# wwPDB X-ray Structure Validation Summary Report (i)

May 29, 2020 – 06:38 am BST

| | | |
|---|---|---|
| PDB ID | : | 5C0X |
| Title | : | Structure of a 12-subunit nuclear exosome complex bound to structured RNA |
| Authors | : | Makino, D.L.; Conti, E. |
| Deposited on | : | 2015-06-12 |
| Resolution | : | 3.81 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

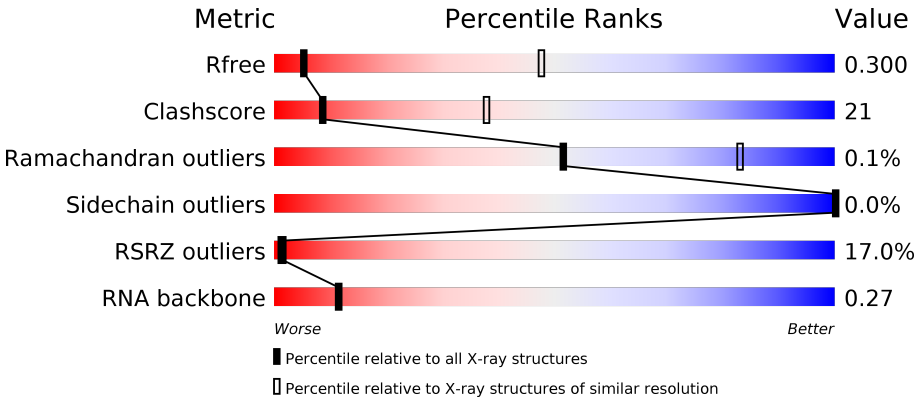
| | | |
|---|---|---|
| MolProbity | : | 4.02b-467 |
| Xtriage (Phenix) | : | 1.13 |
| EDS | : | 2.11 |
| Percentile statistics | : | 20191225.v01 (using entries in the PDB archive December 25th 2019) |
| Refmac | : | 5.8.0158 |
| CCP4 | : | 7.0.044 (Gargrove) |
| Ideal geometry (proteins) | : | Engh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

# 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.81 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 | 1231 (4.04-3.60) |
| Clashscore | 141614 | 1031 (4.02-3.62) |
| Ramachandran outliers | 138981 | 1261 (4.04-3.60) |
| Sidechain outliers | 138945 | 1255 (4.04-3.60) |
| RSRZ outliers | 127900 | 1139 (4.04-3.60) |
| RNA backbone | 3102 | 1037 (4.62-3.00) |

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 1 | A | 305 | 7%, 77%, 21%, · |
| 2 | B | 248 | 8%, 76%, 22%, · |
| 3 | C | 394 | 7%, 61%, 25%, 14% |
| 4 | D | 245 | 5%, 74%, 17%, 9% |

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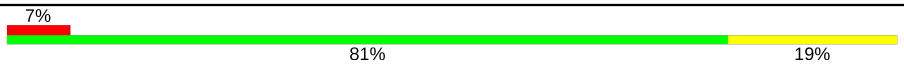
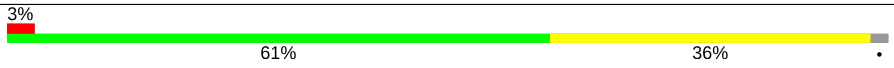
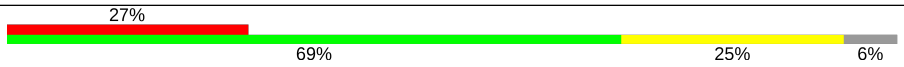
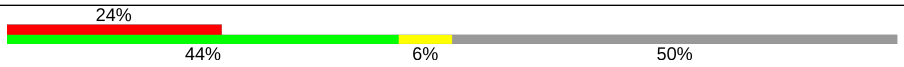
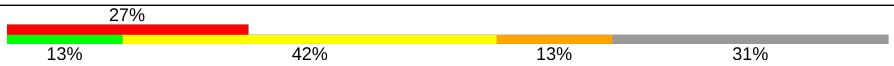
| Mol | Chain | Length | Quality of chain |
|---|---|---|---|
| 5 | E | 267 |   |
| 6 | F | 250 |   |
| 7 | G | 243 |   |
| 8 | H | 361 |   |
| 9 | I | 295 |   |
| 10 | J | 1003 |   |
| 11 | K | 695 |   |
| 12 | R | 45 |   |

## 2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 27816 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 Exosome complex component RRP45.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | A | 299 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2304 | 1444 | 393 | 451 | 16 | | | |

- Molecule 2 is a protein called Exosome complex component SKI6.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 2 | B | 244 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1886 | 1177 | 335 | 366 | 8 | | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| B | -1 | GLY | - | expression tag | UNP P46948 |
| B | 0 | HIS | - | expression tag | UNP P46948 |

- Molecule 3 is a protein called Exosome complex component RRP43.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 3 | C | 339 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 2589 | 1640 | 441 | 497 | 11 | | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| C | 102 | SER | ALA | engineered mutation | UNP P25359 |
| C | 363 | MET | VAL | engineered mutation | UNP P25359 |

- Molecule 4 is a protein called Exosome complex component RRP46.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 4 | D | 223 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 1701 | 1072 | 285 | 334 | 10 | | | |

There are 22 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| D | -21 | GLY | - | expression tag | UNP P53256 |
| D | -20 | HIS | - | expression tag | UNP P53256 |
| D | -19 | GLY | - | expression tag | UNP P53256 |
| D | -18 | ASN | - | expression tag | UNP P53256 |
| D | -17 | ASN | - | expression tag | UNP P53256 |
| D | -16 | LYS | - | expression tag | UNP P53256 |
| D | -15 | GLU | - | expression tag | UNP P53256 |
| D | -14 | PRO | - | expression tag | UNP P53256 |
| D | -13 | ASN | - | expression tag | UNP P53256 |
| D | -12 | THR | - | expression tag | UNP P53256 |
| D | -11 | LYS | - | expression tag | UNP P53256 |
| D | -10 | ASN | - | expression tag | UNP P53256 |
| D | -9 | ARG | - | expression tag | UNP P53256 |
| D | -8 | LEU | - | expression tag | UNP P53256 |
| D | -7 | ASP | - | expression tag | UNP P53256 |
| D | -6 | SER | - | expression tag | UNP P53256 |
| D | -5 | ALA | - | expression tag | UNP P53256 |
| D | -4 | GLU | - | expression tag | UNP P53256 |
| D | -3 | LYS | - | expression tag | UNP P53256 |
| D | -2 | LYS | - | expression tag | UNP P53256 |
| D | -1 | LYS | - | expression tag | UNP P53256 |
| D | 0 | LYS | - | expression tag | UNP P53256 |

- Molecule 5 is a protein called Exosome complex component RRP42.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 5 | E | 267 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 2050 | 1308 | 338 | 399 | 5 | | | |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| E | -1 | GLY | - | expression tag | UNP Q12277 |
| E | 0 | HIS | - | expression tag | UNP Q12277 |
| E | 138 | ILE | VAL | engineered mutation | UNP Q12277 |

- Molecule 6 is a protein called Exosome complex component MTR3.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 6 | F | 215 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1638 | 1023 | 273 | 332 | 10 | | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| F | 75 | SER | THR | engineered mutation | UNP P48240 |
| F | 161 | THR | MET | engineered mutation | UNP P48240 |

- Molecule 7 is a protein called Exosome complex component RRP40.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 7 | G | 237 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1792 | 1143 | 295 | 344 | 10 | | | |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| G | -2 | GLY | - | expression tag | UNP Q08285 |
| G | -1 | PRO | - | expression tag | UNP Q08285 |
| G | 0 | HIS | - | expression tag | UNP Q08285 |

- Molecule 8 is a protein called Exosome complex component RRP4.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 8 | H | 293 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2236 | 1393 | 403 | 428 | 12 | | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| H | -1 | ARG | - | expression tag | UNP P38792 |
| H | 0 | SER | - | expression tag | UNP P38792 |

- Molecule 9 is a protein called Exosome complex component CSL4.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 9 | I | 222 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1653 | 1034 | 287 | 325 | 7 | | | |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| I | -2 | GLY | - | expression tag | UNP P53859 |
| I | -1 | PRO | - | expression tag | UNP P53859 |
| I | 0 | HIS | - | expression tag | UNP P53859 |

- Molecule 10 is a protein called Exosome complex exonuclease DIS3.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 10 | J | 944 | Total | C | N | O | S | 0 | 1 | 0 |
| | | | 7427 | 4693 | 1304 | 1395 | 35 | | | |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| J | -1 | GLY | - | expression tag | UNP Q08162 |
| J | 0 | ALA | - | expression tag | UNP Q08162 |
| J | 171 | ASN | ASP | engineered mutation | UNP Q08162 |
| J | 551 | ASN | ASP | engineered mutation | UNP Q08162 |

- Molecule 11 is a protein called Exosome complex exonuclease RRP6.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 11 | K | 350 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1982 | 1212 | 379 | 389 | 2 | | | |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|---|---|---|---|---|---|
| K | -1 | GLY | - | expression tag | UNP Q12149 |
| K | 0 | ALA | - | expression tag | UNP Q12149 |
| K | 2 | ALA | THR | engineered mutation | UNP Q12149 |
| K | 296 | ASN | ASP | engineered mutation | UNP Q12149 |

- Molecule 12 is a RNA chain called RNA synthetic.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|---|---|---|---|---|---|---|---|---|---|---|
| 12 | R | 31 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 557 | 244 | 71 | 211 | 31 | | | |

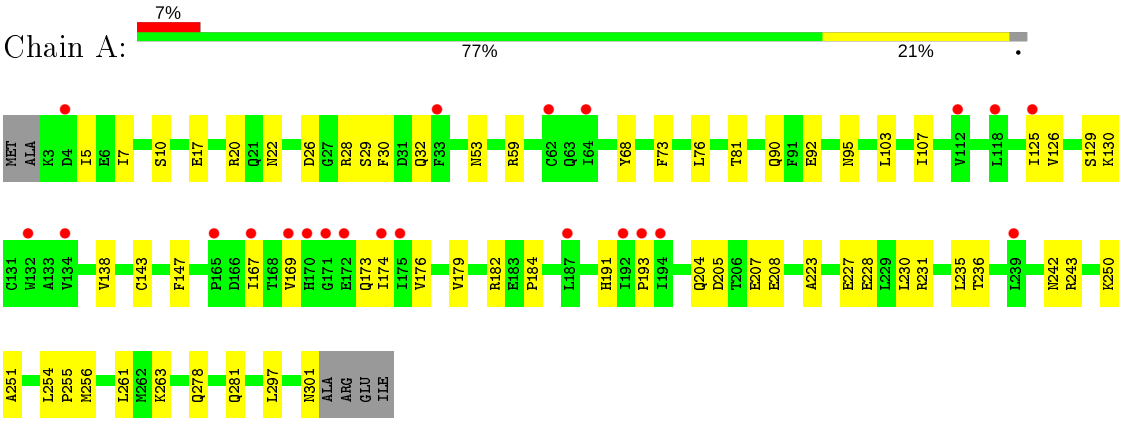
- Molecule 13 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|---|---|---|---|---|---|---|
| 13 | J | 1 | Total | Zn | 0 | 0 |
| | | | 1 | 1 | | |

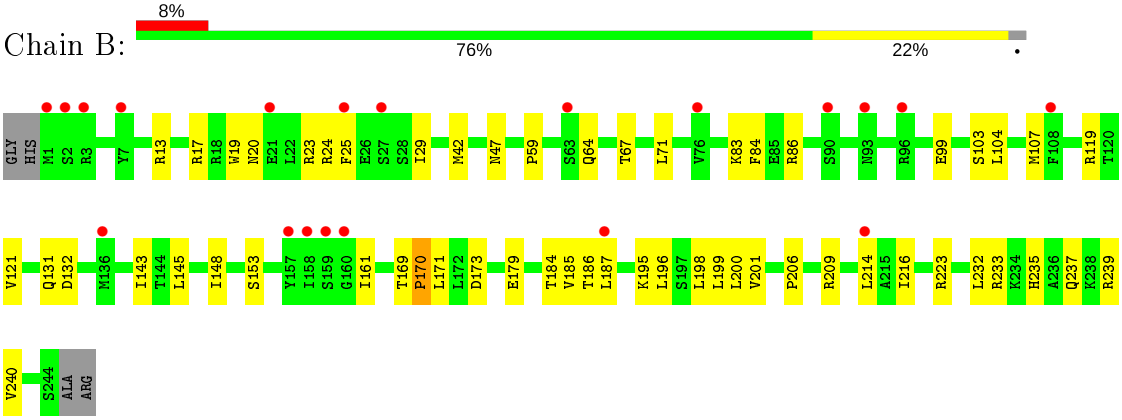
# 3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

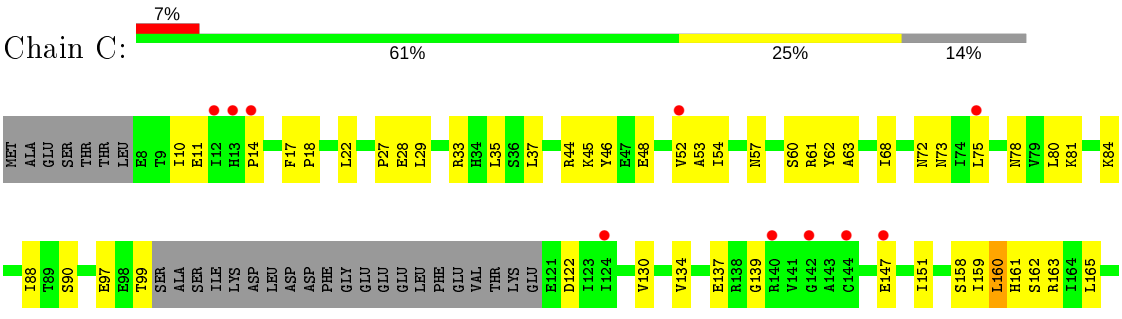
- Molecule 1: Exosome complex component RRP45

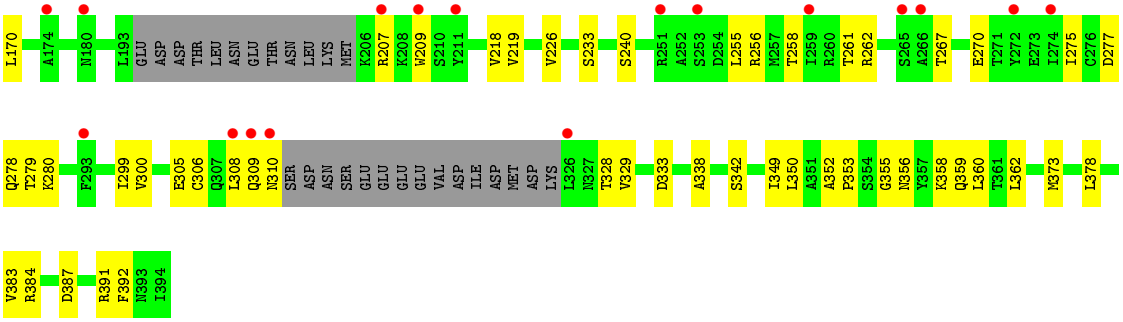



- Molecule 2: Exosome complex component SKI6

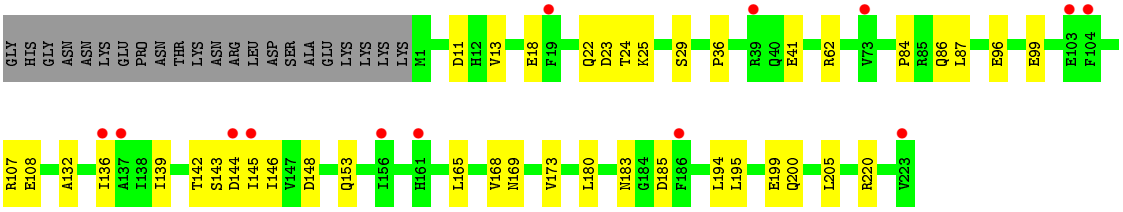



- Molecule 3: Exosome complex component RRP43

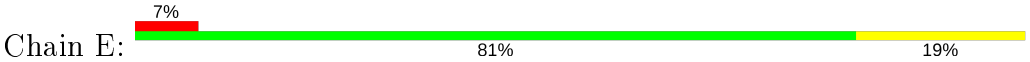


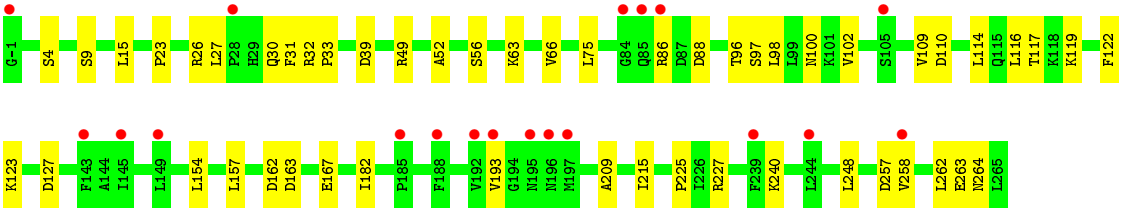



• Molecule 4: Exosome complex component RRP46

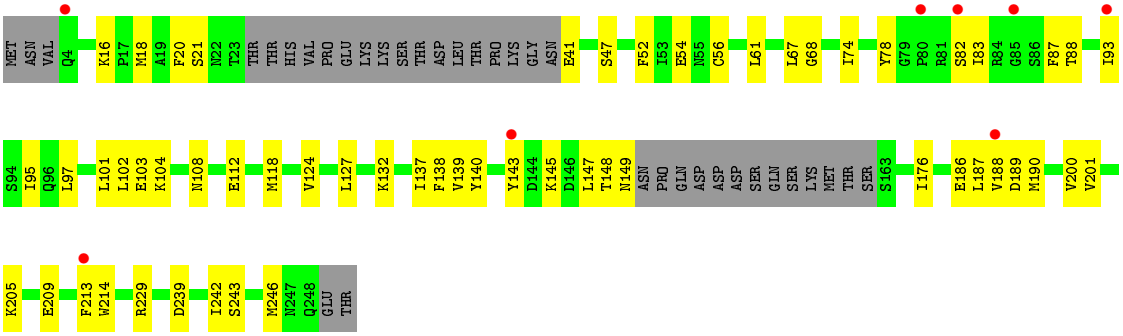




• Molecule 5: Exosome complex component RRP42

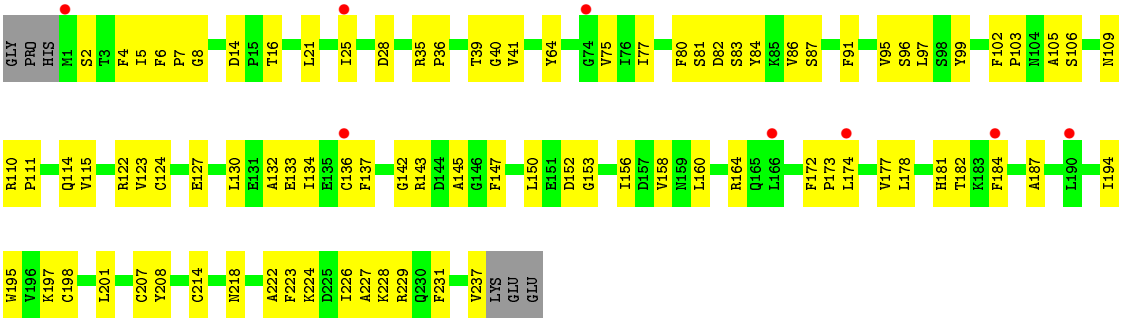



• Molecule 6: Exosome complex component MTR3

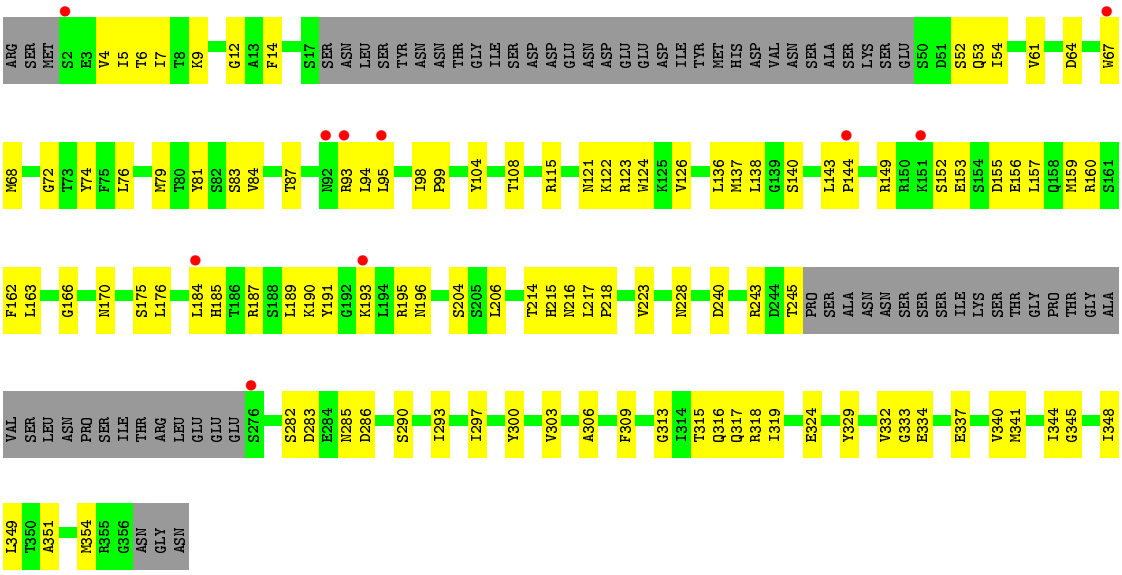




• Molecule 7: Exosome complex component RRP40



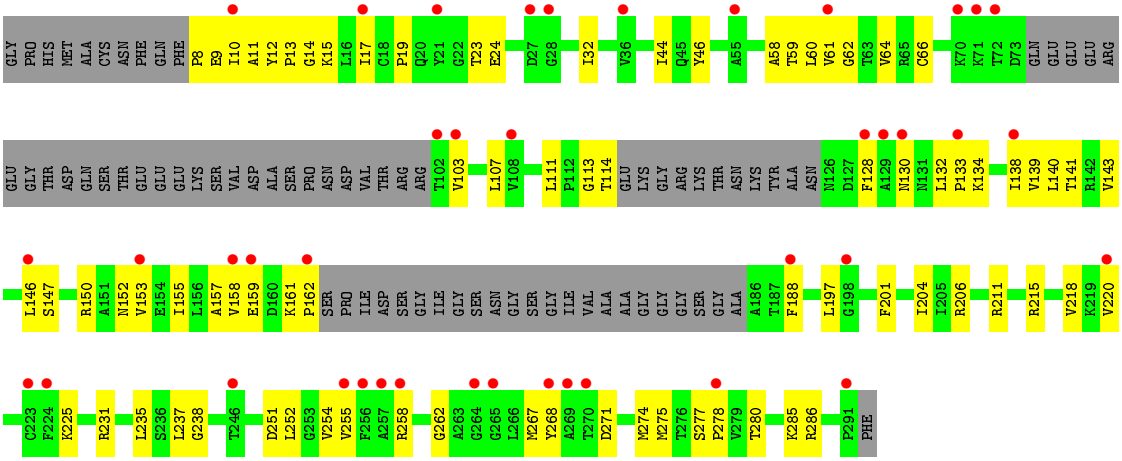
• Molecule 8: Exosome complex component RRP4

Chain H:

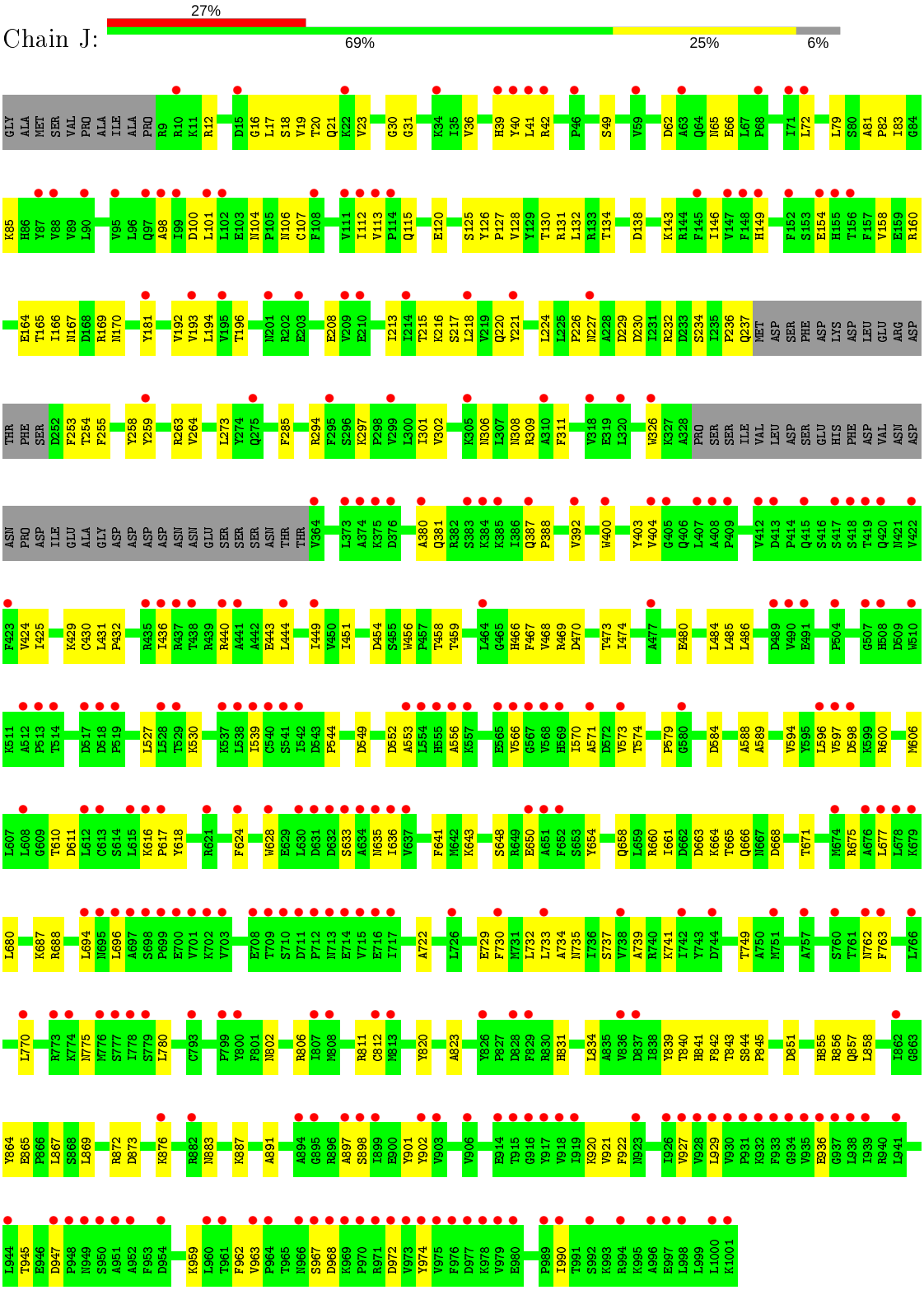
• Molecule 9: Exosome complex component CSL4

Chain I:

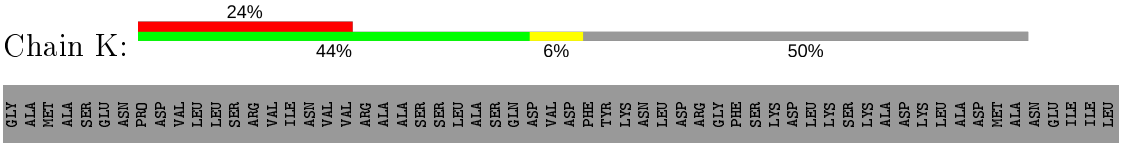
• Molecule 10: Exosome complex exonuclease DIS3

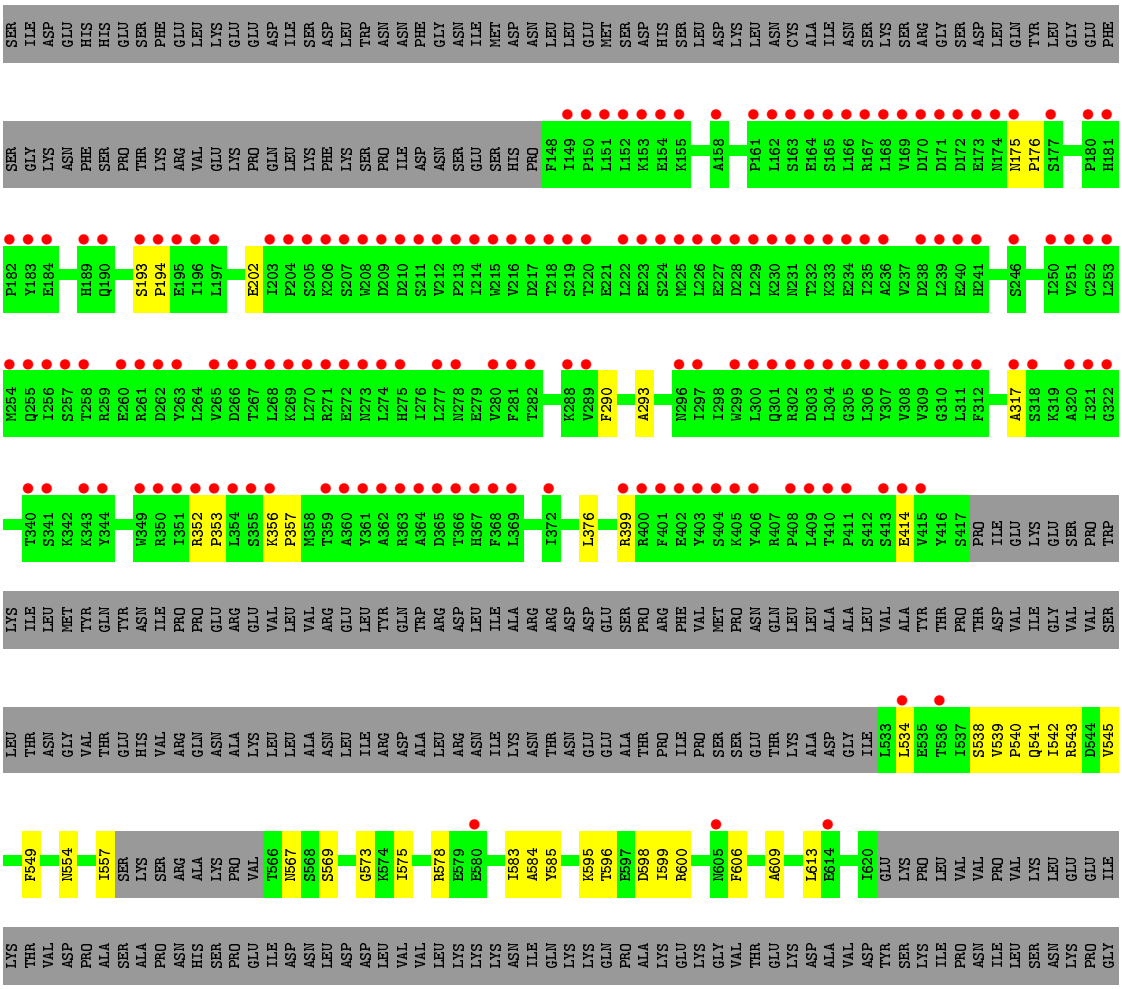
Chain J:




• Molecule 11: Exosome complex exonuclease RRP6

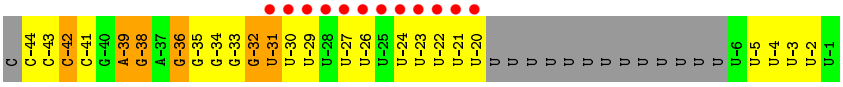
Chain K:





• Molecule 12: RNA synthetic

Chain R:

# 4 Data and refinement statistics (i)

| Property | Value | Source |
|---|---|---|
| Space group | P 21 21 21 | Depositor |
| Cell constants<br>a, b, c, $\alpha$, $\beta$, $\gamma$ | 106.15Å 177.39Å 299.90Å<br>90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 57.89 – 3.81<br>57.89 – 3.81 | Depositor<br>EDS |
| % Data completeness<br>(in resolution range) | 81.5 (57.89-3.81)<br>81.6 (57.89-3.81) | Depositor<br>EDS |
| $R_{merge}$ | 0.16 | Depositor |
| $R_{sym}$ | (Not available) | Depositor |
| $< I/\sigma(I) >$ [1] | 1.21 (at 3.77Å) | Xtriage |
| Refinement program | PHENIX | Depositor |
| R, $R_{free}$ | 0.295 , 0.300<br>0.295 , 0.300 | Depositor<br>DCC |
| $R_{free}$ test set | 2292 reflections (5.00%) | wwPDB-VP |
| Wilson B-factor (Å$^2$) | 159.6 | Xtriage |
| Anisotropy | 0.528 | Xtriage |
| Bulk solvent $k_{sol}$(e/Å$^3$), $B_{sol}$(Å$^2$) | 0.29 , 181.6 | EDS |
| L-test for twinning[2] | $< \|L\| > = 0.40$, $< L^2 > = 0.22$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| $F_o$,$F_c$ correlation | 0.89 | EDS |
| Total number of atoms | 27816 | wwPDB-VP |
| Average B, all atoms (Å$^2$) | 270.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.39% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

# 5 Model quality

## 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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 | 0.25 | 0/2340 | 0.37 | 0/3161 |
| 2 | B | 0.28 | 0/1910 | 0.43 | 0/2579 |
| 3 | C | 0.25 | 0/2629 | 0.41 | 0/3569 |
| 4 | D | 0.23 | 0/1722 | 0.40 | 0/2339 |
| 5 | E | 0.24 | 0/2093 | 0.39 | 1/2849 (0.0%) |
| 6 | F | 0.24 | 0/1660 | 0.40 | 0/2241 |
| 7 | G | 0.25 | 0/1828 | 0.43 | 0/2486 |
| 8 | H | 0.26 | 0/2269 | 0.40 | 0/3066 |
| 9 | I | 0.22 | 0/1676 | 0.43 | 0/2277 |
| 10 | J | 0.28 | 0/7575 | 0.40 | 1/10290 (0.0%) |
| 11 | K | 0.30 | 0/2001 | 0.56 | 0/2778 |
| 12 | R | 0.26 | 0/615 | 0.70 | 0/951 |
| All | All | 0.26 | 0/28318 | 0.43 | 2/38586 (0.0%) |

There are no bond length outliers.

All (2) bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed($^o$) | Ideal($^o$) |
|---|---|---|---|---|---|---|---|
| 10 | J | 947 | ASP | CB-CG-OD2 | 5.20 | 122.97 | 118.30 |
| 5 | E | 110 | ASP | CB-CG-OD2 | 5.12 | 122.91 | 118.30 |

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|---|---|---|---|---|---|---|
| 1 | A | 2304 | 0 | 2265 | 85 | 0 |
| 2 | B | 1886 | 0 | 1904 | 59 | 0 |
| 3 | C | 2589 | 0 | 2607 | 135 | 0 |
| 4 | D | 1701 | 0 | 1755 | 39 | 3 |
| 5 | E | 2050 | 0 | 2063 | 74 | 1 |
| 6 | F | 1638 | 0 | 1590 | 108 | 0 |
| 7 | G | 1792 | 0 | 1747 | 133 | 1 |
| 8 | H | 2236 | 0 | 2215 | 159 | 4 |
| 9 | I | 1653 | 0 | 1616 | 142 | 0 |
| 10 | J | 7427 | 0 | 7352 | 284 | 0 |
| 11 | K | 1982 | 0 | 1255 | 45 | 2 |
| 12 | R | 557 | 0 | 281 | 45 | 1 |
| 13 | J | 1 | 0 | 0 | 0 | 0 |
| All | All | 27816 | 0 | 26650 | 1120 | 6 |

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 1120 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) |
|---|---|---|---|
| 5:E:257:ASP:CB | 8:H:4:VAL:HG21 | 1.35 | 1.57 |
| 10:J:467:PHE:CZ | 10:J:469:ARG:O | 1.63 | 1.50 |
| 5:E:257:ASP:CB | 8:H:4:VAL:CG2 | 2.08 | 1.30 |
| 10:J:467:PHE:CZ | 10:J:469:ARG:C | 2.04 | 1.29 |
| 1:A:242:ASN:HB3 | 10:J:872:ARG:NH2 | 1.45 | 1.28 |

The worst 5 of 6 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

| Atom-1 | Atom-2 | Interatomic distance (Å) | Clash overlap (Å) |
|---|---|---|---|
| 4:D:200:GLN:NE2 | 8:H:329:TYR:CE1[1_655] | 1.52 | 0.68 |
| 7:G:229:ARG:NH1 | 12:R:-39:A:N6[4_545] | 1.88 | 0.32 |
| 8:H:245:THR:C | 11:K:202:GLU:O[1_455] | 1.88 | 0.32 |
| 5:E:162:ASP:OD1 | 11:K:543:ARG:NH2[3_554] | 1.97 | 0.23 |
| 4:D:200:GLN:NE2 | 8:H:329:TYR:CD1[1_655] | 1.98 | 0.22 |

## 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 | 297/305 (97%) | 290 (98%) | 7 (2%) | 0 | 100 | 100 |
| 2 | B | 242/248 (98%) | 237 (98%) | 4 (2%) | 1 (0%) | 34 | 70 |
| 3 | C | 332/394 (84%) | 312 (94%) | 19 (6%) | 1 (0%) | 41 | 74 |
| 4 | D | 222/245 (91%) | 218 (98%) | 4 (2%) | 0 | 100 | 100 |
| 5 | E | 266/267 (100%) | 250 (94%) | 16 (6%) | 0 | 100 | 100 |
| 6 | F | 209/250 (84%) | 197 (94%) | 12 (6%) | 0 | 100 | 100 |
| 7 | G | 235/243 (97%) | 226 (96%) | 9 (4%) | 0 | 100 | 100 |
| 8 | H | 287/361 (80%) | 278 (97%) | 8 (3%) | 1 (0%) | 41 | 74 |
| 9 | I | 214/295 (72%) | 208 (97%) | 6 (3%) | 0 | 100 | 100 |
| 10 | J | 939/1003 (94%) | 899 (96%) | 39 (4%) | 1 (0%) | 51 | 83 |
| 11 | K | 344/695 (50%) | 330 (96%) | 14 (4%) | 0 | 100 | 100 |
| All | All | 3587/4306 (83%) | 3445 (96%) | 138 (4%) | 4 (0%) | 51 | 83 |

All (4) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 8 | H | 333 | GLY |
| 2 | B | 170 | PRO |
| 10 | J | 598 | ASP |
| 3 | C | 18 | PRO |

### 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 | 255/266 (96%) | 255 (100%) | 0 | 100 | 100 |
| 2 | B | 210/219 (96%) | 210 (100%) | 0 | 100 | 100 |
| 3 | C | 282/350 (81%) | 281 (100%) | 1 (0%) | 91 | 95 |
| 4 | D | 196/216 (91%) | 196 (100%) | 0 | 100 | 100 |
| 5 | E | 238/241 (99%) | 238 (100%) | 0 | 100 | 100 |
| 6 | F | 181/219 (83%) | 181 (100%) | 0 | 100 | 100 |
| 7 | G | 194/211 (92%) | 194 (100%) | 0 | 100 | 100 |
| 8 | H | 243/313 (78%) | 243 (100%) | 0 | 100 | 100 |
| 9 | I | 174/242 (72%) | 174 (100%) | 0 | 100 | 100 |
| 10 | J | 816/901 (91%) | 816 (100%) | 0 | 100 | 100 |
| 11 | K | 81/636 (13%) | 81 (100%) | 0 | 100 | 100 |
| All | All | 2870/3814 (75%) | 2869 (100%) | 1 (0%) | 100 | 100 |

All (1) residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 3 | C | 160 | LEU |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 3 | C | 73 | ASN |
| 10 | J | 855 | HIS |
| 6 | F | 206 | ASN |
| 2 | B | 237 | GLN |
| 6 | F | 49 | HIS |

### 5.3.3 RNA

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|---|---|---|---|---|
| 12 | R | 29/45 (64%) | 15 (51%) | 0 |

5 of 15 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|---|---|---|---|
| 12 | R | -42 | C |
| 12 | R | -39 | A |

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| Mol | Chain | Res | Type |
|---|---|---|---|
| 12 | R | -38 | G |
| 12 | R | -36 | G |
| 12 | R | -32 | G |

There are no RNA pucker outliers to report.

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

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

## 5.5 Carbohydrates

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

# 6 Fit of model and data

## 6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, $95^{th}$ 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 | 299/305 (98%) | 0.35 | 22 (7%) 14 11 | 168, 206, 270, 304 | 0 |
| 2 | B | 244/248 (98%) | 0.58 | 20 (8%) 11 9 | 162, 209, 280, 314 | 0 |
| 3 | C | 339/394 (86%) | 0.51 | 27 (7%) 12 10 | 205, 234, 301, 333 | 0 |
| 4 | D | 223/245 (91%) | 0.44 | 13 (5%) 23 18 | 170, 206, 259, 300 | 0 |
| 5 | E | 267/267 (100%) | 0.47 | 19 (7%) 16 12 | 179, 216, 267, 309 | 0 |
| 6 | F | 215/250 (86%) | 0.34 | 8 (3%) 41 33 | 189, 221, 266, 308 | 0 |
| 7 | G | 237/243 (97%) | 0.19 | 8 (3%) 45 37 | 167, 203, 253, 283 | 0 |
| 8 | H | 293/361 (81%) | 0.21 | 10 (3%) 45 37 | 175, 209, 263, 286 | 0 |
| 9 | I | 222/295 (75%) | 0.94 | 41 (18%) 1 1 | 205, 244, 291, 345 | 0 |
| 10 | J | 944/1003 (94%) | 1.46 | 274 (29%) 0 0 | 238, 377, 429, 458 | 0 |
| 11 | K | 350/695 (50%) | 2.51 | 170 (48%) 0 0 | 227, 378, 404, 428 | 0 |
| 12 | R | 31/45 (68%) | 3.37 | 12 (38%) 0 0 | 265, 295, 398, 401 | 0 |
| All | All | 3664/4351 (84%) | 0.93 | 624 (17%) 1 1 | 162, 242, 405, 458 | 0 |

The worst 5 of 624 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|---|---|---|---|---|
| 11 | K | 270 | LEU | 16.1 |
| 10 | J | 553 | ALA | 15.2 |
| 12 | R | -27 | U | 14.3 |
| 12 | R | -26 | U | 13.5 |
| 12 | R | -28 | U | 13.2 |

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

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

## 6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

## 6.4 Ligands (i)

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

| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å$^2$) | Q<0.9 |
|---|---|---|---|---|---|---|---|---|
| 13 | ZN | J | 1101 | 1/1 | 0.73 | 0.04 | 298,298,298,298 | 0 |

## 6.5 Other polymers (i)

There are no such residues in this entry.