Supplementary material

for

Two conformational states in the crystal structure of the *Homo sapiens* cytoplasmic ribosomal decoding A site.

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Supplementary Table 1. Crystal data and statistics of data collection.

	Low resolution dataset	High resolution dataset
Crystal data		
Space group	$P2_12_12$	$P2_12_12$
Unit cell (Å)	a = 46.1, b = 47.2, c = 56.7	a = 46.1, b = 47.4, c = 56.8
Z^a	1	1
Data collection		
Beamline	BM16 of ESRF	ID14-1 of ESRF
Wavelength (Å)	0.9795	0.9340
Resolution (Å)	57.0-2.8	29.0-2.3
of the outer shell (Å)	3.0-2.8	2.4-2.3
Observed reflections	66140	16221
Unique reflections	3304	4878
Completeness (%)	100.0	83.1
in the outer shell (%)	100.0	78.5
R_{merge}^b (%)	14.3	11.7
in the outer shell (%)	42.8	29.2

[a] Number of dsRNA in the asymmetric unit.

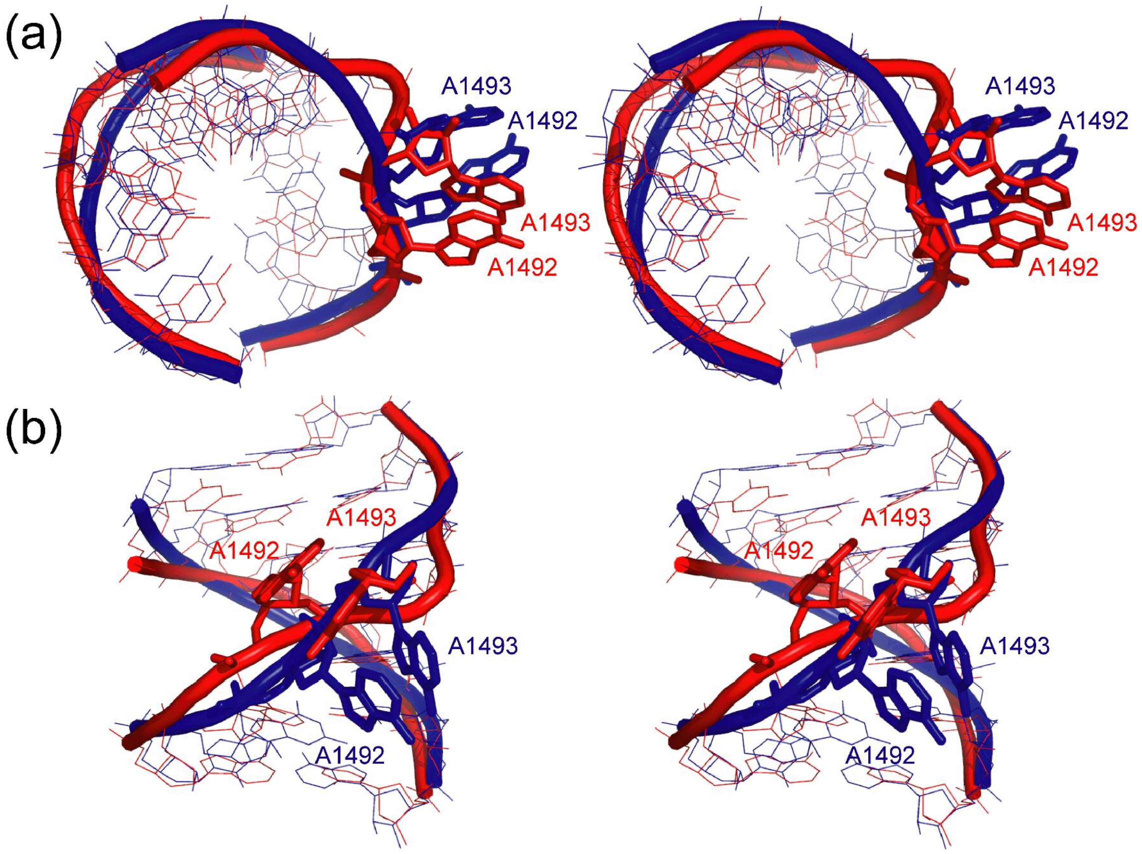
[b] $R_{\text{merge}} = 100 \times \Sigma_{hklj}|I_{hklj} - \langle I_{hklj}\rangle| / \Sigma_{hklj}\langle I_{hklj}\rangle$.

Supplementary Table 2. Statistics of structure refinement.

	High resolution dataset
Resolution range (Å)	10-2.3 ($F_o > 3\sigma$)
Used reflections	4823
R-factor^a (%)	24.7
R_{free}^b	28.2
Number of DNA atoms	920
Number of cations	3 $[\text{Co(NH}_3)_6]^{3+}$, 2 hexa-hydrated Mg^{2+}
Number of water molecules	51
R.m.s. deviation	
Bond length (Å)	0.005
Bond angles (°)	1.1
Improper angles (°)	1.8

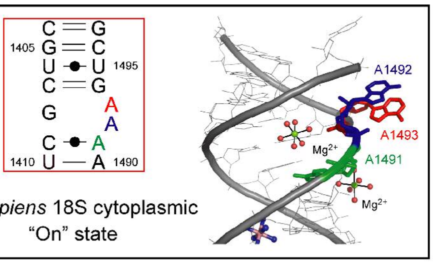
[a] R-factor $= 100 \times \Sigma||F_o| - |F_c|| / \Sigma|F_o|$, where $|F_o|$ and $|F_c|$ are optimally scaled observed and calculated structure factor amplitudes, respectively.

[b] Calculated using a random set containing 10% of observations that were not included throughout refinement.



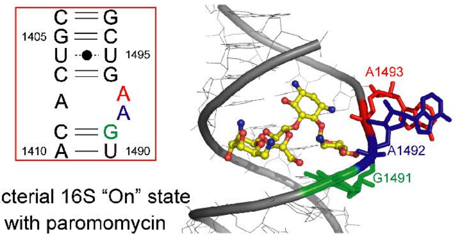
Supplementary Figure 1. Stereoviews of superimposition between “on” states of the *H. sapiens* cytoplasmic (red) and the bacterial A site (blue; PDB ID: 1J7T) (8) from two different angles.

(a)



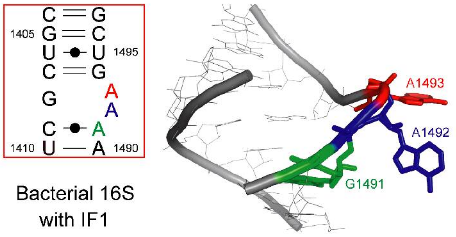
H. sapiens 18S cytoplasmic
“On” state

(b)



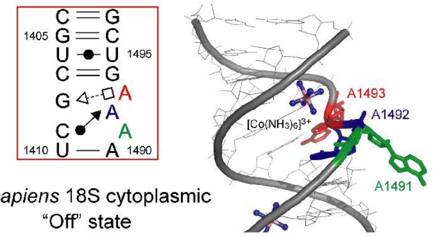
Bacterial 16S “On” state
with paromomycin

(c)



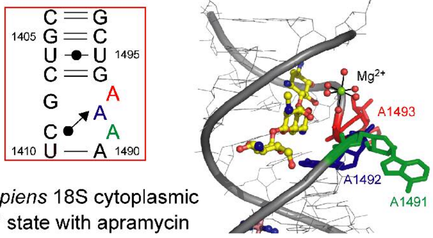
Bacterial 16S
with IF1

(d)



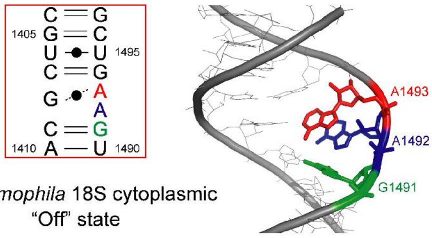
H. sapiens 18S cytoplasmic
“Off” state

(e)



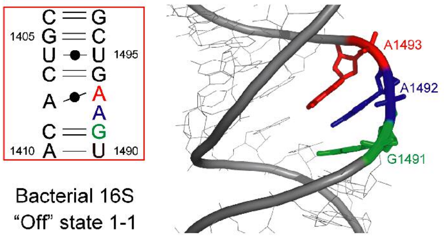
H. sapiens 18S cytoplasmic
“Off” state with apramycin

(f)



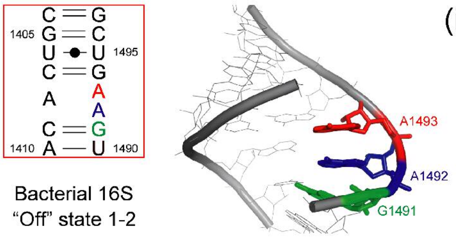
T. thermophila 18S cytoplasmic
“Off” state

(g)



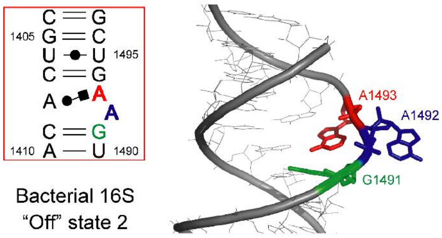
Bacterial 16S
“Off” state 1-1

(h)



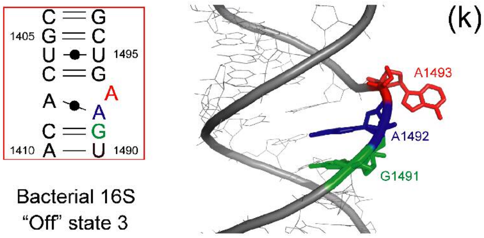
Bacterial 16S
“Off” state 1-2

(i)



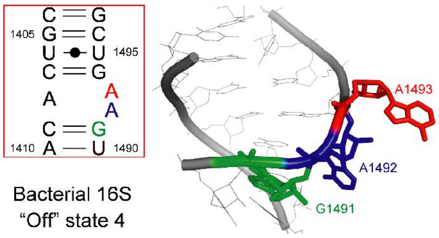
Bacterial 16S
“Off” state 2

(j)



Bacterial 16S
“Off” state 3

(k)



Bacterial 16S
“Off” state 4

Supplementary Figure 2. Secondary and tertiary structures of the A site in the “on” and “off” states. (a) The “on” state of the *H. sapiens* 18S cytoplasmic A site. (b) The “on” state of the bacterial 16S A site in complex with paromomycin (PDB ID: 1J7T (2.5 Å)) (8). No “on” state of the bacterial 16S A site has been observed without drug except in presence of the initiation factor IF1 shown in (c) which displays the bacterial 16S A site in complex with initiation factor IF1 (PDB ID: 1HR0 (3.2 Å)) (45). (d) The “off” state of the *H. sapiens* 18S cytoplasmic A site. (e) The “off” state of the *H. sapiens* 18S cytoplasmic A site in complex with apramycin (2.8 Å) (Kondo. J., François, B., Urzhumtsev, A. and Westhof, E. Submitted). (f) The “off” state of the *T. thermophila* cytoplasmic A site (PDB ID: 1FYO). (g-k) Five “off” states of the bacterial 16S A site (PDB ID: 1J5E (3.05 Å), 2AVY (3.46 Å), 2ET8 (2.5 Å), 1T0E (1.7 Å), 1N34 (3.8 Å)) (2, 5, 7, 12, 14). The “on” and “off” states found in the present crystal structure are in black frame.