



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 05:44 am GMT

PDB ID : 4Z32
Title : Crystal Structure of the FERM-SH2 Domains of Jak2
Authors : McNally, R.; Eck, M.J.
Deposited on : 2015-03-30
Resolution : 3.04 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

<http://wwpdb.org/validation/2016/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) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

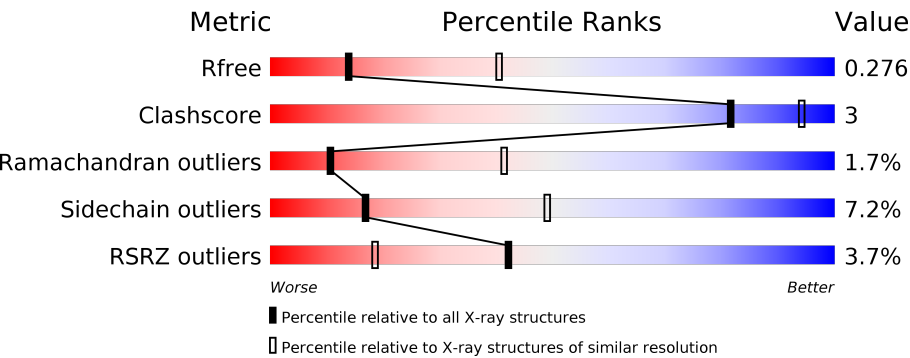
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.04 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} | 100719 | 2176 (3.08-3.00) |
| Clashscore | 112137 | 2542 (3.08-3.00) |
| Ramachandran outliers | 110173 | 2458 (3.08-3.00) |
| Sidechain outliers | 110143 | 2461 (3.08-3.00) |
| RSRZ outliers | 101464 | 2202 (3.08-3.00) |

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 | 497 | <div><div>%</div><div><div></div><div>75%</div><div>13%</div><div>•</div><div>11%</div></div></div> |
| 1 | B | 497 | <div><div>%</div><div><div></div><div>73%</div><div>14%</div><div>•</div><div>11%</div></div></div> |
| 1 | C | 497 | <div><div>6%</div><div><div></div><div>70%</div><div>13%</div><div>•</div><div>16%</div></div></div> |
| 1 | D | 497 | <div><div>3%</div><div><div></div><div>71%</div><div>12%</div><div>•</div><div>16%</div></div></div> |
| 1 | E | 497 | <div><div>%</div><div><div></div><div>73%</div><div>12%</div><div>•</div><div>14%</div></div></div> |
| 1 | F | 497 | <div><div>%</div><div><div></div><div>73%</div><div>13%</div><div>•</div><div>12%</div></div></div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 1 | G | 497 | <div><div></div><div>4%</div><div>74%</div><div>8%</div><div>17%</div></div> |
| 1 | H | 497 | <div><div></div><div>7%</div><div>72%</div><div>9%</div><div>19%</div></div> |

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 27929 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 Tyrosine-protein kinase JAK2.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|---------|-------|
| 1 | A | 441 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3624 | 2334 | 622 | 646 | 22 | | | |
| 1 | B | 441 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3624 | 2334 | 622 | 646 | 22 | | | |
| 1 | C | 418 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3433 | 2211 | 588 | 612 | 22 | | | |
| 1 | D | 417 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3423 | 2208 | 587 | 606 | 22 | | | |
| 1 | E | 427 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3516 | 2271 | 602 | 622 | 21 | | | |
| 1 | F | 436 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3586 | 2311 | 616 | 637 | 22 | | | |
| 1 | G | 411 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3375 | 2179 | 578 | 597 | 21 | | | |
| 1 | H | 405 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 3336 | 2154 | 573 | 588 | 21 | | | |

There are 88 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| A | 30 | GLY | - | expression tag | UNP O60674 |
| A | 517 | LEU | - | expression tag | UNP O60674 |
| A | 518 | GLU | - | expression tag | UNP O60674 |
| A | 519 | HIS | - | expression tag | UNP O60674 |
| A | 520 | HIS | - | expression tag | UNP O60674 |
| A | 521 | HIS | - | expression tag | UNP O60674 |
| A | 522 | HIS | - | expression tag | UNP O60674 |
| A | 523 | HIS | - | expression tag | UNP O60674 |
| A | 524 | HIS | - | expression tag | UNP O60674 |
| A | 525 | HIS | - | expression tag | UNP O60674 |
| A | 526 | HIS | - | expression tag | UNP O60674 |
| B | 30 | GLY | - | expression tag | UNP O60674 |
| B | 517 | LEU | - | expression tag | UNP O60674 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| B | 518 | GLU | - | expression tag | UNP O60674 |
| B | 519 | HIS | - | expression tag | UNP O60674 |
| B | 520 | HIS | - | expression tag | UNP O60674 |
| B | 521 | HIS | - | expression tag | UNP O60674 |
| B | 522 | HIS | - | expression tag | UNP O60674 |
| B | 523 | HIS | - | expression tag | UNP O60674 |
| B | 524 | HIS | - | expression tag | UNP O60674 |
| B | 525 | HIS | - | expression tag | UNP O60674 |
| B | 526 | HIS | - | expression tag | UNP O60674 |
| C | 30 | GLY | - | expression tag | UNP O60674 |
| C | 517 | LEU | - | expression tag | UNP O60674 |
| C | 518 | GLU | - | expression tag | UNP O60674 |
| C | 519 | HIS | - | expression tag | UNP O60674 |
| C | 520 | HIS | - | expression tag | UNP O60674 |
| C | 521 | HIS | - | expression tag | UNP O60674 |
| C | 522 | HIS | - | expression tag | UNP O60674 |
| C | 523 | HIS | - | expression tag | UNP O60674 |
| C | 524 | HIS | - | expression tag | UNP O60674 |
| C | 525 | HIS | - | expression tag | UNP O60674 |
| C | 526 | HIS | - | expression tag | UNP O60674 |
| D | 30 | GLY | - | expression tag | UNP O60674 |
| D | 517 | LEU | - | expression tag | UNP O60674 |
| D | 518 | GLU | - | expression tag | UNP O60674 |
| D | 519 | HIS | - | expression tag | UNP O60674 |
| D | 520 | HIS | - | expression tag | UNP O60674 |
| D | 521 | HIS | - | expression tag | UNP O60674 |
| D | 522 | HIS | - | expression tag | UNP O60674 |
| D | 523 | HIS | - | expression tag | UNP O60674 |
| D | 524 | HIS | - | expression tag | UNP O60674 |
| D | 525 | HIS | - | expression tag | UNP O60674 |
| D | 526 | HIS | - | expression tag | UNP O60674 |
| E | 30 | GLY | - | expression tag | UNP O60674 |
| E | 517 | LEU | - | expression tag | UNP O60674 |
| E | 518 | GLU | - | expression tag | UNP O60674 |
| E | 519 | HIS | - | expression tag | UNP O60674 |
| E | 520 | HIS | - | expression tag | UNP O60674 |
| E | 521 | HIS | - | expression tag | UNP O60674 |
| E | 522 | HIS | - | expression tag | UNP O60674 |
| E | 523 | HIS | - | expression tag | UNP O60674 |
| E | 524 | HIS | - | expression tag | UNP O60674 |
| E | 525 | HIS | - | expression tag | UNP O60674 |
| E | 526 | HIS | - | expression tag | UNP O60674 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| F | 30 | GLY | - | expression tag | UNP O60674 |
| F | 517 | LEU | - | expression tag | UNP O60674 |
| F | 518 | GLU | - | expression tag | UNP O60674 |
| F | 519 | HIS | - | expression tag | UNP O60674 |
| F | 520 | HIS | - | expression tag | UNP O60674 |
| F | 521 | HIS | - | expression tag | UNP O60674 |
| F | 522 | HIS | - | expression tag | UNP O60674 |
| F | 523 | HIS | - | expression tag | UNP O60674 |
| F | 524 | HIS | - | expression tag | UNP O60674 |
| F | 525 | HIS | - | expression tag | UNP O60674 |
| F | 526 | HIS | - | expression tag | UNP O60674 |
| G | 30 | GLY | - | expression tag | UNP O60674 |
| G | 517 | LEU | - | expression tag | UNP O60674 |
| G | 518 | GLU | - | expression tag | UNP O60674 |
| G | 519 | HIS | - | expression tag | UNP O60674 |
| G | 520 | HIS | - | expression tag | UNP O60674 |
| G | 521 | HIS | - | expression tag | UNP O60674 |
| G | 522 | HIS | - | expression tag | UNP O60674 |
| G | 523 | HIS | - | expression tag | UNP O60674 |
| G | 524 | HIS | - | expression tag | UNP O60674 |
| G | 525 | HIS | - | expression tag | UNP O60674 |
| G | 526 | HIS | - | expression tag | UNP O60674 |
| H | 30 | GLY | - | expression tag | UNP O60674 |
| H | 517 | LEU | - | expression tag | UNP O60674 |
| H | 518 | GLU | - | expression tag | UNP O60674 |
| H | 519 | HIS | - | expression tag | UNP O60674 |
| H | 520 | HIS | - | expression tag | UNP O60674 |
| H | 521 | HIS | - | expression tag | UNP O60674 |
| H | 522 | HIS | - | expression tag | UNP O60674 |
| H | 523 | HIS | - | expression tag | UNP O60674 |
| H | 524 | HIS | - | expression tag | UNP O60674 |
| H | 525 | HIS | - | expression tag | UNP O60674 |
| H | 526 | HIS | - | expression tag | UNP O60674 |

- Molecule 2 is water.

| Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|----------------|---------|---------|
| 2 | A | 5 | Total O 5 5 | 0 | 0 |
| 2 | B | 4 | Total O 4 4 | 0 | 0 |
| 2 | D | 1 | Total O 1 1 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---------|---------|
| 2 | E | 1 | Total | O | 0 | 0 |
| | | | 1 | 1 | | |
| 2 | F | 1 | Total | O | 0 | 0 |
| | | | 1 | 1 | | |

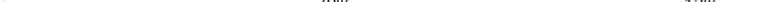
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

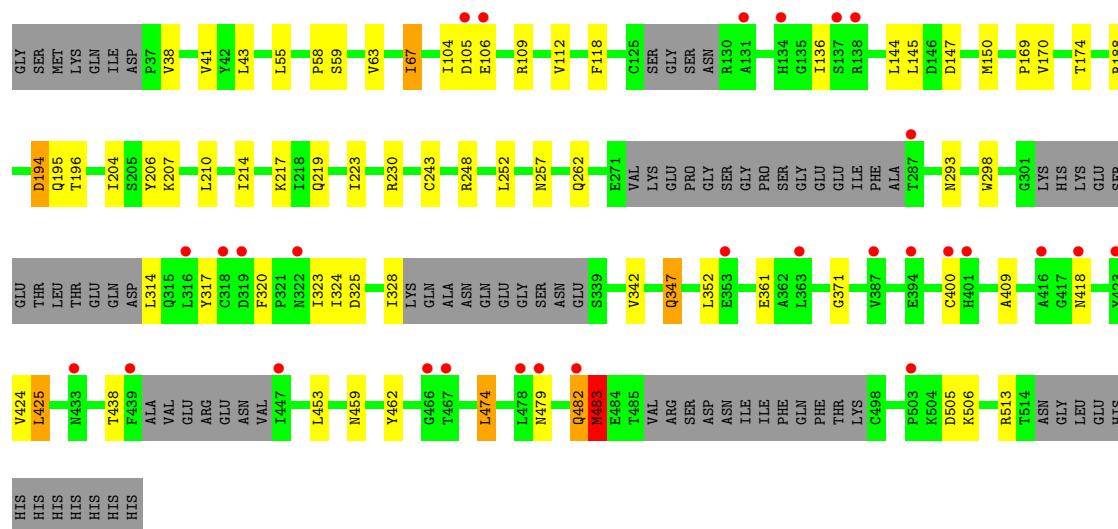
Chain A: 

Chain B:

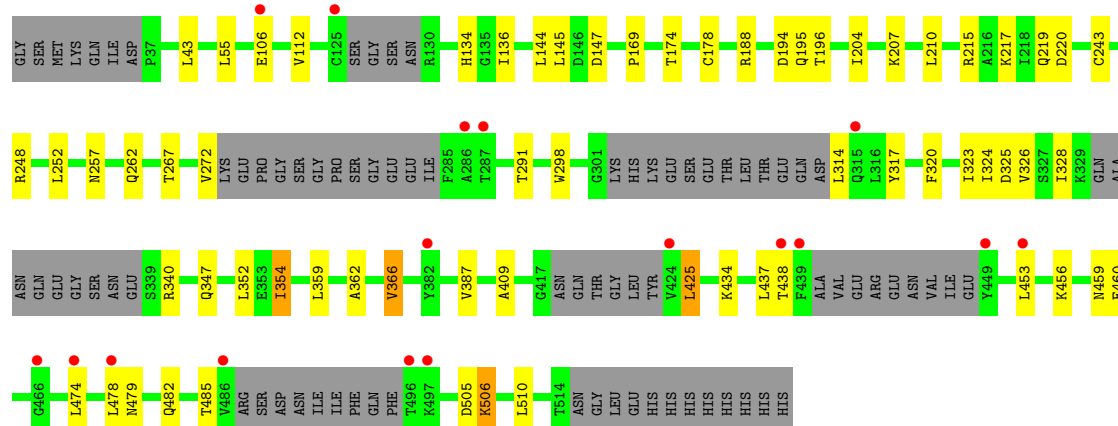
73% 14% 11%

GLY SER MET MET LYS GLN ILE ASP P37 V38 Y42 L43 S50 S55 L55 P58 S59 T78 I104 D105 E106 S107 T108 R109 V112 L113 C125 G125 GLY SER GLY ASN R130 H134 G135 I136 S137 R138 L144 L145 D146 D147 R158 P169 V170 T174 R188 I189 D194 Q195 T196 Y201 T204 K207 R215 A216 K217 T218 Q219 R226 R234 R248 L252 W257 Q262 T267 V272 LYS GLU PRO GLY SER GLY PRO SER SER GLY GLY ILE T291 G294 W298 G301 LYS HIS GLY LYS T324 L314 L316 L316 L324 K329 GLN ALA ASN ASN GLU GLY GLY SER ASN GLU S339 S347 E355 L356 A362 C400 A409 N418 Q419 L425 K434 Y435 T438 V441 E444 L453 L454 T455 K456 E460 E461 Y462 N470 L474

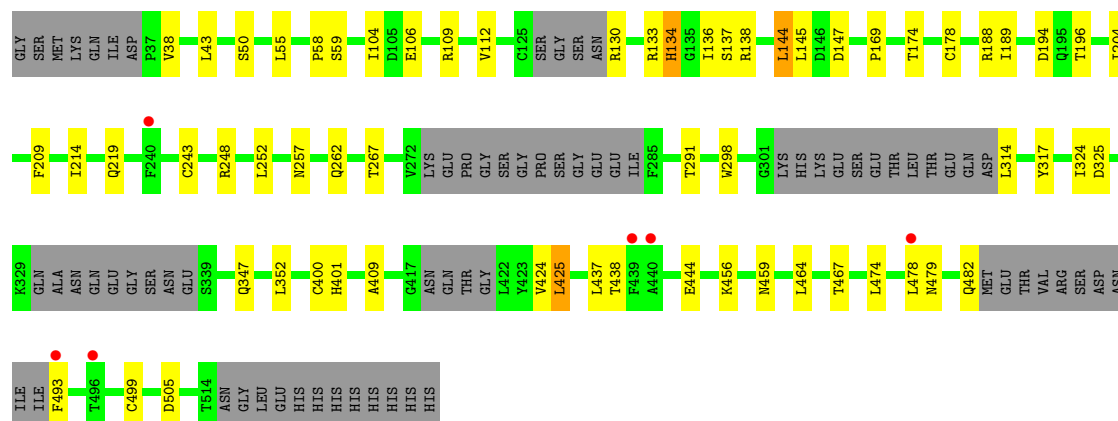
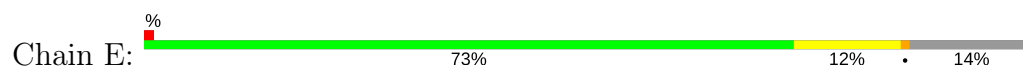
Chain C:  6% 70% 13% 16%



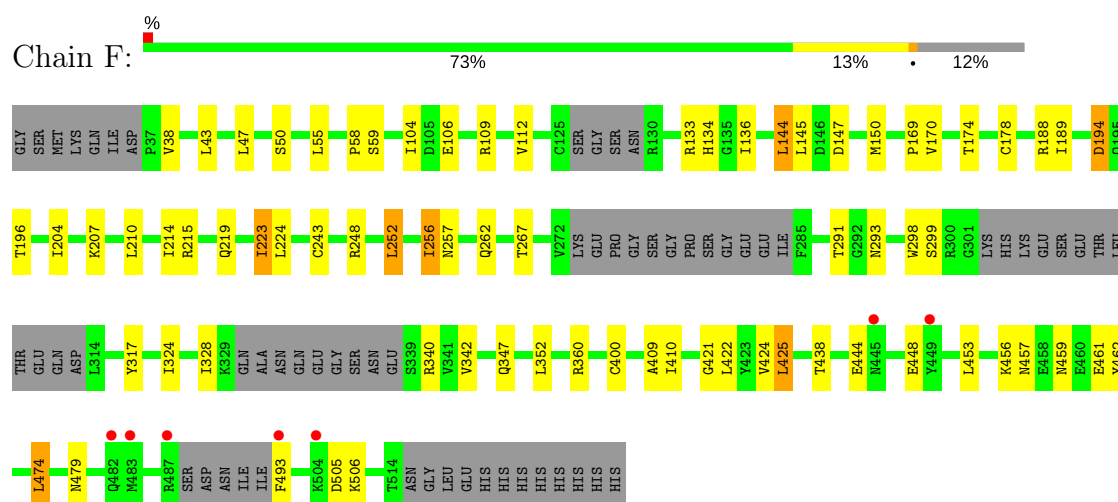
• Molecule 1: Tyrosine-protein kinase JAK2



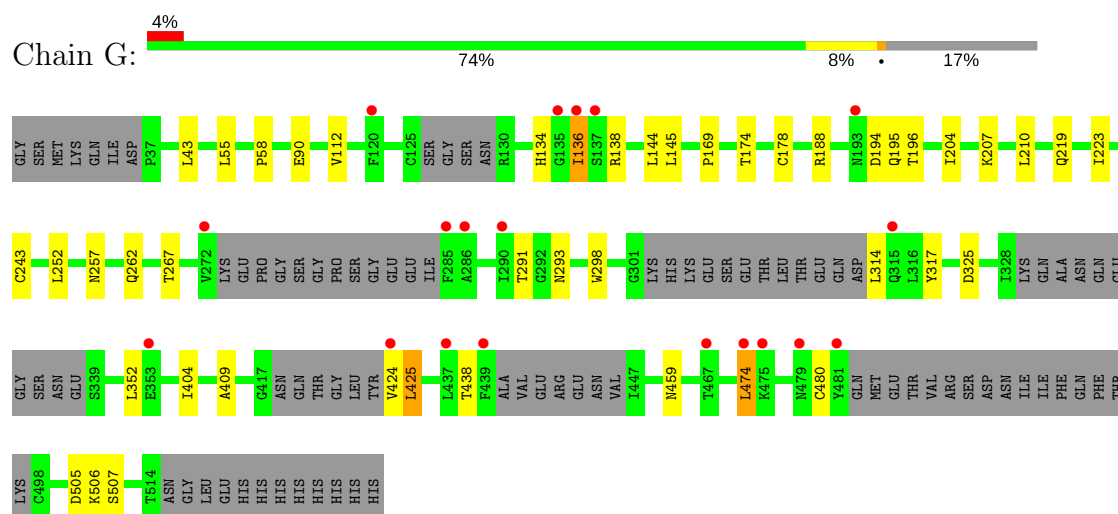
• Molecule 1: Tyrosine-protein kinase JAK2



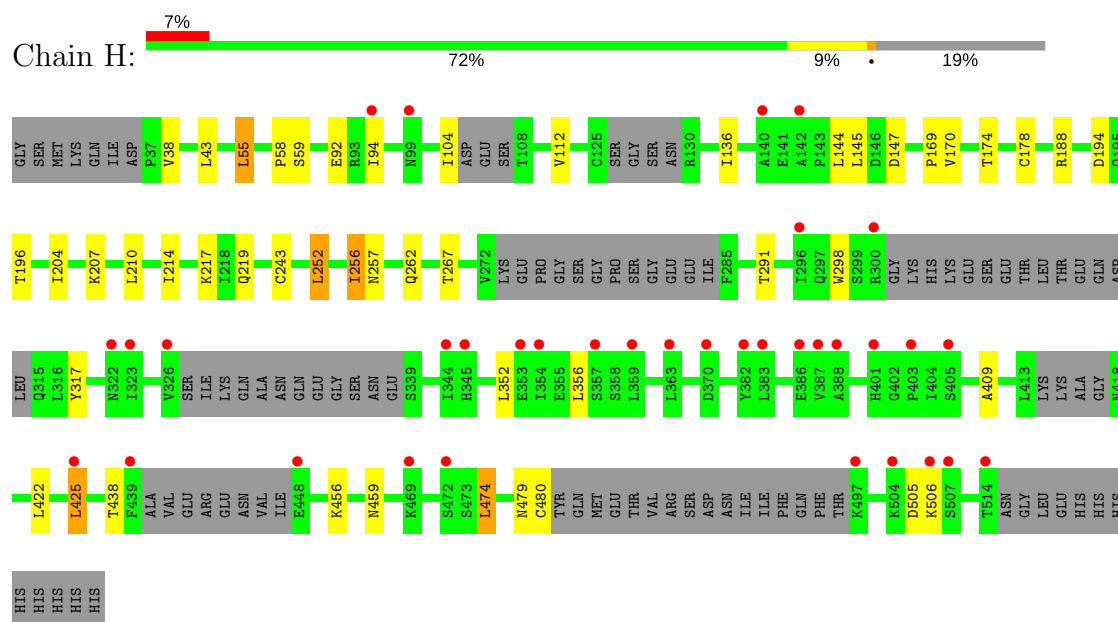
• Molecule 1: Tyrosine-protein kinase JAK2



• Molecule 1: Tyrosine-protein kinase JAK2



• Molecule 1: Tyrosine-protein kinase JAK2



4 Data and refinement statistics

| Property | Value | Source |
|---|---|------------------|
| Space group | P 1 21 1 | Depositor |
| Cell constants a, b, c, α , β , γ | 118.19Å 188.74Å 118.58Å 90.00° 113.87° 90.00° | Depositor |
| Resolution (Å) | 42.95 – 3.04 47.19 – 3.00 | Depositor EDS |
| % Data completeness (in resolution range) | 96.2 (42.95-3.04) 95.3 (47.19-3.00) | Depositor EDS |
| R_{merge} | 0.07 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 2.01 (at 3.01Å) | Xtriage |
| Refinement program | PHENIX (phenix.refine: 1.9_1692) | Depositor |
| R, R_{free} | 0.257 , 0.276 0.257 , 0.276 | Depositor DCC |
| R_{free} test set | 4306 reflections (4.91%) | DCC |
| Wilson B-factor (Å ²) | 67.8 | Xtriage |
| Anisotropy | 0.315 | Xtriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.30 , 43.2 | EDS |
| L-test for twinning ² | $\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$ | Xtriage |
| Estimated twinning fraction | 0.116 for l,-k,h | Xtriage |
| F_o, F_c correlation | 0.91 | EDS |
| Total number of atoms | 27929 | wwPDB-VP |
| Average B, all atoms (Å ²) | 88.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 34.10 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 7.1980e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 | 0.39 | 0/3713 | 0.59 | 0/5015 |
| 1 | B | 0.39 | 0/3713 | 0.61 | 0/5015 |
| 1 | C | 0.39 | 0/3517 | 0.59 | 0/4748 |
| 1 | D | 0.38 | 0/3506 | 0.58 | 0/4730 |
| 1 | E | 0.39 | 0/3603 | 0.58 | 0/4863 |
| 1 | F | 0.39 | 0/3674 | 0.59 | 0/4960 |
| 1 | G | 0.39 | 0/3458 | 0.59 | 0/4667 |
| 1 | H | 0.38 | 0/3418 | 0.58 | 0/4613 |
| All | All | 0.39 | 0/28602 | 0.59 | 0/38611 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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 | 3624 | 0 | 3603 | 24 | 0 |
| 1 | B | 3624 | 0 | 3603 | 28 | 0 |
| 1 | C | 3433 | 0 | 3406 | 29 | 0 |
| 1 | D | 3423 | 0 | 3409 | 23 | 0 |
| 1 | E | 3516 | 0 | 3496 | 21 | 0 |
| 1 | F | 3586 | 0 | 3565 | 28 | 0 |
| 1 | G | 3375 | 0 | 3354 | 12 | 0 |
| 1 | H | 3336 | 0 | 3311 | 13 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 2 | A | 5 | 0 | 0 | 0 | 0 |
| 2 | B | 4 | 0 | 0 | 0 | 0 |
| 2 | D | 1 | 0 | 0 | 0 | 0 |
| 2 | E | 1 | 0 | 0 | 0 | 0 |
| 2 | F | 1 | 0 | 0 | 0 | 0 |
| All | All | 27929 | 0 | 27747 | 165 | 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 3.

All (165) 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) |
|------------------|------------------|--------------------------|-------------------|
| 1:C:41:VAL:HG21 | 1:C:67:ILE:HD11 | 1.42 | 1.01 |
| 1:H:252:LEU:O | 1:H:256:ILE:HD13 | 1.75 | 0.87 |
| 1:F:252:LEU:O | 1:F:256:ILE:HD13 | 1.76 | 0.86 |
| 1:B:147:ASP:HB3 | 1:B:248:ARG:HH12 | 1.42 | 0.84 |
| 1:F:207:LYS:HA | 1:F:210:LEU:HD12 | 1.61 | 0.83 |
| 1:A:207:LYS:HA | 1:A:210:LEU:HD12 | 1.62 | 0.81 |
| 1:G:207:LYS:HA | 1:G:210:LEU:HD12 | 1.66 | 0.76 |
| 1:C:248:ARG:HH12 | 1:D:195:GLN:HG2 | 1.51 | 0.74 |
| 1:H:207:LYS:HA | 1:H:210:LEU:HD12 | 1.68 | 0.74 |
| 1:F:147:ASP:HB3 | 1:F:248:ARG:HH22 | 1.53 | 0.72 |
| 1:C:41:VAL:HG21 | 1:C:67:ILE:CD1 | 2.19 | 0.71 |
| 1:B:267:THR:HG22 | 1:B:291:THR:HG22 | 1.72 | 0.71 |
| 1:D:267:THR:HG22 | 1:D:291:THR:HG22 | 1.72 | 0.70 |
| 1:A:267:THR:HG22 | 1:A:291:THR:HG22 | 1.74 | 0.70 |
| 1:F:267:THR:HG22 | 1:F:291:THR:HG22 | 1.73 | 0.70 |
| 1:E:267:THR:HG22 | 1:E:291:THR:HG22 | 1.73 | 0.69 |
| 1:C:147:ASP:HB3 | 1:C:248:ARG:HH22 | 1.58 | 0.69 |
| 1:F:147:ASP:HB3 | 1:F:248:ARG:NH2 | 2.08 | 0.68 |
| 1:F:133:ARG:HG3 | 1:F:144:LEU:HA | 1.77 | 0.67 |
| 1:G:267:THR:HG22 | 1:G:291:THR:HG22 | 1.77 | 0.66 |
| 1:B:147:ASP:HB3 | 1:B:248:ARG:NH1 | 2.11 | 0.65 |
| 1:D:328:ILE:HD11 | 1:D:366:VAL:HG21 | 1.78 | 0.65 |
| 1:D:326:VAL:HG11 | 1:D:366:VAL:HG12 | 1.80 | 0.64 |
| 1:B:147:ASP:CB | 1:B:248:ARG:HH12 | 2.09 | 0.63 |
| 1:C:147:ASP:HB3 | 1:C:248:ARG:NH2 | 2.13 | 0.63 |
| 1:E:400:CYS:HA | 1:E:425:LEU:HB3 | 1.81 | 0.62 |
| 1:D:425:LEU:HD21 | 1:D:478:LEU:HD11 | 1.83 | 0.60 |
| 1:G:195:GLN:HE22 | 1:H:147:ASP:HB2 | 1.65 | 0.60 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:C:195:GLN:HE22 | 1:D:147:ASP:HB2 | 1.66 | 0.60 |
| 1:D:362:ALA:O | 1:D:366:VAL:HG22 | 2.02 | 0.60 |
| 1:E:204:ILE:HD13 | 1:F:47:LEU:HB3 | 1.83 | 0.60 |
| 1:E:178:CYS:SG | 1:E:214:ILE:HD13 | 2.41 | 0.60 |
| 1:H:409:ALA:HB1 | 1:H:438:THR:HG21 | 1.83 | 0.59 |
| 1:E:50:SER:HB2 | 1:F:189:ILE:HG12 | 1.85 | 0.59 |
| 1:G:425:LEU:HD11 | 1:G:474:LEU:HD22 | 1.85 | 0.58 |
| 1:B:147:ASP:CB | 1:B:248:ARG:NH1 | 2.66 | 0.57 |
| 1:B:441:VAL:HG11 | 1:B:491:ILE:HG21 | 1.86 | 0.57 |
| 1:E:133:ARG:HG3 | 1:E:144:LEU:HA | 1.87 | 0.56 |
| 1:B:434:LYS:HD3 | 1:B:453:LEU:HD11 | 1.88 | 0.56 |
| 1:D:409:ALA:HB1 | 1:D:438:THR:HG21 | 1.87 | 0.56 |
| 1:F:409:ALA:HB1 | 1:F:438:THR:HG21 | 1.89 | 0.55 |
| 1:D:207:LYS:HA | 1:D:210:LEU:HD12 | 1.89 | 0.54 |
| 1:E:189:ILE:HG12 | 1:F:50:SER:HB2 | 1.89 | 0.54 |
| 1:F:178:CYS:HB3 | 1:F:210:LEU:HD23 | 1.91 | 0.53 |
| 1:A:272:VAL:HG21 | 1:A:354:ILE:HG23 | 1.89 | 0.53 |
| 1:A:194:ASP:O | 1:B:248:ARG:NH2 | 2.35 | 0.53 |
| 1:A:50:SER:HB3 | 1:B:189:ILE:HG12 | 1.91 | 0.52 |
| 1:F:207:LYS:HB3 | 1:F:215:ARG:HG3 | 1.91 | 0.52 |
| 1:B:409:ALA:HB1 | 1:B:438:THR:HG21 | 1.91 | 0.52 |
| 1:E:409:ALA:HB1 | 1:E:438:THR:HG21 | 1.90 | 0.52 |
| 1:H:169:PRO:HG2 | 1:H:174:THR:HG21 | 1.92 | 0.52 |
| 1:D:169:PRO:HG2 | 1:D:174:THR:HG21 | 1.92 | 0.51 |
| 1:C:206:TYR:HE1 | 1:C:230:ARG:HG2 | 1.75 | 0.51 |
| 1:C:409:ALA:HB1 | 1:C:438:THR:HG21 | 1.92 | 0.51 |
| 1:A:419:GLN:HB3 | 1:A:422:LEU:HD12 | 1.92 | 0.51 |
| 1:D:366:VAL:HG23 | 1:D:387:VAL:HG11 | 1.92 | 0.51 |
| 1:C:169:PRO:HG2 | 1:C:174:THR:HG21 | 1.93 | 0.51 |
| 1:A:147:ASP:HB2 | 1:B:195:GLN:HE22 | 1.75 | 0.51 |
| 1:G:169:PRO:HG2 | 1:G:174:THR:HG21 | 1.92 | 0.51 |
| 1:B:356:LEU:HD13 | 1:B:362:ALA:HA | 1.92 | 0.50 |
| 1:C:425:LEU:HD11 | 1:C:474:LEU:HD22 | 1.92 | 0.50 |
| 1:B:169:PRO:HG2 | 1:B:174:THR:HG21 | 1.93 | 0.50 |
| 1:E:38:VAL:HG12 | 1:E:109:ARG:HG2 | 1.94 | 0.50 |
| 1:A:178:CYS:HB3 | 1:A:210:LEU:HD23 | 1.92 | 0.50 |
| 1:G:409:ALA:HB1 | 1:G:438:THR:HG21 | 1.93 | 0.50 |
| 1:C:43:LEU:HD11 | 1:C:55:LEU:HD13 | 1.94 | 0.50 |
| 1:B:435:TYR:HE1 | 1:B:456:LYS:HG3 | 1.77 | 0.50 |
| 1:G:178:CYS:HB3 | 1:G:210:LEU:HD23 | 1.94 | 0.50 |
| 1:D:43:LEU:HD11 | 1:D:55:LEU:HD13 | 1.94 | 0.49 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:E:425:LEU:HD21 | 1:E:478:LEU:HD21 | 1.93 | 0.49 |
| 1:A:169:PRO:HG2 | 1:A:174:THR:HG21 | 1.93 | 0.49 |
| 1:B:38:VAL:HG23 | 1:B:109:ARG:HG2 | 1.94 | 0.49 |
| 1:F:43:LEU:HD11 | 1:F:55:LEU:HD13 | 1.94 | 0.49 |
| 1:F:169:PRO:HG2 | 1:F:174:THR:HG21 | 1.94 | 0.49 |
| 1:G:43:LEU:HD11 | 1:G:55:LEU:HD13 | 1.94 | 0.49 |
| 1:H:178:CYS:HB3 | 1:H:210:LEU:HD23 | 1.94 | 0.49 |
| 1:C:293:ASN:HA | 1:C:513:ARG:HD2 | 1.95 | 0.49 |
| 1:A:409:ALA:HB1 | 1:A:438:THR:HG21 | 1.93 | 0.49 |
| 1:E:169:PRO:HG2 | 1:E:174:THR:HG21 | 1.93 | 0.49 |
| 1:H:43:LEU:HD11 | 1:H:55:LEU:HD23 | 1.93 | 0.49 |
| 1:B:147:ASP:CG | 1:B:248:ARG:NH1 | 2.67 | 0.48 |
| 1:A:400:CYS:HB2 | 1:A:425:LEU:HD13 | 1.96 | 0.48 |
| 1:B:170:VAL:HG12 | 1:B:217:LYS:HD2 | 1.96 | 0.48 |
| 1:C:38:VAL:HG12 | 1:C:109:ARG:HG2 | 1.95 | 0.48 |
| 1:D:506:LYS:HA | 1:D:510:LEU:HD12 | 1.96 | 0.48 |
| 1:A:43:LEU:HD11 | 1:A:55:LEU:HD13 | 1.96 | 0.48 |
| 1:F:400:CYS:HB2 | 1:F:425:LEU:HD13 | 1.95 | 0.48 |
| 1:F:457:ASN:HB2 | 1:F:461:GLU:H | 1.79 | 0.47 |
| 1:E:43:LEU:HD11 | 1:E:55:LEU:HD13 | 1.95 | 0.47 |
| 1:D:317:TYR:CZ | 1:D:352:LEU:HB2 | 2.50 | 0.47 |
| 1:B:400:CYS:HB2 | 1:B:425:LEU:HD13 | 1.97 | 0.47 |
| 1:B:43:LEU:HD11 | 1:B:55:LEU:HD13 | 1.97 | 0.47 |
| 1:F:317:TYR:CZ | 1:F:352:LEU:HB2 | 2.49 | 0.47 |
| 1:B:42:TYR:HB3 | 1:B:113:LEU:HD23 | 1.97 | 0.47 |
| 1:C:207:LYS:HA | 1:C:210:LEU:HD12 | 1.97 | 0.47 |
| 1:E:317:TYR:CZ | 1:E:352:LEU:HB2 | 2.50 | 0.47 |
| 1:H:267:THR:HG22 | 1:H:291:THR:HG22 | 1.95 | 0.47 |
| 1:B:207:LYS:HZ1 | 1:B:226:ARG:HH11 | 1.62 | 0.47 |
| 1:B:461:GLU:HG3 | 1:B:470:ASN:HB3 | 1.97 | 0.47 |
| 1:C:400:CYS:HB2 | 1:C:425:LEU:HD13 | 1.96 | 0.47 |
| 1:C:482:GLN:O | 1:C:483:MET:HB2 | 2.15 | 0.47 |
| 1:H:425:LEU:HD11 | 1:H:474:LEU:HD22 | 1.97 | 0.47 |
| 1:A:441:VAL:HG21 | 1:A:491:ILE:HG12 | 1.96 | 0.46 |
| 1:C:324:ILE:HD11 | 1:C:347:GLN:HA | 1.98 | 0.46 |
| 1:B:324:ILE:HD11 | 1:B:347:GLN:HA | 1.97 | 0.46 |
| 1:D:324:ILE:HD11 | 1:D:347:GLN:HA | 1.97 | 0.46 |
| 1:E:147:ASP:HB3 | 1:E:248:ARG:NH2 | 2.29 | 0.46 |
| 1:F:324:ILE:HD11 | 1:F:347:GLN:HA | 1.96 | 0.46 |
| 1:G:317:TYR:CZ | 1:G:352:LEU:HB2 | 2.50 | 0.46 |
| 1:A:317:TYR:CZ | 1:A:352:LEU:HB2 | 2.50 | 0.46 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:A:324:ILE:HD11 | 1:A:347:GLN:HA | 1.97 | 0.46 |
| 1:C:118:PHE:CZ | 1:C:371:GLY:HA3 | 2.51 | 0.46 |
| 1:D:320:PHE:HA | 1:D:323:ILE:HD12 | 1.98 | 0.46 |
| 1:E:324:ILE:HD11 | 1:E:347:GLN:HA | 1.97 | 0.45 |
| 1:B:425:LEU:HD11 | 1:B:474:LEU:HD22 | 1.99 | 0.45 |
| 1:A:189:ILE:HG12 | 1:B:50:SER:HB3 | 1.97 | 0.45 |
| 1:C:317:TYR:CZ | 1:C:352:LEU:HB2 | 2.52 | 0.45 |
| 1:F:38:VAL:HG12 | 1:F:109:ARG:HG2 | 1.98 | 0.45 |
| 1:A:425:LEU:HD11 | 1:A:474:LEU:HD22 | 1.98 | 0.45 |
| 1:H:92:GLU:HB3 | 1:H:94:ILE:HD12 | 1.98 | 0.45 |
| 1:B:201:TYR:CE2 | 1:B:234:ARG:HD3 | 2.52 | 0.44 |
| 1:E:424:VAL:HB | 1:E:438:THR:HG23 | 1.99 | 0.44 |
| 1:C:63:VAL:O | 1:C:67:ILE:HG22 | 2.18 | 0.44 |
| 1:F:425:LEU:HD11 | 1:F:474:LEU:HD22 | 2.00 | 0.44 |
| 1:A:461:GLU:O | 1:A:462:TYR:HB2 | 2.18 | 0.43 |
| 1:B:435:TYR:HB2 | 1:B:454:ILE:HB | 2.00 | 0.43 |
| 1:A:272:VAL:CG2 | 1:A:354:ILE:HG23 | 2.49 | 0.43 |
| 1:D:340:ARG:HD3 | 1:D:359:LEU:HB3 | 2.01 | 0.43 |
| 1:H:317:TYR:CZ | 1:H:352:LEU:HB2 | 2.54 | 0.43 |
| 1:D:178:CYS:HB3 | 1:D:210:LEU:HD23 | 2.01 | 0.43 |
| 1:F:424:VAL:HB | 1:F:438:THR:HG23 | 2.01 | 0.43 |
| 1:G:134:HIS:HB2 | 1:G:507:SER:O | 2.19 | 0.43 |
| 1:G:424:VAL:HB | 1:G:438:THR:HG23 | 2.01 | 0.42 |
| 1:F:400:CYS:HA | 1:F:425:LEU:HB3 | 2.01 | 0.42 |
| 1:C:248:ARG:NH1 | 1:D:195:GLN:HG2 | 2.29 | 0.42 |
| 1:F:170:VAL:HG13 | 1:F:214:ILE:HD13 | 2.01 | 0.42 |
| 1:C:170:VAL:HG13 | 1:C:214:ILE:HD13 | 2.02 | 0.42 |
| 1:D:267:THR:HG22 | 1:D:291:THR:CG2 | 2.46 | 0.42 |
| 1:C:194:ASP:OD2 | 1:D:248:ARG:HG2 | 2.20 | 0.42 |
| 1:E:204:ILE:HD12 | 1:E:209:PHE:CZ | 2.55 | 0.42 |
| 1:H:59:SER:HA | 1:H:104:ILE:HG22 | 2.02 | 0.42 |
| 1:E:248:ARG:HD2 | 1:F:194:ASP:HB2 | 2.02 | 0.42 |
| 1:C:170:VAL:HG12 | 1:C:217:LYS:HD2 | 2.02 | 0.42 |
| 1:A:59:SER:HA | 1:A:104:ILE:HG22 | 2.03 | 0.41 |
| 1:D:434:LYS:HE3 | 1:D:453:LEU:HD13 | 2.01 | 0.41 |
| 1:F:328:ILE:HG12 | 1:F:342:VAL:HG22 | 2.03 | 0.41 |
| 1:H:170:VAL:HG13 | 1:H:214:ILE:HD13 | 2.01 | 0.41 |
| 1:C:320:PHE:HA | 1:C:323:ILE:HD12 | 2.02 | 0.41 |
| 1:A:170:VAL:HG13 | 1:A:214:ILE:HD13 | 2.02 | 0.41 |
| 1:F:223:ILE:HD13 | 1:F:224:LEU:HG | 2.02 | 0.41 |
| 1:G:136:ILE:C | 1:G:138:ARG:H | 2.24 | 0.41 |

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| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|------------------|------------------|--------------------------|-------------------|
| 1:F:59:SER:HA | 1:F:104:ILE:HG22 | 2.02 | 0.41 |
| 1:E:401:HIS:HE1 | 1:E:499:CYS:O | 2.03 | 0.41 |
| 1:C:424:VAL:HB | 1:C:438:THR:HG23 | 2.02 | 0.40 |
| 1:C:59:SER:HA | 1:C:104:ILE:HG22 | 2.03 | 0.40 |
| 1:C:328:ILE:HG12 | 1:C:342:VAL:HG22 | 2.02 | 0.40 |
| 1:E:267:THR:HG22 | 1:E:291:THR:CG2 | 2.48 | 0.40 |
| 1:A:328:ILE:HG12 | 1:A:342:VAL:HG22 | 2.02 | 0.40 |
| 1:B:59:SER:HA | 1:B:104:ILE:HG22 | 2.03 | 0.40 |
| 1:D:272:VAL:HG21 | 1:D:354:ILE:HG12 | 2.04 | 0.40 |
| 1:F:267:THR:HG22 | 1:F:291:THR:CG2 | 2.48 | 0.40 |
| 1:A:424:VAL:HB | 1:A:438:THR:HG23 | 2.04 | 0.40 |
| 1:A:400:CYS:HA | 1:A:425:LEU:HB3 | 2.04 | 0.40 |
| 1:C:400:CYS:HA | 1:C:425:LEU:HB3 | 2.03 | 0.40 |
| 1:E:59:SER:HA | 1:E:104:ILE:HG22 | 2.03 | 0.40 |

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 | 431/497 (87%) | 399 (93%) | 23 (5%) | 9 (2%) | 8 | 35 |
| 1 | B | 431/497 (87%) | 400 (93%) | 20 (5%) | 11 (3%) | 6 | 29 |
| 1 | C | 404/497 (81%) | 375 (93%) | 21 (5%) | 8 (2%) | 9 | 36 |
| 1 | D | 401/497 (81%) | 378 (94%) | 20 (5%) | 3 (1%) | 25 | 64 |
| 1 | E | 413/497 (83%) | 388 (94%) | 18 (4%) | 7 (2%) | 11 | 41 |
| 1 | F | 424/497 (85%) | 393 (93%) | 22 (5%) | 9 (2%) | 8 | 35 |
| 1 | G | 395/497 (80%) | 372 (94%) | 19 (5%) | 4 (1%) | 18 | 56 |
| 1 | H | 387/497 (78%) | 362 (94%) | 21 (5%) | 4 (1%) | 18 | 56 |
| All | All | 3286/3976 (83%) | 3067 (93%) | 164 (5%) | 55 (2%) | 11 | 41 |

All (55) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 136 | ILE |
| 1 | B | 106 | GLU |
| 1 | B | 136 | ILE |
| 1 | C | 106 | GLU |
| 1 | C | 136 | ILE |
| 1 | C | 483 | MET |
| 1 | D | 136 | ILE |
| 1 | E | 106 | GLU |
| 1 | E | 136 | ILE |
| 1 | F | 106 | GLU |
| 1 | F | 136 | ILE |
| 1 | F | 462 | TYR |
| 1 | G | 136 | ILE |
| 1 | H | 136 | ILE |
| 1 | A | 462 | TYR |
| 1 | B | 134 | HIS |
| 1 | C | 347 | GLN |
| 1 | A | 194 | ASP |
| 1 | B | 444 | GLU |
| 1 | B | 462 | TYR |
| 1 | B | 489 | ASP |
| 1 | C | 462 | TYR |
| 1 | E | 134 | HIS |
| 1 | F | 134 | HIS |
| 1 | A | 106 | GLU |
| 1 | A | 134 | HIS |
| 1 | A | 196 | THR |
| 1 | A | 444 | GLU |
| 1 | A | 489 | ASP |
| 1 | B | 194 | ASP |
| 1 | B | 196 | THR |
| 1 | B | 294 | GLY |
| 1 | B | 485 | THR |
| 1 | C | 196 | THR |
| 1 | D | 196 | THR |
| 1 | E | 194 | ASP |
| 1 | E | 196 | THR |
| 1 | E | 444 | GLU |
| 1 | F | 194 | ASP |
| 1 | F | 196 | THR |
| 1 | F | 421 | GLY |
| 1 | F | 444 | GLU |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | G | 196 | THR |
| 1 | H | 196 | THR |
| 1 | D | 194 | ASP |
| 1 | G | 194 | ASP |
| 1 | H | 194 | ASP |
| 1 | C | 194 | ASP |
| 1 | B | 58 | PRO |
| 1 | C | 58 | PRO |
| 1 | A | 58 | PRO |
| 1 | E | 58 | PRO |
| 1 | F | 58 | PRO |
| 1 | H | 58 | PRO |
| 1 | G | 58 | PRO |

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 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 | 398/446 (89%) | 371 (93%) | 27 (7%) | 18 | 52 |
| 1 | B | 398/446 (89%) | 368 (92%) | 30 (8%) | 16 | 47 |
| 1 | C | 377/446 (84%) | 349 (93%) | 28 (7%) | 16 | 48 |
| 1 | D | 376/446 (84%) | 345 (92%) | 31 (8%) | 13 | 43 |
| 1 | E | 385/446 (86%) | 358 (93%) | 27 (7%) | 18 | 51 |
| 1 | F | 393/446 (88%) | 363 (92%) | 30 (8%) | 15 | 47 |
| 1 | G | 370/446 (83%) | 347 (94%) | 23 (6%) | 21 | 56 |
| 1 | H | 366/446 (82%) | 341 (93%) | 25 (7%) | 18 | 52 |
| All | All | 3063/3568 (86%) | 2842 (93%) | 221 (7%) | 17 | 49 |

All (221) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 112 | VAL |
| 1 | A | 134 | HIS |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 144 | LEU |
| 1 | A | 145 | LEU |
| 1 | A | 188 | ARG |
| 1 | A | 200 | ILE |
| 1 | A | 204 | ILE |
| 1 | A | 219 | GLN |
| 1 | A | 223 | ILE |
| 1 | A | 243 | CYS |
| 1 | A | 252 | LEU |
| 1 | A | 262 | GLN |
| 1 | A | 285 | PHE |
| 1 | A | 298 | TRP |
| 1 | A | 314 | LEU |
| 1 | A | 325 | ASP |
| 1 | A | 360 | ARG |
| 1 | A | 425 | LEU |
| 1 | A | 448 | GLU |
| 1 | A | 459 | ASN |
| 1 | A | 460 | GLU |
| 1 | A | 474 | LEU |
| 1 | A | 479 | ASN |
| 1 | A | 482 | GLN |
| 1 | A | 493 | PHE |
| 1 | A | 505 | ASP |
| 1 | A | 506 | LYS |
| 1 | B | 38 | VAL |
| 1 | B | 78 | THR |
| 1 | B | 105 | ASP |
| 1 | B | 108 | THR |
| 1 | B | 112 | VAL |
| 1 | B | 144 | LEU |
| 1 | B | 145 | LEU |
| 1 | B | 158 | ARG |
| 1 | B | 188 | ARG |
| 1 | B | 204 | ILE |
| 1 | B | 215 | ARG |
| 1 | B | 219 | GLN |
| 1 | B | 234 | ARG |
| 1 | B | 252 | LEU |
| 1 | B | 257 | ASN |
| 1 | B | 262 | GLN |
| 1 | B | 298 | TRP |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | B | 314 | LEU |
| 1 | B | 316 | LEU |
| 1 | B | 339 | SER |
| 1 | B | 355 | GLU |
| 1 | B | 419 | GLN |
| 1 | B | 425 | LEU |
| 1 | B | 460 | GLU |
| 1 | B | 474 | LEU |
| 1 | B | 479 | ASN |
| 1 | B | 484 | GLU |
| 1 | B | 485 | THR |
| 1 | B | 505 | ASP |
| 1 | B | 506 | LYS |
| 1 | C | 67 | ILE |
| 1 | C | 105 | ASP |
| 1 | C | 112 | VAL |
| 1 | C | 144 | LEU |
| 1 | C | 145 | LEU |
| 1 | C | 150 | MET |
| 1 | C | 188 | ARG |
| 1 | C | 204 | ILE |
| 1 | C | 219 | GLN |
| 1 | C | 223 | ILE |
| 1 | C | 243 | CYS |
| 1 | C | 252 | LEU |
| 1 | C | 257 | ASN |
| 1 | C | 262 | GLN |
| 1 | C | 298 | TRP |
| 1 | C | 314 | LEU |
| 1 | C | 325 | ASP |
| 1 | C | 361 | GLU |
| 1 | C | 418 | ASN |
| 1 | C | 425 | LEU |
| 1 | C | 453 | LEU |
| 1 | C | 459 | ASN |
| 1 | C | 474 | LEU |
| 1 | C | 479 | ASN |
| 1 | C | 482 | GLN |
| 1 | C | 483 | MET |
| 1 | C | 505 | ASP |
| 1 | C | 506 | LYS |
| 1 | D | 106 | GLU |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | D | 112 | VAL |
| 1 | D | 134 | HIS |
| 1 | D | 144 | LEU |
| 1 | D | 145 | LEU |
| 1 | D | 188 | ARG |
| 1 | D | 204 | ILE |
| 1 | D | 215 | ARG |
| 1 | D | 217 | LYS |
| 1 | D | 219 | GLN |
| 1 | D | 220 | ASP |
| 1 | D | 243 | CYS |
| 1 | D | 252 | LEU |
| 1 | D | 257 | ASN |
| 1 | D | 262 | GLN |
| 1 | D | 298 | TRP |
| 1 | D | 314 | LEU |
| 1 | D | 325 | ASP |
| 1 | D | 354 | ILE |
| 1 | D | 366 | VAL |
| 1 | D | 425 | LEU |
| 1 | D | 437 | LEU |
| 1 | D | 456 | LYS |
| 1 | D | 459 | ASN |
| 1 | D | 460 | GLU |
| 1 | D | 474 | LEU |
| 1 | D | 479 | ASN |
| 1 | D | 482 | GLN |
| 1 | D | 485 | THR |
| 1 | D | 505 | ASP |
| 1 | D | 506 | LYS |
| 1 | E | 112 | VAL |
| 1 | E | 130 | ARG |
| 1 | E | 134 | HIS |
| 1 | E | 137 | SER |
| 1 | E | 138 | ARG |
| 1 | E | 144 | LEU |
| 1 | E | 145 | LEU |
| 1 | E | 188 | ARG |
| 1 | E | 219 | GLN |
| 1 | E | 243 | CYS |
| 1 | E | 252 | LEU |
| 1 | E | 257 | ASN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | E | 262 | GLN |
| 1 | E | 298 | TRP |
| 1 | E | 314 | LEU |
| 1 | E | 325 | ASP |
| 1 | E | 425 | LEU |
| 1 | E | 437 | LEU |
| 1 | E | 456 | LYS |
| 1 | E | 459 | ASN |
| 1 | E | 464 | LEU |
| 1 | E | 467 | THR |
| 1 | E | 474 | LEU |
| 1 | E | 479 | ASN |
| 1 | E | 482 | GLN |
| 1 | E | 493 | PHE |
| 1 | E | 505 | ASP |
| 1 | F | 112 | VAL |
| 1 | F | 144 | LEU |
| 1 | F | 145 | LEU |
| 1 | F | 150 | MET |
| 1 | F | 188 | ARG |
| 1 | F | 204 | ILE |
| 1 | F | 219 | GLN |
| 1 | F | 223 | ILE |
| 1 | F | 243 | CYS |
| 1 | F | 252 | LEU |
| 1 | F | 256 | ILE |
| 1 | F | 257 | ASN |
| 1 | F | 262 | GLN |
| 1 | F | 293 | ASN |
| 1 | F | 298 | TRP |
| 1 | F | 299 | SER |
| 1 | F | 340 | ARG |
| 1 | F | 360 | ARG |
| 1 | F | 410 | ILE |
| 1 | F | 422 | LEU |
| 1 | F | 425 | LEU |
| 1 | F | 448 | GLU |
| 1 | F | 453 | LEU |
| 1 | F | 456 | LYS |
| 1 | F | 459 | ASN |
| 1 | F | 474 | LEU |
| 1 | F | 479 | ASN |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | F | 493 | PHE |
| 1 | F | 505 | ASP |
| 1 | F | 506 | LYS |
| 1 | G | 90 | GLU |
| 1 | G | 112 | VAL |
| 1 | G | 144 | LEU |
| 1 | G | 145 | LEU |
| 1 | G | 188 | ARG |
| 1 | G | 204 | ILE |
| 1 | G | 219 | GLN |
| 1 | G | 223 | ILE |
| 1 | G | 243 | CYS |
| 1 | G | 252 | LEU |
| 1 | G | 257 | ASN |
| 1 | G | 262 | GLN |
| 1 | G | 293 | ASN |
| 1 | G | 298 | TRP |
| 1 | G | 314 | LEU |
| 1 | G | 325 | ASP |
| 1 | G | 404 | ILE |
| 1 | G | 425 | LEU |
| 1 | G | 459 | ASN |
| 1 | G | 474 | LEU |
| 1 | G | 480 | CYS |
| 1 | G | 505 | ASP |
| 1 | G | 506 | LYS |
| 1 | H | 38 | VAL |
| 1 | H | 55 | LEU |
| 1 | H | 112 | VAL |
| 1 | H | 144 | LEU |
| 1 | H | 145 | LEU |
| 1 | H | 188 | ARG |
| 1 | H | 204 | ILE |
| 1 | H | 217 | LYS |
| 1 | H | 219 | GLN |
| 1 | H | 243 | CYS |
| 1 | H | 252 | LEU |
| 1 | H | 256 | ILE |
| 1 | H | 257 | ASN |
| 1 | H | 262 | GLN |
| 1 | H | 298 | TRP |
| 1 | H | 356 | LEU |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | H | 422 | LEU |
| 1 | H | 425 | LEU |
| 1 | H | 456 | LYS |
| 1 | H | 459 | ASN |
| 1 | H | 474 | LEU |
| 1 | H | 479 | ASN |
| 1 | H | 480 | CYS |
| 1 | H | 505 | ASP |
| 1 | H | 506 | LYS |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A | 238 | GLN |
| 1 | A | 418 | ASN |
| 1 | B | 175 | GLN |
| 1 | B | 195 | GLN |
| 1 | B | 257 | ASN |
| 1 | B | 322 | ASN |
| 1 | B | 419 | GLN |
| 1 | C | 195 | GLN |
| 1 | C | 322 | ASN |
| 1 | C | 457 | ASN |
| 1 | D | 238 | GLN |
| 1 | D | 322 | ASN |
| 1 | D | 433 | ASN |
| 1 | E | 238 | GLN |
| 1 | E | 433 | ASN |
| 1 | E | 463 | ASN |
| 1 | F | 195 | GLN |
| 1 | F | 322 | ASN |
| 1 | F | 482 | GLN |
| 1 | G | 175 | GLN |
| 1 | G | 195 | GLN |
| 1 | G | 451 | HIS |
| 1 | H | 418 | ASN |

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 carbohydrates 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 ⓘ

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.

| Mol | Chain | Analysed | <RSRZ> | #RSRZ > 2 | | OWAB(Å ²) | Q < 0.9 |
|-----|-------|-----------------|--------|-----------|-------|-----------------------|---------|
| 1 | A | 441/497 (88%) | 0.09 | 6 (1%) | 75 49 | 33, 64, 120, 158 | 0 |
| 1 | B | 441/497 (88%) | 0.05 | 5 (1%) | 80 55 | 32, 64, 116, 134 | 0 |
| 1 | C | 418/497 (84%) | 0.43 | 29 (6%) | 18 6 | 52, 104, 152, 167 | 0 |
| 1 | D | 417/497 (83%) | 0.26 | 17 (4%) | 38 16 | 44, 86, 149, 165 | 0 |
| 1 | E | 427/497 (85%) | 0.12 | 6 (1%) | 75 49 | 40, 77, 138, 183 | 0 |
| 1 | F | 436/497 (87%) | 0.14 | 7 (1%) | 72 44 | 34, 73, 127, 167 | 0 |
| 1 | G | 411/497 (82%) | 0.34 | 19 (4%) | 33 14 | 48, 99, 156, 181 | 0 |
| 1 | H | 405/497 (81%) | 0.56 | 35 (8%) | 11 4 | 56, 114, 160, 176 | 0 |
| All | All | 3396/3976 (85%) | 0.24 | 124 (3%) | 42 18 | 32, 82, 149, 183 | 0 |

All (124) RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | D | 496 | THR | 5.4 |
| 1 | H | 363 | LEU | 5.0 |
| 1 | E | 493 | PHE | 4.9 |
| 1 | C | 482 | GLN | 4.6 |
| 1 | C | 416 | ALA | 4.6 |
| 1 | B | 418 | ASN | 4.4 |
| 1 | F | 483 | MET | 4.4 |
| 1 | H | 323 | ILE | 4.2 |
| 1 | C | 423 | TYR | 4.1 |
| 1 | C | 138 | ARG | 4.0 |
| 1 | C | 479 | ASN | 4.0 |
| 1 | H | 140 | ALA | 4.0 |
| 1 | G | 137 | SER | 3.9 |
| 1 | H | 388 | ALA | 3.8 |
| 1 | D | 315 | GLN | 3.7 |
| 1 | C | 105 | ASP | 3.7 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | A | 493 | PHE | 3.7 |
| 1 | C | 106 | GLU | 3.7 |
| 1 | H | 344 | ILE | 3.6 |
| 1 | D | 106 | GLU | 3.6 |
| 1 | C | 418 | ASN | 3.5 |
| 1 | H | 506 | LYS | 3.5 |
| 1 | F | 487 | ARG | 3.5 |
| 1 | G | 467 | THR | 3.5 |
| 1 | C | 387 | VAL | 3.4 |
| 1 | H | 322 | ASN | 3.4 |
| 1 | C | 318 | CYS | 3.4 |
| 1 | H | 353 | GLU | 3.3 |
| 1 | F | 493 | PHE | 3.3 |
| 1 | D | 286 | ALA | 3.3 |
| 1 | D | 438 | THR | 3.2 |
| 1 | G | 285 | PHE | 3.2 |
| 1 | H | 448 | GLU | 3.2 |
| 1 | H | 296 | ILE | 3.1 |
| 1 | F | 449 | TYR | 3.1 |
| 1 | A | 492 | ILE | 3.1 |
| 1 | D | 486 | VAL | 3.1 |
| 1 | G | 120 | PHE | 3.1 |
| 1 | A | 490 | ASN | 3.1 |
| 1 | C | 466 | GLY | 3.0 |
| 1 | C | 433 | ASN | 3.0 |
| 1 | H | 326 | VAL | 3.0 |
| 1 | F | 504 | LYS | 3.0 |
| 1 | C | 131 | ALA | 3.0 |
| 1 | C | 467 | THR | 3.0 |
| 1 | C | 400 | CYS | 3.0 |
| 1 | F | 482 | GLN | 2.9 |
| 1 | H | 386 | GLU | 2.9 |
| 1 | H | 387 | VAL | 2.9 |
| 1 | C | 439 | PHE | 2.8 |
| 1 | E | 439 | PHE | 2.8 |
| 1 | C | 353 | GLU | 2.8 |
| 1 | G | 481 | TYR | 2.8 |
| 1 | D | 424 | VAL | 2.8 |
| 1 | G | 272 | VAL | 2.7 |
| 1 | H | 370 | ASP | 2.7 |
| 1 | D | 478 | LEU | 2.7 |
| 1 | D | 382 | TYR | 2.7 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | C | 478 | LEU | 2.7 |
| 1 | D | 449 | TYR | 2.7 |
| 1 | H | 142 | ALA | 2.7 |
| 1 | H | 357 | SER | 2.7 |
| 1 | G | 424 | VAL | 2.7 |
| 1 | G | 136 | ILE | 2.7 |
| 1 | D | 497 | LYS | 2.7 |
| 1 | C | 319 | ASP | 2.7 |
| 1 | H | 359 | LEU | 2.7 |
| 1 | G | 135 | GLY | 2.7 |
| 1 | C | 363 | LEU | 2.7 |
| 1 | H | 405 | SER | 2.6 |
| 1 | G | 286 | ALA | 2.6 |
| 1 | H | 514 | THR | 2.6 |
| 1 | H | 401 | HIS | 2.6 |
| 1 | H | 425 | LEU | 2.6 |
| 1 | H | 469 | LYS | 2.5 |
| 1 | G | 193 | ASN | 2.5 |
| 1 | G | 353 | GLU | 2.4 |
| 1 | H | 497 | LYS | 2.4 |
| 1 | A | 486 | VAL | 2.4 |
| 1 | H | 99 | ASN | 2.4 |
| 1 | F | 445 | ASN | 2.3 |
| 1 | B | 461 | GLU | 2.3 |
| 1 | H | 507 | SER | 2.2 |
| 1 | D | 125 | CYS | 2.2 |
| 1 | G | 474 | LEU | 2.2 |
| 1 | H | 94 | ILE | 2.2 |
| 1 | G | 315 | GLN | 2.2 |
| 1 | C | 322 | ASN | 2.2 |
| 1 | D | 287 | THR | 2.2 |
| 1 | A | 491 | ILE | 2.2 |
| 1 | B | 488 | SER | 2.2 |
| 1 | H | 354 | ILE | 2.2 |
| 1 | C | 287 | THR | 2.2 |
| 1 | E | 496 | THR | 2.2 |
| 1 | G | 479 | ASN | 2.2 |
| 1 | C | 137 | SER | 2.1 |
| 1 | C | 401 | HIS | 2.1 |
| 1 | E | 478 | LEU | 2.1 |
| 1 | E | 440 | ALA | 2.1 |
| 1 | G | 290 | ILE | 2.1 |

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| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 1 | C | 503 | PRO | 2.1 |
| 1 | B | 138 | ARG | 2.1 |
| 1 | H | 504 | LYS | 2.1 |
| 1 | C | 134 | HIS | 2.1 |
| 1 | C | 447 | ILE | 2.1 |
| 1 | C | 316 | LEU | 2.1 |
| 1 | C | 394 | GLU | 2.1 |
| 1 | G | 475 | LYS | 2.1 |
| 1 | G | 437 | LEU | 2.1 |
| 1 | D | 474 | LEU | 2.1 |
| 1 | D | 439 | PHE | 2.1 |
| 1 | H | 300 | ARG | 2.1 |
| 1 | A | 285 | PHE | 2.0 |
| 1 | H | 439 | PHE | 2.0 |
| 1 | E | 240 | PHE | 2.0 |
| 1 | H | 345 | HIS | 2.0 |
| 1 | H | 472 | SER | 2.0 |
| 1 | H | 383 | LEU | 2.0 |
| 1 | D | 466 | GLY | 2.0 |
| 1 | H | 403 | PRO | 2.0 |
| 1 | H | 382 | TYR | 2.0 |
| 1 | G | 439 | PHE | 2.0 |
| 1 | B | 483 | MET | 2.0 |
| 1 | D | 453 | LEU | 2.0 |

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 carbohydrates 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.