Dec 11, 2022 – 01:38 am GMT

PDB ID : 6R7Q
EMDB ID : EMD-4745
Title : Structure of XBP1u-paused ribosome nascent chain complex with Sec61.
Authors : Shanmuganathan, V.; Cheng, J.; Braunger, K.; Berninghausen, O.; Beatrix, B.; Beckmann, R.
Deposited on : 2019-03-29
Resolution : 3.90 Å (reported)
Based on initial model : ?

This is a Full wwPDB EM Validation Report for a publicly released PDB 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 ☰ symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references ☰) were used in the production of this report:

- EMDB validation analysis : 0.0.1.dev43
- MolProbity : 4.02b-467
- Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
- MapQ : 1.9.9
- Ideal geometry (proteins) : Engh & Huber (2001)
- Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
- Validation Pipeline (wwPDB-VP) : 2.31.3
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 3.90 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>
<th>Whole archive (#Entries)</th>
<th>EM structures (#Entries)</th>
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<tr>
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<tr>
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The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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%. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

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<tr>
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<td>ZZ</td>
<td>29</td>
<td>83% 97% 17%</td>
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</table>
2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 219898 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 40S ribosomal protein S30.
  
<table>
<thead>
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<th>Atoms</th>
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<th>Trace</th>
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<tr>
<td>1</td>
<td>AA</td>
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<td>Total C N O S</td>
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<td>0</td>
</tr>
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<td></td>
<td>443 274 97 71 1</td>
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<td>0</td>
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</tbody>
</table>

- Molecule 2 is a protein called 40S ribosomal protein S7.
  
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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<td></td>
<td></td>
<td>1488 952 271 264 1</td>
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</tbody>
</table>

- Molecule 3 is a protein called 40S ribosomal protein S8.
  
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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</thead>
<tbody>
<tr>
<td>3</td>
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<td>0</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>1686 1058 332 291 5</td>
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</table>

There is a discrepancy between the modelled and reference sequences:

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<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
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<td>GLY</td>
<td>conflict</td>
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- Molecule 4 is a protein called Ribosomal protein S9 (Predicted).
  
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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</thead>
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<tr>
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<td></td>
<td></td>
<td>1525 969 306 248 2</td>
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- Molecule 5 is a protein called Ribosomal protein S11.
  
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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</thead>
<tbody>
<tr>
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<td>EE</td>
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<td>Total C N O S</td>
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<td>0</td>
</tr>
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<td></td>
<td></td>
<td>1175 749 222 198 6</td>
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- Molecule 6 is a protein called Ribosomal protein S28.
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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<td>6</td>
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<td>Total C N O S</td>
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- Molecule 7 is a protein called uS10.

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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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</thead>
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<td>100</td>
<td>Total C N O S</td>
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<td>0</td>
</tr>
<tr>
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<td></td>
<td></td>
<td>795 498 152 141 4</td>
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- Molecule 8 is a protein called eS21.

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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>8</td>
<td>HH</td>
<td>83</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
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<td></td>
<td></td>
<td>636 393 117 121 5</td>
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- Molecule 9 is a protein called uS13.

<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>9</td>
<td>II</td>
<td>144</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
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<td></td>
<td></td>
<td>1190 746 241 202 1</td>
<td></td>
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</table>

- Molecule 10 is a protein called 40S ribosomal protein S27.

<table>
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<th>Residues</th>
<th>Atoms</th>
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<th>Trace</th>
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<tbody>
<tr>
<td>10</td>
<td>JJ</td>
<td>83</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>651 408 121 115 7</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 11 is a protein called eS17.

<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>KK</td>
<td>132</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1068 670 199 195 4</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 12 is a protein called eS26.

<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>LL</td>
<td>101</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>814 507 170 132 5</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 13 is a protein called uS11.
Molecule 14 is a protein called eS31.

Molecule 15 is a protein called X-box-binding protein 1.

There is a discrepancy between the modelled and reference sequences:

Molecule 16 is a RNA chain called P-tRNA.

Molecule 17 is a RNA chain called E-tRNA.

Molecule 18 is a RNA chain called messenger RNA.

Molecule 19 is a RNA chain called 28S 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>19</td>
<td>5</td>
<td>3543</td>
<td>Total C N O P</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>75972 33833 13910 24686 3543</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 20 is a protein called ribosomal protein RACK1.

<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>6</td>
<td>313</td>
<td>Total C N O S</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>2436 1535 424 465 12</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 21 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>
<tbody>
<tr>
<td>21</td>
<td>7</td>
<td>120</td>
<td>Total C N O P</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>2558 1141 456 842 119</td>
<td>0</td>
<td>0</td>
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</tbody>
</table>

- Molecule 22 is a RNA chain called 5.8S ribosomal RNA.

<table>
<thead>
<tr>
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<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>22</td>
<td>8</td>
<td>151</td>
<td>Total C N O S</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>3208 1432 564 1062 150</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 23 is a protein called uS14.

<table>
<thead>
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<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>23</td>
<td>9</td>
<td>55</td>
<td>Total C N O S</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>459 286 94 74 5</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 24 is a protein called eS24.

<table>
<thead>
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<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>24</td>
<td>NN</td>
<td>124</td>
<td>Total C N O S</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1011 640 198 168 5</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 25 is a protein called ribosomal protein eS25.

<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>OO</td>
<td>75</td>
<td>Total C N O S</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>598 382 111 104 1</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 26 is a protein called eS19.
There is a discrepancy between the modelled and reference sequences:

<table>
<thead>
<tr>
<th>Chain</th>
<th>Residue</th>
<th>Modelled</th>
<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>PP</td>
<td>119</td>
<td>GLY</td>
<td>TRP</td>
<td>conflict</td>
<td>UNP G1TN62</td>
</tr>
</tbody>
</table>

- Molecule 27 is a protein called ribosomal protein uS15.

<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>QQ</td>
<td>149</td>
<td>Total C N O S 1202 770 228 203 1</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 28 is a protein called 40S ribosomal protein S12.

<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>RR</td>
<td>117</td>
<td>Total C N O S 908 570 161 169 8</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 29 is a protein called uL2.

<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>A</td>
<td>248</td>
<td>Total C N O S 1898 1189 389 314 6</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 30 is a protein called uL3.

<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>B</td>
<td>394</td>
<td>Total C N O S 3172 2020 597 542 13</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 31 is a protein called uL4.

<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>C</td>
<td>362</td>
<td>Total C N O S 2883 1812 577 480 14</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 32 is a protein called 60S ribosomal protein L5.
- Molecule 33 is a protein called 60S ribosomal protein L6.

<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>D</td>
<td>293</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>2391 1512 438 427 14</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 34 is a protein called uL30.

<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>E</td>
<td>216</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1729 1115 329 282 3</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 35 is a protein called eL8.

<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>35</td>
<td>G</td>
<td>233</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1879 1199 361 315 4</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

There is a discrepancy between the modelled and reference sequences:

<table>
<thead>
<tr>
<th>Chain</th>
<th>Residue</th>
<th>Modelled</th>
<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>G</td>
<td>244</td>
<td>GLY</td>
<td>CYS</td>
<td>conflict</td>
<td>UNP G1STW0</td>
</tr>
</tbody>
</table>

- Molecule 36 is a protein called uL6.

<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>36</td>
<td>H</td>
<td>190</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1516 954 284 272 6</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 37 is a protein called Ribosomal protein L10 (Predicted).

<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>37</td>
<td>I</td>
<td>205</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1664 1056 321 274 13</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 38 is a protein called Ribosomal protein L11.
- Molecule 39 is a RNA chain called 18S 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>39</td>
<td>K</td>
<td>1698</td>
<td>Total C N O P</td>
<td>36249 16180 6508 11864 1697</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 40 is a protein called 60S ribosomal protein L13.

<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>40</td>
<td>L</td>
<td>210</td>
<td>Total C N O S</td>
<td>1702 1065 354 279 4</td>
<td>0 0</td>
</tr>
</tbody>
</table>

There are 9 discrepancies between the modelled and reference sequences:

<table>
<thead>
<tr>
<th>Chain</th>
<th>Residue</th>
<th>Modelled</th>
<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>L</td>
<td>47</td>
<td>ALA</td>
<td>-</td>
<td>insertion</td>
<td>UNP G1TPV0</td>
</tr>
<tr>
<td>L</td>
<td>48</td>
<td>PRO</td>
<td>-</td>
<td>insertion</td>
<td>UNP G1TPV0</td>
</tr>
<tr>
<td>L</td>
<td>49</td>
<td>ARG</td>
<td>-</td>
<td>insertion</td>
<td>UNP G1TPV0</td>
</tr>
<tr>
<td>L</td>
<td>50</td>
<td>PRO</td>
<td>-</td>
<td>insertion</td>
<td>UNP G1TPV0</td>
</tr>
<tr>
<td>L</td>
<td>51</td>
<td>ALA</td>
<td>-</td>
<td>insertion</td>
<td>UNP G1TPV0</td>
</tr>
<tr>
<td>L</td>
<td>52</td>
<td>ALA</td>
<td>-</td>
<td>insertion</td>
<td>UNP G1TPV0</td>
</tr>
<tr>
<td>L</td>
<td>53</td>
<td>GLY</td>
<td>-</td>
<td>insertion</td>
<td>UNP G1TPV0</td>
</tr>
<tr>
<td>L</td>
<td>54</td>
<td>PRO</td>
<td>-</td>
<td>insertion</td>
<td>UNP G1TPV0</td>
</tr>
<tr>
<td>L</td>
<td>55</td>
<td>ILE</td>
<td>-</td>
<td>insertion</td>
<td>UNP G1TPV0</td>
</tr>
</tbody>
</table>

- Molecule 41 is a protein called Ribosomal protein L14.

<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>41</td>
<td>M</td>
<td>138</td>
<td>Total C N O S</td>
<td>1137 727 221 182 7</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 42 is a protein called Ribosomal protein L15.

<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>N</td>
<td>203</td>
<td>Total C N O S</td>
<td>1701 1072 359 266 4</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 43 is a protein called uL13.
• Molecule 44 is a protein called uL22.

<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>P</td>
<td>153</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1242 777 241 215 9</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

• Molecule 45 is a protein called eL18.

<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>Q</td>
<td>187</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1515 946 315 250 4</td>
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</tbody>
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There are 16 discrepancies between the modelled and reference sequences:

<table>
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<th>Residue</th>
<th>Modelled</th>
<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Q</td>
<td>6</td>
<td>ARG</td>
<td>LEU</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>14</td>
<td>ARG</td>
<td>TRP</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>23</td>
<td>ILE</td>
<td>MET</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>24</td>
<td>TYR</td>
<td>CYS</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>38</td>
<td>ARG</td>
<td>HIS</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>57</td>
<td>ASN</td>
<td>LYS</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>66</td>
<td>MET</td>
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<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>74</td>
<td>GLY</td>
<td>ASP</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>75</td>
<td>ARG</td>
<td>PRO</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>86</td>
<td>VAL</td>
<td>ILE</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>110</td>
<td>ARG</td>
<td>HIS</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>117</td>
<td>GLY</td>
<td>GLU</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>124</td>
<td>ASP</td>
<td>HIS</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>150</td>
<td>ARG</td>
<td>GLN</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
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<td>172</td>
<td>ARG</td>
<td>GLY</td>
<td>conflict</td>
<td>UNP G1TX70</td>
</tr>
<tr>
<td>Q</td>
<td>184</td>
<td>ARG</td>
<td>TRP</td>
<td>conflict</td>
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• Molecule 46 is a protein called eL19.

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<td>1508 933 328 238 9</td>
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• Molecule 47 is a protein called eL20.
- Molecule 48 is a protein called eL21.

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- Molecule 49 is a protein called eL22.

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<td>809 519 141 147 2</td>
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- Molecule 50 is a protein called eL14.

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<td></td>
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<td>979 618 184 172 5</td>
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- Molecule 51 is a protein called Ribosomal protein L24.

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<td></td>
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<td>860 538 174 144 4</td>
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- Molecule 52 is a protein called uL23.

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<td></td>
<td></td>
<td>967 618 181 167 1</td>
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- Molecule 53 is a protein called Ribosomal protein L26.

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<td></td>
<td></td>
<td>1115 700 226 186 3</td>
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- Molecule 54 is a protein called 60S ribosomal protein L27.
- Molecule 55 is a protein called eS10.

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- Molecule 56 is a protein called uL15.

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<td>1162    734 239 185 4</td>
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- Molecule 57 is a protein called eL29.

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- Molecule 58 is a protein called eL30.

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- Molecule 59 is a protein called eL31.

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- Molecule 60 is a protein called eL32.

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<td>1053    667 216 165 5</td>
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- Molecule 61 is a protein called eL33.
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- Molecule 62 is a protein called eL34.
- Molecule 63 is a protein called uL29.
- Molecule 64 is a protein called 60S ribosomal protein L36.
- Molecule 65 is a protein called Ribosomal protein L37.
- Molecule 66 is a protein called eL38.
- Molecule 67 is a protein called eL39.
- Molecule 68 is a protein called eL40.
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- Molecule 69 is a protein called 60s ribosomal protein l41.

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- Molecule 70 is a protein called eL42.

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<td>851 533 174 138 6</td>
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- Molecule 71 is a protein called ribosomal protein eL43.

<table>
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- Molecule 72 is a protein called uS2.

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- Molecule 73 is a protein called eL28.

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<th>Atoms</th>
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<td></td>
<td></td>
<td></td>
<td>994 616 205 167 6</td>
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- Molecule 74 is a protein called 60S acidic ribosomal protein P0.

<table>
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<th>Atoms</th>
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<td></td>
<td></td>
<td>1507 959 263 276 9</td>
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- Molecule 75 is a protein called uL11.
Molecule 76 is a protein called 40S ribosomal protein S3a.

Molecule 77 is a protein called uS5.

Molecule 78 is a protein called Ribosomal protein S3.

Molecule 79 is a protein called 40S ribosomal protein S4.

There are 4 discrepancies between the modelled and reference sequences:

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<th>Actual</th>
<th>Comment</th>
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Molecule 80 is a protein called Ribosomal protein S5.

Molecule 81 is a protein called 40S ribosomal protein S6.
• Molecule 82 is a protein called Ribosomal protein S15a.

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<td>1034 659 193 176 6</td>
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• Molecule 83 is a protein called Ribosomal protein S16.

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• Molecule 84 is a protein called Ribosomal protein S23.

<table>
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• Molecule 85 is a protein called uS19.

<table>
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>85</td>
<td>WW</td>
<td>120</td>
<td>Total C N O S</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>997 635 187 168 7</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

• Molecule 86 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.

<table>
<thead>
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<tr>
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<td></td>
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<td></td>
<td></td>
<td>3313 2181 535 576 21</td>
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<td>0</td>
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There is a discrepancy between the modelled and reference sequences:

<table>
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<tr>
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<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
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</thead>
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<tr>
<td>XX</td>
<td>145</td>
<td>SER</td>
<td>THR</td>
<td>conflict</td>
<td>UNP P38377</td>
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• Molecule 87 is a protein called Protein transport protein Sec61 subunit gamma.
- Molecule 88 is a protein called Protein transport protein Sec61 subunit beta.

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<th>AltConf</th>
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<td>88</td>
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<td>229 157 36 34 2</td>
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- Molecule 89 is ZINC ION (three-letter code: ZN) (formula: Zn).

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<td>Total Zn</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>m</td>
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<td>Total Zn</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>o</td>
<td>1</td>
<td>Total Zn</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td>p</td>
<td>1</td>
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- Molecule 90 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

<table>
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<td>V</td>
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<td>Total Mg</td>
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Continued on next page...
Continued from previous page...

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<th>Atoms</th>
<th>AltConf</th>
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</thead>
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<td>1 0</td>
</tr>
<tr>
<td>90</td>
<td>e</td>
<td>1</td>
<td>Total Mg 1</td>
<td>1 0</td>
</tr>
<tr>
<td>90</td>
<td>g</td>
<td>1</td>
<td>Total Mg 1</td>
<td>1 0</td>
</tr>
<tr>
<td>90</td>
<td>j</td>
<td>1</td>
<td>Total Mg 1</td>
<td>1 0</td>
</tr>
<tr>
<td>90</td>
<td>y</td>
<td>1</td>
<td>Total Mg 1</td>
<td>1 0</td>
</tr>
</tbody>
</table>
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 and atom inclusion in map density. 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. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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: 40S ribosomal protein S30

Chain AA:

- Molecule 2: 40S ribosomal protein S7

Chain BB:

- Molecule 3: 40S ribosomal protein S8

Chain CC:

- Molecule 4: Ribosomal protein S9 (Predicted)

Chain DD:
• Molecule 5: Ribosomal protein S11

Chain EE:

• Molecule 6: Ribosomal protein S28

Chain FF:

• Molecule 7: uS10

Chain GG:

• Molecule 8: eS21

Chain HH:
- Molecule 9: uS13

Chain II:

- Molecule 10: 40S ribosomal protein S27

Chain JJ:

- Molecule 11: eS17

Chain KK:

- Molecule 12: eS26

Chain LL:

- Molecule 13: uS11

Chain MM:
• Molecule 14: eS31

Chain 0:

84% 99%

• Molecule 15: X-box-binding protein 1

Chain 1:

67% 46%

• Molecule 16: P-tRNA

Chain 2:

71% 43%

• Molecule 17: E-tRNA

Chain 3:

72% 21%

• Molecule 18: messenger RNA

Chain 4:

67% 33%
- Molecule 19: 28S ribosomal RNA
• Molecule 20: ribosomal protein RACK1

Chain 6:
- Molecule 21: 5S ribosomal RNA

Chain 7:

- Molecule 22: 5.8S ribosomal RNA

Chain 8:

- Molecule 23: uS14

Chain 9:

- Molecule 24: eS24

Chain NN:
• Molecule 25: ribosomal protein eS25

Chain OO:

• Molecule 26: eS19

Chain PP:

• Molecule 27: ribosomal protein uS15

Chain QQ:

• Molecule 28: 40S ribosomal protein S12

Chain RR:

• Molecule 29: uL2

Chain A:
• Molecule 30: uL3

Chain B:

• Molecule 31: uL4

Chain C:

• Molecule 32: 60S ribosomal protein L5

Chain D:

• Molecule 33: 60S ribosomal protein L6

Chain E:

• Molecule 34: uL30
- Molecule 40: 60S ribosomal protein L13

Chain L:

- Molecule 41: Ribosomal protein L14

Chain M:

- Molecule 42: Ribosomal protein L15

Chain N:

- Molecule 43: uL13

Chain O:

- Molecule 44: uL22

Chain P:

- Molecule 45: eL18
• Molecule 52: uL23
Chain X:

• Molecule 53: Ribosomal protein L26
Chain Y:

• Molecule 54: 60S ribosomal protein L27
Chain Z:

• Molecule 55: eS10
Chain SS:

• Molecule 56: uL15
Chain a:

• Molecule 57: eL29
Chain b:
• Molecule 58: eL30
Chain c: 13% 99%

• Molecule 59: eL31
Chain d: 17% 97%

• Molecule 60: eL32
Chain e: 7% 98%

• Molecule 61: eL33
Chain f: 9% 97%

• Molecule 62: eL34
Chain g: 11% 97%

• Molecule 63: uL29
Chain h: 17% 100%
- Molecule 64: 60S ribosomal protein L36
- Molecule 65: Ribosomal protein L37
- Molecule 66: eL38
- Molecule 67: eL39
- Molecule 68: eL40
- Molecule 69: 60s ribosomal protein L41
- Molecule 70: eL42
• Molecule 71: ribosomal protein eL43

• Molecule 72: uS2

• Molecule 73: eL28

• Molecule 74: 60S acidic ribosomal protein P0
• Molecule 75: uL11

Chain t: 100%

• Molecule 76: 40S ribosomal protein S3a

Chain u: 38% 97%

• Molecule 77: uS5

Chain v: 37% 99%

• Molecule 78: Ribosomal protein S3
Molecule 79: 40S ribosomal protein S4

Molecule 80: Ribosomal protein S5
• Molecule 81: 40S ribosomal protein S6

Chain z:

• Molecule 82: Ribosomal protein S15a

Chain TT:

• Molecule 83: Ribosomal protein S16

Chain UU:

• Molecule 84: Ribosomal protein S23

Chain VV:
- Molecule 85: uS19

Chain WW:

- Molecule 86: Protein transport protein Sec61 subunit alpha isoform 1

Chain XX:
• Molecule 87: Protein transport protein Sec61 subunit gamma

Chain YY:

• Molecule 88: Protein transport protein Sec61 subunit beta

Chain ZZ:
## 4 Experimental information

<table>
<thead>
<tr>
<th>Property</th>
<th>Value</th>
<th>Source</th>
</tr>
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<td>EM 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>12749</td>
<td>Depositor</td>
</tr>
<tr>
<td>Resolution determination method</td>
<td>FSC 0.143 CUT-OFF</td>
<td>Depositor</td>
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<tr>
<td>CTF correction method</td>
<td>NONE</td>
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<tr>
<td>Microscope</td>
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<tr>
<td>Voltage (kV)</td>
<td>300</td>
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<tr>
<td>Electron dose ( e^-/\AA^2 )</td>
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<td>Maximum defocus (nm)</td>
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<td>Magnification</td>
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<td>Pixel spacing (Å)</td>
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</tbody>
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5  Model quality

5.1  Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

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>
<th>Chain</th>
<th>Bond lengths</th>
<th>Bond angles</th>
</tr>
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<tr>
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<td>RMSZ</td>
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</tr>
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</tr>
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<td>3</td>
<td>CC</td>
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<td>5</td>
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<td>V</td>
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<td>Y</td>
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<td>Z</td>
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<td>0/1130</td>
</tr>
<tr>
<td>55</td>
<td>SS</td>
<td>0.31</td>
<td>0/834</td>
</tr>
<tr>
<td>56</td>
<td>a</td>
<td>0.61</td>
<td>0/1191</td>
</tr>
<tr>
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<td>b</td>
<td>0.40</td>
<td>0/861</td>
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<td>58</td>
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<td>0.53</td>
<td>0/771</td>
</tr>
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<td>d</td>
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<td>60</td>
<td>e</td>
<td>0.58</td>
<td>0/1071</td>
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<td>f</td>
<td>0.63</td>
<td>0/895</td>
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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.
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There are no chirality outliers.

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5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.
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.

<table>
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<tr>
<th>Mol</th>
<th>Chain</th>
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<th>Favoured</th>
<th>Allowed</th>
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<th>Percentiles</th>
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<tr>
<td>86</td>
<td>XX</td>
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All (16) Ramachandran outliers are listed below:

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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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<tr>
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<th>Rotameric</th>
<th>Outliers</th>
<th>Percentiles</th>
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<tr>
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<td>57 75</td>
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<tr>
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5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.
5.6 Ligand geometry

Of 305 ligands modelled in this entry, 305 are monoatomic - leaving 0 for Mogul analysis.
There are no bond length outliers.
There are no bond angle outliers.
There are no chirality outliers.
There are no torsion outliers.
There are no ring outliers.
No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

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6 Map visualisation

This section contains visualisations of the EMDB entry EMD-4745. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

6.1.1 Primary map

The images above show the map projected in three orthogonal directions.

6.2 Central slices

6.2.1 Primary map

The images above show the map projected in three orthogonal directions.
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices

6.3.1 Primary map

The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views

6.4.1 Primary map

The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.
6.5 Mask visualisation

This section was not generated. No masks/segmentation were deposited.
7 Map analysis

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution

The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.
7.2 Volume estimate

The volume at the recommended contour level is 1111 nm$^3$; this corresponds to an approximate mass of 1003 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.
7.3 Rotationally averaged power spectrum

*Reported resolution corresponds to spatial frequency of 0.256 Å⁻¹
8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC

*Reported resolution corresponds to spatial frequency of 0.256 Å\(^{-1}\)
8.2 Resolution estimates

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<th>Estimation criterion (FSC cut-off)</th>
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<td>Unmasked-calculated*</td>
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*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-4745 and PDB model 6R7Q. Per-residue inclusion information can be found in section 3 on page 23.

9.1 Map-model overlay

The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.
9.2 Q-score mapped to coordinate model

The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.08).
9.4 Atom inclusion

At the recommended contour level, 67% of all backbone atoms, 58% of all non-hydrogen atoms, are inside the map.
### 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.08) and Q-score for the entire model and for each chain.

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