

Whole Genome Sequence of *Dermacoccus abyssi* MT1.1 Isolated from the Challenger Deep of the Mariana Trench Reveals Phenazine Biosynthesis Locus and Environmental Adaptation Factors

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Abstract

Dermacoccus abyssi strain MT1.1^T is a piezotolerant actinobacterium that was isolated from Mariana Trench sediment collected at a depth of 10898 m. The organism was found to produce ten dermacozines (A–J) that belonged to a new phenazine family and which displayed various biological activities such as radical scavenging and cytotoxicity. Here we report on the isolation and identification of a new dermacozine compound, dermacozine M, the chemical structure of which was determined using 1D and 2D-NMR, and high resolution MS. A whole genome sequence of the strain contained six secondary metabolite-biosynthetic

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gene clusters (BGCs), including one responsible for the biosynthesis of a family of phenazine compounds. A pathway leading to the biosynthesis of dermacozines is proposed.

Bioinformatic analyses of key stress-related genes provide an insight into how the organism adapted to the environmental conditions that prevail in the deep-sea.

Keywords

Mariana Trench; *Dermacoccus* strain MT1.1^T; Dermacozines; Genome sequencing; Biosynthetic gene clusters

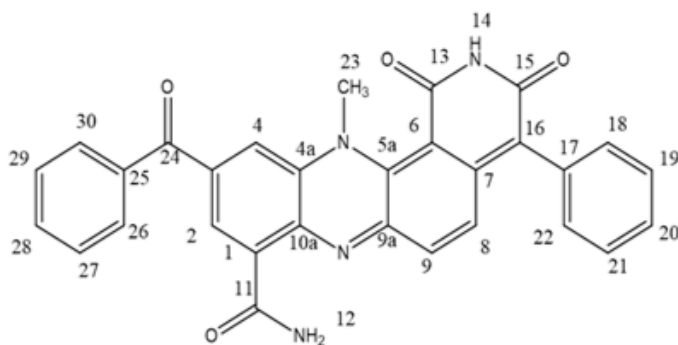


Fig. S1. Dermacozine M Atoms Numbering

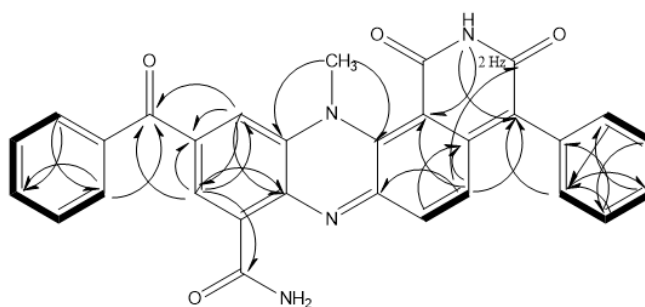


Fig. S2. HMBC and COSY correlations of Dermacozine M

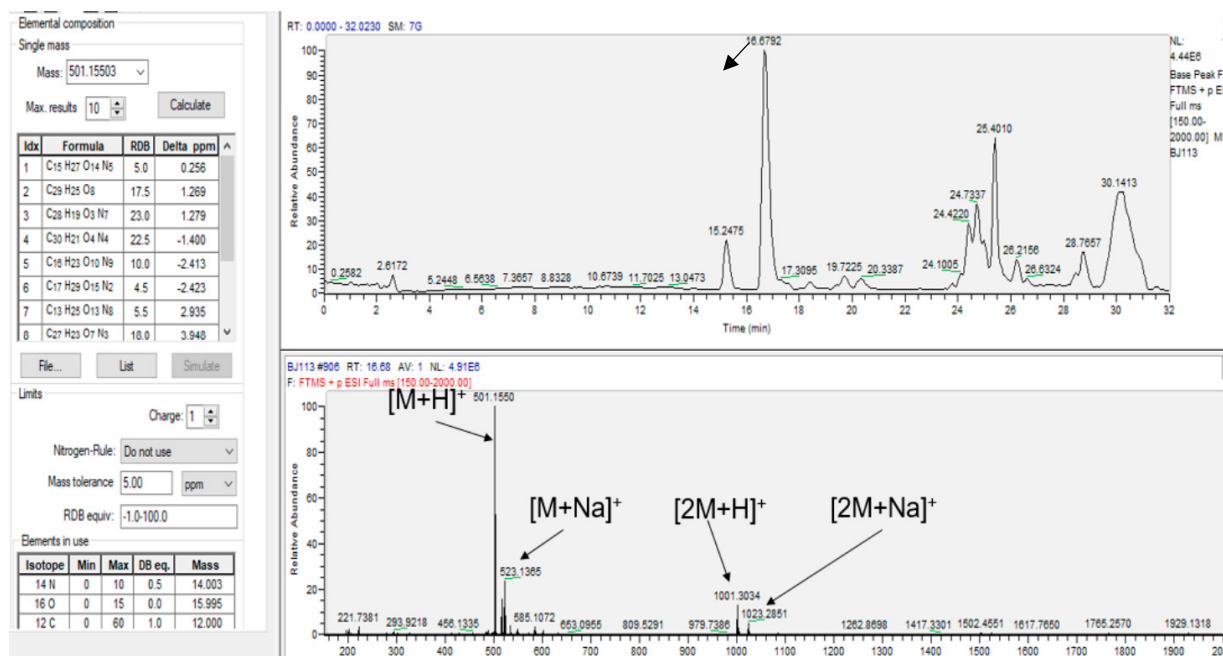


Fig. S3. LC MS data and formula of Dermacozine M (Orbitrap, HRESMIS)

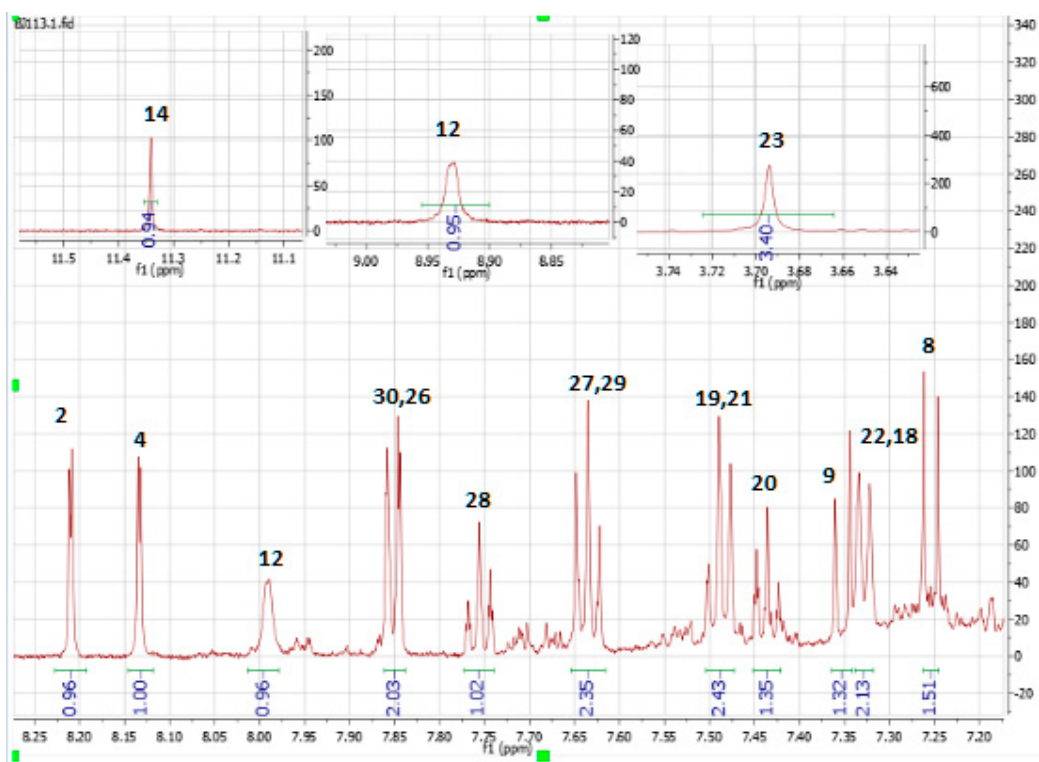


Fig. S4. ^1H NMR of Dermacozine M ($\text{DMSO}-d_6$, 600 MHz)

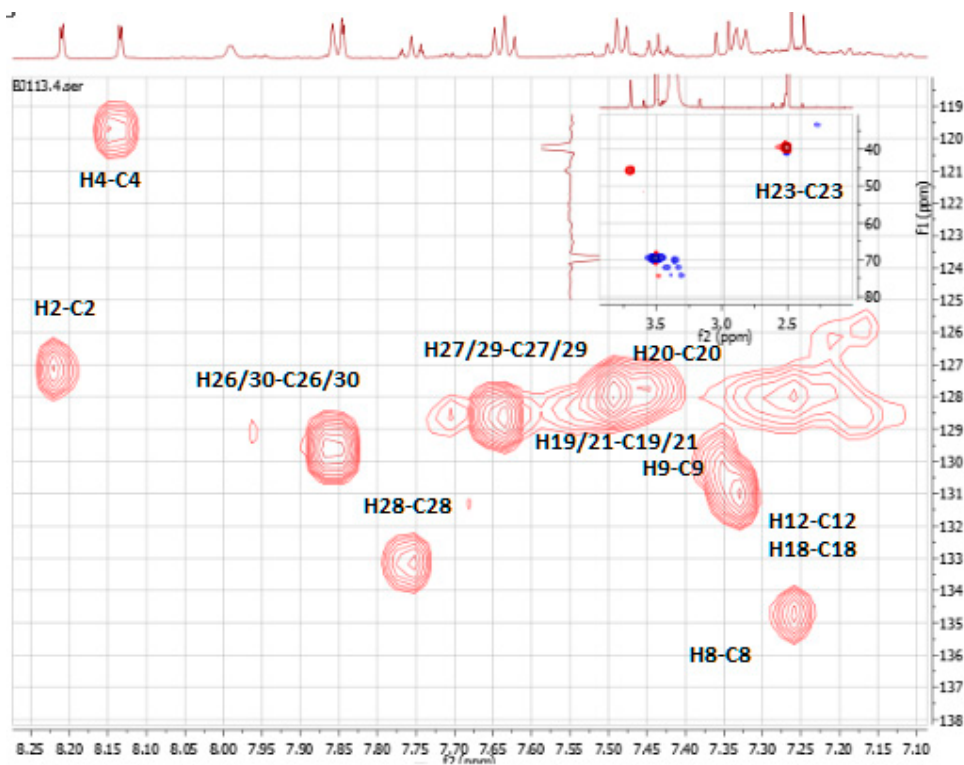


Fig. S5. HSQC spectrum of Dermacozine M ($\text{DMSO}-d_6$, 600 MHz)

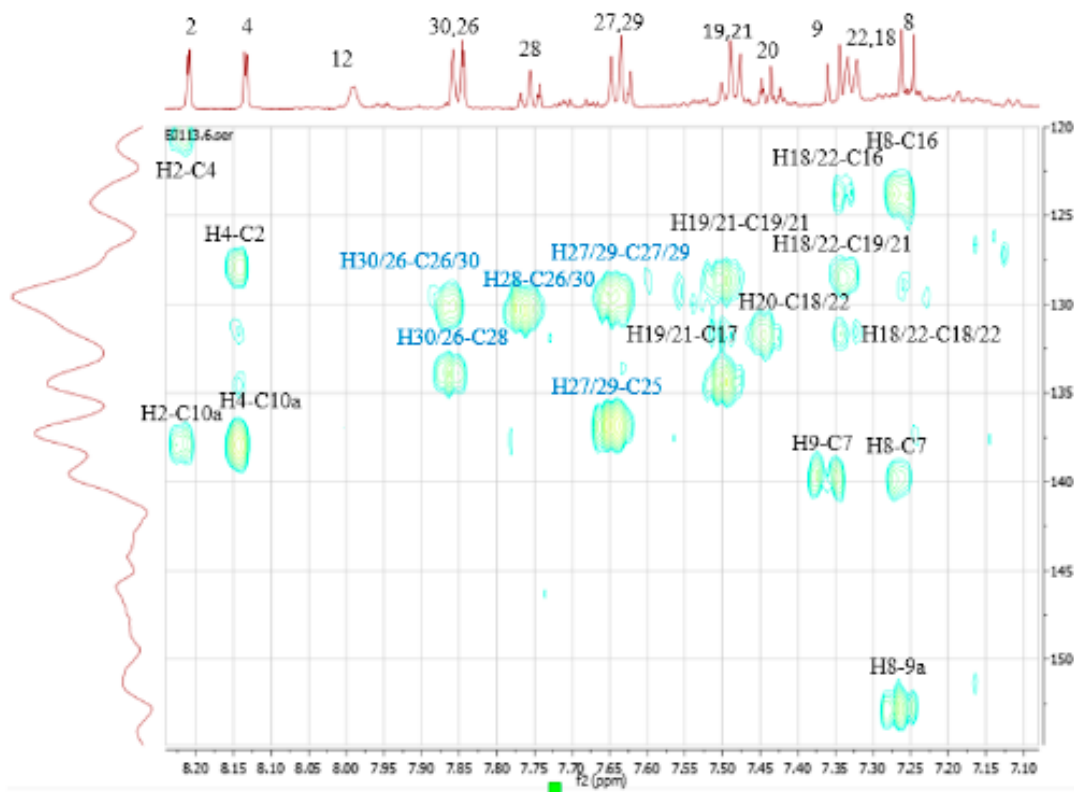


Fig. S6. HMBC (7 Hz) spectrum of Dermacozone M (DMSO- d_6 , 600 MHz)

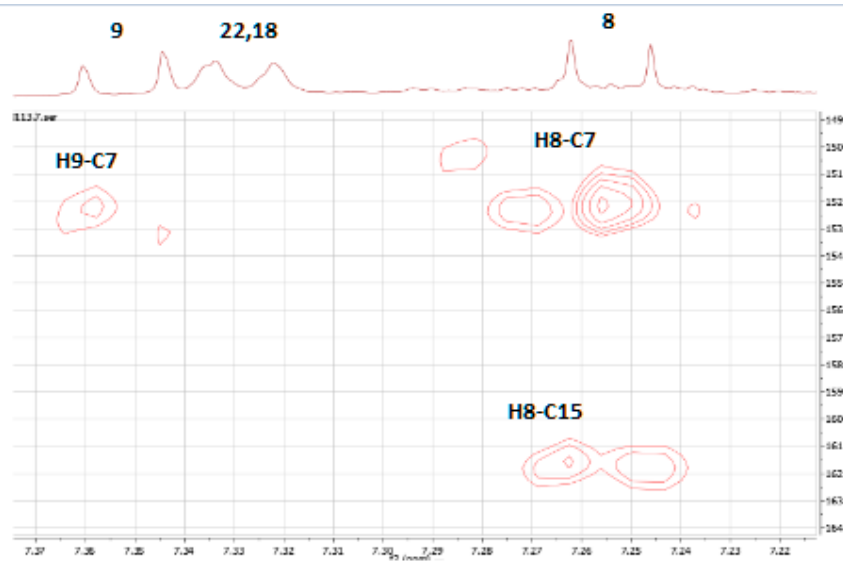


Fig. S7. HMBC (2 Hz) spectrum of Dermacozone M (DMSO- d_6 , 600 MHz) showing H8-C15 correlation

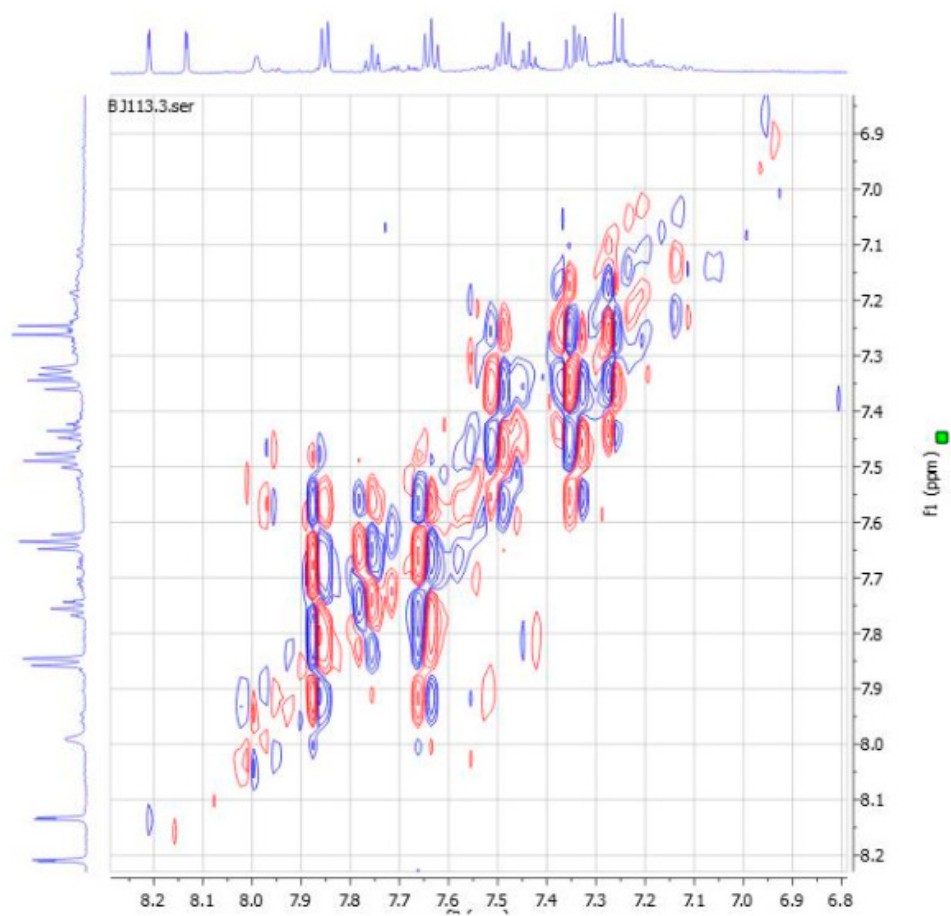


Fig. S8. DQF-COSY Spectrum of Dermacozine M (DMSO-*d*₆, 600 MHz)

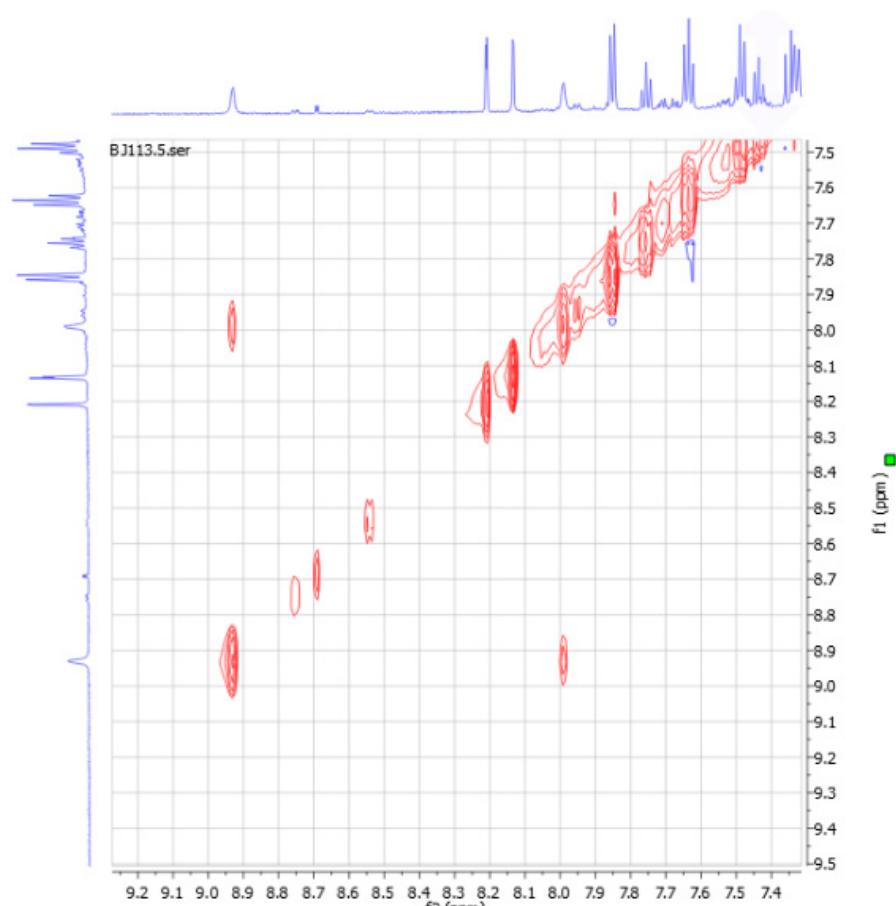


Fig. S9. NOESY spectrum of Dermacozine M showing correlation of the -NH protons of the carboxamide group (12) (DMSO- d_6 , 600 MHz)

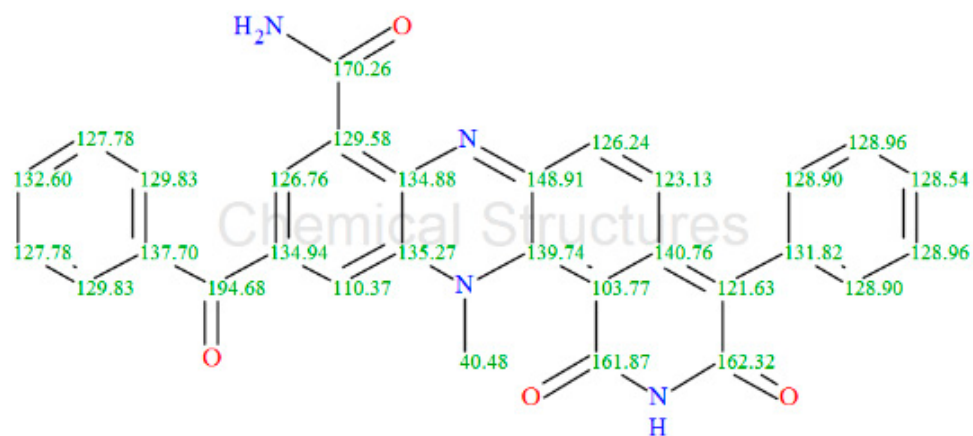


Fig. S10. ACD Labs ^{13}C chemical shift prediction simulating the missing C13 carbonyl chemical shift

Table S1. Putative cold shock and osmotic stress response genes identified in the genome of *D. abyssi* MT1.1^T.

Stress response	Protein	Gene	GenBank ID
Cold Shock	Cold-shock protein	<i>csp</i> s	WP_118912295 WP_118912768
	Chaperonin GroEL	<i>groL</i>	WP_118913312 WP_118913486
	ATP-dependent chaperone ClpB	<i>clpB</i>	WP_118914595
	Co-chaperone GroES	<i>groES</i>	WP_118913311
	DEAD/DEAH box helicase	<i>deaD</i>	WP_118914699 WP_118913081
Osmotic stress	Choline dehydrogenase	<i>betA</i>	WP_118913227
	Betaine/Carnitine/Choline Transporter (BCCT family transporter)		WP_118912156 WP_118913228 WP_118913588
	Glycine/betaine ABC transporter substrate-binding protein	<i>opuA</i>	WP_118914940
	Aquaporin	<i>aqua</i>	WP_118912896
	Aspartate-semialdehyde dehydrogenase	<i>asd</i>	WP_118914342 WP_118914341
	Thiol reductant ABC exporter subunit CydC	<i>cydC</i>	WP_118912958
	Thiol reductant ABC exporter subunit CydD	<i>cydD</i>	WP_118912957
	Malate dehydrogenase	<i>mdh</i>	WP_118912226
	single-stranded DNA-binding protein	<i>ssb</i>	WP_118914057
	ABC transporter permease		WP_118912686 WP_118912989
	Metal ABC transporter permease		WP_118912641
	Amino acid ABC transporter permease		WP_118912632
	Branched-chain amino acid ABC transporter permease		WP_047310547
	Protein translocase subunit SecF	<i>secF</i>	WP_118913201
	Protein translocase subunit SecD	<i>secD</i>	WP_118913202

Table S2. Oxidative stress response and respiration-related genes in the genome of *D. abyssi* MT1.1^T.

Stress response	Protein	Gene	GenBank ID
Oxidative stress	Superoxide dismutase	<i>sodN</i>	WP_047310274
	Catalase	-	WP_118912840
	Thioredoxin	<i>trxA</i>	WP_118914664
	Thioredoxin-disulfide reductase	<i>trxB</i>	WP_118914013
	Peroxiredoxin	-	WP_047312091

	OsmC family peroxiredoxin	<i>osmC</i>	WP_118913166
	NAD(P)H-quinone oxidoreductase	-	WP_118914329
	Alkyl hydroperoxide reductase	-	WP_118912925
	Glutathione <i>S</i> -transferase family protein	-	WP_118913584
	Arsenate reductase	<i>arsC</i>	WP_118913813
	Glutaredoxin family protein	-	WP_118914221
Respiration			
	Cytochrome <i>d</i> ubiquinol oxidase subunit I	<i>cydA</i>	WP_118912949
	Cytochrome <i>d</i> ubiquinol oxidase subunit II	<i>cydB</i>	WP_118912950
	Cytochrome <i>c</i> oxidase subunit I	<i>ctad</i>	WP_118913146
	Cytochrome <i>c</i> oxidase subunit II	<i>coxb</i>	WP_118913145
	Cytochrome <i>c</i> oxidase subunit IV	-	WP_118913147
	cytochrome c oxidase assembly protein	-	WP_118912928
Respiratory-related			
	Arsenate reductase	<i>arsc</i>	WP_118913813
	Ferredoxin reductase	-	WP_118914278
	NADH-quinone oxidoreductase subunit A	<i>nuoA</i>	WP_118912274
	NADH-quinone oxidoreductase subunit B	<i>nuoB</i>	-
	NADH-quinone oxidoreductase subunit C	<i>nuoC</i>	WP_118912273
	NADH-quinone oxidoreductase subunit D	<i>nuoD</i>	WP_118915078
	NADH-quinone oxidoreductase subunit F	<i>nuoF</i>	-
	NADH-quinone oxidoreductase subunit H	<i>nuoH</i>	WP_118912336
	NADH-quinone oxidoreductase subunit I	<i>nuoI</i>	WP_082128608
	NADH-quinone oxidoreductase subunit J	<i>nuoJ</i>	WP_118912272
	NADH-quinone oxidoreductase subunit K	<i>nuoK</i>	WP_047310431
	NADH-quinone oxidoreductase subunit L	<i>nuoL</i>	WP_118912271
	NADH-quinone oxidoreductase subunit M	<i>nuoM</i>	WP_118912335
	NADH-quinone oxidoreductase subunit N	<i>nuoN</i>	-
	Glycerol-3-phosphate dehydrogenase		WP_118912897
	NAD(P)-dependent glycerol-3-phosphate dehydrogenase		WP_118912765
	L-lactate dehydrogenase	-	WP_118912189
	Formate dehydrogenase	-	WP_118912882
	Succinate dehydrogenase	-	WP_118913370
	Succinate dehydrogenase/fumarate reductase iron-sulfur subunit	-	WP_118913372
	Fumarate reductase/succinate dehydrogenase flavoprotein subunit	-	WP_118913371

Table S3. Genes responsible for cell wall/membrane alteration and carbon starvation in the genome of *D. abyssi* MT1.1^T.

Stress response	Protein	Gene	GenBank ID
Membrane/cell wall alteration	Beta-ketoacyl	<i>fabF</i>	WP_118912631
	3-oxoacyl-ACP reductase	<i>fabG</i>	WP_118912254
	Ketoacyl-ACP synthase III	<i>fabH</i>	WP_118912630
	enoyl	<i>fabI</i>	WP_118912407

	Enoyl-ACP reductase	-	WP_118912704
	Enoyl-CoA hydratase	-	WP_118912167
	Long-chain fatty acid-CoA ligase	-	WP_118912679
	Acyl-CoA desaturase	-	WP_118914883
	Acyl dehydratase	-	WP_118913070
	3-hydroxyacyl-CoA dehydrogenase	-	WP_118912252
	Phytoene/squalene synthase family protein	-	WP_118913237
	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	<i>murA</i>	WP_118912784
	Phosphopantetheinyl transferase	-	WP_118913279
Carbon starvation	Carbon starvation protein A	<i>csta</i>	WP_118914698
	Glycogen synthase	<i>glga</i>	WP_118913041
	Glycogen debranching enzyme	<i>glgx</i>	WP_118912402
			WP_118913222
	Glycogen/starch/alpha-glucan phosphorylase	-	WP_118914122
	Carbonic anhydrase	-	WP_118914411
			WP_118912225
	Carbon-nitrogen hydrolase family	-	WP_118915142
			WP_118912927

Table S4. Putative organic matter-hydrolyzing enzymes identified in the genome of *D. abyssi* MT1.1^T.

Enzymes	GenBank ID
Protease	
aminopeptidase P family protein	WP_118912327
aminopeptidase N	WP_118912267
M48 family peptidase	WP_118912322
M1 family peptidase	WP_118912863
M50 family peptidase	WP_118913143
S9 family peptidase	WP_118913024
alpha/beta hydrolase	WP_118912940
Polysaccharase	
Glycogen/starch/alpha-glucan phosphorylase	WP_118914411
beta-N-acetylhexosaminidase	WP_118913310
Polysaccharide deacetylase	WP_118914959
Polysaccharide deacetylase family protein	WP_118914361
Peptidoglycan endopeptidase	WP_118913505
alpha-amylase	WP_118914957
Carbohydrate kinase	WP_118912216
Glucosidase	WP_118913090
Galactokinase	WP_118912975

beta- <i>N</i> -acetylhexosaminidase	WP_118913310
Purine catabolism	
Purine-nucleoside phosphorylase	WP_118913393
hypoxanthine phosphoribosyltransferase	WP_118914540
Allantoin	
Allantoin permease	WP_118913617
Allantoate amidohydrolase	WP_118913007
