

S7 Table. Ribosome-S-F cryo-EM data collection and refinement statistics.

Data collection			
Magnification	105,000		
Voltage (kV)	300		
Electron Microscope	Krios-GIF-K3		
Defocus (um)	-1.0 to -2.5		
Energy filter width (eV)	20		
Pixel size (Å) ^a	0.848 (0.424)		
Total dose (e ⁻ / Å ²)	46		
Number of frames	40		
Number of micrographs	3,054		
Initial particle images (no.)	648,714		
Final particle images (no.)	430,291		
Refinement	70S P-site-tRNA	70S E-site-tRNA	70S Empty
Total Particles (no.)	53,114	109,944	135,858
<u>GS-FSC Resolution (0.143, Å)^b</u>			
50S	2.50	2.37	2.35
30S Core	2.72	2.59	2.55
30S Head	2.66	2.52	2.57
<u>Model composition</u>			
Chains	53	53	51
Protein residues	5,500	5,512	5,510
Nucleotides	4,447	4,442	4,358
Streptothricin-F	2	0	1
<u>r.m.s.d.</u>			
Bond lengths (Å)	0.004	0.004	0.003
Bond angles (°)	0.622	0.621	0.588
Validation	70S P-site-tRNA	70S E-site-tRNA	70S Empty
MolProbity score	1.72	1.66	1.64
Clash score	5.07	4.71	4.45
<u>Ramachandran plot</u>			
Favored (%)	97.22	97.23	97.47
Allowed (%)	2.63	2.64	2.33
Disallowed (%)	0.15	0.13	0.20
CC Mask	0.91	0.91	0.91

^aSuper-resolution stacks processed in 0.75 resolution instead of 0.5 during motion correction

^bGold-Standard Fourier Shell Correlation; refinements split into three regions for each structure.