



wwPDB EM Validation Summary Report ⓘ

Nov 5, 2024 – 12:58 PM EST

PDB ID : 7MPI
EMDB ID : EMD-23934
Title : Stm1 bound vacant 80S structure isolated from cbf5-D95A
Authors : Rai, J.; Zhao, Y.; Li, H.
Deposited on : 2021-05-04
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

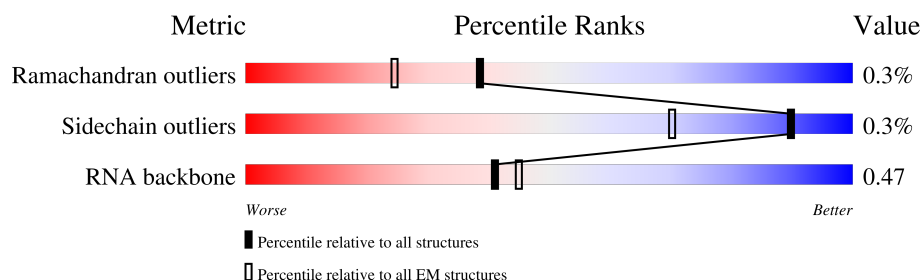
1 Overall quality at a glance

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.



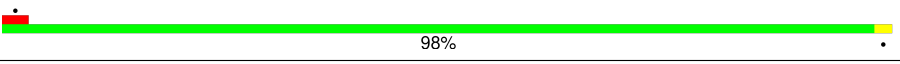
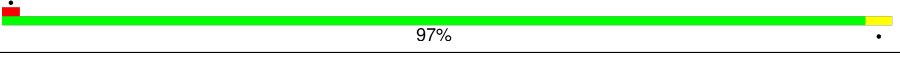
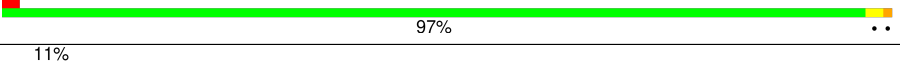
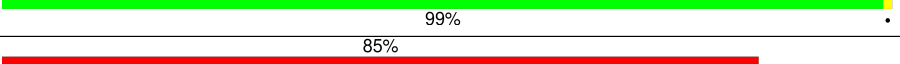
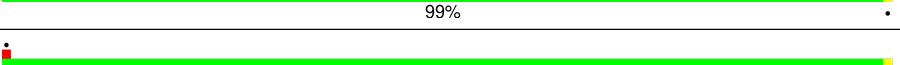
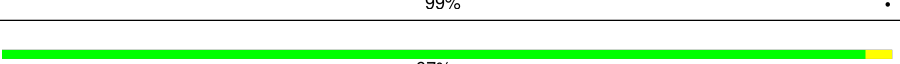
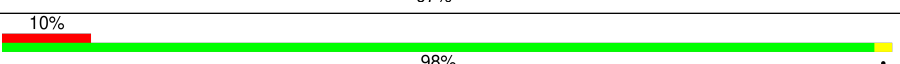
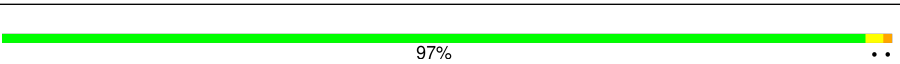
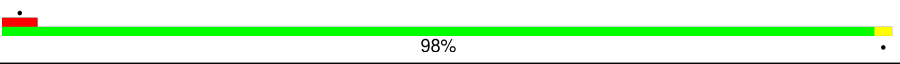
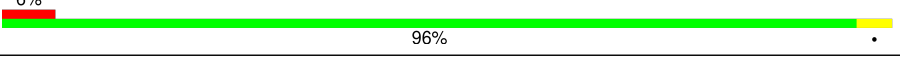
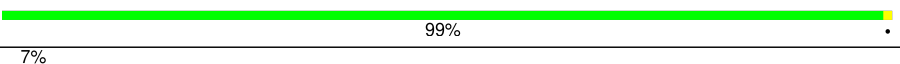
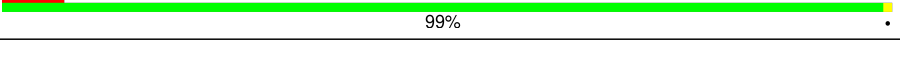
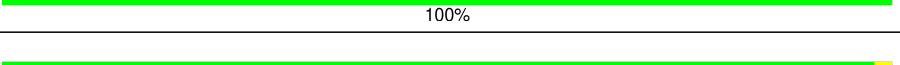
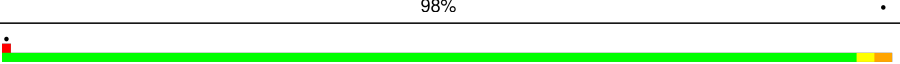
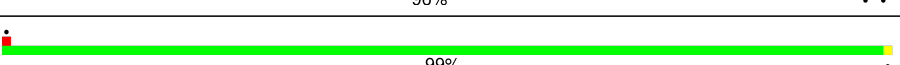
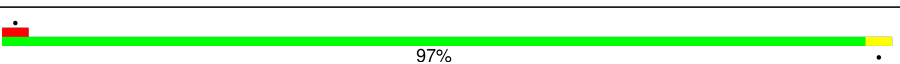
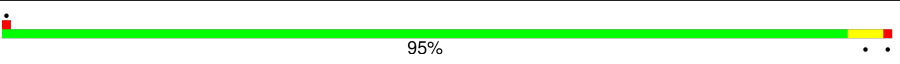
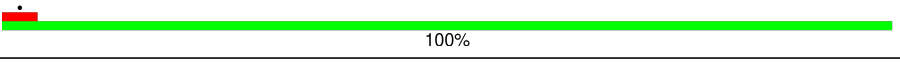
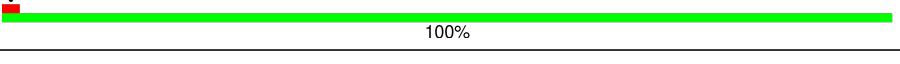
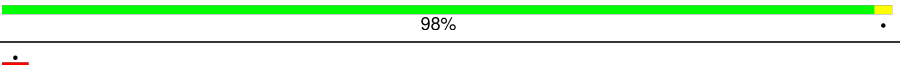
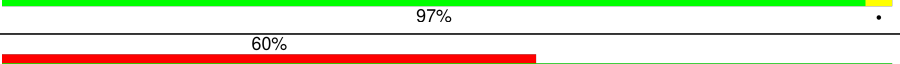
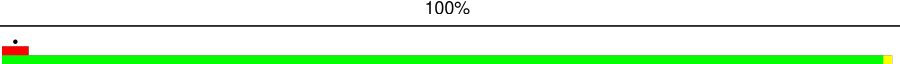
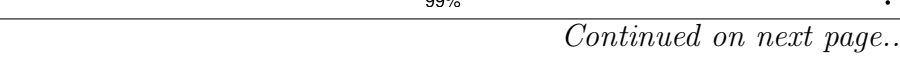


Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	BA	206	
2	BB	214	
3	BC	217	
4	BD	223	
5	BE	260	
6	BF	206	
7	BG	226	
8	BH	184	

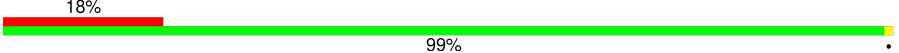

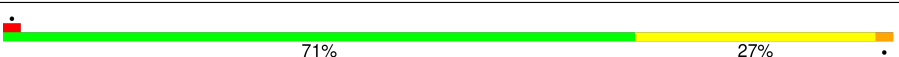
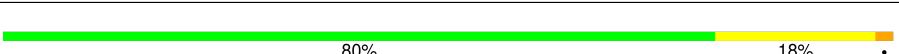
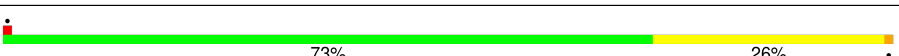
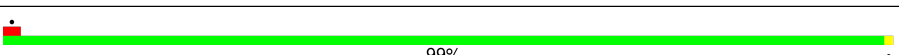
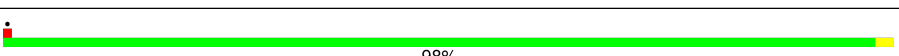
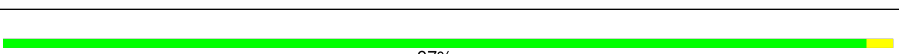
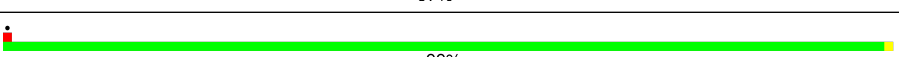
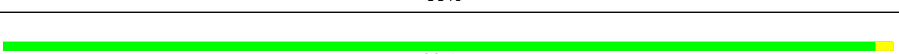
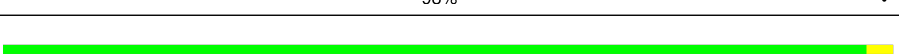
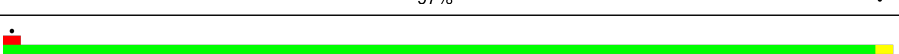
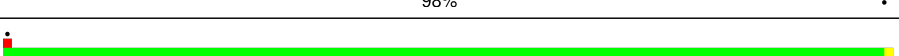
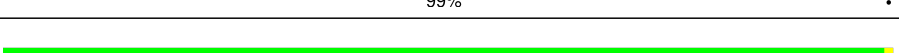
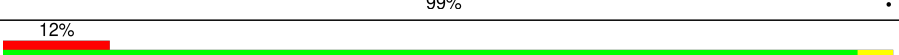
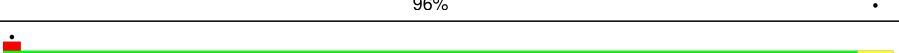
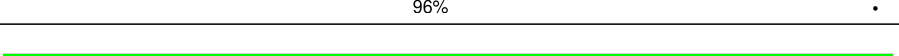
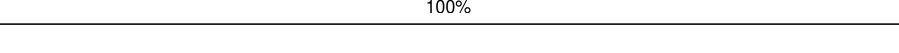
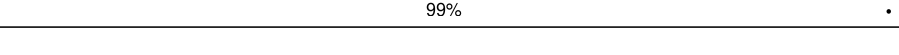
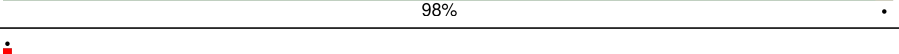
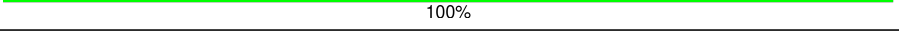
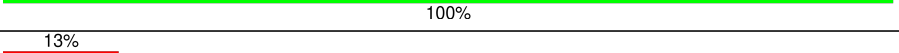
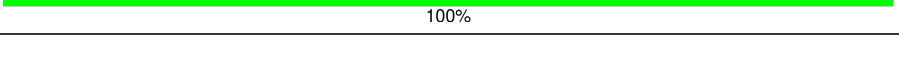
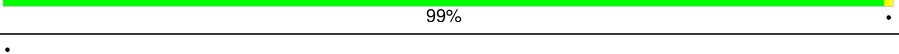
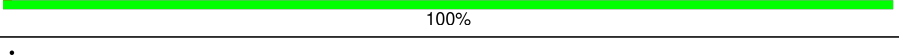
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Mol	Chain	Length	Quality of chain
9	BI	188	 98%
10	BJ	185	 97%
11	BK	96	 97%
12	BL	155	 11%99%
13	BM	121	 85%99%
14	BN	150	 99%
15	BO	127	 97%
16	BP	124	 10%98%
17	BQ	141	 97%
18	BR	121	 98%
19	BS	145	 6%96%
20	BT	141	 99%
21	BU	107	 7%99%
22	BV	87	 100%
23	BW	129	 98%
24	BX	144	 96%
25	BY	134	 99%
26	BZ	69	 97%
27	Ba	97	 95%
28	Bb	81	 100%
29	Bc	63	 100%
30	Bd	53	 98%
31	Be	60	 97%
32	Bf	57	 60%100%
33	Bg	312	 99%


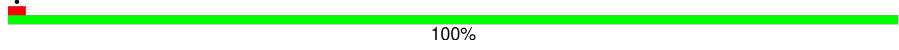
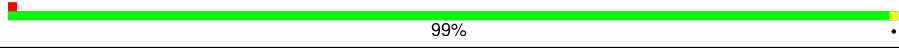
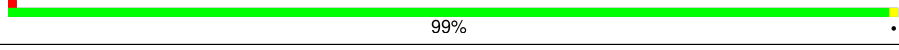
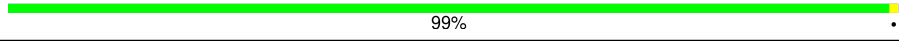
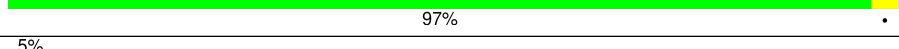
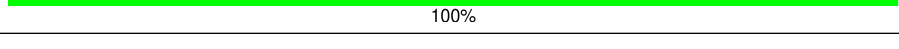
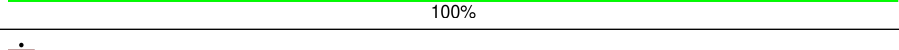
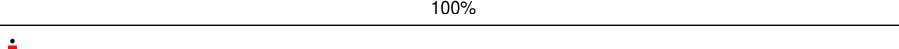
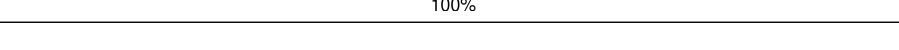
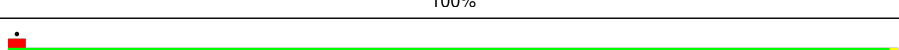
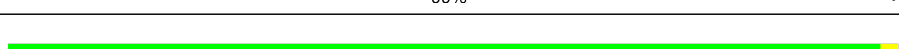

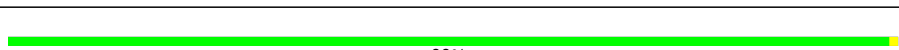
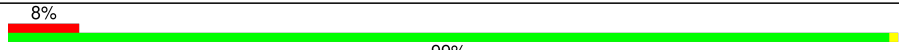
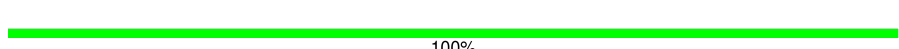
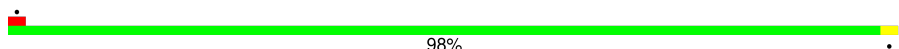

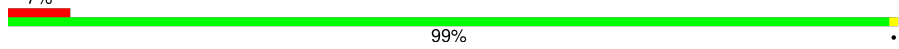
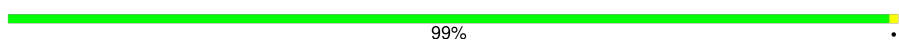

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Mol	Chain	Length	Quality of chain
34	Bh	89	
35	B5	1781	
36	A1	3137	
37	A3	121	
38	A4	158	
39	AA	247	
40	AB	386	
41	AC	361	
42	AD	292	
43	AE	156	
44	AF	222	
45	AG	230	
46	AH	190	
47	AI	205	
48	AJ	169	
49	AL	193	
50	AM	136	
51	AN	203	
52	AO	197	
53	AP	175	
54	AQ	185	
55	AR	188	
56	AS	172	
57	AT	159	
58	AU	100	

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Mol	Chain	Length	Quality of chain
59	AV	136	 100%
60	AW	63	 100%
61	AX	121	 99%
62	AY	126	 99%
63	AZ	135	 99%
64	Aa	148	 97%
65	Ab	58	 100%
66	Ac	97	 100%
67	Ad	109	 100%
68	Ae	127	 100%
69	Af	106	 100%
70	Ag	112	 99%
71	Ah	119	 98%
72	Ai	99	 99%
73	Aj	87	 99%
74	Ak	77	 99%
75	Al	50	 100%
76	Am	52	 98%
77	An	25	 100%
78	Ao	105	 99%
79	Ap	91	 99%

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
35	3AU	B5	1191	X	-	-	-
35	G7M	B5	1575	X	-	-	-

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 199433 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 protein called 40S ribosomal protein S0-A.

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

- Molecule 2 is a protein called 40S ribosomal protein S1-A.

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

- Molecule 3 is a protein called 40S ribosomal protein S2.

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

- Molecule 4 is a protein called 40S ribosomal protein S3.

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

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

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

- Molecule 6 is a protein called 40S ribosomal protein S5.

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

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

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

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

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

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	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
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 10 is a protein called 40S ribosomal protein S9-A.

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

- Molecule 11 is a protein called 40S ribosomal protein S10-A.

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

- Molecule 12 is a protein called 40S ribosomal protein S11-A.

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

- Molecule 13 is a protein called 40S ribosomal protein S12.

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

- Molecule 14 is a protein called 40S ribosomal protein S13.

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

- Molecule 15 is a protein called 40S ribosomal protein S14-A.

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

- Molecule 16 is a protein called 40S ribosomal protein S15.

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

- Molecule 17 is a protein called 40S ribosomal protein S16-A.

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

- Molecule 18 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	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 19 is a protein called 40S ribosomal protein S18-A.

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

- Molecule 20 is a protein called 40S ribosomal protein S19-A.

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

- Molecule 21 is a protein called 40S ribosomal protein S20.

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

- Molecule 22 is a protein called 40S ribosomal protein S21-A.

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

- Molecule 23 is a protein called 40S ribosomal protein S22-A.

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

- Molecule 24 is a protein called 40S ribosomal protein S23-A.

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

- Molecule 25 is a protein called 40S ribosomal protein S24-A.

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

- Molecule 26 is a protein called 40S ribosomal protein S25-A.

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

- Molecule 27 is a protein called 40S ribosomal protein S26-B.

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

- Molecule 28 is a protein called 40S ribosomal protein S27-A.

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

- Molecule 29 is a protein called 40S ribosomal protein S28-A.

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

- Molecule 30 is a protein called 40S ribosomal protein S29-A.

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

- Molecule 31 is a protein called 40S ribosomal protein S30-A.

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

- Molecule 32 is a protein called 40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	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 33 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

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

- Molecule 34 is a protein called Suppressor protein STM1.

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

- Molecule 35 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	B5	1781	Total	C	N	O	P	1	0
			37849	16931	6657	12480	1781		

- Molecule 36 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	A1	3137	Total	C	N	O	P	0	0
			67139	30012	12094	21896	3137		

- Molecule 37 is a RNA chain called 5s rRNA.

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

- Molecule 38 is a RNA chain called 5.8 S rRNA.

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

- Molecule 39 is a protein called 60S ribosomal protein L2-A.

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

- Molecule 40 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	AB	386	Total	C	N	O	S	0	0
			3078	1953	584	533	8		

- Molecule 41 is a protein called 60S ribosomal protein L4-A.

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

- Molecule 42 is a protein called 60S ribosomal protein L5.

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

- Molecule 43 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 44 is a protein called 60S ribosomal protein L7-A.

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

- Molecule 45 is a protein called 60S ribosomal protein L8-A.

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

- Molecule 46 is a protein called 60S ribosomal protein L9-A.

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

- Molecule 47 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	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 48 is a protein called 60S ribosomal protein L11-A.

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

- Molecule 49 is a protein called 60S ribosomal protein L13-A.

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

- Molecule 50 is a protein called 60S ribosomal protein L14-A.

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

- Molecule 51 is a protein called 60S ribosomal protein L15-A.

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

- Molecule 52 is a protein called 60S ribosomal protein L16-A.

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

- Molecule 53 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	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 54 is a protein called 60S ribosomal protein L18-A.

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

- Molecule 55 is a protein called 60S ribosomal protein L19-A.

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

- Molecule 56 is a protein called 60S ribosomal protein L20-A.

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

- Molecule 57 is a protein called 60S ribosomal protein L21-A.

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

- Molecule 58 is a protein called 60S ribosomal protein L22-A.

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

- Molecule 59 is a protein called 60S ribosomal protein L23-A.

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

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

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

- Molecule 61 is a protein called 60S ribosomal protein L25.

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

- Molecule 62 is a protein called 60S ribosomal protein L26-A.

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

- Molecule 63 is a protein called 60S ribosomal protein L27-A.

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

- Molecule 64 is a protein called 60S ribosomal protein L28.

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

- Molecule 65 is a protein called 60S ribosomal protein L29.

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

- Molecule 66 is a protein called 60S ribosomal protein L30.

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

- Molecule 67 is a protein called 60S ribosomal protein L31-A.

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

- Molecule 68 is a protein called 60S ribosomal protein L32.

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

- Molecule 69 is a protein called 60S ribosomal protein L33-A.

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

- Molecule 70 is a protein called 60S ribosomal protein L34-A.

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

- Molecule 71 is a protein called 60S ribosomal protein L35-A.

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

- Molecule 72 is a protein called 60S ribosomal protein L36-A.

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

- Molecule 73 is a protein called 60S ribosomal protein L37-A.

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

- Molecule 74 is a protein called 60S ribosomal protein L38.

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

- Molecule 75 is a protein called 60S ribosomal protein L39.

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

- Molecule 76 is a protein called 60S ribosomal protein L40-A.

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

- Molecule 77 is a protein called 60S ribosomal protein L41-A.

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

- Molecule 78 is a protein called 60S ribosomal protein L42-A.

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

- Molecule 79 is a protein called 60S ribosomal protein L43-A.

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

- Molecule 80 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
80	BD	1	Total	Mg	0
			1	1	
80	BJ	1	Total	Mg	0
			1	1	
80	BL	1	Total	Mg	0
			1	1	
80	B5	91	Total	Mg	0
			91	91	
80	A1	242	Total	Mg	0
			242	242	
80	A3	2	Total	Mg	0
			2	2	
80	A4	9	Total	Mg	0
			9	9	
80	AB	3	Total	Mg	0
			3	3	
80	AG	1	Total	Mg	0
			1	1	
80	AL	1	Total	Mg	0
			1	1	
80	AN	2	Total	Mg	0
			2	2	
80	AO	1	Total	Mg	0
			1	1	
80	AP	1	Total	Mg	0
			1	1	
80	AR	1	Total	Mg	0
			1	1	
80	AX	1	Total	Mg	0
			1	1	
80	Ae	4	Total	Mg	0
			4	4	
80	Af	2	Total	Mg	0
			2	2	
80	Aj	2	Total	Mg	0
			2	2	

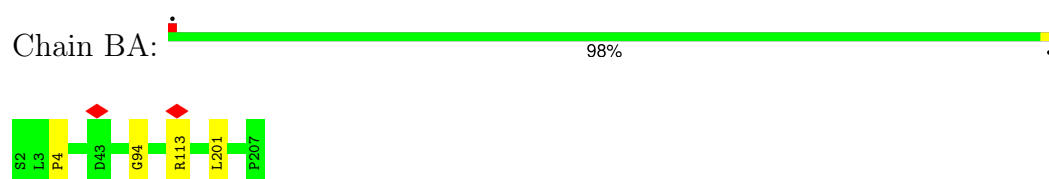
- Molecule 81 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

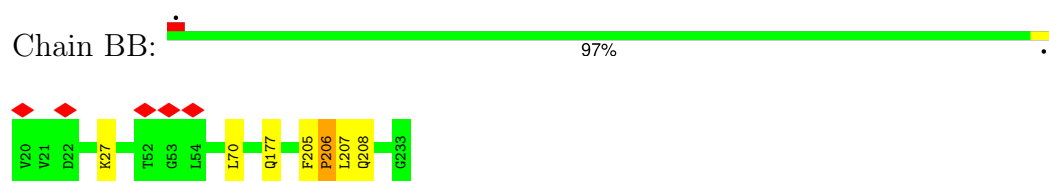
3 Residue-property plots [i](#)

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.

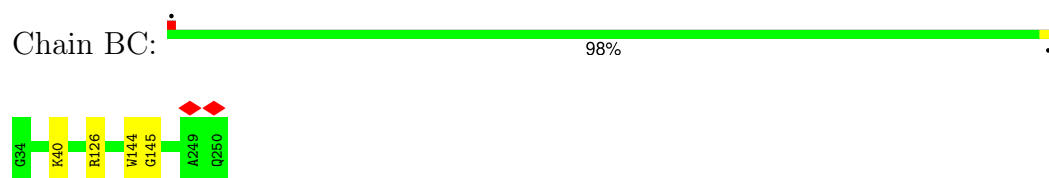
- Molecule 1: 40S ribosomal protein S0-A



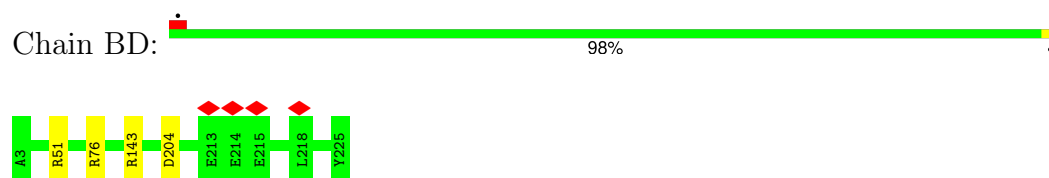
- Molecule 2: 40S ribosomal protein S1-A



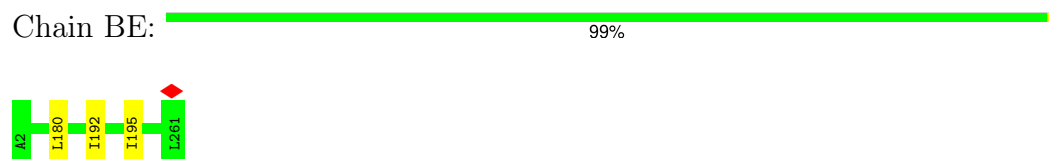
- Molecule 3: 40S ribosomal protein S2



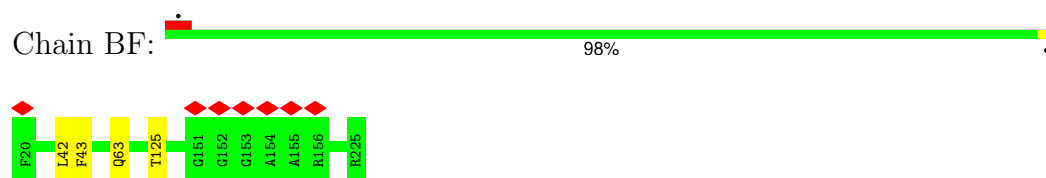
- Molecule 4: 40S ribosomal protein S3



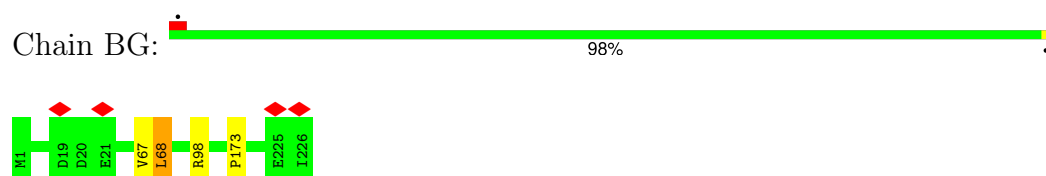
- Molecule 5: 40S ribosomal protein S4-A



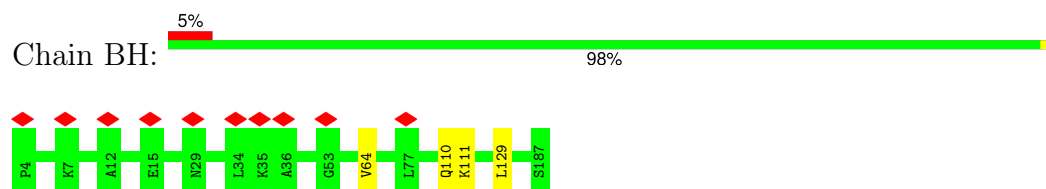
- Molecule 6: 40S ribosomal protein S5



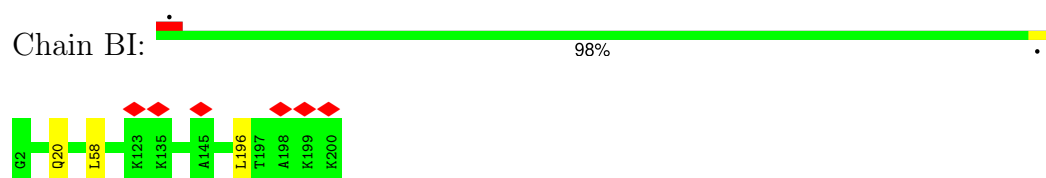
- Molecule 7: 40S ribosomal protein S6-A



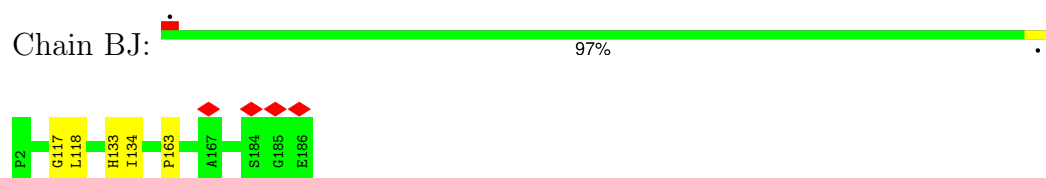
- Molecule 8: 40S ribosomal protein S7-A



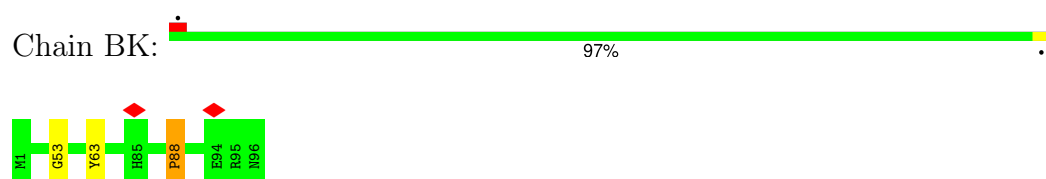
- Molecule 9: 40S ribosomal protein S8-A



- Molecule 10: 40S ribosomal protein S9-A

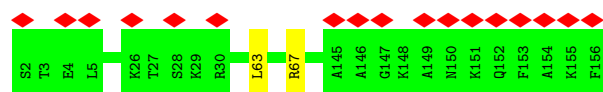


- Molecule 11: 40S ribosomal protein S10-A

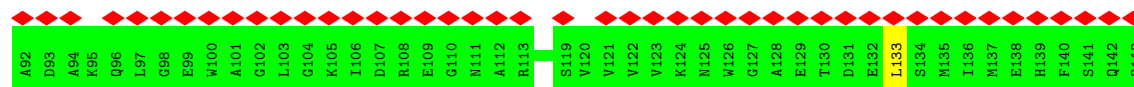
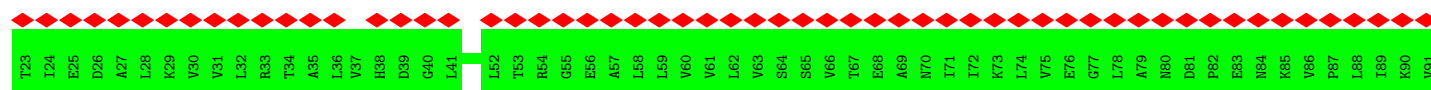
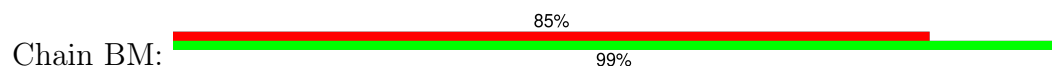


- Molecule 12: 40S ribosomal protein S11-A

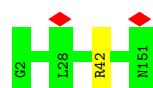




- Molecule 13: 40S ribosomal protein S12



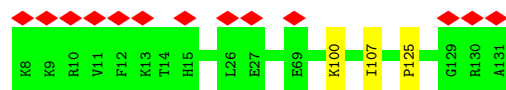
- Molecule 14: 40S ribosomal protein S13



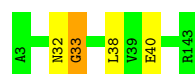
- Molecule 15: 40S ribosomal protein S14-A



- Molecule 16: 40S ribosomal protein S15

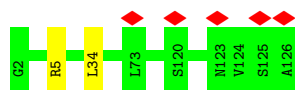


- Molecule 17: 40S ribosomal protein S16-A



- Molecule 18: 40S ribosomal protein S17-A

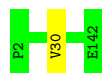




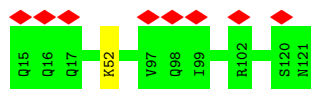
- Molecule 19: 40S ribosomal protein S18-A



- Molecule 20: 40S ribosomal protein S19-A



- Molecule 21: 40S ribosomal protein S20



- Molecule 22: 40S ribosomal protein S21-A



There are no outlier residues recorded for this chain.

- Molecule 23: 40S ribosomal protein S22-A

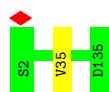


- Molecule 24: 40S ribosomal protein S23-A



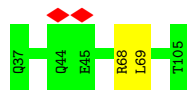
- Molecule 25: 40S ribosomal protein S24-A





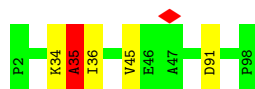
- Molecule 26: 40S ribosomal protein S25-A

Chain BZ: 97%



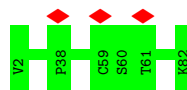
- Molecule 27: 40S ribosomal protein S26-B

Chain Ba: 95%



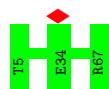
- Molecule 28: 40S ribosomal protein S27-A

Chain Bb: 100%



- Molecule 29: 40S ribosomal protein S28-A

Chain Bc: 100%



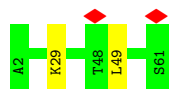
- Molecule 30: 40S ribosomal protein S29-A

Chain Bd: 98%

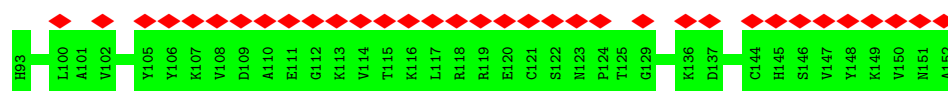


- Molecule 31: 40S ribosomal protein S30-A

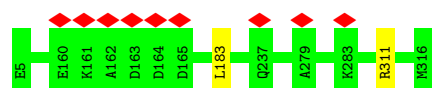
Chain Be: 97%



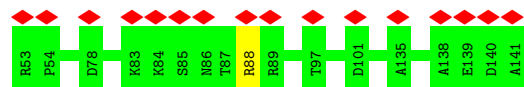
- Molecule 32: 40S ribosomal protein S31



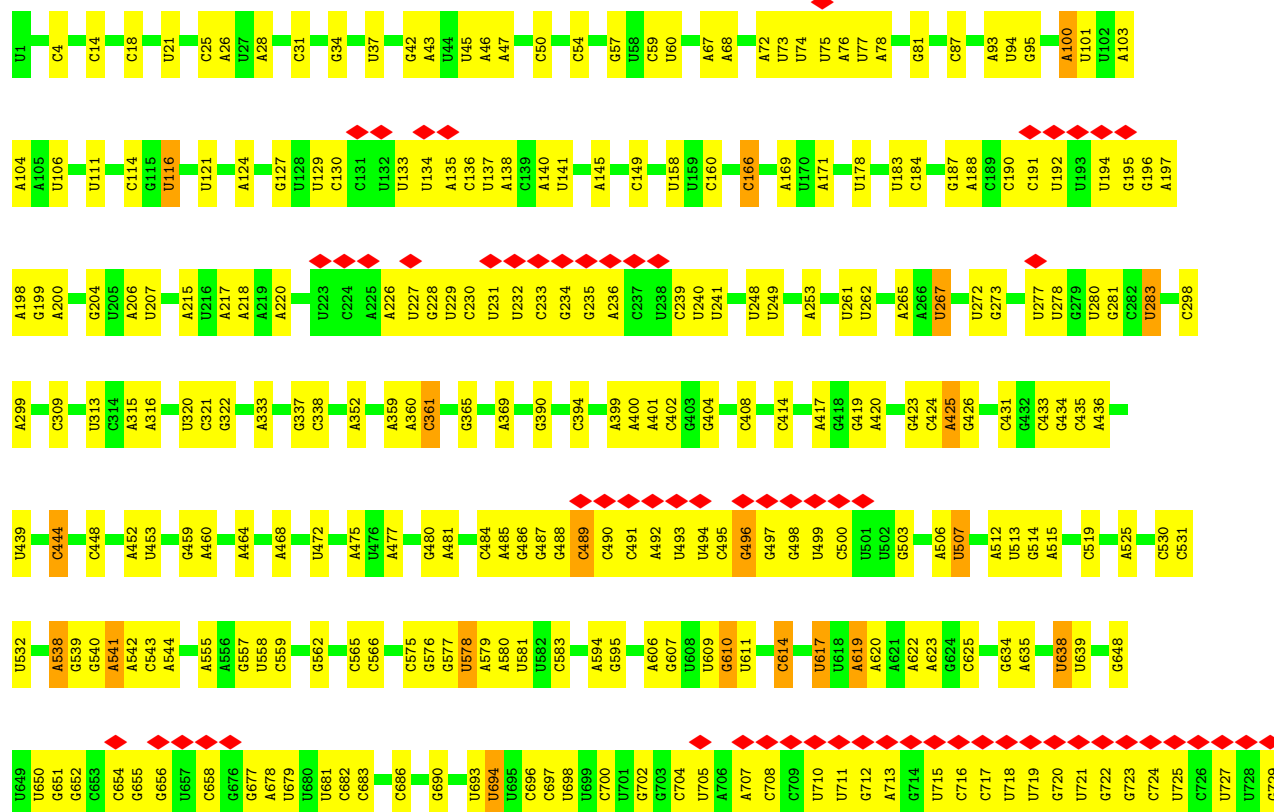
- Molecule 33: Guanine nucleotide-binding protein subunit beta-like protein

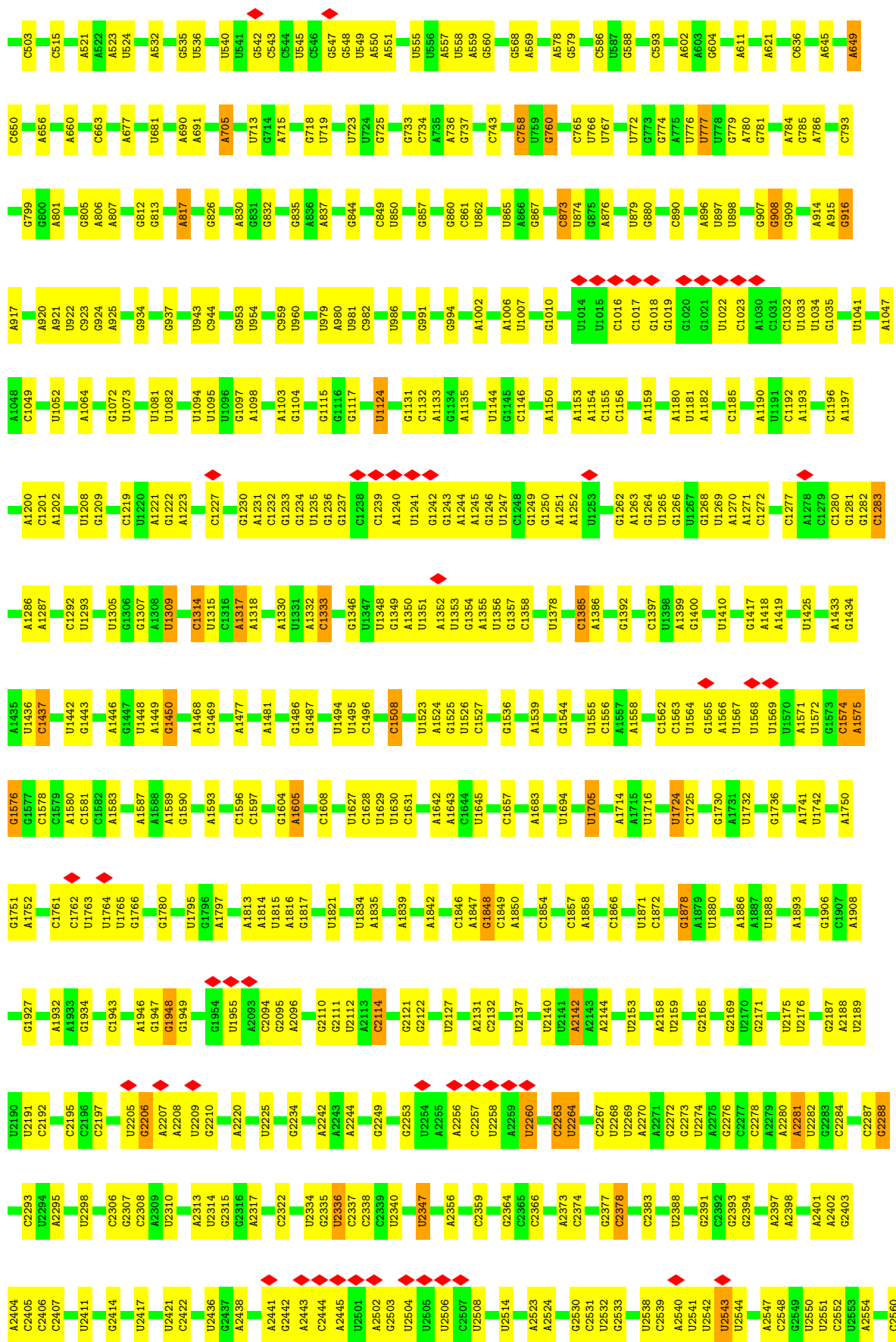


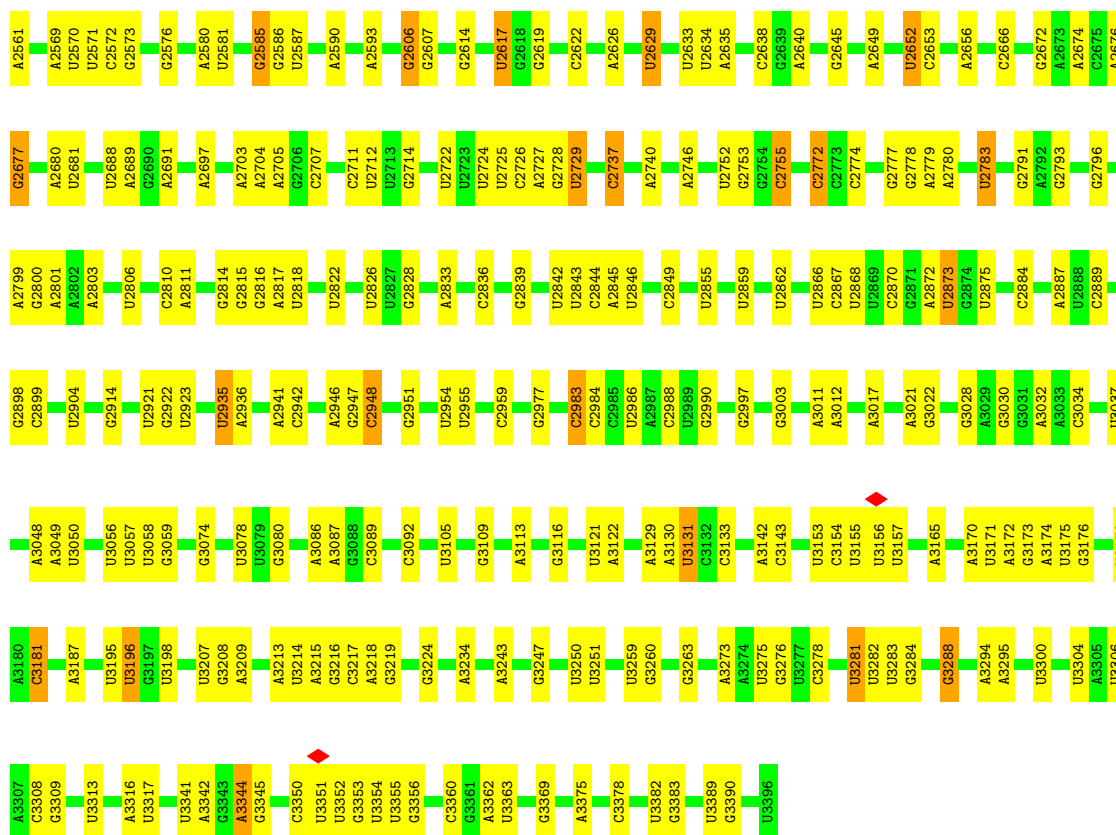
- Molecule 34: Suppressor protein STM1



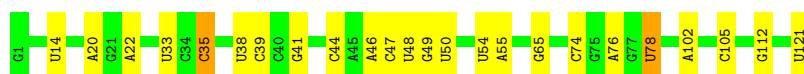
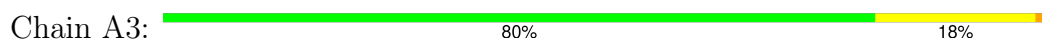
- Molecule 35: 18S rRNA







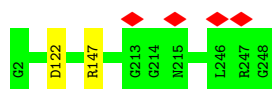
• Molecule 37: 5s rRNA



• Molecule 38: 5.8 S rRNA



• Molecule 39: 60S ribosomal protein L2-A



• Molecule 40: 60S ribosomal protein L3

Chain AB:  98%



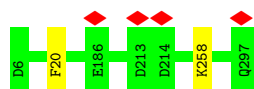
- Molecule 41: 60S ribosomal protein L4-A

Chain AC:  97%



- Molecule 42: 60S ribosomal protein L5

Chain AD:  99%



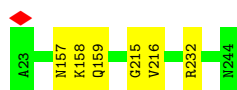
- Molecule 43: 60S ribosomal protein L6-A

Chain AE:  98%



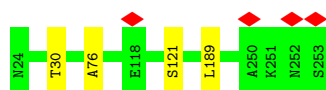
- Molecule 44: 60S ribosomal protein L7-A

Chain AF:  97%



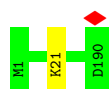
- Molecule 45: 60S ribosomal protein L8-A

Chain AG:  98%



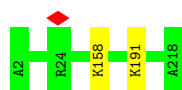
- Molecule 46: 60S ribosomal protein L9-A

Chain AH:  99%



- Molecule 47: 60S ribosomal protein L10

Chain AI:  99%



- Molecule 48: 60S ribosomal protein L11-A

Chain AJ:  96%



- Molecule 49: 60S ribosomal protein L13-A

Chain AL:  96%



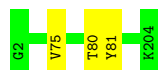
- Molecule 50: 60S ribosomal protein L14-A

Chain AM:  100%

There are no outlier residues recorded for this chain.

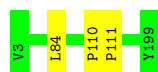
- Molecule 51: 60S ribosomal protein L15-A

Chain AN:  99%



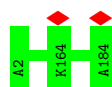
- Molecule 52: 60S ribosomal protein L16-A

Chain AO:  98%



- Molecule 53: 60S ribosomal protein L17-A

Chain AP:  100%



- Molecule 54: 60S ribosomal protein L18-A

Chain AQ:  100%

There are no outlier residues recorded for this chain.

- Molecule 55: 60S ribosomal protein L19-A

Chain AR:  13%  100%



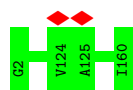
- Molecule 56: 60S ribosomal protein L20-A

Chain AS:  99%



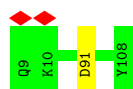
- Molecule 57: 60S ribosomal protein L21-A

Chain AT:  100%



- Molecule 58: 60S ribosomal protein L22-A

Chain AU:  99%



- Molecule 59: 60S ribosomal protein L23-A

Chain AV:  100%



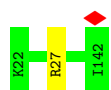
- Molecule 60: 60S ribosomal protein L24-A

Chain AW:  100%



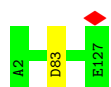
- Molecule 61: 60S ribosomal protein L25

Chain AX:  99%



- Molecule 62: 60S ribosomal protein L26-A

Chain AY:  99%



- Molecule 63: 60S ribosomal protein L27-A

Chain AZ:  99%



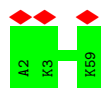
- Molecule 64: 60S ribosomal protein L28

Chain Aa:  97%



- Molecule 65: 60S ribosomal protein L29

Chain Ab:  5% 100%



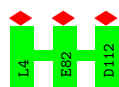
- Molecule 66: 60S ribosomal protein L30

Chain Ac:  100%

There are no outlier residues recorded for this chain.

- Molecule 67: 60S ribosomal protein L31-A

Chain Ad:  100%



- Molecule 68: 60S ribosomal protein L32

Chain Ae:  100%



- Molecule 69: 60S ribosomal protein L33-A

Chain Af:  100%

There are no outlier residues recorded for this chain.

- Molecule 70: 60S ribosomal protein L34-A

Chain Ag:  99%



- Molecule 71: 60S ribosomal protein L35-A

Chain Ah:  98%



- Molecule 72: 60S ribosomal protein L36-A

Chain Ai:  99%



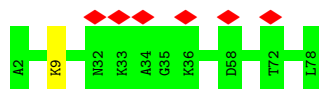
- Molecule 73: 60S ribosomal protein L37-A

Chain Aj:  99%



- Molecule 74: 60S ribosomal protein L38

Chain Ak:  8% 99%



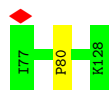
- Molecule 75: 60S ribosomal protein L39

Chain Al:  100%

There are no outlier residues recorded for this chain.

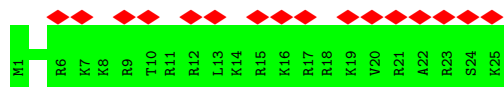
- Molecule 76: 60S ribosomal protein L40-A

Chain Am:  98%



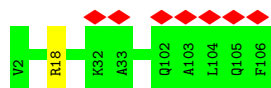
- Molecule 77: 60S ribosomal protein L41-A

Chain An:  64%



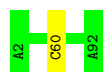
- Molecule 78: 60S ribosomal protein L42-A

Chain Ao:  7%



- Molecule 79: 60S ribosomal protein L43-A

Chain Ap:  99%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	404065	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	0.062	Depositor
Minimum map value	-0.005	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0065	Depositor
Map size (Å)	463.968, 463.968, 463.968	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.074, 1.074, 1.074	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, HIC, 1MA, 3AU, MG, 5MC, G7M, OMU, OMC, A2M, MA6, ZN, OMG, 4AC

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	BA	0.44	0/1653	0.63	1/2261 (0.0%)
2	BB	0.43	0/1735	0.75	1/2335 (0.0%)
3	BC	0.43	0/1665	0.67	1/2263 (0.0%)
4	BD	0.40	0/1759	0.61	1/2368 (0.0%)
5	BE	0.41	0/2109	0.66	2/2839 (0.1%)
6	BF	0.40	0/1629	0.64	0/2202
7	BG	0.38	0/1844	0.66	0/2464
8	BH	0.39	0/1506	0.72	1/2028 (0.0%)
9	BI	0.43	0/1514	0.69	2/2021 (0.1%)
10	BJ	0.41	0/1519	0.66	1/2035 (0.0%)
11	BK	0.64	2/837 (0.2%)	1.05	4/1131 (0.4%)
12	BL	0.46	0/1272	0.61	1/1712 (0.1%)
13	BM	0.29	0/921	0.72	1/1245 (0.1%)
14	BN	0.44	0/1215	0.65	1/1638 (0.1%)
15	BO	0.42	0/952	0.77	1/1279 (0.1%)
16	BP	0.46	0/1012	0.72	1/1356 (0.1%)
17	BQ	0.48	0/1125	0.68	1/1510 (0.1%)
18	BR	0.35	0/984	0.66	1/1318 (0.1%)
19	BS	0.45	0/1211	0.73	2/1628 (0.1%)
20	BT	0.49	0/1113	0.71	0/1494
21	BU	0.37	0/865	0.66	0/1169
22	BV	0.50	0/692	0.64	0/932
23	BW	0.56	1/1038 (0.1%)	0.72	0/1395
24	BX	0.45	0/1139	0.76	1/1518 (0.1%)
25	BY	0.45	0/1087	0.66	1/1449 (0.1%)
26	BZ	0.43	0/566	0.74	1/761 (0.1%)
27	Ba	0.46	0/782	0.77	3/1047 (0.3%)
28	Bb	0.39	0/620	0.65	0/838
29	Bc	0.38	0/499	0.67	0/670
30	Bd	0.47	0/452	0.62	0/600
31	Be	0.35	0/483	0.56	1/643 (0.2%)
32	Bf	0.28	0/462	0.65	0/617

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Bg	0.41	0/2454	0.69	2/3340 (0.1%)
34	Bh	0.32	0/678	0.61	0/905
35	B5	0.80	3/41700 (0.0%)	1.21	345/64963 (0.5%)
36	A1	1.03	0/74123	1.15	407/115559 (0.4%)
37	A3	0.87	0/2883	1.07	11/4491 (0.2%)
38	A4	1.14	0/3745	1.16	16/5828 (0.3%)
39	AA	0.44	0/1912	0.61	1/2569 (0.0%)
40	AB	0.57	1/3136 (0.0%)	0.65	1/4213 (0.0%)
41	AC	0.54	1/2800 (0.0%)	0.69	2/3790 (0.1%)
42	AD	0.37	0/2390	0.59	0/3225
43	AE	0.51	0/1260	0.68	1/1694 (0.1%)
44	AF	0.56	0/1821	0.66	1/2451 (0.0%)
45	AG	0.46	0/1830	0.61	1/2469 (0.0%)
46	AH	0.46	0/1531	0.61	0/2062
47	AI	0.37	0/1708	0.60	1/2290 (0.0%)
48	AJ	0.35	0/1374	0.71	3/1842 (0.2%)
49	AL	0.53	1/1568 (0.1%)	0.66	1/2106 (0.0%)
50	AM	0.49	0/1068	0.53	0/1438
51	AN	0.57	0/1757	0.63	0/2354
52	AO	0.59	0/1585	0.62	1/2128 (0.0%)
53	AP	0.54	0/1410	0.60	0/1893
54	AQ	0.47	0/1465	0.58	0/1965
55	AR	0.43	0/1538	0.53	0/2050
56	AS	0.58	0/1481	0.66	1/1990 (0.1%)
57	AT	0.46	0/1300	0.64	0/1743
58	AU	0.45	0/812	0.70	1/1099 (0.1%)
59	AV	0.51	0/1018	0.67	0/1369
60	AW	0.53	0/533	0.58	0/707
61	AX	0.53	0/983	0.69	1/1325 (0.1%)
62	AY	0.53	0/1004	0.66	1/1341 (0.1%)
63	AZ	0.43	0/1118	0.62	0/1497
64	Aa	0.49	0/1204	0.67	3/1612 (0.2%)
65	Ab	0.35	0/473	0.56	0/629
66	Ac	0.45	0/751	0.62	0/1008
67	Ad	0.53	0/904	0.58	0/1213
68	Ae	0.56	0/1041	0.60	0/1394
69	Af	0.64	0/868	0.62	0/1168
70	Ag	0.50	0/890	0.62	1/1189 (0.1%)
71	Ah	0.48	0/978	0.58	0/1301
72	Ai	0.39	0/778	0.66	0/1034
73	Aj	0.54	0/696	0.67	1/923 (0.1%)
74	Ak	0.40	0/618	0.66	0/826
75	Al	0.46	0/443	0.56	0/588

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Am	0.48	0/423	0.66	1/562 (0.2%)
77	An	0.32	0/234	0.59	0/300
78	Ao	0.35	0/860	0.66	1/1136 (0.1%)
79	Ap	0.49	0/701	0.70	1/934 (0.1%)
All	All	0.79	9/212107 (0.0%)	1.00	836/311279 (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
1	BA	0	1
2	BB	0	5
3	BC	0	2
5	BE	0	1
6	BF	0	2
7	BG	0	1
8	BH	0	2
9	BI	0	1
10	BJ	0	3
11	BK	0	2
15	BO	0	1
16	BP	0	1
17	BQ	0	3
19	BS	0	2
20	BT	0	1
24	BX	0	5
26	BZ	0	1
27	Ba	0	2
35	B5	4	0
40	AB	0	1
41	AC	0	4
42	AD	0	1
43	AE	0	1
44	AF	0	3
45	AG	0	3
46	AH	0	1
48	AJ	0	3
49	AL	0	2
51	AN	0	2
52	AO	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
56	AS	0	1
63	AZ	0	1
71	Ah	0	1
72	Ai	0	1
All	All	4	62

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	BK	88	PRO	CG-CD	-12.00	1.11	1.50
40	AB	16	PHE	C-N	-8.40	1.14	1.34
11	BK	88	PRO	CB-CG	-6.52	1.17	1.50
49	AL	54	LEU	C-N	-6.14	1.20	1.34
23	BW	115	GLU	CG-CD	-5.79	1.43	1.51

The worst 5 of 836 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	A1	266	A	O5'-P-OP1	-31.81	72.53	110.70
36	A1	266	A	OP1-P-OP2	-27.23	78.76	119.60
36	A1	1948	G	O5'-P-OP2	-25.38	80.24	110.70
36	A1	1948	G	O5'-P-OP1	-22.31	83.93	110.70
36	A1	266	A	O5'-P-OP2	19.73	134.38	110.70

All (4) chirality outliers are listed below:

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

5 of 62 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	BA	94	GLY	Peptide
2	BB	177	GLN	Peptide
2	BB	205	PHE	Peptide
2	BB	206	PRO	Peptide
2	BB	27	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	
1	BA	204/206 (99%)	181 (89%)	22 (11%)	1 (0%)	25	54
2	BB	212/214 (99%)	176 (83%)	34 (16%)	2 (1%)	14	40
3	BC	215/217 (99%)	199 (93%)	15 (7%)	1 (0%)	25	54
4	BD	221/223 (99%)	207 (94%)	14 (6%)	0	100	100
5	BE	258/260 (99%)	228 (88%)	30 (12%)	0	100	100
6	BF	204/206 (99%)	186 (91%)	17 (8%)	1 (0%)	25	54
7	BG	224/226 (99%)	205 (92%)	16 (7%)	3 (1%)	10	32
8	BH	182/184 (99%)	166 (91%)	15 (8%)	1 (0%)	25	54
9	BI	184/188 (98%)	149 (81%)	35 (19%)	0	100	100
10	BJ	183/185 (99%)	165 (90%)	17 (9%)	1 (0%)	25	54
11	BK	94/96 (98%)	77 (82%)	17 (18%)	0	100	100
12	BL	153/155 (99%)	138 (90%)	15 (10%)	0	100	100
13	BM	119/121 (98%)	85 (71%)	34 (29%)	0	100	100
14	BN	148/150 (99%)	139 (94%)	9 (6%)	0	100	100
15	BO	125/127 (98%)	109 (87%)	15 (12%)	1 (1%)	16	43
16	BP	122/124 (98%)	100 (82%)	21 (17%)	1 (1%)	16	43
17	BQ	139/141 (99%)	127 (91%)	11 (8%)	1 (1%)	19	46
18	BR	117/121 (97%)	111 (95%)	6 (5%)	0	100	100
19	BS	143/145 (99%)	129 (90%)	13 (9%)	1 (1%)	19	46
20	BT	139/141 (99%)	127 (91%)	12 (9%)	0	100	100
21	BU	105/107 (98%)	98 (93%)	7 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	BV	83/87 (95%)	72 (87%)	11 (13%)	0	100	100
23	BW	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
24	BX	142/144 (99%)	118 (83%)	21 (15%)	3 (2%)	5	21
25	BY	132/134 (98%)	124 (94%)	8 (6%)	0	100	100
26	BZ	67/69 (97%)	61 (91%)	6 (9%)	0	100	100
27	Ba	95/97 (98%)	74 (78%)	19 (20%)	2 (2%)	5	21
28	Bb	79/81 (98%)	68 (86%)	11 (14%)	0	100	100
29	Bc	61/63 (97%)	58 (95%)	3 (5%)	0	100	100
30	Bd	51/53 (96%)	51 (100%)	0	0	100	100
31	Be	58/60 (97%)	51 (88%)	7 (12%)	0	100	100
32	Bf	53/57 (93%)	36 (68%)	17 (32%)	0	100	100
33	Bg	310/312 (99%)	276 (89%)	34 (11%)	0	100	100
34	Bh	87/89 (98%)	78 (90%)	9 (10%)	0	100	100
39	AA	245/247 (99%)	232 (95%)	13 (5%)	0	100	100
40	AB	383/386 (99%)	368 (96%)	14 (4%)	1 (0%)	37	64
41	AC	359/361 (99%)	321 (89%)	36 (10%)	2 (1%)	22	49
42	AD	290/292 (99%)	267 (92%)	22 (8%)	1 (0%)	37	64
43	AE	152/156 (97%)	142 (93%)	10 (7%)	0	100	100
44	AF	220/222 (99%)	206 (94%)	12 (6%)	2 (1%)	14	40
45	AG	228/230 (99%)	210 (92%)	18 (8%)	0	100	100
46	AH	188/190 (99%)	176 (94%)	12 (6%)	0	100	100
47	AI	201/205 (98%)	185 (92%)	16 (8%)	0	100	100
48	AJ	167/169 (99%)	146 (87%)	21 (13%)	0	100	100
49	AL	191/193 (99%)	171 (90%)	17 (9%)	3 (2%)	8	27
50	AM	134/136 (98%)	128 (96%)	6 (4%)	0	100	100
51	AN	201/203 (99%)	185 (92%)	15 (8%)	1 (0%)	25	54
52	AO	195/197 (99%)	188 (96%)	6 (3%)	1 (0%)	25	54
53	AP	171/175 (98%)	164 (96%)	7 (4%)	0	100	100
54	AQ	183/185 (99%)	175 (96%)	8 (4%)	0	100	100
55	AR	186/188 (99%)	178 (96%)	8 (4%)	0	100	100
56	AS	170/172 (99%)	162 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
57	AT	157/159 (99%)	148 (94%)	9 (6%)	0	100	100
58	AU	98/100 (98%)	93 (95%)	5 (5%)	0	100	100
59	AV	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
60	AW	61/63 (97%)	59 (97%)	2 (3%)	0	100	100
61	AX	119/121 (98%)	114 (96%)	5 (4%)	0	100	100
62	AY	124/126 (98%)	115 (93%)	9 (7%)	0	100	100
63	AZ	133/135 (98%)	121 (91%)	11 (8%)	1 (1%)	16	43
64	Aa	146/148 (99%)	129 (88%)	16 (11%)	1 (1%)	19	46
65	Ab	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
66	Ac	95/97 (98%)	90 (95%)	5 (5%)	0	100	100
67	Ad	107/109 (98%)	103 (96%)	4 (4%)	0	100	100
68	Ae	125/127 (98%)	121 (97%)	4 (3%)	0	100	100
69	Af	104/106 (98%)	101 (97%)	3 (3%)	0	100	100
70	Ag	110/112 (98%)	105 (96%)	5 (4%)	0	100	100
71	Ah	117/119 (98%)	109 (93%)	7 (6%)	1 (1%)	14	40
72	Ai	97/99 (98%)	89 (92%)	8 (8%)	0	100	100
73	Aj	85/87 (98%)	77 (91%)	8 (9%)	0	100	100
74	Ak	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
75	Al	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
76	Am	50/52 (96%)	46 (92%)	4 (8%)	0	100	100
77	An	23/25 (92%)	23 (100%)	0	0	100	100
78	Ao	103/105 (98%)	96 (93%)	7 (7%)	0	100	100
79	Ap	89/91 (98%)	83 (93%)	6 (7%)	0	100	100
All	All	10956/11121 (98%)	10008 (91%)	915 (8%)	33 (0%)	38	64

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
24	BX	97	ASP
41	AC	339	LEU
44	AF	159	GLN
49	AL	48	PRO
51	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	
1	BA	173/173 (100%)	172 (99%)	1 (1%)	84	90
2	BB	191/191 (100%)	191 (100%)	0	100	100
3	BC	176/176 (100%)	176 (100%)	0	100	100
4	BD	182/182 (100%)	179 (98%)	3 (2%)	58	76
5	BE	221/221 (100%)	221 (100%)	0	100	100
6	BF	173/173 (100%)	172 (99%)	1 (1%)	84	90
7	BG	193/193 (100%)	192 (100%)	1 (0%)	86	91
8	BH	165/165 (100%)	165 (100%)	0	100	100
9	BI	150/150 (100%)	150 (100%)	0	100	100
10	BJ	158/158 (100%)	158 (100%)	0	100	100
11	BK	89/89 (100%)	88 (99%)	1 (1%)	70	83
12	BL	136/136 (100%)	135 (99%)	1 (1%)	81	89
13	BM	98/98 (100%)	98 (100%)	0	100	100
14	BN	127/127 (100%)	127 (100%)	0	100	100
15	BO	96/96 (100%)	95 (99%)	1 (1%)	73	85
16	BP	104/104 (100%)	104 (100%)	0	100	100
17	BQ	117/117 (100%)	117 (100%)	0	100	100
18	BR	110/110 (100%)	109 (99%)	1 (1%)	75	86
19	BS	128/128 (100%)	127 (99%)	1 (1%)	79	88
20	BT	113/113 (100%)	113 (100%)	0	100	100
21	BU	100/100 (100%)	99 (99%)	1 (1%)	73	85
22	BV	74/74 (100%)	74 (100%)	0	100	100
23	BW	110/110 (100%)	109 (99%)	1 (1%)	75	86
24	BX	119/119 (100%)	119 (100%)	0	100	100
25	BY	112/112 (100%)	112 (100%)	0	100	100
26	BZ	61/61 (100%)	61 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
27	Ba	83/83 (100%)	83 (100%)	0	100	100
28	Bb	70/70 (100%)	70 (100%)	0	100	100
29	Bc	56/56 (100%)	56 (100%)	0	100	100
30	Bd	47/47 (100%)	46 (98%)	1 (2%)	48	69
31	Be	51/51 (100%)	50 (98%)	1 (2%)	50	71
32	Bf	49/49 (100%)	49 (100%)	0	100	100
33	Bg	256/257 (100%)	256 (100%)	0	100	100
34	Bh	68/68 (100%)	67 (98%)	1 (2%)	60	77
39	AA	189/189 (100%)	188 (100%)	1 (0%)	86	91
40	AB	321/321 (100%)	318 (99%)	3 (1%)	75	86
41	AC	288/288 (100%)	286 (99%)	2 (1%)	81	89
42	AD	241/241 (100%)	241 (100%)	0	100	100
43	AE	134/134 (100%)	133 (99%)	1 (1%)	81	89
44	AF	186/186 (100%)	186 (100%)	0	100	100
45	AG	189/189 (100%)	189 (100%)	0	100	100
46	AH	170/170 (100%)	170 (100%)	0	100	100
47	AI	176/176 (100%)	175 (99%)	1 (1%)	84	90
48	AJ	147/147 (100%)	146 (99%)	1 (1%)	81	89
49	AL	154/154 (100%)	154 (100%)	0	100	100
50	AM	107/107 (100%)	107 (100%)	0	100	100
51	AN	175/175 (100%)	175 (100%)	0	100	100
52	AO	160/160 (100%)	160 (100%)	0	100	100
53	AP	141/141 (100%)	141 (100%)	0	100	100
54	AQ	150/150 (100%)	150 (100%)	0	100	100
55	AR	153/153 (100%)	153 (100%)	0	100	100
56	AS	156/156 (100%)	156 (100%)	0	100	100
57	AT	136/136 (100%)	136 (100%)	0	100	100
58	AU	87/87 (100%)	87 (100%)	0	100	100
59	AV	104/104 (100%)	104 (100%)	0	100	100
60	AW	55/55 (100%)	55 (100%)	0	100	100
61	AX	105/105 (100%)	105 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	AY	109/109 (100%)	109 (100%)	0	100	100
63	AZ	115/115 (100%)	115 (100%)	0	100	100
64	Aa	118/118 (100%)	118 (100%)	0	100	100
65	Ab	46/46 (100%)	46 (100%)	0	100	100
66	Ac	81/81 (100%)	81 (100%)	0	100	100
67	Ad	96/96 (100%)	96 (100%)	0	100	100
68	Ae	109/109 (100%)	109 (100%)	0	100	100
69	Af	90/90 (100%)	90 (100%)	0	100	100
70	Ag	95/95 (100%)	95 (100%)	0	100	100
71	Ah	104/104 (100%)	104 (100%)	0	100	100
72	Ai	81/81 (100%)	81 (100%)	0	100	100
73	Aj	70/70 (100%)	70 (100%)	0	100	100
74	Ak	68/68 (100%)	67 (98%)	1 (2%)	60	77
75	Al	45/45 (100%)	45 (100%)	0	100	100
76	Am	47/47 (100%)	47 (100%)	0	100	100
77	An	23/23 (100%)	23 (100%)	0	100	100
78	Ao	90/90 (100%)	90 (100%)	0	100	100
79	Ap	71/71 (100%)	71 (100%)	0	100	100
All	All	9338/9339 (100%)	9312 (100%)	26 (0%)	90	94

5 of 26 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	Be	29	LYS
40	AB	93	VAL
48	AJ	60	ARG
39	AA	147	ARG
40	AB	300	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
19	BS	71	GLN
47	AI	209	ASN
59	AV	98	ASN

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Mol	Chain	Res	Type
55	AR	134	HIS
6	BF	95	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
35	B5	1774/1781 (99%)	525 (29%)	11 (0%)
36	A1	3131/3137 (99%)	726 (23%)	17 (0%)
37	A3	120/121 (99%)	19 (15%)	0
38	A4	156/158 (98%)	34 (21%)	1 (0%)
All	All	5181/5197 (99%)	1304 (25%)	29 (0%)

5 of 1304 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
35	B5	4	C
35	B5	25	C
35	B5	26	A
35	B5	34	G
35	B5	42	G

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
36	A1	439	C
36	A1	3121	U
36	A1	916	G
36	A1	2111	G
36	A1	873	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
36	A2M	A1	1449	80,36	18,25,26	0.91	0	20,36,39	1.42	2 (10%)
36	OMC	A1	2197	36	19,22,23	0.78	0	25,31,34	0.77	0
36	OMG	A1	2619	36	19,26,27	0.86	1 (5%)	21,38,41	1.11	3 (14%)
36	5MC	A1	2870	36	19,22,23	1.35	2 (10%)	26,32,35	1.17	3 (11%)
36	A2M	A1	1133	36	18,25,26	0.92	1 (5%)	20,36,39	1.53	3 (15%)
36	OMG	A1	867	80,36	19,26,27	0.91	1 (5%)	21,38,41	1.25	3 (14%)
36	OMU	A1	898	36	19,22,23	1.41	4 (21%)	25,31,34	1.89	5 (20%)
36	OMG	A1	805	36	19,26,27	0.97	1 (5%)	21,38,41	1.16	3 (14%)
36	UR3	A1	2634	80,36	19,22,23	0.98	1 (5%)	26,32,35	1.62	3 (11%)
35	OMG	B5	562	35	19,26,27	1.01	1 (5%)	21,38,41	1.13	2 (9%)
35	A2M	B5	974	35	18,25,26	0.83	0	20,36,39	1.52	3 (15%)
35	OMG	B5	1428	80,35	19,26,27	0.92	1 (5%)	21,38,41	1.12	2 (9%)
35	MA6	B5	1781	35	19,26,27	1.00	2 (10%)	18,38,41	2.11	5 (27%)
36	OMC	A1	663	36	19,22,23	0.97	2 (10%)	25,31,34	0.88	0
36	A2M	A1	817	80,36	18,25,26	0.91	0	20,36,39	1.53	3 (15%)
35	A2M	B5	436	35	18,25,26	0.90	0	20,36,39	1.23	3 (15%)
35	4AC	B5	1773	35	21,24,25	1.17	3 (14%)	28,34,37	2.89	6 (21%)
35	OMU	B5	1269	80,35	19,22,23	1.31	4 (21%)	25,31,34	1.96	7 (28%)
35	OMC	B5	1007	35	19,22,23	0.82	0	25,31,34	0.87	1 (4%)
36	OMC	A1	1437	80,36	19,22,23	0.95	1 (5%)	25,31,34	1.55	5 (20%)
36	OMG	A1	2288	36	19,26,27	0.90	1 (5%)	21,38,41	1.19	3 (14%)
36	A2M	A1	2946	80,36	18,25,26	0.79	0	20,36,39	1.49	4 (20%)
36	OMU	A1	2421	36	19,22,23	1.27	4 (21%)	25,31,34	1.74	5 (20%)
36	OMU	A1	2417	36	19,22,23	1.30	4 (21%)	25,31,34	1.78	4 (16%)
36	OMG	A1	2791	36	19,26,27	0.88	1 (5%)	21,38,41	1.13	2 (9%)
35	OMU	B5	578	35	19,22,23	1.29	4 (21%)	25,31,34	1.82	4 (16%)
35	MA6	B5	1782	35	19,26,27	0.97	1 (5%)	18,38,41	1.99	4 (22%)
36	OMC	A1	2959	36	19,22,23	0.83	1 (5%)	25,31,34	1.01	1 (4%)
35	A2M	B5	796	35	18,25,26	0.88	0	20,36,39	1.29	2 (10%)
35	A2M	B5	420	35	18,25,26	0.82	0	20,36,39	1.42	3 (15%)
35	OMG	B5	1572	35	19,26,27	0.96	1 (5%)	21,38,41	1.07	2 (9%)
36	OMC	A1	650	36	19,22,23	0.88	2 (10%)	25,31,34	0.81	0
36	A2M	A1	807	36	18,25,26	0.84	0	20,36,39	1.41	2 (10%)
36	OMU	A1	2921	36	19,22,23	1.23	3 (15%)	25,31,34	1.89	6 (24%)
36	OMC	A1	2948	36	19,22,23	0.86	1 (5%)	25,31,34	1.18	3 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
36	A2M	A1	2640	36	18,25,26	0.80	0	20,36,39	1.19	2 (10%)
36	OMU	A1	2724	36	19,22,23	1.28	4 (21%)	25,31,34	1.88	5 (20%)
36	OMG	A1	2793	36	19,26,27	0.88	1 (5%)	21,38,41	1.13	2 (9%)
36	5MC	A1	2278	80,36	19,22,23	1.55	3 (15%)	26,32,35	1.35	5 (19%)
35	OMC	B5	1639	35	19,22,23	0.79	1 (5%)	25,31,34	0.89	1 (4%)
36	OMC	A1	2337	36	19,22,23	0.87	2 (10%)	25,31,34	1.19	2 (8%)
35	OMC	B5	414	35	19,22,23	0.89	2 (10%)	25,31,34	0.89	1 (4%)
36	A2M	A1	2280	36	18,25,26	0.82	0	20,36,39	1.38	2 (10%)
36	1MA	A1	645	80,36	17,25,26	1.34	2 (11%)	17,37,40	1.20	3 (17%)
35	A2M	B5	619	80,35	18,25,26	0.81	0	20,36,39	1.36	3 (15%)
35	OMG	B5	1271	35	19,26,27	0.91	1 (5%)	21,38,41	1.02	2 (9%)
35	OMG	B5	1126	35	19,26,27	0.91	1 (5%)	21,38,41	1.09	3 (14%)
36	A2M	A1	649	36	18,25,26	0.78	0	20,36,39	1.13	2 (10%)
35	A2M	B5	100	80,35	18,25,26	0.92	1 (5%)	20,36,39	1.43	4 (20%)
35	4AC	B5	1280	35	21,24,25	1.10	1 (4%)	28,34,37	1.60	6 (21%)
36	OMG	A1	1450	36	19,26,27	1.09	1 (5%)	21,38,41	1.00	2 (9%)
36	OMU	A1	2347	36	19,22,23	1.42	4 (21%)	25,31,34	1.93	6 (24%)
36	A2M	A1	876	36	18,25,26	0.87	0	20,36,39	1.24	2 (10%)
36	A2M	A1	2281	36	18,25,26	0.79	0	20,36,39	1.85	3 (15%)
36	OMG	A1	2922	36	19,26,27	0.84	1 (5%)	21,38,41	1.05	1 (4%)
35	A2M	B5	28	80,35	18,25,26	0.81	0	20,36,39	1.42	4 (20%)
36	OMG	A1	908	80,36	19,26,27	0.96	1 (5%)	21,38,41	1.38	4 (19%)
36	OMU	A1	1888	36	19,22,23	1.42	4 (21%)	25,31,34	2.00	5 (20%)
35	G7M	B5	1575	35	20,26,27	2.55	4 (20%)	16,39,42	1.12	1 (6%)
35	A2M	B5	541	35	18,25,26	0.83	0	20,36,39	1.23	3 (15%)
36	OMG	A1	2815	36	19,26,27	0.88	1 (5%)	21,38,41	1.20	4 (19%)
36	A2M	A1	2220	36	18,25,26	0.83	0	20,36,39	1.35	2 (10%)
36	OMU	A1	2729	36	19,22,23	1.41	4 (21%)	25,31,34	1.82	6 (24%)
40	HIC	AB	243	40	8,11,12	1.46	1 (12%)	5,14,16	0.75	0
35	3AU	B5	1191	35	24,28,29	0.48	0	30,40,43	0.70	0
36	1MA	A1	2142	36	17,25,26	1.42	2 (11%)	17,37,40	1.38	3 (17%)

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
36	A2M	A1	1449	80,36	-	0/5/27/28	0/3/3/3
36	OMC	A1	2197	36	-	6/9/27/28	0/2/2/2
36	OMG	A1	2619	36	-	0/5/27/28	0/3/3/3
36	5MC	A1	2870	36	-	4/7/25/26	0/2/2/2
36	A2M	A1	1133	36	-	0/5/27/28	0/3/3/3
36	OMG	A1	867	80,36	-	1/5/27/28	0/3/3/3
36	OMU	A1	898	36	-	0/9/27/28	0/2/2/2
36	OMG	A1	805	36	-	1/5/27/28	0/3/3/3
36	UR3	A1	2634	80,36	-	0/7/25/26	0/2/2/2
35	OMG	B5	562	35	-	0/5/27/28	0/3/3/3
35	A2M	B5	974	35	-	0/5/27/28	0/3/3/3
35	OMG	B5	1428	80,35	-	4/5/27/28	0/3/3/3
35	MA6	B5	1781	35	-	5/7/29/30	0/3/3/3
36	OMC	A1	663	36	-	0/9/27/28	0/2/2/2
36	A2M	A1	817	80,36	-	1/5/27/28	0/3/3/3
35	A2M	B5	436	35	-	0/5/27/28	0/3/3/3
35	4AC	B5	1773	35	-	3/11/29/30	0/2/2/2
35	OMU	B5	1269	80,35	-	3/9/27/28	0/2/2/2
35	OMC	B5	1007	35	-	0/9/27/28	0/2/2/2
36	OMC	A1	1437	80,36	-	2/9/27/28	0/2/2/2
36	OMG	A1	2288	36	-	2/5/27/28	0/3/3/3
36	A2M	A1	2946	80,36	-	1/5/27/28	0/3/3/3
36	OMU	A1	2421	36	-	0/9/27/28	0/2/2/2
36	OMU	A1	2417	36	-	1/9/27/28	0/2/2/2
36	OMG	A1	2791	36	-	0/5/27/28	0/3/3/3
35	OMU	B5	578	35	-	3/9/27/28	0/2/2/2
35	MA6	B5	1782	35	-	2/7/29/30	0/3/3/3
36	OMC	A1	2959	36	-	0/9/27/28	0/2/2/2
35	A2M	B5	796	35	-	0/5/27/28	0/3/3/3
35	A2M	B5	420	35	-	0/5/27/28	0/3/3/3
35	OMG	B5	1572	35	-	0/5/27/28	0/3/3/3
36	OMC	A1	650	36	-	0/9/27/28	0/2/2/2
36	A2M	A1	807	36	-	1/5/27/28	0/3/3/3
36	OMU	A1	2921	36	-	0/9/27/28	0/2/2/2
36	OMC	A1	2948	36	-	0/9/27/28	0/2/2/2
36	A2M	A1	2640	36	-	0/5/27/28	0/3/3/3
36	OMU	A1	2724	36	-	0/9/27/28	0/2/2/2
36	OMG	A1	2793	36	-	0/5/27/28	0/3/3/3
36	5MC	A1	2278	80,36	-	0/7/25/26	0/2/2/2
35	OMC	B5	1639	35	-	0/9/27/28	0/2/2/2
36	OMC	A1	2337	36	-	0/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	OMC	B5	414	35	-	0/9/27/28	0/2/2/2
36	A2M	A1	2280	36	-	0/5/27/28	0/3/3/3
36	1MA	A1	645	80,36	-	0/3/25/26	0/3/3/3
35	A2M	B5	619	80,35	-	2/5/27/28	0/3/3/3
35	OMG	B5	1271	35	-	0/5/27/28	0/3/3/3
35	OMG	B5	1126	35	-	1/5/27/28	0/3/3/3
36	A2M	A1	649	36	-	2/5/27/28	0/3/3/3
35	A2M	B5	100	80,35	-	2/5/27/28	0/3/3/3
35	4AC	B5	1280	35	-	4/11/29/30	0/2/2/2
36	OMG	A1	1450	36	-	2/5/27/28	0/3/3/3
36	OMU	A1	2347	36	-	2/9/27/28	0/2/2/2
36	A2M	A1	876	36	-	0/5/27/28	0/3/3/3
36	A2M	A1	2281	36	-	1/5/27/28	0/3/3/3
36	OMG	A1	2922	36	-	0/5/27/28	0/3/3/3
35	A2M	B5	28	80,35	-	1/5/27/28	0/3/3/3
36	OMG	A1	908	80,36	-	3/5/27/28	0/3/3/3
36	OMU	A1	1888	36	-	0/9/27/28	0/2/2/2
35	G7M	B5	1575	35	3/3/5/5	2/3/25/26	0/3/3/3
35	A2M	B5	541	35	-	3/5/27/28	0/3/3/3
36	OMG	A1	2815	36	-	0/5/27/28	0/3/3/3
36	A2M	A1	2220	36	-	1/5/27/28	0/3/3/3
36	OMU	A1	2729	36	-	3/9/27/28	0/2/2/2
40	HIC	AB	243	40	-	0/5/6/8	0/1/1/1
35	3AU	B5	1191	35	1/1/7/7	2/16/34/35	0/2/2/2
36	1MA	A1	2142	36	-	2/3/25/26	0/3/3/3

The worst 5 of 90 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	B5	1575	G7M	C8-N9	7.75	1.47	1.33
35	B5	1575	G7M	C8-N7	6.32	1.44	1.33
36	A1	2278	5MC	C5-C4	5.45	1.48	1.44
36	A1	2142	1MA	C2-N3	4.70	1.34	1.28
36	A1	2870	5MC	C5-C4	4.53	1.47	1.44

The worst 5 of 196 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B5	1773	4AC	N4-C4-N3	11.03	131.77	113.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
35	B5	1773	4AC	C5-C4-N4	-8.28	108.99	122.94
36	A1	2634	UR3	C4-N3-C2	-6.10	119.67	124.58
35	B5	1782	MA6	C2-N1-C6	6.09	122.82	116.84
35	B5	1781	MA6	C2-N1-C6	5.70	122.43	116.84

All (4) chirality outliers are listed below:

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

5 of 73 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
35	B5	28	A2M	C1'-C2'-O2'-CM'
35	B5	619	A2M	O4'-C4'-C5'-O5'
35	B5	1280	4AC	N3-C4-N4-C7
35	B5	1280	4AC	C5-C4-N4-C7
35	B5	1280	4AC	O7-C7-N4-C4

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 368 ligands modelled in this entry, 368 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
36	A1	5
53	AP	1
9	BI	1
35	B5	1
43	AE	1
47	AI	1
32	Bf	1
18	BR	1
38	A4	1
22	BV	1
49	AL	1
40	AB	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	26.01
1	AP	155:GLU	C	164:LYS	N	23.68
1	A1	1955:U	O3'	2093:A	P	22.93
1	BI	123:LYS	C	135:LYS	N	19.36
1	A1	1023:C	O3'	1030:A	P	17.87

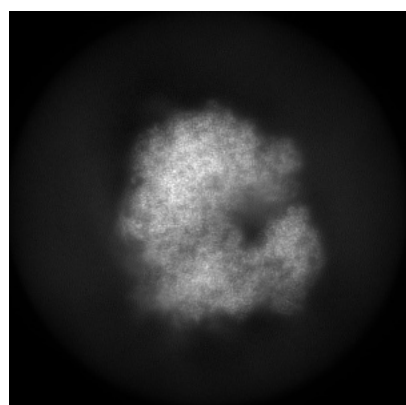
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-23934. These allow visual inspection of the internal detail of the map and identification of artifacts.

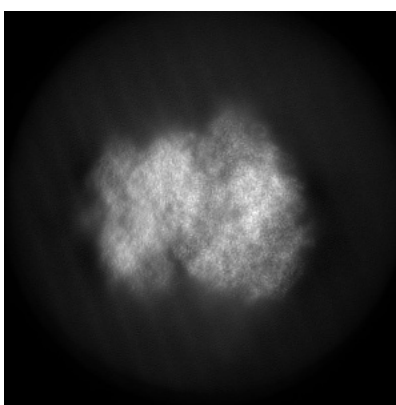
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

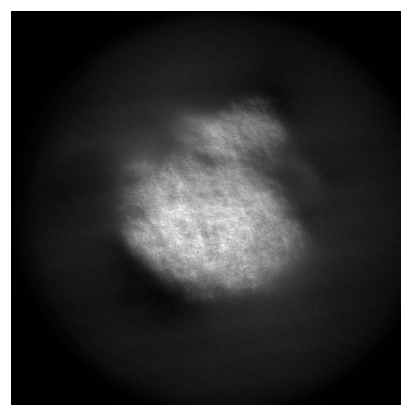
6.1.1 Primary map



X



Y

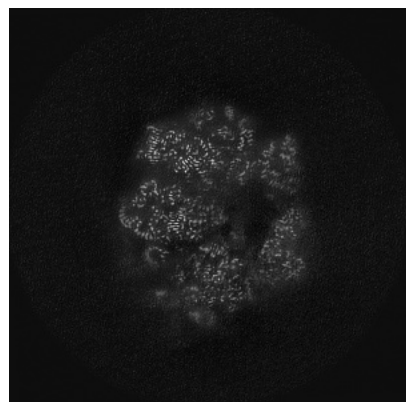


Z

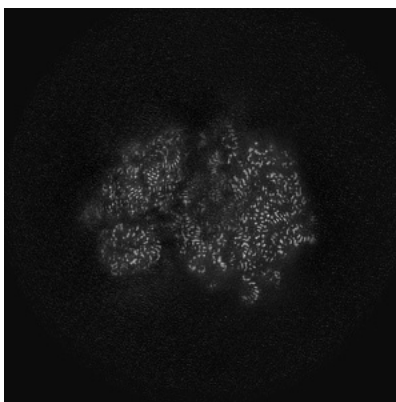
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

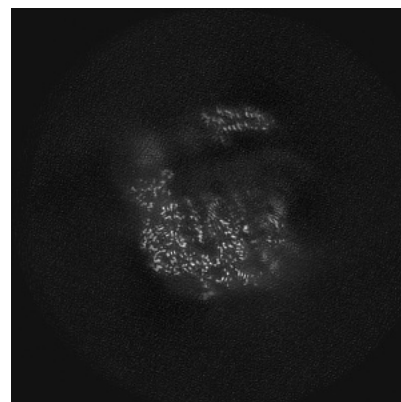
6.2.1 Primary map



X Index: 216



Y Index: 216

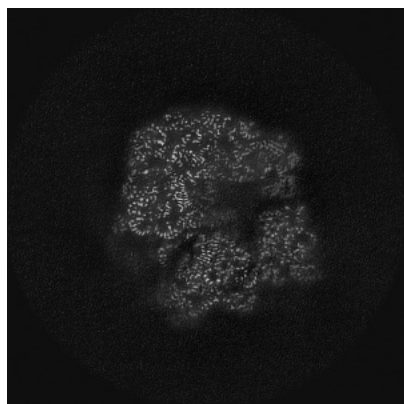


Z Index: 216

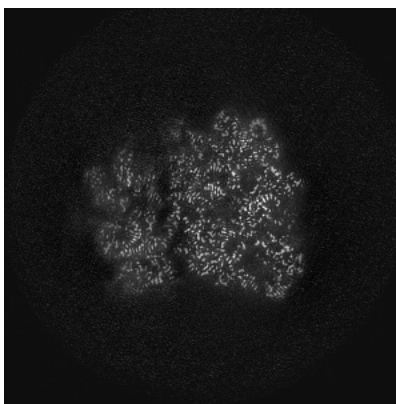
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

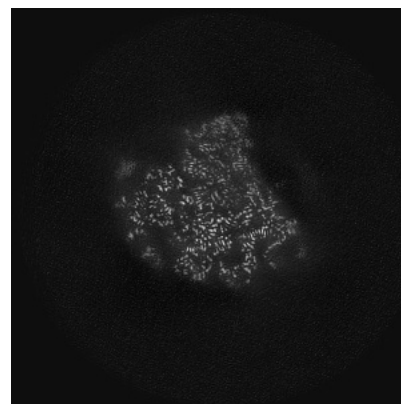
6.3.1 Primary map



X Index: 236



Y Index: 192

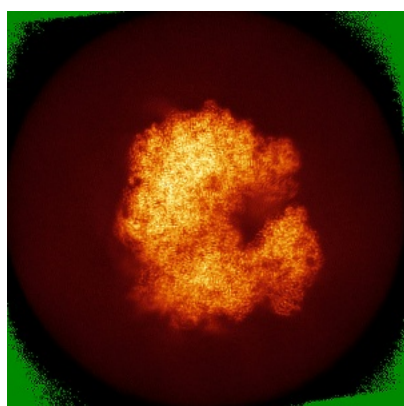


Z Index: 266

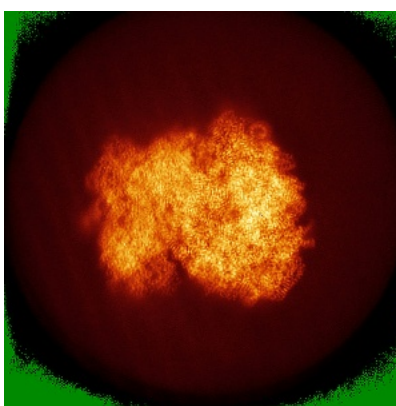
The images above show the largest variance slices of the map in three orthogonal directions.

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

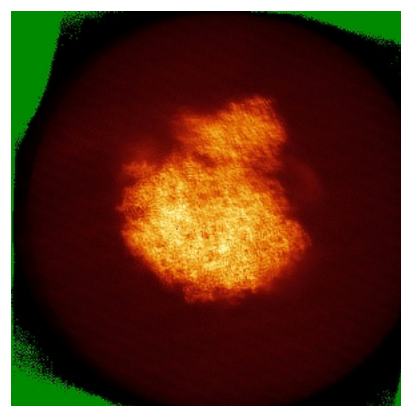
6.4.1 Primary map



X



Y

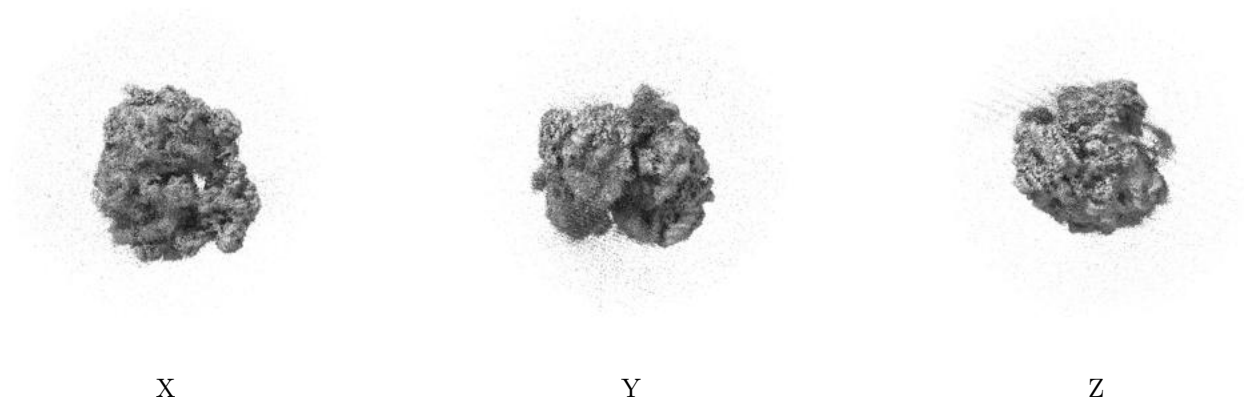


Z

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 0.0065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

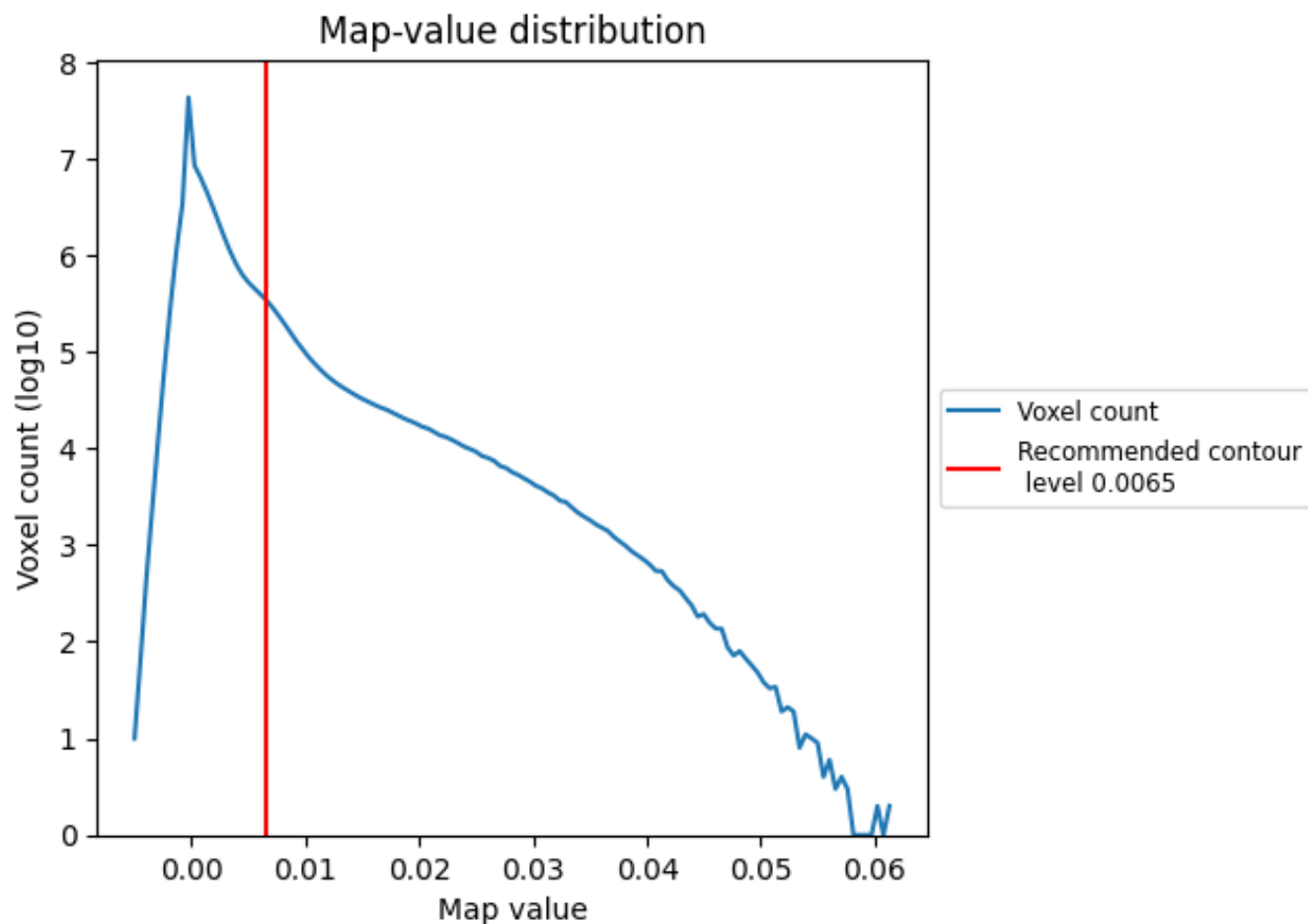
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

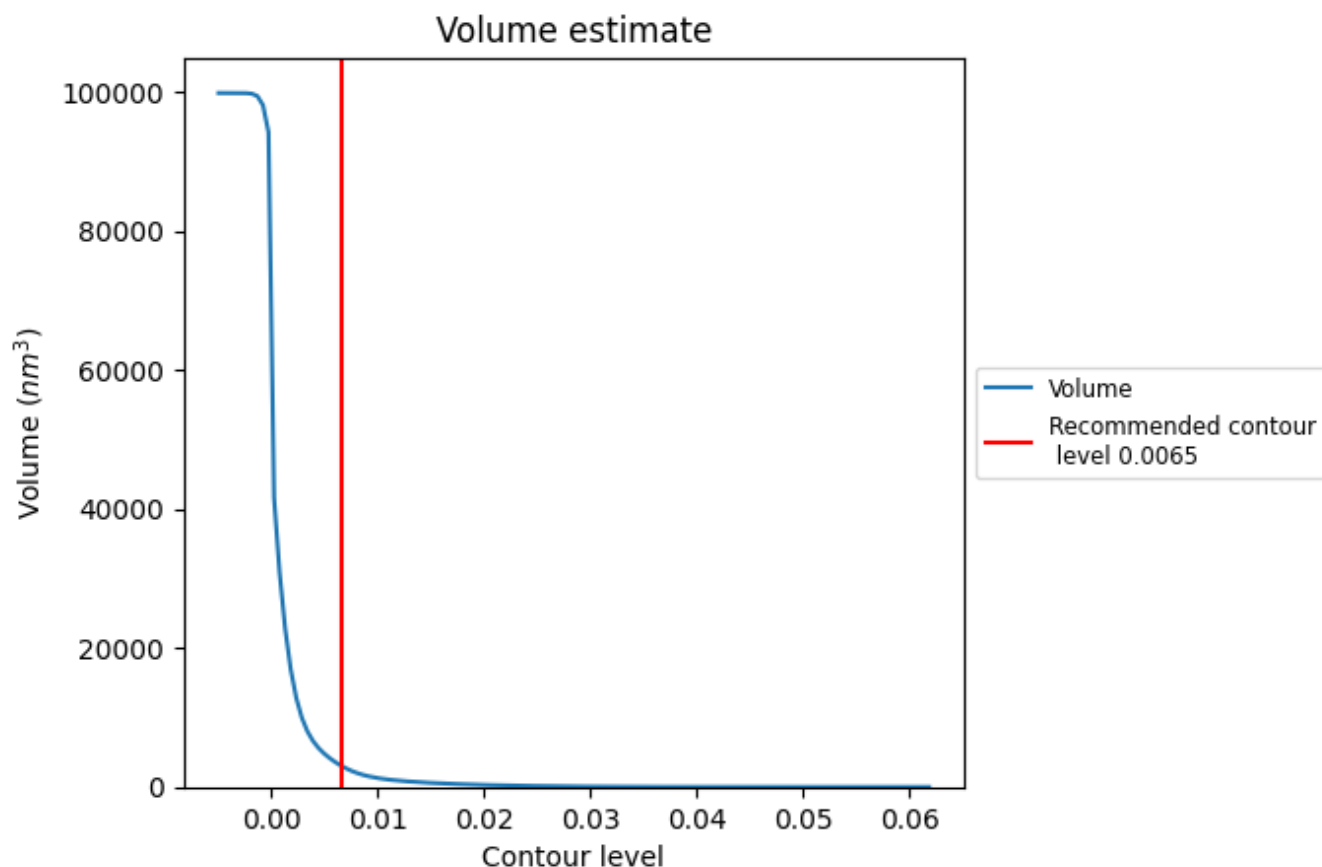
This section contains the results of statistical analysis of the map.

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.

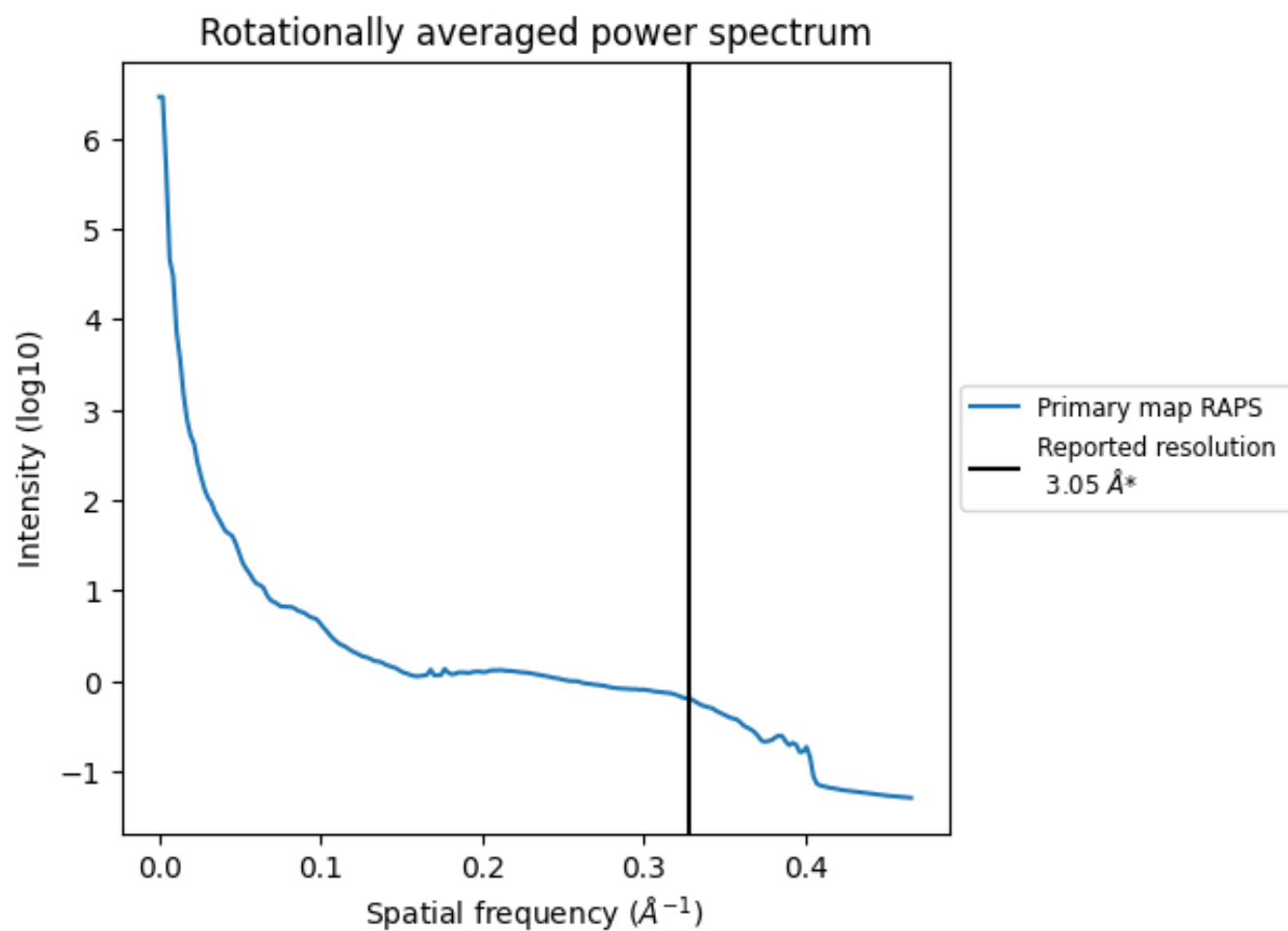
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3102 nm^3 ; this corresponds to an approximate mass of 2802 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

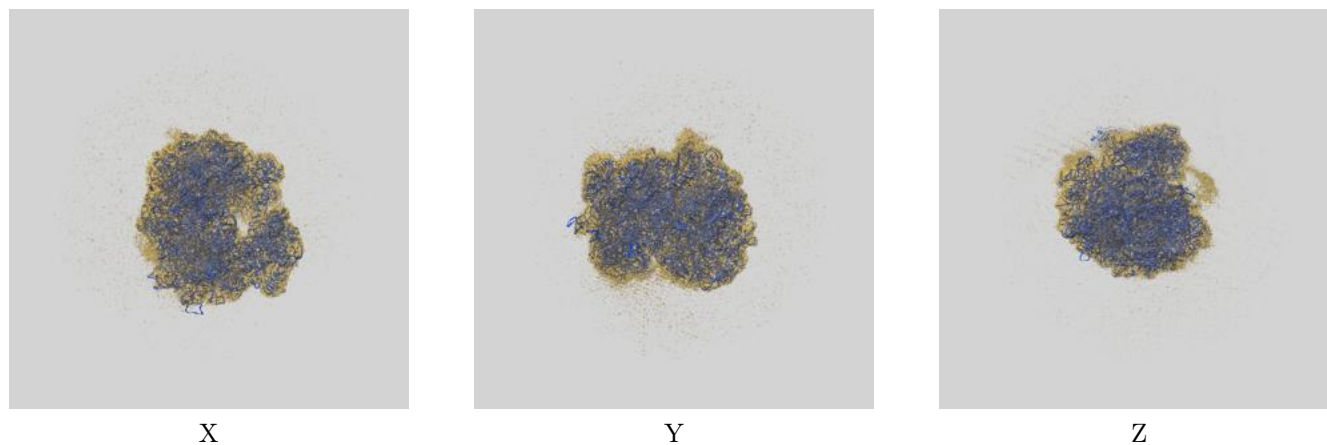
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

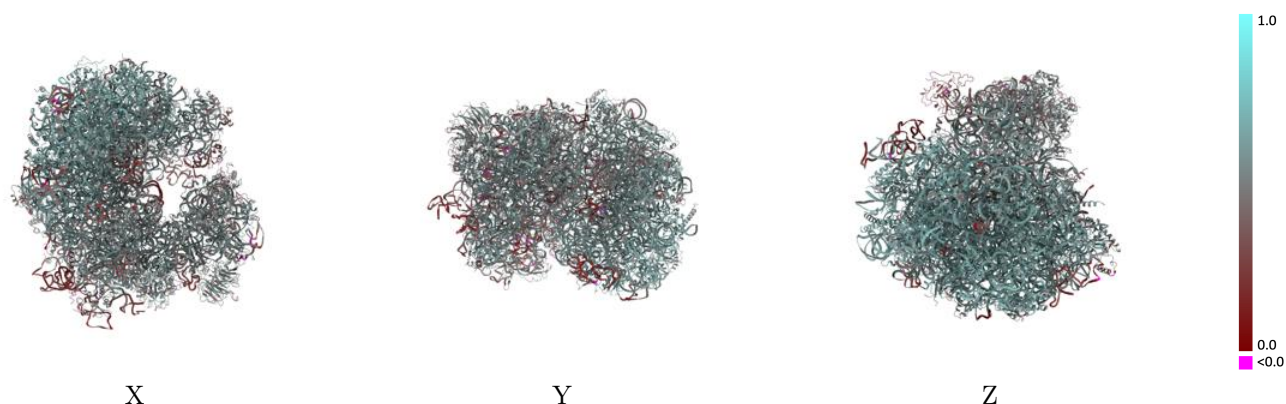
This section contains information regarding the fit between EMDB map EMD-23934 and PDB model 7MPI. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



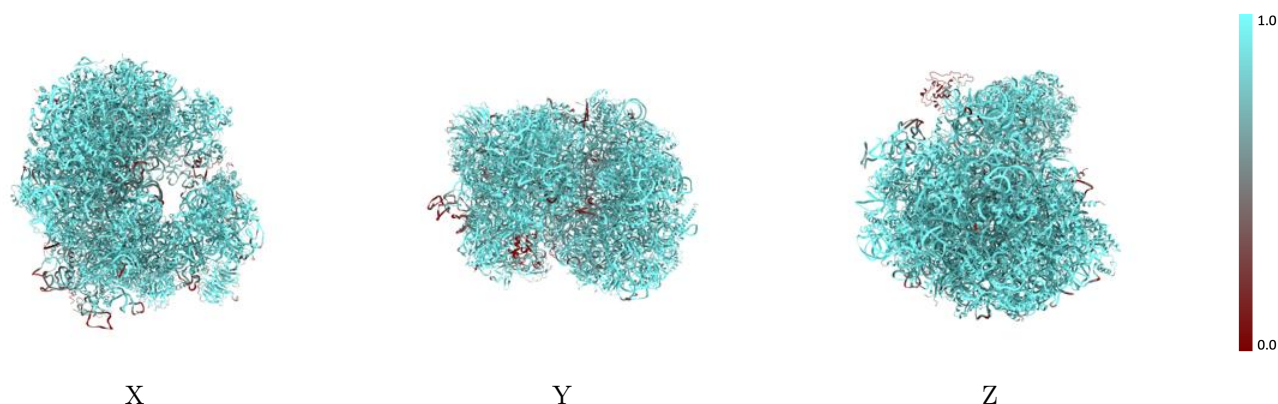
The images above show the 3D surface view of the map at the recommended contour level 0.0065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



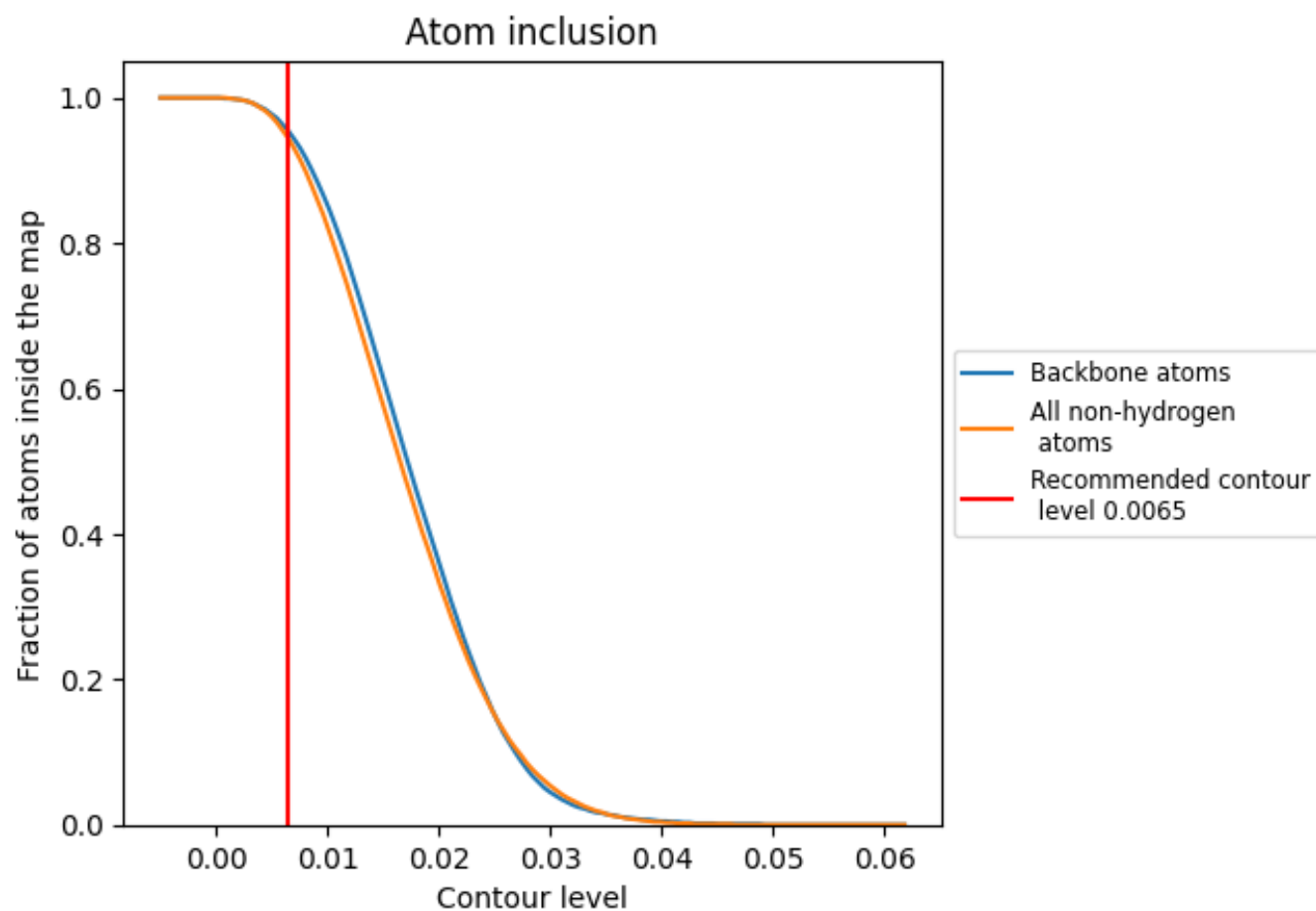
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0065).







































































9.4 Atom inclusion ⓘ



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 (0.0065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9440	 0.5380
A1	 0.9690	 0.5660
A3	 0.9990	 0.5510
A4	 0.9910	 0.6160
AA	 0.9470	 0.5690
AB	 0.9820	 0.6220
AC	 0.9770	 0.6070
AD	 0.9240	 0.4860
AE	 0.9620	 0.5840
AF	 0.9800	 0.6140
AG	 0.9630	 0.5480
AH	 0.9660	 0.5790
AI	 0.9510	 0.4970
AJ	 0.7920	 0.3910
AL	 0.9510	 0.5870
AM	 0.9810	 0.6080
AN	 0.9880	 0.6150
AO	 0.9880	 0.6260
AP	 0.9750	 0.6280
AQ	 0.9890	 0.6130
AR	 0.8470	 0.5280
AS	 0.9830	 0.6170
AT	 0.9630	 0.5730
AU	 0.9080	 0.5180
AV	 0.9520	 0.6040
AW	 0.9430	 0.6020
AX	 0.9700	 0.5920
AY	 0.9760	 0.6000
AZ	 0.9800	 0.5340
Aa	 0.9890	 0.6040
Ab	 0.9160	 0.5150
Ac	 0.9770	 0.5290
Ad	 0.9430	 0.5940
Ae	 0.9860	 0.6280
Af	 0.9950	 0.6500









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Chain	Atom inclusion	Q-score
Ag	 0.9680	 0.5780
Ah	 0.9780	 0.5920
Ai	 0.9340	 0.5470
Aj	 0.9970	 0.6350
Ak	 0.8350	 0.4790
Al	 0.9930	 0.6250
Am	 0.9650	 0.5860
An	 0.3630	 0.3240
Ao	 0.8770	 0.4870
Ap	 0.9580	 0.5750
B5	 0.9270	 0.4810
BA	 0.9310	 0.5120
BB	 0.9320	 0.4700
BC	 0.9540	 0.5270
BD	 0.9460	 0.4950
BE	 0.9800	 0.5210
BF	 0.9410	 0.4940
BG	 0.8930	 0.4890
BH	 0.8310	 0.4440
BI	 0.9340	 0.5110
BJ	 0.9670	 0.5120
BK	 0.9480	 0.4480
BL	 0.8760	 0.5080
BM	 0.1450	 0.2070
BN	 0.9450	 0.5220
BO	 0.9640	 0.4950
BP	 0.8480	 0.4610
BQ	 0.9690	 0.5320
BR	 0.7970	 0.4450
BS	 0.8920	 0.4910
BT	 0.9360	 0.5340
BU	 0.8760	 0.4500
BV	 0.9340	 0.5380
BW	 0.9860	 0.5530
BX	 0.9530	 0.5330
BY	 0.9500	 0.5150
BZ	 0.8710	 0.4960
Ba	 0.9660	 0.5260
Bb	 0.9070	 0.5020
Bc	 0.9370	 0.5010
Bd	 0.9930	 0.5480
Be	 0.9170	 0.4960

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Chain	Atom inclusion	Q-score
Bf	 0.3650	 0.2290
Bg	 0.9080	 0.4920
Bh	 0.6980	 0.3680