



wwPDB EM Validation Summary Report ⓘ

Jul 21, 2025 – 09:18 PM EDT

PDB ID : 8VVS / pdb_00008vvs
EMDB ID : EMD-43567
Title : Post-decoding post-hydrolysis state obtained from merged datasets of elongation inhibitor-treated mammalian ribosomes
Authors : Loerch, S.; Petrossian, E.; Smith, P.R.; Campbell, Z.T.
Deposited on : 2024-01-31
Resolution : 3.10 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

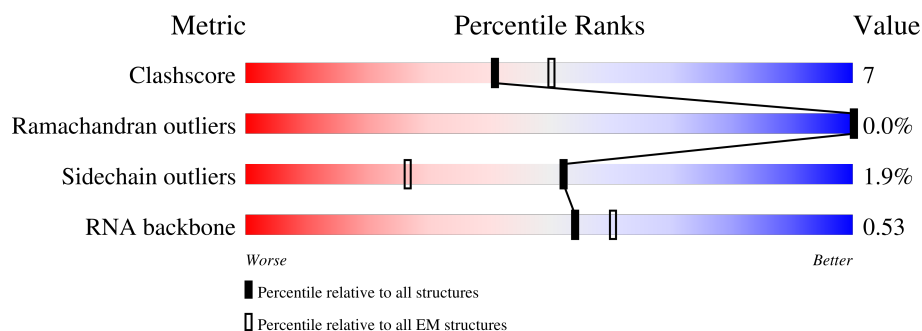
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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) | EM structures (#Entries) |
|-----------------------|-----------------------------|-----------------------------|
| Clashscore | 210492 | 15764 |
| Ramachandran outliers | 207382 | 16835 |
| Sidechain outliers | 206894 | 16415 |
| RNA backbone | 6643 | 2191 |

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 1 | A | 257 | |
| 2 | B | 403 | |
| 3 | C | 413 | |
| 4 | D | 297 | |
| 5 | E | 291 | |
| 6 | F | 249 | |
| 7 | G | 319 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 8 | H | 192 | |
| 9 | I | 214 | |
| 10 | J | 178 | |
| 11 | K | 211 | |
| 12 | L | 218 | |
| 13 | M | 204 | |
| 14 | N | 203 | |
| 15 | O | 213 | |
| 16 | P | 188 | |
| 17 | Q | 212 | |
| 18 | R | 224 | |
| 19 | S | 160 | |
| 20 | T | 128 | |
| 21 | U | 140 | |
| 22 | V | 157 | |
| 23 | W | 156 | |
| 24 | X | 145 | |
| 25 | Y | 136 | |
| 26 | Z | 148 | |
| 27 | AA | 245 | |
| 28 | BA | 115 | |
| 29 | CA | 125 | |
| 30 | DA | 135 | |
| 31 | EA | 110 | |
| 32 | FA | 129 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 33 | GA | 123 | |
| 34 | HA | 105 | |
| 35 | IA | 97 | |
| 36 | JA | 70 | |
| 37 | KA | 51 | |
| 38 | LA | 128 | |
| 39 | MA | 25 | |
| 40 | NA | 106 | |
| 41 | OA | 92 | |
| 42 | PA | 137 | |
| 43 | RA | 165 | |
| 44 | SA | 76 | |
| 45 | TA | 76 | |
| 46 | UA | 75 | |
| 47 | VA | 12 | |
| 48 | WA | 3584 | |
| 49 | XA | 120 | |
| 50 | YA | 156 | |
| 51 | ZA | 1869 | |
| 52 | AB | 295 | |
| 53 | BB | 264 | |
| 54 | CB | 293 | |
| 55 | DB | 281 | |
| 56 | EB | 263 | |
| 57 | FB | 204 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 58 | GB | 249 | |
| 59 | HB | 432 | |
| 60 | IB | 208 | |
| 61 | JB | 194 | |
| 62 | KB | 165 | |
| 63 | LB | 158 | |
| 64 | MB | 132 | |
| 65 | NB | 151 | |
| 66 | OB | 151 | |
| 67 | PB | 145 | |
| 68 | QB | 172 | |
| 69 | RB | 135 | |
| 70 | SB | 152 | |
| 71 | TB | 145 | |
| 72 | UB | 119 | |
| 73 | VB | 83 | |
| 74 | WB | 130 | |
| 75 | XB | 143 | |
| 76 | YB | 131 | |
| 77 | ZB | 124 | |
| 78 | AC | 115 | |
| 79 | BC | 84 | |
| 80 | CC | 69 | |
| 81 | DC | 56 | |
| 82 | EC | 133 | |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 83 | FC | 188 | |
| 84 | GC | 317 | |
| 85 | IC | 4 | |
| 86 | b | 318 | |
| 87 | c | 14 | |
| 88 | HC | 462 | |

2 Entry composition

There are 95 unique types of molecules in this entry. The entry contains 220703 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 uL2.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 1 | A | 250 | Total | C | N | O | S | 0 | 0 |
| | | | 1914 | 1199 | 392 | 317 | 6 | | |

- Molecule 2 is a protein called uL3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 2 | B | 397 | Total | C | N | O | S | 0 | 0 |
| | | | 3196 | 2035 | 603 | 545 | 13 | | |

- Molecule 3 is a protein called uL4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 3 | C | 362 | Total | C | N | O | S | 0 | 0 |
| | | | 2883 | 1812 | 577 | 480 | 14 | | |

- Molecule 4 is a protein called uL18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 4 | D | 294 | Total | C | N | O | S | 0 | 0 |
| | | | 2395 | 1514 | 439 | 428 | 14 | | |

- Molecule 5 is a protein called L6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 5 | E | 228 | Total | C | N | O | S | 0 | 0 |
| | | | 1823 | 1173 | 349 | 298 | 3 | | |

- Molecule 6 is a protein called uL30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 6 | F | 227 | Total | C | N | O | S | 0 | 0 |
| | | | 1897 | 1217 | 366 | 305 | 9 | | |

- Molecule 7 is a protein called L7A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 7 | G | 229 | Total | C | N | O | S | 0 | 0 |
| | | | 1850 | 1181 | 356 | 309 | 4 | | |

- Molecule 8 is a protein called L9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 8 | H | 190 | Total | C | N | O | S | 0 | 0 |
| | | | 1516 | 954 | 284 | 272 | 6 | | |

- Molecule 9 is a protein called L10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 9 | I | 205 | Total | C | N | O | S | 0 | 0 |
| | | | 1664 | 1056 | 321 | 274 | 13 | | |

- Molecule 10 is a protein called uL5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 10 | J | 171 | Total | C | N | O | S | 0 | 0 |
| | | | 1372 | 867 | 256 | 243 | 6 | | |

- Molecule 11 is a protein called eL13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 11 | K | 210 | Total | C | N | O | S | 0 | 0 |
| | | | 1702 | 1065 | 354 | 279 | 4 | | |

There are 9 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|-----------|------------|
| K | 46 | ILE | - | insertion | UNP G1TPV0 |
| K | 47 | ALA | - | insertion | UNP G1TPV0 |
| K | 48 | PRO | - | insertion | UNP G1TPV0 |
| K | 49 | ARG | - | insertion | UNP G1TPV0 |
| K | 50 | PRO | - | insertion | UNP G1TPV0 |
| K | 51 | ALA | - | insertion | UNP G1TPV0 |
| K | 52 | ALA | - | insertion | UNP G1TPV0 |
| K | 53 | GLY | - | insertion | UNP G1TPV0 |
| K | 54 | PRO | - | insertion | UNP G1TPV0 |

- Molecule 12 is a protein called eL14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 12 | L | 138 | Total | C | N | O | S | 0 | 0 |
| | | | 1137 | 727 | 221 | 182 | 7 | | |

- Molecule 13 is a protein called eL15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 13 | M | 203 | Total | C | N | O | S | 0 | 0 |
| | | | 1701 | 1072 | 359 | 266 | 4 | | |

- Molecule 14 is a protein called uL13.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 14 | N | 199 | Total | C | N | O | S | 0 | 0 |
| | | | 1630 | 1051 | 319 | 255 | 5 | | |

- Molecule 15 is a protein called uL22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 15 | O | 156 | Total | C | N | O | S | 0 | 0 |
| | | | 1266 | 793 | 245 | 219 | 9 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| O | 43 | SER | ALA | conflict | UNP G1TVT6 |

- Molecule 16 is a protein called eL18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 16 | P | 187 | Total | C | N | O | S | 0 | 0 |
| | | | 1515 | 946 | 315 | 250 | 4 | | |

There are 12 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| P | 4 | ASP | ASN | conflict | UNP G1TFE0 |
| P | 14 | ARG | TRP | conflict | UNP G1TFE0 |
| P | 53 | MET | LEU | conflict | UNP G1TFE0 |
| P | 58 | ARG | TRP | conflict | UNP G1TFE0 |
| P | 75 | ARG | GLN | conflict | UNP G1TFE0 |
| P | 80 | ALA | PRO | conflict | UNP G1TFE0 |
| P | 86 | VAL | ILE | conflict | UNP G1TFE0 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| P | 104 | ARG | HIS | conflict | UNP G1TFE0 |
| P | 110 | ARG | CYS | conflict | UNP G1TFE0 |
| P | 137 | VAL | GLY | conflict | UNP G1TFE0 |
| P | 157 | GLY | ARG | conflict | UNP G1TFE0 |
| P | 181 | ARG | TRP | conflict | UNP G1TFE0 |

- Molecule 17 is a protein called eL19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 17 | Q | 180 | Total | C | N | O | S | 0 | 0 |
| | | | 1508 | 933 | 328 | 238 | 9 | | |

- Molecule 18 is a protein called eL20.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 18 | R | 176 | Total | C | N | O | S | 0 | 0 |
| | | | 1462 | 930 | 285 | 236 | 11 | | |

- Molecule 19 is a protein called eL21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 19 | S | 159 | Total | C | N | O | S | 0 | 0 |
| | | | 1298 | 823 | 252 | 217 | 6 | | |

- Molecule 20 is a protein called eL22.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 20 | T | 101 | Total | C | N | O | S | 0 | 0 |
| | | | 826 | 530 | 144 | 150 | 2 | | |

There are 11 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| T | 18 | LEU | VAL | conflict | UNP G1TSG1 |
| T | 32 | GLY | ARG | conflict | UNP G1TSG1 |
| T | 36 | ALA | GLU | conflict | UNP G1TSG1 |
| T | 39 | PHE | SER | conflict | UNP G1TSG1 |
| T | 54 | GLY | ARG | conflict | UNP G1TSG1 |
| T | 60 | VAL | ALA | conflict | UNP G1TSG1 |
| T | 62 | SER | THR | conflict | UNP G1TSG1 |
| T | 63 | LEU | ILE | conflict | UNP G1TSG1 |

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| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| T | 97 | ARG | HIS | conflict | UNP G1TSG1 |
| T | 106 | THR | SER | conflict | UNP G1TSG1 |
| T | 126 | GLU | ASP | conflict | UNP G1TSG1 |

- Molecule 21 is a protein called L23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 21 | U | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1004 | 631 | 191 | 177 | 5 | | |

- Molecule 22 is a protein called uL24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 22 | V | 110 | Total | C | N | O | S | 0 | 0 |
| | | | 887 | 555 | 179 | 149 | 4 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| V | 78 | SER | PHE | conflict | UNP G1SE28 |

- Molecule 23 is a protein called uL23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 23 | W | 118 | Total | C | N | O | S | 0 | 0 |
| | | | 967 | 618 | 181 | 167 | 1 | | |

- Molecule 24 is a protein called L26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 24 | X | 134 | Total | C | N | O | S | 0 | 0 |
| | | | 1115 | 700 | 226 | 186 | 3 | | |

- Molecule 25 is a protein called L27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 25 | Y | 135 | Total | C | N | O | S | 0 | 0 |
| | | | 1107 | 714 | 208 | 182 | 3 | | |

- Molecule 26 is a protein called uL15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 26 | Z | 147 | Total | C | N | O | S | 0 | 0 |
| | | | 1162 | 734 | 239 | 185 | 4 | | |

- Molecule 27 is a protein called L29.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 27 | AA | 107 | Total | C | N | O | S | 0 | 0 |
| | | | 873 | 542 | 195 | 133 | 3 | | |

- Molecule 28 is a protein called eL30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 28 | BA | 99 | Total | C | N | O | S | 0 | 0 |
| | | | 769 | 486 | 135 | 141 | 7 | | |

- Molecule 29 is a protein called L31.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 29 | CA | 108 | Total | C | N | O | S | 0 | 0 |
| | | | 893 | 563 | 172 | 156 | 2 | | |

- Molecule 30 is a protein called L32.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 30 | DA | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1064 | 673 | 220 | 166 | 5 | | |

- Molecule 31 is a protein called eL33.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 31 | EA | 109 | Total | C | N | O | S | 0 | 0 |
| | | | 876 | 555 | 174 | 143 | 4 | | |

- Molecule 32 is a protein called L34.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 32 | FA | 114 | Total | C | N | O | S | 0 | 0 |
| | | | 906 | 566 | 187 | 147 | 6 | | |

- Molecule 33 is a protein called L35.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 33 | GA | 121 | Total | C | N | O | S | 0 | 0 |
| | | | 1008 | 637 | 203 | 167 | 1 | | |

- Molecule 34 is a protein called L36.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 34 | HA | 102 | Total | C | N | O | S | 0 | 0 |
| | | | 830 | 520 | 176 | 129 | 5 | | |

- Molecule 35 is a protein called L37.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 35 | IA | 87 | Total | C | N | O | S | 0 | 0 |
| | | | 716 | 440 | 159 | 112 | 5 | | |

- Molecule 36 is a protein called eL38.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 36 | JA | 69 | Total | C | N | O | S | 0 | 0 |
| | | | 569 | 366 | 103 | 99 | 1 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| JA | 24 | LYS | ASN | conflict | UNP G1U001 |

- Molecule 37 is a protein called eL39.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 37 | KA | 50 | Total | C | N | O | S | 0 | 0 |
| | | | 447 | 286 | 96 | 64 | 1 | | |

- Molecule 38 is a protein called eL40.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 38 | LA | 52 | Total | C | N | O | S | 0 | 0 |
| | | | 429 | 266 | 90 | 67 | 6 | | |

- Molecule 39 is a protein called eL41.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 39 | MA | 25 | Total | C | N | O | S | 0 | 0 |
| | | | 239 | 145 | 64 | 27 | 3 | | |

- Molecule 40 is a protein called eL42.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 40 | NA | 104 | Total | C | N | O | S | 0 | 0 |
| | | | 851 | 533 | 174 | 138 | 6 | | |

- Molecule 41 is a protein called eL43.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 41 | OA | 91 | Total | C | N | O | S | 0 | 0 |
| | | | 708 | 445 | 136 | 120 | 7 | | |

- Molecule 42 is a protein called L28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 42 | PA | 124 | Total | C | N | O | S | 0 | 0 |
| | | | 994 | 616 | 205 | 167 | 6 | | |

- Molecule 43 is a protein called L12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 43 | RA | 153 | Total | C | N | O | S | 0 | 0 |
| | | | 1160 | 722 | 218 | 217 | 3 | | |

- Molecule 44 is a RNA chain called P-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 44 | SA | 76 | Total | C | N | O | P | 0 | 0 |
| | | | 1622 | 726 | 300 | 521 | 75 | | |

- Molecule 45 is a RNA chain called E-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 45 | TA | 76 | Total | C | N | O | P | 0 | 0 |
| | | | 1615 | 722 | 286 | 532 | 75 | | |

- Molecule 46 is a RNA chain called A-site tRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|----|---------|-------|
| 46 | UA | 75 | Total | C | N | O | P | 0 | 0 |
| | | | 1596 | 713 | 285 | 523 | 75 | | |

- Molecule 47 is a RNA chain called mRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|----|---------|-------|
| 47 | VA | 12 | Total | C | N | O | P | 0 | 0 |
| | | | 251 | 113 | 41 | 85 | 12 | | |

- Molecule 48 is a RNA chain called 28S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|-------|
| 48 | WA | 3578 | Total | C | N | O | P | 0 | 0 |
| | | | 76735 | 34173 | 14061 | 24923 | 3578 | | |

- Molecule 49 is a RNA chain called 5S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|-------|
| 49 | XA | 119 | Total | C | N | O | P | 0 | 0 |
| | | | 2538 | 1132 | 454 | 834 | 118 | | |

There are 7 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|-------------|
| XA | 2 | U | N | conflict | GB X06789.1 |
| XA | 36 | C | N | conflict | GB X06789.1 |
| XA | 102 | U | N | conflict | GB X06789.1 |
| XA | 112 | U | N | conflict | GB X06789.1 |
| XA | 114 | U | N | conflict | GB X06789.1 |
| XA | 119 | U | C | conflict | GB X06789.1 |
| XA | 120 | U | N | conflict | GB X06789.1 |

- Molecule 50 is a RNA chain called 5.8S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|------|-----|---------|-------|
| 50 | YA | 156 | Total | C | N | O | P | 0 | 0 |
| | | | 3314 | 1480 | 585 | 1094 | 155 | | |

- Molecule 51 is a RNA chain called 18S rRNA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-------|------|-------|------|---------|-------|
| 51 | ZA | 1716 | Total | C | N | O | P | 0 | 0 |
| | | | 36623 | 16347 | 6572 | 11989 | 1715 | | |

- Molecule 52 is a protein called RPSA.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 52 | AB | 217 | Total | C | N | O | S | 0 | 0 |
| | | | 1710 | 1086 | 300 | 316 | 8 | | |

- Molecule 53 is a protein called S3A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 53 | BB | 213 | Total | C | N | O | S | 0 | 0 |
| | | | 1729 | 1098 | 309 | 308 | 14 | | |

- Molecule 54 is a protein called eS1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 54 | CB | 220 | Total | C | N | O | S | 0 | 0 |
| | | | 1707 | 1105 | 293 | 300 | 9 | | |

- Molecule 55 is a protein called S3.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 55 | DB | 228 | Total | C | N | O | S | 0 | 0 |
| | | | 1768 | 1126 | 318 | 316 | 8 | | |

- Molecule 56 is a protein called S4.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 56 | EB | 262 | Total | C | N | O | S | 0 | 0 |
| | | | 2076 | 1324 | 386 | 358 | 8 | | |

There are 4 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| EB | 25 | GLY | SER | conflict | UNP G1TK17 |
| EB | 51 | ARG | LYS | conflict | UNP G1TK17 |
| EB | 78 | THR | ALA | conflict | UNP G1TK17 |
| EB | 156 | VAL | MET | conflict | UNP G1TK17 |

- Molecule 57 is a protein called S5.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 57 | FB | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1471 | 921 | 277 | 266 | 7 | | |

- Molecule 58 is a protein called eS6.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 58 | GB | 237 | Total | C | N | O | S | 0 | 0 |
| | | | 1923 | 1200 | 387 | 329 | 7 | | |

- Molecule 59 is a protein called eS7.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 59 | HB | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1489 | 952 | 271 | 265 | 1 | | |

- Molecule 60 is a protein called S8.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 60 | IB | 206 | Total | C | N | O | S | 0 | 0 |
| | | | 1686 | 1058 | 332 | 291 | 5 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| IB | 47 | ARG | GLY | conflict | UNP G1TJW1 |

- Molecule 61 is a protein called S9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 61 | JB | 185 | Total | C | N | O | S | 0 | 0 |
| | | | 1525 | 969 | 306 | 248 | 2 | | |

- Molecule 62 is a protein called S10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 62 | KB | 96 | Total | C | N | O | S | 0 | 0 |
| | | | 810 | 530 | 143 | 131 | 6 | | |

- Molecule 63 is a protein called S11.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 63 | LB | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1180 | 752 | 223 | 199 | 6 | | |

- Molecule 64 is a protein called S12.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 64 | MB | 117 | Total | C | N | O | S | 0 | 0 |
| | | | 908 | 570 | 161 | 169 | 8 | | |

- Molecule 65 is a protein called uS15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 65 | NB | 149 | Total | C | N | O | S | 0 | 0 |
| | | | 1202 | 770 | 228 | 203 | 1 | | |

- Molecule 66 is a protein called S14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 66 | OB | 136 | Total | C | N | O | S | 0 | 0 |
| | | | 1016 | 621 | 199 | 190 | 6 | | |

- Molecule 67 is a protein called S15.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 67 | PB | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1058 | 670 | 201 | 180 | 7 | | |

- Molecule 68 is a protein called uS9.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 68 | QB | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1128 | 717 | 213 | 195 | 3 | | |

- Molecule 69 is a protein called eS17.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 69 | RB | 132 | Total | C | N | O | S | 0 | 0 |
| | | | 1068 | 670 | 199 | 195 | 4 | | |

- Molecule 70 is a protein called S18.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 70 | SB | 144 | Total | C | N | O | S | 0 | 0 |
| | | | 1190 | 746 | 241 | 202 | 1 | | |

- Molecule 71 is a protein called S19.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 71 | TB | 142 | Total | C | N | O | S | 0 | 0 |
| | | | 1104 | 693 | 212 | 196 | 3 | | |

- Molecule 72 is a protein called uS10.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 72 | UB | 102 | Total | C | N | O | S | 0 | 0 |
| | | | 808 | 507 | 154 | 143 | 4 | | |

- Molecule 73 is a protein called S21.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 73 | VB | 83 | Total | C | N | O | S | 0 | 0 |
| | | | 636 | 393 | 117 | 121 | 5 | | |

There are 7 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| VB | 3 | ASN | SER | conflict | UNP G1TM82 |
| VB | 4 | ASP | ASN | conflict | UNP G1TM82 |
| VB | 33 | GLN | PRO | conflict | UNP G1TM82 |
| VB | 50 | PHE | SER | conflict | UNP G1TM82 |
| VB | 75 | ALA | SER | conflict | UNP G1TM82 |
| VB | 76 | ASP | HIS | conflict | UNP G1TM82 |
| VB | 81 | LYS | GLN | conflict | UNP G1TM82 |

- Molecule 74 is a protein called S15A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 74 | WB | 129 | Total | C | N | O | S | 0 | 0 |
| | | | 1034 | 659 | 193 | 176 | 6 | | |

- Molecule 75 is a protein called S23.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 75 | XB | 141 | Total | C | N | O | S | 0 | 0 |
| | | | 1098 | 693 | 219 | 183 | 3 | | |

- Molecule 76 is a protein called S24.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 76 | YB | 124 | Total | C | N | O | S | 0 | 0 |
| | | | 1011 | 640 | 198 | 168 | 5 | | |

- Molecule 77 is a protein called eS25.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 77 | ZB | 85 | Total | C | N | O | S | 0 | 0 |
| | | | 683 | 439 | 128 | 115 | 1 | | |

- Molecule 78 is a protein called S26.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 78 | AC | 101 | Total | C | N | O | S | 0 | 0 |
| | | | 814 | 507 | 170 | 132 | 5 | | |

There are 3 discrepancies between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| AC | 28 | ARG | CYS | conflict | UNP G1TFE8 |
| AC | 56 | ALA | VAL | conflict | UNP G1TFE8 |
| AC | 109 | ARG | PRO | conflict | UNP G1TFE8 |

- Molecule 79 is a protein called S27.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 79 | BC | 83 | Total | C | N | O | S | 0 | 0 |
| | | | 651 | 408 | 121 | 115 | 7 | | |

- Molecule 80 is a protein called S28.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 80 | CC | 62 | Total | C | N | O | S | 0 | 0 |
| | | | 488 | 297 | 97 | 92 | 2 | | |

- Molecule 81 is a protein called uS14.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 81 | DC | 55 | Total | C | N | O | S | 0 | 0 |
| | | | 459 | 286 | 94 | 74 | 5 | | |

- Molecule 82 is a protein called S30.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|-------|
| 82 | EC | 55 | Total | C | N | O | S | 0 | 0 |
| | | | 443 | 274 | 97 | 71 | 1 | | |

- Molecule 83 is a protein called S27A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|-------|
| 83 | FC | 69 | Total | C | N | O | S | 0 | 0 |
| | | | 564 | 357 | 105 | 95 | 7 | | |

- Molecule 84 is a protein called RACK1.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|----|---------|-------|
| 84 | GC | 313 | Total | C | N | O | S | 0 | 0 |
| | | | 2436 | 1535 | 424 | 465 | 12 | | |

- Molecule 85 is a protein called peptide.

| Mol | Chain | Residues | Atoms | | | | AltConf | Trace |
|-----|-------|----------|-------|----|---|---|---------|-------|
| 85 | IC | 4 | Total | C | N | O | 0 | 0 |
| | | | 20 | 12 | 4 | 4 | | |

- Molecule 86 is a protein called RPLP0.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|-------|
| 86 | b | 167 | Total | C | N | O | S | 0 | 0 |
| | | | 1279 | 813 | 228 | 229 | 9 | | |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment | Reference |
|-------|---------|----------|--------|----------|------------|
| b | 82 | LEU | ILE | conflict | UNP G1SPK4 |

- Molecule 87 is a protein called RPLP peptide.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|----|----|----|---|---------|-------|
| 87 | c | 14 | Total | C | N | O | S | 0 | 0 |
| | | | 110 | 66 | 14 | 29 | 1 | | |

- Molecule 88 is a protein called eukaryotic elongation factor 1 A.

| Mol | Chain | Residues | Atoms | | | | | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|-------|
| 88 | HC | 223 | Total | C | N | O | S | 0 | 0 |
| | | | 1664 | 1048 | 299 | 308 | 9 | | |

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|-----|---------|
| 89 | A | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 89 | I | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 89 | O | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 89 | P | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 89 | U | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 89 | Z | 2 | Total | Mg | 0 |
| | | | 2 | 2 | |
| 89 | FA | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 89 | IA | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 89 | SA | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 89 | WA | 158 | Total | Mg | 0 |
| | | | 158 | 158 | |
| 89 | XA | 3 | Total | Mg | 0 |
| | | | 3 | 3 | |
| 89 | YA | 2 | Total | Mg | 0 |
| | | | 2 | 2 | |
| 89 | ZA | 61 | Total | Mg | 0 |
| | | | 61 | 61 | |
| 89 | AC | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |
| 89 | HC | 1 | Total | Mg | 0 |
| | | | 1 | 1 | |

- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn).

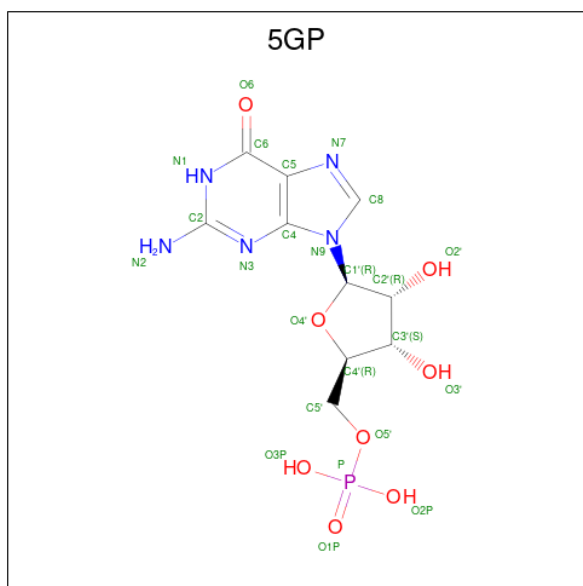
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 90 | FA | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 90 | IA | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |

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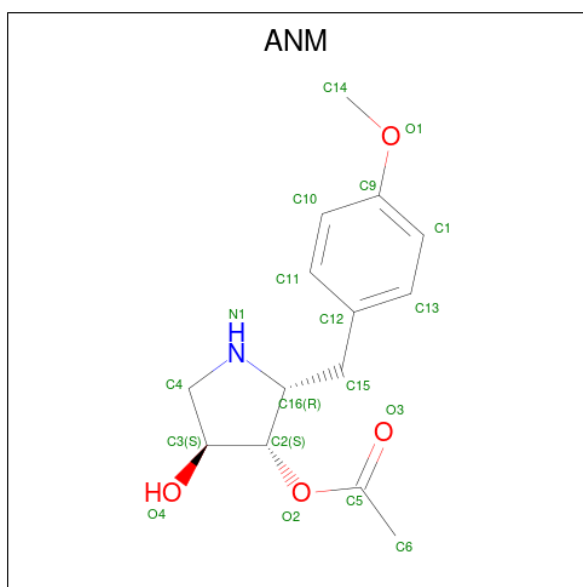
| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|----|---------|
| 90 | LA | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 90 | NA | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 90 | OA | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 90 | AC | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 90 | DC | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |
| 90 | FC | 1 | Total | Zn | 0 |
| | | | 1 | 1 | |

- Molecule 91 is GUANOSINE-5'-MONOPHOSPHATE (CCD ID: 5GP) (formula: $C_{10}H_{14}N_5O_8P$).



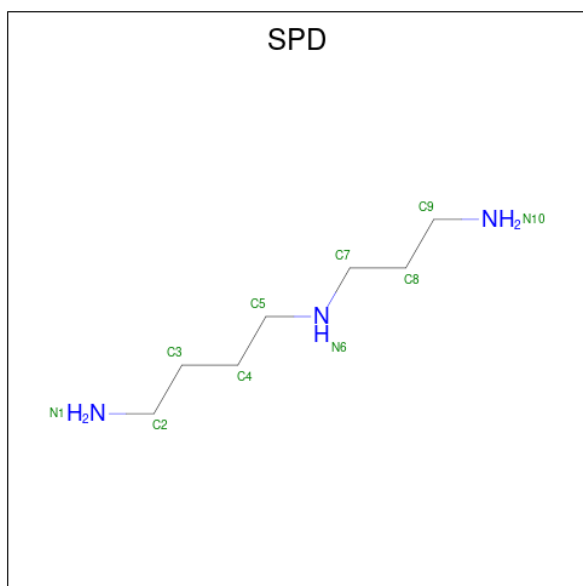
| Mol | Chain | Residues | Atoms | | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---|---------|
| 91 | UA | 1 | Total | C | N | O | P | 0 |
| | | | 24 | 10 | 5 | 8 | 1 | |

- Molecule 92 is ANISOMYCIN (CCD ID: ANM) (formula: $C_{14}H_{19}NO_4$).



| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|----|---|---|---------|
| 92 | WA | 1 | Total | C | N | O | 0 |
| | | | 19 | 14 | 1 | 4 | |

- Molecule 93 is SPERMIDINE (CCD ID: SPD) (formula: $C_7H_{19}N_3$).



| Mol | Chain | Residues | Atoms | | | AltConf |
|-----|-------|----------|-------|---|---|---------|
| 93 | WA | 1 | Total | C | N | 0 |
| | | | 10 | 7 | 3 | |
| 93 | WA | 1 | Total | C | N | 0 |
| | | | 10 | 7 | 3 | |
| 93 | WA | 1 | Total | C | N | 0 |
| | | | 10 | 7 | 3 | |

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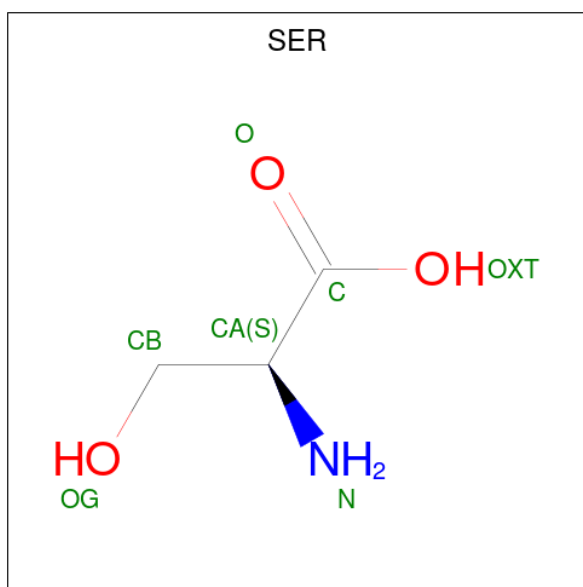
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| Mol | Chain | Residues | Atoms | | | AltConf |
|-----|-------|----------|-------|---|---|---------|
| 93 | ZA | 1 | Total | C | N | 0 |
| | | | 10 | 7 | 3 | |

- Molecule 94 is POTASSIUM ION (CCD ID: K) (formula: K).

| Mol | Chain | Residues | Atoms | | AltConf |
|-----|-------|----------|-------|---|---------|
| 94 | WA | 1 | Total | K | 0 |
| | | | 1 | 1 | |

- Molecule 95 is SERINE (CCD ID: SER) (formula: C₃H₇NO₃).




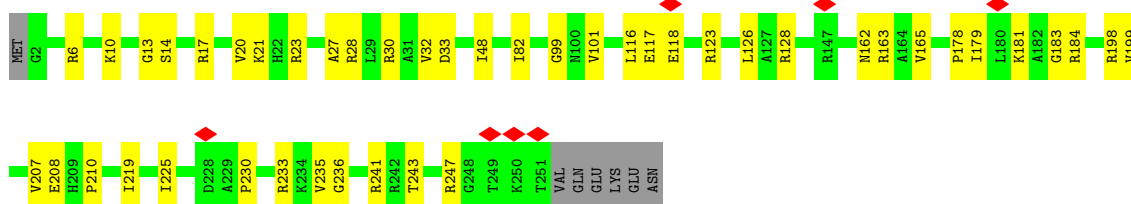
| Mol | Chain | Residues | Atoms | | | | AltConf |
|-----|-------|----------|-------|---|---|---|---------|
| 95 | HC | 1 | Total | C | N | O | 0 |
| | | | 6 | 3 | 1 | 2 | |

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

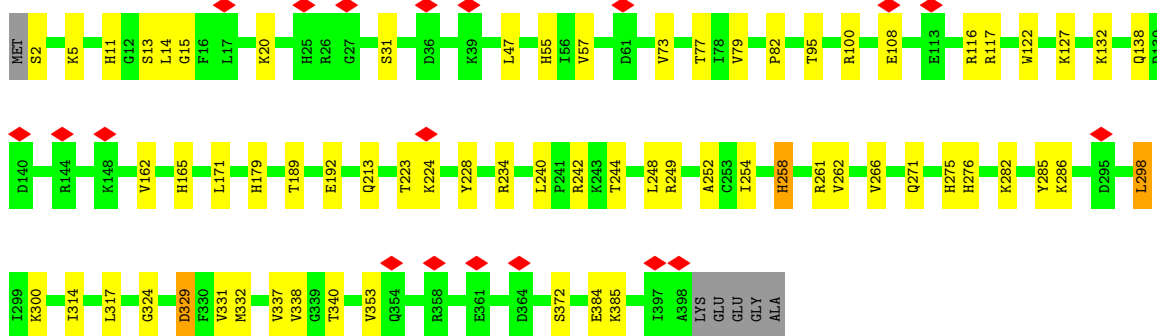
• Molecule 1: uL2

Chain A: 




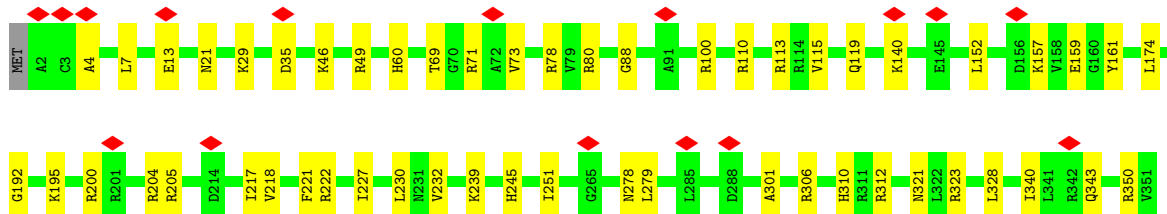
• Molecule 2: uL3

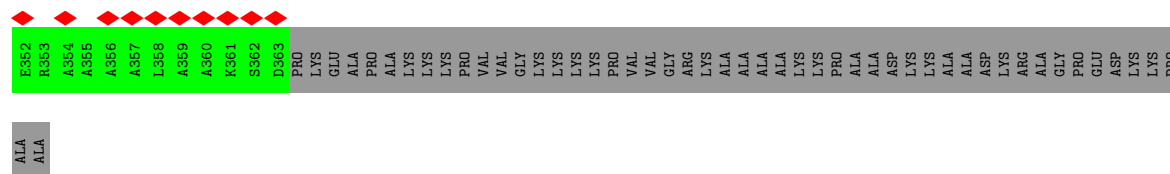
Chain B: 



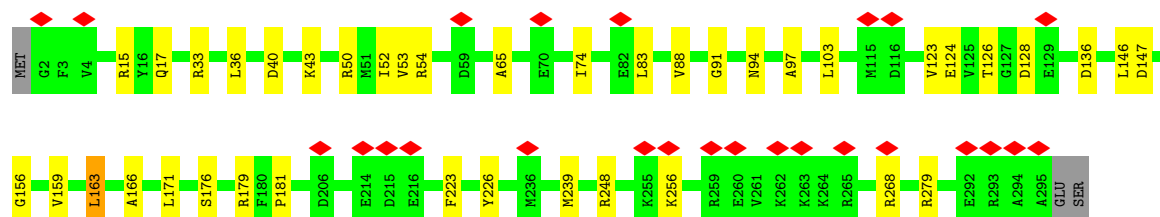
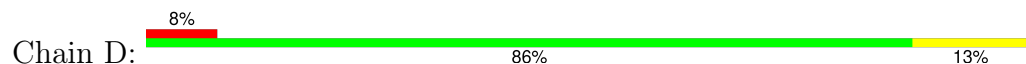
• Molecule 3: uL4

Chain C: 

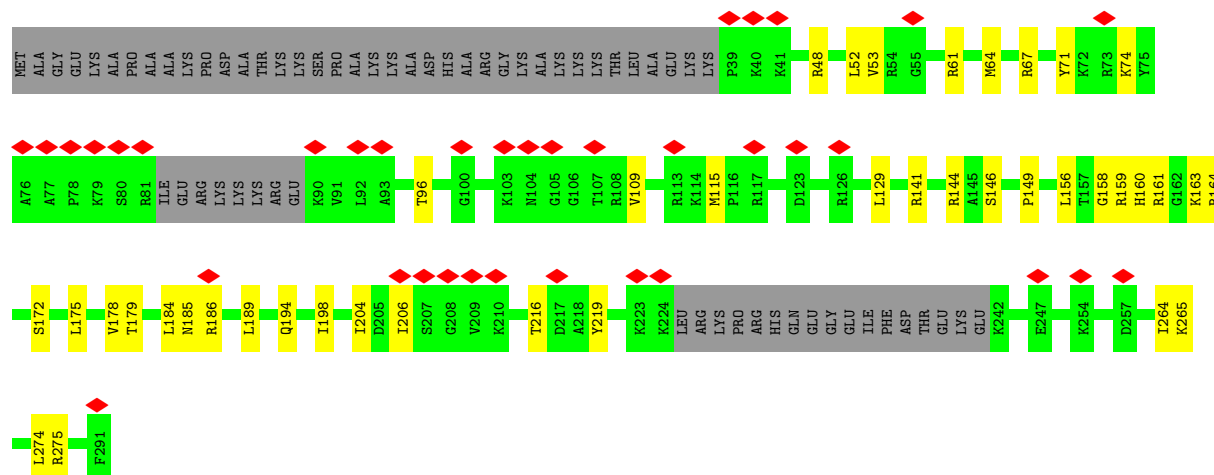




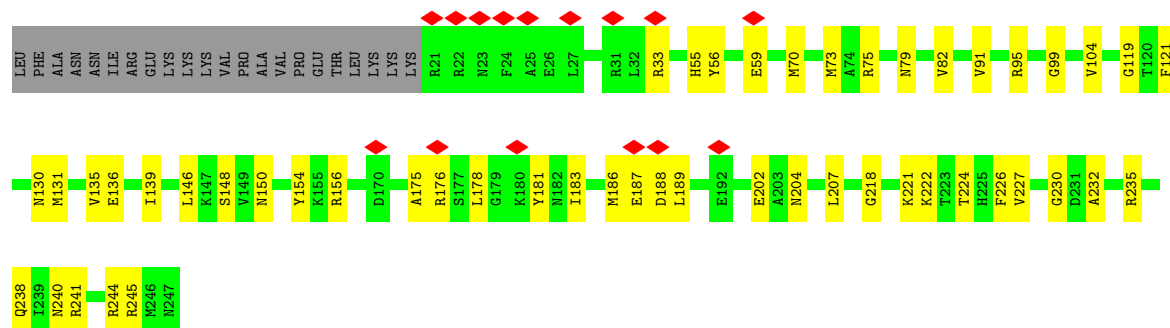
• Molecule 4: uL18



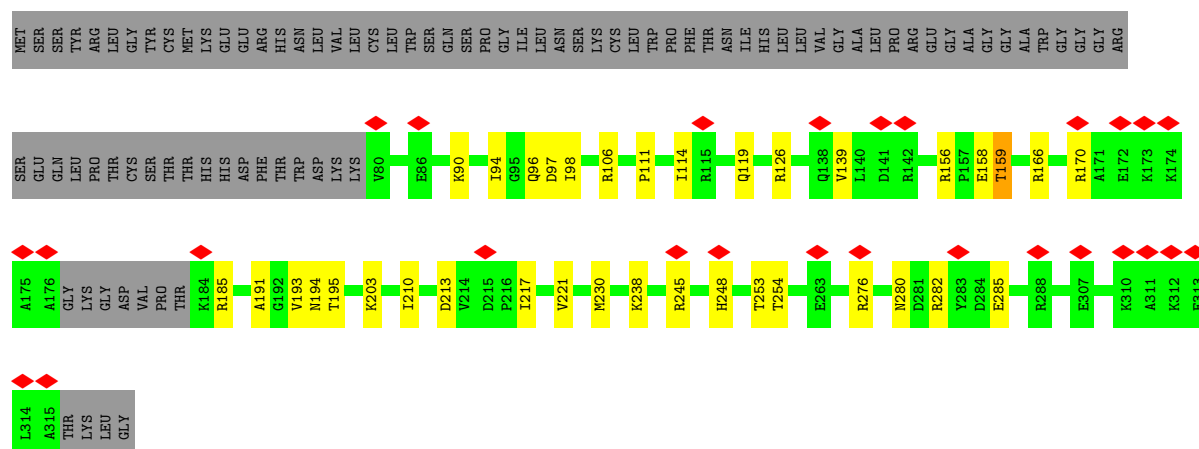
• Molecule 5: L6



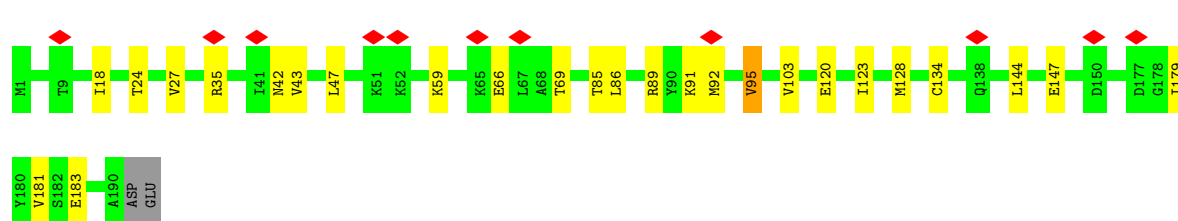
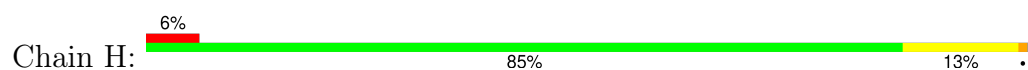
• Molecule 6: uL30



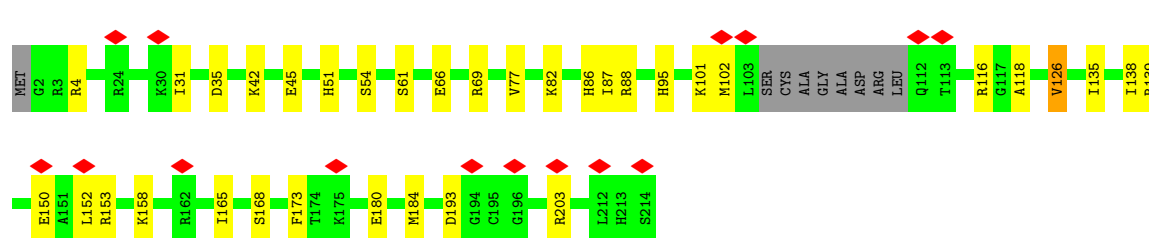
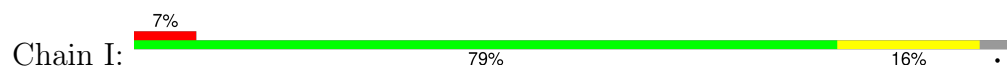
• Molecule 7: L7A



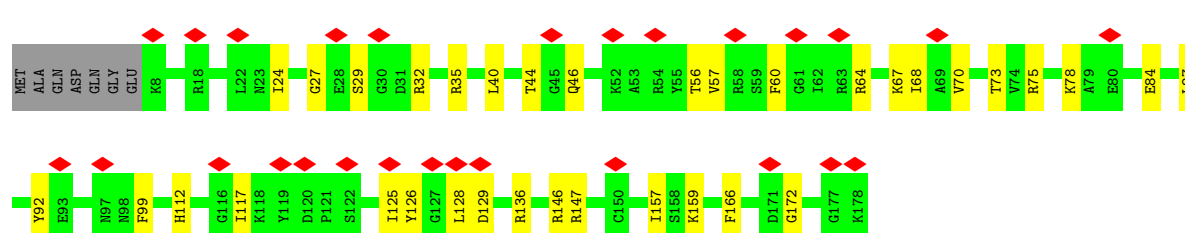
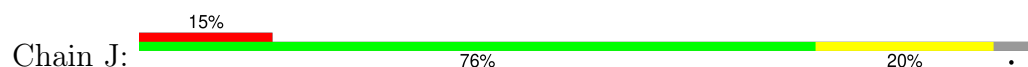
- Molecule 8: L9



- Molecule 9: L10

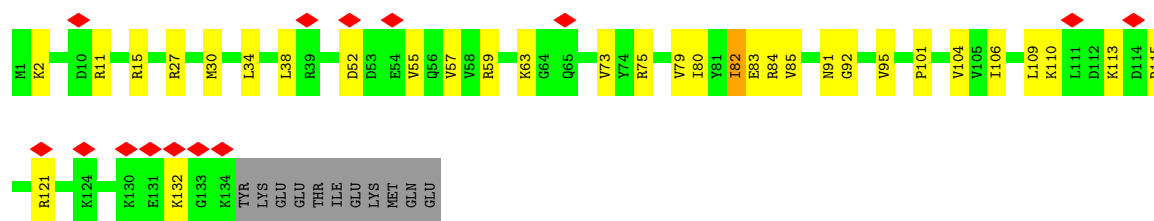


- Molecule 10: uL5

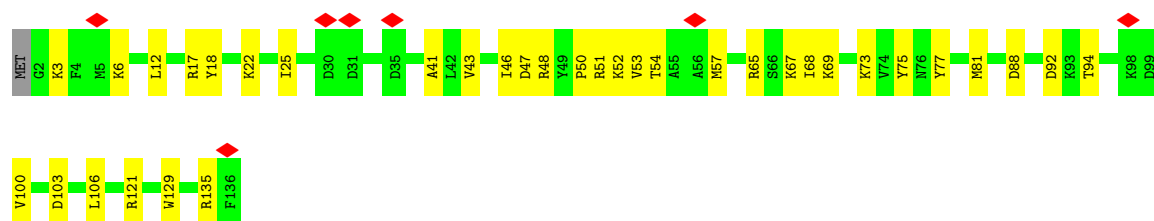
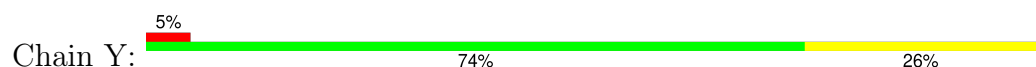


- Molecule 11: eL13

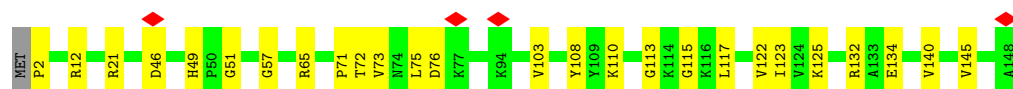
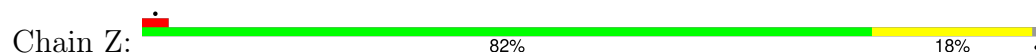




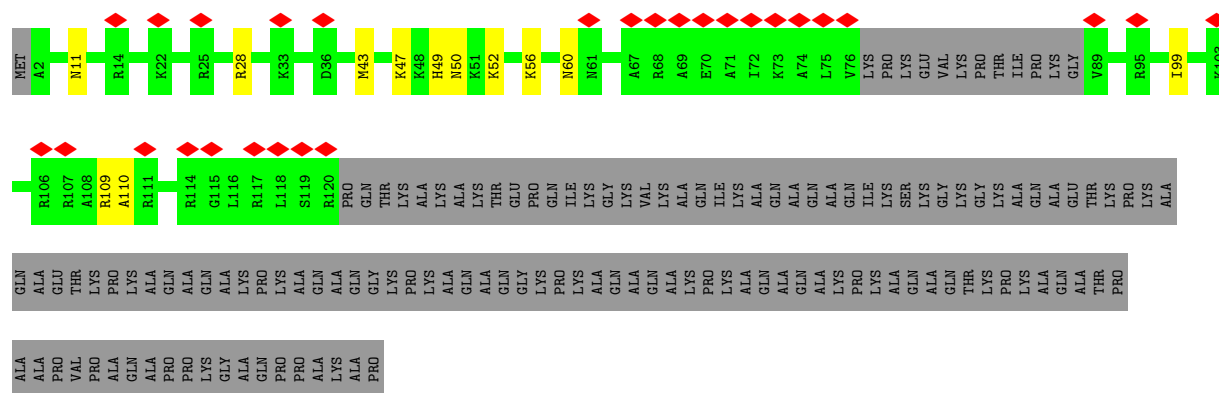
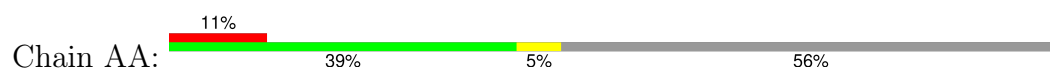
• Molecule 25: L27



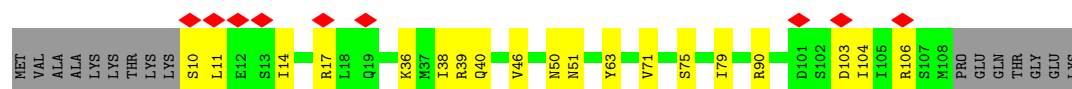
• Molecule 26: uL15



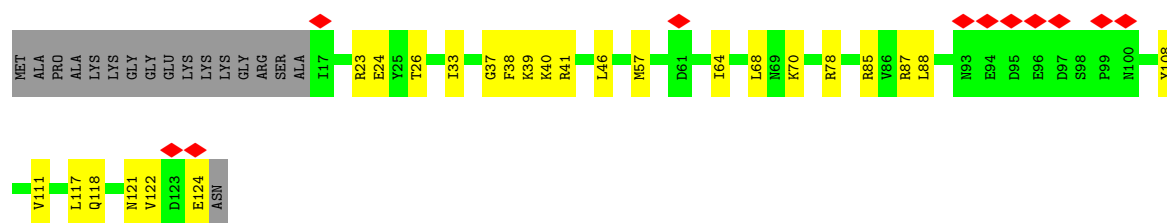
• Molecule 27: L29



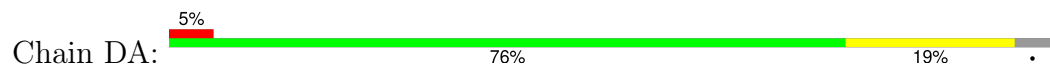
• Molecule 28: eL30



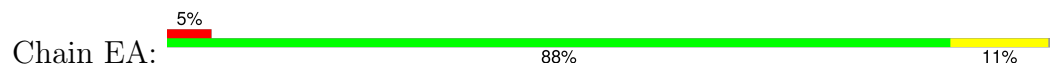
• Molecule 29: L31



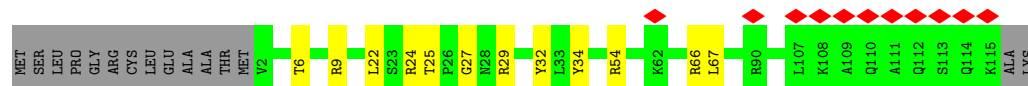
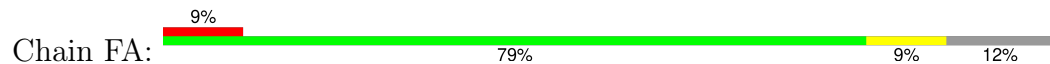
- Molecule 30: L32



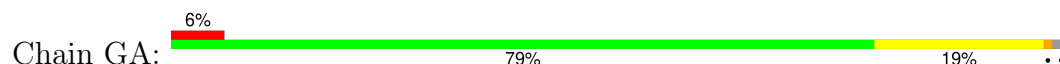
- Molecule 31: eL33



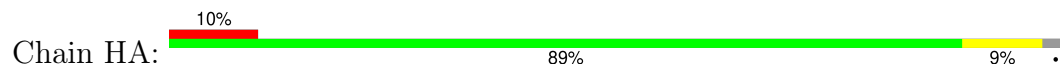
- Molecule 32: L34



- Molecule 33: L35



- Molecule 34: L36

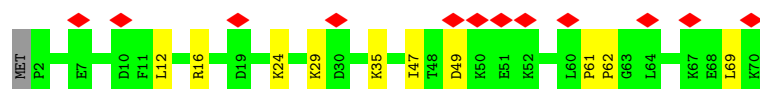
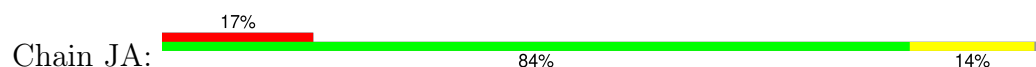


- Molecule 35: L37

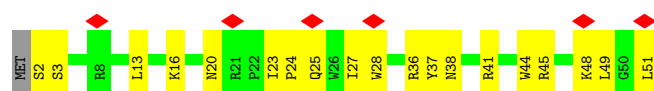




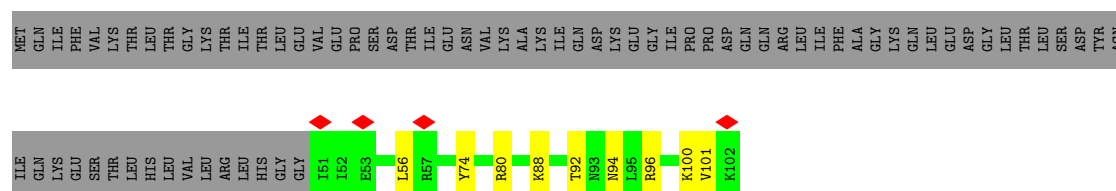
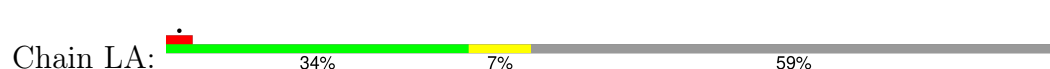
- Molecule 36: eL38



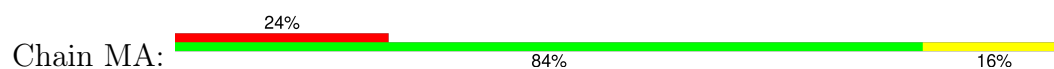
- Molecule 37: eL39



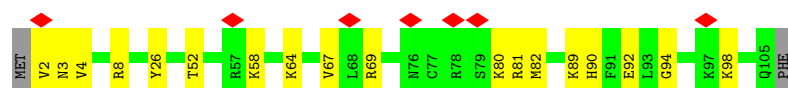
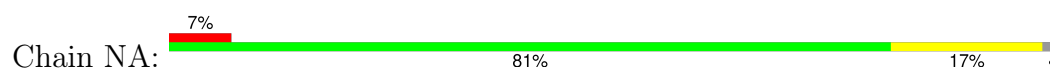
- Molecule 38: eL40



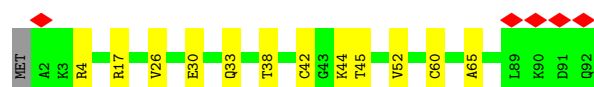
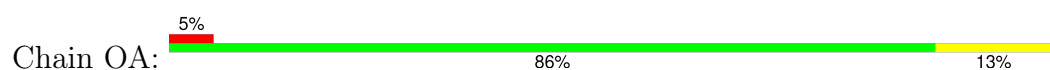
- Molecule 39: eL41



- Molecule 40: eL42

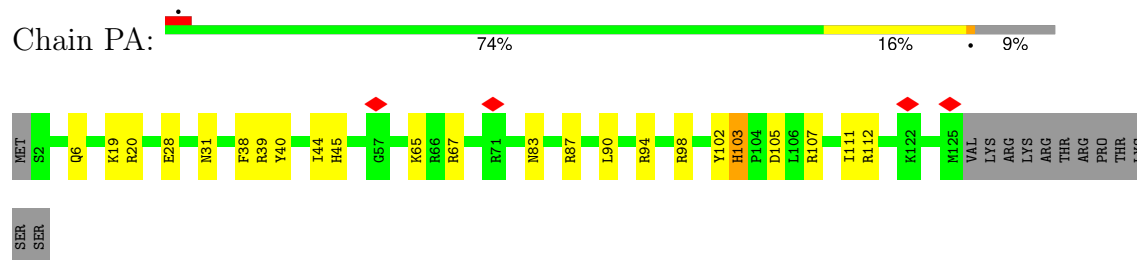


- Molecule 41: eL43



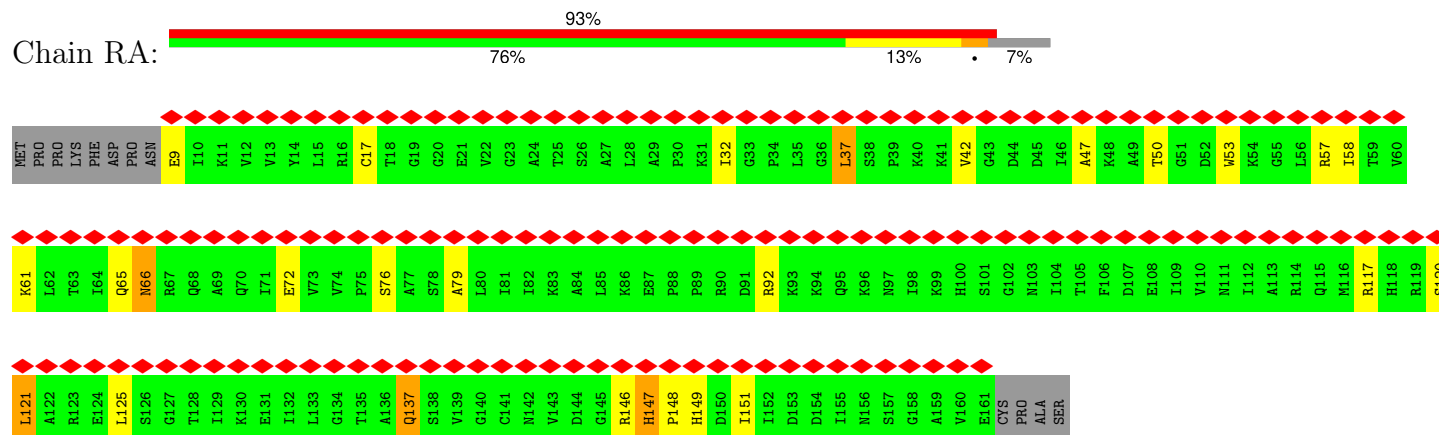
- Molecule 42: L28

Chain PA:



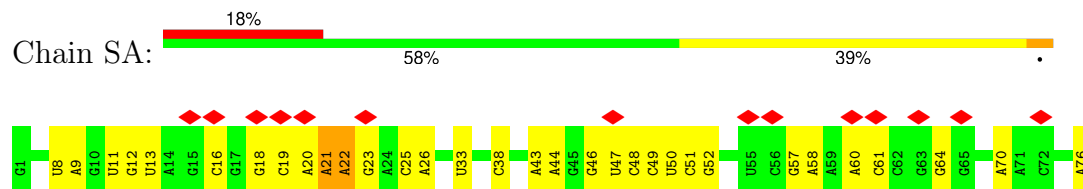
- Molecule 43: L12

Chain RA:



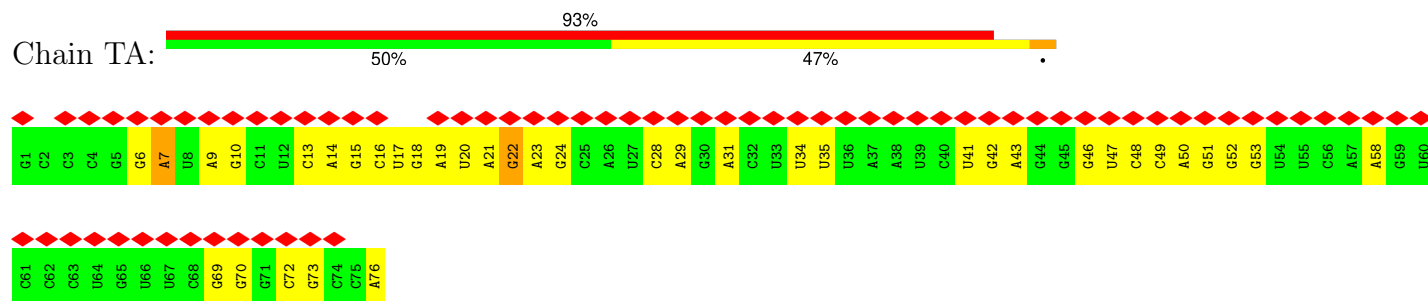
- Molecule 44: P-site tRNA

Chain SA:



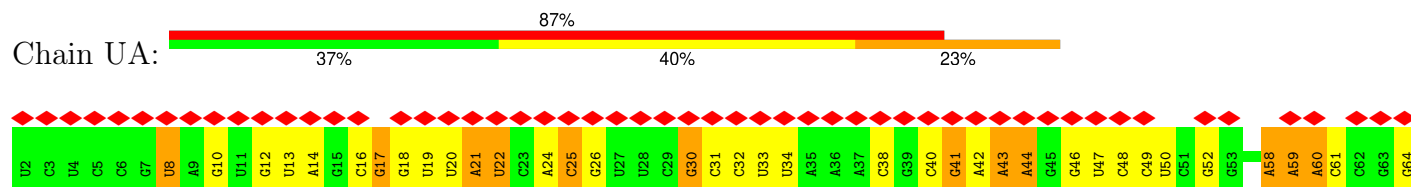
- Molecule 45: E-site tRNA

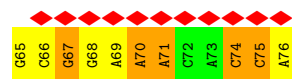
Chain TA:



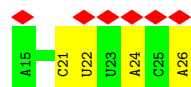
- Molecule 46: A-site tRNA

Chain UA:

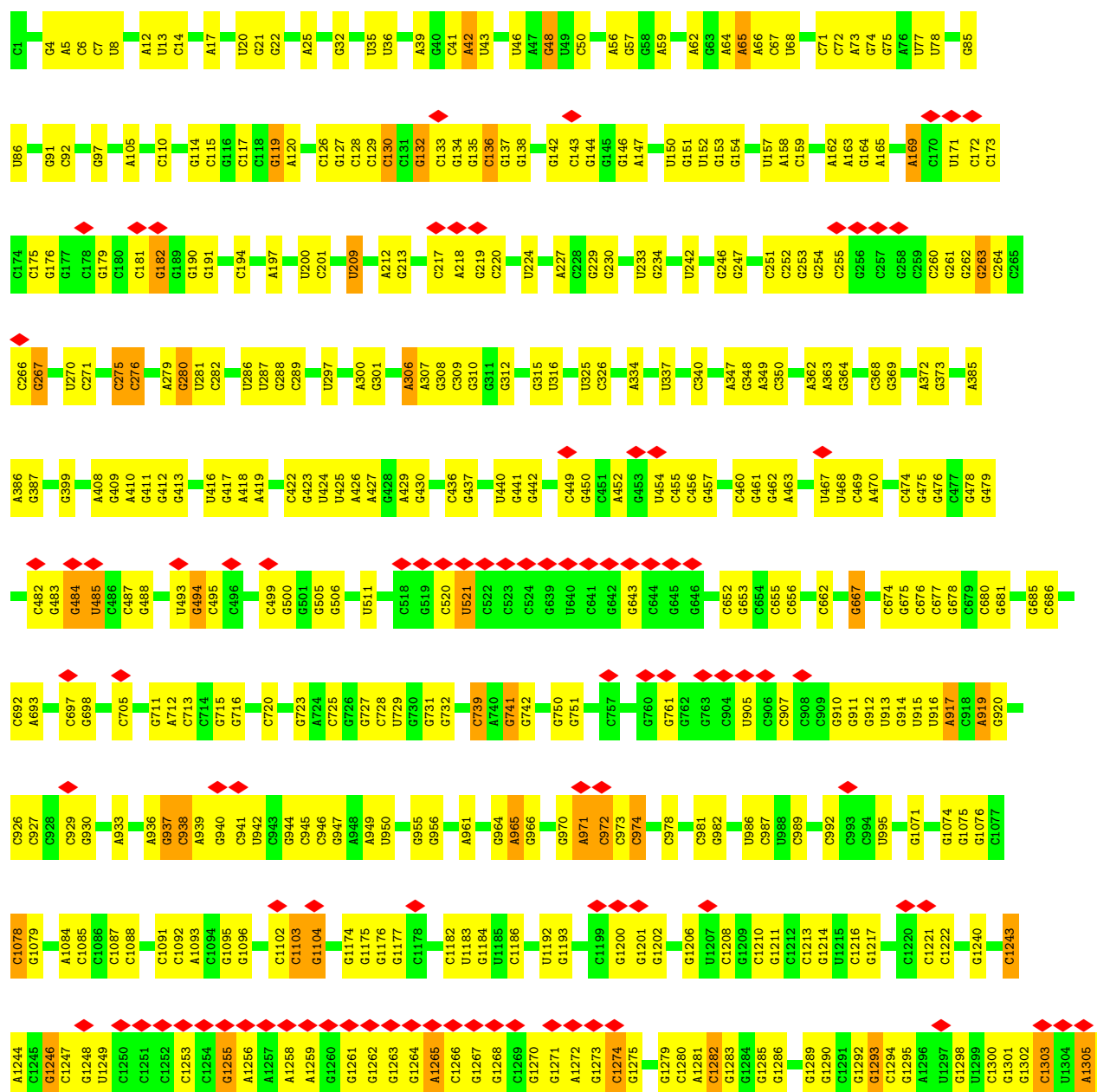




• Molecule 47: mRNA

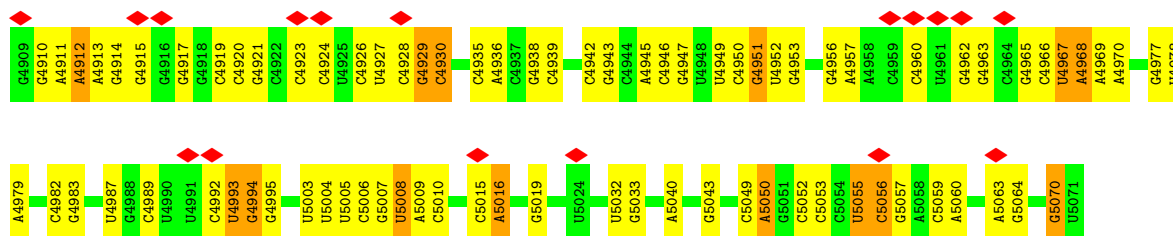


• Molecule 48: 28S rRNA





| | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| G4654 | U4653 | A4451 | A4327 | C4127 | G3948 | A3863 | C3767 | A3655 | U2845 | G2744 |
| U4654 | U4654 | U4454 | G4328 | A4128 | A3949 | A3864 | C3763 | A3656 | A2846 | A2745 |
| U4557 | U4557 | C4455 | C4329 | A4129 | C3950 | G3870 | C3763 | G3661 | A2847 | A2746 |
| C4562 | C4562 | U4459 | G4332 | A4130 | A3951 | C3871 | G3767 | A3664 | G2850 | A2747 |
| U4565 | U4565 | U4460 | G4333 | U4234 | U3952 | C3872 | C3772 | A3665 | A2851 | U2748 |
| A4566 | A4566 | U4461 | C4334 | A4235 | G3953 | A3873 | U3772 | G3666 | C2751 | U2749 |
| U4568 | U4568 | C4463 | A4338 | A4236 | A3954 | C3874 | C3773 | C3667 | G2857 | C2750 |
| G4569 | G4569 | A4466 | C4343 | C4239 | A3954 | G3875 | U3774 | A3667 | C2858 | G2752 |
| G4572 | G4572 | U4467 | C4348 | C4240 | A4064 | G3876 | U3775 | C3672 | G2864 | G2758 |
| G4575 | G4575 | C4468 | U4349 | C4241 | U4065 | A3877 | A3776 | G3673 | G2865 | A2759 |
| U4576 | U4576 | U4469 | G4349 | C4242 | C4066 | A3879 | A3777 | G3674 | G2866 | G2760 |
| G4577 | G4577 | C4468 | A4350 | A4253 | C4066 | C3880 | G3778 | C3675 | A2866 | G2762 |
| U4578 | U4578 | C4351 | C4352 | G4256 | G4067 | G3881 | G3779 | G3683 | U2871 | U2761 |
| G4579 | G4579 | U4355 | A4356 | U4262 | U4068 | G3882 | A3785 | G3686 | A2883 | G2763 |
| U4580 | U4580 | U4356 | C4356 | C4263 | U4069 | G3883 | A3786 | C3687 | G2886 | A2766 |
| U4581 | U4581 | A4368 | A4368 | G4265 | U4070 | G3891 | A3787 | G3688 | A2887 | G2678 |
| A4586 | A4586 | G4372 | G4375 | U4267 | U4071 | A3892 | U3788 | C3689 | C2892 | U2771 |
| U4587 | U4587 | G4375 | G4379 | G4268 | U4072 | G3893 | A3797 | U3689 | A2896 | G2773 |
| G4588 | G4588 | A4375 | A4379 | G4269 | U4073 | C3894 | U3798 | G3691 | A2897 | G2779 |
| C4589 | C4589 | U4503 | A4509 | A4270 | G4078 | A3896 | U3800 | A3694 | G2898 | U2689 |
| A4592 | A4592 | C4510 | A4380 | A4273 | A4079 | G3899 | U3804 | U3699 | G2899 | G2779 |
| U4596 | U4596 | U4511 | A4381 | C4164 | G4082 | G3902 | U3807 | G3700 | C2899 | G2780 |
| C4597 | C4597 | A4382 | U4382 | U4165 | G4083 | A3903 | G3808 | C3781 | G2901 | C2782 |
| G4602 | G4602 | U4513 | A4389 | C4166 | U4084 | U4085 | A3809 | U3709 | C2902 | G2783 |
| U4706 | U4706 | A4514 | C4389 | C4167 | U4085 | G3909 | C3810 | C3710 | G2903 | U2702 |
| A4707 | A4707 | A4515 | A4390 | G4168 | G4088 | A3910 | G3811 | A3713 | G2904 | U2703 |
| U4711 | U4711 | A4520 | C4391 | C4171 | G4089 | C3912 | G3812 | A3714 | A3598 | C2704 |
| C4716 | C4716 | A4613 | A4392 | A4172 | G4090 | C3913 | G3813 | A3715 | G3599 | C2705 |
| U4717 | U4717 | U4396 | A4396 | C4173 | G4091 | U3914 | U3816 | A3719 | C3600 | G2706 |
| G4718 | G4718 | U4620 | U4397 | A4174 | G4092 | G3915 | G3817 | A3720 | A3601 | C2707 |
| A4719 | A4719 | G4624 | A4398 | G4175 | G4095 | U3916 | A3818 | A3721 | G3602 | G2708 |
| C4722 | C4722 | U4629 | G4402 | U4176 | G4096 | U3917 | A3819 | G3722 | U3609 | U2709 |
| U4873 | U4873 | G4630 | G4403 | C4302 | G4097 | G3918 | U3820 | A3726 | A3610 | U2710 |
| A4884 | A4884 | U4631 | U4406 | U4303 | G4097 | C3919 | G3821 | A3727 | G3511 | C2711 |
| G4885 | G4885 | C4632 | U4407 | U4304 | G4097 | U3919 | G3821 | G3724 | A3612 | C2712 |
| U4887 | U4887 | U4408 | U4408 | C4305 | C4098 | G3920 | G3821 | A3725 | A3613 | G2713 |
| C4888 | C4888 | A4415 | C4415 | A4306 | G4099 | G3920 | G3825 | A3726 | G3617 | C2713 |
| A4889 | A4889 | G4415 | U4307 | U4307 | G4099 | A4100 | U3840 | A3726 | G3617 | U2709 |
| C4890 | C4890 | U4439 | U4308 | U4308 | G4099 | A4101 | G3841 | A3726 | A3626 | C2721 |
| A4895 | A4895 | U4441 | U4308 | U4190 | G4099 | C3926 | U3842 | A3726 | G3627 | G2722 |
| G4899 | G4899 | U4421 | U4421 | U4191 | G4109 | C3926 | U3845 | A3726 | G3628 | G2723 |
| C4901 | C4901 | U4541 | U4422 | U4192 | G4110 | C3926 | U3846 | A3726 | C2816 | U2727 |
| G4906 | G4906 | C4423 | C4423 | G4193 | G4111 | C3926 | A3847 | A3726 | G2824 | G2728 |
| A4907 | A4907 | A4424 | A4424 | C4194 | C4111 | C3926 | U3850 | A3726 | U2828 | U2732 |
| U4908 | U4908 | G4450 | G4450 | C4195 | C4112 | C3926 | A3851 | A3726 | G2829 | C2733 |
| | | | | C4201 | U4113 | C3926 | U3857 | A3726 | U2830 | G2734 |
| | | | | A4546 | C4114 | C3926 | A3858 | A3726 | A2837 | C2735 |
| | | | | A4550 | U4115 | C3926 | A3858 | A3726 | A2838 | U2736 |
| | | | | C4446 | C4116 | C3926 | A3858 | A3726 | A2839 | G2737 |
| | | | | A4551 | C4117 | C3926 | A3858 | A3726 | A2839 | G2738 |
| | | | | G4652 | C4117 | C3926 | A3858 | A3726 | A2839 | G2738 |
| | | | | A4653 | C4118 | C3926 | A3858 | A3726 | A2839 | G2738 |
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• Molecule 49: 5S rRNA

Chain XA: 71% 23% 5%



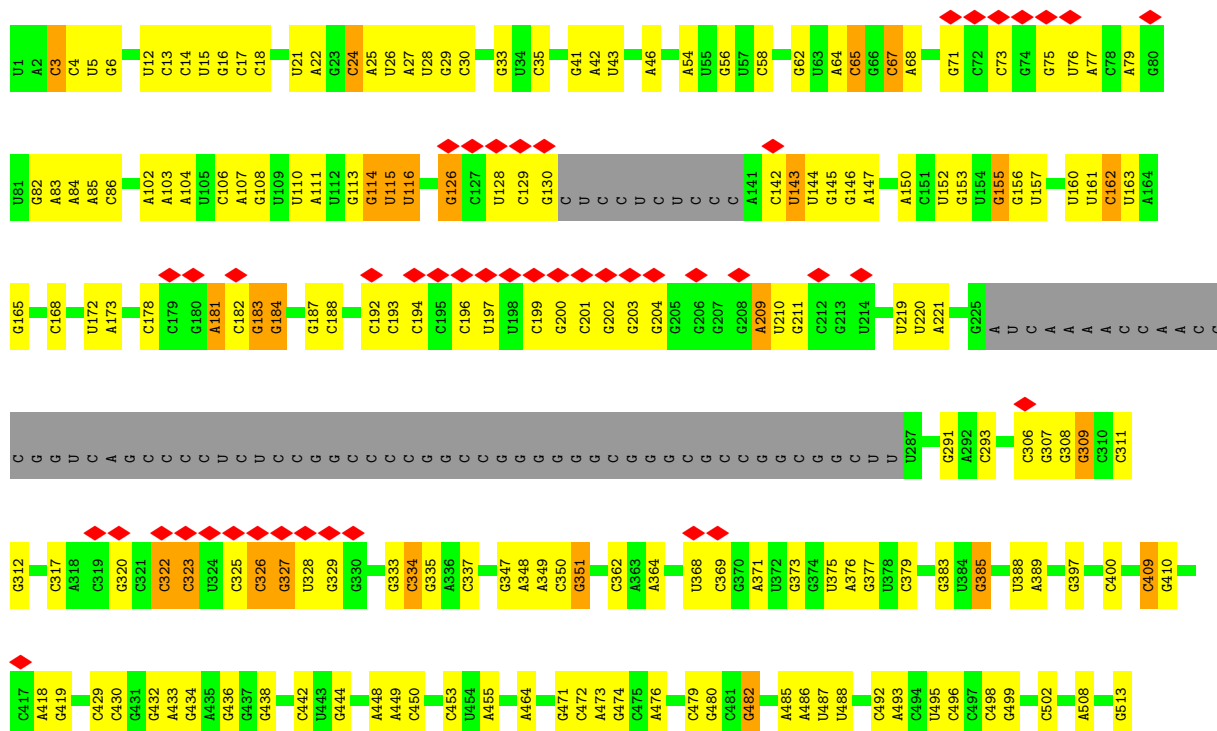
• Molecule 50: 5.8S rRNA

Chain YA: 10% 55% 38% 6%

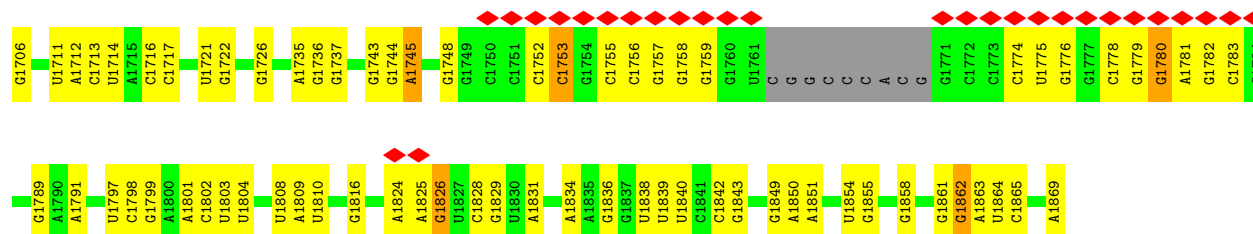


• Molecule 51: 18S rRNA

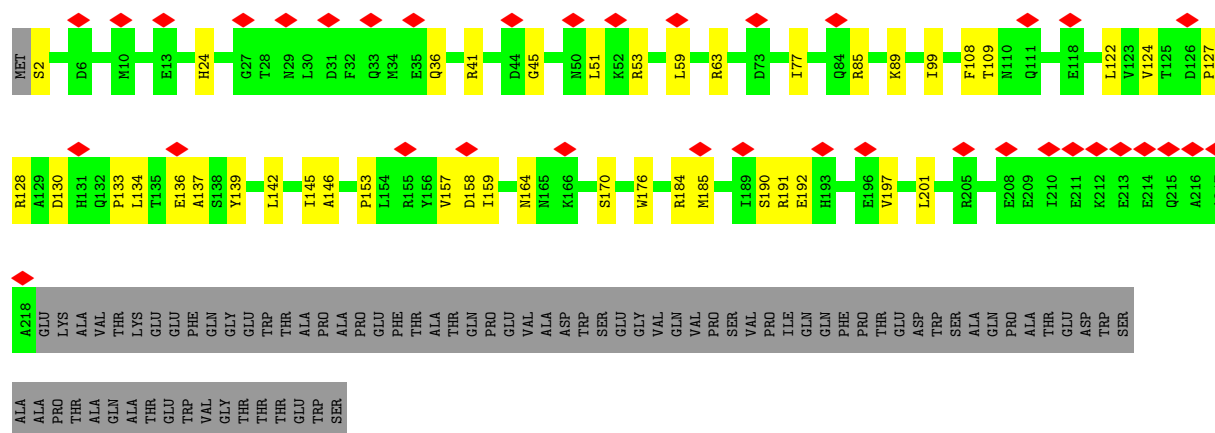
Chain ZA: 10% 51% 36% 6% 8%



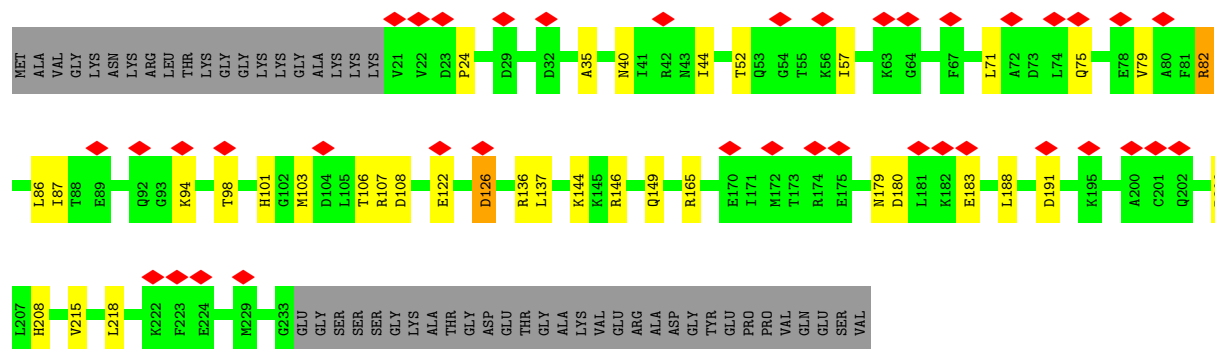




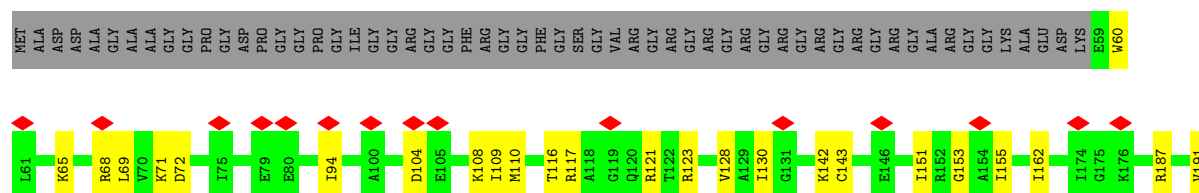
• Molecule 52: RPSA

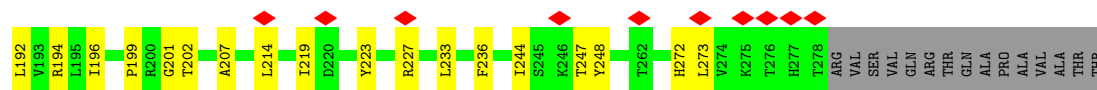


• Molecule 53: S3A

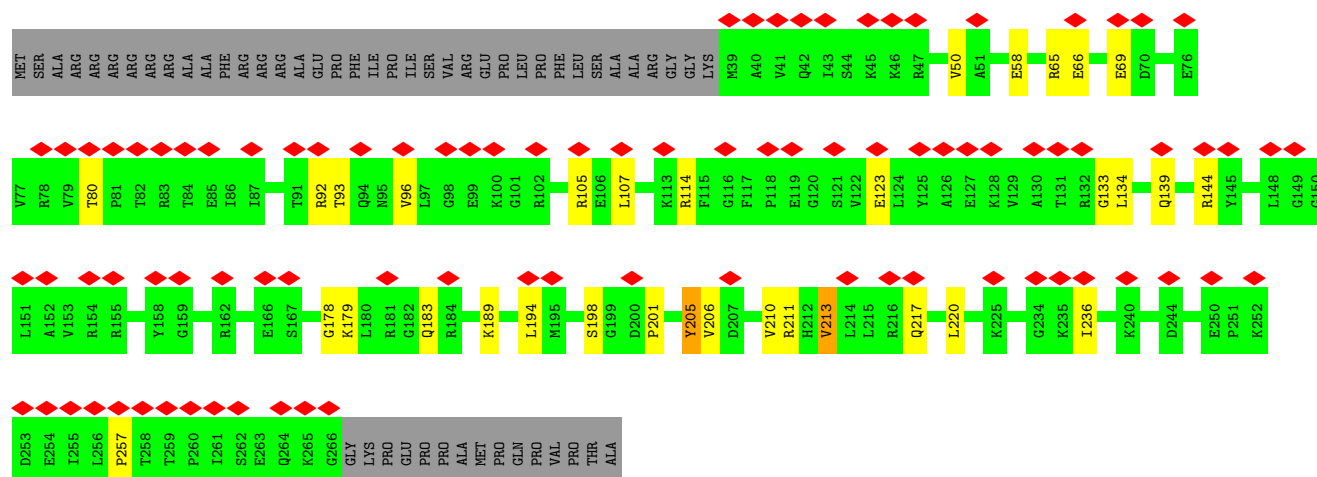


• Molecule 54: eS1

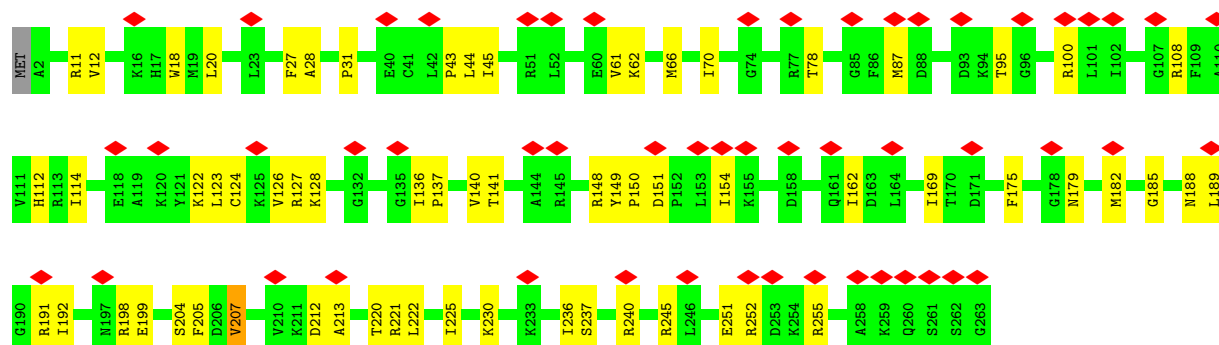
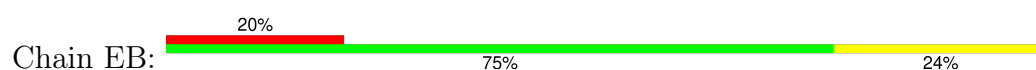




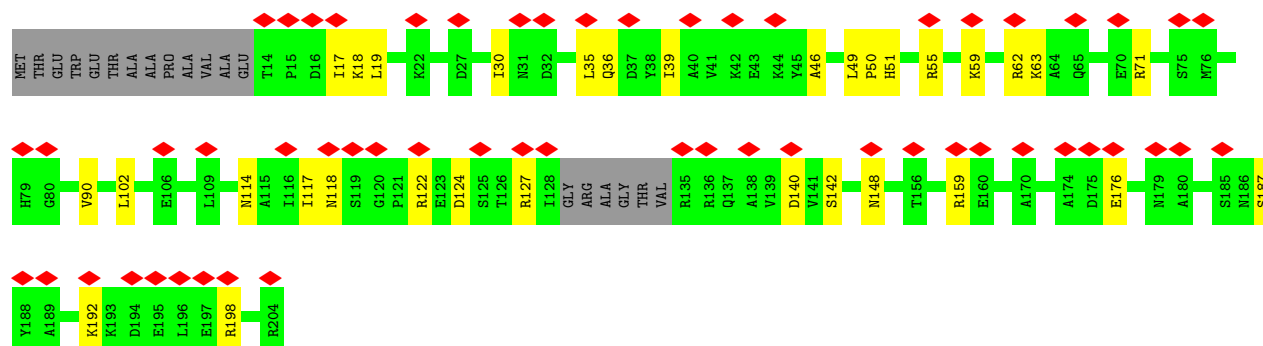
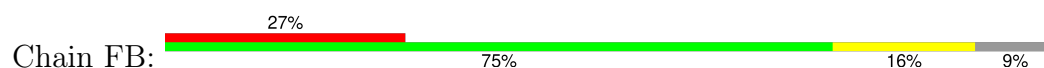
• Molecule 55: S3



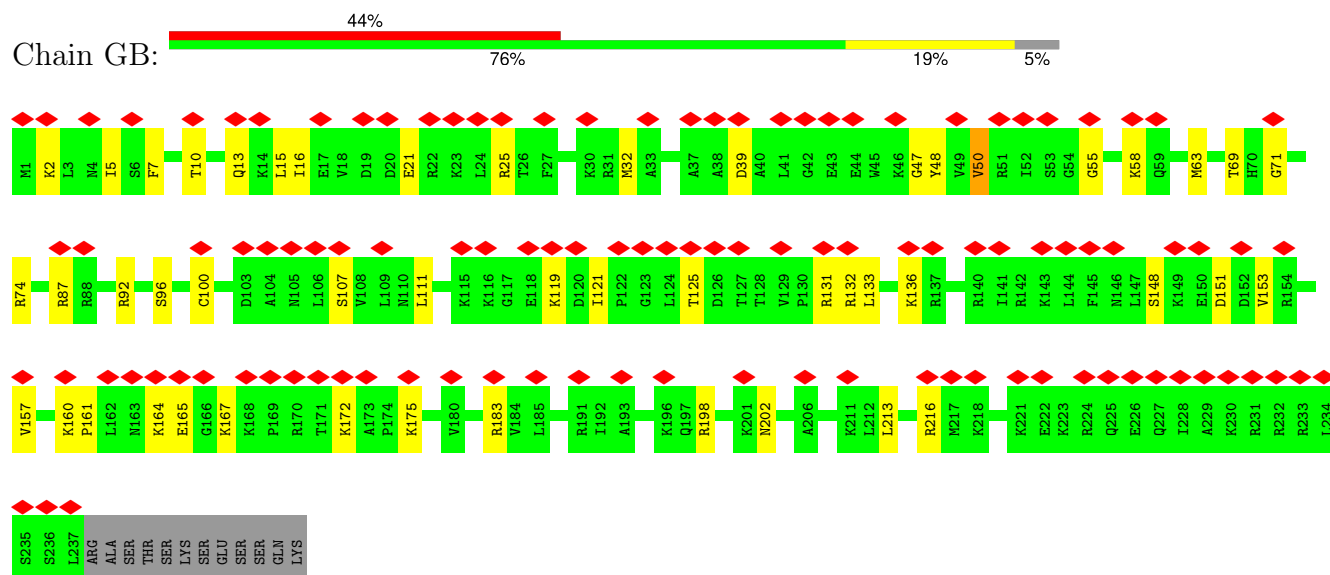
• Molecule 56: S4



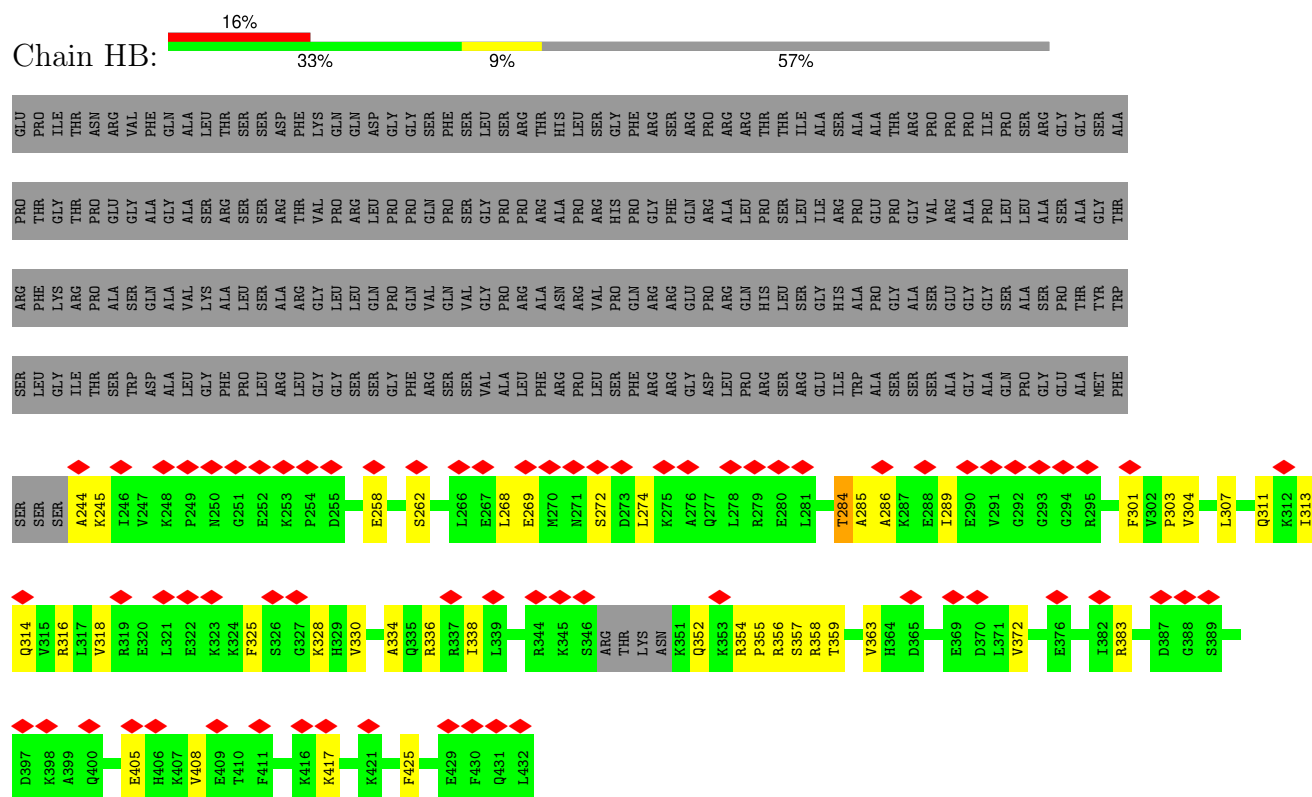
• Molecule 57: S5



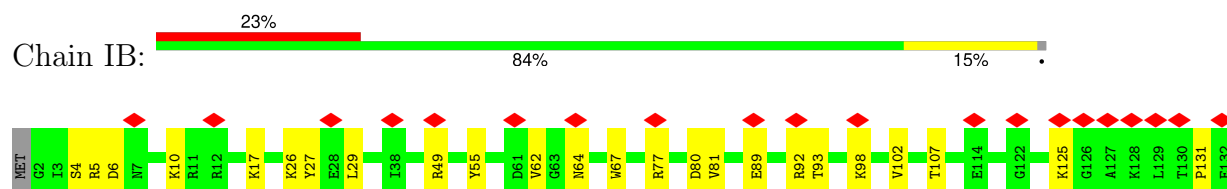
- Molecule 58: eS6

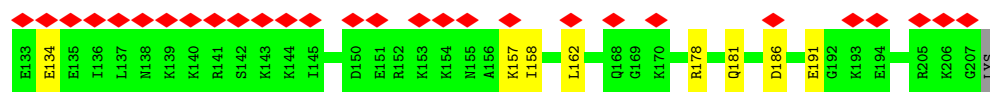


- Molecule 59: eS7

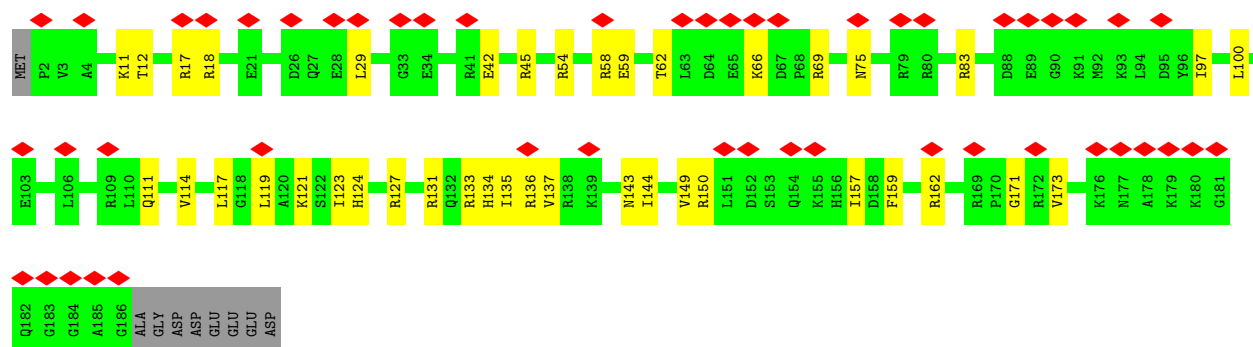
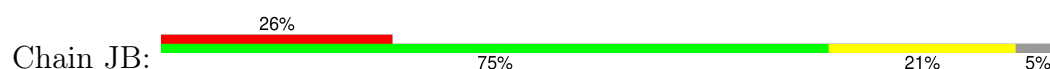


- Molecule 60: S8

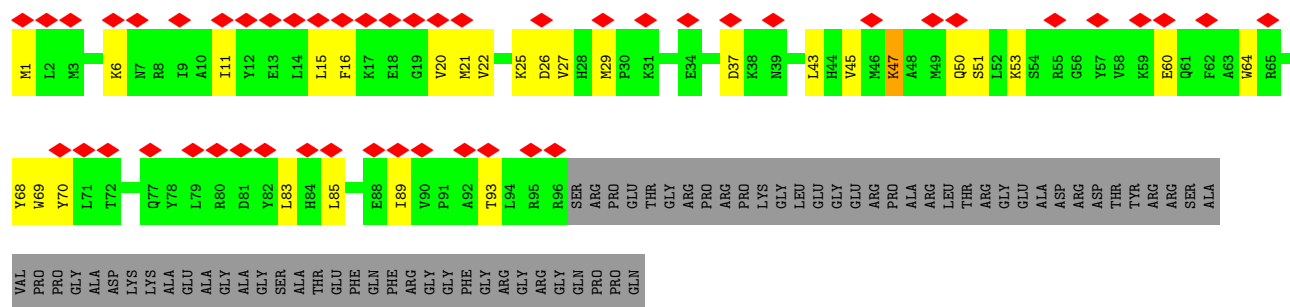
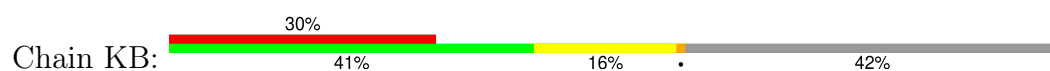




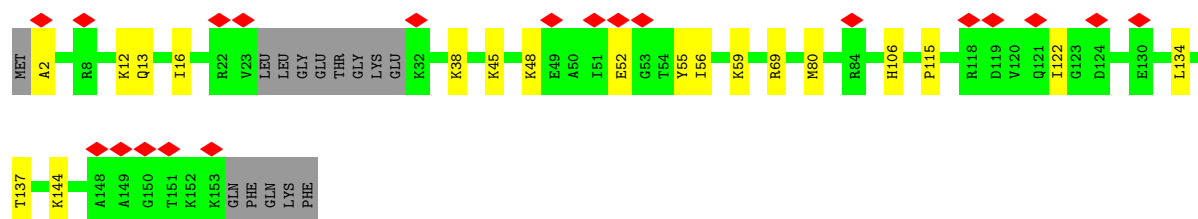
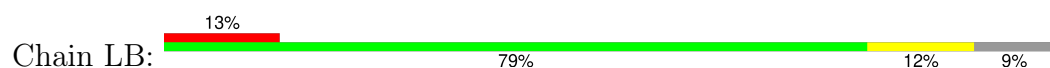
• Molecule 61: S9



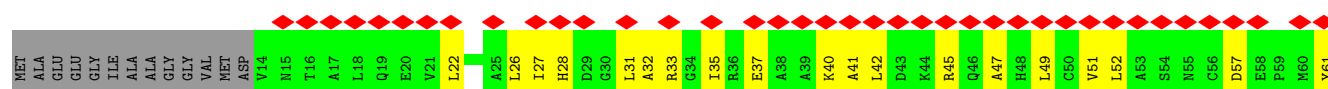
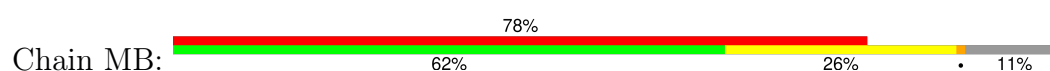
• Molecule 62: S10

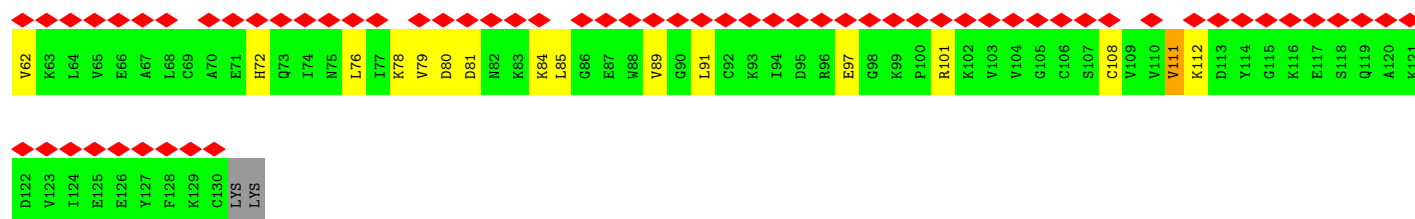


• Molecule 63: S11

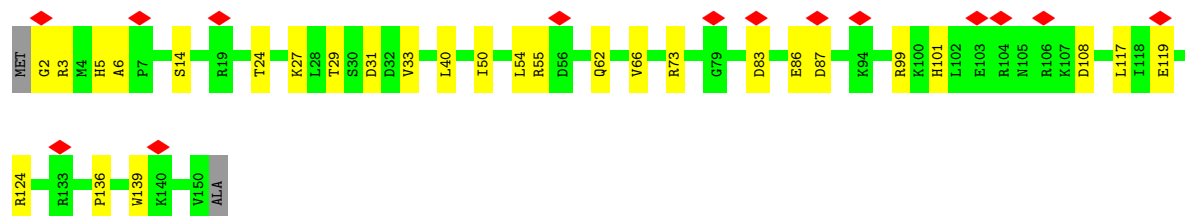
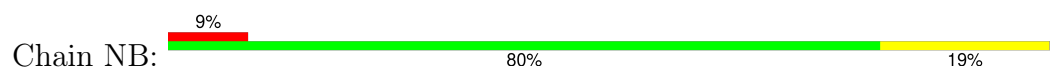


• Molecule 64: S12

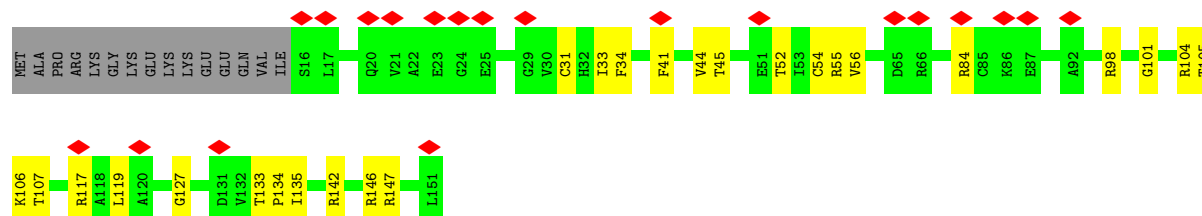
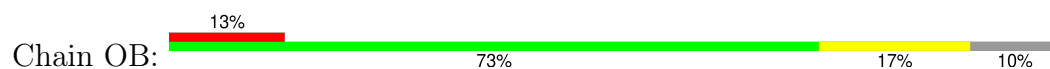




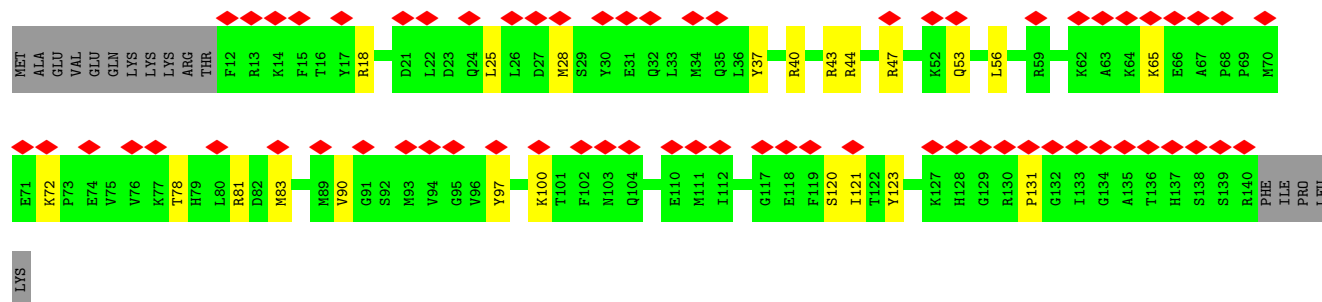
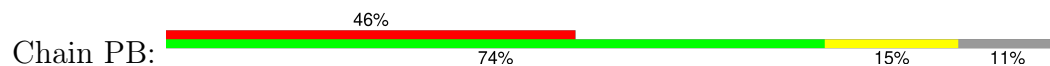
• Molecule 65: uS15



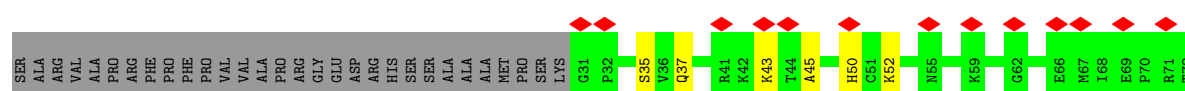
• Molecule 66: S14

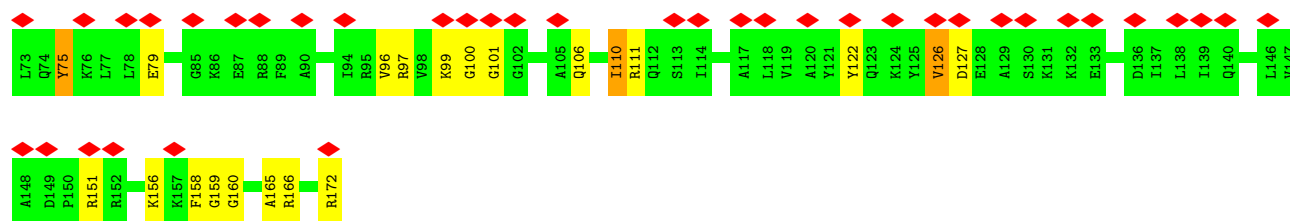


• Molecule 67: S15

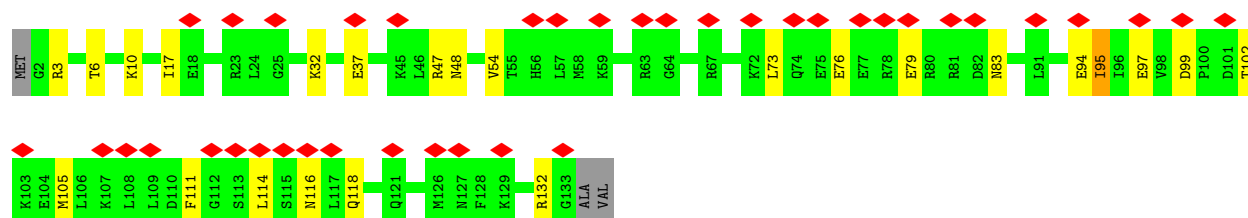
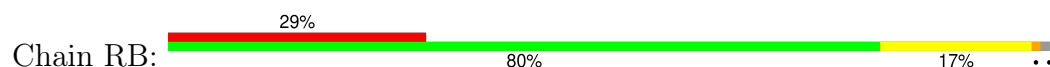


• Molecule 68: uS9

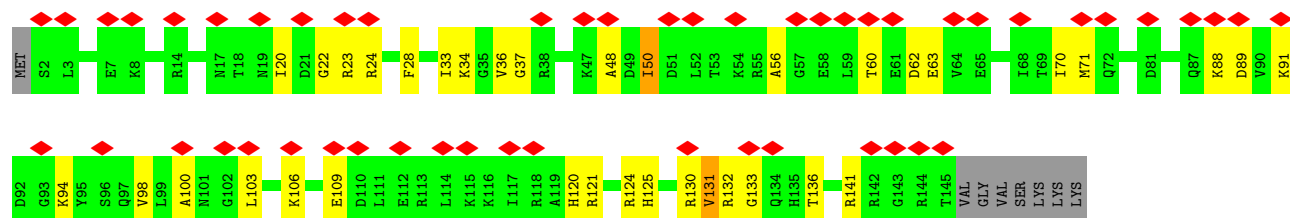




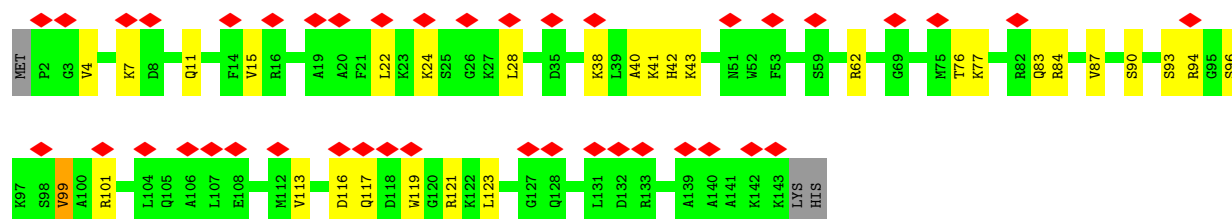
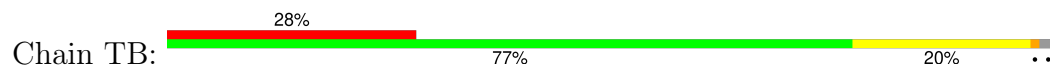
• Molecule 69: eS17



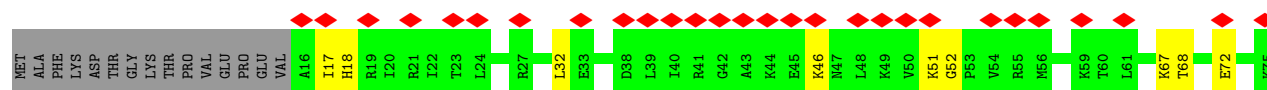
• Molecule 70: S18

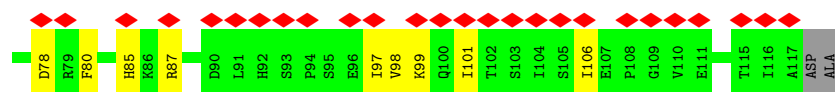


• Molecule 71: S19

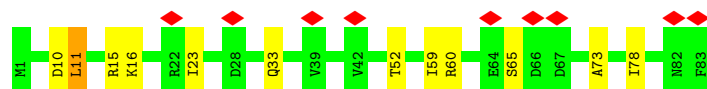
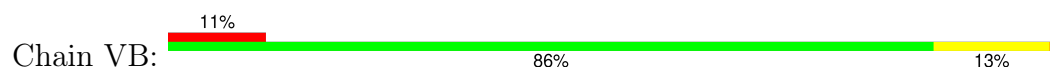


• Molecule 72: uS10

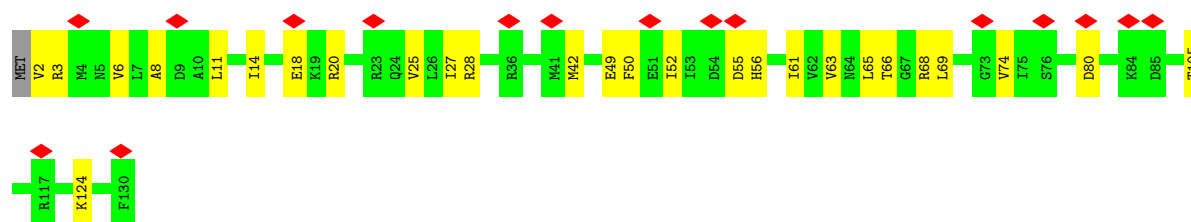
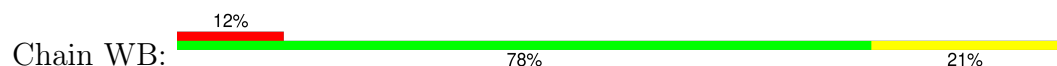




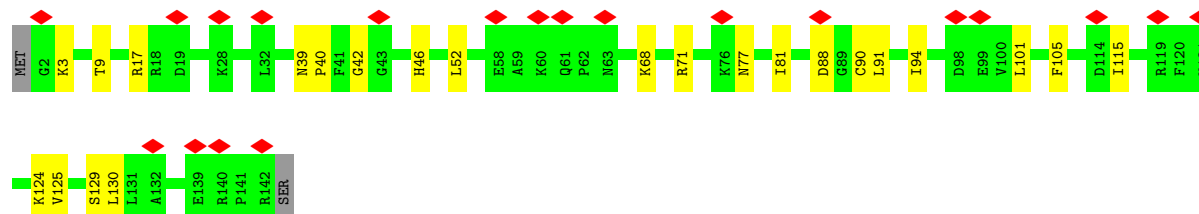
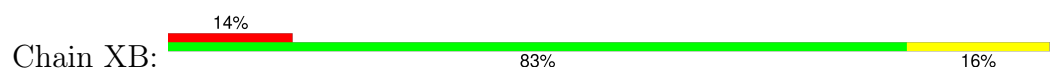
- Molecule 73: S21



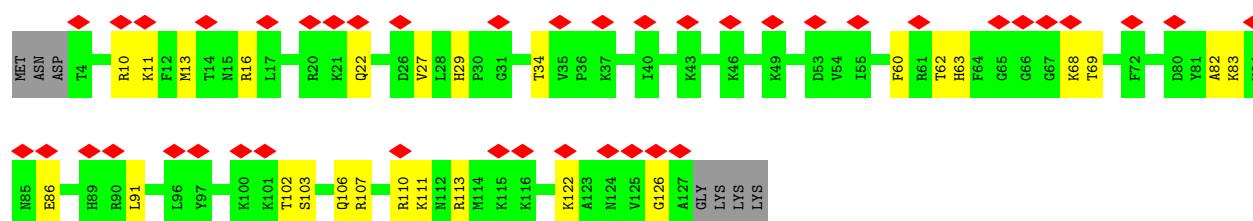
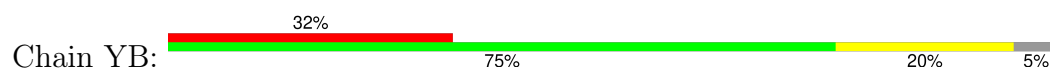
- Molecule 74: S15A



- Molecule 75: S23



- Molecule 76: S24

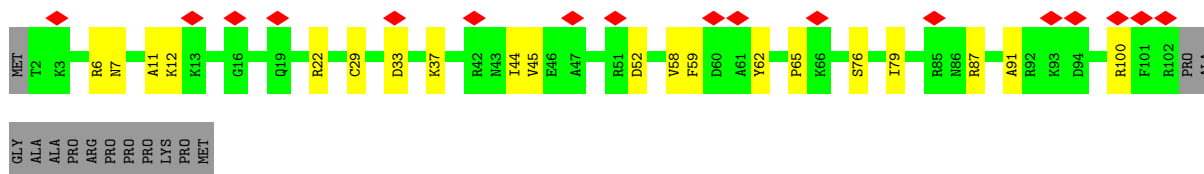


- Molecule 77: eS25

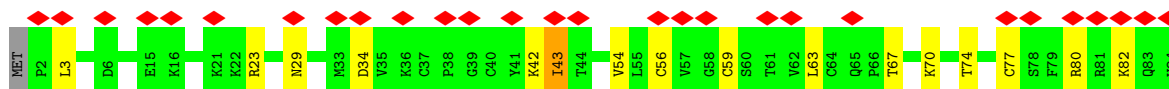
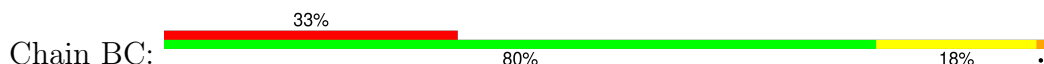




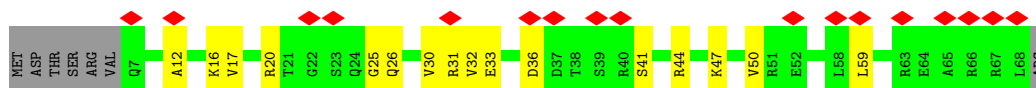
- Molecule 78: S26



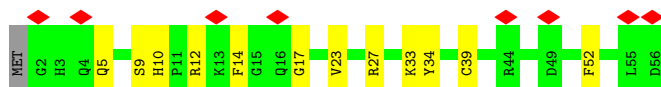
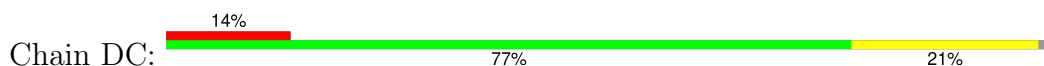
- Molecule 79: S27



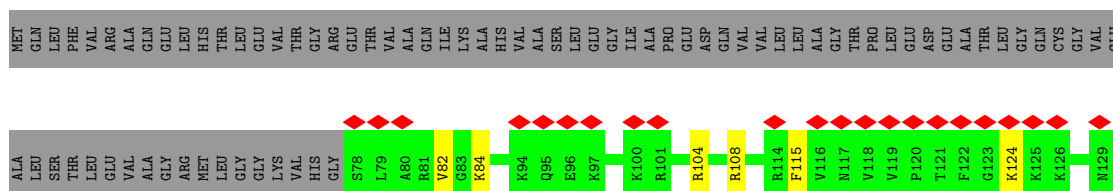
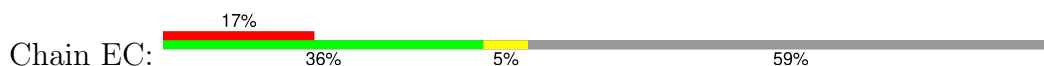
- Molecule 80: S28



- Molecule 81: uS14



- Molecule 82: S30



- Molecule 83: S27A



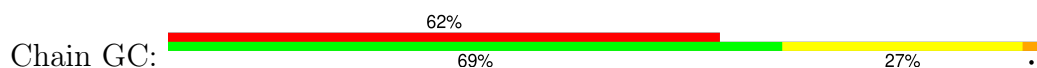
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 HIS
 PRO
 LEU
 TYR
 GLN
 GLY
 SER
 PRO
 ILE
 TRP
 CYS
 GLY
 ARG
 LEU
 ARG
 GLY
 GLY
 ALA
 LEU
 PHE
 GLY
 GLY
 GLY
 ALA
 GLY
 LYS
 PRO
 ARG
 GLY
 PRO
 ASP
 PHE
 LEU
 PHE
 ASP
 PRO
 SER
 SER
 ALA
 ARG
 ARG
 TRP
 ALA
 ARG
 HIS
 GLN
 ASP
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 ASP
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 ARG
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 ASN
 PRO
 TYR
 GLY

GLU
 ASP
 HIS
 HIS
 ALA
 ARG
 GLY
 ILE
 PRO
 ASP
 PRO
 GLN
 GLN
 ARG
 LEU
 PHE
 ILE
 ALA
 GLY
 LYS
 GLN
 LEU
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 ASP
 GLY
 ARG
 THR
 LEU
 SER
 ASP
 TYR
 ASN
 ILE
 GLN
 LYS
 LEU
 SER
 THR
 LEU
 HIS
 VAL
 LEU
 LEU
 ARG
 LEU
 ARG
 GLY
 GLY
 ALA
 LYS
 LYS
 ASP
 LYS
 K82
 K83
 S84
 Y85
 T86
 T87
 P88

K89
 K90
 N91
 K92
 H93
 K94
 R95
 K96
 K97
 V98
 K99
 L100
 A101
 V102
 L103
 Y104
 Y105
 Y106
 K107
 V108
 D109
 E110
 N111
 K112
 K113
 T114
 S115
 R116
 L117
 R118
 R119
 C121
 C122
 S123
 D124
 E125
 C126
 G127
 A128
 G129
 V130
 F131
 M132
 A133
 S134
 H135
 F136
 D137
 R138
 H139
 Y140
 C141
 G142
 K143
 C144
 C145
 L146
 T147
 Y148

C149
 F150
 ASN
 LYS
 PRO
 GLU
 ASP
 LYS

• Molecule 84: RACK1



MET
 T2
 E3
 Q4
 M5
 T6
 L7
 R8
 G9
 T10
 L11
 G13
 V18
 T19
 Q20
 I21
 A22
 Q26
 F27
 P28
 D29
 G95
 M30
 I31
 L32
 S33
 A34
 S35
 R36
 D37
 K38
 T39
 I40
 I41
 M42
 W43
 K44
 L45
 T46
 R47
 D48
 E49
 T50
 N51
 Y52
 G53
 I54
 R57
 R60
 G61
 H62
 S63
 S67
 D68
 V69

V70
 I71
 S72
 D73
 D74
 G75
 F76
 F77
 A78
 L79
 S82
 W83
 D84
 G85
 T86
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 W90
 D91
 L92
 T93
 T94
 G95
 T96
 T97
 T98
 R99
 R100
 F101
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 G103
 H104
 T105
 K106
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 V108
 L109
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 V111
 A112
 F113
 S114
 S115
 D116
 N117
 R118
 Q119
 I120
 V121
 S122
 G123
 S124
 R125
 D126
 K127
 T128
 I129
 K130

L131
 W132
 N133
 T134
 L135
 G136
 V137
 C138
 K139
 Y140
 T141
 V142
 Q143
 D144
 E145
 W150
 V151
 S152
 R155
 F156
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 P158
 N159
 S160
 S161
 N162
 P163
 I164
 I165
 V166
 S167
 C168
 D171
 V174
 K175
 V176
 W177
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 L179
 A180
 N181
 C182
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 L184
 K185
 N186
 T187
 H188
 I189
 G190
 H191
 T192
 G193
 Y194
 L195
 N196

T197
 V198
 T199
 V200
 S201
 P202
 D203
 G204
 S205
 L206
 C207
 A208
 S209
 G210
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 G214
 Q215
 A216
 W217
 L218
 W219
 D220
 L221
 N222
 E223
 G224
 K225
 H226
 L227
 Y228
 T229
 L230
 D231
 G232
 G233
 D234
 N237
 A238
 L239
 C240
 F241
 S242
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 T252
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 P254
 S255
 I256
 K257
 I258
 W259

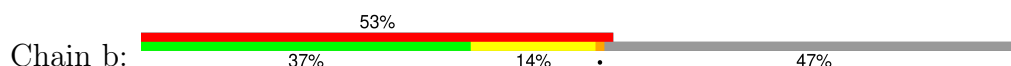
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 S276
 T277
 S278
 S279
 K280
 A281
 E282
 C286
 S288
 L289
 A290
 W291
 S292
 A293
 D294
 G295
 Q296
 T297
 L298
 F299
 A300
 G301
 Y302
 T303
 D304
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 V307
 R308
 V309
 W310
 Q311
 V312
 T313
 T314
 GLY
 THR
 ARG

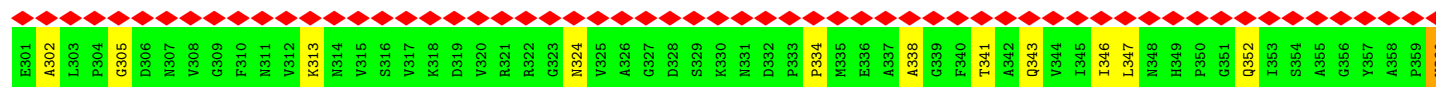
• Molecule 85: peptide



A195
 H196
 F197
 D198

• Molecule 86: RPLP0





| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| L421 | G422 | R423 | F424 | A425 | V426 | D427 | D428 | M429 | R430 | T431 | T432 | V433 | A434 | V435 | G436 | V437 | L438 | K439 | A440 | V441 | D442 | K443 | K444 | A445 | A446 | G447 | A448 | G449 | K450 | V451 | T452 | K453 | S454 | A455 | Q456 | K457 | A458 | Q459 | K460 | A461 | K462 | | | | | | | | | | | | | | | | | | |
| L361 | D362 | C363 | H364 | T365 | A366 | H367 | L368 | M369 | C370 | K371 | F372 | A373 | E374 | L375 | K376 | E377 | K378 | L379 | D380 | R381 | R382 | S383 | G384 | K385 | K386 | L387 | E388 | D389 | G390 | P391 | K392 | F393 | L394 | K395 | S396 | G397 | D398 | A399 | A400 | I401 | V402 | D403 | M404 | V405 | P406 | G407 | K408 | P409 | M410 | C411 | V412 | E413 | S414 | F415 | S416 | D417 | Y418 | P419 | P420 |

4 Experimental information

| Property | Value | Source |
|--------------------------------------|---|-----------|
| EM reconstruction method | SINGLE PARTICLE | Depositor |
| Imposed symmetry | POINT, Not provided | |
| Number of particles used | 6359 | Depositor |
| Resolution determination method | FSC 0.143 CUT-OFF | Depositor |
| CTF correction method | PHASE FLIPPING AND AMPLITUDE CORRECTION | Depositor |
| Microscope | FEI TITAN KRIOS | Depositor |
| Voltage (kV) | 300 | Depositor |
| Electron dose ($e^-/\text{\AA}^2$) | 75 | Depositor |
| Minimum defocus (nm) | 500 | Depositor |
| Maximum defocus (nm) | 2500 | Depositor |
| Magnification | Not provided | |
| Image detector | GATAN K3 (6k x 4k) | Depositor |
| Maximum map value | 33.575 | Depositor |
| Minimum map value | -21.832 | Depositor |
| Average map value | 0.004 | Depositor |
| Map value standard deviation | 1.513 | Depositor |
| Recommended contour level | 6.5 | Depositor |
| Map size (Å) | 686.87994, 686.87994, 686.87994 | wwPDB |
| Map dimensions | 648, 648, 648 | wwPDB |
| Map angles (°) | 90.0, 90.0, 90.0 | wwPDB |
| Pixel spacing (Å) | 1.06, 1.06, 1.06 | Depositor |

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, SPD, MG, ANM, K, 5GP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|-------------|-------------|-------------|
| | | RMSZ | $\# Z > 5$ | RMSZ | $\# Z > 5$ |
| 1 | A | 0.12 | 0/1952 | 0.28 | 0/2617 |
| 2 | B | 0.12 | 0/3264 | 0.28 | 0/4371 |
| 3 | C | 0.11 | 0/2937 | 0.25 | 0/3946 |
| 4 | D | 0.10 | 0/2441 | 0.24 | 0/3269 |
| 5 | E | 0.11 | 0/1859 | 0.26 | 0/2491 |
| 6 | F | 0.12 | 0/1933 | 0.26 | 0/2577 |
| 7 | G | 0.11 | 0/1881 | 0.25 | 0/2532 |
| 8 | H | 0.11 | 0/1535 | 0.27 | 0/2063 |
| 9 | I | 0.11 | 0/1702 | 0.24 | 0/2272 |
| 10 | J | 0.10 | 0/1395 | 0.28 | 0/1863 |
| 11 | K | 0.10 | 0/1733 | 0.24 | 0/2316 |
| 12 | L | 0.11 | 0/1158 | 0.25 | 0/1547 |
| 13 | M | 0.12 | 0/1746 | 0.27 | 0/2338 |
| 14 | N | 0.13 | 0/1662 | 0.29 | 0/2222 |
| 15 | O | 0.12 | 0/1292 | 0.28 | 0/1733 |
| 16 | P | 0.11 | 0/1539 | 0.29 | 0/2054 |
| 17 | Q | 0.11 | 0/1524 | 0.25 | 0/2013 |
| 18 | R | 0.12 | 0/1501 | 0.29 | 0/2012 |
| 19 | S | 0.11 | 0/1326 | 0.24 | 0/1770 |
| 20 | T | 0.11 | 0/840 | 0.31 | 0/1127 |
| 21 | U | 0.12 | 0/1018 | 0.28 | 0/1364 |
| 22 | V | 0.11 | 0/900 | 0.26 | 0/1194 |
| 23 | W | 0.11 | 0/984 | 0.26 | 0/1323 |
| 24 | X | 0.10 | 0/1132 | 0.23 | 0/1504 |
| 25 | Y | 0.11 | 0/1130 | 0.23 | 0/1507 |
| 26 | Z | 0.11 | 0/1191 | 0.26 | 0/1590 |
| 27 | AA | 0.09 | 0/886 | 0.20 | 0/1171 |
| 28 | BA | 0.10 | 0/779 | 0.22 | 0/1044 |
| 29 | CA | 0.12 | 0/908 | 0.28 | 0/1223 |
| 30 | DA | 0.10 | 0/1082 | 0.24 | 0/1443 |
| 31 | EA | 0.12 | 0/895 | 0.27 | 0/1198 |
| 32 | FA | 0.11 | 0/916 | 0.26 | 0/1220 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|---------|-------------|----------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 33 | GA | 0.09 | 0/1016 | 0.23 | 0/1341 |
| 34 | HA | 0.09 | 0/841 | 0.23 | 0/1112 |
| 35 | IA | 0.12 | 0/731 | 0.27 | 0/966 |
| 36 | JA | 0.10 | 0/575 | 0.26 | 0/761 |
| 37 | KA | 0.11 | 0/459 | 0.27 | 0/608 |
| 38 | LA | 0.10 | 0/435 | 0.28 | 0/575 |
| 39 | MA | 0.10 | 0/240 | 0.19 | 0/305 |
| 40 | NA | 0.11 | 0/864 | 0.24 | 0/1140 |
| 41 | OA | 0.12 | 0/718 | 0.32 | 0/953 |
| 42 | PA | 0.12 | 0/1010 | 0.29 | 0/1354 |
| 43 | RA | 0.12 | 0/1174 | 0.32 | 0/1582 |
| 44 | SA | 0.10 | 0/1815 | 0.24 | 0/2828 |
| 45 | TA | 0.09 | 0/1804 | 0.22 | 0/2810 |
| 46 | UA | 0.13 | 0/1783 | 0.32 | 0/2776 |
| 47 | VA | 0.09 | 0/279 | 0.21 | 0/431 |
| 48 | WA | 0.12 | 0/85839 | 0.25 | 0/133881 |
| 49 | XA | 0.11 | 0/2836 | 0.20 | 0/4421 |
| 50 | YA | 0.11 | 0/3701 | 0.23 | 0/5766 |
| 51 | ZA | 0.11 | 0/40949 | 0.24 | 0/63819 |
| 52 | AB | 0.10 | 0/1747 | 0.25 | 0/2374 |
| 53 | BB | 0.10 | 0/1756 | 0.25 | 0/2350 |
| 54 | CB | 0.12 | 0/1744 | 0.29 | 0/2358 |
| 55 | DB | 0.10 | 0/1796 | 0.25 | 0/2417 |
| 56 | EB | 0.11 | 0/2118 | 0.30 | 0/2849 |
| 57 | FB | 0.11 | 0/1492 | 0.29 | 0/2005 |
| 58 | GB | 0.10 | 0/1946 | 0.25 | 0/2590 |
| 59 | HB | 0.11 | 0/1511 | 0.28 | 0/2022 |
| 60 | IB | 0.11 | 0/1715 | 0.26 | 0/2287 |
| 61 | JB | 0.10 | 0/1550 | 0.27 | 0/2069 |
| 62 | KB | 0.11 | 0/834 | 0.28 | 0/1125 |
| 63 | LB | 0.11 | 0/1200 | 0.26 | 0/1604 |
| 64 | MB | 0.10 | 0/918 | 0.27 | 0/1233 |
| 65 | NB | 0.10 | 0/1226 | 0.23 | 0/1649 |
| 66 | OB | 0.11 | 0/1029 | 0.27 | 0/1380 |
| 67 | PB | 0.12 | 0/1079 | 0.28 | 0/1441 |
| 68 | QB | 0.12 | 0/1146 | 0.29 | 0/1534 |
| 69 | RB | 0.10 | 0/1082 | 0.25 | 0/1452 |
| 70 | SB | 0.10 | 0/1208 | 0.29 | 0/1618 |
| 71 | TB | 0.11 | 0/1123 | 0.25 | 0/1504 |
| 72 | UB | 0.11 | 0/818 | 0.28 | 0/1099 |
| 73 | VB | 0.10 | 0/643 | 0.25 | 0/860 |
| 74 | WB | 0.12 | 0/1051 | 0.30 | 0/1406 |
| 75 | XB | 0.10 | 0/1116 | 0.24 | 0/1490 |

| Mol | Chain | Bond lengths | | Bond angles | |
|-----|-------|--------------|----------|-------------|----------|
| | | RMSZ | # Z >5 | RMSZ | # Z >5 |
| 76 | YB | 0.11 | 0/1028 | 0.28 | 0/1366 |
| 77 | ZB | 0.11 | 0/691 | 0.32 | 0/922 |
| 78 | AC | 0.10 | 0/828 | 0.27 | 0/1109 |
| 79 | BC | 0.09 | 0/665 | 0.23 | 0/891 |
| 80 | CC | 0.10 | 0/490 | 0.26 | 0/656 |
| 81 | DC | 0.10 | 0/470 | 0.25 | 0/623 |
| 82 | EC | 0.08 | 0/447 | 0.24 | 0/587 |
| 83 | FC | 0.09 | 0/576 | 0.23 | 0/764 |
| 84 | GC | 0.11 | 0/2493 | 0.32 | 0/3394 |
| 85 | IC | 0.06 | 0/19 | 0.14 | 0/25 |
| 86 | b | 0.14 | 0/1296 | 0.31 | 0/1745 |
| 87 | c | 0.12 | 0/111 | 0.29 | 0/145 |
| 88 | HC | 0.11 | 0/1694 | 0.30 | 0/2287 |
| All | All | 0.11 | 0/236766 | 0.25 | 0/347573 |

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1 | A | 1914 | 0 | 2013 | 35 | 0 |
| 2 | B | 3196 | 0 | 3339 | 51 | 0 |
| 3 | C | 2883 | 0 | 3053 | 37 | 0 |
| 4 | D | 2395 | 0 | 2427 | 30 | 0 |
| 5 | E | 1823 | 0 | 1995 | 31 | 0 |
| 6 | F | 1897 | 0 | 2021 | 36 | 0 |
| 7 | G | 1850 | 0 | 1991 | 23 | 0 |
| 8 | H | 1516 | 0 | 1597 | 15 | 0 |
| 9 | I | 1664 | 0 | 1712 | 23 | 0 |
| 10 | J | 1372 | 0 | 1412 | 21 | 0 |
| 11 | K | 1702 | 0 | 1820 | 26 | 0 |
| 12 | L | 1137 | 0 | 1211 | 24 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 13 | M | 1701 | 0 | 1749 | 34 | 0 |
| 14 | N | 1630 | 0 | 1778 | 32 | 0 |
| 15 | O | 1266 | 0 | 1302 | 16 | 0 |
| 16 | P | 1515 | 0 | 1634 | 30 | 0 |
| 17 | Q | 1508 | 0 | 1664 | 24 | 0 |
| 18 | R | 1462 | 0 | 1508 | 24 | 0 |
| 19 | S | 1298 | 0 | 1366 | 21 | 0 |
| 20 | T | 826 | 0 | 852 | 17 | 0 |
| 21 | U | 1004 | 0 | 1063 | 15 | 0 |
| 22 | V | 887 | 0 | 935 | 11 | 0 |
| 23 | W | 967 | 0 | 1040 | 10 | 0 |
| 24 | X | 1115 | 0 | 1205 | 19 | 0 |
| 25 | Y | 1107 | 0 | 1182 | 22 | 0 |
| 26 | Z | 1162 | 0 | 1209 | 23 | 0 |
| 27 | AA | 873 | 0 | 949 | 8 | 0 |
| 28 | BA | 769 | 0 | 803 | 11 | 0 |
| 29 | CA | 893 | 0 | 932 | 16 | 0 |
| 30 | DA | 1064 | 0 | 1160 | 21 | 0 |
| 31 | EA | 876 | 0 | 912 | 12 | 0 |
| 32 | FA | 906 | 0 | 998 | 7 | 0 |
| 33 | GA | 1008 | 0 | 1142 | 18 | 0 |
| 34 | HA | 830 | 0 | 916 | 6 | 0 |
| 35 | IA | 716 | 0 | 750 | 17 | 0 |
| 36 | JA | 569 | 0 | 637 | 8 | 0 |
| 37 | KA | 447 | 0 | 480 | 13 | 0 |
| 38 | LA | 429 | 0 | 465 | 6 | 0 |
| 39 | MA | 239 | 0 | 289 | 4 | 0 |
| 40 | NA | 851 | 0 | 920 | 13 | 0 |
| 41 | OA | 708 | 0 | 757 | 9 | 0 |
| 42 | PA | 994 | 0 | 1051 | 16 | 0 |
| 43 | RA | 1160 | 0 | 1218 | 15 | 0 |
| 44 | SA | 1622 | 0 | 825 | 12 | 0 |
| 45 | TA | 1615 | 0 | 820 | 18 | 0 |
| 46 | UA | 1596 | 0 | 810 | 17 | 0 |
| 47 | VA | 251 | 0 | 128 | 1 | 0 |
| 48 | WA | 76735 | 0 | 38762 | 933 | 0 |
| 49 | XA | 2538 | 0 | 1286 | 27 | 0 |
| 50 | YA | 3314 | 0 | 1683 | 35 | 0 |
| 51 | ZA | 36623 | 0 | 18504 | 464 | 0 |
| 52 | AB | 1710 | 0 | 1711 | 26 | 0 |
| 53 | BB | 1729 | 0 | 1803 | 21 | 0 |
| 54 | CB | 1707 | 0 | 1793 | 29 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 55 | DB | 1768 | 0 | 1863 | 21 | 0 |
| 56 | EB | 2076 | 0 | 2177 | 37 | 0 |
| 57 | FB | 1471 | 0 | 1522 | 23 | 0 |
| 58 | GB | 1923 | 0 | 2089 | 38 | 0 |
| 59 | HB | 1489 | 0 | 1582 | 25 | 0 |
| 60 | IB | 1686 | 0 | 1772 | 21 | 0 |
| 61 | JB | 1525 | 0 | 1640 | 34 | 0 |
| 62 | KB | 810 | 0 | 836 | 20 | 0 |
| 63 | LB | 1180 | 0 | 1254 | 14 | 0 |
| 64 | MB | 908 | 0 | 939 | 19 | 0 |
| 65 | NB | 1202 | 0 | 1289 | 19 | 0 |
| 66 | OB | 1016 | 0 | 1039 | 20 | 0 |
| 67 | PB | 1058 | 0 | 1104 | 15 | 0 |
| 68 | QB | 1128 | 0 | 1195 | 20 | 0 |
| 69 | RB | 1068 | 0 | 1121 | 16 | 0 |
| 70 | SB | 1190 | 0 | 1249 | 28 | 0 |
| 71 | TB | 1104 | 0 | 1138 | 21 | 0 |
| 72 | UB | 808 | 0 | 878 | 14 | 0 |
| 73 | VB | 636 | 0 | 637 | 8 | 0 |
| 74 | WB | 1034 | 0 | 1080 | 20 | 0 |
| 75 | XB | 1098 | 0 | 1167 | 15 | 0 |
| 76 | YB | 1011 | 0 | 1083 | 18 | 0 |
| 77 | ZB | 683 | 0 | 761 | 8 | 0 |
| 78 | AC | 814 | 0 | 864 | 16 | 0 |
| 79 | BC | 651 | 0 | 672 | 8 | 0 |
| 80 | CC | 488 | 0 | 514 | 11 | 0 |
| 81 | DC | 459 | 0 | 449 | 9 | 0 |
| 82 | EC | 443 | 0 | 492 | 8 | 0 |
| 83 | FC | 564 | 0 | 577 | 7 | 0 |
| 84 | GC | 2436 | 0 | 2393 | 47 | 0 |
| 85 | IC | 20 | 0 | 10 | 0 | 0 |
| 86 | b | 1279 | 0 | 1343 | 29 | 0 |
| 87 | c | 110 | 0 | 83 | 4 | 0 |
| 88 | HC | 1664 | 0 | 1721 | 27 | 0 |
| 89 | A | 1 | 0 | 0 | 0 | 0 |
| 89 | AC | 1 | 0 | 0 | 0 | 0 |
| 89 | FA | 1 | 0 | 0 | 0 | 0 |
| 89 | HC | 1 | 0 | 0 | 0 | 0 |
| 89 | I | 1 | 0 | 0 | 0 | 0 |
| 89 | IA | 1 | 0 | 0 | 0 | 0 |
| 89 | O | 1 | 0 | 0 | 0 | 0 |
| 89 | P | 1 | 0 | 0 | 0 | 0 |

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| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|--------|----------|----------|---------|--------------|
| 89 | SA | 1 | 0 | 0 | 0 | 0 |
| 89 | U | 1 | 0 | 0 | 0 | 0 |
| 89 | WA | 158 | 0 | 0 | 0 | 0 |
| 89 | XA | 3 | 0 | 0 | 0 | 0 |
| 89 | YA | 2 | 0 | 0 | 0 | 0 |
| 89 | Z | 2 | 0 | 0 | 0 | 0 |
| 89 | ZA | 61 | 0 | 0 | 0 | 0 |
| 90 | AC | 1 | 0 | 0 | 0 | 0 |
| 90 | DC | 1 | 0 | 0 | 0 | 0 |
| 90 | FA | 1 | 0 | 0 | 0 | 0 |
| 90 | FC | 1 | 0 | 0 | 0 | 0 |
| 90 | IA | 1 | 0 | 0 | 0 | 0 |
| 90 | LA | 1 | 0 | 0 | 0 | 0 |
| 90 | NA | 1 | 0 | 0 | 0 | 0 |
| 90 | OA | 1 | 0 | 0 | 0 | 0 |
| 91 | UA | 24 | 0 | 11 | 0 | 0 |
| 92 | WA | 19 | 0 | 18 | 0 | 0 |
| 93 | WA | 30 | 0 | 57 | 1 | 0 |
| 93 | ZA | 10 | 0 | 19 | 0 | 0 |
| 94 | WA | 1 | 0 | 0 | 0 | 0 |
| 95 | HC | 6 | 0 | 4 | 0 | 0 |
| All | All | 220703 | 0 | 164224 | 2507 | 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 7.

The worst 5 of 2507 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) |
|------------------|-----------------|--------------------------|-------------------|
| 46:UA:8:U:H3 | 46:UA:14:A:H62 | 1.07 | 1.03 |
| 48:WA:1446:G:H1 | 48:WA:2113:U:H3 | 1.02 | 1.00 |
| 48:WA:2847:A:H61 | 48:WA:3845:C:N4 | 1.57 | 1.00 |
| 48:WA:1249:U:H3 | 48:WA:1268:G:H1 | 1.07 | 0.99 |
| 51:ZA:197:U:H3 | 51:ZA:202:G:H1 | 0.98 | 0.97 |

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

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

| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|-----------|---------|----------|-------------|-----|
| 1 | A | 248/257 (96%) | 236 (95%) | 12 (5%) | 0 | 100 | 100 |
| 2 | B | 395/403 (98%) | 385 (98%) | 10 (2%) | 0 | 100 | 100 |
| 3 | C | 360/413 (87%) | 348 (97%) | 12 (3%) | 0 | 100 | 100 |
| 4 | D | 292/297 (98%) | 286 (98%) | 6 (2%) | 0 | 100 | 100 |
| 5 | E | 222/291 (76%) | 217 (98%) | 5 (2%) | 0 | 100 | 100 |
| 6 | F | 225/249 (90%) | 219 (97%) | 6 (3%) | 0 | 100 | 100 |
| 7 | G | 225/319 (70%) | 220 (98%) | 5 (2%) | 0 | 100 | 100 |
| 8 | H | 188/192 (98%) | 183 (97%) | 5 (3%) | 0 | 100 | 100 |
| 9 | I | 201/214 (94%) | 196 (98%) | 5 (2%) | 0 | 100 | 100 |
| 10 | J | 169/178 (95%) | 168 (99%) | 1 (1%) | 0 | 100 | 100 |
| 11 | K | 208/211 (99%) | 202 (97%) | 6 (3%) | 0 | 100 | 100 |
| 12 | L | 136/218 (62%) | 132 (97%) | 4 (3%) | 0 | 100 | 100 |
| 13 | M | 201/204 (98%) | 196 (98%) | 5 (2%) | 0 | 100 | 100 |
| 14 | N | 197/203 (97%) | 195 (99%) | 2 (1%) | 0 | 100 | 100 |
| 15 | O | 154/213 (72%) | 151 (98%) | 3 (2%) | 0 | 100 | 100 |
| 16 | P | 185/188 (98%) | 180 (97%) | 5 (3%) | 0 | 100 | 100 |
| 17 | Q | 178/212 (84%) | 175 (98%) | 3 (2%) | 0 | 100 | 100 |
| 18 | R | 174/224 (78%) | 166 (95%) | 8 (5%) | 0 | 100 | 100 |
| 19 | S | 157/160 (98%) | 152 (97%) | 5 (3%) | 0 | 100 | 100 |
| 20 | T | 99/128 (77%) | 95 (96%) | 4 (4%) | 0 | 100 | 100 |
| 21 | U | 133/140 (95%) | 128 (96%) | 5 (4%) | 0 | 100 | 100 |
| 22 | V | 106/157 (68%) | 103 (97%) | 3 (3%) | 0 | 100 | 100 |
| 23 | W | 116/156 (74%) | 114 (98%) | 2 (2%) | 0 | 100 | 100 |
| 24 | X | 132/145 (91%) | 128 (97%) | 4 (3%) | 0 | 100 | 100 |
| 25 | Y | 133/136 (98%) | 131 (98%) | 2 (2%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|---------------|------------|---------|----------|-------------|-----|
| 26 | Z | 145/148 (98%) | 143 (99%) | 2 (1%) | 0 | 100 | 100 |
| 27 | AA | 103/245 (42%) | 101 (98%) | 2 (2%) | 0 | 100 | 100 |
| 28 | BA | 97/115 (84%) | 96 (99%) | 1 (1%) | 0 | 100 | 100 |
| 29 | CA | 106/125 (85%) | 104 (98%) | 2 (2%) | 0 | 100 | 100 |
| 30 | DA | 127/135 (94%) | 122 (96%) | 5 (4%) | 0 | 100 | 100 |
| 31 | EA | 107/110 (97%) | 106 (99%) | 1 (1%) | 0 | 100 | 100 |
| 32 | FA | 112/129 (87%) | 111 (99%) | 1 (1%) | 0 | 100 | 100 |
| 33 | GA | 119/123 (97%) | 117 (98%) | 2 (2%) | 0 | 100 | 100 |
| 34 | HA | 100/105 (95%) | 95 (95%) | 5 (5%) | 0 | 100 | 100 |
| 35 | IA | 85/97 (88%) | 83 (98%) | 2 (2%) | 0 | 100 | 100 |
| 36 | JA | 67/70 (96%) | 65 (97%) | 2 (3%) | 0 | 100 | 100 |
| 37 | KA | 48/51 (94%) | 46 (96%) | 2 (4%) | 0 | 100 | 100 |
| 38 | LA | 50/128 (39%) | 50 (100%) | 0 | 0 | 100 | 100 |
| 39 | MA | 23/25 (92%) | 23 (100%) | 0 | 0 | 100 | 100 |
| 40 | NA | 102/106 (96%) | 98 (96%) | 4 (4%) | 0 | 100 | 100 |
| 41 | OA | 89/92 (97%) | 85 (96%) | 4 (4%) | 0 | 100 | 100 |
| 42 | PA | 122/137 (89%) | 119 (98%) | 3 (2%) | 0 | 100 | 100 |
| 43 | RA | 151/165 (92%) | 140 (93%) | 11 (7%) | 0 | 100 | 100 |
| 52 | AB | 215/295 (73%) | 211 (98%) | 4 (2%) | 0 | 100 | 100 |
| 53 | BB | 211/264 (80%) | 207 (98%) | 4 (2%) | 0 | 100 | 100 |
| 54 | CB | 218/293 (74%) | 214 (98%) | 4 (2%) | 0 | 100 | 100 |
| 55 | DB | 226/281 (80%) | 225 (100%) | 1 (0%) | 0 | 100 | 100 |
| 56 | EB | 260/263 (99%) | 251 (96%) | 9 (4%) | 0 | 100 | 100 |
| 57 | FB | 181/204 (89%) | 174 (96%) | 7 (4%) | 0 | 100 | 100 |
| 58 | GB | 235/249 (94%) | 233 (99%) | 2 (1%) | 0 | 100 | 100 |
| 59 | HB | 181/432 (42%) | 175 (97%) | 6 (3%) | 0 | 100 | 100 |
| 60 | IB | 204/208 (98%) | 201 (98%) | 3 (2%) | 0 | 100 | 100 |
| 61 | JB | 183/194 (94%) | 180 (98%) | 3 (2%) | 0 | 100 | 100 |
| 62 | KB | 94/165 (57%) | 92 (98%) | 2 (2%) | 0 | 100 | 100 |
| 63 | LB | 140/158 (89%) | 138 (99%) | 2 (1%) | 0 | 100 | 100 |
| 64 | MB | 115/132 (87%) | 109 (95%) | 6 (5%) | 0 | 100 | 100 |

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| Mol | Chain | Analysed | Favoured | Allowed | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|----------|-------------|-----|
| 65 | NB | 147/151 (97%) | 146 (99%) | 1 (1%) | 0 | 100 | 100 |
| 66 | OB | 134/151 (89%) | 128 (96%) | 6 (4%) | 0 | 100 | 100 |
| 67 | PB | 127/145 (88%) | 123 (97%) | 4 (3%) | 0 | 100 | 100 |
| 68 | QB | 140/172 (81%) | 135 (96%) | 5 (4%) | 0 | 100 | 100 |
| 69 | RB | 130/135 (96%) | 126 (97%) | 4 (3%) | 0 | 100 | 100 |
| 70 | SB | 142/152 (93%) | 139 (98%) | 3 (2%) | 0 | 100 | 100 |
| 71 | TB | 140/145 (97%) | 135 (96%) | 4 (3%) | 1 (1%) | 19 | 51 |
| 72 | UB | 100/119 (84%) | 96 (96%) | 4 (4%) | 0 | 100 | 100 |
| 73 | VB | 81/83 (98%) | 79 (98%) | 2 (2%) | 0 | 100 | 100 |
| 74 | WB | 127/130 (98%) | 123 (97%) | 4 (3%) | 0 | 100 | 100 |
| 75 | XB | 139/143 (97%) | 136 (98%) | 3 (2%) | 0 | 100 | 100 |
| 76 | YB | 122/131 (93%) | 119 (98%) | 3 (2%) | 0 | 100 | 100 |
| 77 | ZB | 83/124 (67%) | 83 (100%) | 0 | 0 | 100 | 100 |
| 78 | AC | 99/115 (86%) | 96 (97%) | 3 (3%) | 0 | 100 | 100 |
| 79 | BC | 81/84 (96%) | 80 (99%) | 1 (1%) | 0 | 100 | 100 |
| 80 | CC | 60/69 (87%) | 60 (100%) | 0 | 0 | 100 | 100 |
| 81 | DC | 53/56 (95%) | 53 (100%) | 0 | 0 | 100 | 100 |
| 82 | EC | 53/133 (40%) | 51 (96%) | 2 (4%) | 0 | 100 | 100 |
| 83 | FC | 67/188 (36%) | 63 (94%) | 4 (6%) | 0 | 100 | 100 |
| 84 | GC | 311/317 (98%) | 301 (97%) | 10 (3%) | 0 | 100 | 100 |
| 85 | IC | 2/4 (50%) | 2 (100%) | 0 | 0 | 100 | 100 |
| 86 | b | 162/318 (51%) | 150 (93%) | 11 (7%) | 1 (1%) | 22 | 53 |
| 87 | c | 12/14 (86%) | 11 (92%) | 1 (8%) | 0 | 100 | 100 |
| 88 | HC | 221/462 (48%) | 209 (95%) | 12 (5%) | 0 | 100 | 100 |
| All | All | 11783/14293 (82%) | 11464 (97%) | 317 (3%) | 2 (0%) | 100 | 100 |

All (2) Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 71 | TB | 119 | TRP |
| 86 | b | 225 | VAL |

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 PDB entries followed by that with respect to all EM entries.

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

| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|---------------|------------|----------|-------------|-----|
| 1 | A | 192/199 (96%) | 191 (100%) | 1 (0%) | 86 | 92 |
| 2 | B | 344/348 (99%) | 336 (98%) | 8 (2%) | 45 | 70 |
| 3 | C | 302/337 (90%) | 300 (99%) | 2 (1%) | 81 | 90 |
| 4 | D | 247/250 (99%) | 246 (100%) | 1 (0%) | 89 | 94 |
| 5 | E | 201/251 (80%) | 199 (99%) | 2 (1%) | 73 | 86 |
| 6 | F | 198/218 (91%) | 198 (100%) | 0 | 100 | 100 |
| 7 | G | 197/273 (72%) | 194 (98%) | 3 (2%) | 60 | 80 |
| 8 | H | 169/171 (99%) | 166 (98%) | 3 (2%) | 54 | 76 |
| 9 | I | 175/181 (97%) | 173 (99%) | 2 (1%) | 70 | 84 |
| 10 | J | 144/149 (97%) | 143 (99%) | 1 (1%) | 81 | 90 |
| 11 | K | 175/176 (99%) | 171 (98%) | 4 (2%) | 45 | 70 |
| 12 | L | 117/161 (73%) | 117 (100%) | 0 | 100 | 100 |
| 13 | M | 171/172 (99%) | 167 (98%) | 4 (2%) | 45 | 70 |
| 14 | N | 171/173 (99%) | 171 (100%) | 0 | 100 | 100 |
| 15 | O | 137/190 (72%) | 137 (100%) | 0 | 100 | 100 |
| 16 | P | 164/165 (99%) | 162 (99%) | 2 (1%) | 67 | 83 |
| 17 | Q | 159/191 (83%) | 159 (100%) | 0 | 100 | 100 |
| 18 | R | 157/192 (82%) | 153 (98%) | 4 (2%) | 42 | 69 |
| 19 | S | 139/140 (99%) | 137 (99%) | 2 (1%) | 62 | 81 |
| 20 | T | 91/114 (80%) | 91 (100%) | 0 | 100 | 100 |
| 21 | U | 103/107 (96%) | 102 (99%) | 1 (1%) | 73 | 86 |
| 22 | V | 89/126 (71%) | 87 (98%) | 2 (2%) | 47 | 71 |
| 23 | W | 106/134 (79%) | 105 (99%) | 1 (1%) | 75 | 88 |
| 24 | X | 124/135 (92%) | 120 (97%) | 4 (3%) | 34 | 63 |
| 25 | Y | 117/118 (99%) | 116 (99%) | 1 (1%) | 75 | 88 |
| 26 | Z | 119/120 (99%) | 118 (99%) | 1 (1%) | 79 | 89 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|----------------|------------|----------|-------------|-----|
| 27 | AA | 87/184 (47%) | 86 (99%) | 1 (1%) | 70 | 84 |
| 28 | BA | 85/98 (87%) | 83 (98%) | 2 (2%) | 44 | 70 |
| 29 | CA | 98/110 (89%) | 97 (99%) | 1 (1%) | 73 | 86 |
| 30 | DA | 115/121 (95%) | 115 (100%) | 0 | 100 | 100 |
| 31 | EA | 88/89 (99%) | 88 (100%) | 0 | 100 | 100 |
| 32 | FA | 98/109 (90%) | 95 (97%) | 3 (3%) | 35 | 63 |
| 33 | GA | 109/110 (99%) | 106 (97%) | 3 (3%) | 38 | 66 |
| 34 | HA | 86/89 (97%) | 86 (100%) | 0 | 100 | 100 |
| 35 | IA | 74/80 (92%) | 73 (99%) | 1 (1%) | 62 | 81 |
| 36 | JA | 64/65 (98%) | 64 (100%) | 0 | 100 | 100 |
| 37 | KA | 47/48 (98%) | 46 (98%) | 1 (2%) | 48 | 72 |
| 38 | LA | 48/116 (41%) | 46 (96%) | 2 (4%) | 25 | 56 |
| 39 | MA | 24/24 (100%) | 24 (100%) | 0 | 100 | 100 |
| 40 | NA | 92/94 (98%) | 92 (100%) | 0 | 100 | 100 |
| 41 | OA | 74/75 (99%) | 73 (99%) | 1 (1%) | 62 | 81 |
| 42 | PA | 108/121 (89%) | 106 (98%) | 2 (2%) | 52 | 75 |
| 43 | RA | 126/137 (92%) | 118 (94%) | 8 (6%) | 15 | 42 |
| 52 | AB | 180/244 (74%) | 180 (100%) | 0 | 100 | 100 |
| 53 | BB | 194/231 (84%) | 192 (99%) | 2 (1%) | 73 | 86 |
| 54 | CB | 186/225 (83%) | 185 (100%) | 1 (0%) | 86 | 92 |
| 55 | DB | 190/232 (82%) | 186 (98%) | 4 (2%) | 48 | 72 |
| 56 | EB | 224/225 (100%) | 219 (98%) | 5 (2%) | 47 | 71 |
| 57 | FB | 158/170 (93%) | 157 (99%) | 1 (1%) | 84 | 91 |
| 58 | GB | 207/218 (95%) | 203 (98%) | 4 (2%) | 52 | 75 |
| 59 | HB | 165/360 (46%) | 161 (98%) | 4 (2%) | 44 | 70 |
| 60 | IB | 178/180 (99%) | 176 (99%) | 2 (1%) | 70 | 84 |
| 61 | JB | 161/168 (96%) | 159 (99%) | 2 (1%) | 67 | 83 |
| 62 | KB | 87/136 (64%) | 86 (99%) | 1 (1%) | 70 | 84 |
| 63 | LB | 130/142 (92%) | 128 (98%) | 2 (2%) | 60 | 80 |
| 64 | MB | 99/108 (92%) | 93 (94%) | 6 (6%) | 15 | 43 |
| 65 | NB | 130/131 (99%) | 129 (99%) | 1 (1%) | 79 | 89 |

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| Mol | Chain | Analysed | Rotameric | Outliers | Percentiles | |
|-----|-------|-------------------|-------------|----------|-------------|-----|
| 66 | OB | 106/119 (89%) | 105 (99%) | 1 (1%) | 75 | 88 |
| 67 | PB | 115/130 (88%) | 111 (96%) | 4 (4%) | 31 | 61 |
| 68 | QB | 117/140 (84%) | 114 (97%) | 3 (3%) | 41 | 68 |
| 69 | RB | 119/121 (98%) | 116 (98%) | 3 (2%) | 42 | 69 |
| 70 | SB | 125/132 (95%) | 123 (98%) | 2 (2%) | 58 | 79 |
| 71 | TB | 112/116 (97%) | 109 (97%) | 3 (3%) | 40 | 67 |
| 72 | UB | 93/107 (87%) | 90 (97%) | 3 (3%) | 34 | 63 |
| 73 | VB | 67/67 (100%) | 65 (97%) | 2 (3%) | 36 | 64 |
| 74 | WB | 112/113 (99%) | 111 (99%) | 1 (1%) | 75 | 88 |
| 75 | XB | 113/115 (98%) | 109 (96%) | 4 (4%) | 31 | 61 |
| 76 | YB | 107/113 (95%) | 107 (100%) | 0 | 100 | 100 |
| 77 | ZB | 75/102 (74%) | 74 (99%) | 1 (1%) | 65 | 82 |
| 78 | AC | 88/98 (90%) | 87 (99%) | 1 (1%) | 70 | 84 |
| 79 | BC | 75/76 (99%) | 73 (97%) | 2 (3%) | 40 | 67 |
| 80 | CC | 55/62 (89%) | 55 (100%) | 0 | 100 | 100 |
| 81 | DC | 48/49 (98%) | 47 (98%) | 1 (2%) | 48 | 72 |
| 82 | EC | 46/106 (43%) | 45 (98%) | 1 (2%) | 47 | 71 |
| 83 | FC | 62/154 (40%) | 59 (95%) | 3 (5%) | 21 | 51 |
| 84 | GC | 272/275 (99%) | 250 (92%) | 22 (8%) | 9 | 33 |
| 86 | b | 138/258 (54%) | 126 (91%) | 12 (9%) | 8 | 31 |
| 87 | c | 12/12 (100%) | 12 (100%) | 0 | 100 | 100 |
| 88 | HC | 179/379 (47%) | 164 (92%) | 15 (8%) | 9 | 32 |
| All | All | 10256/12075 (85%) | 10063 (98%) | 193 (2%) | 52 | 75 |

5 of 193 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 68 | QB | 110 | ILE |
| 83 | FC | 135 | HIS |
| 69 | RB | 99 | ASP |
| 74 | WB | 105 | THR |
| 84 | GC | 54 | ILE |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 64 | MB | 75 | ASN |
| 78 | AC | 72 | HIS |
| 68 | QB | 37 | GLN |
| 75 | XB | 61 | GLN |
| 84 | GC | 222 | ASN |

5.3.3 RNA ⓘ

| Mol | Chain | Analysed | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 44 | SA | 75/76 (98%) | 16 (21%) | 3 (4%) |
| 45 | TA | 75/76 (98%) | 15 (20%) | 0 |
| 46 | UA | 74/75 (98%) | 37 (50%) | 1 (1%) |
| 47 | VA | 11/12 (91%) | 3 (27%) | 0 |
| 48 | WA | 3556/3584 (99%) | 603 (16%) | 20 (0%) |
| 49 | XA | 118/120 (98%) | 9 (7%) | 0 |
| 50 | YA | 155/156 (99%) | 33 (21%) | 0 |
| 51 | ZA | 1707/1869 (91%) | 326 (19%) | 8 (0%) |
| All | All | 5771/5968 (96%) | 1042 (18%) | 32 (0%) |

5 of 1042 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 44 | SA | 9 | A |
| 44 | SA | 16 | C |
| 44 | SA | 18 | G |
| 44 | SA | 19 | C |
| 44 | SA | 20 | A |

5 of 32 RNA pucker outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|------|------|
| 51 | ZA | 870 | A |
| 51 | ZA | 890 | U |
| 48 | WA | 1806 | A |
| 48 | WA | 1677 | C |
| 51 | ZA | 1137 | 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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 252 ligands modelled in this entry, 245 are monoatomic - leaving 7 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

| Mol | Type | Chain | Res | Link | Bond lengths | | | Bond angles | | |
|-----|------|-------|------|------|--------------|------|-------------|-------------|------|-------------|
| | | | | | Counts | RMSZ | $\# Z > 2$ | Counts | RMSZ | $\# Z > 2$ |
| 93 | SPD | WA | 5246 | - | 9,9,9 | 0.26 | 0 | 8,8,8 | 0.29 | 0 |
| 91 | 5GP | UA | 101 | 46 | 22,26,26 | 1.23 | 2 (9%) | 24,40,40 | 1.28 | 4 (16%) |
| 93 | SPD | ZA | 1944 | - | 9,9,9 | 0.26 | 0 | 8,8,8 | 0.29 | 0 |
| 93 | SPD | WA | 5244 | - | 9,9,9 | 0.27 | 0 | 8,8,8 | 0.34 | 0 |
| 92 | ANM | WA | 5243 | 94 | 20,20,20 | 4.07 | 7 (35%) | 24,27,27 | 1.40 | 2 (8%) |
| 93 | SPD | WA | 5245 | - | 9,9,9 | 0.28 | 0 | 8,8,8 | 0.30 | 0 |
| 95 | SER | HC | 502 | - | 4,5,6 | 0.59 | 0 | 1,5,7 | 0.54 | 0 |

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

| Mol | Type | Chain | Res | Link | Chirals | Torsions | Rings |
|-----|------|-------|------|------|---------|------------|---------|
| 93 | SPD | WA | 5246 | - | - | 1/7/7/7 | - |
| 91 | 5GP | UA | 101 | 46 | - | 5/6/26/26 | 0/3/3/3 |
| 93 | SPD | ZA | 1944 | - | - | 1/7/7/7 | - |
| 93 | SPD | WA | 5244 | - | - | 1/7/7/7 | - |
| 92 | ANM | WA | 5243 | 94 | - | 6/10/23/23 | 0/2/2/2 |
| 93 | SPD | WA | 5245 | - | - | 1/7/7/7 | - |
| 95 | SER | HC | 502 | - | - | 1/2/4/6 | - |

The worst 5 of 9 bond length outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|-------|--------|-------------|----------|
| 92 | WA | 5243 | ANM | C3-C2 | -11.78 | 1.32 | 1.53 |

Continued on next page...

Continued from previous page...

| Mol | Chain | Res | Type | Atoms | Z | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|--------|-------|-------------|----------|
| 92 | WA | 5243 | ANM | C16-N1 | -8.84 | 1.30 | 1.47 |
| 92 | WA | 5243 | ANM | C2-C16 | 7.40 | 1.68 | 1.53 |
| 91 | UA | 101 | 5GP | C5-C6 | -4.12 | 1.39 | 1.47 |
| 92 | WA | 5243 | ANM | C4-C3 | 4.00 | 1.58 | 1.53 |

The worst 5 of 6 bond angle outliers are listed below:

| Mol | Chain | Res | Type | Atoms | Z | Observed(°) | Ideal(°) |
|-----|-------|------|------|----------|-------|-------------|----------|
| 92 | WA | 5243 | ANM | O2-C5-C6 | 5.19 | 120.35 | 111.09 |
| 91 | UA | 101 | 5GP | C8-N7-C5 | 2.89 | 107.48 | 102.55 |
| 91 | UA | 101 | 5GP | C5-C6-N1 | 2.88 | 119.56 | 114.07 |
| 91 | UA | 101 | 5GP | C2-N1-C6 | -2.34 | 120.83 | 125.11 |
| 92 | WA | 5243 | ANM | C2-O2-C5 | -2.12 | 114.43 | 117.72 |

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

| Mol | Chain | Res | Type | Atoms |
|-----|-------|------|------|---------------|
| 91 | UA | 101 | 5GP | C5'-O5'-P-O1P |
| 92 | WA | 5243 | ANM | C6-C5-O2-C2 |
| 92 | WA | 5243 | ANM | O3-C5-O2-C2 |
| 92 | WA | 5243 | ANM | C10-C9-O1-C14 |
| 92 | WA | 5243 | ANM | C1-C9-O1-C14 |

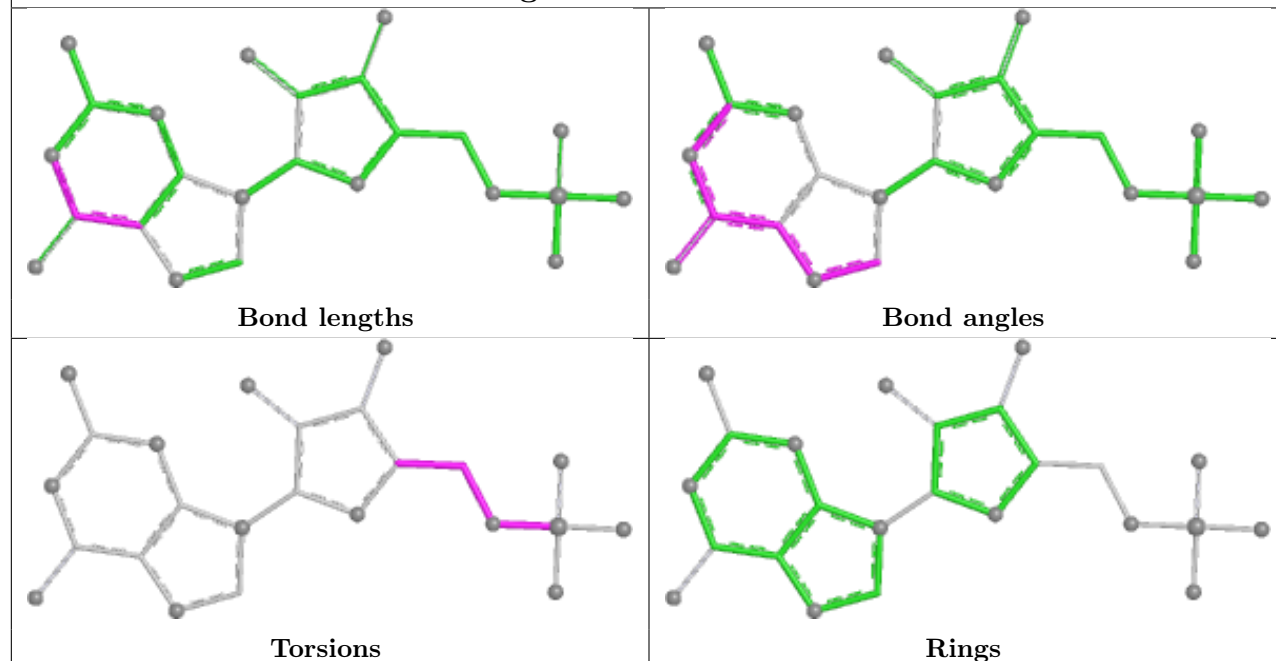
There are no ring outliers.

1 monomer is involved in 1 short contact:

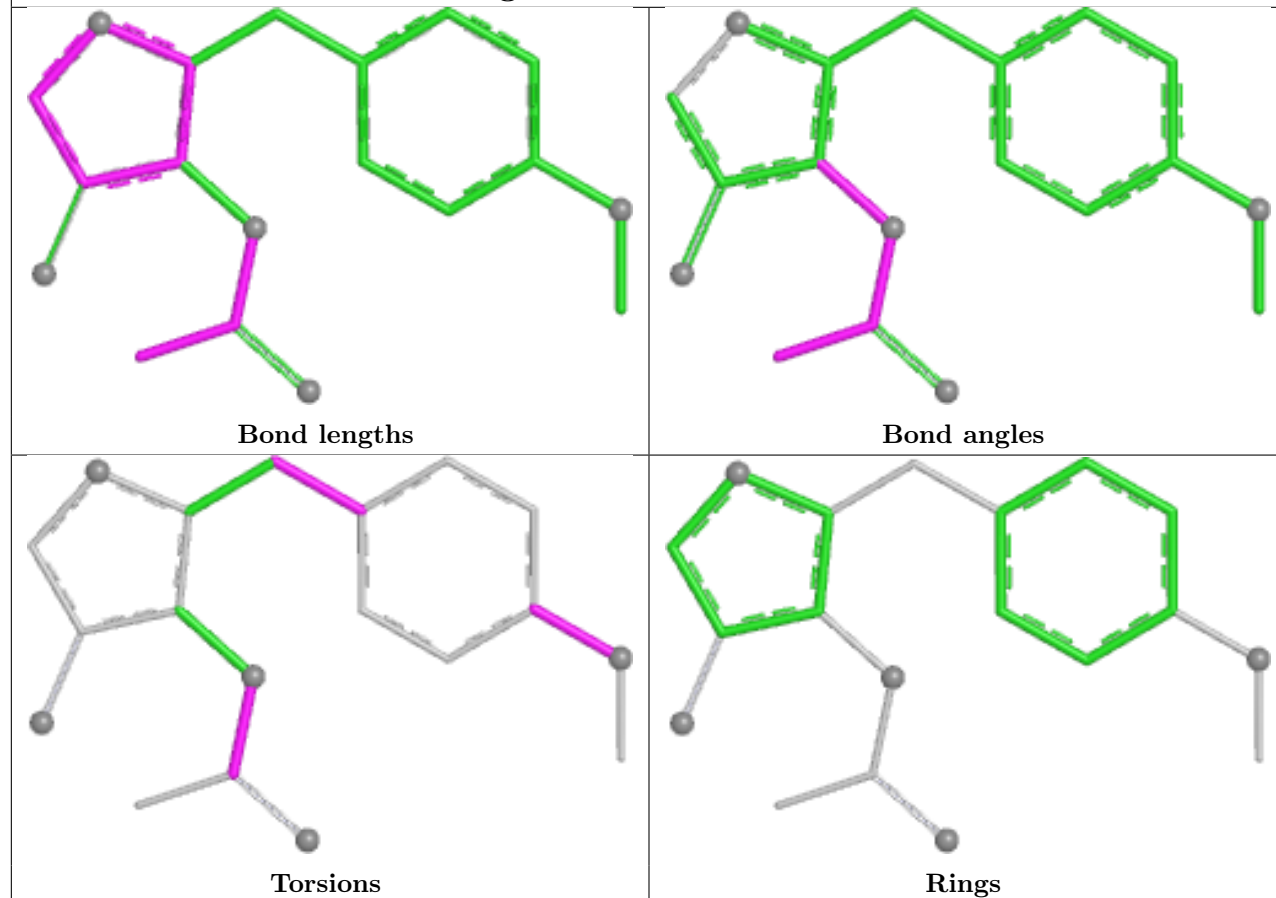
| Mol | Chain | Res | Type | Clashes | Symm-Clashes |
|-----|-------|------|------|---------|--------------|
| 93 | WA | 5244 | SPD | 1 | 0 |

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand 5GP UA 101



Ligand ANM WA 5243



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

| Mol | Chain | Number of breaks |
|-----|-------|------------------|
| 48 | WA | 21 |
| 86 | b | 2 |

The worst 5 of 23 chain breaks are listed below:

| Model | Chain | Residue-1 | Atom-1 | Residue-2 | Atom-2 | Distance (Å) |
|-------|-------|-----------|--------|-----------|--------|--------------|
| 1 | WA | 2118:C | O3' | 2260:C | P | 37.06 |
| 1 | WA | 1225:G | O3' | 1239:G | P | 20.73 |
| 1 | WA | 996:C | O3' | 1070:G | P | 17.80 |
| 1 | WA | 4779:C | O3' | 4861:C | P | 17.50 |
| 1 | WA | 763:G | O3' | 904:C | P | 16.92 |

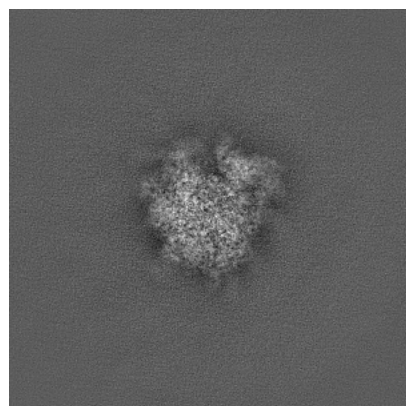
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43567. These allow visual inspection of the internal detail of the map and identification of artifacts.

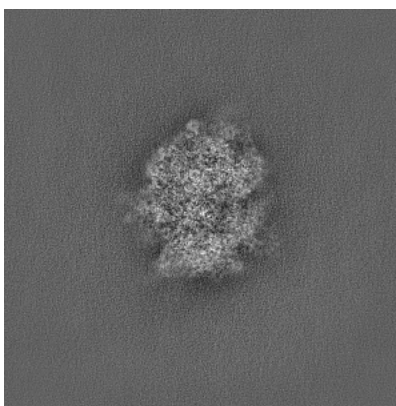
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

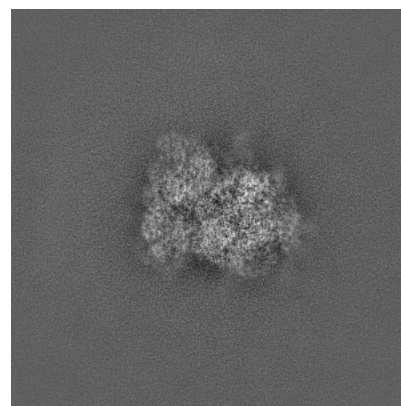
6.1.1 Primary map



X

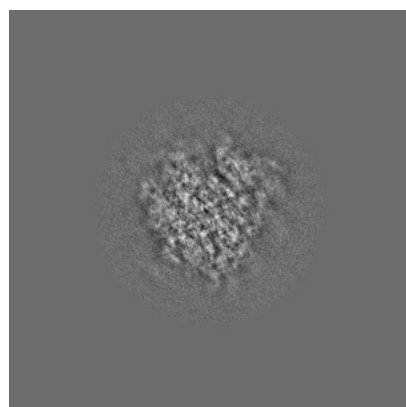


Y

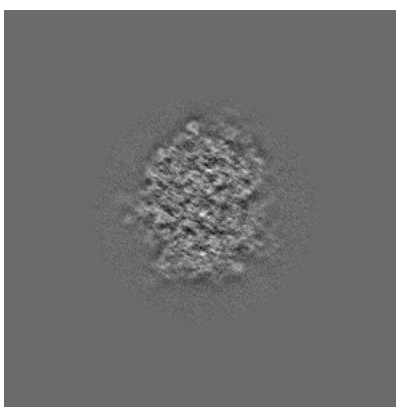


Z

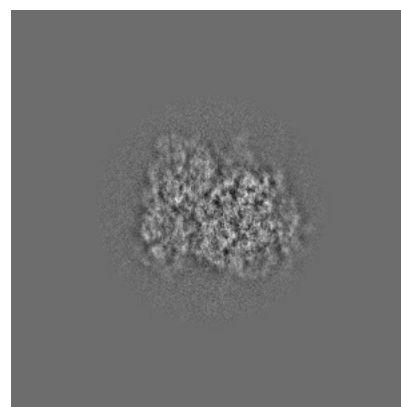
6.1.2 Raw map



X



Y

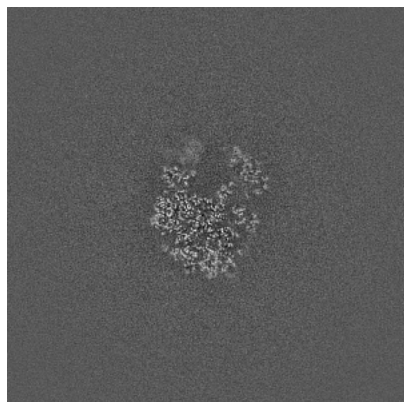


Z

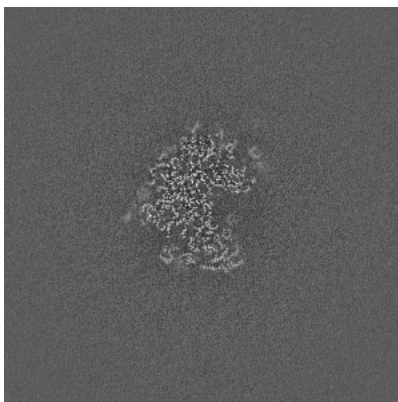
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

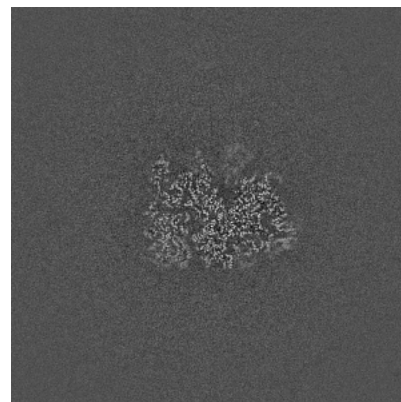
6.2.1 Primary map



X Index: 324

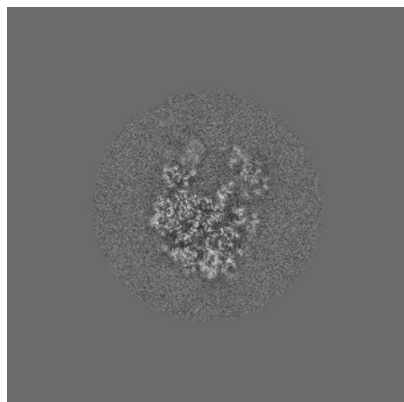


Y Index: 324

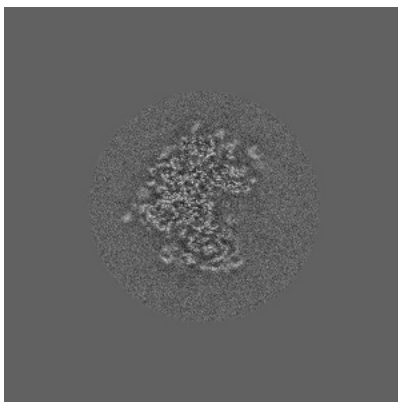


Z Index: 324

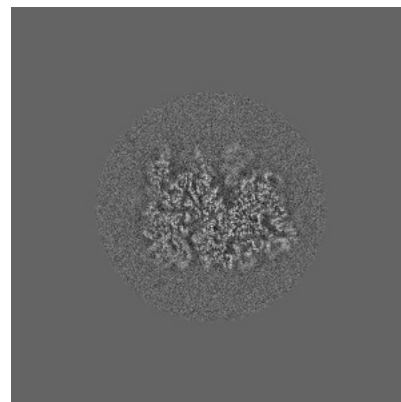
6.2.2 Raw map



X Index: 324



Y Index: 324

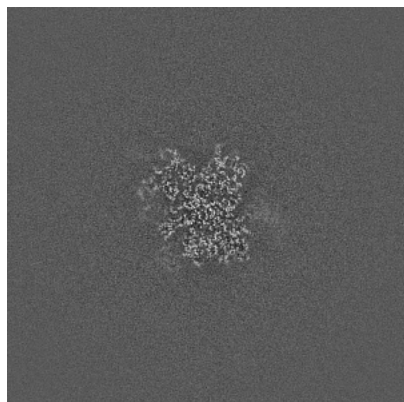


Z Index: 324

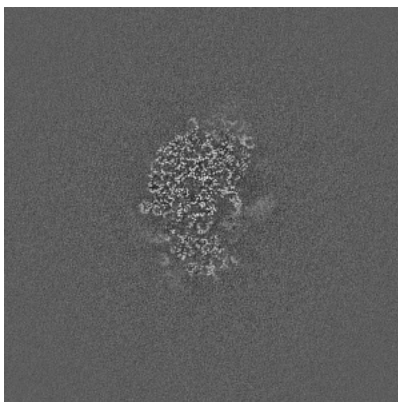
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

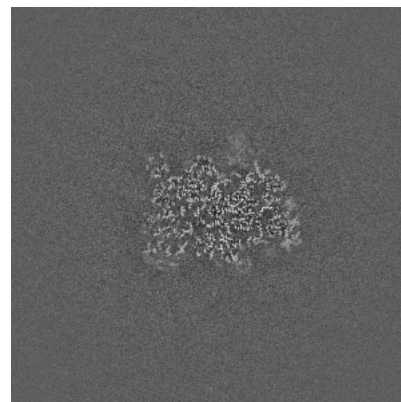
6.3.1 Primary map



X Index: 377

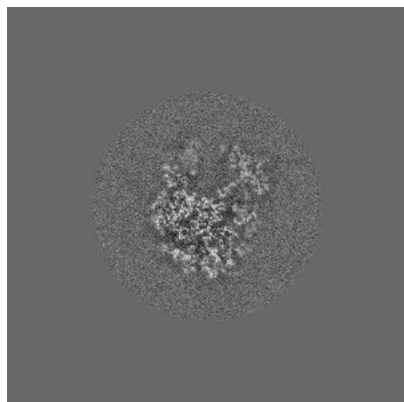


Y Index: 301

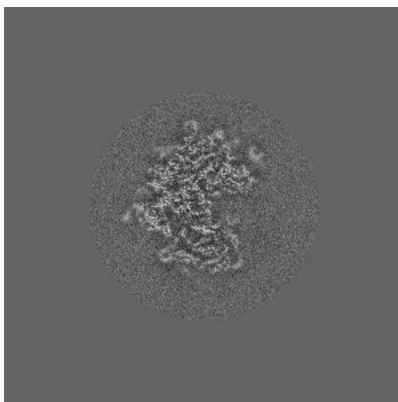


Z Index: 311

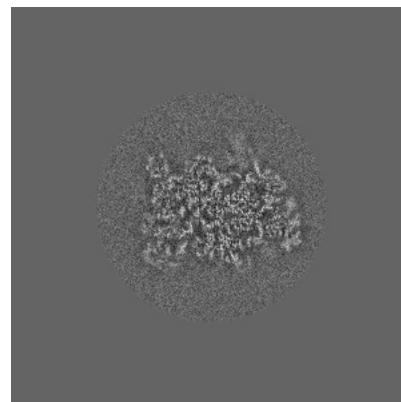
6.3.2 Raw map



X Index: 322



Y Index: 327

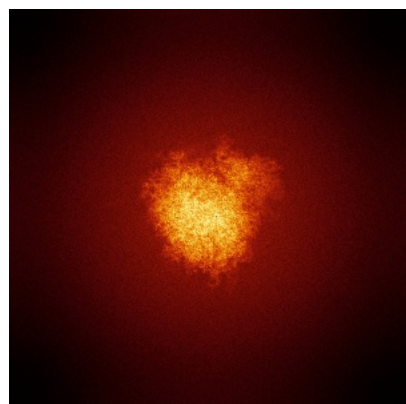


Z Index: 311

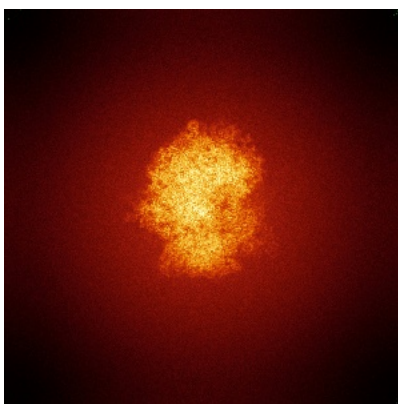
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

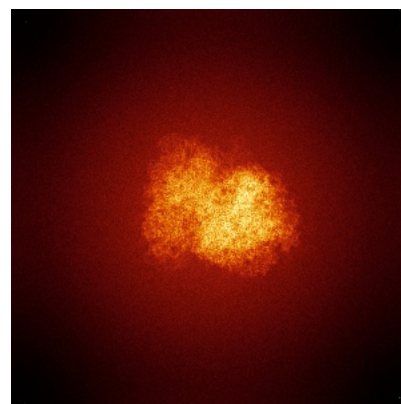
6.4.1 Primary map



X

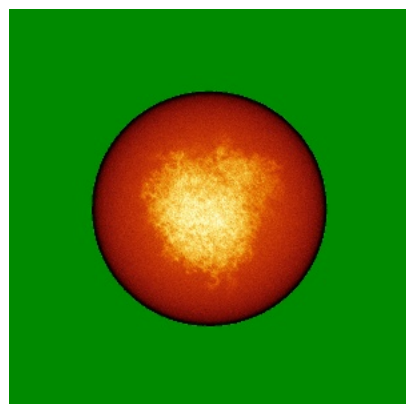


Y

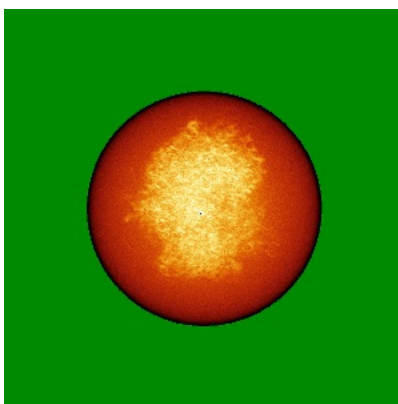


Z

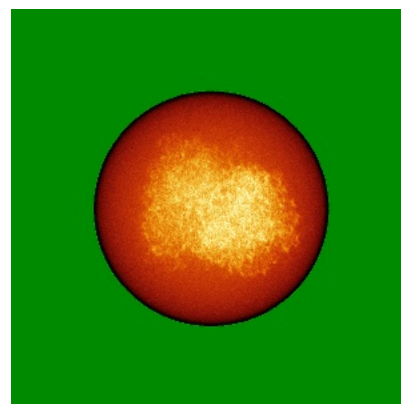
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 6.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

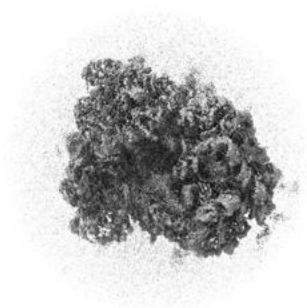
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

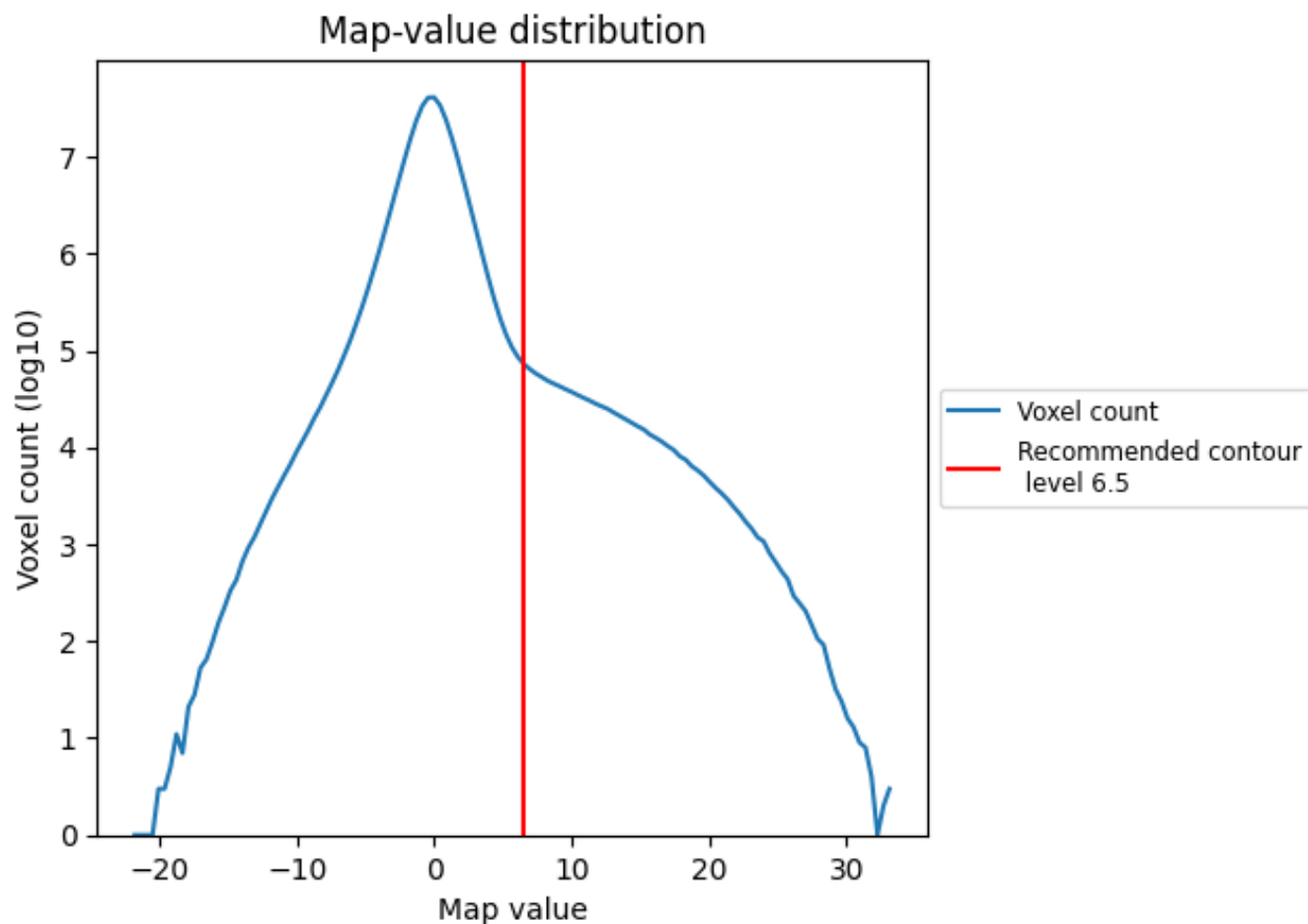
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

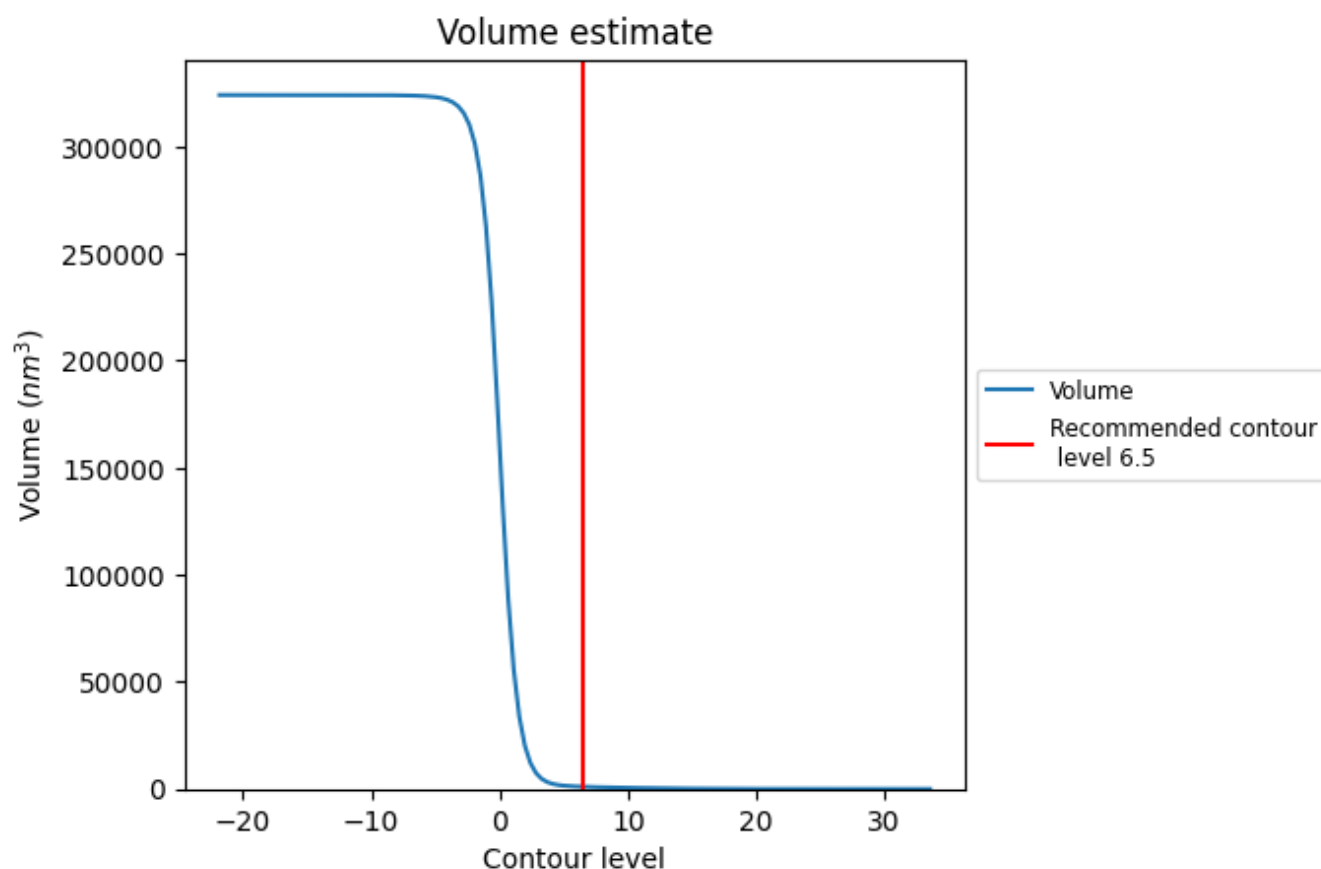
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

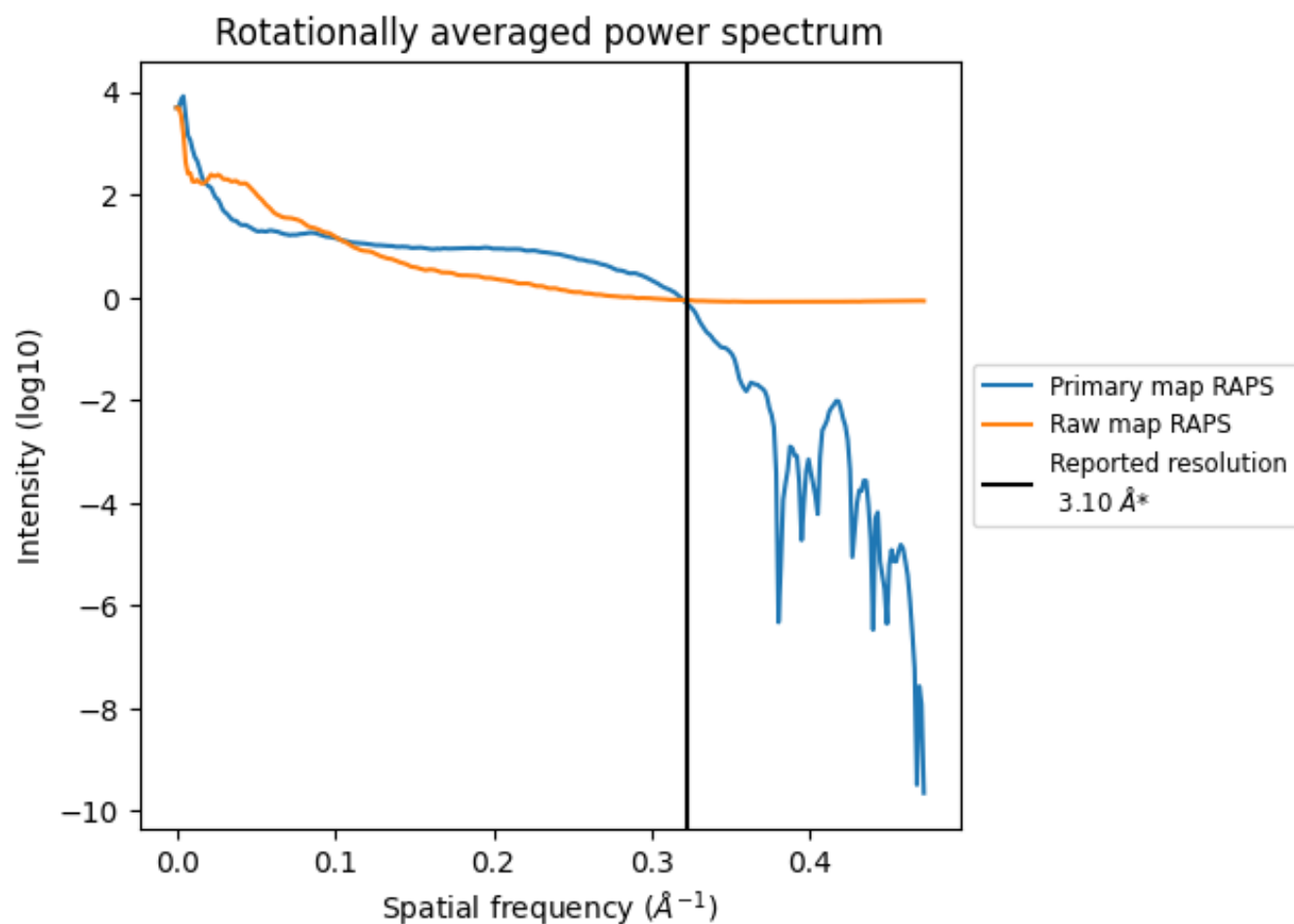
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1042 nm^3 ; this corresponds to an approximate mass of 941 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

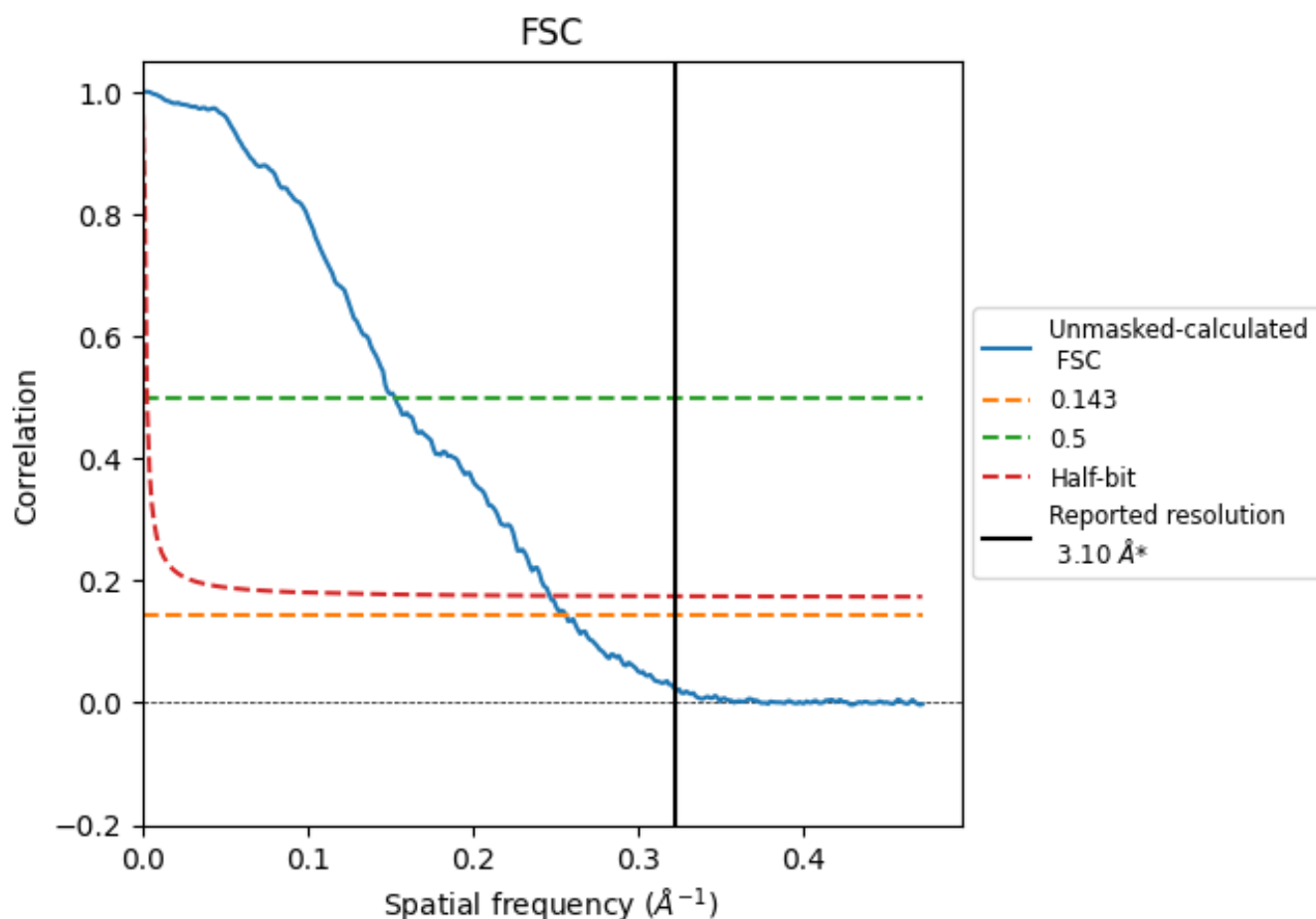


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

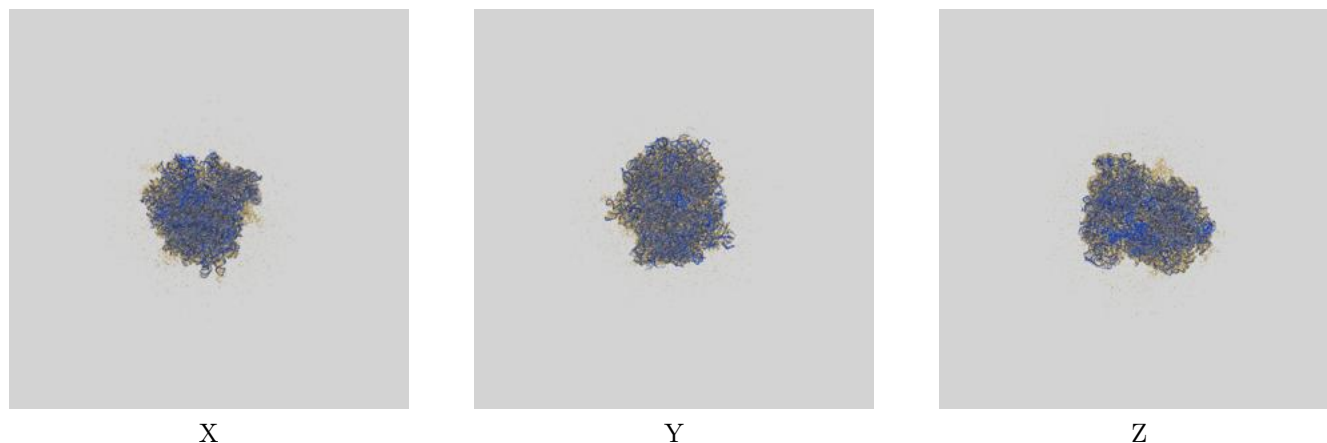
| Resolution estimate (Å) | Estimation criterion (FSC cut-off) | | |
|---------------------------|------------------------------------|------|----------|
| | 0.143 | 0.5 | Half-bit |
| Reported by author | 3.10 | - | - |
| Author-provided FSC curve | - | - | - |
| Unmasked-calculated* | 3.90 | 6.55 | 4.06 |

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.90 differs from the reported value 3.1 by more than 10 %

9 Map-model fit [i](#)

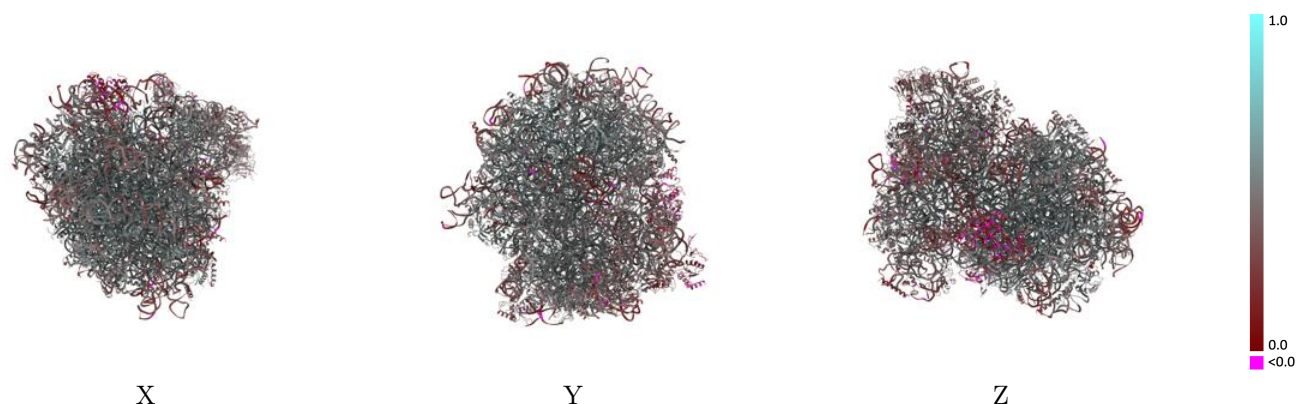
This section contains information regarding the fit between EMDB map EMD-43567 and PDB model 8VVS. Per-residue inclusion information can be found in section 3 on page 26.

9.1 Map-model overlay [i](#)



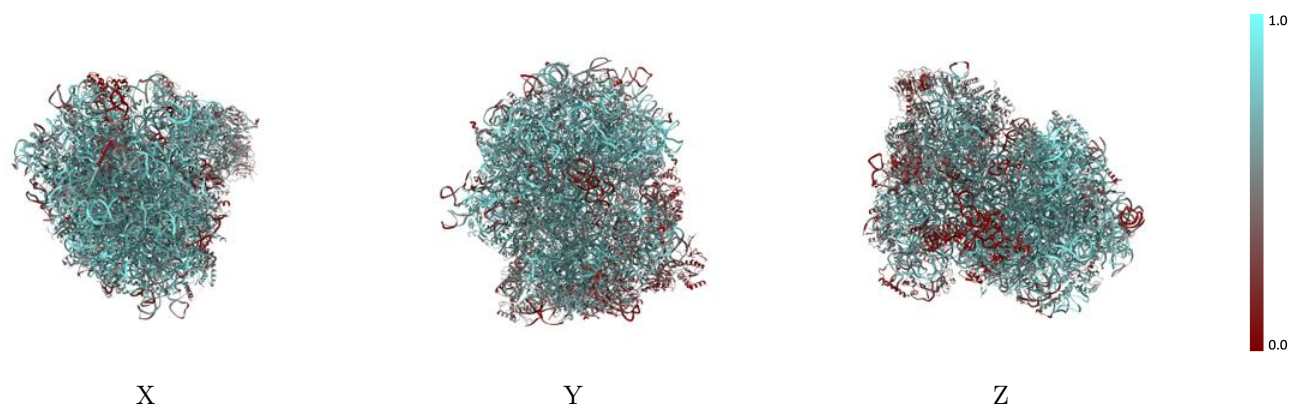
The images above show the 3D surface view of the map at the recommended contour level 6.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



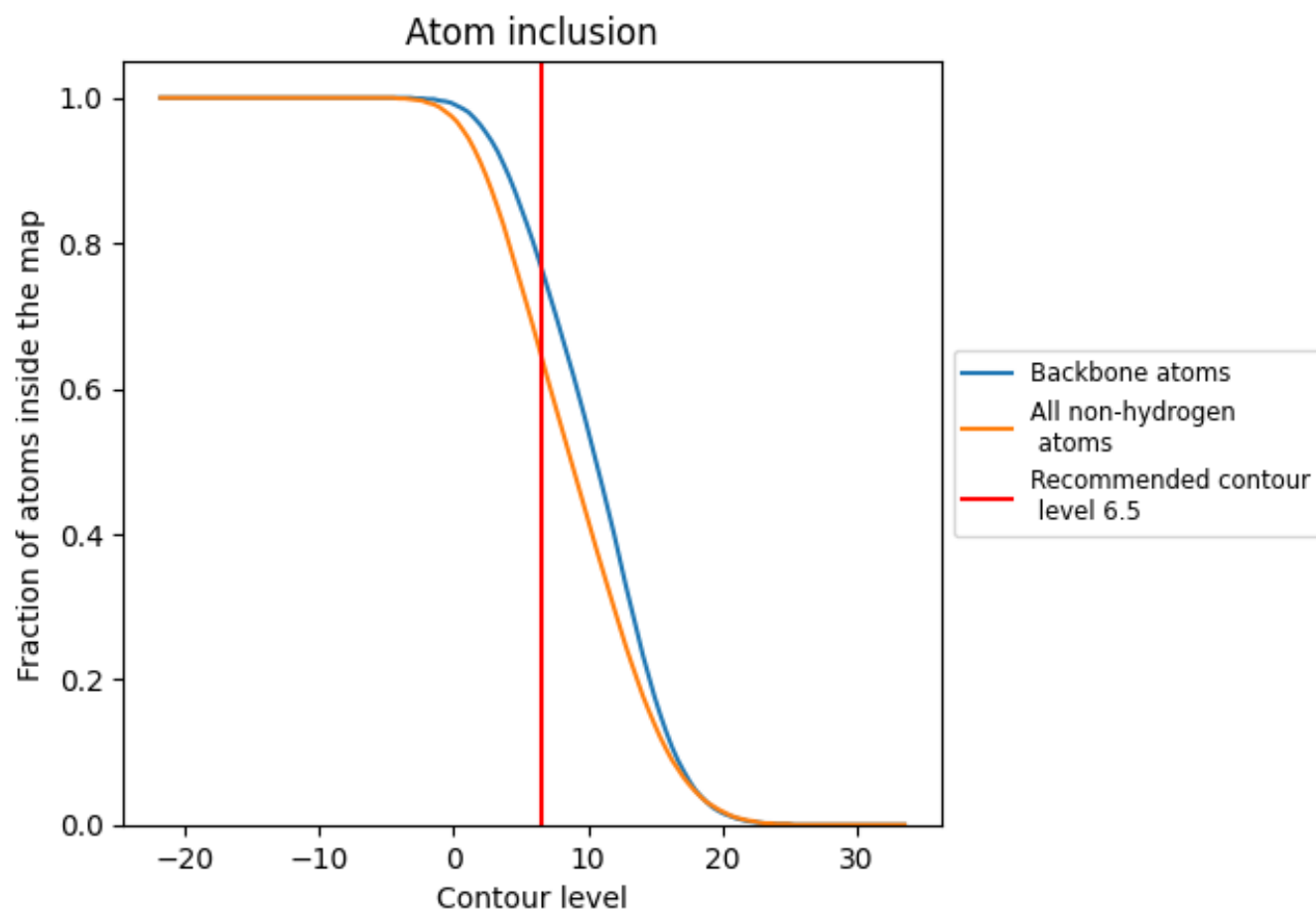
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (6.5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 77% of all backbone atoms, 65% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ





















































































The table lists the average atom inclusion at the recommended contour level (6.5) and Q-score for the entire model and for each chain.

| Chain | Atom inclusion | Q-score |
|-------|--|--|
| All |  0.6460 |  0.4470 |
| A |  0.6850 |  0.5250 |
| AA |  0.5240 |  0.4290 |
| AB |  0.5640 |  0.4480 |
| AC |  0.5950 |  0.4800 |
| B |  0.6640 |  0.5000 |
| BA |  0.6370 |  0.4740 |
| BB |  0.5470 |  0.4620 |
| BC |  0.4960 |  0.4430 |
| C |  0.6580 |  0.5050 |
| CA |  0.6370 |  0.4870 |
| CB |  0.5790 |  0.4700 |
| CC |  0.4830 |  0.4270 |
| D |  0.6490 |  0.4570 |
| DA |  0.6690 |  0.5140 |
| DB |  0.4440 |  0.4000 |
| DC |  0.5360 |  0.4510 |
| E |  0.5860 |  0.4560 |
| EA |  0.6590 |  0.5230 |
| EB |  0.5430 |  0.4600 |
| EC |  0.4440 |  0.3890 |
| F |  0.6400 |  0.4970 |
| FA |  0.6370 |  0.4940 |
| FB |  0.4920 |  0.4150 |
| FC |  0.1510 |  0.2610 |
| G |  0.5960 |  0.4450 |
| GA |  0.6280 |  0.4750 |
| GB |  0.4160 |  0.3710 |
| GC |  0.3270 |  0.3460 |
| H |  0.6140 |  0.4700 |
| HA |  0.6240 |  0.4600 |
| HB |  0.4550 |  0.3990 |
| HC |  0.0940 |  0.2990 |
| I |  0.6600 |  0.5050 |
| IA |  0.6960 |  0.5230 |



























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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| IB |  0.5400 |  0.4470 |
| IC |  0.4500 |  0.4450 |
| J |  0.5850 |  0.4410 |
| JA |  0.5550 |  0.4330 |
| JB |  0.5490 |  0.4390 |
| K |  0.6270 |  0.4870 |
| KA |  0.6230 |  0.4920 |
| KB |  0.4160 |  0.3740 |
| L |  0.6270 |  0.4650 |
| LA |  0.6710 |  0.5040 |
| LB |  0.5980 |  0.4910 |
| M |  0.6990 |  0.5240 |
| MA |  0.6190 |  0.4880 |
| MB |  0.1710 |  0.2180 |
| N |  0.6630 |  0.4960 |
| NA |  0.6490 |  0.5150 |
| NB |  0.6130 |  0.4650 |
| O |  0.6530 |  0.5080 |
| OA |  0.6490 |  0.5070 |
| OB |  0.5720 |  0.4590 |
| P |  0.6760 |  0.5120 |
| PA |  0.6630 |  0.5020 |
| PB |  0.4030 |  0.3730 |
| Q |  0.6320 |  0.4700 |
| QB |  0.4780 |  0.4160 |
| R |  0.6550 |  0.4970 |
| RA |  0.0190 |  0.1040 |
| RB |  0.4910 |  0.4190 |
| S |  0.6370 |  0.4920 |
| SA |  0.5680 |  0.4020 |
| SB |  0.4790 |  0.4040 |
| T |  0.5610 |  0.4300 |
| TA |  0.1550 |  0.2340 |
| TB |  0.4980 |  0.4050 |
| U |  0.6480 |  0.5110 |
| UA |  0.1610 |  0.2630 |
| UB |  0.4050 |  0.3770 |
| V |  0.4820 |  0.3960 |
| VA |  0.4820 |  0.4170 |
| VB |  0.5850 |  0.4520 |
| W |  0.6310 |  0.4740 |
| WA |  0.7500 |  0.4610 |

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| Chain | Atom inclusion | Q-score |
|-------|--|--|
| WB |  0.6060 |  0.4800 |
| X |  0.6350 |  0.4820 |
| XA |  0.8460 |  0.4940 |
| XB |  0.5810 |  0.4850 |
| Y |  0.6570 |  0.4800 |
| YA |  0.7580 |  0.4690 |
| YB |  0.4740 |  0.4100 |
| Z |  0.7070 |  0.5150 |
| ZA |  0.6920 |  0.4370 |
| ZB |  0.3880 |  0.3790 |
| b |  0.0410 |  0.1270 |
| c |  0.0090 |  0.1480 |