PDB ID : 6ZMO
EMDB ID : EMD-11299
Title : SARS-CoV-2 Nsp1 bound to the human LYAR-80S-eEF1a ribosome complex
Authors : Thoms, M.; Buschauer, R.; Ameismeier, M.; Denk, T.; Kratzat, H.; Mackens-Kiani, T.; Cheng, J.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2020-07-03
Resolution : 3.10 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 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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2
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 3.10 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>
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<tr>
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<th>Value</th>
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<td>Sidechain outliers</td>
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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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<td>LE</td>
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<td>8% 80% 18%</td>
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<tr>
<td>88</td>
<td>i</td>
<td>180</td>
<td>18% 82%</td>
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</table>
2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 230351 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 RNA chain called 28S ribosomal RNA.

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<th>Residues</th>
<th>Atoms</th>
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</table>

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

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</table>

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

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- Molecule 4 is a protein called 60S ribosomal protein L8.

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- Molecule 5 is a protein called 60S ribosomal protein L3.

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- Molecule 6 is a protein called 60S ribosomal protein L4.

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<th>Atoms</th>
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- Molecule 7 is a protein called 60S ribosomal protein L5.

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- Molecule 8 is a protein called 60S ribosomal protein L6.

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- Molecule 9 is a protein called 60S ribosomal protein L7.

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- Molecule 10 is a protein called 60S ribosomal protein L7a.

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- Molecule 11 is a protein called 60S ribosomal protein L9.

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- Molecule 12 is a protein called 60S ribosomal protein L10-like.

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- Molecule 13 is a protein called 60S ribosomal protein L11.

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- Molecule 14 is a protein called 60S ribosomal protein L13.
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- Molecule 15 is a protein called 60S ribosomal protein L14.

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- Molecule 16 is a protein called 60S ribosomal protein L15.

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<td>203</td>
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- Molecule 17 is a protein called 60S ribosomal protein L13a.

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- Molecule 18 is a protein called 60S ribosomal protein L17.

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- Molecule 19 is a protein called 60S ribosomal protein L18.

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- Molecule 20 is a protein called 60S ribosomal protein L19.

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<tr>
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<td>LR</td>
<td>187</td>
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<td>0</td>
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<td>1566 971 336 250 9</td>
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- Molecule 21 is a protein called 60S ribosomal protein L18a.
• Molecule 22 is a protein called 60S ribosomal protein L21.

• Molecule 23 is a protein called 60S ribosomal protein L22.

• Molecule 24 is a protein called 60S ribosomal protein L23.

• Molecule 25 is a protein called 60S ribosomal protein L24.

• Molecule 26 is a protein called 60S ribosomal protein L23a.

• Molecule 27 is a protein called 60S ribosomal protein L26.

• Molecule 28 is a protein called 60S ribosomal protein L27.
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<td>0</td>
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<td></td>
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<td>1107 714 208 182 3</td>
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- Molecule 29 is a protein called 60S ribosomal protein L27a.

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- Molecule 30 is a protein called 60S ribosomal protein L29.

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<td></td>
<td></td>
<td>876 546 189 137 4</td>
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- Molecule 31 is a protein called 60S ribosomal protein L30.

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<td>764 485 135 138 6</td>
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- Molecule 32 is a protein called 60S ribosomal protein L31.

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<td>0</td>
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<td>888 560 171 155 2</td>
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- Molecule 33 is a protein called 60S ribosomal protein L32.

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<td>1053 667 216 165 5</td>
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- Molecule 34 is a protein called 60S ribosomal protein L35a.

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<td>0</td>
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<td></td>
<td>876 555 174 144 3</td>
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- Molecule 35 is a protein called 60S ribosomal protein L34.
- Molecule 36 is a protein called 60S ribosomal protein L35.

<table>
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<td>1015 641 205 168 1</td>
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- Molecule 37 is a protein called 60S ribosomal protein L36.

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<td></td>
<td></td>
<td>832 521 177 129 5</td>
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- Molecule 38 is a protein called 60S ribosomal protein L37.

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<td></td>
<td>705 434 155 111 5</td>
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- Molecule 39 is a protein called 60S ribosomal protein L38.

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<td></td>
<td>569 366 103 99 1</td>
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- Molecule 40 is a protein called 60S ribosomal protein L39.

<table>
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<td>444 281 98 64 1</td>
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- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

<table>
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<td>429 266 90 67 6</td>
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- Molecule 42 is a protein called 60S ribosomal protein L41.
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- Molecule 43 is a protein called 60S ribosomal protein L36a.

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- Molecule 44 is a protein called 60S ribosomal protein L37a.

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- Molecule 45 is a protein called 60S ribosomal protein L28.

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- Molecule 46 is a protein called 60S acidic ribosomal protein P0.

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<td>1496 952 259 276 9</td>
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- Molecule 47 is a protein called 60S ribosomal protein L12.

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<th>Atoms</th>
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<tr>
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<td>1046 652 191 199 4</td>
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- Molecule 48 is a protein called 60S ribosomal protein L10a.

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<tr>
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<td></td>
<td></td>
<td>1741 1113 312 307 9</td>
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- Molecule 49 is a RNA chain called 18S ribosomal RNA.
- Molecule 50 is a protein called 40S ribosomal protein SA.

<table>
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- Molecule 51 is a protein called 40S ribosomal protein S3a.

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- Molecule 52 is a protein called 40S ribosomal protein S3.

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- Molecule 53 is a protein called 40S ribosomal protein S4, X isoform.

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- Molecule 54 is a protein called 40S ribosomal protein S5.

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<tr>
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- Molecule 55 is a protein called 40S ribosomal protein S7.

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- Molecule 56 is a protein called 40S ribosomal protein S8.
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- Molecule 57 is a protein called 40S ribosomal protein S10.
- Molecule 58 is a protein called 40S ribosomal protein S11.
- Molecule 59 is a protein called 40S ribosomal protein S15.
- Molecule 60 is a protein called 40S ribosomal protein S16.
- Molecule 61 is a protein called 40S ribosomal protein S17.
- Molecule 62 is a protein called 40S ribosomal protein S18.
- Molecule 63 is a protein called 40S ribosomal protein S19.
• Molecule 64 is a protein called 40S ribosomal protein S20.

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• Molecule 65 is a protein called 40S ribosomal protein S21.

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• Molecule 66 is a protein called 40S ribosomal protein S23.

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• Molecule 67 is a protein called 40S ribosomal protein S26.

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<td>C N O S</td>
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<td></td>
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<td>821 512 171 133</td>
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• Molecule 68 is a protein called 40S ribosomal protein S28.

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• Molecule 69 is a protein called 40S ribosomal protein S29.

<table>
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</tr>
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<td></td>
<td></td>
<td>C N O S</td>
<td></td>
<td></td>
</tr>
<tr>
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<td></td>
<td></td>
<td>459 286 94 74</td>
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• Molecule 70 is a protein called Receptor of activated protein C kinase 1.
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<tr>
<td>70</td>
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- Molecule 71 is a protein called 40S ribosomal protein S2.

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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>71</td>
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- Molecule 72 is a protein called 40S ribosomal protein S6.

<table>
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
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<tr>
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</table>

- Molecule 73 is a protein called 40S ribosomal protein S9.

<table>
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
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- Molecule 74 is a protein called 40S ribosomal protein S12.

<table>
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<th>Atoms</th>
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<tr>
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<td>940 590 164 177 9</td>
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- Molecule 75 is a protein called 40S ribosomal protein S13.

<table>
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- Molecule 76 is a protein called 40S ribosomal protein S14.

<table>
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<td>1049 642 204 197 6</td>
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- Molecule 77 is a protein called 40S ribosomal protein S15a.
<table>
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<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>77</td>
<td>SW</td>
<td>129</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1034 659 193 176 6</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 78 is a protein called 40S ribosomal protein S24.

<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>78</td>
<td>SY</td>
<td>131</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1065 673 209 178 5</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 79 is a protein called 40S ribosomal protein S25.

<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>79</td>
<td>SZ</td>
<td>75</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>598 382 111 104 1</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 80 is a protein called 40S ribosomal protein S27.

<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>80</td>
<td>Sb</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 81 is a protein called 40S ribosomal protein S30.

<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>81</td>
<td>Se</td>
<td>58</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>443 271 98 73 1</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 82 is a protein called Ubiquitin-40S ribosomal protein S27a.

<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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</thead>
<tbody>
<tr>
<td>82</td>
<td>Sf</td>
<td>67</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>548 346 102 93 7</td>
<td></td>
<td></td>
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- Molecule 83 is a protein called Proliferation-associated protein 2G4.

<table>
<thead>
<tr>
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<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>83</td>
<td>CA</td>
<td>354</td>
<td>Total C N O S</td>
<td>4</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>2764 1744 475 528 17</td>
<td></td>
<td></td>
</tr>
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</table>

- Molecule 84 is a RNA chain called tRNA.
<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
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<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>84</td>
<td>CB</td>
<td>87</td>
<td>Total C N O P</td>
<td>1858 828 332 611 87</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 85 is a RNA chain called tRNA.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>85</td>
<td>CC</td>
<td>75</td>
<td>Total C N O P</td>
<td>1589 710 279 525 75</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 86 is a protein called Elongation factor 1-alpha 1.

<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>86</td>
<td>CD</td>
<td>440</td>
<td>Total C N O S</td>
<td>3371 2143 581 630 17</td>
<td>0</td>
</tr>
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</table>

- Molecule 87 is a protein called Cell growth-regulating nucleolar protein.

<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>87</td>
<td>CE</td>
<td>72</td>
<td>Total C N O</td>
<td>603 395 105 103</td>
<td>0</td>
</tr>
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</table>

- Molecule 88 is a protein called Non-structural protein 1.

<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>88</td>
<td>i</td>
<td>33</td>
<td>Total C N O S</td>
<td>263 160 47 55 1</td>
<td>0</td>
</tr>
</tbody>
</table>

- Molecule 89 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>
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</thead>
<tbody>
<tr>
<td>89</td>
<td>L5</td>
<td>212</td>
<td>Total Mg</td>
<td>212</td>
</tr>
<tr>
<td>89</td>
<td>L7</td>
<td>3</td>
<td>Total Mg</td>
<td>3</td>
</tr>
<tr>
<td>89</td>
<td>L8</td>
<td>4</td>
<td>Total Mg</td>
<td>4</td>
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<tr>
<td>89</td>
<td>LA</td>
<td>1</td>
<td>Total Mg</td>
<td>1</td>
</tr>
<tr>
<td>89</td>
<td>LI</td>
<td>1</td>
<td>Total Mg</td>
<td>1</td>
</tr>
<tr>
<td>89</td>
<td>LP</td>
<td>1</td>
<td>Total Mg</td>
<td>1</td>
</tr>
</tbody>
</table>

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

<table>
<thead>
<tr>
<th>Mol</th>
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<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
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</thead>
<tbody>
<tr>
<td>89</td>
<td>LV</td>
<td>1</td>
<td>Total</td>
<td>Mg</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>89</td>
<td>Le</td>
<td>2</td>
<td>Total</td>
<td>Mg</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>2</td>
<td>2</td>
</tr>
<tr>
<td>89</td>
<td>Lg</td>
<td>1</td>
<td>Total</td>
<td>Mg</td>
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<tr>
<td></td>
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<td>1</td>
<td>1</td>
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<td>89</td>
<td>S2</td>
<td>28</td>
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<td>Mg</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>28</td>
<td>28</td>
</tr>
<tr>
<td>89</td>
<td>SG</td>
<td>1</td>
<td>Total</td>
<td>Mg</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>89</td>
<td>SO</td>
<td>1</td>
<td>Total</td>
<td>Mg</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
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<td>1</td>
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</table>

- Molecule 90 is ZINC ION (three-letter code: ZN) (formula: Zn).

<table>
<thead>
<tr>
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<th>Residues</th>
<th>Atoms</th>
<th>AltConf</th>
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<tbody>
<tr>
<td>90</td>
<td>Lg</td>
<td>1</td>
<td>Total</td>
<td>Zn</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>90</td>
<td>Lj</td>
<td>1</td>
<td>Total</td>
<td>Zn</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>90</td>
<td>Lm</td>
<td>1</td>
<td>Total</td>
<td>Zn</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>90</td>
<td>Lo</td>
<td>1</td>
<td>Total</td>
<td>Zn</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>90</td>
<td>Lp</td>
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<td>Total</td>
<td>Zn</td>
</tr>
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</tr>
<tr>
<td>90</td>
<td>Sa</td>
<td>1</td>
<td>Total</td>
<td>Zn</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>90</td>
<td>Sd</td>
<td>1</td>
<td>Total</td>
<td>Zn</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>90</td>
<td>Sf</td>
<td>1</td>
<td>Total</td>
<td>Zn</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1</td>
<td>1</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: 28S ribosomal RNA
Molecule 2: 5S ribosomal RNA

Chain L7:

Molecule 3: 5.8S ribosomal RNA

Chain L8:
• Molecule 4: 60S ribosomal protein L8

Chain LA:

• Molecule 5: 60S ribosomal protein L3

Chain LB:

• Molecule 6: 60S ribosomal protein L4

Chain LC:

• Molecule 7: 60S ribosomal protein L5

Chain LD:

• Molecule 8: 60S ribosomal protein L6

Chain LE:

• Molecule 9: 60S ribosomal protein L7

Chain LF:
• Molecule 10: 60S ribosomal protein L7a

Chain LG:

• Molecule 11: 60S ribosomal protein L9

Chain LH:

• Molecule 12: 60S ribosomal protein L10-like

Chain LI:

• Molecule 13: 60S ribosomal protein L11

Chain LJ:

• Molecule 14: 60S ribosomal protein L13

Chain LL:

• Molecule 15: 60S ribosomal protein L14

Chain LM:
• Molecule 16: 60S ribosomal protein L15

Chain LN:

• Molecule 17: 60S ribosomal protein L13a

Chain LO:

• Molecule 18: 60S ribosomal protein L17

Chain LP:

• Molecule 19: 60S ribosomal protein L18

Chain LQ:

• Molecule 20: 60S ribosomal protein L19

Chain LR:

• Molecule 21: 60S ribosomal protein L18a

Chain LS:

• Molecule 22: 60S ribosomal protein L21
Chain LT:

- Molecule 23: 60S ribosomal protein L22

Chain LU:

- Molecule 24: 60S ribosomal protein L23

Chain LV:

- Molecule 25: 60S ribosomal protein L24

Chain LW:

- Molecule 26: 60S ribosomal protein L23a

Chain LX:

- Molecule 27: 60S ribosomal protein L26

Chain LZ:

- Molecule 28: 60S ribosomal protein L27
• Molecule 29: 60S ribosomal protein L27a

Chain La:

• Molecule 30: 60S ribosomal protein L29

Chain Lb:

• Molecule 31: 60S ribosomal protein L30

Chain Lc:

• Molecule 32: 60S ribosomal protein L31

Chain Ld:

• Molecule 33: 60S ribosomal protein L32

Chain Le:

• Molecule 34: 60S ribosomal protein L35a

Chain Lf:
- Molecule 35: 60S ribosomal protein L34

Chain Lg:

- Molecule 36: 60S ribosomal protein L35

Chain Lh:

- Molecule 37: 60S ribosomal protein L36

Chain Li:

- Molecule 38: 60S ribosomal protein L37

Chain Lj:

- Molecule 39: 60S ribosomal protein L38

Chain Lk:

- Molecule 40: 60S ribosomal protein L39

Chain Li:

- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm:
- Molecule 42: 60S ribosomal protein L41

Chain Ln:

- Molecule 43: 60S ribosomal protein L36a

Chain Lo:

- Molecule 44: 60S ribosomal protein L37a

Chain Lp:

- Molecule 45: 60S ribosomal protein L28

Chain Lr:

- Molecule 46: 60S acidic ribosomal protein P0

Chain Ls:
- Molecule 47: 60S ribosomal protein L12

Chain Lt:

- Molecule 48: 60S ribosomal protein L10a

Chain Lz:

- Molecule 49: 18S ribosomal RNA

Chain S2:
• Molecule 50: 40S ribosomal protein SA

Chain SA:

• Molecule 51: 40S ribosomal protein S3a

Chain SB:

• Molecule 52: 40S ribosomal protein S3

Chain SD:

• Molecule 53: 40S ribosomal protein S4, X isoform

Chain SE:

• Molecule 54: 40S ribosomal protein S5

Chain SF:

• Molecule 55: 40S ribosomal protein S7

Chain SH:
• Molecule 56: 40S ribosomal protein S8

Chain SI:

• Molecule 57: 40S ribosomal protein S10

Chain SK:

• Molecule 58: 40S ribosomal protein S11

Chain SL:

• Molecule 59: 40S ribosomal protein S15

Chain SP:

• Molecule 60: 40S ribosomal protein S16

Chain SQ:

• Molecule 61: 40S ribosomal protein S17

Chain SR:

• Molecule 62: 40S ribosomal protein S18
Chain SS:

- Molecule 63: 40S ribosomal protein S19

Chain ST:

- Molecule 64: 40S ribosomal protein S20

Chain SU:

- Molecule 65: 40S ribosomal protein S21

Chain SV:

- Molecule 66: 40S ribosomal protein S23

Chain SX:

- Molecule 67: 40S ribosomal protein S26

Chain Sa:

- Molecule 68: 40S ribosomal protein S28
• Molecule 69: 40S ribosomal protein S29

Chain Sd:

• Molecule 70: Receptor of activated protein C kinase 1

Chain Sg:

• Molecule 71: 40S ribosomal protein S2

Chain SC:

• Molecule 72: 40S ribosomal protein S6

Chain SG:

• Molecule 73: 40S ribosomal protein S9

Chain SJ:

• Molecule 74: 40S ribosomal protein S12

Chain SM:
- Molecule 75: 40S ribosomal protein S13

Chain SN:

- Molecule 76: 40S ribosomal protein S14

Chain SO:

- Molecule 77: 40S ribosomal protein S15a

Chain SW:

- Molecule 78: 40S ribosomal protein S24

Chain SY:

- Molecule 79: 40S ribosomal protein S25

Chain SZ:

- Molecule 80: 40S ribosomal protein S27

Chain Sb:
• Molecule 81: 40S ribosomal protein S30

Chain Se:

• Molecule 82: Ubiquitin-40S ribosomal protein S27a

Chain Sf:

• Molecule 83: Proliferation-associated protein 2G4

Chain CA:
• Molecule 84: tRNA

Chain CB:

• Molecule 85: tRNA

Chain CC:

• Molecule 86: Elongation factor 1-alpha 1

Chain CD:

• Molecule 87: Cell growth-regulating nucleolar protein

Chain CE:
• Molecule 88: Non-structural protein 1

Chain i:

[Visual representation of protein chain with percentage distribution]
### 4 Experimental information

<table>
<thead>
<tr>
<th>Property</th>
<th>Value</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>EM reconstruction method</td>
<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>11417</td>
<td>Depositor</td>
</tr>
<tr>
<td>Resolution determination method</td>
<td>FSC 0.143 CUT-OFF</td>
<td>Depositor</td>
</tr>
<tr>
<td>CTF correction method</td>
<td>PHASE FLIPPING AND AMPLITUDE CORRECTION</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>44.8</td>
<td>Depositor</td>
</tr>
<tr>
<td>Minimum defocus (nm)</td>
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<td>Depositor</td>
</tr>
<tr>
<td>Magnification</td>
<td>Not provided</td>
<td>Depositor</td>
</tr>
<tr>
<td>Image detector</td>
<td>GATAN K2 SUMMIT (4k x 4k)</td>
<td>Depositor</td>
</tr>
<tr>
<td>Maximum map value</td>
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<td>Depositor</td>
</tr>
<tr>
<td>Minimum map value</td>
<td>-0.150</td>
<td>Depositor</td>
</tr>
<tr>
<td>Average map value</td>
<td>0.003</td>
<td>Depositor</td>
</tr>
<tr>
<td>Map value standard deviation</td>
<td>0.018</td>
<td>Depositor</td>
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<tr>
<td>Recommended contour level</td>
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<td>Depositor</td>
</tr>
<tr>
<td>Map size (Å)</td>
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<td>wwPDB</td>
</tr>
<tr>
<td>Map dimensions</td>
<td>400, 400, 400</td>
<td>wwPDB</td>
</tr>
<tr>
<td>Map angles (°)</td>
<td>90.0, 90.0, 90.0</td>
<td>wwPDB</td>
</tr>
<tr>
<td>Pixel spacing (Å)</td>
<td>1.059, 1.059, 1.059</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: MG, ZN

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></th>
<th>Bond angles</th>
<th></th>
</tr>
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<tbody>
<tr>
<td></td>
<td></td>
<td>RMSZ</td>
<td>#</td>
<td>Z</td>
<td>&gt;5</td>
</tr>
<tr>
<td>1</td>
<td>L5</td>
<td>1.11</td>
<td>11/89595 (0.0%)</td>
<td>1.21</td>
<td>735/139686 (0.5%)</td>
</tr>
<tr>
<td>2</td>
<td>L7</td>
<td>0.97</td>
<td>0/2861</td>
<td>1.14</td>
<td>16/4459 (0.4%)</td>
</tr>
<tr>
<td>3</td>
<td>L8</td>
<td>1.10</td>
<td>0/3701</td>
<td>1.12</td>
<td>13/5766 (0.2%)</td>
</tr>
<tr>
<td>4</td>
<td>LA</td>
<td>0.63</td>
<td>0/1936</td>
<td>0.71</td>
<td>2/2596 (0.1%)</td>
</tr>
<tr>
<td>5</td>
<td>LB</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.

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

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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.

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All (32) 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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<th>Rotameric</th>
<th>Outliers</th>
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<tr>
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<td>244 (99%)</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 264 ligands modelled in this entry, 264 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

There are no chain breaks in this entry.
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-11299. 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

![Image of largest variance slices with X Index: 178, Y Index: 194, Z Index: 224]

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

### 6.4 Orthogonal standard-deviation projections (False-color)

#### 6.4.1 Primary map

![Image of map standard deviation projections with false color in X, Y, Z]

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.
6.5 Orthogonal surface views

6.5.1 Primary map

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.6 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 2071 nm³; this corresponds to an approximate mass of 1871 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

![Rotationally averaged power spectrum](image)

*Reported resolution corresponds to spatial frequency of 0.323 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 0.323 Å\(^{-1}\)*
### 8.2 Resolution estimates

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<th>Estimation criterion (FSC cut-off)</th>
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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-11299 and PDB model 6ZMO. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay

The images above show the 3D surface view of the map at the recommended contour level 0.05 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 (0.05).
9.4 Atom inclusion

At the recommended contour level, 89% of all backbone atoms, 88% 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 (0.05) and Q-score for the entire model and for each chain.

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