

Figure S1. Circular dichroism of SAAP-148 and its analogues recorded on a JASCO J-1500 spectropolarimeter and analyzed using BeStSel server.

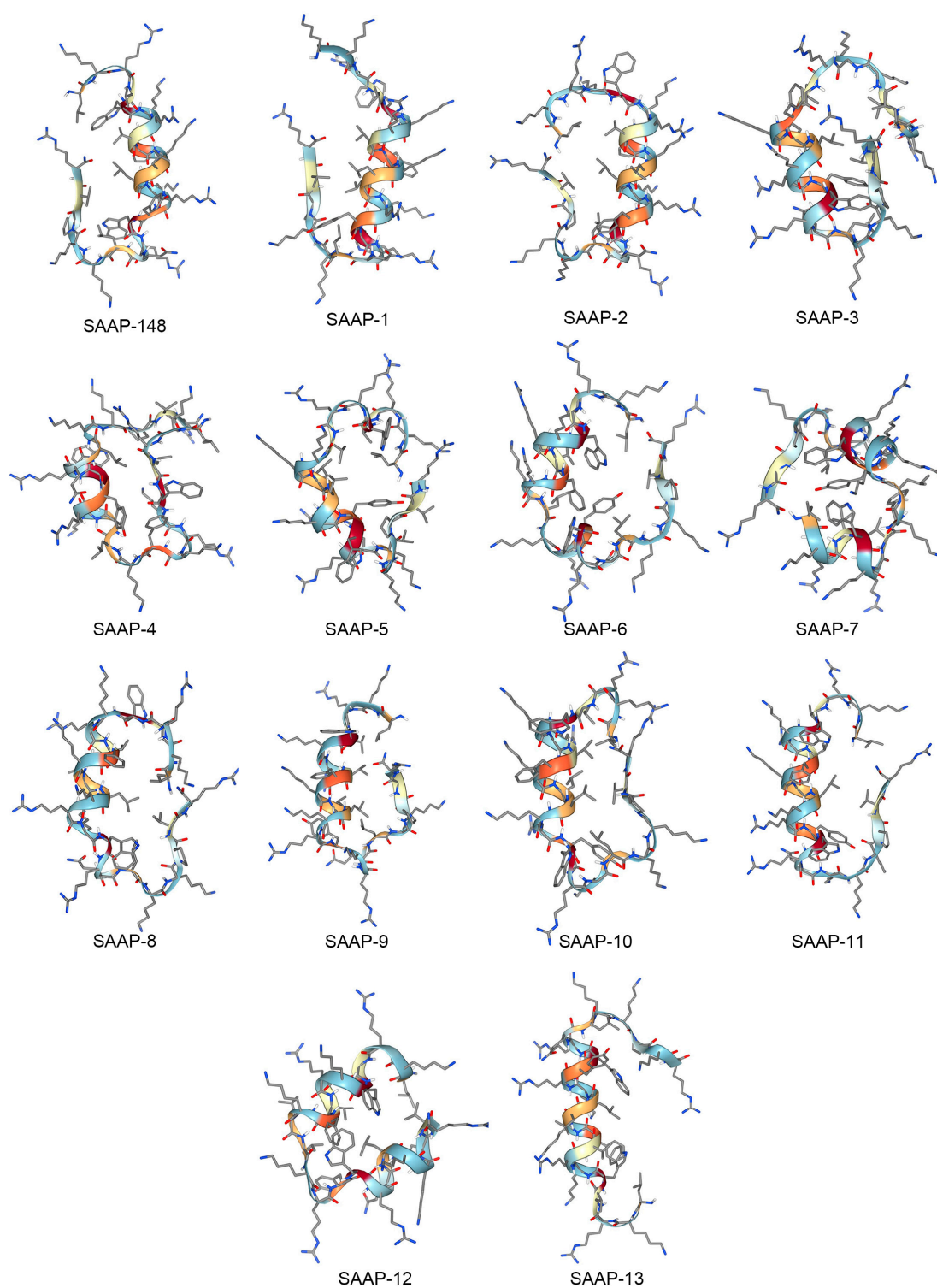


Figure S2. 3D structure of SAAP-148 and its analogues predicted using PEP-FOLD4 servers (<https://bioserv.rpbs.univ-paris-diderot.fr/services/PEP-FOLD4/> Parameter settings: Generator:ts3, Number of models:200,Use Debye-Huckel contribution:Yes,Solvent pH:7,Ionic strength(mM):150)

**Table S1.** The percentage of secondary structure found for each peptide in 30  $\mu$ M SDS. Secondary structure was calculated using BeStSel server.

Peptides	$\alpha$ -Helix	$\beta$ -Antiparallel	$\beta$ -Parallel	Turn	Others
LL-37	100	0	0	0	0
SAAP-148	93.5	6.5	0	0	0
SAAP-1	93.5	6.5	0	0	0
SAAP-2	93.5	6.5	0	0	0
SAAP-3	100	0	0	0	0
SAAP-4	50.9	45.5	0	0	3.6
SAAP-5	100	0	0	0	0
SAAP-6	84.4	15.6	0	0	0
SAAP-7	48.3	48.3	0	0	3.4
SAAP-8	100	0	0	0	0
SAAP-9	100	0	0	0	0
SAAP-10	100	0	0	0	0
SAAP-11	100	0	0	0	0
SAAP-12	100	0	0	0	0
SAAP-13	98.8	0	0	0	1.2



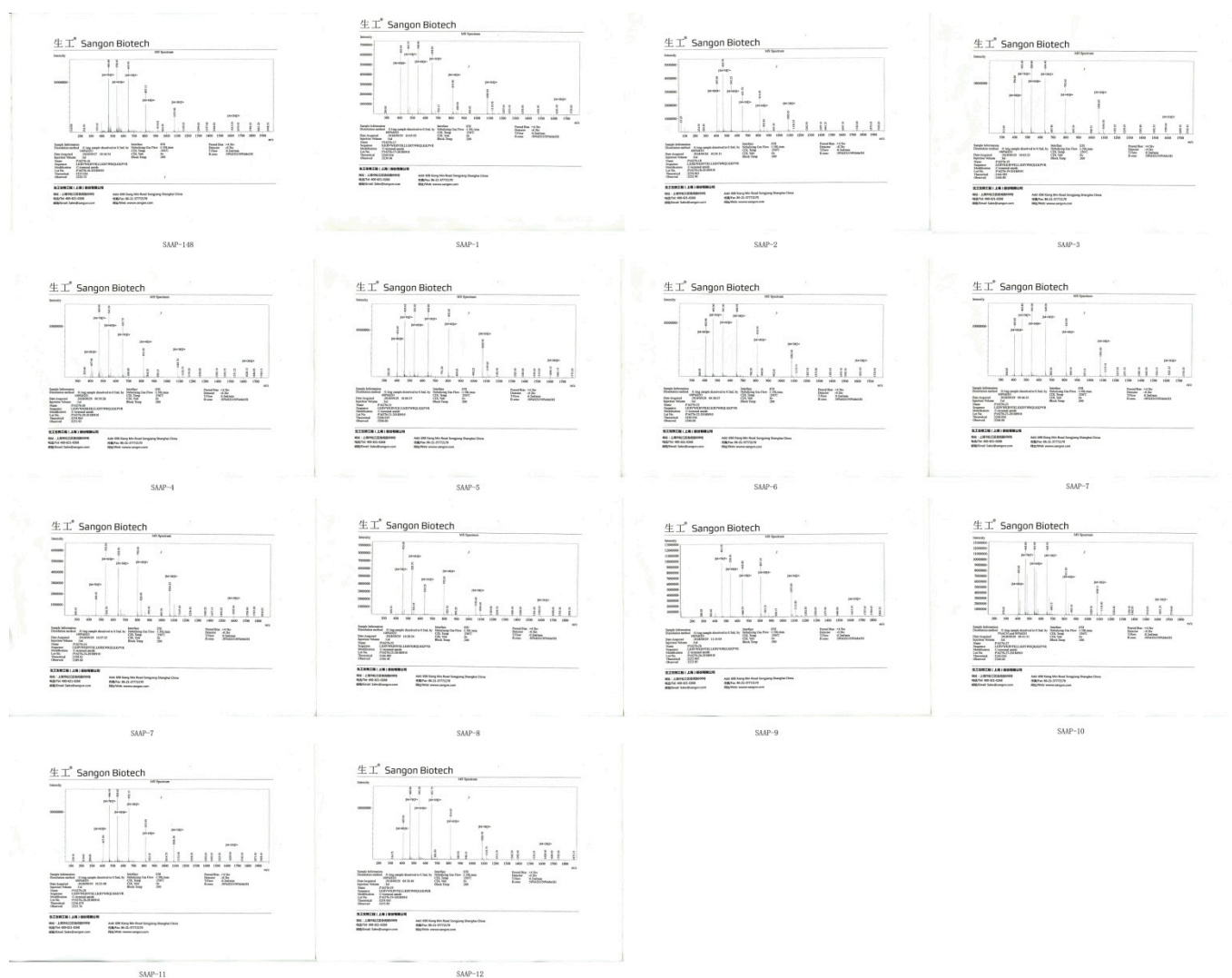


Figure S4. The ESI-MS of all AMPs