

Table S4. Tertiary structure quality assessment scores of the 50S ribosomal protein L7/L12-adjuvanted vaccine construct structures

Structure	RMSD (Å) ^{a)}	Overall quality ^{b)}	Residues in most favorable region (%) ^{c)}
Alphafold v2-predicted	-	50.49	73.10
Chimera 1.17.1-energy minimized	0.42	86	60.70
GalaxyRefine-refined_model 1	1.29	85.08	89.10
GalaxyRefine-refined_model 2	1.29	83.9	87.40
GalaxyRefine-refined_model 3	1.3	85.59	88.00
GalaxyRefine-refined_model 4 ^{d)}	1.26	91.02	92.80
GalaxyRefine-refined_model 5	1.29	81.82	88.00

RMSD, root-mean-square deviation.

^{a)}Relative to the raw structure (Alphafold-predicted); determined using UCSF Chimera 1.17.1. ^{b)}Identified using ERRAT, available in SAVES v6.0 (<https://saves.mbi.ucla.edu>); high resolution structures quality >95%, lower resolution structures quality >91%. ^{c)}Identified using Procheck, available in SAVES v6.0; good quality structures >90% residues in most favorable regions. ^{d)}GalaxyRefine-refined_model 4, the highest-scoring model from the quality assessments, emerged as the best representative structure of the vaccine construct.