



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 02:40 AM UTC

PDB ID : 1IBM / pdb\_00001ibm  
Title : STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH A MESSENGER RNA FRAGMENT AND COGNATE TRANSFER RNA ANTICODON STEM-LOOP BOUND AT THE A SITE  
Authors : Ogle, J.M.; Brodersen, D.E.; Clemons Jr., W.M.; Tarry, M.J.; Carter, A.P.; Ramakrishnan, V.  
Deposited on : 2001-03-28  
Resolution : 3.31 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

|                                |   |                                                                  |
|--------------------------------|---|------------------------------------------------------------------|
| MolProbity                     | : | 4-5-2 with Phenix2.0                                             |
| Xtriage (Phenix)               | : | 2.0                                                              |
| EDS                            | : | 3.0                                                              |
| Percentile statistics          | : | 20250101.v01 (using entries in the PDB archive January 1st 2025) |
| CCP4                           | : | 9.0.010 (Gargrove)                                               |
| Density-Fitness                | : | 1.0.12                                                           |
| Ideal geometry (proteins)      | : | Engl & Huber (2001)                                              |
| Ideal geometry (DNA, RNA)      | : | Parkinson et al. (1996)                                          |
| Validation Pipeline (wwPDB-VP) | : | 2.49                                                             |

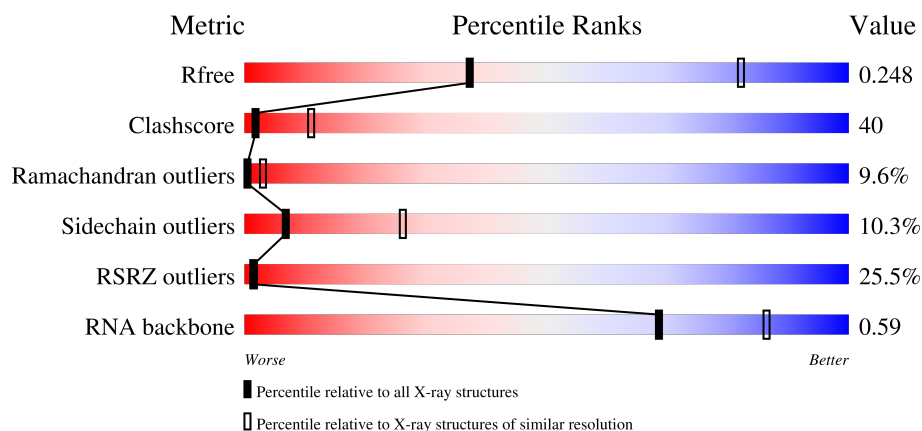
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.31 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<br>(#Entries) | Similar resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-------------------------------------------------------|
| $R_{free}$            | 180053                      | 1153 (3.34-3.30)                                      |
| Clashscore            | 190562                      | 1193 (3.34-3.30)                                      |
| Ramachandran outliers | 187476                      | 1172 (3.34-3.30)                                      |
| Sidechain outliers    | 187428                      | 1171 (3.34-3.30)                                      |
| RSRZ outliers         | 180081                      | 1153 (3.34-3.30)                                      |
| RNA backbone          | 3983                        | 1067 (3.64-3.00)                                      |

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . 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     | 1522   | <div> <div>20%</div> <div>27%</div> <div>59%</div> <div>11%</div> <div>..</div> </div>               |
| 2   | X     | 6      | <div> <div>50%</div> <div>67%</div> <div>33%</div> </div>                                            |
| 3   | Y     | 15     | <div> <div>33%</div> <div>33%</div> <div>27%</div> <div>7%</div> <div>7%</div> <div>27%</div> </div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 4   | Z     | 4      |                  |
| 5   | B     | 256    |                  |
| 6   | C     | 239    |                  |
| 7   | D     | 209    |                  |
| 8   | E     | 162    |                  |
| 9   | F     | 101    |                  |
| 10  | G     | 156    |                  |
| 11  | H     | 138    |                  |
| 12  | I     | 128    |                  |
| 13  | J     | 105    |                  |
| 14  | K     | 129    |                  |
| 15  | L     | 135    |                  |
| 16  | M     | 126    |                  |
| 17  | N     | 61     |                  |
| 18  | O     | 89     |                  |
| 19  | P     | 88     |                  |
| 20  | Q     | 105    |                  |
| 21  | R     | 88     |                  |
| 22  | S     | 93     |                  |
| 23  | T     | 106    |                  |
| 24  | V     | 26     |                  |

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

| Mol | Type | Chain | Res  | Chirality | Geometry | Clashes | Electron density |
|-----|------|-------|------|-----------|----------|---------|------------------|
| 25  | MG   | A     | 1624 | -         | -        | -       | X                |
| 25  | MG   | A     | 1628 | -         | -        | -       | X                |

## 2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 52160 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 RNA chain called 16S RIBOSOMAL RNA.

| Mol | Chain | Residues | Atoms |       |      |       |      | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|---------|-------|
| 1   | A     | 1507     | Total | C     | N    | O     | P    | 0       | 0       | 0     |
|     |       |          | 32391 | 14418 | 6002 | 10465 | 1506 |         |         |       |

- Molecule 2 is a RNA chain called P-SITE MESSENGER RNA FRAGMENT.

| Mol | Chain | Residues | Atoms |    |    |    |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|---------|-------|
| 2   | X     | 6        | Total | C  | N  | O  | P | 0       | 0       | 0     |
|     |       |          | 117   | 54 | 14 | 44 | 5 |         |         |       |

- Molecule 3 is a RNA chain called ANTICODON STEM-LOOP OF PHENYLALANINE TRANSFER RNA.

| Mol | Chain | Residues | Atoms |     |    |    |    | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|---------|-------|
| 3   | Y     | 11       | Total | C   | N  | O  | P  | 0       | 0       | 0     |
|     |       |          | 233   | 106 | 44 | 73 | 10 |         |         |       |

- Molecule 4 is a RNA chain called A-SITE MESSENGER RNA FRAGMENT.

| Mol | Chain | Residues | Atoms |    |   |    |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|----|---|----|---|---------|---------|-------|
| 4   | Z     | 4        | Total | C  | N | O  | P | 0       | 0       | 0     |
|     |       |          | 77    | 36 | 8 | 30 | 3 |         |         |       |

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S2.

| Mol | Chain | Residues | Atoms |      |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 5   | B     | 234      | Total | C    | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1900  | 1213 | 341 | 341 | 5 |         |         |       |

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S3.

| Mol | Chain | Residues | Atoms |      |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 6   | C     | 206      | Total | C    | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1612  | 1016 | 314 | 281 | 1 |         |         |       |

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S4.

| Mol | Chain | Residues | Atoms |      |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 7   | D     | 208      | Total | C    | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1703  | 1066 | 339 | 291 | 7 |         |         |       |

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S5.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 8   | E     | 150      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1146  | 724 | 217 | 201 | 4 |         |         |       |

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S6.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 9   | F     | 101      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 843   | 531 | 155 | 154 | 3 |         |         |       |

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S7.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 10  | G     | 155      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1257  | 781 | 252 | 218 | 6 |         |         |       |

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S8.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 11  | H     | 138      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1116  | 705 | 215 | 193 | 3 |         |         |       |

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S9.

| Mol | Chain | Residues | Atoms |     |     |     |  | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|---------|-------|
| 12  | I     | 127      | Total | C   | N   | O   |  | 0       | 0       | 0     |
|     |       |          | 1011  | 639 | 198 | 174 |  |         |         |       |

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S10.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 13  | J     | 98       | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 792   | 498 | 156 | 137 | 1 |         |         |       |

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S11.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 14  | K     | 119      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 885   | 549 | 168 | 165 | 3 |         |         |       |

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S12.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 15  | L     | 124      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 970   | 611 | 195 | 163 | 1 |         |         |       |

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S13.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 16  | M     | 118      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 937   | 579 | 193 | 163 | 2 |         |         |       |

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S14.

| Mol | Chain | Residues | Atoms |     |     |    |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|---------|-------|
| 17  | N     | 60       | Total | C   | N   | O  | S | 0       | 0       | 0     |
|     |       |          | 492   | 312 | 104 | 72 | 4 |         |         |       |

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S15.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 18  | O     | 88       | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 734   | 459 | 147 | 126 | 2 |         |         |       |

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S16.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 19  | P     | 83       | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 700   | 443 | 139 | 117 | 1 |         |         |       |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment  | Reference   |
|-------|---------|----------|--------|----------|-------------|
| P     | ?       | -        | PHE    | conflict | GB 12056104 |
| P     | ?       | -        | HIS    | conflict | GB 12056104 |
| P     | ?       | -        | TYR    | conflict | GB 12056104 |

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S17.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 20  | Q     | 104      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 857   | 547 | 161 | 147 | 2 |         |         |       |

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN S18.

| Mol | Chain | Residues | Atoms |     |     |    |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|---------|-------|
| 21  | R     | 73       | Total | C   | N   | O  | S | 0       | 0       | 0     |
|     |       |          | 597   | 380 | 118 | 99 |   |         |         |       |

- Molecule 22 is a protein called 30S RIBOSOMAL PROTEIN S19.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 22  | S     | 87       | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 697   | 444 | 130 | 121 | 2 |         |         |       |

- Molecule 23 is a protein called 30S RIBOSOMAL PROTEIN S20.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 23  | T     | 99       | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 763   | 470 | 162 | 129 | 2 |         |         |       |

- Molecule 24 is a protein called 30S RIBOSOMAL PROTEIN THX.

| Mol | Chain | Residues | Atoms |     |    |    | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|---------|-------|
| 24  | V     | 24       | Total | C   | N  | O  | 0       | 0       | 0     |
|     |       |          | 208   | 128 | 50 | 30 |         |         |       |

- Molecule 25 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms |     | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|---------|---------|
| 25  | A     | 118      | Total | Mg  | 0       | 0       |
|     |       |          | 118   | 118 |         |         |
| 25  | D     | 1        | Total | Mg  | 0       | 0       |
|     |       |          | 1     | 1   |         |         |

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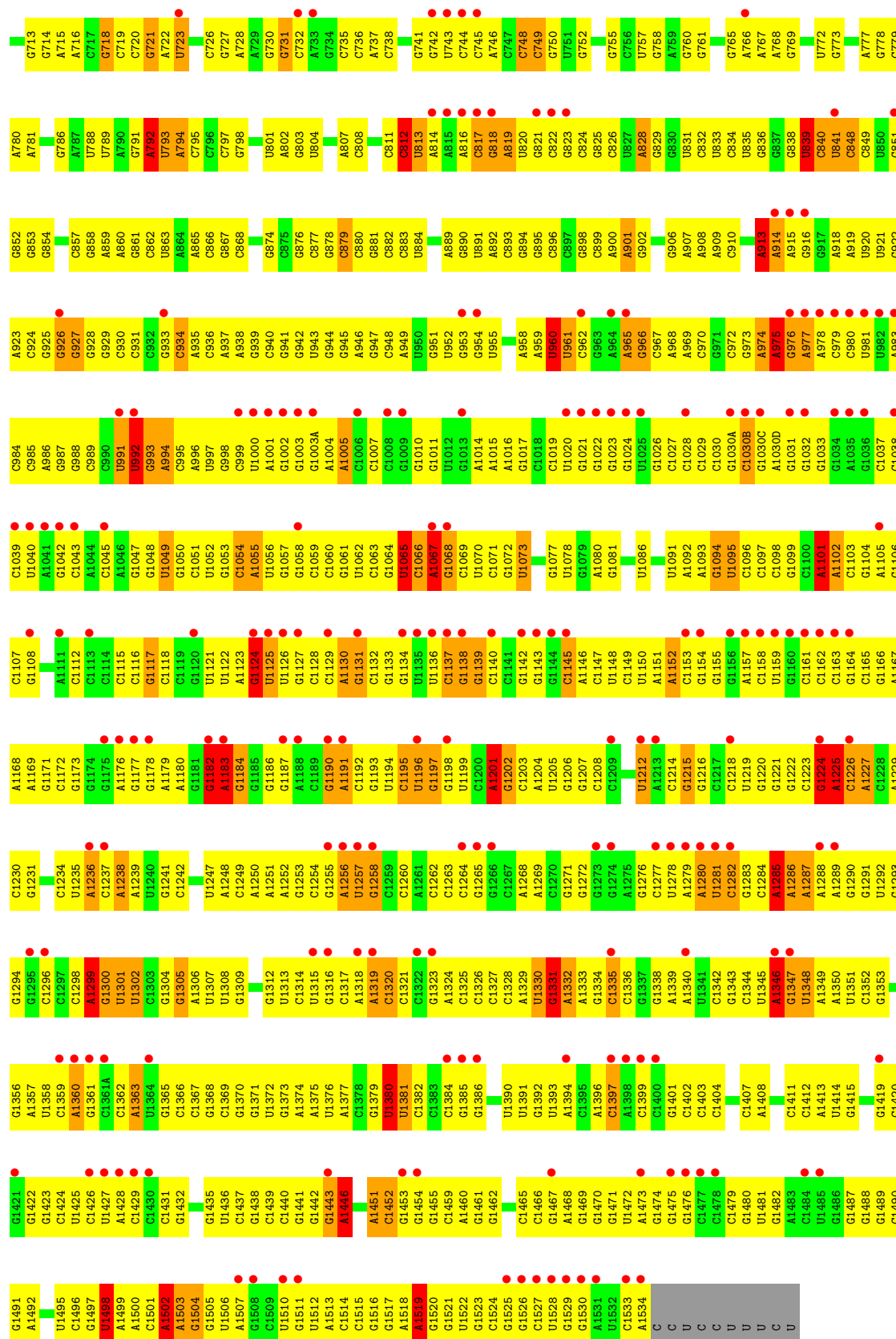
| Mol | Chain | Residues | Atoms      |         | ZeroOcc | AltConf |
|-----|-------|----------|------------|---------|---------|---------|
| 25  | H     | 1        | Total<br>1 | Mg<br>1 | 0       | 0       |

- Molecule 26 is ZINC ION (CCD ID: ZN) (formula: Zn).

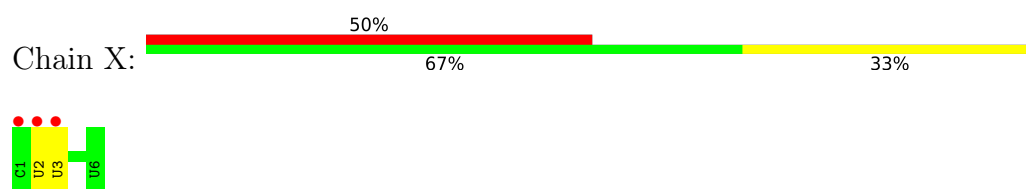
| Mol | Chain | Residues | Atoms      |         | ZeroOcc | AltConf |
|-----|-------|----------|------------|---------|---------|---------|
| 26  | D     | 1        | Total<br>1 | Zn<br>1 | 0       | 0       |
| 26  | N     | 1        | Total<br>1 | Zn<br>1 | 0       | 0       |



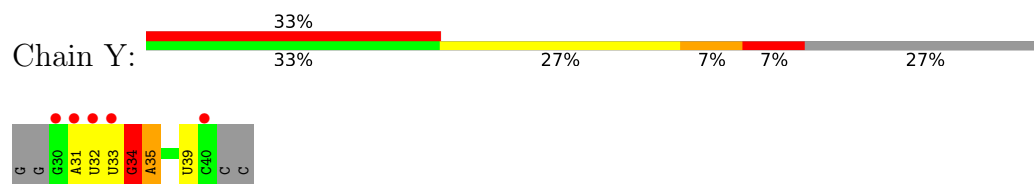




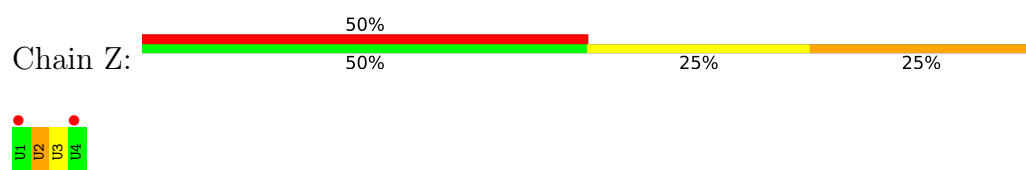
• Molecule 2: P-SITE MESSENGER RNA FRAGMENT



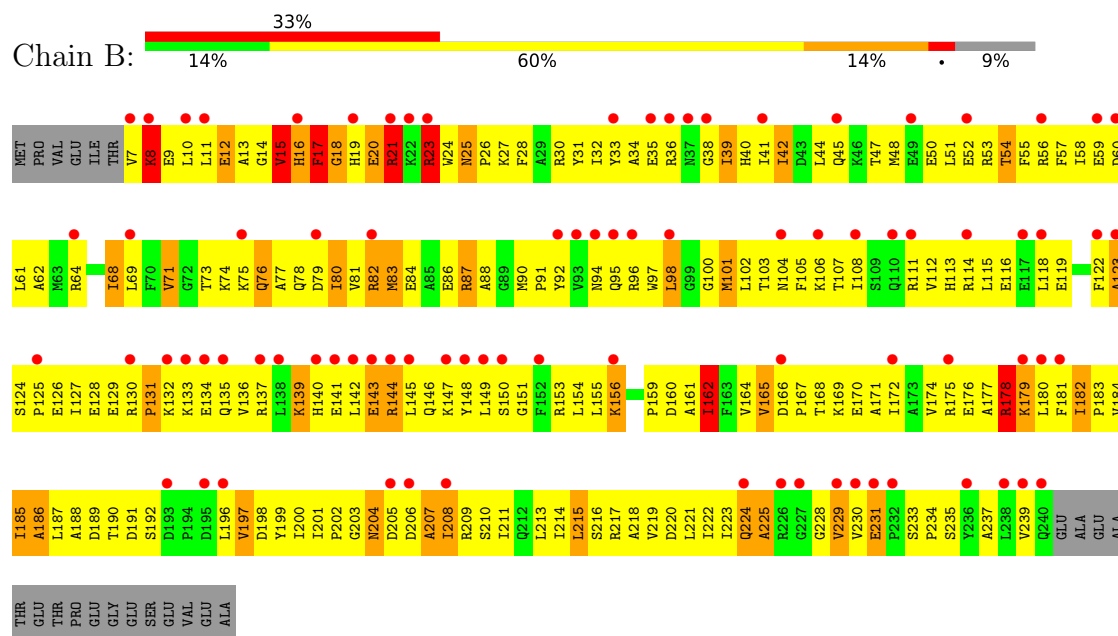
• Molecule 3: ANTICODON STEM-LOOP OF PHENYLALANINE TRANSFER RNA



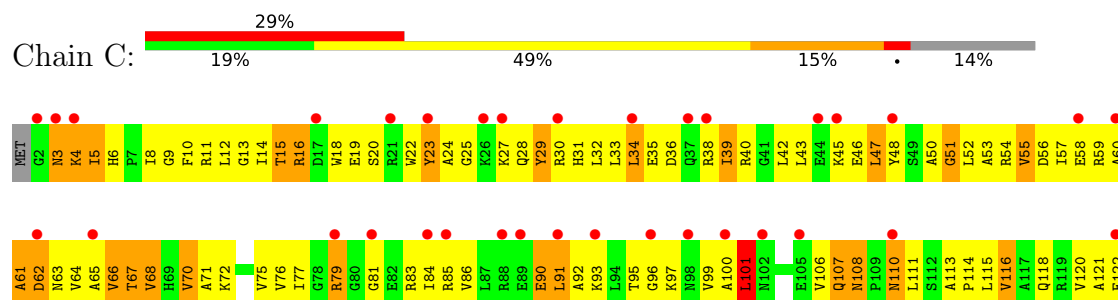
• Molecule 4: A-SITE MESSENGER RNA FRAGMENT

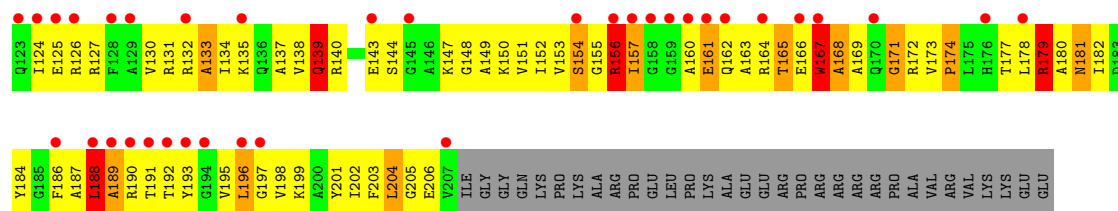


• Molecule 5: 30S RIBOSOMAL PROTEIN S2

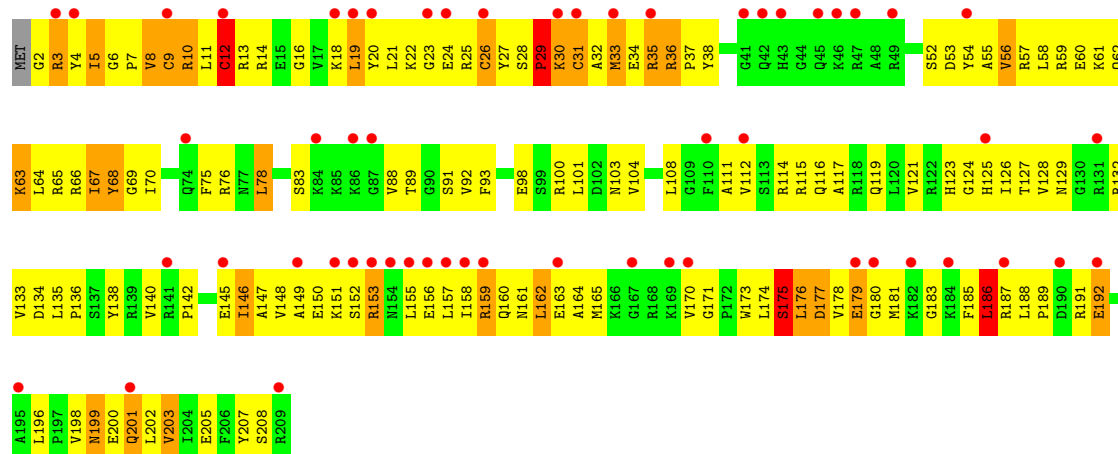


• Molecule 6: 30S RIBOSOMAL PROTEIN S3

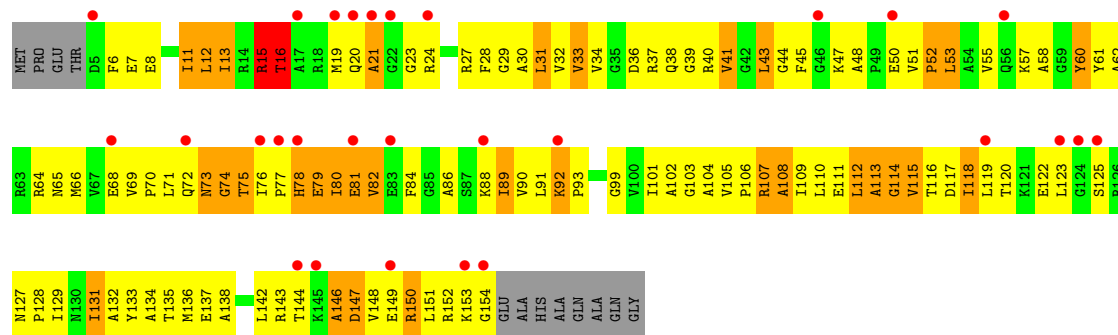




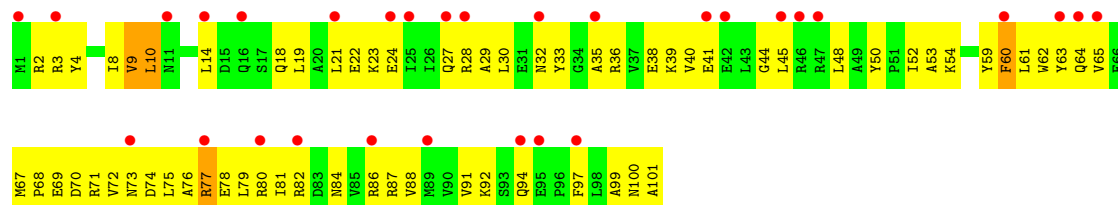
● Molecule 7: 30S RIBOSOMAL PROTEIN S4



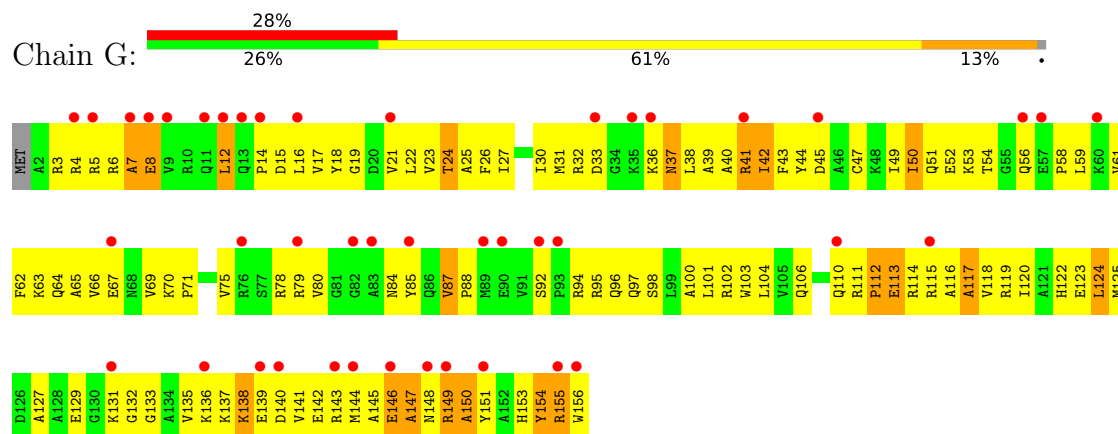
● Molecule 8: 30S RIBOSOMAL PROTEIN S5



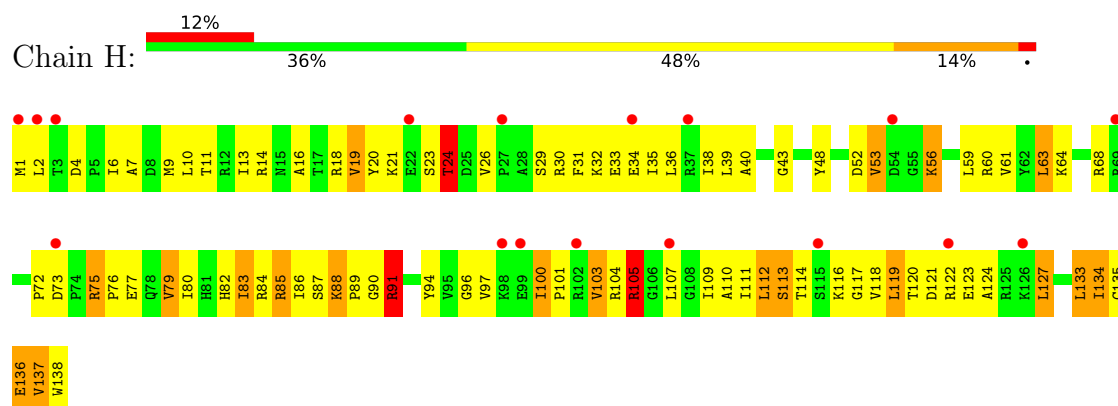
● Molecule 9: 30S RIBOSOMAL PROTEIN S6



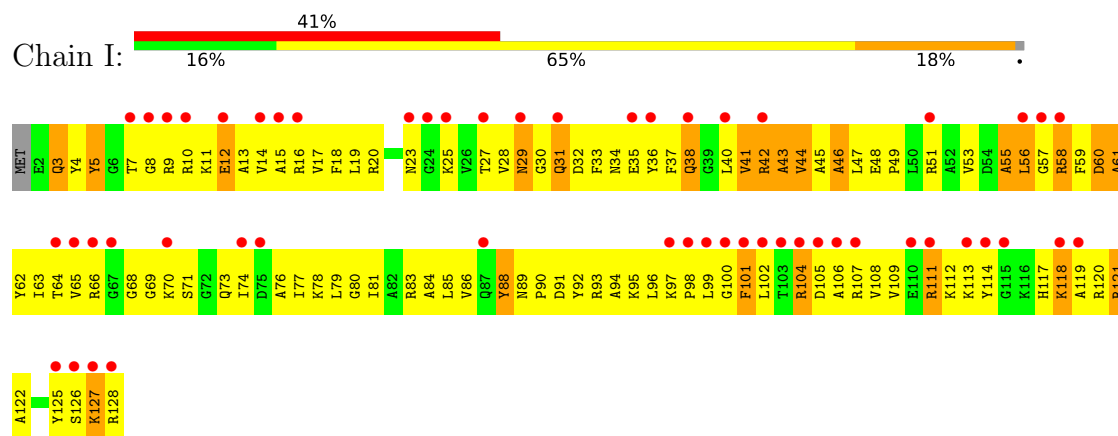
• Molecule 10: 30S RIBOSOMAL PROTEIN S7



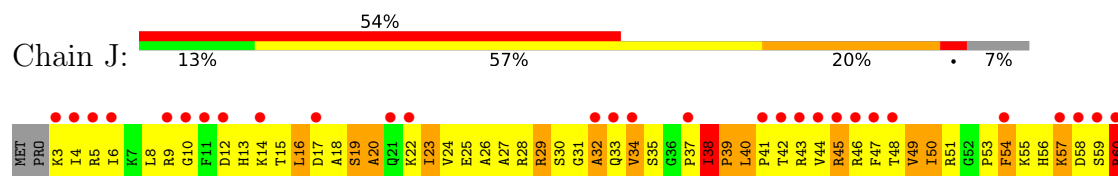
• Molecule 11: 30S RIBOSOMAL PROTEIN S8

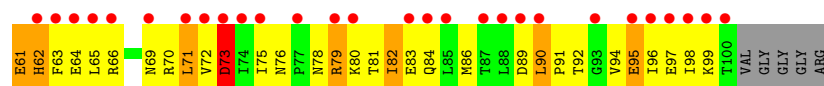


• Molecule 12: 30S RIBOSOMAL PROTEIN S9

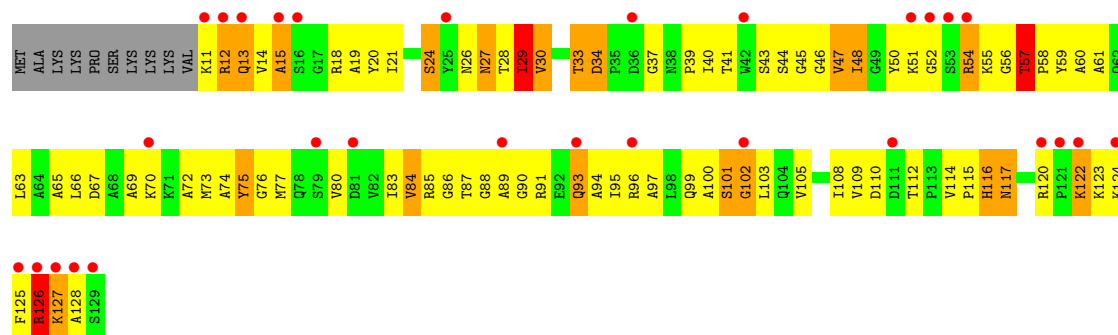


• Molecule 13: 30S RIBOSOMAL PROTEIN S10

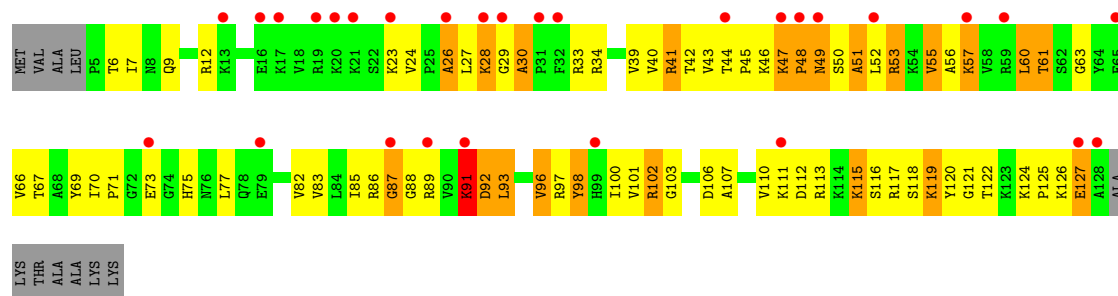




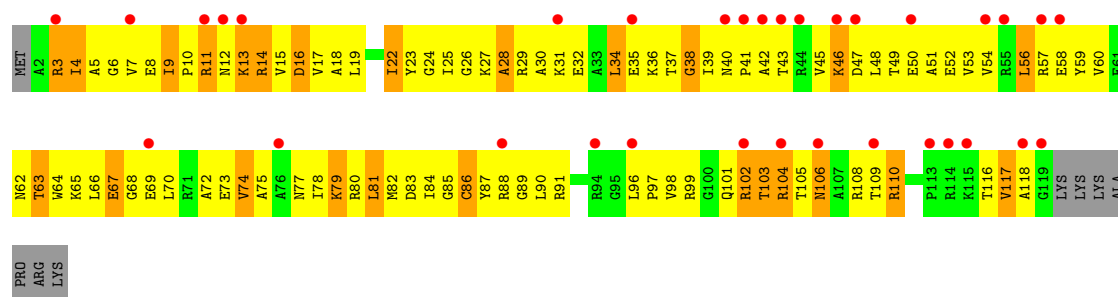
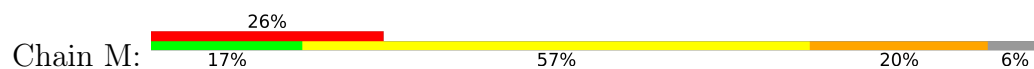
• Molecule 14: 30S RIBOSOMAL PROTEIN S11



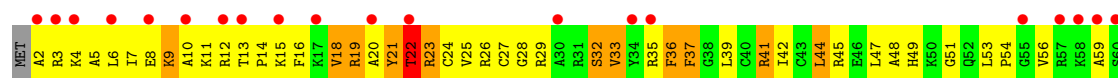
• Molecule 15: 30S RIBOSOMAL PROTEIN S12



• Molecule 16: 30S RIBOSOMAL PROTEIN S13



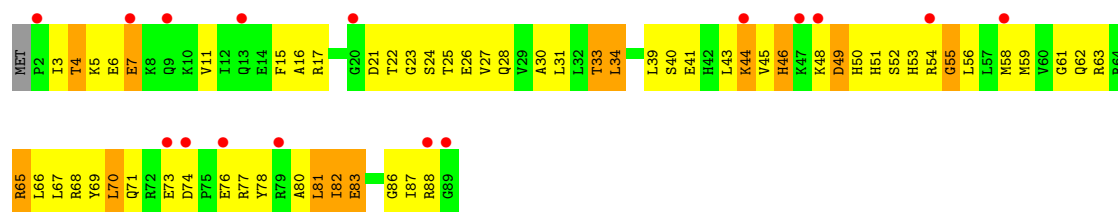
• Molecule 17: 30S RIBOSOMAL PROTEIN S14



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## • Molecule 18: 30S RIBOSOMAL PROTEIN S15

Chain O: 18% 30% 54% 15%



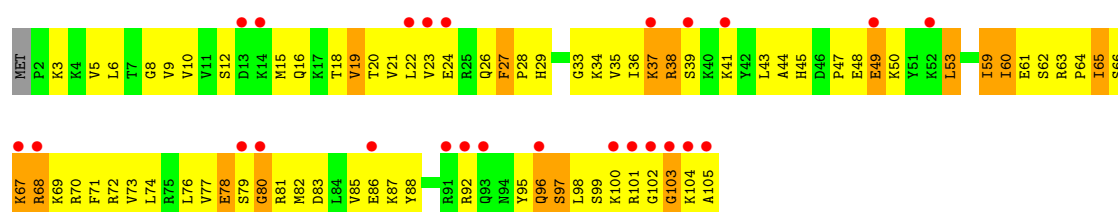
## • Molecule 19: 30S RIBOSOMAL PROTEIN S16

Chain P: 15% 34% 50% 10% 6%



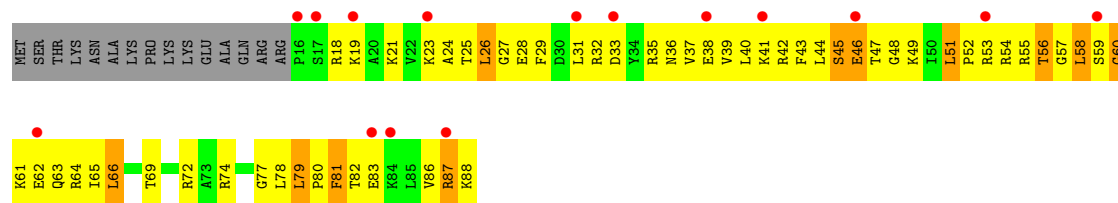
## • Molecule 20: 30S RIBOSOMAL PROTEIN S17

Chain Q: 24% 27% 57% 15%



## • Molecule 21: 30S RIBOSOMAL PROTEIN S18

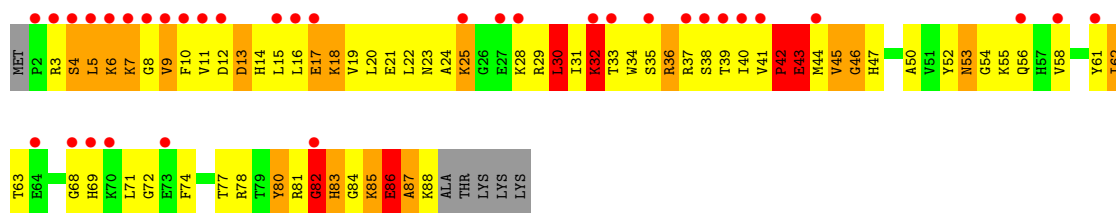
Chain R: 17% 18% 52% 13% 17%



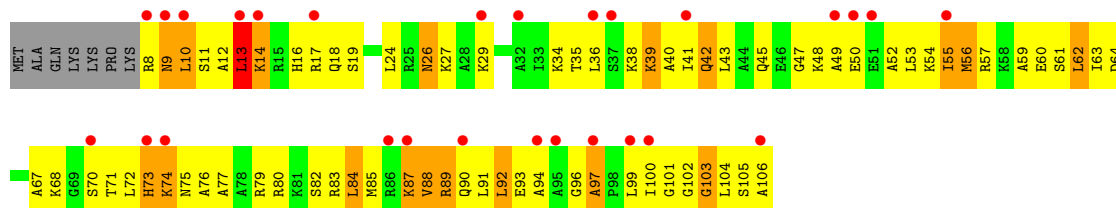
## • Molecule 22: 30S RIBOSOMAL PROTEIN S19

Chain S: 38% 19% 48% 19% 6% 6%





● Molecule 23: 30S RIBOSOMAL PROTEIN S20



● Molecule 24: 30S RIBOSOMAL PROTEIN THX





## 4 Data and refinement statistics

| Property                                                                | Value                                                       | Source           |
|-------------------------------------------------------------------------|-------------------------------------------------------------|------------------|
| Space group                                                             | P 41 21 2                                                   | Depositor        |
| Cell constants<br>a, b, c, $\alpha$ , $\beta$ , $\gamma$                | 401.57Å 401.57Å 176.11Å<br>90.00° 90.00° 90.00°             | Depositor        |
| Resolution (Å)                                                          | 316.23 – 3.31<br>283.96 – 3.31                              | Depositor<br>EDS |
| % Data completeness<br>(in resolution range)                            | 90.6 (316.23-3.31)<br>90.6 (283.96-3.31)                    | Depositor<br>EDS |
| $R_{merge}$                                                             | (Not available)                                             | Depositor        |
| $R_{sym}$                                                               | 0.12                                                        | Depositor        |
| $\langle I/\sigma(I) \rangle$ <sup>1</sup>                              | 3.34 (at 3.33Å)                                             | Xtriage          |
| Refinement program                                                      | CNS                                                         | Depositor        |
| R, $R_{free}$                                                           | 0.231 , 0.286<br>0.204 , 0.248                              | Depositor<br>DCC |
| $R_{free}$ test set                                                     | 9648 reflections (5.03%)                                    | wwPDB-VP         |
| Wilson B-factor (Å <sup>2</sup> )                                       | 76.8                                                        | Xtriage          |
| Anisotropy                                                              | 0.204                                                       | Xtriage          |
| Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> ) | 0.45 , 999.0                                                | EDS              |
| L-test for twinning <sup>2</sup>                                        | $\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$ | Xtriage          |
| Estimated twinning fraction                                             | No twinning to report.                                      | Xtriage          |
| $F_o, F_c$ correlation                                                  | 0.86                                                        | EDS              |
| Total number of atoms                                                   | 52160                                                       | wwPDB-VP         |
| Average B, all atoms (Å <sup>2</sup> )                                  | 68.0                                                        | wwPDB-VP         |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.54% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 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     | 0.46         | 0/36259        | 0.73        | 67/56593 (0.1%)  |
| 2   | X     | 0.49         | 0/128          | 0.72        | 0/196            |
| 3   | Y     | 0.41         | 0/261          | 0.77        | 1/405 (0.2%)     |
| 4   | Z     | 0.43         | 0/84           | 0.83        | 0/128            |
| 5   | B     | 0.41         | 0/1935         | 1.02        | 9/2609 (0.3%)    |
| 6   | C     | 0.45         | 0/1636         | 0.96        | 5/2205 (0.2%)    |
| 7   | D     | 0.51         | 2/1733 (0.1%)  | 1.02        | 8/2318 (0.3%)    |
| 8   | E     | 0.61         | 0/1162         | 1.20        | 12/1564 (0.8%)   |
| 9   | F     | 0.41         | 0/856          | 0.92        | 2/1154 (0.2%)    |
| 10  | G     | 0.43         | 0/1276         | 0.99        | 6/1709 (0.4%)    |
| 11  | H     | 0.60         | 0/1136         | 1.22        | 13/1527 (0.9%)   |
| 12  | I     | 0.43         | 0/1029         | 1.01        | 4/1378 (0.3%)    |
| 13  | J     | 0.43         | 0/805          | 1.07        | 7/1082 (0.6%)    |
| 14  | K     | 0.54         | 0/900          | 0.98        | 2/1213 (0.2%)    |
| 15  | L     | 0.51         | 0/986          | 1.10        | 5/1320 (0.4%)    |
| 16  | M     | 0.46         | 0/947          | 1.01        | 5/1270 (0.4%)    |
| 17  | N     | 0.45         | 0/501          | 1.19        | 5/664 (0.8%)     |
| 18  | O     | 0.51         | 0/745          | 0.92        | 3/992 (0.3%)     |
| 19  | P     | 0.59         | 0/716          | 1.16        | 4/963 (0.4%)     |
| 20  | Q     | 0.60         | 0/870          | 1.18        | 8/1159 (0.7%)    |
| 21  | R     | 0.44         | 0/603          | 1.05        | 8/799 (1.0%)     |
| 22  | S     | 0.42         | 0/712          | 1.05        | 6/956 (0.6%)     |
| 23  | T     | 0.54         | 0/765          | 1.11        | 6/1007 (0.6%)    |
| 24  | V     | 0.52         | 0/212          | 0.93        | 0/277            |
| All | All   | 0.47         | 2/56257 (0.0%) | 0.84        | 186/83488 (0.2%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1   | A     | 1                   | 29                  |

All (2) bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|-----|------|-------|-------|-------------|----------|
| 7   | D     | 201 | GLN  | C-N   | -6.22 | 1.25        | 1.33     |
| 7   | D     | 199 | ASN  | C-N   | -5.82 | 1.26        | 1.33     |

The worst 5 of 186 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms       | Z     | Observed(°) | Ideal(°) |
|-----|-------|-----|------|-------------|-------|-------------|----------|
| 1   | A     | 181 | G    | C2'-C3'-O3' | 13.64 | 129.96      | 109.50   |
| 1   | A     | 559 | A    | C2'-C3'-O3' | 13.19 | 129.29      | 109.50   |
| 1   | A     | 575 | G    | C2'-C3'-O3' | 13.17 | 129.25      | 109.50   |
| 1   | A     | 366 | C    | C2'-C3'-O3' | 13.10 | 129.15      | 109.50   |
| 1   | A     | 243 | A    | C2'-C3'-O3' | 12.04 | 127.56      | 109.50   |

All (1) chirality outliers are listed below:

| Mol | Chain | Res | Type | Atom |
|-----|-------|-----|------|------|
| 1   | A     | 366 | C    | C3'  |

5 of 29 planarity outliers are listed below:

| Mol | Chain | Res    | Type | Group     |
|-----|-------|--------|------|-----------|
| 1   | A     | 190(F) | G    | Sidechain |
| 1   | A     | 197    | A    | Sidechain |
| 1   | A     | 24     | U    | Sidechain |
| 1   | A     | 249    | U    | Sidechain |
| 1   | A     | 37     | U    | Sidechain |

## 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     | 32391 | 0        | 16349    | 1276    | 0            |
| 2   | X     | 117   | 0        | 64       | 3       | 0            |
| 3   | Y     | 233   | 0        | 120      | 10      | 0            |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 4   | Z     | 77    | 0        | 42       | 4       | 0            |
| 5   | B     | 1900  | 0        | 1951     | 304     | 0            |
| 6   | C     | 1612  | 0        | 1677     | 256     | 0            |
| 7   | D     | 1703  | 0        | 1764     | 175     | 0            |
| 8   | E     | 1146  | 0        | 1207     | 133     | 0            |
| 9   | F     | 843   | 0        | 857      | 89      | 0            |
| 10  | G     | 1257  | 0        | 1296     | 139     | 0            |
| 11  | H     | 1116  | 0        | 1177     | 114     | 0            |
| 12  | I     | 1011  | 0        | 1043     | 170     | 0            |
| 13  | J     | 792   | 0        | 835      | 148     | 0            |
| 14  | K     | 885   | 0        | 904      | 94      | 0            |
| 15  | L     | 970   | 0        | 1057     | 120     | 0            |
| 16  | M     | 937   | 0        | 995      | 130     | 0            |
| 17  | N     | 492   | 0        | 529      | 79      | 0            |
| 18  | O     | 734   | 0        | 771      | 67      | 0            |
| 19  | P     | 700   | 0        | 720      | 61      | 0            |
| 20  | Q     | 857   | 0        | 930      | 104     | 0            |
| 21  | R     | 597   | 0        | 668      | 85      | 0            |
| 22  | S     | 697   | 0        | 723      | 125     | 0            |
| 23  | T     | 763   | 0        | 861      | 96      | 0            |
| 24  | V     | 208   | 0        | 221      | 14      | 0            |
| 25  | A     | 118   | 0        | 0        | 0       | 0            |
| 25  | D     | 1     | 0        | 0        | 0       | 0            |
| 25  | H     | 1     | 0        | 0        | 0       | 0            |
| 26  | D     | 1     | 0        | 0        | 0       | 0            |
| 26  | N     | 1     | 0        | 0        | 0       | 0            |
| All | All   | 52160 | 0        | 36761    | 3519    | 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 40.

The worst 5 of 3519 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:A:1397:C:OP2  | 8:E:24:ARG:NH2   | 1.62                     | 1.27              |
| 5:B:84:GLU:HB3  | 5:B:219:VAL:HG21 | 1.25                     | 1.18              |
| 6:C:14:ILE:HG22 | 6:C:15:THR:H     | 1.12                     | 1.15              |
| 1:A:1443:G:H5'' | 1:A:1446:A:H5'   | 1.31                     | 1.11              |
| 7:D:36:ARG:H    | 7:D:37:PRO:HD3   | 0.95                     | 1.11              |

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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

| Mol | Chain | Analysed        | Favoured   | Allowed   | Outliers  | Percentiles |     |
|-----|-------|-----------------|------------|-----------|-----------|-------------|-----|
| 5   | B     | 232/256 (91%)   | 143 (62%)  | 59 (25%)  | 30 (13%)  | 0           | 1   |
| 6   | C     | 204/239 (85%)   | 125 (61%)  | 49 (24%)  | 30 (15%)  | 0           | 1   |
| 7   | D     | 206/209 (99%)   | 139 (68%)  | 49 (24%)  | 18 (9%)   | 0           | 4   |
| 8   | E     | 148/162 (91%)   | 114 (77%)  | 24 (16%)  | 10 (7%)   | 1           | 7   |
| 9   | F     | 99/101 (98%)    | 81 (82%)   | 17 (17%)  | 1 (1%)    | 12          | 41  |
| 10  | G     | 153/156 (98%)   | 104 (68%)  | 37 (24%)  | 12 (8%)   | 1           | 5   |
| 11  | H     | 136/138 (99%)   | 112 (82%)  | 19 (14%)  | 5 (4%)    | 2           | 17  |
| 12  | I     | 125/128 (98%)   | 85 (68%)   | 25 (20%)  | 15 (12%)  | 0           | 1   |
| 13  | J     | 96/105 (91%)    | 58 (60%)   | 23 (24%)  | 15 (16%)  | 0           | 1   |
| 14  | K     | 117/129 (91%)   | 84 (72%)   | 18 (15%)  | 15 (13%)  | 0           | 1   |
| 15  | L     | 122/135 (90%)   | 84 (69%)   | 24 (20%)  | 14 (12%)  | 0           | 2   |
| 16  | M     | 116/126 (92%)   | 74 (64%)   | 28 (24%)  | 14 (12%)  | 0           | 1   |
| 17  | N     | 58/61 (95%)     | 38 (66%)   | 14 (24%)  | 6 (10%)   | 0           | 2   |
| 18  | O     | 86/89 (97%)     | 58 (67%)   | 23 (27%)  | 5 (6%)    | 1           | 9   |
| 19  | P     | 81/88 (92%)     | 59 (73%)   | 20 (25%)  | 2 (2%)    | 4           | 24  |
| 20  | Q     | 102/105 (97%)   | 83 (81%)   | 12 (12%)  | 7 (7%)    | 1           | 7   |
| 21  | R     | 71/88 (81%)     | 50 (70%)   | 17 (24%)  | 4 (6%)    | 1           | 10  |
| 22  | S     | 85/93 (91%)     | 55 (65%)   | 17 (20%)  | 13 (15%)  | 0           | 1   |
| 23  | T     | 97/106 (92%)    | 57 (59%)   | 30 (31%)  | 10 (10%)  | 0           | 2   |
| 24  | V     | 22/26 (85%)     | 16 (73%)   | 6 (27%)   | 0         | 100         | 100 |
| All | All   | 2356/2540 (93%) | 1619 (69%) | 511 (22%) | 226 (10%) | 0           | 3   |

5 of 226 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 5   | B     | 16  | HIS  |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 5   | B     | 17  | PHE  |
| 5   | B     | 20  | GLU  |
| 5   | B     | 21  | ARG  |
| 5   | B     | 24  | TRP  |

### 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 |    |
|-----|-------|----------------|-----------|----------|-------------|----|
| 5   | B     | 202/220 (92%)  | 181 (90%) | 21 (10%) | 7           | 25 |
| 6   | C     | 160/188 (85%)  | 142 (89%) | 18 (11%) | 5           | 22 |
| 7   | D     | 180/181 (99%)  | 162 (90%) | 18 (10%) | 7           | 27 |
| 8   | E     | 115/123 (94%)  | 94 (82%)  | 21 (18%) | 2           | 8  |
| 9   | F     | 90/90 (100%)   | 86 (96%)  | 4 (4%)   | 25          | 54 |
| 10  | G     | 126/127 (99%)  | 118 (94%) | 8 (6%)   | 16          | 44 |
| 11  | H     | 119/119 (100%) | 104 (87%) | 15 (13%) | 4           | 19 |
| 12  | I     | 98/99 (99%)    | 91 (93%)  | 7 (7%)   | 13          | 40 |
| 13  | J     | 87/92 (95%)    | 78 (90%)  | 9 (10%)  | 7           | 26 |
| 14  | K     | 90/99 (91%)    | 76 (84%)  | 14 (16%) | 2           | 12 |
| 15  | L     | 104/111 (94%)  | 95 (91%)  | 9 (9%)   | 9           | 33 |
| 16  | M     | 94/101 (93%)   | 83 (88%)  | 11 (12%) | 5           | 21 |
| 17  | N     | 49/50 (98%)    | 45 (92%)  | 4 (8%)   | 10          | 36 |
| 18  | O     | 79/80 (99%)    | 71 (90%)  | 8 (10%)  | 7           | 27 |
| 19  | P     | 72/74 (97%)    | 66 (92%)  | 6 (8%)   | 10          | 35 |
| 20  | Q     | 96/97 (99%)    | 88 (92%)  | 8 (8%)   | 10          | 35 |
| 21  | R     | 64/77 (83%)    | 61 (95%)  | 3 (5%)   | 23          | 52 |
| 22  | S     | 75/80 (94%)    | 63 (84%)  | 12 (16%) | 2           | 12 |
| 23  | T     | 76/82 (93%)    | 68 (90%)  | 8 (10%)  | 6           | 25 |
| 24  | V     | 19/21 (90%)    | 18 (95%)  | 1 (5%)   | 20          | 49 |

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| Mol | Chain | Analysed        | Rotameric  | Outliers  | Percentiles |
|-----|-------|-----------------|------------|-----------|-------------|
| All | All   | 1995/2111 (94%) | 1790 (90%) | 205 (10%) | 7 26        |

5 of 205 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 13  | J     | 49  | VAL  |
| 15  | L     | 98  | TYR  |
| 23  | T     | 39  | LYS  |
| 13  | J     | 79  | ARG  |
| 14  | K     | 84  | VAL  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 11  | H     | 82  | HIS  |
| 13  | J     | 84  | GLN  |
| 22  | S     | 69  | HIS  |
| 21  | R     | 36  | ASN  |
| 12  | I     | 23  | ASN  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1   | A     | 1506/1522 (98%) | 205 (13%)         | 70 (4%)         |
| 2   | X     | 5/6 (83%)       | 0                 | 0               |
| 3   | Y     | 10/15 (66%)     | 2 (20%)           | 1 (10%)         |
| 4   | Z     | 3/4 (75%)       | 1 (33%)           | 0               |
| All | All   | 1524/1547 (98%) | 208 (13%)         | 71 (4%)         |

5 of 208 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | A     | 8   | A    |
| 1   | A     | 9   | G    |
| 1   | A     | 31  | G    |
| 1   | A     | 32  | A    |
| 1   | A     | 39  | G    |

5 of 71 RNA pucker outliers are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 1   | A     | 1224 | G    |
| 1   | A     | 1281 | U    |
| 1   | A     | 1347 | G    |
| 1   | A     | 428  | G    |
| 1   | A     | 372  | C    |

## 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](#)

Of 122 ligands modelled in this entry, 122 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [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, 95<sup>th</sup> 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 <sup>2</sup> ) | Q<0.9 |
|-----|-------|-----------------|--------|---------------|-----------------------|-------|
| 1   | A     | 1507/1522 (99%) | 1.10   | 300 (19%) 3 3 | 16, 53, 140, 201      | 0     |
| 2   | X     | 6/6 (100%)      | 3.95   | 3 (50%) 0 0   | 59, 71, 178, 201      | 0     |
| 3   | Y     | 11/15 (73%)     | 1.65   | 5 (45%) 0 0   | 66, 90, 182, 190      | 0     |
| 4   | Z     | 4/4 (100%)      | 1.45   | 2 (50%) 0 0   | 71, 77, 89, 119       | 0     |
| 5   | B     | 234/256 (91%)   | 1.64   | 85 (36%) 1 1  | 19, 87, 173, 201      | 0     |
| 6   | C     | 206/239 (86%)   | 1.61   | 69 (33%) 1 1  | 22, 80, 160, 201      | 0     |
| 7   | D     | 208/209 (99%)   | 1.23   | 56 (26%) 1 1  | 17, 60, 145, 180      | 0     |
| 8   | E     | 150/162 (92%)   | 1.02   | 28 (18%) 3 3  | 17, 48, 107, 201      | 0     |
| 9   | F     | 101/101 (100%)  | 1.49   | 30 (29%) 1 1  | 35, 88, 148, 185      | 0     |
| 10  | G     | 155/156 (99%)   | 1.22   | 43 (27%) 1 1  | 27, 70, 150, 201      | 0     |
| 11  | H     | 138/138 (100%)  | 0.54   | 17 (12%) 8 7  | 5, 39, 108, 136       | 0     |
| 12  | I     | 127/128 (99%)   | 1.89   | 53 (41%) 0 0  | 19, 82, 144, 184      | 0     |
| 13  | J     | 98/105 (93%)    | 2.62   | 57 (58%) 0 0  | 30, 107, 188, 201     | 0     |
| 14  | K     | 119/129 (92%)   | 1.75   | 29 (24%) 2 1  | 12, 54, 130, 201      | 0     |
| 15  | L     | 124/135 (91%)   | 1.17   | 29 (23%) 2 2  | 16, 57, 144, 187      | 0     |
| 16  | M     | 118/126 (93%)   | 1.29   | 33 (27%) 1 1  | 32, 70, 144, 170      | 0     |
| 17  | N     | 60/61 (98%)     | 1.83   | 21 (35%) 1 1  | 39, 70, 140, 201      | 0     |
| 18  | O     | 88/89 (98%)     | 1.07   | 16 (18%) 3 3  | 7, 56, 145, 201       | 0     |
| 19  | P     | 83/88 (94%)     | 0.93   | 13 (15%) 5 4  | 10, 41, 101, 150      | 0     |
| 20  | Q     | 104/105 (99%)   | 1.31   | 25 (24%) 2 1  | 10, 43, 157, 201      | 0     |
| 21  | R     | 73/88 (82%)     | 1.19   | 15 (20%) 2 3  | 32, 66, 166, 201      | 0     |
| 22  | S     | 87/93 (93%)     | 1.90   | 35 (40%) 0 0  | 54, 99, 176, 201      | 0     |
| 23  | T     | 99/106 (93%)    | 1.35   | 27 (27%) 1 1  | 15, 50, 123, 156      | 0     |
| 24  | V     | 24/26 (92%)     | 1.60   | 8 (33%) 1 1   | 26, 59, 128, 179      | 0     |

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| Mol | Chain | Analysed        | <RSRZ> | #RSRZ>2                     | OWAB(Å <sup>2</sup> ) | Q<0.9 |
|-----|-------|-----------------|--------|-----------------------------|-----------------------|-------|
| All | All   | 3924/4087 (96%) | 1.29   | 999 (25%) <b>1</b> <b>1</b> | 5, 60, 152, 201       | 0     |

The worst 5 of 999 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 14  | K     | 128 | ALA  | 37.5 |
| 14  | K     | 129 | SER  | 33.2 |
| 18  | O     | 89  | GLY  | 12.8 |
| 23  | T     | 9   | ASN  | 12.7 |
| 10  | G     | 13  | GLN  | 11.4 |

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

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

## 6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> ) | Q<0.9 |
|-----|------|-------|------|-------|------|------|----------------------------|-------|
| 25  | MG   | A     | 1624 | 1/1   | 0.62 | 0.56 | 27,27,27,27                | 1     |
| 25  | MG   | A     | 1636 | 1/1   | 0.66 | 0.18 | 27,27,27,27                | 1     |
| 25  | MG   | A     | 1626 | 1/1   | 0.73 | 0.19 | 27,27,27,27                | 1     |
| 25  | MG   | A     | 1654 | 1/1   | 0.76 | 0.31 | 27,27,27,27                | 1     |
| 25  | MG   | A     | 1628 | 1/1   | 0.77 | 0.52 | 27,27,27,27                | 1     |
| 25  | MG   | A     | 1561 | 1/1   | 0.77 | 0.40 | 27,27,27,27                | 0     |
| 25  | MG   | A     | 1622 | 1/1   | 0.77 | 0.18 | 27,27,27,27                | 0     |
| 25  | MG   | A     | 1655 | 1/1   | 0.77 | 0.36 | 27,27,27,27                | 1     |
| 25  | MG   | A     | 1618 | 1/1   | 0.79 | 0.15 | 27,27,27,27                | 1     |
| 25  | MG   | A     | 1649 | 1/1   | 0.79 | 0.22 | 27,27,27,27                | 1     |
| 25  | MG   | A     | 1640 | 1/1   | 0.82 | 0.46 | 27,27,27,27                | 1     |
| 25  | MG   | A     | 1589 | 1/1   | 0.83 | 0.34 | 27,27,27,27                | 0     |
| 25  | MG   | A     | 210  | 1/1   | 0.83 | 0.20 | 27,27,27,27                | 1     |

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| Mol | Type | Chain | Res  | Atoms | RSCC | RSR  | B-factors( $\text{\AA}^2$ ) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-----------------------------|-------|
| 25  | MG   | A     | 1565 | 1/1   | 0.83 | 0.34 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1574 | 1/1   | 0.83 | 0.33 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1641 | 1/1   | 0.85 | 0.39 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1548 | 1/1   | 0.85 | 0.30 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1606 | 1/1   | 0.86 | 0.20 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1560 | 1/1   | 0.87 | 0.37 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1597 | 1/1   | 0.87 | 0.25 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1579 | 1/1   | 0.87 | 0.16 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1627 | 1/1   | 0.88 | 0.16 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1545 | 1/1   | 0.88 | 0.26 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1613 | 1/1   | 0.88 | 0.29 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1562 | 1/1   | 0.88 | 0.20 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1656 | 1/1   | 0.88 | 0.14 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1621 | 1/1   | 0.89 | 0.25 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1591 | 1/1   | 0.89 | 0.32 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1652 | 1/1   | 0.89 | 0.10 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 87   | 1/1   | 0.89 | 0.27 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1639 | 1/1   | 0.89 | 0.32 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1550 | 1/1   | 0.89 | 0.22 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1620 | 1/1   | 0.90 | 0.33 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1558 | 1/1   | 0.90 | 0.29 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1576 | 1/1   | 0.91 | 0.25 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1593 | 1/1   | 0.91 | 0.27 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1566 | 1/1   | 0.91 | 0.16 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1598 | 1/1   | 0.91 | 0.23 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1582 | 1/1   | 0.91 | 0.20 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1575 | 1/1   | 0.91 | 0.28 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 214  | 1/1   | 0.92 | 0.12 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1547 | 1/1   | 0.92 | 0.22 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1581 | 1/1   | 0.92 | 0.08 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1637 | 1/1   | 0.92 | 0.17 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1615 | 1/1   | 0.92 | 0.23 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1594 | 1/1   | 0.92 | 0.40 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1625 | 1/1   | 0.93 | 0.09 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1604 | 1/1   | 0.93 | 0.07 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1569 | 1/1   | 0.93 | 0.24 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1607 | 1/1   | 0.93 | 0.24 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1609 | 1/1   | 0.93 | 0.13 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1611 | 1/1   | 0.93 | 0.15 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1638 | 1/1   | 0.93 | 0.24 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 86   | 1/1   | 0.93 | 0.23 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1564 | 1/1   | 0.93 | 0.14 | 27,27,27,27                 | 0     |

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| Mol | Type | Chain | Res  | Atoms | RSCC | RSR  | B-factors( $\text{\AA}^2$ ) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-----------------------------|-------|
| 25  | MG   | A     | 1617 | 1/1   | 0.93 | 0.29 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1644 | 1/1   | 0.93 | 0.17 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1555 | 1/1   | 0.93 | 0.27 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1584 | 1/1   | 0.93 | 0.32 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1585 | 1/1   | 0.93 | 0.27 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1556 | 1/1   | 0.93 | 0.34 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1603 | 1/1   | 0.93 | 0.24 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1583 | 1/1   | 0.94 | 0.10 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1573 | 1/1   | 0.94 | 0.29 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1546 | 1/1   | 0.94 | 0.24 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1587 | 1/1   | 0.94 | 0.28 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1568 | 1/1   | 0.94 | 0.27 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 71   | 1/1   | 0.94 | 0.26 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1552 | 1/1   | 0.94 | 0.34 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1645 | 1/1   | 0.94 | 0.08 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1646 | 1/1   | 0.94 | 0.34 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1580 | 1/1   | 0.94 | 0.21 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1557 | 1/1   | 0.94 | 0.21 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1572 | 1/1   | 0.94 | 0.09 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1629 | 1/1   | 0.94 | 0.17 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1630 | 1/1   | 0.94 | 0.32 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1602 | 1/1   | 0.95 | 0.13 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1578 | 1/1   | 0.95 | 0.25 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1590 | 1/1   | 0.95 | 0.13 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1571 | 1/1   | 0.95 | 0.18 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1619 | 1/1   | 0.95 | 0.29 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1648 | 1/1   | 0.95 | 0.09 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1592 | 1/1   | 0.95 | 0.17 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 211  | 1/1   | 0.95 | 0.32 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1653 | 1/1   | 0.95 | 0.23 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1549 | 1/1   | 0.95 | 0.33 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1623 | 1/1   | 0.95 | 0.08 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1612 | 1/1   | 0.95 | 0.08 | 27,27,27,27                 | 0     |
| 25  | MG   | D     | 215  | 1/1   | 0.95 | 0.11 | 27,27,27,27                 | 0     |
| 25  | MG   | H     | 213  | 1/1   | 0.95 | 0.06 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1642 | 1/1   | 0.96 | 0.18 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1567 | 1/1   | 0.96 | 0.06 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1651 | 1/1   | 0.96 | 0.13 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1577 | 1/1   | 0.96 | 0.10 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1634 | 1/1   | 0.96 | 0.08 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1616 | 1/1   | 0.97 | 0.14 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1643 | 1/1   | 0.97 | 0.14 | 27,27,27,27                 | 1     |

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| Mol | Type | Chain | Res  | Atoms | RSCC | RSR  | B-factors( $\text{\AA}^2$ ) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-----------------------------|-------|
| 25  | MG   | A     | 1605 | 1/1   | 0.97 | 0.06 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1554 | 1/1   | 0.97 | 0.33 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1559 | 1/1   | 0.97 | 0.16 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1647 | 1/1   | 0.97 | 0.08 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1631 | 1/1   | 0.97 | 0.30 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1632 | 1/1   | 0.97 | 0.08 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1633 | 1/1   | 0.97 | 0.32 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1608 | 1/1   | 0.97 | 0.08 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1595 | 1/1   | 0.97 | 0.11 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1610 | 1/1   | 0.97 | 0.15 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1601 | 1/1   | 0.97 | 0.20 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1570 | 1/1   | 0.97 | 0.36 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1588 | 1/1   | 0.97 | 0.20 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1599 | 1/1   | 0.97 | 0.21 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1586 | 1/1   | 0.98 | 0.05 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1563 | 1/1   | 0.98 | 0.12 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1614 | 1/1   | 0.98 | 0.25 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1650 | 1/1   | 0.98 | 0.18 | 27,27,27,27                 | 1     |
| 25  | MG   | A     | 1635 | 1/1   | 0.98 | 0.14 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1551 | 1/1   | 0.98 | 0.35 | 27,27,27,27                 | 0     |
| 26  | ZN   | D     | 506  | 1/1   | 0.98 | 0.20 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1600 | 1/1   | 0.99 | 0.11 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1596 | 1/1   | 0.99 | 0.43 | 27,27,27,27                 | 0     |
| 25  | MG   | A     | 1553 | 1/1   | 0.99 | 0.35 | 27,27,27,27                 | 0     |
| 26  | ZN   | N     | 507  | 1/1   | 1.00 | 0.02 | 27,27,27,27                 | 1     |

## 6.5 Other polymers

There are no such residues in this entry.