



wwPDB EM Validation Summary Report ⓘ

Nov 5, 2024 – 12:47 PM EST

PDB ID : 7N8B
EMDB ID : EMD-24235
Title : Cycloheximide bound vacant 80S structure isolated from cbf5-D95A
Authors : Rai, J.; Zhao, Y.; Li, H.
Deposited on : 2021-06-14
Resolution : 3.05 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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

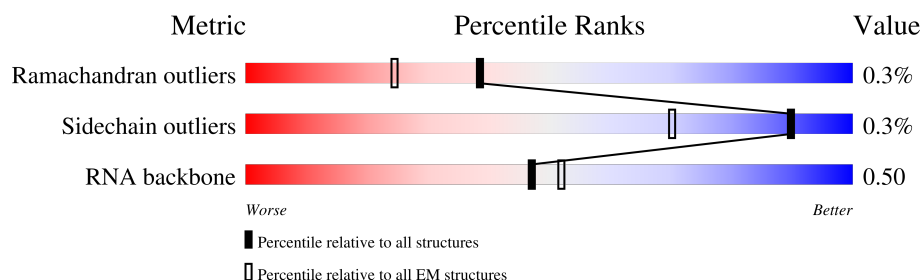
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.05 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



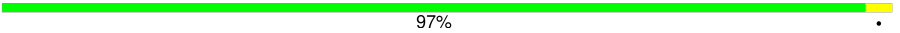
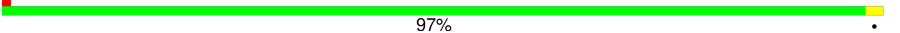
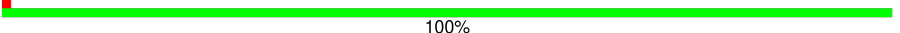
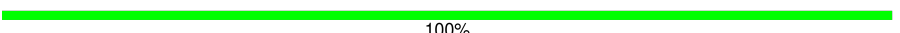

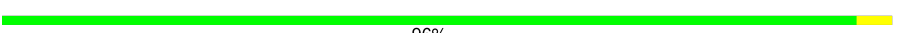









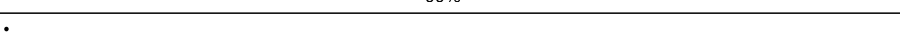
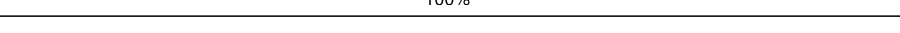
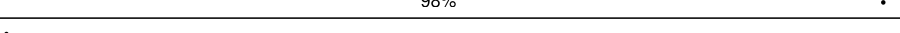
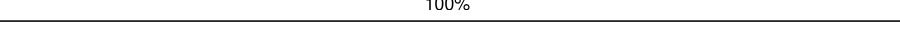
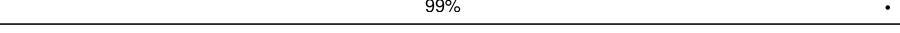
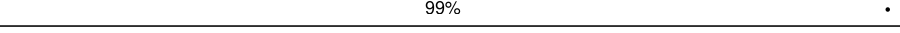
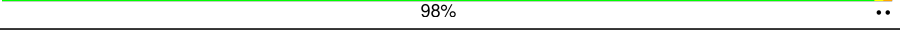
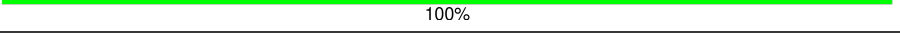
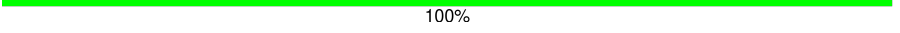
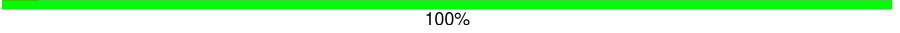
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	A1	3156	
2	A3	121	
3	A4	158	
4	AA	247	
5	AB	386	
6	AC	361	
7	AD	292	
8	AE	156	

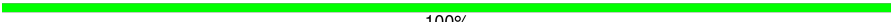
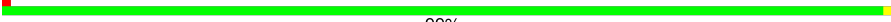













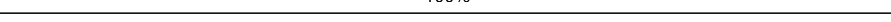
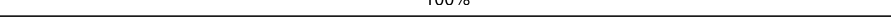
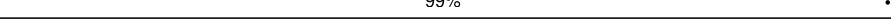
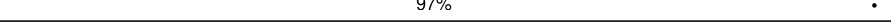
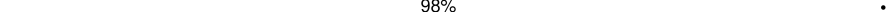
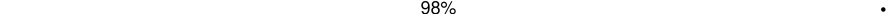
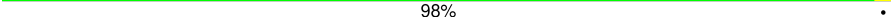

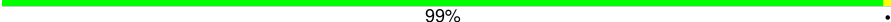
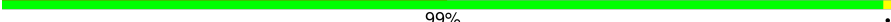
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Mol	Chain	Length	Quality of chain
9	AF	222	 97% .
10	AG	230	 97% .
11	AH	190	 100% .
12	AI	205	 100% .
13	AJ	169	 5% 98% ..
14	AL	193	 96% .
15	AM	136	 99% .
16	AN	203	 99% .
17	AO	197	 98% ..
18	AP	175	 99% .
19	AQ	185	 99% .
20	AR	188	 7% 99% .
21	AS	172	 99% .
22	AT	159	 99% .
23	AU	100	 99% .
24	AV	136	 100% .
25	AW	63	 98% .
26	AX	121	 100% .
27	AY	126	 99% .
28	AZ	135	 99% .
29	Aa	148	 98% ..
30	Ab	58	 100% .
31	Ac	97	 100% .
32	Ad	109	 100% .
33	Ae	127	 100% .

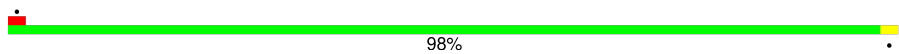
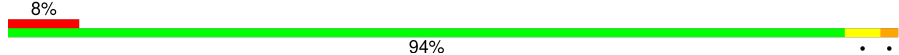
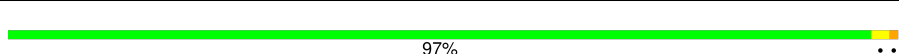
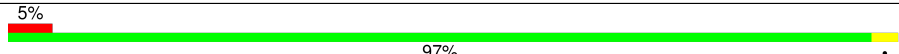
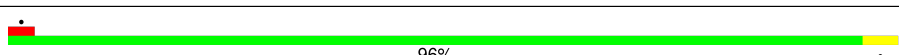
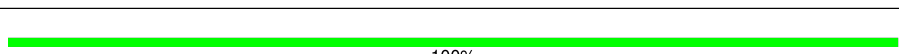
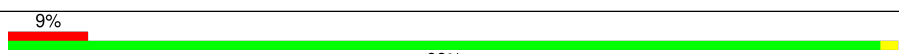
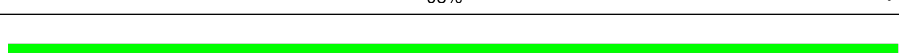
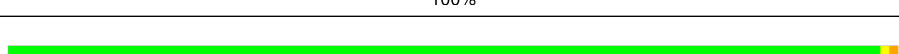
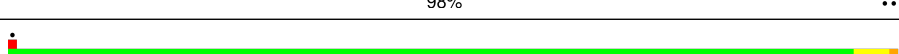
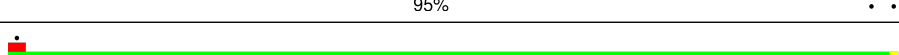
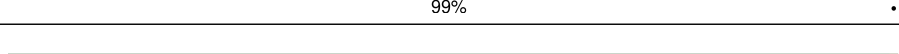
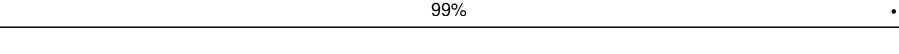
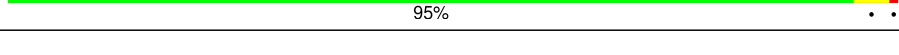
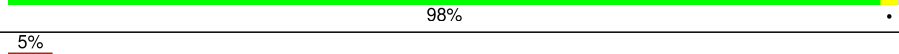
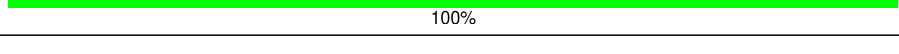
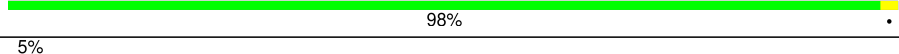
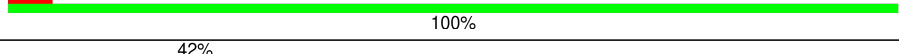
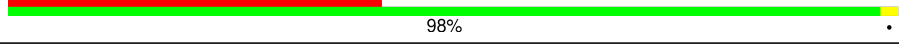
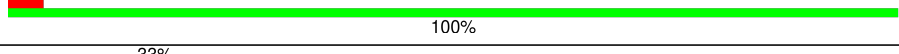
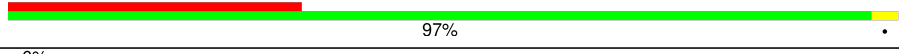
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Mol	Chain	Length	Quality of chain
34	Af	106	 100%
35	Ag	112	 99%
36	Ah	119	 98%
37	Ai	99	 98%
38	Aj	87	 100%
39	Ak	77	 100%
40	Al	50	 98%
41	Am	52	 98%
42	An	25	 100%
43	Ao	105	 100%
44	Ap	91	 98%
45	BA	206	 98%
46	BB	214	 96%
47	BC	217	 98%
48	BD	223	 100%
49	BE	260	 100%
50	BF	206	 99%
51	BG	226	 97%
52	BH	184	 98%
53	BI	188	 98%
54	BJ	185	 98%
55	BK	96	 100%
56	BL	155	 99%
57	BM	121	 99%
58	BN	150	 100%

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Mol	Chain	Length	Quality of chain
59	BO	127	
60	BP	124	
61	BQ	141	
62	BR	121	
63	BS	145	
64	BT	141	
65	BU	107	
66	BV	87	
67	BW	129	
68	BX	144	
69	BY	134	
70	BZ	69	
71	Ba	97	
72	Bb	81	
73	Bc	63	
74	Bd	53	
75	Be	60	
76	Bf	57	
77	Bg	312	
78	Bh	89	
79	B5	1783	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
79	3AU	B5	1191	X	-	-	-
79	G7M	B5	1575	X	-	-	-

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 199900 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 25S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A1	3156	Total	C	N	O	P	0	0
			67535	30189	12152	22038	3156		

- Molecule 2 is a RNA chain called 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A3	121	Total	C	N	O	P	0	0
			2579	1152	461	845	121		

- Molecule 3 is a RNA chain called 5.8S.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A4	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 4 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AA	247	Total	C	N	O	S	0	0
			1878	1170	381	326	1		

- Molecule 5 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AB	386	Total	C	N	O	S	0	0
			3079	1954	584	533	8		

- Molecule 6 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AC	361	Total	C	N	O	S	0	0
			2748	1729	522	494	3		

- Molecule 7 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AD	292	Total	C	N	O	S	0	0
			2341	1478	408	453	2		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AE	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	LEU	deletion	UNP Q02326
AE	?	-	THR	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	GLU	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326
AE	?	-	GLU	deletion	UNP Q02326
AE	?	-	ALA	deletion	UNP Q02326
AE	?	-	ASN	deletion	UNP Q02326
AE	?	-	LEU	deletion	UNP Q02326
AE	?	-	PHE	deletion	UNP Q02326
AE	?	-	PRO	deletion	UNP Q02326
AE	?	-	GLU	deletion	UNP Q02326
AE	?	-	GLN	deletion	UNP Q02326
AE	?	-	GLN	deletion	UNP Q02326
AE	?	-	ASN	deletion	UNP Q02326
AE	?	-	LYS	deletion	UNP Q02326

- Molecule 9 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AF	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 10 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AG	230	Total	C	N	O	S	0	0
			1798	1149	323	323	3		

- Molecule 11 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AH	190	Total	C	N	O	S	0	0
			1510	957	273	276	4		

- Molecule 12 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AI	205	Total	C	N	O	S	0	0
			1672	1063	316	288	5		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AI	?	-	MET	deletion	UNP P41805
AI	?	-	LEU	deletion	UNP P41805
AI	?	-	SER	deletion	UNP P41805
AI	?	-	CYS	deletion	UNP P41805
AI	?	-	ALA	deletion	UNP P41805
AI	?	-	GLY	deletion	UNP P41805
AI	?	-	ALA	deletion	UNP P41805
AI	?	-	ASP	deletion	UNP P41805
AI	?	-	ARG	deletion	UNP P41805
AI	?	-	LEU	deletion	UNP P41805
AI	?	-	GLN	deletion	UNP P41805
AI	?	-	GLN	deletion	UNP P41805

- Molecule 13 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AJ	169	Total	C	N	O	S	0	0
			1353	847	253	249	4		

- Molecule 14 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	AL	193	Total	C	N	O	0	0
			1543	962	315	266		

- Molecule 15 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AM	136	Total	C	N	O	S	0	0
			1053	675	199	177	2		

- Molecule 16 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AN	203	Total	C	N	O	S	0	0
			1720	1077	361	281	1		

- Molecule 17 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AO	197	Total	C	N	O	S	197	0
			1555	1003	289	262	1		

- Molecule 18 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AP	175	Total	C	N	O		0	0
			1388	862	277	249			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	VAL	deletion	UNP P05740
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	LYS	deletion	UNP P05740
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	ALA	deletion	UNP P05740
AP	?	-	GLU	deletion	UNP P05740
AP	?	-	LYS	deletion	UNP P05740

- Molecule 19 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AQ	185	Total	C	N	O	S	0	0
			1441	908	290	241	2		

- Molecule 20 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	AR	188	Total	C	N	O		
			1521	935	326	260	0	0

- Molecule 21 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AS	172	Total	C	N	O	S		
			1445	930	267	244	4	0	0

- Molecule 22 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AT	159	Total	C	N	O	S		
			1276	805	246	221	4	0	0

- Molecule 23 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	AU	100	Total	C	N	O		
			796	516	131	149	0	0

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AV	136	Total	C	N	O	S		
			1003	628	189	179	7	0	0

- Molecule 25 is a protein called 60S ribosomal protein L24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AW	63	Total	C	N	O	S		
			521	336	102	82	1	0	0

- Molecule 26 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AX	121	Total	C	N	O	S		
			968	623	170	173	2	0	0

- Molecule 27 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	AY	126	Total	C	N	O	0	0
			993	625	192	176		

- Molecule 28 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	AZ	135	Total	C	N	O	0	0
			1092	710	202	180		

- Molecule 29 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Aa	148	Total	C	N	O	S	0	0
			1173	749	231	190	3		

- Molecule 30 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
30	Ab	58	Total	C	N	O	0	0
			462	289	100	73		

- Molecule 31 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ac	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 32 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Ad	109	Total	C	N	O	S	0	0
			890	565	168	156	1		

- Molecule 33 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ae	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 34 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Af	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 35 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ag	112	Total	C	N	O	S	0	0
			880	545	179	152	4		

- Molecule 36 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ah	119	Total	C	N	O	S	0	0
			969	615	186	167	1		

- Molecule 37 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ai	99	Total	C	N	O	S	0	0
			771	481	156	132	2		

- Molecule 38 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Aj	87	Total	C	N	O	S	0	0
			681	414	148	114	5		

- Molecule 39 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
39	Ak	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 40 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Al	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 41 is a protein called 60S ribosomal protein L40-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Am	52	Total	C	N	O	S	0	0
			417	259	86	67	5		

- Molecule 42 is a protein called 60S ribosomal protein L41-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	An	25	Total	C	N	O	S	0	0
			233	142	63	27	1		

- Molecule 43 is a protein called 60S ribosomal protein L42-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Ao	105	Total	C	N	O	S	0	0
			847	534	170	138	5		

- Molecule 44 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ap	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 45 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BA	206	Total	C	N	O	S	0	0
			1612	1034	285	291	2		

- Molecule 46 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	BB	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 47 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BC	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 48 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	BD	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 49 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	BE	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 50 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	BF	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 51 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	BG	226	Total	C	N	O	S	0	0
			1820	1142	350	325	3		

- Molecule 52 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
52	BH	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 53 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BI	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BI	?	-	LYS	deletion	UNP P0CX39
BI	?	-	LYS	deletion	UNP P0CX39
BI	?	-	ASN	deletion	UNP P0CX39
BI	?	-	VAL	deletion	UNP P0CX39
BI	?	-	LYS	deletion	UNP P0CX39
BI	?	-	GLU	deletion	UNP P0CX39

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Chain	Residue	Modelled	Actual	Comment	Reference
BI	?	-	GLU	deletion	UNP P0CX39
BI	?	-	GLU	deletion	UNP P0CX39
BI	?	-	THR	deletion	UNP P0CX39
BI	?	-	VAL	deletion	UNP P0CX39
BI	?	-	ALA	deletion	UNP P0CX39

- Molecule 54 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BJ	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 55 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BK	96	Total	C	N	O	S	0	0
			817	529	133	153	2		

- Molecule 56 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BL	155	Total	C	N	O	S	0	0
			1244	798	235	208	3		

- Molecule 57 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BM	121	Total	C	N	O	S	0	0
			913	574	162	175	2		

- Molecule 58 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	BN	150	Total	C	N	O	S	0	0
			1192	759	224	207	2		

- Molecule 59 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	BO	127	Total	C	N	O	S	0	0
			941	578	186	174	3		

- Molecule 60 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	BP	124	Total	C	N	O	S	0	0
			991	631	187	166	7		

- Molecule 61 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	BQ	141	Total	C	N	O	S	0	0
			1105	708	203	194			

- Molecule 62 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	BR	121	Total	C	N	O	S	0	0
			975	611	183	179	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
BR	?	-	SER	deletion	UNP P02407
BR	?	-	ASN	deletion	UNP P02407
BR	?	-	GLY	deletion	UNP P02407
BR	?	-	VAL	deletion	UNP P02407

- Molecule 63 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BS	145	Total	C	N	O	S	0	0
			1192	743	237	210	2		

- Molecule 64 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BT	141	Total	C	N	O	S	0	0
			1095	685	206	202	2		

- Molecule 65 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BU	107	Total	C	N	O	S	0	0
			855	539	156	159	1		

- Molecule 66 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	BV	87	Total	C	N	O	S	0	0
			684	420	125	137	2		

- Molecule 67 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BW	129	Total	C	N	O	S	0	0
			1021	650	188	180	3		

- Molecule 68 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BX	144	Total	C	N	O	S	0	0
			1121	708	220	191	2		

- Molecule 69 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	BY	134	Total	C	N	O	S	0	0
			1073	676	208	189			

- Molecule 70 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BZ	69	Total	C	N	O	S	0	0
			558	357	103	98			

- Molecule 71 is a protein called 40S ribosomal protein S26-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Ba	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 72 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Bb	81	Total	C	N	O	S	0	0
			610	382	110	113	5		

- Molecule 73 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	Bc	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 74 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	Bd	53	Total	C	N	O	S	0	0
			442	274	92	72	4		

- Molecule 75 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Be	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 76 is a protein called 40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Bf	57	Total	C	N	O	S	0	0
			454	288	86	77	3		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Bf	97	ALA	LYS	conflict	UNP P05759
Bf	?	-	CYS	deletion	UNP P05759
Bf	?	-	GLY	deletion	UNP P05759
Bf	?	-	ALA	deletion	UNP P05759

- Molecule 77 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Bg	312	Total	C	N	O	S	0	0
			2401	1522	410	461	8		

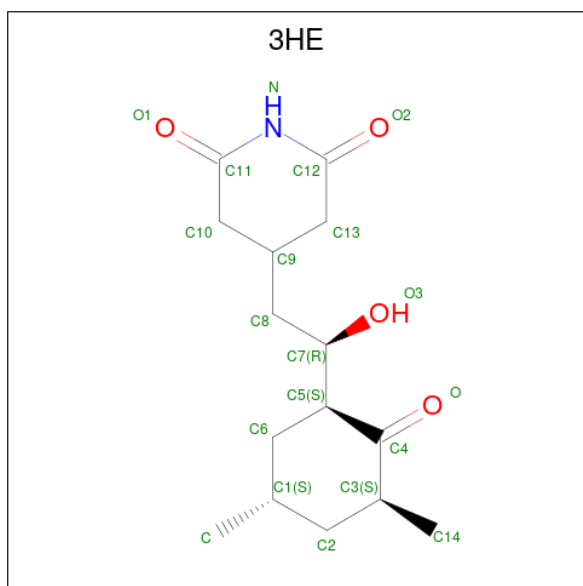
- Molecule 78 is a protein called Suppressor protein STM1.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Bh	89	Total	C	N	O		0	0
			675	391	137	147			

- Molecule 79 is a RNA chain called 18S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	B5	1783	Total	C	N	O	P	1	0
			37891	16950	6664	12494	1783		

- Molecule 80 is 4-{(2R)-2-[(1S,3S,5S)-3,5-dimethyl-2-oxocyclohexyl]-2-hydroxyethyl}piperidine-2,6-dione (three-letter code: 3HE) (formula: C₁₅H₂₃NO₄).



Mol	Chain	Residues	Atoms				AltConf
80	A1	1	Total	C	N	O	0
			20	15	1	4	

- Molecule 81 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
81	A1	247	Total	Mg	0
			247	247	
81	A3	5	Total	Mg	0
			5	5	
81	A4	9	Total	Mg	0
			9	9	
81	AB	4	Total	Mg	0
			4	4	
81	AC	1	Total	Mg	0
			1	1	
81	AG	1	Total	Mg	0
			1	1	
81	AL	3	Total	Mg	0
			3	3	

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Mol	Chain	Residues	Atoms		AltConf
81	AN	1	Total 1	Mg 1	0
81	AO	1	Total 1	Mg 1	0
81	AP	1	Total 1	Mg 1	0
81	AR	1	Total 1	Mg 1	0
81	AV	1	Total 1	Mg 1	0
81	Aa	1	Total 1	Mg 1	0
81	Ae	2	Total 2	Mg 2	0
81	Af	1	Total 1	Mg 1	0
81	Aj	1	Total 1	Mg 1	0
81	BE	1	Total 1	Mg 1	0
81	BG	1	Total 1	Mg 1	0
81	BJ	1	Total 1	Mg 1	0
81	Ba	1	Total 1	Mg 1	0
81	B5	90	Total 90	Mg 90	0

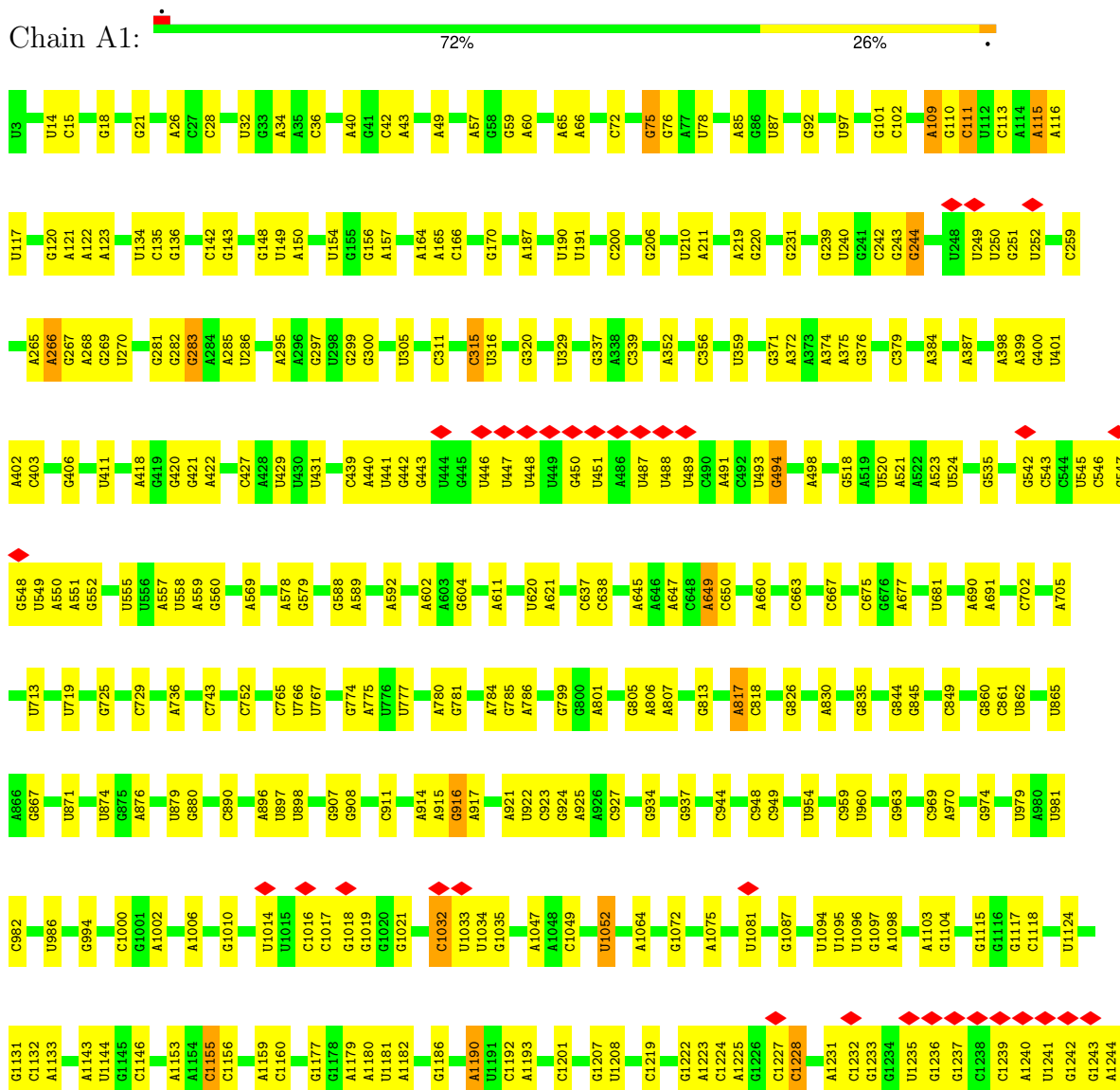
- Molecule 82 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
82	Ao	1	Total 1	Zn 1	0
82	Bb	1	Total 1	Zn 1	0

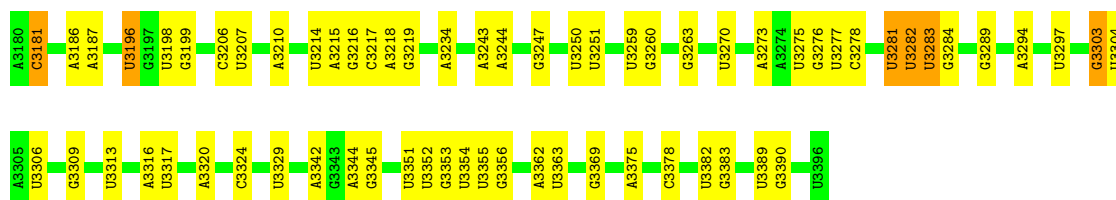
3 Residue-property plots

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: 25S

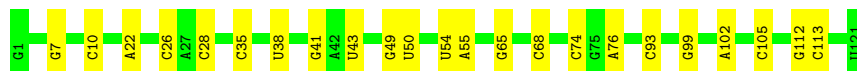






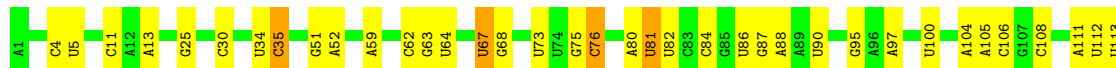
• Molecule 2: 5S

Chain A3: 81% 19%



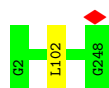
• Molecule 3: 5.8S

Chain A4: 72% 26%



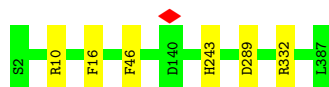
• Molecule 4: 60S ribosomal protein L2-A

Chain AA: 100%



• Molecule 5: 60S ribosomal protein L3

Chain AB: 98%



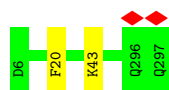
• Molecule 6: 60S ribosomal protein L4-A

Chain AC: 98%



• Molecule 7: 60S ribosomal protein L5

Chain AD: 99%



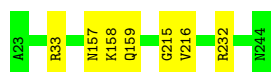
- Molecule 8: 60S ribosomal protein L6-A

Chain AE: 99%



- Molecule 9: 60S ribosomal protein L7-A

Chain AF: 97%



- Molecule 10: 60S ribosomal protein L8-A

Chain AG: 97%



- Molecule 11: 60S ribosomal protein L9-A

Chain AH: 100%



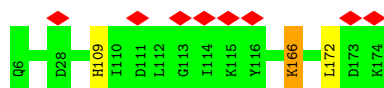
- Molecule 12: 60S ribosomal protein L10

Chain AI: 100%



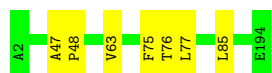
- Molecule 13: 60S ribosomal protein L11-A

Chain AJ: 5%



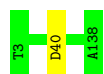
- Molecule 14: 60S ribosomal protein L13-A

Chain AL:  96% .



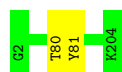
- Molecule 15: 60S ribosomal protein L14-A

Chain AM:  99% .



- Molecule 16: 60S ribosomal protein L15-A

Chain AN:  99% .



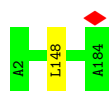
- Molecule 17: 60S ribosomal protein L16-A

Chain AO:  98% ..



- Molecule 18: 60S ribosomal protein L17-A

Chain AP:  99% .



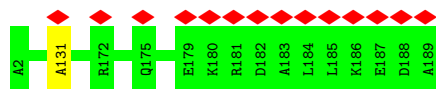
- Molecule 19: 60S ribosomal protein L18-A

Chain AQ:  99% .



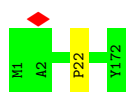
- Molecule 20: 60S ribosomal protein L19-A

Chain AR:  99% .



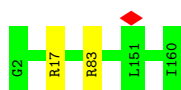
- Molecule 21: 60S ribosomal protein L20-A

Chain AS:  99%



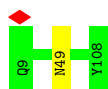
- Molecule 22: 60S ribosomal protein L21-A

Chain AT:  99%



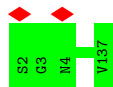
- Molecule 23: 60S ribosomal protein L22-A

Chain AU:  99%



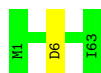
- Molecule 24: 60S ribosomal protein L23-A

Chain AV:  100%



- Molecule 25: 60S ribosomal protein L24-A

Chain AW:  98%



- Molecule 26: 60S ribosomal protein L25

Chain AX:  100%



- Molecule 27: 60S ribosomal protein L26-A

Chain AY:  99%



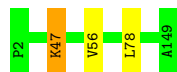
- Molecule 28: 60S ribosomal protein L27-A

Chain AZ:  99%



- Molecule 29: 60S ribosomal protein L28

Chain Aa:  98%



- Molecule 30: 60S ribosomal protein L29

Chain Ab:  100%



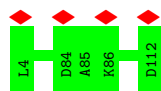
- Molecule 31: 60S ribosomal protein L30

Chain Ac:  100%



- Molecule 32: 60S ribosomal protein L31-A

Chain Ad:  100%



- Molecule 33: 60S ribosomal protein L32

Chain Ae:  100%



- Molecule 34: 60S ribosomal protein L33-A

Chain Af:  100%

There are no outlier residues recorded for this chain.

- Molecule 35: 60S ribosomal protein L34-A

Chain Ag:  99%



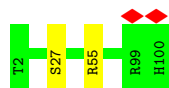
- Molecule 36: 60S ribosomal protein L35-A

Chain Ah:  98%



- Molecule 37: 60S ribosomal protein L36-A

Chain Ai:  98%



- Molecule 38: 60S ribosomal protein L37-A

Chain Aj:  100%



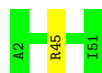
- Molecule 39: 60S ribosomal protein L38

Chain Ak:  100%

There are no outlier residues recorded for this chain.

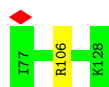
- Molecule 40: 60S ribosomal protein L39

Chain Al:  98%



- Molecule 41: 60S ribosomal protein L40-A

Chain Am:  98%



- Molecule 42: 60S ribosomal protein L41-A

Chain An:  100%

There are no outlier residues recorded for this chain.

- Molecule 43: 60S ribosomal protein L42-A

Chain Ao:  100%



- Molecule 44: 60S ribosomal protein L43-A

Chain Ap:  98%



- Molecule 45: 40S ribosomal protein S0-A

Chain BA:  98%



- Molecule 46: 40S ribosomal protein S1-A

Chain BB:  96%



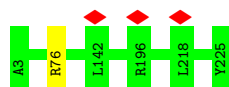
- Molecule 47: 40S ribosomal protein S2

Chain BC:  98%



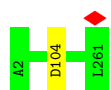
- Molecule 48: 40S ribosomal protein S3

Chain BD:  100%



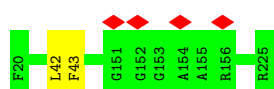
- Molecule 49: 40S ribosomal protein S4-A

Chain BE:  100%



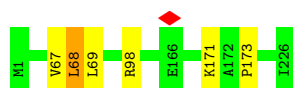
- Molecule 50: 40S ribosomal protein S5

Chain BF:  99%



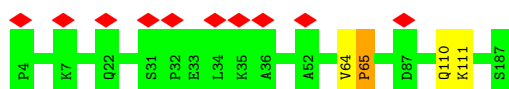
- Molecule 51: 40S ribosomal protein S6-A

Chain BG:  97%



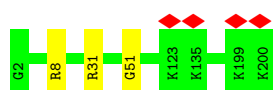
- Molecule 52: 40S ribosomal protein S7-A

Chain BH:  98%



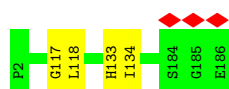
- Molecule 53: 40S ribosomal protein S8-A

Chain BI:  98%



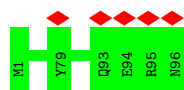
- Molecule 54: 40S ribosomal protein S9-A

Chain BJ:  98%



- Molecule 55: 40S ribosomal protein S10-A

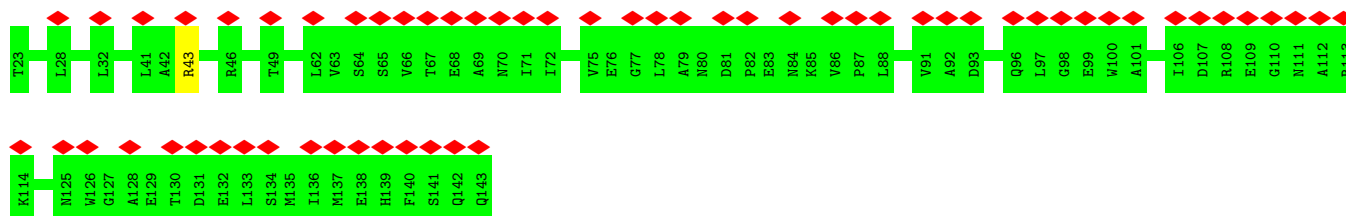
Chain BK:  100%



- Molecule 56: 40S ribosomal protein S11-A



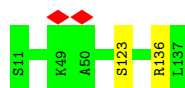
- Molecule 57: 40S ribosomal protein S12



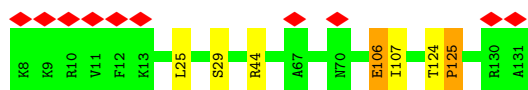
- Molecule 58: 40S ribosomal protein S13



- Molecule 59: 40S ribosomal protein S14-A

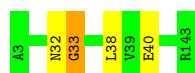


- Molecule 60: 40S ribosomal protein S15

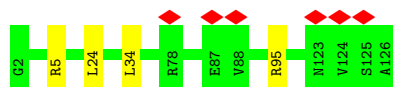


- Molecule 61: 40S ribosomal protein S16-A

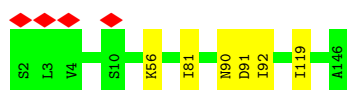




- Molecule 62: 40S ribosomal protein S17-A



- Molecule 63: 40S ribosomal protein S18-A

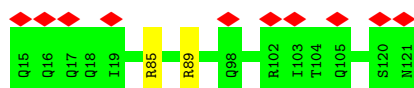


- Molecule 64: 40S ribosomal protein S19-A



There are no outlier residues recorded for this chain.

- Molecule 65: 40S ribosomal protein S20



- Molecule 66: 40S ribosomal protein S21-A



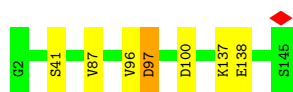
There are no outlier residues recorded for this chain.

- Molecule 67: 40S ribosomal protein S22-A



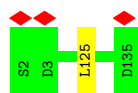
- Molecule 68: 40S ribosomal protein S23-A





- Molecule 69: 40S ribosomal protein S24-A

Chain BY: 99%



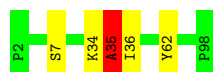
- Molecule 70: 40S ribosomal protein S25-A

Chain BZ: 99%



- Molecule 71: 40S ribosomal protein S26-B

Chain Ba: 95%



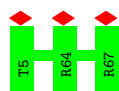
- Molecule 72: 40S ribosomal protein S27-A

Chain Bb: 98%



- Molecule 73: 40S ribosomal protein S28-A

Chain Bc: 5% 100%



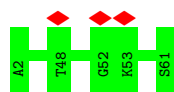
- Molecule 74: 40S ribosomal protein S29-A

Chain Bd: 98%

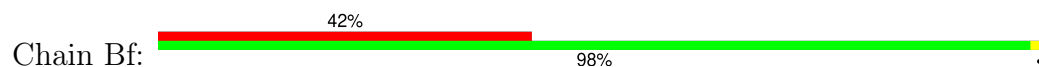


- Molecule 75: 40S ribosomal protein S30-A

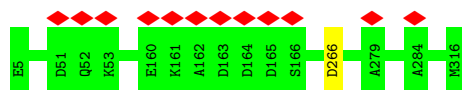
Chain Be: 5% 100%



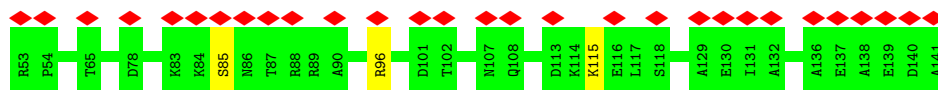
- Molecule 76: 40S ribosomal protein S31



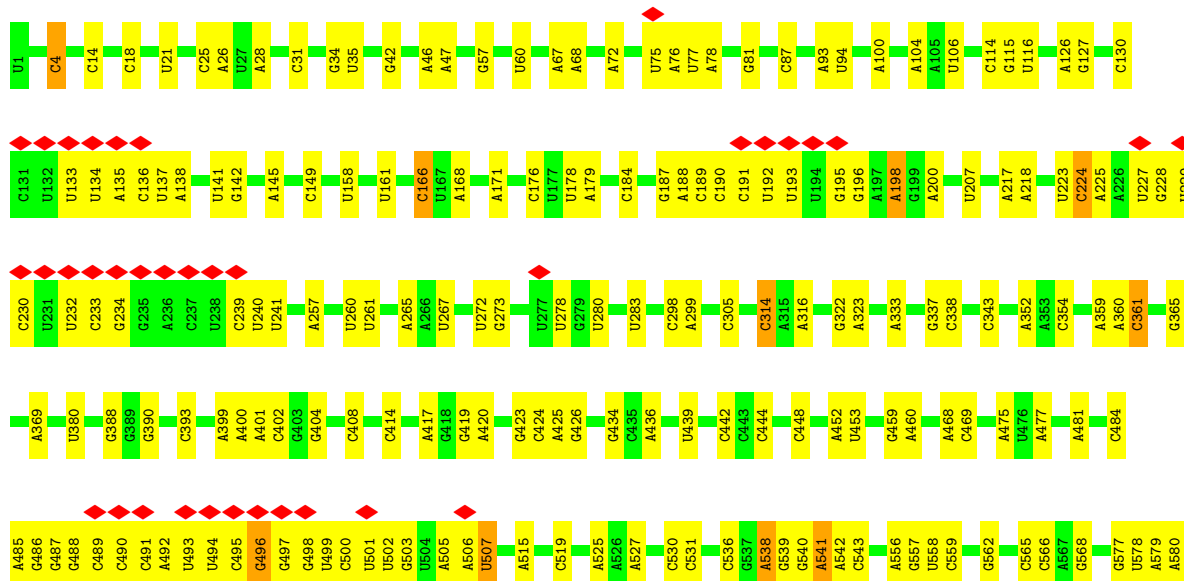
- Molecule 77: Guanine nucleotide-binding protein subunit beta-like protein

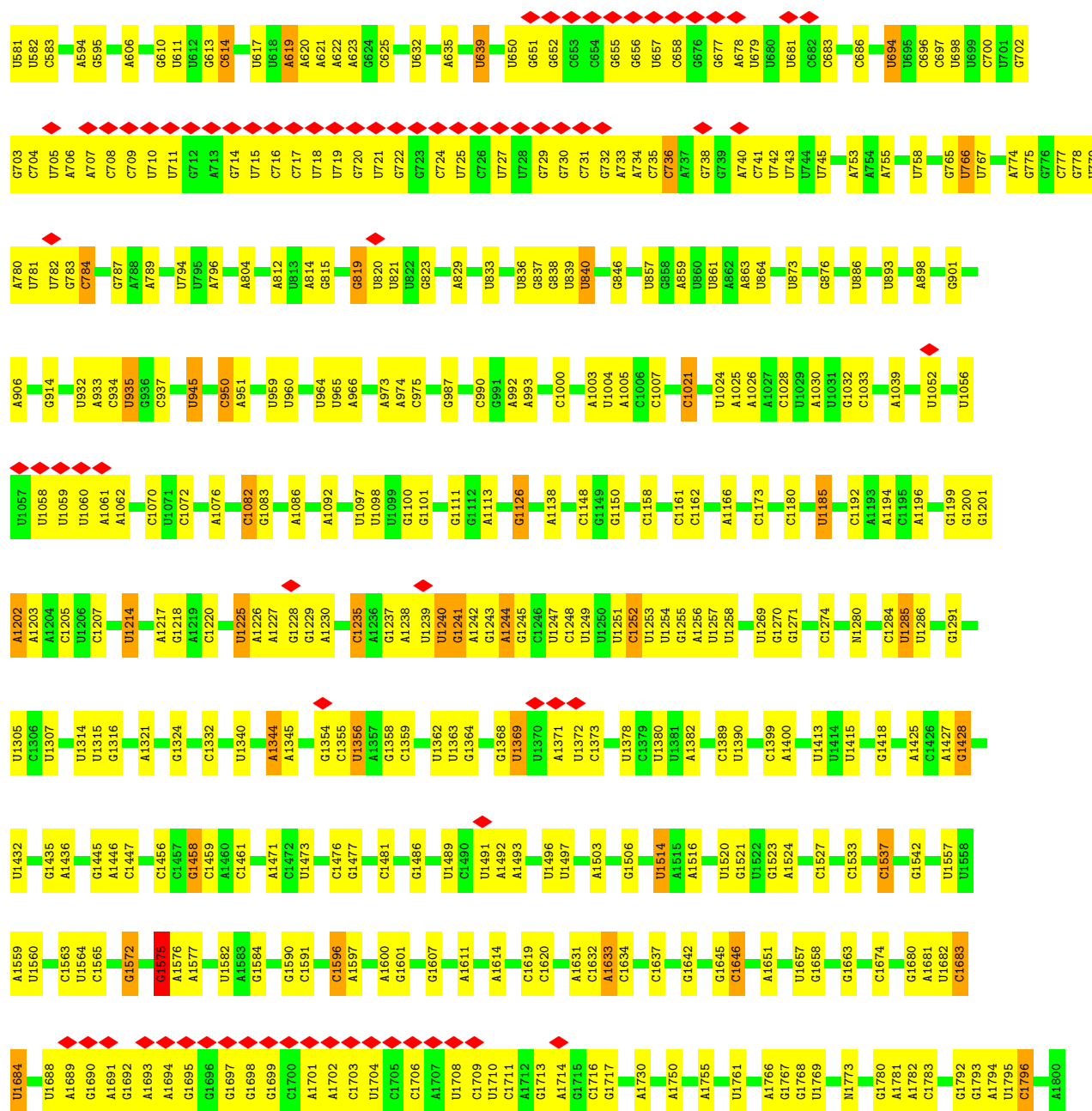


- Molecule 78: Suppressor protein STM1



- Molecule 79: 18S RIBOSOMAL RNA





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	178990	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	61	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.233	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	455.75998, 455.75998, 455.75998	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.055, 1.055, 1.055	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MG, 3AU, OMU, UR3, 3HE, 5MC, G7M, 1MA, 4AC, OMG, A2M, ZN, OMC, HIC, 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	A1	1.02	2/74562 (0.0%)	1.14	436/116239 (0.4%)
2	A3	0.86	0/2883	1.06	13/4491 (0.3%)
3	A4	1.09	0/3745	1.14	25/5828 (0.4%)
4	AA	0.55	0/1912	0.65	1/2569 (0.0%)
5	AB	0.59	0/3137	0.66	4/4215 (0.1%)
6	AC	0.54	1/2800 (0.0%)	0.66	1/3790 (0.0%)
7	AD	0.44	0/2390	0.58	0/3225
8	AE	0.51	0/1260	0.59	0/1694
9	AF	0.54	0/1821	0.64	2/2451 (0.1%)
10	AG	0.50	0/1830	0.62	3/2469 (0.1%)
11	AH	0.52	0/1531	0.62	0/2062
12	AI	0.42	0/1708	0.57	0/2290
13	AJ	0.36	0/1374	0.63	1/1842 (0.1%)
14	AL	0.54	0/1568	0.63	1/2106 (0.0%)
15	AM	0.55	0/1068	0.62	1/1438 (0.1%)
16	AN	0.62	0/1757	0.68	0/2354
17	AO	0.56	0/1585	0.58	1/2128 (0.0%)
18	AP	0.53	0/1410	0.56	1/1893 (0.1%)
19	AQ	0.50	0/1465	0.61	1/1965 (0.1%)
20	AR	0.46	0/1538	0.54	0/2050
21	AS	0.60	0/1481	0.65	0/1990
22	AT	0.52	0/1300	0.63	0/1743
23	AU	0.48	0/812	0.64	0/1099
24	AV	0.52	0/1018	0.62	0/1369
25	AW	0.53	0/533	0.62	1/707 (0.1%)
26	AX	0.56	0/983	0.61	0/1325
27	AY	0.55	0/1004	0.70	1/1341 (0.1%)
28	AZ	0.51	0/1118	0.65	0/1497
29	Aa	0.54	0/1204	0.71	2/1612 (0.1%)
30	Ab	0.39	0/473	0.53	0/629
31	Ac	0.49	0/751	0.56	0/1008
32	Ad	0.56	0/904	0.58	0/1213

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Ae	0.53	0/1041	0.55	0/1394
34	Af	0.61	0/868	0.56	0/1168
35	Ag	0.56	0/890	0.66	2/1189 (0.2%)
36	Ah	0.49	0/978	0.56	0/1301
37	Ai	0.47	0/778	0.66	0/1034
38	Aj	0.60	0/696	0.63	0/923
39	Ak	0.51	0/618	0.65	0/826
40	Al	0.55	0/443	0.73	1/588 (0.2%)
41	Am	0.53	0/423	0.56	0/562
42	An	0.33	0/234	0.51	0/300
43	Ao	0.45	0/860	0.62	0/1136
44	Ap	0.52	0/701	0.67	0/934
45	BA	0.42	0/1653	0.60	2/2261 (0.1%)
46	BB	0.43	0/1735	0.71	2/2335 (0.1%)
47	BC	0.47	1/1665 (0.1%)	0.66	1/2263 (0.0%)
48	BD	0.42	0/1759	0.64	0/2368
49	BE	0.48	0/2109	0.67	1/2839 (0.0%)
50	BF	0.42	0/1629	0.62	0/2202
51	BG	0.42	0/1844	0.63	3/2464 (0.1%)
52	BH	0.40	0/1506	0.71	0/2028
53	BI	0.46	1/1514 (0.1%)	0.63	0/2021
54	BJ	0.43	0/1519	0.65	1/2035 (0.0%)
55	BK	0.45	0/837	0.71	0/1131
56	BL	0.47	0/1272	0.55	0/1712
57	BM	0.31	0/921	0.67	0/1245
58	BN	0.46	0/1215	0.63	0/1638
59	BO	0.43	0/952	0.67	0/1279
60	BP	0.47	0/1012	0.71	2/1356 (0.1%)
61	BQ	0.44	0/1125	0.67	1/1510 (0.1%)
62	BR	0.36	0/984	0.64	1/1318 (0.1%)
63	BS	0.45	0/1211	0.67	1/1628 (0.1%)
64	BT	0.48	0/1113	0.71	0/1494
65	BU	0.42	0/865	0.66	2/1169 (0.2%)
66	BV	0.48	0/692	0.61	0/932
67	BW	0.52	0/1038	0.66	1/1395 (0.1%)
68	BX	0.48	0/1139	0.74	1/1518 (0.1%)
69	BY	0.48	0/1087	0.66	1/1449 (0.1%)
70	BZ	0.39	0/566	0.70	1/761 (0.1%)
71	Ba	0.46	0/782	0.73	1/1047 (0.1%)
72	Bb	0.41	0/620	0.66	1/838 (0.1%)
73	Bc	0.39	0/499	0.71	0/670
74	Bd	0.48	0/452	0.64	0/600
75	Be	0.40	0/483	0.53	0/643

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Bf	0.33	0/462	0.69	0/617
77	Bg	0.39	0/2454	0.65	1/3340 (0.0%)
78	Bh	0.28	0/678	0.54	0/905
79	B5	0.81	0/41746	1.15	315/65032 (0.5%)
All	All	0.79	5/212593 (0.0%)	0.98	837/312030 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	AC	0	2
7	AD	0	1
8	AE	0	1
9	AF	0	3
10	AG	0	4
13	AJ	0	2
14	AL	0	2
16	AN	0	1
17	AO	0	1
20	AR	0	1
21	AS	0	1
22	AT	0	1
28	AZ	0	1
36	Ah	0	1
37	Ai	0	1
45	BA	0	1
46	BB	0	4
47	BC	0	1
50	BF	0	2
51	BG	0	1
52	BH	0	3
53	BI	0	2
54	BJ	0	2
59	BO	0	1
60	BP	0	4
61	BQ	0	3
63	BS	0	3
67	BW	0	1
68	BX	0	5
71	Ba	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
76	Bf	0	1
78	Bh	0	1
79	B5	4	0
All	All	4	61

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
47	BC	111	VAL	CB-CG1	-5.29	1.41	1.52
53	BI	31	ARG	C-N	-5.22	1.22	1.34
1	A1	300	G	N9-C8	-5.16	1.34	1.37
1	A1	1835	A	C6-N1	-5.16	1.31	1.35
6	AC	230	VAL	CB-CG1	-5.13	1.42	1.52

The worst 5 of 837 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	266	A	O5'-P-OP1	-29.63	75.14	110.70
1	A1	266	A	OP1-P-OP2	-28.49	76.86	119.60
1	A1	266	A	O5'-P-OP2	18.43	132.82	110.70
79	B5	1537	C	N1-C2-O2	13.61	127.07	118.90
1	A1	1948	G	OP1-P-OP2	13.40	139.70	119.60

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
79	B5	1191	3AU	C12
79	B5	1575	G7M	C3',C2',C4'

5 of 61 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	AC	131	VAL	Peptide
6	AC	318	LEU	Peptide
7	AD	43	LYS	Peptide
8	AE	67	GLY	Peptide
9	AF	158	LYS	Peptide

5.2 Too-close contacts

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	AA	245/247 (99%)	232 (95%)	13 (5%)	0	100	100
5	AB	383/386 (99%)	363 (95%)	20 (5%)	0	100	100
6	AC	359/361 (99%)	326 (91%)	31 (9%)	2 (1%)	22	49
7	AD	290/292 (99%)	272 (94%)	17 (6%)	1 (0%)	37	64
8	AE	152/156 (97%)	139 (91%)	13 (9%)	0	100	100
9	AF	220/222 (99%)	207 (94%)	11 (5%)	2 (1%)	14	40
10	AG	228/230 (99%)	216 (95%)	12 (5%)	0	100	100
11	AH	188/190 (99%)	171 (91%)	17 (9%)	0	100	100
12	AI	201/205 (98%)	187 (93%)	14 (7%)	0	100	100
13	AJ	167/169 (99%)	147 (88%)	20 (12%)	0	100	100
14	AL	191/193 (99%)	165 (86%)	22 (12%)	4 (2%)	5	21
15	AM	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
16	AN	201/203 (99%)	186 (92%)	14 (7%)	1 (0%)	25	54
17	AO	195/197 (99%)	191 (98%)	2 (1%)	2 (1%)	13	38
18	AP	171/175 (98%)	163 (95%)	8 (5%)	0	100	100
19	AQ	183/185 (99%)	177 (97%)	6 (3%)	0	100	100
20	AR	186/188 (99%)	176 (95%)	10 (5%)	0	100	100
21	AS	170/172 (99%)	161 (95%)	9 (5%)	0	100	100
22	AT	157/159 (99%)	146 (93%)	11 (7%)	0	100	100
23	AU	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
24	AV	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
25	AW	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
26	AX	119/121 (98%)	115 (97%)	4 (3%)	0	100	100
27	AY	124/126 (98%)	116 (94%)	8 (6%)	0	100	100
28	AZ	133/135 (98%)	123 (92%)	9 (7%)	1 (1%)	16	43

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	Aa	146/148 (99%)	126 (86%)	18 (12%)	2 (1%)	9	30
30	Ab	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
31	Ac	95/97 (98%)	94 (99%)	1 (1%)	0	100	100
32	Ad	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
33	Ae	125/127 (98%)	120 (96%)	5 (4%)	0	100	100
34	Af	104/106 (98%)	100 (96%)	4 (4%)	0	100	100
35	Ag	110/112 (98%)	107 (97%)	3 (3%)	0	100	100
36	Ah	117/119 (98%)	107 (92%)	9 (8%)	1 (1%)	14	40
37	Ai	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
38	Aj	85/87 (98%)	82 (96%)	3 (4%)	0	100	100
39	Ak	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
40	Al	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
41	Am	50/52 (96%)	48 (96%)	2 (4%)	0	100	100
42	An	23/25 (92%)	23 (100%)	0	0	100	100
43	Ao	103/105 (98%)	93 (90%)	10 (10%)	0	100	100
44	Ap	89/91 (98%)	82 (92%)	6 (7%)	1 (1%)	12	35
45	BA	204/206 (99%)	185 (91%)	18 (9%)	1 (0%)	25	54
46	BB	212/214 (99%)	186 (88%)	24 (11%)	2 (1%)	14	40
47	BC	215/217 (99%)	197 (92%)	17 (8%)	1 (0%)	25	54
48	BD	221/223 (99%)	207 (94%)	14 (6%)	0	100	100
49	BE	258/260 (99%)	240 (93%)	18 (7%)	0	100	100
50	BF	204/206 (99%)	185 (91%)	19 (9%)	0	100	100
51	BG	224/226 (99%)	209 (93%)	13 (6%)	2 (1%)	14	40
52	BH	182/184 (99%)	166 (91%)	14 (8%)	2 (1%)	12	35
53	BI	184/188 (98%)	156 (85%)	28 (15%)	0	100	100
54	BJ	183/185 (99%)	168 (92%)	14 (8%)	1 (0%)	25	54
55	BK	94/96 (98%)	77 (82%)	17 (18%)	0	100	100
56	BL	153/155 (99%)	145 (95%)	8 (5%)	0	100	100
57	BM	119/121 (98%)	93 (78%)	26 (22%)	0	100	100
58	BN	148/150 (99%)	140 (95%)	8 (5%)	0	100	100
59	BO	125/127 (98%)	110 (88%)	15 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
60	BP	122/124 (98%)	101 (83%)	19 (16%)	2 (2%)	8	27
61	BQ	139/141 (99%)	131 (94%)	7 (5%)	1 (1%)	19	46
62	BR	117/121 (97%)	106 (91%)	10 (8%)	1 (1%)	14	40
63	BS	143/145 (99%)	128 (90%)	13 (9%)	2 (1%)	9	30
64	BT	139/141 (99%)	125 (90%)	14 (10%)	0	100	100
65	BU	105/107 (98%)	100 (95%)	5 (5%)	0	100	100
66	BV	83/87 (95%)	78 (94%)	5 (6%)	0	100	100
67	BW	127/129 (98%)	117 (92%)	9 (7%)	1 (1%)	16	43
68	BX	142/144 (99%)	120 (84%)	20 (14%)	2 (1%)	9	30
69	BY	132/134 (98%)	124 (94%)	8 (6%)	0	100	100
70	BZ	67/69 (97%)	61 (91%)	6 (9%)	0	100	100
71	Ba	95/97 (98%)	76 (80%)	16 (17%)	3 (3%)	3	14
72	Bb	79/81 (98%)	72 (91%)	7 (9%)	0	100	100
73	Bc	61/63 (97%)	57 (93%)	4 (7%)	0	100	100
74	Bd	51/53 (96%)	47 (92%)	4 (8%)	0	100	100
75	Be	58/60 (97%)	53 (91%)	5 (9%)	0	100	100
76	Bf	53/57 (93%)	39 (74%)	14 (26%)	0	100	100
77	Bg	310/312 (99%)	275 (89%)	35 (11%)	0	100	100
78	Bh	87/89 (98%)	81 (93%)	6 (7%)	0	100	100
All	All	10956/11121 (98%)	10091 (92%)	827 (8%)	38 (0%)	38	64

5 of 38 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	AC	339	LEU
9	AF	159	GLN
14	AL	48	PRO
14	AL	63	VAL
16	AN	81	TYR

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	AA	189/189 (100%)	189 (100%)	0	100	100
5	AB	321/321 (100%)	319 (99%)	2 (1%)	84	90
6	AC	288/288 (100%)	287 (100%)	1 (0%)	91	94
7	AD	241/241 (100%)	241 (100%)	0	100	100
8	AE	134/134 (100%)	134 (100%)	0	100	100
9	AF	186/186 (100%)	186 (100%)	0	100	100
10	AG	189/189 (100%)	189 (100%)	0	100	100
11	AH	170/170 (100%)	170 (100%)	0	100	100
12	AI	176/176 (100%)	175 (99%)	1 (1%)	84	90
13	AJ	147/147 (100%)	146 (99%)	1 (1%)	81	89
14	AL	154/154 (100%)	154 (100%)	0	100	100
15	AM	107/107 (100%)	107 (100%)	0	100	100
16	AN	175/175 (100%)	175 (100%)	0	100	100
17	AO	160/160 (100%)	160 (100%)	0	100	100
18	AP	141/141 (100%)	141 (100%)	0	100	100
19	AQ	150/150 (100%)	150 (100%)	0	100	100
20	AR	153/153 (100%)	153 (100%)	0	100	100
21	AS	156/156 (100%)	156 (100%)	0	100	100
22	AT	136/136 (100%)	135 (99%)	1 (1%)	81	89
23	AU	87/87 (100%)	86 (99%)	1 (1%)	70	83
24	AV	104/104 (100%)	104 (100%)	0	100	100
25	AW	55/55 (100%)	55 (100%)	0	100	100
26	AX	105/105 (100%)	105 (100%)	0	100	100
27	AY	109/109 (100%)	109 (100%)	0	100	100
28	AZ	115/115 (100%)	115 (100%)	0	100	100
29	Aa	118/118 (100%)	118 (100%)	0	100	100
30	Ab	46/46 (100%)	46 (100%)	0	100	100
31	Ac	81/81 (100%)	81 (100%)	0	100	100
32	Ad	96/96 (100%)	96 (100%)	0	100	100
33	Ae	109/109 (100%)	109 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Af	90/90 (100%)	90 (100%)	0	100	100
35	Ag	95/95 (100%)	95 (100%)	0	100	100
36	Ah	104/104 (100%)	104 (100%)	0	100	100
37	Ai	81/81 (100%)	80 (99%)	1 (1%)	67	82
38	Aj	70/70 (100%)	70 (100%)	0	100	100
39	Ak	68/68 (100%)	68 (100%)	0	100	100
40	Al	45/45 (100%)	45 (100%)	0	100	100
41	Am	47/47 (100%)	46 (98%)	1 (2%)	48	69
42	An	23/23 (100%)	23 (100%)	0	100	100
43	Ao	90/90 (100%)	90 (100%)	0	100	100
44	Ap	71/71 (100%)	70 (99%)	1 (1%)	62	79
45	BA	173/173 (100%)	172 (99%)	1 (1%)	84	90
46	BB	191/191 (100%)	190 (100%)	1 (0%)	86	91
47	BC	176/176 (100%)	176 (100%)	0	100	100
48	BD	182/182 (100%)	181 (100%)	1 (0%)	86	91
49	BE	221/221 (100%)	221 (100%)	0	100	100
50	BF	173/173 (100%)	173 (100%)	0	100	100
51	BG	193/193 (100%)	192 (100%)	1 (0%)	86	91
52	BH	165/165 (100%)	165 (100%)	0	100	100
53	BI	150/150 (100%)	150 (100%)	0	100	100
54	BJ	158/158 (100%)	158 (100%)	0	100	100
55	BK	89/89 (100%)	89 (100%)	0	100	100
56	BL	136/136 (100%)	135 (99%)	1 (1%)	81	89
57	BM	98/98 (100%)	97 (99%)	1 (1%)	73	85
58	BN	127/127 (100%)	127 (100%)	0	100	100
59	BO	96/96 (100%)	95 (99%)	1 (1%)	73	85
60	BP	104/104 (100%)	103 (99%)	1 (1%)	73	85
61	BQ	117/117 (100%)	117 (100%)	0	100	100
62	BR	110/110 (100%)	108 (98%)	2 (2%)	54	74
63	BS	128/128 (100%)	128 (100%)	0	100	100
64	BT	113/113 (100%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
65	BU	100/100 (100%)	100 (100%)	0	100	100
66	BV	74/74 (100%)	74 (100%)	0	100	100
67	BW	110/110 (100%)	110 (100%)	0	100	100
68	BX	119/119 (100%)	119 (100%)	0	100	100
69	BY	112/112 (100%)	112 (100%)	0	100	100
70	BZ	61/61 (100%)	61 (100%)	0	100	100
71	Ba	83/83 (100%)	83 (100%)	0	100	100
72	Bb	70/70 (100%)	69 (99%)	1 (1%)	62	79
73	Bc	56/56 (100%)	56 (100%)	0	100	100
74	Bd	47/47 (100%)	46 (98%)	1 (2%)	48	69
75	Be	51/51 (100%)	51 (100%)	0	100	100
76	Bf	49/49 (100%)	49 (100%)	0	100	100
77	Bg	256/257 (100%)	256 (100%)	0	100	100
78	Bh	68/68 (100%)	66 (97%)	2 (3%)	37	62
All	All	9338/9339 (100%)	9314 (100%)	24 (0%)	90	94

5 of 24 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
56	BL	67	ARG
60	BP	44	ARG
59	BO	136	ARG
62	BR	5	ARG
23	AU	49	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
6	AC	320	ASN
23	AU	49	ASN
46	BB	146	GLN
50	BF	63	GLN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A1	3150/3156 (99%)	694 (22%)	13 (0%)
2	A3	120/121 (99%)	15 (12%)	0
3	A4	156/158 (98%)	34 (21%)	2 (1%)
79	B5	1775/1783 (99%)	458 (25%)	14 (0%)
All	All	5201/5218 (99%)	1201 (23%)	29 (0%)

5 of 1201 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A1	14	U
1	A1	18	G
1	A1	21	G
1	A1	26	A
1	A1	34	A

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	A4	81	U
79	B5	1633	A
79	B5	272	U
79	B5	1344	A
79	B5	224	C

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

66 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	$\# Z > 2$
79	A2M	B5	619	79,81	18,25,26	0.85	0	20,36,39	1.48	3 (15%)
79	3AU	B5	1191	79	24,28,29	0.48	0	30,40,43	0.70	0
1	A2M	A1	817	81,1	18,25,26	0.86	0	20,36,39	1.72	3 (15%)
1	OMC	A1	1437	81,1	19,22,23	0.91	1 (5%)	25,31,34	1.49	5 (20%)
79	OMC	B5	414	79	19,22,23	0.82	0	25,31,34	0.88	1 (4%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	UR3	A1	2634	81,1	19,22,23	0.96	2 (10%)	26,32,35	1.92	4 (15%)
1	OMG	A1	2288	1	19,26,27	0.95	1 (5%)	21,38,41	1.08	2 (9%)
1	A2M	A1	807	1	18,25,26	0.87	0	20,36,39	1.48	3 (15%)
1	A2M	A1	649	1	18,25,26	0.77	0	20,36,39	1.36	2 (10%)
1	OMU	A1	2724	1	19,22,23	1.34	4 (21%)	25,31,34	1.85	5 (20%)
1	OMG	A1	2791	1	19,26,27	0.93	1 (5%)	21,38,41	1.17	2 (9%)
1	OMU	A1	2347	1	19,22,23	1.46	4 (21%)	25,31,34	1.92	7 (28%)
1	OMG	A1	2922	1	19,26,27	0.91	1 (5%)	21,38,41	1.03	2 (9%)
1	1MA	A1	2142	81,1	17,25,26	1.39	2 (11%)	17,37,40	1.32	3 (17%)
79	A2M	B5	100	79,81	18,25,26	0.85	0	20,36,39	1.21	2 (10%)
1	OMG	A1	2793	1	19,26,27	0.92	1 (5%)	21,38,41	1.13	2 (9%)
1	OMG	A1	2619	1	19,26,27	0.87	1 (5%)	21,38,41	1.02	2 (9%)
1	A2M	A1	2946	81,1	18,25,26	0.90	0	20,36,39	1.46	3 (15%)
79	A2M	B5	436	79	18,25,26	0.80	0	20,36,39	1.28	3 (15%)
1	OMU	A1	2417	1	19,22,23	1.34	4 (21%)	25,31,34	1.77	5 (20%)
1	OMC	A1	650	1	19,22,23	0.87	2 (10%)	25,31,34	0.89	1 (4%)
79	A2M	B5	796	79	18,25,26	0.86	0	20,36,39	1.42	4 (20%)
1	OMU	A1	2421	1	19,22,23	1.34	3 (15%)	25,31,34	1.87	4 (16%)
1	OMC	A1	2337	1	19,22,23	0.94	2 (10%)	25,31,34	1.03	1 (4%)
79	OMG	B5	1572	79	19,26,27	0.94	1 (5%)	21,38,41	1.08	2 (9%)
79	OMG	B5	1428	79,81	19,26,27	0.89	1 (5%)	21,38,41	0.98	1 (4%)
1	OMC	A1	2197	1	19,22,23	0.81	0	25,31,34	0.79	0
1	A2M	A1	876	1	18,25,26	0.90	0	20,36,39	1.19	2 (10%)
1	OMG	A1	805	1	19,26,27	0.96	1 (5%)	21,38,41	1.07	1 (4%)
1	A2M	A1	2220	1	18,25,26	0.81	0	20,36,39	1.53	3 (15%)
79	OMU	B5	578	79	19,22,23	1.24	4 (21%)	25,31,34	1.85	6 (24%)
1	5MC	A1	2870	81,1	19,22,23	1.07	3 (15%)	26,32,35	1.35	3 (11%)
79	OMG	B5	1271	79	19,26,27	0.95	1 (5%)	21,38,41	1.04	2 (9%)
1	OMG	A1	867	81,1	19,26,27	0.92	1 (5%)	21,38,41	1.15	3 (14%)
79	G7M	B5	1575	79	20,26,27	2.65	4 (20%)	16,39,42	1.14	1 (6%)
79	4AC	B5	1773	79	21,24,25	1.01	1 (4%)	28,34,37	1.38	6 (21%)
1	A2M	A1	1133	1	18,25,26	0.87	1 (5%)	20,36,39	1.48	4 (20%)
79	A2M	B5	420	79	18,25,26	0.82	0	20,36,39	1.43	4 (20%)
1	OMU	A1	1888	1	19,22,23	1.41	4 (21%)	25,31,34	1.98	5 (20%)
1	OMG	A1	2815	1	19,26,27	0.96	1 (5%)	21,38,41	1.28	3 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	A2M	A1	2281	1	18,25,26	0.79	0	20,36,39	2.10	4 (20%)
1	1MA	A1	645	81,1	17,25,26	1.38	2 (11%)	17,37,40	1.24	3 (17%)
79	OMC	B5	1007	79	19,22,23	0.83	1 (5%)	25,31,34	0.97	1 (4%)
79	OMU	B5	1269	79,81	19,22,23	1.40	4 (21%)	25,31,34	1.95	6 (24%)
79	MA6	B5	1781	79	19,26,27	1.10	2 (10%)	18,38,41	2.11	3 (16%)
79	A2M	B5	974	79	18,25,26	0.83	0	20,36,39	1.22	2 (10%)
79	OMC	B5	1639	79	19,22,23	0.82	0	25,31,34	0.79	0
79	4AC	B5	1280	79	21,24,25	1.16	3 (14%)	28,34,37	1.71	3 (10%)
79	A2M	B5	541	79	18,25,26	0.80	0	20,36,39	1.32	3 (15%)
79	MA6	B5	1782	79	19,26,27	0.96	1 (5%)	18,38,41	2.04	3 (16%)
1	OMU	A1	898	1	19,22,23	1.42	4 (21%)	25,31,34	1.77	4 (16%)
1	OMU	A1	2729	1	19,22,23	1.40	3 (15%)	25,31,34	1.72	6 (24%)
1	OMC	A1	2959	1	19,22,23	0.89	1 (5%)	25,31,34	0.99	1 (4%)
1	A2M	A1	1449	81,1	18,25,26	0.86	0	20,36,39	1.14	1 (5%)
1	OMG	A1	1450	1	19,26,27	0.96	1 (5%)	21,38,41	1.17	2 (9%)
1	A2M	A1	2280	1	18,25,26	0.87	0	20,36,39	1.26	2 (10%)
79	OMG	B5	562	79	19,26,27	0.93	1 (5%)	21,38,41	1.13	3 (14%)
5	HIC	AB	243	5	8,11,12	1.44	1 (12%)	5,14,16	0.73	0
1	A2M	A1	2640	1	18,25,26	0.83	0	20,36,39	1.09	2 (10%)
79	OMG	B5	1126	79	19,26,27	0.96	1 (5%)	21,38,41	1.05	2 (9%)
79	A2M	B5	28	79,81	18,25,26	0.88	0	20,36,39	1.26	2 (10%)
1	5MC	A1	2278	81,1	19,22,23	1.31	3 (15%)	26,32,35	1.32	4 (15%)
1	OMC	A1	663	1	19,22,23	0.90	2 (10%)	25,31,34	0.85	0
1	OMC	A1	2948	1	19,22,23	0.92	2 (10%)	25,31,34	1.01	2 (8%)
1	OMU	A1	2921	1	19,22,23	1.34	4 (21%)	25,31,34	1.87	5 (20%)
1	OMG	A1	908	81,1	19,26,27	0.93	1 (5%)	21,38,41	1.41	3 (14%)

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
79	A2M	B5	619	79,81	-	2/5/27/28	0/3/3/3
79	3AU	B5	1191	79	1/1/7/7	3/16/34/35	0/2/2/2
1	A2M	A1	817	81,1	-	2/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OMC	A1	1437	81,1	-	2/9/27/28	0/2/2/2
79	OMC	B5	414	79	-	0/9/27/28	0/2/2/2
1	UR3	A1	2634	81,1	-	0/7/25/26	0/2/2/2
1	OMG	A1	2288	1	-	2/5/27/28	0/3/3/3
1	A2M	A1	807	1	-	1/5/27/28	0/3/3/3
1	A2M	A1	649	1	-	1/5/27/28	0/3/3/3
1	OMU	A1	2724	1	-	0/9/27/28	0/2/2/2
1	OMG	A1	2791	1	-	0/5/27/28	0/3/3/3
1	OMU	A1	2347	1	-	2/9/27/28	0/2/2/2
1	OMG	A1	2922	1	-	0/5/27/28	0/3/3/3
1	1MA	A1	2142	81,1	-	2/3/25/26	0/3/3/3
79	A2M	B5	100	79,81	-	1/5/27/28	0/3/3/3
1	OMG	A1	2793	1	-	0/5/27/28	0/3/3/3
1	OMG	A1	2619	1	-	1/5/27/28	0/3/3/3
1	A2M	A1	2946	81,1	-	0/5/27/28	0/3/3/3
79	A2M	B5	436	79	-	0/5/27/28	0/3/3/3
1	OMU	A1	2417	1	-	2/9/27/28	0/2/2/2
1	OMC	A1	650	1	-	0/9/27/28	0/2/2/2
79	A2M	B5	796	79	-	0/5/27/28	0/3/3/3
1	OMU	A1	2421	1	-	0/9/27/28	0/2/2/2
1	OMC	A1	2337	1	-	1/9/27/28	0/2/2/2
79	OMG	B5	1572	79	-	0/5/27/28	0/3/3/3
79	OMG	B5	1428	79,81	-	3/5/27/28	0/3/3/3
1	OMC	A1	2197	1	-	6/9/27/28	0/2/2/2
1	A2M	A1	876	1	-	0/5/27/28	0/3/3/3
1	OMG	A1	805	1	-	0/5/27/28	0/3/3/3
1	A2M	A1	2220	1	-	0/5/27/28	0/3/3/3
79	OMU	B5	578	79	-	0/9/27/28	0/2/2/2
79	G7M	B5	1575	79	3/3/5/5	2/3/25/26	0/3/3/3
1	5MC	A1	2870	81,1	-	6/7/25/26	0/2/2/2
1	OMG	A1	867	81,1	-	0/5/27/28	0/3/3/3
79	OMG	B5	1271	79	-	1/5/27/28	0/3/3/3
79	4AC	B5	1773	79	-	2/11/29/30	0/2/2/2
1	A2M	A1	1133	1	-	0/5/27/28	0/3/3/3
79	A2M	B5	420	79	-	0/5/27/28	0/3/3/3
1	OMU	A1	1888	1	-	0/9/27/28	0/2/2/2
1	OMG	A1	2815	1	-	0/5/27/28	0/3/3/3
1	A2M	A1	2281	1	-	2/5/27/28	0/3/3/3
1	1MA	A1	645	81,1	-	0/3/25/26	0/3/3/3
79	OMC	B5	1007	79	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
79	OMU	B5	1269	79,81	-	2/9/27/28	0/2/2/2
79	MA6	B5	1781	79	-	1/7/29/30	0/3/3/3
79	A2M	B5	974	79	-	0/5/27/28	0/3/3/3
79	OMC	B5	1639	79	-	0/9/27/28	0/2/2/2
79	4AC	B5	1280	79	-	4/11/29/30	0/2/2/2
79	A2M	B5	541	79	-	2/5/27/28	0/3/3/3
79	MA6	B5	1782	79	-	4/7/29/30	0/3/3/3
1	OMU	A1	898	1	-	0/9/27/28	0/2/2/2
1	OMU	A1	2729	1	-	2/9/27/28	0/2/2/2
1	OMC	A1	2959	1	-	0/9/27/28	0/2/2/2
1	A2M	A1	1449	81,1	-	0/5/27/28	0/3/3/3
1	OMG	A1	1450	1	-	2/5/27/28	0/3/3/3
1	A2M	A1	2280	1	-	0/5/27/28	0/3/3/3
79	OMG	B5	562	79	-	0/5/27/28	0/3/3/3
5	HIC	AB	243	5	-	2/5/6/8	0/1/1/1
1	A2M	A1	2640	1	-	0/5/27/28	0/3/3/3
79	OMG	B5	1126	79	-	2/5/27/28	0/3/3/3
79	A2M	B5	28	79,81	-	0/5/27/28	0/3/3/3
1	5MC	A1	2278	81,1	-	0/7/25/26	0/2/2/2
1	OMC	A1	663	1	-	0/9/27/28	0/2/2/2
1	OMC	A1	2948	1	-	0/9/27/28	0/2/2/2
1	OMU	A1	2921	1	-	0/9/27/28	0/2/2/2
1	OMG	A1	908	81,1	-	3/5/27/28	0/3/3/3

The worst 5 of 89 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
79	B5	1575	G7M	C8-N9	8.06	1.47	1.33
79	B5	1575	G7M	C8-N7	6.44	1.44	1.33
79	B5	1575	G7M	C5-C4	4.28	1.47	1.39
1	A1	2142	1MA	C2-N3	4.13	1.33	1.28
1	A1	2278	5MC	C5-C4	3.98	1.47	1.44

The worst 5 of 182 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	2634	UR3	C4-N3-C2	-7.58	118.48	124.58
79	B5	1280	4AC	N4-C4-N3	6.49	124.41	113.87
79	B5	1781	MA6	C2-N1-C6	6.26	122.98	116.84
79	B5	1782	MA6	C2-N1-C6	5.98	122.70	116.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A1	2281	A2M	O4'-C1'-N9	5.66	116.25	108.75

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
79	B5	1191	3AU	C12
79	B5	1575	G7M	C3'
79	B5	1575	G7M	C2'
79	B5	1575	G7M	C4'

5 of 68 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	AB	243	HIC	CA-CB-CG-ND1
5	AB	243	HIC	CA-CB-CG-CD2
1	A1	908	OMG	C1'-C2'-O2'-CM2
1	A1	1437	OMC	C1'-C2'-O2'-CM2
1	A1	1450	OMG	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 377 ligands modelled in this entry, 376 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
80	3HE	A1	3401	-	21,21,21	0.43	0	23,30,30	0.76	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
80	3HE	A1	3401	-	-	0/8/36/36	0/2/2/2

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	A1	6
79	B5	2
18	AP	1
53	BI	1
8	AE	1
12	AI	1
62	BR	1
76	Bf	1
3	A4	1
66	BV	1

The worst 5 of 16 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	1253:U	O3'	1260:A	P	26.34
1	AP	155:GLU	C	164:LYS	N	24.32
1	BI	123:LYS	C	135:LYS	N	18.64

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A1	1955:U	O3'	2093:A	P	18.09
1	B5	658:C	O3'	676:G	P	17.61

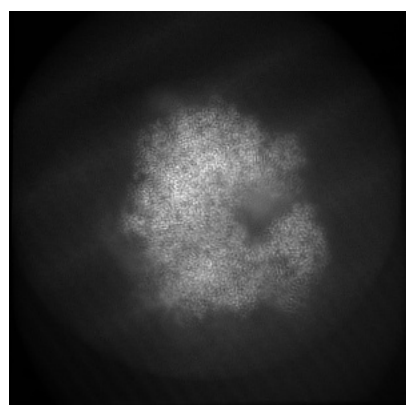
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24235. These allow visual inspection of the internal detail of the map and identification of artifacts.

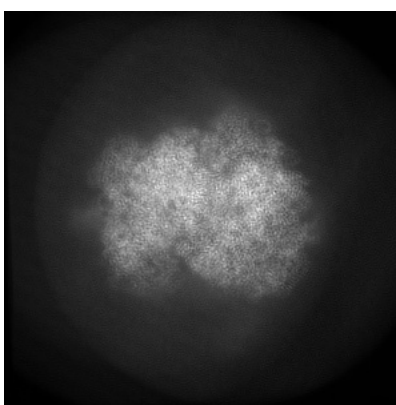
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

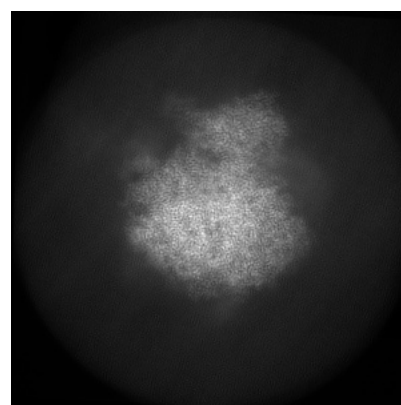
6.1.1 Primary map



X



Y

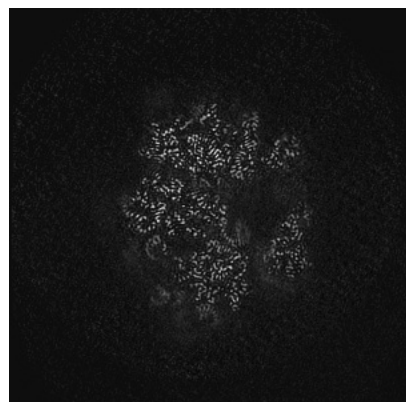


Z

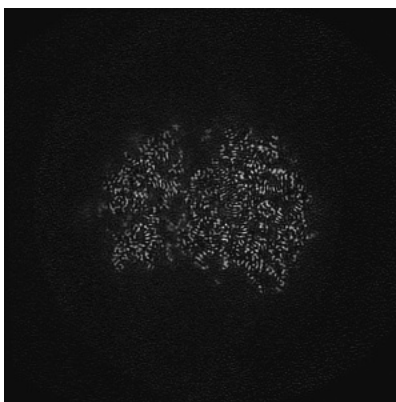
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

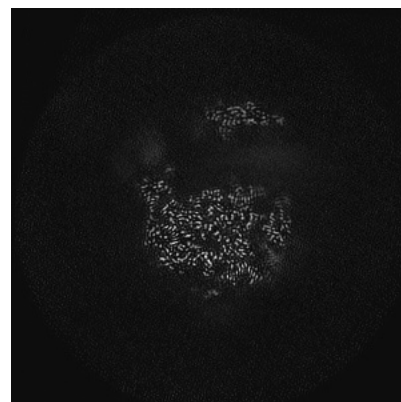
6.2.1 Primary map



X Index: 216



Y Index: 216

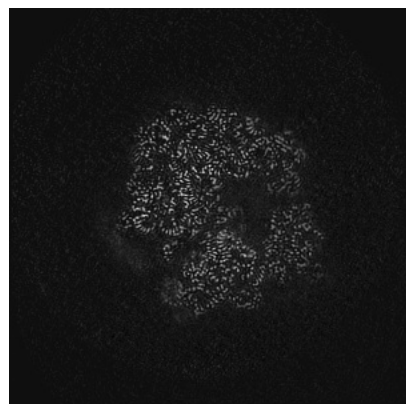


Z Index: 216

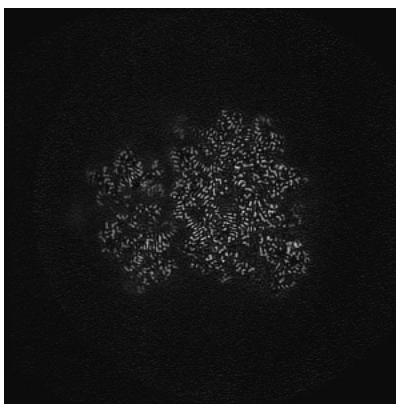
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

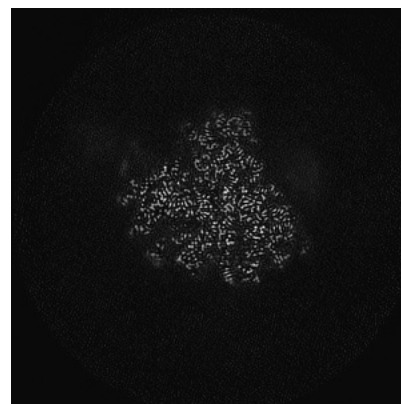
6.3.1 Primary map



X Index: 240



Y Index: 199

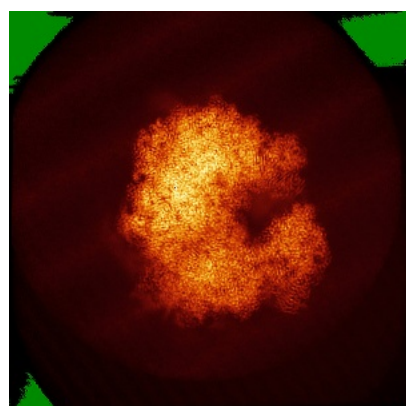


Z Index: 265

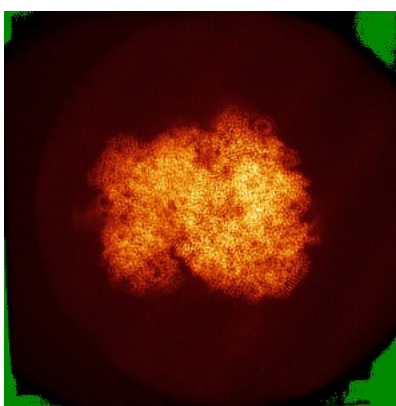
The images above show the largest variance slices of the map in three orthogonal directions.

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

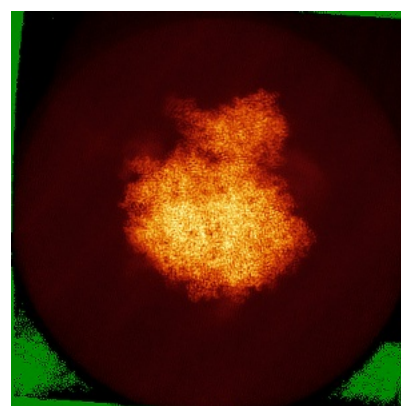
6.4.1 Primary map



X



Y

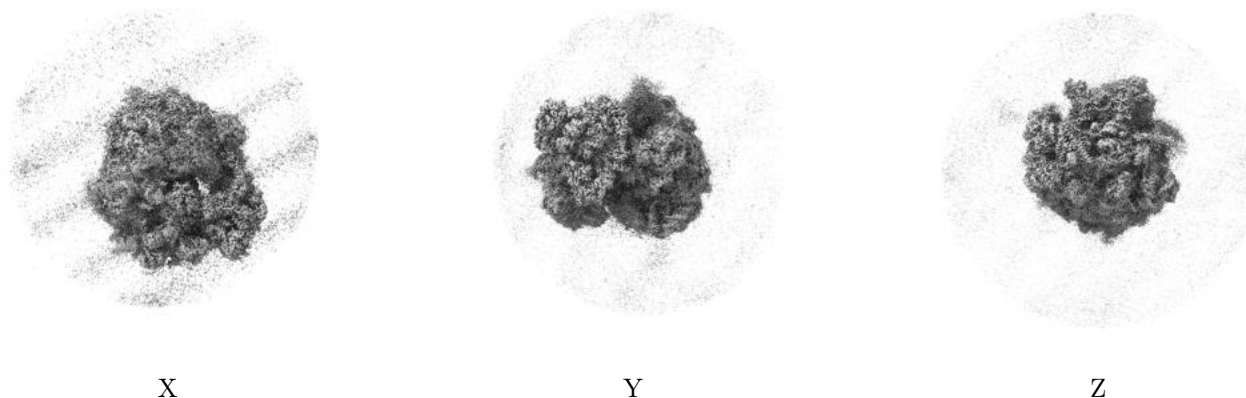


Z

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 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

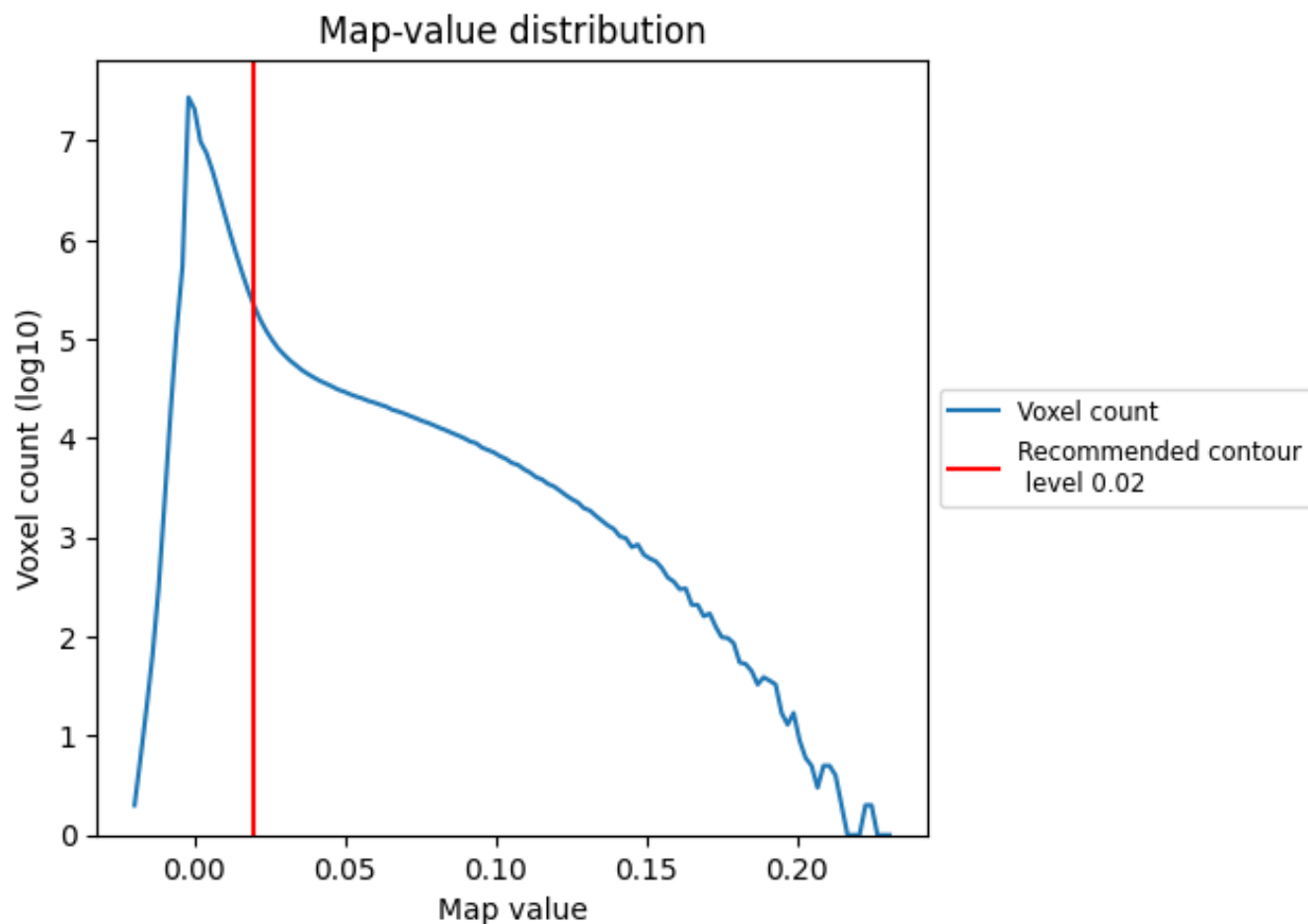
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

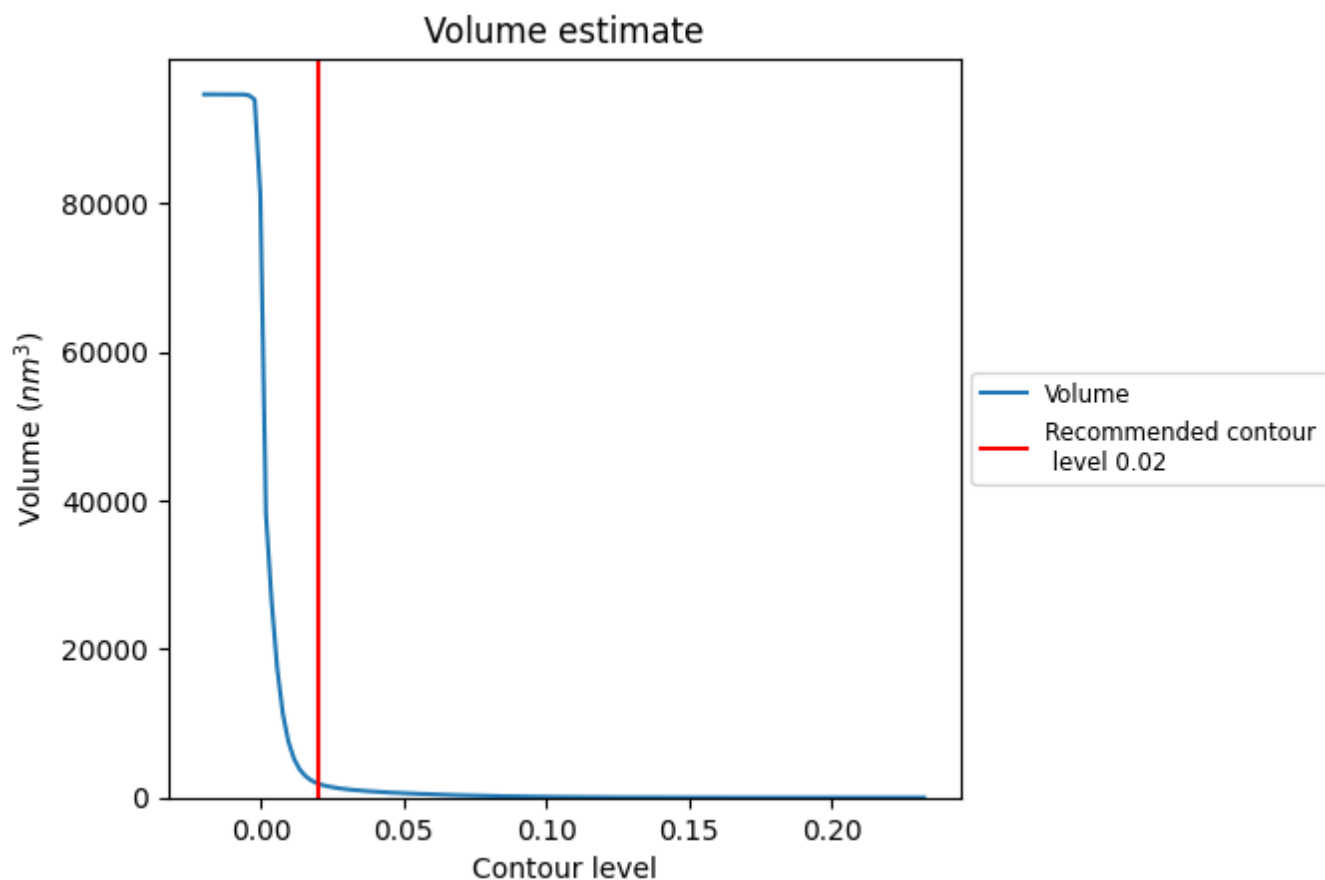
This section contains the results of statistical analysis of the map.

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.

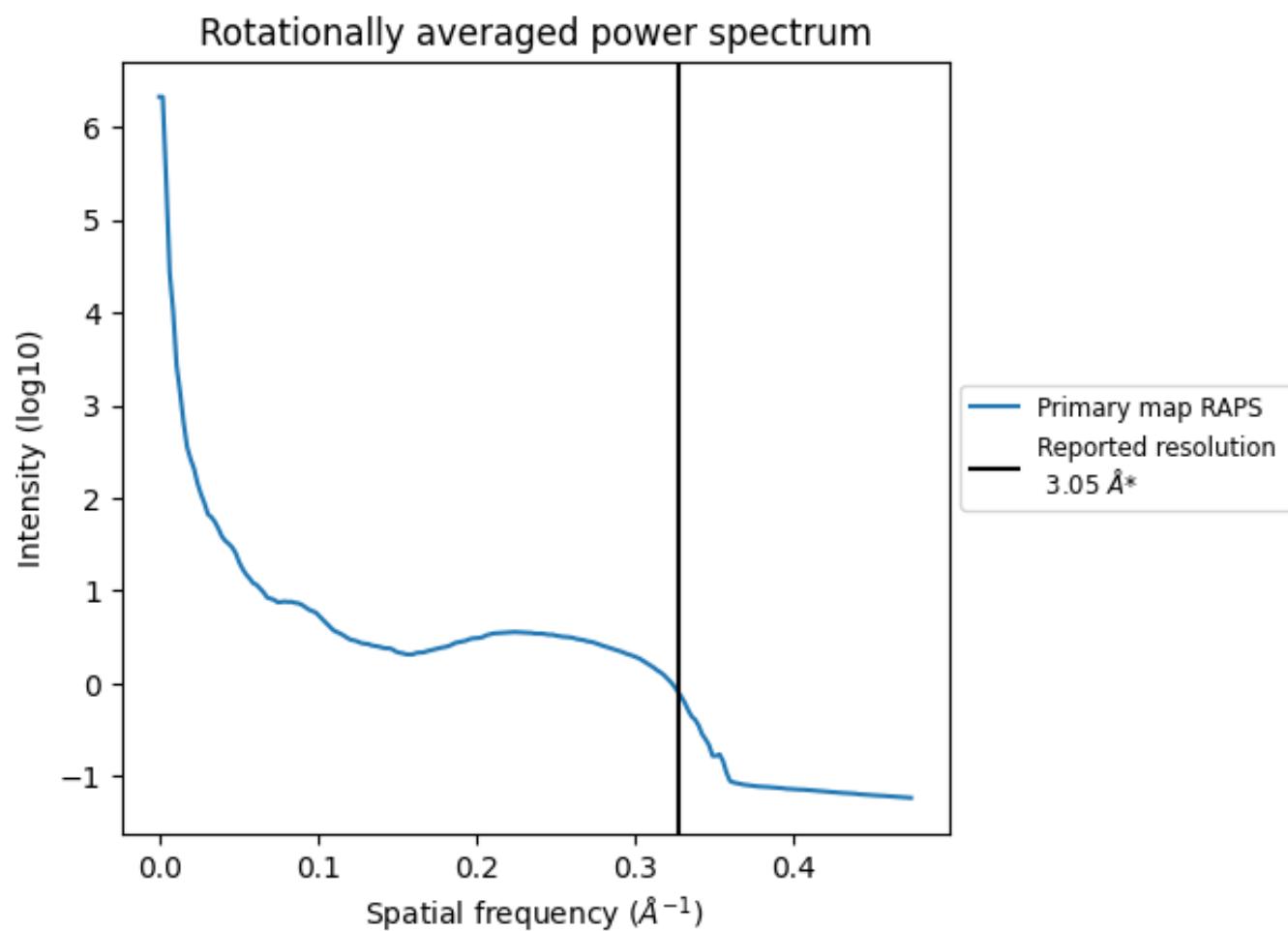
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1915 nm^3 ; this corresponds to an approximate mass of 1730 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 0.328 Å⁻¹

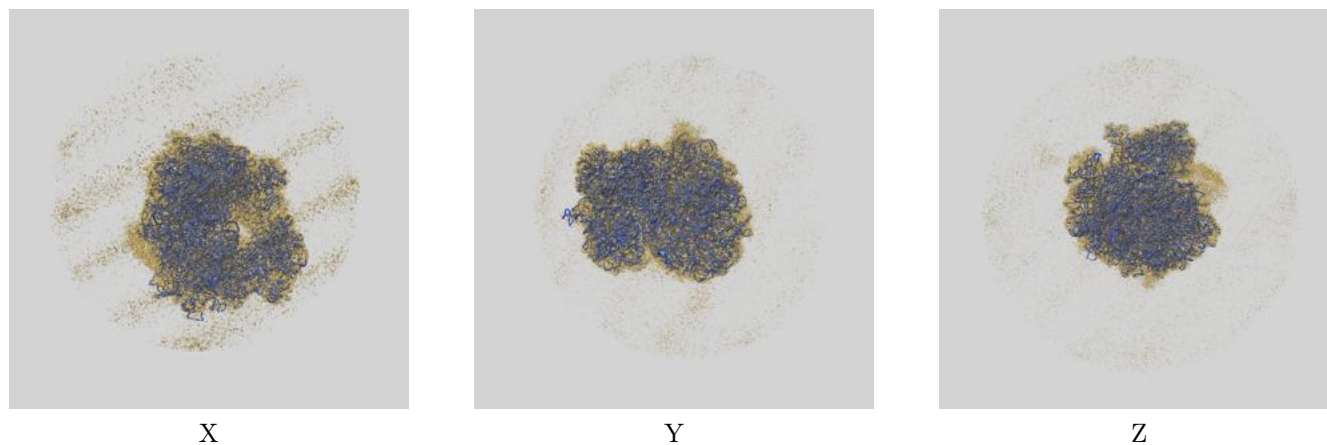
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

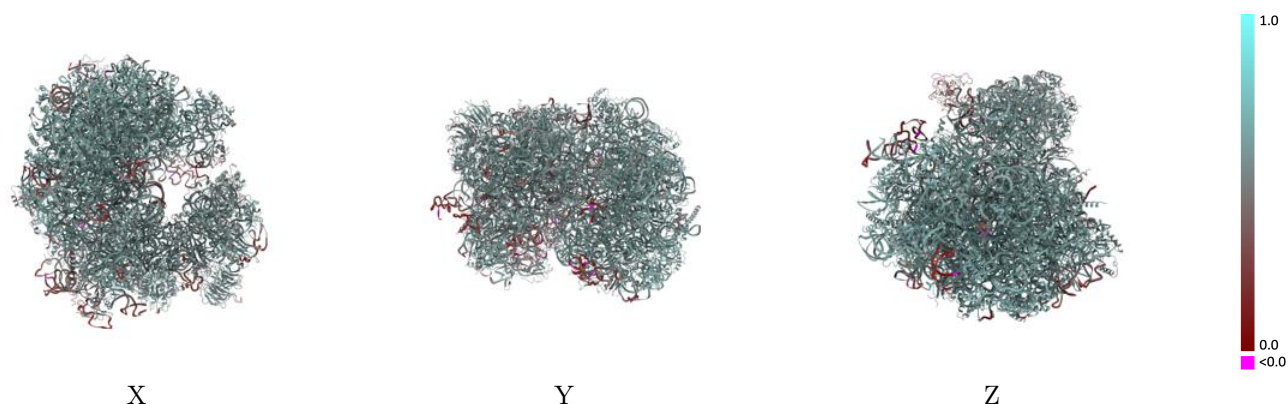
This section contains information regarding the fit between EMDB map EMD-24235 and PDB model 7N8B. Per-residue inclusion information can be found in [section 3](#) on [page 21](#).

9.1 Map-model overlay [i](#)



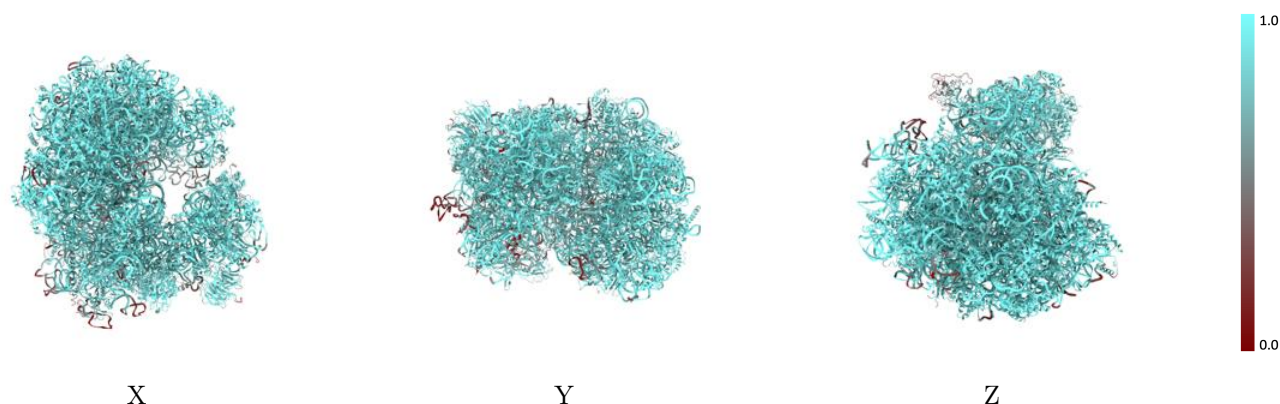
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



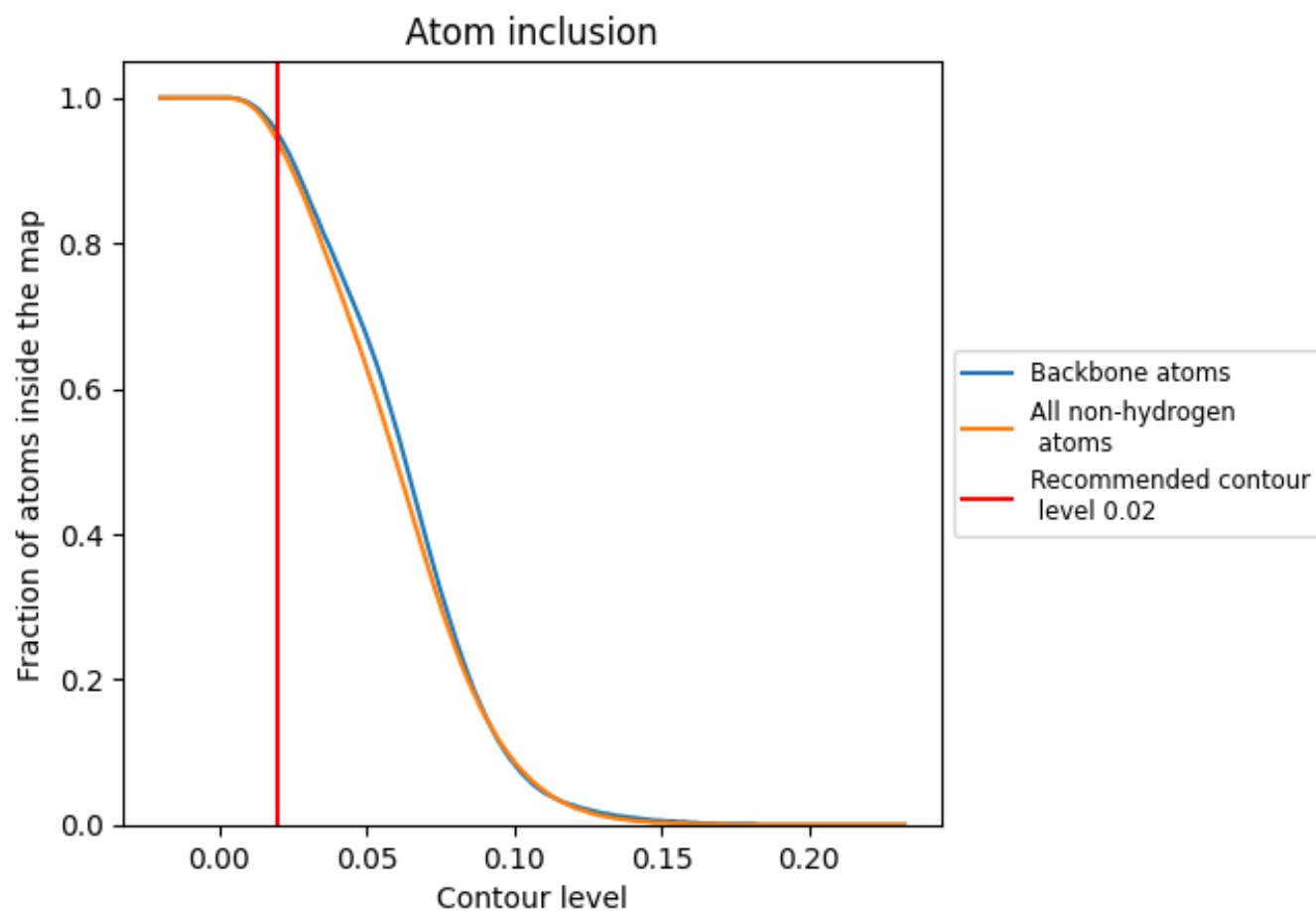
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 94% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9400	 0.5700
A1	 0.9630	 0.5830
A3	 0.9940	 0.5940
A4	 0.9880	 0.6100
AA	 0.9820	 0.6150
AB	 0.9800	 0.6200
AC	 0.9750	 0.6080
AD	 0.9270	 0.5640
AE	 0.9600	 0.6000
AF	 0.9690	 0.6050
AG	 0.9430	 0.5870
AH	 0.9600	 0.5970
AI	 0.9480	 0.5810
AJ	 0.8730	 0.5080
AL	 0.9540	 0.6060
AM	 0.9710	 0.6100
AN	 0.9900	 0.6270
AO	 0.9770	 0.6120
AP	 0.9750	 0.6210
AQ	 0.9830	 0.6200
AR	 0.8830	 0.5390
AS	 0.9730	 0.6120
AT	 0.9690	 0.5970
AU	 0.9450	 0.5640
AV	 0.9740	 0.6090
AW	 0.9960	 0.6260
AX	 0.9680	 0.6080
AY	 0.9650	 0.6120
AZ	 0.9640	 0.5910
Aa	 0.9640	 0.6110
Ab	 0.9470	 0.5820
Ac	 0.9550	 0.5880
Ad	 0.9290	 0.6100
Ae	 0.9800	 0.6220
Af	 0.9940	 0.6330









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Chain	Atom inclusion	Q-score
Ag	 0.9580	 0.5980
Ah	 0.9740	 0.6150
Ai	 0.9330	 0.5620
Aj	 0.9800	 0.6190
Ak	 0.9300	 0.5730
Al	 0.9810	 0.6250
Am	 0.9400	 0.5890
An	 0.8870	 0.4910
Ao	 0.9470	 0.5910
Ap	 0.9690	 0.5960
B5	 0.9190	 0.5340
BA	 0.9460	 0.5750
BB	 0.9170	 0.5570
BC	 0.9600	 0.5870
BD	 0.9040	 0.5250
BE	 0.9540	 0.5950
BF	 0.9150	 0.5450
BG	 0.9210	 0.5630
BH	 0.8100	 0.5110
BI	 0.9430	 0.5740
BJ	 0.9280	 0.5730
BK	 0.8260	 0.4820
BL	 0.8710	 0.5500
BM	 0.3920	 0.2640
BN	 0.9490	 0.5790
BO	 0.9220	 0.5500
BP	 0.8380	 0.5160
BQ	 0.9480	 0.5790
BR	 0.8430	 0.5110
BS	 0.8920	 0.5350
BT	 0.9320	 0.5630
BU	 0.8130	 0.5050
BV	 0.9430	 0.5860
BW	 0.9730	 0.6070
BX	 0.9690	 0.5950
BY	 0.9130	 0.5750
BZ	 0.8780	 0.5410
Ba	 0.9380	 0.5700
Bb	 0.9190	 0.5710
Bc	 0.8660	 0.5190
Bd	 0.9790	 0.5790
Be	 0.9080	 0.5480

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Chain	Atom inclusion	Q-score
Bf	 0.4530	 0.2350
Bg	 0.8660	 0.5390
Bh	 0.5370	 0.3250