**Supplementary file 3**. RNAP conformational changes.

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| structure | reference  structure | PyMOL aligna | PyMOL rms\_curb | | | | |  | align | | rms\_cur |
|  |  | structural  corec | structural core | overall  (-structural core) | clampd | 'shelf-jawe | lobe-Si1f |  | BHg | | |
| E70 | RPo | 0.647 Å  (1273 Cs) | 0.839 Å  (1356 Cs) | 2.480  (1804) | 3.396  3.3°  open | 1.735  2.7°  twisted open | 2.912  3.4°  DNA-> |  | 0.484  (33) | 0.55  (35) | |
| TraR-E70(I) | RPo | 0.454  (1249) | 0.673  (1380) | 4.931  (1817) | 2.880  3.6°  open | 2.675  4.1°  open | 10.213  18°  ->TraR |  | 0.81  (30) | 1.478  (35) | |
| H |  | 0.873  (1355) | 4.567  (1806) | 1.413  1.8°  roll-CCW | 1.755  2.7°  open | 9.993  17°  ->TraR |  | 0.764  (30) | 1.485  (35) | |
| PDB 5w1s-A (TraR-E70 complex A)h | TraR1 | 0.632  (1251) | 0.871  (1377) | 6.323  (1646) | 3.837  5.7°  open | 2.523  3.2°  closed | 13.968  24°  TraR-> |  |  |  | |
| RPo |  | 0.604  (1256) | 3.354  (1638) | 5.906  7.8°  open | 2.211  1.8°  twisted open | 3.912  6.1°  TraR-> |  | 0.585  (35) | 0.585  (35) | |
| H |  | 0.680  (1241) | 2.699  (1629) | 3.226  4.4°  open | 2.030  0.86° | 5.007  8.1°  TraR-> |  |  |  | |
| 4yg2a | 0.344  (1306) | 0.541  (1482) | 1.089  (1648) | 1.587  1.7°  open | 1.174  1.2° | 1.351  2.4°  TraR-> |  |  |  | |
| PDB 5w1s-B (TraR-E70 complex B)h | TraR1 | 0.731  (1279) | 0.963  (1369) | 5.780  (1637) | 2.583  4.8°  open | 2.948  3.7°  closed | 12.498  22°  TraR-> |  |  |  | |
| RPo |  | 0.938  (1370) | 2.865  (1635) | 4.376  5.7°  open | 2.826  3.9°  twisted | 2.955  5.7°  DNA-> |  | 0.509  (33) | 0.576  (35) | |
| H |  | 0.989  (1355) | 2.7  (1627) | 2.256  3.4°  roll-CCW | 2.365  1.8°  closed | 4.998  8.8°  TraR-> |  |  |  | |
| 4yg2b | 0.358  (1283) | 0.47  (1372) | 0.73  (1638) | 0.864  0.89° | 0.887  1.2° | 0.622  1.2° |  |  |  | |
| PDB 4yg2-A (E70 complex A)i | RPo |  |  |  |  |  |  |  | 0.519  (35) | 0.519  (35) | |
| PDB 4yg2-B (E70 complex B)i | RPo |  |  |  |  |  |  |  | 0.415  (31) | 0.568  (35) | |

aThe structure in the first column (structure) was aligned to the structure in the second column (reference structure) by C atoms only using the PyMOL align command, which superimposes the two structures using an algorithm that rejects outliers (such as in flexible loops, etc.) to minimize the root-mean-square deviation (rmsd) while maximizing the number of aligned atoms. The entries list the resulting rmsd (Å, top row) and the number of Catoms aligned (in parentheses). For the clamp, lobe-Si1, and 'shelf-jaw entries, the rotational angle and axis between the elements was calculated using the PyMOL script draw\_rotation\_axis.py (<https://pymolwiki.org/index.php/RotationAxis>). The rotation angle is listed in the second row. The direction of movement (from the target structure to the reference structure) is denoted below.

bThe structures/structural elements denoted were compared (but not aligned) by C atoms only using the PyMOL rms\_cur command, which calculates the rmsd for all of the specified atoms (no outliers removed).

c*Eco* RNAP structural core: I, II,  (1-27, 147-152, 445-455, 520-713, 786-828, 1060-1240), ' (343-368, 421-786), .

d*Eco* RNAP clamp:  (1319-1342), ' (1-342, 1318-1344), 70 (92-137, 353-449).

e*Eco* RNAP 'shelf-jaw: ' (787-931, 1135-1315).

f*Eco* RNAP lobe-Si1:  (153-444).

g*Eco* RNAP BH: ' (769-803).

h(Molodtsov et al., 2018).

i(Murakami, 2013).