Full wwPDB/EMDataBank EM Map/Model Validation Report

Feb 19, 2018 – 08:22 pm GMT

PDB ID : 4V4N
EMDB ID: : EMD-5691
Title : Structure of the Methanococcus jannaschii ribosome-SecYEBeta channel complex
Authors : Menetret, J.F.; Park, E.; Gumbart, J.C.; Ludtke, S.J.; Li, W.; Whynot, A.; Rapoport, T.A.; Akey, C.W.
Deposited on : 2013-06-17
Resolution : 9.00 Å (reported)
Based on PDB ID : 3J2L, 3J21, 3J20, 1RHZ

This is a Full wwPDB/EMDataBank EM Map/Model Validation Report for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the i symbol.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30686
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

**ELECTRON MICROSCOPY**

The reported resolution of this entry is 9.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.

<table>
<thead>
<tr>
<th>Metric</th>
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<th>EM structures (#Entries)</th>
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<td>1886</td>
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<tr>
<td>Ramachandran outliers</td>
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<td>Sidechain outliers</td>
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<td>1531</td>
</tr>
<tr>
<td>RNA backbone</td>
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The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for >3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%.

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<td>BV</td>
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</table>
2 Entry composition

There are 67 unique types of molecules in this entry. The entry contains 171094 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Preprotein translocase subunit SecE.

<table>
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<th>Atoms</th>
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<td>N</td>
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<td></td>
<td>O</td>
<td>85</td>
<td></td>
</tr>
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- Molecule 2 is a protein called Preprotein translocase subunit SecG.

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- Molecule 3 is a protein called 50S ribosomal protein L39E.

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<td>O</td>
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- Molecule 4 is a protein called 50S ribosomal protein L19E.

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- Molecule 5 is a protein called 50S ribosomal protein L22P.

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- Molecule 6 is a protein called 50S ribosomal protein L23P.

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</tbody>
</table>
- Molecule 7 is a protein called 50S ribosomal protein L24P.

<table>
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<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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<td>7</td>
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<td>C 637 N 195 O 172 S 4</td>
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- Molecule 8 is a protein called 50S ribosomal protein L29P.

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<th>Atoms</th>
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<td>66</td>
<td>Total</td>
<td>C 338 N 105 O 99 S 4</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 9 is a protein called Protein translocase subunit SecY.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>9</td>
<td>AX</td>
<td>432</td>
<td>Total</td>
<td>C 521 N 559 O 19 S 19</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 10 is a RNA chain called E-tRNA.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>10</td>
<td>B1</td>
<td>77</td>
<td>Total</td>
<td>C 303 N 334 O 533 P 76</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 11 is a RNA chain called 16S ribosomal RNA.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>11</td>
<td>B2</td>
<td>1495</td>
<td>Total</td>
<td>C 10387 N 5954 O 14297 P 1494</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 12 is a protein called 30S ribosomal protein L7AE.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>12</td>
<td>B3</td>
<td>123</td>
<td>Total</td>
<td>C 181 N 155 O 599 S 939</td>
<td>0</td>
</tr>
<tr>
<td>12</td>
<td>AG</td>
<td>123</td>
<td>Total</td>
<td>C 181 N 155 O 599 S 939</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 13 is a protein called 30S ribosomal protein S3AE.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>13</td>
<td>BA</td>
<td>190</td>
<td>Total</td>
<td>C 274 N 273 O 1007 S 1559</td>
<td>0</td>
</tr>
</tbody>
</table>
- Molecule 14 is a protein called 30S ribosomal protein S2P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>14</td>
<td>BB</td>
<td>202</td>
<td>Total C N O S</td>
<td>1623 1046 282 290 5</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 15 is a protein called 30S ribosomal protein S3P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>15</td>
<td>BC</td>
<td>186</td>
<td>Total C N O S</td>
<td>1460 933 271 252 4</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 16 is a protein called 30S ribosomal protein S4P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>16</td>
<td>BD</td>
<td>172</td>
<td>Total C N O S</td>
<td>1434 902 273 255 4</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 17 is a protein called 30S ribosomal protein S4E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>17</td>
<td>BE</td>
<td>241</td>
<td>Total C N O S</td>
<td>1976 1277 355 339 5</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 18 is a protein called 30S ribosomal protein S5P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>18</td>
<td>BF</td>
<td>217</td>
<td>Total C N O S</td>
<td>1717 1084 319 306 8</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 19 is a protein called 30S ribosomal protein S6E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>19</td>
<td>BG</td>
<td>125</td>
<td>Total C N O S</td>
<td>984 623 180 179 2</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 20 is a protein called 30S ribosomal protein S7P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>20</td>
<td>BH</td>
<td>215</td>
<td>Total C N O S</td>
<td>1736 1100 326 302 8</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 21 is a protein called 30S ribosomal protein S8P.
<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>21</td>
<td>BI</td>
<td>129</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1028 668 178 180 2</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 22 is a protein called 30S ribosomal protein S8E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>22</td>
<td>BJ</td>
<td>127</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1004 622 207 174 1</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 23 is a protein called 30S ribosomal protein S9P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>23</td>
<td>BK</td>
<td>135</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1072 671 205 190 6</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 24 is a protein called 30S ribosomal protein S10P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>24</td>
<td>BL</td>
<td>102</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>822 507 159 152 4</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 25 is a protein called 30S ribosomal protein S11P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>25</td>
<td>BM</td>
<td>133</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1004 623 200 179 2</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 26 is a protein called 30S ribosomal protein S12P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>26</td>
<td>BN</td>
<td>145</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1141 722 223 193 3</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 27 is a protein called 30S ribosomal protein S13P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>27</td>
<td>BO</td>
<td>148</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1189 746 237 200 6</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 28 is a protein called 30S ribosomal protein S14P.
<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>28</td>
<td>BP</td>
<td>56</td>
<td>Total C N O S</td>
<td>462 292 95 69 6</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 29 is a protein called 30S ribosomal protein S15P/S13E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>29</td>
<td>BQ</td>
<td>158</td>
<td>Total C N O S</td>
<td>1310 834 250 221 5</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 30 is a protein called 30S ribosomal protein S17P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>30</td>
<td>BR</td>
<td>113</td>
<td>Total C N O S</td>
<td>934 592 177 160 5</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 31 is a protein called 30S ribosomal protein S17E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>31</td>
<td>BS</td>
<td>67</td>
<td>Total C N O S</td>
<td>556 353 105 95 3</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 32 is a protein called 30S ribosomal protein S19P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>32</td>
<td>BT</td>
<td>111</td>
<td>Total C N O S</td>
<td>924 594 173 151 6</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 33 is a protein called 30S ribosomal protein S19E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>33</td>
<td>BU</td>
<td>144</td>
<td>Total C N O S</td>
<td>1176 758 212 205 1</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 34 is a protein called 30S ribosomal protein S24E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>34</td>
<td>BV</td>
<td>99</td>
<td>Total C N O S</td>
<td>823 532 134 154 3</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 35 is a protein called 30S ribosomal protein S27E.
<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
</table>
| 35  | BW    | 63       | Total C N O S
|     |       |          | 478 306 85 81 6 | 0      | 0     |

- Molecule 36 is a protein called 30S ribosomal protein S28E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
</table>
| 36  | BX    | 71       | Total C N O S
|     |       |          | 568 345 115 107 1 | 0      | 0     |

- Molecule 37 is a protein called 30S ribosomal protein S27AE.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
</table>
| 37  | BY    | 50       | Total C N O S
|     |       |          | 409 262 75 66 6 | 0      | 0     |

- Molecule 38 is a RNA chain called 23S ribosomal RNA.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
</table>
| 38  | A1    | 2969     | Total C N O P
|     |       |          | 63885 28427 11905 20589 2964 | 0      | 0     |

- Molecule 39 is a RNA chain called 5S ribosomal RNA.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
</table>
| 39  | A3    | 126      | Total C N O P
|     |       |          | 2691 1199 492 875 125 | 0      | 0     |

- Molecule 40 is a protein called 50S ribosomal protein L14E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
</table>
| 40  | A5    | 81       | Total C N O S
|     |       |          | 614 386 119 108 1 | 0      | 0     |
| 40  | AK    | 81       | Total C N O S
|     |       |          | 614 386 119 108 1 | 0      | 0     |

- Molecule 41 is a protein called 50S ribosomal protein L1P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
</table>
| 41  | AA    | 216      | Total C N O S
|     |       |          | 1677 1068 300 304 5 | 0      | 0     |

- Molecule 42 is a protein called 50S ribosomal protein L31E.
- Molecule 43 is a protein called 50S ribosomal protein L2.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>42</td>
<td>Aa</td>
<td>82</td>
<td>Total C N O</td>
<td>677 444 126 107</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 44 is a protein called 50S ribosomal protein L32E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>44</td>
<td>Ab</td>
<td>127</td>
<td>Total C N O S</td>
<td>1075 689 217 168 1</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 45 is a protein called 50S ribosomal protein L3P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>45</td>
<td>AC</td>
<td>342</td>
<td>Total C N O S</td>
<td>2717 1741 495 467 14</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 46 is a protein called 50S ribosomal protein L4P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>46</td>
<td>AD</td>
<td>255</td>
<td>Total C N O S</td>
<td>2026 1288 391 342 5</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 47 is a protein called 50S ribosomal protein L34E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>47</td>
<td>Ad</td>
<td>89</td>
<td>Total C N O S</td>
<td>740 463 158 108 11</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 48 is a protein called 50S ribosomal protein L5P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>48</td>
<td>AE</td>
<td>186</td>
<td>Total C N O S</td>
<td>1489 937 278 265 9</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 49 is a protein called 50S ribosomal protein L37E.
• Molecule 50 is a protein called 50S ribosomal protein L6P.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>49</td>
<td>Ae</td>
<td>62</td>
<td>Total</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>C 506</td>
<td>N 312</td>
<td>O 111</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>N 78 5</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

• Molecule 51 is a protein called 50S ribosomal protein L40E.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>50</td>
<td>AF</td>
<td>184</td>
<td>Total</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>C 1476</td>
<td>N 956</td>
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<td></td>
<td>N 252 2</td>
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<td></td>
<td></td>
<td>O 266 2</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

• Molecule 52 is a protein called 50S ribosomal protein L11P.

<table>
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<tr>
<th>Mol</th>
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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<td>Ag</td>
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</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>C 372</td>
<td></td>
<td></td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>N 236 4</td>
<td></td>
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<tr>
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<td></td>
<td></td>
<td>O 56 4</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

• Molecule 53 is a protein called 50S ribosomal protein L41E.

<table>
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<td></td>
<td></td>
<td></td>
<td>C 989</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>N 635 4</td>
<td></td>
<td></td>
</tr>
<tr>
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<td></td>
<td></td>
<td>O 164 6</td>
<td></td>
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</tr>
</tbody>
</table>

• Molecule 54 is a protein called 50S ribosomal protein L13P.

<table>
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<tr>
<td></td>
<td></td>
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<td>C 230</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>N 147 1</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>O 54 1</td>
<td></td>
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</tr>
</tbody>
</table>

• Molecule 55 is a protein called 50S ribosomal protein L37AE.

<table>
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<tbody>
<tr>
<td>55</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>C 590</td>
<td></td>
<td></td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>N 368 5</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>O 122 5</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

• Molecule 56 is a protein called 50S ribosomal protein L14P.
Molecule 57 is a protein called 50S ribosomal protein L44E.

Molecule 58 is a protein called 50S ribosomal protein P0/L10E.

Molecule 59 is a protein called 50S ribosomal protein L15P.

Molecule 60 is a protein called 50S ribosomal protein L15E.

Molecule 61 is a protein called 50S ribosomal protein L10E/L16.

Molecule 62 is a protein called 50S ribosomal protein L18P.

Molecule 63 is a protein called 50S ribosomal protein L18E.
- Molecule 64 is a protein called 50S ribosomal protein L21E.

<table>
<thead>
<tr>
<th>Mol</th>
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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<tbody>
<tr>
<td>64</td>
<td>AR</td>
<td>95</td>
<td>Total C N O S</td>
<td>787 501 160 125 1</td>
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</table>

- Molecule 65 is a protein called 50S ribosomal protein L24E.

<table>
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<td>65</td>
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- Molecule 66 is a protein called 50S ribosomal protein L30P.

<table>
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<th>Atoms</th>
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<th>Trace</th>
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<tr>
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<td>AY</td>
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<td>Total C N O S</td>
<td>1243 788 235 213 7</td>
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- Molecule 67 is a protein called 50S ribosomal protein L30E.

<table>
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<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>67</td>
<td>AZ</td>
<td>99</td>
<td>Total C N O S</td>
<td>754 489 121 142 2</td>
<td>0</td>
</tr>
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</table>
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Preprotein translocase subunit SecE

Chain A7:

- Molecule 2: Preprotein translocase subunit SecG

Chain A8:

- Molecule 3: 50S ribosomal protein L39E

Chain Af:

- Molecule 4: 50S ribosomal protein L19E

Chain AQ:

- Molecule 5: 50S ribosomal protein L22P

Chain AS:
• Molecule 6: 50S ribosomal protein L23P

Chain AT:

• Molecule 7: 50S ribosomal protein L24P

Chain AU:

• Molecule 8: 50S ribosomal protein L29P

Chain AW:

• Molecule 9: Protein translocase subunit SecY

Chain AX:

• Molecule 10: E-tRNA

Chain B1:

• Molecule 11: 16S ribosomal RNA
• Molecule 12: 30S ribosomal protein L7AE

Chain B3:

• Molecule 12: 30S ribosomal protein L7AE

Chain AG:

• Molecule 13: 30S ribosomal protein S3AE

Chain BA:
- Molecule 14: 30S ribosomal protein S2P

Chain BB: 68% 30%

- Molecule 15: 30S ribosomal protein S3P

Chain BC: 75% 22%

- Molecule 16: 30S ribosomal protein S4P

Chain BD: 74% 20% 5%

- Molecule 17: 30S ribosomal protein S4E

Chain BE: 68% 27% 5%

- Molecule 18: 30S ribosomal protein S5P

Chain BF: 73% 21% 6%
- Molecule 19: 30S ribosomal protein S6E

Chain BG:

- Molecule 20: 30S ribosomal protein S7P

Chain BH:

- Molecule 21: 30S ribosomal protein S8P

Chain BI:

- Molecule 22: 30S ribosomal protein S8E

Chain BJ:

- Molecule 23: 30S ribosomal protein S9P

Chain BK:
• Molecule 24: 30S ribosomal protein S10P

Chain BL:

• Molecule 25: 30S ribosomal protein S11P

Chain BM:

• Molecule 26: 30S ribosomal protein S12P

Chain BN:

• Molecule 27: 30S ribosomal protein S13P

Chain BO:

• Molecule 28: 30S ribosomal protein S14P

Chain BP:

• Molecule 29: 30S ribosomal protein S15P/S13E
Chain BQ:

- Molecule 30: 30S ribosomal protein S17P

Chain BR:

- Molecule 31: 30S ribosomal protein S17E

Chain BS:

- Molecule 32: 30S ribosomal protein S19P

Chain BT:

- Molecule 33: 30S ribosomal protein S19E

Chain BU:

- Molecule 34: 30S ribosomal protein S24E

Chain BV:

- Molecule 35: 30S ribosomal protein S27E
Chain BW:

- Molecule 36: 30S ribosomal protein S28E

Chain BX:

- Molecule 37: 30S ribosomal protein S27AE

Chain BY:

- Molecule 38: 23S ribosomal RNA

Chain A1:
• Molecule 39: 5S ribosomal RNA

Chain A3:

• Molecule 40: 50S ribosomal protein L14E

Chain A5:

• Molecule 40: 50S ribosomal protein L14E
### Chain AK:

- Molecule 41: 50S ribosomal protein L1P

### Chain AA:

- Molecule 42: 50S ribosomal protein L31E

### Chain Aa:

- Molecule 43: 50S ribosomal protein L2

### Chain AB:

- Molecule 44: 50S ribosomal protein L32E

### Chain Ac:

- Molecule 45: 50S ribosomal protein L3P
• Molecule 46: 50S ribosomal protein L4P

Chain AD:

• Molecule 47: 50S ribosomal protein L34E

Chain Ad:

• Molecule 48: 50S ribosomal protein L5P

Chain AE:

• Molecule 49: 50S ribosomal protein L37E

Chain Ae:

• Molecule 50: 50S ribosomal protein L6P

Chain AF:
- Molecule 51: 50S ribosomal protein L40E

Chain Ag:

- Molecule 52: 50S ribosomal protein L11P

Chain AH:

- Molecule 53: 50S ribosomal protein L41E

Chain Ah:

- Molecule 54: 50S ribosomal protein L13P

Chain AI:

- Molecule 55: 50S ribosomal protein L37AE

Chain Ai:

- Molecule 56: 50S ribosomal protein L14P

Chain AJ:
• Molecule 57: 50S ribosomal protein L44E
Chain Aj:

• Molecule 58: 50S ribosomal protein P0/L10E
Chain Ak:

• Molecule 59: 50S ribosomal protein L15P
Chain AL:

• Molecule 60: 50S ribosomal protein L15E
Chain AM:

• Molecule 61: 50S ribosomal protein L10E/L16
Chain AN:

• Molecule 62: 50S ribosomal protein L18P
Chain AO: 68% 28%

• Molecule 63: 50S ribosomal protein L18E

Chain AP: 72% 23%

• Molecule 64: 50S ribosomal protein L21E

Chain AR: 69% 25%

• Molecule 65: 50S ribosomal protein L24E

Chain AV: 65% 29% 6%

• Molecule 66: 50S ribosomal protein L30P

Chain AY: 76% 21%

• Molecule 67: 50S ribosomal protein L30E

Chain AZ: 73% 21%
### 4 Experimental information

<table>
<thead>
<tr>
<th>Property</th>
<th>Value</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>Reconstruction method</td>
<td>SINGLE PARTICLE</td>
<td>Depositor</td>
</tr>
<tr>
<td>Imposed symmetry</td>
<td>POINT, C1</td>
<td>Depositor</td>
</tr>
<tr>
<td>Number of particles used</td>
<td>37000</td>
<td>Depositor</td>
</tr>
<tr>
<td>Resolution determination method</td>
<td>FSC 0.5 CUT-OFF</td>
<td>Depositor</td>
</tr>
<tr>
<td>CTF correction method</td>
<td>per micrograph</td>
<td>Depositor</td>
</tr>
<tr>
<td>Microscope</td>
<td>FEI TECNAI F20</td>
<td>Depositor</td>
</tr>
<tr>
<td>Voltage (kV)</td>
<td>200</td>
<td>Depositor</td>
</tr>
<tr>
<td>Electron dose ($e^-/\text{Å}^2$)</td>
<td>20</td>
<td>Depositor</td>
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<tr>
<td>Minimum defocus (nm)</td>
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<td>Depositor</td>
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<td>Maximum defocus (nm)</td>
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<tr>
<td>Magnification</td>
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</tr>
<tr>
<td>Image detector</td>
<td>KODAK SO-163 FILM</td>
<td>Depositor</td>
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</table>
## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with \(|Z| > 5\) is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

<table>
<thead>
<tr>
<th>Mol</th>
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<th>Bond lengths</th>
<th>Bond angles</th>
</tr>
</thead>
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<td></td>
<td></td>
<td>RMSZ</td>
<td>#(</td>
</tr>
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<td>1.64</td>
<td>2/534 (0.4%)</td>
</tr>
<tr>
<td>10</td>
<td>B1</td>
<td>3.41</td>
<td>257/1840 (14.0%)</td>
</tr>
<tr>
<td>11</td>
<td>B2</td>
<td>3.43</td>
<td>4996/35963 (13.9%)</td>
</tr>
<tr>
<td>12</td>
<td>AG</td>
<td>1.71</td>
<td>4/951 (0.4%)</td>
</tr>
<tr>
<td>12</td>
<td>B3</td>
<td>1.62</td>
<td>3/951 (0.3%)</td>
</tr>
<tr>
<td>13</td>
<td>BA</td>
<td>1.74</td>
<td>21/1585 (1.3%)</td>
</tr>
<tr>
<td>14</td>
<td>BB</td>
<td>1.72</td>
<td>15/1654 (0.9%)</td>
</tr>
<tr>
<td>15</td>
<td>BC</td>
<td>1.82</td>
<td>18/1481 (1.2%)</td>
</tr>
<tr>
<td>16</td>
<td>BD</td>
<td>1.77</td>
<td>14/1457 (1.0%)</td>
</tr>
<tr>
<td>17</td>
<td>BE</td>
<td>1.76</td>
<td>25/2025 (1.2%)</td>
</tr>
<tr>
<td>18</td>
<td>BF</td>
<td>1.81</td>
<td>29/1746 (1.7%)</td>
</tr>
<tr>
<td>19</td>
<td>BG</td>
<td>1.72</td>
<td>9/999 (0.9%)</td>
</tr>
<tr>
<td>2</td>
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<td>1.75</td>
<td>1/263 (0.4%)</td>
</tr>
<tr>
<td>20</td>
<td>BH</td>
<td>1.79</td>
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<td>BI</td>
<td>1.77</td>
<td>13/1049 (1.2%)</td>
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<tr>
<td>22</td>
<td>BJ</td>
<td>1.83</td>
<td>14/1013 (1.4%)</td>
</tr>
<tr>
<td>23</td>
<td>BK</td>
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<td>10/1088 (0.9%)</td>
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<tr>
<td>24</td>
<td>BL</td>
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<tr>
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<td>BM</td>
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<td>16/1022 (1.6%)</td>
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<td>26</td>
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<tr>
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<td>BQ</td>
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<tr>
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<td>37</td>
<td>BY</td>
<td>1.66</td>
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</tr>
<tr>
<td>38</td>
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<td>9848/71524 (13.8%)</td>
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<tr>
<td>39</td>
<td>A3</td>
<td>3.37</td>
<td>408/3007 (13.6%)</td>
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</table>
Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.
<table>
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<tr>
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<th>#Planarity outliers</th>
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<td>2</td>
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<tr>
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</tr>
<tr>
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<td>BD</td>
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</tr>
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</tr>
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<td>18</td>
<td>BF</td>
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<td>BG</td>
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<td>4</td>
</tr>
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<td>1</td>
</tr>
<tr>
<td>20</td>
<td>BH</td>
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<td>13</td>
</tr>
<tr>
<td>21</td>
<td>BI</td>
<td>0</td>
<td>3</td>
</tr>
<tr>
<td>22</td>
<td>BJ</td>
<td>0</td>
<td>6</td>
</tr>
<tr>
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<td>7</td>
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<tr>
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<td>1</td>
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| 11 | B2 | 235 | G | C2-N3 | 7.68 | 1.38 | 1.32 |
| 11 | B2 | 389 | G | N1-C2 | 7.68 | 1.43 | 1.37 |
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| 11 | B2 | 1466 | G | C2-N2 | 7.68 | 1.42 | 1.34 |
| 38 | A1 | 43 | G | N9-C4 | -7.68 | 1.31 | 1.38 |
| 38 | A1 | 1027 | A | N3-C4 | 7.68 | 1.39 | 1.34 |
| 38 | A1 | 1207 | G | N3-C4 | -7.68 | 1.30 | 1.35 |
| 38 | A1 | 1641 | G | C2-N2 | 7.68 | 1.42 | 1.34 |
| 38 | A1 | 1946 | G | P-O5' | -7.68 | 1.52 | 1.59 |
| 38 | A1 | 1985 | G | N9-C8 | 7.68 | 1.43 | 1.37 |
| 38 | A1 | 1976 | C | C2-N3 | 7.68 | 1.38 | 1.32 |
| 38 | A1 | 542 | G | O3'-P | -7.68 | 1.51 | 1.61 |
| 11 | B2 | 537 | G | N3-C4 | 7.68 | 1.40 | 1.35 |
| 11 | B2 | 974 | G | C2-N3 | 7.68 | 1.38 | 1.32 |
| 11 | B2 | 1006 | C | C4-N4 | 7.68 | 1.40 | 1.33 |
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| 38 | A1 | 2195 | G | C2'-C1' | -7.68 | 1.45 | 1.53 |
| 38 | A1 | 2459 | G | C5'-C4' | 7.68 | 1.60 | 1.51 |
| 38 | A1 | 2685 | G | C5-C4 | 7.68 | 1.43 | 1.38 |
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| 38 | A1 | 212 | A | C6-N1 | 7.67 | 1.41 | 1.35 |
| 38 | A1 | 1306 | A | N1-C2 | -7.67 | 1.27 | 1.34 |
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| 38 | A1 | 2599 | C | C4-C5 | 7.67 | 1.49 | 1.43 |
| 38 | A1 | 527 | G | N9-C8 | 7.67 | 1.43 | 1.37 |
| 38 | A1 | 2068 | U | C2'-C1' | -7.67 | 1.45 | 1.53 |
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| 11 | B2 | 858 | A | C6-N6 | 7.67 | 1.40 | 1.33 |
| 38 | A1 | 905 | G | O3'-P | -7.67 | 1.51 | 1.61 |
| 38 | A1 | 1429 | A | C6-N1 | 7.67 | 1.41 | 1.35 |
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38  | A1  | 1425 | U   | N3-C4 | 6.12 | 1.44 | 1.38
38  | A1  | 2791 | C   | O4'-C1' | 6.12 | 1.49 | 1.41
38  | A1  | 2873 | G   | P-O5' | -6.12 | 1.53 | 1.59
10  | B1  | 32   | A   | C4'-O4' | 6.12 | 1.53 | 1.45
38  | A1  | 229  | G   | C2-N3 | 6.12 | 1.37 | 1.32
38  | A1  | 702  | G   | N9-C4 | -6.12 | 1.33 | 1.38
38  | A1  | 1891 | C   | C4-C5 | 6.12 | 1.47 | 1.43
38  | A1  | 2149 | U   | C2-N3 | 6.12 | 1.42 | 1.37
38  | A1  | 2707 | G   | O3'-P | -6.12 | 1.53 | 1.61
11  | B2  | 463  | G   | C8-N7 | -6.12 | 1.27 | 1.30
11  | B2  | 621  | G   | C2'-C1' | -6.12 | 1.46 | 1.53
11  | B2  | 995  | G   | C6-N1 | 6.12 | 1.43 | 1.39
11  | B2  | 1093 | C   | C4-N4 | 6.12 | 1.39 | 1.33
11  | B2  | 1326 | G   | C4'-C3' | 6.12 | 1.59 | 1.53
38  | A1  | 393  | C   | C4'-C3' | 6.12 | 1.59 | 1.53
38  | A1  | 706  | U   | C4-C5 | 6.12 | 1.49 | 1.43
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38 | A1 | 1259 | G | C2'-C1'   | -5.42 | 1.47 | 1.53 |
38 | A1 | 1307 | C | C4-C5      | 5.42 | 1.47 | 1.43 |
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| 38 | A1  | 2045 | C | C4-C5-C6 | 8.29  | 121.55 | 117.40 |
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| 38 | A1  | 1251 | G | O4'-C1'-N9 | 8.29  | 114.83 | 108.20 |
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| 38 | A1  | 2586 | A | C5-C6-N6 | -8.29 | 117.07 | 123.70 |
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| 38 | A1  | 2129 | G | C8-N9-C4 | -8.29 | 103.08 | 106.40 |
| 38 | A1  | 2170 | C | C4-C5-C6 | 8.29  | 121.55 | 117.40 |
| 38 | A1  | 2679 | A | C6-N1-C2 | -8.29 | 113.03 | 118.60 |
| 38 | A1  | 1251 | G | C5-C6-N6 | -8.29 | 119.83 | 123.60 |
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| 11 | B2  | 977  | G | N1-C2-N3 | -8.28 | 118.93 | 123.90 |
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| 38 | A1  | 1810 | G | N3-C2-N2 | 8.28  | 119.90 | 119.90 |
| 38 | A1  | 2280 | G | C1'-O4'-C4' | 8.28  | 116.53 | 109.90 |
| 38 | A1  | 2330 | A | N1-C6-N6 | 8.28  | 123.57 | 118.60 |
| 38 | A1  | 2406 | C | C2-N3-C4 | 8.28  | 124.04 | 119.90 |
| 39 | A3  | 49 | A | N1-C2-N3 | -8.28 | 125.16 | 129.30 |
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| 11 | B2  | 886  | G | C5-N7-C8 | 8.28  | 108.44 | 104.30 |
| 38 | A1  | 878  | G | N9-C4-C5 | -8.28 | 102.09 | 105.40 |
| 38 | A1  | 1495 | A | O4'-C1'-N9 | 8.28  | 114.82 | 108.20 |
| 38 | A1  | 2046 | C | C2-N1-C1' | 8.28  | 127.91 | 118.80 |
| 10 | B1  | 11  | C | C5-C6-N1 | 8.28  | 125.14 | 121.00 |
| 11 | B2  | 459  | G | N1-C2-N3 | -8.28 | 118.94 | 123.90 |
| 11 | B2  | 859  | A | N1-C6-N6 | 8.28  | 123.56 | 118.60 |
| 38 | A1  | 121  | G | N3-C2-N2 | 8.28  | 125.69 | 119.90 |
| 38 | A1  | 2301 | C | P-O5'-C5' | 8.28  | 134.14 | 120.90 |
| 11 | B2  | 663  | G | N1-C2-N3 | -8.27 | 118.94 | 123.90 |
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38 | A1 | 2165 | A | N3-C4-C5 | -7.74 | 121.38 | 126.80 |
38 | A1 | 2789 | G | O4'-C1'-N9 | 7.74 | 114.39 | 108.20 |
38 | A1 | 3038 | A | C5-C6-N6 | -7.74 | 117.50 | 123.70 |
38 | A3 | 831 | C | O4'-C1'-N1 | 7.74 | 114.39 | 108.20 |
38 | A1 | 1064 | G | C5-C6-O6 | -7.74 | 123.95 | 128.60 |
38 | A1 | 2362 | U | N1-C2-O2 | -7.74 | 117.38 | 122.80 |
38 | A1 | 831 | C | O4'-C1'-N1 | 7.74 | 114.39 | 108.20 |
11 | B2 | 506 | G | C4-C5-C6 | 7.74 | 123.44 | 118.80 |
11 | B2 | 1089 | C | N3-C4-N4 | 7.74 | 123.42 | 118.00 |
38 | A1 | 1470 | C | N3-C4-N4 | 7.74 | 123.42 | 118.00 |
38 | A1 | 2588 | C | O4'-C1'-N1 | 7.74 | 114.39 | 108.20 |
11 | B2 | 443 | C | OP1-P-OP2 | -7.74 | 107.99 | 119.60 |
38 | A1 | 180 | A | C5-C6-N1 | -7.74 | 113.83 | 117.70 |
38 | A1 | 638 | A | C5-C6-N1 | -7.74 | 113.83 | 117.70 |
38 | A1 | 1185 | A | C4-C5-C6 | 7.74 | 120.87 | 117.00 |
11 | B2 | 505 | U | C5-C6-N1 | 7.74 | 126.57 | 122.70 |
11 | B2 | 748 | A | C5-C6-N6 | -7.74 | 117.51 | 123.70 |
38 | A1 | 707 | U | C5-C4-O4 | -7.74 | 117.51 | 123.70 |
38 | A1 | 766 | G | C4-C5-N7 | -7.74 | 117.51 | 123.70 |
38 | A1 | 1625 | A | C5-C6-N1 | -7.74 | 117.51 | 123.70 |
38 | A1 | 2365 | G | N9-C4-C5 | -7.74 | 117.51 | 123.70 |
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22 | BJ | 73 | ARG | NE-CZ-NH2 | -7.74 | 117.51 | 123.70 |
38 | A1 | 921 | C | C5-C4-N4 | -7.74 | 117.51 | 123.70 |
38 | A1 | 946 | U | P-O3'-C3' | 7.74 | 128.98 | 119.70 |
38 | A1 | 1406 | G | N1-C2-N3 | -7.74 | 119.25 | 123.90 |
38 | A1 | 2630 | C | O4'-C1'-N1 | 7.74 | 114.39 | 108.20 |
38 | A1 | 2680 | A | N9-C4-C5 | 7.74 | 108.89 | 105.80 |
38 | A1 | 1232 | G | N9-C4-C5 | 7.74 | 108.89 | 105.40 |
38 | A1 | 2318 | G | C5-C6-O6 | -7.73 | 123.96 | 128.60 |
38 | A1 | 2595 | C | O4'-C1'-N1 | 7.73 | 114.39 | 108.20 |
11 | B2 | 403 | C | C5-C6-N1 | 7.73 | 124.87 | 121.00 |
11 | B2 | 777 | G | N3-C2-N2 | 7.73 | 125.31 | 119.90 |
11 | B2 | 884 | G | N3-C4-N9 | 7.73 | 130.64 | 126.00 |
11 | B2 | 1156 | G | P-O3'-C3' | 7.73 | 128.98 | 119.70 |
11 | B2 | 1424 | A | N1-C2-N3 | -7.73 | 119.25 | 123.90 |
38 | A1 | 499 | A | N1-C6-N6 | 7.73 | 123.24 | 118.60 |

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| 38  | A1  | 2071| C   | N3-C2-O2 | 6.81 | 126.66 | 121.90 |
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| 62  | AO  | 7   | TYR | CB-CG-CD2 | -6.80 | 116.92 | 121.00 |
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| 27  | BO  | 9   | ARG | NE-CZ-NH1 | 6.80 | 123.70 | 120.30 |
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14 | BB | 69 | ALA | N-CA-CB | 5.36 | 117.60 | 110.10
16 | BD | 170 | MET | CG-SD-CE | 5.36 | 108.77 | 100.20
33 | BU | 25 | GLU | CB-CA-C | -5.36 | 99.69 | 110.40
38 | A1 | 440 | A | C2-N3-C4 | -5.36 | 107.92 | 110.60
38 | A1 | 485 | G | N3-C4-C5 | -5.36 | 119.76 | 121.90
38 | A1 | 920 | G | N9-C4-C5 | -5.36 | 103.26 | 105.40
38 | A1 | 1209 | A | C5-C6-N1 | -5.36 | 115.02 | 117.70
38 | A1 | 1422 | G | N1-C2-N3 | -5.36 | 120.69 | 123.90
38 | A1 | 1461 | G | N3-C4-N9 | -5.36 | 122.78 | 126.00
38 | A1 | 1775 | G | O4'-C1'-N9 | 5.36 | 112.49 | 108.20
38 | A1 | 2126 | G | C8-N9-C1' | 5.36 | 133.97 | 127.00
38 | A1 | 2178 | A | N7-C8-N9 | -5.36 | 111.12 | 113.80
38 | A1 | 2295 | C | N3-C4-C5 | -5.36 | 119.76 | 121.90
38 | A1 | 2393 | G | O4'-C1'-N9 | 5.36 | 112.49 | 108.20
38 | A1 | 2853 | A | O4'-C1'-N9 | 5.36 | 112.49 | 108.20
10 | B1 | 77 | A | C4-C5-C6 | 5.36 | 119.68 | 117.00
11 | B2 | 29 | G | O4'-C1'-N9 | 5.36 | 112.48 | 108.20
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38 | A1 | 320 | C | P-O5'-C5' | 5.36 | 129.47 | 120.90
38 | A1 | 843 | C | N3-C4-C5 | -5.36 | 119.76 | 121.90
38 | A1 | 984 | U | C6-N1-C2 | -5.36 | 117.79 | 121.00
38 | A1 | 1382 | C | O4'-C1'-N1 | 5.36 | 112.48 | 108.20
38 | A1 | 1456 | U | C4-C5-C6 | 5.36 | 122.91 | 119.70
38 | A1 | 2135 | C | N3-C2-O2 | -5.36 | 118.15 | 121.90
38 | A1 | 2255 | C | N3-C4-N4 | 5.36 | 121.75 | 118.00
38 | A1 | 2581 | G | N7-C8-N9 | 5.36 | 115.78 | 113.10
38 | A1 | 2635 | C | N3-C4-N4 | 5.36 | 121.75 | 118.00
43 | AB | 109 | TYR | CB-CG-CD1 | 5.36 | 124.21 | 121.00
11 | B2 | 1332 | C | C5'-C4'-O4' | 5.36 | 115.52 | 109.10
38 | A1 | 86 | G | C4-C5-C6 | 5.36 | 122.01 | 118.80
38 | A1 | 101 | G | O5'-P-OP1 | 5.36 | 117.12 | 110.70
38 | A1 | 786 | G | N7-C8-N9 | -5.36 | 110.42 | 113.10
45 | AC | 68 | MET | CG-SD-CE | -5.36 | 91.63 | 100.20
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38 | A1 | 1533 | G | C8-N9-C1' | 5.22 | 133.78 | 127.00
38 | A1 | 1848 | A | P-O5'-C5' | -5.22 | 112.55 | 120.90
38 | A1 | 2376 | A | N9-C4-C5 | -5.22 | 103.71 | 105.80
1 | A7 | 66 | LYS | N-CA-CB | 5.22 | 119.99 | 110.60
3 | Af | 3 | ARG | NE-CZ-NH2 | -5.22 | 117.69 | 120.30
9 | AX | 277 | TYR | CB-CG-CD1 | -5.22 | 117.87 | 121.00
11 | B2 | 268 | C | C5-C6-N1 | 5.22 | 123.61 | 121.00
11 | B2 | 855 | C | N1-C2-O2 | 5.22 | 122.03 | 118.90
11 | B2 | 904 | G | N3-C2-N2 | 5.22 | 123.55 | 119.90
11 | B2 | 961 | U | C5'-C4'-O4' | 5.22 | 115.36 | 109.10
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38 | A1 | 2335 | G | C4-C5-N7 | 5.05 | 112.82 | 110.80
41 | AA | 194 | ARG | C-N-CA | 5.05 | 132.92 | 122.30
11 | B2 | 848 | G | O4'-C1'-N9 | 5.05 | 112.24 | 108.20
11 | B2 | 1099 | A | N9-C4-C5 | 5.05 | 107.82 | 105.80
11 | B2 | 1493 | C | C3'-C2'-C1' | 5.05 | 105.54 | 101.50
24 | BL | 47 | ILE | N-CA-C | -5.05 | 97.36 | 111.00
38 | A1 | 416 | A | N3-C4-C5 | -5.05 | 123.26 | 126.80
38 | A1 | 671 | G | C3'-C2'-C1' | -5.05 | 97.46 | 101.50
38 | A1 | 2132 | C | C6-N1-C2 | -5.05 | 118.28 | 120.30
38 | A1 | 2449 | A | C4-C5-C6 | 5.05 | 119.53 | 117.00
59 | AL | 36 | MET | CG-SD-CE | -5.05 | 92.11 | 100.20
66 | AY | 16 | LYS | CB-CG-CD | 5.05 | 124.74 | 111.60
4 | AQ | 21 | ARG | NE-CZ-NH1 | -5.05 | 117.77 | 120.30
11 | B2 | 42 | G | C4-C5-C6 | 5.05 | 121.83 | 118.80
11 | B2 | 93 | A | C5'-C4'-O4' | 5.05 | 115.16 | 109.10
11 | B2 | 278 | A | C5-N7-C8 | 5.05 | 106.42 | 103.90
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11 | B2 | 431 | U | N3-C2-O2 | 5.05 | 125.74 | 122.20
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11 | B2 | 1278 | A | C5-N7-C8 | 5.05 | 106.43 | 103.90
14 | BB | 155 | PRO | N-CD-CG | 5.05 | 110.78 | 103.20
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38 | A1 | 1012 | G | C5-N7-C8 | 5.05 | 106.83 | 104.30
38 | A1 | 1452 | G | N1-C2-N2 | -5.05 | 111.65 | 116.20
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38 | A1 | 2179 | G | O4'-C1'-N9 | 5.05 | 112.24 | 108.20
38 | A1 | 2496 | G | C4-C5-N7 | -5.05 | 108.78 | 110.80
38 | A1 | 2513 | C | C6-N1-C2 | -5.05 | 118.28 | 120.30
38 | A1 | 2591 | A | C5'-C4'-C3' | -5.05 | 107.92 | 116.00
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41 | AA | 67 | ASP | CB-CG-OD1 | -5.05 | 113.75 | 118.30
57 | Aj | 10 | TYR | CB-CG-CG2 | -5.05 | 117.97 | 121.00
58 | Ak | 133 | PRO | N-CA-CB | 5.05 | 109.36 | 103.30
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5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

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The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (554) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

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<tr>
<th>Atom-1</th>
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<th>Interatomic distance (Å)</th>
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There are no symmetry-related clash(es).
### 5.3 Torsion angles

#### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

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<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Analysed</th>
<th>Favoured</th>
<th>Allowed</th>
<th>Outliers</th>
<th>Percentiles</th>
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<td>139 (94%)</td>
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<td>3  (2%)</td>
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### 5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.
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5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.