



wwPDB EM Validation Summary Report ⓘ

Jun 25, 2026 – 08:36 AM EDT

PDB ID : 6MTE / pdb_00006mte
EMDB ID : EMD-9242
Title : Rabbit 80S ribosome with eEF2 and SERBP1 (rotated state)
Authors : Brown, A.; Baird, M.R.; Yip, M.C.J.; Murray, J.; Shao, S.
Deposited on : 2018-10-19
Resolution : 3.40 Å(reported)
Based on initial model : 5LZV

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

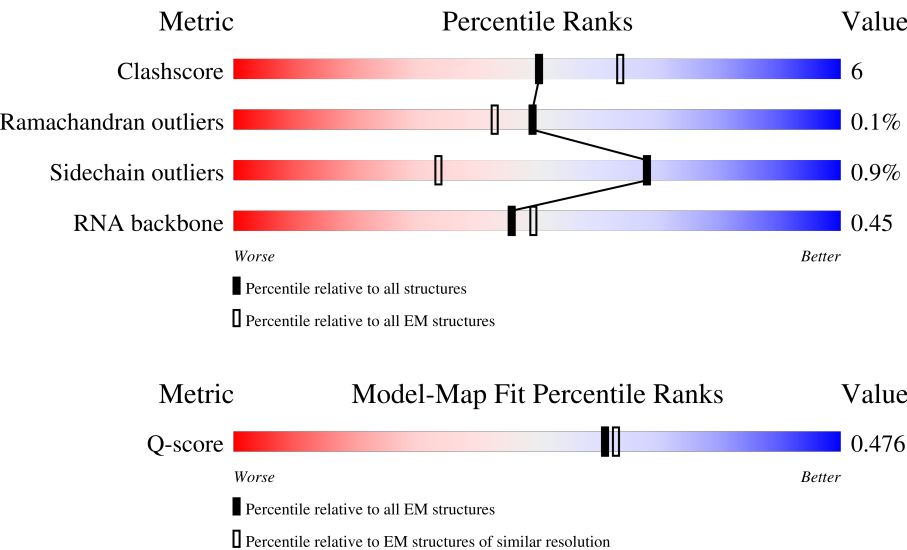
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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.



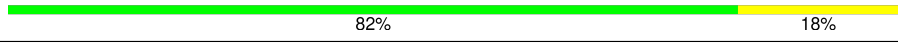
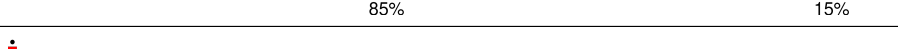
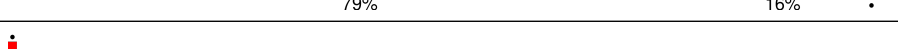
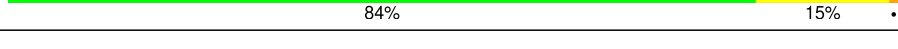
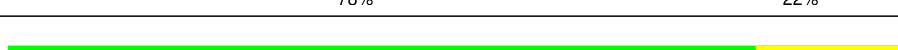
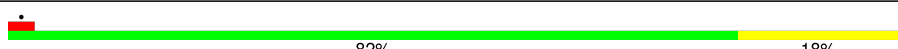
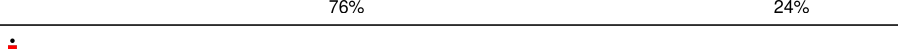
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	5	3597	
2	7	120	
3	8	151	

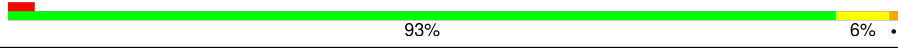
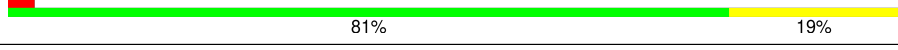
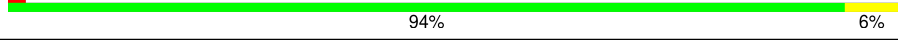
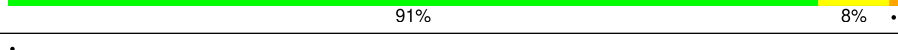
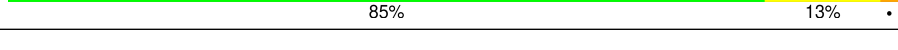
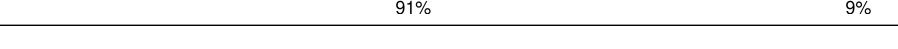
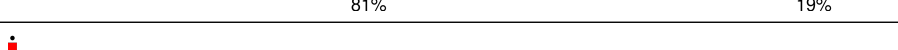
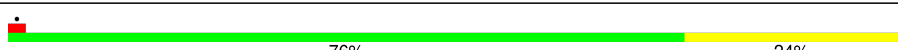
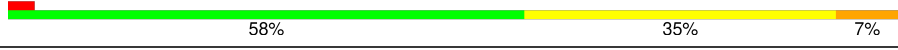
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Mol	Chain	Length	Quality of chain
4	A	248	
5	B	394	
6	C	362	
7	D	293	
8	E	291	
9	F	225	
10	G	319	
11	H	190	
12	I	214	
13	J	170	
14	L	210	
15	M	138	
16	N	203	
17	O	199	
18	P	153	
19	Q	187	
20	R	180	
21	S	176	
22	T	159	
23	U	99	
24	V	131	
25	W	157	
26	X	118	
27	Y	134	
28	Z	135	

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Mol	Chain	Length	Quality of chain
29	a	147	
30	b	245	
31	c	98	
32	d	107	
33	e	128	
34	f	109	
35	g	114	
36	h	122	
37	i	102	
38	j	86	
39	k	69	
40	l	50	
41	m	52	
42	n	25	
43	o	103	
44	p	91	
45	r	124	
46	s	196	
47	t	153	
48	v	848	
49	w	55	
50	9	1698	
51	AA	217	
52	BB	213	
53	CC	221	

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Mol	Chain	Length	Quality of chain
54	DD	228	
55	EE	262	
56	FF	204	
57	GG	237	
58	HH	194	
59	II	206	
60	JJ	185	
61	KK	96	
62	LL	158	
63	MM	117	
64	NN	149	
65	OO	136	
66	PP	125	
67	QQ	142	
68	RR	132	
69	SS	144	
70	TT	141	
71	UU	100	
72	VV	83	
73	WW	129	
74	XX	141	
75	YY	124	
76	ZZ	75	
77	aa	101	
78	bb	83	

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Mol	Chain	Length	Quality of chain
79	cc	62	
80	dd	55	
81	ee	55	
82	ff	68	
83	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
1	B8W	5	4185	-	X	-	-

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 220739 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 28S rRNA.

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

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

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

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

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

- Molecule 4 is a protein called uL2.

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

- Molecule 5 is a protein called uL3.

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

- Molecule 6 is a protein called uL4.

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

- Molecule 7 is a protein called uL18.

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

- Molecule 8 is a protein called eL6.

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

- Molecule 9 is a protein called uL30.

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

- Molecule 10 is a protein called eL8.

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

- Molecule 11 is a protein called uL6.

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

- Molecule 12 is a protein called uL16.

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

- Molecule 13 is a protein called uL5.

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

- Molecule 14 is a protein called eL13.

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

- Molecule 15 is a protein called eL14.

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

- Molecule 16 is a protein called eL15.

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

- Molecule 17 is a protein called uL13.

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

- Molecule 18 is a protein called uL22.

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

- Molecule 19 is a protein called eL18.

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

- Molecule 20 is a protein called eL19.

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

- Molecule 21 is a protein called eL20.

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

- Molecule 22 is a protein called eL21.

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

- Molecule 23 is a protein called eL22.

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

- Molecule 24 is a protein called uL14.

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

- Molecule 25 is a protein called eL24.

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

- Molecule 26 is a protein called uL23.

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

- Molecule 27 is a protein called uL24.

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

- Molecule 28 is a protein called eL27.

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

- Molecule 29 is a protein called uL15.

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

- Molecule 30 is a protein called eL29.

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

- Molecule 31 is a protein called eL30.

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

- Molecule 32 is a protein called eL31.

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

- Molecule 33 is a protein called eL32.

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

- Molecule 34 is a protein called eL33.

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

- Molecule 35 is a protein called eL34.

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

- Molecule 36 is a protein called uL29.

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

- Molecule 37 is a protein called eL36.

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

- Molecule 38 is a protein called eL37.

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

- Molecule 39 is a protein called eL38.

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

- Molecule 40 is a protein called eL39.

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

- Molecule 41 is a protein called eL40.

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

- Molecule 42 is a protein called eL41.

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

- Molecule 43 is a protein called eL42.

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

- Molecule 44 is a protein called eL43.

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

- Molecule 45 is a protein called eL28.

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

- Molecule 46 is a protein called uL10.

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

- Molecule 47 is a protein called uL11.

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

- Molecule 48 is a protein called eEF2.

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

- Molecule 49 is a protein called SERBP1.

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

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

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

- Molecule 51 is a protein called uS2.

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

- Molecule 52 is a protein called eS1.

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

- Molecule 53 is a protein called uS5.

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

- Molecule 54 is a protein called uS3.

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

- Molecule 55 is a protein called eS4.

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

- Molecule 56 is a protein called uS7.

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

- Molecule 57 is a protein called eS6.

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

- Molecule 58 is a protein called eS7.

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

- Molecule 59 is a protein called eS8.

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

- Molecule 60 is a protein called uS4.

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

- Molecule 61 is a protein called eS10.

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

- Molecule 62 is a protein called uS17.

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

- Molecule 63 is a protein called eS12.

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

- Molecule 64 is a protein called uS15.

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

- Molecule 65 is a protein called uS11.

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

- Molecule 66 is a protein called uS19.

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

- Molecule 67 is a protein called uS9.

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

- Molecule 68 is a protein called eS17.

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

- Molecule 69 is a protein called uS13.

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

- Molecule 70 is a protein called eS19.

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

- Molecule 71 is a protein called uS10.

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

- Molecule 72 is a protein called eS21.

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

- Molecule 73 is a protein called uS8.

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

- Molecule 74 is a protein called uS12.

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

- Molecule 75 is a protein called eS24.

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

- Molecule 76 is a protein called eS25.

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

- Molecule 77 is a protein called eS26.

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

- Molecule 78 is a protein called eS27.

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

- Molecule 79 is a protein called eS28.

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

- Molecule 80 is a protein called uS14.

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

- Molecule 81 is a protein called eS30.

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

- Molecule 82 is a protein called eS31.

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

- Molecule 83 is a protein called RACK1.

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

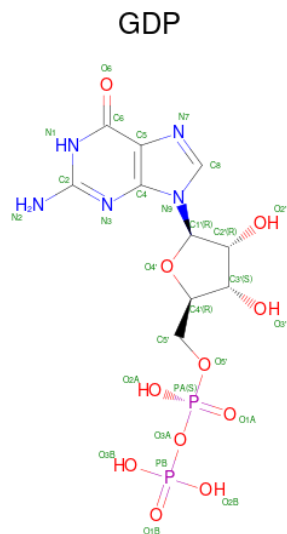
- Molecule 84 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 85 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 86 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).

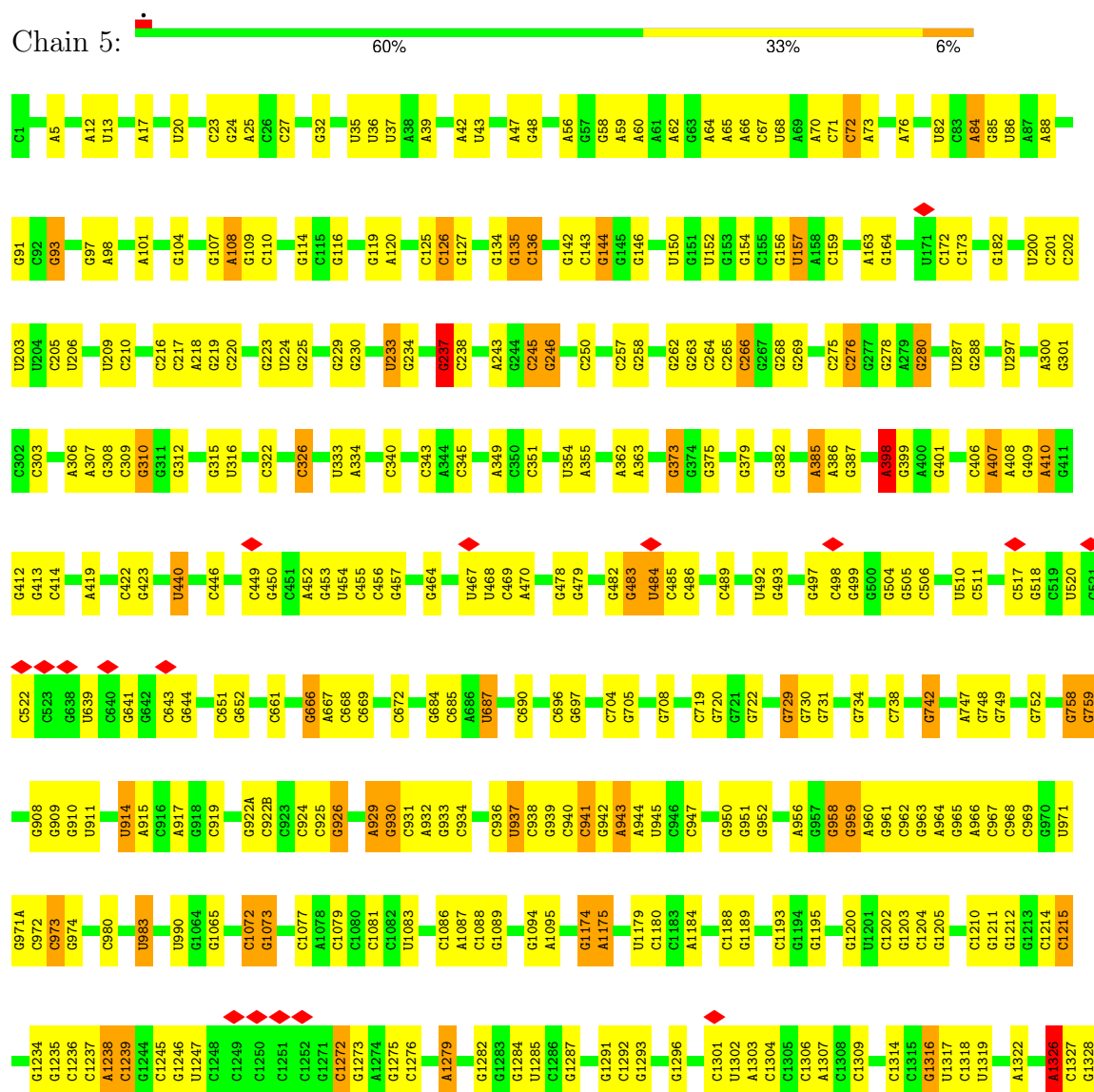


Mol	Chain	Residues	Atoms					AltConf
86	v	1	Total	C	N	O	P	0
			28	10	5	11	2	

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: 28S rRNA

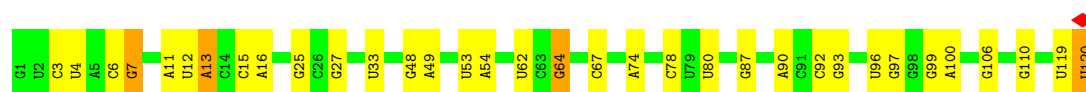


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C2804	U2708	C2588	U2490	A2389	C2289	G2050	A1968	U1866	A1767	G1641	G1517	G1415	C1332
G2809	C2709	C2589	C2492	A2390	G2294	G2052	G1961	G1869	C1768	C1645	A1518	G1416	A1333
U2810	G2710	A2600	U2493	G2394	G2297	G2055	A1962	C1870	G1769	A1646	C1521	G1419	A1337
G2811	G2711	G2602	U2494	A2396	G2298	G2056	G1963	A1871	A1770	A1420	G1522	A1420	G1338
C2814	G2714	C2397	U2398	A2398	U2299	C2062	A1964	G1872	U1771	U1649	A1523	G1426	C1344
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G2827	G2722	G2405	U2507	U2404	U2304	U2070	U1971	U1882	A1775	U1659	U1538	C1429	U1348
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G2835	A2725	G2617	A2507	A2406	G2306	C2072	G1975	G1895	A1547	G1670	A1547	C1436	G1351
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G2846	U2740	U2630	G2521	A2417	G2316	U2084	A1983	U1905	C1679	A1679	C1566	C1444	G1361
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A3604	U2773	C2667	U2554	G2451	A2349	G2105	C2011	A1932	G1826	A1743	G1604	C1480	A1392
C3605	A2783	C2670	C2558	G2459	U2350	A2107	C1935	C1938	G1827	U1748	G1605	C1481	G1393
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	A4702	A4702	C4599	A4511	U4403	U4404	A4219	U3967	G3897	C3781	C3673
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				U4572	U4465	G4382	C4175		G3945	A3849	A3733
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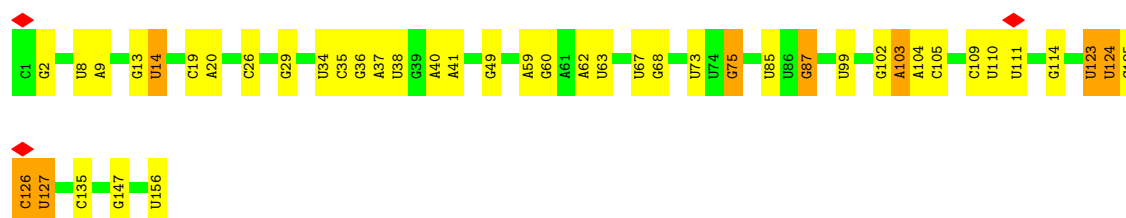
- Molecule 2: 5S rRNA

Chain 7: 



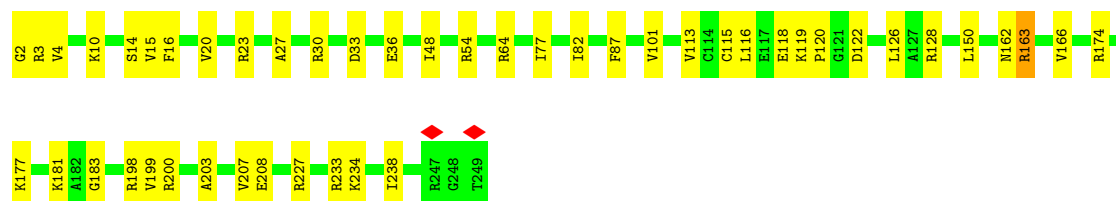
- Molecule 3: 5.8S rRNA

Chain 8: 



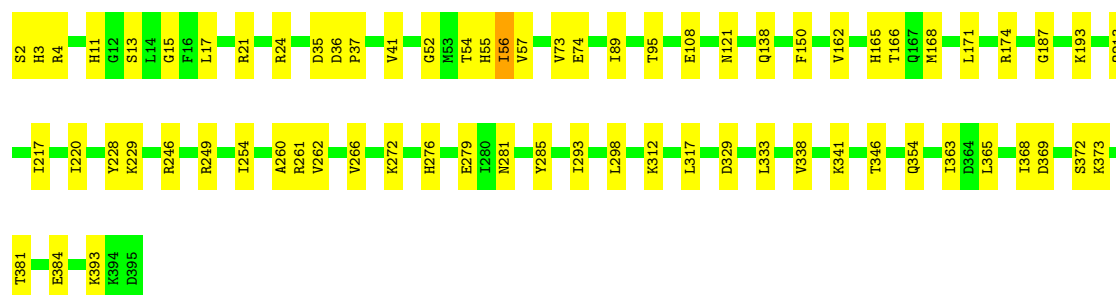
- Molecule 4: uL2

Chain A: 



- Molecule 5: uL3

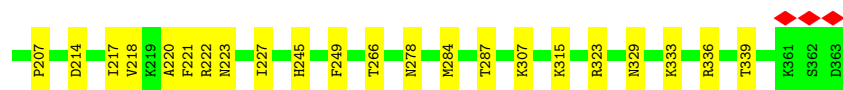
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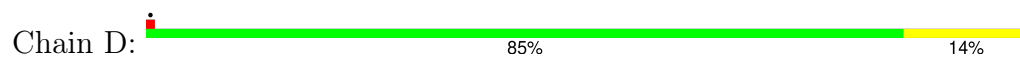
- Molecule 6: uL4

Chain C: 

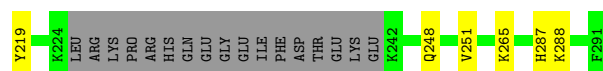
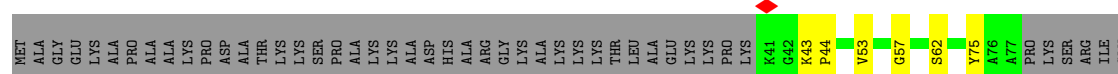




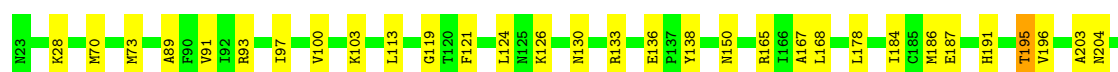
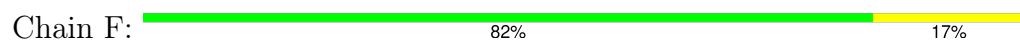
• Molecule 7: uL18



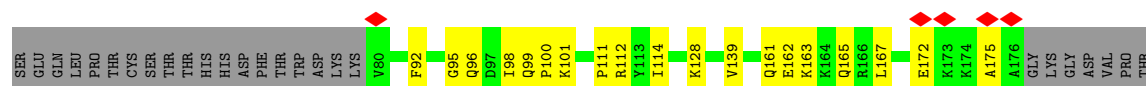
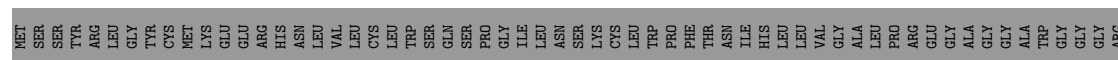
• Molecule 8: eL6



• Molecule 9: uL30

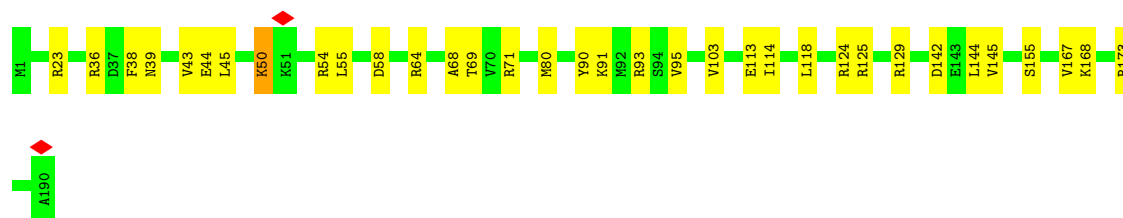
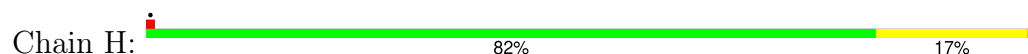


• Molecule 10: eL8

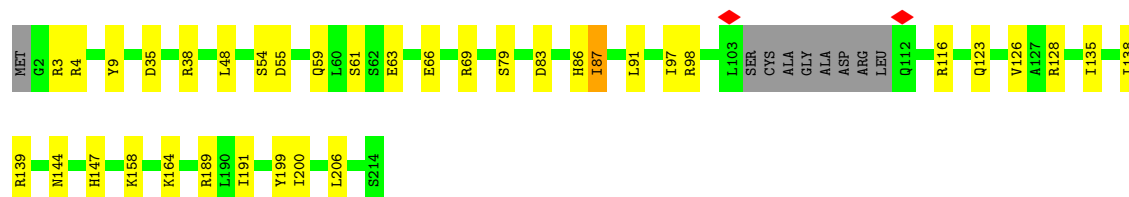
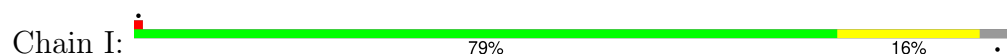




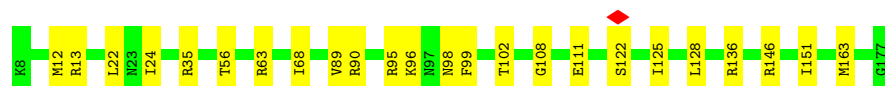
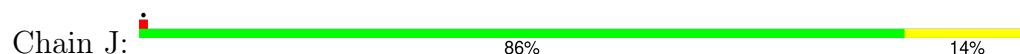
• Molecule 11: uL6



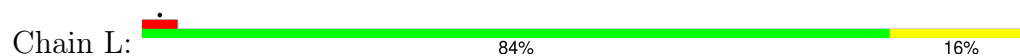
• Molecule 12: uL16



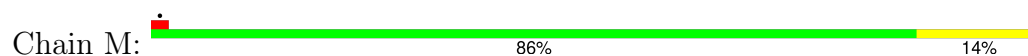
• Molecule 13: uL5



• Molecule 14: eL13



• Molecule 15: eL14



- Molecule 16: eL15

Chain N:  76% 24%



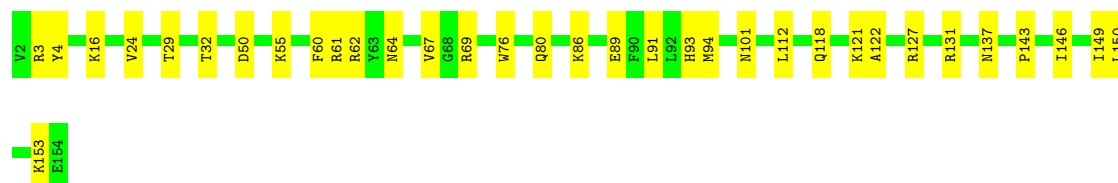
- Molecule 17: uL13

Chain O:  84% 15%



- Molecule 18: uL22

Chain P:  78% 22%



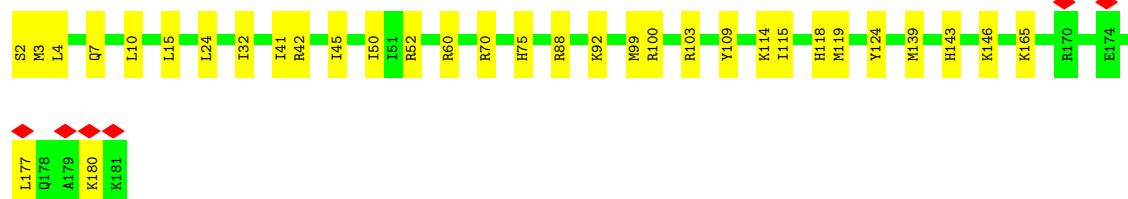
- Molecule 19: eL18

Chain Q:  84% 16%



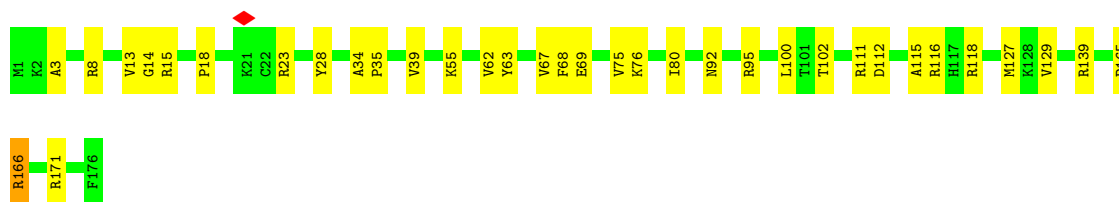
- Molecule 20: eL19

Chain R:  82% 18%

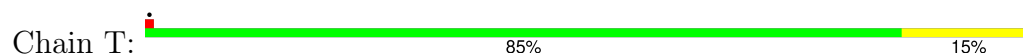


- Molecule 21: eL20

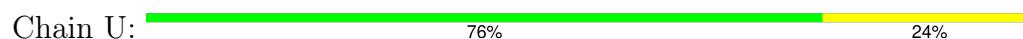
Chain S:  80% 19%



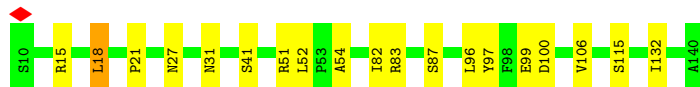
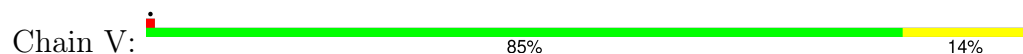
- Molecule 22: eL21



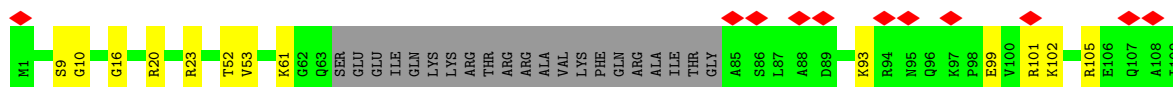
- Molecule 23: eL22



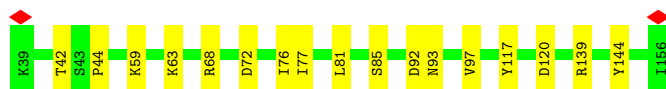
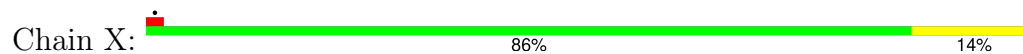
- Molecule 24: uL14



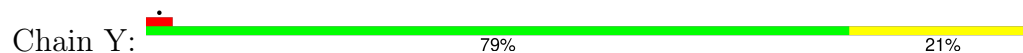
- Molecule 25: eL24



- Molecule 26: uL23



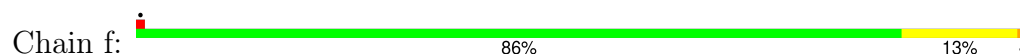
- Molecule 27: uL24







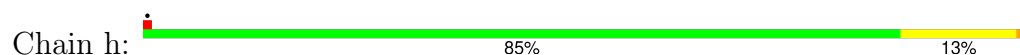
● Molecule 34: eL33



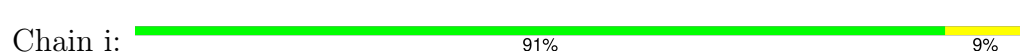
● Molecule 35: eL34



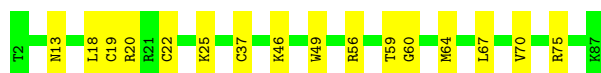
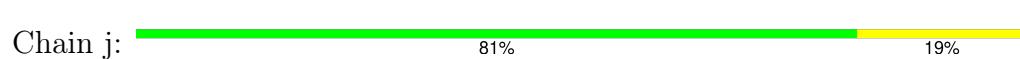
● Molecule 36: uL29



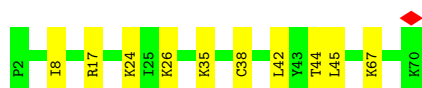
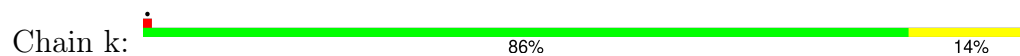
● Molecule 37: eL36



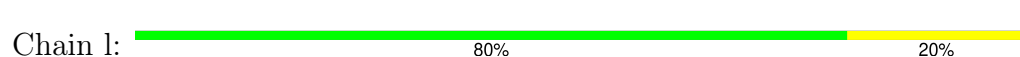
● Molecule 38: eL37



● Molecule 39: eL38



● Molecule 40: eL39





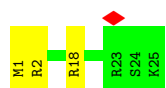
• Molecule 41: eL40

Chain m: 65% 33%



• Molecule 42: eL41

Chain n: 88% 12%



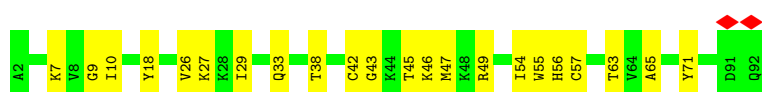
• Molecule 43: eL42

Chain o: 90% 10%



• Molecule 44: eL43

Chain p: 76% 24%



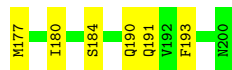
• Molecule 45: eL28

Chain r: 84% 16%

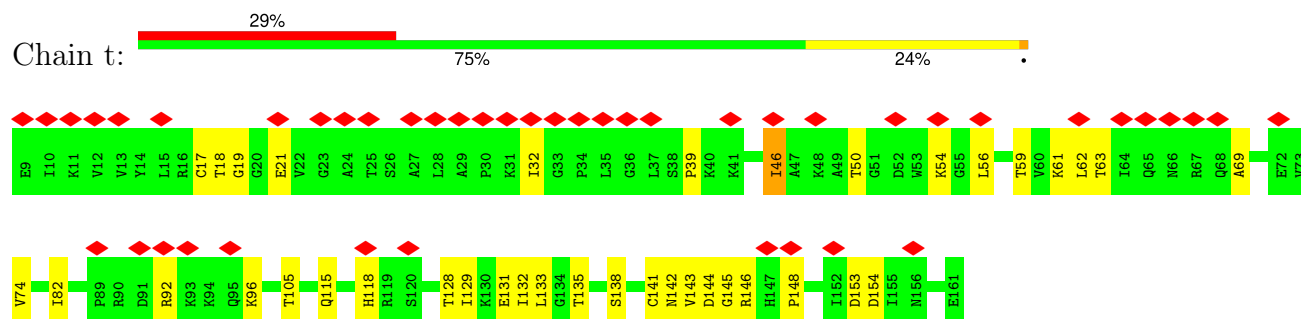


• Molecule 46: uL10

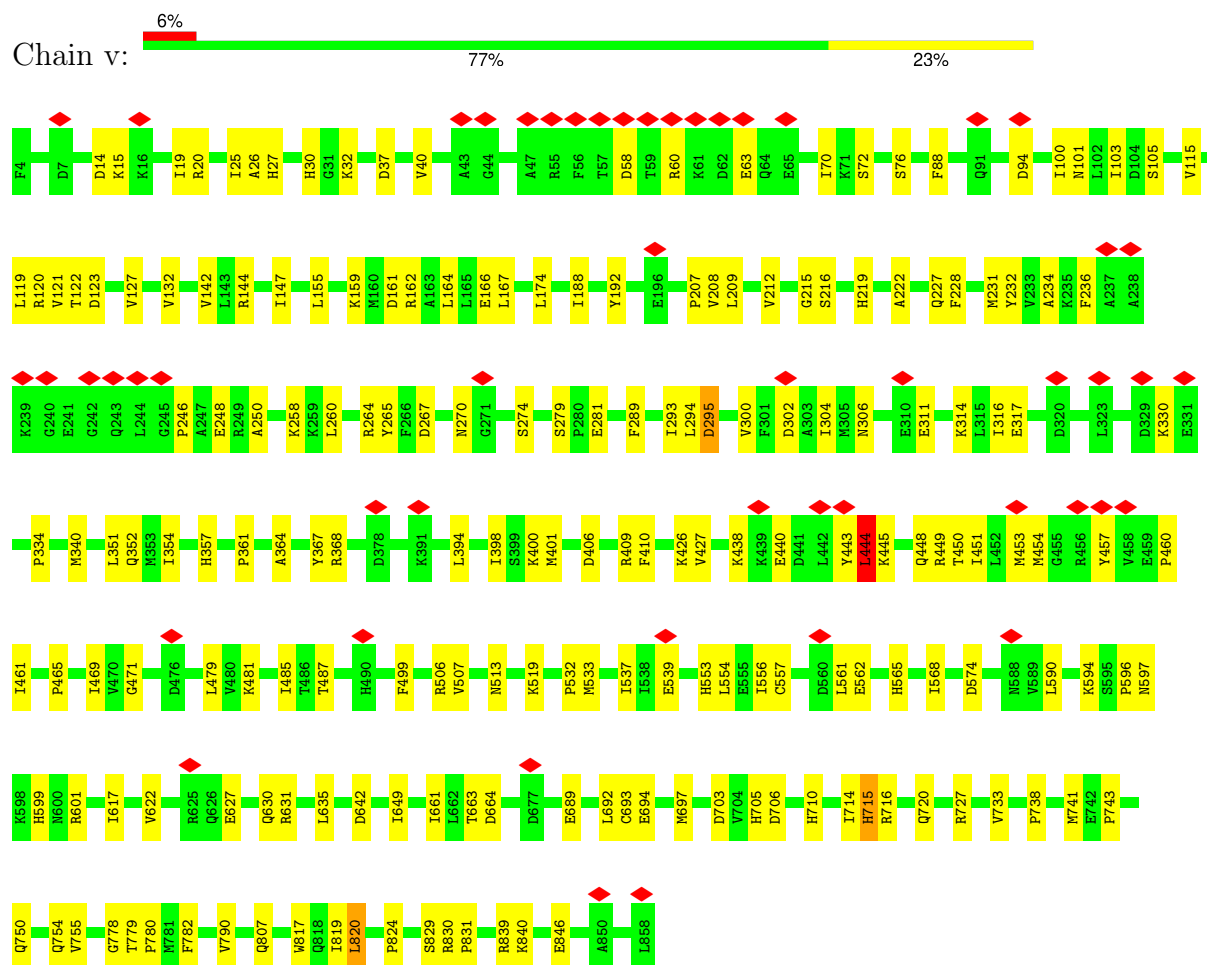
Chain s: 82% 18%



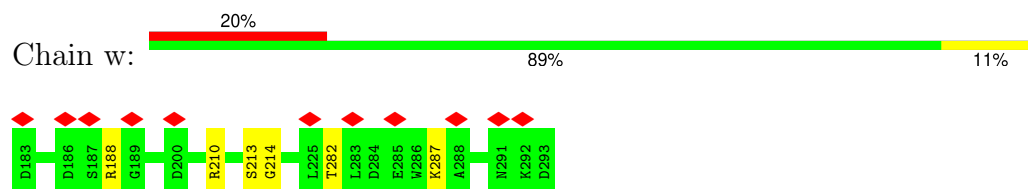
- Molecule 47: uL11



- Molecule 48: eEF2

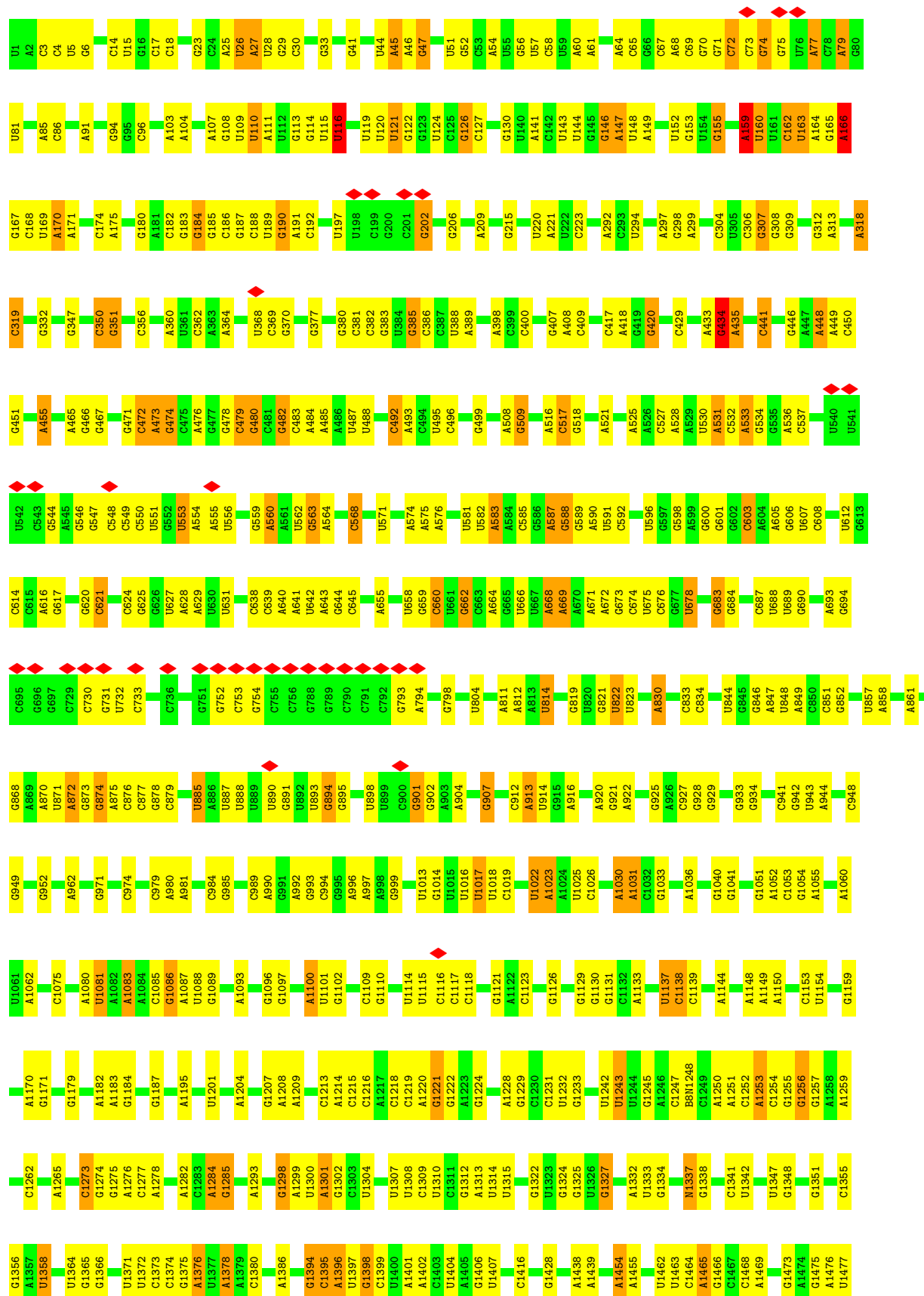


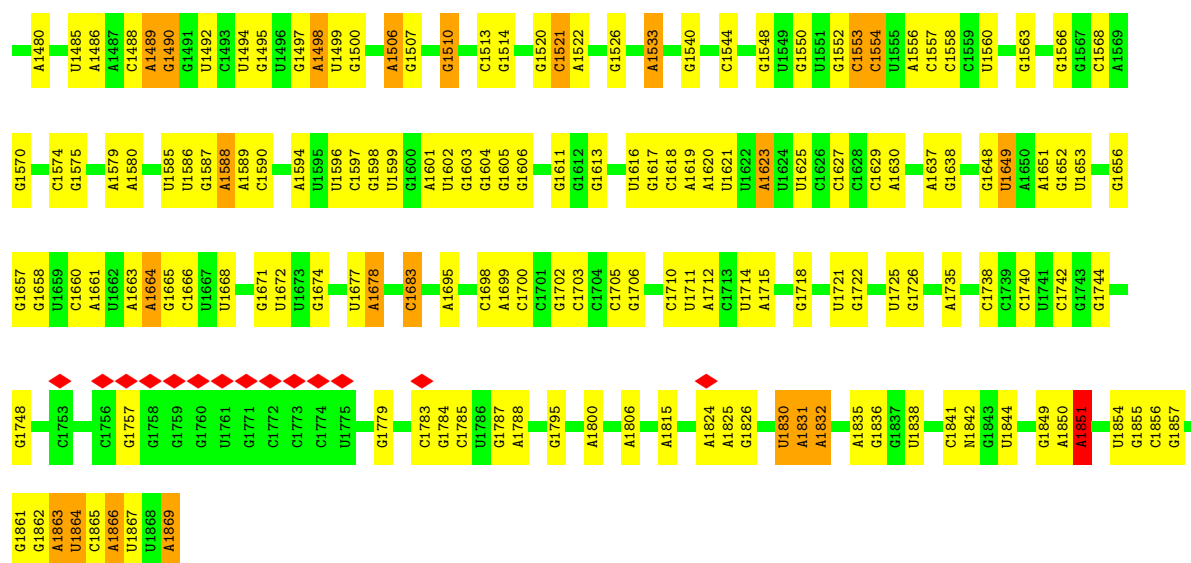
- Molecule 49: SERBP1



- Molecule 50: 18S rRNA

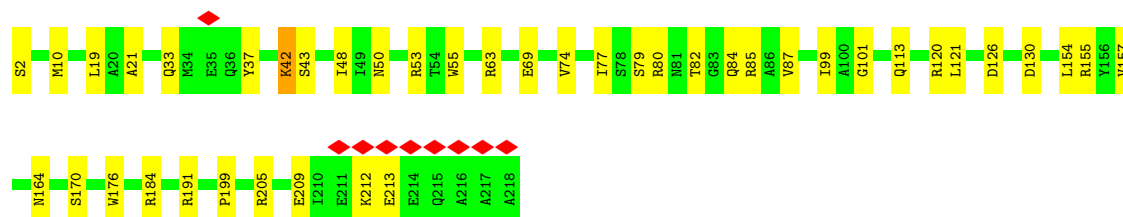






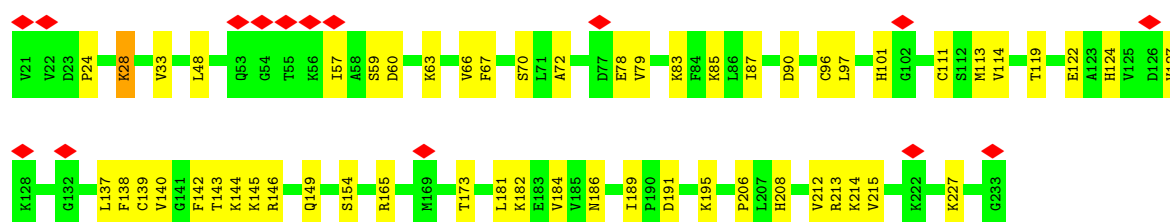
• Molecule 51: uS2

Chain AA: 81% 19%



• Molecule 52: eS1

Chain BB: 7% 74% 25%



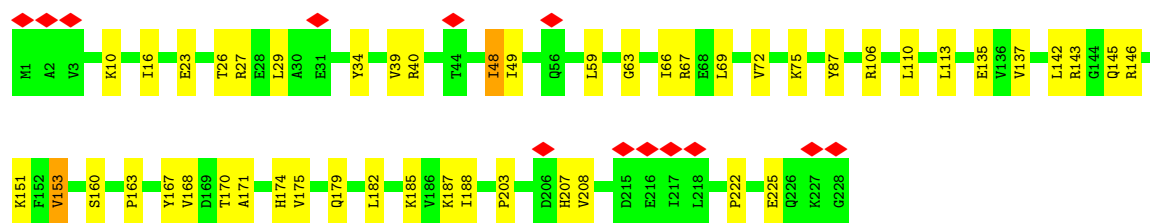
• Molecule 53: uS5

Chain CC: 88% 12%

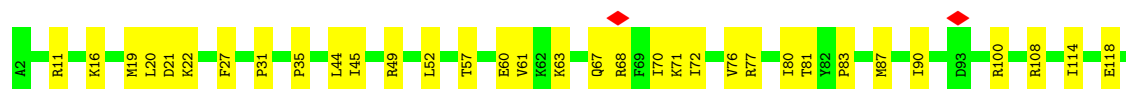
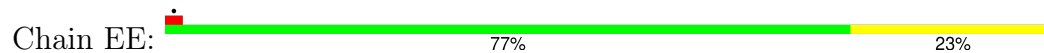


• Molecule 54: uS3

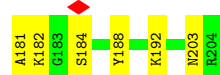
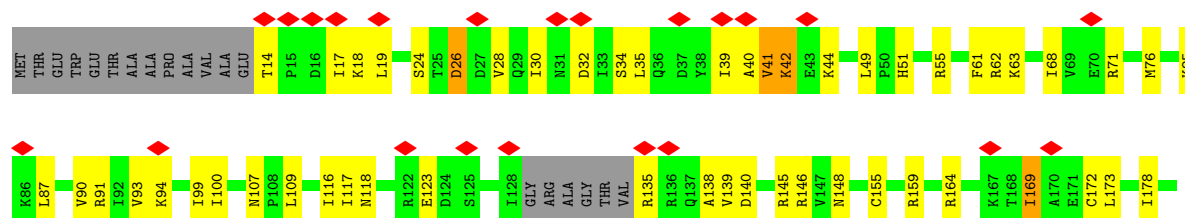
Chain DD: 6% 79% 20%



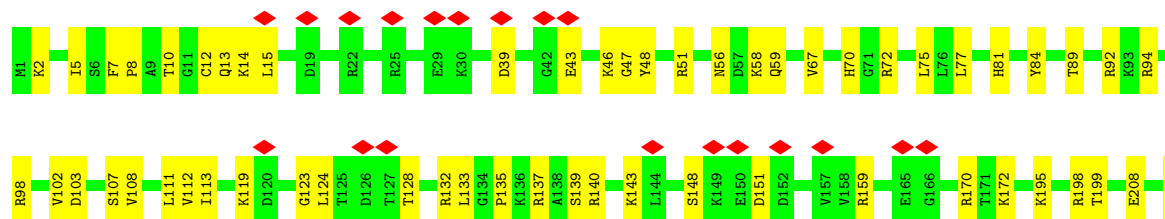
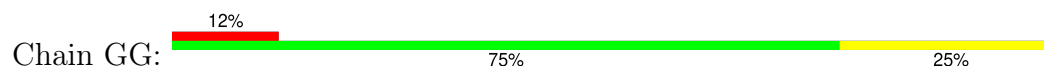
• Molecule 55: eS4



• Molecule 56: uS7



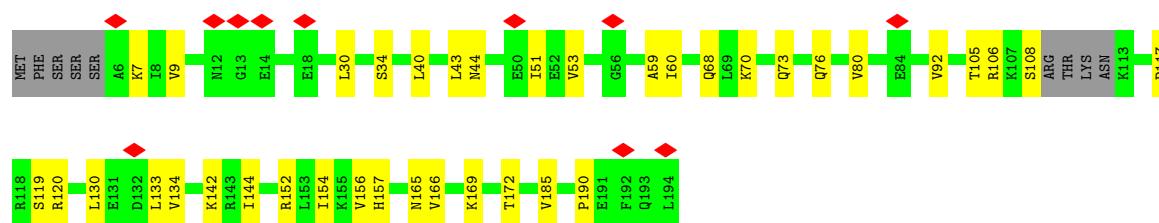
• Molecule 57: eS6



• Molecule 58: eS7

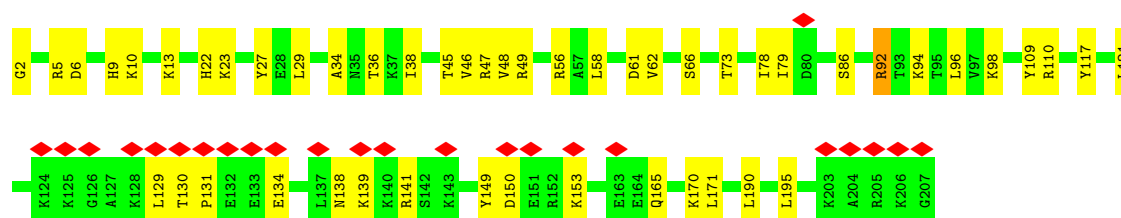


Chain HH: 



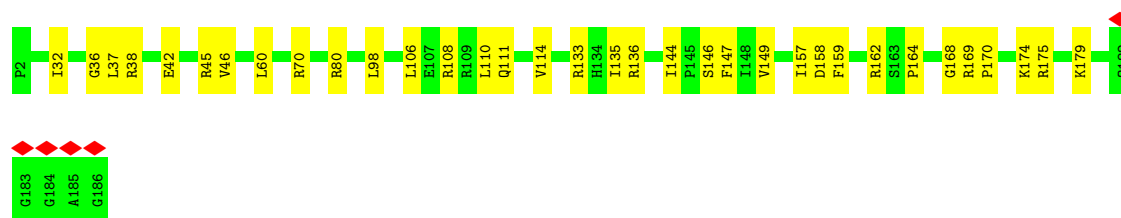
- Molecule 59: eS8

Chain II: 



- Molecule 60: uS4

Chain JJ: 



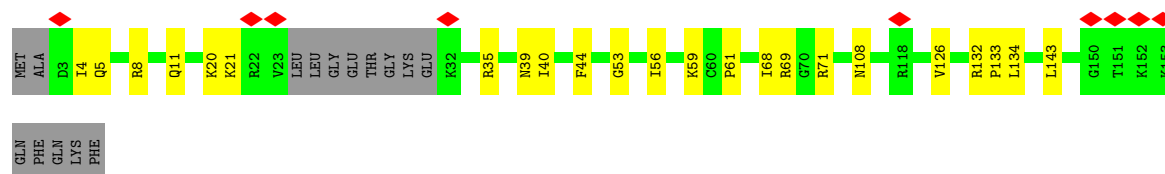
- Molecule 61: eS10

Chain KK: 

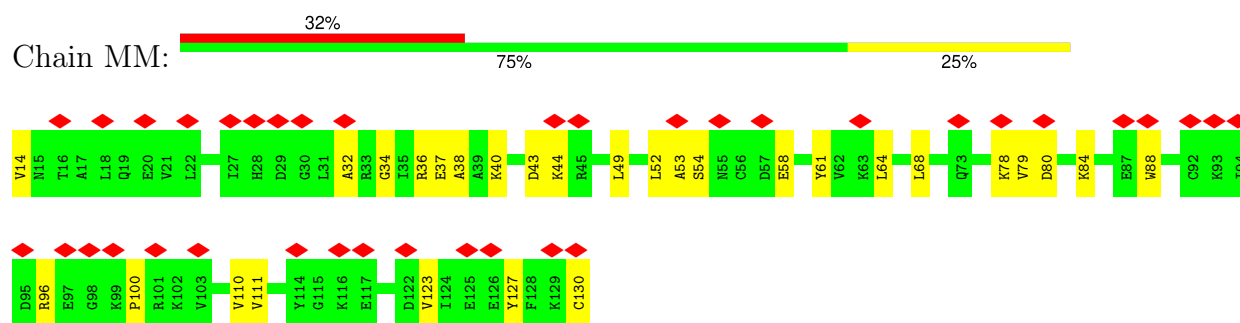


- Molecule 62: uS17

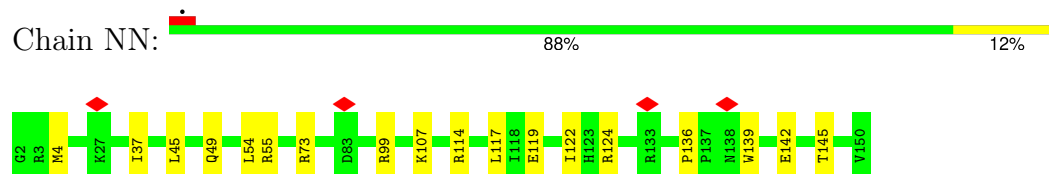
Chain LL: 



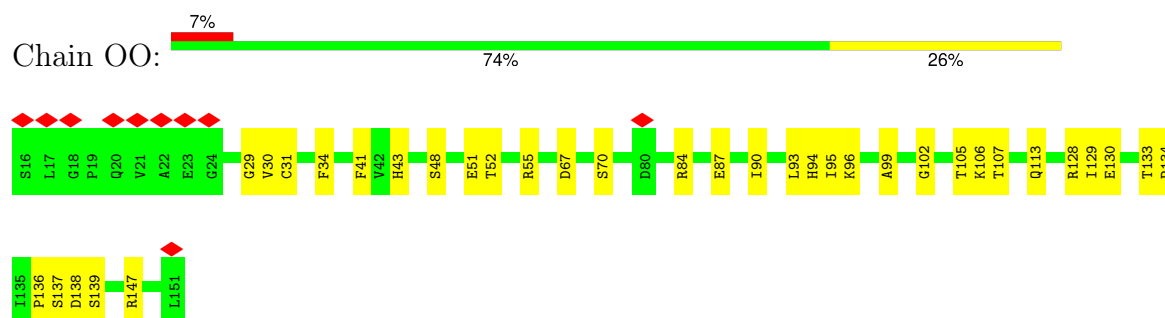
- Molecule 63: eS12



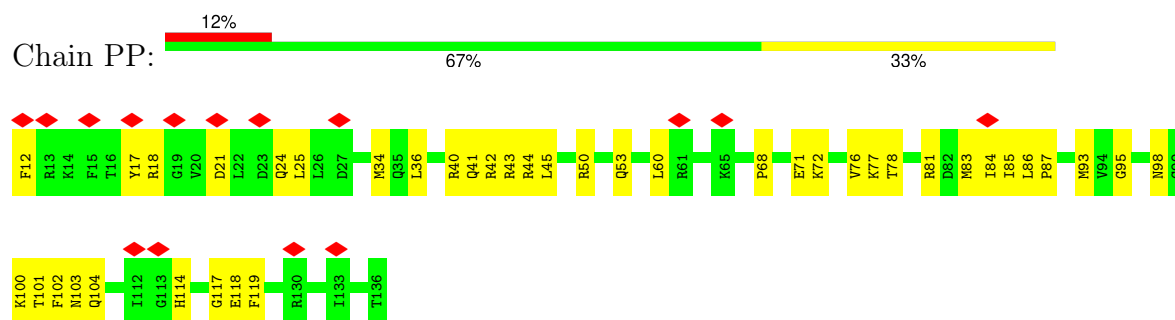
• Molecule 64: uS15



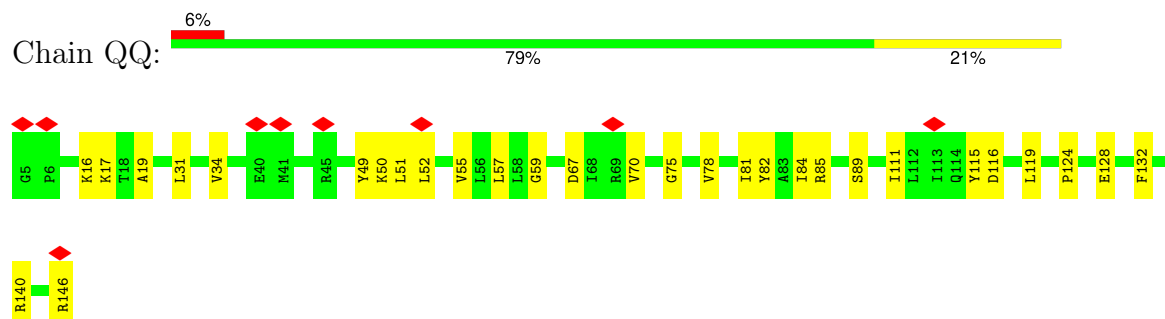
• Molecule 65: uS11



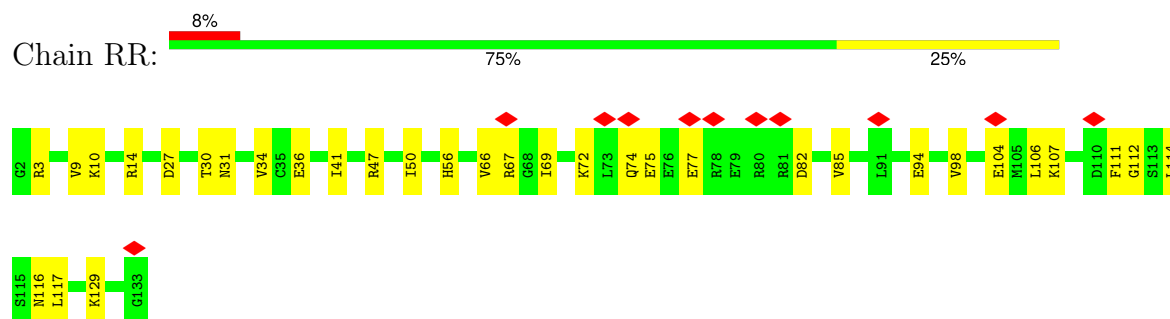
• Molecule 66: uS19



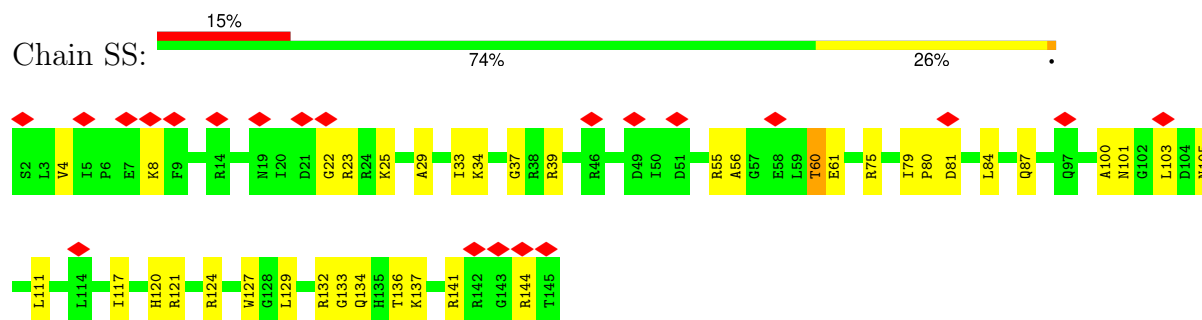
• Molecule 67: uS9



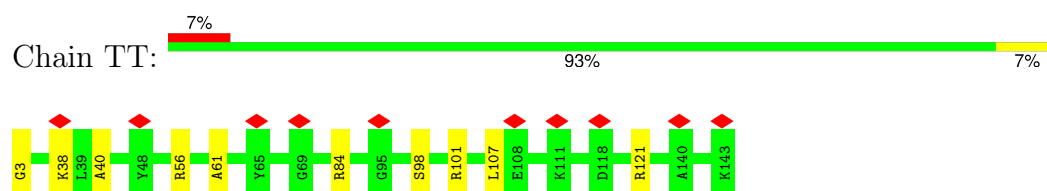
- Molecule 68: eS17



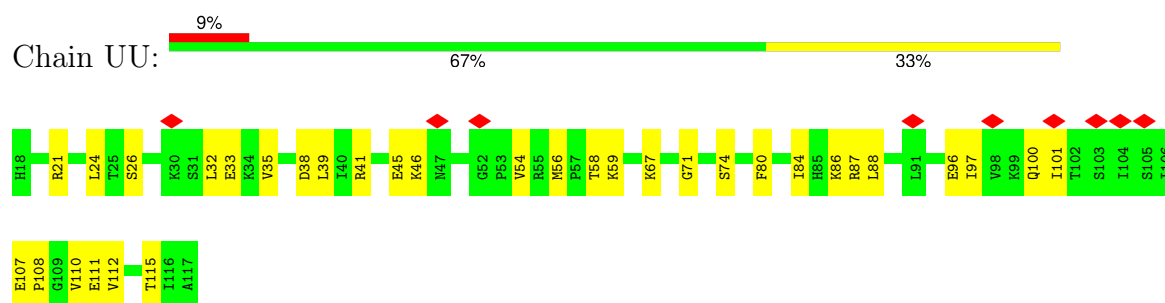
- Molecule 69: uS13



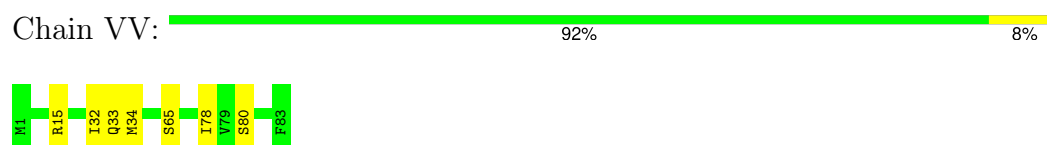
- Molecule 70: eS19



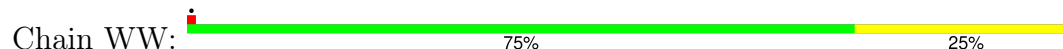
- Molecule 71: uS10



- Molecule 72: eS21

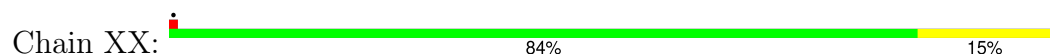


- Molecule 73: uS8

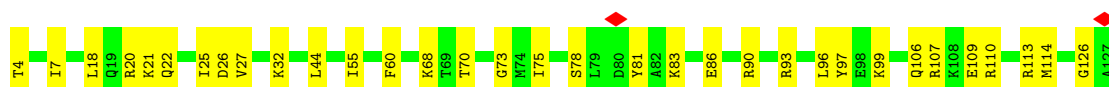
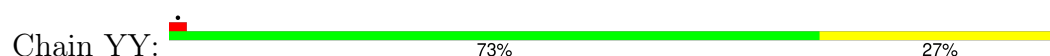




- Molecule 74: uS12



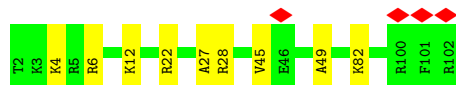
- Molecule 75: eS24



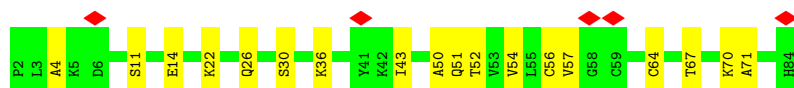
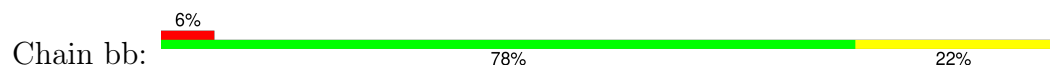
- Molecule 76: eS25



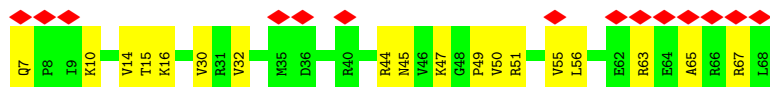
- Molecule 77: eS26



- Molecule 78: eS27

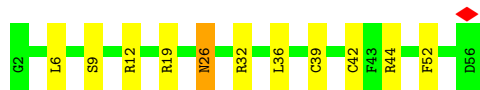


- Molecule 79: eS28



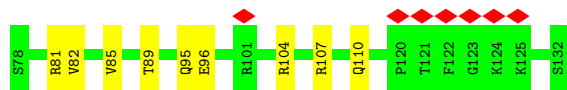
- Molecule 80: uS14

Chain dd:  80% 18%



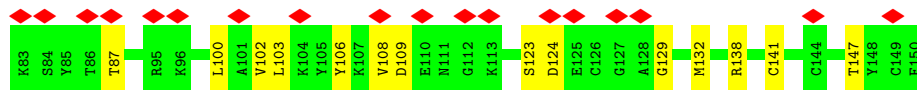
- Molecule 81: eS30

Chain ee:  13% 84% 16%



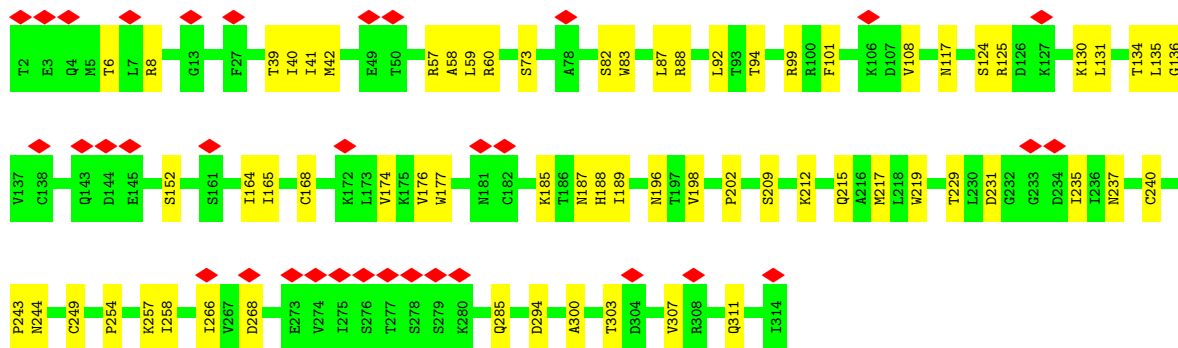
- Molecule 82: eS31

Chain ff:  26% 79% 21%



- Molecule 83: RACK1

Chain gg:  11% 79% 21%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	133480	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.679	Depositor
Minimum map value	-0.386	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.08	Depositor
Map size (Å)	536.0, 536.0, 536.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.34, 1.34, 1.34	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	5	0.40	3/83819 (0.0%)	0.45	7/130590 (0.0%)
2	7	0.39	0/2858	0.39	0/4455
3	8	0.39	0/3559	0.41	0/5543
4	A	0.45	0/1936	0.68	1/2596 (0.0%)
5	B	0.44	0/3240	0.67	2/4339 (0.0%)
6	C	0.43	0/2927	0.64	1/3932 (0.0%)
7	D	0.34	0/2437	0.57	0/3264
8	E	0.34	0/1762	0.65	1/2362 (0.0%)
9	F	0.43	0/1911	0.66	0/2549
10	G	0.36	0/1910	0.61	0/2569
11	H	0.46	0/1535	0.67	0/2063
12	I	0.42	0/1702	0.59	0/2272
13	J	0.33	0/1385	0.64	0/1852
14	L	0.38	0/1733	0.69	2/2316 (0.1%)
15	M	0.39	0/1158	0.62	0/1547
16	N	0.45	0/1746	0.67	0/2338
17	O	0.46	0/1662	0.69	1/2222 (0.0%)
18	P	0.41	0/1268	0.65	0/1700
19	Q	0.43	0/1539	0.66	0/2054
20	R	0.38	0/1524	0.68	0/2013
21	S	0.46	0/1501	0.65	0/2012
22	T	0.39	0/1326	0.59	0/1770
23	U	0.30	0/823	0.68	0/1104
24	V	0.42	0/993	0.62	0/1332
25	W	0.39	0/829	0.67	0/1099
26	X	0.38	0/984	0.62	2/1323 (0.2%)
27	Y	0.37	0/1132	0.63	0/1504
28	Z	0.37	0/1130	0.58	0/1507
29	a	0.44	0/1191	0.65	1/1590 (0.1%)
30	b	0.32	0/861	0.62	0/1138

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	c	0.35	0/771	0.57	0/1034
32	d	0.38	0/903	0.63	1/1216 (0.1%)
33	e	0.42	0/1071	0.59	0/1429
34	f	0.46	0/895	0.72	0/1198
35	g	0.40	0/916	0.67	0/1220
36	h	0.36	0/1021	0.60	0/1348
37	i	0.33	0/841	0.64	0/1112
38	j	0.42	0/720	0.67	0/952
39	k	0.33	0/575	0.57	0/761
40	l	0.40	0/459	0.63	0/608
41	m	0.45	0/425	0.73	0/561
42	n	0.33	0/240	0.74	0/305
43	o	0.38	0/855	0.60	0/1128
44	p	0.39	0/718	0.65	0/953
45	r	0.41	0/1010	0.67	0/1354
46	s	0.28	0/1530	0.61	0/2064
47	t	0.31	0/1174	0.81	1/1582 (0.1%)
48	v	0.35	0/6736	0.72	4/9094 (0.0%)
49	w	0.29	0/447	0.63	0/592
50	9	0.33	0/39723	0.44	2/61870 (0.0%)
51	AA	0.35	0/1747	0.66	0/2374
52	BB	0.30	0/1756	0.71	0/2350
53	CC	0.40	0/1753	0.65	0/2369
54	DD	0.33	0/1796	0.67	0/2417
55	EE	0.34	0/2118	0.68	0/2849
56	FF	0.29	0/1492	0.76	5/2005 (0.2%)
57	GG	0.27	0/1946	0.73	1/2590 (0.0%)
58	HH	0.31	0/1510	0.65	0/2022
59	II	0.36	1/1715 (0.1%)	0.68	0/2287
60	JJ	0.36	0/1550	0.67	2/2069 (0.1%)
61	KK	0.32	0/834	0.67	0/1125
62	LL	0.37	0/1195	0.61	0/1597
63	MM	0.28	0/918	0.68	0/1233
64	NN	0.31	0/1226	0.55	0/1649
65	OO	0.28	0/1029	0.63	0/1380
66	PP	0.29	0/1045	0.68	0/1396
67	QQ	0.26	0/1146	0.64	0/1534
68	RR	0.26	0/1082	0.62	0/1452
69	SS	0.28	0/1208	0.71	0/1618
70	TT	0.24	0/1115	0.60	0/1493
71	UU	0.29	0/805	0.63	0/1081
72	VV	0.39	0/643	0.62	0/860
73	WW	0.44	0/1051	0.72	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
74	XX	0.41	0/1116	0.66	0/1490
75	YY	0.26	0/1028	0.63	0/1366
76	ZZ	0.27	0/604	0.68	0/810
77	aa	0.32	0/828	0.61	0/1109
78	bb	0.28	0/665	0.58	0/891
79	cc	0.24	0/490	0.52	0/656
80	dd	0.32	0/470	0.62	0/623
81	ee	0.30	0/447	0.58	0/587
82	ff	0.24	0/567	0.63	0/753
83	gg	0.25	0/2493	0.60	0/3394
All	All	0.37	4/232799 (0.0%)	0.54	34/340171 (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	C	0	1
8	E	0	2
9	F	0	1
10	G	0	1
11	H	0	1
16	N	0	3
21	S	0	1
22	T	0	1
32	d	0	1
35	g	0	1
46	s	0	1
47	t	0	1
48	v	0	4
51	AA	0	2
54	DD	0	1
55	EE	0	1
56	FF	0	1
59	II	0	1
66	PP	0	1
69	SS	0	1
71	UU	0	1
72	VV	0	1
74	XX	0	1
83	gg	0	1
All	All	0	31

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	II	130	THR	C-N	7.32	1.40	1.33
1	5	3785	A2M	O3'-P	5.52	1.61	1.56
1	5	4523	A2M	O3'-P	5.28	1.61	1.56
1	5	1534	A2M	O3'-P	5.12	1.61	1.56

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	4056	A	OP1-P-O3'	-9.35	79.94	108.00
1	5	4056	A	OP2-P-O3'	-7.13	86.61	108.00
4	A	15	VAL	N-CA-C	-6.30	106.56	113.43
57	GG	67	VAL	N-CA-C	-6.02	106.94	112.96
6	C	76	ILE	N-CA-C	-5.85	104.39	109.19

There are no chirality outliers.

5 of 31 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	C	73	VAL	Peptide
8	E	178	VAL	Peptide
8	E	179	THR	Peptide
9	F	195	THR	Peptide
10	G	215	ASP	Peptide

5.2 Too-close contacts [i](#)

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	5	77254	0	38805	588	0
2	7	2558	0	1296	20	0
3	8	3209	0	1631	23	0
4	A	1898	0	1993	36	0
5	B	3172	0	3310	44	0
6	C	2884	0	3054	42	0
7	D	2391	0	2424	33	0
8	E	1729	0	1887	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	F	1875	0	1995	27	0
10	G	1879	0	2027	24	0
11	H	1516	0	1597	28	0
12	I	1664	0	1712	23	0
13	J	1362	0	1399	16	0
14	L	1702	0	1820	26	0
15	M	1137	0	1211	14	0
16	N	1701	0	1749	34	0
17	O	1630	0	1778	22	0
18	P	1242	0	1274	26	0
19	Q	1515	0	1634	22	0
20	R	1508	0	1664	21	0
21	S	1462	0	1508	29	0
22	T	1298	0	1366	17	0
23	U	809	0	833	16	0
24	V	979	0	1039	13	0
25	W	816	0	856	12	0
26	X	967	0	1040	11	0
27	Y	1115	0	1205	19	0
28	Z	1107	0	1182	15	0
29	a	1162	0	1209	25	0
30	b	848	0	920	8	0
31	c	761	0	794	5	0
32	d	888	0	930	12	0
33	e	1053	0	1147	7	0
34	f	876	0	912	11	0
35	g	906	0	999	6	0
36	h	1013	0	1147	13	0
37	i	830	0	916	7	0
38	j	705	0	737	14	0
39	k	569	0	637	6	0
40	l	447	0	480	8	0
41	m	430	0	466	14	0
42	n	239	0	289	3	0
43	o	842	0	913	8	0
44	p	708	0	756	16	0
45	r	994	0	1051	16	0
46	s	1507	0	1564	18	0
47	t	1160	0	1218	19	0
48	v	6628	0	6713	113	0
49	w	440	0	402	5	0
50	9	36291	0	18322	331	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	AA	1710	0	1708	28	0
52	BB	1729	0	1803	39	0
53	CC	1716	0	1806	18	0
54	DD	1768	0	1866	33	0
55	EE	2076	0	2177	34	0
56	FF	1471	0	1522	44	0
57	GG	1923	0	2089	45	0
58	HH	1488	0	1582	23	0
59	II	1686	0	1772	41	0
60	JJ	1525	0	1640	24	0
61	KK	810	0	836	18	0
62	LL	1175	0	1249	20	0
63	MM	908	0	939	17	0
64	NN	1202	0	1289	11	0
65	OO	1016	0	1039	24	0
66	PP	1025	0	1074	28	0
67	QQ	1128	0	1195	21	0
68	RR	1068	0	1121	22	0
69	SS	1190	0	1249	27	0
70	TT	1097	0	1132	8	0
71	UU	795	0	862	21	0
72	VV	636	0	637	5	0
73	WW	1034	0	1080	23	0
74	XX	1098	0	1167	13	0
75	YY	1011	0	1083	24	0
76	ZZ	598	0	656	17	0
77	aa	814	0	863	8	0
78	bb	651	0	672	14	0
79	cc	488	0	514	14	0
80	dd	459	0	452	12	0
81	ee	443	0	492	6	0
82	ff	555	0	567	10	0
83	gg	2436	0	2393	40	0
84	5	200	0	0	0	0
84	7	7	0	0	0	0
84	8	6	0	0	0	0
84	9	78	0	0	0	0
84	A	1	0	0	0	0
84	P	1	0	0	0	0
84	TT	1	0	0	0	0
84	V	1	0	0	0	0
84	a	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	j	1	0	0	0	0
84	v	1	0	0	0	0
85	KK	1	0	0	0	0
85	aa	1	0	0	0	0
85	ff	1	0	0	0	0
85	g	1	0	0	0	0
85	j	1	0	0	0	0
85	m	1	0	0	0	0
85	o	1	0	0	0	0
85	p	1	0	0	0	0
86	v	28	0	12	2	0
All	All	220739	0	166349	2093	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 6.

The worst 5 of 2093 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)
1:5:4296:B8H:C5	1:5:4296:B8H:C4	1.82	1.57
1:5:3762:B8H:C4	1:5:3762:B8H:C5	1.83	1.56
1:5:1860:B8H:C4	1:5:1860:B8H:C5	1.82	1.56
1:5:1860:B8H:C6	1:5:1860:B8H:N1	1.68	1.54
1:5:3762:B8H:C6	1:5:3762:B8H:N1	1.68	1.53

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
4	A	246/248 (99%)	221 (90%)	25 (10%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	B	392/394 (100%)	365 (93%)	27 (7%)	0	100	100
6	C	359/362 (99%)	339 (94%)	20 (6%)	0	100	100
7	D	291/293 (99%)	279 (96%)	12 (4%)	0	100	100
8	E	208/291 (72%)	198 (95%)	10 (5%)	0	100	100
9	F	223/225 (99%)	212 (95%)	10 (4%)	1 (0%)	30	59
10	G	229/319 (72%)	219 (96%)	10 (4%)	0	100	100
11	H	188/190 (99%)	171 (91%)	17 (9%)	0	100	100
12	I	201/214 (94%)	191 (95%)	10 (5%)	0	100	100
13	J	168/170 (99%)	160 (95%)	8 (5%)	0	100	100
14	L	208/210 (99%)	198 (95%)	8 (4%)	2 (1%)	12	40
15	M	136/138 (99%)	125 (92%)	11 (8%)	0	100	100
16	N	201/203 (99%)	190 (94%)	11 (6%)	0	100	100
17	O	197/199 (99%)	191 (97%)	6 (3%)	0	100	100
18	P	151/153 (99%)	146 (97%)	5 (3%)	0	100	100
19	Q	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
20	R	178/180 (99%)	173 (97%)	5 (3%)	0	100	100
21	S	174/176 (99%)	164 (94%)	9 (5%)	1 (1%)	21	50
22	T	157/159 (99%)	153 (98%)	3 (2%)	1 (1%)	21	50
23	U	97/99 (98%)	92 (95%)	5 (5%)	0	100	100
24	V	129/131 (98%)	127 (98%)	2 (2%)	0	100	100
25	W	96/157 (61%)	89 (93%)	7 (7%)	0	100	100
26	X	116/118 (98%)	108 (93%)	8 (7%)	0	100	100
27	Y	132/134 (98%)	127 (96%)	5 (4%)	0	100	100
28	Z	133/135 (98%)	128 (96%)	5 (4%)	0	100	100
29	a	145/147 (99%)	137 (94%)	8 (6%)	0	100	100
30	b	100/245 (41%)	95 (95%)	5 (5%)	0	100	100
31	c	96/98 (98%)	88 (92%)	8 (8%)	0	100	100
32	d	105/107 (98%)	97 (92%)	8 (8%)	0	100	100
33	e	126/128 (98%)	119 (94%)	7 (6%)	0	100	100
34	f	107/109 (98%)	102 (95%)	5 (5%)	0	100	100
35	g	112/114 (98%)	108 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	h	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
37	i	100/102 (98%)	97 (97%)	3 (3%)	0	100	100
38	j	84/86 (98%)	77 (92%)	7 (8%)	0	100	100
39	k	67/69 (97%)	66 (98%)	1 (2%)	0	100	100
40	l	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
41	m	49/52 (94%)	46 (94%)	2 (4%)	1 (2%)	6	25
42	n	23/25 (92%)	23 (100%)	0	0	100	100
43	o	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
44	p	89/91 (98%)	87 (98%)	2 (2%)	0	100	100
45	r	122/124 (98%)	116 (95%)	6 (5%)	0	100	100
46	s	194/196 (99%)	178 (92%)	16 (8%)	0	100	100
47	t	151/153 (99%)	128 (85%)	22 (15%)	1 (1%)	18	47
48	v	843/848 (99%)	774 (92%)	68 (8%)	1 (0%)	48	78
49	w	51/55 (93%)	46 (90%)	5 (10%)	0	100	100
51	AA	215/217 (99%)	206 (96%)	9 (4%)	0	100	100
52	BB	211/213 (99%)	203 (96%)	8 (4%)	0	100	100
53	CC	219/221 (99%)	206 (94%)	13 (6%)	0	100	100
54	DD	226/228 (99%)	216 (96%)	10 (4%)	0	100	100
55	EE	260/262 (99%)	244 (94%)	16 (6%)	0	100	100
56	FF	181/204 (89%)	162 (90%)	19 (10%)	0	100	100
57	GG	235/237 (99%)	224 (95%)	11 (5%)	0	100	100
58	HH	181/194 (93%)	173 (96%)	8 (4%)	0	100	100
59	II	204/206 (99%)	185 (91%)	19 (9%)	0	100	100
60	JJ	183/185 (99%)	180 (98%)	3 (2%)	0	100	100
61	KK	94/96 (98%)	86 (92%)	8 (8%)	0	100	100
62	LL	139/158 (88%)	131 (94%)	8 (6%)	0	100	100
63	MM	115/117 (98%)	101 (88%)	14 (12%)	0	100	100
64	NN	147/149 (99%)	138 (94%)	9 (6%)	0	100	100
65	OO	134/136 (98%)	123 (92%)	11 (8%)	0	100	100
66	PP	123/125 (98%)	118 (96%)	5 (4%)	0	100	100
67	QQ	140/142 (99%)	132 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	RR	130/132 (98%)	121 (93%)	9 (7%)	0	100	100
69	SS	142/144 (99%)	135 (95%)	7 (5%)	0	100	100
70	TT	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
71	UU	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
72	VV	81/83 (98%)	76 (94%)	5 (6%)	0	100	100
73	WW	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
74	XX	139/141 (99%)	132 (95%)	4 (3%)	3 (2%)	5	24
75	YY	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
76	ZZ	73/75 (97%)	70 (96%)	3 (4%)	0	100	100
77	aa	99/101 (98%)	90 (91%)	9 (9%)	0	100	100
78	bb	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
79	cc	60/62 (97%)	57 (95%)	3 (5%)	0	100	100
80	dd	53/55 (96%)	48 (91%)	5 (9%)	0	100	100
81	ee	53/55 (96%)	50 (94%)	3 (6%)	0	100	100
82	ff	66/68 (97%)	55 (83%)	11 (17%)	0	100	100
83	gg	311/313 (99%)	282 (91%)	29 (9%)	0	100	100
All	All	12409/13005 (95%)	11674 (94%)	724 (6%)	11 (0%)	49	78

5 of 11 Ramachandran outliers are listed below:

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

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	A	190/190 (100%)	186 (98%)	4 (2%)	47	64
5	B	342/342 (100%)	336 (98%)	6 (2%)	51	67
6	C	301/301 (100%)	300 (100%)	1 (0%)	86	84
7	D	247/247 (100%)	246 (100%)	1 (0%)	84	83
8	E	190/251 (76%)	188 (99%)	2 (1%)	65	74
9	F	196/196 (100%)	195 (100%)	1 (0%)	81	81
10	G	200/272 (74%)	197 (98%)	3 (2%)	57	69
11	H	169/169 (100%)	169 (100%)	0	100	100
12	I	175/181 (97%)	173 (99%)	2 (1%)	65	74
13	J	143/143 (100%)	142 (99%)	1 (1%)	76	78
14	L	175/175 (100%)	174 (99%)	1 (1%)	78	80
15	M	117/117 (100%)	117 (100%)	0	100	100
16	N	171/171 (100%)	170 (99%)	1 (1%)	78	80
17	O	171/171 (100%)	168 (98%)	3 (2%)	51	67
18	P	134/134 (100%)	134 (100%)	0	100	100
19	Q	164/164 (100%)	164 (100%)	0	100	100
20	R	159/159 (100%)	159 (100%)	0	100	100
21	S	157/157 (100%)	155 (99%)	2 (1%)	61	71
22	T	139/139 (100%)	138 (99%)	1 (1%)	76	78
23	U	89/89 (100%)	89 (100%)	0	100	100
24	V	101/101 (100%)	100 (99%)	1 (1%)	68	75
25	W	82/126 (65%)	82 (100%)	0	100	100
26	X	106/106 (100%)	105 (99%)	1 (1%)	70	76
27	Y	124/124 (100%)	122 (98%)	2 (2%)	55	68
28	Z	117/117 (100%)	113 (97%)	4 (3%)	32	57
29	a	119/119 (100%)	118 (99%)	1 (1%)	73	77
30	b	84/184 (46%)	84 (100%)	0	100	100
31	c	84/84 (100%)	83 (99%)	1 (1%)	63	72
32	d	98/98 (100%)	97 (99%)	1 (1%)	68	75
33	e	114/114 (100%)	114 (100%)	0	100	100
34	f	88/88 (100%)	86 (98%)	2 (2%)	44	63
35	g	98/98 (100%)	96 (98%)	2 (2%)	48	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	h	109/109 (100%)	107 (98%)	2 (2%)	51	67
37	i	86/86 (100%)	86 (100%)	0	100	100
38	j	73/73 (100%)	73 (100%)	0	100	100
39	k	64/64 (100%)	64 (100%)	0	100	100
40	l	47/47 (100%)	47 (100%)	0	100	100
41	m	47/47 (100%)	46 (98%)	1 (2%)	47	64
42	n	24/24 (100%)	24 (100%)	0	100	100
43	o	91/91 (100%)	91 (100%)	0	100	100
44	p	74/74 (100%)	74 (100%)	0	100	100
45	r	108/108 (100%)	108 (100%)	0	100	100
46	s	164/164 (100%)	161 (98%)	3 (2%)	51	67
47	t	126/126 (100%)	124 (98%)	2 (2%)	55	68
48	v	722/722 (100%)	714 (99%)	8 (1%)	65	74
49	w	46/46 (100%)	46 (100%)	0	100	100
51	AA	180/181 (99%)	180 (100%)	0	100	100
52	BB	194/194 (100%)	191 (98%)	3 (2%)	57	69
53	CC	187/187 (100%)	187 (100%)	0	100	100
54	DD	190/190 (100%)	187 (98%)	3 (2%)	55	68
55	EE	224/224 (100%)	219 (98%)	5 (2%)	45	63
56	FF	158/170 (93%)	155 (98%)	3 (2%)	50	66
57	GG	207/207 (100%)	205 (99%)	2 (1%)	68	75
58	HH	165/174 (95%)	164 (99%)	1 (1%)	78	80
59	II	178/178 (100%)	177 (99%)	1 (1%)	78	80
60	JJ	161/161 (100%)	161 (100%)	0	100	100
61	KK	87/87 (100%)	86 (99%)	1 (1%)	65	74
62	LL	130/142 (92%)	129 (99%)	1 (1%)	73	77
63	MM	99/99 (100%)	98 (99%)	1 (1%)	68	75
64	NN	130/130 (100%)	129 (99%)	1 (1%)	73	77
65	OO	106/106 (100%)	106 (100%)	0	100	100
66	PP	111/111 (100%)	109 (98%)	2 (2%)	51	67
67	QQ	117/117 (100%)	117 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	RR	119/119 (100%)	118 (99%)	1 (1%)	73	77
69	SS	125/125 (100%)	123 (98%)	2 (2%)	55	68
70	TT	111/111 (100%)	111 (100%)	0	100	100
71	UU	92/92 (100%)	92 (100%)	0	100	100
72	VV	67/67 (100%)	67 (100%)	0	100	100
73	WW	112/112 (100%)	111 (99%)	1 (1%)	70	76
74	XX	113/113 (100%)	111 (98%)	2 (2%)	51	67
75	YY	107/107 (100%)	107 (100%)	0	100	100
76	ZZ	66/66 (100%)	65 (98%)	1 (2%)	57	69
77	aa	88/88 (100%)	88 (100%)	0	100	100
78	bb	75/75 (100%)	75 (100%)	0	100	100
79	cc	55/55 (100%)	55 (100%)	0	100	100
80	dd	48/48 (100%)	47 (98%)	1 (2%)	47	64
81	ee	46/46 (100%)	45 (98%)	1 (2%)	45	63
82	ff	61/61 (100%)	61 (100%)	0	100	100
83	gg	272/272 (100%)	270 (99%)	2 (1%)	76	78
All	All	10806/11123 (97%)	10711 (99%)	95 (1%)	68	76

5 of 95 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
48	v	537	ILE
56	FF	76	MET
48	v	779	THR
54	DD	142	LEU
57	GG	102	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 103 such sidechains are listed below:

Mol	Chain	Res	Type
48	v	544	HIS
56	FF	114	ASN
83	gg	76	GLN
48	v	764	ASN
55	EE	50	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3554/3597 (98%)	833 (23%)	59 (1%)
2	7	119/120 (99%)	14 (11%)	0
3	8	149/151 (98%)	25 (16%)	1 (0%)
50	9	1682/1698 (99%)	390 (23%)	18 (1%)
All	All	5504/5566 (98%)	1262 (22%)	78 (1%)

5 of 1262 RNA backbone outliers are listed below:

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

5 of 78 RNA pucker outliers are listed below:

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

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	PSU	5	4628	1	18,21,22	1.15	3 (16%)	21,30,33	2.23	5 (23%)
1	OMC	5	3887	1	19,22,23	2.87	7 (36%)	25,31,34	0.96	1 (4%)
1	OMG	5	3792	1	23,26,27	2.44	8 (34%)	32,38,41	2.06	9 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	OMU	9	116	50	19,22,23	2.93	7 (36%)	25,31,34	1.86	5 (20%)
1	7MG	5	4550	1	23,26,27	3.27	10 (43%)	27,39,42	2.09	10 (37%)
1	7MG	5	2522	1	23,26,27	3.24	10 (43%)	27,39,42	2.11	9 (33%)
1	PSU	5	1582	1	18,21,22	1.10	1 (5%)	21,30,33	1.85	4 (19%)
1	BGH	5	3899	1,84	25,29,30	4.21	15 (60%)	30,43,46	2.68	14 (46%)
1	MHG	5	4371	1	29,32,33	3.69	11 (37%)	34,46,49	2.43	12 (35%)
50	OMC	9	1710	50	19,22,23	2.96	7 (36%)	25,31,34	0.95	1 (4%)
1	5MC	5	3782	1	19,22,23	3.69	8 (42%)	26,32,35	1.05	1 (3%)
50	OMC	9	517	50	19,22,23	2.85	7 (36%)	25,31,34	0.65	0
50	PSU	9	822	50	18,21,22	1.05	2 (11%)	21,30,33	2.07	5 (23%)
1	B9B	5	1574	1	25,28,29	3.75	10 (40%)	35,40,43	2.27	12 (34%)
50	B8N	9	1248	50,84	25,29,30	3.09	7 (28%)	28,42,45	2.00	7 (25%)
1	OMG	5	4870	1	23,26,27	2.39	8 (34%)	32,38,41	1.85	8 (25%)
50	OMC	9	1703	50	19,22,23	2.95	7 (36%)	25,31,34	0.86	1 (4%)
1	OMG	5	1522	1	23,26,27	2.36	8 (34%)	32,38,41	1.98	8 (25%)
1	B9B	5	2754	1,84	25,28,29	3.77	9 (36%)	35,40,43	2.43	13 (37%)
1	B8K	5	4690	1	24,28,29	4.86	17 (70%)	29,42,45	2.85	11 (37%)
1	5MC	5	4335	1	19,22,23	3.89	8 (42%)	26,32,35	1.19	3 (11%)
50	5MC	9	1374	50	19,22,23	3.92	8 (42%)	26,32,35	1.35	3 (11%)
1	A2M	5	398	1	22,25,26	3.93	11 (50%)	30,36,39	2.28	10 (33%)
50	A2M	9	1031	50	22,25,26	3.88	11 (50%)	30,36,39	2.50	12 (40%)
1	UR3	5	1866	1	19,22,23	2.55	6 (31%)	26,32,35	1.58	5 (19%)
1	PSU	5	2508	1	18,21,22	1.03	1 (5%)	21,30,33	1.79	4 (19%)
1	PSU	5	4403	1	18,21,22	1.04	1 (5%)	21,30,33	1.99	4 (19%)
1	PSU	5	4636	1	18,21,22	1.08	2 (11%)	21,30,33	2.12	5 (23%)
1	B9H	5	2786	1	21,25,26	2.99	3 (14%)	22,35,38	1.79	3 (13%)
1	OMG	5	4196	1	23,26,27	2.35	8 (34%)	32,38,41	1.93	8 (25%)
1	A2M	5	4571	1	22,25,26	3.93	11 (50%)	30,36,39	2.44	13 (43%)
50	UR3	9	1830	50	19,22,23	2.75	7 (36%)	26,32,35	1.81	5 (19%)
1	PSU	5	1683	1	18,21,22	1.13	2 (11%)	21,30,33	1.97	4 (19%)
50	MA6	9	1851	50	23,26,27	1.49	4 (17%)	33,38,41	2.70	12 (36%)
1	A2M	5	3825	1	22,25,26	3.93	11 (50%)	30,36,39	2.35	11 (36%)
1	OMU	5	4620	1	19,22,23	2.74	7 (36%)	25,31,34	1.95	5 (20%)
1	PSU	5	3729	1	18,21,22	1.10	1 (5%)	21,30,33	1.87	4 (19%)
50	PSU	9	119	50	18,21,22	0.96	1 (5%)	21,30,33	1.71	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	PSU	9	612	50	18,21,22	1.00	1 (5%)	21,30,33	1.87	5 (23%)
50	4AC	9	1337	50	21,24,25	3.17	9 (42%)	28,34,37	1.27	4 (14%)
1	OMU	5	4306	1	19,22,23	2.83	8 (42%)	25,31,34	1.86	5 (20%)
1	7MG	5	1605	1	23,26,27	3.25	10 (43%)	27,39,42	2.18	9 (33%)
1	1MA	5	4415	1	21,25,26	2.69	5 (23%)	30,37,40	1.88	5 (16%)
1	UR3	5	4597	1	19,22,23	2.56	7 (36%)	26,32,35	1.47	4 (15%)
1	OMG	5	1883	1	23,26,27	2.44	8 (34%)	32,38,41	2.07	7 (21%)
1	PSU	5	4450	1,84	18,21,22	1.09	3 (16%)	21,30,33	2.12	5 (23%)
1	PSU	5	4531	1	18,21,22	1.11	3 (16%)	21,30,33	2.05	5 (23%)
50	5MU	9	814	50	19,22,23	4.93	7 (36%)	27,32,35	3.58	12 (44%)
41	MLZ	m	72	41	8,9,10	0.78	0	4,9,11	0.78	0
1	B8W	5	4129	1	23,26,27	3.38	10 (43%)	33,38,41	5.88	21 (63%)
1	UR3	5	4530	1	19,22,23	2.71	7 (36%)	26,32,35	1.70	5 (19%)
50	MA6	9	1850	50	23,26,27	1.50	5 (21%)	33,38,41	2.79	13 (39%)
50	6MZ	9	1832	50,84	22,25,26	3.01	5 (22%)	29,36,39	4.08	12 (41%)
1	M7A	5	4564	1	19,25,26	1.61	4 (21%)	25,37,40	3.97	8 (32%)
1	1MA	5	1322	1,84	21,25,26	2.57	5 (23%)	30,37,40	1.85	5 (16%)
1	A2M	5	3718	1	22,25,26	3.94	13 (59%)	30,36,39	2.17	10 (33%)
50	A2M	9	27	50,84	22,25,26	3.89	10 (45%)	30,36,39	2.48	13 (43%)
1	OMG	5	4623	1	23,26,27	2.40	9 (39%)	32,38,41	1.96	8 (25%)
1	OMG	5	4637	1	23,26,27	2.36	8 (34%)	32,38,41	1.83	8 (25%)
1	OMG	5	4494	1	23,26,27	2.41	9 (39%)	32,38,41	1.89	9 (28%)
50	E3C	9	568	50	19,23,24	3.37	6 (31%)	21,33,36	2.46	6 (28%)
1	A2M	5	1326	1	22,25,26	3.90	13 (59%)	30,36,39	2.29	9 (30%)
3	OMU	8	14	1,3	19,22,23	2.88	7 (36%)	25,31,34	1.97	7 (28%)
1	OMG	5	373	1	23,26,27	2.41	9 (39%)	32,38,41	1.99	10 (31%)
1	B8W	5	4185	1	23,26,27	3.38	11 (47%)	33,38,41	5.67	23 (69%)
1	A2M	5	2363	1,84	22,25,26	3.99	10 (45%)	30,36,39	2.52	12 (40%)
1	B8H	5	1860	1	19,22,23	6.83	6 (31%)	21,32,35	2.39	5 (23%)
1	PSU	5	3764	1	18,21,22	1.05	1 (5%)	21,30,33	1.81	4 (19%)
50	A2M	9	166	50	22,25,26	3.87	11 (50%)	30,36,39	2.50	11 (36%)
50	A2M	9	484	50	22,25,26	3.88	12 (54%)	30,36,39	2.29	10 (33%)
50	PSU	9	1081	50	18,21,22	1.08	2 (11%)	21,30,33	1.91	5 (23%)
1	I4U	5	4194	1	20,24,25	5.01	13 (65%)	27,34,37	1.82	4 (14%)
1	A2M	5	1524	1	22,25,26	3.90	12 (54%)	30,36,39	2.63	12 (40%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	PSU	9	1243	50,84	18,21,22	1.10	1 (5%)	21,30,33	1.97	4 (19%)
1	B9B	5	237	1	25,28,29	3.78	9 (36%)	35,40,43	2.58	14 (40%)
1	2MG	5	1517	1	23,26,27	2.90	7 (30%)	33,38,41	2.48	10 (30%)
1	OMC	5	2861	1	19,22,23	2.85	7 (36%)	25,31,34	0.91	1 (4%)
1	OMC	5	3909	1	19,22,23	2.85	7 (36%)	25,31,34	1.31	3 (12%)
50	PSU	9	823	50	18,21,22	1.11	2 (11%)	21,30,33	1.95	4 (19%)
50	A2M	9	159	50	22,25,26	3.94	10 (45%)	30,36,39	2.52	13 (43%)
1	E6G	5	4355	1	24,27,28	3.60	12 (50%)	34,39,42	2.53	14 (41%)
1	P7G	5	3880	1	24,28,29	3.52	10 (41%)	25,41,44	1.33	2 (8%)
1	A2M	5	3785	1	22,25,26	3.86	13 (59%)	30,36,39	2.56	12 (40%)
1	P4U	5	1348	1,84	21,24,25	3.28	7 (33%)	28,33,36	1.94	3 (10%)
1	5MC	5	4447	1	19,22,23	3.85	8 (42%)	26,32,35	1.13	1 (3%)
50	OMG	9	644	50	23,26,27	2.41	9 (39%)	32,38,41	1.87	8 (25%)
1	B8Q	5	1456	1	18,22,23	2.75	5 (27%)	21,32,35	1.90	4 (19%)
50	OMG	9	683	50	23,26,27	2.37	9 (39%)	32,38,41	1.85	9 (28%)
1	B8T	5	4671	1	19,22,23	3.01	8 (42%)	25,31,34	0.95	1 (4%)
1	E7G	5	1797	1	24,27,28	3.26	11 (45%)	28,40,43	2.33	10 (35%)
1	B8K	5	3897	1	24,28,29	4.76	17 (70%)	29,42,45	2.61	12 (41%)
1	PSU	5	4500	1	18,21,22	1.08	3 (16%)	21,30,33	2.06	5 (23%)
1	PSU	5	4442	1	18,21,22	1.08	3 (16%)	21,30,33	1.98	5 (23%)
48	DDE	v	715	48	18,20,21	1.03	1 (5%)	17,28,30	1.21	3 (17%)
1	5MU	5	4083	1	19,22,23	4.71	7 (36%)	27,32,35	3.46	9 (33%)
1	A2M	5	4523	1,84	22,25,26	3.91	12 (54%)	30,36,39	2.36	11 (36%)
1	6MZ	5	4220	1	22,25,26	2.89	7 (31%)	29,36,39	4.01	12 (41%)
1	A2M	5	1871	1,84	22,25,26	3.90	12 (54%)	30,36,39	2.44	10 (33%)
6	MLZ	C	333	6	8,9,10	0.84	0	4,9,11	0.70	0
1	OMG	5	1625	1,84	23,26,27	2.38	8 (34%)	32,38,41	1.94	9 (28%)
1	2MG	5	4872	1	23,26,27	2.83	9 (39%)	33,38,41	3.26	16 (48%)
1	A2M	5	3723	1	22,25,26	3.94	12 (54%)	30,36,39	2.27	9 (30%)
1	OMC	5	2422	1,84	19,22,23	2.88	7 (36%)	25,31,34	1.00	1 (4%)
1	B8W	5	4472	1	23,26,27	3.41	12 (52%)	33,38,41	5.38	21 (63%)
50	4AC	9	1842	50	21,24,25	3.11	10 (47%)	28,34,37	1.21	4 (14%)
50	OMC	9	174	50	19,22,23	2.97	7 (36%)	25,31,34	0.83	1 (4%)
50	OMG	9	509	50,84	23,26,27	2.39	9 (39%)	32,38,41	1.88	8 (25%)
1	OMG	5	4370	1	23,26,27	2.38	9 (39%)	32,38,41	1.89	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
50	B8Q	9	1219	50	18,22,23	2.94	4 (22%)	21,32,35	2.24	7 (33%)
1	A2M	5	2401	1,84	22,25,26	3.91	12 (54%)	30,36,39	2.53	11 (36%)
1	OMG	5	2424	1	23,26,27	2.43	9 (39%)	32,38,41	1.85	8 (25%)
1	OMG	5	2050	1	23,26,27	2.40	8 (34%)	32,38,41	1.85	8 (25%)
1	OMC	5	2365	1	19,22,23	2.84	7 (36%)	25,31,34	0.70	0
1	B8W	5	4529	1,84	23,26,27	3.36	11 (47%)	33,38,41	5.87	22 (66%)
50	M7A	9	1806	50	19,25,26	1.62	2 (10%)	25,37,40	3.94	8 (32%)
50	A2M	9	668	50,84	22,25,26	3.92	11 (50%)	30,36,39	2.43	14 (46%)
1	B8H	5	3762	1	19,22,23	6.86	6 (31%)	21,32,35	2.63	5 (23%)
1	OMC	5	3701	1,84	19,22,23	2.82	7 (36%)	25,31,34	0.75	0
1	OMG	5	1316	1	23,26,27	2.40	9 (39%)	32,38,41	1.99	8 (25%)
1	PSU	5	3715	1	18,21,22	1.05	1 (5%)	21,30,33	1.83	4 (19%)
1	A2M	5	1534	1,84	22,25,26	3.93	13 (59%)	30,36,39	2.51	12 (40%)
1	B8W	5	2380	1	23,26,27	3.34	12 (52%)	33,38,41	5.62	18 (54%)
1	B8H	5	4296	1	19,22,23	6.87	6 (31%)	21,32,35	2.64	5 (23%)
50	A2M	9	1678	50	22,25,26	3.91	11 (50%)	30,36,39	2.39	10 (33%)
1	OMG	5	2364	1	23,26,27	2.40	9 (39%)	32,38,41	1.95	7 (21%)
1	OMC	5	4536	1	19,22,23	2.83	7 (36%)	25,31,34	1.07	2 (8%)
1	OMC	5	2804	1	19,22,23	2.87	7 (36%)	25,31,34	0.83	0
1	2MG	5	729	1	23,26,27	2.84	7 (30%)	33,38,41	2.20	8 (24%)
1	PSU	5	4293	1	18,21,22	1.11	2 (11%)	21,30,33	1.88	3 (14%)
1	B8T	5	4483	1	19,22,23	3.02	8 (42%)	25,31,34	1.07	2 (8%)
1	OMG	5	2773	1	23,26,27	2.42	9 (39%)	32,38,41	1.88	8 (25%)
1	OMC	5	3869	1	19,22,23	2.81	7 (36%)	25,31,34	0.85	1 (4%)
1	E7G	5	2297	1	24,27,28	3.11	11 (45%)	28,40,43	2.24	9 (32%)
1	A2M	5	3867	1	22,25,26	3.95	12 (54%)	30,36,39	2.32	12 (40%)
1	PSU	5	1677	1	18,21,22	1.12	3 (16%)	21,30,33	2.04	6 (28%)
1	I4U	5	1659	1	20,24,25	5.00	14 (70%)	27,34,37	2.22	3 (11%)
50	OMU	9	121	50	19,22,23	3.00	8 (42%)	25,31,34	1.87	5 (20%)
1	P7G	5	1909	1	24,28,29	3.70	11 (45%)	25,41,44	1.28	2 (8%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	5	4628	1	-	0/7/25/26	0/2/2/2
1	OMC	5	3887	1	-	1/9/27/28	0/2/2/2
1	OMG	5	3792	1	-	2/9/27/28	0/3/3/3
50	OMU	9	116	50	-	3/9/27/28	0/2/2/2
1	7MG	5	4550	1	-	0/7/37/38	0/3/3/3
1	7MG	5	2522	1	-	0/7/37/38	0/3/3/3
1	PSU	5	1582	1	-	2/7/25/26	0/2/2/2
1	BGH	5	3899	1,84	-	2/13/43/44	0/3/3/3
1	MHG	5	4371	1	-	5/16/46/47	0/3/3/3
50	OMC	9	1710	50	-	0/9/27/28	0/2/2/2
1	5MC	5	3782	1	-	0/7/25/26	0/2/2/2
50	OMC	9	517	50	-	2/9/27/28	0/2/2/2
50	PSU	9	822	50	-	2/7/25/26	0/2/2/2
1	B9B	5	1574	1	-	3/11/29/30	0/3/3/3
50	B8N	9	1248	50,84	-	2/16/34/35	0/2/2/2
1	OMG	5	4870	1	-	4/9/27/28	0/3/3/3
50	OMC	9	1703	50	-	2/9/27/28	0/2/2/2
1	OMG	5	1522	1	-	0/9/27/28	0/3/3/3
1	B9B	5	2754	1,84	-	1/11/29/30	0/3/3/3
1	B8K	5	4690	1	-	0/11/41/42	0/3/3/3
1	5MC	5	4335	1	-	0/7/25/26	0/2/2/2
50	5MC	9	1374	50	-	0/7/25/26	0/2/2/2
1	A2M	5	398	1	-	2/9/27/28	0/3/3/3
50	A2M	9	1031	50	-	0/9/27/28	0/3/3/3
1	UR3	5	1866	1	-	1/7/25/26	0/2/2/2
1	PSU	5	2508	1	-	0/7/25/26	0/2/2/2
1	PSU	5	4403	1	-	2/7/25/26	0/2/2/2
1	PSU	5	4636	1	-	4/7/25/26	0/2/2/2
1	B9H	5	2786	1	-	3/12/47/48	0/2/2/2
1	OMG	5	4196	1	-	0/9/27/28	0/3/3/3
1	A2M	5	4571	1	-	0/9/27/28	0/3/3/3
50	UR3	9	1830	50	-	4/7/25/26	0/2/2/2
1	PSU	5	1683	1	-	0/7/25/26	0/2/2/2
50	MA6	9	1851	50	-	3/11/29/30	0/3/3/3
1	A2M	5	3825	1	-	0/9/27/28	0/3/3/3
1	OMU	5	4620	1	-	0/9/27/28	0/2/2/2
1	PSU	5	3729	1	-	2/7/25/26	0/2/2/2
50	PSU	9	119	50	-	2/7/25/26	0/2/2/2
50	PSU	9	612	50	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	4AC	9	1337	50	-	0/11/29/30	0/2/2/2
1	OMU	5	4306	1	-	1/9/27/28	0/2/2/2
1	7MG	5	1605	1	-	0/7/37/38	0/3/3/3
1	1MA	5	4415	1	-	2/7/25/26	0/3/3/3
1	UR3	5	4597	1	-	0/7/25/26	0/2/2/2
1	OMG	5	1883	1	-	0/9/27/28	0/3/3/3
1	PSU	5	4450	1,84	-	3/7/25/26	0/2/2/2
1	PSU	5	4531	1	-	0/7/25/26	0/2/2/2
50	5MU	9	814	50	-	0/7/25/26	0/2/2/2
41	MLZ	m	72	41	-	3/7/8/10	-
1	B8W	5	4129	1	-	2/9/27/28	0/3/3/3
1	UR3	5	4530	1	-	1/7/25/26	0/2/2/2
50	MA6	9	1850	50	-	1/11/29/30	0/3/3/3
50	6MZ	9	1832	50,84	-	2/9/27/28	0/3/3/3
1	M7A	5	4564	1	-	0/7/37/38	0/3/3/3
1	1MA	5	1322	1,84	-	0/7/25/26	0/3/3/3
1	A2M	5	3718	1	-	0/9/27/28	0/3/3/3
50	A2M	9	27	50,84	-	0/9/27/28	0/3/3/3
1	OMG	5	4623	1	-	0/9/27/28	0/3/3/3
1	OMG	5	4637	1	-	3/9/27/28	0/3/3/3
1	OMG	5	4494	1	-	2/9/27/28	0/3/3/3
50	E3C	9	568	50	-	4/9/44/45	0/2/2/2
1	A2M	5	1326	1	-	0/9/27/28	0/3/3/3
3	OMU	8	14	1,3	-	1/9/27/28	0/2/2/2
1	OMG	5	373	1	-	1/9/27/28	0/3/3/3
1	B8W	5	4185	1	-	4/9/27/28	0/3/3/3
1	A2M	5	2363	1,84	-	0/9/27/28	0/3/3/3
1	B8H	5	1860	1	-	2/7/25/26	0/2/2/2
1	PSU	5	3764	1	-	2/7/25/26	0/2/2/2
50	A2M	9	166	50	-	2/9/27/28	0/3/3/3
50	A2M	9	484	50	-	0/9/27/28	0/3/3/3
50	PSU	9	1081	50	-	3/7/25/26	0/2/2/2
1	I4U	5	4194	1	-	4/9/29/30	0/2/2/2
1	A2M	5	1524	1	-	1/9/27/28	0/3/3/3
50	PSU	9	1243	50,84	-	2/7/25/26	0/2/2/2
1	B9B	5	237	1	-	4/11/29/30	0/3/3/3
1	2MG	5	1517	1	-	0/9/27/28	0/3/3/3
1	OMC	5	2861	1	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	5	3909	1	-	1/9/27/28	0/2/2/2
50	PSU	9	823	50	-	0/7/25/26	0/2/2/2
50	A2M	9	159	50	-	3/9/27/28	0/3/3/3
1	E6G	5	4355	1	-	5/10/28/29	0/3/3/3
1	P7G	5	3880	1	-	3/10/40/41	0/3/3/3
1	A2M	5	3785	1	-	3/9/27/28	0/3/3/3
1	P4U	5	1348	1,84	-	4/10/29/30	0/2/2/2
1	5MC	5	4447	1	-	4/7/25/26	0/2/2/2
50	OMG	9	644	50	-	1/9/27/28	0/3/3/3
1	B8Q	5	1456	1	-	2/7/42/43	0/2/2/2
50	OMG	9	683	50	-	2/9/27/28	0/3/3/3
1	B8T	5	4671	1	-	0/7/27/28	0/2/2/2
1	E7G	5	1797	1	-	3/9/39/40	0/3/3/3
1	B8K	5	3897	1	-	3/11/41/42	0/3/3/3
1	PSU	5	4500	1	-	3/7/25/26	0/2/2/2
1	PSU	5	4442	1	-	0/7/25/26	0/2/2/2
48	DDE	v	715	48	-	14/20/21/23	0/1/1/1
1	5MU	5	4083	1	-	6/7/25/26	0/2/2/2
1	A2M	5	4523	1,84	-	2/9/27/28	0/3/3/3
1	6MZ	5	4220	1	-	0/9/27/28	0/3/3/3
1	A2M	5	1871	1,84	-	0/9/27/28	0/3/3/3
6	MLZ	C	333	6	-	2/7/8/10	-
1	OMG	5	1625	1,84	-	3/9/27/28	0/3/3/3
1	2MG	5	4872	1	-	1/9/27/28	0/3/3/3
1	A2M	5	3723	1	-	0/9/27/28	0/3/3/3
1	OMC	5	2422	1,84	-	0/9/27/28	0/2/2/2
1	B8W	5	4472	1	-	2/9/27/28	0/3/3/3
50	4AC	9	1842	50	-	0/11/29/30	0/2/2/2
50	OMC	9	174	50	-	0/9/27/28	0/2/2/2
50	OMG	9	509	50,84	-	0/9/27/28	0/3/3/3
1	OMG	5	4370	1	-	0/9/27/28	0/3/3/3
50	B8Q	9	1219	50	-	0/7/42/43	0/2/2/2
1	A2M	5	2401	1,84	-	2/9/27/28	0/3/3/3
1	OMG	5	2424	1	-	2/9/27/28	0/3/3/3
1	OMG	5	2050	1	-	0/9/27/28	0/3/3/3
1	OMC	5	2365	1	-	0/9/27/28	0/2/2/2
1	B8W	5	4529	1,84	-	2/9/27/28	0/3/3/3
50	M7A	9	1806	50	-	0/7/37/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	A2M	9	668	50,84	-	5/9/27/28	0/3/3/3
1	B8H	5	3762	1	-	0/7/25/26	0/2/2/2
1	OMC	5	3701	1,84	-	4/9/27/28	0/2/2/2
1	OMG	5	1316	1	-	0/9/27/28	0/3/3/3
1	PSU	5	3715	1	-	0/7/25/26	0/2/2/2
1	A2M	5	1534	1,84	-	1/9/27/28	0/3/3/3
1	B8W	5	2380	1	-	5/9/27/28	0/3/3/3
1	B8H	5	4296	1	-	1/7/25/26	0/2/2/2
50	A2M	9	1678	50	-	0/9/27/28	0/3/3/3
1	OMG	5	2364	1	-	2/9/27/28	0/3/3/3
1	OMC	5	4536	1	-	0/9/27/28	0/2/2/2
1	OMC	5	2804	1	-	0/9/27/28	0/2/2/2
1	2MG	5	729	1	-	2/9/27/28	0/3/3/3
1	PSU	5	4293	1	-	0/7/25/26	0/2/2/2
1	B8T	5	4483	1	-	2/7/27/28	0/2/2/2
1	OMG	5	2773	1	-	0/9/27/28	0/3/3/3
1	OMC	5	3869	1	-	0/9/27/28	0/2/2/2
1	E7G	5	2297	1	-	1/9/39/40	0/3/3/3
1	A2M	5	3867	1	-	4/9/27/28	0/3/3/3
1	PSU	5	1677	1	-	2/7/25/26	0/2/2/2
1	I4U	5	1659	1	-	2/9/29/30	0/2/2/2
50	OMU	9	121	50	-	2/9/27/28	0/2/2/2
1	P7G	5	1909	1	-	3/10/40/41	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)
1	5	4296	B8H	C6-C5	-16.02	1.12	1.35
1	5	3762	B8H	C6-C5	-15.66	1.12	1.35
1	5	1860	B8H	C6-C5	-15.66	1.12	1.35
1	5	4296	B8H	C4-N3	-14.97	1.10	1.38
1	5	3762	B8H	C4-N3	-14.81	1.11	1.38

The worst 5 of 1007 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	4529	B8W	N2-C2-N3	18.96	145.65	117.22
1	5	4129	B8W	N2-C2-N3	18.81	145.43	117.22
1	5	4185	B8W	N2-C2-N3	18.58	145.08	117.22
1	5	2380	B8W	N2-C2-N3	18.53	145.01	117.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	5	4472	B8W	N2-C2-N3	17.71	143.78	117.22

There are no chirality outliers.

5 of 213 torsion outliers are listed below:

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

There are no ring outliers.

51 monomers are involved in 82 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	5	3887	OMC	1	0
50	9	116	OMU	1	0
1	5	2522	7MG	1	0
1	5	3899	BGH	1	0
1	5	1574	B9B	2	0
1	5	2754	B9B	1	0
1	5	398	A2M	2	0
50	9	1031	A2M	2	0
1	5	4196	OMG	1	0
1	5	4571	A2M	1	0
50	9	1830	UR3	1	0
50	9	1851	MA6	1	0
1	5	4620	OMU	1	0
50	9	1337	4AC	2	0
1	5	4306	OMU	1	0
1	5	1605	7MG	1	0
1	5	1883	OMG	1	0
50	9	814	5MU	1	0
41	m	72	MLZ	2	0
50	9	1832	6MZ	1	0
1	5	3718	A2M	1	0
50	9	27	A2M	2	0
1	5	4623	OMG	1	0
1	5	1326	A2M	2	0
3	8	14	OMU	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	5	373	OMG	1	0
1	5	2363	A2M	2	0
1	5	1860	B8H	6	0
50	9	166	A2M	1	0
1	5	237	B9B	1	0
1	5	1517	2MG	1	0
50	9	159	A2M	2	0
50	9	683	OMG	1	0
1	5	1797	E7G	1	0
1	5	3897	B8K	1	0
1	5	4500	PSU	1	0
48	v	715	DDE	2	0
1	5	4523	A2M	2	0
1	5	1871	A2M	1	0
6	C	333	MLZ	1	0
1	5	1625	OMG	1	0
1	5	4872	2MG	1	0
1	5	3723	A2M	4	0
1	5	2422	OMC	1	0
50	9	509	OMG	1	0
1	5	3762	B8H	6	0
1	5	1316	OMG	1	0
1	5	2380	B8W	1	0
1	5	4296	B8H	6	0
50	9	1678	A2M	3	0
1	5	729	2MG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
86	GDP	v	900	-	29,30,30	1.16	4 (13%)	45,47,47	1.78	7 (15%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
86	GDP	v	900	-	-	0/16/32/32	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
86	v	900	GDP	C6-N1	-2.62	1.34	1.38
86	v	900	GDP	C5-C4	2.56	1.45	1.38
86	v	900	GDP	C4-N9	-2.43	1.31	1.38
86	v	900	GDP	C5-N7	-2.26	1.34	1.39

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
86	v	900	GDP	C5-C4-N3	-5.51	119.62	128.39
86	v	900	GDP	C2-N3-C4	4.96	120.85	112.30
86	v	900	GDP	N9-C4-N3	3.98	133.91	125.95
86	v	900	GDP	C6-C5-N7	3.68	136.99	130.29
86	v	900	GDP	C4-C5-N7	-2.64	106.49	110.67

There are no chirality outliers.

There are no torsion outliers.

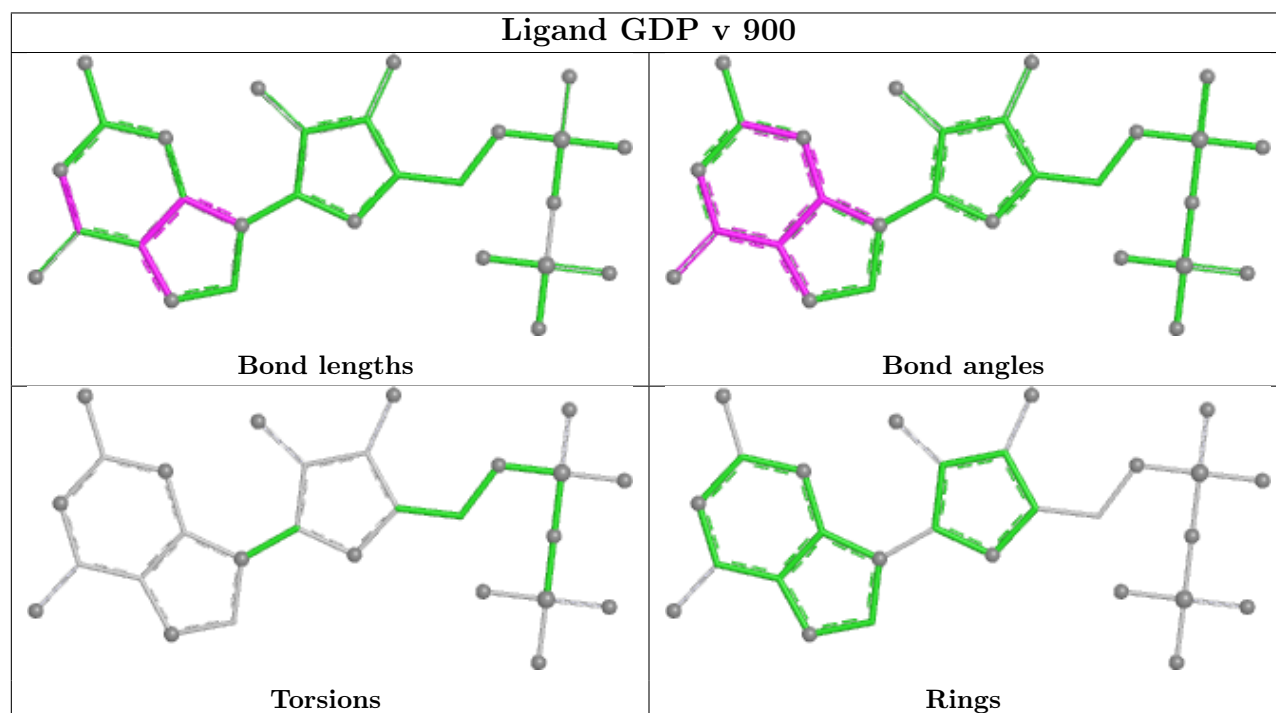
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
86	v	900	GDP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

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

The worst 5 of 70 chain breaks are listed below:

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

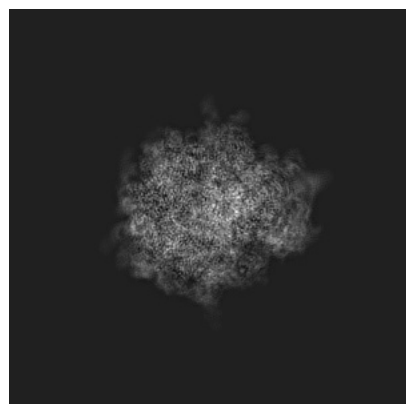
6 Map visualisation [i](#)

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

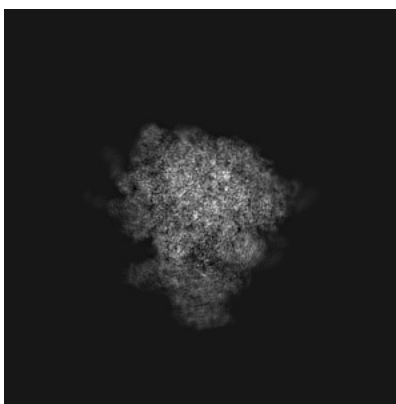
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

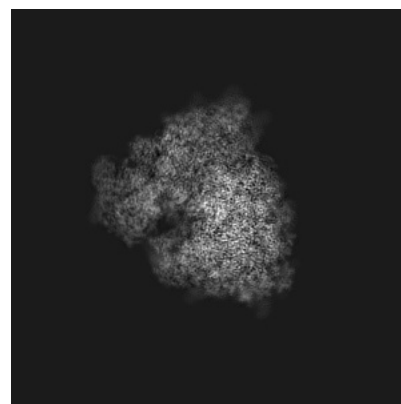
6.1.1 Primary map



X

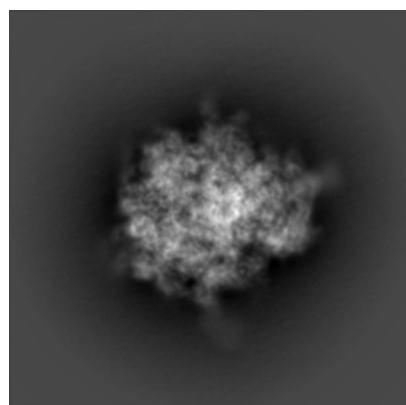


Y

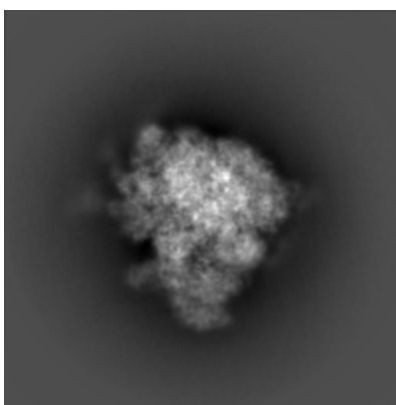


Z

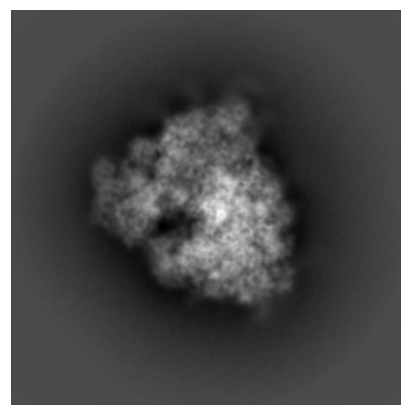
6.1.2 Raw map



X



Y

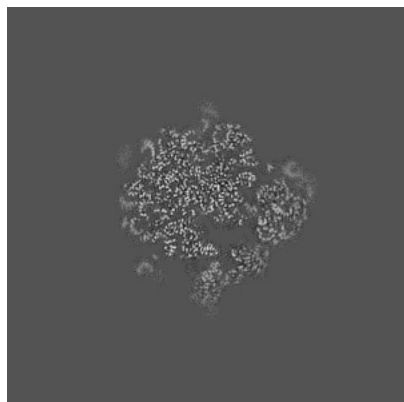


Z

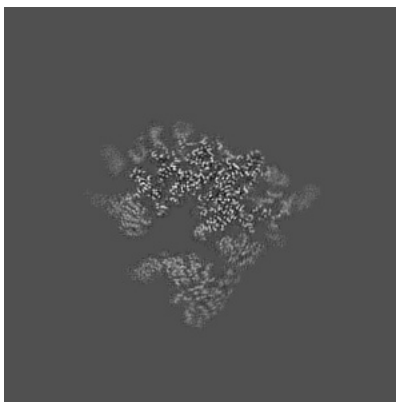
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

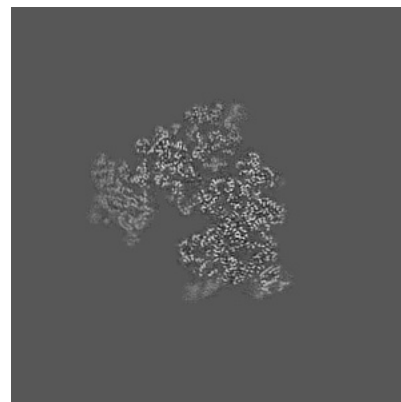
6.2.1 Primary map



X Index: 200

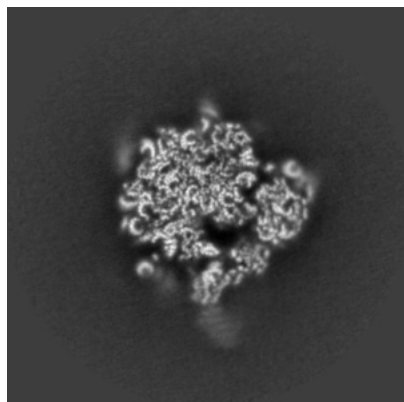


Y Index: 200

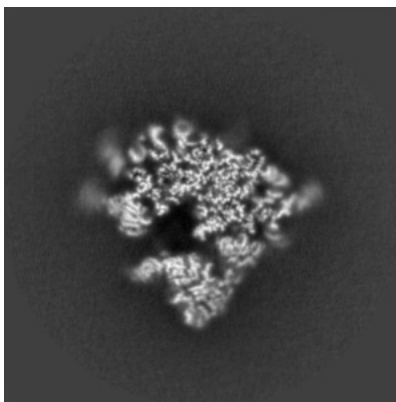


Z Index: 200

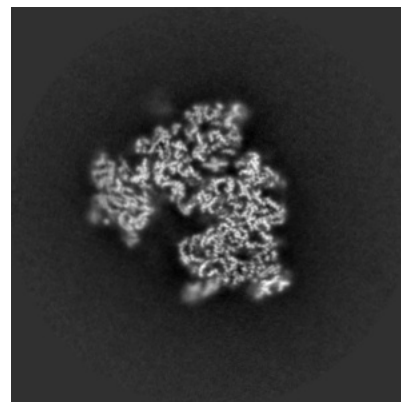
6.2.2 Raw map



X Index: 200



Y Index: 200

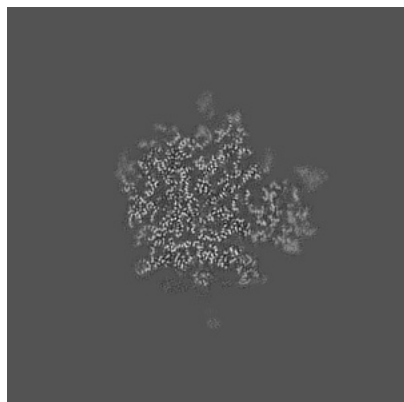


Z Index: 200

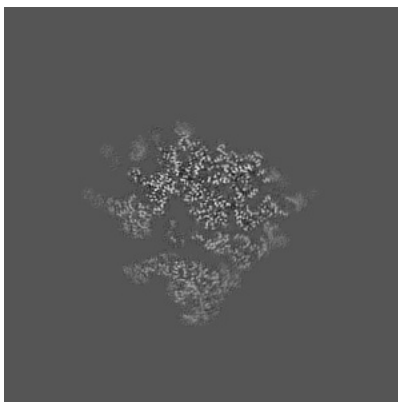
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

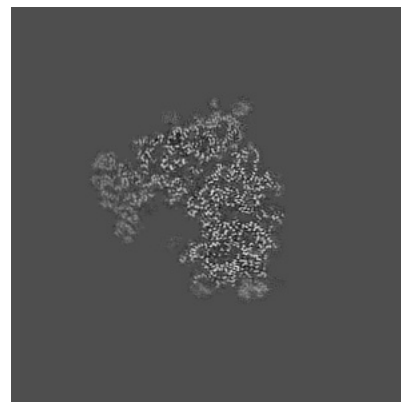
6.3.1 Primary map



X Index: 213

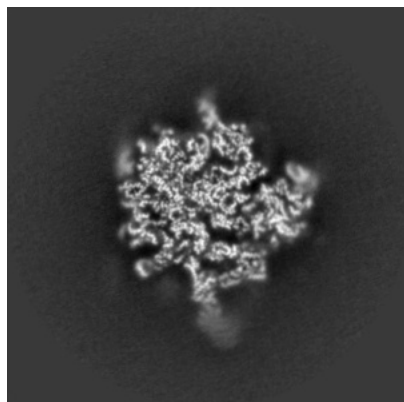


Y Index: 206

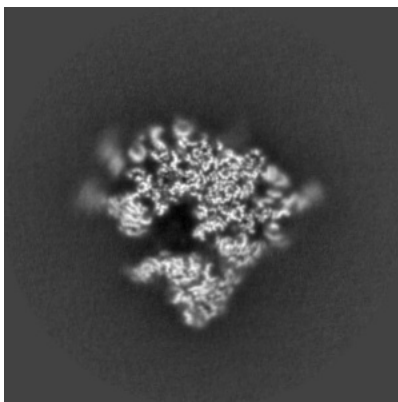


Z Index: 210

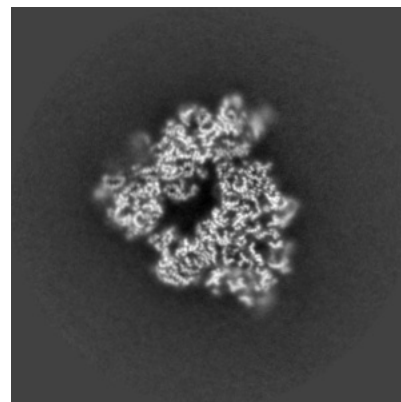
6.3.2 Raw map



X Index: 206



Y Index: 201

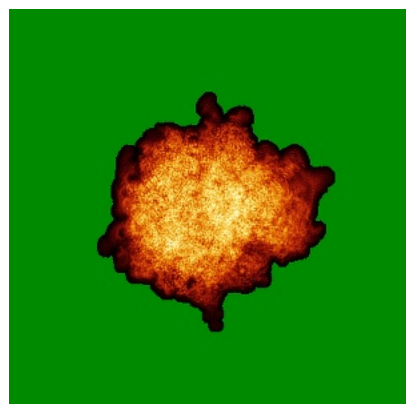


Z Index: 176

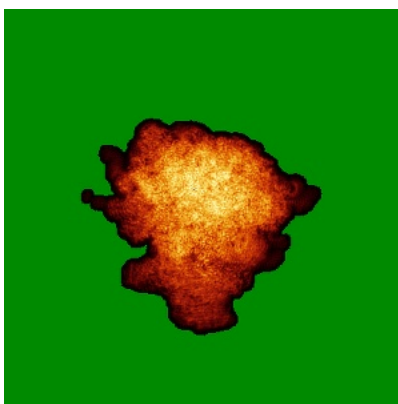
The images above show the largest variance slices of the map in three orthogonal directions.

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

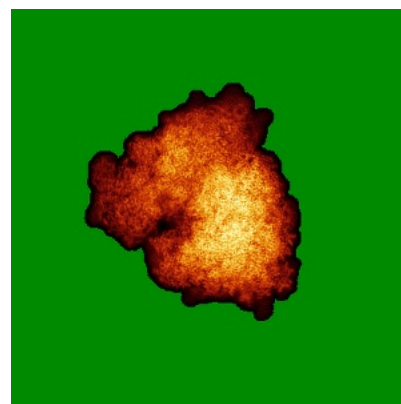
6.4.1 Primary map



X

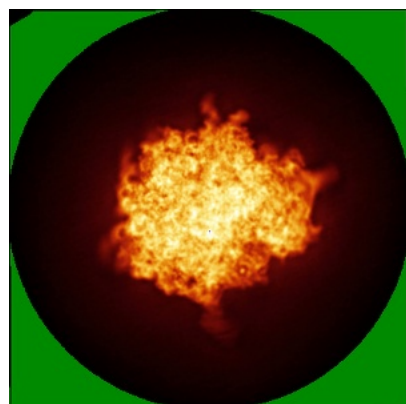


Y

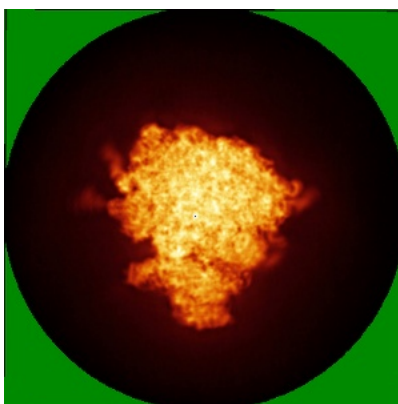


Z

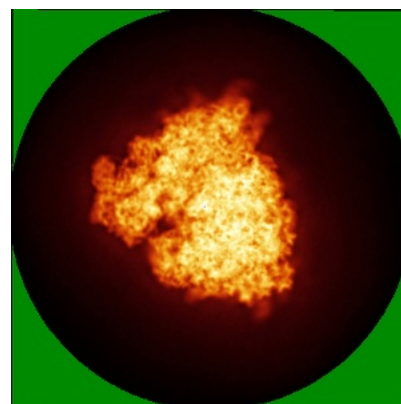
6.4.2 Raw map



X



Y

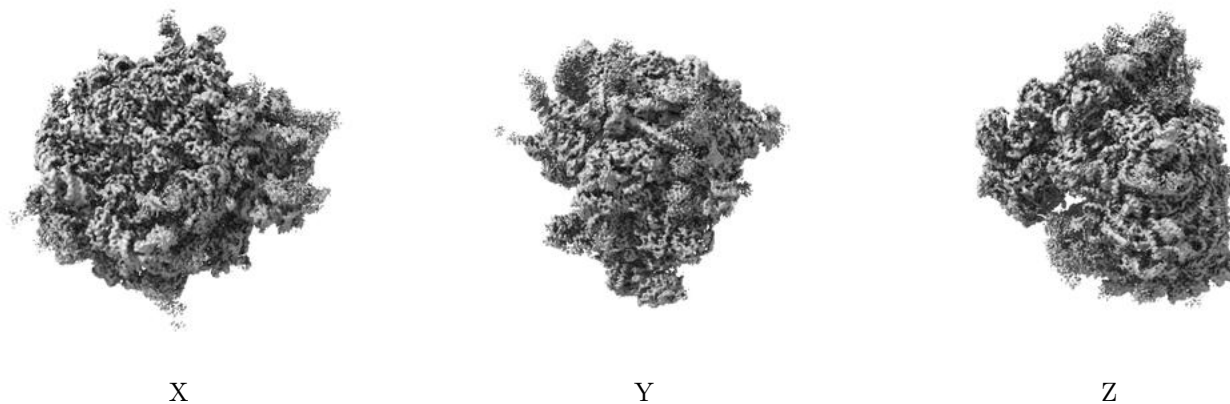


Z

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

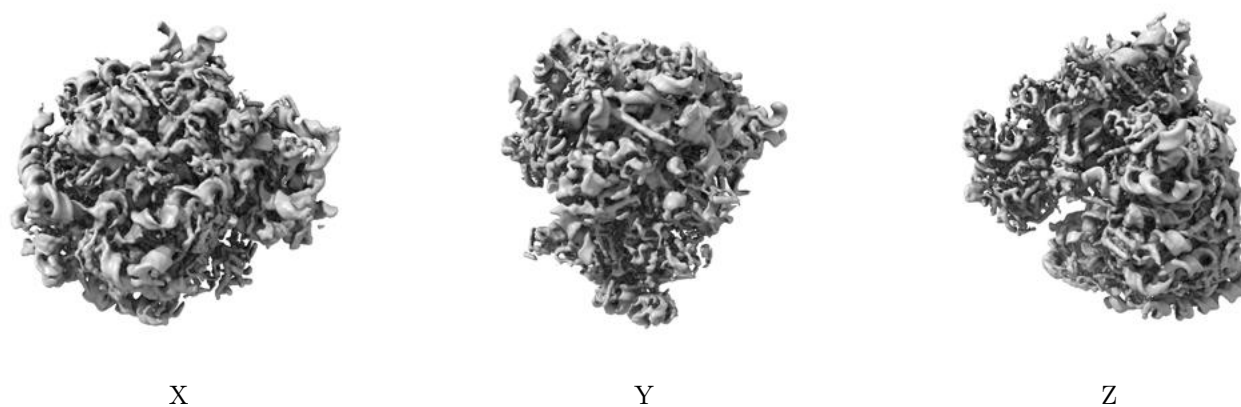
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

6.5.2 Raw map



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

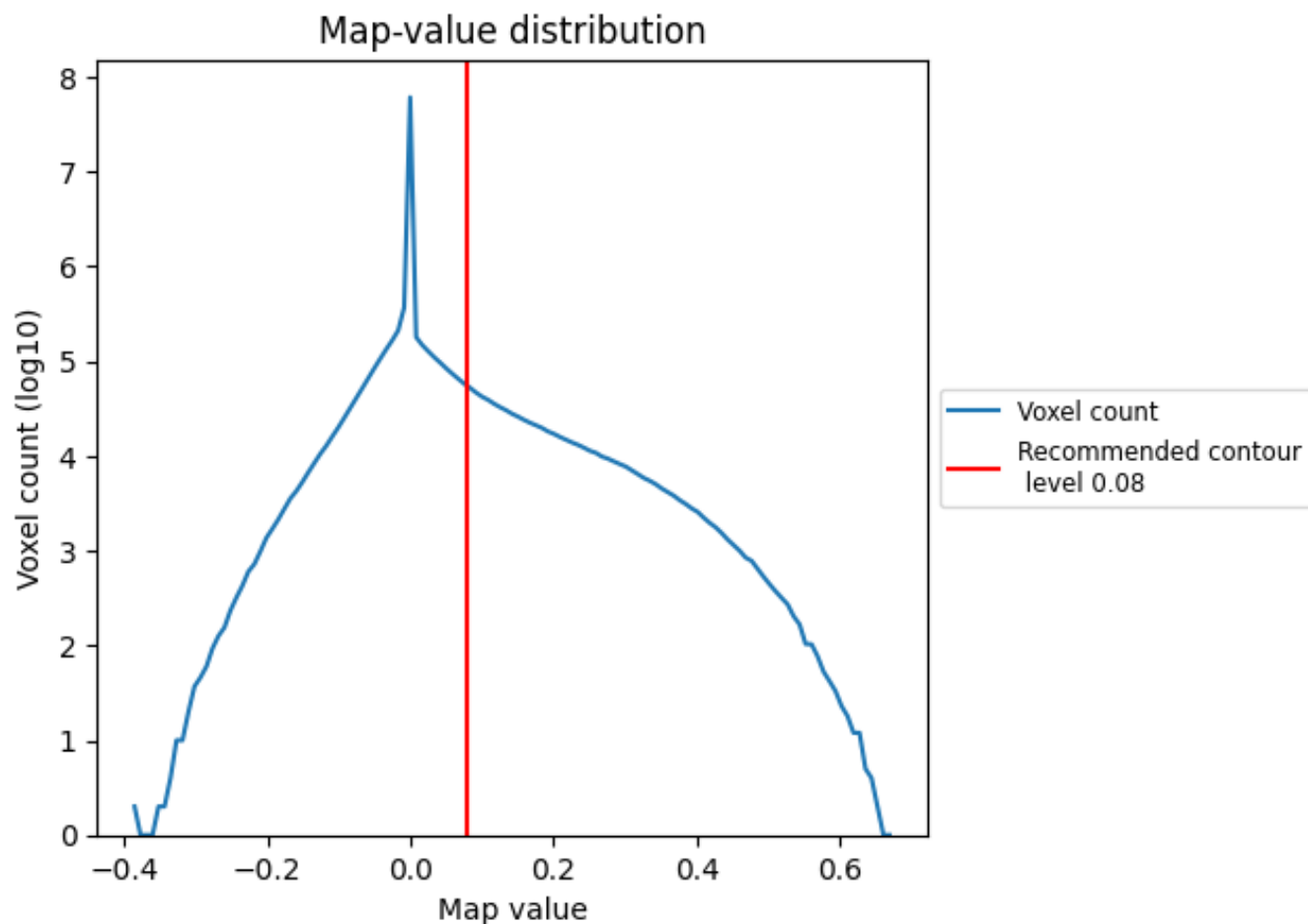
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

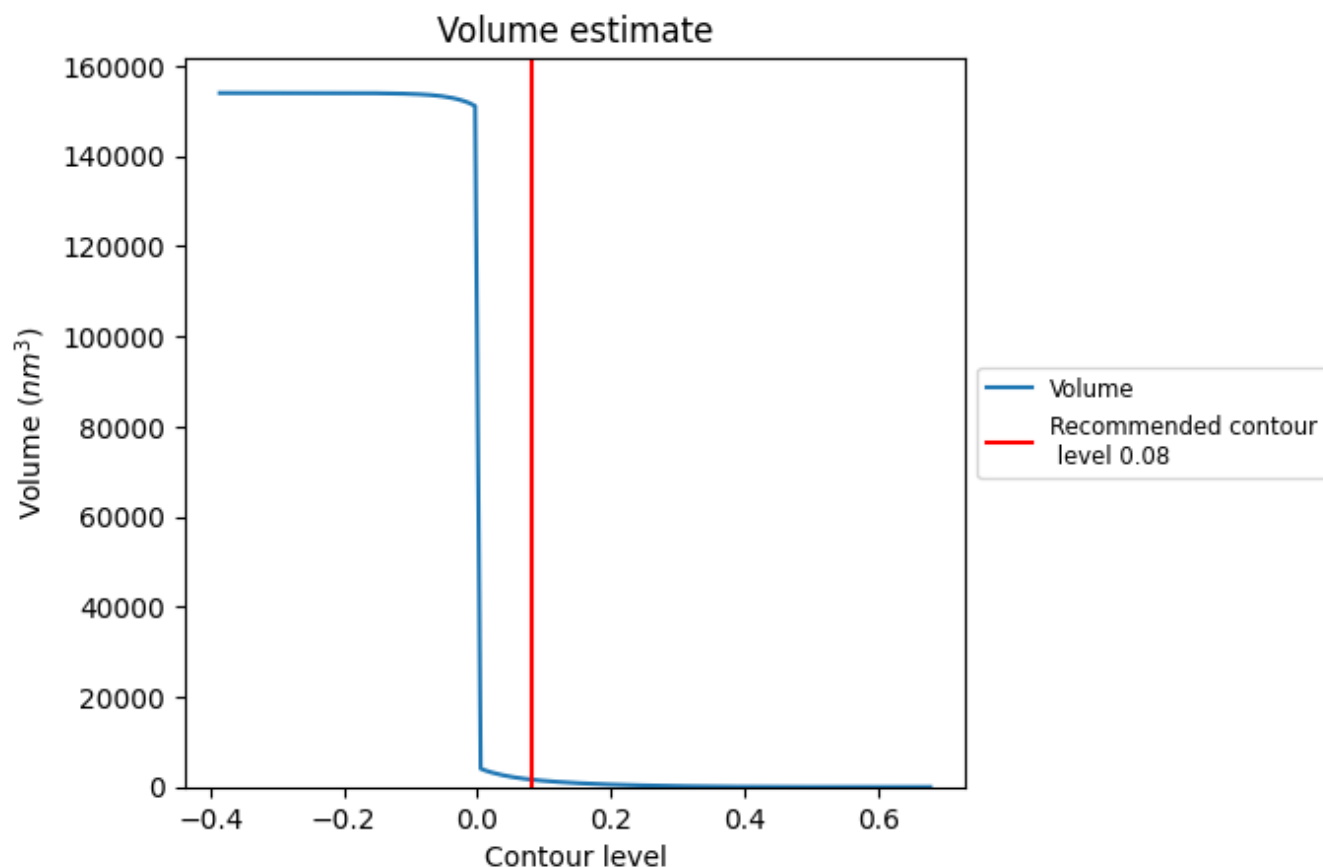
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

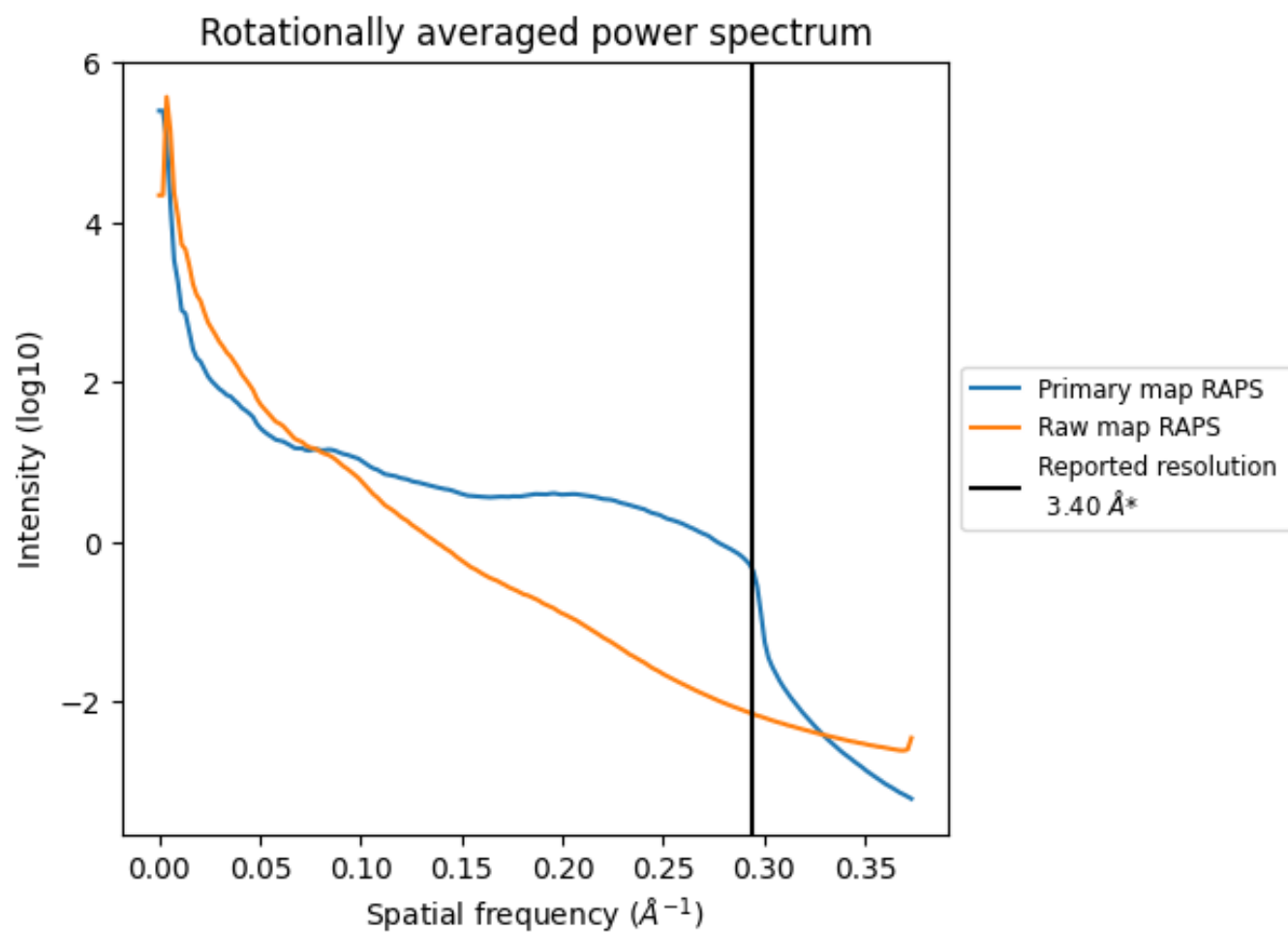
7.2 Volume estimate [i](#)



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

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

7.3 Rotationally averaged power spectrum ⓘ

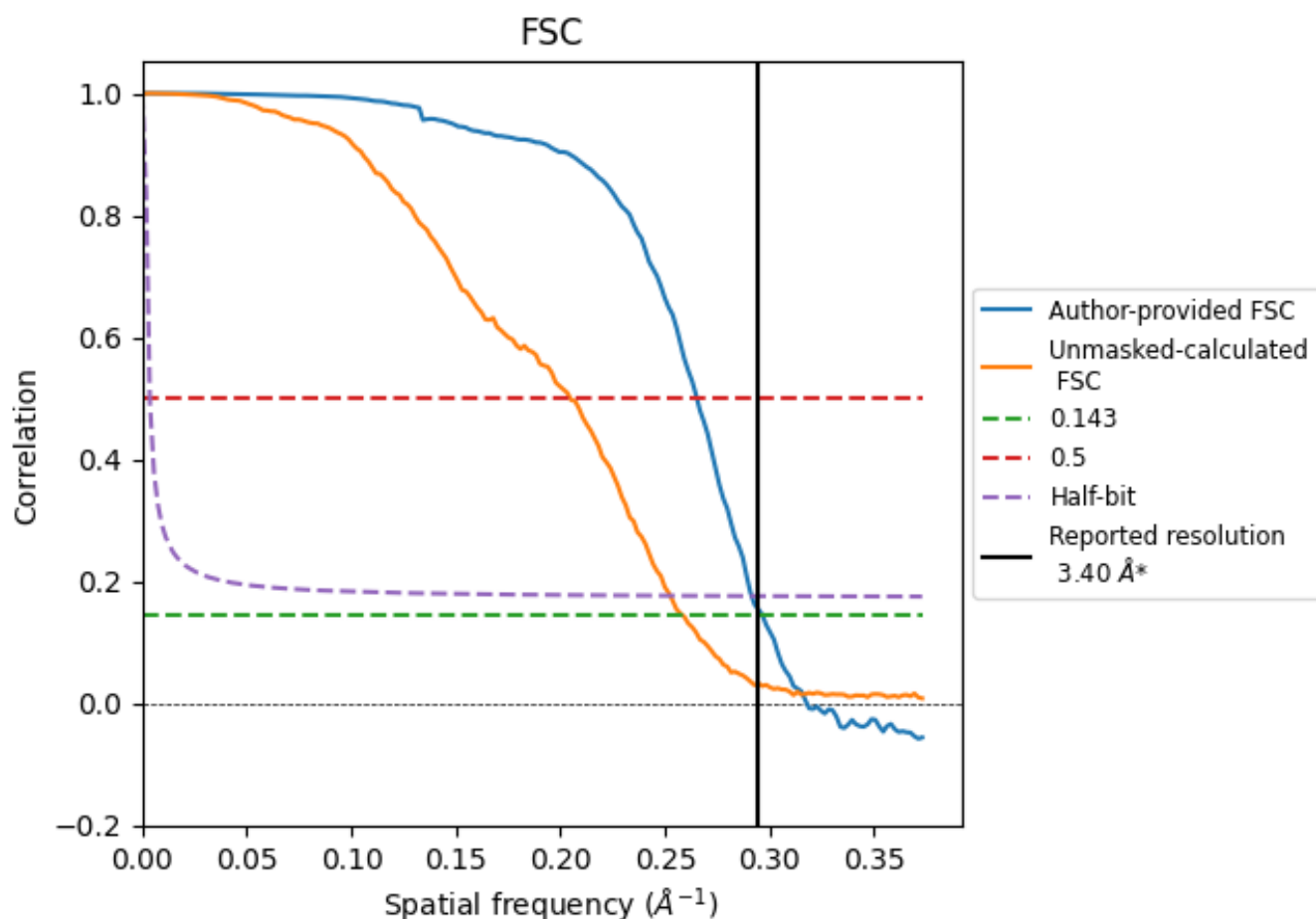


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

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 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

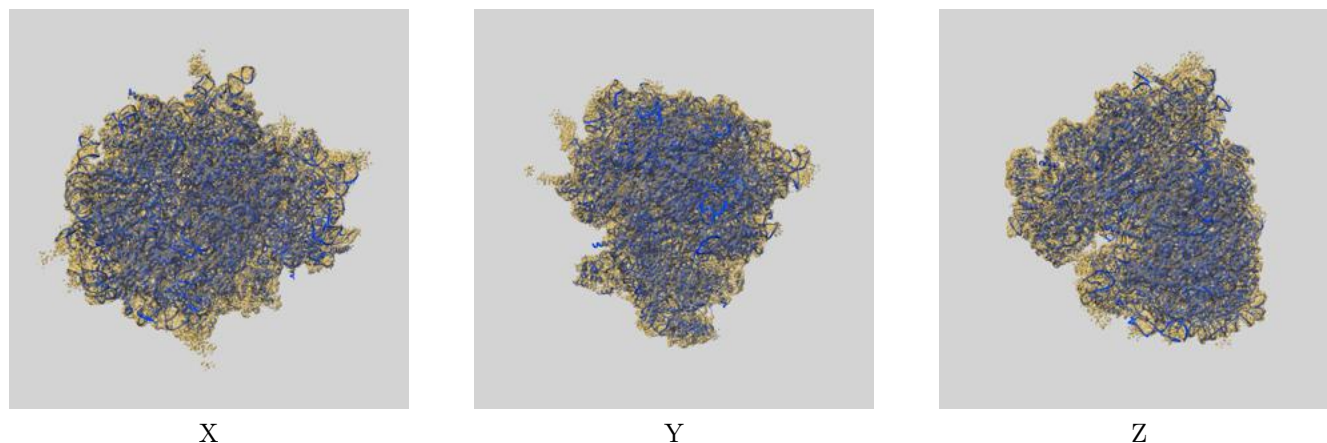
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.37	3.77	3.43
Unmasked-calculated*	3.86	4.89	3.96

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.86 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

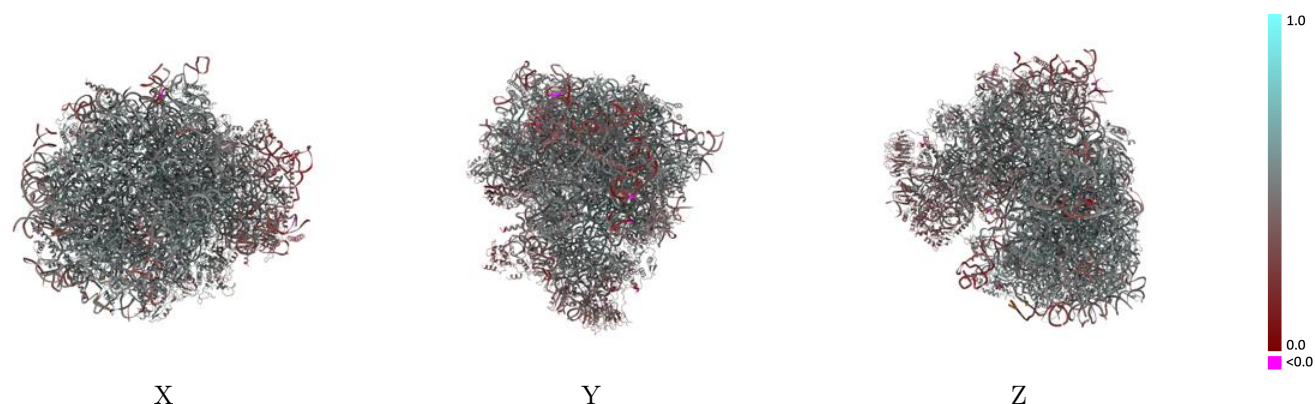
This section contains information regarding the fit between EMDB map EMD-9242 and PDB model 6MTE. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



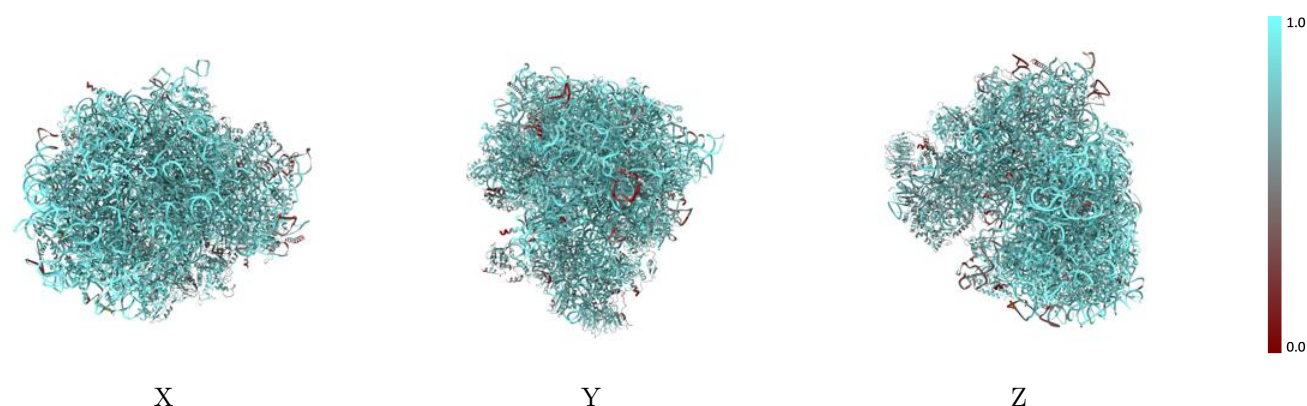
The images above show the 3D surface view of the map at the recommended contour level 0.08 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



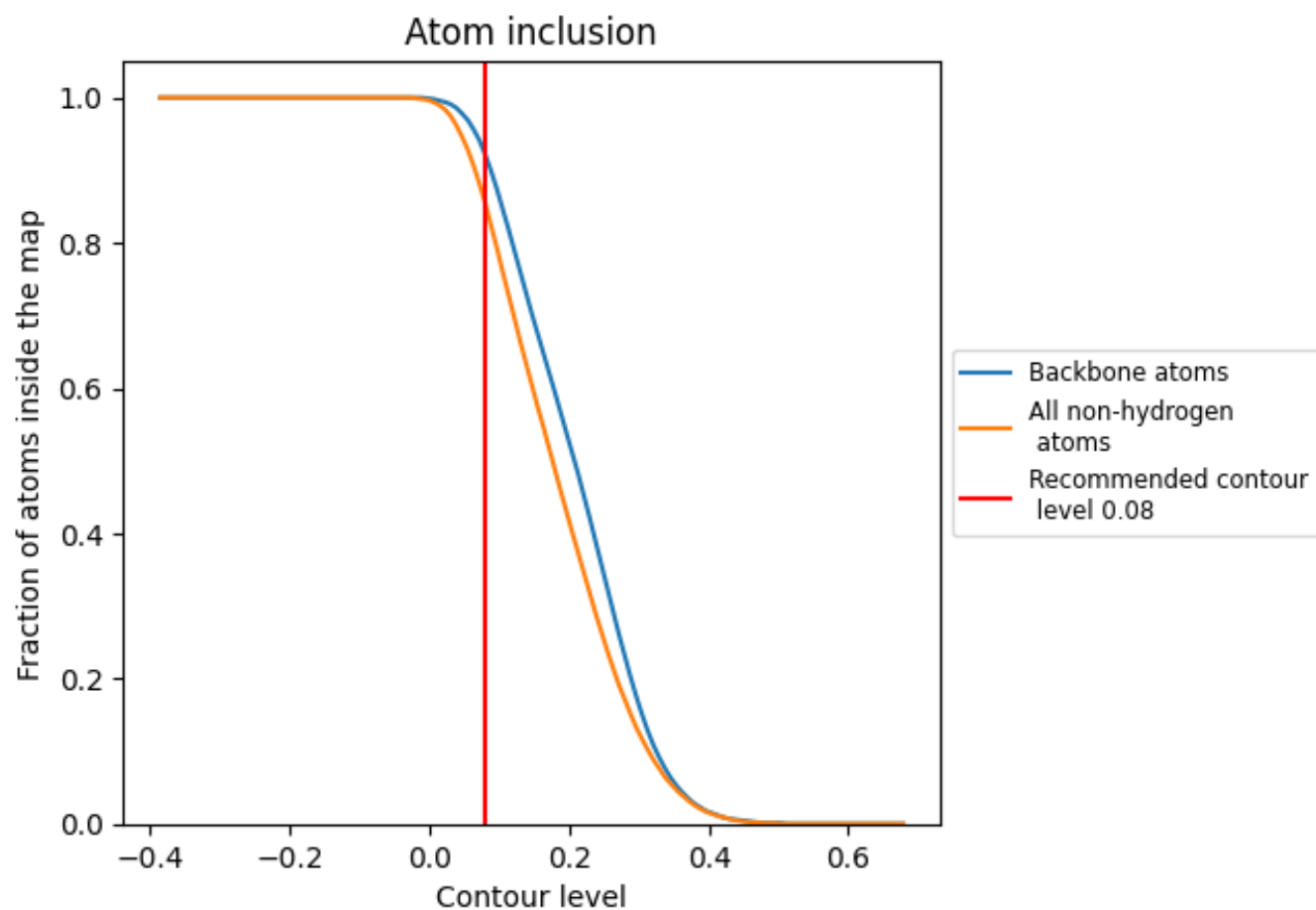
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.08).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 85% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.08) and Q-score for the entire model and for each chain.

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



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

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