



Full wwPDB EM Validation Report ⓘ

Apr 1, 2025 – 09:12 PM EDT

PDB ID : 8CXB / pdb_00008cxb
EMDB ID : EMD-24276
Title : Human PA28-20S (PA28-4a3b)
Authors : Zhao, J.; Makhija, S.; Huang, B.; Cheng, Y.
Deposited on : 2022-05-20
Resolution : 2.90 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.dev117
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.42

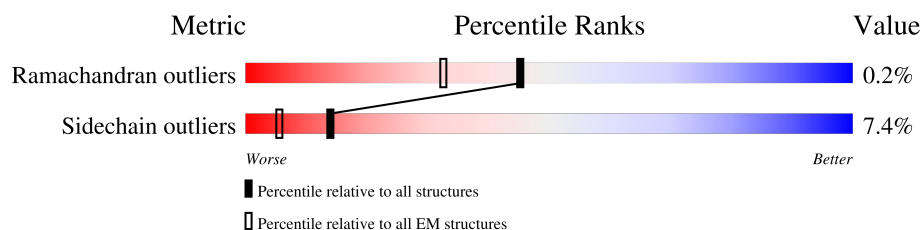
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.






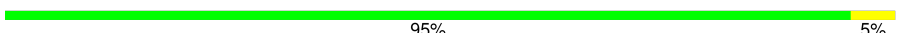











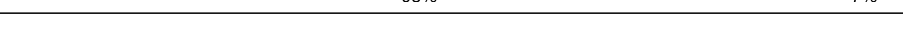
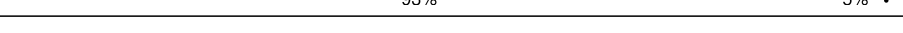








| Metric | Whole archive (#Entries) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Ramachandran outliers | 207382 | 16835 |
| Sidechain outliers | 206894 | 16415 |

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 $\leq 5\%$.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | c | 239 | |
| 1 | e | 239 | |
| 1 | g | 239 | |
| 2 | d | 249 | |
| 2 | f | 249 | |
| 2 | h | 249 | |
| 2 | i | 249 | |
| 3 | A | 234 | |
| 3 | O | 234 | |
| 4 | B | 261 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|---|
| 4 | P | 261 |  92% 5% • |
| 5 | C | 248 |  89% 6% 5% |
| 5 | Q | 248 |  90% 5% 5% |
| 6 | D | 241 |  95% 5% |
| 6 | R | 241 |  91% 7% • |
| 7 | E | 263 |  86% 5% 9% |
| 7 | S | 263 |  85% 5% 10% |
| 8 | F | 255 |  87% 7% 6% |
| 8 | T | 255 |  89% 5% 6% |
| 9 | G | 246 |  89% 8% • |
| 9 | U | 246 |  93% 6% • |
| 10 | H | 277 |  74% 5% 20% |
| 10 | V | 277 |  74% 6% 20% |
| 11 | I | 205 |  89% 10% |
| 11 | W | 205 |  93% 7% |
| 12 | J | 201 |  93% 5% • |
| 12 | X | 201 |  92% 5% • |
| 13 | K | 263 |  72% • 24% |
| 13 | Y | 263 |  70% 6% 24% |
| 14 | L | 241 |  83% 5% 12% |
| 14 | Z | 241 |  85% • 12% |
| 15 | M | 264 |  77% • 19% |
| 15 | a | 264 |  76% 6% 19% |
| 16 | N | 239 |  81% • 15% |
| 16 | b | 239 |  82% • 15% |

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 57967 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Proteasome activator complex subunit 2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 1 | c | 214 | Total | C | N | O | S | 0 | 0 |
| | | | 1666 | 1080 | 281 | 301 | 4 | | |
| 1 | e | 213 | Total | C | N | O | S | 0 | 0 |
| | | | 1661 | 1077 | 280 | 300 | 4 | | |
| 1 | g | 214 | Total | C | N | O | S | 0 | 0 |
| | | | 1666 | 1080 | 281 | 301 | 4 | | |

- Molecule 2 is a protein called Proteasome activator complex subunit 1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 2 | d | 211 | Total | C | N | O | S | 0 | 0 |
| | | | 1634 | 1054 | 281 | 295 | 4 | | |
| 2 | f | 204 | Total | C | N | O | S | 0 | 0 |
| | | | 1590 | 1025 | 274 | 287 | 4 | | |
| 2 | h | 211 | Total | C | N | O | S | 0 | 0 |
| | | | 1636 | 1058 | 283 | 289 | 6 | | |
| 2 | i | 211 | Total | C | N | O | S | 0 | 0 |
| | | | 1630 | 1053 | 282 | 289 | 6 | | |

- Molecule 3 is a protein called Proteasome subunit alpha type-2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 3 | A | 229 | Total | C | N | O | S | 0 | 0 |
| | | | 1696 | 1101 | 294 | 295 | 6 | | |
| 3 | O | 229 | Total | C | N | O | S | 0 | 0 |
| | | | 1678 | 1089 | 290 | 293 | 6 | | |

- Molecule 4 is a protein called Proteasome subunit alpha type-4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 4 | B | 249 | Total | C | N | O | S | 0 | 0 |
| | | | 1793 | 1146 | 318 | 319 | 10 | | |

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| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 4 | P | 251 | Total | C | N | O | S | 0 | 0 |
| | | | 1843 | 1174 | 328 | 331 | 10 | | |

- Molecule 5 is a protein called Proteasome subunit alpha type-7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 5 | C | 235 | Total | C | N | O | S | 0 | 0 |
| | | | 1703 | 1082 | 314 | 302 | 5 | | |
| 5 | Q | 236 | Total | C | N | O | S | 0 | 0 |
| | | | 1723 | 1095 | 320 | 303 | 5 | | |

- Molecule 6 is a protein called Proteasome subunit alpha type-5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 6 | D | 241 | Total | C | N | O | S | 0 | 0 |
| | | | 1751 | 1116 | 301 | 322 | 12 | | |
| 6 | R | 235 | Total | C | N | O | S | 0 | 0 |
| | | | 1693 | 1076 | 292 | 314 | 11 | | |

- Molecule 7 is a protein called Proteasome subunit alpha type-1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 7 | E | 239 | Total | C | N | O | S | 0 | 0 |
| | | | 1810 | 1144 | 331 | 324 | 11 | | |
| 7 | S | 237 | Total | C | N | O | S | 0 | 0 |
| | | | 1759 | 1119 | 329 | 301 | 10 | | |

- Molecule 8 is a protein called Proteasome subunit alpha type-3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 8 | F | 240 | Total | C | N | O | S | 0 | 0 |
| | | | 1785 | 1145 | 313 | 316 | 11 | | |
| 8 | T | 239 | Total | C | N | O | S | 0 | 0 |
| | | | 1784 | 1143 | 314 | 317 | 10 | | |

- Molecule 9 is a protein called Proteasome subunit alpha type-6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 9 | G | 239 | Total | C | N | O | S | 0 | 0 |
| | | | 1769 | 1133 | 305 | 319 | 12 | | |
| 9 | U | 242 | Total | C | N | O | S | 0 | 0 |
| | | | 1789 | 1146 | 307 | 323 | 13 | | |

- Molecule 10 is a protein called Proteasome subunit beta type-7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 10 | H | 222 | Total | C | N | O | S | 0 | 0 |
| | | | 1609 | 1023 | 276 | 299 | 11 | | |
| 10 | V | 222 | Total | C | N | O | S | 0 | 0 |
| | | | 1612 | 1023 | 274 | 304 | 11 | | |

- Molecule 11 is a protein called Proteasome subunit beta type-3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 11 | I | 204 | Total | C | N | O | S | 0 | 0 |
| | | | 1564 | 1003 | 264 | 278 | 19 | | |
| 11 | W | 204 | Total | C | N | O | S | 0 | 0 |
| | | | 1559 | 1000 | 264 | 277 | 18 | | |

- Molecule 12 is a protein called Proteasome subunit beta type-2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12 | J | 197 | Total | C | N | O | S | 0 | 0 |
| | | | 1544 | 998 | 265 | 272 | 9 | | |
| 12 | X | 196 | Total | C | N | O | S | 0 | 0 |
| | | | 1535 | 990 | 264 | 273 | 8 | | |

- Molecule 13 is a protein called Proteasome subunit beta type-5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 13 | K | 200 | Total | C | N | O | S | 0 | 0 |
| | | | 1525 | 968 | 273 | 275 | 9 | | |
| 13 | Y | 200 | Total | C | N | O | S | 0 | 0 |
| | | | 1532 | 970 | 272 | 281 | 9 | | |

- Molecule 14 is a protein called Proteasome subunit beta type-1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 14 | L | 213 | Total | C | N | O | S | 0 | 0 |
| | | | 1599 | 1022 | 279 | 288 | 10 | | |
| 14 | Z | 213 | Total | C | N | O | S | 0 | 0 |
| | | | 1593 | 1022 | 281 | 280 | 10 | | |

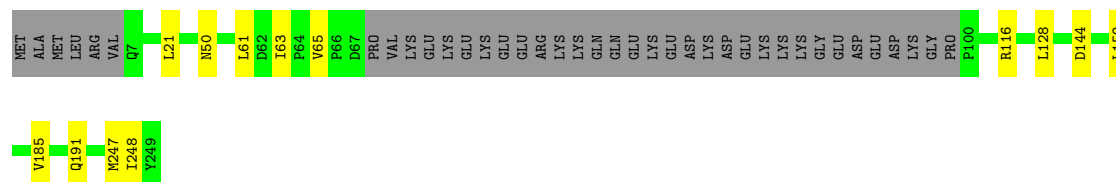
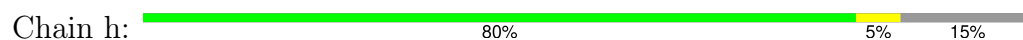
- Molecule 15 is a protein called Proteasome subunit beta type-4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 15 | M | 215 | Total | C | N | O | S | 0 | 0 |
| | | | 1643 | 1043 | 289 | 299 | 12 | | |
| 15 | a | 215 | Total | C | N | O | S | 0 | 0 |
| | | | 1624 | 1034 | 288 | 290 | 12 | | |

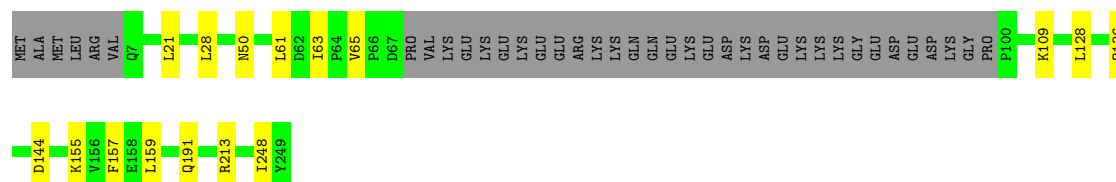
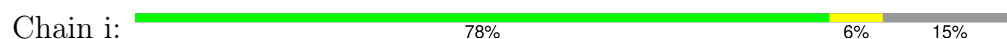
- Molecule 16 is a protein called Proteasome subunit beta type-6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 16 | N | 202 | Total | C | N | O | S | 0 | 0 |
| | | | 1491 | 939 | 258 | 282 | 12 | | |
| 16 | b | 202 | Total | C | N | O | S | 0 | 0 |
| | | | 1478 | 934 | 258 | 274 | 12 | | |

- Molecule 2: Proteasome activator complex subunit 1



- Molecule 2: Proteasome activator complex subunit 1



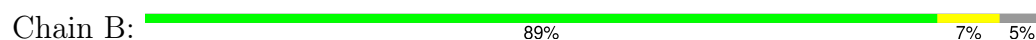
- Molecule 3: Proteasome subunit alpha type-2



- Molecule 3: Proteasome subunit alpha type-2



- Molecule 4: Proteasome subunit alpha type-4

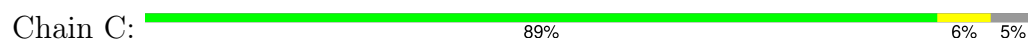


- Molecule 4: Proteasome subunit alpha type-4

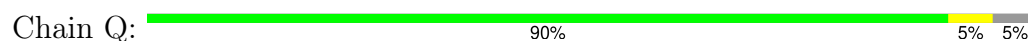




- Molecule 5: Proteasome subunit alpha type-7



- Molecule 5: Proteasome subunit alpha type-7



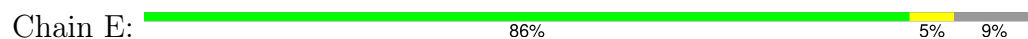
- Molecule 6: Proteasome subunit alpha type-5



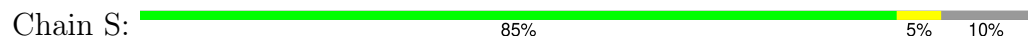
- Molecule 6: Proteasome subunit alpha type-5



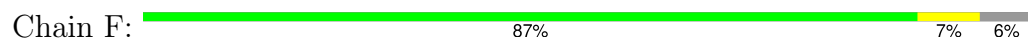
- Molecule 7: Proteasome subunit alpha type-1



- Molecule 7: Proteasome subunit alpha type-1



- Molecule 8: Proteasome subunit alpha type-3





- Molecule 8: Proteasome subunit alpha type-3

Chain T: 89% 5% 6%



- Molecule 9: Proteasome subunit alpha type-6

Chain G: 89% 8% .



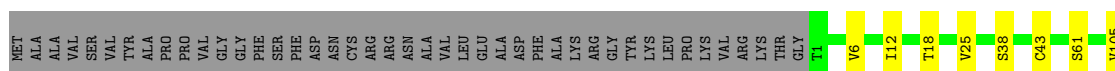
- Molecule 9: Proteasome subunit alpha type-6

Chain U: 93% 6% .



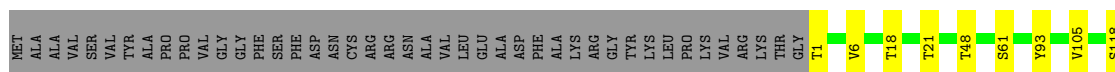
- Molecule 10: Proteasome subunit beta type-7

Chain H: 74% 5% 20%



- Molecule 10: Proteasome subunit beta type-7

Chain V: 74% 6% 20%



- Molecule 11: Proteasome subunit beta type-3

Chain I: 89% 10%



- Molecule 11: Proteasome subunit beta type-3

Chain W: 93% 7%



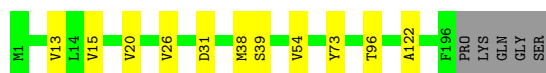
- Molecule 12: Proteasome subunit beta type-2

Chain J: 93% 5% .



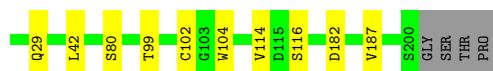
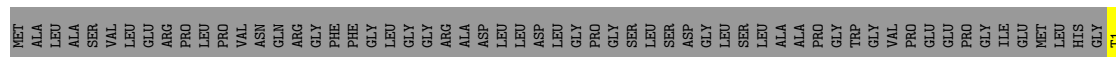
- Molecule 12: Proteasome subunit beta type-2

Chain X: 92% 5% .



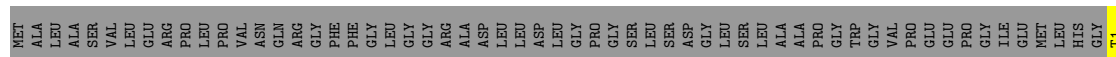
- Molecule 13: Proteasome subunit beta type-5

Chain K: 72% . 24%



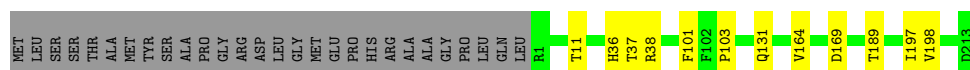
- Molecule 13: Proteasome subunit beta type-5

Chain Y: 70% 6% 24%




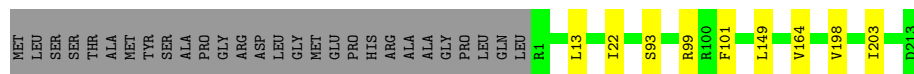
- Molecule 14: Proteasome subunit beta type-1

Chain L: 83% 5% 12%




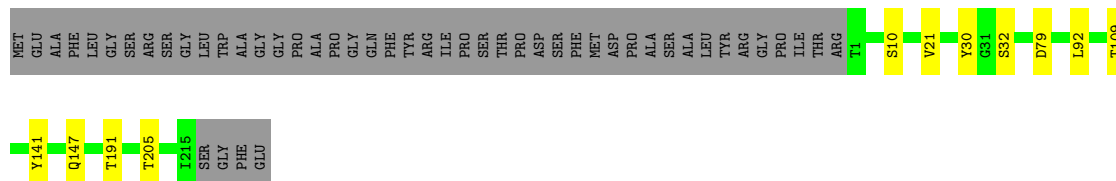
- Molecule 14: Proteasome subunit beta type-1

Chain Z:  85% 12%



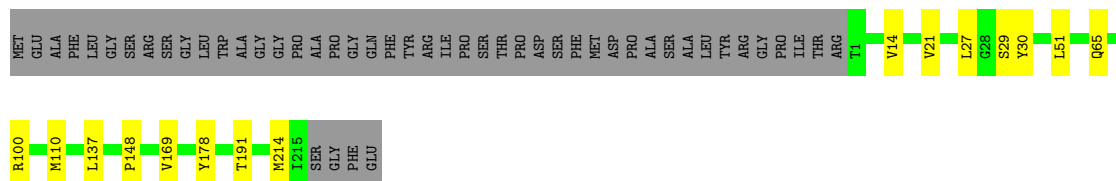
- Molecule 15: Proteasome subunit beta type-4

Chain M:  77% 19%




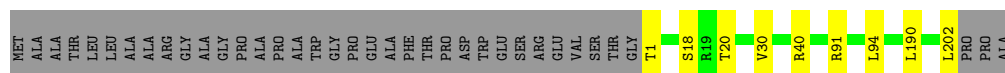
- Molecule 15: Proteasome subunit beta type-4

Chain a:  76% 6% 19%




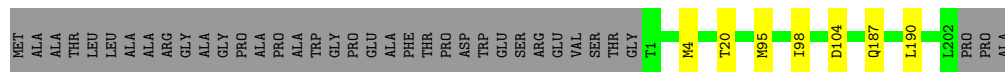
- Molecule 16: Proteasome subunit beta type-6

Chain N:  81% 15%



- Molecule 16: Proteasome subunit beta type-6

Chain b:  82% 15%



4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 135937 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI POLARA 300 | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 43 | Depositor |
| Minimum defocus (nm) | 1300 | Depositor |
| Maximum defocus (nm) | 2000 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K2 SUMMIT (4k x 4k) | Depositor |

5 Model quality

5.1 Standard geometry

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 | c | 0.54 | 0/1700 | 0.78 | 0/2310 |
| 1 | e | 0.54 | 0/1695 | 0.79 | 0/2303 |
| 1 | g | 0.54 | 0/1700 | 0.76 | 0/2310 |
| 2 | d | 0.52 | 0/1665 | 0.82 | 1/2258 (0.0%) |
| 2 | f | 0.53 | 0/1620 | 0.80 | 0/2196 |
| 2 | h | 0.52 | 0/1667 | 0.79 | 0/2258 |
| 2 | i | 0.53 | 0/1661 | 0.78 | 0/2251 |
| 3 | A | 0.63 | 0/1735 | 0.86 | 1/2362 (0.0%) |
| 3 | O | 0.61 | 0/1717 | 0.83 | 1/2339 (0.0%) |
| 4 | B | 0.61 | 0/1821 | 0.87 | 1/2477 (0.0%) |
| 4 | P | 0.59 | 0/1872 | 0.83 | 0/2541 |
| 5 | C | 0.61 | 0/1729 | 0.85 | 1/2356 (0.0%) |
| 5 | Q | 0.59 | 0/1749 | 0.82 | 0/2380 |
| 6 | D | 0.65 | 0/1780 | 0.86 | 1/2417 (0.0%) |
| 6 | R | 0.61 | 0/1720 | 0.79 | 0/2336 |
| 7 | E | 0.64 | 0/1845 | 0.84 | 0/2504 |
| 7 | S | 0.63 | 0/1794 | 0.86 | 0/2437 |
| 8 | F | 0.64 | 0/1820 | 0.82 | 0/2464 |
| 8 | T | 0.64 | 0/1819 | 0.81 | 1/2463 (0.0%) |
| 9 | G | 0.62 | 0/1802 | 0.86 | 1/2449 (0.0%) |
| 9 | U | 0.59 | 0/1823 | 0.82 | 0/2478 |
| 10 | H | 0.65 | 0/1636 | 0.91 | 2/2223 (0.1%) |
| 10 | V | 0.64 | 0/1639 | 0.85 | 1/2228 (0.0%) |
| 11 | I | 0.61 | 0/1593 | 0.87 | 0/2149 |
| 11 | W | 0.62 | 0/1588 | 0.88 | 0/2144 |
| 12 | J | 0.60 | 0/1577 | 0.86 | 0/2138 |
| 12 | X | 0.61 | 0/1567 | 0.84 | 0/2124 |
| 13 | K | 0.65 | 0/1556 | 0.86 | 0/2104 |
| 13 | Y | 0.63 | 0/1563 | 0.84 | 0/2115 |
| 14 | L | 0.66 | 0/1629 | 0.88 | 2/2201 (0.1%) |
| 14 | Z | 0.65 | 0/1623 | 0.87 | 1/2192 (0.0%) |
| 15 | M | 0.63 | 0/1676 | 0.87 | 0/2272 |
| 15 | a | 0.66 | 0/1657 | 0.86 | 1/2250 (0.0%) |
| 16 | N | 0.67 | 0/1517 | 0.86 | 0/2056 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|-----------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 16 | b | 0.65 | 0/1504 | 0.86 | 1/2038 (0.0%) |
| All | All | 0.61 | 0/59059 | 0.84 | 16/80123 (0.0%) |

There are no bond length outliers.

All (16) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|-----|------|---------|-------|-------------|----------|
| 10 | H | 188 | PRO | CA-N-CD | -7.59 | 100.87 | 111.50 |
| 14 | Z | 101 | PHE | CB-CA-C | 7.23 | 124.87 | 110.40 |
| 2 | d | 157 | PHE | CB-CA-C | -6.87 | 96.67 | 110.40 |
| 5 | C | 12 | PRO | N-CA-C | -6.79 | 94.46 | 112.10 |
| 10 | H | 188 | PRO | N-CA-CB | -6.50 | 95.45 | 102.60 |
| 16 | b | 104 | ASP | CB-CA-C | -6.47 | 97.46 | 110.40 |
| 6 | D | 17 | PRO | N-CA-C | -6.26 | 95.83 | 112.10 |
| 4 | B | 14 | PRO | N-CA-C | -6.19 | 96.02 | 112.10 |
| 3 | A | 14 | PRO | N-CA-C | -6.09 | 96.27 | 112.10 |
| 14 | L | 101 | PHE | CB-CA-C | 5.70 | 121.80 | 110.40 |
| 8 | T | 122 | TYR | CB-CA-C | 5.43 | 121.25 | 110.40 |
| 10 | V | 93 | TYR | CB-CA-C | 5.28 | 120.95 | 110.40 |
| 14 | L | 103 | PRO | N-CA-C | 5.27 | 125.81 | 112.10 |
| 3 | O | 75 | TYR | CB-CA-C | -5.15 | 100.10 | 110.40 |
| 15 | a | 178 | TYR | CB-CA-C | -5.11 | 100.19 | 110.40 |
| 9 | G | 9 | PHE | CB-CA-C | 5.07 | 120.54 | 110.40 |

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

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 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.

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|------------|---------|----------|-------------|-----|
| 1 | c | 210/239 (88%) | 209 (100%) | 1 (0%) | 0 | 100 | 100 |
| 1 | e | 209/239 (87%) | 206 (99%) | 2 (1%) | 1 (0%) | 25 | 56 |
| 1 | g | 210/239 (88%) | 210 (100%) | 0 | 0 | 100 | 100 |
| 2 | d | 207/249 (83%) | 204 (99%) | 3 (1%) | 0 | 100 | 100 |
| 2 | f | 200/249 (80%) | 197 (98%) | 3 (2%) | 0 | 100 | 100 |
| 2 | h | 207/249 (83%) | 204 (99%) | 2 (1%) | 1 (0%) | 25 | 56 |
| 2 | i | 207/249 (83%) | 205 (99%) | 2 (1%) | 0 | 100 | 100 |
| 3 | A | 227/234 (97%) | 224 (99%) | 3 (1%) | 0 | 100 | 100 |
| 3 | O | 227/234 (97%) | 226 (100%) | 1 (0%) | 0 | 100 | 100 |
| 4 | B | 247/261 (95%) | 241 (98%) | 6 (2%) | 0 | 100 | 100 |
| 4 | P | 249/261 (95%) | 245 (98%) | 3 (1%) | 1 (0%) | 30 | 60 |
| 5 | C | 233/248 (94%) | 230 (99%) | 3 (1%) | 0 | 100 | 100 |
| 5 | Q | 234/248 (94%) | 232 (99%) | 2 (1%) | 0 | 100 | 100 |
| 6 | D | 239/241 (99%) | 231 (97%) | 8 (3%) | 0 | 100 | 100 |
| 6 | R | 233/241 (97%) | 232 (100%) | 1 (0%) | 0 | 100 | 100 |
| 7 | E | 237/263 (90%) | 233 (98%) | 4 (2%) | 0 | 100 | 100 |
| 7 | S | 235/263 (89%) | 230 (98%) | 5 (2%) | 0 | 100 | 100 |
| 8 | F | 238/255 (93%) | 238 (100%) | 0 | 0 | 100 | 100 |
| 8 | T | 237/255 (93%) | 236 (100%) | 1 (0%) | 0 | 100 | 100 |
| 9 | G | 237/246 (96%) | 232 (98%) | 4 (2%) | 1 (0%) | 30 | 60 |
| 9 | U | 240/246 (98%) | 239 (100%) | 1 (0%) | 0 | 100 | 100 |
| 10 | H | 220/277 (79%) | 215 (98%) | 3 (1%) | 2 (1%) | 14 | 43 |
| 10 | V | 220/277 (79%) | 217 (99%) | 1 (0%) | 2 (1%) | 14 | 43 |
| 11 | I | 202/205 (98%) | 197 (98%) | 5 (2%) | 0 | 100 | 100 |
| 11 | W | 202/205 (98%) | 198 (98%) | 3 (2%) | 1 (0%) | 25 | 56 |
| 12 | J | 195/201 (97%) | 191 (98%) | 3 (2%) | 1 (0%) | 25 | 56 |
| 12 | X | 194/201 (96%) | 189 (97%) | 4 (2%) | 1 (0%) | 25 | 56 |
| 13 | K | 198/263 (75%) | 196 (99%) | 2 (1%) | 0 | 100 | 100 |
| 13 | Y | 198/263 (75%) | 196 (99%) | 2 (1%) | 0 | 100 | 100 |
| 14 | L | 211/241 (88%) | 209 (99%) | 2 (1%) | 0 | 100 | 100 |
| 14 | Z | 211/241 (88%) | 208 (99%) | 3 (1%) | 0 | 100 | 100 |
| 15 | M | 213/264 (81%) | 209 (98%) | 3 (1%) | 1 (0%) | 25 | 56 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|----------|-------------|-----|
| 15 | a | 213/264 (81%) | 205 (96%) | 7 (3%) | 1 (0%) | 25 | 56 |
| 16 | N | 200/239 (84%) | 196 (98%) | 4 (2%) | 0 | 100 | 100 |
| 16 | b | 200/239 (84%) | 197 (98%) | 3 (2%) | 0 | 100 | 100 |
| All | All | 7640/8589 (89%) | 7527 (98%) | 100 (1%) | 13 (0%) | 45 | 73 |

All (13) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | e | 236 | PRO |
| 10 | H | 171 | SER |
| 10 | H | 188 | PRO |
| 10 | V | 171 | SER |
| 2 | h | 247 | MET |
| 15 | M | 10 | SER |
| 12 | X | 122 | ALA |
| 9 | G | 11 | ARG |
| 12 | J | 122 | ALA |
| 11 | W | 29 | ILE |
| 15 | a | 214 | MET |
| 10 | V | 188 | PRO |
| 4 | P | 59 | VAL |

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.

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|-------------|----|
| 1 | c | 172/212 (81%) | 162 (94%) | 10 (6%) | 17 | 46 |
| 1 | e | 172/212 (81%) | 161 (94%) | 11 (6%) | 14 | 41 |
| 1 | g | 172/212 (81%) | 170 (99%) | 2 (1%) | 67 | 89 |
| 2 | d | 168/224 (75%) | 160 (95%) | 8 (5%) | 21 | 54 |
| 2 | f | 166/224 (74%) | 156 (94%) | 10 (6%) | 16 | 44 |
| 2 | h | 170/224 (76%) | 158 (93%) | 12 (7%) | 12 | 36 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|----------|-------------|----|
| 2 | i | 168/224 (75%) | 152 (90%) | 16 (10%) | 7 | 22 |
| 3 | A | 158/191 (83%) | 147 (93%) | 11 (7%) | 12 | 36 |
| 3 | O | 155/191 (81%) | 148 (96%) | 7 (4%) | 23 | 56 |
| 4 | B | 159/221 (72%) | 142 (89%) | 17 (11%) | 5 | 17 |
| 4 | P | 171/221 (77%) | 160 (94%) | 11 (6%) | 14 | 41 |
| 5 | C | 152/211 (72%) | 139 (91%) | 13 (9%) | 8 | 27 |
| 5 | Q | 157/211 (74%) | 145 (92%) | 12 (8%) | 11 | 32 |
| 6 | D | 173/203 (85%) | 163 (94%) | 10 (6%) | 17 | 46 |
| 6 | R | 164/203 (81%) | 148 (90%) | 16 (10%) | 6 | 21 |
| 7 | E | 181/224 (81%) | 168 (93%) | 13 (7%) | 12 | 35 |
| 7 | S | 169/224 (75%) | 156 (92%) | 13 (8%) | 10 | 31 |
| 8 | F | 167/212 (79%) | 150 (90%) | 17 (10%) | 6 | 19 |
| 8 | T | 168/212 (79%) | 157 (94%) | 11 (6%) | 14 | 40 |
| 9 | G | 175/210 (83%) | 157 (90%) | 18 (10%) | 6 | 19 |
| 9 | U | 177/210 (84%) | 163 (92%) | 14 (8%) | 10 | 30 |
| 10 | H | 165/228 (72%) | 148 (90%) | 17 (10%) | 6 | 19 |
| 10 | V | 166/228 (73%) | 152 (92%) | 14 (8%) | 9 | 28 |
| 11 | I | 164/174 (94%) | 143 (87%) | 21 (13%) | 3 | 11 |
| 11 | W | 162/174 (93%) | 149 (92%) | 13 (8%) | 10 | 30 |
| 12 | J | 156/171 (91%) | 146 (94%) | 10 (6%) | 14 | 41 |
| 12 | X | 156/171 (91%) | 146 (94%) | 10 (6%) | 14 | 41 |
| 13 | K | 146/202 (72%) | 135 (92%) | 11 (8%) | 11 | 33 |
| 13 | Y | 147/202 (73%) | 130 (88%) | 17 (12%) | 4 | 14 |
| 14 | L | 161/199 (81%) | 151 (94%) | 10 (6%) | 15 | 43 |
| 14 | Z | 160/199 (80%) | 152 (95%) | 8 (5%) | 20 | 52 |
| 15 | M | 166/215 (77%) | 156 (94%) | 10 (6%) | 16 | 44 |
| 15 | a | 160/215 (74%) | 147 (92%) | 13 (8%) | 9 | 29 |
| 16 | N | 149/181 (82%) | 140 (94%) | 9 (6%) | 16 | 44 |
| 16 | b | 145/181 (80%) | 139 (96%) | 6 (4%) | 26 | 60 |
| All | All | 5717/7216 (79%) | 5296 (93%) | 421 (7%) | 14 | 34 |

All (421) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | c | 16 | GLN |
| 1 | c | 17 | VAL |
| 1 | c | 22 | GLN |
| 1 | c | 32 | LEU |
| 1 | c | 41 | ILE |
| 1 | c | 57 | LEU |
| 1 | c | 109 | PRO |
| 1 | c | 134 | ASP |
| 1 | c | 193 | GLU |
| 1 | c | 238 | MET |
| 2 | d | 25 | THR |
| 2 | d | 46 | GLU |
| 2 | d | 63 | ILE |
| 2 | d | 65 | VAL |
| 2 | d | 104 | VAL |
| 2 | d | 128 | LEU |
| 2 | d | 136 | GLN |
| 2 | d | 248 | ILE |
| 1 | e | 41 | ILE |
| 1 | e | 47 | LEU |
| 1 | e | 94 | LEU |
| 1 | e | 103 | LEU |
| 1 | e | 107 | VAL |
| 1 | e | 116 | GLU |
| 1 | e | 134 | ASP |
| 1 | e | 184 | VAL |
| 1 | e | 186 | ASP |
| 1 | e | 207 | LEU |
| 1 | e | 224 | LEU |
| 2 | f | 11 | GLN |
| 2 | f | 21 | LEU |
| 2 | f | 29 | LEU |
| 2 | f | 39 | GLU |
| 2 | f | 46 | GLU |
| 2 | f | 63 | ILE |
| 2 | f | 136 | GLN |
| 2 | f | 144 | ASP |
| 2 | f | 159 | LEU |
| 2 | f | 241 | ARG |
| 3 | A | 5 | TYR |
| 3 | A | 19 | VAL |
| 3 | A | 43 | VAL |
| 3 | A | 44 | VAL |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 3 | A | 64 | VAL |
| 3 | A | 73 | LEU |
| 3 | A | 126 | VAL |
| 3 | A | 136 | CYS |
| 3 | A | 187 | ILE |
| 3 | A | 207 | ILE |
| 3 | A | 218 | ARG |
| 4 | B | 6 | ASP |
| 4 | B | 9 | THR |
| 4 | B | 21 | VAL |
| 4 | B | 28 | ILE |
| 4 | B | 33 | THR |
| 4 | B | 35 | LEU |
| 4 | B | 44 | LEU |
| 4 | B | 61 | PHE |
| 4 | B | 76 | VAL |
| 4 | B | 105 | ILE |
| 4 | B | 128 | ARG |
| 4 | B | 134 | LEU |
| 4 | B | 177 | GLN |
| 4 | B | 216 | LEU |
| 4 | B | 217 | THR |
| 4 | B | 223 | THR |
| 4 | B | 224 | VAL |
| 5 | C | 7 | ILE |
| 5 | C | 35 | VAL |
| 5 | C | 41 | VAL |
| 5 | C | 59 | VAL |
| 5 | C | 65 | LEU |
| 5 | C | 69 | VAL |
| 5 | C | 89 | VAL |
| 5 | C | 107 | ILE |
| 5 | C | 108 | THR |
| 5 | C | 148 | ASP |
| 5 | C | 168 | VAL |
| 5 | C | 186 | LEU |
| 5 | C | 191 | VAL |
| 6 | D | 46 | VAL |
| 6 | D | 47 | CYS |
| 6 | D | 54 | ILE |
| 6 | D | 78 | MET |
| 6 | D | 81 | LEU |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 6 | D | 107 | MET |
| 6 | D | 113 | THR |
| 6 | D | 163 | VAL |
| 6 | D | 165 | CYS |
| 6 | D | 188 | SER |
| 7 | E | 14 | SER |
| 7 | E | 30 | LYS |
| 7 | E | 101 | ARG |
| 7 | E | 122 | ARG |
| 7 | E | 123 | TYR |
| 7 | E | 139 | ASP |
| 7 | E | 147 | THR |
| 7 | E | 150 | SER |
| 7 | E | 173 | GLU |
| 7 | E | 174 | ARG |
| 7 | E | 184 | LEU |
| 7 | E | 222 | THR |
| 7 | E | 237 | GLU |
| 8 | F | 9 | LEU |
| 8 | F | 35 | THR |
| 8 | F | 37 | ILE |
| 8 | F | 53 | VAL |
| 8 | F | 66 | LEU |
| 8 | F | 69 | VAL |
| 8 | F | 71 | ARG |
| 8 | F | 80 | LEU |
| 8 | F | 96 | SER |
| 8 | F | 142 | VAL |
| 8 | F | 151 | ILE |
| 8 | F | 174 | THR |
| 8 | F | 179 | LEU |
| 8 | F | 181 | MET |
| 8 | F | 186 | CYS |
| 8 | F | 192 | GLU |
| 8 | F | 215 | TRP |
| 9 | G | 13 | ILE |
| 9 | G | 17 | SER |
| 9 | G | 61 | LEU |
| 9 | G | 66 | VAL |
| 9 | G | 78 | CYS |
| 9 | G | 112 | ASP |
| 9 | G | 115 | CYS |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 9 | G | 120 | ASP |
| 9 | G | 124 | VAL |
| 9 | G | 126 | THR |
| 9 | G | 128 | ASN |
| 9 | G | 131 | MET |
| 9 | G | 137 | CYS |
| 9 | G | 154 | CYS |
| 9 | G | 166 | THR |
| 9 | G | 170 | VAL |
| 9 | G | 173 | THR |
| 9 | G | 217 | VAL |
| 10 | H | 6 | VAL |
| 10 | H | 12 | ILE |
| 10 | H | 18 | THR |
| 10 | H | 25 | VAL |
| 10 | H | 38 | SER |
| 10 | H | 43 | CYS |
| 10 | H | 61 | SER |
| 10 | H | 105 | VAL |
| 10 | H | 106 | THR |
| 10 | H | 143 | ARG |
| 10 | H | 171 | SER |
| 10 | H | 181 | ASN |
| 10 | H | 182 | LYS |
| 10 | H | 183 | LEU |
| 10 | H | 188 | PRO |
| 10 | H | 194 | LYS |
| 10 | H | 213 | THR |
| 11 | I | 19 | VAL |
| 11 | I | 33 | MET |
| 11 | I | 36 | THR |
| 11 | I | 52 | LEU |
| 11 | I | 57 | THR |
| 11 | I | 70 | LEU |
| 11 | I | 79 | ARG |
| 11 | I | 85 | THR |
| 11 | I | 98 | ARG |
| 11 | I | 104 | THR |
| 11 | I | 121 | CYS |
| 11 | I | 126 | ILE |
| 11 | I | 134 | ASP |
| 11 | I | 136 | VAL |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 11 | I | 145 | MET |
| 11 | I | 158 | ASP |
| 11 | I | 177 | ASP |
| 11 | I | 182 | MET |
| 11 | I | 184 | VAL |
| 11 | I | 190 | GLU |
| 11 | I | 196 | THR |
| 12 | J | 26 | VAL |
| 12 | J | 74 | GLU |
| 12 | J | 76 | SER |
| 12 | J | 78 | THR |
| 12 | J | 96 | THR |
| 12 | J | 102 | LEU |
| 12 | J | 118 | MET |
| 12 | J | 144 | ASP |
| 12 | J | 145 | ARG |
| 12 | J | 148 | THR |
| 13 | K | 1 | THR |
| 13 | K | 29 | GLN |
| 13 | K | 42 | LEU |
| 13 | K | 80 | SER |
| 13 | K | 99 | THR |
| 13 | K | 102 | CYS |
| 13 | K | 104 | TRP |
| 13 | K | 114 | VAL |
| 13 | K | 116 | SER |
| 13 | K | 182 | ASP |
| 13 | K | 187 | VAL |
| 14 | L | 11 | THR |
| 14 | L | 36 | HIS |
| 14 | L | 37 | THR |
| 14 | L | 38 | ARG |
| 14 | L | 131 | GLN |
| 14 | L | 164 | VAL |
| 14 | L | 169 | ASP |
| 14 | L | 189 | THR |
| 14 | L | 197 | ILE |
| 14 | L | 198 | VAL |
| 15 | M | 21 | VAL |
| 15 | M | 30 | TYR |
| 15 | M | 32 | SER |
| 15 | M | 79 | ASP |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 15 | M | 92 | LEU |
| 15 | M | 109 | THR |
| 15 | M | 141 | TYR |
| 15 | M | 147 | GLN |
| 15 | M | 191 | THR |
| 15 | M | 205 | THR |
| 16 | N | 1 | THR |
| 16 | N | 18 | SER |
| 16 | N | 20 | THR |
| 16 | N | 30 | VAL |
| 16 | N | 40 | ARG |
| 16 | N | 91 | ARG |
| 16 | N | 94 | LEU |
| 16 | N | 190 | LEU |
| 16 | N | 202 | LEU |
| 3 | O | 43 | VAL |
| 3 | O | 44 | VAL |
| 3 | O | 50 | LYS |
| 3 | O | 73 | LEU |
| 3 | O | 131 | VAL |
| 3 | O | 135 | ILE |
| 3 | O | 155 | PHE |
| 4 | P | 9 | THR |
| 4 | P | 25 | MET |
| 4 | P | 44 | LEU |
| 4 | P | 64 | LYS |
| 4 | P | 123 | GLN |
| 4 | P | 132 | VAL |
| 4 | P | 150 | SER |
| 4 | P | 185 | THR |
| 4 | P | 190 | LEU |
| 4 | P | 217 | THR |
| 4 | P | 223 | THR |
| 5 | Q | 23 | GLN |
| 5 | Q | 27 | LYS |
| 5 | Q | 54 | GLN |
| 5 | Q | 67 | ASP |
| 5 | Q | 77 | THR |
| 5 | Q | 83 | VAL |
| 5 | Q | 103 | THR |
| 5 | Q | 107 | ILE |
| 5 | Q | 172 | LEU |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 5 | Q | 191 | VAL |
| 5 | Q | 206 | ILE |
| 5 | Q | 225 | ILE |
| 6 | R | 10 | ARG |
| 6 | R | 46 | VAL |
| 6 | R | 47 | CYS |
| 6 | R | 54 | ILE |
| 6 | R | 58 | LEU |
| 6 | R | 59 | MET |
| 6 | R | 91 | LYS |
| 6 | R | 108 | THR |
| 6 | R | 119 | LEU |
| 6 | R | 121 | LEU |
| 6 | R | 139 | VAL |
| 6 | R | 156 | MET |
| 6 | R | 165 | CYS |
| 6 | R | 190 | THR |
| 6 | R | 210 | LEU |
| 6 | R | 234 | LEU |
| 7 | S | 5 | GLN |
| 7 | S | 16 | GLN |
| 7 | S | 18 | ARG |
| 7 | S | 35 | THR |
| 7 | S | 39 | LYS |
| 7 | S | 60 | GLN |
| 7 | S | 64 | LEU |
| 7 | S | 120 | THR |
| 7 | S | 130 | VAL |
| 7 | S | 133 | LEU |
| 7 | S | 150 | SER |
| 7 | S | 222 | THR |
| 7 | S | 228 | ASP |
| 8 | T | 35 | THR |
| 8 | T | 41 | CYS |
| 8 | T | 69 | VAL |
| 8 | T | 94 | GLU |
| 8 | T | 100 | SER |
| 8 | T | 142 | VAL |
| 8 | T | 154 | SER |
| 8 | T | 156 | VAL |
| 8 | T | 181 | MET |
| 8 | T | 182 | LYS |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 8 | T | 215 | TRP |
| 9 | U | 49 | VAL |
| 9 | U | 66 | VAL |
| 9 | U | 73 | THR |
| 9 | U | 78 | CYS |
| 9 | U | 80 | MET |
| 9 | U | 81 | THR |
| 9 | U | 84 | THR |
| 9 | U | 90 | GLN |
| 9 | U | 112 | ASP |
| 9 | U | 131 | MET |
| 9 | U | 170 | VAL |
| 9 | U | 173 | THR |
| 9 | U | 200 | THR |
| 9 | U | 215 | ILE |
| 10 | V | 1 | THR |
| 10 | V | 6 | VAL |
| 10 | V | 18 | THR |
| 10 | V | 21 | THR |
| 10 | V | 48 | THR |
| 10 | V | 61 | SER |
| 10 | V | 105 | VAL |
| 10 | V | 118 | SER |
| 10 | V | 119 | THR |
| 10 | V | 182 | LYS |
| 10 | V | 184 | ASP |
| 10 | V | 197 | THR |
| 10 | V | 212 | LEU |
| 10 | V | 216 | ILE |
| 11 | W | 2 | ILE |
| 11 | W | 19 | VAL |
| 11 | W | 57 | THR |
| 11 | W | 70 | LEU |
| 11 | W | 98 | ARG |
| 11 | W | 131 | VAL |
| 11 | W | 134 | ASP |
| 11 | W | 136 | VAL |
| 11 | W | 137 | VAL |
| 11 | W | 141 | CYS |
| 11 | W | 176 | ARG |
| 11 | W | 186 | VAL |
| 11 | W | 195 | THR |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 12 | X | 13 | VAL |
| 12 | X | 15 | VAL |
| 12 | X | 20 | VAL |
| 12 | X | 26 | VAL |
| 12 | X | 31 | ASP |
| 12 | X | 38 | MET |
| 12 | X | 39 | SER |
| 12 | X | 54 | VAL |
| 12 | X | 73 | TYR |
| 12 | X | 96 | THR |
| 13 | Y | 1 | THR |
| 13 | Y | 30 | THR |
| 13 | Y | 40 | TYR |
| 13 | Y | 41 | LEU |
| 13 | Y | 44 | THR |
| 13 | Y | 58 | LEU |
| 13 | Y | 97 | MET |
| 13 | Y | 102 | CYS |
| 13 | Y | 104 | TRP |
| 13 | Y | 107 | ARG |
| 13 | Y | 119 | ASN |
| 13 | Y | 121 | ILE |
| 13 | Y | 133 | VAL |
| 13 | Y | 138 | VAL |
| 13 | Y | 179 | VAL |
| 13 | Y | 187 | VAL |
| 13 | Y | 194 | ASP |
| 14 | Z | 13 | LEU |
| 14 | Z | 22 | ILE |
| 14 | Z | 93 | SER |
| 14 | Z | 99 | ARG |
| 14 | Z | 149 | LEU |
| 14 | Z | 164 | VAL |
| 14 | Z | 198 | VAL |
| 14 | Z | 203 | ILE |
| 15 | a | 14 | VAL |
| 15 | a | 21 | VAL |
| 15 | a | 27 | LEU |
| 15 | a | 29 | SER |
| 15 | a | 30 | TYR |
| 15 | a | 51 | LEU |
| 15 | a | 65 | GLN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 15 | a | 100 | ARG |
| 15 | a | 110 | MET |
| 15 | a | 137 | LEU |
| 15 | a | 148 | PRO |
| 15 | a | 169 | VAL |
| 15 | a | 191 | THR |
| 16 | b | 4 | MET |
| 16 | b | 20 | THR |
| 16 | b | 95 | MET |
| 16 | b | 98 | ILE |
| 16 | b | 187 | GLN |
| 16 | b | 190 | LEU |
| 2 | h | 21 | LEU |
| 2 | h | 50 | ASN |
| 2 | h | 61 | LEU |
| 2 | h | 63 | ILE |
| 2 | h | 65 | VAL |
| 2 | h | 116 | ARG |
| 2 | h | 128 | LEU |
| 2 | h | 144 | ASP |
| 2 | h | 159 | LEU |
| 2 | h | 185 | VAL |
| 2 | h | 191 | GLN |
| 2 | h | 248 | ILE |
| 2 | i | 21 | LEU |
| 2 | i | 28 | LEU |
| 2 | i | 50 | ASN |
| 2 | i | 61 | LEU |
| 2 | i | 63 | ILE |
| 2 | i | 65 | VAL |
| 2 | i | 109 | LYS |
| 2 | i | 128 | LEU |
| 2 | i | 136 | GLN |
| 2 | i | 144 | ASP |
| 2 | i | 155 | LYS |
| 2 | i | 157 | PHE |
| 2 | i | 159 | LEU |
| 2 | i | 191 | GLN |
| 2 | i | 213 | ARG |
| 2 | i | 248 | ILE |
| 1 | g | 41 | ILE |
| 1 | g | 50 | ASP |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (77) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | c | 38 | GLN |
| 1 | c | 45 | GLN |
| 1 | c | 126 | GLN |
| 1 | c | 151 | ASN |
| 2 | d | 138 | GLN |
| 2 | d | 147 | ASN |
| 2 | f | 138 | GLN |
| 2 | f | 147 | ASN |
| 3 | A | 122 | GLN |
| 4 | B | 146 | GLN |
| 4 | B | 149 | GLN |
| 4 | B | 230 | GLN |
| 6 | D | 13 | ASN |
| 6 | D | 227 | HIS |
| 7 | E | 31 | GLN |
| 7 | E | 68 | ASN |
| 9 | G | 24 | GLN |
| 9 | G | 53 | GLN |
| 9 | G | 128 | ASN |
| 11 | I | 17 | ASN |
| 12 | J | 87 | ASN |
| 12 | J | 168 | GLN |
| 13 | K | 10 | HIS |
| 13 | K | 29 | GLN |
| 13 | K | 162 | GLN |
| 14 | L | 77 | HIS |
| 14 | L | 80 | ASN |
| 15 | M | 81 | HIS |
| 15 | M | 147 | GLN |
| 15 | M | 157 | GLN |
| 15 | M | 188 | GLN |
| 15 | M | 213 | HIS |
| 16 | N | 66 | HIS |
| 16 | N | 106 | GLN |
| 16 | N | 110 | GLN |
| 3 | O | 108 | GLN |
| 3 | O | 168 | ASN |
| 4 | P | 109 | GLN |
| 4 | P | 123 | GLN |
| 4 | P | 230 | GLN |
| 5 | Q | 54 | GLN |

Continued on next page...

Continued from previous page...

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 6 | R | 182 | GLN |
| 6 | R | 227 | HIS |
| 7 | S | 16 | GLN |
| 7 | S | 68 | ASN |
| 9 | U | 24 | GLN |
| 9 | U | 53 | GLN |
| 9 | U | 147 | GLN |
| 10 | V | 80 | ASN |
| 11 | W | 6 | ASN |
| 12 | X | 82 | ASN |
| 12 | X | 87 | ASN |
| 12 | X | 132 | HIS |
| 13 | Y | 29 | GLN |
| 13 | Y | 119 | ASN |
| 14 | Z | 80 | ASN |
| 14 | Z | 108 | ASN |
| 14 | Z | 131 | GLN |
| 14 | Z | 152 | GLN |
| 14 | Z | 157 | ASN |
| 15 | a | 81 | HIS |
| 16 | b | 193 | GLN |
| 2 | h | 27 | ASN |
| 2 | h | 138 | GLN |
| 2 | h | 147 | ASN |
| 2 | h | 191 | GLN |
| 2 | i | 11 | GLN |
| 2 | i | 27 | ASN |
| 2 | i | 138 | GLN |
| 2 | i | 147 | ASN |
| 2 | i | 173 | GLN |
| 2 | i | 191 | GLN |
| 2 | i | 199 | GLN |
| 1 | g | 16 | GLN |
| 1 | g | 38 | GLN |
| 1 | g | 126 | GLN |
| 1 | g | 127 | HIS |

5.3.3 RNA ⓘ

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 oligosaccharides 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 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24276. 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 [i](#)

This section was not generated.

6.2 Central slices [i](#)

This section was not generated.

6.3 Largest variance slices [i](#)

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

This section was not generated.

6.5 Orthogonal surface views [i](#)

This section was not generated.

6.6 Mask visualisation [i](#)

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 ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit

This section was not generated.