

MariClus: your one-stop platform for information on marine natural products, their gene clusters and producing organisms

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MariClus

Dashboard

Species

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Tutorial

Search for species, clusters, molecules, articles...

Search

Salinispora tropica

Back to species

General

Taxonomy

Bacteria / Terrabacteria group / Actinomycetota / Actinomycetes / Micromonosporales / Micromonosporaceae / Salinispora

Description

This species produces the chemicals salinosporamide A and B which may be useful for cancer treatment.

Pubmed ID





19550008

Biosynthesis of the salinosporamide A polyketide synthase substrate chloroethylmalonyl-coenzyme A from S-adenosyl-L-methionine

17563368

Genome sequencing reveals complex secondary metabolome in the marine actinomycete Salinispora tropica

Collection









   

Genome accession

GCF_000016425.1

FASTA

Search:

Contig	Start	End	#genes in cluster	Type	Predicted product																																																																																																																																																																				
 NC_009380.1	653599	698397	41	T1PKS	<div>Show all molecules for this cluster</div>																																																																																																																																																																				
 NC_009380.1	736985	779496	38	NRP																																																																																																																																																																					
 NC_009380.1	1016172	1031000	12	NAGGN																																																																																																																																																																					
 NC_009380.1	1131284	1180343	31	transAT_PKS-like	<div>Cum. BLAST score: 22414 Known cluster coverage: 7%  salinosporamide A  Cum. BLAST score: 17472 Known cluster coverage: 90.48%  salinosporamide A  Cluster Information BGC Cluster BGC00001145 Source salinosporamide A Type NRP-Polyketide Number of proteins with BLAST hits to this cluster out of total genes in cluster 19 / 21 (90.48%) Cumulative BLAST score 17472.0 Genes <table><thead><tr><th>Gene</th><th>Annotation</th></tr></thead><tbody><tr><td>ABP73634.1</td><td>SalU</td></tr><tr><td>ABP73635.1</td><td>SalT</td></tr><tr><td>ABP73636.1</td><td>SalS</td></tr><tr><td>ABP73637.1</td><td>SalRll</td></tr><tr><td>ABP73638.1</td><td>SalQ</td></tr><tr><td>ABP73639.1</td><td>SalRll</td></tr><tr><td>ABP73640.1</td><td>SalO</td></tr><tr><td>ABP73641.1</td><td>SalN</td></tr><tr><td>ABP73642.1</td><td>SalM</td></tr><tr><td>ABP73643.1</td><td>SalL</td></tr><tr><td>ABP73644.1</td><td>SalK</td></tr><tr><td>ABP73645.1</td><td>SalA</td></tr><tr><td>ABP73646.1</td><td>SalB</td></tr><tr><td>ABP73647.1</td><td>SalC</td></tr><tr><td>ABP73648.1</td><td>SalD</td></tr><tr><td>ABP73649.1</td><td>SalE</td></tr><tr><td>ABP73650.1</td><td>SalF</td></tr><tr><td>ABP73651.1</td><td>SalG</td></tr><tr><td>ABP73652.1</td><td>SalH</td></tr><tr><td>ABP73653.1</td><td>SalI</td></tr><tr><td>ABP73654.1</td><td>SalJ</td></tr></tbody></table> Blast Hits <table><thead><tr><th>Query Gene</th><th>Subject Gene</th><th>% Identity</th><th>Blast Score</th><th>% Coverage</th><th>E-value</th></tr></thead><tbody><tr><td>STROP_RS05145</td><td>ABP73653.1</td><td>100</td><td>531</td><td>98.58156028368793</td><td>1.47e-193</td></tr><tr><td>STROP_RS05150</td><td>ABP73652.1</td><td>100</td><td>1148</td><td>100.0</td><td>0.0</td></tr><tr><td>STROP_RS05155</td><td>ABP73651.1</td><td>100</td><td>927</td><td>100.0</td><td>0.0</td></tr><tr><td>STROP_RS05160</td><td>ABP73650.1</td><td>100</td><td>578</td><td>100.0</td><td>5.85e-212</td></tr><tr><td>STROP_RS05165</td><td>ABP73649.1</td><td>100</td><td>160</td><td>100.0</td><td>1.53e-53</td></tr><tr><td>STROP_RS05170</td><td>ABP73648.1</td><td>100</td><td>840</td><td>96.11764705882354</td><td>6.95e-311</td></tr><tr><td>STROP_RS05175</td><td>ABP73647.1</td><td>100</td><td>1198</td><td>100.0</td><td>0.0</td></tr><tr><td>STROP_RS05180</td><td>ABP73646.1</td><td>100</td><td>1232</td><td>100.0</td><td>0.0</td></tr><tr><td>STROP_RS05185</td><td>ABP73645.1</td><td>99</td><td>3996</td><td>100.0</td><td>0.0</td></tr><tr><td>STROP_RS05190</td><td>ABP73644.1</td><td>100</td><td>551</td><td>96.89655172412794</td><td>2.69e-201</td></tr><tr><td>STROP_RS05195</td><td>ABP73643.1</td><td>100</td><td>576</td><td>100.0</td><td>2.68e-211</td></tr><tr><td>STROP_RS05200</td><td>ABP73642.1</td><td>100</td><td>497</td><td>100.0</td><td>5.51e-181</td></tr><tr><td>STROP_RS05205</td><td>ABP73641.1</td><td>100</td><td>522</td><td>100.0</td><td>1.31e-190</td></tr><tr><td>STROP_RS05210</td><td>ABP73640.1</td><td>100</td><td>578</td><td>100.0</td><td>2.04e-212</td></tr><tr><td>STROP_RS05215</td><td>ABP73639.1</td><td>100</td><td>419</td><td>100.0</td><td>6.9e-151</td></tr><tr><td>STROP_RS05220</td><td>ABP73638.1</td><td>100</td><td>2221</td><td>100.0</td><td>0.0</td></tr><tr><td>STROP_RS05225</td><td>ABP73637.1</td><td>100</td><td>656</td><td>100.0</td><td>6.28e-241</td></tr><tr><td>STROP_RS05230</td><td>ABP73636.1</td><td>100</td><td>305</td><td>100.0</td><td>3.37e-108</td></tr><tr><td>STROP_RS05235</td><td>ABP73635.1</td><td>100</td><td>537</td><td>100.0</td><td>1.94e-196</td></tr></tbody></table><div>Show all molecules for this cluster</div></div>	Gene	Annotation	ABP73634.1	SalU	ABP73635.1	SalT	ABP73636.1	SalS	ABP73637.1	SalRll	ABP73638.1	SalQ	ABP73639.1	SalRll	ABP73640.1	SalO	ABP73641.1	SalN	ABP73642.1	SalM	ABP73643.1	SalL	ABP73644.1	SalK	ABP73645.1	SalA	ABP73646.1	SalB	ABP73647.1	SalC	ABP73648.1	SalD	ABP73649.1	SalE	ABP73650.1	SalF	ABP73651.1	SalG	ABP73652.1	SalH	ABP73653.1	SalI	ABP73654.1	SalJ	Query Gene	Subject Gene	% Identity	Blast Score	% Coverage	E-value	STROP_RS05145	ABP73653.1	100	531	98.58156028368793	1.47e-193	STROP_RS05150	ABP73652.1	100	1148	100.0	0.0	STROP_RS05155	ABP73651.1	100	927	100.0	0.0	STROP_RS05160	ABP73650.1	100	578	100.0	5.85e-212	STROP_RS05165	ABP73649.1	100	160	100.0	1.53e-53	STROP_RS05170	ABP73648.1	100	840	96.11764705882354	6.95e-311	STROP_RS05175	ABP73647.1	100	1198	100.0	0.0	STROP_RS05180	ABP73646.1	100	1232	100.0	0.0	STROP_RS05185	ABP73645.1	99	3996	100.0	0.0	STROP_RS05190	ABP73644.1	100	551	96.89655172412794	2.69e-201	STROP_RS05195	ABP73643.1	100	576	100.0	2.68e-211	STROP_RS05200	ABP73642.1	100	497	100.0	5.51e-181	STROP_RS05205	ABP73641.1	100	522	100.0	1.31e-190	STROP_RS05210	ABP73640.1	100	578	100.0	2.04e-212	STROP_RS05215	ABP73639.1	100	419	100.0	6.9e-151	STROP_RS05220	ABP73638.1	100	2221	100.0	0.0	STROP_RS05225	ABP73637.1	100	656	100.0	6.28e-241	STROP_RS05230	ABP73636.1	100	305	100.0	3.37e-108	STROP_RS05235	ABP73635.1	100	537	100.0	1.94e-196
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Supplementary Figure S1. MariClus database view of the species details for *Salinispora tropica*. The page shows the information about the species, such as its taxonomic lineage, genome assembly, publications and culture collection number. It also shows the list of clusters and molecules predicted for the species. The molecule Salinosporamide A is highlighted in the table as this was our search query. The evidence for the second occurrence of the molecule in this species has been expanded, showing more information about the corresponding MIBiG cluster, the number of BLAST hits and the scores of each hit to the MIBiG cluster. The user can access the antiSMASH pages of the cluster and the molecule by clicking on the icons. The view is limited to the clusters of interest.

Taxonomy Browser

Selected taxa	
Terrabacteria group	Pseudomonadota (purple photosynthetic bacteria and relatives)
FCB group	PVC group
Thermodesulfobacteriota	
Campylobacterota (e-proteobacteria)	Euryarchaeota (euryarchaeotes)
TACK group	Enter one or more taxonomic names
Taxonomic name	Genomes
▼ <i>Bacteria</i> (bacteria)	1,594,016
> <i>FCB group</i>	63,407
> <i>Pseudomonadota</i> (proteobacteria)	981,346
> <i>Terrabacteria group</i>	398,002
> <i>Thermodesulfobacteriota</i>	3,772
> <i>Campylobacterota</i> (e-proteobacteria)	92,269
> <i>PVC group</i>	14,413
▼ <i>Archaea</i> (archaea)	15,322
> <i>TACK group</i>	3,321
> <i>Euryarchaeota</i> (euryarchaeotes)	4,711

Supplementary Figure S2. NCBI taxonomy browser results for the top 8 phyla of the MariClus database. The table shows the taxonomic names and the number of genomes in each phylum. The Pseudomonadota and Terrabacteria group together account for more than 80% of all entries in the bacteria superkingdom (Sayers *et al.* 2022)[16].

References

Sayers, Eric W., Evan E. Bolton, J. Rodney Brister, Kathi Canese, Jessica Chan, Donald C. Comeau, Ryan Connor, et al. 2022. "Database Resources of the National Center for Biotechnology Information." *Nucleic Acids Research* 50 (D1): D20–26. <https://doi.org/10.1093/nar/gkab1112>.