

Identification of antimicrobial peptides from the microalgae *Tetraselmis suecica* (Kylin) Butcher, and bactericidal activity improvement.

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Supplementary Material

Table S1. Identity percentage of the sequences identified according BLAST search in NCBI, within *Tetraselmis* genera (Tax id:).

#	Peptide	% Identity	NCBI accession number	Protein	Organism
1	AQ-1749	100	AMP43327	beta" subunit of RNA polymerase (chloroplast)	<i>Tetraselmis</i> sp. CCMP 881
2	AQ-1750	100	CAA87754	NADH dehydrogenase subunit 5 (mitochondrion)	<i>Tetraselmis subcordiformis</i>
3	AQ-1751	--	--	--	--
4	AQ-1752	80	AML77346	putative LOV domain-containing protein	<i>Tetraselmis chui</i>
5	AQ-1753	80	ABA02341	photosystem II reaction center protein D1 (chloroplast)	<i>Tetraselmis suecica</i>
6	AQ-1754	83	AMP43289	apocytochrome f of cytochrome b6/f complex (chloroplast)	<i>Tetraselmis</i> sp. CCMP 881
7	AQ-1755	--	--	--	--
8	AQ-1756	80	AYF56515	heat shock protein 100	<i>Tetraselmis suecica</i>
9	AQ-1757	80	BAJ21550	beta-tubulin	<i>Tetraselmis chui</i>
10	AQ-1758	80	ABA02340	ATP synthase CF1 beta chain (chloroplast)	<i>Tetraselmis suecica</i>
11	AQ-1759	57	AML76832	putative LOV domain-containing protein	<i>Tetraselmis cordiformis</i>
12	AQ-1760	80	ABA02339	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit (chloroplast)	<i>Tetraselmis suecica</i>
13	AQ-1761	60	AFQ38466	ammonium transporter	<i>Tetraselmis chui</i>
14	AQ-1762	80	CAH59454	proton-translocating inorganic pyrophosphatase	<i>Tetraselmis suecica</i>
15	AQ-1763	60	AML77286	putative LOV domain-containing protein	<i>Tetraselmis striata</i>
16	AQ-1764	--	--	--	--
17	AQ-1765	60	AAO47330	high affinity phosphate transporter	<i>Tetraselmis chui</i>
18	AQ-1766	60	ABA02341	photosystem II reaction center protein D1	<i>Tetraselmis suecica</i>

19	AQ-1767	70	AMP43301	CP47 chlorophyll apoprotein of photosystem II (chloroplast)	<i>Tetraselmis sp.</i> CCMP 881
20	AQ-1768	--	--	--	--
21	AQ-1769	100	AFK27534.	cytochrome c oxidase subunit 2	<i>Tetraselmis gracilis</i>
22	AQ-1770	--	--	--	--
23	AQ-1771	--	--	--	--
24	AQ-1772	--	--	--	--

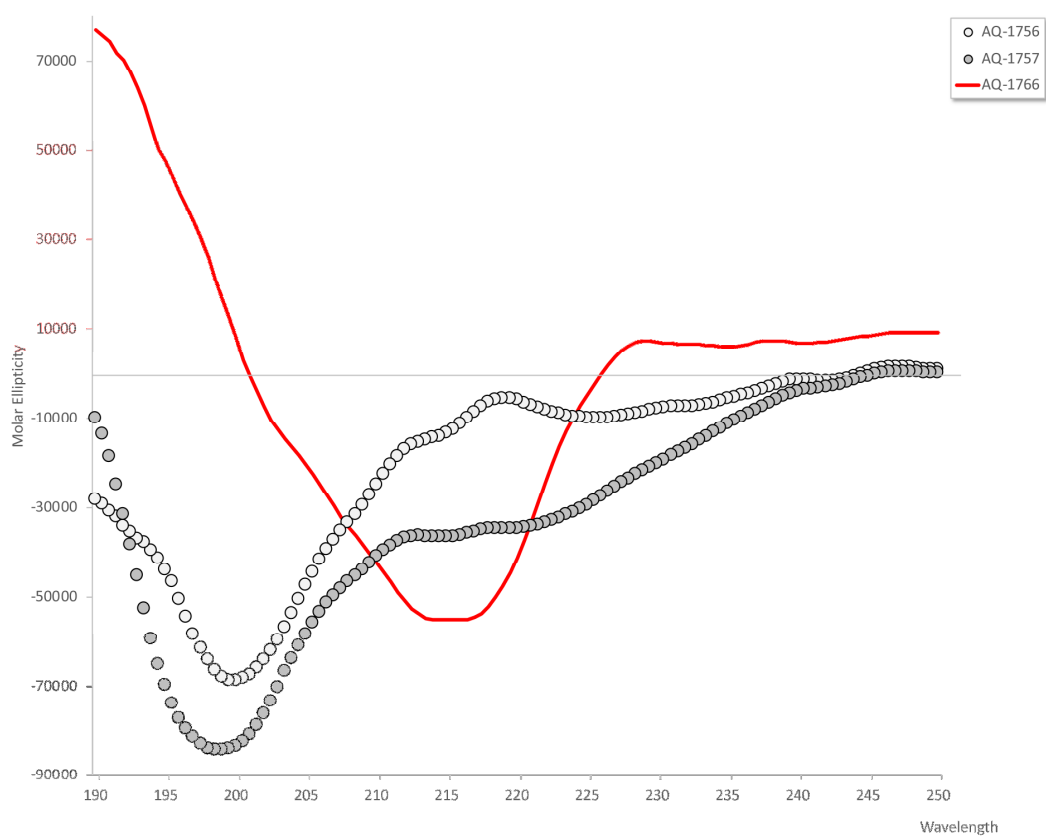


Figure S1. Circular dichroism of the peptides AQ-1755, AQ-1757 and AQ-1766. The spectra were performed in TFE 30%.

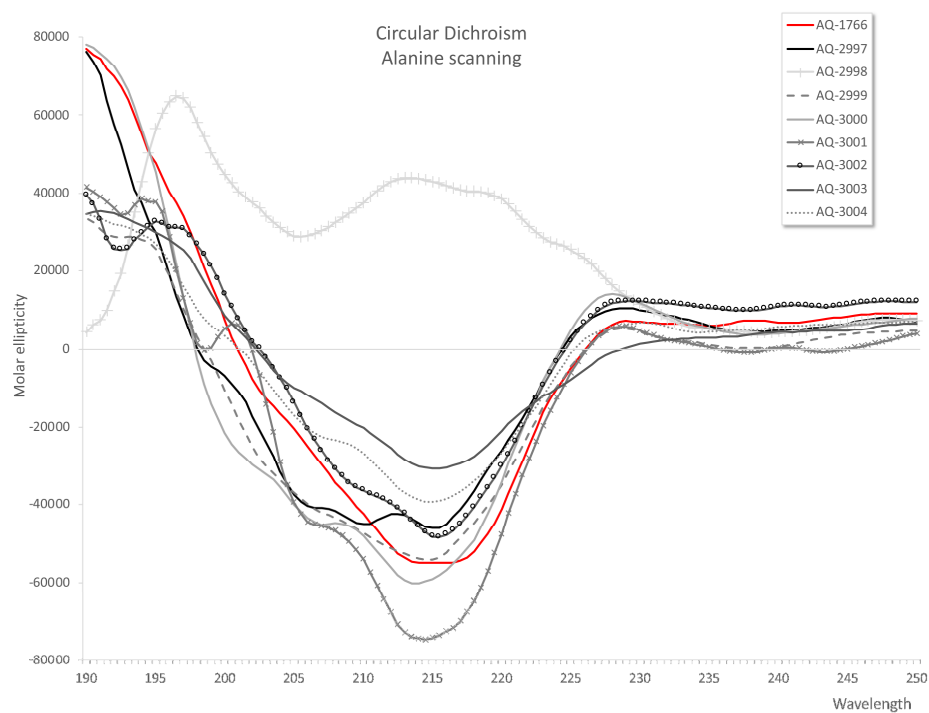
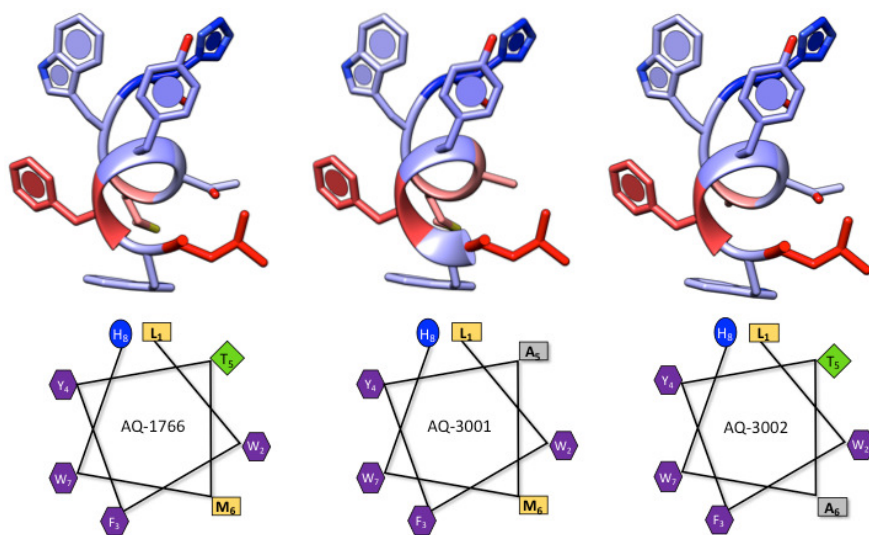


Figure S2. Circular dichroism of the peptide AQ-1766 (red line), and the analogous with alanine replacements (Table 2) . The spectra were performed in TFE 30%.



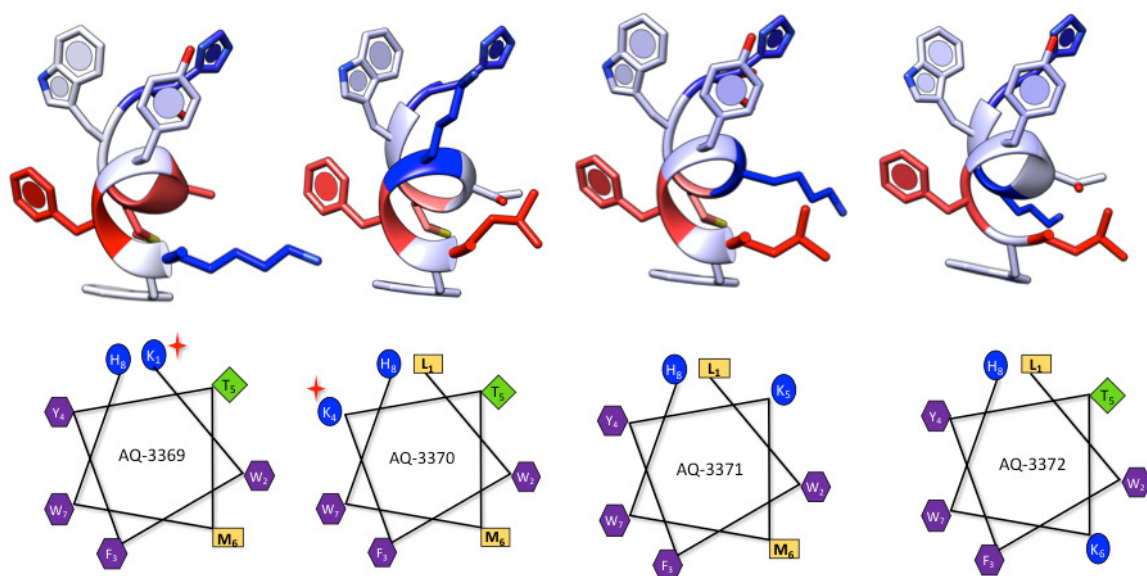


Figure S3. 3D and 2D representaton of active peptides: PEPFOLD3 prediction structures colored according to Kite & Doolittle hydrophobicity as implemented in Chimera, and helical wheel representations for each peptide modified from pepwheel of EMBOSS suite. Red stars indicate the lysine residues in the same face of the helix with the the other basic residue histidine.