

Title: Genome-resolved insight into the reservoir of antibiotic resistance genes in aquatic microbial community

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Supplementary Table S1. Summary of ARG identification tools and databases used in this study.

Tool	Database	Approach	Input
RGI	CARD	BLASTp	Protein sequence
AMRFinder (NCBI)	The Bacterial Antimicrobial Resistance Reference Gene Database	BLASTp & HMM scan	Protein sequence
DeepARG	DeepARG-DB	deep-learning	Protein sequence
ResFinder	ResFinder	BLASTn	Nucleotide sequence
sraX	CARD & ARGminer & BacMet	BLASTx	Nucleotide sequence
ABRicate	ARG-ANNOT	BLASTn	Nucleotide sequence

Supplementary Table S2. Reference genes and the mutation position for each of ARGs that confirm resistance due to mutation events.

Gene symbol	Gene name	# genes	Reference gene	Mutation position	Ref.
rpoB	DNA-directed RNA polymerase subunit beta	20	NP_215181	L511R	https://card.mcmaster.ca/ontology/39867
			CCP43410.1	D516G	
				H526T, E250G	
rpsL	30S ribosomal protein S12	43	WP_003910993	K43R	https://card.mcmaster.ca/ontology/39979
				K88R	
rpsA	30S ribosomal protein S1	3	WP_016810233	D123A	https://card.mcmaster.ca/ontology/42776
			CCP44394	Δ438A	
				A412V	

gyrA	DNA gyrase subunit A (Topoisomerase)	7	WP_023644204 WP_000116442	A90V, D94G G79C, S81L	https://card.mcmaster.ca/ontology/39879 , https://card.mcmaster.ca/ontology/40507
parC	Topoisomerase IV subunit A	2	WP_000202252	S84L, D105E	https://card.mcmaster.ca/ontology/40508
LpxC	UDP-3-O-acyl-N-acetylglucosamine deacetylase	4	AJF83452	P30L	https://card.mcmaster.ca/ontology/40184
murA	UDP-N-acetylglucosamine enolpyruvyl transferase	3	CCE36834	C117D	https://card.mcmaster.ca/ontology/40467

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15 **Supplementary Table S3.** Taxonomy of the Caspian Sea antibiotic resistant MAGs. The percent of completeness and contamination of these MAGs
 16 with their estimated genome size, GC content and taxonomic assignments are listed.

Genome id	Estimated Genome size (Mbp)	GC content %	Completeness %	Contamination %	Taxonomy
casp150-mb.136	5.97	60.52	92.52	3.42	p__Acidobacteriota;c__Acidobacteriae;o__Bryobacterales; f__UBA6623;g__s__
casp150-mb.154	4.72	60.73	95.67	1.83	p__Acidobacteriota;c__Acidobacteriae;o__Bryobacterales; f__UBA6623;g__s__
casp40-mb.95	4.78	60.70	95.25	3.89	p__Acidobacteriota;c__Acidobacteriae;o__Bryobacterales; f__UBA6623;g__s__
casp150-mb.205	3.67	65.10	93.68	4.27	p__Acidobacteriota;c__Viciniabacteria;o__Viciniabacterales; f__UBA2999;g__s__
casp150-mb.299	5.01	65.49	90.6	3.42	p__Acidobacteriota;c__Viciniabacteria;o__Viciniabacterales; f__UBA8438;g__UBA8438;s__
casp15-mb.71	1.76	51.25	87.09	2.56	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__BACL27;s__
casp15-mb.93	1.59	51.73	90.62	3.68	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__BACL27;s__
casp150-mb.152	1.62	47.79	89.32	0.85	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__BACL27;s__
casp150-mb.247	1.62	50.47	78.66	3.42	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__BACL27;s__
casp15-mb.34	2.42	63.76	93.16	1.28	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino5;s__
casp15-mb.84	2.49	63.73	98.29	3.85	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino5;s__
casp150-mb.11	2.55	63.57	97.44	3.94	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino5;s__
casp150-mb.170	2.37	63.76	93.16	2.14	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino5;s__
casp150-mb.321	2.22	66.30	91.45	3.85	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino5;s__
casp40-mb.212	2.56	63.64	96.58	1.28	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino5;s__

casp40-mb.94	2.26	66.38	82.34	3.85	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino5;s__
casp15-mb.191	2.29	55.83	94.02	1.28	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino5;s__Casp-actino5 sp001510385
casp40-mb.42	2.24	55.86	94.02	1.28	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino5;s__Casp-actino5 sp001510385
casp15-mb.86	2.41	62.32	83.59	0.85	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino8;s__
casp150-mb.228	2.37	62.35	80.6	0.85	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino8;s__
casp40-mb.149	2.39	62.35	83.16	0.85	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino8;s__
casp150-mb.258	2.37	52.60	97.61	3.07	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino8;s__Casp-actino8 sp001510335
casp40-mb.115	2.49	52.61	96.3	2.14	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino8;s__Casp-actino8 sp001510335
casp150-mb.41	2.51	62.73	94.02	2.99	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino8;s__Casp-actino8 sp001510455
casp40-mb.285	2.42	62.86	94.02	1.71	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Casp-actino8;s__Casp-actino8 sp001510455
casp40-mb.234	2.93	62.53	93.16	2.56	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__Ilumatobacter;s__
casp15-mb.62	1.79	52.06	88.08	0.95	p__Actinobacteriota;c__Acidimicrobiia;o__Microtrichales; f__Ilumatobacteraceae;g__UBA3006;s__UBA3006 sp001438985
casp150-mb.29	1.37	31.31	75.21	2.14	p__Actinobacteriota;c__Acidimicrobiia;o__TMED189; f__TMED189;g__TMED189;s__
casp150-mb.86	2.04	58.36	95.73	3.56	p__Actinobacteriota;c__Acidimicrobiia;o__UBA5794; f__UBA5794;g__UBA5794;s__
casp15-mb.16	3.49	67.58	70.15	0.05	p__Actinobacteriota;c__Actinobacteria;o__Mycobacteriales; f__Mycobacteriaceae;g__Mycolicibacterium;s__
casp150-mb.119	4.18	67.64	96.53	1.61	p__Actinobacteriota;c__Actinobacteria;o__Mycobacteriales; f__Mycobacteriaceae;g__Mycolicibacterium;s__Mycolicibacterium sp001510415
casp40-mb.75	4.14	67.64	97.15	0.94	p__Actinobacteriota;c__Actinobacteria;o__Mycobacteriales; f__Mycobacteriaceae;g__Mycolicibacterium;s__Mycolicibacterium sp001510415
casp40-mb.59	1.37	44.99	67.91	1.94	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__AcAMD- 5;g__AcAMD-5;s__

casp150-mb.328	1.41	38.22	64.81	0.59	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__AcAMD-5;g__ATZT02;s__
casp15-mb.194	1.51	45.04	89.92	1.23	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicales;g__AAA044-D11;s__AAA044-D11 sp002340925
casp150-mb.71	1.47	45.06	86.95	0.66	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicales;g__AAA044-D11;s__AAA044-D11 sp002340925
casp40-mb.60	1.52	45.07	90.19	1.89	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicales;g__AAA044-D11;s__AAA044-D11 sp002340925
casp40-mb.83	1.49	44.37	83.65	0.86	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicales;g__MAG-120802;s__
casp15-mb.46	1.42	40.84	71.59	0.79	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicales;g__Nanopelagicales;s__Nanopelagicales sp001437855
casp150-mb.270	1.38	40.74	66.2	2.81	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicales;g__Nanopelagicales;s__Nanopelagicales sp001437855
casp40-mb.272	1.41	40.76	74.4	0.7	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicales;g__Nanopelagicales;s__Nanopelagicales sp001437855
casp150-mb.195	1.58	47.47	88.52	0.7	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__Nanopelagicales;g__Planktophilia;s__
casp40-mb.119	2.15	58.63	94.61	0.81	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__S36-B12;g__GCA-2737125;s__
casp15-mb.155	3.15	61.17	76.47	2.34	p__Actinobacteriota;c__Actinobacteria;o__Nanopelagicales; f__S36-B12;g__S36-B12;s__
casp150-mb.221	2.26	57.90	82.84	2.42	p__Chloroflexota;c__Dehalococcoidia;o__SAR202; f__;g__;s__
casp150-mb.66	2.03	67.82	51.91	4.13	p__Chloroflexota;c__Dehalococcoidia;o__UBA2979; f__UBA2979;g__;s__
casp15-mb.81	5.10	55.29	63.68	3.12	p__Cyanobacteria;c__Cyanobacteriia;o__Phormidiales; f__Phormidiales;g__;s__
casp40-mb.69	5.13	55.14	87.27	1.63	p__Cyanobacteria;c__Cyanobacteriia;o__Phormidiales; f__Phormidiales;g__;s__
casp40-mb.232	4.97	59.24	57.97	0.72	p__Cyanobacteria;c__Cyanobacteriia;o__Phormidiales; f__Phormidiales;g__PCC-6406;s__
casp150-mb.31	3.22	63.95	97.8	2.2	p__Gemmatimonadota;c__Gemmatimonadetes;o__Gemmatimonadales; f__Gemmatimonadaceae;g__Fen-1231;s__
casp150-mb.298	3.42	64.13	97.8	4.4	p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23; f__UBA6960;g__;s__
casp40-mb.311	3.36	64.19	98.9	4.95	p__Gemmatimonadota;c__Gemmatimonadetes;o__SG8-23; f__UBA6960;g__;s__
casp40-mb.18	5.71	54.89	79.83	1.2	p__Latescibacterota;c__UBA2968;o__UBA2968; f__GCA-2709665;g__;s__

casp150-mb.130	1.32	32.31	55.12	0.99	p__Patescibacteria;c__WWE3;o__f__g__s__
casp15-mb.10	2.91	68.66	50.24	3.98	p__Planctomycetota;c__Phycisphaerae;o__Phycisphaerales; f__SM1A02;g__s__
casp150-mb.166	2.63	50.54	96.15	0	p__Planctomycetota;c__Phycisphaerae;o__Phycisphaerales; f__SM1A02;g__s__
casp150-mb.294	2.47	65.75	88.35	1.14	p__Planctomycetota;c__Phycisphaerae;o__Phycisphaerales; f__SM1A02;g__s__
casp150-mb.65	1.88	57.34	95.45	0	p__Planctomycetota;c__Phycisphaerae;o__Phycisphaerales; f__SM1A02;g__s__
casp40-mb.123	2.34	65.79	96.59	1.14	p__Planctomycetota;c__Phycisphaerae;o__Phycisphaerales; f__SM1A02;g__s__
casp150-mb.61	3.49	61.40	86.53	1.24	p__Planctomycetota;c__Phycisphaerae;o__Phycisphaerales; f__SM1A02;g__UBA12014;s__
casp40-mb.35	3.43	61.37	93.62	2.01	p__Planctomycetota;c__Phycisphaerae;o__Phycisphaerales; f__SM1A02;g__UBA12014;s__
casp150-mb.46	10.14	58.42	96.48	3.45	p__Planctomycetota;c__Planctomycetes;o__Pirellulales; f__Pirellulaceae;g__GCA-2726245;s__
casp150-mb.201	3.50	68.03	90.74	1.72	p__Planctomycetota;c__Planctomycetes;o__Pirellulales; f__UBA1268;g__s__
casp150-mb.45	4.88	63.56	70.35	2.4	p__Planctomycetota;c__Planctomycetes;o__Pirellulales; f__UBA1268;g__s__
casp40-mb.39	3.64	68.10	97.63	1.15	p__Planctomycetota;c__Planctomycetes;o__Pirellulales; f__UBA1268;g__s__
casp150-mb.69	12.39	58.04	62.5	1.79	p__Planctomycetota;c__Planctomycetes;o__Planctomycetales; f__Planctomycetaceae;g__s__
casp40-mb.109	6.07	54.52	97.69	1.19	p__Planctomycetota;c__Planctomycetes;o__Planctomycetales; f__Planctomycetaceae;g__s__
casp40-mb.51	7.60	56.59	64.69	1.25	p__Planctomycetota;c__Planctomycetes;o__Planctomycetales; f__Planctomycetaceae;g__s__
casp150-mb.290	2.57	54.76	95.16	1.08	p__Planctomycetota;c__UBA1135;o__UBA1135;f__UBA1135;g__GCA- 2746235;s__
casp40-mb.240	2.61	54.82	94.09	1.08	p__Planctomycetota;c__UBA1135;o__UBA1135;f__UBA1135;g__GCA- 2746235;s__
casp15-mb.161	4.81	70.44	95.45	1.14	p__Planctomycetota;c__UBA1135;o__UBA2386;f__UBA2386;g__s__
casp40-mb.29	4.76	70.34	89.2	0	p__Planctomycetota;c__UBA1135;o__UBA2386;f__UBA2386;g__s__
casp150-mb.133	3.20	67.01	71.35	3.01	p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales; f__Caulobacteraceae;g__Brevundimonas;s__

casp40-mb.174	3.13	66.89	85.68	1.1	p__Proteobacteria;c__Alphaproteobacteria;o__Caulobacterales; f__Caulobacteraceae;g__Brevundimonas;s__
casp40-mb.87	4.49	56.96	71.02	3.75	p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales_A; f__g__s__
casp40-mb.99	3.93	68.36	97.85	1.08	p__Proteobacteria;c__Alphaproteobacteria;o__SP197; f__SP197;g__s__
casp40-mb.200	2.54	41.23	43.86	0.43	p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales; f__Emcibacteraceae;g__UBA4441;s__
casp150-mb.269	2.17	66.77	75.46	1.2	p__Proteobacteria;c__Alphaproteobacteria;o__UBA2966; f__g__s__
casp150-mb.97	2.60	66.74	98.1	1.92	p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales; f__SG8-39;g__RBG-16-66-20;s__
casp40-mb.55	2.56	66.81	80.6	4.72	p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales; f__SG8-39;g__RBG-16-66-20;s__
casp150-mb.292	2.63	67.41	88.63	1.53	p__Proteobacteria;c__Gammaproteobacteria;o__Burkholderiales; f__SG8-39;g__SG8-39;s__
casp15-mb.175	2.57	39.10	91.2	0.29	p__Proteobacteria;c__Gammaproteobacteria;o__Francisellales; f__Francisellaceae;g__Caedibacter;s__
casp40-mb.114	4.60	52.76	94.8	4.28	p__Proteobacteria;c__Gammaproteobacteria;o__Ga0077536; f__Ga0077536;g__UBA11873;s__
casp150-mb.297	1.54	60.75	92.49	1.17	p__Proteobacteria;c__Gammaproteobacteria;o__Ga0077554; f__Ga0077554;g__s__
casp40-mb.214	2.18	52.07	81	0.66	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Halieaceae;g__IMCC3088;s__
casp15-mb.124	2.08	52.15	71.43	1.49	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Halieaceae;g__IMCC3088;s__IMCC3088 sp003520285
casp15-mb.181	3.24	52.64	79.8	3.33	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Halieaceae;g__Luminiphilus;s__
casp40-mb.140	5.42	58.42	87.98	4.69	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__HTCC2089;g__s__
casp150-mb.241	2.82	42.21	75.66	1.4	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter johnsonii
casp40-mb.142	2.76	42.52	59.01	0.83	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter johnsonii
casp150-mb.169	3.60	38.87	98.18	1.73	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter venetianus
casp40-mb.215	3.67	38.99	98.53	0.79	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Moraxellaceae;g__Acinetobacter;s__Acinetobacter venetianus
casp15-mb.5	2.89	52.11	94.81	2.16	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Pseudohongiellaceae;g__OM182;s__

casp15-mb.167	3.91	54.77	95	1.17	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Pseudohongiellaceae;g__UBA9145;s__
casp150-mb.100	4.76	51.60	94.63	1.98	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Pseudohongiellaceae;g__UBA9145;s__
casp150-mb.148	3.33	49.18	94.07	1.79	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Pseudohongiellaceae;g__UBA9145;s__
casp40-mb.220	3.90	54.83	90.06	1.94	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Pseudohongiellaceae;g__UBA9145;s__
casp40-mb.61	3.41	49.18	94.07	1.23	p__Proteobacteria;c__Gammaproteobacteria;o__Pseudomonadales; f__Pseudohongiellaceae;g__UBA9145;s__
casp150-mb.9	4.00	54.45	89.06	2.81	p__Proteobacteria;c__Gammaproteobacteria;o__Woeseiales; f__Woeseiaceae;g__SZUA-117;s__
casp40-mb.225	3.71	54.45	88.41	2.51	p__Proteobacteria;c__Gammaproteobacteria;o__Woeseiales; f__Woeseiaceae;g__SZUA-117;s__
casp150-mb.222	2.16	61.65	97.97	0.68	p__Verrucomicrobiota;c__Verrucomicrobiae;o__Chthoniobacterales; f__;g__;s__
casp40-mb.44	2.08	61.78	97.8	1.01	p__Verrucomicrobiota;c__Verrucomicrobiae;o__Chthoniobacterales; f__;g__;s__

18 **Supplementary Table S4.** List of β -lactamase containing genomes in the Caspian Sea MAGs and their
 19 taxonomic affiliation. There are 40 β -lactamase genes detected in 30 Caspian Sea MAGs.

Genome id	Gene id	β -lactamase class	Class	Order
casp150-mb.136	EEKHDION 03010	class B	Acidobacteriae	Bryobacterales
casp150-mb.154	EOCCHKBK 01016	class B	Acidobacteriae	Bryobacterales
	EOCCHKBK 03411	class B		
casp40-mb.95	OICPLIJP 01112	class B	Acidobacteriae	Bryobacterales
	OICPLIJP 03168	class B		
casp150-mb.119	KIBDMIMN 02996	class A	Actinobacteria	Mycobacteriales
casp40-mb.75	BGPOMPEL 02839	class A	Actinobacteria	Mycobacteriales
casp150-mb.133	IBHFGKKE 00487	class A	Alphaproteobacteria	Caulobacterales
casp40-mb.174	LEECDGGH 01667	class A	Alphaproteobacteria	Caulobacterales
casp40-mb.200	IKHHLIND 00205	class D	Alphaproteobacteria	Sphingomonadales
casp150-mb.66	IFOMPFBH 00010	class A	Dehalococcoidia	UBA2979
casp15-mb.175	EBJODPFO 00650	class A	Gammaproteobacteria	Francisellales
casp15-mb.167	ADILNDBO 00237	class B	Gammaproteobacteria	Pseudomonadales
casp150-mb.100	POANLGLH 03091	class B	Gammaproteobacteria	Pseudomonadales
	POANLGLH 03261	class B		
casp150-mb.148	JKEJJGBH 00119	class A	Gammaproteobacteria	Pseudomonadales
casp150-mb.169	HNBACKAMJ 00045	class C	Gammaproteobacteria	Pseudomonadales
	HNBACKAMJ 00307	class D		
casp150-mb.241	HMCNMLOA 00746	class D	Gammaproteobacteria	Pseudomonadales
casp40-mb.142	FCMKGLIF 00920	class D	Gammaproteobacteria	Pseudomonadales
casp40-mb.215	IAHFBJBJ 00371	class D	Gammaproteobacteria	Pseudomonadales

	IAHFBJBJ 00481	class C		
casp40-mb.220	GPCFOBLN 01961	class B	Gammaproteobacteria	Pseudomonadales
casp40-mb.61	GHFBJIFD 00366	class A	Gammaproteobacteria	Pseudomonadales
casp150-mb.9	MFLPOMFE 01486	class D	Gammaproteobacteria	Woeseiales
casp40-mb.225	CLDJHIBN 02085	class D	Gammaproteobacteria	Woeseiales
casp150-mb.31	CFBKJOIE 01731	class B	Gemmatimonadetes	Gemmatimonadales
casp150-mb.298	NPIGMJFH 02028	class B	Gemmatimonadetes	SG8-23
casp40-mb.311	OAPKMILO 00770	class A	Gemmatimonadetes	SG8-23
	OAPKMILO 01670	class B		
casp150-mb.46	AIEJOLAH 07624	class B	Planctomycetes	Pirellulales
casp150-mb.69	BIDOACPM 03738	class B	Planctomycetes	Planctomycetales
casp40-mb.109	PCMHCDEH 03871	class B	Planctomycetes	Planctomycetales
casp40-mb.51	CDIDJOII 03913	class B	Planctomycetes	Planctomycetales
casp150-mb.205	KEACKLOE 00888	class B	Vicinamibacteria	Vicinamibacterales
	KEACKLOE 02795	class B		
casp150-mb.299	BNEENLPF 00151	class B	Vicinamibacteria	Vicinamibacterales
	BNEENLPF 02856	class B		
	BNEENLPF 03106	class B		
	BNEENLPF 03234	class B		

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