



## wwPDB EM Validation Summary Report ⓘ

Nov 2, 2024 – 08:40 pm GMT

PDB ID : 6Q8Y  
EMDB ID : EMD-4474  
Title : Cryo-EM structure of the mRNA translating and degrading yeast 80S ribosome-Xrn1 nuclease complex  
Authors : Tesina, P.; Heckel, E.; Cheng, J.; Buschauer, R.; Kater, L.; Berninghausen, O.; Becker, T.; Beckmann, R.  
Deposited on : 2018-12-16  
Resolution : 3.10 Å(reported)

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

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

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

EMDB validation analysis : 0.0.1.dev113  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

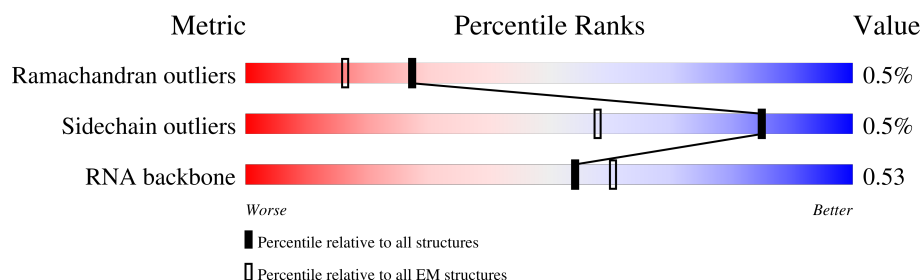
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.10 Å.

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



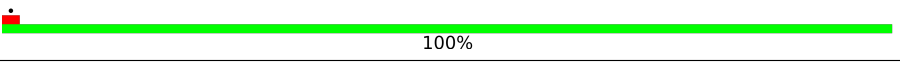
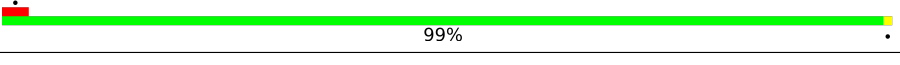
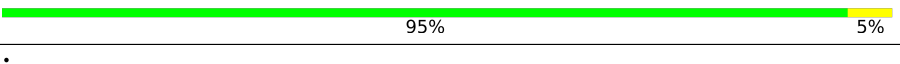
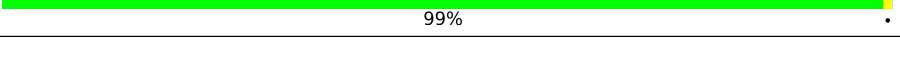
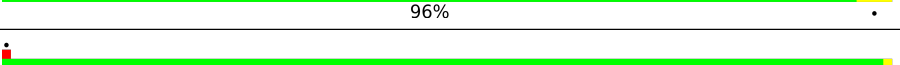
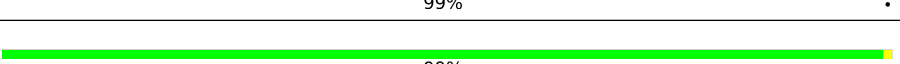
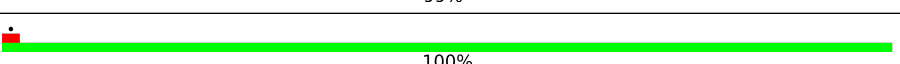
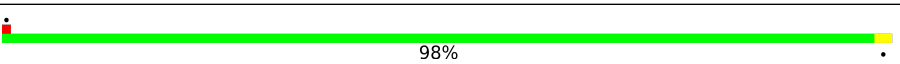
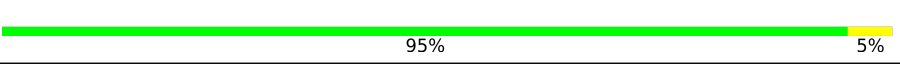
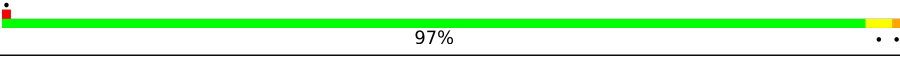
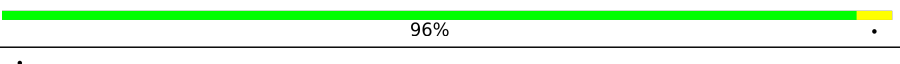
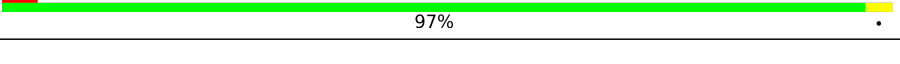
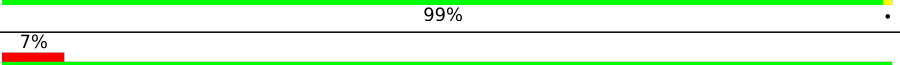
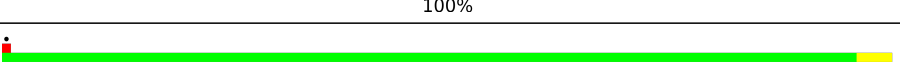
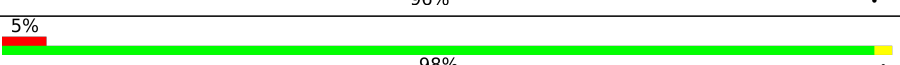
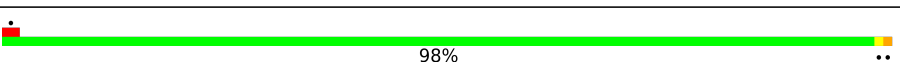
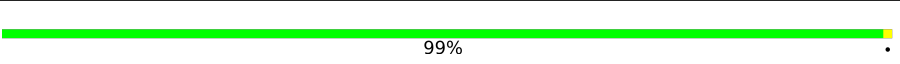
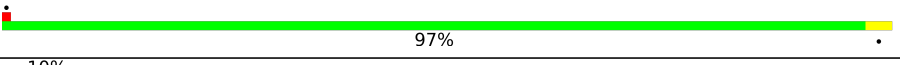
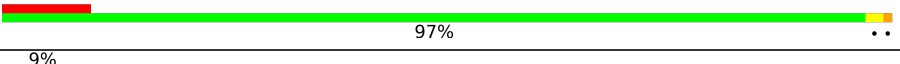
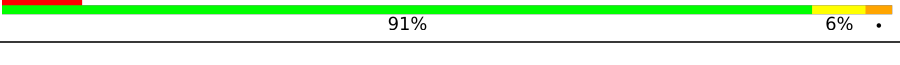
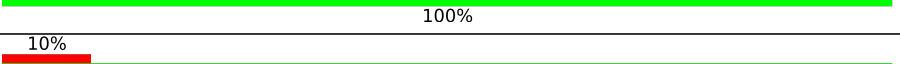
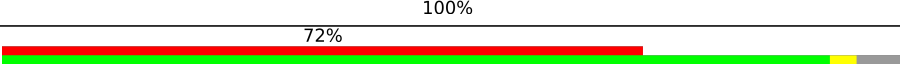
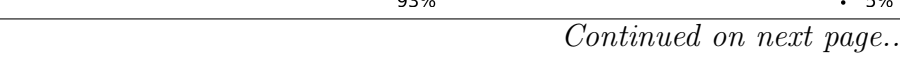


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	2	1797	67% 29%
2	AA	233	97%
3	AB	136	99%
4	AC	100	94% 5%
5	AD	191	99%
6	AE	67	7% 100%
7	AF	87	98%
8	AG	169	99%

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Mol	Chain	Length	Quality of chain
9	AH	121	 100%
10	AI	77	 99%
11	AJ	193	 95% 5%
12	AK	126	 99%
13	AL	50	 96%
14	AM	136	 99%
15	AN	135	 99%
16	AO	52	 100%
17	AP	105	 98%
18	AQ	203	 95% 5%
19	AR	148	 97%
20	AS	25	 96%
21	AT	91	 97%
22	AU	197	 99%
23	AV	58	 7% 100%
24	AW	252	 96%
25	AX	183	 5% 98%
26	a	87	 98%
27	b	129	 99%
28	c	144	 97%
29	d	132	 10% 97%
30	e	97	 9% 91% 6%
31	f	81	 100%
32	g	60	 10% 100%
33	z	916	 72% 93% 5%

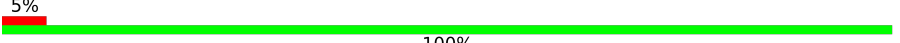


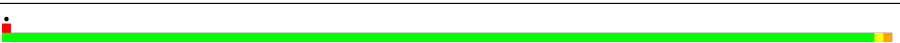

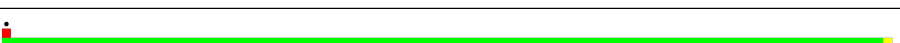

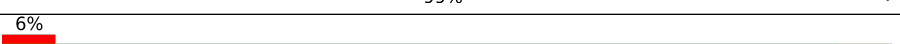
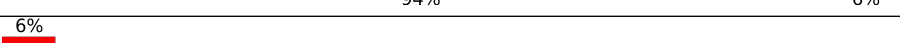
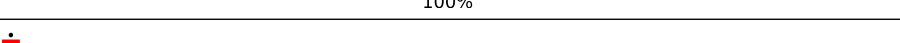
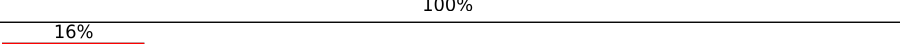
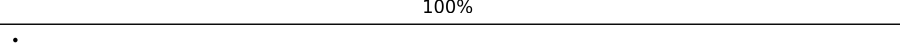
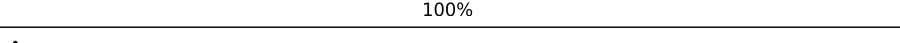
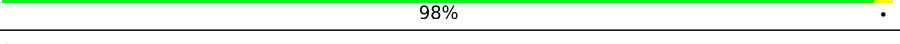
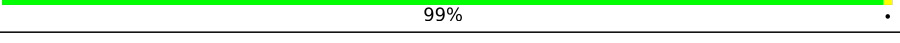
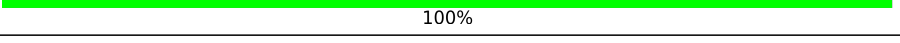
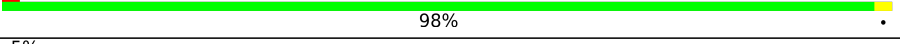
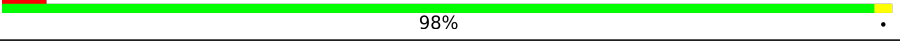
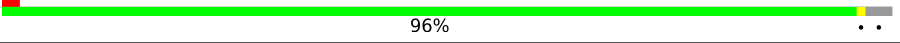

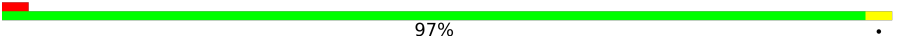
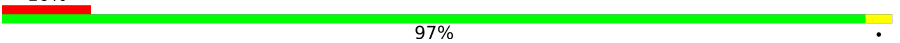
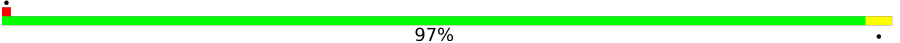
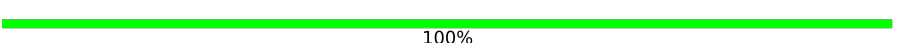
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Mol	Chain	Length	Quality of chain
34	l	17	
35	n	76	
36	m	75	
37	AY	97	
38	BA	386	
39	BB	185	
40	BC	109	
41	BD	220	
42	BE	361	
43	BF	188	
44	BG	127	
45	BH	172	
46	BI	296	
47	BJ	159	
48	BK	106	
49	BL	100	
50	BM	175	
51	BN	112	
52	BO	222	
53	BP	119	
54	BQ	3396	
55	BR	121	
56	BS	158	
57	A	223	
58	B	206	

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Mol	Chain	Length	Quality of chain
59	C	96	 5% 100%
60	D	121	 12% 98%
61	E	121	 9% 99%
62	F	141	 98%
63	G	125	 98%
64	H	139	 99%
65	J	107	 5% 99%
66	K	70	 6% 94% 6%
67	L	63	 6% 100%
68	M	53	 100%
69	N	51	 16% 100%
70	O	318	 100%
71	P	219	 98%
72	Q	214	 99%
73	R	220	 100%
74	S	260	 98%
75	T	226	 5% 98%
76	U	184	 96%
77	V	199	 7% 88% 6% 6%
78	W	178	 97%
79	X	155	 10% 97%
80	Y	150	 97%
81	Z	127	 100%
82	I	143	 99%

## 2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 209410 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
1	2	1767	Total	C	N	O	P	0	0
			37645	16830	6656	12392	1767		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	1570	G	A	conflict	GB 1329886537

- Molecule 2 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 3 is a protein called 60S ribosomal protein L23-A.

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

- Molecule 4 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 5 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 6 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AE	67	Total	C	N	O	S	0	0
			543	349	106	87	1		

- Molecule 7 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 8 is a protein called 60S ribosomal protein L11-B.

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

- Molecule 9 is a protein called 60S ribosomal protein L25.

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

- Molecule 10 is a protein called 60S ribosomal protein L38.

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

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

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

- Molecule 12 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	AK	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 13 is a protein called 60S ribosomal protein L39.

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

- Molecule 14 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 15 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AN	135	Total	C	N	O	S	0	0
			1092	710	202	180			

- Molecule 16 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 17 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 18 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 19 is a protein called 60S ribosomal protein L28.

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

- Molecule 20 is a protein called 60S ribosomal protein L41-B.



Mol	Chain	Residues	Atoms					AltConf	Trace
20	AS	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 21 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 22 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 23 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AV	58	Total	C	N	O	S	0	0
			462	289	100	73			

- Molecule 24 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 25 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AX	183	Total	C	N	O	S	0	0
			1420	882	281	257			

- Molecule 26 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	a	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 27 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 28 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	d	132	Total	C	N	O	S	0	0
			1060	669	206	185			

- Molecule 30 is a protein called 40S ribosomal protein S26-B.

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

- Molecule 31 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 32 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	g	60	Total	C	N	O	S	0	0
			473	297	98	77	1		

- Molecule 33 is a protein called 5'-3' exoribonuclease 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	z	874	Total	C	N	O	S	0	0
			7181	4639	1194	1320	28		

- Molecule 34 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	l	17	Total	C	N	O	P	0	0
			367	164	70	116	17		

- Molecule 35 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	n	76	Total	C	N	O	P	0	0
			1621	723	291	531	76		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	74	C	-	insertion	GB 1329886529
n	75	C	-	insertion	GB 1329886529
n	76	A	-	insertion	GB 1329886529

- Molecule 36 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	m	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	11	C	U	conflict	GB 176418

- Molecule 37 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	AY	97	Total	C	N	O	S	0	0
			742	479	124	138	1		

- Molecule 38 is a protein called 60S ribosomal protein L3.

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

- Molecule 39 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 41 is a protein called 60S ribosomal protein L10.

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

- Molecule 42 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 43 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
43	BF	188	Total	C	N	O	0	0
			1521	935	326	260		

- Molecule 44 is a protein called 60S ribosomal protein L32.

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

- Molecule 45 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L5.

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

- Molecule 47 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 48 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BL	100	Total	C	N	O	S	0	0
			796	516	131	149			

- Molecule 50 is a protein called 60S ribosomal protein L6-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 54 is a RNA chain called 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BQ	3161	Total	C	N	O	P	0	0
			67610	30200	12186	22063	3161		

- Molecule 55 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 56 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BS	158	Total	C	N	O	P	0	0
			3352	1500	586	1108	158		

- Molecule 57 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 58 is a protein called Rps5p.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	B	206	Total	C	N	O	S	0	0
			1603	1004	297	299	3		

- Molecule 59 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	C	96	Total	C	N	O	S	0	0
			813	527	133	151	2		

- Molecule 60 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	D	121	Total	C	N	O	S	0	0
			877	552	153	170	2		

- Molecule 61 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	E	121	Total	C	N	O	S	0	0
			957	611	176	163	7		

- Molecule 62 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	F	141	Total	C	N	O	S	0	0
			1099	704	202	193			

- Molecule 63 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	G	125	Total	C	N	O	S	0	0
			1001	625	188	186	2		

- Molecule 64 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	H	139	Total	C	N	O	S	0	0
			1143	716	222	203	2		

- Molecule 65 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	J	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 66 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	K	70	Total	C	N	O	S	0	0
			563	360	104	99			

- Molecule 67 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	L	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 68 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 69 is a protein called Ubiquitin-40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	N	51	Total	C	N	O	S	0	0
			397	249	73	71	4		

- Molecule 70 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	O	318	Total	C	N	O	S	0	0
			2436	1541	418	469	8		

- Molecule 71 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	P	219	Total	C	N	O	S	0	0
			1691	1082	296	311	2		

- Molecule 72 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Q	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 73 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	R	220	Total	C	N	O	S	0	0
			1671	1072	297	300	2		

- Molecule 74 is a protein called 40S ribosomal protein S4-A.



Mol	Chain	Residues	Atoms					AltConf	Trace
74	S	260	Total	C	N	O	S	0	0
			2061	1309	389	360	3		

- Molecule 75 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	T	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 76 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
76	U	179	Total	C	N	O	0	0
			1442	926	259	257		

- Molecule 77 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	V	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 78 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	W	178	Total	C	N	O	S	0	0
			1434	905	276	252	1		

- Molecule 79 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	X	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 80 is a protein called 40S ribosomal protein S13.

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

- Molecule 81 is a protein called 40S ribosomal protein S14-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Z	127	Total	C	N	O	S	0	0
			891	545	182	163	1		

- Molecule 82 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	I	143	Total	C	N	O	S	0	0
			1101	688	204	207	2		

- Molecule 83 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
83	AF	1	Total	Zn	0
			1	1	
83	AO	1	Total	Zn	0
			1	1	
83	AP	1	Total	Zn	0
			1	1	
83	AT	1	Total	Zn	0
			1	1	
83	e	1	Total	Zn	0
			1	1	
83	BN	1	Total	Zn	0
			1	1	
83	M	1	Total	Zn	0
			1	1	
83	N	1	Total	Zn	0
			1	1	

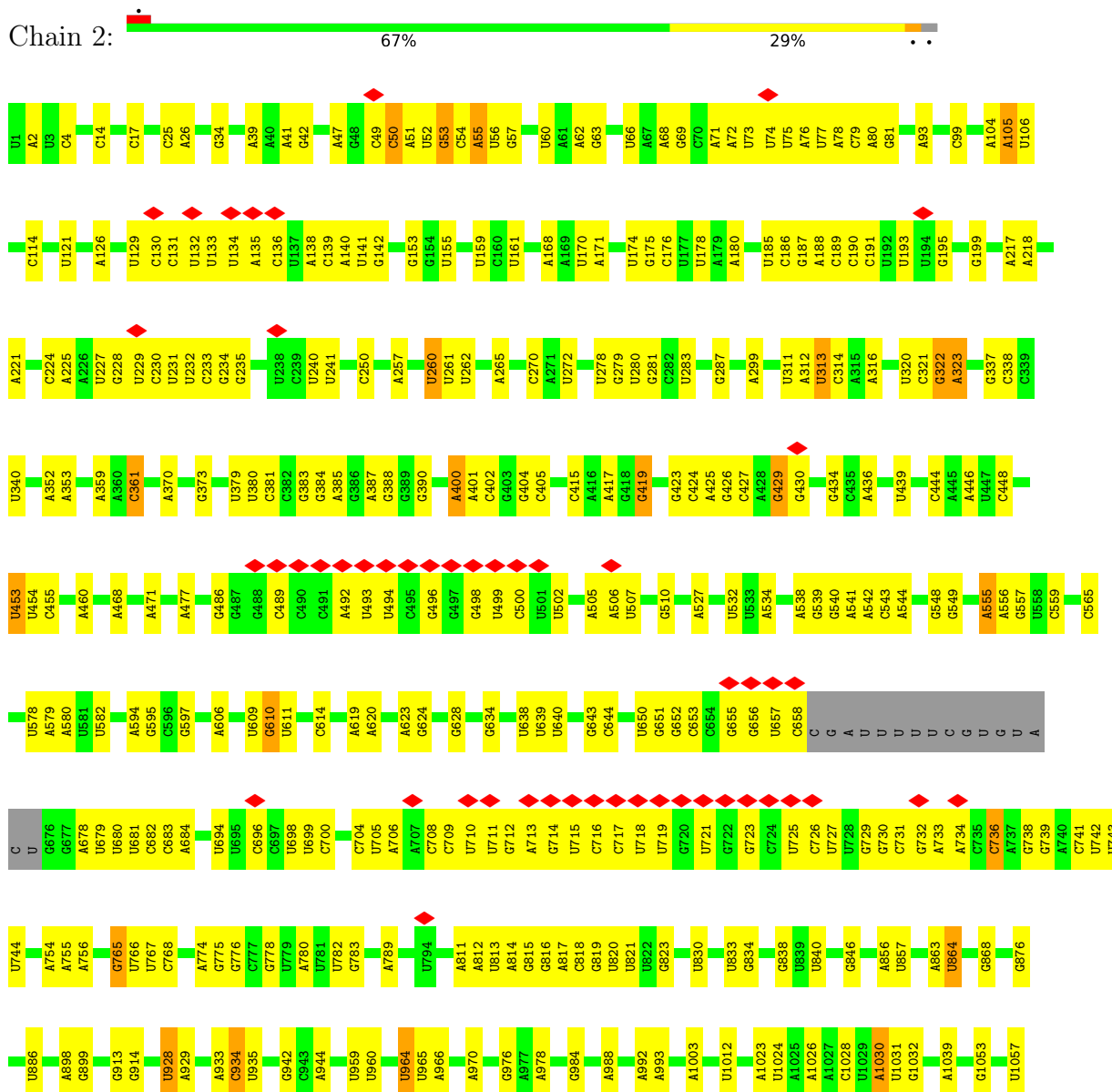
- Molecule 84 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

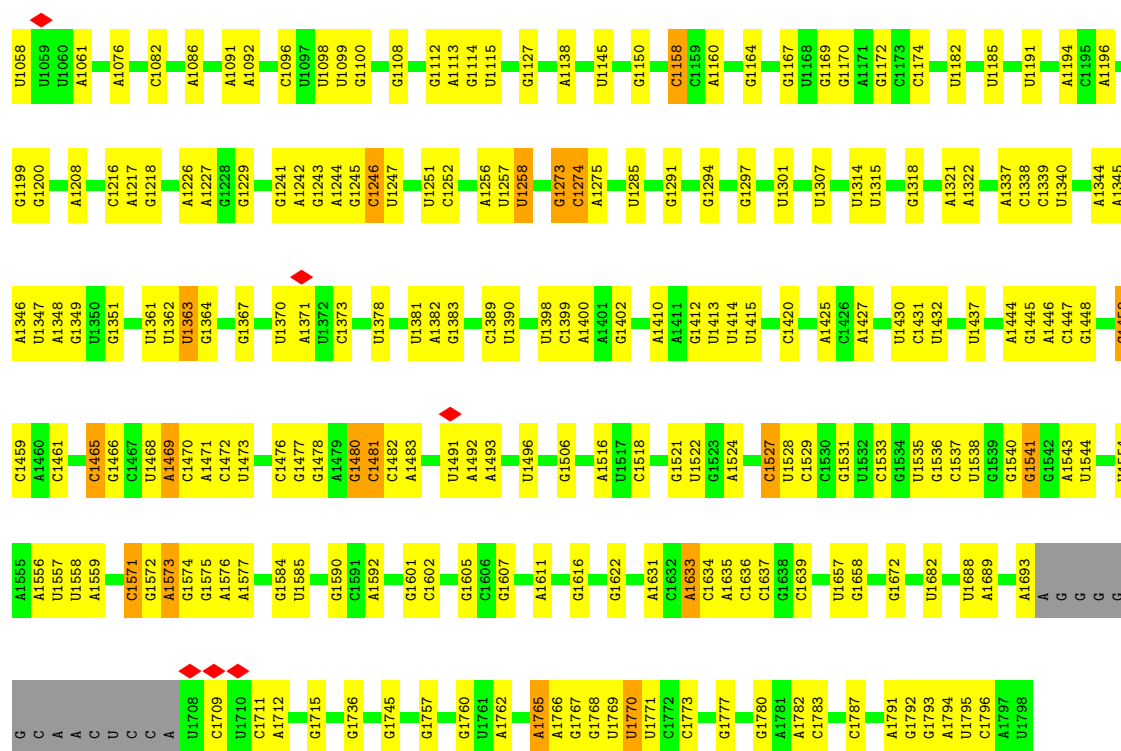
Mol	Chain	Residues	Atoms		AltConf
84	z	1	Total	Mg	0
			1	1	
84	l	1	Total	Mg	0
			1	1	

### 3 Residue-property plots

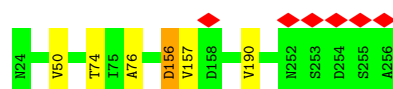
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: 18S ribosomal RNA

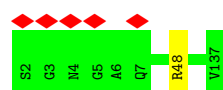




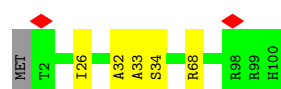
• Molecule 2: 60S ribosomal protein L8-A



• Molecule 3: 60S ribosomal protein L23-A



• Molecule 4: 60S ribosomal protein L36-A

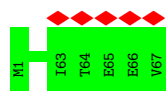


• Molecule 5: 60S ribosomal protein L9-A





- Molecule 6: 60S ribosomal protein L24-A



- Molecule 7: 60S ribosomal protein L37-A



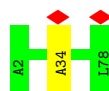
- Molecule 8: 60S ribosomal protein L11-B



- Molecule 9: 60S ribosomal protein L25



- Molecule 10: 60S ribosomal protein L38

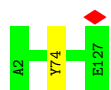


- Molecule 11: 60S ribosomal protein L13-A



- Molecule 12: 60S ribosomal protein L26-A

Chain AK:  99%



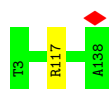
- Molecule 13: 60S ribosomal protein L39

Chain AL:  96%



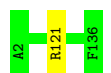
- Molecule 14: 60S ribosomal protein L14-A

Chain AM:  99%



- Molecule 15: 60S ribosomal protein L27-A

Chain AN:  99%



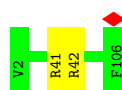
- Molecule 16: Ubiquitin-60S ribosomal protein L40

Chain AO:  100%



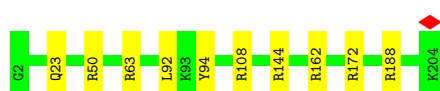
- Molecule 17: 60S ribosomal protein L42-A

Chain AP:  98%



- Molecule 18: 60S ribosomal protein L15-A

Chain AQ:  95%



- Molecule 19: 60S ribosomal protein L28

Chain AR:  97%



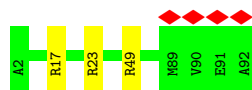
- Molecule 20: 60S ribosomal protein L41-B

Chain AS:  96%



- Molecule 21: 60S ribosomal protein L43-A

Chain AT:  97%



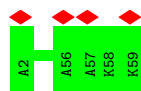
- Molecule 22: 60S ribosomal protein L16-A

Chain AU:  99%



- Molecule 23: 60S ribosomal protein L29

Chain AV:  7% 100%



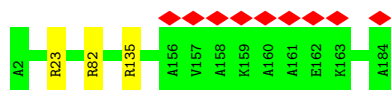
- Molecule 24: 60S ribosomal protein L2-A

Chain AW:  96%

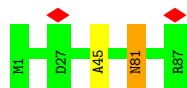


- Molecule 25: 60S ribosomal protein L17-A

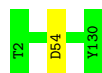
Chain AX:  5% 98%



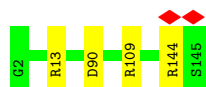
- Molecule 26: 40S ribosomal protein S21-A



- Molecule 27: 40S ribosomal protein S22-A



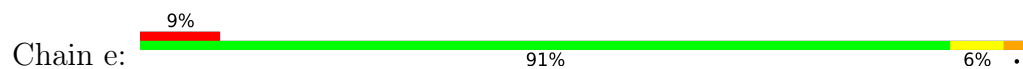
- Molecule 28: 40S ribosomal protein S23-A



- Molecule 29: 40S ribosomal protein S24-A



- Molecule 30: 40S ribosomal protein S26-B



- Molecule 31: 40S ribosomal protein S27-A

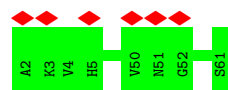


There are no outlier residues recorded for this chain.

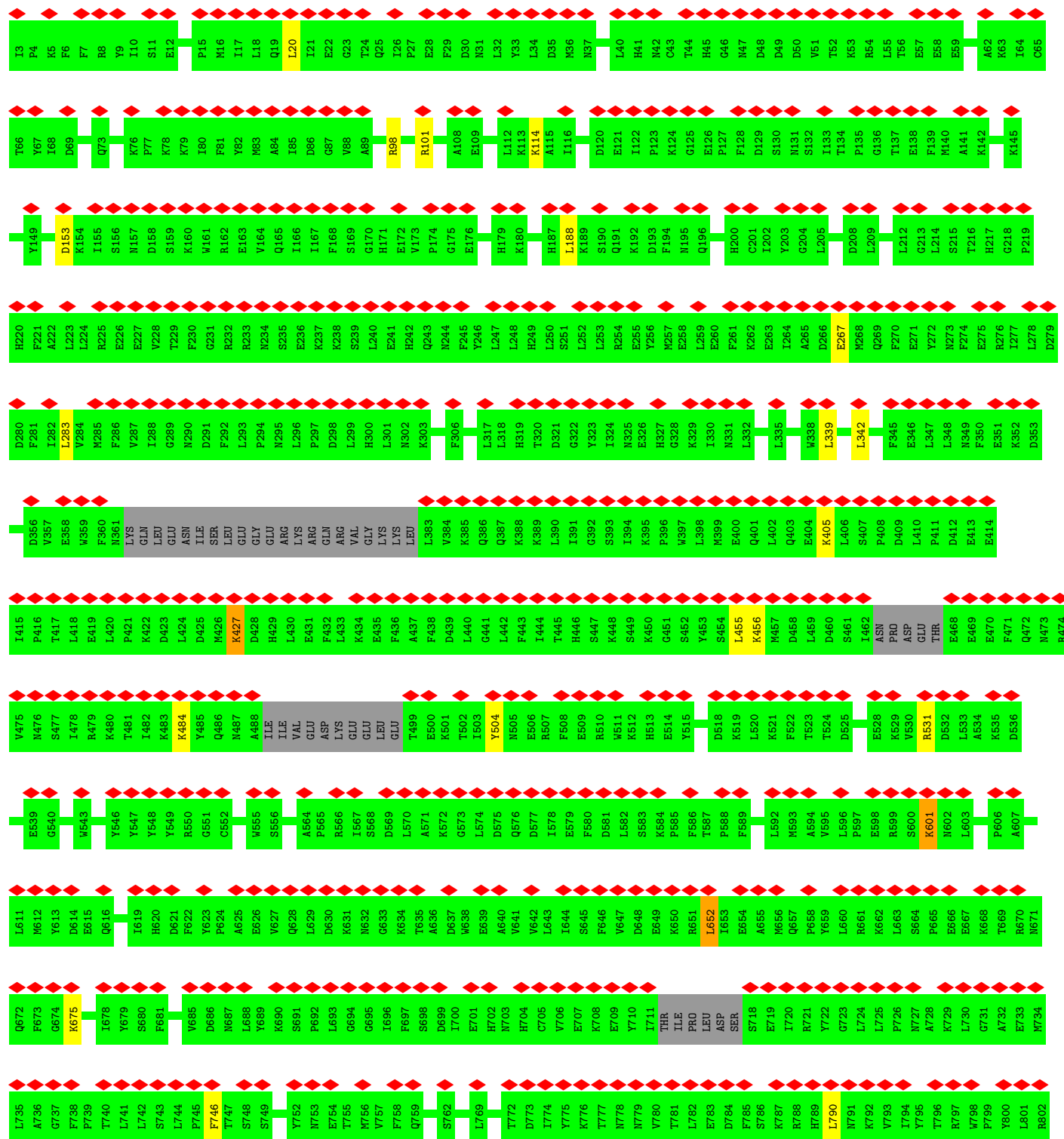
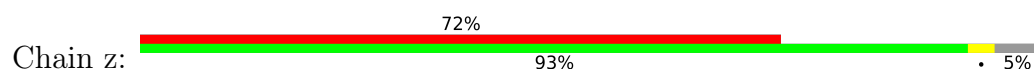
- Molecule 32: 40S ribosomal protein S30-A





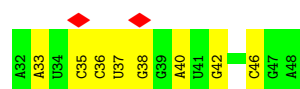


• Molecule 33: 5'-3' exoribonuclease 1

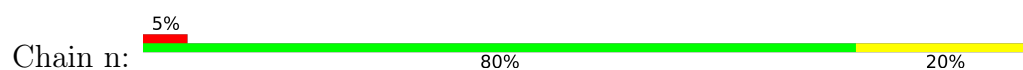




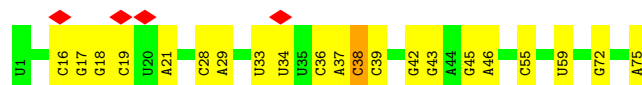
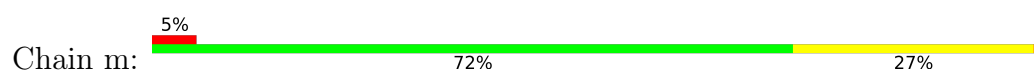
- Molecule 34: mRNA



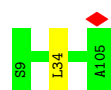
- Molecule 35: P-site tRNA



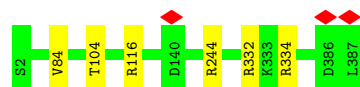
- Molecule 36: E-site tRNA



- Molecule 37: 60S ribosomal protein L30



- Molecule 38: 60S ribosomal protein L3



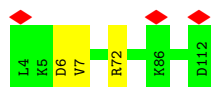
- Molecule 39: 60S ribosomal protein L18-A





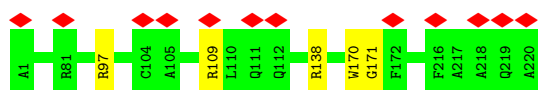
- Molecule 40: 60S ribosomal protein L31-A

Chain BC: 97%



- Molecule 41: 60S ribosomal protein L10

Chain BD: 98%



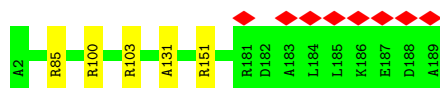
- Molecule 42: 60S ribosomal protein L4-A

Chain BE: 98%



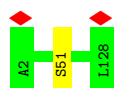
- Molecule 43: 60S ribosomal protein L19-A

Chain BF: 97%



- Molecule 44: 60S ribosomal protein L32

Chain BG: 99%



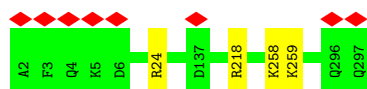
- Molecule 45: 60S ribosomal protein L20-A

Chain BH: 100%



- Molecule 46: 60S ribosomal protein L5

Chain BI:  99%



- Molecule 47: 60S ribosomal protein L21-A

Chain BJ:  97%



- Molecule 48: 60S ribosomal protein L33-A

Chain BK:  100%

There are no outlier residues recorded for this chain.

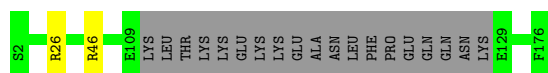
- Molecule 49: 60S ribosomal protein L22-A

Chain BL:  100%



- Molecule 50: 60S ribosomal protein L6-A

Chain BM:  88% 11%



- Molecule 51: 60S ribosomal protein L34-A

Chain BN:  98%



- Molecule 52: 60S ribosomal protein L7-A

Chain BO:  98%




- Molecule 53: 60S ribosomal protein L35-A

Chain BP:  93% 6%



A3279	U3151	G2950	C2825	A2656	U2497	C2420	G2272	G2111	C1869	A1729	G1565
U3287	U3152	A2968	G2828	U2665	U2498	U2434	U2273	U2112	G	G1730	A1566
G3289	C2988	C2969	G2828	C2666	A2500	G2435	U2274	A2113	G	A1741	U1567
U3283	U3155	G2961	C2836	A2674	U2501	U2436	A2281	C2114	C	A1750	U1568
A3295	U3156	G2964	U2842	G2677	A2502	A2458	U2282	G2121	G	G1761	U1569
A3294	U3157	A2969	A2845	A2678	U2513	A2459	G2283	G2122	G	C1762	U1570
U3304	U3170	A2970	U2846	A2679	U2514	C2444	C2284	A2131	G	A1760	U1571
A3305	A3171	A2971	A2847	U2680	A2515	A2445	C2285	C2132	U	C1763	U1572
U3306	A3172	G2972	A2847	U2681	G2522	U2446	G2307	A2138	U	G1576	G1573
U3313	G3173	G2977	C2857	A2689	A2523	G2450	U2310	A2139	U	G1577	
A3316	U3174	U2978	U2860	A2690	A2524	G2451	A2313	A2142	U	C1578	
U3317	U3175	U2979	C2867	A2691	G2530	G	U2314	G2145	G	U1764	
G3318	G3176	C2983	A2870	A2694	C2531	U	G2315	C2146	G	U1765	
U3319	U3179	A3180	G2871	A2703	U2538	G	A2321	A2147	C	G1766	
A3344	G3181	G2990	U2872	A2704	A2539	A	C2322	U2148	U	G1770	
G3345	A3186	U2996	U2873	G2714	U2541	A	U2334	A2149	U	G1780	
U3346	A3187	G2997	C2876	A2715	U2542	U	U2335	G2157	G	G1790	
A3347	A3188	A3012	A2880	U2716	G2549	A	G2336	U2158	U	G1796	
G3348	G3206	A3012	C2881	C2726	U2552	G	U2340	G2165	G	A1797	
C3349	U3207	G3022	C2881	C2727	C2553	U	C2354	G2169	G	G1808	
U3351	G3208	U3023	A2887	U2728	A2554	G	G2355	G2170	U	A1809	
U3352	A3209	U3047	U2888	U2729	C2560	G	C2362	A2178	U	G1813	
G3353	A3210	A3048	C2889	C2737	A2561	A	C2366	C2179	G	A1814	
U3354	C3217	A3049	C2894	A2740	A2562	G	C2371	A2188	U	U1620	
U3355	A3218	U3056	G2898	C2741	U2570	G	A2373	G2192	G	U1815	
G3356	G3220	U3057	C2894	C2742	U2571	U	C2374	C2193	C	A1816	
A3362	G3224	U3058	A2911	G2753	C2572	U	G2375	G2197	U	G1817	
G3369	G3241	U3078	G2912	U2753	G2585	C	G2376	G2201	G	U1818	
A3372	G3242	U3079	G2913	A2762	C2586	C	A2377	U2205	G	U1820	
A3375	A3243	G3030	U2915	C2772	C2589	C	C2376	G2206	U	U1821	
C3378	A3244	A3086	U2923	C2773	A2593	U	U2388	A2208	C	A1835	
U3382	G3246	C3089	C2928	G2777	A2595	G	C2389	G2207	C	U1836	
G3383	G3247	C3092	U2935	A2800	C2600	U	G2393	A2209	U	U1837	
G3386	U3259	C3117	A2936	A2801	G2606	A	A2397	U2210	C	A1840	
G3390	G3263	G3128	G2937	A2802	G2607	A	A2398	G2210	U	A1842	
U3386	A3268	A3129	C2938	A2804	G2619	U	A2402	C2237	A	C1843	
	U3269	A3130	A2941	A2804	G2620	C	G2403	A2243	C	G1844	
	U3270	U3131	C2942	C2810	C2627	A	A2404	A2244	U	C1845	
	G3271	U3131	G2945	A2813	A2635	U	C2407	G2249	C	C1846	
	C3272	G3140	A2946	G2816	C2644	C	U2411	A2256	U	C1849	
	U3276	A3141	G2947	A2817	C2644	U	U2411	A2257	C	A1850	
	G3277	C3142	U2948		U2852	A	A2419		C	A1858	
	C3278	C3143	U2949			C2495			C	C1866	
						C2496			C	G1868	

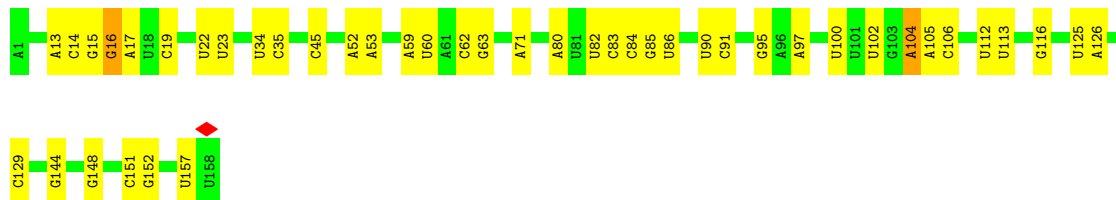
- Molecule 55: 5S ribosomal RNA

Chain BR:  80% 19%



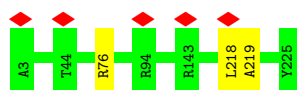
- Molecule 56: 5.8S ribosomal RNA

Chain BS:  72% 27%



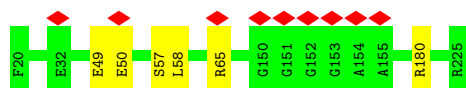
- Molecule 57: 40S ribosomal protein S3

Chain A:  99%



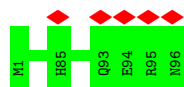
- Molecule 58: Rps5p

Chain B:  97%



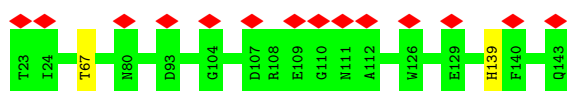
- Molecule 59: 40S ribosomal protein S10-A

Chain C:  5% 100%

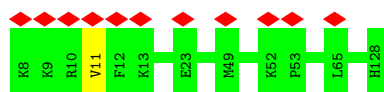


- Molecule 60: 40S ribosomal protein S12

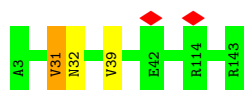
Chain D:  12% 98%



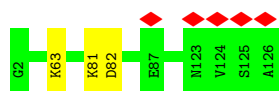
- Molecule 61: 40S ribosomal protein S15



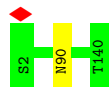
- Molecule 62: 40S ribosomal protein S16-A



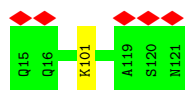
- Molecule 63: 40S ribosomal protein S17-A



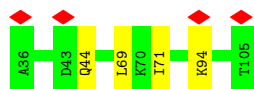
- Molecule 64: 40S ribosomal protein S18-A



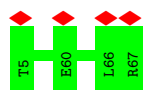
- Molecule 65: 40S ribosomal protein S20



- Molecule 66: 40S ribosomal protein S25-A

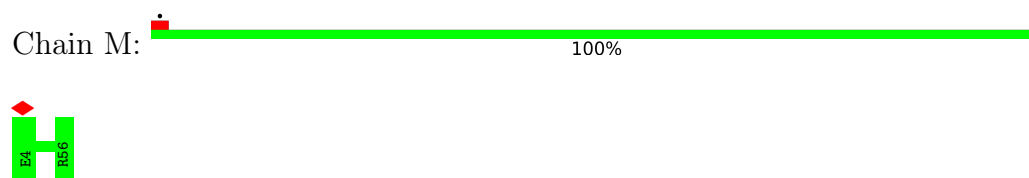


- Molecule 67: 40S ribosomal protein S28-A

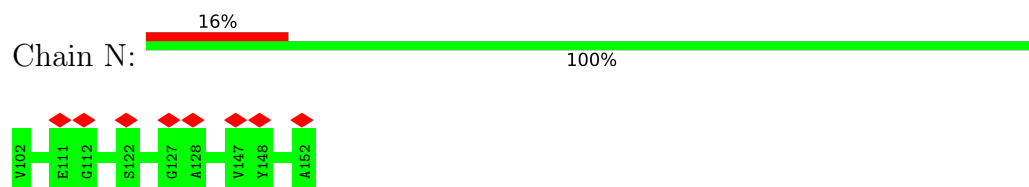




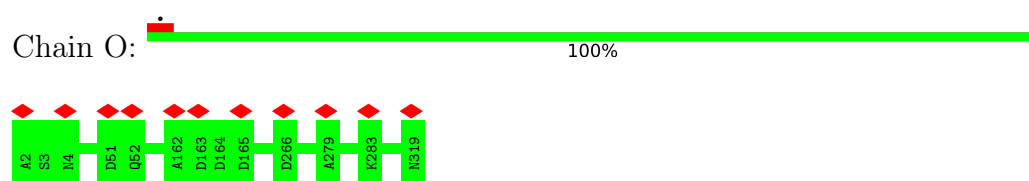
- Molecule 68: 40S ribosomal protein S29-A



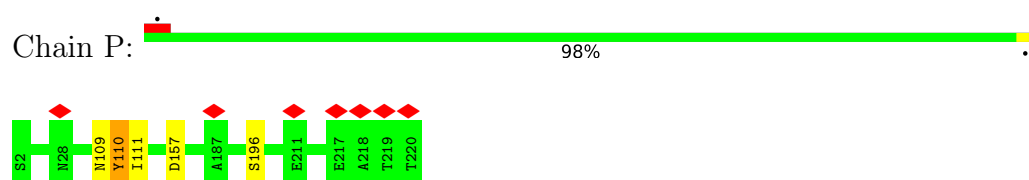
- Molecule 69: Ubiquitin-40S ribosomal protein S31



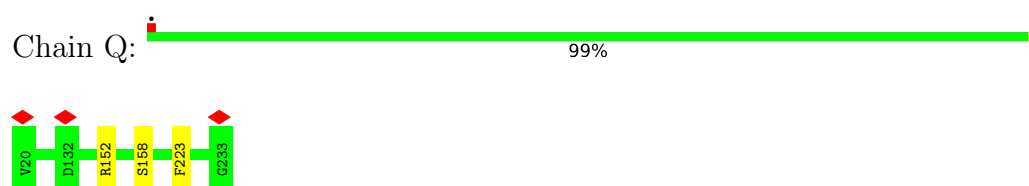
- Molecule 70: Guanine nucleotide-binding protein subunit beta-like protein



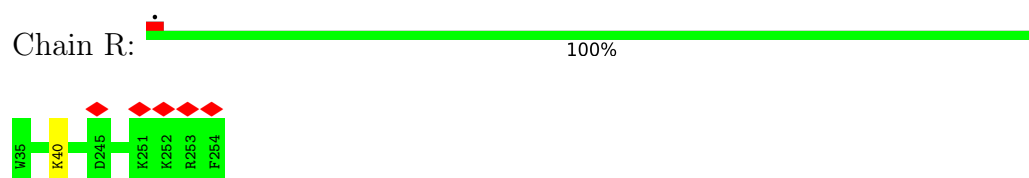
- Molecule 71: 40S ribosomal protein S0-A



- Molecule 72: 40S ribosomal protein S1-A

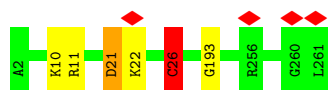


- Molecule 73: 40S ribosomal protein S2

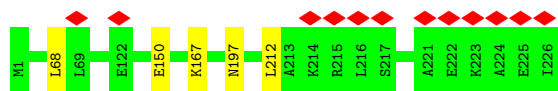


- Molecule 74: 40S ribosomal protein S4-A

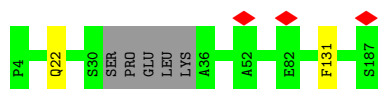




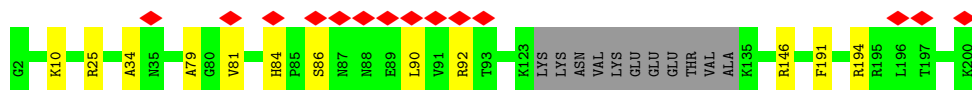
- Molecule 75: 40S ribosomal protein S6-A



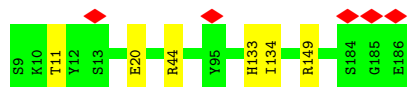
- Molecule 76: 40S ribosomal protein S7-A



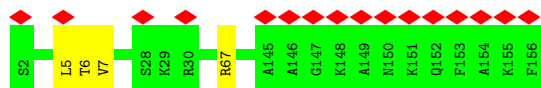
- Molecule 77: 40S ribosomal protein S8-A



- Molecule 78: 40S ribosomal protein S9-A



- Molecule 79: 40S ribosomal protein S11-A



- Molecule 80: 40S ribosomal protein S13



- Molecule 81: 40S ribosomal protein S14-B

Chain Z:  100%

There are no outlier residues recorded for this chain.

- Molecule 82: 40S ribosomal protein S19-A

Chain I:  99% .



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	217000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.470	Depositor
Minimum map value	-0.232	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.019	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	433.6, 433.6, 433.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	1.09	8/42103 (0.0%)	1.12	119/65603 (0.2%)
2	AA	0.65	1/1836 (0.1%)	0.66	0/2481
3	AB	0.70	0/1018	0.75	2/1369 (0.1%)
4	AC	0.56	0/778	0.70	0/1034
5	AD	0.59	0/1539	0.68	0/2073
6	AE	0.72	0/555	0.67	0/738
7	AF	0.88	0/696	0.92	2/923 (0.2%)
8	AG	0.48	0/1374	0.66	0/1842
9	AH	0.72	0/979	0.70	0/1321
10	AI	0.57	0/618	0.64	0/826
11	AJ	0.73	0/1568	0.82	4/2106 (0.2%)
12	AK	0.68	0/1004	0.72	0/1341
13	AL	0.79	0/443	0.90	2/588 (0.3%)
14	AM	0.60	0/1068	0.73	1/1438 (0.1%)
15	AN	0.69	0/1118	0.63	0/1497
16	AO	0.58	0/423	0.73	0/562
17	AP	0.70	0/860	0.74	2/1136 (0.2%)
18	AQ	0.94	0/1757	0.92	9/2354 (0.4%)
19	AR	0.79	0/1204	0.79	3/1612 (0.2%)
20	AS	0.73	0/234	1.04	1/300 (0.3%)
21	AT	0.80	0/701	0.82	1/934 (0.1%)
22	AU	0.75	0/1585	0.70	2/2128 (0.1%)
23	AV	0.57	0/473	0.66	0/629
24	AW	0.84	1/1948 (0.1%)	0.87	11/2617 (0.4%)
25	AX	0.74	0/1443	0.79	4/1944 (0.2%)
26	a	0.60	0/693	0.69	0/935
27	b	0.71	0/1038	0.67	0/1395
28	c	0.66	0/1139	0.78	2/1518 (0.1%)
29	d	0.48	0/1074	0.71	0/1431
30	e	0.68	0/782	0.98	3/1047 (0.3%)
31	f	0.55	0/620	0.67	0/838
32	g	0.44	0/481	0.65	0/640

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	z	0.37	0/7362	0.69	6/9944 (0.1%)
34	l	0.69	0/411	0.95	0/639
35	n	0.76	0/1811	1.03	4/2821 (0.1%)
36	m	0.54	0/1773	0.99	2/2759 (0.1%)
37	AY	0.67	0/750	0.67	1/1008 (0.1%)
38	BA	0.77	1/3146 (0.0%)	0.75	3/4228 (0.1%)
39	BB	0.70	0/1465	0.80	3/1965 (0.2%)
40	BC	0.70	0/890	0.76	1/1196 (0.1%)
41	BD	0.62	0/1807	0.71	1/2425 (0.0%)
42	BE	0.74	1/2800 (0.0%)	0.73	2/3790 (0.1%)
43	BF	0.70	0/1538	0.79	4/2050 (0.2%)
44	BG	0.74	1/1041 (0.1%)	0.73	0/1394
45	BH	0.72	0/1481	0.70	0/1990
46	BI	0.56	0/2425	0.63	1/3271 (0.0%)
47	BJ	0.71	0/1300	0.73	2/1743 (0.1%)
48	BK	0.85	0/868	0.74	0/1168
49	BL	0.56	0/812	0.56	0/1099
50	BM	0.56	0/1260	0.65	1/1694 (0.1%)
51	BN	0.82	0/890	0.79	2/1189 (0.2%)
52	BO	0.74	0/1821	0.68	2/2451 (0.1%)
53	BP	0.65	0/978	0.78	5/1301 (0.4%)
54	BQ	1.43	82/75679 (0.1%)	1.24	287/117989 (0.2%)
55	BR	1.08	0/2883	1.03	2/4491 (0.0%)
56	BS	1.47	4/3745 (0.1%)	1.21	6/5829 (0.1%)
57	A	0.46	0/1759	0.60	1/2368 (0.0%)
58	B	0.43	0/1623	0.65	1/2195 (0.0%)
59	C	0.40	0/833	0.56	0/1126
60	D	0.35	0/885	0.65	0/1202
61	E	0.39	0/978	0.66	0/1315
62	F	0.52	0/1119	0.64	0/1503
63	G	0.45	0/1011	0.68	0/1355
64	H	0.39	0/1162	0.68	0/1564
65	J	0.44	0/865	0.61	0/1169
66	K	0.38	0/571	0.74	1/768 (0.1%)
67	L	0.46	0/499	0.72	0/670
68	M	0.54	0/452	0.64	0/600
69	N	0.32	0/404	0.64	0/542
70	O	0.35	0/2489	0.58	0/3389
71	P	0.52	0/1732	0.65	0/2371
72	Q	0.53	0/1735	0.71	0/2335
73	R	0.62	0/1702	0.68	0/2310
74	S	0.57	0/2102	0.68	2/2829 (0.1%)
75	T	0.44	0/1823	0.71	0/2439

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
76	U	0.46	0/1465	0.62	0/1971
77	V	0.63	1/1514 (0.1%)	0.81	3/2021 (0.1%)
78	W	0.53	0/1456	0.74	1/1949 (0.1%)
79	X	0.76	0/1239	0.70	1/1673 (0.1%)
80	Y	0.65	0/1215	0.77	2/1638 (0.1%)
81	Z	0.63	0/901	0.80	0/1217
82	I	0.46	0/1119	0.59	0/1504
All	All	1.07	100/224741 (0.0%)	1.03	515/329657 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	AA	0	3
4	AC	0	2
5	AD	0	1
10	AI	0	1
11	AJ	0	1
18	AQ	0	1
19	AR	0	1
21	AT	0	1
26	a	0	1
27	b	0	1
29	d	0	3
30	e	0	7
33	z	0	5
40	BC	0	1
41	BD	0	3
42	BE	0	1
46	BI	0	1
52	BO	0	1
53	BP	0	2
57	A	0	1
58	B	0	2
61	E	0	1
64	H	0	1
66	K	0	1
71	P	0	2
72	Q	0	2
74	S	0	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
75	T	0	3
76	U	0	1
77	V	0	6
78	W	0	2
79	X	0	1
80	Y	0	1
All	All	0	62

The worst 5 of 100 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
54	BQ	1835	A	N9-C4	-6.43	1.33	1.37
54	BQ	906	A	N9-C4	-6.40	1.34	1.37
54	BQ	42	C	C4-C5	-6.31	1.38	1.43
54	BQ	2145	A	C8-N7	-6.31	1.27	1.31
54	BQ	3344	A	N9-C4	-6.07	1.34	1.37

The worst 5 of 515 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	BQ	3152	U	C2-N1-C1'	10.51	130.31	117.70
54	BQ	406	G	O4'-C1'-N9	9.53	115.82	108.20
54	BQ	1303	A	C1'-C2'-O2'	-9.52	82.04	110.60
54	BQ	895	A	N9-C4-C5	-9.39	102.04	105.80
54	BQ	3344	A	N1-C6-N6	9.33	124.20	118.60

There are no chirality outliers.

5 of 62 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	AA	156	ASP	Peptide
2	AA	74	THR	Peptide
2	AA	76	ALA	Peptide
4	AC	26	ILE	Peptide
4	AC	32	ALA	Peptide

## 5.2 Too-close contacts

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



## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	AA	231/233 (99%)	204 (88%)	25 (11%)	2 (1%)	14	45
3	AB	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
4	AC	97/100 (97%)	90 (93%)	5 (5%)	2 (2%)	5	25
5	AD	189/191 (99%)	175 (93%)	13 (7%)	1 (0%)	25	58
6	AE	65/67 (97%)	61 (94%)	4 (6%)	0	100	100
7	AF	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
8	AG	167/169 (99%)	154 (92%)	12 (7%)	1 (1%)	22	53
9	AH	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
10	AI	75/77 (97%)	69 (92%)	6 (8%)	0	100	100
11	AJ	191/193 (99%)	168 (88%)	19 (10%)	4 (2%)	5	25
12	AK	124/126 (98%)	123 (99%)	1 (1%)	0	100	100
13	AL	48/50 (96%)	45 (94%)	3 (6%)	0	100	100
14	AM	134/136 (98%)	121 (90%)	13 (10%)	0	100	100
15	AN	133/135 (98%)	117 (88%)	16 (12%)	0	100	100
16	AO	50/52 (96%)	47 (94%)	3 (6%)	0	100	100
17	AP	103/105 (98%)	92 (89%)	11 (11%)	0	100	100
18	AQ	201/203 (99%)	184 (92%)	16 (8%)	1 (0%)	25	58
19	AR	146/148 (99%)	125 (86%)	19 (13%)	2 (1%)	9	34
20	AS	23/25 (92%)	23 (100%)	0	0	100	100
21	AT	89/91 (98%)	81 (91%)	8 (9%)	0	100	100
22	AU	195/197 (99%)	188 (96%)	7 (4%)	0	100	100
23	AV	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
24	AW	250/252 (99%)	238 (95%)	12 (5%)	0	100	100
25	AX	181/183 (99%)	174 (96%)	7 (4%)	0	100	100
26	a	85/87 (98%)	70 (82%)	13 (15%)	2 (2%)	5	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	b	127/129 (98%)	123 (97%)	4 (3%)	0	100	100
28	c	142/144 (99%)	125 (88%)	16 (11%)	1 (1%)	19	51
29	d	130/132 (98%)	112 (86%)	16 (12%)	2 (2%)	8	33
30	e	95/97 (98%)	73 (77%)	21 (22%)	1 (1%)	12	39
31	f	79/81 (98%)	69 (87%)	10 (13%)	0	100	100
32	g	58/60 (97%)	49 (84%)	9 (16%)	0	100	100
33	z	864/916 (94%)	783 (91%)	80 (9%)	1 (0%)	48	79
37	AY	95/97 (98%)	94 (99%)	1 (1%)	0	100	100
38	BA	384/386 (100%)	354 (92%)	30 (8%)	0	100	100
39	BB	183/185 (99%)	169 (92%)	14 (8%)	0	100	100
40	BC	107/109 (98%)	97 (91%)	9 (8%)	1 (1%)	14	45
41	BD	218/220 (99%)	198 (91%)	19 (9%)	1 (0%)	25	58
42	BE	359/361 (99%)	322 (90%)	35 (10%)	2 (1%)	22	53
43	BF	186/188 (99%)	173 (93%)	12 (6%)	1 (0%)	25	58
44	BG	125/127 (98%)	122 (98%)	3 (2%)	0	100	100
45	BH	170/172 (99%)	159 (94%)	11 (6%)	0	100	100
46	BI	294/296 (99%)	271 (92%)	22 (8%)	1 (0%)	37	68
47	BJ	157/159 (99%)	140 (89%)	15 (10%)	2 (1%)	10	36
48	BK	104/106 (98%)	97 (93%)	7 (7%)	0	100	100
49	BL	98/100 (98%)	87 (89%)	11 (11%)	0	100	100
50	BM	152/175 (87%)	144 (95%)	8 (5%)	0	100	100
51	BN	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
52	BO	220/222 (99%)	206 (94%)	13 (6%)	1 (0%)	25	58
53	BP	117/119 (98%)	110 (94%)	5 (4%)	2 (2%)	7	30
57	A	221/223 (99%)	205 (93%)	16 (7%)	0	100	100
58	B	204/206 (99%)	167 (82%)	34 (17%)	3 (2%)	8	33
59	C	94/96 (98%)	79 (84%)	15 (16%)	0	100	100
60	D	119/121 (98%)	81 (68%)	37 (31%)	1 (1%)	16	48
61	E	119/121 (98%)	98 (82%)	21 (18%)	0	100	100
62	F	139/141 (99%)	120 (86%)	16 (12%)	3 (2%)	5	24
63	G	123/125 (98%)	103 (84%)	18 (15%)	2 (2%)	8	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
64	H	137/139 (99%)	117 (85%)	20 (15%)	0	100	100
65	J	105/107 (98%)	94 (90%)	11 (10%)	0	100	100
66	K	68/70 (97%)	56 (82%)	11 (16%)	1 (2%)	8	33
67	L	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
68	M	51/53 (96%)	50 (98%)	1 (2%)	0	100	100
69	N	49/51 (96%)	38 (78%)	11 (22%)	0	100	100
70	O	316/318 (99%)	294 (93%)	22 (7%)	0	100	100
71	P	217/219 (99%)	191 (88%)	23 (11%)	3 (1%)	9	34
72	Q	212/214 (99%)	179 (84%)	32 (15%)	1 (0%)	25	58
73	R	218/220 (99%)	196 (90%)	21 (10%)	1 (0%)	25	58
74	S	258/260 (99%)	225 (87%)	31 (12%)	2 (1%)	16	48
75	T	224/226 (99%)	199 (89%)	24 (11%)	1 (0%)	30	63
76	U	175/184 (95%)	160 (91%)	15 (9%)	0	100	100
77	V	184/199 (92%)	158 (86%)	25 (14%)	1 (0%)	25	58
78	W	176/178 (99%)	144 (82%)	30 (17%)	2 (1%)	12	39
79	X	153/155 (99%)	140 (92%)	12 (8%)	1 (1%)	19	51
80	Y	148/150 (99%)	138 (93%)	10 (7%)	0	100	100
81	Z	125/127 (98%)	112 (90%)	13 (10%)	0	100	100
82	I	141/143 (99%)	131 (93%)	9 (6%)	1 (1%)	19	51
All	All	11782/12024 (98%)	10635 (90%)	1093 (9%)	54 (0%)	27	58

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	AA	156	ASP
2	AA	157	VAL
11	AJ	62	THR
42	BE	339	LEU
53	BP	91	ALA

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	AA	187/191 (98%)	186 (100%)	1 (0%)	86	92
3	AB	104/104 (100%)	104 (100%)	0	100	100
4	AC	81/82 (99%)	80 (99%)	1 (1%)	67	83
5	AD	171/171 (100%)	171 (100%)	0	100	100
6	AE	56/59 (95%)	56 (100%)	0	100	100
7	AF	70/70 (100%)	70 (100%)	0	100	100
8	AG	147/147 (100%)	147 (100%)	0	100	100
9	AH	104/105 (99%)	104 (100%)	0	100	100
10	AI	68/68 (100%)	68 (100%)	0	100	100
11	AJ	154/154 (100%)	153 (99%)	1 (1%)	84	91
12	AK	109/109 (100%)	108 (99%)	1 (1%)	75	88
13	AL	45/45 (100%)	45 (100%)	0	100	100
14	AM	107/107 (100%)	107 (100%)	0	100	100
15	AN	115/115 (100%)	114 (99%)	1 (1%)	75	88
16	AO	47/47 (100%)	47 (100%)	0	100	100
17	AP	90/90 (100%)	90 (100%)	0	100	100
18	AQ	175/175 (100%)	174 (99%)	1 (1%)	84	91
19	AR	118/118 (100%)	117 (99%)	1 (1%)	79	89
20	AS	23/23 (100%)	23 (100%)	0	100	100
21	AT	71/71 (100%)	70 (99%)	1 (1%)	62	81
22	AU	160/160 (100%)	160 (100%)	0	100	100
23	AV	46/46 (100%)	46 (100%)	0	100	100
24	AW	193/194 (100%)	192 (100%)	1 (0%)	86	92
25	AX	140/145 (97%)	140 (100%)	0	100	100
26	a	74/74 (100%)	74 (100%)	0	100	100
27	b	110/110 (100%)	110 (100%)	0	100	100
28	c	119/119 (100%)	118 (99%)	1 (1%)	79	89
29	d	111/111 (100%)	111 (100%)	0	100	100
30	e	83/83 (100%)	82 (99%)	1 (1%)	67	83
31	f	70/70 (100%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	g	50/51 (98%)	50 (100%)	0	100	100
33	z	783/842 (93%)	766 (98%)	17 (2%)	47	71
37	AY	81/81 (100%)	81 (100%)	0	100	100
38	BA	320/322 (99%)	317 (99%)	3 (1%)	75	88
39	BB	150/150 (100%)	150 (100%)	0	100	100
40	BC	92/96 (96%)	92 (100%)	0	100	100
41	BD	184/186 (99%)	184 (100%)	0	100	100
42	BE	288/288 (100%)	288 (100%)	0	100	100
43	BF	153/153 (100%)	153 (100%)	0	100	100
44	BG	109/109 (100%)	109 (100%)	0	100	100
45	BH	156/156 (100%)	156 (100%)	0	100	100
46	BI	244/244 (100%)	243 (100%)	1 (0%)	89	94
47	BJ	136/136 (100%)	135 (99%)	1 (1%)	81	90
48	BK	90/90 (100%)	90 (100%)	0	100	100
49	BL	87/87 (100%)	87 (100%)	0	100	100
50	BM	134/152 (88%)	133 (99%)	1 (1%)	81	90
51	BN	95/95 (100%)	94 (99%)	1 (1%)	70	84
52	BO	186/186 (100%)	185 (100%)	1 (0%)	86	92
53	BP	104/104 (100%)	103 (99%)	1 (1%)	73	86
57	A	182/182 (100%)	181 (100%)	1 (0%)	86	92
58	B	172/173 (99%)	172 (100%)	0	100	100
59	C	88/89 (99%)	88 (100%)	0	100	100
60	D	89/98 (91%)	88 (99%)	1 (1%)	70	84
61	E	100/103 (97%)	100 (100%)	0	100	100
62	F	115/117 (98%)	114 (99%)	1 (1%)	75	88
63	G	113/113 (100%)	112 (99%)	1 (1%)	75	88
64	H	124/124 (100%)	124 (100%)	0	100	100
65	J	100/100 (100%)	99 (99%)	1 (1%)	73	86
66	K	61/61 (100%)	60 (98%)	1 (2%)	58	79
67	L	56/56 (100%)	56 (100%)	0	100	100
68	M	47/47 (100%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	N	43/43 (100%)	43 (100%)	0	100	100
70	O	259/261 (99%)	259 (100%)	0	100	100
71	P	177/184 (96%)	176 (99%)	1 (1%)	84	91
72	Q	191/191 (100%)	191 (100%)	0	100	100
73	R	180/180 (100%)	180 (100%)	0	100	100
74	S	219/221 (99%)	215 (98%)	4 (2%)	54	76
75	T	188/193 (97%)	187 (100%)	1 (0%)	86	92
76	U	160/165 (97%)	159 (99%)	1 (1%)	84	91
77	V	150/160 (94%)	149 (99%)	1 (1%)	81	90
78	W	152/152 (100%)	151 (99%)	1 (1%)	81	90
79	X	129/136 (95%)	128 (99%)	1 (1%)	79	89
80	Y	127/127 (100%)	126 (99%)	1 (1%)	79	89
81	Z	81/96 (84%)	81 (100%)	0	100	100
82	I	112/115 (97%)	112 (100%)	0	100	100
All	All	10005/10178 (98%)	9951 (100%)	54 (0%)	85	92

5 of 54 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	BA	104	THR
52	BO	93	ASN
76	U	22	GLN
38	BA	116	ARG
47	BJ	139	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
59	C	9	ASN
76	U	110	GLN
65	J	48	HIS
70	O	268	GLN
77	V	87	ASN

### 5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1763/1797 (98%)	508 (28%)	66 (3%)
34	l	16/17 (94%)	8 (50%)	0
35	n	75/76 (98%)	13 (17%)	0
36	m	74/75 (98%)	21 (28%)	0
54	BQ	3158/3396 (92%)	644 (20%)	92 (2%)
55	BR	120/121 (99%)	22 (18%)	3 (2%)
56	BS	157/158 (99%)	37 (23%)	4 (2%)
All	All	5363/5640 (95%)	1253 (23%)	165 (3%)

5 of 1253 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	4	C
1	2	17	C
1	2	25	C
1	2	26	A

5 of 165 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	BQ	1820	U
54	BQ	2971	A
54	BQ	1913	A
54	BQ	2495	C
54	BQ	3243	A

## 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 10 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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



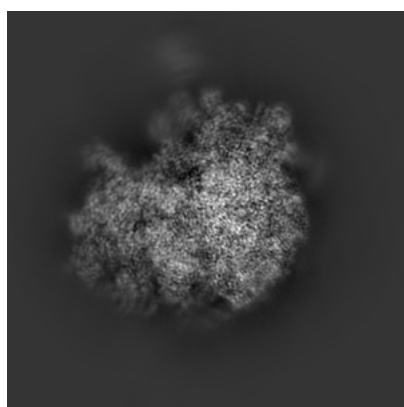
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4474. These allow visual inspection of the internal detail of the map and identification of artifacts.

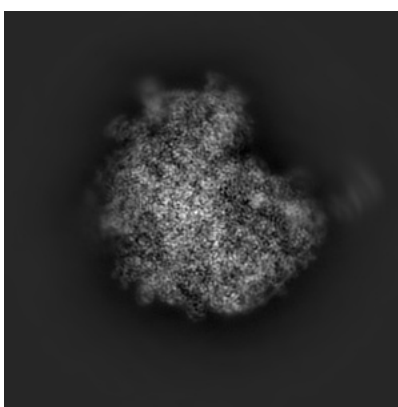
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

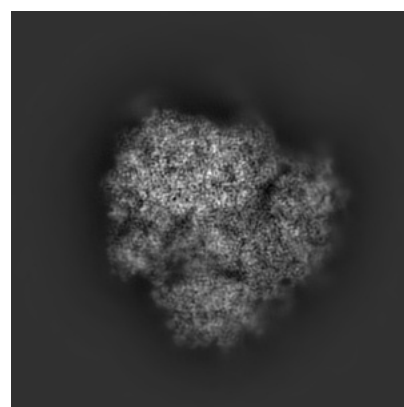
#### 6.1.1 Primary map



X



Y

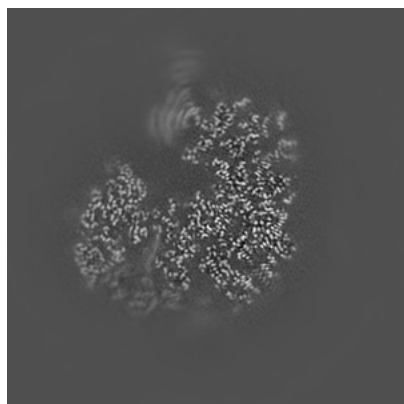


Z

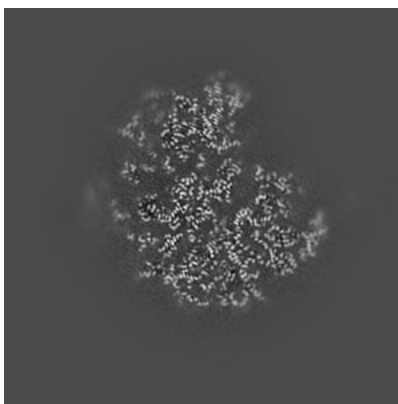
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

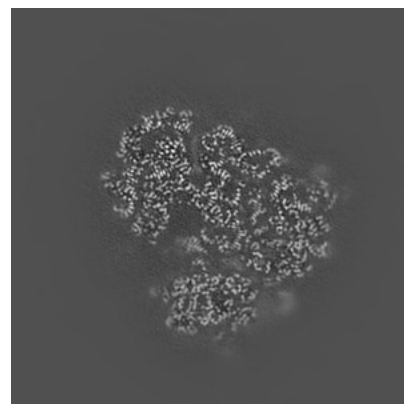
#### 6.2.1 Primary map



X Index: 200



Y Index: 200

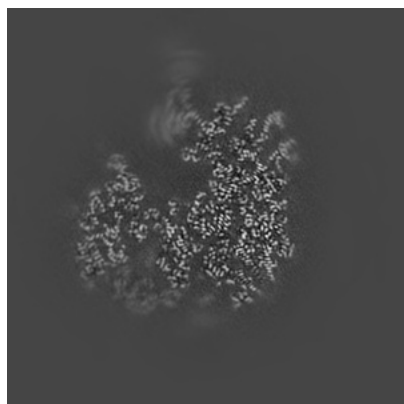


Z Index: 200

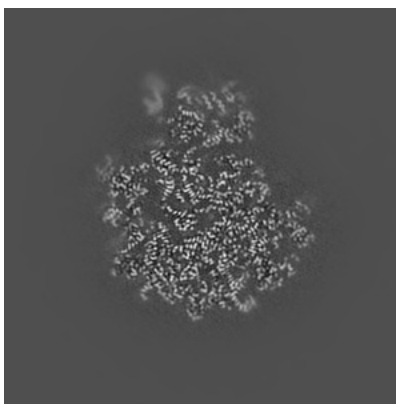
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

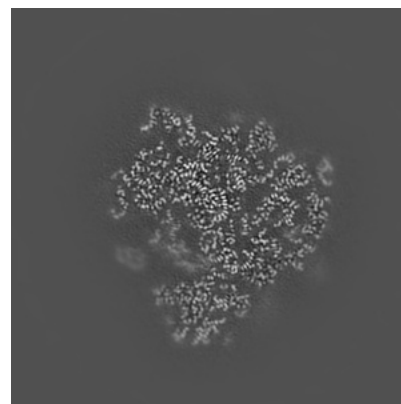
### 6.3.1 Primary map



X Index: 203



Y Index: 226

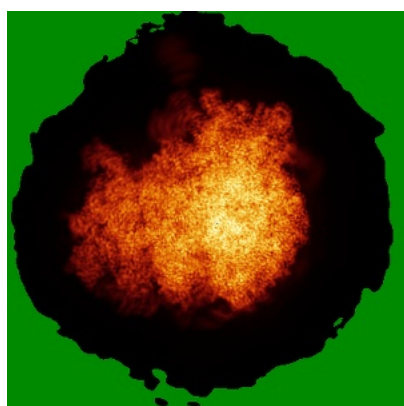


Z Index: 180

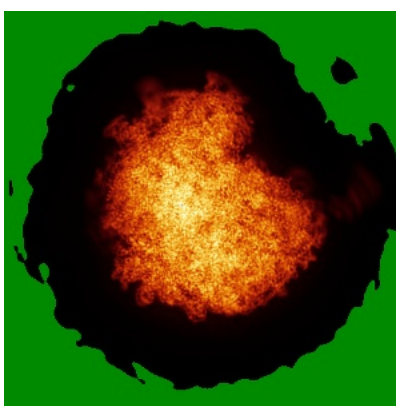
The images above show the largest variance slices of the map in three orthogonal directions.

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

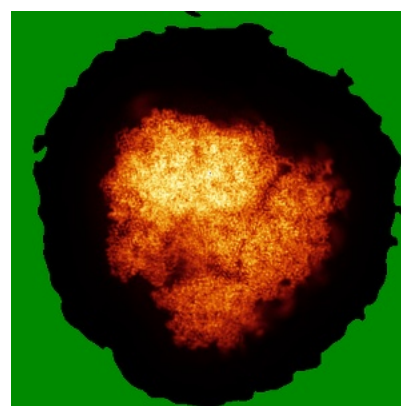
### 6.4.1 Primary map



X



Y



Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

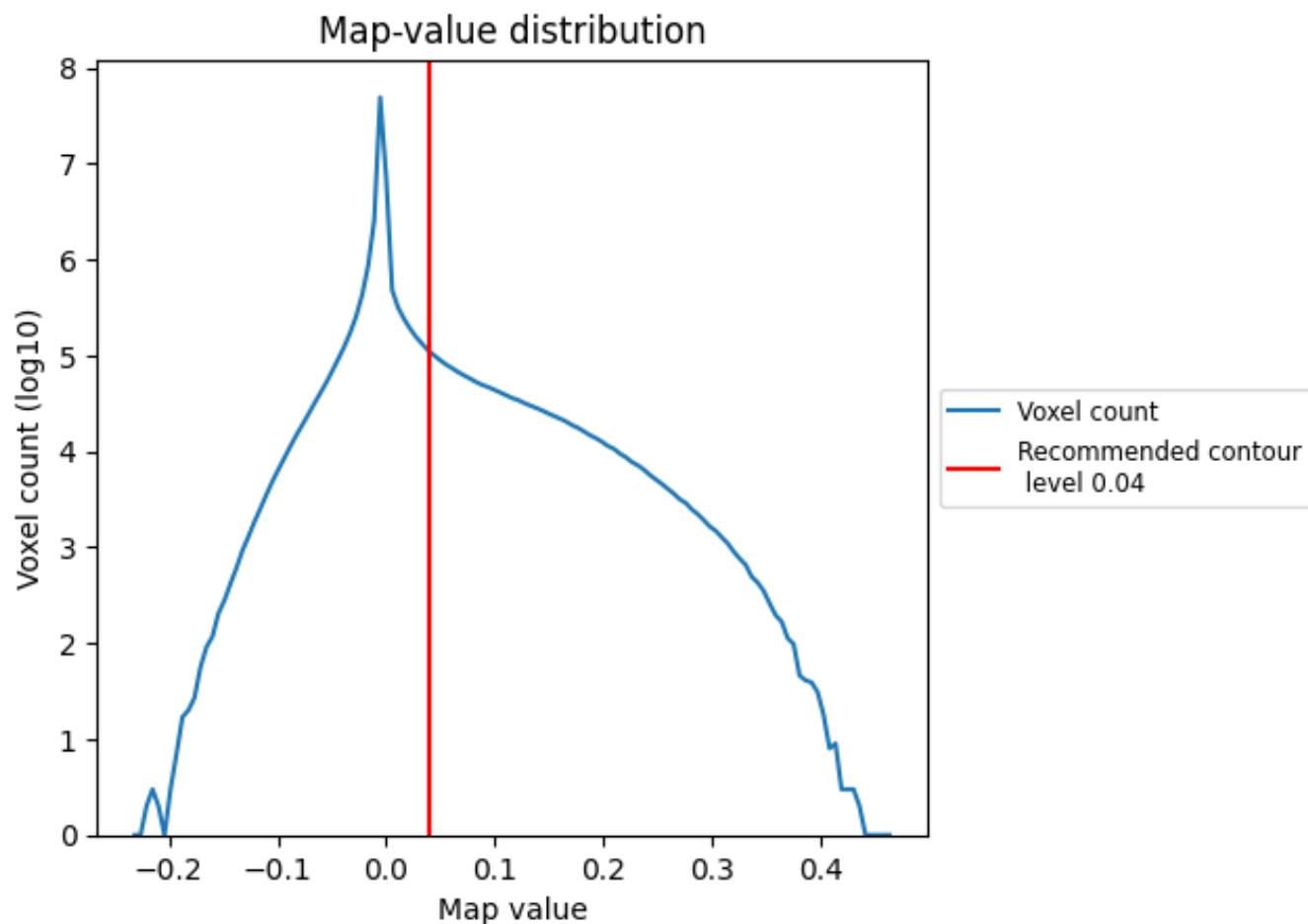
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

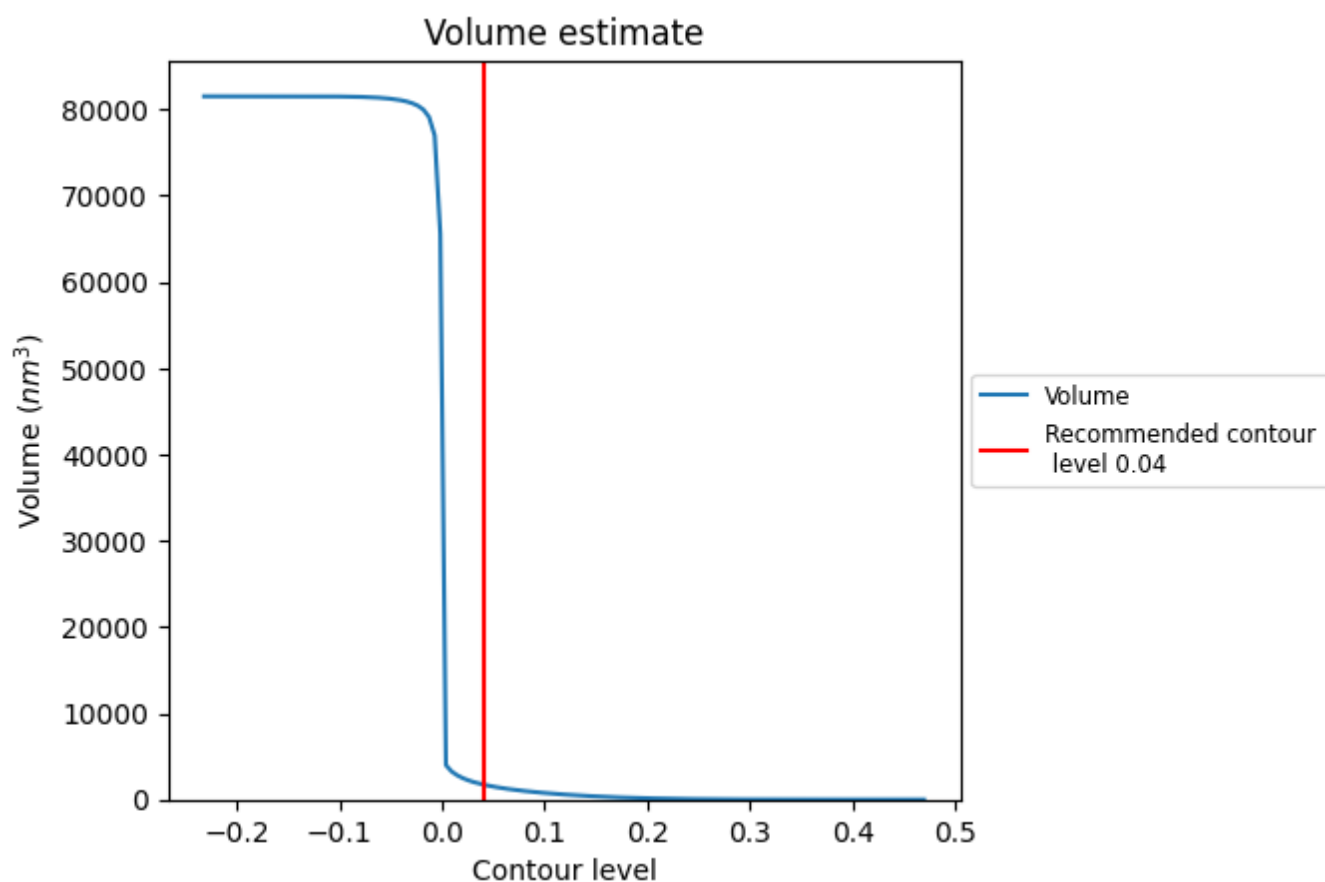
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

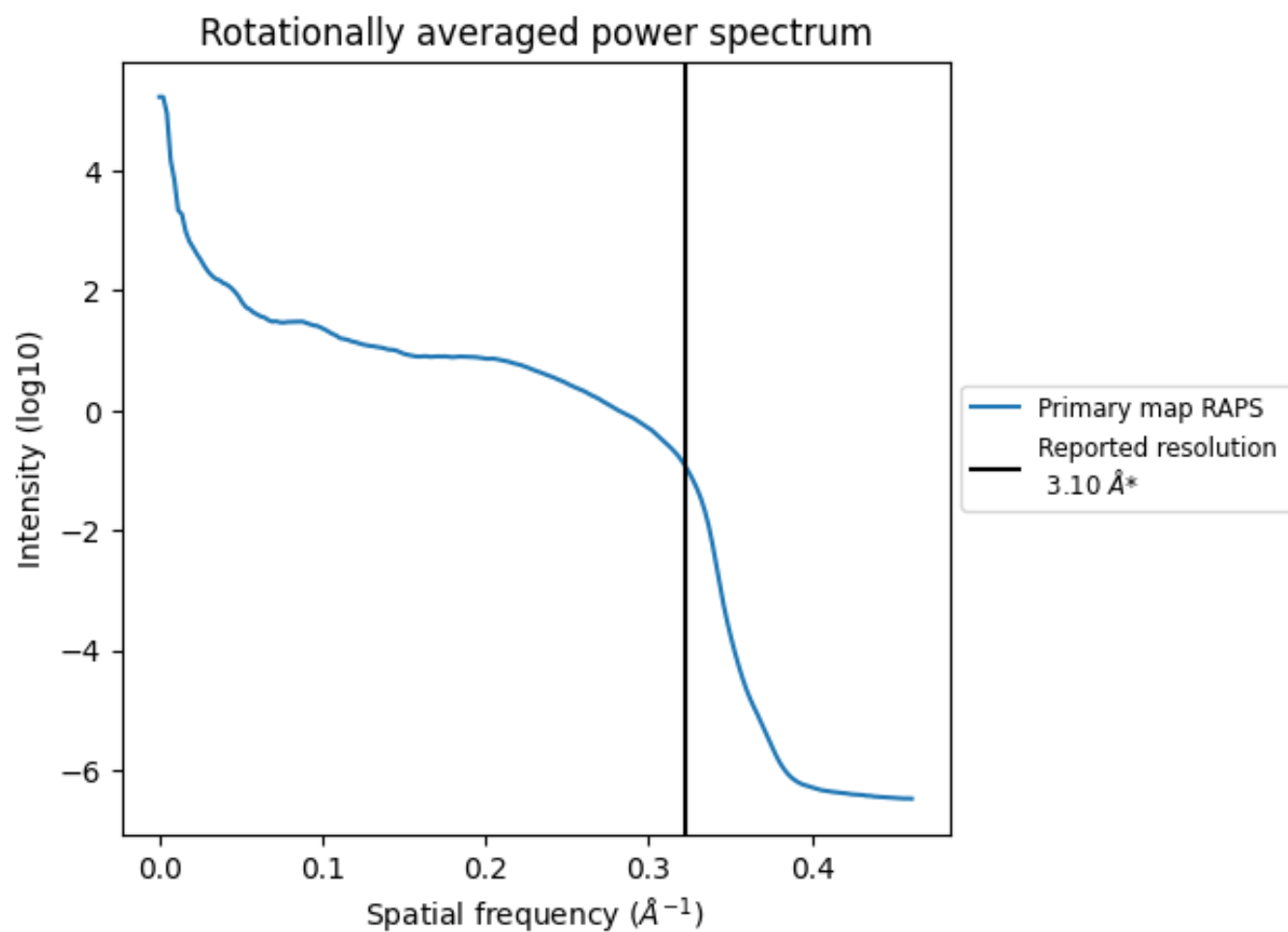
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1744 nm<sup>3</sup>; this corresponds to an approximate mass of 1575 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ

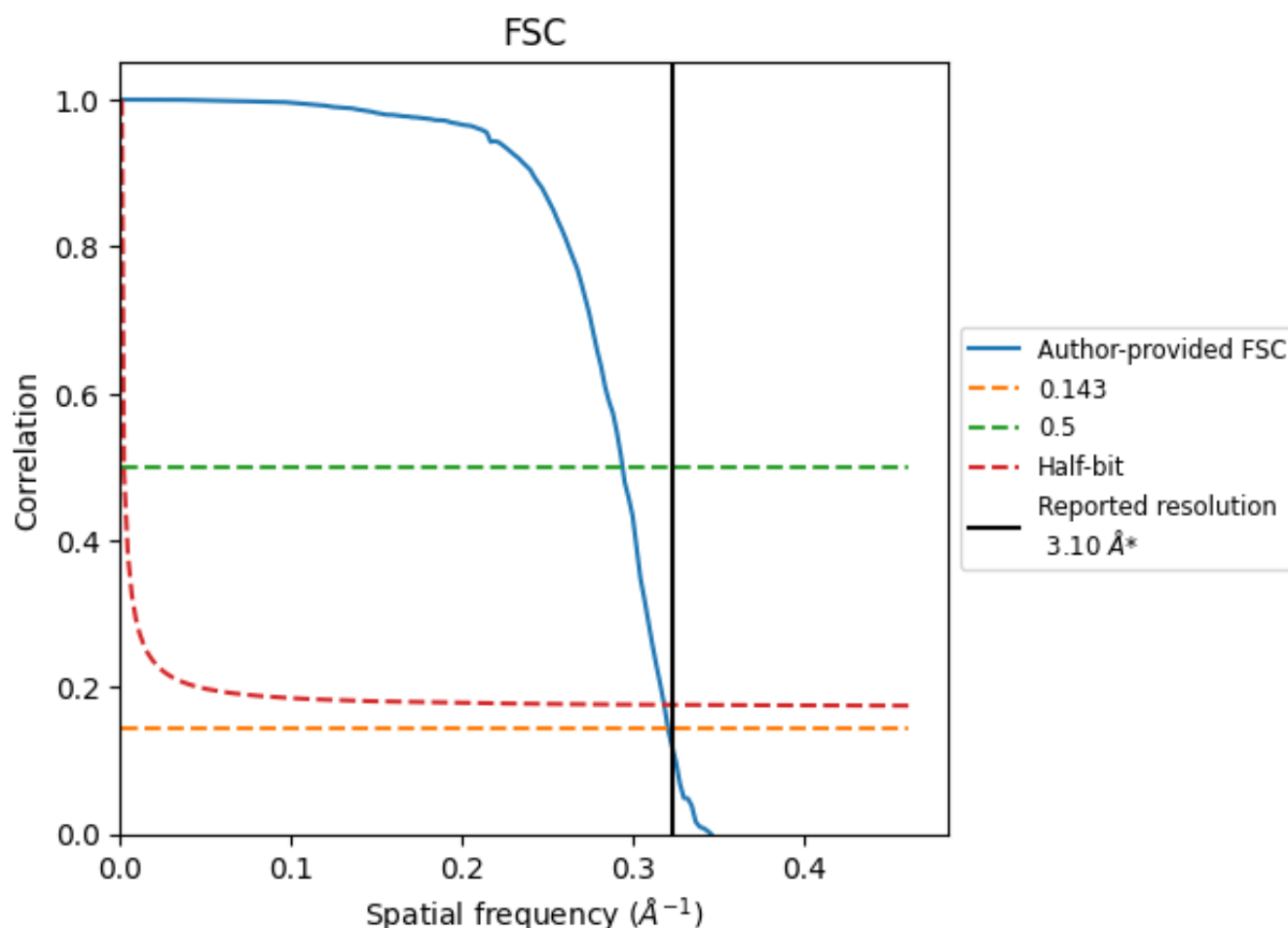


\*Reported resolution corresponds to spatial frequency of 0.323 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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 [i](#)



\*Reported resolution corresponds to spatial frequency of 0.323 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.12	3.40	3.14
Unmasked-calculated*	-	-	-

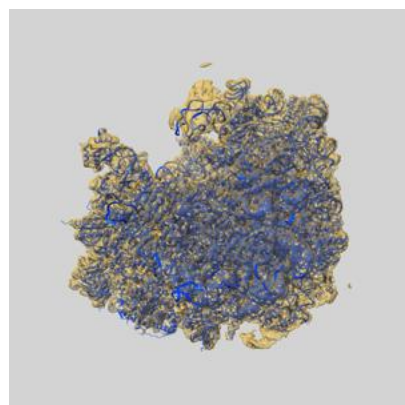
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



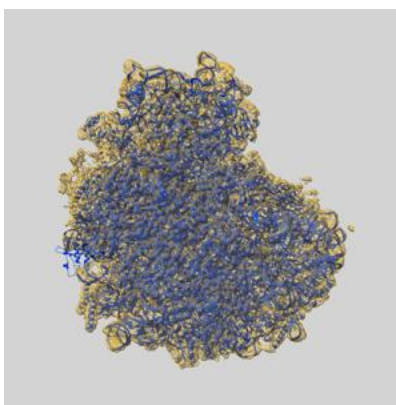
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4474 and PDB model 6Q8Y. Per-residue inclusion information can be found in section 3 on page 19.

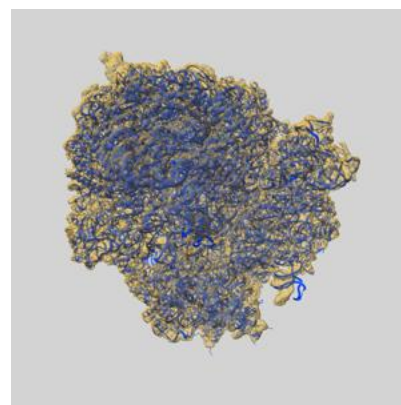
### 9.1 Map-model overlay [i](#)



X



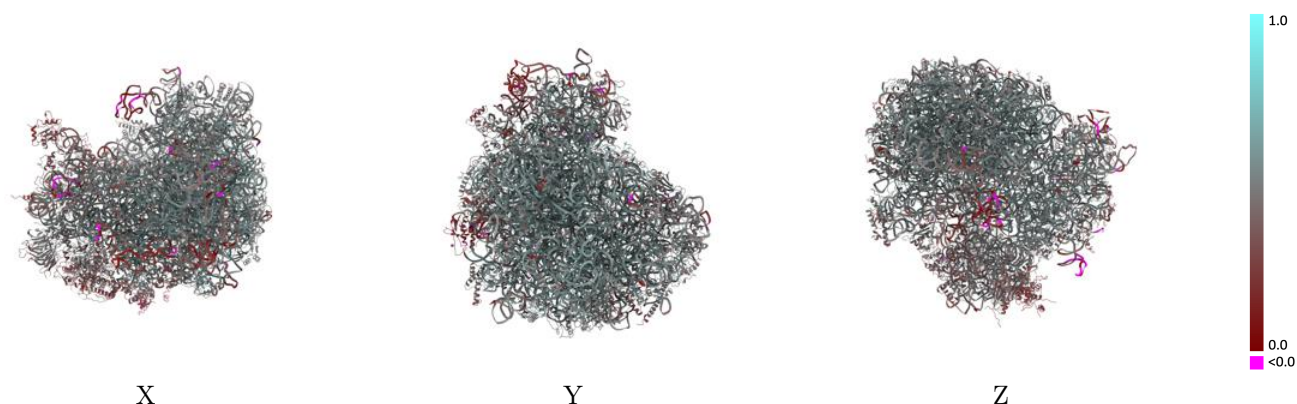
Y



Z

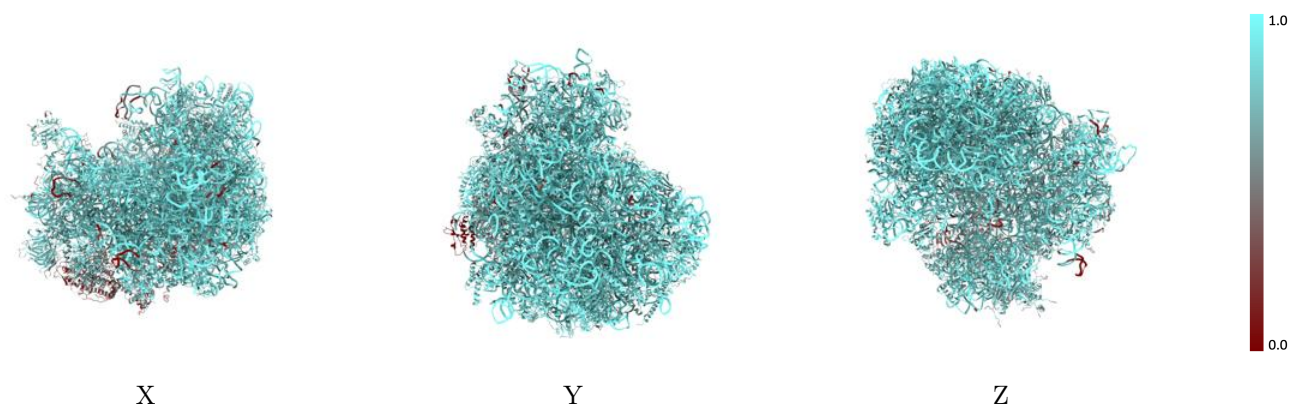
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



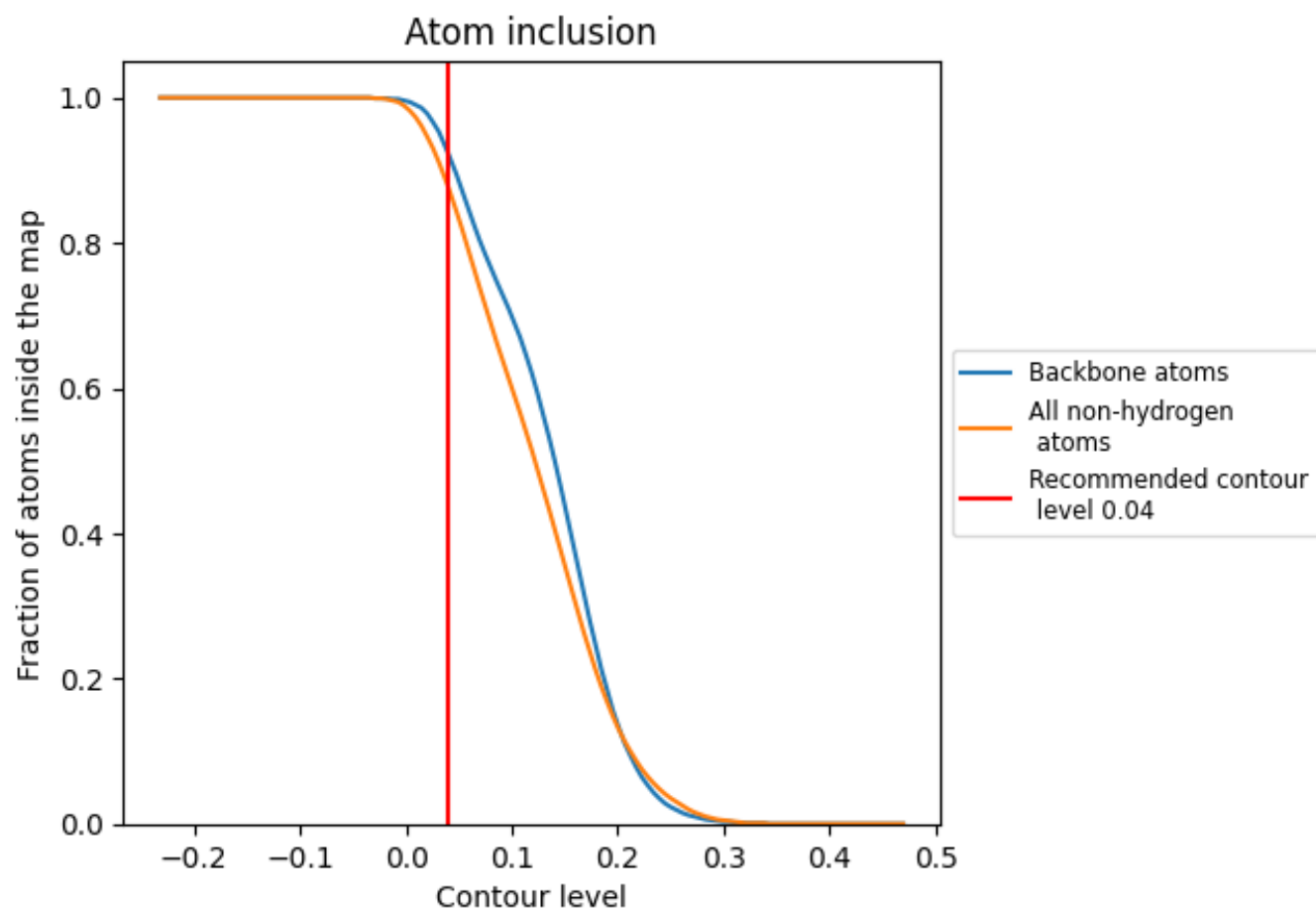
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



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 (0.04).







































































## 9.4 Atom inclusion ⓘ



At the recommended contour level, 92% of all backbone atoms, 88% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8770	 0.4840
2	 0.9310	 0.4700
A	 0.8000	 0.4360
AA	 0.8540	 0.4920
AB	 0.8430	 0.5260
AC	 0.8460	 0.4920
AD	 0.8400	 0.4890
AE	 0.8330	 0.5120
AF	 0.8980	 0.5580
AG	 0.8160	 0.4490
AH	 0.8720	 0.5240
AI	 0.8100	 0.4740
AJ	 0.8720	 0.5100
AK	 0.8760	 0.5100
AL	 0.8720	 0.5360
AM	 0.8700	 0.4830
AN	 0.8760	 0.5090
AO	 0.8490	 0.5030
AP	 0.8340	 0.5250
AQ	 0.8770	 0.5510
AR	 0.8810	 0.5320
AS	 0.7920	 0.5220
AT	 0.8390	 0.5320
AU	 0.8670	 0.5120
AV	 0.8030	 0.4750
AW	 0.8750	 0.5530
AX	 0.8690	 0.5180
AY	 0.8640	 0.5170
B	 0.7710	 0.4210
BA	 0.8840	 0.5280
BB	 0.8820	 0.5210
BC	 0.8530	 0.5110
BD	 0.8040	 0.4710
BE	 0.8830	 0.5210
BF	 0.8230	 0.4880















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Chain	Atom inclusion	Q-score
BG	 0.8650	 0.5330
BH	 0.8520	 0.5090
BI	 0.8420	 0.4480
BJ	 0.8500	 0.5060
BK	 0.8870	 0.5440
BL	 0.8630	 0.4760
BM	 0.8620	 0.4890
BN	 0.8700	 0.5320
BO	 0.8740	 0.5020
BP	 0.8670	 0.5070
BQ	 0.9600	 0.5200
BR	 0.9820	 0.4980
BS	 0.9720	 0.5500
C	 0.7510	 0.3850
D	 0.6740	 0.2640
E	 0.7540	 0.3870
F	 0.8240	 0.4640
G	 0.7890	 0.4330
H	 0.7920	 0.4120
I	 0.8080	 0.4130
J	 0.7360	 0.4070
K	 0.8010	 0.3730
L	 0.7500	 0.4470
M	 0.8770	 0.4910
N	 0.7090	 0.2760
O	 0.7880	 0.4260
P	 0.8280	 0.4600
Q	 0.8230	 0.4760
R	 0.8310	 0.4910
S	 0.8350	 0.4980
T	 0.7900	 0.4180
U	 0.8130	 0.4330
V	 0.7850	 0.4590
W	 0.8120	 0.4480
X	 0.8110	 0.5070
Y	 0.8390	 0.5020
Z	 0.8820	 0.5040
a	 0.8360	 0.4730
b	 0.8700	 0.5270
c	 0.8270	 0.5180
d	 0.7740	 0.4190
e	 0.7590	 0.4340

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Chain	Atom inclusion	Q-score
f	 0.8450	 0.4920
g	 0.7830	 0.4470
l	 0.6680	 0.3580
m	 0.8190	 0.3660
n	 0.9080	 0.4430
z	 0.2310	 0.2590