



wwPDB EM Validation Summary Report ⓘ

Aug 3, 2026 – 12:54 pm BST

PDB ID : 9SRB / pdb_00009srb
EMDB ID : EMD-55136
Title : Cryo-EM structure of P. abyssi 70S ribosome in complex with hibernation factor HibA and SBDS
Authors : Madru, C.M.; Bourgeois, G.B.; Mechulam, Y.M.; Schmitt, E.S.
Deposited on : 2025-09-24
Resolution : 2.30 Å(reported)

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

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

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:

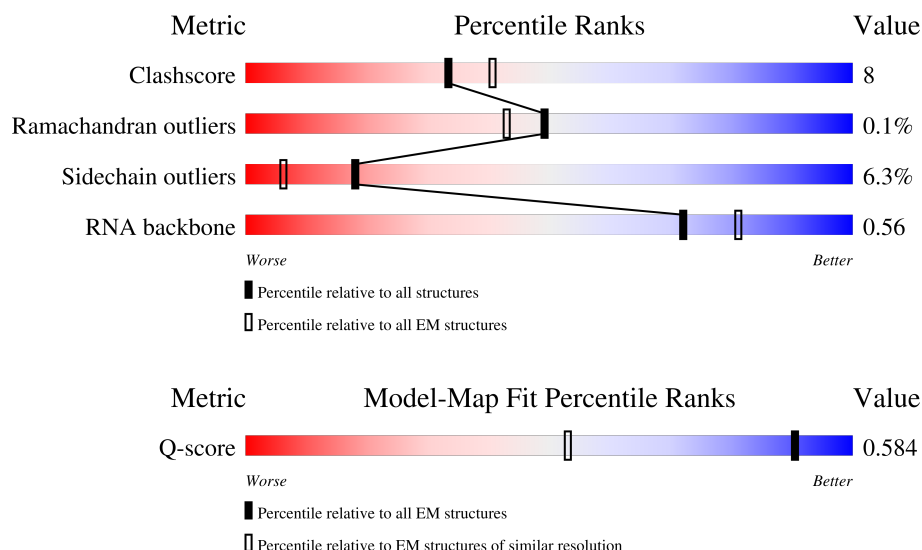
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

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 2.30 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	4254 (1.80 - 2.80)

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	1	3018	
2	2	1512	
3	3	128	

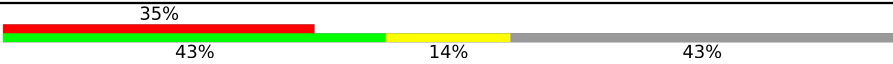
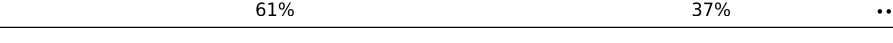
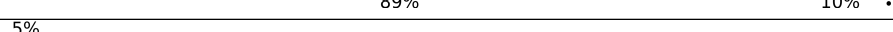
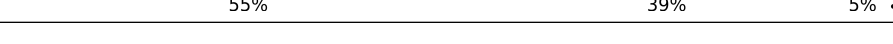
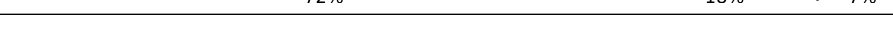
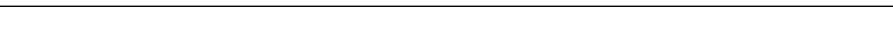
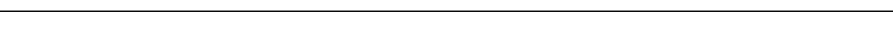
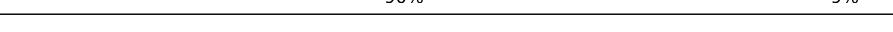
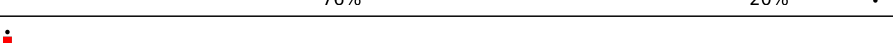
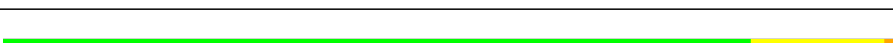
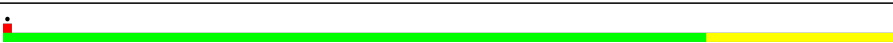
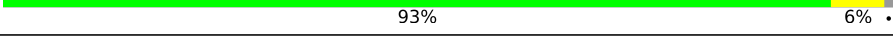
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	A	236	
5	H	392	
6	AA	199	
7	AB	202	
8	AC	63	
9	AD	180	
10	AE	243	
11	AF	236	
12	AG	125	
13	AH	215	
14	AI	130	
15	AJ	127	
16	AK	135	
17	AL	102	
18	AM	137	
19	AN	147	
20	AP	56	
21	AQ	158	
22	AR	113	
23	AS	67	
24	AU	150	
25	AV	99	
25	B6	99	
26	AW	65	
27	AX	71	

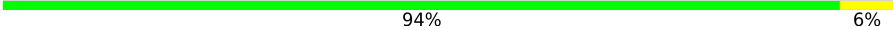
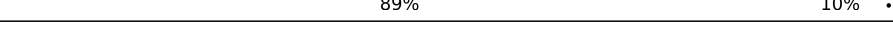
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
28	AY	51	
29	AZ	210	
30	A0	37	
31	A3	123	
31	B4	123	
31	BG	123	
32	AT	132	
33	AO	148	
34	BB	239	
35	BY	155	
36	BO	203	
37	BC	361	
38	B5	82	
38	BK	82	
39	BL	147	
40	Bf	51	
41	BU	121	
42	Bb	130	
43	Be	62	
44	BE	188	
45	Ba	94	
46	BT	86	
47	BW	68	
48	Bi	83	
49	BI	142	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
50	BR	97	 86% 12% ..
51	BQ	151	 83% 15% ..
52	BV	67	 85% 9% 6%
53	Bj	94	 94% 6%
54	BD	255	 86% 13% .
55	BF	184	 81% 18% ..
56	BZ	99	 77% 21% ..
57	BP	120	 89% 11%
58	BM	194	 89% 10% .
59	BS	155	 87% 12% .
60	Bd	91	 90% 10%
61	BN	181	 81% 17% .
62	Bg	51	 78% 16% 6%
63	Bc	87	 89% 10% .
64	BJ	141	 86% 13% .
65	Bl	77	 84% 16%
66	Bk	65	 85% 12% .
67	BA	219	 48% 58% 39% ..

2 Entry composition

There are 69 unique types of molecules in this entry. The entry contains 173872 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 rRNA 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	3018	Total	C	N	O	P	0	0
			65181	29055	12094	21014	3018		

- Molecule 2 is a RNA chain called rRNA 16S.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1496	Total	C	N	O	P	0	0
			32291	14408	5957	10430	1496		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	126	Total	C	N	O	P	0	0
			2703	1203	498	876	126		

- Molecule 4 is a protein called Ribosome maturation protein SDO1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	235	Total	C	N	O	S	0	0
			1900	1216	334	346	4		

- Molecule 5 is a protein called Dehydrogenase.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	386	Total	C	N	O	S	0	0
			3074	1962	535	567	10		

- Molecule 6 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AA	188	Total	C	N	O	S	0	0
			1531	993	268	266	4		

- Molecule 7 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AB	196	Total	C	N	O	S	0	0
			1571	1017	269	281	4		

- Molecule 8 is a protein called Zn-ribbon RNA-binding protein involved in translation.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AC	57	Total	C	N	O	S	0	0
			449	285	80	76	8		

- Molecule 9 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AD	173	Total	C	N	O	S	0	0
			1452	913	280	255	4		

- Molecule 10 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AE	242	Total	C	N	O	S	0	0
			1983	1281	358	339	5		

- Molecule 11 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AF	229	Total	C	N	O	S	0	0
			1808	1147	334	320	7		

- Molecule 12 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AG	124	Total	C	N	O	S	0	0
			977	621	178	176	2		

- Molecule 13 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AH	214	Total	C	N	O	S	0	0
			1725	1095	323	300	7		

- Molecule 14 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AI	129	Total	C	N	O	S	0	0
			1034	668	184	180	2		

- Molecule 15 is a protein called 30S ribosomal protein S8e.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AJ	125	Total	C	N	O	S	0	0
			986	612	205	169			

- Molecule 16 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AK	135	Total	C	N	O	S	0	0
			1073	673	207	189	4		

- Molecule 17 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AL	100	Total	C	N	O	S	0	0
			809	502	157	147	3		

- Molecule 18 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AM	127	Total	C	N	O	S	0	0
			955	591	190	172	2		

- Molecule 19 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AN	146	Total	C	N	O	S	0	0
			1148	727	224	194	3		

- Molecule 20 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AP	55	Total	C	N	O	S	0	0
			455	288	95	67	5		

- Molecule 21 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AQ	157	Total	C	N	O	S	0	0
			1305	833	249	219	4		

- Molecule 22 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AR	108	Total	C	N	O	S	0	0
			893	567	173	150	3		

- Molecule 23 is a protein called 30S ribosomal protein S17e.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AS	64	Total	C	N	O	S	0	0
			541	343	104	93	1		

- Molecule 24 is a protein called 30S ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AU	149	Total	C	N	O		0	0
			1223	790	221	212			

- Molecule 25 is a protein called 30S ribosomal protein S24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AV	96	Total	C	N	O	S	0	0
			808	528	129	148	3		
25	B6	94	Total	C	N	O	S	0	0
			790	516	125	146	3		

- Molecule 26 is a protein called 30S ribosomal protein S27e.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AW	61	Total	C	N	O	S	0	0
			470	294	91	80	5		

- Molecule 27 is a protein called 30S ribosomal protein S28e.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	AX	65	Total	C	N	O	0	0
			516	316	103	97		

- Molecule 28 is a protein called 30S ribosomal protein S27ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AY	29	Total	C	N	O	S	0	0
			227	141	44	37	5		

- Molecule 29 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AZ	196	Total	C	N	O	S	0	0
			1541	983	284	270	4		

- Molecule 30 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	A0	36	Total	C	N	O	S	0	0
			343	218	84	39	2		

- Molecule 31 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A3	122	Total	C	N	O	S	0	0
			933	594	156	180	3		
31	BG	122	Total	C	N	O	S	0	0
			932	594	156	179	3		
31	B4	122	Total	C	N	O	S	0	0
			933	594	156	180	3		

- Molecule 32 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AT	130	Total	C	N	O	S	0	0
			1057	675	201	174	7		

- Molecule 33 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AO	138	Total	C	N	O	S	0	0
			1116	700	221	190	5		

- Molecule 34 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BB	238	Total	C	N	O	S	0	0
			1838	1163	354	317	4		

- Molecule 35 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BY	154	Total	C	N	O	S	0	0
			1235	783	234	212	6		

- Molecule 36 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BO	198	Total	C	N	O	S	0	0
			1607	1024	302	279	2		

- Molecule 37 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BC	360	Total	C	N	O	S	0	0
			2870	1843	522	494	11		

- Molecule 38 is a protein called Large ribosomal subunit protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	B5	81	Total	C	N	O	S	0	0
			614	388	116	108	2		
38	BK	80	Total	C	N	O	S	0	0
			607	383	115	107	2		

- Molecule 39 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BL	147	Total	C	N	O	S	0	0
			1149	720	224	202	3		

- Molecule 40 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Bf	50	Total	C	N	O	S	0	0
			435	275	99	60	1		

- Molecule 41 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BU	121	Total	C	N	O	S	0	0
			1011	638	198	170	5		

- Molecule 42 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Bb	129	Total	C	N	O	S	0	0
			1095	702	221	171	1		

- Molecule 43 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Be	61	Total	C	N	O	S	0	0
			503	312	112	75	4		

- Molecule 44 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	BE	185	Total	C	N	O	S	0	0
			1485	934	277	265	9		

- Molecule 45 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ba	94	Total	C	N	O	S	0	0
			778	503	147	127	1		

- Molecule 46 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BT	86	Total	C	N	O	S	0	0
			696	451	118	126	1		

- Molecule 47 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BW	68	Total	C	N	O	S	0	0
			565	349	111	99	6		

- Molecule 48 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Bi	82	Total	C	N	O	S	0	0
			620	389	129	97	5		

- Molecule 49 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BI	142	Total	C	N	O	S	0	0
			1148	734	217	194	3		

- Molecule 50 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BR	96	Total	C	N	O	S	0	0
			797	507	164	125	1		

- Molecule 51 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BQ	150	Total	C	N	O	S	0	0
			1265	795	261	203	6		

- Molecule 52 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	BV	63	Total	C	N	O	S	0	0
			532	339	103	84	6		

- Molecule 53 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Bj	94	Total	C	N	O	S	0	0
			789	502	163	119	5		

- Molecule 54 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BD	255	Total	C	N	O	S	0	0
			2026	1290	388	343	5		

- Molecule 55 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BF	183	Total	C	N	O	S	0	0
			1456	943	251	261	1		

- Molecule 56 is a protein called Large ribosomal subunit protein eL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
56	BZ	98	Total	C	N	O		
			749	486	122	141	0	0

- Molecule 57 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
57	BP	120	Total	C	N	O	S	
			971	610	188	170	3	0

- Molecule 58 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms				AltConf	Trace
58	BM	193	Total	C	N	O	S	
			1588	1014	318	251	5	0

- Molecule 59 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
59	BS	154	Total	C	N	O	S	
			1247	786	246	211	4	0

- Molecule 60 is a protein called Large ribosomal subunit protein eL34.

Mol	Chain	Residues	Atoms				AltConf	Trace
60	Bd	91	Total	C	N	O	S	
			759	477	163	109	10	0

- Molecule 61 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms				AltConf	Trace
61	BN	178	Total	C	N	O	S	
			1452	920	281	246	5	0

- Molecule 62 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms				AltConf	Trace
62	Bg	48	Total	C	N	O	S	
			387	243	80	60	4	0

- Molecule 63 is a protein called Large ribosomal subunit protein eL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Bc	87	Total	C	N	O	S	0	0
			684	435	132	115	2		

- Molecule 64 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BJ	140	Total	C	N	O	S	0	0
			1066	664	214	185	3		

- Molecule 65 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Bl	77	Total	C	N	O	S	0	0
			659	425	120	113	1		

- Molecule 66 is a protein called C2H2-type domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Bk	63	Total	C	N	O	S	0	0
			528	339	108	78	3		

- Molecule 67 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BA	215	Total	C	N	O	S	0	0
			1675	1065	301	304	5		

- Molecule 68 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
68	1	164	Total	Mg	0
			164	164	
68	2	65	Total	Mg	0
			65	65	
68	3	1	Total	Mg	0
			1	1	
68	AD	1	Total	Mg	0
			1	1	
68	AK	1	Total	Mg	0
			1	1	
68	AN	1	Total	Mg	0
			1	1	

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
68	BB	2	Total 2	Mg 2	0
68	Bb	1	Total 1	Mg 1	0
68	BD	1	Total 1	Mg 1	0
68	BM	1	Total 1	Mg 1	0
68	BS	1	Total 1	Mg 1	0
68	Bc	1	Total 1	Mg 1	0

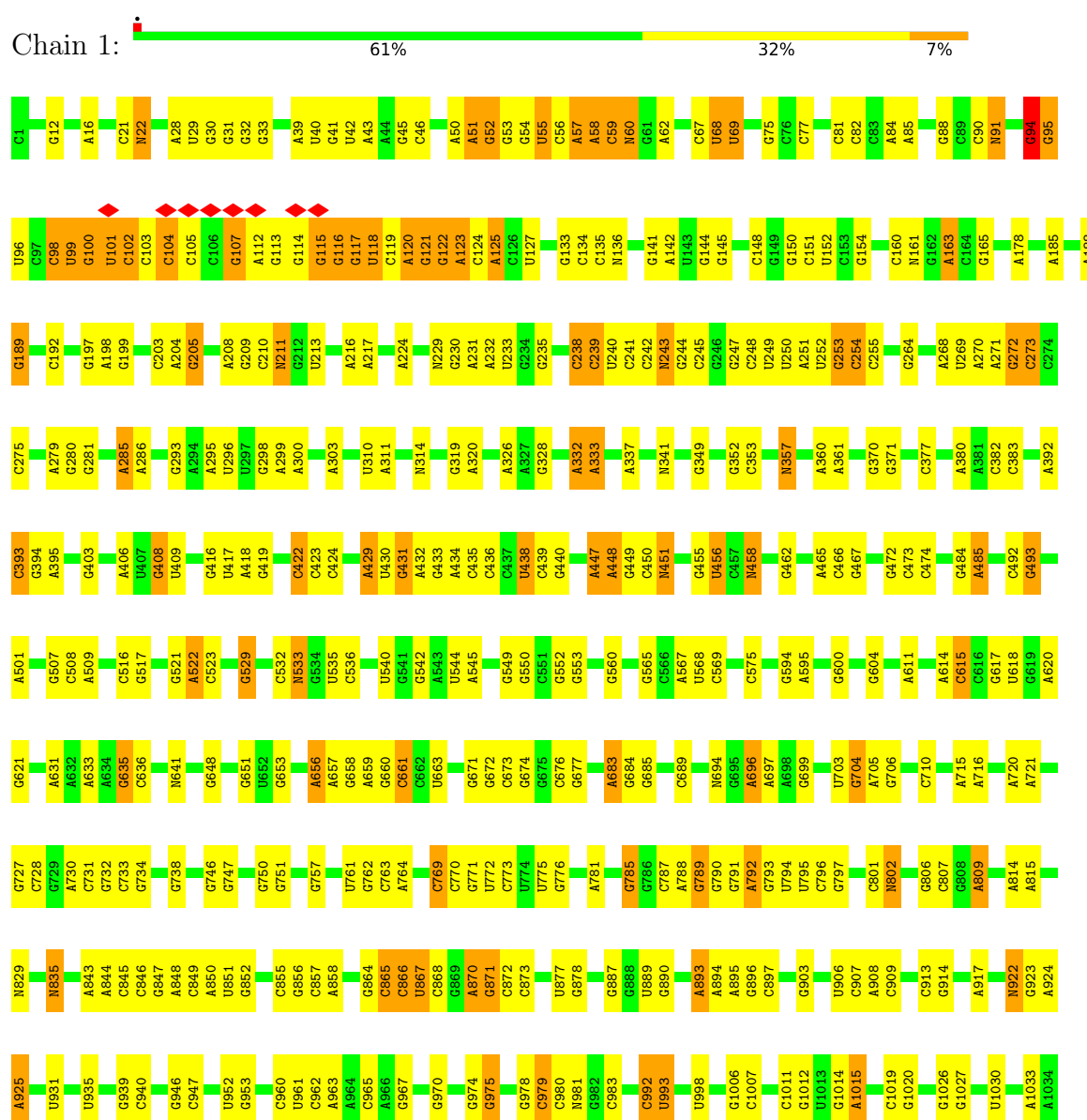
- Molecule 69 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
69	AC	2	Total 2	Zn 2	0
69	AF	1	Total 1	Zn 1	0
69	AP	1	Total 1	Zn 1	0
69	AR	1	Total 1	Zn 1	0
69	AW	1	Total 1	Zn 1	0
69	Be	1	Total 1	Zn 1	0
69	Bi	1	Total 1	Zn 1	0
69	BV	1	Total 1	Zn 1	0
69	Bj	1	Total 1	Zn 1	0
69	Bd	1	Total 1	Zn 1	0
69	Bg	1	Total 1	Zn 1	0
69	Bk	1	Total 1	Zn 1	0

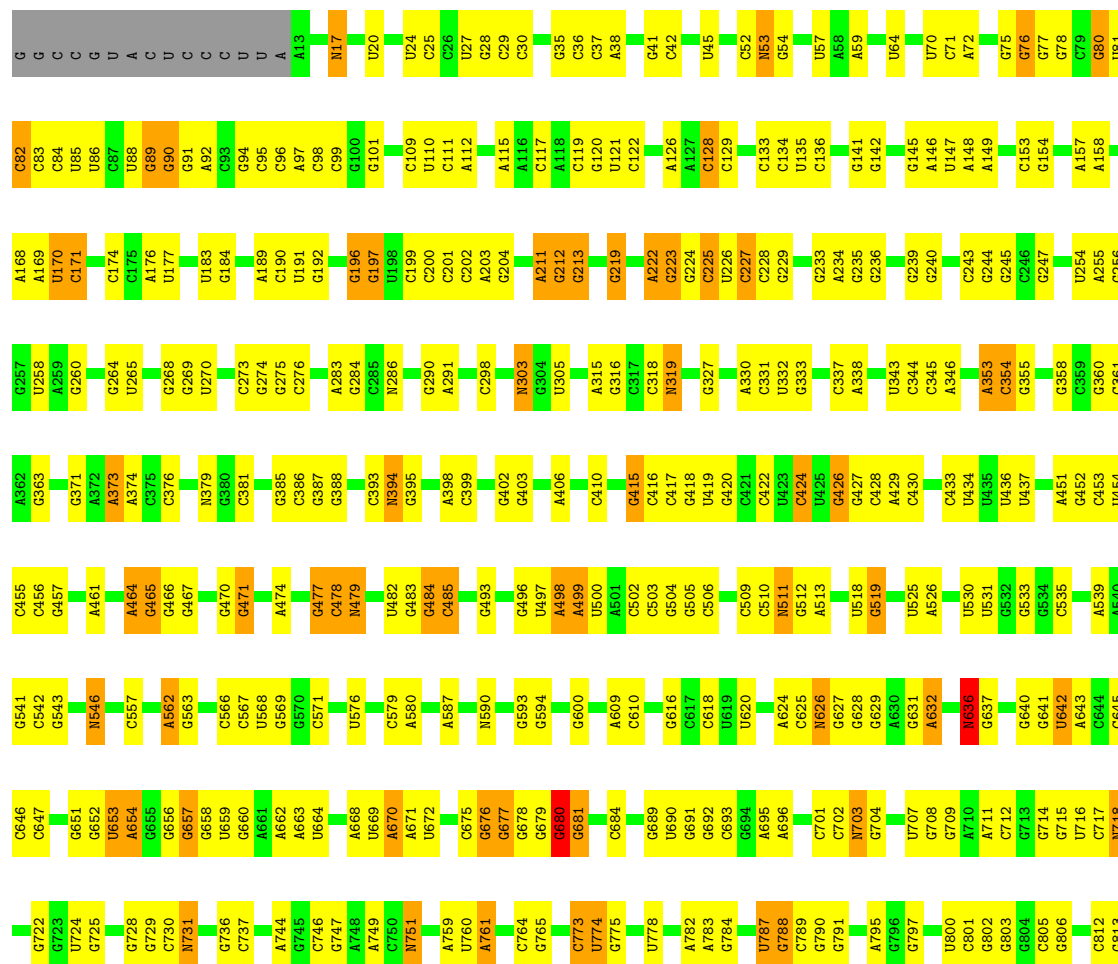
3 Residue-property plots

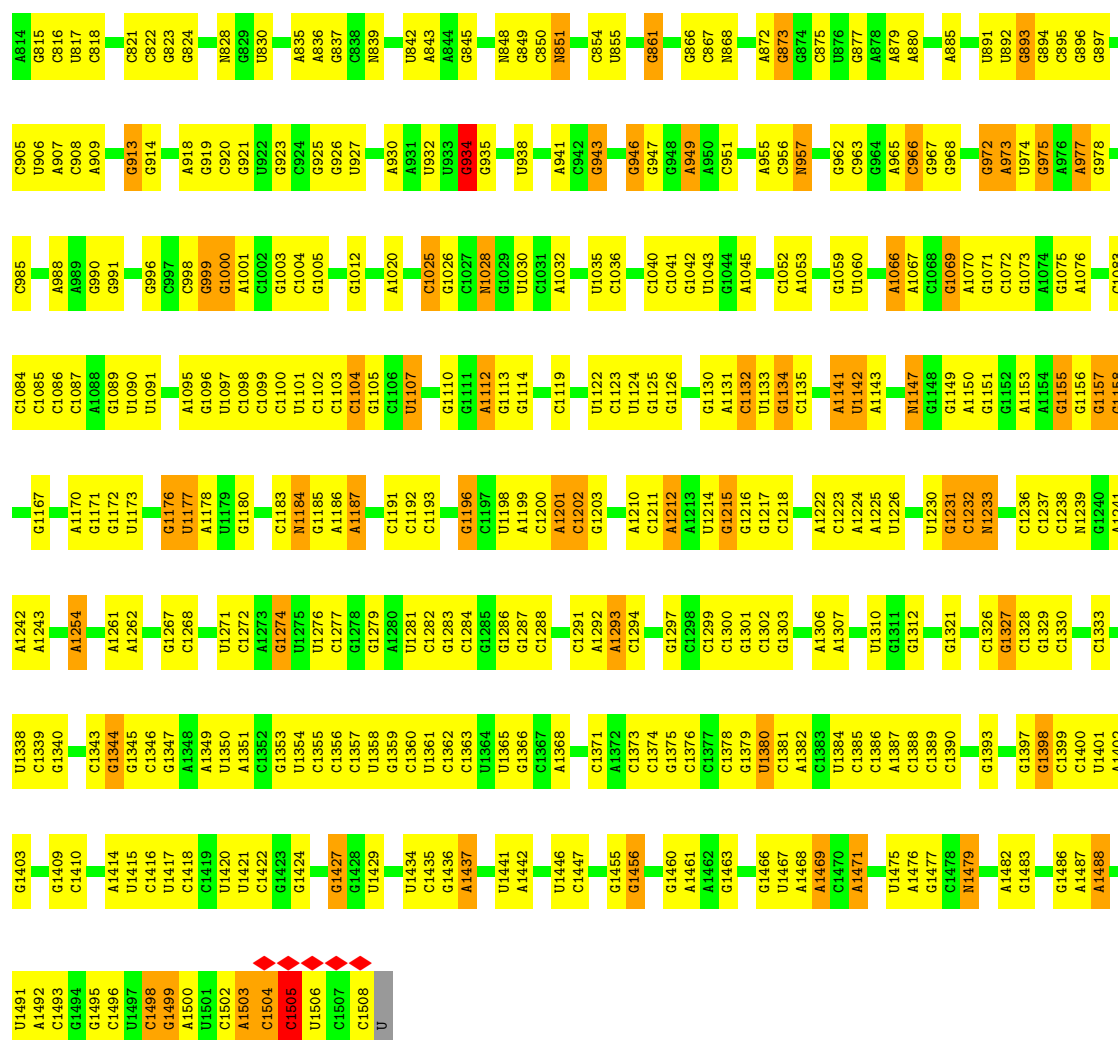
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: rRNA 23S









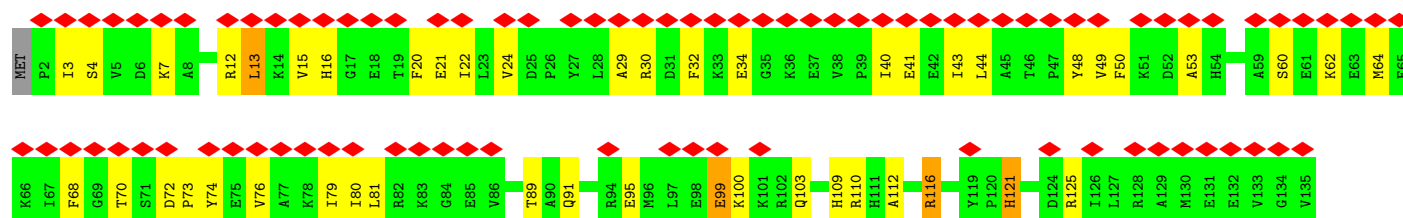
• Molecule 3: rRNA 5S

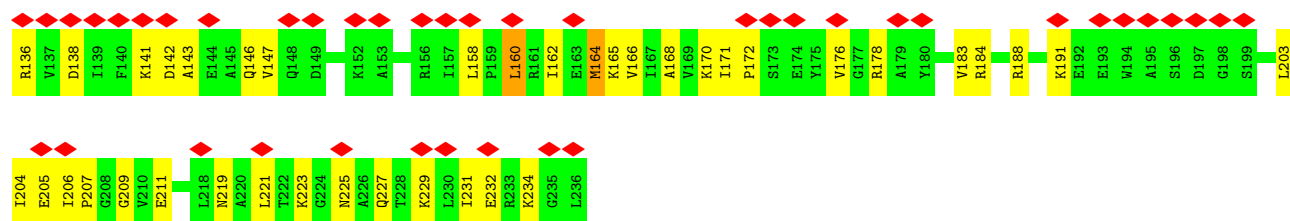
Chain 3: 69% 24% 5%



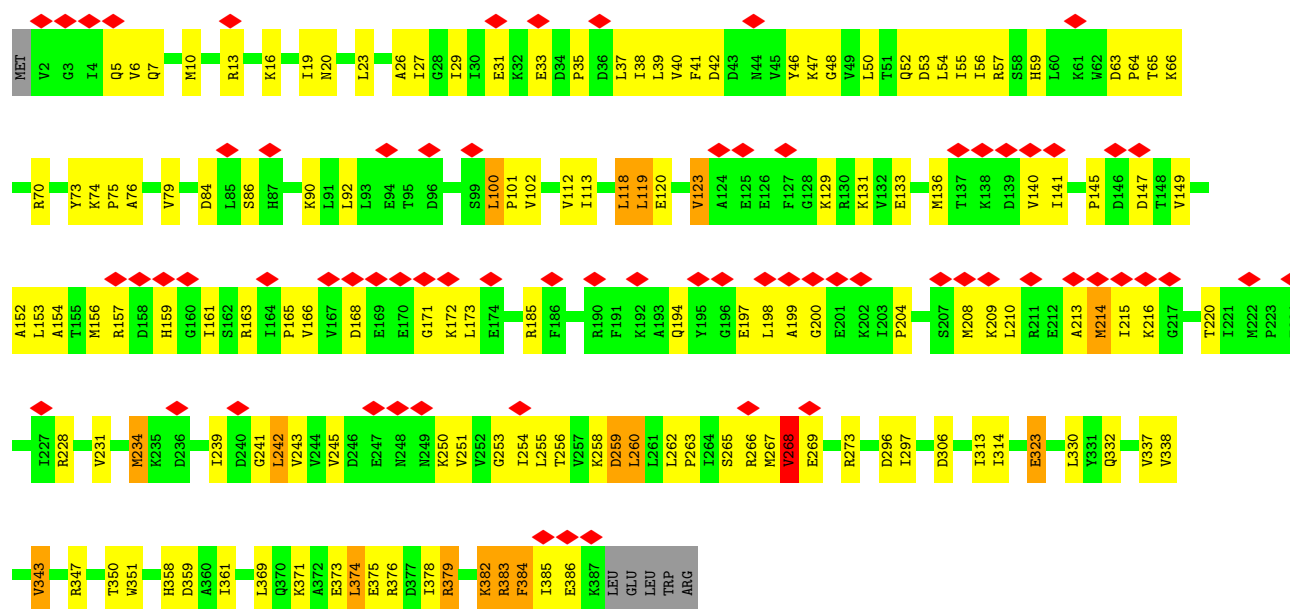
• Molecule 4: Ribosome maturation protein SDO1 homolog

Chain A: 55% 63% 34%

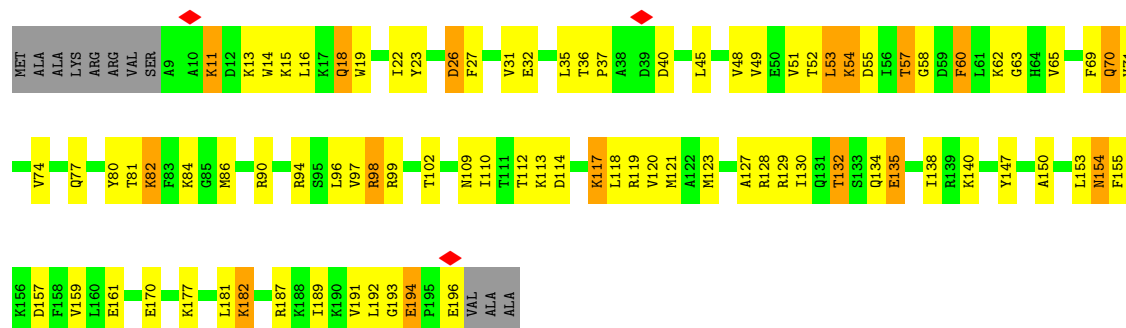




• Molecule 5: Dehydrogenase



• Molecule 6: 30S ribosomal protein S3Ae



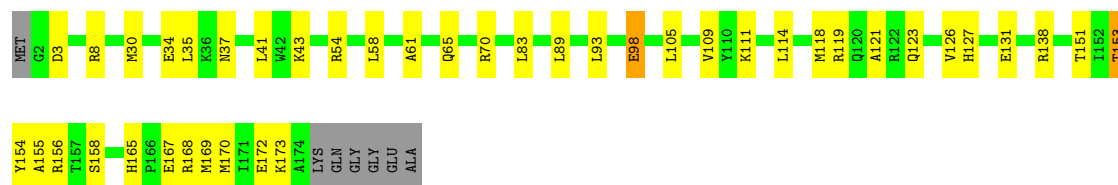
• Molecule 7: 30S ribosomal protein S2



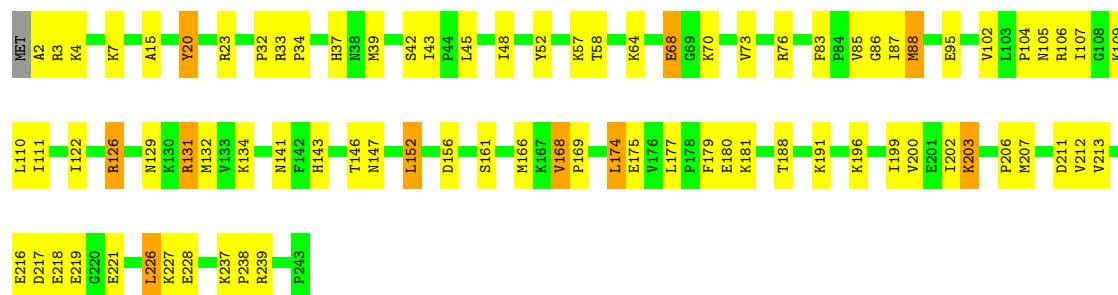
- Molecule 8: Zn-ribbon RNA-binding protein involved in translation



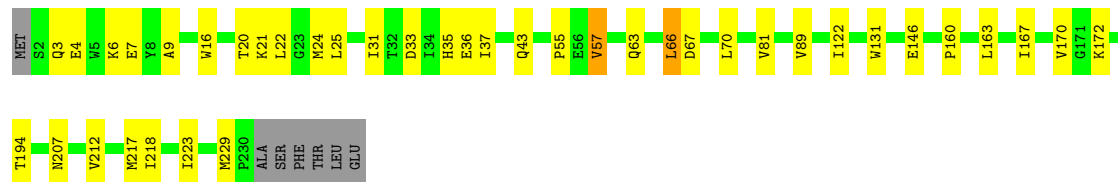
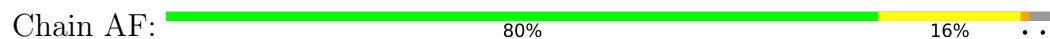
- Molecule 9: 30S ribosomal protein S4



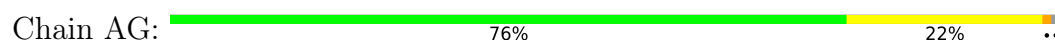
- Molecule 10: 30S ribosomal protein S4e

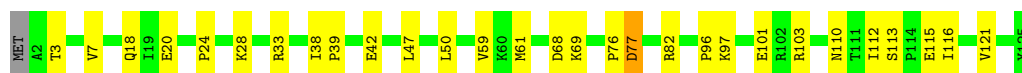


- Molecule 11: 30S ribosomal protein S5



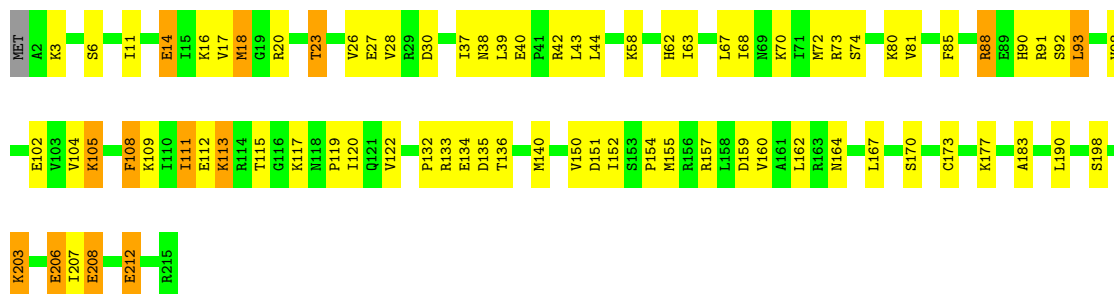
- Molecule 12: 30S ribosomal protein S6e





- Molecule 13: 30S ribosomal protein S7

Chain AH: 63% 31% 6%



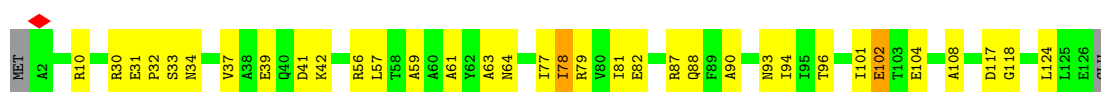
- Molecule 14: 30S ribosomal protein S8

Chain AI: 75% 24%



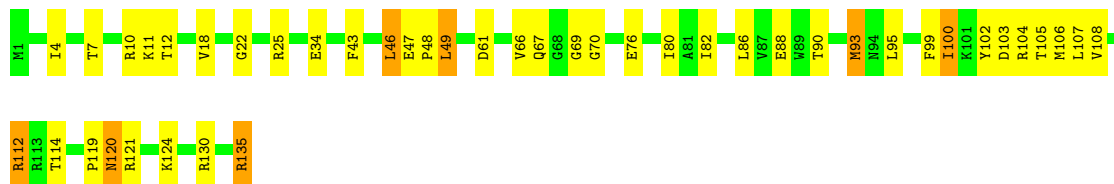
- Molecule 15: 30S ribosomal protein S8e

Chain AJ: 72% 25%



- Molecule 16: 30S ribosomal protein S9

Chain AK: 67% 27% 5%



- Molecule 17: 30S ribosomal protein S10

Chain AL: 59% 32% 7%





- Molecule 18: 30S ribosomal protein S11

Chain AM: 64% 24% 5% 7%



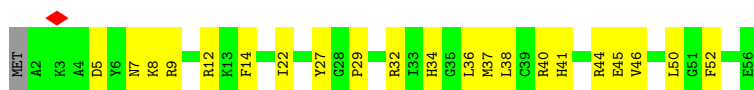
- Molecule 19: 30S ribosomal protein S12

Chain AN: 86% 12% ..



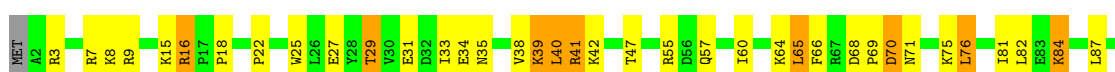
- Molecule 20: 30S ribosomal protein S14 type Z

Chain AP: 61% 38% .



- Molecule 21: 30S ribosomal protein S15

Chain AQ: 62% 30% 8% .



- Molecule 22: Small ribosomal subunit protein uS17

Chain AR: 72% 22% . .



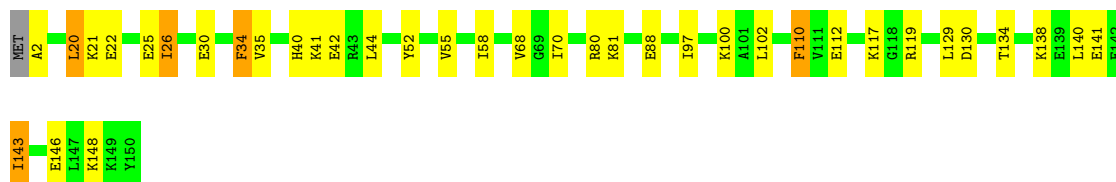
- Molecule 23: 30S ribosomal protein S17e

Chain AS: 57% 34% . .



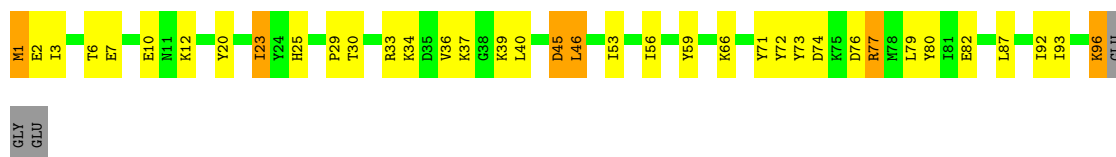
- Molecule 24: 30S ribosomal protein S19e

Chain AU: 75% 21% . .



- Molecule 25: 30S ribosomal protein S24e

Chain AV: 60% 31% 6% .



- Molecule 25: 30S ribosomal protein S24e

Chain B6: 82% 10% 5% .



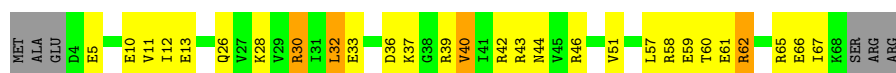
- Molecule 26: 30S ribosomal protein S27e

Chain AW: 51% 38% 5% 6%



- Molecule 27: 30S ribosomal protein S28e

Chain AX: 52% 34% 6% 8%



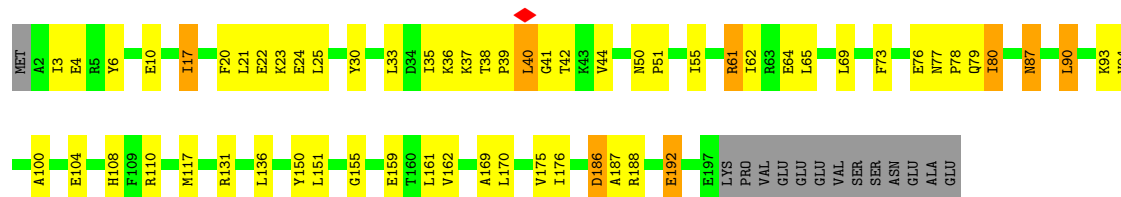
- Molecule 28: 30S ribosomal protein S27ae

Chain AY: 35% 43% 14% 43%



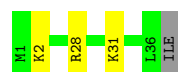
- Molecule 29: 30S ribosomal protein S3

Chain AZ: 64% 25% 7%



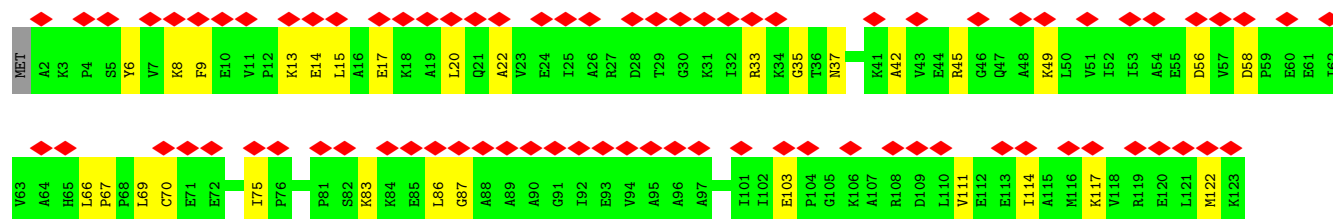
- Molecule 30: Small ribosomal subunit protein eS32

Chain A0: 89% 8%



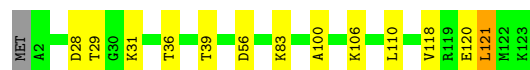
- Molecule 31: 50S ribosomal protein L7Ae

Chain A3: 64% 75% 24%



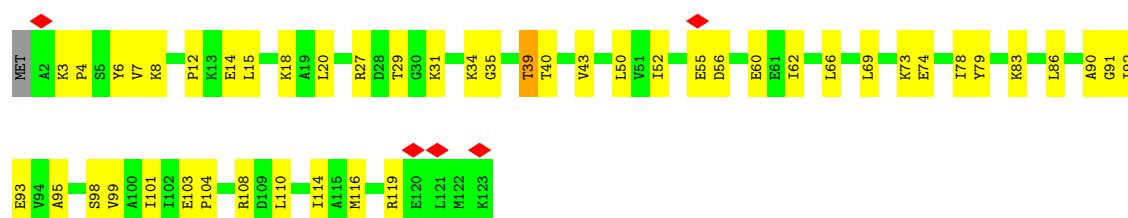
- Molecule 31: 50S ribosomal protein L7Ae

Chain BG: 89% 10%

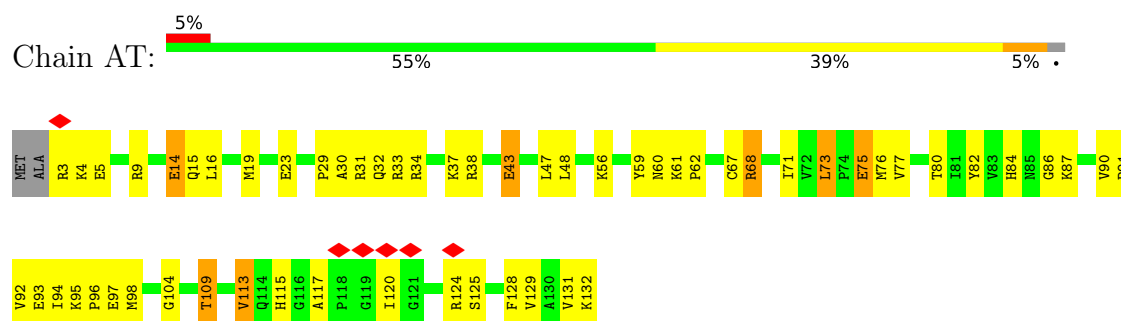


- Molecule 31: 50S ribosomal protein L7Ae

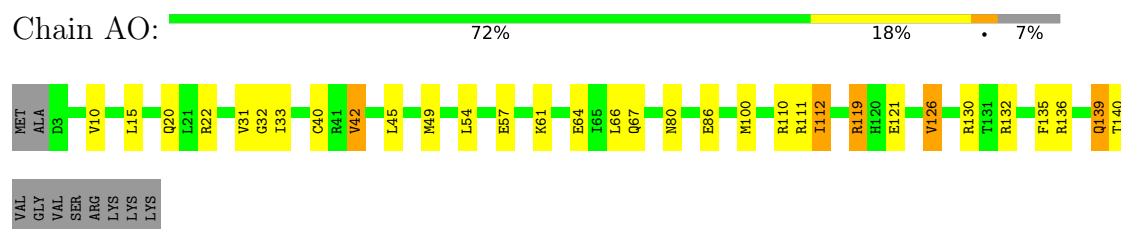
Chain B4: 61% 37%



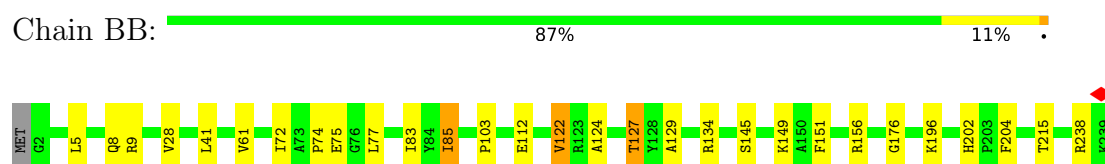
- Molecule 32: 30S ribosomal protein S19



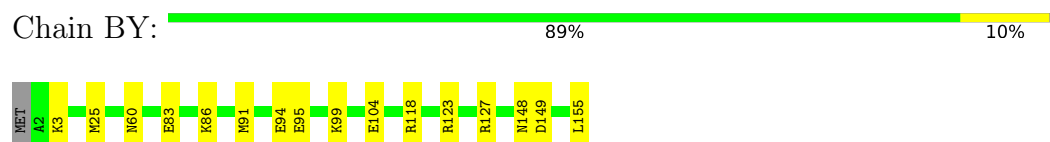
- Molecule 33: 30S ribosomal protein S13



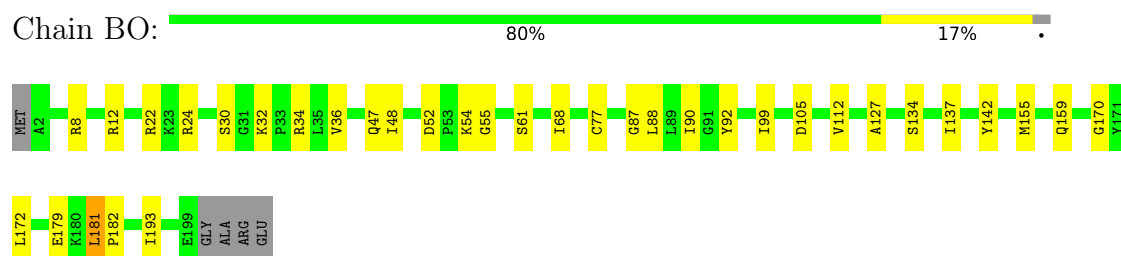
- Molecule 34: Large ribosomal subunit protein uL2



- Molecule 35: Large ribosomal subunit protein uL30

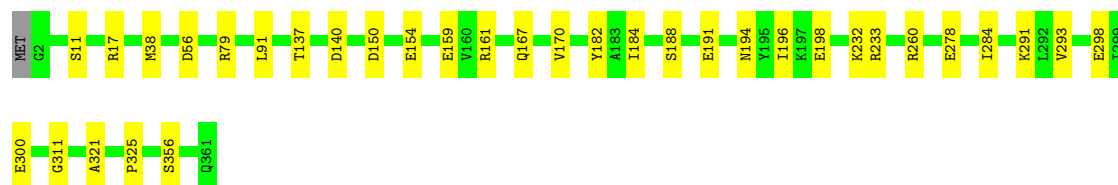


- Molecule 36: Large ribosomal subunit protein uL18



- Molecule 37: Large ribosomal subunit protein uL3





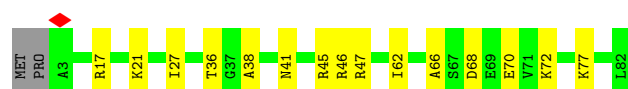
- Molecule 38: Large ribosomal subunit protein eL14

Chain B5: 76% 20% . .



- Molecule 38: Large ribosomal subunit protein eL14

Chain BK: 79% 18% .



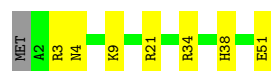
- Molecule 39: Large ribosomal subunit protein uL15

Chain BL: 84% 15% .



- Molecule 40: Large ribosomal subunit protein eL39

Chain Bf: 84% 14% .



- Molecule 41: Large ribosomal subunit protein uL24

Chain BU: 79% 21%



- Molecule 42: Large ribosomal subunit protein eL32

Chain Bb: 92% 7% .



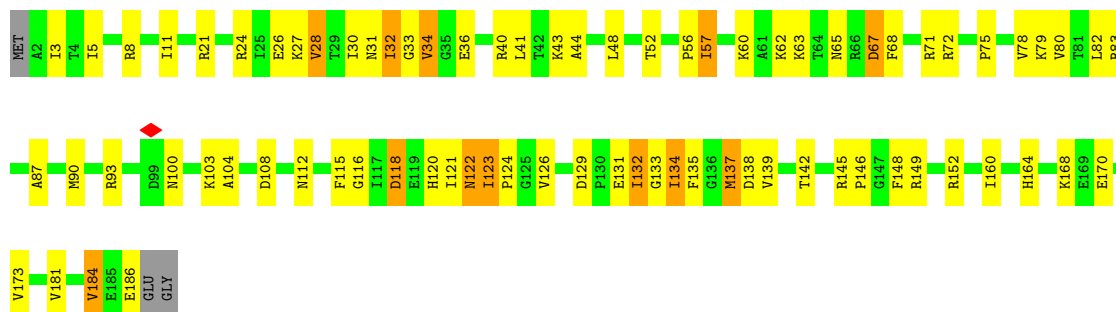
- Molecule 43: Large ribosomal subunit protein eL37

Chain Be:  81% 18%



- Molecule 44: Large ribosomal subunit protein uL5

Chain BE:  57% 35% 6%



- Molecule 45: Large ribosomal subunit protein eL31

Chain Ba:  82% 18%



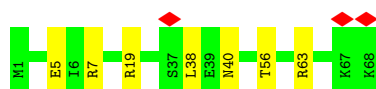
- Molecule 46: Large ribosomal subunit protein uL23

Chain BT:  87% 12%



- Molecule 47: Large ribosomal subunit protein uL29

Chain BW:  90% 10%



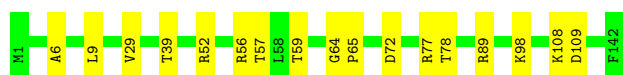
- Molecule 48: Large ribosomal subunit protein eL43

Chain Bi:  93% 6%



- Molecule 49: Large ribosomal subunit protein uL13

Chain BI:  88% 12%



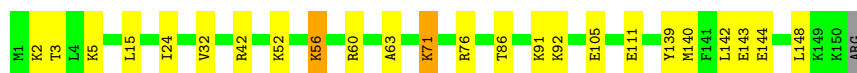
- Molecule 50: Large ribosomal subunit protein eL21

Chain BR:  86% 12% ..



- Molecule 51: Large ribosomal subunit protein eL19

Chain BQ:  83% 15% ..

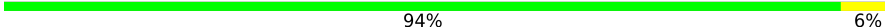


- Molecule 52: Large ribosomal subunit protein eL24

Chain BV:  85% 9% 6%



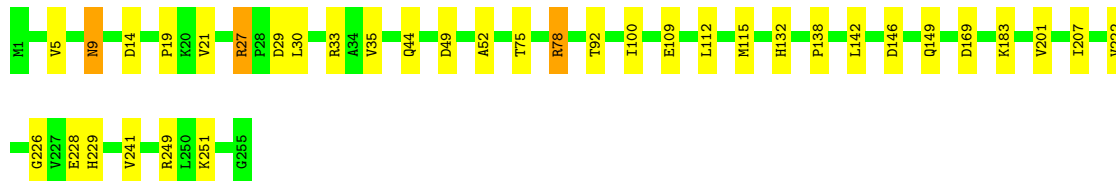
- Molecule 53: Large ribosomal subunit protein eL42

Chain Bj:  94% 6%



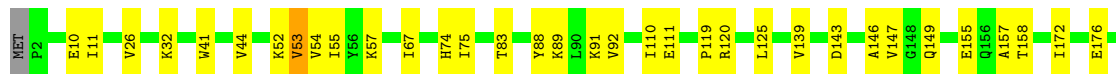
- Molecule 54: Large ribosomal subunit protein uL4

Chain BD:  86% 13% .



- Molecule 55: Large ribosomal subunit protein uL6

Chain BF:  81% 18% ..



F184

- Molecule 56: Large ribosomal subunit protein eL30

Chain BZ:  77% 21% ..



- Molecule 57: Large ribosomal subunit protein eL18

Chain BP:  89% 11%



- Molecule 58: Large ribosomal subunit protein eL15

Chain BM:  89% 10% .



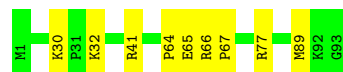
- Molecule 59: Large ribosomal subunit protein uL22

Chain BS:  87% 12% .



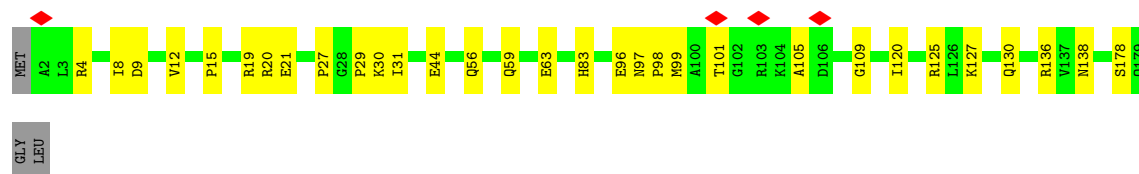
- Molecule 60: Large ribosomal subunit protein eL34

Chain Bd:  90% 10%



- Molecule 61: Large ribosomal subunit protein uL16

Chain BN:  81% 17% .



- Molecule 62: Large ribosomal subunit protein eL40

Chain Bg:  78% 16% 6%



- Molecule 63: Large ribosomal subunit protein eL33

Chain Bc:  89% 10%



- Molecule 64: Large ribosomal subunit protein uL14

Chain BJ:  86% 13%



- Molecule 65: Large ribosomal subunit protein eL20

Chain Bl:  84% 16%



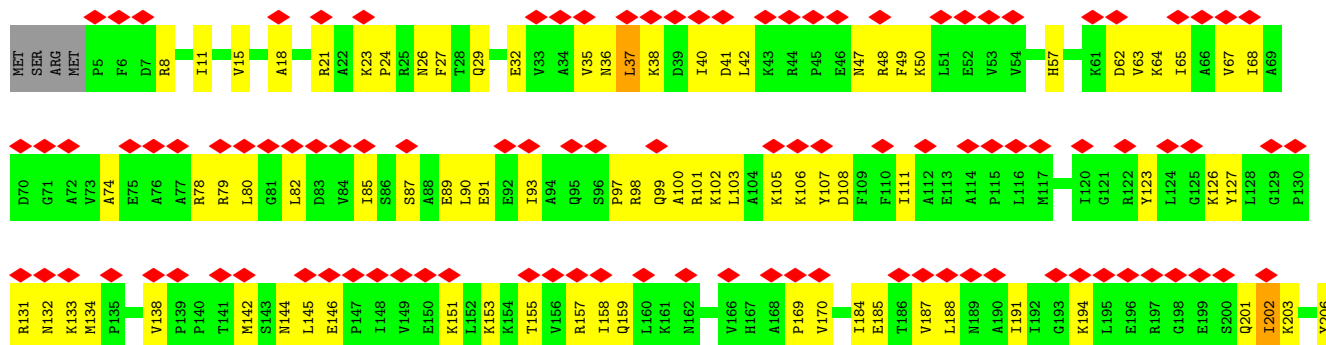
- Molecule 66: C2H2-type domain-containing protein

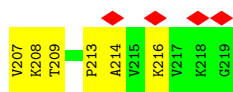
Chain Bk:  85% 12%



- Molecule 67: Large ribosomal subunit protein uL1

Chain BA:  48% 58% 39%





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.014	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.0009	Depositor
Map size (Å)	302.04, 302.04, 302.04	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83900005, 0.83900005, 0.83900005	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 4AC, B8H, OMU, 6MZ, OMC, A2M, 5MC, MA6, UR3, MG, ZN, OMG, LHH

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	1	0.17	2/70601 (0.0%)	0.31	2/110066 (0.0%)
2	2	0.19	2/34435 (0.0%)	0.38	0/53681
3	3	0.15	0/2995	0.34	0/4669
4	A	0.13	0/1934	0.35	0/2598
5	H	0.12	0/3120	0.32	0/4209
6	AA	0.24	0/1557	0.43	0/2087
7	AB	0.17	0/1602	0.31	0/2165
8	AC	0.19	0/463	0.35	0/628
9	AD	0.13	0/1476	0.28	0/1980
10	AE	0.18	0/2032	0.36	0/2742
11	AF	0.14	0/1838	0.28	0/2478
12	AG	0.12	0/993	0.28	0/1329
13	AH	0.17	0/1762	0.37	0/2366
14	AI	0.14	0/1055	0.31	0/1415
15	AJ	0.13	0/995	0.28	0/1327
16	AK	0.14	0/1089	0.39	0/1459
17	AL	0.19	0/817	0.35	0/1097
18	AM	0.14	0/973	0.38	0/1311
19	AN	0.12	0/1165	0.27	0/1547
20	AP	0.13	0/465	0.30	0/613
21	AQ	0.15	0/1333	0.35	0/1791
22	AR	0.18	0/916	0.33	0/1237
23	AS	0.12	0/548	0.24	0/725
24	AU	0.19	0/1253	0.33	0/1689
25	AV	0.17	0/826	0.34	0/1108
25	B6	0.10	0/808	0.27	0/1086
26	AW	0.13	0/476	0.31	0/641
27	AX	0.13	0/518	0.33	0/694
28	AY	0.12	0/235	0.36	0/315
29	AZ	0.16	0/1563	0.32	0/2099
30	A0	0.14	0/349	0.28	0/451
31	A3	0.11	0/945	0.34	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
31	B4	0.16	0/945	0.36	0/1274
31	BG	0.11	0/944	0.25	0/1274
32	AT	0.16	0/1077	0.35	0/1439
33	AO	0.17	0/1135	0.35	0/1526
34	BB	0.13	0/1882	0.28	0/2538
35	BY	0.11	0/1254	0.26	0/1677
36	BO	0.12	0/1645	0.27	0/2209
37	BC	0.12	0/2933	0.27	0/3943
38	B5	0.11	0/619	0.29	0/830
38	BK	0.11	0/611	0.28	0/819
39	BL	0.12	0/1167	0.30	0/1552
40	Bf	0.12	0/443	0.25	0/589
41	BU	0.11	0/1027	0.26	0/1368
42	Bb	0.12	0/1120	0.25	0/1494
43	Be	0.13	0/514	0.26	0/676
44	BE	0.17	0/1509	0.37	0/2022
45	Ba	0.12	0/793	0.26	0/1064
46	BT	0.12	0/705	0.24	0/945
47	BW	0.09	0/566	0.21	0/747
48	Bi	0.10	0/630	0.26	0/839
49	BI	0.12	0/1166	0.25	0/1559
50	BR	0.11	0/819	0.23	0/1098
51	BQ	0.11	0/1281	0.22	0/1689
52	BV	0.11	0/547	0.26	0/729
53	Bj	0.10	0/807	0.23	0/1070
54	BD	0.11	0/2069	0.25	0/2787
55	BF	0.11	0/1485	0.25	0/2003
56	BZ	0.11	0/759	0.25	0/1023
57	BP	0.11	0/984	0.24	0/1314
58	BM	0.12	0/1627	0.24	0/2170
59	BS	0.13	0/1275	0.28	0/1715
60	Bd	0.13	0/778	0.28	0/1036
61	BN	0.12	0/1483	0.25	0/1992
62	Bg	0.09	0/396	0.22	0/526
63	Bc	0.11	0/693	0.27	0/926
64	BJ	0.12	0/1080	0.25	0/1456
65	Bl	0.11	0/669	0.28	0/886
66	Bk	0.13	0/538	0.25	0/709
67	BA	0.12	0/1700	0.29	0/2288
All	All	0.16	4/182812 (0.0%)	0.32	2/268678 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	94	G	O3'-P	-9.21	1.47	1.61
1	1	96	U	C1'-N1	5.73	1.57	1.48
2	2	830	OMU	O3'-P	5.05	1.61	1.56
2	2	373	A2M	O3'-P	5.00	1.61	1.56

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2408	G	C4'-C3'-O3'	-8.62	96.46	109.40
1	1	1306	G	C2'-C3'-O3'	6.03	122.74	113.70

There are no chirality outliers.

There are no planarity outliers.

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	1	65181	0	32949	761	0
2	2	32291	0	16339	543	0
3	3	2703	0	1375	30	0
4	A	1900	0	1968	57	0
5	H	3074	0	3190	109	0
6	AA	1531	0	1623	54	0
7	AB	1571	0	1630	44	0
8	AC	449	0	435	18	0
9	AD	1452	0	1521	26	0
10	AE	1983	0	2058	47	0
11	AF	1808	0	1879	24	0
12	AG	977	0	1037	19	0
13	AH	1725	0	1780	56	0
14	AI	1034	0	1069	24	0
15	AJ	986	0	1070	19	0
16	AK	1073	0	1133	31	0
17	AL	809	0	859	26	0
18	AM	955	0	981	32	0
19	AN	1148	0	1248	12	0
20	AP	455	0	475	18	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	AQ	1305	0	1388	41	0
22	AR	893	0	912	13	0
23	AS	541	0	573	16	0
24	AU	1223	0	1263	25	0
25	AV	808	0	832	20	0
25	B6	790	0	806	11	0
26	AW	470	0	495	20	0
27	AX	516	0	544	15	0
28	AY	227	0	207	6	0
29	AZ	1541	0	1624	41	0
30	A0	343	0	407	3	0
31	A3	933	0	982	19	0
31	B4	933	0	982	26	0
31	BG	932	0	982	9	0
32	AT	1057	0	1131	35	0
33	AO	1116	0	1152	20	0
34	BB	1838	0	1903	21	0
35	BY	1235	0	1314	12	0
36	BO	1607	0	1638	22	0
37	BC	2870	0	3021	20	0
38	B5	614	0	671	13	0
38	BK	607	0	663	10	0
39	BL	1149	0	1218	20	0
40	Bf	435	0	494	6	0
41	BU	1011	0	1078	20	0
42	Bb	1095	0	1190	7	0
43	Be	503	0	533	9	0
44	BE	1485	0	1539	52	0
45	Ba	778	0	851	12	0
46	BT	696	0	758	7	0
47	BW	565	0	628	5	0
48	Bi	620	0	668	3	0
49	BI	1148	0	1237	14	0
50	BR	797	0	835	9	0
51	BQ	1265	0	1392	18	0
52	BV	532	0	523	6	0
53	Bj	789	0	842	2	0
54	BD	2026	0	2131	28	0
55	BF	1456	0	1514	22	0
56	BZ	749	0	796	14	0
57	BP	971	0	1039	6	0
58	BM	1588	0	1683	15	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	BS	1247	0	1280	12	0
60	Bd	759	0	825	8	0
61	BN	1452	0	1491	22	0
62	Bg	387	0	397	6	0
63	Bc	684	0	748	6	0
64	BJ	1066	0	1133	13	0
65	Bl	659	0	702	9	0
66	Bk	528	0	575	6	0
67	BA	1675	0	1787	59	0
68	1	164	0	0	0	0
68	2	65	0	0	0	0
68	3	1	0	0	0	0
68	AD	1	0	0	0	0
68	AK	1	0	0	0	0
68	AN	1	0	0	0	0
68	BB	2	0	0	0	0
68	BD	1	0	0	0	0
68	BM	1	0	0	0	0
68	BS	1	0	0	0	0
68	Bb	1	0	0	0	0
68	Bc	1	0	0	0	0
69	AC	2	0	0	0	0
69	AF	1	0	0	0	0
69	AP	1	0	0	0	0
69	AR	1	0	0	0	0
69	AW	1	0	0	0	0
69	BV	1	0	0	0	0
69	Bd	1	0	0	0	0
69	Be	1	0	0	0	0
69	Bg	1	0	0	0	0
69	Bi	1	0	0	0	0
69	Bj	1	0	0	0	0
69	Bk	1	0	0	0	0
All	All	173872	0	127996	2463	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 8.

The worst 5 of 2463 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)
1:1:117:G:O2'	1:1:118:U:OP1	1.67	1.12
1:1:2408:G:C8	1:1:2410:G:N7	2.16	1.12
1:1:100:G:N2	1:1:119:C:O2	1.82	1.12
1:1:2585:4AC:H5	1:1:2597:G:H1	1.18	1.01
1:1:2608:4AC:H5	1:1:2613:G:H1	1.21	1.00

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	233/236 (99%)	227 (97%)	6 (3%)	0	100	100
5	H	384/392 (98%)	371 (97%)	12 (3%)	1 (0%)	36	46
6	AA	186/199 (94%)	185 (100%)	1 (0%)	0	100	100
7	AB	194/202 (96%)	192 (99%)	2 (1%)	0	100	100
8	AC	55/63 (87%)	53 (96%)	2 (4%)	0	100	100
9	AD	171/180 (95%)	167 (98%)	4 (2%)	0	100	100
10	AE	240/243 (99%)	234 (98%)	6 (2%)	0	100	100
11	AF	227/236 (96%)	221 (97%)	6 (3%)	0	100	100
12	AG	122/125 (98%)	118 (97%)	4 (3%)	0	100	100
13	AH	212/215 (99%)	210 (99%)	2 (1%)	0	100	100
14	AI	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
15	AJ	123/127 (97%)	122 (99%)	1 (1%)	0	100	100
16	AK	133/135 (98%)	131 (98%)	1 (1%)	1 (1%)	16	20
17	AL	98/102 (96%)	97 (99%)	1 (1%)	0	100	100
18	AM	125/137 (91%)	120 (96%)	4 (3%)	1 (1%)	16	20
19	AN	144/147 (98%)	144 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	AP	53/56 (95%)	53 (100%)	0	0	100	100
21	AQ	155/158 (98%)	154 (99%)	1 (1%)	0	100	100
22	AR	106/113 (94%)	104 (98%)	2 (2%)	0	100	100
23	AS	62/67 (92%)	62 (100%)	0	0	100	100
24	AU	147/150 (98%)	145 (99%)	2 (1%)	0	100	100
25	AV	94/99 (95%)	94 (100%)	0	0	100	100
25	B6	92/99 (93%)	91 (99%)	1 (1%)	0	100	100
26	AW	59/65 (91%)	58 (98%)	1 (2%)	0	100	100
27	AX	63/71 (89%)	62 (98%)	1 (2%)	0	100	100
28	AY	27/51 (53%)	22 (82%)	5 (18%)	0	100	100
29	AZ	194/210 (92%)	190 (98%)	3 (2%)	1 (0%)	24	31
30	A0	34/37 (92%)	34 (100%)	0	0	100	100
31	A3	120/123 (98%)	111 (92%)	9 (8%)	0	100	100
31	B4	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
31	BG	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
32	AT	128/132 (97%)	126 (98%)	2 (2%)	0	100	100
33	AO	136/148 (92%)	132 (97%)	4 (3%)	0	100	100
34	BB	236/239 (99%)	229 (97%)	6 (2%)	1 (0%)	30	38
35	BY	152/155 (98%)	151 (99%)	1 (1%)	0	100	100
36	BO	196/203 (97%)	195 (100%)	1 (0%)	0	100	100
37	BC	358/361 (99%)	350 (98%)	8 (2%)	0	100	100
38	B5	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
38	BK	78/82 (95%)	76 (97%)	2 (3%)	0	100	100
39	BL	145/147 (99%)	139 (96%)	6 (4%)	0	100	100
40	Bf	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	BU	119/121 (98%)	119 (100%)	0	0	100	100
42	Bb	127/130 (98%)	127 (100%)	0	0	100	100
43	Be	59/62 (95%)	58 (98%)	1 (2%)	0	100	100
44	BE	183/188 (97%)	180 (98%)	3 (2%)	0	100	100
45	Ba	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
46	BT	84/86 (98%)	83 (99%)	1 (1%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	BW	66/68 (97%)	66 (100%)	0	0	100	100
48	Bi	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
49	BI	140/142 (99%)	137 (98%)	3 (2%)	0	100	100
50	BR	94/97 (97%)	94 (100%)	0	0	100	100
51	BQ	148/151 (98%)	147 (99%)	1 (1%)	0	100	100
52	BV	61/67 (91%)	60 (98%)	1 (2%)	0	100	100
53	Bj	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
54	BD	253/255 (99%)	250 (99%)	3 (1%)	0	100	100
55	BF	181/184 (98%)	181 (100%)	0	0	100	100
56	BZ	96/99 (97%)	95 (99%)	1 (1%)	0	100	100
57	BP	118/120 (98%)	118 (100%)	0	0	100	100
58	BM	191/194 (98%)	189 (99%)	2 (1%)	0	100	100
59	BS	152/155 (98%)	149 (98%)	3 (2%)	0	100	100
60	Bd	89/91 (98%)	88 (99%)	1 (1%)	0	100	100
61	BN	176/181 (97%)	172 (98%)	4 (2%)	0	100	100
62	Bg	46/51 (90%)	46 (100%)	0	0	100	100
63	Bc	85/87 (98%)	84 (99%)	1 (1%)	0	100	100
64	BJ	138/141 (98%)	138 (100%)	0	0	100	100
65	Bl	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
66	Bk	61/65 (94%)	61 (100%)	0	0	100	100
67	BA	213/219 (97%)	207 (97%)	6 (3%)	0	100	100
All	All	8995/9316 (97%)	8834 (98%)	156 (2%)	5 (0%)	49	60

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	H	268	VAL
16	AK	120	ASN
29	AZ	61	ARG
18	AM	124	ASP
34	BB	122	VAL

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	201/202 (100%)	185 (92%)	16 (8%)	11	15
5	H	332/338 (98%)	303 (91%)	29 (9%)	9	12
6	AA	160/167 (96%)	123 (77%)	37 (23%)	1	1
7	AB	168/173 (97%)	135 (80%)	33 (20%)	1	1
8	AC	50/55 (91%)	46 (92%)	4 (8%)	11	15
9	AD	156/160 (98%)	149 (96%)	7 (4%)	24	37
10	AE	213/214 (100%)	186 (87%)	27 (13%)	4	5
11	AF	192/198 (97%)	184 (96%)	8 (4%)	26	40
12	AG	107/108 (99%)	104 (97%)	3 (3%)	38	56
13	AH	183/184 (100%)	161 (88%)	22 (12%)	5	5
14	AI	106/107 (99%)	102 (96%)	4 (4%)	29	44
15	AJ	101/103 (98%)	96 (95%)	5 (5%)	22	33
16	AK	111/111 (100%)	98 (88%)	13 (12%)	5	6
17	AL	89/91 (98%)	75 (84%)	14 (16%)	2	2
18	AM	94/104 (90%)	81 (86%)	13 (14%)	3	4
19	AN	120/121 (99%)	116 (97%)	4 (3%)	33	50
20	AP	45/46 (98%)	44 (98%)	1 (2%)	45	65
21	AQ	142/143 (99%)	122 (86%)	20 (14%)	3	3
22	AR	97/102 (95%)	86 (89%)	11 (11%)	5	7
23	AS	58/61 (95%)	52 (90%)	6 (10%)	7	8
24	AU	126/127 (99%)	105 (83%)	21 (17%)	2	2
25	AV	88/90 (98%)	74 (84%)	14 (16%)	2	2
25	B6	86/90 (96%)	83 (96%)	3 (4%)	32	48
26	AW	53/56 (95%)	43 (81%)	10 (19%)	1	1
27	AX	55/60 (92%)	42 (76%)	13 (24%)	1	1
28	AY	22/42 (52%)	22 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	AZ	155/168 (92%)	136 (88%)	19 (12%)	4	5
30	A0	34/35 (97%)	34 (100%)	0	100	100
31	A3	98/99 (99%)	96 (98%)	2 (2%)	48	67
31	B4	98/99 (99%)	89 (91%)	9 (9%)	8	11
31	BG	98/99 (99%)	97 (99%)	1 (1%)	68	82
32	AT	113/114 (99%)	93 (82%)	20 (18%)	2	2
33	AO	115/123 (94%)	97 (84%)	18 (16%)	2	2
34	BB	188/189 (100%)	186 (99%)	2 (1%)	65	81
35	BY	132/133 (99%)	131 (99%)	1 (1%)	73	86
36	BO	167/170 (98%)	162 (97%)	5 (3%)	36	53
37	BC	306/307 (100%)	304 (99%)	2 (1%)	76	87
38	B5	65/66 (98%)	60 (92%)	5 (8%)	12	16
38	BK	64/66 (97%)	62 (97%)	2 (3%)	35	52
39	BL	118/118 (100%)	115 (98%)	3 (2%)	42	60
40	Bf	46/47 (98%)	46 (100%)	0	100	100
41	BU	109/109 (100%)	109 (100%)	0	100	100
42	Bb	117/118 (99%)	116 (99%)	1 (1%)	70	84
43	Be	52/53 (98%)	51 (98%)	1 (2%)	50	69
44	BE	158/160 (99%)	139 (88%)	19 (12%)	5	5
45	Ba	84/84 (100%)	84 (100%)	0	100	100
46	BT	77/77 (100%)	75 (97%)	2 (3%)	40	59
47	BW	63/63 (100%)	61 (97%)	2 (3%)	34	51
48	Bi	61/62 (98%)	61 (100%)	0	100	100
49	BI	122/122 (100%)	122 (100%)	0	100	100
50	BR	86/87 (99%)	84 (98%)	2 (2%)	44	63
51	BQ	132/133 (99%)	129 (98%)	3 (2%)	44	63
52	BV	54/58 (93%)	54 (100%)	0	100	100
53	Bj	83/84 (99%)	81 (98%)	2 (2%)	43	62
54	BD	212/212 (100%)	206 (97%)	6 (3%)	38	56
55	BF	156/157 (99%)	154 (99%)	2 (1%)	61	77
56	BZ	79/80 (99%)	75 (95%)	4 (5%)	21	32

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	BP	102/102 (100%)	99 (97%)	3 (3%)	37	55
58	BM	160/161 (99%)	160 (100%)	0	100	100
59	BS	130/131 (99%)	129 (99%)	1 (1%)	73	86
60	Bd	82/82 (100%)	81 (99%)	1 (1%)	63	79
61	BN	149/151 (99%)	149 (100%)	0	100	100
62	Bg	37/39 (95%)	37 (100%)	0	100	100
63	Bc	74/74 (100%)	73 (99%)	1 (1%)	59	76
64	BJ	108/109 (99%)	107 (99%)	1 (1%)	70	84
65	Bl	72/72 (100%)	70 (97%)	2 (3%)	38	56
66	Bk	55/57 (96%)	55 (100%)	0	100	100
67	BA	182/186 (98%)	176 (97%)	6 (3%)	33	50
All	All	7748/7909 (98%)	7262 (94%)	486 (6%)	18	23

5 of 486 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
18	AM	102	ILE
51	BQ	111	GLU
24	AU	58	ILE
50	BR	77	VAL
31	B4	29	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 167 such sidechains are listed below:

Mol	Chain	Res	Type
51	BQ	58	GLN
59	BS	45	ASN
52	BV	57	GLN
56	BZ	21	ASN
61	BN	38	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3016/3018 (99%)	442 (14%)	20 (0%)
2	2	1495/1512 (98%)	209 (13%)	20 (1%)

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	3	125/128 (97%)	13 (10%)	1 (0%)
All	All	4636/4658 (99%)	664 (14%)	41 (0%)

5 of 664 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	12	G
1	1	28	A
1	1	39	A
1	1	51	A
1	1	52	G

5 of 41 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	2	669	U
2	2	1141	A
2	2	676	G
2	2	842	U
2	2	1157	G

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

159 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	5MC	2	535	2	18,22,23	0.94	2 (11%)	26,32,35	1.14	2 (7%)
1	5MC	1	2162	1	18,22,23	0.95	2 (11%)	26,32,35	1.11	2 (7%)
2	OMU	2	64	2	19,22,23	1.24	3 (15%)	26,31,34	1.75	5 (19%)
1	4AC	1	1885	1	21,24,25	1.02	2 (9%)	29,34,37	1.32	4 (13%)
2	OMU	2	774	2	19,22,23	1.26	3 (15%)	26,31,34	1.77	4 (15%)
1	4AC	1	341	1	21,24,25	1.02	2 (9%)	29,34,37	1.35	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	4AC	2	590	2	21,24,25	1.02	2 (9%)	29,34,37	1.34	4 (13%)
1	OMU	1	2784	1	19,22,23	1.20	3 (15%)	26,31,34	1.71	5 (19%)
1	OMG	1	2138	1	23,26,27	1.20	3 (13%)	33,38,41	1.93	6 (18%)
1	4AC	1	922	1	21,24,25	1.04	2 (9%)	29,34,37	1.39	4 (13%)
1	4AC	1	2287	1	21,24,25	1.01	2 (9%)	29,34,37	1.37	4 (13%)
2	OMU	2	1177	2	19,22,23	1.22	3 (15%)	26,31,34	1.71	4 (15%)
1	4AC	1	2585	1	21,24,25	1.06	2 (9%)	29,34,37	1.72	6 (20%)
1	4AC	1	1068	1	21,24,25	1.03	2 (9%)	29,34,37	1.34	4 (13%)
2	4AC	2	868	2	21,24,25	1.04	2 (9%)	29,34,37	1.33	5 (17%)
2	4AC	2	1233	2	21,24,25	1.01	2 (9%)	29,34,37	1.39	4 (13%)
2	MA6	2	1487	2	23,26,27	1.47	4 (17%)	34,38,41	2.11	10 (29%)
1	4AC	1	1594	68,1	21,24,25	1.02	2 (9%)	29,34,37	1.34	4 (13%)
2	6MZ	2	1469	68,2	22,25,26	1.50	4 (18%)	30,36,39	2.19	10 (33%)
2	4AC	2	319	2	21,24,25	1.03	2 (9%)	29,34,37	1.33	4 (13%)
2	4AC	2	1479	2	21,24,25	1.01	2 (9%)	29,34,37	1.34	4 (13%)
1	5MC	1	2203	1	18,22,23	0.95	2 (11%)	26,32,35	1.11	2 (7%)
2	4AC	2	303	2	21,24,25	1.02	2 (9%)	29,34,37	1.35	4 (13%)
2	4AC	2	718	2	21,24,25	1.01	2 (9%)	29,34,37	1.39	4 (13%)
2	4AC	2	286	2	21,24,25	1.03	2 (9%)	29,34,37	1.39	4 (13%)
2	UR3	2	1467	2	19,22,23	0.95	0	26,32,35	1.44	1 (3%)
2	4AC	2	1028	2	21,24,25	1.02	2 (9%)	29,34,37	1.34	4 (13%)
1	4AC	1	2062	1	21,24,25	1.02	2 (9%)	29,34,37	1.34	4 (13%)
1	4AC	1	2083	1	21,24,25	1.04	2 (9%)	29,34,37	1.27	4 (13%)
1	4AC	1	2865	1	21,24,25	1.02	2 (9%)	29,34,37	1.33	4 (13%)
2	4AC	2	17	2	21,24,25	1.01	2 (9%)	29,34,37	1.35	4 (13%)
1	4AC	1	1554	1	21,24,25	1.02	2 (9%)	29,34,37	1.34	4 (13%)
1	4AC	1	641	1	21,24,25	1.03	2 (9%)	29,34,37	1.35	4 (13%)
1	4AC	1	1962	1	21,24,25	1.02	2 (9%)	29,34,37	1.35	4 (13%)
1	5MC	1	2733	1	18,22,23	0.97	2 (11%)	26,32,35	1.28	3 (11%)
1	4AC	1	1755	1	21,24,25	1.04	2 (9%)	29,34,37	1.56	4 (13%)
1	4AC	1	2642	1	21,24,25	1.02	2 (9%)	29,34,37	1.31	4 (13%)
2	OMC	2	846	2	19,22,23	0.81	0	26,31,34	0.79	0
1	4AC	1	2925	1	21,24,25	1.04	2 (9%)	29,34,37	1.33	5 (17%)
1	4AC	1	1878	1	21,24,25	1.01	2 (9%)	29,34,37	1.51	4 (13%)
1	4AC	1	1065	1	21,24,25	1.02	2 (9%)	29,34,37	1.37	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	4AC	1	2136	1	21,24,25	1.03	2 (9%)	29,34,37	1.35	4 (13%)
2	OMG	2	1069	2	23,26,27	1.21	3 (13%)	33,38,41	1.93	6 (18%)
2	OMU	2	787	2	19,22,23	1.23	3 (15%)	26,31,34	1.84	5 (19%)
1	4AC	1	1557	1	21,24,25	1.01	2 (9%)	29,34,37	1.31	4 (13%)
2	OMG	2	471	2	23,26,27	1.21	3 (13%)	33,38,41	1.90	6 (18%)
1	4AC	1	2966	1	21,24,25	1.02	2 (9%)	29,34,37	1.35	4 (13%)
1	4AC	1	22	1	21,24,25	1.04	2 (9%)	29,34,37	1.32	5 (17%)
1	4AC	1	451	1	21,24,25	1.02	2 (9%)	29,34,37	1.35	4 (13%)
1	4AC	1	2329	1	21,24,25	1.03	2 (9%)	29,34,37	1.36	4 (13%)
1	5MC	1	2163	1	18,22,23	0.95	2 (11%)	26,32,35	1.10	2 (7%)
1	4AC	1	229	1	21,24,25	1.04	2 (9%)	29,34,37	1.32	4 (13%)
2	4AC	2	511	2	21,24,25	1.03	2 (9%)	29,34,37	1.39	4 (13%)
1	4AC	1	243	1	21,24,25	1.02	2 (9%)	29,34,37	1.36	4 (13%)
2	A2M	2	373	2	22,25,26	1.46	4 (18%)	31,36,39	2.05	8 (25%)
1	4AC	1	1934	1	21,24,25	1.01	2 (9%)	29,34,37	1.38	4 (13%)
1	4AC	1	1695	1	21,24,25	1.02	2 (9%)	29,34,37	1.35	4 (13%)
1	5MC	1	2183	1	18,22,23	0.95	2 (11%)	26,32,35	1.12	2 (7%)
1	4AC	1	533	1	21,24,25	1.03	2 (9%)	29,34,37	1.35	4 (13%)
2	OMC	2	129	2	19,22,23	0.81	0	26,31,34	0.81	0
1	4AC	1	2027	1	21,24,25	1.03	2 (9%)	29,34,37	1.34	4 (13%)
1	4AC	1	2992	1	21,24,25	1.04	2 (9%)	29,34,37	0.87	2 (6%)
2	4AC	2	731	2	21,24,25	1.02	2 (9%)	29,34,37	1.40	4 (13%)
2	OMC	2	773	2	19,22,23	0.84	0	26,31,34	0.94	1 (3%)
1	OMG	1	328	1	23,26,27	1.21	3 (13%)	33,38,41	1.95	7 (21%)
1	OMG	1	789	1	23,26,27	1.20	3 (13%)	33,38,41	1.95	6 (18%)
1	4AC	1	694	1	21,24,25	1.02	2 (9%)	29,34,37	1.33	4 (13%)
2	LHH	2	1041	2	22,25,26	0.34	0	29,35,38	0.49	1 (3%)
2	OMC	2	1040	2	19,22,23	1.17	2 (10%)	26,31,34	0.92	1 (3%)
2	LHH	2	250	2	22,25,26	0.31	0	29,35,38	0.47	0
1	4AC	1	1765	1	21,24,25	1.04	2 (9%)	29,34,37	1.36	4 (13%)
1	4AC	1	1938	1	21,24,25	1.03	2 (9%)	29,34,37	1.33	4 (13%)
1	OMG	1	2147	1	23,26,27	1.21	3 (13%)	33,38,41	1.94	6 (18%)
1	OMG	1	2144	1	23,26,27	1.20	3 (13%)	33,38,41	1.93	6 (18%)
1	4AC	1	802	1	21,24,25	1.00	2 (9%)	29,34,37	1.38	4 (13%)
2	5MC	2	875	2	18,22,23	0.96	2 (11%)	26,32,35	1.17	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MC	1	2093	1	18,22,23	0.95	2 (11%)	26,32,35	1.11	2 (7%)
1	4AC	1	1048	1	21,24,25	1.03	2 (9%)	29,34,37	1.39	4 (13%)
2	4AC	2	703	2	21,24,25	0.98	2 (9%)	29,34,37	2.22	2 (6%)
2	4AC	2	626	2	21,24,25	1.02	2 (9%)	29,34,37	1.42	4 (13%)
2	4AC	2	1184	2	21,24,25	1.06	2 (9%)	29,34,37	1.59	3 (10%)
2	5MC	2	1374	2	18,22,23	0.97	2 (11%)	26,32,35	1.14	3 (11%)
1	OMG	1	2678	1	23,26,27	1.20	3 (13%)	33,38,41	1.96	6 (18%)
1	4AC	1	2249	1	21,24,25	1.04	2 (9%)	29,34,37	1.38	4 (13%)
1	4AC	1	1293	1	21,24,25	1.02	2 (9%)	29,34,37	1.37	4 (13%)
1	4AC	1	2545	1	21,24,25	1.02	2 (9%)	29,34,37	1.38	4 (13%)
1	4AC	1	2937	68,1	21,24,25	1.03	2 (9%)	29,34,37	1.56	4 (13%)
2	OMG	2	519	2	23,26,27	1.21	3 (13%)	33,38,41	1.95	6 (18%)
1	4AC	1	2608	1	21,24,25	1.05	2 (9%)	29,34,37	1.73	5 (17%)
1	4AC	1	2960	1	21,24,25	1.02	2 (9%)	29,34,37	1.29	4 (13%)
3	4AC	3	32	3	21,24,25	1.02	2 (9%)	29,34,37	1.37	4 (13%)
1	4AC	1	1667	1	21,24,25	1.02	2 (9%)	29,34,37	1.33	4 (13%)
1	4AC	1	1460	1	21,24,25	1.02	2 (9%)	29,34,37	1.37	4 (13%)
1	4AC	1	1621	1	21,24,25	1.02	2 (9%)	29,34,37	1.33	4 (13%)
2	4AC	2	851	2	21,24,25	1.04	2 (9%)	29,34,37	1.30	5 (17%)
1	4AC	1	835	1	21,24,25	1.03	2 (9%)	29,34,37	1.34	4 (13%)
1	4AC	1	1550	1	21,24,25	1.02	2 (9%)	29,34,37	1.36	4 (13%)
1	4AC	1	3004	1	21,24,25	1.03	2 (9%)	29,34,37	1.30	4 (13%)
1	4AC	1	2908	1	21,24,25	1.03	2 (9%)	29,34,37	1.30	4 (13%)
2	B8H	2	938	2	19,22,23	0.80	1 (5%)	22,32,35	0.85	0
1	A2M	1	1055	1	22,25,26	1.47	4 (18%)	31,36,39	2.07	8 (25%)
1	4AC	1	60	1	21,24,25	1.04	2 (9%)	29,34,37	1.36	4 (13%)
1	OMG	1	923	68,1	23,26,27	1.19	3 (13%)	33,38,41	1.95	7 (21%)
2	OMU	2	20	2	19,22,23	1.22	2 (10%)	26,31,34	1.77	5 (19%)
1	4AC	1	2001	1	21,24,25	1.03	2 (9%)	29,34,37	1.33	4 (13%)
1	4AC	1	829	1	21,24,25	1.02	2 (9%)	29,34,37	1.32	4 (13%)
2	4AC	2	839	2	21,24,25	1.02	2 (9%)	29,34,37	1.37	4 (13%)
2	OMU	2	830	2	19,22,23	1.25	3 (15%)	26,31,34	1.74	5 (19%)
2	OMU	2	1380	2	19,22,23	1.26	4 (21%)	26,31,34	1.71	5 (19%)
2	4AC	2	379	2	21,24,25	1.01	2 (9%)	29,34,37	1.39	4 (13%)
2	OMG	2	873	2	23,26,27	1.20	3 (13%)	33,38,41	1.97	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MA6	2	1488	2	23,26,27	1.48	4 (17%)	34,38,41	2.13	9 (26%)
1	4AC	1	1873	1	21,24,25	1.02	2 (9%)	29,34,37	1.31	4 (13%)
2	OMG	2	680	2	23,26,27	1.24	3 (13%)	33,38,41	2.08	6 (18%)
1	4AC	1	91	1	21,24,25	1.03	2 (9%)	29,34,37	1.44	4 (13%)
2	5MC	2	1496	2	18,22,23	0.93	2 (11%)	26,32,35	1.09	2 (7%)
1	4AC	1	161	1	21,24,25	1.02	2 (9%)	29,34,37	1.33	4 (13%)
2	5MC	2	1505	2	18,22,23	0.97	2 (11%)	26,32,35	1.13	2 (7%)
2	4AC	2	1239	2	21,24,25	1.03	2 (9%)	29,34,37	1.36	4 (13%)
2	4AC	2	848	2	21,24,25	1.02	2 (9%)	29,34,37	1.35	4 (13%)
2	4AC	2	957	2	21,24,25	1.03	2 (9%)	29,34,37	1.36	4 (13%)
2	OMG	2	657	2	23,26,27	1.27	3 (13%)	33,38,41	2.01	6 (18%)
2	4AC	2	828	2	21,24,25	1.02	2 (9%)	29,34,37	1.35	4 (13%)
2	5MC	2	1202	2	18,22,23	0.93	1 (5%)	26,32,35	1.01	2 (7%)
1	4AC	1	357	1	21,24,25	1.01	2 (9%)	29,34,37	1.36	4 (13%)
2	OMG	2	934	2	23,26,27	1.22	3 (13%)	33,38,41	1.97	6 (18%)
2	4AC	2	751	2	21,24,25	1.02	2 (9%)	29,34,37	1.32	4 (13%)
1	4AC	1	1780	1	21,24,25	1.02	1 (4%)	29,34,37	1.55	4 (13%)
2	4AC	2	1147	2	21,24,25	1.00	2 (9%)	29,34,37	1.46	4 (13%)
2	4AC	2	394	2	21,24,25	1.05	2 (9%)	29,34,37	1.55	4 (13%)
2	OMG	2	467	2	23,26,27	1.20	3 (13%)	33,38,41	1.95	6 (18%)
1	4AC	1	1867	1	21,24,25	1.03	2 (9%)	29,34,37	1.35	4 (13%)
2	4AC	2	479	2	21,24,25	1.02	2 (9%)	29,34,37	1.43	4 (13%)
1	4AC	1	1222	68,1	21,24,25	1.02	2 (9%)	29,34,37	1.32	4 (13%)
2	4AC	2	636	2	21,24,25	1.05	2 (9%)	29,34,37	2.16	6 (20%)
2	5MC	2	1498	2	18,22,23	0.93	2 (11%)	26,32,35	1.41	5 (19%)
2	OMC	2	1376	2	19,22,23	0.81	0	26,31,34	0.79	0
1	4AC	1	981	1	21,24,25	1.01	2 (9%)	29,34,37	1.28	4 (13%)
1	4AC	1	314	1	21,24,25	1.03	2 (9%)	29,34,37	1.33	4 (13%)
1	4AC	1	1243	1	21,24,25	1.03	2 (9%)	29,34,37	1.36	4 (13%)
1	4AC	1	1662	1	21,24,25	1.01	2 (9%)	29,34,37	1.38	4 (13%)
1	5MC	1	2198	1	18,22,23	0.94	2 (11%)	26,32,35	1.13	2 (7%)
1	4AC	1	2548	1	21,24,25	1.02	2 (9%)	29,34,37	1.35	4 (13%)
1	4AC	1	2570	1	21,24,25	1.01	2 (9%)	29,34,37	1.36	4 (13%)
1	4AC	1	1617	1	21,24,25	1.01	2 (9%)	29,34,37	1.36	4 (13%)
2	4AC	2	546	2	21,24,25	1.01	2 (9%)	29,34,37	1.33	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	4AC	1	2495	1	21,24,25	1.03	2 (9%)	29,34,37	1.33	4 (13%)
1	4AC	1	2718	1	21,24,25	1.01	2 (9%)	29,34,37	1.34	4 (13%)
1	4AC	1	211	1	21,24,25	1.03	2 (9%)	29,34,37	1.33	4 (13%)
2	4AC	2	53	2	21,24,25	1.00	2 (9%)	29,34,37	1.43	4 (13%)
1	4AC	1	136	1	21,24,25	1.01	2 (9%)	29,34,37	1.32	4 (13%)
1	LHH	1	616	1	22,25,26	0.30	0	29,35,38	0.46	0
2	OMG	2	913	2	23,26,27	1.20	3 (13%)	33,38,41	1.93	6 (18%)
2	5MC	2	1025	2	18,22,23	0.95	2 (11%)	26,32,35	1.15	3 (11%)
1	A2M	1	2173	1	22,25,26	1.44	4 (18%)	31,36,39	2.10	10 (32%)
1	OMC	1	615	1	19,22,23	0.82	0	26,31,34	0.95	1 (3%)
1	4AC	1	458	1	21,24,25	1.02	2 (9%)	29,34,37	1.36	4 (13%)
2	5MC	2	693	2	18,22,23	0.95	2 (11%)	26,32,35	1.12	2 (7%)
1	OMC	1	1948	1	19,22,23	0.81	0	26,31,34	0.77	0

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	5MC	2	535	2	-	0/7/25/26	0/2/2/2
1	5MC	1	2162	1	-	0/7/25/26	0/2/2/2
2	OMU	2	64	2	-	0/9/27/28	0/2/2/2
1	4AC	1	1885	1	-	0/11/29/30	0/2/2/2
2	OMU	2	774	2	-	0/9/27/28	0/2/2/2
1	4AC	1	341	1	-	0/11/29/30	0/2/2/2
2	4AC	2	590	2	-	0/11/29/30	0/2/2/2
1	OMU	1	2784	1	-	0/9/27/28	0/2/2/2
1	OMG	1	2138	1	-	0/9/27/28	0/3/3/3
1	4AC	1	922	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2287	1	-	0/11/29/30	0/2/2/2
2	OMU	2	1177	2	-	1/9/27/28	0/2/2/2
1	4AC	1	2585	1	-	3/11/29/30	0/2/2/2
1	4AC	1	1068	1	-	0/11/29/30	0/2/2/2
2	4AC	2	868	2	-	0/11/29/30	0/2/2/2
2	4AC	2	1233	2	-	0/11/29/30	0/2/2/2
2	MA6	2	1487	2	-	0/11/29/30	0/3/3/3
1	4AC	1	1594	68,1	-	0/11/29/30	0/2/2/2
2	6MZ	2	1469	68,2	-	0/9/27/28	0/3/3/3
2	4AC	2	319	2	-	0/11/29/30	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	4AC	2	1479	2	-	0/11/29/30	0/2/2/2
1	5MC	1	2203	1	-	0/7/25/26	0/2/2/2
2	4AC	2	303	2	-	0/11/29/30	0/2/2/2
2	4AC	2	718	2	-	0/11/29/30	0/2/2/2
2	4AC	2	286	2	-	0/11/29/30	0/2/2/2
2	UR3	2	1467	2	-	0/7/25/26	0/2/2/2
2	4AC	2	1028	2	-	0/11/29/30	0/2/2/2
1	4AC	1	2062	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2083	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2865	1	-	0/11/29/30	0/2/2/2
2	4AC	2	17	2	-	0/11/29/30	0/2/2/2
1	4AC	1	1554	1	-	0/11/29/30	0/2/2/2
1	4AC	1	641	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1962	1	-	0/11/29/30	0/2/2/2
1	5MC	1	2733	1	-	4/7/25/26	0/2/2/2
1	4AC	1	1755	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2642	1	-	0/11/29/30	0/2/2/2
2	OMC	2	846	2	-	0/9/27/28	0/2/2/2
1	4AC	1	2925	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1878	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1065	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2136	1	-	0/11/29/30	0/2/2/2
2	OMG	2	1069	2	-	1/9/27/28	0/3/3/3
2	OMU	2	787	2	-	6/9/27/28	0/2/2/2
1	4AC	1	1557	1	-	0/11/29/30	0/2/2/2
2	OMG	2	471	2	-	0/9/27/28	0/3/3/3
1	4AC	1	2966	1	-	0/11/29/30	0/2/2/2
1	4AC	1	22	1	-	0/11/29/30	0/2/2/2
1	4AC	1	451	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2329	1	-	0/11/29/30	0/2/2/2
1	5MC	1	2163	1	-	0/7/25/26	0/2/2/2
1	4AC	1	229	1	-	0/11/29/30	0/2/2/2
2	4AC	2	511	2	-	0/11/29/30	0/2/2/2
1	4AC	1	243	1	-	0/11/29/30	0/2/2/2
2	A2M	2	373	2	-	0/9/27/28	0/3/3/3
1	4AC	1	1934	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1695	1	-	0/11/29/30	0/2/2/2
1	5MC	1	2183	1	-	0/7/25/26	0/2/2/2
1	4AC	1	533	1	-	0/11/29/30	0/2/2/2
2	OMC	2	129	2	-	0/9/27/28	0/2/2/2
1	4AC	1	2027	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2992	1	-	2/11/29/30	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	4AC	2	731	2	-	0/11/29/30	0/2/2/2
2	OMC	2	773	2	-	0/9/27/28	0/2/2/2
1	OMG	1	328	1	-	0/9/27/28	0/3/3/3
1	OMG	1	789	1	-	2/9/27/28	0/3/3/3
1	4AC	1	694	1	-	0/11/29/30	0/2/2/2
2	LHH	2	1041	2	-	0/13/31/32	0/2/2/2
2	OMC	2	1040	2	-	0/9/27/28	0/2/2/2
2	LHH	2	250	2	-	1/13/31/32	0/2/2/2
1	4AC	1	1765	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1938	1	-	0/11/29/30	0/2/2/2
1	OMG	1	2147	1	-	3/9/27/28	0/3/3/3
1	OMG	1	2144	1	-	1/9/27/28	0/3/3/3
1	4AC	1	802	1	-	0/11/29/30	0/2/2/2
2	5MC	2	875	2	-	0/7/25/26	0/2/2/2
1	5MC	1	2093	1	-	0/7/25/26	0/2/2/2
1	4AC	1	1048	1	-	0/11/29/30	0/2/2/2
2	4AC	2	703	2	-	3/11/29/30	0/2/2/2
2	4AC	2	626	2	-	0/11/29/30	0/2/2/2
2	4AC	2	1184	2	-	0/11/29/30	0/2/2/2
2	5MC	2	1374	2	-	2/7/25/26	0/2/2/2
1	OMG	1	2678	1	-	1/9/27/28	0/3/3/3
1	4AC	1	2249	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1293	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2545	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2937	68,1	-	1/11/29/30	0/2/2/2
2	OMG	2	519	2	-	0/9/27/28	0/3/3/3
1	4AC	1	2608	1	-	3/11/29/30	0/2/2/2
1	4AC	1	2960	1	-	0/11/29/30	0/2/2/2
3	4AC	3	32	3	-	0/11/29/30	0/2/2/2
1	4AC	1	1667	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1460	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1621	1	-	0/11/29/30	0/2/2/2
2	4AC	2	851	2	-	0/11/29/30	0/2/2/2
1	4AC	1	835	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1550	1	-	0/11/29/30	0/2/2/2
1	4AC	1	3004	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2908	1	-	0/11/29/30	0/2/2/2
2	B8H	2	938	2	-	0/7/25/26	0/2/2/2
1	A2M	1	1055	1	-	1/9/27/28	0/3/3/3
1	4AC	1	60	1	-	0/11/29/30	0/2/2/2
1	OMG	1	923	68,1	-	2/9/27/28	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMU	2	20	2	-	6/9/27/28	0/2/2/2
1	4AC	1	2001	1	-	0/11/29/30	0/2/2/2
1	4AC	1	829	1	-	0/11/29/30	0/2/2/2
2	4AC	2	839	2	-	0/11/29/30	0/2/2/2
2	OMU	2	830	2	-	0/9/27/28	0/2/2/2
2	OMU	2	1380	2	-	2/9/27/28	0/2/2/2
2	4AC	2	379	2	-	0/11/29/30	0/2/2/2
2	OMG	2	873	2	-	1/9/27/28	0/3/3/3
2	MA6	2	1488	2	-	1/11/29/30	0/3/3/3
1	4AC	1	1873	1	-	0/11/29/30	0/2/2/2
2	OMG	2	680	2	-	1/9/27/28	0/3/3/3
1	4AC	1	91	1	-	0/11/29/30	0/2/2/2
2	5MC	2	1496	2	-	0/7/25/26	0/2/2/2
1	4AC	1	161	1	-	0/11/29/30	0/2/2/2
2	5MC	2	1505	2	-	2/7/25/26	0/2/2/2
2	4AC	2	1239	2	-	0/11/29/30	0/2/2/2
2	4AC	2	848	2	-	0/11/29/30	0/2/2/2
2	4AC	2	957	2	-	0/11/29/30	0/2/2/2
2	OMG	2	657	2	-	0/9/27/28	0/3/3/3
2	4AC	2	828	2	-	0/11/29/30	0/2/2/2
2	5MC	2	1202	2	-	1/7/25/26	0/2/2/2
1	4AC	1	357	1	-	0/11/29/30	0/2/2/2
2	OMG	2	934	2	-	2/9/27/28	0/3/3/3
2	4AC	2	751	2	-	2/11/29/30	0/2/2/2
1	4AC	1	1780	1	-	0/11/29/30	0/2/2/2
2	4AC	2	1147	2	-	0/11/29/30	0/2/2/2
2	4AC	2	394	2	-	0/11/29/30	0/2/2/2
2	OMG	2	467	2	-	0/9/27/28	0/3/3/3
1	4AC	1	1867	1	-	0/11/29/30	0/2/2/2
2	4AC	2	479	2	-	0/11/29/30	0/2/2/2
1	4AC	1	1222	68,1	-	0/11/29/30	0/2/2/2
2	4AC	2	636	2	-	2/11/29/30	0/2/2/2
2	5MC	2	1498	2	-	5/7/25/26	0/2/2/2
2	OMC	2	1376	2	-	1/9/27/28	0/2/2/2
1	4AC	1	981	1	-	0/11/29/30	0/2/2/2
1	4AC	1	314	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1243	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1662	1	-	0/11/29/30	0/2/2/2
1	5MC	1	2198	1	-	0/7/25/26	0/2/2/2
1	4AC	1	2548	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2570	1	-	0/11/29/30	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	4AC	1	1617	1	-	0/11/29/30	0/2/2/2
2	4AC	2	546	2	-	0/11/29/30	0/2/2/2
1	4AC	1	2495	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2718	1	-	0/11/29/30	0/2/2/2
1	4AC	1	211	1	-	0/11/29/30	0/2/2/2
2	4AC	2	53	2	-	0/11/29/30	0/2/2/2
1	4AC	1	136	1	-	0/11/29/30	0/2/2/2
1	LHH	1	616	1	-	0/13/31/32	0/2/2/2
2	OMG	2	913	2	-	1/9/27/28	0/3/3/3
2	5MC	2	1025	2	-	0/7/25/26	0/2/2/2
1	A2M	1	2173	1	-	0/9/27/28	0/3/3/3
1	OMC	1	615	1	-	1/9/27/28	0/2/2/2
1	4AC	1	458	1	-	0/11/29/30	0/2/2/2
2	5MC	2	693	2	-	0/7/25/26	0/2/2/2
1	OMC	1	1948	1	-	0/9/27/28	0/2/2/2

The worst 5 of 331 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1469	6MZ	C5-C4	4.66	1.47	1.39
2	2	1488	MA6	C5-C4	4.60	1.47	1.39
2	2	1487	MA6	C5-C4	4.54	1.47	1.39
1	1	1055	A2M	C5-C4	4.44	1.47	1.39
2	2	373	A2M	C5-C4	4.44	1.47	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	703	4AC	N4-C4-N3	8.33	127.82	113.85
2	2	703	4AC	C5-C4-N4	-7.74	109.48	122.92
2	2	657	OMG	C5-C4-N3	-6.66	117.66	128.46
2	2	680	OMG	C5-C4-N3	-6.57	117.81	128.46
1	1	1055	A2M	C5-C4-N3	-6.38	118.42	126.75

There are no chirality outliers.

5 of 65 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	2147	OMG	C3'-C4'-C5'-O5'
1	1	2585	4AC	O4'-C1'-N1-C2
1	1	2585	4AC	O4'-C1'-N1-C6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
1	1	2608	4AC	O4'-C1'-N1-C2
1	1	2608	4AC	O4'-C1'-N1-C6

There are no ring outliers.

88 monomers are involved in 128 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	774	OMU	2	0
1	1	922	4AC	1	0
1	1	2287	4AC	4	0
2	2	1177	OMU	1	0
1	1	2585	4AC	3	0
1	1	1068	4AC	1	0
2	2	1233	4AC	1	0
1	1	1594	4AC	1	0
2	2	1469	6MZ	1	0
2	2	319	4AC	1	0
2	2	1479	4AC	1	0
2	2	303	4AC	1	0
2	2	718	4AC	1	0
2	2	1028	4AC	1	0
1	1	2062	4AC	1	0
1	1	2865	4AC	1	0
2	2	17	4AC	1	0
1	1	1755	4AC	2	0
1	1	2925	4AC	1	0
1	1	1878	4AC	1	0
1	1	1065	4AC	2	0
1	1	2136	4AC	1	0
2	2	1069	OMG	1	0
2	2	471	OMG	1	0
1	1	22	4AC	1	0
1	1	451	4AC	3	0
1	1	2329	4AC	1	0
2	2	511	4AC	1	0
1	1	243	4AC	1	0
2	2	373	A2M	1	0
1	1	1934	4AC	2	0
1	1	533	4AC	1	0
2	2	129	OMC	1	0
1	1	2027	4AC	1	0
1	1	2992	4AC	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	731	4AC	1	0
2	2	773	OMC	1	0
1	1	789	OMG	1	0
1	1	1765	4AC	1	0
1	1	2144	OMG	1	0
1	1	802	4AC	2	0
1	1	1048	4AC	2	0
2	2	703	4AC	6	0
2	2	626	4AC	2	0
2	2	1184	4AC	2	0
1	1	2678	OMG	1	0
1	1	2249	4AC	2	0
1	1	2545	4AC	1	0
2	2	519	OMG	2	0
1	1	2608	4AC	3	0
3	3	32	4AC	1	0
1	1	1667	4AC	4	0
1	1	1460	4AC	1	0
2	2	851	4AC	2	0
1	1	835	4AC	1	0
1	1	1550	4AC	2	0
1	1	3004	4AC	1	0
1	1	60	4AC	1	0
1	1	2001	4AC	1	0
2	2	1380	OMU	2	0
2	2	680	OMG	1	0
1	1	91	4AC	1	0
2	2	1505	5MC	1	0
2	2	957	4AC	1	0
2	2	657	OMG	3	0
2	2	1202	5MC	2	0
1	1	357	4AC	1	0
2	2	934	OMG	2	0
1	1	1780	4AC	1	0
2	2	1147	4AC	1	0
2	2	394	4AC	2	0
1	1	1867	4AC	1	0
2	2	479	4AC	2	0
2	2	636	4AC	4	0
2	2	1376	OMC	1	0
1	1	1662	4AC	1	0
1	1	2198	5MC	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	2548	4AC	1	0
1	1	2570	4AC	1	0
1	1	1617	4AC	3	0
2	2	546	4AC	3	0
1	1	2718	4AC	1	0
1	1	211	4AC	1	0
2	2	53	4AC	1	0
2	2	913	OMG	1	0
2	2	1025	5MC	1	0
1	1	615	OMC	1	0
1	1	458	4AC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 253 ligands modelled in this entry, 253 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
1	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	107:G	O3'	112:A	P	12.79

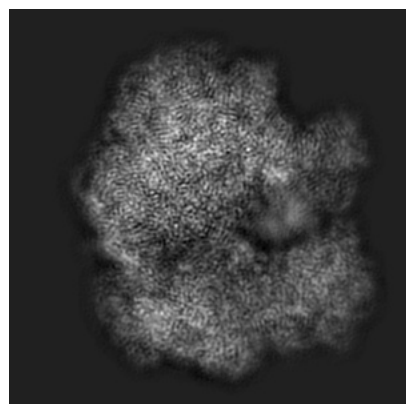
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55136. These allow visual inspection of the internal detail of the map and identification of artifacts.

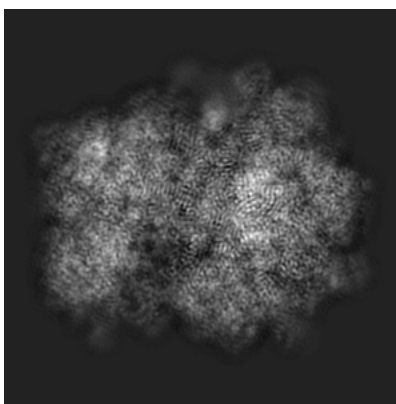
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

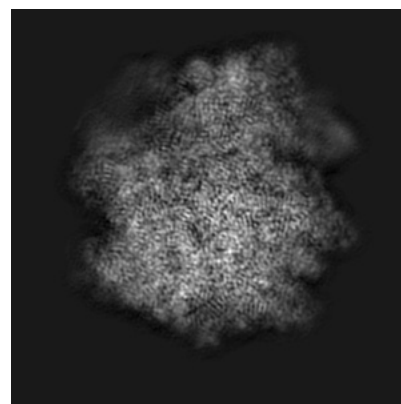
6.1.1 Primary map



X

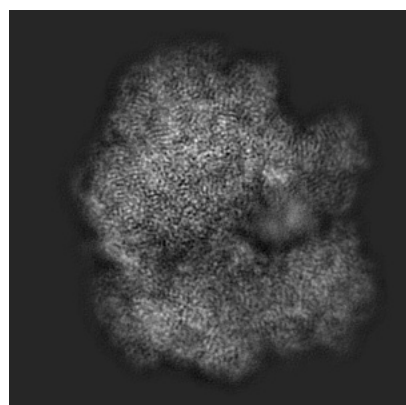


Y

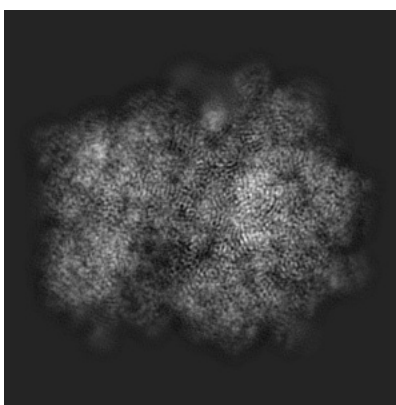


Z

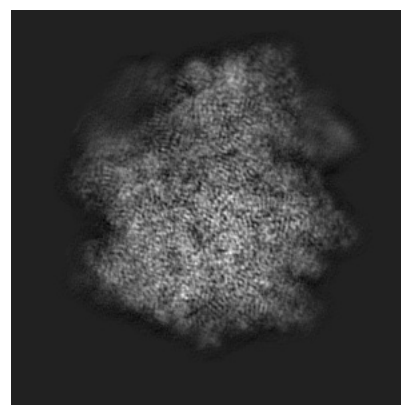
6.1.2 Raw map



X



Y

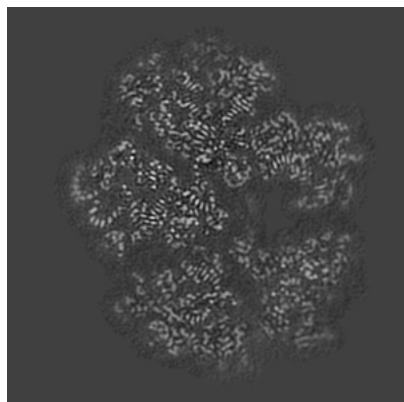


Z

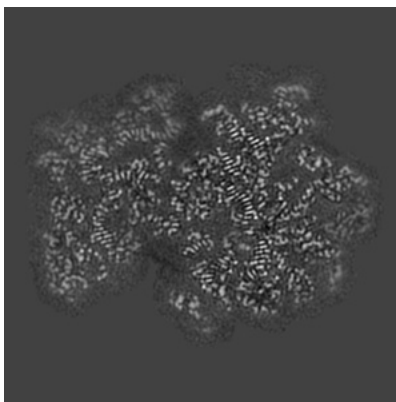
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

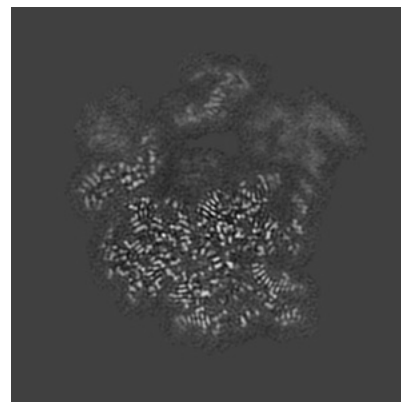
6.2.1 Primary map



X Index: 180

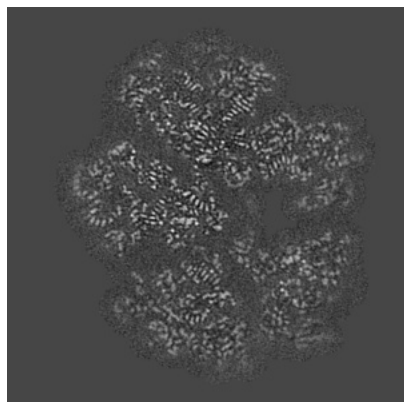


Y Index: 180

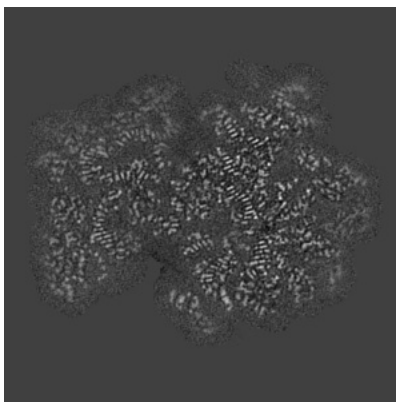


Z Index: 180

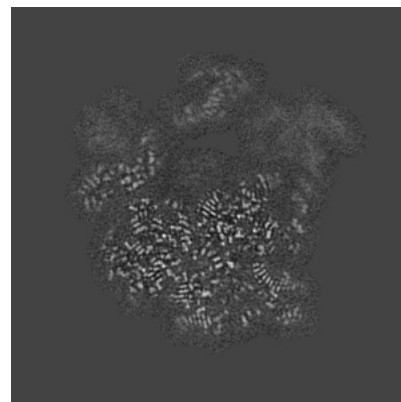
6.2.2 Raw map



X Index: 180



Y Index: 180

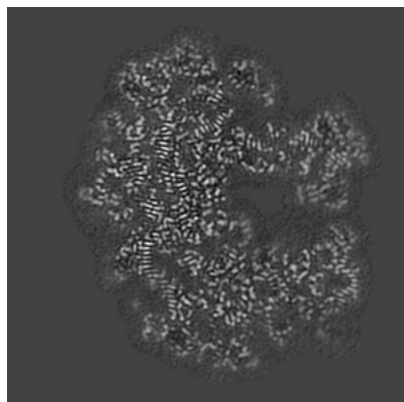


Z Index: 180

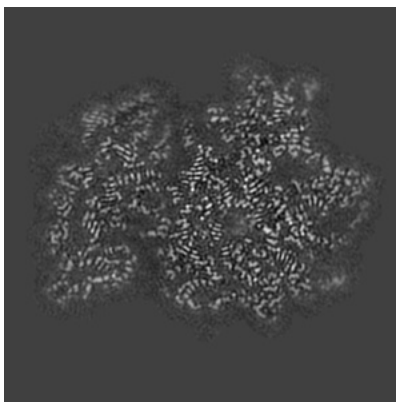
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

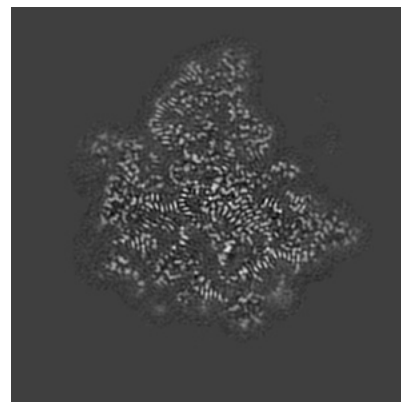
6.3.1 Primary map



X Index: 196

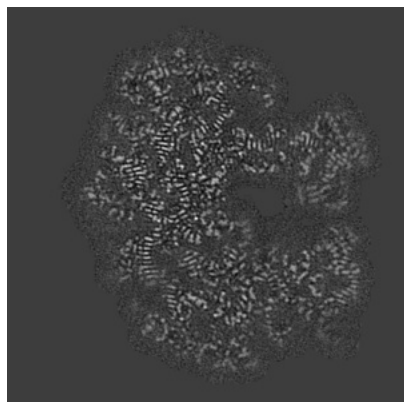


Y Index: 170

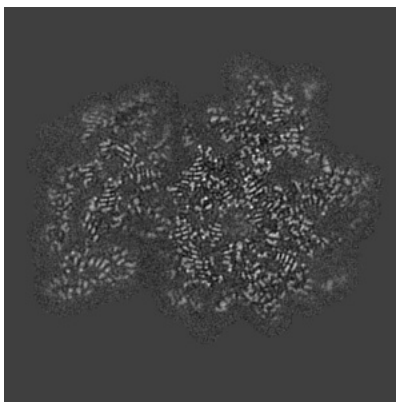


Z Index: 232

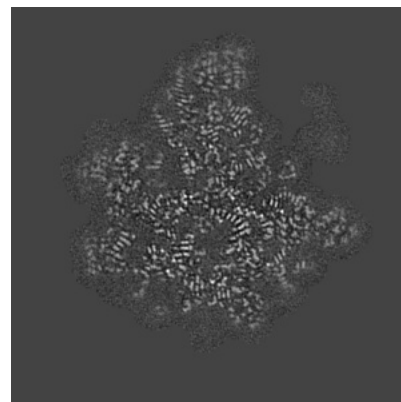
6.3.2 Raw map



X Index: 195



Y Index: 171

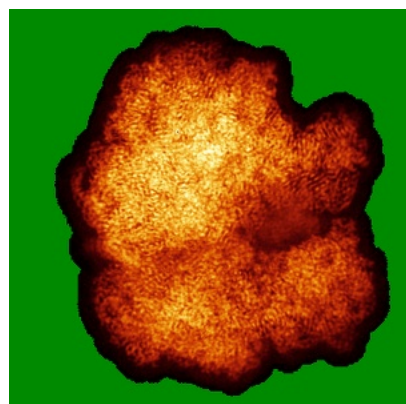


Z Index: 224

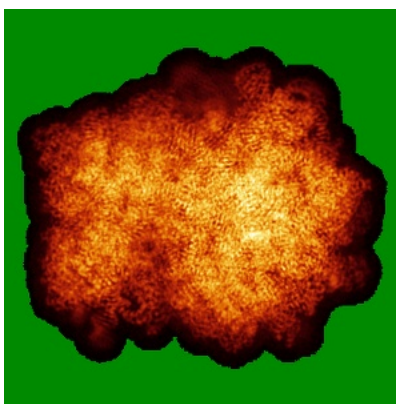
The images above show the largest variance slices of the map in three orthogonal directions.

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

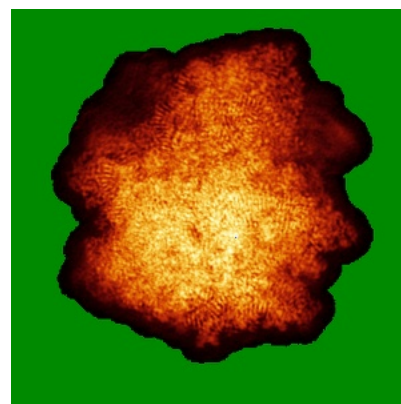
6.4.1 Primary map



X

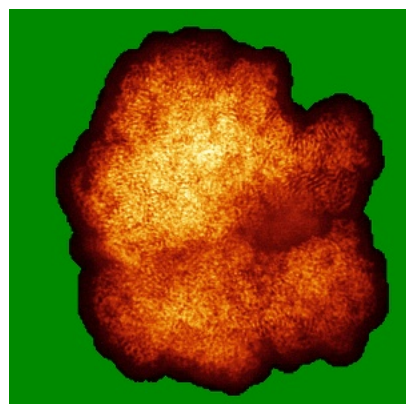


Y

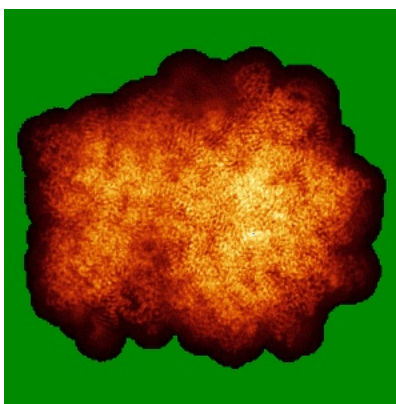


Z

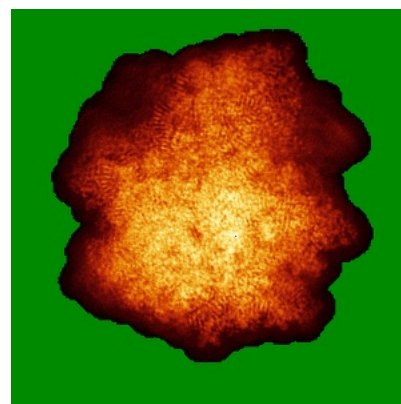
6.4.2 Raw map



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](#)

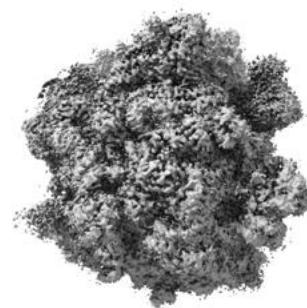
6.5.1 Primary map



X



Y



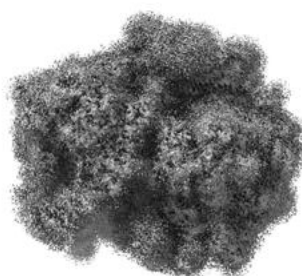
Z

The images above show the 3D surface view of the map at the recommended contour level 0.0009. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

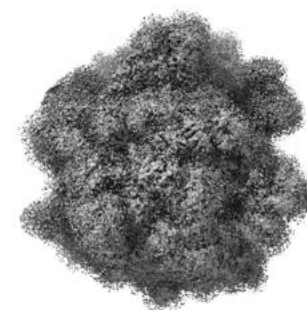
6.5.2 Raw map



X



Y



Z

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.

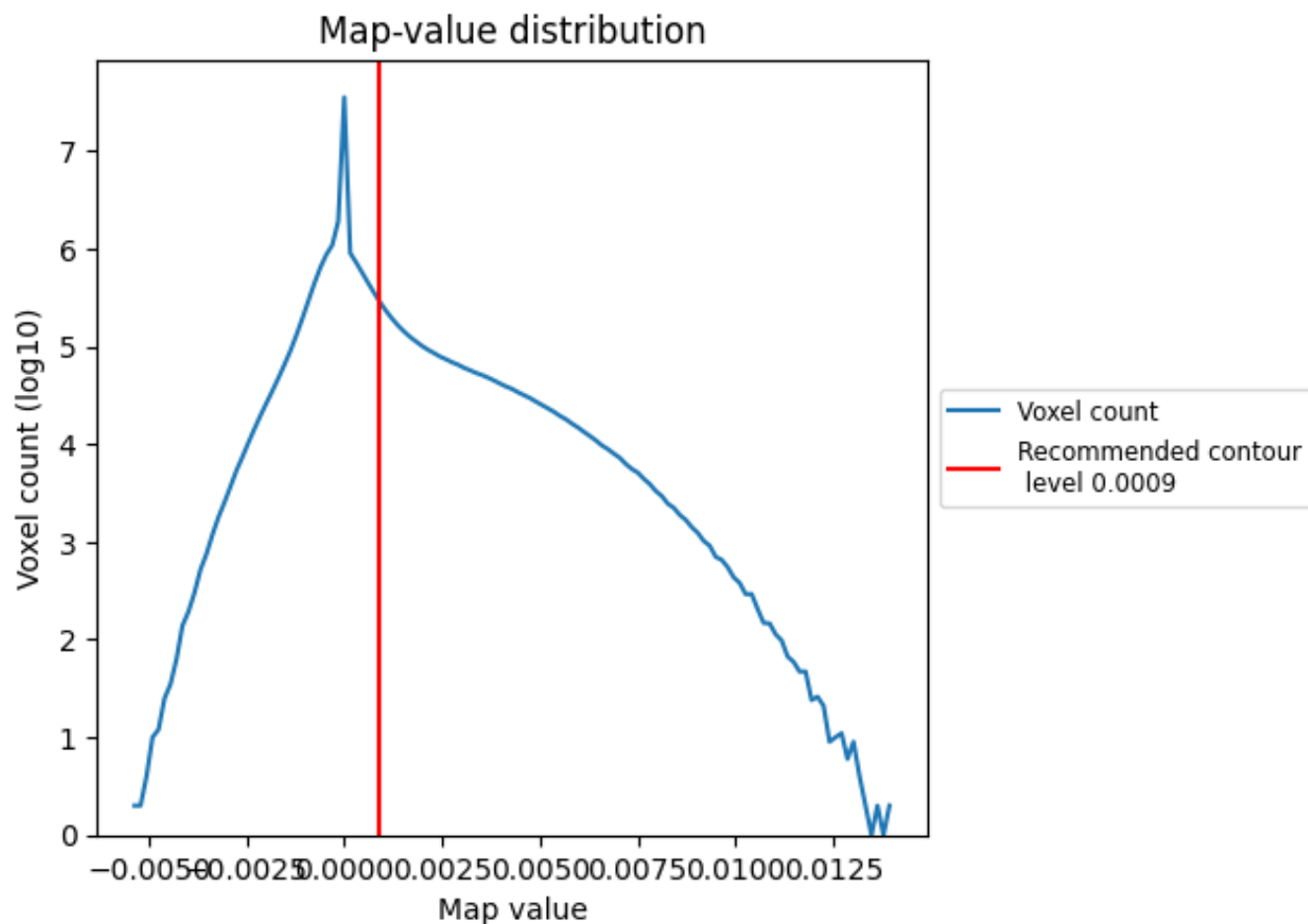
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

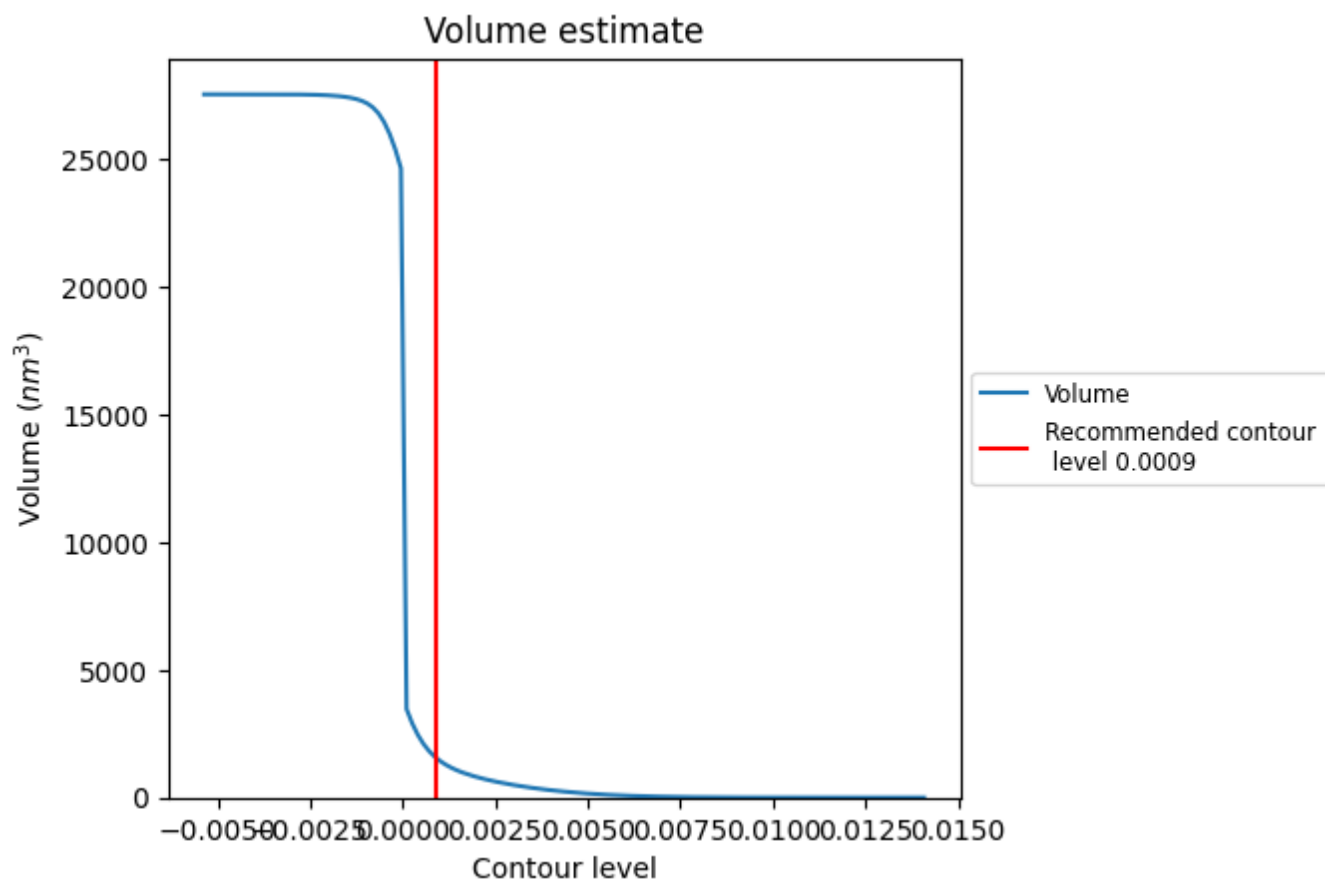
This section contains the results of statistical analysis of the map.

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.

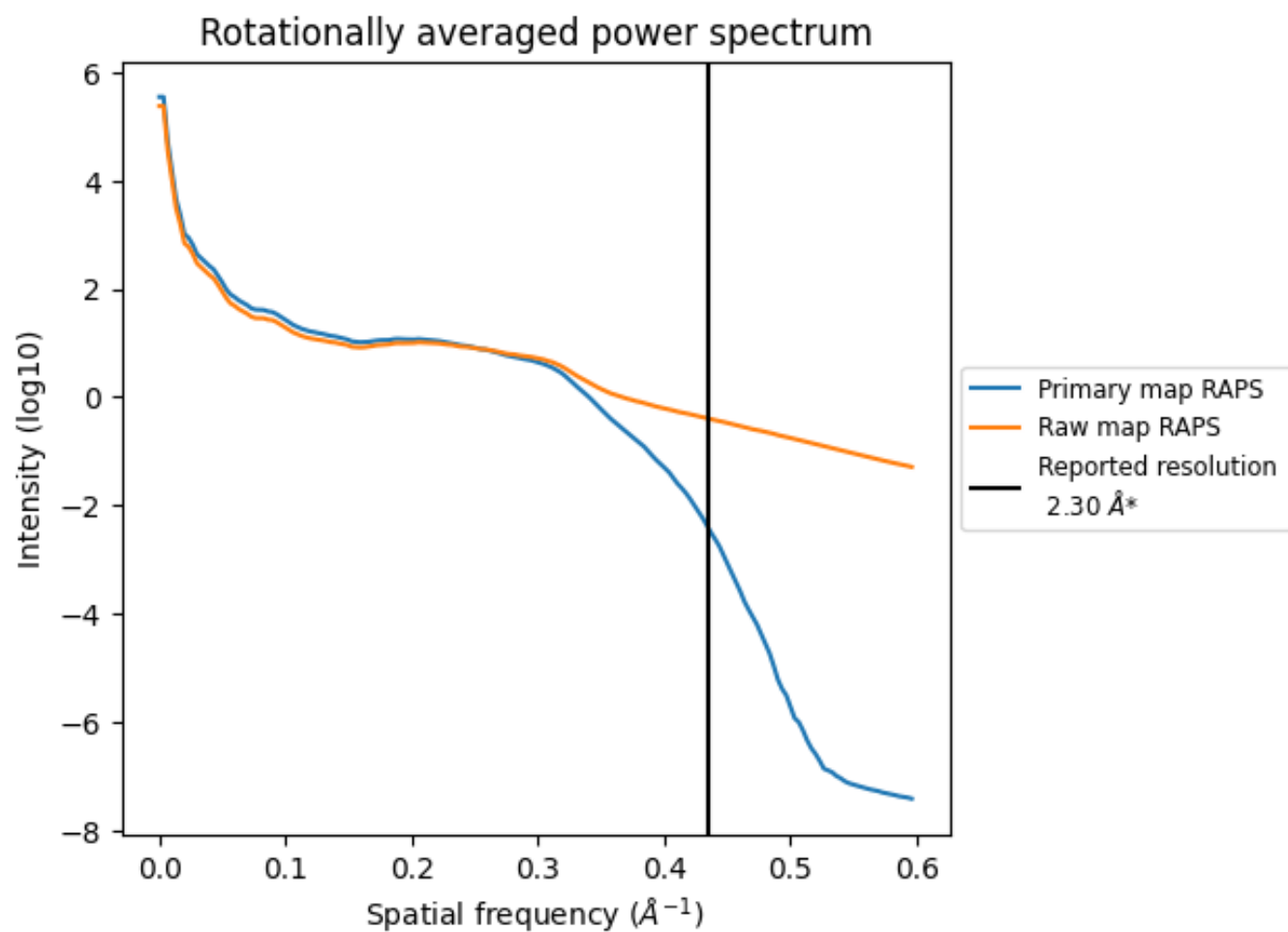
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1563 nm^3 ; this corresponds to an approximate mass of 1412 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 ⓘ

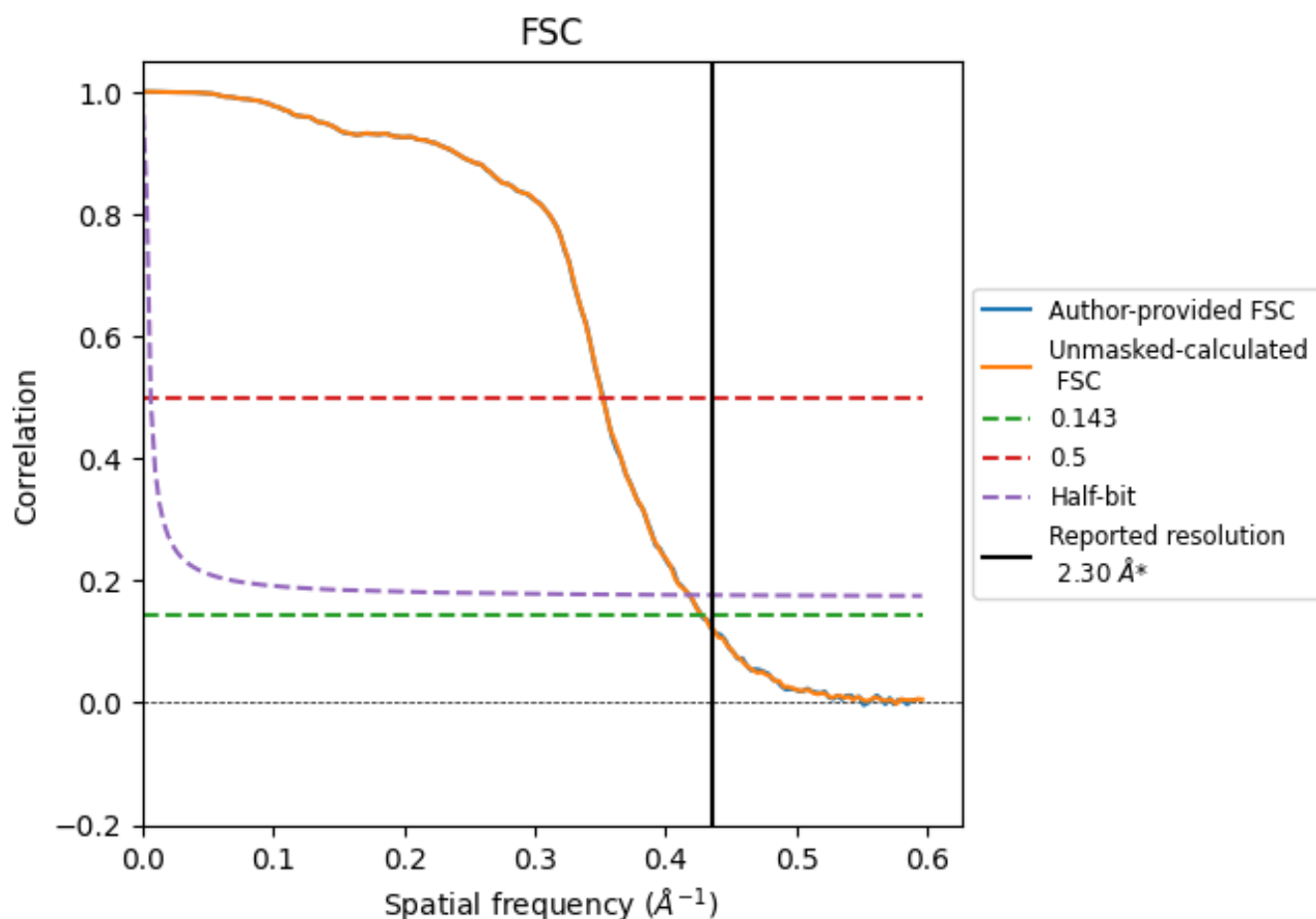


*Reported resolution corresponds to spatial frequency of 0.435 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.435 Å⁻¹

8.2 Resolution estimates [i](#)

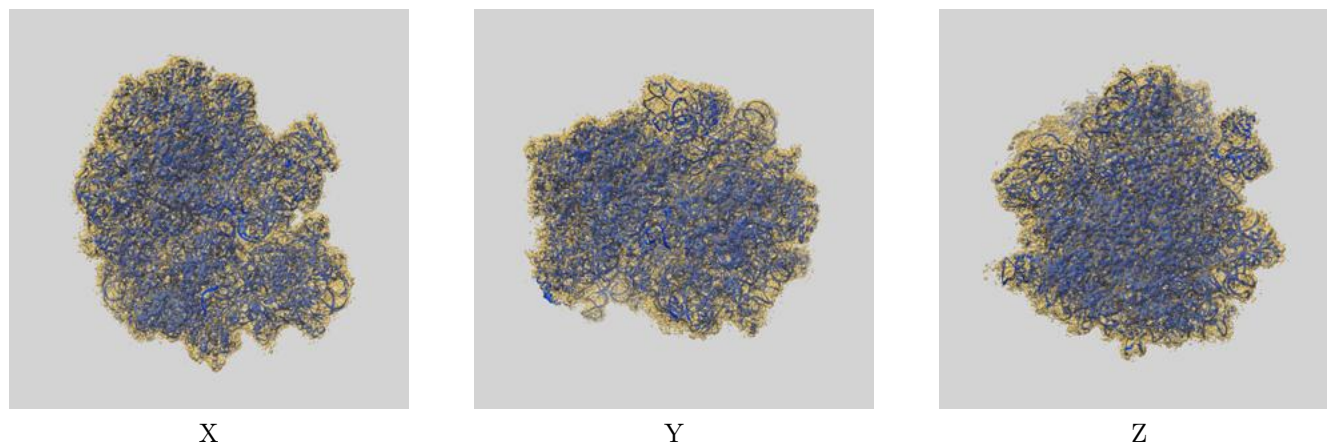
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.30	-	-
Author-provided FSC curve	2.34	2.84	2.39
Unmasked-calculated*	2.34	2.84	2.39

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

9 Map-model fit [i](#)

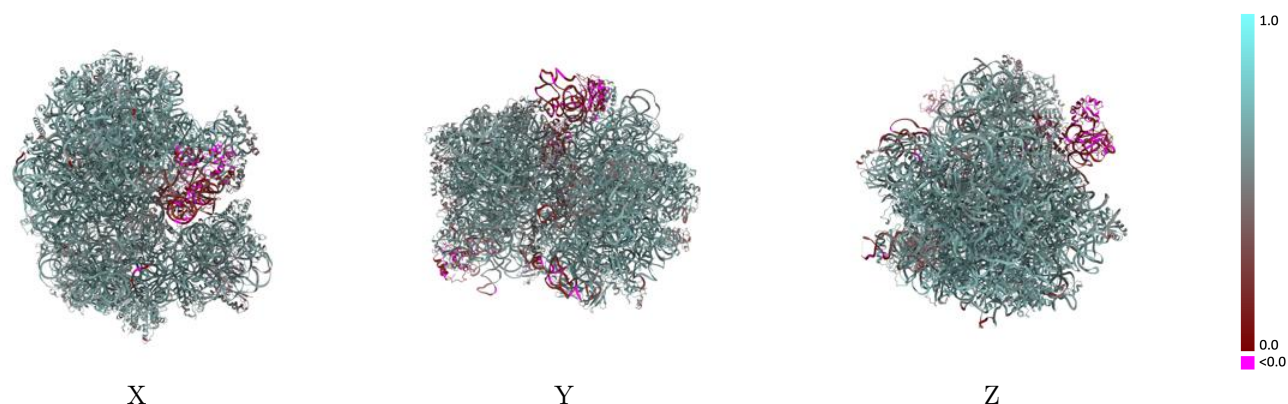
This section contains information regarding the fit between EMDB map EMD-55136 and PDB model 9SRB. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

9.1 Map-model overlay [i](#)



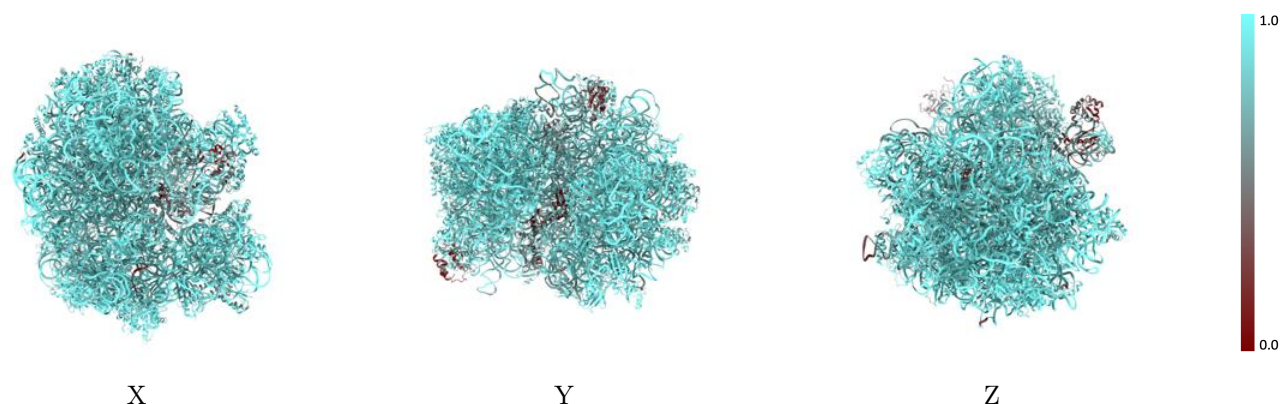
The images above show the 3D surface view of the map at the recommended contour level 0.0009 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



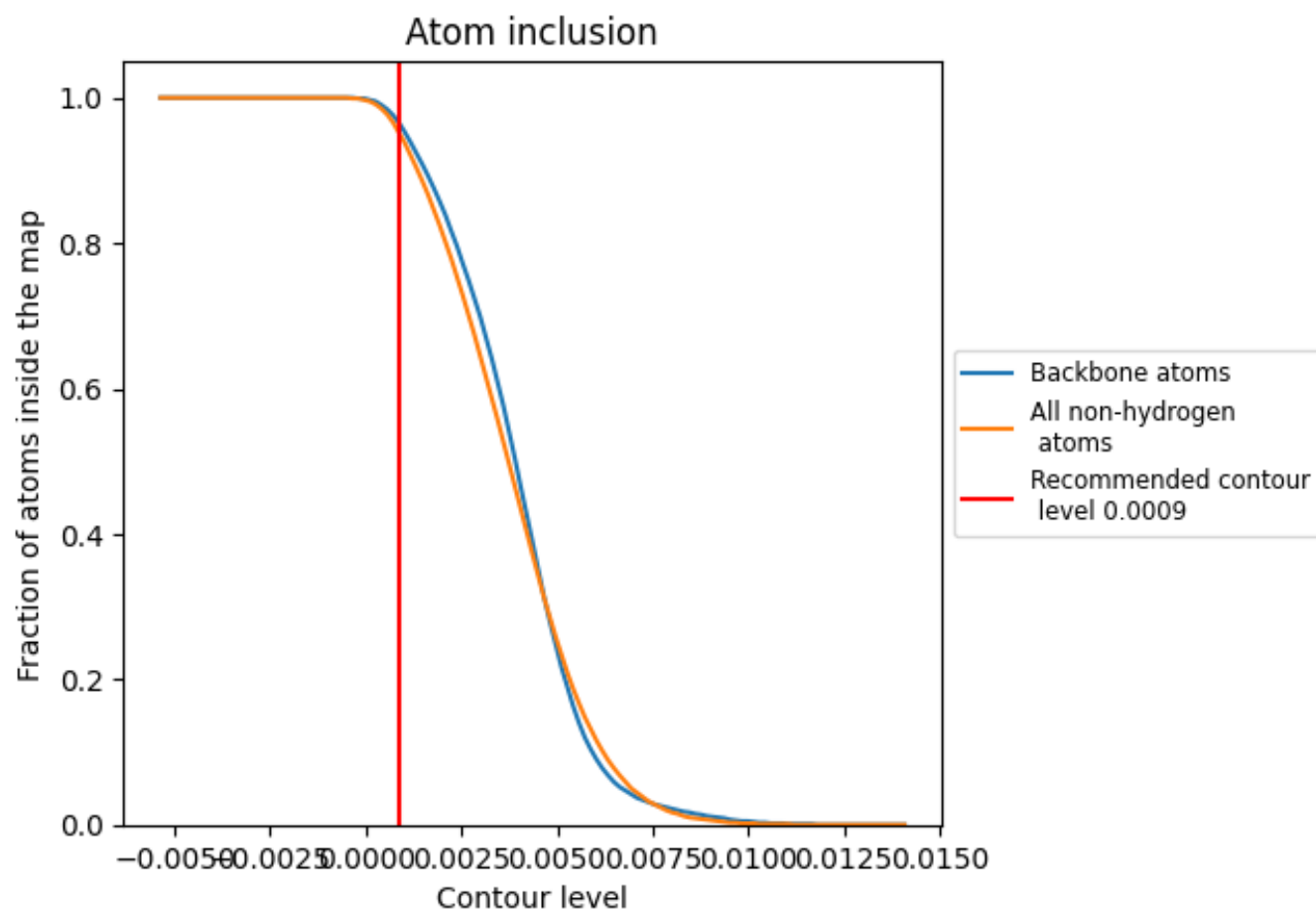
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0009).

9.4 Atom inclusion ⓘ



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.0009) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9490	 0.5840
1	 0.9750	 0.6010
2	 0.9880	 0.6010
3	 0.9980	 0.6030
A	 0.3810	 0.4020
A0	 0.9500	 0.6260
A3	 0.3100	 0.1270
AA	 0.8820	 0.5190
AB	 0.9620	 0.5690
AC	 0.9500	 0.5650
AD	 0.9590	 0.5870
AE	 0.9760	 0.5950
AF	 0.9700	 0.5980
AG	 0.9250	 0.5570
AH	 0.9530	 0.5770
AI	 0.9850	 0.6250
AJ	 0.9590	 0.6080
AK	 0.9590	 0.5750
AL	 0.8780	 0.5100
AM	 0.9070	 0.5590
AN	 0.9480	 0.5950
AO	 0.9440	 0.5750
AP	 0.9520	 0.5860
AQ	 0.9380	 0.5720
AR	 0.9630	 0.6110
AS	 0.9660	 0.5390
AT	 0.9260	 0.5590
AU	 0.9710	 0.5810
AV	 0.9420	 0.5670
AW	 0.9520	 0.5400
AX	 0.9490	 0.5740
AY	 0.3810	 0.1070
AZ	 0.9140	 0.5370
B4	 0.8290	 0.4190
B5	 0.9820	 0.5940



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
B6	 0.7840	 0.5600
BA	 0.4530	 0.0690
BB	 0.9750	 0.6470
BC	 0.9750	 0.6440
BD	 0.9850	 0.6360
BE	 0.9040	 0.5040
BF	 0.9690	 0.5960
BG	 0.9600	 0.5830
BI	 0.9750	 0.6440
BJ	 0.9620	 0.6480
BK	 0.9680	 0.5620
BL	 0.9570	 0.6090
BM	 0.9920	 0.6560
BN	 0.9540	 0.6090
BO	 0.9610	 0.5600
BP	 0.9820	 0.6390
BQ	 0.9770	 0.6350
BR	 0.9820	 0.6400
BS	 0.9870	 0.6420
BT	 0.9810	 0.6220
BU	 0.9750	 0.6220
BV	 0.9820	 0.6410
BW	 0.9100	 0.5680
BY	 0.9850	 0.6340
BZ	 0.9460	 0.5690
Ba	 0.9630	 0.6100
Bb	 0.9800	 0.6450
Bc	 0.9750	 0.6410
Bd	 0.9770	 0.6280
Be	 0.9920	 0.6560
Bf	 0.9980	 0.6530
Bg	 0.9890	 0.6190
Bi	 0.9700	 0.6410
Bj	 0.9590	 0.6230
Bk	 0.9670	 0.6060
Bl	 0.9810	 0.5890
H	 0.6550	 0.3180