



wwPDB EM Validation Summary Report ⓘ

Aug 3, 2026 – 01:46 pm BST

PDB ID : 9SRC / pdb_00009src
EMDB ID : EMD-55137
Title : Cryo-EM structure of P. abyssi 70S ribosome in complex with hibernation factor HibA in PTC conformation
Authors : Madru, C.M.; Bourgeois, G.B.; Mechulam, Y.M.; Schmitt, E.S.
Deposited on : 2025-09-24
Resolution : 2.10 Å(reported)
Based on initial model : .

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:

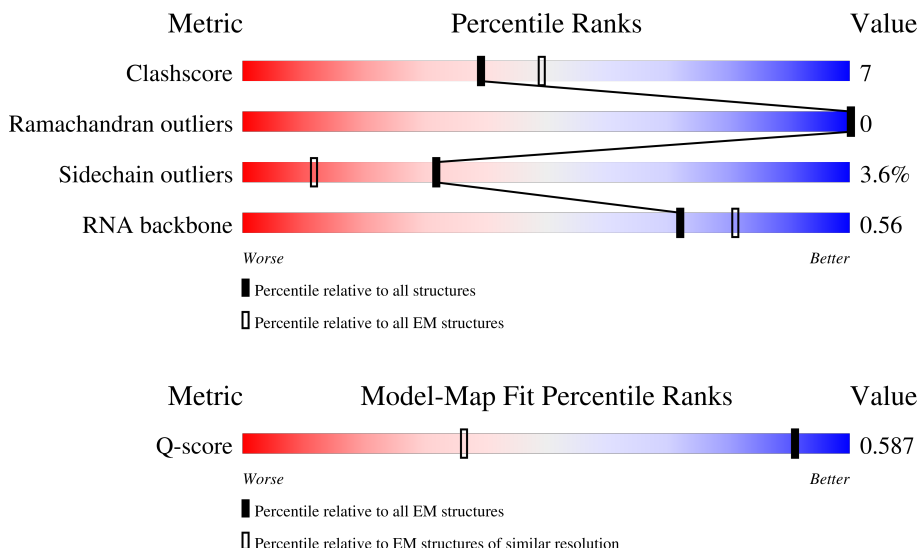
EMDB validation analysis : 0.0.1.dev133
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal 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 2.10 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	2317 (1.60 - 2.60)

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.

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1	1	3018	
2	2	1512	
3	3	128	

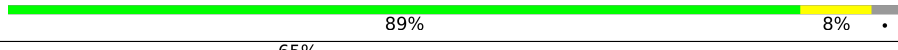
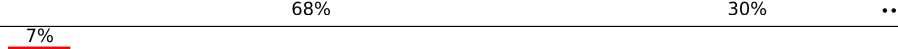
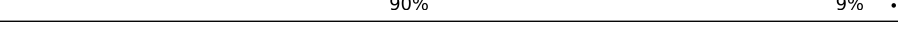
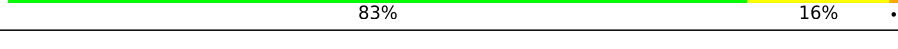
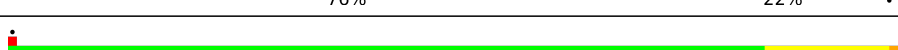
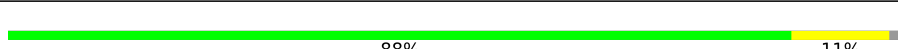
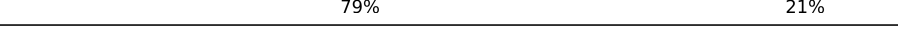
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Mol	Chain	Length	Quality of chain
4	H	392	
5	AA	199	
6	AB	202	
7	AC	63	
8	AD	180	
9	AE	243	
10	AF	236	
11	AG	125	
12	AH	215	
13	AI	130	
14	AJ	127	
15	AK	135	
16	AL	102	
17	AM	137	
18	AN	147	
19	AP	56	
20	AQ	158	
21	AR	113	
22	AS	67	
23	AU	150	
24	AV	99	
24	B6	99	
25	AW	65	
26	AX	71	
27	AY	51	

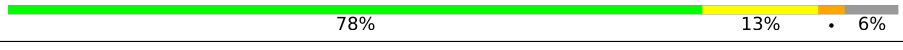
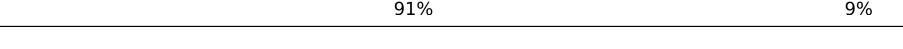
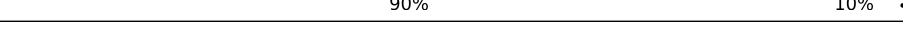
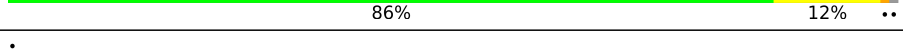
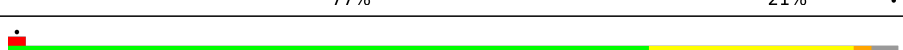
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Mol	Chain	Length	Quality of chain
28	AZ	210	
29	A0	37	
30	A3	123	
30	B4	123	
30	BG	123	
31	AT	132	
32	AO	148	
33	BB	239	
34	BY	155	
35	BO	203	
36	BC	361	
37	B5	82	
37	BK	82	
38	BL	147	
39	Bf	51	
40	BU	121	
41	Bb	130	
42	Be	62	
43	BE	188	
44	Ba	94	
45	BT	86	
46	BW	68	
47	Bi	83	
48	BI	142	
49	BR	97	

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Mol	Chain	Length	Quality of chain
50	BQ	151	
51	BV	67	
52	Bj	94	
53	BD	255	
54	BF	184	
55	BZ	99	
56	BP	120	
57	BM	194	
58	BS	155	
59	Bd	91	
60	BN	181	
61	Bg	51	
62	Bc	87	
63	BJ	141	
64	Bl	77	
65	Bk	65	

2 Entry composition [i](#)

There are 67 unique types of molecules in this entry. The entry contains 170465 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 Dehydrogenase.

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

- Molecule 5 is a protein called 30S ribosomal protein S3Ae.

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

- Molecule 6 is a protein called 30S ribosomal protein S2.

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

- Molecule 7 is a protein called Zn-ribbon RNA-binding protein involved in translation.

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

- Molecule 8 is a protein called 30S ribosomal protein S4.

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

- Molecule 9 is a protein called 30S ribosomal protein S4e.

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

- Molecule 10 is a protein called 30S ribosomal protein S5.

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

- Molecule 11 is a protein called 30S ribosomal protein S6e.

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

- Molecule 12 is a protein called 30S ribosomal protein S7.

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

- Molecule 13 is a protein called 30S ribosomal protein S8.

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

- Molecule 14 is a protein called 30S ribosomal protein S8e.

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

- Molecule 15 is a protein called 30S ribosomal protein S9.

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

- Molecule 16 is a protein called 30S ribosomal protein S10.

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

- Molecule 17 is a protein called 30S ribosomal protein S11.

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

- Molecule 18 is a protein called 30S ribosomal protein S12.

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

- Molecule 19 is a protein called 30S ribosomal protein S14 type Z.

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

- Molecule 20 is a protein called 30S ribosomal protein S15.

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

- Molecule 21 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AR	107	Total	C	N	O	S	0	0
			884	562	172	147	3		

- Molecule 22 is a protein called 30S ribosomal protein S17e.

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

- Molecule 23 is a protein called 30S ribosomal protein S19e.

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

- Molecule 24 is a protein called 30S ribosomal protein S24e.

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

- Molecule 25 is a protein called 30S ribosomal protein S27e.

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

- Molecule 26 is a protein called 30S ribosomal protein S28e.

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

- Molecule 27 is a protein called 30S ribosomal protein S27ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AY	49	Total	C	N	O	S	0	0
			400	257	76	62	5		

- Molecule 28 is a protein called 30S ribosomal protein S3.

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

- Molecule 29 is a protein called Small ribosomal subunit protein eS32.

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

- Molecule 30 is a protein called 50S ribosomal protein L7Ae.

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

- Molecule 31 is a protein called 30S ribosomal protein S19.

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

- Molecule 32 is a protein called 30S ribosomal protein S13.

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

- Molecule 33 is a protein called Large ribosomal subunit protein uL2.

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

- Molecule 34 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 35 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 36 is a protein called Large ribosomal subunit protein uL3.

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

- Molecule 37 is a protein called Large ribosomal subunit protein eL14.

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

- Molecule 38 is a protein called Large ribosomal subunit protein uL15.

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

- Molecule 39 is a protein called Large ribosomal subunit protein eL39.

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

- Molecule 40 is a protein called Large ribosomal subunit protein uL24.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL32.

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

- Molecule 42 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 43 is a protein called Large ribosomal subunit protein uL5.

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

- Molecule 44 is a protein called Large ribosomal subunit protein eL31.

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

- Molecule 45 is a protein called Large ribosomal subunit protein uL23.

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

- Molecule 46 is a protein called Large ribosomal subunit protein uL29.

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

- Molecule 47 is a protein called Large ribosomal subunit protein eL43.

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

- Molecule 48 is a protein called Large ribosomal subunit protein uL13.

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

- Molecule 49 is a protein called Large ribosomal subunit protein eL21.

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

- Molecule 50 is a protein called Large ribosomal subunit protein eL19.

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

- Molecule 51 is a protein called Large ribosomal subunit protein eL24.

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

- Molecule 52 is a protein called Large ribosomal subunit protein eL42.

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

- Molecule 53 is a protein called Large ribosomal subunit protein uL4.

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

- Molecule 54 is a protein called Large ribosomal subunit protein uL6.

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

- Molecule 55 is a protein called Large ribosomal subunit protein eL30.

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

- Molecule 56 is a protein called Large ribosomal subunit protein eL18.

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

- Molecule 57 is a protein called Large ribosomal subunit protein eL15.

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

- Molecule 58 is a protein called Large ribosomal subunit protein uL22.

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

- Molecule 59 is a protein called Large ribosomal subunit protein eL34.

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

- Molecule 60 is a protein called Large ribosomal subunit protein uL16.

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

- Molecule 61 is a protein called Large ribosomal subunit protein eL40.

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

- Molecule 62 is a protein called Large ribosomal subunit protein eL33.

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

- Molecule 63 is a protein called Large ribosomal subunit protein uL14.

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

- Molecule 64 is a protein called Large ribosomal subunit protein eL20.

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

- Molecule 65 is a protein called C2H2-type domain-containing protein.

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

- Molecule 66 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
66	1	166	Total	Mg	0
			166	166	
66	2	68	Total	Mg	0
			68	68	
66	3	1	Total	Mg	0
			1	1	
66	AK	1	Total	Mg	0
			1	1	
66	AN	1	Total	Mg	0
			1	1	
66	AR	1	Total	Mg	0
			1	1	
66	BB	2	Total	Mg	0
			2	2	
66	Bb	1	Total	Mg	0
			1	1	
66	BD	1	Total	Mg	0
			1	1	
66	BM	1	Total	Mg	0
			1	1	
66	BS	1	Total	Mg	0
			1	1	

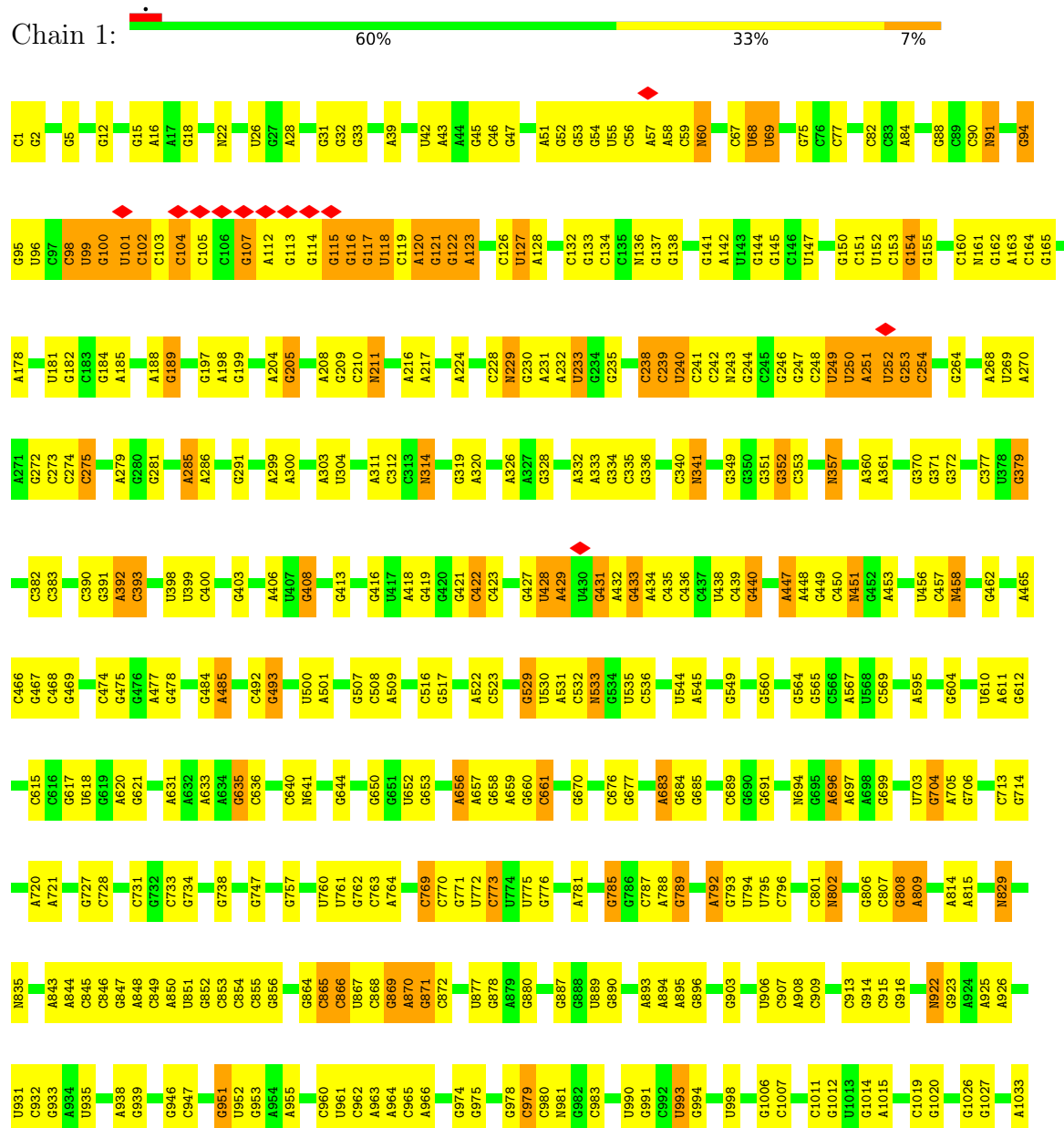
- Molecule 67 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

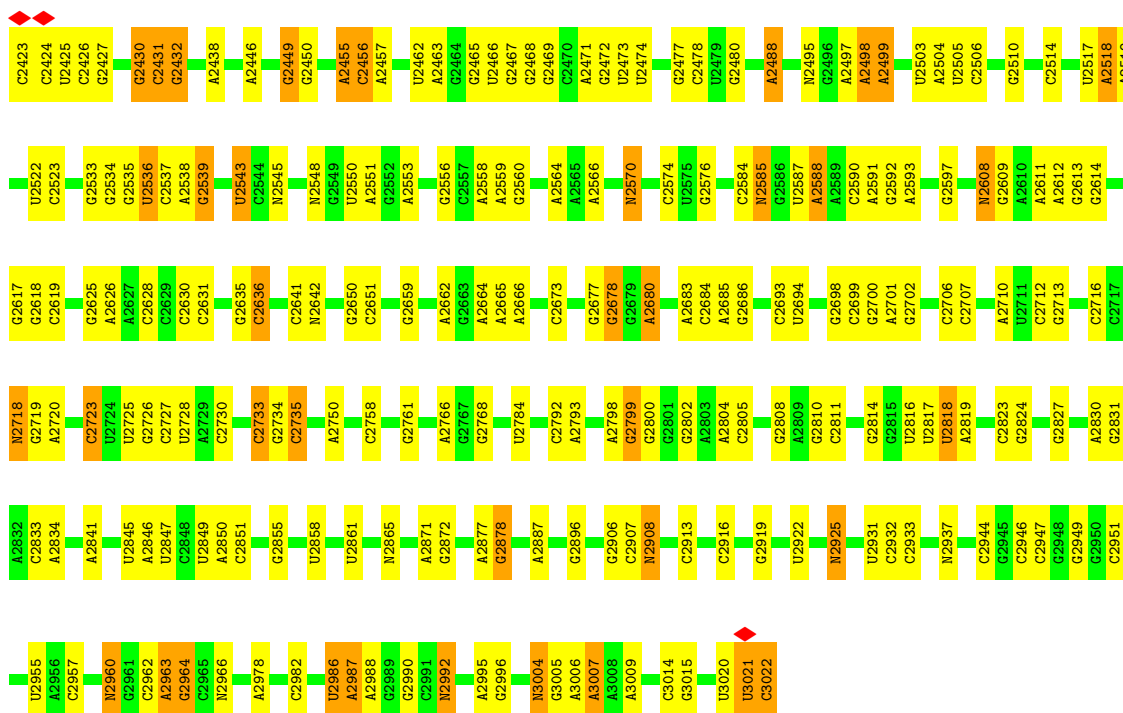
3 Residue-property plots

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

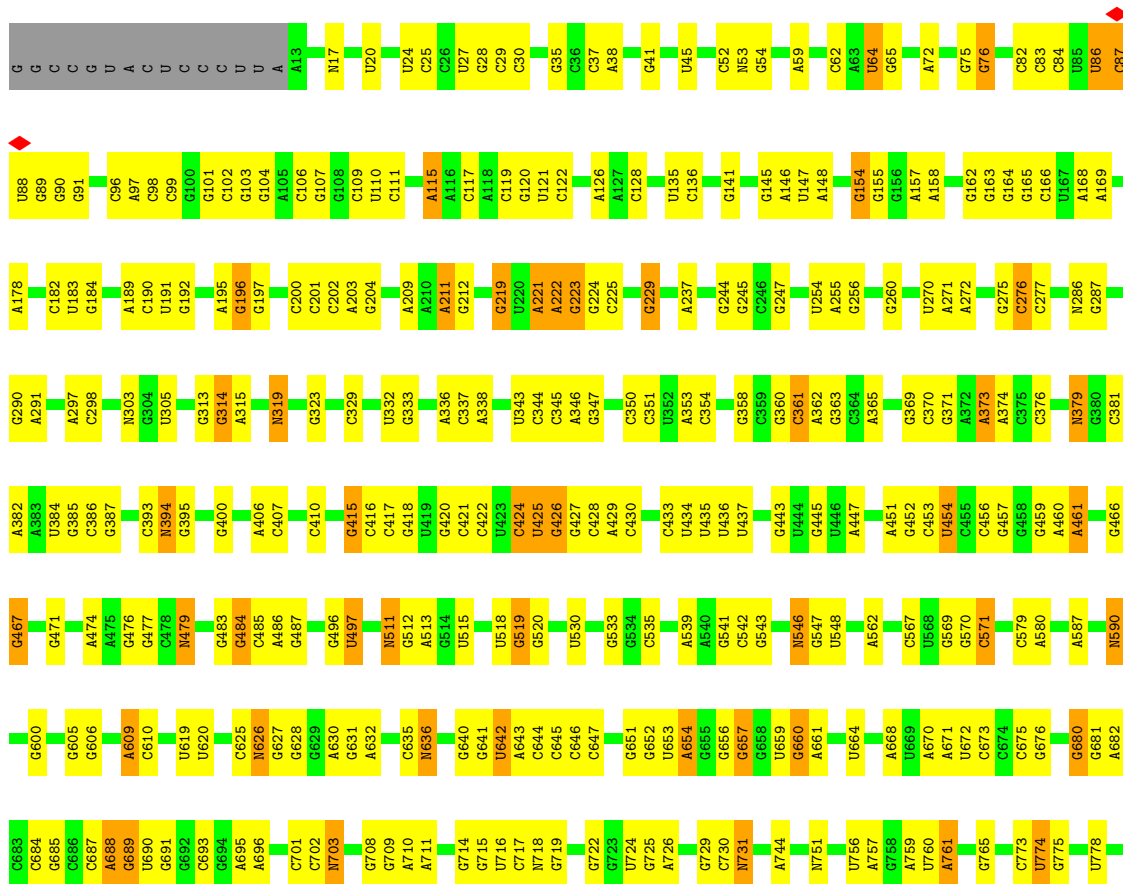


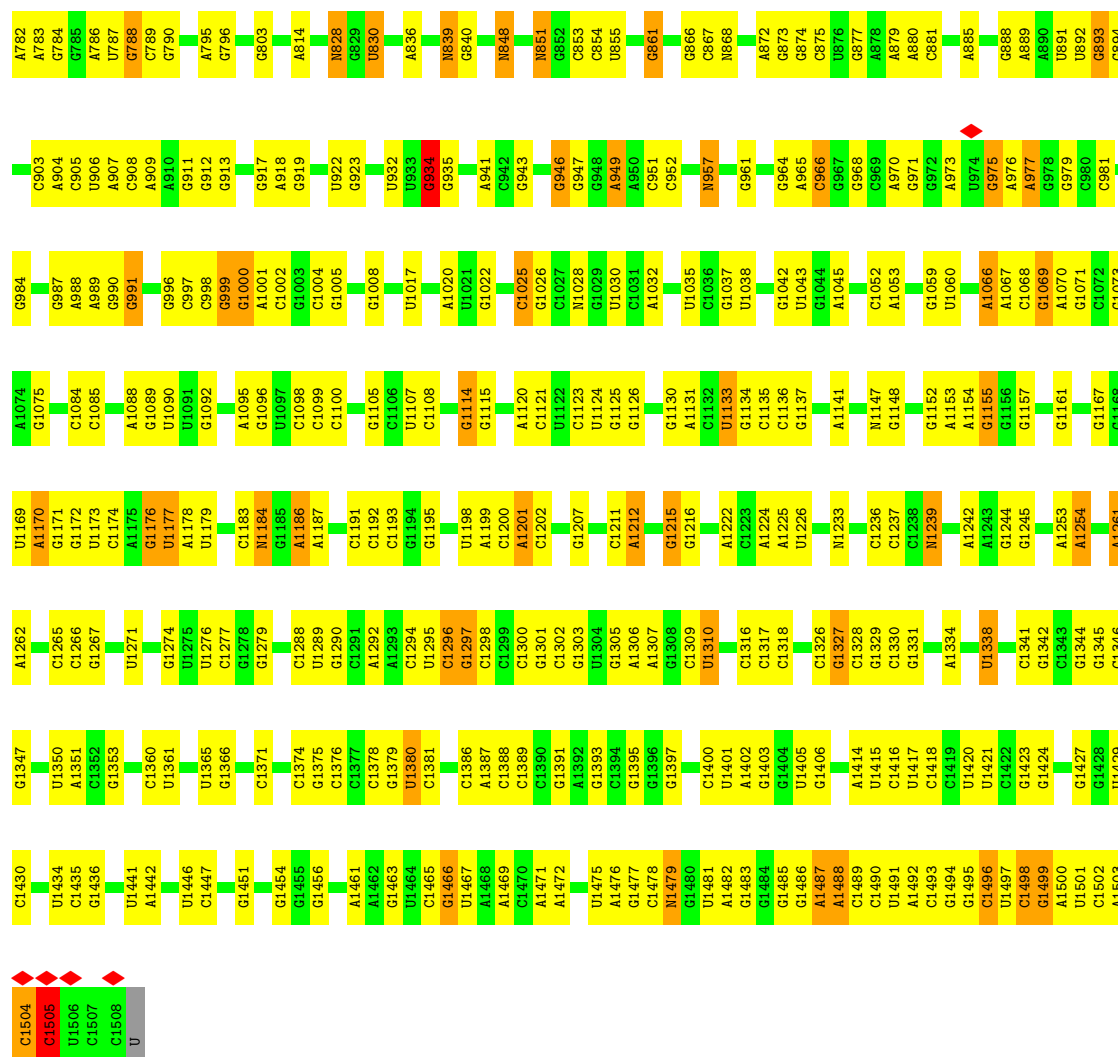




• Molecule 2: rRNA 16S

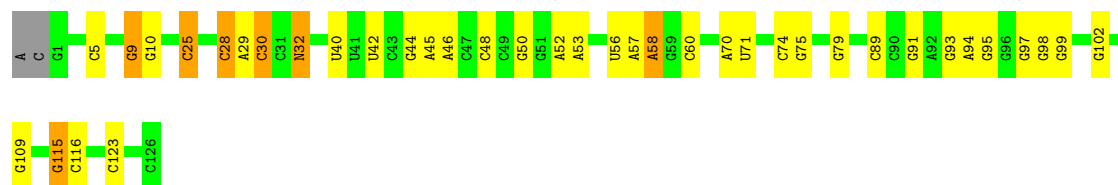
Chain 2: 55% 37% 6% .





• Molecule 3: rRNA 5S

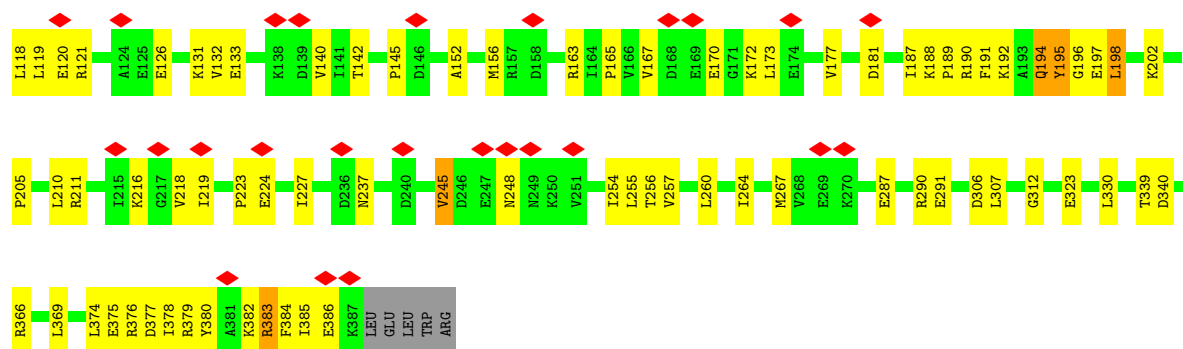
Chain 3: 68% 25% 5% •



• Molecule 4: Dehydrogenase

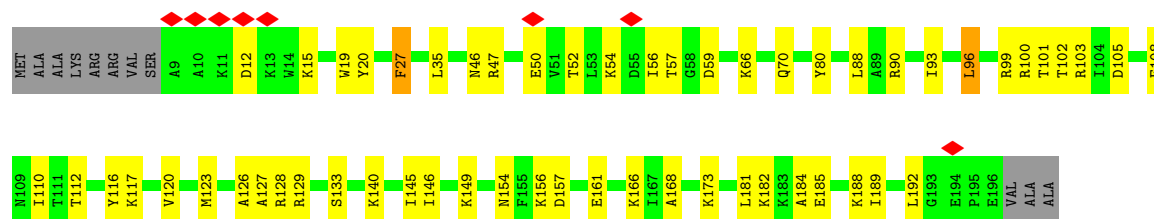
Chain H: 8% 71% 26% ••





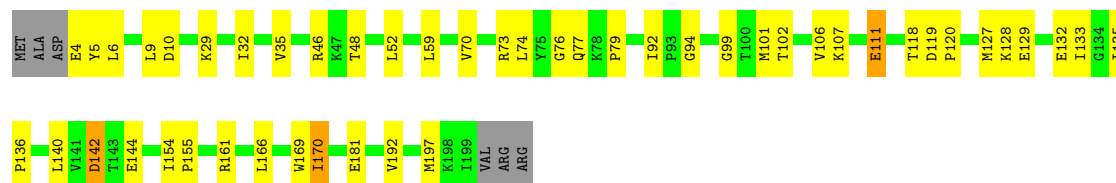
• Molecule 5: 30S ribosomal protein S3Ae

Chain AA: 66% 28% 6%



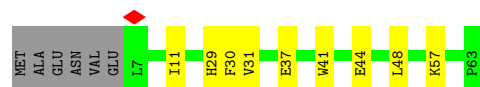
• Molecule 6: 30S ribosomal protein S2

Chain AB: 73% 22% 6%



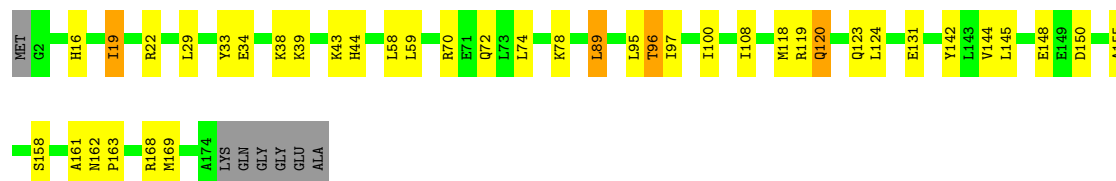
• Molecule 7: Zn-ribbon RNA-binding protein involved in translation

Chain AC: 76% 14% 10%

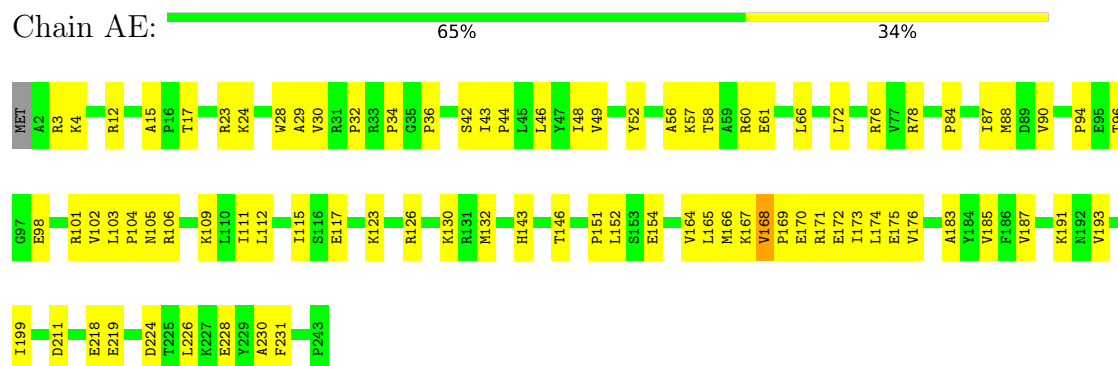


• Molecule 8: 30S ribosomal protein S4

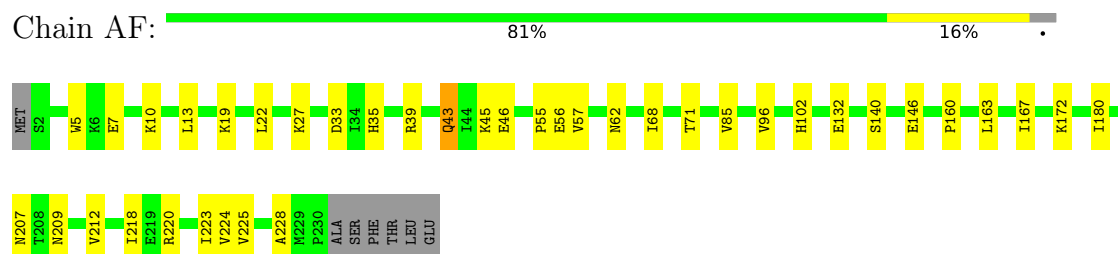
Chain AD: 74% 20% 6%



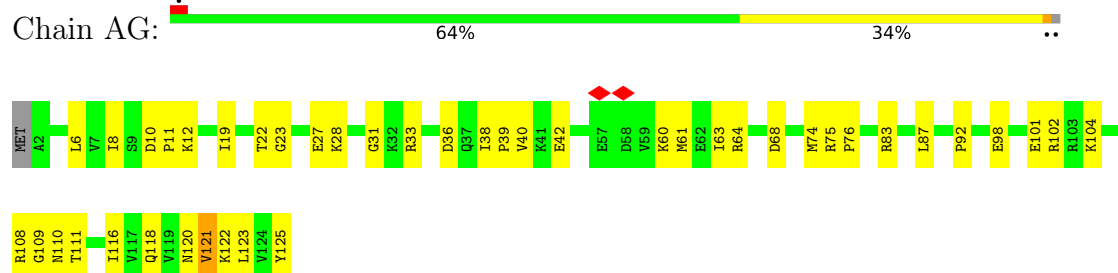
- Molecule 9: 30S ribosomal protein S4e



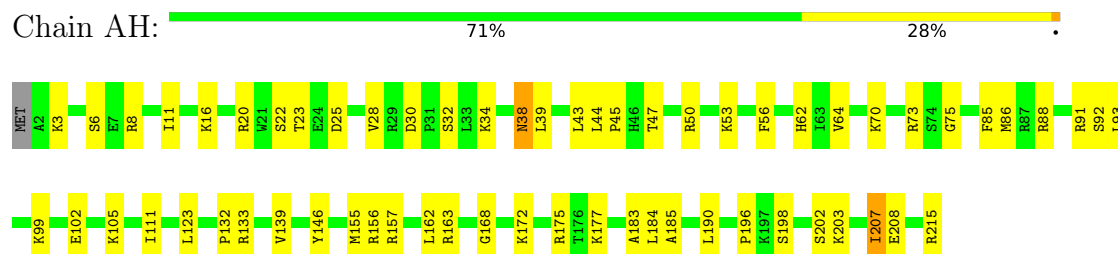
- Molecule 10: 30S ribosomal protein S5



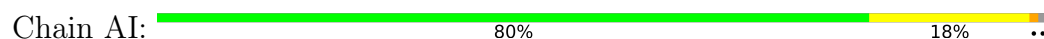
- Molecule 11: 30S ribosomal protein S6e

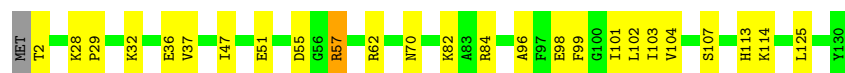


- Molecule 12: 30S ribosomal protein S7



- Molecule 13: 30S ribosomal protein S8





- Molecule 14: 30S ribosomal protein S8e

Chain AJ: 70% 28% ..



- Molecule 15: 30S ribosomal protein S9

Chain AK: 73% 27% .



- Molecule 16: 30S ribosomal protein S10

Chain AL: 6% 73% 22% . .



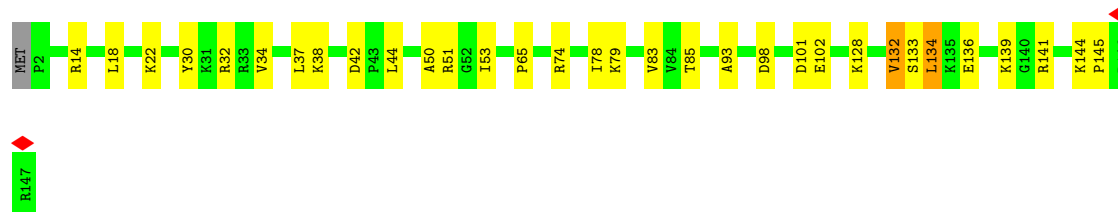
- Molecule 17: 30S ribosomal protein S11

Chain AM: 77% 15% 7% .



- Molecule 18: 30S ribosomal protein S12

Chain AN: 78% 20% ..



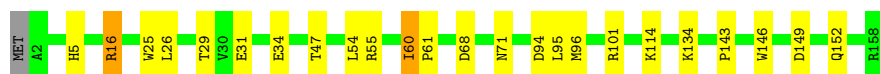
- Molecule 19: 30S ribosomal protein S14 type Z

Chain AP:  79% 18% ..



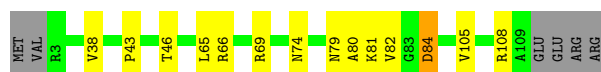
- Molecule 20: 30S ribosomal protein S15

Chain AQ:  84% 14% ..



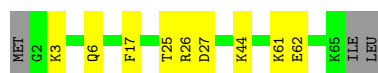
- Molecule 21: 30S ribosomal protein S17

Chain AR:  82% 12% 5%



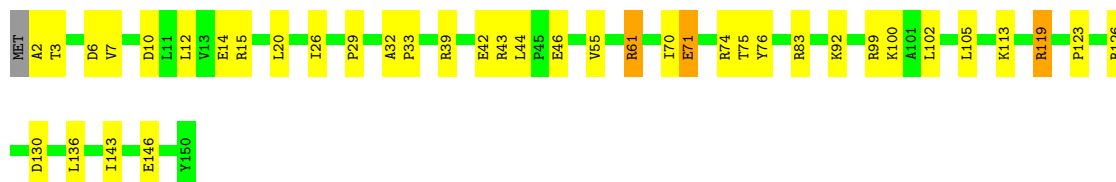
- Molecule 22: 30S ribosomal protein S17e

Chain AS:  82% 13% .



- Molecule 23: 30S ribosomal protein S19e

Chain AU:  73% 24% ..



- Molecule 24: 30S ribosomal protein S24e

Chain AV:  70% 23% . .



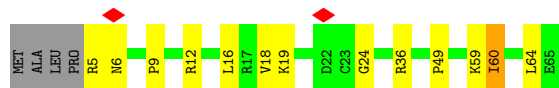
- Molecule 24: 30S ribosomal protein S24e

Chain B6:  72% 23% 5%



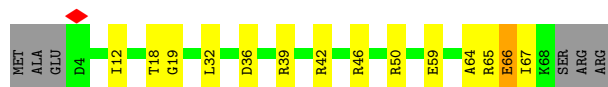
- Molecule 25: 30S ribosomal protein S27e

Chain AW: 74% 18% 6%



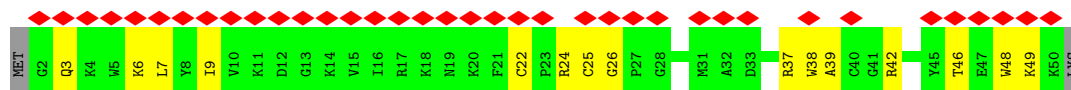
- Molecule 26: 30S ribosomal protein S28e

Chain AX: 72% 18% 8%



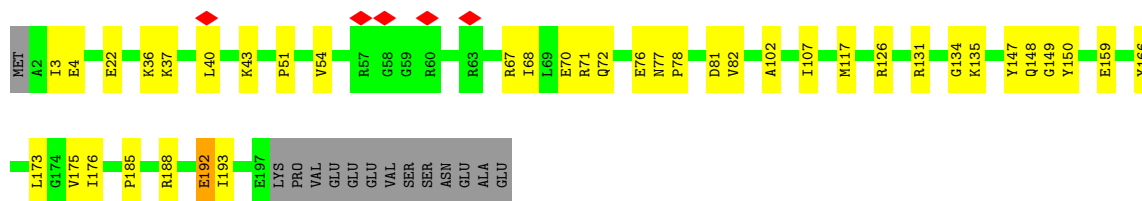
- Molecule 27: 30S ribosomal protein S27ae

Chain AY: 73% 67% 29%



- Molecule 28: 30S ribosomal protein S3

Chain AZ: 75% 18% 7%



- Molecule 29: Small ribosomal subunit protein eS32

Chain A0: 89% 8%



- Molecule 30: 50S ribosomal protein L7Ae

Chain A3: 65% 68% 30%



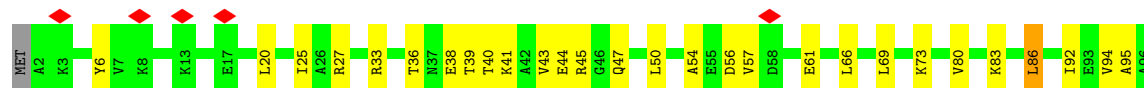
- Molecule 30: 50S ribosomal protein L7Ae

Chain BG: 80% 19%



- Molecule 30: 50S ribosomal protein L7Ae

Chain B4: 7% 64% 33%



- Molecule 31: 30S ribosomal protein S19

Chain AT: 5% 67% 30%



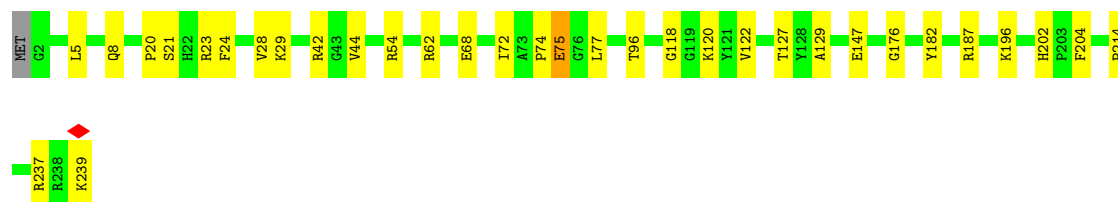
- Molecule 32: 30S ribosomal protein S13

Chain AO: 63% 28% 7%



- Molecule 33: Large ribosomal subunit protein uL2

Chain BB: 86% 13%



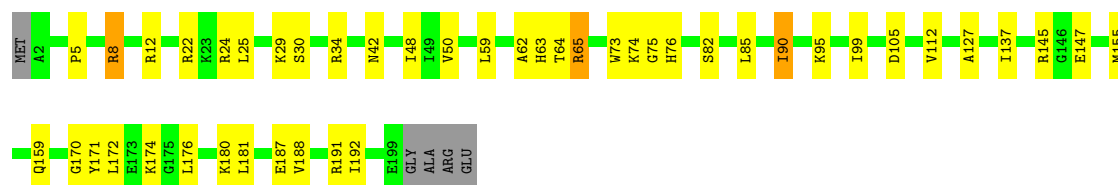
- Molecule 34: Large ribosomal subunit protein uL30

Chain BY: 90% 9% .



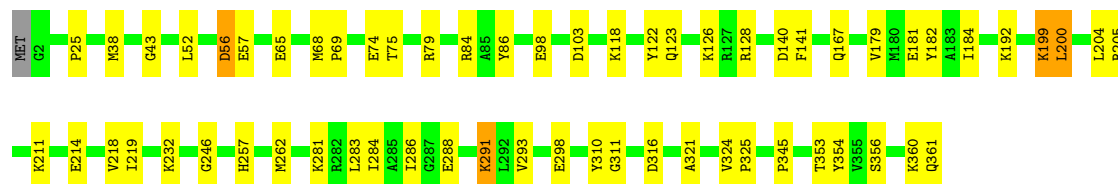
- Molecule 35: Large ribosomal subunit protein uL18

Chain BO: 75% 21% ..



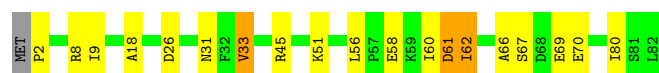
- Molecule 36: Large ribosomal subunit protein uL3

Chain BC: 83% 16% .



- Molecule 37: Large ribosomal subunit protein eL14

Chain B5: 76% 20% ..



- Molecule 37: Large ribosomal subunit protein eL14

Chain BK: 78% 20% .



- Molecule 38: Large ribosomal subunit protein uL15

Chain BL:  83% 16%



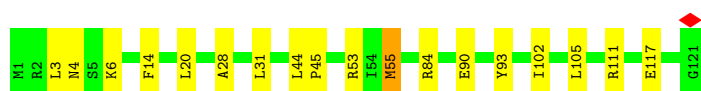
- Molecule 39: Large ribosomal subunit protein eL39

Chain Bf:  76% 22%



- Molecule 40: Large ribosomal subunit protein uL24

Chain BU:  85% 14%



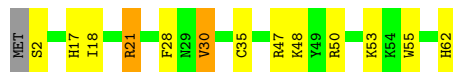
- Molecule 41: Large ribosomal subunit protein eL32

Chain Bb:  88% 11%



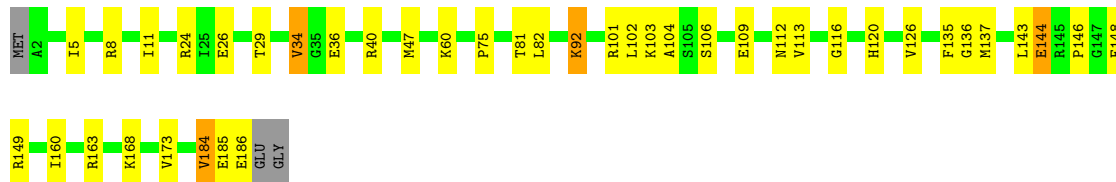
- Molecule 42: Large ribosomal subunit protein eL37

Chain Be:  77% 18%



- Molecule 43: Large ribosomal subunit protein uL5

Chain BE:  77% 20%



- Molecule 44: Large ribosomal subunit protein eL31

Chain Ba:  79% 21%



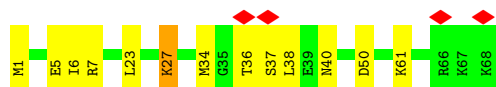
- Molecule 45: Large ribosomal subunit protein uL23

Chain BT:  92% 7%



- Molecule 46: Large ribosomal subunit protein uL29

Chain BW:  6% 81% 18%



- Molecule 47: Large ribosomal subunit protein eL43

Chain Bi:  88% 11%



- Molecule 48: Large ribosomal subunit protein uL13

Chain BI:  78% 21%



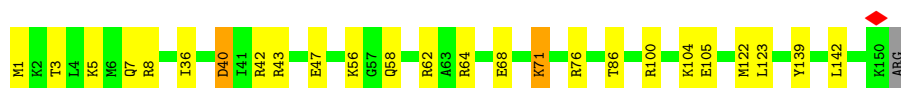
- Molecule 49: Large ribosomal subunit protein eL21

Chain BR:  87% 12%



- Molecule 50: Large ribosomal subunit protein eL19

Chain BQ:  83% 15%



- Molecule 51: Large ribosomal subunit protein eL24

Chain BV:  78% 13% 6%



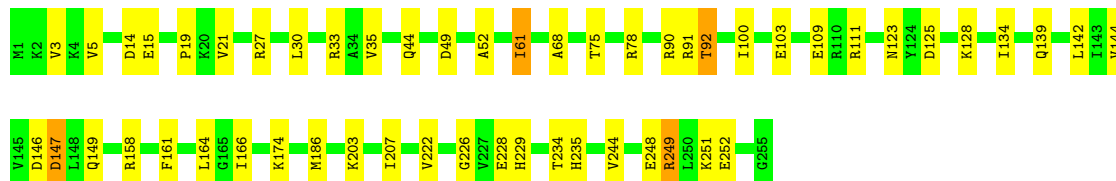
- Molecule 52: Large ribosomal subunit protein eL42

Chain Bj:  91% 9%



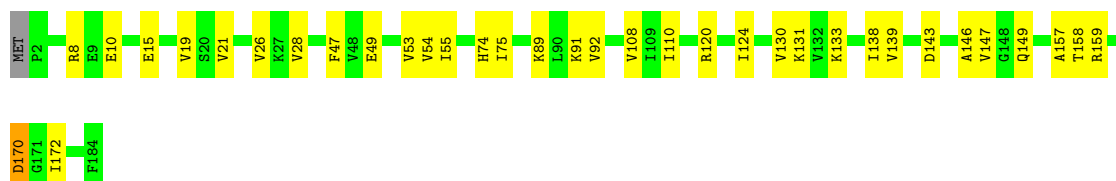
- Molecule 53: Large ribosomal subunit protein uL4

Chain BD:  79% 19%



- Molecule 54: Large ribosomal subunit protein uL6

Chain BF:  80% 18%



- Molecule 55: Large ribosomal subunit protein eL30

Chain BZ:  77% 21%



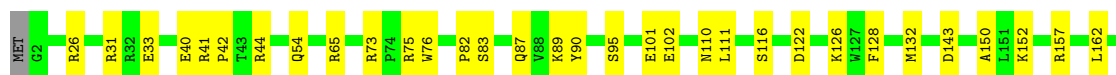
- Molecule 56: Large ribosomal subunit protein eL18

Chain BP:  81% 19%



- Molecule 57: Large ribosomal subunit protein eL15

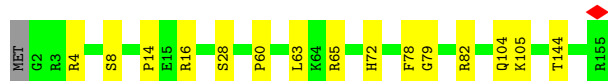
Chain BM:  82% 17%



K194

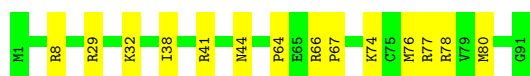
- Molecule 58: Large ribosomal subunit protein uL22

Chain BS:  90% 10%



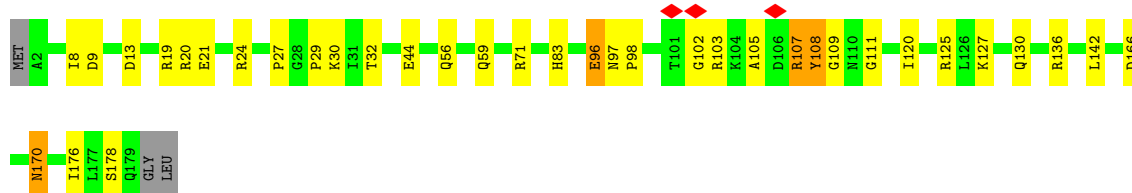
- Molecule 59: Large ribosomal subunit protein eL34

Chain Bd:  85% 15%



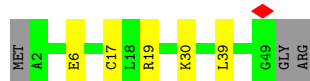
- Molecule 60: Large ribosomal subunit protein uL16

Chain BN:  78% 18%



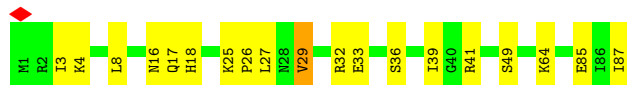
- Molecule 61: Large ribosomal subunit protein eL40

Chain Bg:  84% 10% 6%



- Molecule 62: Large ribosomal subunit protein eL33

Chain Bc:  78% 21%

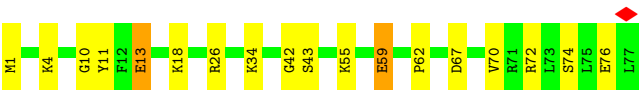
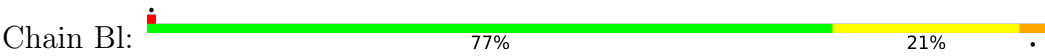


- Molecule 63: Large ribosomal subunit protein uL14

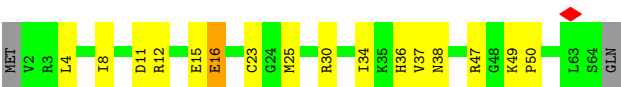
Chain BJ:  86% 12%



● Molecule 64: Large ribosomal subunit protein eL20



● Molecule 65: C2H2-type domain-containing protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	24000	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	0.016	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.00095	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: UR3, OMC, 5MC, MG, ZN, LHH, B8H, 4AC, A2M, 6MZ, OMU, OMG, MA6

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	0.22	1/70601 (0.0%)	0.31	0/110066
2	2	0.18	0/34435	0.27	0/53681
3	3	0.17	0/2995	0.27	0/4669
4	H	0.19	0/3120	0.44	2/4209 (0.0%)
5	AA	0.12	0/1557	0.28	0/2087
6	AB	0.12	0/1602	0.27	0/2165
7	AC	0.12	0/463	0.26	0/628
8	AD	0.14	0/1476	0.25	0/1980
9	AE	0.17	0/2032	0.32	0/2742
10	AF	0.15	0/1838	0.28	0/2478
11	AG	0.13	0/993	0.31	0/1329
12	AH	0.13	0/1762	0.29	0/2366
13	AI	0.16	0/1055	0.27	0/1415
14	AJ	0.13	0/995	0.25	0/1327
15	AK	0.15	0/1089	0.29	0/1459
16	AL	0.15	0/817	0.29	0/1097
17	AM	0.14	0/973	0.30	0/1311
18	AN	0.15	0/1165	0.27	0/1547
19	AP	0.13	0/465	0.26	0/613
20	AQ	0.12	0/1333	0.27	0/1791
21	AR	0.13	0/907	0.27	0/1225
22	AS	0.12	0/548	0.22	0/725
23	AU	0.14	0/1253	0.28	0/1689
24	AV	0.14	0/826	0.27	0/1108
24	B6	0.11	0/808	0.27	0/1086
25	AW	0.11	0/476	0.23	0/641
26	AX	0.12	0/518	0.29	0/694
27	AY	0.11	0/412	0.30	0/549
28	AZ	0.13	0/1563	0.29	0/2099
29	A0	0.17	0/349	0.32	0/451
30	A3	0.12	0/945	0.33	0/1274
30	B4	0.13	0/945	0.32	0/1274

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
30	BG	0.13	0/944	0.27	0/1274
31	AT	0.20	0/1077	0.33	0/1439
32	AO	0.13	0/1135	0.34	0/1526
33	BB	0.19	0/1882	0.30	0/2538
34	BY	0.17	0/1254	0.27	0/1677
35	BO	0.15	0/1645	0.26	0/2209
36	BC	0.18	0/2933	0.29	0/3943
37	B5	0.14	0/619	0.27	0/830
37	BK	0.13	0/611	0.36	0/819
38	BL	0.16	0/1167	0.28	0/1552
39	Bf	0.18	0/443	0.27	0/589
40	BU	0.29	0/1027	0.38	0/1368
41	Bb	0.17	0/1120	0.27	0/1494
42	Be	0.19	0/514	0.28	0/676
43	BE	0.13	0/1509	0.28	0/2022
44	Ba	0.16	0/793	0.26	0/1064
45	BT	0.16	0/705	0.26	0/945
46	BW	0.13	0/566	0.25	0/747
47	Bi	0.16	0/630	0.32	0/839
48	BI	0.17	0/1166	0.26	0/1559
49	BR	0.18	0/819	0.26	0/1098
50	BQ	0.17	0/1281	0.27	0/1689
51	BV	0.18	0/547	0.27	0/729
52	Bj	0.16	0/807	0.24	0/1070
53	BD	0.17	0/2069	0.29	0/2787
54	BF	0.15	0/1485	0.25	0/2003
55	BZ	0.15	0/759	0.30	0/1023
56	BP	0.16	0/984	0.27	0/1314
57	BM	0.19	0/1627	0.29	0/2170
58	BS	0.18	0/1275	0.31	0/1715
59	Bd	0.17	0/778	0.27	0/1036
60	BN	0.16	0/1483	0.26	0/1992
61	Bg	0.14	0/396	0.24	0/526
62	Bc	0.17	0/693	0.31	0/926
63	BJ	0.18	0/1080	0.28	0/1456
64	Bl	0.14	0/669	0.27	0/886
65	Bk	0.18	0/538	0.27	0/709
All	All	0.19	1/179346 (0.0%)	0.30	2/264014 (0.0%)

All (1) bond length outliers are listed below:

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	96	U	C1'-N1	5.75	1.57	1.48

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	H	377	ASP	O-C-N	-11.25	107.35	122.43
4	H	383	ARG	N-CA-C	6.29	120.56	113.01

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	726	0
2	2	32291	0	16342	429	0
3	3	2703	0	1375	29	0
4	H	3074	0	3190	83	0
5	AA	1531	0	1623	38	0
6	AB	1571	0	1630	30	0
7	AC	449	0	435	4	0
8	AD	1452	0	1521	29	0
9	AE	1983	0	2060	55	0
10	AF	1808	0	1879	26	0
11	AG	977	0	1037	29	0
12	AH	1725	0	1780	45	0
13	AI	1034	0	1069	18	0
14	AJ	986	0	1070	24	0
15	AK	1073	0	1133	28	0
16	AL	809	0	859	20	0
17	AM	955	0	981	24	0
18	AN	1148	0	1248	20	0
19	AP	455	0	475	10	0
20	AQ	1305	0	1388	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	AR	884	0	906	10	0
22	AS	541	0	573	8	0
23	AU	1223	0	1263	22	0
24	AV	808	0	832	17	0
24	B6	790	0	806	13	0
25	AW	470	0	495	9	0
26	AX	516	0	544	13	0
27	AY	400	0	401	11	0
28	AZ	1541	0	1624	22	0
29	A0	343	0	407	2	0
30	A3	933	0	982	27	0
30	B4	933	0	982	28	0
30	BG	932	0	982	14	0
31	AT	1057	0	1131	30	0
32	AO	1116	0	1152	26	0
33	BB	1838	0	1903	23	0
34	BY	1235	0	1314	10	0
35	BO	1607	0	1638	31	0
36	BC	2870	0	3020	38	0
37	B5	614	0	671	15	0
37	BK	607	0	663	11	0
38	BL	1149	0	1218	22	0
39	Bf	435	0	494	9	0
40	BU	1011	0	1078	13	0
41	Bb	1095	0	1190	10	0
42	Be	503	0	533	12	0
43	BE	1485	0	1539	27	0
44	Ba	778	0	851	12	0
45	BT	696	0	758	5	0
46	BW	565	0	628	9	0
47	Bi	620	0	668	6	0
48	BI	1148	0	1237	20	0
49	BR	797	0	835	10	0
50	BQ	1265	0	1392	21	0
51	BV	532	0	523	10	0
52	Bj	789	0	842	3	0
53	BD	2026	0	2131	37	0
54	BF	1456	0	1514	21	0
55	BZ	749	0	796	14	0
56	BP	971	0	1039	13	0
57	BM	1588	0	1683	21	0
58	BS	1247	0	1280	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
59	Bd	759	0	825	10	0
60	BN	1452	0	1491	27	0
61	Bg	387	0	397	4	0
62	Bc	684	0	748	12	0
63	BJ	1066	0	1133	12	0
64	Bl	659	0	702	12	0
65	Bk	528	0	575	12	0
66	1	166	0	0	0	0
66	2	68	0	0	0	0
66	3	1	0	0	0	0
66	AK	1	0	0	0	0
66	AN	1	0	0	0	0
66	AR	1	0	0	0	0
66	BB	2	0	0	0	0
66	BD	1	0	0	0	0
66	BM	1	0	0	0	0
66	BS	1	0	0	0	0
66	Bb	1	0	0	0	0
67	AC	2	0	0	0	0
67	AF	1	0	0	0	0
67	AP	1	0	0	0	0
67	AR	1	0	0	0	0
67	AW	1	0	0	0	0
67	BV	1	0	0	0	0
67	Bd	1	0	0	0	0
67	Be	1	0	0	0	0
67	Bg	1	0	0	0	0
67	Bi	1	0	0	0	0
67	Bj	1	0	0	0	0
67	Bk	1	0	0	0	0
All	All	170465	0	124433	2098	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 7.

The worst 5 of 2098 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)
4:H:384:PHE:CZ	26:AX:65:ARG:NH1	1.74	1.45
1:1:107:G:N2	1:1:112:A:N7	1.85	1.20
1:1:107:G:N2	1:1:112:A:C8	2.14	1.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:100:G:N2	1:1:119:C:O2	1.82	1.12
1:1:117:G:O2'	1:1:118:U:OP1	1.67	1.12

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	H	384/392 (98%)	369 (96%)	15 (4%)	0	100	100
5	AA	186/199 (94%)	181 (97%)	5 (3%)	0	100	100
6	AB	194/202 (96%)	194 (100%)	0	0	100	100
7	AC	55/63 (87%)	53 (96%)	2 (4%)	0	100	100
8	AD	171/180 (95%)	169 (99%)	2 (1%)	0	100	100
9	AE	240/243 (99%)	233 (97%)	7 (3%)	0	100	100
10	AF	227/236 (96%)	221 (97%)	6 (3%)	0	100	100
11	AG	122/125 (98%)	116 (95%)	6 (5%)	0	100	100
12	AH	212/215 (99%)	205 (97%)	7 (3%)	0	100	100
13	AI	127/130 (98%)	124 (98%)	3 (2%)	0	100	100
14	AJ	123/127 (97%)	122 (99%)	1 (1%)	0	100	100
15	AK	133/135 (98%)	129 (97%)	4 (3%)	0	100	100
16	AL	98/102 (96%)	96 (98%)	2 (2%)	0	100	100
17	AM	125/137 (91%)	120 (96%)	5 (4%)	0	100	100
18	AN	144/147 (98%)	143 (99%)	1 (1%)	0	100	100
19	AP	53/56 (95%)	52 (98%)	1 (2%)	0	100	100
20	AQ	155/158 (98%)	151 (97%)	4 (3%)	0	100	100
21	AR	105/113 (93%)	101 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	AS	62/67 (92%)	59 (95%)	3 (5%)	0	100	100
23	AU	147/150 (98%)	145 (99%)	2 (1%)	0	100	100
24	AV	94/99 (95%)	93 (99%)	1 (1%)	0	100	100
24	B6	92/99 (93%)	92 (100%)	0	0	100	100
25	AW	59/65 (91%)	57 (97%)	2 (3%)	0	100	100
26	AX	63/71 (89%)	61 (97%)	2 (3%)	0	100	100
27	AY	47/51 (92%)	42 (89%)	5 (11%)	0	100	100
28	AZ	194/210 (92%)	189 (97%)	5 (3%)	0	100	100
29	A0	34/37 (92%)	34 (100%)	0	0	100	100
30	A3	120/123 (98%)	113 (94%)	7 (6%)	0	100	100
30	B4	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
30	BG	120/123 (98%)	119 (99%)	1 (1%)	0	100	100
31	AT	128/132 (97%)	126 (98%)	2 (2%)	0	100	100
32	AO	136/148 (92%)	127 (93%)	9 (7%)	0	100	100
33	BB	236/239 (99%)	227 (96%)	9 (4%)	0	100	100
34	BY	152/155 (98%)	151 (99%)	1 (1%)	0	100	100
35	BO	196/203 (97%)	193 (98%)	3 (2%)	0	100	100
36	BC	358/361 (99%)	348 (97%)	10 (3%)	0	100	100
37	B5	79/82 (96%)	77 (98%)	2 (2%)	0	100	100
37	BK	78/82 (95%)	74 (95%)	4 (5%)	0	100	100
38	BL	145/147 (99%)	138 (95%)	7 (5%)	0	100	100
39	Bf	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
40	BU	119/121 (98%)	119 (100%)	0	0	100	100
41	Bb	127/130 (98%)	127 (100%)	0	0	100	100
42	Be	59/62 (95%)	58 (98%)	1 (2%)	0	100	100
43	BE	183/188 (97%)	182 (100%)	1 (0%)	0	100	100
44	Ba	92/94 (98%)	92 (100%)	0	0	100	100
45	BT	84/86 (98%)	84 (100%)	0	0	100	100
46	BW	66/68 (97%)	65 (98%)	1 (2%)	0	100	100
47	Bi	80/83 (96%)	76 (95%)	4 (5%)	0	100	100
48	BI	140/142 (99%)	135 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
49	BR	94/97 (97%)	94 (100%)	0	0	100	100
50	BQ	148/151 (98%)	147 (99%)	1 (1%)	0	100	100
51	BV	61/67 (91%)	60 (98%)	1 (2%)	0	100	100
52	Bj	92/94 (98%)	92 (100%)	0	0	100	100
53	BD	253/255 (99%)	249 (98%)	4 (2%)	0	100	100
54	BF	181/184 (98%)	181 (100%)	0	0	100	100
55	BZ	96/99 (97%)	93 (97%)	3 (3%)	0	100	100
56	BP	118/120 (98%)	118 (100%)	0	0	100	100
57	BM	191/194 (98%)	189 (99%)	2 (1%)	0	100	100
58	BS	152/155 (98%)	149 (98%)	3 (2%)	0	100	100
59	Bd	89/91 (98%)	89 (100%)	0	0	100	100
60	BN	176/181 (97%)	169 (96%)	7 (4%)	0	100	100
61	Bg	46/51 (90%)	46 (100%)	0	0	100	100
62	Bc	85/87 (98%)	84 (99%)	1 (1%)	0	100	100
63	BJ	138/141 (98%)	138 (100%)	0	0	100	100
64	Bl	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
65	Bk	61/65 (94%)	60 (98%)	1 (2%)	0	100	100
All	All	8568/8861 (97%)	8378 (98%)	190 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	H	332/338 (98%)	312 (94%)	20 (6%)	17	15
5	AA	160/167 (96%)	153 (96%)	7 (4%)	25	26
6	AB	168/173 (97%)	161 (96%)	7 (4%)	26	28
7	AC	50/55 (91%)	47 (94%)	3 (6%)	17	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	AD	156/160 (98%)	149 (96%)	7 (4%)	24	25
9	AE	213/214 (100%)	205 (96%)	8 (4%)	29	32
10	AF	192/198 (97%)	187 (97%)	5 (3%)	40	46
11	AG	107/108 (99%)	102 (95%)	5 (5%)	23	24
12	AH	183/184 (100%)	176 (96%)	7 (4%)	29	32
13	AI	106/107 (99%)	103 (97%)	3 (3%)	38	43
14	AJ	101/103 (98%)	98 (97%)	3 (3%)	36	41
15	AK	111/111 (100%)	107 (96%)	4 (4%)	31	34
16	AL	89/91 (98%)	82 (92%)	7 (8%)	11	9
17	AM	94/104 (90%)	93 (99%)	1 (1%)	65	74
18	AN	120/121 (99%)	117 (98%)	3 (2%)	42	48
19	AP	45/46 (98%)	43 (96%)	2 (4%)	25	26
20	AQ	142/143 (99%)	138 (97%)	4 (3%)	38	43
21	AR	96/102 (94%)	93 (97%)	3 (3%)	35	39
22	AS	58/61 (95%)	58 (100%)	0	100	100
23	AU	126/127 (99%)	117 (93%)	9 (7%)	13	11
24	AV	88/90 (98%)	81 (92%)	7 (8%)	11	8
24	B6	86/90 (96%)	83 (96%)	3 (4%)	32	35
25	AW	53/56 (95%)	51 (96%)	2 (4%)	29	32
26	AX	55/60 (92%)	50 (91%)	5 (9%)	9	6
27	AY	40/42 (95%)	37 (92%)	3 (8%)	12	10
28	AZ	155/168 (92%)	150 (97%)	5 (3%)	34	38
29	A0	34/35 (97%)	33 (97%)	1 (3%)	37	42
30	A3	98/99 (99%)	93 (95%)	5 (5%)	21	21
30	B4	98/99 (99%)	88 (90%)	10 (10%)	7	4
30	BG	98/99 (99%)	97 (99%)	1 (1%)	68	76
31	AT	113/114 (99%)	107 (95%)	6 (5%)	20	19
32	AO	115/123 (94%)	107 (93%)	8 (7%)	14	11
33	BB	188/189 (100%)	185 (98%)	3 (2%)	55	64
34	BY	132/133 (99%)	131 (99%)	1 (1%)	73	81
35	BO	167/170 (98%)	160 (96%)	7 (4%)	26	28

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	BC	306/307 (100%)	299 (98%)	7 (2%)	44	51
37	B5	65/66 (98%)	61 (94%)	4 (6%)	16	14
37	BK	64/66 (97%)	61 (95%)	3 (5%)	23	24
38	BL	118/118 (100%)	114 (97%)	4 (3%)	32	35
39	Bf	46/47 (98%)	45 (98%)	1 (2%)	45	53
40	BU	109/109 (100%)	108 (99%)	1 (1%)	70	78
41	Bb	117/118 (99%)	115 (98%)	2 (2%)	53	62
42	Be	52/53 (98%)	50 (96%)	2 (4%)	29	32
43	BE	158/160 (99%)	151 (96%)	7 (4%)	25	26
44	Ba	84/84 (100%)	81 (96%)	3 (4%)	31	34
45	BT	77/77 (100%)	75 (97%)	2 (3%)	40	46
46	BW	63/63 (100%)	60 (95%)	3 (5%)	23	23
47	Bi	61/62 (98%)	60 (98%)	1 (2%)	55	64
48	BI	122/122 (100%)	119 (98%)	3 (2%)	42	48
49	BR	86/87 (99%)	85 (99%)	1 (1%)	63	72
50	BQ	132/133 (99%)	129 (98%)	3 (2%)	44	51
51	BV	54/58 (93%)	52 (96%)	2 (4%)	30	33
52	Bj	83/84 (99%)	80 (96%)	3 (4%)	31	34
53	BD	212/212 (100%)	206 (97%)	6 (3%)	38	43
54	BF	156/157 (99%)	153 (98%)	3 (2%)	50	58
55	BZ	79/80 (99%)	76 (96%)	3 (4%)	29	32
56	BP	102/102 (100%)	99 (97%)	3 (3%)	37	42
57	BM	160/161 (99%)	158 (99%)	2 (1%)	61	69
58	BS	130/131 (99%)	128 (98%)	2 (2%)	57	65
59	Bd	82/82 (100%)	81 (99%)	1 (1%)	63	72
60	BN	149/151 (99%)	142 (95%)	7 (5%)	23	24
61	Bg	37/39 (95%)	37 (100%)	0	100	100
62	Bc	74/74 (100%)	70 (95%)	4 (5%)	20	18
63	BJ	108/109 (99%)	103 (95%)	5 (5%)	24	25
64	Bl	72/72 (100%)	70 (97%)	2 (3%)	38	43
65	Bk	55/57 (96%)	54 (98%)	1 (2%)	51	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	7382/7521 (98%)	7116 (96%)	266 (4%)	32 34

5 of 266 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	BP	110	ASN
60	BN	32	THR
30	B4	69	LEU
21	AR	82	VAL
20	AQ	60	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 156 such sidechains are listed below:

Mol	Chain	Res	Type
53	BD	44	GLN
60	BN	59	GLN
53	BD	214	HIS
57	BM	97	GLN
60	BN	170	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	3016/3018 (99%)	479 (15%)	22 (0%)
2	2	1495/1512 (98%)	186 (12%)	2 (0%)
3	3	125/128 (97%)	14 (11%)	0
All	All	4636/4658 (99%)	679 (14%)	24 (0%)

5 of 679 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	5	G
1	1	12	G
1	1	28	A
1	1	39	A
1	1	43	A

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1364	C
1	1	2367	G
1	1	2341	G
1	1	2455	A
1	1	250	U

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

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
1	5MC	1	2162	1	18,22,23	0.93	2 (11%)	26,32,35	1.18	3 (11%)
2	4AC	2	1028	2	21,24,25	1.02	2 (9%)	29,34,37	1.34	4 (13%)
1	4AC	1	229	1	21,24,25	1.03	2 (9%)	29,34,37	1.30	4 (13%)
2	LHH	2	250	2	22,25,26	0.31	0	29,35,38	0.50	0
1	4AC	1	802	1	21,24,25	1.01	2 (9%)	29,34,37	1.44	4 (13%)
1	4AC	1	2545	1	21,24,25	1.02	2 (9%)	29,34,37	1.35	4 (13%)
1	4AC	1	2908	1	21,24,25	1.01	2 (9%)	29,34,37	1.29	4 (13%)
1	4AC	1	2062	1	21,24,25	1.00	2 (9%)	29,34,37	1.29	4 (13%)
1	4AC	1	451	1	21,24,25	1.01	2 (9%)	29,34,37	1.32	4 (13%)
1	4AC	1	22	1	21,24,25	1.04	2 (9%)	29,34,37	1.33	4 (13%)
1	OMC	1	1948	1	19,22,23	0.81	0	26,31,34	0.82	1 (3%)
1	4AC	1	2960	1	21,24,25	1.01	2 (9%)	29,34,37	1.33	4 (13%)
2	OMC	2	1040	2	19,22,23	0.81	0	26,31,34	0.78	0
2	OMG	2	680	2	23,26,27	1.21	3 (13%)	33,38,41	1.94	6 (18%)
1	4AC	1	922	1	21,24,25	1.05	2 (9%)	29,34,37	1.45	4 (13%)
2	4AC	2	731	2	21,24,25	1.03	2 (9%)	29,34,37	1.37	4 (13%)
1	OMC	1	615	1	19,22,23	0.81	0	26,31,34	0.82	1 (3%)
1	4AC	1	2865	1	21,24,25	1.02	2 (9%)	29,34,37	1.28	4 (13%)
2	UR3	2	1467	2	19,22,23	0.94	0	26,32,35	1.44	2 (7%)
2	4AC	2	868	2	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	17	2	21,24,25	1.01	2 (9%)	29,34,37	1.35	4 (13%)
2	OMU	2	20	2	19,22,23	1.23	2 (10%)	26,31,34	1.79	5 (19%)
2	5MC	2	1374	2	18,22,23	0.92	2 (11%)	26,32,35	1.11	2 (7%)
2	4AC	2	590	2	21,24,25	1.01	2 (9%)	29,34,37	1.35	4 (13%)
2	4AC	2	1239	2	21,24,25	1.03	2 (9%)	29,34,37	1.33	4 (13%)
1	4AC	1	314	1	21,24,25	1.03	2 (9%)	29,34,37	1.28	4 (13%)
1	4AC	1	1667	1	21,24,25	1.00	2 (9%)	29,34,37	1.35	4 (13%)
1	4AC	1	2925	1	21,24,25	1.02	2 (9%)	29,34,37	1.34	4 (13%)
2	4AC	2	379	2	21,24,25	1.01	2 (9%)	29,34,37	1.35	4 (13%)
2	4AC	2	303	2	21,24,25	1.02	2 (9%)	29,34,37	1.34	4 (13%)
1	4AC	1	2495	1	21,24,25	1.02	2 (9%)	29,34,37	1.31	4 (13%)
1	4AC	1	2585	1	21,24,25	1.06	2 (9%)	29,34,37	1.81	5 (17%)
1	5MC	1	2733	1	18,22,23	0.97	2 (11%)	26,32,35	1.23	3 (11%)
2	5MC	2	1202	2	18,22,23	0.93	2 (11%)	26,32,35	1.16	3 (11%)
1	4AC	1	2718	1	21,24,25	1.02	2 (9%)	29,34,37	1.34	4 (13%)
1	4AC	1	1885	1	21,24,25	1.02	2 (9%)	29,34,37	1.32	4 (13%)
1	4AC	1	1222	66,1	21,24,25	1.03	2 (9%)	29,34,37	1.31	4 (13%)
1	4AC	1	1962	1	21,24,25	1.01	2 (9%)	29,34,37	1.37	4 (13%)
1	4AC	1	2287	1	21,24,25	1.01	2 (9%)	29,34,37	1.41	4 (13%)
2	4AC	2	839	2	21,24,25	1.02	2 (9%)	29,34,37	1.33	4 (13%)
2	4AC	2	636	2	21,24,25	1.02	2 (9%)	29,34,37	1.39	4 (13%)
1	4AC	1	1068	1	21,24,25	1.04	2 (9%)	29,34,37	1.39	4 (13%)
1	4AC	1	641	1	21,24,25	1.03	2 (9%)	29,34,37	1.34	4 (13%)
2	OMU	2	1177	2	19,22,23	1.23	3 (15%)	26,31,34	1.74	5 (19%)
1	4AC	1	835	1	21,24,25	1.03	2 (9%)	29,34,37	1.36	4 (13%)
1	4AC	1	60	1	21,24,25	1.02	2 (9%)	29,34,37	1.44	4 (13%)
1	4AC	1	1765	1	21,24,25	1.02	2 (9%)	29,34,37	1.34	4 (13%)
2	4AC	2	703	2	21,24,25	1.02	1 (4%)	29,34,37	1.44	4 (13%)
2	5MC	2	1505	2	18,22,23	0.97	2 (11%)	26,32,35	1.15	3 (11%)
1	5MC	1	2198	1	18,22,23	0.92	2 (11%)	26,32,35	1.21	3 (11%)
2	4AC	2	286	2	21,24,25	1.01	2 (9%)	29,34,37	1.30	4 (13%)
1	4AC	1	1460	1	21,24,25	1.01	2 (9%)	29,34,37	1.37	4 (13%)
2	5MC	2	693	2	18,22,23	0.94	2 (11%)	26,32,35	1.17	3 (11%)
1	4AC	1	1867	1	21,24,25	1.02	2 (9%)	29,34,37	1.37	4 (13%)
2	A2M	2	373	2	22,25,26	1.45	4 (18%)	31,36,39	2.08	8 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	4AC	1	2992	1	21,24,25	1.04	2 (9%)	29,34,37	0.90	1 (3%)
2	OMU	2	830	2	19,22,23	1.25	3 (15%)	26,31,34	1.68	4 (15%)
1	4AC	1	829	1	21,24,25	1.02	2 (9%)	29,34,37	1.37	4 (13%)
2	OMC	2	846	2	19,22,23	0.81	0	26,31,34	0.81	0
1	4AC	1	1048	1	21,24,25	1.03	2 (9%)	29,34,37	1.36	4 (13%)
2	5MC	2	1025	2	18,22,23	0.95	2 (11%)	26,32,35	1.17	2 (7%)
1	5MC	1	2163	1	18,22,23	0.93	2 (11%)	26,32,35	1.12	2 (7%)
2	OMG	2	467	2	23,26,27	1.20	3 (13%)	33,38,41	1.96	6 (18%)
1	5MC	1	2093	1	18,22,23	0.94	2 (11%)	26,32,35	1.13	2 (7%)
1	4AC	1	2642	1	21,24,25	1.01	2 (9%)	29,34,37	1.30	4 (13%)
2	4AC	2	957	2	21,24,25	1.01	2 (9%)	29,34,37	1.35	4 (13%)
1	4AC	1	357	1	21,24,25	1.01	2 (9%)	29,34,37	1.38	4 (13%)
1	4AC	1	458	1	21,24,25	1.01	2 (9%)	29,34,37	1.34	5 (17%)
2	OMU	2	787	2	19,22,23	1.21	2 (10%)	26,31,34	1.77	5 (19%)
2	OMG	2	657	2	23,26,27	1.22	3 (13%)	33,38,41	1.92	6 (18%)
2	MA6	2	1487	2	23,26,27	1.46	5 (21%)	34,38,41	2.11	10 (29%)
1	4AC	1	341	1	21,24,25	1.03	2 (9%)	29,34,37	1.30	5 (17%)
2	LHH	2	1041	2	22,25,26	0.31	0	29,35,38	0.49	0
1	LHH	1	616	1	22,25,26	0.32	0	29,35,38	0.48	0
1	4AC	1	2136	1	21,24,25	1.02	2 (9%)	29,34,37	1.39	4 (13%)
1	4AC	1	211	1	21,24,25	1.01	2 (9%)	29,34,37	1.34	4 (13%)
2	OMG	2	934	2	23,26,27	1.20	3 (13%)	33,38,41	1.99	6 (18%)
1	4AC	1	2548	1	21,24,25	1.00	2 (9%)	29,34,37	1.32	4 (13%)
1	4AC	1	533	1	21,24,25	1.02	2 (9%)	29,34,37	1.31	5 (17%)
2	4AC	2	1479	2	21,24,25	1.00	2 (9%)	29,34,37	1.30	5 (17%)
2	4AC	2	828	2	21,24,25	1.00	2 (9%)	29,34,37	1.33	4 (13%)
2	4AC	2	626	2	21,24,25	1.00	2 (9%)	29,34,37	1.38	4 (13%)
1	OMG	1	923	66,1	23,26,27	1.22	3 (13%)	33,38,41	1.90	6 (18%)
3	4AC	3	32	3	21,24,25	1.01	2 (9%)	29,34,37	1.38	4 (13%)
1	4AC	1	1554	1	21,24,25	1.01	2 (9%)	29,34,37	1.35	4 (13%)
1	OMG	1	2678	1	23,26,27	1.22	3 (13%)	33,38,41	1.90	6 (18%)
1	A2M	1	1055	1	22,25,26	1.44	4 (18%)	31,36,39	2.12	9 (29%)
2	4AC	2	851	2	21,24,25	1.03	2 (9%)	29,34,37	1.28	4 (13%)
2	OMG	2	519	2	23,26,27	1.21	3 (13%)	33,38,41	1.96	5 (15%)
1	4AC	1	694	1	21,24,25	1.00	2 (9%)	29,34,37	1.30	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	B8H	2	938	2	19,22,23	0.57	0	22,32,35	0.64	0
1	4AC	1	1550	1	21,24,25	1.01	2 (9%)	29,34,37	1.35	4 (13%)
2	4AC	2	1147	2	21,24,25	1.02	2 (9%)	29,34,37	1.44	4 (13%)
1	4AC	1	1755	1	21,24,25	1.00	2 (9%)	29,34,37	1.58	4 (13%)
1	4AC	1	1594	66,1	21,24,25	1.02	2 (9%)	29,34,37	1.33	4 (13%)
1	4AC	1	1934	1	21,24,25	1.01	2 (9%)	29,34,37	1.38	4 (13%)
1	4AC	1	161	1	21,24,25	1.00	2 (9%)	29,34,37	1.37	4 (13%)
2	6MZ	2	1469	2,66	22,25,26	1.48	4 (18%)	30,36,39	2.20	9 (30%)
1	OMG	1	2147	1	23,26,27	1.20	3 (13%)	33,38,41	1.91	6 (18%)
1	OMU	1	2784	1	19,22,23	1.23	3 (15%)	26,31,34	1.75	5 (19%)
1	4AC	1	1878	1	21,24,25	1.01	2 (9%)	29,34,37	1.50	4 (13%)
2	4AC	2	546	2	21,24,25	1.02	2 (9%)	29,34,37	1.36	4 (13%)
2	5MC	2	1498	2	18,22,23	0.96	2 (11%)	26,32,35	1.26	3 (11%)
1	4AC	1	2083	1	21,24,25	1.04	2 (9%)	29,34,37	1.29	5 (17%)
1	4AC	1	2001	1	21,24,25	1.06	2 (9%)	29,34,37	1.51	4 (13%)
2	OMG	2	1069	2	23,26,27	1.21	3 (13%)	33,38,41	1.90	6 (18%)
1	4AC	1	91	1	21,24,25	1.01	2 (9%)	29,34,37	1.35	4 (13%)
1	4AC	1	1621	1	21,24,25	1.02	2 (9%)	29,34,37	1.30	4 (13%)
2	OMC	2	773	2	19,22,23	0.82	0	26,31,34	0.90	1 (3%)
2	5MC	2	1496	2	18,22,23	0.93	2 (11%)	26,32,35	1.18	3 (11%)
1	4AC	1	1695	1	21,24,25	1.02	2 (9%)	29,34,37	1.37	4 (13%)
1	5MC	1	2183	1	18,22,23	0.94	2 (11%)	26,32,35	1.13	2 (7%)
1	OMG	1	2138	1	23,26,27	1.22	3 (13%)	33,38,41	1.91	6 (18%)
2	5MC	2	875	2	18,22,23	0.93	2 (11%)	26,32,35	1.20	3 (11%)
2	5MC	2	535	2	18,22,23	0.93	2 (11%)	26,32,35	1.13	2 (7%)
1	4AC	1	1557	1	21,24,25	1.02	2 (9%)	29,34,37	1.26	4 (13%)
1	4AC	1	1065	1	21,24,25	1.02	2 (9%)	29,34,37	1.42	4 (13%)
1	4AC	1	2027	1	21,24,25	1.02	2 (9%)	29,34,37	1.34	4 (13%)
1	4AC	1	243	1	21,24,25	1.01	2 (9%)	29,34,37	1.35	4 (13%)
1	4AC	1	1873	1	21,24,25	1.03	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%)
2	OMG	2	913	2	23,26,27	1.20	3 (13%)	33,38,41	1.93	5 (15%)
2	4AC	2	718	2	21,24,25	0.99	2 (9%)	29,34,37	1.39	4 (13%)
1	5MC	1	2203	1	18,22,23	0.93	2 (11%)	26,32,35	1.13	2 (7%)
2	4AC	2	1184	2	21,24,25	1.01	2 (9%)	29,34,37	1.38	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	OMG	2	471	2	23,26,27	1.22	3 (13%)	33,38,41	1.92	6 (18%)
1	4AC	1	1780	1	21,24,25	1.03	2 (9%)	29,34,37	1.55	4 (13%)
1	4AC	1	1662	1	21,24,25	1.00	2 (9%)	29,34,37	1.36	4 (13%)
2	OMG	2	873	2	23,26,27	1.22	3 (13%)	33,38,41	1.95	6 (18%)
1	4AC	1	2937	66,1	21,24,25	1.03	2 (9%)	29,34,37	1.55	4 (13%)
1	OMG	1	2144	1	23,26,27	1.22	3 (13%)	33,38,41	1.93	6 (18%)
2	4AC	2	751	2	21,24,25	1.01	2 (9%)	29,34,37	1.31	4 (13%)
1	OMG	1	789	1	23,26,27	1.23	3 (13%)	33,38,41	1.94	6 (18%)
1	4AC	1	2966	1	21,24,25	1.04	2 (9%)	29,34,37	1.36	4 (13%)
1	4AC	1	2329	1	21,24,25	1.01	2 (9%)	29,34,37	1.41	4 (13%)
2	MA6	2	1488	2	23,26,27	1.47	5 (21%)	34,38,41	2.09	10 (29%)
2	4AC	2	394	2	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	1.34	4 (13%)
1	4AC	1	1243	1	21,24,25	1.04	2 (9%)	29,34,37	1.36	4 (13%)
1	4AC	1	981	1	21,24,25	1.01	2 (9%)	29,34,37	1.28	4 (13%)
2	4AC	2	53	2	21,24,25	1.00	2 (9%)	29,34,37	1.38	4 (13%)
1	A2M	1	2173	1	22,25,26	1.44	4 (18%)	31,36,39	2.05	8 (25%)
1	4AC	1	136	1	21,24,25	1.01	2 (9%)	29,34,37	1.33	4 (13%)
1	OMG	1	328	1	23,26,27	1.22	3 (13%)	33,38,41	1.93	6 (18%)
1	4AC	1	2608	1	21,24,25	1.06	2 (9%)	29,34,37	1.77	6 (20%)
2	OMU	2	774	2	19,22,23	1.24	3 (15%)	26,31,34	1.73	4 (15%)
2	OMU	2	64	2	19,22,23	1.22	4 (21%)	26,31,34	1.68	4 (15%)
1	4AC	1	3004	1	21,24,25	1.03	2 (9%)	29,34,37	1.28	4 (13%)
1	4AC	1	2249	1	21,24,25	1.04	2 (9%)	29,34,37	1.39	4 (13%)
2	OMU	2	1380	2	19,22,23	1.29	4 (21%)	26,31,34	1.76	4 (15%)
2	4AC	2	1233	2	21,24,25	1.02	2 (9%)	29,34,37	1.36	4 (13%)
2	4AC	2	319	2	21,24,25	1.01	2 (9%)	29,34,37	1.39	4 (13%)
2	4AC	2	848	2	21,24,25	0.99	2 (9%)	29,34,37	1.42	4 (13%)
1	4AC	1	1938	1	21,24,25	1.03	2 (9%)	29,34,37	1.33	4 (13%)
2	4AC	2	511	2	21,24,25	1.05	2 (9%)	29,34,37	1.38	4 (13%)
2	OMC	2	129	2	19,22,23	0.80	0	26,31,34	0.83	0
2	4AC	2	479	2	21,24,25	1.02	2 (9%)	29,34,37	1.40	4 (13%)
2	OMC	2	1376	2	19,22,23	0.81	0	26,31,34	0.77	0
1	4AC	1	2570	1	21,24,25	1.02	2 (9%)	29,34,37	1.38	4 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MC	1	2162	1	-	0/7/25/26	0/2/2/2
2	4AC	2	1028	2	-	0/11/29/30	0/2/2/2
1	4AC	1	229	1	-	0/11/29/30	0/2/2/2
2	LHH	2	250	2	-	0/13/31/32	0/2/2/2
1	4AC	1	802	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	2908	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2062	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	22	1	-	0/11/29/30	0/2/2/2
1	OMC	1	1948	1	-	0/9/27/28	0/2/2/2
1	4AC	1	2960	1	-	0/11/29/30	0/2/2/2
2	OMC	2	1040	2	-	0/9/27/28	0/2/2/2
2	OMG	2	680	2	-	0/9/27/28	0/3/3/3
1	4AC	1	922	1	-	0/11/29/30	0/2/2/2
2	4AC	2	731	2	-	0/11/29/30	0/2/2/2
1	OMC	1	615	1	-	0/9/27/28	0/2/2/2
1	4AC	1	2865	1	-	0/11/29/30	0/2/2/2
2	UR3	2	1467	2	-	0/7/25/26	0/2/2/2
2	4AC	2	868	2	-	0/11/29/30	0/2/2/2
2	4AC	2	17	2	-	0/11/29/30	0/2/2/2
2	OMU	2	20	2	-	6/9/27/28	0/2/2/2
2	5MC	2	1374	2	-	2/7/25/26	0/2/2/2
2	4AC	2	590	2	-	0/11/29/30	0/2/2/2
2	4AC	2	1239	2	-	0/11/29/30	0/2/2/2
1	4AC	1	314	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1667	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2925	1	-	0/11/29/30	0/2/2/2
2	4AC	2	379	2	-	0/11/29/30	0/2/2/2
2	4AC	2	303	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	2585	1	-	3/11/29/30	0/2/2/2
1	5MC	1	2733	1	-	4/7/25/26	0/2/2/2
2	5MC	2	1202	2	-	1/7/25/26	0/2/2/2
1	4AC	1	2718	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1885	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1222	66,1	-	0/11/29/30	0/2/2/2
1	4AC	1	1962	1	-	0/11/29/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	4AC	1	2287	1	-	0/11/29/30	0/2/2/2
2	4AC	2	839	2	-	0/11/29/30	0/2/2/2
2	4AC	2	636	2	-	0/11/29/30	0/2/2/2
1	4AC	1	1068	1	-	0/11/29/30	0/2/2/2
1	4AC	1	641	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	835	1	-	0/11/29/30	0/2/2/2
1	4AC	1	60	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1765	1	-	0/11/29/30	0/2/2/2
2	4AC	2	703	2	-	0/11/29/30	0/2/2/2
2	5MC	2	1505	2	-	2/7/25/26	0/2/2/2
1	5MC	1	2198	1	-	0/7/25/26	0/2/2/2
2	4AC	2	286	2	-	0/11/29/30	0/2/2/2
1	4AC	1	1460	1	-	0/11/29/30	0/2/2/2
2	5MC	2	693	2	-	0/7/25/26	0/2/2/2
1	4AC	1	1867	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	2992	1	-	3/11/29/30	0/2/2/2
2	OMU	2	830	2	-	0/9/27/28	0/2/2/2
1	4AC	1	829	1	-	1/11/29/30	0/2/2/2
2	OMC	2	846	2	-	0/9/27/28	0/2/2/2
1	4AC	1	1048	1	-	0/11/29/30	0/2/2/2
2	5MC	2	1025	2	-	0/7/25/26	0/2/2/2
1	5MC	1	2163	1	-	0/7/25/26	0/2/2/2
2	OMG	2	467	2	-	0/9/27/28	0/3/3/3
1	5MC	1	2093	1	-	0/7/25/26	0/2/2/2
1	4AC	1	2642	1	-	0/11/29/30	0/2/2/2
2	4AC	2	957	2	-	0/11/29/30	0/2/2/2
1	4AC	1	357	1	-	0/11/29/30	0/2/2/2
1	4AC	1	458	1	-	0/11/29/30	0/2/2/2
2	OMU	2	787	2	-	0/9/27/28	0/2/2/2
2	OMG	2	657	2	-	0/9/27/28	0/3/3/3
2	MA6	2	1487	2	-	0/11/29/30	0/3/3/3
1	4AC	1	341	1	-	0/11/29/30	0/2/2/2
2	LHH	2	1041	2	-	0/13/31/32	0/2/2/2
1	LHH	1	616	1	-	0/13/31/32	0/2/2/2
1	4AC	1	2136	1	-	0/11/29/30	0/2/2/2
1	4AC	1	211	1	-	0/11/29/30	0/2/2/2
2	OMG	2	934	2	-	2/9/27/28	0/3/3/3
1	4AC	1	2548	1	-	0/11/29/30	0/2/2/2
1	4AC	1	533	1	-	0/11/29/30	0/2/2/2
2	4AC	2	1479	2	-	0/11/29/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	4AC	2	828	2	-	0/11/29/30	0/2/2/2
2	4AC	2	626	2	-	0/11/29/30	0/2/2/2
1	OMG	1	923	66,1	-	2/9/27/28	0/3/3/3
3	4AC	3	32	3	-	0/11/29/30	0/2/2/2
1	4AC	1	1554	1	-	0/11/29/30	0/2/2/2
1	OMG	1	2678	1	-	1/9/27/28	0/3/3/3
1	A2M	1	1055	1	-	0/9/27/28	0/3/3/3
2	4AC	2	851	2	-	0/11/29/30	0/2/2/2
2	OMG	2	519	2	-	0/9/27/28	0/3/3/3
1	4AC	1	694	1	-	0/11/29/30	0/2/2/2
2	B8H	2	938	2	-	1/7/25/26	0/2/2/2
1	4AC	1	1550	1	-	0/11/29/30	0/2/2/2
2	4AC	2	1147	2	-	0/11/29/30	0/2/2/2
1	4AC	1	1755	1	-	2/11/29/30	0/2/2/2
1	4AC	1	1594	66,1	-	0/11/29/30	0/2/2/2
1	4AC	1	1934	1	-	0/11/29/30	0/2/2/2
1	4AC	1	161	1	-	0/11/29/30	0/2/2/2
2	6MZ	2	1469	2,66	-	0/9/27/28	0/3/3/3
1	OMG	1	2147	1	-	3/9/27/28	0/3/3/3
1	OMU	1	2784	1	-	0/9/27/28	0/2/2/2
1	4AC	1	1878	1	-	0/11/29/30	0/2/2/2
2	4AC	2	546	2	-	0/11/29/30	0/2/2/2
2	5MC	2	1498	2	-	3/7/25/26	0/2/2/2
1	4AC	1	2083	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2001	1	-	0/11/29/30	0/2/2/2
2	OMG	2	1069	2	-	2/9/27/28	0/3/3/3
1	4AC	1	91	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1621	1	-	0/11/29/30	0/2/2/2
2	OMC	2	773	2	-	0/9/27/28	0/2/2/2
2	5MC	2	1496	2	-	0/7/25/26	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	OMG	1	2138	1	-	0/9/27/28	0/3/3/3
2	5MC	2	875	2	-	0/7/25/26	0/2/2/2
2	5MC	2	535	2	-	0/7/25/26	0/2/2/2
1	4AC	1	1557	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	2027	1	-	0/11/29/30	0/2/2/2
1	4AC	1	243	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1873	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1293	1	-	0/11/29/30	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMG	2	913	2	-	1/9/27/28	0/3/3/3
2	4AC	2	718	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	1184	2	-	0/11/29/30	0/2/2/2
2	OMG	2	471	2	-	0/9/27/28	0/3/3/3
1	4AC	1	1780	1	-	0/11/29/30	0/2/2/2
1	4AC	1	1662	1	-	0/11/29/30	0/2/2/2
2	OMG	2	873	2	-	1/9/27/28	0/3/3/3
1	4AC	1	2937	66,1	-	1/11/29/30	0/2/2/2
1	OMG	1	2144	1	-	0/9/27/28	0/3/3/3
2	4AC	2	751	2	-	0/11/29/30	0/2/2/2
1	OMG	1	789	1	-	4/9/27/28	0/3/3/3
1	4AC	1	2966	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2329	1	-	0/11/29/30	0/2/2/2
2	MA6	2	1488	2	-	2/11/29/30	0/3/3/3
2	4AC	2	394	2	-	0/11/29/30	0/2/2/2
1	4AC	1	1617	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	981	1	-	0/11/29/30	0/2/2/2
2	4AC	2	53	2	-	0/11/29/30	0/2/2/2
1	A2M	1	2173	1	-	0/9/27/28	0/3/3/3
1	4AC	1	136	1	-	0/11/29/30	0/2/2/2
1	OMG	1	328	1	-	0/9/27/28	0/3/3/3
1	4AC	1	2608	1	-	3/11/29/30	0/2/2/2
2	OMU	2	774	2	-	0/9/27/28	0/2/2/2
2	OMU	2	64	2	-	0/9/27/28	0/2/2/2
1	4AC	1	3004	1	-	0/11/29/30	0/2/2/2
1	4AC	1	2249	1	-	0/11/29/30	0/2/2/2
2	OMU	2	1380	2	-	0/9/27/28	0/2/2/2
2	4AC	2	1233	2	-	0/11/29/30	0/2/2/2
2	4AC	2	319	2	-	0/11/29/30	0/2/2/2
2	4AC	2	848	2	-	0/11/29/30	0/2/2/2
1	4AC	1	1938	1	-	0/11/29/30	0/2/2/2
2	4AC	2	511	2	-	0/11/29/30	0/2/2/2
2	OMC	2	129	2	-	0/9/27/28	0/2/2/2
2	4AC	2	479	2	-	0/11/29/30	0/2/2/2
2	OMC	2	1376	2	-	0/9/27/28	0/2/2/2
1	4AC	1	2570	1	-	0/11/29/30	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	4.54	1.47	1.39
2	2	1488	MA6	C5-C4	4.42	1.47	1.39
2	2	373	A2M	C5-C4	4.37	1.47	1.39
1	1	1055	A2M	C5-C4	4.36	1.47	1.39
2	2	1487	MA6	C5-C4	4.33	1.47	1.39

The worst 5 of 639 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1055	A2M	C5-C4-N3	-6.47	118.31	126.75
2	2	373	A2M	C5-C4-N3	-6.37	118.43	126.75
2	2	657	OMG	C5-C4-N3	-6.32	118.21	128.46
2	2	680	OMG	C5-C4-N3	-6.31	118.23	128.46
1	1	2173	A2M	C5-C4-N3	-6.30	118.53	126.75

There are no chirality outliers.

5 of 51 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
1	1	2608	4AC	O4'-C1'-N1-C2
1	1	2608	4AC	O4'-C1'-N1-C6

There are no ring outliers.

84 monomers are involved in 118 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	229	4AC	1	0
1	1	802	4AC	2	0
1	1	2908	4AC	1	0
1	1	451	4AC	1	0
1	1	2960	4AC	1	0
2	2	680	OMG	1	0
1	1	922	4AC	1	0
2	2	731	4AC	2	0
2	2	590	4AC	1	0
2	2	1239	4AC	1	0
1	1	314	4AC	1	0
1	1	1667	4AC	2	0
1	1	2925	4AC	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	379	4AC	2	0
1	1	2585	4AC	3	0
1	1	2718	4AC	2	0
1	1	2287	4AC	2	0
2	2	839	4AC	1	0
2	2	636	4AC	2	0
2	2	1177	OMU	1	0
1	1	60	4AC	1	0
1	1	1765	4AC	1	0
2	2	703	4AC	3	0
2	2	1505	5MC	1	0
1	1	2198	5MC	1	0
1	1	1867	4AC	1	0
2	2	373	A2M	2	0
1	1	2992	4AC	1	0
2	2	830	OMU	1	0
1	1	829	4AC	2	0
2	2	1025	5MC	1	0
2	2	467	OMG	1	0
2	2	957	4AC	1	0
1	1	357	4AC	1	0
1	1	458	4AC	1	0
2	2	657	OMG	1	0
2	2	1487	MA6	2	0
1	1	341	4AC	1	0
1	1	2136	4AC	1	0
1	1	211	4AC	1	0
2	2	934	OMG	1	0
1	1	533	4AC	1	0
2	2	1479	4AC	1	0
2	2	828	4AC	1	0
2	2	626	4AC	3	0
3	3	32	4AC	2	0
1	1	2678	OMG	1	0
1	1	1055	A2M	2	0
2	2	851	4AC	1	0
2	2	519	OMG	1	0
1	1	1550	4AC	3	0
1	1	1755	4AC	2	0
1	1	1594	4AC	1	0
1	1	1934	4AC	2	0
1	1	1878	4AC	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	2	546	4AC	1	0
1	1	2001	4AC	2	0
2	2	1069	OMG	1	0
1	1	91	4AC	1	0
2	2	1496	5MC	1	0
1	1	1695	4AC	1	0
1	1	2183	5MC	1	0
1	1	1065	4AC	3	0
1	1	2027	4AC	1	0
1	1	1293	4AC	1	0
2	2	1184	4AC	2	0
1	1	1780	4AC	3	0
1	1	1662	4AC	1	0
1	1	789	OMG	2	0
1	1	2329	4AC	1	0
2	2	1488	MA6	3	0
2	2	394	4AC	2	0
1	1	1617	4AC	2	0
1	1	2608	4AC	2	0
2	2	774	OMU	2	0
2	2	64	OMU	1	0
1	1	3004	4AC	1	0
2	2	1380	OMU	2	0
2	2	319	4AC	1	0
2	2	848	4AC	1	0
2	2	511	4AC	2	0
2	2	479	4AC	1	0
2	2	1376	OMC	1	0
1	1	2570	4AC	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 257 ligands modelled in this entry, 257 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	11.57

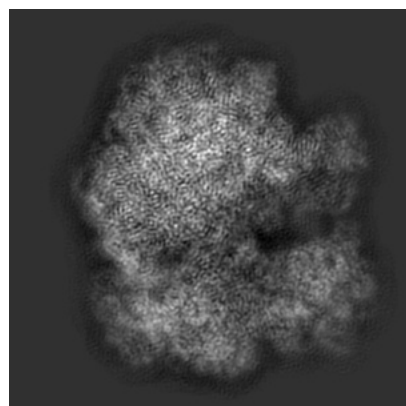
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55137. These allow visual inspection of the internal detail of the map and identification of artifacts.

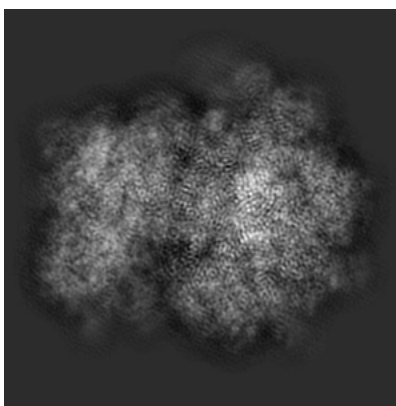
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

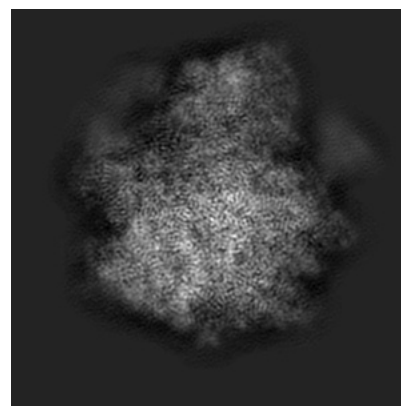
6.1.1 Primary map



X

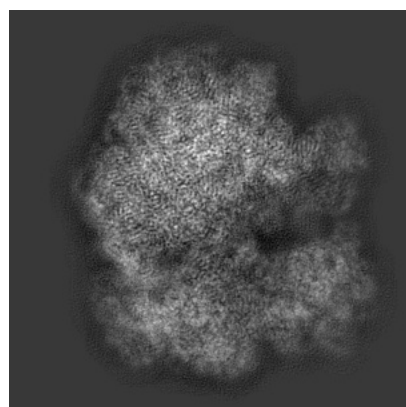


Y

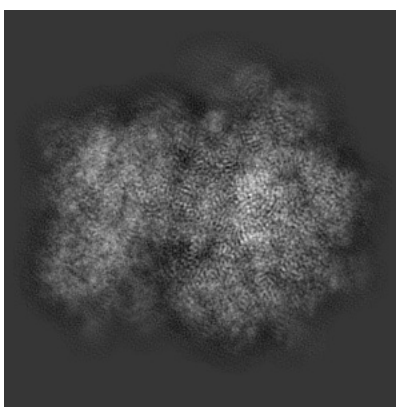


Z

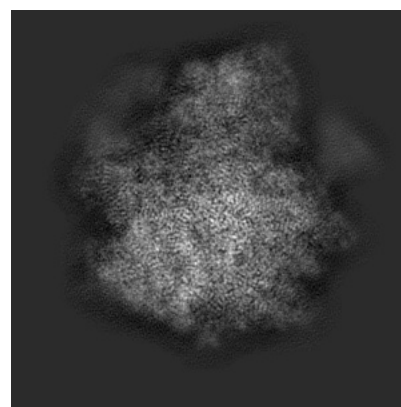
6.1.2 Raw map



X



Y

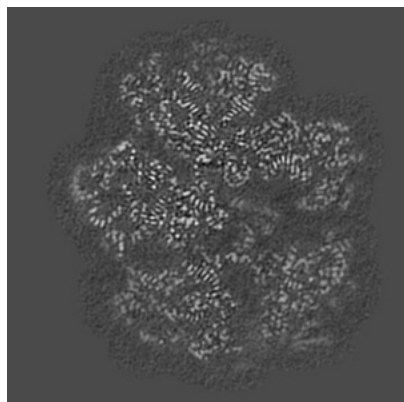


Z

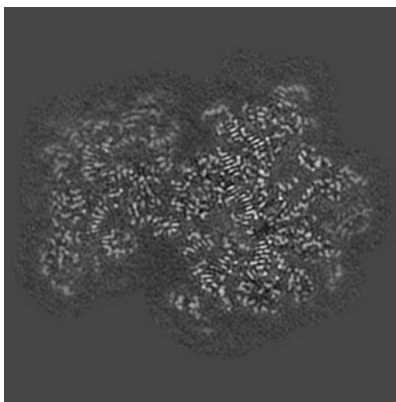
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

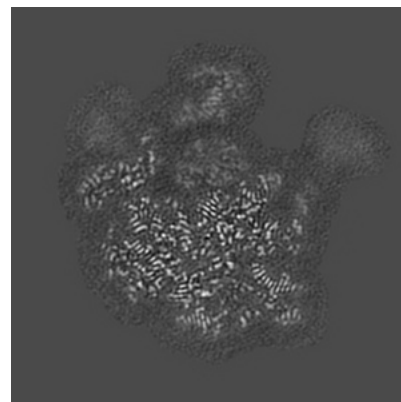
6.2.1 Primary map



X Index: 180

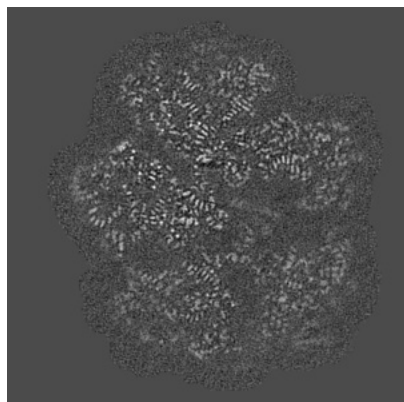


Y Index: 180

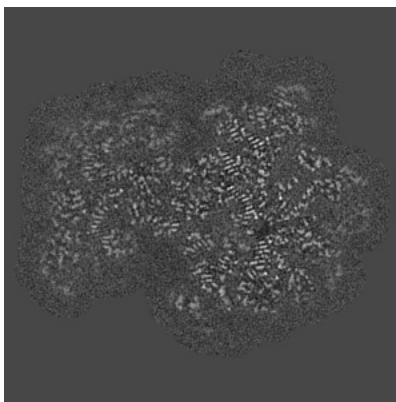


Z Index: 180

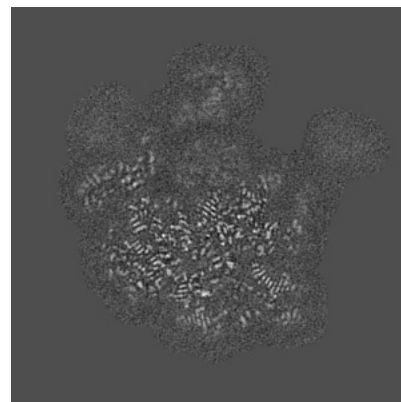
6.2.2 Raw map



X Index: 180



Y Index: 180

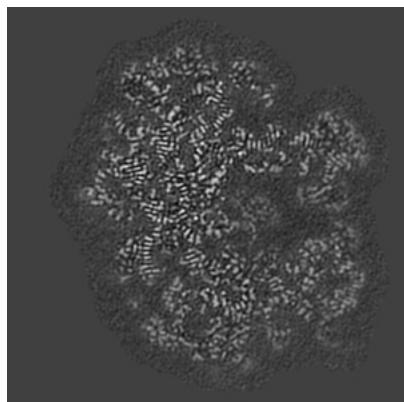


Z Index: 180

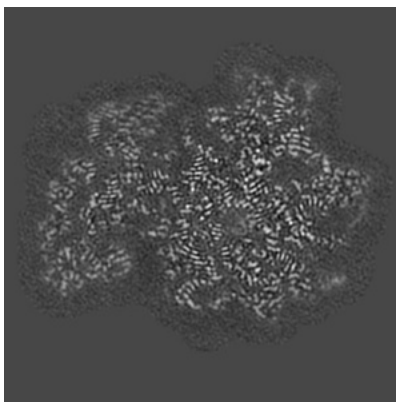
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

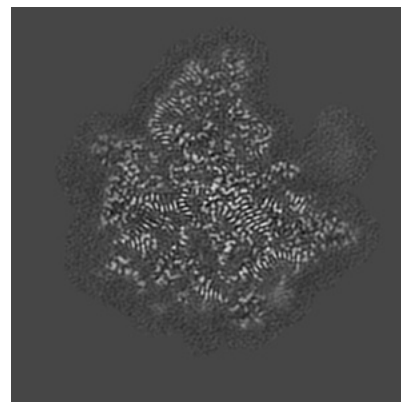
6.3.1 Primary map



X Index: 195

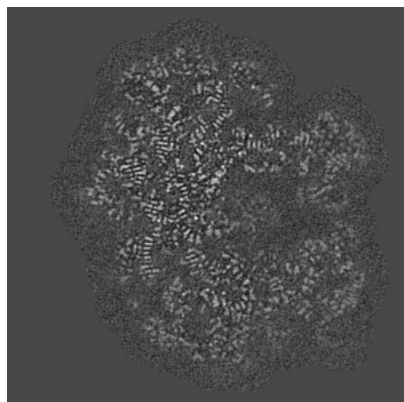


Y Index: 170

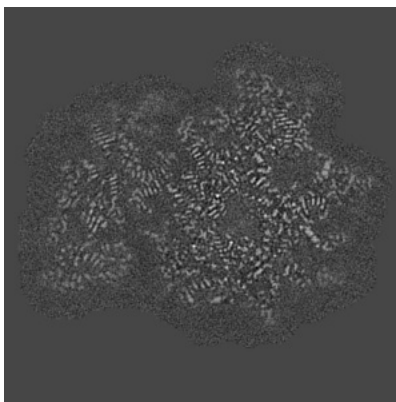


Z Index: 232

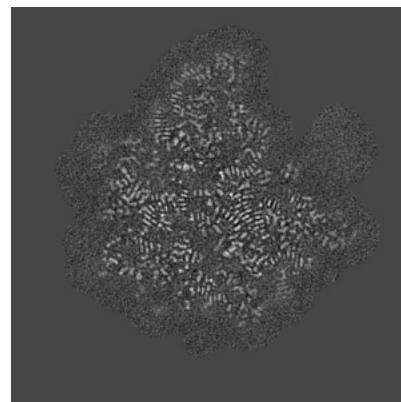
6.3.2 Raw map



X Index: 195



Y Index: 166

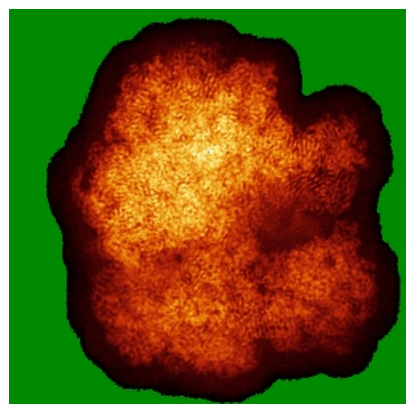


Z Index: 229

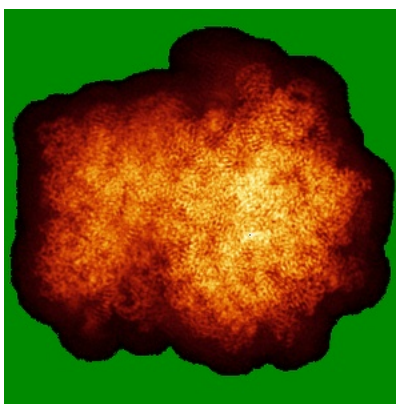
The images above show the largest variance slices of the map in three orthogonal directions.

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

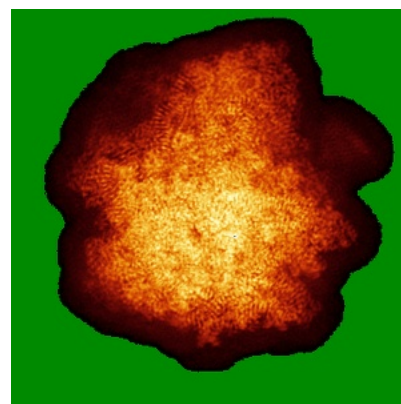
6.4.1 Primary map



X

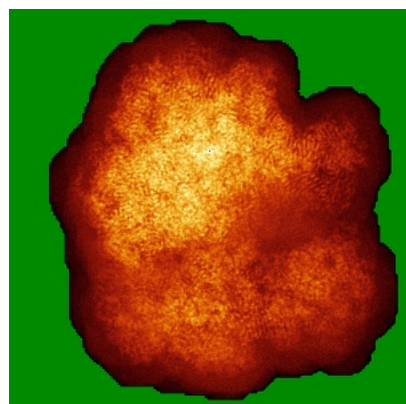


Y

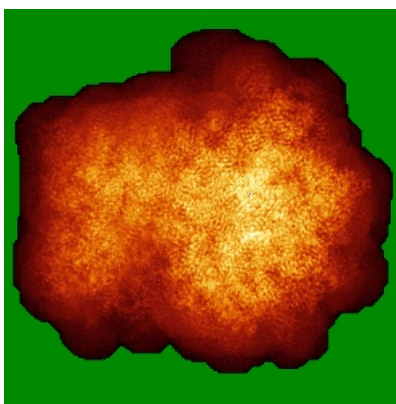


Z

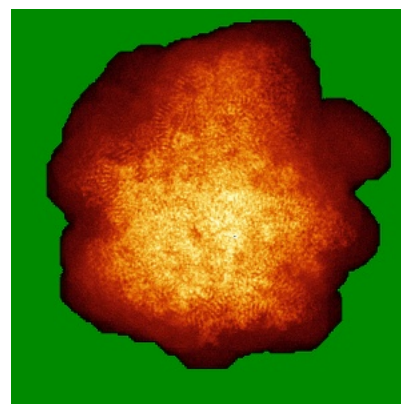
6.4.2 Raw map



X



Y

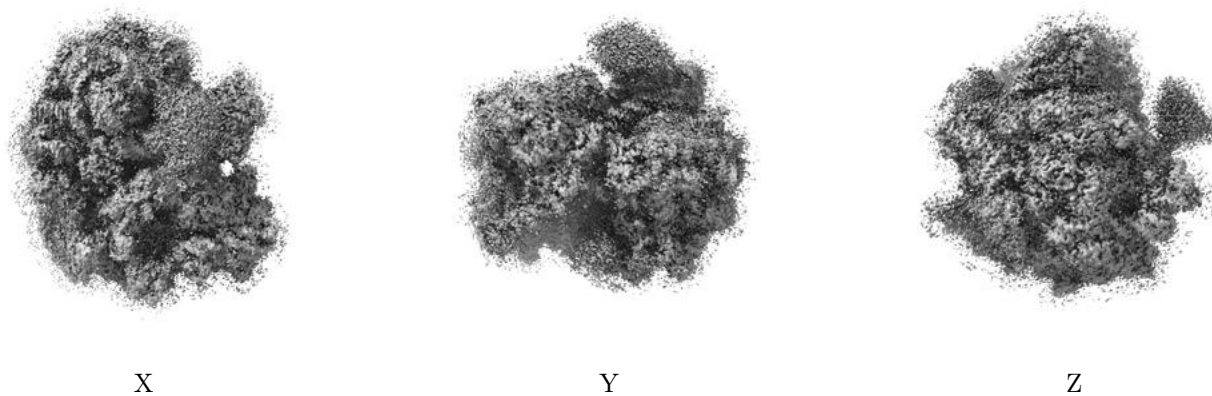


Z

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.

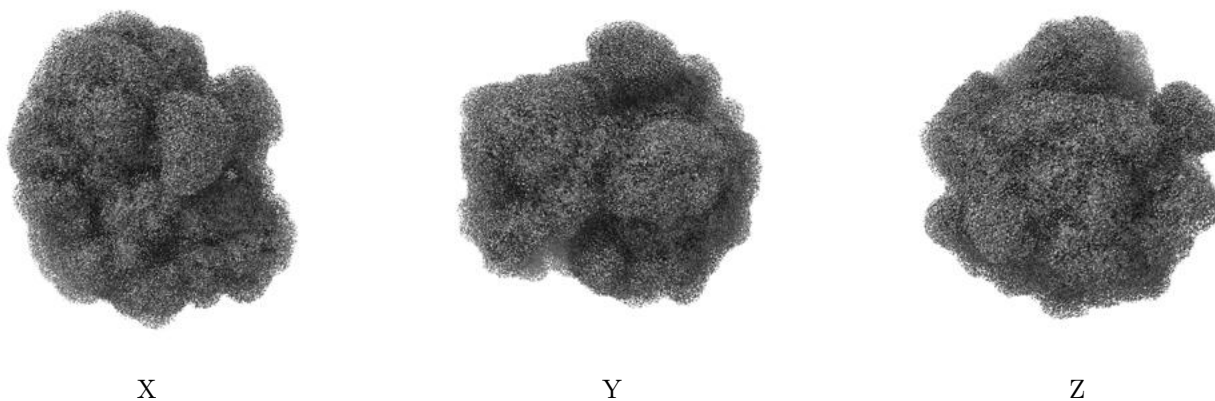
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00095. 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.

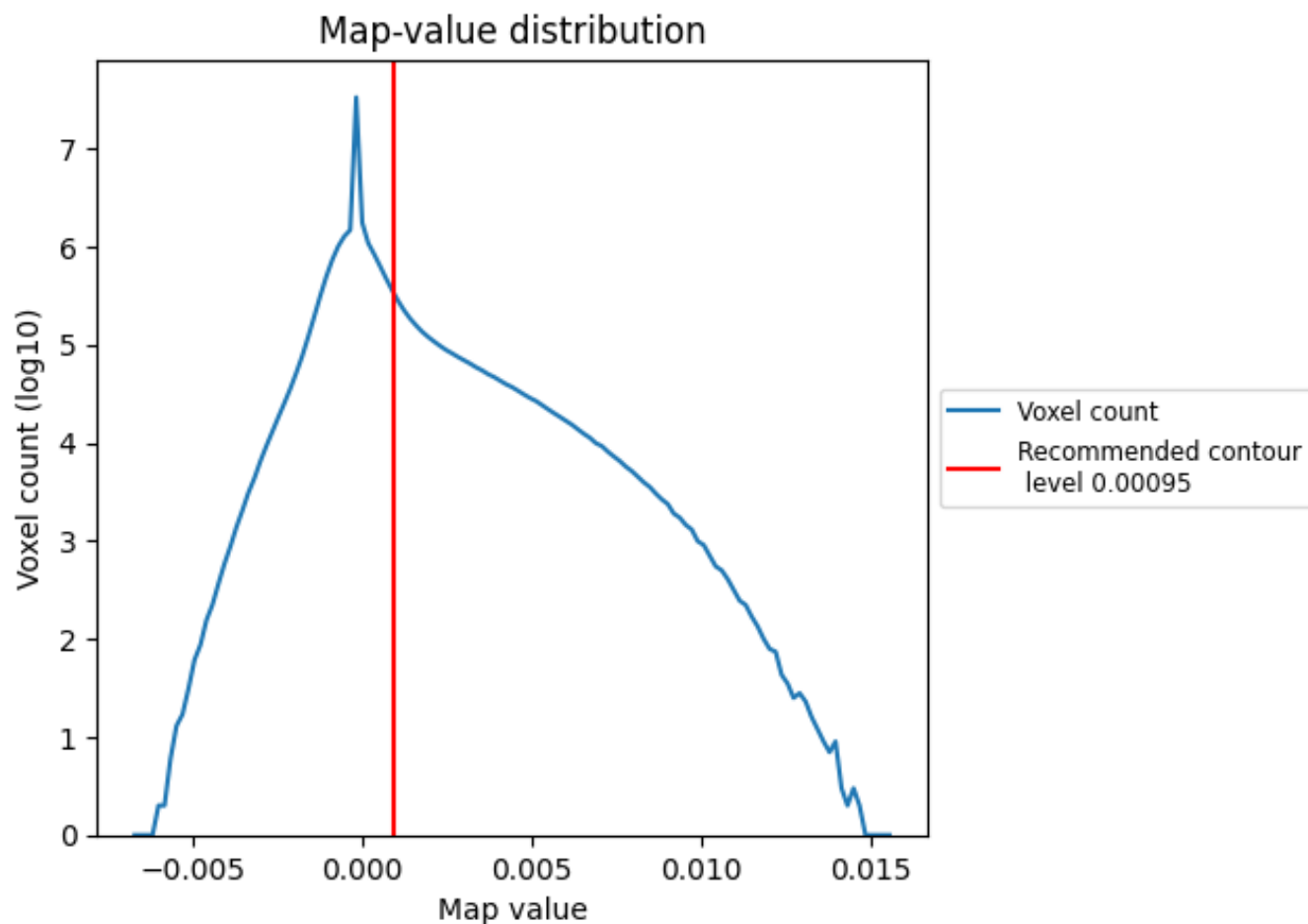
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

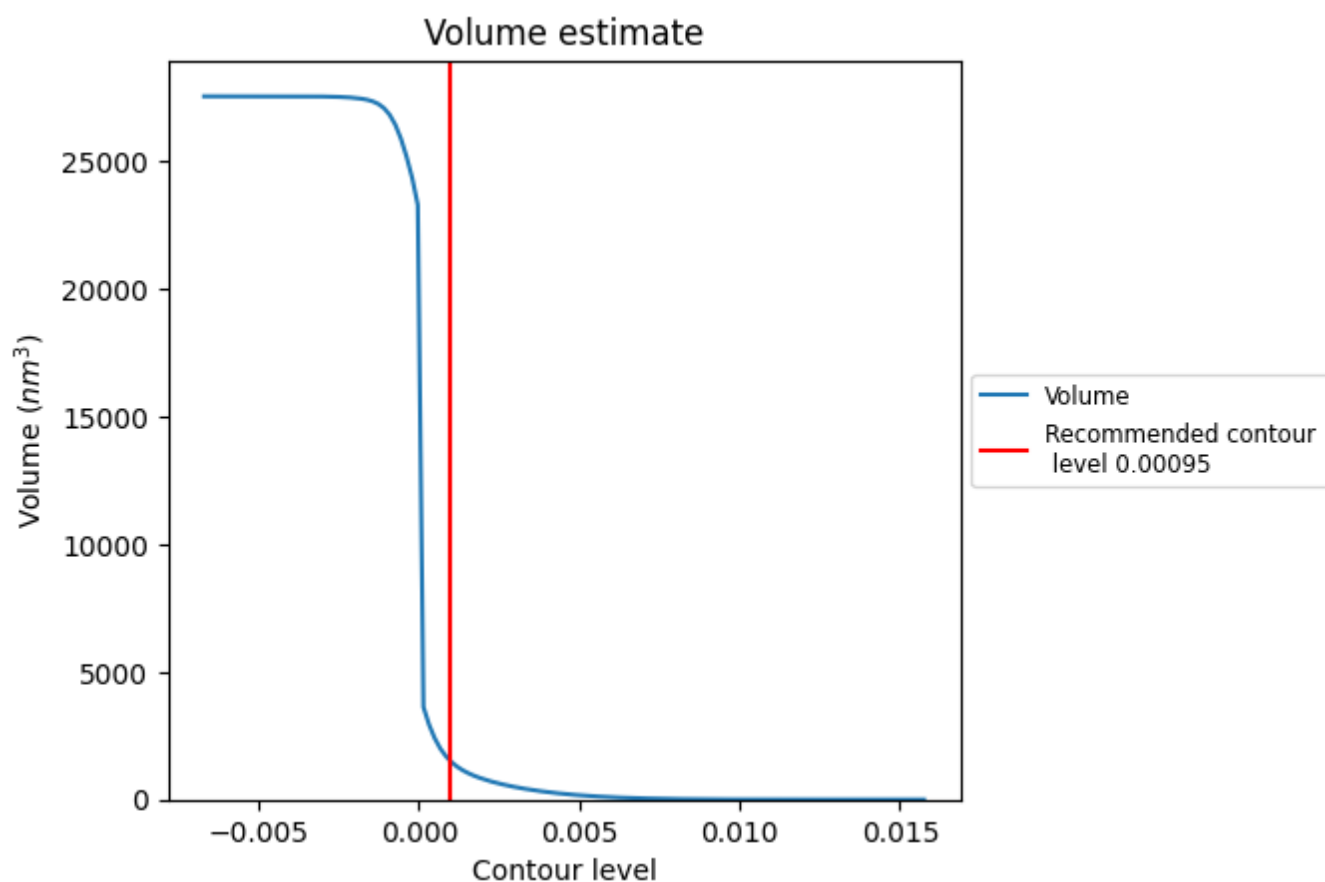
This section contains the results of statistical analysis of the map.

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.

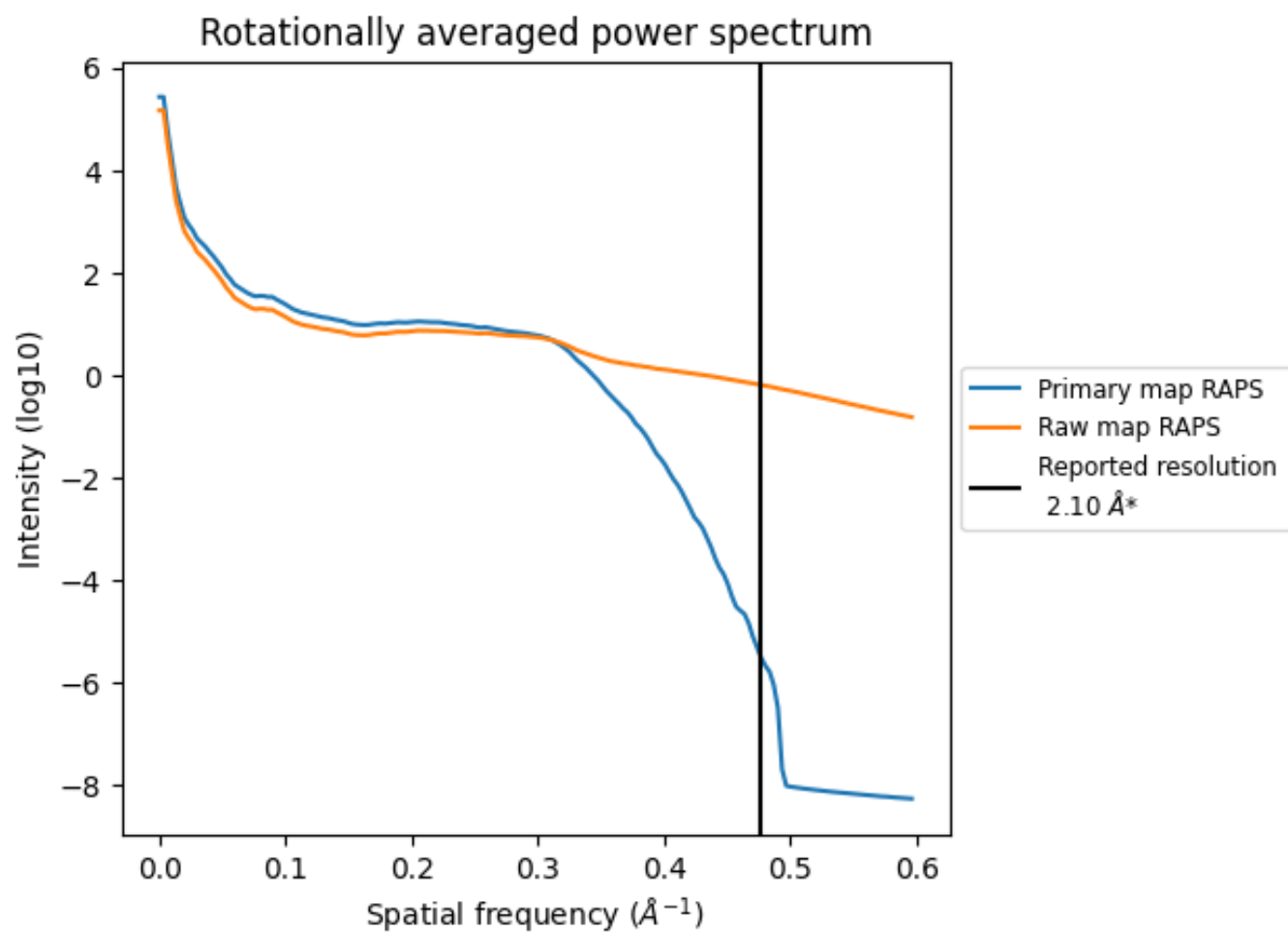
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1560 nm^3 ; this corresponds to an approximate mass of 1409 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 ⓘ

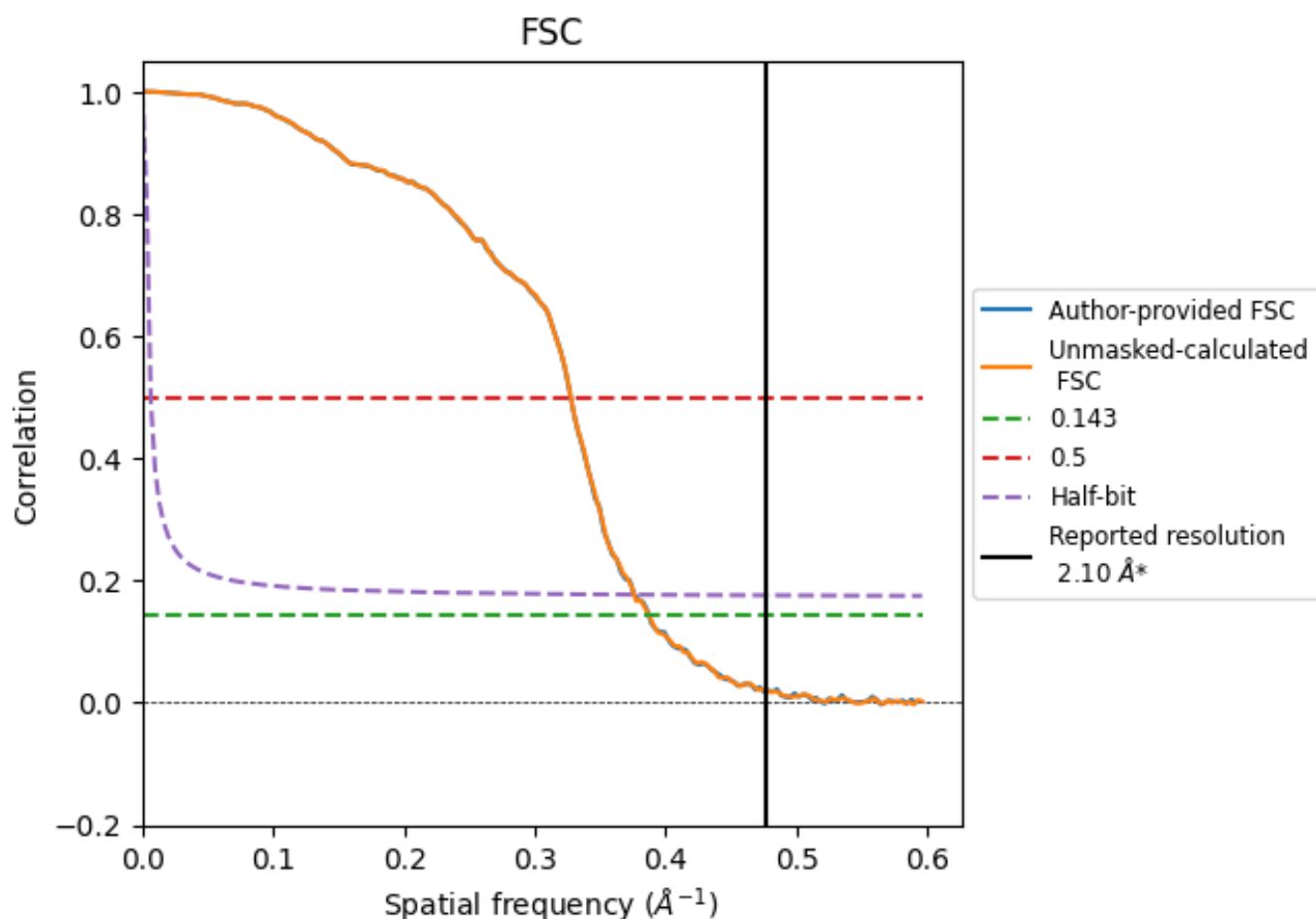


*Reported resolution corresponds to spatial frequency of 0.476 $\text{\AA}^{-1}$

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 $0.476 \text{ \AA}^{-1}$

8.2 Resolution estimates

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.10	-	-
Author-provided FSC curve	2.58	3.05	2.66
Unmasked-calculated*	2.58	3.05	2.66

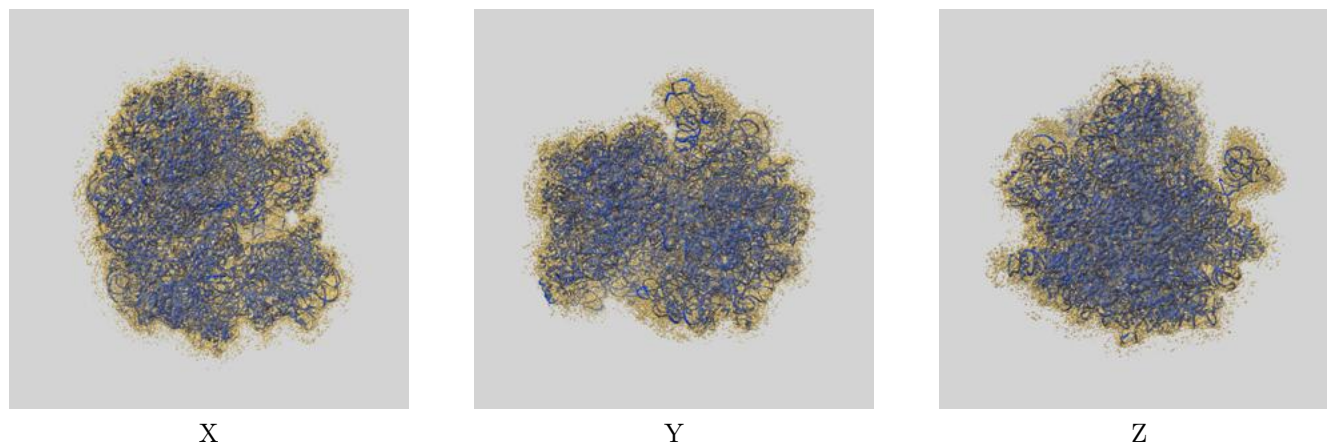
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 2.58 differs from the reported value 2.1 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.58 differs from the reported value 2.1 by more than 10 %

9 Map-model fit [i](#)

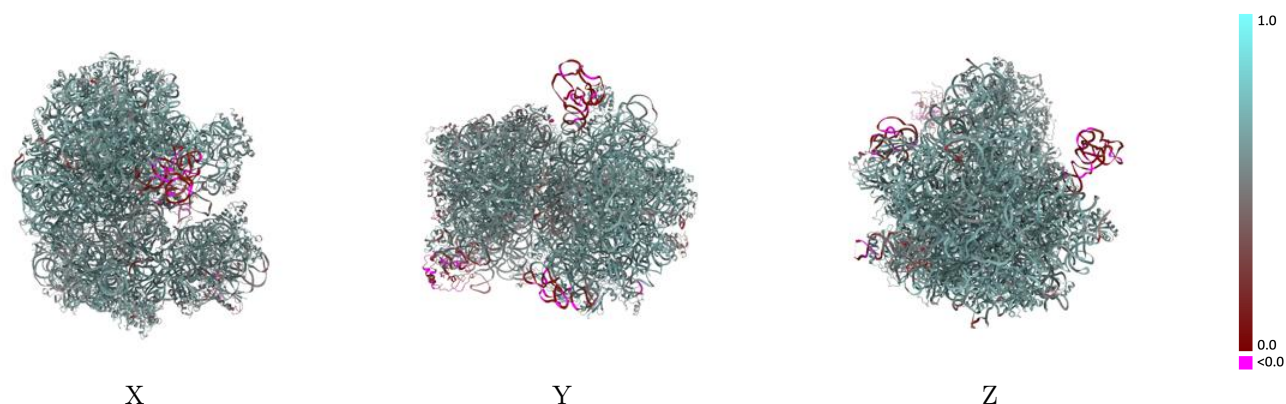
This section contains information regarding the fit between EMDB map EMD-55137 and PDB model 9SRC. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



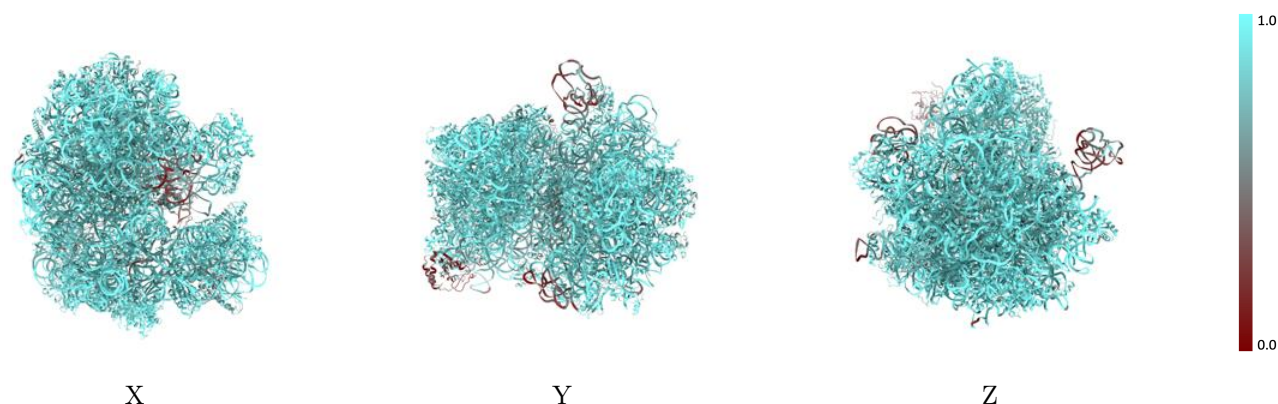
The images above show the 3D surface view of the map at the recommended contour level 0.00095 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



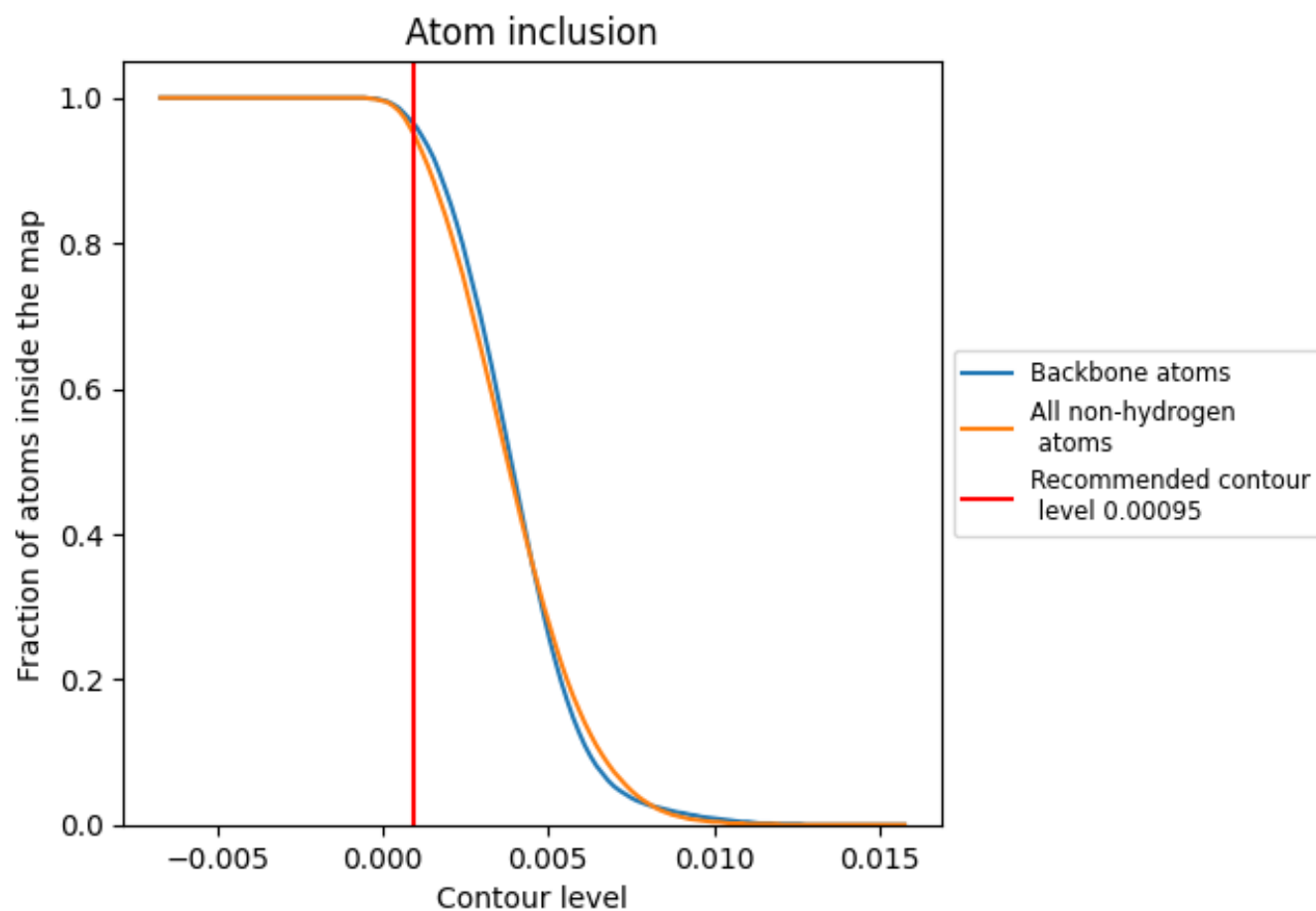
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.00095).

9.4 Atom inclusion [i](#)



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 (0.00095) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9500	 0.5870
1	 0.9580	 0.5980
2	 0.9790	 0.5850
3	 0.9940	 0.5990
A0	 0.9750	 0.6480
A3	 0.3140	 0.1390
AA	 0.8690	 0.5040
AB	 0.9580	 0.5550
AC	 0.9640	 0.5770
AD	 0.9630	 0.5960
AE	 0.9590	 0.5610
AF	 0.9740	 0.6070
AG	 0.8960	 0.4970
AH	 0.9450	 0.5670
AI	 0.9710	 0.6070
AJ	 0.9490	 0.5800
AK	 0.9640	 0.5690
AL	 0.8580	 0.4930
AM	 0.9250	 0.5500
AN	 0.9460	 0.6000
AO	 0.9220	 0.5370
AP	 0.9170	 0.5590
AQ	 0.9300	 0.5570
AR	 0.9490	 0.5900
AS	 0.9370	 0.5400
AT	 0.8830	 0.5220
AU	 0.9590	 0.5680
AV	 0.9200	 0.5220
AW	 0.9060	 0.4980
AX	 0.9130	 0.5300
AY	 0.1810	 0.1380
AZ	 0.8780	 0.5100
B4	 0.7540	 0.4060
B5	 0.9700	 0.5870
B6	 0.7810	 0.5550



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Chain	Atom inclusion	Q-score
BB	 0.9780	 0.6470
BC	 0.9760	 0.6390
BD	 0.9830	 0.6350
BE	 0.9270	 0.5470
BF	 0.9410	 0.6010
BG	 0.9540	 0.5930
BI	 0.9740	 0.6360
BJ	 0.9780	 0.6390
BK	 0.9490	 0.5650
BL	 0.9660	 0.6090
BM	 0.9920	 0.6520
BN	 0.9510	 0.6160
BO	 0.9690	 0.5910
BP	 0.9900	 0.6320
BQ	 0.9700	 0.6270
BR	 0.9820	 0.6440
BS	 0.9780	 0.6380
BT	 0.9800	 0.6190
BU	 0.9660	 0.6150
BV	 0.9760	 0.6320
BW	 0.8950	 0.5720
BY	 0.9810	 0.6350
BZ	 0.9200	 0.5660
Ba	 0.9590	 0.6060
Bb	 0.9820	 0.6420
Bc	 0.9810	 0.6390
Bd	 0.9700	 0.6260
Be	 0.9980	 0.6470
Bf	 0.9980	 0.6410
Bg	 0.9730	 0.6230
Bi	 0.9560	 0.6400
Bj	 0.9720	 0.6320
Bk	 0.9610	 0.6050
Bl	 0.9280	 0.5970
H	 0.7590	 0.5310