wwPDB EM Validation Summary Report (i)

Dec 11, 2022 – 05:17 pm GMT

PDB ID	:	6SWA
EMDB ID	:	EMD-10321
Title	:	Mus musculus brain neocortex ribosome 60S bound to Ebp1
Authors	:	Kraushar, M.L.; Sprink, T.
Deposited on	:	2019-09-20
Resolution	:	3.10 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

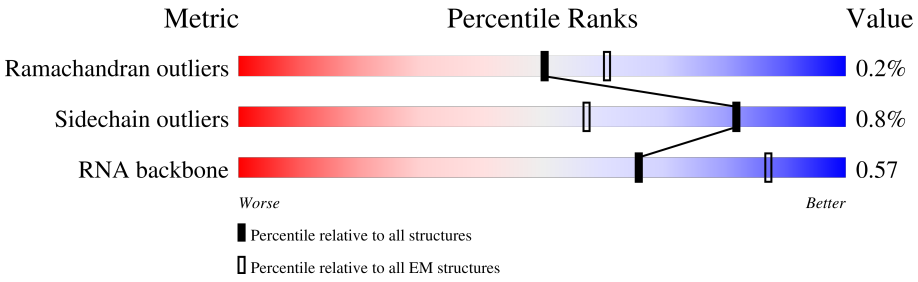
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
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	A	252	7% 99% .
2	B	394	6% 99% .
3	C	363	9% 100%
4	D	294	11% 100%
5	E	194	18% 99% .
6	F	234	11% 100%
7	G	234	18% 99% .
8	H	191	6% 100%

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Mol	Chain	Length	Quality of chain
9	I	211	11% 99%
10	J	169	21% 99%
11	K	205	17% 100%
12	L	139	5% 100%
13	M	203	100%
14	N	195	99%
15	O	153	5% 100%
16	P	185	6% 100%
17	Q	175	99%
18	R	157	6% 99%
19	S	101	17% 99%
20	T	129	6% 99%
21	U	62	11% 100%
22	V	118	12% 98%
23	W	127	5% 99%
24	X	134	10% 98%
25	Y	147	5% 100%
26	Z	68	18% 100%
27	a	97	6% 100%
28	b	106	10% 99%
29	c	129	8% 99%
30	d	109	5% 100%
31	e	114	8% 98%
32	f	122	10% 100%
33	g	98	17% 100%

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Mol	Chain	Length	Quality of chain
34	h	84	100%
35	i	69	23% 100%
36	j	50	14% 100%
37	k	50	8% 98%
38	l	25	16% 100%
39	m	105	16% 100%
40	n	91	11% 100%
41	o	184	15% 99%
42	p	122	6% 99%
43	q	3612	9% 84% 16%
44	r	157	11% 79% 21%
45	s	119	87% 13%
46	t	353	58% 92% 7%

2 Entry composition (i)

There are 48 unique types of molecules in this entry. The entry contains 138160 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 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	252	1930	1209	395	320	6	0	0

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	394	3178	2024	597	543	14	0	0

- Molecule 3 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	363	2897	1822	578	482	15	0	0

- Molecule 4 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	D	294	2395	1509	442	430	14	0	0

- Molecule 5 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	E	194	1576	1008	296	270	2	0	0

- Molecule 6 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	F	234	1947	1251	375	313	8	0	0

- Molecule 7 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	234	Total	C	N	O	S	0	0
			1879	1197	361	317	4		

- Molecule 8 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	191	Total	C	N	O	S	0	0
			1527	960	285	276	6		

- Molecule 9 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	208	Total	C	N	O	S	0	0
			1692	1074	327	278	13		

- Molecule 10 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	169	Total	C	N	O	S	0	0
			1353	855	252	240	6		

- Molecule 11 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	205	Total	C	N	O	S	0	0
			1660	1038	342	276	4		

- Molecule 12 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	139	Total	C	N	O	S	0	0
			1143	732	221	183	7		

- Molecule 13 is a protein called 60S ribosomal protein L15.

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

- Molecule 14 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	195	Total	C	N	O	S	0	0
			1599	1029	314	250	6		

- Molecule 15 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 16 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	185	Total	C	N	O	S	0	0
			1504	941	312	247	4		

- Molecule 17 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	175	Total	C	N	O	S	0	0
			1447	920	283	233	11		

- Molecule 18 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	157	Total	C	N	O	S	0	0
			1284	815	251	213	5		

- Molecule 19 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	101	Total	C	N	O	S	0	0
			826	529	145	150	2		

- Molecule 20 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	129	Total	C	N	O	S	0	0
			969	613	182	169	5		

- Molecule 21 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	62	Total	C	N	O	S	0	0
			520	332	102	84	2		

- Molecule 22 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	118	Total	C	N	O	S	0	0
			966	618	181	166	1		

- Molecule 23 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	127	Total	C	N	O	S	0	0
			1064	668	216	177	3		

- Molecule 24 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	134	Total	C	N	O	S	0	0
			1103	712	207	181	3		

- Molecule 25 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	147	Total	C	N	O	S	0	0
			1164	736	239	185	4		

- Molecule 26 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	68	Total	C	N	O	S	0	0
			558	344	122	90	2		

- Molecule 27 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	a	97	Total	C	N	O	S	0	0
			753	478	133	135	7		

- Molecule 28 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	b	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

- Molecule 29 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	c	129	Total	C	N	O	S	0	0
			1064	673	220	166	5		

- Molecule 30 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	d	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 31 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	e	114	Total	C	N	O	S	0	0
			906	565	187	148	6		

- Molecule 32 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	f	122	Total	C	N	O	S	0	0
			1015	643	204	167	1		

- Molecule 33 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	98	Total	C	N	O	S	0	0
			802	499	168	130	5		

- Molecule 34 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	h	84	Total	C	N	O	S	0	0
			689	423	152	109	5		

- Molecule 35 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	69	Total	C	N	O	S	0	0
			568	365	103	99	1		

- Molecule 36 is a protein called Ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	j	50	Total	C	N	O	S	0	0
			443	281	98	63	1		

- Molecule 37 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	k	50	Total	C	N	O	S	0	0
			411	254	87	64	6		

- Molecule 38 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	l	25	Total	C	N	O	S	0	0
			240	145	64	28	3		

- Molecule 39 is a protein called Ribosomal protein L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	m	105	Total	C	N	O	S	0	0
			863	542	175	140	6		

- Molecule 40 is a protein called Ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	n	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 41 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	o	184	Total	C	N	O	S	0	0
			1542	955	332	246	9		

- Molecule 42 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	p	122	Total	C	N	O	S	0	0
			980	606	204	165	5		

- Molecule 43 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	q	3612	Total	C	N	O	P	0	0
			77430	34484	14158	25176	3612		

- Molecule 44 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	r	157	Total	C	N	O	P	0	0
			3337	1489	587	1104	157		

- Molecule 45 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	s	119	Total	C	N	O	P	0	0
			2541	1132	454	836	119		

- Molecule 46 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	t	353	Total	C	N	O	S	0	0
			2739	1729	470	523	17		

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

Mol	Chain	Residues	Atoms		AltConf
47	B	1	Total	Mg	0
			1	1	
47	K	1	Total	Mg	0
			1	1	
47	M	1	Total	Mg	0
			1	1	
47	P	1	Total	Mg	0
			1	1	
47	W	1	Total	Mg	0
			1	1	
47	b	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms	AltConf
47	c	1	Total Mg 1 1	0
47	l	1	Total Mg 1 1	0
47	q	223	Total Mg 223 223	0
47	r	7	Total Mg 7 7	0
47	s	9	Total Mg 9 9	0

- Molecule 48 is ZINC ION (three-letter code: ZN) (formula: Zn).

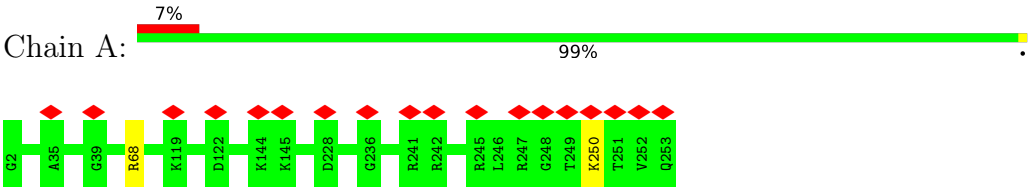
Mol	Chain	Residues	Atoms	AltConf
48	h	1	Total Zn 1 1	0
48	m	1	Total Zn 1 1	0
48	n	1	Total Zn 1 1	0

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.

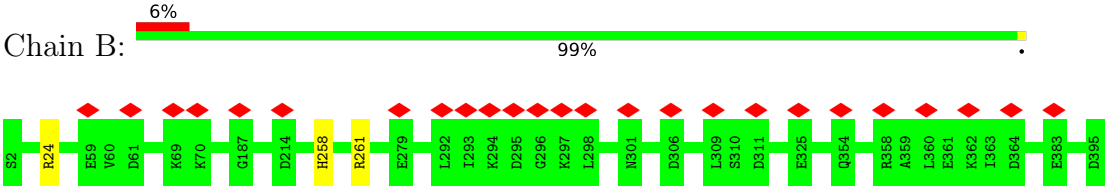
• Molecule 1: 60S ribosomal protein L8

Chain A:



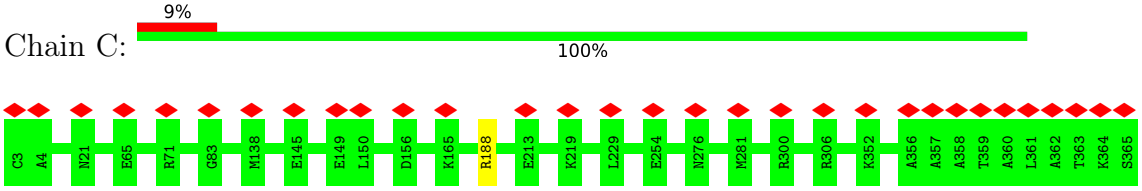
• Molecule 2: 60S ribosomal protein L3

Chain B:



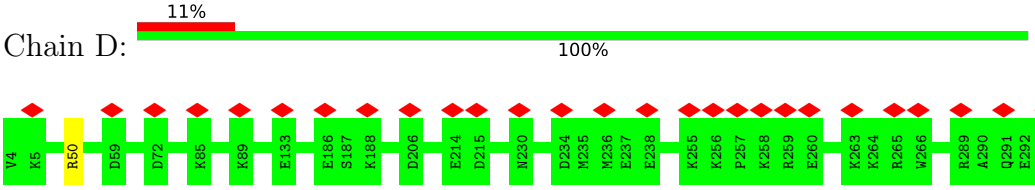
• Molecule 3: 60S ribosomal protein L4

Chain C:



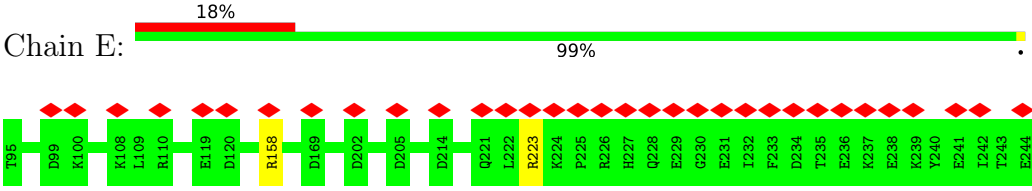
• Molecule 4: 60S ribosomal protein L5

Chain D:



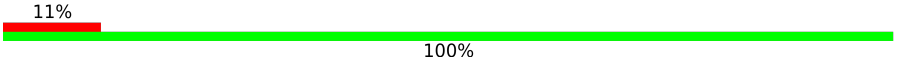
• Molecule 5: 60S ribosomal protein L6

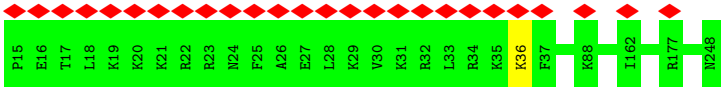
Chain E:



• Molecule 6: 60S ribosomal protein L7

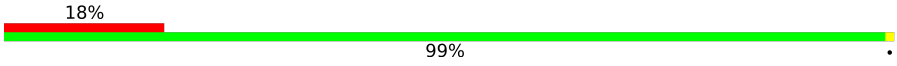
Chain F:





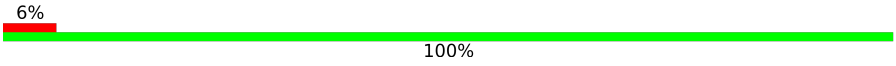
• Molecule 7: 60S ribosomal protein L7a

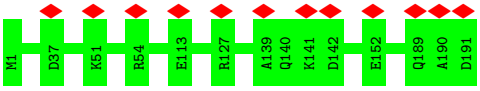
Chain G:



• Molecule 8: 60S ribosomal protein L9

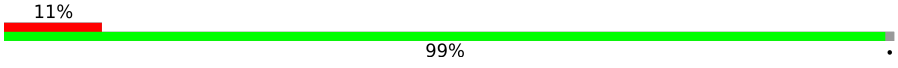
Chain H:

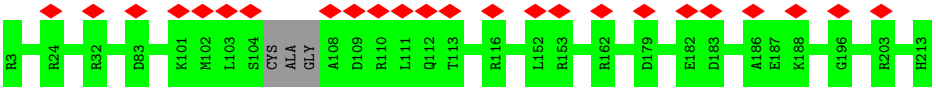




• Molecule 9: 60S ribosomal protein L10

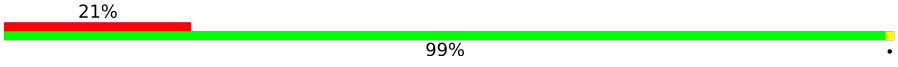
Chain I:

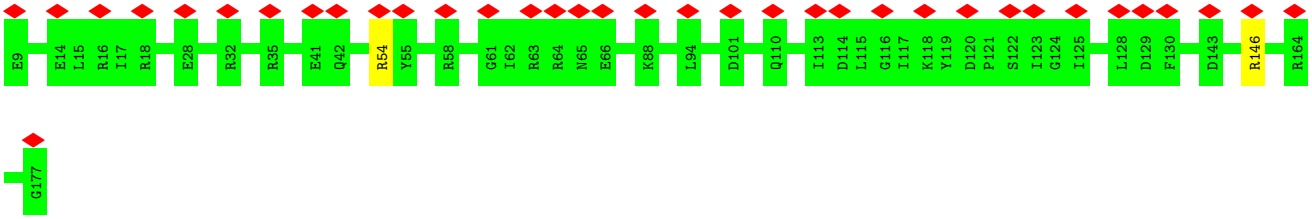




• Molecule 10: 60S ribosomal protein L11

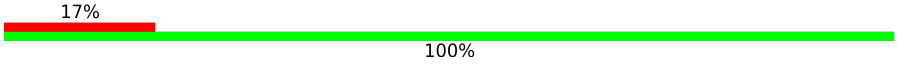
Chain J:

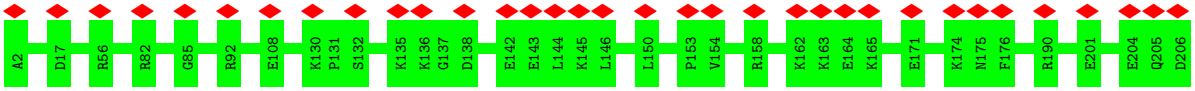




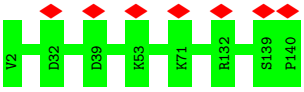
• Molecule 11: 60S ribosomal protein L13

Chain K:

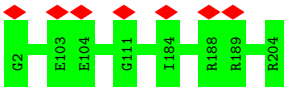




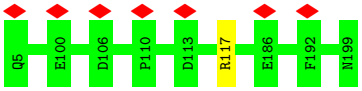
• Molecule 12: 60S ribosomal protein L14



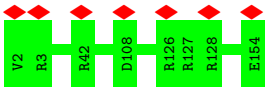
• Molecule 13: 60S ribosomal protein L15



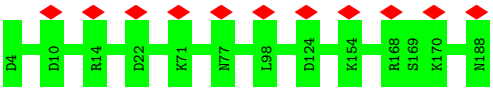
• Molecule 14: 60S ribosomal protein L13a



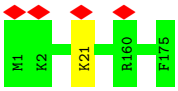
• Molecule 15: 60S ribosomal protein L17



• Molecule 16: 60S ribosomal protein L18

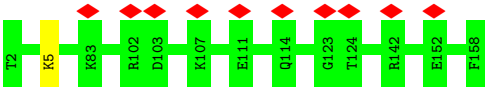


• Molecule 17: 60S ribosomal protein L18a



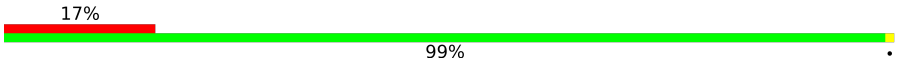
• Molecule 18: 60S ribosomal protein L21

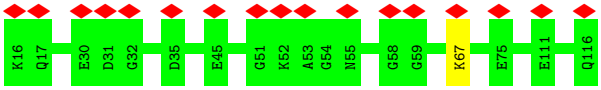
Chain R:



• Molecule 19: 60S ribosomal protein L22

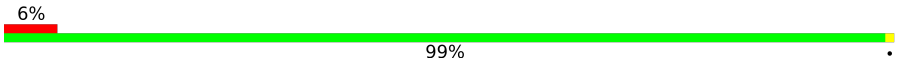
Chain S:

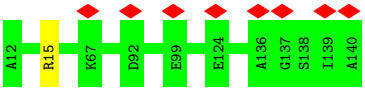




• Molecule 20: 60S ribosomal protein L23

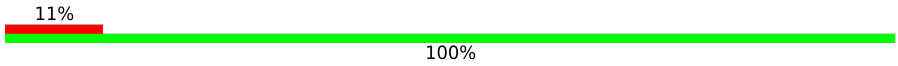
Chain T:

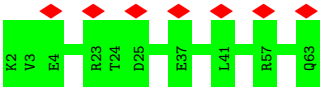




• Molecule 21: 60S ribosomal protein L24

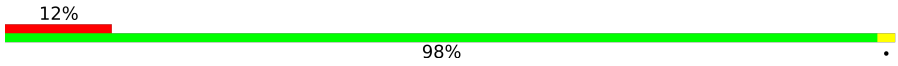
Chain U:

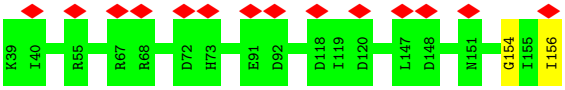




• Molecule 22: 60S ribosomal protein L23a

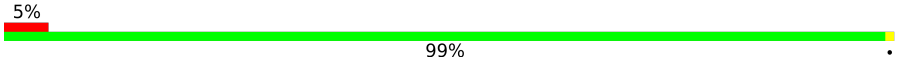
Chain V:

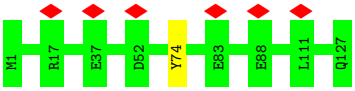




• Molecule 23: Ribosomal protein L26

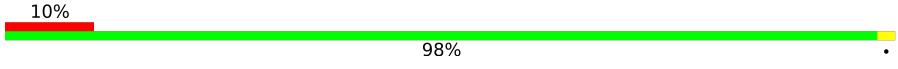
Chain W:

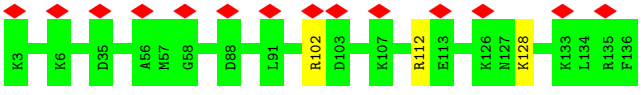




• Molecule 24: 60S ribosomal protein L27

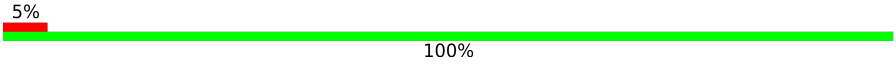
Chain X:

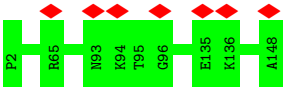




• Molecule 25: 60S ribosomal protein L27a

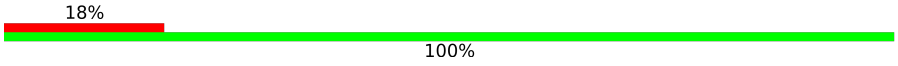
Chain Y:

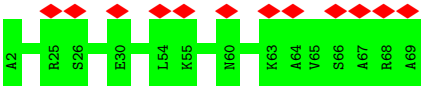




• Molecule 26: 60S ribosomal protein L29

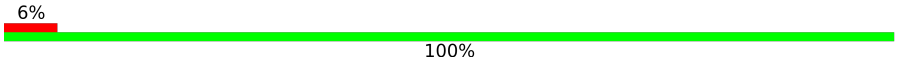
Chain Z:

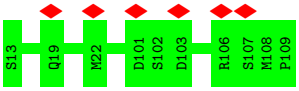




• Molecule 27: 60S ribosomal protein L30

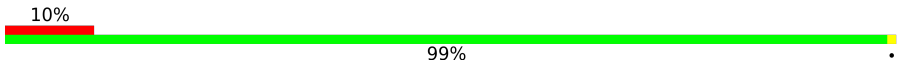
Chain a:

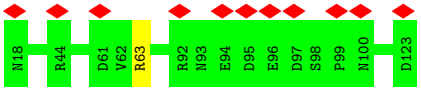




• Molecule 28: 60S ribosomal protein L31

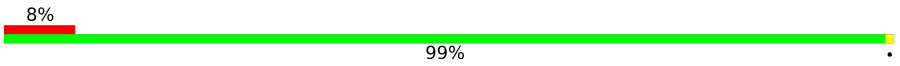
Chain b:

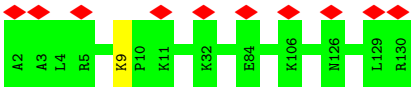




• Molecule 29: 60S ribosomal protein L32

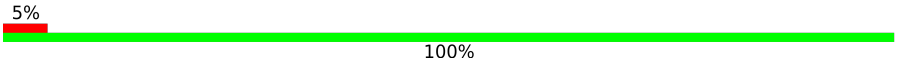
Chain c:

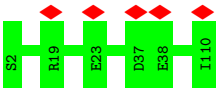




• Molecule 30: 60S ribosomal protein L35a

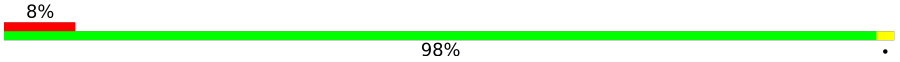
Chain d:

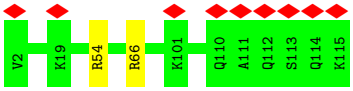




• Molecule 31: 60S ribosomal protein L34

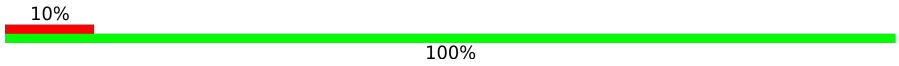
Chain e:

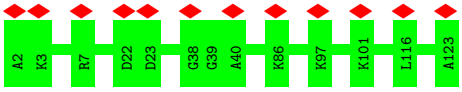




• Molecule 32: 60S ribosomal protein L35

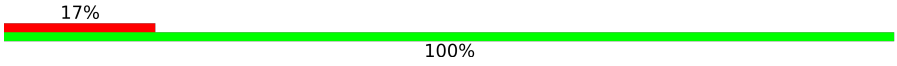
Chain f:

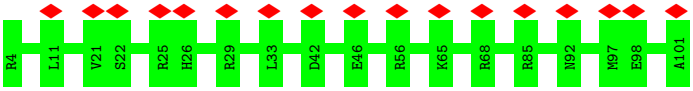




• Molecule 33: 60S ribosomal protein L36

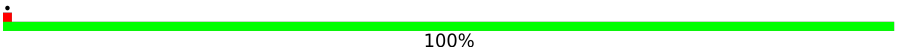
Chain g:





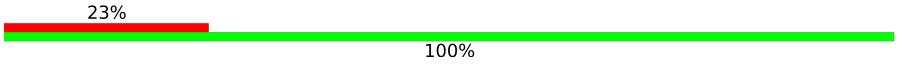
• Molecule 34: 60S ribosomal protein L37

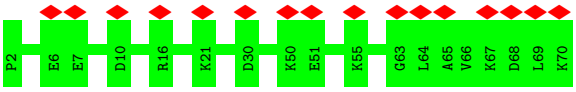
Chain h:



• Molecule 35: 60S ribosomal protein L38

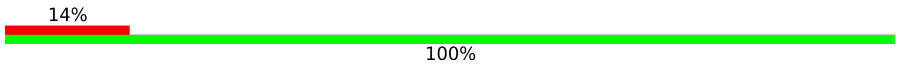
Chain i:

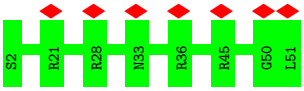




• Molecule 36: Ribosomal protein L39

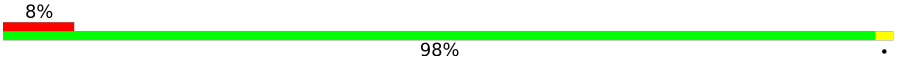
Chain j:

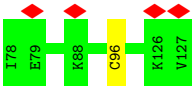




• Molecule 37: 60S ribosomal protein L40

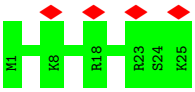
Chain k:





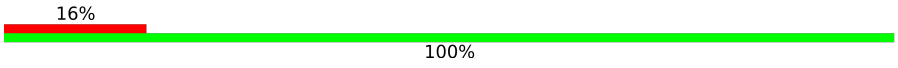
• Molecule 38: 60S ribosomal protein L41

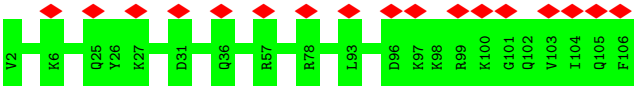
Chain l:



• Molecule 39: Ribosomal protein L36A

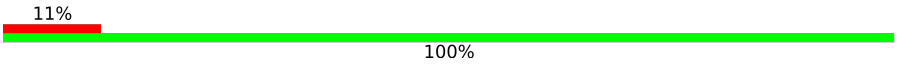
Chain m:

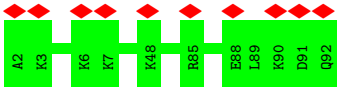




• Molecule 40: Ribosomal protein L37a

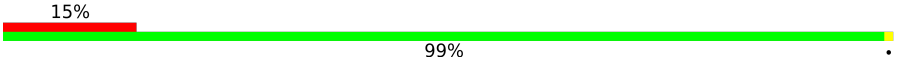
Chain n:

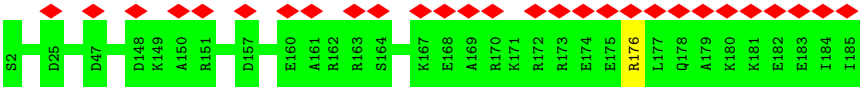




• Molecule 41: 60S ribosomal protein L19

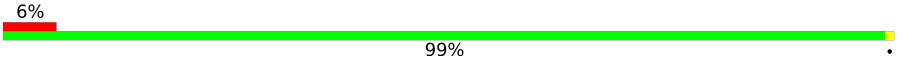
Chain o:

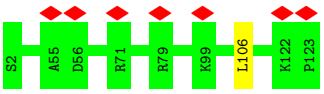




• Molecule 42: 60S ribosomal protein L28

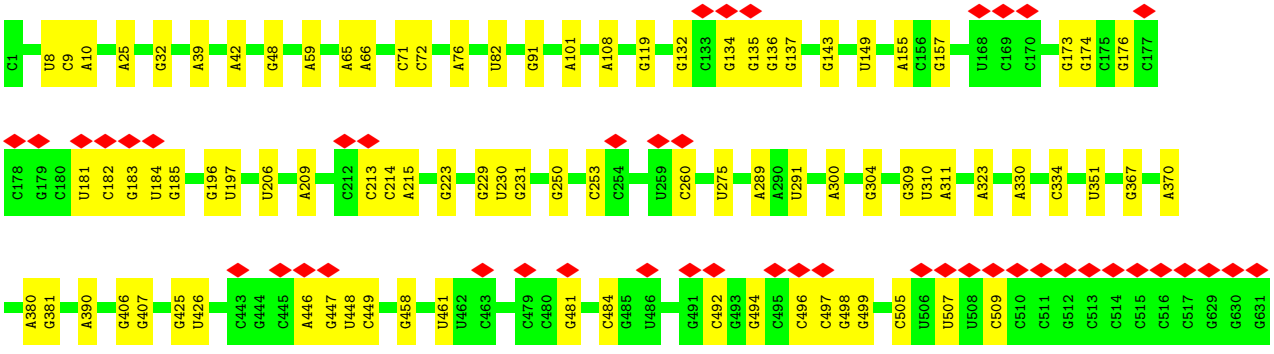
Chain p:

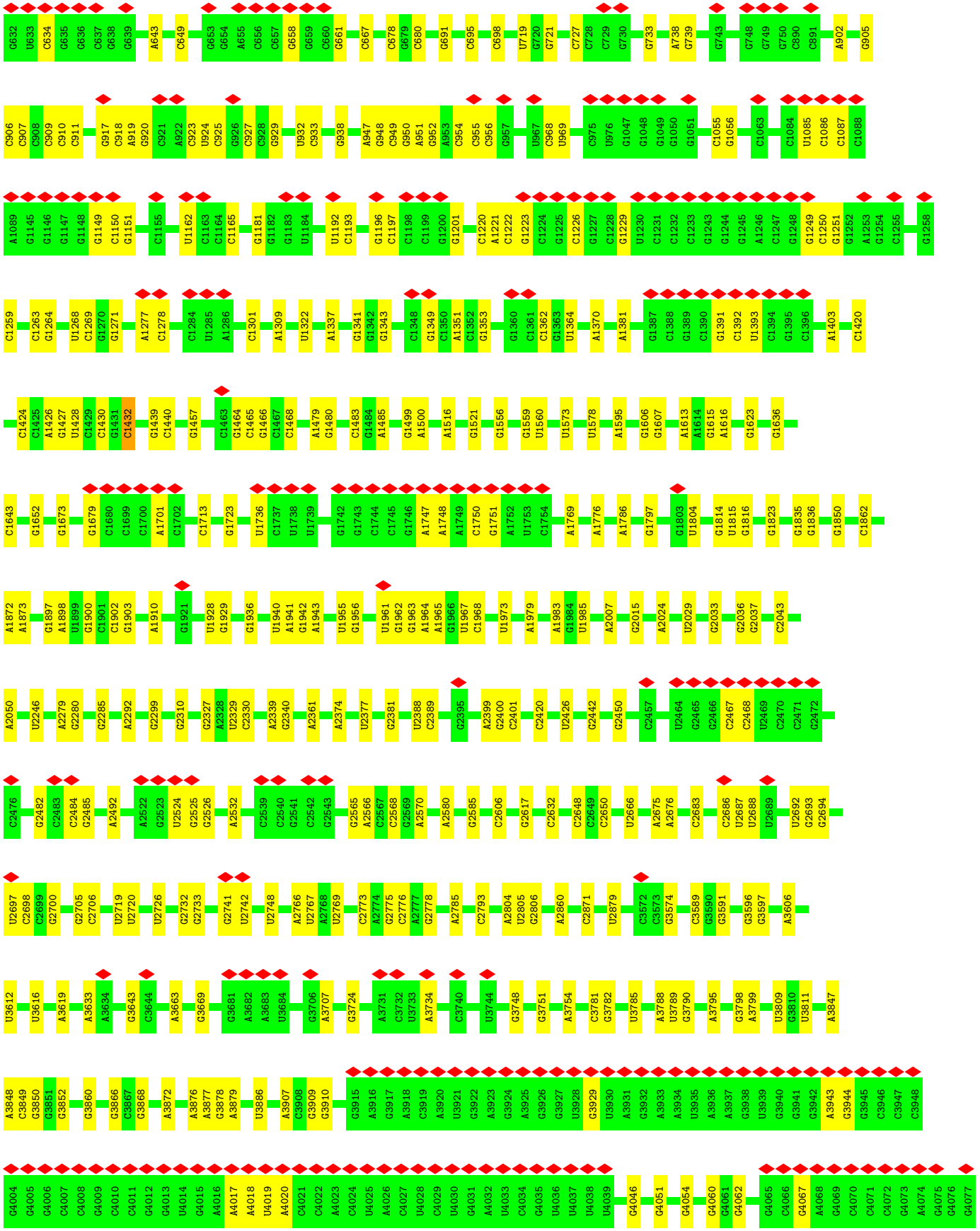


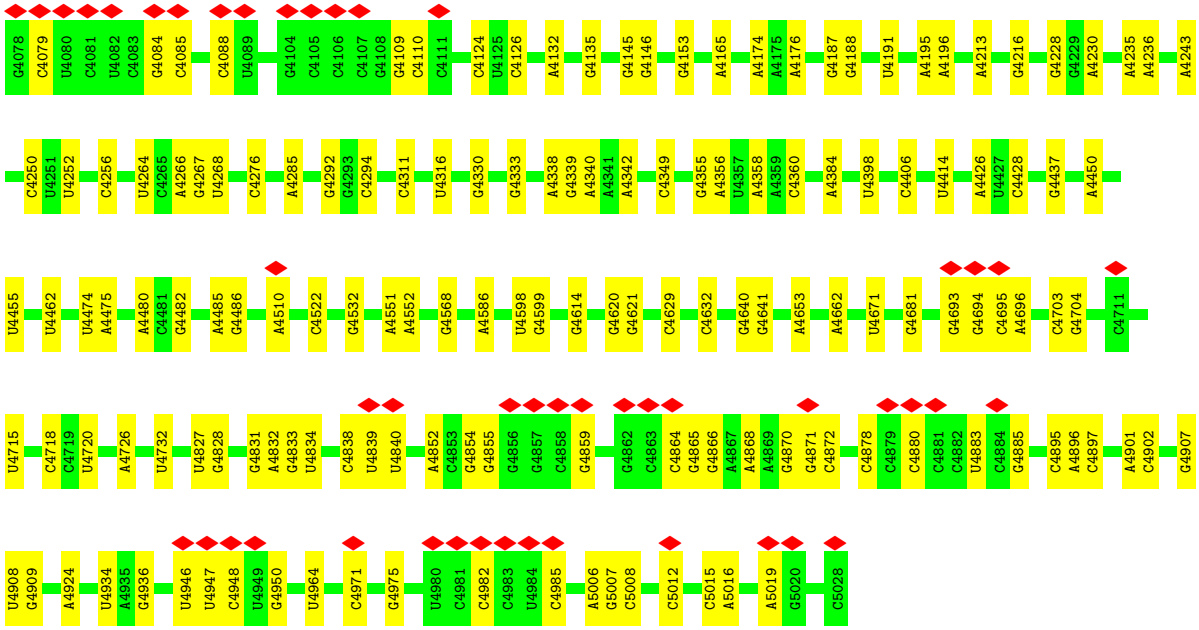


• Molecule 43: 28S ribosomal RNA

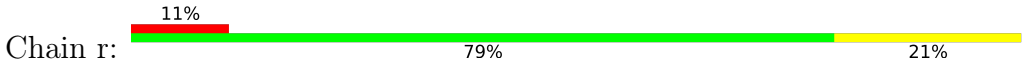
Chain q:

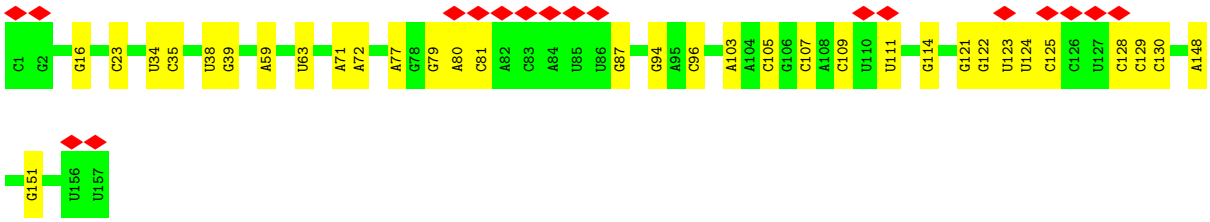



G632 U633 C634 G635 G636 C637 G638 G639 A643 C649 G653 G654 A655 C656 C657 G658 G659 C660 G661 C667 C678 G679 C680 G691 C695 C698 U719 G720 G721 C727 C728 C729 G730 G733 A738 G739 G743 G748 G749 G750 C890 C891 A902 G905
C906 C907 C908 C909 C910 C911 G917 C918 A919 G920 C921 A922 C923 U924 C925 G926 C927 G928 G929 U932 C933 G938 A947 G948 C949 G950 A951 G952 A953 C954 C955 C956 G957 U967 C968 U969 C975 U976 G1047 G1048 G1049 G1050 G1051 C1055 G1056 C1063 C1084 U1085 C1086 C1087 C1088
A1089 C1145 G1146 G1147 G1148 G1149 C1150 G1151 C1155 U1162 C1163 C1164 C1165 G1181 G1182 G1183 U1184 U1192 C1193 G1196 C1197 C1198 C1199 G1200 G1201 C1220 A1221 C1222 G1223 C1224 G1225 C1226 G1227 C1228 G1229 U1230 C1231 C1232 C1233 G1243 G1244 G1245 A1246 C1247 G1248 G1249 C1250 G1251 G1252 A1253 G1254 C1255 G1258
C1259 C1263 G1264 U1268 C1269 G1270 G1271 A1277 C1278 C1284 U1285 A1286 C1301 A1309 U1322 A1337 G1341 G1342 G1343 C1348 G1349 C1350 A1351 C1352 G1353 G1360 C1361 C1362 G1363 U1364 A1370 A1381 G1387 C1388 G1389 C1390 G1391 C1392 U1393 C1394 G1395 C1396 A1403 C1420
C1424 C1425 A1426 G1427 U1428 C1429 C1430 G1431 C1432 G1439 C1440 G1457 G1463 G1464 C1465 G1466 C1467 C1468 A1479 G1480 C1483 G1484 A1485 G1499 A1500 A1516 G1521 G1556 G1559 U1560 U1573 U1578 A1595 G1606 G1607 A1613 A1614 G1615 A1616 G1623 G1636
C1643 G1652 G1673 G1679 C1680 C1699 C1700 A1701 C1702 C1713 G1723 U1736 C1737 U1738 U1739 G1742 G1743 C1744 C1745 G1746 A1747 A1748 C1749 C1750 G1751 A1752 U1753 C1754 A1769 A1776 A1786 G1797 G1803 U1804 G1814 U1815 G1816 G1823 G1835 G1836 G1850 C1862
A1872 A1873 G1897 A1898 U1899 G1900 C1901 C1902 G1903 A1910 G1921 U1928 G1929 G1936 U1940 A1941 G1942 A1943 U1955 G1956 U1961 G1962 G1963 A1964 A1965 G1966 U1967 C1968 U1973 A1979 A1983 G1984 U1985 A2007 G2015 A2024 U2029 G2033 G2036 G2037 C2043
A2050 U2246 A2279 C2280 G2285 A2292 G2299 G2310 G2327 A2328 U2329 C2330 A2339 G2340 A2361 A2374 U2377 G2381 U2388 C2389 G2395 A2399 G2400 C2401 C2420 U2426 G2442 G2450 C2457 U2464 G2465 G2466 C2467 C2468 U2469 C2470 C2471 G2472
C2476 G2482 C2483 C2484 G2485 A2492 A2522 G2523 U2524 G2525 G2526 A2532 C2539 C2540 G2541 C2542 G2543 G2565 A2566 C2567 C2568 G2569 A2570 A2580 G2585 C2606 G2617 C2632 C2648 C2649 C2650 U2666 A2675 A2676 C2683 C2686 U2687 U2688 U2689 U2692 G2693 G2694
U2697 C2698 C2699 G2700 G2705 C2706 U2719 U2720 U2726 G2732 G2733 G2741 U2742 U2748 A2766 U2767 A2768 U2769 C2773 A2774 G2775 C2776 A2777 G2778 A2785 C2793 A2804 U2805 G2806 A2860 C2871 U2879 C3572 C3573 G3574 C3589 G3590 G3591 G3596 G3597 A3606
U3612 U3616 A3619 A3633 A3634 G3643 C3644 A3663 G3669 G3681 A3682 A3683 U3684 G3706 A3707 G3724 A3731 C3732 U3733 A3734 C3740 U3744 G3748 G3751 A3754 C3781 G3782 U3785 A3788 U3789 G3790 A3795 G3798 A3799 U3809 G3810 U3811 A3847
A3848 C3849 G3850 G3851 G3852 G3860 G3866 C3867 G3868 A3872 A3876 A3877 G3878 A3879 U3886 A3907 C3908 G3909 G3910 G3915 A3916 G3917 A3918 C3919 A3920 U3921 G3922 A3923 G3924 A3925 G3926 G3927 U3928 G3929 U3930 A3931 G3932 A3933 A3934 U3935 A3936 A3937 G3938 U3939 G3940 G3941 G3942 A3943 G3944 G3945 C3946 C3947 C3948
G4004 G4005 G4006 C4007 C4008 G4009 C4010 C4011 G4012 G4013 U4014 G4015 A4016 A4017 A4018 U4019 A4020 C4021 C4022 A4023 C4024 U4025 A4026 C4027 U4028 C4029 U4030 G4031 A4032 U4033 C4034 G4035 U4036 U4037 U4038 U4039 G4046 G4051 G4054 G4060 G4061 G4062 G4065 C4066 G4067 A4068 G4069 C4070 C4071 C4072 G4073 A4074 G4075 G4076 G4077

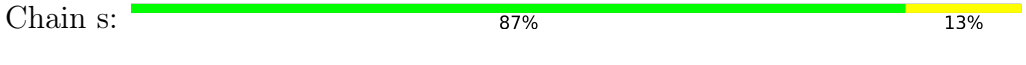


• Molecule 44: 5.8S ribosomal RNA

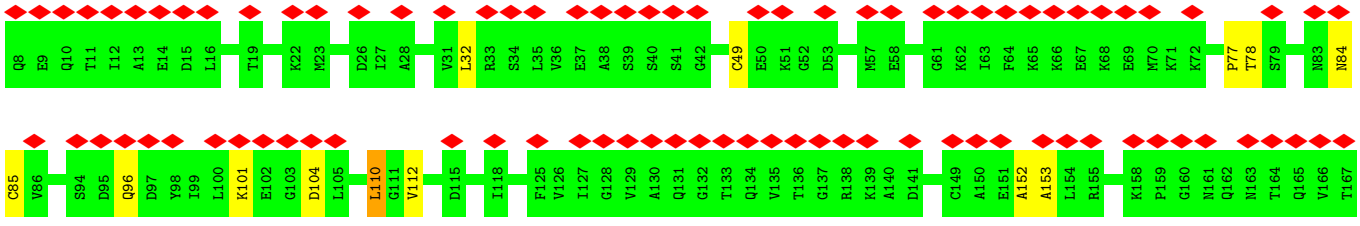


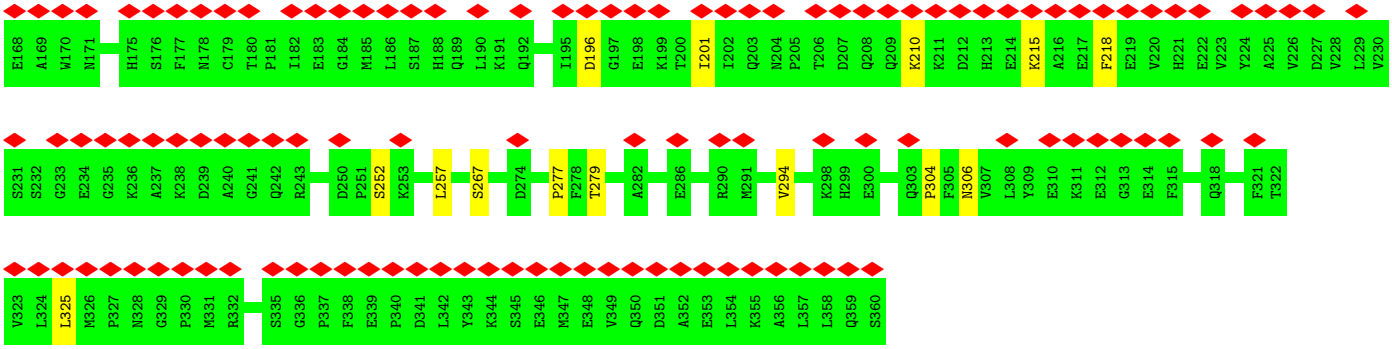


• Molecule 45: 5S ribosomal RNA



• Molecule 46: Proliferation-associated protein 2G4




E168 A169 W170 N171 H175 S176 F177 N178 C179 T180 P181 I182 E183 G184 M185 L186 S187 H188 Q189 L190 K191 Q192 I195 D196 G197 E198 K199 T200 I201 I202 Q203 N204 P205 T206 D207 Q208 Q209 K210 K211 D212 H213 E214 K215 A216 E217 F218 E219 V220 H221 E222 V223 Y224 A225 V226 D227 V228 L229 V230
S231 S232 G233 E234 G235 K236 A237 K238 D239 A240 G241 Q242 R243 D250 P251 S252 K253 L257 S267 D274 P277 F278 T279 A282 E286 R290 M291 V294 K298 H299 E300 Q303 P304 F305 N306 V307 L308 Y309 E310 K311 E312 G313 E314 F315 Q318 F321 T322
V323 L324 L325 M326 P327 N328 G329 P330 M331 R332 S335 G336 P337 F338 E339 P340 D341 L342 Y343 K344 S345 E346 M347 E348 V349 Q350 D351 A352 E353 L354 K355 A356 L357 L358 Q359 S360

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	208206	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 ($e^-/Å^2$)	31.78	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	31000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	20.986	Depositor
Minimum map value	-10.475	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.898	Depositor
Recommended contour level	4.0	Depositor
Map size (Å)	477.612, 477.612, 477.612	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3267, 1.3267, 1.3267	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.24	0/1968	0.44	0/2639
2	B	0.24	0/3245	0.42	0/4343
3	C	0.23	0/2951	0.39	0/3961
4	D	0.24	0/2440	0.39	0/3266
5	E	0.24	0/1607	0.43	0/2159
6	F	0.24	0/1983	0.38	0/2641
7	G	0.24	0/1913	0.42	0/2577
8	H	0.25	0/1545	0.44	0/2076
9	I	0.24	0/1730	0.40	0/2311
10	J	0.24	0/1376	0.41	0/1841
11	K	0.24	0/1691	0.41	0/2264
12	L	0.24	0/1165	0.39	0/1558
13	M	0.23	0/1746	0.39	0/2338
14	N	0.24	0/1629	0.39	0/2178
15	O	0.23	0/1268	0.41	0/1700
16	P	0.23	0/1528	0.40	0/2038
17	Q	0.24	0/1486	0.42	0/1994
18	R	0.24	0/1312	0.41	0/1752
19	S	0.25	0/840	0.43	0/1126
20	T	0.25	0/983	0.42	0/1319
21	U	0.24	0/533	0.37	0/710
22	V	0.24	0/983	0.41	0/1323
23	W	0.26	0/1081	0.42	0/1439
24	X	0.25	0/1126	0.39	0/1502
25	Y	0.24	0/1193	0.40	0/1593
26	Z	0.23	0/568	0.37	0/750
27	a	0.24	0/764	0.41	0/1026
28	b	0.23	0/894	0.43	0/1204
29	c	0.23	0/1082	0.40	0/1443
30	d	0.25	0/895	0.43	0/1198
31	e	0.24	0/916	0.42	0/1221
32	f	0.23	0/1023	0.38	0/1350

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	g	0.23	0/813	0.38	0/1078
34	h	0.26	0/703	0.44	0/929
35	i	0.24	0/574	0.41	0/760
36	j	0.22	0/453	0.39	0/599
37	k	0.30	0/417	0.46	0/553
38	l	0.21	0/241	0.32	0/305
39	m	0.24	0/877	0.40	0/1156
40	n	0.24	0/718	0.40	0/953
41	o	0.22	0/1558	0.36	0/2059
42	p	0.23	0/995	0.45	1/1333 (0.1%)
43	q	0.17	0/86618	0.74	13/135116 (0.0%)
44	r	0.16	0/3726	0.74	0/5804
45	s	0.19	0/2839	0.76	1/4425 (0.0%)
46	t	0.28	0/2786	0.51	0/3753
All	All	0.20	0/148782	0.65	15/219663 (0.0%)

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
2	B	0	1

There are no bond length outliers.

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
43	q	909	C	N1-C2-O2	10.02	124.91	118.90
43	q	909	C	N3-C2-O2	-9.96	114.93	121.90
43	q	2650	C	N3-C2-O2	-6.87	117.09	121.90
43	q	667	C	N3-C2-O2	-6.85	117.11	121.90
43	q	2388	U	C2-N1-C1'	6.76	125.81	117.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	258	HIS	Peptide

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 (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	A	250/252 (99%)	234 (94%)	16 (6%)	0	100	100
2	B	392/394 (100%)	377 (96%)	15 (4%)	0	100	100
3	C	361/363 (99%)	344 (95%)	17 (5%)	0	100	100
4	D	292/294 (99%)	283 (97%)	9 (3%)	0	100	100
5	E	192/194 (99%)	178 (93%)	14 (7%)	0	100	100
6	F	232/234 (99%)	223 (96%)	9 (4%)	0	100	100
7	G	232/234 (99%)	228 (98%)	4 (2%)	0	100	100
8	H	189/191 (99%)	181 (96%)	8 (4%)	0	100	100
9	I	204/211 (97%)	200 (98%)	4 (2%)	0	100	100
10	J	167/169 (99%)	161 (96%)	6 (4%)	0	100	100
11	K	203/205 (99%)	185 (91%)	18 (9%)	0	100	100
12	L	137/139 (99%)	128 (93%)	9 (7%)	0	100	100
13	M	201/203 (99%)	197 (98%)	4 (2%)	0	100	100
14	N	193/195 (99%)	186 (96%)	7 (4%)	0	100	100
15	O	151/153 (99%)	147 (97%)	4 (3%)	0	100	100
16	P	183/185 (99%)	173 (94%)	10 (6%)	0	100	100
17	Q	173/175 (99%)	166 (96%)	7 (4%)	0	100	100
18	R	155/157 (99%)	149 (96%)	6 (4%)	0	100	100
19	S	99/101 (98%)	96 (97%)	3 (3%)	0	100	100
20	T	127/129 (98%)	127 (100%)	0	0	100	100
21	U	60/62 (97%)	60 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
22	V	116/118 (98%)	113 (97%)	2 (2%)	1 (1%)	17 52
23	W	125/127 (98%)	124 (99%)	1 (1%)	0	100 100
24	X	132/134 (98%)	128 (97%)	4 (3%)	0	100 100
25	Y	145/147 (99%)	140 (97%)	5 (3%)	0	100 100
26	Z	66/68 (97%)	61 (92%)	5 (8%)	0	100 100
27	a	95/97 (98%)	95 (100%)	0	0	100 100
28	b	104/106 (98%)	101 (97%)	3 (3%)	0	100 100
29	c	127/129 (98%)	121 (95%)	6 (5%)	0	100 100
30	d	107/109 (98%)	105 (98%)	2 (2%)	0	100 100
31	e	112/114 (98%)	108 (96%)	4 (4%)	0	100 100
32	f	120/122 (98%)	117 (98%)	3 (2%)	0	100 100
33	g	96/98 (98%)	91 (95%)	5 (5%)	0	100 100
34	h	82/84 (98%)	79 (96%)	3 (4%)	0	100 100
35	i	67/69 (97%)	65 (97%)	2 (3%)	0	100 100
36	j	48/50 (96%)	47 (98%)	1 (2%)	0	100 100
37	k	48/50 (96%)	46 (96%)	2 (4%)	0	100 100
38	l	23/25 (92%)	23 (100%)	0	0	100 100
39	m	103/105 (98%)	95 (92%)	8 (8%)	0	100 100
40	n	89/91 (98%)	87 (98%)	2 (2%)	0	100 100
41	o	182/184 (99%)	181 (100%)	1 (0%)	0	100 100
42	p	120/122 (98%)	110 (92%)	10 (8%)	0	100 100
46	t	351/353 (99%)	296 (84%)	43 (12%)	12 (3%)	3 21
All	All	6651/6742 (99%)	6356 (96%)	282 (4%)	13 (0%)	50 79

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
46	t	96	GLN
46	t	153	ALA
46	t	294	VAL
46	t	32	LEU
46	t	152	ALA

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	194/194 (100%)	192 (99%)	2 (1%)	76 90
2	B	342/342 (100%)	340 (99%)	2 (1%)	86 94
3	C	305/305 (100%)	304 (100%)	1 (0%)	92 96
4	D	247/247 (100%)	246 (100%)	1 (0%)	91 96
5	E	176/176 (100%)	174 (99%)	2 (1%)	73 89
6	F	204/204 (100%)	203 (100%)	1 (0%)	88 94
7	G	199/199 (100%)	197 (99%)	2 (1%)	76 90
8	H	170/170 (100%)	170 (100%)	0	100 100
9	I	178/179 (99%)	178 (100%)	0	100 100
10	J	142/142 (100%)	140 (99%)	2 (1%)	67 86
11	K	172/172 (100%)	172 (100%)	0	100 100
12	L	118/118 (100%)	118 (100%)	0	100 100
13	M	171/171 (100%)	171 (100%)	0	100 100
14	N	168/168 (100%)	167 (99%)	1 (1%)	86 94
15	O	134/134 (100%)	134 (100%)	0	100 100
16	P	163/163 (100%)	163 (100%)	0	100 100
17	Q	155/155 (100%)	154 (99%)	1 (1%)	86 94
18	R	137/137 (100%)	136 (99%)	1 (1%)	84 93
19	S	91/91 (100%)	90 (99%)	1 (1%)	73 89
20	T	100/100 (100%)	99 (99%)	1 (1%)	76 90
21	U	54/54 (100%)	54 (100%)	0	100 100
22	V	106/106 (100%)	105 (99%)	1 (1%)	78 91
23	W	119/119 (100%)	118 (99%)	1 (1%)	81 92
24	X	117/117 (100%)	114 (97%)	3 (3%)	46 74
25	Y	120/120 (100%)	120 (100%)	0	100 100
26	Z	58/58 (100%)	58 (100%)	0	100 100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
27	a	82/82 (100%)	82 (100%)	0	100 100
28	b	97/97 (100%)	96 (99%)	1 (1%)	76 90
29	c	115/115 (100%)	114 (99%)	1 (1%)	78 91
30	d	88/88 (100%)	88 (100%)	0	100 100
31	e	98/98 (100%)	96 (98%)	2 (2%)	55 80
32	f	109/109 (100%)	109 (100%)	0	100 100
33	g	85/85 (100%)	85 (100%)	0	100 100
34	h	71/71 (100%)	71 (100%)	0	100 100
35	i	64/64 (100%)	64 (100%)	0	100 100
36	j	47/47 (100%)	47 (100%)	0	100 100
37	k	46/46 (100%)	45 (98%)	1 (2%)	52 78
38	l	24/24 (100%)	24 (100%)	0	100 100
39	m	93/93 (100%)	93 (100%)	0	100 100
40	n	74/74 (100%)	74 (100%)	0	100 100
41	o	163/163 (100%)	162 (99%)	1 (1%)	86 94
42	p	106/106 (100%)	106 (100%)	0	100 100
46	t	297/302 (98%)	281 (95%)	16 (5%)	22 53
All	All	5799/5805 (100%)	5754 (99%)	45 (1%)	82 92

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	o	176	ARG
46	t	112	VAL
46	t	49	CYS
46	t	101	LYS
46	t	201	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 77 such sidechains are listed below:

Mol	Chain	Res	Type
27	a	51	ASN
42	p	100	ASN
30	d	80	ASN
36	j	25	GLN

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Mol	Chain	Res	Type
46	t	193	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
43	q	3600/3612 (99%)	569 (15%)	0
44	r	156/157 (99%)	33 (21%)	0
45	s	118/119 (99%)	15 (12%)	0
All	All	3874/3888 (99%)	617 (15%)	0

5 of 617 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
43	q	8	U
43	q	9	C
43	q	10	A
43	q	25	A
43	q	32	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 250 ligands modelled in this entry, 250 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
43	q	11

The worst 5 of 11 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	q	4734:C	O3'	4818:G	P	19.70
1	q	3948:C	O3'	4004:G	P	18.35
1	q	1202:G	O3'	1216:G	P	17.70
1	q	517:C	O3'	629:G	P	17.04
1	q	2881:G	O3'	3569:C	P	16.97

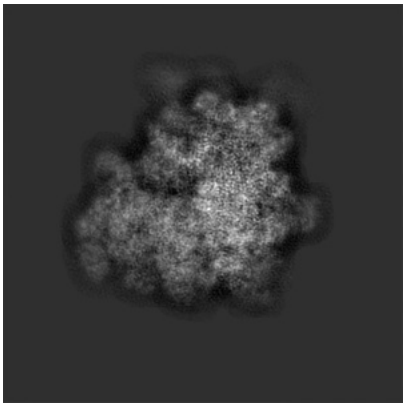
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-10321. These allow visual inspection of the internal detail of the map and identification of artifacts.

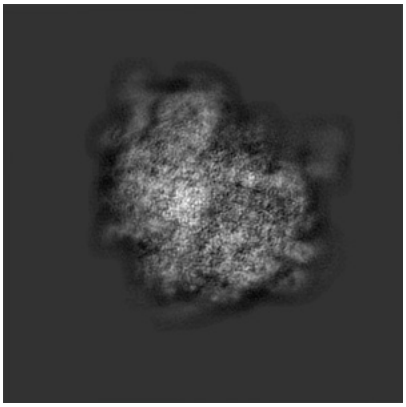
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

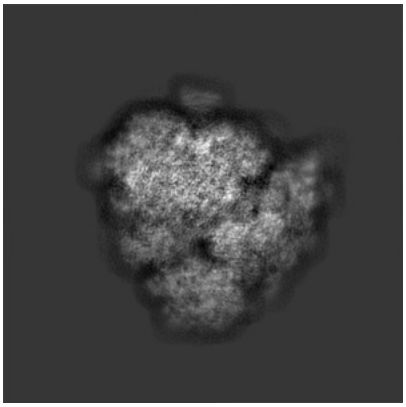
6.1.1 Primary map



X



Y

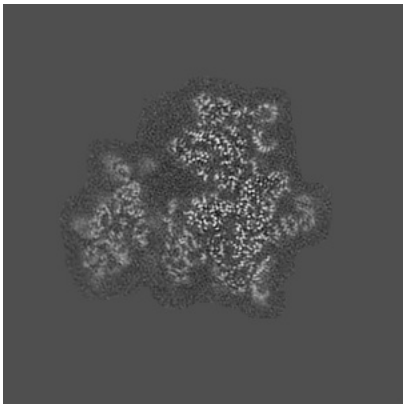


Z

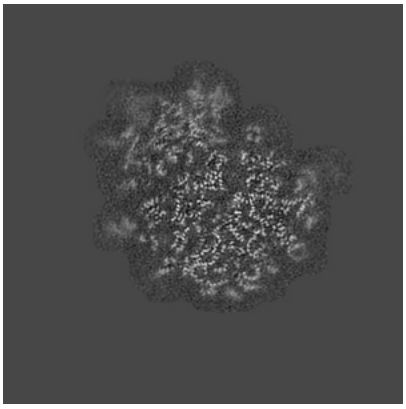
The images above show the map projected in three orthogonal directions.

6.2 Central slices

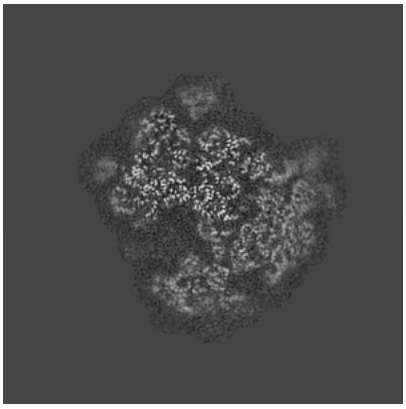
6.2.1 Primary map



X Index: 180



Y Index: 180

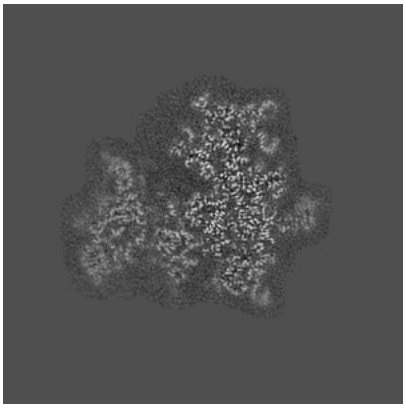


Z Index: 180

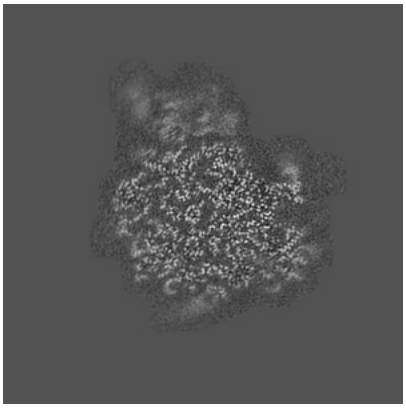
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

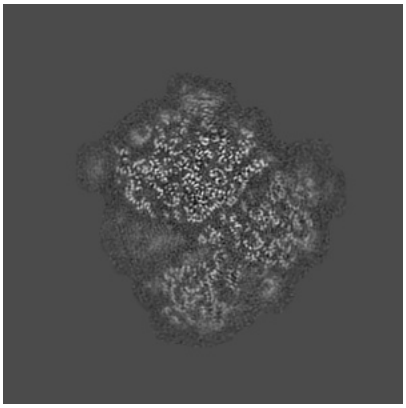
6.3.1 Primary map



X Index: 184



Y Index: 206

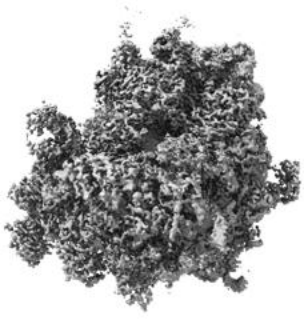


Z Index: 165

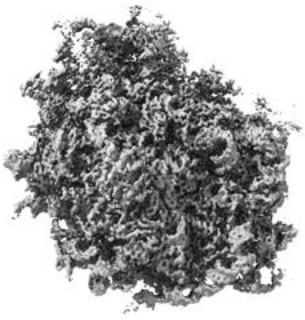
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X



Y

Z

The images above show the 3D surface view of the map at the recommended contour level 4.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

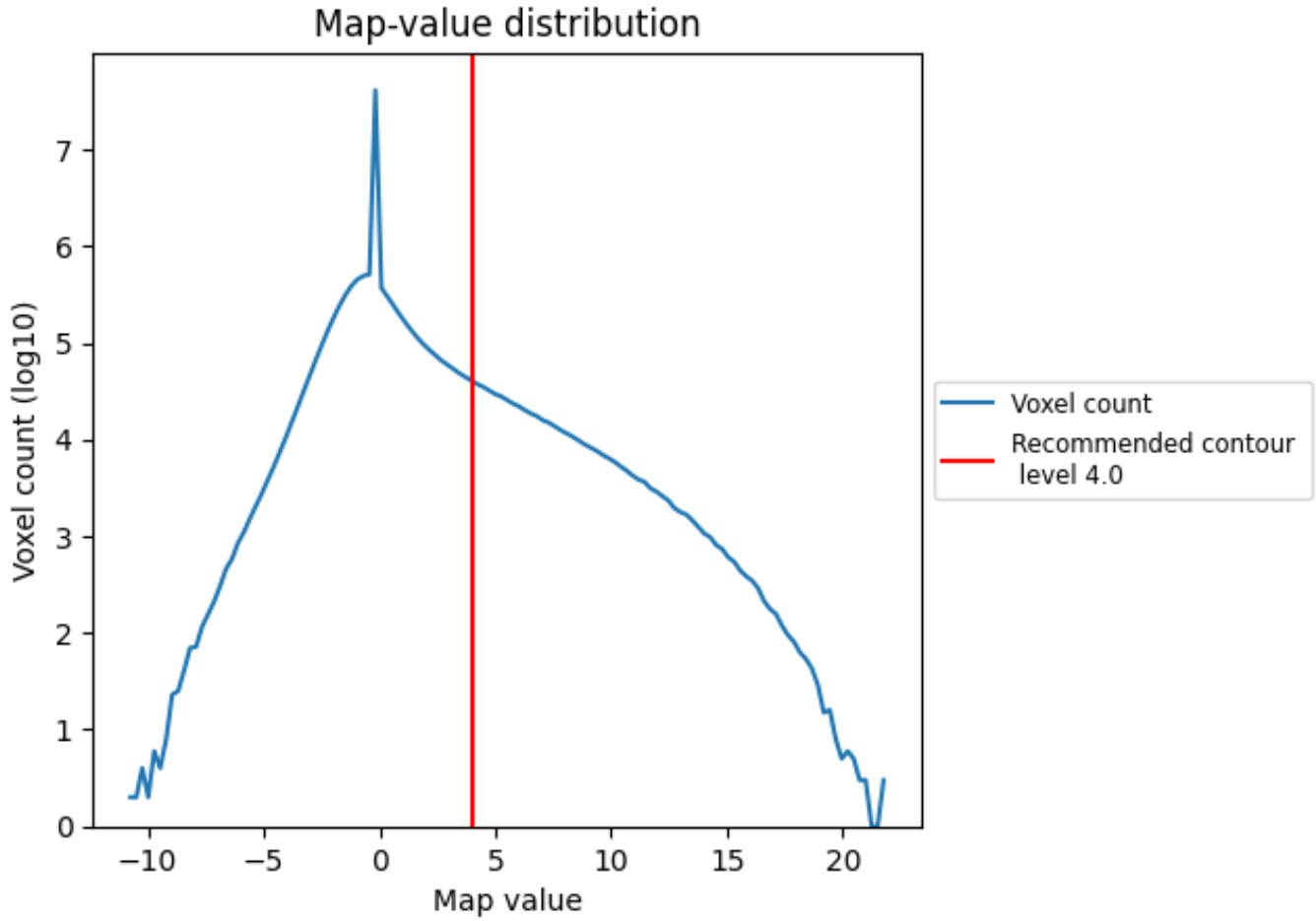
6.5 Mask visualisation (i)

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

7 Map analysis

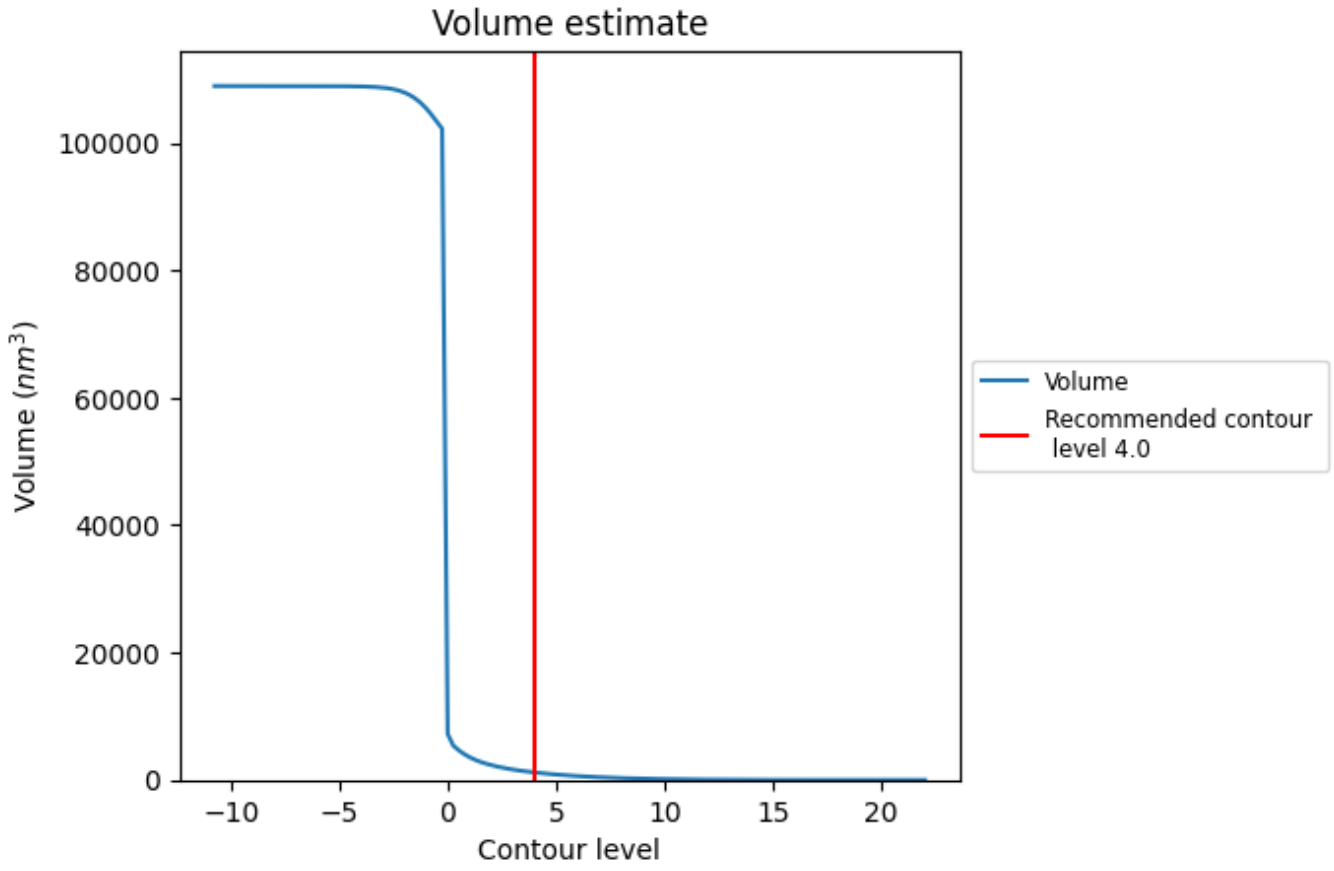
This section contains the results of statistical analysis of the map.

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.

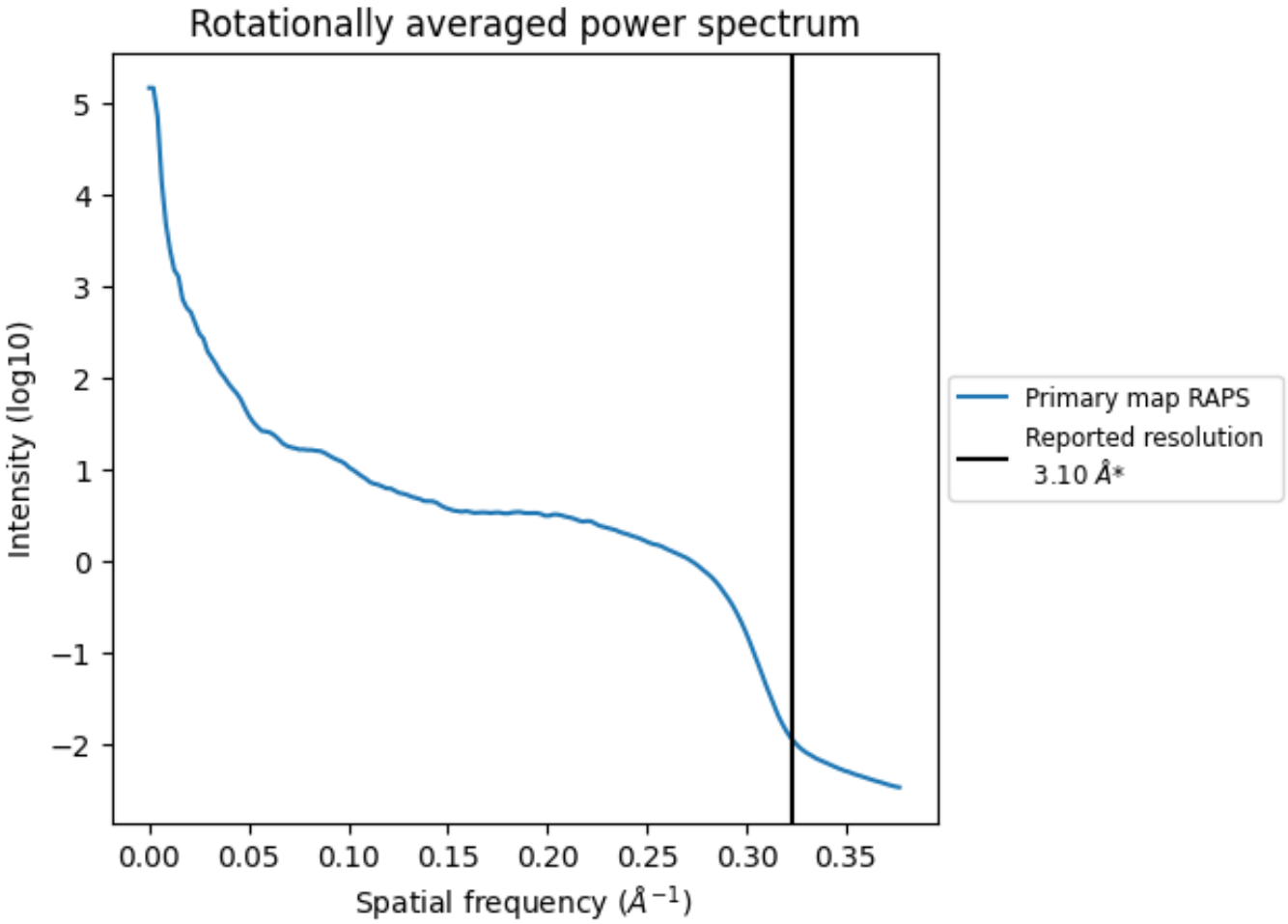
7.2 Volume estimate (i)



The volume at the recommended contour level is 1181 nm^3; this corresponds to an approximate mass of 1066 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 (i)



*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

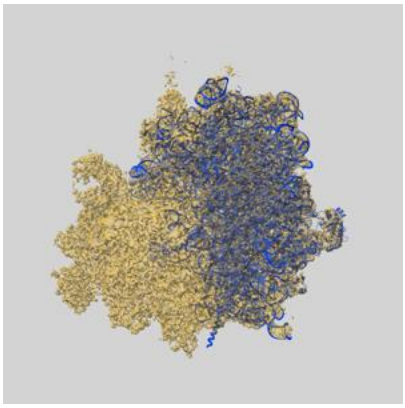
8 Fourier-Shell correlation (i)

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

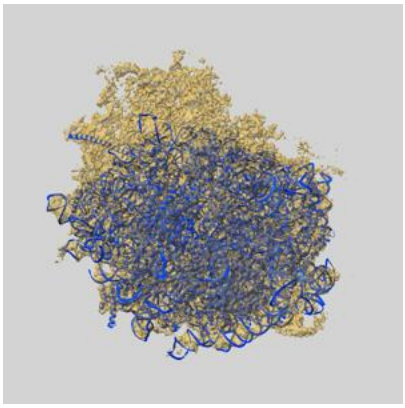
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-10321 and PDB model 6SWA. Per-residue inclusion information can be found in section 3 on page 13.

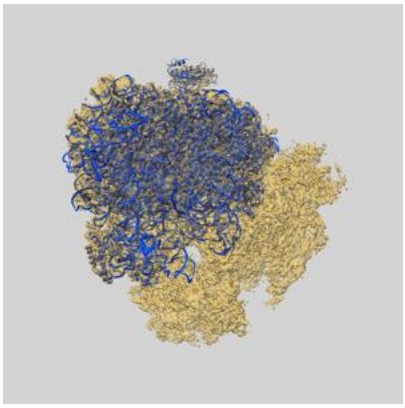
9.1 Map-model overlay



X



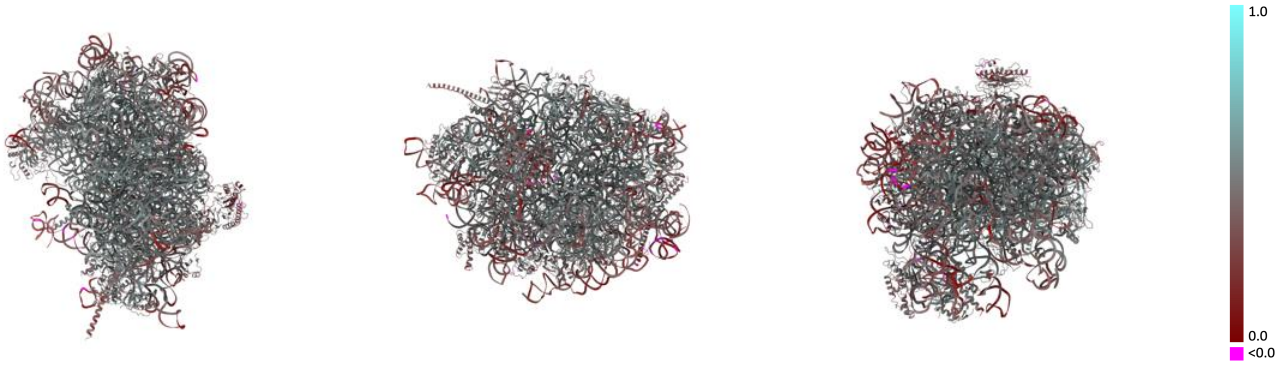
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 4.0 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.

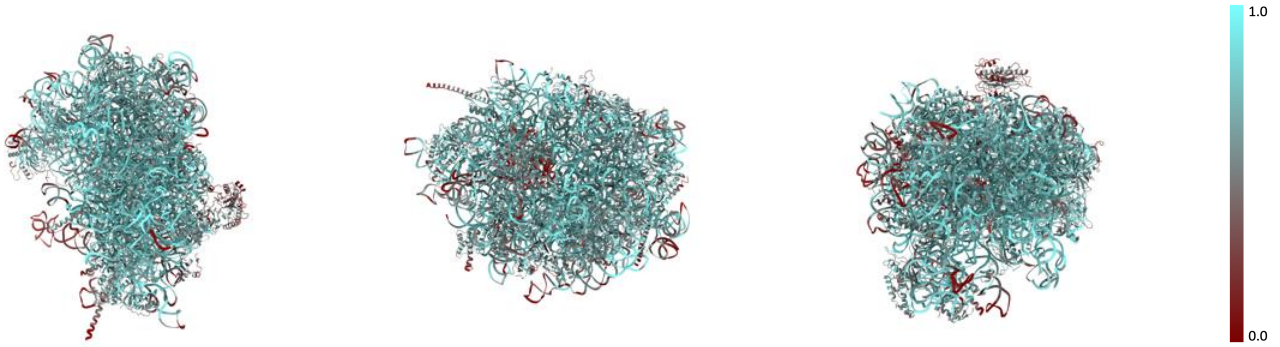
9.2 Q-score mapped to coordinate model



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.

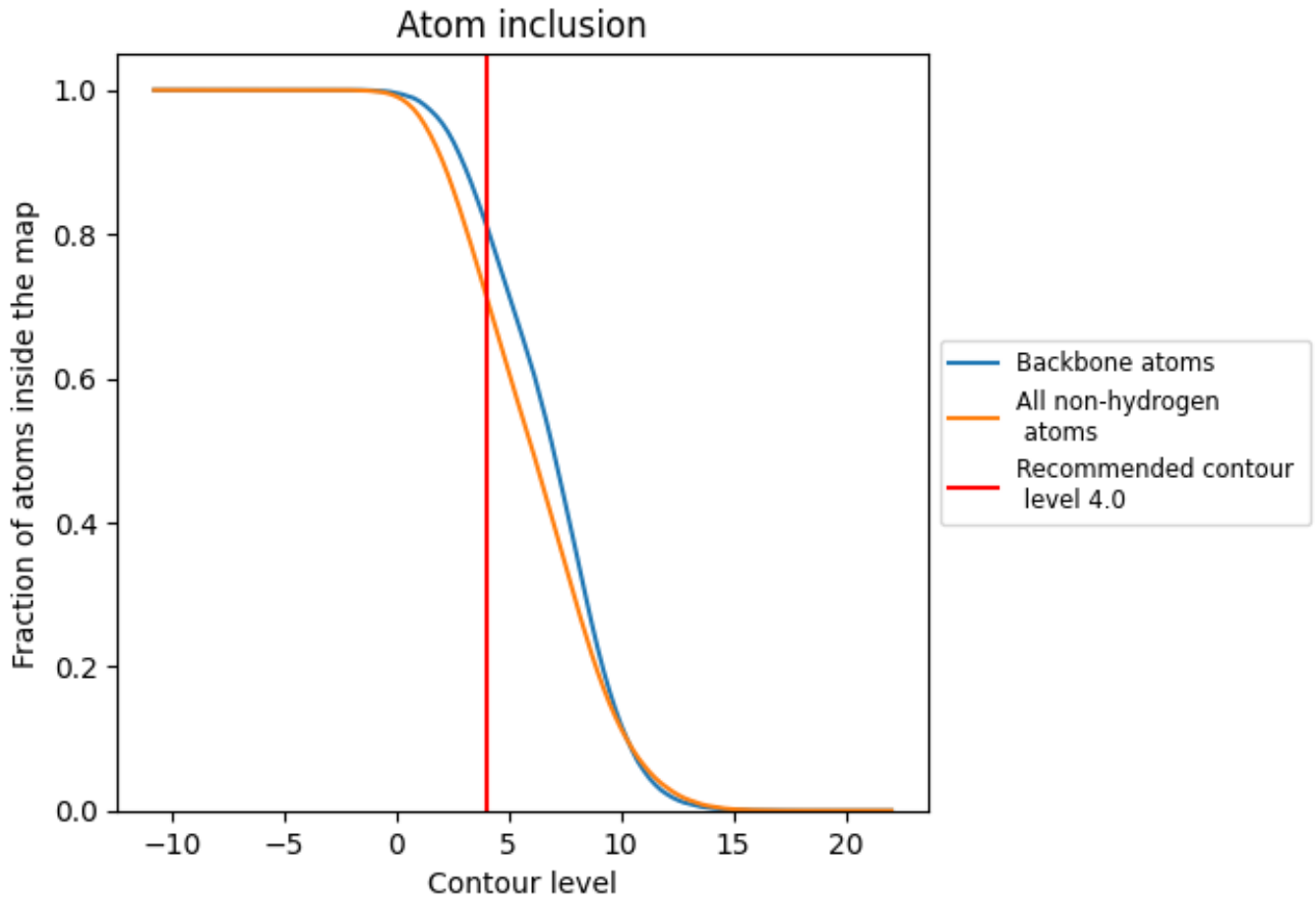
9.3 Atom inclusion mapped to coordinate model



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 (4.0).

9.4 Atom inclusion (i)



At the recommended contour level, 81% of all backbone atoms, 72% 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 (4.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7150	0.4490
A	0.6636	0.5130
B	0.6899	0.4960
C	0.6604	0.4890
D	0.6308	0.4440
E	0.5983	0.4340
F	0.6438	0.4610
G	0.5703	0.4360
H	0.6736	0.4930
I	0.6634	0.4830
J	0.5724	0.4320
K	0.6134	0.4400
L	0.7086	0.4760
M	0.7014	0.5120
N	0.7219	0.5030
O	0.6949	0.5040
P	0.6715	0.4920
Q	0.7168	0.5030
R	0.6709	0.4940
S	0.5743	0.4270
T	0.6642	0.5130
U	0.6587	0.5030
V	0.6294	0.4860
W	0.6839	0.4920
X	0.6314	0.4690
Y	0.6956	0.4970
Z	0.5867	0.4410
a	0.6522	0.4680
b	0.6631	0.5010
c	0.6650	0.5090
d	0.7399	0.5250
e	0.6582	0.4800
f	0.6116	0.4600
g	0.6065	0.4410
h	0.7275	0.5100

Continued on next page...

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Chain	Atom inclusion	Q-score
i	0.5360	0.4350
j	0.6469	0.4920
k	0.6952	0.5210
l	0.5591	0.4800
m	0.6158	0.4820
n	0.6386	0.4910
o	0.6176	0.4670
p	0.6971	0.4760
q	0.7608	0.4320
r	0.7554	0.4330
s	0.8475	0.4600
t	0.3543	0.3660