



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2018 – 02:10 pm GMT

PDB ID : 4V6C
Title : Crystal structure of the E. coli 70S ribosome in an intermediate state of ratcheting
Authors : Zhang, W.; Dunkle, J.A.; Cate, J.H.D.
Deposited on : 2009-06-27
Resolution : 3.19 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : trunk31020
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk31020

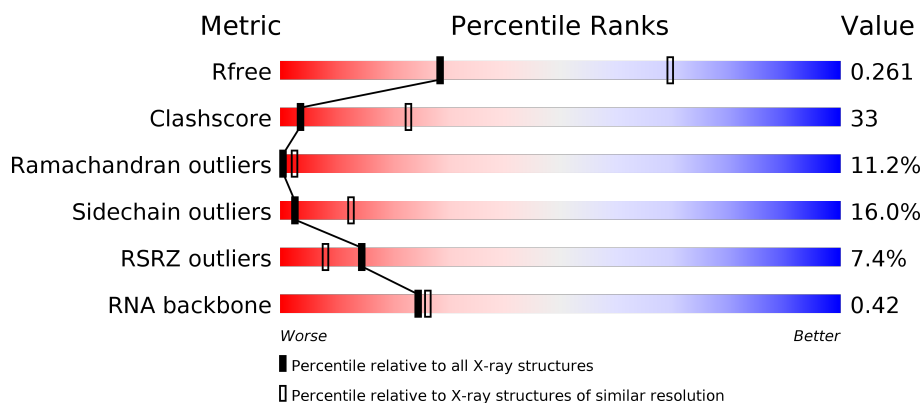
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.19 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} | 111664 | 1121 (3.22-3.18) |
| Clashscore | 122126 | 1091 (3.20-3.20) |
| Ramachandran outliers | 120053 | 1074 (3.20-3.20) |
| Sidechain outliers | 120020 | 1073 (3.20-3.20) |
| RSRZ outliers | 108989 | 1083 (3.22-3.18) |
| RNA backbone | 2636 | 1107 (3.60-2.80) |

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 | AB | 241 | <div> <div>6%</div> <div>18% 49% 21% 10%</div> </div> |
| 1 | CB | 241 | <div> <div>5%</div> <div>23% 53% 14% 10%</div> </div> |
| 2 | AC | 233 | <div> <div>0%</div> <div>33% 43% 10% 12%</div> </div> |
| 2 | CC | 233 | <div> <div>5%</div> <div>34% 41% 12% 12%</div> </div> |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 3 | AD | 206 | |
| 3 | CD | 206 | |
| 4 | AE | 167 | |
| 4 | CE | 167 | |
| 5 | AF | 135 | |
| 5 | CF | 135 | |
| 6 | AG | 179 | |
| 6 | CG | 179 | |
| 7 | AH | 130 | |
| 7 | CH | 130 | |
| 8 | AI | 130 | |
| 8 | CI | 130 | |
| 9 | AJ | 103 | |
| 9 | CJ | 103 | |
| 10 | AK | 129 | |
| 10 | CK | 129 | |
| 11 | AL | 124 | |
| 11 | CL | 124 | |
| 12 | AM | 118 | |
| 12 | CM | 118 | |
| 13 | AN | 101 | |
| 13 | CN | 101 | |
| 14 | AO | 89 | |
| 14 | CO | 89 | |
| 15 | AP | 82 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 15 | CP | 82 | |
| 16 | AQ | 84 | |
| 16 | CQ | 84 | |
| 17 | AR | 75 | |
| 17 | CR | 75 | |
| 18 | AS | 92 | |
| 18 | CS | 92 | |
| 19 | AT | 87 | |
| 19 | CT | 87 | |
| 20 | AU | 71 | |
| 20 | CU | 71 | |
| 21 | AA | 1533 | |
| 22 | BA | 2903 | |
| 22 | DA | 2903 | |
| 23 | BB | 118 | |
| 24 | BC | 273 | |
| 24 | DC | 273 | |
| 25 | BD | 209 | |
| 25 | DD | 209 | |
| 26 | BE | 201 | |
| 26 | DE | 201 | |
| 27 | BF | 179 | |
| 27 | DF | 179 | |
| 28 | BG | 177 | |
| 28 | DG | 177 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 29 | BH | 149 | |
| 29 | DH | 149 | |
| 30 | BI | 142 | |
| 30 | DI | 142 | |
| 31 | BJ | 142 | |
| 31 | DJ | 142 | |
| 32 | BK | 123 | |
| 32 | DK | 123 | |
| 33 | BL | 144 | |
| 33 | DL | 144 | |
| 34 | BM | 136 | |
| 34 | DM | 136 | |
| 35 | BN | 127 | |
| 35 | DN | 127 | |
| 36 | BO | 117 | |
| 36 | DO | 117 | |
| 37 | BP | 115 | |
| 37 | DP | 115 | |
| 38 | BQ | 118 | |
| 38 | DQ | 118 | |
| 39 | BR | 103 | |
| 39 | DR | 103 | |
| 40 | BS | 110 | |
| 40 | DS | 110 | |
| 41 | BT | 100 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 41 | DT | 100 | |
| 42 | BU | 104 | |
| 42 | DU | 104 | |
| 43 | BV | 94 | |
| 43 | DV | 94 | |
| 44 | BW | 85 | |
| 44 | DW | 85 | |
| 45 | BX | 78 | |
| 45 | DX | 78 | |
| 46 | BY | 63 | |
| 46 | DY | 63 | |
| 47 | BZ | 59 | |
| 47 | DZ | 59 | |
| 48 | B0 | 57 | |
| 48 | D0 | 57 | |
| 49 | B1 | 55 | |
| 49 | D1 | 55 | |
| 50 | B2 | 46 | |
| 50 | D2 | 46 | |
| 51 | B3 | 65 | |
| 51 | D3 | 65 | |
| 52 | B4 | 38 | |
| 52 | D4 | 38 | |
| 53 | CA | 1530 | |
| 54 | DB | 117 | |

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 |
|-----|------|-------|------|-----------|----------|---------|------------------|
| 55 | MG | BA | 3057 | - | - | - | X |
| 55 | MG | CA | 1619 | - | - | - | X |
| 55 | MG | CA | 1624 | - | - | - | X |
| 55 | MG | DA | 3002 | - | - | - | X |
| 55 | MG | DA | 3003 | - | - | - | X |
| 55 | MG | DA | 3005 | - | - | - | X |
| 55 | MG | DA | 3010 | - | - | - | X |
| 55 | MG | DA | 3013 | - | - | - | X |
| 55 | MG | DA | 3020 | - | - | - | X |
| 55 | MG | DA | 3027 | - | - | - | X |
| 55 | MG | DA | 3039 | - | - | - | X |
| 55 | MG | DA | 3063 | - | - | - | X |
| 55 | MG | DA | 3064 | - | - | - | X |
| 55 | MG | DA | 3065 | - | - | - | X |
| 55 | MG | DA | 3098 | - | - | - | X |
| 55 | MG | DA | 3110 | - | - | - | X |
| 55 | MG | DA | 3129 | - | - | - | X |
| 55 | MG | DA | 3132 | - | - | - | X |
| 55 | MG | DA | 3134 | - | - | - | X |
| 55 | MG | DJ | 201 | - | - | - | X |

2 Entry composition [i](#)

There are 57 unique types of molecules in this entry. The entry contains 284450 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 30S ribosomal protein S2.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 1 | AB | 218 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1704 | 1081 | 305 | 311 | 7 | | | |
| 1 | CB | 218 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1704 | 1081 | 305 | 311 | 7 | | | |

- Molecule 2 is a protein called 30S ribosomal protein S3.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 2 | AC | 206 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1624 | 1028 | 305 | 288 | 3 | | | |
| 2 | CC | 206 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1624 | 1028 | 305 | 288 | 3 | | | |

- Molecule 3 is a protein called 30S ribosomal protein S4.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 3 | AD | 205 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1643 | 1026 | 315 | 298 | 4 | | | |
| 3 | CD | 205 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1643 | 1026 | 315 | 298 | 4 | | | |

- Molecule 4 is a protein called 30S ribosomal protein S5.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 4 | AE | 150 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1105 | 687 | 211 | 201 | 6 | | | |
| 4 | CE | 150 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1105 | 687 | 211 | 201 | 6 | | | |

- Molecule 5 is a protein called 30S ribosomal protein S6.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 5 | AF | 100 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 817 | 515 | 148 | 148 | 6 | | | |
| 5 | CF | 100 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 817 | 515 | 148 | 148 | 6 | | | |

- Molecule 6 is a protein called 30S ribosomal protein S7.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 6 | AG | 151 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1181 | 735 | 227 | 215 | 4 | | | |
| 6 | CG | 150 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1174 | 730 | 226 | 214 | 4 | | | |

- Molecule 7 is a protein called 30S ribosomal protein S8.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 7 | AH | 129 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 979 | 616 | 173 | 184 | 6 | | | |
| 7 | CH | 129 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 979 | 616 | 173 | 184 | 6 | | | |

- Molecule 8 is a protein called 30S ribosomal protein S9.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 8 | AI | 127 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1022 | 634 | 206 | 179 | 3 | | | |
| 8 | CI | 127 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1022 | 634 | 206 | 179 | 3 | | | |

- Molecule 9 is a protein called 30S ribosomal protein S10.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 9 | AJ | 98 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 786 | 493 | 150 | 142 | 1 | | | |
| 9 | CJ | 98 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 786 | 493 | 150 | 142 | 1 | | | |

- Molecule 10 is a protein called 30S ribosomal protein S11.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 10 | AK | 117 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 877 | 540 | 174 | 160 | 3 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 10 | CK | 117 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 877 | 540 | 174 | 160 | 3 | | | |

- Molecule 11 is a protein called 30S ribosomal protein S12.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 11 | AL | 123 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 955 | 590 | 196 | 165 | 4 | | | |
| 11 | CL | 123 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 955 | 590 | 196 | 165 | 4 | | | |

- Molecule 12 is a protein called 30S ribosomal protein S13.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 12 | AM | 114 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 883 | 546 | 178 | 156 | 3 | | | |
| 12 | CM | 113 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 876 | 541 | 177 | 155 | 3 | | | |

- Molecule 13 is a protein called 30S ribosomal protein S14.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 13 | AN | 96 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 774 | 483 | 160 | 128 | 3 | | | |
| 13 | CN | 95 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 769 | 480 | 159 | 127 | 3 | | | |

- Molecule 14 is a protein called 30S ribosomal protein S15.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 14 | AO | 88 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 714 | 439 | 144 | 130 | 1 | | | |
| 14 | CO | 88 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 714 | 439 | 144 | 130 | 1 | | | |

- Molecule 15 is a protein called 30S ribosomal protein S16.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 15 | AP | 82 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 649 | 406 | 128 | 114 | 1 | | | |
| 15 | CP | 80 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 638 | 400 | 126 | 111 | 1 | | | |

- Molecule 16 is a protein called 30S ribosomal protein S17.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 16 | AQ | 80 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 648 | 411 | 121 | 113 | 3 | | | |
| 16 | CQ | 80 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 648 | 411 | 121 | 113 | 3 | | | |

- Molecule 17 is a protein called 30S ribosomal protein S18.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---------|---------|-------|
| 17 | AR | 55 | Total | C | N | O | 0 | 0 | 0 |
| | | | 455 | 288 | 86 | 81 | | | |
| 17 | CR | 55 | Total | C | N | O | 0 | 0 | 0 |
| | | | 455 | 288 | 86 | 81 | | | |

- Molecule 18 is a protein called 30S ribosomal protein S19.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 18 | AS | 79 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 637 | 408 | 120 | 107 | 2 | | | |
| 18 | CS | 79 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 637 | 408 | 120 | 107 | 2 | | | |

- Molecule 19 is a protein called 30S ribosomal protein S20.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 19 | AT | 85 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 665 | 411 | 137 | 114 | 3 | | | |
| 19 | CT | 85 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 665 | 411 | 137 | 114 | 3 | | | |

- Molecule 20 is a protein called 30S ribosomal protein S21.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 20 | AU | 51 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 425 | 265 | 86 | 73 | 1 | | | |
| 20 | CU | 51 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 425 | 265 | 86 | 73 | 1 | | | |

- Molecule 21 is a RNA chain called 16S rRNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|---------|-------|
| 21 | AA | 1533 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 32895 | 14671 | 6036 | 10655 | 1533 | | | |

- Molecule 22 is a RNA chain called 23S rRNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|---------|-------|
| 22 | BA | 2854 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 61274 | 27334 | 11279 | 19807 | 2854 | | | |
| 22 | DA | 2841 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 60995 | 27210 | 11229 | 19715 | 2841 | | | |

- Molecule 23 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|---------|-------|
| 23 | BB | 118 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 2529 | 1126 | 464 | 821 | 118 | | | |

- Molecule 24 is a protein called 50S ribosomal protein L2.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 24 | BC | 271 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2082 | 1288 | 423 | 364 | 7 | | | |
| 24 | DC | 271 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2082 | 1288 | 423 | 364 | 7 | | | |

- Molecule 25 is a protein called 50S ribosomal protein L3.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 25 | BD | 209 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1565 | 979 | 288 | 294 | 4 | | | |
| 25 | DD | 209 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1565 | 979 | 288 | 294 | 4 | | | |

- Molecule 26 is a protein called 50S ribosomal protein L4.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 26 | BE | 201 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1552 | 974 | 283 | 290 | 5 | | | |
| 26 | DE | 201 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1552 | 974 | 283 | 290 | 5 | | | |

- Molecule 27 is a protein called 50S ribosomal protein L5.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 27 | BF | 177 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1410 | 899 | 249 | 256 | 6 | | | |
| 27 | DF | 178 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1420 | 905 | 251 | 258 | 6 | | | |

- Molecule 28 is a protein called 50S ribosomal protein L6.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 28 | BG | 176 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1323 | 832 | 243 | 246 | 2 | | | |
| 28 | DG | 176 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1323 | 832 | 243 | 246 | 2 | | | |

- Molecule 29 is a protein called 50S ribosomal protein L9.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 29 | BH | 149 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1111 | 699 | 197 | 214 | 1 | | | |
| 29 | DH | 149 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1111 | 699 | 197 | 214 | 1 | | | |

- Molecule 30 is a protein called 50S ribosomal protein L11.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 30 | BI | 141 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1032 | 651 | 179 | 196 | 6 | | | |
| 30 | DI | 141 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1032 | 651 | 179 | 196 | 6 | | | |

- Molecule 31 is a protein called 50S ribosomal protein L13.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 31 | BJ | 142 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1129 | 714 | 212 | 199 | 4 | | | |
| 31 | DJ | 142 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1129 | 714 | 212 | 199 | 4 | | | |

- Molecule 32 is a protein called 50S ribosomal protein L14.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 32 | BK | 122 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 938 | 587 | 180 | 165 | 6 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 32 | DK | 122 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 938 | 587 | 180 | 165 | 6 | | | |

- Molecule 33 is a protein called 50S ribosomal protein L15.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 33 | BL | 143 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1045 | 649 | 206 | 189 | 1 | | | |
| 33 | DL | 143 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1045 | 649 | 206 | 189 | 1 | | | |

- Molecule 34 is a protein called 50S ribosomal protein L16.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 34 | BM | 136 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1074 | 686 | 205 | 177 | 6 | | | |
| 34 | DM | 136 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1074 | 686 | 205 | 177 | 6 | | | |

- Molecule 35 is a protein called 50S ribosomal protein L17.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 35 | BN | 120 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 960 | 593 | 196 | 166 | 5 | | | |
| 35 | DN | 120 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 960 | 593 | 196 | 166 | 5 | | | |

- Molecule 36 is a protein called 50S ribosomal protein L18.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 36 | BO | 116 | Total | C | N | O | 0 | 0 | 0 |
| | | | 892 | 552 | 178 | 162 | | | |
| 36 | DO | 116 | Total | C | N | O | 0 | 0 | 0 |
| | | | 892 | 552 | 178 | 162 | | | |

- Molecule 37 is a protein called 50S ribosomal protein L19.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 37 | BP | 114 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 917 | 574 | 179 | 163 | 1 | | | |
| 37 | DP | 114 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 917 | 574 | 179 | 163 | 1 | | | |

- Molecule 38 is a protein called 50S ribosomal protein L20.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 38 | BQ | 117 | Total | C | N | O | 0 | 0 | 0 |
| | | | 947 | 604 | 192 | 151 | | | |
| 38 | DQ | 117 | Total | C | N | O | 0 | 0 | 0 |
| | | | 947 | 604 | 192 | 151 | | | |

- Molecule 39 is a protein called 50S ribosomal protein L21.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 39 | BR | 103 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 816 | 516 | 153 | 145 | 2 | | | |
| 39 | DR | 103 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 816 | 516 | 153 | 145 | 2 | | | |

- Molecule 40 is a protein called 50S ribosomal protein L22.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 40 | BS | 110 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 857 | 532 | 166 | 156 | 3 | | | |
| 40 | DS | 110 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 857 | 532 | 166 | 156 | 3 | | | |

- Molecule 41 is a protein called 50S ribosomal protein L23.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 41 | BT | 93 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 738 | 466 | 139 | 131 | 2 | | | |
| 41 | DT | 93 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 738 | 466 | 139 | 131 | 2 | | | |

- Molecule 42 is a protein called 50S ribosomal protein L24.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 42 | BU | 102 | Total | C | N | O | 0 | 0 | 0 |
| | | | 779 | 492 | 146 | 141 | | | |
| 42 | DU | 102 | Total | C | N | O | 0 | 0 | 0 |
| | | | 779 | 492 | 146 | 141 | | | |

- Molecule 43 is a protein called 50S ribosomal protein L25.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 43 | BV | 94 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 753 | 479 | 137 | 134 | 3 | | | |
| 43 | DV | 94 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 753 | 479 | 137 | 134 | 3 | | | |

- Molecule 44 is a protein called 50S ribosomal protein L27.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 44 | BW | 79 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 596 | 367 | 120 | 108 | 1 | | | |
| 44 | DW | 79 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 596 | 367 | 120 | 108 | 1 | | | |

- Molecule 45 is a protein called 50S ribosomal protein L28.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 45 | BX | 77 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 625 | 388 | 129 | 106 | 2 | | | |
| 45 | DX | 77 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 625 | 388 | 129 | 106 | 2 | | | |

- Molecule 46 is a protein called 50S ribosomal protein L29.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 46 | BY | 63 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 509 | 313 | 99 | 95 | 2 | | | |
| 46 | DY | 63 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 509 | 313 | 99 | 95 | 2 | | | |

- Molecule 47 is a protein called 50S ribosomal protein L30.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 47 | BZ | 58 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 449 | 281 | 87 | 79 | 2 | | | |
| 47 | DZ | 58 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 449 | 281 | 87 | 79 | 2 | | | |

- Molecule 48 is a protein called 50S ribosomal protein L32.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 48 | B0 | 56 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 444 | 269 | 94 | 80 | 1 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 48 | D0 | 56 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 444 | 269 | 94 | 80 | 1 | | | |

- Molecule 49 is a protein called 50S ribosomal protein L33.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|--|---------|---------|-------|
| 49 | B1 | 50 | Total | C | N | O | | 0 | 0 | 0 |
| | | | 409 | 263 | 75 | 71 | | | | |
| 49 | D1 | 50 | Total | C | N | O | | 0 | 0 | 0 |
| | | | 409 | 263 | 75 | 71 | | | | |

- Molecule 50 is a protein called 50S ribosomal protein L34.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 50 | B2 | 46 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 377 | 228 | 90 | 57 | 2 | | | |
| 50 | D2 | 46 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 377 | 228 | 90 | 57 | 2 | | | |

- Molecule 51 is a protein called 50S ribosomal protein L35.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|---------|-------|
| 51 | B3 | 64 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 504 | 323 | 105 | 74 | 2 | | | |
| 51 | D3 | 64 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 504 | 323 | 105 | 74 | 2 | | | |

- Molecule 52 is a protein called 50S ribosomal protein L36.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 52 | B4 | 38 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 302 | 185 | 65 | 48 | 4 | | | |
| 52 | D4 | 38 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 302 | 185 | 65 | 48 | 4 | | | |

- Molecule 53 is a RNA chain called 16S rRNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|---------|-------|
| 53 | CA | 1530 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 32831 | 14642 | 6024 | 10635 | 1530 | | | |

- Molecule 54 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|---------|-------|
| 54 | DB | 117 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 2507 | 1116 | 459 | 815 | 117 | | | |

- Molecule 55 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|-----|---------|---------|
| 55 | BB | 4 | Total | Mg | 0 | 0 |
| | | | 4 | 4 | | |
| 55 | BA | 137 | Total | Mg | 0 | 0 |
| | | | 137 | 137 | | |
| 55 | CA | 42 | Total | Mg | 0 | 0 |
| | | | 42 | 42 | | |
| 55 | DJ | 1 | Total | Mg | 0 | 0 |
| | | | 1 | 1 | | |
| 55 | AA | 43 | Total | Mg | 0 | 0 |
| | | | 43 | 43 | | |
| 55 | DA | 135 | Total | Mg | 0 | 0 |
| | | | 135 | 135 | | |
| 55 | DB | 1 | Total | Mg | 0 | 0 |
| | | | 1 | 1 | | |

- Molecule 56 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---------|---------|
| 56 | B4 | 1 | Total | Zn | 0 | 0 |
| | | | 1 | 1 | | |
| 56 | D4 | 1 | Total | Zn | 0 | 0 |
| | | | 1 | 1 | | |

- Molecule 57 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|---|---------|---------|
| 57 | AE | 1 | Total | O | 0 | 0 |
| | | | 1 | 1 | | |
| 57 | AL | 3 | Total | O | 0 | 0 |
| | | | 3 | 3 | | |
| 57 | AN | 6 | Total | O | 0 | 0 |
| | | | 6 | 6 | | |
| 57 | AT | 2 | Total | O | 0 | 0 |
| | | | 2 | 2 | | |
| 57 | AU | 1 | Total | O | 0 | 0 |
| | | | 1 | 1 | | |

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| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|--------------|----------|---------|---------|
| 57 | AA | 195 | Total 195 | O 195 | 0 | 0 |
| 57 | BA | 610 | Total 610 | O 610 | 0 | 0 |
| 57 | BB | 20 | Total 20 | O 20 | 0 | 0 |
| 57 | BC | 10 | Total 10 | O 10 | 0 | 0 |
| 57 | BD | 2 | Total 2 | O 2 | 0 | 0 |
| 57 | BL | 4 | Total 4 | O 4 | 0 | 0 |
| 57 | BN | 3 | Total 3 | O 3 | 0 | 0 |
| 57 | BQ | 1 | Total 1 | O 1 | 0 | 0 |
| 57 | BT | 2 | Total 2 | O 2 | 0 | 0 |
| 57 | B0 | 1 | Total 1 | O 1 | 0 | 0 |
| 57 | B2 | 1 | Total 1 | O 1 | 0 | 0 |
| 57 | B3 | 3 | Total 3 | O 3 | 0 | 0 |
| 57 | B4 | 3 | Total 3 | O 3 | 0 | 0 |
| 57 | CE | 5 | Total 5 | O 5 | 0 | 0 |
| 57 | CI | 1 | Total 1 | O 1 | 0 | 0 |
| 57 | CL | 1 | Total 1 | O 1 | 0 | 0 |
| 57 | CN | 3 | Total 3 | O 3 | 0 | 0 |
| 57 | CT | 3 | Total 3 | O 3 | 0 | 0 |
| 57 | CU | 2 | Total 2 | O 2 | 0 | 0 |
| 57 | CA | 192 | Total 192 | O 192 | 0 | 0 |
| 57 | DA | 599 | Total 599 | O 599 | 0 | 0 |

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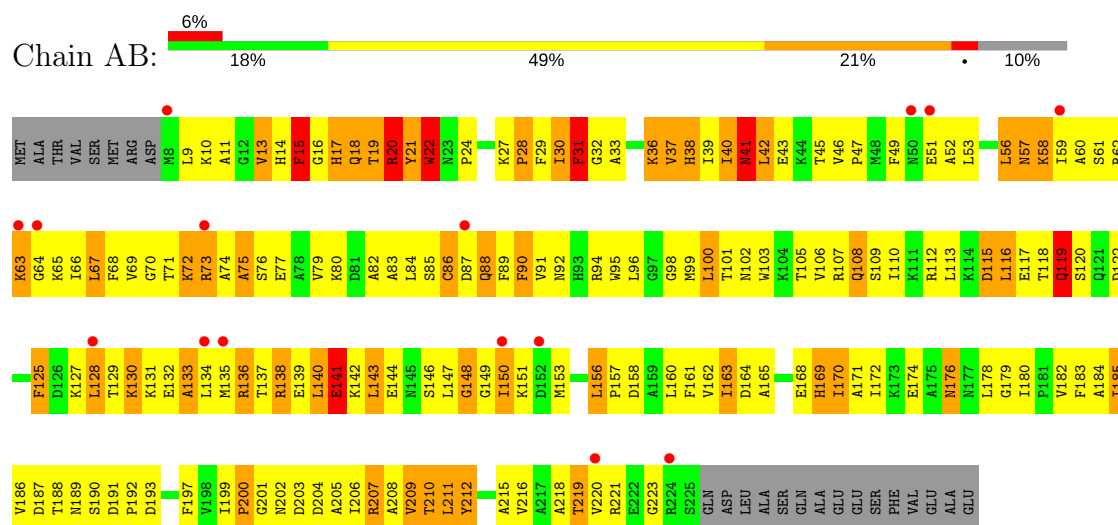
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| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------------|---------|---------|---------|
| 57 | DB | 4 | Total 4 | O 4 | 0 | 0 |
| 57 | DC | 13 | Total 13 | O 13 | 0 | 0 |
| 57 | DD | 4 | Total 4 | O 4 | 0 | 0 |
| 57 | DE | 3 | Total 3 | O 3 | 0 | 0 |
| 57 | DJ | 3 | Total 3 | O 3 | 0 | 0 |
| 57 | DL | 5 | Total 5 | O 5 | 0 | 0 |
| 57 | DN | 2 | Total 2 | O 2 | 0 | 0 |
| 57 | DT | 2 | Total 2 | O 2 | 0 | 0 |
| 57 | DU | 1 | Total 1 | O 1 | 0 | 0 |
| 57 | DV | 1 | Total 1 | O 1 | 0 | 0 |
| 57 | D2 | 1 | Total 1 | O 1 | 0 | 0 |
| 57 | D3 | 1 | Total 1 | O 1 | 0 | 0 |
| 57 | D4 | 4 | Total 4 | O 4 | 0 | 0 |

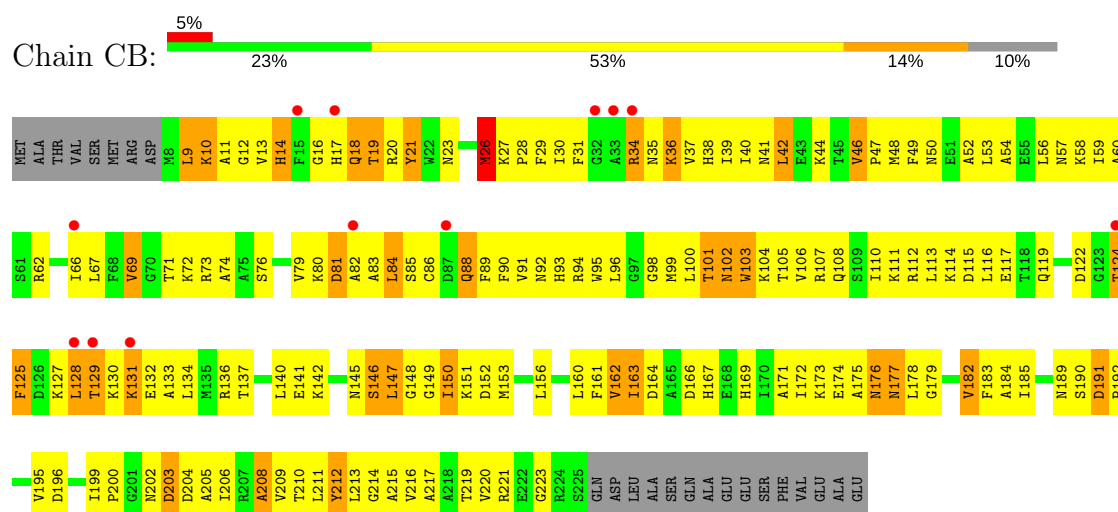
3 Residue-property plots

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: 30S ribosomal protein S2

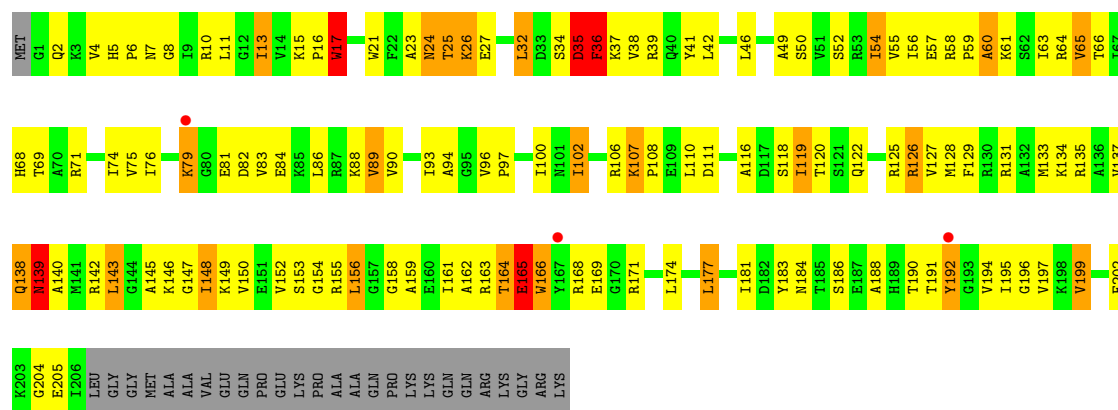


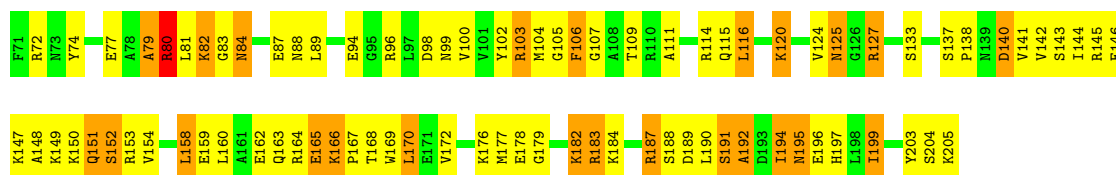
• Molecule 1: 30S ribosomal protein S2



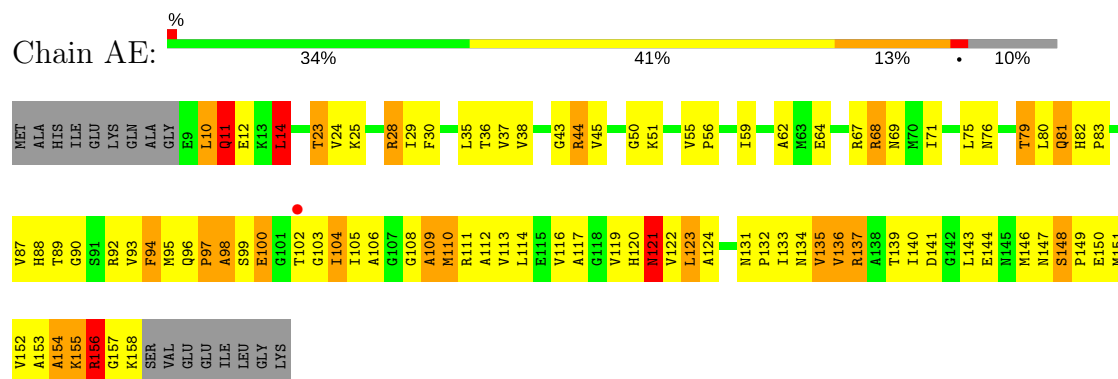
• Molecule 2: 30S ribosomal protein S3



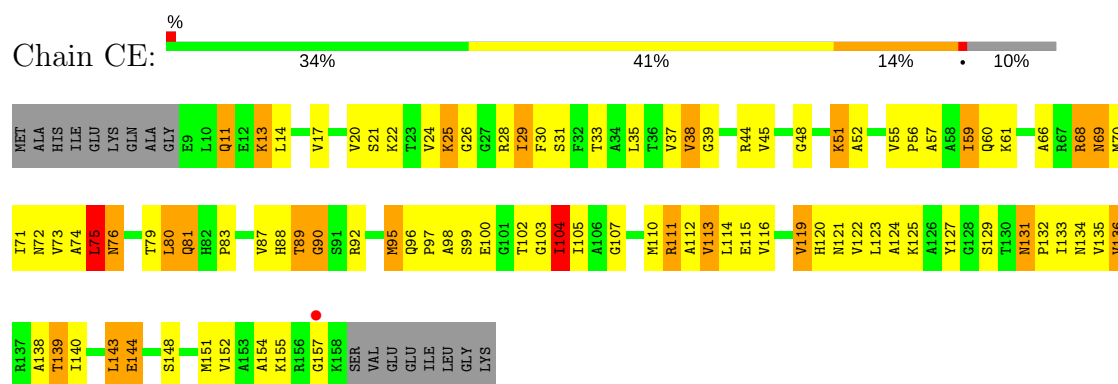




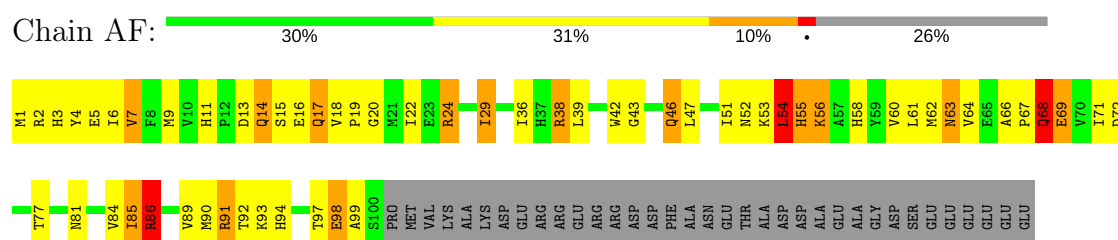
• Molecule 4: 30S ribosomal protein S5



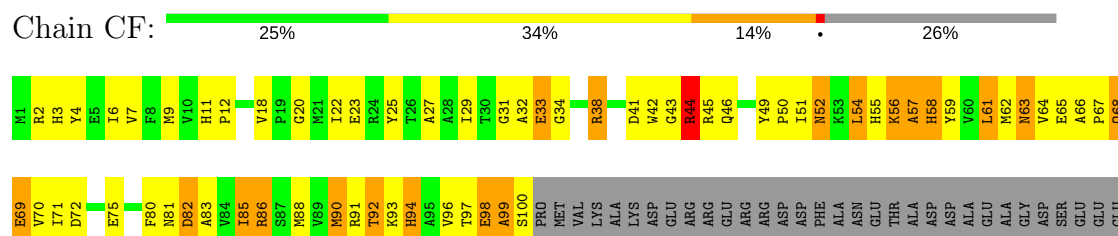
• Molecule 4: 30S ribosomal protein S5



• Molecule 5: 30S ribosomal protein S6

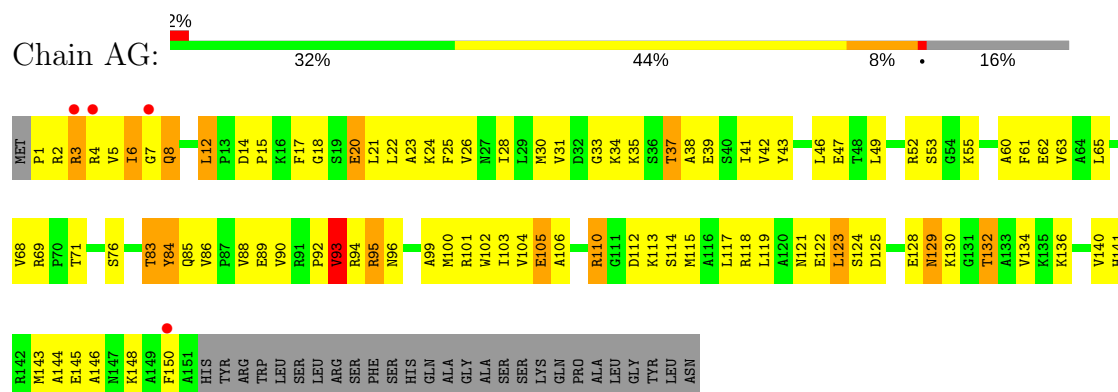


• Molecule 5: 30S ribosomal protein S6

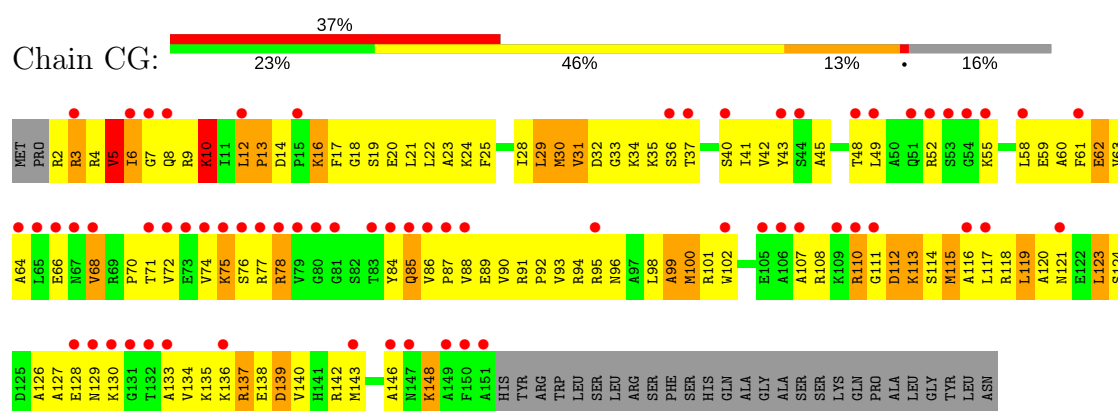


GLU
GLU
GLU

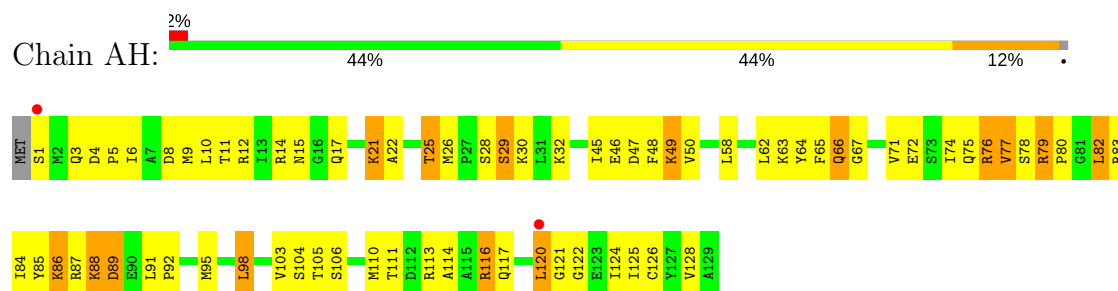
• Molecule 6: 30S ribosomal protein S7



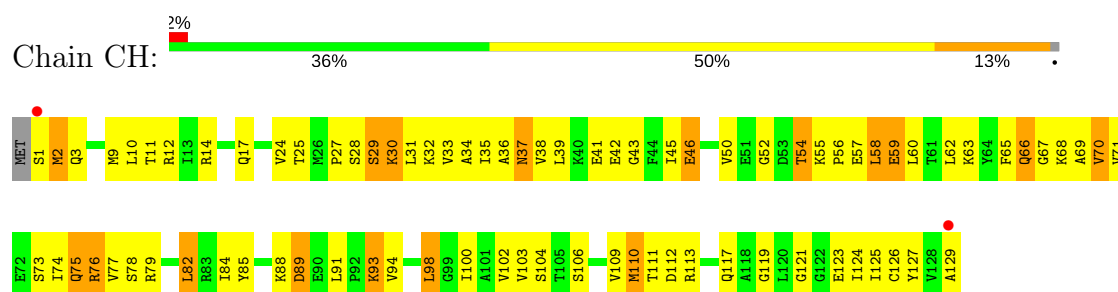
• Molecule 6: 30S ribosomal protein S7



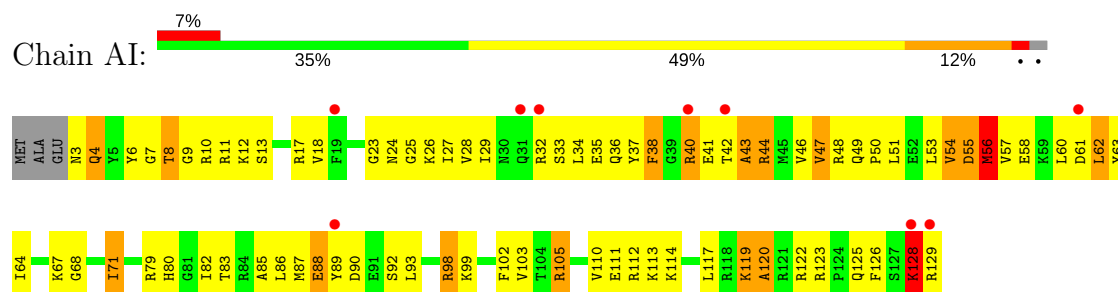
• Molecule 7: 30S ribosomal protein S8



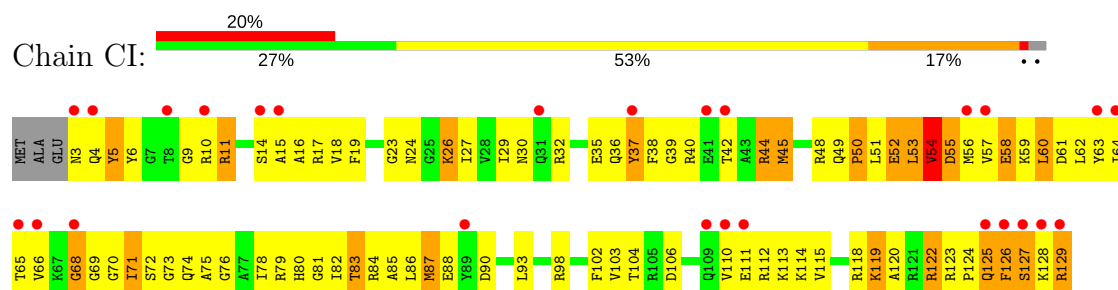
• Molecule 7: 30S ribosomal protein S8



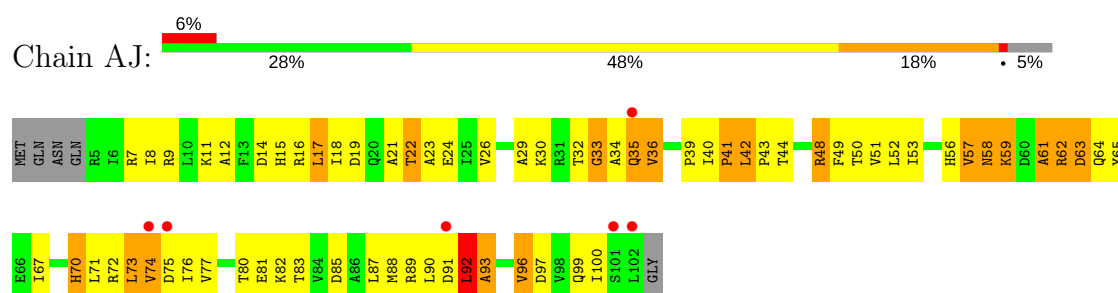
- Molecule 8: 30S ribosomal protein S9



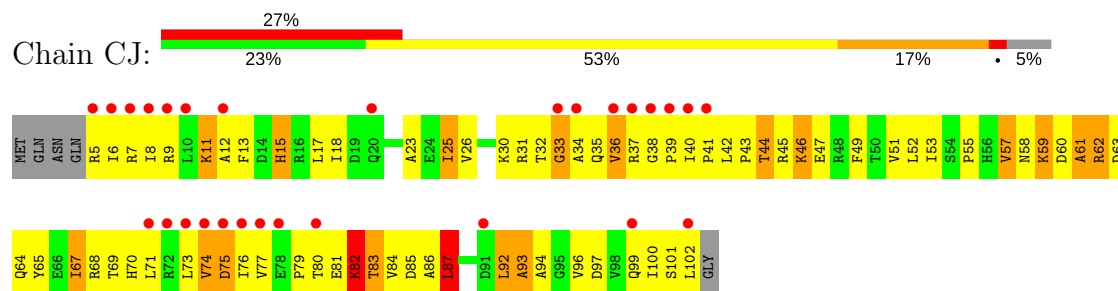
- Molecule 8: 30S ribosomal protein S9



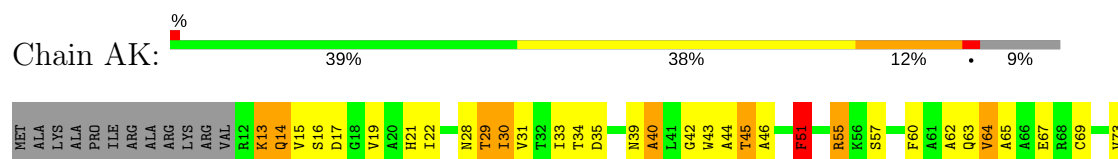
- Molecule 9: 30S ribosomal protein S10



- Molecule 9: 30S ribosomal protein S10



- Molecule 10: 30S ribosomal protein S11

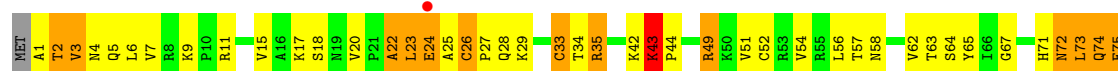
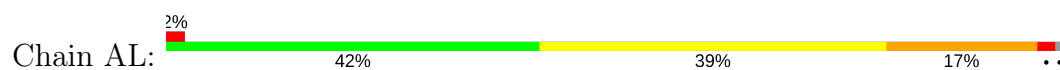




- Molecule 10: 30S ribosomal protein S11



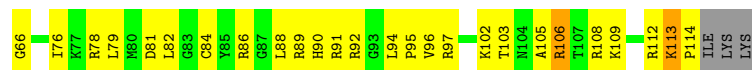
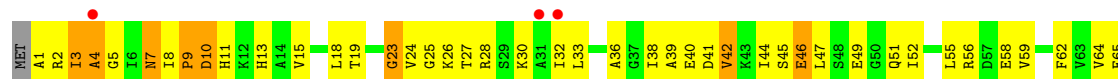
- Molecule 11: 30S ribosomal protein S12



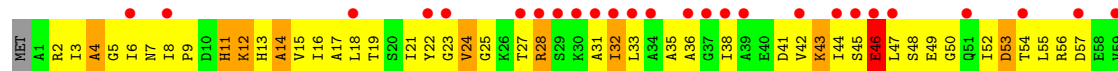
- Molecule 11: 30S ribosomal protein S12



- Molecule 12: 30S ribosomal protein S13

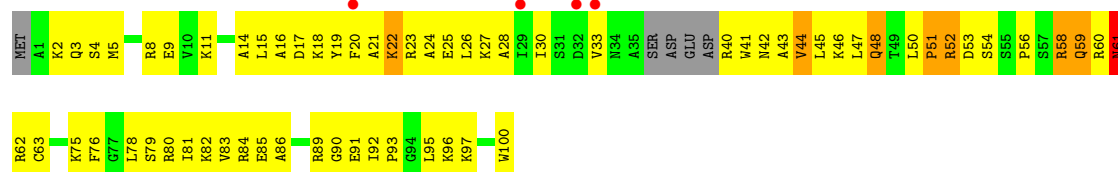


- Molecule 12: 30S ribosomal protein S13





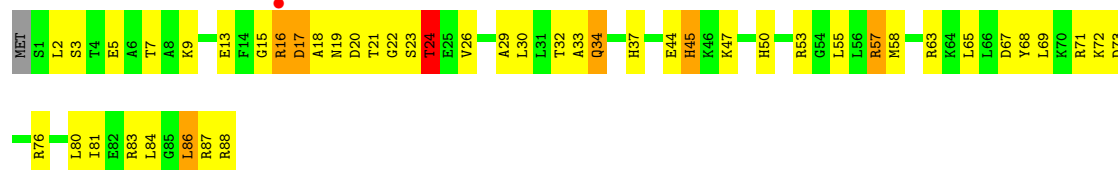
- Molecule 13: 30S ribosomal protein S14



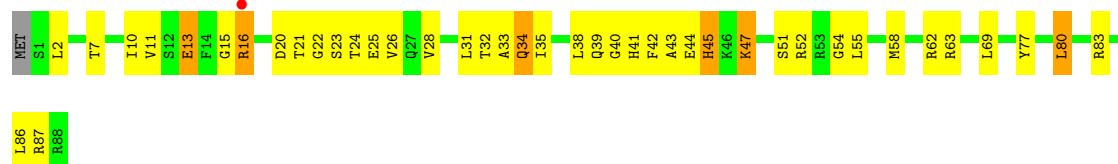
- Molecule 13: 30S ribosomal protein S14



- Molecule 14: 30S ribosomal protein S15



- Molecule 14: 30S ribosomal protein S15



- Molecule 15: 30S ribosomal protein S16

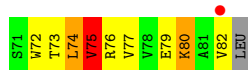
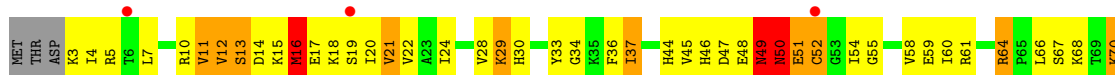




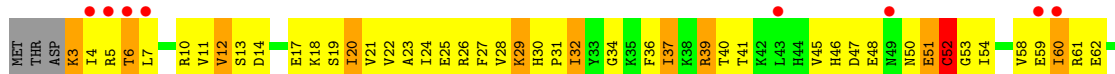
• Molecule 15: 30S ribosomal protein S16



• Molecule 16: 30S ribosomal protein S17



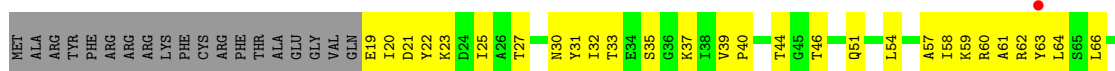
• Molecule 16: 30S ribosomal protein S17

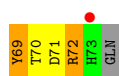


• Molecule 17: 30S ribosomal protein S18

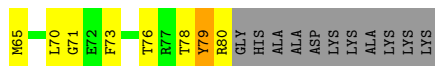
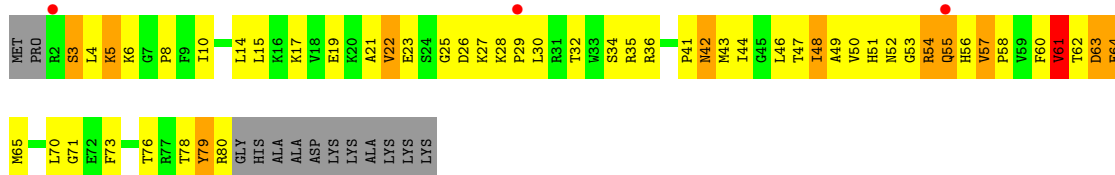


• Molecule 17: 30S ribosomal protein S18

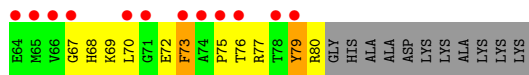
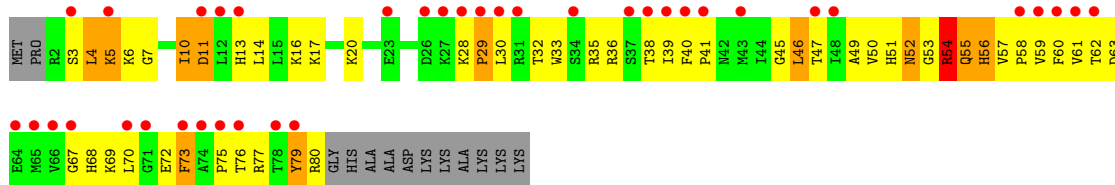




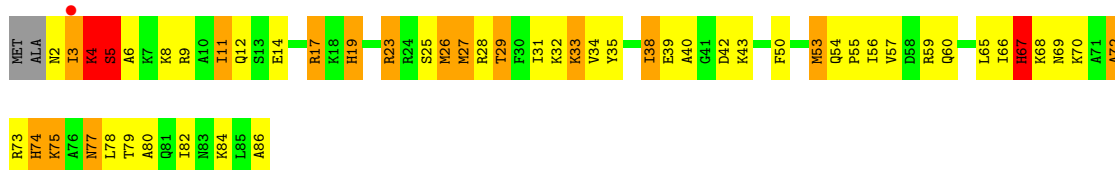
• Molecule 18: 30S ribosomal protein S19



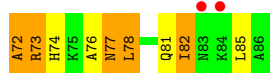
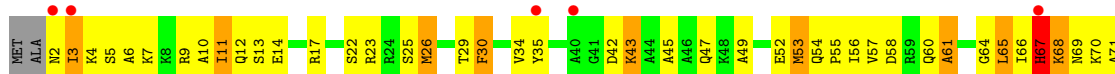
• Molecule 18: 30S ribosomal protein S19



• Molecule 19: 30S ribosomal protein S20



• Molecule 19: 30S ribosomal protein S20



• Molecule 20: 30S ribosomal protein S21



ALA
ARG
GLU
ASN
ALA
ARG
ARG
THR
ARG
LEU
TYR

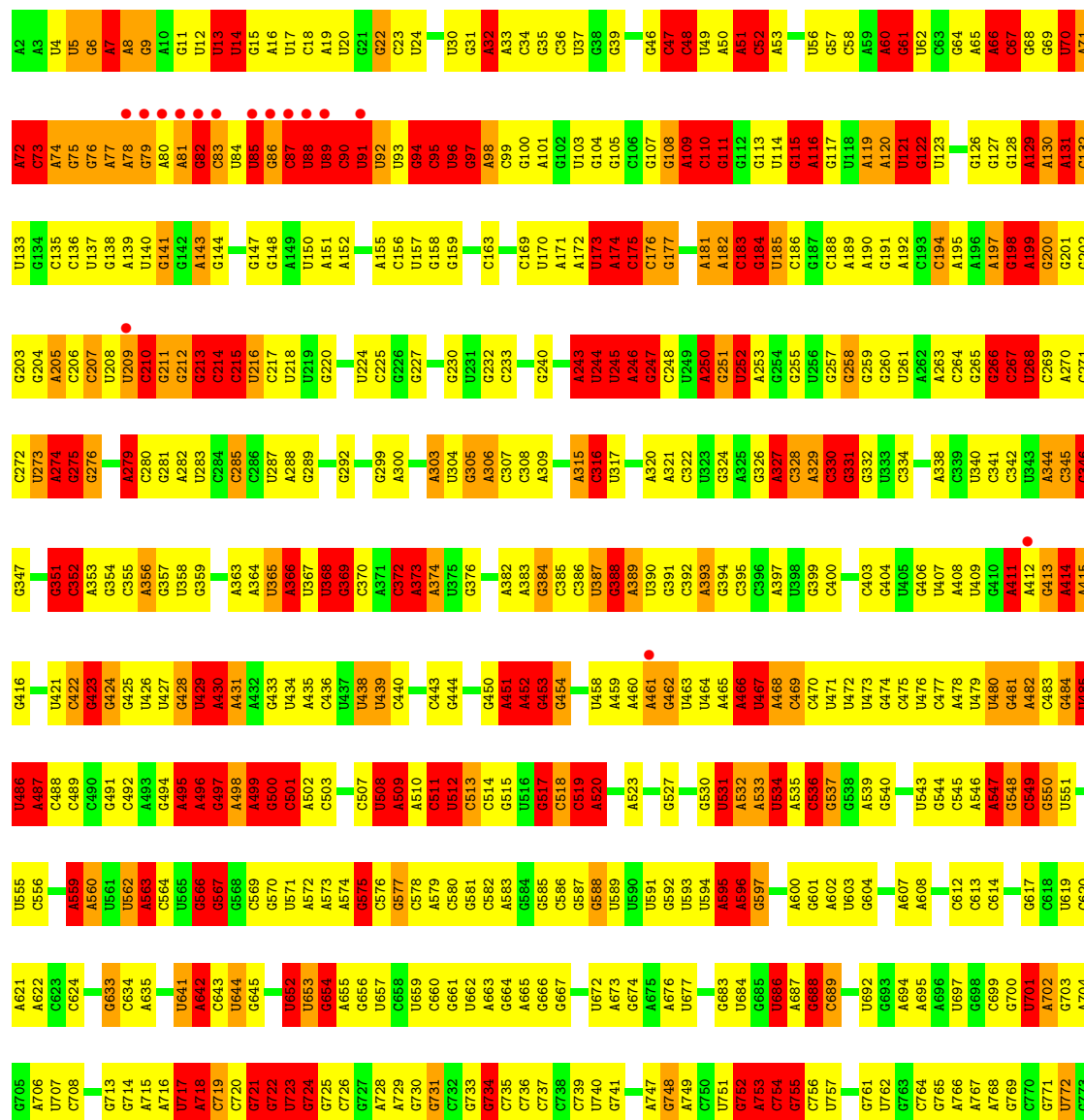
- Molecule 20: 30S ribosomal protein S21

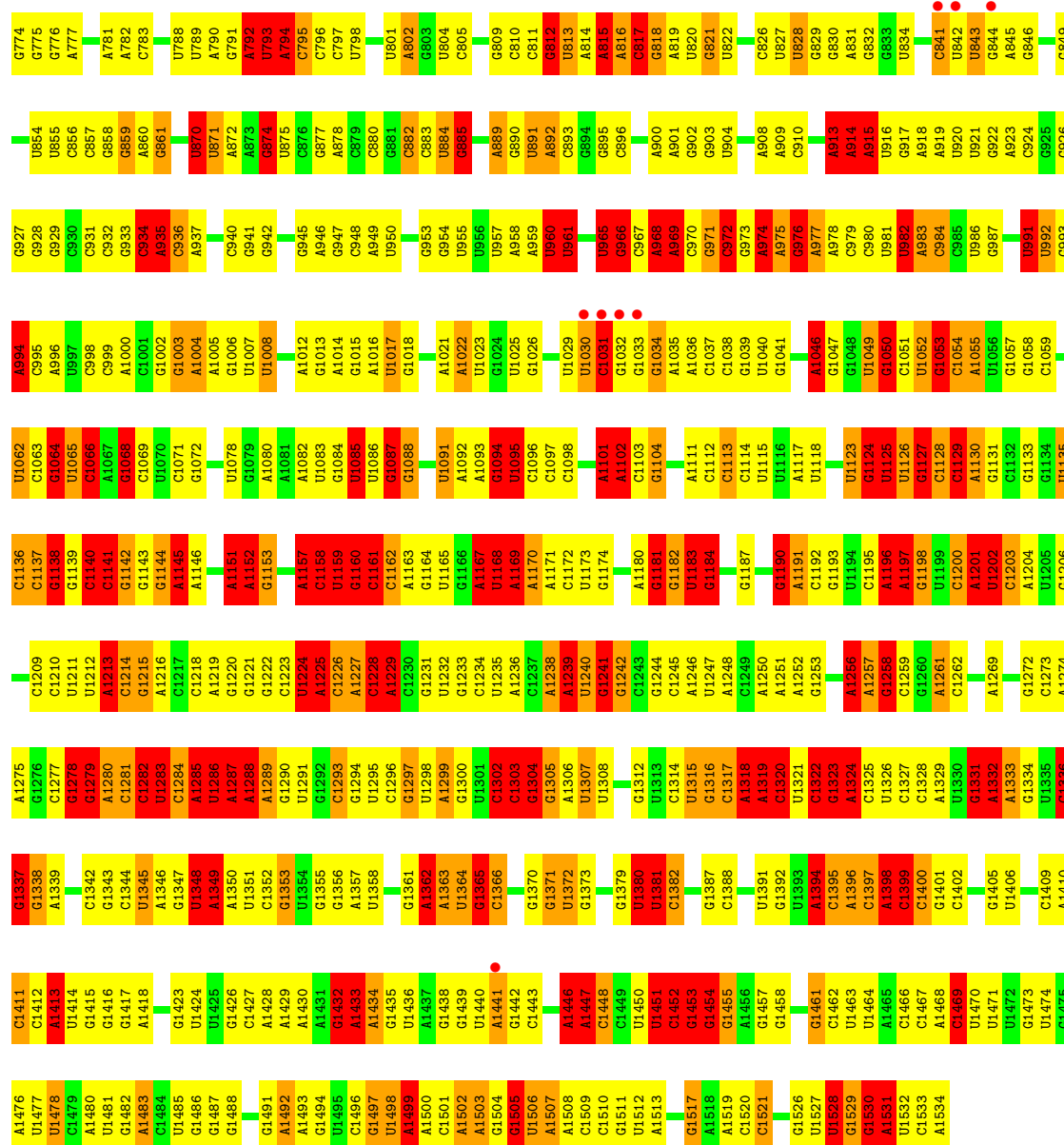


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|-----|-----|-----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | PRO | VAL | I3 | K4 | E7 | N8 | E9 | P10 | D11 | V13 | L14 | L15 | R16 | R17 | F18 | K19 | R20 | S21 | C22 | C23 | K24 | A25 | G26 | L28 | A29 | E30 | V31 | R32 | R33 | K34 | F36 | Y37 | E38 | K39 | P40 | T41 | T42 | E43 | R44 | K45 | K53 | ARG | HIS | ALA | LYS | LYS | LEU | ALA | ALA | ALA | ARG | ARG |
|-----|-----|-----|----|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

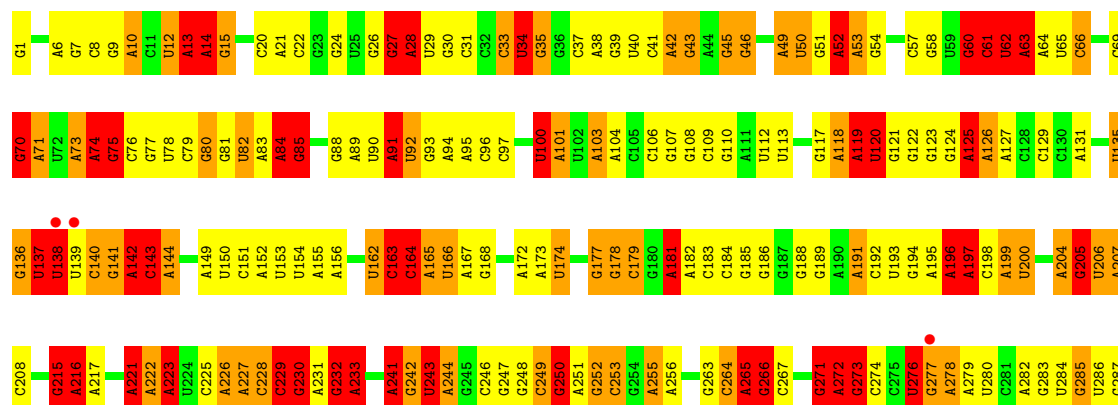
THR
ARG
LEU
TYR

- Molecule 21: 16S rRNA





• Molecule 22: 23S rRNA



| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
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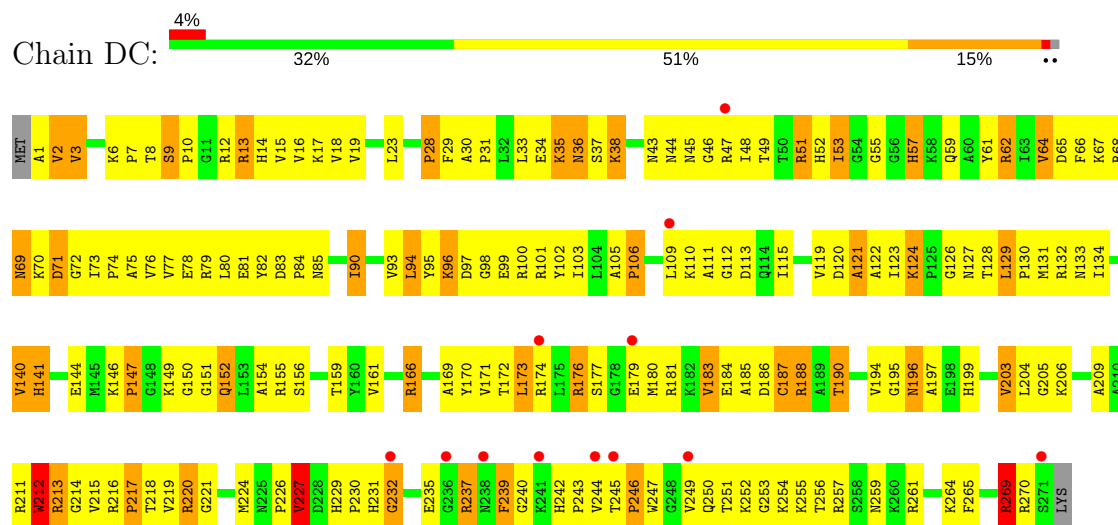


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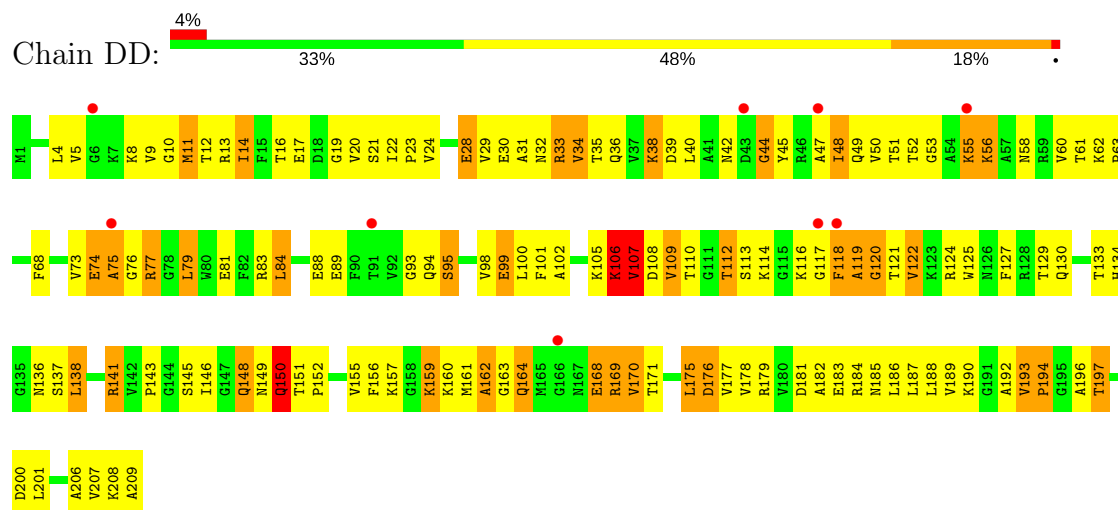
• Molecule 24: 50S ribosomal protein L2



• Molecule 25: 50S ribosomal protein L3

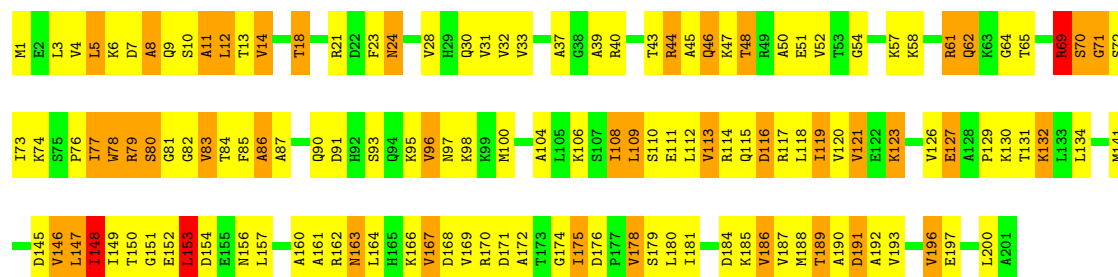


• Molecule 25: 50S ribosomal protein L3



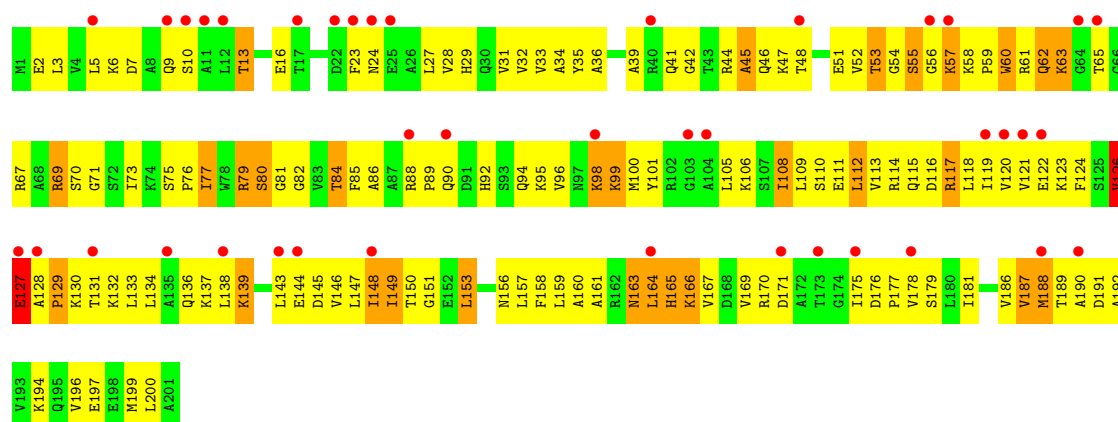
• Molecule 26: 50S ribosomal protein L4

Chain BE:  32% 46% 20% .



• Molecule 26: 50S ribosomal protein L4

Chain DE:  29% 55% 14% .



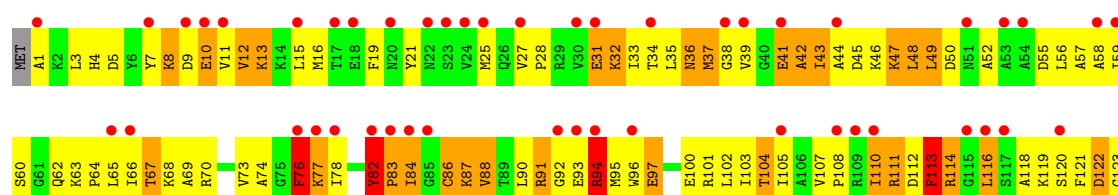
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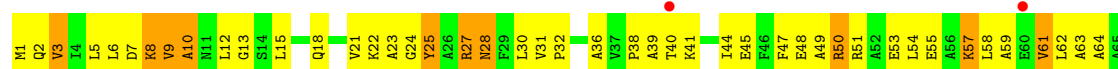
Chain BF:  44% 40% 13% ..

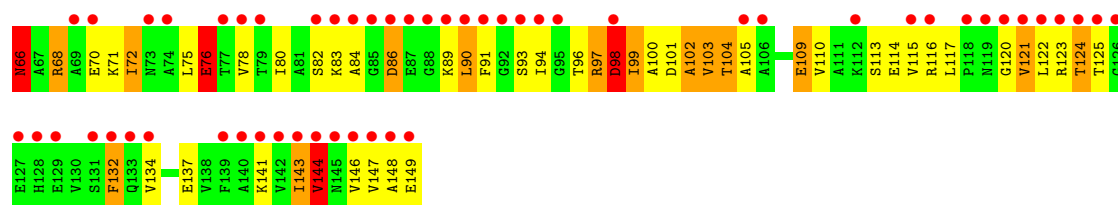


• Molecule 27: 50S ribosomal protein L5

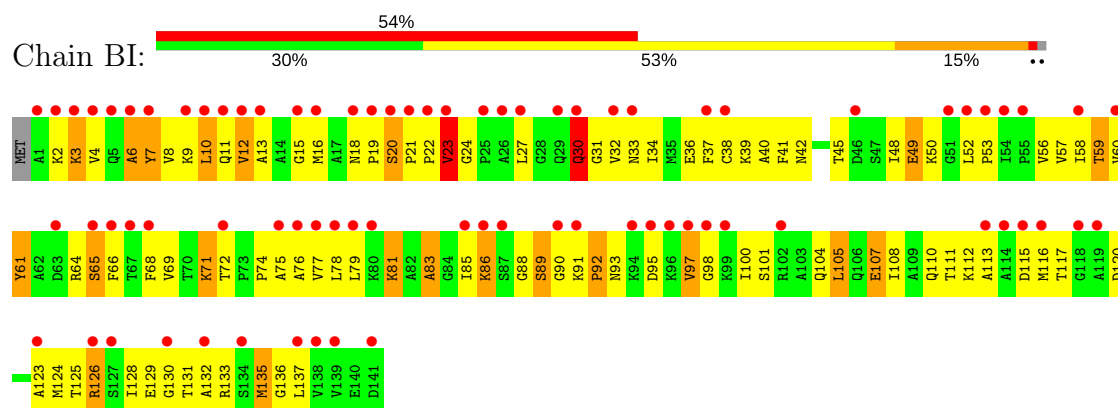
Chain DF:  26% 47% 23% ..



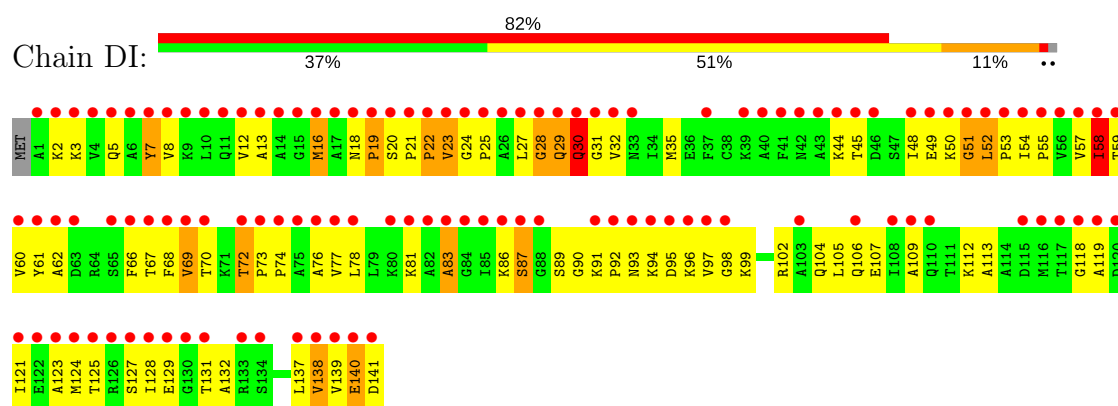




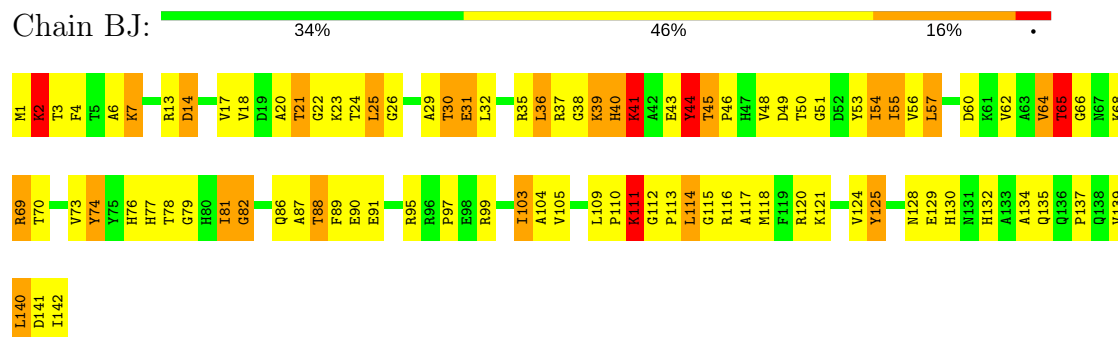
• Molecule 30: 50S ribosomal protein L11



• Molecule 30: 50S ribosomal protein L11

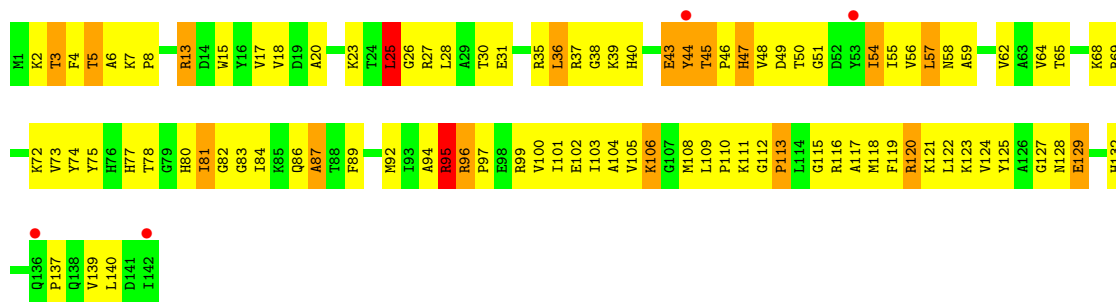


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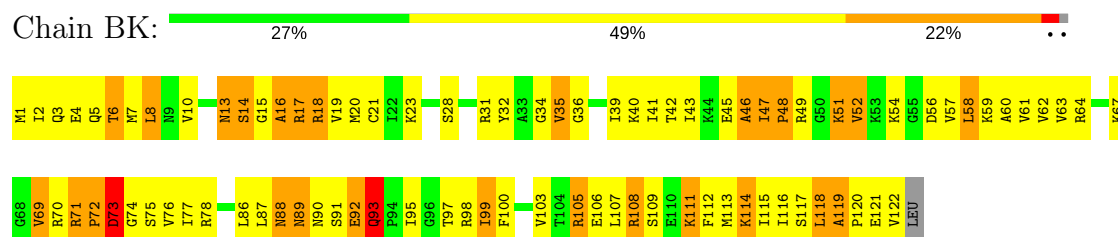


• Molecule 31: 50S ribosomal protein L13

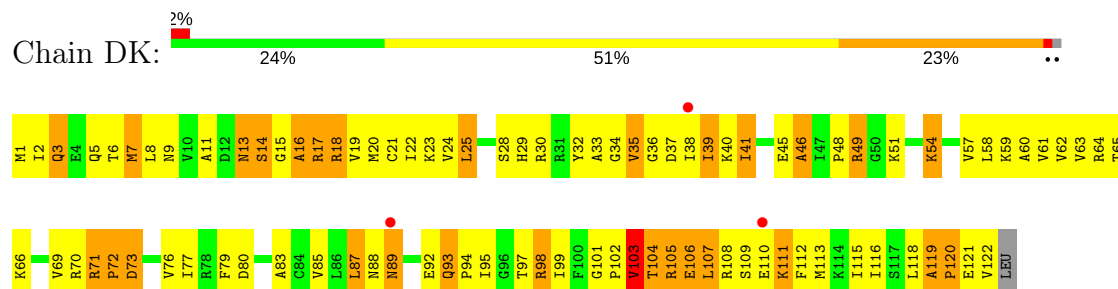




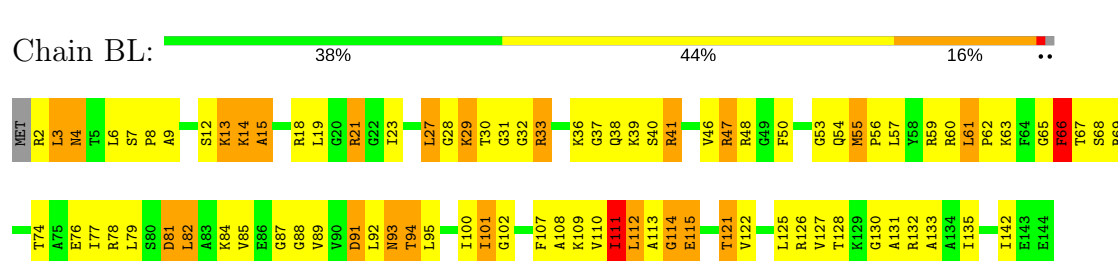
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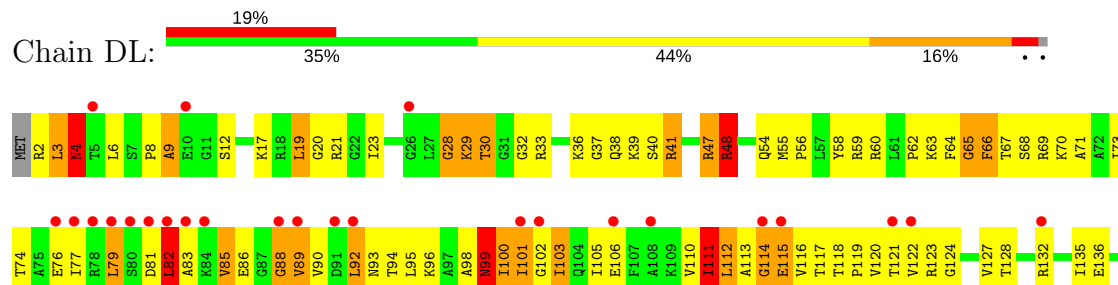
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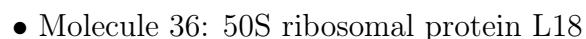
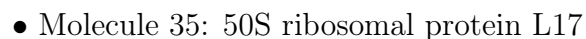
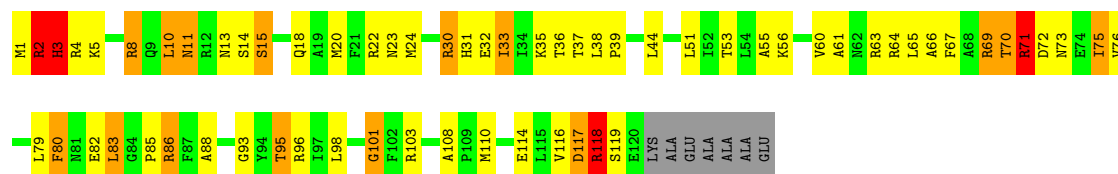
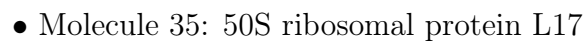
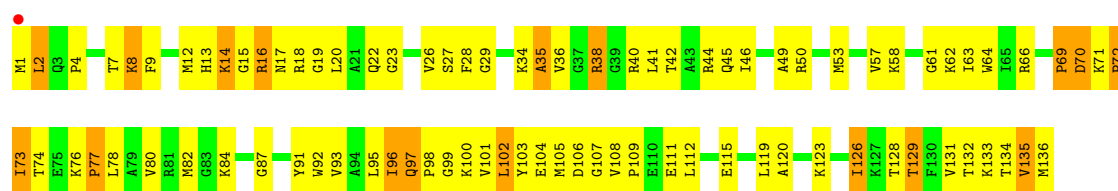
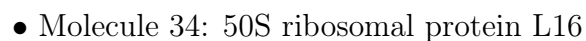
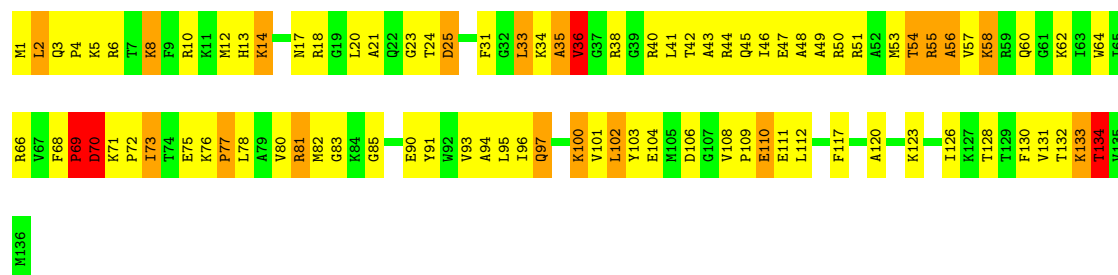
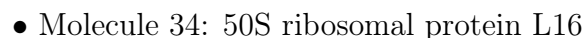


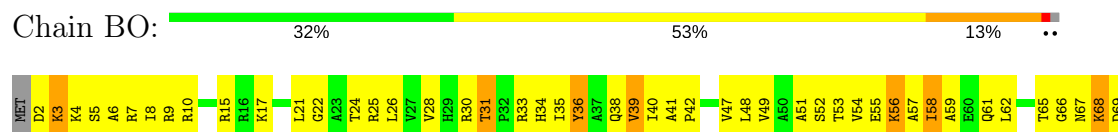
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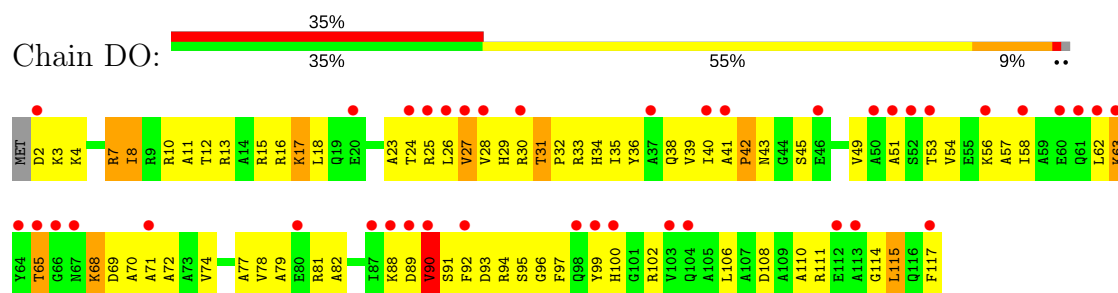
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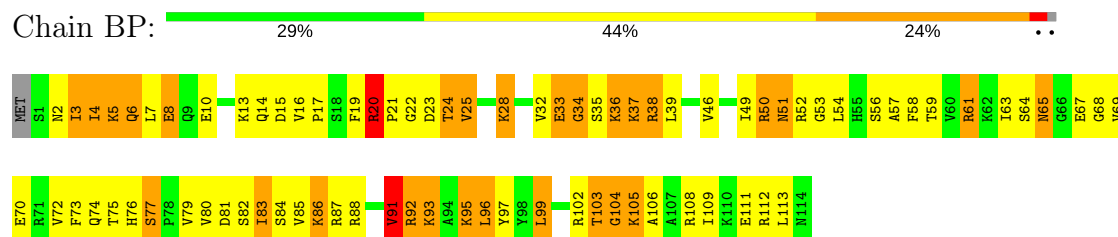




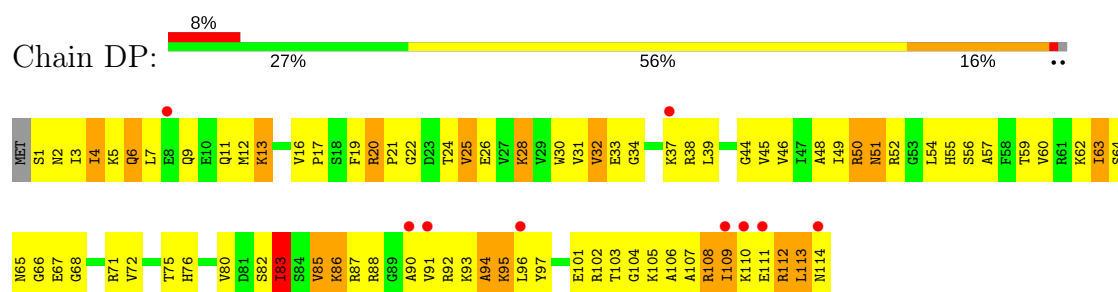
- Molecule 36: 50S ribosomal protein L18



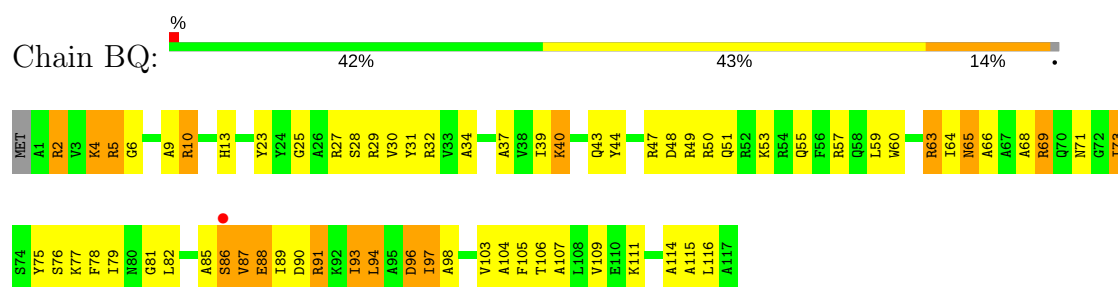
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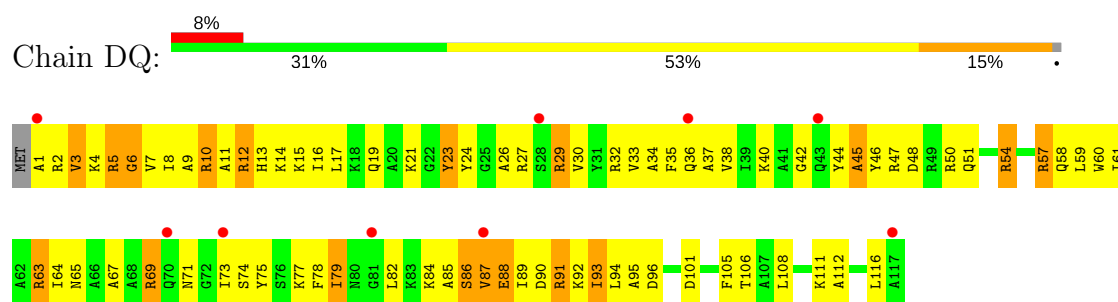
- Molecule 37: 50S ribosomal protein L19



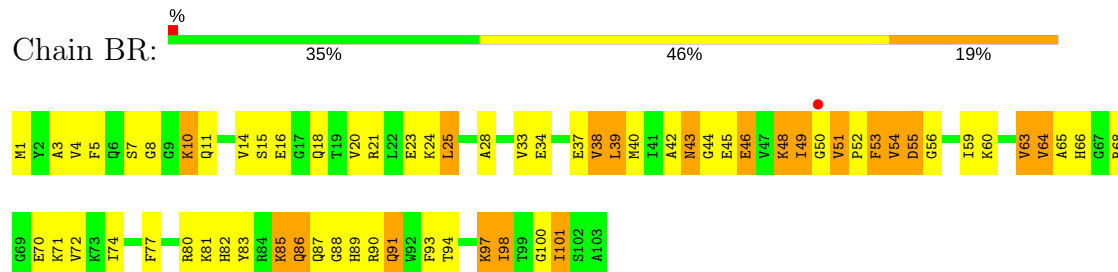
- Molecule 38: 50S ribosomal protein L20



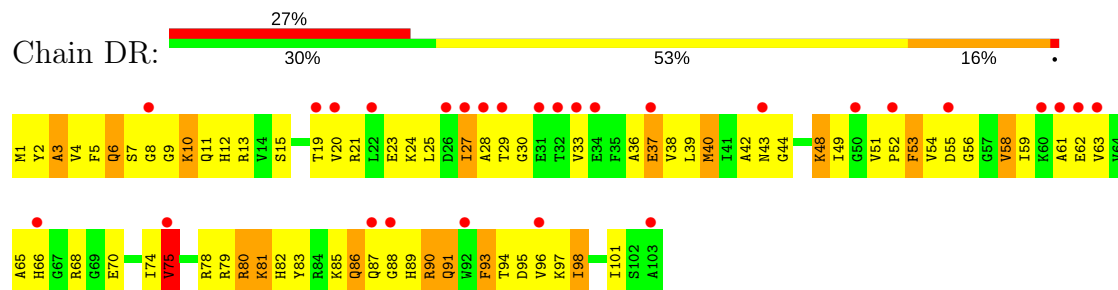
- Molecule 38: 50S ribosomal protein L20



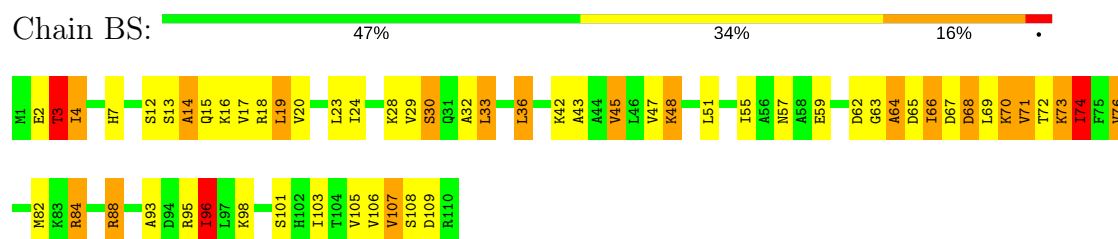
- Molecule 39: 50S ribosomal protein L21



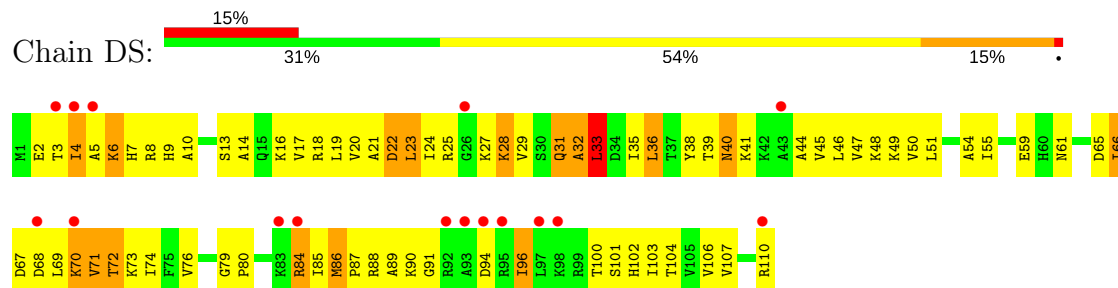
- Molecule 39: 50S ribosomal protein L21



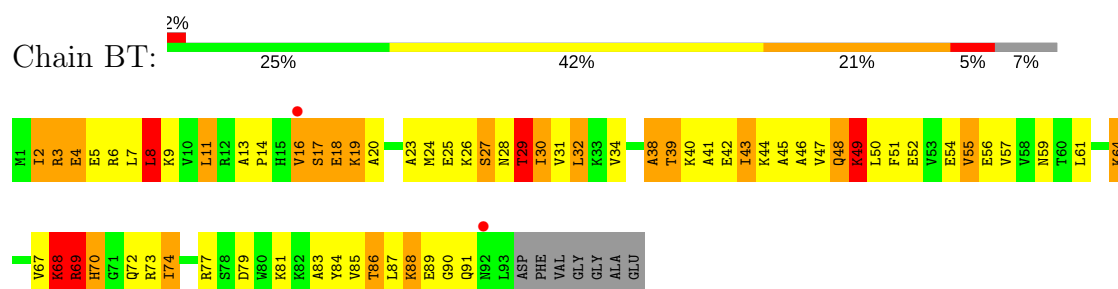
- Molecule 40: 50S ribosomal protein L22



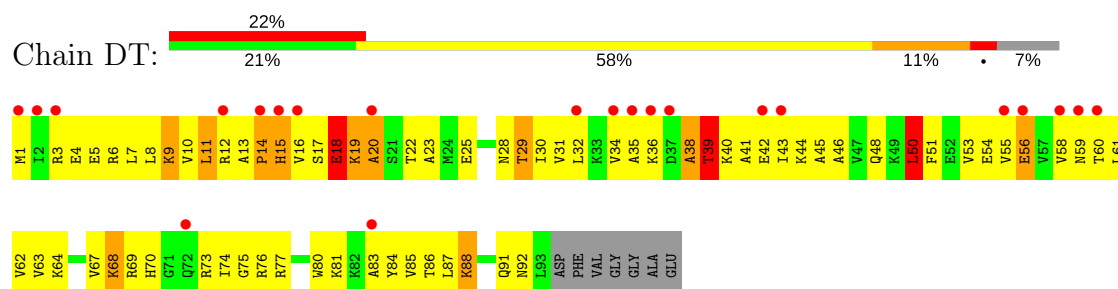
- Molecule 40: 50S ribosomal protein L22



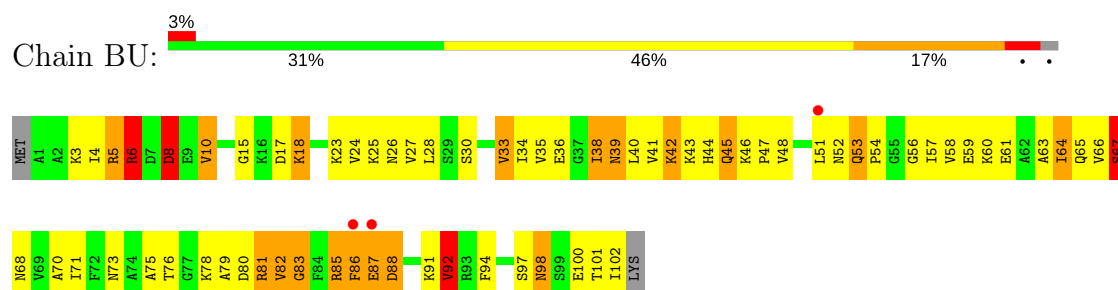
- Molecule 41: 50S ribosomal protein L23



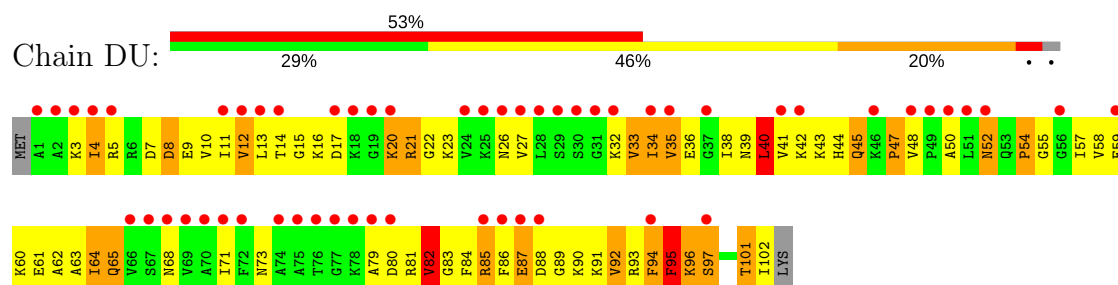
• Molecule 41: 50S ribosomal protein L23



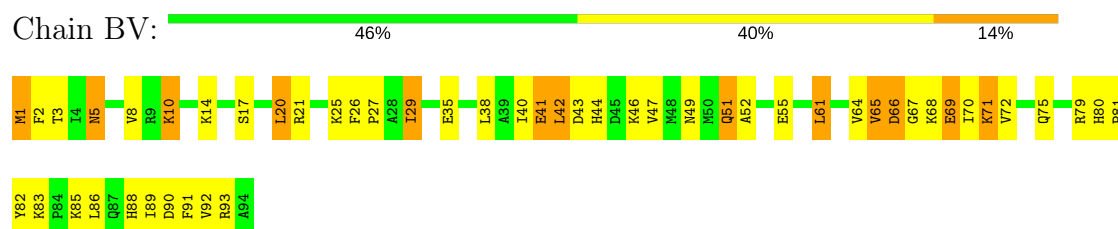
• Molecule 42: 50S ribosomal protein L24



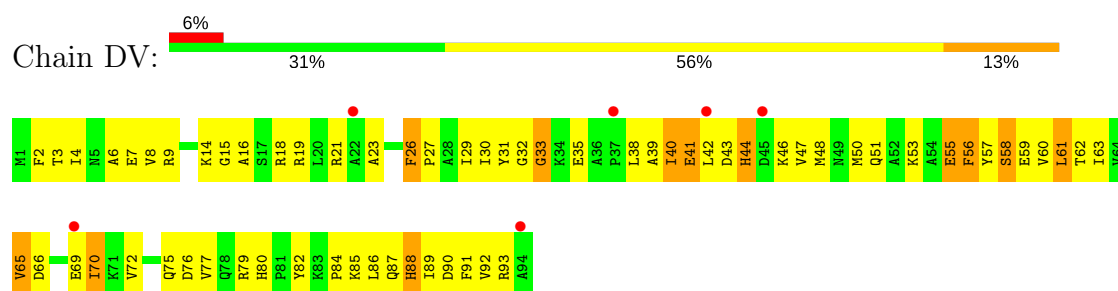
• Molecule 42: 50S ribosomal protein L24



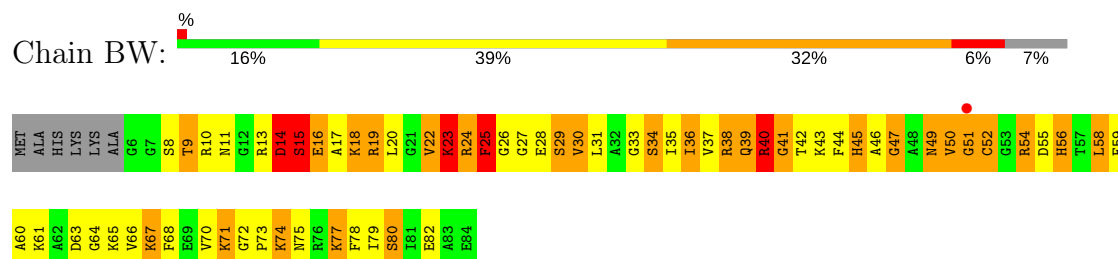
• Molecule 43: 50S ribosomal protein L25



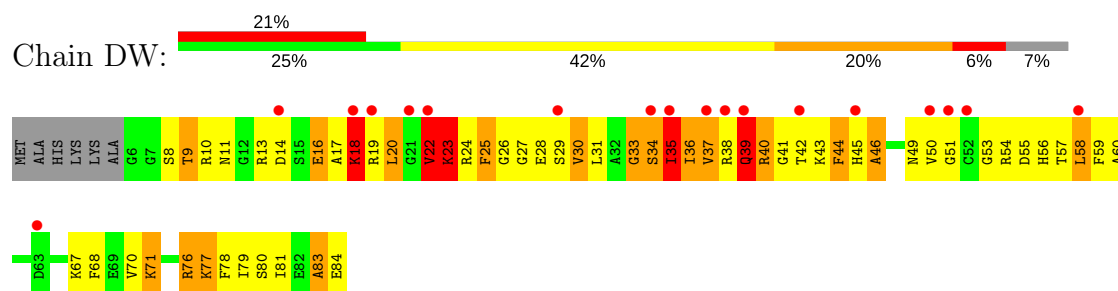
• Molecule 43: 50S ribosomal protein L25



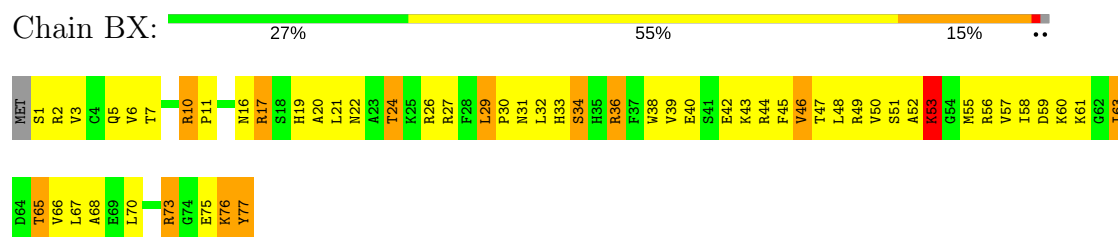
- Molecule 44: 50S ribosomal protein L27



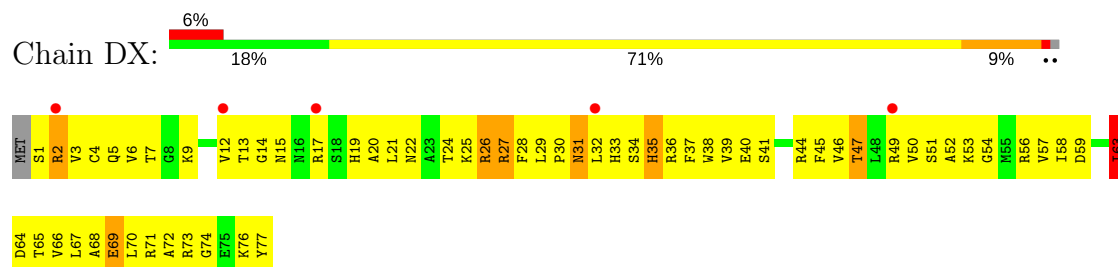
- Molecule 44: 50S ribosomal protein L27



- Molecule 45: 50S ribosomal protein L28



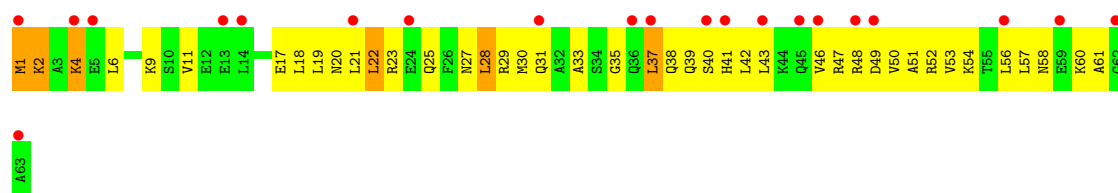
- Molecule 45: 50S ribosomal protein L28



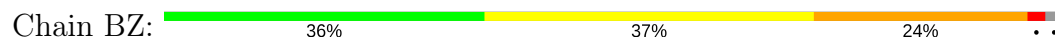
- Molecule 46: 50S ribosomal protein L29



- Molecule 46: 50S ribosomal protein L29



- Molecule 47: 50S ribosomal protein L30



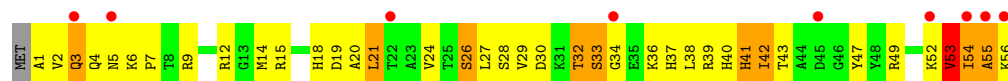
- Molecule 47: 50S ribosomal protein L30



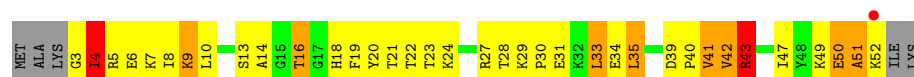
- Molecule 48: 50S ribosomal protein L32



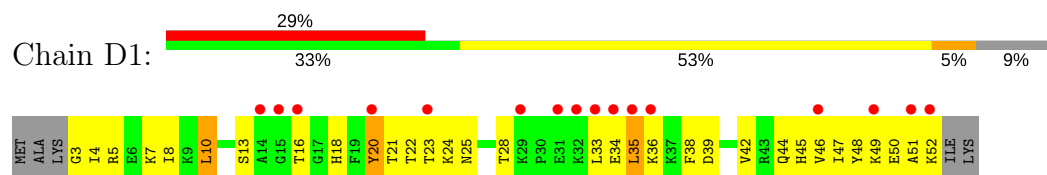
- Molecule 48: 50S ribosomal protein L32



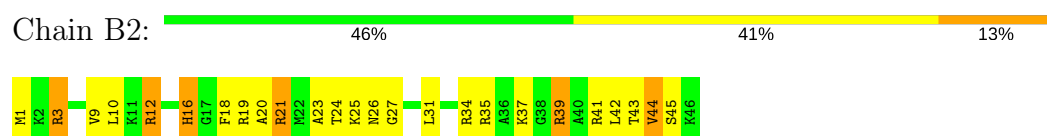
- Molecule 49: 50S ribosomal protein L33



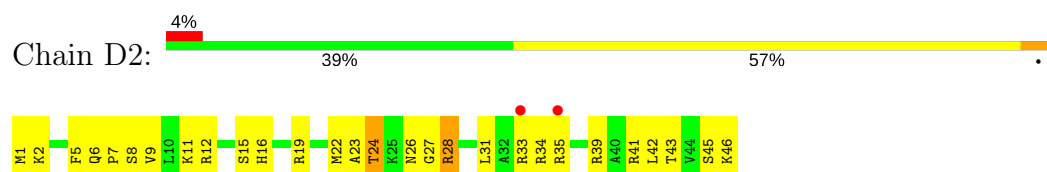
- Molecule 49: 50S ribosomal protein L33



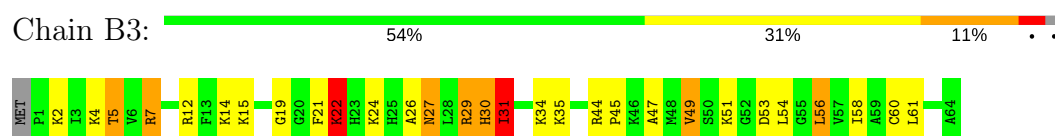
- Molecule 50: 50S ribosomal protein L34



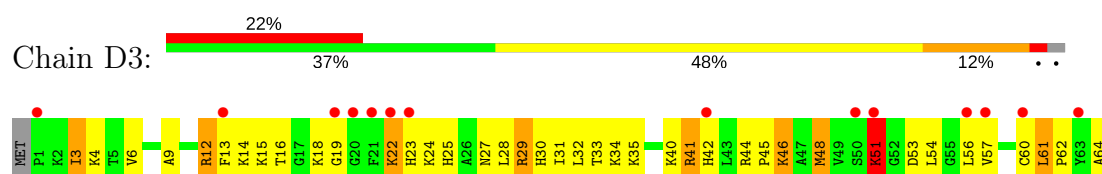
- Molecule 50: 50S ribosomal protein L34



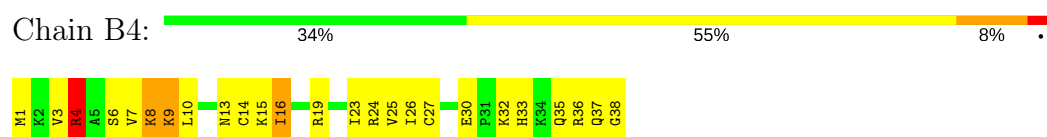
- Molecule 51: 50S ribosomal protein L35



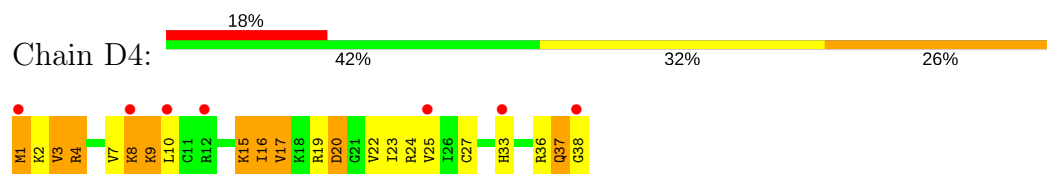
- Molecule 51: 50S ribosomal protein L35



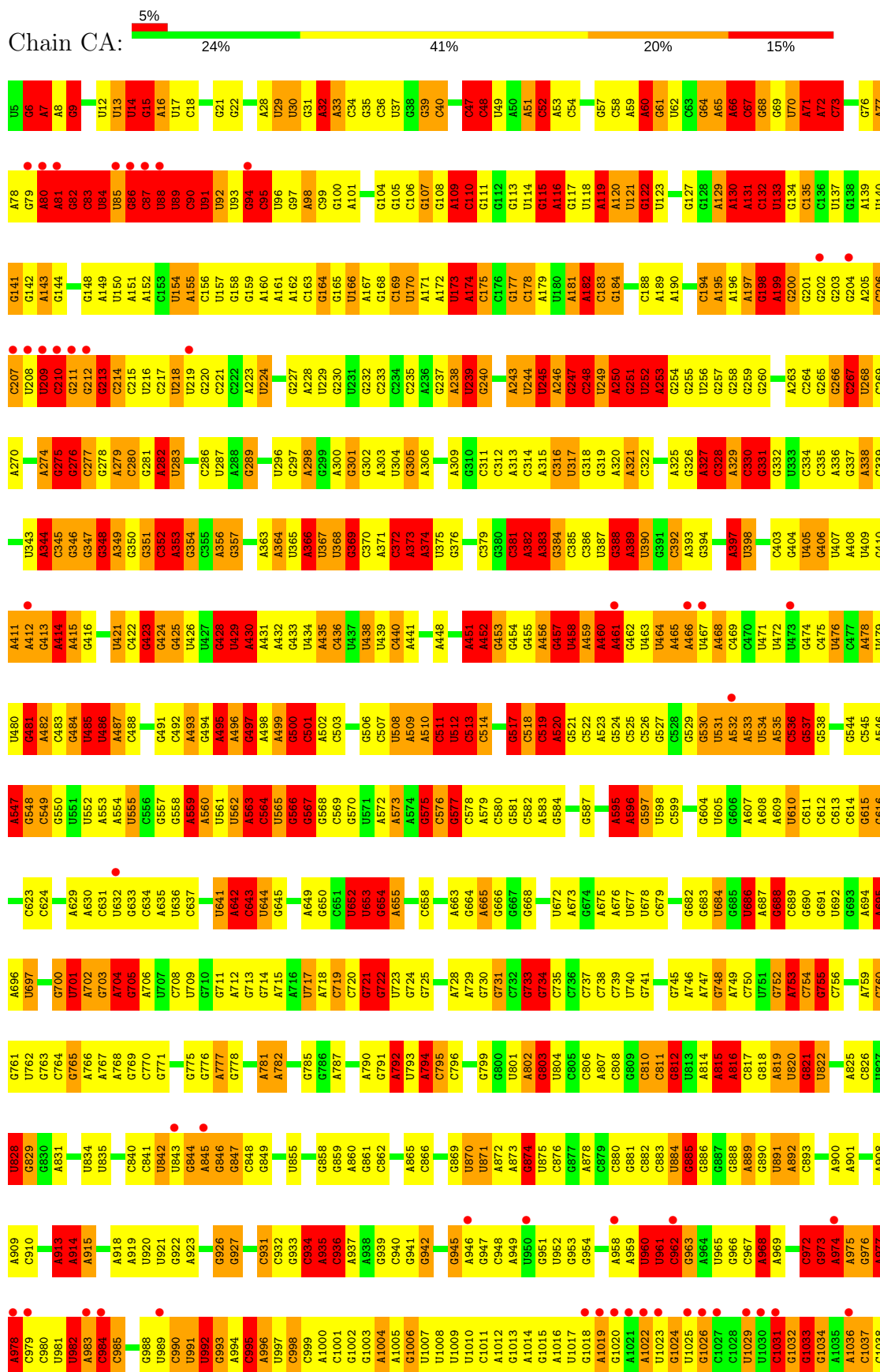
- Molecule 52: 50S ribosomal protein L36

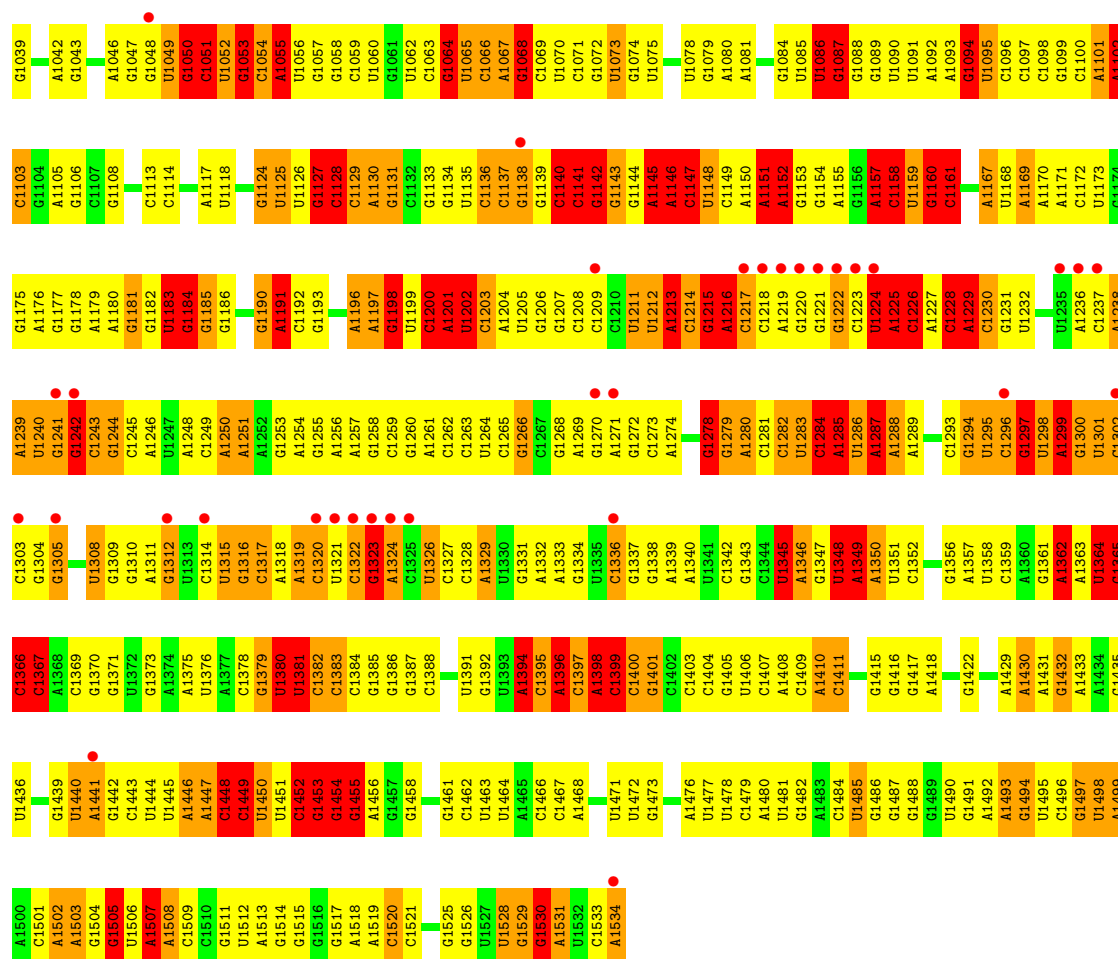


- Molecule 52: 50S ribosomal protein L36

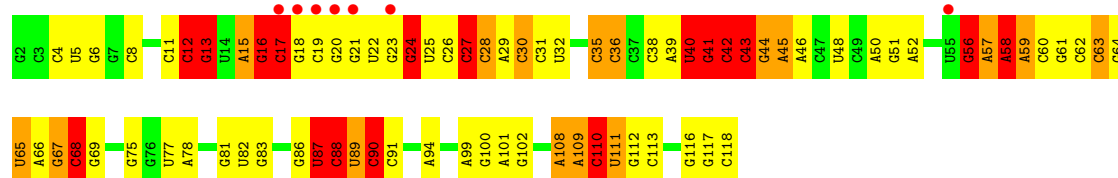


- Molecule 53: 16S rRNA





● Molecule 54: 5S rRNA



4 Data and refinement statistics

| Property | Value | Source |
|---|---|------------------|
| Space group | P 21 21 21 | Depositor |
| Cell constants a, b, c, α , β , γ | 211.89Å 434.93Å 622.92Å 90.00° 90.00° 90.00° | Depositor |
| Resolution (Å) | 39.88 – 3.19 39.88 – 3.19 | Depositor EDS |
| % Data completeness (in resolution range) | 95.8 (39.88-3.19) 95.8 (39.88-3.19) | Depositor EDS |
| R_{merge} | 0.17 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 1.53 (at 3.18Å) | Xtriage |
| Refinement program | PHENIX ?, PHENIX (phenix.refine) | Depositor |
| R, R_{free} | 0.195 , 0.252 0.207 , 0.261 | Depositor DCC |
| R_{free} test set | 18197 reflections (2.01%) | wwPDB-VP |
| Wilson B-factor (Å ²) | 63.6 | Xtriage |
| Anisotropy | 0.258 | Xtriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.24 , 74.7 | EDS |
| L-test for twinning ² | $\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$ | Xtriage |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| F_o, F_c correlation | 0.92 | EDS |
| Total number of atoms | 284450 | wwPDB-VP |
| Average B, all atoms (Å ²) | 98.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.53% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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 | AB | 0.30 | 0/1735 | 0.52 | 0/2338 |
| 1 | CB | 0.27 | 0/1735 | 0.49 | 0/2338 |
| 2 | AC | 0.30 | 0/1651 | 0.53 | 1/2225 (0.0%) |
| 2 | CC | 0.25 | 0/1651 | 0.45 | 0/2225 |
| 3 | AD | 0.31 | 0/1665 | 0.52 | 0/2227 |
| 3 | CD | 0.39 | 0/1665 | 0.60 | 0/2227 |
| 4 | AE | 0.36 | 0/1118 | 0.63 | 1/1504 (0.1%) |
| 4 | CE | 0.34 | 0/1118 | 0.54 | 0/1504 |
| 5 | AF | 0.32 | 0/835 | 0.49 | 0/1128 |
| 5 | CF | 0.28 | 0/835 | 0.50 | 0/1128 |
| 6 | AG | 0.27 | 0/1195 | 0.48 | 0/1602 |
| 6 | CG | 0.25 | 0/1187 | 0.46 | 0/1591 |
| 7 | AH | 0.33 | 0/989 | 0.55 | 0/1326 |
| 7 | CH | 0.28 | 0/989 | 0.50 | 0/1326 |
| 8 | AI | 0.27 | 0/1034 | 0.49 | 0/1375 |
| 8 | CI | 0.24 | 0/1034 | 0.43 | 0/1375 |
| 9 | AJ | 0.29 | 0/796 | 0.53 | 0/1077 |
| 9 | CJ | 0.24 | 0/796 | 0.48 | 0/1077 |
| 10 | AK | 0.31 | 0/893 | 0.56 | 0/1205 |
| 10 | CK | 0.29 | 0/893 | 0.50 | 0/1205 |
| 11 | AL | 0.39 | 0/969 | 0.69 | 0/1300 |
| 11 | CL | 0.32 | 0/969 | 0.57 | 0/1300 |
| 12 | AM | 0.26 | 0/892 | 0.49 | 0/1193 |
| 12 | CM | 0.20 | 0/884 | 0.41 | 0/1181 |
| 13 | AN | 0.30 | 0/785 | 0.54 | 0/1043 |
| 13 | CN | 0.22 | 0/780 | 0.39 | 0/1036 |
| 14 | AO | 0.30 | 0/722 | 0.49 | 0/964 |
| 14 | CO | 0.26 | 0/722 | 0.45 | 0/964 |
| 15 | AP | 0.30 | 0/659 | 0.50 | 0/884 |
| 15 | CP | 0.30 | 0/648 | 0.51 | 0/870 |
| 16 | AQ | 0.39 | 0/657 | 0.59 | 0/881 |
| 16 | CQ | 0.31 | 0/657 | 0.51 | 0/881 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-----------------|-------------|--------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 17 | AR | 0.30 | 0/462 | 0.50 | 0/621 |
| 17 | CR | 0.30 | 0/462 | 0.47 | 0/621 |
| 18 | AS | 0.28 | 0/652 | 0.49 | 0/877 |
| 18 | CS | 0.21 | 0/652 | 0.43 | 0/877 |
| 19 | AT | 0.35 | 0/671 | 0.56 | 0/888 |
| 19 | CT | 0.27 | 0/671 | 0.50 | 0/888 |
| 20 | AU | 0.39 | 0/430 | 0.54 | 0/570 |
| 20 | CU | 0.39 | 0/430 | 0.63 | 0/570 |
| 21 | AA | 0.55 | 1/36834 (0.0%) | 1.38 | 581/57462 (1.0%) |
| 22 | BA | 0.78 | 12/68626 (0.0%) | 1.59 | 1420/107056 (1.3%) |
| 22 | DA | 0.50 | 0/68314 | 1.35 | 1136/106569 (1.1%) |
| 23 | BB | 0.71 | 0/2828 | 1.50 | 45/4410 (1.0%) |
| 24 | BC | 0.44 | 0/2121 | 0.70 | 1/2852 (0.0%) |
| 24 | DC | 0.31 | 0/2121 | 0.53 | 0/2852 |
| 25 | BD | 0.53 | 0/1586 | 0.76 | 1/2134 (0.0%) |
| 25 | DD | 0.30 | 0/1586 | 0.56 | 0/2134 |
| 26 | BE | 0.43 | 0/1571 | 0.64 | 0/2113 |
| 26 | DE | 0.26 | 0/1571 | 0.47 | 0/2113 |
| 27 | BF | 0.33 | 0/1434 | 0.54 | 0/1926 |
| 27 | DF | 0.23 | 0/1444 | 0.47 | 0/1937 |
| 28 | BG | 0.40 | 0/1343 | 0.64 | 0/1816 |
| 28 | DG | 0.24 | 0/1343 | 0.48 | 0/1816 |
| 29 | BH | 0.31 | 0/1122 | 0.50 | 0/1515 |
| 29 | DH | 0.28 | 0/1122 | 0.50 | 0/1515 |
| 30 | BI | 0.23 | 0/1046 | 0.47 | 0/1410 |
| 30 | DI | 0.21 | 0/1046 | 0.43 | 0/1410 |
| 31 | BJ | 0.57 | 0/1152 | 0.80 | 1/1551 (0.1%) |
| 31 | DJ | 0.28 | 0/1152 | 0.55 | 1/1551 (0.1%) |
| 32 | BK | 0.51 | 0/947 | 0.77 | 0/1268 |
| 32 | DK | 0.33 | 0/947 | 0.56 | 0/1268 |
| 33 | BL | 0.43 | 0/1054 | 0.75 | 0/1403 |
| 33 | DL | 0.27 | 0/1054 | 0.52 | 0/1403 |
| 34 | BM | 0.50 | 0/1093 | 0.70 | 0/1460 |
| 34 | DM | 0.27 | 0/1093 | 0.46 | 0/1460 |
| 35 | BN | 0.47 | 0/973 | 0.70 | 0/1301 |
| 35 | DN | 0.28 | 0/973 | 0.50 | 0/1301 |
| 36 | BO | 0.42 | 0/902 | 0.63 | 0/1209 |
| 36 | DO | 0.22 | 0/902 | 0.42 | 0/1209 |
| 37 | BP | 0.50 | 0/929 | 0.73 | 0/1242 |
| 37 | DP | 0.30 | 0/929 | 0.50 | 0/1242 |
| 38 | BQ | 0.57 | 0/960 | 0.73 | 0/1278 |
| 38 | DQ | 0.29 | 0/960 | 0.46 | 0/1278 |
| 39 | BR | 0.60 | 1/829 (0.1%) | 0.75 | 0/1107 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|------------------|-------------|--------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 39 | DR | 0.28 | 0/829 | 0.49 | 0/1107 |
| 40 | BS | 0.53 | 0/864 | 0.72 | 0/1156 |
| 40 | DS | 0.29 | 0/864 | 0.52 | 0/1156 |
| 41 | BT | 0.46 | 0/744 | 0.74 | 0/994 |
| 41 | DT | 0.24 | 0/744 | 0.48 | 0/994 |
| 42 | BU | 0.44 | 0/787 | 0.70 | 0/1051 |
| 42 | DU | 0.25 | 0/787 | 0.47 | 0/1051 |
| 43 | BV | 0.42 | 0/766 | 0.58 | 0/1025 |
| 43 | DV | 0.25 | 0/766 | 0.43 | 0/1025 |
| 44 | BW | 0.56 | 0/603 | 0.87 | 0/797 |
| 44 | DW | 0.26 | 0/603 | 0.48 | 0/797 |
| 45 | BX | 0.42 | 0/635 | 0.70 | 1/848 (0.1%) |
| 45 | DX | 0.27 | 0/635 | 0.55 | 0/848 |
| 46 | BY | 0.35 | 0/510 | 0.65 | 0/677 |
| 46 | DY | 0.22 | 0/510 | 0.45 | 0/677 |
| 47 | BZ | 0.51 | 0/453 | 0.77 | 0/605 |
| 47 | DZ | 0.26 | 0/453 | 0.49 | 0/605 |
| 48 | B0 | 0.45 | 0/450 | 0.71 | 0/599 |
| 48 | D0 | 0.28 | 0/450 | 0.51 | 0/599 |
| 49 | B1 | 0.40 | 0/416 | 0.63 | 0/554 |
| 49 | D1 | 0.27 | 0/416 | 0.46 | 0/554 |
| 50 | B2 | 0.46 | 0/380 | 0.73 | 0/498 |
| 50 | D2 | 0.28 | 0/380 | 0.50 | 0/498 |
| 51 | B3 | 0.45 | 0/513 | 0.69 | 0/676 |
| 51 | D3 | 0.27 | 0/513 | 0.51 | 0/676 |
| 52 | B4 | 0.55 | 0/303 | 0.78 | 0/397 |
| 52 | D4 | 0.27 | 0/303 | 0.49 | 0/397 |
| 53 | CA | 0.50 | 0/36762 | 1.32 | 542/57350 (0.9%) |
| 54 | DB | 0.44 | 0/2803 | 1.26 | 34/4371 (0.8%) |
| All | All | 0.55 | 14/306737 (0.0%) | 1.26 | 3765/458565 (0.8%) |

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 |
|-----|-------|---------------------|---------------------|
| 25 | BD | 0 | 1 |
| 32 | BK | 0 | 1 |
| 35 | BN | 0 | 1 |
| 51 | B3 | 0 | 1 |
| All | All | 0 | 4 |

The worst 5 of 14 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|--------|-------------|----------|
| 22 | BA | 1142 | A | N9-C4 | -10.15 | 1.31 | 1.37 |
| 22 | BA | 2451 | A | C8-N7 | 8.00 | 1.37 | 1.31 |
| 22 | BA | 2447 | G | N9-C4 | 7.71 | 1.44 | 1.38 |
| 22 | BA | 984 | A | N9-C4 | -6.87 | 1.33 | 1.37 |
| 22 | BA | 1142 | A | C8-N7 | 6.70 | 1.36 | 1.31 |

The worst 5 of 3765 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|------------|--------|-------------|----------|
| 22 | BA | 2447 | G | C6-N1-C2 | -18.49 | 114.00 | 125.10 |
| 22 | BA | 919 | U | N1-C2-O2 | 18.00 | 135.40 | 122.80 |
| 22 | BA | 919 | U | C2-N1-C1' | 16.54 | 137.55 | 117.70 |
| 22 | BA | 302 | C | N1-C1'-C2' | -16.46 | 92.60 | 114.00 |
| 22 | BA | 805 | G | P-O3'-C3' | 15.12 | 137.85 | 119.70 |

There are no chirality outliers.

All (4) planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|---------|
| 51 | B3 | 29 | ARG | Peptide |
| 25 | BD | 9 | VAL | Peptide |
| 32 | BK | 15 | GLY | Peptide |
| 35 | BN | 101 | GLY | Peptide |

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 | AB | 1704 | 0 | 1732 | 221 | 0 |
| 1 | CB | 1704 | 0 | 1732 | 174 | 0 |
| 2 | AC | 1624 | 0 | 1699 | 112 | 0 |
| 2 | CC | 1624 | 0 | 1699 | 143 | 0 |
| 3 | AD | 1643 | 0 | 1710 | 151 | 0 |
| 3 | CD | 1643 | 0 | 1710 | 152 | 0 |
| 4 | AE | 1105 | 0 | 1148 | 132 | 0 |
| 4 | CE | 1105 | 0 | 1148 | 99 | 0 |

Continued on next page...

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 5 | AF | 817 | 0 | 808 | 73 | 0 |
| 5 | CF | 817 | 0 | 808 | 66 | 0 |
| 6 | AG | 1181 | 0 | 1240 | 87 | 0 |
| 6 | CG | 1174 | 0 | 1230 | 136 | 0 |
| 7 | AH | 979 | 0 | 1034 | 74 | 0 |
| 7 | CH | 979 | 0 | 1034 | 88 | 0 |
| 8 | AI | 1022 | 0 | 1070 | 83 | 0 |
| 8 | CI | 1022 | 0 | 1070 | 98 | 0 |
| 9 | AJ | 786 | 0 | 828 | 74 | 0 |
| 9 | CJ | 786 | 0 | 828 | 97 | 0 |
| 10 | AK | 877 | 0 | 887 | 89 | 0 |
| 10 | CK | 877 | 0 | 887 | 78 | 0 |
| 11 | AL | 955 | 0 | 1019 | 89 | 0 |
| 11 | CL | 955 | 0 | 1019 | 89 | 0 |
| 12 | AM | 883 | 0 | 944 | 74 | 0 |
| 12 | CM | 876 | 0 | 937 | 107 | 0 |
| 13 | AN | 774 | 0 | 827 | 76 | 0 |
| 13 | CN | 769 | 0 | 822 | 82 | 0 |
| 14 | AO | 714 | 0 | 737 | 54 | 0 |
| 14 | CO | 714 | 0 | 737 | 36 | 0 |
| 15 | AP | 649 | 0 | 666 | 52 | 0 |
| 15 | CP | 638 | 0 | 656 | 67 | 0 |
| 16 | AQ | 648 | 0 | 691 | 75 | 0 |
| 16 | CQ | 648 | 0 | 691 | 61 | 0 |
| 17 | AR | 455 | 0 | 478 | 25 | 0 |
| 17 | CR | 455 | 0 | 478 | 35 | 0 |
| 18 | AS | 637 | 0 | 665 | 52 | 0 |
| 18 | CS | 637 | 0 | 665 | 75 | 0 |
| 19 | AT | 665 | 0 | 714 | 72 | 0 |
| 19 | CT | 665 | 0 | 714 | 52 | 0 |
| 20 | AU | 425 | 0 | 449 | 88 | 0 |
| 20 | CU | 425 | 0 | 449 | 80 | 0 |
| 21 | AA | 32895 | 0 | 16553 | 1203 | 0 |
| 22 | BA | 61274 | 0 | 30819 | 1932 | 0 |
| 22 | DA | 60995 | 0 | 30679 | 3174 | 0 |
| 23 | BB | 2529 | 0 | 1281 | 63 | 0 |
| 24 | BC | 2082 | 0 | 2157 | 213 | 0 |
| 24 | DC | 2082 | 0 | 2157 | 210 | 0 |
| 25 | BD | 1565 | 0 | 1616 | 186 | 0 |
| 25 | DD | 1565 | 0 | 1616 | 179 | 0 |
| 26 | BE | 1552 | 0 | 1619 | 127 | 0 |
| 26 | DE | 1552 | 0 | 1619 | 172 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 27 | BF | 1410 | 0 | 1447 | 124 | 0 |
| 27 | DF | 1420 | 0 | 1460 | 170 | 0 |
| 28 | BG | 1323 | 0 | 1374 | 169 | 0 |
| 28 | DG | 1323 | 0 | 1374 | 137 | 0 |
| 29 | BH | 1111 | 0 | 1148 | 107 | 0 |
| 29 | DH | 1111 | 0 | 1148 | 102 | 0 |
| 30 | BI | 1032 | 0 | 1088 | 108 | 0 |
| 30 | DI | 1032 | 0 | 1088 | 77 | 0 |
| 31 | BJ | 1129 | 0 | 1162 | 154 | 0 |
| 31 | DJ | 1129 | 0 | 1162 | 141 | 0 |
| 32 | BK | 938 | 0 | 1012 | 99 | 0 |
| 32 | DK | 938 | 0 | 1012 | 111 | 0 |
| 33 | BL | 1045 | 0 | 1117 | 117 | 0 |
| 33 | DL | 1045 | 0 | 1117 | 115 | 0 |
| 34 | BM | 1074 | 0 | 1157 | 102 | 0 |
| 34 | DM | 1074 | 0 | 1157 | 96 | 0 |
| 35 | BN | 960 | 0 | 1000 | 82 | 0 |
| 35 | DN | 960 | 0 | 1000 | 122 | 0 |
| 36 | BO | 892 | 0 | 923 | 74 | 0 |
| 36 | DO | 892 | 0 | 923 | 75 | 0 |
| 37 | BP | 917 | 0 | 965 | 131 | 0 |
| 37 | DP | 917 | 0 | 965 | 112 | 0 |
| 38 | BQ | 947 | 0 | 1022 | 124 | 0 |
| 38 | DQ | 947 | 0 | 1022 | 131 | 0 |
| 39 | BR | 816 | 0 | 839 | 91 | 0 |
| 39 | DR | 816 | 0 | 839 | 91 | 0 |
| 40 | BS | 857 | 0 | 922 | 67 | 0 |
| 40 | DS | 857 | 0 | 922 | 76 | 0 |
| 41 | BT | 738 | 0 | 807 | 117 | 0 |
| 41 | DT | 738 | 0 | 807 | 98 | 0 |
| 42 | BU | 779 | 0 | 834 | 57 | 0 |
| 42 | DU | 779 | 0 | 834 | 89 | 0 |
| 43 | BV | 753 | 0 | 780 | 45 | 0 |
| 43 | DV | 753 | 0 | 780 | 64 | 0 |
| 44 | BW | 596 | 0 | 610 | 187 | 0 |
| 44 | DW | 596 | 0 | 610 | 111 | 0 |
| 45 | BX | 625 | 0 | 655 | 61 | 0 |
| 45 | DX | 625 | 0 | 655 | 63 | 0 |
| 46 | BY | 509 | 0 | 543 | 55 | 0 |
| 46 | DY | 509 | 0 | 543 | 58 | 0 |
| 47 | BZ | 449 | 0 | 491 | 39 | 0 |
| 47 | DZ | 449 | 0 | 491 | 43 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 48 | B0 | 444 | 0 | 461 | 22 | 0 |
| 48 | D0 | 444 | 0 | 461 | 53 | 0 |
| 49 | B1 | 409 | 0 | 440 | 44 | 0 |
| 49 | D1 | 409 | 0 | 440 | 31 | 0 |
| 50 | B2 | 377 | 0 | 418 | 29 | 0 |
| 50 | D2 | 377 | 0 | 418 | 41 | 0 |
| 51 | B3 | 504 | 0 | 574 | 41 | 0 |
| 51 | D3 | 504 | 0 | 574 | 58 | 0 |
| 52 | B4 | 302 | 0 | 340 | 32 | 0 |
| 52 | D4 | 302 | 0 | 340 | 29 | 0 |
| 53 | CA | 32831 | 0 | 16521 | 1452 | 0 |
| 54 | DB | 2507 | 0 | 1270 | 121 | 0 |
| 55 | AA | 43 | 0 | 0 | 0 | 0 |
| 55 | BA | 137 | 0 | 0 | 0 | 0 |
| 55 | BB | 4 | 0 | 0 | 0 | 0 |
| 55 | CA | 42 | 0 | 0 | 0 | 0 |
| 55 | DA | 135 | 0 | 0 | 0 | 0 |
| 55 | DB | 1 | 0 | 0 | 0 | 0 |
| 55 | DJ | 1 | 0 | 0 | 0 | 0 |
| 56 | B4 | 1 | 0 | 0 | 0 | 0 |
| 56 | D4 | 1 | 0 | 0 | 0 | 0 |
| 57 | AA | 195 | 0 | 0 | 2 | 0 |
| 57 | AE | 1 | 0 | 0 | 0 | 0 |
| 57 | AL | 3 | 0 | 0 | 0 | 0 |
| 57 | AN | 6 | 0 | 0 | 0 | 0 |
| 57 | AT | 2 | 0 | 0 | 0 | 0 |
| 57 | AU | 1 | 0 | 0 | 0 | 0 |
| 57 | B0 | 1 | 0 | 0 | 0 | 0 |
| 57 | B2 | 1 | 0 | 0 | 0 | 0 |
| 57 | B3 | 3 | 0 | 0 | 0 | 0 |
| 57 | B4 | 3 | 0 | 0 | 0 | 0 |
| 57 | BA | 610 | 0 | 0 | 24 | 0 |
| 57 | BB | 20 | 0 | 0 | 1 | 0 |
| 57 | BC | 10 | 0 | 0 | 0 | 0 |
| 57 | BD | 2 | 0 | 0 | 1 | 0 |
| 57 | BL | 4 | 0 | 0 | 1 | 0 |
| 57 | BN | 3 | 0 | 0 | 0 | 0 |
| 57 | BQ | 1 | 0 | 0 | 0 | 0 |
| 57 | BT | 2 | 0 | 0 | 1 | 0 |
| 57 | CA | 192 | 0 | 0 | 8 | 0 |
| 57 | CE | 5 | 0 | 0 | 0 | 0 |
| 57 | CI | 1 | 0 | 0 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 57 | CL | 1 | 0 | 0 | 0 | 0 |
| 57 | CN | 3 | 0 | 0 | 0 | 0 |
| 57 | CT | 3 | 0 | 0 | 0 | 0 |
| 57 | CU | 2 | 0 | 0 | 0 | 0 |
| 57 | D2 | 1 | 0 | 0 | 1 | 0 |
| 57 | D3 | 1 | 0 | 0 | 0 | 0 |
| 57 | D4 | 4 | 0 | 0 | 0 | 0 |
| 57 | DA | 599 | 0 | 0 | 9 | 0 |
| 57 | DB | 4 | 0 | 0 | 0 | 0 |
| 57 | DC | 13 | 0 | 0 | 1 | 0 |
| 57 | DD | 4 | 0 | 0 | 0 | 0 |
| 57 | DE | 3 | 0 | 0 | 0 | 0 |
| 57 | DJ | 3 | 0 | 0 | 0 | 0 |
| 57 | DL | 5 | 0 | 0 | 0 | 0 |
| 57 | DN | 2 | 0 | 0 | 2 | 0 |
| 57 | DT | 2 | 0 | 0 | 1 | 0 |
| 57 | DU | 1 | 0 | 0 | 0 | 0 |
| 57 | DV | 1 | 0 | 0 | 0 | 0 |
| All | All | 284450 | 0 | 190838 | 15808 | 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 33.

The worst 5 of 15808 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) |
|-------------------|--------------------|--------------------------|-------------------|
| 38:BQ:63:ARG:NH1 | 38:BQ:96:ASP:HA | 1.49 | 1.26 |
| 22:DA:1439:A:C2 | 22:DA:1552:A:C6 | 2.32 | 1.17 |
| 22:DA:1439:A:N1 | 22:DA:1552:A:C5 | 2.12 | 1.17 |
| 27:BF:35:LEU:HB3 | 27:BF:153:ILE:HG22 | 1.19 | 1.16 |
| 33:BL:93:ASN:HD22 | 33:BL:94:THR:N | 1.44 | 1.16 |

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 | |
|-----|-------|---------------|-----------|----------|----------|-------------|----|
| 1 | AB | 216/241 (90%) | 131 (61%) | 49 (23%) | 36 (17%) | 0 | 1 |
| 1 | CB | 216/241 (90%) | 149 (69%) | 47 (22%) | 20 (9%) | 1 | 4 |
| 2 | AC | 204/233 (88%) | 151 (74%) | 35 (17%) | 18 (9%) | 1 | 4 |
| 2 | CC | 204/233 (88%) | 144 (71%) | 41 (20%) | 19 (9%) | 1 | 4 |
| 3 | AD | 203/206 (98%) | 140 (69%) | 36 (18%) | 27 (13%) | 0 | 1 |
| 3 | CD | 203/206 (98%) | 142 (70%) | 39 (19%) | 22 (11%) | 0 | 3 |
| 4 | AE | 148/167 (89%) | 107 (72%) | 25 (17%) | 16 (11%) | 0 | 3 |
| 4 | CE | 148/167 (89%) | 111 (75%) | 21 (14%) | 16 (11%) | 0 | 3 |
| 5 | AF | 98/135 (73%) | 74 (76%) | 15 (15%) | 9 (9%) | 1 | 4 |
| 5 | CF | 98/135 (73%) | 68 (69%) | 18 (18%) | 12 (12%) | 0 | 2 |
| 6 | AG | 149/179 (83%) | 108 (72%) | 34 (23%) | 7 (5%) | 2 | 19 |
| 6 | CG | 148/179 (83%) | 99 (67%) | 35 (24%) | 14 (10%) | 1 | 4 |
| 7 | AH | 127/130 (98%) | 93 (73%) | 30 (24%) | 4 (3%) | 4 | 30 |
| 7 | CH | 127/130 (98%) | 96 (76%) | 20 (16%) | 11 (9%) | 1 | 4 |
| 8 | AI | 125/130 (96%) | 84 (67%) | 31 (25%) | 10 (8%) | 1 | 6 |
| 8 | CI | 125/130 (96%) | 90 (72%) | 21 (17%) | 14 (11%) | 0 | 2 |
| 9 | AJ | 96/103 (93%) | 67 (70%) | 18 (19%) | 11 (12%) | 0 | 2 |
| 9 | CJ | 96/103 (93%) | 55 (57%) | 24 (25%) | 17 (18%) | 0 | 0 |
| 10 | AK | 115/129 (89%) | 85 (74%) | 21 (18%) | 9 (8%) | 1 | 7 |
| 10 | CK | 115/129 (89%) | 85 (74%) | 22 (19%) | 8 (7%) | 1 | 8 |
| 11 | AL | 121/124 (98%) | 87 (72%) | 20 (16%) | 14 (12%) | 0 | 2 |
| 11 | CL | 121/124 (98%) | 85 (70%) | 29 (24%) | 7 (6%) | 2 | 14 |
| 12 | AM | 112/118 (95%) | 89 (80%) | 16 (14%) | 7 (6%) | 1 | 11 |
| 12 | CM | 111/118 (94%) | 60 (54%) | 38 (34%) | 13 (12%) | 0 | 2 |
| 13 | AN | 92/101 (91%) | 56 (61%) | 24 (26%) | 12 (13%) | 0 | 1 |
| 13 | CN | 91/101 (90%) | 60 (66%) | 26 (29%) | 5 (6%) | 2 | 16 |
| 14 | AO | 86/89 (97%) | 63 (73%) | 20 (23%) | 3 (4%) | 4 | 27 |
| 14 | CO | 86/89 (97%) | 62 (72%) | 20 (23%) | 4 (5%) | 2 | 19 |
| 15 | AP | 80/82 (98%) | 58 (72%) | 14 (18%) | 8 (10%) | 0 | 3 |
| 15 | CP | 78/82 (95%) | 50 (64%) | 17 (22%) | 11 (14%) | 0 | 1 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|----|
| 16 | AQ | 78/84 (93%) | 51 (65%) | 15 (19%) | 12 (15%) | 0 | 1 |
| 16 | CQ | 78/84 (93%) | 59 (76%) | 10 (13%) | 9 (12%) | 0 | 2 |
| 17 | AR | 53/75 (71%) | 40 (76%) | 11 (21%) | 2 (4%) | 3 | 24 |
| 17 | CR | 53/75 (71%) | 39 (74%) | 12 (23%) | 2 (4%) | 3 | 24 |
| 18 | AS | 77/92 (84%) | 59 (77%) | 9 (12%) | 9 (12%) | 0 | 2 |
| 18 | CS | 77/92 (84%) | 46 (60%) | 24 (31%) | 7 (9%) | 1 | 4 |
| 19 | AT | 83/87 (95%) | 56 (68%) | 20 (24%) | 7 (8%) | 1 | 5 |
| 19 | CT | 83/87 (95%) | 59 (71%) | 16 (19%) | 8 (10%) | 1 | 4 |
| 20 | AU | 49/71 (69%) | 25 (51%) | 13 (26%) | 11 (22%) | 0 | 0 |
| 20 | CU | 49/71 (69%) | 21 (43%) | 11 (22%) | 17 (35%) | 0 | 0 |
| 24 | BC | 269/273 (98%) | 194 (72%) | 50 (19%) | 25 (9%) | 1 | 4 |
| 24 | DC | 269/273 (98%) | 174 (65%) | 63 (23%) | 32 (12%) | 0 | 2 |
| 25 | BD | 207/209 (99%) | 146 (70%) | 27 (13%) | 34 (16%) | 0 | 1 |
| 25 | DD | 207/209 (99%) | 132 (64%) | 43 (21%) | 32 (16%) | 0 | 1 |
| 26 | BE | 199/201 (99%) | 155 (78%) | 24 (12%) | 20 (10%) | 0 | 3 |
| 26 | DE | 199/201 (99%) | 130 (65%) | 46 (23%) | 23 (12%) | 0 | 2 |
| 27 | BF | 175/179 (98%) | 134 (77%) | 25 (14%) | 16 (9%) | 1 | 4 |
| 27 | DF | 176/179 (98%) | 98 (56%) | 43 (24%) | 35 (20%) | 0 | 0 |
| 28 | BG | 174/177 (98%) | 111 (64%) | 38 (22%) | 25 (14%) | 0 | 1 |
| 28 | DG | 174/177 (98%) | 106 (61%) | 38 (22%) | 30 (17%) | 0 | 0 |
| 29 | BH | 147/149 (99%) | 68 (46%) | 47 (32%) | 32 (22%) | 0 | 0 |
| 29 | DH | 147/149 (99%) | 75 (51%) | 54 (37%) | 18 (12%) | 0 | 2 |
| 30 | BI | 139/142 (98%) | 84 (60%) | 41 (30%) | 14 (10%) | 0 | 3 |
| 30 | DI | 139/142 (98%) | 81 (58%) | 39 (28%) | 19 (14%) | 0 | 1 |
| 31 | BJ | 140/142 (99%) | 107 (76%) | 21 (15%) | 12 (9%) | 1 | 5 |
| 31 | DJ | 140/142 (99%) | 91 (65%) | 38 (27%) | 11 (8%) | 1 | 6 |
| 32 | BK | 120/123 (98%) | 86 (72%) | 15 (12%) | 19 (16%) | 0 | 1 |
| 32 | DK | 120/123 (98%) | 80 (67%) | 20 (17%) | 20 (17%) | 0 | 1 |
| 33 | BL | 141/144 (98%) | 101 (72%) | 32 (23%) | 8 (6%) | 2 | 15 |
| 33 | DL | 141/144 (98%) | 81 (57%) | 40 (28%) | 20 (14%) | 0 | 1 |
| 34 | BM | 134/136 (98%) | 97 (72%) | 22 (16%) | 15 (11%) | 0 | 2 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|----|
| 34 | DM | 134/136 (98%) | 92 (69%) | 29 (22%) | 13 (10%) | 1 | 4 |
| 35 | BN | 118/127 (93%) | 92 (78%) | 17 (14%) | 9 (8%) | 1 | 7 |
| 35 | DN | 118/127 (93%) | 72 (61%) | 30 (25%) | 16 (14%) | 0 | 1 |
| 36 | BO | 114/117 (97%) | 91 (80%) | 12 (10%) | 11 (10%) | 1 | 4 |
| 36 | DO | 114/117 (97%) | 77 (68%) | 30 (26%) | 7 (6%) | 1 | 13 |
| 37 | BP | 112/115 (97%) | 77 (69%) | 18 (16%) | 17 (15%) | 0 | 1 |
| 37 | DP | 112/115 (97%) | 68 (61%) | 27 (24%) | 17 (15%) | 0 | 1 |
| 38 | BQ | 115/118 (98%) | 100 (87%) | 9 (8%) | 6 (5%) | 2 | 17 |
| 38 | DQ | 115/118 (98%) | 80 (70%) | 25 (22%) | 10 (9%) | 1 | 4 |
| 39 | BR | 101/103 (98%) | 80 (79%) | 13 (13%) | 8 (8%) | 1 | 6 |
| 39 | DR | 101/103 (98%) | 70 (69%) | 21 (21%) | 10 (10%) | 1 | 3 |
| 40 | BS | 108/110 (98%) | 86 (80%) | 16 (15%) | 6 (6%) | 2 | 15 |
| 40 | DS | 108/110 (98%) | 76 (70%) | 23 (21%) | 9 (8%) | 1 | 5 |
| 41 | BT | 91/100 (91%) | 52 (57%) | 24 (26%) | 15 (16%) | 0 | 1 |
| 41 | DT | 91/100 (91%) | 46 (50%) | 31 (34%) | 14 (15%) | 0 | 1 |
| 42 | BU | 100/104 (96%) | 69 (69%) | 15 (15%) | 16 (16%) | 0 | 1 |
| 42 | DU | 100/104 (96%) | 51 (51%) | 26 (26%) | 23 (23%) | 0 | 0 |
| 43 | BV | 92/94 (98%) | 77 (84%) | 13 (14%) | 2 (2%) | 7 | 39 |
| 43 | DV | 92/94 (98%) | 61 (66%) | 23 (25%) | 8 (9%) | 1 | 4 |
| 44 | BW | 77/85 (91%) | 30 (39%) | 24 (31%) | 23 (30%) | 0 | 0 |
| 44 | DW | 77/85 (91%) | 33 (43%) | 27 (35%) | 17 (22%) | 0 | 0 |
| 45 | BX | 75/78 (96%) | 56 (75%) | 14 (19%) | 5 (7%) | 1 | 10 |
| 45 | DX | 75/78 (96%) | 47 (63%) | 20 (27%) | 8 (11%) | 0 | 3 |
| 46 | BY | 61/63 (97%) | 38 (62%) | 16 (26%) | 7 (12%) | 0 | 2 |
| 46 | DY | 61/63 (97%) | 42 (69%) | 14 (23%) | 5 (8%) | 1 | 6 |
| 47 | BZ | 56/59 (95%) | 45 (80%) | 9 (16%) | 2 (4%) | 4 | 26 |
| 47 | DZ | 56/59 (95%) | 34 (61%) | 16 (29%) | 6 (11%) | 0 | 3 |
| 48 | B0 | 54/57 (95%) | 41 (76%) | 9 (17%) | 4 (7%) | 1 | 8 |
| 48 | D0 | 54/57 (95%) | 39 (72%) | 8 (15%) | 7 (13%) | 0 | 1 |
| 49 | B1 | 48/55 (87%) | 36 (75%) | 7 (15%) | 5 (10%) | 0 | 3 |
| 49 | D1 | 48/55 (87%) | 37 (77%) | 7 (15%) | 4 (8%) | 1 | 5 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|------------|------------|------------|-------------|----|
| 50 | B2 | 44/46 (96%) | 39 (89%) | 4 (9%) | 1 (2%) | 7 | 38 |
| 50 | D2 | 44/46 (96%) | 31 (70%) | 10 (23%) | 3 (7%) | 1 | 10 |
| 51 | B3 | 62/65 (95%) | 53 (86%) | 5 (8%) | 4 (6%) | 1 | 11 |
| 51 | D3 | 62/65 (95%) | 39 (63%) | 18 (29%) | 5 (8%) | 1 | 6 |
| 52 | B4 | 36/38 (95%) | 31 (86%) | 2 (6%) | 3 (8%) | 1 | 5 |
| 52 | D4 | 36/38 (95%) | 23 (64%) | 7 (19%) | 6 (17%) | 0 | 1 |
| All | All | 11238/11970 (94%) | 7646 (68%) | 2332 (21%) | 1260 (11%) | 0 | 2 |

5 of 1260 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | AB | 18 | GLN |
| 1 | AB | 20 | ARG |
| 1 | AB | 40 | ILE |
| 1 | AB | 75 | ALA |
| 1 | AB | 119 | GLN |

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 | AB | 180/199 (90%) | 138 (77%) | 42 (23%) | 1 | 4 |
| 1 | CB | 180/199 (90%) | 155 (86%) | 25 (14%) | 4 | 18 |
| 2 | AC | 170/190 (90%) | 139 (82%) | 31 (18%) | 2 | 9 |
| 2 | CC | 170/190 (90%) | 152 (89%) | 18 (11%) | 7 | 30 |
| 3 | AD | 172/173 (99%) | 144 (84%) | 28 (16%) | 2 | 12 |
| 3 | CD | 172/173 (99%) | 138 (80%) | 34 (20%) | 1 | 8 |
| 4 | AE | 113/126 (90%) | 94 (83%) | 19 (17%) | 2 | 11 |
| 4 | CE | 113/126 (90%) | 93 (82%) | 20 (18%) | 2 | 10 |
| 5 | AF | 87/116 (75%) | 74 (85%) | 13 (15%) | 3 | 15 |
| 5 | CF | 87/116 (75%) | 74 (85%) | 13 (15%) | 3 | 15 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|-------------|----|
| 6 | AG | 124/147 (84%) | 109 (88%) | 15 (12%) | 5 | 24 |
| 6 | CG | 123/147 (84%) | 99 (80%) | 24 (20%) | 1 | 8 |
| 7 | AH | 104/105 (99%) | 88 (85%) | 16 (15%) | 3 | 14 |
| 7 | CH | 104/105 (99%) | 90 (86%) | 14 (14%) | 4 | 19 |
| 8 | AI | 105/107 (98%) | 88 (84%) | 17 (16%) | 2 | 12 |
| 8 | CI | 105/107 (98%) | 91 (87%) | 14 (13%) | 4 | 20 |
| 9 | AJ | 86/90 (96%) | 72 (84%) | 14 (16%) | 2 | 12 |
| 9 | CJ | 86/90 (96%) | 77 (90%) | 9 (10%) | 7 | 31 |
| 10 | AK | 90/99 (91%) | 71 (79%) | 19 (21%) | 1 | 6 |
| 10 | CK | 90/99 (91%) | 78 (87%) | 12 (13%) | 4 | 20 |
| 11 | AL | 103/104 (99%) | 81 (79%) | 22 (21%) | 1 | 6 |
| 11 | CL | 103/104 (99%) | 84 (82%) | 19 (18%) | 2 | 9 |
| 12 | AM | 92/96 (96%) | 88 (96%) | 4 (4%) | 32 | 68 |
| 12 | CM | 91/96 (95%) | 80 (88%) | 11 (12%) | 5 | 24 |
| 13 | AN | 79/84 (94%) | 73 (92%) | 6 (8%) | 14 | 49 |
| 13 | CN | 79/84 (94%) | 67 (85%) | 12 (15%) | 3 | 15 |
| 14 | AO | 76/77 (99%) | 69 (91%) | 7 (9%) | 10 | 36 |
| 14 | CO | 76/77 (99%) | 70 (92%) | 6 (8%) | 13 | 46 |
| 15 | AP | 65/65 (100%) | 54 (83%) | 11 (17%) | 2 | 11 |
| 15 | CP | 65/65 (100%) | 53 (82%) | 12 (18%) | 2 | 9 |
| 16 | AQ | 74/78 (95%) | 61 (82%) | 13 (18%) | 2 | 10 |
| 16 | CQ | 74/78 (95%) | 63 (85%) | 11 (15%) | 3 | 15 |
| 17 | AR | 48/65 (74%) | 45 (94%) | 3 (6%) | 20 | 56 |
| 17 | CR | 48/65 (74%) | 46 (96%) | 2 (4%) | 32 | 69 |
| 18 | AS | 70/79 (89%) | 62 (89%) | 8 (11%) | 6 | 27 |
| 18 | CS | 70/79 (89%) | 62 (89%) | 8 (11%) | 6 | 27 |
| 19 | AT | 65/66 (98%) | 48 (74%) | 17 (26%) | 0 | 2 |
| 19 | CT | 65/66 (98%) | 54 (83%) | 11 (17%) | 2 | 11 |
| 20 | AU | 44/61 (72%) | 32 (73%) | 12 (27%) | 0 | 1 |
| 20 | CU | 44/61 (72%) | 34 (77%) | 10 (23%) | 1 | 4 |
| 24 | BC | 216/218 (99%) | 173 (80%) | 43 (20%) | 1 | 7 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 24 | DC | 216/218 (99%) | 188 (87%) | 28 (13%) | 4 | 21 |
| 25 | BD | 164/164 (100%) | 136 (83%) | 28 (17%) | 2 | 11 |
| 25 | DD | 164/164 (100%) | 140 (85%) | 24 (15%) | 3 | 16 |
| 26 | BE | 165/165 (100%) | 125 (76%) | 40 (24%) | 1 | 3 |
| 26 | DE | 165/165 (100%) | 150 (91%) | 15 (9%) | 10 | 37 |
| 27 | BF | 148/150 (99%) | 128 (86%) | 20 (14%) | 4 | 19 |
| 27 | DF | 149/150 (99%) | 122 (82%) | 27 (18%) | 2 | 10 |
| 28 | BG | 137/138 (99%) | 107 (78%) | 30 (22%) | 1 | 5 |
| 28 | DG | 137/138 (99%) | 119 (87%) | 18 (13%) | 4 | 21 |
| 29 | BH | 114/114 (100%) | 96 (84%) | 18 (16%) | 3 | 13 |
| 29 | DH | 114/114 (100%) | 96 (84%) | 18 (16%) | 3 | 13 |
| 30 | BI | 109/110 (99%) | 91 (84%) | 18 (16%) | 2 | 12 |
| 30 | DI | 109/110 (99%) | 102 (94%) | 7 (6%) | 19 | 56 |
| 31 | BJ | 116/116 (100%) | 89 (77%) | 27 (23%) | 1 | 4 |
| 31 | DJ | 116/116 (100%) | 104 (90%) | 12 (10%) | 8 | 32 |
| 32 | BK | 103/104 (99%) | 84 (82%) | 19 (18%) | 2 | 9 |
| 32 | DK | 103/104 (99%) | 87 (84%) | 16 (16%) | 3 | 14 |
| 33 | BL | 102/103 (99%) | 79 (78%) | 23 (22%) | 1 | 4 |
| 33 | DL | 102/103 (99%) | 88 (86%) | 14 (14%) | 4 | 19 |
| 34 | BM | 109/109 (100%) | 87 (80%) | 22 (20%) | 1 | 7 |
| 34 | DM | 109/109 (100%) | 99 (91%) | 10 (9%) | 10 | 36 |
| 35 | BN | 100/103 (97%) | 83 (83%) | 17 (17%) | 2 | 11 |
| 35 | DN | 100/103 (97%) | 85 (85%) | 15 (15%) | 3 | 15 |
| 36 | BO | 86/87 (99%) | 69 (80%) | 17 (20%) | 1 | 8 |
| 36 | DO | 86/87 (99%) | 78 (91%) | 8 (9%) | 10 | 36 |
| 37 | BP | 99/100 (99%) | 78 (79%) | 21 (21%) | 1 | 6 |
| 37 | DP | 99/100 (99%) | 90 (91%) | 9 (9%) | 10 | 37 |
| 38 | BQ | 89/90 (99%) | 74 (83%) | 15 (17%) | 2 | 11 |
| 38 | DQ | 89/90 (99%) | 78 (88%) | 11 (12%) | 5 | 23 |
| 39 | BR | 84/84 (100%) | 65 (77%) | 19 (23%) | 1 | 4 |
| 39 | DR | 84/84 (100%) | 71 (84%) | 13 (16%) | 3 | 14 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|------------|-------------|----|
| 40 | BS | 93/93 (100%) | 73 (78%) | 20 (22%) | 1 | 6 |
| 40 | DS | 93/93 (100%) | 76 (82%) | 17 (18%) | 2 | 9 |
| 41 | BT | 80/84 (95%) | 61 (76%) | 19 (24%) | 1 | 3 |
| 41 | DT | 80/84 (95%) | 74 (92%) | 6 (8%) | 15 | 49 |
| 42 | BU | 83/85 (98%) | 66 (80%) | 17 (20%) | 1 | 6 |
| 42 | DU | 83/85 (98%) | 74 (89%) | 9 (11%) | 7 | 29 |
| 43 | BV | 78/78 (100%) | 61 (78%) | 17 (22%) | 1 | 5 |
| 43 | DV | 78/78 (100%) | 66 (85%) | 12 (15%) | 3 | 14 |
| 44 | BW | 59/63 (94%) | 42 (71%) | 17 (29%) | 0 | 1 |
| 44 | DW | 59/63 (94%) | 44 (75%) | 15 (25%) | 0 | 2 |
| 45 | BX | 67/68 (98%) | 53 (79%) | 14 (21%) | 1 | 6 |
| 45 | DX | 67/68 (98%) | 58 (87%) | 9 (13%) | 4 | 20 |
| 46 | BY | 55/55 (100%) | 43 (78%) | 12 (22%) | 1 | 5 |
| 46 | DY | 55/55 (100%) | 52 (94%) | 3 (6%) | 24 | 62 |
| 47 | BZ | 48/49 (98%) | 32 (67%) | 16 (33%) | 0 | 0 |
| 47 | DZ | 48/49 (98%) | 41 (85%) | 7 (15%) | 3 | 16 |
| 48 | B0 | 47/48 (98%) | 43 (92%) | 4 (8%) | 12 | 42 |
| 48 | D0 | 47/48 (98%) | 40 (85%) | 7 (15%) | 3 | 15 |
| 49 | B1 | 45/49 (92%) | 36 (80%) | 9 (20%) | 1 | 7 |
| 49 | D1 | 45/49 (92%) | 41 (91%) | 4 (9%) | 11 | 38 |
| 50 | B2 | 38/38 (100%) | 31 (82%) | 7 (18%) | 2 | 9 |
| 50 | D2 | 38/38 (100%) | 34 (90%) | 4 (10%) | 7 | 31 |
| 51 | B3 | 51/52 (98%) | 44 (86%) | 7 (14%) | 4 | 19 |
| 51 | D3 | 51/52 (98%) | 42 (82%) | 9 (18%) | 2 | 10 |
| 52 | B4 | 34/34 (100%) | 30 (88%) | 4 (12%) | 6 | 26 |
| 52 | D4 | 34/34 (100%) | 29 (85%) | 5 (15%) | 3 | 16 |
| All | All | 9331/9756 (96%) | 7837 (84%) | 1494 (16%) | 2 | 12 |

5 of 1494 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 39 | BR | 10 | LYS |
| 49 | B1 | 41 | VAL |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 39 | DR | 75 | VAL |
| 40 | BS | 4 | ILE |
| 43 | BV | 41 | GLU |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 333 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 42 | BU | 52 | ASN |
| 2 | CC | 184 | ASN |
| 42 | DU | 45 | GLN |
| 43 | BV | 51 | GLN |
| 48 | B0 | 4 | GLN |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 21 | AA | 1532/1533 (99%) | 471 (30%) | 241 (15%) |
| 22 | BA | 2850/2903 (98%) | 800 (28%) | 404 (14%) |
| 22 | DA | 2838/2903 (97%) | 1022 (36%) | 515 (18%) |
| 23 | BB | 117/118 (99%) | 29 (24%) | 19 (16%) |
| 53 | CA | 1529/1530 (99%) | 512 (33%) | 238 (15%) |
| 54 | DB | 116/117 (99%) | 36 (31%) | 19 (16%) |
| All | All | 8982/9104 (98%) | 2870 (31%) | 1436 (15%) |

5 of 2870 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 21 | AA | 5 | U |
| 21 | AA | 6 | G |
| 21 | AA | 7 | A |
| 21 | AA | 8 | A |
| 21 | AA | 9 | G |

5 of 1436 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 23 | BB | 24 | G |
| 53 | CA | 874 | G |
| 22 | DA | 2311 | A |
| 53 | CA | 15 | G |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 53 | CA | 366 | A |

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](#)

Of 365 ligands modelled in this entry, 365 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, 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 | AB | 218/241 (90%) | 0.18 | 15 (6%) 17 9 | 85, 115, 146, 164 | 0 |
| 1 | CB | 218/241 (90%) | 0.33 | 12 (5%) 25 14 | 90, 125, 152, 170 | 0 |
| 2 | AC | 206/233 (88%) | -0.35 | 3 (1%) 73 61 | 57, 83, 116, 147 | 0 |
| 2 | CC | 206/233 (88%) | 0.39 | 11 (5%) 26 14 | 83, 129, 170, 188 | 0 |
| 3 | AD | 205/206 (99%) | -0.24 | 7 (3%) 45 30 | 50, 87, 137, 176 | 0 |
| 3 | CD | 205/206 (99%) | -0.37 | 3 (1%) 73 61 | 41, 63, 102, 148 | 0 |
| 4 | AE | 150/167 (89%) | -0.31 | 1 (0%) 87 81 | 51, 70, 116, 147 | 0 |
| 4 | CE | 150/167 (89%) | -0.06 | 1 (0%) 87 81 | 65, 87, 122, 144 | 0 |
| 5 | AF | 100/135 (74%) | -0.16 | 0 100 100 | 60, 90, 125, 142 | 0 |
| 5 | CF | 100/135 (74%) | 0.06 | 0 100 100 | 65, 113, 147, 158 | 0 |
| 6 | AG | 151/179 (84%) | 0.03 | 4 (2%) 56 41 | 69, 108, 139, 157 | 0 |
| 6 | CG | 150/179 (83%) | 1.93 | 66 (44%) 0 0 | 98, 173, 223, 233 | 0 |
| 7 | AH | 129/130 (99%) | -0.52 | 2 (1%) 72 59 | 49, 71, 106, 133 | 0 |
| 7 | CH | 129/130 (99%) | -0.21 | 2 (1%) 72 59 | 63, 100, 133, 159 | 0 |
| 8 | AI | 127/130 (97%) | 0.22 | 9 (7%) 16 9 | 56, 115, 166, 189 | 0 |
| 8 | CI | 127/130 (97%) | 1.17 | 26 (20%) 1 0 | 127, 174, 225, 239 | 0 |
| 9 | AJ | 98/103 (95%) | 0.07 | 6 (6%) 21 11 | 59, 97, 152, 160 | 0 |
| 9 | CJ | 98/103 (95%) | 1.66 | 28 (28%) 0 0 | 122, 160, 189, 201 | 0 |
| 10 | AK | 117/129 (90%) | -0.13 | 1 (0%) 84 76 | 43, 88, 124, 137 | 0 |
| 10 | CK | 117/129 (90%) | -0.01 | 0 100 100 | 57, 99, 130, 151 | 0 |
| 11 | AL | 123/124 (99%) | -0.35 | 2 (1%) 72 59 | 33, 54, 96, 135 | 0 |
| 11 | CL | 123/124 (99%) | 0.01 | 2 (1%) 72 59 | 47, 74, 110, 135 | 0 |
| 12 | AM | 114/118 (96%) | 0.10 | 3 (2%) 56 41 | 70, 117, 155, 177 | 0 |
| 12 | CM | 113/118 (95%) | 2.48 | 62 (54%) 0 0 | 220, 351, 413, 434 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|------------------|--------|----------------|-----------------------|-------|
| 13 | AN | 96/101 (95%) | -0.15 | 4 (4%) 36 23 | 59, 86, 136, 158 | 0 |
| 13 | CN | 95/101 (94%) | 1.46 | 22 (23%) 0 0 | 102, 191, 256, 269 | 0 |
| 14 | AO | 88/89 (98%) | -0.43 | 1 (1%) 80 69 | 48, 75, 106, 128 | 0 |
| 14 | CO | 88/89 (98%) | 0.12 | 1 (1%) 80 69 | 72, 109, 141, 167 | 0 |
| 15 | AP | 82/82 (100%) | -0.21 | 3 (3%) 41 27 | 55, 79, 129, 174 | 0 |
| 15 | CP | 80/82 (97%) | 0.22 | 3 (3%) 40 26 | 64, 96, 133, 152 | 0 |
| 16 | AQ | 80/84 (95%) | 0.15 | 4 (5%) 29 16 | 38, 73, 112, 144 | 0 |
| 16 | CQ | 80/84 (95%) | 0.64 | 9 (11%) 5 3 | 54, 96, 117, 131 | 0 |
| 17 | AR | 55/75 (73%) | 0.09 | 3 (5%) 25 14 | 56, 80, 129, 146 | 0 |
| 17 | CR | 55/75 (73%) | 0.22 | 2 (3%) 42 28 | 57, 89, 131, 170 | 0 |
| 18 | AS | 79/92 (85%) | 0.26 | 3 (3%) 40 26 | 79, 110, 152, 161 | 0 |
| 18 | CS | 79/92 (85%) | 2.47 | 38 (48%) 0 0 | 250, 307, 359, 371 | 0 |
| 19 | AT | 85/87 (97%) | -0.22 | 1 (1%) 79 67 | 51, 81, 114, 133 | 0 |
| 19 | CT | 85/87 (97%) | 0.66 | 7 (8%) 11 6 | 79, 125, 161, 177 | 0 |
| 20 | AU | 51/71 (71%) | 0.27 | 1 (1%) 65 51 | 60, 104, 138, 148 | 0 |
| 20 | CU | 51/71 (71%) | 0.09 | 1 (1%) 65 51 | 63, 97, 143, 153 | 0 |
| 21 | AA | 1533/1533 (100%) | -0.49 | 23 (1%) 73 61 | 34, 72, 169, 235 | 0 |
| 22 | BA | 2854/2903 (98%) | -0.46 | 66 (2%) 60 47 | 13, 33, 142, 320 | 0 |
| 22 | DA | 2841/2903 (97%) | 0.43 | 146 (5%) 28 16 | 59, 119, 216, 320 | 0 |
| 23 | BB | 118/118 (100%) | -0.57 | 0 100 100 | 18, 47, 75, 99 | 0 |
| 24 | BC | 271/273 (99%) | -0.44 | 9 (3%) 46 30 | 20, 43, 83, 142 | 0 |
| 24 | DC | 271/273 (99%) | 0.22 | 12 (4%) 34 21 | 63, 94, 128, 153 | 0 |
| 25 | BD | 209/209 (100%) | -0.69 | 0 100 100 | 13, 29, 72, 96 | 0 |
| 25 | DD | 209/209 (100%) | 0.37 | 9 (4%) 35 22 | 68, 108, 141, 168 | 0 |
| 26 | BE | 201/201 (100%) | -0.64 | 0 100 100 | 15, 42, 87, 124 | 0 |
| 26 | DE | 201/201 (100%) | 1.10 | 40 (19%) 1 0 | 89, 191, 252, 282 | 0 |
| 27 | BF | 177/179 (98%) | -0.31 | 0 100 100 | 32, 67, 116, 132 | 0 |
| 27 | DF | 178/179 (99%) | 1.75 | 64 (35%) 0 0 | 125, 209, 220, 232 | 0 |
| 28 | BG | 176/177 (99%) | -0.43 | 0 100 100 | 27, 57, 103, 128 | 0 |
| 28 | DG | 176/177 (99%) | 1.29 | 40 (22%) 0 0 | 120, 165, 207, 220 | 0 |
| 29 | BH | 149/149 (100%) | 2.09 | 59 (39%) 0 0 | 42, 178, 213, 217 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|----------------|--------|---------------|-----------------------|-------|
| 29 | DH | 149/149 (100%) | 2.48 | 56 (37%) 0 0 | 104, 173, 208, 219 | 0 |
| 30 | BI | 141/142 (99%) | 2.89 | 77 (54%) 0 0 | 199, 245, 286, 294 | 0 |
| 30 | DI | 141/142 (99%) | 5.04 | 117 (82%) 0 0 | 264, 305, 323, 331 | 0 |
| 31 | BJ | 142/142 (100%) | -0.68 | 0 100 100 | 12, 25, 57, 111 | 0 |
| 31 | DJ | 142/142 (100%) | 0.20 | 4 (2%) 53 39 | 76, 110, 134, 153 | 0 |
| 32 | BK | 122/123 (99%) | -0.67 | 0 100 100 | 20, 32, 76, 121 | 0 |
| 32 | DK | 122/123 (99%) | 0.10 | 3 (2%) 57 43 | 71, 93, 127, 142 | 0 |
| 33 | BL | 143/144 (99%) | -0.69 | 0 100 100 | 13, 38, 74, 100 | 0 |
| 33 | DL | 143/144 (99%) | 1.09 | 28 (19%) 1 0 | 80, 150, 189, 202 | 0 |
| 34 | BM | 136/136 (100%) | -0.71 | 0 100 100 | 14, 30, 61, 99 | 0 |
| 34 | DM | 136/136 (100%) | 0.12 | 1 (0%) 87 81 | 73, 117, 143, 161 | 0 |
| 35 | BN | 120/127 (94%) | -0.70 | 0 100 100 | 14, 28, 44, 97 | 0 |
| 35 | DN | 120/127 (94%) | 0.56 | 7 (5%) 23 12 | 89, 121, 152, 171 | 0 |
| 36 | BO | 116/117 (99%) | -0.52 | 0 100 100 | 30, 46, 73, 101 | 0 |
| 36 | DO | 116/117 (99%) | 1.53 | 41 (35%) 0 0 | 146, 178, 207, 216 | 0 |
| 37 | BP | 114/115 (99%) | -0.58 | 0 100 100 | 22, 39, 90, 131 | 0 |
| 37 | DP | 114/115 (99%) | 0.37 | 9 (7%) 12 7 | 80, 108, 135, 143 | 0 |
| 38 | BQ | 117/118 (99%) | -0.68 | 1 (0%) 84 76 | 9, 22, 46, 96 | 0 |
| 38 | DQ | 117/118 (99%) | 0.67 | 9 (7%) 13 7 | 87, 112, 154, 191 | 0 |
| 39 | BR | 103/103 (100%) | -0.60 | 1 (0%) 82 73 | 11, 33, 75, 91 | 0 |
| 39 | DR | 103/103 (100%) | 1.22 | 28 (27%) 0 0 | 85, 135, 170, 190 | 0 |
| 40 | BS | 110/110 (100%) | -0.78 | 0 100 100 | 14, 23, 57, 118 | 0 |
| 40 | DS | 110/110 (100%) | 0.81 | 16 (14%) 2 1 | 76, 120, 154, 170 | 0 |
| 41 | BT | 93/100 (93%) | -0.17 | 2 (2%) 62 48 | 28, 51, 112, 140 | 0 |
| 41 | DT | 93/100 (93%) | 1.34 | 22 (23%) 0 0 | 132, 189, 223, 233 | 0 |
| 42 | BU | 102/104 (98%) | -0.26 | 3 (2%) 51 37 | 29, 54, 100, 155 | 0 |
| 42 | DU | 102/104 (98%) | 2.20 | 55 (53%) 0 0 | 153, 202, 250, 283 | 0 |
| 43 | BV | 94/94 (100%) | -0.68 | 0 100 100 | 17, 39, 79, 105 | 0 |
| 43 | DV | 94/94 (100%) | 0.46 | 6 (6%) 19 10 | 113, 143, 165, 179 | 0 |
| 44 | BW | 79/85 (92%) | -0.27 | 1 (1%) 77 65 | 18, 39, 94, 127 | 0 |
| 44 | DW | 79/85 (92%) | 1.30 | 18 (22%) 0 0 | 99, 157, 191, 201 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|-------------------|--------|----------------|-----------------------|-------|
| 45 | BX | 77/78 (98%) | -0.53 | 0 100 100 | 23, 43, 80, 104 | 0 |
| 45 | DX | 77/78 (98%) | 0.57 | 5 (6%) 19 10 | 84, 124, 170, 177 | 0 |
| 46 | BY | 63/63 (100%) | -0.19 | 1 (1%) 72 59 | 41, 68, 113, 128 | 0 |
| 46 | DY | 63/63 (100%) | 1.40 | 21 (33%) 0 0 | 180, 226, 268, 278 | 0 |
| 47 | BZ | 58/59 (98%) | -0.67 | 0 100 100 | 13, 27, 56, 97 | 0 |
| 47 | DZ | 58/59 (98%) | 0.63 | 7 (12%) 4 2 | 97, 143, 180, 187 | 0 |
| 48 | B0 | 56/57 (98%) | -0.80 | 0 100 100 | 12, 29, 61, 113 | 0 |
| 48 | D0 | 56/57 (98%) | 1.05 | 9 (16%) 1 1 | 84, 128, 163, 172 | 0 |
| 49 | B1 | 50/55 (90%) | -0.19 | 1 (2%) 65 51 | 29, 50, 91, 116 | 0 |
| 49 | D1 | 50/55 (90%) | 1.64 | 16 (32%) 0 0 | 110, 143, 159, 168 | 0 |
| 50 | B2 | 46/46 (100%) | -0.65 | 0 100 100 | 20, 30, 49, 131 | 0 |
| 50 | D2 | 46/46 (100%) | 0.76 | 2 (4%) 35 22 | 87, 115, 137, 147 | 0 |
| 51 | B3 | 64/65 (98%) | -0.74 | 0 100 100 | 15, 30, 43, 62 | 0 |
| 51 | D3 | 64/65 (98%) | 1.16 | 14 (21%) 0 0 | 93, 126, 150, 169 | 0 |
| 52 | B4 | 38/38 (100%) | -0.56 | 0 100 100 | 19, 33, 62, 87 | 0 |
| 52 | D4 | 38/38 (100%) | 0.92 | 7 (18%) 1 0 | 84, 127, 158, 161 | 0 |
| 53 | CA | 1530/1530 (100%) | 0.15 | 82 (5%) 26 14 | 44, 100, 246, 325 | 0 |
| 54 | DB | 117/117 (100%) | 0.51 | 7 (5%) 22 12 | 108, 175, 209, 221 | 0 |
| All | All | 20431/21074 (96%) | 0.16 | 1514 (7%) 14 8 | 9, 93, 219, 434 | 0 |

The worst 5 of 1514 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|------|------|------|
| 29 | DH | 92 | GLY | 21.3 |
| 22 | BA | 2154 | A | 18.7 |
| 30 | BI | 2 | LYS | 16.5 |
| 30 | DI | 58 | ILE | 16.0 |
| 29 | DH | 91 | PHE | 15.0 |

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 carbohydrates 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, 95th 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 |
|-----|------|-------|------|-------|-------|------|----------------------------|-------|
| 55 | MG | DJ | 201 | 1/1 | -0.26 | 3.56 | 242,242,242,242 | 0 |
| 55 | MG | DA | 3065 | 1/1 | 0.08 | 2.49 | 221,221,221,221 | 0 |
| 55 | MG | DA | 3013 | 1/1 | 0.23 | 0.57 | 211,211,211,211 | 0 |
| 55 | MG | DA | 3132 | 1/1 | 0.31 | 0.76 | 216,216,216,216 | 0 |
| 55 | MG | DA | 3064 | 1/1 | 0.41 | 3.06 | 204,204,204,204 | 0 |
| 55 | MG | DA | 3003 | 1/1 | 0.46 | 1.02 | 210,210,210,210 | 0 |
| 55 | MG | DA | 3006 | 1/1 | 0.47 | 0.20 | 200,200,200,200 | 0 |
| 55 | MG | CA | 1624 | 1/1 | 0.48 | 0.75 | 120,120,120,120 | 0 |
| 55 | MG | DA | 3074 | 1/1 | 0.49 | 0.14 | 194,194,194,194 | 0 |
| 55 | MG | DA | 3050 | 1/1 | 0.52 | 0.19 | 209,209,209,209 | 0 |
| 55 | MG | DA | 3063 | 1/1 | 0.52 | 1.08 | 191,191,191,191 | 0 |
| 55 | MG | BA | 3056 | 1/1 | 0.54 | 0.36 | 187,187,187,187 | 0 |
| 55 | MG | DA | 3005 | 1/1 | 0.54 | 0.84 | 208,208,208,208 | 0 |
| 55 | MG | DA | 3039 | 1/1 | 0.55 | 0.47 | 220,220,220,220 | 0 |
| 55 | MG | DA | 3110 | 1/1 | 0.55 | 1.25 | 181,181,181,181 | 0 |
| 55 | MG | CA | 1636 | 1/1 | 0.59 | 0.26 | 171,171,171,171 | 0 |
| 55 | MG | DA | 3027 | 1/1 | 0.60 | 1.18 | 195,195,195,195 | 0 |
| 55 | MG | DA | 3134 | 1/1 | 0.61 | 0.42 | 198,198,198,198 | 0 |
| 55 | MG | AA | 1611 | 1/1 | 0.62 | 0.23 | 176,176,176,176 | 0 |
| 55 | MG | DA | 3002 | 1/1 | 0.63 | 0.91 | 179,179,179,179 | 0 |
| 55 | MG | BA | 3015 | 1/1 | 0.64 | 0.36 | 221,221,221,221 | 0 |
| 55 | MG | DA | 3121 | 1/1 | 0.64 | 0.22 | 97,97,97,97 | 0 |
| 55 | MG | DA | 3007 | 1/1 | 0.65 | 0.30 | 198,198,198,198 | 0 |
| 55 | MG | DA | 3109 | 1/1 | 0.65 | 0.38 | 165,165,165,165 | 0 |
| 55 | MG | DA | 3018 | 1/1 | 0.66 | 0.19 | 194,194,194,194 | 0 |
| 55 | MG | DA | 3099 | 1/1 | 0.66 | 0.15 | 142,142,142,142 | 0 |
| 55 | MG | DA | 3042 | 1/1 | 0.66 | 0.36 | 139,139,139,139 | 0 |
| 55 | MG | DA | 3125 | 1/1 | 0.67 | 0.18 | 77,77,77,77 | 0 |
| 55 | MG | CA | 1603 | 1/1 | 0.67 | 0.23 | 169,169,169,169 | 0 |
| 55 | MG | CA | 1616 | 1/1 | 0.68 | 0.27 | 192,192,192,192 | 0 |
| 55 | MG | DA | 3089 | 1/1 | 0.68 | 0.15 | 169,169,169,169 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(Å ²) | Q<0.9 |
|-----|------|-------|------|-------|------|------|----------------------------|-------|
| 55 | MG | DA | 3010 | 1/1 | 0.68 | 1.13 | 200,200,200,200 | 0 |
| 55 | MG | DA | 3098 | 1/1 | 0.68 | 0.44 | 158,158,158,158 | 0 |
| 55 | MG | DA | 3107 | 1/1 | 0.68 | 0.26 | 169,169,169,169 | 0 |
| 55 | MG | DA | 3060 | 1/1 | 0.69 | 0.33 | 198,198,198,198 | 0 |
| 55 | MG | DA | 3020 | 1/1 | 0.70 | 0.69 | 207,207,207,207 | 0 |
| 55 | MG | DA | 3033 | 1/1 | 0.70 | 0.14 | 113,113,113,113 | 0 |
| 55 | MG | DA | 3094 | 1/1 | 0.71 | 0.20 | 172,172,172,172 | 0 |
| 55 | MG | DA | 3100 | 1/1 | 0.72 | 0.18 | 171,171,171,171 | 0 |
| 55 | MG | DA | 3129 | 1/1 | 0.72 | 1.27 | 194,194,194,194 | 0 |
| 55 | MG | CA | 1629 | 1/1 | 0.72 | 0.10 | 174,174,174,174 | 0 |
| 55 | MG | DA | 3084 | 1/1 | 0.72 | 0.16 | 178,178,178,178 | 0 |
| 55 | MG | DA | 3127 | 1/1 | 0.73 | 0.33 | 97,97,97,97 | 0 |
| 55 | MG | DA | 3046 | 1/1 | 0.73 | 0.14 | 173,173,173,173 | 0 |
| 55 | MG | DA | 3135 | 1/1 | 0.75 | 0.26 | 162,162,162,162 | 0 |
| 55 | MG | CA | 1602 | 1/1 | 0.75 | 0.15 | 120,120,120,120 | 0 |
| 55 | MG | DA | 3108 | 1/1 | 0.77 | 0.12 | 103,103,103,103 | 0 |
| 55 | MG | DA | 3040 | 1/1 | 0.78 | 0.17 | 117,117,117,117 | 0 |
| 55 | MG | CA | 1619 | 1/1 | 0.78 | 0.44 | 180,180,180,180 | 0 |
| 55 | MG | BA | 3048 | 1/1 | 0.79 | 0.10 | 144,144,144,144 | 0 |
| 55 | MG | DA | 3052 | 1/1 | 0.79 | 0.15 | 110,110,110,110 | 0 |
| 55 | MG | DA | 3044 | 1/1 | 0.79 | 0.13 | 138,138,138,138 | 0 |
| 55 | MG | BB | 201 | 1/1 | 0.80 | 0.45 | 187,187,187,187 | 0 |
| 55 | MG | BA | 3057 | 1/1 | 0.80 | 0.51 | 219,219,219,219 | 0 |
| 55 | MG | DA | 3085 | 1/1 | 0.80 | 0.43 | 169,169,169,169 | 0 |
| 55 | MG | DA | 3034 | 1/1 | 0.80 | 0.23 | 105,105,105,105 | 0 |
| 55 | MG | DA | 3070 | 1/1 | 0.80 | 0.35 | 209,209,209,209 | 0 |
| 55 | MG | DA | 3048 | 1/1 | 0.80 | 0.17 | 128,128,128,128 | 0 |
| 55 | MG | DA | 3015 | 1/1 | 0.81 | 0.84 | 183,183,183,183 | 0 |
| 55 | MG | DA | 3075 | 1/1 | 0.82 | 1.63 | 207,207,207,207 | 0 |
| 55 | MG | DA | 3029 | 1/1 | 0.82 | 0.55 | 205,205,205,205 | 0 |
| 55 | MG | DA | 3119 | 1/1 | 0.82 | 0.09 | 86,86,86,86 | 0 |
| 55 | MG | DA | 3126 | 1/1 | 0.82 | 0.44 | 164,164,164,164 | 0 |
| 55 | MG | DA | 3049 | 1/1 | 0.83 | 0.14 | 99,99,99,99 | 0 |
| 55 | MG | AA | 1618 | 1/1 | 0.83 | 0.12 | 68,68,68,68 | 0 |
| 55 | MG | DA | 3051 | 1/1 | 0.83 | 0.14 | 140,140,140,140 | 0 |
| 55 | MG | AA | 1636 | 1/1 | 0.83 | 0.61 | 164,164,164,164 | 0 |
| 55 | MG | DA | 3131 | 1/1 | 0.83 | 1.37 | 204,204,204,204 | 0 |
| 55 | MG | DA | 3008 | 1/1 | 0.83 | 0.11 | 100,100,100,100 | 0 |
| 55 | MG | DA | 3123 | 1/1 | 0.83 | 0.09 | 99,99,99,99 | 0 |
| 55 | MG | DA | 3111 | 1/1 | 0.83 | 0.20 | 166,166,166,166 | 0 |
| 55 | MG | DA | 3077 | 1/1 | 0.83 | 0.20 | 159,159,159,159 | 0 |
| 55 | MG | BA | 3004 | 1/1 | 0.83 | 0.16 | 155,155,155,155 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-----------------------------|-------|
| 55 | MG | AA | 1603 | 1/1 | 0.83 | 0.13 | 124,124,124,124 | 0 |
| 55 | MG | CA | 1640 | 1/1 | 0.84 | 0.20 | 161,161,161,161 | 0 |
| 55 | MG | DA | 3080 | 1/1 | 0.84 | 0.09 | 74,74,74,74 | 0 |
| 55 | MG | CA | 1632 | 1/1 | 0.84 | 0.16 | 160,160,160,160 | 0 |
| 55 | MG | DA | 3058 | 1/1 | 0.84 | 0.36 | 171,171,171,171 | 0 |
| 55 | MG | CA | 1617 | 1/1 | 0.85 | 0.23 | 220,220,220,220 | 0 |
| 55 | MG | CA | 1610 | 1/1 | 0.85 | 0.18 | 145,145,145,145 | 0 |
| 55 | MG | DA | 3062 | 1/1 | 0.85 | 0.08 | 113,113,113,113 | 0 |
| 55 | MG | DA | 3059 | 1/1 | 0.85 | 0.53 | 188,188,188,188 | 0 |
| 55 | MG | CA | 1605 | 1/1 | 0.85 | 0.16 | 48,48,48,48 | 0 |
| 55 | MG | BA | 3049 | 1/1 | 0.85 | 0.16 | 104,104,104,104 | 0 |
| 55 | MG | DA | 3115 | 1/1 | 0.85 | 0.22 | 151,151,151,151 | 0 |
| 55 | MG | CA | 1627 | 1/1 | 0.86 | 0.24 | 166,166,166,166 | 0 |
| 55 | MG | CA | 1638 | 1/1 | 0.86 | 0.15 | 155,155,155,155 | 0 |
| 55 | MG | CA | 1623 | 1/1 | 0.86 | 0.21 | 96,96,96,96 | 0 |
| 55 | MG | DA | 3083 | 1/1 | 0.86 | 0.14 | 144,144,144,144 | 0 |
| 55 | MG | DA | 3093 | 1/1 | 0.86 | 0.16 | 121,121,121,121 | 0 |
| 55 | MG | DA | 3031 | 1/1 | 0.86 | 0.13 | 113,113,113,113 | 0 |
| 55 | MG | DA | 3087 | 1/1 | 0.86 | 0.16 | 87,87,87,87 | 0 |
| 55 | MG | CA | 1635 | 1/1 | 0.86 | 0.14 | 76,76,76,76 | 0 |
| 55 | MG | CA | 1607 | 1/1 | 0.86 | 0.18 | 154,154,154,154 | 0 |
| 55 | MG | DA | 3061 | 1/1 | 0.86 | 0.40 | 160,160,160,160 | 0 |
| 55 | MG | AA | 1616 | 1/1 | 0.87 | 0.08 | 126,126,126,126 | 0 |
| 55 | MG | DA | 3028 | 1/1 | 0.87 | 0.16 | 162,162,162,162 | 0 |
| 55 | MG | DA | 3072 | 1/1 | 0.87 | 0.24 | 80,80,80,80 | 0 |
| 55 | MG | CA | 1622 | 1/1 | 0.87 | 0.09 | 169,169,169,169 | 0 |
| 55 | MG | DA | 3041 | 1/1 | 0.87 | 0.17 | 77,77,77,77 | 0 |
| 55 | MG | CA | 1634 | 1/1 | 0.87 | 0.11 | 112,112,112,112 | 0 |
| 55 | MG | BA | 3035 | 1/1 | 0.88 | 0.35 | 168,168,168,168 | 0 |
| 55 | MG | DA | 3037 | 1/1 | 0.88 | 0.22 | 176,176,176,176 | 0 |
| 55 | MG | BA | 3070 | 1/1 | 0.88 | 0.11 | 164,164,164,164 | 0 |
| 55 | MG | DA | 3026 | 1/1 | 0.88 | 0.17 | 145,145,145,145 | 0 |
| 55 | MG | AA | 1624 | 1/1 | 0.88 | 0.12 | 101,101,101,101 | 0 |
| 55 | MG | DA | 3117 | 1/1 | 0.88 | 0.13 | 67,67,67,67 | 0 |
| 55 | MG | DA | 3057 | 1/1 | 0.88 | 0.15 | 104,104,104,104 | 0 |
| 55 | MG | AA | 1619 | 1/1 | 0.88 | 0.46 | 165,165,165,165 | 0 |
| 55 | MG | BA | 3091 | 1/1 | 0.88 | 0.08 | 47,47,47,47 | 0 |
| 55 | MG | CA | 1612 | 1/1 | 0.88 | 0.33 | 117,117,117,117 | 0 |
| 55 | MG | DA | 3014 | 1/1 | 0.89 | 0.24 | 151,151,151,151 | 0 |
| 55 | MG | CA | 1611 | 1/1 | 0.89 | 0.16 | 108,108,108,108 | 0 |
| 55 | MG | DA | 3004 | 1/1 | 0.89 | 0.17 | 118,118,118,118 | 0 |
| 55 | MG | CA | 1630 | 1/1 | 0.89 | 0.11 | 121,121,121,121 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-----------------------------|-------|
| 55 | MG | AA | 1641 | 1/1 | 0.89 | 0.17 | 131,131,131,131 | 0 |
| 55 | MG | DA | 3032 | 1/1 | 0.89 | 0.17 | 71,71,71,71 | 0 |
| 55 | MG | DA | 3101 | 1/1 | 0.89 | 0.36 | 127,127,127,127 | 0 |
| 55 | MG | DA | 3047 | 1/1 | 0.89 | 0.11 | 82,82,82,82 | 0 |
| 55 | MG | DA | 3092 | 1/1 | 0.89 | 0.19 | 157,157,157,157 | 0 |
| 55 | MG | CA | 1608 | 1/1 | 0.89 | 0.17 | 60,60,60,60 | 0 |
| 55 | MG | BA | 3058 | 1/1 | 0.89 | 0.23 | 164,164,164,164 | 0 |
| 55 | MG | DA | 3096 | 1/1 | 0.89 | 0.19 | 107,107,107,107 | 0 |
| 55 | MG | BA | 3001 | 1/1 | 0.90 | 0.12 | 109,109,109,109 | 0 |
| 55 | MG | DA | 3017 | 1/1 | 0.90 | 0.23 | 86,86,86,86 | 0 |
| 55 | MG | AA | 1608 | 1/1 | 0.90 | 0.11 | 106,106,106,106 | 0 |
| 55 | MG | BA | 3080 | 1/1 | 0.90 | 0.08 | 31,31,31,31 | 0 |
| 55 | MG | DA | 3011 | 1/1 | 0.90 | 0.16 | 126,126,126,126 | 0 |
| 55 | MG | CA | 1615 | 1/1 | 0.90 | 0.25 | 136,136,136,136 | 0 |
| 55 | MG | BA | 3093 | 1/1 | 0.90 | 0.16 | 110,110,110,110 | 0 |
| 55 | MG | AA | 1630 | 1/1 | 0.90 | 0.11 | 163,163,163,163 | 0 |
| 55 | MG | DA | 3104 | 1/1 | 0.90 | 0.20 | 109,109,109,109 | 0 |
| 55 | MG | DA | 3079 | 1/1 | 0.90 | 0.47 | 184,184,184,184 | 0 |
| 55 | MG | CA | 1621 | 1/1 | 0.90 | 0.15 | 40,40,40,40 | 0 |
| 55 | MG | AA | 1613 | 1/1 | 0.90 | 0.12 | 102,102,102,102 | 0 |
| 55 | MG | DA | 3023 | 1/1 | 0.90 | 0.13 | 71,71,71,71 | 0 |
| 55 | MG | DA | 3001 | 1/1 | 0.90 | 0.08 | 109,109,109,109 | 0 |
| 55 | MG | BA | 3094 | 1/1 | 0.90 | 0.06 | 37,37,37,37 | 0 |
| 55 | MG | BA | 3063 | 1/1 | 0.91 | 0.11 | 42,42,42,42 | 0 |
| 55 | MG | DA | 3122 | 1/1 | 0.91 | 0.17 | 113,113,113,113 | 0 |
| 55 | MG | CA | 1614 | 1/1 | 0.91 | 0.57 | 178,178,178,178 | 0 |
| 55 | MG | CA | 1618 | 1/1 | 0.91 | 0.14 | 90,90,90,90 | 0 |
| 55 | MG | DA | 3043 | 1/1 | 0.91 | 0.15 | 104,104,104,104 | 0 |
| 55 | MG | DA | 3105 | 1/1 | 0.91 | 0.17 | 62,62,62,62 | 0 |
| 55 | MG | CA | 1639 | 1/1 | 0.91 | 0.16 | 149,149,149,149 | 0 |
| 55 | MG | BA | 3046 | 1/1 | 0.91 | 0.13 | 23,23,23,23 | 0 |
| 55 | MG | BA | 3003 | 1/1 | 0.91 | 0.10 | 63,63,63,63 | 0 |
| 55 | MG | DA | 3120 | 1/1 | 0.91 | 0.12 | 84,84,84,84 | 0 |
| 55 | MG | DA | 3124 | 1/1 | 0.91 | 0.32 | 165,165,165,165 | 0 |
| 55 | MG | CA | 1601 | 1/1 | 0.91 | 0.10 | 124,124,124,124 | 0 |
| 55 | MG | DA | 3066 | 1/1 | 0.91 | 0.10 | 94,94,94,94 | 0 |
| 55 | MG | DA | 3053 | 1/1 | 0.91 | 0.14 | 59,59,59,59 | 0 |
| 55 | MG | BA | 3089 | 1/1 | 0.91 | 0.15 | 134,134,134,134 | 0 |
| 55 | MG | CA | 1626 | 1/1 | 0.91 | 0.19 | 40,40,40,40 | 0 |
| 55 | MG | BA | 3137 | 1/1 | 0.91 | 0.36 | 188,188,188,188 | 0 |
| 55 | MG | DA | 3116 | 1/1 | 0.91 | 0.27 | 154,154,154,154 | 0 |
| 55 | MG | BA | 3060 | 1/1 | 0.92 | 0.34 | 129,129,129,129 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-----------------------------|-------|
| 55 | MG | DA | 3055 | 1/1 | 0.92 | 0.06 | 75,75,75,75 | 0 |
| 55 | MG | BA | 3092 | 1/1 | 0.92 | 0.18 | 75,75,75,75 | 0 |
| 55 | MG | BA | 3113 | 1/1 | 0.92 | 0.09 | 60,60,60,60 | 0 |
| 56 | ZN | D4 | 101 | 1/1 | 0.92 | 0.07 | 156,156,156,156 | 0 |
| 55 | MG | DA | 3016 | 1/1 | 0.92 | 0.16 | 169,169,169,169 | 0 |
| 55 | MG | BA | 3100 | 1/1 | 0.92 | 0.11 | 47,47,47,47 | 0 |
| 55 | MG | DA | 3036 | 1/1 | 0.92 | 0.09 | 97,97,97,97 | 0 |
| 55 | MG | BA | 3037 | 1/1 | 0.92 | 0.32 | 171,171,171,171 | 0 |
| 55 | MG | CA | 1628 | 1/1 | 0.92 | 1.03 | 204,204,204,204 | 0 |
| 55 | MG | DA | 3088 | 1/1 | 0.92 | 0.16 | 160,160,160,160 | 0 |
| 55 | MG | CA | 1625 | 1/1 | 0.92 | 0.30 | 118,118,118,118 | 0 |
| 55 | MG | AA | 1615 | 1/1 | 0.92 | 0.18 | 164,164,164,164 | 0 |
| 55 | MG | DB | 201 | 1/1 | 0.92 | 0.08 | 117,117,117,117 | 0 |
| 55 | MG | DA | 3130 | 1/1 | 0.92 | 0.37 | 102,102,102,102 | 0 |
| 55 | MG | CA | 1620 | 1/1 | 0.92 | 0.31 | 172,172,172,172 | 0 |
| 55 | MG | BA | 3088 | 1/1 | 0.92 | 0.19 | 81,81,81,81 | 0 |
| 55 | MG | BA | 3132 | 1/1 | 0.92 | 0.39 | 202,202,202,202 | 0 |
| 55 | MG | BA | 3136 | 1/1 | 0.92 | 0.17 | 150,150,150,150 | 0 |
| 55 | MG | CA | 1613 | 1/1 | 0.93 | 0.08 | 96,96,96,96 | 0 |
| 55 | MG | BA | 3077 | 1/1 | 0.93 | 0.22 | 90,90,90,90 | 0 |
| 55 | MG | BA | 3112 | 1/1 | 0.93 | 0.15 | 121,121,121,121 | 0 |
| 55 | MG | BA | 3053 | 1/1 | 0.93 | 0.10 | 30,30,30,30 | 0 |
| 55 | MG | DA | 3114 | 1/1 | 0.93 | 0.09 | 95,95,95,95 | 0 |
| 55 | MG | BA | 3029 | 1/1 | 0.93 | 0.16 | 43,43,43,43 | 0 |
| 55 | MG | DA | 3097 | 1/1 | 0.93 | 0.16 | 110,110,110,110 | 0 |
| 55 | MG | DA | 3073 | 1/1 | 0.93 | 0.13 | 141,141,141,141 | 0 |
| 55 | MG | CA | 1606 | 1/1 | 0.93 | 0.11 | 64,64,64,64 | 0 |
| 55 | MG | AA | 1640 | 1/1 | 0.93 | 0.13 | 109,109,109,109 | 0 |
| 55 | MG | BA | 3007 | 1/1 | 0.93 | 0.09 | 67,67,67,67 | 0 |
| 55 | MG | BB | 202 | 1/1 | 0.93 | 0.10 | 67,67,67,67 | 0 |
| 55 | MG | DA | 3118 | 1/1 | 0.93 | 0.14 | 77,77,77,77 | 0 |
| 55 | MG | DA | 3068 | 1/1 | 0.94 | 0.08 | 65,65,65,65 | 0 |
| 55 | MG | DA | 3082 | 1/1 | 0.94 | 0.12 | 83,83,83,83 | 0 |
| 55 | MG | BA | 3120 | 1/1 | 0.94 | 0.26 | 156,156,156,156 | 0 |
| 55 | MG | DA | 3133 | 1/1 | 0.94 | 0.09 | 84,84,84,84 | 0 |
| 55 | MG | AA | 1614 | 1/1 | 0.94 | 0.07 | 55,55,55,55 | 0 |
| 55 | MG | BA | 3116 | 1/1 | 0.94 | 0.13 | 133,133,133,133 | 0 |
| 55 | MG | DA | 3102 | 1/1 | 0.94 | 0.18 | 83,83,83,83 | 0 |
| 55 | MG | DA | 3112 | 1/1 | 0.94 | 0.11 | 148,148,148,148 | 0 |
| 55 | MG | DA | 3106 | 1/1 | 0.94 | 0.17 | 69,69,69,69 | 0 |
| 55 | MG | DA | 3035 | 1/1 | 0.94 | 0.15 | 87,87,87,87 | 0 |
| 55 | MG | BA | 3072 | 1/1 | 0.94 | 0.36 | 94,94,94,94 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-----------------------------|-------|
| 55 | MG | DA | 3030 | 1/1 | 0.94 | 0.17 | 144,144,144,144 | 0 |
| 55 | MG | DA | 3071 | 1/1 | 0.94 | 0.11 | 64,64,64,64 | 0 |
| 55 | MG | DA | 3086 | 1/1 | 0.94 | 0.23 | 122,122,122,122 | 0 |
| 55 | MG | DA | 3024 | 1/1 | 0.94 | 0.04 | 85,85,85,85 | 0 |
| 55 | MG | BA | 3026 | 1/1 | 0.94 | 0.59 | 152,152,152,152 | 0 |
| 55 | MG | BA | 3086 | 1/1 | 0.94 | 0.12 | 45,45,45,45 | 0 |
| 55 | MG | BB | 203 | 1/1 | 0.94 | 0.10 | 37,37,37,37 | 0 |
| 55 | MG | BA | 3119 | 1/1 | 0.94 | 0.12 | 88,88,88,88 | 0 |
| 55 | MG | DA | 3054 | 1/1 | 0.94 | 0.10 | 75,75,75,75 | 0 |
| 55 | MG | AA | 1628 | 1/1 | 0.94 | 0.32 | 96,96,96,96 | 0 |
| 55 | MG | DA | 3025 | 1/1 | 0.94 | 0.17 | 108,108,108,108 | 0 |
| 55 | MG | BA | 3124 | 1/1 | 0.94 | 0.09 | 39,39,39,39 | 0 |
| 55 | MG | AA | 1639 | 1/1 | 0.94 | 0.10 | 96,96,96,96 | 0 |
| 55 | MG | BA | 3087 | 1/1 | 0.95 | 0.12 | 13,13,13,13 | 0 |
| 55 | MG | AA | 1623 | 1/1 | 0.95 | 0.16 | 70,70,70,70 | 0 |
| 55 | MG | DA | 3067 | 1/1 | 0.95 | 0.09 | 70,70,70,70 | 0 |
| 55 | MG | BA | 3121 | 1/1 | 0.95 | 0.10 | 12,12,12,12 | 0 |
| 55 | MG | BA | 3002 | 1/1 | 0.95 | 0.10 | 81,81,81,81 | 0 |
| 55 | MG | AA | 1620 | 1/1 | 0.95 | 0.10 | 107,107,107,107 | 0 |
| 55 | MG | AA | 1602 | 1/1 | 0.95 | 0.12 | 121,121,121,121 | 0 |
| 55 | MG | DA | 3045 | 1/1 | 0.95 | 0.16 | 102,102,102,102 | 0 |
| 55 | MG | AA | 1629 | 1/1 | 0.95 | 0.16 | 58,58,58,58 | 0 |
| 55 | MG | AA | 1605 | 1/1 | 0.95 | 0.06 | 123,123,123,123 | 0 |
| 55 | MG | BA | 3134 | 1/1 | 0.95 | 0.54 | 137,137,137,137 | 0 |
| 55 | MG | BA | 3019 | 1/1 | 0.95 | 0.07 | 39,39,39,39 | 0 |
| 55 | MG | AA | 1635 | 1/1 | 0.95 | 0.13 | 64,64,64,64 | 0 |
| 55 | MG | CA | 1604 | 1/1 | 0.95 | 0.07 | 71,71,71,71 | 0 |
| 55 | MG | DA | 3081 | 1/1 | 0.95 | 0.15 | 141,141,141,141 | 0 |
| 55 | MG | BA | 3069 | 1/1 | 0.95 | 0.07 | 14,14,14,14 | 0 |
| 55 | MG | DA | 3128 | 1/1 | 0.95 | 0.21 | 153,153,153,153 | 0 |
| 55 | MG | BA | 3117 | 1/1 | 0.95 | 0.19 | 23,23,23,23 | 0 |
| 55 | MG | AA | 1626 | 1/1 | 0.95 | 0.18 | 39,39,39,39 | 0 |
| 55 | MG | BA | 3031 | 1/1 | 0.95 | 0.13 | 11,11,11,11 | 0 |
| 55 | MG | AA | 1643 | 1/1 | 0.95 | 0.05 | 35,35,35,35 | 0 |
| 55 | MG | BA | 3065 | 1/1 | 0.95 | 0.08 | 26,26,26,26 | 0 |
| 55 | MG | BA | 3098 | 1/1 | 0.95 | 0.20 | 60,60,60,60 | 0 |
| 55 | MG | DA | 3095 | 1/1 | 0.95 | 0.14 | 114,114,114,114 | 0 |
| 55 | MG | CA | 1637 | 1/1 | 0.95 | 0.20 | 100,100,100,100 | 0 |
| 55 | MG | AA | 1604 | 1/1 | 0.95 | 0.10 | 98,98,98,98 | 0 |
| 55 | MG | DA | 3069 | 1/1 | 0.95 | 0.07 | 79,79,79,79 | 0 |
| 55 | MG | CA | 1631 | 1/1 | 0.96 | 0.18 | 92,92,92,92 | 0 |
| 55 | MG | BA | 3126 | 1/1 | 0.96 | 0.14 | 21,21,21,21 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-----------------------------|-------|
| 55 | MG | AA | 1607 | 1/1 | 0.96 | 0.11 | 62,62,62,62 | 0 |
| 55 | MG | DA | 3038 | 1/1 | 0.96 | 0.24 | 97,97,97,97 | 0 |
| 55 | MG | CA | 1642 | 1/1 | 0.96 | 0.06 | 78,78,78,78 | 0 |
| 55 | MG | AA | 1631 | 1/1 | 0.96 | 0.06 | 165,165,165,165 | 0 |
| 55 | MG | BA | 3005 | 1/1 | 0.96 | 0.09 | 86,86,86,86 | 0 |
| 55 | MG | AA | 1621 | 1/1 | 0.96 | 0.08 | 139,139,139,139 | 0 |
| 55 | MG | AA | 1601 | 1/1 | 0.96 | 0.09 | 82,82,82,82 | 0 |
| 55 | MG | BA | 3010 | 1/1 | 0.96 | 0.07 | 29,29,29,29 | 0 |
| 55 | MG | BA | 3030 | 1/1 | 0.96 | 0.08 | 57,57,57,57 | 0 |
| 55 | MG | DA | 3113 | 1/1 | 0.96 | 0.08 | 59,59,59,59 | 0 |
| 55 | MG | BA | 3067 | 1/1 | 0.96 | 0.10 | 21,21,21,21 | 0 |
| 55 | MG | AA | 1617 | 1/1 | 0.96 | 0.09 | 83,83,83,83 | 0 |
| 55 | MG | CA | 1641 | 1/1 | 0.96 | 0.08 | 68,68,68,68 | 0 |
| 55 | MG | AA | 1606 | 1/1 | 0.96 | 0.14 | 38,38,38,38 | 0 |
| 55 | MG | DA | 3019 | 1/1 | 0.96 | 0.14 | 161,161,161,161 | 0 |
| 55 | MG | BA | 3105 | 1/1 | 0.96 | 0.23 | 16,16,16,16 | 0 |
| 55 | MG | CA | 1633 | 1/1 | 0.96 | 0.07 | 61,61,61,61 | 0 |
| 55 | MG | BA | 3011 | 1/1 | 0.96 | 0.19 | 120,120,120,120 | 0 |
| 55 | MG | BA | 3032 | 1/1 | 0.96 | 0.11 | 31,31,31,31 | 0 |
| 55 | MG | DA | 3091 | 1/1 | 0.96 | 0.13 | 95,95,95,95 | 0 |
| 56 | ZN | B4 | 101 | 1/1 | 0.96 | 0.09 | 51,51,51,51 | 0 |
| 55 | MG | BA | 3079 | 1/1 | 0.96 | 0.07 | 99,99,99,99 | 0 |
| 55 | MG | BA | 3039 | 1/1 | 0.96 | 0.08 | 9,9,9,9 | 0 |
| 55 | MG | BA | 3111 | 1/1 | 0.96 | 0.06 | 47,47,47,47 | 0 |
| 55 | MG | BA | 3016 | 1/1 | 0.96 | 0.05 | 64,64,64,64 | 0 |
| 55 | MG | BA | 3130 | 1/1 | 0.96 | 0.13 | 8,8,8,8 | 0 |
| 55 | MG | BA | 3062 | 1/1 | 0.96 | 0.34 | 193,193,193,193 | 0 |
| 55 | MG | BA | 3051 | 1/1 | 0.96 | 0.09 | 71,71,71,71 | 0 |
| 55 | MG | DA | 3103 | 1/1 | 0.96 | 0.12 | 62,62,62,62 | 0 |
| 55 | MG | DA | 3021 | 1/1 | 0.97 | 0.23 | 66,66,66,66 | 0 |
| 55 | MG | AA | 1637 | 1/1 | 0.97 | 0.08 | 85,85,85,85 | 0 |
| 55 | MG | BA | 3082 | 1/1 | 0.97 | 0.07 | 30,30,30,30 | 0 |
| 55 | MG | DA | 3022 | 1/1 | 0.97 | 0.24 | 155,155,155,155 | 0 |
| 55 | MG | AA | 1638 | 1/1 | 0.97 | 0.08 | 29,29,29,29 | 0 |
| 55 | MG | AA | 1625 | 1/1 | 0.97 | 0.05 | 67,67,67,67 | 0 |
| 55 | MG | DA | 3056 | 1/1 | 0.97 | 0.14 | 103,103,103,103 | 0 |
| 55 | MG | BA | 3044 | 1/1 | 0.97 | 0.09 | 34,34,34,34 | 0 |
| 55 | MG | BA | 3073 | 1/1 | 0.97 | 0.12 | 12,12,12,12 | 0 |
| 55 | MG | BB | 204 | 1/1 | 0.97 | 0.10 | 40,40,40,40 | 0 |
| 55 | MG | BA | 3071 | 1/1 | 0.97 | 0.35 | 132,132,132,132 | 0 |
| 55 | MG | BA | 3075 | 1/1 | 0.97 | 0.24 | 119,119,119,119 | 0 |
| 55 | MG | BA | 3045 | 1/1 | 0.97 | 0.19 | 21,21,21,21 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-----------------------------|-------|
| 55 | MG | DA | 3009 | 1/1 | 0.97 | 0.18 | 107,107,107,107 | 0 |
| 55 | MG | BA | 3024 | 1/1 | 0.97 | 0.13 | 16,16,16,16 | 0 |
| 55 | MG | AA | 1632 | 1/1 | 0.97 | 0.07 | 81,81,81,81 | 0 |
| 55 | MG | BA | 3114 | 1/1 | 0.97 | 0.13 | 86,86,86,86 | 0 |
| 55 | MG | BA | 3085 | 1/1 | 0.97 | 0.14 | 116,116,116,116 | 0 |
| 55 | MG | DA | 3090 | 1/1 | 0.97 | 0.13 | 90,90,90,90 | 0 |
| 55 | MG | BA | 3012 | 1/1 | 0.97 | 0.15 | 8,8,8,8 | 0 |
| 55 | MG | BA | 3023 | 1/1 | 0.97 | 0.11 | 11,11,11,11 | 0 |
| 55 | MG | BA | 3036 | 1/1 | 0.98 | 0.14 | 11,11,11,11 | 0 |
| 55 | MG | AA | 1634 | 1/1 | 0.98 | 0.08 | 59,59,59,59 | 0 |
| 55 | MG | BA | 3074 | 1/1 | 0.98 | 0.07 | 59,59,59,59 | 0 |
| 55 | MG | AA | 1627 | 1/1 | 0.98 | 0.25 | 86,86,86,86 | 0 |
| 55 | MG | BA | 3068 | 1/1 | 0.98 | 0.11 | 11,11,11,11 | 0 |
| 55 | MG | BA | 3122 | 1/1 | 0.98 | 0.06 | 64,64,64,64 | 0 |
| 55 | MG | BA | 3081 | 1/1 | 0.98 | 0.08 | 32,32,32,32 | 0 |
| 55 | MG | BA | 3095 | 1/1 | 0.98 | 0.08 | 38,38,38,38 | 0 |
| 55 | MG | AA | 1612 | 1/1 | 0.98 | 0.10 | 60,60,60,60 | 0 |
| 55 | MG | BA | 3050 | 1/1 | 0.98 | 0.12 | 16,16,16,16 | 0 |
| 55 | MG | BA | 3129 | 1/1 | 0.98 | 0.10 | 31,31,31,31 | 0 |
| 55 | MG | BA | 3083 | 1/1 | 0.98 | 0.11 | 42,42,42,42 | 0 |
| 55 | MG | BA | 3033 | 1/1 | 0.98 | 0.09 | 9,9,9,9 | 0 |
| 55 | MG | BA | 3061 | 1/1 | 0.98 | 0.21 | 171,171,171,171 | 0 |
| 55 | MG | BA | 3055 | 1/1 | 0.98 | 0.08 | 25,25,25,25 | 0 |
| 55 | MG | BA | 3018 | 1/1 | 0.98 | 0.07 | 35,35,35,35 | 0 |
| 55 | MG | DA | 3076 | 1/1 | 0.98 | 0.24 | 167,167,167,167 | 0 |
| 55 | MG | BA | 3131 | 1/1 | 0.98 | 0.18 | 17,17,17,17 | 0 |
| 55 | MG | BA | 3078 | 1/1 | 0.98 | 0.07 | 26,26,26,26 | 0 |
| 55 | MG | BA | 3076 | 1/1 | 0.98 | 0.15 | 16,16,16,16 | 0 |
| 55 | MG | BA | 3127 | 1/1 | 0.98 | 0.17 | 43,43,43,43 | 0 |
| 55 | MG | BA | 3014 | 1/1 | 0.98 | 0.20 | 64,64,64,64 | 0 |
| 55 | MG | BA | 3038 | 1/1 | 0.98 | 0.19 | 30,30,30,30 | 0 |
| 55 | MG | BA | 3041 | 1/1 | 0.98 | 0.15 | 19,19,19,19 | 0 |
| 55 | MG | BA | 3118 | 1/1 | 0.98 | 0.07 | 13,13,13,13 | 0 |
| 55 | MG | BA | 3034 | 1/1 | 0.98 | 0.14 | 8,8,8,8 | 0 |
| 55 | MG | BA | 3084 | 1/1 | 0.98 | 0.17 | 58,58,58,58 | 0 |
| 55 | MG | DA | 3078 | 1/1 | 0.98 | 0.20 | 68,68,68,68 | 0 |
| 55 | MG | DA | 3012 | 1/1 | 0.98 | 0.20 | 75,75,75,75 | 0 |
| 55 | MG | BA | 3047 | 1/1 | 0.98 | 0.16 | 20,20,20,20 | 0 |
| 55 | MG | BA | 3109 | 1/1 | 0.98 | 0.15 | 13,13,13,13 | 0 |
| 55 | MG | BA | 3123 | 1/1 | 0.98 | 0.15 | 10,10,10,10 | 0 |
| 55 | MG | AA | 1609 | 1/1 | 0.98 | 0.19 | 71,71,71,71 | 0 |
| 55 | MG | BA | 3115 | 1/1 | 0.98 | 0.13 | 49,49,49,49 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-----------------------------|-------|
| 55 | MG | BA | 3106 | 1/1 | 0.98 | 0.16 | 37,37,37,37 | 0 |
| 55 | MG | BA | 3096 | 1/1 | 0.98 | 0.04 | 40,40,40,40 | 0 |
| 55 | MG | AA | 1622 | 1/1 | 0.98 | 0.14 | 30,30,30,30 | 0 |
| 55 | MG | BA | 3017 | 1/1 | 0.98 | 0.12 | 9,9,9,9 | 0 |
| 55 | MG | BA | 3099 | 1/1 | 0.98 | 0.10 | 82,82,82,82 | 0 |
| 55 | MG | BA | 3028 | 1/1 | 0.98 | 0.20 | 100,100,100,100 | 0 |
| 55 | MG | BA | 3090 | 1/1 | 0.98 | 0.05 | 28,28,28,28 | 0 |
| 55 | MG | BA | 3125 | 1/1 | 0.98 | 0.69 | 162,162,162,162 | 0 |
| 55 | MG | BA | 3022 | 1/1 | 0.98 | 0.07 | 37,37,37,37 | 0 |
| 55 | MG | BA | 3040 | 1/1 | 0.98 | 0.15 | 27,27,27,27 | 0 |
| 55 | MG | CA | 1609 | 1/1 | 0.98 | 0.11 | 83,83,83,83 | 0 |
| 55 | MG | BA | 3043 | 1/1 | 0.99 | 0.05 | 17,17,17,17 | 0 |
| 55 | MG | AA | 1610 | 1/1 | 0.99 | 0.07 | 33,33,33,33 | 0 |
| 55 | MG | BA | 3059 | 1/1 | 0.99 | 0.07 | 36,36,36,36 | 0 |
| 55 | MG | BA | 3006 | 1/1 | 0.99 | 0.06 | 32,32,32,32 | 0 |
| 55 | MG | BA | 3052 | 1/1 | 0.99 | 0.10 | 25,25,25,25 | 0 |
| 55 | MG | BA | 3104 | 1/1 | 0.99 | 0.10 | 22,22,22,22 | 0 |
| 55 | MG | AA | 1633 | 1/1 | 0.99 | 0.10 | 78,78,78,78 | 0 |
| 55 | MG | BA | 3108 | 1/1 | 0.99 | 0.16 | 30,30,30,30 | 0 |
| 55 | MG | BA | 3107 | 1/1 | 0.99 | 0.13 | 11,11,11,11 | 0 |
| 55 | MG | BA | 3020 | 1/1 | 0.99 | 0.29 | 16,16,16,16 | 0 |
| 55 | MG | BA | 3110 | 1/1 | 0.99 | 0.21 | 11,11,11,11 | 0 |
| 55 | MG | BA | 3042 | 1/1 | 0.99 | 0.15 | 18,18,18,18 | 0 |
| 55 | MG | BA | 3021 | 1/1 | 0.99 | 0.06 | 17,17,17,17 | 0 |
| 55 | MG | BA | 3133 | 1/1 | 0.99 | 0.21 | 103,103,103,103 | 0 |
| 55 | MG | BA | 3027 | 1/1 | 0.99 | 0.11 | 31,31,31,31 | 0 |
| 55 | MG | BA | 3025 | 1/1 | 0.99 | 0.12 | 21,21,21,21 | 0 |
| 55 | MG | BA | 3102 | 1/1 | 0.99 | 0.08 | 36,36,36,36 | 0 |
| 55 | MG | BA | 3066 | 1/1 | 0.99 | 0.10 | 18,18,18,18 | 0 |
| 55 | MG | BA | 3097 | 1/1 | 0.99 | 0.07 | 18,18,18,18 | 0 |
| 55 | MG | BA | 3064 | 1/1 | 0.99 | 0.08 | 38,38,38,38 | 0 |
| 55 | MG | BA | 3013 | 1/1 | 0.99 | 0.14 | 8,8,8,8 | 0 |
| 55 | MG | BA | 3054 | 1/1 | 0.99 | 0.09 | 14,14,14,14 | 0 |
| 55 | MG | AA | 1642 | 1/1 | 0.99 | 0.14 | 40,40,40,40 | 0 |
| 55 | MG | BA | 3101 | 1/1 | 0.99 | 0.12 | 27,27,27,27 | 0 |
| 55 | MG | BA | 3008 | 1/1 | 0.99 | 0.12 | 17,17,17,17 | 0 |
| 55 | MG | BA | 3103 | 1/1 | 0.99 | 0.14 | 60,60,60,60 | 0 |
| 55 | MG | BA | 3128 | 1/1 | 0.99 | 0.10 | 18,18,18,18 | 0 |
| 55 | MG | BA | 3135 | 1/1 | 0.99 | 0.12 | 12,12,12,12 | 0 |
| 55 | MG | BA | 3009 | 1/1 | 1.00 | 0.09 | 13,13,13,13 | 0 |

6.5 Other polymers [i](#)

There are no such residues in this entry.