



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 05:21 PM UTC

PDB ID : 2ZJR / pdb\_00002zjr  
Title : Refined native structure of the large ribosomal subunit (50S) from *Deinococcus radiodurans*  
Authors : Harms, J.M.; Wilson, D.N.; Schluenzen, F.; Connell, S.R.; Stachelhaus, T.; Zaborowska, Z.; Spahn, C.M.T.; Fucini, P.  
Deposited on : 2008-03-08  
Resolution : 2.91 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

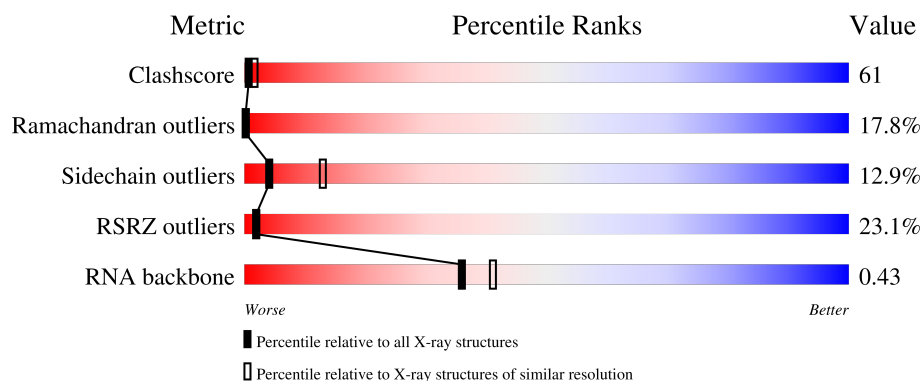
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

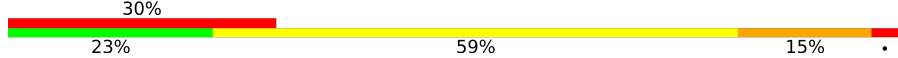
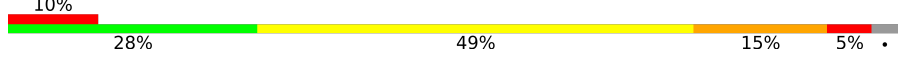
The reported resolution of this entry is 2.91 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



| Metric                | Whole archive<br>(#Entries) | Similar resolution<br>(#Entries, resolution range(Å)) |
|-----------------------|-----------------------------|-------------------------------------------------------|
| Clashscore            | 190562                      | 3213 (2.94-2.90)                                      |
| Ramachandran outliers | 187476                      | 3128 (2.94-2.90)                                      |
| Sidechain outliers    | 187428                      | 3130 (2.94-2.90)                                      |
| RSRZ outliers         | 180081                      | 2995 (2.94-2.90)                                      |
| RNA backbone          | 3983                        | 1016 (3.12-2.72)                                      |

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

| Mol | Chain | Length | Quality of chain                                                                     |
|-----|-------|--------|--------------------------------------------------------------------------------------|
| 1   | X     | 2880   |  |
| 2   | Y     | 123    |  |
| 3   | A     | 274    |  |
| 4   | B     | 211    |  |
| 5   | C     | 205    |  |

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| Mol | Chain | Length | Quality of chain |
|-----|-------|--------|------------------|
| 6   | D     | 180    |                  |
| 7   | E     | 185    |                  |
| 8   | F     | 144    |                  |
| 9   | G     | 174    |                  |
| 10  | H     | 134    |                  |
| 11  | I     | 156    |                  |
| 12  | J     | 142    |                  |
| 13  | K     | 116    |                  |
| 14  | L     | 114    |                  |
| 15  | M     | 166    |                  |
| 16  | N     | 118    |                  |
| 17  | O     | 100    |                  |
| 18  | P     | 134    |                  |
| 19  | Q     | 95     |                  |
| 20  | R     | 115    |                  |
| 21  | S     | 237    |                  |
| 22  | T     | 91     |                  |
| 23  | U     | 81     |                  |
| 24  | V     | 67     |                  |
| 25  | W     | 55     |                  |
| 26  | Z     | 60     |                  |
| 27  | 1     | 55     |                  |
| 28  | 2     | 47     |                  |
| 29  | 3     | 66     |                  |
| 30  | 4     | 37     |                  |

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

| Mol | Type | Chain | Res  | Chirality | Geometry | Clashes | Electron density |
|-----|------|-------|------|-----------|----------|---------|------------------|
| 31  | MG   | X     | 2884 | -         | -        | -       | X                |

## 2 Entry composition

There are 31 unique types of molecules in this entry. The entry contains 83819 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called ribosomal 23S RNA.

| Mol | Chain | Residues | Atoms |       |       |       |      | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-------|-------|-------|------|---------|---------|-------|
| 1   | X     | 2686     | Total | C     | N     | O     | P    | 0       | 0       | 0     |
|     |       |          | 57651 | 25718 | 10642 | 18606 | 2685 |         |         |       |

- Molecule 2 is a RNA chain called ribosomal 5S RNA.

| Mol | Chain | Residues | Atoms |      |     |     |     | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|-----|---------|---------|-------|
| 2   | Y     | 122      | Total | C    | N   | O   | P   | 0       | 0       | 0     |
|     |       |          | 2598  | 1161 | 476 | 840 | 121 |         |         |       |

- Molecule 3 is a protein called 50S ribosomal protein L2.

| Mol | Chain | Residues | Atoms |      |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|------|-----|-----|---|---------|---------|-------|
| 3   | A     | 240      | Total | C    | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1826  | 1137 | 366 | 321 | 2 |         |         |       |

- Molecule 4 is a protein called 50S ribosomal protein L3.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 4   | B     | 205      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1539  | 965 | 295 | 271 | 8 |         |         |       |

- Molecule 5 is a protein called 50S ribosomal protein L4.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 5   | C     | 197      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1506  | 935 | 287 | 282 | 2 |         |         |       |

- Molecule 6 is a protein called 50S ribosomal protein L5.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 6   | D     | 177      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1400  | 892 | 247 | 254 | 7 |         |         |       |

- Molecule 7 is a protein called 50S ribosomal protein L6.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 7   | E     | 171      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1286  | 812 | 237 | 236 | 1 |         |         |       |

- Molecule 8 is a protein called 50S ribosomal protein L11.

| Mol | Chain | Residues | Atoms |     |    |    |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 8   | F     | 71       | Total | C   | N  | O  | S | 0       | 0       | 0     |
|     |       |          | 503   | 310 | 91 | 99 | 3 |         |         |       |

- Molecule 9 is a protein called 50S ribosomal protein L13.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 9   | G     | 142      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1114  | 704 | 209 | 198 | 3 |         |         |       |

- Molecule 10 is a protein called 50S ribosomal protein L14.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 10  | H     | 134      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 997   | 614 | 198 | 180 | 5 |         |         |       |

- Molecule 11 is a protein called 50S ribosomal protein L15.

| Mol | Chain | Residues | Atoms |     |     |     |  | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|---------|-------|
| 11  | I     | 141      | Total | C   | N   | O   |  | 0       | 0       | 0     |
|     |       |          | 1067  | 655 | 216 | 196 |  |         |         |       |

- Molecule 12 is a protein called 50S ribosomal protein L16.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 12  | J     | 136      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1090  | 696 | 202 | 185 | 7 |         |         |       |

There is a discrepancy between the modelled and reference sequences:

| Chain | Residue | Modelled | Actual | Comment               | Reference  |
|-------|---------|----------|--------|-----------------------|------------|
| J     | 1       | MET      | -      | initiating methionine | UNP Q9RXJ5 |

- Molecule 13 is a protein called 50S ribosomal protein L17.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 13  | K     | 113      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 878   | 541 | 178 | 157 | 2 |         |         |       |

- Molecule 14 is a protein called 50S ribosomal protein L18.

| Mol | Chain | Residues | Atoms |     |     |     |  | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|---------|-------|
| 14  | L     | 104      | Total | C   | N   | O   |  | 0       | 0       | 0     |
|     |       |          | 779   | 476 | 161 | 142 |  |         |         |       |

- Molecule 15 is a protein called 50S ribosomal protein L19.

| Mol | Chain | Residues | Atoms |     |     |     |  | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|---------|-------|
| 15  | M     | 108      | Total | C   | N   | O   |  | 0       | 0       | 0     |
|     |       |          | 871   | 543 | 172 | 156 |  |         |         |       |

- Molecule 16 is a protein called 50S ribosomal protein L20.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 16  | N     | 117      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 978   | 608 | 210 | 159 | 1 |         |         |       |

- Molecule 17 is a protein called 50S ribosomal protein L21.

| Mol | Chain | Residues | Atoms |     |     |     |  | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|--|---------|---------|-------|
| 17  | O     | 94       | Total | C   | N   | O   |  | 0       | 0       | 0     |
|     |       |          | 741   | 465 | 139 | 137 |  |         |         |       |

- Molecule 18 is a protein called 50S ribosomal protein L22.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 18  | P     | 127      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1014  | 639 | 199 | 174 | 2 |         |         |       |

- Molecule 19 is a protein called 50S ribosomal protein L23.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 19  | Q     | 93       | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 726   | 458 | 136 | 130 | 2 |         |         |       |

- Molecule 20 is a protein called 50S ribosomal protein L24.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 20  | R     | 110      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 825   | 513 | 160 | 151 | 1 |         |         |       |

- Molecule 21 is a protein called 50S ribosomal protein L25.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 21  | S     | 175      | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 1345  | 849 | 236 | 254 | 6 |         |         |       |

- Molecule 22 is a protein called 50S ribosomal protein L27.

| Mol | Chain | Residues | Atoms |     |     |     |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|-----|---|---------|---------|-------|
| 22  | T     | 84       | Total | C   | N   | O   | S | 0       | 0       | 0     |
|     |       |          | 625   | 393 | 122 | 109 | 1 |         |         |       |

- Molecule 23 is a protein called 50S ribosomal protein L28.

| Mol | Chain | Residues | Atoms |     |     |    | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---------|---------|-------|
| 23  | U     | 72       | Total | C   | N   | O  | 0       | 0       | 0     |
|     |       |          | 552   | 341 | 116 | 95 |         |         |       |

- Molecule 24 is a protein called 50S ribosomal protein L29.

| Mol | Chain | Residues | Atoms |     |     |    |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|-----|----|---|---------|---------|-------|
| 24  | V     | 66       | Total | C   | N   | O  | S | 0       | 0       | 0     |
|     |       |          | 533   | 327 | 107 | 96 | 3 |         |         |       |

- Molecule 25 is a protein called 50S ribosomal protein L30.

| Mol | Chain | Residues | Atoms |     |    |    |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 25  | W     | 55       | Total | C   | N  | O  | S | 0       | 0       | 0     |
|     |       |          | 424   | 264 | 82 | 76 | 2 |         |         |       |

- Molecule 26 is a protein called 50S ribosomal protein L32.

| Mol | Chain | Residues | Atoms |     |    |    |   | ZeroOcc | AltConf | Trace |
|-----|-------|----------|-------|-----|----|----|---|---------|---------|-------|
| 26  | Z     | 58       | Total | C   | N  | O  | S | 0       | 0       | 0     |
|     |       |          | 457   | 281 | 94 | 77 | 5 |         |         |       |

- Molecule 27 is a protein called 50S ribosomal protein L33.



| Mol | Chain | Residues | Atoms            | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------------|---------|---------|-------|
| 27  | 1     | 53       | Total C<br>53 53 | 0       | 0       | 53    |

- Molecule 28 is a protein called 50S ribosomal protein L34.

| Mol | Chain | Residues | Atoms            | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------------|---------|---------|-------|
| 28  | 2     | 46       | Total C<br>46 46 | 0       | 0       | 46    |

- Molecule 29 is a protein called 50S ribosomal protein L35.

| Mol | Chain | Residues | Atoms            | ZeroOcc | AltConf | Trace |
|-----|-------|----------|------------------|---------|---------|-------|
| 29  | 3     | 63       | Total C<br>63 63 | 0       | 0       | 63    |

- Molecule 30 is a protein called 50S ribosomal protein L36.

| Mol | Chain | Residues | Atoms                            | ZeroOcc | AltConf | Trace |
|-----|-------|----------|----------------------------------|---------|---------|-------|
| 30  | 4     | 37       | Total C N O S<br>297 179 66 47 5 | 0       | 0       | 0     |

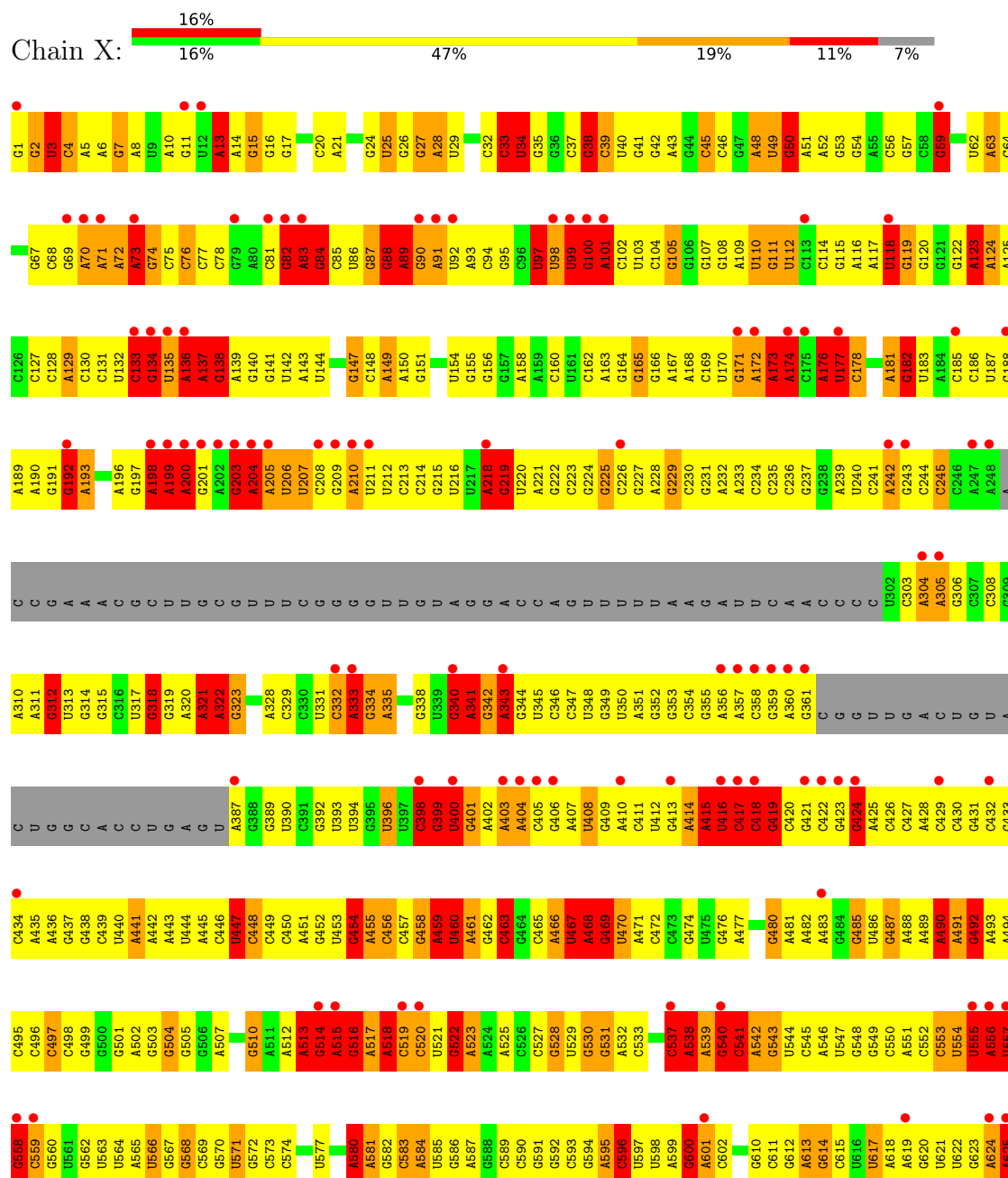
- Molecule 31 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

| Mol | Chain | Residues | Atoms             | ZeroOcc | AltConf |
|-----|-------|----------|-------------------|---------|---------|
| 31  | X     | 30       | Total Mg<br>30 30 | 0       | 0       |
| 31  | Y     | 5        | Total Mg<br>5 5   | 0       | 0       |

### 3 Residue-property plots

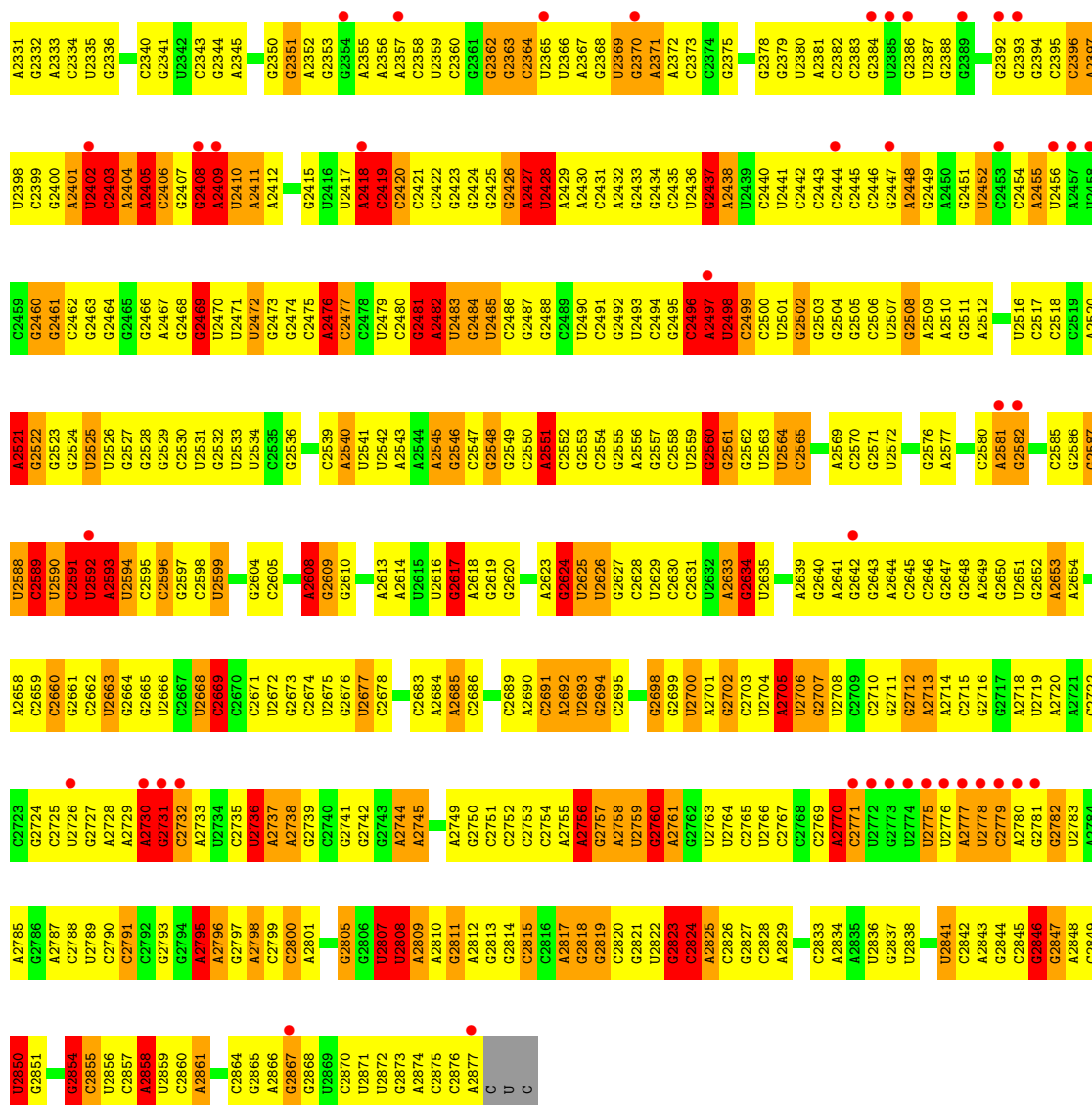
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

#### • Molecule 1: ribosomal 23S RNA

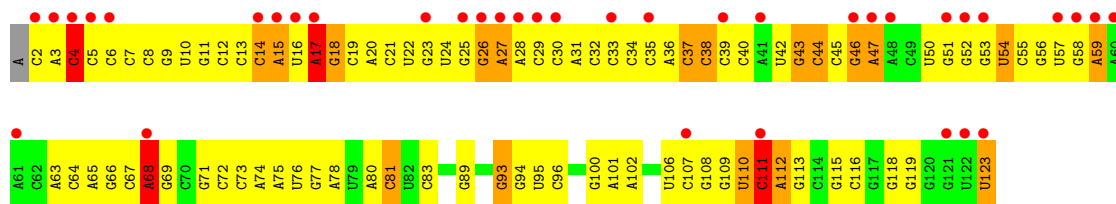




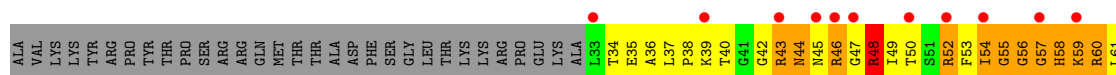
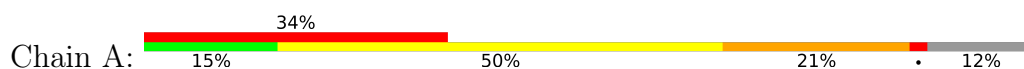
|       |       |       |       |       |       |       |       |       |       |       |       |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| G2269 | U2208 | U2088 | C2027 | U1967 | G     | U1843 | C1780 | G1713 | C1648 | A1582 | C1517 |
| U2270 | G2209 | C2069 | C2028 | G1968 | G     | C1844 | C1781 | A1714 | U1648 | A1583 | C1518 |
| C2271 | G2029 | U2090 | G2029 | G1969 | U     | A1845 | A1782 | G1715 | U1651 | A1584 | G1519 |
| C2272 | U2030 | C     | U2030 | G1970 | C     | A1846 | G1783 | G1716 | U1652 | A1585 | G1520 |
| C2273 | A2031 | U     | A2031 | C1971 | C     | G1847 | C1784 | A1718 | U1655 | A1586 | U1521 |
| C2274 | G2032 | G     | G2032 | C1972 | U     | U1848 | A1785 | A1719 | C1655 | A1587 | A1522 |
| U2275 | C2033 | C     | C2033 | C1973 | A1910 | G1849 | C1786 | G1719 | U1656 | A1588 | A1523 |
| C2276 | A2034 | U     | A2034 | U1974 | A1911 | G1850 | U1787 | U1722 | U1657 | A1589 | A1524 |
| C2277 | G2035 | U     | G2035 | U1975 | A1912 | A1851 | C1788 | G1723 | A1658 | U1525 | A1525 |
| A2278 | U1976 | A     | U1976 | U1976 | C     | C1852 | G1789 | U1724 | G1659 | U1526 | A1526 |
| G2279 | C2036 | G     | C2036 | C1977 | C     | C1853 | G1790 | G1725 | G1660 | U1527 | A1527 |
| G2280 | A2037 | G     | A2037 | U1914 | A1915 | G1854 | C1791 | C1726 | C1661 | A1528 | A1528 |
| A2281 | G2038 | G     | G2038 | C1978 | G1916 | G1855 | C1792 | C1727 | G1662 | C1529 | A1529 |
| C2282 | A2040 | U     | A2040 | A1980 | C1917 | U1856 | A1793 | U1728 | C1663 | U1530 | A1530 |
| C2283 | A2041 | A     | A2041 | A1981 | G1918 | G1857 | A1794 | A1728 | G1664 | A1531 | A1531 |
| U2284 | A2042 | G     | A2042 | C1982 | A1919 | C1858 | C1795 | C1729 | U1666 | A1532 | A1532 |
| G2285 | A2043 | U     | A2043 | U1983 | A1920 | A1859 | U1799 | C1731 | A1667 | G1533 | G1533 |
| U2286 | G2044 | U     | G2044 | A1984 | A1921 | A1860 | A1799 | U1732 | G1668 | G1536 | G1536 |
| G2287 | A2045 | G     | A2045 | G1985 | U1922 | G1861 | C1800 | U1733 | A1669 | U1537 | U1537 |
| A2288 | C2046 | G     | C2046 | G1986 | U1923 | C1862 | A1801 | G1734 | A1670 | U1538 | U1538 |
| U2289 | G2047 | A     | G2047 | G1987 | C1925 | U1924 | A1802 | C1735 | G1671 | U1539 | U1539 |
| G2290 | C2048 | G     | C2048 | C1988 | U1926 | G1864 | G1803 | G1736 | A1672 | C1540 | C1540 |
| C2291 | U2049 | C     | U2049 | U1990 | U1927 | G1865 | U1804 | C1737 | C1673 | U1541 | G1541 |
| G2292 | G2050 | C     | G2050 | C1991 | U1928 | A1866 | G1805 | U1738 | C1674 | G1542 | G1542 |
| C2293 | U2051 | U     | U2051 | G1992 | U1929 | A1867 | G1806 | U1738 | C1675 | G1543 | G1543 |
| U2294 | G2052 | U     | G2052 | G1993 | C1930 | A1868 | A1807 | U1741 | U1676 | A1544 | A1544 |
| G2295 | A2053 | G     | A2053 | U1994 | U1933 | A1869 | C1808 | G1742 | U1677 | U1547 | U1547 |
| U2296 | C2054 | C     | C2054 | G1995 | U1934 | U1870 | G1809 | G1743 | C1678 | U1548 | U1548 |
| G2297 | G2055 | G     | G2055 | U1996 | A1996 | A1871 | U1810 | C1744 | U1679 | U1549 | U1549 |
| C2298 | C2056 | A     | C2056 | A1997 | A1935 | A1872 | A1811 | G1745 | U1680 | C1549 | C1549 |
| U2299 | U2057 | A     | U2057 | A1998 | A1936 | A1873 | U1812 | A1746 | A1681 | C1550 | C1550 |
| C2300 | U2058 | C     | U2058 | U1999 | G1937 | G1874 | A1813 | U1747 | A1682 | U1551 | U1551 |
| A2301 | G2059 | C     | G2059 | U2000 | U1938 | C1875 | G1814 | U1748 | G1683 | C1552 | C1552 |
| G2302 | C2061 | U     | C2061 | A2002 | C1940 | C1876 | G1815 | G1749 | G1684 | G1553 | G1553 |
| C2303 | U2062 | G     | U2062 | A2003 | U1944 | C1877 | G1816 | U1750 | A1685 | A1554 | A1554 |
| U2304 | A2063 | G     | A2063 | U2004 | C1945 | C1878 | U1817 | A1753 | A1686 | U1555 | U1555 |
| G2305 | C2064 | C     | C2064 | U2005 | U1946 | U1881 | U1819 | G1754 | C1687 | A1556 | A1556 |
| A2306 | A2065 | C     | A2065 | U2006 | U1947 | G1882 | G1820 | G1755 | U1688 | G1557 | G1557 |
| C2307 | U2066 | U     | U2066 | G2006 | G1947 | A1883 | A1821 | C1756 | U1689 | C1558 | C1558 |
| U2308 | C2067 | U     | C2067 | G2007 | C1948 | A1884 | G1822 | C1756 | U1690 | A1559 | A1559 |
| G2309 | U2068 | U     | U2068 | C2008 | C1948 | A1885 | G1823 | C1757 | G1691 | A1560 | A1560 |
| C2310 | U2069 | U     | U2069 | U2009 | A1949 | G1886 | C1824 | U1757 | C1692 | A1561 | A1561 |
| A2311 | G2070 | G     | G2070 | G2010 | C1950 | G1887 | C1825 | G1762 | A1693 | G1562 | G1562 |
| G2312 | C2071 | G     | C2071 | U2011 | G1951 | C1888 | U1826 | G1763 | U1697 | U1563 | U1563 |
| U2313 | C2072 | G     | U2072 | A2012 | A1952 | G     | G1827 | A1764 | C1697 | U1564 | U1564 |
| A2314 | A2073 | U     | A2073 | A2013 | A1953 | C     | C1830 | C1765 | C1698 | A1569 | A1569 |
| C2315 | U2074 | U     | U2074 | A2014 | A1954 | U     | G1831 | U1766 | A1699 | C1570 | C1570 |
| G2316 | G2075 | C     | G2075 | G2015 | G1955 | C     | G1832 | C1767 | C1700 | G1571 | G1571 |
| U2317 | U2076 | G     | U2076 | A2016 | G1956 | G     | U1833 | U1770 | C1701 | C1572 | C1572 |
| C2318 | G2077 | U     | G2077 | U2017 | C1957 | U     | U1834 | A1771 | G1704 | G1573 | G1573 |
| U2319 | U2078 | G     | U2078 | G2018 | U1958 | A     | G1834 | C1772 | U1705 | A1574 | A1574 |
| G2320 | A2079 | G     | A2079 | C2019 | U1959 | A     | C1835 | C1773 | U1706 | C1575 | C1575 |
| U2321 | U2080 | A     | U2080 | G2020 | A1960 | C     | C1836 | C1774 | A1707 | G1576 | G1576 |
| C2322 | U2081 | G     | U2081 | C2021 | A1961 | U     | G1837 | A1775 | C1708 | G1577 | G1577 |
| G2323 | G2082 | G     | G2082 | C2022 | C1962 | A     | G1838 | A1776 | U1709 | U1578 | U1578 |
| U2324 | C2083 | C     | U2083 | C2023 | G1963 | U     | A1839 | A1777 | C1710 | G1579 | G1579 |
| A2325 | G2084 | A     | G2084 | U2024 | U1964 | A     | A1840 | A1778 | U1711 | U1580 | U1580 |
| C2326 | U2085 | A     | U2085 | A2025 | U1965 | A     | G1841 | A1779 | C1712 | C1581 | C1581 |
| U2327 | C2086 | C     | C2086 | C2026 | C1966 | C     | G1842 | C1779 |       |       |       |
| G2328 | U2087 | C     | U2087 |       |       |       |       |       |       |       |       |

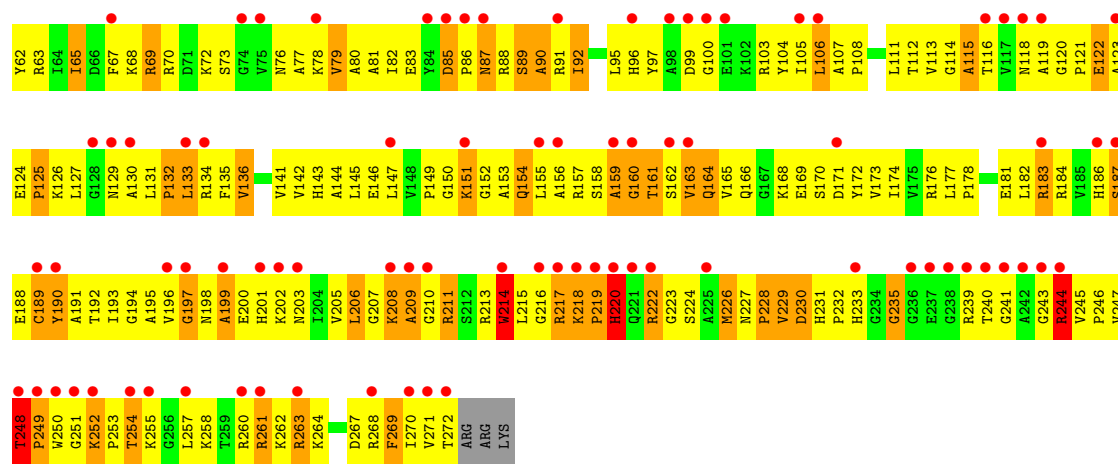


### • Molecule 2: ribosomal 5S RNA

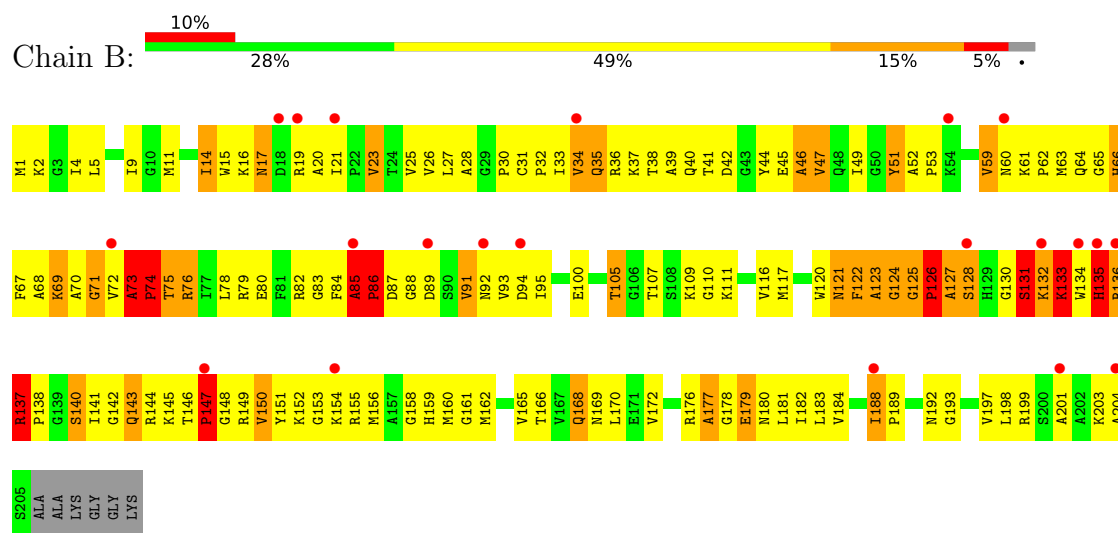


### • Molecule 3: 50S ribosomal protein L2

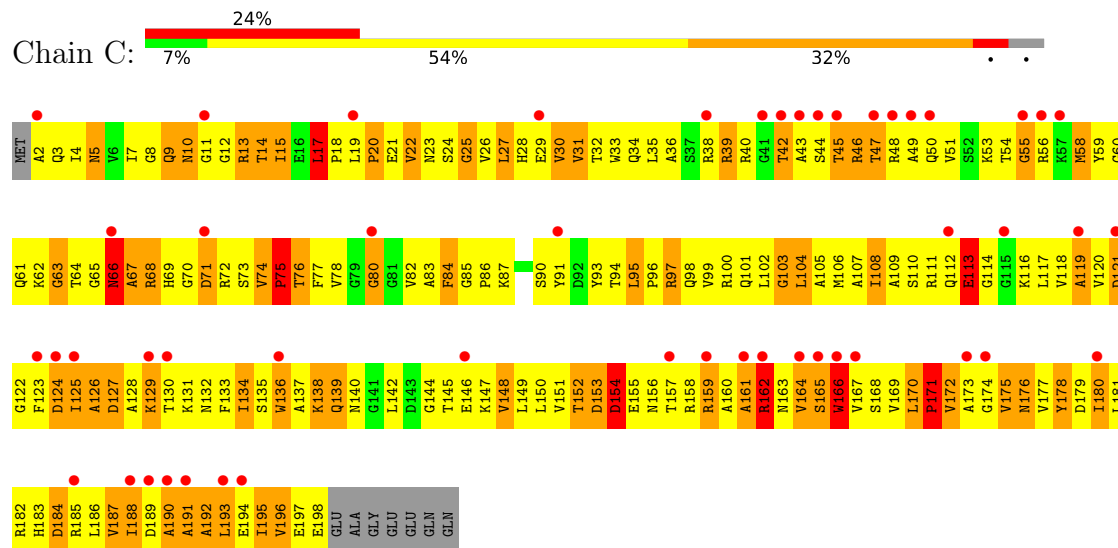




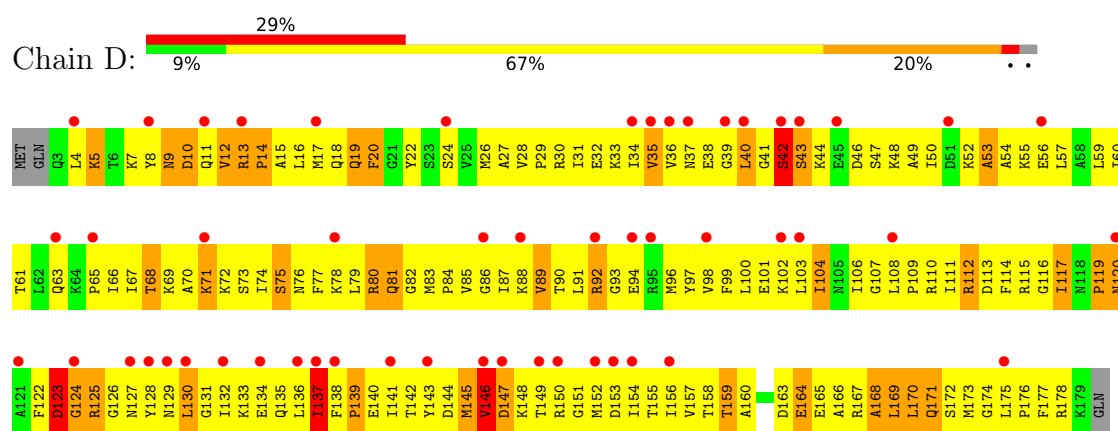
• Molecule 4: 50S ribosomal protein L3



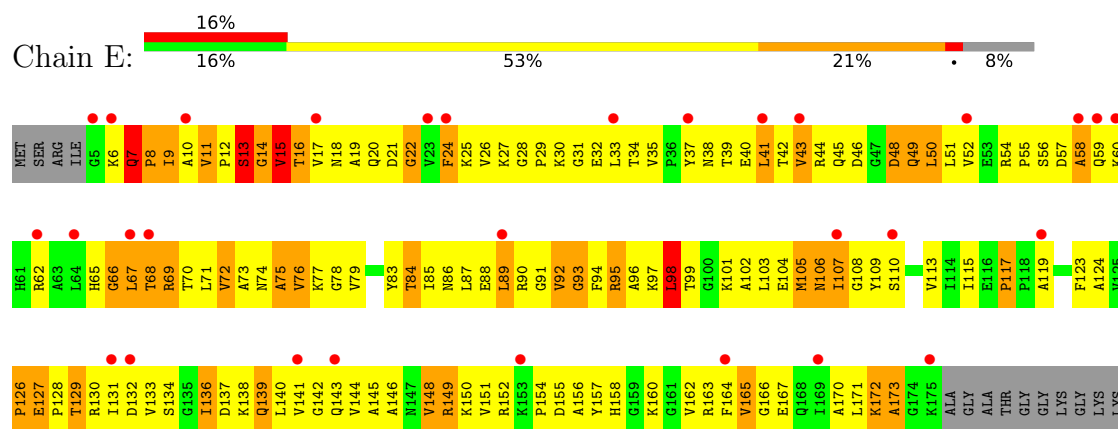
• Molecule 5: 50S ribosomal protein L4



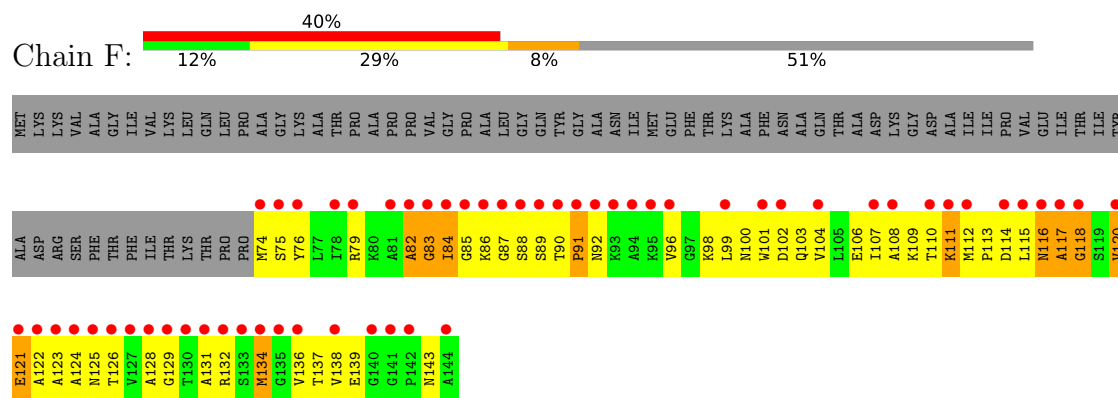
• Molecule 6: 50S ribosomal protein L5



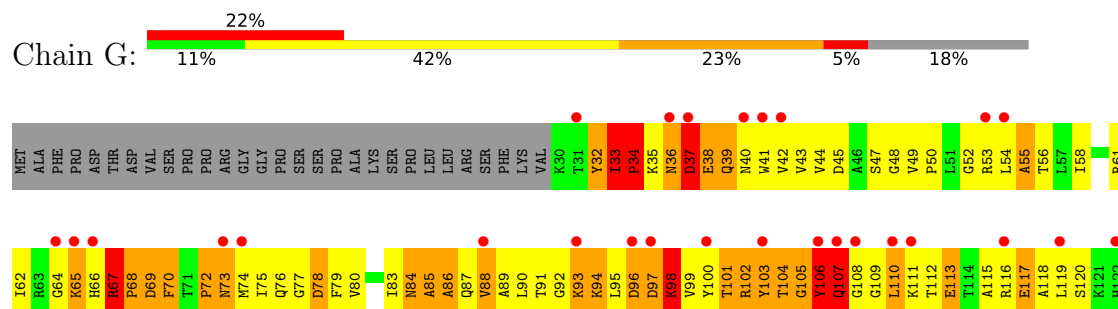
• Molecule 7: 50S ribosomal protein L6



• Molecule 8: 50S ribosomal protein L11

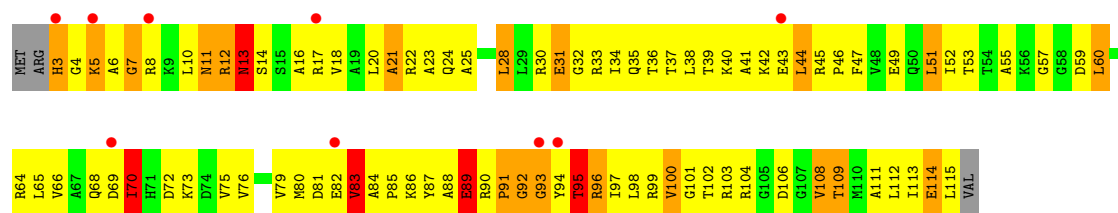


• Molecule 9: 50S ribosomal protein L13

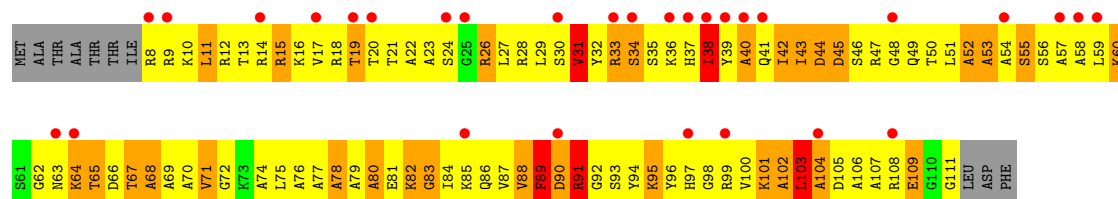




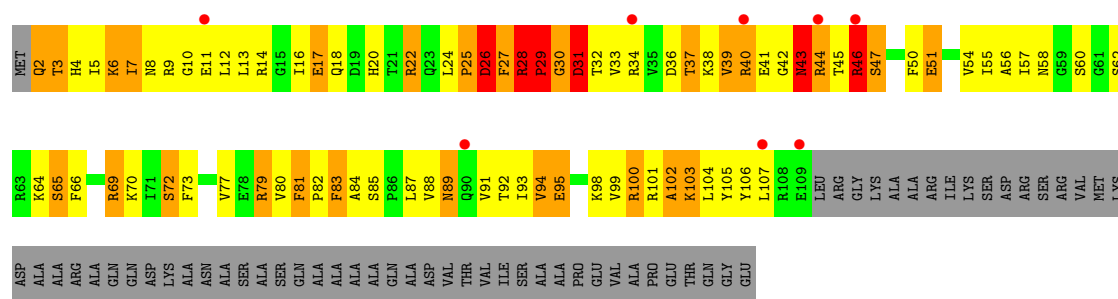




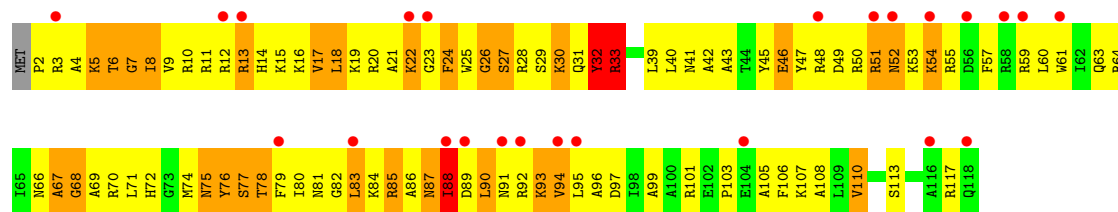
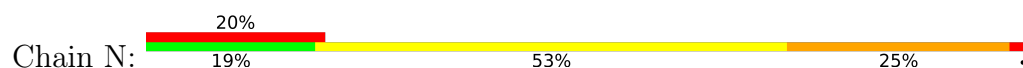
• Molecule 14: 50S ribosomal protein L18



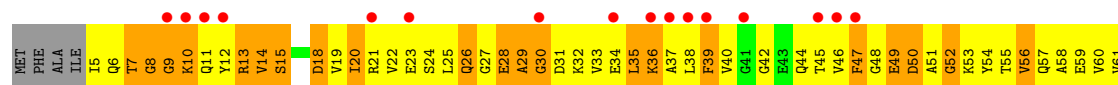
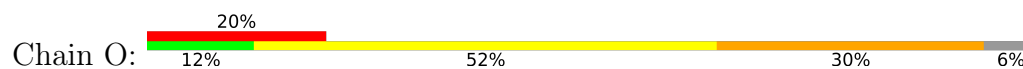
• Molecule 15: 50S ribosomal protein L19

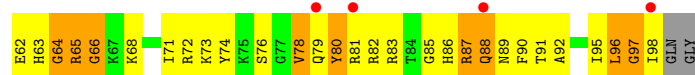


• Molecule 16: 50S ribosomal protein L20

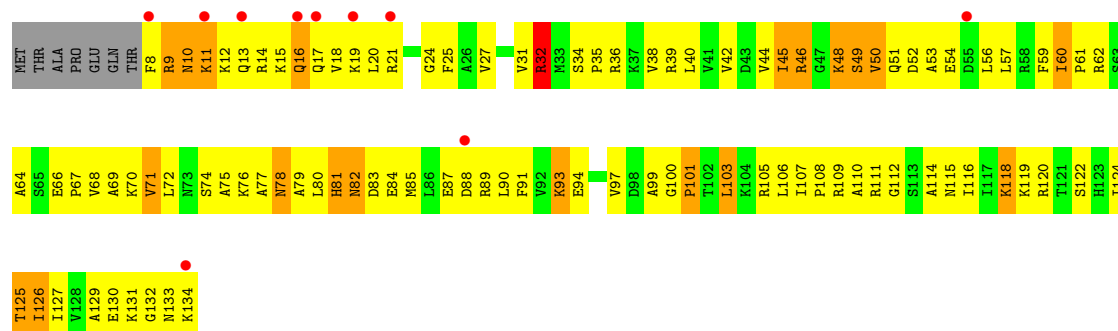


• Molecule 17: 50S ribosomal protein L21

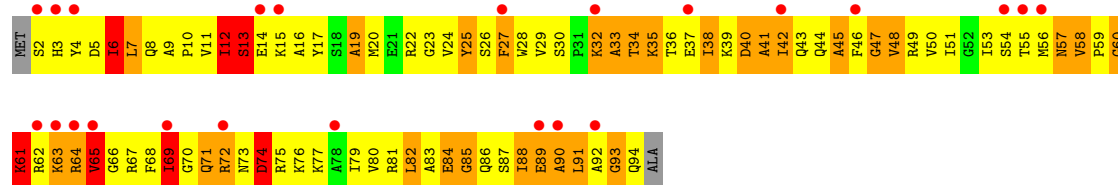




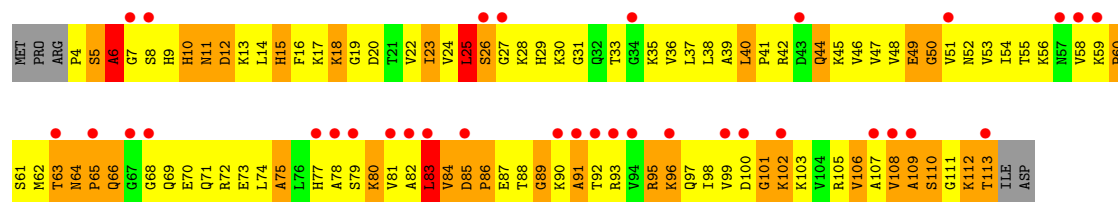
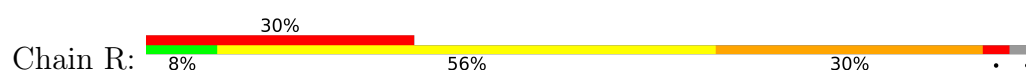
• Molecule 18: 50S ribosomal protein L22



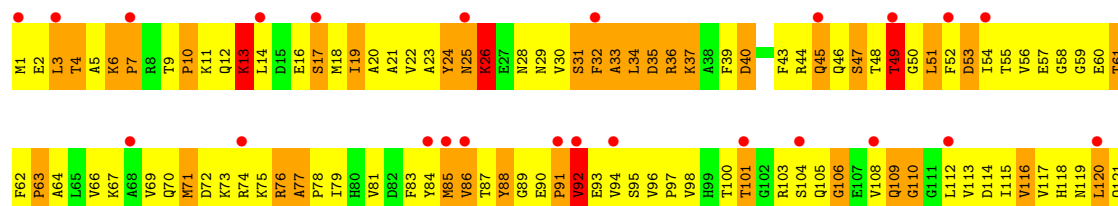
• Molecule 19: 50S ribosomal protein L23

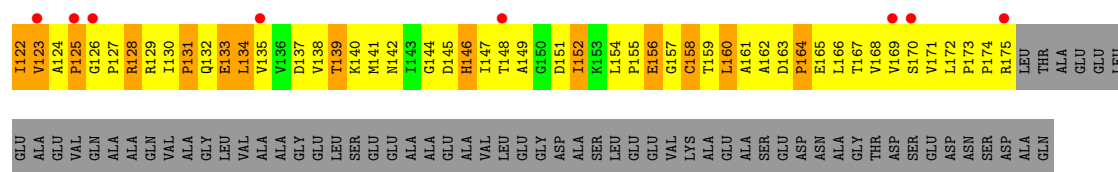


• Molecule 20: 50S ribosomal protein L24

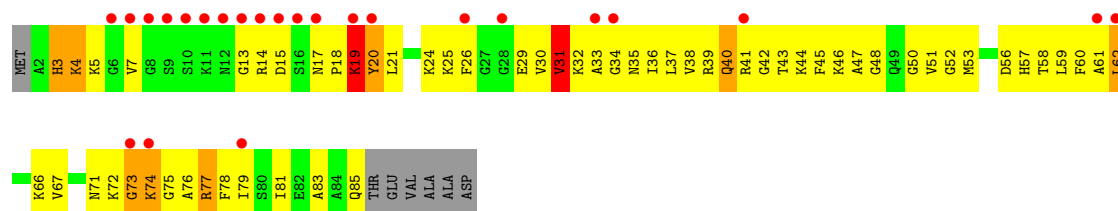


• Molecule 21: 50S ribosomal protein L25

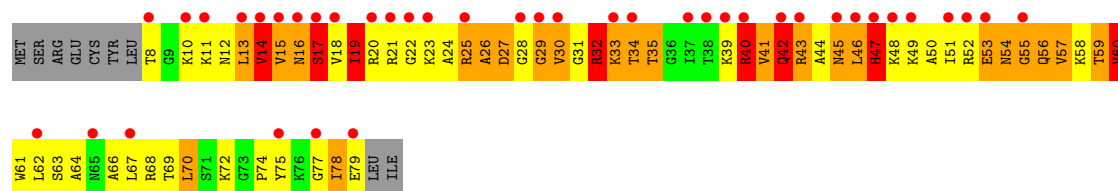




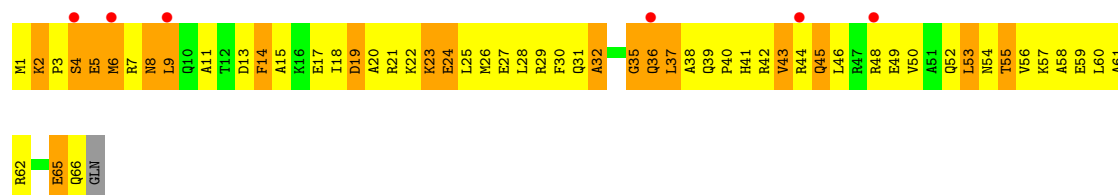
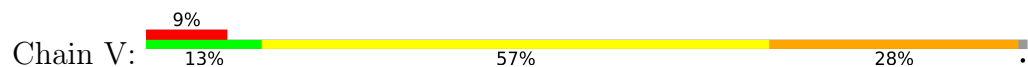
• Molecule 22: 50S ribosomal protein L27



• Molecule 23: 50S ribosomal protein L28



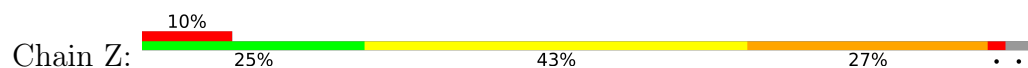
• Molecule 24: 50S ribosomal protein L29

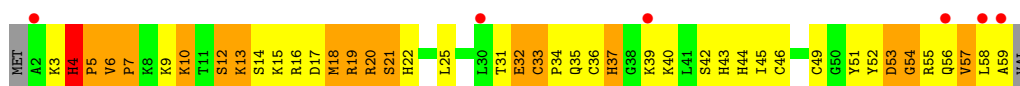


• Molecule 25: 50S ribosomal protein L30

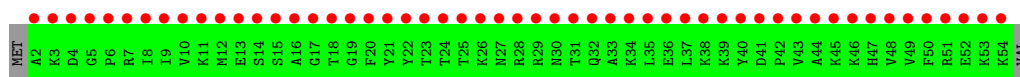


• Molecule 26: 50S ribosomal protein L32

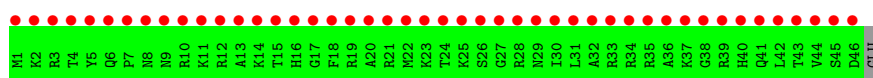




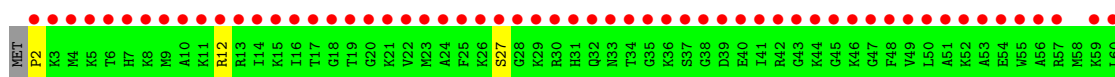
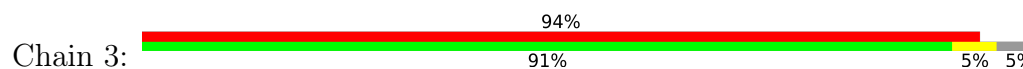
- Molecule 27: 50S ribosomal protein L33



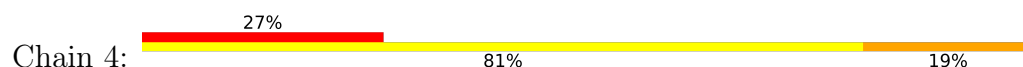
- Molecule 28: 50S ribosomal protein L34



- Molecule 29: 50S ribosomal protein L35



- Molecule 30: 50S ribosomal protein L36



## 4 Data and refinement statistics

| Property                                                                | Value                                                       | Source           |
|-------------------------------------------------------------------------|-------------------------------------------------------------|------------------|
| Space group                                                             | I 2 2 2                                                     | Depositor        |
| Cell constants<br>a, b, c, $\alpha$ , $\beta$ , $\gamma$                | 169.90Å 408.90Å 694.50Å<br>90.00° 90.00° 90.00°             | Depositor        |
| Resolution (Å)                                                          | 29.90 – 2.91<br>29.90 – 2.91                                | Depositor<br>EDS |
| % Data completeness<br>(in resolution range)                            | 94.1 (29.90-2.91)<br>94.3 (29.90-2.91)                      | Depositor<br>EDS |
| $R_{merge}$                                                             | (Not available)                                             | Depositor        |
| $R_{sym}$                                                               | (Not available)                                             | Depositor        |
| $\langle I/\sigma(I) \rangle$ <sup>1</sup>                              | 1.56 (at 2.90Å)                                             | Xtriage          |
| Refinement program                                                      | CNS                                                         | Depositor        |
| R, $R_{free}$                                                           | 0.277 , 0.311<br>0.264 , (Not available)                    | Depositor<br>DCC |
| $R_{free}$ test set                                                     | No test flags present.                                      | wwPDB-VP         |
| Wilson B-factor (Å <sup>2</sup> )                                       | 52.9                                                        | Xtriage          |
| Anisotropy                                                              | 0.101                                                       | Xtriage          |
| Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> ) | 0.18 , 37.9                                                 | EDS              |
| L-test for twinning <sup>2</sup>                                        | $\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$ | Xtriage          |
| Estimated twinning fraction                                             | No twinning to report.                                      | Xtriage          |
| $F_o, F_c$ correlation                                                  | 0.87                                                        | EDS              |
| Total number of atoms                                                   | 83819                                                       | wwPDB-VP         |
| Average B, all atoms (Å <sup>2</sup> )                                  | 43.0                                                        | wwPDB-VP         |

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.87% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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   | X     | 0.63         | 73/64561 (0.1%) | 1.11        | 646/100708 (0.6%) |
| 2   | Y     | 0.38         | 0/2904          | 0.73        | 1/4525 (0.0%)     |
| 3   | A     | 0.62         | 1/1862 (0.1%)   | 1.22        | 25/2510 (1.0%)    |
| 4   | B     | 0.91         | 0/1567          | 1.46        | 25/2105 (1.2%)    |
| 5   | C     | 0.74         | 0/1529          | 1.30        | 20/2070 (1.0%)    |
| 6   | D     | 0.53         | 0/1419          | 1.06        | 5/1903 (0.3%)     |
| 7   | E     | 0.55         | 0/1308          | 1.16        | 16/1771 (0.9%)    |
| 8   | F     | 0.94         | 1/508 (0.2%)    | 1.74        | 15/683 (2.2%)     |
| 9   | G     | 0.74         | 1/1138 (0.1%)   | 1.40        | 15/1539 (1.0%)    |
| 10  | H     | 0.98         | 1/1007 (0.1%)   | 1.35        | 12/1352 (0.9%)    |
| 11  | I     | 0.71         | 1/1081 (0.1%)   | 1.29        | 15/1448 (1.0%)    |
| 12  | J     | 0.72         | 0/1113          | 1.27        | 13/1486 (0.9%)    |
| 13  | K     | 1.11         | 0/886           | 1.42        | 11/1188 (0.9%)    |
| 14  | L     | 0.58         | 1/785 (0.1%)    | 1.22        | 5/1048 (0.5%)     |
| 15  | M     | 0.94         | 0/884           | 1.83        | 17/1186 (1.4%)    |
| 16  | N     | 0.68         | 0/994           | 1.18        | 12/1323 (0.9%)    |
| 17  | O     | 0.64         | 0/750           | 1.12        | 4/1000 (0.4%)     |
| 18  | P     | 0.93         | 0/1027          | 1.35        | 13/1373 (0.9%)    |
| 19  | Q     | 0.71         | 0/737           | 1.26        | 11/988 (1.1%)     |
| 20  | R     | 0.59         | 0/835           | 1.26        | 12/1121 (1.1%)    |
| 21  | S     | 0.56         | 0/1370          | 1.08        | 12/1862 (0.6%)    |
| 22  | T     | 0.60         | 0/633           | 1.07        | 2/838 (0.2%)      |
| 23  | U     | 0.67         | 0/556           | 1.29        | 10/741 (1.3%)     |
| 24  | V     | 0.50         | 0/537           | 1.05        | 5/714 (0.7%)      |
| 25  | W     | 0.65         | 0/426           | 1.24        | 5/568 (0.9%)      |
| 26  | Z     | 0.90         | 0/469           | 1.42        | 9/629 (1.4%)      |
| 30  | 4     | 0.52         | 0/298           | 0.91        | 0/390             |
| All | All   | 0.66         | 79/91184 (0.1%) | 1.14        | 936/137069 (0.7%) |

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

| Mol | Chain | #Chirality outliers | #Planarity outliers |
|-----|-------|---------------------|---------------------|
| 1   | X     | 0                   | 225                 |
| 2   | Y     | 0                   | 4                   |
| 9   | G     | 0                   | 1                   |
| 16  | N     | 0                   | 1                   |
| 19  | Q     | 0                   | 1                   |
| All | All   | 0                   | 232                 |

The worst 5 of 79 bond length outliers are listed below:

| Mol | Chain | Res  | Type | Atoms   | Z     | Observed(Å) | Ideal(Å) |
|-----|-------|------|------|---------|-------|-------------|----------|
| 1   | X     | 1123 | G    | C3'-O3' | 13.47 | 1.62        | 1.42     |
| 1   | X     | 2322 | U    | C3'-O3' | 11.40 | 1.59        | 1.42     |
| 1   | X     | 1123 | G    | C4'-C3' | 10.34 | 1.68        | 1.52     |
| 1   | X     | 100  | G    | C3'-O3' | 9.24  | 1.57        | 1.43     |
| 1   | X     | 1187 | A    | C3'-O3' | 8.91  | 1.55        | 1.42     |

The worst 5 of 936 bond angle outliers are listed below:

| Mol | Chain | Res  | Type | Atoms      | Z      | Observed(°) | Ideal(°) |
|-----|-------|------|------|------------|--------|-------------|----------|
| 15  | M     | 28   | ARG  | CA-C-N     | 26.56  | 153.03      | 119.84   |
| 15  | M     | 28   | ARG  | C-N-CA     | 26.56  | 153.03      | 119.84   |
| 1   | X     | 1055 | A    | N9-C1'-C2' | -24.20 | 75.70       | 112.00   |
| 1   | X     | 513  | A    | N9-C1'-C2' | 21.26  | 145.90      | 114.00   |
| 1   | X     | 2297 | G    | N9-C1'-C2' | 20.18  | 142.27      | 112.00   |

There are no chirality outliers.

5 of 232 planarity outliers are listed below:

| Mol | Chain | Res | Type | Group     |
|-----|-------|-----|------|-----------|
| 1   | X     | 13  | A    | Sidechain |
| 1   | X     | 15  | G    | Sidechain |
| 1   | X     | 32  | C    | Sidechain |
| 1   | X     | 34  | U    | Sidechain |
| 1   | X     | 59  | G    | Sidechain |

## 5.2 Too-close contacts ⓘ

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

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

| Mol | Chain | Non-H | H(model) | H(added) | Clashes | Symm-Clashes |
|-----|-------|-------|----------|----------|---------|--------------|
| 1   | X     | 57651 | 0        | 29047    | 3657    | 0            |
| 2   | Y     | 2598  | 0        | 1328     | 162     | 0            |
| 3   | A     | 1826  | 0        | 1885     | 402     | 0            |
| 4   | B     | 1539  | 0        | 1600     | 267     | 0            |
| 5   | C     | 1506  | 0        | 1525     | 394     | 0            |
| 6   | D     | 1400  | 0        | 1481     | 391     | 0            |
| 7   | E     | 1286  | 0        | 1336     | 256     | 0            |
| 8   | F     | 503   | 0        | 520      | 99      | 0            |
| 9   | G     | 1114  | 0        | 1144     | 274     | 0            |
| 10  | H     | 997   | 0        | 1046     | 157     | 0            |
| 11  | I     | 1067  | 0        | 1103     | 283     | 0            |
| 12  | J     | 1090  | 0        | 1125     | 261     | 0            |
| 13  | K     | 878   | 0        | 930      | 123     | 0            |
| 14  | L     | 779   | 0        | 820      | 243     | 0            |
| 15  | M     | 871   | 0        | 894      | 202     | 0            |
| 16  | N     | 978   | 0        | 1020     | 226     | 0            |
| 17  | O     | 741   | 0        | 756      | 195     | 0            |
| 18  | P     | 1014  | 0        | 1096     | 156     | 0            |
| 19  | Q     | 726   | 0        | 753      | 193     | 0            |
| 20  | R     | 825   | 0        | 881      | 269     | 0            |
| 21  | S     | 1345  | 0        | 1372     | 309     | 0            |
| 22  | T     | 625   | 0        | 655      | 102     | 0            |
| 23  | U     | 552   | 0        | 604      | 207     | 0            |
| 24  | V     | 533   | 0        | 558      | 113     | 0            |
| 25  | W     | 424   | 0        | 470      | 68      | 0            |
| 26  | Z     | 457   | 0        | 464      | 73      | 0            |
| 27  | 1     | 53    | 0        | 0        | 0       | 0            |
| 28  | 2     | 46    | 0        | 0        | 0       | 0            |
| 29  | 3     | 63    | 0        | 0        | 3       | 0            |
| 30  | 4     | 297   | 0        | 330      | 70      | 0            |
| 31  | X     | 30    | 0        | 0        | 0       | 0            |
| 31  | Y     | 5     | 0        | 0        | 0       | 0            |
| All | All   | 83819 | 0        | 54743    | 8365    | 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 61.

The worst 5 of 8365 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



| Atom-1         | Atom-2          | Interatomic distance (Å) | Clash overlap (Å) |
|----------------|-----------------|--------------------------|-------------------|
| 1:X:135:U:H2'  | 1:X:136:A:C8    | 1.59                     | 1.37              |
| 1:X:2195:C:C5  | 1:X:2196:U:C5   | 2.22                     | 1.28              |
| 1:X:623:G:N2   | 1:X:626:A:C2    | 2.01                     | 1.26              |
| 1:X:1053:G:H2' | 1:X:1054:C:C6   | 1.71                     | 1.25              |
| 1:X:333:A:H3'  | 5:C:162:ARG:NH2 | 1.49                     | 1.24              |

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

| Mol | Chain | Analysed      | Favoured  | Allowed  | Outliers | Percentiles |   |
|-----|-------|---------------|-----------|----------|----------|-------------|---|
| 3   | A     | 238/274 (87%) | 147 (62%) | 53 (22%) | 38 (16%) | 0           | 0 |
| 4   | B     | 203/211 (96%) | 147 (72%) | 31 (15%) | 25 (12%) | 0           | 0 |
| 5   | C     | 195/205 (95%) | 99 (51%)  | 48 (25%) | 48 (25%) | 0           | 0 |
| 6   | D     | 175/180 (97%) | 91 (52%)  | 59 (34%) | 25 (14%) | 0           | 0 |
| 7   | E     | 169/185 (91%) | 100 (59%) | 39 (23%) | 30 (18%) | 0           | 0 |
| 8   | F     | 69/144 (48%)  | 45 (65%)  | 19 (28%) | 5 (7%)   | 1           | 2 |
| 9   | G     | 140/174 (80%) | 80 (57%)  | 28 (20%) | 32 (23%) | 0           | 0 |
| 10  | H     | 132/134 (98%) | 114 (86%) | 11 (8%)  | 7 (5%)   | 1           | 4 |
| 11  | I     | 139/156 (89%) | 62 (45%)  | 33 (24%) | 44 (32%) | 0           | 0 |
| 12  | J     | 134/142 (94%) | 74 (55%)  | 36 (27%) | 24 (18%) | 0           | 0 |
| 13  | K     | 111/116 (96%) | 85 (77%)  | 12 (11%) | 14 (13%) | 0           | 0 |
| 14  | L     | 102/114 (90%) | 55 (54%)  | 22 (22%) | 25 (24%) | 0           | 0 |
| 15  | M     | 106/166 (64%) | 71 (67%)  | 21 (20%) | 14 (13%) | 0           | 0 |
| 16  | N     | 115/118 (98%) | 72 (63%)  | 25 (22%) | 18 (16%) | 0           | 0 |
| 17  | O     | 92/100 (92%)  | 57 (62%)  | 16 (17%) | 19 (21%) | 0           | 0 |
| 18  | P     | 125/134 (93%) | 94 (75%)  | 20 (16%) | 11 (9%)  | 0           | 1 |

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| Mol | Chain | Analysed        | Favoured   | Allowed   | Outliers  | Percentiles |   |
|-----|-------|-----------------|------------|-----------|-----------|-------------|---|
| 19  | Q     | 91/95 (96%)     | 44 (48%)   | 23 (25%)  | 24 (26%)  | 0           | 0 |
| 20  | R     | 108/115 (94%)   | 60 (56%)   | 24 (22%)  | 24 (22%)  | 0           | 0 |
| 21  | S     | 173/237 (73%)   | 94 (54%)   | 40 (23%)  | 39 (22%)  | 0           | 0 |
| 22  | T     | 82/91 (90%)     | 48 (58%)   | 20 (24%)  | 14 (17%)  | 0           | 0 |
| 23  | U     | 70/81 (86%)     | 35 (50%)   | 18 (26%)  | 17 (24%)  | 0           | 0 |
| 24  | V     | 64/67 (96%)     | 32 (50%)   | 20 (31%)  | 12 (19%)  | 0           | 0 |
| 25  | W     | 53/55 (96%)     | 42 (79%)   | 6 (11%)   | 5 (9%)    | 0           | 1 |
| 26  | Z     | 56/60 (93%)     | 41 (73%)   | 7 (12%)   | 8 (14%)   | 0           | 0 |
| 30  | 4     | 35/37 (95%)     | 17 (49%)   | 9 (26%)   | 9 (26%)   | 0           | 0 |
| All | All   | 2977/3391 (88%) | 1806 (61%) | 640 (22%) | 531 (18%) | 0           | 0 |

5 of 531 Ramachandran outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 3   | A     | 60  | ARG  |
| 3   | A     | 187 | SER  |
| 3   | A     | 209 | ALA  |
| 3   | A     | 217 | ARG  |
| 3   | A     | 220 | HIS  |

### 5.3.2 Protein sidechains ⓘ

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

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

| Mol | Chain | Analysed      | Rotameric | Outliers | Percentiles |    |
|-----|-------|---------------|-----------|----------|-------------|----|
| 3   | A     | 185/215 (86%) | 164 (89%) | 21 (11%) | 5           | 17 |
| 4   | B     | 155/157 (99%) | 138 (89%) | 17 (11%) | 6           | 19 |
| 5   | C     | 157/163 (96%) | 134 (85%) | 23 (15%) | 3           | 10 |
| 6   | D     | 153/156 (98%) | 134 (88%) | 19 (12%) | 4           | 14 |
| 7   | E     | 136/144 (94%) | 122 (90%) | 14 (10%) | 7           | 22 |
| 8   | F     | 51/107 (48%)  | 49 (96%)  | 2 (4%)   | 28          | 61 |
| 9   | G     | 118/146 (81%) | 101 (86%) | 17 (14%) | 3           | 10 |

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| Mol | Chain | Analysed        | Rotameric  | Outliers  | Percentiles |    |
|-----|-------|-----------------|------------|-----------|-------------|----|
| 10  | H     | 103/103 (100%)  | 88 (85%)   | 15 (15%)  | 3           | 10 |
| 11  | I     | 108/121 (89%)   | 91 (84%)   | 17 (16%)  | 2           | 8  |
| 12  | J     | 110/116 (95%)   | 96 (87%)   | 14 (13%)  | 4           | 14 |
| 13  | K     | 90/93 (97%)     | 74 (82%)   | 16 (18%)  | 2           | 6  |
| 14  | L     | 74/82 (90%)     | 56 (76%)   | 18 (24%)  | 1           | 2  |
| 15  | M     | 94/134 (70%)    | 79 (84%)   | 15 (16%)  | 2           | 8  |
| 16  | N     | 96/97 (99%)     | 84 (88%)   | 12 (12%)  | 4           | 14 |
| 17  | O     | 75/79 (95%)     | 68 (91%)   | 7 (9%)    | 8           | 26 |
| 18  | P     | 109/115 (95%)   | 99 (91%)   | 10 (9%)   | 8           | 26 |
| 19  | Q     | 75/76 (99%)     | 64 (85%)   | 11 (15%)  | 3           | 10 |
| 20  | R     | 91/96 (95%)     | 80 (88%)   | 11 (12%)  | 5           | 15 |
| 21  | S     | 149/192 (78%)   | 130 (87%)  | 19 (13%)  | 4           | 13 |
| 22  | T     | 62/67 (92%)     | 58 (94%)   | 4 (6%)    | 15          | 42 |
| 23  | U     | 57/66 (86%)     | 41 (72%)   | 16 (28%)  | 0           | 1  |
| 24  | V     | 54/55 (98%)     | 50 (93%)   | 4 (7%)    | 13          | 36 |
| 25  | W     | 48/48 (100%)    | 44 (92%)   | 4 (8%)    | 10          | 30 |
| 26  | Z     | 51/53 (96%)     | 45 (88%)   | 6 (12%)   | 5           | 16 |
| 30  | 4     | 35/35 (100%)    | 33 (94%)   | 2 (6%)    | 18          | 48 |
| All | All   | 2436/2716 (90%) | 2122 (87%) | 314 (13%) | 4           | 13 |

5 of 314 residues with a non-rotameric sidechain are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 18  | P     | 103 | LEU  |
| 23  | U     | 32  | ARG  |
| 19  | Q     | 7   | LEU  |
| 21  | S     | 4   | THR  |
| 24  | V     | 37  | LEU  |

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 99 such sidechains are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 16  | N     | 72  | HIS  |
| 19  | Q     | 73  | ASN  |
| 16  | N     | 91  | ASN  |

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| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 18  | P     | 78  | ASN  |
| 20  | R     | 44  | GLN  |

### 5.3.3 RNA ⓘ

| Mol | Chain | Analysed        | Backbone Outliers | Pucker Outliers |
|-----|-------|-----------------|-------------------|-----------------|
| 1   | X     | 2680/2880 (93%) | 706 (26%)         | 324 (12%)       |
| 2   | Y     | 121/123 (98%)   | 25 (20%)          | 1 (0%)          |
| All | All   | 2801/3003 (93%) | 731 (26%)         | 325 (11%)       |

5 of 731 RNA backbone outliers are listed below:

| Mol | Chain | Res | Type |
|-----|-------|-----|------|
| 1   | X     | 2   | G    |
| 1   | X     | 4   | C    |
| 1   | X     | 13  | A    |
| 1   | X     | 14  | A    |
| 1   | X     | 25  | U    |

5 of 325 RNA pucker outliers are listed below:

| Mol | Chain | Res  | Type |
|-----|-------|------|------|
| 1   | X     | 1923 | U    |
| 1   | X     | 2476 | A    |
| 1   | X     | 1975 | G    |
| 1   | X     | 2237 | C    |
| 1   | X     | 2608 | A    |

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 35 ligands modelled in this entry, 35 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

| Mol | Chain | Analysed        | <RSRZ> | #RSRZ>2        | OWAB(Å <sup>2</sup> ) | Q<0.9 |
|-----|-------|-----------------|--------|----------------|-----------------------|-------|
| 1   | X     | 2686/2880 (93%) | 1.00   | 470 (17%) 4 3  | 3, 38, 98, 118        | 0     |
| 2   | Y     | 122/123 (99%)   | 1.46   | 37 (30%) 1 1   | 24, 67, 89, 101       | 0     |
| 3   | A     | 240/274 (87%)   | 1.97   | 94 (39%) 1 0   | 17, 53, 65, 71        | 0     |
| 4   | B     | 205/211 (97%)   | 0.63   | 21 (10%) 12 10 | 2, 21, 43, 56         | 0     |
| 5   | C     | 197/205 (96%)   | 1.41   | 50 (25%) 1 1   | 14, 43, 58, 66        | 0     |
| 6   | D     | 177/180 (98%)   | 1.47   | 53 (29%) 1 1   | 50, 60, 67, 69        | 0     |
| 7   | E     | 171/185 (92%)   | 1.15   | 30 (17%) 4 3   | 38, 53, 64, 68        | 0     |
| 8   | F     | 71/144 (49%)    | 3.28   | 57 (80%) 0 0   | 0, 77, 83, 85         | 0     |
| 9   | G     | 142/174 (81%)   | 1.58   | 38 (26%) 1 1   | 24, 39, 53, 63        | 0     |
| 10  | H     | 134/134 (100%)  | 0.39   | 5 (3%) 45 36   | 3, 17, 33, 42         | 0     |
| 11  | I     | 141/156 (90%)   | 2.10   | 55 (39%) 1 0   | 21, 52, 62, 71        | 0     |
| 12  | J     | 136/142 (95%)   | 1.35   | 31 (22%) 2 2   | 28, 43, 60, 65        | 0     |
| 13  | K     | 113/116 (97%)   | 0.47   | 9 (7%) 18 15   | 2, 10, 24, 34         | 0     |
| 14  | L     | 104/114 (91%)   | 1.63   | 30 (28%) 1 1   | 38, 51, 58, 63        | 0     |
| 15  | M     | 108/166 (65%)   | 0.50   | 8 (7%) 20 17   | 3, 18, 43, 55         | 0     |
| 16  | N     | 117/118 (99%)   | 1.30   | 24 (20%) 2 2   | 5, 37, 54, 61         | 0     |
| 17  | O     | 94/100 (94%)    | 1.23   | 20 (21%) 2 2   | 22, 47, 59, 64        | 0     |
| 18  | P     | 127/134 (94%)   | 0.49   | 10 (7%) 18 15  | 4, 18, 47, 59         | 0     |
| 19  | Q     | 93/95 (97%)     | 1.32   | 23 (24%) 2 1   | 29, 42, 56, 68        | 0     |
| 20  | R     | 110/115 (95%)   | 1.71   | 34 (30%) 1 1   | 35, 46, 61, 65        | 0     |
| 21  | S     | 175/237 (73%)   | 1.32   | 32 (18%) 3 3   | 49, 58, 64, 68        | 0     |
| 22  | T     | 84/91 (92%)     | 1.65   | 24 (28%) 1 1   | 26, 44, 59, 70        | 0     |
| 23  | U     | 72/81 (88%)     | 2.51   | 40 (55%) 0 0   | 41, 53, 63, 67        | 0     |
| 24  | V     | 66/67 (98%)     | 0.81   | 6 (9%) 15 12   | 38, 52, 65, 67        | 0     |

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| Mol | Chain | Analysed        | <RSRZ> | #RSRZ>2        | OWAB(Å <sup>2</sup> ) | Q<0.9 |
|-----|-------|-----------------|--------|----------------|-----------------------|-------|
| 25  | W     | 55/55 (100%)    | 0.62   | 5 (9%) 15 12   | 21, 37, 49, 64        | 0     |
| 26  | Z     | 58/60 (96%)     | 0.76   | 6 (10%) 12 10  | 4, 16, 38, 44         | 0     |
| 27  | 1     | 53/55 (96%)     | 16.45  | 53 (100%) 0 0  | 37, 47, 56, 60        | 0     |
| 28  | 2     | 46/47 (97%)     | 14.59  | 46 (100%) 0 0  | 11, 27, 34, 37        | 0     |
| 29  | 3     | 63/66 (95%)     | 14.36  | 62 (98%) 0 0   | 21, 36, 46, 48        | 0     |
| 30  | 4     | 37/37 (100%)    | 1.46   | 10 (27%) 1 1   | 44, 52, 58, 59        | 0     |
| All | All   | 5997/6562 (91%) | 1.55   | 1383 (23%) 2 2 | 0, 43, 84, 118        | 0     |

The worst 5 of 1383 RSRZ outliers are listed below:

| Mol | Chain | Res | Type | RSRZ |
|-----|-------|-----|------|------|
| 27  | 1     | 7   | ARG  | 58.4 |
| 27  | 1     | 40  | TYR  | 49.4 |
| 29  | 3     | 22  | VAL  | 42.9 |
| 27  | 1     | 50  | PHE  | 35.6 |
| 27  | 1     | 6   | PRO  | 32.0 |

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

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

## 6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 6.4 Ligands ⓘ

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

| Mol | Type | Chain | Res  | Atoms | RSCC | RSR  | B-factors(Å <sup>2</sup> ) | Q<0.9 |
|-----|------|-------|------|-------|------|------|----------------------------|-------|
| 31  | MG   | X     | 2884 | 1/1   | 0.62 | 0.52 | 55,55,55,55                | 0     |
| 31  | MG   | Y     | 126  | 1/1   | 0.62 | 0.19 | 25,25,25,25                | 0     |
| 31  | MG   | X     | 2890 | 1/1   | 0.69 | 0.40 | 49,49,49,49                | 0     |
| 31  | MG   | X     | 2881 | 1/1   | 0.69 | 0.32 | 59,59,59,59                | 0     |

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| Mol | Type | Chain | Res  | Atoms | RSCC | RSR  | B-factors( $\text{\AA}^2$ ) | Q<0.9 |
|-----|------|-------|------|-------|------|------|-----------------------------|-------|
| 31  | MG   | X     | 2883 | 1/1   | 0.74 | 0.22 | 49,49,49,49                 | 0     |
| 31  | MG   | X     | 2887 | 1/1   | 0.74 | 0.12 | 3,3,3,3                     | 0     |
| 31  | MG   | X     | 2910 | 1/1   | 0.75 | 0.24 | 19,19,19,19                 | 0     |
| 31  | MG   | X     | 2882 | 1/1   | 0.76 | 0.20 | 12,12,12,12                 | 0     |
| 31  | MG   | X     | 2905 | 1/1   | 0.76 | 0.21 | 6,6,6,6                     | 0     |
| 31  | MG   | Y     | 128  | 1/1   | 0.77 | 0.12 | 41,41,41,41                 | 0     |
| 31  | MG   | X     | 2908 | 1/1   | 0.79 | 0.33 | 17,17,17,17                 | 0     |
| 31  | MG   | X     | 2899 | 1/1   | 0.79 | 0.28 | 19,19,19,19                 | 0     |
| 31  | MG   | Y     | 127  | 1/1   | 0.80 | 0.09 | 12,12,12,12                 | 0     |
| 31  | MG   | X     | 2907 | 1/1   | 0.81 | 0.24 | 58,58,58,58                 | 0     |
| 31  | MG   | X     | 2897 | 1/1   | 0.81 | 0.32 | 3,3,3,3                     | 0     |
| 31  | MG   | X     | 2886 | 1/1   | 0.82 | 0.17 | 41,41,41,41                 | 0     |
| 31  | MG   | X     | 2903 | 1/1   | 0.82 | 0.07 | 24,24,24,24                 | 0     |
| 31  | MG   | Y     | 124  | 1/1   | 0.82 | 0.25 | 26,26,26,26                 | 0     |
| 31  | MG   | X     | 2895 | 1/1   | 0.83 | 0.31 | 3,3,3,3                     | 0     |
| 31  | MG   | X     | 2898 | 1/1   | 0.83 | 0.29 | 3,3,3,3                     | 0     |
| 31  | MG   | X     | 2892 | 1/1   | 0.84 | 0.18 | 22,22,22,22                 | 0     |
| 31  | MG   | X     | 2893 | 1/1   | 0.85 | 0.11 | 13,13,13,13                 | 0     |
| 31  | MG   | X     | 2896 | 1/1   | 0.87 | 0.13 | 3,3,3,3                     | 0     |
| 31  | MG   | X     | 2909 | 1/1   | 0.89 | 0.07 | 3,3,3,3                     | 0     |
| 31  | MG   | X     | 2888 | 1/1   | 0.89 | 0.10 | 3,3,3,3                     | 0     |
| 31  | MG   | X     | 2885 | 1/1   | 0.90 | 0.24 | 56,56,56,56                 | 0     |
| 31  | MG   | X     | 2906 | 1/1   | 0.91 | 0.18 | 13,13,13,13                 | 0     |
| 31  | MG   | X     | 2902 | 1/1   | 0.92 | 0.17 | 60,60,60,60                 | 0     |
| 31  | MG   | Y     | 125  | 1/1   | 0.92 | 0.20 | 9,9,9,9                     | 0     |
| 31  | MG   | X     | 2894 | 1/1   | 0.92 | 0.49 | 15,15,15,15                 | 0     |
| 31  | MG   | X     | 2900 | 1/1   | 0.92 | 0.39 | 3,3,3,3                     | 0     |
| 31  | MG   | X     | 2901 | 1/1   | 0.92 | 0.29 | 3,3,3,3                     | 0     |
| 31  | MG   | X     | 2904 | 1/1   | 0.94 | 0.12 | 3,3,3,3                     | 0     |
| 31  | MG   | X     | 2891 | 1/1   | 0.95 | 0.29 | 12,12,12,12                 | 0     |
| 31  | MG   | X     | 2889 | 1/1   | 0.96 | 0.22 | 3,3,3,3                     | 0     |

## 6.5 Other polymers

There are no such residues in this entry.