

A. Bacterial families		Total sum of spectra	Average BGP_02	Average BGP_03	Average BGP_04	Average BGP_05a	Average BGP_05b	Average BGP_07	Average BGP_09	Average BGP_10	Average BGP_X1	Average BGP_X2	Average BGP_X3	Total amount of
<i>Bacillaceae</i>	F	37541	381 ± 67	954 ± 159	1178 ± 95	1501 ± 247	1159 ± 368	882 ± 95	760 ± 109	875 ± 151	536 ± 95	893 ± 63	268 ± 144	%of all microorganisms 6.7%
	P	264	3 ± 3	3 ± 2	4 ± 2	19 ± 8	17 ± 10	8 ± 4	5 ± 3	1 ± 1	4 ± 3	1 ± 2	2 ± 3	%of phage proteins for this family 0.7%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Enterobacteriaceae</i>	F	19308	159 ± 12	543 ± 103	495 ± 125	587 ± 209	431 ± 139	594 ± 50	308 ± 45	350 ± 81	384 ± 105	373 ± 51	604 ± 751	%of all microorganisms 3.4%
	P	538	4 ± 1	2 ± 1	3 ± 1	17 ± 8	7 ± 5	4 ± 2	69 ± 17	4 ± 3	22 ± 4	2 ± 1	2 ± 2	%of phage proteins for this family 2.8%
	C	71	1 ± 1	0 ± 0	10 ± 3	1 ± 1	0 ± 1	0 ± 0	0 ± 0	0 ± 1	1 ± 1	2 ± 2	0 ± 0	%of CRISPR proteins for this family 0.4%
<i>Thermoanaerobacteraceae</i>	F	11565	692 ± 482	24 ± 9	108 ± 45	540 ± 155	373 ± 135	68 ± 12	348 ± 84	456 ± 180	47 ± 29	229 ± 36	8 ± 7	%of all microorganisms 2.1%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family 0.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Desulfovibrionaceae</i>	F	9585	102 ± 32	474 ± 167	180 ± 54	94 ± 25	91 ± 34	481 ± 153	82 ± 17	304 ± 95	226 ± 95	138 ± 84	226 ± 230	%of all microorganisms 1.7%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family 0.0%
	C	1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 1	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Thermotogaceae</i>	F	8618	16 ± 4	24 ± 6	42 ± 10	1043 ± 153	917 ± 233	16 ± 5	18 ± 5	10 ± 4	22 ± 4	28 ± 17	19 ± 11	%of all microorganisms 1.5%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family 0.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Spirochaetaceae</i>	F	7847	53 ± 23	82 ± 8	156 ± 17	104 ± 28	101 ± 11	347 ± 86	47 ± 5	765 ± 318	141 ± 22	131 ± 14	35 ± 42	%of all microorganisms 1.4%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family 0.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Rhizobiaceae</i>	F	7406	43 ± 30	192 ± 41	325 ± 25	224 ± 78	209 ± 21	109 ± 25	127 ± 29	191 ± 38	205 ± 74	164 ± 33	62 ± 64	%of all microorganisms 1.3%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family 0.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Clostridiaceae</i>	F	7279	75 ± 24	288 ± 21	212 ± 42	432 ± 65	333 ± 96	145 ± 32	46 ± 9	73 ± 2	72 ± 40	111 ± 14	33 ± 22	%of all microorganisms 1.3%
	P	166	0 ± 0	0 ± 0	0 ± 0	31 ± 19	11 ± 4	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family 2.3%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Streptococcaceae</i>	F	3675	219 ± 163	130 ± 27	45 ± 13	88 ± 31	57 ± 15	68 ± 20	40 ± 22	64 ± 30	33 ± 16	159 ± 133	18 ± 12	%of all microorganisms 0.7%
	P	10	0 ± 0	0 ± 1	1 ± 1	0 ± 0	0 ± 1	1 ± 1	1 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 1	%of phage proteins for this family 0.3%
	C	3	0 ± 0	0 ± 0	0 ± 0	1 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.1%
<i>Mycobacteriaceae</i>	F	2561	46 ± 12	143 ± 42	81 ± 13	97 ± 18	91 ± 45	48 ± 8	31 ± 9	19 ± 4	30 ± 10	33 ± 16	24 ± 15	%of all microorganisms 0.5%
	P	27	0 ± 1	0 ± 0	0 ± 0	1 ± 1	1 ± 1	1 ± 1	1 ± 1	0 ± 0	1 ± 1	3 ± 3	0 ± 1	%of phage proteins for this family 1.1%
	C	59	0 ± 0	6 ± 4	2 ± 1	0 ± 0	0 ± 0	5 ± 3	0 ± 0	0 ± 1	0 ± 0	1 ± 2	1 ± 1	%of CRISPR proteins for this family 2.3%
<i>Enterococcaceae</i>	F	2512	2 ± 2	13 ± 4	215 ± 54	48 ± 25	40 ± 13	53 ± 17	108 ± 21	16 ± 10	66 ± 12	58 ± 24	10 ± 9	%of all microorganisms 0.4%
	P	3	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	1 ± 1	%of phage proteins for this family 0.1%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Pseudomonadaceae</i>	F	1875	14 ± 3	49 ± 12	57 ± 9	35 ± 3	37 ± 6	86 ± 5	42 ± 36	59 ± 20	51 ± 21	31 ± 9	9 ± 5	%of all microorganisms 0.3%
	P	283	1 ± 1	1 ± 1	1 ± 1	39 ± 15	28 ± 16	2 ± 2	0 ± 0	0 ± 0	0 ± 1	0 ± 1	0 ± 0	%of phage proteins for this family 15.1%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Vibrionaceae</i>	F	1649	6 ± 2	40 ± 18	33 ± 6	123 ± 24	92 ± 32	27 ± 4	5 ± 2	9 ± 1	14 ± 7	25 ± 14	40 ± 38	%of all microorganisms 0.3%
	P	36	0 ± 0	3 ± 2	1 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	2 ± 2	4 ± 2	%of phage proteins for this family 2.2%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Pasteurellaceae</i>	F	1347	21 ± 5	51 ± 15	39 ± 9	27 ± 14	38 ± 15	65 ± 24	8 ± 2	28 ± 10	14 ± 8	23 ± 8	24 ± 24	%of all microorganisms 0.2%
	P	8	1 ± 1	1 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 1	%of phage proteins for this family 0.6%
	C	27	0 ± 0	5 ± 4	2 ± 2	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 1	%of CRISPR proteins for this family 2.0%
<i>Streptomyetaceae</i>	F	1000	10 ± 7	54 ± 1	30 ± 8	26 ± 11	35 ± 10	26 ± 8	9 ± 1	20 ± 10	21 ± 3	15 ± 5	5 ± 3	%of all microorganisms 0.2%
	P	10	0 ± 0	0 ± 0	0 ± 0	2 ± 2	1 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 1	0 ± 0	%of phage proteins for this family 1.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Acholeplasmataceae</i>	F	894	18 ± 2	27 ± 9	21 ± 1	35 ± 20	21 ± 6	18 ± 3	24 ± 3	9 ± 2	19 ± 3	20 ± 14	11 ± 6	%of all microorganisms 0.2%
	P	89	0 ± 0	0 ± 0	0 ± 0	7 ± 2	7 ± 3	5 ± 3	4 ± 2	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family 10.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Chlamydiaceae</i>	F	529	3 ± 2	20 ± 8	7 ± 1	39 ± 6	28 ± 3	6 ± 5	5 ± 2	1 ± 1	8 ± 6	11 ± 12	4 ± 2	%of all microorganisms 0.1%
	P	47	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 1	0 ± 0	10 ± 4	2 ± 1	0 ± 0	0 ± 0	%of phage proteins for this family 8.9%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Burkholderiaceae</i>	F	436	1 ± 1	36 ± 9	18 ± 9	21 ± 9	12 ± 4	5 ± 3	1 ± 1	2 ± 1	4 ± 1	6 ± 5	4 ± 2	%of all microorganisms 0.1%
	P	9	1 ± 3	0 ± 0	0 ± 0	1 ± 1	0 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 1	0 ± 0	%of phage proteins for this family 2.1%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.0%
<i>Neisseriaceae</i>	F	323	5 ± 6	21 ± 3	3 ± 2	5 ± 3	5 ± 5	9 ± 3	1 ± 1	1 ± 1	1 ± 1	18 ± 19	13 ± 12	%of all microorganisms 0.1%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family 0.0%
	C	3	0 ± 0	1 ± 1	0 ± 0	0 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 0.9%
<i>Chlorobiaceae</i>	F	298	2 ± 2	16 ± 9	15 ± 2	9 ± 3	8 ± 2	6 ± 4	4 ± 1	3 ± 2	5 ± 1	6 ± 1	1 ± 1	%of all microorganisms 0.1%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family 0.0%
	C	8	0 ± 0	2 ± 2	0 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family 2.7%

Thermaceae	F	237	1 ± 1	3 ± 3	7 ± 1	19 ± 7	15 ± 9	2 ± 2	3 ± 2	2 ± 2	4 ± 1	3 ± 2	2 ± 3	%of all microorganisms	0.0%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	4	0 ± 1	0 ± 0	1 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	1.7%
Listeriaceae	F	217	1 ± 1	11 ± 7	5 ± 2	5 ± 4	1 ± 1	5 ± 3	11 ± 5	8 ± 4	3 ± 1	7 ± 5	1 ± 2	%of all microorganisms	0.0%
	P	2	0 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.9%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.0%
Geobacteraceae	F	141	9 ± 11	6 ± 5	1 ± 1	5 ± 6	3 ± 1	1 ± 1	5 ± 4	1 ± 1	1 ± 1	3 ± 3	2 ± 2	%of all microorganisms	0.0%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	1	0 ± 0	0 ± 0	0 ± 0	0 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.7%
Rhodospirillaceae	F	72	1 ± 1	7 ± 5	2 ± 3	2 ± 3	1 ± 1	2 ± 3	1 ± 1	0 ± 0	1 ± 1	1 ± 1	1 ± 1	%of all microorganisms	0.0%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	7	0 ± 0	0 ± 0	0 ± 1	0 ± 0	0 ± 0	2 ± 2	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	9.7%
Bdellovibrionaceae	F	12	0 ± 0	0 ± 1	0 ± 0	0 ± 1	1 ± 1	0 ± 0	0 ± 1	0 ± 1	1 ± 1	0 ± 1	0 ± 0	%of all microorganisms	0.0%
	P	3	1 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	25.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.0%
Halomonadaceae	F	7	0 ± 1	0 ± 0	0 ± 0	1 ± 1	0 ± 1	1 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of all microorganisms	0.0%
	P	74	0 ± 1	0 ± 0	0 ± 0	9 ± 7	9 ± 8	0 ± 0	0 ± 0	0 ± 1	0 ± 0	0 ± 1	0 ± 0	%of phage proteins for this family	1057.1%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.0%
Spiroplasmataceae	F	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of all microorganisms	0.0%
	P	1	0 ± 0	0 ± 0	0 ± 0	0 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.0%
Sum of considered bacteria	F	126934	1879 ± 895	3206 ± 692	3272 ± 548	5106 ± 1150	4094 ± 1206	3067 ± 569	2033 ± 414	3265 ± 968	1905 ± 558	2485 ± 582	1422 ± 1408	%of all microorganisms	22.6%
	P	1570	11 ± 10	10 ± 6	9 ± 6	124 ± 62	80 ± 48	20 ± 12	79 ± 23	15 ± 8	28 ± 9	9 ± 10	9 ± 9	%of phage proteins for this family	1.2%
	C	184	1 ± 1	14 ± 9	14 ± 8	2 ± 3	0 ± 1	7 ± 5	3 ± 1	1 ± 2	1 ± 1	3 ± 4	1 ± 2	%of CRISPR proteins for this family	0.1%

B. Archaeal families	Total sum of spectra	Average BGP_02	Average BGP_03	Average BGP_04	Average BGP_05a	Average BGP_05b	Average BGP_07	Average BGP_09	Average BGP_10	Average BGP_X1	Average BGP_X2	Average BGP_X3	Total amount of		
Methanosarcinaceae	F	22754	359 ± 95	1722 ± 395	1030 ± 438	227 ± 25	218 ± 36	366 ± 26	411 ± 53	379 ± 114	398 ± 81	498 ± 217	81 ± 82	%of all microorganisms	4.0%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.0%
Methanocaldococcaceae	F	14127	236 ± 194	673 ± 28	475 ± 94	367 ± 82	284 ± 96	270 ± 48	217 ± 32	322 ± 49	183 ± 71	374 ± 213	132 ± 105	%of all microorganisms	2.5%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	263	1 ± 1	1 ± 1	1 ± 1	35 ± 13	15 ± 6	0 ± 1	0 ± 0	13 ± 4	0 ± 0	1 ± 1	0 ± 1	%of CRISPR proteins for this family	1.9%
Archaeoglobaceae	F	5601	141 ± 99	195 ± 56	147 ± 35	171 ± 20	193 ± 10	64 ± 28	143 ± 31	96 ± 22	62 ± 21	116 ± 54	72 ± 85	%of all microorganisms	1.0%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	18	0 ± 0	0 ± 0	5 ± 2	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.3%
Methanomicrobiaceae	F	4637	22 ± 12	98 ± 20	84 ± 17	182 ± 27	131 ± 58	26 ± 5	203 ± 51	79 ± 8	112 ± 21	223 ± 105	1 ± 1	%of all microorganisms	0.8%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.0%
Methanobacteriaceae	F	2891	88 ± 86	119 ± 38	42 ± 12	64 ± 21	51 ± 28	39 ± 7	57 ± 32	62 ± 22	23 ± 1	63 ± 48	117 ± 116	%of all microorganisms	0.5%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.0%
Methanococcaceae	F	2162	44 ± 34	103 ± 23	40 ± 12	74 ± 23	67 ± 15	10 ± 2	66 ± 19	31 ± 9	20 ± 3	84 ± 87	2 ± 2	%of all microorganisms	0.4%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.0%
Thermococcaceae	F	1945	12 ± 8	37 ± 9	35 ± 14	127 ± 17	112 ± 39	10 ± 5	46 ± 3	13 ± 4	59 ± 6	22 ± 13	16 ± 17	%of all microorganisms	0.3%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	132	0 ± 0	1 ± 1	9 ± 7	13 ± 7	8 ± 5	0 ± 0	2 ± 1	0 ± 0	1 ± 1	0 ± 1	0 ± 0	%of CRISPR proteins for this family	6.8%
Halobacteriaceae	F	588	5 ± 3	20 ± 9	11 ± 7	25 ± 19	23 ± 13	2 ± 3	21 ± 15	3 ± 2	3 ± 1	32 ± 33	2 ± 3	%of all microorganisms	0.1%
	P	2	0 ± 0	0 ± 0	0 ± 0	0 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 1	%of phage proteins for this family	0.3%
	C	43	0 ± 1	0 ± 0	0 ± 0	4 ± 2	5 ± 1	0 ± 0	0 ± 0	2 ± 2	0 ± 0	1 ± 1	0 ± 0	%of CRISPR proteins for this family	7.3%
Sulfolobaceae	F	339	8 ± 3	9 ± 2	12 ± 3	11 ± 2	11 ± 7	6 ± 3	4 ± 1	6 ± 4	10 ± 2	7 ± 1	2 ± 1	%of all microorganisms	0.1%
	P	2	0 ± 0	0 ± 0	0 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.6%
	C	1	0 ± 0	0 ± 0	0 ± 1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.3%
Thermoproteaceae	F	80	0 ± 1	2 ± 1	2 ± 1	5 ± 1	3 ± 2	3 ± 2	1 ± 1	0 ± 0	1 ± 1	2 ± 2	3 ± 2	%of all microorganisms	0.0%
	P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of phage proteins for this family	0.0%
	C	1	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 1	0 ± 0	0 ± 0	%of CRISPR proteins for this family	1.3%
Haloarculaceae	F	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of all microorganisms	0.0%
	P	63	0 ± 0	0 ± 0	1 ± 1	0 ± 0	0 ± 0	0 ± 0	2 ± 1	1 ± 1	10 ± 8	1 ± 1	2 ± 3	%of phage proteins for this family	0.0%
	C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	%of CRISPR proteins for this family	0.0%
Sum of considered archaea	F	55124	915 ± 536	2977 ± 580	1876.3 ± 633	1251.3 ± 237	1091.8 ± 305	794.5 ± 129	1168.3 ± 238	990.75 ± 234	870.25 ± 207	1420 ± 773	426 ± 414	%of all microorganisms	9.8%
	P	67	0 ± 0	0 ± 0	1.25 ± 1.3	0.25 ± 0.5	0 ± 0	0 ± 0	1.75 ± 0.5	0.75 ± 1	9.75 ± 8.1	1 ± 0.8	2 ± 4	%of phage proteins for this family	0.1%
	C	458	1 ± 1.5	1.75 ± 1.8	14.25 ± 9.4	51.25 ± 22	27.5 ± 12	0.25 ± 0.5	1.5 ± 1	14.5 ± 6.3	0.75 ± 1.1	1.5 ± 2	0.25 ± 0.5	%of CRISPR proteins for this family	0.8%

C. Others		Total sum of spectra	Average BGP_02	Average BGP_03	Average BGP_04	Average BGP_05a	Average BGP_05b	Average BGP_07	Average BGP_09	Average BGP_10	Average BGP_X1	Average BGP_X2	Average BGP_X3	Total amount of
F	348885	6845 ± 1273	11948 ± 1753	8775 ± 1383	13245 ± 2432	10335 ± 2670	7455 ± 366	5947 ± 400	5942 ± 1002	5816 ± 1395	7253 ± 1418	3662	2406	%of all microorganisms 62.0%
P	7703	48 ± 20	115 ± 12	156 ± 74	627 ± 178	470 ± 187	110 ± 7	76 ± 18	49 ± 8	190 ± 149	70 ± 18	15	10	%of phage proteins for this family 2.2%
C	2611	14 ± 7	151 ± 55	71 ± 50	205 ± 22	173 ± 44	4 ± 2	3 ± 2	15 ± 9	2 ± 2	12 ± 15	3	5	%of CRISPR proteins for this family 0.7%
F	31447	477 ± 148	1139 ± 336	731 ± 73	1062 ± 225	798 ± 253	836 ± 37	591 ± 75	501 ± 31	546 ± 44	762 ± 171	420	252	%of all microorganisms 5.6%
P	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0	0	%of phage proteins for this family 0.0%
C	0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0 ± 0	0	0	%of CRISPR proteins for this family 0.0%

D. Overall		Total sum of spectra	Average BGP_02	Average BGP_03	Average BGP_04	Average BGP_05a	Average BGP_05b	Average BGP_07	Average BGP_09	Average BGP_10	Average BGP_X1	Average BGP_X2	Average BGP_X3	Total amount of
F	562390	10116 ± 2228	19270 ± 3006	14655 ± 2402	20664 ± 3631	16319 ± 4223	12151 ± 609	9739 ± 617	10698 ± 1986	9137 ± 2078	11920 ± 2436	5930 ± 3638		%of all microorganisms 100.0%
P	9340	59 ± 25	125 ± 11	166 ± 70	751 ± 200	550 ± 191	130 ± 7	157 ± 10	65 ± 12	228 ± 149	80 ± 20	26 ± 15		%of phage proteins for this family 1.7%
C	3253	16 ± 9	166 ± 63	100 ± 64	258 ± 22	201 ± 48	11 ± 4	8 ± 3	30 ± 10	4 ± 3	17 ± 17	4 ± 6		%of CRISPR proteins for this family 0.6%