



wwPDB EM Validation Summary Report ⓘ

Jun 24, 2026 – 05:14 AM EDT

PDB ID : 6MTC / pdb_00006mtc
EMDB ID : EMD-9239
Title : Rabbit 80S ribosome with Z-site tRNA and IFRD2 (unrotated 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:

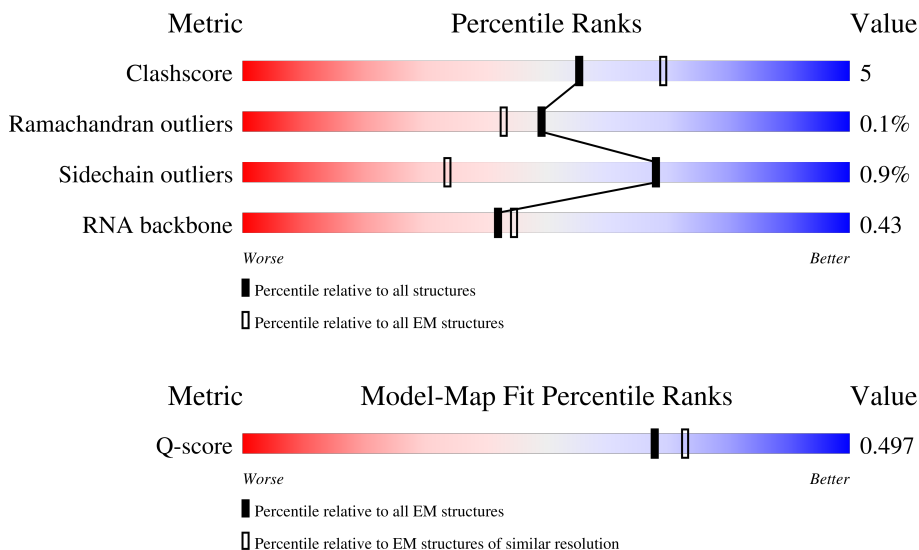
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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.

























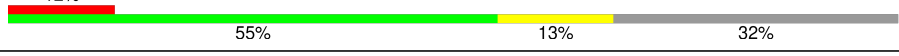


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	4	75	
2	5	3597	
3	7	120	










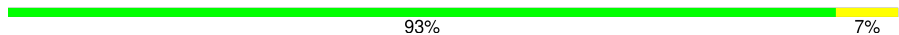















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Mol	Chain	Length	Quality of chain
4	8	151	
5	A	248	
6	B	394	
7	C	362	
8	D	293	
9	E	291	
10	F	225	
11	G	319	
12	H	190	
13	I	214	
14	J	170	
15	L	210	
16	M	138	
17	N	203	
18	O	199	
19	P	153	
20	Q	187	
21	R	180	
22	S	176	
23	T	159	
24	U	99	
25	V	131	
26	W	157	
27	X	118	
28	Y	134	




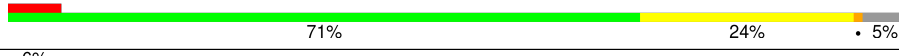
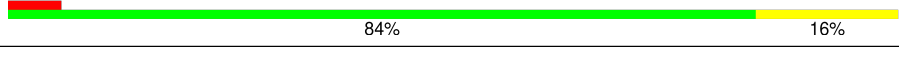



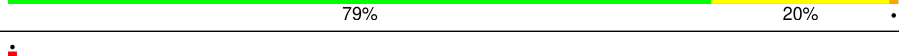
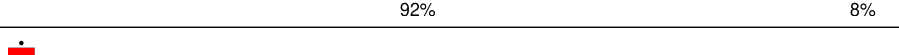
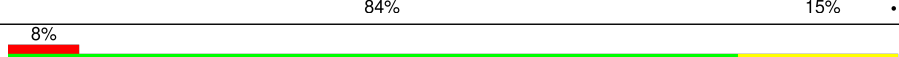
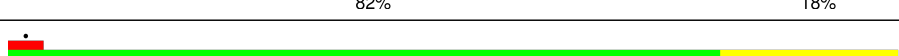

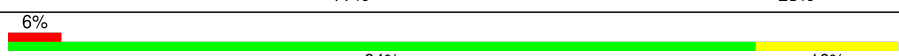
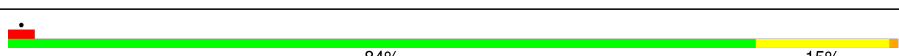
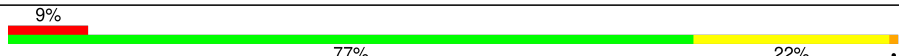





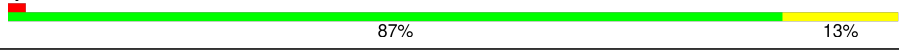
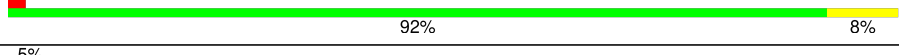
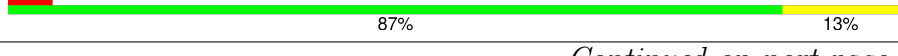

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Mol	Chain	Length	Quality of chain
29	Z	135	 80% 19%
30	a	147	 82% 18%
31	b	245	 5% 39% 58%
32	c	98	 92% 8%
33	d	107	 83% 17%
34	e	128	 88% 12%
35	f	109	 84% 16%
36	g	114	 84% 16%
37	h	122	 92% 8%
38	i	102	 93% 7%
39	j	86	 88% 12%
40	k	69	 80% 17%
41	l	50	 82% 16%
42	m	52	 73% 27%
43	n	25	 64% 36%
44	o	103	 88% 12%
45	p	91	 84% 16%
46	r	124	 85% 15%
47	u	206	 45% 71% 28%
48	v	441	 11% 70% 10% 20%
49	9	1698	 5% 61% 33% 6%
50	AA	217	 80% 20%
51	BB	213	 77% 23%
52	CC	221	 81% 19%
53	DD	228	 9% 80% 19%

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Mol	Chain	Length	Quality of chain
54	EE	262	 80% 19%
55	FF	204	 74% 16% 9%
56	GG	237	 78% 21%
57	HH	194	 71% 24% 5%
58	II	206	 84% 16%
59	JJ	185	 84% 16%
60	KK	96	 73% 26%
61	LL	158	 77% 13% 9%
62	MM	117	 79% 20%
63	NN	149	 92% 8%
64	OO	136	 84% 15%
65	PP	120	 82% 18%
66	QQ	142	 80% 20%
67	RR	132	 77% 23%
68	SS	144	 84% 16%
69	TT	141	 84% 15%
70	UU	100	 77% 22%
71	VV	83	 77% 23%
72	WW	129	 78% 22%
73	XX	141	 84% 14%
74	YY	124	 87% 12%
75	ZZ	75	 88% 12%
76	aa	101	 87% 13%
77	bb	83	 92% 8%
78	cc	62	 87% 13%

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Mol	Chain	Length	Quality of chain
79	dd	55	
80	ee	55	
81	ff	68	
82	gg	313	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	B8W	5	4185	-	X	-	-

2 Entry composition [i](#)

There are 84 unique types of molecules in this entry. The entry contains 216975 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 Z-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	4	75	1593	712	281	526	74	0	0

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	5	3597	77254	34469	14127	25061	3597	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	7	120	2558	1141	456	842	119	0	0

- Molecule 4 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	8	151	3209	1433	564	1062	150	0	0

- Molecule 5 is a protein called 60S ribosomal protein L8.

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

- Molecule 6 is a protein called 60S ribosomal protein L3.

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

- Molecule 7 is a protein called 60S ribosomal protein L4.

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

- Molecule 8 is a protein called 60S ribosomal protein L5.

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

- Molecule 9 is a protein called 60S ribosomal protein L6.

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

- Molecule 10 is a protein called 60S ribosomal protein L7.

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

- Molecule 11 is a protein called 60S ribosomal protein L7a.

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

- Molecule 12 is a protein called 60S ribosomal protein L9.

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

- Molecule 13 is a protein called 60S ribosomal protein L10.

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

- Molecule 14 is a protein called 60S ribosomal protein L11.

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

- Molecule 15 is a protein called 60S ribosomal protein L13.

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

- Molecule 16 is a protein called 60S ribosomal protein L14.

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

- Molecule 17 is a protein called 60S Ribosomal protein L15.

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

- Molecule 18 is a protein called 60S ribosomal protein L13a.

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

- Molecule 19 is a protein called 60S ribosomal protein L17.

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

- Molecule 20 is a protein called 60S ribosomal protein L18.

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

- Molecule 21 is a protein called 60S ribosomal protein L19.

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

- Molecule 22 is a protein called 60S ribosomal protein L18a.

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

- Molecule 23 is a protein called 60S ribosomal protein L21.

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

- Molecule 24 is a protein called 60S ribosomal protein L22.

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

- Molecule 25 is a protein called 60S ribosomal protein L23.

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

- Molecule 26 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	W	106	860	538	174	144	4	0	0

- Molecule 27 is a protein called 60S ribosomal protein L23a.

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

- Molecule 28 is a protein called 60S ribosomal protein L26.

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

- Molecule 29 is a protein called 60S ribosomal protein L27.

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

- Molecule 30 is a protein called 60S ribosomal protein L27a.

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

- Molecule 31 is a protein called 60S ribosomal protein L29.

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

- Molecule 32 is a protein called 60S ribosomal protein L30.

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

- Molecule 33 is a protein called 60S ribosomal protein L31.

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

- Molecule 34 is a protein called 60S ribosomal protein L32.

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

- Molecule 35 is a protein called 60S ribosomal protein L35a.

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

- Molecule 36 is a protein called 60S ribosomal protein L34.

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

- Molecule 37 is a protein called 60S ribosomal protein L35.

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

- Molecule 38 is a protein called 60S ribosomal protein L36.

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

- Molecule 39 is a protein called 60S ribosomal protein L37.

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

- Molecule 40 is a protein called 60S ribosomal protein L38.

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

- Molecule 41 is a protein called 60S ribosomal protein L39.

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

- Molecule 42 is a protein called 60S ribosomal protein L40.

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

- Molecule 43 is a protein called 60S ribosomal protein L41.

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

- Molecule 44 is a protein called 60S ribosomal protein L36a.

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

- Molecule 45 is a protein called 60S ribosomal protein L37a.

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

- Molecule 46 is a protein called 60S ribosomal protein L28.

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

- Molecule 47 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	u	206	Total	C	N	O	S	0	0
			1654	1058	297	291	8		

- Molecule 48 is a protein called Interferon-related developmental regulator 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	v	354	Total	C	N	O	S	0	0
			2737	1725	493	506	13		

- Molecule 49 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
49	9	1698	36291	16217	6509	11868	1697	0	0

- Molecule 50 is a protein called 40S ribosomal protein SA.

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

- Molecule 51 is a protein called 40S ribosomal protein S3a.

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

- Molecule 52 is a protein called 40S ribosomal protein S2.

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

- Molecule 53 is a protein called 40S ribosomal protein S3.

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

- Molecule 54 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 55 is a protein called 40S ribosomal protein S5.

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

- Molecule 56 is a protein called 40S ribosomal protein S6.

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

- Molecule 57 is a protein called 40S ribosomal protein S7.

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

- Molecule 58 is a protein called 40S ribosomal protein S8.

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

- Molecule 59 is a protein called 40S ribosomal protein S9.

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

- Molecule 60 is a protein called 40S ribosomal protein S10.

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

- Molecule 61 is a protein called 40S ribosomal protein S11.

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

- Molecule 62 is a protein called 40S ribosomal protein S12.

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

- Molecule 63 is a protein called 40S ribosomal protein S13.

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

- Molecule 64 is a protein called 40S ribosomal protein S14.

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

- Molecule 65 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
65	PP	120	997	635	187	168	7	0	0

- Molecule 66 is a protein called 40S ribosomal protein S16.

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

- Molecule 67 is a protein called 40S ribosomal protein S17.

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

- Molecule 68 is a protein called 40S ribosomal protein S18.

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

- Molecule 69 is a protein called 40S ribosomal protein S19.

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

- Molecule 70 is a protein called 40S ribosomal protein S20.

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

- Molecule 71 is a protein called 40S ribosomal protein S21.

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

- Molecule 72 is a protein called 40S ribosomal protein S15a.

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

- Molecule 73 is a protein called 40S ribosomal protein S23.

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

- Molecule 74 is a protein called 40S ribosomal protein S24.

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

- Molecule 75 is a protein called 40S ribosomal protein S25.

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

- Molecule 76 is a protein called 40S ribosomal protein S26.

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

- Molecule 77 is a protein called 40S ribosomal protein S27.

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

- Molecule 78 is a protein called 40S ribosomal protein S28.

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

- Molecule 79 is a protein called 40S ribosomal protein S29.

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

- Molecule 80 is a protein called 40S ribosomal protein S30.

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

- Molecule 81 is a protein called 40S ribosomal protein S27a.

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

- Molecule 82 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	5	199	Total	Mg	0
			199	199	
83	7	7	Total	Mg	0
			7	7	
83	8	6	Total	Mg	0
			6	6	

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Mol	Chain	Residues	Atoms		AltConf
83	A	1	Total 1	Mg 1	0
83	B	1	Total 1	Mg 1	0
83	P	2	Total 2	Mg 2	0
83	V	1	Total 1	Mg 1	0
83	j	1	Total 1	Mg 1	0
83	9	77	Total 77	Mg 77	0
83	LL	1	Total 1	Mg 1	0
83	TT	1	Total 1	Mg 1	0

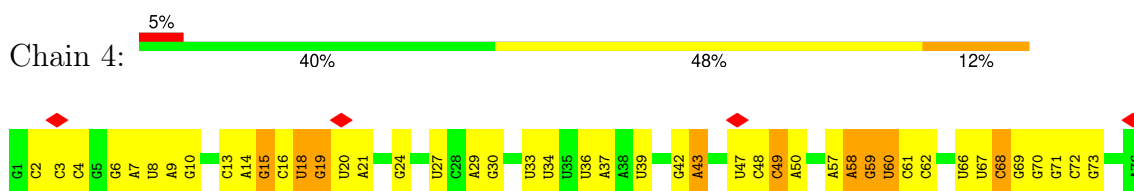
- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

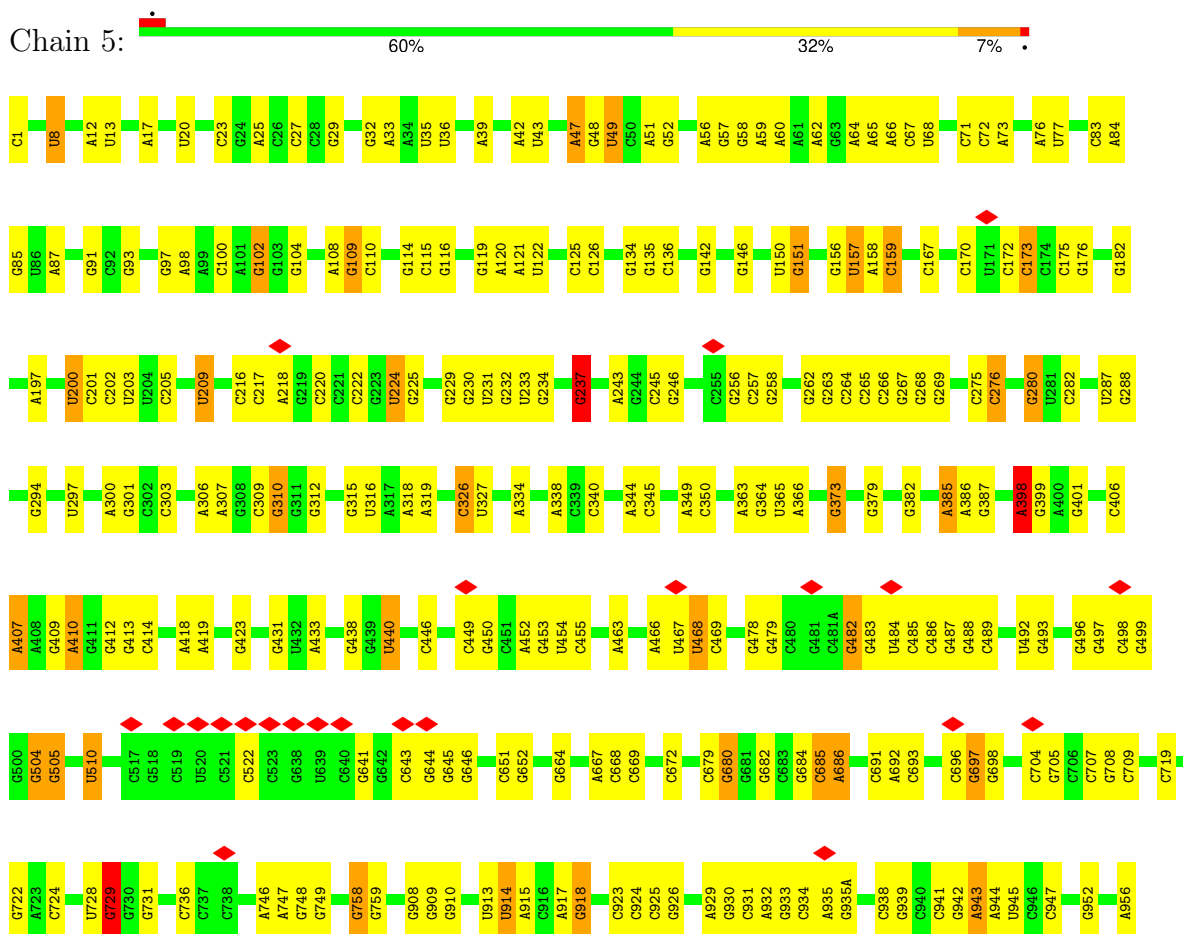
3 Residue-property plots

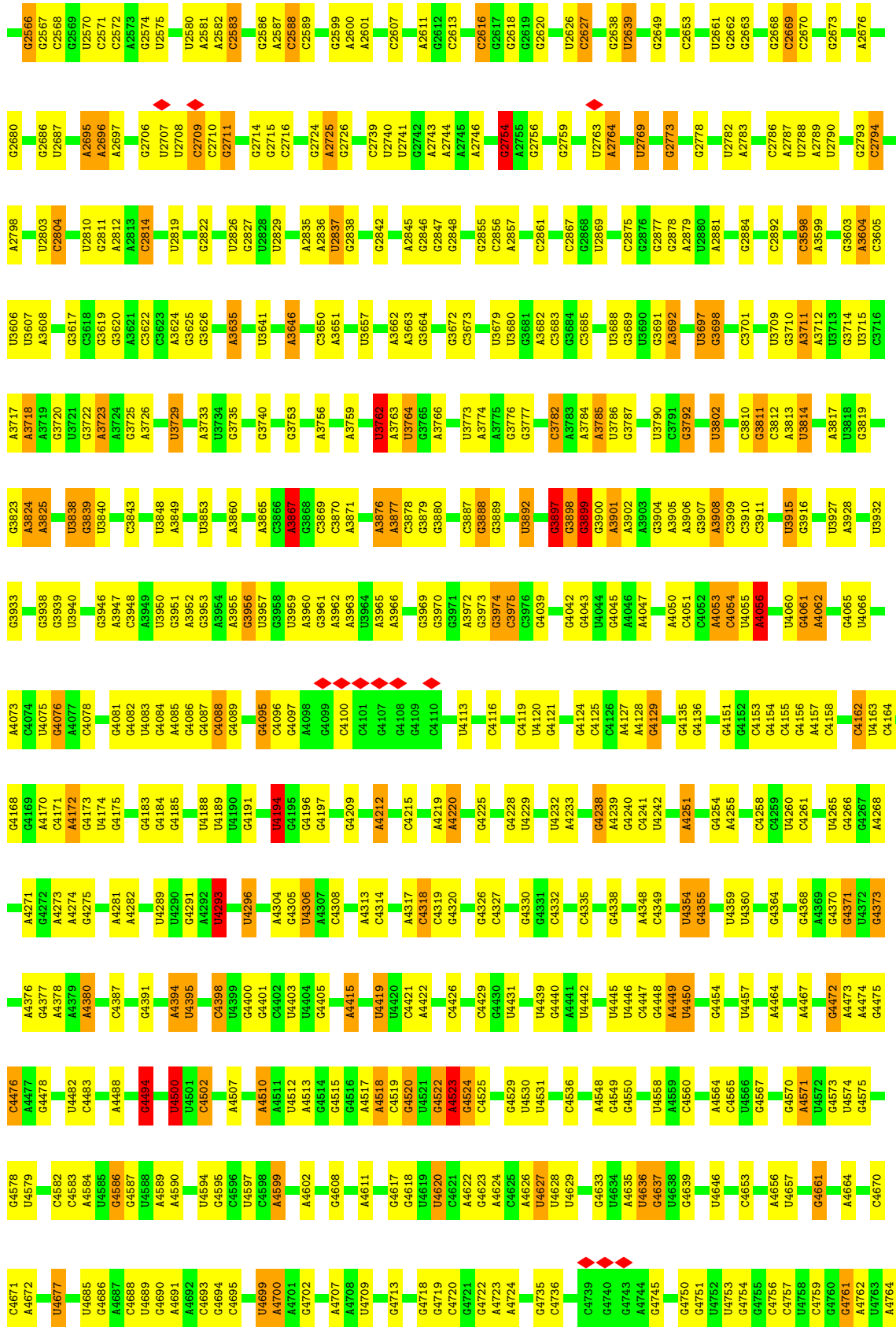
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

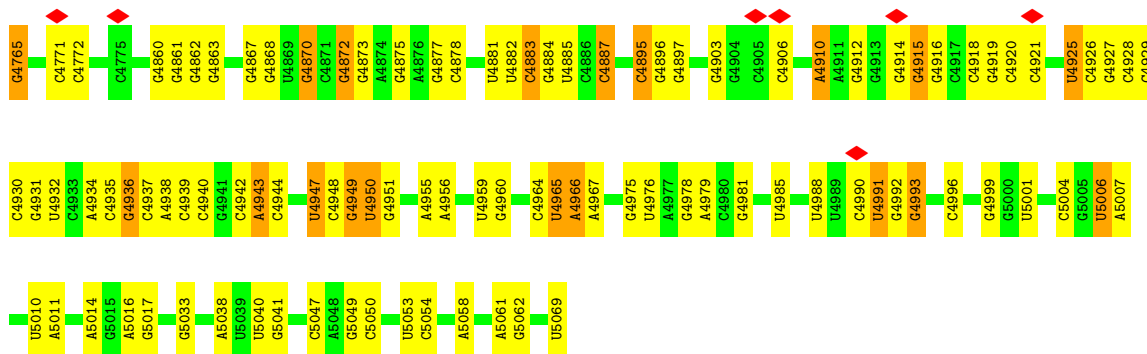
• Molecule 1: Z-site tRNA



• Molecule 2: 28S rRNA



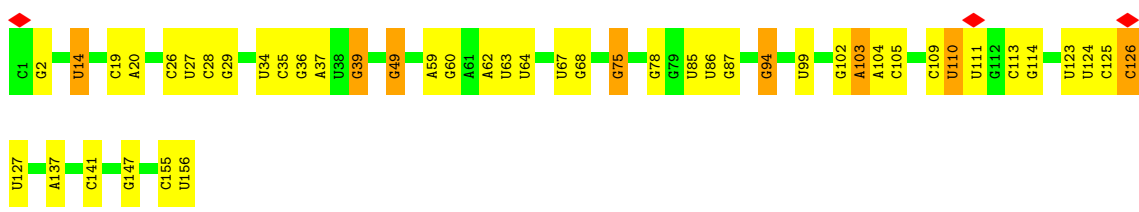




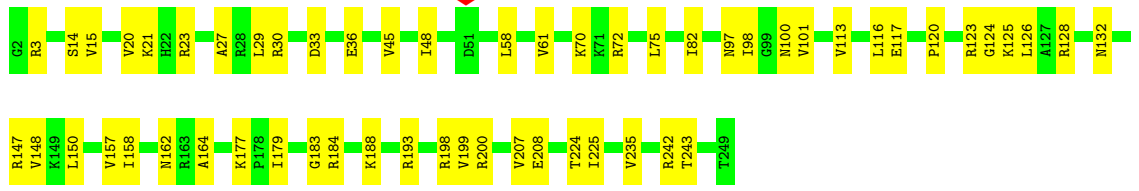
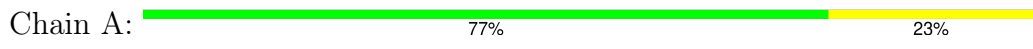
• Molecule 3: 5S rRNA



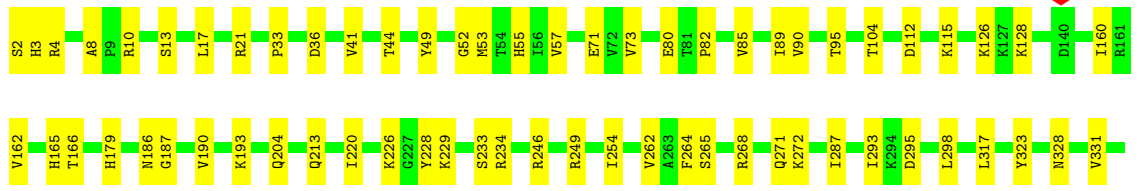
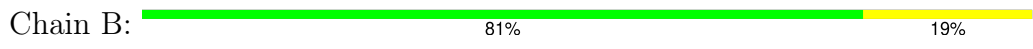
• Molecule 4: 5.8S rRNA



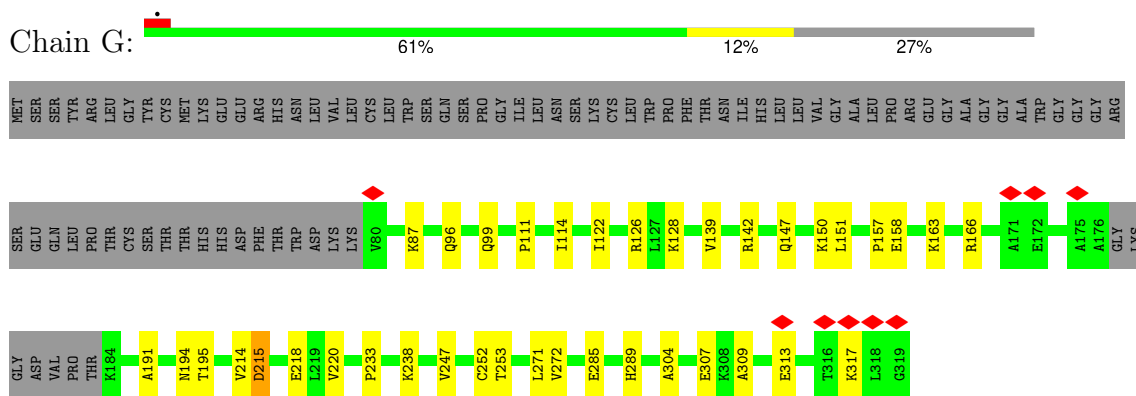
• Molecule 5: 60S ribosomal protein L8



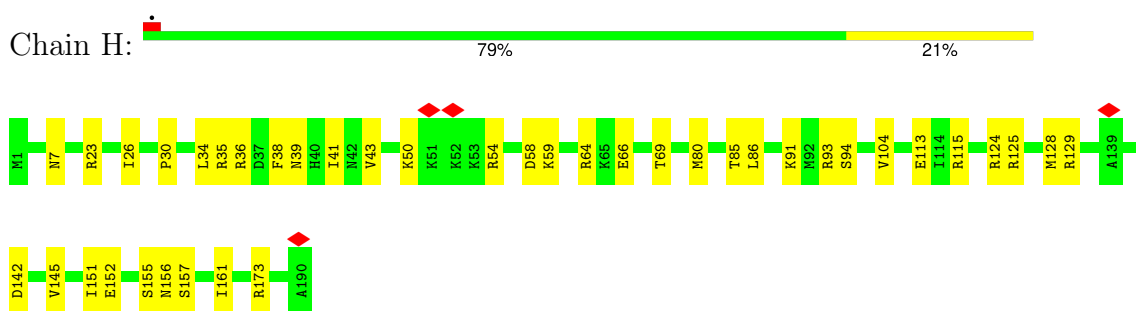
• Molecule 6: 60S ribosomal protein L3



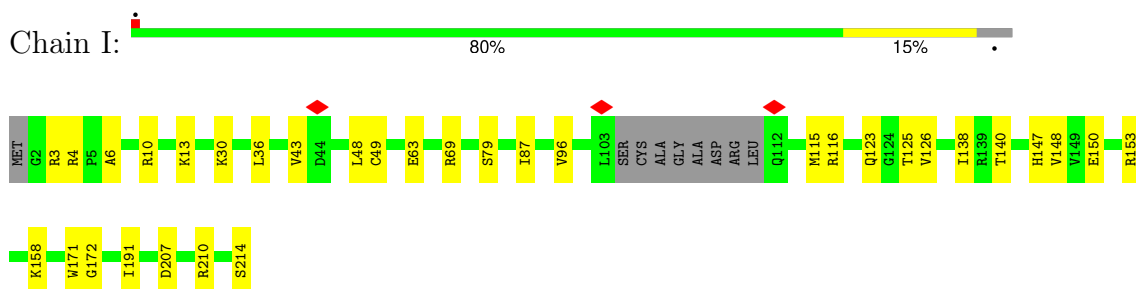
• Molecule 11: 60S ribosomal protein L7a



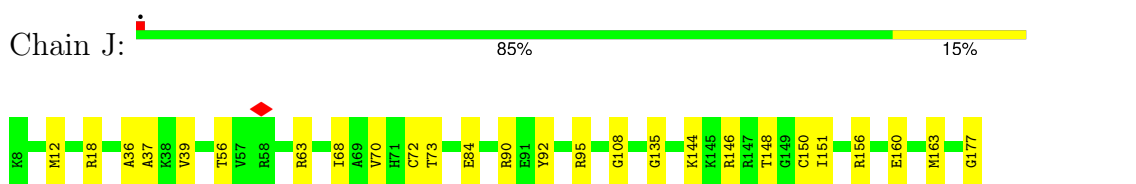
• Molecule 12: 60S ribosomal protein L9



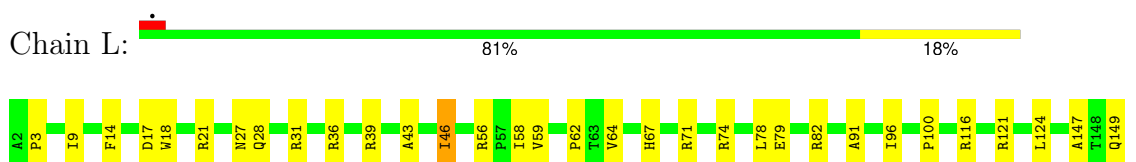
• Molecule 13: 60S ribosomal protein L10

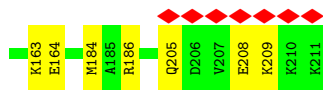


• Molecule 14: 60S ribosomal protein L11

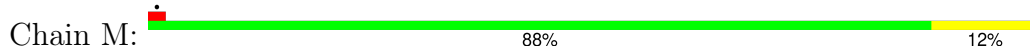


• Molecule 15: 60S ribosomal protein L13

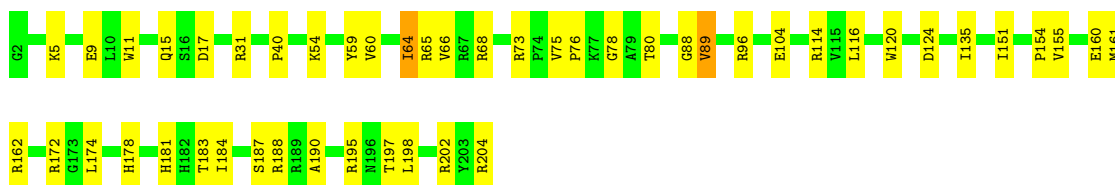




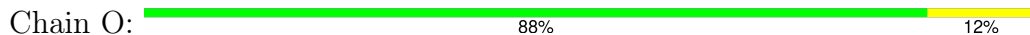
- Molecule 16: 60S ribosomal protein L14



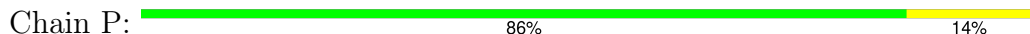
- Molecule 17: 60S Ribosomal protein L15



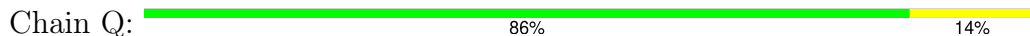
- Molecule 18: 60S ribosomal protein L13a



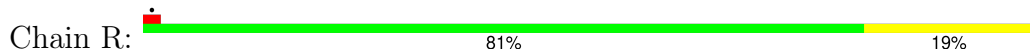
- Molecule 19: 60S ribosomal protein L17



- Molecule 20: 60S ribosomal protein L18

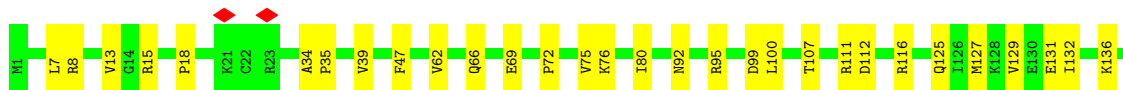
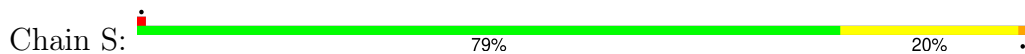


- Molecule 21: 60S ribosomal protein L19

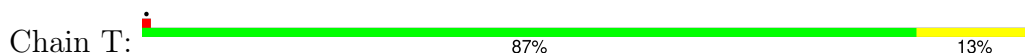




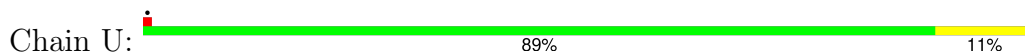
• Molecule 22: 60S ribosomal protein L18a



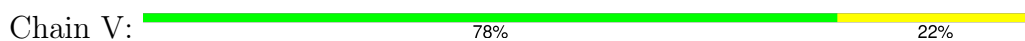
• Molecule 23: 60S ribosomal protein L21



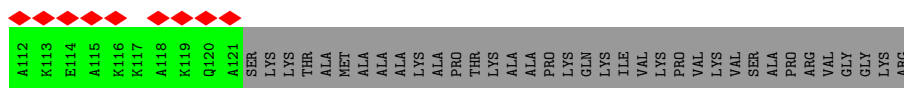
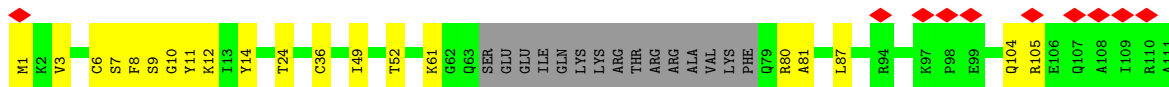
• Molecule 24: 60S ribosomal protein L22




• Molecule 25: 60S ribosomal protein L23

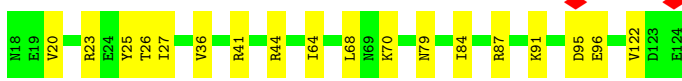


• Molecule 26: 60S ribosomal protein L24




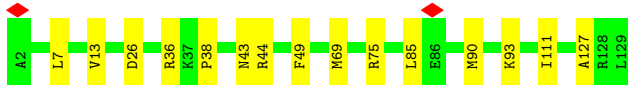
• Molecule 27: 60S ribosomal protein L23a

Chain d:  83% 17%




- Molecule 34: 60S ribosomal protein L32

Chain e:  88% 12%




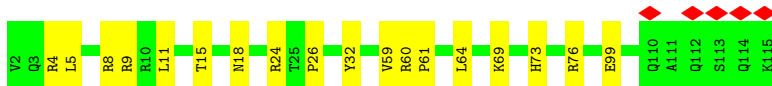
- Molecule 35: 60S ribosomal protein L35a

Chain f:  84% 16%




- Molecule 36: 60S ribosomal protein L34

Chain g:  84% 16%



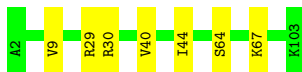
- Molecule 37: 60S ribosomal protein L35

Chain h:  92% 8%




- Molecule 38: 60S ribosomal protein L36

Chain i:  93% 7%

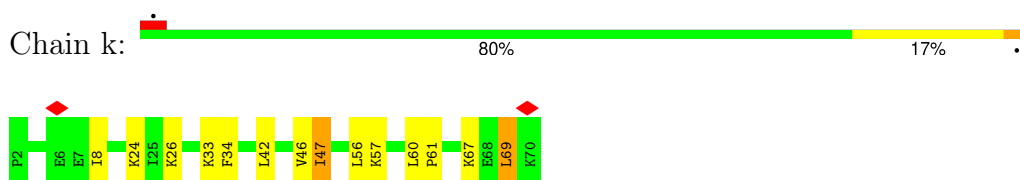


- Molecule 39: 60S ribosomal protein L37

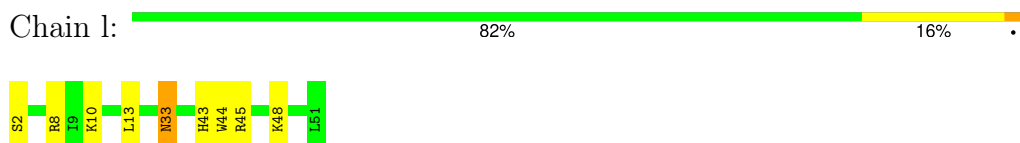
Chain j:  88% 12%



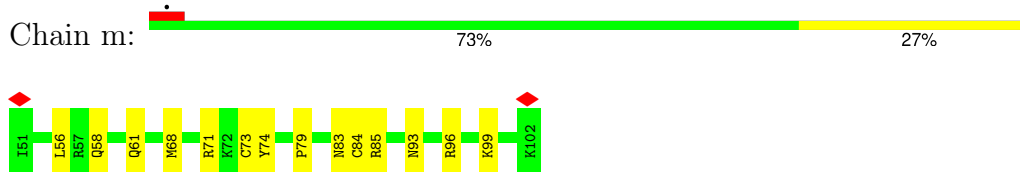
- Molecule 40: 60S ribosomal protein L38



- Molecule 41: 60S ribosomal protein L39



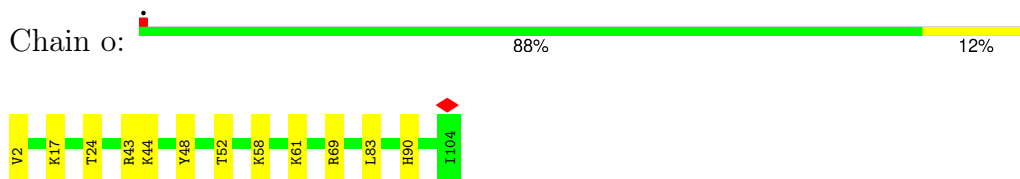
- Molecule 42: 60S ribosomal protein L40



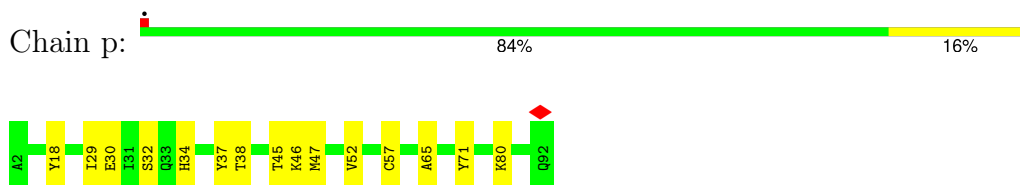
- Molecule 43: 60S ribosomal protein L41



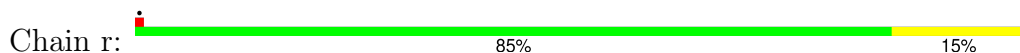
- Molecule 44: 60S ribosomal protein L36a

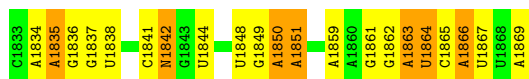


- Molecule 45: 60S ribosomal protein L37a

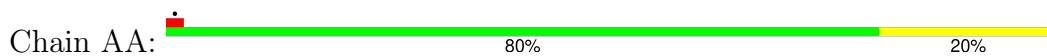


- Molecule 46: 60S ribosomal protein L28

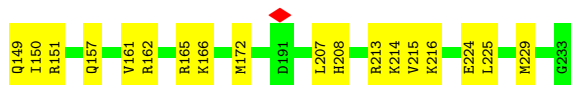
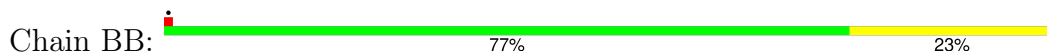




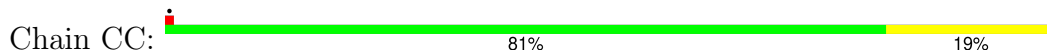
- Molecule 50: 40S ribosomal protein SA



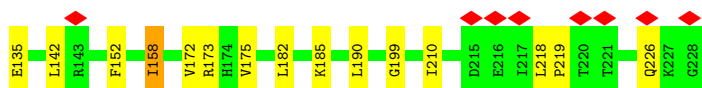
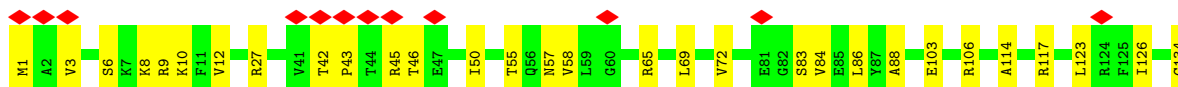
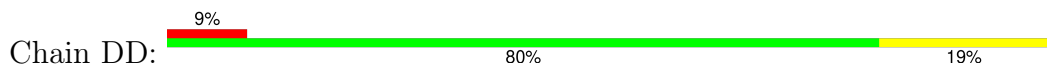
- Molecule 51: 40S ribosomal protein S3a



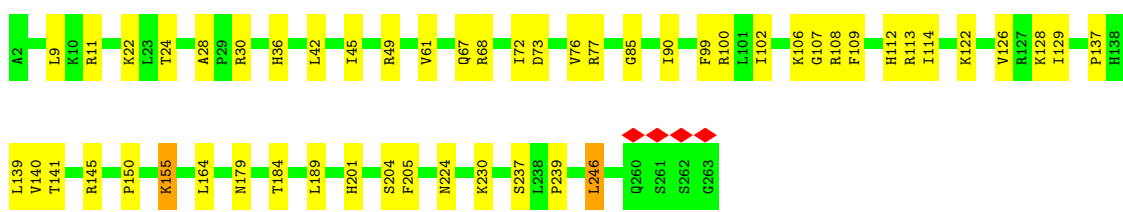
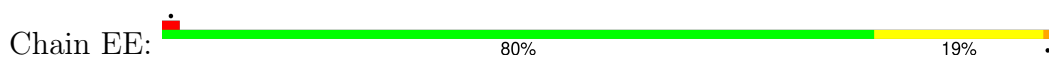
- Molecule 52: 40S ribosomal protein S2



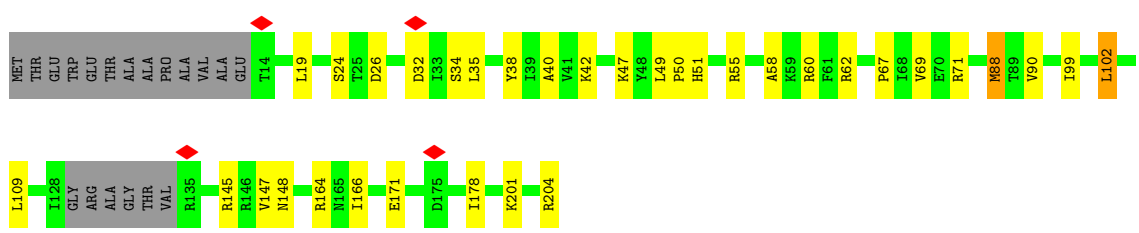
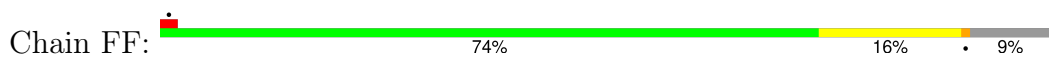
- Molecule 53: 40S ribosomal protein S3



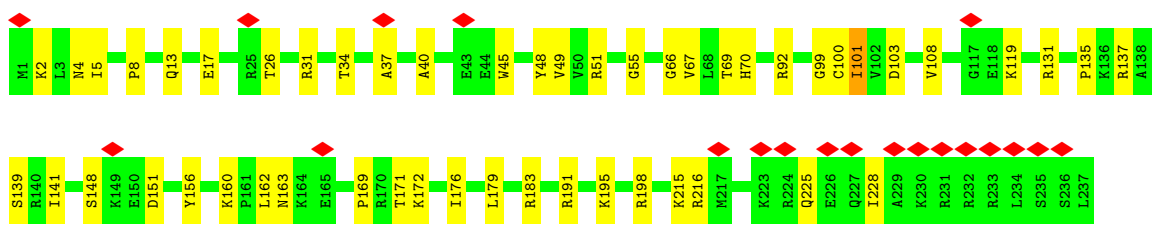
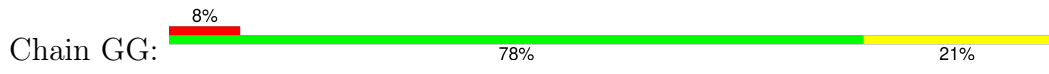
- Molecule 54: 40S ribosomal protein S4, X isoform



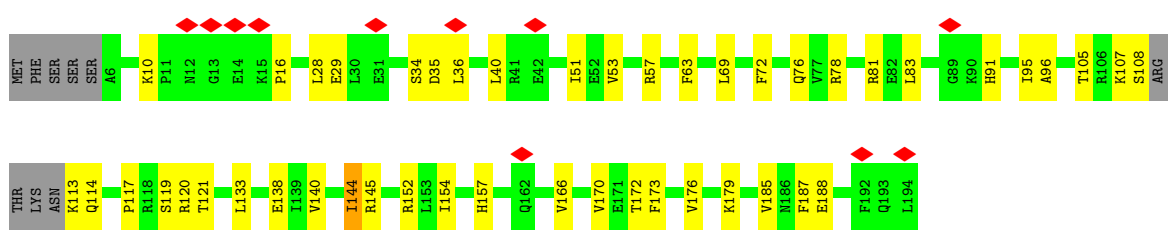
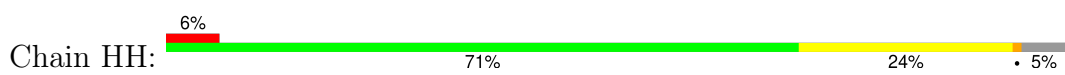
• Molecule 55: 40S ribosomal protein S5



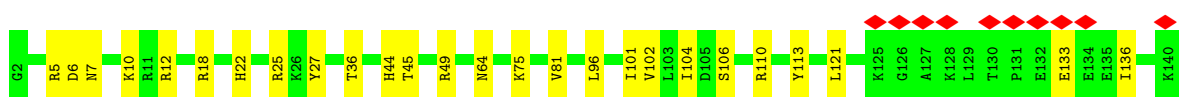
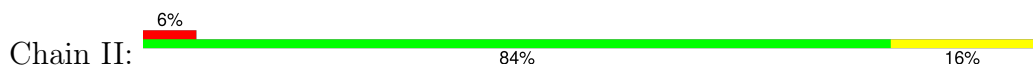
• Molecule 56: 40S ribosomal protein S6



• Molecule 57: 40S ribosomal protein S7

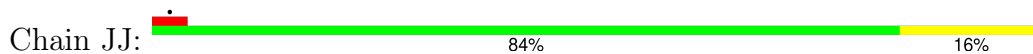


• Molecule 58: 40S ribosomal protein S8

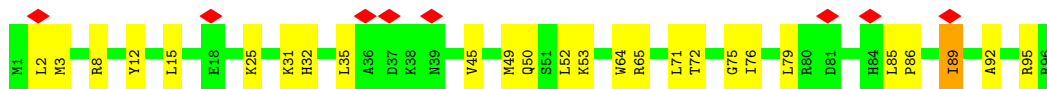
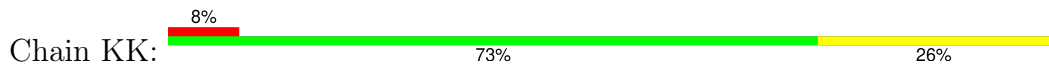




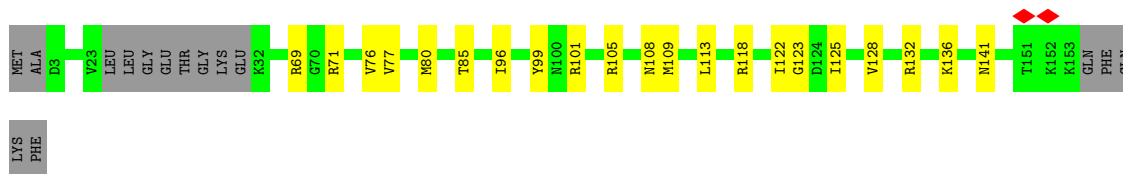
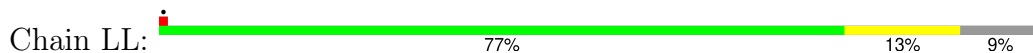
• Molecule 59: 40S ribosomal protein S9



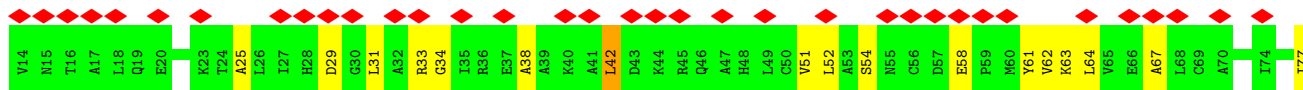
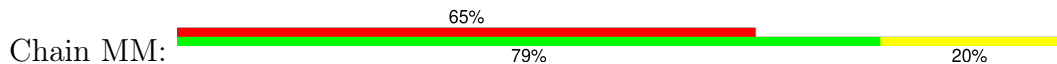
• Molecule 60: 40S ribosomal protein S10



• Molecule 61: 40S ribosomal protein S11




• Molecule 62: 40S ribosomal protein S12



• Molecule 63: 40S ribosomal protein S13




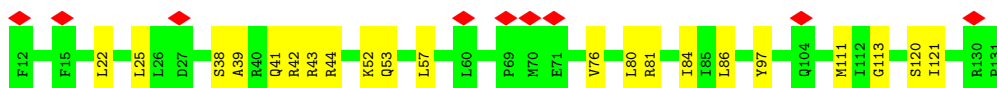
• Molecule 64: 40S ribosomal protein S14

Chain OO:  84% 15%




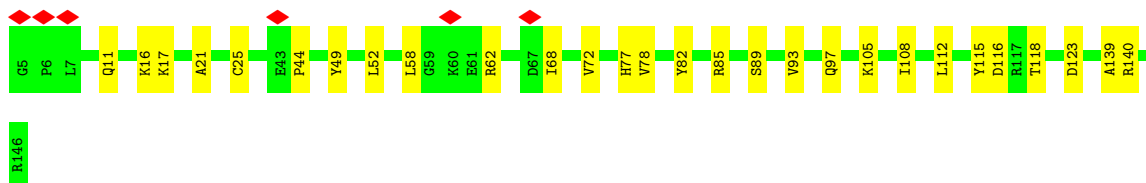
- Molecule 65: 40S ribosomal protein S15

Chain PP:  8% 82% 18%




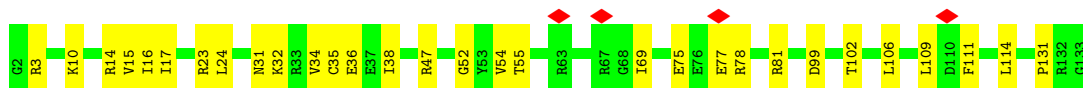
- Molecule 66: 40S ribosomal protein S16

Chain QQ:  80% 20%




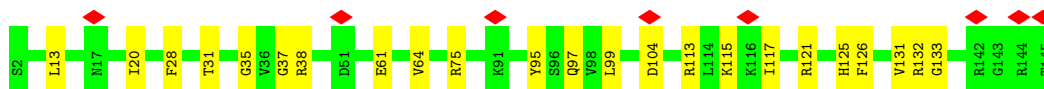
- Molecule 67: 40S ribosomal protein S17

Chain RR:  77% 23%




- Molecule 68: 40S ribosomal protein S18

Chain SS:  6% 84% 16%




- Molecule 69: 40S ribosomal protein S19

Chain TT:  84% 15%

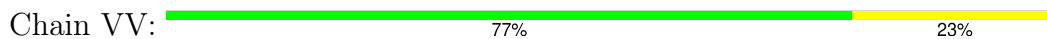


- Molecule 70: 40S ribosomal protein S20

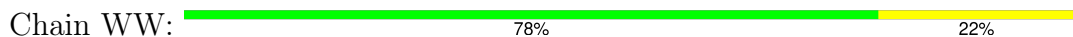
Chain UU:  9% 77% 22%



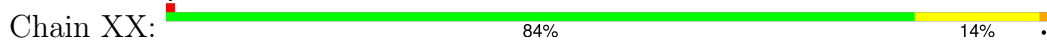
- Molecule 71: 40S ribosomal protein S21



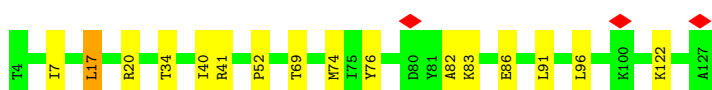
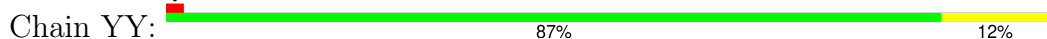
- Molecule 72: 40S ribosomal protein S15a



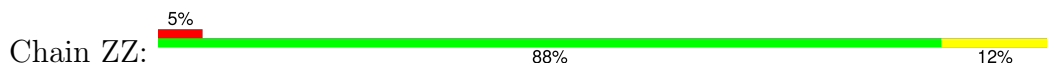
- Molecule 73: 40S ribosomal protein S23



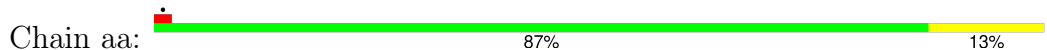
- Molecule 74: 40S ribosomal protein S24



- Molecule 75: 40S ribosomal protein S25



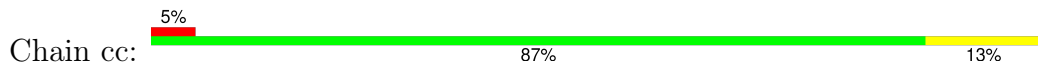
- Molecule 76: 40S ribosomal protein S26



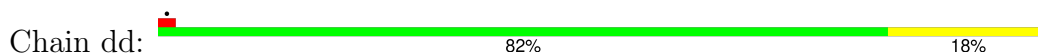
- Molecule 77: 40S ribosomal protein S27



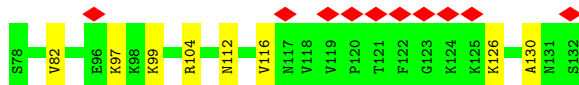
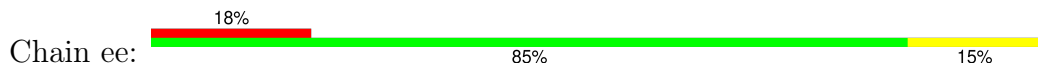
• Molecule 78: 40S ribosomal protein S28



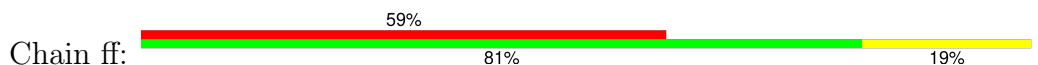
• Molecule 79: 40S ribosomal protein S29



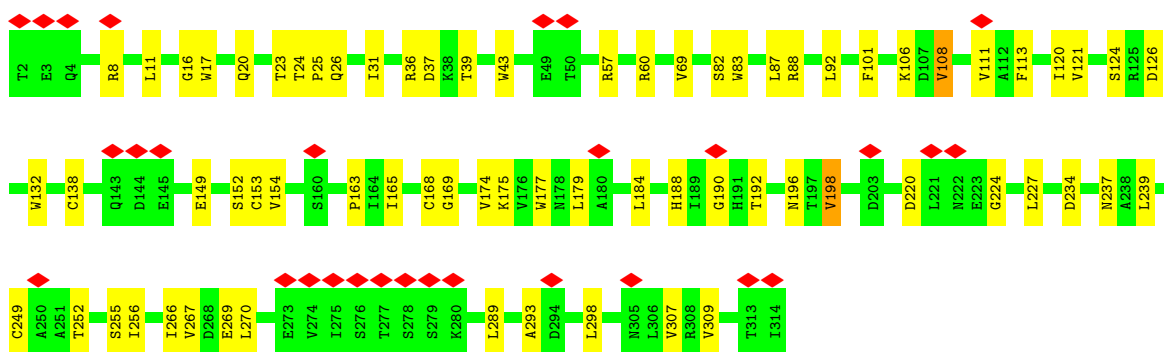
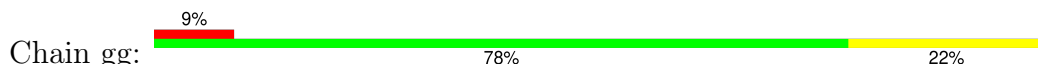
• Molecule 80: 40S ribosomal protein S30



• Molecule 81: 40S ribosomal protein S27a



• Molecule 82: Receptor of activated protein C kinase 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	74031	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	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	1.018	Depositor
Minimum map value	-0.622	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.1	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: B8H, 6MZ, PSU, I4U, 4AC, E3C, MG, OMC, MLZ, B8W, OMU, B9H, UR3, E7G, B8K, B8N, 5MC, A2M, P4U, B9B, 7MG, P7G, MA6, ZN, M7A, BGH, 2MG, OMG, B8T, E6G, 1MA, MHG, 5MU, B8Q

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	4	0.22	0/1779	0.45	0/2771
2	5	0.45	3/83825 (0.0%)	0.50	11/130614 (0.0%)
3	7	0.42	0/2858	0.42	0/4455
4	8	0.45	0/3559	0.46	0/5543
5	A	0.54	0/1936	0.76	1/2596 (0.0%)
6	B	0.48	0/3240	0.68	0/4339
7	C	0.49	0/2927	0.65	0/3932
8	D	0.39	0/2437	0.59	2/3264 (0.1%)
9	E	0.39	0/1762	0.64	1/2362 (0.0%)
10	F	0.49	0/1911	0.72	0/2549
11	G	0.43	0/1910	0.66	0/2569
12	H	0.43	0/1535	0.69	0/2063
13	I	0.43	0/1702	0.58	0/2272
14	J	0.39	0/1385	0.71	0/1852
15	L	0.42	0/1733	0.67	0/2316
16	M	0.44	0/1158	0.67	0/1547
17	N	0.52	0/1746	0.70	2/2338 (0.1%)
18	O	0.48	0/1662	0.67	0/2222
19	P	0.49	0/1268	0.67	0/1700
20	Q	0.49	0/1539	0.72	0/2054
21	R	0.47	0/1524	0.74	1/2013 (0.0%)
22	S	0.50	0/1501	0.68	0/2012
23	T	0.47	0/1326	0.66	0/1770
24	U	0.36	0/823	0.69	0/1104
25	V	0.46	0/993	0.63	0/1332
26	W	0.41	0/873	0.74	0/1158
27	X	0.43	0/984	0.61	0/1323
28	Y	0.42	0/1132	0.68	0/1504
29	Z	0.43	0/1130	0.63	0/1507
30	a	0.51	0/1191	0.63	0/1590

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	b	0.37	0/861	0.67	0/1138
32	c	0.46	0/771	0.66	0/1034
33	d	0.43	0/903	0.71	0/1216
34	e	0.48	0/1071	0.63	0/1429
35	f	0.50	0/895	0.70	0/1198
36	g	0.45	0/916	0.71	0/1220
37	h	0.41	0/1021	0.65	0/1348
38	i	0.40	0/841	0.64	0/1112
39	j	0.49	0/720	0.72	0/952
40	k	0.45	1/575 (0.2%)	0.65	1/761 (0.1%)
41	l	0.51	0/459	0.74	0/608
42	m	0.44	0/425	0.74	0/561
43	n	0.43	0/240	0.77	0/305
44	o	0.43	0/855	0.57	0/1128
45	p	0.48	0/718	0.66	0/953
46	r	0.50	0/1010	0.70	0/1354
47	u	0.29	0/1680	0.75	3/2255 (0.1%)
48	v	0.32	0/2779	0.72	0/3751
49	9	0.38	0/39723	0.47	0/61870
50	AA	0.42	0/1747	0.67	0/2374
51	BB	0.42	0/1756	0.72	0/2350
52	CC	0.43	0/1753	0.69	0/2369
53	DD	0.32	0/1796	0.67	2/2417 (0.1%)
54	EE	0.39	0/2118	0.66	0/2849
55	FF	0.39	0/1492	0.69	1/2005 (0.0%)
56	GG	0.33	0/1946	0.65	0/2590
57	HH	0.35	0/1510	0.70	0/2022
58	II	0.42	0/1715	0.68	0/2287
59	JJ	0.37	0/1550	0.62	0/2069
60	KK	0.32	0/834	0.73	2/1125 (0.2%)
61	LL	0.43	0/1195	0.64	0/1597
62	MM	0.30	0/918	0.72	2/1233 (0.2%)
63	NN	0.42	0/1226	0.70	0/1649
64	OO	0.45	0/1029	0.67	1/1380 (0.1%)
65	PP	0.36	0/1017	0.67	0/1358
66	QQ	0.34	0/1146	0.65	0/1534
67	RR	0.36	0/1082	0.70	0/1452
68	SS	0.31	0/1208	0.69	2/1618 (0.1%)
69	TT	0.32	0/1115	0.60	0/1493
70	UU	0.33	0/805	0.65	0/1081
71	VV	0.42	0/643	0.63	0/860
72	WW	0.46	0/1051	0.73	0/1406
73	XX	0.40	0/1116	0.68	2/1490 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
74	YY	0.34	0/1028	0.57	0/1366
75	ZZ	0.29	0/604	0.56	0/810
76	aa	0.47	1/828 (0.1%)	0.70	0/1109
77	bb	0.37	0/665	0.63	0/891
78	cc	0.34	0/490	0.61	0/656
79	dd	0.36	0/470	0.59	0/623
80	ee	0.32	0/447	0.66	0/587
81	ff	0.25	0/567	0.58	0/753
82	gg	0.29	0/2493	0.63	0/3394
All	All	0.42	5/229172 (0.0%)	0.57	34/335661 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	B	0	1
7	C	0	1
11	G	0	1
12	H	0	1
15	L	0	2
17	N	0	3
18	O	0	1
23	T	0	1
31	b	0	1
33	d	0	1
40	k	0	1
47	u	0	2
52	CC	0	1
54	EE	0	1
71	VV	0	1
72	WW	0	1
73	XX	0	1
81	ff	0	1
All	All	0	22

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
40	k	61	PRO	CA-C	5.65	1.55	1.52
2	5	4523	A2M	O3'-P	5.64	1.61	1.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	3785	A2M	O3'-P	5.22	1.61	1.56
76	aa	98	PRO	CA-C	-5.20	1.48	1.52
2	5	1534	A2M	O3'-P	5.04	1.61	1.56

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	4056	A	OP1-P-O3'	-9.67	78.98	108.00
64	OO	137	SER	N-CA-C	-6.58	103.72	111.03
2	5	4056	A	OP2-P-O3'	-6.48	88.57	108.00
5	A	15	VAL	N-CA-C	-6.26	106.61	113.43
40	k	61	PRO	O-C-N	6.13	124.03	121.15

There are no chirality outliers.

5 of 22 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	B	55	HIS	Peptide
7	C	73	VAL	Peptide
11	G	215	ASP	Peptide
12	H	50	LYS	Peptide
15	L	46	ILE	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	4	1593	0	809	11	0
2	5	77254	0	38800	555	0
3	7	2558	0	1296	17	0
4	8	3209	0	1631	25	0
5	A	1898	0	1993	41	0
6	B	3172	0	3310	54	0
7	C	2884	0	3054	36	0
8	D	2391	0	2424	29	0
9	E	1729	0	1887	20	0
10	F	1875	0	1995	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	G	1879	0	2027	29	0
12	H	1516	0	1595	28	0
13	I	1664	0	1712	19	0
14	J	1362	0	1399	16	0
15	L	1702	0	1820	29	0
16	M	1137	0	1209	12	0
17	N	1701	0	1749	33	0
18	O	1630	0	1778	17	0
19	P	1242	0	1274	17	0
20	Q	1515	0	1634	21	0
21	R	1508	0	1664	27	0
22	S	1462	0	1508	25	0
23	T	1298	0	1366	16	0
24	U	809	0	833	7	0
25	V	979	0	1039	21	0
26	W	860	0	903	17	0
27	X	967	0	1040	9	0
28	Y	1115	0	1205	16	0
29	Z	1107	0	1182	15	0
30	a	1162	0	1209	20	0
31	b	848	0	920	8	0
32	c	761	0	794	4	0
33	d	888	0	930	11	0
34	e	1053	0	1147	12	0
35	f	876	0	912	12	0
36	g	906	0	998	11	0
37	h	1013	0	1147	10	0
38	i	830	0	916	6	0
39	j	705	0	737	8	0
40	k	569	0	637	8	0
41	l	447	0	480	8	0
42	m	430	0	466	10	0
43	n	239	0	289	10	0
44	o	842	0	913	9	0
45	p	708	0	756	12	0
46	r	994	0	1051	12	0
47	u	1654	0	1760	33	0
48	v	2737	0	2782	24	0
49	9	36291	0	18321	273	0
50	AA	1710	0	1708	29	0
51	BB	1729	0	1803	35	0
52	CC	1716	0	1806	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	DD	1768	0	1866	31	0
54	EE	2076	0	2177	32	0
55	FF	1471	0	1522	24	0
56	GG	1923	0	2089	40	0
57	HH	1488	0	1582	29	0
58	II	1686	0	1772	21	0
59	JJ	1525	0	1640	21	0
60	KK	810	0	836	18	0
61	LL	1175	0	1249	16	0
62	MM	908	0	939	16	0
63	NN	1202	0	1289	11	0
64	OO	1016	0	1039	16	0
65	PP	997	0	1045	13	0
66	QQ	1128	0	1195	19	0
67	RR	1068	0	1121	21	0
68	SS	1190	0	1249	15	0
69	TT	1097	0	1132	20	0
70	UU	795	0	862	14	0
71	VV	636	0	637	12	0
72	WW	1034	0	1080	24	0
73	XX	1098	0	1167	16	0
74	YY	1011	0	1083	10	0
75	ZZ	598	0	656	8	0
76	aa	814	0	865	9	0
77	bb	651	0	672	5	0
78	cc	488	0	514	6	0
79	dd	459	0	449	10	0
80	ee	443	0	492	6	0
81	ff	555	0	566	11	0
82	gg	2436	0	2393	44	0
83	5	199	0	0	0	0
83	7	7	0	0	0	0
83	8	6	0	0	0	0
83	9	77	0	0	0	0
83	A	1	0	0	0	0
83	B	1	0	0	0	0
83	LL	1	0	0	0	0
83	P	2	0	0	0	0
83	TT	1	0	0	0	0
83	V	1	0	0	0	0
83	j	1	0	0	0	0
84	aa	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	dd	1	0	0	0	0
84	ff	1	0	0	0	0
84	g	1	0	0	0	0
84	j	1	0	0	0	0
84	m	1	0	0	0	0
84	o	1	0	0	0	0
84	p	1	0	0	0	0
All	All	216975	0	161796	1824	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 1824 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1860:B8H:C4	2:5:1860:B8H:C5	1.82	1.57
2:5:4296:B8H:C5	2:5:4296:B8H:C4	1.83	1.56
2:5:1860:B8H:C6	2:5:1860:B8H:N1	1.68	1.54
2:5:3762:B8H:C6	2:5:3762:B8H:N1	1.68	1.54
2:5:3762:B8H:C4	2:5:3762:B8H:C5	1.82	1.54

There are no symmetry-related clashes.

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	
5	A	246/248 (99%)	218 (89%)	28 (11%)	0	100	100
6	B	392/394 (100%)	364 (93%)	27 (7%)	1 (0%)	36	65
7	C	359/362 (99%)	343 (96%)	16 (4%)	0	100	100
8	D	291/293 (99%)	277 (95%)	14 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	E	208/291 (72%)	193 (93%)	15 (7%)	0	100	100
10	F	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
11	G	229/319 (72%)	221 (96%)	8 (4%)	0	100	100
12	H	188/190 (99%)	179 (95%)	9 (5%)	0	100	100
13	I	201/214 (94%)	194 (96%)	7 (4%)	0	100	100
14	J	168/170 (99%)	166 (99%)	2 (1%)	0	100	100
15	L	208/210 (99%)	200 (96%)	7 (3%)	1 (0%)	24	54
16	M	136/138 (99%)	130 (96%)	6 (4%)	0	100	100
17	N	201/203 (99%)	186 (92%)	15 (8%)	0	100	100
18	O	197/199 (99%)	193 (98%)	4 (2%)	0	100	100
19	P	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
20	Q	185/187 (99%)	173 (94%)	12 (6%)	0	100	100
21	R	178/180 (99%)	172 (97%)	6 (3%)	0	100	100
22	S	174/176 (99%)	164 (94%)	9 (5%)	1 (1%)	21	50
23	T	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
24	U	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
25	V	129/131 (98%)	122 (95%)	7 (5%)	0	100	100
26	W	102/157 (65%)	97 (95%)	5 (5%)	0	100	100
27	X	116/118 (98%)	110 (95%)	6 (5%)	0	100	100
28	Y	132/134 (98%)	128 (97%)	4 (3%)	0	100	100
29	Z	133/135 (98%)	126 (95%)	6 (4%)	1 (1%)	16	44
30	a	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
31	b	100/245 (41%)	93 (93%)	7 (7%)	0	100	100
32	c	96/98 (98%)	89 (93%)	7 (7%)	0	100	100
33	d	105/107 (98%)	95 (90%)	9 (9%)	1 (1%)	12	40
34	e	126/128 (98%)	118 (94%)	8 (6%)	0	100	100
35	f	107/109 (98%)	105 (98%)	2 (2%)	0	100	100
36	g	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
37	h	120/122 (98%)	120 (100%)	0	0	100	100
38	i	100/102 (98%)	94 (94%)	6 (6%)	0	100	100
39	j	84/86 (98%)	75 (89%)	9 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	k	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
41	l	48/50 (96%)	41 (85%)	7 (15%)	0	100	100
42	m	49/52 (94%)	43 (88%)	5 (10%)	1 (2%)	6	25
43	n	23/25 (92%)	23 (100%)	0	0	100	100
44	o	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
45	p	89/91 (98%)	84 (94%)	5 (6%)	0	100	100
46	r	122/124 (98%)	117 (96%)	5 (4%)	0	100	100
47	u	204/206 (99%)	173 (85%)	29 (14%)	2 (1%)	12	40
48	v	348/441 (79%)	320 (92%)	28 (8%)	0	100	100
50	AA	215/217 (99%)	201 (94%)	14 (6%)	0	100	100
51	BB	211/213 (99%)	200 (95%)	11 (5%)	0	100	100
52	CC	219/221 (99%)	212 (97%)	7 (3%)	0	100	100
53	DD	226/228 (99%)	217 (96%)	9 (4%)	0	100	100
54	EE	260/262 (99%)	243 (94%)	17 (6%)	0	100	100
55	FF	181/204 (89%)	172 (95%)	9 (5%)	0	100	100
56	GG	235/237 (99%)	226 (96%)	9 (4%)	0	100	100
57	HH	181/194 (93%)	172 (95%)	9 (5%)	0	100	100
58	II	204/206 (99%)	192 (94%)	12 (6%)	0	100	100
59	JJ	183/185 (99%)	177 (97%)	6 (3%)	0	100	100
60	KK	94/96 (98%)	86 (92%)	8 (8%)	0	100	100
61	LL	139/158 (88%)	132 (95%)	7 (5%)	0	100	100
62	MM	115/117 (98%)	102 (89%)	13 (11%)	0	100	100
63	NN	147/149 (99%)	136 (92%)	11 (8%)	0	100	100
64	OO	134/136 (98%)	126 (94%)	8 (6%)	0	100	100
65	PP	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
66	QQ	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
67	RR	130/132 (98%)	125 (96%)	5 (4%)	0	100	100
68	SS	142/144 (99%)	134 (94%)	8 (6%)	0	100	100
69	TT	139/141 (99%)	132 (95%)	7 (5%)	0	100	100
70	UU	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
71	VV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
72	WW	127/129 (98%)	121 (95%)	6 (5%)	0	100	100
73	XX	139/141 (99%)	130 (94%)	7 (5%)	2 (1%)	9	31
74	YY	122/124 (98%)	119 (98%)	3 (2%)	0	100	100
75	ZZ	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
76	aa	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
77	bb	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
78	cc	60/62 (97%)	58 (97%)	2 (3%)	0	100	100
79	dd	53/55 (96%)	52 (98%)	1 (2%)	0	100	100
80	ee	53/55 (96%)	51 (96%)	2 (4%)	0	100	100
81	ff	66/68 (97%)	58 (88%)	8 (12%)	0	100	100
82	gg	311/313 (99%)	279 (90%)	32 (10%)	0	100	100
All	All	11723/12395 (95%)	11060 (94%)	653 (6%)	10 (0%)	49	78

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
42	m	73	CYS
6	B	295	ASP
33	d	96	GLU
47	u	61	PRO
47	u	198	TRP

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	
5	A	190/190 (100%)	188 (99%)	2 (1%)	65	74
6	B	342/342 (100%)	340 (99%)	2 (1%)	78	80
7	C	301/301 (100%)	299 (99%)	2 (1%)	76	78
8	D	247/247 (100%)	246 (100%)	1 (0%)	84	83
9	E	190/251 (76%)	186 (98%)	4 (2%)	47	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	F	196/196 (100%)	194 (99%)	2 (1%)	68	75
11	G	200/272 (74%)	199 (100%)	1 (0%)	81	81
12	H	169/169 (100%)	168 (99%)	1 (1%)	78	80
13	I	175/181 (97%)	172 (98%)	3 (2%)	53	67
14	J	143/143 (100%)	143 (100%)	0	100	100
15	L	175/175 (100%)	173 (99%)	2 (1%)	65	74
16	M	117/117 (100%)	117 (100%)	0	100	100
17	N	171/171 (100%)	169 (99%)	2 (1%)	63	72
18	O	171/171 (100%)	170 (99%)	1 (1%)	78	80
19	P	134/134 (100%)	133 (99%)	1 (1%)	76	78
20	Q	164/164 (100%)	164 (100%)	0	100	100
21	R	159/159 (100%)	159 (100%)	0	100	100
22	S	157/157 (100%)	155 (99%)	2 (1%)	61	71
23	T	139/139 (100%)	138 (99%)	1 (1%)	76	78
24	U	89/89 (100%)	89 (100%)	0	100	100
25	V	101/101 (100%)	101 (100%)	0	100	100
26	W	86/126 (68%)	86 (100%)	0	100	100
27	X	106/106 (100%)	105 (99%)	1 (1%)	70	76
28	Y	124/124 (100%)	123 (99%)	1 (1%)	73	77
29	Z	117/117 (100%)	116 (99%)	1 (1%)	70	76
30	a	119/119 (100%)	119 (100%)	0	100	100
31	b	84/184 (46%)	84 (100%)	0	100	100
32	c	84/84 (100%)	83 (99%)	1 (1%)	63	72
33	d	98/98 (100%)	98 (100%)	0	100	100
34	e	114/114 (100%)	113 (99%)	1 (1%)	70	76
35	f	88/88 (100%)	88 (100%)	0	100	100
36	g	98/98 (100%)	95 (97%)	3 (3%)	35	59
37	h	109/109 (100%)	109 (100%)	0	100	100
38	i	86/86 (100%)	85 (99%)	1 (1%)	63	72
39	j	73/73 (100%)	72 (99%)	1 (1%)	59	70
40	k	64/64 (100%)	63 (98%)	1 (2%)	55	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	l	47/47 (100%)	46 (98%)	1 (2%)	47	64
42	m	47/47 (100%)	47 (100%)	0	100	100
43	n	24/24 (100%)	24 (100%)	0	100	100
44	o	91/91 (100%)	91 (100%)	0	100	100
45	p	74/74 (100%)	74 (100%)	0	100	100
46	r	108/108 (100%)	107 (99%)	1 (1%)	70	76
47	u	186/186 (100%)	183 (98%)	3 (2%)	55	68
48	v	289/355 (81%)	284 (98%)	5 (2%)	53	67
50	AA	180/181 (99%)	179 (99%)	1 (1%)	78	80
51	BB	194/194 (100%)	192 (99%)	2 (1%)	68	75
52	CC	187/187 (100%)	181 (97%)	6 (3%)	34	58
53	DD	190/190 (100%)	189 (100%)	1 (0%)	81	81
54	EE	224/224 (100%)	223 (100%)	1 (0%)	84	83
55	FF	158/170 (93%)	156 (99%)	2 (1%)	61	71
56	GG	207/207 (100%)	206 (100%)	1 (0%)	81	81
57	HH	165/174 (95%)	161 (98%)	4 (2%)	43	62
58	II	178/178 (100%)	177 (99%)	1 (1%)	78	80
59	JJ	161/161 (100%)	161 (100%)	0	100	100
60	KK	87/87 (100%)	86 (99%)	1 (1%)	65	74
61	LL	130/142 (92%)	129 (99%)	1 (1%)	73	77
62	MM	99/99 (100%)	98 (99%)	1 (1%)	68	75
63	NN	130/130 (100%)	130 (100%)	0	100	100
64	OO	106/106 (100%)	106 (100%)	0	100	100
65	PP	109/109 (100%)	108 (99%)	1 (1%)	70	76
66	QQ	117/117 (100%)	116 (99%)	1 (1%)	70	76
67	RR	119/119 (100%)	119 (100%)	0	100	100
68	SS	125/125 (100%)	125 (100%)	0	100	100
69	TT	111/111 (100%)	109 (98%)	2 (2%)	51	67
70	UU	92/92 (100%)	89 (97%)	3 (3%)	33	57
71	VV	67/67 (100%)	65 (97%)	2 (3%)	36	59
72	WW	112/112 (100%)	110 (98%)	2 (2%)	51	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	XX	113/113 (100%)	112 (99%)	1 (1%)	70	76
74	YY	107/107 (100%)	106 (99%)	1 (1%)	70	76
75	ZZ	66/66 (100%)	66 (100%)	0	100	100
76	aa	88/88 (100%)	88 (100%)	0	100	100
77	bb	75/75 (100%)	75 (100%)	0	100	100
78	cc	55/55 (100%)	54 (98%)	1 (2%)	51	67
79	dd	48/48 (100%)	48 (100%)	0	100	100
80	ee	46/46 (100%)	46 (100%)	0	100	100
81	ff	61/61 (100%)	61 (100%)	0	100	100
82	gg	272/272 (100%)	269 (99%)	3 (1%)	65	74
All	All	10225/10604 (96%)	10138 (99%)	87 (1%)	68	76

5 of 87 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
53	DD	158	ILE
66	QQ	93	VAL
55	FF	102	LEU
57	HH	144	ILE
70	UU	54	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

Mol	Chain	Res	Type
55	FF	74	ASN
66	QQ	80	GLN
55	FF	82	ASN
58	II	168	GLN
73	XX	61	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	4	74/75 (98%)	35 (47%)	1 (1%)
2	5	3558/3597 (98%)	899 (25%)	68 (1%)
3	7	119/120 (99%)	14 (11%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	8	149/151 (98%)	27 (18%)	1 (0%)
49	9	1682/1698 (99%)	391 (23%)	20 (1%)
All	All	5582/5641 (98%)	1366 (24%)	90 (1%)

5 of 1366 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	4	2	C
1	4	3	C
1	4	4	C
1	4	8	U
1	4	9	A

5 of 90 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	5	4075	U
49	9	140	U
2	5	4232	U
2	5	4884	G
49	9	553	U

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

137 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
2	PSU	5	4403	2	18,21,22	0.99	1 (5%)	21,30,33	2.00	6 (28%)
49	OMC	9	517	49	19,22,23	2.86	7 (36%)	25,31,34	1.01	1 (4%)
2	OMG	5	1625	2,83	23,26,27	2.33	8 (34%)	32,38,41	1.93	8 (25%)
2	A2M	5	2363	2,83	22,25,26	3.98	13 (59%)	30,36,39	2.44	12 (40%)
2	PSU	5	4442	2	18,21,22	1.08	2 (11%)	21,30,33	2.08	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMG	5	2364	2	23,26,27	2.37	8 (34%)	32,38,41	1.96	7 (21%)
2	A2M	5	1524	2	22,25,26	3.95	12 (54%)	30,36,39	2.65	14 (46%)
2	B9B	5	237	2	25,28,29	3.81	9 (36%)	35,40,43	2.64	14 (40%)
49	OMU	9	116	49	19,22,23	2.82	7 (36%)	25,31,34	1.87	5 (20%)
2	OMG	5	4494	2	23,26,27	2.43	9 (39%)	32,38,41	1.97	11 (34%)
2	OMC	5	4536	2	19,22,23	2.77	7 (36%)	25,31,34	1.02	1 (4%)
49	M7A	9	1806	49	19,25,26	1.62	2 (10%)	25,37,40	3.88	8 (32%)
49	PSU	9	1243	49	18,21,22	1.22	2 (11%)	21,30,33	1.43	4 (19%)
2	2MG	5	4872	2	23,26,27	2.84	9 (39%)	33,38,41	3.31	16 (48%)
2	B8W	5	4529	2,83	23,26,27	3.35	11 (47%)	33,38,41	5.90	22 (66%)
2	OMG	5	3792	2	23,26,27	2.41	8 (34%)	32,38,41	2.05	9 (28%)
2	B8K	5	3897	2	24,28,29	4.73	17 (70%)	29,42,45	2.73	14 (48%)
2	OMG	5	4196	2	23,26,27	2.37	8 (34%)	32,38,41	1.92	8 (25%)
2	1MA	5	4415	2	21,25,26	2.66	5 (23%)	30,37,40	1.80	5 (16%)
2	PSU	5	3729	2	18,21,22	1.08	2 (11%)	21,30,33	1.84	4 (19%)
2	A2M	5	2401	2,83	22,25,26	3.92	13 (59%)	30,36,39	2.36	9 (30%)
2	OMC	5	2861	2	19,22,23	2.85	7 (36%)	25,31,34	1.07	2 (8%)
2	A2M	5	1534	2,83	22,25,26	3.97	12 (54%)	30,36,39	2.48	13 (43%)
2	UR3	5	4597	2	19,22,23	2.62	6 (31%)	26,32,35	1.57	5 (19%)
2	2MG	5	1517	2	23,26,27	2.91	7 (30%)	33,38,41	2.60	9 (27%)
2	PSU	5	3764	2	18,21,22	1.03	1 (5%)	21,30,33	1.70	4 (19%)
49	B8Q	9	1219	49,83	18,22,23	2.89	5 (27%)	21,32,35	2.63	7 (33%)
49	B8N	9	1248	49	25,29,30	3.08	7 (28%)	28,42,45	2.05	7 (25%)
2	OMG	5	1883	2	23,26,27	2.47	8 (34%)	32,38,41	2.06	9 (28%)
2	OMC	5	3701	2,83	19,22,23	2.77	7 (36%)	25,31,34	0.83	0
49	OMC	9	1710	49	19,22,23	2.93	7 (36%)	25,31,34	1.15	2 (8%)
2	PSU	5	2508	2	18,21,22	1.01	1 (5%)	21,30,33	1.69	4 (19%)
2	A2M	5	398	2	22,25,26	3.92	11 (50%)	30,36,39	2.35	10 (33%)
49	A2M	9	1031	49	22,25,26	3.94	12 (54%)	30,36,39	2.41	10 (33%)
2	A2M	5	1326	2	22,25,26	3.94	13 (59%)	30,36,39	2.32	9 (30%)
2	I4U	5	1659	2	20,24,25	4.95	13 (65%)	27,34,37	2.02	3 (11%)
2	E6G	5	4355	2	24,27,28	3.61	11 (45%)	34,39,42	2.64	13 (38%)
2	OMC	5	2422	2,83	19,22,23	2.91	7 (36%)	25,31,34	0.78	1 (4%)
2	MHG	5	4371	2	29,32,33	3.66	11 (37%)	34,46,49	2.46	12 (35%)
49	OMG	9	683	49	23,26,27	2.42	9 (39%)	32,38,41	1.99	9 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	A2M	5	3723	2	22,25,26	3.97	12 (54%)	30,36,39	2.28	8 (26%)
2	A2M	5	1871	2,83	22,25,26	3.92	12 (54%)	30,36,39	2.42	10 (33%)
2	OMC	5	3909	2	19,22,23	2.83	7 (36%)	25,31,34	0.66	0
49	PSU	9	823	49	18,21,22	1.06	2 (11%)	21,30,33	1.82	4 (19%)
2	7MG	5	2522	2	23,26,27	3.17	10 (43%)	27,39,42	2.18	9 (33%)
2	PSU	5	1582	2	18,21,22	1.18	2 (11%)	21,30,33	1.94	4 (19%)
2	BGH	5	3899	2,83	25,29,30	4.11	15 (60%)	30,43,46	2.70	16 (53%)
2	B9B	5	2754	2,83	25,28,29	3.74	9 (36%)	35,40,43	2.46	10 (28%)
49	4AC	9	1337	49	21,24,25	3.14	10 (47%)	28,34,37	1.18	4 (14%)
2	UR3	5	4530	2	19,22,23	2.69	7 (36%)	26,32,35	1.67	6 (23%)
2	A2M	5	4571	2	22,25,26	3.93	11 (50%)	30,36,39	2.40	10 (33%)
2	B8K	5	4690	2	24,28,29	4.92	17 (70%)	29,42,45	2.80	13 (44%)
49	A2M	9	668	49,83	22,25,26	3.96	11 (50%)	30,36,39	2.40	13 (43%)
2	OMC	5	3887	2	19,22,23	2.74	7 (36%)	25,31,34	0.88	1 (4%)
2	PSU	5	4531	2	18,21,22	1.11	2 (11%)	21,30,33	2.01	5 (23%)
49	OMG	9	644	49	23,26,27	2.37	8 (34%)	32,38,41	1.95	8 (25%)
2	P7G	5	3880	2	24,28,29	3.54	10 (41%)	25,41,44	1.48	3 (12%)
49	MA6	9	1850	49	23,26,27	1.58	5 (21%)	33,38,41	2.86	11 (33%)
2	I4U	5	4194	2	20,24,25	4.96	13 (65%)	27,34,37	1.88	5 (18%)
2	5MU	5	4083	2	19,22,23	4.71	7 (36%)	27,32,35	3.76	11 (40%)
2	OMG	5	2773	2	23,26,27	2.39	9 (39%)	32,38,41	1.82	8 (25%)
2	OMC	5	2365	2	19,22,23	2.88	7 (36%)	25,31,34	0.94	0
2	B8H	5	3762	2	19,22,23	6.84	6 (31%)	21,32,35	2.54	5 (23%)
49	OMU	9	121	49	19,22,23	2.89	7 (36%)	25,31,34	1.99	6 (24%)
2	OMG	5	2424	2	23,26,27	2.45	9 (39%)	32,38,41	1.89	8 (25%)
2	A2M	5	4523	2,83	22,25,26	3.92	12 (54%)	30,36,39	2.43	12 (40%)
2	B8H	5	1860	2	19,22,23	6.83	6 (31%)	21,32,35	2.45	5 (23%)
49	PSU	9	612	49	18,21,22	0.98	2 (11%)	21,30,33	1.79	5 (23%)
2	B8H	5	4296	2	19,22,23	6.89	7 (36%)	21,32,35	2.62	5 (23%)
7	MLZ	C	333	7	8,9,10	0.87	0	4,9,11	0.78	0
2	PSU	5	4500	2	18,21,22	1.05	3 (16%)	21,30,33	2.07	6 (28%)
49	OMG	9	509	49,83	23,26,27	2.37	9 (39%)	32,38,41	1.81	7 (21%)
49	5MC	9	1374	49	19,22,23	3.73	8 (42%)	26,32,35	1.04	1 (3%)
49	A2M	9	166	49	22,25,26	3.92	10 (45%)	30,36,39	2.48	10 (33%)
2	OMG	5	1316	2	23,26,27	2.41	9 (39%)	32,38,41	1.97	10 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	5	3715	2	18,21,22	1.03	1 (5%)	21,30,33	1.76	4 (19%)
49	5MU	9	814	49	19,22,23	4.84	7 (36%)	27,32,35	3.53	11 (40%)
2	M7A	5	4564	2	19,25,26	1.60	2 (10%)	25,37,40	4.04	7 (28%)
2	OMG	5	4870	2	23,26,27	2.42	9 (39%)	32,38,41	1.98	9 (28%)
2	2MG	5	729	2	23,26,27	2.90	7 (30%)	33,38,41	2.31	8 (24%)
2	P4U	5	1348	2,83	21,24,25	3.29	7 (33%)	28,33,36	1.87	3 (10%)
2	B9H	5	2786	2	21,25,26	2.91	3 (14%)	22,35,38	1.83	3 (13%)
49	PSU	9	119	49	18,21,22	0.97	1 (5%)	21,30,33	1.73	4 (19%)
49	PSU	9	1081	49	18,21,22	1.09	3 (16%)	21,30,33	1.78	4 (19%)
2	PSU	5	1677	2	18,21,22	1.19	3 (16%)	21,30,33	2.07	5 (23%)
49	MA6	9	1851	49	23,26,27	1.52	4 (17%)	33,38,41	2.73	12 (36%)
2	5MC	5	4447	2	19,22,23	3.85	8 (42%)	26,32,35	1.20	2 (7%)
49	OMC	9	174	49	19,22,23	2.90	7 (36%)	25,31,34	0.72	0
2	A2M	5	3785	2	22,25,26	3.87	13 (59%)	30,36,39	2.51	11 (36%)
2	OMC	5	3869	2	19,22,23	2.78	7 (36%)	25,31,34	0.81	0
49	UR3	9	1830	49	19,22,23	2.60	6 (31%)	26,32,35	1.88	5 (19%)
2	B8Q	5	1456	2	18,22,23	2.77	5 (27%)	21,32,35	1.95	5 (23%)
2	A2M	5	3718	2	22,25,26	3.97	13 (59%)	30,36,39	2.14	10 (33%)
2	6MZ	5	4220	2	22,25,26	2.94	7 (31%)	29,36,39	4.11	12 (41%)
49	A2M	9	159	49	22,25,26	3.94	11 (50%)	30,36,39	2.41	13 (43%)
2	B8W	5	2380	2	23,26,27	3.34	12 (52%)	33,38,41	5.70	19 (57%)
2	OMG	5	2050	2	23,26,27	2.40	8 (34%)	32,38,41	1.83	8 (25%)
2	E7G	5	2297	2	24,27,28	3.15	11 (45%)	28,40,43	2.25	9 (32%)
2	7MG	5	4550	2	23,26,27	3.20	10 (43%)	27,39,42	2.16	11 (40%)
2	A2M	5	3825	2	22,25,26	3.93	11 (50%)	30,36,39	2.44	11 (36%)
2	5MC	5	3782	2	19,22,23	3.65	8 (42%)	26,32,35	1.13	2 (7%)
2	OMG	5	4623	2	23,26,27	2.39	9 (39%)	32,38,41	1.88	8 (25%)
2	UR3	5	1866	2	19,22,23	2.46	6 (31%)	26,32,35	1.56	5 (19%)
2	OMU	5	4306	2	19,22,23	2.69	7 (36%)	25,31,34	1.94	5 (20%)
2	PSU	5	4450	2,83	18,21,22	1.07	2 (11%)	21,30,33	2.24	6 (28%)
2	A2M	5	3867	2	22,25,26	3.98	11 (50%)	30,36,39	2.27	10 (33%)
2	PSU	5	4628	2	18,21,22	1.08	3 (16%)	21,30,33	2.25	5 (23%)
49	A2M	9	1678	49	22,25,26	3.97	12 (54%)	30,36,39	2.44	12 (40%)
2	PSU	5	4293	2	18,21,22	1.09	2 (11%)	21,30,33	1.89	4 (19%)
49	4AC	9	1842	49	21,24,25	3.07	10 (47%)	28,34,37	1.34	4 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
49	A2M	9	27	49,83	22,25,26	3.97	13 (59%)	30,36,39	2.35	10 (33%)
2	B8T	5	4483	2	19,22,23	3.01	8 (42%)	25,31,34	1.15	2 (8%)
42	MLZ	m	72	42	8,9,10	0.79	0	4,9,11	0.85	0
2	OMC	5	2804	2	19,22,23	2.84	7 (36%)	25,31,34	0.91	1 (4%)
49	E3C	9	568	49	19,23,24	3.45	6 (31%)	21,33,36	2.81	6 (28%)
2	OMG	5	4370	2	23,26,27	2.41	8 (34%)	32,38,41	1.91	7 (21%)
2	B8W	5	4472	2	23,26,27	3.34	12 (52%)	33,38,41	5.35	22 (66%)
2	P7G	5	1909	2	24,28,29	3.70	10 (41%)	25,41,44	1.56	3 (12%)
2	B8W	5	4129	2	23,26,27	3.33	11 (47%)	33,38,41	5.43	21 (63%)
2	PSU	5	4636	2	18,21,22	1.14	2 (11%)	21,30,33	2.11	5 (23%)
49	PSU	9	822	49	18,21,22	1.04	1 (5%)	21,30,33	1.94	5 (23%)
2	OMG	5	4637	2	23,26,27	2.30	8 (34%)	32,38,41	1.92	8 (25%)
49	OMC	9	1703	49	19,22,23	2.95	7 (36%)	25,31,34	0.73	0
49	A2M	9	484	49	22,25,26	3.86	12 (54%)	30,36,39	2.40	11 (36%)
2	5MC	5	4335	2	19,22,23	3.82	8 (42%)	26,32,35	1.22	3 (11%)
2	OMG	5	373	2	23,26,27	2.41	9 (39%)	32,38,41	2.04	10 (31%)
2	OMU	5	4620	2	19,22,23	2.72	7 (36%)	25,31,34	2.05	6 (24%)
2	B8T	5	4671	2	19,22,23	3.05	8 (42%)	25,31,34	0.89	1 (4%)
2	B9B	5	1574	2	25,28,29	3.74	9 (36%)	35,40,43	2.41	15 (42%)
2	PSU	5	1683	2	18,21,22	1.22	2 (11%)	21,30,33	1.99	4 (19%)
2	E7G	5	1797	2	24,27,28	3.23	11 (45%)	28,40,43	2.31	9 (32%)
2	B8W	5	4185	2	23,26,27	3.40	12 (52%)	33,38,41	5.48	22 (66%)
2	1MA	5	1322	2,83	21,25,26	2.49	5 (23%)	30,37,40	1.93	6 (20%)
49	6MZ	9	1832	49,83	22,25,26	3.04	5 (22%)	29,36,39	4.20	13 (44%)
4	OMU	8	14	4,2	19,22,23	2.83	7 (36%)	25,31,34	2.05	6 (24%)
2	OMG	5	1522	2	23,26,27	2.37	8 (34%)	32,38,41	1.98	8 (25%)
2	7MG	5	1605	2	23,26,27	3.23	10 (43%)	27,39,42	2.17	9 (33%)

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
2	PSU	5	4403	2	-	2/7/25/26	0/2/2/2
49	OMC	9	517	49	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMG	5	1625	2,83	-	3/9/27/28	0/3/3/3
2	A2M	5	2363	2,83	-	0/9/27/28	0/3/3/3
2	PSU	5	4442	2	-	0/7/25/26	0/2/2/2
2	OMG	5	2364	2	-	2/9/27/28	0/3/3/3
2	A2M	5	1524	2	-	2/9/27/28	0/3/3/3
2	B9B	5	237	2	-	5/11/29/30	0/3/3/3
49	OMU	9	116	49	-	2/9/27/28	0/2/2/2
2	OMG	5	4494	2	-	3/9/27/28	0/3/3/3
2	OMC	5	4536	2	-	0/9/27/28	0/2/2/2
49	M7A	9	1806	49	-	0/7/37/38	0/3/3/3
49	PSU	9	1243	49	-	2/7/25/26	0/2/2/2
2	2MG	5	4872	2	-	2/9/27/28	0/3/3/3
2	B8W	5	4529	2,83	-	3/9/27/28	0/3/3/3
2	OMG	5	3792	2	-	2/9/27/28	0/3/3/3
2	B8K	5	3897	2	-	3/11/41/42	0/3/3/3
2	OMG	5	4196	2	-	0/9/27/28	0/3/3/3
2	1MA	5	4415	2	-	2/7/25/26	0/3/3/3
2	PSU	5	3729	2	-	2/7/25/26	0/2/2/2
2	A2M	5	2401	2,83	-	0/9/27/28	0/3/3/3
2	OMC	5	2861	2	-	1/9/27/28	0/2/2/2
2	A2M	5	1534	2,83	-	1/9/27/28	0/3/3/3
2	UR3	5	4597	2	-	0/7/25/26	0/2/2/2
2	2MG	5	1517	2	-	0/9/27/28	0/3/3/3
2	PSU	5	3764	2	-	1/7/25/26	0/2/2/2
49	B8Q	9	1219	49,83	-	1/7/42/43	0/2/2/2
49	B8N	9	1248	49	-	4/16/34/35	0/2/2/2
2	OMG	5	1883	2	-	0/9/27/28	0/3/3/3
2	OMC	5	3701	2,83	-	5/9/27/28	0/2/2/2
49	OMC	9	1710	49	-	0/9/27/28	0/2/2/2
2	PSU	5	2508	2	-	0/7/25/26	0/2/2/2
2	A2M	5	398	2	-	2/9/27/28	0/3/3/3
49	A2M	9	1031	49	-	0/9/27/28	0/3/3/3
2	A2M	5	1326	2	-	0/9/27/28	0/3/3/3
2	I4U	5	1659	2	-	2/9/29/30	0/2/2/2
2	E6G	5	4355	2	-	4/10/28/29	0/3/3/3
2	OMC	5	2422	2,83	-	0/9/27/28	0/2/2/2
2	MHG	5	4371	2	-	8/16/46/47	0/3/3/3
49	OMG	9	683	49	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	A2M	5	3723	2	-	0/9/27/28	0/3/3/3
2	A2M	5	1871	2,83	-	0/9/27/28	0/3/3/3
2	OMC	5	3909	2	-	0/9/27/28	0/2/2/2
49	PSU	9	823	49	-	0/7/25/26	0/2/2/2
2	7MG	5	2522	2	-	0/7/37/38	0/3/3/3
2	PSU	5	1582	2	-	2/7/25/26	0/2/2/2
2	BGH	5	3899	2,83	-	3/13/43/44	0/3/3/3
2	B9B	5	2754	2,83	-	4/11/29/30	0/3/3/3
49	4AC	9	1337	49	-	1/11/29/30	0/2/2/2
2	UR3	5	4530	2	-	1/7/25/26	0/2/2/2
2	A2M	5	4571	2	-	0/9/27/28	0/3/3/3
2	B8K	5	4690	2	-	0/11/41/42	0/3/3/3
49	A2M	9	668	49,83	-	3/9/27/28	0/3/3/3
2	OMC	5	3887	2	-	1/9/27/28	0/2/2/2
2	PSU	5	4531	2	-	0/7/25/26	0/2/2/2
49	OMG	9	644	49	-	1/9/27/28	0/3/3/3
2	P7G	5	3880	2	-	3/10/40/41	0/3/3/3
49	MA6	9	1850	49	-	0/11/29/30	0/3/3/3
2	I4U	5	4194	2	-	3/9/29/30	0/2/2/2
2	5MU	5	4083	2	-	0/7/25/26	0/2/2/2
2	OMG	5	2773	2	-	0/9/27/28	0/3/3/3
2	OMC	5	2365	2	-	2/9/27/28	0/2/2/2
2	B8H	5	3762	2	-	2/7/25/26	0/2/2/2
49	OMU	9	121	49	-	2/9/27/28	0/2/2/2
2	OMG	5	2424	2	-	2/9/27/28	0/3/3/3
2	A2M	5	4523	2,83	-	2/9/27/28	0/3/3/3
2	B8H	5	1860	2	-	0/7/25/26	0/2/2/2
49	PSU	9	612	49	-	0/7/25/26	0/2/2/2
2	B8H	5	4296	2	-	0/7/25/26	0/2/2/2
7	MLZ	C	333	7	-	2/7/8/10	-
2	PSU	5	4500	2	-	3/7/25/26	0/2/2/2
49	OMG	9	509	49,83	-	1/9/27/28	0/3/3/3
49	5MC	9	1374	49	-	0/7/25/26	0/2/2/2
49	A2M	9	166	49	-	2/9/27/28	0/3/3/3
2	OMG	5	1316	2	-	0/9/27/28	0/3/3/3
2	PSU	5	3715	2	-	0/7/25/26	0/2/2/2
49	5MU	9	814	49	-	1/7/25/26	0/2/2/2
2	M7A	5	4564	2	-	0/7/37/38	0/3/3/3
2	OMG	5	4870	2	-	3/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2MG	5	729	2	-	2/9/27/28	0/3/3/3
2	P4U	5	1348	2,83	-	2/10/29/30	0/2/2/2
2	B9H	5	2786	2	-	2/12/47/48	0/2/2/2
49	PSU	9	119	49	-	1/7/25/26	0/2/2/2
49	PSU	9	1081	49	-	1/7/25/26	0/2/2/2
2	PSU	5	1677	2	-	0/7/25/26	0/2/2/2
49	MA6	9	1851	49	-	4/11/29/30	0/3/3/3
2	5MC	5	4447	2	-	4/7/25/26	0/2/2/2
49	OMC	9	174	49	-	0/9/27/28	0/2/2/2
2	A2M	5	3785	2	-	4/9/27/28	0/3/3/3
2	OMC	5	3869	2	-	0/9/27/28	0/2/2/2
49	UR3	9	1830	49	-	2/7/25/26	0/2/2/2
2	B8Q	5	1456	2	-	0/7/42/43	0/2/2/2
2	A2M	5	3718	2	-	0/9/27/28	0/3/3/3
2	6MZ	5	4220	2	-	2/9/27/28	0/3/3/3
49	A2M	9	159	49	-	3/9/27/28	0/3/3/3
2	B8W	5	2380	2	-	4/9/27/28	0/3/3/3
2	OMG	5	2050	2	-	0/9/27/28	0/3/3/3
2	E7G	5	2297	2	-	2/9/39/40	0/3/3/3
2	7MG	5	4550	2	-	0/7/37/38	0/3/3/3
2	A2M	5	3825	2	-	0/9/27/28	0/3/3/3
2	5MC	5	3782	2	-	0/7/25/26	0/2/2/2
2	OMG	5	4623	2	-	0/9/27/28	0/3/3/3
2	UR3	5	1866	2	-	1/7/25/26	0/2/2/2
2	OMU	5	4306	2	-	0/9/27/28	0/2/2/2
2	PSU	5	4450	2,83	-	2/7/25/26	0/2/2/2
2	A2M	5	3867	2	-	2/9/27/28	0/3/3/3
2	PSU	5	4628	2	-	0/7/25/26	0/2/2/2
49	A2M	9	1678	49	-	0/9/27/28	0/3/3/3
2	PSU	5	4293	2	-	1/7/25/26	0/2/2/2
49	4AC	9	1842	49	-	0/11/29/30	0/2/2/2
49	A2M	9	27	49,83	-	0/9/27/28	0/3/3/3
2	B8T	5	4483	2	-	0/7/27/28	0/2/2/2
42	MLZ	m	72	42	-	3/7/8/10	-
2	OMC	5	2804	2	-	0/9/27/28	0/2/2/2
49	E3C	9	568	49	-	6/9/44/45	0/2/2/2
2	OMG	5	4370	2	-	0/9/27/28	0/3/3/3
2	B8W	5	4472	2	-	2/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	P7G	5	1909	2	-	2/10/40/41	0/3/3/3
2	B8W	5	4129	2	-	3/9/27/28	0/3/3/3
2	PSU	5	4636	2	-	3/7/25/26	0/2/2/2
49	PSU	9	822	49	-	2/7/25/26	0/2/2/2
2	OMG	5	4637	2	-	2/9/27/28	0/3/3/3
49	OMC	9	1703	49	-	2/9/27/28	0/2/2/2
49	A2M	9	484	49	-	0/9/27/28	0/3/3/3
2	5MC	5	4335	2	-	0/7/25/26	0/2/2/2
2	OMG	5	373	2	-	1/9/27/28	0/3/3/3
2	OMU	5	4620	2	-	1/9/27/28	0/2/2/2
2	B8T	5	4671	2	-	0/7/27/28	0/2/2/2
2	B9B	5	1574	2	-	3/11/29/30	0/3/3/3
2	PSU	5	1683	2	-	0/7/25/26	0/2/2/2
2	E7G	5	1797	2	-	3/9/39/40	0/3/3/3
2	B8W	5	4185	2	-	4/9/27/28	0/3/3/3
2	1MA	5	1322	2,83	-	0/7/25/26	0/3/3/3
49	6MZ	9	1832	49,83	-	2/9/27/28	0/3/3/3
4	OMU	8	14	4,2	-	1/9/27/28	0/2/2/2
2	OMG	5	1522	2	-	0/9/27/28	0/3/3/3
2	7MG	5	1605	2	-	0/7/37/38	0/3/3/3

The worst 5 of 1048 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	4296	B8H	C6-C5	-16.16	1.12	1.35
2	5	1860	B8H	C6-C5	-15.85	1.12	1.35
2	5	3762	B8H	C6-C5	-15.80	1.12	1.35
2	5	4296	B8H	C4-N3	-14.94	1.10	1.38
2	5	1860	B8H	C4-N3	-14.82	1.11	1.38

The worst 5 of 1011 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	2380	B8W	N2-C2-N3	19.07	145.81	117.22
2	5	4529	B8W	N2-C2-N3	18.80	145.41	117.22
2	5	4185	B8W	N2-C2-N3	18.44	144.87	117.22
2	5	4472	B8W	N2-C2-N3	18.00	144.22	117.22
2	5	4129	B8W	N2-C2-N3	17.96	144.15	117.22

There are no chirality outliers.

5 of 190 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	C	333	MLZ	N-CA-CB-CG
7	C	333	MLZ	C-CA-CB-CG
2	5	237	B9B	C5-C6-O6-C61
2	5	237	B9B	N1-C6-O6-C61
2	5	237	B9B	O4'-C4'-C5'-O5'

There are no ring outliers.

54 monomers are involved in 79 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	5	1524	A2M	1	0
2	5	237	B9B	1	0
49	9	116	OMU	1	0
2	5	4494	OMG	1	0
2	5	3897	B8K	1	0
2	5	1517	2MG	1	0
2	5	1883	OMG	1	0
2	5	398	A2M	2	0
49	9	1031	A2M	1	0
2	5	1326	A2M	2	0
2	5	2422	OMC	1	0
2	5	3723	A2M	3	0
2	5	1871	A2M	1	0
2	5	2522	7MG	1	0
2	5	3899	BGH	1	0
2	5	2754	B9B	1	0
2	5	4571	A2M	1	0
49	9	1850	MA6	1	0
2	5	4194	I4U	1	0
2	5	2773	OMG	1	0
2	5	3762	B8H	6	0
2	5	4523	A2M	2	0
2	5	1860	B8H	6	0
2	5	4296	B8H	6	0
7	C	333	MLZ	1	0
2	5	4500	PSU	1	0
49	9	509	OMG	1	0
49	9	166	A2M	1	0
2	5	1316	OMG	1	0
49	9	814	5MU	1	0
2	5	729	2MG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
49	9	174	OMC	1	0
2	5	3718	A2M	2	0
2	5	4220	6MZ	2	0
49	9	159	A2M	2	0
2	5	2380	B8W	1	0
2	5	3825	A2M	1	0
2	5	3782	5MC	1	0
2	5	1866	UR3	1	0
2	5	3867	A2M	1	0
49	9	1678	A2M	1	0
2	5	4293	PSU	1	0
49	9	1842	4AC	1	0
49	9	27	A2M	1	0
2	5	2804	OMC	1	0
2	5	4472	B8W	1	0
2	5	4129	B8W	1	0
2	5	373	OMG	1	0
2	5	4620	OMU	1	0
2	5	1574	B9B	3	0
2	5	1322	1MA	1	0
49	9	1832	6MZ	1	0
4	8	14	OMU	1	0
2	5	1605	7MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 305 ligands modelled in this entry, 305 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	5	43
49	9	18
4	8	1

The worst 5 of 62 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	5	2113:G	O3'	2258:C	P	40.50
1	5	1252:C	O3'	1271:G	P	34.93
1	5	1219:G	O3'	1233:G	P	21.40
1	5	1405:C	O3'	1406:G	P	20.69
1	5	1406(C):G	O3'	1411:C	P	20.19

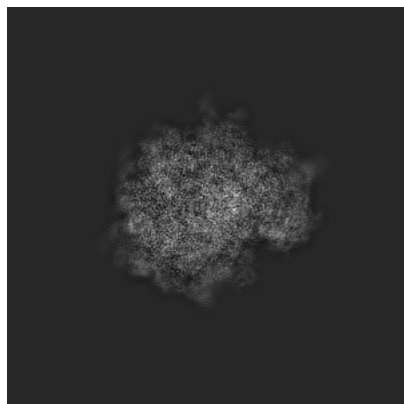
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9239. These allow visual inspection of the internal detail of the map and identification of artifacts.

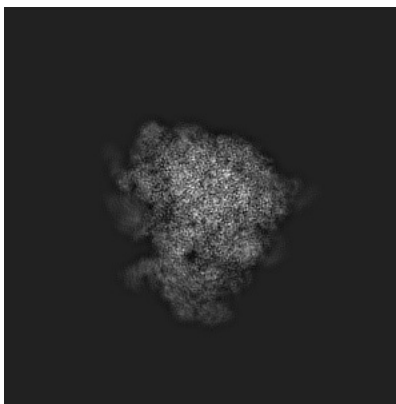
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

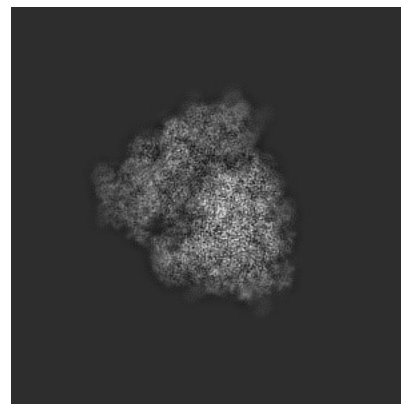
6.1.1 Primary map



X

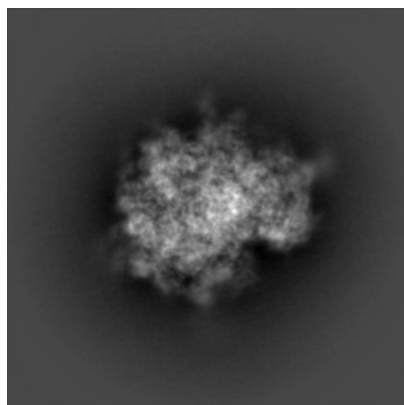


Y

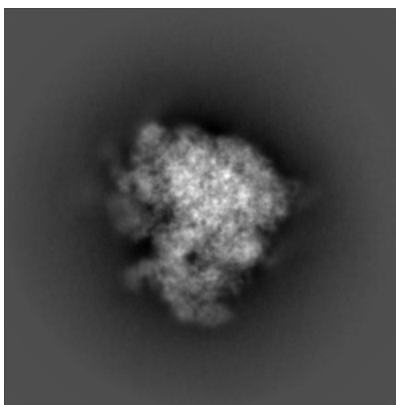


Z

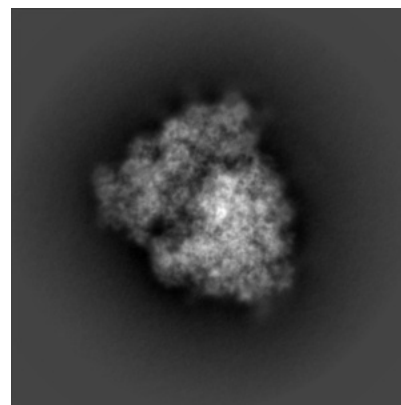
6.1.2 Raw map



X



Y

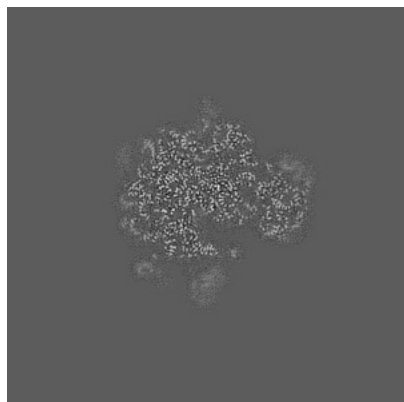


Z

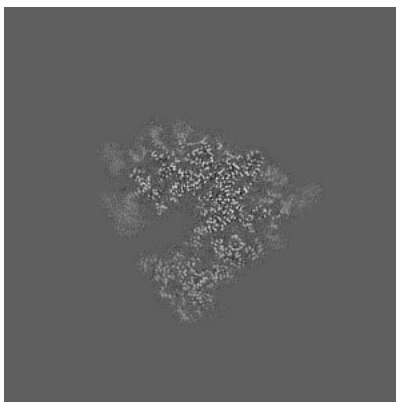
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

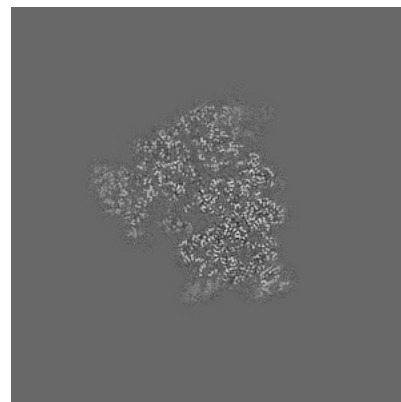
6.2.1 Primary map



X Index: 200

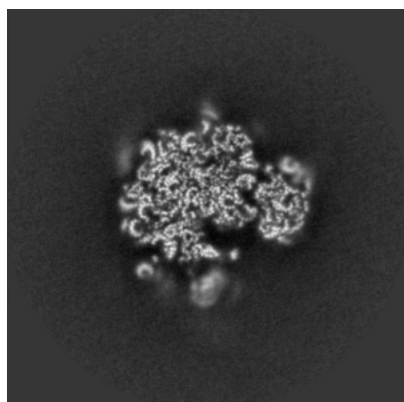


Y Index: 200

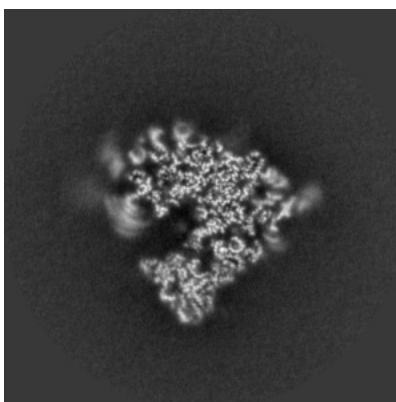


Z Index: 200

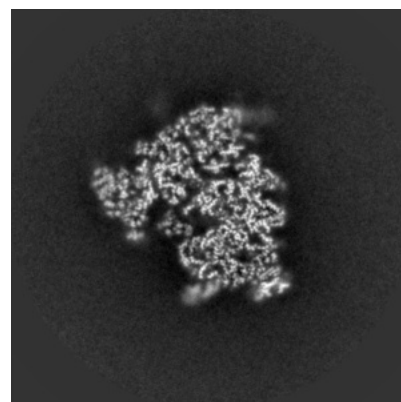
6.2.2 Raw map



X Index: 200



Y Index: 200

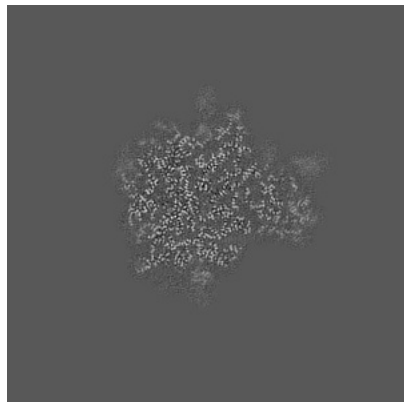


Z Index: 200

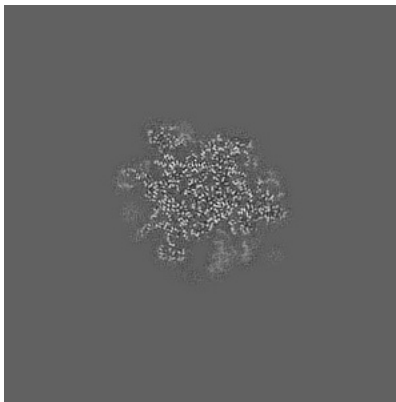
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

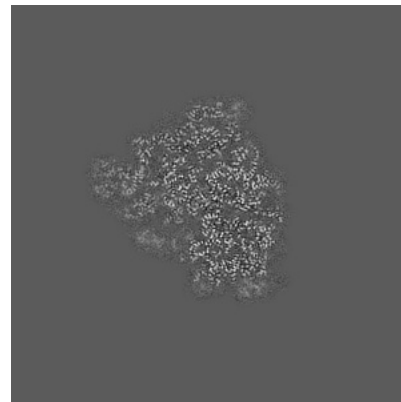
6.3.1 Primary map



X Index: 213

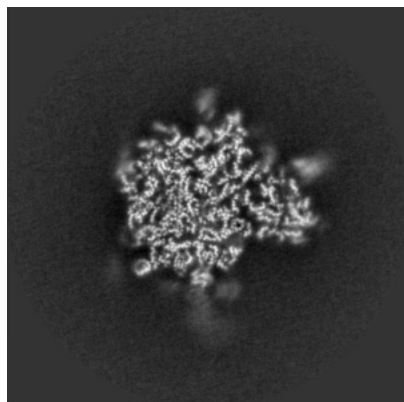


Y Index: 160

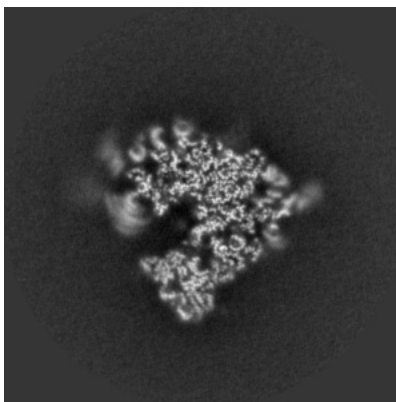


Z Index: 211

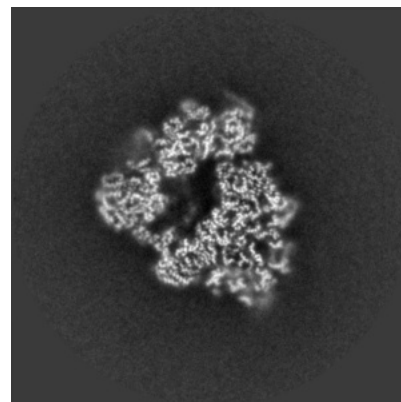
6.3.2 Raw map



X Index: 213



Y Index: 201

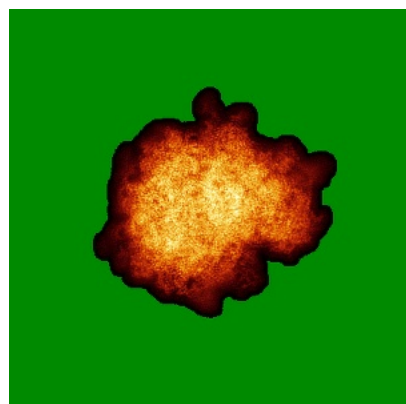


Z Index: 176

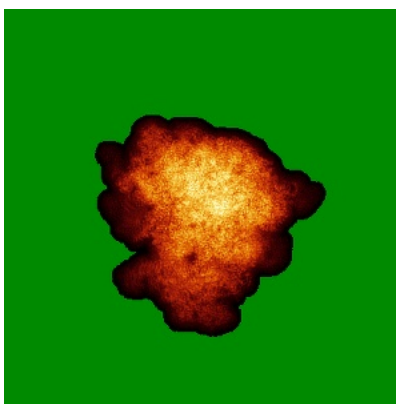
The images above show the largest variance slices of the map in three orthogonal directions.

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

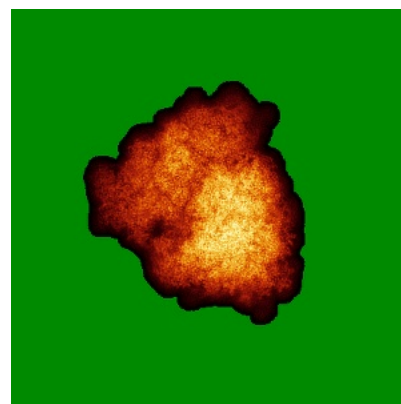
6.4.1 Primary map



X

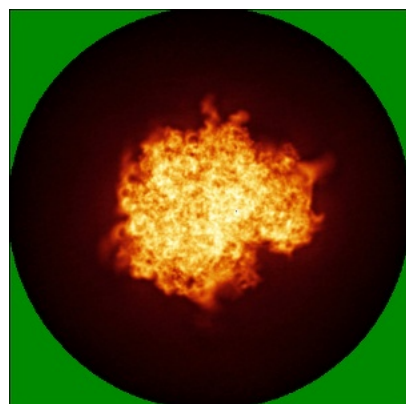


Y

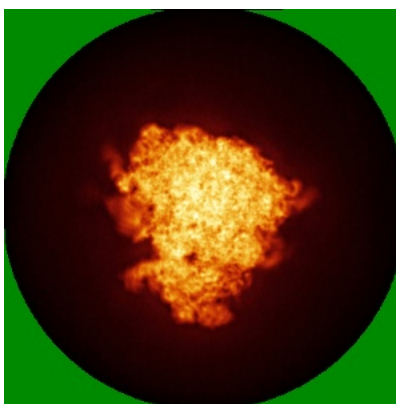


Z

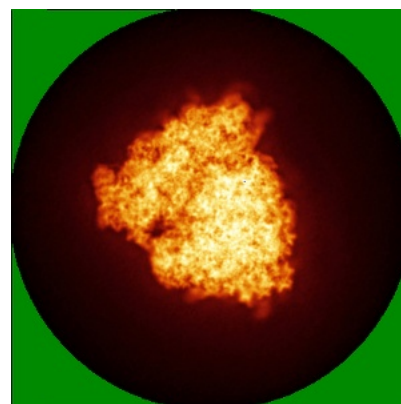
6.4.2 Raw map



X



Y

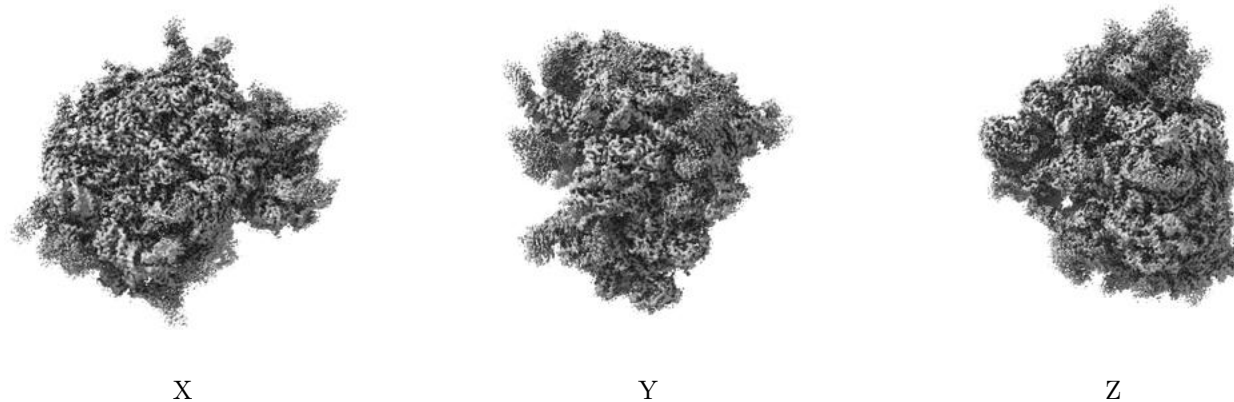


Z

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.

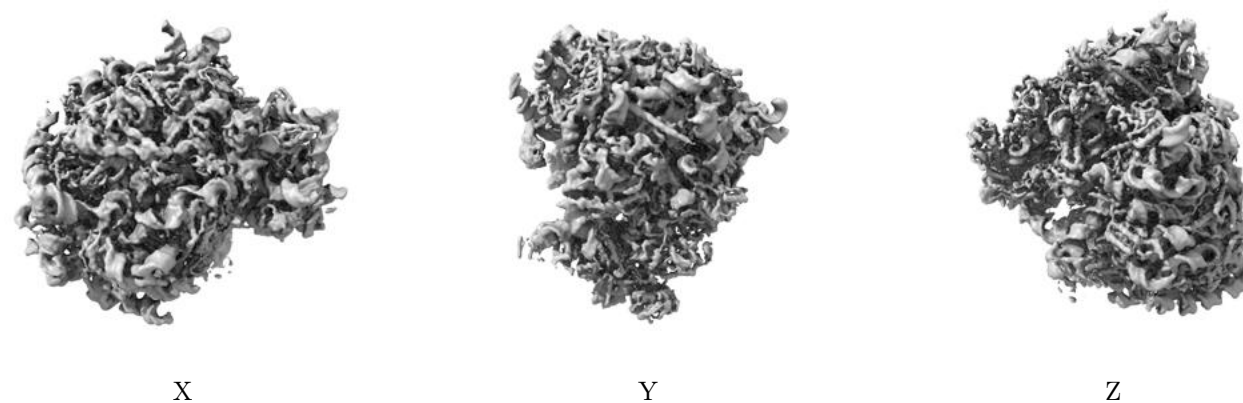
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. 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.

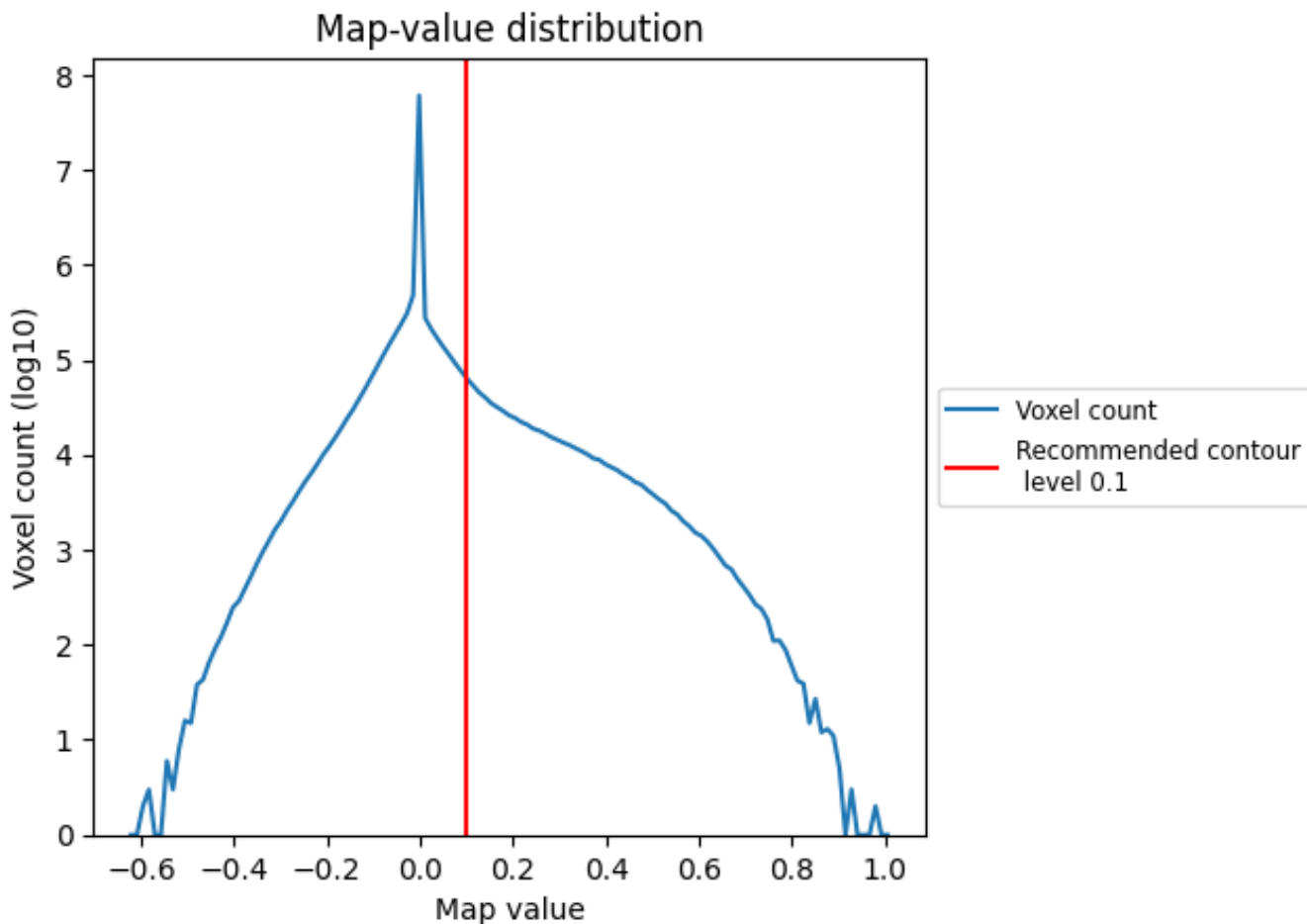
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

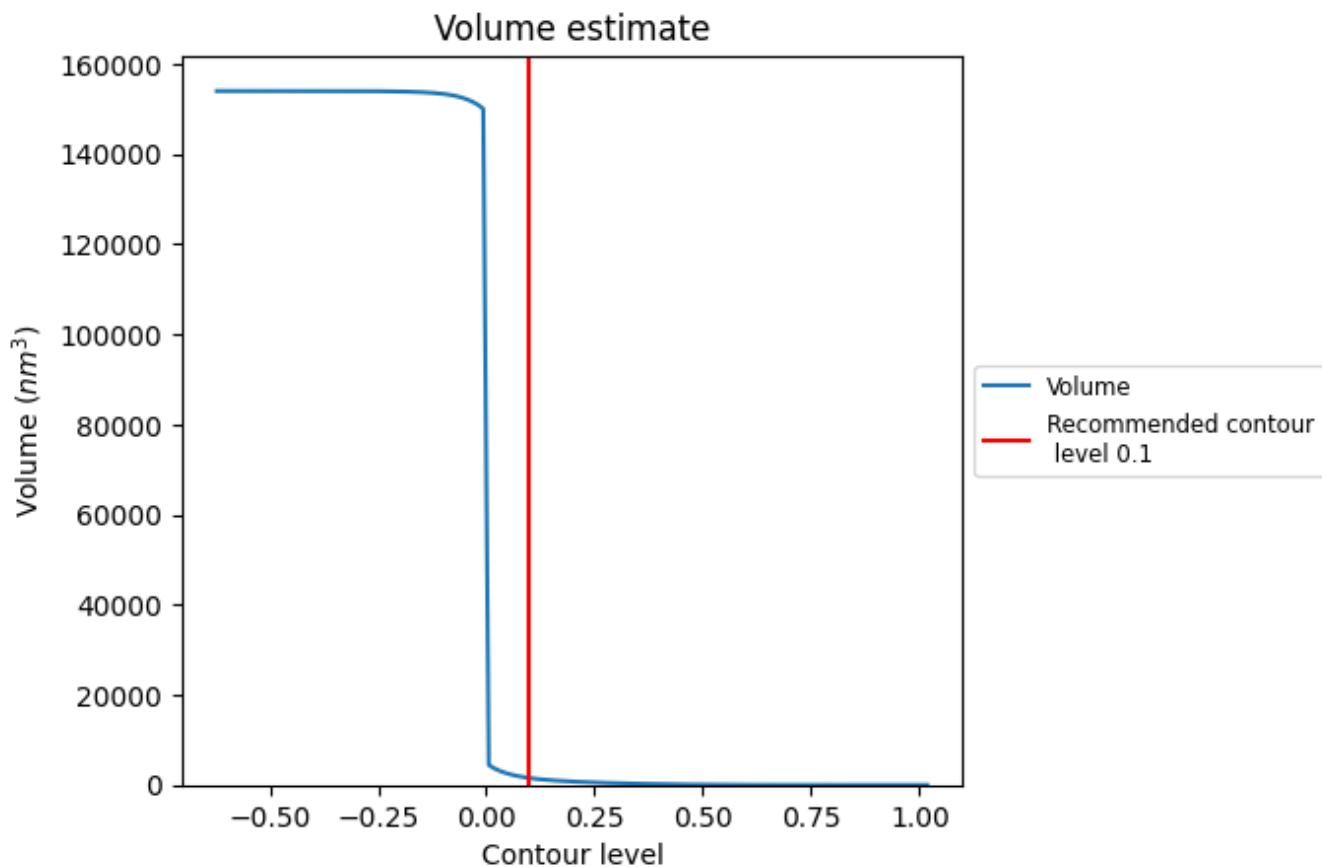
This section contains the results of statistical analysis of the map.

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.

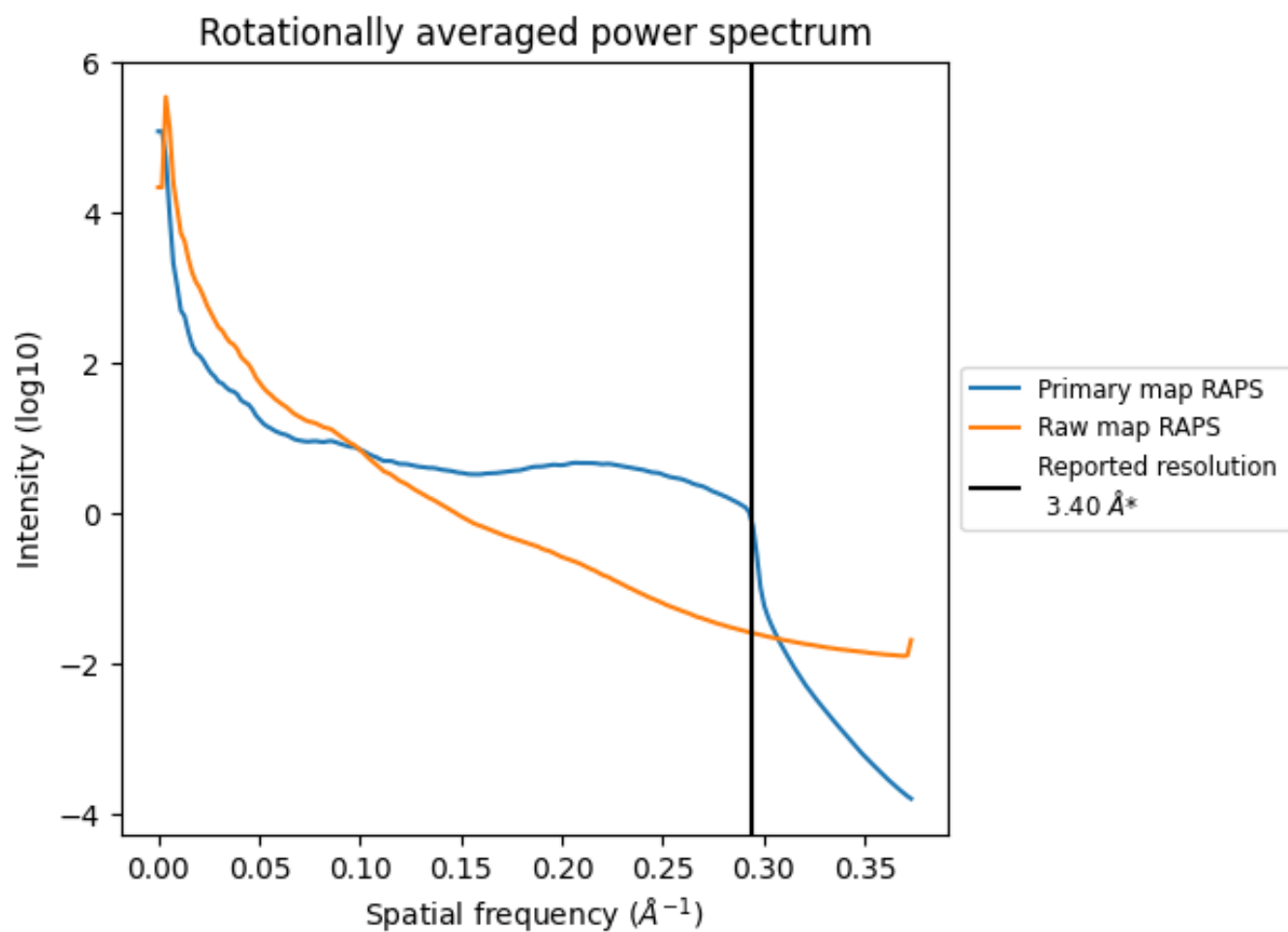
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 1528 nm³; this corresponds to an approximate mass of 1381 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

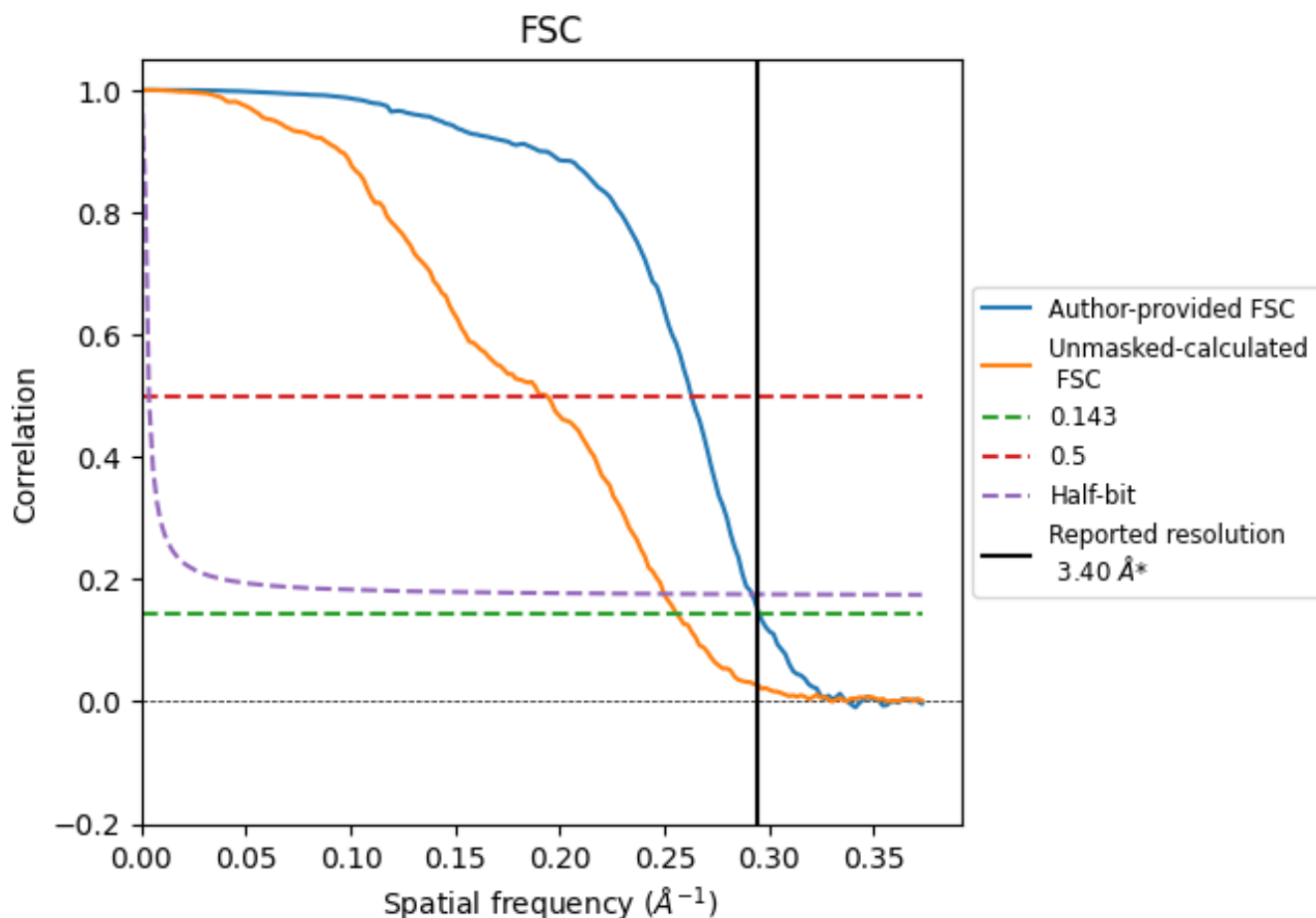


*Reported resolution corresponds to spatial frequency of 0.294 \AA^{-1}

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 Å⁻¹

8.2 Resolution estimates [i](#)

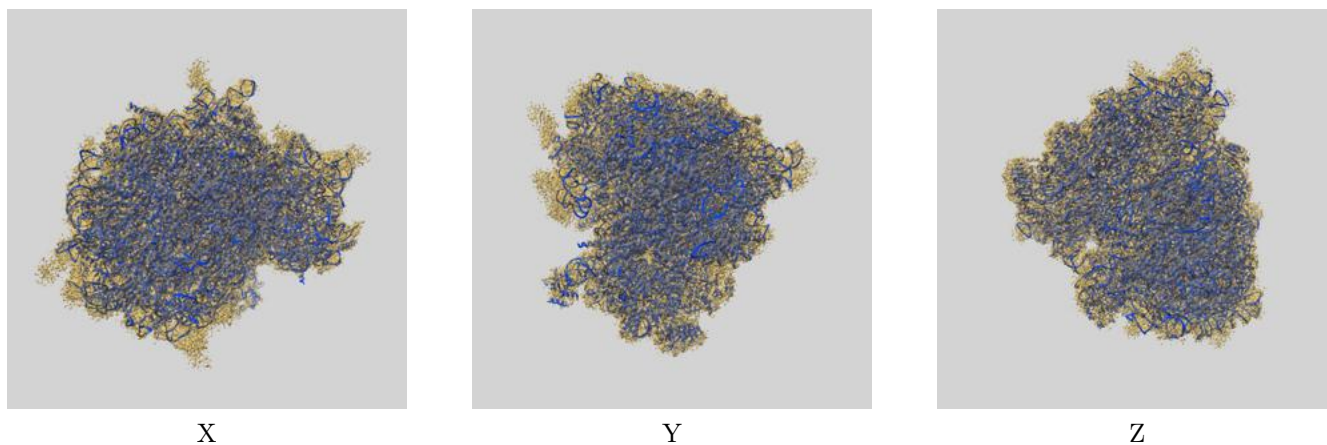
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.39	3.81	3.43
Unmasked-calculated*	3.91	5.16	4.00

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

9 Map-model fit [i](#)

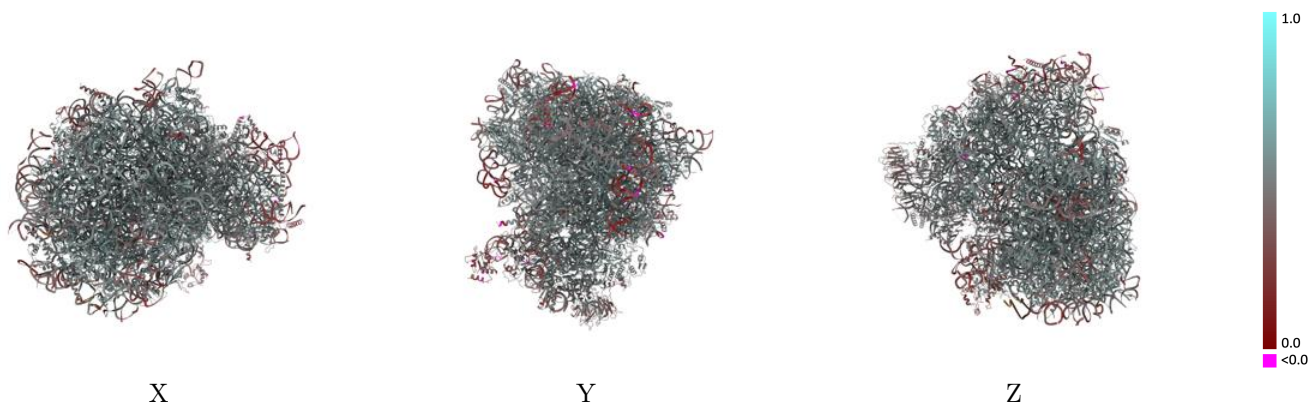
This section contains information regarding the fit between EMDB map EMD-9239 and PDB model 6MTC. Per-residue inclusion information can be found in section [3](#) on page [20](#).

9.1 Map-model overlay [i](#)



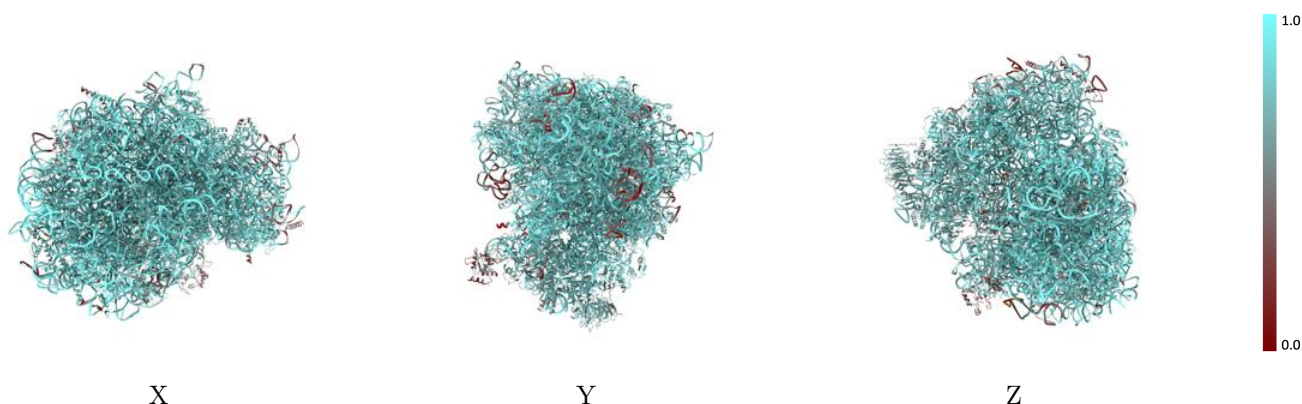
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



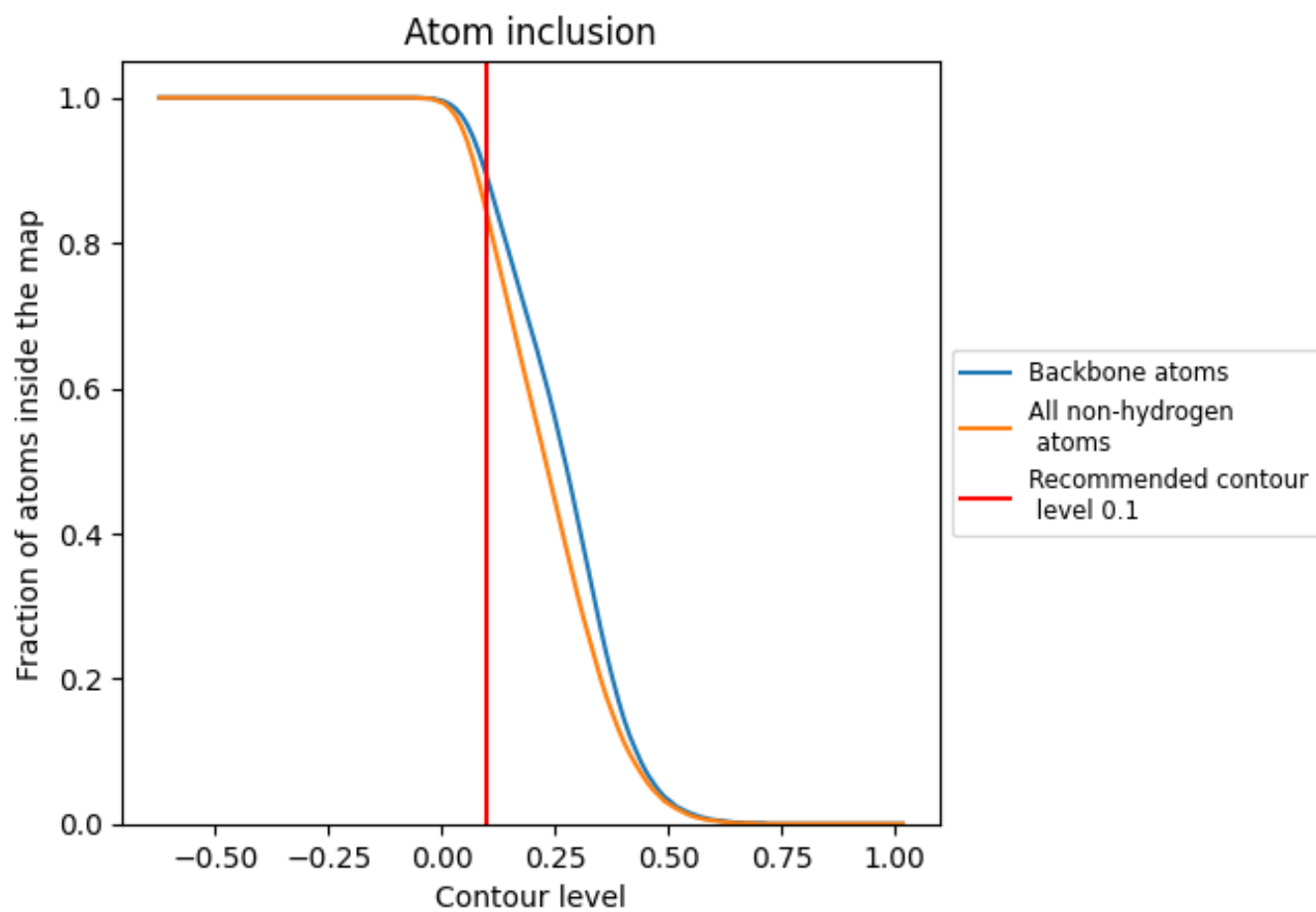
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 84% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8410	 0.4970
4	 0.7290	 0.3350
5	 0.8830	 0.4920
7	 0.9390	 0.5210
8	 0.9060	 0.5060
9	 0.8690	 0.4760
A	 0.8870	 0.5620
AA	 0.8130	 0.5150
B	 0.8750	 0.5500
BB	 0.8030	 0.5210
C	 0.8650	 0.5490
CC	 0.8270	 0.5240
D	 0.8500	 0.5240
DD	 0.6920	 0.4640
E	 0.8410	 0.5280
EE	 0.8100	 0.5260
F	 0.8570	 0.5460
FF	 0.7740	 0.4930
G	 0.7970	 0.5110
GG	 0.7180	 0.4660
H	 0.8200	 0.5310
HH	 0.7300	 0.4720
I	 0.8510	 0.5440
II	 0.7890	 0.5150
J	 0.7900	 0.5020
JJ	 0.8080	 0.5050
KK	 0.6710	 0.4350
L	 0.8270	 0.5300
LL	 0.8150	 0.5350
M	 0.8470	 0.5280
MM	 0.3100	 0.2620
N	 0.8930	 0.5620
NN	 0.8410	 0.5300
O	 0.8540	 0.5430
OO	 0.8070	 0.5220















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Chain	Atom inclusion	Q-score
P	0.8640	0.5490
PP	0.6710	0.4330
Q	0.8690	0.5540
QQ	0.7400	0.4770
R	0.8120	0.5210
RR	0.7500	0.4860
S	0.8660	0.5520
SS	0.7220	0.4680
T	0.8460	0.5380
TT	0.7430	0.4740
U	0.7830	0.4850
UU	0.6810	0.4460
V	0.8580	0.5550
VV	0.8020	0.5250
W	0.6940	0.4530
WW	0.8550	0.5380
X	0.8300	0.5330
XX	0.8230	0.5300
Y	0.8530	0.5390
YY	0.7810	0.4960
Z	0.8610	0.5320
ZZ	0.7050	0.4620
a	0.8730	0.5560
aa	0.8330	0.5420
b	0.7490	0.4890
bb	0.7870	0.5180
c	0.8360	0.5290
cc	0.7380	0.5060
d	0.8310	0.5300
dd	0.8080	0.4980
e	0.8730	0.5590
ee	0.6950	0.4890
f	0.8910	0.5620
ff	0.3810	0.3280
g	0.8310	0.5430
gg	0.6390	0.4170
h	0.8260	0.5280
i	0.8350	0.5250
j	0.9020	0.5550
k	0.7680	0.5130
l	0.8430	0.5460
m	0.8540	0.5360

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Chain	Atom inclusion	Q-score
n	 0.7940	 0.5270
o	 0.8530	 0.5500
p	 0.8390	 0.5540
r	 0.8840	 0.5490
u	 0.4540	 0.3420
v	 0.6270	 0.4620