

Title	Genome mining coupled with OSMAC-based cultivation reveal differential production of surugamide A by the marine sponge isolate <i>Streptomyces</i> sp. SM17 when compared to its terrestrial relative <i>S. albidoflavus</i> J1074
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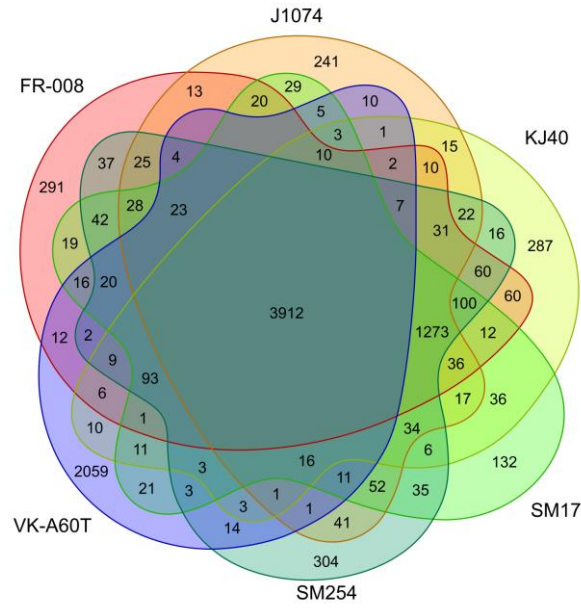
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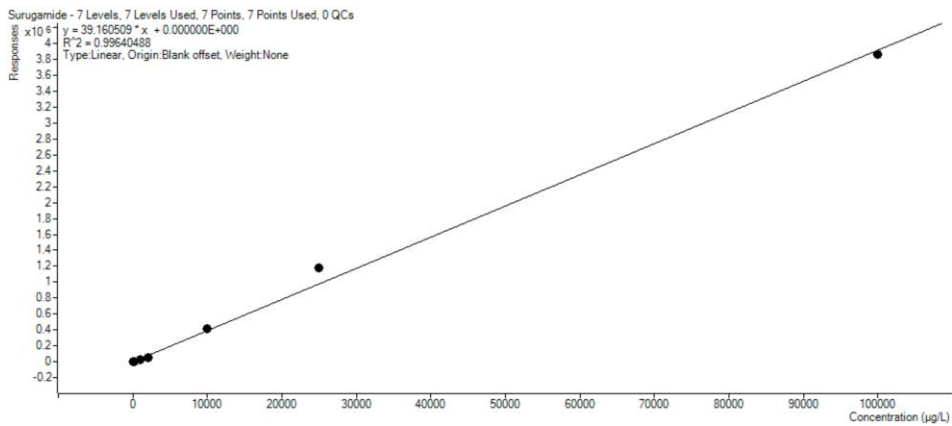
## Supplementary Tables and Figures

**Table S1.** Genome statistics determined using the Prokka program, of the *Streptomyces* isolates genomes obtained from GenBank and determined to belong to the *albidoflavus* phylogroup.

Isolate	Number of bases	Number of CDSs	rRNA	tRNA	tmRNA
FR-008	7,090,955	6,126	21	79	1
J1074	6,841,649	5,847	21	77	1
KJ40	7,070,328	6,057	21	78	1
SM17	6,975,788	5,972	21	78	1
SM254	7,170,504	6,182	21	77	1



**Figure S1.** Venn diagram representing the presence/absence of groups of orthologous genes in the *albidoflavus* phylogroup genomes (namely strains FR-008, J1074, KJ40, SM17, and SM254), also including the *Streptomyces koyangensis* VK-A60T genome.



**Figure S2.** Calibration curve for surugamide A, determined using LC-MS and pure surugamide A at seven concentrations (0.1, 0.2, 1, 2, 10, 25, 100 mg/L).