



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 28, 2023 – 12:12 AM EDT

PDB ID : 3KYM
Title : Crystal structure of Li33 IgG2 di-Fab
Authors : Silvian, L.F.; Pepinsky, R.B.; Walus, L.
Deposited on : 2009-12-06
Resolution : 2.62 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 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:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

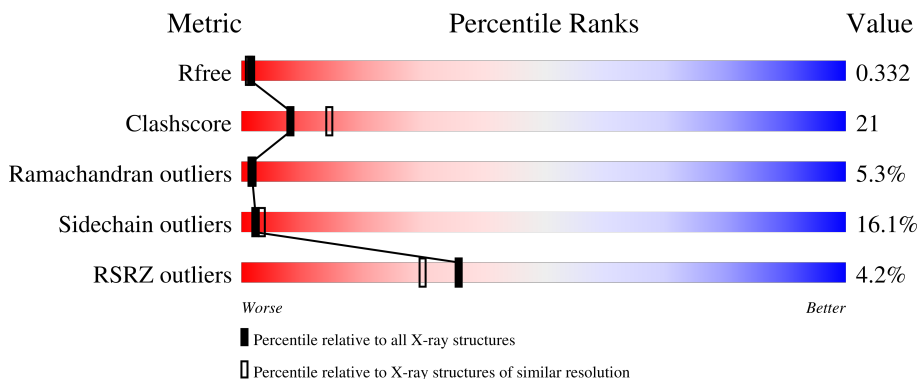
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.62 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.



| Metric | Whole archive (#Entries) | Similar resolution (#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|---|
| R_{free} | 130704 | 3797 (2.64-2.60) |
| Clashscore | 141614 | 4168 (2.64-2.60) |
| Ramachandran outliers | 138981 | 4093 (2.64-2.60) |
| Sidechain outliers | 138945 | 4093 (2.64-2.60) |
| RSRZ outliers | 127900 | 3731 (2.64-2.60) |

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 of the lower 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 $\leq 5\%$. 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.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|-------------------|
| 1 | A | 214 | 5% 62% 33% 5% |
| 1 | C | 214 | 2% 62% 31% 6% |
| 1 | E | 214 | 60% 31% 8% |
| 1 | G | 214 | 67% 28% . |
| 1 | I | 214 | 5% 57% 38% . |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | K | 214 | |
| 1 | M | 214 | |
| 1 | O | 214 | |
| 2 | B | 227 | |
| 2 | D | 227 | |
| 2 | F | 227 | |
| 2 | H | 227 | |
| 2 | J | 227 | |
| 2 | L | 227 | |
| 2 | N | 227 | |
| 2 | P | 227 | |

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 26358 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 Light Chain Li33 IgG2.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|---------------|-----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 1 | A | 213 | Total 1640 | C 1026 | N 277 | O 332 | S 5 | 0 | 0 | 0 |
| 1 | C | 213 | Total 1640 | C 1026 | N 277 | O 332 | S 5 | 0 | 0 | 0 |
| 1 | E | 213 | Total 1640 | C 1026 | N 277 | O 332 | S 5 | 0 | 0 | 0 |
| 1 | G | 213 | Total 1640 | C 1026 | N 277 | O 332 | S 5 | 0 | 0 | 0 |
| 1 | I | 213 | Total 1640 | C 1026 | N 277 | O 332 | S 5 | 0 | 0 | 0 |
| 1 | K | 209 | Total 1605 | C 1001 | N 273 | O 326 | S 5 | 0 | 0 | 0 |
| 1 | M | 208 | Total 1597 | C 1000 | N 268 | O 324 | S 5 | 0 | 0 | 0 |
| 1 | O | 213 | Total 1640 | C 1026 | N 277 | O 332 | S 5 | 0 | 0 | 0 |

- Molecule 2 is a protein called Heavy Chain Li33 IgG2.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|---------------|-----------|----------|----------|--------|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 2 | B | 220 | Total 1672 | C 1057 | N 283 | O 325 | S 7 | 0 | 0 | 0 |
| 2 | D | 220 | Total 1672 | C 1057 | N 283 | O 325 | S 7 | 0 | 0 | 0 |
| 2 | F | 219 | Total 1663 | C 1051 | N 281 | O 324 | S 7 | 0 | 0 | 0 |
| 2 | H | 219 | Total 1663 | C 1051 | N 281 | O 324 | S 7 | 0 | 0 | 0 |
| 2 | J | 219 | Total 1663 | C 1051 | N 281 | O 324 | S 7 | 0 | 0 | 0 |
| 2 | L | 219 | Total 1663 | C 1051 | N 281 | O 324 | S 7 | 0 | 0 | 0 |

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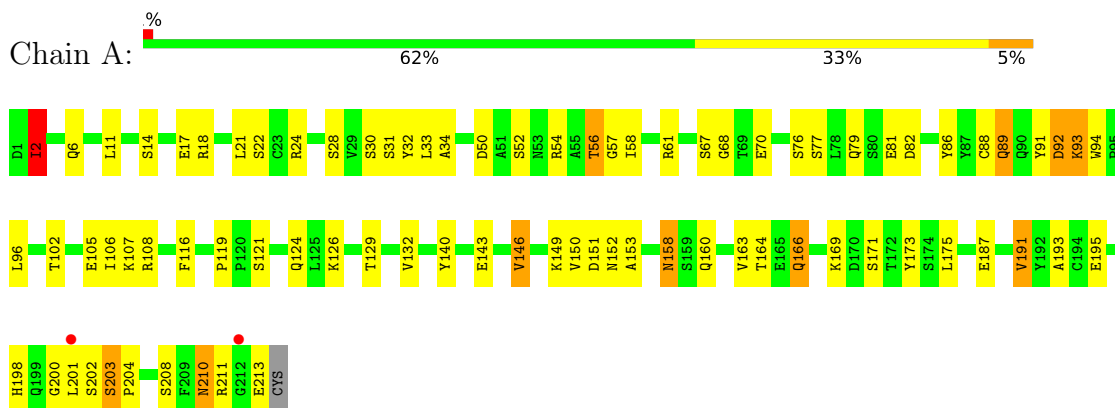
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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| | | | Total | C | N | O | S | | | |
| 2 | N | 219 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1663 | 1051 | 281 | 324 | 7 | | | |
| 2 | P | 219 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1657 | 1048 | 278 | 324 | 7 | | | |

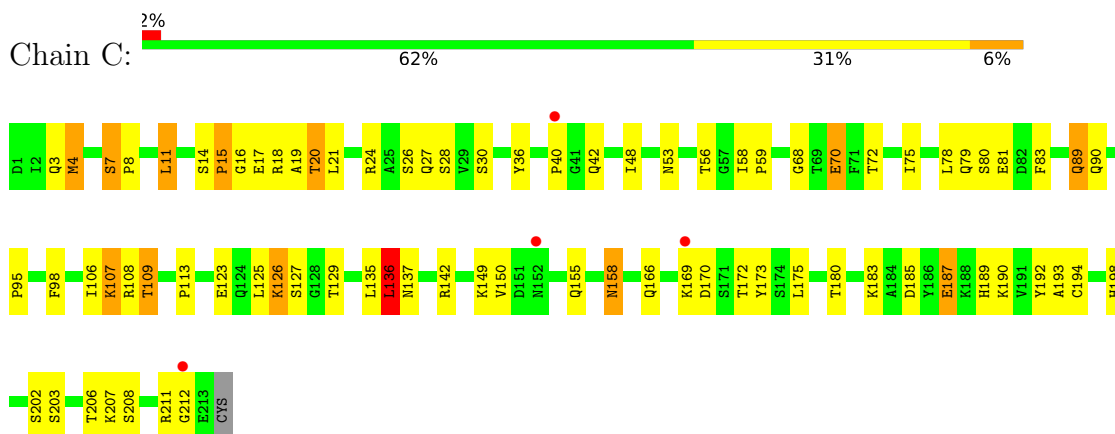
3 Residue-property plots [i](#)

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 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.

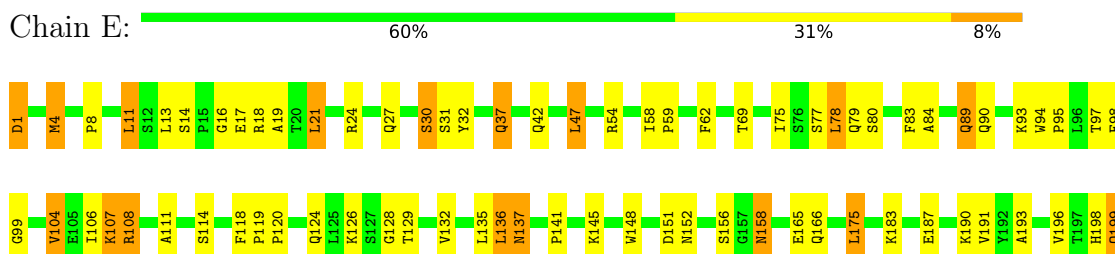
• Molecule 1: Light Chain Li33 IgG2



• Molecule 1: Light Chain Li33 IgG2



• Molecule 1: Light Chain Li33 IgG2

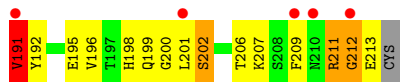




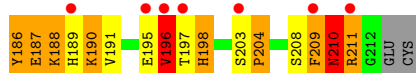
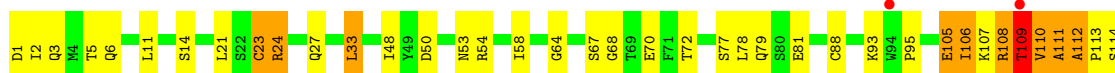
- Molecule 1: Light Chain Li33 IgG2



- Molecule 1: Light Chain Li33 IgG2

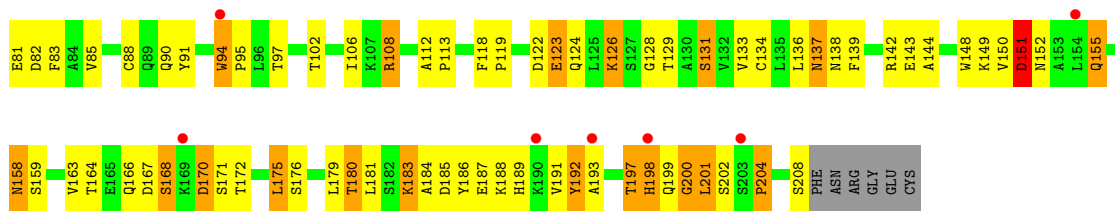


- Molecule 1: Light Chain Li33 IgG2

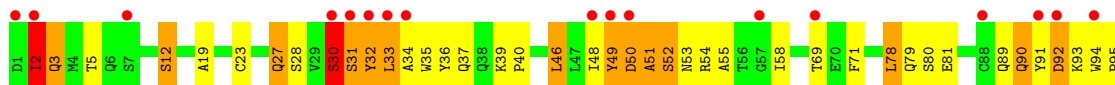


- Molecule 1: Light Chain Li33 IgG2



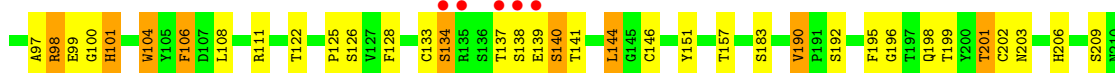
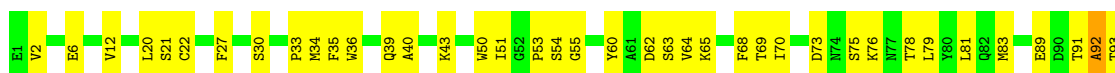


• Molecule 1: Light Chain Li33 IgG2



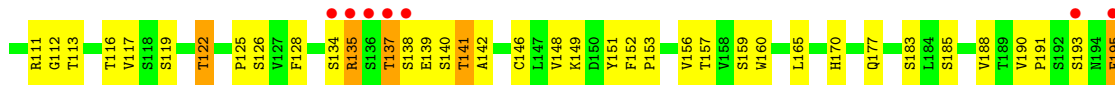
CYS

• Molecule 2: Heavy Chain Li33 IgG2



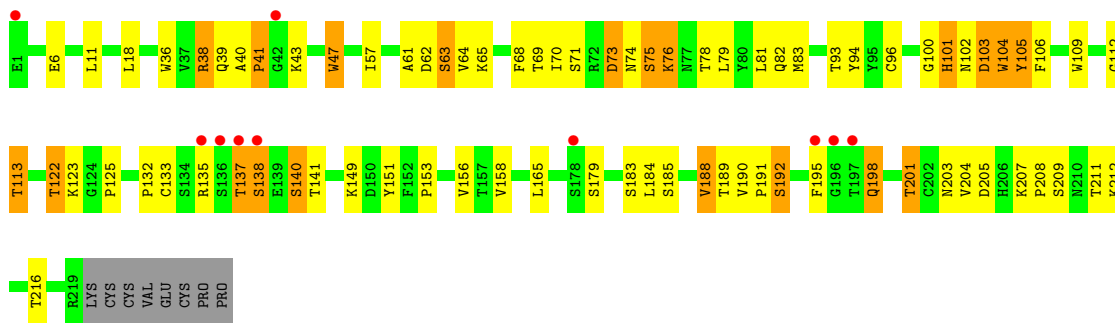
T211 K212 V213 D214 E6 K215 G100 V12 L20 S21 C22 F27 S30 P33 M34 F35 W36 Q39 A40 K43 W60 I51 G52 P53 S54 G55 Y60 A61 D62 S63 V64 K65 F68 T69 I70 D73 M74 S75 K76 N77 T78 L79 Y80 L81 E83 D86 T91 A92 T93

• Molecule 2: Heavy Chain Li33 IgG2

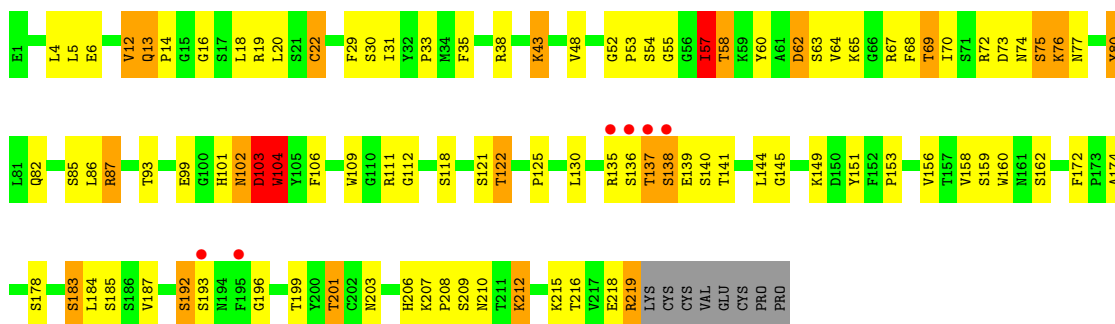


G196 T197 Q198 T199 Y200 C202 N203 D205 H206 S209 H210 K212 T211 T216 R219 K220 CYS E138 CYS S140 VAL G113 CYS PRO

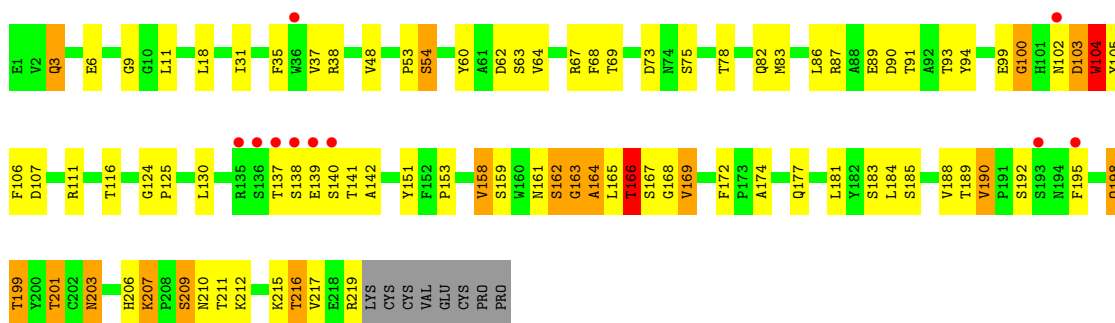
• Molecule 2: Heavy Chain Li33 IgG2



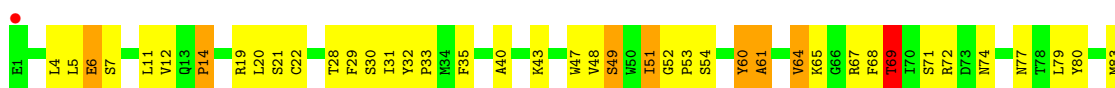
• Molecule 2: Heavy Chain Li33 IgG2

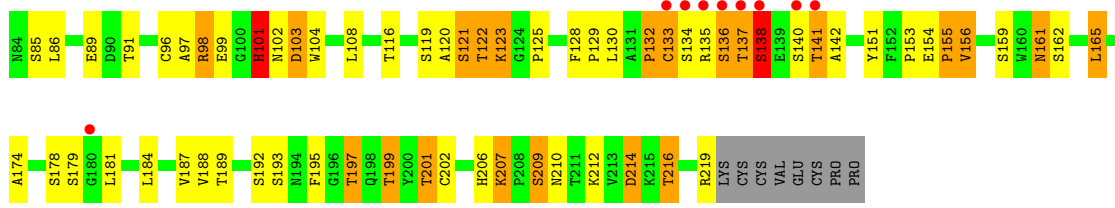


• Molecule 2: Heavy Chain Li33 IgG2

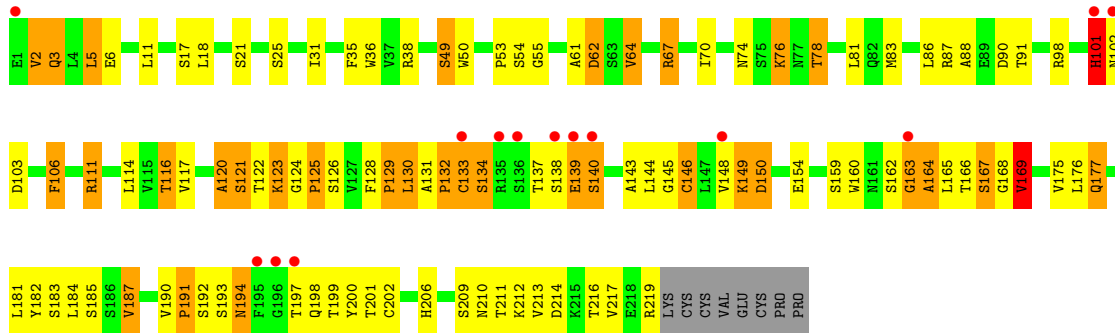


• Molecule 2: Heavy Chain Li33 IgG2

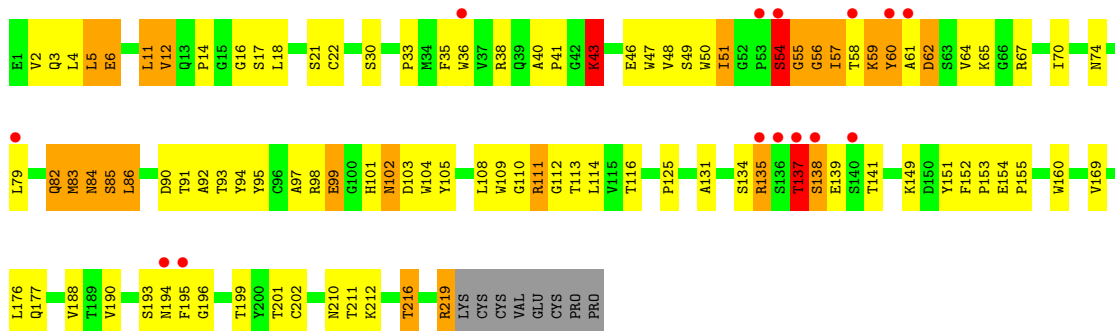




● Molecule 2: Heavy Chain Li33 IgG2



● Molecule 2: Heavy Chain Li33 IgG2



4 Data and refinement statistics i

| Property | Value | Source |
|---|---|------------------|
| Space group | P 1 | Depositor |
| Cell constants a, b, c, α , β , γ | 91.67Å 109.55Å 118.43Å 61.46° 79.29° 87.59° | Depositor |
| Resolution (Å) | 19.96 – 2.62 19.95 – 2.62 | Depositor EDS |
| % Data completeness (in resolution range) | 97.0 (19.96-2.62) 97.0 (19.95-2.62) | Depositor EDS |
| R_{merge} | 0.06 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 2.35 (at 2.63Å) | Xtrriage |
| Refinement program | REFMAC 5.5.0088 | Depositor |
| R, R_{free} | 0.259 , 0.339 0.256 , 0.332 | Depositor DCC |
| R_{free} test set | 5749 reflections (4.98%) | wwPDB-VP |
| Wilson B-factor (Å ²) | 42.2 | Xtrriage |
| Anisotropy | 0.184 | Xtrriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.33 , 54.9 | EDS |
| L-test for twinning ² | $\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$ | Xtrriage |
| Estimated twinning fraction | 0.008 for -h,k,k-l | Xtrriage |
| F_o, F_c correlation | 0.90 | EDS |
| Total number of atoms | 26358 | wwPDB-VP |
| Average B, all atoms (Å ²) | 48.0 | wwPDB-VP |

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.80% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality i

5.1 Standard geometry i

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).

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|----------------|-------------|----------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 1 | A | 0.57 | 0/1676 | 0.74 | 0/2275 |
| 1 | C | 0.56 | 0/1676 | 0.69 | 1/2275 (0.0%) |
| 1 | E | 0.63 | 0/1676 | 0.76 | 1/2275 (0.0%) |
| 1 | G | 0.67 | 0/1676 | 0.76 | 0/2275 |
| 1 | I | 0.64 | 0/1676 | 0.79 | 0/2275 |
| 1 | K | 0.66 | 0/1638 | 0.87 | 0/2220 |
| 1 | M | 0.58 | 0/1632 | 0.77 | 1/2217 (0.0%) |
| 1 | O | 0.63 | 0/1676 | 0.75 | 0/2275 |
| 2 | B | 0.61 | 0/1716 | 0.76 | 0/2338 |
| 2 | D | 0.59 | 1/1716 (0.1%) | 0.72 | 0/2338 |
| 2 | F | 0.64 | 0/1707 | 0.76 | 1/2327 (0.0%) |
| 2 | H | 0.64 | 0/1707 | 0.79 | 0/2327 |
| 2 | J | 0.63 | 0/1707 | 0.77 | 0/2327 |
| 2 | L | 0.62 | 0/1707 | 0.76 | 0/2327 |
| 2 | N | 0.59 | 0/1707 | 0.78 | 1/2327 (0.0%) |
| 2 | P | 0.61 | 0/1701 | 0.77 | 0/2320 |
| All | All | 0.62 | 1/26994 (0.0%) | 0.77 | 5/36718 (0.0%) |

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.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1 | G | 0 | 1 |
| 1 | K | 0 | 2 |
| 2 | H | 0 | 1 |
| All | All | 0 | 4 |

All (1) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 2 | D | 202 | CYS | CB-SG | -6.20 | 1.71 | 1.82 |

All (5) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-----------|-------|-------------|----------|
| 1 | C | 136 | LEU | CA-CB-CG | 6.63 | 130.54 | 115.30 |
| 1 | E | 47 | LEU | CA-CB-CG | 5.61 | 128.21 | 115.30 |
| 2 | N | 114 | LEU | CA-CB-CG | 5.22 | 127.31 | 115.30 |
| 1 | M | 78 | LEU | CA-CB-CG | 5.12 | 127.08 | 115.30 |
| 2 | F | 38 | ARG | NE-CZ-NH2 | -5.09 | 117.75 | 120.30 |

There are no chirality outliers.

All (4) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 1 | G | 7 | SER | Peptide |
| 2 | H | 103 | ASP | Peptide |
| 1 | K | 109 | THR | Peptide |
| 1 | K | 114 | SER | Peptide |

5.2 Too-close contacts [i](#)

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.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 1640 | 0 | 1589 | 47 | 0 |
| 1 | C | 1640 | 0 | 1589 | 56 | 0 |
| 1 | E | 1640 | 0 | 1589 | 67 | 0 |
| 1 | G | 1640 | 0 | 1589 | 46 | 0 |
| 1 | I | 1640 | 0 | 1589 | 73 | 0 |
| 1 | K | 1605 | 0 | 1556 | 115 | 0 |
| 1 | M | 1597 | 0 | 1552 | 114 | 0 |
| 1 | O | 1640 | 0 | 1589 | 71 | 0 |
| 2 | B | 1672 | 0 | 1622 | 57 | 0 |
| 2 | D | 1672 | 0 | 1622 | 57 | 0 |
| 2 | F | 1663 | 0 | 1609 | 61 | 0 |
| 2 | H | 1663 | 0 | 1609 | 81 | 0 |
| 2 | J | 1663 | 0 | 1609 | 74 | 0 |
| 2 | L | 1663 | 0 | 1609 | 84 | 0 |
| 2 | N | 1663 | 0 | 1609 | 109 | 0 |
| 2 | P | 1657 | 0 | 1598 | 100 | 0 |
| All | All | 26358 | 0 | 25529 | 1105 | 0 |

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 21.

The worst 5 of 1105 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|----------------|-----------------|--------------------------|-------------------|
| 2:H:76:LYS:HE2 | 1:M:32:TYR:CE2 | 1.45 | 1.48 |
| 2:N:102:ASN:N | 2:N:103:ASP:HB2 | 1.16 | 1.43 |
| 2:N:102:ASN:H | 2:N:103:ASP:CB | 1.45 | 1.28 |
| 2:H:76:LYS:HE2 | 1:M:32:TYR:CZ | 1.74 | 1.23 |
| 2:P:56:GLY:CA | 2:P:57:ILE:HG12 | 1.76 | 1.15 |

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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.

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|----|
| 1 | A | 211/214 (99%) | 190 (90%) | 17 (8%) | 4 (2%) | 8 | 14 |
| 1 | C | 211/214 (99%) | 183 (87%) | 24 (11%) | 4 (2%) | 8 | 14 |
| 1 | E | 211/214 (99%) | 195 (92%) | 14 (7%) | 2 (1%) | 17 | 33 |
| 1 | G | 211/214 (99%) | 190 (90%) | 19 (9%) | 2 (1%) | 17 | 33 |
| 1 | I | 211/214 (99%) | 183 (87%) | 19 (9%) | 9 (4%) | 2 | 3 |
| 1 | K | 205/214 (96%) | 151 (74%) | 33 (16%) | 21 (10%) | 0 | 0 |
| 1 | M | 206/214 (96%) | 173 (84%) | 20 (10%) | 13 (6%) | 1 | 1 |
| 1 | O | 211/214 (99%) | 178 (84%) | 17 (8%) | 16 (8%) | 1 | 1 |
| 2 | B | 218/227 (96%) | 185 (85%) | 26 (12%) | 7 (3%) | 4 | 5 |
| 2 | D | 218/227 (96%) | 187 (86%) | 23 (11%) | 8 (4%) | 3 | 4 |
| 2 | F | 217/227 (96%) | 191 (88%) | 18 (8%) | 8 (4%) | 3 | 4 |
| 2 | H | 217/227 (96%) | 184 (85%) | 22 (10%) | 11 (5%) | 2 | 2 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|-----------|----------|-------------|---|
| 2 | J | 217/227 (96%) | 178 (82%) | 24 (11%) | 15 (7%) | 1 | 1 |
| 2 | L | 217/227 (96%) | 175 (81%) | 22 (10%) | 20 (9%) | 1 | 0 |
| 2 | N | 217/227 (96%) | 169 (78%) | 24 (11%) | 24 (11%) | 0 | 0 |
| 2 | P | 217/227 (96%) | 170 (78%) | 29 (13%) | 18 (8%) | 1 | 0 |
| All | All | 3415/3528 (97%) | 2882 (84%) | 351 (10%) | 182 (5%) | 2 | 2 |

5 of 182 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 202 | SER |
| 2 | B | 101 | HIS |
| 2 | B | 134 | SER |
| 2 | B | 140 | SER |
| 2 | D | 135 | ARG |

5.3.2 Protein sidechains [i](#)

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 1 | A | 184/185 (100%) | 151 (82%) | 33 (18%) | 2 | 2 |
| 1 | C | 184/185 (100%) | 159 (86%) | 25 (14%) | 3 | 5 |
| 1 | E | 184/185 (100%) | 154 (84%) | 30 (16%) | 2 | 3 |
| 1 | G | 184/185 (100%) | 157 (85%) | 27 (15%) | 3 | 4 |
| 1 | I | 184/185 (100%) | 164 (89%) | 20 (11%) | 6 | 11 |
| 1 | K | 180/185 (97%) | 144 (80%) | 36 (20%) | 1 | 2 |
| 1 | M | 180/185 (97%) | 145 (81%) | 35 (19%) | 1 | 2 |
| 1 | O | 184/185 (100%) | 163 (89%) | 21 (11%) | 5 | 9 |
| 2 | B | 186/193 (96%) | 160 (86%) | 26 (14%) | 3 | 5 |
| 2 | D | 186/193 (96%) | 160 (86%) | 26 (14%) | 3 | 5 |
| 2 | F | 185/193 (96%) | 155 (84%) | 30 (16%) | 2 | 3 |
| 2 | H | 185/193 (96%) | 151 (82%) | 34 (18%) | 1 | 2 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|-----------|-------------|---|
| 2 | J | 185/193 (96%) | 155 (84%) | 30 (16%) | 2 | 3 |
| 2 | L | 185/193 (96%) | 147 (80%) | 38 (20%) | 1 | 1 |
| 2 | N | 185/193 (96%) | 152 (82%) | 33 (18%) | 2 | 2 |
| 2 | P | 184/193 (95%) | 155 (84%) | 29 (16%) | 2 | 3 |
| All | All | 2945/3024 (97%) | 2472 (84%) | 473 (16%) | 2 | 3 |

5 of 473 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | I | 6 | GLN |
| 1 | O | 213 | GLU |
| 1 | K | 23 | CYS |
| 1 | O | 132 | VAL |
| 2 | N | 76 | LYS |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 2 | L | 177 | GLN |
| 2 | N | 102 | ASN |
| 2 | L | 206 | HIS |
| 1 | M | 138 | ASN |
| 1 | O | 137 | ASN |

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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.

| Mol | Chain | Analysed | <RSRZ> | #RSRZ > 2 | OWAB(Å ²) | Q < 0.9 |
|-----|-------|-----------------|--------|----------------|-----------------------|---------|
| 1 | A | 213/214 (99%) | -0.13 | 2 (0%) 84 82 | 27, 47, 64, 73 | 0 |
| 1 | C | 213/214 (99%) | 0.17 | 4 (1%) 66 62 | 40, 57, 68, 75 | 0 |
| 1 | E | 213/214 (99%) | -0.26 | 0 100 100 | 25, 39, 53, 64 | 0 |
| 1 | G | 213/214 (99%) | -0.34 | 1 (0%) 91 89 | 18, 35, 49, 66 | 0 |
| 1 | I | 213/214 (99%) | 0.10 | 10 (4%) 31 25 | 18, 41, 74, 83 | 0 |
| 1 | K | 209/214 (97%) | 0.37 | 21 (10%) 7 4 | 26, 49, 89, 100 | 0 |
| 1 | M | 208/214 (97%) | 0.22 | 8 (3%) 40 34 | 33, 55, 72, 78 | 0 |
| 1 | O | 213/214 (99%) | 0.20 | 19 (8%) 9 6 | 27, 46, 73, 83 | 0 |
| 2 | B | 220/227 (96%) | -0.05 | 5 (2%) 60 55 | 29, 47, 67, 76 | 0 |
| 2 | D | 220/227 (96%) | 0.09 | 11 (5%) 28 23 | 37, 47, 70, 81 | 0 |
| 2 | F | 219/227 (96%) | 0.08 | 10 (4%) 32 26 | 25, 42, 61, 73 | 0 |
| 2 | H | 219/227 (96%) | -0.05 | 6 (2%) 54 49 | 28, 38, 65, 72 | 0 |
| 2 | J | 219/227 (96%) | 0.08 | 10 (4%) 32 26 | 26, 44, 67, 77 | 0 |
| 2 | L | 219/227 (96%) | 0.21 | 10 (4%) 32 26 | 31, 50, 71, 85 | 0 |
| 2 | N | 219/227 (96%) | 0.42 | 14 (6%) 19 15 | 32, 56, 80, 86 | 0 |
| 2 | P | 219/227 (96%) | 0.31 | 14 (6%) 19 15 | 35, 51, 74, 78 | 0 |
| All | All | 3449/3528 (97%) | 0.09 | 145 (4%) 36 30 | 18, 47, 72, 100 | 0 |

The worst 5 of 145 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 2 | D | 136 | SER | 8.9 |
| 2 | F | 136 | SER | 7.8 |
| 2 | F | 137 | THR | 7.5 |
| 2 | N | 195 | PHE | 6.8 |
| 2 | N | 136 | SER | 6.2 |

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.