wwPDB EM Validation Summary Report ⓘ

Jul 15, 2024 – 08:10 pm BST

PDB ID	:	7ZS5
EMDB ID	:	EMD-14926
Title	:	Structure of 60S ribosomal subunit from S. cerevisiae with eIF6 and tRNA
Authors	:	Best, K.M.; Ikeuchi, K.; Kater, L.; Best, D.M.; Musial, J.; Matsuo, Y.; Berninghausen, O.; Becker, T.; Inada, T.; Beckmann, R.
Deposited on	:	2022-05-06
Resolution	:	3.20 Å(reported)
Based on initial models	:	6HD7, 6SNT, 1G62

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:

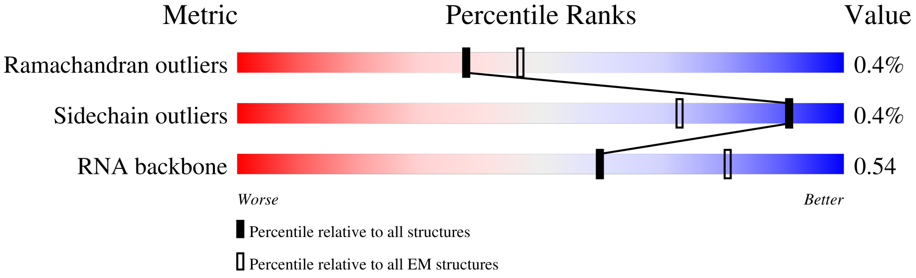
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

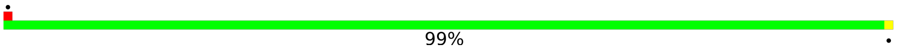
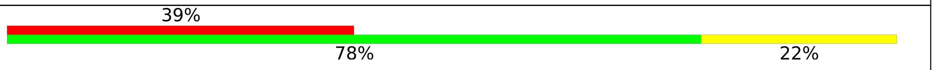
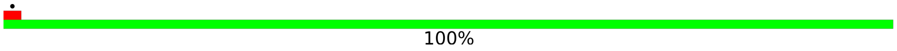
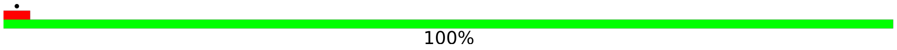
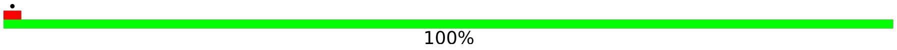
The reported resolution of this entry is 3.20 Å.

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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	1	3396	
2	3	121	
3	4	158	
4	A	224	
5	2	76	
6	BA	105	
7	BB	91	
8	BC	252	

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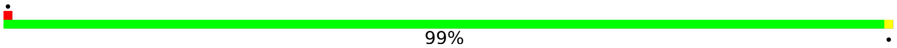
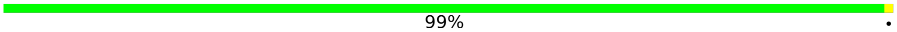
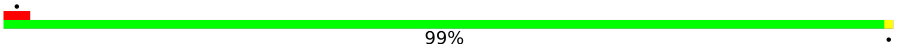
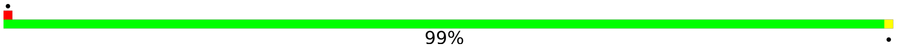
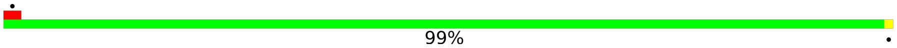
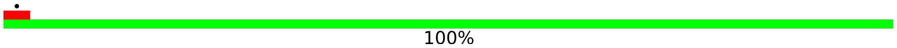
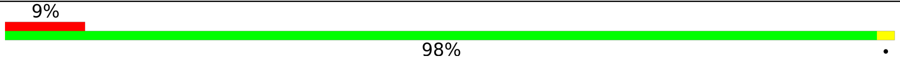
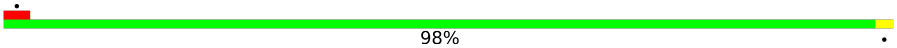
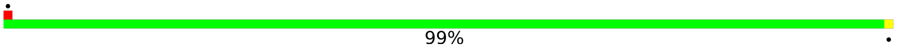
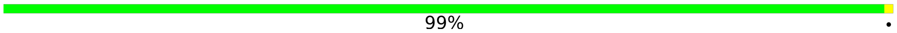
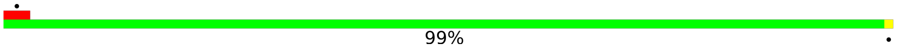
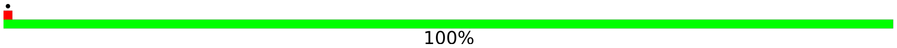
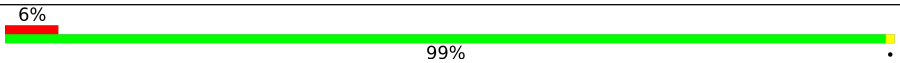
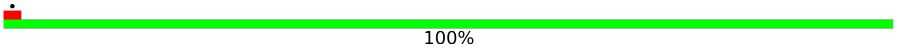
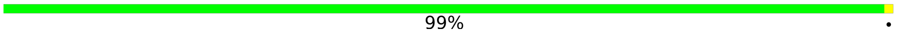
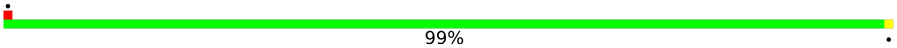
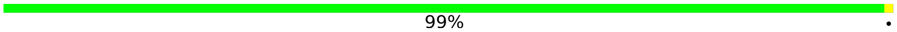
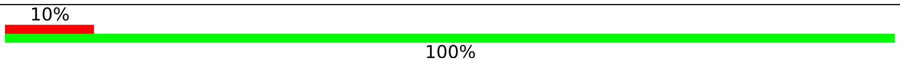
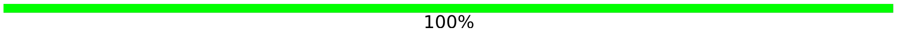
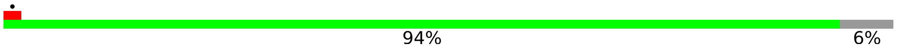
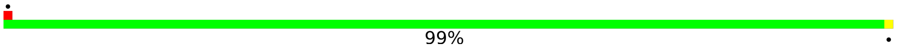
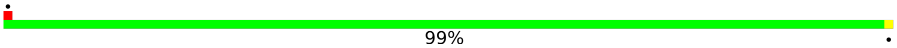
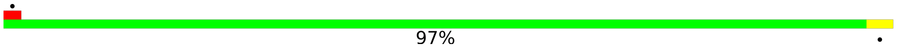
Mol	Chain	Length	Quality of chain
9	BD	386	 99%
10	BE	361	 99%
11	BF	296	 99%
12	BG	176	 89% 11%
13	BH	222	 99%
14	BI	233	 99%
15	BJ	191	 100%
16	BL	169	 9% 98%
17	BM	193	 98%
18	BN	136	 99%
19	BO	203	 100%
20	BP	197	 99%
21	BQ	183	 99%
22	BR	185	 100%
23	BS	160	 6% 99%
24	BT	172	 100%
25	BU	159	 99%
26	BV	100	 99%
27	BW	136	 99%
28	BX	69	 10% 100%
29	BY	121	 100%
30	BZ	127	 94% 6%
31	Ba	135	 99%
32	Bb	148	 99%
33	Bc	58	 97%

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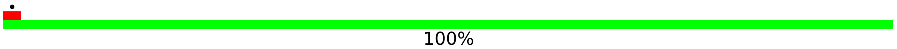
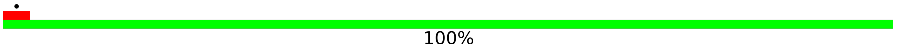
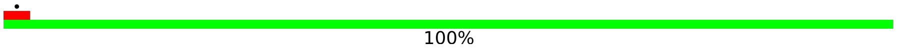
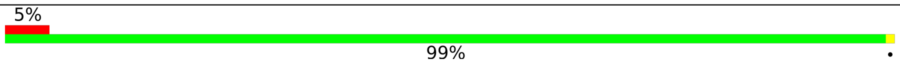
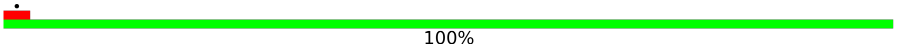
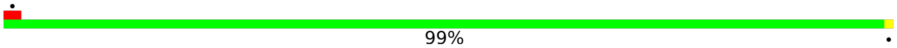
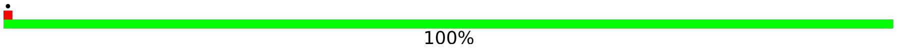
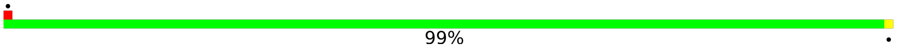
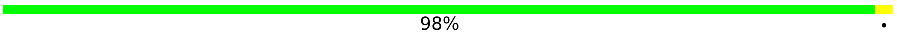
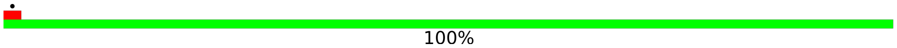
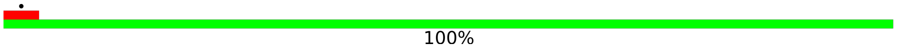
Mol	Chain	Length	Quality of chain
34	Bd	97	
35	Be	109	
36	Bf	127	
37	Bg	106	
38	Bh	112	
39	Bi	119	
40	Bj	99	
41	Bk	87	
42	Bl	77	
43	Bm	50	
44	Bn	52	
45	BK	220	

2 Entry composition ⓘ

There are 47 unique types of molecules in this entry. The entry contains 127849 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 RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	3248	69452	31022	12494	22688	3248	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	3	121	2579	1152	461	845	121	0	0

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	4	158	3353	1500	586	1109	158	0	0

- Molecule 4 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	A	224	1633	1019	279	328	7	0	0

- Molecule 5 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	2	76	1619	722	288	533	76	0	0

- Molecule 6 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	BA	105	847	534	170	138	5	0	0

- Molecule 7 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	BB	91	694	429	138	121	6	0	0

- Molecule 8 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	BC	252	1914	1191	388	334	1	0	0

- Molecule 9 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	BD	386	3075	1950	584	533	8	0	0

- Molecule 10 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	BE	361	2748	1729	522	494	3	0	0

- Molecule 11 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	BF	296	2375	1501	414	458	2	0	0

- Molecule 12 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	BG	156	1239	800	222	216	1	0	0

- Molecule 13 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	BH	222	1784	1151	324	308	1	0	0

- Molecule 14 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
14	BI	233	1804	1151	323	327	3	0	0

- Molecule 15 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
15	BJ	191	1518	963	274	277	4	0	0

- Molecule 16 is a protein called 60S ribosomal protein L11-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	BL	169	1353	847	253	249	4	0	0

- Molecule 17 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	BM	193	1543	962	315	266	0	0

- Molecule 18 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	BN	136	1053	675	199	177	2	0	0

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	BO	203	1720	1077	361	281	1	0	0

- Molecule 20 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	BP	197	1555	1003	289	262	1	0	0

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	BQ	183	1420	882	281	257	0	0

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	BR	185	1441	908	290	241	2	0	0

- Molecule 23 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
23	BS	160	1286	797	269	220	0	0

- Molecule 24 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	BT	172	1445	930	267	244	4	0	0

- Molecule 25 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	BU	159	1276	805	246	221	4	0	0

- Molecule 26 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	BV	100	796	516	131	149	0	0

- Molecule 27 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
27	BW	136	1003	628	189	179	7	0	0

- Molecule 28 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	BX	69	553	355	108	89	1	0	0

- Molecule 29 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	BY	121	964	620	169	173	2	0	0

- Molecule 30 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	BZ	120	939	591	179	169	0	0

- Molecule 31 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
31	Ba	135	1092	710	202	180	0	0

- Molecule 32 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
32	Bb	148	1173	749	231	190	3	0	0

- Molecule 33 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
33	Bc	58	462	289	100	73	0	0

- Molecule 34 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	Bd	97	743	479	124	139	1	0	0

- Molecule 35 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Be	109	Total	C	N	O	S	0	0
			876	556	167	152	1		

- Molecule 36 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Bf	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 37 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Bg	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 38 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Bh	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 39 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Bi	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 40 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Bj	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 41 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Bk	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 42 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
42	Bl	77	612	391	115	106	0	0

- Molecule 43 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
43	Bm	50	436	272	97	65	2	0	0

- Molecule 44 is a protein called 60S ribosomal protein L40-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
44	Bn	52	417	259	86	67	5	0	0

- Molecule 45 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
45	BK	220	1770	1121	335	307	7	0	0

- Molecule 46 is UNKNOWN (three-letter code: UNK) (formula: $C_4H_9NO_2$).

Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
46	1	14	70	42	14	14	0
			Total	C	N	O	
46	BE	2	10	6	2	2	0
			Total	C	N	O	
46	BQ	4	20	12	4	4	0
			Total	C	N	O	
46	Bm	3	15	9	3	3	0

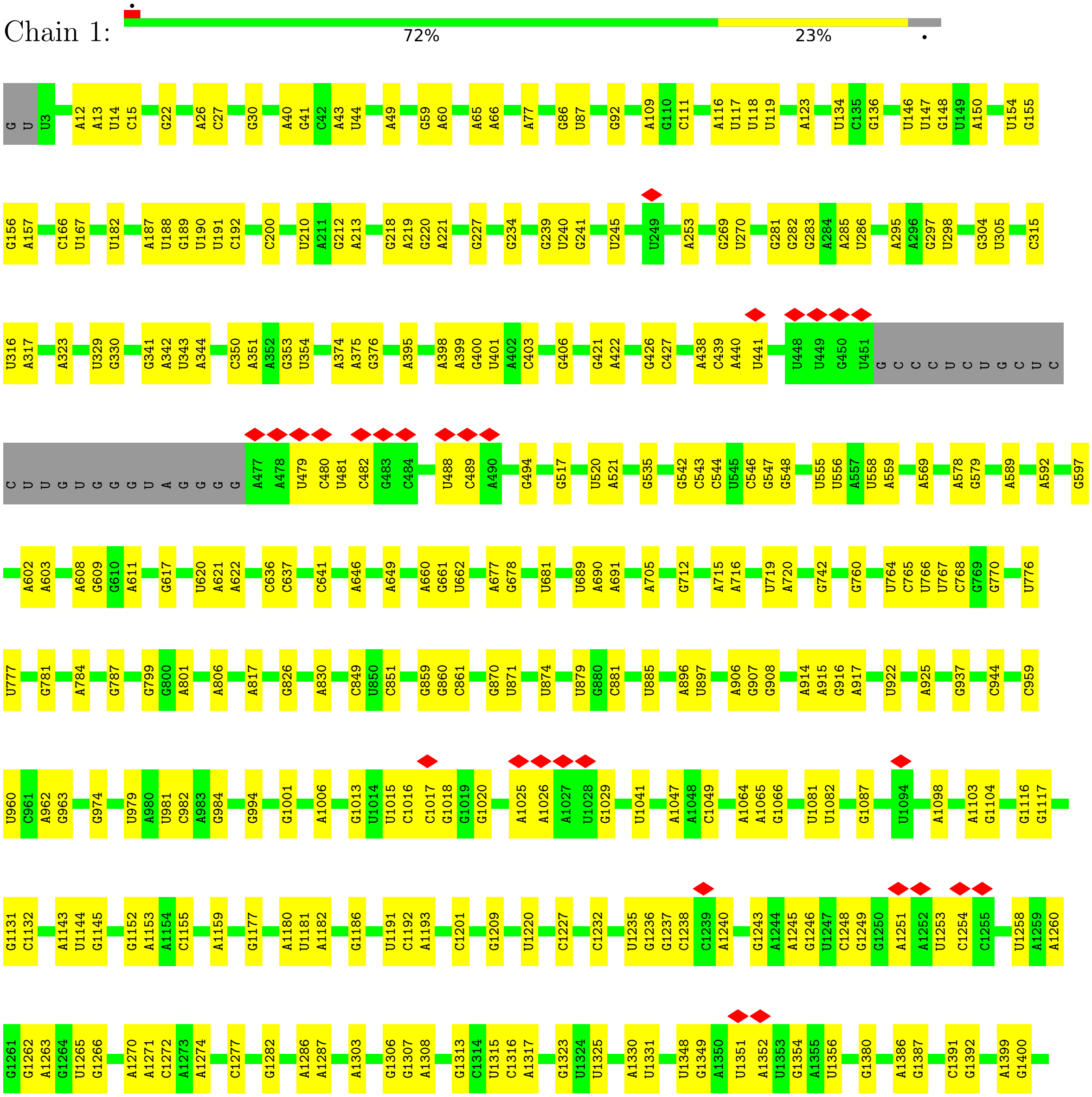
- Molecule 47 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

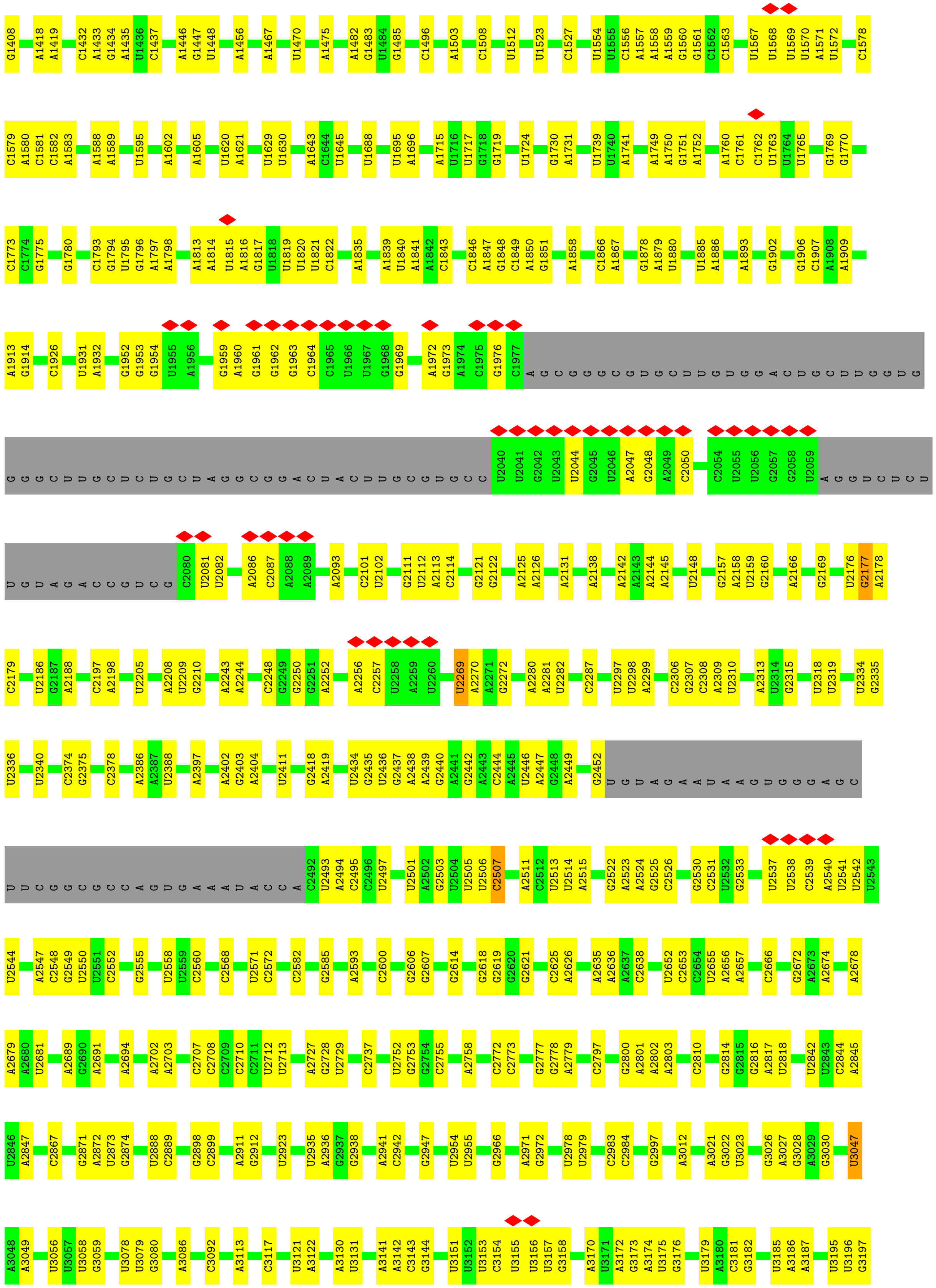
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
47	2	1	1	1	0

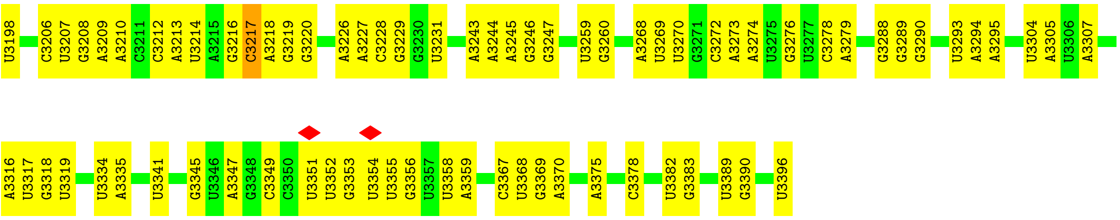
3 Residue-property plots

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 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: 25S ribosomal RNA

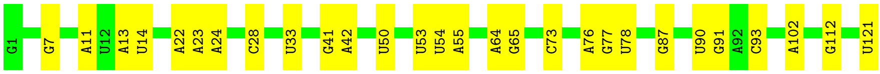



G1408 A1418 A1419 C1432 G1433 G1434 A1435 U1436 C1437 A1446 G1447 U1448 A1456 A1467 U1470 A1475 A1482 G1483 U1484 G1485 C1496 A1503 C1508 U1512 U1523 C1527 U1554 U1555 C1556 A1557 A1558 A1559 G1560 G1561 C1562 C1563 U1567 U1568 U1569 U1570 A1571 U1572 C1578
C1579 A1580 C1581 C1582 A1583 A1588 G1589 U1595 A1602 A1605 U1620 A1621 U1629 U1630 A1643 C1644 U1645 U1688 U1695 A1696 A1715 U1716 U1717 G1718 G1719 U1724 G1730 A1731 U1739 U1740 A1741 A1749 A1750 G1751 A1752 A1760 C1761 C1762 U1763 U1764 U1765 G1769 G1770
C1773 C1774 G1775 G1780 C1793 G1794 U1795 G1796 A1797 A1798 A1813 A1814 U1815 A1816 G1817 U1818 U1819 U1820 U1821 C1822 A1835 A1839 U1840 A1841 A1842 C1843 C1846 A1847 G1848 C1849 A1850 G1851 A1858 C1866 A1867 G1878 A1879 U1880 U1885 A1886 A1893 G1902 G1906 C1907 A1908 A1909
A1913 G1914 C1926 U1931 A1932 G1952 G1953 G1954 U1955 A1956 G1959 A1960 G1961 G1962 G1963 C1964 C1965 U1966 U1967 G1968 G1969 A1972 G1973 A1974 C1975 G1976 C1977 A G C G G G C G U G C U U G G U G G A C U G C U U G G U G
G G G C U U G C U C U G C U A G G C G G A C U A C U U G C G U G C C U2040 U2041 G2042 U2043 U2044 G2045 U2046 A2047 G2048 A2049 C2050 C2054 U2055 U2056 G2057 G2058 U2059 A G G U C C U C U
U G U A G A C C G U C G C2080 U2081 U2082 A2086 C2087 A2088 A2089 A2093 C2101 U2102 G2111 U2112 A2113 C2114 G2121 G2122 A2125 A2126 A2131 A2138 A2142 A2143 A2144 A2145 U2148 G2157 A2158 U2159 G2160 A2166 G2169 U2176 G2177 A2178
C2179 U2186 G2187 A2188 C2197 A2198 U2205 A2208 U2209 G2210 A2243 A2244 C2248 G2249 G2250 G2251 A2252 A2256 C2257 U2258 A2259 U2260 U2269 A2270 A2271 G2272 A2280 A2281 U2282 C2287 U2297 U2298 A2299 C2306 G2307 C2308 A2309 U2310 A2313 U2314 G2315 U2318 U2319 U2334 G2335
U2336 U2340 C2374 G2375 C2378 A2386 A2387 U2388 A2397 A2402 G2403 A2404 U2411 G2418 A2419 U2434 G2435 U2436 G2437 A2438 A2439 G2440 A2441 G2442 A2443 C2444 A2445 U2446 A2447 G2448 A2449 G2452 U G U A G A A U A A G U G G G A G C
U U C G G C G C C A G U G A A A U A C C A C2492 U2493 A2494 C2495 C2496 U2497 U2501 A2502 G2503 U2504 U2505 U2506 C2507 A2511 C2512 U2513 U2514 A2515 G2522 A2523 A2524 G2525 C2526 G2530 C2531 U2532 G2533 U2537 U2538 C2539 A2540 U2541 U2542 U2543
U2544 A2547 C2548 G2549 U2550 U2551 C2552 G2555 U2558 U2559 C2560 C2568 U2571 C2572 C2582 G2585 A2593 C2600 G2606 G2607 G2614 G2618 G2619 G2620 G2621 C2625 A2626 A2635 A2636 A2637 C2638 U2652 C2653 C2654 U2655 A2656 A2657 C2666 G2672 A2673 A2674 A2678
A2679 A2680 U2681 A2689 G2690 A2691 A2694 A2702 A2703 C2707 C2708 C2709 C2710 C2711 U2712 U2713 A2727 G2728 U2729 C2737 U2752 G2753 G2754 C2755 A2758 C2772 C2773 G2777 G2778 A2779 C2797 G2800 A2801 A2802 A2803 C2810 G2814 G2815 G2816 A2817 U2818 U2842 U2843 C2844 A2845
U2846 A2847 C2867 G2871 A2872 U2873 G2874 U2888 C2889 G2898 C2899 A2911 G2912 U2923 U2935 A2936 G2937 G2938 A2941 C2942 G2947 U2954 U2955 G2966 A2971 G2972 U2978 U2979 C2983 C2984 G2997 A3012 A3021 G3022 U3023 G3026 A3027 G3028 A3029 G3030 U3047
A3048 A3049 U3056 U3057 U3058 G3059 U3078 U3079 G3080 A3086 C3092 A3113 C3117 U3121 A3122 A3130 U3131 A3141 A3142 C3143 G3144 U3151 U3152 U3153 C3154 U3155 U3156 U3157 G3158 A3170 U3171 A3172 G3173 A3174 U3175 G3176 U3179 A3180 C3181 G3182 U3185 A3186 A3187 U3195 U3196 G3197



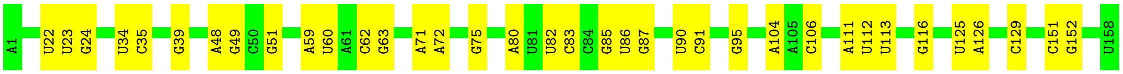
- Molecule 2: 5S ribosomal RNA

Chain 3:



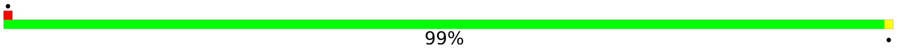
- Molecule 3: 5.8S ribosomal RNA

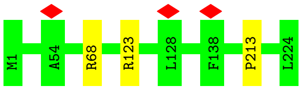
Chain 4:



- Molecule 4: Eukaryotic translation initiation factor 6

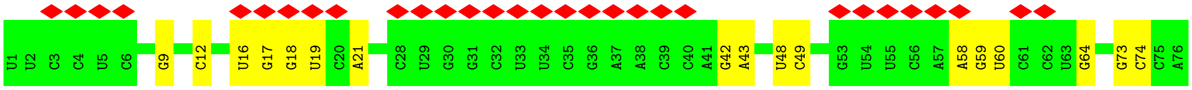
Chain A:





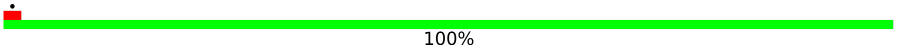
- Molecule 5: tRNA

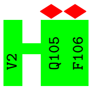
Chain 2:



- Molecule 6: 60S ribosomal protein L42-A

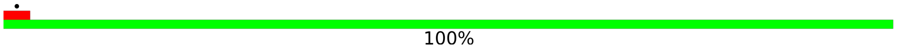
Chain BA:

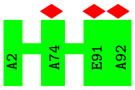




- Molecule 7: 60S ribosomal protein L43-A

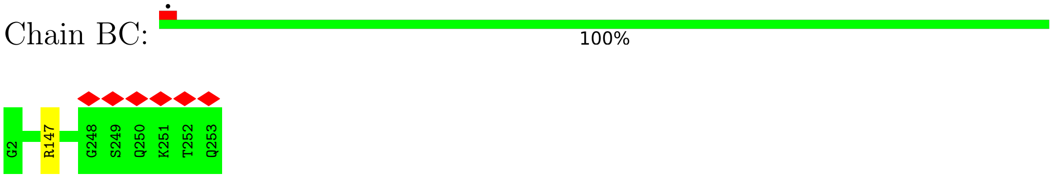
Chain BB:





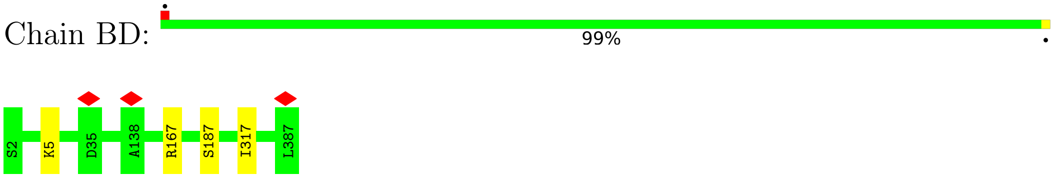
- Molecule 8: 60S ribosomal protein L2-A

Chain BC:



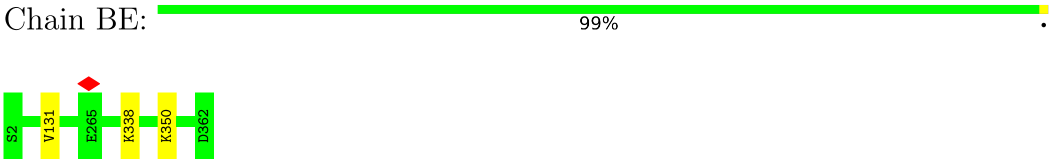
- Molecule 9: 60S ribosomal protein L3

Chain BD:



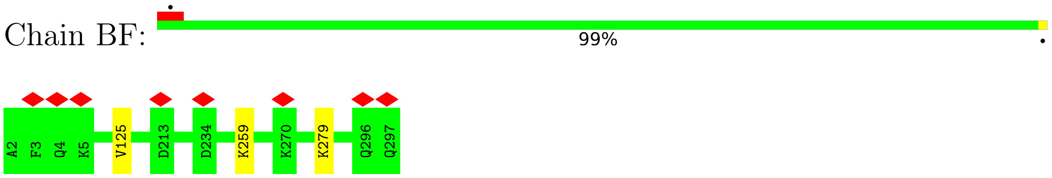
- Molecule 10: 60S ribosomal protein L4-A

Chain BE:



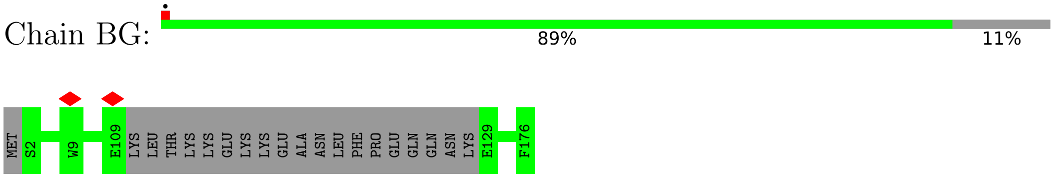
- Molecule 11: 60S ribosomal protein L5

Chain BF:



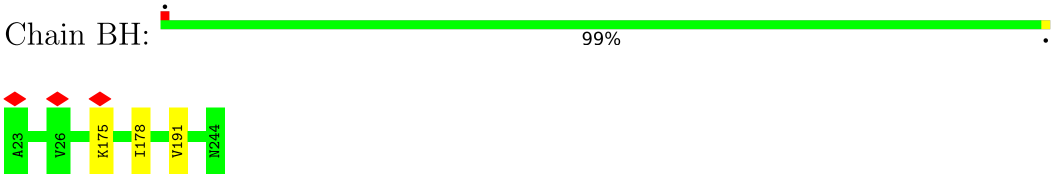
- Molecule 12: 60S ribosomal protein L6-A

Chain BG:



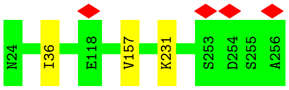
- Molecule 13: 60S ribosomal protein L7-A

Chain BH:



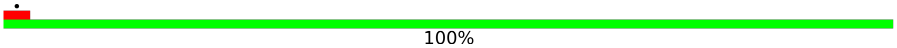
- Molecule 14: 60S ribosomal protein L8-A

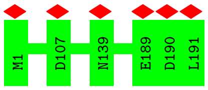
Chain BI:



- Molecule 15: 60S ribosomal protein L9-A

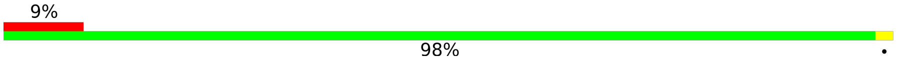
Chain BJ:

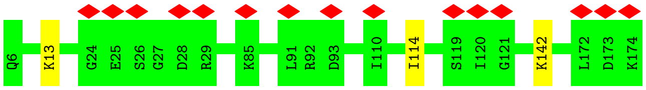




- Molecule 16: 60S ribosomal protein L11-B

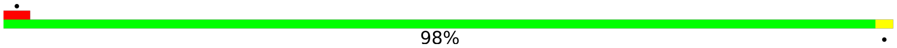
Chain BL:

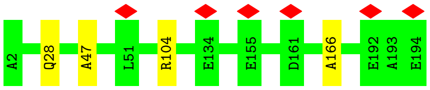




- Molecule 17: 60S ribosomal protein L13-A

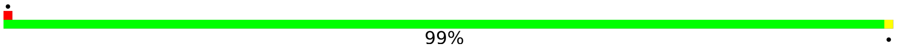
Chain BM:

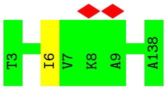




- Molecule 18: 60S ribosomal protein L14-A

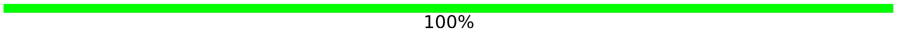
Chain BN:

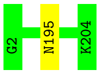




- Molecule 19: 60S ribosomal protein L15-A

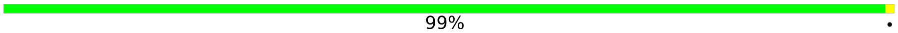
Chain BO:

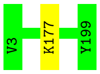




- Molecule 20: 60S ribosomal protein L16-A

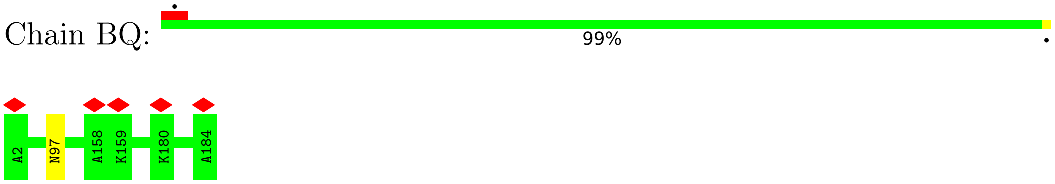
Chain BP:





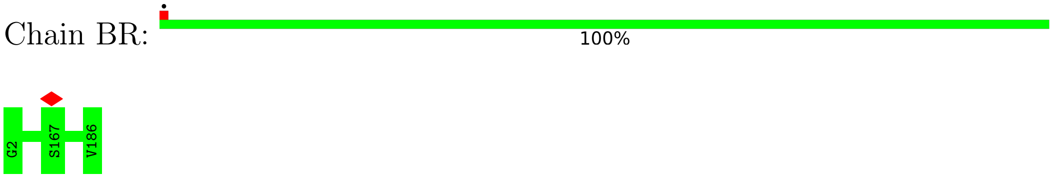
- Molecule 21: 60S ribosomal protein L17-A

Chain BQ:



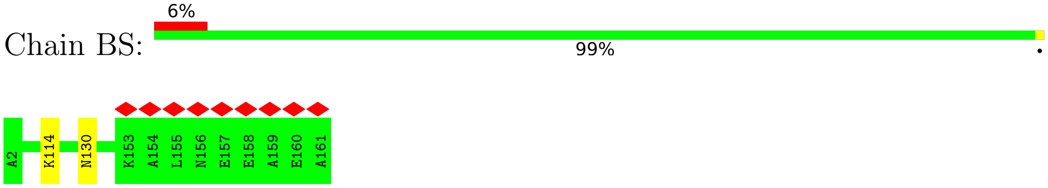
- Molecule 22: 60S ribosomal protein L18-A

Chain BR:



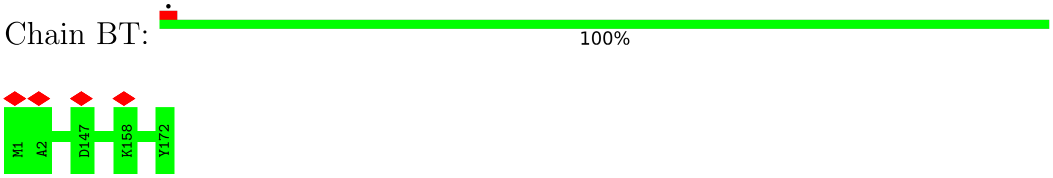
- Molecule 23: 60S ribosomal protein L19-A

Chain BS:



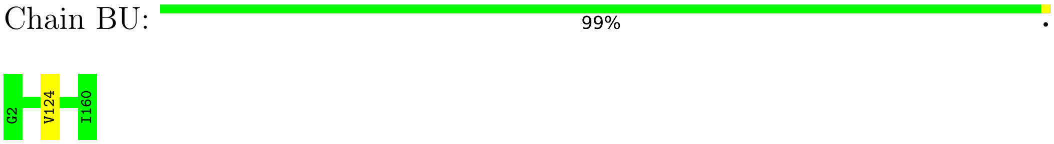
- Molecule 24: 60S ribosomal protein L20-A

Chain BT:



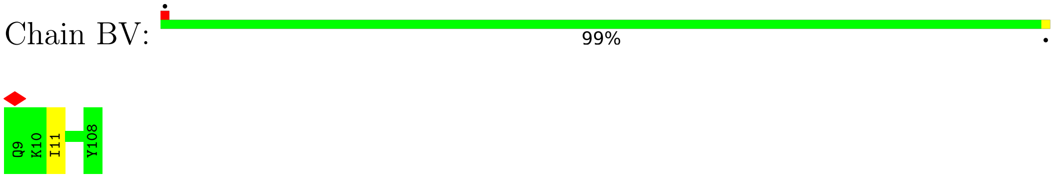
- Molecule 25: 60S ribosomal protein L21-A

Chain BU:



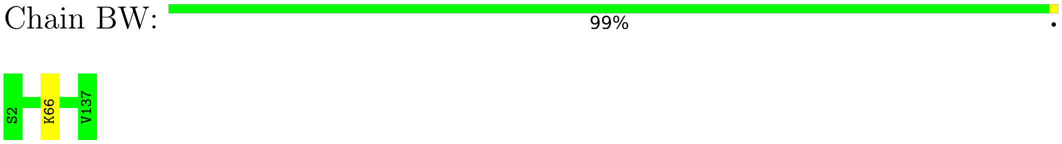
- Molecule 26: 60S ribosomal protein L22-A

Chain BV:



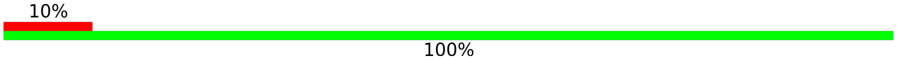
- Molecule 27: 60S ribosomal protein L23-A

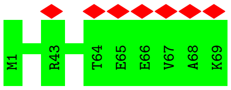
Chain BW:



- Molecule 28: 60S ribosomal protein L24-A

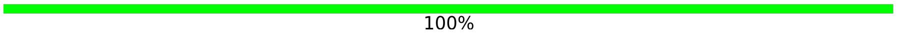
Chain BX:





- Molecule 29: 60S ribosomal protein L25

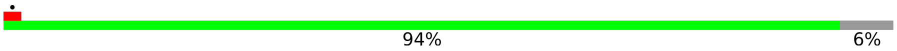
Chain BY:

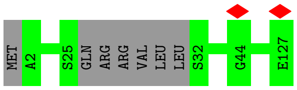


There are no outlier residues recorded for this chain.

- Molecule 30: 60S ribosomal protein L26-A

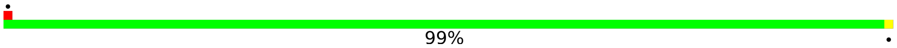
Chain BZ:

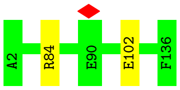




- Molecule 31: 60S ribosomal protein L27-A

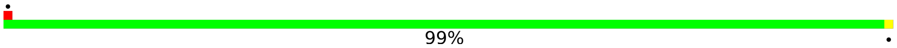
Chain Ba:

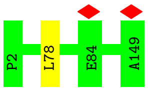




- Molecule 32: 60S ribosomal protein L28

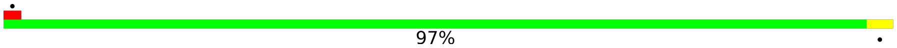
Chain Bb:

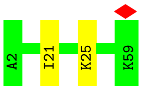




- Molecule 33: 60S ribosomal protein L29

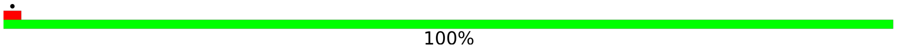
Chain Bc:

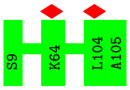




- Molecule 34: 60S ribosomal protein L30

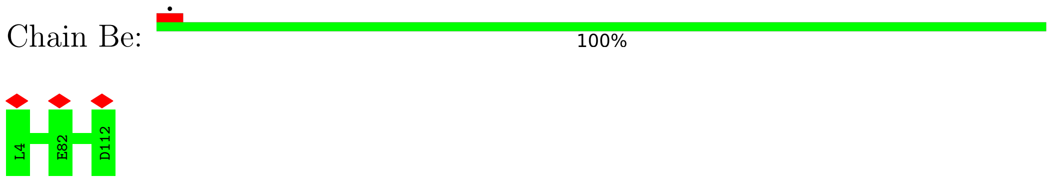
Chain Bd:





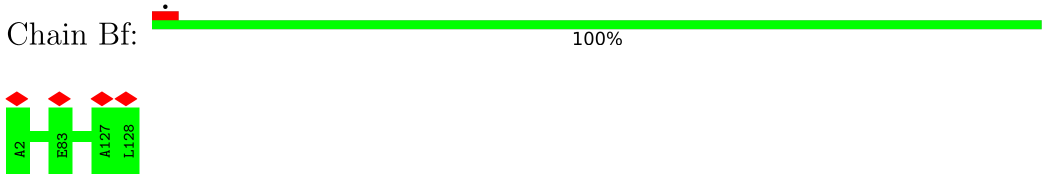
- Molecule 35: 60S ribosomal protein L31-A

Chain Be:



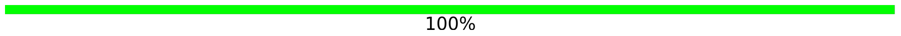
- Molecule 36: 60S ribosomal protein L32

Chain Bf:



- Molecule 37: 60S ribosomal protein L33-A

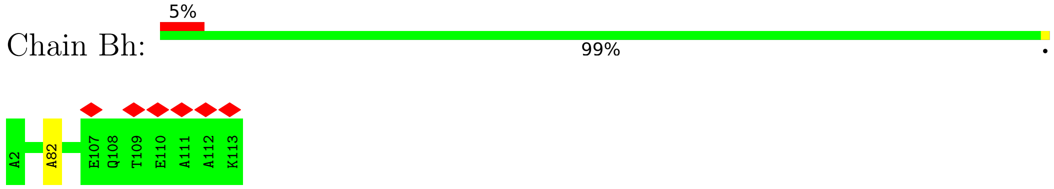
Chain Bg:



There are no outlier residues recorded for this chain.

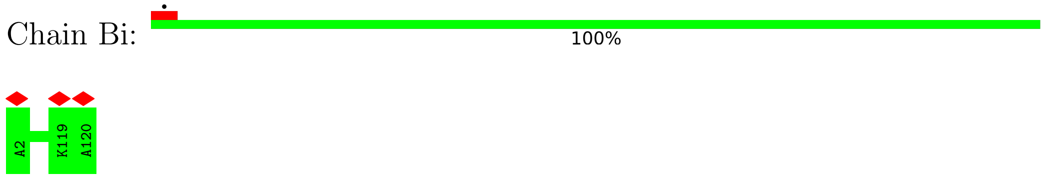
- Molecule 38: 60S ribosomal protein L34-A

Chain Bh:



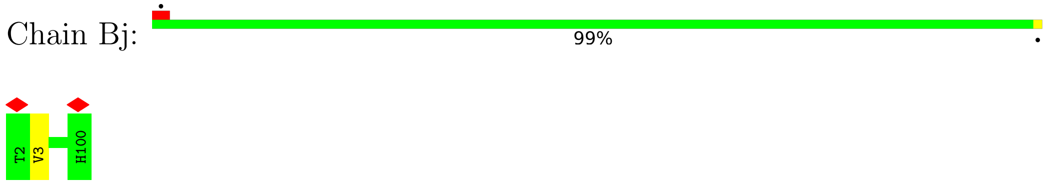
- Molecule 39: 60S ribosomal protein L35-A

Chain Bi:



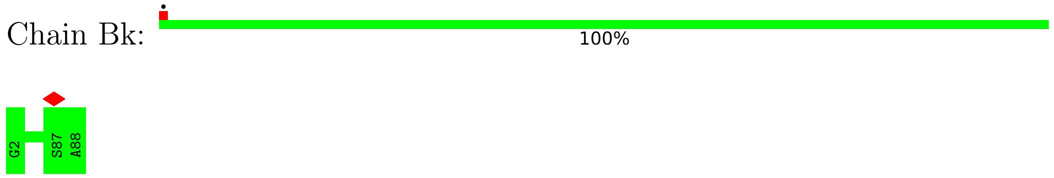
- Molecule 40: 60S ribosomal protein L36-A

Chain Bj:



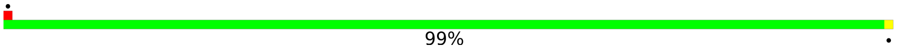
- Molecule 41: 60S ribosomal protein L37-A

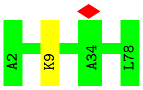
Chain Bk:



- Molecule 42: 60S ribosomal protein L38

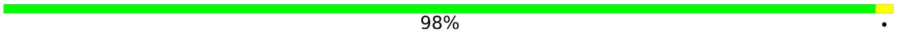
Chain Bl:

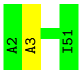




- Molecule 43: 60S ribosomal protein L39

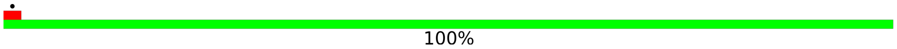
Chain Bm:

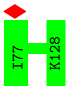




- Molecule 44: 60S ribosomal protein L40-A

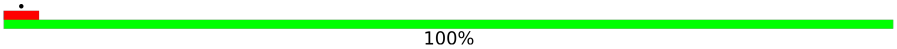
Chain Bn:

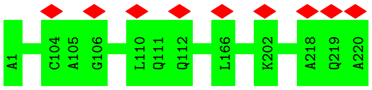




- Molecule 45: 60S ribosomal protein L10

Chain BK:





4 Experimental information ⓘ

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	25072	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{Å}^2$)	43.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	3.151	Depositor
Minimum map value	-1.485	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.070	Depositor
Recommended contour level	0.3	Depositor
Map size (Å)	585.19995, 585.19995, 585.19995	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.045, 1.045, 1.045	Depositor

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	1	0.20	0/77733	0.79	25/121186 (0.0%)
2	3	0.18	0/2883	0.77	2/4491 (0.0%)
3	4	0.23	1/3746 (0.0%)	0.77	2/5832 (0.0%)
4	A	0.25	0/1653	0.56	1/2255 (0.0%)
5	2	0.19	0/1808	0.83	1/2816 (0.0%)
6	BA	0.26	0/860	0.55	0/1136
7	BB	0.24	0/701	0.59	0/934
8	BC	0.25	0/1948	0.55	0/2617
9	BD	0.24	0/3146	0.52	0/4228
10	BE	0.24	0/2800	0.52	0/3790
11	BF	0.24	0/2425	0.51	0/3271
12	BG	0.25	0/1260	0.50	0/1694
13	BH	0.25	0/1821	0.51	0/2451
14	BI	0.25	0/1836	0.50	0/2481
15	BJ	0.25	0/1539	0.52	0/2073
16	BL	0.27	0/1374	0.60	0/1842
17	BM	0.25	0/1568	0.57	0/2106
18	BN	0.24	0/1068	0.53	0/1438
19	BO	0.23	0/1757	0.57	0/2354
20	BP	0.25	0/1585	0.50	0/2128
21	BQ	0.25	0/1443	0.58	0/1944
22	BR	0.24	0/1465	0.55	0/1965
23	BS	0.24	0/1303	0.54	0/1740
24	BT	0.25	0/1481	0.54	0/1990
25	BU	0.24	0/1300	0.53	0/1743
26	BV	0.25	0/812	0.50	0/1099
27	BW	0.28	0/1018	0.57	0/1369
28	BX	0.27	0/565	0.58	0/752
29	BY	0.25	0/979	0.52	0/1321
30	BZ	0.24	0/949	0.55	0/1266
31	Ba	0.25	0/1118	0.49	0/1497
32	Bb	0.25	0/1204	0.58	0/1612

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Bc	0.26	0/473	0.56	0/629
34	Bd	0.27	0/751	0.50	0/1008
35	Be	0.24	0/890	0.54	0/1196
36	Bf	0.24	0/1041	0.53	0/1394
37	Bg	0.25	0/868	0.54	0/1168
38	Bh	0.24	0/890	0.55	0/1189
39	Bi	0.24	0/978	0.53	0/1301
40	Bj	0.24	0/778	0.56	0/1034
41	Bk	0.24	0/696	0.57	0/923
42	Bl	0.25	0/618	0.57	0/826
43	Bm	0.30	0/443	0.61	0/588
44	Bn	0.27	0/423	0.63	0/562
45	BK	0.25	0/1807	0.55	0/2425
All	All	0.22	1/137804 (0.0%)	0.71	31/203664 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	4	75	G	N7-C5	-6.73	1.35	1.39

The worst 5 of 31 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	213	PRO	CA-N-CD	-7.86	100.49	111.50
5	2	12	C	N3-C2-O2	-7.08	116.94	121.90
1	1	2708	C	N3-C2-O2	-6.72	117.19	121.90
1	1	2446	U	C2-N1-C1'	6.65	125.68	117.70
1	1	2507	C	C2-N1-C1'	6.45	125.89	118.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	222/224 (99%)	218 (98%)	4 (2%)	0	100	100
6	BA	103/105 (98%)	101 (98%)	2 (2%)	0	100	100
7	BB	89/91 (98%)	87 (98%)	2 (2%)	0	100	100
8	BC	250/252 (99%)	247 (99%)	3 (1%)	0	100	100
9	BD	384/386 (100%)	375 (98%)	6 (2%)	3 (1%)	19	58
10	BE	359/361 (99%)	343 (96%)	14 (4%)	2 (1%)	25	64
11	BF	294/296 (99%)	288 (98%)	4 (1%)	2 (1%)	22	61
12	BG	152/176 (86%)	151 (99%)	1 (1%)	0	100	100
13	BH	220/222 (99%)	213 (97%)	5 (2%)	2 (1%)	17	56
14	BI	231/233 (99%)	225 (97%)	4 (2%)	2 (1%)	17	56
15	BJ	189/191 (99%)	186 (98%)	3 (2%)	0	100	100
16	BL	167/169 (99%)	154 (92%)	12 (7%)	1 (1%)	25	64
17	BM	191/193 (99%)	179 (94%)	9 (5%)	3 (2%)	9	43
18	BN	134/136 (98%)	130 (97%)	3 (2%)	1 (1%)	22	61
19	BO	201/203 (99%)	198 (98%)	3 (2%)	0	100	100
20	BP	195/197 (99%)	191 (98%)	4 (2%)	0	100	100
21	BQ	181/183 (99%)	175 (97%)	6 (3%)	0	100	100
22	BR	183/185 (99%)	178 (97%)	5 (3%)	0	100	100
23	BS	158/160 (99%)	155 (98%)	3 (2%)	0	100	100
24	BT	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
25	BU	157/159 (99%)	150 (96%)	6 (4%)	1 (1%)	25	64
26	BV	98/100 (98%)	92 (94%)	5 (5%)	1 (1%)	15	54
27	BW	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
28	BX	67/69 (97%)	65 (97%)	2 (3%)	0	100	100
29	BY	119/121 (98%)	118 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	BZ	116/127 (91%)	113 (97%)	3 (3%)	0	100	100
31	Ba	133/135 (98%)	128 (96%)	4 (3%)	1 (1%)	19	58
32	Bb	146/148 (99%)	140 (96%)	5 (3%)	1 (1%)	22	61
33	Bc	56/58 (97%)	55 (98%)	0	1 (2%)	8	41
34	Bd	95/97 (98%)	95 (100%)	0	0	100	100
35	Be	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
36	Bf	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
37	Bg	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
38	Bh	110/112 (98%)	108 (98%)	1 (1%)	1 (1%)	17	56
39	Bi	117/119 (98%)	114 (97%)	3 (3%)	0	100	100
40	Bj	97/99 (98%)	91 (94%)	5 (5%)	1 (1%)	15	54
41	Bk	85/87 (98%)	85 (100%)	0	0	100	100
42	Bl	75/77 (97%)	73 (97%)	2 (3%)	0	100	100
43	Bm	48/50 (96%)	47 (98%)	0	1 (2%)	7	37
44	Bn	50/52 (96%)	50 (100%)	0	0	100	100
45	BK	218/220 (99%)	209 (96%)	9 (4%)	0	100	100
All	All	6330/6443 (98%)	6148 (97%)	158 (2%)	24 (0%)	38	69

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	BF	259	LYS
17	BM	28	GLN
17	BM	166	ALA
31	Ba	102	GLU
38	Bh	82	ALA

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	
4	A	177/192 (92%)	175 (99%)	2 (1%)	73	88
6	BA	90/90 (100%)	90 (100%)	0	100	100
7	BB	71/71 (100%)	71 (100%)	0	100	100
8	BC	193/194 (100%)	192 (100%)	1 (0%)	88	95
9	BD	320/322 (99%)	319 (100%)	1 (0%)	92	96
10	BE	288/288 (100%)	287 (100%)	1 (0%)	92	96
11	BF	244/244 (100%)	243 (100%)	1 (0%)	91	95
12	BG	134/153 (88%)	134 (100%)	0	100	100
13	BH	186/186 (100%)	185 (100%)	1 (0%)	88	95
14	BI	187/191 (98%)	186 (100%)	1 (0%)	88	95
15	BJ	171/171 (100%)	171 (100%)	0	100	100
16	BL	147/147 (100%)	145 (99%)	2 (1%)	67	86
17	BM	154/154 (100%)	153 (99%)	1 (1%)	86	94
18	BN	107/107 (100%)	107 (100%)	0	100	100
19	BO	175/175 (100%)	174 (99%)	1 (1%)	86	94
20	BP	160/160 (100%)	159 (99%)	1 (1%)	86	94
21	BQ	140/145 (97%)	139 (99%)	1 (1%)	84	94
22	BR	150/150 (100%)	150 (100%)	0	100	100
23	BS	131/131 (100%)	129 (98%)	2 (2%)	65	85
24	BT	156/156 (100%)	156 (100%)	0	100	100
25	BU	136/136 (100%)	136 (100%)	0	100	100
26	BV	87/87 (100%)	87 (100%)	0	100	100
27	BW	104/104 (100%)	103 (99%)	1 (1%)	76	90
28	BX	56/60 (93%)	56 (100%)	0	100	100
29	BY	104/105 (99%)	104 (100%)	0	100	100
30	BZ	103/110 (94%)	103 (100%)	0	100	100
31	Ba	115/115 (100%)	114 (99%)	1 (1%)	78	91
32	Bb	118/118 (100%)	118 (100%)	0	100	100
33	Bc	46/46 (100%)	45 (98%)	1 (2%)	52	79
34	Bd	81/81 (100%)	81 (100%)	0	100	100
35	Be	92/96 (96%)	92 (100%)	0	100	100
36	Bf	109/109 (100%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	Bg	90/90 (100%)	90 (100%)	0	100	100
38	Bh	95/95 (100%)	95 (100%)	0	100	100
39	Bi	104/104 (100%)	104 (100%)	0	100	100
40	Bj	81/81 (100%)	81 (100%)	0	100	100
41	Bk	70/70 (100%)	70 (100%)	0	100	100
42	Bl	68/68 (100%)	67 (98%)	1 (2%)	65	85
43	Bm	45/45 (100%)	45 (100%)	0	100	100
44	Bn	47/47 (100%)	47 (100%)	0	100	100
45	BK	184/186 (99%)	184 (100%)	0	100	100
All	All	5316/5380 (99%)	5296 (100%)	20 (0%)	91	95

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	BS	114	LYS
31	Ba	84	ARG
42	Bl	9	LYS
33	Bc	25	LYS
13	BH	175	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
24	BT	46	GLN
27	BW	47	ASN
45	BK	208	ASN
28	BX	33	ASN
44	Bn	119	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3243/3396 (95%)	755 (23%)	79 (2%)
2	3	120/121 (99%)	27 (22%)	3 (2%)
3	4	157/158 (99%)	34 (21%)	3 (1%)
5	2	75/76 (98%)	16 (21%)	0
All	All	3595/3751 (95%)	832 (23%)	85 (2%)

5 of 832 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	12	A
1	1	13	A
1	1	15	C
1	1	22	G
1	1	26	A

5 of 85 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	2538	U
1	1	3216	G
1	1	2549	G
1	1	3022	G
1	1	3246	G

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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 24 ligands modelled in this entry, 23 are unknown and 1 is 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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

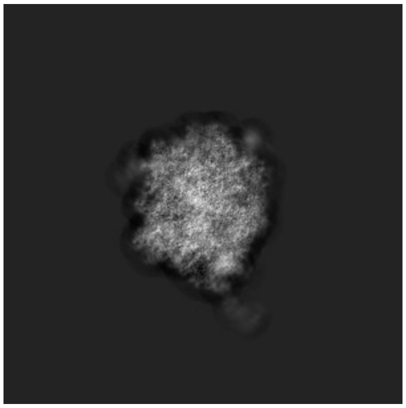
6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-14926. These allow visual inspection of the internal detail of the map and identification of artifacts.

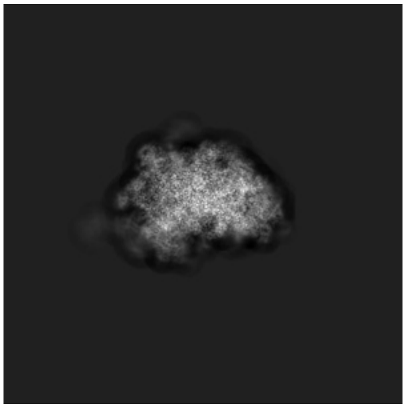
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections ⓘ

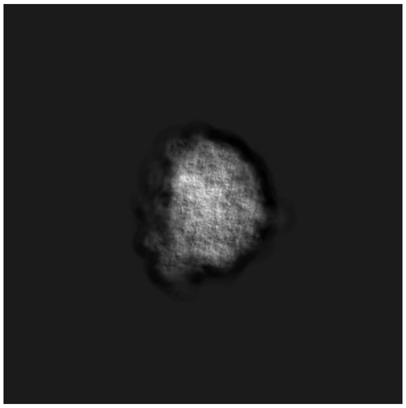
6.1.1 Primary map



X

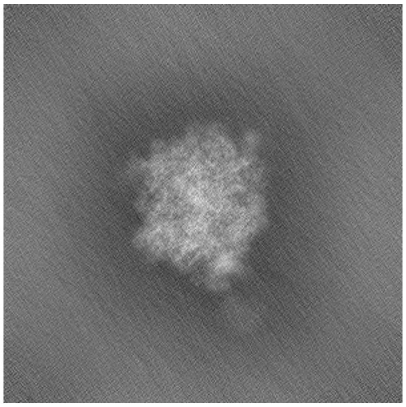


Y

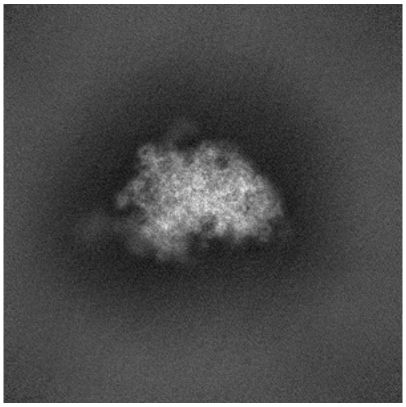


Z

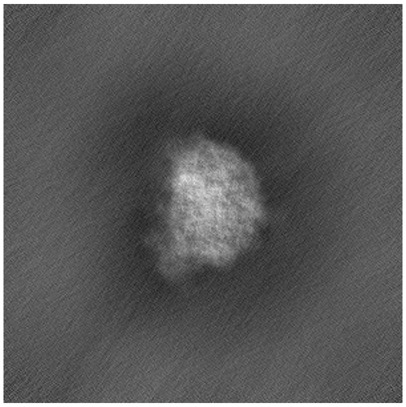
6.1.2 Raw map



X



Y

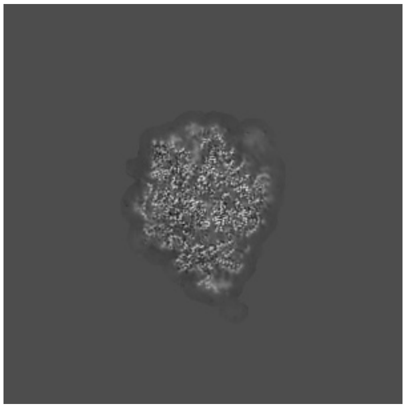


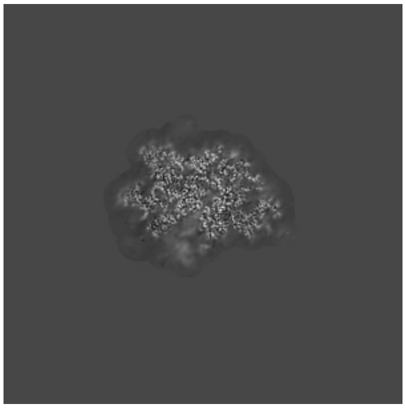
Z

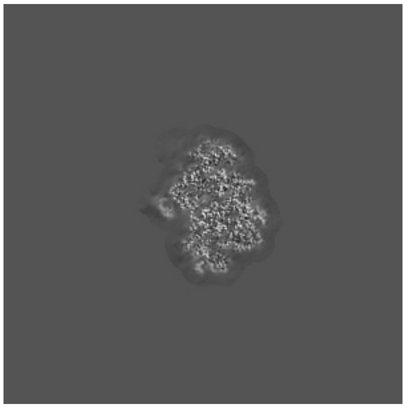
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

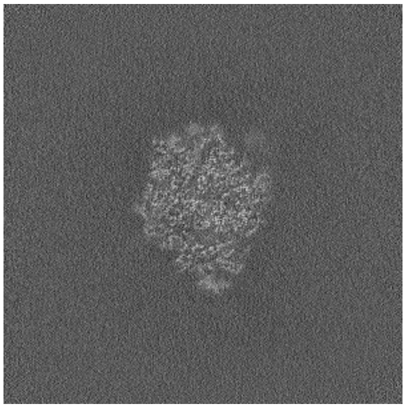
6.2.1 Primary map

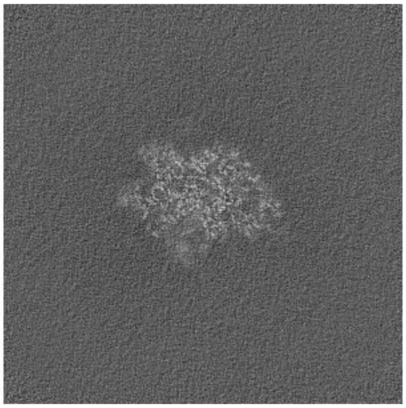

X Index: 280

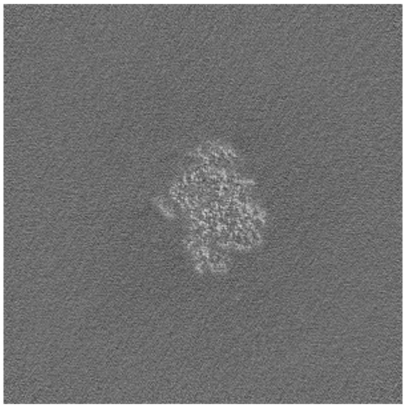

Y Index: 280


Z Index: 280

6.2.2 Raw map


X Index: 280

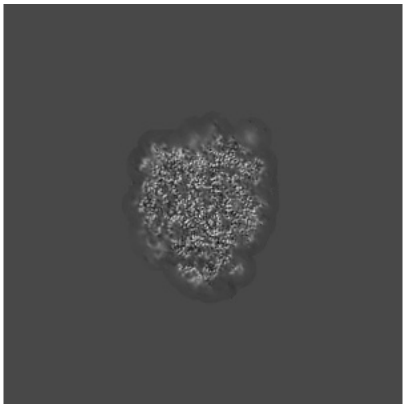

Y Index: 280

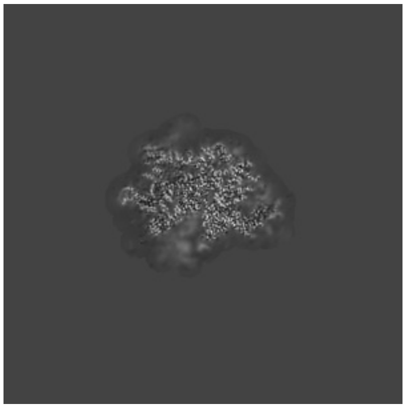

Z Index: 280

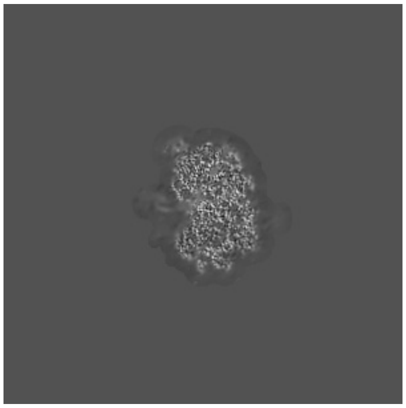
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices

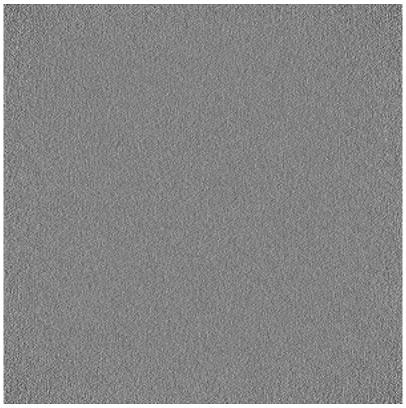
6.3.1 Primary map

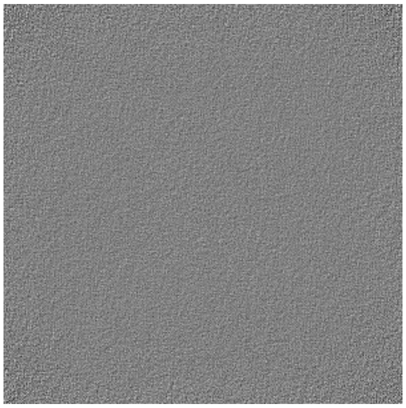

X Index: 300

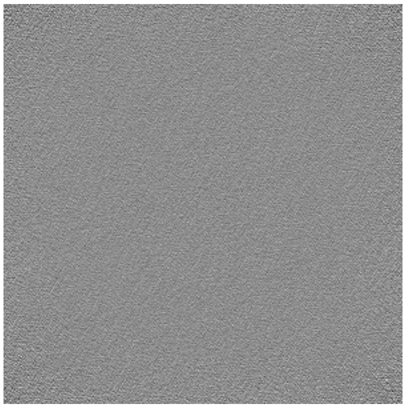

Y Index: 275


Z Index: 271

6.3.2 Raw map


X Index: 0

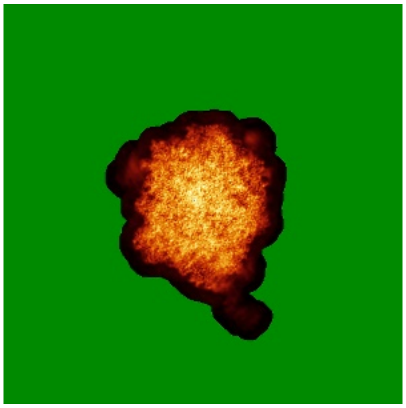

Y Index: 0

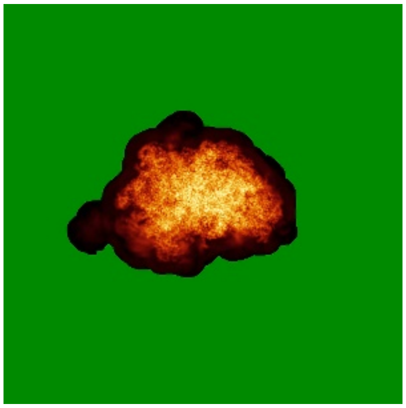

Z Index: 0

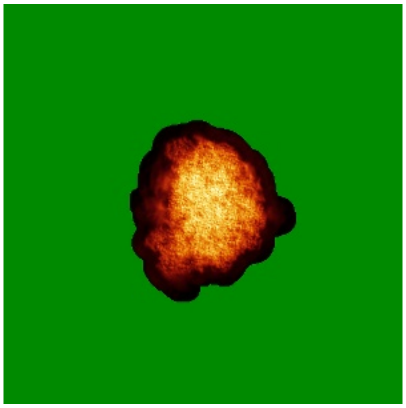
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color)

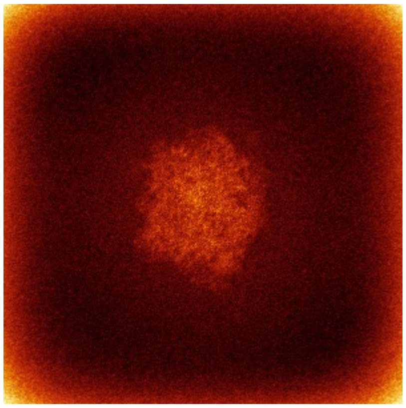
6.4.1 Primary map

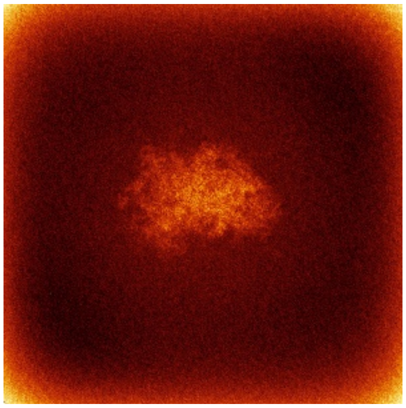

X

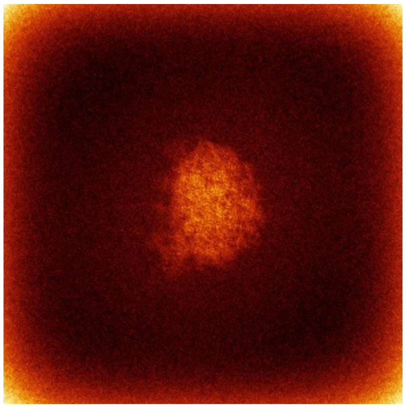

Y


Z

6.4.2 Raw map


X


Y


Z

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

6.5 Orthogonal surface views

6.5.1 Primary map


X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map


X Y Z

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

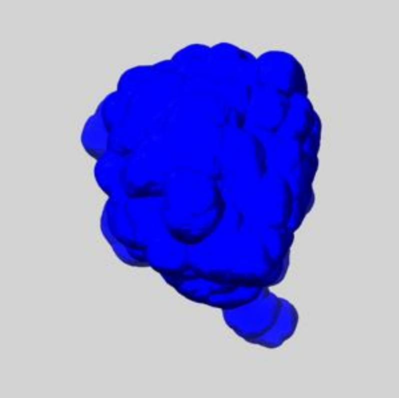
6.6 Mask visualisation

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

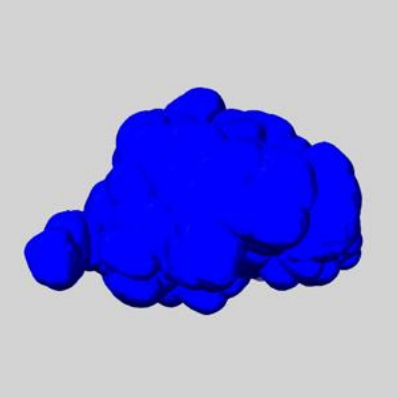
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

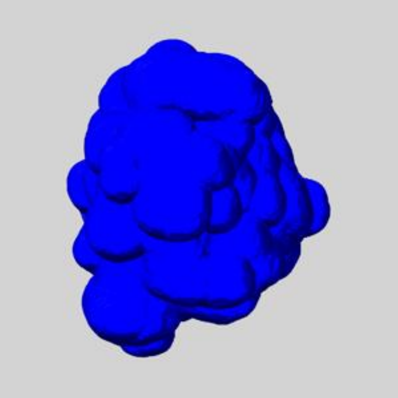
6.6.1 emd_14926_msk_1.map



X



Y

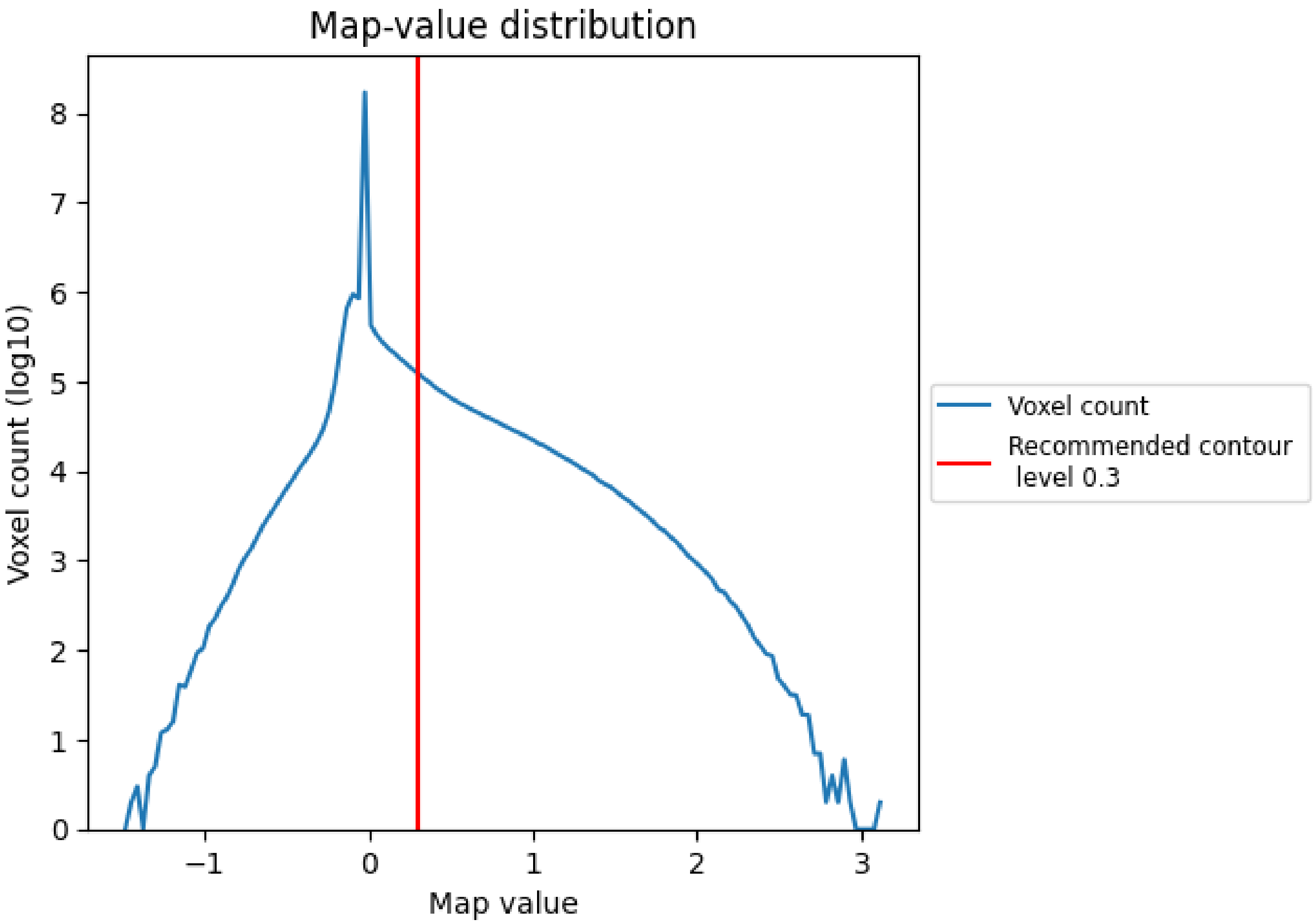


Z

7 Map analysis ⓘ

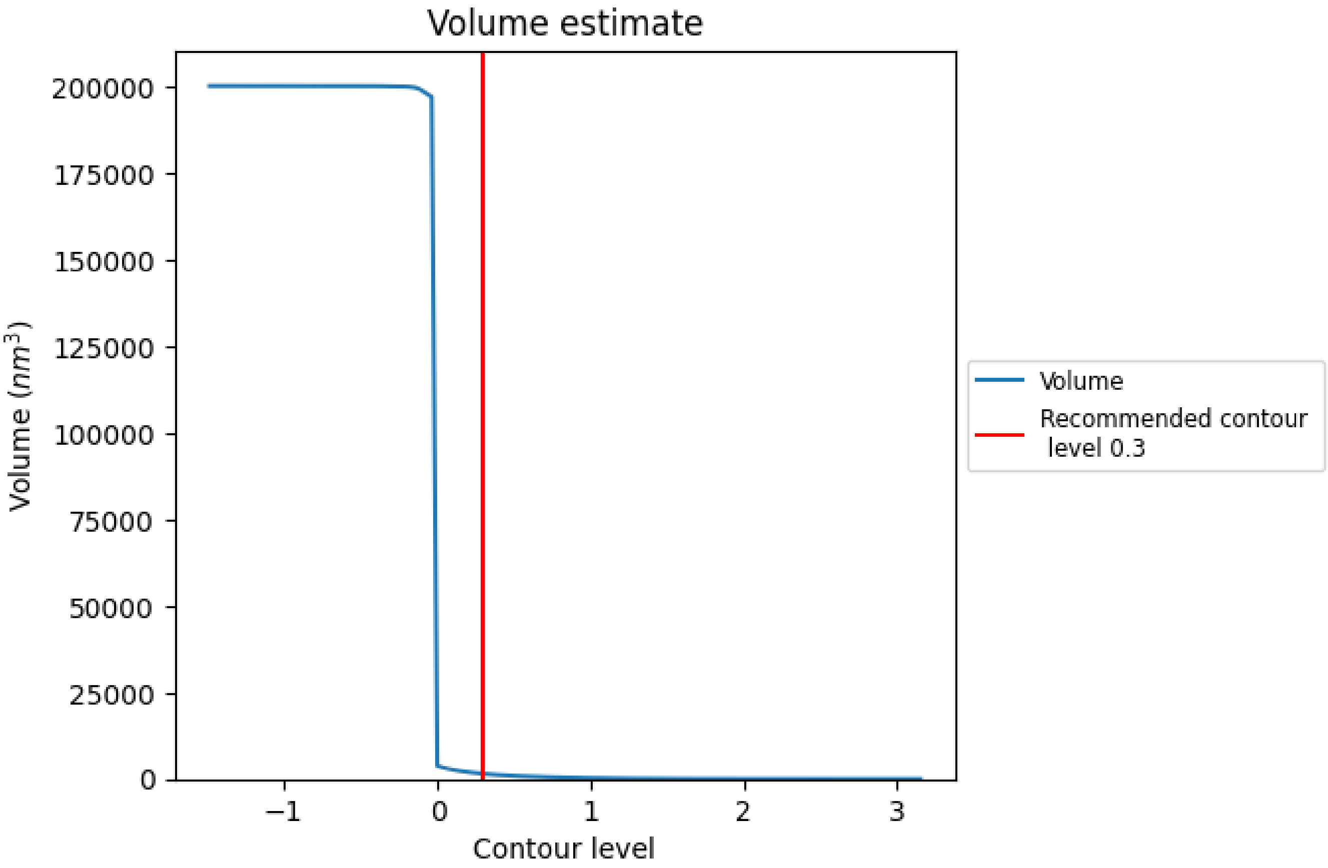
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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.

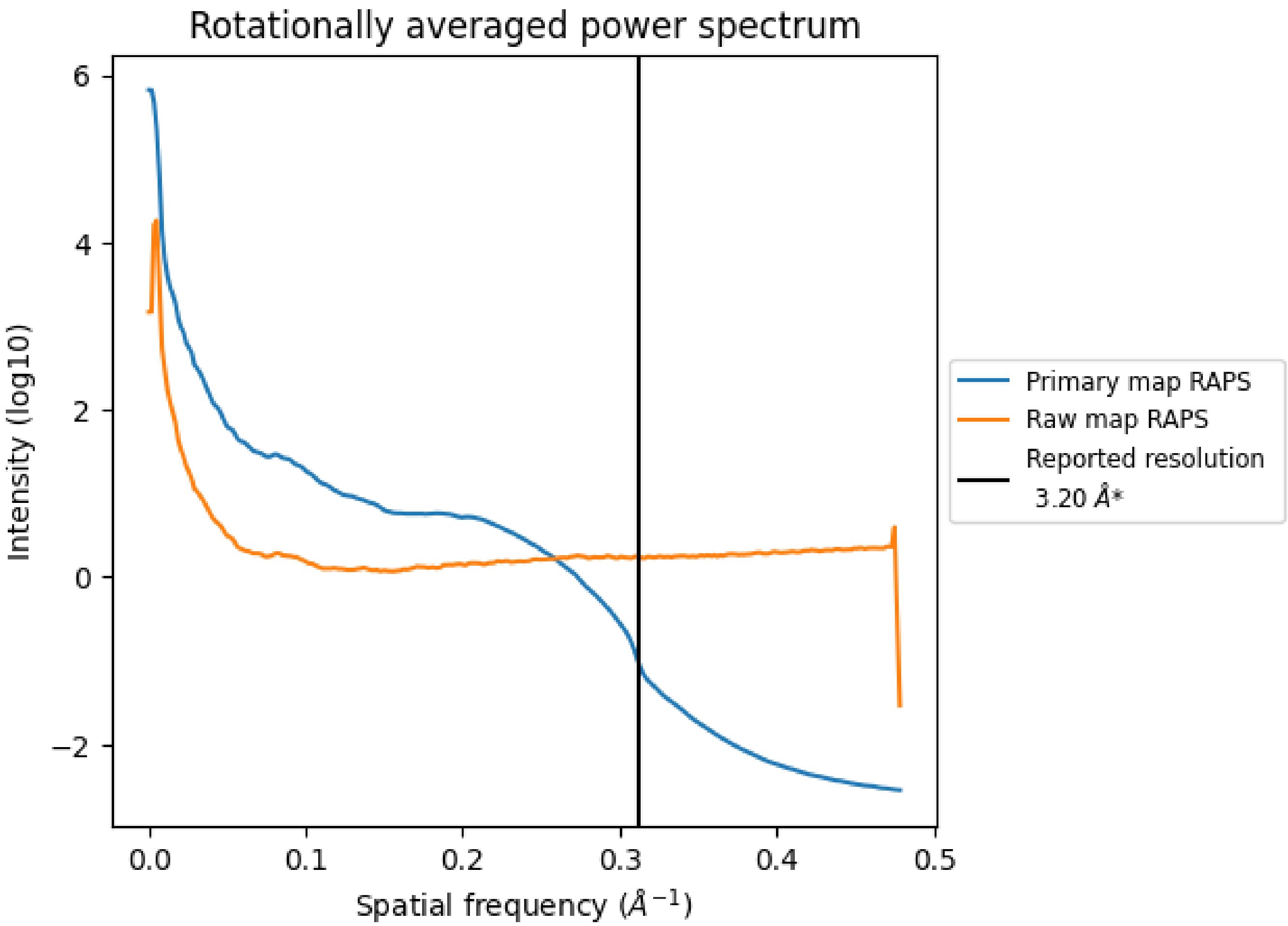
7.2 Volume estimate (i)



The volume at the recommended contour level is 1499 nm^3; this corresponds to an approximate mass of 1354 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 ⓘ

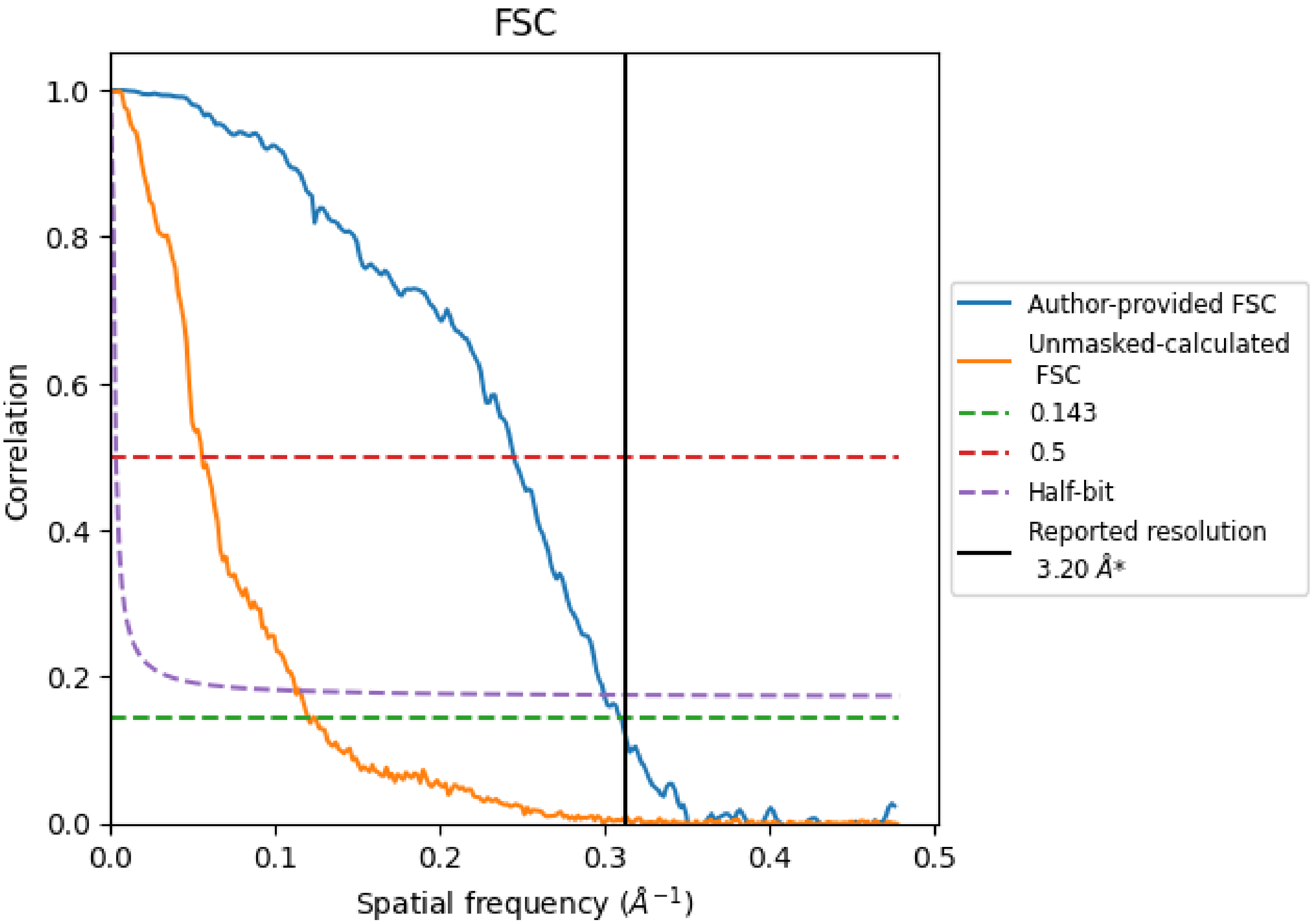


*Reported resolution corresponds to spatial frequency of 0.312 Å^{-1}

8 Fourier-Shell correlation ⓘ

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

8.1 FSC ⓘ



*Reported resolution corresponds to spatial frequency of 0.312 $Å^{-1}$

8.2 Resolution estimates ⓘ

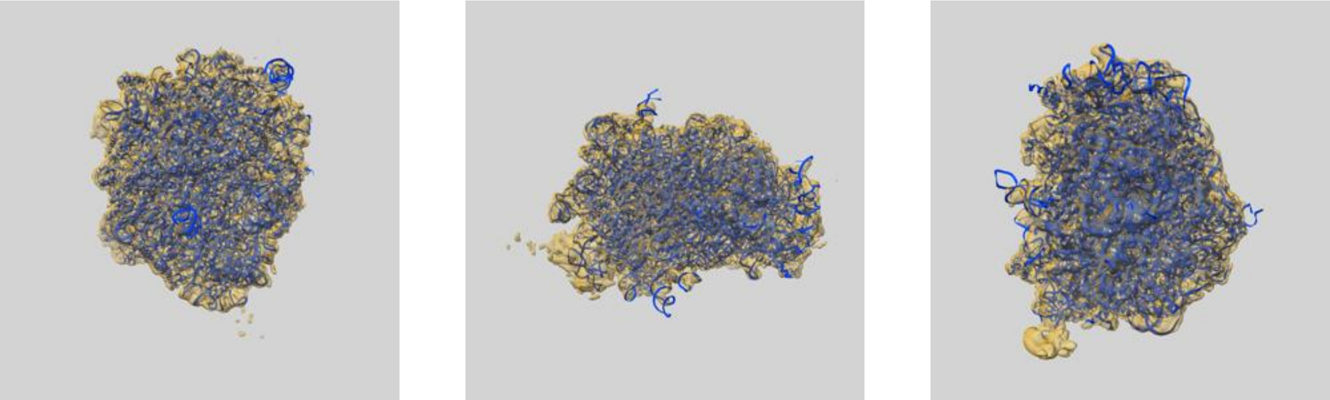
Resolution estimate (Å)	**Estimation criterion (FSC cut-off)**		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.22	4.08	3.34
Unmasked-calculated*	8.33	17.99	8.90

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.33 differs from the reported value 3.2 by more than 10 %

9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-14926 and PDB model 7ZS5. Per-residue inclusion information can be found in section 3 on page 12.

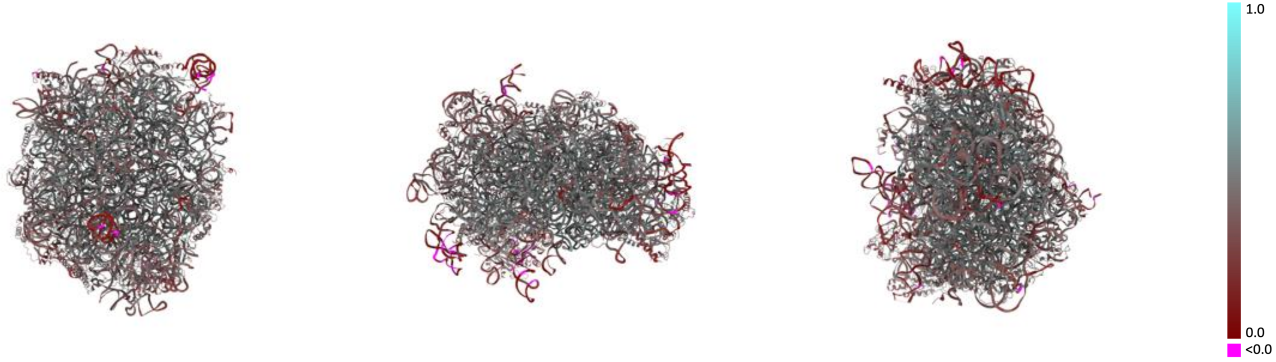
9.1 Map-model overlay



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

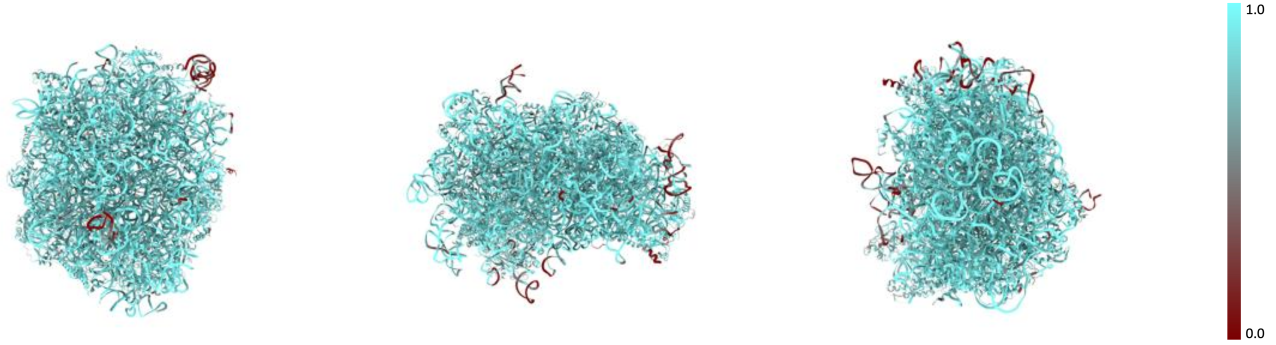
9.2 Q-score mapped to coordinate model ⓘ



X Y Z

The images above show the model with each residue coloured according 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.

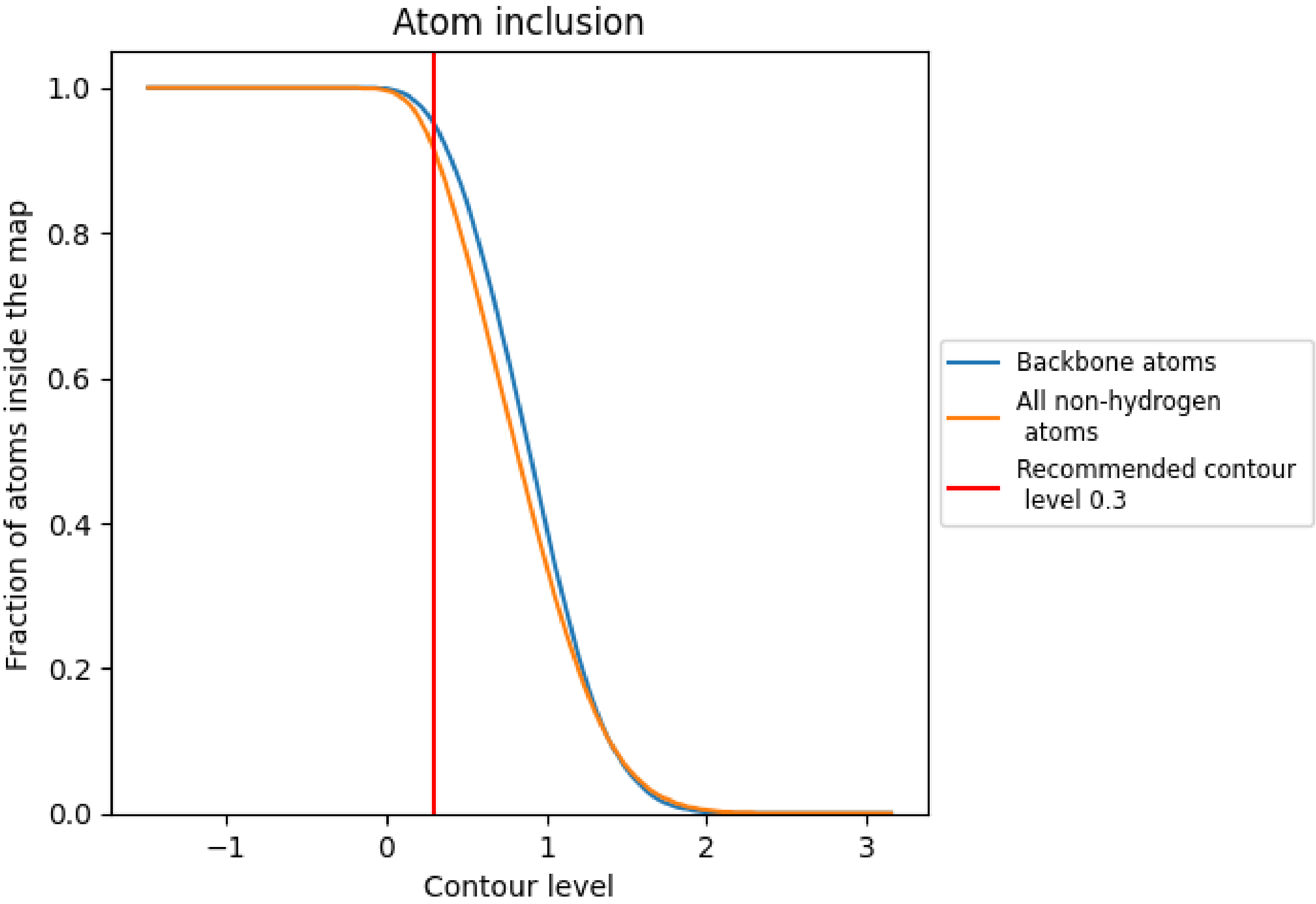
9.3 Atom inclusion mapped to coordinate model ⓘ



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.3).

9.4 Atom inclusion ⓘ



At the recommended contour level, 95% of all backbone atoms, 91% 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 (0.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9140	0.4210
1	0.9390	0.4160
2	0.5330	0.1110
3	0.9620	0.4120
4	0.9780	0.4490
A	0.8320	0.3510
BA	0.8560	0.4560
BB	0.9190	0.4630
BC	0.9110	0.4740
BD	0.9180	0.4570
BE	0.9190	0.4580
BF	0.8490	0.3730
BG	0.8310	0.3830
BH	0.8890	0.4470
BI	0.8770	0.3950
BJ	0.8560	0.4280
BK	0.8610	0.4220
BL	0.8000	0.3220
BM	0.8720	0.4410
BN	0.8470	0.3940
BO	0.9440	0.4970
BP	0.9230	0.4640
BQ	0.9130	0.4430
BR	0.8930	0.4620
BS	0.8820	0.4380
BT	0.8730	0.4500
BU	0.8740	0.4400
BV	0.8820	0.4000
BW	0.9140	0.4720
BX	0.8550	0.4210
BY	0.9400	0.4720
BZ	0.8700	0.4380
Ba	0.8710	0.4240
Bb	0.9110	0.4600
Bc	0.8940	0.4210

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Chain	**Atom inclusion**	**Q-score**
Bd	🟦 0.8540	⬛ 0.4150
Be	🟦 0.8810	⬛ 0.4630
Bf	🟦 0.8880	⬛ 0.4570
Bg	🟦 0.9030	⬛ 0.4710
Bh	🟦 0.8720	⬛ 0.4410
Bi	🟦 0.9120	⬛ 0.4320
Bj	🟦 0.8730	⬛ 0.4210
Bk	🟦 0.9450	⬛ 0.5100
Bl	🟦 0.7910	⬛ 0.4030
Bm	🟦 0.9120	⬛ 0.4690
Bn	🟦 0.9130	⬛ 0.4600