

## Supporting Information:

Movie 1: An example of the flipping of A1492 and A1493 in the context of the 30S ribosomal subunit (simulation S1). Ribosomal RNA is shown in violet. Ribosomal proteins are shown in maroon. Small subunit rRNA A1493 (cyan) and A1492 (green) flip in and out of the decoding helix (H44). Hexa-hydrated magnesium is shown in translucent. The movie displays a minute fraction of the total simulation ( $< 1/1,000^{\text{th}}$ ).

Movie 2: Gentamicin unbinding from the ribosomal A site (simulation S2). Ring I (white), ring II (orange) and ring III (yellow) of gentamicin probe the non-specific energy landscape near the binding site. As in movie 1, movie 2 displays a minute fraction of the total simulation ( $< 1/1,000^{\text{th}}$ ).

## Forcefield parameters for MgW<sub>6</sub> (GROMACS)

[ moleculetype ]

```
; molname      nrexcl
MO6             1
```

[ atoms ]

```
; nr  type  resnr  residue  atom  cgnr  charge  mass
  1  amber99_33  1  MO6    MG    1    +2.0   24.30000
  2  amber99_42  1      MO6   O1    2    -0.834  16.00000
  3  amber99_27  1      MO6   H11   2     0.417   4.00800
  4  amber99_27  1      MO6   H12   2     0.417   4.00800
  5  amber99_42  1      MO6   O2    3    -0.834  16.00000
  6  amber99_27  1      MO6   H21   3     0.417   4.00800
  7  amber99_27  1      MO6   H22   3     0.417   4.00800
  8  amber99_42  1      MO6   O3    4    -0.834  16.00000
  9  amber99_27  1      MO6   H31   4     0.417   4.00800
 10  amber99_27  1      MO6   H32   4     0.417   4.00800
 11  amber99_42  1      MO6   O4    5    -0.834  16.00000
 12  amber99_27  1      MO6   H41   5     0.417   4.00800
 13  amber99_27  1      MO6   H42   5     0.417   4.00800
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14	amber99_42	1	MO6	O5	6	-0.834	16.00000
15	amber99_27	1	MO6	H51	6	0.417	4.00800
16	amber99_27	1	MO6	H52	6	0.417	4.00800
17	amber99_42	1	MO6	O6	7	-0.834	16.00000
18	amber99_27	1	MO6	H61	7	0.417	4.00800
19	amber99_27	1	MO6	H62	7	0.417	4.00800

[ bonds ]

;i	j		funct	length	force.c.		
1	2	1	0.204	343092.8	0.204	243092.8	
1	5	1	0.204	343092.8	0.204	243092.8	
1	8	1	0.204	343092.8	0.204	243092.8	
1	11	1	0.204	343092.8	0.204	243092.8	
1	14	1	0.204	343092.8	0.204	243092.8	
1	17	1	0.204	343092.8	0.204	243092.8	
2	3	1	0.1	345000	0.1	345000	
2	4	1	0.1	345000	0.1	345000	
5	6	1	0.1	345000	0.1	345000	
5	7	1	0.1	345000	0.1	345000	
8	9	1	0.1	345000	0.1	345000	
8	10	1	0.1	345000	0.1	345000	
11	12	1	0.1	345000	0.1	345000	
11	13	1	0.1	345000	0.1	345000	
14	15	1	0.1	345000	0.1	345000	
14	16	1	0.1	345000	0.1	345000	
17	18	1	0.1	345000	0.1	345000	
17	19	1	0.1	345000	0.1	345000	

[ angles ]

;i	j	k	funct	angle	force.c.		
11	1	17	1	180.00	583	180.00	383
2	1	5	1	180.00	583	180.00	383
8	1	14	1	180.00	583	180.00	383
2	1	8	1	90.00	583	90.00	383
2	1	11	1	90.00	583	90.00	383
2	1	14	1	90.00	583	90.00	383
2	1	17	1	90.00	583	90.00	383
5	1	8	1	90.00	583	90.00	383
5	1	11	1	90.00	583	90.00	383
5	1	14	1	90.00	583	90.00	383
5	1	17	1	90.00	583	90.00	383
3	2	4	1	109.47	383	109.47	383

6	5	7	1	109.47383	109.47383
9	8	10	1	109.47383	109.47383
12	11	13	1	109.47383	109.47383
15	14	16	1	109.47383	109.47383
18	17	19	1	109.47383	109.47383

[ dihedrals ]

; ai	aj	ak	al	funct	q0	kq
5	2	14	8	2	0.0	1.8e+02
11	17	2	5	2	0.0	1.8e+02
11	17	14	8	2	0.0	1.8e+02