

Supplementary Material

***Anianabacter salinae* gen. nov., sp. nov. ASV31^T, a facultative alkaliphilic and extremely halotolerant bacterium isolated from brine of a millennial continental saltern**

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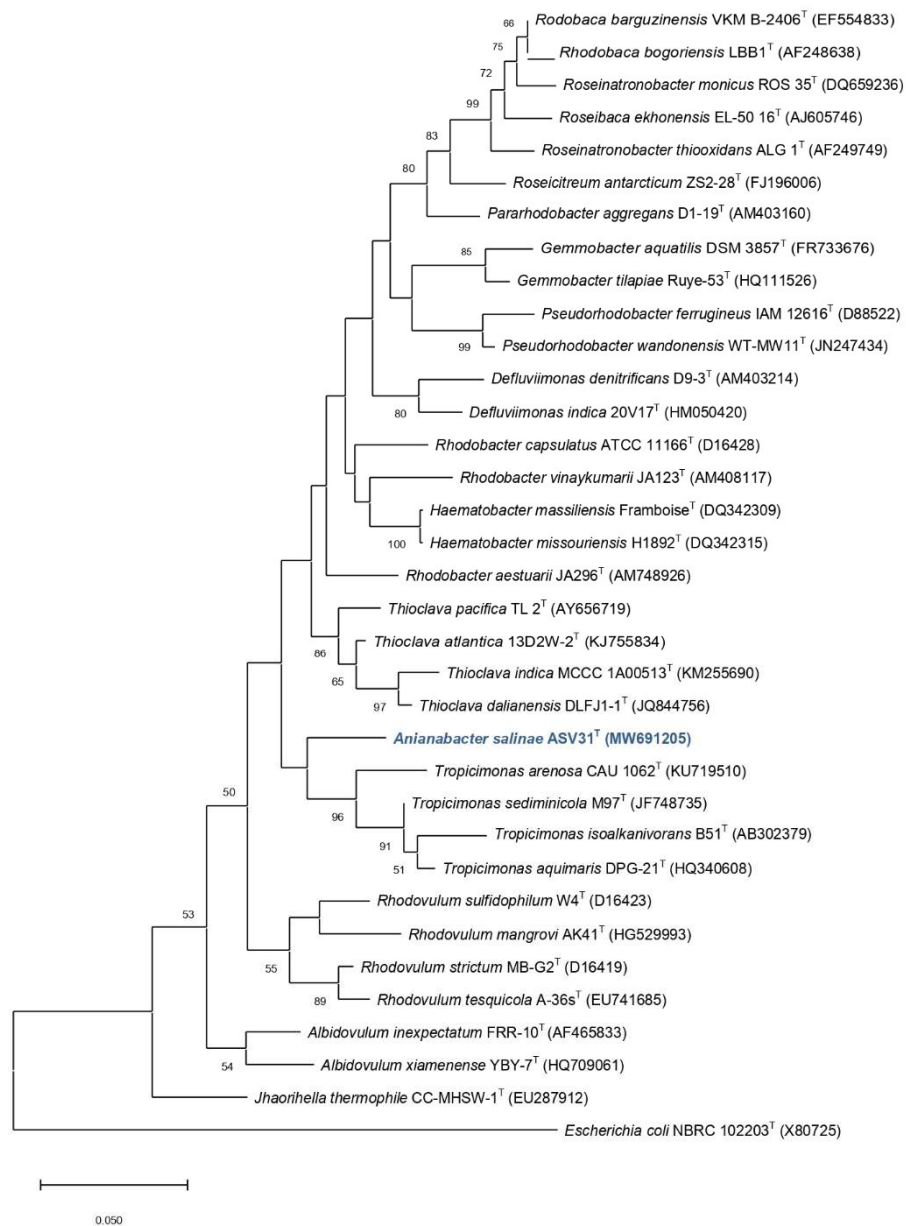


Figure S1. Maximum-likelihood phylogenetic tree based on 16S rRNA gene sequences showing the relationships between *Anianabacter salinae* ASV31^T and other strains of *Rhodobacteraceae* family. Only bootstrap values (expressed as percentages of 1000 replications) greater than 50% are shown at branching points. *Escherichia coli* NBRC 102203^T was used as the outgroup. Bar, 0.05 substitutions per nucleotide position.

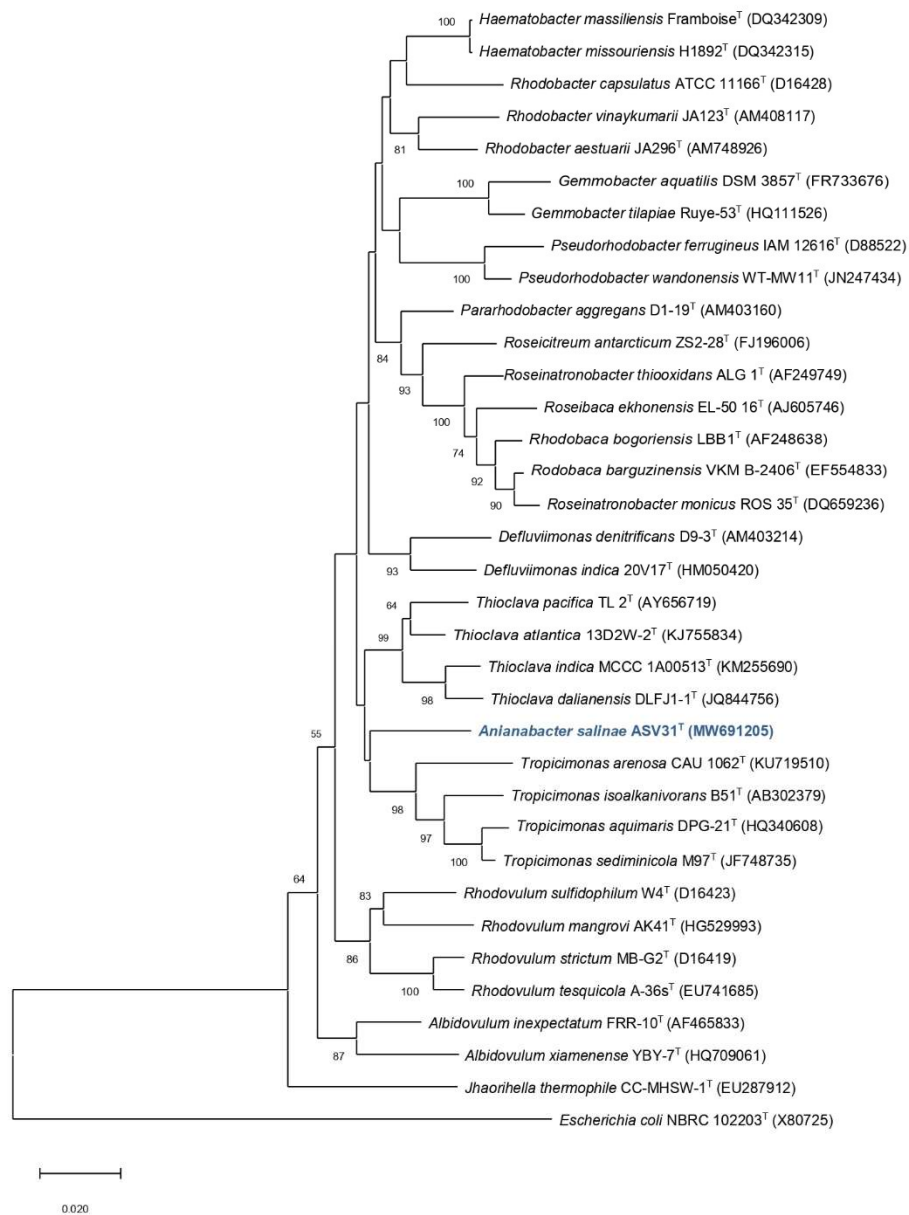


Figure S2. Minimum evolution phylogenetic tree based on 16S rRNA gene sequences showing the relationships between *Anianabacter salinae* ASV31^T and other species of *Rhodobacteraceae* family. Only bootstrap values (expressed as percentages of 1000 replications) greater than 50% are shown at branching points. *Escherichia coli* NBRC 102203^T was used as the outgroup. Bar, 0.02 substitutions per nucleotide position.



Figure. S3. *Anianabacter salinae* ASV31^T growth on marine agar medium. Colony morphology and colour are shown.

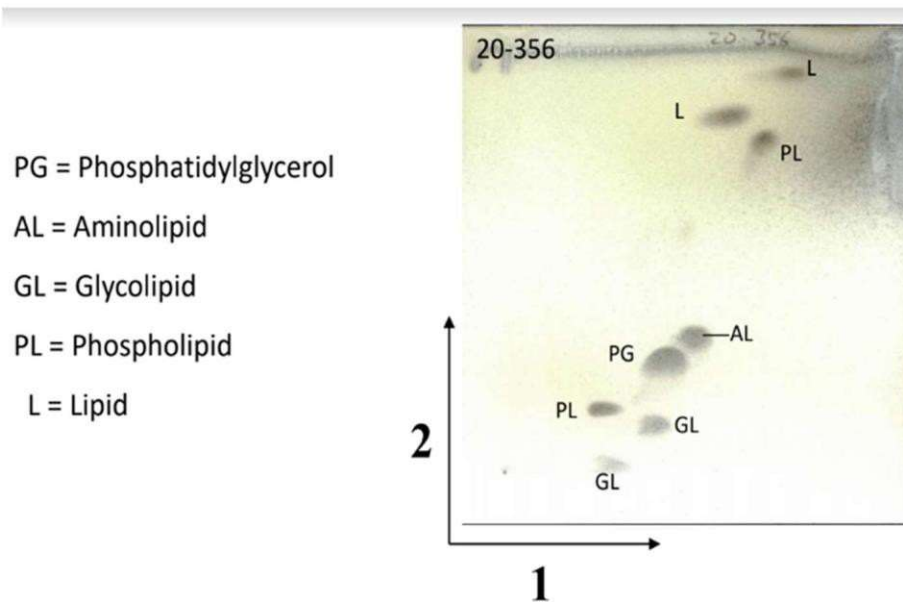


Figure S4. Thin-layer chromatogram of polar lipids of *Anianabacter salinae* ASV31^T.

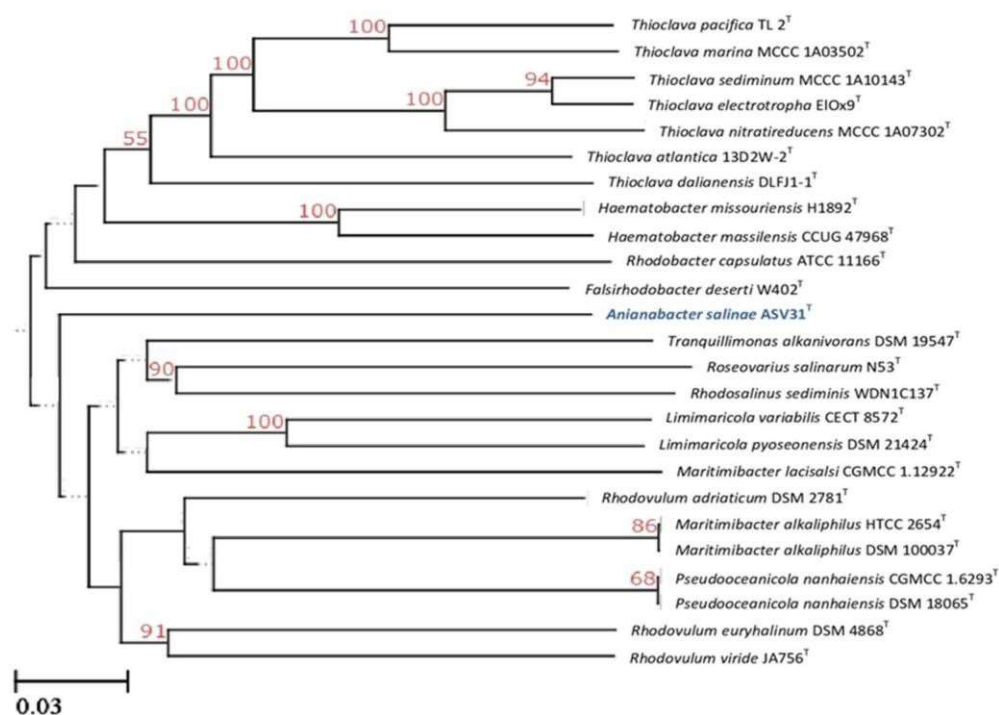
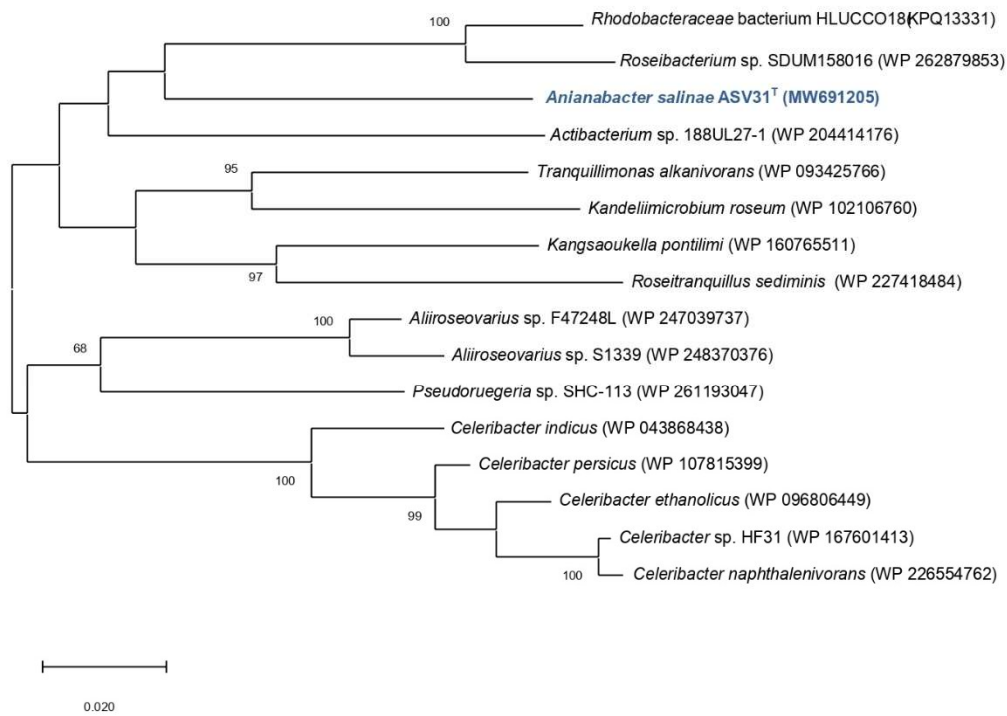


Figure S5. Whole-genome-based taxonomic tree, showing the position of the strain ASV31^T and related strains of *Rhodobacteraceae* family. Bootstrap values greater than 50% in the clade nodes are shown. Bar, 0.03 substitutions per nucleotide position.

A



B

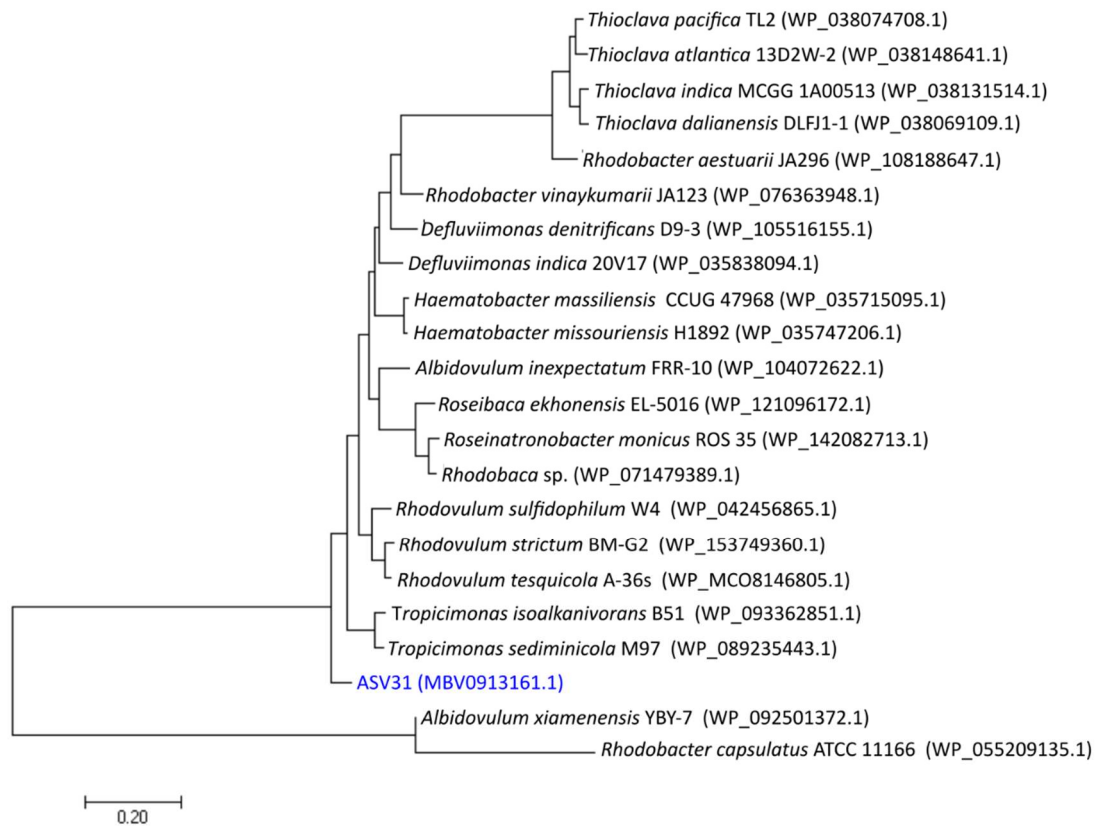
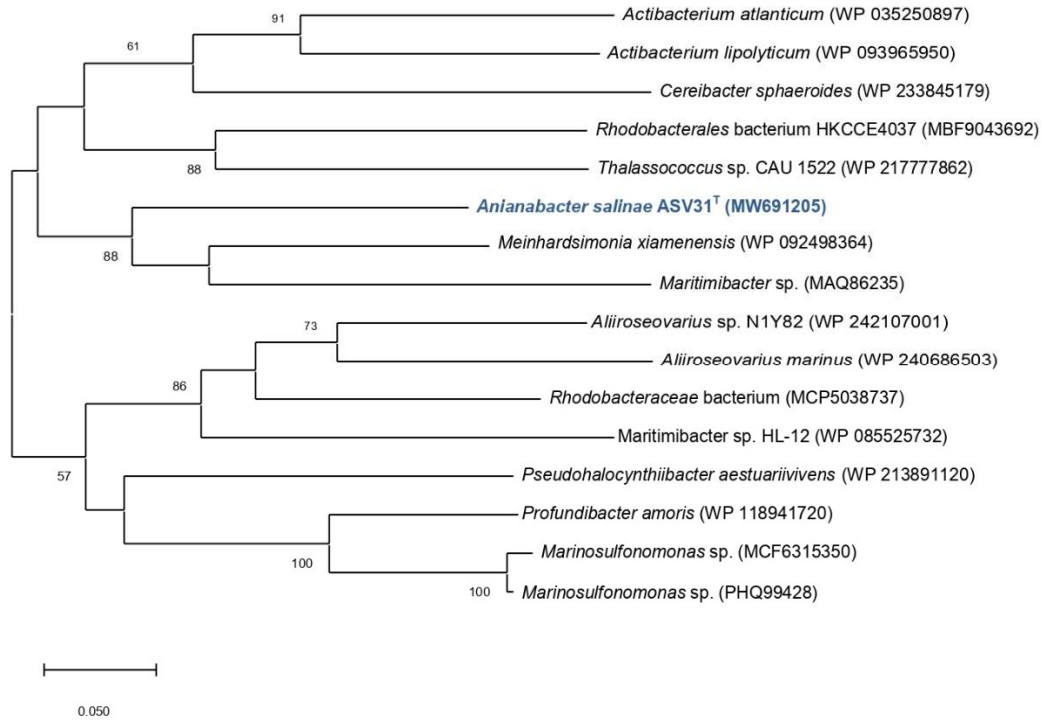


Figure S6. RpoC-based maximum-likelihood tree: A, performed with the most similar amino acidic sequences; B, performed with sequences from representatives of the *Rhodobacteraceae* family. Tree was generated using MEGA X. Only bootstrap values (expressed as percentages of 1000 replications) greater than 50% are shown at branching points. The scale bar indicates the number of substitutions per site

A



B

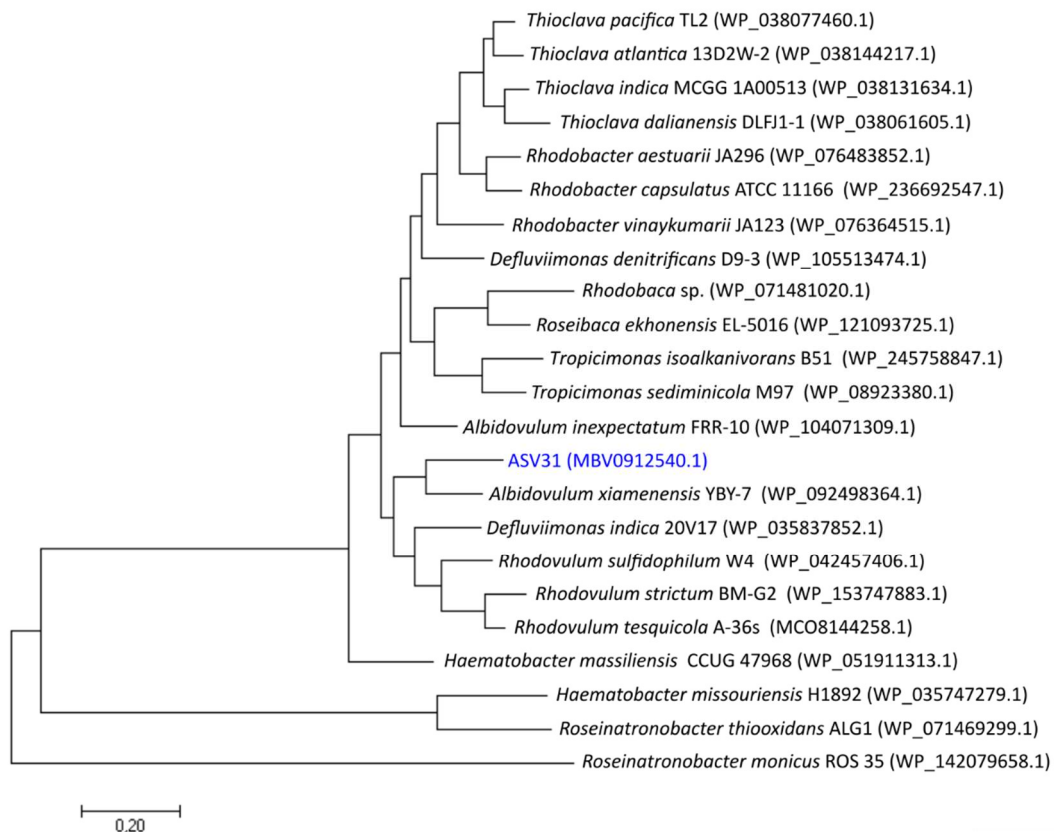
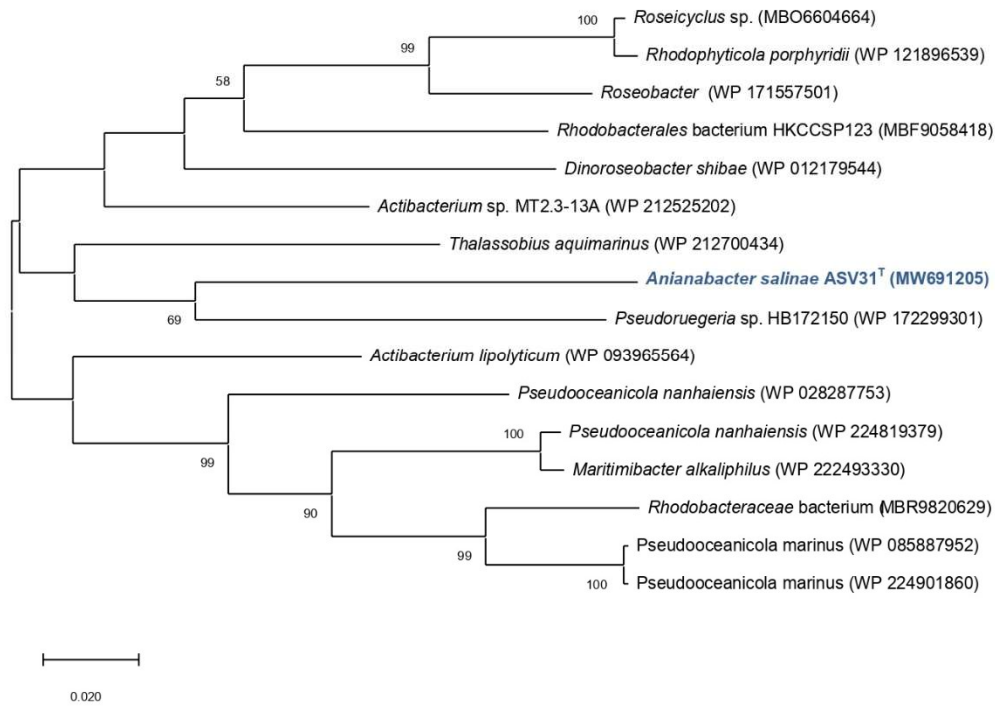


Figure S7. Acyl-CoA synthetase-based maximum-likelihood tree: A, performed with the most similar amino acid sequences; B, performed with sequences from representatives of the *Rhodobacteraceae* family. Tree was generated using MEGA X. Only bootstrap values (expressed as percentages of 1000 replications) greater than 50% are shown at branching points. The scale bar indicates the number of substitutions per site.

A



B

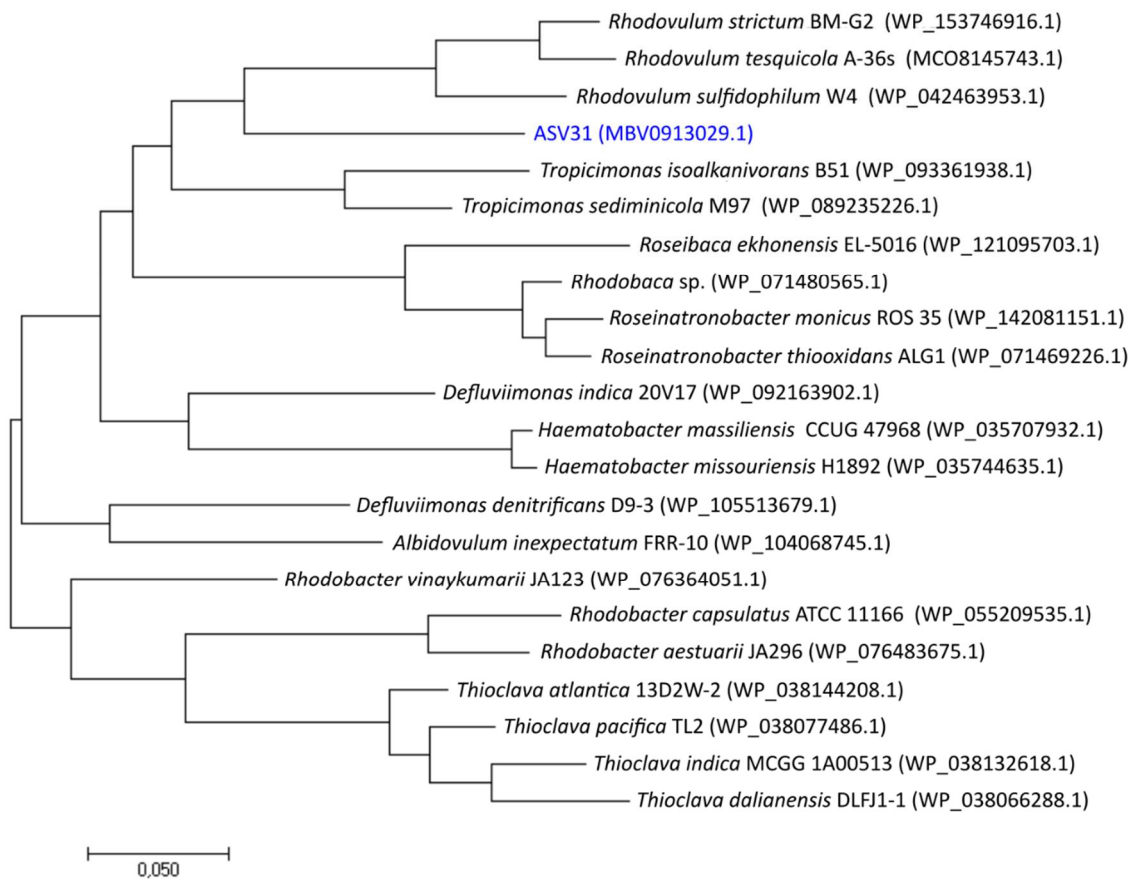


Figure S8. 2-oxoglutarate dehydrogenase-based maximum likelihood tree; A, performed with the most similar amino acidic sequences, B, performed with sequences from representatives of the *Rhodobacteraceae* family. Tree was generated using MEGA X. Only bootstrap values (expressed as percentages of 1000 replications) greater than 50% are shown at branching points. The scale bar indicates the number of substitutions per site.

Table S1. AAI and POCP matrix from pairwise whole-genome comparison. The heat map shows AAI and POCP values between strain ASV31^T and type species of the closest genera in family *Rhodobacteraceae*. The darkest the green colour the higher the percentage of similarity.

AAI		POCP																																		
		<i>Ananabacter salinae</i> ASV31 ^T	<i>Haematobacter mazziliensis</i> CCUG 47968 ^T	<i>Haematobacter missouriensis</i> H1892 ^T	<i>Rhodobacter aestuarii</i> DSM 19945 ^T	<i>Rhodobacter blasticus</i> DSM 2131 ^T	<i>Rhodobacter capsulatus</i> DSM 1710 ^T	<i>Rhodobacter flagellatus</i> SYSU G03088 ^T	<i>Rhodobacter maris</i> JA276 ^T	<i>Rhodobacter sediminicola</i> JA983 ^T	<i>Rhodobacter thermarum</i> YIM 73036 ^T	<i>Rhodobacter viridis</i> JA737 ^T	<i>Rhodobacter xinxiangensis</i> TJ48 ^T	<i>Rhodovulum algae</i> LMG 29228 ^T	<i>Rhodovulum adriaticum</i> DSM 2781 ^T	<i>Rhodovulum bhavnagarense</i> DSM 24766 ^T	<i>Rhodovulum euryhalinum</i> DSM 4868 ^T	<i>Rhodovulum imhoffii</i> DSM 18064 ^T	<i>Rhodovulum marinum</i> DSM 18063 ^T	<i>Rhodovulum robiginosum</i> DSM 12329 ^T	<i>Rhodovulum steppense</i> DSM 21153 ^T	<i>Rhodovulum strictum</i> DSM 11289 ^T	<i>Rhodovulum sulfidophilum</i> DSM 1374 ^T	<i>Rhodovulum viride</i> JA756 ^T	<i>Rhodovulum visakhapatnamense</i> JA181 ^T	<i>Thioclava arenaosa</i> CAU 1312 ^T	<i>Thioclava atlantica</i> 13D2W-2 ^T	<i>Thioclava dalienensis</i> CGMCC 1.12325 ^T	<i>Thioclava electrotropha</i> Elox9 ^T	<i>Thioclava indica</i> DT23-4 ^T	<i>Thioclava marina</i> 11.10-0-13 ^T	<i>Thioclava nitrareducens</i> 25B10-4 ^T	<i>Thioclava pacifica</i> DSM 10166 ^T	<i>Thioclava sediminum</i> TAW-CT134 ^T	<i>Tropicimonas isokanivorans</i> DSM 19548 ^T	<i>Tropicimonas sediminicola</i> DSM 29339 ^T
<i>Ananabacter salinae</i> ASV31 ^T	100	50	49	53	58	53	58	53	54	58	53	49	54	60	57	59	58	58	62	56	55	54	54	55	58	56	55	54	56	58	55	56	55	52	55	
<i>Haematobacter mazziliensis</i> CCUG 47968 ^T	60	100	86	50	54	52	50	53	56	57	51	57	51	50	51	52	52	54	50	53	53	51	50	53	54	56	54	50	53	54	52	56	51	48	47	
<i>Haematobacter missouriensis</i> H1892 ^T	60	92	100	50	51	51	51	51	56	53	57	56	51	50	51	51	53	53	50	52	53	51	51	54	53	55	53	50	52	53	51	54	50	49	47	
<i>Rhodobacter aestuarii</i> DSM 19945 ^T	61	61	61	100	61	74	56	77	59	56	73	49	56	58	57	59	58	57	58	57	59	56	57	58	66	61	58	60	62	65	58	65	61	51	51	
<i>Rhodobacter blasticus</i> DSM 2131 ^T	62	62	62	64	100	64	71	63	63	71	63	54	56	59	59	61	60	58	60	59	61	57	57	58	62	59	56	56	59	61	57	60	57	53	54	
<i>Rhodobacter capsulatus</i> DSM 1710 ^T	61	62	61	78	64	100	58	77	60	58	81	51	56	59	58	60	59	57	58	58	58	58	58	59	66	60	58	58	61	64	57	63	59	49	50	
<i>Rhodobacter flagellatus</i> SYSU G03088 ^T	62	62	62	63	73	64	100	56	59	86	56	52	52	56	57	58	58	57	59	57	58	53	53	54	59	56	54	54	57	59	55	58	55	52	53	
<i>Rhodobacter maris</i> JA276 ^T	61	61	61	82	64	78	63	100	59	57	75	50	56	59	58	58	58	59	57	58	59	57	59	61	65	62	59	59	62	65	59	65	60	51	51	
<i>Rhodobacter sediminicola</i> JA983 ^T	63	64	64	64	67	65	68	64	100	60	58	55	57	58	60	62	61	58	60	61	62	58	56	61	59	58	54	56	58	59	55	57	56	55	52	
<i>Rhodobacter thermarum</i> YIM 73036 ^T	62	62	62	63	72	63	86	63	68	100	57	52	52	57	58	59	58	57	60	57	58	53	53	57	59	58	55	54	58	59	57	59	55	53	53	
<i>Rhodobacter viridis</i> JA737 ^T	61	61	61	78	64	89	63	78	64	63	100	50	54	57	56	58	57	56	57	56	57	56	58	54	56	57	65	60	57	61	64	57	62	59	49	50
<i>Rhodobacter xinxiangensis</i> TJ48 ^T	60	63	63	61	64	61	64	61	66	63	61	100	48	48	49	50	50	49	49	49	49	49	48	49	50	62	51	52	50	51	53	50	52	51	45	46
<i>Rhodovulum algae</i> LMG 29228 ^T	64	61	62	62	62	62	62	62	63	62	62	60	100	63	61	66	61	64	62	64	63	85	78	77	56	54	52	52	54	56	52	55	53	50	51	
<i>Rhodovulum adriaticum</i> DSM 2781 ^T	65	61	61	62	63	63	62	62	64	63	62	61	73	100	77	71	67	71	69	68	67	64	63	65	61	59	54	55	58	60	56	60	56	53	53	
<i>Rhodovulum bhavnagarense</i> DSM 24766 ^T	65	62	62	62	63	62	63	63	65	63	62	61	73	83	100	69	69	68	68	69	67	62	61	64	62	58	54	53	57	59	55	59	54	54	52	
<i>Rhodovulum euryhalinum</i> DSM 4868 ^T	65	62	62	62	64	63	63	63	65	64	62	61	74	76	76	100	68	78	72	77	77	68	69	71	61	58	54	57	58	61	56	60	57	56	57	
<i>Rhodovulum imhoffii</i> DSM 18064 ^T	64	62	62	62	62	62	62	62	65	62	61	61	70	71	72	71	100	65	69	65	67	63	62	65	64	58	54	55	58	60	56	59	56	55	52	
<i>Rhodovulum marinum</i> DSM 18063 ^T	66	62	62	62	63	63	63	63	64	63	62	61	74	77	77	83	72	100	70	75	72	65	67	69	61	59	55	56	58	62	58	62	57	55	56	
<i>Rhodovulum robiginosum</i> DSM 12329 ^T	66	61	62	62	63	63	63	62	65	63	62	61	71	75	74	75	73	75	100	67	67	62	62	65	62	60	54	58	58	62	58	60	59	58	58	
<i>Rhodovulum steppense</i> DSM 21153 ^T	65	62	62	62	63	62	63	63	65	63	62	61	73	75	75	83	71	81	73	100	81	65	65	69	60	58	53	54	56	60	55	57	55	53	54	
<i>Rhodovulum strictum</i> DSM 11289 ^T	64	62	61	62	63	62	64	63	66	64	62	61	73	75	75	82	70	80	73	90	100	64	65	69	60	58	53	53	55	58	54	59	54	55	53	
<i>Rhodovulum sulfidophilum</i> DSM 1374 ^T	64	61	61	62	62	62	62	62	64	62	62	60	92	73	73	75	70	74	72	74	73	100	79	78	56	54	52	52	55	56	52	56	53	50	52	
<i>Rhodovulum viride</i> JA756 ^T	64	61	61	62	63	63	62	63	64	62	62	60	87	74	73	75	70	75	72	74	74	87	100	86	55	54	53	53	54	56	53	55	53	51	52	
<i>Rhodovulum visakhapatnamense</i> JA181 ^T	64	62	62	62	63	62	63	65	63	62	61	86	73	74	75	70	75	72	75	74	87	95	100	65	58	55	55	56	58	55	58	55	55	53	53	
<i>Thioclava arenaosa</i> CAU 1312 ^T	63	63	62	71	64	71	64	71	65	64	71	63	63	64	64	64	63	64	64	64	63	63	63	100	67	62	65	69	75	65	73	67	53	55		
<i>Thioclava atlantica</i> 13D2W-2 ^T	62	62	62	68	63	68	62	68	63	62	68	61	62	61	63	63	62	63	63	63	62	62	62	63	71	100	70	78	71	78	78	78	55	55		
<i>Thioclava dalienensis</i> CGMCC 1.12325 ^T	61	60	60	66	61	67	61	66	62	61	66	60	60	62	62	61	61	62	62	62	62	61	61	62	70	71	100	69	70	68	69	69	53	52		
<i>Thioclava electrotropha</i> Elox9 ^T	61	60	60	67	62	67	61	67	62	61	67	60	62	62	62	62	62	62	62	62	62	62	62	71	81	76	100	72	78	83	77	91	53	54		
<i>Thioclava indica</i> DT23-4 ^T	60	60	60	68	62	68	62	68	62	62	67	60	61	62	62	62	62	62	62	62	62	62	61	61	61	71	77	79	77	100	76	73	74	73	53	55
<i>Thioclava marina</i> 11.10-0-13 ^T	62	61	61	69	63	69	63	69	63	62	68	61	62	63	63	63	62	63	63	63	63	62	62	63	73	83	76	84	79	100	77	88	80	54	55	
<i>Thioclava nitrareducens</i> 25B10-4 ^T	61	60	60	67	62	67	62	67	62	61	67	60	61	63	62	62	62	62	62	62	62	62	61	61	61	71	81	76	93	77	83	100	76	83	54	53
<i>Thioclava pacifica</i> DSM 10166 ^T	61	62	61	69	62	69	62	69	64	62	68	61	62	63	63	63	62	63	63	63	63	62	62	63	73	83	77	83	78	94	82	100	79	54	55	
<i>Thioclava sediminum</i> TAW-CT134 ^T	61	60	60	68	62	67	61	67	62	61	67	60	61	62	62	62	61	62	62	62	62	62	62	71	81	76	98	77	84	94	84	100	53	55		
<i>Tropicimonas isokanivorans</i> DSM 19548 ^T	62	59	59	60	60	59	61	60	62	61	59	58	61	65	64	64	65	64	65	64	64	62	62	63	62	61	60	60	60	60	61	61	60	100	64	
<i>Tropicimonas sediminicola</i> DSM 29339 ^T	62	59	59	60	61	60	61	60	61	61	60	58	62	64	64	64	63	64	54	64	63	62	63	63	62	61	60	60	60	61	60	61	60	75	100	

Table S2. Presence and absence of subsystems in strain ASV31^T compared to its closest relatives (*Thioclava pacifica* DSM 10166^T, *Rhodovulum algae* LMG 29228^T, *Tropicimonas isoalkanivorans* B51^T and *Haematobacter massiliensis* CCUG 47968^T).

Only present in ASV31 ^T (not in relatives)			
Category	Subcategory	Subsystem	Role
Amino Acids and Derivatives	Aromatic amino acids and derivatives	Aromatic amino acid degradation	2-oxo-hepta-3-ene-1,7-dioic acid hydratase (EC 4.2.-.-)
			Homoprotocatechuate degradative operon repressor
	Alanine, serine, and glycine	Glycine and Serine Utilization	Cystathionine gamma-lyase (EC 4.4.1.1)
	Arginine; urea cycle, polyamines	Urea carboxylase and Allophanate hydrolase cluster	Allophanate hydrolase (EC 3.5.1.54)
Carbohydrates	Central carbohydrate metabolism	Pyruvate metabolism II: acetyl-CoA, acetogenesis from pyruvate	Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4)
Clustering-based subsystems	May be related to ADP-phosphoribose and NAD-dependent acetylation	CBSS-216591.1.peg.168	MaoC domain protein dehydratase
	Clustering-based subsystems	CBSS-292415.3.peg.2341	Major facilitator superfamily (MFS) transporter
	no subcategory	CBSS-296591.1.peg.2330	Alpha-1,3-N-acetylgalactosamine transferase PgIA (EC 2.4.1.-)
			Lipid carrier : UDP-N-acetylgalactosaminyltransferase (EC 2.4.1.-)
			Putative glycosyltransferase
	tRNA sulfuration	CBSS-89187.3.peg.2957	hypothetical protein SKA53_09994
Cofactors, Vitamins, Prosthetic Groups, Pigments	Tetrapyrroles	Cobalamin synthesis	Cobalt-precorrin-6x reductase (EC 1.3.1.54)
Fatty Acids, Lipids, and Isoprenoids	Fatty acids	Fatty Acid Biosynthesis FASII	Biotin carboxyl carrier protein
Membrane Transport	TRAP transporters	TRAP Transporter unknown substrate 4	TRAP dicarboxylate transporter, DctM subunit, unknown substrate 4
			TRAP dicarboxylate transporter, DctQ subunit, unknown substrate 4
			TRAP transporter solute receptor, unknown substrate 4
		TRAP Transporter unknown substrate 7	TRAP dicarboxylate transporter, DctQ subunit, unknown substrate 7
			TRAP transporter solute receptor, unknown substrate 7

Metabolism of Aromatic Compounds	no subcategory	Aromatic Amin Catabolism	3,4-dihydroxyphenylacetate 2,3-dioxygenase (EC 1.13.11.15)
	Peripheral pathways for catabolism of aromatic compounds	Benzoate degradation	Ortho-halobenzoate 1,2-dioxygenase alpha-ISP protein OhbB
			Ortho-halobenzoate 1,2-dioxygenase beta-ISP protein OhbA
	Metabolism of central aromatic intermediates	Catechol branch of beta-ketoadipate pathway	Catechol 1,2-dioxygenase (EC 1.13.11.1)
		Central meta-cleavage pathway of aromatic compound degradation	Muconolactone isomerase (EC 5.3.3.4), putative
Miscellaneous	no subcategory	Lignin degradation fragments	3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogenases
			4-carboxy-4-hydroxy-2-oxoadipate aldolase (EC 4.1.3.17)
Nitrogen Metabolism	no subcategory	Cyanate hydrolysis	Cyanate ABC transporter, ATP-binding protein
			Cyanate ABC transporter, permease protein
			Cyanate ABC transporter, substrate binding protein
Protein Metabolism	Protein processing and modification	N-linked Glycosylation in Bacteria	Alpha-1,4-N-acetylgalactosamine transferase PglI (EC 2.4.1.-)
			Phospholipid-lipopolysaccharide ABC transporter
Regulation and Cell signalling	no subcategory	cAMP signalling in bacteria	3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17)
Respiration	Electron accepting reactions	Anaerobic respiratory reductases	Vanillate O-demethylase oxidoreductase (EC 1.14.13.-)
	no subcategory	Carbon monoxide dehydrogenase maturation factors	Carbon monoxide oxidation accessory protein CoxD
		Soluble cytochromes and functionally related electron carriers	Carbon monoxide oxidation accessory protein CoxE
RNA Metabolism	RNA processing and modification	RNA methylation	tRNA (adenine37-N(6))-methyltransferase TrmN6 (EC 2.1.1.223)
Stress Response	Periplasmic Stress	Periplasmic Stress Response	Outer membrane protein H precursor
Virulence, Disease and Defence	Resistance to antibiotics and toxic compounds	Zinc resistance	Response regulator of zinc sigma-54-dependent two-component system

Only present in all relatives (not in ASV31 ^T)			
Category	Subcategory	Subsystem	Role
Amino Acids and Derivatives	no subcategory	Creatine and Creatinine Degradation	Cytosine deaminase (EC 3.5.4.1)
	Lysine, threonine, methionine, and cysteine	Cysteine Biosynthesis	Cysteine synthase (EC 2.5.1.47)
Carbohydrates	CO2 fixation	CO2 uptake, carboxysome	Ribulose biphosphate carboxylase large chain (EC 4.1.1.39)
			Ribulose biphosphate carboxylase small chain (EC 4.1.1.39)
			RuBisCO operon transcriptional regulator CbbR
	Sugar alcohols	Glycerol and Glycerol-3-phosphate Uptake and Utilization	Glycerol-3-phosphate ABC transporter, permease protein UgpE (TC 3.A.1.1.3)
	Central carbohydrate metabolism	Glycolysis and Gluconeogenesis	Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11)
			Fructose-bisphosphate aldolase class II (EC 4.1.2.13)
Clustering-based subsystems	no subcategory	LMPTP YfkJ cluster	Low molecular weight protein tyrosine phosphatase (EC 3.1.3.48)
Cofactors, Vitamins, Prosthetic Groups, Pigments	Coenzyme A	Coenzyme A Biosynthesis	Pantoate--beta-alanine ligase (EC 6.3.2.1)
Membrane Transport	Cation transporters	Magnesium transport	Magnesium and cobalt transport protein CorA
Miscellaneous	no subcategory	Broadly distributed proteins not in subsystems	YciL protein
Motility and Chemotaxis	Flagellar motility in Prokaryota	Flagellar motility	Flagellar L-ring protein FlgH
			Flagellar biosynthesis protein FlhA
			Flagellar biosynthesis protein FlhB
			Flagellar biosynthesis protein FliR
			Flagellar motor rotation protein MotA
			Flagellar motor switch protein FliN
			Flagellum-specific ATP synthase FliI
		Flagellum in Campylobacter	Flagellar basal-body rod protein FlgB
			Flagellar basal-body rod protein FlgC
			Flagellar hook-basal body complex protein FliE
			Flagellin protein FlaA
Phages, Prophages, Transposable elements,	Gene Transfer Agent (GTA)	Gene Transfer Agent	Gene Transfer Agent (GTA) ORFG06

Plasmids			
Phosphorus Metabolism	no subcategory	Phosphate metabolism	Probable low-affinity inorganic phosphate transporter
Protein Metabolism	Protein biosynthesis	tRNAs	tRNA-Ala-CGC

Table S3. CAZyme types present in ASV31^T strain.

CAZyme category	Families	Known CAZyme activities
Auxiliary Activity (AA)	2	manganese peroxidase (EC 1.11.1.13); versatile peroxidase (EC 1.11.1.16); lignin peroxidase (EC 1.11.1.14); peroxidase (EC 1.11.1.-); cytochrome-c peroxidase (EC 1.11.1.5); ascorbate peroxidase (EC 1.11.1.11)
	3	cellobiose dehydrogenase (EC 1.1.99.18); glucose 1-oxidase (EC 1.1.3.4); aryl alcohol oxidase (EC 1.1.3.7); alcohol oxidase (EC 1.1.3.13); pyranose oxidase (EC 1.1.3.10); glucose 1-dehydrogenase (FAD, quinone) (EC 1.1.5.9); pyranose dehydrogenase (EC 1.1.99.29); oligosaccharide dehydrogenase (FAD) (EC 1.1.5.-)
	3_2	ecdysone oxidase (EC 1.1.3.16); glucose 1-oxidase (EC 1.1.3.4); aryl alcohol oxidase (EC 1.1.3.7); oligosaccharide dehydrogenase (FAD) (EC 1.1.5.-); glucose 1-dehydrogenase (FAD, quinone) (EC 1.1.5.9); pyranose dehydrogenase (EC 1.1.99.29)
	4	vanillyl-alcohol oxidase (EC 1.1.3.38)
	6	1,4-benzoquinone reductase (EC 1.6.5.6)
	7	glucooligosaccharide oxidase (EC 1.1.3.-); chitooligosaccharide oxidase (EC 1.1.3.-); celooligosaccharide dehydrogenase (EC 1.1.99.-)
Carbohydrate-Binding Module (CBM)	48	Modules of approx. 100 residues with glycogen-binding function, appended to GH13 modules. Also found in the beta subunit (glycogen-binding) of AMP-activated protein kinases (AMPK)
Carbohydrate Esterase (CE)	1	acetyl xylan esterase (EC 3.1.1.72); cinnamoyl esterase (EC 3.1.1.-); feruloyl esterase (EC 3.1.1.73); carboxylesterase (EC 3.1.1.1); S-formylglutathione hydrolase (EC 3.1.2.12); diacylglycerol O-acyltransferase (EC 2.3.1.20); trehalose 6-O-mycophyltransferase (EC 2.3.1.122)
	4	acetyl xylan esterase (EC 3.1.1.72); chitin deacetylase (EC 3.5.1.41); chitooligosaccharide deacetylase (EC 3.5.1.-); peptidoglycan GlcNAc deacetylase (EC 3.5.1.-); peptidoglycan N-acetylmuramic acid deacetylase (EC 3.5.1.-)
	11	UDP-3-O-acyl N-acetylglucosamine deacetylase (EC 3.5.1.108)
	14	N-acetyl-1-D-myo-inositol-2-amino-2-deoxy- α -D-glucopyranoside deacetylase (EC 3.5.1.89); diacetylchitobiose deacetylase (EC 3.5.1.-); mycothiol S-conjugate amidase (EC 3.5.1.-)
Glycoside Hydrolase (GH)	1	β -glucosidase (EC 3.2.1.21); β -galactosidase (EC 3.2.1.23); β -mannosidase (EC 3.2.1.25); β -glucuronidase (EC 3.2.1.31); β -xylosidase (EC 3.2.1.37); β -D-fucosidase (EC 3.2.1.38); phlorizin hydrolase (EC 3.2.1.62); exo- β -1,4-glucanase (EC 3.2.1.74); 6-phospho- β -galactosidase (EC 3.2.1.85); 6-phospho- β -glucosidase (EC 3.2.1.86); strictosidine β -glucosidase (EC 3.2.1.105); lactase (EC 3.2.1.108); amygdalin β -glucosidase (EC 3.2.1.117); prunasin β -glucosidase (EC 3.2.1.118); vicianin hydrolase (EC 3.2.1.119); raucaffricine β -glucosidase (EC 3.2.1.125); thioglucosidase (EC 3.2.1.147); β -primeverosidase (EC 3.2.1.149); isoflavonoid 7-O- β -apiosyl- β -glucosidase (EC 3.2.1.161); ABA-specific β -glucosidase (EC 3.2.1.175); DIMBOA β -glucosidase (EC 3.2.1.182); β -glycosidase (EC 3.2.1.-); hydroxyisourate hydrolase (EC 3.-.-.-); β -rutosidase / α -L-rhamnose-(1,6)- β -D-glucosidase (EC 3.2.1.-); protodioscin 26-O- β -D-glucosidase (EC 3.2.1.186)
	3	β -glucosidase (EC 3.2.1.21); xylan 1,4- β -xylosidase (EC 3.2.1.37); β -glucosylceramidase (EC 3.2.1.45); β -N-acetylhexosaminidase (EC 3.2.1.52); α -L-arabinofuranosidase (EC 3.2.1.55); glucan 1,4- β -glucosidase (EC 3.2.1.74); isoprimeverose-producing oligoxyloglucan hydrolase (EC 3.2.1.120); coniferin β -glucosidase (EC 3.2.1.126); exo-1,3-1,4-glucanase (EC 3.2.1.-); β -N-acetylglucosaminide phosphorylases (EC 2.4.1.-); β -1,2-glucosidase (EC 3.2.1.-); β -1,3-glucosidase (EC 3.2.1.-); xyloglucan-specific exo- β -1,4-glucanase / exo-xyloglucanase (EC 3.2.1.155); stevioside- β -1,2-glucosidase (EC 3.2.1.-); lichenase / endo- β -1,3-1,4-glucanase (EC 3.2.1.73); protodioscin 26-O- β -D-glucosidase (EC 3.2.1.186); β -glucuronidase (EC 3.2.1.31)
	13_9	[retaining] a-1,4-glucan branching enzyme (EC 2.4.1.18)
	13_11	[retaining] 4-a-glucanotransferase / amyloamylase (EC 2.4.1.25); a-glycosidase (EC 3.2.1.-); [retaining] isoamylase (EC 3.2.1.68)
	13_18	[retaining] sucrose 6(F)-phosphate phosphorylase (EC 2.4.1.329); Glucosylglycerate phosphorylase (EC 2.4.1.352); [retaining] glucosylglycerol phosphorylase (EC 2.4.1.359); [retaining] sucrose phosphorylase (EC 2.4.1.7)
	23	lysozyme type G (EC 3.2.1.17); peptidoglycan lyase (EC 4.2.2.n1) also known in the literature as peptidoglycan lytic transglycosylase; chitinase (EC 3.2.1.14)
	102	peptidoglycan lytic transglycosylase (EC 3.2.1.-)
	103	peptidoglycan lytic transglycosylase (EC 3.2.1.-)
	105	unsaturated rhamnogalacturonyl hydrolase (EC 3.2.1.172); d-4,5-unsaturated β -glucuronyl hydrolase (EC 3.2.1.-); d-4,5-unsaturated α -galacturonidase (EC 3.2.1.-)
	108	N-acetylmuramidase (EC 3.2.1.17)
	109	α -N-acetylglactosaminidase (EC 3.2.1.49); β -N-acetylhexosaminidase (EC 3.2.1.52)

GlycosylTransferase (GT)	2	cellulose synthase (EC 2.4.1.12); chitin synthase (EC 2.4.1.16); dolichyl-phosphate β -D-mannosyltransferase (EC 2.4.1.83); dolichyl-phosphate β -glucosyltransferase (EC 2.4.1.117); N-acetylglucosaminyltransferase (EC 2.4.1.-); N-acetylgalactosaminyltransferase (EC 2.4.1.-); hyaluronan synthase (EC 2.4.1.212); chitin oligosaccharide synthase (EC 2.4.1.-); β -1,3-glucan synthase (EC 2.4.1.34); β -1,4-mannan synthase (EC 2.4.1.-); β -mannosylphosphodecaprenol-mannooligosaccharide α -1,6-mannosyltransferase (EC 2.4.1.199); UDP-Galf: rhamnopyranosyl-N-acetylglucosaminyl-PP-decaprenol β -1,4/1,5-galactofuranosyltransferase (EC 2.4.1.287); UDP-Galf: galactofuranosyl-galactofuranosyl-rhamnosyl-N-acetylglucosaminyl-PP-decaprenol β -1,5/1,6-galactofuranosyltransferase (EC 2.4.1.288); dTDP-L-Rha: N-acetylglucosaminyl-PP-decaprenol α -1,3-L-rhamnosyltransferase (EC 2.4.1.289); alternating β -1,3/4-N-acetylmannan synthase (2.4.1.-); UDP-GlcA: N-acetylglucosaminyl-proteoglycan β -1,4-glucuronosyltransferase (EC 2.4.1.225)
	4	sucrose synthase (EC 2.4.1.13); sucrose-phosphate synthase (EC 2.4.1.14); α -glucosyltransferase (EC 2.4.1.52); lipopolysaccharide N-acetylglucosaminyltransferase (EC 2.4.1.56); phosphatidylinositol α -mannosyltransferase (EC 2.4.1.57); GDP-Man: Man1GlcNAc2-PP-dolichol α -1,3-mannosyltransferase (EC 2.4.1.132); GDP-Man: Man3GlcNAc2-PP-dolichol/Man4GlcNAc2-PP-dolichol α -1,2-mannosyltransferase (EC 2.4.1.131); digalactosyldiacylglycerol synthase (EC 2.4.1.141); 1,2-diacylglycerol 3-glucosyltransferase (EC 2.4.1.157); diglucosyl diacylglycerol synthase (EC 2.4.1.208); trehalose phosphorylase (EC 2.4.1.231); NDP-Glc: α -glucose α -glucosyltransferase / α , α -trehalose synthase (EC 2.4.1.245); GDP-Man: Man2GlcNAc2-PP-dolichol α -1,6-mannosyltransferase (EC 2.4.1.257); UDP-GlcNAc: 2-
	5	deoxystreptamine α -N-acetylglucosaminyltransferase (EC 2.4.1.283); UDP-GlcNAc: ribostamycin α -N-acetylglucosaminyltransferase (EC 2.4.1.285); UDP-Gal α -galactosyltransferase (EC 2.4.1.-); UDP-Xyl α -xylosyltransferase (EC 2.4.2.-); UDP-GlcA α -glucuronyltransferase (EC 2.4.1.-); UDP-Glc α -glucosyltransferase (EC 2.4.1.-); UDP-GalNAc: GalNAc-PP-Und α -1,3-N-acetylgalactosaminyltransferase (EC 2.4.1.306); UDP-GalNAc: N,N'-diacetyl bacillosaminyl-PP-Und α -1,3-N-acetylgalactosaminyltransferase (EC 2.4.1.290); ADP-dependent α -maltose-1-phosphate synthase (2.4.1.342); [retaining] UDP-GlcNAc: polypeptide α -N-acetylglucosaminyltransferase (EC 2.4.1.-); UDP-GlcNAc: α -N-acetylglucosaminyltransferase (EC 2.4.1.-)
	8	UDP-Glc: glycogen glucosyltransferase (EC 2.4.1.11); ADP-Glc: starch glucosyltransferase (EC 2.4.1.21); NDP-Glc: starch glucosyltransferase (EC 2.4.1.242); UDP-Glc: α -1,3-glucan synthase (EC 2.4.1.183) UDP-Glc: α -1,4-glucan synthase (EC 2.4.1.-)
	14	lipopolysaccharide α -1,3-galactosyltransferase (EC 2.4.1.44); UDP-Glc: (glucosyl)lipopolysaccharide α -1,2-glucosyltransferase (EC 2.4.1.-); lipopolysaccharide glucosyltransferase 1 (EC 2.4.1.58); glycogenin glucosyltransferase (EC 2.4.1.186); inositol 1- α -galactosyltransferase (galactinol synthase) (EC 2.4.1.123); homogalacturonan α -1,4-galacturonosyltransferase (EC 2.4.1.43); UDP-GlcA: xylan α -glucuronyltransferase (EC 2.4.1.-); UDP-Gal: glucoside α -1,3-galactosyltransferase (EC 2.4.1.-)
	19	β -1,3-galactosyl-O-glycosyl-glycoprotein β -1,6-N-acetylglucosaminyltransferase (EC 2.4.1.102); N-acetylactosaminide β -1,6-N-acetylglucosaminyltransferase (EC 2.4.1.150); protein O- β -xylosyltransferase (EC 2.4.2.26); UDP-GlcA: arabinogalactan β -glucuronosyltransferase (EC 2.4.1.-)
	20	lipid-A-disaccharide synthase (EC 2.4.1.182).
	28	α , α -trehalose-phosphate synthase [UDP-forming] (EC 2.4.1.15); Glucosylglycerol-phosphate synthase (EC 2.4.1.213); trehalose-6-P phosphatase (EC 3.1.3.12); [retaining] GDP-valeniol: validamine 7-phosphate valeniolyltransferase (EC 2.-.-.-)
	30	1,2-diacylglycerol 3- β -galactosyltransferase (EC 2.4.1.46); 1,2-diacylglycerol 3- β -glucosyltransferase (EC 2.4.1.157); UDP-GlcNAc: Und-PP-MurAc-pentapeptide β -N-acetylglucosaminyltransferase (EC 2.4.1.227); digalactosyldiacylglycerol synthase (EC 2.4.1.241)
	35	CMP- β -KDO: α -3-deoxy-D-manno-octulosonic-acid (KDO) transferase (EC 2.4.99.-).
	51	glycogen or starch phosphorylase (EC 2.4.1.1).
	81	murein polymerase (EC 2.4.1.129).
	83	NDP-Glc: glucosyl-3-phosphoglycerate synthase (EC 2.4.1.266); NDP-Man: mannosyl-3-phosphoglycerate synthase (EC 2.4.1.217); ADP-Glc: glucosyl-2-glycerate synthase (EC 2.4.1.-); mannosyl-3-phosphoglycerate synthase / [retaining] GDP-Man: 3-phosphoglycerate α -mannosyltransferase (EC 2.4.1.217)
107		undecaprenyl phosphate- α -L-Ara4N: 4-amino-4-deoxy- β -L-arabinosyltransferase (EC 2.4.2.43); dodecaprenyl phosphate- β -galacturonic acid: lipopolysaccharide core α -galacturonosyl transferase (EC 2.4.1.-)