



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 07:32 PM EST

PDB ID : 4V6V
EMDB ID : EMD-5562
Title : Tetracycline resistance protein Tet(O) bound to the ribosome
Authors : Li, W.; Atkinson, G.C.; Thakor, N.S.; Allas, U.; Lu, C.; Chan, K.Y.; Tenson, T.; Schulten, K.; Wilson, K.S.; Hauryliuk, V.; Frank, J.
Deposited on : 2013-02-25
Resolution : 9.80 Å (reported)
Based on initial models : 2I2V, 2I2U

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:

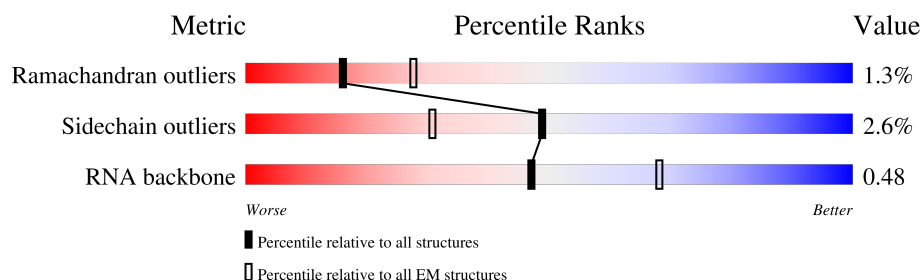
EMDB validation analysis : 0.0.1.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.3

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 9.80 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	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	AJ	103	
2	AK	128	
3	AL	123	
4	AM	117	
5	AN	100	
6	AO	88	
7	AP	82	
8	AQ	83	






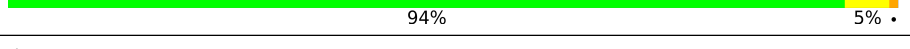
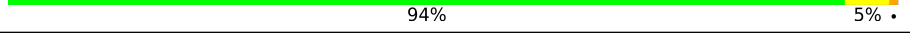
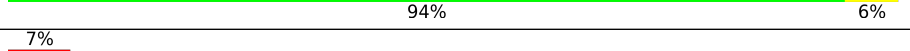
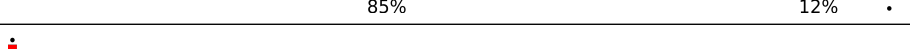
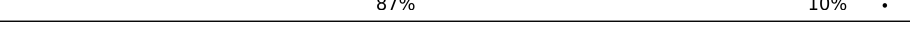
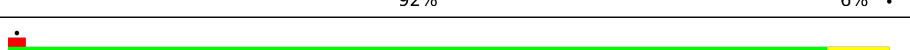
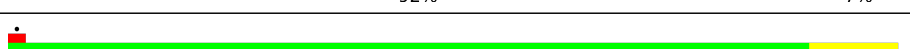
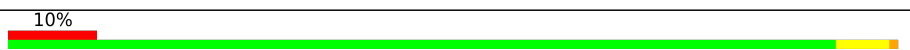

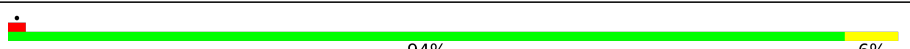



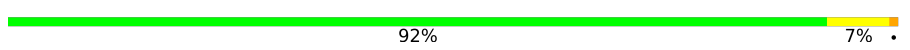

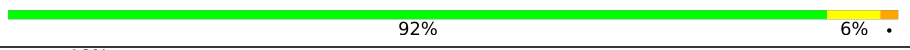
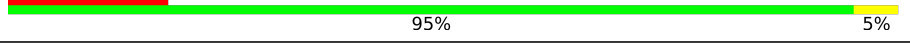
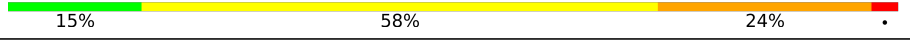
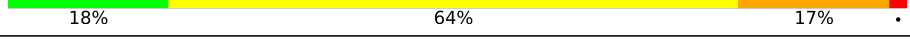

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Mol	Chain	Length	Quality of chain
9	AR	74	
10	AS	91	
11	AB	240	
12	AT	86	
13	AU	70	
14	AC	232	
15	AD	205	
16	AE	166	
17	AF	135	
18	AG	178	
19	AH	129	
20	AI	129	
21	A1	639	
22	AA	1542	
23	A2	47	
24	A3	77	
25	BC	234	
26	BJ	164	
27	BK	141	
28	BN	142	
29	BO	123	
30	BP	144	
31	BQ	136	
32	BR	127	
33	BS	117	

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Mol	Chain	Length	Quality of chain
34	BT	114	 89% 11% .
35	BD	272	 88% 11% .
36	BU	117	 85% 13% .
37	BV	103	 88% 12% .
38	BW	110	 90% 8% .
39	BX	100	 94% 5% .
40	BY	103	 94% 5% .
41	BZ	94	 94% 6% .
42	B0	84	 7% 85% 12% .
43	B1	77	 87% 10% .
44	B2	63	 92% 6% .
45	BE	209	 92% 7% .
46	B3	58	 90% 10% .
47	B4	70	 10% 93% 6% .
48	B5	56	 82% 18% .
49	B6	54	 94% 6% .
50	B7	46	 80% 20% .
51	B8	64	 89% 9% .
52	B9	38	 87% 13% .
53	BF	201	 92% 7% .
54	BG	178	 88% 11% .
55	BH	176	 92% 6% .
56	BL	149	 18% 95% 5% .
57	BA	2904	 15% 58% 24% .
58	Ba	120	 18% 64% 17% .

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 154956 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 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AJ	103	Total	C	N	O	S	0	0
			794	483	158	151	2		

- Molecule 2 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AK	128	Total	C	N	O	S	0	0
			923	553	196	171	3		

- Molecule 3 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AL	123	Total	C	N	O	S	0	0
			923	558	196	165	4		

- Molecule 4 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AM	117	Total	C	N	O	S	0	0
			876	530	183	160	3		

- Molecule 5 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AN	100	Total	C	N	O	S	0	0
			771	465	164	139	3		

- Molecule 6 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AO	88	Total	C	N	O	S	0	0
			690	414	146	129	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AO	79	ARG	GLN	conflict	UNP P0ADZ4

- Molecule 7 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AP	82	Total	C	N	O	S	0	0
			620	377	128	114	1		

- Molecule 8 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AQ	83	Total	C	N	O	S	0	0
			657	410	124	120	3		

- Molecule 9 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AR	74	Total	C	N	O	S	0	0
			603	372	123	107	1		

- Molecule 10 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AS	91	Total	C	N	O	S	0	0
			708	445	139	122	2		

- Molecule 11 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AB	240	Total	C	N	O	S	0	0
			1805	1113	332	352	8		

- Molecule 12 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AT	86	Total	C	N	O	S	0	0
			636	380	138	115	3		

- Molecule 13 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AU	70	Total	C	N	O	S	0	0
			564	340	125	98	1		

- Molecule 14 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AC	232	Total	C	N	O	S	0	0
			1761	1088	346	323	4		

- Molecule 15 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AD	205	Total	C	N	O	S	0	0
			1587	970	315	298	4		

- Molecule 16 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AE	166	Total	C	N	O	S	0	0
			1182	718	232	226	6		

- Molecule 17 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AF	135	Total	C	N	O	S	0	0
			1061	637	198	219	7		

- Molecule 18 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AG	178	Total	C	N	O	S	0	0
			1347	821	269	253	4		

- Molecule 19 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AH	129	Total	C	N	O	S	0	0
			948	585	173	184	6		

- Molecule 20 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AI	129	Total	C	N	O	S	0	0
			1000	606	208	183	3		

- Molecule 21 is a protein called Tetracycline resistance protein TetO.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	A1	639	Total	C	N	O	S	0	0
			4989	3146	850	966	27		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A1	227	ILE	THR	conflict	UNP P10952

- Molecule 22 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AA	1542	Total	C	N	O	P	0	0
			33089	14767	6064	10717	1541		

- Molecule 23 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	A2	47	Total	C	N	O	P	0	0
			993	445	167	335	46		

- Molecule 24 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	A3	77	Total	C	N	O	P	S	0	0
			1640	734	297	533	75	1		

- Molecule 25 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	BC	234	Total	C	N	O	S	0	0
			1733	1081	315	330	7		

- Molecule 26 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	BJ	164	Total	C	N	O	S	0	0
			1233	776	220	231	6		

- Molecule 27 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	BK	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 28 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	BN	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 29 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	BO	123	Total	C	N	O	S	0	0
			947	593	181	167	6		

- Molecule 30 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	BP	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 31 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	BQ	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 32 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	BR	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

- Molecule 33 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	BS	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- Molecule 34 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	BT	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 35 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	BD	272	Total	C	N	O	S	0	0
			2092	1294	425	366	7		

- Molecule 36 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	BU	117	Total	C	N	O		0	0
			947	604	192	151			

- Molecule 37 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BV	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 38 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	BW	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 39 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	BX	100	Total	C	N	O	S	0	0
			787	496	146	143	2		

- Molecule 40 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	BY	103	Total	C	N	O		
			789	498	148	143	0	0

- Molecule 41 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	BZ	94	Total	C	N	O	S		
			753	479	137	134	3	0	0

- Molecule 42 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	B0	84	Total	C	N	O	S		
			634	391	129	113	1	0	0

- Molecule 43 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	B1	77	Total	C	N	O	S		
			625	388	129	106	2	0	0

- Molecule 44 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	B2	63	Total	C	N	O	S		
			509	313	99	95	2	0	0

- Molecule 45 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	BE	209	Total	C	N	O	S		
			1565	979	288	294	4	0	0

- Molecule 46 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	B3	58	Total	C	N	O	S		
			449	281	87	79	2	0	0

- Molecule 47 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	B4	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 48 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	B5	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 49 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	B6	54	Total	C	N	O	S	0	0
			441	284	81	76			

- Molecule 50 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	B7	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 51 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B8	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 52 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B9	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 53 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	BF	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 54 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	BG	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 55 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	BH	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 56 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	BL	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 57 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	BA	2904	Total	C	N	O	P	0	0
			62351	27824	11469	20155	2903		

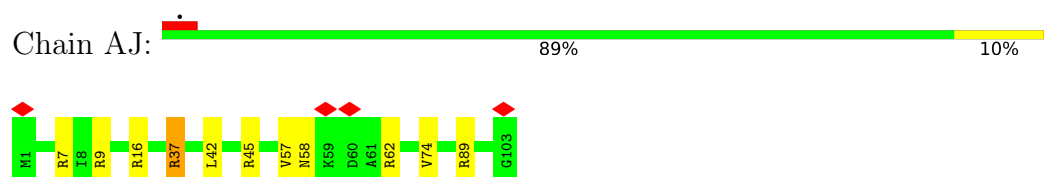
- Molecule 58 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Ba	120	Total	C	N	O	P	0	0
			2566	1144	468	835	119		

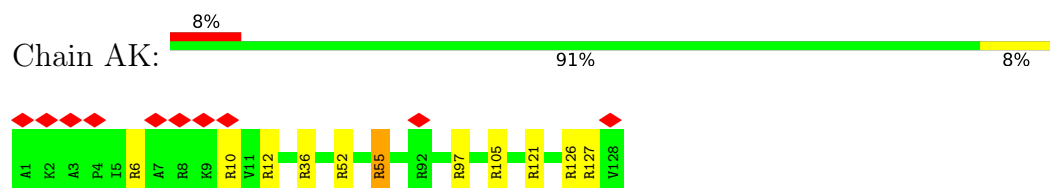
3 Residue-property plots [i](#)

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.

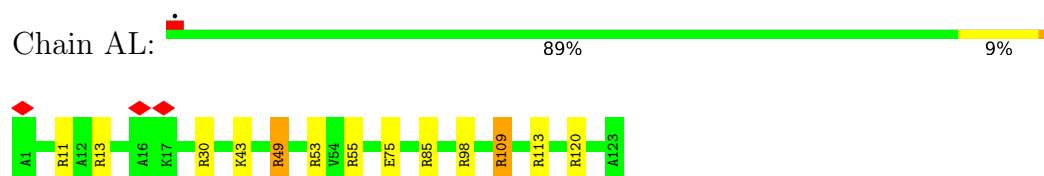
- Molecule 1: 30S ribosomal protein S10



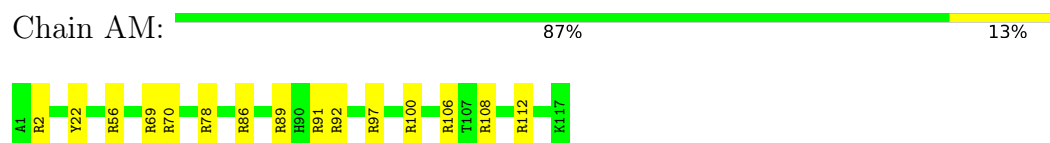
- Molecule 2: 30S ribosomal protein S11



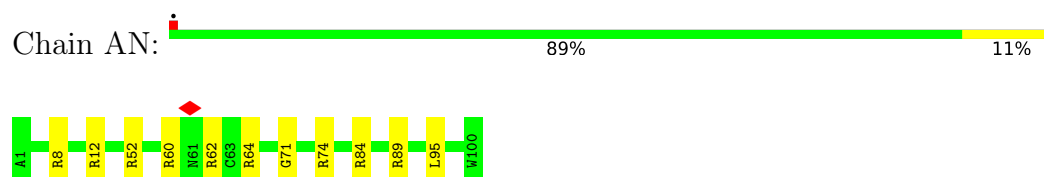
- Molecule 3: 30S ribosomal protein S12



- Molecule 4: 30S ribosomal protein S13

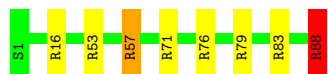


- Molecule 5: 30S ribosomal protein S14



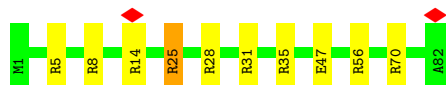
- Molecule 6: 30S ribosomal protein S15

Chain AO:  91% 7% ..



- Molecule 7: 30S ribosomal protein S16

Chain AP:  88% 11% .




- Molecule 8: 30S ribosomal protein S17

Chain AQ:  93% 6% .




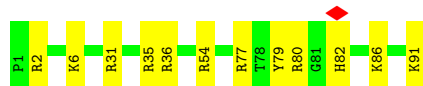
- Molecule 9: 30S ribosomal protein S18

Chain AR:  7% 82% 16% .



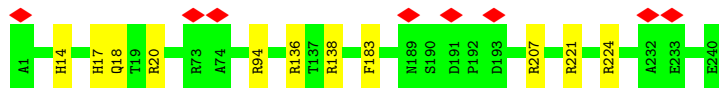
- Molecule 10: 30S ribosomal protein S19

Chain AS:  87% 13%



- Molecule 11: 30S ribosomal protein S2

Chain AB:  95% 5%

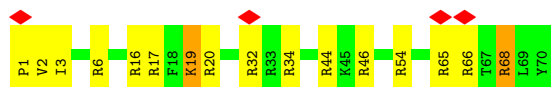
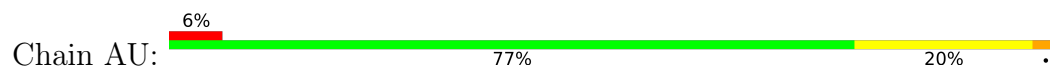


- Molecule 12: 30S ribosomal protein S20

Chain AT:  93% 7%



- Molecule 13: 30S ribosomal protein S21



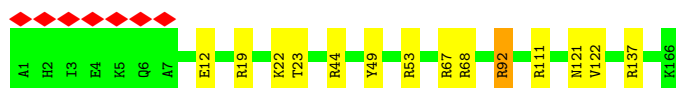
- Molecule 14: 30S ribosomal protein S3



- Molecule 15: 30S ribosomal protein S4



- Molecule 16: 30S ribosomal protein S5



- Molecule 17: 30S ribosomal protein S6



- Molecule 18: 30S ribosomal protein S7



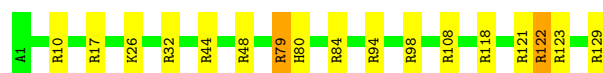
- Molecule 19: 30S ribosomal protein S8

Chain AH:  93% 6%



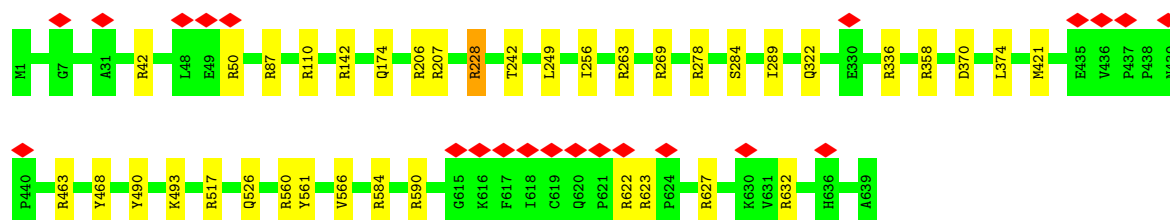
- Molecule 20: 30S ribosomal protein S9

Chain AI:  87% 12%




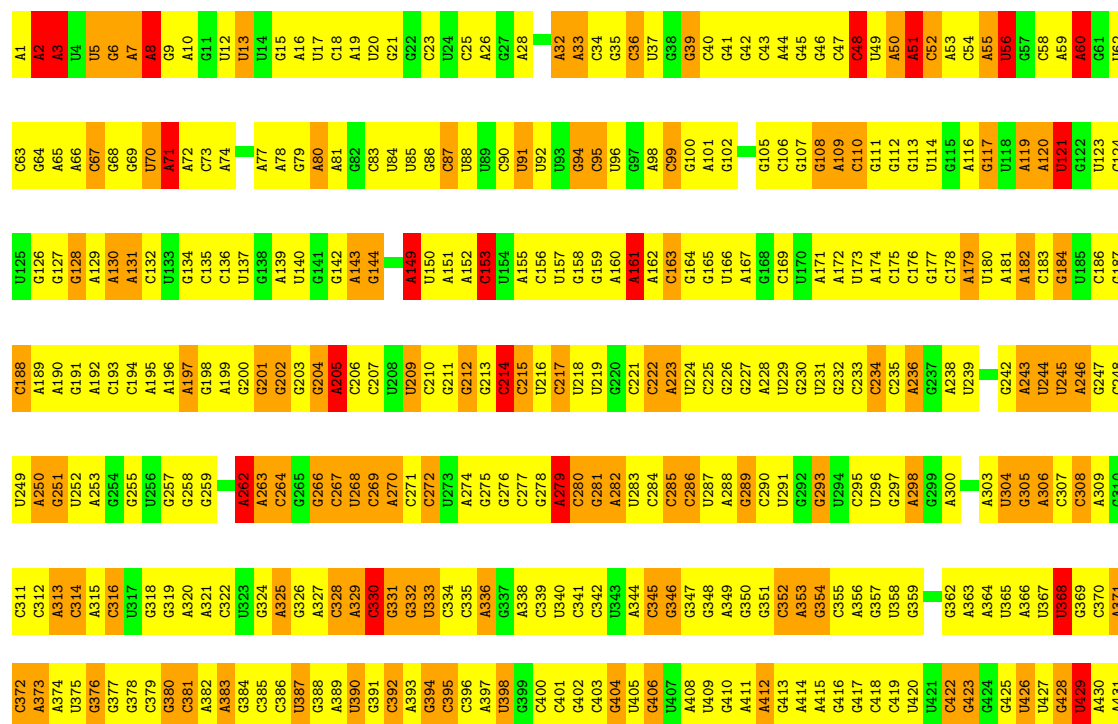
- Molecule 21: Tetracycline resistance protein TetO

Chain A1:  94% 6%

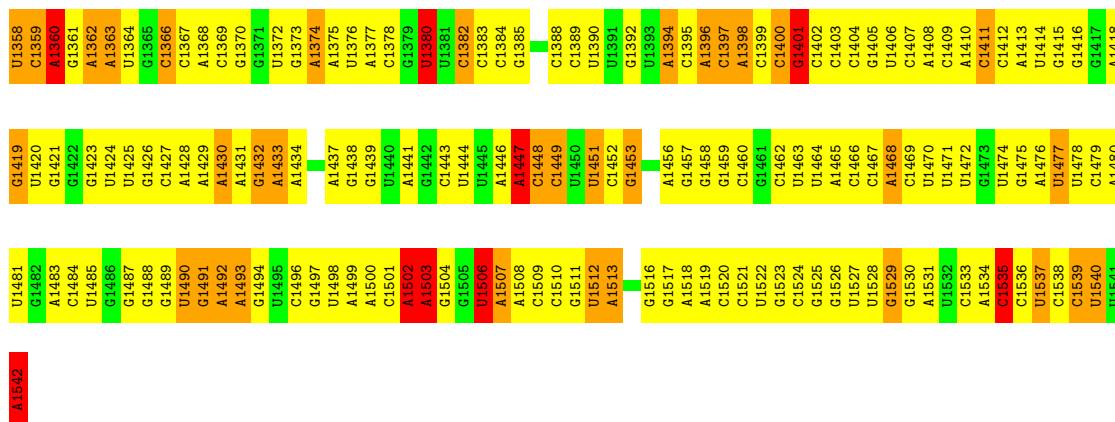


- Molecule 22: 16S ribosomal RNA

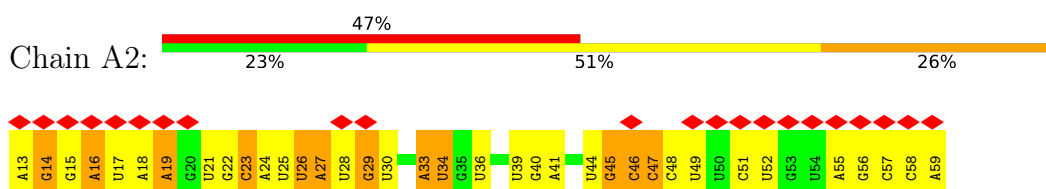
Chain AA:  15% 58% 24%



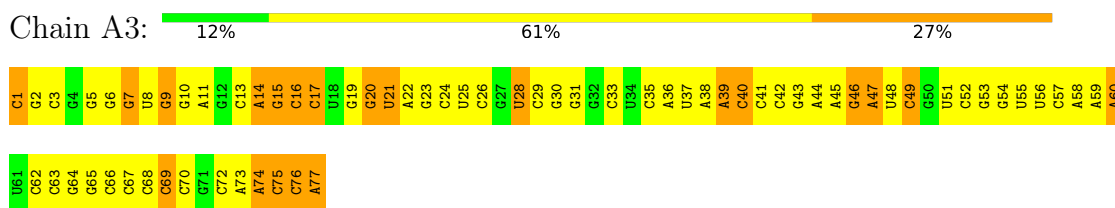
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A1239	G1178	C1115	U1052	C990	C930	C868	C807	G746	U686	A621	C557	A496	U434
G1240	A1179	U1116	G1053	U991	C931	G869	C808	A747	A687	C622	G558	G497	A435
G1241	A1180	U1117	C1054	U992	C932	U870	G809	G748	G688	C623	A559	A498	C436
G1242		U1118	A1055	G993	G933	U871	C810	A749	C689	C624	A560	A499	U437
G1243	U1183	C1119	U1056	A994	C934	A872	C811	C750	G690	U625	U561	G500	U438
G1244	G1184	C1120		C995	A935	A873	C812	U751	G691	G626	U562	C501	U439
A1245	G1185	U1121	C1059	A996	C936	G874	U813	G752	U692	G627	A563	A502	C440
C1246	G1186	U1122	U1060	U997	A937	U875	A814	A753	G693	G628	C564	C503	A441
U1247	G1187	U1123		C998	A938	G876	A815	G754	A694	A629	U565	C504	G442
A1248	A1188	U1124	C1063	C999	G939	G877	A816	C755	A695	A630	G566	G505	C443
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A1250	G1190	C1128	U1065	C1001	G941	C879	G818	U757	U697	G632	G568	C507	G445
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G1253	G1193	A1131	G1068	A1005	G944	U820	U822	G760	G700	A635	U571	A510	A448
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G1260	C1201	C1140	U1076	G1013	U952	G890	G829	A768	C708	C643	A579	C518	U458
A1261	U1202	C1141	G1077	U1014	G953	U891	G830	G769	U709	G644	C580	C519	A459
C1262	G1203	G1142		G1015	G954	A892	A831	C770	G710	G645	G581	A520	A460
C1263	A1204	A1143	A1016	U1016	U955	C893	G832	G771	G711	A646	C582	G521	A461
U1264	U1205	G1144	A1081	U1017	U956	G894	G833	U772	A712	C647	A583	C522	G462
G1265	C1206	A1145	A1082	G1018	U957	G895	U834	G773	G713	A648	G584	A523	U463
G1266	G1207	C1146	U1083	A1019	A958	C896	U835	G774	G714	A649	G585	G524	U464
C1267	C1208	U1147	G1084	G1020	A959	C897	G836	G775	A715	G650	C586	C525	A465
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G1270	C1211	C1150	G1087	U1023	G962	A900	C839	G778	A718	G654	U591	C528	A468
A1271	U1211	A1151	C1088	G1024	G963	A901	C840	G779	C719	A655	G592	G529	C469
C1272	U1212	A1152	G1089	U1025	A964	G902	C841		C720		U593	G530	C470
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A1275	G1215	G1155	A1091	C1028	C967	U905	G844	G783	U723	C660	A596	A533	U473
G1276	C1216	A1156	A1092	U1029	C967	U906	A845	A784	G724	G661	G597	U534	G474
C1277	C1217	G1156	A1093	U1093	A968	A906	A846	G785	G725	U662	U598	A535	C475
U1278	C1218	A1157	G1084	U1030	A969	A907	G846	G786	G726	A663	C599	C536	U476
A1279	A1219	C1158	U1095	C1031	C970	A908	G847	A787	G727	G664	A600	C477	C477
G1279	U1219	U1159	C1096	G1032	C971	A909	C848	U788	A728	G665	G601	A539	A478
A1280	G1220	C1160	C1097	G1033	G972	A910	G849	U789	A729	G666	A602	G540	U479
C1281	G1221	G1161	C1098	G1034	C973	U911		U790	G730		U603	G541	U480
C1282	G1222	C1162	C1099	A1035	A974	A912	G852	G791	G731	G670		G542	G481
U1283	C1223	A1163	C1100	A1036	A975	A913	C853	G792	C732	G671	A607	U543	A482
A1284	U1224	G1164	A1101	C1037	G976	A914	C854	A792	C733	U672	A608	G544	C483
A1285	U1225	G1165	C1102	C1038	A977	A915	U855	U793	G734	A673	A609	C545	C484
G1286	A1226	G1166	C1103	G1039	A978	A916	C856	A794	G735	G674	U610	A546	U485
A1287	C1227	U1167	G1104	U1040	C979	A918	C857	C795	C736	A675	C611	A547	U486
U1288	A1228	A1168	A1105	U1041	A919	A919	G858	G796	C737	A676	C612	G548	U487
A1289	C1229	U1169	C1106	A1042	U981	U920	C859	C797	C738	A677	C613	C549	C488
C1290	C1230	A1169	C1107	G1043	U982	U921	A860	U798	C739	U677	C614	G550	C489
U1291	G1231	A1170	G1108	A1044	U983	G922	G861	G799	U740	C679	G615	U551	C490
C1292	A1232	C1171	C1109	C1045	C984	A923	U862	G800	U741	C680	G616	U552	C491
G1293	C1233	C1172	A1173	A1046	C985	C924	U863	U801	G742	A681	C517	A553	C492
C1294	A1234	U1174	A1110	G1047	U986	G925	A864	A802	G742	C592	G618	A554	C493
U1295	C1235	G1175	C1112		C987	C926	A865		A742				
G1296	A1236												
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										</			



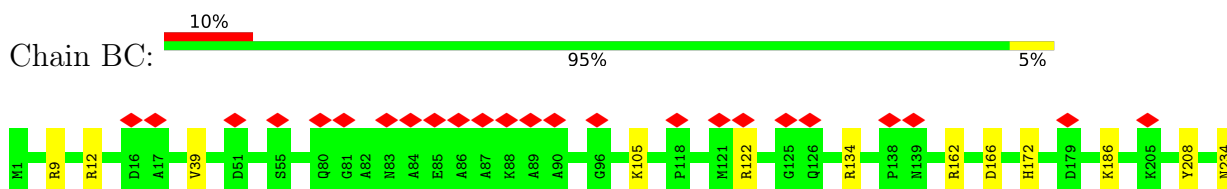
- Molecule 23: mRNA



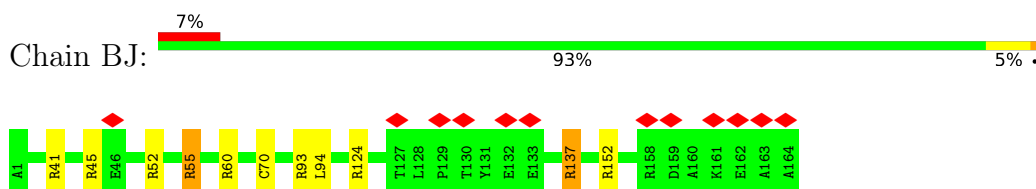
- Molecule 24: P-tRNA



- Molecule 25: 50S ribosomal protein L1

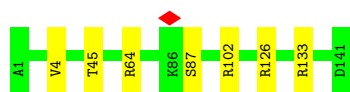


- Molecule 26: 50S ribosomal protein L10

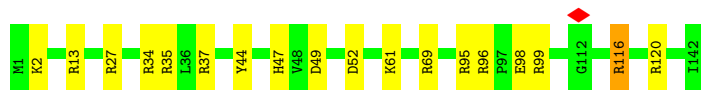


- Molecule 27: 50S ribosomal protein L11

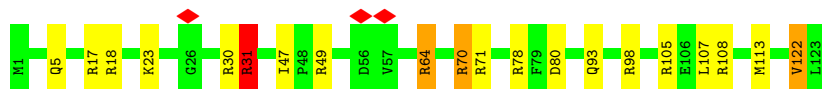
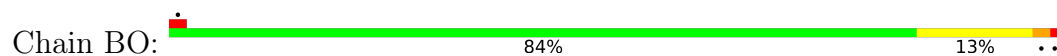




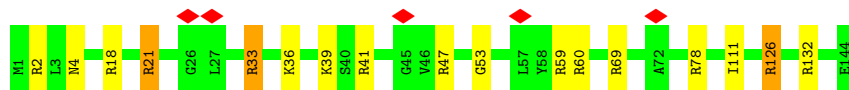
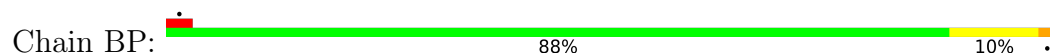
- Molecule 28: 50S ribosomal protein L13



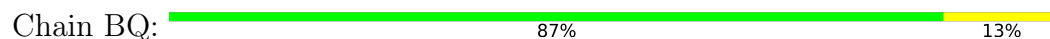
- Molecule 29: 50S ribosomal protein L14



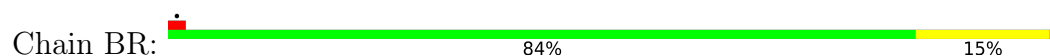
- Molecule 30: 50S ribosomal protein L15



- Molecule 31: 50S ribosomal protein L16




- Molecule 32: 50S ribosomal protein L17

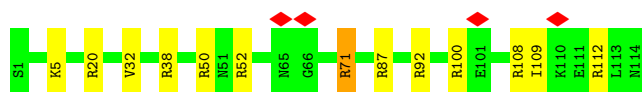


- Molecule 33: 50S ribosomal protein L18



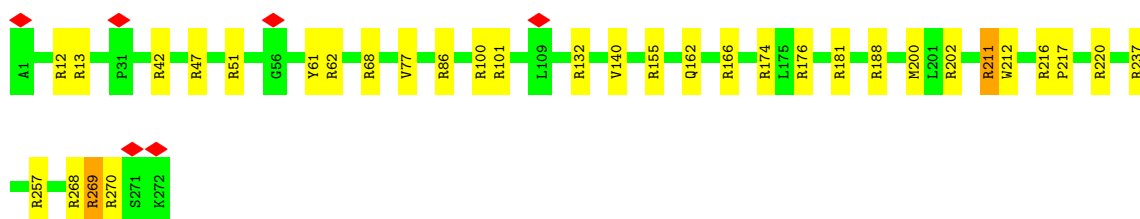
- Molecule 34: 50S ribosomal protein L19

Chain BT:  89% 11% .




- Molecule 35: 50S ribosomal protein L2

Chain BD:  88% 11% .




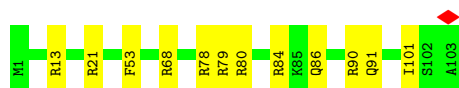
- Molecule 36: 50S ribosomal protein L20

Chain BU:  85% 13% .



- Molecule 37: 50S ribosomal protein L21

Chain BV:  88% 12% .



- Molecule 38: 50S ribosomal protein L22

Chain BW:  90% 8% .



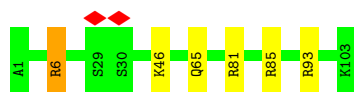
- Molecule 39: 50S ribosomal protein L23

Chain BX:  94% 5% .



- Molecule 40: 50S ribosomal protein L24

Chain BY:  94% 5% .



- Molecule 41: 50S ribosomal protein L25

Chain BZ: 94% 6%



- Molecule 42: 50S ribosomal protein L27

Chain B0: 7% 85% 12% .



- Molecule 43: 50S ribosomal protein L28

Chain B1: 87% 10% .



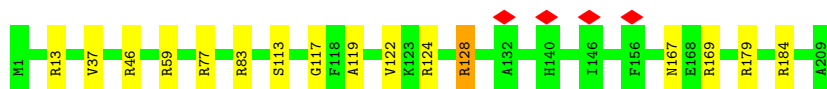
- Molecule 44: 50S ribosomal protein L29

Chain B2: 92% 6% .



- Molecule 45: 50S ribosomal protein L3

Chain BE: 92% 7% .

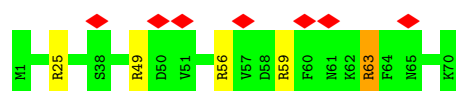


- Molecule 46: 50S ribosomal protein L30

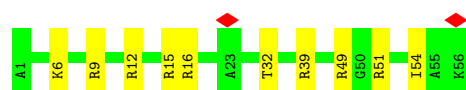
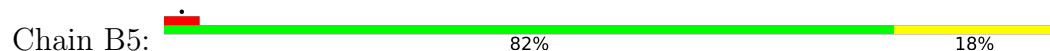
Chain B3: 90% 10% .



- Molecule 47: 50S ribosomal protein L31



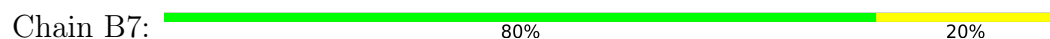
- Molecule 48: 50S ribosomal protein L32



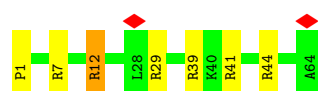
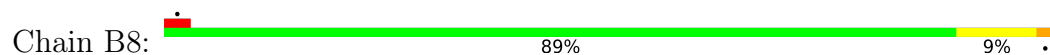
- Molecule 49: 50S ribosomal protein L33



- Molecule 50: 50S ribosomal protein L34



- Molecule 51: 50S ribosomal protein L35




- Molecule 52: 50S ribosomal protein L36



- Molecule 53: 50S ribosomal protein L4



- Molecule 54: 50S ribosomal protein L5

Chain BG:  88% 11% .



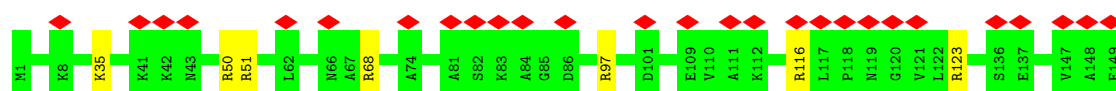
- Molecule 55: 50S ribosomal protein L6

Chain BH:  92% 6% .




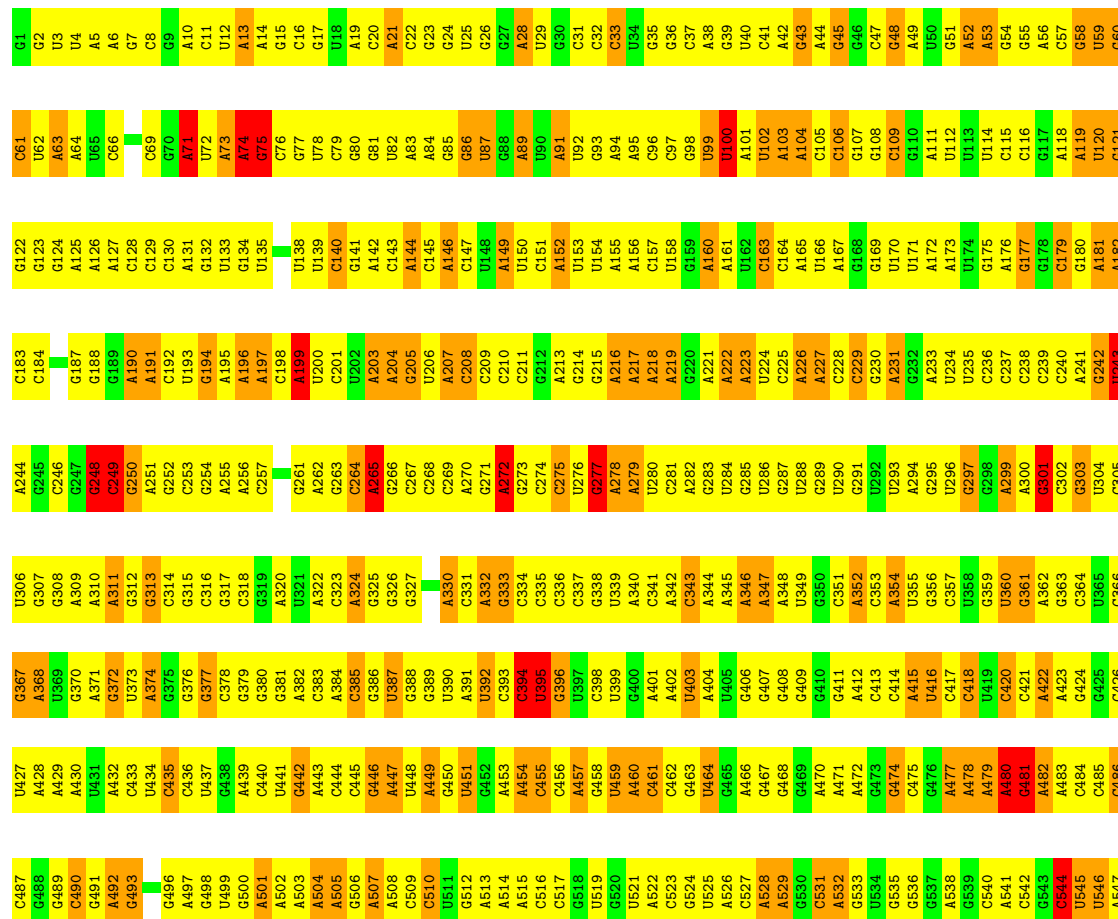
- Molecule 56: 50S ribosomal protein L9

Chain BL:  18% 95% 5% .



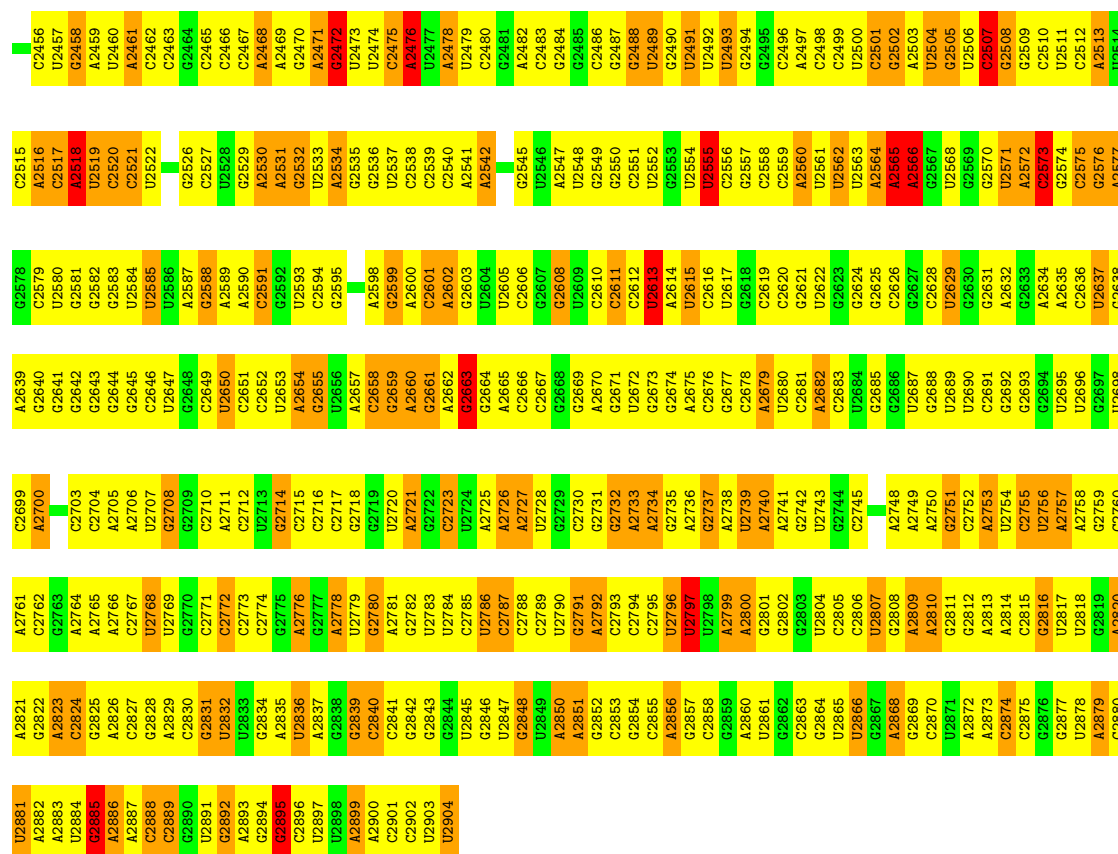
- Molecule 57: 23S ribosomal RNA

Chain BA:  15% 58% 24% .



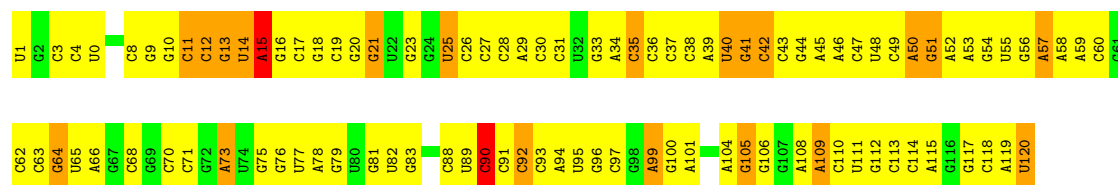


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A2268	G2269	A2270	G2271	G2272	A2273	A2274	G2275	G2276	G2277	A2278	G2279	G2280	A2281	G2282	G2283	A2284	G2285	G2286	A2287	G2288	G2289	G2290	G2291		G2294	G2295	G2296	G2297	A2298	G2299	G2300	G2301	G2302	G2303	G2304	G2305	G2306	G2307	G2308	A2309	G2310	A2311	G2312	G2313	A2314		A2317			U2320	U2321	A2322	G2323	G2324	G2325	A2326	G2327	A2328	G2329	G2330																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
A2205	C2206	C2207	C2208	G2209	G2210	A2211	A2212	G2213	G2214	C2215	G2216		U2219	G2220	G2221	C2222	G2223	G2224	A2225	C2226	G2227	G2228	G2229	G2230	G2231	G2232	G2233	G2234	G2235	G2236	G2237	G2301	G2302	G2303	G2304	G2305	G2306	G2307	G2308	A2309	G2310	G2311	G2312	G2313	A2314		G2317	G2320	G2321	G2322	G2323	G2324	G2325	G2326	G2327	A2328	G2329	G2330																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
G2144	C2145	C2146	A2147	G2148	G2149	C2150	G2151	G2152	A2153	A2154	G2155		A2158	G2159	G2160	C2161	G2162	A2163	C2164	G2165	A2166	G2167	G2168	A2169		A2170	A2171	G2172	A2173	C2174	C2175	A2176	C2177	G2178	C2179	A2180	G2181	A2182	A2183	A2184	G2185	G2186	G2187	G2188	G2189	G2190	A2191	G2192	G2193	G2194	G2195	G2196	G2197	G2198	G2199	G2200																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
A2082	G2083	G2084	G2085	G2086	G2087	A2088	G2089	A2090	G2091	G2092	G2093	A2094	A2095	G2096	A2097	G2098	G2099	G2100	A2101	G2102	C2103	G2104	G2105	G2106	G2107	A2108	G2109	G2110	G2111	G2112	G2113	A2114	G2115	G2116	A2117	G2118	A2119	G2120	G2121	G2122		A2126	G2127	G2128	G2129	G2130	G2131	G2132	G2133	A2134	G2135	G2136	G2137	G2138	G2139	G2140	G2141	A2142	G2143																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
U2022	C2023	G2024	C2025	G2026	G2027	G2028	G2029	A2030	G2031	G2032	A2033	G2034	G2035	A2036	G2037	G2038	G2039	G2040	U2041	A2042	C2043	C2044	G2045	G2046	C2047	G2048	G2049	G2050	A2051	A2052	G2053	A2054	G2055	G2056	G2057	A2058	G2059	A2060	G2061	A2062	G2063	C2064	G2065	C2066	G2067	U2068	G2069	A2070	A2071	C2072	G2073	A2074	G2075	G2076	A2077	C2078	U2079	A2080	U2081																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
A1960	C1961	C1962	U1963	G1964	G1965	A1966	G1967	G1968	G1969	G1970	G1971	G1972	G1973	C1974	G1975	G1976	A1977	A1978		A1981		U1982	C1985	C1986	A1987	G1988	G1989	C1990	U1991	G1992	G1993	C1994	G1995	U1996	G1997	A1998	G1999	C2000	C2001	G2002	A2003	G2004	A2005	C2006	G2007	U2008	A2009	G2010	U2011	G2012	A2013	A2014	G1954	A1955	U2016	G2017	G2018	A2019	A2020	C2021																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
U1898	A1899	A1900	A1901	G1902	G1903	G1904	G1905	G1906	G1907	G1908	G1909	G1910	U1911	A1912	A1913	G1914	3TD1915	A1916	U1917	A1918	A1919	C1920	G1921	G1922	U1923	C1924	G1925	U1926	A1927	A1928	G1929	G1930	U1931	A1932	G1933	C1934	G1935	A1936	A1937	A1938	U1939	U1940	C1941	C1942	U1943	U1944	G1945	U1946	G1947	G1948		A1952	A1953	G1954	U1955	U1956	C1957	G1958	G1959																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
C1838	G1839	G1840	U1841	G1842	G1843	C1844	G1845	G1846	A1847	A1848	G1849	G1850	U1851	U1852	A1853	A1854	U1855	U1856	G1857	A1858	U1859	G1860	G1861	G1862	G1863	U1864	U1865	A1866	G1867	C1868	G1869	C1870	A1871	A1872	G1873	C1874	G1875	A1876	A1877	G1878	C1879	U1880	C1881	U1882	U1883	A1884	U1885	U1886	C1887	G1888	A1889	A1890	G1891	C1892	C1893	C1894	G1895	C1896	G1897																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
U1778	U1779	U1780	U1781	U1782	A1783	A1784	A1785	A1786	A1787	C1788	A1789	C1790	A1791	G1792	A1793	A1794	C1795	U1796	G1797	U1798	G1799	C1800	A1801	A1802	A1803	C1804	U1805	C1806	G1807	A1808	A1809	A1810	G1811	U1812	G1813	G1814	A1815	C1816	G1817	U1818	A1819	U1820	A1821	C1822	G1823	U1824	U1825	G1826	U1827	G1828	A1829	C1830	G1831	C1832	C1833	U1834	G1835	C1836	C1837																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																															
A1585	C1586	U1587	A1588	G1589	C1600	G1601	U1602	A1603	G1604	C1605	A1606	G1607	A1608	A1609	A1610	C1611	C1612	G1613	A1614	C1615	A1616	C1617	A1618	G1619	G1620	U1621	G1622	U1623	A1624	C1625	A1626	G1627	G1628	U1629	A1630	G1631	A1632	G1633	A1634	A1635	U1636	U1637	C1638	C1639	A1640	A1641	C1642	G1643	C1644	U1645	C1646	U1647	G1648	U1649	A1650	A1651	A1652	G1653	A1654	U1655																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
C1656	U1657	C1658	G1659	G1660	G1661	U1662	U1663	A1664	A1665	G1666	G1667	A1668	A1669	C1670	U1671	A1672	G1673	G1674	C1675	A1676	A1677	C1678	A1679	U1680	G1681	G1682	U1683	C1684	C1685	A1686	G1687	U1688	A1689	A1690	C1691	U1692	U1693	C1694	G1695	G1696	G1697	A1698	C1699	A1700	A1701	G1702	G1703	C1704	A1705	C1706	G1707	U1708	U1709	G1710	A1711	U1712	A1713	U1714	G1715	U1716																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
A1717	G1718	G1719	U1720	G1721	A1722	G1723	G1724	G1725	C1726	C1727	G1728	U1729	C1730	G1731	C1732	G1733	G1734	A1735	U1736	G1737	U1738	A1739	A1740	C1741	U1742	G1743	A1744	A1745	A1746	U1747	C1748	A1749	U1750	U1751	G1752	G1753	A1754	A1755	G1756	A1757	U1758	A1759	C1760	C1761	A1762	C1763	C1764	U1765		C1768	U1769	G1770	C1771	U1772	A1773	C1774	G1775	U1776	U1777	G1778	U1779	C1780	C1781	C1782	C1783	C1784	C1785	C1786	C1787	C1788	C1789	C1790	C1791	C1792	C1793	C1794	C1795	C1796	C1797	C1798	C1799	C1800	C1801	C1802	C1803	C1804	C1805	C1806	C1807	C1808	C1809	C1810	C1811	C1812	C1813	C1814	C1815	C1816	C1817	C1818	C1819	C1820	C1821	C1822	C1823	C1824	C1825	C1826	C1827	C1828	C1829	C1830	C1831	C1832	C1833	C1834	C1835	C1836	C1837	C1838	C1839	C1840	C1841	C1842	C1843	C1844	C1845	C1846	C1847	C1848	C1849	C1850	C1851	C1852	C1853	C1854	C1855	C1856	C1857	C1858	C1859	C1860	C1861	C1862	C1863	C1864	C1865	C1866	C1867	C1868	C1869	C1870	C1871	C1872	C1873	C1874	C1875	C1876	C1877	C1878	C1879	C1880	C1881	C1882	C1883	C1884	C1885	C1886	C1887	C1888	C1889	C1890	C1891	C1892	C1893	C1894	C1895	C1896	C1897	C1898	C1899	C1900	C1901	C1902	C1903	C1904	C1905	C1906	C1907	C1908	C1909	C1910	C1911	C1912	C1913	C1914	C1915	C1916	C1917	C1918	C1919	C1920	C1921	C1922	C1923	C1924	C1925	C1926	C1927	C1928	C1929	C1930	C1931	C1932	C1933	C1934	C1935	C1936	C1937	C1938	C1939	C1940	C1941	C1942	C1943	C1944	C1945	C1946	C1947	C1948	C1949	C1950	C1951	C1952	C1953	C1954	C1955	C1956	C1957	C1958	C1959	C1960	C1961	C1962	C1963	C1964	C1965	C1966	C1967	C1968	C1969	C1970	C1971	C1972	C1973	C1974	C1975	C1976	C1977	C1978	C1979	C1980	C1981	C1982	C1983	C1984	C1985	C1986	C1987	C1988	C1989	C1990	C1991	C1992	C1993	C1994	C1995	C1996	C1997	C1998	C1999	C2000	C2001	C2002	C2003	C2004	C2005	C2006	C2007	C2008	C2009	C2010	C2011	C2012	C2013	C2014	C2015	C2016	C2017	C2018	C2019	C2020	C2021	C2022	C2023	C2024	C2025	C2026	C2027	C2028	C2029	C2030	C2031	C2032	C2033	C2034	C2035	C2036	C2037	C2038	C2039	C2040	C2041	C2042	C2043	C2044	C2045	C2046	C2047	C2048	C2049	C2050	C2051	C2052	C2053	C2054	C2055	C2056	C2057	C2058	C2059	C2060	C2061	C2062	C2063	C2064	C2065	C2066	C2067	C2068	C2069	C2070	C2071	C2072	C2073	C2074	C2075	C2076	C2077	C2078	C2079	C2080	C2081	C2082	C2083	C2084	C2085	C2086	C2087	C2088	C2089	C2090	C2091	C2092	C2093	C2094	C2095	C2096	C2097	C2098	C2099	C2100	C2101	C2102	C2103	C2104	C2105	C2106	C2107	C2108	C2109	C2110	C2111	C2112	C2113	C2114	C2115	C2116	C2117	C2118	C2119	C2120	C2121	C2122	C2123	C2124	C2125	C2126	C2127	C2128	C2129	C2130	C2131	C2132	C2133	C2134	C2135	C2136	C2137	C2138	C2139	C2140	C2141	C2142	C2143	C2144	C2145	C2146	C2147	C2148	C2149	C2150	C2151	C2152	C2153	C2154	C2155	C2156	C2157	C2158	C2159	C2160	C2161	C2162	C2163	C2164	C2165	C2166	C2167	C2168	C2169	C2170	C2171	C2172	C2173	C2174	C2175	C2176	C2177	C2178	C2179	C2180	C2181	C2182	C2183	C2184	C2185	C2186	C2187	C2188	C2189	C2190	C2191	C2192	C2193	C2194	C2195	C2196	C2197	C2198	C2199	C2200	C2201	C2202	C2203	C2204	C2205	C2206	C2207	C2208	C2209	C2210	C2211	C2212	C2213	C2214	C2215	C2216	C2217	C2218	C2219	C2220	C2221	C2222	C2223	C2224	C2225	C2226	C2227	C2228	C2229	C2230	C2231	C2232	C2233	C2234	C2235	C2236	C2237	C2238	C2239	C2240	C2241	C2242	C2243	C2244	C2245	C2246	C2247	C2248	C2249	C2250	C2251	C2252	C2253	C2254	C2255	C2256	C2257	C2258	C2259	C2260	C2261	C2262	C2263	C2264	C2265	C2266	C2267	C2268	C2269	C2270	C2271	C2272	C2273	C2274	C2275	C2276	C2277	C2278	C2279	C2280	C2281	C2282	C2283	C2284	C2285	C2286	C2287	C2288	C2289	C2290	C2291	C2292	C2293	C2294	C2295	C2296	C2297	C2298	C2299	C2300	C2301	C2302	C2303	C2304



• Molecule 58: 5S ribosomal RNA

Chain Ba: 18% 64% 17%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	98000	Depositor
Resolution determination method	FSC	Depositor
CTF correction method	group defocus	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	Not provided	
Maximum map value	253.190	Depositor
Minimum map value	-113.794	Depositor
Average map value	4.829	Depositor
Map value standard deviation	25.951	Depositor
Recommended contour level	22.0	Depositor
Map size (\AA)	365.85, 365.85, 365.85	wwPDB
Map dimensions	135, 135, 135	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	2.71, 2.71, 2.71	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 7MG, PSU, 4SU, 1MG, 5MC, OMU, 2MG, 2MA, H2U, 5MU, 3TD, 6MZ, UR3, 4OC, OMG, OMC, 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	AJ	0.75	0/742	1.26	7/941 (0.7%)
2	AK	0.79	0/856	1.39	14/1069 (1.3%)
3	AL	0.79	0/873	1.30	12/1110 (1.1%)
4	AM	0.79	0/817	1.45	20/1022 (2.0%)
5	AN	0.82	0/715	1.37	10/883 (1.1%)
6	AO	0.76	0/646	1.22	8/813 (1.0%)
7	AP	0.83	0/572	1.39	11/711 (1.5%)
8	AQ	0.72	0/636	1.16	6/822 (0.7%)
9	AR	0.92	0/568	1.46	12/713 (1.7%)
10	AS	0.77	0/687	1.27	10/880 (1.1%)
11	AB	0.74	0/1703	1.07	9/2161 (0.4%)
12	AT	0.75	0/574	1.25	12/694 (1.7%)
13	AU	0.94	0/520	1.61	15/636 (2.4%)
14	AC	0.75	0/1669	1.15	16/2122 (0.8%)
15	AD	0.80	0/1497	1.29	19/1890 (1.0%)
16	AE	0.73	0/1110	1.14	9/1405 (0.6%)
17	AF	0.79	0/1001	1.23	11/1268 (0.9%)
18	AG	0.79	0/1263	1.33	16/1590 (1.0%)
19	AH	0.72	0/896	1.11	7/1141 (0.6%)
20	AI	0.85	0/940	1.37	19/1180 (1.6%)
21	A1	0.76	0/4864	1.12	24/6363 (0.4%)
22	AA	1.47	6/36769 (0.0%)	2.38	2673/57354 (4.7%)
23	A2	1.48	0/1108	2.31	71/1724 (4.1%)
24	A3	1.49	0/1717	2.41	129/2675 (4.8%)
25	BC	0.68	0/1748	0.98	4/2355 (0.2%)
26	BJ	0.73	0/1247	1.15	10/1679 (0.6%)
27	BK	0.67	0/1046	1.00	4/1410 (0.3%)
28	BN	0.75	0/1152	1.11	11/1551 (0.7%)
29	BO	0.74	0/956	1.20	13/1279 (1.0%)
30	BP	0.79	0/1062	1.36	15/1413 (1.1%)
31	BQ	0.78	0/1093	1.24	13/1460 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BR	0.79	0/1021	1.35	17/1364 (1.2%)
33	BS	0.76	0/910	1.23	14/1219 (1.1%)
34	BT	0.77	0/929	1.25	10/1242 (0.8%)
35	BD	0.75	0/2131	1.25	32/2863 (1.1%)
36	BU	0.80	0/960	1.29	15/1278 (1.2%)
37	BV	0.76	0/829	1.18	9/1107 (0.8%)
38	BW	0.67	0/864	1.10	12/1156 (1.0%)
39	BX	0.69	0/794	1.10	3/1060 (0.3%)
40	BY	0.69	0/797	1.04	4/1062 (0.4%)
41	BZ	0.73	0/766	1.11	6/1025 (0.6%)
42	B0	0.79	0/642	1.25	8/848 (0.9%)
43	B1	0.79	0/635	1.37	13/848 (1.5%)
44	B2	0.71	0/510	1.17	6/677 (0.9%)
45	BE	0.72	0/1586	1.14	15/2134 (0.7%)
46	B3	0.72	0/453	1.29	9/605 (1.5%)
47	B4	0.75	0/559	1.06	5/745 (0.7%)
48	B5	0.79	0/450	1.38	9/599 (1.5%)
49	B6	0.73	0/448	1.02	3/594 (0.5%)
50	B7	0.84	0/380	1.47	10/498 (2.0%)
51	B8	0.76	0/513	1.28	9/676 (1.3%)
52	B9	0.71	0/303	1.16	3/397 (0.8%)
53	BF	0.71	0/1571	1.09	13/2113 (0.6%)
54	BG	0.77	0/1444	1.18	10/1937 (0.5%)
55	BH	0.72	0/1343	1.08	7/1816 (0.4%)
56	BL	0.70	0/1122	1.05	8/1515 (0.5%)
57	BA	1.47	5/69280 (0.0%)	2.39	5083/108078 (4.7%)
58	Ba	1.46	0/2869	2.35	208/4474 (4.6%)
All	All	1.28	11/165156 (0.0%)	2.11	8751/244244 (3.6%)

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
3	AL	0	1
6	AO	0	1
7	AP	0	1
9	AR	0	1
10	AS	0	1
15	AD	0	1
18	AG	0	2

Continued on next page...

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Mol	Chain	#Chirality outliers	#Planarity outliers
21	A1	0	2
22	AA	0	350
23	A2	0	5
24	A3	0	15
26	BJ	0	1
28	BN	0	2
29	BO	0	1
32	BR	0	1
34	BT	0	1
35	BD	0	1
36	BU	0	2
38	BW	0	1
40	BY	0	1
42	B0	0	1
51	B8	0	1
55	BH	0	2
57	BA	0	660
58	Ba	0	15
All	All	0	1070

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
22	AA	1223	C	C4-N4	-5.72	1.28	1.33
22	AA	1226	C	O3'-P	-5.66	1.54	1.61
22	AA	1432	G	C2-N2	-5.45	1.29	1.34
57	BA	823	C	C4-N4	-5.35	1.29	1.33
22	AA	1497	G	C2-N2	-5.32	1.29	1.34

The worst 5 of 8751 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	AE	111	ARG	NE-CZ-NH1	15.27	127.93	120.30
57	BA	1073	A	N1-C6-N6	-14.45	109.93	118.60
26	BJ	55	ARG	NE-CZ-NH1	14.31	127.46	120.30
57	BA	423	A	N1-C6-N6	-14.03	110.18	118.60
7	AP	70	ARG	NE-CZ-NH1	13.34	126.97	120.30

There are no chirality outliers.

5 of 1070 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	AL	109	ARG	Sidechain
6	AO	88	ARG	Sidechain
7	AP	25	ARG	Sidechain
9	AR	2	ARG	Sidechain
10	AS	79	TYR	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AJ	794	0	803	0	0
2	AK	923	0	912	0	0
3	AL	923	0	954	0	0
4	AM	876	0	910	0	0
5	AN	771	0	777	0	0
6	AO	690	0	691	0	0
7	AP	620	0	611	0	0
8	AQ	657	0	687	0	0
9	AR	603	0	602	0	0
10	AS	708	0	732	0	0
11	AB	1805	0	1750	0	0
12	AT	636	0	652	0	0
13	AU	564	0	579	0	0
14	AC	1761	0	1793	0	0
15	AD	1587	0	1596	0	0
16	AE	1182	0	1185	0	0
17	AF	1061	0	971	0	0
18	AG	1347	0	1347	0	0
19	AH	948	0	975	0	0
20	AI	1000	0	1011	0	0
21	A1	4989	0	4915	0	0
22	AA	33089	0	16668	0	0
23	A2	993	0	501	0	0
24	A3	1640	0	845	0	0
25	BC	1733	0	1824	0	0
26	BJ	1233	0	1283	0	0
27	BK	1032	0	1088	0	0
28	BN	1129	0	1162	0	0
29	BO	947	0	1023	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	BP	1053	0	1129	0	0
31	BQ	1074	0	1157	0	0
32	BR	1008	0	1045	0	0
33	BS	900	0	935	0	0
34	BT	917	0	965	0	0
35	BD	2092	0	2170	0	0
36	BU	947	0	1022	0	0
37	BV	816	0	839	0	0
38	BW	857	0	922	0	0
39	BX	787	0	846	0	0
40	BY	789	0	847	0	0
41	BZ	753	0	780	0	0
42	B0	634	0	656	0	0
43	B1	625	0	655	0	0
44	B2	509	0	543	0	0
45	BE	1565	0	1616	0	0
46	B3	449	0	491	0	0
47	B4	549	0	552	0	0
48	B5	444	0	461	0	0
49	B6	441	0	485	0	0
50	B7	377	0	418	0	0
51	B8	504	0	574	0	0
52	B9	302	0	343	0	0
53	BF	1552	0	1619	0	0
54	BG	1420	0	1460	0	0
55	BH	1323	0	1374	0	0
56	BL	1111	0	1148	0	0
57	BA	62351	0	31378	0	0
58	Ba	2566	0	1302	0	0
All	All	154956	0	106579	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

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	AJ	44/103 (43%)	40 (91%)	1 (2%)	3 (7%)	1	15
2	AK	57/128 (44%)	52 (91%)	5 (9%)	0	100	100
3	AL	64/123 (52%)	54 (84%)	8 (12%)	2 (3%)	4	27
4	AM	56/117 (48%)	51 (91%)	4 (7%)	1 (2%)	8	40
5	AN	41/100 (41%)	37 (90%)	3 (7%)	1 (2%)	6	33
6	AO	44/88 (50%)	43 (98%)	1 (2%)	0	100	100
7	AP	34/82 (42%)	31 (91%)	3 (9%)	0	100	100
8	AQ	52/83 (63%)	48 (92%)	4 (8%)	0	100	100
9	AR	36/74 (49%)	34 (94%)	2 (6%)	0	100	100
10	AS	54/91 (59%)	53 (98%)	1 (2%)	0	100	100
11	AB	123/240 (51%)	114 (93%)	7 (6%)	2 (2%)	9	44
12	AT	32/86 (37%)	30 (94%)	2 (6%)	0	100	100
13	AU	24/70 (34%)	18 (75%)	3 (12%)	3 (12%)	0	5
14	AC	126/232 (54%)	122 (97%)	4 (3%)	0	100	100
15	AD	107/205 (52%)	102 (95%)	5 (5%)	0	100	100
16	AE	89/166 (54%)	84 (94%)	4 (4%)	1 (1%)	14	52
17	AF	65/135 (48%)	61 (94%)	4 (6%)	0	100	100
18	AG	84/178 (47%)	79 (94%)	5 (6%)	0	100	100
19	AH	77/129 (60%)	70 (91%)	7 (9%)	0	100	100
20	AI	69/129 (54%)	63 (91%)	6 (9%)	0	100	100
21	A1	434/639 (68%)	390 (90%)	38 (9%)	6 (1%)	11	46
25	BC	232/234 (99%)	213 (92%)	18 (8%)	1 (0%)	34	72
26	BJ	162/164 (99%)	158 (98%)	3 (2%)	1 (1%)	25	66
27	BK	139/141 (99%)	133 (96%)	6 (4%)	0	100	100
28	BN	140/142 (99%)	131 (94%)	9 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	BO	121/123 (98%)	107 (88%)	11 (9%)	3 (2%)	5	32
30	BP	142/144 (99%)	127 (89%)	13 (9%)	2 (1%)	11	46
31	BQ	134/136 (98%)	126 (94%)	6 (4%)	2 (2%)	10	46
32	BR	125/127 (98%)	112 (90%)	11 (9%)	2 (2%)	9	44
33	BS	115/117 (98%)	115 (100%)	0	0	100	100
34	BT	112/114 (98%)	107 (96%)	3 (3%)	2 (2%)	8	40
35	BD	270/272 (99%)	252 (93%)	15 (6%)	3 (1%)	14	52
36	BU	115/117 (98%)	108 (94%)	5 (4%)	2 (2%)	9	42
37	BV	101/103 (98%)	94 (93%)	4 (4%)	3 (3%)	4	28
38	BW	108/110 (98%)	103 (95%)	4 (4%)	1 (1%)	17	57
39	BX	98/100 (98%)	83 (85%)	12 (12%)	3 (3%)	4	27
40	BY	101/103 (98%)	97 (96%)	4 (4%)	0	100	100
41	BZ	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
42	B0	82/84 (98%)	72 (88%)	6 (7%)	4 (5%)	2	20
43	B1	75/77 (97%)	69 (92%)	5 (7%)	1 (1%)	12	48
44	B2	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
45	BE	207/209 (99%)	181 (87%)	20 (10%)	6 (3%)	4	29
46	B3	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
47	B4	68/70 (97%)	62 (91%)	6 (9%)	0	100	100
48	B5	54/56 (96%)	50 (93%)	3 (6%)	1 (2%)	8	38
49	B6	52/54 (96%)	51 (98%)	1 (2%)	0	100	100
50	B7	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
51	B8	62/64 (97%)	61 (98%)	1 (2%)	0	100	100
52	B9	36/38 (95%)	31 (86%)	3 (8%)	2 (6%)	2	19
53	BF	199/201 (99%)	186 (94%)	7 (4%)	6 (3%)	4	28
54	BG	176/178 (99%)	155 (88%)	15 (8%)	6 (3%)	3	26
55	BH	174/176 (99%)	157 (90%)	14 (8%)	3 (2%)	9	42
56	BL	147/149 (99%)	133 (90%)	13 (9%)	1 (1%)	22	63
All	All	5512/7062 (78%)	5089 (92%)	349 (6%)	74 (1%)	16	48

5 of 74 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	A1	242	THR
21	A1	493	LYS
32	BR	13	ASN
35	BD	140	VAL
42	B0	40	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AJ	90/90 (100%)	88 (98%)	2 (2%)	52	71
2	AK	98/98 (100%)	97 (99%)	1 (1%)	76	86
3	AL	103/103 (100%)	102 (99%)	1 (1%)	76	86
4	AM	95/95 (100%)	95 (100%)	0	100	100
5	AN	83/83 (100%)	82 (99%)	1 (1%)	71	83
6	AO	76/76 (100%)	74 (97%)	2 (3%)	46	66
7	AP	65/65 (100%)	64 (98%)	1 (2%)	65	80
8	AQ	77/77 (100%)	75 (97%)	2 (3%)	46	66
9	AR	64/64 (100%)	62 (97%)	2 (3%)	40	62
10	AS	78/78 (100%)	74 (95%)	4 (5%)	24	48
11	AB	198/198 (100%)	196 (99%)	2 (1%)	76	86
12	AT	65/65 (100%)	65 (100%)	0	100	100
13	AU	60/60 (100%)	58 (97%)	2 (3%)	38	61
14	AC	189/189 (100%)	181 (96%)	8 (4%)	30	54
15	AD	172/172 (100%)	168 (98%)	4 (2%)	50	70
16	AE	125/125 (100%)	119 (95%)	6 (5%)	25	51
17	AF	116/116 (100%)	111 (96%)	5 (4%)	29	53
18	AG	146/146 (100%)	143 (98%)	3 (2%)	53	72
19	AH	104/104 (100%)	101 (97%)	3 (3%)	42	64
20	AI	106/106 (100%)	102 (96%)	4 (4%)	33	57

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
21	A1	568/568 (100%)	559 (98%)	9 (2%)	62	79
25	BC	181/181 (100%)	174 (96%)	7 (4%)	32	56
26	BJ	122/122 (100%)	120 (98%)	2 (2%)	62	79
27	BK	109/109 (100%)	106 (97%)	3 (3%)	43	65
28	BN	116/116 (100%)	110 (95%)	6 (5%)	23	48
29	BO	104/104 (100%)	95 (91%)	9 (9%)	10	31
30	BP	103/103 (100%)	96 (93%)	7 (7%)	16	41
31	BQ	109/109 (100%)	105 (96%)	4 (4%)	34	58
32	BR	103/103 (100%)	100 (97%)	3 (3%)	42	64
33	BS	87/87 (100%)	86 (99%)	1 (1%)	73	84
34	BT	99/99 (100%)	97 (98%)	2 (2%)	55	74
35	BD	217/217 (100%)	212 (98%)	5 (2%)	50	70
36	BU	89/89 (100%)	86 (97%)	3 (3%)	37	60
37	BV	84/84 (100%)	83 (99%)	1 (1%)	71	83
38	BW	93/93 (100%)	90 (97%)	3 (3%)	39	61
39	BX	84/84 (100%)	83 (99%)	1 (1%)	71	83
40	BY	84/84 (100%)	82 (98%)	2 (2%)	49	69
41	BZ	78/78 (100%)	77 (99%)	1 (1%)	69	81
42	B0	62/62 (100%)	56 (90%)	6 (10%)	8	27
43	B1	67/67 (100%)	66 (98%)	1 (2%)	65	80
44	B2	55/55 (100%)	54 (98%)	1 (2%)	59	77
45	BE	164/164 (100%)	163 (99%)	1 (1%)	86	92
46	B3	48/48 (100%)	48 (100%)	0	100	100
47	B4	62/62 (100%)	61 (98%)	1 (2%)	62	79
48	B5	47/47 (100%)	45 (96%)	2 (4%)	29	53
49	B6	48/48 (100%)	48 (100%)	0	100	100
50	B7	38/38 (100%)	37 (97%)	1 (3%)	46	66
51	B8	51/51 (100%)	51 (100%)	0	100	100
52	B9	34/34 (100%)	34 (100%)	0	100	100
53	BF	165/165 (100%)	161 (98%)	4 (2%)	49	69
54	BG	149/149 (100%)	141 (95%)	8 (5%)	22	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
55	BH	137/137 (100%)	132 (96%)	5 (4%)	35	59
56	BL	114/114 (100%)	114 (100%)	0	100	100
All	All	5781/5781 (100%)	5629 (97%)	152 (3%)	49	66

5 of 152 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
38	BW	60	HIS
54	BG	103	ILE
40	BY	46	LYS
45	BE	128	ARG
55	BH	154	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	AA	1538/1542 (99%)	194 (12%)	57 (3%)
23	A2	46/47 (97%)	13 (28%)	1 (2%)
24	A3	75/77 (97%)	12 (16%)	2 (2%)
57	BA	2899/2904 (99%)	404 (13%)	115 (3%)
58	Ba	119/120 (99%)	11 (9%)	0
All	All	4677/4690 (99%)	634 (13%)	175 (3%)

5 of 634 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
22	AA	2	A
22	AA	3	A
22	AA	5	U
22	AA	6	G
22	AA	7	A

5 of 175 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
57	BA	1325	U
57	BA	2062	A

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Mol	Chain	Res	Type
57	BA	1393	A
57	BA	1653	G
57	BA	2248	C

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

39 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	$\# Z > 2$
57	PSU	BA	955	57	18,21,22	0.80	0	22,30,33	1.08	2 (9%)
57	2MG	BA	2445	57	18,26,27	0.96	2 (11%)	16,38,41	1.31	2 (12%)
24	4SU	A3	8	24	18,21,22	1.39	1 (5%)	26,30,33	1.16	2 (7%)
22	5MC	AA	1407	22	18,22,23	0.59	0	26,32,35	1.38	4 (15%)
22	MA6	AA	1518	22	19,26,27	0.94	1 (5%)	18,38,41	0.89	0
22	MA6	AA	1519	22	19,26,27	0.95	2 (10%)	18,38,41	0.93	0
57	PSU	BA	2457	57	18,21,22	0.79	0	22,30,33	1.14	2 (9%)
57	PSU	BA	746	57	18,21,22	0.80	0	22,30,33	1.22	3 (13%)
22	5MC	AA	967	22	18,22,23	0.61	0	26,32,35	1.44	4 (15%)
22	4OC	AA	1402	22	20,23,24	0.65	0	26,32,35	1.22	2 (7%)
57	5MC	BA	1962	57	18,22,23	0.57	0	26,32,35	1.51	5 (19%)
57	6MZ	BA	1618	57	18,25,26	0.93	0	16,36,39	1.47	2 (12%)
22	PSU	AA	516	22	18,21,22	0.81	0	22,30,33	1.24	2 (9%)
24	PSU	A3	56	24	18,21,22	0.84	0	22,30,33	1.12	2 (9%)
22	UR3	AA	1498	22	19,22,23	0.71	0	26,32,35	1.01	2 (7%)
57	2MA	BA	2503	57	17,25,26	1.21	3 (17%)	17,37,40	1.60	3 (17%)
57	7MG	BA	2069	57	22,26,27	4.62	2 (9%)	29,39,42	1.41	1 (3%)
24	5MU	A3	55	24	19,22,23	0.67	0	28,32,35	1.33	4 (14%)
22	2MG	AA	1516	22	18,26,27	0.93	1 (5%)	16,38,41	1.14	2 (12%)
57	OMG	BA	2251	57	18,26,27	1.01	1 (5%)	19,38,41	1.32	3 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
57	5MU	BA	1939	57	19,22,23	0.72	0	28,32,35	1.31	3 (10%)
57	3TD	BA	1915	57	18,22,23	0.83	0	22,32,35	1.42	3 (13%)
57	PSU	BA	1917	57	18,21,22	0.78	0	22,30,33	1.13	2 (9%)
57	2MG	BA	1835	57	18,26,27	0.98	1 (5%)	16,38,41	1.15	2 (12%)
57	PSU	BA	1911	57	18,21,22	0.83	0	22,30,33	1.03	2 (9%)
57	H2U	BA	2449	57	18,21,22	1.14	2 (11%)	21,30,33	1.07	0
22	2MG	AA	966	22	18,26,27	1.00	2 (11%)	16,38,41	1.28	2 (12%)
57	1MG	BA	745	57	18,26,27	1.08	2 (11%)	19,39,42	1.10	1 (5%)
24	OMC	A3	33	24	19,22,23	0.70	0	26,31,34	1.09	1 (3%)
57	PSU	BA	2605	57	18,21,22	0.87	0	22,30,33	1.27	3 (13%)
57	5MU	BA	747	57	19,22,23	0.72	0	28,32,35	1.34	3 (10%)
57	OMU	BA	2552	57	19,22,23	0.60	0	26,31,34	0.91	1 (3%)
22	2MG	AA	1207	22	18,26,27	1.01	2 (11%)	16,38,41	1.11	2 (12%)
57	PSU	BA	2504	57	18,21,22	0.78	0	22,30,33	1.15	2 (9%)
57	PSU	BA	2580	57	18,21,22	0.82	0	22,30,33	1.50	4 (18%)
22	7MG	AA	527	22	22,26,27	4.55	2 (9%)	29,39,42	1.47	2 (6%)
57	OMC	BA	2498	57	19,22,23	0.76	0	26,31,34	1.25	1 (3%)
57	6MZ	BA	2030	57	18,25,26	0.92	1 (5%)	16,36,39	1.41	2 (12%)
24	H2U	A3	21	24	18,21,22	1.04	2 (11%)	21,30,33	0.83	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
57	PSU	BA	955	57	-	0/7/25/26	0/2/2/2
57	2MG	BA	2445	57	-	0/5/27/28	0/3/3/3
24	4SU	A3	8	24	-	0/7/25/26	0/2/2/2
22	5MC	AA	1407	22	-	0/7/25/26	0/2/2/2
22	MA6	AA	1518	22	-	0/7/29/30	0/3/3/3
22	MA6	AA	1519	22	-	0/7/29/30	0/3/3/3
57	PSU	BA	2457	57	-	0/7/25/26	0/2/2/2
57	PSU	BA	746	57	-	0/7/25/26	0/2/2/2
22	5MC	AA	967	22	-	0/7/25/26	0/2/2/2
22	4OC	AA	1402	22	-	0/9/29/30	0/2/2/2
57	5MC	BA	1962	57	-	0/7/25/26	0/2/2/2
57	6MZ	BA	1618	57	-	0/5/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
22	PSU	AA	516	22	-	0/7/25/26	0/2/2/2
24	PSU	A3	56	24	-	2/7/25/26	0/2/2/2
22	UR3	AA	1498	22	-	0/7/25/26	0/2/2/2
57	2MA	BA	2503	57	-	1/3/25/26	0/3/3/3
57	7MG	BA	2069	57	-	0/7/37/38	0/3/3/3
24	5MU	A3	55	24	-	0/7/25/26	0/2/2/2
22	2MG	AA	1516	22	-	0/5/27/28	0/3/3/3
57	OMG	BA	2251	57	-	0/5/27/28	0/3/3/3
57	5MU	BA	1939	57	-	0/7/25/26	0/2/2/2
57	3TD	BA	1915	57	-	1/7/25/26	0/2/2/2
57	PSU	BA	1917	57	-	0/7/25/26	0/2/2/2
57	2MG	BA	1835	57	-	0/5/27/28	0/3/3/3
57	PSU	BA	1911	57	-	0/7/25/26	0/2/2/2
57	H2U	BA	2449	57	-	0/7/38/39	0/2/2/2
22	2MG	AA	966	22	-	0/5/27/28	0/3/3/3
57	1MG	BA	745	57	-	0/3/25/26	0/3/3/3
24	OMC	A3	33	24	-	0/9/27/28	0/2/2/2
57	PSU	BA	2605	57	-	0/7/25/26	0/2/2/2
57	5MU	BA	747	57	-	0/7/25/26	0/2/2/2
57	OMU	BA	2552	57	-	0/9/27/28	0/2/2/2
22	2MG	AA	1207	22	-	0/5/27/28	0/3/3/3
57	PSU	BA	2504	57	-	2/7/25/26	0/2/2/2
57	PSU	BA	2580	57	-	0/7/25/26	0/2/2/2
22	7MG	AA	527	22	-	1/7/37/38	0/3/3/3
57	OMC	BA	2498	57	-	1/9/27/28	0/2/2/2
57	6MZ	BA	2030	57	-	1/5/27/28	0/3/3/3
24	H2U	A3	21	24	-	1/7/38/39	0/2/2/2

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	BA	2069	7MG	C8-N9	-21.38	1.34	1.46
22	AA	527	7MG	C8-N9	-21.04	1.34	1.46
24	A3	8	4SU	C5-C4	-4.96	1.36	1.42
57	BA	2449	H2U	C4-N3	-3.07	1.32	1.37
57	BA	2449	H2U	C2-N3	-2.94	1.32	1.38

The worst 5 of 83 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	BA	2069	7MG	N9-C8-N7	6.06	112.04	103.38
22	AA	527	7MG	N9-C8-N7	5.81	111.68	103.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	BA	2503	2MA	C5-C6-N1	4.24	121.33	114.02
57	BA	1618	6MZ	C9-N6-C6	4.04	126.35	122.87
57	BA	1915	3TD	C6-C5-C4	3.86	120.89	118.22

There are no chirality outliers.

5 of 10 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A3	56	PSU	O4'-C1'-C5-C4
57	BA	2504	PSU	O4'-C1'-C5-C4
57	BA	2504	PSU	O4'-C4'-C5'-O5'
24	A3	56	PSU	O4'-C1'-C5-C6
57	BA	1915	3TD	O4'-C1'-C5-C6

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

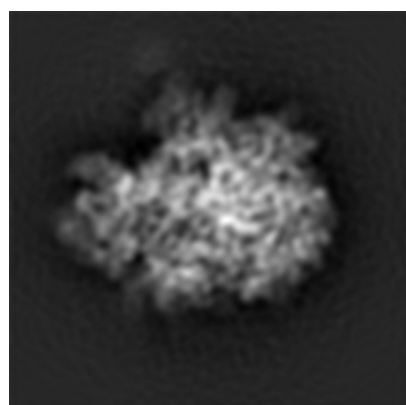
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5562. These allow visual inspection of the internal detail of the map and identification of artifacts.

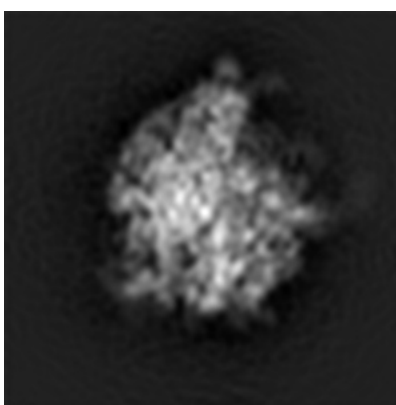
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

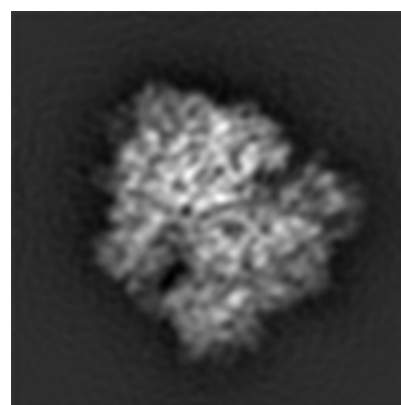
6.1.1 Primary map



X



Y

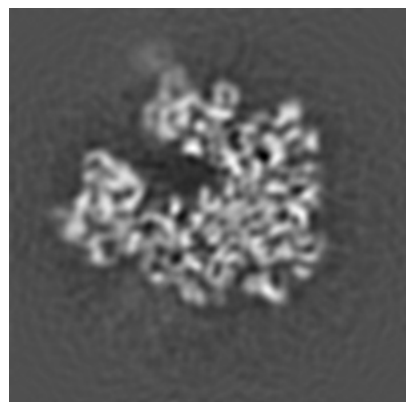


Z

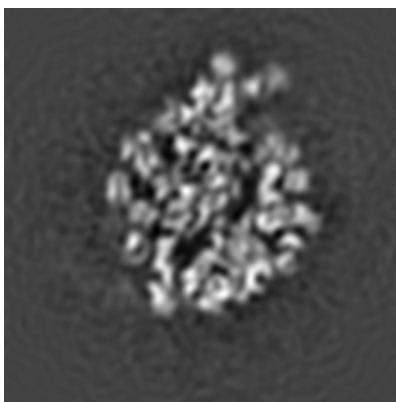
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

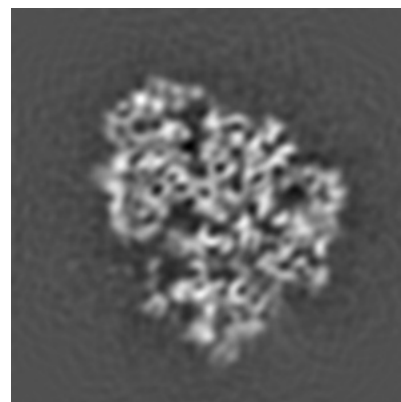
6.2.1 Primary map



X Index: 67



Y Index: 67

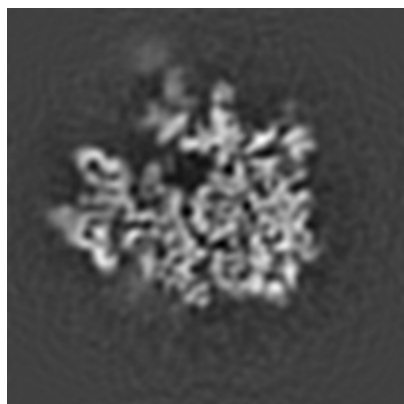


Z Index: 67

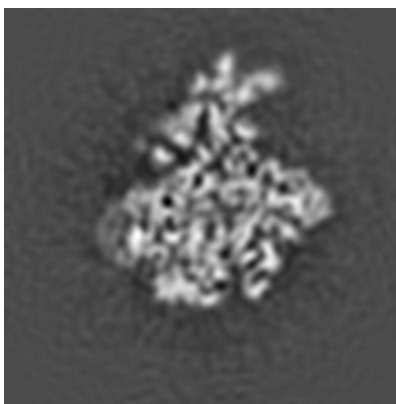
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

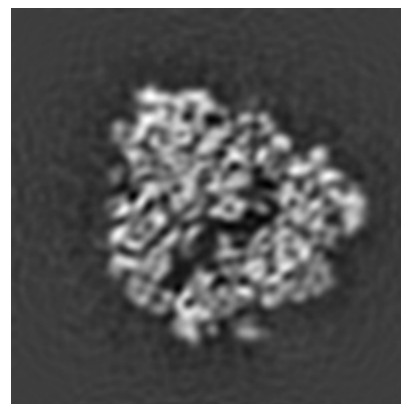
6.3.1 Primary map



X Index: 70



Y Index: 71

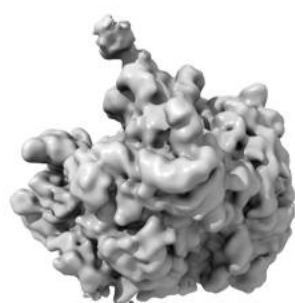


Z Index: 73

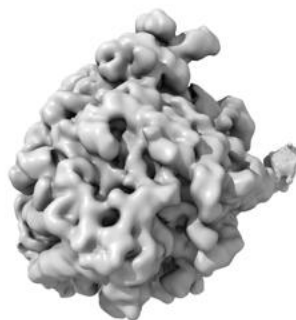
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

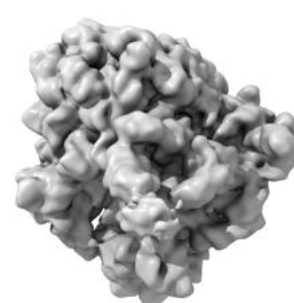
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 22.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

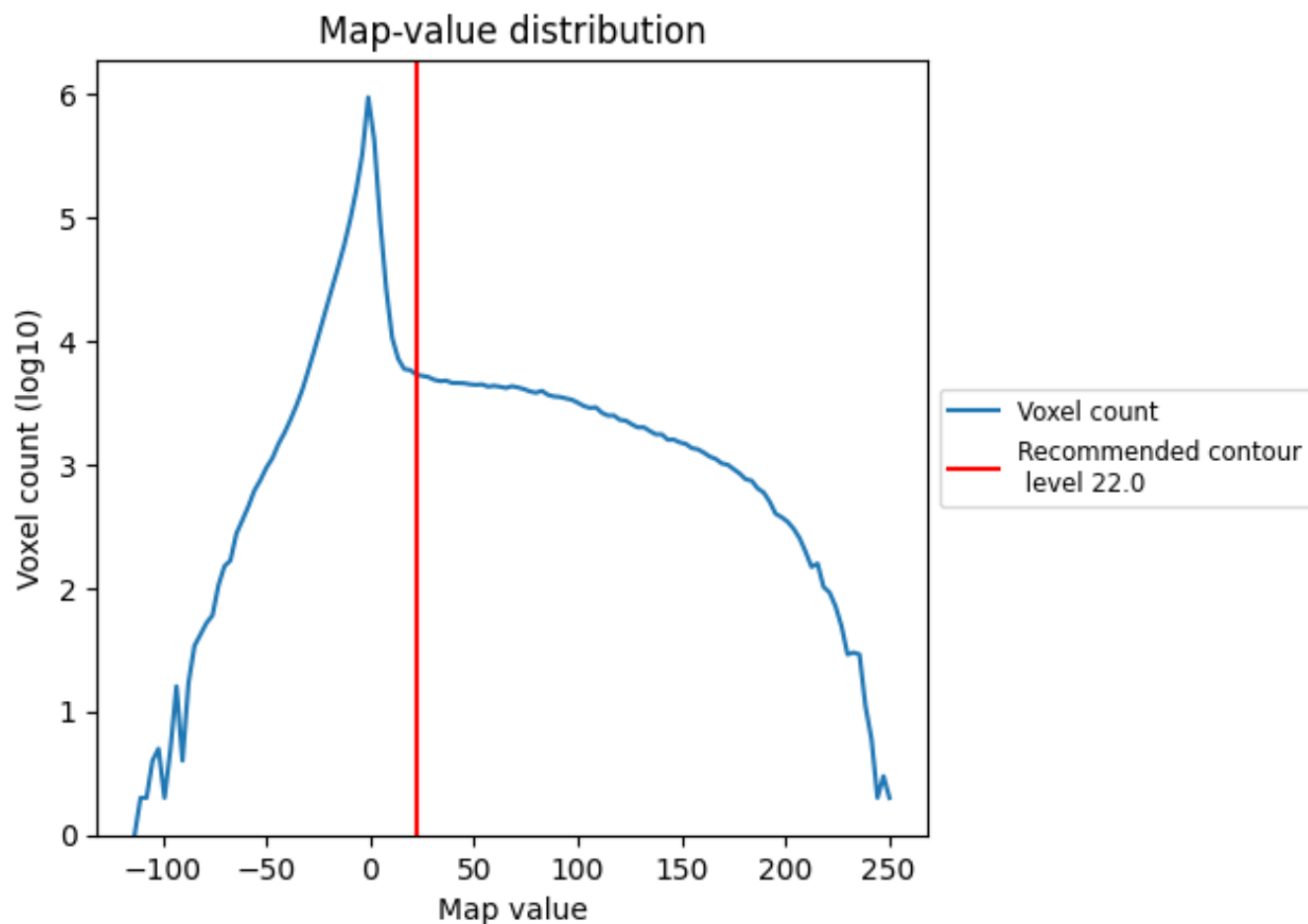
6.5 Mask visualisation

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

7 Map analysis [i](#)

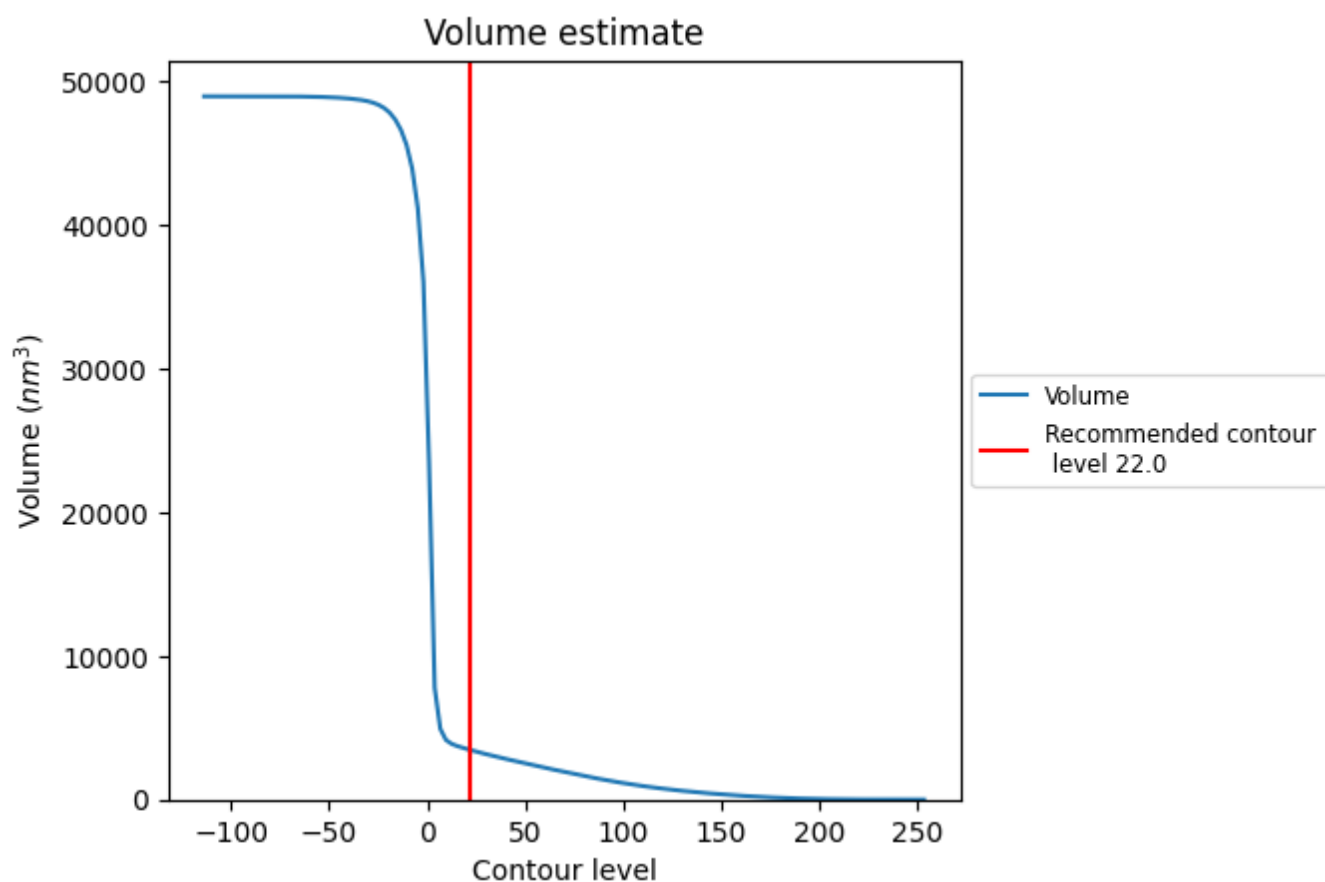
This section contains the results of statistical analysis of the map.

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.

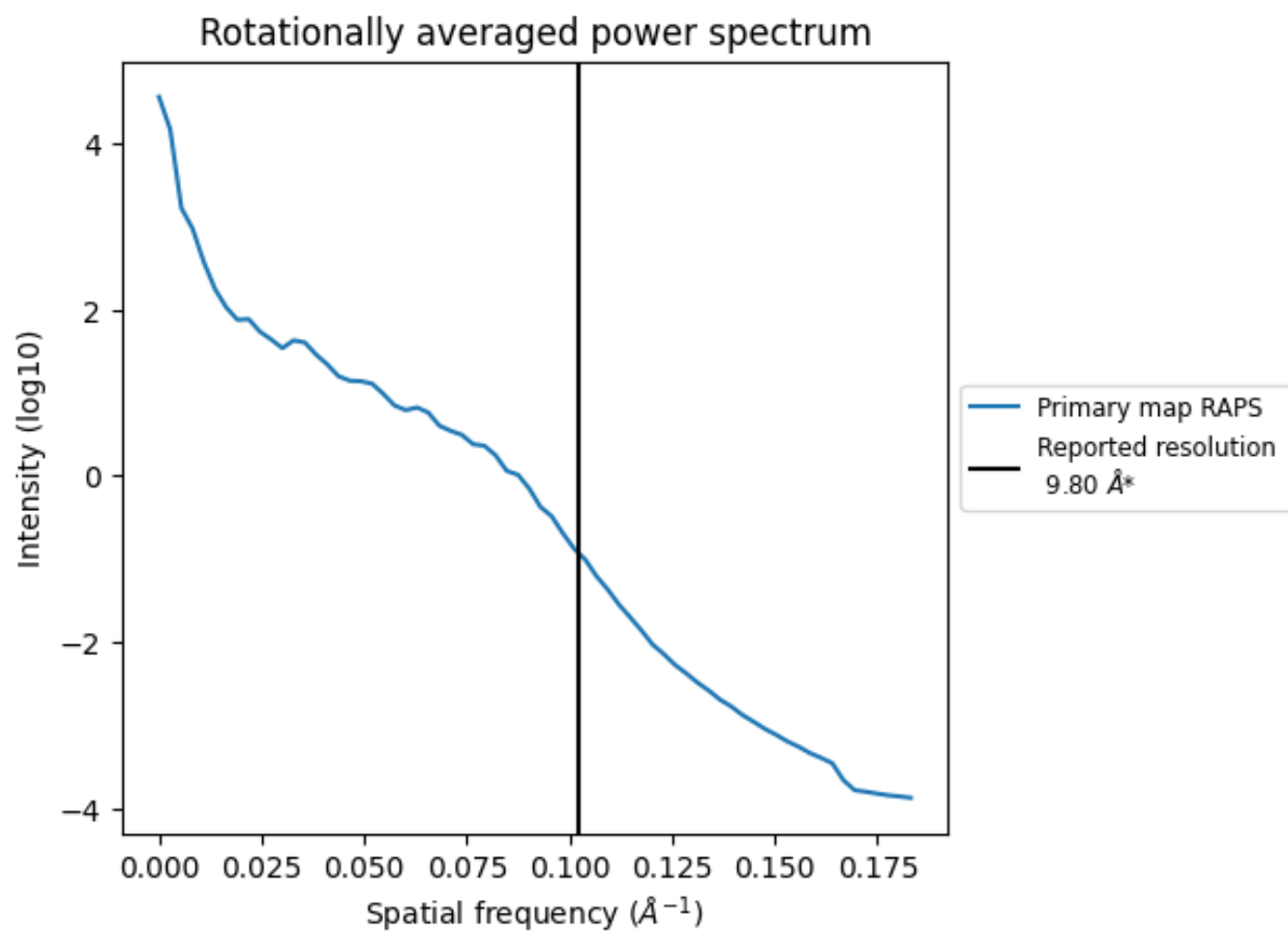
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3450 nm³; this corresponds to an approximate mass of 3116 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 0.102 Å⁻¹

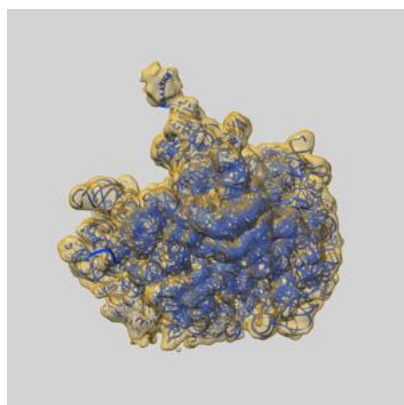
8 Fourier-Shell correlation

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

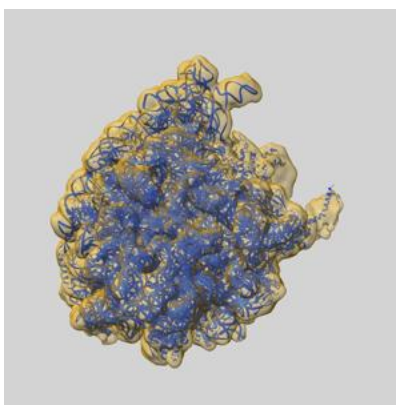
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5562 and PDB model 4V6V. Per-residue inclusion information can be found in section [3](#) on page [14](#).

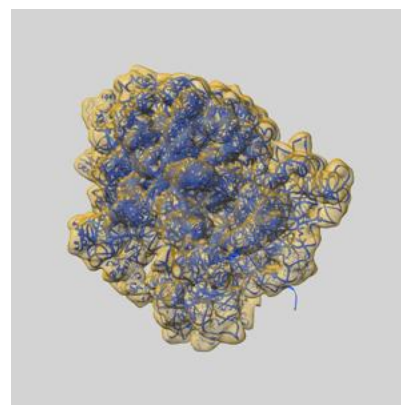
9.1 Map-model overlay [i](#)



X



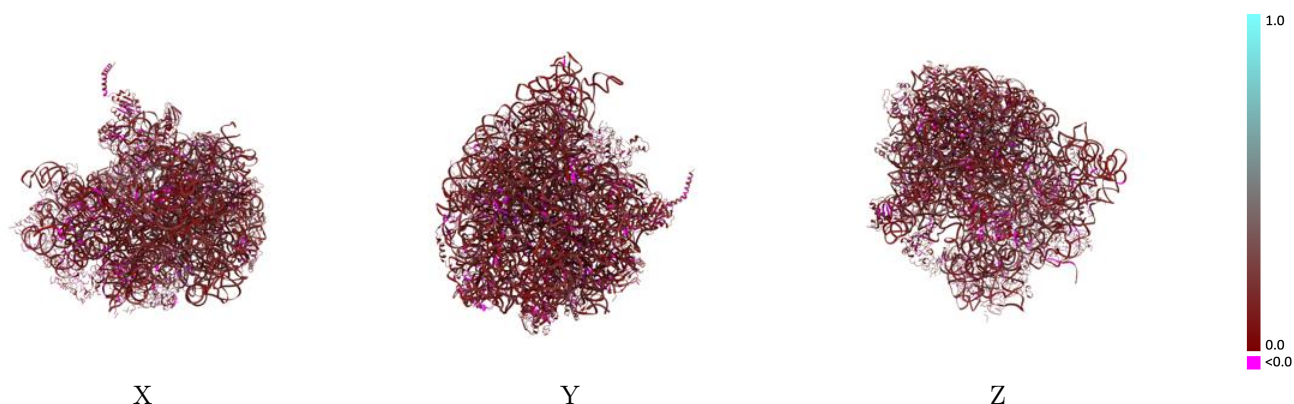
Y



Z

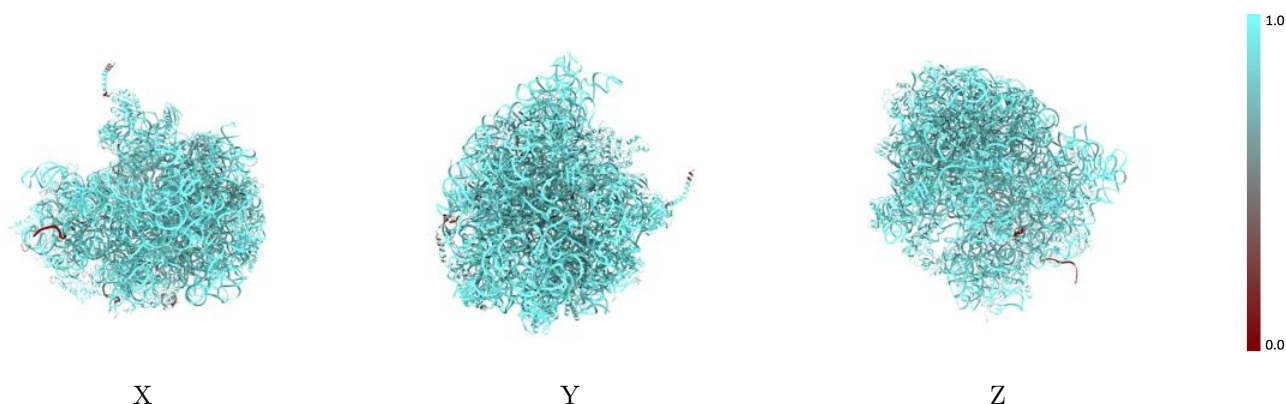
The images above show the 3D surface view of the map at the recommended contour level 22.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



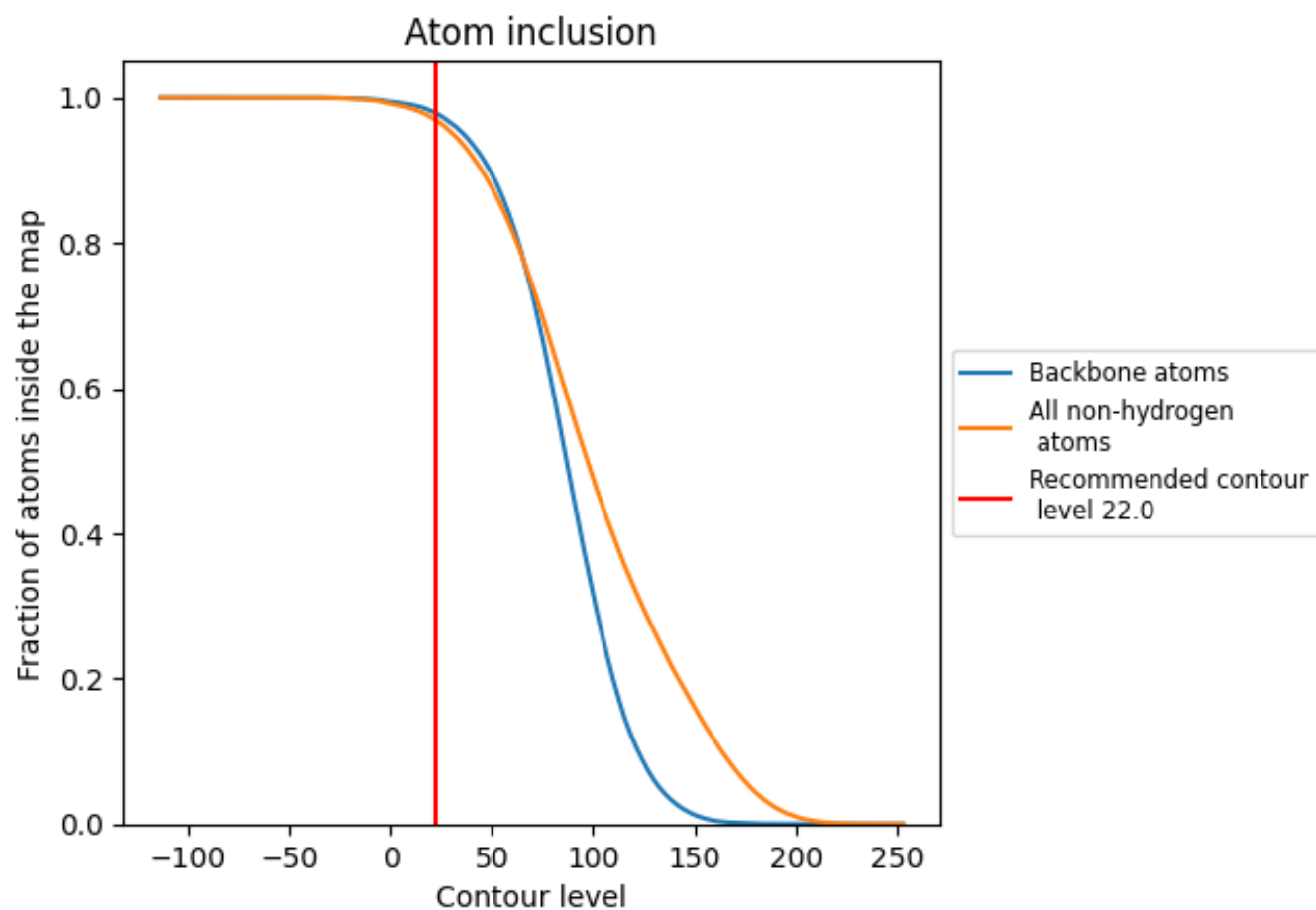
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (22.0).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 97% 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 (22.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9696	 0.1260
A1	 0.9128	 0.1120
A2	 0.4663	 0.0110
A3	 0.9835	 0.1530
AA	 0.9952	 0.1430
AB	 0.9200	 0.1050
AC	 0.9112	 0.0970
AD	 0.9759	 0.0960
AE	 0.8845	 0.0850
AF	 0.8217	 0.0930
AG	 0.9593	 0.1070
AH	 0.9559	 0.1020
AI	 0.9749	 0.0840
AJ	 0.9584	 0.0780
AK	 0.8947	 0.0910
AL	 0.9258	 0.0940
AM	 0.9716	 0.1100
AN	 0.9473	 0.0640
AO	 0.9804	 0.1040
AP	 0.9732	 0.0620
AQ	 0.9626	 0.1070
AR	 0.9092	 0.0770
AS	 0.9538	 0.0810
AT	 0.9614	 0.1110
AU	 0.8745	 0.0990
B0	 0.8997	 0.0370
B1	 0.9551	 0.0880
B2	 0.9658	 0.1380
B3	 0.9657	 0.1170
B4	 0.8848	 0.0850
B5	 0.9299	 0.0630
B6	 0.9538	 0.0900
B7	 0.9268	 0.0670
B8	 0.9430	 0.0620
B9	 0.9521	 0.0520



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Chain	Atom inclusion	Q-score
BA	 0.9933	 0.1450
BC	 0.8759	 0.0490
BD	 0.9383	 0.0750
BE	 0.9415	 0.0870
BF	 0.9724	 0.0950
BG	 0.9732	 0.0890
BH	 0.9807	 0.1240
BJ	 0.8872	 0.0810
BK	 0.9785	 0.0960
BL	 0.7427	 0.1000
BN	 0.9591	 0.0980
BO	 0.9100	 0.0960
BP	 0.9512	 0.0750
BQ	 0.9501	 0.0920
BR	 0.9515	 0.0900
BS	 0.9759	 0.0940
BT	 0.9347	 0.1020
BU	 0.9659	 0.0980
BV	 0.9398	 0.0990
BW	 0.9246	 0.0900
BX	 0.9598	 0.0890
BY	 0.9601	 0.1060
BZ	 0.9729	 0.1180
Ba	 0.9957	 0.1520