



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:33 PM GMT

PDB ID : 4V5O
Title : CRYSTAL STRUCTURE OF THE EUKARYOTIC 40S RIBOSOMAL SUB-UNIT IN COMPLEX WITH INITIATION FACTOR 1.
Authors : Rabl, J.; Leibundgut, M.; Ataide, S.F.; Haag, A.; Ban, N.
Deposited on : 2010-11-26
Resolution : 3.93 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

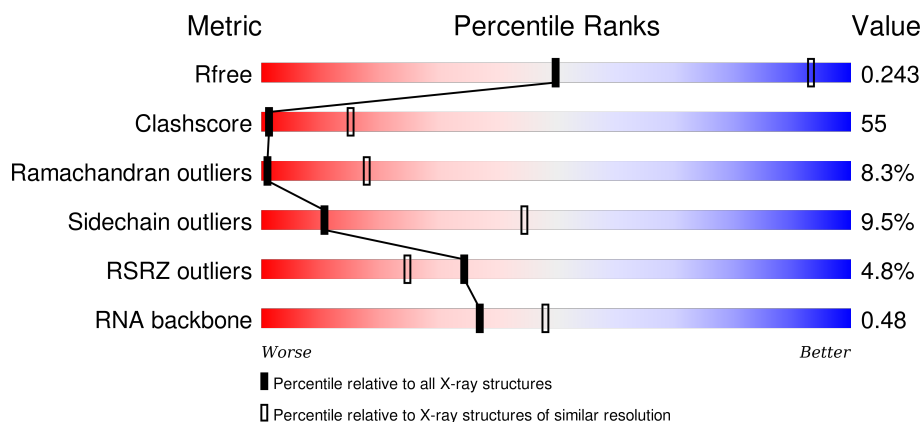
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.93 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} | 91344 | 1007 (4.34-3.54) |
| Clashscore | 102246 | 1042 (4.30-3.58) |
| Ramachandran outliers | 100387 | 1000 (4.30-3.58) |
| Sidechain outliers | 100360 | 1021 (4.32-3.56) |
| RSRZ outliers | 91569 | 1011 (4.34-3.54) |
| RNA backbone | 2183 | 1079 (5.04-2.80) |

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 | A1 | 68 | <div> <div>31%</div> <div>51%</div> <div>16%</div> <div>•</div> </div> |
| 1 | B1 | 68 | <div> <div>26%</div> <div>59%</div> <div>13%</div> <div>•</div> </div> |
| 2 | A2 | 208 | <div> <div>27%</div> <div>20%</div> <div>66%</div> <div>13%</div> </div> |
| 2 | B2 | 208 | <div> <div>7%</div> <div>19%</div> <div>67%</div> <div>13%</div> </div> |

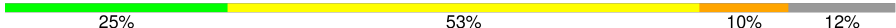

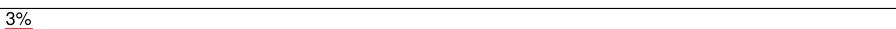
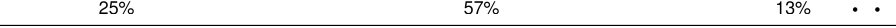
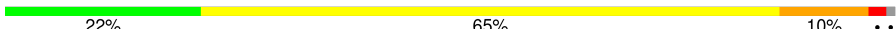

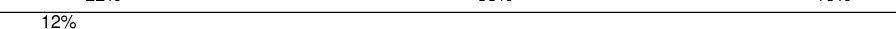



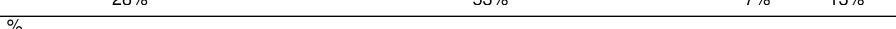

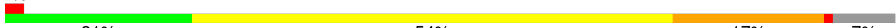
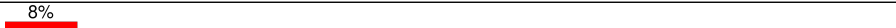
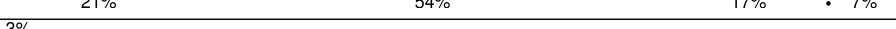

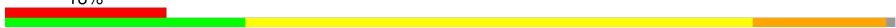
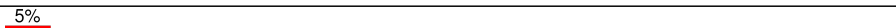
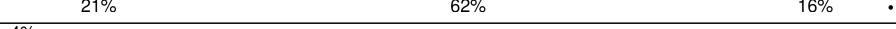
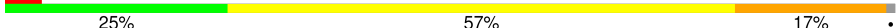



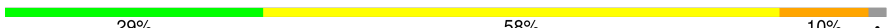

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 3 | A3 | 197 | |
| 3 | B3 | 197 | |
| 4 | A4 | 265 | |
| 4 | B4 | 265 | |
| 5 | A5 | 119 | |
| 5 | B5 | 119 | |
| 6 | A6 | 81 | |
| 6 | B6 | 81 | |
| 7 | A7 | 162 | |
| 7 | B7 | 162 | |
| 8 | A8 | 143 | |
| 8 | B8 | 143 | |
| 9 | A9 | 189 | |
| 9 | B9 | 189 | |
| 10 | AA | 1753 | |
| 10 | BA | 1753 | |
| 11 | AB | 241 | |
| 11 | BB | 241 | |
| 12 | AC | 243 | |
| 12 | BC | 243 | |
| 13 | AD | 181 | |
| 13 | BD | 181 | |
| 14 | AE | 296 | |
| 14 | BE | 296 | |
| 15 | AF | 101 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|--|
| 15 | BF | 101 |  |
| 16 | AG | 200 |  |
| 16 | BG | 200 |  |
| 17 | AH | 130 |  |
| 17 | BH | 130 |  |
| 18 | AI | 145 |  |
| 18 | BI | 145 |  |
| 19 | AJ | 120 |  |
| 19 | BJ | 120 |  |
| 20 | AK | 151 |  |
| 20 | BK | 151 |  |
| 21 | AL | 142 |  |
| 21 | BL | 142 |  |
| 22 | AM | 155 |  |
| 22 | BM | 155 |  |
| 23 | AN | 55 |  |
| 23 | BN | 55 |  |
| 24 | AO | 153 |  |
| 24 | BO | 153 |  |
| 25 | AP | 149 |  |
| 25 | BP | 149 |  |
| 26 | AQ | 157 |  |
| 26 | BQ | 157 |  |
| 27 | AR | 343 |  |
| 27 | BR | 343 |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 28 | AS | 144 | |
| 28 | BS | 144 | |
| 29 | AT | 155 | |
| 29 | BT | 155 | |
| 30 | AU | 126 | |
| 30 | BU | 126 | |
| 31 | AV | 130 | |
| 31 | BV | 130 | |
| 32 | AW | 260 | |
| 32 | BW | 260 | |
| 33 | AX | 80 | |
| 33 | BX | 80 | |
| 34 | AY | 293 | |
| 34 | BY | 293 | |
| 35 | AZ | 97 | |
| 35 | BZ | 97 | |

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 |
|-----|------|-------|------|-----------|----------|---------|------------------|
| 36 | MG | AA | 1815 | - | - | - | X |
| 36 | MG | AA | 1851 | - | - | - | X |
| 36 | MG | AA | 1856 | - | - | - | X |
| 36 | MG | AA | 1868 | - | - | - | X |
| 36 | MG | AA | 1874 | - | - | - | X |
| 36 | MG | AA | 1881 | - | - | - | X |
| 36 | MG | AA | 1889 | - | - | - | X |
| 36 | MG | BA | 1803 | - | - | - | X |
| 36 | MG | BA | 1810 | - | - | - | X |
| 36 | MG | BA | 1815 | - | - | - | X |

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| Mol | Type | Chain | Res | Chirality | Geometry | Clashes | Electron density |
|-----|------|-------|------|-----------|----------|---------|------------------|
| 36 | MG | BA | 1873 | - | - | - | X |
| 36 | MG | BA | 1888 | - | - | - | X |

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 157632 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 RIBOSOMAL PROTEIN S28E CONTAINING PROTEIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|---------|-------|
| 1 | A1 | 67 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 519 | 312 | 105 | 98 | 4 | | | |
| 1 | B1 | 67 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 519 | 312 | 105 | 98 | 4 | | | |

- Molecule 2 is a protein called 40S RIBOSOMAL PROTEIN S8.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 2 | A2 | 207 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1693 | 1057 | 336 | 296 | 4 | | | |
| 2 | B2 | 207 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1693 | 1057 | 336 | 296 | 4 | | | |

- Molecule 3 is a protein called RPS7E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 3 | A3 | 196 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1048 | 286 | 294 | 1 | | | |
| 3 | B3 | 196 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1629 | 1048 | 286 | 294 | 1 | | | |

- Molecule 4 is a protein called 40S RIBOSOMAL PROTEIN S3A.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 4 | A4 | 215 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1724 | 1090 | 314 | 316 | 4 | | | |
| 4 | B4 | 215 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1724 | 1090 | 314 | 316 | 4 | | | |

- Molecule 5 is a protein called RIBOSOMAL PROTEIN S26E CONTAINING PROTEIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 5 | A5 | 98 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 797 | 485 | 170 | 136 | 6 | | | |
| 5 | B5 | 98 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 797 | 485 | 170 | 136 | 6 | | | |

- Molecule 6 is a protein called RPS27E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 6 | A6 | 80 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 632 | 398 | 110 | 116 | 8 | | | |
| 6 | B6 | 80 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 632 | 398 | 110 | 116 | 8 | | | |

There are 28 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| B6 | 54 | CYS | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 55 | GLU | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 56 | LYS | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 57 | CYS | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 58 | SER | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 59 | ALA | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 60 | ILE | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 61 | LEU | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 62 | CYS | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 63 | LYS | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 64 | PRO | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 65 | THR | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 66 | GLY | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 67 | GLY | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 68 | LYS | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 69 | VAL | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 70 | GLN | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 71 | ILE | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 72 | GLN | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 73 | ALA | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 74 | GLY | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 75 | CYS | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 76 | ALA | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 77 | PHE | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 78 | LYS | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 79 | ILE | - | EXPRESSION TAG | UNP Q22CK0 |
| B6 | 80 | LYS | - | EXPRESSION TAG | UNP Q22CK0 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| B6 | 81 | ASN | - | EXPRESSION TAG | UNP Q22CK0 |

- Molecule 7 is a protein called PLECTIN/S10 DOMAIN CONTAINING PROTEIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 7 | A7 | 104 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 859 | 560 | 142 | 155 | 2 | | | |
| 7 | B7 | 104 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 859 | 560 | 142 | 155 | 2 | | | |

- Molecule 8 is a protein called RPS25E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 8 | A8 | 93 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 725 | 460 | 135 | 128 | 2 | | | |
| 8 | B8 | 93 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 725 | 460 | 135 | 128 | 2 | | | |

- Molecule 9 is a protein called RPS31E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 9 | A9 | 98 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 742 | 479 | 139 | 119 | 5 | | | |
| 9 | B9 | 98 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 742 | 479 | 139 | 119 | 5 | | | |

- Molecule 10 is a RNA chain called 18S RRNA.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|---------|-------|
| 10 | AA | 1745 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 37231 | 16654 | 6651 | 12181 | 1745 | | | |
| 10 | BA | 1745 | Total | C | N | O | P | 0 | 0 | 0 |
| | | | 37231 | 16654 | 6651 | 12181 | 1745 | | | |

- Molecule 11 is a protein called RPS0E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|---------|-------|
| 11 | AB | 204 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1642 | 1039 | 288 | 304 | 11 | | | |
| 11 | BB | 204 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1642 | 1039 | 288 | 304 | 11 | | | |

- Molecule 12 is a protein called KH DOMAIN CONTAINING PROTEIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 12 | AC | 229 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1820 | 1173 | 320 | 319 | 8 | | | |
| 12 | BC | 229 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1820 | 1173 | 320 | 319 | 8 | | | |

- Molecule 13 is a protein called RIBOSOMAL PROTEIN S4 CONTAINING PROTEIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 13 | AD | 179 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1475 | 931 | 286 | 252 | 6 | | | |
| 13 | BD | 179 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1475 | 931 | 286 | 252 | 6 | | | |

- Molecule 14 is a protein called RIBOSOMAL PROTEIN S5 CONTAINING PROTEIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 14 | AE | 230 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1827 | 1176 | 323 | 325 | 3 | | | |
| 14 | BE | 230 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1827 | 1176 | 323 | 325 | 3 | | | |

- Molecule 15 is a protein called EIF1.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 15 | AF | 89 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 736 | 465 | 131 | 137 | 3 | | | |
| 15 | BF | 89 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 736 | 465 | 131 | 137 | 3 | | | |

- Molecule 16 is a protein called RIBOSOMAL PROTEIN S7 CONTAINING PROTEIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 16 | AG | 192 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1520 | 961 | 281 | 270 | 8 | | | |
| 16 | BG | 192 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1520 | 961 | 281 | 270 | 8 | | | |

- Molecule 17 is a protein called RIBOSOMAL PROTEIN S8 CONTAINING PROTEIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 17 | AH | 129 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1040 | 671 | 184 | 180 | 5 | | | |
| 17 | BH | 129 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1040 | 671 | 184 | 180 | 5 | | | |

- Molecule 18 is a protein called RPS16E, 40S RIBOSOMAL PROTEIN RPS16E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 18 | AI | 143 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1135 | 715 | 217 | 198 | 5 | | | |
| 18 | BI | 143 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1135 | 715 | 217 | 198 | 5 | | | |

- Molecule 19 is a protein called RIBOSOMAL PROTEIN S10 CONTAINING PROTEIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 19 | AJ | 105 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 833 | 525 | 150 | 152 | 6 | | | |
| 19 | BJ | 105 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 833 | 525 | 150 | 152 | 6 | | | |

- Molecule 20 is a protein called RPS14E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 20 | AK | 140 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1063 | 654 | 206 | 197 | 6 | | | |
| 20 | BK | 140 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1063 | 654 | 206 | 197 | 6 | | | |

- Molecule 21 is a protein called 40S RIBOSOMAL PROTEIN S12.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 21 | AL | 141 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1097 | 691 | 221 | 180 | 5 | | | |
| 21 | BL | 141 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1097 | 691 | 221 | 180 | 5 | | | |

- Molecule 22 is a protein called RPS18E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 22 | AM | 154 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1239 | 780 | 237 | 216 | 6 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 22 | BM | 154 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1239 | 780 | 237 | 216 | 6 | | | |

- Molecule 23 is a protein called RPS29E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 23 | AN | 53 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 447 | 278 | 91 | 72 | 6 | | | |
| 23 | BN | 53 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 447 | 278 | 91 | 72 | 6 | | | |

There are 2 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| BN | 54 | TYR | - | EXPRESSION TAG | UNP Q22MB0 |
| BN | 55 | ARG | - | EXPRESSION TAG | UNP Q22MB0 |

- Molecule 24 is a protein called RPS13E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 24 | AO | 150 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1214 | 782 | 228 | 200 | 4 | | | |
| 24 | BO | 150 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1214 | 782 | 228 | 200 | 4 | | | |

- Molecule 25 is a protein called RPS24E.

| Mol | Chain | Residues | Atoms | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---------|---------|-------|
| 25 | AP | 148 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1197 | 763 | 221 | 213 | | | |
| 25 | BP | 148 | Total | C | N | O | 0 | 0 | 0 |
| | | | 1197 | 763 | 221 | 213 | | | |

- Molecule 26 is a protein called RIBOSOMAL PROTEIN S17 CONTAINING PROTEIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 26 | AQ | 157 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1275 | 818 | 235 | 217 | 5 | | | |
| 26 | BQ | 157 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1275 | 818 | 235 | 217 | 5 | | | |

- Molecule 27 is a protein called RACK1.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 27 | AR | 338 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2682 | 1711 | 462 | 501 | 8 | | | |
| 27 | BR | 338 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2682 | 1711 | 462 | 501 | 8 | | | |

- Molecule 28 is a protein called RPS15E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 28 | AS | 125 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 985 | 632 | 173 | 176 | 4 | | | |
| 28 | BS | 125 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 985 | 632 | 173 | 176 | 4 | | | |

- Molecule 29 is a protein called RPS19E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 29 | AT | 150 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1211 | 769 | 227 | 213 | 2 | | | |
| 29 | BT | 150 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1211 | 769 | 227 | 213 | 2 | | | |

- Molecule 30 is a protein called RIBOSOMAL PROTEIN L7AE CONTAINING PROTEIN.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 30 | AU | 124 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 952 | 599 | 166 | 182 | 5 | | | |
| 30 | BU | 124 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 952 | 599 | 166 | 182 | 5 | | | |

- Molecule 31 is a protein called RPS17E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 31 | AV | 121 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 979 | 619 | 182 | 176 | 2 | | | |
| 31 | BV | 121 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 979 | 619 | 182 | 176 | 2 | | | |

- Molecule 32 is a protein called 40S RIBOSOMAL PROTEIN S4.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 32 | AW | 259 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2079 | 1322 | 383 | 370 | 4 | | | |

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| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 32 | BW | 259 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 2079 | 1322 | 383 | 370 | 4 | | | |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------------|------------|
| BW | 1 | MET | - | EXPRESSION TAG | UNP P0C233 |
| BW | 70 | GLN | GLY | CONFLICT | UNP P0C233 |
| BW | 236 | SER | LEU | CONFLICT | UNP P0C233 |
| BW | 237 | TRP | TYR | CONFLICT | UNP P0C233 |

- Molecule 33 is a protein called RPS30E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|---------|-------|
| 33 | AX | 68 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 554 | 350 | 113 | 90 | 1 | | | |
| 33 | BX | 68 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 554 | 350 | 113 | 90 | 1 | | | |

- Molecule 34 is a protein called RPS6E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|---------|-------|
| 34 | AY | 235 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1868 | 1184 | 347 | 326 | 11 | | | |
| 34 | BY | 235 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 1868 | 1184 | 347 | 326 | 11 | | | |

- Molecule 35 is a protein called RPS21E.

| Mol | Chain | Residues | Atoms | | | | | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 35 | AZ | 97 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 747 | 458 | 139 | 146 | 4 | | | |
| 35 | BZ | 97 | Total | C | N | O | S | 0 | 0 | 0 |
| | | | 747 | 458 | 139 | 146 | 4 | | | |

- Molecule 36 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------|----|---------|---------|
| 36 | AA | 90 | Total | Mg | 0 | 0 |
| | | | 90 | 90 | | |
| 36 | B4 | 1 | Total | Mg | 0 | 0 |
| | | | 1 | 1 | | |

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| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|-------------|----------|---------|---------|
| 36 | BA | 89 | Total 89 | Mg 89 | 0 | 0 |
| 36 | BD | 1 | Total 1 | Mg 1 | 0 | 0 |
| 36 | A4 | 1 | Total 1 | Mg 1 | 0 | 0 |
| 36 | BW | 1 | Total 1 | Mg 1 | 0 | 0 |
| 36 | AL | 1 | Total 1 | Mg 1 | 0 | 0 |

- Molecule 37 is ZINC ION (three-letter code: ZN) (formula: Zn).

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|------------|---------|---------|---------|
| 37 | B5 | 1 | Total 1 | Zn 1 | 0 | 0 |
| 37 | BN | 1 | Total 1 | Zn 1 | 0 | 0 |
| 37 | B9 | 1 | Total 1 | Zn 1 | 0 | 0 |
| 37 | A6 | 1 | Total 1 | Zn 1 | 0 | 0 |
| 37 | AN | 1 | Total 1 | Zn 1 | 0 | 0 |
| 37 | A5 | 1 | Total 1 | Zn 1 | 0 | 0 |
| 37 | A9 | 1 | Total 1 | Zn 1 | 0 | 0 |
| 37 | B6 | 1 | Total 1 | Zn 1 | 0 | 0 |

- Molecule 38 is water.

| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|--------------|----------|---------|---------|
| 38 | A2 | 2 | Total 2 | O 2 | 0 | 0 |
| 38 | A4 | 2 | Total 2 | O 2 | 0 | 0 |
| 38 | A5 | 1 | Total 1 | O 1 | 0 | 0 |
| 38 | AA | 516 | Total 516 | O 516 | 0 | 0 |

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| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|--------------|----------|---------|---------|
| 38 | AC | 1 | Total 1 | O 1 | 0 | 0 |
| 38 | AD | 4 | Total 4 | O 4 | 0 | 0 |
| 38 | AE | 3 | Total 3 | O 3 | 0 | 0 |
| 38 | AL | 3 | Total 3 | O 3 | 0 | 0 |
| 38 | AM | 4 | Total 4 | O 4 | 0 | 0 |
| 38 | AO | 1 | Total 1 | O 1 | 0 | 0 |
| 38 | AP | 1 | Total 1 | O 1 | 0 | 0 |
| 38 | AQ | 2 | Total 2 | O 2 | 0 | 0 |
| 38 | AT | 4 | Total 4 | O 4 | 0 | 0 |
| 38 | AW | 4 | Total 4 | O 4 | 0 | 0 |
| 38 | AY | 4 | Total 4 | O 4 | 0 | 0 |
| 38 | B2 | 2 | Total 2 | O 2 | 0 | 0 |
| 38 | B4 | 2 | Total 2 | O 2 | 0 | 0 |
| 38 | B5 | 1 | Total 1 | O 1 | 0 | 0 |
| 38 | BA | 512 | Total 512 | O 512 | 0 | 0 |
| 38 | BC | 2 | Total 2 | O 2 | 0 | 0 |
| 38 | BD | 2 | Total 2 | O 2 | 0 | 0 |
| 38 | BE | 5 | Total 5 | O 5 | 0 | 0 |
| 38 | BK | 1 | Total 1 | O 1 | 0 | 0 |
| 38 | BL | 2 | Total 2 | O 2 | 0 | 0 |
| 38 | BM | 6 | Total 6 | O 6 | 0 | 0 |

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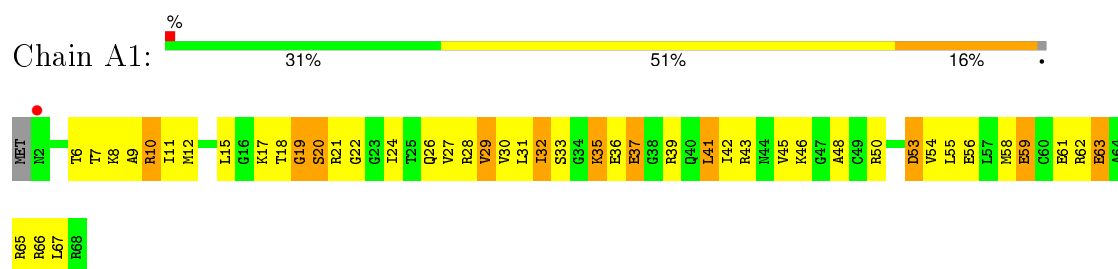
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| Mol | Chain | Residues | Atoms | | ZeroOcc | AltConf |
|-----|-------|----------|------------|--------|---------|---------|
| 38 | BO | 1 | Total 1 | O 1 | 0 | 0 |
| 38 | BP | 1 | Total 1 | O 1 | 0 | 0 |
| 38 | BQ | 1 | Total 1 | O 1 | 0 | 0 |
| 38 | BT | 6 | Total 6 | O 6 | 0 | 0 |
| 38 | BW | 5 | Total 5 | O 5 | 0 | 0 |
| 38 | BY | 3 | Total 3 | O 3 | 0 | 0 |

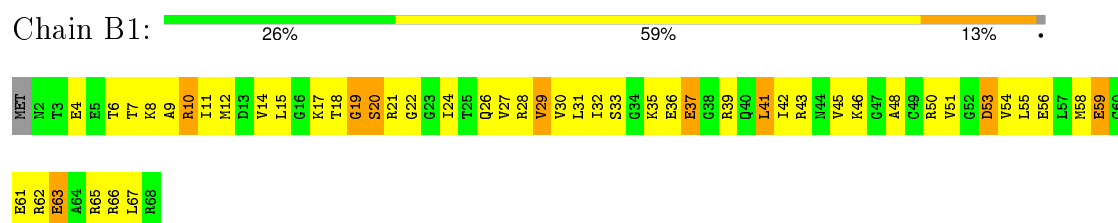
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

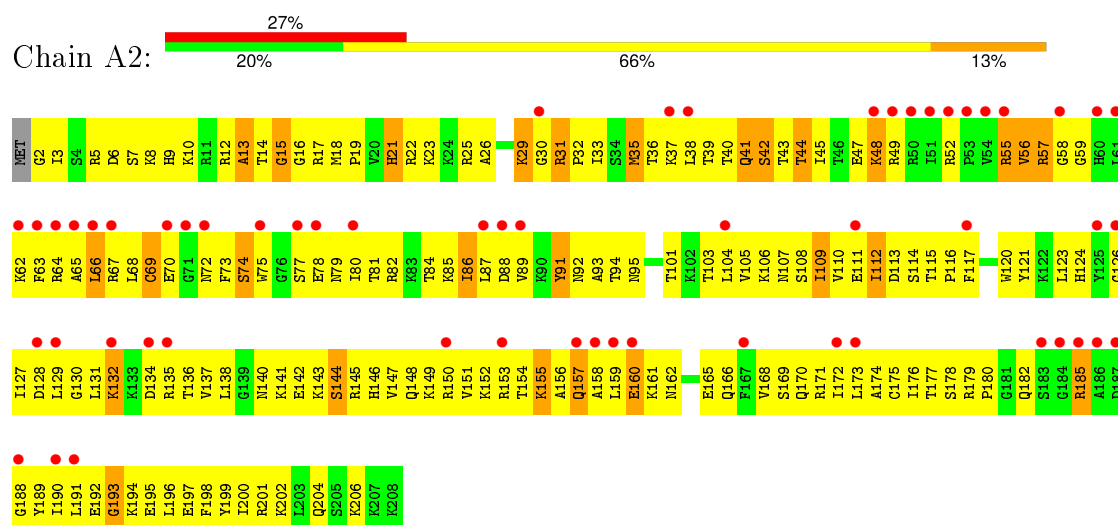
• Molecule 1: RIBOSOMAL PROTEIN S28E CONTAINING PROTEIN



• Molecule 1: RIBOSOMAL PROTEIN S28E CONTAINING PROTEIN

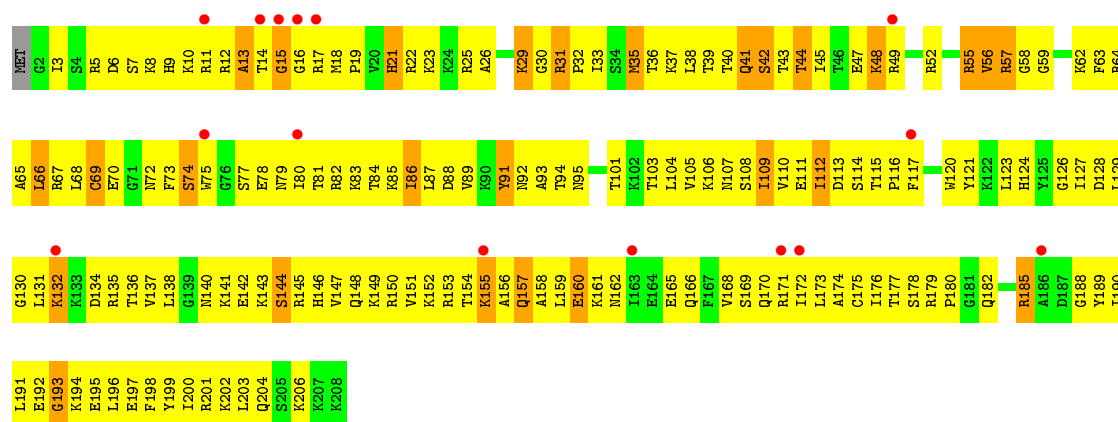


• Molecule 2: 40S RIBOSOMAL PROTEIN S8

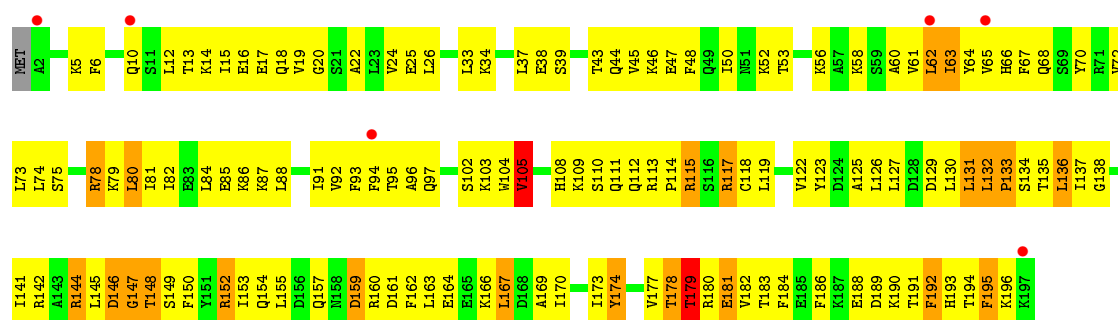


• Molecule 2: 40S RIBOSOMAL PROTEIN S8

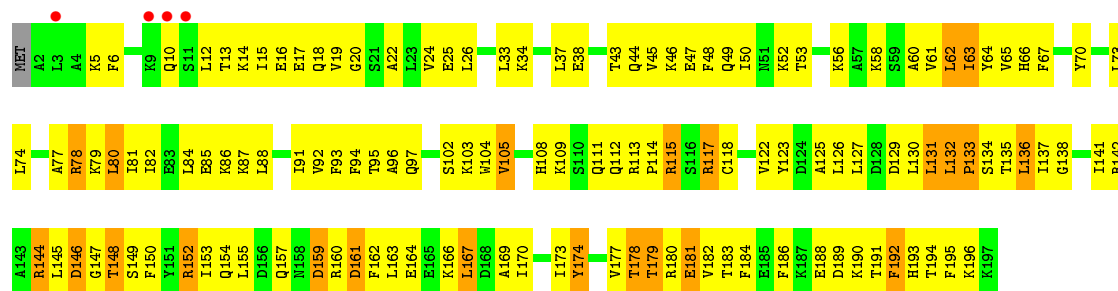




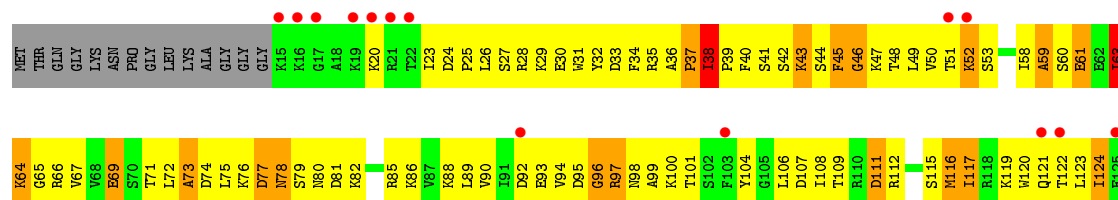
• Molecule 3: RPS7E

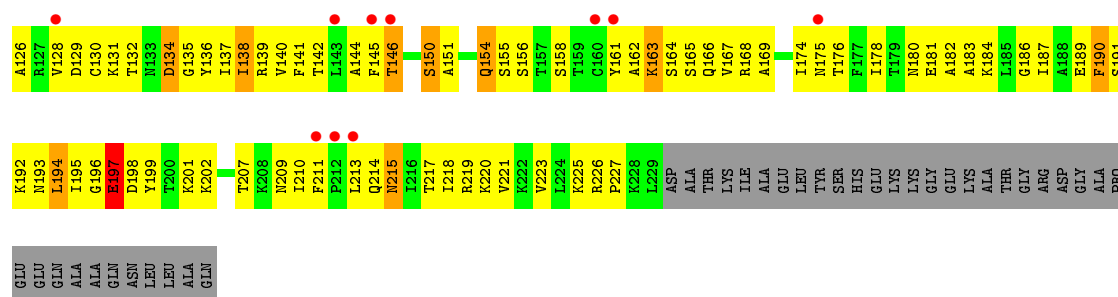


• Molecule 3: RPS7E

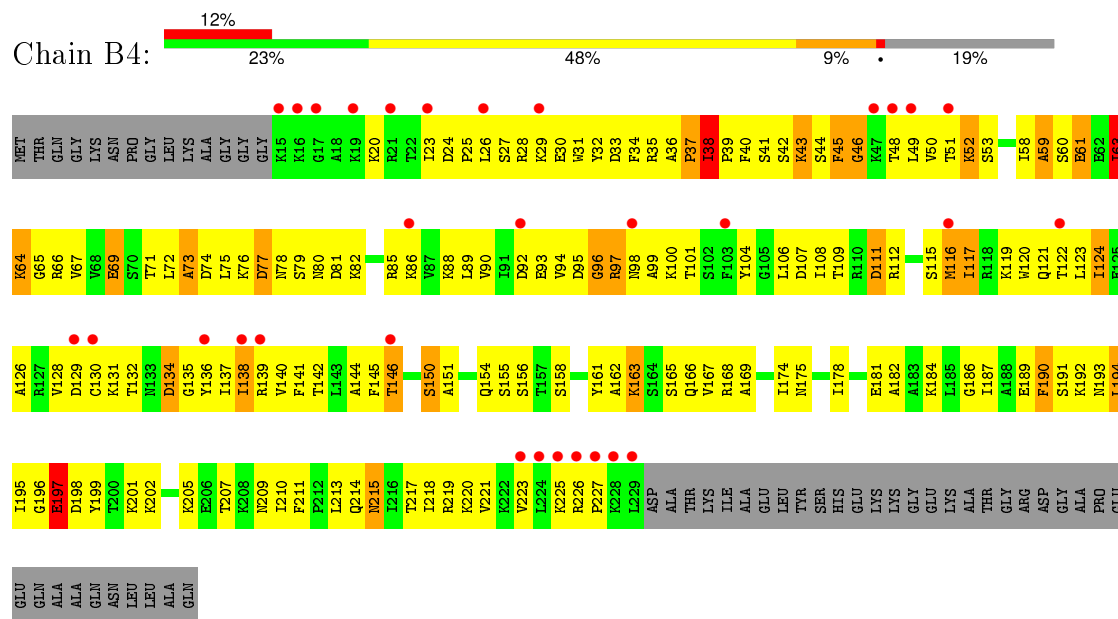


• Molecule 4: 40S RIBOSOMAL PROTEIN S3A

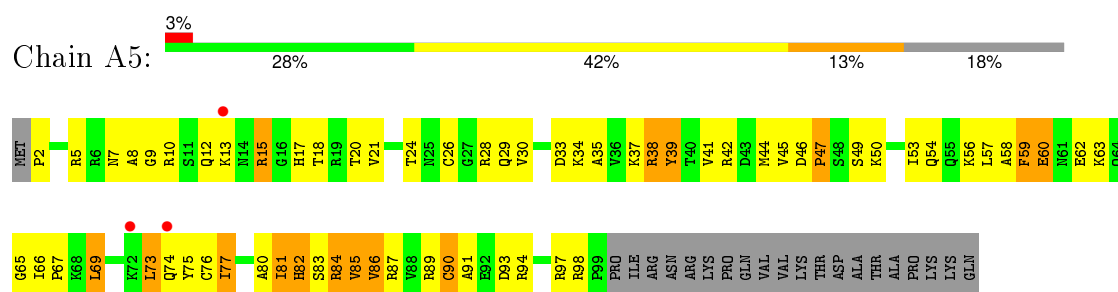




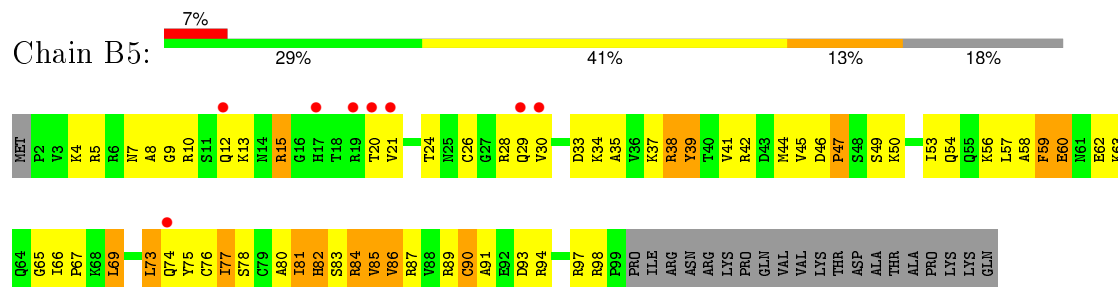
• Molecule 4: 40S RIBOSOMAL PROTEIN S3A



• Molecule 5: RIBOSOMAL PROTEIN S26E CONTAINING PROTEIN



• Molecule 5: RIBOSOMAL PROTEIN S26E CONTAINING PROTEIN



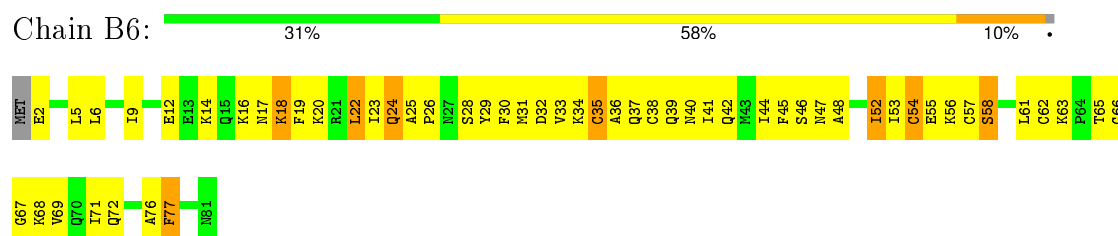
• Molecule 6: RPS27E

Chain A6:



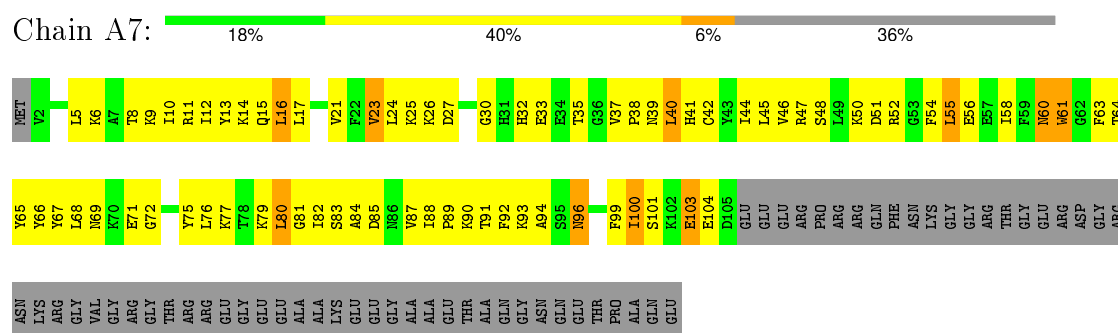
- Molecule 6: RPS27E

Chain B6:



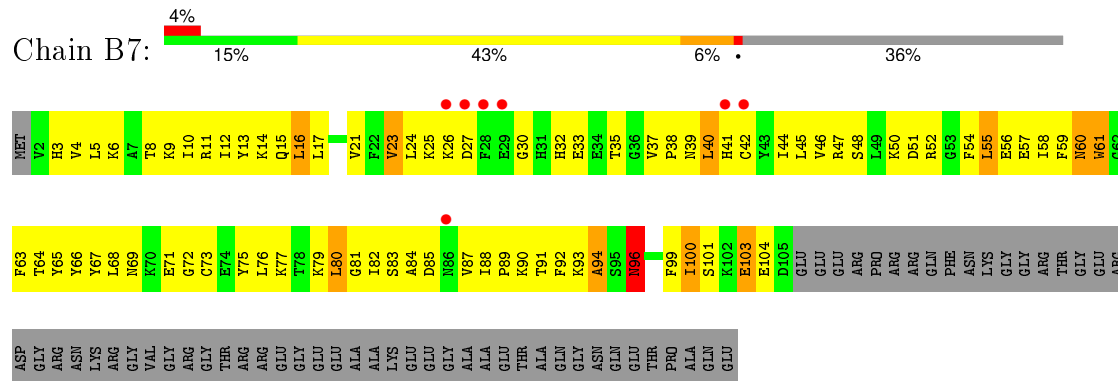
- Molecule 7: PLECTIN/S10 DOMAIN CONTAINING PROTEIN

Chain A7:



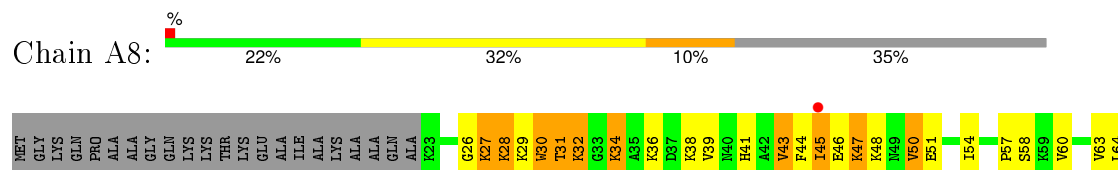
- Molecule 7: PLECTIN/S10 DOMAIN CONTAINING PROTEIN

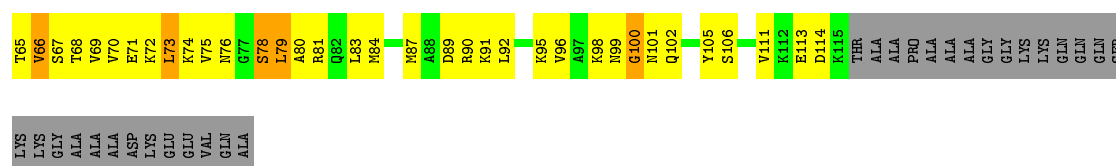
Chain B7:



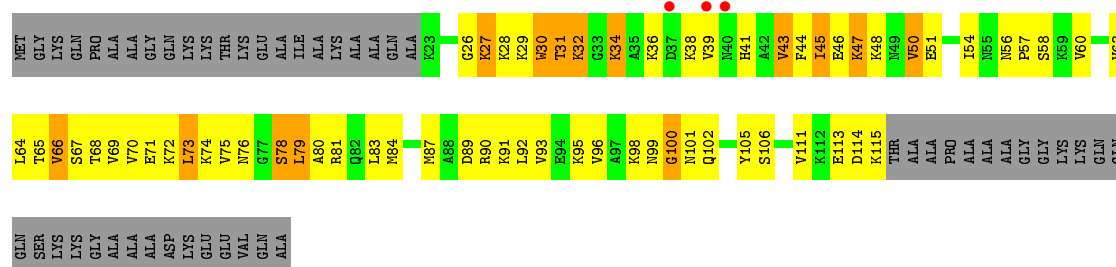
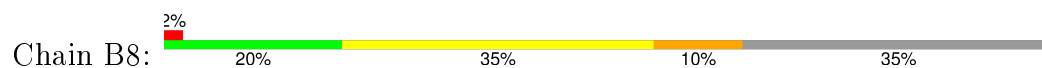
- Molecule 8: RPS25E

Chain A8:

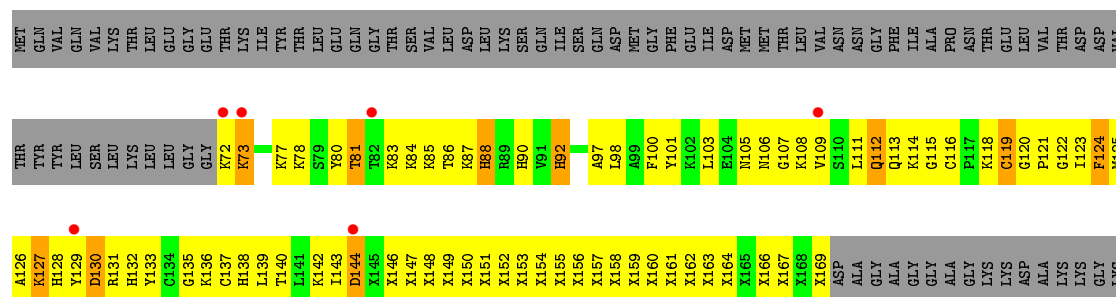




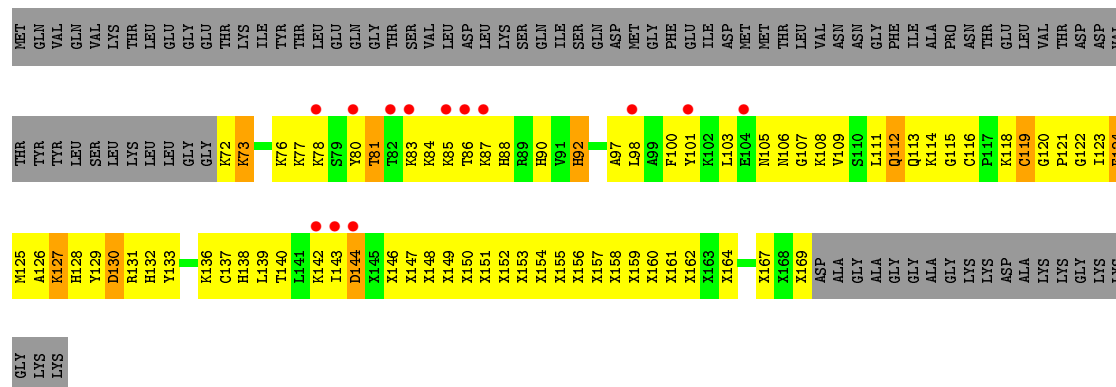
• Molecule 8: RPS25E



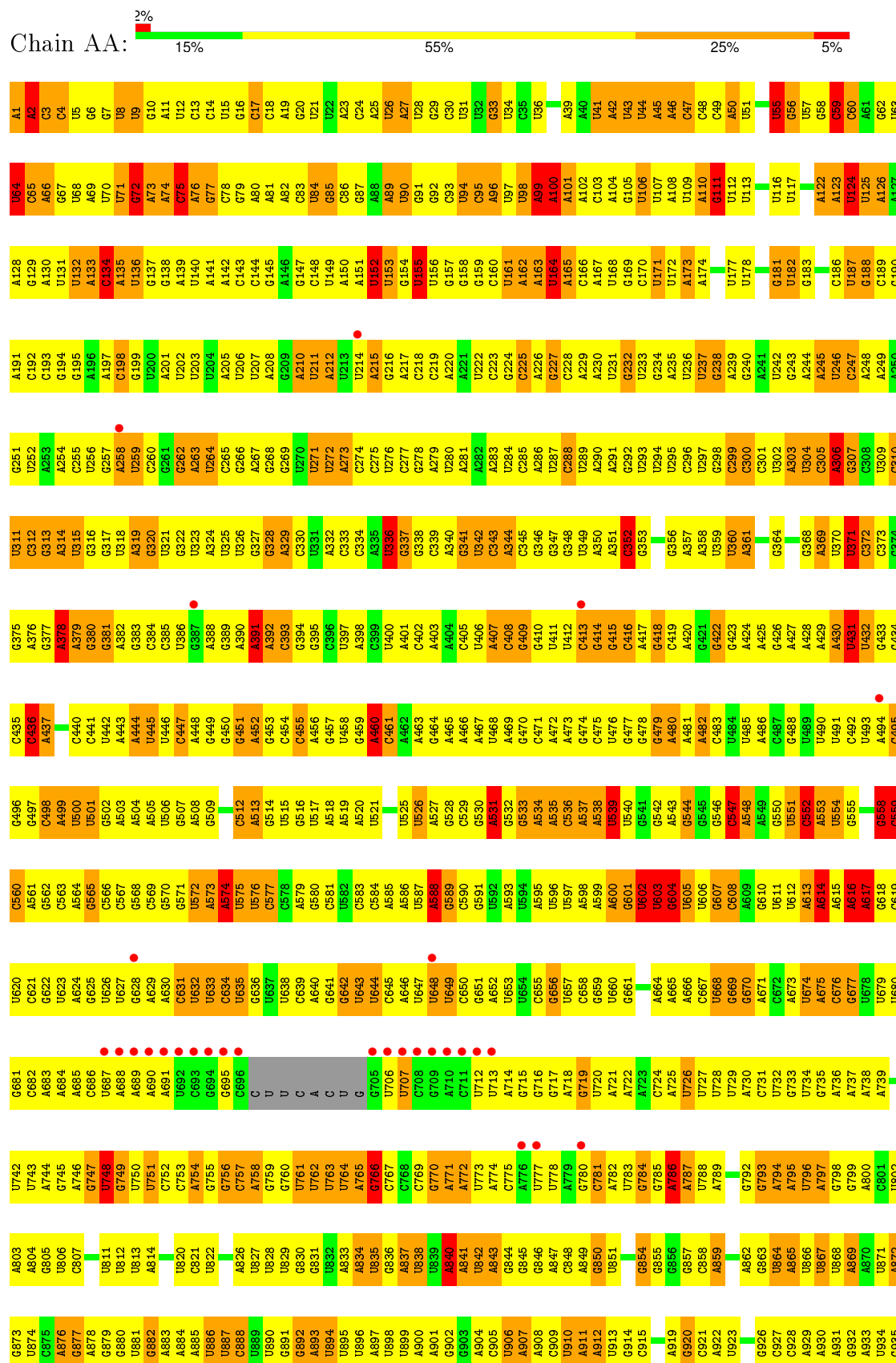
• Molecule 9: RPS31E

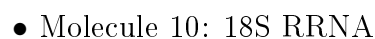


• Molecule 9: RPS31E

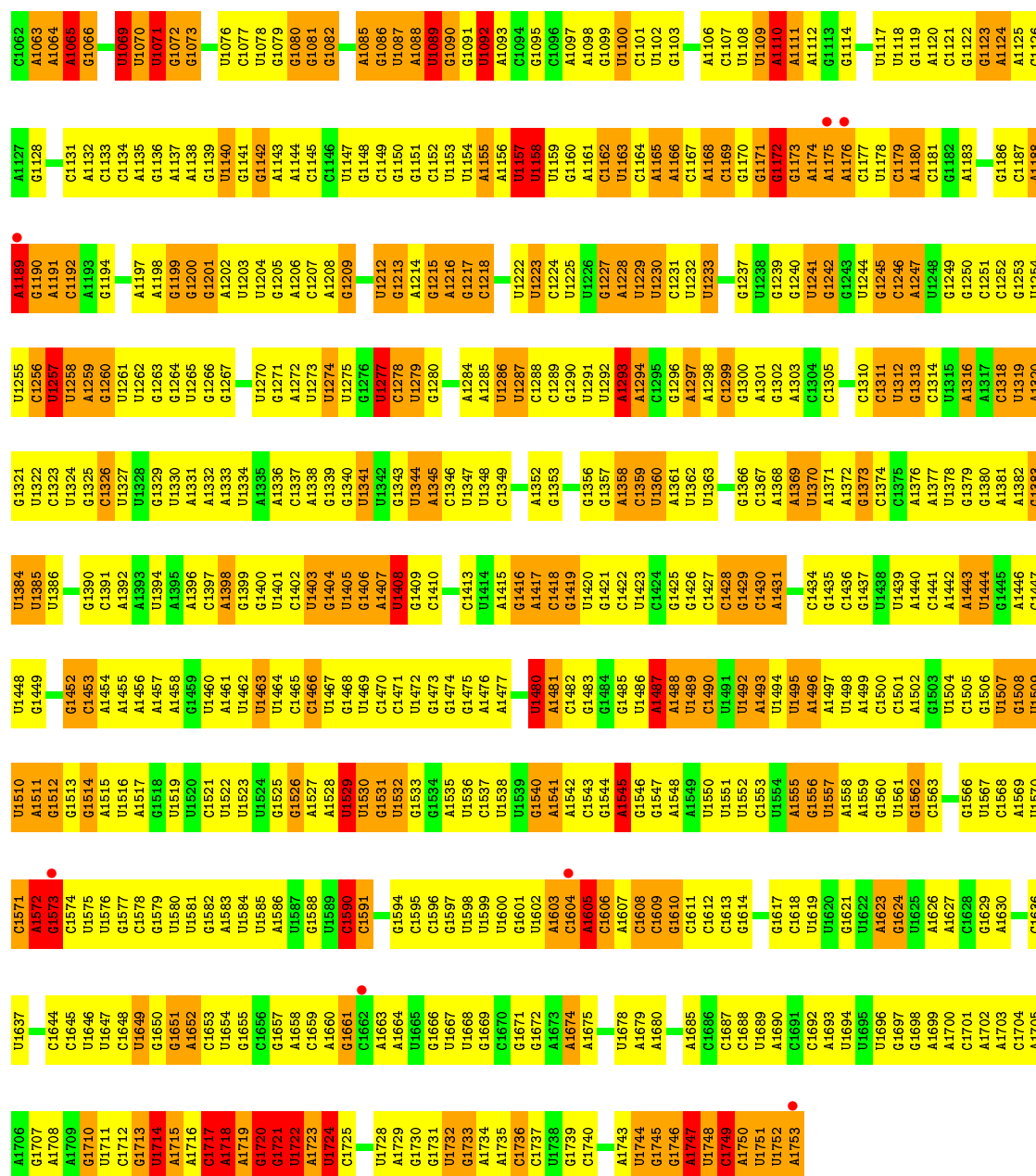


• Molecule 10: 18S RRNA

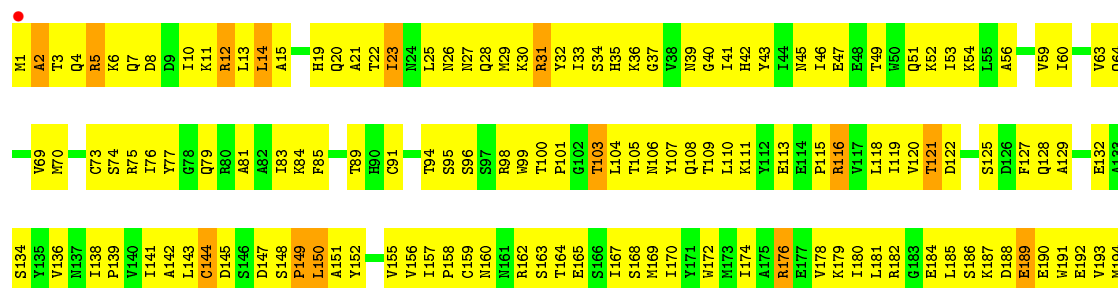


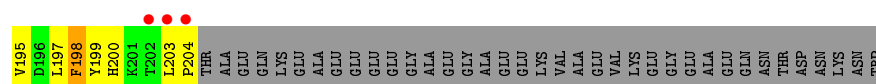


| | | | | | | | | | | | | | | | |
|-------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| U1000 | U837 | A872 | U802 | U742 | U679 | C619 | G558 | G496 | C436 | C373 | U309 | A249 | C189 | A127 | U64 |
| A1001 | U838 | G873 | A803 | U743 | U680 | U620 | C569 | G497 | A437 | G374 | C310 | A250 | G190 | A128 | C65 |
| U1002 | U939 | U874 | A804 | U744 | G681 | G821 | C561 | C498 | A438 | G375 | U311 | A251 | A191 | G129 | A66 |
| A1003 | C875 | C875 | G805 | A744 | G682 | G622 | A561 | A499 | U439 | A376 | C312 | U252 | C192 | A130 | G67 |
| A1004 | A876 | A876 | U806 | G745 | A683 | U623 | G562 | U500 | C440 | G377 | G313 | A253 | G193 | U131 | U68 |
| A1005 | G877 | G877 | C807 | A746 | A684 | A624 | C563 | U501 | C441 | A378 | A314 | A254 | G194 | U132 | A69 |
| C1006 | A878 | A878 | C907 | G747 | A685 | G625 | A564 | G502 | U442 | A379 | U315 | C255 | G195 | A133 | U70 |
| U1007 | U748 | U748 | U811 | U748 | C886 | U626 | G565 | A503 | A443 | G380 | G316 | U256 | A196 | A133 | U71 |
| A1008 | A879 | G880 | U812 | G749 | C887 | U627 | C566 | A504 | A444 | G381 | G317 | G257 | A197 | C134 | G72 |
| U1009 | U881 | U881 | U813 | U750 | A688 | G628 | C567 | A505 | U445 | A382 | U318 | A258 | C198 | U136 | A73 |
| A1010 | C947 | G882 | A814 | U751 | A689 | A629 | G568 | U506 | U446 | G383 | A319 | U259 | G199 | G137 | A74 |
| G1013 | A848 | A848 | U820 | C752 | C690 | A630 | C569 | G507 | C447 | C384 | G320 | C260 | U200 | G138 | C75 |
| A1014 | A850 | A850 | C821 | A754 | A691 | C631 | G570 | A508 | A448 | C385 | U321 | C261 | A201 | A139 | A76 |
| C1015 | A951 | U886 | U822 | A755 | U692 | U632 | G571 | G509 | G449 | U386 | G322 | G262 | U202 | U140 | G77 |
| U1016 | A952 | U887 | G831 | G756 | C693 | U633 | U572 | C512 | G450 | G387 | U323 | A263 | U203 | A141 | C78 |
| C1017 | C953 | C888 | U832 | G756 | A694 | C634 | A573 | A513 | G451 | A388 | A324 | U264 | U204 | A142 | G79 |
| G1018 | G954 | U889 | U828 | C757 | G695 | U635 | A574 | G514 | A452 | G389 | U325 | C265 | A205 | C143 | A80 |
| G1019 | A855 | U890 | U829 | A758 | C696 | G636 | U575 | U515 | G453 | A390 | U326 | G266 | U206 | C144 | A81 |
| G1020 | A856 | G891 | U830 | G759 | C | U637 | U576 | U516 | C454 | A391 | G327 | A267 | U207 | G145 | A82 |
| U1022 | G958 | G892 | G831 | G760 | U | U638 | C577 | U517 | A455 | A392 | G328 | G268 | A208 | A146 | C83 |
| G1025 | G962 | U895 | U833 | U761 | U | U639 | C580 | U518 | A456 | C393 | A329 | G269 | G209 | G147 | U84 |
| C1026 | G963 | U896 | U834 | U762 | C | A640 | C581 | A519 | G457 | G394 | C330 | U270 | A210 | C148 | C85 |
| U1027 | G964 | U897 | A837 | U763 | A | G641 | U587 | A520 | U458 | G395 | U331 | U271 | U211 | U149 | C86 |
| G1028 | G965 | A898 | U838 | U764 | U | U642 | C583 | A521 | G459 | C396 | A332 | U272 | A212 | A150 | C87 |
| A1030 | U967 | A900 | U839 | U765 | C | U643 | U584 | U522 | A460 | U397 | C333 | A273 | U213 | A151 | A88 |
| A1031 | C968 | A901 | G846 | A765 | U | U644 | C585 | C523 | C461 | U398 | C334 | C274 | U214 | U152 | A89 |
| U1032 | A969 | G902 | U847 | C766 | G | U645 | C586 | U524 | A462 | C399 | A335 | C275 | A215 | U153 | U90 |
| A1033 | A970 | G903 | U848 | C767 | U705 | C650 | C590 | U525 | A463 | U400 | U336 | U276 | G216 | G154 | G91 |
| C1034 | A971 | A904 | U849 | U773 | U712 | C651 | C591 | U526 | G464 | U411 | C342 | C277 | A217 | G155 | G92 |
| A1035 | C972 | C905 | G844 | A774 | U713 | A652 | U592 | U527 | A465 | U412 | U343 | C278 | C218 | U156 | C93 |
| U1036 | A973 | U906 | G845 | C775 | A714 | U653 | A593 | A531 | G470 | U413 | U344 | C279 | C219 | G157 | U94 |
| G1037 | C974 | A907 | G846 | A776 | G715 | U654 | U594 | G532 | C471 | U414 | C345 | C284 | G224 | A162 | A99 |
| U1038 | G975 | C974 | A847 | U777 | G716 | C655 | A595 | G533 | A472 | U415 | C346 | C285 | C225 | A163 | A100 |
| C1039 | A976 | U910 | C948 | U778 | G717 | G656 | U596 | A534 | A473 | C413 | G346 | A286 | A226 | U164 | A101 |
| C1040 | U977 | A911 | A849 | A779 | A718 | U657 | U597 | A535 | G474 | C414 | G347 | U287 | A227 | A165 | A102 |
| A1041 | C978 | A912 | G850 | C780 | G719 | C658 | A598 | C536 | C475 | G415 | G348 | C288 | G228 | C166 | C103 |
| G1042 | A979 | U913 | U851 | C781 | U720 | G659 | A599 | A537 | U476 | C416 | U349 | U289 | A229 | A167 | A104 |
| U1043 | G980 | G914 | U852 | A782 | A721 | U660 | A600 | A538 | G477 | C417 | A350 | A290 | A230 | U168 | G105 |
| C1044 | A981 | C915 | U853 | U783 | A722 | G661 | G601 | U539 | G478 | C418 | A351 | A291 | U231 | G169 | U106 |
| G1045 | U982 | C915 | G854 | C784 | A723 | U662 | U602 | U540 | G479 | C419 | C352 | C292 | G232 | C170 | U107 |
| C1046 | A983 | G920 | G855 | G785 | C724 | G663 | U603 | G541 | A480 | C420 | G353 | U293 | U233 | U171 | A108 |
| C1047 | C984 | C921 | G856 | A786 | A725 | A664 | G604 | G542 | A481 | C421 | A357 | U294 | A234 | U172 | U109 |
| A1048 | C985 | A922 | G857 | A787 | U726 | A665 | U605 | A543 | C482 | G422 | A358 | U295 | A235 | A173 | A110 |
| C1049 | G986 | U923 | C858 | U788 | U727 | A666 | U606 | G544 | C483 | G423 | C359 | C296 | U236 | A174 | G111 |
| C1050 | U987 | U914 | C859 | A789 | U728 | C667 | G607 | G545 | U484 | A424 | U359 | U297 | U237 | U174 | U112 |
| G1051 | C988 | G926 | A859 | A789 | U729 | U668 | C608 | G546 | U485 | A425 | U360 | G298 | G238 | U177 | U116 |
| U1052 | G989 | C927 | A862 | G792 | A730 | G669 | A609 | C547 | A486 | C426 | A361 | C299 | A239 | U178 | U117 |
| A1053 | U990 | C928 | G863 | G793 | C731 | G670 | G610 | C548 | C487 | A427 | G362 | C300 | G240 | C179 | U120 |
| U1054 | A991 | A929 | U864 | A794 | U732 | A671 | U611 | A549 | G488 | A428 | G363 | C301 | A241 | G180 | A121 |
| G1055 | G992 | A930 | A865 | A795 | G733 | C672 | U612 | G550 | U489 | A429 | G364 | U302 | U242 | G181 | U122 |
| A1056 | U993 | A931 | U866 | U796 | U734 | A673 | A613 | U551 | C490 | A430 | A303 | U304 | G243 | U182 | G183 |
| C1057 | C994 | G932 | U867 | A797 | G735 | U674 | A614 | C552 | U491 | U431 | G368 | U305 | A245 | G184 | A123 |
| A1058 | U995 | A933 | U868 | G798 | A736 | A675 | A615 | A553 | C492 | U432 | A369 | C306 | U246 | C186 | U124 |
| A1059 | U996 | G934 | A869 | G799 | A737 | C676 | A616 | U554 | U493 | G433 | U370 | U307 | G247 | U187 | G125 |
| A1060 | A997 | G935 | A870 | A800 | A738 | G677 | A617 | G555 | A494 | G434 | C372 | C308 | A248 | G188 | A126 |
| U1061 | C997 | U936 | U871 | C801 | A739 | U678 | G618 | G556 | C495 | C435 | | | | | |

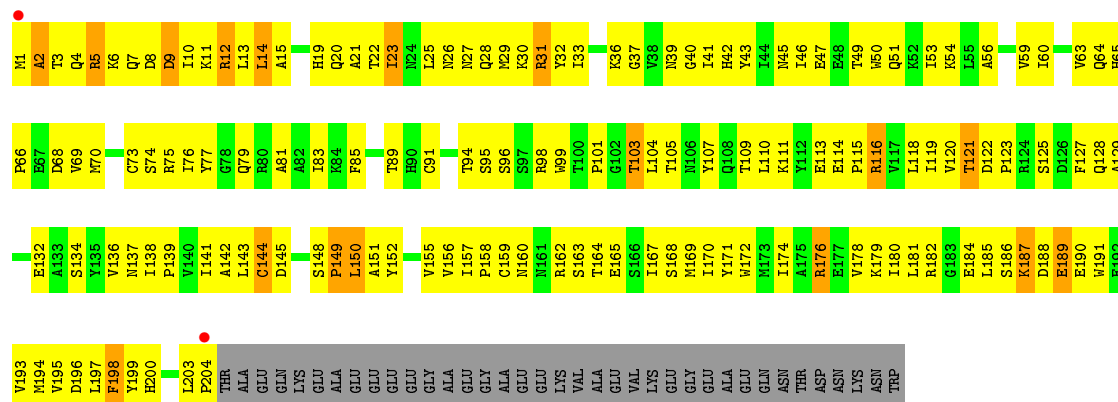


• Molecule 11: RPS0E

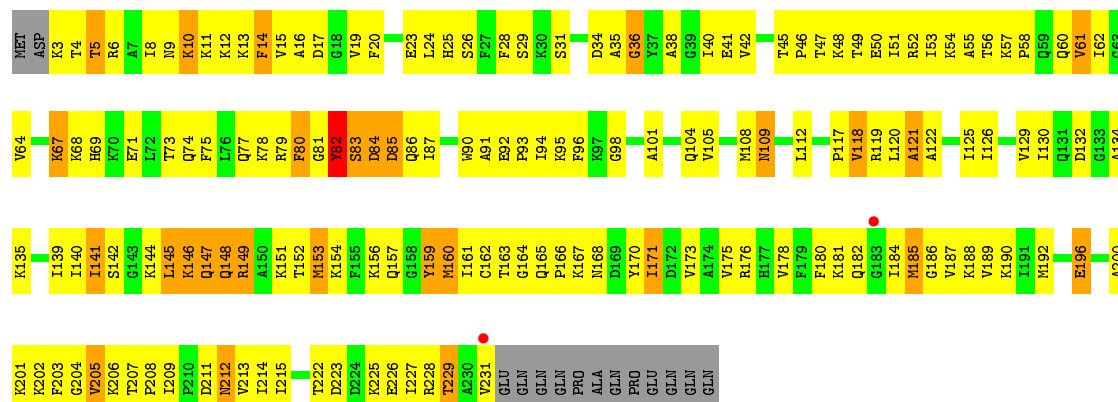




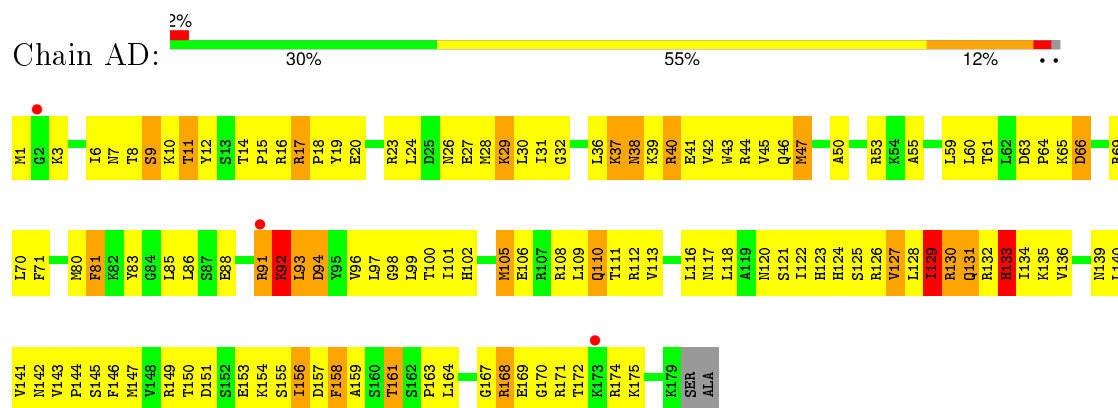
• Molecule 11: RPS0E



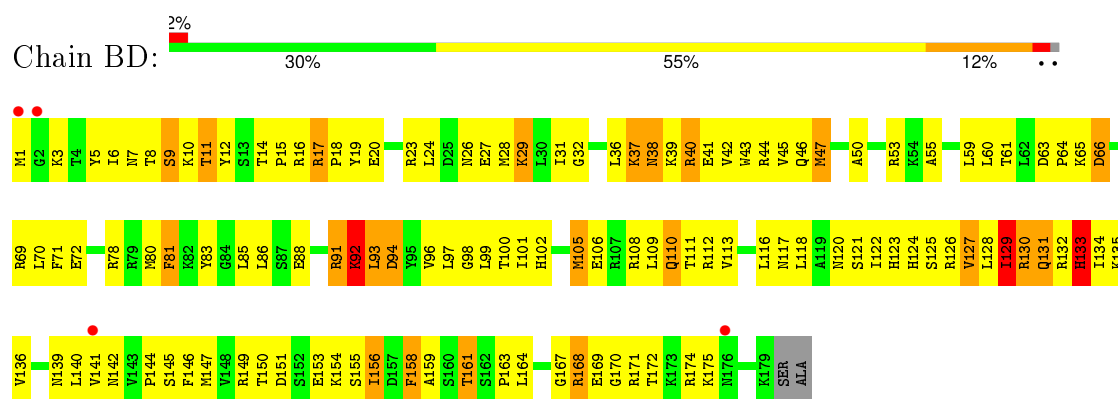
• Molecule 12: KH DOMAIN CONTAINING PROTEIN



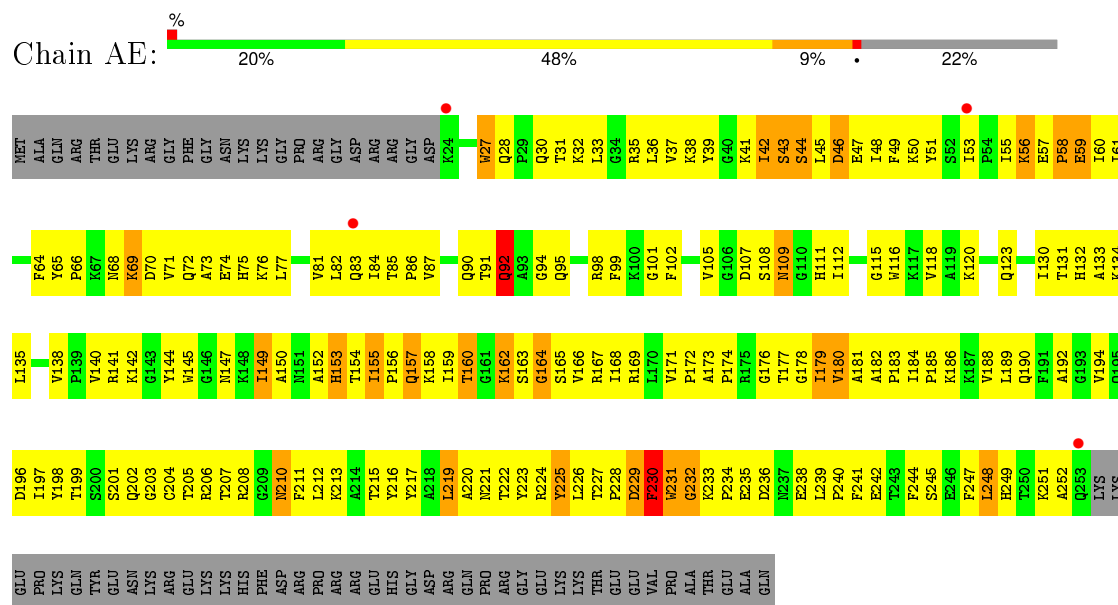
• Molecule 13: RIBOSOMAL PROTEIN S4 CONTAINING PROTEIN



• Molecule 13: RIBOSOMAL PROTEIN S4 CONTAINING PROTEIN

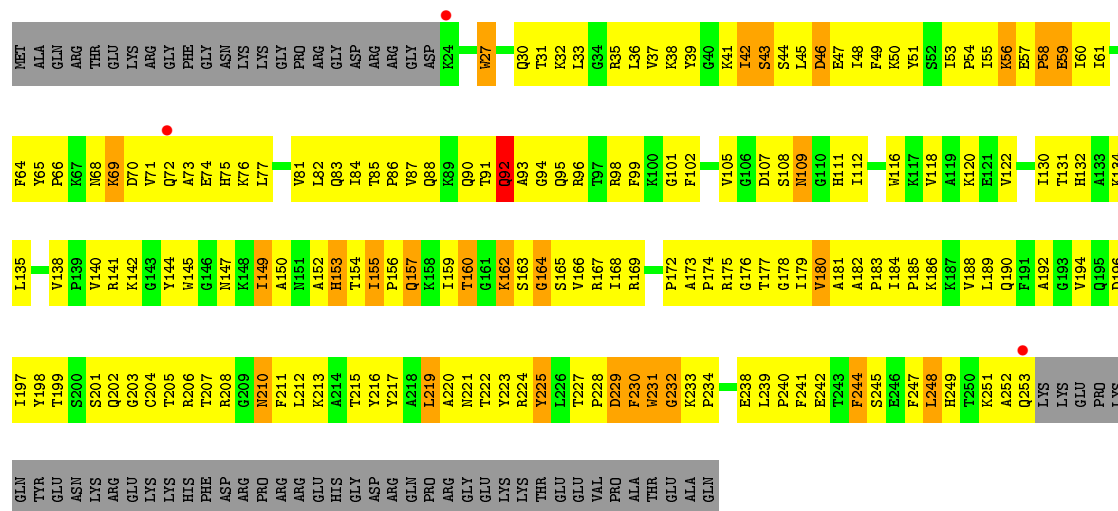


• Molecule 14: RIBOSOMAL PROTEIN S5 CONTAINING PROTEIN

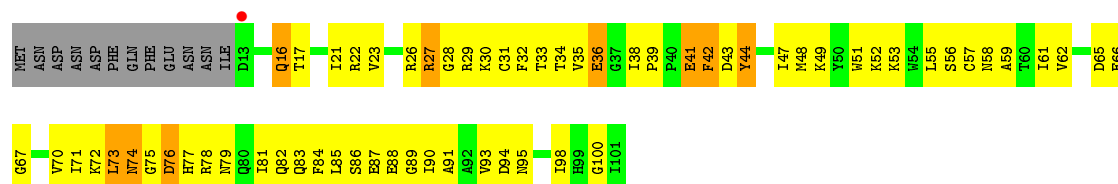


• Molecule 14: RIBOSOMAL PROTEIN S5 CONTAINING PROTEIN

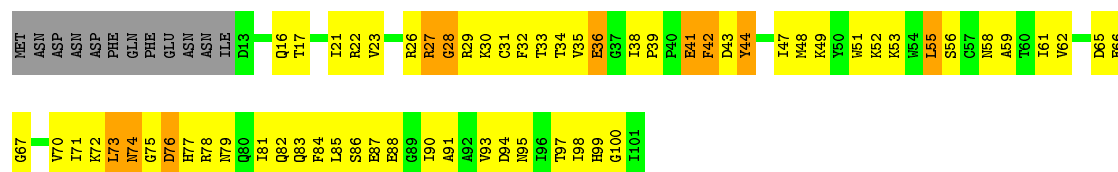
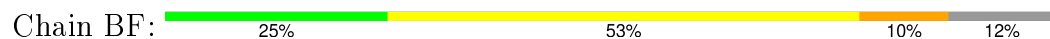




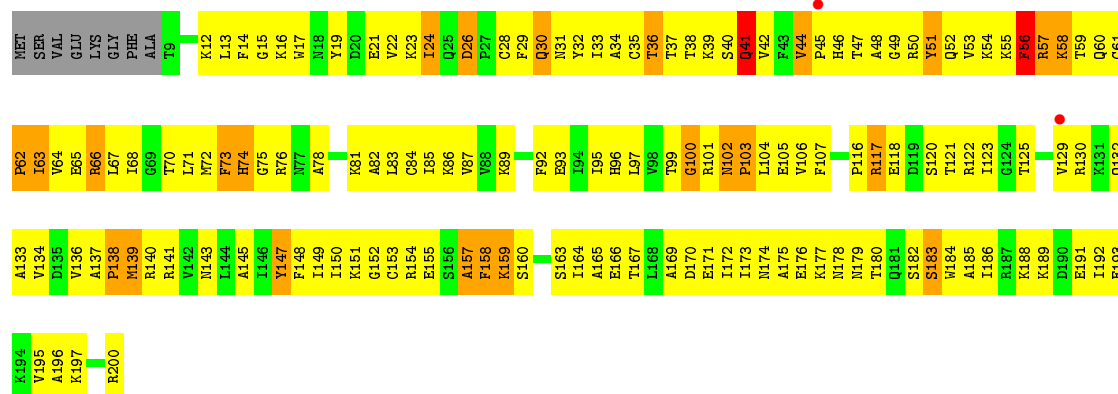
• Molecule 15: EIF1



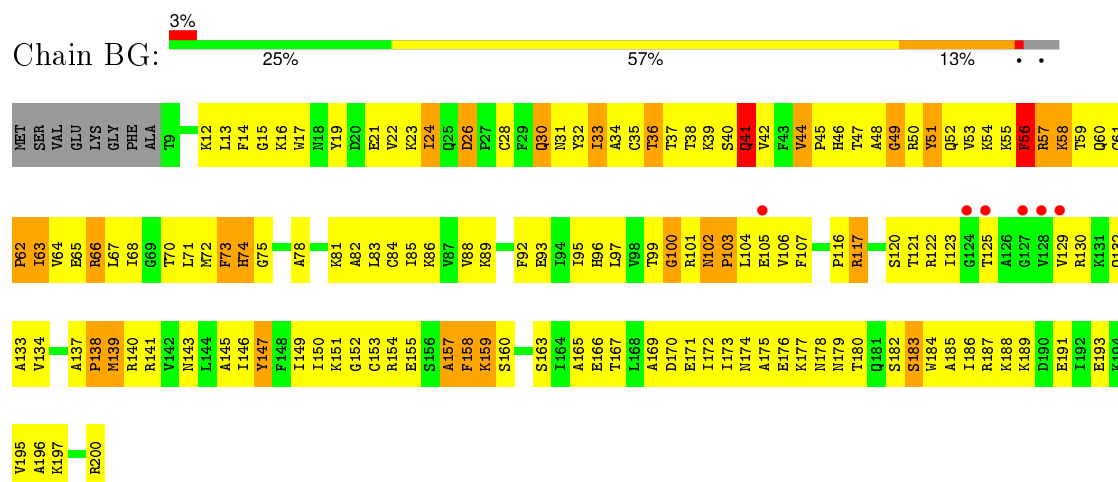
• Molecule 15: EIF1



• Molecule 16: RIBOSOMAL PROTEIN S7 CONTAINING PROTEIN



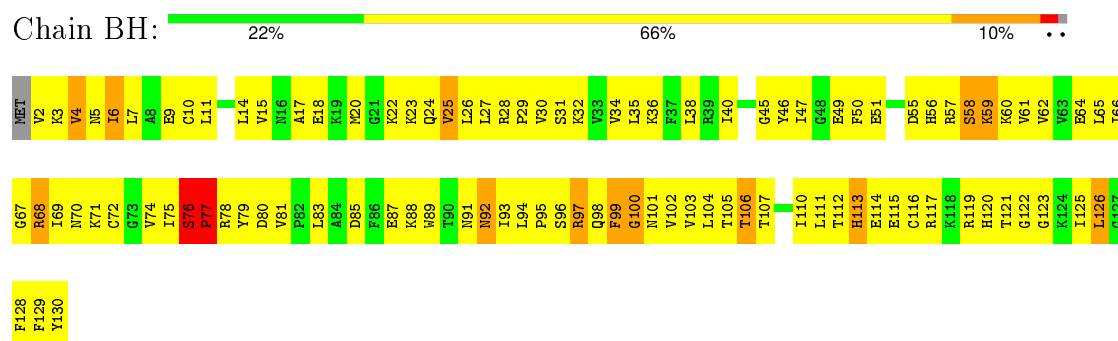
• Molecule 16: RIBOSOMAL PROTEIN S7 CONTAINING PROTEIN



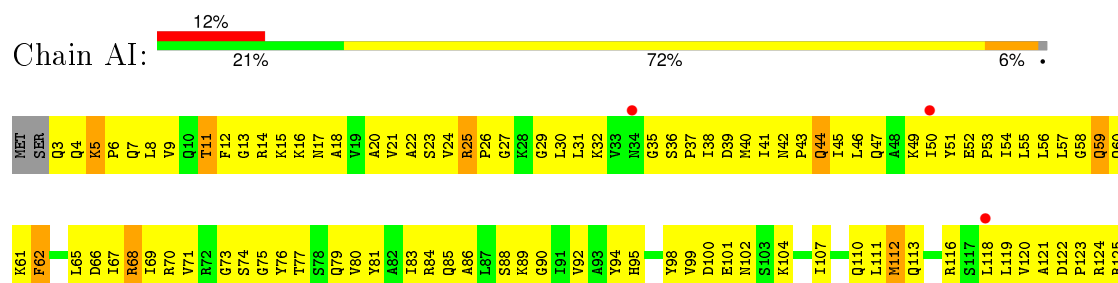
• Molecule 17: RIBOSOMAL PROTEIN S8 CONTAINING PROTEIN

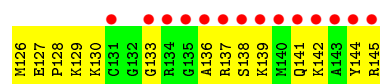


• Molecule 17: RIBOSOMAL PROTEIN S8 CONTAINING PROTEIN

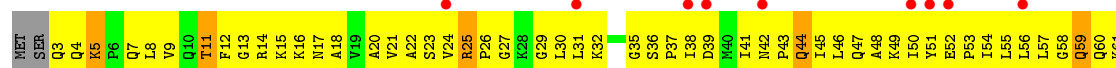


• Molecule 18: RPS16E, 40S RIBOSOMAL PROTEIN RPS16E

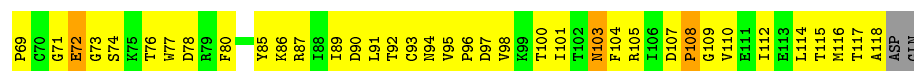




• Molecule 18: RPS16E, 40S RIBOSOMAL PROTEIN RPS16E



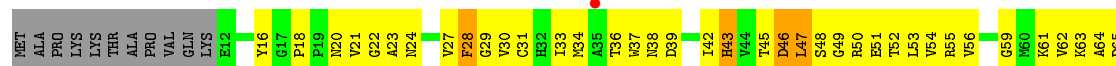
• Molecule 19: RIBOSOMAL PROTEIN S10 CONTAINING PROTEIN



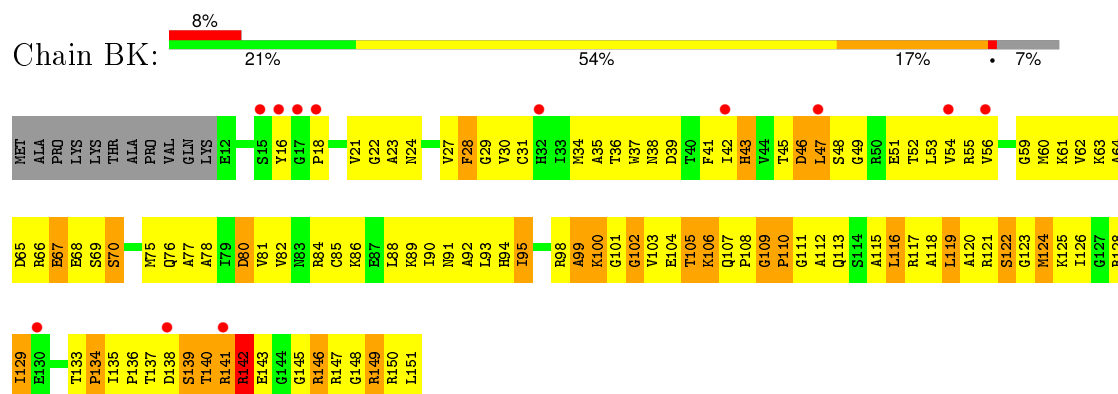
• Molecule 19: RIBOSOMAL PROTEIN S10 CONTAINING PROTEIN



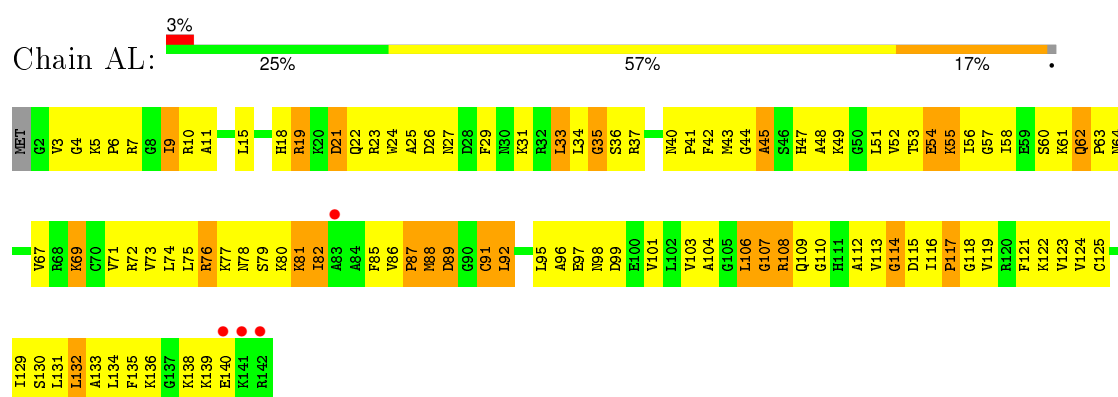
• Molecule 20: RPS14E



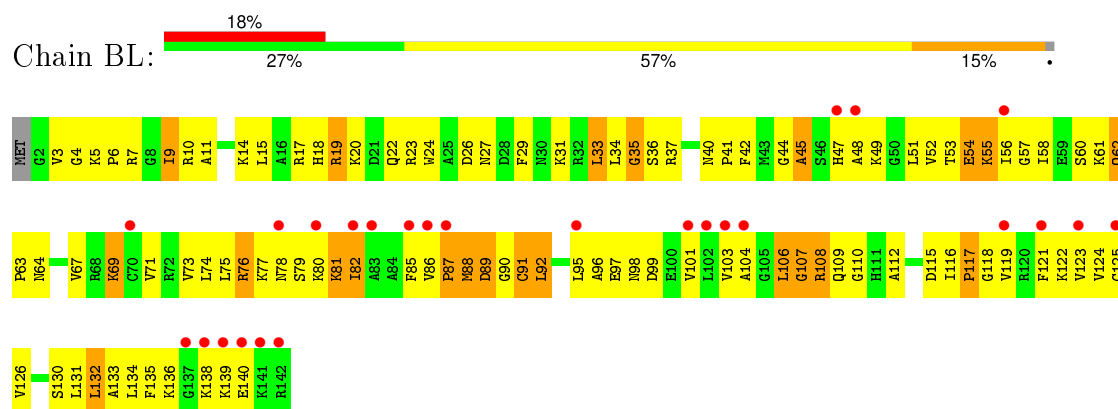
- Molecule 20: RPS14E



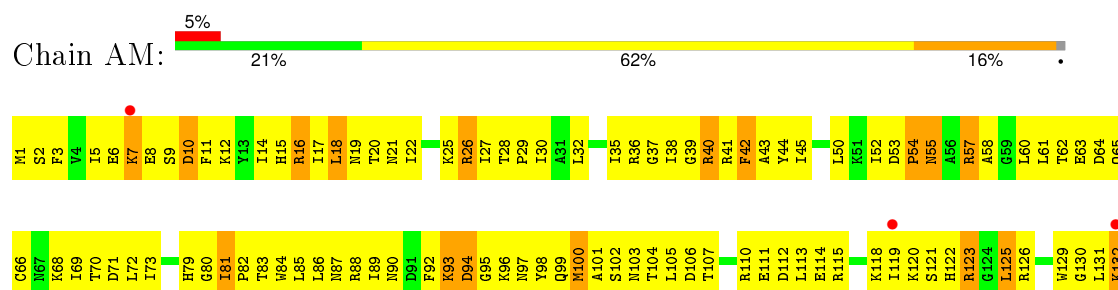
- Molecule 21: 40S RIBOSOMAL PROTEIN S12



- Molecule 21: 40S RIBOSOMAL PROTEIN S12

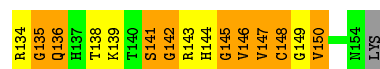
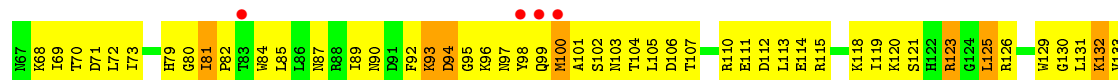
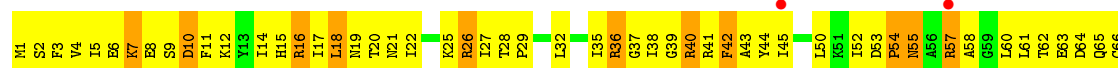


- Molecule 22: RPS18E

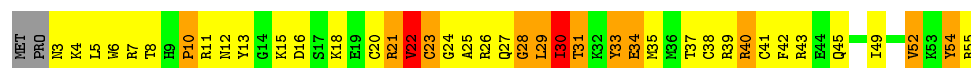




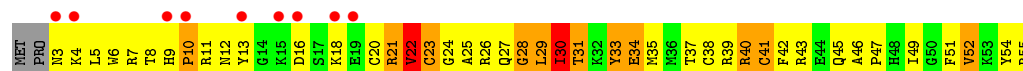
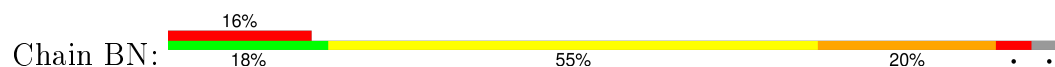
• Molecule 22: RPS18E



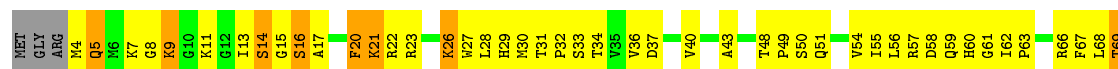
• Molecule 23: RPS29E



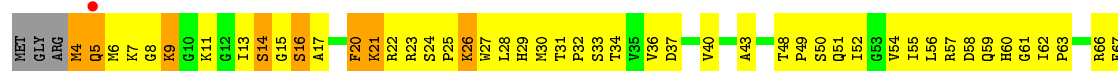
• Molecule 23: RPS29E



• Molecule 24: RPS13E

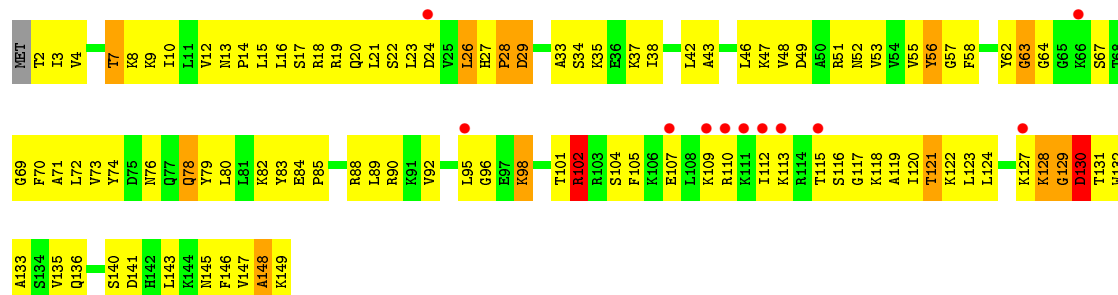


• Molecule 24: RPS13E

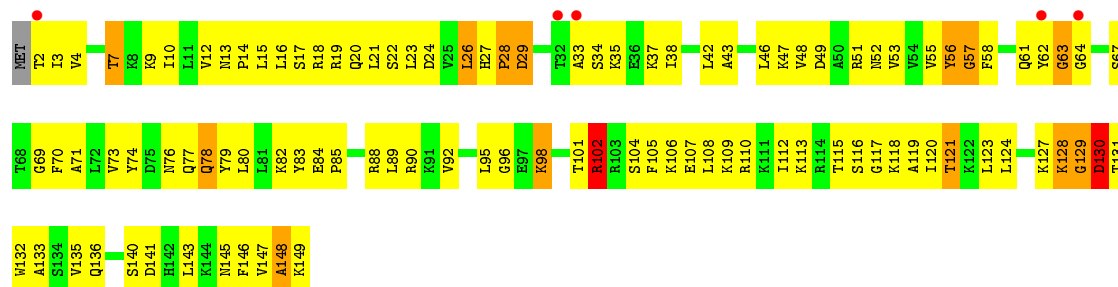




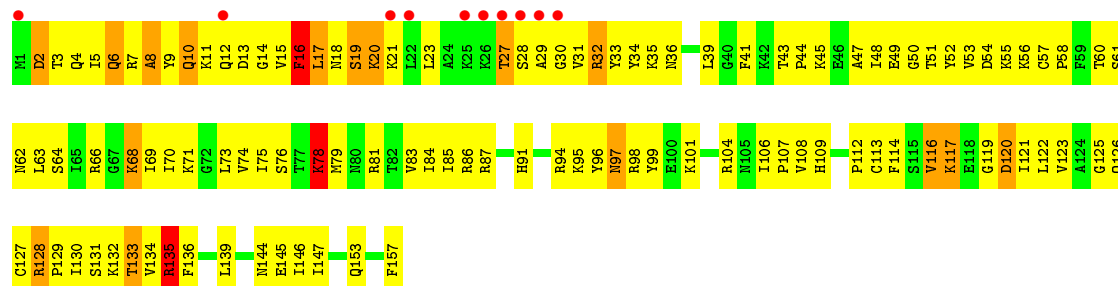
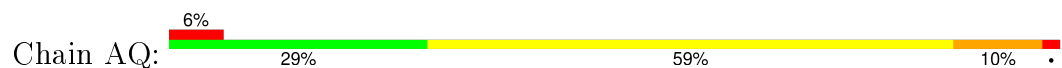
• Molecule 25: RPS24E



• Molecule 25: RPS24E

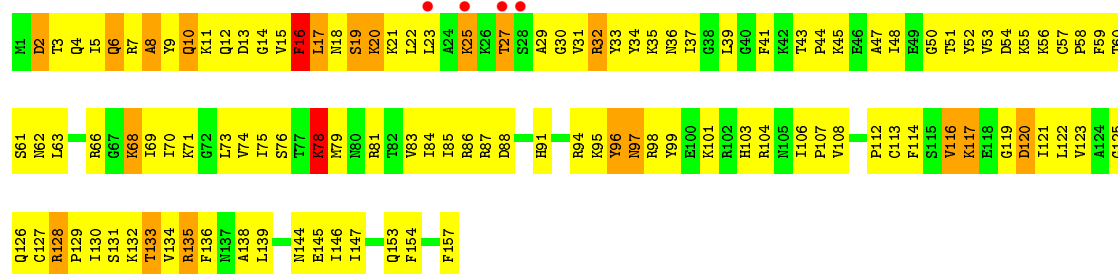


• Molecule 26: RIBOSOMAL PROTEIN S17 CONTAINING PROTEIN

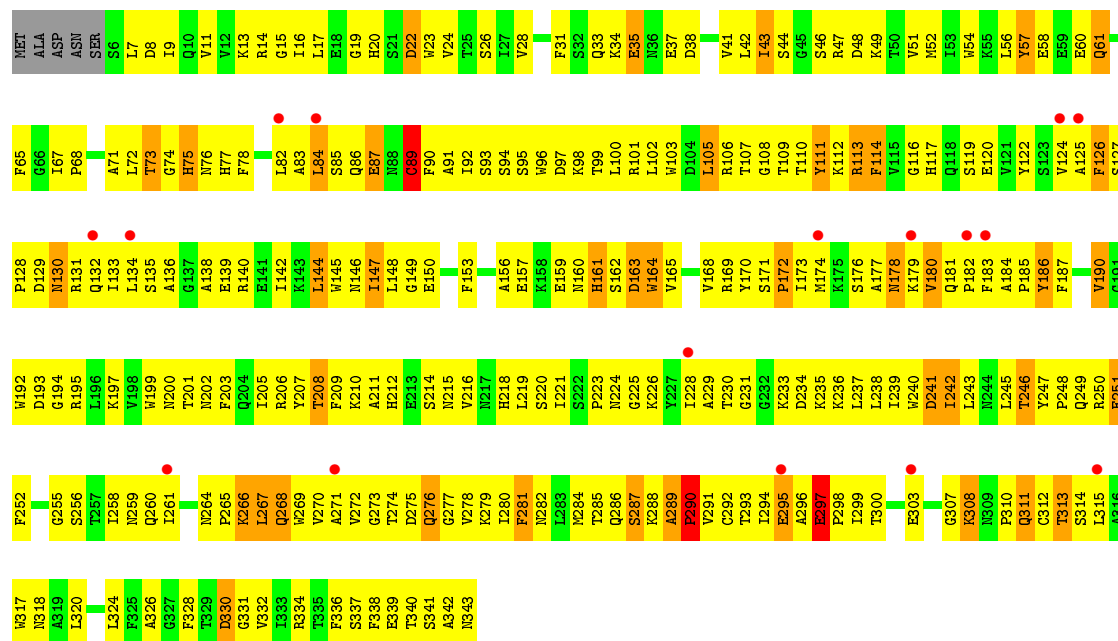


• Molecule 26: RIBOSOMAL PROTEIN S17 CONTAINING PROTEIN

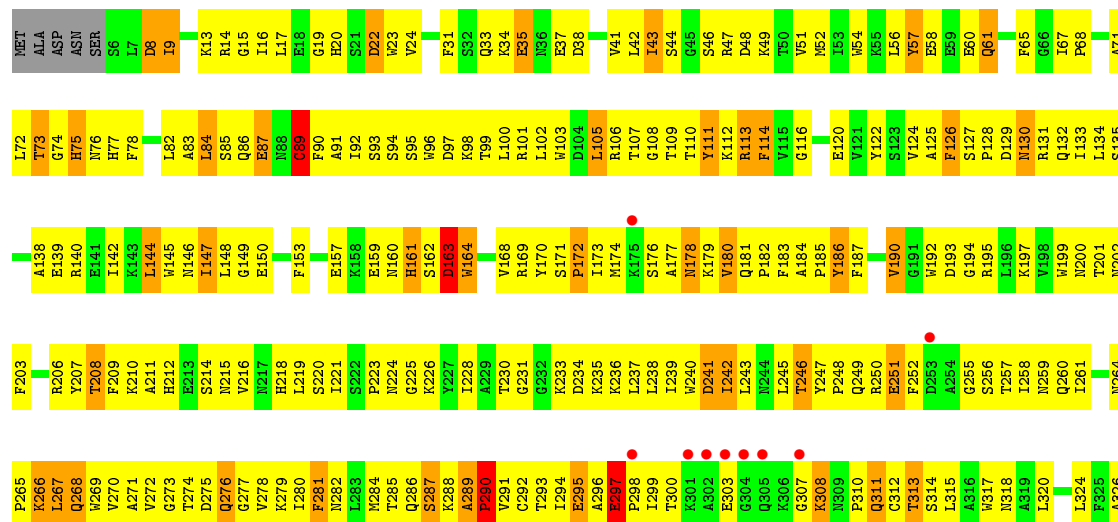


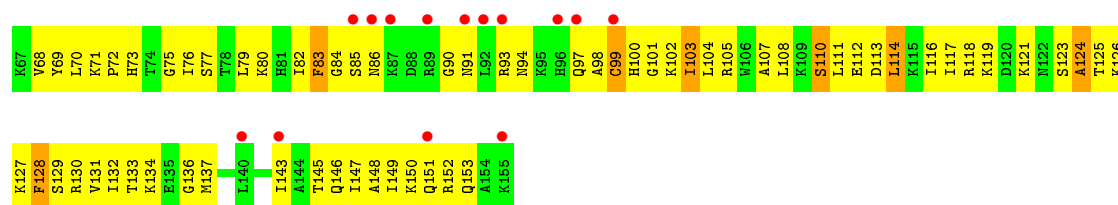


• Molecule 27: RACK1

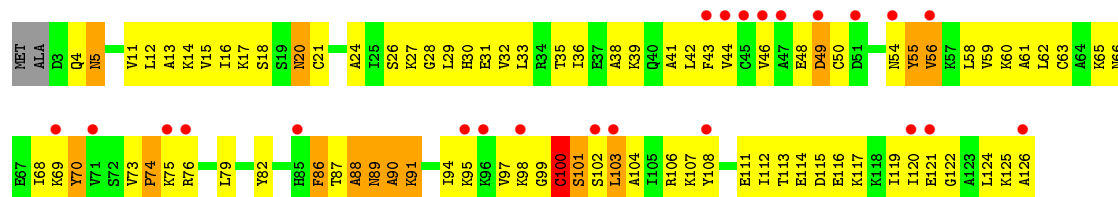


• Molecule 27: RACK1

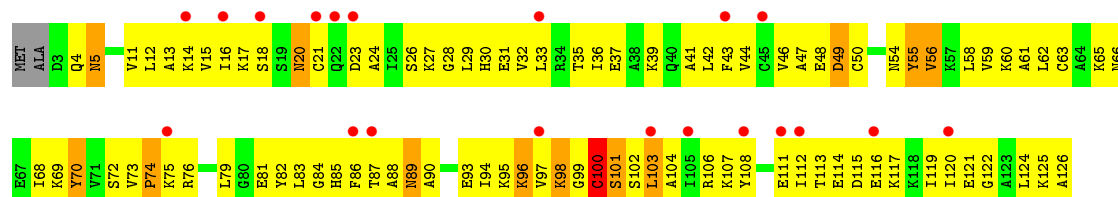




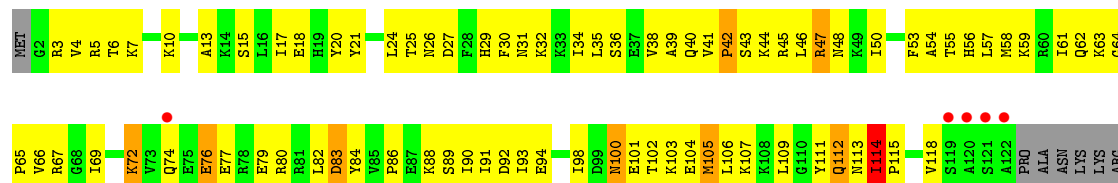
• Molecule 30: RIBOSOMAL PROTEIN L7AE CONTAINING PROTEIN



• Molecule 30: RIBOSOMAL PROTEIN L7AE CONTAINING PROTEIN

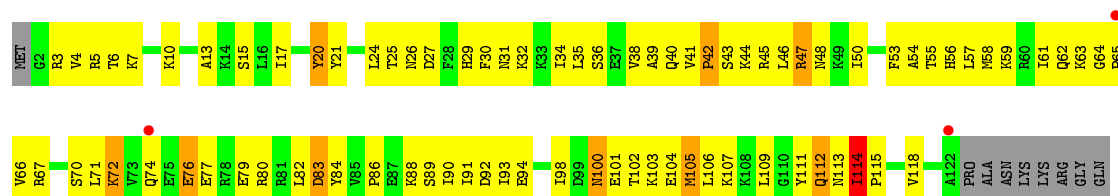


• Molecule 31: RPS17E



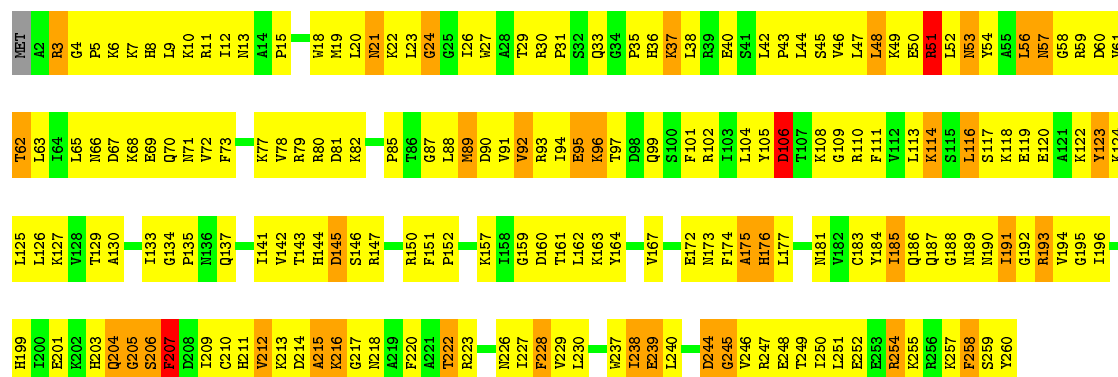
GLY
GLN

• Molecule 31: RPS17E

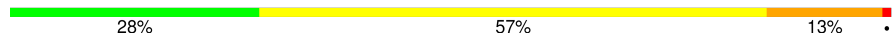


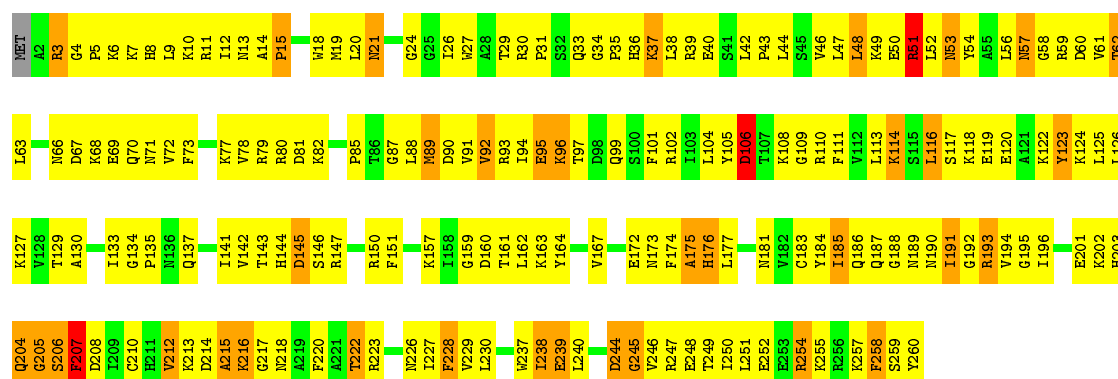
• Molecule 32: 40S RIBOSOMAL PROTEIN S4

Chain AW: 



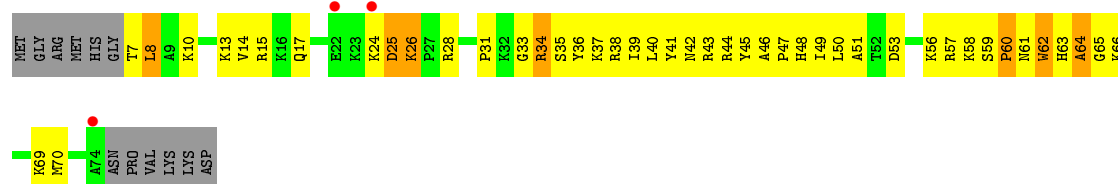
• Molecule 32: 40S RIBOSOMAL PROTEIN S4

Chain BW: 



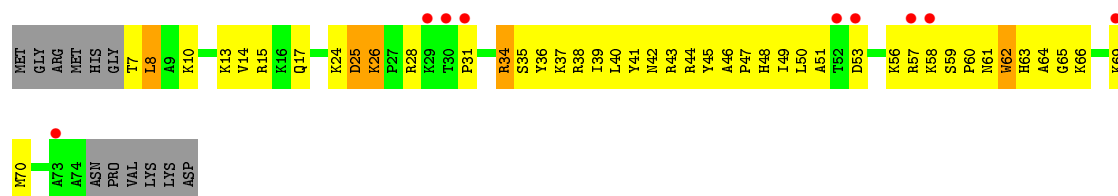
• Molecule 33: RPS30E

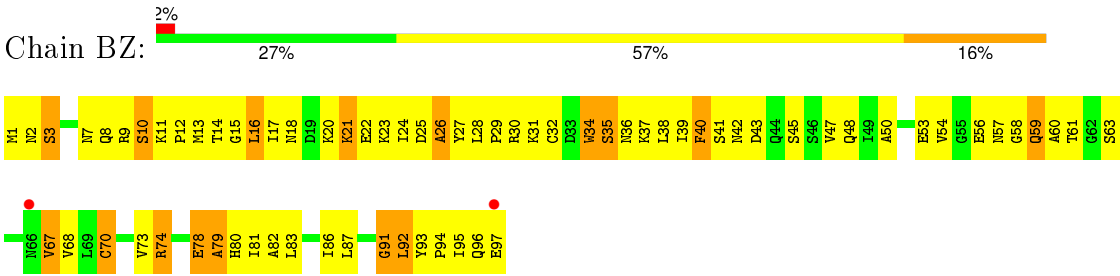
Chain AX: 



• Molecule 33: RPS30E

Chain BX: 





4 Data and refinement statistics

| Property | Value | Source |
|---|---|------------------|
| Space group | C 1 2 1 | Depositor |
| Cell constants a, b, c, α , β , γ | 320.52Å 362.21Å 412.11Å 90.00° 109.61° 90.00° | Depositor |
| Resolution (Å) | 25.00 – 3.93 97.05 – 3.93 | Depositor EDS |
| % Data completeness (in resolution range) | 85.1 (25.00-3.93) 85.1 (97.05-3.93) | Depositor EDS |
| R_{merge} | 0.15 | Depositor |
| R_{sym} | (Not available) | Depositor |
| $\langle I/\sigma(I) \rangle$ ¹ | 2.24 (at 3.89Å) | Xtriage |
| Refinement program | CNS 1.3 | Depositor |
| R, R_{free} | 0.206 , 0.243 0.209 , 0.243 | Depositor DCC |
| R_{free} test set | 6686 reflections (2.00%) | DCC |
| Wilson B-factor (Å ²) | 126.5 | Xtriage |
| Anisotropy | 0.335 | Xtriage |
| Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²) | 0.22 , 99.6 | EDS |
| Estimated twinning fraction | No twinning to report. | Xtriage |
| L-test for twinning ² | $\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$ | Xtriage |
| Outliers | 0 of 364650 reflections | Xtriage |
| F_o, F_c correlation | 0.89 | EDS |
| Total number of atoms | 157632 | wwPDB-VP |
| Average B, all atoms (Å ²) | 148.0 | wwPDB-VP |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.78% 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, 0.375 respectively for untwinned datasets, and 0.333, 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 | A1 | 0.38 | 0/518 | 0.74 | 0/688 |
| 1 | B1 | 0.37 | 0/518 | 0.73 | 0/688 |
| 2 | A2 | 0.38 | 0/1717 | 0.70 | 1/2288 (0.0%) |
| 2 | B2 | 0.39 | 0/1717 | 0.71 | 1/2288 (0.0%) |
| 3 | A3 | 0.41 | 0/1656 | 0.70 | 0/2223 |
| 3 | B3 | 0.42 | 0/1656 | 0.71 | 0/2223 |
| 4 | A4 | 0.40 | 0/1748 | 0.71 | 1/2340 (0.0%) |
| 4 | B4 | 0.40 | 0/1748 | 0.71 | 1/2340 (0.0%) |
| 5 | A5 | 0.42 | 0/807 | 0.77 | 0/1077 |
| 5 | B5 | 0.43 | 0/807 | 0.77 | 0/1077 |
| 6 | A6 | 0.46 | 0/640 | 0.71 | 0/855 |
| 6 | B6 | 0.48 | 0/640 | 0.71 | 0/855 |
| 7 | A7 | 0.40 | 0/879 | 0.73 | 0/1183 |
| 7 | B7 | 0.43 | 0/879 | 0.73 | 0/1183 |
| 8 | A8 | 0.38 | 0/732 | 0.66 | 0/974 |
| 8 | B8 | 0.37 | 0/732 | 0.65 | 0/974 |
| 9 | A9 | 0.39 | 0/605 | 0.69 | 0/799 |
| 9 | B9 | 0.39 | 0/605 | 0.69 | 0/799 |
| 10 | AA | 0.59 | 6/41668 (0.0%) | 0.86 | 69/64931 (0.1%) |
| 10 | BA | 0.58 | 6/41668 (0.0%) | 0.86 | 70/64931 (0.1%) |
| 11 | AB | 0.41 | 0/1676 | 0.66 | 0/2273 |
| 11 | BB | 0.40 | 0/1676 | 0.66 | 0/2273 |
| 12 | AC | 0.43 | 0/1855 | 0.71 | 0/2490 |
| 12 | BC | 0.42 | 0/1855 | 0.71 | 0/2490 |
| 13 | AD | 0.43 | 0/1498 | 0.69 | 0/1998 |
| 13 | BD | 0.41 | 0/1498 | 0.68 | 0/1998 |
| 14 | AE | 0.47 | 0/1873 | 0.75 | 1/2533 (0.0%) |
| 14 | BE | 0.46 | 0/1873 | 0.74 | 1/2533 (0.0%) |
| 15 | AF | 0.43 | 0/751 | 0.68 | 0/1010 |
| 15 | BF | 0.44 | 0/751 | 0.68 | 0/1010 |
| 16 | AG | 0.45 | 0/1546 | 0.71 | 0/2079 |
| 16 | BG | 0.45 | 0/1546 | 0.71 | 0/2079 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|------------------|-------------|-------------------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 17 | AH | 0.48 | 0/1058 | 0.83 | 0/1421 |
| 17 | BH | 0.49 | 0/1058 | 0.85 | 1/1421 (0.1%) |
| 18 | AI | 0.42 | 0/1151 | 0.68 | 0/1540 |
| 18 | BI | 0.41 | 0/1151 | 0.68 | 0/1540 |
| 19 | AJ | 0.38 | 0/842 | 0.77 | 0/1133 |
| 19 | BJ | 0.39 | 0/842 | 0.77 | 0/1133 |
| 20 | AK | 0.42 | 0/1078 | 0.73 | 0/1452 |
| 20 | BK | 0.41 | 0/1078 | 0.73 | 0/1452 |
| 21 | AL | 0.41 | 0/1114 | 0.73 | 0/1485 |
| 21 | BL | 0.43 | 0/1114 | 0.74 | 0/1485 |
| 22 | AM | 0.37 | 0/1260 | 0.67 | 0/1690 |
| 22 | BM | 0.39 | 0/1260 | 0.67 | 0/1690 |
| 23 | AN | 0.46 | 0/457 | 0.74 | 0/608 |
| 23 | BN | 0.49 | 0/457 | 0.75 | 0/608 |
| 24 | AO | 0.43 | 0/1238 | 0.74 | 1/1658 (0.1%) |
| 24 | BO | 0.41 | 0/1238 | 0.73 | 1/1658 (0.1%) |
| 25 | AP | 0.41 | 0/1215 | 0.70 | 0/1626 |
| 25 | BP | 0.41 | 0/1215 | 0.69 | 0/1626 |
| 26 | AQ | 0.46 | 0/1298 | 0.74 | 0/1741 |
| 26 | BQ | 0.44 | 0/1298 | 0.74 | 0/1741 |
| 27 | AR | 0.38 | 0/2750 | 0.69 | 0/3726 |
| 27 | BR | 0.38 | 0/2750 | 0.69 | 0/3726 |
| 28 | AS | 0.37 | 0/1003 | 0.65 | 1/1342 (0.1%) |
| 28 | BS | 0.39 | 0/1003 | 0.66 | 1/1342 (0.1%) |
| 29 | AT | 0.43 | 0/1233 | 0.66 | 0/1656 |
| 29 | BT | 0.42 | 0/1233 | 0.66 | 0/1656 |
| 30 | AU | 0.35 | 0/961 | 0.63 | 0/1288 |
| 30 | BU | 0.35 | 0/961 | 0.62 | 0/1288 |
| 31 | AV | 0.40 | 0/992 | 0.69 | 0/1326 |
| 31 | BV | 0.42 | 0/992 | 0.68 | 0/1326 |
| 32 | AW | 0.42 | 0/2119 | 0.74 | 0/2849 |
| 32 | BW | 0.42 | 0/2119 | 0.73 | 0/2849 |
| 33 | AX | 0.36 | 0/566 | 0.70 | 0/753 |
| 33 | BX | 0.36 | 0/566 | 0.71 | 0/753 |
| 34 | AY | 0.38 | 0/1895 | 0.67 | 0/2523 |
| 34 | BY | 0.38 | 0/1895 | 0.67 | 0/2523 |
| 35 | AZ | 0.42 | 0/755 | 0.75 | 0/1013 |
| 35 | BZ | 0.42 | 0/755 | 0.76 | 0/1013 |
| All | All | 0.51 | 12/166308 (0.0%) | 0.79 | 150/241142 (0.1%) |

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 |
|-----|-------|---------------------|---------------------|
| 5 | A5 | 0 | 1 |
| 5 | B5 | 0 | 1 |
| 10 | AA | 1 | 70 |
| 10 | BA | 1 | 74 |
| 26 | BQ | 0 | 1 |
| 27 | AR | 0 | 1 |
| 27 | BR | 0 | 1 |
| All | All | 2 | 149 |

The worst 5 of 12 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|-------|-------------|----------|
| 10 | AA | 1109 | U | O3'-P | 7.44 | 1.70 | 1.61 |
| 10 | BA | 1 | A | OP3-P | -7.12 | 1.52 | 1.61 |
| 10 | AA | 1 | A | OP3-P | -6.89 | 1.52 | 1.61 |
| 10 | BA | 1109 | U | O3'-P | -6.87 | 1.52 | 1.61 |
| 10 | AA | 1721 | G | O3'-P | 6.41 | 1.68 | 1.61 |

The worst 5 of 150 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|------------|-------|-------------|----------|
| 10 | AA | 1718 | A | N9-C1'-C2' | 11.64 | 129.13 | 114.00 |
| 10 | BA | 1718 | A | N9-C1'-C2' | 11.45 | 128.89 | 114.00 |
| 10 | BA | 1749 | C | N1-C1'-C2' | 10.71 | 127.93 | 114.00 |
| 10 | BA | 391 | A | N9-C1'-C2' | 10.52 | 127.67 | 114.00 |
| 10 | AA | 391 | A | N9-C1'-C2' | 10.36 | 127.47 | 114.00 |

All (2) chirality outliers are listed below:

| Mol | Chain | Res | Type | Atom |
|-----|-------|------|------|------|
| 10 | AA | 1718 | A | C1' |
| 10 | BA | 1718 | A | C1' |

5 of 149 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group |
|-----|-------|-----|------|-----------|
| 5 | A5 | 39 | TYR | Sidechain |
| 10 | AA | 43 | U | Sidechain |
| 10 | AA | 55 | U | Sidechain |
| 10 | AA | 59 | C | Sidechain |
| 10 | AA | 64 | U | Sidechain |

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 | A1 | 519 | 0 | 550 | 78 | 0 |
| 1 | B1 | 519 | 0 | 550 | 80 | 0 |
| 2 | A2 | 1693 | 0 | 1795 | 257 | 0 |
| 2 | B2 | 1693 | 0 | 1795 | 265 | 0 |
| 3 | A3 | 1629 | 0 | 1708 | 185 | 0 |
| 3 | B3 | 1629 | 0 | 1708 | 178 | 0 |
| 4 | A4 | 1724 | 0 | 1822 | 197 | 0 |
| 4 | B4 | 1724 | 0 | 1822 | 191 | 0 |
| 5 | A5 | 797 | 0 | 836 | 121 | 0 |
| 5 | B5 | 797 | 0 | 837 | 108 | 0 |
| 6 | A6 | 632 | 0 | 646 | 88 | 0 |
| 6 | B6 | 632 | 0 | 646 | 97 | 0 |
| 7 | A7 | 859 | 0 | 860 | 123 | 0 |
| 7 | B7 | 859 | 0 | 860 | 129 | 0 |
| 8 | A8 | 725 | 0 | 795 | 134 | 0 |
| 8 | B8 | 725 | 0 | 795 | 124 | 0 |
| 9 | A9 | 742 | 0 | 785 | 148 | 0 |
| 9 | B9 | 742 | 0 | 787 | 134 | 0 |
| 10 | AA | 37231 | 0 | 18715 | 3075 | 0 |
| 10 | BA | 37231 | 0 | 18715 | 3021 | 0 |
| 11 | AB | 1642 | 0 | 1653 | 207 | 0 |
| 11 | BB | 1642 | 0 | 1653 | 216 | 0 |
| 12 | AC | 1820 | 0 | 1920 | 241 | 0 |
| 12 | BC | 1820 | 0 | 1920 | 236 | 0 |
| 13 | AD | 1475 | 0 | 1571 | 213 | 0 |
| 13 | BD | 1475 | 0 | 1571 | 211 | 0 |
| 14 | AE | 1827 | 0 | 1861 | 287 | 0 |
| 14 | BE | 1827 | 0 | 1861 | 282 | 0 |
| 15 | AF | 736 | 0 | 722 | 78 | 0 |
| 15 | BF | 736 | 0 | 722 | 88 | 0 |
| 16 | AG | 1520 | 0 | 1572 | 231 | 0 |
| 16 | BG | 1520 | 0 | 1572 | 231 | 0 |
| 17 | AH | 1040 | 0 | 1096 | 166 | 0 |
| 17 | BH | 1040 | 0 | 1096 | 170 | 0 |
| 18 | AI | 1135 | 0 | 1204 | 159 | 0 |
| 18 | BI | 1135 | 0 | 1204 | 146 | 0 |
| 19 | AJ | 833 | 0 | 903 | 82 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 19 | BJ | 833 | 0 | 903 | 81 | 0 |
| 20 | AK | 1063 | 0 | 1088 | 184 | 0 |
| 20 | BK | 1063 | 0 | 1088 | 178 | 0 |
| 21 | AL | 1097 | 0 | 1169 | 138 | 0 |
| 21 | BL | 1097 | 0 | 1169 | 135 | 0 |
| 22 | AM | 1239 | 0 | 1288 | 192 | 0 |
| 22 | BM | 1239 | 0 | 1288 | 192 | 0 |
| 23 | AN | 447 | 0 | 446 | 74 | 0 |
| 23 | BN | 447 | 0 | 446 | 81 | 0 |
| 24 | AO | 1214 | 0 | 1322 | 131 | 0 |
| 24 | BO | 1214 | 0 | 1322 | 131 | 0 |
| 25 | AP | 1197 | 0 | 1285 | 152 | 0 |
| 25 | BP | 1197 | 0 | 1285 | 142 | 0 |
| 26 | AQ | 1275 | 0 | 1354 | 213 | 0 |
| 26 | BQ | 1275 | 0 | 1354 | 199 | 0 |
| 27 | AR | 2682 | 0 | 2629 | 355 | 0 |
| 27 | BR | 2682 | 0 | 2629 | 327 | 0 |
| 28 | AS | 985 | 0 | 1026 | 114 | 0 |
| 28 | BS | 985 | 0 | 1026 | 122 | 0 |
| 29 | AT | 1211 | 0 | 1265 | 159 | 0 |
| 29 | BT | 1211 | 0 | 1265 | 162 | 0 |
| 30 | AU | 952 | 0 | 993 | 107 | 0 |
| 30 | BU | 952 | 0 | 993 | 124 | 0 |
| 31 | AV | 979 | 0 | 1041 | 136 | 0 |
| 31 | BV | 979 | 0 | 1041 | 141 | 0 |
| 32 | AW | 2079 | 0 | 2151 | 286 | 0 |
| 32 | BW | 2079 | 0 | 2151 | 293 | 0 |
| 33 | AX | 554 | 0 | 604 | 64 | 0 |
| 33 | BX | 554 | 0 | 604 | 72 | 0 |
| 34 | AY | 1868 | 0 | 1999 | 256 | 0 |
| 34 | BY | 1868 | 0 | 1999 | 242 | 0 |
| 35 | AZ | 747 | 0 | 758 | 107 | 0 |
| 35 | BZ | 747 | 0 | 758 | 109 | 0 |
| 36 | A4 | 1 | 0 | 0 | 0 | 0 |
| 36 | AA | 90 | 0 | 0 | 0 | 0 |
| 36 | AL | 1 | 0 | 0 | 0 | 0 |
| 36 | B4 | 1 | 0 | 0 | 0 | 0 |
| 36 | BA | 89 | 0 | 0 | 0 | 0 |
| 36 | BD | 1 | 0 | 0 | 0 | 0 |
| 36 | BW | 1 | 0 | 0 | 0 | 0 |
| 37 | A5 | 1 | 0 | 0 | 0 | 0 |
| 37 | A6 | 1 | 0 | 0 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 37 | A9 | 1 | 0 | 0 | 0 | 0 |
| 37 | AN | 1 | 0 | 0 | 0 | 0 |
| 37 | B5 | 1 | 0 | 0 | 0 | 0 |
| 37 | B6 | 1 | 0 | 0 | 0 | 0 |
| 37 | B9 | 1 | 0 | 0 | 0 | 0 |
| 37 | BN | 1 | 0 | 0 | 0 | 0 |
| 38 | A2 | 2 | 0 | 0 | 0 | 0 |
| 38 | A4 | 2 | 0 | 0 | 0 | 0 |
| 38 | A5 | 1 | 0 | 0 | 0 | 0 |
| 38 | AA | 516 | 0 | 0 | 14 | 0 |
| 38 | AC | 1 | 0 | 0 | 0 | 0 |
| 38 | AD | 4 | 0 | 0 | 0 | 0 |
| 38 | AE | 3 | 0 | 0 | 0 | 0 |
| 38 | AL | 3 | 0 | 0 | 0 | 0 |
| 38 | AM | 4 | 0 | 0 | 1 | 0 |
| 38 | AO | 1 | 0 | 0 | 0 | 0 |
| 38 | AP | 1 | 0 | 0 | 0 | 0 |
| 38 | AQ | 2 | 0 | 0 | 0 | 0 |
| 38 | AT | 4 | 0 | 0 | 0 | 0 |
| 38 | AW | 4 | 0 | 0 | 0 | 0 |
| 38 | AY | 4 | 0 | 0 | 0 | 0 |
| 38 | B2 | 2 | 0 | 0 | 0 | 0 |
| 38 | B4 | 2 | 0 | 0 | 0 | 0 |
| 38 | B5 | 1 | 0 | 0 | 0 | 0 |
| 38 | BA | 512 | 0 | 0 | 5 | 0 |
| 38 | BC | 2 | 0 | 0 | 0 | 0 |
| 38 | BD | 2 | 0 | 0 | 0 | 0 |
| 38 | BE | 5 | 0 | 0 | 0 | 0 |
| 38 | BK | 1 | 0 | 0 | 0 | 0 |
| 38 | BL | 2 | 0 | 0 | 0 | 0 |
| 38 | BM | 6 | 0 | 0 | 0 | 0 |
| 38 | BO | 1 | 0 | 0 | 0 | 0 |
| 38 | BP | 1 | 0 | 0 | 0 | 0 |
| 38 | BQ | 1 | 0 | 0 | 0 | 0 |
| 38 | BT | 6 | 0 | 0 | 0 | 0 |
| 38 | BW | 5 | 0 | 0 | 0 | 0 |
| 38 | BY | 3 | 0 | 0 | 0 | 0 |
| All | All | 157632 | 0 | 122867 | 15283 | 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 55.

The worst 5 of 15283 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) |
|-------------------|-----------------|--------------------------|-------------------|
| 10:AA:604:G:H1 | 10:AA:1080:G:N2 | 1.23 | 1.36 |
| 4:A4:207:THR:HG21 | 4:A4:213:LEU:HG | 1.21 | 1.21 |
| 10:BA:604:G:H1 | 10:BA:1080:G:N2 | 1.40 | 1.19 |
| 21:AL:9:ILE:HD12 | 21:AL:9:ILE:H | 1.02 | 1.18 |
| 10:AA:534:A:H3' | 10:AA:535:A:H5' | 1.18 | 1.18 |

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|----|
| 1 | A1 | 65/68 (96%) | 45 (69%) | 11 (17%) | 9 (14%) | 0 | 6 |
| 1 | B1 | 65/68 (96%) | 44 (68%) | 12 (18%) | 9 (14%) | 0 | 6 |
| 2 | A2 | 205/208 (99%) | 147 (72%) | 38 (18%) | 20 (10%) | 1 | 14 |
| 2 | B2 | 205/208 (99%) | 146 (71%) | 39 (19%) | 20 (10%) | 1 | 14 |
| 3 | A3 | 194/197 (98%) | 159 (82%) | 25 (13%) | 10 (5%) | 2 | 31 |
| 3 | B3 | 194/197 (98%) | 159 (82%) | 24 (12%) | 11 (6%) | 2 | 28 |
| 4 | A4 | 213/265 (80%) | 161 (76%) | 33 (16%) | 19 (9%) | 1 | 16 |
| 4 | B4 | 213/265 (80%) | 161 (76%) | 34 (16%) | 18 (8%) | 1 | 17 |
| 5 | A5 | 96/119 (81%) | 66 (69%) | 20 (21%) | 10 (10%) | 1 | 12 |
| 5 | B5 | 96/119 (81%) | 65 (68%) | 21 (22%) | 10 (10%) | 1 | 12 |
| 6 | A6 | 78/81 (96%) | 57 (73%) | 15 (19%) | 6 (8%) | 1 | 20 |
| 6 | B6 | 78/81 (96%) | 57 (73%) | 15 (19%) | 6 (8%) | 1 | 20 |
| 7 | A7 | 102/162 (63%) | 78 (76%) | 17 (17%) | 7 (7%) | 1 | 24 |
| 7 | B7 | 102/162 (63%) | 78 (76%) | 17 (17%) | 7 (7%) | 1 | 24 |
| 8 | A8 | 91/143 (64%) | 71 (78%) | 13 (14%) | 7 (8%) | 1 | 20 |
| 8 | B8 | 91/143 (64%) | 71 (78%) | 13 (14%) | 7 (8%) | 1 | 20 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|----------|----------|-------------|----|
| 9 | A9 | 72/189 (38%) | 50 (69%) | 17 (24%) | 5 (7%) | 1 | 24 |
| 9 | B9 | 72/189 (38%) | 50 (69%) | 17 (24%) | 5 (7%) | 1 | 24 |
| 11 | AB | 202/241 (84%) | 168 (83%) | 28 (14%) | 6 (3%) | 5 | 45 |
| 11 | BB | 202/241 (84%) | 167 (83%) | 28 (14%) | 7 (4%) | 4 | 42 |
| 12 | AC | 227/243 (93%) | 177 (78%) | 31 (14%) | 19 (8%) | 1 | 17 |
| 12 | BC | 227/243 (93%) | 176 (78%) | 32 (14%) | 19 (8%) | 1 | 17 |
| 13 | AD | 177/181 (98%) | 132 (75%) | 36 (20%) | 9 (5%) | 2 | 31 |
| 13 | BD | 177/181 (98%) | 130 (73%) | 38 (22%) | 9 (5%) | 2 | 31 |
| 14 | AE | 228/296 (77%) | 170 (75%) | 40 (18%) | 18 (8%) | 1 | 19 |
| 14 | BE | 228/296 (77%) | 172 (75%) | 39 (17%) | 17 (8%) | 1 | 21 |
| 15 | AF | 87/101 (86%) | 70 (80%) | 12 (14%) | 5 (6%) | 2 | 28 |
| 15 | BF | 87/101 (86%) | 70 (80%) | 12 (14%) | 5 (6%) | 2 | 28 |
| 16 | AG | 190/200 (95%) | 141 (74%) | 33 (17%) | 16 (8%) | 1 | 17 |
| 16 | BG | 190/200 (95%) | 142 (75%) | 31 (16%) | 17 (9%) | 1 | 16 |
| 17 | AH | 127/130 (98%) | 98 (77%) | 24 (19%) | 5 (4%) | 4 | 38 |
| 17 | BH | 127/130 (98%) | 98 (77%) | 26 (20%) | 3 (2%) | 7 | 50 |
| 18 | AI | 141/145 (97%) | 111 (79%) | 25 (18%) | 5 (4%) | 4 | 42 |
| 18 | BI | 141/145 (97%) | 110 (78%) | 26 (18%) | 5 (4%) | 4 | 42 |
| 19 | AJ | 103/120 (86%) | 89 (86%) | 6 (6%) | 8 (8%) | 1 | 20 |
| 19 | BJ | 103/120 (86%) | 89 (86%) | 6 (6%) | 8 (8%) | 1 | 20 |
| 20 | AK | 138/151 (91%) | 96 (70%) | 28 (20%) | 14 (10%) | 1 | 13 |
| 20 | BK | 138/151 (91%) | 95 (69%) | 27 (20%) | 16 (12%) | 0 | 9 |
| 21 | AL | 139/142 (98%) | 106 (76%) | 17 (12%) | 16 (12%) | 0 | 9 |
| 21 | BL | 139/142 (98%) | 106 (76%) | 18 (13%) | 15 (11%) | 0 | 11 |
| 22 | AM | 152/155 (98%) | 109 (72%) | 22 (14%) | 21 (14%) | 0 | 6 |
| 22 | BM | 152/155 (98%) | 110 (72%) | 21 (14%) | 21 (14%) | 0 | 6 |
| 23 | AN | 51/55 (93%) | 30 (59%) | 11 (22%) | 10 (20%) | 0 | 3 |
| 23 | BN | 51/55 (93%) | 31 (61%) | 11 (22%) | 9 (18%) | 0 | 3 |
| 24 | AO | 148/153 (97%) | 112 (76%) | 20 (14%) | 16 (11%) | 0 | 11 |
| 24 | BO | 148/153 (97%) | 113 (76%) | 19 (13%) | 16 (11%) | 0 | 11 |
| 25 | AP | 146/149 (98%) | 115 (79%) | 20 (14%) | 11 (8%) | 1 | 21 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|------------|------------|----------|-------------|----|
| 25 | BP | 146/149 (98%) | 115 (79%) | 20 (14%) | 11 (8%) | 1 | 21 |
| 26 | AQ | 155/157 (99%) | 115 (74%) | 26 (17%) | 14 (9%) | 1 | 16 |
| 26 | BQ | 155/157 (99%) | 112 (72%) | 27 (17%) | 16 (10%) | 1 | 12 |
| 27 | AR | 336/343 (98%) | 255 (76%) | 48 (14%) | 33 (10%) | 1 | 14 |
| 27 | BR | 336/343 (98%) | 256 (76%) | 48 (14%) | 32 (10%) | 1 | 15 |
| 28 | AS | 123/144 (85%) | 91 (74%) | 25 (20%) | 7 (6%) | 2 | 28 |
| 28 | BS | 123/144 (85%) | 90 (73%) | 25 (20%) | 8 (6%) | 1 | 26 |
| 29 | AT | 148/155 (96%) | 114 (77%) | 17 (12%) | 17 (12%) | 0 | 9 |
| 29 | BT | 148/155 (96%) | 113 (76%) | 20 (14%) | 15 (10%) | 1 | 13 |
| 30 | AU | 122/126 (97%) | 91 (75%) | 20 (16%) | 11 (9%) | 1 | 16 |
| 30 | BU | 122/126 (97%) | 89 (73%) | 22 (18%) | 11 (9%) | 1 | 16 |
| 31 | AV | 119/130 (92%) | 94 (79%) | 16 (13%) | 9 (8%) | 1 | 20 |
| 31 | BV | 119/130 (92%) | 96 (81%) | 14 (12%) | 9 (8%) | 1 | 20 |
| 32 | AW | 257/260 (99%) | 193 (75%) | 40 (16%) | 24 (9%) | 1 | 16 |
| 32 | BW | 257/260 (99%) | 195 (76%) | 38 (15%) | 24 (9%) | 1 | 16 |
| 33 | AX | 66/80 (82%) | 48 (73%) | 12 (18%) | 6 (9%) | 1 | 16 |
| 33 | BX | 66/80 (82%) | 48 (73%) | 12 (18%) | 6 (9%) | 1 | 16 |
| 34 | AY | 233/293 (80%) | 188 (81%) | 31 (13%) | 14 (6%) | 2 | 27 |
| 34 | BY | 233/293 (80%) | 187 (80%) | 32 (14%) | 14 (6%) | 2 | 27 |
| 35 | AZ | 95/97 (98%) | 70 (74%) | 13 (14%) | 12 (13%) | 0 | 8 |
| 35 | BZ | 95/97 (98%) | 69 (73%) | 14 (15%) | 12 (13%) | 0 | 8 |
| All | All | 10052/11358 (88%) | 7627 (76%) | 1588 (16%) | 837 (8%) | 1 | 18 |

5 of 837 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1 | A1 | 20 | SER |
| 1 | A1 | 35 | LYS |
| 1 | A1 | 37 | GLU |
| 1 | A1 | 59 | GLU |
| 1 | A1 | 63 | GLU |

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 | A1 | 56/57 (98%) | 53 (95%) | 3 (5%) | 27 | 67 |
| 1 | B1 | 56/57 (98%) | 53 (95%) | 3 (5%) | 27 | 67 |
| 2 | A2 | 184/185 (100%) | 171 (93%) | 13 (7%) | 18 | 58 |
| 2 | B2 | 184/185 (100%) | 171 (93%) | 13 (7%) | 18 | 58 |
| 3 | A3 | 182/183 (100%) | 164 (90%) | 18 (10%) | 10 | 43 |
| 3 | B3 | 182/183 (100%) | 165 (91%) | 17 (9%) | 11 | 46 |
| 4 | A4 | 191/225 (85%) | 166 (87%) | 25 (13%) | 5 | 30 |
| 4 | B4 | 191/225 (85%) | 166 (87%) | 25 (13%) | 5 | 30 |
| 5 | A5 | 88/107 (82%) | 80 (91%) | 8 (9%) | 12 | 47 |
| 5 | B5 | 88/107 (82%) | 80 (91%) | 8 (9%) | 12 | 47 |
| 6 | A6 | 71/72 (99%) | 67 (94%) | 4 (6%) | 26 | 65 |
| 6 | B6 | 71/72 (99%) | 67 (94%) | 4 (6%) | 26 | 65 |
| 7 | A7 | 94/136 (69%) | 84 (89%) | 10 (11%) | 8 | 39 |
| 7 | B7 | 94/136 (69%) | 84 (89%) | 10 (11%) | 8 | 39 |
| 8 | A8 | 80/109 (73%) | 68 (85%) | 12 (15%) | 3 | 25 |
| 8 | B8 | 80/109 (73%) | 68 (85%) | 12 (15%) | 3 | 25 |
| 9 | A9 | 64/138 (46%) | 56 (88%) | 8 (12%) | 6 | 32 |
| 9 | B9 | 64/138 (46%) | 56 (88%) | 8 (12%) | 6 | 32 |
| 11 | AB | 183/211 (87%) | 167 (91%) | 16 (9%) | 13 | 49 |
| 11 | BB | 183/211 (87%) | 167 (91%) | 16 (9%) | 13 | 49 |
| 12 | AC | 197/210 (94%) | 178 (90%) | 19 (10%) | 10 | 44 |
| 12 | BC | 197/210 (94%) | 179 (91%) | 18 (9%) | 12 | 47 |
| 13 | AD | 161/162 (99%) | 137 (85%) | 24 (15%) | 4 | 25 |
| 13 | BD | 161/162 (99%) | 137 (85%) | 24 (15%) | 4 | 25 |
| 14 | AE | 194/250 (78%) | 171 (88%) | 23 (12%) | 6 | 34 |
| 14 | BE | 194/250 (78%) | 171 (88%) | 23 (12%) | 6 | 34 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|-----------|----------|-------------|----|
| 15 | AF | 80/92 (87%) | 72 (90%) | 8 (10%) | 9 | 42 |
| 15 | BF | 80/92 (87%) | 71 (89%) | 9 (11%) | 7 | 37 |
| 16 | AG | 163/169 (96%) | 147 (90%) | 16 (10%) | 10 | 43 |
| 16 | BG | 163/169 (96%) | 146 (90%) | 17 (10%) | 9 | 40 |
| 17 | AH | 116/117 (99%) | 101 (87%) | 15 (13%) | 5 | 31 |
| 17 | BH | 116/117 (99%) | 102 (88%) | 14 (12%) | 6 | 33 |
| 18 | AI | 120/122 (98%) | 115 (96%) | 5 (4%) | 36 | 72 |
| 18 | BI | 120/122 (98%) | 115 (96%) | 5 (4%) | 36 | 72 |
| 19 | AJ | 98/111 (88%) | 93 (95%) | 5 (5%) | 29 | 68 |
| 19 | BJ | 98/111 (88%) | 93 (95%) | 5 (5%) | 29 | 68 |
| 20 | AK | 112/121 (93%) | 96 (86%) | 16 (14%) | 4 | 27 |
| 20 | BK | 112/121 (93%) | 96 (86%) | 16 (14%) | 4 | 27 |
| 21 | AL | 113/114 (99%) | 101 (89%) | 12 (11%) | 8 | 39 |
| 21 | BL | 113/114 (99%) | 102 (90%) | 11 (10%) | 10 | 43 |
| 22 | AM | 134/135 (99%) | 121 (90%) | 13 (10%) | 10 | 43 |
| 22 | BM | 134/135 (99%) | 121 (90%) | 13 (10%) | 10 | 43 |
| 23 | AN | 47/49 (96%) | 41 (87%) | 6 (13%) | 5 | 31 |
| 23 | BN | 47/49 (96%) | 41 (87%) | 6 (13%) | 5 | 31 |
| 24 | AO | 134/136 (98%) | 127 (95%) | 7 (5%) | 29 | 68 |
| 24 | BO | 134/136 (98%) | 127 (95%) | 7 (5%) | 29 | 68 |
| 25 | AP | 133/134 (99%) | 124 (93%) | 9 (7%) | 20 | 59 |
| 25 | BP | 133/134 (99%) | 124 (93%) | 9 (7%) | 20 | 59 |
| 26 | AQ | 141/141 (100%) | 125 (89%) | 16 (11%) | 7 | 37 |
| 26 | BQ | 141/141 (100%) | 126 (89%) | 15 (11%) | 8 | 39 |
| 27 | AR | 291/295 (99%) | 261 (90%) | 30 (10%) | 9 | 41 |
| 27 | BR | 291/295 (99%) | 260 (89%) | 31 (11%) | 8 | 39 |
| 28 | AS | 105/117 (90%) | 102 (97%) | 3 (3%) | 50 | 79 |
| 28 | BS | 105/117 (90%) | 101 (96%) | 4 (4%) | 40 | 75 |
| 29 | AT | 129/134 (96%) | 117 (91%) | 12 (9%) | 11 | 46 |
| 29 | BT | 129/134 (96%) | 116 (90%) | 13 (10%) | 9 | 42 |
| 30 | AU | 103/104 (99%) | 97 (94%) | 6 (6%) | 25 | 64 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-----------------|------------|-----------|-------------|----|
| 30 | BU | 103/104 (99%) | 99 (96%) | 4 (4%) | 39 | 74 |
| 31 | AV | 108/115 (94%) | 100 (93%) | 8 (7%) | 17 | 56 |
| 31 | BV | 108/115 (94%) | 99 (92%) | 9 (8%) | 14 | 51 |
| 32 | AW | 226/227 (100%) | 196 (87%) | 30 (13%) | 5 | 30 |
| 32 | BW | 226/227 (100%) | 197 (87%) | 29 (13%) | 5 | 31 |
| 33 | AX | 57/67 (85%) | 55 (96%) | 2 (4%) | 43 | 77 |
| 33 | BX | 57/67 (85%) | 55 (96%) | 2 (4%) | 43 | 77 |
| 34 | AY | 201/244 (82%) | 187 (93%) | 14 (7%) | 19 | 58 |
| 34 | BY | 201/244 (82%) | 187 (93%) | 14 (7%) | 19 | 58 |
| 35 | AZ | 82/82 (100%) | 76 (93%) | 6 (7%) | 17 | 57 |
| 35 | BZ | 82/82 (100%) | 76 (93%) | 6 (7%) | 17 | 57 |
| All | All | 8876/9742 (91%) | 8034 (90%) | 842 (10%) | 11 | 44 |

5 of 842 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 32 | AW | 106 | ASP |
| 4 | B4 | 134 | ASP |
| 30 | BU | 20 | ASN |
| 32 | AW | 212 | VAL |
| 2 | B2 | 35 | MET |

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 276 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 31 | AV | 48 | ASN |
| 4 | B4 | 175 | ASN |
| 30 | BU | 7 | GLN |
| 32 | AW | 53 | ASN |
| 34 | AY | 206 | ASN |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 10 | AA | 1743/1753 (99%) | 452 (25%) | 194 (11%) |
| 10 | BA | 1743/1753 (99%) | 453 (25%) | 194 (11%) |

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| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| All | All | 3486/3506 (99%) | 905 (25%) | 388 (11%) |

5 of 905 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 10 | AA | 2 | A |
| 10 | AA | 3 | C |
| 10 | AA | 4 | C |
| 10 | AA | 9 | U |
| 10 | AA | 17 | C |

5 of 388 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 10 | AA | 1555 | A |
| 10 | BA | 164 | U |
| 10 | BA | 1443 | A |
| 10 | AA | 1605 | A |
| 10 | BA | 41 | U |

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 192 ligands modelled in this entry, 192 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 | A1 | 67/68 (98%) | -0.25 | 1 (1%) 76 66 | 99, 157, 220, 262 | 0 |
| 1 | B1 | 67/68 (98%) | -0.50 | 0 100 100 | 99, 157, 220, 262 | 0 |
| 2 | A2 | 207/208 (99%) | 1.21 | 57 (27%) 1 1 | 96, 144, 194, 231 | 0 |
| 2 | B2 | 207/208 (99%) | 0.61 | 15 (7%) 18 12 | 98, 145, 194, 231 | 0 |
| 3 | A3 | 196/197 (99%) | 0.02 | 6 (3%) 52 40 | 82, 138, 187, 267 | 0 |
| 3 | B3 | 196/197 (99%) | -0.07 | 4 (2%) 68 57 | 75, 138, 186, 266 | 0 |
| 4 | A4 | 215/265 (81%) | 0.63 | 24 (11%) 7 6 | 80, 146, 201, 228 | 0 |
| 4 | B4 | 215/265 (81%) | 0.78 | 31 (14%) 3 4 | 77, 145, 202, 229 | 0 |
| 5 | A5 | 98/119 (82%) | 0.13 | 3 (3%) 52 40 | 71, 124, 201, 246 | 0 |
| 5 | B5 | 98/119 (82%) | 0.55 | 8 (8%) 14 10 | 68, 124, 201, 246 | 0 |
| 6 | A6 | 80/81 (98%) | 0.12 | 0 100 100 | 86, 130, 172, 187 | 0 |
| 6 | B6 | 80/81 (98%) | -0.22 | 0 100 100 | 86, 128, 172, 186 | 0 |
| 7 | A7 | 104/162 (64%) | -0.10 | 0 100 100 | 100, 150, 201, 249 | 0 |
| 7 | B7 | 104/162 (64%) | 0.22 | 7 (6%) 21 14 | 104, 151, 199, 249 | 0 |
| 8 | A8 | 93/143 (65%) | 0.10 | 1 (1%) 82 74 | 112, 159, 219, 255 | 0 |
| 8 | B8 | 93/143 (65%) | 0.13 | 3 (3%) 51 38 | 110, 159, 219, 256 | 0 |
| 9 | A9 | 73/189 (38%) | 0.28 | 6 (8%) 14 10 | 146, 185, 238, 253 | 0 |
| 9 | B9 | 73/189 (38%) | 0.63 | 13 (17%) 2 2 | 148, 186, 238, 254 | 0 |
| 10 | AA | 1745/1753 (99%) | 0.11 | 32 (1%) 71 61 | 80, 134, 291, 454 | 0 |
| 10 | BA | 1745/1753 (99%) | 0.09 | 31 (1%) 71 61 | 80, 134, 291, 454 | 0 |
| 11 | AB | 204/241 (84%) | -0.27 | 4 (1%) 68 57 | 82, 136, 177, 225 | 0 |
| 11 | BB | 204/241 (84%) | -0.02 | 2 (0%) 84 77 | 78, 136, 177, 224 | 0 |
| 12 | AC | 229/243 (94%) | -0.18 | 2 (0%) 85 79 | 89, 131, 194, 244 | 0 |
| 12 | BC | 229/243 (94%) | -0.31 | 0 100 100 | 87, 132, 195, 246 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|----------------|--------|---------------|-----------------------|-------|
| 13 | AD | 179/181 (98%) | 0.20 | 3 (1%) 73 62 | 77, 122, 182, 214 | 0 |
| 13 | BD | 179/181 (98%) | -0.01 | 4 (2%) 65 54 | 82, 125, 184, 215 | 0 |
| 14 | AE | 230/296 (77%) | 0.03 | 4 (1%) 73 62 | 62, 114, 194, 243 | 0 |
| 14 | BE | 230/296 (77%) | -0.13 | 3 (1%) 79 70 | 65, 116, 194, 244 | 0 |
| 15 | AF | 89/101 (88%) | -0.28 | 1 (1%) 82 74 | 87, 136, 190, 230 | 0 |
| 15 | BF | 89/101 (88%) | -0.33 | 0 100 100 | 86, 137, 190, 229 | 0 |
| 16 | AG | 192/200 (96%) | 0.05 | 2 (1%) 84 77 | 86, 140, 191, 286 | 0 |
| 16 | BG | 192/200 (96%) | -0.10 | 6 (3%) 52 40 | 86, 140, 191, 287 | 0 |
| 17 | AH | 129/130 (99%) | -0.18 | 0 100 100 | 65, 105, 154, 194 | 0 |
| 17 | BH | 129/130 (99%) | -0.07 | 0 100 100 | 62, 106, 154, 193 | 0 |
| 18 | AI | 143/145 (98%) | 0.59 | 17 (11%) 6 5 | 87, 135, 188, 222 | 0 |
| 18 | BI | 143/145 (98%) | 0.68 | 14 (9%) 10 7 | 87, 135, 189, 221 | 0 |
| 19 | AJ | 105/120 (87%) | -0.11 | 1 (0%) 84 77 | 84, 132, 199, 218 | 0 |
| 19 | BJ | 105/120 (87%) | -0.05 | 1 (0%) 84 77 | 86, 133, 198, 218 | 0 |
| 20 | AK | 140/151 (92%) | 0.08 | 3 (2%) 67 55 | 93, 144, 191, 223 | 0 |
| 20 | BK | 140/151 (92%) | 0.50 | 12 (8%) 13 10 | 90, 144, 192, 224 | 0 |
| 21 | AL | 141/142 (99%) | 0.20 | 4 (2%) 56 44 | 71, 126, 169, 213 | 0 |
| 21 | BL | 141/142 (99%) | 0.94 | 26 (18%) 2 2 | 74, 128, 169, 212 | 0 |
| 22 | AM | 154/155 (99%) | 0.44 | 7 (4%) 37 27 | 94, 154, 204, 233 | 0 |
| 22 | BM | 154/155 (99%) | 0.34 | 6 (3%) 43 32 | 95, 155, 205, 233 | 0 |
| 23 | AN | 53/55 (96%) | 0.24 | 0 100 100 | 83, 124, 156, 193 | 0 |
| 23 | BN | 53/55 (96%) | 0.81 | 9 (16%) 2 3 | 83, 126, 157, 192 | 0 |
| 24 | AO | 150/153 (98%) | -0.14 | 0 100 100 | 73, 124, 223, 287 | 0 |
| 24 | BO | 150/153 (98%) | 0.06 | 2 (1%) 79 70 | 71, 124, 222, 288 | 0 |
| 25 | AP | 148/149 (99%) | 0.32 | 11 (7%) 17 12 | 92, 141, 168, 200 | 0 |
| 25 | BP | 148/149 (99%) | 0.07 | 5 (3%) 49 37 | 94, 141, 170, 200 | 0 |
| 26 | AQ | 157/157 (100%) | 0.14 | 10 (6%) 23 15 | 69, 129, 214, 227 | 0 |
| 26 | BQ | 157/157 (100%) | 0.22 | 4 (2%) 61 48 | 65, 128, 208, 258 | 0 |
| 27 | AR | 338/343 (98%) | 0.20 | 16 (4%) 35 26 | 93, 146, 218, 268 | 0 |
| 27 | BR | 338/343 (98%) | -0.02 | 9 (2%) 58 46 | 94, 145, 209, 245 | 0 |
| 28 | AS | 125/144 (86%) | 0.09 | 5 (4%) 42 31 | 117, 165, 222, 245 | 0 |

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| Mol | Chain | Analysed | <RSRZ> | #RSRZ>2 | OWAB(Å ²) | Q<0.9 |
|-----|-------|-------------------|--------|----------------|-----------------------|-------|
| 28 | BS | 125/144 (86%) | 1.58 | 45 (36%) 0 1 | 119, 165, 222, 245 | 0 |
| 29 | AT | 150/155 (96%) | 1.02 | 25 (16%) 2 3 | 80, 152, 191, 230 | 0 |
| 29 | BT | 150/155 (96%) | 0.71 | 21 (14%) 4 4 | 79, 151, 192, 229 | 0 |
| 30 | AU | 124/126 (98%) | 0.68 | 23 (18%) 2 2 | 117, 177, 213, 227 | 0 |
| 30 | BU | 124/126 (98%) | 0.98 | 20 (16%) 3 3 | 136, 185, 221, 250 | 0 |
| 31 | AV | 121/130 (93%) | -0.15 | 5 (4%) 41 30 | 78, 143, 206, 254 | 0 |
| 31 | BV | 121/130 (93%) | 0.21 | 3 (2%) 61 48 | 76, 142, 206, 253 | 0 |
| 32 | AW | 259/260 (99%) | -0.19 | 0 100 100 | 84, 125, 166, 200 | 0 |
| 32 | BW | 259/260 (99%) | -0.42 | 0 100 100 | 87, 126, 167, 199 | 0 |
| 33 | AX | 68/80 (85%) | 0.40 | 3 (4%) 38 27 | 106, 155, 242, 271 | 0 |
| 33 | BX | 68/80 (85%) | 0.74 | 9 (13%) 4 4 | 107, 158, 243, 271 | 0 |
| 34 | AY | 235/293 (80%) | 0.82 | 42 (17%) 2 2 | 108, 159, 237, 316 | 0 |
| 34 | BY | 235/293 (80%) | 0.48 | 26 (11%) 7 6 | 110, 159, 237, 315 | 0 |
| 35 | AZ | 97/97 (100%) | -0.20 | 0 100 100 | 74, 129, 185, 209 | 0 |
| 35 | BZ | 97/97 (100%) | -0.36 | 2 (2%) 67 55 | 77, 129, 184, 210 | 0 |
| All | All | 13676/14864 (92%) | 0.18 | 659 (4%) 34 25 | 62, 139, 215, 454 | 0 |

The worst 5 of 659 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 10 | BA | 213 | U | 12.5 |
| 10 | BA | 211 | U | 11.9 |
| 4 | B4 | 229 | LEU | 9.8 |
| 34 | AY | 235 | VAL | 9.8 |
| 4 | B4 | 15 | LYS | 9.4 |

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

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

6.3 Carbohydrates ⓘ

There are no 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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 | LLDF | B-factors(Å ²) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-------|----------------------------|-------|
| 36 | MG | BA | 1888 | 1/1 | 0.84 | 2.05 | 31.30 | 227,227,227,227 | 0 |
| 36 | MG | BA | 1873 | 1/1 | 0.77 | 0.59 | 17.20 | 218,218,218,218 | 0 |
| 36 | MG | AA | 1889 | 1/1 | 0.90 | 0.71 | 15.96 | 200,200,200,200 | 0 |
| 36 | MG | AA | 1851 | 1/1 | 0.95 | 0.31 | 10.10 | 187,187,187,187 | 0 |
| 36 | MG | AA | 1874 | 1/1 | 0.82 | 0.30 | 5.77 | 194,194,194,194 | 0 |
| 36 | MG | AA | 1815 | 1/1 | 0.96 | 0.39 | 5.08 | 144,144,144,144 | 0 |
| 36 | MG | BA | 1815 | 1/1 | 0.98 | 0.33 | 4.60 | 155,155,155,155 | 0 |
| 36 | MG | BA | 1810 | 1/1 | 0.93 | 0.42 | 4.12 | 188,188,188,188 | 0 |
| 36 | MG | AA | 1868 | 1/1 | 0.81 | 1.00 | 2.98 | 197,197,197,197 | 0 |
| 36 | MG | AA | 1881 | 1/1 | 0.95 | 0.29 | 2.65 | 198,198,198,198 | 0 |
| 36 | MG | BA | 1803 | 1/1 | 0.94 | 0.40 | 2.53 | 169,169,169,169 | 0 |
| 36 | MG | AA | 1856 | 1/1 | 0.91 | 0.75 | 1.91 | 182,182,182,182 | 0 |
| 36 | MG | BA | 1859 | 1/1 | 0.86 | 0.26 | 1.06 | 194,194,194,194 | 0 |
| 36 | MG | AA | 1810 | 1/1 | 0.97 | 0.28 | 0.60 | 175,175,175,175 | 0 |
| 36 | MG | BA | 1865 | 1/1 | 0.87 | 0.19 | 0.46 | 183,183,183,183 | 0 |
| 36 | MG | BA | 1868 | 1/1 | 0.92 | 0.20 | -0.34 | 208,208,208,208 | 0 |
| 37 | ZN | B6 | 500 | 1/1 | 0.99 | 0.13 | -0.59 | 108,108,108,108 | 0 |
| 36 | MG | AA | 1802 | 1/1 | 0.90 | 0.19 | -0.59 | 175,175,175,175 | 0 |
| 36 | MG | BA | 1851 | 1/1 | 0.85 | 0.17 | -0.66 | 169,169,169,169 | 0 |
| 36 | MG | BA | 1825 | 1/1 | 0.84 | 0.13 | -0.67 | 153,153,153,153 | 0 |
| 37 | ZN | B5 | 500 | 1/1 | 0.99 | 0.16 | -0.90 | 87,87,87,87 | 0 |
| 36 | MG | BA | 1802 | 1/1 | 0.92 | 0.11 | -0.98 | 169,169,169,169 | 0 |
| 37 | ZN | A6 | 500 | 1/1 | 0.99 | 0.11 | -1.17 | 118,118,118,118 | 0 |
| 37 | ZN | AN | 500 | 1/1 | 1.00 | 0.12 | -1.40 | 105,105,105,105 | 0 |
| 37 | ZN | B9 | 500 | 1/1 | 0.95 | 0.06 | -1.43 | 247,247,247,247 | 0 |
| 37 | ZN | BN | 500 | 1/1 | 0.99 | 0.12 | -1.43 | 113,113,113,113 | 0 |
| 36 | MG | BA | 1814 | 1/1 | 0.91 | 0.11 | -1.55 | 214,214,214,214 | 0 |
| 37 | ZN | A5 | 500 | 1/1 | 0.99 | 0.11 | -1.55 | 95,95,95,95 | 0 |
| 37 | ZN | A9 | 500 | 1/1 | 0.99 | 0.10 | -1.75 | 169,169,169,169 | 0 |
| 36 | MG | BA | 1833 | 1/1 | 0.93 | 0.14 | -2.03 | 172,172,172,172 | 0 |
| 36 | MG | BA | 1884 | 1/1 | 0.81 | 0.13 | -2.16 | 219,219,219,219 | 0 |
| 36 | MG | AA | 1818 | 1/1 | 0.96 | 0.13 | -2.36 | 121,121,121,121 | 0 |
| 36 | MG | BA | 1831 | 1/1 | 0.97 | 0.14 | -2.59 | 115,115,115,115 | 0 |
| 36 | MG | AA | 1819 | 1/1 | 0.98 | 0.12 | -2.64 | 136,136,136,136 | 0 |
| 36 | MG | AA | 1803 | 1/1 | 0.95 | 0.08 | -2.78 | 147,147,147,147 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | LLDF | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-------|-----------------------------|-------|
| 36 | MG | AA | 1831 | 1/1 | 0.96 | 0.20 | -3.01 | 111,111,111,111 | 0 |
| 36 | MG | AA | 1865 | 1/1 | 0.93 | 0.11 | -3.28 | 184,184,184,184 | 0 |
| 36 | MG | AA | 1814 | 1/1 | 0.88 | 0.07 | -3.53 | 197,197,197,197 | 0 |
| 36 | MG | BA | 1818 | 1/1 | 0.98 | 0.07 | -4.02 | 111,111,111,111 | 0 |
| 36 | MG | AA | 1816 | 1/1 | 0.98 | 0.09 | -4.32 | 96,96,96,96 | 0 |
| 36 | MG | AA | 1887 | 1/1 | 0.91 | 0.08 | -4.61 | 198,198,198,198 | 0 |
| 36 | MG | BA | 1880 | 1/1 | 0.87 | 0.09 | -5.19 | 193,193,193,193 | 0 |
| 36 | MG | BA | 1819 | 1/1 | 0.97 | 0.12 | -5.71 | 122,122,122,122 | 0 |
| 36 | MG | B4 | 301 | 1/1 | 0.88 | 0.07 | - | 165,165,165,165 | 0 |
| 36 | MG | AA | 1882 | 1/1 | 0.77 | 0.43 | - | 181,181,181,181 | 0 |
| 36 | MG | AA | 1834 | 1/1 | 0.82 | 0.24 | - | 182,182,182,182 | 0 |
| 36 | MG | AA | 1822 | 1/1 | 0.95 | 0.14 | - | 139,139,139,139 | 0 |
| 36 | MG | BA | 1813 | 1/1 | 0.97 | 0.07 | - | 187,187,187,187 | 0 |
| 36 | MG | BA | 1863 | 1/1 | 0.97 | 0.12 | - | 166,166,166,166 | 0 |
| 36 | MG | BA | 1842 | 1/1 | 0.63 | 0.50 | - | 210,210,210,210 | 0 |
| 36 | MG | AA | 1817 | 1/1 | 0.98 | 0.19 | - | 126,126,126,126 | 0 |
| 36 | MG | AA | 1846 | 1/1 | 0.93 | 0.14 | - | 161,161,161,161 | 0 |
| 36 | MG | BA | 1882 | 1/1 | 0.93 | 0.59 | - | 196,196,196,196 | 0 |
| 36 | MG | BA | 1849 | 1/1 | 0.63 | 0.23 | - | 198,198,198,198 | 0 |
| 36 | MG | AA | 1806 | 1/1 | 0.89 | 0.14 | - | 151,151,151,151 | 0 |
| 36 | MG | BA | 1885 | 1/1 | 0.95 | 0.23 | - | 161,161,161,161 | 0 |
| 36 | MG | BA | 1845 | 1/1 | 0.69 | 0.23 | - | 225,225,225,225 | 0 |
| 36 | MG | AA | 1811 | 1/1 | 0.94 | 0.11 | - | 154,154,154,154 | 0 |
| 36 | MG | AA | 1835 | 1/1 | 0.90 | 0.15 | - | 159,159,159,159 | 0 |
| 36 | MG | BA | 1821 | 1/1 | 0.91 | 0.11 | - | 160,160,160,160 | 0 |
| 36 | MG | BW | 301 | 1/1 | 0.81 | 0.13 | - | 166,166,166,166 | 0 |
| 36 | MG | BA | 1857 | 1/1 | 0.95 | 0.18 | - | 130,130,130,130 | 0 |
| 36 | MG | BA | 1840 | 1/1 | 0.95 | 0.14 | - | 128,128,128,128 | 0 |
| 36 | MG | AA | 1832 | 1/1 | 0.90 | 0.07 | - | 189,189,189,189 | 0 |
| 36 | MG | AA | 1858 | 1/1 | 0.83 | 0.08 | - | 162,162,162,162 | 0 |
| 36 | MG | AA | 1880 | 1/1 | 0.94 | 0.09 | - | 193,193,193,193 | 0 |
| 36 | MG | A4 | 301 | 1/1 | 0.96 | 0.16 | - | 174,174,174,174 | 0 |
| 36 | MG | AA | 1862 | 1/1 | 0.97 | 0.06 | - | 191,191,191,191 | 0 |
| 36 | MG | BA | 1841 | 1/1 | 0.96 | 0.11 | - | 129,129,129,129 | 0 |
| 36 | MG | AA | 1852 | 1/1 | 0.79 | 0.10 | - | 173,173,173,173 | 0 |
| 36 | MG | AA | 1857 | 1/1 | 0.94 | 0.09 | - | 140,140,140,140 | 0 |
| 36 | MG | AA | 1878 | 1/1 | 0.90 | 0.10 | - | 160,160,160,160 | 0 |
| 36 | MG | BA | 1878 | 1/1 | 0.79 | 0.17 | - | 177,177,177,177 | 0 |
| 36 | MG | BA | 1877 | 1/1 | 0.91 | 0.13 | - | 177,177,177,177 | 0 |
| 36 | MG | AA | 1833 | 1/1 | 0.97 | 0.10 | - | 135,135,135,135 | 0 |
| 36 | MG | BA | 1827 | 1/1 | 0.89 | 0.23 | - | 199,199,199,199 | 0 |
| 36 | MG | BA | 1828 | 1/1 | 0.95 | 0.18 | - | 145,145,145,145 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | LLDF | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|------|-------|------|------|------|-----------------------------|-------|
| 36 | MG | AA | 1888 | 1/1 | 0.74 | 0.30 | - | 205,205,205,205 | 0 |
| 36 | MG | AA | 1805 | 1/1 | 0.94 | 0.49 | - | 175,175,175,175 | 0 |
| 36 | MG | AA | 1886 | 1/1 | 0.88 | 0.21 | - | 148,148,148,148 | 0 |
| 36 | MG | BA | 1854 | 1/1 | 0.77 | 0.26 | - | 189,189,189,189 | 0 |
| 36 | MG | BA | 1808 | 1/1 | 0.97 | 0.48 | - | 140,140,140,140 | 0 |
| 36 | MG | AA | 1807 | 1/1 | 0.89 | 0.07 | - | 194,194,194,194 | 0 |
| 36 | MG | BA | 1887 | 1/1 | 0.78 | 0.35 | - | 206,206,206,206 | 0 |
| 36 | MG | AA | 1869 | 1/1 | 0.84 | 0.32 | - | 209,209,209,209 | 0 |
| 36 | MG | BA | 1838 | 1/1 | 0.79 | 0.47 | - | 172,172,172,172 | 0 |
| 36 | MG | BA | 1836 | 1/1 | 0.81 | 0.36 | - | 175,175,175,175 | 0 |
| 36 | MG | BA | 1806 | 1/1 | 0.90 | 0.22 | - | 168,168,168,168 | 0 |
| 36 | MG | AA | 1844 | 1/1 | 0.92 | 0.36 | - | 166,166,166,166 | 0 |
| 36 | MG | BA | 1835 | 1/1 | 0.87 | 0.24 | - | 187,187,187,187 | 0 |
| 36 | MG | AA | 1873 | 1/1 | 0.90 | 0.57 | - | 196,196,196,196 | 0 |
| 36 | MG | BA | 1860 | 1/1 | 0.92 | 0.07 | - | 177,177,177,177 | 0 |
| 36 | MG | AA | 1809 | 1/1 | 0.80 | 0.40 | - | 193,193,193,193 | 0 |
| 36 | MG | AA | 1837 | 1/1 | 0.92 | 0.12 | - | 149,149,149,149 | 0 |
| 36 | MG | BA | 1811 | 1/1 | 0.89 | 0.22 | - | 170,170,170,170 | 0 |
| 36 | MG | AA | 1871 | 1/1 | 0.82 | 0.37 | - | 201,201,201,201 | 0 |
| 36 | MG | BA | 1867 | 1/1 | 0.67 | 0.14 | - | 180,180,180,180 | 0 |
| 36 | MG | BA | 1832 | 1/1 | 0.95 | 0.03 | - | 194,194,194,194 | 0 |
| 36 | MG | AA | 1876 | 1/1 | 0.79 | 0.14 | - | 180,180,180,180 | 0 |
| 36 | MG | BA | 1847 | 1/1 | 0.74 | 0.26 | - | 204,204,204,204 | 0 |
| 36 | MG | BA | 1817 | 1/1 | 0.94 | 0.07 | - | 134,134,134,134 | 0 |
| 36 | MG | BA | 1843 | 1/1 | 0.79 | 0.22 | - | 196,196,196,196 | 0 |
| 36 | MG | BA | 1829 | 1/1 | 0.82 | 0.12 | - | 163,163,163,163 | 0 |
| 36 | MG | AA | 1860 | 1/1 | 0.90 | 0.12 | - | 176,176,176,176 | 0 |
| 36 | MG | BA | 1883 | 1/1 | 0.77 | 0.61 | - | 187,187,187,187 | 0 |
| 36 | MG | AA | 1829 | 1/1 | 0.97 | 0.05 | - | 160,160,160,160 | 0 |
| 36 | MG | AA | 1848 | 1/1 | 0.84 | 0.13 | - | 183,183,183,183 | 0 |
| 36 | MG | AA | 1839 | 1/1 | 0.92 | 0.12 | - | 143,143,143,143 | 0 |
| 36 | MG | BA | 1820 | 1/1 | 0.81 | 0.15 | - | 170,170,170,170 | 0 |
| 36 | MG | BA | 1834 | 1/1 | 0.90 | 0.14 | - | 138,138,138,138 | 0 |
| 36 | MG | AA | 1804 | 1/1 | 0.95 | 0.12 | - | 150,150,150,150 | 0 |
| 36 | MG | AA | 1864 | 1/1 | 0.92 | 0.17 | - | 176,176,176,176 | 0 |
| 36 | MG | AA | 1825 | 1/1 | 0.98 | 0.13 | - | 115,115,115,115 | 0 |
| 36 | MG | AA | 1867 | 1/1 | 0.98 | 0.07 | - | 193,193,193,193 | 0 |
| 36 | MG | BA | 1872 | 1/1 | 0.76 | 0.62 | - | 200,200,200,200 | 0 |
| 36 | MG | BD | 201 | 1/1 | 0.92 | 0.61 | - | 233,233,233,233 | 0 |
| 36 | MG | BA | 1816 | 1/1 | 0.94 | 0.14 | - | 127,127,127,127 | 0 |
| 36 | MG | BA | 1871 | 1/1 | 0.78 | 0.19 | - | 209,209,209,209 | 0 |
| 36 | MG | AA | 1859 | 1/1 | 0.79 | 0.09 | - | 193,193,193,193 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | LLDF | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|------|-------|------|------|------|-----------------------------|-------|
| 36 | MG | AA | 1855 | 1/1 | 0.80 | 0.60 | - | 214,214,214,214 | 0 |
| 36 | MG | BA | 1856 | 1/1 | 0.93 | 0.11 | - | 173,173,173,173 | 0 |
| 36 | MG | AA | 1870 | 1/1 | 0.73 | 0.42 | - | 195,195,195,195 | 0 |
| 36 | MG | AA | 1861 | 1/1 | 0.84 | 0.21 | - | 204,204,204,204 | 0 |
| 36 | MG | AA | 1885 | 1/1 | 0.93 | 0.20 | - | 223,223,223,223 | 0 |
| 36 | MG | BA | 1848 | 1/1 | 0.87 | 0.36 | - | 206,206,206,206 | 0 |
| 36 | MG | BA | 1822 | 1/1 | 0.90 | 0.13 | - | 151,151,151,151 | 0 |
| 36 | MG | AA | 1824 | 1/1 | 0.90 | 0.06 | - | 148,148,148,148 | 0 |
| 36 | MG | AA | 1821 | 1/1 | 0.96 | 0.18 | - | 144,144,144,144 | 0 |
| 36 | MG | BA | 1839 | 1/1 | 0.95 | 0.11 | - | 140,140,140,140 | 0 |
| 36 | MG | AA | 1879 | 1/1 | 0.87 | 0.22 | - | 193,193,193,193 | 0 |
| 36 | MG | AA | 1828 | 1/1 | 0.97 | 0.14 | - | 133,133,133,133 | 0 |
| 36 | MG | BA | 1875 | 1/1 | 0.17 | 0.44 | - | 193,193,193,193 | 0 |
| 36 | MG | AA | 1820 | 1/1 | 0.91 | 0.14 | - | 157,157,157,157 | 0 |
| 36 | MG | BA | 1852 | 1/1 | 0.90 | 0.21 | - | 170,170,170,170 | 0 |
| 36 | MG | AA | 1866 | 1/1 | 0.76 | 0.17 | - | 197,197,197,197 | 0 |
| 36 | MG | AA | 1826 | 1/1 | 0.89 | 0.11 | - | 155,155,155,155 | 0 |
| 36 | MG | BA | 1824 | 1/1 | 0.84 | 0.08 | - | 172,172,172,172 | 0 |
| 36 | MG | BA | 1855 | 1/1 | 0.56 | 0.80 | - | 275,275,275,275 | 0 |
| 36 | MG | AA | 1890 | 1/1 | 0.84 | 0.11 | - | 218,218,218,218 | 0 |
| 36 | MG | AA | 1850 | 1/1 | 0.88 | 0.17 | - | 185,185,185,185 | 0 |
| 36 | MG | AA | 1863 | 1/1 | 0.88 | 0.12 | - | 183,183,183,183 | 0 |
| 36 | MG | BA | 1804 | 1/1 | 0.94 | 0.10 | - | 191,191,191,191 | 0 |
| 36 | MG | BA | 1812 | 1/1 | 0.96 | 0.66 | - | 166,166,166,166 | 0 |
| 36 | MG | BA | 1805 | 1/1 | 0.98 | 0.10 | - | 150,150,150,150 | 0 |
| 36 | MG | BA | 1866 | 1/1 | 0.84 | 0.30 | - | 186,186,186,186 | 0 |
| 36 | MG | BA | 1809 | 1/1 | 0.95 | 0.19 | - | 172,172,172,172 | 0 |
| 36 | MG | AA | 1823 | 1/1 | 0.91 | 0.20 | - | 130,130,130,130 | 0 |
| 36 | MG | AL | 201 | 1/1 | 0.85 | 0.17 | - | 182,182,182,182 | 0 |
| 36 | MG | BA | 1837 | 1/1 | 0.76 | 0.26 | - | 178,178,178,178 | 0 |
| 36 | MG | BA | 1864 | 1/1 | 0.90 | 0.16 | - | 182,182,182,182 | 0 |
| 36 | MG | AA | 1883 | 1/1 | 0.78 | 0.40 | - | 209,209,209,209 | 0 |
| 36 | MG | BA | 1889 | 1/1 | 0.87 | 0.13 | - | 209,209,209,209 | 0 |
| 36 | MG | AA | 1812 | 1/1 | 0.89 | 0.54 | - | 173,173,173,173 | 0 |
| 36 | MG | BA | 1858 | 1/1 | 0.93 | 0.05 | - | 163,163,163,163 | 0 |
| 36 | MG | BA | 1876 | 1/1 | 0.75 | 0.25 | - | 184,184,184,184 | 0 |
| 36 | MG | AA | 1813 | 1/1 | 0.79 | 0.12 | - | 191,191,191,191 | 0 |
| 36 | MG | AA | 1854 | 1/1 | 0.88 | 0.14 | - | 158,158,158,158 | 0 |
| 36 | MG | BA | 1826 | 1/1 | 0.91 | 0.08 | - | 185,185,185,185 | 0 |
| 36 | MG | BA | 1861 | 1/1 | 0.91 | 0.18 | - | 181,181,181,181 | 0 |
| 36 | MG | AA | 1841 | 1/1 | 0.82 | 0.21 | - | 170,170,170,170 | 0 |
| 36 | MG | AA | 1838 | 1/1 | 0.90 | 0.12 | - | 144,144,144,144 | 0 |

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| Mol | Type | Chain | Res | Atoms | RSCC | RSR | LLDF | B-factors(\AA^2) | Q<0.9 |
|-----|------|-------|------|-------|------|------|------|-----------------------------|-------|
| 36 | MG | BA | 1862 | 1/1 | 0.88 | 0.07 | - | 177,177,177,177 | 0 |
| 36 | MG | BA | 1879 | 1/1 | 0.88 | 0.41 | - | 221,221,221,221 | 0 |
| 36 | MG | AA | 1875 | 1/1 | 0.89 | 0.28 | - | 152,152,152,152 | 0 |
| 36 | MG | BA | 1869 | 1/1 | 0.89 | 0.15 | - | 188,188,188,188 | 0 |
| 36 | MG | AA | 1853 | 1/1 | 0.97 | 0.09 | - | 177,177,177,177 | 0 |
| 36 | MG | BA | 1846 | 1/1 | 0.95 | 0.07 | - | 147,147,147,147 | 0 |
| 36 | MG | AA | 1843 | 1/1 | 0.93 | 0.09 | - | 182,182,182,182 | 0 |
| 36 | MG | BA | 1801 | 1/1 | 0.85 | 0.12 | - | 186,186,186,186 | 0 |
| 36 | MG | BA | 1823 | 1/1 | 0.94 | 0.14 | - | 123,123,123,123 | 0 |
| 36 | MG | BA | 1830 | 1/1 | 0.91 | 0.34 | - | 204,204,204,204 | 0 |
| 36 | MG | BA | 1886 | 1/1 | 0.76 | 0.22 | - | 214,214,214,214 | 0 |
| 36 | MG | AA | 1845 | 1/1 | 0.84 | 0.21 | - | 193,193,193,193 | 0 |
| 36 | MG | AA | 1849 | 1/1 | 0.97 | 0.21 | - | 159,159,159,159 | 0 |
| 36 | MG | BA | 1870 | 1/1 | 0.90 | 0.10 | - | 205,205,205,205 | 0 |
| 36 | MG | AA | 1801 | 1/1 | 0.96 | 0.06 | - | 160,160,160,160 | 0 |
| 36 | MG | BA | 1807 | 1/1 | 0.70 | 0.39 | - | 210,210,210,210 | 0 |
| 36 | MG | BA | 1874 | 1/1 | 0.97 | 0.38 | - | 164,164,164,164 | 0 |
| 36 | MG | AA | 1830 | 1/1 | 0.87 | 0.16 | - | 183,183,183,183 | 0 |
| 36 | MG | AA | 1872 | 1/1 | 0.91 | 0.32 | - | 196,196,196,196 | 0 |
| 36 | MG | BA | 1881 | 1/1 | 0.83 | 0.09 | - | 149,149,149,149 | 0 |
| 36 | MG | BA | 1850 | 1/1 | 0.89 | 0.48 | - | 221,221,221,221 | 0 |
| 36 | MG | BA | 1844 | 1/1 | 0.98 | 0.08 | - | 157,157,157,157 | 0 |
| 36 | MG | AA | 1842 | 1/1 | 0.92 | 0.12 | - | 175,175,175,175 | 0 |
| 36 | MG | AA | 1847 | 1/1 | 0.93 | 0.27 | - | 186,186,186,186 | 0 |
| 36 | MG | AA | 1884 | 1/1 | 0.91 | 0.47 | - | 190,190,190,190 | 0 |
| 36 | MG | BA | 1853 | 1/1 | 0.86 | 0.09 | - | 194,194,194,194 | 0 |
| 36 | MG | AA | 1827 | 1/1 | 0.94 | 0.43 | - | 178,178,178,178 | 0 |
| 36 | MG | AA | 1836 | 1/1 | 0.84 | 0.17 | - | 166,166,166,166 | 0 |
| 36 | MG | AA | 1840 | 1/1 | 0.98 | 0.09 | - | 124,124,124,124 | 0 |
| 36 | MG | AA | 1808 | 1/1 | 0.96 | 0.35 | - | 136,136,136,136 | 0 |
| 36 | MG | AA | 1877 | 1/1 | 0.98 | 0.20 | - | 170,170,170,170 | 0 |

6.5 Other polymers

There are no such residues in this entry.