Full wwPDB EM Validation Report

Nov 6, 2022 – 12:10 PM EST

PDB ID : 7TUT
EMDB ID : EMD-26133
Title : Structure of the rabbit 80S ribosome stalled on a 4-TMD Rhodopsin intermediate in complex with the multipass translocon
Authors : Kim, M.K.; Lewis, A.J.O.; Keenan, R.J.; Hegde, R.S.
Deposited on : 2022-02-03
Resolution : 3.88 Å (reported)

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
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) : 2.31.2
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 3.88 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>
</tr>
</thead>
<tbody>
<tr>
<td>Ramachandran outliers</td>
<td>154571</td>
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<tr>
<td>Sidechain outliers</td>
<td>154315</td>
<td>3826</td>
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<td>RNA backbone</td>
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</table>

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 \( \geq 3, 2, 1 \) 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.

<table>
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<tr>
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<td>C</td>
<td>413</td>
<td>87% 12%</td>
</tr>
<tr>
<td>3</td>
<td>D</td>
<td>297</td>
<td>99%</td>
</tr>
<tr>
<td>4</td>
<td>E</td>
<td>291</td>
<td>79% 20%</td>
</tr>
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<td>5</td>
<td>F</td>
<td>247</td>
<td>91% 9%</td>
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<td>6</td>
<td>G</td>
<td>319</td>
<td>73% 27%</td>
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<td>H</td>
<td>192</td>
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</tr>
<tr>
<td>8</td>
<td>I</td>
<td>214</td>
<td>96%</td>
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<table>
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<tr>
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<td>d</td>
<td>125</td>
<td>84% 14%</td>
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<td>e</td>
<td>135</td>
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<td>f</td>
<td>110</td>
<td>99%</td>
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<tr>
<td>31</td>
<td>g</td>
<td>116</td>
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<td>h</td>
<td>123</td>
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<tr>
<td>33</td>
<td>i</td>
<td>105</td>
<td>97%</td>
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<td>l</td>
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<td>m</td>
<td>102</td>
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<tr>
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<td>n</td>
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<td>o</td>
<td>106</td>
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</tr>
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<td>p</td>
<td>92</td>
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<td>q</td>
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<td>137</td>
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<tr>
<td>51</td>
<td>5</td>
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</tr>
<tr>
<td>54</td>
<td>8</td>
<td>188</td>
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</tr>
<tr>
<td>55</td>
<td>K</td>
<td>3543</td>
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</tr>
<tr>
<td>56</td>
<td>9</td>
<td>129</td>
<td><img src="#" alt="Quality" /> 26% <img src="#" alt="Quality" /> 82% <img src="#" alt="Quality" /> 16%</td>
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</tbody>
</table>
2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 267107 atoms, of which 114508 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 uL2.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>248</td>
<td>Total C H N O S</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>3891 1189 1993 389 314 6</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 2 is a protein called uL4.

<table>
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>C</td>
<td>362</td>
<td>Total C H N O S</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>5936 1812 3053 577 480 14</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 3 is a protein called uL18.

<table>
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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</thead>
<tbody>
<tr>
<td>3</td>
<td>D</td>
<td>293</td>
<td>Total C H N O S</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>4815 1512 2424 438 427 14</td>
<td>0</td>
<td>0</td>
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</tbody>
</table>

- Molecule 4 is a protein called eL6.

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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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</thead>
<tbody>
<tr>
<td>4</td>
<td>E</td>
<td>233</td>
<td>Total C H N O S</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>3908 1206 2031 357 311 3</td>
<td>0</td>
<td>0</td>
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</tbody>
</table>

- Molecule 5 is a protein called uL30.

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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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</thead>
<tbody>
<tr>
<td>5</td>
<td>F</td>
<td>225</td>
<td>Total C H N O S</td>
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<td></td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>3870 1205 1995 358 303 9</td>
<td>0</td>
<td>0</td>
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</table>

There are 4 discrepancies between the modelled and reference sequences:

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<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
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</thead>
<tbody>
<tr>
<td>F</td>
<td>61</td>
<td>ARG</td>
<td>GLY</td>
<td>conflict</td>
<td>UNP G1TUB1</td>
</tr>
<tr>
<td>F</td>
<td>93</td>
<td>ARG</td>
<td>GLY</td>
<td>conflict</td>
<td>UNP G1TUB1</td>
</tr>
<tr>
<td>F</td>
<td>131</td>
<td>MET</td>
<td>VAL</td>
<td>conflict</td>
<td>UNP G1TUB1</td>
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<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>F</td>
<td>153</td>
<td>ILE</td>
<td>VAL</td>
<td>conflict</td>
<td>UNP G1TUB1</td>
</tr>
</tbody>
</table>

- Molecule 6 is a protein called eL8.

<table>
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<th>Trace</th>
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<tbody>
<tr>
<td>6</td>
<td>G</td>
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<td>Total C</td>
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<td></td>
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<td>H</td>
<td>1199</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>N</td>
<td>2027</td>
<td></td>
</tr>
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<td></td>
<td></td>
<td></td>
<td>S</td>
<td>315</td>
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There is a discrepancy between the modelled and reference sequences:

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<th>Reference</th>
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<td>CYS</td>
<td>conflict</td>
<td>UNP G1STW0</td>
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- Molecule 7 is a protein called uL6.

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<td></td>
<td></td>
<td>S</td>
<td>272</td>
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- Molecule 8 is a protein called uL16.

<table>
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<th>Atoms</th>
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<th>Trace</th>
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<td>O</td>
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<td></td>
<td></td>
<td></td>
<td>S</td>
<td>274</td>
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</table>

- Molecule 9 is a protein called uL5.

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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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<td>N</td>
<td>1399</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>S</td>
<td>241</td>
<td></td>
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- Molecule 10 is a protein called eL13.

<table>
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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<td>Total C</td>
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<td>0</td>
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<td>N</td>
<td>1820</td>
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There are 9 discrepancies between the modelled and reference sequences:

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<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
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<tbody>
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<td>L</td>
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<td>ILE</td>
<td>-</td>
<td>insertion</td>
<td>UNP G1TPV0</td>
</tr>
</tbody>
</table>

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Continued from previous page...

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<th>Actual</th>
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<th>Reference</th>
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- Molecule 11 is a protein called eL14.

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<th>Trace</th>
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<td>11</td>
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- Molecule 12 is a protein called eL15.

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<th>Atoms</th>
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<td>12</td>
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There is a discrepancy between the modelled and reference sequences:

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<th>Actual</th>
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<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>N</td>
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- Molecule 13 is a protein called uL13.

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<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
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- Molecule 14 is a protein called uL22.

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<th>Atoms</th>
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- Molecule 15 is a protein called eL18.
Molecule 16 is a protein called eL19.

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<th>AltConf</th>
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<tbody>
<tr>
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There are 3 discrepancies between the modelled and reference sequences:

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<th>Reference</th>
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</thead>
<tbody>
<tr>
<td>R</td>
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<td>GLN</td>
<td>conflict</td>
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<tr>
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<td>UNP G1TJR3</td>
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Molecule 17 is a protein called eL20.

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<th>Trace</th>
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<tbody>
<tr>
<td>17</td>
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<tr>
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<td></td>
<td>2970 930 1508 285 236 11</td>
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Molecule 18 is a protein called eL21.

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<tbody>
<tr>
<td>18</td>
<td>T</td>
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Molecule 19 is a protein called eL22.

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<tbody>
<tr>
<td>19</td>
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<td></td>
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<td>1690 534 856 146 152 2</td>
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There are 11 discrepancies between the modelled and reference sequences:

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<td>U</td>
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<td>LEU</td>
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<td>UNP G1TSG1</td>
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<tr>
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<td>ARG</td>
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<td>GLU</td>
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<td>UNP G1TSG1</td>
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<tr>
<td>U</td>
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<td>PHE</td>
<td>SER</td>
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<td>UNP G1TSG1</td>
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<td>ARG</td>
<td>conflict</td>
<td>UNP G1TSG1</td>
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<table>
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<tr>
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<tr>
<td>U</td>
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<td>ILE</td>
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<td>U</td>
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<td>THR</td>
<td>SER</td>
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<tr>
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- Molecule 20 is a protein called uL14.

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<tbody>
<tr>
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- Molecule 21 is a protein called eL24.

<table>
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- Molecule 22 is a protein called eL23.

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<td>H</td>
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<td></td>
<td></td>
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- Molecule 23 is a protein called uL24.

<table>
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<tbody>
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- Molecule 24 is a protein called eL27.

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- Molecule 25 is a protein called uL15.
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- Molecule 26 is a protein called eL29.
- Molecule 27 is a protein called eL30.
- Molecule 28 is a protein called eL31.
- Molecule 29 is a protein called eL32.
- Molecule 30 is a protein called eL33.
- Molecule 31 is a protein called eL34.
- Molecule 32 is a protein called eL35.
- Molecule 33 is a protein called eL36.

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<th>Chain</th>
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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- Molecule 34 is a protein called eL37.

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<th>Atoms</th>
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</thead>
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- Molecule 35 is a protein called eL38.

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<td>Total C H N O S</td>
<td>1443 434 738 155 111 5</td>
<td>0 0</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>k</td>
<td>24</td>
<td>LYS</td>
<td>ASN</td>
<td>conflict</td>
<td>UNP G1U001</td>
</tr>
</tbody>
</table>

- Molecule 36 is a protein called eL39.

<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>l</td>
<td>50</td>
<td>Total C H N O S</td>
<td>927 286 480 96 64 1</td>
<td>0 0</td>
</tr>
</tbody>
</table>

- Molecule 37 is a protein called eL40.

<table>
<thead>
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<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>m</td>
<td>52</td>
<td>Total C H N O S</td>
<td>895 266 466 90 67 6</td>
<td>0 0</td>
</tr>
</tbody>
</table>

There are 9 discrepancies between the modelled and reference sequences:

<table>
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<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>m</td>
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<td>MET</td>
<td>-</td>
<td>initiating methionine</td>
<td>UNP A0A2K5PSA0</td>
</tr>
</tbody>
</table>

Continued on next page...
Continued from previous page...

<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>m</td>
<td>2</td>
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<td>-</td>
<td>expression tag</td>
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<tr>
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<td>-</td>
<td>expression tag</td>
<td>UNP A0A2K5PSA0</td>
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<tr>
<td>m</td>
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<td>PRO</td>
<td>-</td>
<td>expression tag</td>
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<tr>
<td>m</td>
<td>5</td>
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<td>-</td>
<td>expression tag</td>
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<tr>
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<td>6</td>
<td>SER</td>
<td>-</td>
<td>expression tag</td>
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- Molecule 38 is a protein called eL41.

<table>
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<tbody>
<tr>
<td>38</td>
<td>n</td>
<td>25</td>
<td>Total C</td>
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<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>H</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>N</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>O</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>S</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>528</td>
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</tr>
<tr>
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</tr>
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<td></td>
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<tr>
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</tbody>
</table>

- Molecule 39 is a protein called eL42.

<table>
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<th>Chain</th>
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<th>Atoms</th>
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</thead>
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<tr>
<td>39</td>
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<td>Total C</td>
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<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>H</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>N</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>O</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>S</td>
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<tr>
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- Molecule 40 is a protein called eL43.

<table>
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<th>Atoms</th>
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<tbody>
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<td>Total C</td>
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<td>0</td>
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<tr>
<td></td>
<td></td>
<td></td>
<td>H</td>
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<td>N</td>
<td></td>
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<td>S</td>
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<td>7</td>
<td></td>
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</tbody>
</table>

- Molecule 41 is a RNA chain called P-site tRNA.

<table>
<thead>
<tr>
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<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
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<tbody>
<tr>
<td>41</td>
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<td>76</td>
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<td></td>
<td></td>
<td>H</td>
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<td>N</td>
<td></td>
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<td></td>
<td>O</td>
<td></td>
<td></td>
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- Molecule 42 is a protein called eL28.

<table>
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<th>Atoms</th>
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<tbody>
<tr>
<td>42</td>
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<td>Total C</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>H</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>N</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>O</td>
<td></td>
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<td>6</td>
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</tbody>
</table>

- Molecule 43 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>43</td>
<td>u</td>
<td>120</td>
<td>Total C</td>
<td>H</td>
<td>N</td>
</tr>
<tr>
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<td></td>
<td></td>
<td>3854</td>
<td>1141</td>
<td>1296</td>
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</tbody>
</table>

There are 7 discrepancies between the modelled and reference sequences:

<table>
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<th>Chain</th>
<th>Residue</th>
<th>Modelled</th>
<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>u</td>
<td>2</td>
<td>U</td>
<td>N</td>
<td>conflict</td>
<td>GB X06789.1</td>
</tr>
<tr>
<td>u</td>
<td>36</td>
<td>C</td>
<td>N</td>
<td>conflict</td>
<td>GB X06789.1</td>
</tr>
<tr>
<td>u</td>
<td>102</td>
<td>U</td>
<td>N</td>
<td>conflict</td>
<td>GB X06789.1</td>
</tr>
<tr>
<td>u</td>
<td>112</td>
<td>U</td>
<td>N</td>
<td>conflict</td>
<td>GB X06789.1</td>
</tr>
<tr>
<td>u</td>
<td>114</td>
<td>U</td>
<td>N</td>
<td>conflict</td>
<td>GB X06789.1</td>
</tr>
<tr>
<td>u</td>
<td>119</td>
<td>U</td>
<td>C</td>
<td>conflict</td>
<td>GB X06789.1</td>
</tr>
<tr>
<td>u</td>
<td>120</td>
<td>U</td>
<td>N</td>
<td>conflict</td>
<td>GB X06789.1</td>
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</tbody>
</table>

- Molecule 44 is a RNA chain called 5.8S 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>44</td>
<td>v</td>
<td>156</td>
<td>Total C</td>
<td>H</td>
<td>N</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>4997</td>
<td>1480</td>
<td>1683</td>
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</table>

- Molecule 45 is a protein called uL3.

<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>45</td>
<td>w</td>
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<td>H</td>
<td>N</td>
</tr>
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<td></td>
<td></td>
<td></td>
<td>6482</td>
<td>2020</td>
<td>3310</td>
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There is a discrepancy between the modelled and reference sequences:

<table>
<thead>
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<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
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</thead>
<tbody>
<tr>
<td>w</td>
<td>1</td>
<td>MET</td>
<td>-</td>
<td>insertion</td>
<td>UNP G1TL06</td>
</tr>
</tbody>
</table>

- Molecule 46 is a protein called Nascent chain.

<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>46</td>
<td>B</td>
<td>70</td>
<td>Total C</td>
<td>H</td>
<td>N</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1054</td>
<td>349</td>
<td>528</td>
</tr>
</tbody>
</table>

- Molecule 47 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.
- Molecule 48 is a protein called Protein transport protein Sec61 subunit beta.

<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>2</td>
<td>29</td>
<td>Total C H N O S</td>
<td>475 157 245 36 35 2</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 49 is a protein called Protein transport protein Sec61 gamma.

<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>3</td>
<td>68</td>
<td>Total C H N O S</td>
<td>1120 355 577 94 89 5</td>
<td>0</td>
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</table>

- Molecule 50 is a protein called Coiled-coil domain containing 47.

<table>
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<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>4</td>
<td>342</td>
<td>Total C H N O S</td>
<td>5595 1738 2817 495 522 23</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 51 is a protein called PAT complex subunit Asterix.

<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>51</td>
<td>5</td>
<td>90</td>
<td>Total C H N O S</td>
<td>1421 456 710 115 128 12</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 52 is a protein called Nicalin.

<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>52</td>
<td>7</td>
<td>521</td>
<td>Total C H N O S</td>
<td>8260 2625 4121 726 771 17</td>
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</tbody>
</table>

- Molecule 53 is a protein called Transmembrane protein 147.

<table>
<thead>
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<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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</thead>
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<tr>
<td>53</td>
<td>6</td>
<td>224</td>
<td>Total C H N O S</td>
<td>3575 1190 1792 277 300 16</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 54 is a protein called Calcium load-activated calcium channel.

<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>54</td>
<td>8</td>
<td>177</td>
<td>Total C H N O S</td>
<td>2884 900 1478 242 252 12</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 55 is a RNA chain called 28S ribosomal RNA.
Molecule 56 is a protein called Obligate partner of TMCO1 insertase.

<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>55</td>
<td>K</td>
<td>3543</td>
<td>Total C, H, N, O, P</td>
<td>114330, 33833, 38358, 13910, 24686, 3543</td>
<td>0</td>
</tr>
</tbody>
</table>

Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

<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>56</td>
<td>9</td>
<td>109</td>
<td>Total C, H, N, O, S</td>
<td>1784, 610, 881, 134, 156, 3</td>
<td>0</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Mol</th>
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<th>Residues</th>
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<tr>
<td>57</td>
<td>C</td>
<td>1</td>
<td>Total Mg</td>
<td>1</td>
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<tr>
<td>57</td>
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</tr>
<tr>
<td>57</td>
<td>I</td>
<td>2</td>
<td>Total Mg</td>
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<td>J</td>
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<td>Total Mg</td>
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</tr>
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<td>57</td>
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<td>u</td>
<td>4</td>
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<td>4</td>
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</tr>
<tr>
<td>57</td>
<td>K</td>
<td>202</td>
<td>Total Mg</td>
<td>202</td>
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</table>

Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

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<thead>
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<th>Atoms</th>
<th>AltConf</th>
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<td>g</td>
<td>1</td>
<td>Total Zn</td>
<td>1</td>
</tr>
<tr>
<td>58</td>
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<tr>
<td>58</td>
<td>m</td>
<td>1</td>
<td>Total Zn</td>
<td>1</td>
</tr>
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</table>

Continued on next page...
Continued from previous page...

<table>
<thead>
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<th>Atoms</th>
<th>AltConf</th>
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</thead>
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<tr>
<td>58</td>
<td>o</td>
<td>1</td>
<td>Total Zn</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1 1 1</td>
<td></td>
</tr>
<tr>
<td>58</td>
<td>p</td>
<td>1</td>
<td>Total Zn</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1 1 1</td>
<td></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: uL2

Chain A:

• Molecule 2: uL4

Chain C:

• Molecule 3: uL18

Chain D:

• Molecule 4: eL6

Chain E:

• Molecule 5: uL30

Chain F:
- Molecule 6: eL8

Chain G:

- Molecule 7: uL6

Chain H:

- Molecule 8: uL16

Chain I:

- Molecule 9: uL5

Chain J:

- Molecule 10: eL13

Chain L:

- Molecule 11: eL14

Chain M:
• Molecule 12: eL15

Chain N: 98%

• Molecule 13: uL13

Chain O: 97%

• Molecule 14: uL22

Chain P: 82% 17%

• Molecule 15: eL18

Chain Q: 99%

• Molecule 16: eL19

Chain R: 79% 21%

• Molecule 17: eL20

Chain S: 99%

• Molecule 18: eL21

Chain T: 99%
- Molecule 19: eL22

Chain U:

- Molecule 20: uL14

Chain V:

- Molecule 21: eL24

Chain W:

- Molecule 22: eL23

Chain X:

- Molecule 23: uL24

Chain Y:

- Molecule 24: eL27

Chain Z:

- Molecule 25: uL15
Chain a:

- Molecule 26: eL29

Chain b:

- Molecule 27: eL30

Chain c:

- Molecule 28: eL31

Chain d:

- Molecule 29: eL32

Chain e:

- Molecule 30: eL33

Chain f:

- Molecule 31: eL34

Chain g:
- Molecule 32: eL35

Chain h:

- Molecule 33: eL36

Chain i:

- Molecule 34: eL37

Chain j:

- Molecule 35: eL38

Chain k:

- Molecule 36: eL39

Chain l:

- Molecule 37: eL40

Chain m:

- Molecule 38: eL41

Chain n:
There are no outlier residues recorded for this chain.

- Molecule 39: eL42
  Chain o:

- Molecule 40: eL43
  Chain p:

- Molecule 41: P-site tRNA
  Chain q:

- Molecule 42: eL28
  Chain r:

- Molecule 43: 5S ribosomal RNA
  Chain u:

- Molecule 44: 5.8S ribosomal RNA
  Chain v:

- Molecule 45: uL3
  Chain w:
• Molecule 46: Nascent chain

Chain B:

Molecule 49: Protein transport protein Sec61 subunit alpha isoform 1

Chain 1:

Molecule 48: Protein transport protein Sec61 subunit beta

Chain 2:

Molecule 49: Protein transport protein Sec61 gamma

Chain 3:

Molecule 50: Coiled-coil domain containing 47

Chain 4:
- Molecule 51: PAT complex subunit Asterix

Chain 5:

- Molecule 52: Nicalin

Chain 7:
- Molecule 53: Transmembrane protein 147

Chain 6:

- Molecule 54: Calcium load-activated calcium channel

Chain 8:

- Molecule 55: 28S ribosomal RNA

Chain K:
- Molecule 56: Obligate partner of TMCO1 insertase

Chain 9:
## 4 Experimental information

<table>
<thead>
<tr>
<th>Property</th>
<th>Value</th>
<th>Source</th>
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<tbody>
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<td>SINGLE PARTICLE</td>
<td>Depositor</td>
</tr>
<tr>
<td>Imposed symmetry</td>
<td>POINT, Not provided</td>
<td>Depositor</td>
</tr>
<tr>
<td>Number of particles used</td>
<td>136812</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>
<td>Depositor</td>
</tr>
<tr>
<td>Microscope</td>
<td>FEI TITAN KRIOS</td>
<td>Depositor</td>
</tr>
<tr>
<td>Voltage (kV)</td>
<td>300</td>
<td>Depositor</td>
</tr>
<tr>
<td>Electron dose ($e^{-}/Å^2$)</td>
<td>54</td>
<td>Depositor</td>
</tr>
<tr>
<td>Minimum defocus (nm)</td>
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<td>Depositor</td>
</tr>
<tr>
<td>Maximum defocus (nm)</td>
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</tr>
<tr>
<td>Magnification</td>
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<td></td>
</tr>
<tr>
<td>Image detector</td>
<td>GATAN K3 BIOQUANTUM (6k x 4k)</td>
<td>Depositor</td>
</tr>
<tr>
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<tr>
<td>Minimum map value</td>
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<tr>
<td>Map value standard deviation</td>
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<td>Recommended contour level</td>
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<tr>
<td>Map size (Å)</td>
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<td>wwPDB</td>
</tr>
<tr>
<td>Map dimensions</td>
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</tr>
<tr>
<td>Map angles (°)</td>
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</tr>
<tr>
<td>Pixel spacing (Å)</td>
<td>1.34, 1.34, 1.34</td>
<td>Depositor</td>
</tr>
</tbody>
</table>
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>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>RMSZ</td>
<td>#</td>
</tr>
<tr>
<td>1</td>
<td>A</td>
<td>0.25</td>
<td>0/1936</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>0.25</td>
<td>0/2937</td>
</tr>
<tr>
<td>3</td>
<td>D</td>
<td>0.26</td>
<td>0/2437</td>
</tr>
<tr>
<td>4</td>
<td>E</td>
<td>0.26</td>
<td>0/1914</td>
</tr>
<tr>
<td>5</td>
<td>F</td>
<td>0.25</td>
<td>0/1911</td>
</tr>
<tr>
<td>6</td>
<td>G</td>
<td>0.25</td>
<td>0/1910</td>
</tr>
<tr>
<td>7</td>
<td>H</td>
<td>0.25</td>
<td>0/1535</td>
</tr>
<tr>
<td>8</td>
<td>I</td>
<td>0.25</td>
<td>0/1702</td>
</tr>
<tr>
<td>9</td>
<td>J</td>
<td>0.26</td>
<td>0/1385</td>
</tr>
<tr>
<td>10</td>
<td>L</td>
<td>0.25</td>
<td>0/1733</td>
</tr>
<tr>
<td>11</td>
<td>M</td>
<td>0.26</td>
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<tr>
<td>12</td>
<td>N</td>
<td>0.25</td>
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<tr>
<td>13</td>
<td>O</td>
<td>0.26</td>
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<tr>
<td>14</td>
<td>P</td>
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<tr>
<td>15</td>
<td>Q</td>
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<td>0/1538</td>
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<td>16</td>
<td>R</td>
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<td>17</td>
<td>S</td>
<td>0.26</td>
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<td>18</td>
<td>T</td>
<td>0.25</td>
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<td>19</td>
<td>U</td>
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<td>20</td>
<td>V</td>
<td>0.26</td>
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<td>21</td>
<td>W</td>
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<td>29</td>
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<td>32</td>
<td>h</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>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>#Chirality outliers</th>
<th>#Planarity outliers</th>
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<tbody>
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There are no bond length outliers.

All (46) bond angle outliers are listed below:

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<th>Mol</th>
<th>Chain</th>
<th>Res</th>
<th>Type</th>
<th>Atoms</th>
<th>Z</th>
<th>Observed(°)</th>
<th>Ideal(°)</th>
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<tr>
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<td>G</td>
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</table>

Continued on next page...
Continued from previous page...

<table>
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<tr>
<th>Mol</th>
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<th>Type</th>
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<td>120.80</td>
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<td>G</td>
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<td>O4'-C1'-N9</td>
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<td>5.18</td>
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<td>N9-C4-C5</td>
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<td>A</td>
<td>O4'-C1'-N9</td>
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</table>
There are no chirality outliers.

All (1) planarity outliers are listed below:

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<th>Res</th>
<th>Type</th>
<th>Group</th>
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<td>234</td>
<td>G</td>
<td>Sidechain</td>
</tr>
</tbody>
</table>

### 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>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Analysed</th>
<th>Favoured</th>
<th>Allowed</th>
<th>Outliers</th>
<th>Percentiles</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
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<td>246/257 (96%)</td>
<td>220 (89%)</td>
<td>26 (11%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>360/413 (87%)</td>
<td>336 (93%)</td>
<td>24 (7%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>3</td>
<td>D</td>
<td>291/297 (98%)</td>
<td>270 (93%)</td>
<td>21 (7%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>4</td>
<td>E</td>
<td>227/291 (78%)</td>
<td>218 (96%)</td>
<td>8 (4%)</td>
<td>1 (0%)</td>
<td>34 71</td>
</tr>
<tr>
<td>5</td>
<td>F</td>
<td>223/247 (90%)</td>
<td>208 (93%)</td>
<td>15 (7%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>6</td>
<td>G</td>
<td>229/319 (72%)</td>
<td>214 (93%)</td>
<td>15 (7%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>7</td>
<td>H</td>
<td>188/192 (98%)</td>
<td>176 (94%)</td>
<td>12 (6%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>8</td>
<td>I</td>
<td>201/214 (94%)</td>
<td>182 (90%)</td>
<td>19 (10%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>9</td>
<td>J</td>
<td>168/178 (94%)</td>
<td>158 (94%)</td>
<td>10 (6%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>10</td>
<td>L</td>
<td>208/211 (99%)</td>
<td>194 (93%)</td>
<td>13 (6%)</td>
<td>1 (0%)</td>
<td>29 67</td>
</tr>
<tr>
<td>11</td>
<td>M</td>
<td>136/218 (62%)</td>
<td>126 (93%)</td>
<td>10 (7%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>12</td>
<td>N</td>
<td>200/204 (98%)</td>
<td>185 (92%)</td>
<td>14 (7%)</td>
<td>1 (0%)</td>
<td>29 67</td>
</tr>
<tr>
<td>13</td>
<td>O</td>
<td>197/203 (97%)</td>
<td>187 (95%)</td>
<td>10 (5%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>14</td>
<td>P</td>
<td>151/184 (82%)</td>
<td>143 (95%)</td>
<td>8 (5%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>15</td>
<td>Q</td>
<td>185/188 (98%)</td>
<td>171 (92%)</td>
<td>14 (8%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>16</td>
<td>R</td>
<td>153/196 (78%)</td>
<td>144 (94%)</td>
<td>9 (6%)</td>
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<td>100 100</td>
</tr>
</tbody>
</table>

Continued on next page...
### Mol Chain Analysed Favoured Allowed Outliers Percentiles

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<th>Mol</th>
<th>Chain</th>
<th>Analysed</th>
<th>Favoured</th>
<th>Allowed</th>
<th>Outliers</th>
<th>Percentiles</th>
</tr>
</thead>
<tbody>
<tr>
<td>17</td>
<td>S</td>
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<td>160 (92%)</td>
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</tr>
<tr>
<td>18</td>
<td>T</td>
<td>157/160 (98%)</td>
<td>139 (88%)</td>
<td>17 (11%)</td>
<td>1 (1%)</td>
<td>25 63</td>
</tr>
<tr>
<td>19</td>
<td>U</td>
<td>100/128 (78%)</td>
<td>90 (90%)</td>
<td>10 (10%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>20</td>
<td>V</td>
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<td>121 (94%)</td>
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</tr>
<tr>
<td>21</td>
<td>W</td>
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</tr>
<tr>
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</tr>
<tr>
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</tr>
<tr>
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<td>92 (96%)</td>
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<td>0</td>
<td>100 100</td>
</tr>
<tr>
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<td>94 (90%)</td>
<td>11 (10%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
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<td>e</td>
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<td>118 (94%)</td>
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<td>0</td>
<td>100 100</td>
</tr>
<tr>
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<td>f</td>
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<td>101 (94%)</td>
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<td>100 100</td>
</tr>
<tr>
<td>31</td>
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<td>106 (95%)</td>
<td>6  (5%)</td>
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<td>100 100</td>
</tr>
<tr>
<td>32</td>
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<td>120/123 (98%)</td>
<td>117 (98%)</td>
<td>3  (2%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
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<td>i</td>
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<td>95 (95%)</td>
<td>5  (5%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
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<td>81 (96%)</td>
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<td>0</td>
<td>100 100</td>
</tr>
<tr>
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<td>100 100</td>
</tr>
<tr>
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<td>39 (81%)</td>
<td>9  (19%)</td>
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<td>100 100</td>
</tr>
<tr>
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<td>m</td>
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<td>100 100</td>
</tr>
<tr>
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<td>100 100</td>
</tr>
<tr>
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<td>o</td>
<td>102/106 (96%)</td>
<td>93 (91%)</td>
<td>9  (9%)</td>
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<td>100 100</td>
</tr>
<tr>
<td>40</td>
<td>p</td>
<td>89/92 (97%)</td>
<td>81 (91%)</td>
<td>8  (9%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>42</td>
<td>r</td>
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</tr>
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<tr>
<td>46</td>
<td>B</td>
<td>68/273 (25%)</td>
<td>56 (82%)</td>
<td>11 (16%)</td>
<td>1 (2%)</td>
<td>10 45</td>
</tr>
<tr>
<td>47</td>
<td>l</td>
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<td>460 (99%)</td>
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<tr>
<td>48</td>
<td>2</td>
<td>27/96 (28%)</td>
<td>27 (100%)</td>
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<td>0</td>
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<tr>
<td>49</td>
<td>3</td>
<td>66/68 (97%)</td>
<td>66 (100%)</td>
<td>0</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>50</td>
<td>4</td>
<td>340/483 (70%)</td>
<td>336 (99%)</td>
<td>3  (1%)</td>
<td>1 (0%)</td>
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</table>

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Continued from previous page...

<table>
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<th>Favoured</th>
<th>Allowed</th>
<th>Outliers</th>
<th>Percentiles</th>
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<td>100 100</td>
</tr>
<tr>
<td>52</td>
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<td>519/563 (92%)</td>
<td>512 (99%)</td>
<td>7 (1%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>53</td>
<td>6</td>
<td>222/224 (99%)</td>
<td>222 (100%)</td>
<td>0</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>54</td>
<td>8</td>
<td>175/188 (93%)</td>
<td>174 (99%)</td>
<td>1 (1%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>56</td>
<td>9</td>
<td>107/129 (83%)</td>
<td>101 (94%)</td>
<td>6 (6%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>All</td>
<td>All</td>
<td>8428/9902 (85%)</td>
<td>7941 (94%)</td>
<td>481 (6%)</td>
<td>6 (0%)</td>
<td>54 84</td>
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</table>

All (6) Ramachandran outliers are listed below:

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<th>Type</th>
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<td>PRO</td>
</tr>
<tr>
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<td>L</td>
<td>64</td>
<td>VAL</td>
</tr>
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<td>4</td>
<td>347</td>
<td>GLY</td>
</tr>
<tr>
<td>18</td>
<td>T</td>
<td>82</td>
<td>GLY</td>
</tr>
<tr>
<td>46</td>
<td>B</td>
<td>242</td>
<td>PRO</td>
</tr>
<tr>
<td>4</td>
<td>E</td>
<td>228</td>
<td>PRO</td>
</tr>
</tbody>
</table>

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.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Analysed</th>
<th>Rotameric</th>
<th>Outliers</th>
<th>Percentiles</th>
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</thead>
<tbody>
<tr>
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<td>A</td>
<td>190/199 (96%)</td>
<td>189 (100%)</td>
<td>1 (0%)</td>
<td>88 93</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>302/337 (90%)</td>
<td>300 (99%)</td>
<td>2 (1%)</td>
<td>84 90</td>
</tr>
<tr>
<td>3</td>
<td>D</td>
<td>247/250 (99%)</td>
<td>247 (100%)</td>
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<td>88 93</td>
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<th>Outliers</th>
<th>Percentiles</th>
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<td>2</td>
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<td>4</td>
<td>306/435 (70%)</td>
<td>303 (99%)</td>
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<td>56</td>
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All (49) residues with a non-rotameric sidechain are listed below:

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Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

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5.3.3 RNA 📫
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<th>Pucker Outliers</th>
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</tr>
<tr>
<td>43</td>
<td>u</td>
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</tr>
<tr>
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<td>v</td>
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<td>37 (23%)</td>
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<td>818 (23%)</td>
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<td>All</td>
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All (885) RNA backbone outliers are listed below:

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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 225 ligands modelled in this entry, 225 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-26133. 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 0.5. 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 4244 nm$^3$; this corresponds to an approximate mass of 3834 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 0.258 Å\(^{-1}\)
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-26133 and PDB model 7TUT. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay

The images above show the 3D surface view of the map at the recommended contour level 0.5 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 (0.5).
9.4 Atom inclusion

At the recommended contour level, 91% of all backbone atoms, 92% 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 (0.5) and Q-score for the entire model and for each chain.

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