YP_006987	5.00E-65					
YP_006987	2.00E-46					
YP_006987	4.00E-48					
YP_006987	1.00E-12					
WP_05029	2.00E-05					
YP_006987	1.00E-47					
YP_006987	4.00E-20				PF15937.2 PrlF_antitoxin	2.30E-10
YP_008125	6.00E-08					
YP_006987	5.00E-22					
YP_006987	1.00E-33					
YP_006987	2.00E-51					
YP_006987	2.00E-42					
YP_006987	4.00E-36					
YP_006987	8.00E-03					
YP_006987	1.00E-23					
YP_006987	5.00E-55					
YP_006987	3.00E-22					
YP_006987	2.00E-15					
YP_006987	2.00E-40					
YP_006987	4.00E-63					
YP_006987	8.00E-19					
YP_006987	1.00E-04					

YP_006987	1.00E-72	Yes		Yes		
YP_006987	3.00E-97					
YP_006987	0.00E+00	Yes	Yes			
YP_006987	6.00E-116					
YP_006987	2.00E-48					
YP_006987	6.00E-70					
YP_006987	3.00E-94					
YP_006987	1.00E-48					
YP_006987	4.00E-36					
YP_006987	5.00E-115					
YP_006987	3.00E-13					
YP_006987	4.00E-32					
YP_006987	7.00E-58					
YP_006987	8.00E-30					
YP_006987	5.00E-80					
YP_007236	3.00E-11					
YP_006987	2.00E-29				PF13744.3 HTH_37	5.10E-18
YP_006987	3.00E-23					

YP_006987	0.00E+00				PF04542.11 Sigma70_r2	5.90E-05
YP_006987	7.00E-139					
YP_006987	7.00E-33					
YP_006987	0.00E+00					
YP_006987	2.00E-87				PF03013.11 Pyr_excise	4.90E-40
YP_006987	7.00E-24					
YP_006987	6.00E-25					
YP_006987	9.00E-03					
YP_006987	3.00E-39					
YP_006987	1.00E-64					
YP_006987	1.00E-138					
YP_006987	3.00E-49					
YP_006987	2.00E-108					

YP_006987	2.00E-79				PF01844.20 HNH	8.70E-07
YP_006987	2.00E-42					
YP_006987	0.00E+00				PF00004.26 AAA	3.10E-13
YP_006987	6.00E-27					
YP_006987	6.00E-44					
YP_006987	1.00E-23					
YP_006987	3.00E-49		Yes			
YP_006987	6.00E-119					
AKJ74681.1	6.00E-14	Yes				
AKJ74681.1	2.00E-20	Yes				
YP_006987	6.00E-180					
YP_006987	1.00E-15					
YP_006987	6.00E-09					
YP_006987	1.00E-03					
YP_006987	6.00E-96					
YP_006987	3.00E-18					

YP_006987	3.00E-21					
YP_006987	5.00E-07					
YP_006987	5.00E-122				PF06693.8 DUF1190	2.90E-36
YP_006987	3.00E-98	Yes	Yes		PF13385.3 Laminin_G_3	1.50E-12
YP_006987	1.00E-80	Yes	Yes			
KOO35119.	6.00E-13				PF13415.3 Kelch_3, PF13964.3 Kelch_6	1.50E-5, 3.70E
		Yes			PF13385.3 Laminin_G_3	6.80E-14
		Yes			PF01344.22 Kelch_1	5.20E-06
YP_006987	2.00E-18	Yes				

					PF01344.22 Kelch_1, PF13964.3 Kelch_6	1.20E-7, 1.40E
YP_006987	2.00E-88					
YP_006987	6.00E-56					
YP_006987	1.00E-38					
YP_006987	1.00E-83					
YP_006987	8.00E-56					
YP_006987	5.00E-100					
YP_006987	3.00E-102					
YP_006987	1.00E-60					
WP_04649	5.00E-09					
KTD71834.	9.00E-11					
YP_007877	9.00E-06					
YP_006987	8.00E-51					
YP_006987	2.00E-52					
YP_006987	4.00E-48					
YP_006987	2.00E-15					
YP_006987	8.00E-37					
YP_006987	2.00E-14					
YP_006987	4.00E-39					

YP_006987	2.00E-60					
YP_006987	2.00E-29					
WP_01326	1.00E-83		Yes		PF01145.22 Band_7	1.00E-27
YP_006987	1.00E-29					
YP_006987	8.00E-03					
YP_006987	1.00E-18					
YP_006987	7.00E-23					
YP_006987	3.00E-41					
YP_006987	1.00E-96					
YP_006987	1.00E-60					
YP_006987	7.00E-16					
YP_006987	5.00E-88					
YP_006987	5.00E-58					
YP_006987	8.00E-46					
YP_006987	0.00E+00				PF06067.8 DUF932	5.10E-37
YP_006987	3.00E-63					
YP_006987	2.00E-28					
YP_006987	1.00E-64					

YP_006987	9.00E-28					
YP_006987	2.00E-37					

HHpred	**E-value**	**Interproscan (Protein family, Domains and repeats)**	**No. of Transmembrane domains (TMHMM)**
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PH stomatin; archaea, trimer, coiled- coil, flotillin, SPFH, membrane fusion, trafficking, transmembrane, membrane protein; 3.20A {Pyrococcus horikoshii}	4.70E-28	Stomatin family (IPR001972), Band 7 domain (IPR001107	1
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_		Protein of unknown function DUF932 (IPR026325)	_
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Modification methylase TAQI; DNA, DNA methyltransferase, target base partner, 5-methylpyr 2(1H)-ONE, base flipping; HET: 5PY 6MA NEA; 1.61A {Thermus aquaticus}	0.31	DNA N-6-adenine-methyltransferase (IPR008593),	_
Nicotinate (nicotinamide) nucleotide adenylyltran; NAD, nucleotidyltransferase, pyridine nucleotide biosynthesi transferase; HET: NXX; 1.70A {Bacillus anthracis}	6.00E-29	Cytidyltransferase-like domain (IPR004821), Rossmann-like alpha/beta/alpha sandwich fold (IPR014729)	_
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Bifunctional RELA/SPOT; HD domain, alpha beta 2-layer sandwich, helix bundle, mangan PPG2':3'P, (P)PPGPP, PPGPP; HET: GDP GPX; 2.10A {Streptococcus dysgalactiae subsp}	1.60E-51	HD domain (IPR006674)	_
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RNA ligase, T4 RNA ligase 1; nucleotidyl transferase, ATP-binding; HET: APC; 2.21A {Bacteriophage T4}	1.10E-83	RNA ligase T4 Rnl1, N-terminal (IPR019039)	_
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PNKP1; RNA repair, kinase, phosphatase, methyltransferase, ligase, binding; 3.30A {Capnocytophaga gingivalis}	2.30E-35	P-loop containing nucleoside triphosphate hydrolase (IPR027417), HAD-like domain (IPR023214)	_
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Serine/threonine protein phosphatase; bacteriophage lambda, Ser/Thr protein phosphatase, ppase, manganese, sulfate, viral protein; 2.15A {Enterobacteria phage lambda}	1.40E-32	Metallo-dependent phosphatase-like (IPR029052) Calcineurin-like phosphoesterase domain, apaH type (IPR004843)	_
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Thermostable DNA ligase; protein-nucleotide complex, cell cycle, cell division, DNA damage, DNA, recombination, DNA repair, DNA replication; HET: AMP; 1.8A {Pyrococcus furiosus}	4.70E-78	DNA ligase, ATP-dependent, central (IPR012310), Nucleic acid-binding, OB-fold (IPR012340)	_
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Phosphohydrolase; glycerophosphodiesterase, metallohydrolase, phosphatase, metal ION; 1.90A {Enterobacter aerogenes}	6.90E-24	Metallo-dependent phosphatase-like (IPR029052) Calcineurin-like phosphoesterase domain, apaH type (IPR004843)	_
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Putative ATP-dependent CLP protease proteolytic S; mitochondrial CLPP, CLP/HSP 100, ATP-dependent protease, HYD; HET: FME; 2.10A {Homo sapiens}	7.00E-42		_
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Deoxycytidylate deaminase; DCMP deaminase, cytidine deaminase, deoxycytidylate deaminas TIM5, hydrolase; HET: DCM DU; 2.60A {Cyanophage s-tim5}	4.70E-36	Deoxycytidylate deaminase-related (IPR015517), Deoxycytidylate deaminase (IPR016473), Cytidine deaminase-like (IPR016193), Cytidine and deoxycytidylate deaminases, zinc-binding (IPR002125)	_
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Major tail protein V; bacteriophage lambda, phage tail, GPV, IG-like domain, viral; NMR {Enterobacteria phage lambda}	1.10E-19	Invasin/intimin cell-adhesion fragments (IPR008964), Bacterial Ig-like, group 2 (IPR003343)	_
		Rossmann-like alpha/beta/alpha sandwich fold (IPR014729), Cytidyltransferase-like domain (IPR004821), NUDIX hydrolase domain-like (IPR015797), NUDIX hydrolase domain (IPR000086)	_
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Nicotinamide-nucleotide adenylyltransferase; two individual domains, hydrolase; HET: AMP; 2.30A {Francisella tularensis}	9.50E-54	Nicotinate phosphoribosyltransferase family (IPR007229), Nicotinamide phosphoribosyl transferase (IPR016471), Quinolinate phosphoribosyl transferase, C-terminal (IPR002638),	_
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Nicotinamide phosphoribosyltransferase; transferase-transferase inhibitor complex; HET: 20P; 1.50A {Homo sapiens}	9.00E-113	Sirtuin family (IPR003000), DHS-like NAD/FAD-binding domain (IPR029035), Sirtuin family, catalytic core domain (IPR026590), Sirtuin family (IPR003000), Sirtuin family, catalytic core small domain (IPR026591) Sirtuin family, catalytic core small domain (IPR026591)	_
		NUDIX hydrolase domain-like (IPR015797), NUDIX hydrolase domain (IPR000086)	_
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Silent information regulator 2; protein-ligand complex, gene regulation; HET: APR; 1.47A {Archaeoglobus fulgidus}	1.30E-62	PIN domain-like (IPR029060), PIN domain (IPR002716), P-loop containing nucleoside triphosphate hydrolase (IPR027417), PhoH-like protein (IPR003714)	_
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CMP/hydroxymethyl CMP hydrolase; CMP N-glycosidase; HET: C5P; 1.55A {Streptomyces rimofaciens}	4.00E-18	_	_
Groes protein; chaperone; HET: ADP; 2.81A {Escherichia coli}	1.50E-38	GroES chaperonin family (IPR020818), GroES-like (IPR011032),	_
Tyrosyl-tRNA synthetase; complex with L-tyrosine, rossmann fold, ligase; HET: BIF TYR; 2.65A {Escherichia coli}	2.00E-101	Aminoacyl-tRNA synthetase, class Ic (IPR002305) Tyrosine-tRNA ligase (IPR002307), Tyrosine-tRNA ligase, bacterial-type (IPR024088), Tyrosine-tRNA ligase, bacterial-type, type 1 (IPR024107), Rossmann-like alpha/beta/alpha sandwich fold (IPR014729), RNA-binding S4 domain (IPR002942)	_
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DCMP deaminase, deoxycytidylate deaminase; hydrolase; HET: DDN; 2.20A {Enterobacteria phage T4}	8.20E-27		_
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DTMP kinase, thymidylate kinase; nucleotide biosynthesis, ATP-binding, nucleotide-binding, poxvirus, transferase; HET: TYD POP; 2.4A {Vaccinia virus copenhagen}	9.60E-19	P-loop containing nucleoside triphosphate hydrolase (IPR027417)	_

Anaerobic ribonucleotide-triphosphate reductase large chain; oxidoreductase, allosteric regulation, substrate specificity; 2.45A {Bacteriophage T4}	2.00E-149	Ribonucleoside-triphosphate reductase, anaerobic (IPR012833), Glycine radical domain (IPR001150)	_
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Pyruvate formate-lyase 1-activating enzyme; adoMet radical, SAM radical, activase, glycyl radical, carbo metabolism, glucose metabolism, iron; HET: MT2 PGE; 2.25A {Escherichia coli}	9.50E-25	Ribonucleoside-triphosphate reductase activating, anaerobic (IPR012837), Aldolase-type TIM barrel (IPR013785)	_
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THG1-like uncharacterized protein; polymerase PALM-like catalytic domain, transferase, GTP and binding; HET: ATP; 2.36A {Bacillus thuringiensis}	1.30E-83	tRNAHis guanylyltransferase Thg1 (IPR007537)	_
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_		Protein of unknown function DUF4326) (IPR025475)	_
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Protein (N-4 cytosine-specific methyltransferase PVU II); type II DNA-(cytosine N4) methyltransferase, amino methylation, selenomethionine; HET: SAH; 2.80A {Proteus vulgaris}	1.40E-45	Restriction/modification DNA-methylase (IPR001091), S-adenosyl-L-methionine-dependent methyltransferase (IPR029063), DNA methylase N-4/N-6 (IPR002941)	_
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_		Nucleotidyltransferase, predicted (IPR018775)	_
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Acyl carrier protein; structural genomics, riken structural genomics/proteomics in RSGI, NPPSFA; 1.50A {Thermus thermophilus}	1.20E-15	Acyl carrier protein (ACP) (IPR003231), Acyl carrier protein-like (IPR009081)	_
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		Ferritin-like superfamily (IPR009078)	_
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Thymidine kinase; transferase, type II, transferase; HET: TTP; 1.83A {Homo sapiens}	2.40E-38		_
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Naegleria gruberi RNA ligase; RNA repair, adenylyltransferase; HET: AMP; 1.69A {Naegleria gruberi}	7.00E-68	RNA ligase, DRB0094 (IPR012646), RNA ligase domain, REL/Rln2 (IPR021122),	_

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RO sixty-related protein, RSR; alpha helical repeats, VON willebrand factor A domain, beta- RNA binding protein; 1.89A {Deinococcus radiodurans}	5.80E-35	Domain of unknown function DUF2828 (IPR024553), Domain of unknown function DUF2828 (IPR024553), von Willebrand factor, type A (IPR002035)	_
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Oxygen-regulated invasion protein ORGB,endolysin; type III secretion system, protein transport; 2.00A {Salmonella typhimurium}, P60_TTH, cell WALL-binding endopeptidase-related protein; hydrolase; HET: NAG NDG; 1.75A {Thermus thermophilus}	3.8E-30, 3.6e-09	LysM domain (IPR018392), Lysozyme domain (IPR023347)	1
_		Ribosomal protein S30Ae/sigma 54 modulation protein (IPR003489),	_
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TRNA CCA-adding enzyme; tRNA nucleotidyltransferase, translation, transferase; HET: ATP; 3.00A {Geobacillus stearothermophilus}	7.60E-70	Poly A polymerase, head domain (IPR002646), tRNA nucleotidyltransferase/poly(A) polymerase, RNA and SrmB- binding domain (IPR032828)	_
NDX1; nudix protein, diadenosine polyphosphate, AP6A, thermus THER HB8, hydrolase, riken structural genomics/proteomics initia RSGI; 1.70A {Thermus thermophilus}	5.70E-25	NUDIX hydrolase domain-like (IPR015797), NUDIX hydrolase domain (IPR000086), NUDIX hydrolase (IPR020476)	_
Glutaredoxin 3; GSH, oxidoreductase; HET: CSU GSH; 1.58A {Alkaliphilus oremlandii}	3.20E-21	Glutaredoxin (IPR002109), Thioredoxin-like fold (IPR012336)	_
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Glutamyl-tRNA(Gln) amidotransferase subunit E; ligase, ligase/RNA complex; 3.15A {Methanothermobacterthermautotrophicus}	2.60E-39	Macro domain (IPR002589)	_
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		P-loop containing nucleoside triphosphate hydrolase (IPR027417)	_
Conserved hypothetical protein protein BT1257; structural genomics, PSI, PROT structure initiative; HET: MSE; 1.25A {Bacteroides thetaiotaomicron}	1.50E-40	Tail sheath protein (IPR007067)	_
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Sheath; pyocin, bacteriocin, sheath, structural protein; 3.50A {Pseudomonas aeruginosa}	1.10E-53	Restriction endonuclease, FokI, C-terminal/endonuclease I, core (IPR011578), TnsA endonuclease, N-terminal (IPR014833)	_
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		P-loop containing nucleoside triphosphate hydrolase (IPR027417), AAA+ ATPase domain (IPR003593)	_
Transposon TN7 transposition protein TNSA; protein-protein complex, mixed alpha-beta, DNA binding prote; 1.85A {Escherichia coli}	6.10E-26	Putative metallopeptidase domain (IPR025154), Putative metallopeptidase domain (IPR025154), VWA-like domain (IPR018698), von Willebrand factor, type A (IPR002035)	1

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Microneme protein 2; A/I domain, cell adhesion, hydrolase; 2.05A {Toxoplasma gondii}	2.60E-10	Thymidylate synthase (IPR000398), Thymidylate synthase/dCMP hydroxymethylase domain (IPR023451)	_
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_		Domain of unknown function DUF4376 (IPR025484)	_
		Parallel beta-helix repeat (IPR006626)	_
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ORF135, CTP pyrophosphohydrolase; NMR {Escherichia coli}	6.90E-23	NUDIX hydrolase domain-like (IPR015797), NUDIX hydrolase domain (IPR000086)	_
Tail connector protein GP15; bacteriophage T4, phage tail terminator protein, viral; 2.70A {Enterobacteria phage T4}	3.20E-71	Myoviridae tail sheath stabiliser (IPR031997)	_
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CLPA protein; AAA+, N-terminal domain, CLPS, crystal, binding mechanism, hydrolase; HET: ADP; 2.25A {Escherichia coli} SCOP	8.00E-101	ClpA/B family (IPR001270), Clp, N-terminal (IPR004176), P-loop containing nucleoside triphosphate hydrolase (IPR027417), AAA+ ATPase domain (IPR003593), Clp ATPase, C-terminal (IPR019489)	_
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Tail lysozyme; GP25-like fold, initiation of sheath polymerization, basepla component, T4 GP18, T4 GP53, T4 GP6, hydrolase; 2.47A {Enterobacteria phage T4}	1.50E-31	GpW/Gp25/anti-adapter protein IraD (IPR007048)	_
Lysozyme; direct methods, lanthinide binding sites, hydrolase; 1.04A {Enterobacteria phage P22}	1.80E-41	Glycoside hydrolase, family 24 (IPR002196), T4-type lysozyme (IPR001165), Lysozyme-like domain (IPR023346), Lysozyme domain (IPR023347)	_
beta-barrel, OB-fold, beta-helix, type VI secretion system C spike, secreted outside of the cell, toxin; HET: TAM; 3.32A {Pseudomonas aeruginosa}	1.70E-36	Glycoside hydrolase, family 24 (IPR002196),Gp5 N-terminal (IPR006531), Lysozyme-like domain (IPR023346), Lysozyme domain (IPR023347)	_
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Tail protein X, GPX; LYSM, phage tail, viral protein; NMR {Enterobacteria phage P2}	0.019	Baseplate wedge protein gp53, bacteriophage T4 (IPR022607)	_

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Exonuclease, putative; adenosine triphosphate, bacterial proteins, DNA breaks, DOUB stranded, DNA repair, DNA repair enzymes; HET: ADP; 2.61A {Thermotoga maritima}	9.70E-41	Metallo-dependent phosphatase-like (IPR029052), Calcineurin-like phosphoesterase domain, lpxH type (IPR024654)	_
DNA double-strand break repair RAD50 ATPase; DNA repair, ABC transporter ATPase domain-like; HET: DNA ADP; 2.70A {Methanocaldococcus jannaschii}	3.40E-35	P-loop containing nucleoside triphosphate hydrolase (IPR027417),	_
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Portal protein GP20; viral protein; 3.63A {Enterobacteria phage T4}	6.00E-129	Structural protein of head Gp20 (IPR010823)	_
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_		Peptidase U9, T4 prohead protease (IPR005082)	_
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Head vertex protein GP24; bacteriophage T4, capsid protein, bacteriophage, virus, HK97, MAD, viral protein; 2.90A {Enterobacteria phage T4}	8.00E-108	Capsid protein, T4-like bacteriophage (IPR010762)	_
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Structure-specific endonuclease subunit SLX1; DNA repair, GIY-YIG, homogolous recombination, HYD; 1.78A {Candida glabrata}	3.30E-05	Bacteriophage T5, Orf172 DNA-binding (IPR018306)	_
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DNA polymerase, GP43; difluorotoluene nucleoside; HET: DNA DOC DGT; 1.73A {Enterobacteria phage RB69}	4.00E-130	DNA-directed DNA polymerase, family B (IPR006172), DNA-directed DNA polymerase, family B, multifunctional domain (IPR006134), DNA polymerase, palm domain (IPR023211)	_
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Hypothetical protein AQ_1665; structural genomics, protein structure initi midwest center for structural genomics, PSI, MCSG, unknown; 2.40A {Aquifex aeolicus}	1.40E-26	Metallo-dependent phosphatase-like (IPR029052), Calcineurin-like phosphoesterase domain, apaH type (IPR004843)	_

		Putative regulatory protein, FmdB, Zinc ribbon domain (IPR013429)	_
Groes protein; chaperone; HET: ADP; 2.81A {Escherichia coli}	1.50E-41	GroES chaperonin family (IPR020818), GroES-like (IPR011032)	_
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Ribonuclease H, RNAse H; BPT4 RNAse H, 5'-3' exonuclease, hydrolase, endonuclease; 1.50A {Enterobacteria phage T4}	1.40E-57	PIN domain-like (IPR029060), 5'-3' exonuclease, alpha-helical arch, N-terminal (IPR020046)	_
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Terminase, DNA packaging protein GP17; large terminase, alternative initiation, ATP-binding, DNA-binding, hydrolase, nuclease; HET: DNA; 2.80A {Bacteriophage T4}	2.60E-50	P-loop containing nucleoside triphosphate hydrolase (IPR027417), Terminase, large subunit (IPR004921)	_
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		Bacteriophage T4, Gp32, single-stranded DNA-binding (IPR012339), Nucleic acid-binding, OB-fold (IPR012340)	_
		DNA recombination and repair protein RecA (IPR013765), P-loop containing nucleoside triphosphate hydrolase (IPR027417), DNA recombination and repair protein RecA, monomer-monomer interface (IPR020587)	_

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DNA polymerase III epsilon subunit; DNA polymerase proofreading domain, transferase; HET: DNA U5P; 1.60A {Escherichia coli}	1.60E-30	Putative quorum-sensing-regulated virulence factor (IPR024530), Ribonuclease H-like domain (IPR012337), Exonuclease, RNase T/DNA polymerase III (IPR013520)	_
DAR protein, ATP-dependent DNA helicase UVSW; ATP-dependant helicase, T4-bacteriophage, recombination, hydrolase; 2.70A {Enterobacteria phage T4}	8.30E-61	P-loop containing nucleoside triphosphate hydrolase (IPR027417), Helicase superfamily 1/2, ATP-binding domain (IPR014001), Helicase/UvrB, N-terminal (IPR006935), Helicase, C-terminal (IPR001650)	_
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		S-adenosyl-L-methionine-dependent methyltransferase (IPR029063)	_
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Replicative DNA helicase; RECA-type helicase, ATP binding, D binding, replication; HET: ADP; 3.30A {Aquifex aeolicus}	8.80E-58	P-loop containing nucleoside triphosphate hydrolase (IPR027417), P-loop containing nucleoside triphosphate hydrolase (IPR027417)	_
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Exodeoxyribonuclease 8; exonuclease, recombination, hydrolase; 2.80A {Escherichia coli}	2.50E-17	Restriction endonuclease type II-like (IPR011335)	_
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Ribonucleoside-diphosphate reductase 1 subunit alpha; oxidoreductase, DNA replication, allosteric enzyme, nucleotide-binding; HET: NIY; 2.10A {Escherichia coli}	1.00E-187	ATP-cone domain (IPR005144), Ribonucleotide reductase large subunit, C-terminal (IPR000788), Ribonucleotide reductase, class I , alpha subunit (IPR013346), Ribonucleotide reductase R1 subunit, N-terminal (IPR008926), Ribonucleotide reductase large subunit, N-terminal (IPR013509)	_
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Ribonucleotide reductase R2; radical protein, DI iron, oxidoreductase; 1.42A {Escherichia coli}	3.90E-89	Ribonucleotide reductase small subunit (IPR000358), Ferritin-like superfamily (IPR009078) Ribonucleotide reductase-related (IPR012348)	_
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Putative NTP pyrophosphohydrolase; structural genomics, joint center for structural genomics, J protein structure initiative; 1.78A {Exiguobacterium sibiricum 255-15}	1.30E-42	Phosphoribosyl-ATP pyrophosphohydrolase-like (IPR021130), NTP pyrophosphohydrolase-like domain (IPR023292),	_
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Dihydrofolate reductase; DHFR, NADP, oxidoreductase; 2.00A {Geobacillus stearothermophilus}	2.70E-39	Dihydrofolate reductase (IPR012259), Dihydrofolate reductase-like domain (IPR024072) Dihydrofolate reductase domain (IPR001796)	_
Ribonuclease HI, RNAse HI; hydrolase, endoribonuclease; 2.00A {Shewanella oneidensis}	6.20E-36	Ribonuclease H-like domain (IPR012337) Ribonuclease H domain (IPR002156)	_
ATP-dependent DNA helicase DDA; RECA-like domain, SH3 domain, PIN-tower interface, coupling hydrolysis to DNA unwinding, ssDNA; 3.30A {Enterobacteria phage T4}	1.30E-45	P-loop containing nucleoside triphosphate hydrolase (IPR027417), UvrD-like helicase C-terminal domain	_
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Protein (translation initiation factor IF3); gene regulation; NMR {Escherichia coli}	3.70E-30	Translation initiation factor 3, N-terminal (IPR019814), Translation initiation factor 3, C-terminal (IPR019815)	_
ATP-dependent CLP protease adapter protein CLPS; adaptor, protein-peptide complex, peptide binding protein; 1.15A {Caulobacter vibrioides}	1.60E-31	Ribosomal protein L7/L12, C-terminal/adaptor protein ClpS-like (IPR014719) Adaptor protein ClpS, core (IPR003769)	_
Uncharacterized protein; chicago center for functional annotation, structural genomic biology, midwest center for structural genomics, MCSG; HET: MSE; 1.73A {Yersinia pestis}	3.50E-28	KTSC domain (IPR025309)	_
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Topoisomerase IV subunit B, DNA topoisomerase 4 S chimera; DNA unwinding, supercoiling, isomerase-DNA complex; HET: DNA; 3.70A {Streptococcus pneumoniae}	1.00E-154		_

DNA topoisomerase 4 subunit A; topoisomerase II fold; HET: DNA; 2.80A {Staphylococcus aureus}	2.00E-142	DNA topoisomerase II, eukaryotic-type (IPR001154), DNA topoisomerase, type IIA, subunit A/C-terminal (IPR002205), DNA topoisomerase, type IIA-like domain (IPR013760), DNA topoisomerase, type IIA, subunit A/ C-terminal, alpha-beta (IPR013758), Arginine repressor C-terminal-like domain (IPR024946)	_
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DNA polymerase III alpha subunit; DNA replication, nucleotidyltransferase, beta, PHP, transferase; HET: DNA; 2.30A {Escherichia coli}	1.80E-49	Bacterial DNA polymerase III, alpha subunit (IPR011708)	_
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		GroES-like (IPR011032)	_
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RFCS; clamp loader, extended AAA-ATPase domain, complex with ADP, replication; HET: ADP; 2.80A {Pyrococcus furiosus}	7.70E-42	P-loop containing nucleoside triphosphate hydrolase (IPR027417) AAA+ ATPase domain (IPR003593)	_
		HAD-like domain (IPR023214)	_
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Transcriptional regulator NADR; NMN, NMN adenylyl transferase, ribosylnicotinamide KINA transferase; HET: NAD; 2.90A {Haemophilus influenzae}	3.70E-45	Bifunctional transcriptional regulator NadR (IPR016429), Rossmann-like alpha/beta/alpha sandwich fold , Cytidyltransferase-like domain (IPR004821), P-loop containing nucleoside triphosphate hydrolase (IPR027417)	_
Nicotinamide riboside transporter PNUC; membrane transport, vitamin transport, nicotinamide riboside transport protein; HET: NNR BOG; 2.80A {Neisseria mucosa atcc 25996}	1.20E-58	Nicotinamide mononucleotide transporter PnuC (IPR006419)	7
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Putative acetylornithine deacetylase; ATP-dependent amine/thiol ligase family, ATP-dependent amine ligase, enzyme-carrier protein complex; HET: ADP GLU; 1.80A {Sulfolobus tokodaii}	1.20E-06	Protein of unknown function DUF4343 (IPR025643)	_
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CLPA protein; AAA+, N-terminal domain, CLPS, crystal, binding mechanism, hydrolase; HET: ADP; 2.25A {Escherichia coli}	9.00E-22		_
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5'(3')-deoxyribonucleotidase, cytosolic type; protein conformation, sequence homology, HA hydrolase, dephosphorylation; 1.08A {Homo sapiens}	1.50E-20	HAD-like domain (IPR023214), 5'(3')-deoxyribonucleotidase (IPR010708)	_
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Putative acetylornithine deacetylase; ATP-dependent amine/thiol ligase family, ATP-dependent amine ligase, enzyme-carrier protein complex; HET: ADP GLU; 1.80A {Sulfolobus tokodaii}	2.30E-13	Protein of unknown function DUF4343 (IPR02	_
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Hypothetical protein TA0108; structural genomics, Conserved hypothetical protein protein, PSI, PR structure initiative; HET: SO4; 1.95A {Thermoplasma acidophilum}	2.00E-44	Peptidyl-tRNA hydrolase II domain (IPR023476), Peptidyl-tRNA hydrolase, PTH2 (IPR002833)	_
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Modification methylase HHAI; base flipping, restriction system, transferase-DNA complex; HET: 5CM 2PR SAH EPE CIT; 1.7A {Haemophilus haemolyticus}	1.30E-64	S-adenosyl-L-methionine-dependent methyltransferase (IPR029063), C-5 cytosine methyltransferase (IPR001525)	_
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		Heat shock protein DnaJ, cysteine-rich domain (IPR001305)	_

HNH homing endonuclease; HNH catalytic motif, helix-turn-helix DNA binding domain, PR complex, DNA binding protein-DNA complex; 2.92A {Bacillus phage SPO1}	5.90E-20	HNH nuclease (IPR003615), Uncharacterised protein family YabK (IPR020115)	_
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		Acyl-CoA N-acyltransferase (IPR016181	_
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Putative secreted protein; phospholipase A2, atomic resolution, internal motion, hydrolase; 1.05A {Streptomyces violaceoruber}	5.50E-13	Campylobacter phage CGC-2007, Cje0229 (IPR010767)	_
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		S-adenosyl-L-methionine-dependent methyltransferase (IPR029063)	_
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BLDD, putative DNA-binding protein; the DNA-binding domain of BLDD; 1.81A {Streptomyces coelicolor}	3.90E-18	Lambda repressor-like, DNA-binding domain (IPR010982), Cro/C1-type helix-turn-helix domain (IPR001387)	_
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Sigma-70, RNA polymerase sigma factor RPOD; switch region, squaramide, transcription-inhibitor complex; HET: 4C6; 3.57A {Escherichia coli}	2.30E-48	RNA polymerase sigma factor, region 2 (IPR013325), RNA polymerase sigma-70 like domain (IPR014284), RNA polymerase sigma-70 region 2 (IPR007627), RNA polymerase sigma factor, region 3/4 (IPR013324)	_
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Endonuclease V; 1.45A {Enterobacteria phage T4}	1.80E-72	T4 endonuclease V (IPR024796)	_
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HNH endonuclease; structural genomics, PSI-biology, protein structure initiati northeast structural genomics consortium (NESG); 2.60A {Geobacter metallireducens}	3.80E-14	HNH endonuclease (IPR002711), HNH nuclease (IPR003615)	_
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26S protease regulatory subunit 8 homolog; hydrolase, AAA-ATPase, ATP-analog, classification; 7.70A {Saccharomyces cerevisiae}	7.30E-28	P-loop containing nucleoside triphosphate hydrolase (IPR027417), P-loop containing nucleoside triphosphate hydrolase (IPR027417), AAA+ ATPase domain (IPR003593), ATPase, AAA-type, core (IPR003959)	_
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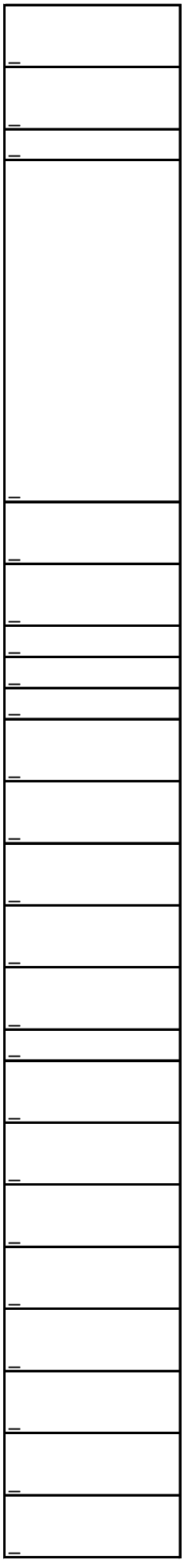
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_		Biofilm formation YgiB (IPR009576)	1
_		Concanavalin A-like lectin/glucanase domain (IPR013320)	_
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Kelch-like protein 3; signaling protein-transferase complex, KLHL3, ubiquitin, ADA protein, protein-binding, kelch repeat; HET: 12P; 1.56A {Homo sapiens}	1.20E-43	Kelch-type beta propeller (IPR015915)	_
SAP-like pentraxin; physiological doubly-stacked heptamer, pentraxin fold, cyclic heptamer, invertebrate lectin, sugar binding protein; 2.30A {Limulus polyphemus}	8.30E-07	Concanavalin A-like lectin/glucanase domain (IPR013320	_
Kelch-like ECH-associated protein 1; beta-propeller, kelch repeat motif, protein binding; HET: MSE; 1.35A {Homo sapiens}	1.20E-40	Kelch-type beta propeller (IPR015915), Kelch repeat type 1 (IPR006652)	_
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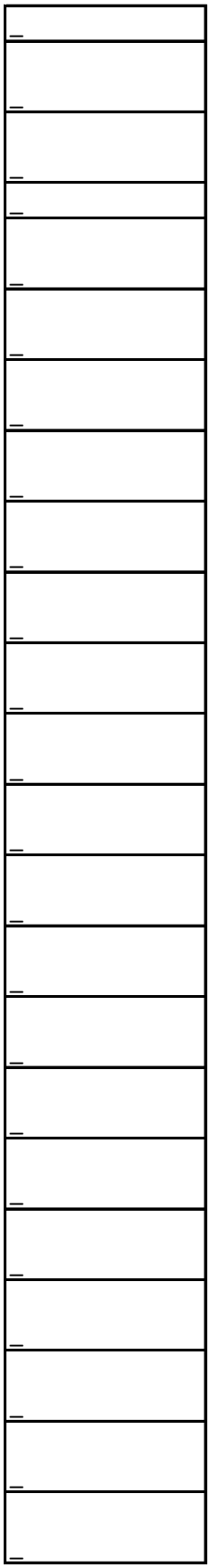
Kelch-like ECH-associated protein 1; beta-propeller, kelch repeat motif, protein binding; HET: MSE; 1.35A {Homo sapiens}	3.20E-40	Kelch-type beta propeller (IPR015915), Kelch repeat type 1 (IPR006652)	_
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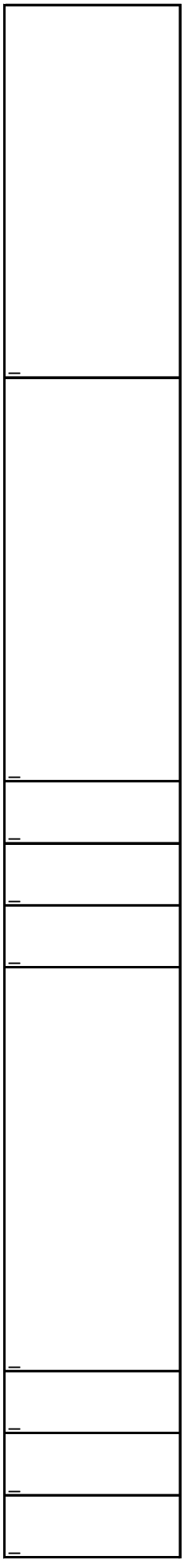
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PH stomatin; archaea, trimer, coiled- coil, flotillin, SPFH, membrane fusion, trafficking, transmembrane, membrane protein; 3.20A {Pyrococcus horikoshii}	4.70E-28	Band 7 domain (IPR001107)	1
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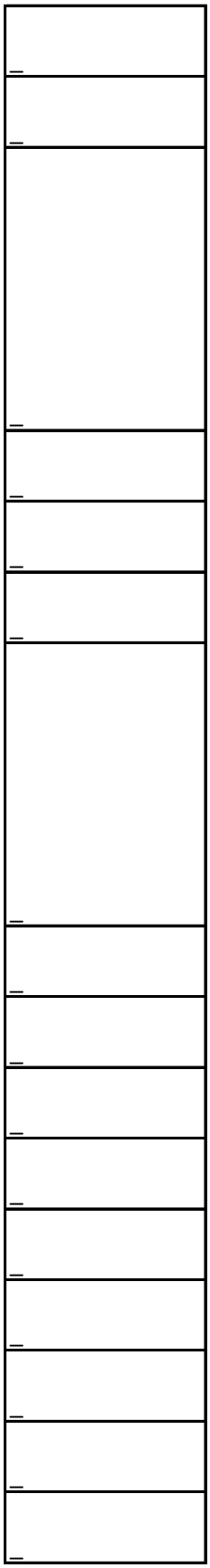
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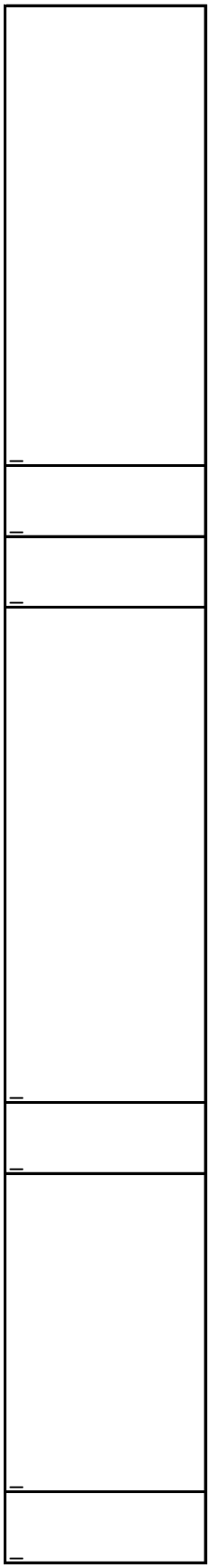
Lipoproteins (LipoP)
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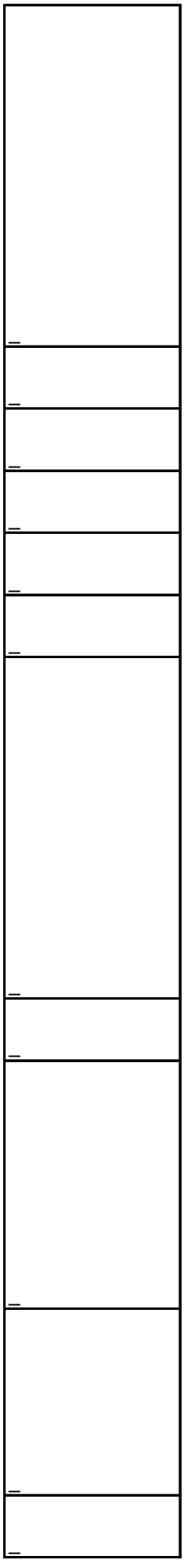


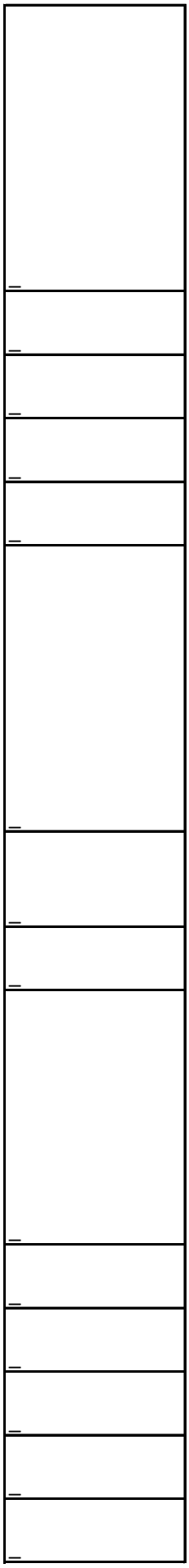






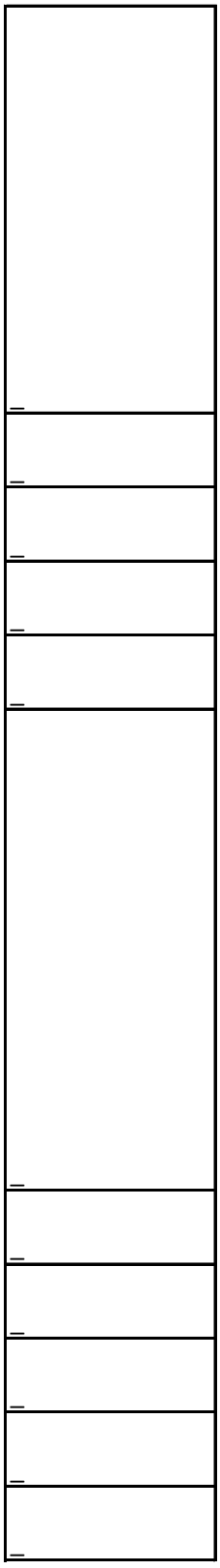




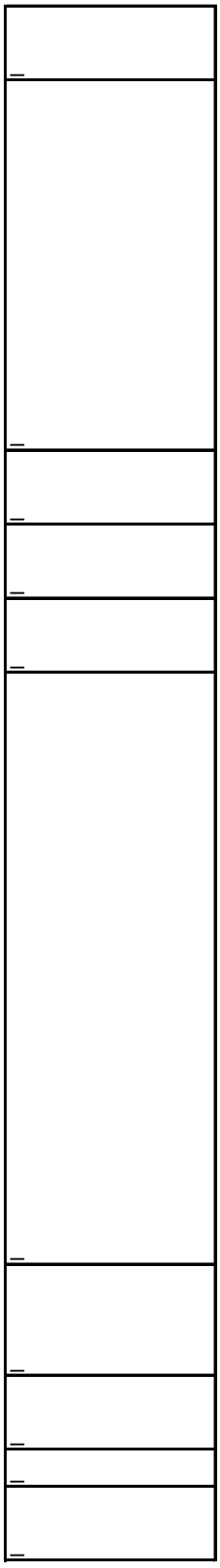


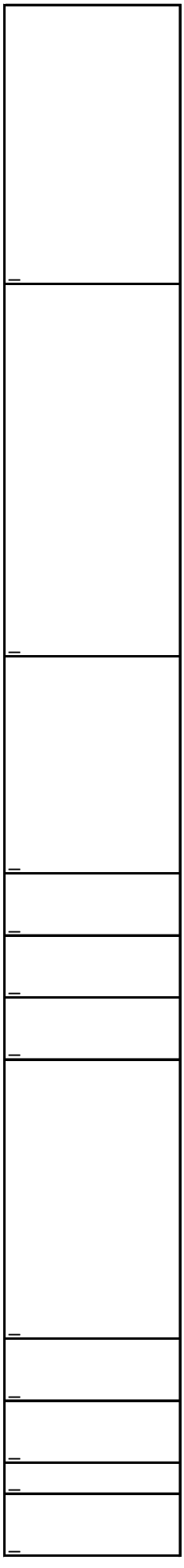
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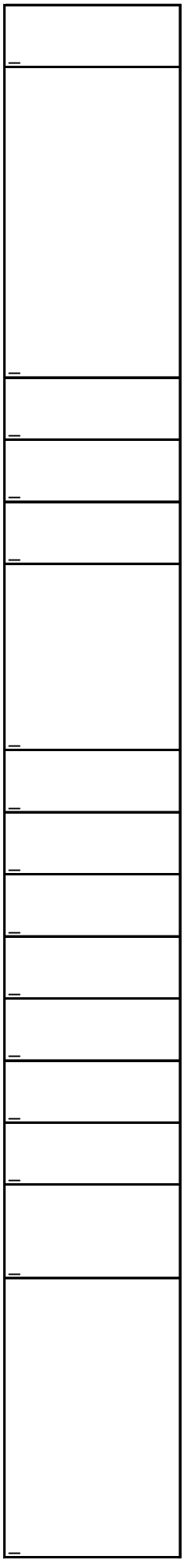
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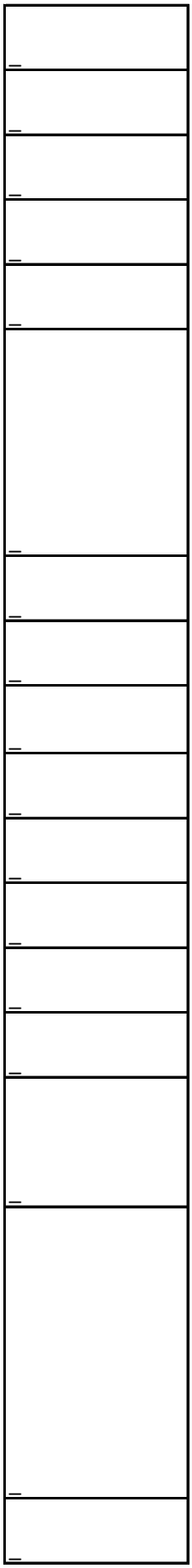


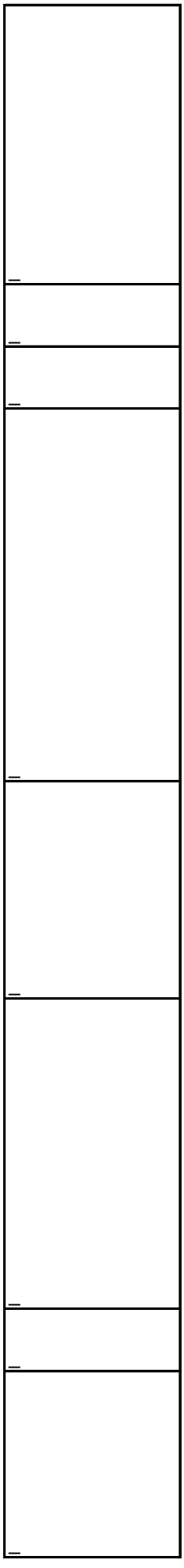
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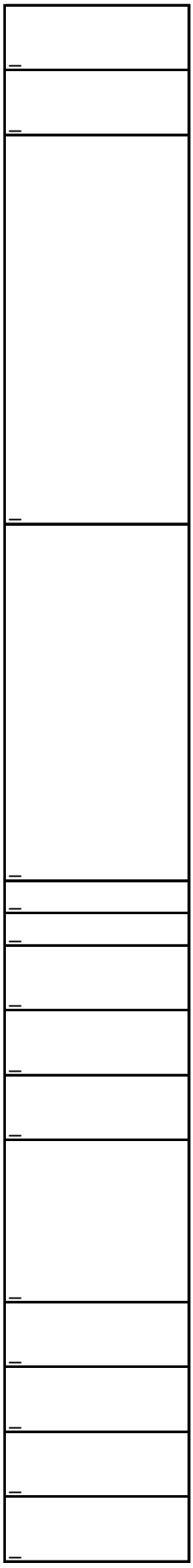


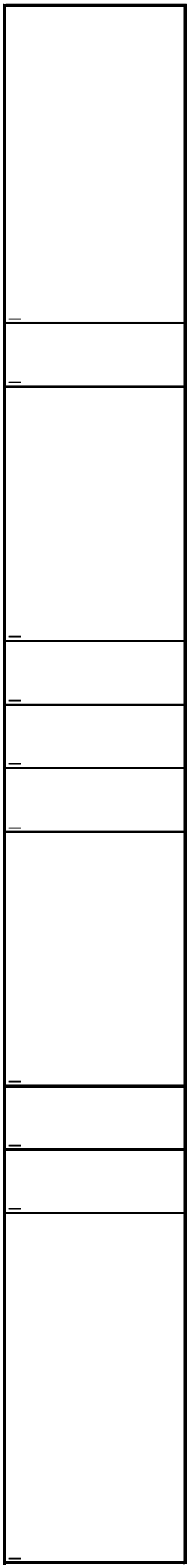


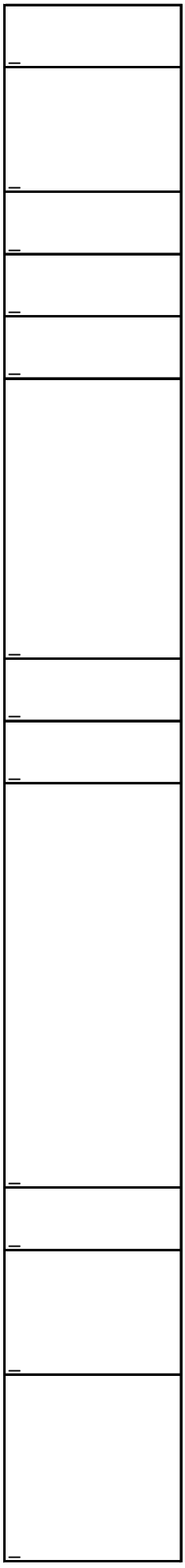


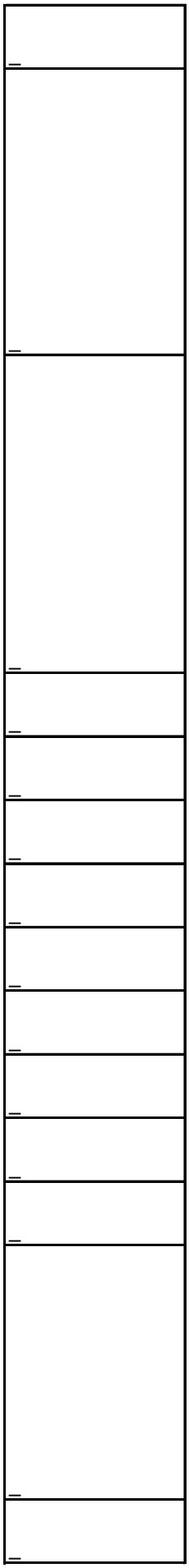


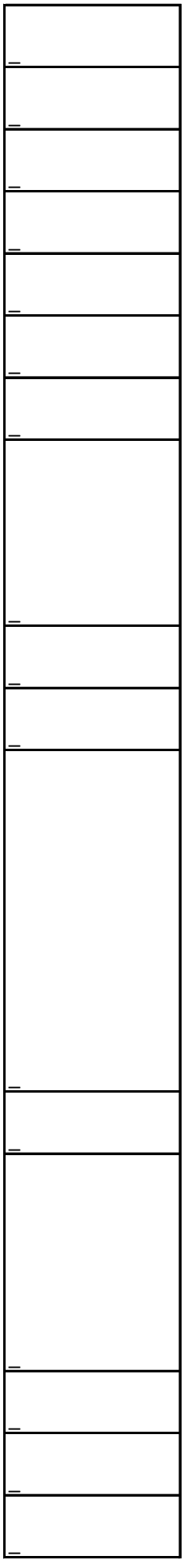


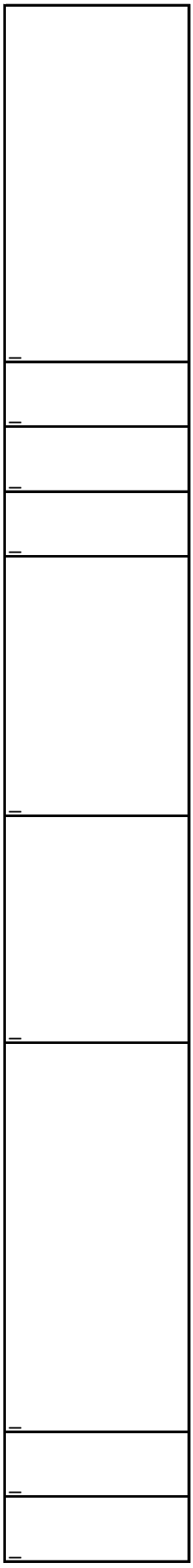


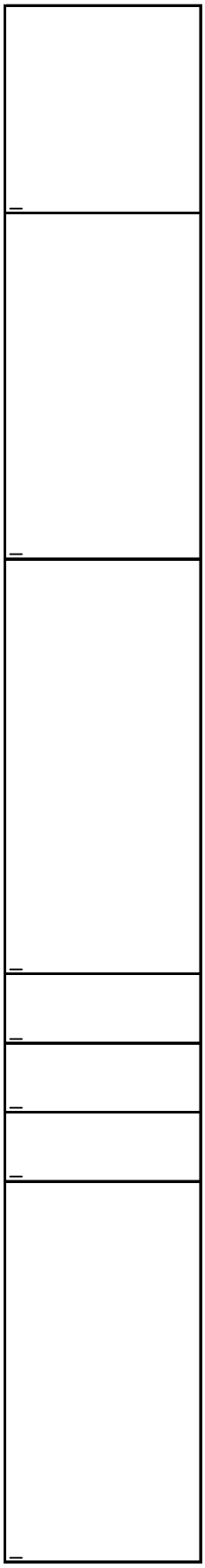


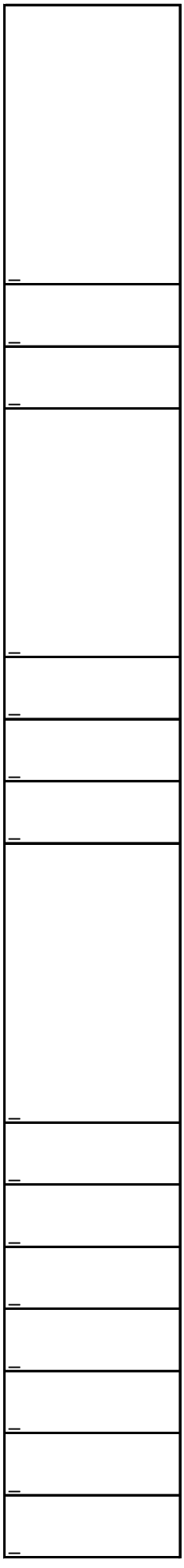


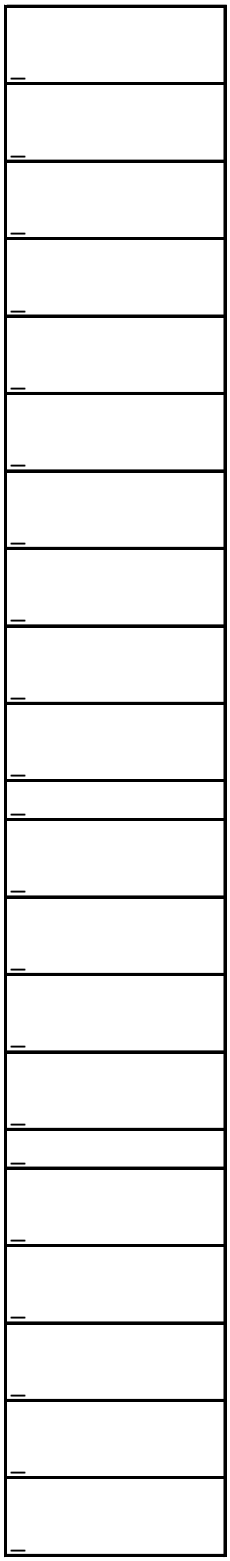


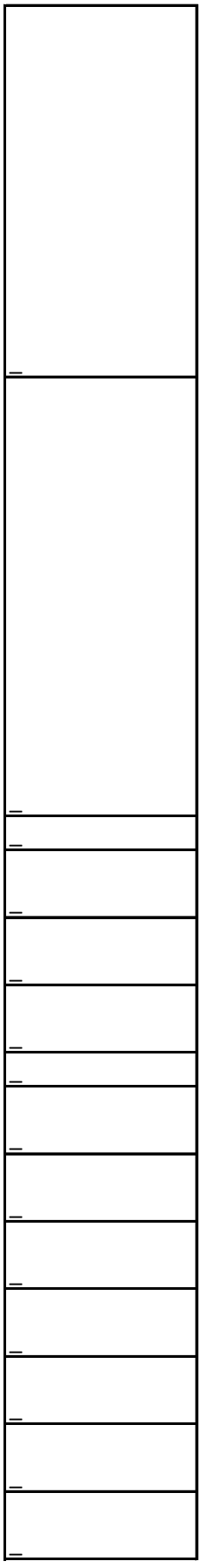


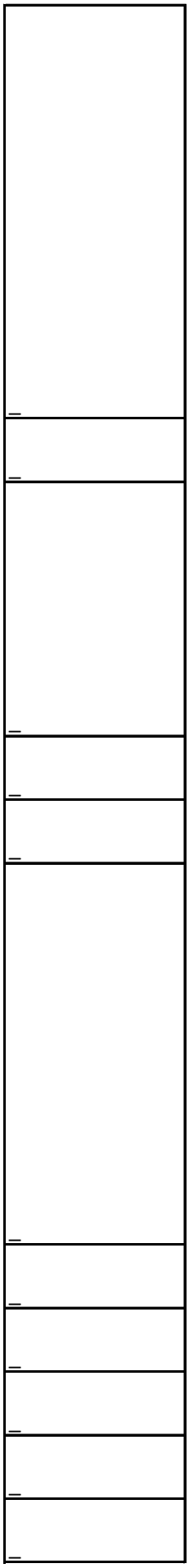


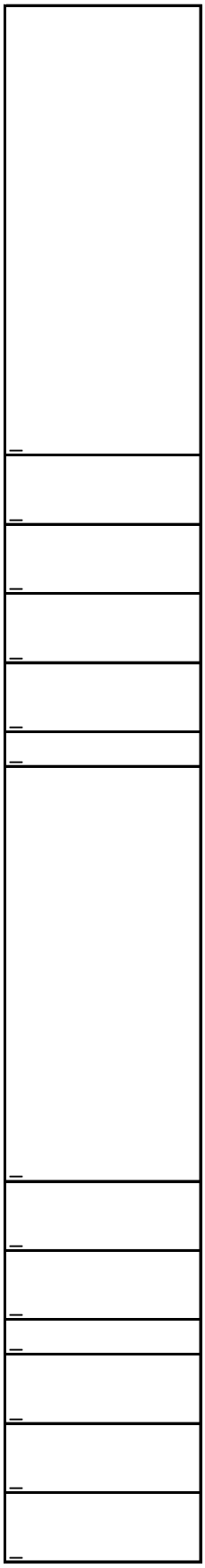


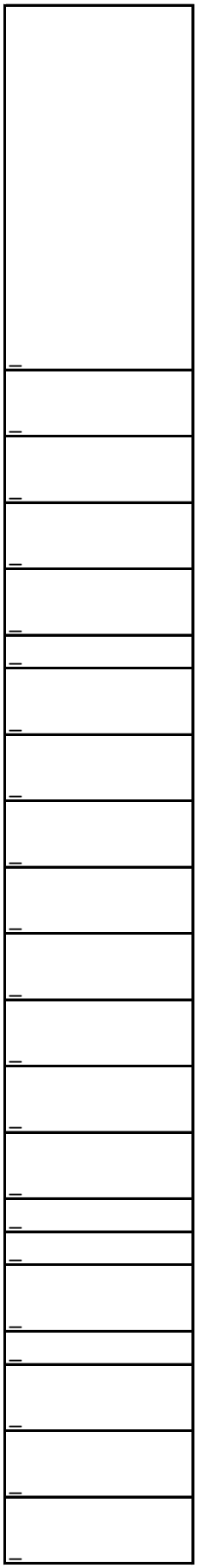


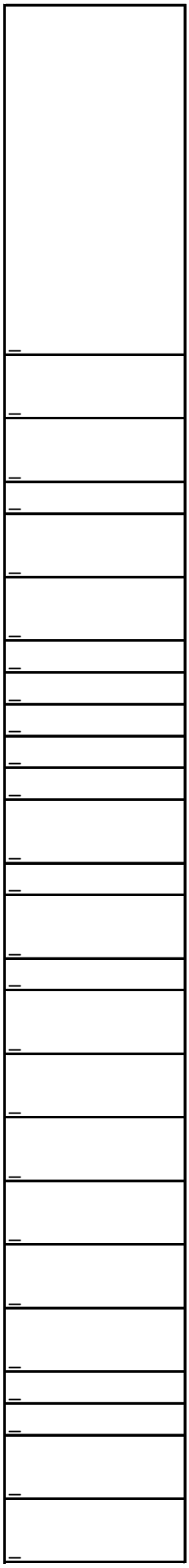


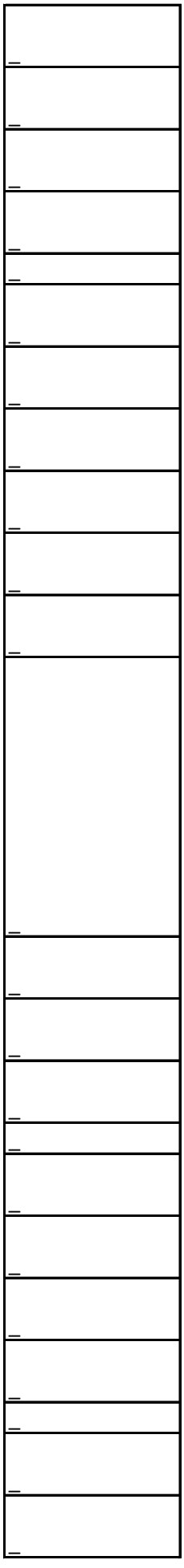




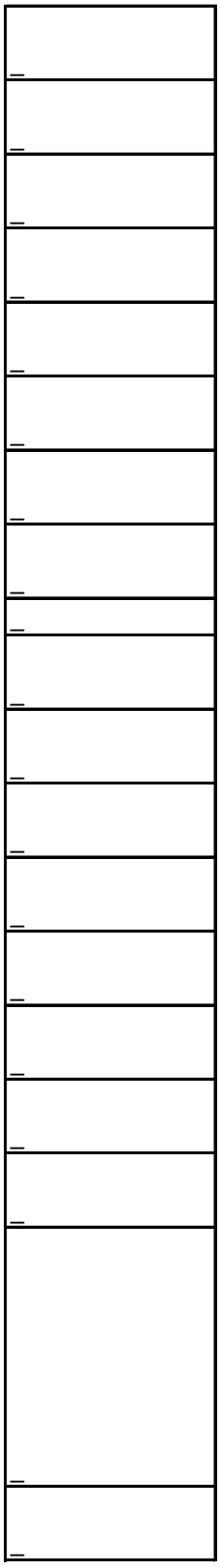


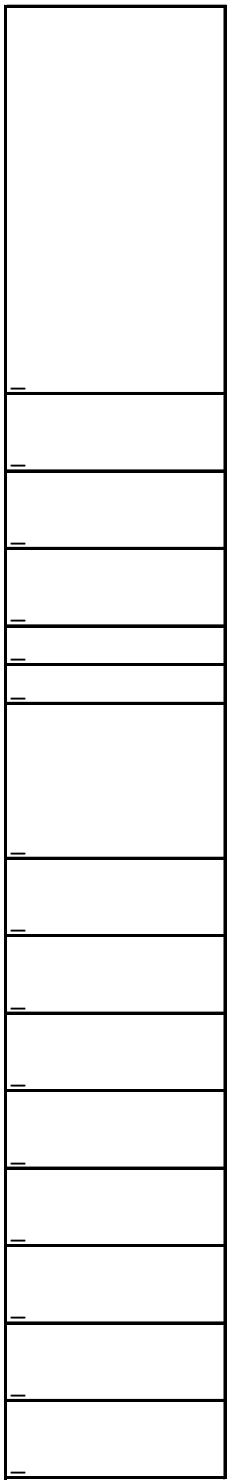


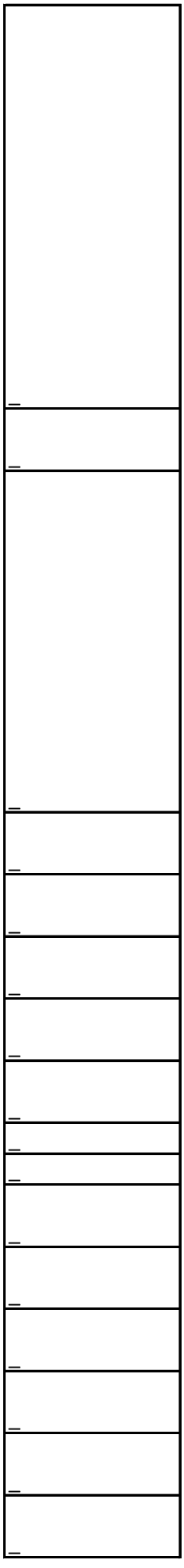




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