



wwPDB EM Validation Summary Report ⓘ

Feb 3, 2025 – 11:42 PM EST

PDB ID : 6MTE
EMDB ID : EMD-9242
Title : Rabbit 80S ribosome with eEF2 and SERBP1 (rotated state)
Authors : Brown, A.; Baird, M.R.; Yip, M.C.J.; Murray, J.; Shao, S.
Deposited on : 2018-10-19
Resolution : 3.40 Å(reported)
Based on initial model : 5LZV

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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
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) : 2.40

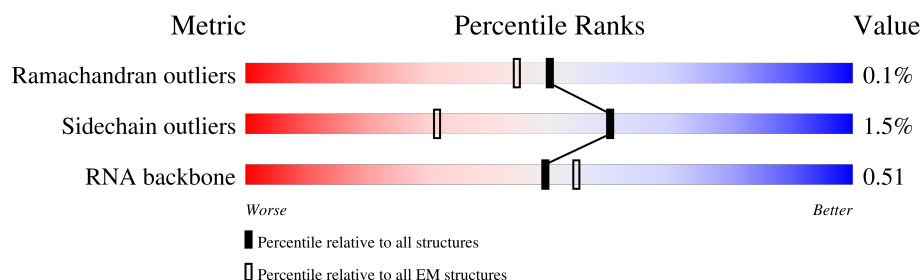
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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.





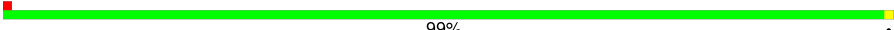
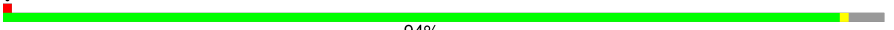






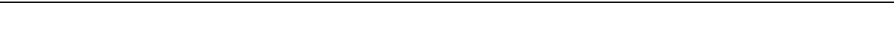

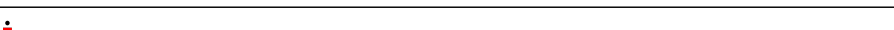
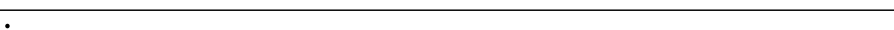
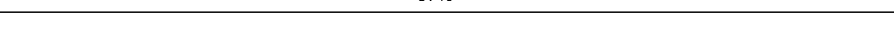
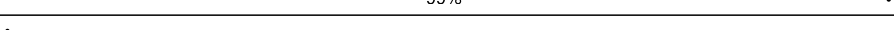
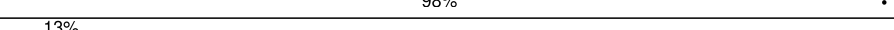

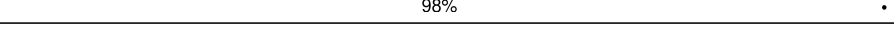
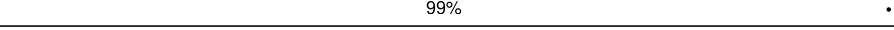
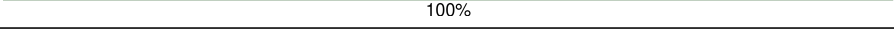
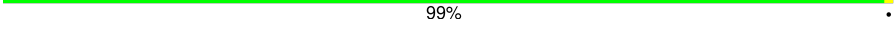

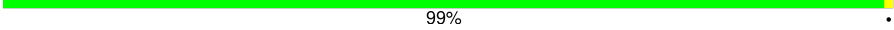
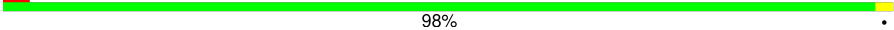
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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 ≥ 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	5	3597	
2	7	120	
3	8	151	
4	A	248	
5	B	394	
6	C	362	
7	D	293	
8	E	291	

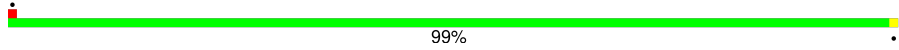
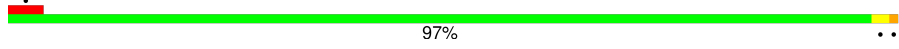
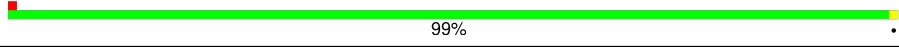
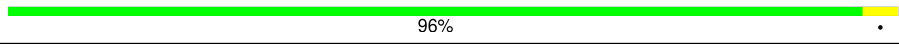
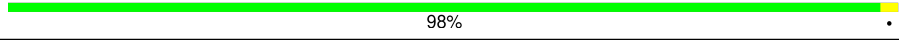
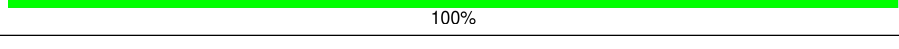
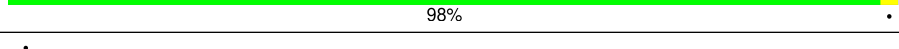
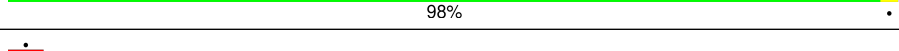
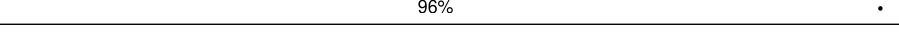
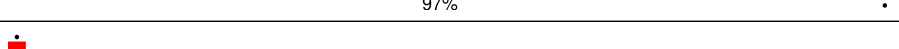
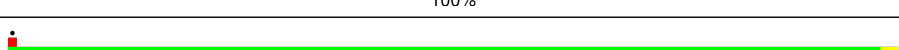
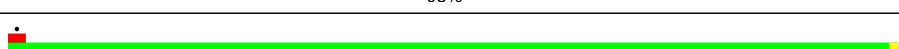
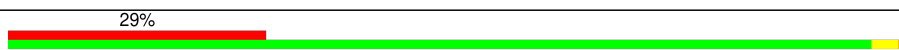
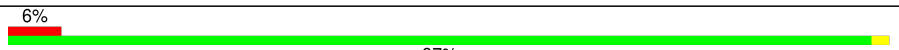
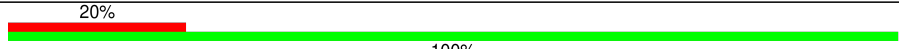

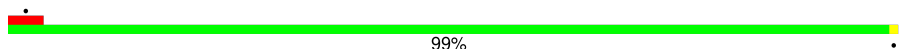
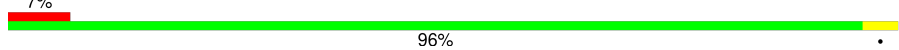
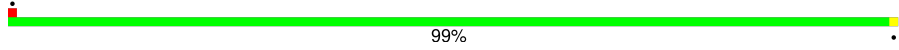
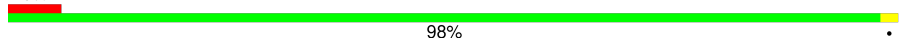
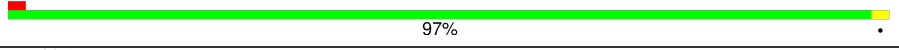
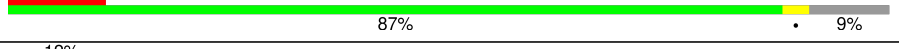
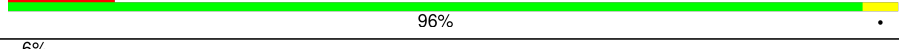
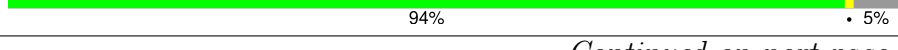

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Mol	Chain	Length	Quality of chain
9	F	225	 99%
10	G	319	 71% 27%
11	H	190	 99%
12	I	214	 94%
13	J	170	 99%
14	L	210	 98%
15	M	138	 99%
16	N	203	 97%
17	O	199	 98%
18	P	153	 98%
19	Q	187	 99%
20	R	180	 99%
21	S	176	 98%
22	T	159	 97%
23	U	99	 99%
24	V	131	 98%
25	W	157	 13% 64% 36%
26	X	118	 98%
27	Y	134	 99%
28	Z	135	 100%
29	a	147	 99%
30	b	245	 42% 58%
31	c	98	 99%
32	d	107	 98%
33	e	128	 98%

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Mol	Chain	Length	Quality of chain
34	f	109	 99%
35	g	114	 97%
36	h	122	 99%
37	i	102	 96%
38	j	86	 98%
39	k	69	 100%
40	l	50	 98%
41	m	52	 98%
42	n	25	 96%
43	o	103	 97%
44	p	91	 100%
45	r	124	 98%
46	s	196	 99%
47	t	153	 29% 97%
48	v	848	 6% 97%
49	w	55	 20% 100%
50	9	1698	 70% 26%
51	AA	217	 99%
52	BB	213	 7% 96%
53	CC	221	 99%
54	DD	228	 6% 98%
55	EE	262	 97%
56	FF	204	 11% 87% 9%
57	GG	237	 12% 96%
58	HH	194	 6% 94% 5%

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Mol	Chain	Length	Quality of chain
59	II	206	
60	JJ	185	
61	KK	96	
62	LL	158	
63	MM	117	
64	NN	149	
65	OO	136	
66	PP	125	
67	QQ	142	
68	RR	132	
69	SS	144	
70	TT	141	
71	UU	100	
72	VV	83	
73	WW	129	
74	XX	141	
75	YY	124	
76	ZZ	75	
77	aa	101	
78	bb	83	
79	cc	62	
80	dd	55	
81	ee	55	
82	ff	68	
83	gg	313	

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 220739 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 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3597	Total	C	N	O	P	0	0
			77254	34469	14127	25061	3597		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	151	Total	C	N	O	P	0	0
			3209	1433	564	1062	150		

- Molecule 4 is a protein called uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 5 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 6 is a protein called uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	362	Total	C	N	O	S	0	0
			2884	1813	577	480	14		

- Molecule 7 is a protein called uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 8 is a protein called eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 9 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 10 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

- Molecule 11 is a protein called uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 12 is a protein called uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 13 is a protein called uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 14 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

- Molecule 15 is a protein called eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 16 is a protein called eL15.

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

- Molecule 17 is a protein called uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 18 is a protein called uL22.

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

- Molecule 19 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

- Molecule 20 is a protein called eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 21 is a protein called eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 22 is a protein called eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 23 is a protein called eL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 24 is a protein called uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 25 is a protein called eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	100	Total	C	N	O	S	0	0
			816	512	164	136	4		

- Molecule 26 is a protein called uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 27 is a protein called uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 28 is a protein called eL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 29 is a protein called uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 30 is a protein called eL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 31 is a protein called eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 32 is a protein called eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 33 is a protein called eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 34 is a protein called eL33.

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

- Molecule 35 is a protein called eL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 37 is a protein called eL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 38 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 39 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 40 is a protein called eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 41 is a protein called eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	m	52	Total	C	N	O	S	0	0
			430	267	90	67	6		

- Molecule 42 is a protein called eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 43 is a protein called eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	o	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 44 is a protein called eL43.

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

- Molecule 45 is a protein called eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 46 is a protein called uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	196	Total	C	N	O	S	0	0
			1507	959	263	276	9		

- Molecule 47 is a protein called uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	t	153	Total	C	N	O	S	0	0
			1160	722	218	217	3		

- Molecule 48 is a protein called eEF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	848	Total	C	N	O	S	0	0
			6628	4211	1138	1235	44		

- Molecule 49 is a protein called SERBP1.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	w	55	Total	C	N	O	0	0
			440	263	87	90		

- Molecule 50 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	9	1698	Total	C	N	O	P	0	0
			36291	16217	6509	11868	1697		

- Molecule 51 is a protein called uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	AA	217	Total	C	N	O	S	0	0
			1710	1086	300	316	8		

- Molecule 52 is a protein called eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BB	213	Total	C	N	O	S	0	0
			1729	1098	309	308	14		

- Molecule 53 is a protein called uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CC	221	Total	C	N	O	S	0	0
			1716	1111	295	301	9		

- Molecule 54 is a protein called uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	DD	228	Total	C	N	O	S	0	0
			1768	1126	318	316	8		

- Molecule 55 is a protein called eS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	EE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 56 is a protein called uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	FF	185	Total	C	N	O	S	0	0
			1471	921	277	266	7		

- Molecule 57 is a protein called eS6.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	GG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 58 is a protein called eS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	HH	185	Total	C	N	O	S	0	0
			1488	952	271	264	1		

- Molecule 59 is a protein called eS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	II	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 60 is a protein called uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	JJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 61 is a protein called eS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	KK	96	Total	C	N	O	S	0	0
			810	530	143	131	6		

- Molecule 62 is a protein called uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	LL	143	Total	C	N	O	S	0	0
			1175	749	222	198	6		

- Molecule 63 is a protein called eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	MM	117	Total	C	N	O	S	0	0
			908	570	161	169	8		

- Molecule 64 is a protein called uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	NN	149	Total	C	N	O	S	0	0
			1202	770	228	203	1		

- Molecule 65 is a protein called uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	OO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 66 is a protein called uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	PP	125	Total	C	N	O	S	0	0
			1025	652	192	174	7		

- Molecule 67 is a protein called uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	QQ	142	Total	C	N	O	S	0	0
			1128	717	213	195	3		

- Molecule 68 is a protein called eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	RR	132	Total	C	N	O	S	0	0
			1068	670	199	195	4		

- Molecule 69 is a protein called uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SS	144	Total	C	N	O	S	0	0
			1190	746	241	202	1		

- Molecule 70 is a protein called eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	TT	141	Total	C	N	O	S	0	0
			1097	688	211	195	3		

- Molecule 71 is a protein called uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	UU	100	Total	C	N	O	S	0	0
			795	498	152	141	4		

- Molecule 72 is a protein called eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	VV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 73 is a protein called uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	WW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 74 is a protein called uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	XX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 75 is a protein called eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	YY	124	Total	C	N	O	S	0	0
			1011	640	198	168	5		

- Molecule 76 is a protein called eS25.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	ZZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 77 is a protein called eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	aa	101	Total	C	N	O	S	0	0
			814	507	170	132	5		

- Molecule 78 is a protein called eS27.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	bb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 79 is a protein called eS28.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	cc	62	Total	C	N	O	S	0	0
			488	297	97	92	2		

- Molecule 80 is a protein called uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	dd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 81 is a protein called eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	ee	55	Total	C	N	O	S	0	0
			443	274	97	71	1		

- Molecule 82 is a protein called eS31.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	ff	68	Total	C	N	O	S	0	0
			555	351	103	94	7		

- Molecule 83 is a protein called RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	gg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

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

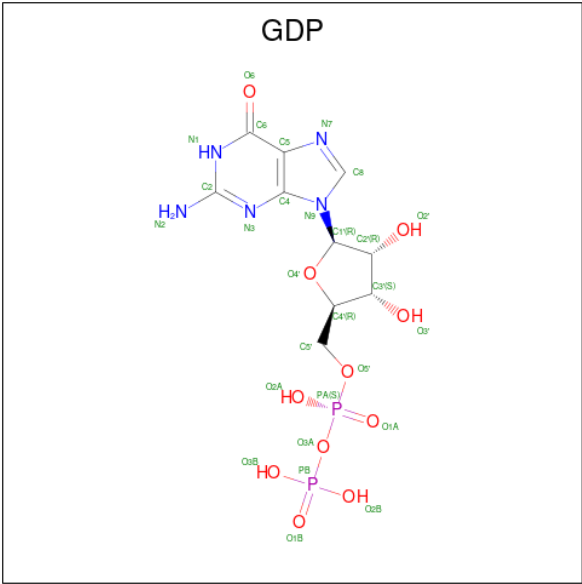
Mol	Chain	Residues	Atoms		AltConf
84	5	200	Total 200	Mg 200	0
84	7	7	Total 7	Mg 7	0
84	8	6	Total 6	Mg 6	0
84	A	1	Total 1	Mg 1	0
84	P	1	Total 1	Mg 1	0
84	V	1	Total 1	Mg 1	0
84	a	1	Total 1	Mg 1	0
84	j	1	Total 1	Mg 1	0
84	v	1	Total 1	Mg 1	0
84	9	78	Total 78	Mg 78	0
84	TT	1	Total 1	Mg 1	0

- Molecule 85 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
85	g	1	Total 1	Zn 1	0
85	j	1	Total 1	Zn 1	0
85	m	1	Total 1	Zn 1	0
85	o	1	Total 1	Zn 1	0
85	p	1	Total 1	Zn 1	0
85	KK	1	Total 1	Zn 1	0
85	aa	1	Total 1	Zn 1	0
85	ff	1	Total 1	Zn 1	0

- Molecule 86 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula:

C₁₀H₁₅N₅O₁₁P₂).

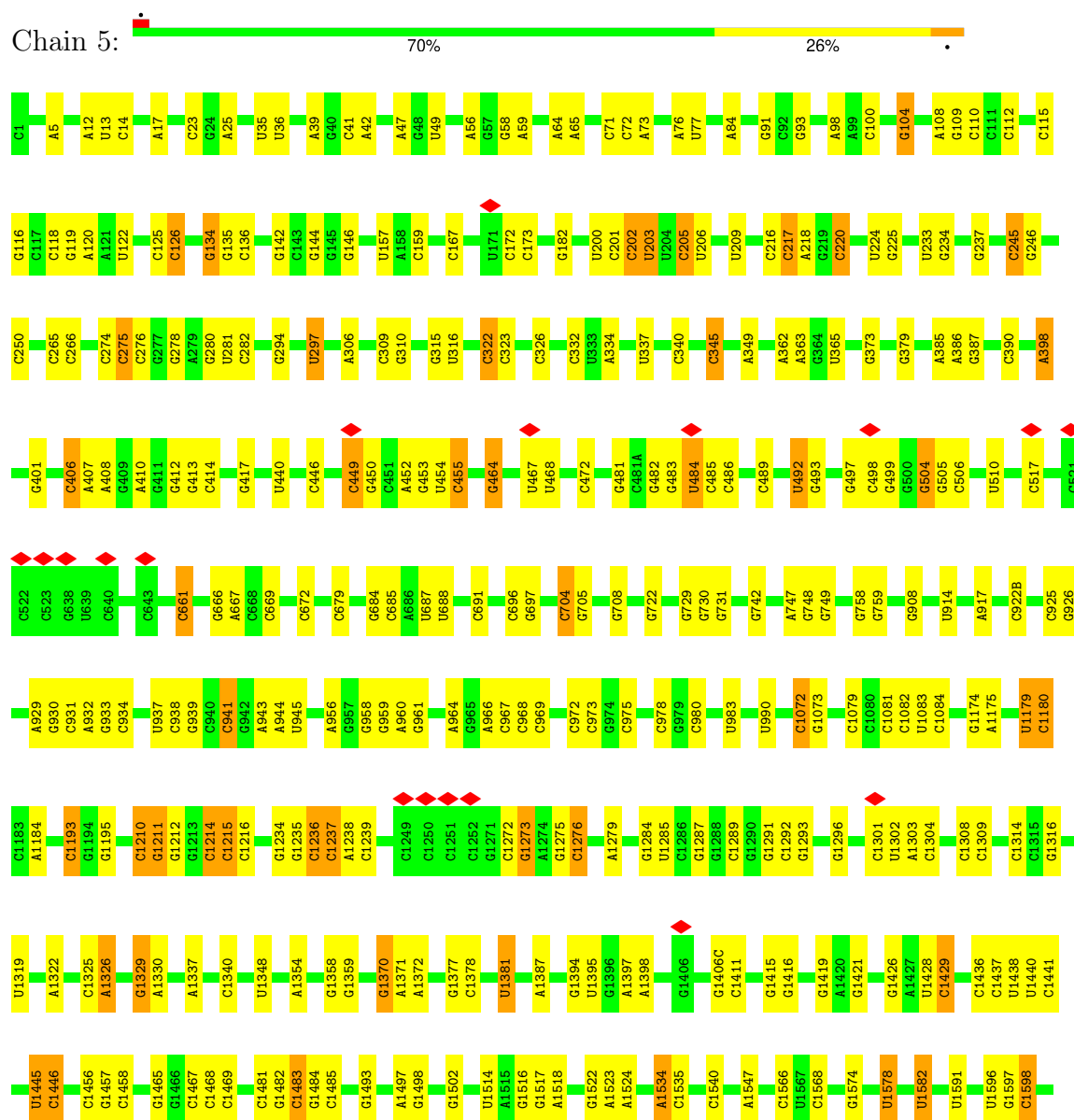


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
86	v	1	28	10	5	11	2	0

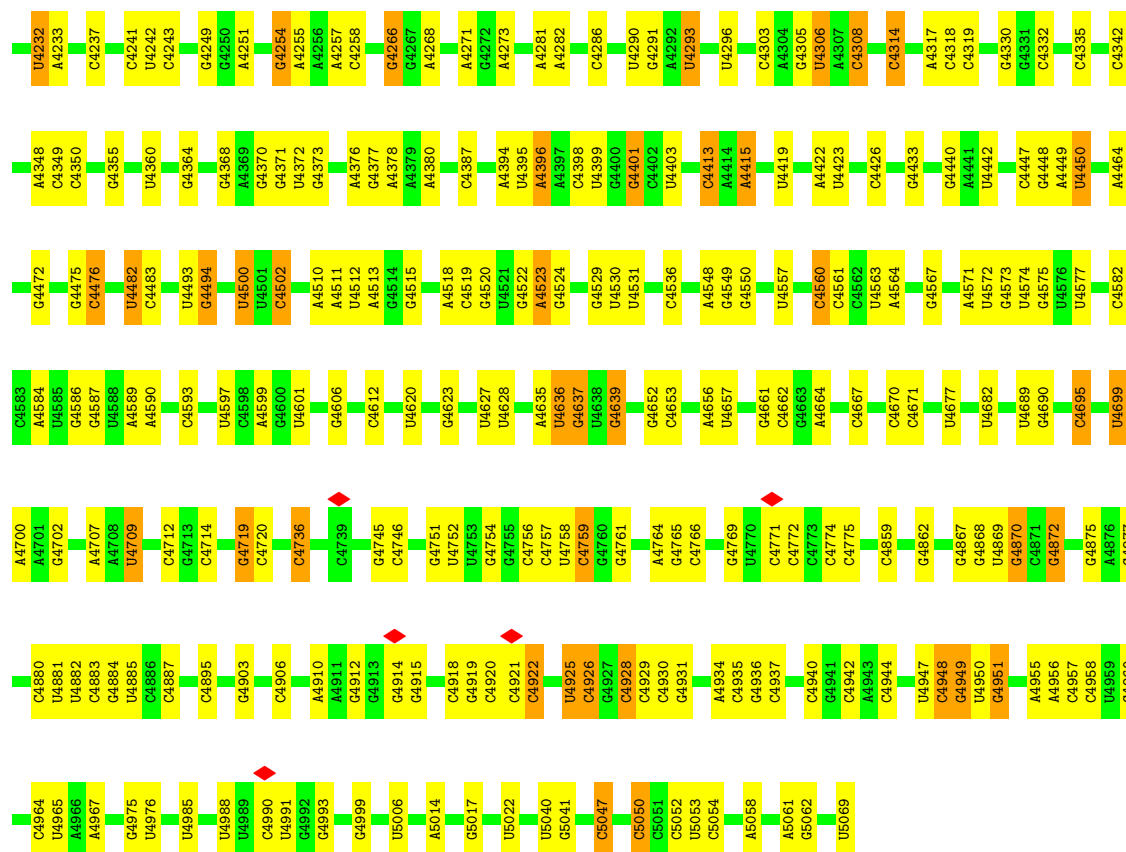
3 Residue-property plots [i](#)

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.

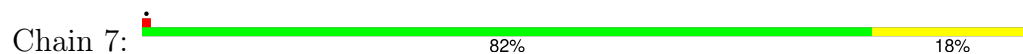
• Molecule 1: 28S rRNA



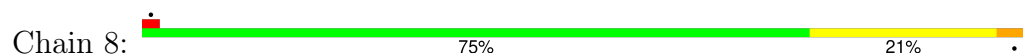
C4100	A3954	U2826	U2554	A2417	C2274	A2029	C1935	U1820	U1602
C4101	A3955	G2827	C2560	A2422	A2279	A2030	G1821	G1821	G1605
C4110	G3956	U2828	C2566	C2423	A2289	U2032	U1822	U1822	U1606
U4111	A3957	G2838	G2567	G2424	C2290	A2033	C1827	C1827	C1607
G4115	U3831	G2842	C2568	U2425	G2294	C2037	G1833	G1833	G1612
C4116	U3838	G2850	U2570	U2432	G2046	G2046	U1834	U1834	A1613
C4119	U3839	A2850	C2571	U2434	G2297	A2047	A1749	A1749	G1624
U4120	U3840	G2855	U2575	G2434	A2300	U2048	G1835	G1835	G1625
A3965	U3851	C2856	U2576	C2441	G2301	G2050	A1751	A1751	G1626
A3966	U3867	C2860	C2583	U2447	G2306	G2052	G1755	G1755	G1627
U3967	G3868	C2861	G2586	U2450	A2307	G1961	U1756	U1756	A1631
U3968	C3869	C2867	C2587	G2453	C1963	C1847	A1632	A1632	A1632
A3969	C3870	G2898	C2588	C2470	A1964	G1853	G1761	G1761	A1634
G3970	C3741	C3603	C2589	G2471	G2314	G1854	C1762	C1762	A1634
G3971	A3876	A3604	C2593	C2474	G2315	G1855	C1763	C1763	A1638
A3972	A3877	C3605	A2600	G2475	G2316	G1965	C1764	C1764	U1639
G3973	A3878	U3606	A2601	C2488	C2319	C1966	A1765	A1765	C1640
G3974	G3879	G3615	A2602	C2489	G2325	U1971	A1766	A1766	G1641
C3975	A3756	U3616	G2622	U2490	A2070	U1974	C1767	C1767	U1649
C3976	A3757	C3622	C2627	C2491	C2072	C1977	C1768	C1768	A1650
G4042	A3760	G3626	C2628	C2502	A2072	C1978	G1769	G1769	G1654
G4043	C3761	U3626	C2629	C2503	C2072	A1979	C1770	C1770	C1655
U4044	A3762	C3630	C2630	C2504	U2084	U1980	C1771	C1771	U1656
G4045	A3763	A3632	C2631	C2505	G2089	C1881	U1772	U1772	U1659
G4046	U3764	G3635	C2632	C2506	U2090	U1882	U1773	U1773	U1660
A4047	G3765	U3636	C2633	C2507	C2091	C1883	C1774	C1774	C1661
A4050	A3773	C3636	C2634	U2508	C2092	C1884	C1775	C1775	C1662
C4051	A3774	A3639	C2635	C2513	C2093	A1888	C1776	C1776	C1663
C4052	G3776	U3640	C2636	C2521	C2094	C1893	C1777	C1777	C1666
A4053	G3777	C3641	C2637	C2522	A2095	C1894	A1780	A1780	U1671
C4054	U3778	C3642	C2638	C2523	G2096	C1899	A1781	A1781	U1671
U4055	G3779	C3643	C2639	C2524	A2097	C1899	A1787	A1787	C1674
A4056	C3780	A3644	C2640	C2525	G2098	C1899	U1791	U1791	C1675
C3909	C3781	C3645	C2641	C2526	C2099	C1899	U1792	U1792	C1676
C3910	A3782	C3646	C2642	C2527	G2100	C1899	G1797	G1797	U1677
C3911	C3783	C3647	C2643	C2528	C2102	G1909	C1800	C1800	C1678
C4057	A3784	U3657	C2644	C2529	A2103	C1915	U1800	U1800	A1679
U4058	A3785	C3658	C2645	C2530	A2104	C1916	A1804	A1804	U1683
C4059	G3786	C3659	C2646	C2531	A2105	C1917	A1805	A1805	A1684
U4060	C3787	C3660	C2647	C2532	G2106	C1918	C1806	C1806	C1685
G4061	G3788	C3661	C2648	C2533	A2107	C1919	C1807	C1807	G1696
C4064	C3792	C3662	C2649	C2534	C2108	C1920	G1691	G1691	U1694
G4065	G3810	C3663	C2650	C2535	G2259	C1921	C1809	C1809	C1694
U4066	C3811	C3664	C2651	C2536	C2260	C1922	U1815	U1815	A1694
U4066	G3812	C3665	C2652	C2537	C2261	C1923	C1812	C1812	G1724
A4073	C3813	C3666	C2653	C2538	C2262	C1924	U1725	U1725	U1725
C4074	C3814	C3667	C2654	C2539	C2263	C1925	U1726	U1726	U1726
U4075	C3815	C3668	C2655	C2540	C2264	C1926	G1818	G1818	
G4076	C3816	C3669	C2656	C2541	C2265	C1927	G1819	G1819	
U4083	C3817	C3670	C2657	C2542	C2266	C1928			
G4084	G3818	C3671	C2658	C2543	U2267	A1929			
A4085	C3819	C3672	C2659	C2544	A2268	U1930			
G4086	C3820	C3673	C2660	C2545	A2269	C1931			
C4087	C3821	C3674	C2661	C2546	U2270	A1932			
C4088	C3822	C3675	C2662	C2547	C2270	A1933			
G4097	C3823	C3676	C2663	C2548	C2271	A1934			
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	C3825	C3678	C2665	C2550	C2273	A1936			
	C3826	C3679	C2666	C2551	C2274	A1937			
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	C3831	C3684	C2671	C2556	C2279	A1942			
	C3832	C3685	C2672	C2557	C2280	A1943			
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	C3836	C3689	C2676	C2561	C2284	A1947			
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	C3860	C3713	C2700	C2585	C2308	A1971			
	C3861	C3714	C2701	C2586	C2309	A1972			
	C3862	C3715	C2702	C2587	C2310	A1973			
	C3863	C3716	C2703	C2588	C2311	A1974			
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	C3865	C3718	C2705	C2590	C2313	A1976			
	C3866	C3719	C2706	C2591	C2314	A1977			
	C3867	C3720	C2707	C2592	C2315	A1978			
	C3868	C3721	C2708	C2593	C2316	A1979			
	C3869	C3722	C2709	C2594	C2317	A1980			
	C3870	C3723	C2710	C2595	C2318	A1981			
	C3871	C3724	C2711	C2596	C2319	A1982			
	C3872	C3725	C2712	C2597	C2320	A1983			
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	C3875	C3728	C2715	C2600	C2323	A1986			
	C3876	C3729	C2716	C2601	C2324	A1987			
	C3877	C3730	C2717	C2602	C2325	A1988			
	C3878	C3731	C2718	C2603	C2326	A1989			
	C3879	C3732	C2719	C2604	C2327	A1990			
	C3880	C3733	C2720	C2605	C2328	A1991			
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	C3882	C3735	C2722	C2607	C2330	A1993			
	C3883	C3736	C2723	C2608	C2331	A1994			
	C3884	C3737	C2724	C2609	C2332	A1995			
	C3885	C3738	C2725	C2610	C2333	A1996			
	C3886	C3739	C2726	C2611	C2334	A1997			
	C3887	C3740	C2727	C2612	C2335	A1998			
	C3888	C3741	C2728	C2613	C2336	A1999			
	C3889	C3742	C2729	C2614	C2337	A2000			
	C3890	C3743	C2730	C2615	C2338	A2001			
	C3891	C3744	C2731	C2616	C2339	A2002			
	C3892	C3745	C2732	C2617	C2340	A2003			
	C3893	C3746	C2733	C2618	C2341	A2004			
	C3894	C3747	C2734	C2619	C2342	A2005			
	C3895	C3748	C2735	C2620	C2343	A2006			
	C3896	C3749	C2736	C2621	C2344	A2007			
	C3897	C3750	C2737	C2622	C2345	A2008			
	C3898	C3751	C2738	C2623	C2346	A2009			
	C3899	C3752	C2739	C2624	C2347	A2010			
	C3900	C3753	C2740	C2625	C2348	A2011			
	C3901	C3754	C2741	C2626	C2349	A2012			
	C3902	C3755	C2742	C2627	C2350	A2013			
	C3903	C3756	C2743	C2628	C2351	A2014			
	C3904	C3757	C2744	C2629	C2352	A2015			
	C3905	C3758	C2745	C2630	C2353	A2016			
	C3906	C3759	C2746	C2631	C2354	A2017			
	C3907	C3760	C2747	C2632	C2355	A2018			
	C3908	C3761	C2748	C2633	C2356	A2019			
	C3909	C3762	C2749	C2634	C2357	A2020			
	C3910	C3763	C2750	C2635	C2358	A2021			
	C3911	C3764	C2751	C2636	C2359	A2022			
	C3912	C3765	C2752	C2637	C2360	A2023			
	C3913	C3766	C2753	C2638	C2361	A2024			
	C3914	C3767	C2754	C2639	C2362	A2025			
	C3915	C3768	C2755	C2640	C2363	A2026			
	C3916	C3769	C2756	C2641	C2364	A2027			
	C3917	C3770	C2757	C2642	C2365	A2028			
	C3918	C3771	C2758	C2643	C2366	A2029			



● Molecule 2: 5S rRNA



● Molecule 3: 5.8S rRNA



● Molecule 4: uL2



- Molecule 5: uL3

Chain B:  98%



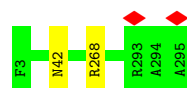
- Molecule 6: uL4

Chain C:  98%



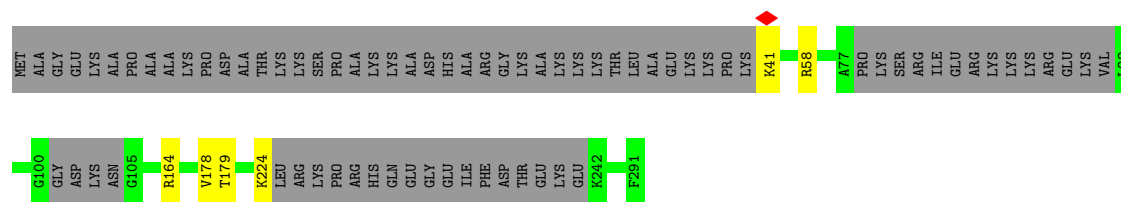
- Molecule 7: uL18

Chain D: 99%



- Molecule 8: eL6

Chain E: 72% . 26%



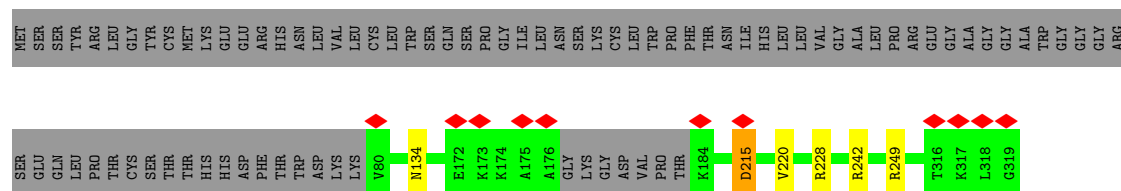
- Molecule 9: uL30

Chain F: 99%



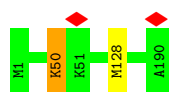
- Molecule 10: eL8

Chain G:  71% . 27%



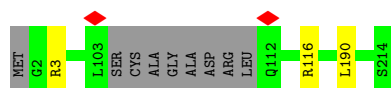
- Molecule 11: uL6

Chain H:  99%



- Molecule 12: uL16

Chain I:  94%



- Molecule 13: uL5

Chain J:  99%



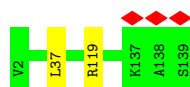
- Molecule 14: eL13

Chain L:  98%



- Molecule 15: eL14

Chain M:  99%



- Molecule 16: eL15

Chain N:  97%



- Molecule 17: uL13

Chain O:  98%



- Molecule 18: uL22

Chain P:  98% .



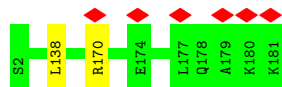
- Molecule 19: eL18

Chain Q:  99% .



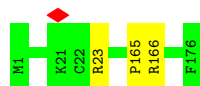
- Molecule 20: eL19

Chain R:  99% .



- Molecule 21: eL20

Chain S:  98% .



- Molecule 22: eL21

Chain T:  97% .



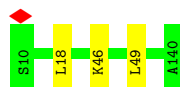
- Molecule 23: eL22

Chain U:  99% .



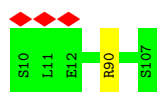
- Molecule 24: uL14

Chain V:  98% .



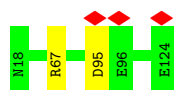
- Molecule 25: eL24

Chain c:  99% .



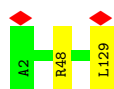
- Molecule 32: eL31

Chain d:  98% .



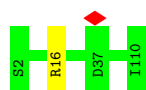
- Molecule 33: eL32

Chain e:  98% .



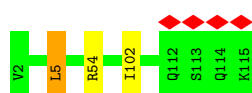
- Molecule 34: eL33

Chain f:  99% .



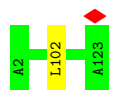
- Molecule 35: eL34

Chain g:  97% ..



- Molecule 36: uL29

Chain h:  99% .



- Molecule 37: eL36

Chain i:  96% .



• Molecule 38: eL37

Chain j:  98% .

• Molecule 39: eL38

Chain k:  100% .

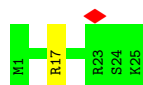
• Molecule 40: eL39

Chain l:  98% .

• Molecule 41: eL40

Chain m:  98% .

• Molecule 42: eL41

Chain n:  96% .

• Molecule 43: eL42

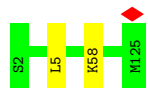
Chain o:  97% .

• Molecule 44: eL43

Chain p:  100% .

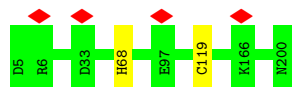
- Molecule 45: eL28

Chain r:  98%



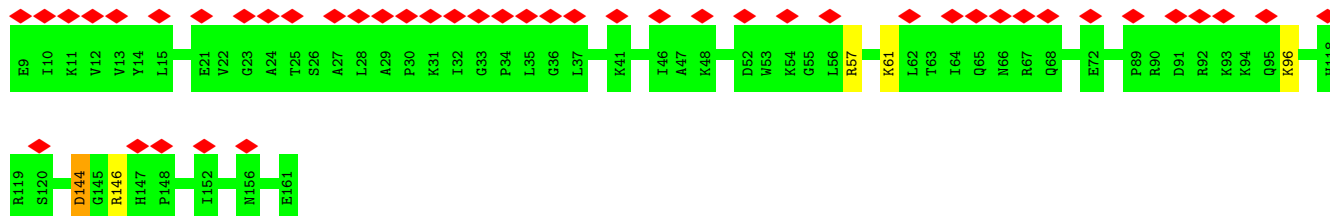
- Molecule 46: uL10

Chain s:  99%



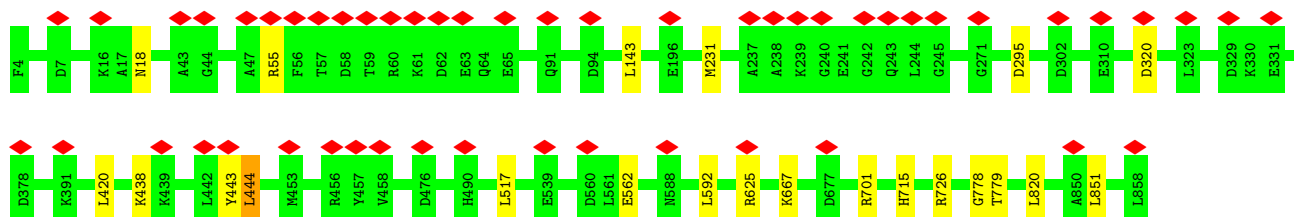
- Molecule 47: uL11

Chain t:  29% 97%



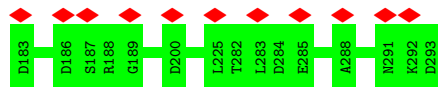
- Molecule 48: eEF2

Chain v:  6% 97%



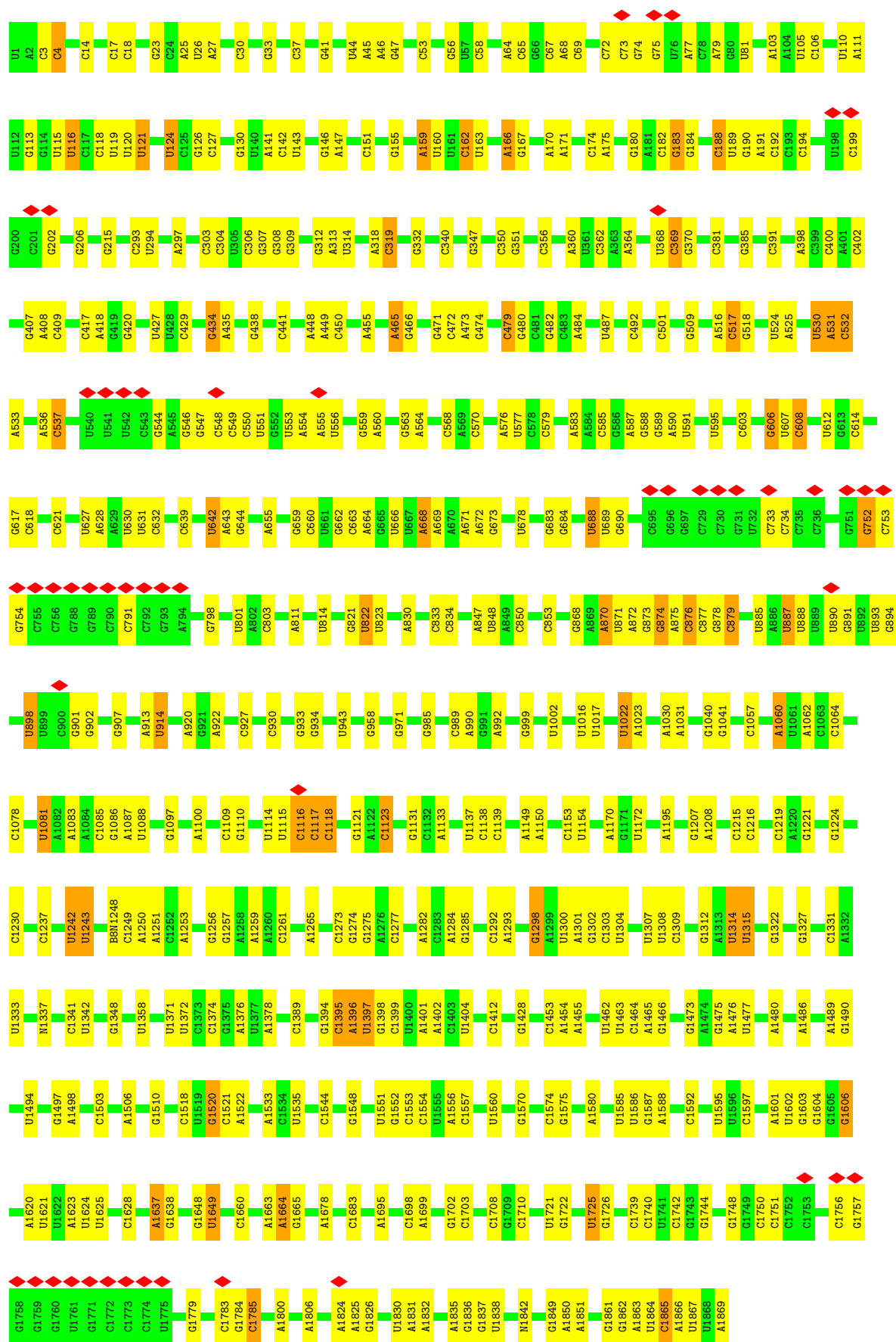
- Molecule 49: SERBP1

Chain w:  20% 100%



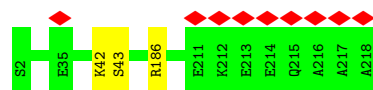
- Molecule 50: 18S rRNA

Chain 9:  70% 26%



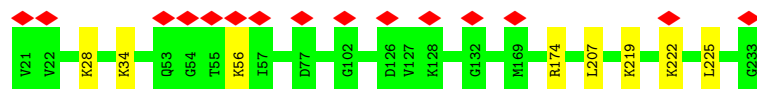
- Molecule 51: uS2

Chain AA:  99%



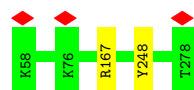
- Molecule 52: eS1

Chain BB:  96%



- Molecule 53: uS5

Chain CC:  99%



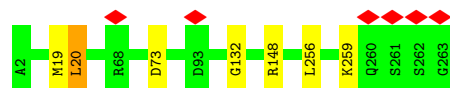
- Molecule 54: uS3

Chain DD:  98%




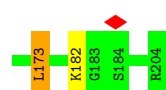
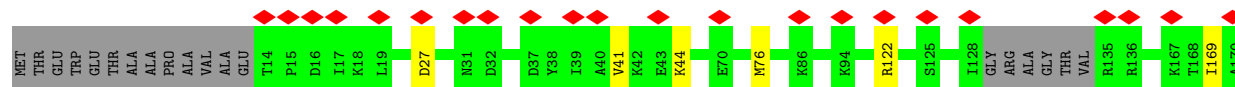
- Molecule 55: eS4

Chain EE:  97%



- Molecule 56: uS7

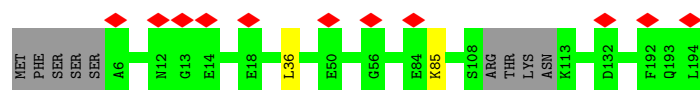
Chain FF:  87% 9%



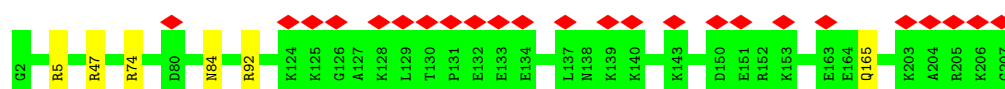
- Molecule 57: eS6



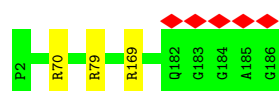
- Molecule 58: eS7



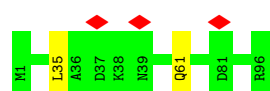
- Molecule 59: eS8



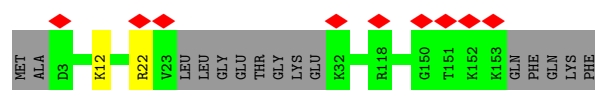
- Molecule 60: uS4



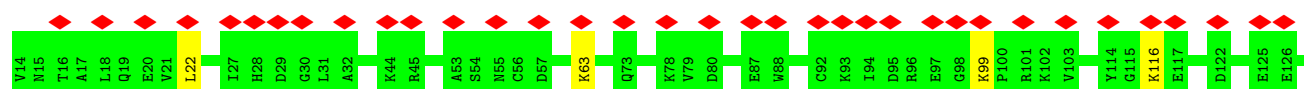
- Molecule 61: eS10



- Molecule 62: uS17



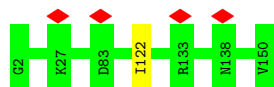
- Molecule 63: eS12





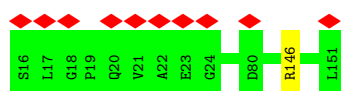
- Molecule 64: uS15

Chain NN: 99%



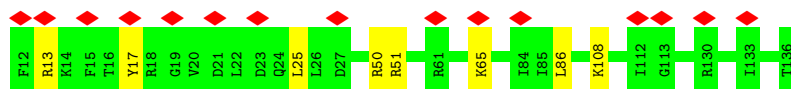
- Molecule 65: uS11

Chain OO: 99%



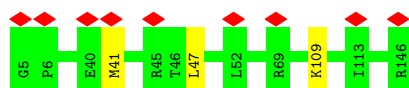
- Molecule 66: uS19

Chain PP: 94% 6%



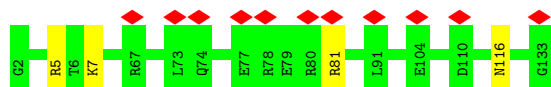
- Molecule 67: uS9

Chain QQ: 98%



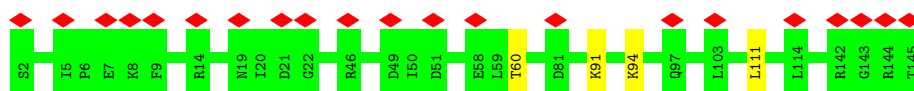
- Molecule 68: eS17

Chain RR: 97%



- Molecule 69: uS13

Chain SS: 97%



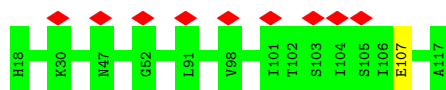
- Molecule 70: eS19

Chain TT:  7% 98%



- Molecule 71: uS10

Chain UU:  9% 99%



- Molecule 72: eS21

Chain VV:  98%



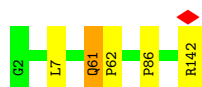
- Molecule 73: uS8

Chain WW:  98%



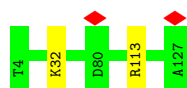
- Molecule 74: uS12

Chain XX:  96%



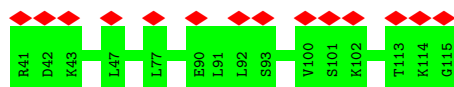
- Molecule 75: eS24

Chain YY:  98%



- Molecule 76: eS25

Chain ZZ:  19% 100%



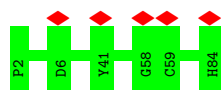
- Molecule 77: eS26

Chain aa:  99% 6% 5%



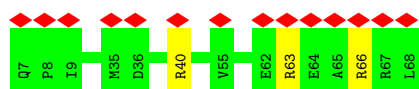
- Molecule 78: eS27

Chain bb:  100% 6% 5%



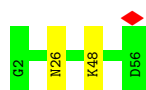
- Molecule 79: eS28

Chain cc:  95% 23% 5%



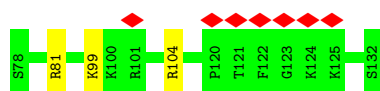
- Molecule 80: uS14

Chain dd:  96% 6% 5%



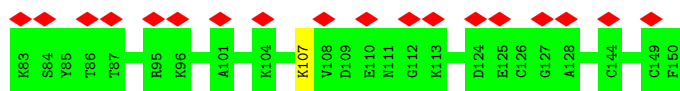
- Molecule 81: eS30

Chain ee:  95% 13% 5%



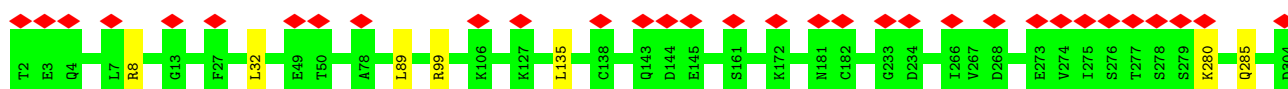
- Molecule 82: eS31

Chain ff:  99% 26% 5%



- Molecule 83: RACK1

Chain gg:  98% 11% 5%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	133480	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 ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.679	Depositor
Minimum map value	-0.386	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	536.0, 536.0, 536.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MC, B8N, MA6, MG, OMG, E7G, 5MU, B9B, 4AC, GDP, 6MZ, M7A, B8H, 7MG, E3C, DDE, 1MA, A2M, 2MG, E6G, MHG, B9H, UR3, B8Q, B8W, PSU, BGH, ZN, OMC, P4U, P7G, B8K, OMU, B8T, MLZ, I4U

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	5	0.80	0/83819	1.15	616/130590 (0.5%)
2	7	0.79	0/2858	1.09	13/4455 (0.3%)
3	8	0.77	0/3559	1.16	39/5543 (0.7%)
4	A	0.51	0/1936	0.62	0/2596
5	B	0.49	0/3240	0.66	2/4339 (0.0%)
6	C	0.47	0/2927	0.62	2/3932 (0.1%)
7	D	0.42	0/2437	0.55	0/3264
8	E	0.39	0/1762	0.64	0/2362
9	F	0.48	0/1911	0.62	0/2549
10	G	0.41	0/1910	0.61	0/2569
11	H	0.50	1/1535 (0.1%)	0.63	0/2063
12	I	0.48	0/1702	0.60	1/2272 (0.0%)
13	J	0.38	0/1385	0.66	1/1852 (0.1%)
14	L	0.42	0/1733	0.63	2/2316 (0.1%)
15	M	0.45	0/1158	0.58	1/1547 (0.1%)
16	N	0.50	0/1746	0.62	0/2338
17	O	0.51	0/1662	0.65	0/2222
18	P	0.49	0/1268	0.61	0/1700
19	Q	0.47	0/1539	0.62	0/2054
20	R	0.41	0/1524	0.65	1/2013 (0.0%)
21	S	0.53	0/1501	0.61	0/2012
22	T	0.47	0/1326	0.57	0/1770
23	U	0.37	0/823	0.64	0/1104
24	V	0.49	0/993	0.63	1/1332 (0.1%)
25	W	0.46	0/829	0.60	0/1099
26	X	0.43	0/984	0.64	1/1323 (0.1%)
27	Y	0.45	0/1132	0.60	0/1504
28	Z	0.46	0/1130	0.59	0/1507
29	a	0.49	0/1191	0.63	0/1590
30	b	0.34	0/861	0.56	0/1138

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	c	0.42	0/771	0.60	0/1034
32	d	0.43	0/903	0.61	0/1216
33	e	0.46	0/1071	0.58	1/1429 (0.1%)
34	f	0.51	0/895	0.68	0/1198
35	g	0.46	0/916	0.63	0/1220
36	h	0.41	0/1021	0.58	0/1348
37	i	0.39	0/841	0.59	1/1112 (0.1%)
38	j	0.46	0/720	0.65	0/952
39	k	0.40	0/575	0.58	0/761
40	l	0.40	0/459	0.61	1/608 (0.2%)
41	m	0.49	0/425	0.68	0/561
42	n	0.33	0/240	0.64	0/305
43	o	0.44	0/855	0.58	1/1128 (0.1%)
44	p	0.46	0/718	0.60	0/953
45	r	0.45	0/1010	0.62	1/1354 (0.1%)
46	s	0.33	0/1530	0.59	0/2064
47	t	0.31	0/1174	0.72	1/1582 (0.1%)
48	v	0.40	0/6736	0.69	8/9094 (0.1%)
49	w	0.33	0/447	0.58	0/592
50	9	0.64	0/39723	1.15	274/61870 (0.4%)
51	AA	0.40	0/1747	0.63	0/2374
52	BB	0.37	0/1756	0.72	4/2350 (0.2%)
53	CC	0.47	0/1753	0.64	0/2369
54	DD	0.38	0/1796	0.65	0/2417
55	EE	0.38	0/2118	0.69	5/2849 (0.2%)
56	FF	0.35	0/1492	0.68	2/2005 (0.1%)
57	GG	0.32	0/1946	0.68	3/2590 (0.1%)
58	HH	0.36	0/1510	0.67	1/2022 (0.0%)
59	II	0.36	0/1715	0.65	0/2287
60	JJ	0.39	0/1550	0.63	0/2069
61	KK	0.39	0/834	0.66	1/1125 (0.1%)
62	LL	0.44	0/1195	0.59	0/1597
63	MM	0.32	0/918	0.64	1/1233 (0.1%)
64	NN	0.36	0/1226	0.58	0/1649
65	OO	0.33	0/1029	0.63	0/1380
66	PP	0.34	0/1045	0.66	2/1396 (0.1%)
67	QQ	0.32	0/1146	0.66	1/1534 (0.1%)
68	RR	0.32	0/1082	0.62	0/1452
69	SS	0.32	0/1208	0.67	0/1618
70	TT	0.30	0/1115	0.59	0/1493
71	UU	0.32	0/805	0.61	0/1081
72	VV	0.41	0/643	0.61	0/860
73	WW	0.48	0/1051	0.69	1/1406 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
74	XX	0.46	0/1116	0.64	1/1490 (0.1%)
75	YY	0.33	0/1028	0.56	0/1366
76	ZZ	0.31	0/604	0.69	0/810
77	aa	0.37	0/828	0.56	0/1109
78	bb	0.33	0/665	0.59	0/891
79	cc	0.32	0/490	0.61	0/656
80	dd	0.40	0/470	0.60	0/623
81	ee	0.36	0/447	0.54	0/587
82	ff	0.32	0/567	0.60	0/753
83	gg	0.32	0/2493	0.64	2/3394 (0.1%)
All	All	0.63	1/232799 (0.0%)	0.97	992/340171 (0.3%)

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
6	C	0	1
8	E	0	2
9	F	0	1
10	G	0	1
11	H	0	1
16	N	0	3
21	S	0	1
22	T	0	1
32	d	0	1
35	g	0	1
46	s	0	1
47	t	0	1
48	v	0	4
51	AA	0	2
54	DD	0	1
55	EE	0	1
56	FF	0	1
59	II	0	1
66	PP	0	1
69	SS	0	1
71	UU	0	1
72	VV	0	1
74	XX	0	1
83	gg	0	1
All	All	0	31

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	H	128	MET	C-N	-5.34	1.21	1.34

The worst 5 of 992 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	9	1116	C	N1-C2-O2	12.69	126.52	118.90
50	9	1116	C	C2-N1-C1'	11.86	131.84	118.80
1	5	4056	A	OP1-P-O3'	-11.48	79.94	105.20
50	9	501	C	N1-C2-O2	11.03	125.52	118.90
1	5	1429	C	N1-C2-O2	10.96	125.47	118.90

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	73	VAL	Peptide
8	E	178	VAL	Peptide
8	E	179	THR	Peptide
9	F	195	THR	Peptide
10	G	215	ASP	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	
4	A	246/248 (99%)	221 (90%)	25 (10%)	0	100	100
5	B	392/394 (100%)	365 (93%)	27 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	C	359/362 (99%)	339 (94%)	20 (6%)	0	100	100
7	D	291/293 (99%)	279 (96%)	12 (4%)	0	100	100
8	E	208/291 (72%)	198 (95%)	10 (5%)	0	100	100
9	F	223/225 (99%)	212 (95%)	10 (4%)	1 (0%)	30	60
10	G	229/319 (72%)	219 (96%)	10 (4%)	0	100	100
11	H	188/190 (99%)	171 (91%)	17 (9%)	0	100	100
12	I	201/214 (94%)	191 (95%)	10 (5%)	0	100	100
13	J	168/170 (99%)	160 (95%)	8 (5%)	0	100	100
14	L	208/210 (99%)	198 (95%)	8 (4%)	2 (1%)	13	39
15	M	136/138 (99%)	125 (92%)	11 (8%)	0	100	100
16	N	201/203 (99%)	190 (94%)	11 (6%)	0	100	100
17	O	197/199 (99%)	191 (97%)	6 (3%)	0	100	100
18	P	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
19	Q	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
20	R	178/180 (99%)	173 (97%)	5 (3%)	0	100	100
21	S	174/176 (99%)	164 (94%)	9 (5%)	1 (1%)	22	50
22	T	157/159 (99%)	153 (98%)	3 (2%)	1 (1%)	22	50
23	U	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
24	V	129/131 (98%)	127 (98%)	2 (2%)	0	100	100
25	W	96/157 (61%)	89 (93%)	7 (7%)	0	100	100
26	X	116/118 (98%)	108 (93%)	8 (7%)	0	100	100
27	Y	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
28	Z	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
29	a	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
30	b	100/245 (41%)	95 (95%)	5 (5%)	0	100	100
31	c	96/98 (98%)	88 (92%)	8 (8%)	0	100	100
32	d	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
33	e	126/128 (98%)	119 (94%)	7 (6%)	0	100	100
34	f	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
35	g	112/114 (98%)	108 (96%)	4 (4%)	0	100	100
36	h	120/122 (98%)	119 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	i	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
38	j	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
39	k	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
40	l	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
41	m	49/52 (94%)	46 (94%)	2 (4%)	1 (2%)	6	25
42	n	23/25 (92%)	23 (100%)	0	0	100	100
43	o	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
44	p	89/91 (98%)	87 (98%)	2 (2%)	0	100	100
45	r	122/124 (98%)	116 (95%)	6 (5%)	0	100	100
46	s	194/196 (99%)	178 (92%)	16 (8%)	0	100	100
47	t	151/153 (99%)	128 (85%)	22 (15%)	1 (1%)	19	47
48	v	843/848 (99%)	774 (92%)	68 (8%)	1 (0%)	48	78
49	w	51/55 (93%)	46 (90%)	5 (10%)	0	100	100
51	AA	215/217 (99%)	206 (96%)	9 (4%)	0	100	100
52	BB	211/213 (99%)	203 (96%)	8 (4%)	0	100	100
53	CC	219/221 (99%)	206 (94%)	13 (6%)	0	100	100
54	DD	226/228 (99%)	216 (96%)	10 (4%)	0	100	100
55	EE	260/262 (99%)	244 (94%)	16 (6%)	0	100	100
56	FF	181/204 (89%)	162 (90%)	19 (10%)	0	100	100
57	GG	235/237 (99%)	224 (95%)	11 (5%)	0	100	100
58	HH	181/194 (93%)	173 (96%)	8 (4%)	0	100	100
59	II	204/206 (99%)	185 (91%)	19 (9%)	0	100	100
60	JJ	183/185 (99%)	180 (98%)	3 (2%)	0	100	100
61	KK	94/96 (98%)	86 (92%)	8 (8%)	0	100	100
62	LL	139/158 (88%)	131 (94%)	8 (6%)	0	100	100
63	MM	115/117 (98%)	101 (88%)	14 (12%)	0	100	100
64	NN	147/149 (99%)	138 (94%)	9 (6%)	0	100	100
65	OO	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
66	PP	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
67	QQ	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
68	RR	130/132 (98%)	121 (93%)	9 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	SS	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
70	TT	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
71	UU	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
72	VV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
73	WW	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
74	XX	139/141 (99%)	132 (95%)	4 (3%)	3 (2%)	5	24
75	YY	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
76	ZZ	73/75 (97%)	70 (96%)	3 (4%)	0	100	100
77	aa	99/101 (98%)	90 (91%)	9 (9%)	0	100	100
78	bb	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
79	cc	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
80	dd	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
81	ee	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
82	ff	66/68 (97%)	55 (83%)	11 (17%)	0	100	100
83	gg	311/313 (99%)	282 (91%)	29 (9%)	0	100	100
All	All	12409/13005 (95%)	11674 (94%)	724 (6%)	11 (0%)	50	78

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
14	L	64	VAL
41	m	73	CYS
74	XX	62	PRO
14	L	63	THR
21	S	166	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	190/190 (100%)	187 (98%)	3 (2%)	58	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	B	342/342 (100%)	338 (99%)	4 (1%)	67	80
6	C	301/301 (100%)	297 (99%)	4 (1%)	65	78
7	D	247/247 (100%)	245 (99%)	2 (1%)	79	87
8	E	190/251 (76%)	186 (98%)	4 (2%)	48	69
9	F	196/196 (100%)	196 (100%)	0	100	100
10	G	200/272 (74%)	194 (97%)	6 (3%)	36	61
11	H	169/169 (100%)	168 (99%)	1 (1%)	84	90
12	I	175/181 (97%)	173 (99%)	2 (1%)	70	81
13	J	143/143 (100%)	143 (100%)	0	100	100
14	L	175/175 (100%)	175 (100%)	0	100	100
15	M	117/117 (100%)	116 (99%)	1 (1%)	75	86
16	N	171/171 (100%)	168 (98%)	3 (2%)	54	73
17	O	171/171 (100%)	167 (98%)	4 (2%)	45	67
18	P	134/134 (100%)	131 (98%)	3 (2%)	47	68
19	Q	164/164 (100%)	162 (99%)	2 (1%)	67	80
20	R	159/159 (100%)	158 (99%)	1 (1%)	84	90
21	S	157/157 (100%)	156 (99%)	1 (1%)	84	90
22	T	139/139 (100%)	137 (99%)	2 (1%)	62	77
23	U	89/89 (100%)	88 (99%)	1 (1%)	70	81
24	V	101/101 (100%)	99 (98%)	2 (2%)	50	70
25	W	82/126 (65%)	82 (100%)	0	100	100
26	X	106/106 (100%)	105 (99%)	1 (1%)	75	86
27	Y	124/124 (100%)	122 (98%)	2 (2%)	58	75
28	Z	117/117 (100%)	117 (100%)	0	100	100
29	a	119/119 (100%)	118 (99%)	1 (1%)	79	87
30	b	84/184 (46%)	82 (98%)	2 (2%)	44	66
31	c	84/84 (100%)	83 (99%)	1 (1%)	67	80
32	d	98/98 (100%)	97 (99%)	1 (1%)	73	83
33	e	114/114 (100%)	113 (99%)	1 (1%)	75	86
34	f	88/88 (100%)	87 (99%)	1 (1%)	70	81
35	g	98/98 (100%)	95 (97%)	3 (3%)	35	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	h	109/109 (100%)	108 (99%)	1 (1%)	75	86
37	i	86/86 (100%)	83 (96%)	3 (4%)	31	56
38	j	73/73 (100%)	71 (97%)	2 (3%)	40	63
39	k	64/64 (100%)	64 (100%)	0	100	100
40	l	47/47 (100%)	47 (100%)	0	100	100
41	m	47/47 (100%)	47 (100%)	0	100	100
42	n	24/24 (100%)	23 (96%)	1 (4%)	25	51
43	o	91/91 (100%)	89 (98%)	2 (2%)	47	68
44	p	74/74 (100%)	74 (100%)	0	100	100
45	r	108/108 (100%)	107 (99%)	1 (1%)	75	86
46	s	164/164 (100%)	163 (99%)	1 (1%)	84	90
47	t	126/126 (100%)	123 (98%)	3 (2%)	44	66
48	v	722/722 (100%)	712 (99%)	10 (1%)	62	77
49	w	46/46 (100%)	46 (100%)	0	100	100
51	AA	180/181 (99%)	179 (99%)	1 (1%)	84	90
52	BB	194/194 (100%)	190 (98%)	4 (2%)	48	69
53	CC	187/187 (100%)	185 (99%)	2 (1%)	70	81
54	DD	190/190 (100%)	186 (98%)	4 (2%)	48	69
55	EE	224/224 (100%)	221 (99%)	3 (1%)	65	78
56	FF	158/170 (93%)	152 (96%)	6 (4%)	28	54
57	GG	207/207 (100%)	199 (96%)	8 (4%)	27	53
58	HH	165/174 (95%)	164 (99%)	1 (1%)	84	90
59	II	178/178 (100%)	173 (97%)	5 (3%)	38	62
60	JJ	161/161 (100%)	158 (98%)	3 (2%)	52	71
61	KK	87/87 (100%)	86 (99%)	1 (1%)	70	81
62	LL	130/142 (92%)	128 (98%)	2 (2%)	60	76
63	MM	99/99 (100%)	96 (97%)	3 (3%)	36	61
64	NN	130/130 (100%)	129 (99%)	1 (1%)	79	87
65	OO	106/106 (100%)	105 (99%)	1 (1%)	75	86
66	PP	111/111 (100%)	106 (96%)	5 (4%)	23	50
67	QQ	117/117 (100%)	115 (98%)	2 (2%)	56	74

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	RR	119/119 (100%)	115 (97%)	4 (3%)	32	57
69	SS	125/125 (100%)	122 (98%)	3 (2%)	44	66
70	TT	111/111 (100%)	108 (97%)	3 (3%)	40	63
71	UU	92/92 (100%)	92 (100%)	0	100	100
72	VV	67/67 (100%)	66 (98%)	1 (2%)	60	76
73	WW	112/112 (100%)	111 (99%)	1 (1%)	75	86
74	XX	113/113 (100%)	112 (99%)	1 (1%)	75	86
75	YY	107/107 (100%)	105 (98%)	2 (2%)	52	71
76	ZZ	66/66 (100%)	66 (100%)	0	100	100
77	aa	88/88 (100%)	87 (99%)	1 (1%)	70	81
78	bb	75/75 (100%)	75 (100%)	0	100	100
79	cc	55/55 (100%)	52 (94%)	3 (6%)	18	44
80	dd	48/48 (100%)	46 (96%)	2 (4%)	25	51
81	ee	46/46 (100%)	43 (94%)	3 (6%)	14	39
82	ff	61/61 (100%)	60 (98%)	1 (2%)	58	75
83	gg	272/272 (100%)	268 (98%)	4 (2%)	60	76
All	All	10806/11123 (97%)	10642 (98%)	164 (2%)	60	76

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
59	II	84	ASN
70	TT	62	ARG
60	JJ	169	ARG
66	PP	51	ARG
77	aa	42	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
7	D	42	ASN
15	M	48	GLN
22	T	69	GLN
55	EE	36	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3520/3597 (97%)	818 (23%)	59 (1%)
2	7	119/120 (99%)	14 (11%)	0
3	8	149/151 (98%)	25 (16%)	1 (0%)
50	9	1670/1698 (98%)	388 (23%)	18 (1%)
All	All	5458/5566 (98%)	1245 (22%)	78 (1%)

5 of 1245 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	5	A
1	5	12	A
1	5	13	U
1	5	17	A
1	5	25	A

5 of 78 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	4936	G
50	9	1137	U
3	8	124	U
50	9	553	U
50	9	1520	G

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

138 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	OMC	5	3869	1	19,22,23	2.81	7 (36%)	25,31,34	0.85	1 (4%)
1	OMG	5	4637	1	19,26,27	2.37	8 (42%)	21,38,41	1.44	4 (19%)
1	5MU	5	4083	1	19,22,23	4.71	7 (36%)	27,32,35	3.46	9 (33%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	5	4447	1	19,22,23	3.85	8 (42%)	26,32,35	1.13	1 (3%)
50	OMC	9	174	50	19,22,23	2.97	7 (36%)	25,31,34	0.83	1 (4%)
50	A2M	9	484	50	18,25,26	4.93	9 (50%)	20,36,39	2.67	3 (15%)
1	B8H	5	3762	1	19,22,23	6.86	6 (31%)	21,32,35	2.63	5 (23%)
1	OMC	5	3887	1	19,22,23	2.87	7 (36%)	25,31,34	0.96	1 (4%)
1	A2M	5	3825	1	18,25,26	4.93	7 (38%)	20,36,39	2.77	5 (25%)
1	B8T	5	4483	1	19,22,23	3.02	8 (42%)	25,31,34	1.07	2 (8%)
50	OMC	9	517	50	19,22,23	2.85	7 (36%)	25,31,34	0.65	0
50	5MC	9	1374	50	19,22,23	3.92	8 (42%)	26,32,35	1.35	3 (11%)
1	E7G	5	1797	1	24,27,28	3.26	11 (45%)	28,40,43	2.33	10 (35%)
1	BGH	5	3899	84,1	25,29,30	4.21	15 (60%)	30,43,46	2.68	14 (46%)
1	A2M	5	2401	84,1	18,25,26	4.91	9 (50%)	20,36,39	2.81	6 (30%)
1	MHG	5	4371	1	29,32,33	3.69	11 (37%)	34,46,49	2.43	12 (35%)
1	OMC	5	3909	1	19,22,23	2.85	7 (36%)	25,31,34	1.31	3 (12%)
1	OMG	5	1522	1	19,26,27	2.39	8 (42%)	21,38,41	1.53	4 (19%)
50	PSU	9	612	50	18,21,22	1.00	1 (5%)	21,30,33	1.87	5 (23%)
1	UR3	5	4597	1	19,22,23	2.56	7 (36%)	26,32,35	1.47	4 (15%)
1	B8H	5	4296	1	19,22,23	6.87	6 (31%)	21,32,35	2.64	5 (23%)
50	4AC	9	1842	50	21,24,25	3.11	10 (47%)	28,34,37	1.21	4 (14%)
1	5MC	5	4335	1	19,22,23	3.89	8 (42%)	26,32,35	1.19	3 (11%)
1	B8K	5	4690	1	24,28,29	4.86	17 (70%)	29,42,45	2.85	11 (37%)
50	5MU	9	814	50	19,22,23	4.93	7 (36%)	27,32,35	3.58	12 (44%)
1	B8W	5	4129	1	18,26,27	4.35	7 (38%)	17,38,41	7.37	10 (58%)
50	4AC	9	1337	50	21,24,25	3.17	9 (42%)	28,34,37	1.27	4 (14%)
1	PSU	5	2508	1	18,21,22	1.03	1 (5%)	21,30,33	1.79	4 (19%)
6	MLZ	C	333	6	8,9,10	0.84	0	4,9,11	0.70	0
1	2MG	5	729	1	18,26,27	2.46	7 (38%)	16,38,41	1.47	4 (25%)
1	OMC	5	4536	1	19,22,23	2.83	7 (36%)	25,31,34	1.07	2 (8%)
1	7MG	5	4550	1	23,26,27	3.27	10 (43%)	27,39,42	2.09	10 (37%)
1	PSU	5	3729	1	18,21,22	1.10	1 (5%)	21,30,33	1.87	4 (19%)
50	OMG	9	644	50	19,26,27	2.42	8 (42%)	21,38,41	1.45	4 (19%)
50	PSU	9	1243	84,50	18,21,22	1.10	1 (5%)	21,30,33	1.97	4 (19%)
50	OMC	9	1710	50	19,22,23	2.96	7 (36%)	25,31,34	0.95	1 (4%)
1	OMC	5	2861	1	19,22,23	2.85	7 (36%)	25,31,34	0.91	1 (4%)
1	5MC	5	3782	1	19,22,23	3.69	8 (42%)	26,32,35	1.05	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	5	4500	1	18,21,22	1.08	3 (16%)	21,30,33	2.06	5 (23%)
1	PSU	5	4450	84,1	18,21,22	1.09	3 (16%)	21,30,33	2.12	5 (23%)
1	OMC	5	3701	84,1	19,22,23	2.82	7 (36%)	25,31,34	0.75	0
1	I4U	5	4194	1	20,24,25	5.01	13 (65%)	27,34,37	1.82	4 (14%)
1	OMG	5	4370	1	19,26,27	2.38	8 (42%)	21,38,41	1.49	4 (19%)
1	OMC	5	2365	1	19,22,23	2.84	7 (36%)	25,31,34	0.70	0
1	PSU	5	4636	1	18,21,22	1.08	2 (11%)	21,30,33	2.12	5 (23%)
1	B9B	5	2754	84,1	20,28,29	5.07	8 (40%)	19,40,43	2.39	7 (36%)
1	P7G	5	1909	1	24,28,29	3.70	11 (45%)	25,41,44	1.28	2 (8%)
1	B8T	5	4671	1	19,22,23	3.01	8 (42%)	25,31,34	0.95	1 (4%)
1	UR3	5	1866	1	19,22,23	2.55	6 (31%)	26,32,35	1.58	5 (19%)
50	OMG	9	683	50	19,26,27	2.42	8 (42%)	21,38,41	1.50	5 (23%)
1	6MZ	5	4220	1	17,25,26	1.78	3 (17%)	15,36,39	2.07	3 (20%)
1	2MG	5	4872	1	18,26,27	2.67	7 (38%)	16,38,41	3.32	6 (37%)
50	A2M	9	668	84,50	18,25,26	4.88	7 (38%)	20,36,39	3.02	7 (35%)
1	A2M	5	3785	1	18,25,26	4.78	10 (55%)	20,36,39	3.09	5 (25%)
48	DDE	v	715	48	15,20,21	1.01	0	11,28,30	1.32	2 (18%)
50	E3C	9	568	50	19,23,24	3.37	6 (31%)	21,33,36	2.46	6 (28%)
50	6MZ	9	1832	84,50	17,25,26	1.55	3 (17%)	15,36,39	1.87	2 (13%)
1	1MA	5	4415	1	17,25,26	3.83	4 (23%)	17,37,40	1.86	3 (17%)
50	B8Q	9	1219	50	18,22,23	2.94	4 (22%)	21,32,35	2.24	7 (33%)
1	M7A	5	4564	1	19,25,26	1.61	4 (21%)	25,37,40	3.97	8 (32%)
50	PSU	9	119	50	18,21,22	0.96	1 (5%)	21,30,33	1.71	5 (23%)
1	A2M	5	2363	84,1	18,25,26	5.02	9 (50%)	20,36,39	2.82	4 (20%)
1	E6G	5	4355	1	19,27,28	4.71	7 (36%)	18,39,42	2.39	6 (33%)
50	PSU	9	823	50	18,21,22	1.11	2 (11%)	21,30,33	1.95	4 (19%)
1	B8H	5	1860	1	19,22,23	6.83	6 (31%)	21,32,35	2.39	5 (23%)
50	UR3	9	1830	50	19,22,23	2.75	7 (36%)	26,32,35	1.81	5 (19%)
1	B8W	5	2380	1	18,26,27	4.23	6 (33%)	17,38,41	7.14	9 (52%)
50	M7A	9	1806	50	19,25,26	1.62	2 (10%)	25,37,40	3.94	8 (32%)
1	PSU	5	4531	1	18,21,22	1.11	3 (16%)	21,30,33	2.05	5 (23%)
1	B9H	5	2786	1	21,25,26	2.99	3 (14%)	22,35,38	1.79	3 (13%)
1	7MG	5	2522	1	23,26,27	3.24	10 (43%)	27,39,42	2.11	9 (33%)
1	A2M	5	4523	84,1	18,25,26	5.04	9 (50%)	20,36,39	2.74	5 (25%)
1	A2M	5	3867	1	18,25,26	4.91	9 (50%)	20,36,39	2.59	4 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	5	4403	1	18,21,22	1.04	1 (5%)	21,30,33	1.99	4 (19%)
1	OMG	5	2050	1	19,26,27	2.39	8 (42%)	21,38,41	1.44	4 (19%)
1	OMG	5	2424	1	19,26,27	2.46	8 (42%)	21,38,41	1.49	4 (19%)
1	OMG	5	4196	1	19,26,27	2.36	8 (42%)	21,38,41	1.45	4 (19%)
1	OMG	5	2773	1	19,26,27	2.45	8 (42%)	21,38,41	1.48	4 (19%)
1	P7G	5	3880	1	24,28,29	3.52	10 (41%)	25,41,44	1.33	2 (8%)
50	A2M	9	1031	50	18,25,26	4.96	8 (44%)	20,36,39	2.92	5 (25%)
1	PSU	5	3764	1	18,21,22	1.05	1 (5%)	21,30,33	1.81	4 (19%)
50	MA6	9	1850	50	19,26,27	1.66	2 (10%)	18,38,41	2.85	3 (16%)
1	UR3	5	4530	1	19,22,23	2.71	7 (36%)	26,32,35	1.70	5 (19%)
1	B9B	5	1574	1	20,28,29	5.06	8 (40%)	19,40,43	2.07	6 (31%)
1	OMU	5	4620	1	19,22,23	2.74	7 (36%)	25,31,34	1.95	5 (20%)
50	A2M	9	166	50	18,25,26	5.02	9 (50%)	20,36,39	2.76	4 (20%)
1	PSU	5	1683	1	18,21,22	1.13	2 (11%)	21,30,33	1.97	4 (19%)
1	OMC	5	2422	84,1	19,22,23	2.88	7 (36%)	25,31,34	1.00	1 (4%)
1	B8W	5	4529	84,1	18,26,27	4.26	7 (38%)	17,38,41	7.41	10 (58%)
1	B9B	5	237	1	20,28,29	5.13	8 (40%)	19,40,43	2.50	5 (26%)
1	OMG	5	373	1	19,26,27	2.42	8 (42%)	21,38,41	1.63	5 (23%)
1	OMG	5	1316	1	19,26,27	2.41	8 (42%)	21,38,41	1.61	4 (19%)
1	A2M	5	3723	1	18,25,26	5.09	9 (50%)	20,36,39	2.61	4 (20%)
1	I4U	5	1659	1	20,24,25	5.00	14 (70%)	27,34,37	2.22	3 (11%)
1	A2M	5	398	1	18,25,26	5.04	9 (50%)	20,36,39	2.56	4 (20%)
1	A2M	5	1534	84,1	18,25,26	4.86	9 (50%)	20,36,39	3.01	5 (25%)
50	B8N	9	1248	84,50	25,29,30	3.09	7 (28%)	28,42,45	2.00	7 (25%)
1	2MG	5	1517	1	18,26,27	2.58	7 (38%)	16,38,41	1.83	5 (31%)
50	PSU	9	1081	50	18,21,22	1.08	2 (11%)	21,30,33	1.91	5 (23%)
1	OMG	5	2364	1	19,26,27	2.42	8 (42%)	21,38,41	1.59	4 (19%)
1	A2M	5	1524	1	18,25,26	4.94	9 (50%)	20,36,39	3.34	6 (30%)
1	7MG	5	1605	1	23,26,27	3.25	10 (43%)	27,39,42	2.18	9 (33%)
1	A2M	5	4571	1	18,25,26	4.98	8 (44%)	20,36,39	2.72	4 (20%)
50	OMU	9	116	50	19,22,23	2.93	7 (36%)	25,31,34	1.86	5 (20%)
3	OMU	8	14	3,1	19,22,23	2.88	7 (36%)	25,31,34	1.97	7 (28%)
1	PSU	5	4442	1	18,21,22	1.08	3 (16%)	21,30,33	1.98	5 (23%)
1	OMG	5	1625	84,1	19,26,27	2.41	8 (42%)	21,38,41	1.46	4 (19%)
1	1MA	5	1322	84,1	17,25,26	3.70	4 (23%)	17,37,40	1.79	3 (17%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	OMU	9	121	50	19,22,23	3.00	8 (42%)	25,31,34	1.87	5 (20%)
50	PSU	9	822	50	18,21,22	1.05	2 (11%)	21,30,33	2.07	5 (23%)
1	E7G	5	2297	1	24,27,28	3.11	11 (45%)	28,40,43	2.24	9 (32%)
50	MA6	9	1851	50	19,26,27	1.69	2 (10%)	18,38,41	2.76	3 (16%)
1	PSU	5	4628	1	18,21,22	1.15	3 (16%)	21,30,33	2.23	5 (23%)
1	A2M	5	1871	84,1	18,25,26	4.92	9 (50%)	20,36,39	2.83	5 (25%)
1	PSU	5	1677	1	18,21,22	1.12	3 (16%)	21,30,33	2.04	6 (28%)
1	B8K	5	3897	1	24,28,29	4.76	17 (70%)	29,42,45	2.61	12 (41%)
50	A2M	9	159	50	18,25,26	5.06	8 (44%)	20,36,39	2.99	5 (25%)
1	OMU	5	4306	1	19,22,23	2.83	8 (42%)	25,31,34	1.86	5 (20%)
41	MLZ	m	72	41	8,9,10	0.78	0	4,9,11	0.78	0
1	OMG	5	4494	1	19,26,27	2.42	8 (42%)	21,38,41	1.51	4 (19%)
50	OMC	9	1703	50	19,22,23	2.95	7 (36%)	25,31,34	0.86	1 (4%)
50	A2M	9	27	84,50	18,25,26	4.89	8 (44%)	20,36,39	2.72	5 (25%)
1	PSU	5	1582	1	18,21,22	1.10	1 (5%)	21,30,33	1.85	4 (19%)
1	B8W	5	4185	1	18,26,27	4.27	7 (38%)	17,38,41	7.23	11 (64%)
1	B8Q	5	1456	1	18,22,23	2.75	5 (27%)	21,32,35	1.90	4 (19%)
1	OMG	5	1883	1	19,26,27	2.44	8 (42%)	21,38,41	1.61	4 (19%)
1	OMC	5	2804	1	19,22,23	2.87	7 (36%)	25,31,34	0.83	0
1	B8W	5	4472	1	18,26,27	4.25	7 (38%)	17,38,41	6.96	9 (52%)
1	PSU	5	3715	1	18,21,22	1.05	1 (5%)	21,30,33	1.83	4 (19%)
1	P4U	5	1348	84,1	21,24,25	3.28	7 (33%)	28,33,36	1.94	3 (10%)
50	A2M	9	1678	50	18,25,26	5.06	9 (50%)	20,36,39	2.86	4 (20%)
50	OMG	9	509	84,50	19,26,27	2.41	8 (42%)	21,38,41	1.40	4 (19%)
1	A2M	5	1326	1	18,25,26	4.85	10 (55%)	20,36,39	2.57	3 (15%)
1	OMG	5	4623	1	19,26,27	2.41	8 (42%)	21,38,41	1.57	4 (19%)
1	OMG	5	4870	1	19,26,27	2.41	7 (36%)	21,38,41	1.49	4 (19%)
1	A2M	5	3718	1	18,25,26	5.01	10 (55%)	20,36,39	2.49	4 (20%)
1	PSU	5	4293	1	18,21,22	1.11	2 (11%)	21,30,33	1.88	3 (14%)
1	OMG	5	3792	1	19,26,27	2.45	8 (42%)	21,38,41	1.57	4 (19%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	5	3869	1	-	0/9/27/28	0/2/2/2
1	OMG	5	4637	1	-	3/5/27/28	0/3/3/3
1	5MU	5	4083	1	-	6/7/25/26	0/2/2/2
1	5MC	5	4447	1	-	4/7/25/26	0/2/2/2
50	OMC	9	174	50	-	0/9/27/28	0/2/2/2
50	A2M	9	484	50	-	0/5/27/28	0/3/3/3
1	B8H	5	3762	1	-	0/7/25/26	0/2/2/2
1	OMC	5	3887	1	-	1/9/27/28	0/2/2/2
1	A2M	5	3825	1	-	0/5/27/28	0/3/3/3
1	B8T	5	4483	1	-	2/7/27/28	0/2/2/2
50	OMC	9	517	50	-	2/9/27/28	0/2/2/2
50	5MC	9	1374	50	-	0/7/25/26	0/2/2/2
1	E7G	5	1797	1	-	3/9/39/40	0/3/3/3
1	BGH	5	3899	84,1	-	2/13/43/44	0/3/3/3
1	A2M	5	2401	84,1	-	2/5/27/28	0/3/3/3
1	MHG	5	4371	1	-	5/16/46/47	0/3/3/3
1	OMC	5	3909	1	-	1/9/27/28	0/2/2/2
1	OMG	5	1522	1	-	0/5/27/28	0/3/3/3
50	PSU	9	612	50	-	0/7/25/26	0/2/2/2
1	UR3	5	4597	1	-	0/7/25/26	0/2/2/2
1	B8H	5	4296	1	-	1/7/25/26	0/2/2/2
50	4AC	9	1842	50	-	0/11/29/30	0/2/2/2
1	5MC	5	4335	1	-	0/7/25/26	0/2/2/2
1	B8K	5	4690	1	-	0/11/41/42	0/3/3/3
50	5MU	9	814	50	-	0/7/25/26	0/2/2/2
1	B8W	5	4129	1	-	2/5/27/28	0/3/3/3
50	4AC	9	1337	50	-	0/11/29/30	0/2/2/2
1	PSU	5	2508	1	-	0/7/25/26	0/2/2/2
6	MLZ	C	333	6	-	2/7/8/10	-
1	2MG	5	729	1	-	2/5/27/28	0/3/3/3
1	OMC	5	4536	1	-	0/9/27/28	0/2/2/2
1	7MG	5	4550	1	-	0/7/37/38	0/3/3/3
1	PSU	5	3729	1	-	2/7/25/26	0/2/2/2
50	OMG	9	644	50	-	1/5/27/28	0/3/3/3
50	PSU	9	1243	84,50	-	2/7/25/26	0/2/2/2
50	OMC	9	1710	50	-	0/9/27/28	0/2/2/2
1	OMC	5	2861	1	-	0/9/27/28	0/2/2/2
1	5MC	5	3782	1	-	0/7/25/26	0/2/2/2
1	PSU	5	4500	1	-	3/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	5	4450	84,1	-	3/7/25/26	0/2/2/2
1	OMC	5	3701	84,1	-	4/9/27/28	0/2/2/2
1	I4U	5	4194	1	-	4/9/29/30	0/2/2/2
1	OMG	5	4370	1	-	0/5/27/28	0/3/3/3
1	OMC	5	2365	1	-	0/9/27/28	0/2/2/2
1	PSU	5	4636	1	-	4/7/25/26	0/2/2/2
1	B9B	5	2754	84,1	-	1/7/29/30	0/3/3/3
1	P7G	5	1909	1	-	3/10/40/41	0/3/3/3
1	B8T	5	4671	1	-	0/7/27/28	0/2/2/2
1	UR3	5	1866	1	-	1/7/25/26	0/2/2/2
50	OMG	9	683	50	-	2/5/27/28	0/3/3/3
1	6MZ	5	4220	1	-	0/5/27/28	0/3/3/3
1	2MG	5	4872	1	-	1/5/27/28	0/3/3/3
50	A2M	9	668	84,50	-	4/5/27/28	0/3/3/3
1	A2M	5	3785	1	-	2/5/27/28	0/3/3/3
48	DDE	v	715	48	-	15/20/21/23	0/1/1/1
50	E3C	9	568	50	-	4/9/44/45	0/2/2/2
50	6MZ	9	1832	84,50	-	2/5/27/28	0/3/3/3
1	1MA	5	4415	1	-	2/3/25/26	0/3/3/3
50	B8Q	9	1219	50	-	0/7/42/43	0/2/2/2
1	M7A	5	4564	1	-	0/7/37/38	0/3/3/3
50	PSU	9	119	50	-	2/7/25/26	0/2/2/2
1	A2M	5	2363	84,1	-	0/5/27/28	0/3/3/3
1	E6G	5	4355	1	-	5/6/28/29	0/3/3/3
50	PSU	9	823	50	-	0/7/25/26	0/2/2/2
1	B8H	5	1860	1	-	2/7/25/26	0/2/2/2
50	UR3	9	1830	50	-	4/7/25/26	0/2/2/2
1	B8W	5	2380	1	-	5/5/27/28	0/3/3/3
50	M7A	9	1806	50	-	0/7/37/38	0/3/3/3
1	PSU	5	4531	1	-	0/7/25/26	0/2/2/2
1	B9H	5	2786	1	-	3/12/47/48	0/2/2/2
1	7MG	5	2522	1	-	0/7/37/38	0/3/3/3
1	A2M	5	4523	84,1	-	2/5/27/28	0/3/3/3
1	A2M	5	3867	1	-	4/5/27/28	0/3/3/3
1	PSU	5	4403	1	-	2/7/25/26	0/2/2/2
1	OMG	5	2050	1	-	0/5/27/28	0/3/3/3
1	OMG	5	2424	1	-	2/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	5	4196	1	-	0/5/27/28	0/3/3/3
1	OMG	5	2773	1	-	0/5/27/28	0/3/3/3
1	P7G	5	3880	1	-	3/10/40/41	0/3/3/3
50	A2M	9	1031	50	-	0/5/27/28	0/3/3/3
1	PSU	5	3764	1	-	2/7/25/26	0/2/2/2
50	MA6	9	1850	50	-	1/7/29/30	0/3/3/3
1	UR3	5	4530	1	-	1/7/25/26	0/2/2/2
1	B9B	5	1574	1	-	3/7/29/30	0/3/3/3
1	OMU	5	4620	1	-	0/9/27/28	0/2/2/2
50	A2M	9	166	50	-	2/5/27/28	0/3/3/3
1	PSU	5	1683	1	-	0/7/25/26	0/2/2/2
1	OMC	5	2422	84,1	-	0/9/27/28	0/2/2/2
1	B8W	5	4529	84,1	-	2/5/27/28	0/3/3/3
1	B9B	5	237	1	-	4/7/29/30	0/3/3/3
1	OMG	5	373	1	-	1/5/27/28	0/3/3/3
1	OMG	5	1316	1	-	0/5/27/28	0/3/3/3
1	A2M	5	3723	1	-	0/5/27/28	0/3/3/3
1	I4U	5	1659	1	-	2/9/29/30	0/2/2/2
1	A2M	5	398	1	-	2/5/27/28	0/3/3/3
1	A2M	5	1534	84,1	-	1/5/27/28	0/3/3/3
50	B8N	9	1248	84,50	-	2/16/34/35	0/2/2/2
1	2MG	5	1517	1	-	0/5/27/28	0/3/3/3
50	PSU	9	1081	50	-	3/7/25/26	0/2/2/2
1	OMG	5	2364	1	-	2/5/27/28	0/3/3/3
1	A2M	5	1524	1	-	0/5/27/28	0/3/3/3
1	7MG	5	1605	1	-	0/7/37/38	0/3/3/3
1	A2M	5	4571	1	-	0/5/27/28	0/3/3/3
50	OMU	9	116	50	-	3/9/27/28	0/2/2/2
3	OMU	8	14	3,1	-	1/9/27/28	0/2/2/2
1	PSU	5	4442	1	-	0/7/25/26	0/2/2/2
1	OMG	5	1625	84,1	-	3/5/27/28	0/3/3/3
1	1MA	5	1322	84,1	-	0/3/25/26	0/3/3/3
50	OMU	9	121	50	-	2/9/27/28	0/2/2/2
50	PSU	9	822	50	-	2/7/25/26	0/2/2/2
1	E7G	5	2297	1	-	1/9/39/40	0/3/3/3
50	MA6	9	1851	50	-	3/7/29/30	0/3/3/3
1	PSU	5	4628	1	-	0/7/25/26	0/2/2/2
1	A2M	5	1871	84,1	-	0/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	5	1677	1	-	2/7/25/26	0/2/2/2
1	B8K	5	3897	1	-	3/11/41/42	0/3/3/3
50	A2M	9	159	50	-	3/5/27/28	0/3/3/3
1	OMU	5	4306	1	-	1/9/27/28	0/2/2/2
41	MLZ	m	72	41	-	3/7/8/10	-
1	OMG	5	4494	1	-	2/5/27/28	0/3/3/3
50	OMC	9	1703	50	-	2/9/27/28	0/2/2/2
50	A2M	9	27	84,50	-	0/5/27/28	0/3/3/3
1	PSU	5	1582	1	-	2/7/25/26	0/2/2/2
1	B8W	5	4185	1	-	4/5/27/28	0/3/3/3
1	B8Q	5	1456	1	-	2/7/42/43	0/2/2/2
1	OMG	5	1883	1	-	0/5/27/28	0/3/3/3
1	OMC	5	2804	1	-	0/9/27/28	0/2/2/2
1	B8W	5	4472	1	-	2/5/27/28	0/3/3/3
1	PSU	5	3715	1	-	0/7/25/26	0/2/2/2
1	P4U	5	1348	84,1	-	4/10/29/30	0/2/2/2
50	A2M	9	1678	50	-	0/5/27/28	0/3/3/3
50	OMG	9	509	84,50	-	0/5/27/28	0/3/3/3
1	A2M	5	1326	1	-	0/5/27/28	0/3/3/3
1	OMG	5	4623	1	-	0/5/27/28	0/3/3/3
1	OMG	5	4870	1	-	4/5/27/28	0/3/3/3
1	A2M	5	3718	1	-	0/5/27/28	0/3/3/3
1	PSU	5	4293	1	-	0/7/25/26	0/2/2/2
1	OMG	5	3792	1	-	2/5/27/28	0/3/3/3

The worst 5 of 930 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	237	B9B	O4'-C1'	18.41	1.65	1.40
1	5	1574	B9B	O4'-C1'	18.07	1.64	1.40
1	5	2754	B9B	O4'-C1'	18.02	1.64	1.40
1	5	3723	A2M	O4'-C1'	17.79	1.64	1.40
1	5	4523	A2M	O4'-C1'	17.66	1.64	1.40

The worst 5 of 643 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	4529	B8W	N2-C2-N3	17.85	145.65	117.79
1	5	4129	B8W	N2-C2-N3	17.71	145.43	117.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	4185	B8W	N2-C2-N3	17.48	145.08	117.79
1	5	2380	B8W	N2-C2-N3	17.43	145.01	117.79
1	5	4472	B8W	N2-C2-N3	16.65	143.78	117.79

There are no chirality outliers.

5 of 211 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	5	237	B9B	C5-C6-O6-C61
1	5	237	B9B	N1-C6-O6-C61
1	5	237	B9B	O4'-C4'-C5'-O5'
1	5	1348	P4U	N3-C4-O4-C41
1	5	1582	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 307 ligands modelled in this entry, 306 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
86	GDP	v	900	-	25,30,30	0.90	1 (4%)	30,47,47	1.39	5 (16%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	GDP	v	900	-	-	0/12/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	v	900	GDP	C6-N1	-2.51	1.34	1.37

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	v	900	GDP	C4'-O4'-C1'	-3.68	106.56	109.92
86	v	900	GDP	C8-N7-C5	2.86	107.41	102.55
86	v	900	GDP	C5-C6-N1	2.28	118.42	114.07
86	v	900	GDP	O4'-C1'-N9	2.22	111.69	108.75
86	v	900	GDP	O6-C6-C5	-2.04	120.27	124.32

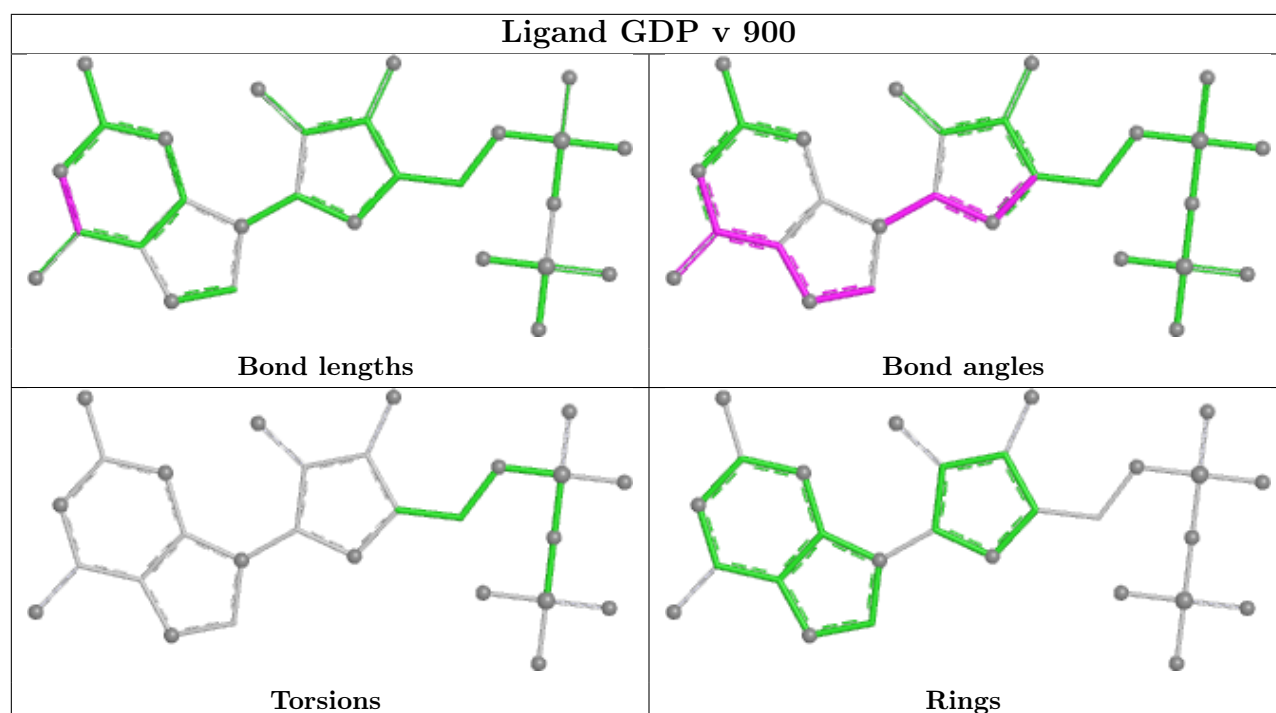
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	49
50	9	18
49	w	1
48	v	1
3	8	1

The worst 5 of 70 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	w	225:LEU	C	282:THR	N	57.95
1	5	2113:G	O3'	2258:C	P	39.61
1	5	1252:C	O3'	1271:G	P	35.94
1	5	1405:C	O3'	1406:G	P	22.80
1	5	1406(C):G	O3'	1411:C	P	20.78

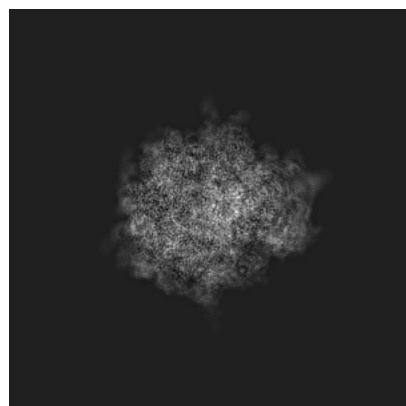
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9242. These allow visual inspection of the internal detail of the map and identification of artifacts.

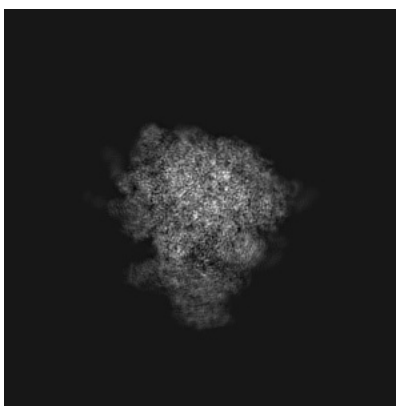
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

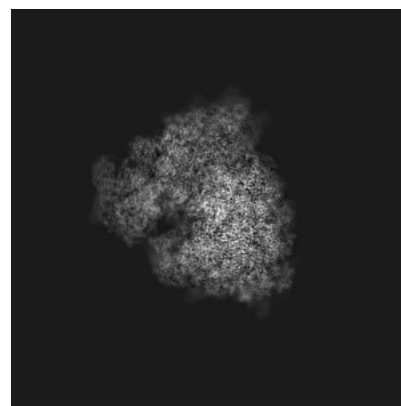
6.1.1 Primary map



X

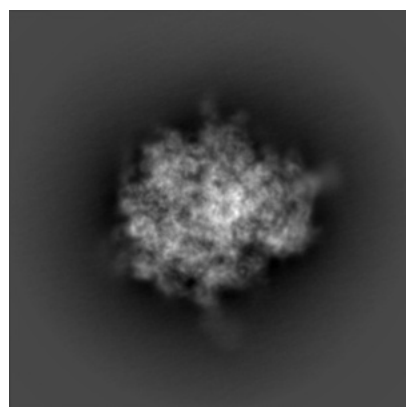


Y

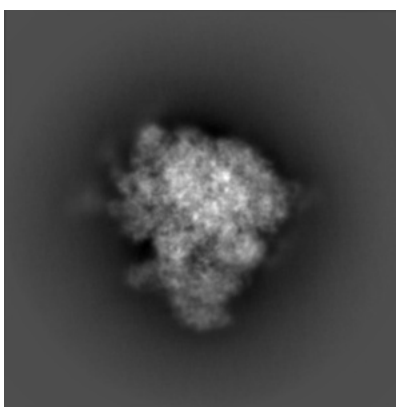


Z

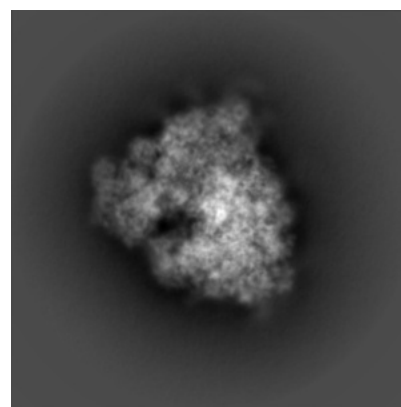
6.1.2 Raw map



X



Y

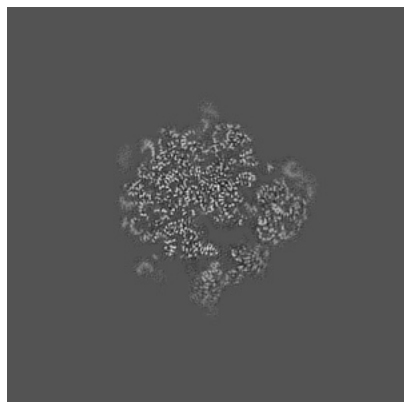


Z

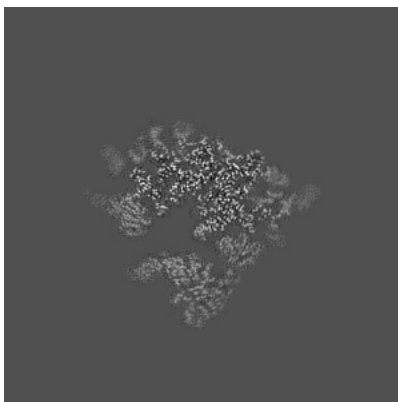
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

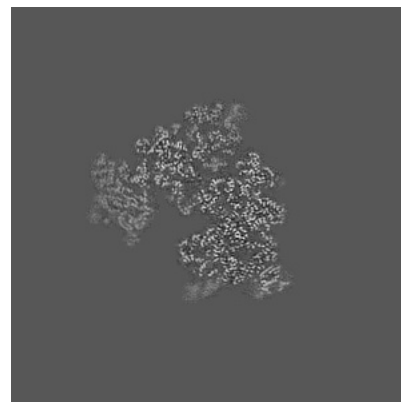
6.2.1 Primary map



X Index: 200

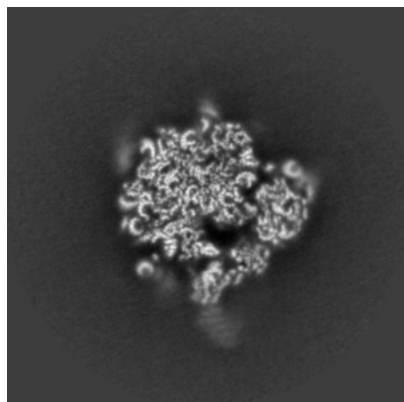


Y Index: 200

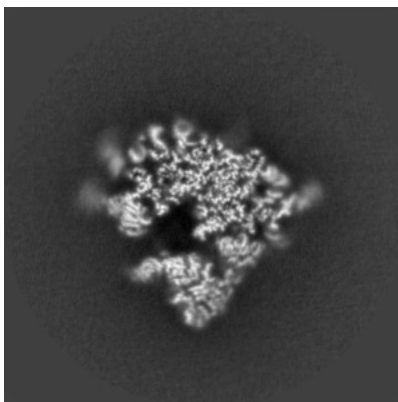


Z Index: 200

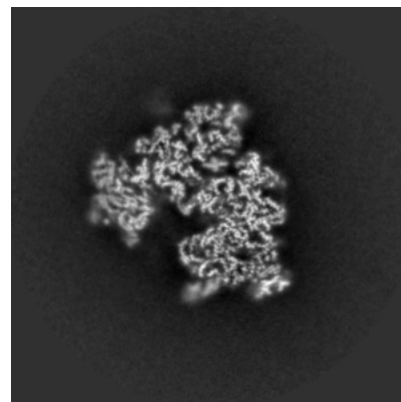
6.2.2 Raw map



X Index: 200



Y Index: 200

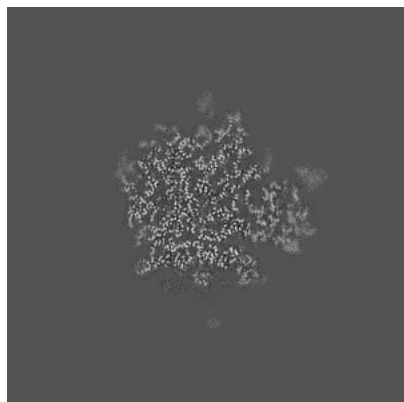


Z Index: 200

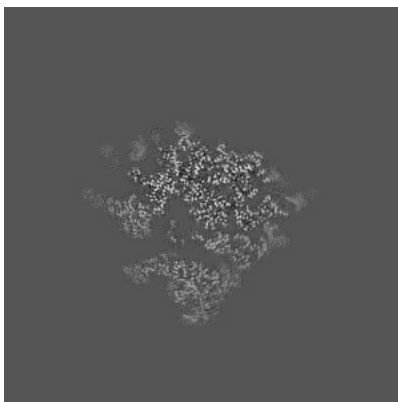
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

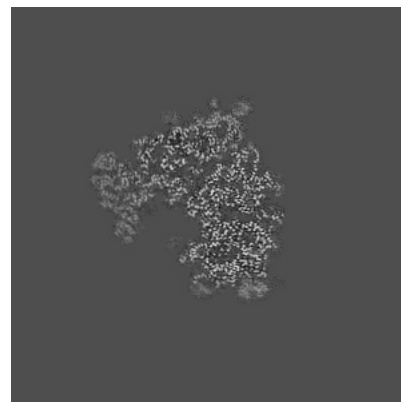
6.3.1 Primary map



X Index: 213

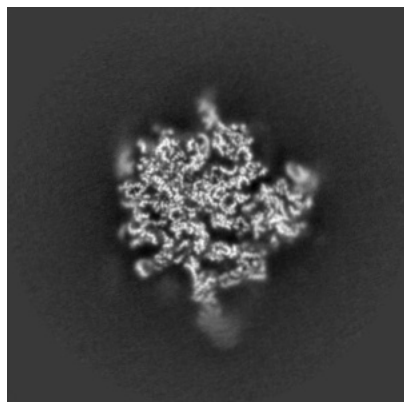


Y Index: 206

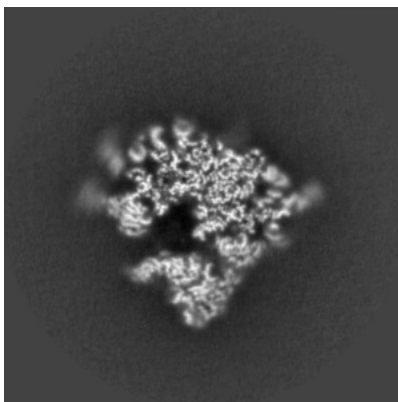


Z Index: 210

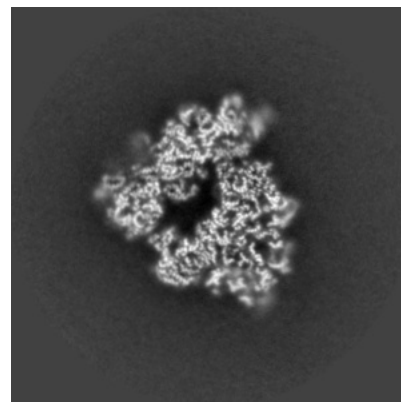
6.3.2 Raw map



X Index: 206



Y Index: 201

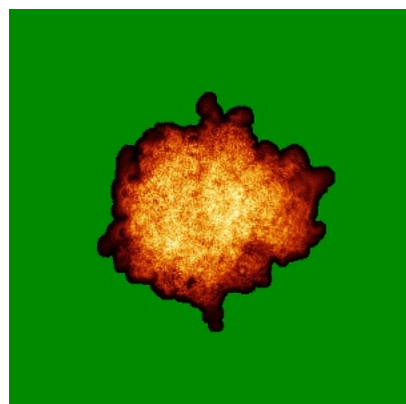


Z Index: 176

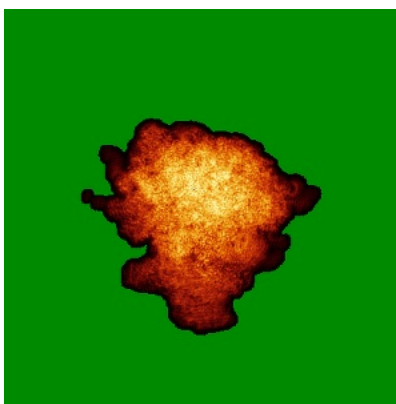
The images above show the largest variance slices of the map in three orthogonal directions.

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

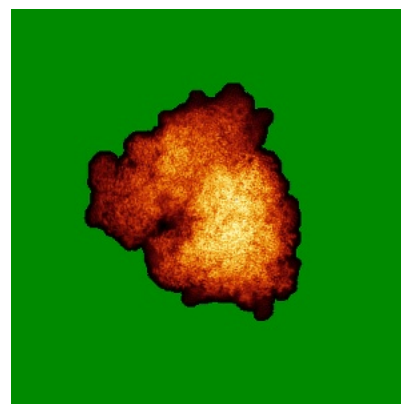
6.4.1 Primary map



X

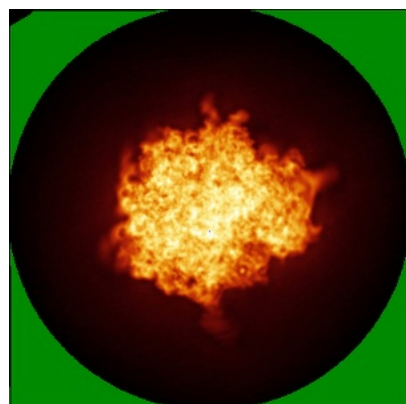


Y

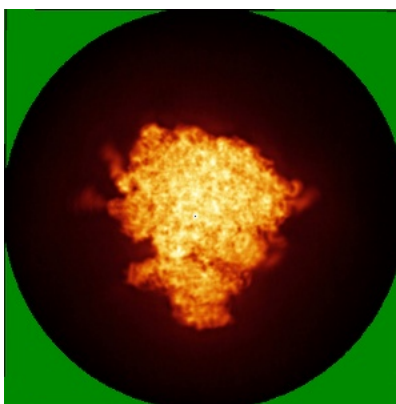


Z

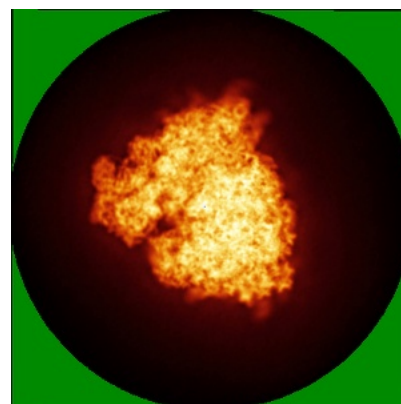
6.4.2 Raw map



X



Y

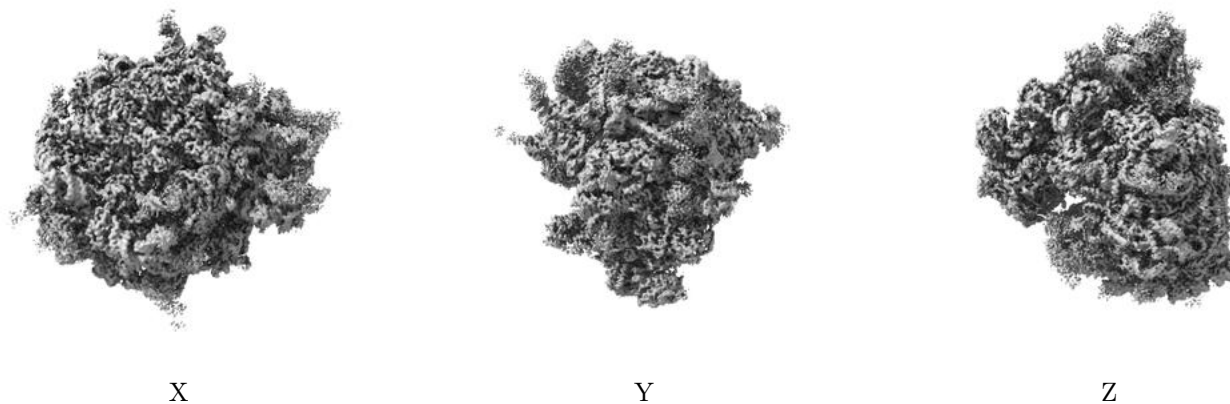


Z

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

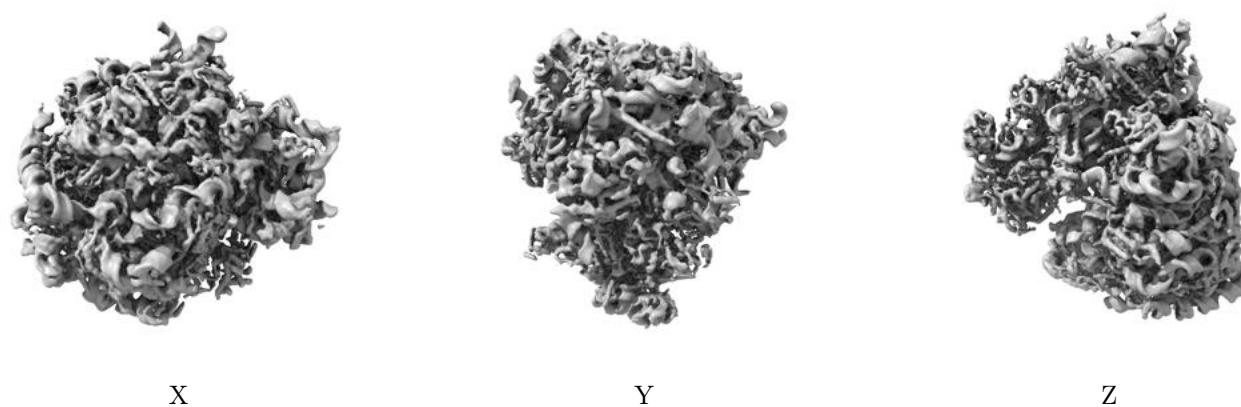
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.08. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

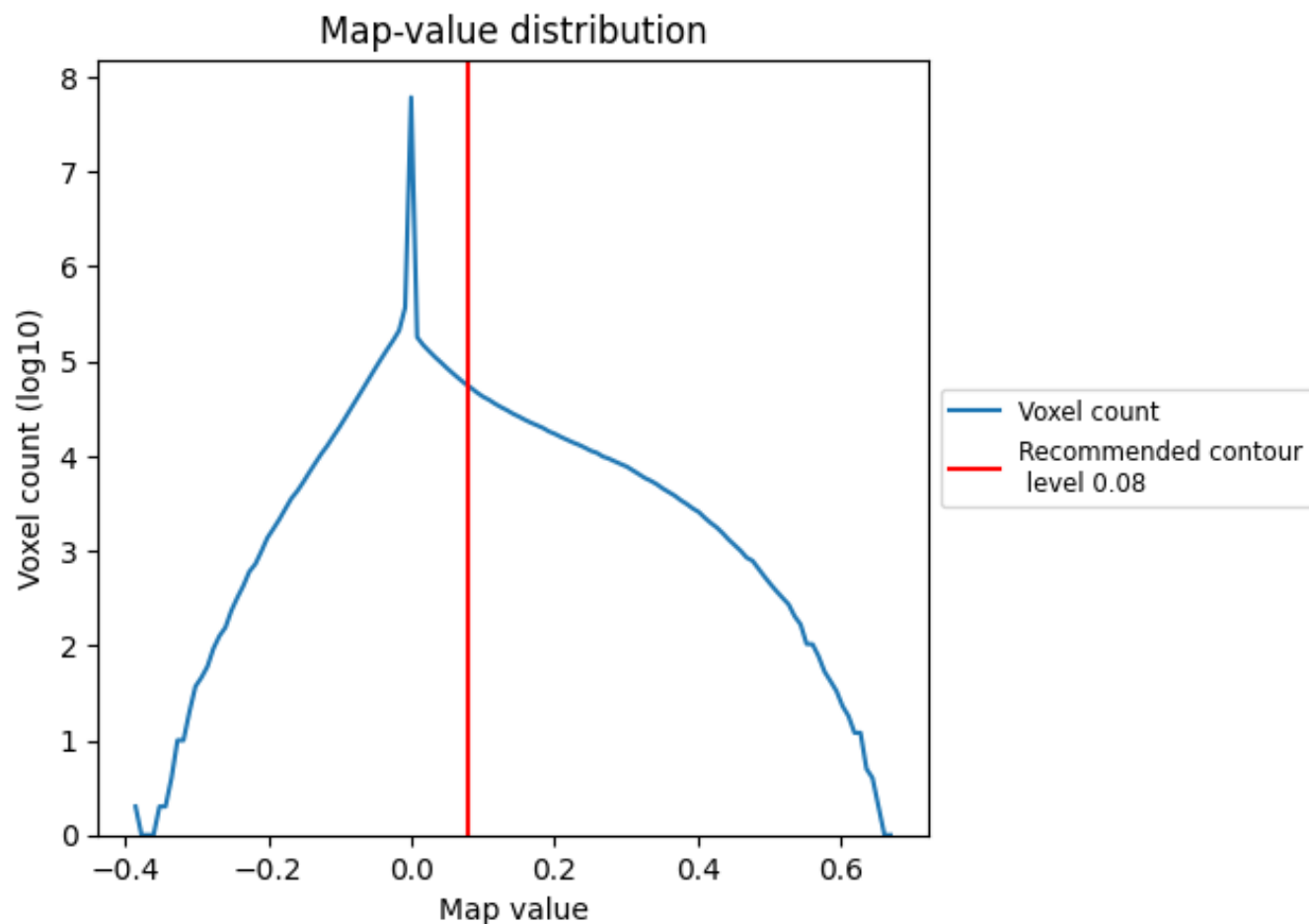
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

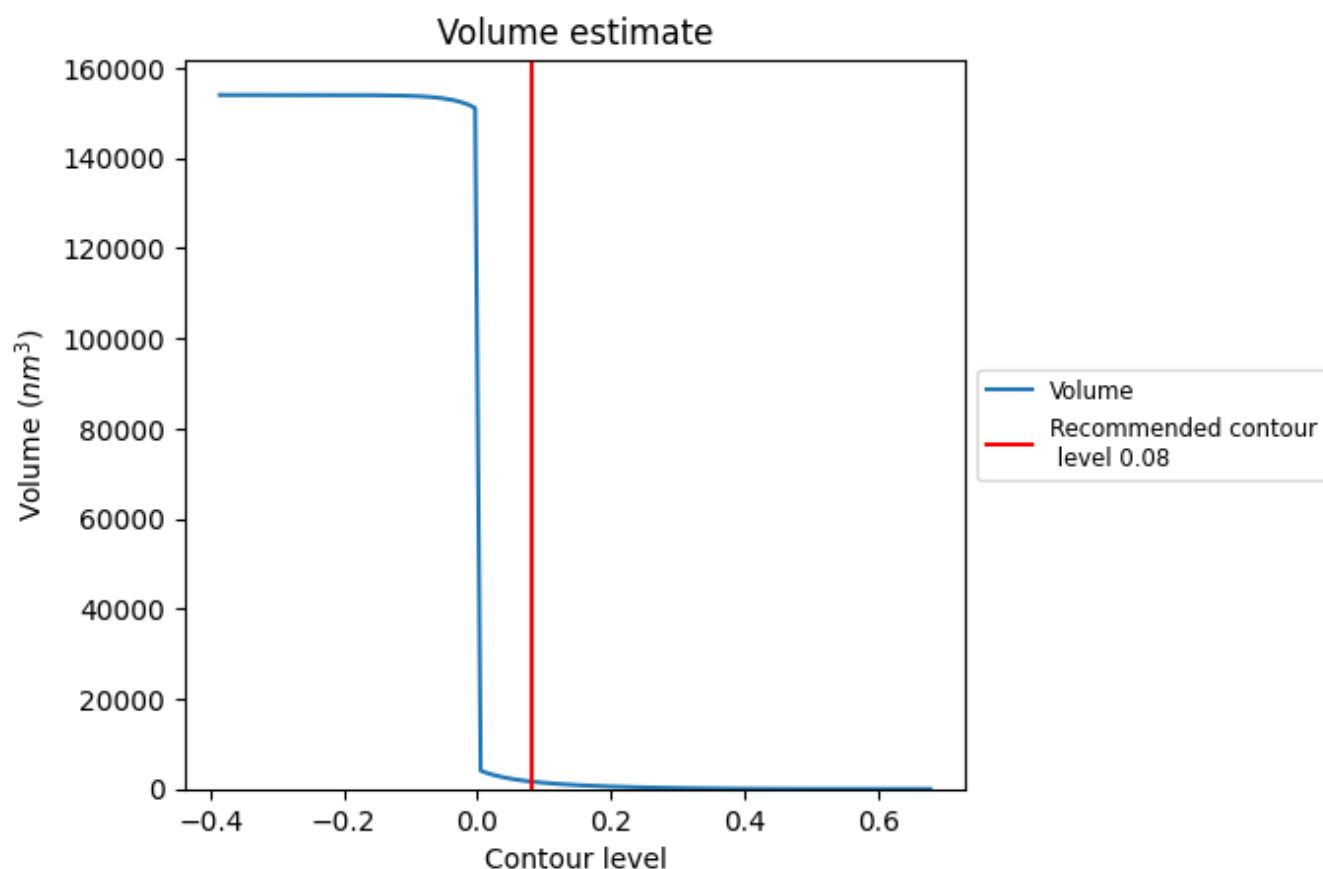
This section contains the results of statistical analysis of the map.

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.

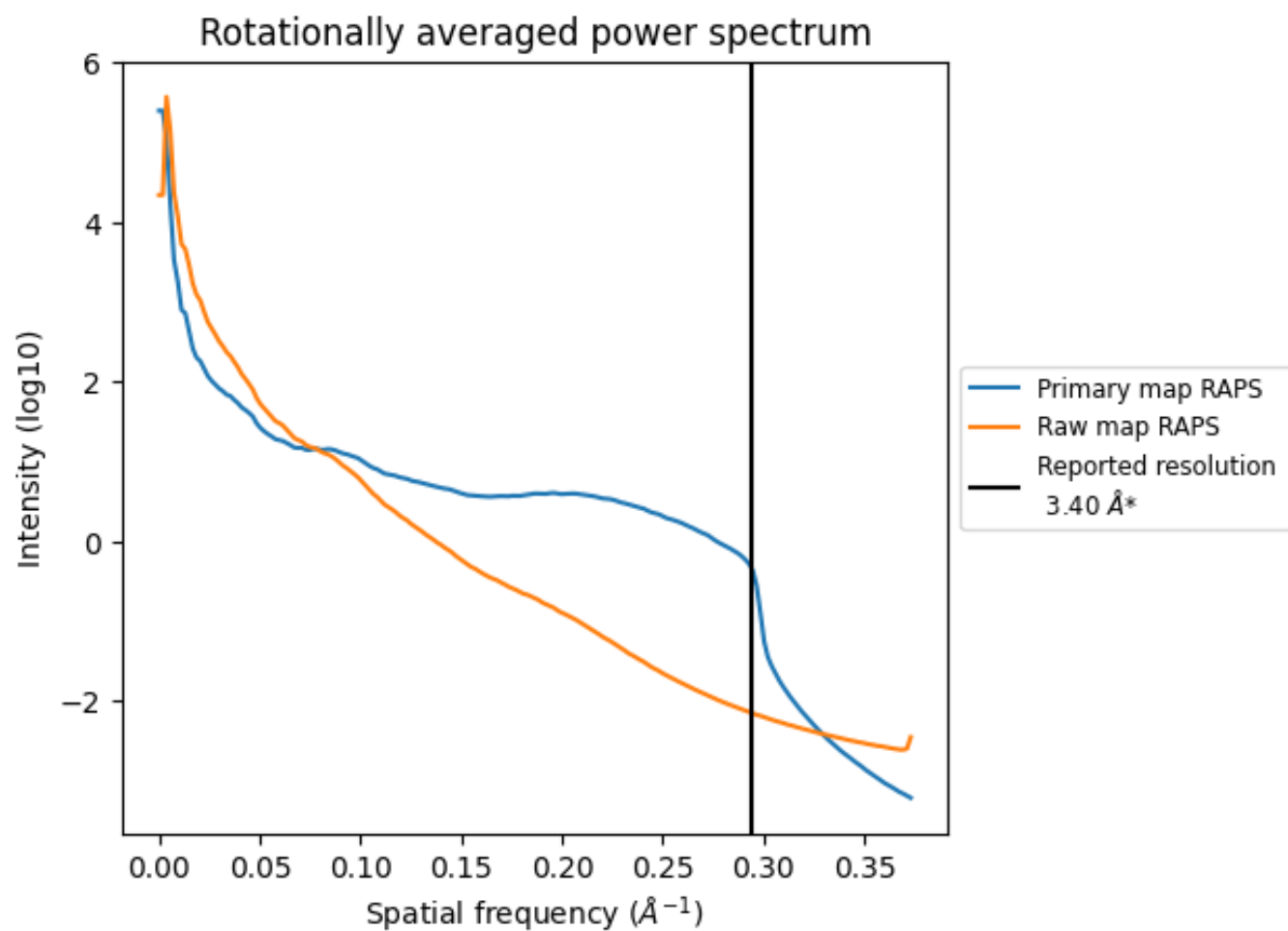
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1651 nm³; this corresponds to an approximate mass of 1492 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 ⓘ

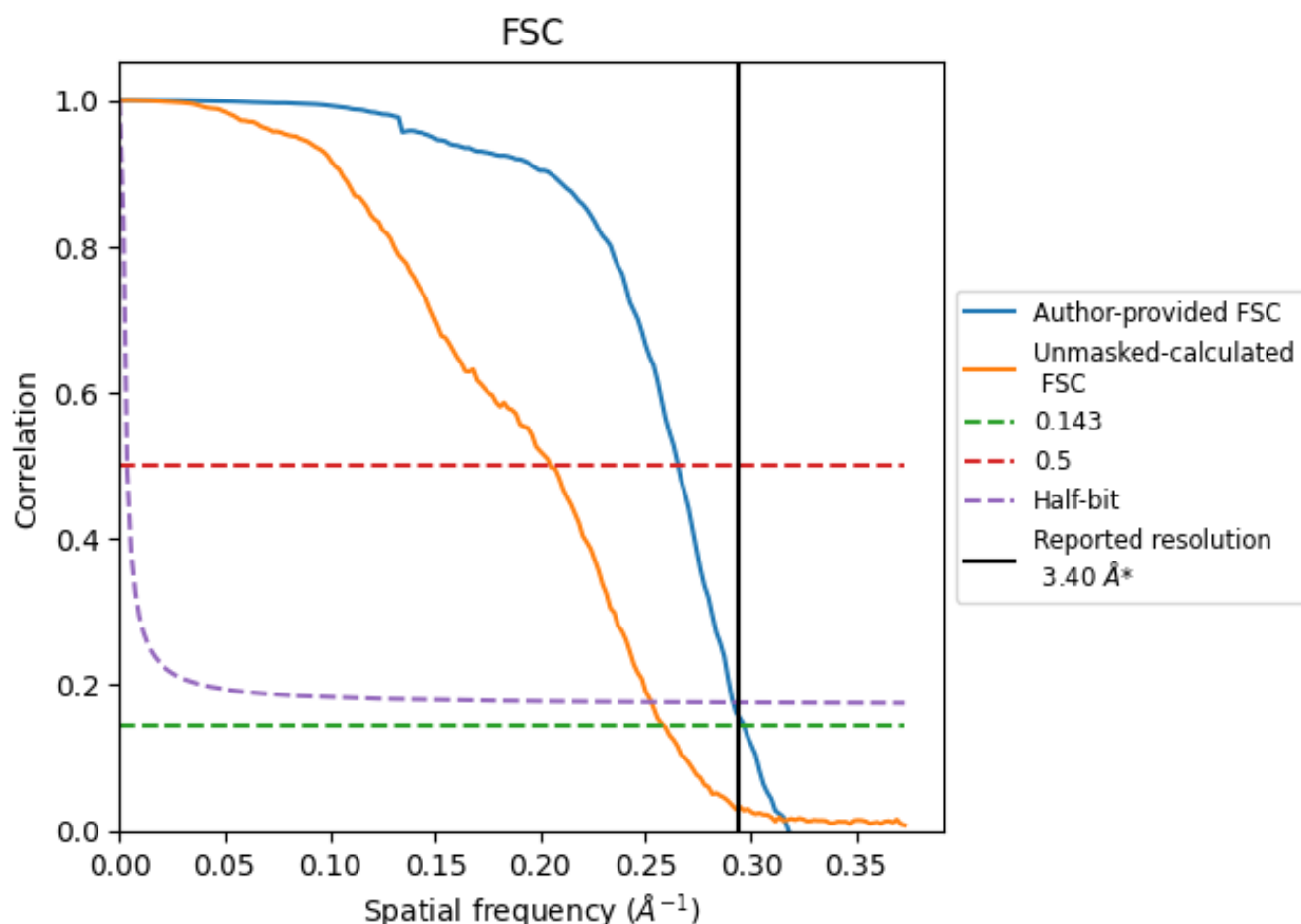


*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

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 0.294 \AA^{-1}

8.2 Resolution estimates [i](#)

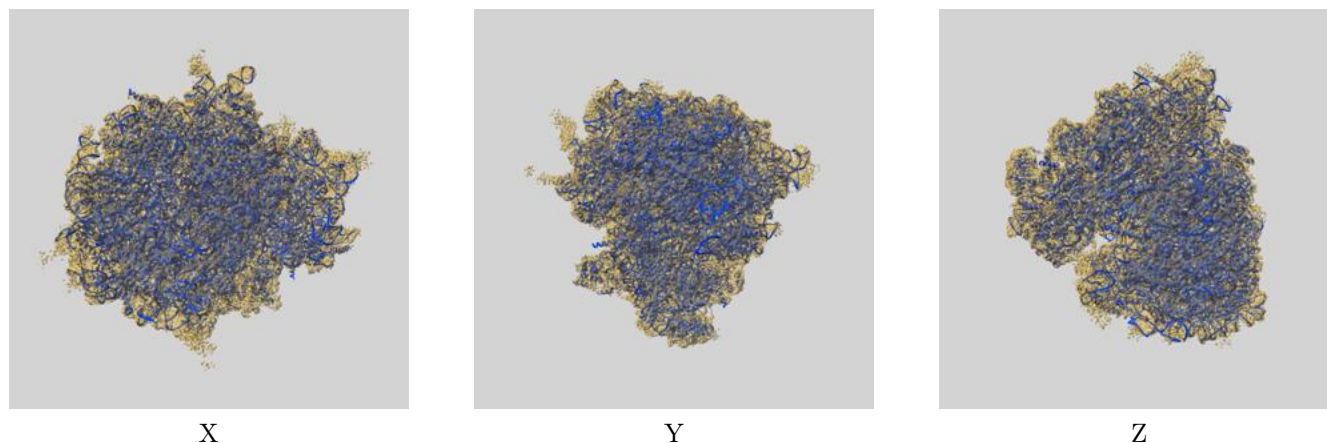
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.37	3.77	3.43
Unmasked-calculated*	3.86	4.89	3.96

*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 3.86 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

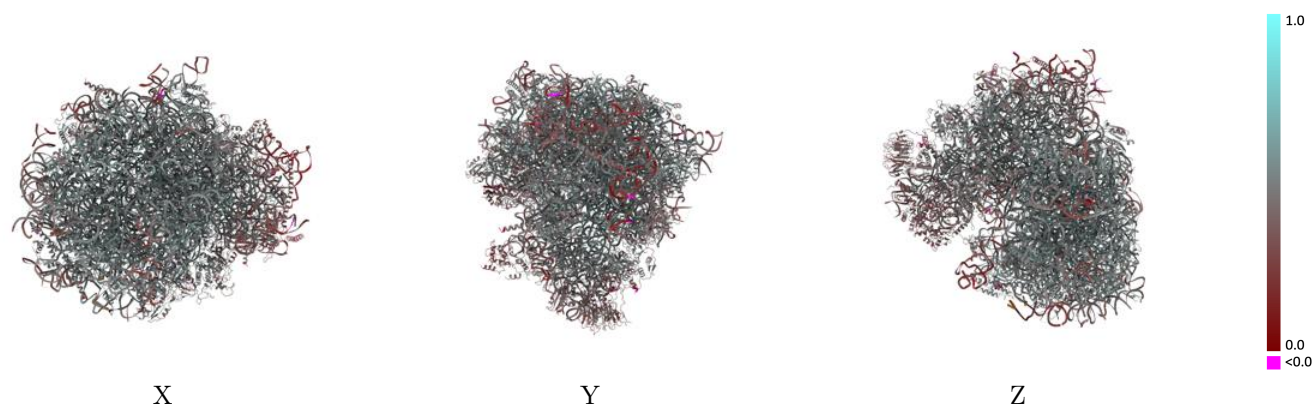
This section contains information regarding the fit between EMDB map EMD-9242 and PDB model 6MTE. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



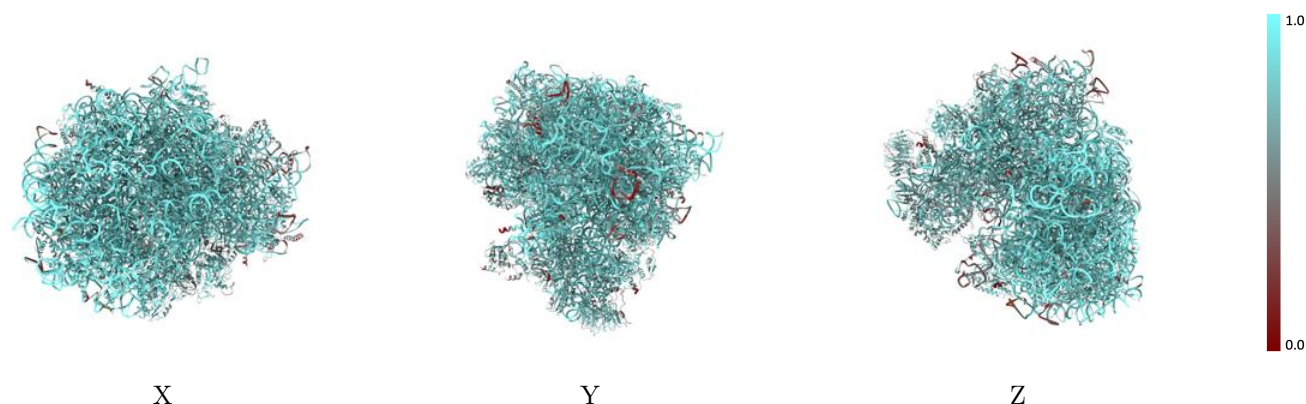
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



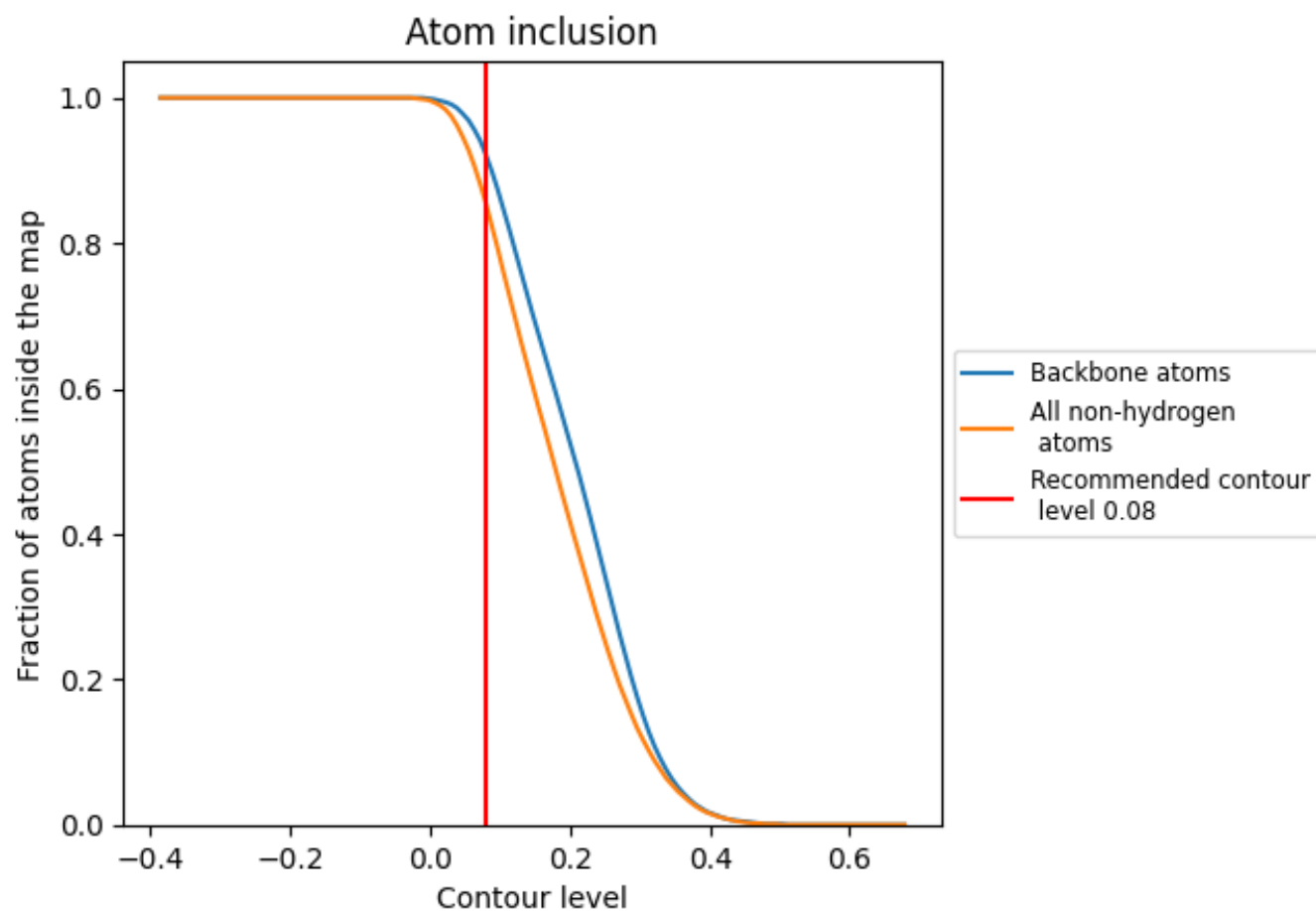
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.08).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 85% 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 (0.08) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8540	 0.4760
5	 0.9160	 0.4870
7	 0.9630	 0.5120
8	 0.9260	 0.4850
9	 0.8930	 0.4420
A	 0.8580	 0.5490
AA	 0.7840	 0.4740
B	 0.8840	 0.5420
BB	 0.7010	 0.4310
C	 0.8660	 0.5310
CC	 0.8250	 0.5120
D	 0.8470	 0.5020
DD	 0.7130	 0.4450
E	 0.8540	 0.5080
EE	 0.7990	 0.4840
F	 0.8580	 0.5320
FF	 0.6030	 0.3480
G	 0.7970	 0.4890
GG	 0.6660	 0.3620
H	 0.8510	 0.5290
HH	 0.7240	 0.4390
I	 0.8530	 0.5330
II	 0.7240	 0.4290
J	 0.8260	 0.4880
JJ	 0.8100	 0.4880
KK	 0.7510	 0.4370
L	 0.8290	 0.5080
LL	 0.7740	 0.4820
M	 0.8610	 0.5280
MM	 0.5280	 0.2930
N	 0.8910	 0.5470
NN	 0.7690	 0.4710
O	 0.8740	 0.5320
OO	 0.7360	 0.4470
P	 0.8560	 0.5340

















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Chain	Atom inclusion	Q-score
PP	 0.6710	 0.3650
Q	 0.8590	 0.5360
QQ	 0.6820	 0.3980
R	 0.8140	 0.5060
RR	 0.6740	 0.4170
S	 0.8830	 0.5440
SS	 0.6520	 0.3520
T	 0.8360	 0.5270
TT	 0.6810	 0.3710
U	 0.8010	 0.4710
UU	 0.7160	 0.4240
V	 0.8540	 0.5480
VV	 0.8140	 0.4980
W	 0.6740	 0.4520
WW	 0.8450	 0.5270
X	 0.8250	 0.5210
XX	 0.8390	 0.5340
Y	 0.8440	 0.5140
YY	 0.7620	 0.4410
Z	 0.8460	 0.5110
ZZ	 0.5710	 0.3140
a	 0.8810	 0.5420
aa	 0.7650	 0.4840
b	 0.7370	 0.4590
bb	 0.7340	 0.4710
c	 0.8090	 0.4910
cc	 0.5720	 0.3790
d	 0.8320	 0.5150
dd	 0.8230	 0.4670
e	 0.8550	 0.5450
ee	 0.7440	 0.4750
f	 0.8910	 0.5500
ff	 0.5900	 0.3200
g	 0.8280	 0.5230
gg	 0.6550	 0.3720
h	 0.8330	 0.5160
i	 0.8180	 0.4960
j	 0.9040	 0.5430
k	 0.8020	 0.4920
l	 0.8430	 0.5220
m	 0.8660	 0.5360
n	 0.7570	 0.5070

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Chain	Atom inclusion	Q-score
o	 0.8400	 0.5420
p	 0.8040	 0.5270
r	 0.8780	 0.5310
s	 0.7500	 0.4490
t	 0.5360	 0.3330
v	 0.7430	 0.4550
w	 0.6220	 0.4480