wwPDB EM Validation Summary Report

Feb 22, 2023 – 09:02 am GMT

PDB ID	:	7ZPQ
EMDB ID	:	EMD-14861
Title	:	Structure of the RQT-bound 80S ribosome from S. cerevisiae (C1)
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	:	2022-04-28
Resolution	:	3.47 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

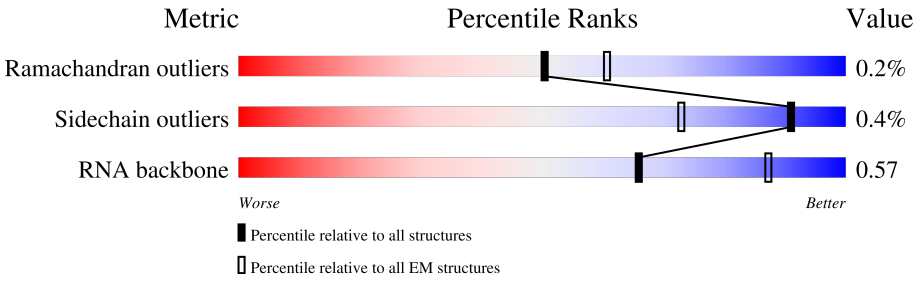
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.32.1

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 3.47 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.



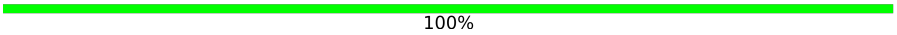
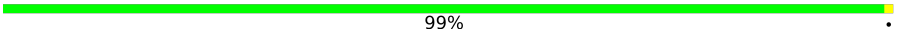
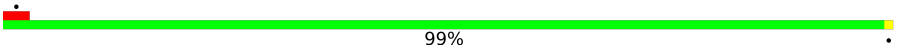
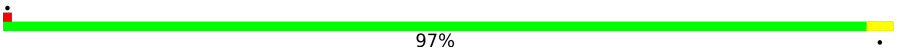
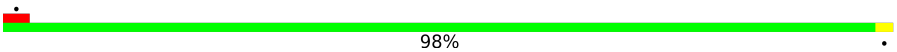
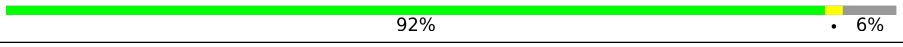
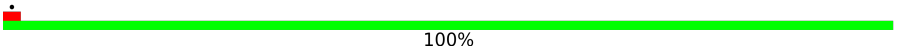
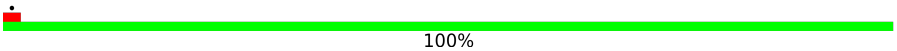
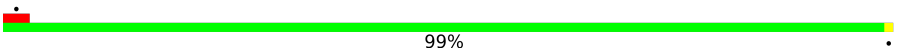
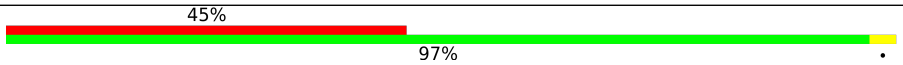
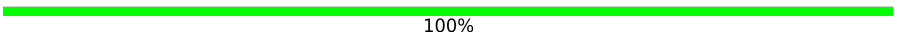
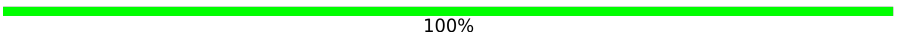
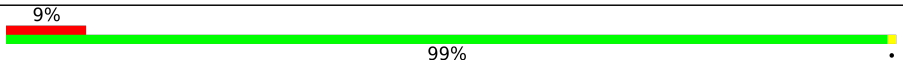
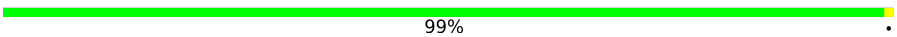
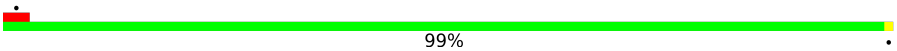
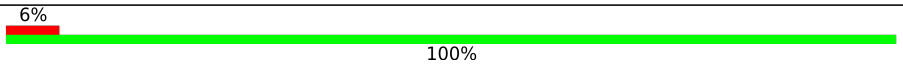
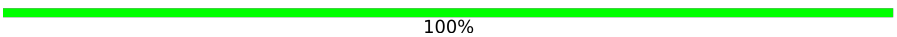
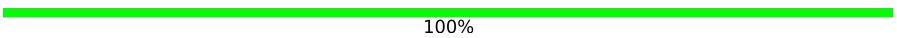
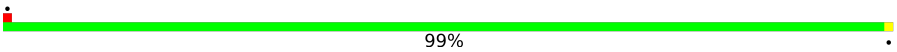
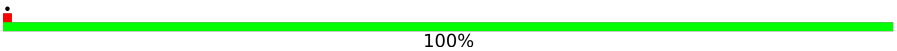
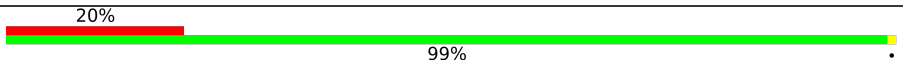
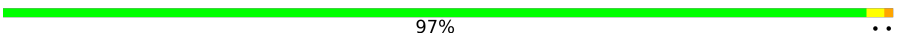
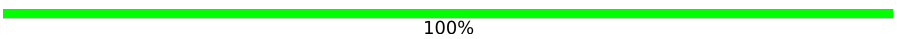
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	2	1798	74% 24%
2	3	158	82% 18%
3	4	121	92% 8%
4	5	3396	78% 16% 6%
5	6	76	7% 84% 16%
6	AA	206	100%
7	AB	255	87% 11%
8	AC	216	100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	AD	222	
10	AE	258	
11	AF	206	
12	AG	228	
13	AH	184	
14	AI	200	
15	AJ	184	
16	AK	92	
17	AL	144	
18	AM	121	
19	AN	150	
20	AO	127	
21	AP	117	
22	AQ	141	
23	AR	136	
24	AS	145	
25	AT	143	
26	AU	100	
27	AV	87	
28	AW	129	
29	AX	144	
30	AY	134	
31	AZ	82	
32	Aa	97	
33	Ab	81	

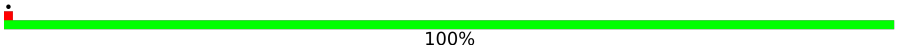
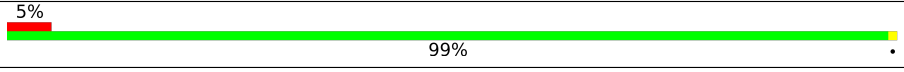
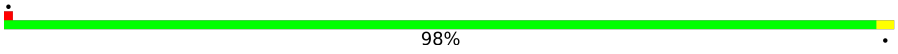
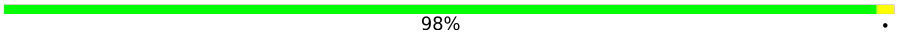
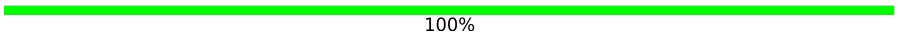
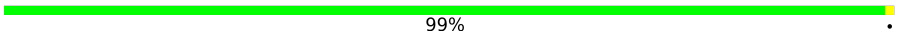
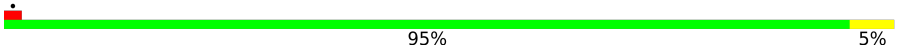
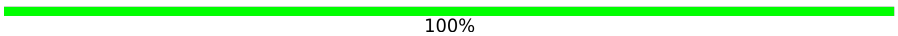
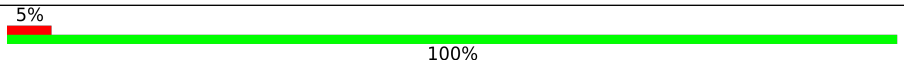
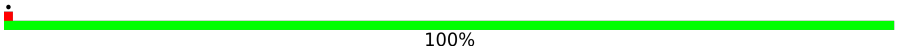
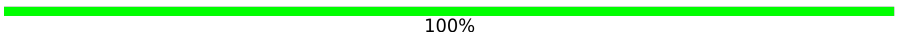
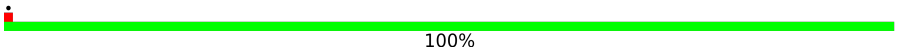
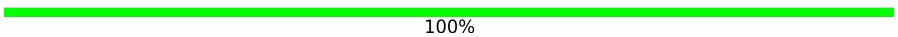
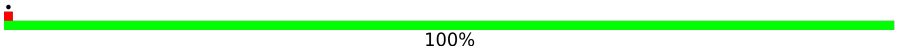
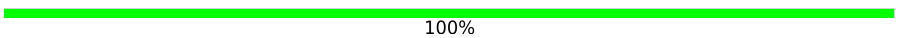
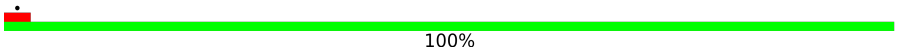
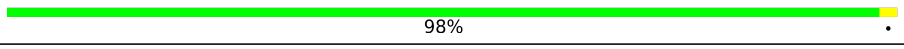
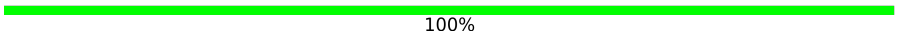
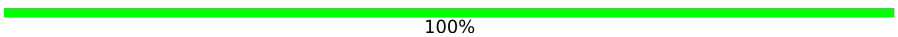
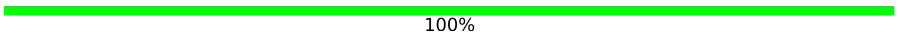
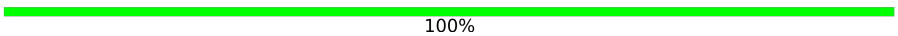
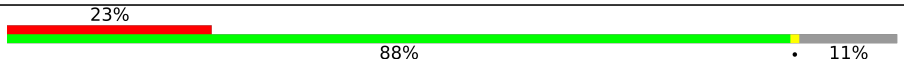
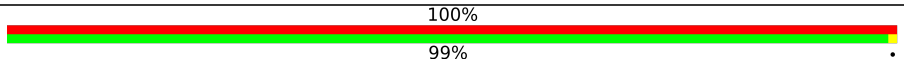
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
34	Ac	63	97%
35	Ad	53	100%
36	Ae	60	100%
37	Af	73	32% 99%
38	Ag	312	8% 100%
39	BA	251	100%
40	BB	386	99%
41	BC	361	100%
42	BD	294	100%
43	BE	176	94% 5%
44	BF	222	100%
45	BG	233	100%
46	BH	191	100%
47	BI	218	100%
48	BJ	169	100%
49	BK	193	98%
50	BL	136	100%
51	BM	203	100%
52	BN	197	98%
53	BO	183	100%
54	BP	185	100%
55	BQ	188	100%
56	BR	171	100%
57	BS	159	99%
58	BT	100	98%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
59	BU	136	
60	BV	126	
61	BW	121	
62	BX	125	
63	BY	135	
64	BZ	148	
65	Ba	58	
66	Bb	96	
67	Bc	109	
68	Bd	127	
69	Be	106	
70	Bf	112	
71	Bg	119	
72	Bh	99	
73	Bi	85	
74	Bj	77	
75	Bk	50	
76	Bl	52	
77	Bm	25	
78	Bn	103	
79	Bo	91	
80	CA	1967	
81	CB	297	
82	CC	530	

2 Entry composition (i)

There are 84 unique types of molecules in this entry. The entry contains 218512 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 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	2	1771	37739	16872	6683	12413	1771	0	0

- Molecule 2 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	3	158	3353	1500	586	1109	158	0	0

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	4	121	2579	1152	461	845	121	0	0

- Molecule 4 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	5	3184	68091	30415	12259	22233	3184	0	0

- Molecule 5 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	6	76	1619	722	288	533	76	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
6	34	U	G	conflict	GB 176436

- Molecule 6 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AA	206	Total	C	N	O	S	0	0
			1603	1030	284	287	2		

- Molecule 7 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AB	226	Total	C	N	O	S	0	0
			1798	1139	330	325	4		

- Molecule 8 is a protein called RPS2 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AC	216	Total	C	N	O	S	0	0
			1626	1042	287	295	2		

- Molecule 9 is a protein called RPS3 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AD	222	Total	C	N	O	S	0	0
			1729	1098	312	313	6		

- Molecule 10 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AE	258	Total	C	N	O	S	0	0
			2056	1308	387	358	3		

- Molecule 11 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AF	206	Total	C	N	O	S	0	0
			1605	1005	299	298	3		

- Molecule 12 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AG	228	Total	C	N	O	S	0	0
			1815	1138	351	323	3		

- Molecule 13 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	AH	184	Total 1473	C 946	N 263	O 264	0	0

- Molecule 14 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AI	187	Total 1476	C 916	N 295	O 263	S 2	0	0

- Molecule 15 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AJ	184	Total 1479	C 935	N 285	O 258	S 1	0	0

- Molecule 16 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AK	92	Total 752	C 487	N 122	O 141	S 2	0	0

- Molecule 17 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AL	144	Total 1159	C 742	N 219	O 195	S 3	0	0

- Molecule 18 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AM	121	Total 875	C 551	N 153	O 169	S 2	0	0

- Molecule 19 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AN	150	Total 1192	C 759	N 224	O 207	S 2	0	0

- Molecule 20 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AO	127	Total	C	N	O	S	0	0
			926	569	185	169	3		

- Molecule 21 is a protein called RPS15 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AP	117	Total	C	N	O	S	0	0
			916	583	171	155	7		

- Molecule 22 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	AQ	141	Total	C	N	O	0	0
			1105	708	203	194		

- Molecule 23 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AR	121	Total	C	N	O	S	0	0
			948	596	179	171	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AR	136	VAL	ASN	conflict	UNP P14127

- Molecule 24 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 25 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AT	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 26 is a protein called RPS20 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AU	100	Total	C	N	O	S	0	0
			797	506	144	146	1		

- Molecule 27 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AV	87	Total	C	N	O	S	0	0
			673	415	125	131	2		

- Molecule 28 is a protein called RPS22A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 29 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 30 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	AY	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 31 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	AZ	82	Total	C	N	O	0	0
			651	416	123	112		

- Molecule 32 is a protein called RPS26B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Aa	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 33 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ab	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 34 is a protein called RPS28A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ac	63	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 35 is a protein called RPS29A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ad	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 36 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ae	60	Total	C	N	O	S	0	0
			472	298	97	76	1		

- Molecule 37 is a protein called RPS31 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Af	73	Total	C	N	O	S	0	0
			556	352	105	95	4		

- Molecule 38 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ag	312	Total	C	N	O	S	0	0
			2383	1514	409	452	8		

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BA	251	Total	C	N	O	S	0	0
			1899	1182	385	331	1		

- Molecule 40 is a protein called 60S ribosomal protein L3.

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

- Molecule 41 is a protein called RPL4A isoform 1.

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

- Molecule 42 is a protein called RPL5 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	BD	294	Total	C	N	O	S	0	0
			2351	1484	410	455	2		

- Molecule 43 is a protein called 60S ribosomal protein L6-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BE	167	Total	C	N	O	S	0	0
			1305	841	234	229	1		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BE	1	MET	-	initiating methionine	UNP P05739
BE	146	ILE	LEU	conflict	UNP P05739
BE	173	MET	LEU	conflict	UNP P05739

- Molecule 44 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BH	191	Total	C	N	O	S	0	0
			1508	957	274	273	4		

- Molecule 47 is a protein called RPL10 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BI	218	Total	C	N	O	S	0	0
			1764	1117	334	306	7		

- Molecule 48 is a protein called RPL11B isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BJ	169	Total	C	N	O	S	0	0
			1350	846	253	247	4		

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	BO	183	Total	C	N	O	0	0
			1416	879	284	253		

- Molecule 54 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	BQ	188	Total	C	N	O	0	0
			1515	932	323	260		

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BR	171	Total	C	N	O	S	0	0
			1437	925	266	243	3		

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 60 is a protein called RPL24A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BV	126	Total	C	N	O	S	0	0
			836	525	165	145	1		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BV	104	GLN	ASN	conflict	UNP A0A6A5PY83
BV	109	GLN	LEU	conflict	UNP A0A6A5PY83
BV	112	ASP	ASN	conflict	UNP A0A6A5PY83
BV	119	ALA	GLU	conflict	UNP A0A6A5PY83

- Molecule 61 is a protein called 60S ribosomal protein L25.

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

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	BX	125	Total	C	N	O	0	0
			984	620	191	173		

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 64 is a protein called 60S ribosomal protein L28.

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

- Molecule 65 is a protein called 60S ribosomal protein L29.

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

- Molecule 66 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bb	96	Total 737	C 476	N 123	O 137	S 1	0	0

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 68 is a protein called RPL32 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Bd	127	Total 1017	C 644	N 205	O 167	S 1	0	0

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bh	99	Total 766	C 478	N 154	O 132	S 2	0	0

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bi	85	Total	C	N	O	S	0	0
			670	408	146	111	5		

- Molecule 74 is a protein called RPL38 isoform 1.

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

- Molecule 75 is a protein called 60S ribosomal protein L39.

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

- Molecule 76 is a protein called 60S ribosomal protein L40-A.

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

- Molecule 77 is a protein called RPL41A isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Bm	25	Total	C	N	O	S	0	0
			229	139	62	27	1		

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bn	103	Total	C	N	O	S	0	0
			824	517	167	135	5		

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 80 is a protein called SLH1 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CA	1742	Total 14008	C 8959	N 2378	O 2596	S 75	0	0

- Molecule 81 is a protein called RQC trigger complex subunit CUE3.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	CB	297	Total 2415	C 1568	N 414	O 427	S 6	0	0

- Molecule 82 is a protein called RQT4 isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CC	114	Total 886	C 539	N 167	O 172	S 8	0	0

- Molecule 83 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	2	84	Total 84	Mg 84	0
83	AQ	1	Total 1	Mg 1	0
83	AT	1	Total 1	Mg 1	0

- Molecule 84 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
84	Ad	1	Total 1	Zn 1	0
84	Af	1	Total 1	Zn 1	0
84	Bf	1	Total 1	Zn 1	0
84	Bi	1	Total 1	Zn 1	0
84	Bl	1	Total 1	Zn 1	0
84	Bn	1	Total 1	Zn 1	0
84	Bo	1	Total 1	Zn 1	0

Continued on next page...

Continued from previous page...

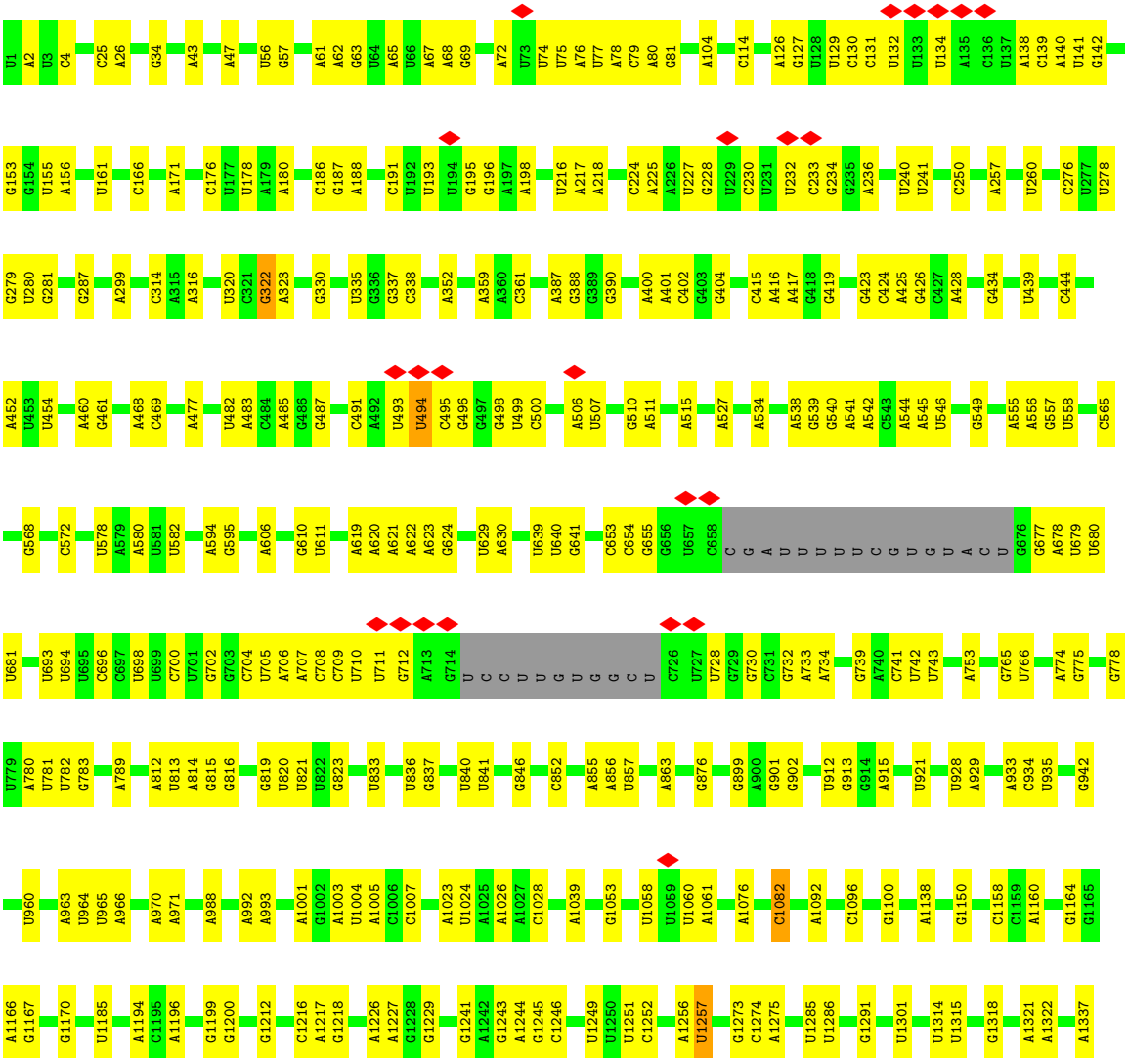
Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
84	CC	2	2	2	0

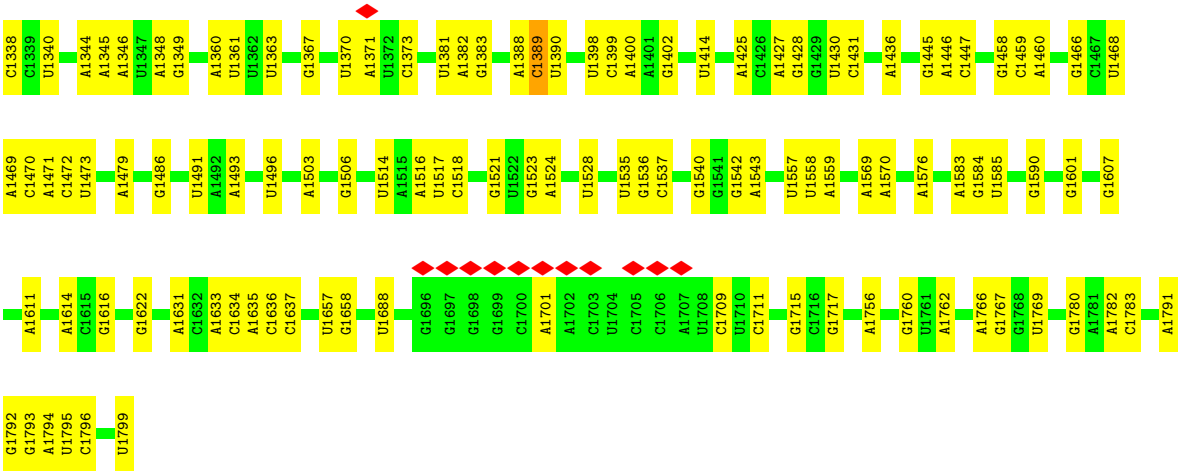
3 Residue-property plots (i)

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: 18S ribosomal RNA

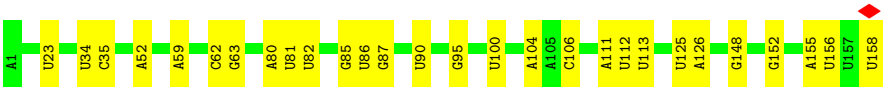
Chain 2:





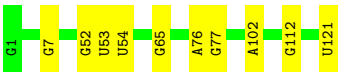
• Molecule 2: 5.8S ribosomal RNA

Chain 3:



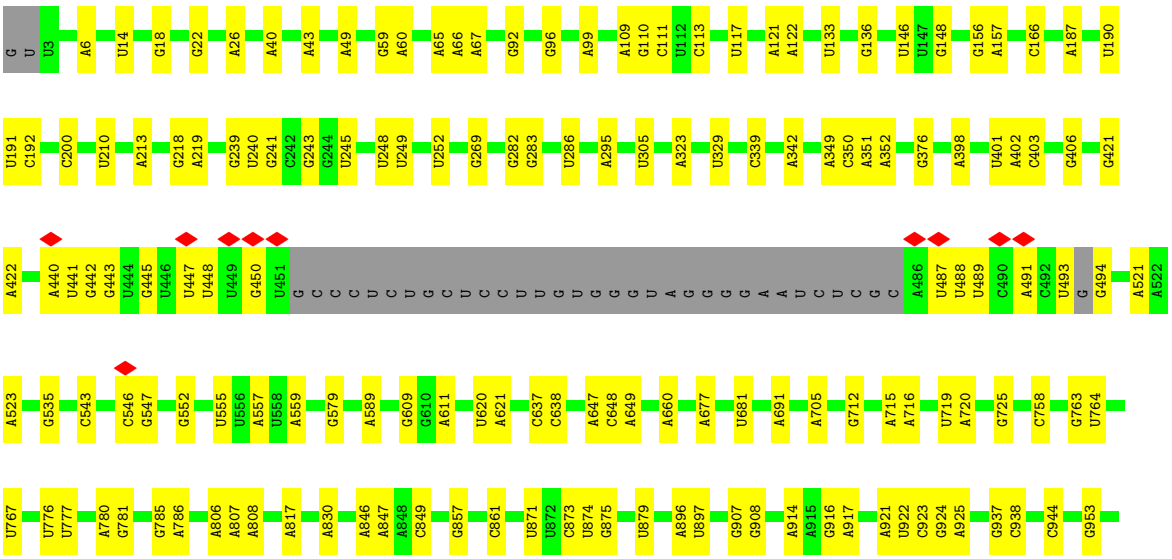
• Molecule 3: 5S ribosomal RNA

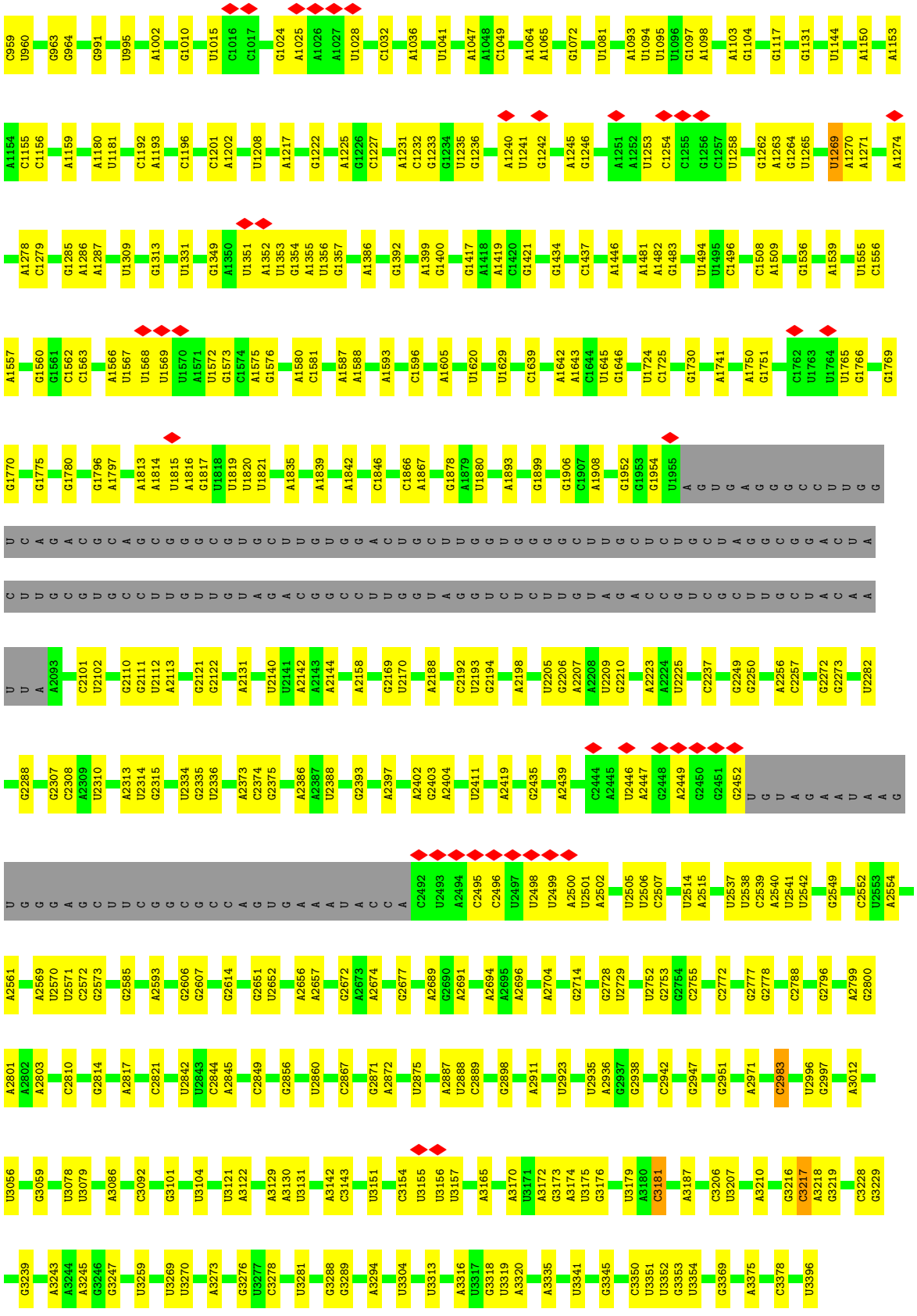
Chain 4:



• Molecule 4: 25S ribosomal RNA

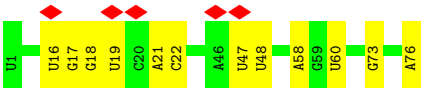
Chain 5:





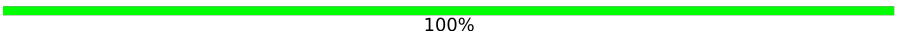
• Molecule 5: tRNA

Chain 6:



• Molecule 6: 40S ribosomal protein S0-A

Chain AA:



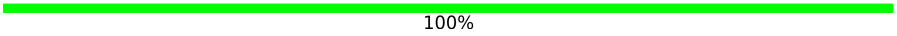
There are no outlier residues recorded for this chain.

• Molecule 7: 40S ribosomal protein S1

Chain AB:

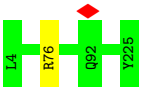
• Molecule 8: RPS2 isoform 1

Chain AC:



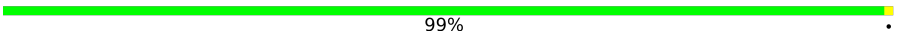
• Molecule 9: RPS3 isoform 1

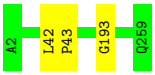
Chain AD:



• Molecule 10: 40S ribosomal protein S4-A

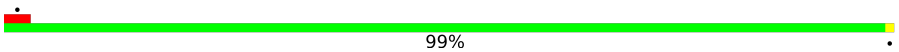
Chain AE:

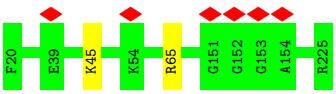




• Molecule 11: Rps5p

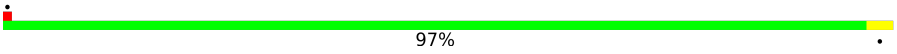
Chain AF:

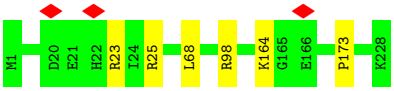




• Molecule 12: 40S ribosomal protein S6-A

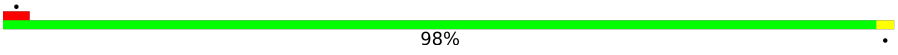
Chain AG:

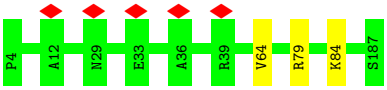




• Molecule 13: 40S ribosomal protein S7-A

Chain AH:



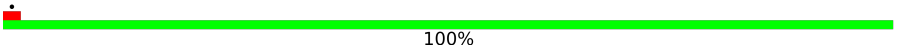


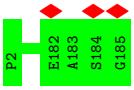
• Molecule 14: 40S ribosomal protein S8

Chain AI:

• Molecule 15: 40S ribosomal protein S9-A

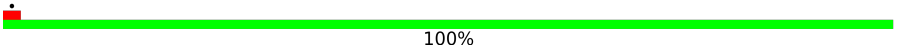
Chain AJ:

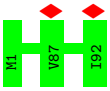




• Molecule 16: 40S ribosomal protein S10-A

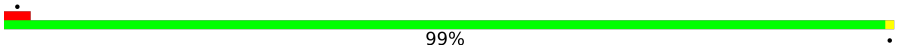
Chain AK:

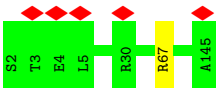




• Molecule 17: 40S ribosomal protein S11-A

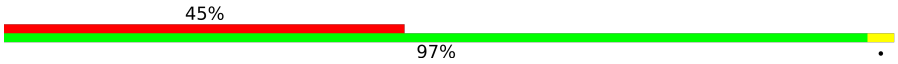
Chain AL:

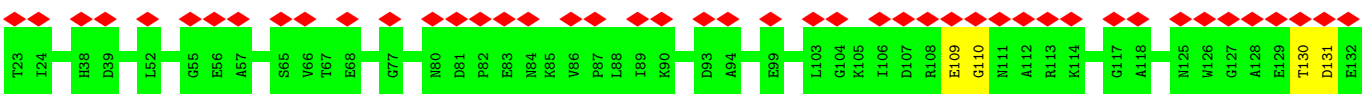


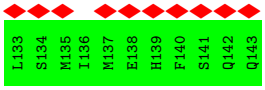


• Molecule 18: 40S ribosomal protein S12

Chain AM:







• Molecule 19: 40S ribosomal protein S13

Chain AN: 

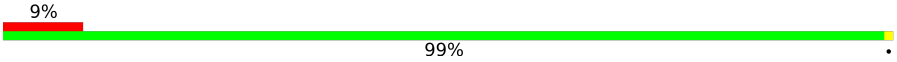
There are no outlier residues recorded for this chain.

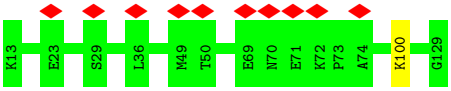
• Molecule 20: 40S ribosomal protein S14-B

Chain AO: 

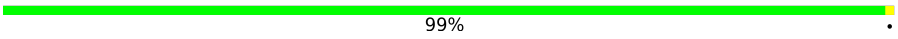
There are no outlier residues recorded for this chain.

• Molecule 21: RPS15 isoform 1

Chain AP: 

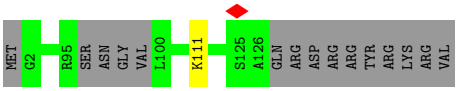


• Molecule 22: 40S ribosomal protein S16-A

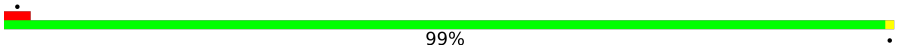
Chain AQ: 

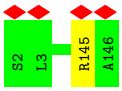
• Molecule 23: 40S ribosomal protein S17-B

Chain AR: 

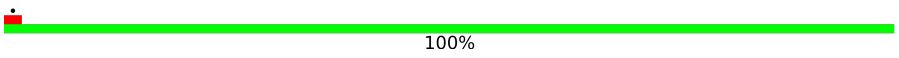


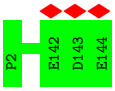
• Molecule 24: 40S ribosomal protein S18-A

Chain AS: 



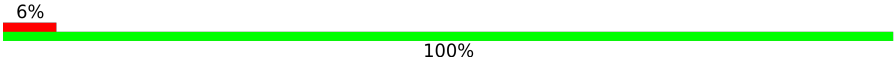
• Molecule 25: 40S ribosomal protein S19-A

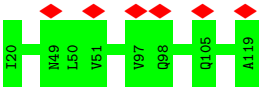
Chain AT: 



• Molecule 26: RPS20 isoform 1

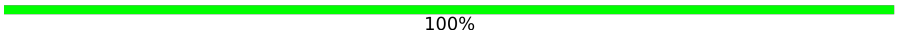
Chain AU:





• Molecule 27: 40S ribosomal protein S21-A

Chain AV:



There are no outlier residues recorded for this chain.

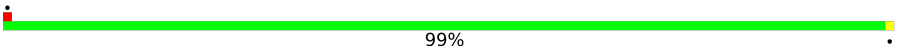
• Molecule 28: RPS22A isoform 1

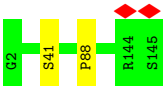
Chain AW:

There are no outlier residues recorded for this chain.

• Molecule 29: 40S ribosomal protein S23-A

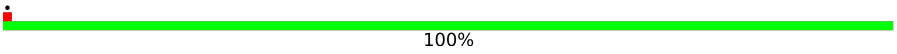
Chain AX:





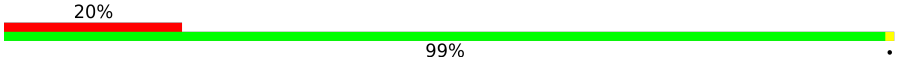
• Molecule 30: 40S ribosomal protein S24-A

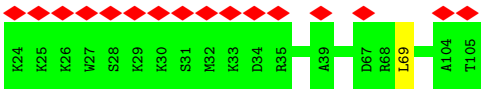
Chain AY:



• Molecule 31: 40S ribosomal protein S25

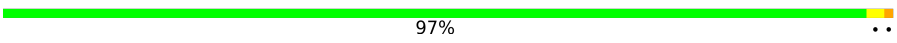
Chain AZ:

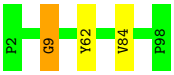




• Molecule 32: RPS26B isoform 1

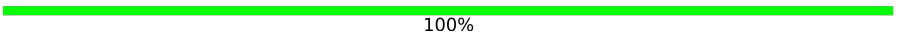
Chain Aa:





• Molecule 33: 40S ribosomal protein S27-A

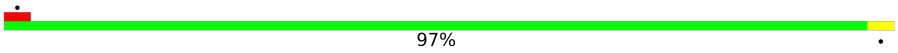
Chain Ab:



There are no outlier residues recorded for this chain.

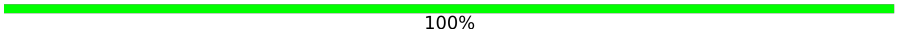
• Molecule 34: RPS28A isoform 1

Chain Ac:



• Molecule 35: RPS29A isoform 1

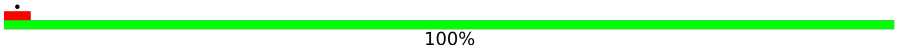
Chain Ad:



There are no outlier residues recorded for this chain.

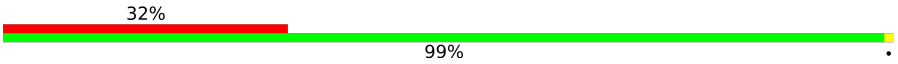
• Molecule 36: 40S ribosomal protein S30-A

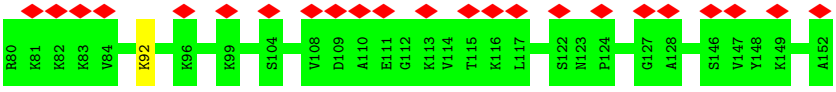
Chain Ae:



• Molecule 37: RPS31 isoform 1

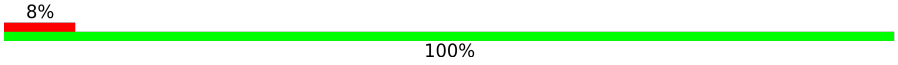
Chain Af:

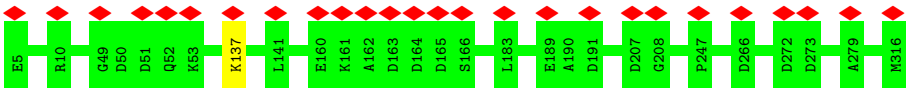




• Molecule 38: Guanine nucleotide-binding protein subunit beta-like protein

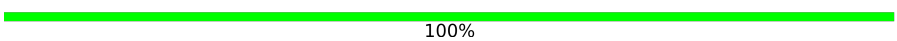
Chain Ag:





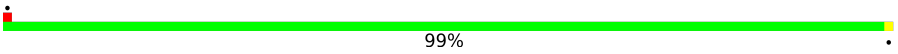
• Molecule 39: 60S ribosomal protein L2-A

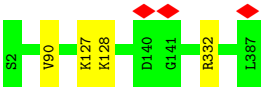
Chain BA:



• Molecule 40: 60S ribosomal protein L3

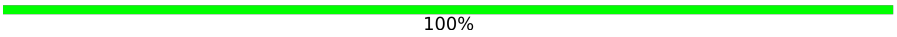
Chain BB:





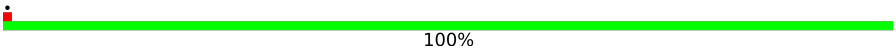
• Molecule 41: RPL4A isoform 1

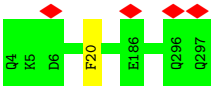
Chain BC:



• Molecule 42: RPL5 isoform 1

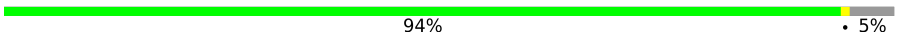
Chain BD:

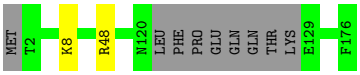




• Molecule 43: 60S ribosomal protein L6-B

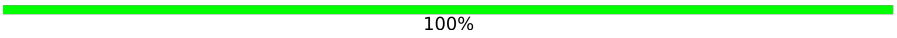
Chain BE:





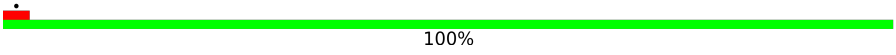
• Molecule 44: 60S ribosomal protein L7-A

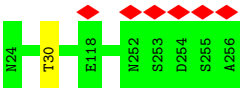
Chain BF:



• Molecule 45: 60S ribosomal protein L8-A

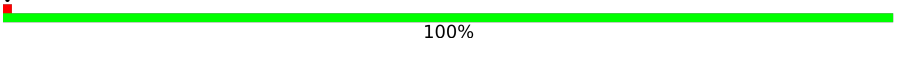
Chain BG:



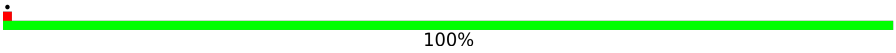


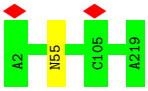
• Molecule 46: 60S ribosomal protein L9-A

Chain BH:

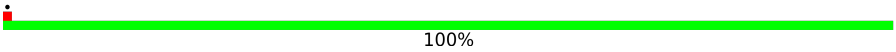


• Molecule 47: RPL10 isoform 1

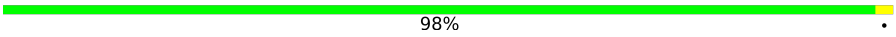
Chain BI: 



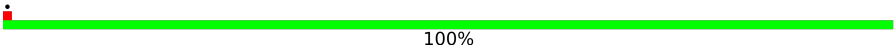
• Molecule 48: RPL11B isoform 1

Chain BJ: 

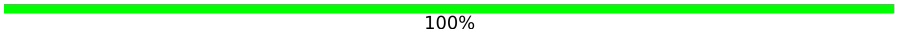
• Molecule 49: 60S ribosomal protein L13-A

Chain BK: 

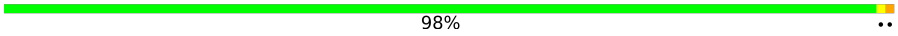
• Molecule 50: 60S ribosomal protein L14-A

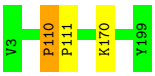
Chain BL: 

• Molecule 51: 60S ribosomal protein L15-A

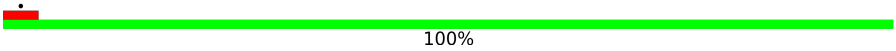
Chain BM: 

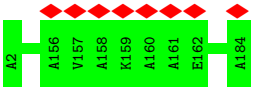
• Molecule 52: 60S ribosomal protein L16-A

Chain BN: 



• Molecule 53: 60S ribosomal protein L17-A

Chain BO: 

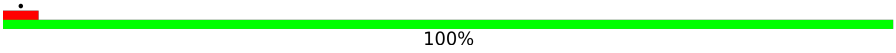


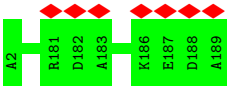
• Molecule 54: 60S ribosomal protein L18-A

Chain BP: 

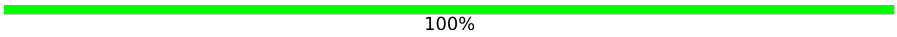
There are no outlier residues recorded for this chain.

• Molecule 55: 60S ribosomal protein L19-A

Chain BQ: 

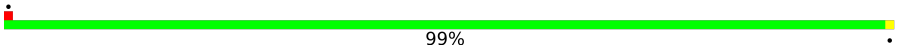


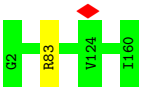
• Molecule 56: 60S ribosomal protein L20-A

Chain BR: 

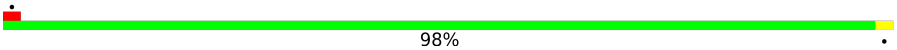
There are no outlier residues recorded for this chain.

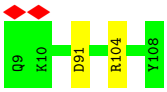
• Molecule 57: 60S ribosomal protein L21-A

Chain BS: 

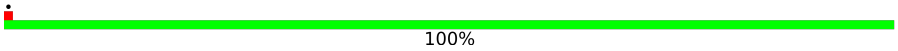


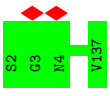
• Molecule 58: 60S ribosomal protein L22-A

Chain BT: 

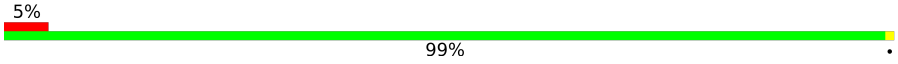


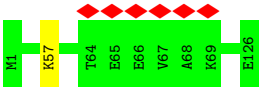
• Molecule 59: 60S ribosomal protein L23-A

Chain BU: 

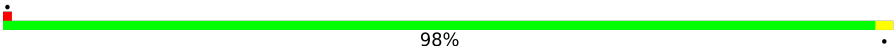


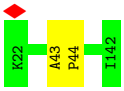
• Molecule 60: RPL24A isoform 1

Chain BV: 

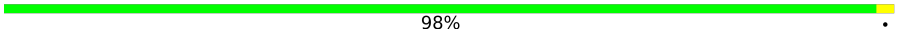


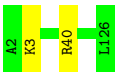
• Molecule 61: 60S ribosomal protein L25

Chain BW: 

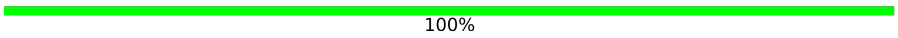


• Molecule 62: 60S ribosomal protein L26-A

Chain BX: 

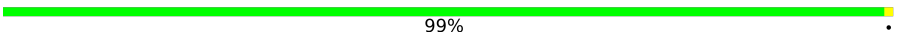


• Molecule 63: 60S ribosomal protein L27-A

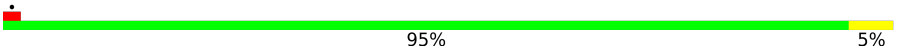
Chain BY: 

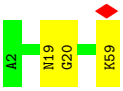
There are no outlier residues recorded for this chain.

• Molecule 64: 60S ribosomal protein L28

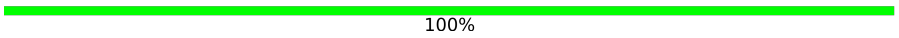
Chain BZ: 

• Molecule 65: 60S ribosomal protein L29

Chain Ba: 

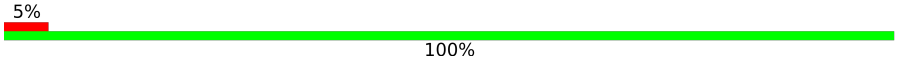


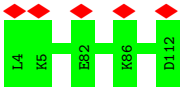
• Molecule 66: 60S ribosomal protein L30

Chain Bb: 

There are no outlier residues recorded for this chain.

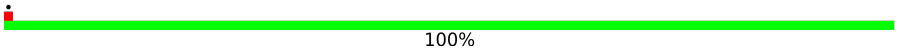
• Molecule 67: 60S ribosomal protein L31-A

Chain Bc: 



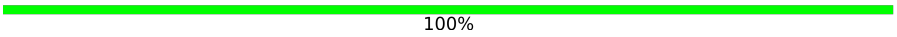
• Molecule 68: RPL32 isoform 1

Chain Bd:



• Molecule 69: 60S ribosomal protein L33-A

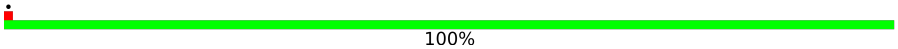
Chain Be:



There are no outlier residues recorded for this chain.

• Molecule 70: 60S ribosomal protein L34-A

Chain Bf:



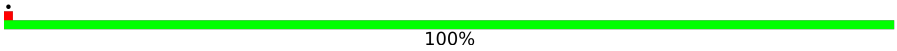
• Molecule 71: 60S ribosomal protein L35-A

Chain Bg:

There are no outlier residues recorded for this chain.

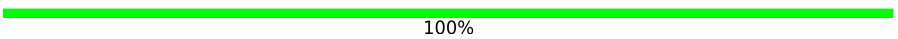
• Molecule 72: 60S ribosomal protein L36-A

Chain Bh:



• Molecule 73: 60S ribosomal protein L37-A

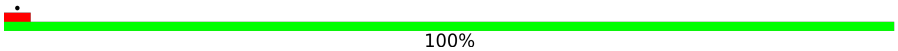
Chain Bi:

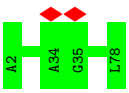


There are no outlier residues recorded for this chain.

• Molecule 74: RPL38 isoform 1

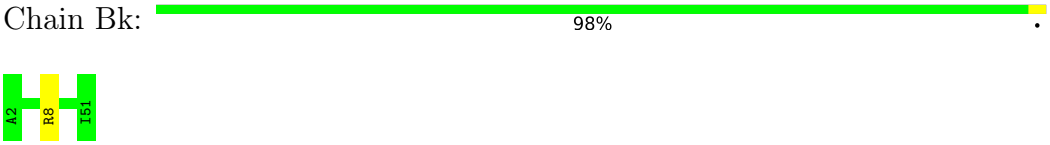
Chain Bj:





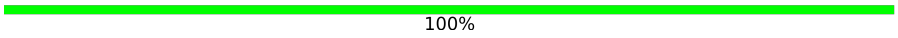
• Molecule 75: 60S ribosomal protein L39

Chain Bk:



• Molecule 76: 60S ribosomal protein L40-A

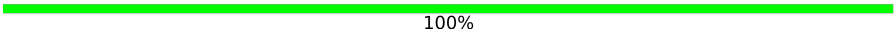
Chain Bl:



There are no outlier residues recorded for this chain.

• Molecule 77: RPL41A isoform 1

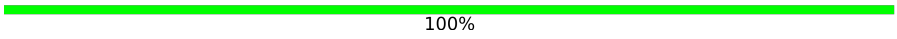
Chain Bm:



There are no outlier residues recorded for this chain.

• Molecule 78: 60S ribosomal protein L42-A

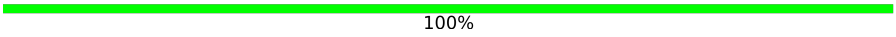
Chain Bn:



There are no outlier residues recorded for this chain.

• Molecule 79: 60S ribosomal protein L43-A

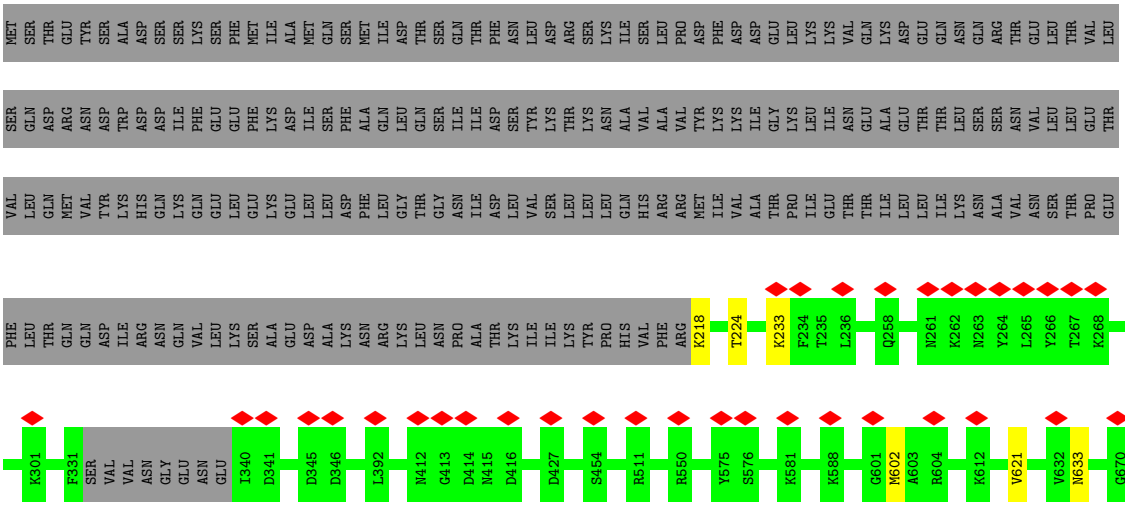
Chain Bo:

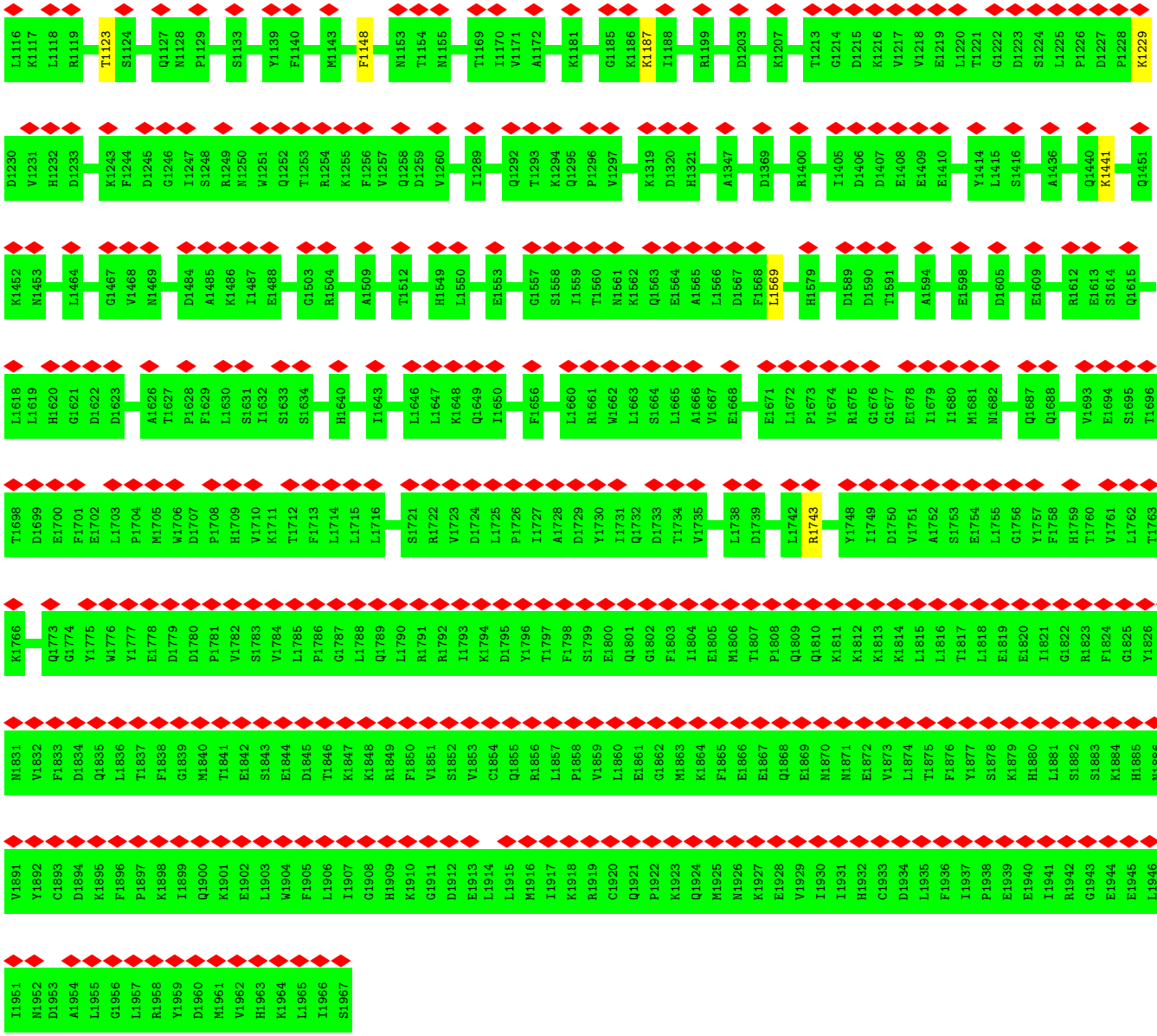


There are no outlier residues recorded for this chain.

• Molecule 80: SLH1 isoform 1

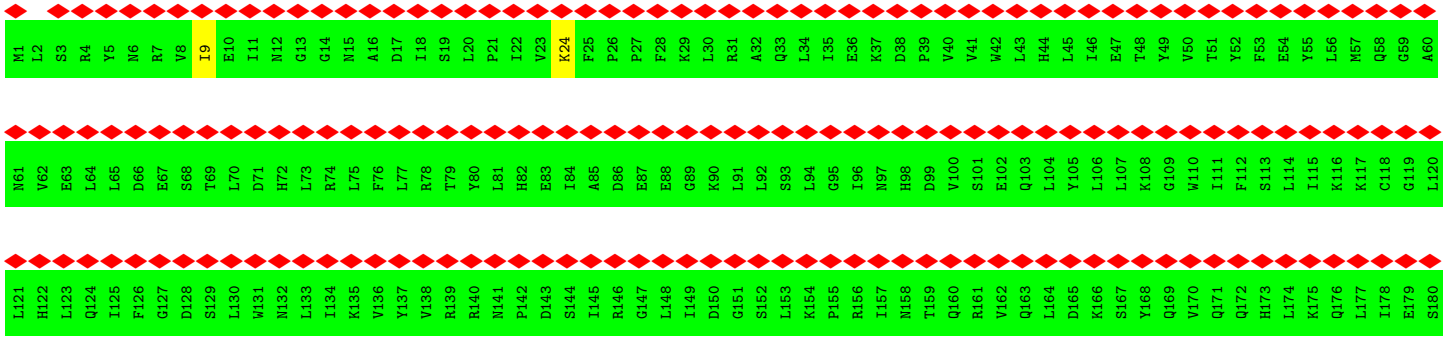
Chain CA:



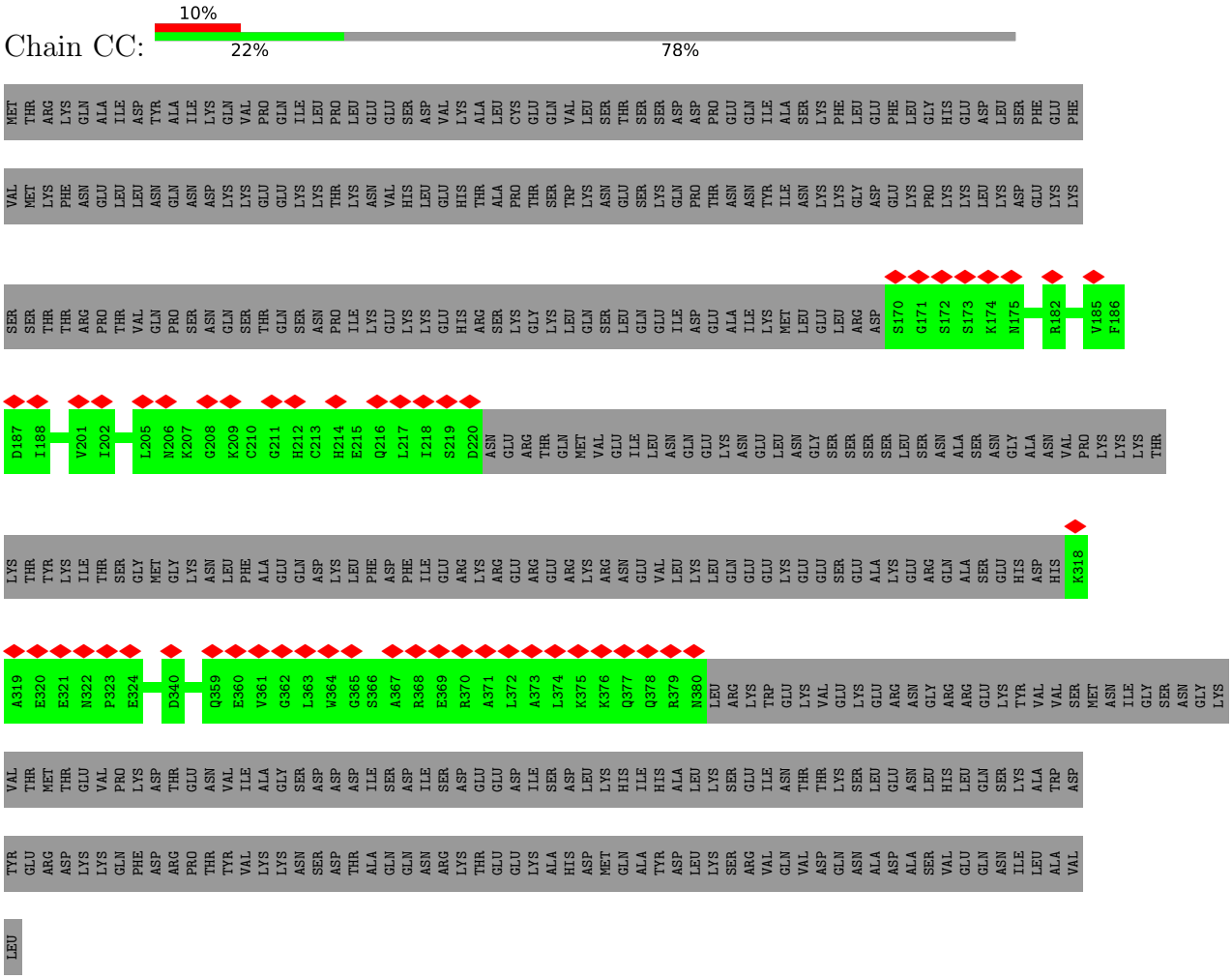


• Molecule 81: RQC trigger complex subunit CUE3

Chain CB:



• Molecule 82: RQT4 isoform 1



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	194186	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 ($e^-/Å^2$)	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	7.920	Depositor
Minimum map value	-1.030	Depositor
Average map value	0.016	Depositor
Map value standard deviation	0.145	Depositor
Recommended contour level	0.4	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 (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	2	0.30	0/42211	0.79	9/65773 (0.0%)
2	3	0.35	0/3746	0.76	1/5832 (0.0%)
3	4	0.31	0/2883	0.75	0/4491
4	5	0.36	0/76214	0.79	17/118821 (0.0%)
5	6	0.17	0/1808	0.75	0/2816
6	AA	0.26	0/1644	0.51	0/2249
7	AB	0.25	0/1823	0.56	0/2447
8	AC	0.26	0/1656	0.49	0/2251
9	AD	0.25	0/1754	0.52	0/2361
10	AE	0.27	0/2097	0.55	1/2823 (0.0%)
11	AF	0.24	0/1625	0.54	0/2197
12	AG	0.25	0/1839	0.57	0/2460
13	AH	0.26	0/1498	0.54	0/2019
14	AI	0.27	0/1501	0.58	0/2006
15	AJ	0.25	0/1504	0.55	0/2016
16	AK	0.24	0/769	0.45	0/1039
17	AL	0.28	0/1185	0.54	0/1598
18	AM	0.24	0/883	0.57	0/1199
19	AN	0.27	0/1215	0.54	0/1638
20	AO	0.27	0/937	0.60	0/1261
21	AP	0.25	0/936	0.55	0/1259
22	AQ	0.25	0/1125	0.53	0/1510
23	AR	0.25	0/957	0.56	0/1283
24	AS	0.25	0/1211	0.54	0/1628
25	AT	0.26	0/1130	0.54	0/1517
26	AU	0.24	0/807	0.52	0/1091
27	AV	0.29	0/682	0.57	0/921
28	AW	0.27	0/1038	0.52	0/1395
29	AX	0.26	0/1139	0.55	0/1518
30	AY	0.26	0/1087	0.54	0/1449
31	AZ	0.24	0/661	0.56	0/888
32	Aa	0.26	0/782	0.67	0/1047

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	Ab	0.25	0/620	0.53	0/838
34	Ac	0.25	0/493	0.59	0/663
35	Ad	0.25	0/452	0.59	0/600
36	Ae	0.27	0/480	0.60	0/639
37	Af	0.26	0/567	0.65	0/764
38	Ag	0.24	0/2436	0.52	0/3318
39	BA	0.28	0/1933	0.57	0/2598
40	BB	0.27	0/3146	0.54	0/4228
41	BC	0.27	0/2800	0.53	0/3790
42	BD	0.27	0/2400	0.51	0/3239
43	BE	0.26	0/1327	0.51	0/1790
44	BF	0.27	0/1821	0.47	0/2451
45	BG	0.27	0/1836	0.48	0/2481
46	BH	0.26	0/1529	0.50	0/2060
47	BI	0.27	0/1801	0.55	0/2416
48	BJ	0.25	0/1371	0.53	0/1838
49	BK	0.27	0/1568	0.58	0/2106
50	BL	0.25	0/1068	0.50	0/1438
51	BM	0.28	0/1757	0.58	0/2354
52	BN	0.28	0/1585	0.50	0/2128
53	BO	0.27	0/1439	0.55	0/1938
54	BP	0.26	0/1465	0.55	0/1965
55	BQ	0.26	0/1532	0.56	0/2043
56	BR	0.29	0/1473	0.52	0/1980
57	BS	0.28	0/1300	0.54	0/1743
58	BT	0.27	0/812	0.53	1/1099 (0.1%)
59	BU	0.28	0/1018	0.54	0/1369
60	BV	0.26	0/850	0.50	0/1152
61	BW	0.28	0/979	0.52	0/1321
62	BX	0.28	0/995	0.54	0/1329
63	BY	0.27	0/1118	0.49	0/1497
64	BZ	0.29	0/1204	0.54	0/1612
65	Ba	0.25	0/473	0.47	0/629
66	Bb	0.27	0/745	0.48	0/1001
67	Bc	0.26	0/890	0.55	0/1196
68	Bd	0.26	0/1038	0.53	0/1390
69	Be	0.29	0/868	0.53	0/1168
70	Bf	0.27	0/890	0.55	0/1189
71	Bg	0.26	0/978	0.50	0/1301
72	Bh	0.25	0/772	0.54	0/1026
73	Bi	0.28	0/685	0.56	0/908
74	Bj	0.27	0/618	0.54	0/826
75	Bk	0.25	0/443	0.58	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
76	Bl	0.26	0/423	0.52	0/562
77	Bm	0.23	0/230	0.69	0/296
78	Bn	0.27	0/836	0.53	0/1104
79	Bo	0.27	0/701	0.57	0/934
80	CA	0.24	0/14309	0.48	1/19348 (0.0%)
81	CB	0.23	0/2463	0.46	0/3324
82	CC	0.23	0/897	0.49	0/1203
All	All	0.31	0/233781	0.69	30/341583 (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
7	AB	0	2
10	AE	0	1
12	AG	0	1
13	AH	0	1
18	AM	0	2
22	AQ	0	1
29	AX	0	2
31	AZ	0	1
32	Aa	0	1
40	BB	0	1
45	BG	0	1
52	BN	0	1
61	BW	0	1
65	Ba	0	2
All	All	0	18

There are no bond length outliers.

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	5	1269	U	C2-N1-C1'	7.71	126.95	117.70
4	5	1269	U	N1-C2-O2	7.19	127.83	122.80
4	5	3217	C	N1-C2-O2	6.90	123.04	118.90
4	5	1269	U	N3-C2-O2	-6.82	117.42	122.20
4	5	922	U	C2-N1-C1'	6.78	125.83	117.70

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	AB	211	HIS	Peptide
7	AB	81	PHE	Peptide
10	AE	42	LEU	Peptide
12	AG	68	LEU	Peptide
13	AH	64	VAL	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
6	AA	204/206 (99%)	192 (94%)	12 (6%)	0	100 100
7	AB	222/255 (87%)	211 (95%)	10 (4%)	1 (0%)	29 66
8	AC	214/216 (99%)	205 (96%)	9 (4%)	0	100 100
9	AD	220/222 (99%)	218 (99%)	2 (1%)	0	100 100
10	AE	256/258 (99%)	245 (96%)	10 (4%)	1 (0%)	34 70
11	AF	204/206 (99%)	195 (96%)	9 (4%)	0	100 100
12	AG	226/228 (99%)	211 (93%)	14 (6%)	1 (0%)	34 70
13	AH	182/184 (99%)	172 (94%)	10 (6%)	0	100 100
14	AI	183/200 (92%)	173 (94%)	8 (4%)	2 (1%)	14 50
15	AJ	182/184 (99%)	173 (95%)	9 (5%)	0	100 100
16	AK	90/92 (98%)	85 (94%)	5 (6%)	0	100 100
17	AL	142/144 (99%)	136 (96%)	6 (4%)	0	100 100
18	AM	119/121 (98%)	95 (80%)	22 (18%)	2 (2%)	9 40
19	AN	148/150 (99%)	141 (95%)	7 (5%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	AO	125/127 (98%)	119 (95%)	6 (5%)	0	100	100
21	AP	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
22	AQ	139/141 (99%)	131 (94%)	8 (6%)	0	100	100
23	AR	117/136 (86%)	112 (96%)	5 (4%)	0	100	100
24	AS	143/145 (99%)	135 (94%)	8 (6%)	0	100	100
25	AT	141/143 (99%)	134 (95%)	7 (5%)	0	100	100
26	AU	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
27	AV	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
28	AW	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
29	AX	142/144 (99%)	129 (91%)	13 (9%)	0	100	100
30	AY	132/134 (98%)	125 (95%)	7 (5%)	0	100	100
31	AZ	80/82 (98%)	75 (94%)	5 (6%)	0	100	100
32	Aa	95/97 (98%)	81 (85%)	11 (12%)	3 (3%)	4	27
33	Ab	79/81 (98%)	73 (92%)	6 (8%)	0	100	100
34	Ac	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
35	Ad	51/53 (96%)	51 (100%)	0	0	100	100
36	Ae	58/60 (97%)	55 (95%)	3 (5%)	0	100	100
37	Af	71/73 (97%)	63 (89%)	8 (11%)	0	100	100
38	Ag	310/312 (99%)	302 (97%)	8 (3%)	0	100	100
39	BA	249/251 (99%)	238 (96%)	10 (4%)	1 (0%)	34	70
40	BB	384/386 (100%)	371 (97%)	12 (3%)	1 (0%)	41	75
41	BC	359/361 (99%)	347 (97%)	11 (3%)	1 (0%)	41	75
42	BD	292/294 (99%)	283 (97%)	8 (3%)	1 (0%)	41	75
43	BE	163/176 (93%)	158 (97%)	5 (3%)	0	100	100
44	BF	220/222 (99%)	215 (98%)	5 (2%)	0	100	100
45	BG	231/233 (99%)	222 (96%)	9 (4%)	0	100	100
46	BH	189/191 (99%)	186 (98%)	3 (2%)	0	100	100
47	BI	216/218 (99%)	214 (99%)	2 (1%)	0	100	100
48	BJ	167/169 (99%)	158 (95%)	9 (5%)	0	100	100
49	BK	191/193 (99%)	178 (93%)	10 (5%)	3 (2%)	9	41
50	BL	134/136 (98%)	132 (98%)	2 (2%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	BM	201/203 (99%)	196 (98%)	5 (2%)	0	100	100
52	BN	195/197 (99%)	189 (97%)	4 (2%)	2 (1%)	15	52
53	BO	181/183 (99%)	175 (97%)	6 (3%)	0	100	100
54	BP	183/185 (99%)	178 (97%)	5 (3%)	0	100	100
55	BQ	186/188 (99%)	184 (99%)	2 (1%)	0	100	100
56	BR	169/171 (99%)	165 (98%)	4 (2%)	0	100	100
57	BS	157/159 (99%)	150 (96%)	7 (4%)	0	100	100
58	BT	98/100 (98%)	98 (100%)	0	0	100	100
59	BU	134/136 (98%)	134 (100%)	0	0	100	100
60	BV	124/126 (98%)	120 (97%)	4 (3%)	0	100	100
61	BW	119/121 (98%)	117 (98%)	1 (1%)	1 (1%)	19	57
62	BX	123/125 (98%)	121 (98%)	2 (2%)	0	100	100
63	BY	133/135 (98%)	131 (98%)	2 (2%)	0	100	100
64	BZ	146/148 (99%)	136 (93%)	8 (6%)	2 (1%)	11	43
65	Ba	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
66	Bb	94/96 (98%)	94 (100%)	0	0	100	100
67	Bc	107/109 (98%)	101 (94%)	6 (6%)	0	100	100
68	Bd	125/127 (98%)	121 (97%)	4 (3%)	0	100	100
69	Be	104/106 (98%)	102 (98%)	2 (2%)	0	100	100
70	Bf	110/112 (98%)	108 (98%)	2 (2%)	0	100	100
71	Bg	117/119 (98%)	115 (98%)	2 (2%)	0	100	100
72	Bh	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
73	Bi	83/85 (98%)	83 (100%)	0	0	100	100
74	Bj	75/77 (97%)	75 (100%)	0	0	100	100
75	Bk	48/50 (96%)	48 (100%)	0	0	100	100
76	Bl	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
77	Bm	23/25 (92%)	23 (100%)	0	0	100	100
78	Bn	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
79	Bo	89/91 (98%)	89 (100%)	0	0	100	100
80	CA	1738/1967 (88%)	1664 (96%)	69 (4%)	5 (0%)	41	75
81	CB	295/297 (99%)	292 (99%)	2 (1%)	1 (0%)	41	75

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
82	CC	110/530 (21%)	106 (96%)	4 (4%)	0	100 100
All	All	13127/14000 (94%)	12615 (96%)	484 (4%)	28 (0%)	50 80

5 of 28 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	AI	10	LYS
32	Aa	84	VAL
52	BN	111[A]	PRO
80	CA	224	THR
80	CA	621	VAL

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
6	AA	170/173 (98%)	170 (100%)	0	100 100
7	AB	200/224 (89%)	200 (100%)	0	100 100
8	AC	175/175 (100%)	175 (100%)	0	100 100
9	AD	182/182 (100%)	181 (100%)	1 (0%)	88 95
10	AE	220/220 (100%)	220 (100%)	0	100 100
11	AF	172/173 (99%)	170 (99%)	2 (1%)	71 87
12	AG	189/195 (97%)	185 (98%)	4 (2%)	53 78
13	AH	163/165 (99%)	161 (99%)	2 (1%)	71 87
14	AI	148/161 (92%)	147 (99%)	1 (1%)	84 93
15	AJ	156/157 (99%)	156 (100%)	0	100 100
16	AK	77/85 (91%)	77 (100%)	0	100 100
17	AL	129/129 (100%)	128 (99%)	1 (1%)	81 92
18	AM	88/98 (90%)	88 (100%)	0	100 100
19	AN	127/127 (100%)	127 (100%)	0	100 100
20	AO	91/96 (95%)	91 (100%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
21	AP	95/98 (97%)	94 (99%)	1 (1%)	73 88
22	AQ	117/117 (100%)	117 (100%)	0	100 100
23	AR	101/124 (82%)	100 (99%)	1 (1%)	76 89
24	AS	128/128 (100%)	127 (99%)	1 (1%)	81 92
25	AT	115/115 (100%)	115 (100%)	0	100 100
26	AU	93/93 (100%)	93 (100%)	0	100 100
27	AV	71/74 (96%)	71 (100%)	0	100 100
28	AW	110/110 (100%)	110 (100%)	0	100 100
29	AX	119/119 (100%)	119 (100%)	0	100 100
30	AY	112/112 (100%)	112 (100%)	0	100 100
31	AZ	67/73 (92%)	67 (100%)	0	100 100
32	Aa	83/83 (100%)	83 (100%)	0	100 100
33	Ab	70/70 (100%)	70 (100%)	0	100 100
34	Ac	55/56 (98%)	53 (96%)	2 (4%)	35 65
35	Ad	47/47 (100%)	47 (100%)	0	100 100
36	Ae	50/51 (98%)	50 (100%)	0	100 100
37	Af	56/64 (88%)	55 (98%)	1 (2%)	59 81
38	Ag	250/257 (97%)	249 (100%)	1 (0%)	91 96
39	BA	190/193 (98%)	190 (100%)	0	100 100
40	BB	321/322 (100%)	319 (99%)	2 (1%)	86 94
41	BC	288/288 (100%)	288 (100%)	0	100 100
42	BD	241/243 (99%)	241 (100%)	0	100 100
43	BE	138/155 (89%)	136 (99%)	2 (1%)	67 85
44	BF	186/186 (100%)	186 (100%)	0	100 100
45	BG	187/191 (98%)	187 (100%)	0	100 100
46	BH	168/171 (98%)	168 (100%)	0	100 100
47	BI	185/185 (100%)	184 (100%)	1 (0%)	88 95
48	BJ	146/147 (99%)	146 (100%)	0	100 100
49	BK	154/154 (100%)	153 (99%)	1 (1%)	86 94
50	BL	107/107 (100%)	107 (100%)	0	100 100
51	BM	175/175 (100%)	174 (99%)	1 (1%)	86 94

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
52	BN	160/160 (100%)	159 (99%)	1 (1%)	86 94
53	BO	138/145 (95%)	138 (100%)	0	100 100
54	BP	150/150 (100%)	150 (100%)	0	100 100
55	BQ	152/153 (99%)	152 (100%)	0	100 100
56	BR	155/155 (100%)	155 (100%)	0	100 100
57	BS	136/136 (100%)	135 (99%)	1 (1%)	84 93
58	BT	87/87 (100%)	86 (99%)	1 (1%)	73 88
59	BU	104/104 (100%)	104 (100%)	0	100 100
60	BV	56/107 (52%)	55 (98%)	1 (2%)	59 81
61	BW	104/105 (99%)	104 (100%)	0	100 100
62	BX	108/108 (100%)	106 (98%)	2 (2%)	57 80
63	BY	115/115 (100%)	115 (100%)	0	100 100
64	BZ	118/118 (100%)	118 (100%)	0	100 100
65	Ba	46/46 (100%)	45 (98%)	1 (2%)	52 77
66	Bb	81/81 (100%)	81 (100%)	0	100 100
67	Bc	92/96 (96%)	92 (100%)	0	100 100
68	Bd	108/109 (99%)	108 (100%)	0	100 100
69	Be	90/90 (100%)	90 (100%)	0	100 100
70	Bf	95/95 (100%)	95 (100%)	0	100 100
71	Bg	104/104 (100%)	104 (100%)	0	100 100
72	Bh	80/81 (99%)	80 (100%)	0	100 100
73	Bi	69/69 (100%)	69 (100%)	0	100 100
74	Bj	68/68 (100%)	68 (100%)	0	100 100
75	Bk	45/45 (100%)	44 (98%)	1 (2%)	52 77
76	Bl	47/47 (100%)	47 (100%)	0	100 100
77	Bm	22/23 (96%)	22 (100%)	0	100 100
78	Bn	87/88 (99%)	87 (100%)	0	100 100
79	Bo	71/71 (100%)	71 (100%)	0	100 100
80	CA	1560/1770 (88%)	1553 (100%)	7 (0%)	91 96
81	CB	266/266 (100%)	264 (99%)	2 (1%)	81 92
82	CC	97/482 (20%)	97 (100%)	0	100 100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	11123/11942 (93%)	11081 (100%)	42 (0%)	91 96

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
60	BV	57	LYS
80	CA	602	MET
62	BX	3	LYS
75	Bk	8	ARG
80	CA	1229	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
47	BI	112	GLN
63	BY	103	GLN
81	CB	103	GLN
59	BU	98	ASN
67	Bc	57	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1768/1798 (98%)	413 (23%)	36 (2%)
2	3	157/158 (99%)	27 (17%)	1 (0%)
3	4	120/121 (99%)	9 (7%)	1 (0%)
4	5	3180/3396 (93%)	530 (16%)	30 (0%)
5	6	75/76 (98%)	12 (16%)	0
All	All	5300/5549 (95%)	991 (18%)	68 (1%)

5 of 991 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	25	C
1	2	26	A
1	2	34	G

5 of 68 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	5	2500	A
4	5	2541	U
4	5	3350	C
1	2	1226	A
1	2	1216	C

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 95 ligands modelled in this entry, 95 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

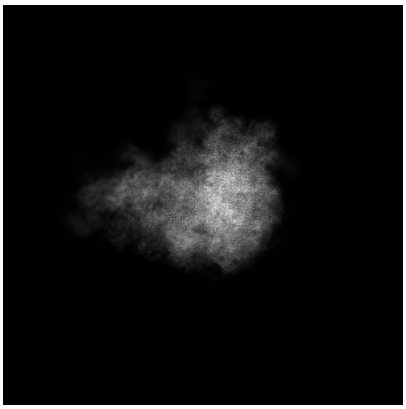
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-14861. These allow visual inspection of the internal detail of the map and identification of artifacts.

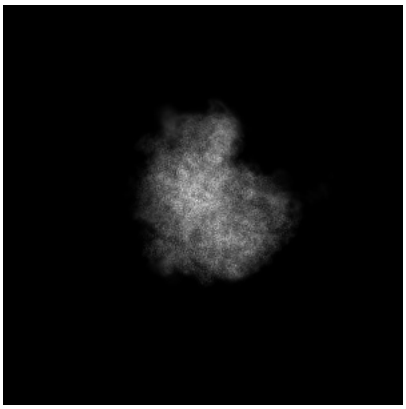
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

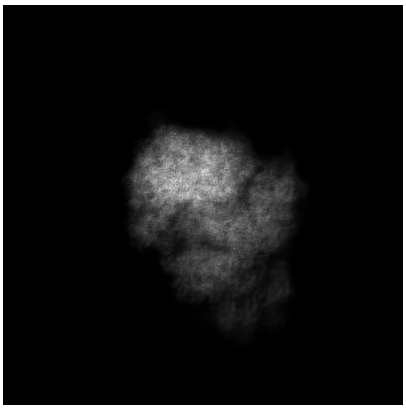
6.1.1 Primary map



X

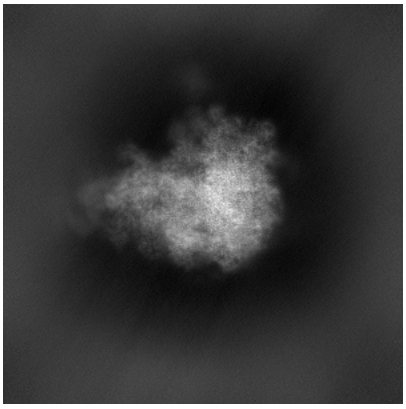


Y

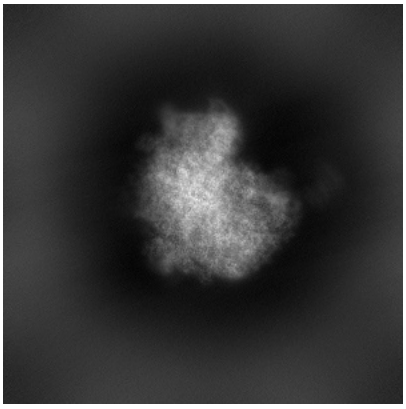


Z

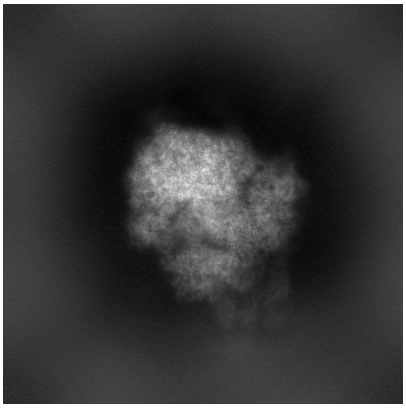
6.1.2 Raw map



X



Y

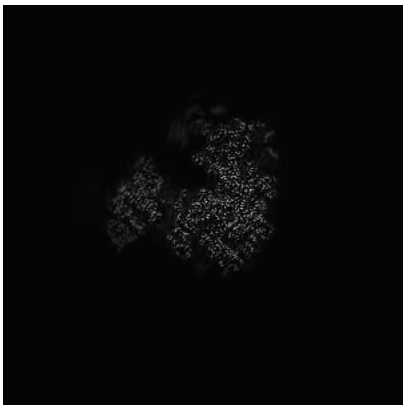


Z

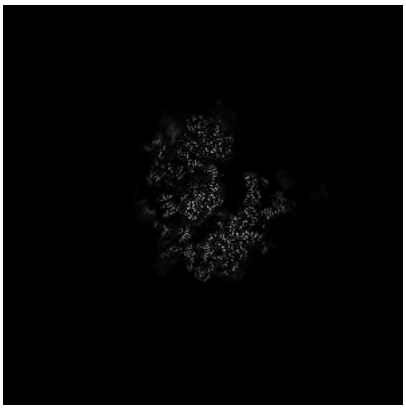
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

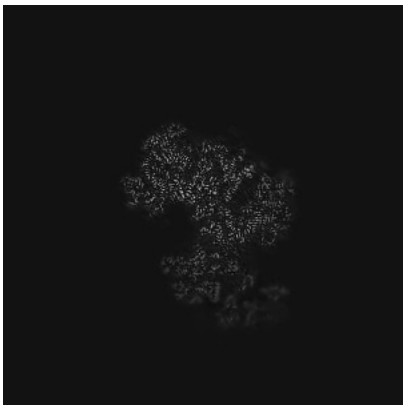
6.2.1 Primary map



X Index: 280

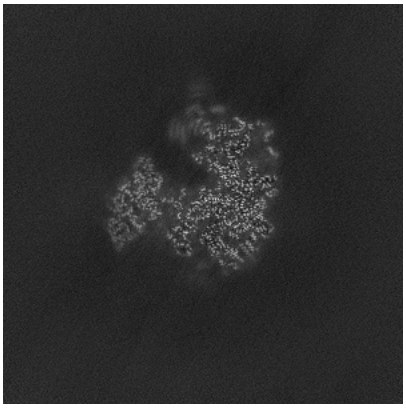


Y Index: 280

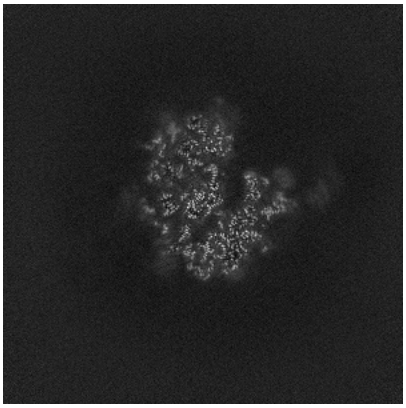


Z Index: 280

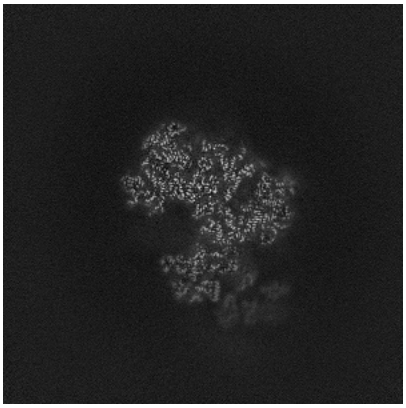
6.2.2 Raw map



X Index: 280



Y Index: 280

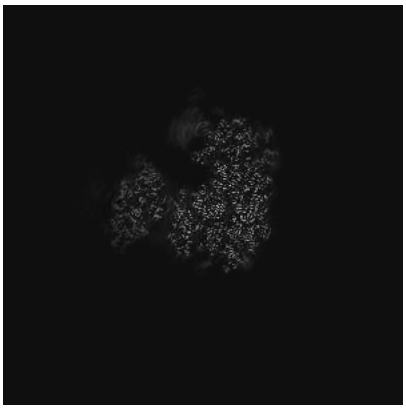


Z Index: 280

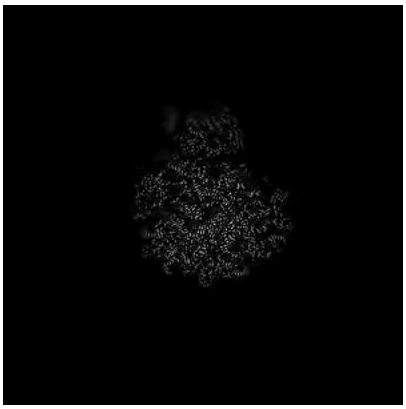
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



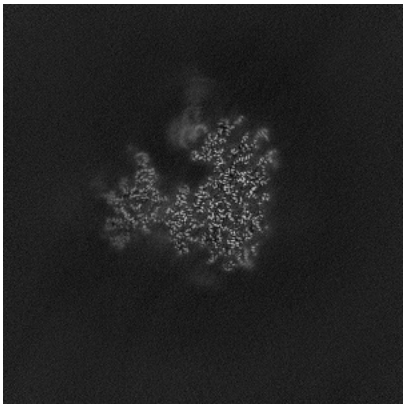
X Index: 285



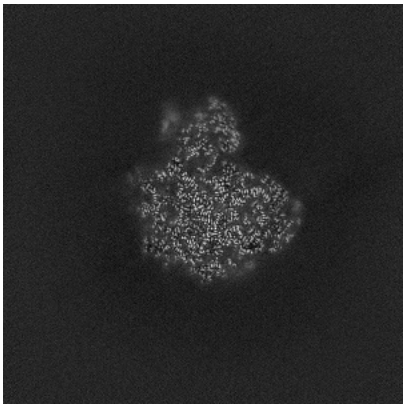
Y Index: 314

Z Index: 300

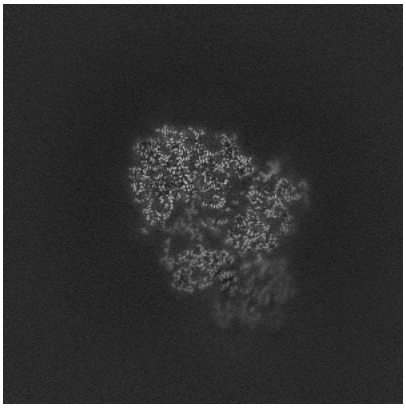
6.3.2 Raw map



X Index: 290



Y Index: 305

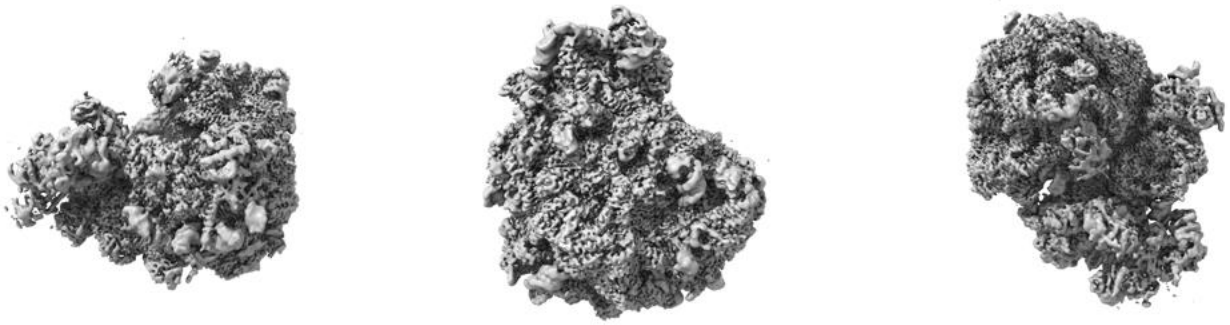


Z Index: 300

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

6.4 Orthogonal surface views (i)

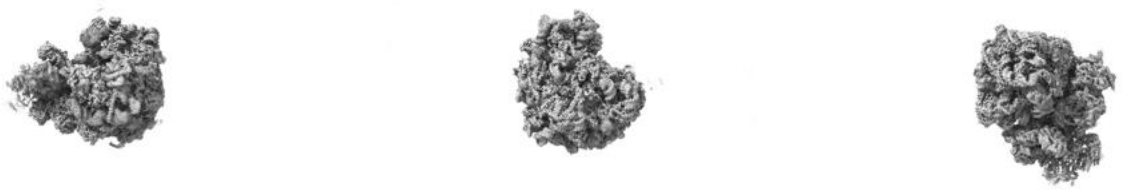
6.4.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

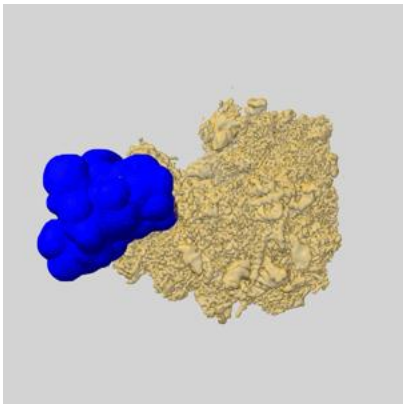
6.5 Mask visualisation

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

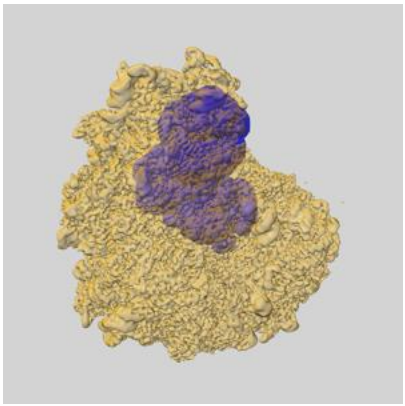
A mask typically either:

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

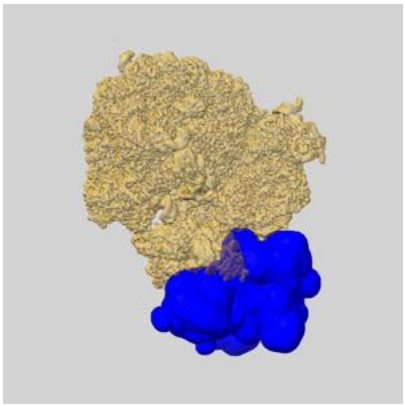
6.5.1 emd_14861_msk_2.map



X

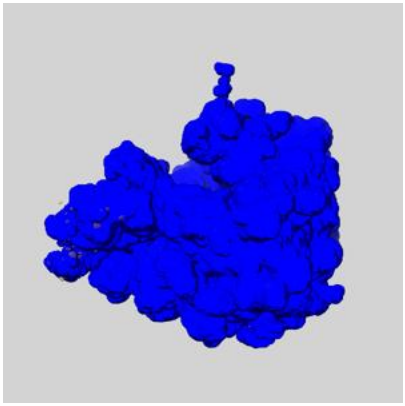


Y

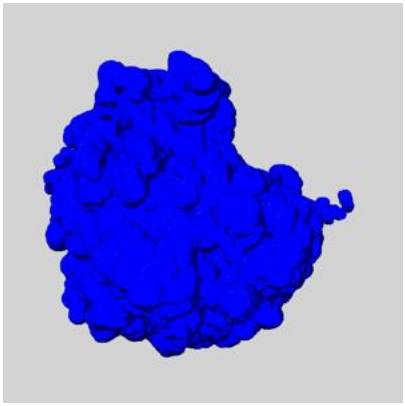


Z

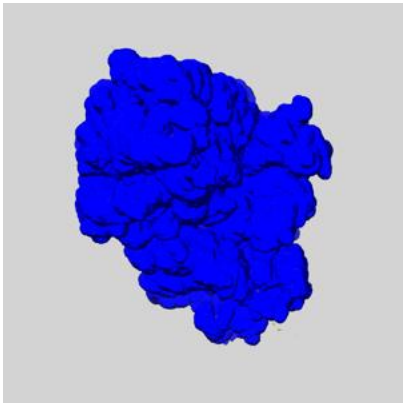
6.5.2 emd_14861_msk_1.map



X



Y

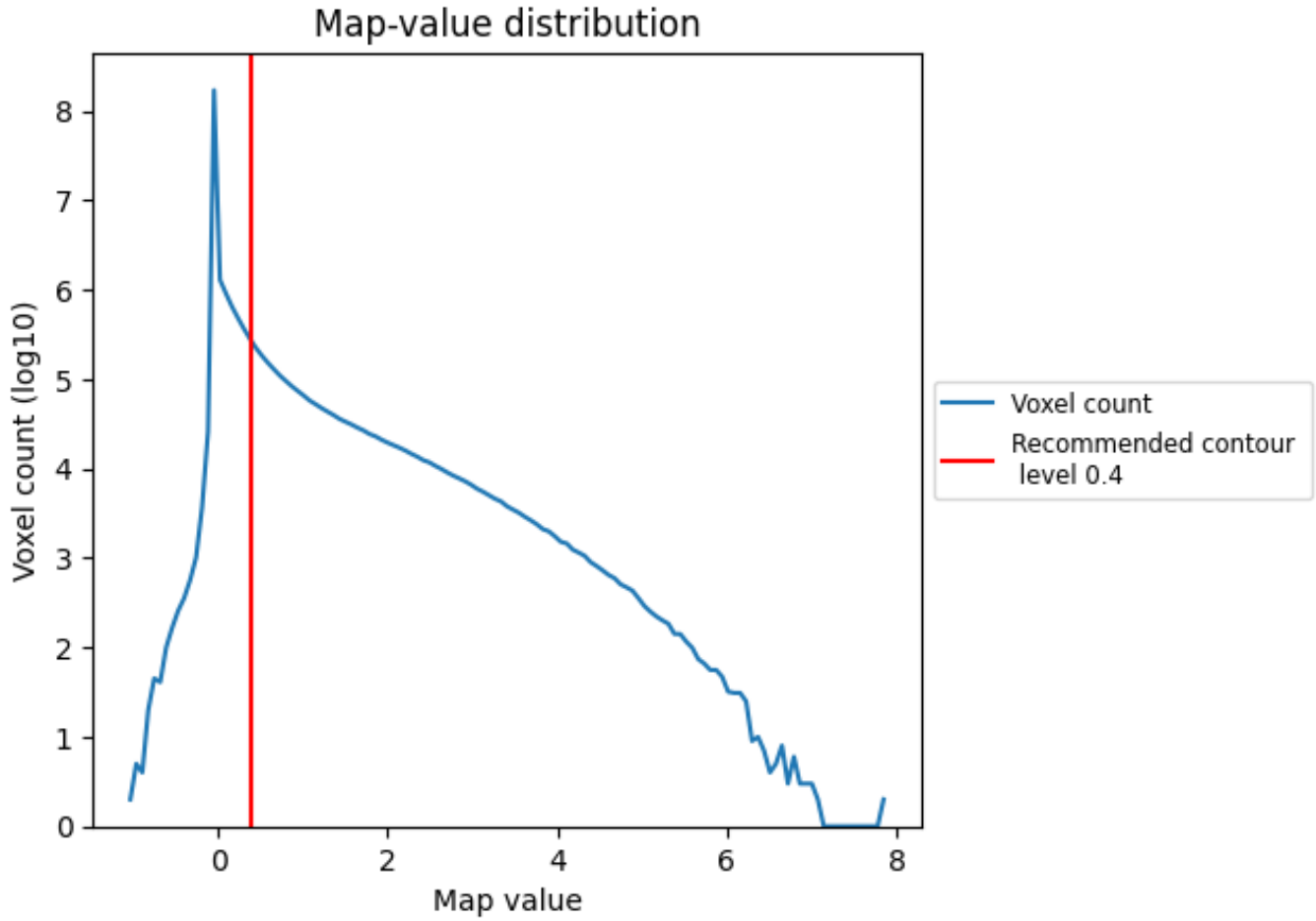


Z

7 Map analysis

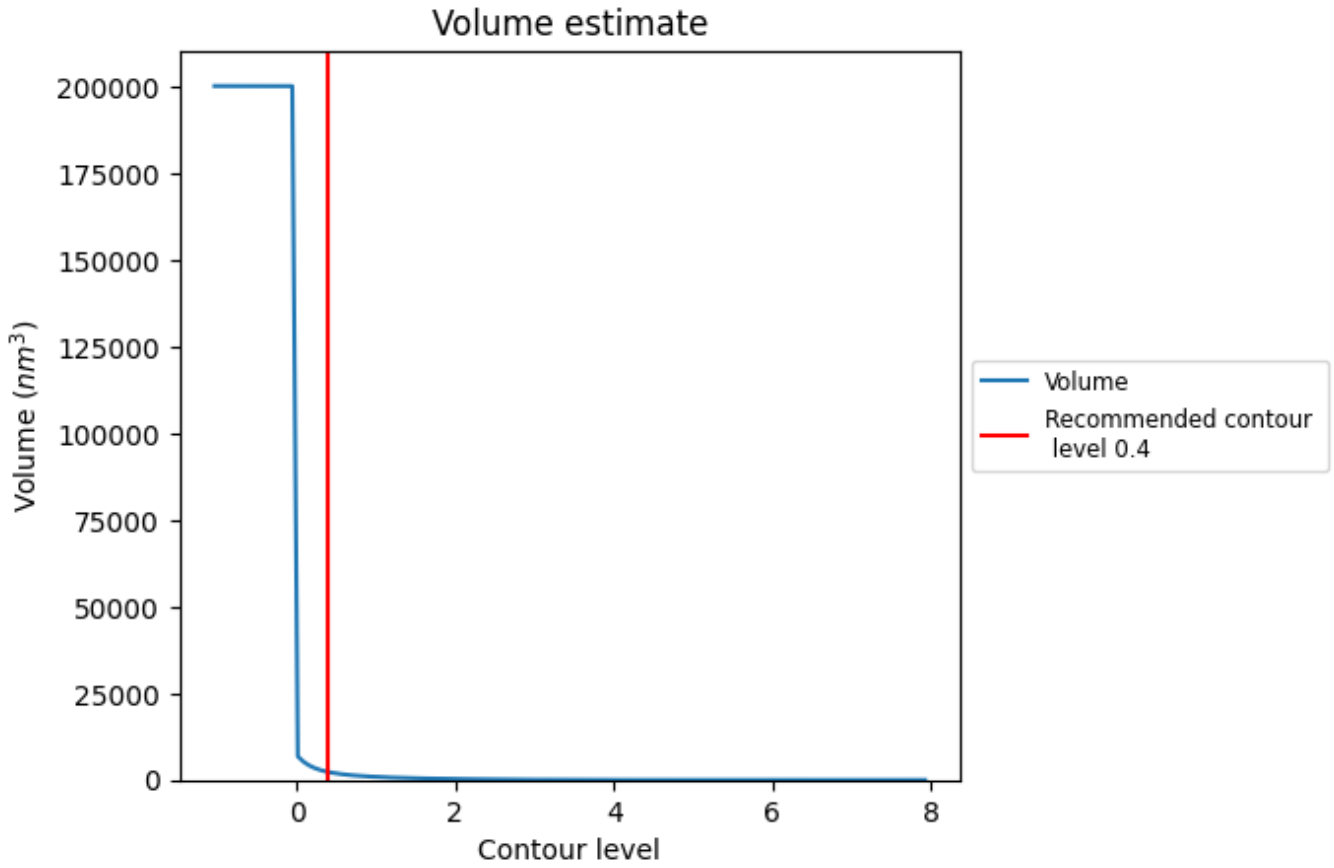
This section contains the results of statistical analysis of the map.

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.

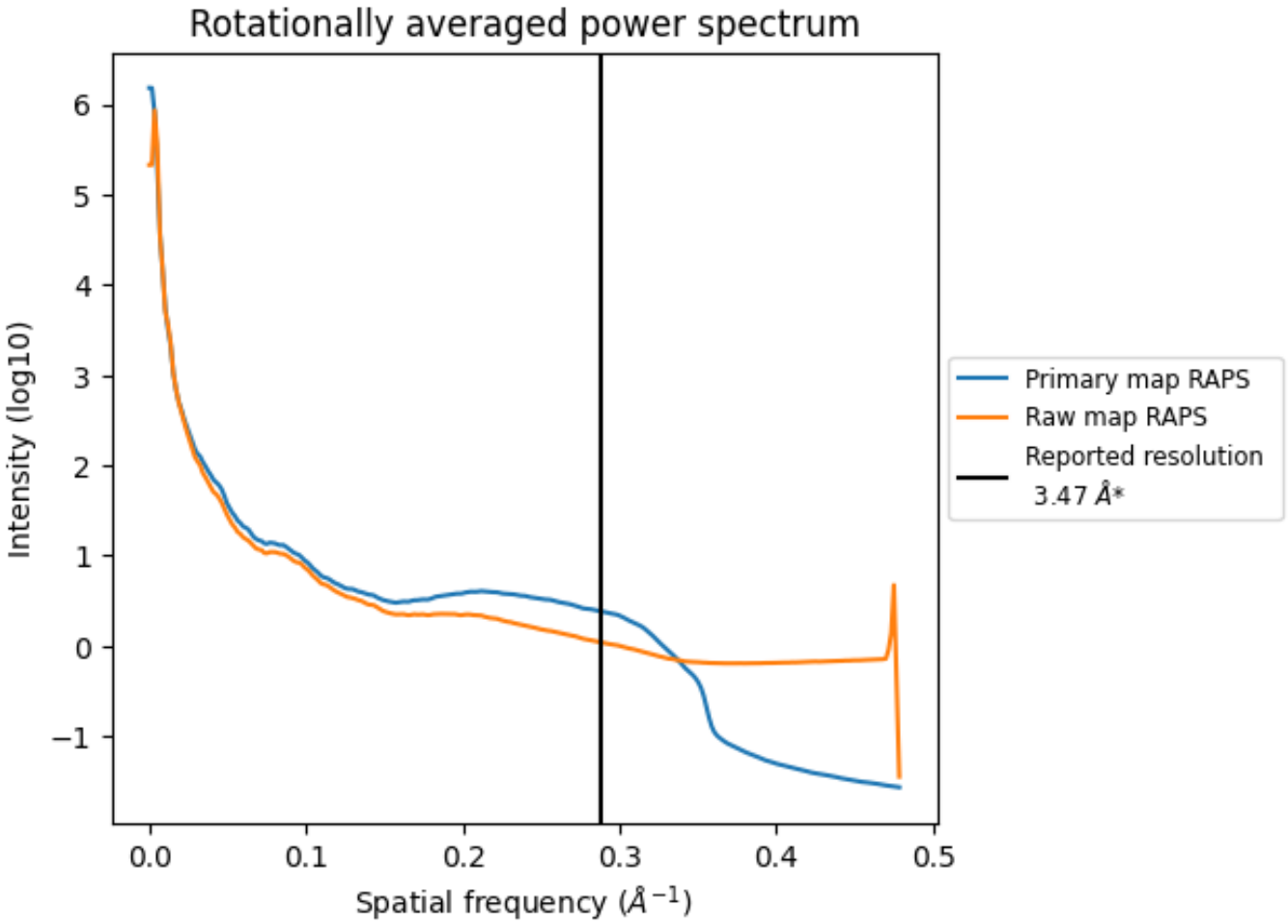
7.2 Volume estimate (i)



The volume at the recommended contour level is 2315 nm^3; this corresponds to an approximate mass of 2091 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)

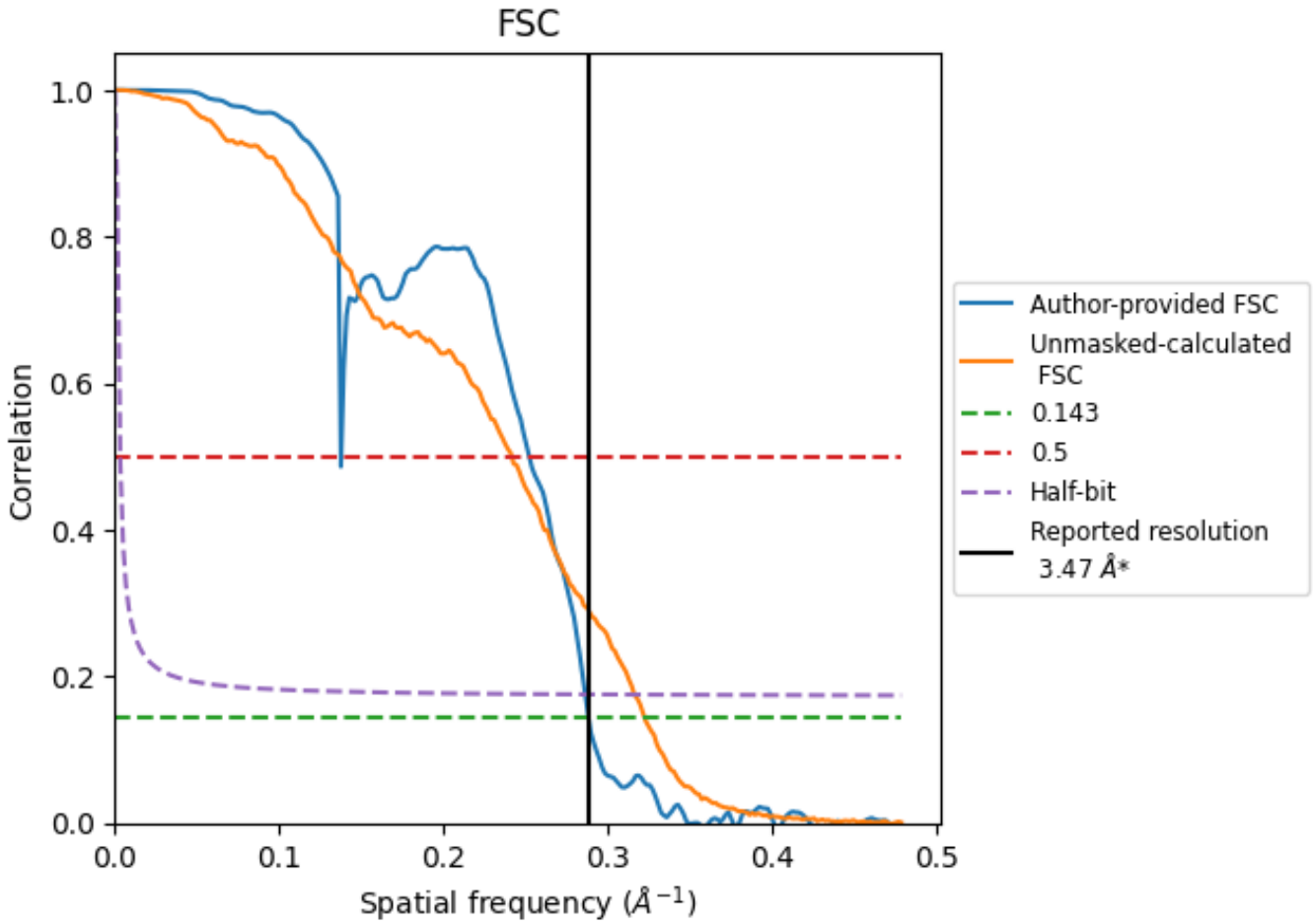


*Reported resolution corresponds to spatial frequency of 0.288 Å^{-1}

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 0.288 $Å^{-1}$

8.2 Resolution estimates (i)

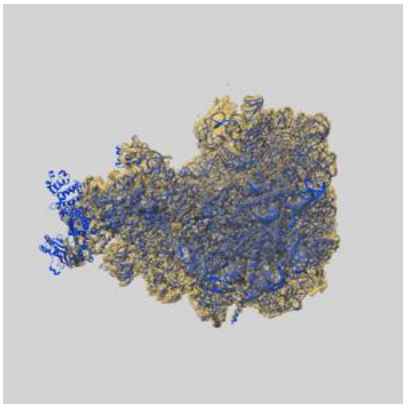
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.47	-	-
Author-provided FSC curve	3.47	7.27	3.49
Unmasked-calculated*	3.10	4.14	3.16

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.10 differs from the reported value 3.47 by more than 10 %

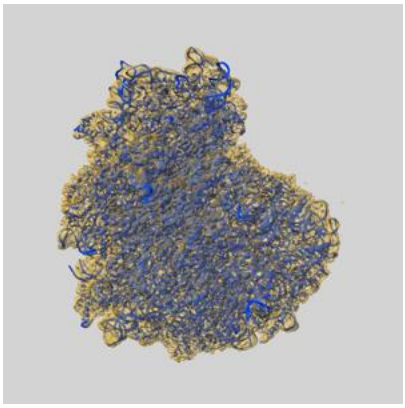
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-14861 and PDB model 7ZPQ. Per-residue inclusion information can be found in section 3 on page 20.

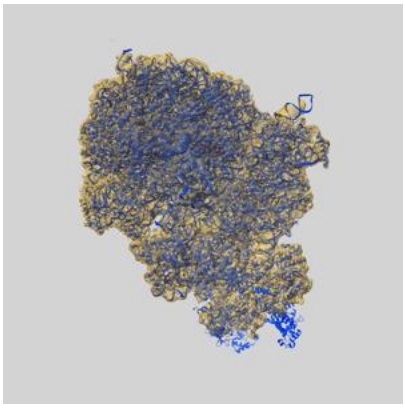
9.1 Map-model overlay



X



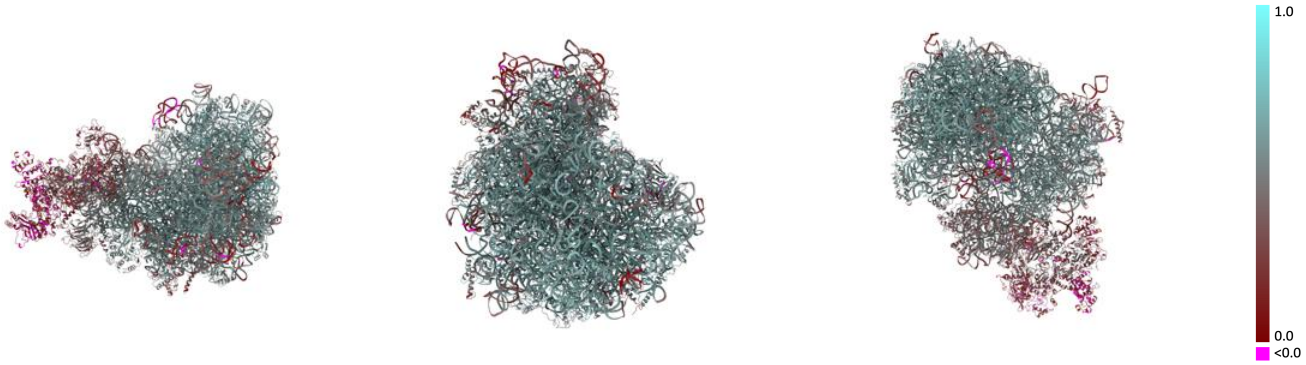
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.4 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.

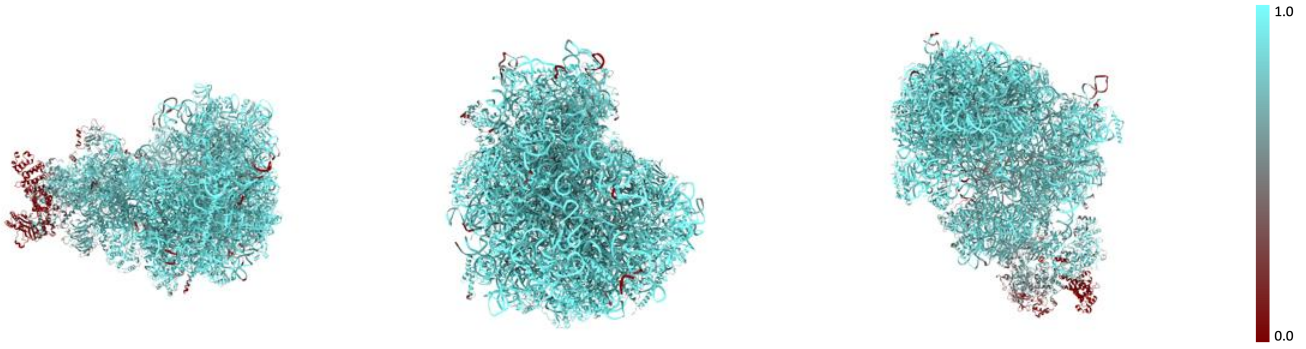
9.2 Q-score mapped to coordinate model



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.

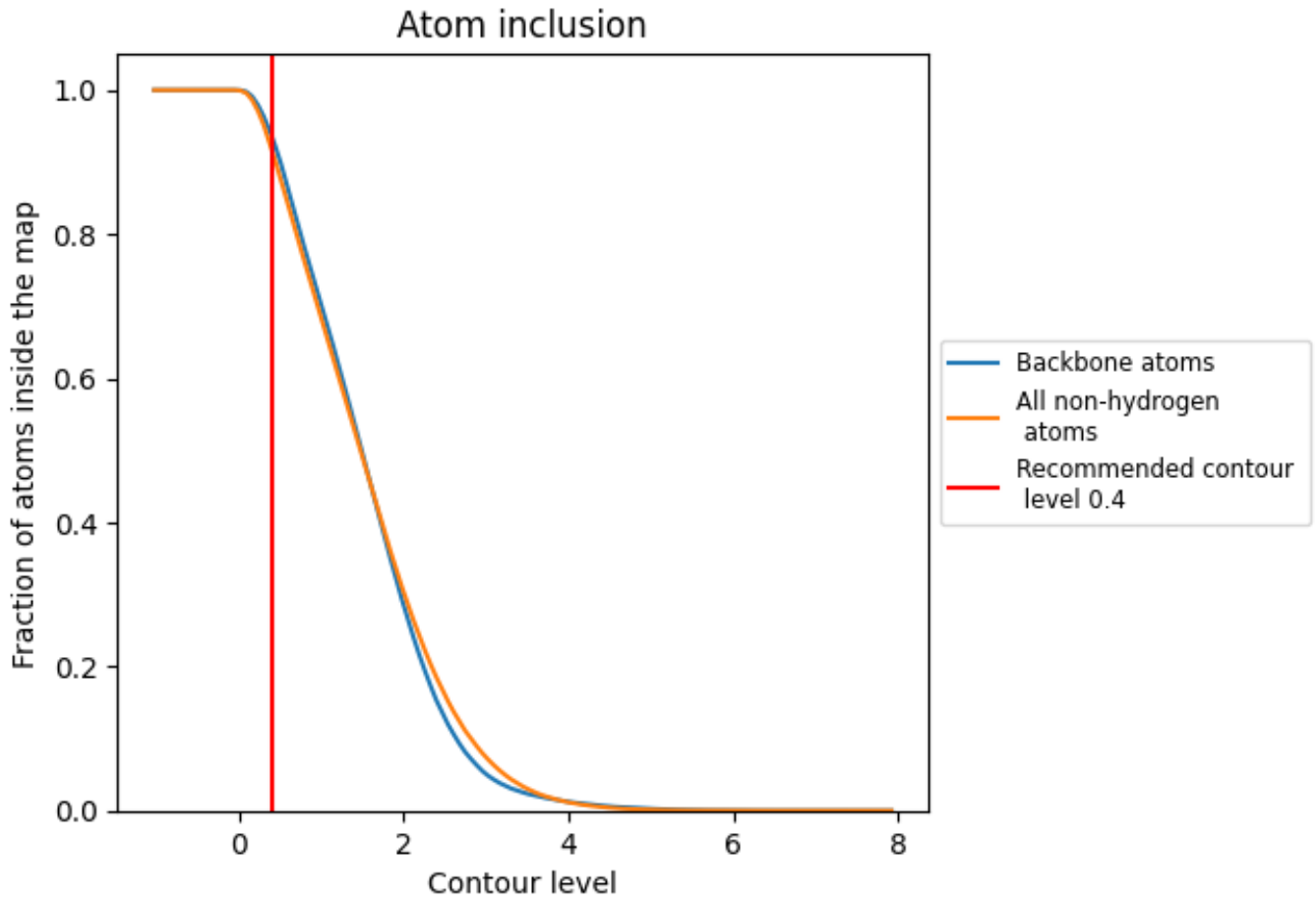
9.3 Atom inclusion mapped to coordinate model



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 (0.4).

9.4 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 92% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9162	0.5220
2	0.9551	0.5070
3	0.9839	0.6030
4	0.9938	0.5830
5	0.9730	0.5810
6	0.7801	0.3420
AA	0.9559	0.5340
AB	0.9371	0.5280
AC	0.9800	0.5800
AD	0.9127	0.4710
AE	0.9690	0.5590
AF	0.8622	0.4420
AG	0.8812	0.4570
AH	0.8740	0.4690
AI	0.9621	0.5670
AJ	0.9363	0.5350
AK	0.8360	0.3770
AL	0.9495	0.5850
AM	0.4243	0.2170
AN	0.9506	0.5690
AO	0.9754	0.5550
AP	0.8034	0.3460
AQ	0.8907	0.4500
AR	0.9089	0.4860
AS	0.8432	0.3680
AT	0.8540	0.3900
AU	0.8402	0.4140
AV	0.9510	0.5510
AW	0.9900	0.6070
AX	0.9607	0.5750
AY	0.9116	0.4900
AZ	0.7104	0.3240
Aa	0.9526	0.5480
Ab	0.9468	0.5290
Ac	0.8879	0.4940

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Ad	0.9599	0.5120
Ae	0.9035	0.5010
Af	0.5809	0.2000
Ag	0.7313	0.3670
BA	0.9880	0.6380
BB	0.9773	0.6060
BC	0.9773	0.6100
BD	0.9314	0.5350
BE	0.9476	0.5500
BF	0.9770	0.6100
BG	0.9368	0.5430
BH	0.9520	0.5660
BI	0.9602	0.5730
BJ	0.9169	0.4780
BK	0.9597	0.5890
BL	0.9698	0.5780
BM	0.9957	0.6420
BN	0.9815	0.6130
BO	0.9577	0.6080
BP	0.9885	0.6210
BQ	0.9271	0.5640
BR	0.9828	0.6130
BS	0.9702	0.5930
BT	0.9271	0.5100
BU	0.9632	0.6130
BV	0.9341	0.5150
BW	0.9650	0.5820
BX	0.9781	0.5910
BY	0.9402	0.5550
BZ	0.9781	0.6210
Ba	0.9447	0.5620
Bb	0.9807	0.5840
Bc	0.9341	0.5730
Bd	0.9859	0.6270
Be	0.9927	0.6410
Bf	0.9613	0.5970
Bg	0.9639	0.5820
Bh	0.9595	0.5670
Bi	0.9938	0.6460
Bj	0.9132	0.5180
Bk	0.9880	0.6270
Bl	0.9480	0.5850

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bm	0.9952	0.6340
Bn	0.9715	0.5940
Bo	0.9836	0.6190
CA	0.6133	0.2420
CB	0.0084	0.1040
CC	0.3933	0.1640