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

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| structure | referencestructure | PyMOL aligna | PyMOL rms\_curb |  | align | rms\_cur |
|  |  | structuralcorec | 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) | 3.3963.3°open | 1.7352.7°twisted open | 2.9123.4°DNA-> |  | 0.484(33) | 0.55(35) |
| TraR-E70(I) | RPo | 0.454(1249) | 0.673(1380) | 4.931(1817) | 2.8803.6°open | 2.6754.1°open | 10.21318°->TraR |  | 0.81(30) | 1.478(35) |
| H |  | 0.873(1355) | 4.567(1806) | 1.4131.8°roll-CCW | 1.7552.7°open | 9.99317°->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) | 3.8375.7°open | 2.5233.2°closed | 13.96824°TraR-> |  |  |  |
| RPo |  | 0.604(1256) | 3.354(1638) | 5.9067.8°open | 2.2111.8°twisted open | 3.9126.1°TraR-> |  | 0.585(35) | 0.585(35) |
| H |  | 0.680(1241) | 2.699(1629) | 3.2264.4°open | 2.0300.86° | 5.0078.1°TraR-> |  |  |  |
| 4yg2a | 0.344(1306) | 0.541(1482) | 1.089(1648) | 1.5871.7°open | 1.1741.2° | 1.3512.4°TraR-> |  |  |  |
| PDB 5w1s-B (TraR-E70 complex B)h | TraR1 | 0.731(1279) | 0.963(1369) | 5.780(1637) | 2.5834.8°open | 2.9483.7°closed | 12.49822°TraR-> |  |  |  |
| RPo |  | 0.938(1370) | 2.865(1635) | 4.3765.7°open | 2.8263.9°twisted | 2.9555.7°DNA-> |  | 0.509(33) | 0.576(35) |
| H |  | 0.989(1355) | 2.7(1627) | 2.2563.4°roll-CCW | 2.3651.8°closed | 4.9988.8°TraR-> |  |  |  |
| 4yg2b | 0.358(1283) | 0.47(1372) | 0.73(1638) | 0.8640.89° | 0.8871.2° | 0.6221.2° |  |  |  |
| 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).