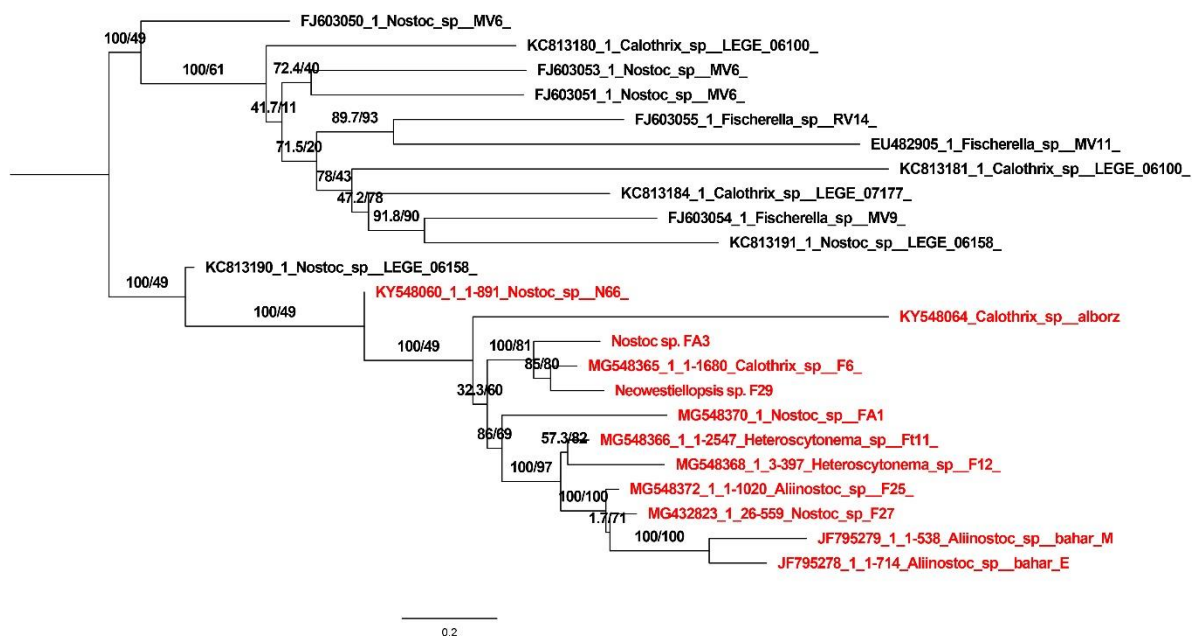


Appendix 1. Oligonucleotide primers of target genes

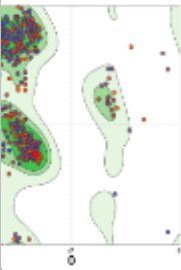
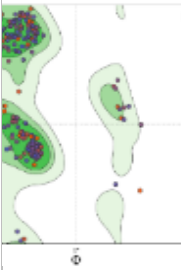
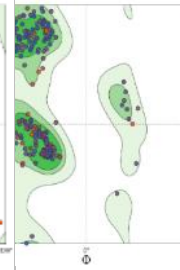
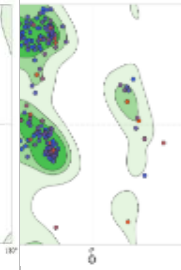
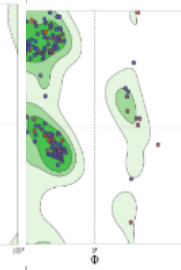

Gene	Sequences
16S rRNA	27F (5'-AGAGTTTGATCCTGGCTCAG-3') 149R (5'-CTTCGCCTCTGTGTGCCTAGGT-3')
PKS	DKF(5'-GTGCCGGTNCRTGNGYYTC-3') DKR(5'-GCGATGGAYCCNCARCARYG-3')
NRPS	MTF2/MTR MTF2 (5'-GCNGGYGGYGCNTAYGTNCC-3') MTR (5'-CCNCGDATYTTNACYTG-3')



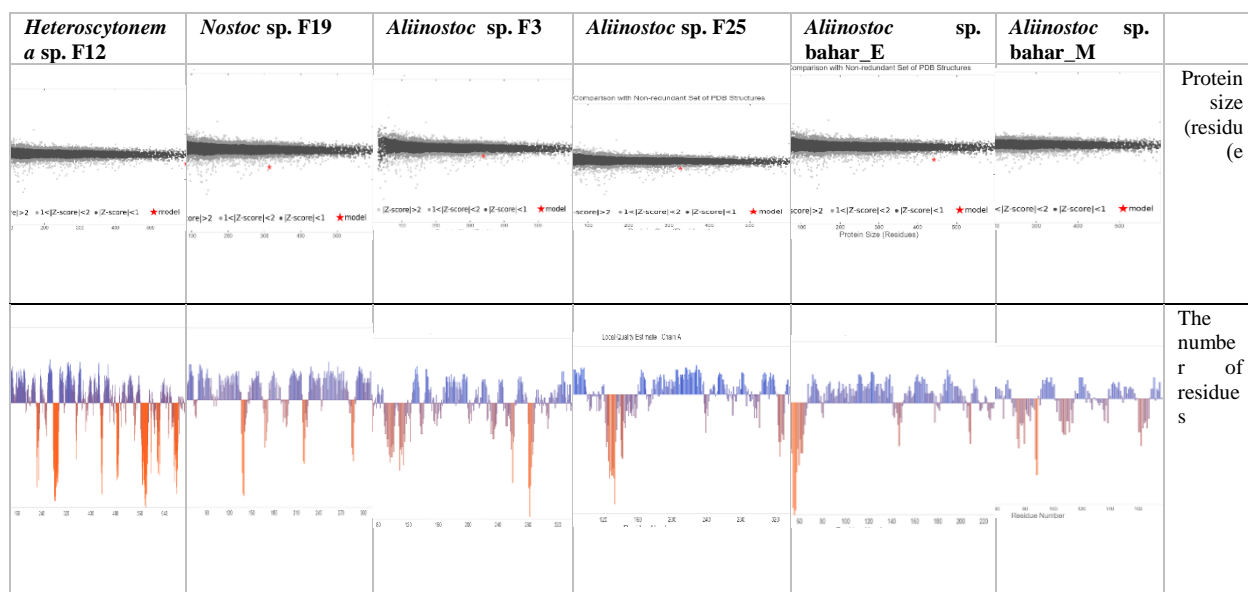
Appendix 2. In the rooted phylogenetic tree of the NRPS gene of the twelve examined strains, the scale shown in the figure indicates 0.2 mutations per amino acid position.

Appendix 3. Quality assessment of the model made of the protein structure of NRPS genes related to twelve cyanobacterial strains based on QMEAN. 3D structure, Ramachandran percentage, and QMEAN and GMQE numerical index provide favorable results.

<i>Heteroscytonema</i> sp. F12	<i>Nostoc</i> sp. F19	<i>Aliinostoc</i> sp. F3	<i>Aliinostoc</i> sp. F25	<i>Aliinostoc</i> sp. bahar_E	<i>Aliinostoc</i> sp. bahar_M	
5u89.1.A	6p1j.1.A	1amu.1.A	6oyf. 1.A	4mz0.1.A	6oyf. 1.A	Template
0.68	0.74	0.79	0.82	0.85	0.81	GMQE

0.67 ± 0.05	0.69 ± 0.05	0.75 ± 0.05	0.80 ± 0.05	0.79 ± 0.05	0.77 ± 0.06	QMEAN DisCo Local
monomer	monomer	Monomer	monomer	Homo-dimer	monomer	Oligo state
						general
93.19%	93.59%	93.18%	95.09%	92.98%	93.22%	Ramachandran percentage

Appendix 4. Statistical distribution of protein structure size and number of NRPS gene residues of twelve cyanobacterial strains.



Appendix 5. The results of the specification of the proposed model for twelve cyanobacterial strains containing the NRPS gene with the SWISS-MODE program

<i>Heteroscytonema</i> sp. F12	[<i>Nostoc</i> sp. F19]	<i>Aliinostoc</i> sp. F3	<i>Aliinostoc</i> sp. F25	<i>Aliinostoc</i> bahar_E	<i>Aliinostoc</i> bahar_M	
5u89.1.A	6p1j.1.A	1amu.1.A	6oyf.1.A	4mz0.1.A	6oyf.1.A	Template

39.14%	38.98%	43.20%	51.38%	61.36%	44.38%	Sequence identity
monomer	monomer	monomer	monomer	Homo-dimer	monomer	Oligo-state
HHblits	HHblits	HHblits	HHblits	X-ray	HHblits	Discovered technique
X-ray, 3.08 Å	X-ray, 2.95 Å	X-ray, 1.90 Å	X-ray, 2.10 Å	X-ray, 2.80 Å	X-ray	Method
0.39	0.39	0.40	0.45	0.48	0.42	Sequence similarity
0.95	1.00	0.99	0.96	1.00	0.99	Covering
Amino acid adenylation domain protein	TXO 2	Gramicidin synthetase1	Txo1	CurL	Txo1	Explanation

