



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:57 PM UTC

PDB ID : 3J5L / pdb_00003j5l
EMDB ID : EMD-5771
Title : Structure of the E. coli 50S subunit with ErmBL nascent chain
Authors : Arenz, S.; Ramu, H.; Gupta, P.; Berninghausen, O.; Beckmann, R.; Vazquez-Laslop, N.; Mankin, A.S.; Wilson, D.N.
Deposited on : 2013-10-23
Resolution : 6.60 Å(reported)
Based on initial model : 3OFR

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:

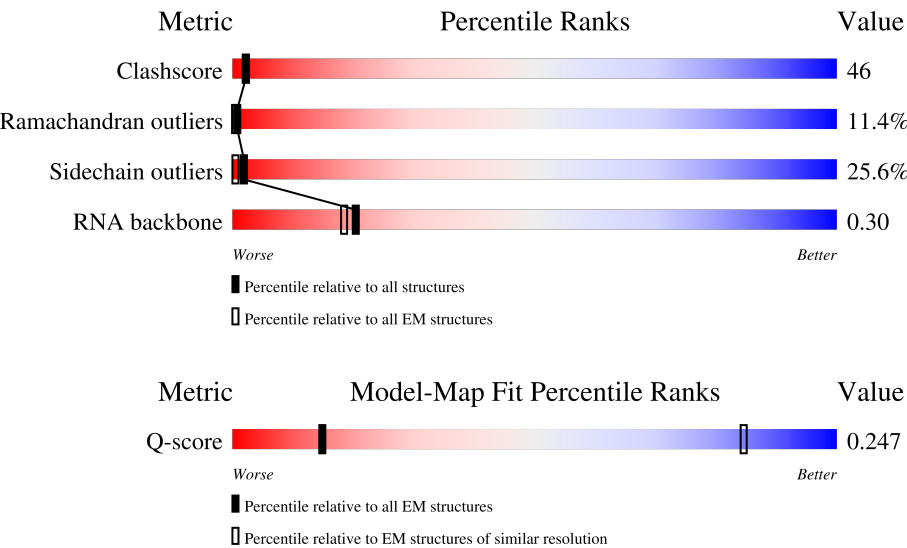
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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:
ELECTRON MICROSCOPY

The reported resolution of this entry is 6.60 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	531 (6.10 - 7.10)

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	0	56	62% 27% 48% 21% .
2	1	50	62% 28% 50% 18% .
3	2	46	43% 43% 37% 17% .

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Mol	Chain	Length	Quality of chain
4	3	64	
5	4	38	
6	5	2	
7	6	10	
8	7	3	
9	A	2904	
10	B	118	
11	C	271	
12	D	209	
13	E	201	
14	F	177	
15	G	176	
16	H	56	
17	I	141	
18	J	142	
19	K	122	
20	L	143	
21	M	136	
22	N	120	
23	O	116	
24	P	114	
25	Q	117	
26	R	103	
27	S	110	
28	T	93	

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Mol	Chain	Length	Quality of chain
29	U	102	82% 19% 53% 27% 2%
30	V	94	65% 45% 43% 13% 1%
31	W	79	61% 14% 38% 38% 10%
32	X	77	60% 18% 56% 23% 1%
33	Y	63	70% 24% 44% 22% 10%
34	Z	58	57% 33% 41% 19% 7%

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 89382 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 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a RNA chain called 5'-R(*CP*(MA6))-3'.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	2	Total	C	N	O	P	0	0
			41	21	8	11	1		

- Molecule 7 is a protein called Erythromycin resistance leader peptide.

Mol	Chain	Residues	Atoms	AltConf	Trace
7	6	8	Total C 8 8	0	8

- Molecule 8 is a RNA chain called 5'-R(*CP*CP*A)-3'.

Mol	Chain	Residues	Atoms	AltConf	Trace
8	7	3	Total C N O P 59 28 11 18 2	0	0

- Molecule 9 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
9	A	2853	Total C N O P 61251 27324 11274 19800 2853	0	0

- Molecule 10 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms	AltConf	Trace
10	B	117	Total C N O P 2506 1116 459 814 117	0	0

- Molecule 11 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms	AltConf	Trace
11	C	271	Total C N O S 2083 1288 423 365 7	0	0

- Molecule 12 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms	AltConf	Trace
12	D	209	Total C N O S 1565 979 288 294 4	0	0

- Molecule 13 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms	AltConf	Trace
13	E	201	Total C N O S 1552 974 283 290 5	0	0

- Molecule 14 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	F	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 15 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 16 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	H	56	Total	C	N	O	S	0	0
			431	275	77	78	1		

- Molecule 17 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 18 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 19 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 20 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 21 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 22 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	N	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 23 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 24 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 25 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 26 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 27 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 28 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	T	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 29 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	U	102	Total	C	N	O	S	0	0
			780	492	146	142			

- Molecule 30 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 31 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	W	79	Total	C	N	O	S	0	0
			596	367	120	108	1		

- Molecule 32 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 33 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

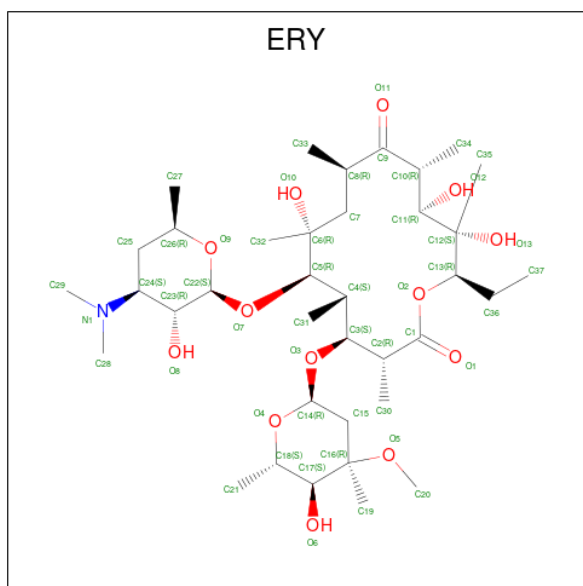
- Molecule 34 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 35 is UNKNOWN LIGAND (CCD ID: UNL) (formula:).

Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
35	5	1	4	2	1	1	0

- Molecule 36 is ERYTHROMYCIN A (CCD ID: ERY) (formula: $C_{37}H_{67}NO_{13}$).

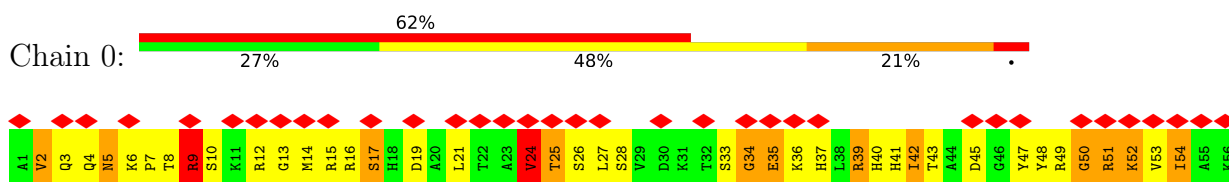


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
36	A	1	51	37	1	13	0

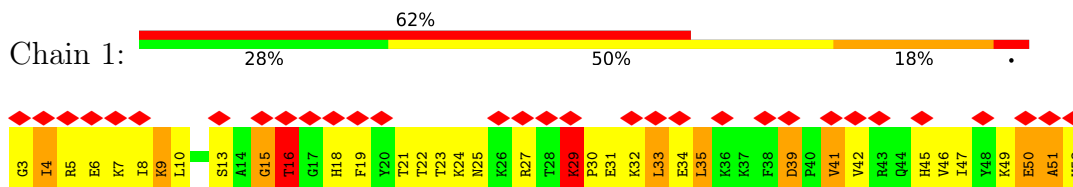
3 Residue-property plots [i](#)

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.

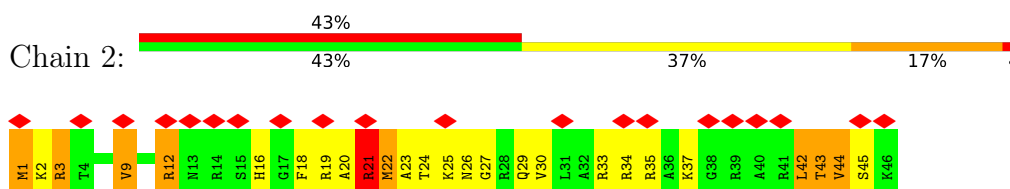
- Molecule 1: 50S ribosomal protein L32



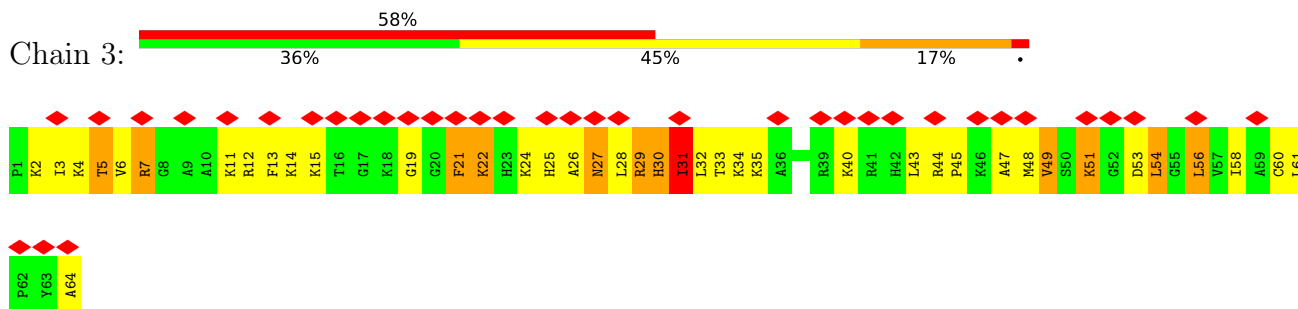
- Molecule 2: 50S ribosomal protein L33



- Molecule 3: 50S ribosomal protein L34

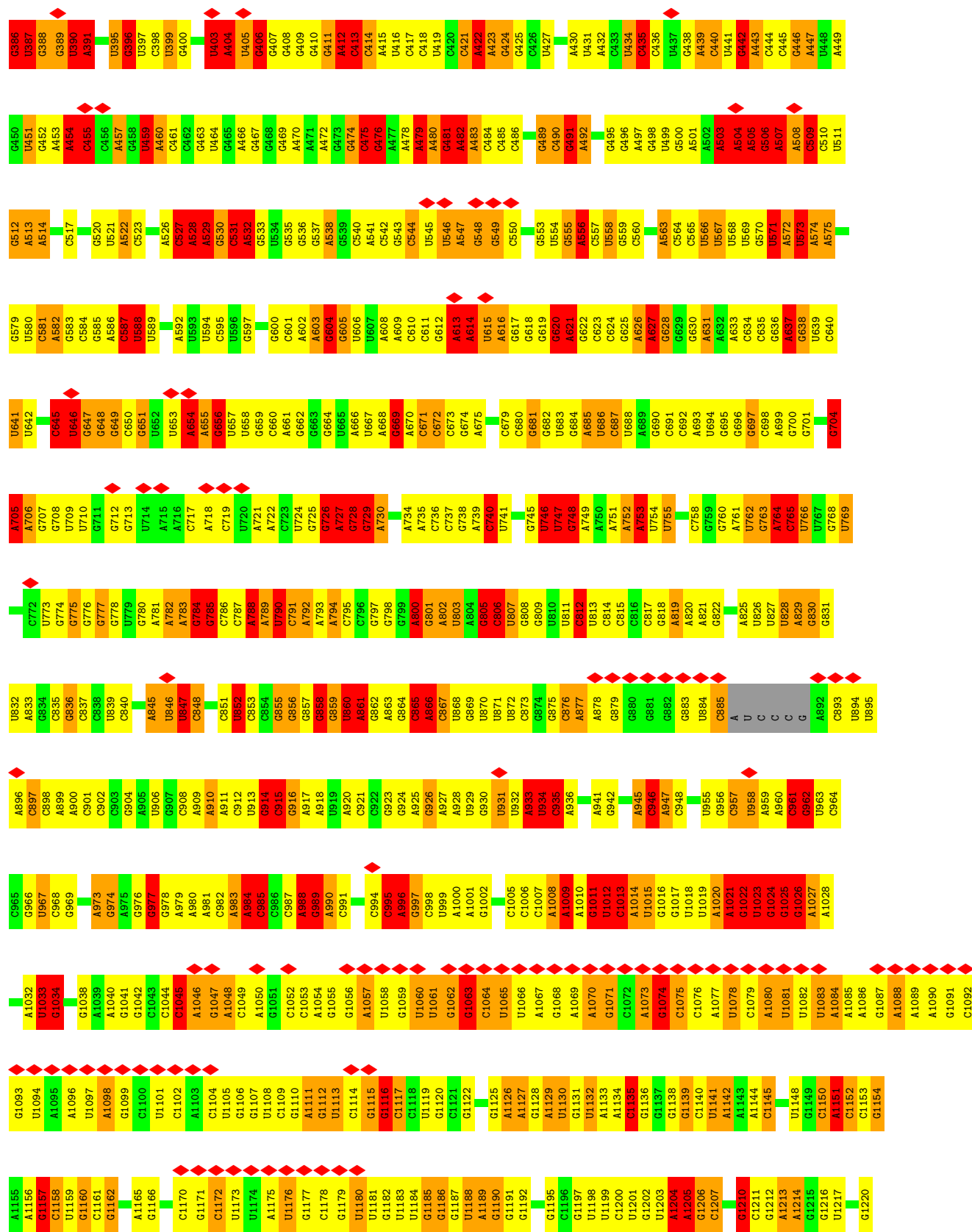


- Molecule 4: 50S ribosomal protein L35



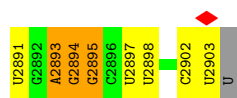
- Molecule 5: 50S ribosomal protein L36



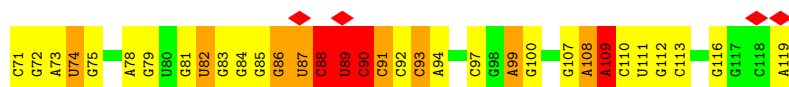
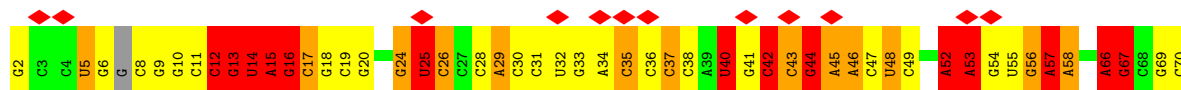
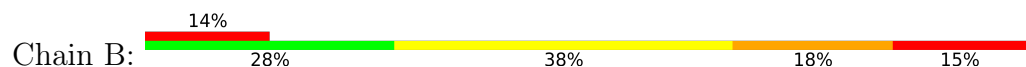


G2002	A1938	C1874	A1809	U1742	G1607	G1540	G1475	U1415	C1349	A1285	C1221
G2006	C1941	G1875	A1810	G1743	A1608	C1541	U1476	G1416	C1350	A1286	U1222
U2007	C1942	A1876	G1813	A1744	A1609	U1542	A1477	U1542	C1351	A1287	G1223
C2008	U1943	G1878	U1745	A1745	A1610	G1543	G1417	G1418	U1352	G1288	U1224
U2011	U1944	G1879	A1814	A1746	C1611	G1681	U1480	A1419	G1356	C1290	A1226
G2012	G1945	U1880	G1815	U1747	C1612	A1545	G1482	A1420	G1357	G1297	U1234
A2013	U1946	C1881	G1816	C1748	G1613	G1546	G1483	G1421	G1358	C1298	G1235
A2014	C1947	U1882	G1817	A1749	G1614	A1553	U1485	G1422	G1359	C1299	G1236
A2015	G1950	U1883	U1818	G1753	C1615	U1554	U1486	G1423	G1360	U1293	A1230
U2016	U1951	A1884	A1819	A1754	A1616	G1555	U1487	G1424	G1361	C1299	G1233
U2017	A1885	U1885	U1820	G1755	C1617	G1556	C1488	G1425	G1362	G1297	U1234
G2018	U1886	U1886	G1822	G1756	A1618	U1557	C1489	G1426	G1364	C1298	G1235
A2019	A1953	G1889	G1823	U1757	U1619	C1558	A1490	A1427	A1365	G1299	G1236
A2020	U1954	U1758	U1824	U1758	U1620	U1559	A1491	C1428	A1366	G1299	G1236
C2021	U1955	A1759	U1825	A1759	A1621	G1560	G1492	A1429	A1367	G1300	A1237
U2022	G1957	C1760	G1695	C1760	A1626	C1561	C1492	G1430	A1367	A1301	G1238
C2023	U1958	G1761	G1696	A1755	G1627	U1562	C1493	A1431	G1368	A1302	G1239
G2024	C1959	U1762	G1697	G1756	G1628	U1563	A1494	G1432	G1369	G1303	U1240
A2025	A1960	G1763	A1698	U1757	U1629	C1564	A1495	A1433	A1370	A1304	A1241
U2026	U1961	C1764	G1699	U1758	A1634	C1565	A1496	A1434	G1371	C1305	U1242
G2027	C1962	G1767	U1700	A1635	U1636	A1566	U1497	G1435	U1372	C1243	C1243
U2028	U1963	U1768	A1701	U1636	U1637	A1567	C1498	G1436	A1373	G1309	A1244
G2029	A1901	U1769	G1702	U1637	A1637	G1568	C1499	U1438	G1374	G1311	G1245
A2030	C1965	G1773	G1703	C1638	C1639	A1569	G1501	U1439	C1375	U1312	A1246
A2031	U1966	A1773	C1706	C1639	A1570	A1570	A1502	U1440	G1377	G1313	A1247
G2032	C1967	C1774	U1707	A1640	A1571	A1572	A1503	G1441	A1378	C1314	G1248
A2033	G1968	U1775	C1708	A1641	A1572	G1573	A1504	U1442	U1379	G1315	U1249
U2034	U1970	G1776	G1709	G1642	G1573	A1574	A1505	U1443	G1380	G1316	C1251
G2035	C1969	U1777	A1711	G1643	C1575	C1575	U1506	G1444	G1381	G1317	G1252
C2036	U1971	U1778	U1712	G1644	C1576	U1575	G1507	G1445	G1382	U1318	A1253
A2037	G1972	U1779	U1713	G1645	U1577	A1583	C1507	G1446	A1383	C1319	A1254
U2038	C1973	U1780	U1714	G1646	C1577	U1578	A1509	C1447	A1384	G1320	U1265
G2039	G1974	U1781	U1715	U1648	U1579	G1579	G1510	G1448	A1385	A1321	G1266
U2042	A1913	U1782	U1716	G1649	A1580	C1585	G1511	G1449	C1386	A1322	C1267
C2043	C1914	U1783	U1717	A1650	G1581	G1581	C1512	G1450	G1387	C1323	U1268
U2044	U1915	A1784	G1718	G1651	G1582	U1582	U1513	C1451	A1392	G1324	G1269
G2049	A1916	U1785	G1719	A1652	A1583	U1584	G1514	G1452	A1393	U1325	A1260
A2051	U1917	A1786	U1720	G1653	U1584	C1585	A1515	A1453	U1394	U1326	C1261
C2050	A1918	U1787	G1721	A1654	C1585	U1586	G1516	C1454	A1395	A1327	C1262
A2052	G1920	C1788	A1722	A1655	C1586	A1587	G1520	G1455	U1396	A1328	U1263
G2053	U1982	U1789	U1725	C1656	U1657	G1587	U1521	G1456	U1397	U1329	A1264
C2054	A1983	G1790	G1726	U1662	U1657	U1588	A1522	U1457	G1398	G1330	A1265
U2055	U1984	U1791	G1727	G1663	U1662	U1589	U1523	G1459	C1398	G1332	G1267
G2056	C1985	G1792	C1728	A1664	A1664	A1590	U1524	U1460	U1400	G1333	A1268
C2057	U1987	C1793	U1729	A1665	A1665	C1591	A1525	C1461	G1401	A1335	A1269
A2060	G1988	C1795	U1730	A1666	A1666	U1592	C1526	C1462	U1402	C1335	C1270
G2061	U1991	U1796	G1731	G1667	G1667	U1594	G1527	C1463	A1403	A1336	G1271
A2062	U1992	G1797	C1732	A1668	A1668	C1595	A1528	G1464	C1404	G1337	A1272
C2063	C1993	U1798	G1733	A1669	A1669	U1599	C1531	G1465	U1405	G1338	U1273
U2064	U1994	U1799	G1734	A1670	A1670	G1600	A1532	U1466	G1407	G1339	A1274
G2065	A1995	G1800	U1735	A1671	U1671	G1601	A1533	U1467	G1408	G1341	A1275
C2066	C1996	U1802	A1736	A1672	A1672	G1602	U1534	U1468	U1409	A1342	A1276
U2067	U1997	A1803	G1737	A1673	A1673	A1603	A1535	A1469	G1410	G1343	G1277
G2068	G1998	G1807	U1738	A1674	A1674	C1604	C1536	G1471	U1411	U1344	G1281
A2069	C2001	A1808	G1740	C1675	C1675	C1605	G1537	G1472	U1412	C1345	U1282
U2068	U2069	G1873	C1741	A1676	A1676	C1606	U1538	U1474	C1414	C1348	A1284

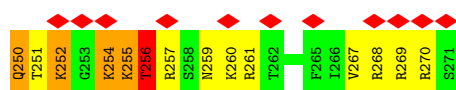
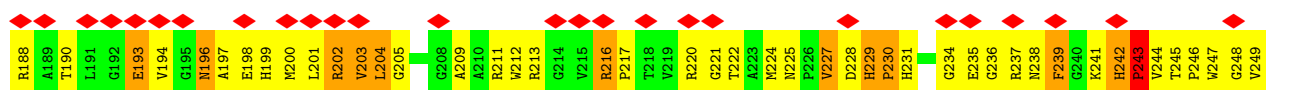
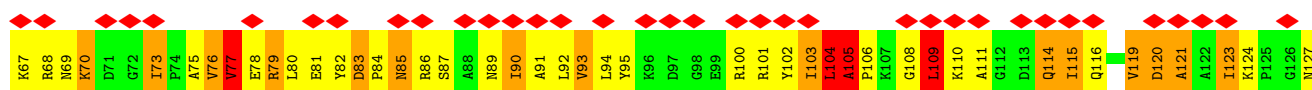
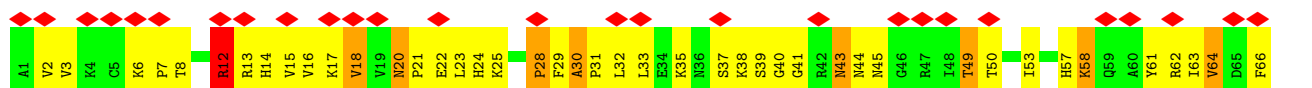
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C2827	A2766	G2639	C2674	U2511	A2448	U2387	A2317	G2193		C2072
G2828	C2702	G2640	C2675	C2512	U2449	A2388	G2318	A2194		U2076
A2829	C2703	G2641	A2577	A2513	U2450	U2389	G2319	A2135		U2077
C2830	A2705	G2642	A2578	C2514	A2451	U2390	U2320	G2136		C2078
G2831	A2706	G2643	C2676	C2515	A2452	U2391	U2321	U2137		U2079
U2832	U2707	G2644	C2677	A2516	A2453	G2392	G2322	G2138		A2080
U2833	G2708	G2645	U2580	C2517	A2454	A2393	G2323	G2139		U2081
G2834		U2646	C2678	A2518	A2455	U2394	G2324	G2140		A2082
A2835	A2711	U2647	U2581	U2519	G2456	C2395	G2325	G2141		C2083
U2836	C2712	G2648	G2583	C2520	G2457	C2396	A2326	G2142		C2084
A2837	U2713	C2649	U2584	C2521	G2458	U2397	A2327	A2143		U2085
G2838	G2714		U2585	U2522	A2459	G2398	A2328	A2144		G2087
C2839	G2715	C2852	U2586	G2523	U2460	U2399	U2329	A2145		A2088
G2840	C2716	U2853	A2587	G2524	A2461	G2400	G2330	G2146		C2089
C2841	G2717	A2854	G2588	G2525	A2462	U2401	G2331	C2147		U2090
G2842	U2718	U2855	A2589	G2526	C2463	U2402	U2332	C2148		A2094
	G2719	U2856	C2590	C2527	G2464	C2403	U2333	G2149		A2095
U2843	A2721	A2857	C2591	U2528	C2465	U2404	A2334	C2150		C2096
G2844	G2722	G2858	U2592	G2529	A2466	U2405	A2335	U2151		U2097
A2845	C2723	G2859	C2593	U2530	C2467	A2406	G2336	G2152		U2098
U2846	U2724	A2860	C2594	A2531	A2468	U2407	U2337	C2153		G2100
A2847		G2661	G2595	U2532	G2469	U2408	C2338	U2154		G2101
G2848	A2725	A2862	A2598	G2533	A2470	C2409	A2339	G2155		G2102
U2849	A2726	G2863	C2599	U2534	A2471	U2410	A2340	G2156		U2099
A2850	U2727	G2864	A2600	U2535	A2472	G2411	G2341	A2157		
A2851	A2728	A2865	C2601	C2536	U2473	A2412	U2342	A		
G2852	G2729	G2866	U2602	C2537	U2474	G2413	U2343	C		
U2853	C2730	C2867	G2603	C2538	A2475	U2414	U2344	G		
G2854	U2731	G2868	U2604	C2539	A2476	G2415	G2345	A		
A2855	G2732	A2869	G2605	U2540	U2477	C2416	A2346	U		
U2856	A2733	A2870	G2606	A2541	A2478	U2417	C2467	U		
G2857	G2734	G2871	U2607	C2542	U2479	G2418	U2348	U		
U2858	A2735	C2872	C2608	G2543	A2480	U2419	G2349	U		
A2859	U2736	G2873	U2609	G2544	U2481	C2420	C2350	U		
		A2799	C2610	U2545	A2482	G2421	A2351	U		
U2860	A2740	C2874	C2611	A2546	G2485	U2422	A2352	U		
G2861	G2741	A2875	C2612	U2547		U2423	G2353	U		
U2862	U2742	C2876	U2613	G2548	U2486	A2424	G2354	U		
G2863	G2743	U2880	A2614	C2550	U2489	U2425	G2355	U		
U2864	U2744	C2881	C2615	U2551	U2490	A2426	C2356	U		
C2865	C2745	A2882	C2616	C2552	U2491	C2427	U2357	U		
U2866	U2746	C2883	U2617	U2553	U2492	G2428	A2358	U		
A2867	G2747	U2884	G2618	C2554	U2493	U2429	G2359	U		
U2868	U2748	C2885	C2619	U2555	G2494	A2430	U2360	U		
G2869	A2749	G2886	C2620	C2556	G2495	U2431	G2361	U		
U2870	U2750	U2887	G2621	U2557	C2496	A2432	G2362	U		
A2871	G2751	G2888	U2622	C2558	A2497	U2433	G2363	U		
U2872	C2752	U2889	G2623	U2562	U2498	A2434	G2364	U		
G2873	U2753	C2890	U2624	U2563	U2499	U2435	G2365	U		
U2874	G2754	A2891	G2625	A2564	U2500	G2436	A2366	U		
A2875	C2755	C2892	U2626	A2565	G2501	U2437	G2367	U		
U2876	U2756	U2893	G2627	A2566	G2502	G2438	G2373	U		
G2877	A2757	C2894	U2628	A2567	A2503	U2439	C2374	U		
U2878	G2758	U2895	G2629	G2568	U2504	A2440	G2308	C2179		
A2879	U2759	C2896	U2630	U2569	U2505	C2441	A2309	U		
U2880	C2760	U2897	A2631	G2570	U2506	U2442	G2310	U		
G2881	U2761	G2898	A2632	U2571	U2507	G2443	A2311	U		
U2882		A2899	G2633	U2572	G2508	C2444	A2312	U		
A2883		C2890	U2634	U2573			G2313	U		
U2884		U2891	G2635	U2574			A2314	U		
G2885		A2892	U2636	U2575			A2184	U		
U2886		C2893		U2576			U2185	U		
A2887		U2894		U2577			G2186	U		
U2888		G2895		U2578			U2187	U		
G2889		A2896		U2579			U2188	U		
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		U2898		U2581			G2190	U		



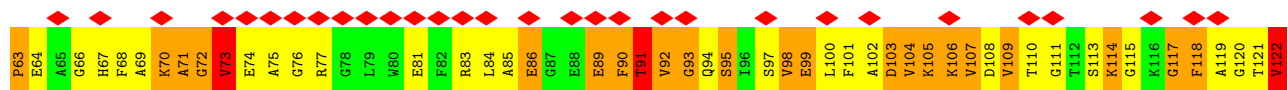
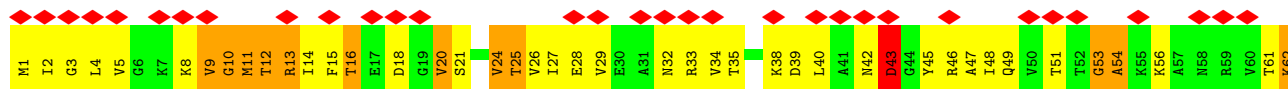
• Molecule 10: 5S ribosomal RNA

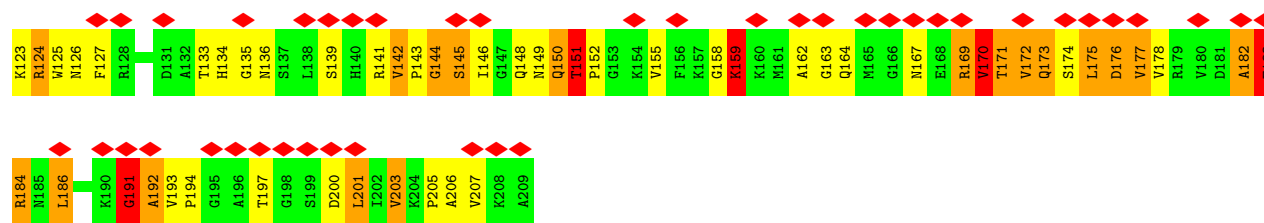


• Molecule 11: 50S ribosomal protein L2

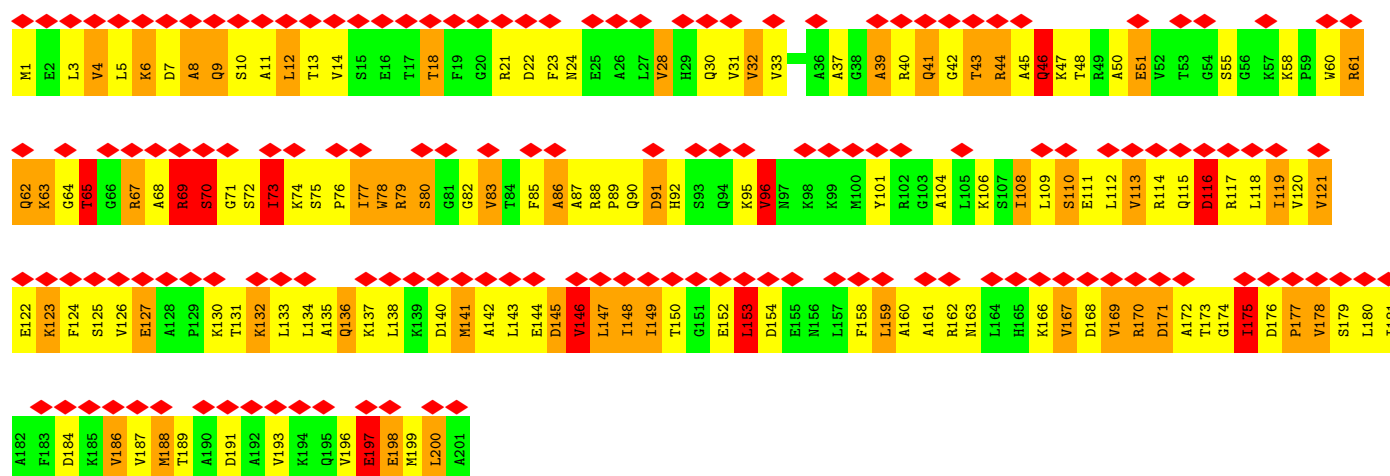
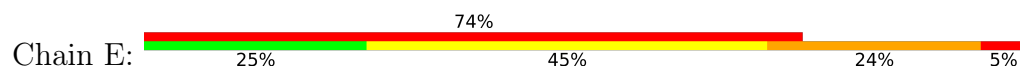


• Molecule 12: 50S ribosomal protein L3

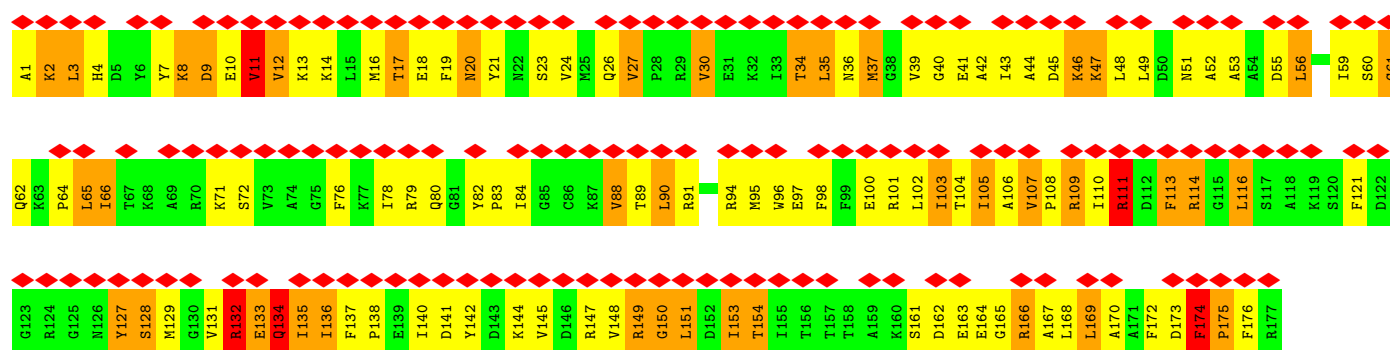
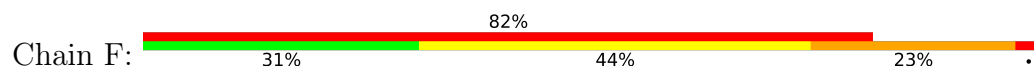




• Molecule 13: 50S ribosomal protein L4

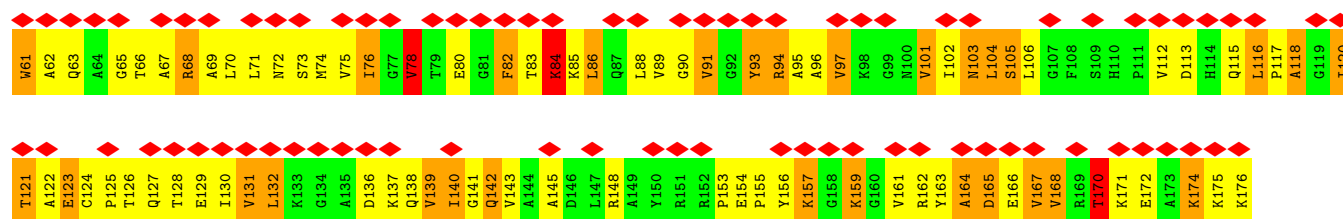


• Molecule 14: 50S ribosomal protein L5



• Molecule 15: 50S ribosomal protein L6

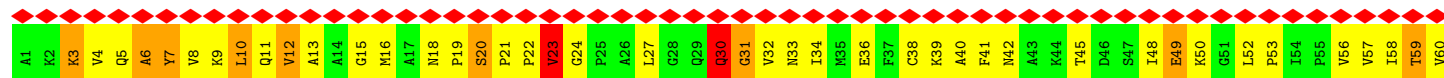




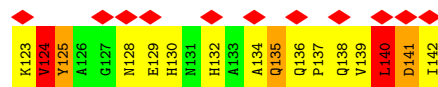
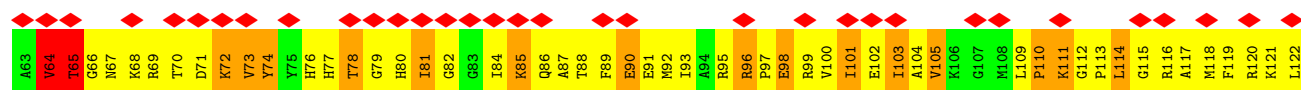
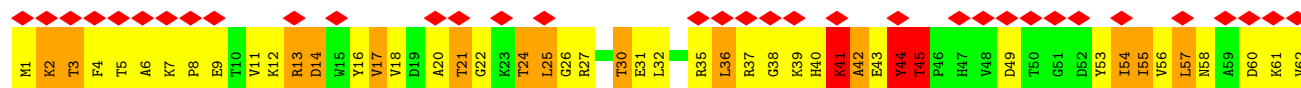
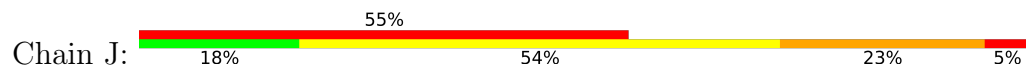
• Molecule 16: 50S ribosomal protein L9



• Molecule 17: 50S ribosomal protein L11



• Molecule 18: 50S ribosomal protein L13

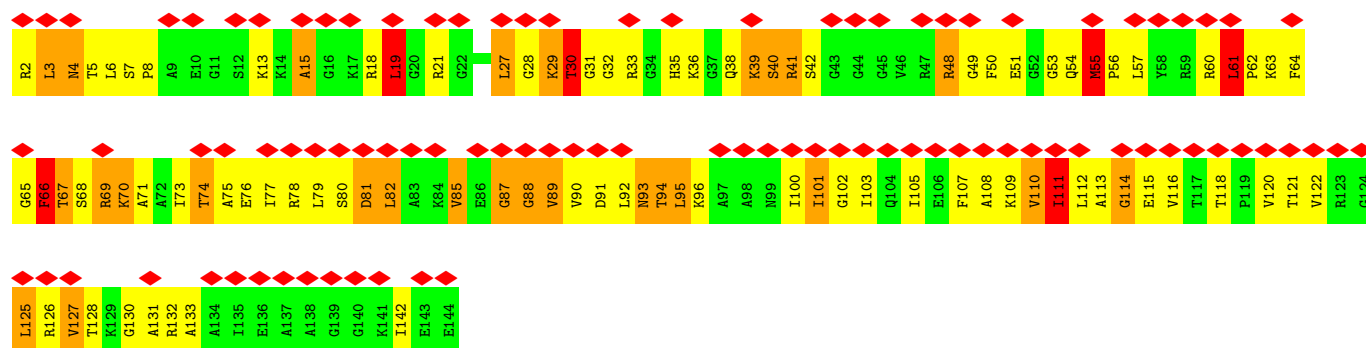


• Molecule 19: 50S ribosomal protein L14

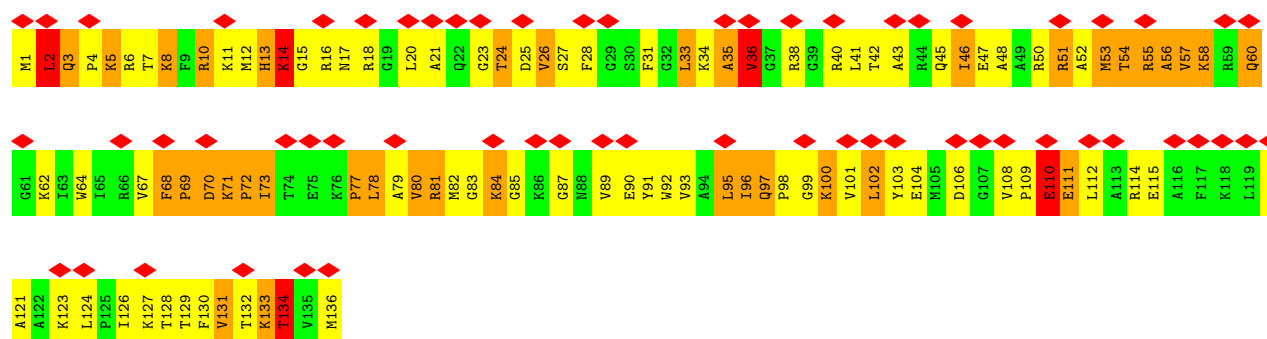
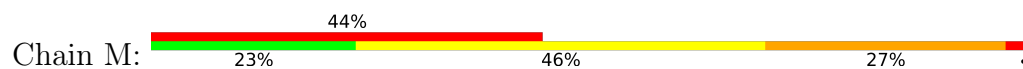




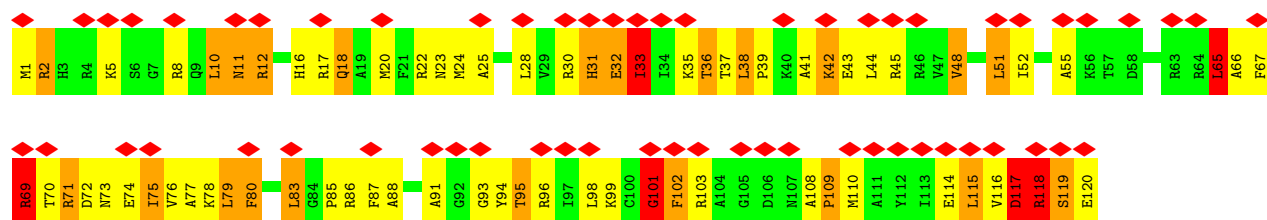
• Molecule 20: 50S ribosomal protein L15



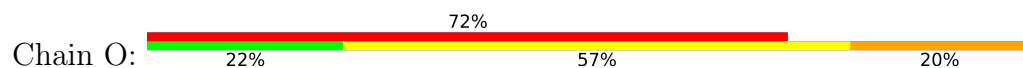
• Molecule 21: 50S ribosomal protein L16

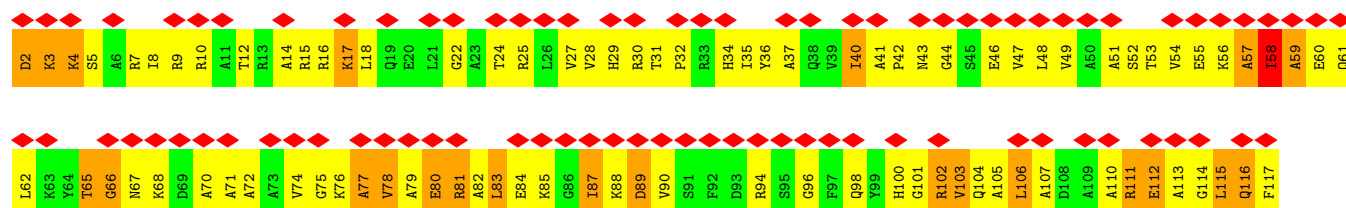


• Molecule 22: 50S ribosomal protein L17

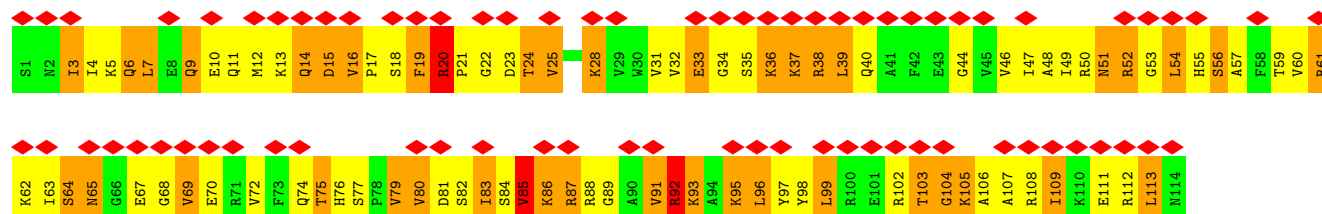
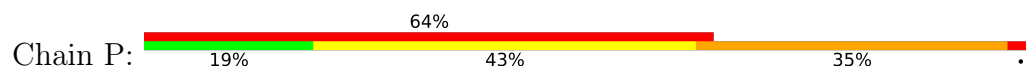


• Molecule 23: 50S ribosomal protein L18

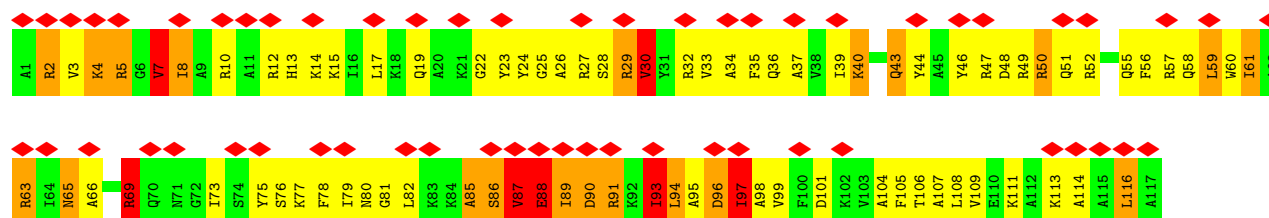




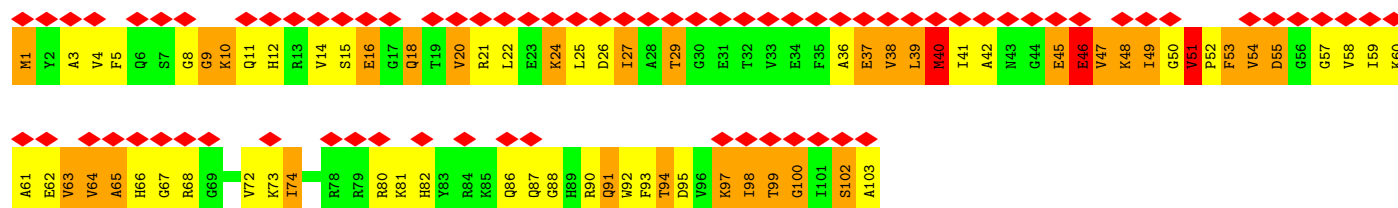
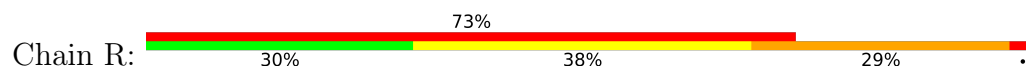
• Molecule 24: 50S ribosomal protein L19



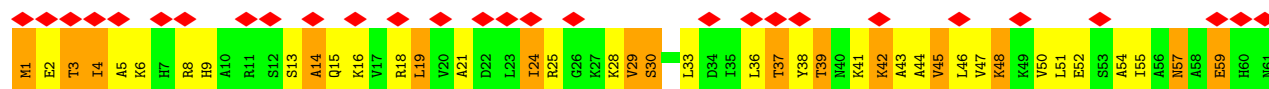
• Molecule 25: 50S ribosomal protein L20



• Molecule 26: 50S ribosomal protein L21

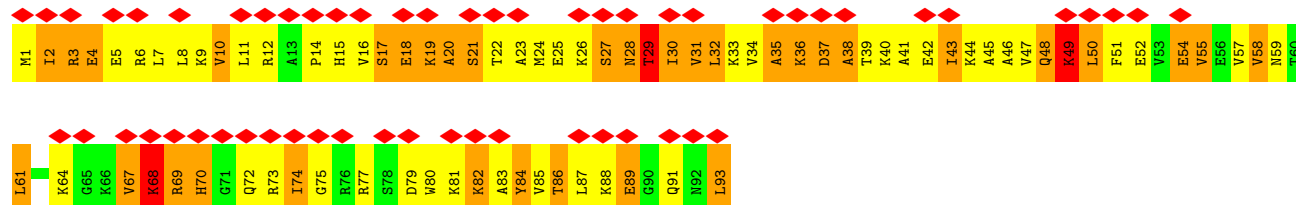
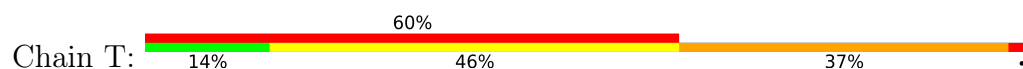


• Molecule 27: 50S ribosomal protein L22

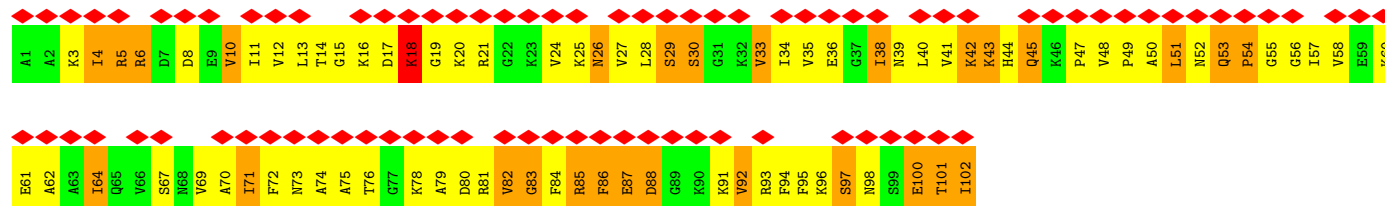
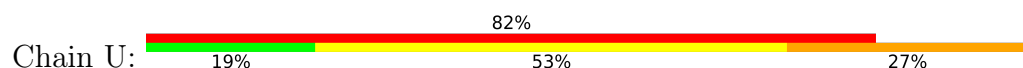




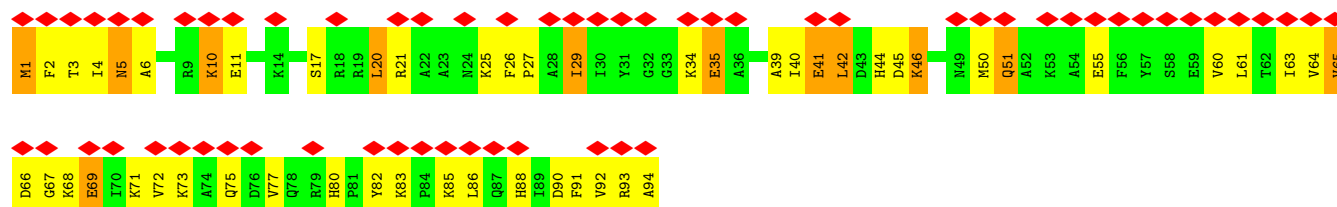
• Molecule 28: 50S ribosomal protein L23



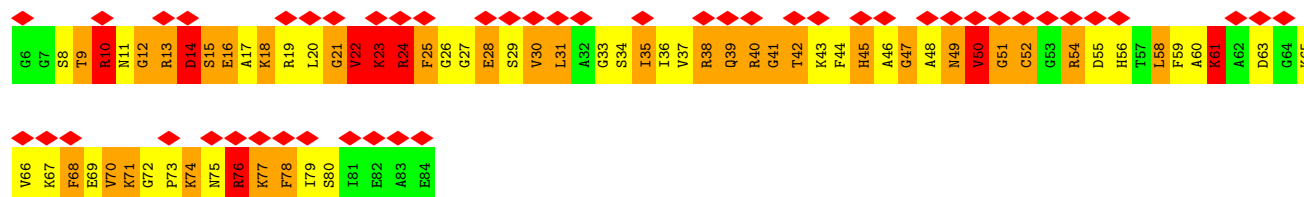
• Molecule 29: 50S ribosomal protein L24



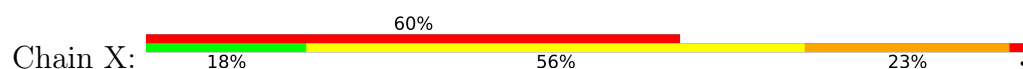
• Molecule 30: 50S ribosomal protein L25

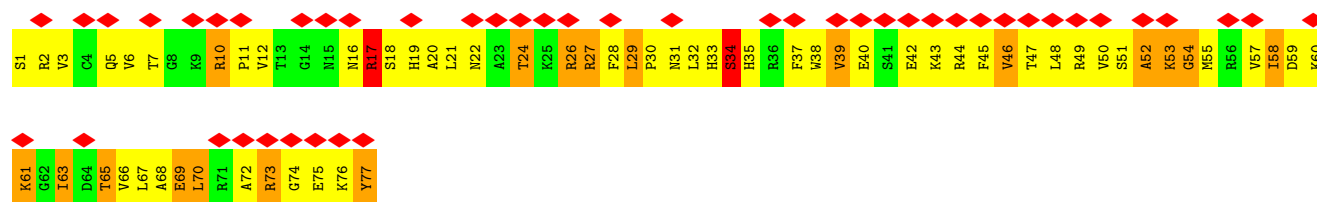


• Molecule 31: 50S ribosomal protein L27

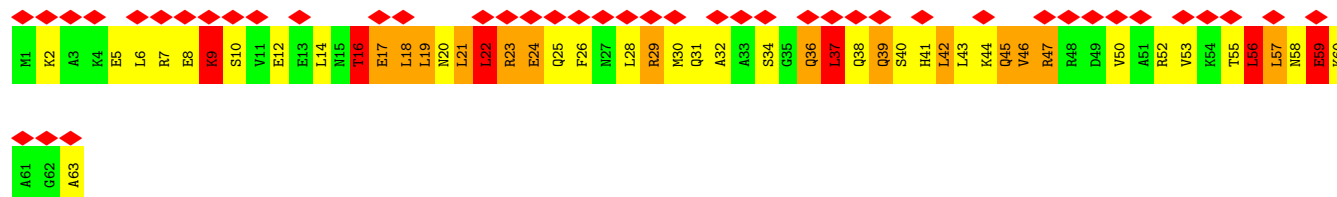
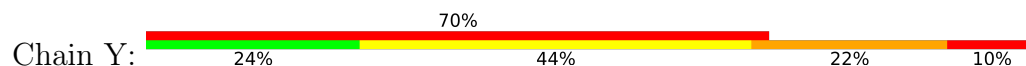


• Molecule 32: 50S ribosomal protein L28

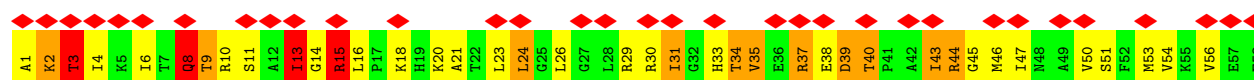




• Molecule 33: 50S ribosomal protein L29



• Molecule 34: 50S ribosomal protein L30



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	349744	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Defocus groups	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	148721	Depositor
Image detector	TVIPS TEMCAM-F416 (4k x 4k)	Depositor
Maximum map value	0.004	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.000	Depositor
Recommended contour level	0.0011	Depositor
Map size ($\text{\AA}$)	390.264, 390.264, 390.264	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0605, 1.0605, 1.0605	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ERY, MA6, UNL

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	0	0.70	0/450	1.10	5/599 (0.8%)
2	1	0.46	0/417	1.03	4/554 (0.7%)
3	2	0.74	0/380	1.06	2/498 (0.4%)
4	3	0.65	0/513	1.08	1/676 (0.1%)
5	4	0.54	0/303	0.97	0/397
6	5	0.27	0/18	0.77	0/26
8	7	0.45	0/65	1.14	1/99 (1.0%)
9	A	0.49	1/68599 (0.0%)	1.21	848/107011 (0.8%)
10	B	0.45	0/2801	1.15	32/4365 (0.7%)
11	C	0.63	0/2122	1.17	13/2852 (0.5%)
12	D	0.80	1/1586 (0.1%)	1.15	8/2134 (0.4%)
13	E	0.65	0/1571	1.05	5/2113 (0.2%)
14	F	0.42	0/1435	0.91	3/1926 (0.2%)
15	G	0.50	0/1343	0.93	2/1816 (0.1%)
16	H	0.40	0/436	0.88	4/586 (0.7%)
17	I	0.35	0/1046	0.88	3/1410 (0.2%)
18	J	0.79	0/1152	1.30	14/1551 (0.9%)
19	K	0.73	0/948	1.19	5/1268 (0.4%)
20	L	0.70	1/1054 (0.1%)	1.24	8/1403 (0.6%)
21	M	0.73	0/1093	1.16	5/1460 (0.3%)
22	N	0.77	0/974	1.17	7/1301 (0.5%)
23	O	0.58	0/902	1.01	4/1209 (0.3%)
24	P	0.67	0/929	1.08	3/1242 (0.2%)
25	Q	0.88	0/960	1.20	7/1278 (0.5%)
26	R	0.78	1/829 (0.1%)	1.17	5/1107 (0.5%)
27	S	0.85	0/864	1.14	2/1156 (0.2%)
28	T	0.65	0/745	1.09	1/994 (0.1%)
29	U	0.58	0/788	1.09	3/1051 (0.3%)
30	V	0.61	0/766	0.95	1/1025 (0.1%)
31	W	0.85	1/603 (0.2%)	1.21	4/797 (0.5%)
32	X	0.58	0/635	1.04	2/848 (0.2%)
33	Y	0.48	0/510	0.90	4/677 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	Z	0.80	0/453	1.30	5/605 (0.8%)
All	All	0.54	5/97290 (0.0%)	1.18	1011/146034 (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
12	D	0	1
18	J	0	1
22	N	0	1
All	All	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	W	50	VAL	CA-CB	6.67	1.63	1.54
20	L	30	THR	CA-CB	6.66	1.62	1.54
26	R	86	GLN	CB-CG	6.54	1.72	1.52
12	D	172	VAL	CA-CB	-5.59	1.49	1.55
9	A	2807	U	C1'-N1	-5.18	1.40	1.48

The worst 5 of 1011 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	2061	G	C4'-C3'-O3'	-16.34	84.89	109.40
9	A	2848	G	P-O3'-C3'	13.27	140.11	120.20
9	A	2505	G	O3'-P-O5'	-13.21	84.18	104.00
9	A	1603	A	P-O3'-C3'	-12.99	100.71	120.20
9	A	627	A	P-O3'-C3'	12.68	139.22	120.20

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
12	D	191	GLY	Peptide
18	J	110	PRO	Peptide
22	N	101	GLY	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	444	0	461	57	0
2	1	410	0	440	73	0
3	2	377	0	418	31	0
4	3	504	0	574	70	0
5	4	302	0	341	47	0
6	5	41	0	27	3	0
7	6	8	0	0	3	0
8	7	59	0	35	3	0
9	A	61251	0	30809	3073	0
10	B	2506	0	1271	107	0
11	C	2083	0	2157	332	0
12	D	1565	0	1616	280	0
13	E	1552	0	1619	205	0
14	F	1411	0	1447	215	0
15	G	1323	0	1374	229	0
16	H	431	0	451	88	0
17	I	1032	0	1088	136	0
18	J	1129	0	1162	225	0
19	K	939	0	1012	158	0
20	L	1045	0	1117	178	0
21	M	1074	0	1157	157	0
22	N	961	0	1000	124	0
23	O	892	0	923	119	0
24	P	917	0	965	192	0
25	Q	947	0	1022	202	0
26	R	816	0	839	151	0
27	S	857	0	922	94	0
28	T	739	0	807	163	0
29	U	780	0	834	102	0
30	V	753	0	780	63	0
31	W	596	0	610	288	0
32	X	625	0	655	113	0
33	Y	509	0	543	79	0
34	Z	449	0	491	51	0
35	5	4	0	0	0	0
36	A	51	0	67	4	0
All	All	89382	0	59034	6838	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 46.

The worst 5 of 6838 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)
24:P:50:ARG:CG	24:P:57:ALA:H	1.24	1.48
24:P:50:ARG:HD2	24:P:51:ASN:N	1.27	1.41
24:P:50:ARG:HG2	24:P:57:ALA:N	1.13	1.40
25:Q:63:ARG:NH1	25:Q:96:ASP:HA	1.37	1.35
12:D:114:LYS:N	12:D:114:LYS:HE3	1.41	1.33

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	0	54/56 (96%)	41 (76%)	9 (17%)	4 (7%)	1	10
2	1	48/50 (96%)	37 (77%)	6 (12%)	5 (10%)	0	6
3	2	44/46 (96%)	37 (84%)	7 (16%)	0	100	100
4	3	62/64 (97%)	53 (86%)	5 (8%)	4 (6%)	1	12
5	4	36/38 (95%)	24 (67%)	9 (25%)	3 (8%)	0	9
11	C	269/271 (99%)	197 (73%)	47 (18%)	25 (9%)	0	8
12	D	207/209 (99%)	141 (68%)	32 (16%)	34 (16%)	0	2
13	E	199/201 (99%)	145 (73%)	34 (17%)	20 (10%)	0	7
14	F	175/177 (99%)	123 (70%)	36 (21%)	16 (9%)	0	8
15	G	174/176 (99%)	111 (64%)	38 (22%)	25 (14%)	0	3
16	H	54/56 (96%)	21 (39%)	13 (24%)	20 (37%)	0	0
17	I	139/141 (99%)	84 (60%)	41 (30%)	14 (10%)	0	7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	J	140/142 (99%)	104 (74%)	24 (17%)	12 (9%)	0	9
19	K	120/122 (98%)	88 (73%)	18 (15%)	14 (12%)	0	4
20	L	141/143 (99%)	100 (71%)	30 (21%)	11 (8%)	1	10
21	M	134/136 (98%)	96 (72%)	18 (13%)	20 (15%)	0	3
22	N	118/120 (98%)	91 (77%)	16 (14%)	11 (9%)	0	8
23	O	114/116 (98%)	85 (75%)	18 (16%)	11 (10%)	0	7
24	P	112/114 (98%)	78 (70%)	20 (18%)	14 (12%)	0	4
25	Q	115/117 (98%)	100 (87%)	7 (6%)	8 (7%)	1	11
26	R	101/103 (98%)	76 (75%)	14 (14%)	11 (11%)	0	6
27	S	108/110 (98%)	89 (82%)	14 (13%)	5 (5%)	2	16
28	T	91/93 (98%)	49 (54%)	26 (29%)	16 (18%)	0	2
29	U	100/102 (98%)	66 (66%)	15 (15%)	19 (19%)	0	2
30	V	92/94 (98%)	75 (82%)	15 (16%)	2 (2%)	5	29
31	W	77/79 (98%)	31 (40%)	22 (29%)	24 (31%)	0	0
32	X	75/77 (97%)	58 (77%)	10 (13%)	7 (9%)	0	8
33	Y	61/63 (97%)	38 (62%)	15 (25%)	8 (13%)	0	4
34	Z	56/58 (97%)	47 (84%)	5 (9%)	4 (7%)	1	11
All	All	3216/3274 (98%)	2285 (71%)	564 (18%)	367 (11%)	1	5

5 of 367 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	51	ARG
1	0	54	ILE
2	1	16	THR
5	4	4	ARG
11	C	77	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	0	47/47 (100%)	36 (77%)	11 (23%)	1	5
2	1	45/45 (100%)	36 (80%)	9 (20%)	1	7
3	2	38/38 (100%)	29 (76%)	9 (24%)	1	4
4	3	51/51 (100%)	42 (82%)	9 (18%)	2	9
5	4	34/34 (100%)	28 (82%)	6 (18%)	2	9
11	C	216/216 (100%)	169 (78%)	47 (22%)	1	6
12	D	164/164 (100%)	131 (80%)	33 (20%)	1	7
13	E	165/165 (100%)	106 (64%)	59 (36%)	0	1
14	F	148/148 (100%)	110 (74%)	38 (26%)	0	3
15	G	137/137 (100%)	99 (72%)	38 (28%)	0	3
16	H	44/44 (100%)	31 (70%)	13 (30%)	0	2
17	I	109/109 (100%)	95 (87%)	14 (13%)	4	15
18	J	116/116 (100%)	87 (75%)	29 (25%)	0	4
19	K	103/103 (100%)	77 (75%)	26 (25%)	0	4
20	L	102/102 (100%)	76 (74%)	26 (26%)	0	3
21	M	109/109 (100%)	78 (72%)	31 (28%)	0	2
22	N	100/100 (100%)	79 (79%)	21 (21%)	1	6
23	O	86/86 (100%)	67 (78%)	19 (22%)	1	6
24	P	99/99 (100%)	64 (65%)	35 (35%)	0	1
25	Q	89/89 (100%)	61 (68%)	28 (32%)	0	2
26	R	84/84 (100%)	59 (70%)	25 (30%)	0	2
27	S	93/93 (100%)	67 (72%)	26 (28%)	0	3
28	T	80/80 (100%)	52 (65%)	28 (35%)	0	1
29	U	83/83 (100%)	66 (80%)	17 (20%)	1	7
30	V	78/78 (100%)	63 (81%)	15 (19%)	1	8
31	W	59/59 (100%)	39 (66%)	20 (34%)	0	1
32	X	67/67 (100%)	51 (76%)	16 (24%)	1	4
33	Y	55/55 (100%)	39 (71%)	16 (29%)	0	2
34	Z	48/48 (100%)	34 (71%)	14 (29%)	0	2
All	All	2649/2649 (100%)	1971 (74%)	678 (26%)	2	3

5 of 678 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	P	80	VAL
28	T	67	VAL
25	Q	8	ILE
24	P	79	VAL
26	R	72	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
18	J	130	HIS
33	Y	15	ASN
22	N	11	ASN
32	X	22	ASN
29	U	65	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	B	115/118 (97%)	37 (32%)	17 (14%)
6	5	1/2 (50%)	0	0
8	7	2/3 (66%)	0	0
9	A	2848/2904 (98%)	986 (34%)	423 (14%)
All	All	2966/3027 (97%)	1023 (34%)	440 (14%)

5 of 1023 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
9	A	10	A
9	A	13	A
9	A	14	A
9	A	15	G
9	A	23	G

5 of 440 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
9	A	1497	U
9	A	1865	U
10	B	108	A
9	A	2728	U
9	A	1554	U

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	$\# Z > 2$
6	MA6	5	76	6,9,35	23,26,27	0.45	0	33,38,41	0.94	1 (3%)

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
6	MA6	5	76	6,9,35	-	0/11/29/30	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
6	5	76	MA6	C2-N1-C6	2.91	118.94	111.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	5	76	MA6	2	0

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 1 is unknown - leaving 1 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
36	ERY	A	9000	-	53,53,53	0.82	1 (1%)	82,82,82	1.69	18 (21%)

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
36	ERY	A	9000	-	-	9/72/107/107	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	A	9000	ERY	C6-C5	2.43	1.59	1.55

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A	9000	ERY	C25-C24-C23	-5.06	102.75	110.02
36	A	9000	ERY	O7-C5-C6	-4.99	100.45	106.40
36	A	9000	ERY	O2-C1-O1	-3.68	117.30	123.95
36	A	9000	ERY	C3-C2-C1	-3.45	102.96	109.93
36	A	9000	ERY	C27-C26-C25	-3.17	108.47	113.27

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
36	A	9000	ERY	C15-C16-O5-C20
36	A	9000	ERY	C19-C16-O5-C20

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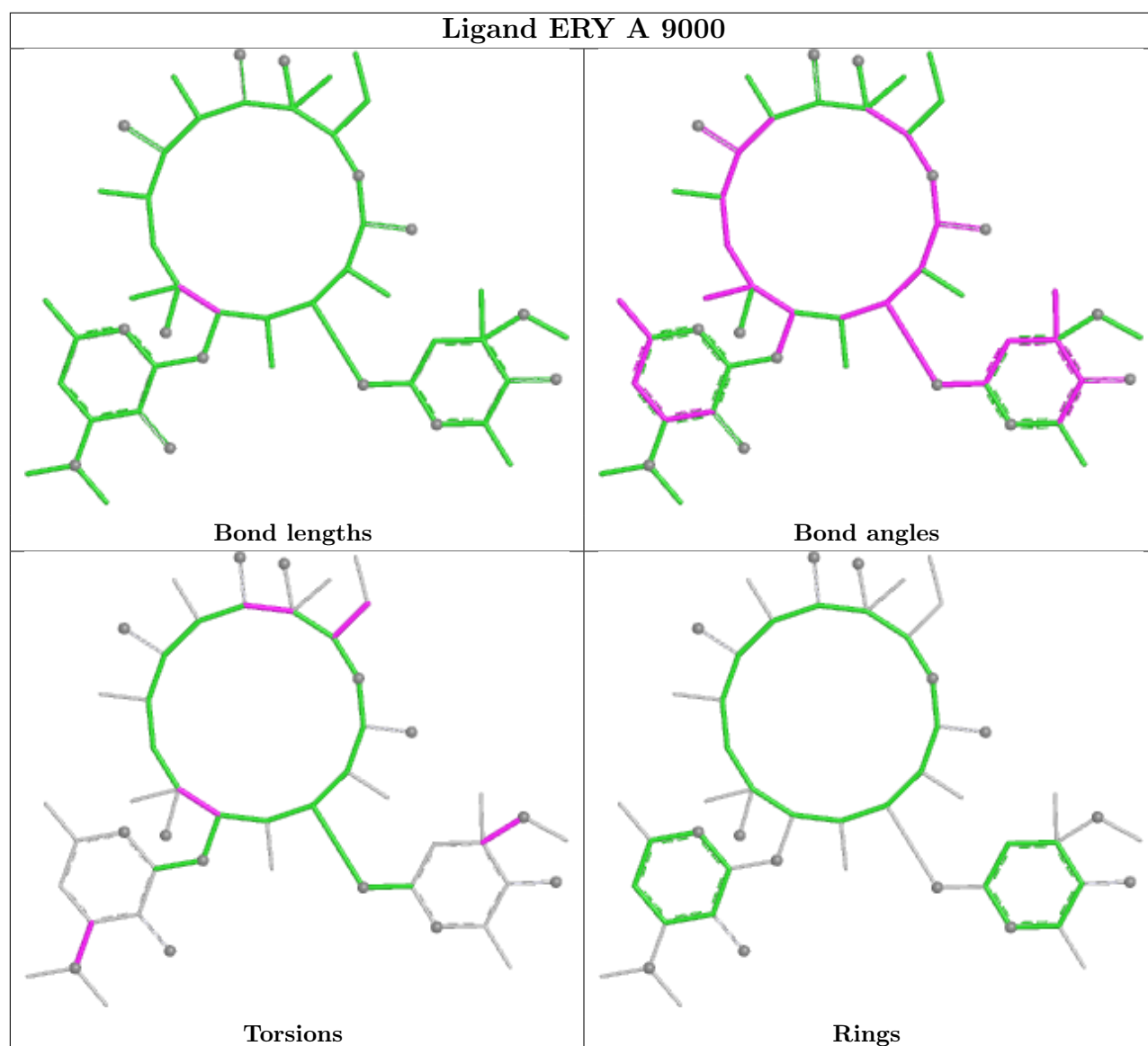
Mol	Chain	Res	Type	Atoms
36	A	9000	ERY	C10-C11-C12-O13
36	A	9000	ERY	C25-C24-N1-C28
36	A	9000	ERY	C4-C5-C6-C32

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	A	9000	ERY	4	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.



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.

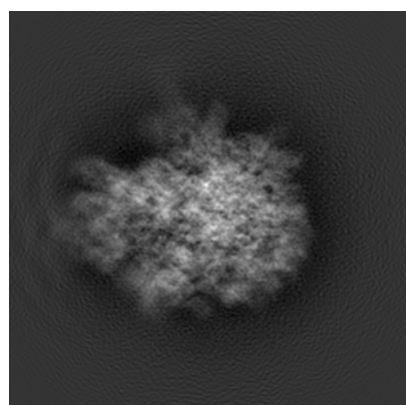
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5771. These allow visual inspection of the internal detail of the map and identification of artifacts.

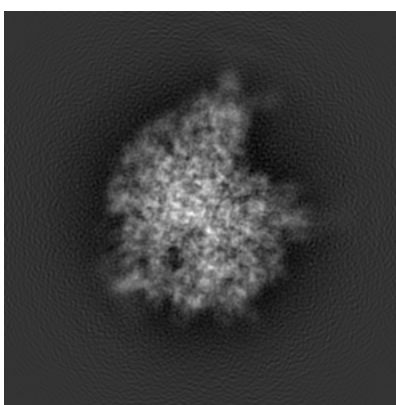
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

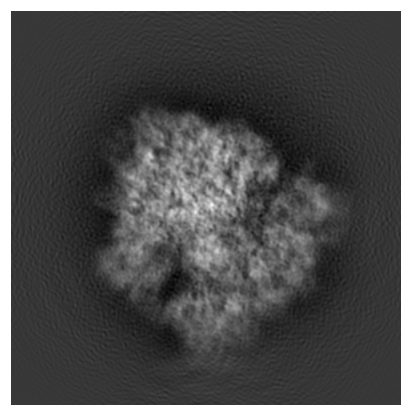
6.1.1 Primary map



X



Y

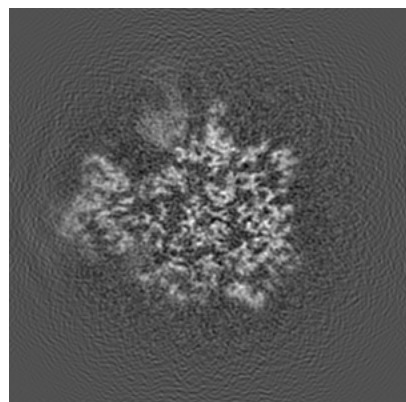


Z

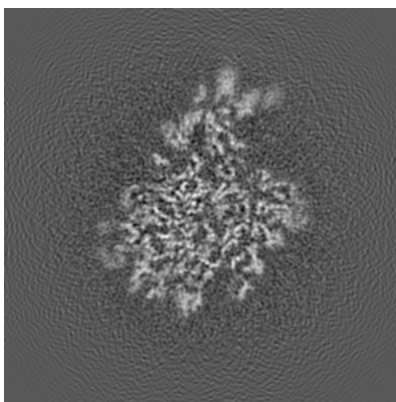
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

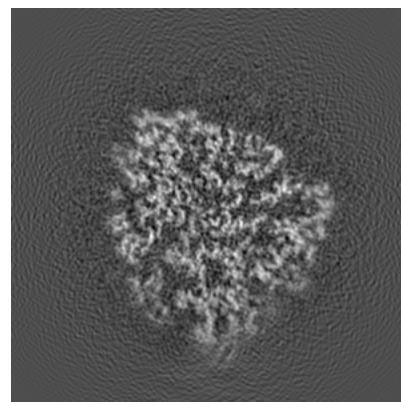
6.2.1 Primary map



X Index: 184



Y Index: 184

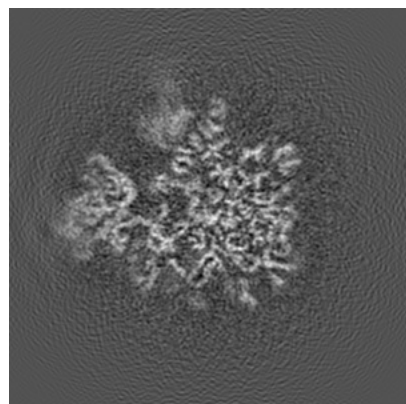


Z Index: 184

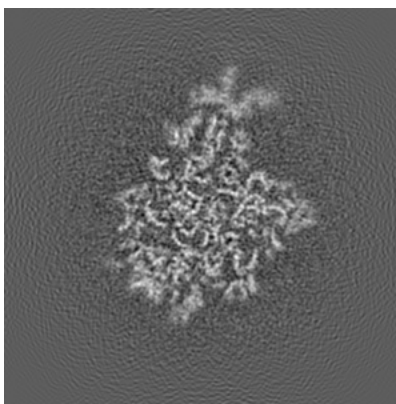
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

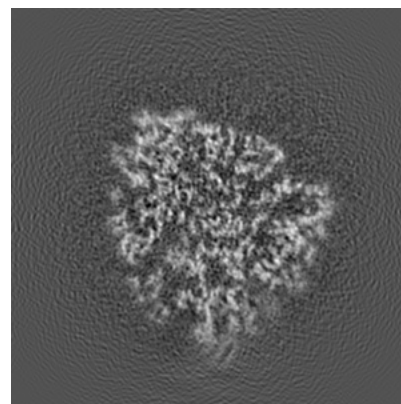
6.3.1 Primary map



X Index: 180



Y Index: 189

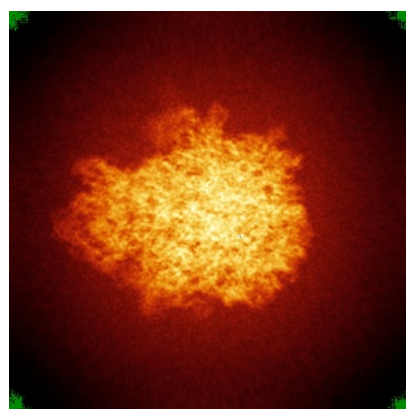


Z Index: 183

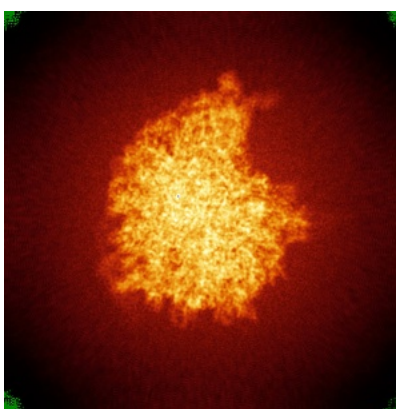
The images above show the largest variance slices of the map in three orthogonal directions.

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

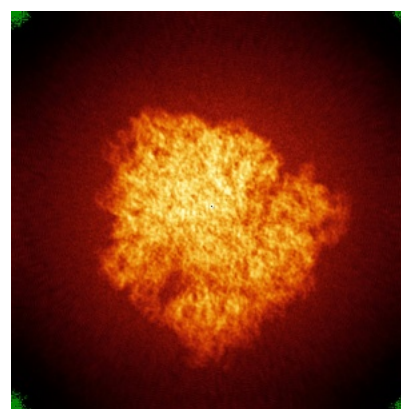
6.4.1 Primary map



X



Y

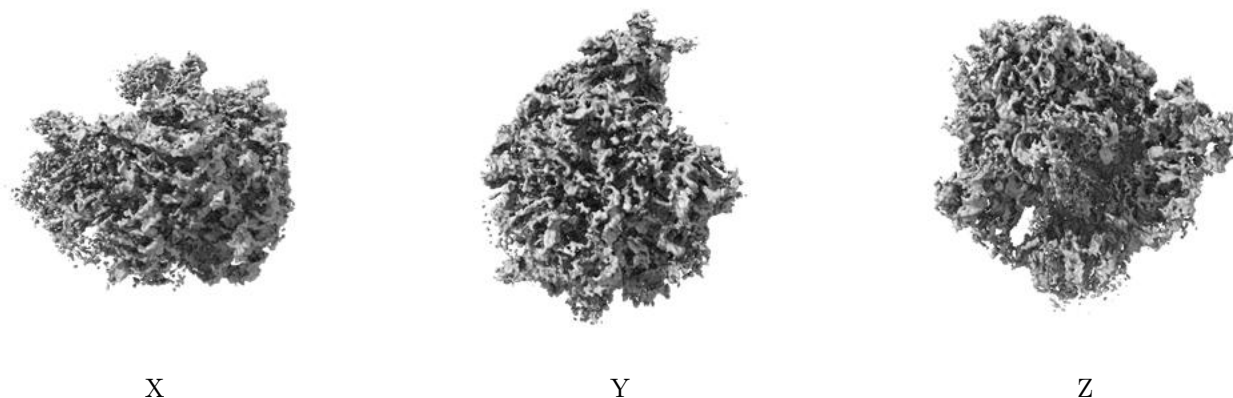


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.0011. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

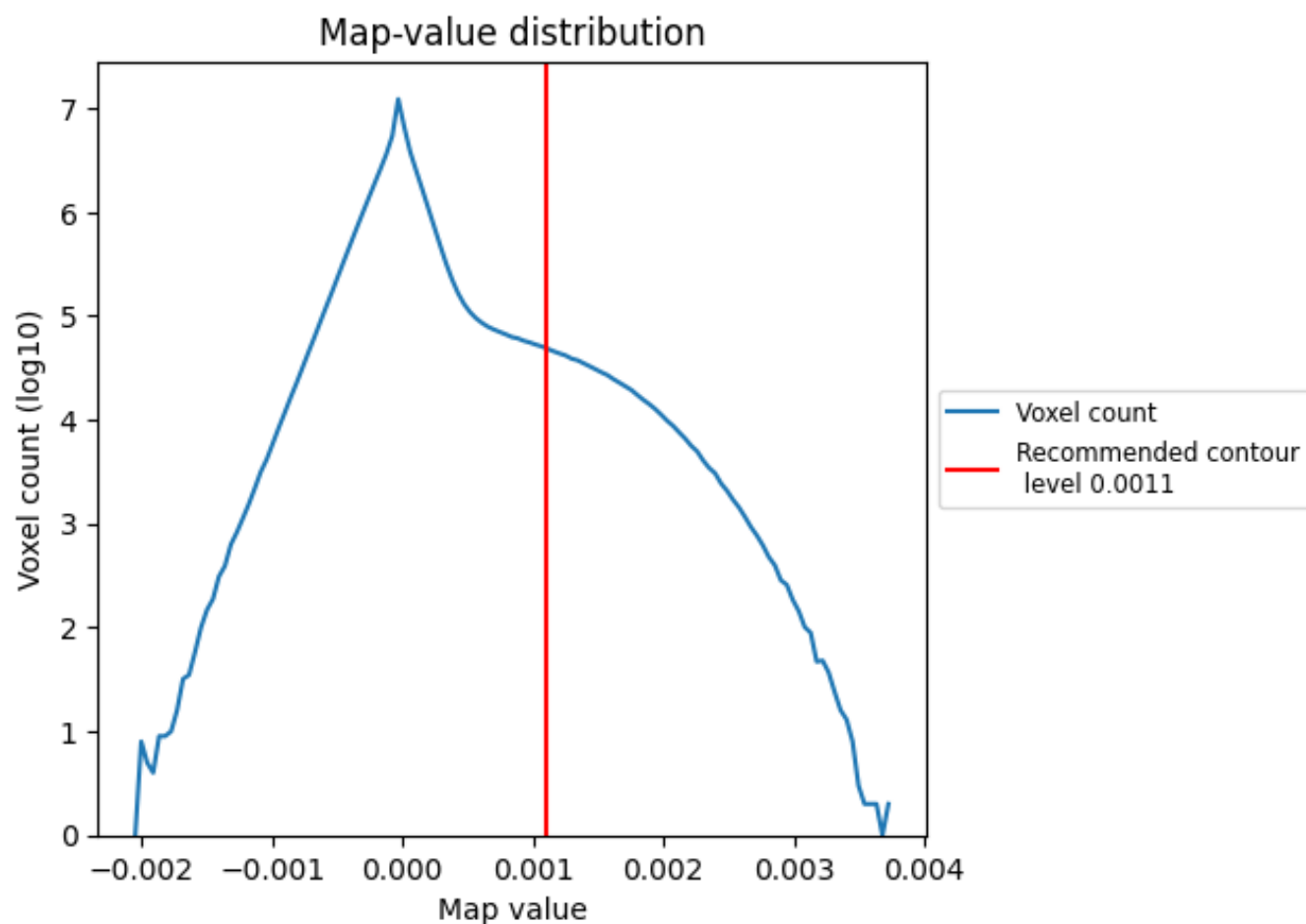
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

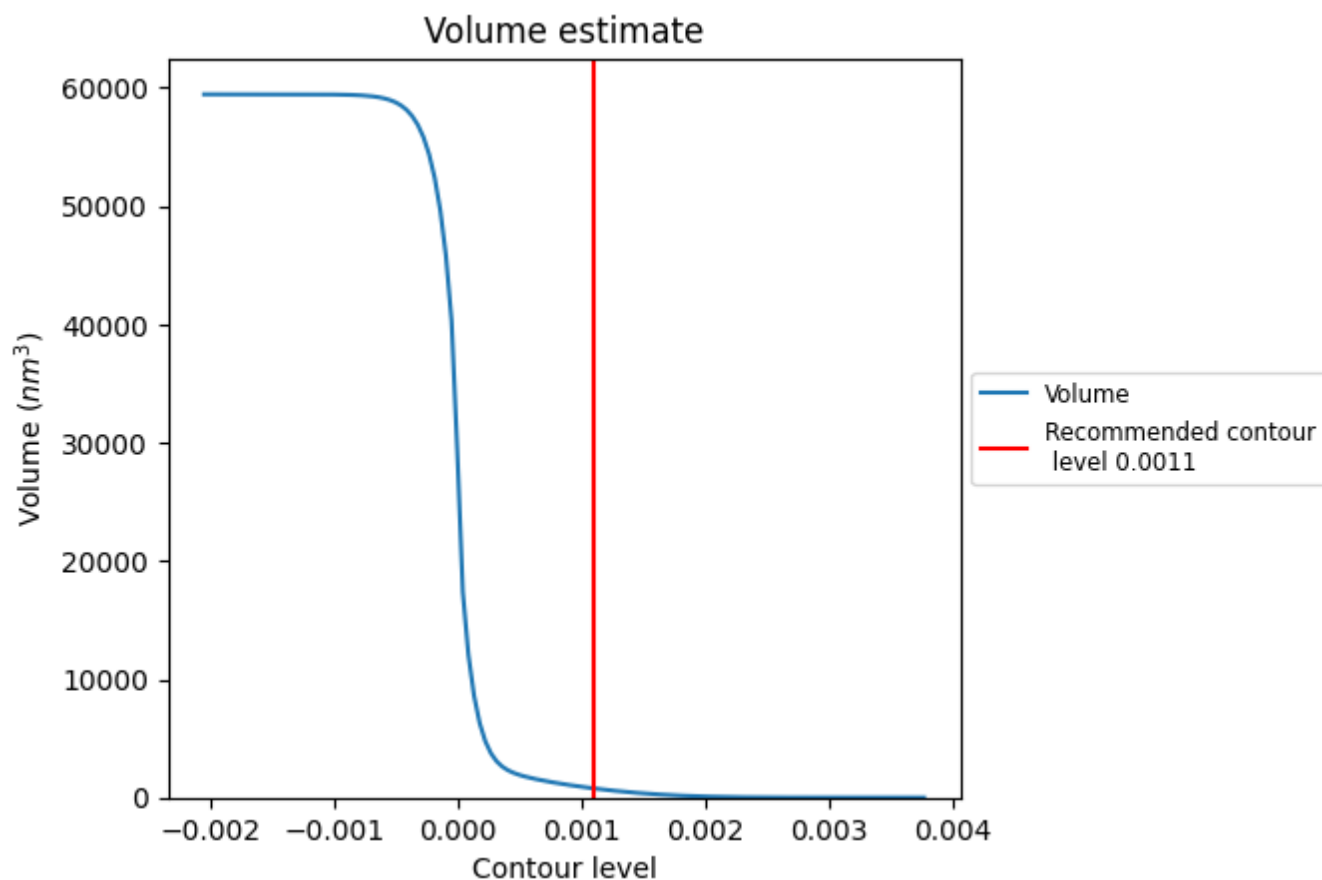
This section contains the results of statistical analysis of the map.

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.

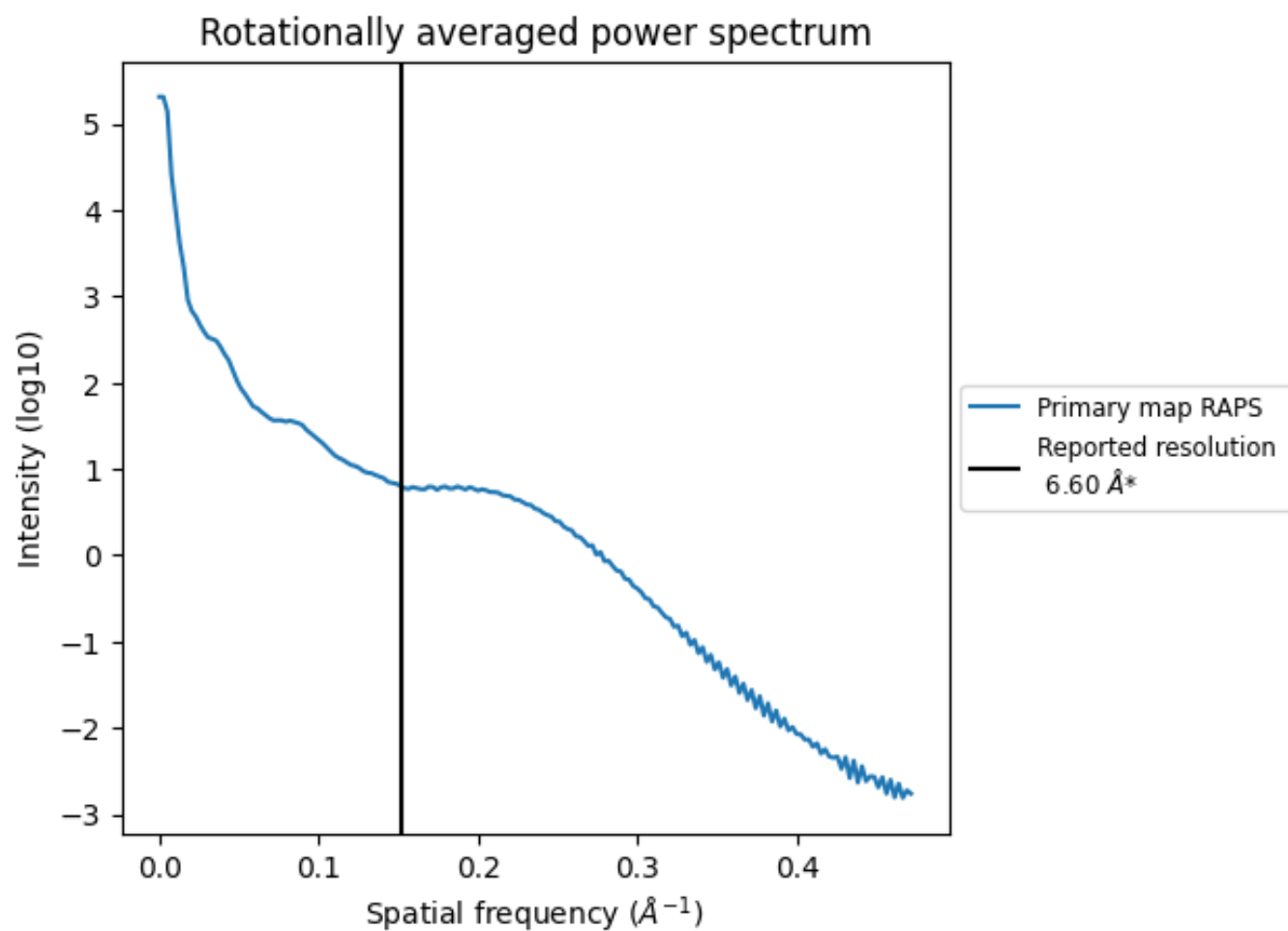
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 776 nm³; this corresponds to an approximate mass of 701 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 0.152 Å⁻¹

8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5771 and PDB model 3J5L. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

This section was not generated.

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

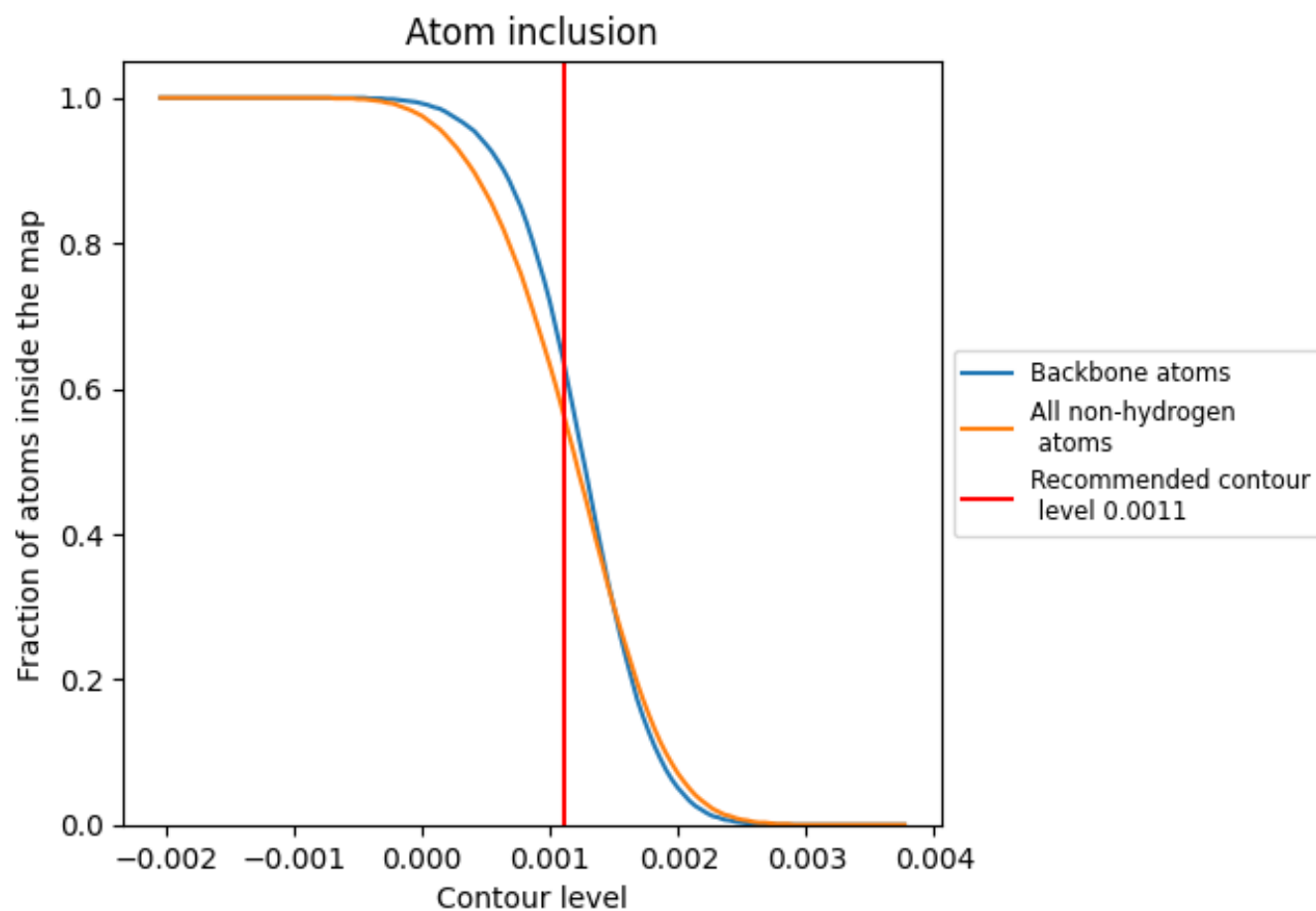


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 64% of all backbone atoms, 57% 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 (0.0011) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5670	 0.2470
0	 0.3640	 0.2200
1	 0.3260	 0.1940
2	 0.4250	 0.2620
3	 0.3690	 0.2420
4	 0.4250	 0.2410
5	 0.4440	 0.2410
6	 0.6250	 0.3380
7	 0.6100	 0.3120
A	 0.6650	 0.2640
B	 0.6360	 0.2360
C	 0.3950	 0.2600
D	 0.3820	 0.2500
E	 0.2490	 0.1960
F	 0.1990	 0.1110
G	 0.2820	 0.1940
H	 0.0900	 0.1270
I	 0.0040	 0.0030
J	 0.3740	 0.2450
K	 0.3490	 0.2320
L	 0.3120	 0.2380
M	 0.4200	 0.2470
N	 0.3990	 0.2410
O	 0.2720	 0.1930
P	 0.3450	 0.2360
Q	 0.3940	 0.2070
R	 0.2660	 0.2300
S	 0.4040	 0.2150
T	 0.3150	 0.2000
U	 0.2130	 0.1780
V	 0.3280	 0.2110
W	 0.3450	 0.2220
X	 0.3790	 0.2340
Y	 0.2940	 0.2020
Z	 0.3390	 0.2070

