



wwPDB EM Validation Summary Report ⓘ

Nov 8, 2022 – 09:52 AM 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:

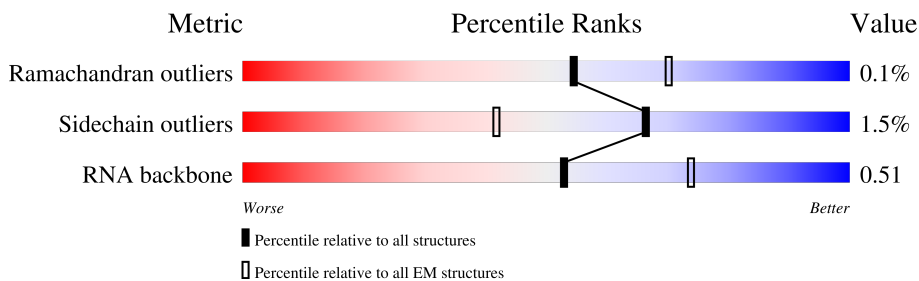
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	

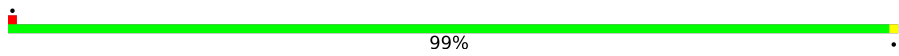
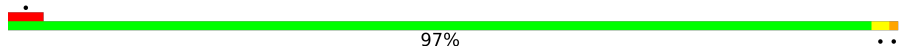
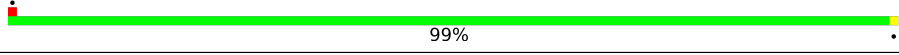
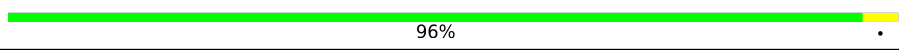
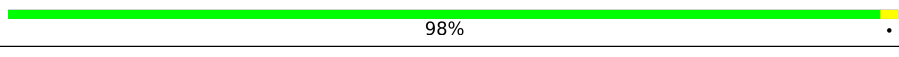
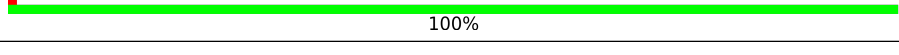
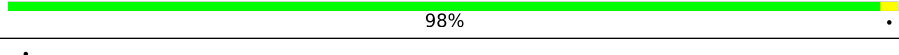
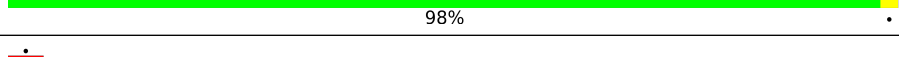
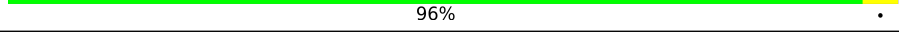
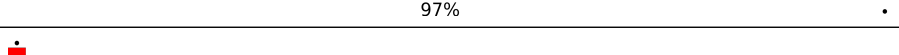
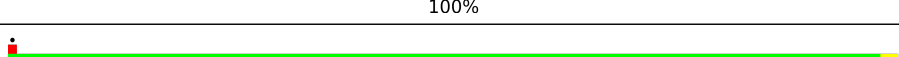
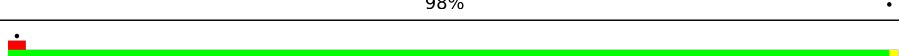
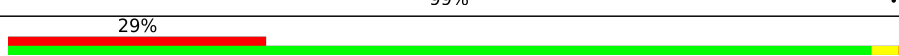
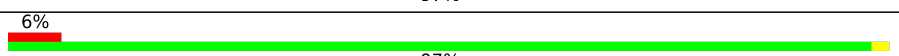
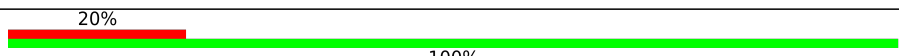
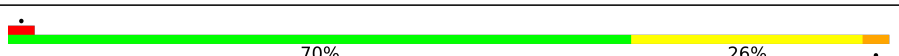
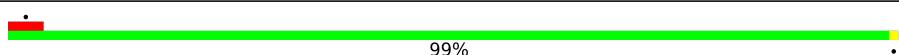
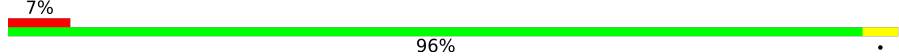
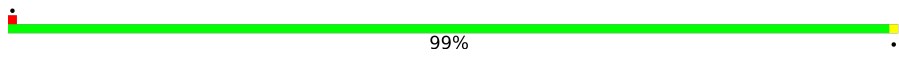
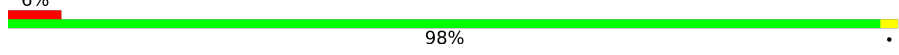
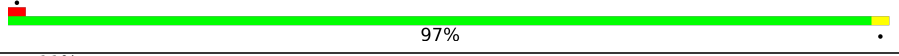
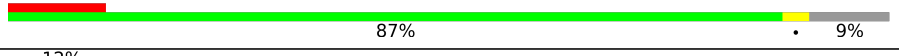
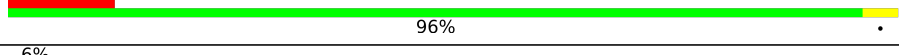
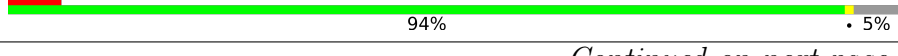

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Mol	Chain	Length	Quality of chain
9	F	225	99%
10	G	319	71% 27%
11	H	190	99%
12	I	214	94%
13	J	170	99%
14	L	210	98%
15	M	138	99%
16	N	203	97%
17	O	199	98%
18	P	153	98%
19	Q	187	99%
20	R	180	99%
21	S	176	98%
22	T	159	97%
23	U	99	99%
24	V	131	98%
25	W	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	12% 97%
60	JJ	185	98%
61	KK	96	98%
62	LL	158	6% 89% 9%
63	MM	117	32% 97%
64	NN	149	99%
65	OO	136	7% 99%
66	PP	125	12% 94% 6%
67	QQ	142	6% 98%
68	RR	132	8% 97%
69	SS	144	15% 97%
70	TT	141	7% 98%
71	UU	100	9% 99%
72	VV	83	98%
73	WW	129	98%
74	XX	141	96%
75	YY	124	98%
76	ZZ	75	19% 100%
77	aa	101	99%
78	bb	83	6% 100%
79	cc	62	23% 95% 5%
80	dd	55	96%
81	ee	55	13% 95% 5%
82	ff	68	26% 99%
83	gg	313	11% 98%

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
			Total	C	N	O	P		
1	5	3597	77254	34469	14127	25061	3597	0	0

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

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

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

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

- Molecule 4 is a protein called uL2.

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

- Molecule 5 is a protein called uL3.

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

- Molecule 6 is a protein called uL4.

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

- Molecule 7 is a protein called uL18.

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

- Molecule 8 is a protein called eL6.

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

- Molecule 9 is a protein called uL30.

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

- Molecule 10 is a protein called eL8.

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

- Molecule 11 is a protein called uL6.

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

- Molecule 12 is a protein called uL16.

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

- Molecule 13 is a protein called uL5.

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

- 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
			Total	C	N	O	S		
21	S	176	1462	930	285	236	11	0	0

- Molecule 22 is a protein called eL21.

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

- Molecule 23 is a protein called eL22.

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

- Molecule 24 is a protein called uL14.

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

- Molecule 25 is a protein called eL24.

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

- Molecule 26 is a protein called uL23.

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

- Molecule 27 is a protein called uL24.

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

- Molecule 28 is a protein called eL27.

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

- Molecule 29 is a protein called uL15.

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

- Molecule 30 is a protein called eL29.

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

- Molecule 31 is a protein called eL30.

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

- Molecule 32 is a protein called eL31.

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

- Molecule 33 is a protein called eL32.

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

- Molecule 34 is a protein called eL33.

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

- 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
			Total	C	N	O	S		
63	MM	117	908	570	161	169	8	0	0

- Molecule 64 is a protein called uS15.

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

- Molecule 65 is a protein called uS11.

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

- Molecule 66 is a protein called uS19.

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

- Molecule 67 is a protein called uS9.

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

- Molecule 68 is a protein called eS17.

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

- Molecule 69 is a protein called uS13.

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

- Molecule 70 is a protein called eS19.

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

- Molecule 71 is a protein called uS10.

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

- Molecule 72 is a protein called eS21.

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

- Molecule 73 is a protein called uS8.

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

- Molecule 74 is a protein called uS12.

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

- Molecule 75 is a protein called eS24.

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

- Molecule 76 is a protein called eS25.

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

- 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).

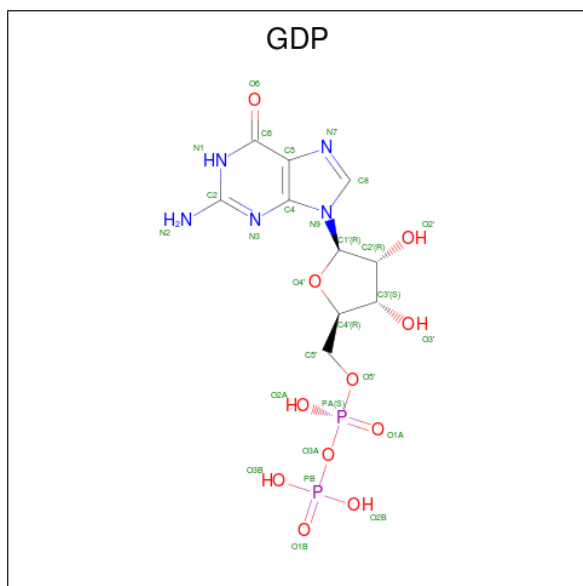
Mol	Chain	Residues	Atoms		AltConf
84	5	200	Total 200	Mg 200	0
84	7	7	Total 7	Mg 7	0
84	8	6	Total 6	Mg 6	0
84	A	1	Total 1	Mg 1	0
84	P	1	Total 1	Mg 1	0
84	V	1	Total 1	Mg 1	0
84	a	1	Total 1	Mg 1	0
84	j	1	Total 1	Mg 1	0
84	v	1	Total 1	Mg 1	0
84	9	78	Total 78	Mg 78	0
84	TT	1	Total 1	Mg 1	0

- 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).

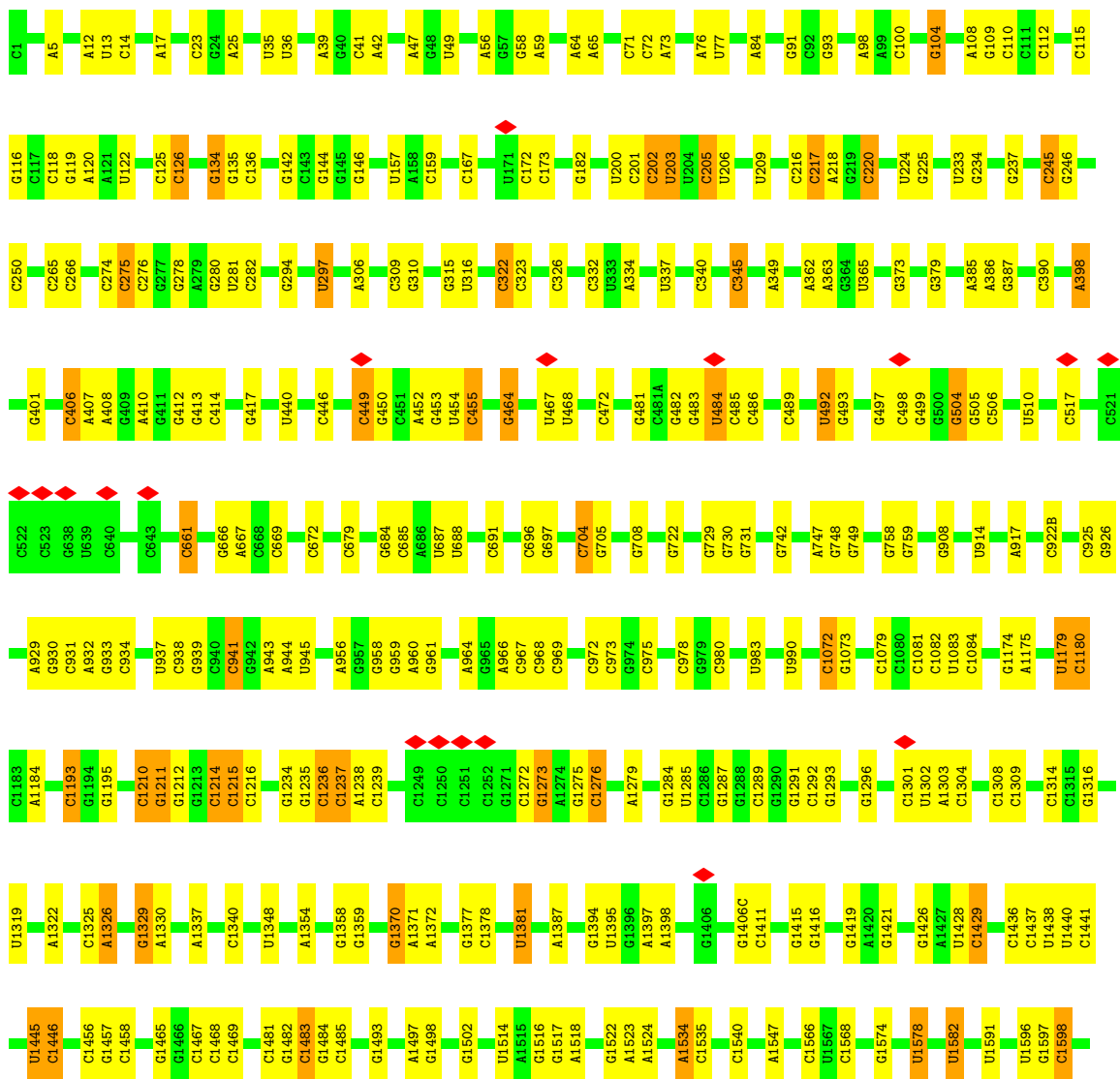


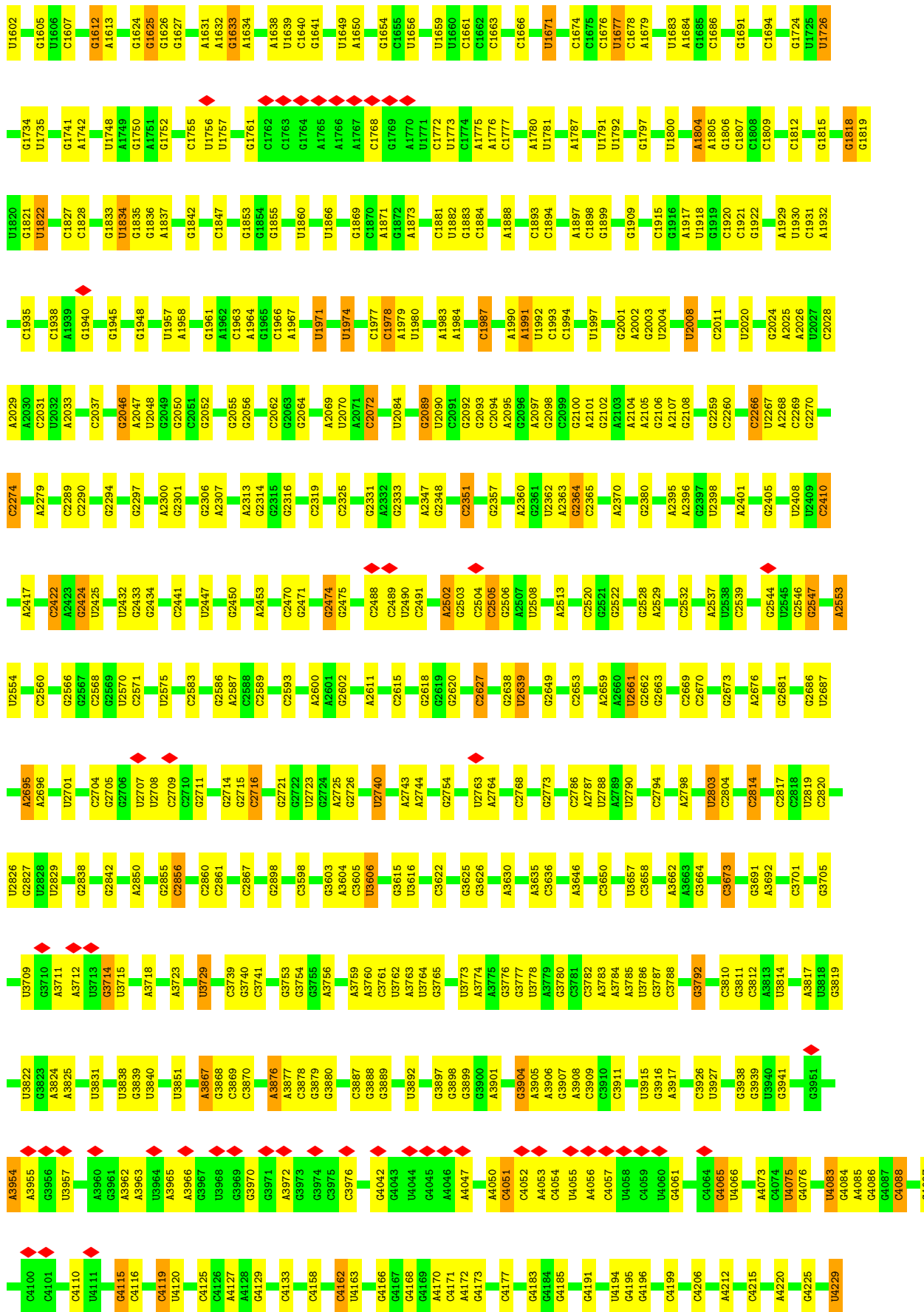
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
86	v	1	28	10	5	11	2	0

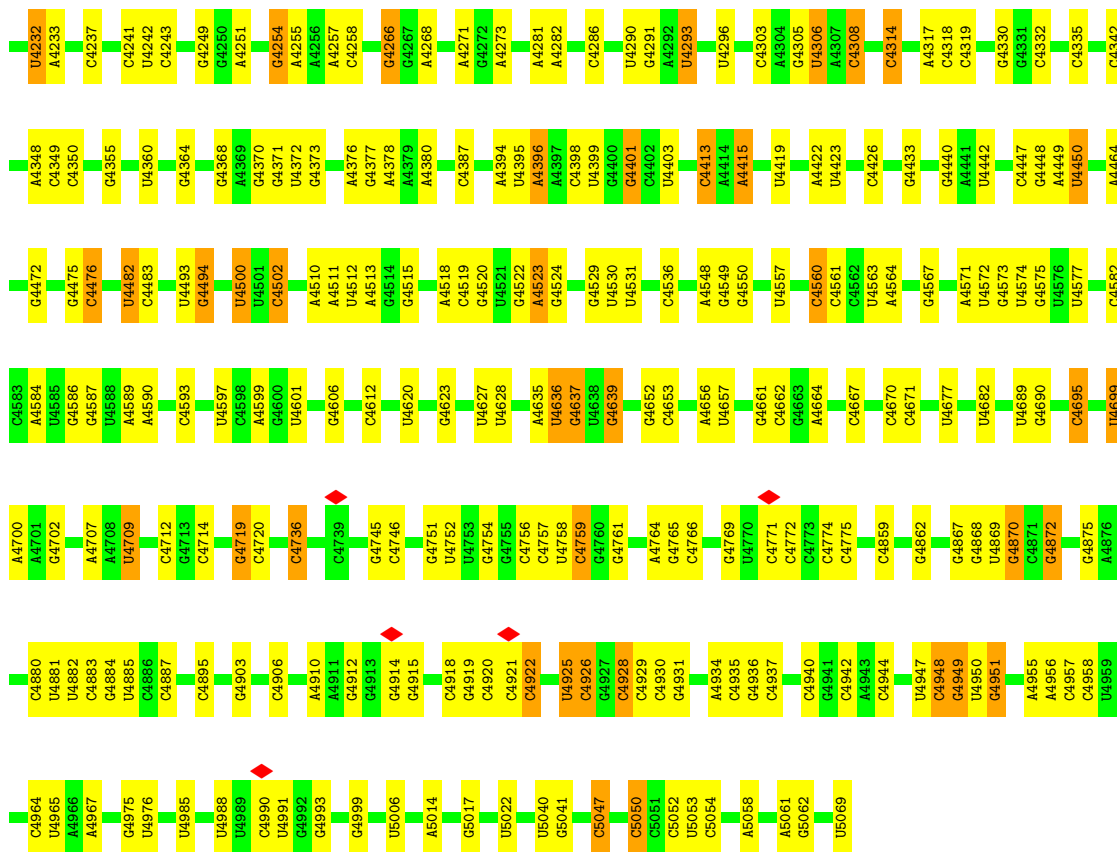
3 Residue-property plots [i](#)

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.

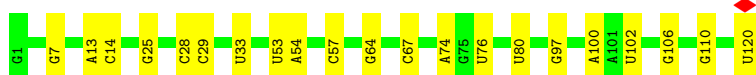
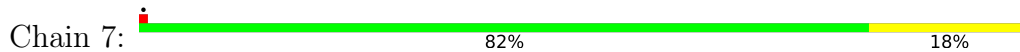
- Molecule 1: 28S rRNA



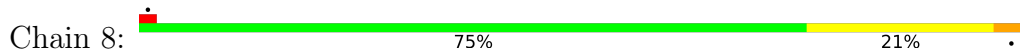




• Molecule 2: 5S rRNA



• Molecule 3: 5.8S rRNA



• Molecule 4: uL2



• Molecule 5: uL3

Chain B:  98%



• Molecule 6: uL4

Chain C:  98%



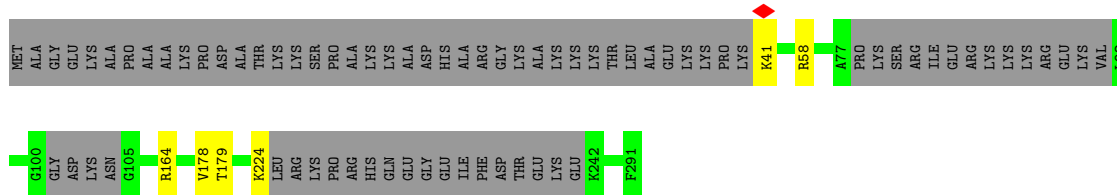
• Molecule 7: uL18

Chain D:  99%



• Molecule 8: eL6

Chain E:  72%



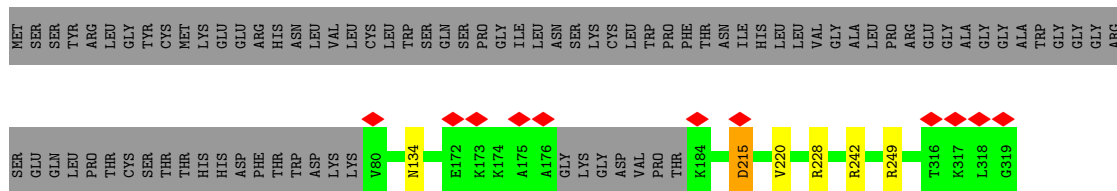
• Molecule 9: uL30

Chain F:  99%



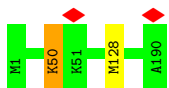
• Molecule 10: eL8

Chain G:  71%



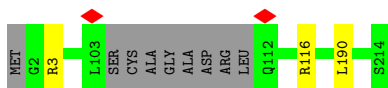
• Molecule 11: uL6

Chain H:  99%



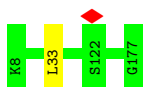
- Molecule 12: uL16

Chain I:  94%



- Molecule 13: uL5

Chain J:  99%



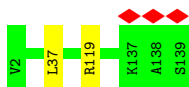
- Molecule 14: eL13

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%



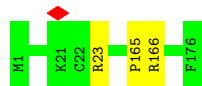
• Molecule 20: eL19

Chain R:  99%



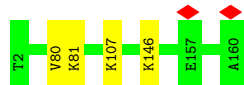
• Molecule 21: eL20

Chain S:  98%



• Molecule 22: eL21

Chain T:  97%



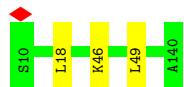
• Molecule 23: eL22

Chain U:  99%



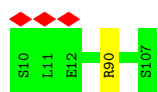
• Molecule 24: uL14

Chain V:  98%



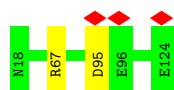
• Molecule 25: eL24

Chain c:  99%



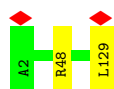
• Molecule 32: eL31

Chain d:  98%



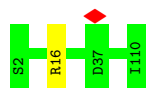
• Molecule 33: eL32

Chain e:  98%



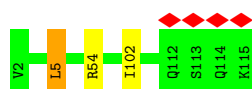
• Molecule 34: eL33

Chain f:  99%



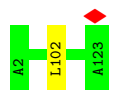
• Molecule 35: eL34

Chain g:  97%



• Molecule 36: uL29

Chain h:  99%



• Molecule 37: eL36

Chain i:  96%



• Molecule 38: eL37

Chain j:  98%

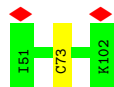
• Molecule 39: eL38

Chain k:  100%

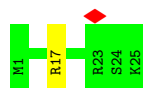
• Molecule 40: eL39

Chain l:  98%

• Molecule 41: eL40

Chain m:  98%

• Molecule 42: eL41

Chain n:  96%

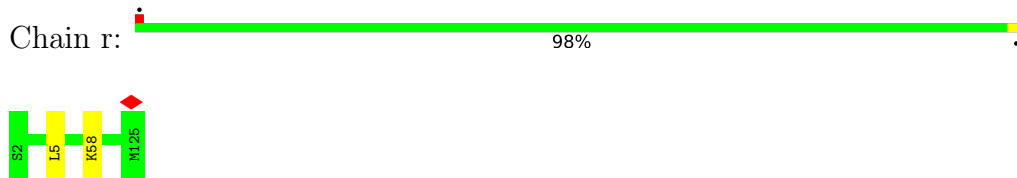
• Molecule 43: eL42

Chain o:  97%

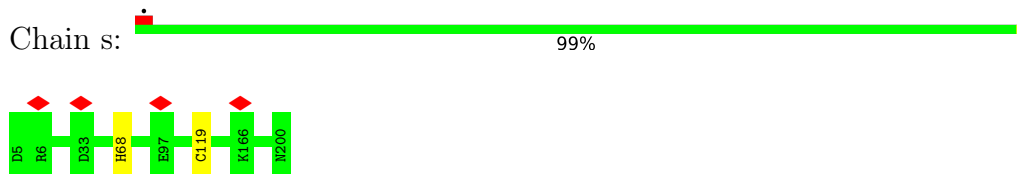
• Molecule 44: eL43

Chain p:  100%

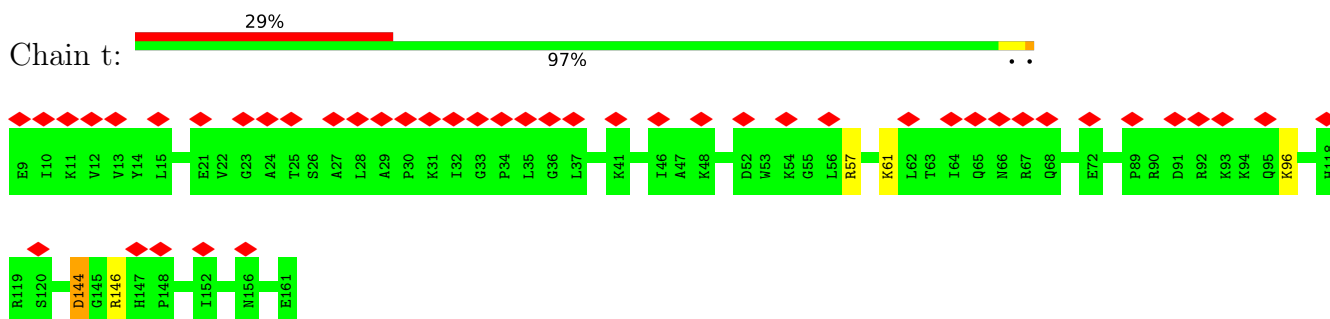
- Molecule 45: eL28



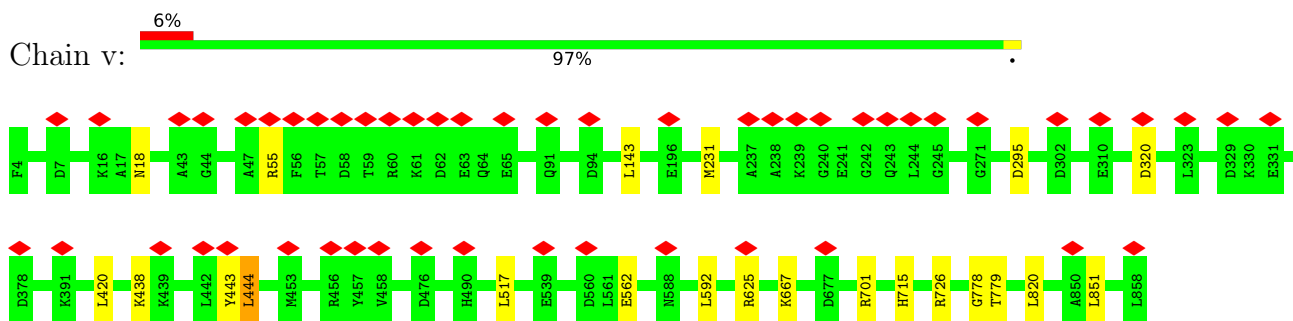
- Molecule 46: uL10



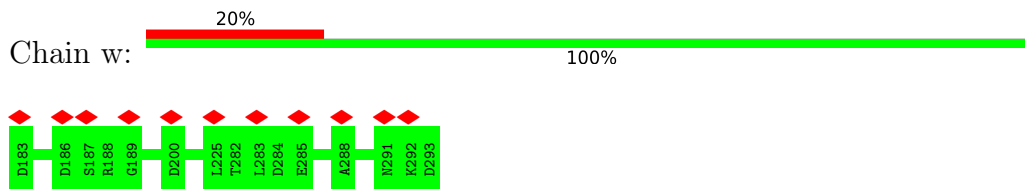
- Molecule 47: uL11



- Molecule 48: eEF2

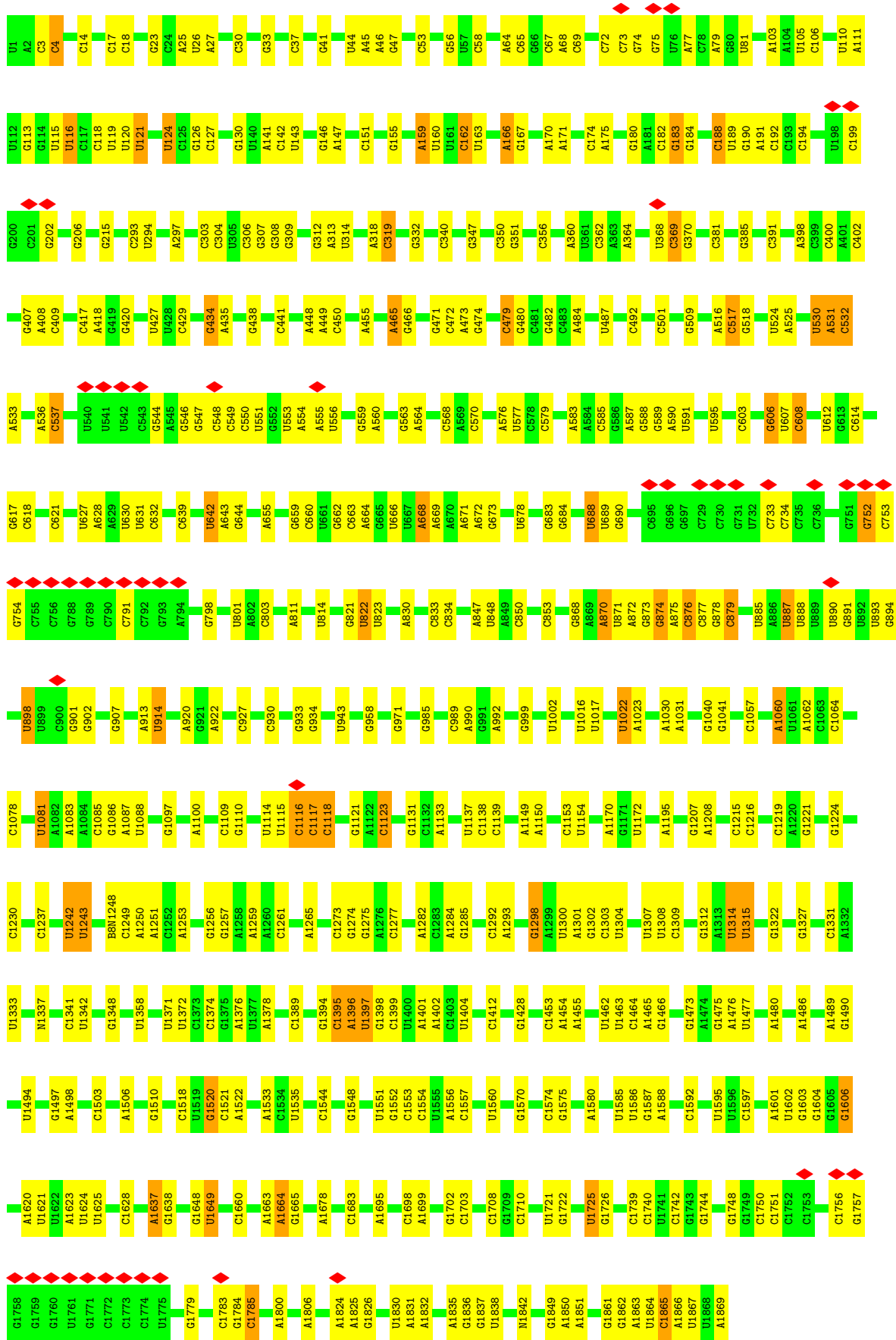


- Molecule 49: SERBP1



- Molecule 50: 18S rRNA





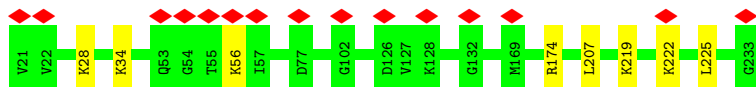
- Molecule 51: uS2

Chain AA:  99%



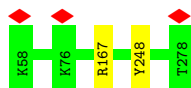
- Molecule 52: eS1

Chain BB:  96%



- Molecule 53: uS5

Chain CC:  99%



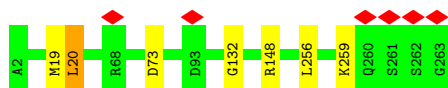
- Molecule 54: uS3

Chain DD:  98%




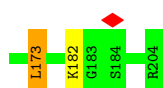
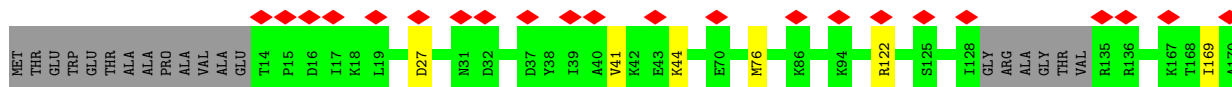
- Molecule 55: eS4

Chain EE:  97%

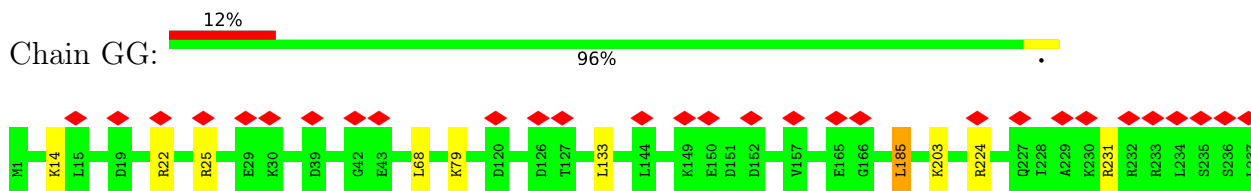


- Molecule 56: uS7

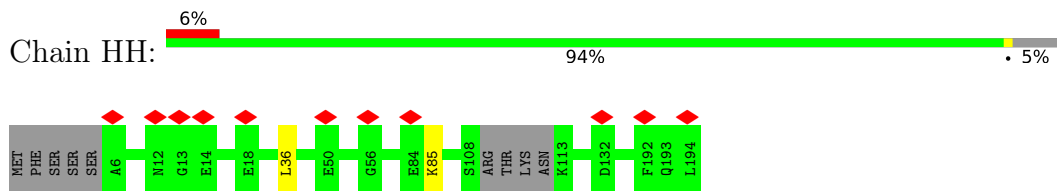
Chain FF:  87% 9%



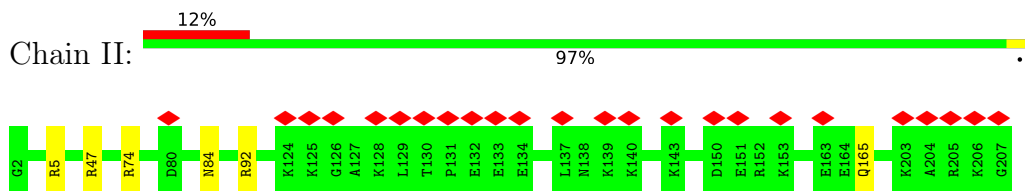
- Molecule 57: eS6



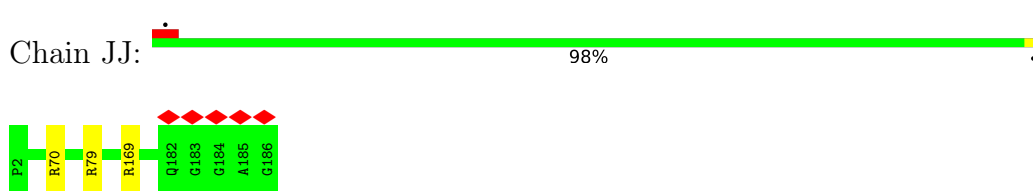
• Molecule 58: eS7



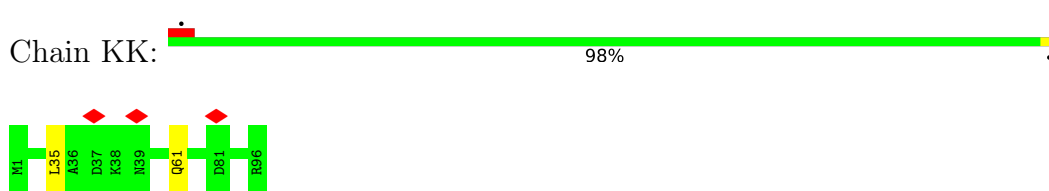
• Molecule 59: eS8



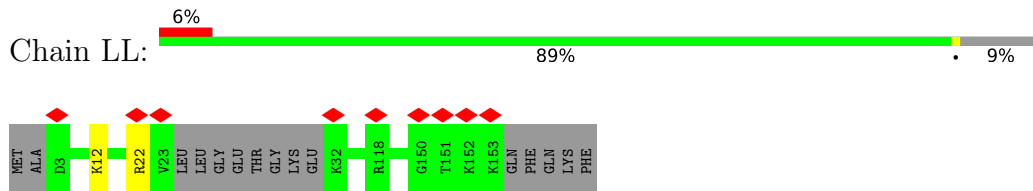
• Molecule 60: uS4



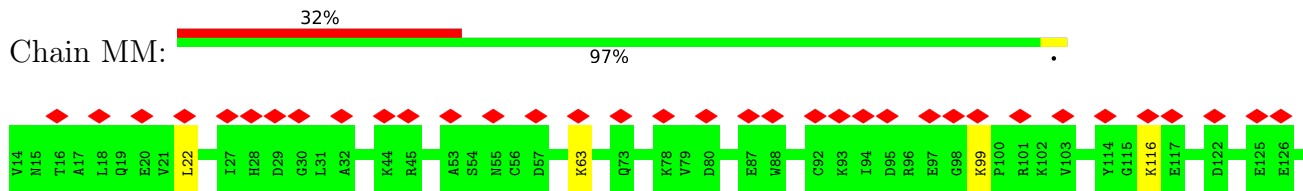
• Molecule 61: eS10



• Molecule 62: uS17

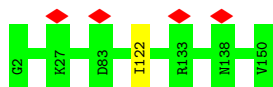


• Molecule 63: eS12

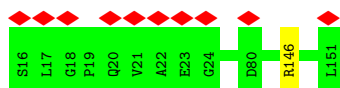




- Molecule 64: uS15



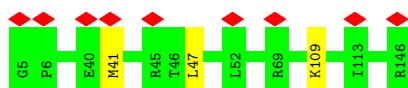
- Molecule 65: uS11



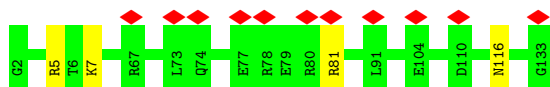
- Molecule 66: uS19



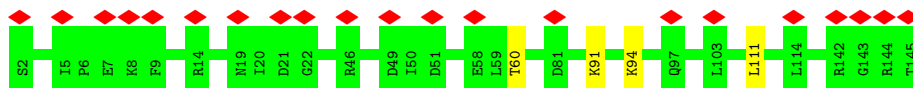
- Molecule 67: uS9



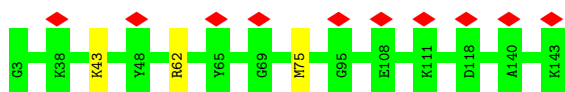
- Molecule 68: eS17



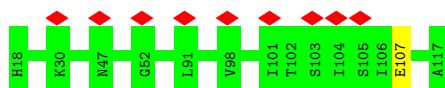
- Molecule 69: uS13



- Molecule 70: eS19



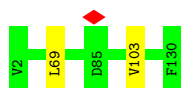
- Molecule 71: uS10



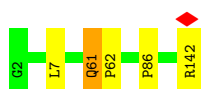
- Molecule 72: eS21



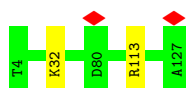
- Molecule 73: uS8



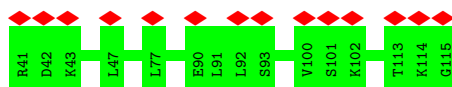
- Molecule 74: uS12



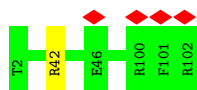
- Molecule 75: eS24



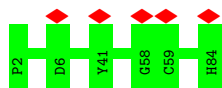
- Molecule 76: eS25



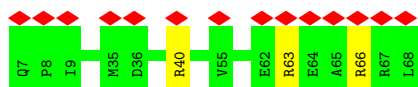
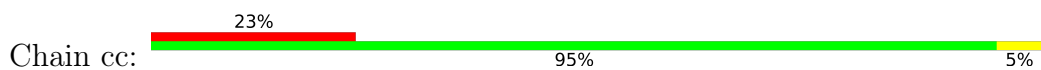
- Molecule 77: eS26



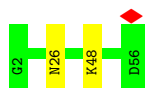
• Molecule 78: eS27



• Molecule 79: eS28



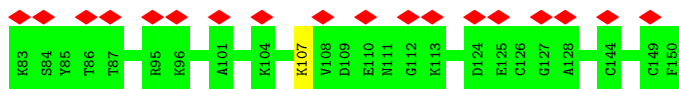
• Molecule 80: uS14



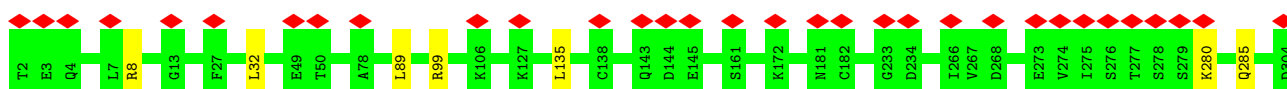
• Molecule 81: eS30



• Molecule 82: eS31



• Molecule 83: RACK1





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 i

5.1 Standard geometry i

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

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%)	34	67
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%)	15	46
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%)	25	57
22	T	157/159 (99%)	153 (98%)	3 (2%)	1 (1%)	25	57
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%)	7	30
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%)	22	55
48	v	843/848 (99%)	774 (92%)	68 (8%)	1 (0%)	51	82
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%)	6	29
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%)	54	82

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 [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	190/190 (100%)	187 (98%)	3 (2%)	62	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	B	342/342 (100%)	338 (99%)	4 (1%)	71	85
6	C	301/301 (100%)	297 (99%)	4 (1%)	69	84
7	D	247/247 (100%)	245 (99%)	2 (1%)	81	91
8	E	190/251 (76%)	186 (98%)	4 (2%)	53	76
9	F	196/196 (100%)	196 (100%)	0	100	100
10	G	200/272 (74%)	194 (97%)	6 (3%)	41	68
11	H	169/169 (100%)	168 (99%)	1 (1%)	86	94
12	I	175/181 (97%)	173 (99%)	2 (1%)	73	86
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%)	78	90
16	N	171/171 (100%)	168 (98%)	3 (2%)	59	79
17	O	171/171 (100%)	167 (98%)	4 (2%)	50	74
18	P	134/134 (100%)	131 (98%)	3 (2%)	52	75
19	Q	164/164 (100%)	162 (99%)	2 (1%)	71	85
20	R	159/159 (100%)	158 (99%)	1 (1%)	86	94
21	S	157/157 (100%)	156 (99%)	1 (1%)	86	94
22	T	139/139 (100%)	137 (99%)	2 (1%)	67	83
23	U	89/89 (100%)	88 (99%)	1 (1%)	73	86
24	V	101/101 (100%)	99 (98%)	2 (2%)	55	77
25	W	82/126 (65%)	82 (100%)	0	100	100
26	X	106/106 (100%)	105 (99%)	1 (1%)	78	90
27	Y	124/124 (100%)	122 (98%)	2 (2%)	62	81
28	Z	117/117 (100%)	117 (100%)	0	100	100
29	a	119/119 (100%)	118 (99%)	1 (1%)	81	91
30	b	84/184 (46%)	82 (98%)	2 (2%)	49	74
31	c	84/84 (100%)	83 (99%)	1 (1%)	71	85
32	d	98/98 (100%)	97 (99%)	1 (1%)	76	88
33	e	114/114 (100%)	113 (99%)	1 (1%)	78	90
34	f	88/88 (100%)	87 (99%)	1 (1%)	73	86
35	g	98/98 (100%)	95 (97%)	3 (3%)	40	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	h	109/109 (100%)	108 (99%)	1 (1%)	78	90
37	i	86/86 (100%)	83 (96%)	3 (4%)	36	65
38	j	73/73 (100%)	71 (97%)	2 (3%)	44	70
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%)	30	59
43	o	91/91 (100%)	89 (98%)	2 (2%)	52	75
44	p	74/74 (100%)	74 (100%)	0	100	100
45	r	108/108 (100%)	107 (99%)	1 (1%)	78	90
46	s	164/164 (100%)	163 (99%)	1 (1%)	86	94
47	t	126/126 (100%)	123 (98%)	3 (2%)	49	74
48	v	722/722 (100%)	712 (99%)	10 (1%)	67	83
49	w	46/46 (100%)	46 (100%)	0	100	100
51	AA	180/181 (99%)	179 (99%)	1 (1%)	86	94
52	BB	194/194 (100%)	190 (98%)	4 (2%)	53	76
53	CC	187/187 (100%)	185 (99%)	2 (1%)	73	86
54	DD	190/190 (100%)	186 (98%)	4 (2%)	53	76
55	EE	224/224 (100%)	221 (99%)	3 (1%)	69	84
56	FF	158/170 (93%)	152 (96%)	6 (4%)	33	61
57	GG	207/207 (100%)	199 (96%)	8 (4%)	32	61
58	HH	165/174 (95%)	164 (99%)	1 (1%)	86	94
59	II	178/178 (100%)	173 (97%)	5 (3%)	43	70
60	JJ	161/161 (100%)	158 (98%)	3 (2%)	57	78
61	KK	87/87 (100%)	86 (99%)	1 (1%)	73	86
62	LL	130/142 (92%)	128 (98%)	2 (2%)	65	82
63	MM	99/99 (100%)	96 (97%)	3 (3%)	41	68
64	NN	130/130 (100%)	129 (99%)	1 (1%)	81	91
65	OO	106/106 (100%)	105 (99%)	1 (1%)	78	90
66	PP	111/111 (100%)	106 (96%)	5 (4%)	27	58
67	QQ	117/117 (100%)	115 (98%)	2 (2%)	60	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	RR	119/119 (100%)	115 (97%)	4 (3%)	37	65
69	SS	125/125 (100%)	122 (98%)	3 (2%)	49	74
70	TT	111/111 (100%)	108 (97%)	3 (3%)	44	70
71	UU	92/92 (100%)	92 (100%)	0	100	100
72	VV	67/67 (100%)	66 (98%)	1 (2%)	65	82
73	WW	112/112 (100%)	111 (99%)	1 (1%)	78	90
74	XX	113/113 (100%)	112 (99%)	1 (1%)	78	90
75	YY	107/107 (100%)	105 (98%)	2 (2%)	57	78
76	ZZ	66/66 (100%)	66 (100%)	0	100	100
77	aa	88/88 (100%)	87 (99%)	1 (1%)	73	86
78	bb	75/75 (100%)	75 (100%)	0	100	100
79	cc	55/55 (100%)	52 (94%)	3 (6%)	21	51
80	dd	48/48 (100%)	46 (96%)	2 (4%)	30	59
81	ee	46/46 (100%)	43 (94%)	3 (6%)	17	46
82	ff	61/61 (100%)	60 (98%)	1 (2%)	62	81
83	gg	272/272 (100%)	268 (98%)	4 (2%)	65	82
All	All	10806/11123 (97%)	10642 (98%)	164 (2%)	66	82

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 [i](#)

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 [i](#)

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	P7G	5	3880	1	24,28,29	3.87	10 (41%)	27,41,44	1.58	3 (11%)
50	4AC	9	1842	50	21,24,25	3.13	10 (47%)	29,34,37	1.16	4 (13%)
1	I4U	5	4194	1	21,24,25	4.95	16 (76%)	27,34,37	1.18	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	A2M	9	1678	50	18,25,26	4.83	9 (50%)	18,36,39	2.59	3 (16%)
1	A2M	5	1326	1	18,25,26	4.64	9 (50%)	18,36,39	2.61	3 (16%)
1	B8H	5	1860	1	19,22,23	6.79	6 (31%)	22,32,35	2.26	5 (22%)
1	B8W	5	4185	1	18,26,27	5.21	8 (44%)	21,38,41	6.11	12 (57%)
1	UR3	5	4597	1	19,22,23	2.53	6 (31%)	26,32,35	1.20	3 (11%)
50	M7A	9	1806	50	20,25,26	2.04	3 (15%)	28,37,40	3.73	8 (28%)
48	DDE	v	715	48	14,20,21	1.02	0	14,28,30	1.24	3 (21%)
1	OMG	5	2424	1	18,26,27	2.51	8 (44%)	19,38,41	1.55	4 (21%)
1	PSU	5	1582	1	18,21,22	1.08	1 (5%)	22,30,33	1.72	4 (18%)
1	6MZ	5	4220	1	18,25,26	2.17	4 (22%)	16,36,39	1.81	3 (18%)
1	MHG	5	4371	1	29,32,33	4.01	11 (37%)	34,46,49	2.28	11 (32%)
1	A2M	5	3825	1	18,25,26	4.71	8 (44%)	18,36,39	2.70	3 (16%)
1	OMG	5	3792	1	18,26,27	2.51	8 (44%)	19,38,41	1.60	4 (21%)
1	5MU	5	4083	1	19,22,23	4.67	7 (36%)	28,32,35	3.47	9 (32%)
1	OMG	5	4370	1	18,26,27	2.43	8 (44%)	19,38,41	1.56	4 (21%)
1	PSU	5	4403	1	18,21,22	1.02	1 (5%)	22,30,33	1.83	4 (18%)
50	E3C	9	568	50	18,23,24	3.37	6 (33%)	21,33,36	2.22	5 (23%)
1	PSU	5	4636	1	18,21,22	1.05	2 (11%)	22,30,33	1.97	4 (18%)
50	A2M	9	27	50,84	18,25,26	4.68	9 (50%)	18,36,39	2.69	4 (22%)
50	5MU	9	814	50	19,22,23	4.87	7 (36%)	28,32,35	3.58	12 (42%)
1	PSU	5	4450	84,1	18,21,22	1.07	3 (16%)	22,30,33	1.96	4 (18%)
1	5MC	5	3782	1	18,22,23	3.56	7 (38%)	26,32,35	1.06	1 (3%)
50	5MC	9	1374	50	18,22,23	3.69	7 (38%)	26,32,35	1.34	3 (11%)
1	1MA	5	4415	1	16,25,26	3.91	4 (25%)	18,37,40	1.78	3 (16%)
1	A2M	5	2401	84,1	18,25,26	4.68	10 (55%)	18,36,39	2.73	4 (22%)
1	B8W	5	4472	1	18,26,27	5.33	8 (44%)	21,38,41	5.88	10 (47%)
1	OMG	5	1316	1	18,26,27	2.46	8 (44%)	19,38,41	1.69	4 (21%)
1	BGH	5	3899	84,1	25,29,30	4.24	16 (64%)	31,43,46	2.57	13 (41%)
1	OMG	5	373	1	18,26,27	2.46	8 (44%)	19,38,41	1.68	5 (26%)
50	B8N	9	1248	50,84	24,29,30	2.79	6 (25%)	29,42,45	1.74	5 (17%)
3	OMU	8	14	3,1	19,22,23	2.84	7 (36%)	26,31,34	1.85	7 (26%)
1	OMC	5	2422	84,1	19,22,23	2.86	7 (36%)	26,31,34	0.98	1 (3%)
1	PSU	5	1683	1	18,21,22	1.11	2 (11%)	22,30,33	1.82	4 (18%)
50	B8Q	9	1219	50	17,22,23	2.92	4 (23%)	22,32,35	2.32	7 (31%)
1	PSU	5	3729	1	18,21,22	1.07	1 (5%)	22,30,33	1.72	4 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	5	4637	1	18,26,27	2.41	8 (44%)	19,38,41	1.49	4 (21%)
50	PSU	9	119	50	18,21,22	0.93	1 (5%)	22,30,33	1.59	4 (18%)
1	A2M	5	1524	1	18,25,26	4.72	10 (55%)	18,36,39	2.75	3 (16%)
1	PSU	5	1677	1	18,21,22	1.12	2 (11%)	22,30,33	1.90	4 (18%)
50	OMG	9	509	50,84	18,26,27	2.46	8 (44%)	19,38,41	1.46	4 (21%)
1	2MG	5	1517	1	18,26,27	2.52	7 (38%)	16,38,41	1.53	4 (25%)
6	MLZ	C	333	6	8,9,10	0.84	0	4,9,11	0.70	0
1	OMU	5	4620	1	19,22,23	2.70	7 (36%)	26,31,34	1.84	5 (19%)
1	B8Q	5	1456	1	17,22,23	2.73	5 (29%)	22,32,35	2.03	4 (18%)
1	OMU	5	4306	1	19,22,23	2.79	8 (42%)	26,31,34	1.75	5 (19%)
50	6MZ	9	1832	50,84	18,25,26	2.23	3 (16%)	16,36,39	1.52	1 (6%)
50	PSU	9	823	50	18,21,22	1.08	1 (5%)	22,30,33	1.81	4 (18%)
1	OMG	5	2364	1	18,26,27	2.47	8 (44%)	19,38,41	1.66	4 (21%)
1	A2M	5	3785	1	18,25,26	4.58	10 (55%)	18,36,39	2.57	3 (16%)
1	B8T	5	4483	1	19,22,23	3.00	8 (42%)	26,31,34	1.05	2 (7%)
50	A2M	9	668	50,84	18,25,26	4.67	8 (44%)	18,36,39	2.70	5 (27%)
1	B8W	5	4529	84,1	18,26,27	5.30	8 (44%)	21,38,41	6.42	10 (47%)
50	OMC	9	1710	50	19,22,23	2.94	7 (36%)	26,31,34	0.93	1 (3%)
1	PSU	5	4442	1	18,21,22	1.06	2 (11%)	22,30,33	1.84	5 (22%)
1	B8W	5	2380	1	18,26,27	5.22	8 (44%)	21,38,41	6.07	7 (33%)
1	PSU	5	4500	1	18,21,22	1.05	3 (16%)	22,30,33	1.91	4 (18%)
1	P7G	5	1909	1	24,28,29	4.12	10 (41%)	27,41,44	1.47	3 (11%)
1	OMC	5	2804	1	19,22,23	2.85	7 (36%)	26,31,34	0.81	0
1	E7G	5	1797	1	24,27,28	3.64	11 (45%)	30,40,43	2.21	10 (33%)
1	E6G	5	4355	1	20,27,28	5.75	9 (45%)	22,39,42	2.14	7 (31%)
1	OMC	5	3701	84,1	19,22,23	2.80	7 (36%)	26,31,34	0.76	0
1	1MA	5	1322	84,1	16,25,26	3.77	4 (25%)	18,37,40	1.76	3 (16%)
50	MA6	9	1851	50	19,26,27	0.98	1 (5%)	18,38,41	2.69	2 (11%)
1	2MG	5	4872	1	18,26,27	2.63	7 (38%)	16,38,41	1.76	4 (25%)
50	OMU	9	116	50	19,22,23	2.88	7 (36%)	26,31,34	1.75	5 (19%)
1	PSU	5	4628	1	18,21,22	1.13	3 (16%)	22,30,33	2.06	5 (22%)
1	A2M	5	398	1	18,25,26	4.82	8 (44%)	18,36,39	2.56	3 (16%)
1	7MG	5	2522	1	22,26,27	3.45	10 (45%)	29,39,42	1.97	8 (27%)
1	B8T	5	4671	1	19,22,23	2.99	8 (42%)	26,31,34	0.96	1 (3%)
1	OMG	5	4623	1	18,26,27	2.46	8 (44%)	19,38,41	1.64	4 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	5	2773	1	18,26,27	2.50	8 (44%)	19,38,41	1.53	4 (21%)
1	7MG	5	4550	1	22,26,27	3.48	10 (45%)	29,39,42	1.95	10 (34%)
1	OMC	5	3909	1	19,22,23	2.84	7 (36%)	26,31,34	1.26	3 (11%)
1	PSU	5	4531	1	18,21,22	1.09	2 (11%)	22,30,33	1.91	5 (22%)
50	MA6	9	1850	50	19,26,27	1.01	1 (5%)	18,38,41	2.81	3 (16%)
1	OMC	5	2861	1	19,22,23	2.83	7 (36%)	26,31,34	0.89	1 (3%)
50	OMC	9	517	50	19,22,23	2.84	7 (36%)	26,31,34	0.65	0
1	A2M	5	2363	84,1	18,25,26	4.80	10 (55%)	18,36,39	2.67	3 (16%)
1	PSU	5	3764	1	18,21,22	1.03	1 (5%)	22,30,33	1.68	4 (18%)
1	UR3	5	4530	1	19,22,23	2.67	6 (31%)	26,32,35	1.43	4 (15%)
1	OMG	5	2050	1	18,26,27	2.44	8 (44%)	19,38,41	1.48	4 (21%)
1	I4U	5	1659	1	21,24,25	4.95	16 (76%)	27,34,37	1.45	2 (7%)
1	7MG	5	1605	1	22,26,27	3.44	10 (45%)	29,39,42	2.05	9 (31%)
1	5MC	5	4335	1	18,22,23	3.61	7 (38%)	26,32,35	1.21	3 (11%)
50	UR3	9	1830	50	19,22,23	2.71	6 (31%)	26,32,35	1.57	4 (15%)
1	OMC	5	2365	1	19,22,23	2.83	7 (36%)	26,31,34	0.69	0
50	OMU	9	121	50	19,22,23	2.95	8 (42%)	26,31,34	1.76	5 (19%)
1	OMG	5	1883	1	18,26,27	2.50	8 (44%)	19,38,41	1.70	4 (21%)
1	A2M	5	4571	1	18,25,26	4.76	8 (44%)	18,36,39	2.68	4 (22%)
1	B9B	5	237	1	21,28,29	6.35	8 (38%)	23,40,43	2.37	7 (30%)
1	A2M	5	4523	84,1	18,25,26	4.82	10 (55%)	18,36,39	2.61	3 (16%)
1	UR3	5	1866	1	19,22,23	2.52	6 (31%)	26,32,35	1.37	4 (15%)
50	PSU	9	1243	50,84	18,21,22	1.07	1 (5%)	22,30,33	1.82	4 (18%)
1	A2M	5	3867	1	18,25,26	4.70	9 (50%)	18,36,39	2.62	4 (22%)
1	B8K	5	4690	1	24,28,29	4.95	16 (66%)	30,42,45	2.71	11 (36%)
1	5MC	5	4447	1	18,22,23	3.66	7 (38%)	26,32,35	1.08	1 (3%)
1	OMG	5	1522	1	18,26,27	2.44	8 (44%)	19,38,41	1.58	4 (21%)
1	OMG	5	4870	1	18,26,27	2.44	8 (44%)	19,38,41	1.53	4 (21%)
50	PSU	9	612	50	18,21,22	0.98	1 (5%)	22,30,33	1.73	4 (18%)
50	4AC	9	1337	50	21,24,25	3.19	9 (42%)	29,34,37	1.23	3 (10%)
1	OMC	5	3869	1	19,22,23	2.79	7 (36%)	26,31,34	0.83	1 (3%)
1	OMG	5	4494	1	18,26,27	2.46	8 (44%)	19,38,41	1.55	4 (21%)
50	OMG	9	644	50	18,26,27	2.47	8 (44%)	19,38,41	1.52	4 (21%)
1	B8K	5	3897	1	24,28,29	4.82	17 (70%)	30,42,45	2.49	12 (40%)
1	A2M	5	3723	1	18,25,26	4.86	9 (50%)	18,36,39	2.59	3 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
41	MLZ	m	72	41	8,9,10	0.77	0	4,9,11	0.78	0
50	A2M	9	166	50	18,25,26	4.79	9 (50%)	18,36,39	2.78	4 (22%)
1	E7G	5	2297	1	24,27,28	3.45	11 (45%)	30,40,43	2.12	9 (30%)
1	A2M	5	1534	84,1	18,25,26	4.66	9 (50%)	18,36,39	2.80	4 (22%)
50	A2M	9	1031	50	18,25,26	4.74	8 (44%)	18,36,39	2.78	4 (22%)
1	B9B	5	1574	1	21,28,29	6.30	9 (42%)	23,40,43	1.91	6 (26%)
1	B8H	5	4296	1	19,22,23	6.83	6 (31%)	22,32,35	2.48	5 (22%)
1	A2M	5	1871	84,1	18,25,26	4.70	9 (50%)	18,36,39	2.76	3 (16%)
1	OMC	5	3887	1	19,22,23	2.86	7 (36%)	26,31,34	0.94	1 (3%)
50	OMC	9	174	50	19,22,23	2.95	7 (36%)	26,31,34	0.81	0
1	PSU	5	2508	1	18,21,22	1.00	1 (5%)	22,30,33	1.66	4 (18%)
1	2MG	5	729	1	18,26,27	2.41	7 (38%)	16,38,41	1.43	4 (25%)
50	A2M	9	159	50	18,25,26	4.83	8 (44%)	18,36,39	2.76	4 (22%)
1	B8W	5	4129	1	18,26,27	5.30	8 (44%)	21,38,41	6.40	10 (47%)
1	M7A	5	4564	1	20,25,26	2.06	4 (20%)	28,37,40	3.76	7 (25%)
50	OMC	9	1703	50	19,22,23	2.94	7 (36%)	26,31,34	0.83	1 (3%)
50	A2M	9	484	50	18,25,26	4.71	9 (50%)	18,36,39	2.72	3 (16%)
50	PSU	9	1081	50	18,21,22	1.06	1 (5%)	22,30,33	1.77	5 (22%)
1	PSU	5	3715	1	18,21,22	1.02	1 (5%)	22,30,33	1.69	4 (18%)
1	OMG	5	1625	84,1	18,26,27	2.45	8 (44%)	19,38,41	1.48	4 (21%)
1	B8H	5	3762	1	19,22,23	6.81	6 (31%)	22,32,35	2.48	5 (22%)
50	PSU	9	822	50	18,21,22	1.03	2 (11%)	22,30,33	1.92	5 (22%)
1	PSU	5	4293	1	18,21,22	1.08	2 (11%)	22,30,33	1.75	3 (13%)
1	OMC	5	4536	1	19,22,23	2.81	7 (36%)	26,31,34	1.04	2 (7%)
50	OMG	9	683	50	18,26,27	2.46	8 (44%)	19,38,41	1.55	5 (26%)
1	OMG	5	4196	1	18,26,27	2.41	8 (44%)	19,38,41	1.49	4 (21%)
1	A2M	5	3718	1	18,25,26	4.79	10 (55%)	18,36,39	2.47	3 (16%)
1	B9B	5	2754	84,1	21,28,29	6.35	9 (42%)	23,40,43	2.05	6 (26%)
1	B9H	5	2786	1	20,25,26	2.98	3 (15%)	22,35,38	1.62	2 (9%)
1	P4U	5	1348	84,1	21,24,25	3.38	8 (38%)	27,33,36	1.26	2 (7%)

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	P7G	5	3880	1	-	2/10/40/41	0/3/3/3
50	4AC	9	1842	50	-	0/11/29/30	0/2/2/2
1	I4U	5	4194	1	-	4/9/29/30	0/2/2/2
50	A2M	9	1678	50	-	0/5/27/28	0/3/3/3
1	A2M	5	1326	1	-	0/5/27/28	0/3/3/3
1	B8H	5	1860	1	-	2/7/25/26	0/2/2/2
1	B8W	5	4185	1	-	4/5/27/28	0/3/3/3
1	UR3	5	4597	1	-	0/7/25/26	0/2/2/2
50	M7A	9	1806	50	-	0/7/37/38	0/3/3/3
48	DDE	v	715	48	-	15/20/21/23	0/1/1/1
1	OMG	5	2424	1	-	2/5/27/28	0/3/3/3
1	PSU	5	1582	1	-	2/7/25/26	0/2/2/2
1	6MZ	5	4220	1	-	0/5/27/28	0/3/3/3
1	MHG	5	4371	1	-	6/16/46/47	0/3/3/3
1	A2M	5	3825	1	-	0/5/27/28	0/3/3/3
1	OMG	5	3792	1	-	2/5/27/28	0/3/3/3
1	5MU	5	4083	1	-	6/7/25/26	0/2/2/2
1	OMG	5	4370	1	-	0/5/27/28	0/3/3/3
1	PSU	5	4403	1	-	2/7/25/26	0/2/2/2
50	E3C	9	568	50	-	4/9/44/45	0/2/2/2
1	PSU	5	4636	1	-	4/7/25/26	0/2/2/2
50	A2M	9	27	50,84	-	0/5/27/28	0/3/3/3
50	5MU	9	814	50	-	0/7/25/26	0/2/2/2
1	PSU	5	4450	84,1	-	4/7/25/26	0/2/2/2
1	5MC	5	3782	1	-	0/7/25/26	0/2/2/2
50	5MC	9	1374	50	-	0/7/25/26	0/2/2/2
1	1MA	5	4415	1	-	2/3/25/26	0/3/3/3
1	A2M	5	2401	84,1	-	2/5/27/28	0/3/3/3
1	B8W	5	4472	1	-	2/5/27/28	0/3/3/3
1	OMG	5	1316	1	-	0/5/27/28	0/3/3/3
1	BGH	5	3899	84,1	-	2/13/43/44	0/3/3/3
1	OMG	5	373	1	-	1/5/27/28	0/3/3/3
50	B8N	9	1248	50,84	-	3/16/34/35	0/2/2/2
3	OMU	8	14	3,1	-	1/9/27/28	0/2/2/2
1	OMC	5	2422	84,1	-	1/9/27/28	0/2/2/2
1	PSU	5	1683	1	-	0/7/25/26	0/2/2/2
50	B8Q	9	1219	50	-	0/7/42/43	0/2/2/2
1	PSU	5	3729	1	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMG	5	4637	1	-	3/5/27/28	0/3/3/3
50	PSU	9	119	50	-	2/7/25/26	0/2/2/2
1	A2M	5	1524	1	-	0/5/27/28	0/3/3/3
1	PSU	5	1677	1	-	2/7/25/26	0/2/2/2
50	OMG	9	509	50,84	-	0/5/27/28	0/3/3/3
1	2MG	5	1517	1	-	0/5/27/28	0/3/3/3
6	MLZ	C	333	6	-	2/7/8/10	-
1	OMU	5	4620	1	-	0/9/27/28	0/2/2/2
1	B8Q	5	1456	1	-	2/7/42/43	0/2/2/2
1	OMU	5	4306	1	-	0/9/27/28	0/2/2/2
50	6MZ	9	1832	50,84	-	2/5/27/28	0/3/3/3
50	PSU	9	823	50	-	0/7/25/26	0/2/2/2
1	OMG	5	2364	1	-	2/5/27/28	0/3/3/3
1	A2M	5	3785	1	-	2/5/27/28	0/3/3/3
1	B8T	5	4483	1	-	2/7/27/28	0/2/2/2
50	A2M	9	668	50,84	-	4/5/27/28	0/3/3/3
1	B8W	5	4529	84,1	-	2/5/27/28	0/3/3/3
50	OMC	9	1710	50	-	0/9/27/28	0/2/2/2
1	PSU	5	4442	1	-	0/7/25/26	0/2/2/2
1	B8W	5	2380	1	-	5/5/27/28	0/3/3/3
1	PSU	5	4500	1	-	3/7/25/26	0/2/2/2
1	P7G	5	1909	1	-	4/10/40/41	0/3/3/3
1	OMC	5	2804	1	-	0/9/27/28	0/2/2/2
1	E7G	5	1797	1	-	3/9/39/40	0/3/3/3
1	E6G	5	4355	1	-	5/6/28/29	0/3/3/3
1	OMC	5	3701	84,1	-	4/9/27/28	0/2/2/2
1	1MA	5	1322	84,1	-	0/3/25/26	0/3/3/3
50	MA6	9	1851	50	-	3/7/29/30	0/3/3/3
1	2MG	5	4872	1	-	2/5/27/28	0/3/3/3
50	OMU	9	116	50	-	3/9/27/28	0/2/2/2
1	PSU	5	4628	1	-	0/7/25/26	0/2/2/2
1	A2M	5	398	1	-	2/5/27/28	0/3/3/3
1	7MG	5	2522	1	-	0/7/37/38	0/3/3/3
1	B8T	5	4671	1	-	0/7/27/28	0/2/2/2
1	OMG	5	4623	1	-	0/5/27/28	0/3/3/3
1	OMG	5	2773	1	-	0/5/27/28	0/3/3/3
1	7MG	5	4550	1	-	0/7/37/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	5	3909	1	-	1/9/27/28	0/2/2/2
1	PSU	5	4531	1	-	0/7/25/26	0/2/2/2
50	MA6	9	1850	50	-	1/7/29/30	0/3/3/3
1	OMC	5	2861	1	-	0/9/27/28	0/2/2/2
50	OMC	9	517	50	-	2/9/27/28	0/2/2/2
1	A2M	5	2363	84,1	-	0/5/27/28	0/3/3/3
1	PSU	5	3764	1	-	2/7/25/26	0/2/2/2
1	UR3	5	4530	1	-	1/7/25/26	0/2/2/2
1	OMG	5	2050	1	-	0/5/27/28	0/3/3/3
1	I4U	5	1659	1	-	2/9/29/30	0/2/2/2
1	7MG	5	1605	1	-	0/7/37/38	0/3/3/3
1	5MC	5	4335	1	-	0/7/25/26	0/2/2/2
50	UR3	9	1830	50	-	4/7/25/26	0/2/2/2
1	OMC	5	2365	1	-	0/9/27/28	0/2/2/2
50	OMU	9	121	50	-	2/9/27/28	0/2/2/2
1	OMG	5	1883	1	-	0/5/27/28	0/3/3/3
1	A2M	5	4571	1	-	0/5/27/28	0/3/3/3
1	B9B	5	237	1	-	4/7/29/30	0/3/3/3
1	A2M	5	4523	84,1	-	2/5/27/28	0/3/3/3
1	UR3	5	1866	1	-	0/7/25/26	0/2/2/2
50	PSU	9	1243	50,84	-	2/7/25/26	0/2/2/2
1	A2M	5	3867	1	-	4/5/27/28	0/3/3/3
1	B8K	5	4690	1	-	0/11/41/42	0/3/3/3
1	5MC	5	4447	1	-	4/7/25/26	0/2/2/2
1	OMG	5	1522	1	-	0/5/27/28	0/3/3/3
1	OMG	5	4870	1	-	4/5/27/28	0/3/3/3
50	PSU	9	612	50	-	0/7/25/26	0/2/2/2
50	4AC	9	1337	50	-	0/11/29/30	0/2/2/2
1	OMC	5	3869	1	-	0/9/27/28	0/2/2/2
1	OMG	5	4494	1	-	2/5/27/28	0/3/3/3
50	OMG	9	644	50	-	1/5/27/28	0/3/3/3
1	B8K	5	3897	1	-	3/11/41/42	0/3/3/3
1	A2M	5	3723	1	-	0/5/27/28	0/3/3/3
41	MLZ	m	72	41	-	3/7/8/10	-
50	A2M	9	166	50	-	2/5/27/28	0/3/3/3
1	E7G	5	2297	1	-	1/9/39/40	0/3/3/3
1	A2M	5	1534	84,1	-	2/5/27/28	0/3/3/3
50	A2M	9	1031	50	-	0/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	B9B	5	1574	1	-	4/7/29/30	0/3/3/3
1	B8H	5	4296	1	-	1/7/25/26	0/2/2/2
1	A2M	5	1871	84,1	-	0/5/27/28	0/3/3/3
1	OMC	5	3887	1	-	1/9/27/28	0/2/2/2
50	OMC	9	174	50	-	0/9/27/28	0/2/2/2
1	PSU	5	2508	1	-	0/7/25/26	0/2/2/2
1	2MG	5	729	1	-	2/5/27/28	0/3/3/3
50	A2M	9	159	50	-	3/5/27/28	0/3/3/3
1	B8W	5	4129	1	-	2/5/27/28	0/3/3/3
1	M7A	5	4564	1	-	0/7/37/38	0/3/3/3
50	OMC	9	1703	50	-	2/9/27/28	0/2/2/2
50	A2M	9	484	50	-	0/5/27/28	0/3/3/3
50	PSU	9	1081	50	-	3/7/25/26	0/2/2/2
1	PSU	5	3715	1	-	0/7/25/26	0/2/2/2
1	OMG	5	1625	84,1	-	3/5/27/28	0/3/3/3
1	B8H	5	3762	1	-	0/7/25/26	0/2/2/2
50	PSU	9	822	50	-	2/7/25/26	0/2/2/2
1	PSU	5	4293	1	-	0/7/25/26	0/2/2/2
1	OMC	5	4536	1	-	0/9/27/28	0/2/2/2
50	OMG	9	683	50	-	2/5/27/28	0/3/3/3
1	OMG	5	4196	1	-	0/5/27/28	0/3/3/3
1	A2M	5	3718	1	-	0/5/27/28	0/3/3/3
1	B9B	5	2754	84,1	-	1/7/29/30	0/3/3/3
1	B9H	5	2786	1	-	3/12/47/48	0/2/2/2
1	P4U	5	1348	84,1	-	4/10/29/30	0/2/2/2

The worst 5 of 938 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	2754	B9B	C2'-C1'	-17.99	1.26	1.53
1	5	1574	B9B	C2'-C1'	-17.90	1.26	1.53
1	5	237	B9B	C2'-C1'	-17.83	1.26	1.53
1	5	237	B9B	O4'-C1'	17.18	1.65	1.41
1	5	1574	B9B	O4'-C1'	16.86	1.64	1.41

The worst 5 of 595 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	4529	B8W	N2-C2-N3	17.10	145.65	117.79
1	5	4129	B8W	N2-C2-N3	16.96	145.43	117.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	4185	B8W	N2-C2-N3	16.75	145.08	117.79
1	5	2380	B8W	N2-C2-N3	16.70	145.01	117.79
1	5	4472	B8W	N2-C2-N3	15.95	143.78	117.79

There are no chirality outliers.

5 of 216 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	C3'-C4'-C5'-O5'
1	5	237	B9B	O4'-C4'-C5'-O5'
1	5	1348	P4U	N3-C4-O4-C41

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides 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	-	24,30,30	0.96	1 (4%)	30,47,47	1.33	4 (13%)

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	-2.63	1.34	1.37

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	v	900	GDP	PA-O3A-PB	-3.89	119.47	132.83
86	v	900	GDP	C5-C6-N1	2.53	118.42	113.95
86	v	900	GDP	C8-N7-C5	2.32	107.41	102.99
86	v	900	GDP	O6-C6-C5	-2.10	120.27	124.37

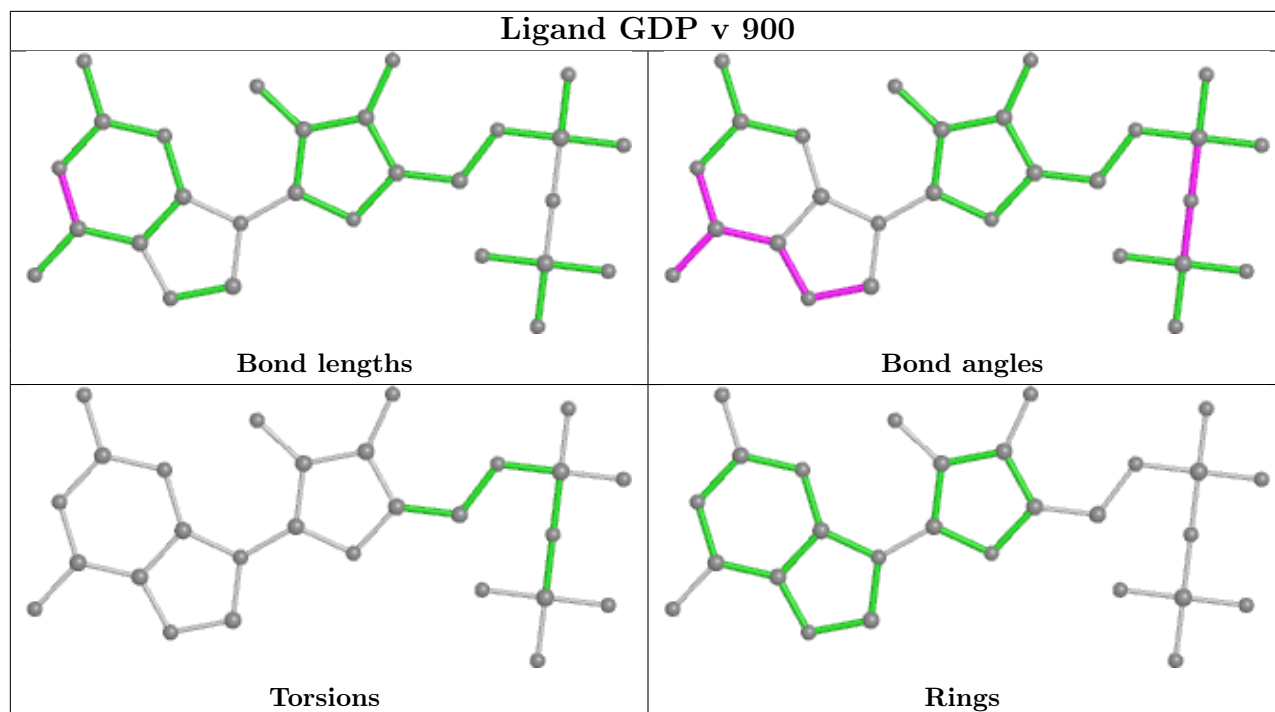
There are no chirality outliers.

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

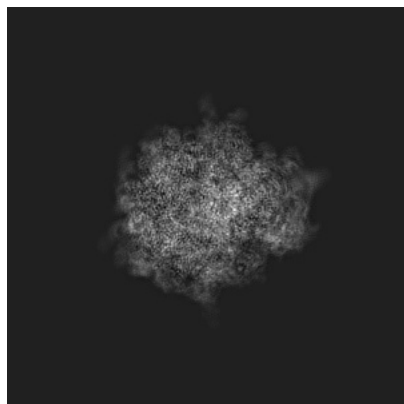
6 Map visualisation [i](#)

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.

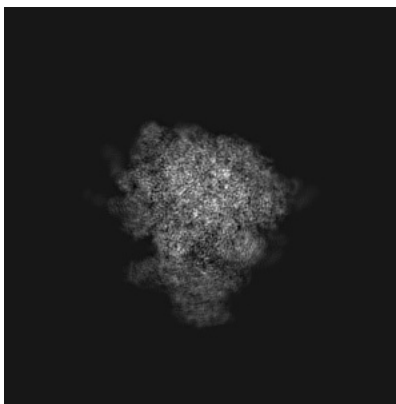
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

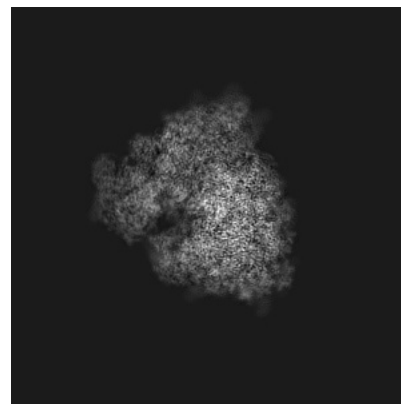
6.1.1 Primary map



X

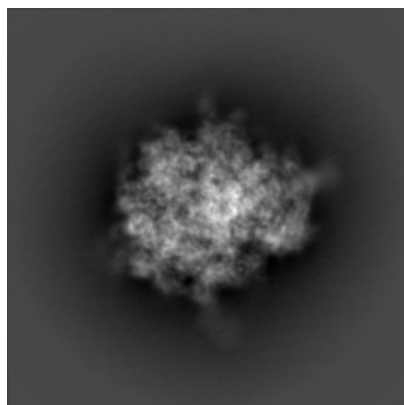


Y

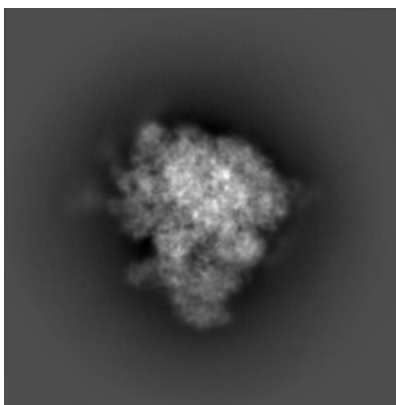


Z

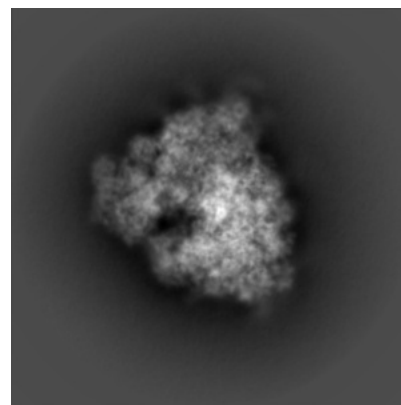
6.1.2 Raw map



X



Y

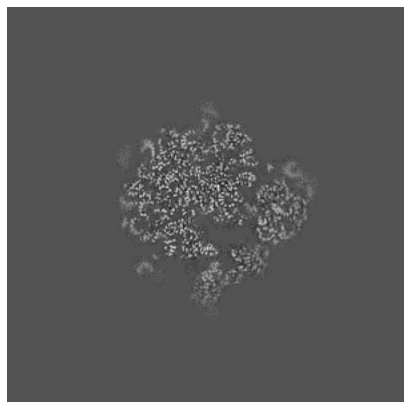


Z

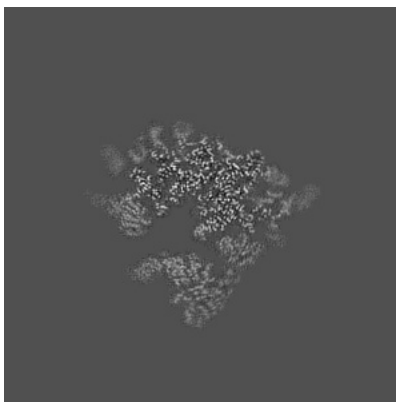
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

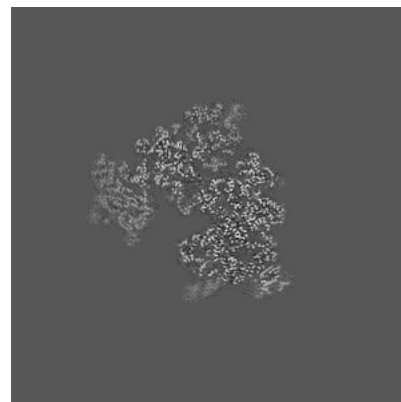
6.2.1 Primary map



X Index: 200

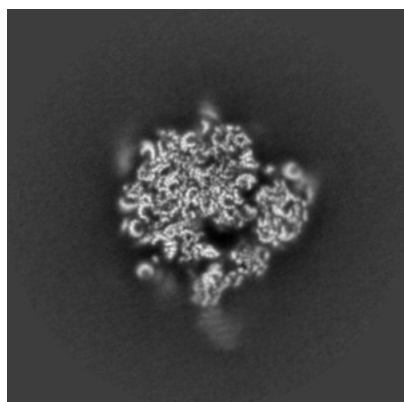


Y Index: 200

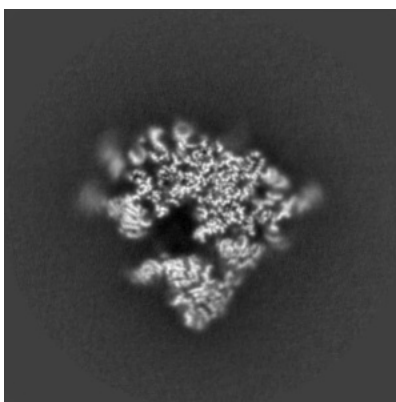


Z Index: 200

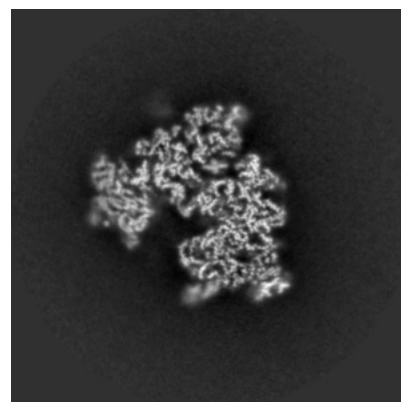
6.2.2 Raw map



X Index: 200



Y Index: 200

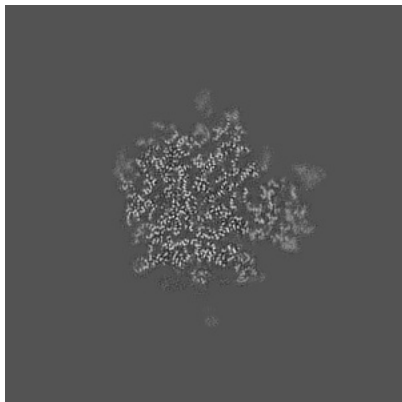


Z Index: 200

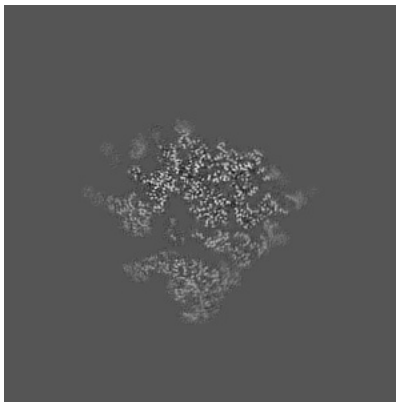
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

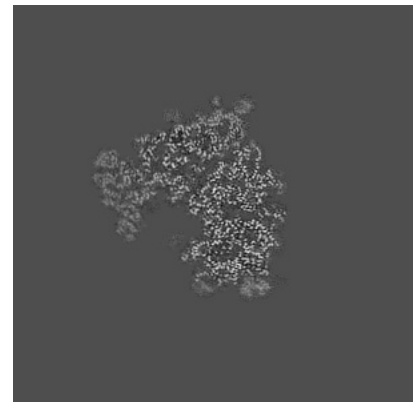
6.3.1 Primary map



X Index: 213

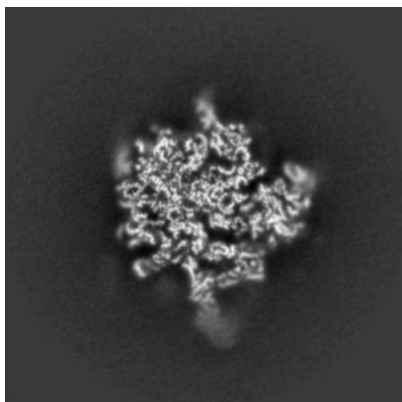


Y Index: 206

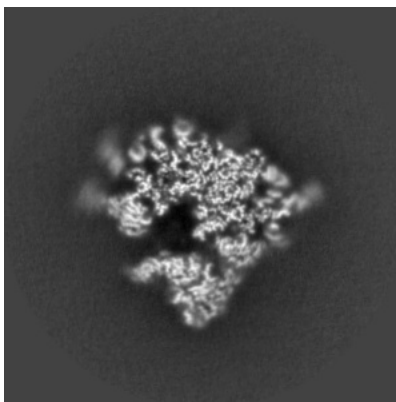


Z Index: 210

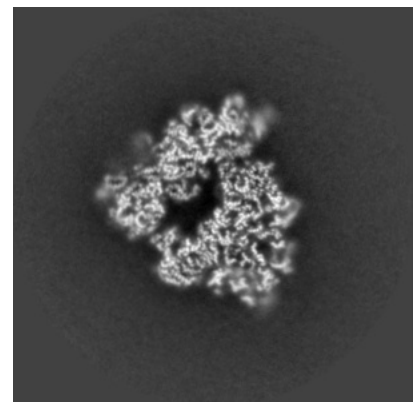
6.3.2 Raw map



X Index: 206



Y Index: 201

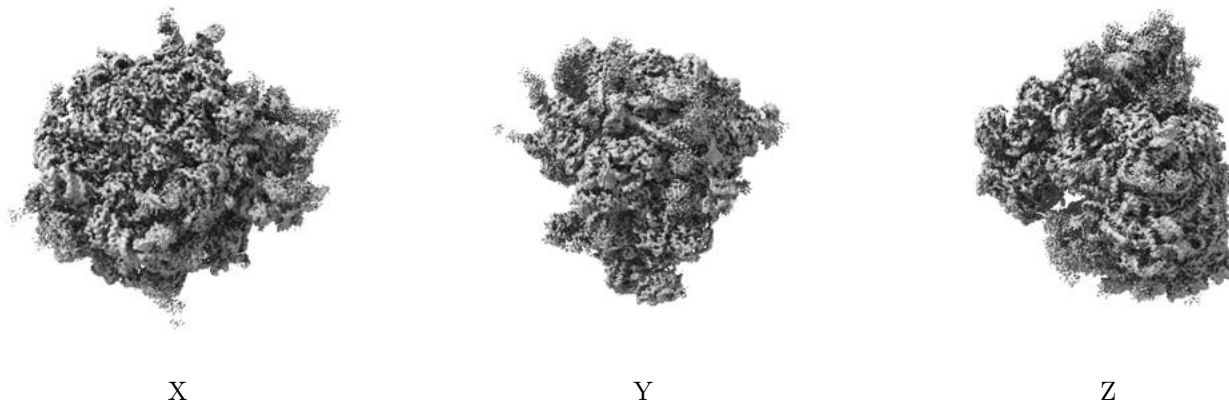


Z Index: 176

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

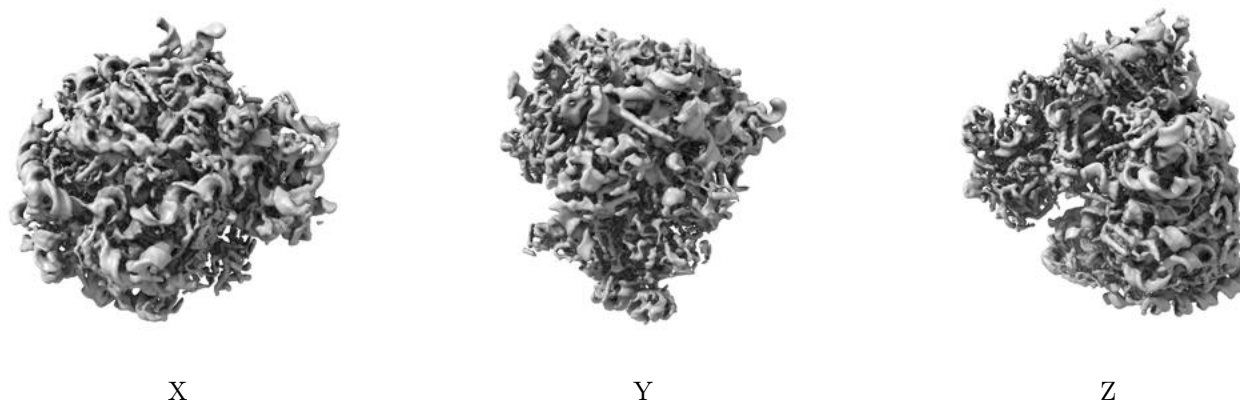
6.4 Orthogonal surface views [i](#)

6.4.1 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.

6.4.2 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.

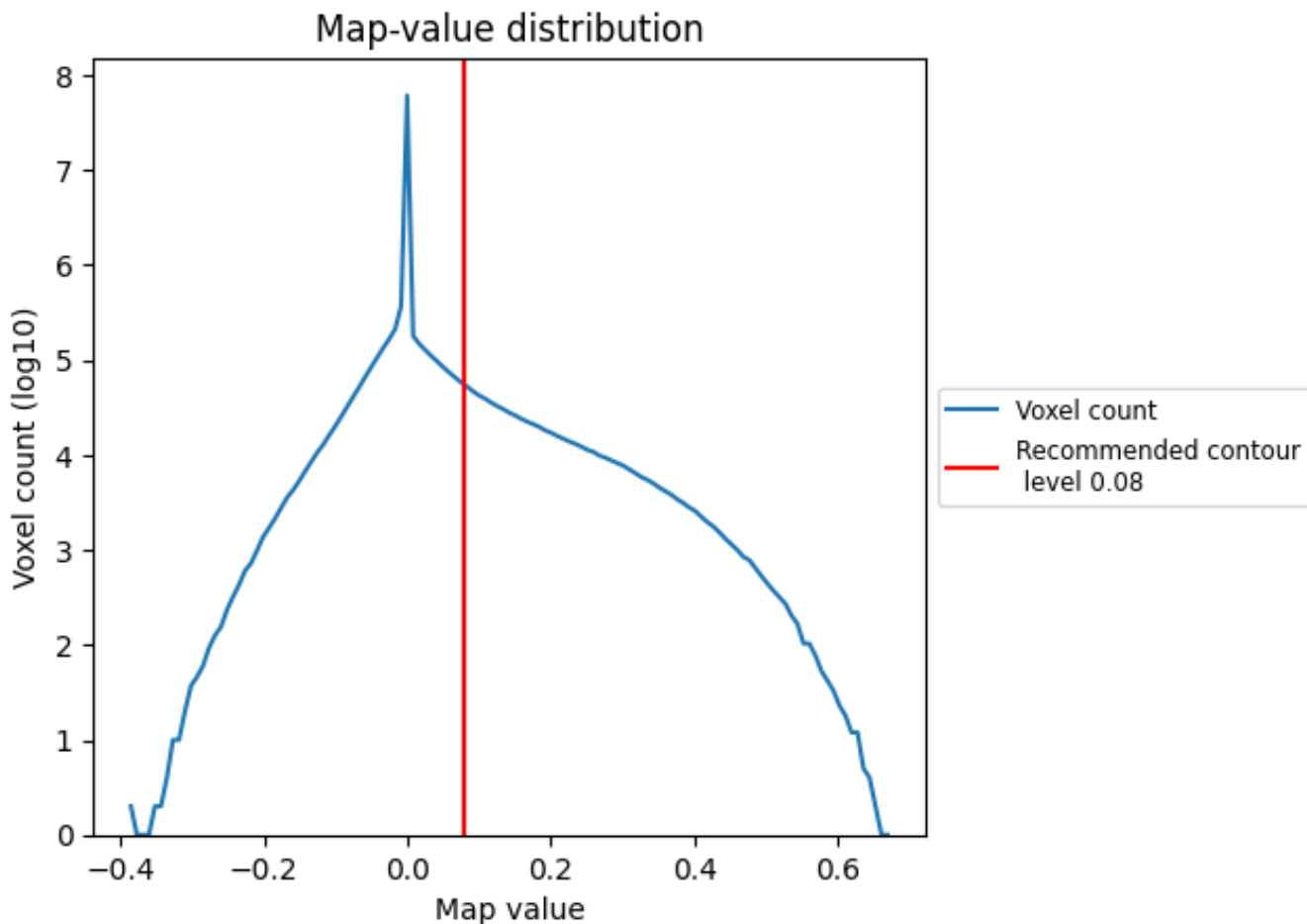
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

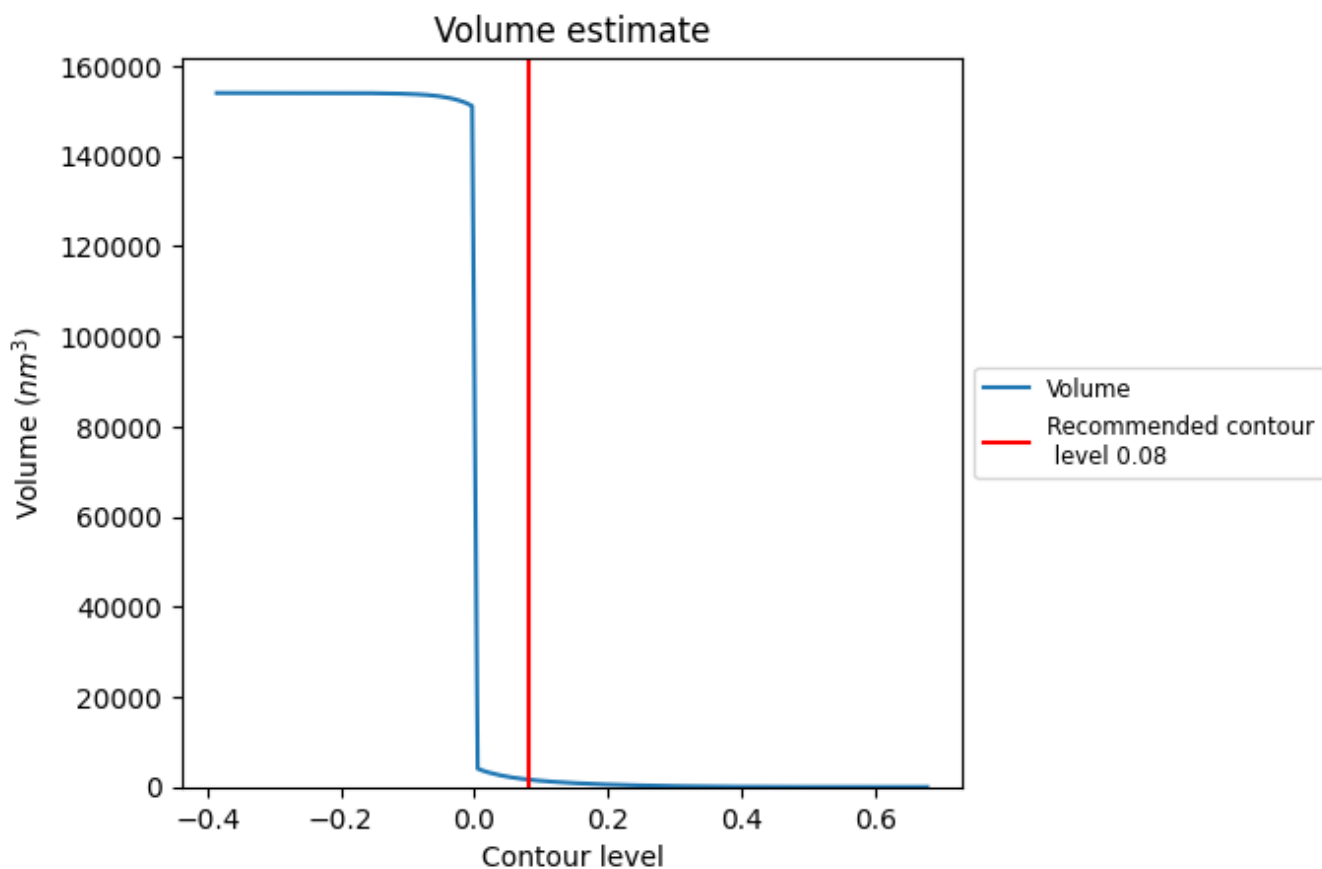
This section contains the results of statistical analysis of the map.

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.

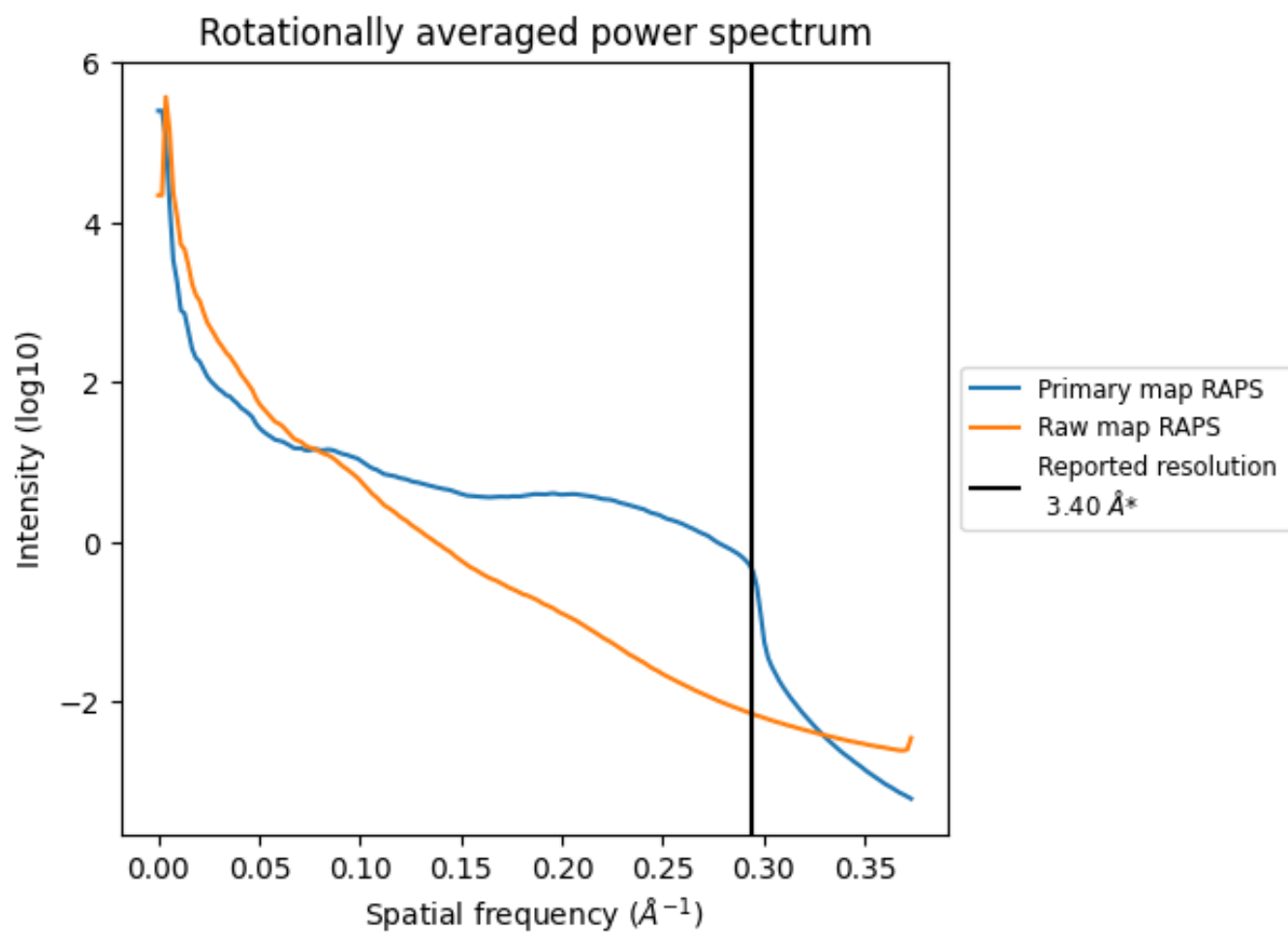
7.2 Volume estimate [i](#)



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 i

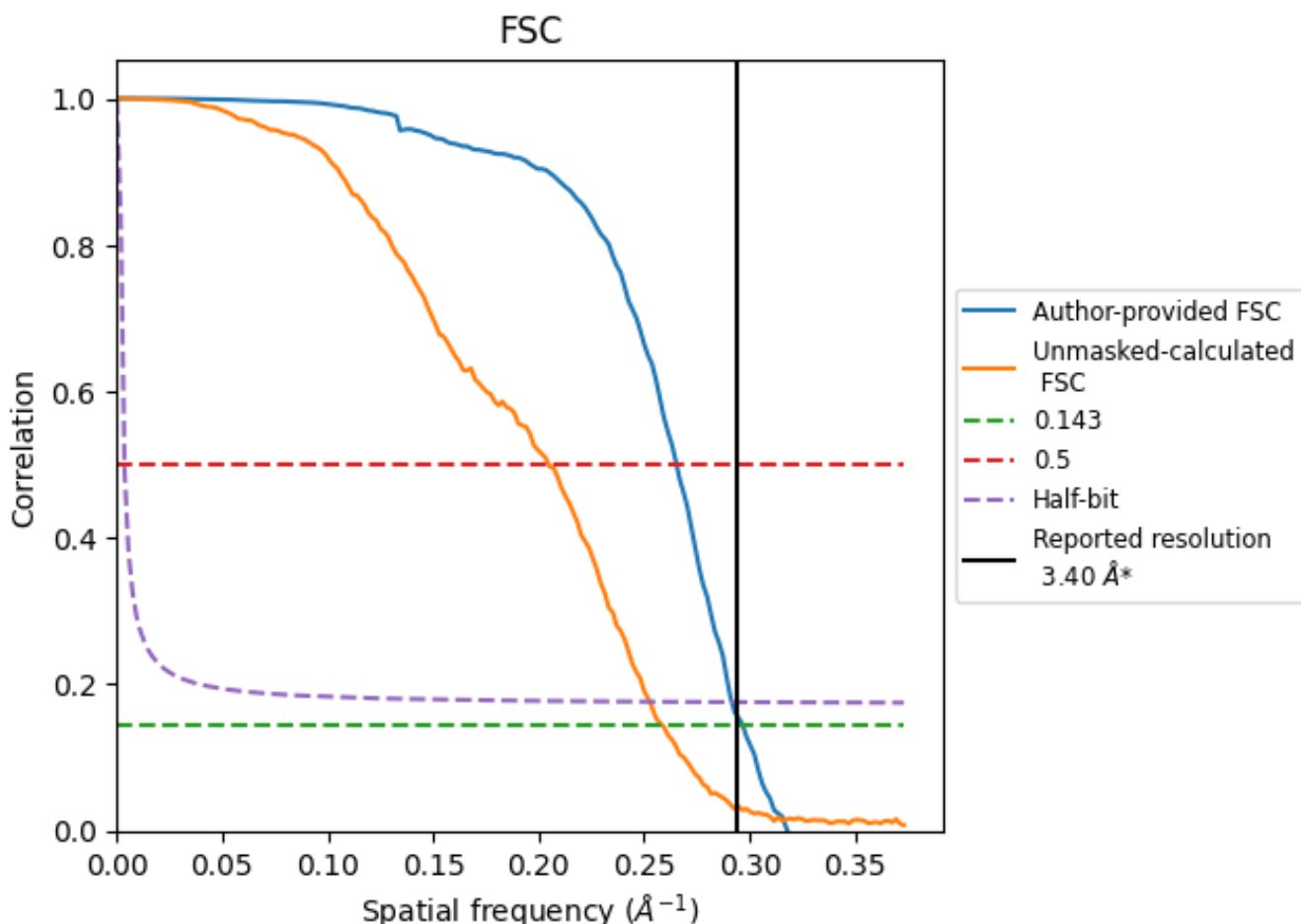


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 Å⁻¹

8.2 Resolution estimates

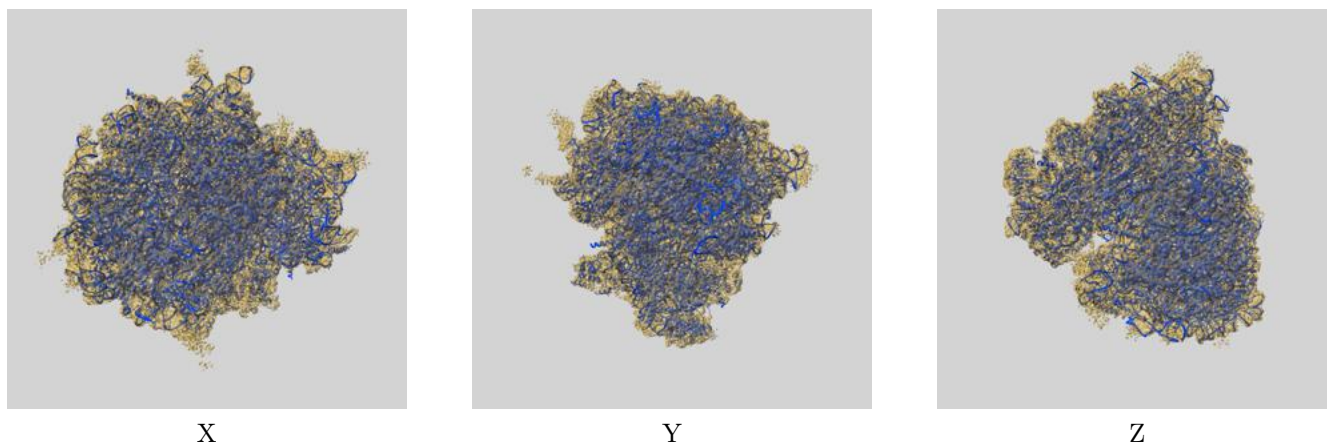
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.37	3.77	3.43
Unmasked-calculated*	3.86	4.89	3.96

*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](#)

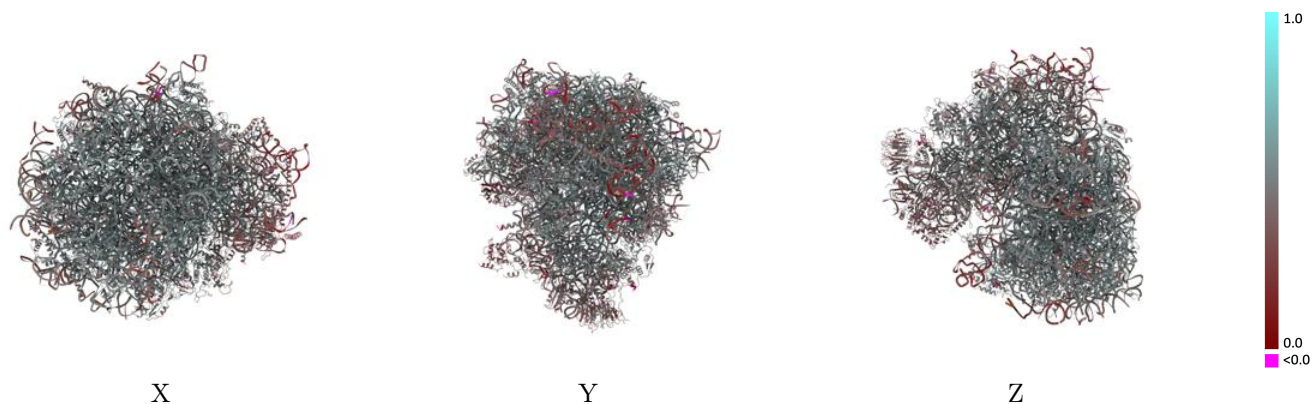
This section contains information regarding the fit between EMDB map EMD-9242 and PDB model 6MTE. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



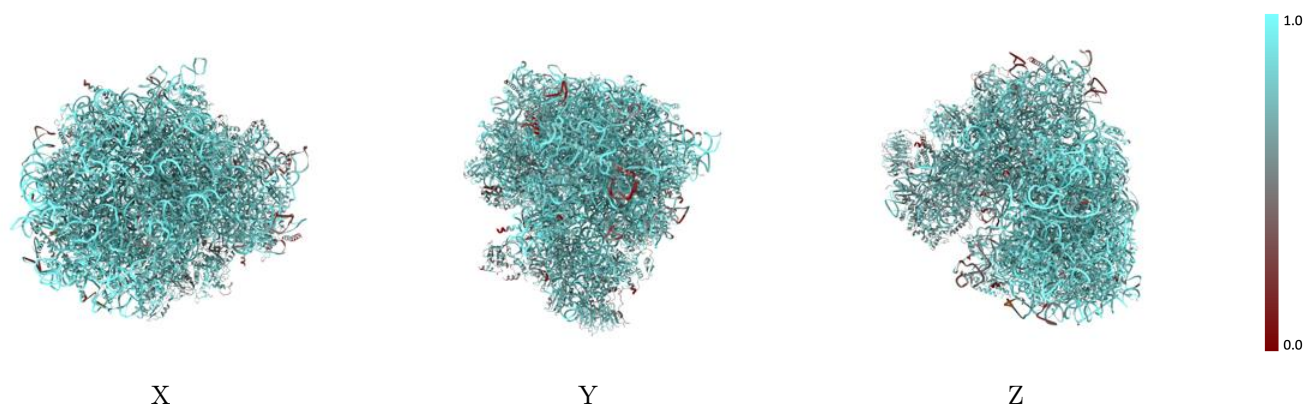
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



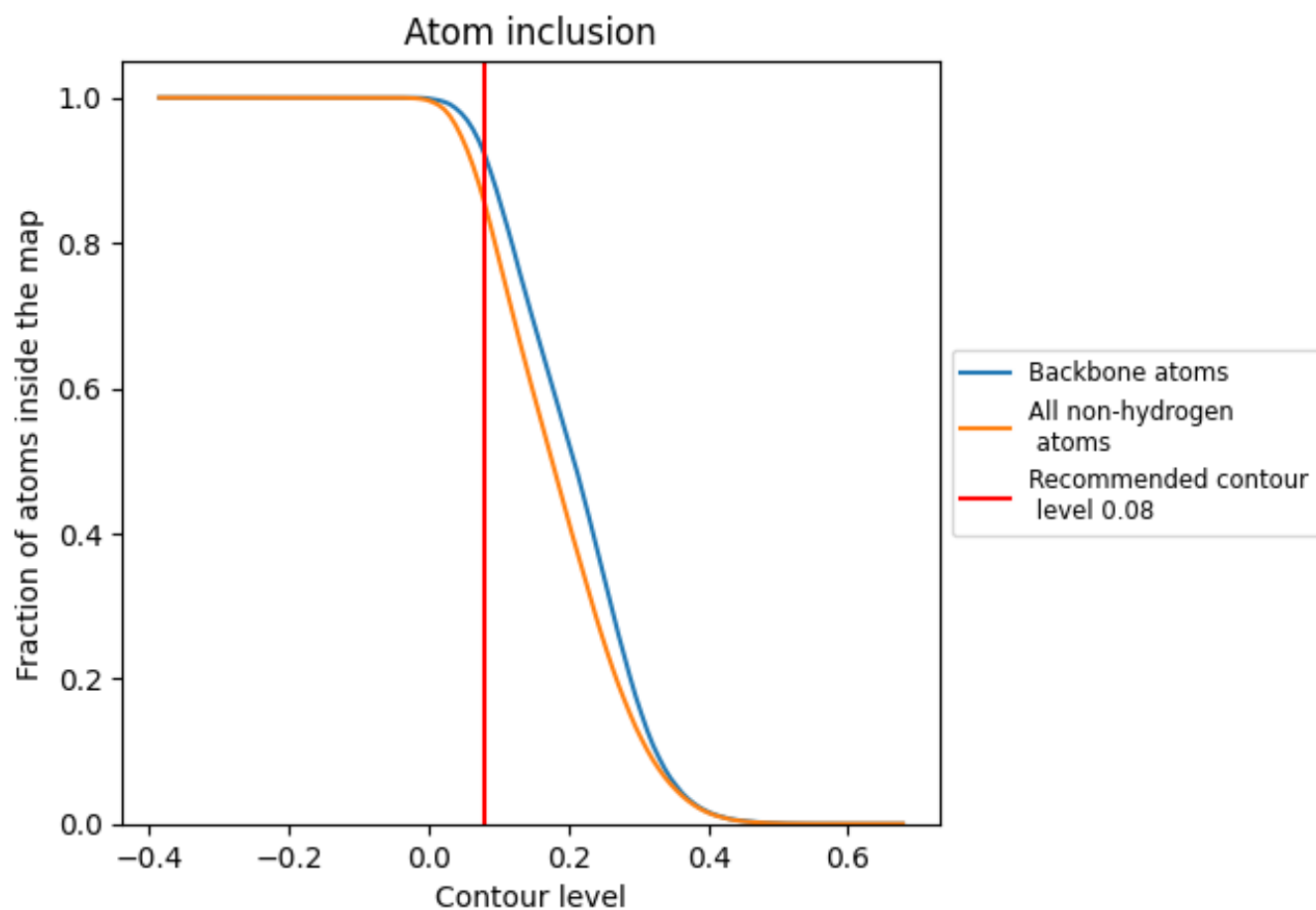
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.8539	 0.4760
5	 0.9157	 0.4870
7	 0.9626	 0.5120
8	 0.9260	 0.4850
9	 0.8930	 0.4420
A	 0.8584	 0.5490
AA	 0.7837	 0.4740
B	 0.8837	 0.5420
BB	 0.7010	 0.4310
C	 0.8661	 0.5310
CC	 0.8254	 0.5120
D	 0.8465	 0.5020
DD	 0.7130	 0.4450
E	 0.8541	 0.5080
EE	 0.7990	 0.4840
F	 0.8583	 0.5320
FF	 0.6034	 0.3480
G	 0.7973	 0.4890
GG	 0.6663	 0.3620
H	 0.8512	 0.5290
HH	 0.7242	 0.4390
I	 0.8525	 0.5330
II	 0.7240	 0.4290
J	 0.8259	 0.4880
JJ	 0.8102	 0.4880
KK	 0.7509	 0.4370
L	 0.8286	 0.5080
LL	 0.7737	 0.4820
M	 0.8608	 0.5280
MM	 0.5280	 0.2930
N	 0.8914	 0.5470
NN	 0.7693	 0.4710
O	 0.8738	 0.5320
OO	 0.7356	 0.4470
P	 0.8558	 0.5340

















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Chain	Atom inclusion	Q-score
PP	0.6707	0.3650
Q	0.8593	0.5360
QQ	0.6822	0.3980
R	0.8140	0.5060
RR	0.6744	0.4170
S	0.8835	0.5440
SS	0.6524	0.3520
T	0.8361	0.5270
TT	0.6807	0.3710
U	0.8015	0.4710
UU	0.7158	0.4240
V	0.8539	0.5480
VV	0.8135	0.4980
W	0.6743	0.4520
WW	0.8446	0.5270
X	0.8245	0.5210
XX	0.8394	0.5340
Y	0.8442	0.5140
YY	0.7625	0.4410
Z	0.8462	0.5110
ZZ	0.5712	0.3140
a	0.8813	0.5420
aa	0.7647	0.4840
b	0.7374	0.4590
bb	0.7340	0.4710
c	0.8091	0.4910
cc	0.5723	0.3790
d	0.8320	0.5150
dd	0.8231	0.4670
e	0.8545	0.5450
ee	0.7441	0.4750
f	0.8907	0.5500
ff	0.5896	0.3200
g	0.8276	0.5230
gg	0.6550	0.3720
h	0.8325	0.5160
i	0.8178	0.4960
j	0.9036	0.5430
k	0.8025	0.4920
l	0.8431	0.5220
m	0.8657	0.5360
n	0.7569	0.5070

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Chain	Atom inclusion	Q-score
o	 0.8397	 0.5420
p	 0.8041	 0.5270
r	 0.8777	 0.5310
s	 0.7502	 0.4490
t	 0.5360	 0.3330
v	 0.7431	 0.4550
w	 0.6215	 0.4480