Full wwPDB X-ray Structure Validation Report

May 29, 2020 – 08:46 am BST

PDB ID : 5UAQ
Title : Escherichia coli RNA polymerase RpoB H526Y mutant
Authors : Molotsov, V.; Scharf, N.T.; Stefan, M.A.; Garcia, G.A.; Murakami, K.S.
Deposited on : 2016-12-19
Resolution : 3.60 Å (reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp
with specific help available everywhere you see the symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11
## 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

**X-RAY DIFFRACTION**

The reported resolution of this entry is 3.60 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>Similar resolution (#Entries, resolution range(Å))</th>
</tr>
</thead>
<tbody>
<tr>
<td>( R_{\text{free}} )</td>
<td>130704</td>
<td>1257 (3.70-3.50)</td>
</tr>
<tr>
<td>Clashscore</td>
<td>141614</td>
<td>1353 (3.70-3.50)</td>
</tr>
<tr>
<td>Ramachandran outliers</td>
<td>138981</td>
<td>1307 (3.70-3.50)</td>
</tr>
<tr>
<td>Sidechain outliers</td>
<td>138945</td>
<td>1307 (3.70-3.50)</td>
</tr>
<tr>
<td>RSRZ outliers</td>
<td>127900</td>
<td>1161 (3.70-3.50)</td>
</tr>
</tbody>
</table>

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower 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 electron density. The numeric value is given above the bar.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Length</th>
<th>Quality of chain</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>329</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>B</td>
<td>329</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>G</td>
<td>329</td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>H</td>
<td>329</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>1342</td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>I</td>
<td>1342</td>
<td></td>
</tr>
</tbody>
</table>

*Continued on next page...*
<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Length</th>
<th>Quality of chain</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>D</td>
<td>1407</td>
<td><img src="image" alt="Quality Bar" /></td>
</tr>
<tr>
<td>3</td>
<td>J</td>
<td>1407</td>
<td><img src="image" alt="Quality Bar" /></td>
</tr>
<tr>
<td>4</td>
<td>E</td>
<td>91</td>
<td><img src="image" alt="Quality Bar" /></td>
</tr>
<tr>
<td>4</td>
<td>K</td>
<td>91</td>
<td><img src="image" alt="Quality Bar" /></td>
</tr>
<tr>
<td>5</td>
<td>F</td>
<td>613</td>
<td><img src="image" alt="Quality Bar" /></td>
</tr>
<tr>
<td>5</td>
<td>L</td>
<td>613</td>
<td><img src="image" alt="Quality Bar" /></td>
</tr>
</tbody>
</table>
2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 55699 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 DNA-directed RNA polymerase subunit alpha.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>ZeroOcc</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>309</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>2403 1505 421 469 8</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>B</td>
<td>217</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1672 1044 295 327 6</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>G</td>
<td>224</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1730 1076 308 340 6</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1</td>
<td>H</td>
<td>217</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>1667 1041 293 327 6</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>ZeroOcc</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>C</td>
<td>1340</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>10572 6634 1839 2056 43</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>I</td>
<td>1340</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>10568 6632 1838 2055 43</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

There are 2 discrepancies between the modelled and reference sequences:

<table>
<thead>
<tr>
<th>Chain</th>
<th>Residue</th>
<th>Modelled</th>
<th>Actual</th>
<th>Comment</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>C</td>
<td>526</td>
<td>TYR</td>
<td>HIS</td>
<td>engineered mutation</td>
<td>UNP P0A8V2</td>
</tr>
<tr>
<td>I</td>
<td>526</td>
<td>TYR</td>
<td>HIS</td>
<td>engineered mutation</td>
<td>UNP P0A8V2</td>
</tr>
</tbody>
</table>

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta’.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>ZeroOcc</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>D</td>
<td>1166</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>9107 5723 1634 1704 46</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>J</td>
<td>1155</td>
<td>Total C N O S</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>9029 5676 1620 1687 46</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.
• Molecule 5 is a protein called RNA polymerase sigma factor RpoD.

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>ZeroOcc</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>4</td>
<td>E</td>
<td>89</td>
<td>Total C</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>N</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>O</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>S</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

• Molecule 6 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>ZeroOcc</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>5</td>
<td>F</td>
<td>467</td>
<td>Total C</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>N</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>O</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>S</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

• Molecule 7 is ZINC ION (three-letter code: ZN) (formula: Zn).

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Residues</th>
<th>Atoms</th>
<th>ZeroOcc</th>
<th>AltConf</th>
<th>Trace</th>
</tr>
</thead>
<tbody>
<tr>
<td>7</td>
<td>J</td>
<td>2</td>
<td>Total Zn</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>7</td>
<td>D</td>
<td>2</td>
<td>Total Zn</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
3  Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density (RSRZ $> 2$). 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: DNA-directed RNA polymerase subunit alpha**

Chain A:

Chain B:
• Molecule 1: DNA-directed RNA polymerase subunit alpha

Chain G:

• Molecule 1: DNA-directed RNA polymerase subunit alpha

Chain H:

• Molecule 2: DNA-directed RNA polymerase subunit beta

Chain C:
• Molecule 2: DNA-directed RNA polymerase subunit beta
Molecule 3: DNA-directed RNA polymerase subunit beta’

Chain D:
Molecule 3: DNA-directed RNA polymerase subunit beta’

Chain J:
[The image contains a detailed diagram of a protein structure, with labeled amino acid positions and annotations for validation purposes.]
• Molecule 4: DNA-directed RNA polymerase subunit omega

Chain E:

- 64%
- 31%

• Molecule 4: DNA-directed RNA polymerase subunit omega

Chain K:

- 53%
- 33%
- 13%

• Molecule 5: RNA polymerase sigma factor RpoD

Chain F:

- 40%
- 31%
- 5%
- 24%
- **Molecule 5**: RNA polymerase sigma factor RpoD

<table>
<thead>
<tr>
<th>Chain L:</th>
</tr>
</thead>
<tbody>
<tr>
<td>36%</td>
</tr>
</tbody>
</table>
## 4 Data and refinement statistics

<table>
<thead>
<tr>
<th>Property</th>
<th>Value</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td>Space group</td>
<td>P 2 1 2 1</td>
<td>Depositor</td>
</tr>
<tr>
<td>Cell constants</td>
<td>a, b, c, α, β, γ</td>
<td>Depositor</td>
</tr>
<tr>
<td>Resolution (Å)</td>
<td>29.90 - 3.60</td>
<td>Depositor</td>
</tr>
<tr>
<td>% Data completeness</td>
<td>93.7 (29.90-3.60)</td>
<td>Depositor</td>
</tr>
<tr>
<td>Refinement program</td>
<td>PHENIX (1.10.1_2155: ???)</td>
<td>Depositor</td>
</tr>
<tr>
<td>Rmerge</td>
<td>(Not available)</td>
<td>Depositor</td>
</tr>
<tr>
<td>Rsym</td>
<td>(Not available)</td>
<td>Depositor</td>
</tr>
<tr>
<td>&lt; I/σ(I) &gt; ^1</td>
<td>2.01 (at 3.56Å)</td>
<td>Xtriage</td>
</tr>
<tr>
<td>Wilson B-factor (Å^2)</td>
<td>142.2</td>
<td>Xtriage</td>
</tr>
<tr>
<td>Anisotropy</td>
<td>0.225</td>
<td>Xtriage</td>
</tr>
<tr>
<td>Bulk solvent κ_{sol} (e/Å^3), B_{sol} (Å^2)</td>
<td>0.27, 91.1</td>
<td>EDS</td>
</tr>
<tr>
<td>L-test for twinning^2</td>
<td>&lt;</td>
<td>L</td>
</tr>
<tr>
<td>Estimated twinning fraction</td>
<td>No twinning to report.</td>
<td>Xtriage</td>
</tr>
<tr>
<td>F_α,F_ε correlation</td>
<td>0.94</td>
<td>EDS</td>
</tr>
<tr>
<td>Total number of atoms</td>
<td>55699</td>
<td>wwPDB-VP</td>
</tr>
<tr>
<td>Average B, all atoms (Å^2)</td>
<td>157.0</td>
<td>wwPDB-VP</td>
</tr>
</tbody>
</table>

Xtriage’s analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.74% of the height of the origin peak. No significant pseudotranslation is detected.*

---

^1 Intensities estimated from amplitudes.

^2 Theoretical values of < |L| >, < L^2 > for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.
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>0.84</td>
<td>4/2435 (0.2%)</td>
</tr>
<tr>
<td>1</td>
<td>B</td>
<td>0.75</td>
<td>1/1692 (0.1%)</td>
</tr>
<tr>
<td>1</td>
<td>G</td>
<td>0.58</td>
<td>0/1751</td>
</tr>
<tr>
<td>1</td>
<td>H</td>
<td>0.59</td>
<td>0/1686</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>1.17</td>
<td>37/10741 (0.3%)</td>
</tr>
<tr>
<td>2</td>
<td>I</td>
<td>0.80</td>
<td>7/10737 (0.1%)</td>
</tr>
<tr>
<td>3</td>
<td>D</td>
<td>1.21</td>
<td>60/9246 (0.6%)</td>
</tr>
<tr>
<td>3</td>
<td>J</td>
<td>1.02</td>
<td>27/9168 (0.3%)</td>
</tr>
<tr>
<td>4</td>
<td>E</td>
<td>0.65</td>
<td>0/693</td>
</tr>
<tr>
<td>4</td>
<td>K</td>
<td>0.38</td>
<td>0/629</td>
</tr>
<tr>
<td>5</td>
<td>F</td>
<td>0.82</td>
<td>2/3857 (0.1%)</td>
</tr>
<tr>
<td>5</td>
<td>L</td>
<td>0.77</td>
<td>3/3872 (0.1%)</td>
</tr>
<tr>
<td>All</td>
<td>All</td>
<td>0.98</td>
<td>141/56507 (0.2%)</td>
</tr>
</tbody>
</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>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>1</td>
<td>G</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>0</td>
<td>11</td>
</tr>
<tr>
<td>2</td>
<td>I</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>3</td>
<td>D</td>
<td>0</td>
<td>12</td>
</tr>
<tr>
<td>3</td>
<td>J</td>
<td>0</td>
<td>9</td>
</tr>
<tr>
<td>5</td>
<td>F</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>5</td>
<td>L</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>All</td>
<td>All</td>
<td>0</td>
<td>39</td>
</tr>
</tbody>
</table>

All (141) bond length outliers are listed below:
<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Res</th>
<th>Type</th>
<th>Atoms</th>
<th>Z</th>
<th>Observed(Å)</th>
<th>Ideal(Å)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2</td>
<td>C</td>
<td>811</td>
<td>ASN</td>
<td>CB-CG</td>
<td>-9.14</td>
<td>1.30</td>
<td>1.51</td>
</tr>
<tr>
<td>1</td>
<td>A</td>
<td>131</td>
<td>CYS</td>
<td>CB-SG</td>
<td>-8.93</td>
<td>1.67</td>
<td>1.82</td>
</tr>
<tr>
<td>3</td>
<td>J</td>
<td>145</td>
<td>VAL</td>
<td>CB-CG2</td>
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There are no chirality outliers.

All (39) planarity outliers are listed below:

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Continued on next page...
5.2 Too-close contacts

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

<table>
<thead>
<tr>
<th>Mol</th>
<th>Chain</th>
<th>Non-H</th>
<th>H(model)</th>
<th>H(added)</th>
<th>Clashes</th>
<th>Symm-Clashes</th>
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</table>
The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 28.

All (3190) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.
<table>
<thead>
<tr>
<th>Atom-1</th>
<th>Atom-2</th>
<th>Interatomic distance (Å)</th>
<th>Clash overlap (Å)</th>
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<td>3:D:1304:ARG:HE</td>
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<td>2:I:1188:ASP:HB2</td>
<td>1.51</td>
<td>0.92</td>
</tr>
<tr>
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<td>2:I:916:SER:HB3</td>
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1:G:92:VAL:O | 1:G:148:ARG:NH2 | 2.25 | 0.68
2:I:26:Tyr:CE2 | 2:I:28:LEU:HB2 | 2.28 | 0.68
1:A:31:LEU:HB2 | 1:A:199:ASP:O | 1.94 | 0.68
1:B:98:VAL:HG11 | 1:B:121:VAL:HG22 | 1.74 | 0.68
3:D:293:ARG:NH1 | 5:F:104:GLU:OE2 | 2.27 | 0.68
3:D:674:THR:OG1 | 3:D:677:GLU:HB2 | 1.94 | 0.68
5:F:247:GLU:HA | 5:F:250:LEU:HD12 | 1.74 | 0.68
2:C:578:TYR:HB3 | 2:C:590:PRO:HG2 | 1.76 | 0.68
2:C:618:GLN:HG3 | 2:C:619:ALA:N | 2.05 | 0.68
3:I:1344:LEU:HB3 | 3:I:1350:ASN:ND2 | 2.08 | 0.68
5:L:101:TYR:O | 5:L:104:GLU:N | 2.26 | 0.68
5:L:281:ARG:O | 5:L:285:ARG:HG3 | 1.93 | 0.68
2:C:656:SER:OG | 2:C:657:THR:N | 2.22 | 0.68
2:C:886:LYS:HE3 | 2:C:916:SER:HB3 | 1.75 | 0.68
3:D:74:LYS:HD2 | 3:D:87:LYS:HD3 | 1.75 | 0.68
3:D:817:HIS:CE1 | 3:D:860:ARG:NE | 2.61 | 0.68
3:I:1147:GLY:O | 3:I:1140:ARG:HB3 | 1.93 | 0.68
1:B:48:LEU:HD12 | 1:B:183:ILE:HD11 | 1.73 | 0.68
3:D:1266:ILE:HD12 | 3:D:1273:ASP:O | 1.94 | 0.68
3:D:1295:ASN:CB | 3:D:1298:VAL:HB | 2.24 | 0.68
2:C:563:THR:OG1 | 2:C:564:PRO:HD2 | 1.93 | 0.68
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3:I:98:ARG:HB3 | 3:I:248:ASP:OD2 | 1.94 | 0.68
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1:A:227:GLN:NE2 | 1:B:9:LEU:O | 2.27 | 0.68
2:C:296:VAL:HB | 2:C:336:LEU:HD12 | 1.75 | 0.68
3:D:709:ARG:O | 3:D:711:GLY:N | 2.27 | 0.68
5:F:306:PHE:HE1 | 5:F:315:TRP:CD2 | 2.11 | 0.68
1:G:79:LEU:HD23 | 1:G:79:LEU:H | 1.59 | 0.68
2:I:890:LYS:HE2 | 2:I:891:GLY:H | 1.58 | 0.68
1:B:29:GLU:HB3 | 1:B:200:LYS:HG3 | 1.74 | 0.68
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2:C:363:LEU:HB3 | 2:C:381:ALA:HB1 | 1.74 | 0.68
3:D:824:PRO:HD3 | 3:D:835:LEU:HB2 | 1.74 | 0.68
3:I:817:HIS:CE1 | 3:I:860:ARG:HE | 2.12 | 0.68
4:K:70:GLN:NE2 | 4:K:74:GLU:OE2 | 2.16 | 0.68

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3:D:1149:ARG:NH2 | 3:D:1153:PRO:HG2 | 2.16 | 0.61
2:1:1246:ARG:HG2 | 2:1:1247:SER:N | 2.15 | 0.61
3:J:30:ILE:HG23 | 3:J:243:PRO:HG3 | 1.82 | 0.61
3:D:316:ILE:HA | 3:D:333:PRO:HA | 1.82 | 0.61
1:A:218:ARG:HG3 | 1:B:231:PHE:O | 2.01 | 0.61
3:D:367:GLY:HA3 | 3:D:448:GLN:HB2 | 1.83 | 0.61
3:J:115:TRP:CE2 | 3:J:1329:THR:HG23 | 2.36 | 0.61
2:C:601:ASP:N | 2:C:601:ASP:OD1 | 2.32 | 0.61
3:J:647:PRO:CG | 3:J:697:MET:HB3 | 2.30 | 0.61
2:C:488:MET:O | 2:C:490:GLN:N | 2.32 | 0.61
1:G:152:TYR:HD1 | 1:G:176:CYS:HB3 | 1.65 | 0.61
2:I:466:VAL:O | 2:I:469:VAL:HG22 | 2.01 | 0.61
5:L:426:LYS:HE2 | 5:L:428:SER:OG | 2.01 | 0.61
5:L:493:LYS:HA | 5:L:496:LYS:HE2 | 1.81 | 0.61
1:B:153:VAL:HB | 1:B:175:ALA:HB3 | 1.82 | 0.60
2:C:316:GLU:H | 2:C:316:GLU:CD | 2.04 | 0.60
2:C:667:LEU:HD21 | 2:C:704:MET:HB2 | 1.82 | 0.60
3:D:762:ASN:OD1 | 3:D:764:ARG:N | 2.33 | 0.60
3:J:361:LEU:HD13 | 3:J:366:CYT:HA | 1.82 | 0.60
1:H:33:ARG:HD2 | 2:I:1081:PRO:HG3 | 1.84 | 0.60
2:I:848:GLU:OE1 | 2:I:886:LYS:NZ | 2.34 | 0.60
3:D:833:GLU:OE2 | 3:D:1247:LYS:NZ | 2.35 | 0.60
2:I:1297:ASP:OD1 | 2:I:1300:GLY:N | 2.25 | 0.60
2:I:346:TYR:OH | 2:I:437:ASN:OD1 | 2.02 | 0.60
2:I:697:LYS:HA | 2:I:795:ALA:HB2 | 1.83 | 0.60
3:J:418:GLU:H | 4:K:45:LYS:HZ2 | 1.47 | 0.60
2:C:156:PHE:CE2 | 2:C:158:ASP:HB2 | 2.37 | 0.60
2:C:510:GLN:OE1 | 2:C:534:GLY:HA2 | 2.00 | 0.60
3:D:1280:VAL:CG1 | 3:D:1304:ARG:HH21 | 2.04 | 0.60
3:D:147:ILE:HG13 | 3:D:147:ILE:O | 2.01 | 0.60
2:C:1246:ARG:NH2 | 2:C:1248:ASP:OD1 | 2.34 | 0.60
3:D:514:THR:OG1 | 3:D:514:THR:O | 2.19 | 0.60
3:J:697:MET:SD | 3:J:741:ALA:HB3 | 2.41 | 0.60
5:L:226:ALA:O | 5:L:229:VAL:HG22 | 2.01 | 0.60
2:C:256:GLU:HB3 | 2:C:261:VAL:HG13 | 1.82 | 0.60
2:C:268:ARG:NH2 | 2:C:270:THR:HG21 | 2.17 | 0.60

Continued on next page...
### Atom-1  |  Atom-2  |  Interatomic distance (Å)  |  Clash overlap (Å)
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2:C:138:ILE:HG22  |  2:C:139:ASN:N  |  2.16  |  0.60
3:D:342:LEU:HD11  |  3:D:1324:SER:HB3  |  1.82  |  0.60
3:D:375:GLU:OE2  |  3:D:378:LYS:HD2  |  2.02  |  0.60
2:I:1247:SER:HB3  |  3:J:375:GLU:O  |  2.01  |  0.60
3:J:536:LEU:HD13  |  3:J:541:LEU:HB2  |  1.83  |  0.60
2:I:122:GLU:OE2  |  3:J:537:Tyr:OH  |  2.19  |  0.60
3:J:988:CYS:SG  |  3:J:889:ASP:N  |  2.75  |  0.60
3:D:115:TRP:CE2  |  3:D:1329:THR:HG23  |  2.37  |  0.60
2:I:678:ARG:HG3  |  2:I:1108:ASN:HD2  |  1.66  |  0.60
2:I:1281:TYR:HE1  |  3:J:484:MET:HE3  |  1.66  |  0.60
2:I:42:ASP:OD2  |  2:I:46:GLN:HB3  |  2.02  |  0.60
2:I:519:ASN:HD21  |  2:I:796:LEU:HD23  |  1.67  |  0.60
5:L:299:LYS:HA  |  5:L:302:PHE:HB3  |  1.83  |  0.60
1:A:249:PHE:HB2  |  1:A:253:LEU:HD12  |  1.82  |  0.60
2:C:344:GLY:HA3  |  2:C:346:Tyr:CZ  |  2.37  |  0.60
2:C:701:GLY:O  |  2:C:1184:THR:N  |  2.25  |  0.60
3:D:810:THR:CG2  |  3:D:893:GLY:HA3  |  2.32  |  0.60
2:C:122:VAL:HG23  |  5:F:472:GLN:HG3  |  1.83  |  0.60
1:B:151:GLY:O  |  1:B:177:TYR:HB2  |  2.02  |  0.60
2:C:150:HIS:CD2  |  2:C:454:ARG:HE  |  2.20  |  0.60
2:C:498:ILE:H  |  2:C:498:ILE:HD12  |  1.66  |  0.60
2:C:590:PRO:HG3  |  2:C:605:TYR:CZ  |  2.36  |  0.60
3:D:363:LEU:HG  |  3:D:363:LEU:O  |  2.02  |  0.60
3:D:641:ILE:HD13  |  3:D:641:ILE:O  |  2.02  |  0.60
2:I:674:ASP:OD1  |  2:I:1109:ILE:N  |  2.34  |  0.60
3:J:495:ASN:ND2  |  3:J:497:GLU:HB2  |  2.17  |  0.60
3:D:1309:ILE:HG13  |  3:D:1310:THR:N  |  2.17  |  0.59
1:G:65:LEU:CD2  |  1:G:65:LEU:H  |  2.15  |  0.59
1:G:228:LEU:HD22  |  1:H:221:ALA:HB1  |  1.84  |  0.59
3:J:521:LYS:NZ  |  3:J:540:GLY:O  |  2.24  |  0.59
5:L:233:ASP:O  |  5:L:236:LYS:HE2  |  2.02  |  0.59
5:L:245:ALA:O  |  5:L:249:ILE:HG13  |  2.01  |  0.59
5:L:486:ARG:HZ  |  5:L:486:ARG:HB2  |  2.31  |  0.59
1:B:73:GLY:HA2  |  1:B:134:THR:CG2  |  2.32  |  0.59

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### Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å)
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1:A:44:ARG:HG3 | 1:A:183:ILE:HG22 | 1.89 | 0.54
2:C:886:LYS:H | 2:C:917:SER:HB3 | 1.73 | 0.54
2:C:1281:TYR:OH | 3:D:431:ARG:O | 2.24 | 0.54
4:E:60:ASN:ND2 | 4:E:63:ILE:HD13 | 2.22 | 0.54
3:J:536:LEU:HD12 | 3:J:542:ALA:HB2 | 1.89 | 0.54
3:J:620:PH:CD1 | 3:J:624:ILE:HD11 | 2.43 | 0.54
5:L:460:ILE:LEO | 5:L:463:LEU:HB2 | 2.08 | 0.54
3:D:362:ARG:H | 3:D:365:GLN:NE2 | 2.06 | 0.54
5:F:343:LYS:O | 5:F:347:ILE:HG13 | 2.08 | 0.54
1:H:91:ARG:HG3 | 1:H:122:GLU:HB3 | 1.90 | 0.54
2:I:673:HIS:CB | 2:I:1109:ILE:HEG22 | 2.36 | 0.54
3:J:905:ARG:CZ | 3:J:910:ASN:HD21 | 2.20 | 0.54
2:C:726:TYR:CE2 | 2:C:728:ASP:HB2 | 2.43 | 0.53
3:D:1158:GLU:HB3 | 3:D:1186:TYR:CE1 | 2.43 | 0.53
3:D:40:LYS:O | 3:D:55:GLY:HA2 | 2.08 | 0.53
5:F:470:MET:CE | 5:F:486:ARG:HH12 | 2.21 | 0.53
2:I:412:GLU:HB3 | 2:I:413:GLU:OE1 | 2.08 | 0.53
3:D:293:ARG:O | 3:D:296:LYS:N | 2.41 | 0.53
3:D:580:TRP:CZ3 | 3:D:589:TYR:HA | 2.44 | 0.53
3:D:824:PRO:HD3 | 3:D:835:LEU:HD13 | 1.91 | 0.53
1:G:67:GLU:O | 1:G:78:ILE:HEB | 2.08 | 0.53
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3:J:442:ILE:HG22 | 3:J:443:GLU:O | 2.08 | 0.53
3:J:623:GLN:O | 3:J:627:THR:HG22 | 2.08 | 0.53
2:I:808:ASN:HB | 3:J:633:ALA:HB2 | 1.72 | 0.53
5:L:561:MET:HG2 | 5:L:576:VAL:HG22 | 1.91 | 0.53

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## Full wwPDB X-ray Structure Validation Report

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5:L:161:LEU:O | 5:L:262:VAL:HG23 | 2.11 | 0.50
2:C:1268:GLN:OE1 | 3:D:352:ARG:HG2 | 2.12 | 0.50
2:C:886:LYS:NZ | 2:C:916:SER:HB3 | 2.26 | 0.50
3:D:188:LEU:O | 3:D:191:SER:OG | 2.25 | 0.50
3:D:839:VAL:HG12 | 3:D:839:VAL:O | 2.12 | 0.50
5:F:120:ALA:HA | 5:F:123:ILE:HD12 | 1.93 | 0.50
1:H:118:ASP:HB2 | 1:H:121:VAL:HG23 | 1.93 | 0.50
1:H:19:VAL:HB | 1:H:23:HIS:CD2 | 2.46 | 0.50
2:I:745:GLU:N | 2:I:1017:GLN:HG3 | 2.26 | 0.50
3:J:355:ILE:HG21 | 3:J:466:MET:HG3 | 1.93 | 0.50
2:C:887:VAL:HB | 2:C:913:VAL:HG22 | 1.92 | 0.50
3:D:1184:ASP:O | 3:D:1186:TYR:N | 2.45 | 0.50
3:D:750:PRO:HA | 3:D:777:HIS:CE1 | 2.47 | 0.50
5:F:478:PRO:HB2 | 5:F:483:LEU:CD1 | 2.41 | 0.50
2:I:157:PHE:CZ | 2:I:431:LYS:HG2 | 2.47 | 0.50
2:I:556:GLY:HA2 | 2:I:659:GLN:O | 2.12 | 0.50
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1:A:114:ASP:N | 1:A:114:ASP:OD1 | 2.44 | 0.50
3:D:114:ILE:HD13 | 3:D:304:ASP:CG | 2.32 | 0.50
3:D:817:HIS:NE2 | 3:D:860:ARG:NH2 | 2.59 | 0.50
3:D:905:ARG:NH1 | 4:E:10:VAL:HG11 | 2.27 | 0.50
1:H:78:ILE:O | 1:H:82:LEU:HG | 2.12 | 0.50
3:J:77:ARG:HB3 | 3:J:80:HIS:CE1 | 2.47 | 0.50
3:J:68:TYR:HA | 3:J:92:VAL:HG23 | 1.93 | 0.50
1:B:16:ILE:HG12 | 1:B:26:VAL:CG1 | 2.41 | 0.50
2:C:1149:TYR:HE2 | 2:C:1180:LYS:SD | 2.35 | 0.50
2:C:1328:LYS:O | 2:C:1332:SER:N | 2.45 | 0.50
2:C:18:ARG:NH1 | 2:C:621:SER:O | 2.45 | 0.50
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### Atom-1 vs Atom-2

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### Interatomic Distance Validation

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<td>2:C:142:GLU:N</td>
<td>2:C:760:ASN:OD1</td>
<td>2.54</td>
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</tr>
<tr>
<td>2:C:836:LEU:CD1</td>
<td>2:C:836:LEU:N</td>
<td>2.82</td>
<td>0.40</td>
</tr>
<tr>
<td>3:D:123:ILE:O</td>
<td>3:D:1234:VAL:C</td>
<td>2.58</td>
<td>0.40</td>
</tr>
<tr>
<td>3:D:205:LEU:O</td>
<td>3:D:205:LEU:HD13</td>
<td>2.22</td>
<td>0.40</td>
</tr>
<tr>
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<td>5:F:505:ILE:HD13</td>
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</tr>
<tr>
<td>5:F:144:LEU:HA</td>
<td>5:F:144:LEU:HD12</td>
<td>1.78</td>
<td>0.40</td>
</tr>
<tr>
<td>1:G:73:GLY:O</td>
<td>1:G:134:THR:HG22</td>
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<td>0.40</td>
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<tr>
<td>2:I:163:LYS:HE3</td>
<td>2:I:163:LYS:HB3</td>
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<tr>
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<td>2:I:645:PHE:HE1</td>
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<td>3:J:856:ILE:CG2</td>
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<tr>
<td>3:J:836:ARG:HG3</td>
<td>3:J:869:CYS:HB3</td>
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</tr>
<tr>
<td>5:L:587:ILE:HA</td>
<td>5:L:590:ILE:CD1</td>
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</tr>
<tr>
<td>1:A:145:LYS:HE3</td>
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<td>1:A:86:LYS:C</td>
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<tr>
<td>1:B:88:LEU:HD12</td>
<td>1:B:88:LEU:HA</td>
<td>1.74</td>
<td>0.40</td>
</tr>
<tr>
<td>2:C:930:ASP:HB3</td>
<td>2:C:1053:TYR:HB2</td>
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<td>0.40</td>
</tr>
<tr>
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<td>2:C:1076:ILE:O</td>
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</tr>
<tr>
<td>2:C:208:ILE:HG21</td>
<td>2:C:208:ILE:HD13</td>
<td>1.79</td>
<td>0.40</td>
</tr>
<tr>
<td>2:C:617:ALA:HB3</td>
<td>2:C:653:MET:CG</td>
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<td>0.40</td>
</tr>
<tr>
<td>2:C:842:ASP:HB2</td>
<td>2:C:1045:GLY:O</td>
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<td>0.40</td>
</tr>
<tr>
<td>3:D:1347:LEU:HG</td>
<td>3:D:1357:ILE:CG2</td>
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<td>0.40</td>
</tr>
</tbody>
</table>

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

<table>
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<tr>
<th>Atom-1</th>
<th>Atom-2</th>
<th>Interatomic distance (Å)</th>
<th>Clash overlap (Å)</th>
</tr>
</thead>
<tbody>
<tr>
<td>3:D:515(ARG):NH2</td>
<td>3:D:717:VAL:HG23</td>
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<td>0.40</td>
</tr>
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<td>3:D:592:VAL:HG22</td>
<td>3:D:592:VAL:H</td>
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<td>0.40</td>
</tr>
<tr>
<td>1:A:316:MET:HB2</td>
<td>5:F:600:HIS:CE1</td>
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<td>0.40</td>
</tr>
<tr>
<td>1:G:38:THR:N</td>
<td>1:H:45:ARG:NH1</td>
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<td>0.40</td>
</tr>
<tr>
<td>2:I:1101:LEU:HD23</td>
<td>3:J:725:MET:SD</td>
<td>2.61</td>
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</tr>
<tr>
<td>2:I:1106:ARG:HE</td>
<td>3:J:731:ARG:HH21</td>
<td>1.70</td>
<td>0.40</td>
</tr>
<tr>
<td>2:I:1247:SER:OG</td>
<td>2:I:1248:THR:N</td>
<td>2.51</td>
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</tr>
<tr>
<td>2:I:41:GLN:NE2</td>
<td>2:I:73:TYR:CE</td>
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<tr>
<td>2:I:861:ALA:HB1</td>
<td>2:I:882:ILE:HD13</td>
<td>2.03</td>
<td>0.40</td>
</tr>
<tr>
<td>2:I:976:ARG:HH12</td>
<td>2:I:990:ASP:HB3</td>
<td>1.86</td>
<td>0.40</td>
</tr>
<tr>
<td>3:J:872:LEU:CD2</td>
<td>3:J:877:VAL:HG11</td>
<td>2.43</td>
<td>0.40</td>
</tr>
<tr>
<td>5:L:112:THR:OG1</td>
<td>5:L:115:GLY:N</td>
<td>2.51</td>
<td>0.40</td>
</tr>
<tr>
<td>5:L:230:VAL:HG13</td>
<td>5:L:231:THR:N</td>
<td>2.36</td>
<td>0.40</td>
</tr>
<tr>
<td>5:L:277:MET:HG3</td>
<td>5:L:362:ASN:HD21</td>
<td>1.86</td>
<td>0.40</td>
</tr>
<tr>
<td>5:L:519:LEU:C</td>
<td>5:L:519:LEU:HD23</td>
<td>2.42</td>
<td>0.40</td>
</tr>
<tr>
<td>5:L:565:ILE:HG22</td>
<td>5:L:566:ASP:OD2</td>
<td>2.21</td>
<td>0.40</td>
</tr>
<tr>
<td>1:A:31:LEU:CD1</td>
<td>1:A:201:LEU:HB2</td>
<td>2.51</td>
<td>0.40</td>
</tr>
<tr>
<td>1:A:76:GLU:HB3</td>
<td>1:A:81:ILE:HG12</td>
<td>2.03</td>
<td>0.40</td>
</tr>
<tr>
<td>1:B:112:ALA:HA</td>
<td>1:B:115:ILE:HG11</td>
<td>2.03</td>
<td>0.40</td>
</tr>
<tr>
<td>1:B:103:ASN:HA</td>
<td>1:B:141:SER:HB2</td>
<td>2.03</td>
<td>0.40</td>
</tr>
<tr>
<td>1:B:215:GLU:HA</td>
<td>1:B:218:ARG:CD</td>
<td>2.51</td>
<td>0.40</td>
</tr>
<tr>
<td>1:B:40:GLY:HA3</td>
<td>1:B:185:TYR:CD1</td>
<td>2.56</td>
<td>0.40</td>
</tr>
<tr>
<td>2:C:1251:TYR:CE1</td>
<td>2:C:1301:ARG:CE</td>
<td>3.04</td>
<td>0.40</td>
</tr>
<tr>
<td>2:C:556:GLY:HA2</td>
<td>2:C:659:GLN:O</td>
<td>2.21</td>
<td>0.40</td>
</tr>
<tr>
<td>2:C:615:VAL:HG21</td>
<td>2:C:645:PHE:CD2</td>
<td>2.57</td>
<td>0.40</td>
</tr>
<tr>
<td>2:C:746:ALA:HA</td>
<td>2:C:974:ARG:HN2</td>
<td>2.34</td>
<td>0.40</td>
</tr>
<tr>
<td>2:C:811:ASN:N</td>
<td>2:C:811:ASN:OD1</td>
<td>2.48</td>
<td>0.40</td>
</tr>
<tr>
<td>2:C:1313:HIS:HD2</td>
<td>3:D:477:GLN:NE2</td>
<td>2.19</td>
<td>0.40</td>
</tr>
<tr>
<td>1:G:14:VAL:HG13</td>
<td>1:G:27:THR:HB</td>
<td>2.03</td>
<td>0.40</td>
</tr>
<tr>
<td>1:H:31:LEU:HB2</td>
<td>1:H:199:ASP:HB2</td>
<td>2.04</td>
<td>0.40</td>
</tr>
</tbody>
</table>
All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

<table>
<thead>
<tr>
<th>Atom-1</th>
<th>Atom-2</th>
<th>Interatomic distance (Å)</th>
<th>Clash overlap (Å)</th>
</tr>
</thead>
<tbody>
<tr>
<td>2:C:44:GLU:OE1</td>
<td>5:F:596:ARG: NH1[4_455]</td>
<td>2.05</td>
<td>0.15</td>
</tr>
<tr>
<td>2:C:940:GLU:OE1</td>
<td>1:H:139:SER: OG[4_455]</td>
<td>2.05</td>
<td>0.15</td>
</tr>
</tbody>
</table>

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 X-ray entries followed by that with respect to entries of similar resolution.

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>
<td>A</td>
<td>305/329 (93%)</td>
<td>271 (89%)</td>
<td>25 (8%)</td>
<td>9 (3%)</td>
<td>4 33</td>
</tr>
<tr>
<td>1</td>
<td>B</td>
<td>213/329 (65%)</td>
<td>191 (90%)</td>
<td>20 (9%)</td>
<td>2 (1%)</td>
<td>17 57</td>
</tr>
<tr>
<td>1</td>
<td>G</td>
<td>222/329 (68%)</td>
<td>182 (82%)</td>
<td>28 (13%)</td>
<td>12 (5%)</td>
<td>21 19</td>
</tr>
<tr>
<td>1</td>
<td>H</td>
<td>213/329 (65%)</td>
<td>193 (91%)</td>
<td>20 (9%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>1338/1342 (100%)</td>
<td>1225 (92%)</td>
<td>103 (8%)</td>
<td>10 (1%)</td>
<td>22 61</td>
</tr>
<tr>
<td>2</td>
<td>I</td>
<td>1338/1342 (100%)</td>
<td>1226 (92%)</td>
<td>100 (8%)</td>
<td>12 (1%)</td>
<td>17 57</td>
</tr>
<tr>
<td>3</td>
<td>D</td>
<td>1162/1407 (83%)</td>
<td>1074 (92%)</td>
<td>79 (7%)</td>
<td>9 (1%)</td>
<td>19 59</td>
</tr>
</tbody>
</table>
Continued from previous page...

<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>3</td>
<td>J</td>
<td>1151/1407 (82%)</td>
<td>1064 (92%)</td>
<td>82 (7%)</td>
<td>5 (0%)</td>
<td>34 71</td>
</tr>
<tr>
<td>4</td>
<td>E</td>
<td>87/91 (96%)</td>
<td>79 (91%)</td>
<td>8 (9%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>4</td>
<td>K</td>
<td>77/91 (85%)</td>
<td>74 (96%)</td>
<td>3 (4%)</td>
<td>0</td>
<td>100 100</td>
</tr>
<tr>
<td>5</td>
<td>F</td>
<td>461/613 (75%)</td>
<td>422 (92%)</td>
<td>37 (8%)</td>
<td>2 (0%)</td>
<td>34 71</td>
</tr>
<tr>
<td>5</td>
<td>L</td>
<td>463/613 (76%)</td>
<td>423 (91%)</td>
<td>39 (8%)</td>
<td>1 (0%)</td>
<td>47 79</td>
</tr>
<tr>
<td>All</td>
<td>All</td>
<td>7030/8222 (86%)</td>
<td>6424 (91%)</td>
<td>544 (8%)</td>
<td>62 (1%)</td>
<td>17 57</td>
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</table>

All (62) Ramachandran outliers are listed below:

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<th>Res</th>
<th>Type</th>
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<tbody>
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<td>29</td>
<td>GLU</td>
</tr>
<tr>
<td>1</td>
<td>A</td>
<td>30</td>
<td>PRO</td>
</tr>
<tr>
<td>1</td>
<td>A</td>
<td>324</td>
<td>ALA</td>
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<td>1</td>
<td>B</td>
<td>232</td>
<td>VAL</td>
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<td>2</td>
<td>C</td>
<td>345</td>
<td>PRO</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>516</td>
<td>ASP</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>519</td>
<td>ASN</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>1159</td>
<td>VAL</td>
</tr>
<tr>
<td>3</td>
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<td>10</td>
<td>ALA</td>
</tr>
<tr>
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<td>G</td>
<td>13</td>
<td>LEU</td>
</tr>
<tr>
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<td>G</td>
<td>14</td>
<td>VAL</td>
</tr>
<tr>
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<td>G</td>
<td>62</td>
<td>ASP</td>
</tr>
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<td>GLU</td>
</tr>
<tr>
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<td>ASP</td>
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<td>VAL</td>
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<td>VAL</td>
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<td>LEU</td>
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<tr>
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<td>I</td>
<td>170</td>
<td>VAL</td>
</tr>
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<td>I</td>
<td>519</td>
<td>ASN</td>
</tr>
<tr>
<td>2</td>
<td>I</td>
<td>761</td>
<td>GLN</td>
</tr>
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<td>J</td>
<td>108</td>
<td>ALA</td>
</tr>
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<td>A</td>
<td>294</td>
<td>ASN</td>
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<td>2</td>
<td>C</td>
<td>697</td>
<td>LYS</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>761</td>
<td>GLN</td>
</tr>
<tr>
<td>3</td>
<td>D</td>
<td>110</td>
<td>PRO</td>
</tr>
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<td>3</td>
<td>D</td>
<td>586</td>
<td>GLY</td>
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<tr>
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<td>G</td>
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<td>VAL</td>
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<tr>
<td>2</td>
<td>I</td>
<td>345</td>
<td>PRO</td>
</tr>
<tr>
<td>1</td>
<td>A</td>
<td>14</td>
<td>VAL</td>
</tr>
</tbody>
</table>

Continued on next page...
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 X-ray entries followed by that with respect to entries of similar resolution.

The Analyzed 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>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>A</td>
<td>268/286 (94%)</td>
<td>249 (93%)</td>
<td>19 (7%)</td>
<td>14</td>
</tr>
<tr>
<td>1</td>
<td>B</td>
<td>184/286 (64%)</td>
<td>166 (90%)</td>
<td>18 (10%)</td>
<td>8</td>
</tr>
<tr>
<td>1</td>
<td>G</td>
<td>191/286 (67%)</td>
<td>179 (94%)</td>
<td>12 (6%)</td>
<td>18</td>
</tr>
<tr>
<td>1</td>
<td>H</td>
<td>183/286 (64%)</td>
<td>165 (90%)</td>
<td>18 (10%)</td>
<td>8</td>
</tr>
<tr>
<td>2</td>
<td>C</td>
<td>1155/1157 (100%)</td>
<td>1046 (91%)</td>
<td>109 (9%)</td>
<td>8</td>
</tr>
<tr>
<td>2</td>
<td>I</td>
<td>1154/1157 (100%)</td>
<td>1046 (91%)</td>
<td>108 (9%)</td>
<td>8</td>
</tr>
<tr>
<td>3</td>
<td>D</td>
<td>975/1168 (84%)</td>
<td>875 (90%)</td>
<td>100 (10%)</td>
<td>7</td>
</tr>
<tr>
<td>3</td>
<td>J</td>
<td>967/1168 (83%)</td>
<td>869 (90%)</td>
<td>98 (10%)</td>
<td>7</td>
</tr>
<tr>
<td>4</td>
<td>E</td>
<td>72/75 (96%)</td>
<td>64 (89%)</td>
<td>8 (11%)</td>
<td>6</td>
</tr>
<tr>
<td>4</td>
<td>K</td>
<td>67/75 (89%)</td>
<td>63 (94%)</td>
<td>4 (6%)</td>
<td>19</td>
</tr>
<tr>
<td>5</td>
<td>F</td>
<td>416/540 (77%)</td>
<td>373 (90%)</td>
<td>43 (10%)</td>
<td>7</td>
</tr>
<tr>
<td>5</td>
<td>L</td>
<td>418/540 (77%)</td>
<td>372 (89%)</td>
<td>46 (11%)</td>
<td>6</td>
</tr>
<tr>
<td>All</td>
<td>All</td>
<td>6050/7024 (86%)</td>
<td>5467 (90%)</td>
<td>583 (10%)</td>
<td>8</td>
</tr>
</tbody>
</table>

All (583) residues with a non-rotameric sidechain are listed below:

<table>
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<tr>
<th>Mol</th>
<th>Chain</th>
<th>Res</th>
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**5.3.3 RNA**

There are no RNA molecules in this entry.

**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 carbohydrates in this entry.

**5.6 Ligand geometry**

Of 6 ligands modelled in this entry, 6 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  Fit of model and data

6.1  Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

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### 6.2 Non-standard residues in protein, DNA, RNA chains

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

### 6.3 Carbohydrates

There are no carbohydrates in this entry.
6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

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6.5 Other polymers

There are no such residues in this entry.