



wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 02:13 PM EST

PDB ID : 4V6P
EMDB ID : EMD-5364
Title : Structural characterization of mRNA-tRNA translocation intermediates (class 4b of the six classes)
Authors : Agirrezabala, X.; Liao, H.; Schreiner, E.; Fu, J.; Ortiz-Meoz, R.F.; Schulten, K.; Green, R.; Frank, J.
Deposited on : 2011-12-08
Resolution : 13.50 Å (reported)
Based on initial model : 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

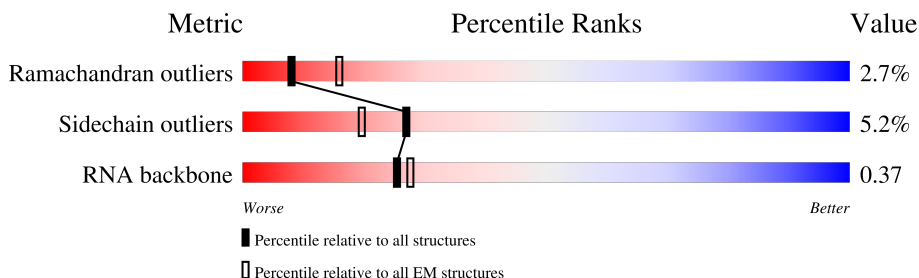
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 13.50 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.





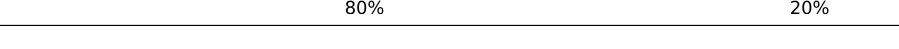
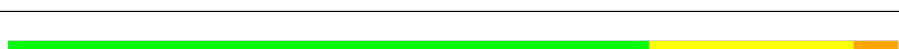



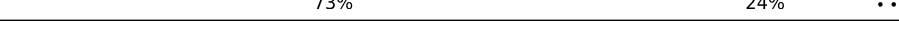



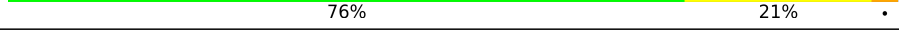

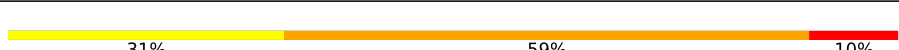


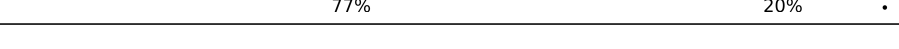







Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	AA	1542	
2	AB	76	
3	AC	47	
4	AD	77	
5	AE	240	
6	AF	232	
7	AG	205	
8	AH	166	

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Mol	Chain	Length	Quality of chain
9	AI	135	
10	AJ	178	
11	AK	129	
12	AL	129	
13	AM	103	
14	AN	128	
15	AO	123	
16	AP	117	
17	AQ	100	
18	AR	88	
19	AS	82	
20	AT	83	
21	AU	74	
22	AV	91	
23	AW	86	
24	AX	70	
25	BA	120	
26	BB	2904	
27	BC	234	
28	BD	272	
29	BE	209	
30	BF	201	
31	BG	178	
32	BH	176	
33	BI	149	

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Mol	Chain	Length	Quality of chain
34	BJ	164	
35	BK	141	
36	BL	142	
37	BM	123	
38	BN	144	
39	BO	136	
40	BP	127	
41	BQ	117	
42	BR	114	
43	BS	117	
44	BT	103	
45	BU	110	
46	BV	100	
47	BW	103	
48	BX	94	
49	BY	84	
50	BZ	77	
51	B0	63	
52	B1	58	
53	B2	70	
54	B3	56	
55	B4	54	
56	B5	46	
57	B6	64	
58	B7	38	

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 152351 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S ribosomal RNA.

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

- Molecule 2 is a RNA chain called A site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	AB	76	Total	C	N	O	P	S	0	0
			1627	731	287	532	75	2		

- Molecule 3 is a RNA chain called mRNA.

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

- Molecule 4 is a RNA chain called P site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	AD	77	Total	C	N	O	P	S	0	0
			1641	734	297	533	76	1		

- Molecule 5 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	240	Total	C	N	O	S	0	0
			1872	1180	332	352	8		

- Molecule 6 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	232	Total	C	N	O	S	0	0
			1822	1149	346	323	4		

- Molecule 7 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 8 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	166	Total	C	N	O	S	0	0
			1225	761	232	226	6		

- Molecule 9 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	135	Total	C	N	O	S	0	0
			1101	677	198	219	7		

- Molecule 10 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	178	Total	C	N	O	S	0	0
			1400	874	269	253	4		

- Molecule 11 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 12 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	129	Total	C	N	O	S	0	0
			1036	642	208	183	3		

- Molecule 13 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	103	Total	C	N	O	S	0	0
			825	514	158	151	2		

- Molecule 14 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	128	Total	C	N	O	S	0	0
			965	595	196	171	3		

- Molecule 15 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 16 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	117	Total	C	N	O	S	0	0
			910	564	183	160	3		

- Molecule 17 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 18 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 19 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 20 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	83	Total	C	N	O	S	0	0
			672	425	124	120	3		

- Molecule 21 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	74	Total	C	N	O	S	0	0
			626	395	123	107	1		

- Molecule 22 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	91	Total	C	N	O	S	0	0
			727	464	139	122	2		

- Molecule 23 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 24 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	70	Total	C	N	O	S	0	0
			590	366	125	98	1		

- Molecule 25 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 26 is a RNA chain called 23S ribosomal RNA.

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

- Molecule 27 is a protein called 50S ribosomal protein L1.

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

- Molecule 28 is a protein called 50S ribosomal protein L2.

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

- Molecule 29 is a protein called 50S ribosomal protein L3.

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

- Molecule 30 is a protein called 50S ribosomal protein L4.

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

- Molecule 31 is a protein called 50S ribosomal protein L5.

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

- Molecule 32 is a protein called 50S ribosomal protein L6.

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

- Molecule 33 is a protein called 50S ribosomal protein L9.

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

- Molecule 34 is a protein called 50S ribosomal protein L10.

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

- Molecule 35 is a protein called 50S ribosomal protein L11.

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

- Molecule 36 is a protein called 50S ribosomal protein L13.

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

- Molecule 37 is a protein called 50S ribosomal protein L14.

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

- Molecule 38 is a protein called 50S ribosomal protein L15.

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

- Molecule 39 is a protein called 50S ribosomal protein L16.

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

- Molecule 40 is a protein called 50S ribosomal protein L17.

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

- Molecule 41 is a protein called 50S ribosomal protein L18.

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

- Molecule 42 is a protein called 50S ribosomal protein L19.

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

- Molecule 43 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	BS	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 44 is a protein called 50S ribosomal protein L21.

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

- Molecule 45 is a protein called 50S ribosomal protein L22.

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

- Molecule 46 is a protein called 50S ribosomal protein L23.

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

- Molecule 47 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	BW	103	Total	C	N	O	S	0	0
			789	498	148	143			

- Molecule 48 is a protein called 50S ribosomal protein L25.

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

- Molecule 49 is a protein called 50S ribosomal protein L27.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	B0	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 52 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	B1	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 53 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	B2	70	Total	C	N	O	S	0	0
			549	339	104	100	6		

- Molecule 54 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	B3	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 55 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
55	B4	54	Total	C	N	O	0	0
			441	284	81	76		

- Molecule 56 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	B5	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

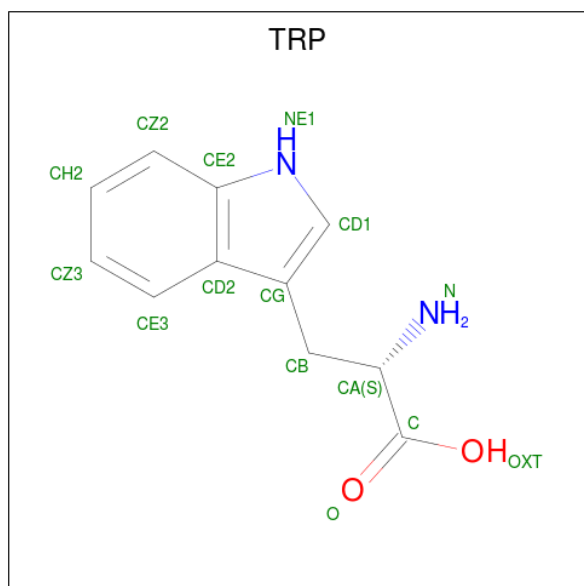
- Molecule 57 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	B6	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 58 is a protein called 50S ribosomal protein L36.

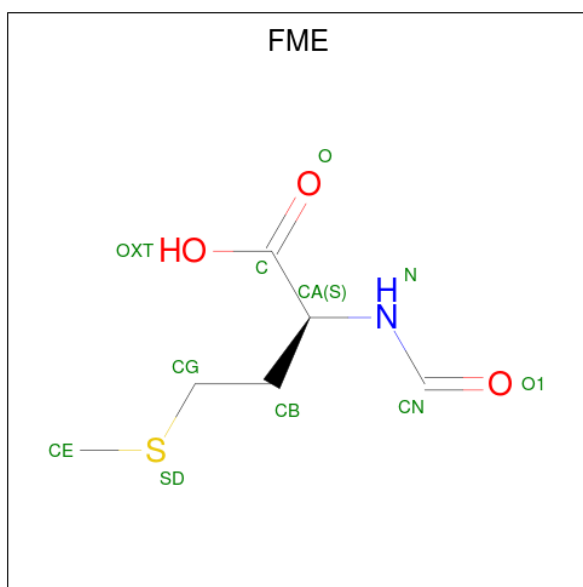
Mol	Chain	Residues	Atoms					AltConf	Trace
58	B7	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 59 is TRYPTOPHAN (three-letter code: TRP) (formula: $C_{11}H_{12}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
59	AB	1	Total	C	N	O	0
			14	11	2	1	

- Molecule 60 is N-FORMYLMETHIONINE (three-letter code: FME) (formula: $C_6H_{11}NO_3S$).

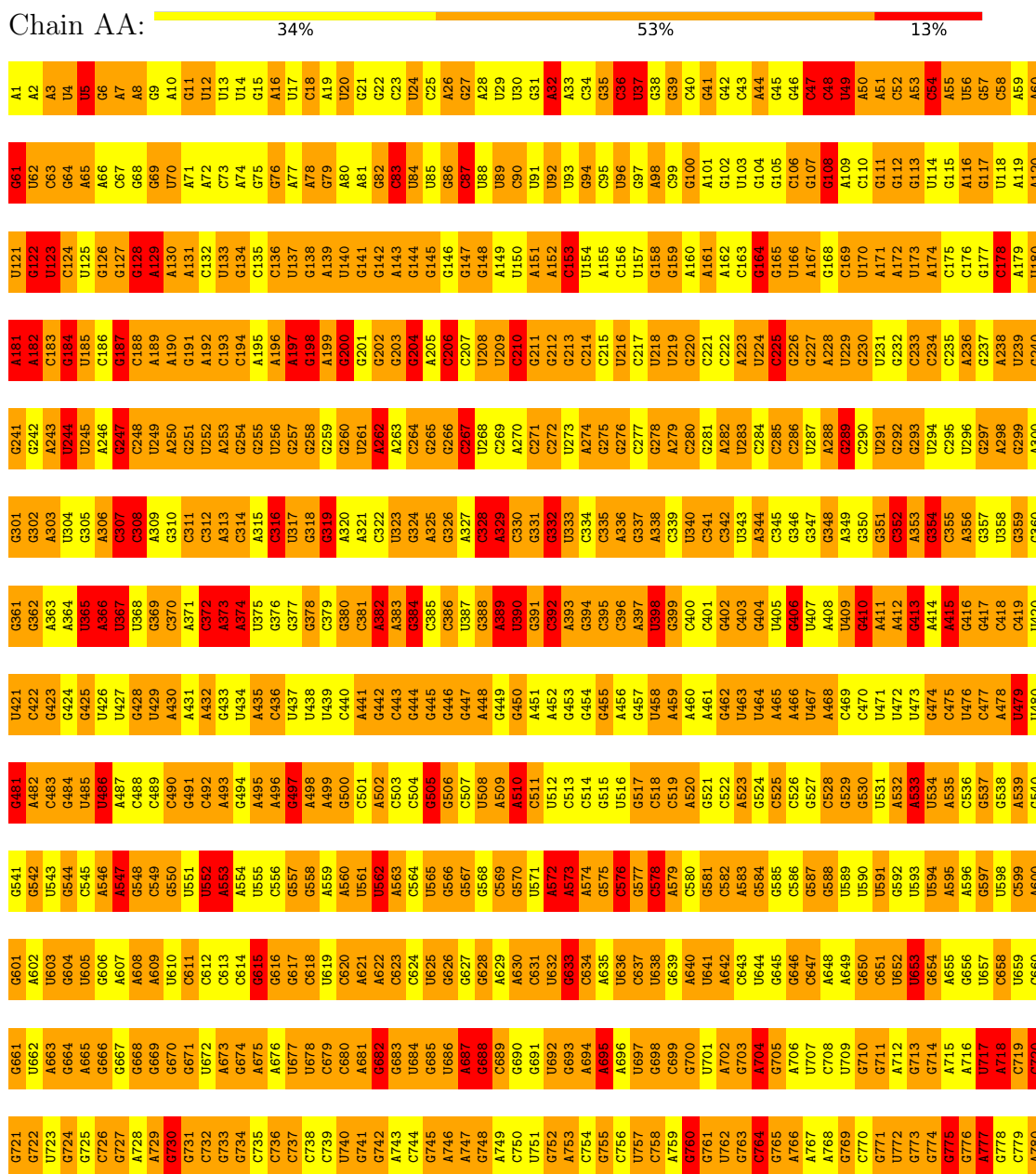


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
60	BB	1	10	6	1	2	1	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S ribosomal RNA



A781	A782	A783	A784	A785	A786	A787	A788	A789	A790	A791	A792	A793	A794	A795	A796	A797	A798	A799	A800	A801	A802	A803	A804	A805	A806	A807	A808	A809	A810	A811	A812	A813	A814	A815	A816	A817	A818	A819	A820	A821	A822	A823	A824	A825	A826	A827	A828	A829	A830	A831	A832	A833	A834	A835	A836	A837	A838	A839	A840
C841	C842	C843	C844	C845	C846	C847	C848	C849	C850	C851	C852	C853	C854	C855	C856	C857	C858	C859	C860	C861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900
A901	A902	A903	A904	A905	A906	A907	A908	A909	A910	A911	A912	A913	A914	A915	A916	A917	A918	A919	A920	A921	A922	A923	A924	A925	A926	A927	A928	A929	A930	A931	A932	A933	A934	A935	A936	A937	A938	A939	A940	A941	A942	A943	A944	A945	A946	A947	A948	A949	A950	A951	A952	A953	A954	A955	A956	A957	A958	A959	A960
U961	U962	U963	U964	U965	U966	U967	U968	U969	U970	U971	U972	U973	U974	U975	U976	U977	U978	U979	U980	U981	U982	U983	U984	U985	U986	U987	U988	U989	U990	U991	U992	U993	U994	U995	U996	U997	U998	U999	C1000	C1001	C1002	C1003	C1004	C1005	C1006	C1007	C1008	C1009	C1010	C1011	C1012	C1013	C1014	C1015	C1016	C1017	C1018	C1019	C1020
A1021	A1022	A1023	A1024	A1025	A1026	A1027	A1028	A1029	A1030	A1031	A1032	A1033	A1034	A1035	A1036	A1037	A1038	A1039	A1040	A1041	A1042	A1043	A1044	A1045	A1046	A1047	A1048	A1049	A1050	A1051	A1052	A1053	A1054	A1055	A1056	A1057	A1058	A1059	A1060	A1061	A1062	A1063	A1064	A1065	A1066	A1067	A1068	A1069	A1070	A1071	A1072	A1073	A1074	A1075	A1076	A1077	A1078	A1079	A1080
A1081	A1082	A1083	A1084	A1085	A1086	A1087	A1088	A1089	A1090	A1091	A1092	A1093	A1094	A1095	A1096	A1097	A1098	A1099	A1100	A1101	A1102	A1103	A1104	A1105	A1106	A1107	A1108	A1109	A1110	A1111	A1112	A1113	A1114	A1115	A1116	A1117	A1118	A1119	A1120	A1121	A1122	A1123	A1124	A1125	A1126	A1127	A1128	A1129	A1130	A1131	A1132	A1133	A1134	A1135	A1136	A1137	A1138	A1139	A1140
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• Molecule 2: A site tRNA

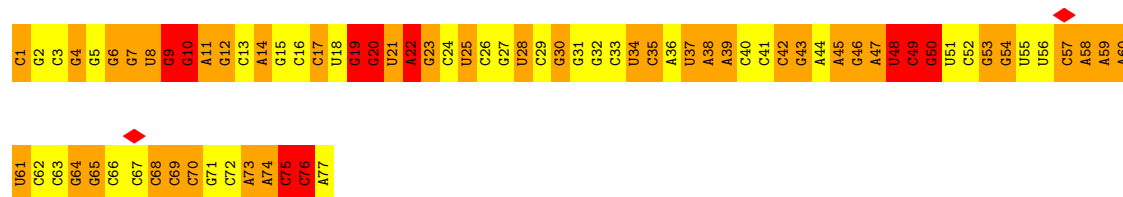


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C61	C62	C63	C64	C65	C66	C67	C68	C69	C70	C71	C72	C73	C74	C75	C76	C77	C78	C79	C80	C81	C82	C83	C84	C85	C86	C87	C88	C89	C90	C91	C92	C93	C94	C95	C96	C97	C98	C99	C100	C101	C102	C103	C104	C105	C106	C107	C108	C109	C110	C111	C112	C113	C114	C115	C116	C117	C118	C119	C120

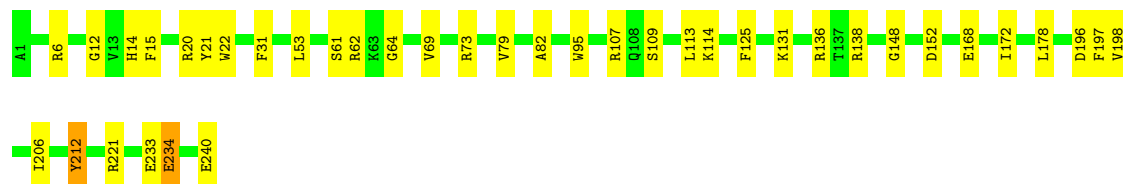
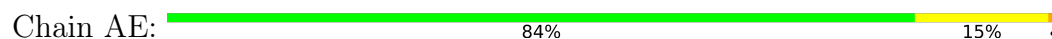
• Molecule 3: mRNA



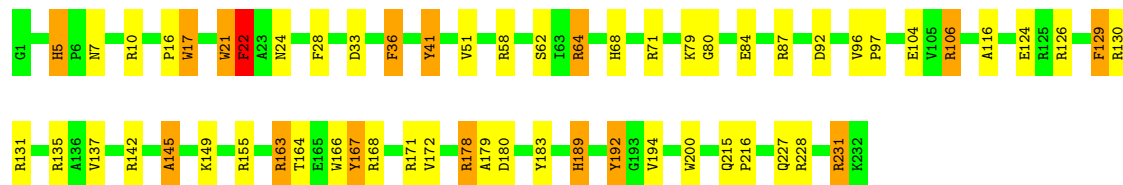
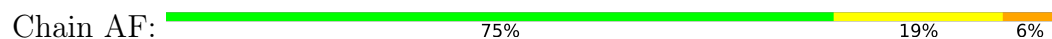
- Molecule 4: P site tRNA



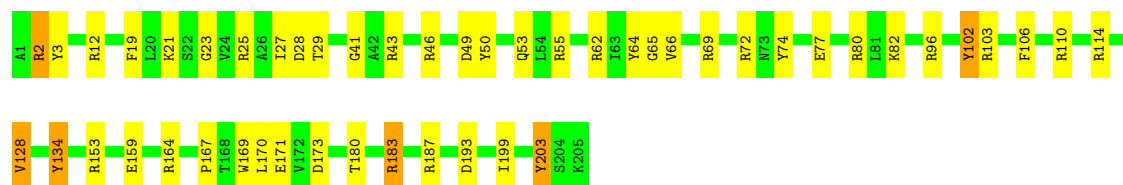
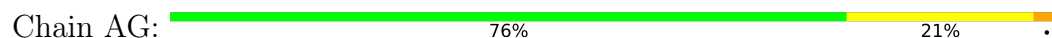
- Molecule 5: 30S ribosomal protein S2



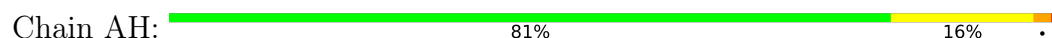
- Molecule 6: 30S ribosomal protein S3



- Molecule 7: 30S ribosomal protein S4

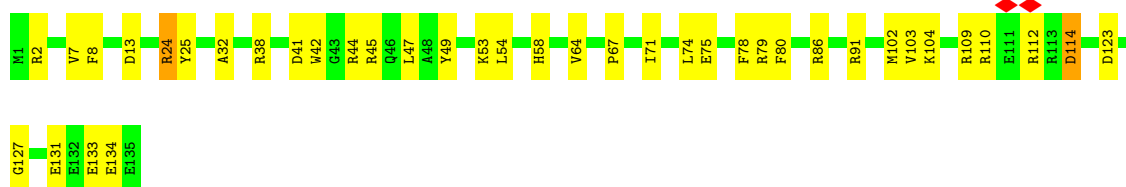


- Molecule 8: 30S ribosomal protein S5

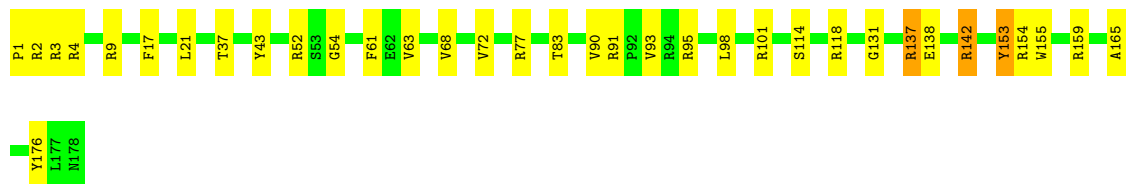
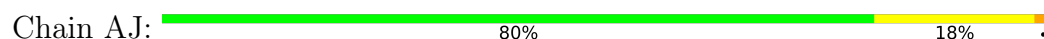




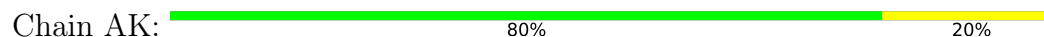
- Molecule 9: 30S ribosomal protein S6



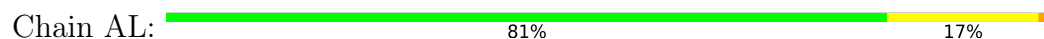
- Molecule 10: 30S ribosomal protein S7



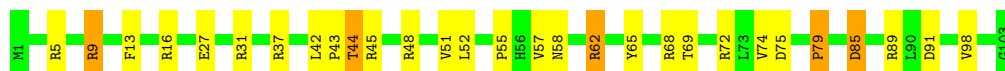
- Molecule 11: 30S ribosomal protein S8



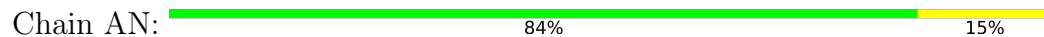
- Molecule 12: 30S ribosomal protein S9



- Molecule 13: 30S ribosomal protein S10



- Molecule 14: 30S ribosomal protein S11

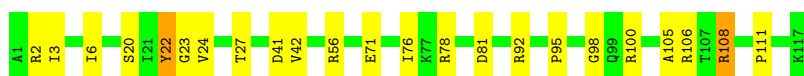
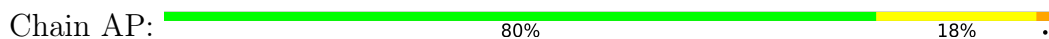




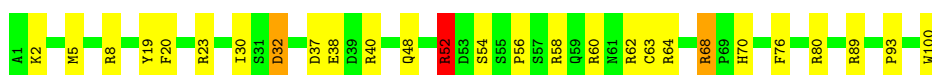
- Molecule 15: 30S ribosomal protein S12



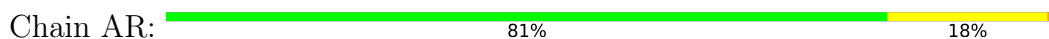
- Molecule 16: 30S ribosomal protein S13



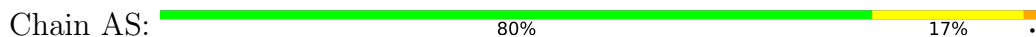
- Molecule 17: 30S ribosomal protein S14



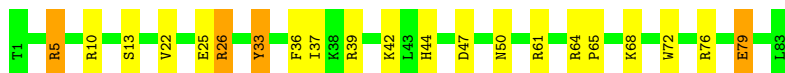
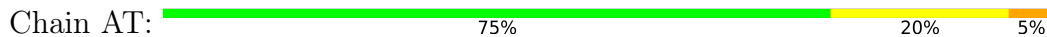
- Molecule 18: 30S ribosomal protein S15



- Molecule 19: 30S ribosomal protein S16

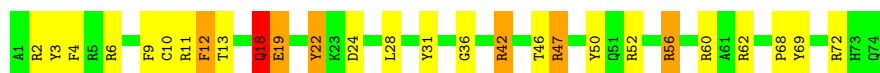


- Molecule 20: 30S ribosomal protein S17

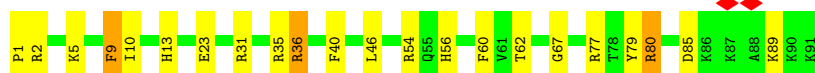
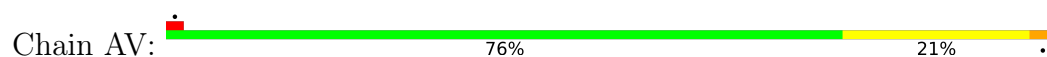


- Molecule 21: 30S ribosomal protein S18

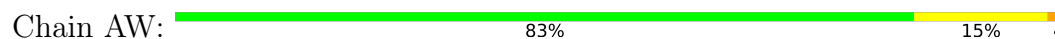




- Molecule 22: 30S ribosomal protein S19



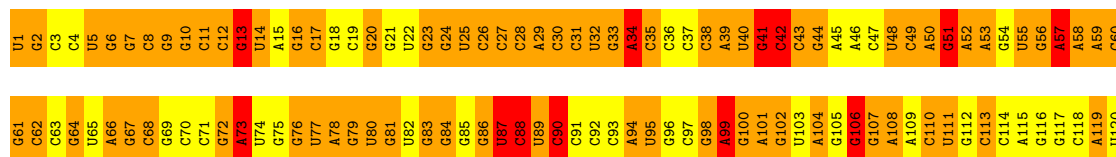
- Molecule 23: 30S ribosomal protein S20



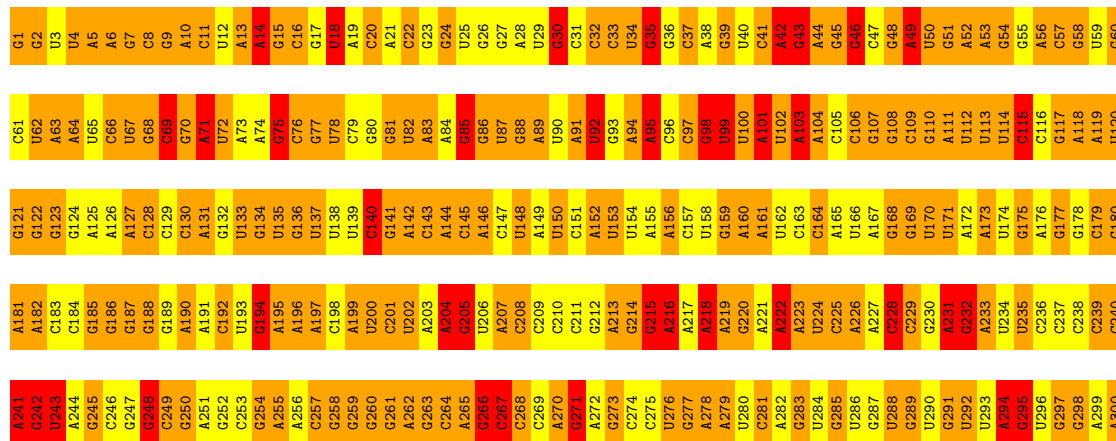
- Molecule 24: 30S ribosomal protein S21



- Molecule 25: 5S ribosomal RNA



- Molecule 26: 23S ribosomal RNA

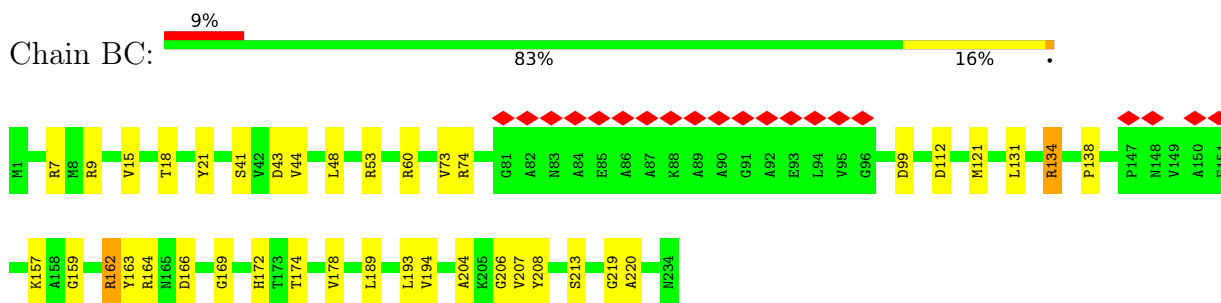


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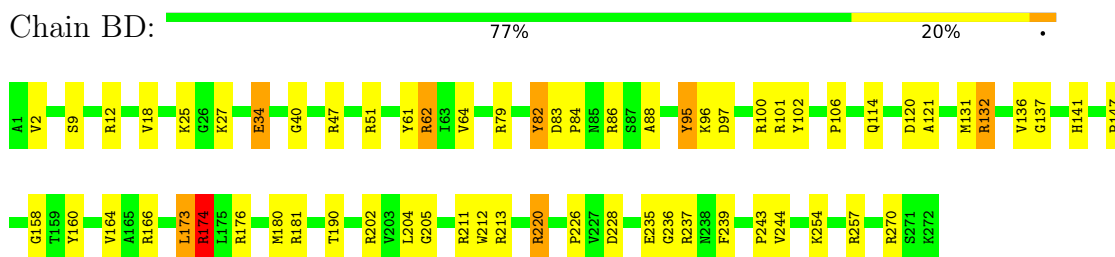
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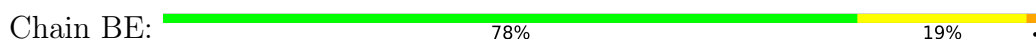
• Molecule 27: 50S ribosomal protein L1

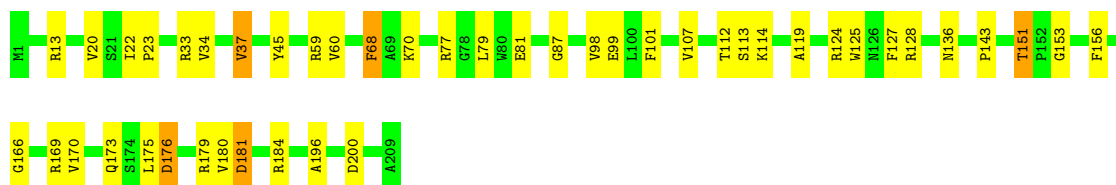


• Molecule 28: 50S ribosomal protein L2



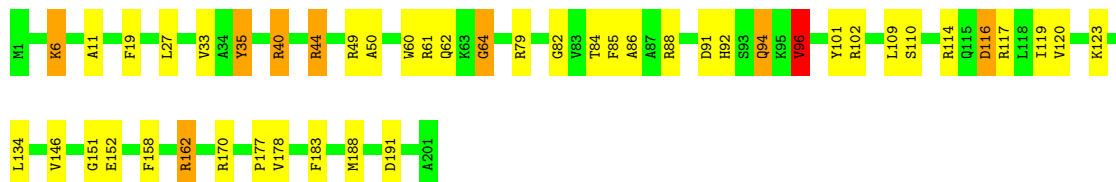
• Molecule 29: 50S ribosomal protein L3





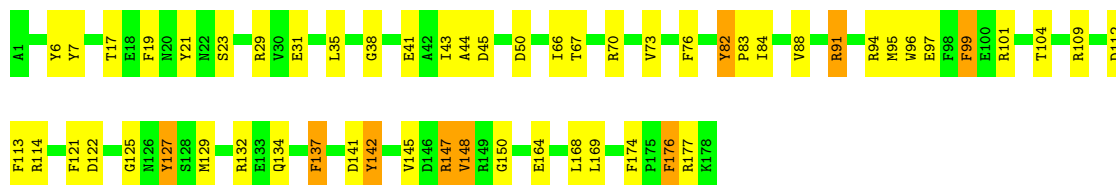
- Molecule 30: 50S ribosomal protein L4

Chain BF: 77% 18% .



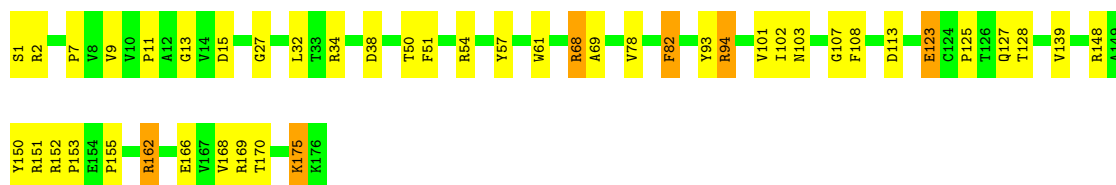
- Molecule 31: 50S ribosomal protein L5

Chain BG: 69% 26% 5% .



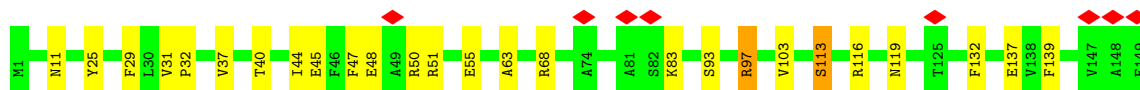
- Molecule 32: 50S ribosomal protein L6

Chain BH: 74% 22% .



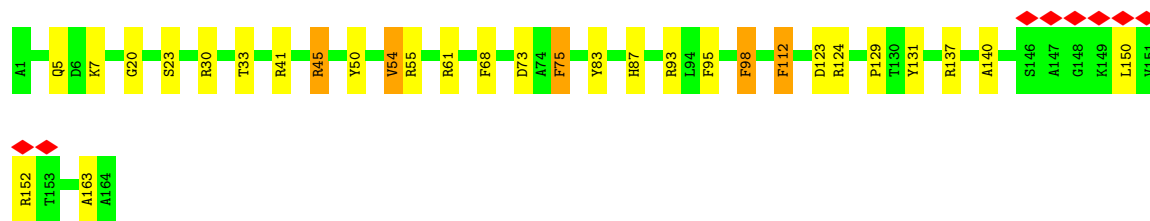
- Molecule 33: 50S ribosomal protein L9

Chain BI: 5% 83% 16% .

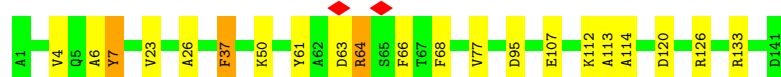
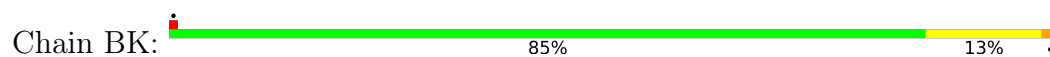


- Molecule 34: 50S ribosomal protein L10

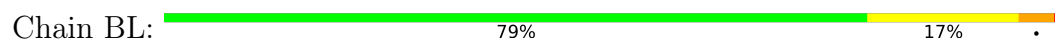
Chain BJ: 5% 82% 15% .



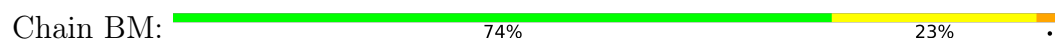
- Molecule 35: 50S ribosomal protein L11



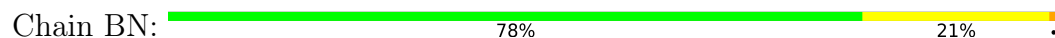
- Molecule 36: 50S ribosomal protein L13



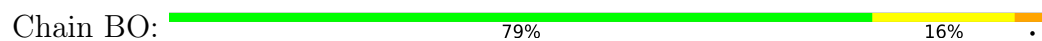
- Molecule 37: 50S ribosomal protein L14



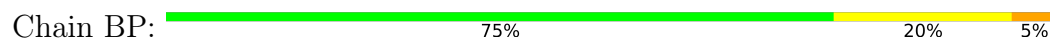
- Molecule 38: 50S ribosomal protein L15

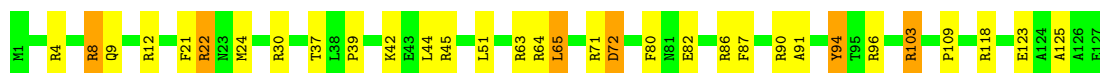


- Molecule 39: 50S ribosomal protein L16

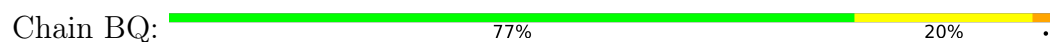


- Molecule 40: 50S ribosomal protein L17





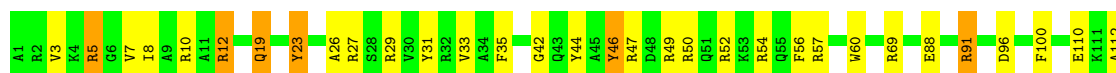
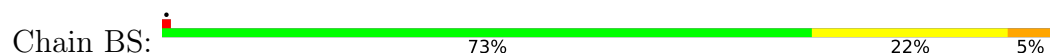
- Molecule 41: 50S ribosomal protein L18



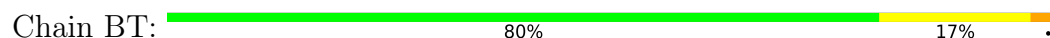
- Molecule 42: 50S ribosomal protein L19



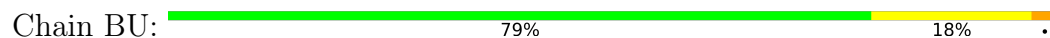
- Molecule 43: 50S ribosomal protein L20



- Molecule 44: 50S ribosomal protein L21

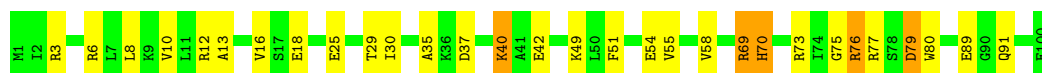


- Molecule 45: 50S ribosomal protein L22

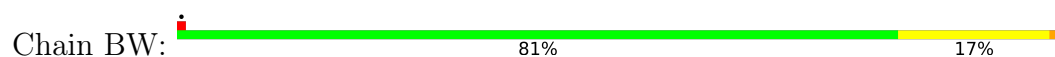


- Molecule 46: 50S ribosomal protein L23

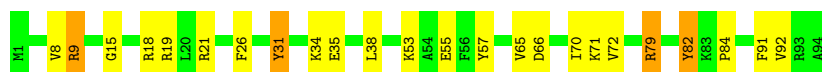
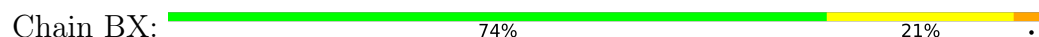




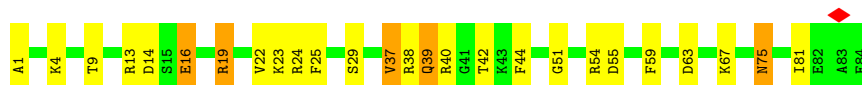
- Molecule 47: 50S ribosomal protein L24



- Molecule 48: 50S ribosomal protein L25



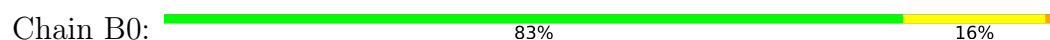
- Molecule 49: 50S ribosomal protein L27



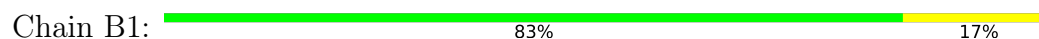
- Molecule 50: 50S ribosomal protein L28



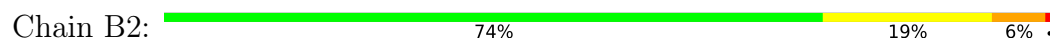
- Molecule 51: 50S ribosomal protein L29

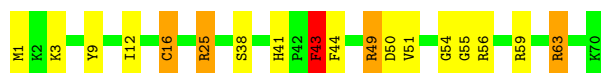


- Molecule 52: 50S ribosomal protein L30

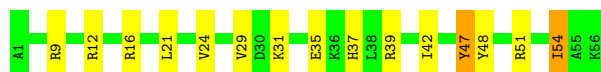
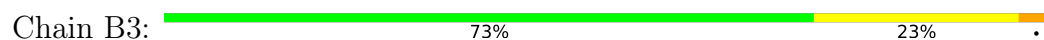


- Molecule 53: 50S ribosomal protein L31

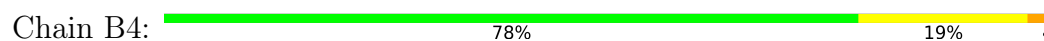




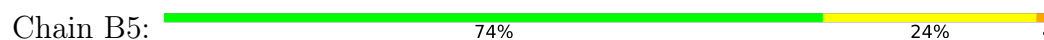
- Molecule 54: 50S ribosomal protein L32



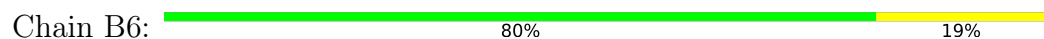
- Molecule 55: 50S ribosomal protein L33



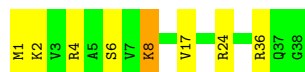
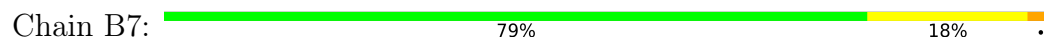
- Molecule 56: 50S ribosomal protein L34



- Molecule 57: 50S ribosomal protein L35



- Molecule 58: 50S ribosomal protein L36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	21000	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Volumes were CTF-corrected in defocus groups	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	25	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	58269	Depositor
Image detector	TVIPS TEMCAM-F415 (4k x 4k)	Depositor
Maximum map value	1.536	Depositor
Minimum map value	-0.480	Depositor
Average map value	0.031	Depositor
Map value standard deviation	0.200	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	375.0, 375.0, 375.0	wwPDB
Map dimensions	250, 250, 250	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.5, 1.5, 1.5	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: OMU, MIA, 7MG, 2MG, 1MG, MA6, OMG, 6MZ, 3TD, CH, 2MA, 4SU, PSU, UR3, H2U, FME, 5MU, 4OC, OMC, 5MC

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	AA	3.07	3842/36769 (10.4%)	3.54	8339/57354 (14.5%)
2	AB	3.16	182/1600 (11.4%)	3.61	372/2492 (14.9%)
3	AC	3.10	124/1108 (11.2%)	3.72	275/1724 (16.0%)
4	AD	3.15	181/1721 (10.5%)	3.52	392/2683 (14.6%)
5	AE	1.46	6/1904 (0.3%)	1.85	30/2565 (1.2%)
6	AF	1.47	6/1852 (0.3%)	2.14	61/2490 (2.4%)
7	AG	1.54	7/1665 (0.4%)	1.95	47/2227 (2.1%)
8	AH	1.48	3/1239 (0.2%)	1.96	33/1664 (2.0%)
9	AI	1.50	5/1121 (0.4%)	1.99	30/1509 (2.0%)
10	AJ	1.51	5/1422 (0.4%)	1.96	30/1908 (1.6%)
11	AK	1.47	6/989 (0.6%)	1.83	20/1326 (1.5%)
12	AL	1.57	2/1048 (0.2%)	1.98	28/1394 (2.0%)
13	AM	1.46	3/835 (0.4%)	2.17	31/1127 (2.8%)
14	AN	1.51	2/982 (0.2%)	1.85	20/1323 (1.5%)
15	AO	1.51	3/969 (0.3%)	2.08	29/1300 (2.2%)
16	AP	1.55	1/919 (0.1%)	1.88	20/1226 (1.6%)
17	AQ	1.45	4/817 (0.5%)	2.05	21/1088 (1.9%)
18	AR	1.50	2/724 (0.3%)	2.03	16/966 (1.7%)
19	AS	1.50	4/659 (0.6%)	2.09	14/884 (1.6%)
20	AT	1.46	2/681 (0.3%)	2.02	24/913 (2.6%)
21	AU	1.68	6/637 (0.9%)	2.13	28/851 (3.3%)
22	AV	1.44	3/744 (0.4%)	1.80	16/995 (1.6%)
23	AW	1.44	0/676	1.87	16/895 (1.8%)
24	AX	1.54	3/598 (0.5%)	2.37	30/792 (3.8%)
25	BA	2.99	281/2869 (9.8%)	3.51	651/4474 (14.6%)
26	BB	3.08	7353/69257 (10.6%)	3.54	15900/108040 (14.7%)
27	BC	1.44	5/1748 (0.3%)	1.89	32/2355 (1.4%)
28	BD	1.55	11/2131 (0.5%)	1.90	52/2863 (1.8%)
29	BE	1.44	3/1586 (0.2%)	1.91	40/2134 (1.9%)
30	BF	1.46	7/1571 (0.4%)	1.94	37/2113 (1.8%)
31	BG	1.58	11/1444 (0.8%)	2.03	47/1937 (2.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	BH	1.57	11/1343 (0.8%)	1.89	39/1816 (2.1%)
33	BI	1.56	7/1122 (0.6%)	1.83	20/1515 (1.3%)
34	BJ	1.49	3/1247 (0.2%)	1.95	37/1679 (2.2%)
35	BK	1.46	3/1046 (0.3%)	1.85	17/1410 (1.2%)
36	BL	1.48	6/1152 (0.5%)	1.94	27/1551 (1.7%)
37	BM	1.49	3/956 (0.3%)	2.06	24/1279 (1.9%)
38	BN	1.52	5/1062 (0.5%)	1.88	26/1413 (1.8%)
39	BO	1.49	4/1093 (0.4%)	1.95	25/1460 (1.7%)
40	BP	1.52	4/1021 (0.4%)	2.12	32/1364 (2.3%)
41	BQ	1.54	4/910 (0.4%)	1.99	23/1219 (1.9%)
42	BR	1.55	5/929 (0.5%)	1.93	26/1242 (2.1%)
43	BS	1.57	10/960 (1.0%)	2.05	33/1278 (2.6%)
44	BT	1.50	3/829 (0.4%)	1.84	16/1107 (1.4%)
45	BU	1.49	1/864 (0.1%)	1.95	26/1156 (2.2%)
46	BV	1.54	3/794 (0.4%)	1.91	18/1060 (1.7%)
47	BW	1.53	1/797 (0.1%)	1.83	15/1062 (1.4%)
48	BX	1.46	3/766 (0.4%)	1.89	22/1025 (2.1%)
49	BY	1.57	4/642 (0.6%)	2.03	20/848 (2.4%)
50	BZ	1.58	2/635 (0.3%)	1.97	14/848 (1.7%)
51	B0	1.43	1/510 (0.2%)	2.10	9/677 (1.3%)
52	B1	1.40	0/453	2.08	9/605 (1.5%)
53	B2	1.45	1/559 (0.2%)	2.02	17/745 (2.3%)
54	B3	1.52	4/450 (0.9%)	1.89	10/599 (1.7%)
55	B4	1.48	0/448	1.91	6/594 (1.0%)
56	B5	1.65	1/380 (0.3%)	2.10	13/498 (2.6%)
57	B6	1.47	0/513	1.90	7/676 (1.0%)
58	B7	1.51	2/303 (0.7%)	2.07	8/397 (2.0%)
All	All	2.69	12164/164069 (7.4%)	3.18	27220/244735 (11.1%)

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	AA	0	881
2	AB	0	40
3	AC	0	28
4	AD	0	42
5	AE	0	3
6	AF	0	11
7	AG	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
8	AH	0	2
9	AI	0	4
10	AJ	0	4
11	AK	0	2
12	AL	0	2
14	AN	0	3
15	AO	0	4
16	AP	0	1
17	AQ	0	4
18	AR	0	1
19	AS	0	2
20	AT	0	1
21	AU	0	3
22	AV	0	2
23	AW	0	1
24	AX	0	2
25	BA	0	75
26	BB	0	1720
27	BC	0	2
28	BD	0	9
29	BE	0	4
30	BF	0	3
31	BG	0	6
32	BH	0	3
33	BI	0	1
34	BJ	0	5
35	BK	0	3
36	BL	0	2
37	BM	0	5
38	BN	0	2
39	BO	0	3
40	BP	0	4
41	BQ	0	6
42	BR	0	4
43	BS	0	6
44	BT	0	4
45	BU	0	5
46	BV	0	2
48	BX	0	4
49	BY	0	5
50	BZ	0	2
51	B0	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
52	B1	0	1
53	B2	0	4
54	B3	0	1
55	B4	0	4
56	B5	0	2
57	B6	0	2
All	All	0	2949

The worst 5 of 12164 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	BB	659	G	N7-C5	18.05	1.50	1.39
26	BB	2104	C	P-O5'	17.37	1.77	1.59
26	BB	2168	G	N7-C5	16.73	1.49	1.39
26	BB	268	C	N1-C6	16.25	1.47	1.37
1	AA	1072	G	P-O5'	16.08	1.75	1.59

The worst 5 of 27220 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	B0	48	ARG	NE-CZ-NH1	24.22	132.41	120.30
26	BB	2494	G	N3-C4-C5	-22.56	117.32	128.60
51	B0	48	ARG	NE-CZ-NH2	-21.50	109.55	120.30
26	BB	93	G	C2-N3-C4	20.63	122.22	111.90
26	BB	1478	G	N1-C6-O6	-20.46	107.62	119.90

There are no chirality outliers.

5 of 2949 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	11	G	Sidechain
1	AA	3	A	Sidechain
1	AA	4	U	Sidechain
1	AA	5	U	Sidechain
1	AA	6	G	Sidechain

5.2 Too-close contacts [i](#)

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	33089	0	16619	0	0
2	AB	1627	0	844	0	0
3	AC	993	0	501	0	0
4	AD	1641	0	840	0	0
5	AE	1872	0	1885	0	0
6	AF	1822	0	1913	0	0
7	AG	1643	0	1710	0	0
8	AH	1225	0	1273	0	0
9	AI	1101	0	1050	0	0
10	AJ	1400	0	1449	0	0
11	AK	979	0	1034	0	0
12	AL	1036	0	1084	0	0
13	AM	825	0	865	0	0
14	AN	965	0	997	0	0
15	AO	955	0	1019	0	0
16	AP	910	0	981	0	0
17	AQ	805	0	847	0	0
18	AR	716	0	742	0	0
19	AS	649	0	666	0	0
20	AT	672	0	716	0	0
21	AU	626	0	651	0	0
22	AV	727	0	769	0	0
23	AW	670	0	722	0	0
24	AX	590	0	631	0	0
25	BA	2566	0	1296	0	0
26	BB	62351	0	31238	0	0
27	BC	1733	0	1824	0	0
28	BD	2092	0	2170	0	0
29	BE	1565	0	1616	0	0
30	BF	1552	0	1619	0	0
31	BG	1420	0	1460	0	0
32	BH	1323	0	1374	0	0
33	BI	1111	0	1148	0	0
34	BJ	1233	0	1283	0	0
35	BK	1032	0	1088	0	0
36	BL	1129	0	1162	0	0
37	BM	947	0	1023	0	0
38	BN	1053	0	1129	0	0
39	BO	1074	0	1157	0	0
40	BP	1008	0	1045	0	0
41	BQ	900	0	935	0	0
42	BR	917	0	965	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
43	BS	947	0	1022	0	0
44	BT	816	0	839	0	0
45	BU	857	0	922	0	0
46	BV	787	0	846	0	0
47	BW	789	0	847	0	0
48	BX	753	0	780	0	0
49	BY	634	0	656	0	0
50	BZ	625	0	655	0	0
51	B0	509	0	543	0	0
52	B1	449	0	491	0	0
53	B2	549	0	552	0	0
54	B3	444	0	461	0	0
55	B4	441	0	485	0	0
56	B5	377	0	418	0	0
57	B6	504	0	574	0	0
58	B7	302	0	343	0	0
59	AB	14	0	9	0	0
60	BB	10	0	10	0	0
All	All	152351	0	103793	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 [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	AE	238/240 (99%)	211 (89%)	24 (10%)	3 (1%)	12	48
6	AF	230/232 (99%)	204 (89%)	20 (9%)	6 (3%)	5	31
7	AG	203/205 (99%)	182 (90%)	17 (8%)	4 (2%)	7	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AH	164/166 (99%)	146 (89%)	15 (9%)	3 (2%)	8	40
9	AI	133/135 (98%)	118 (89%)	12 (9%)	3 (2%)	6	34
10	AJ	176/178 (99%)	163 (93%)	11 (6%)	2 (1%)	14	52
11	AK	127/129 (98%)	116 (91%)	9 (7%)	2 (2%)	9	44
12	AL	127/129 (98%)	118 (93%)	7 (6%)	2 (2%)	9	44
13	AM	101/103 (98%)	92 (91%)	5 (5%)	4 (4%)	3	23
14	AN	126/128 (98%)	111 (88%)	15 (12%)	0	100	100
15	AO	121/123 (98%)	103 (85%)	14 (12%)	4 (3%)	4	26
16	AP	115/117 (98%)	101 (88%)	11 (10%)	3 (3%)	5	31
17	AQ	98/100 (98%)	79 (81%)	13 (13%)	6 (6%)	1	17
18	AR	86/88 (98%)	82 (95%)	3 (4%)	1 (1%)	13	50
19	AS	80/82 (98%)	75 (94%)	4 (5%)	1 (1%)	12	48
20	AT	81/83 (98%)	66 (82%)	14 (17%)	1 (1%)	13	50
21	AU	72/74 (97%)	63 (88%)	6 (8%)	3 (4%)	3	22
22	AV	89/91 (98%)	79 (89%)	6 (7%)	4 (4%)	2	22
23	AW	84/86 (98%)	78 (93%)	4 (5%)	2 (2%)	6	33
24	AX	68/70 (97%)	53 (78%)	13 (19%)	2 (3%)	4	29
27	BC	232/234 (99%)	207 (89%)	20 (9%)	5 (2%)	6	35
28	BD	270/272 (99%)	232 (86%)	30 (11%)	8 (3%)	4	28
29	BE	207/209 (99%)	171 (83%)	31 (15%)	5 (2%)	6	33
30	BF	199/201 (99%)	171 (86%)	16 (8%)	12 (6%)	1	17
31	BG	176/178 (99%)	142 (81%)	24 (14%)	10 (6%)	1	18
32	BH	174/176 (99%)	149 (86%)	22 (13%)	3 (2%)	9	42
33	BI	147/149 (99%)	124 (84%)	21 (14%)	2 (1%)	11	46
34	BJ	162/164 (99%)	147 (91%)	13 (8%)	2 (1%)	13	50
35	BK	139/141 (99%)	126 (91%)	12 (9%)	1 (1%)	22	63
36	BL	140/142 (99%)	112 (80%)	21 (15%)	7 (5%)	2	20
37	BM	121/123 (98%)	104 (86%)	13 (11%)	4 (3%)	4	26
38	BN	142/144 (99%)	121 (85%)	17 (12%)	4 (3%)	5	30
39	BO	134/136 (98%)	116 (87%)	14 (10%)	4 (3%)	4	28
40	BP	125/127 (98%)	116 (93%)	8 (6%)	1 (1%)	19	60

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	BQ	115/117 (98%)	109 (95%)	4 (4%)	2 (2%)	9	42
42	BR	112/114 (98%)	88 (79%)	22 (20%)	2 (2%)	8	40
43	BS	115/117 (98%)	106 (92%)	7 (6%)	2 (2%)	9	42
44	BT	101/103 (98%)	90 (89%)	8 (8%)	3 (3%)	4	28
45	BU	108/110 (98%)	101 (94%)	4 (4%)	3 (3%)	5	30
46	BV	98/100 (98%)	78 (80%)	14 (14%)	6 (6%)	1	17
47	BW	101/103 (98%)	85 (84%)	13 (13%)	3 (3%)	4	28
48	BX	92/94 (98%)	82 (89%)	9 (10%)	1 (1%)	14	52
49	BY	82/84 (98%)	60 (73%)	18 (22%)	4 (5%)	2	20
50	BZ	75/77 (97%)	65 (87%)	6 (8%)	4 (5%)	2	19
51	B0	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	9	44
52	B1	56/58 (97%)	50 (89%)	5 (9%)	1 (2%)	8	40
53	B2	68/70 (97%)	45 (66%)	18 (26%)	5 (7%)	1	14
54	B3	54/56 (96%)	44 (82%)	9 (17%)	1 (2%)	8	38
55	B4	52/54 (96%)	45 (86%)	4 (8%)	3 (6%)	1	18
56	B5	44/46 (96%)	40 (91%)	2 (4%)	2 (4%)	2	22
57	B6	62/64 (97%)	54 (87%)	6 (10%)	2 (3%)	4	26
58	B7	36/38 (95%)	31 (86%)	4 (11%)	1 (3%)	5	30
All	All	6319/6423 (98%)	5506 (87%)	643 (10%)	170 (3%)	8	31

5 of 170 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	AL	86	LEU
13	AM	42	LEU
13	AM	57	VAL
16	AP	22	TYR
21	AU	11	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	
5	AE	198/198 (100%)	191 (96%)	7 (4%)	36	59
6	AF	189/189 (100%)	176 (93%)	13 (7%)	15	40
7	AG	172/172 (100%)	165 (96%)	7 (4%)	30	55
8	AH	125/125 (100%)	119 (95%)	6 (5%)	25	51
9	AI	116/116 (100%)	109 (94%)	7 (6%)	19	44
10	AJ	146/146 (100%)	139 (95%)	7 (5%)	25	51
11	AK	104/104 (100%)	102 (98%)	2 (2%)	57	75
12	AL	106/106 (100%)	104 (98%)	2 (2%)	57	75
13	AM	90/90 (100%)	82 (91%)	8 (9%)	9	30
14	AN	98/98 (100%)	95 (97%)	3 (3%)	40	62
15	AO	103/103 (100%)	95 (92%)	8 (8%)	12	36
16	AP	95/95 (100%)	90 (95%)	5 (5%)	22	47
17	AQ	83/83 (100%)	82 (99%)	1 (1%)	71	83
18	AR	76/76 (100%)	74 (97%)	2 (3%)	46	66
19	AS	65/65 (100%)	63 (97%)	2 (3%)	40	62
20	AT	77/77 (100%)	71 (92%)	6 (8%)	12	36
21	AU	64/64 (100%)	59 (92%)	5 (8%)	12	36
22	AV	78/78 (100%)	72 (92%)	6 (8%)	13	37
23	AW	65/65 (100%)	62 (95%)	3 (5%)	27	52
24	AX	60/60 (100%)	54 (90%)	6 (10%)	7	26
27	BC	181/181 (100%)	171 (94%)	10 (6%)	21	47
28	BD	217/217 (100%)	208 (96%)	9 (4%)	30	55
29	BE	164/164 (100%)	156 (95%)	8 (5%)	25	50
30	BF	165/165 (100%)	157 (95%)	8 (5%)	25	51
31	BG	149/149 (100%)	141 (95%)	8 (5%)	22	47
32	BH	137/137 (100%)	128 (93%)	9 (7%)	16	41
33	BI	114/114 (100%)	108 (95%)	6 (5%)	22	47
34	BJ	122/122 (100%)	118 (97%)	4 (3%)	38	61
35	BK	109/109 (100%)	106 (97%)	3 (3%)	43	65
36	BL	116/116 (100%)	111 (96%)	5 (4%)	29	53
37	BM	104/104 (100%)	97 (93%)	7 (7%)	16	41

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
38	BN	103/103 (100%)	97 (94%)	6 (6%)	20	45
39	BO	109/109 (100%)	101 (93%)	8 (7%)	14	39
40	BP	103/103 (100%)	97 (94%)	6 (6%)	20	45
41	BQ	87/87 (100%)	83 (95%)	4 (5%)	27	52
42	BR	99/99 (100%)	91 (92%)	8 (8%)	11	35
43	BS	89/89 (100%)	87 (98%)	2 (2%)	52	71
44	BT	84/84 (100%)	79 (94%)	5 (6%)	19	44
45	BU	93/93 (100%)	92 (99%)	1 (1%)	73	84
46	BV	84/84 (100%)	75 (89%)	9 (11%)	6	23
47	BW	84/84 (100%)	79 (94%)	5 (6%)	19	44
48	BX	78/78 (100%)	75 (96%)	3 (4%)	33	57
49	BY	62/62 (100%)	60 (97%)	2 (3%)	39	61
50	BZ	67/67 (100%)	63 (94%)	4 (6%)	19	44
51	B0	55/55 (100%)	53 (96%)	2 (4%)	35	59
52	B1	48/48 (100%)	46 (96%)	2 (4%)	30	54
53	B2	62/62 (100%)	57 (92%)	5 (8%)	11	35
54	B3	47/47 (100%)	42 (89%)	5 (11%)	6	24
55	B4	48/48 (100%)	47 (98%)	1 (2%)	53	72
56	B5	38/38 (100%)	37 (97%)	1 (3%)	46	66
57	B6	51/51 (100%)	45 (88%)	6 (12%)	5	20
58	B7	34/34 (100%)	32 (94%)	2 (6%)	19	45
All	All	5213/5213 (100%)	4943 (95%)	270 (5%)	27	48

5 of 270 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
46	BV	91	GLN
48	BX	35	GLU
55	B4	21	THR
23	AW	7	LYS
22	AV	46	LEU

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
1	AA	1538/1542 (99%)	291 (18%)	99 (6%)
2	AB	74/76 (97%)	23 (31%)	6 (8%)
25	BA	119/120 (99%)	16 (13%)	10 (8%)
26	BB	2898/2904 (99%)	544 (18%)	186 (6%)
3	AC	46/47 (97%)	18 (39%)	6 (13%)
4	AD	76/77 (98%)	17 (22%)	4 (5%)
All	All	4751/4766 (99%)	909 (19%)	311 (6%)

5 of 909 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	AA	8	A
1	AA	32	A
1	AA	36	C
1	AA	47	C
1	AA	48	C

5 of 311 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	BB	1778	U
26	BB	2602	A
26	BB	1927	A
26	BB	2223	G
26	BB	2791	G

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

49 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
26	1MG	BB	745	26	18,26,27	1.62	4 (22%)	19,39,42	1.84	6 (31%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PSU	AA	516	1	18,21,22	1.99	7 (38%)	22,30,33	3.00	13 (59%)
1	2MG	AA	1207	1	18,26,27	1.67	5 (27%)	16,38,41	2.04	5 (31%)
26	7MG	BB	2069	26	22,26,27	3.61	6 (27%)	29,39,42	1.82	4 (13%)
26	2MG	BB	2445	26	18,26,27	1.92	4 (22%)	16,38,41	1.23	1 (6%)
1	MA6	AA	1519	1	19,26,27	1.52	4 (21%)	18,38,41	1.54	4 (22%)
2	OMC	AB	32	2	19,22,23	1.20	2 (10%)	26,31,34	1.31	4 (15%)
26	PSU	BB	1917	26	18,21,22	1.98	2 (11%)	22,30,33	1.77	5 (22%)
1	2MG	AA	1516	1	18,26,27	2.24	10 (55%)	16,38,41	1.33	3 (18%)
26	H2U	BB	2449	26	18,21,22	1.51	2 (11%)	21,30,33	1.85	5 (23%)
4	4SU	AD	8	4	18,21,22	2.10	5 (27%)	26,30,33	1.68	7 (26%)
26	PSU	BB	2504	26	18,21,22	1.85	4 (22%)	22,30,33	1.65	5 (22%)
1	MA6	AA	1518	1	19,26,27	1.32	2 (10%)	18,38,41	1.62	5 (27%)
26	OMC	BB	2498	26	19,22,23	1.21	2 (10%)	26,31,34	1.64	5 (19%)
2	MIA	AB	37	2	24,31,32	2.36	9 (37%)	26,44,47	2.16	6 (23%)
1	2MG	AA	966	1	18,26,27	1.16	1 (5%)	16,38,41	1.00	0
4	H2U	AD	21	4	18,21,22	1.57	2 (11%)	21,30,33	1.55	5 (23%)
26	6MZ	BB	1618	26	18,25,26	1.78	6 (33%)	16,36,39	1.68	3 (18%)
2	H2U	AB	20	2	18,21,22	1.56	4 (22%)	21,30,33	1.87	7 (33%)
4	5MU	AD	55	4	19,22,23	1.46	2 (10%)	28,32,35	1.88	7 (25%)
2	5MU	AB	54	2	19,22,23	1.56	4 (21%)	28,32,35	1.93	9 (32%)
1	5MC	AA	967	1	18,22,23	1.39	3 (16%)	26,32,35	1.86	5 (19%)
1	7MG	AA	527	1	22,26,27	4.77	4 (18%)	29,39,42	1.96	7 (24%)
1	UR3	AA	1498	1	19,22,23	1.26	3 (15%)	26,32,35	1.27	3 (11%)
26	5MU	BB	747	26	19,22,23	1.58	4 (21%)	28,32,35	2.85	8 (28%)
26	OMU	BB	2552	26	19,22,23	1.35	3 (15%)	26,31,34	2.28	11 (42%)
1	4OC	AA	1402	1	20,23,24	1.29	2 (10%)	26,32,35	1.12	2 (7%)
2	4SU	AB	8	2	18,21,22	1.37	3 (16%)	26,30,33	1.66	6 (23%)
2	PSU	AB	55	2	18,21,22	1.53	3 (16%)	22,30,33	1.39	4 (18%)
26	2MG	BB	1835	26	18,26,27	1.45	3 (16%)	16,38,41	1.66	5 (31%)
26	5MU	BB	1939	26	19,22,23	1.54	5 (26%)	28,32,35	2.02	8 (28%)
2	7MG	AB	46	2	22,26,27	5.32	4 (18%)	29,39,42	1.92	4 (13%)
26	2MA	BB	2503	26	17,25,26	1.93	4 (23%)	17,37,40	1.26	2 (11%)
26	3TD	BB	1915	26	18,22,23	1.32	2 (11%)	22,32,35	1.20	2 (9%)
26	5MC	BB	1962	26	18,22,23	1.10	2 (11%)	26,32,35	1.52	3 (11%)
26	6MZ	BB	2030	26	18,25,26	1.48	4 (22%)	16,36,39	1.76	3 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	OMG	BB	2251	26	18,26,27	1.70	4 (22%)	19,38,41	1.43	2 (10%)
1	5MC	AA	1407	1	18,22,23	1.27	1 (5%)	26,32,35	1.67	10 (38%)
26	PSU	BB	746	26	18,21,22	1.90	6 (33%)	22,30,33	1.28	3 (13%)
26	PSU	BB	955	26	18,21,22	1.78	5 (27%)	22,30,33	1.70	6 (27%)
4	PSU	AD	56	4	18,21,22	1.48	3 (16%)	22,30,33	1.31	1 (4%)
26	CH	BB	2575	26	16,21,22	1.85	5 (31%)	20,30,33	1.80	5 (25%)
4	OMC	AD	33	4	19,22,23	0.91	0	26,31,34	1.83	5 (19%)
26	PSU	BB	2457	26	18,21,22	2.10	5 (27%)	22,30,33	1.70	4 (18%)
2	H2U	AB	17	2	18,21,22	1.42	2 (11%)	21,30,33	2.16	5 (23%)
2	H2U	AB	16	2	18,21,22	1.22	2 (11%)	21,30,33	2.19	9 (42%)
26	PSU	BB	2580	26	18,21,22	2.07	7 (38%)	22,30,33	1.95	6 (27%)
26	PSU	BB	2605	26	18,21,22	1.98	5 (27%)	22,30,33	2.36	7 (31%)
26	PSU	BB	1911	26	18,21,22	1.80	4 (22%)	22,30,33	1.22	2 (9%)

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
26	1MG	BB	745	26	-	0/3/25/26	0/3/3/3
1	PSU	AA	516	1	-	4/7/25/26	0/2/2/2
1	2MG	AA	1207	1	-	0/5/27/28	0/3/3/3
26	7MG	BB	2069	26	-	0/7/37/38	0/3/3/3
26	2MG	BB	2445	26	-	0/5/27/28	0/3/3/3
1	MA6	AA	1519	1	-	0/7/29/30	0/3/3/3
2	OMC	AB	32	2	-	0/9/27/28	0/2/2/2
26	PSU	BB	1917	26	-	1/7/25/26	0/2/2/2
1	2MG	AA	1516	1	-	0/5/27/28	0/3/3/3
26	H2U	BB	2449	26	-	0/7/38/39	0/2/2/2
4	4SU	AD	8	4	-	0/7/25/26	0/2/2/2
26	PSU	BB	2504	26	-	0/7/25/26	0/2/2/2
1	MA6	AA	1518	1	-	0/7/29/30	0/3/3/3
26	OMC	BB	2498	26	-	0/9/27/28	0/2/2/2
2	MIA	AB	37	2	-	2/11/33/34	0/3/3/3
1	2MG	AA	966	1	-	0/5/27/28	0/3/3/3
4	H2U	AD	21	4	-	3/7/38/39	0/2/2/2
26	6MZ	BB	1618	26	-	0/5/27/28	0/3/3/3
2	H2U	AB	20	2	-	2/7/38/39	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	5MU	AD	55	4	-	0/7/25/26	0/2/2/2
2	5MU	AB	54	2	-	0/7/25/26	0/2/2/2
1	5MC	AA	967	1	-	0/7/25/26	0/2/2/2
1	7MG	AA	527	1	-	1/7/37/38	0/3/3/3
1	UR3	AA	1498	1	-	0/7/25/26	0/2/2/2
26	5MU	BB	747	26	-	0/7/25/26	0/2/2/2
26	OMU	BB	2552	26	-	0/9/27/28	0/2/2/2
1	4OC	AA	1402	1	-	0/9/29/30	0/2/2/2
2	4SU	AB	8	2	-	5/7/25/26	0/2/2/2
2	PSU	AB	55	2	-	2/7/25/26	0/2/2/2
26	2MG	BB	1835	26	-	0/5/27/28	0/3/3/3
26	5MU	BB	1939	26	-	0/7/25/26	0/2/2/2
2	7MG	AB	46	2	-	2/7/37/38	0/3/3/3
26	2MA	BB	2503	26	-	0/3/25/26	0/3/3/3
26	3TD	BB	1915	26	-	0/7/25/26	0/2/2/2
26	5MC	BB	1962	26	-	1/7/25/26	0/2/2/2
26	6MZ	BB	2030	26	-	0/5/27/28	0/3/3/3
26	OMG	BB	2251	26	-	0/5/27/28	0/3/3/3
1	5MC	AA	1407	1	-	0/7/25/26	0/2/2/2
26	PSU	BB	746	26	-	1/7/25/26	0/2/2/2
26	PSU	BB	955	26	-	0/7/25/26	0/2/2/2
4	PSU	AD	56	4	-	0/7/25/26	0/2/2/2
26	CH	BB	2575	26	-	0/5/25/26	0/2/2/2
4	OMC	AD	33	4	-	0/9/27/28	0/2/2/2
26	PSU	BB	2457	26	-	0/7/25/26	0/2/2/2
2	H2U	AB	17	2	-	1/7/38/39	0/2/2/2
2	H2U	AB	16	2	-	0/7/38/39	0/2/2/2
26	PSU	BB	2580	26	-	0/7/25/26	0/2/2/2
26	PSU	BB	2605	26	-	3/7/25/26	0/2/2/2
26	PSU	BB	1911	26	-	1/7/25/26	0/2/2/2

The worst 5 of 185 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	AB	46	7MG	C8-N9	-24.11	1.32	1.46
1	AA	527	7MG	C8-N9	-21.69	1.33	1.46
26	BB	2069	7MG	C8-N9	-15.54	1.37	1.46
2	AB	37	MIA	C2-S10	-8.16	1.68	1.75
26	BB	1917	PSU	C2-N1	7.04	1.46	1.36

The worst 5 of 247 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	BB	747	5MU	C6-C5-C4	9.28	125.79	118.03
1	AA	516	PSU	C6-C5-C4	8.98	124.48	118.20
26	BB	2605	PSU	C6-C5-C4	8.50	124.14	118.20
26	BB	2069	7MG	N9-C8-N7	7.05	113.46	103.38
26	BB	747	5MU	C5M-C5-C6	-7.05	113.44	122.85

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	AA	516	PSU	C2'-C1'-C5-C4
1	AA	516	PSU	C2'-C1'-C5-C6
2	AB	8	4SU	C2'-C1'-N1-C2
2	AB	8	4SU	C2'-C1'-N1-C6
26	BB	746	PSU	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](#)

2 ligands 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	$\# Z > 2$
60	FME	BB	3001	59	8,9,10	1.23	2 (25%)	7,9,11	1.40	1 (14%)
59	TRP	AB	101	2,60	14,15,16	1.99	3 (21%)	13,20,22	2.27	5 (38%)

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
60	FME	BB	3001	59	-	2/7/9/11	-
59	TRP	AB	101	2,60	-	0/5/6/8	0/2/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	AB	101	TRP	OXT-C	-5.01	1.21	1.42
59	AB	101	TRP	CH2-CZ2	3.05	1.43	1.36
59	AB	101	TRP	C-CA	2.83	1.57	1.52
60	BB	3001	FME	CB-CG	2.21	1.60	1.51
60	BB	3001	FME	CE-SD	2.14	1.91	1.78

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	AB	101	TRP	CH2-CZ3-CE3	4.81	127.18	120.44
59	AB	101	TRP	CZ3-CH2-CZ2	-3.88	115.00	120.44
59	AB	101	TRP	CE3-CD2-CE2	-2.82	114.43	118.17
59	AB	101	TRP	CZ2-CE2-CD2	2.30	124.96	120.76
59	AB	101	TRP	CD2-CE2-NE1	-2.04	103.39	107.92

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	BB	3001	FME	O1-CN-N-CA
60	BB	3001	FME	CB-CA-N-CN

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
26	BB	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	BB	2677:G	O3'	2678:C	P	1.76

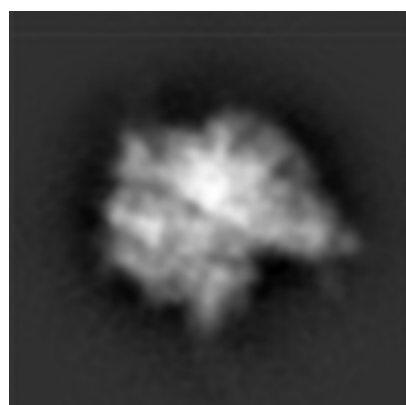
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5364. These allow visual inspection of the internal detail of the map and identification of artifacts.

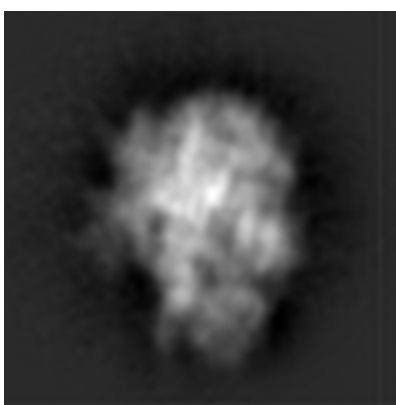
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

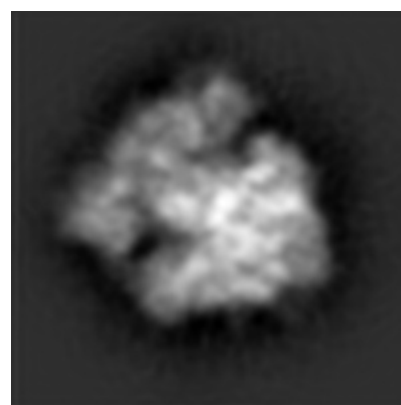
6.1.1 Primary map



X



Y

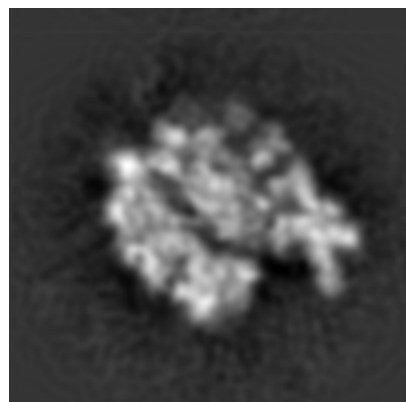


Z

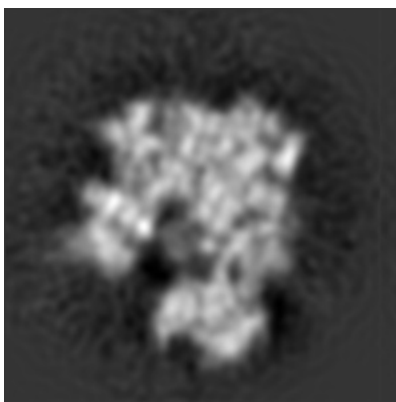
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

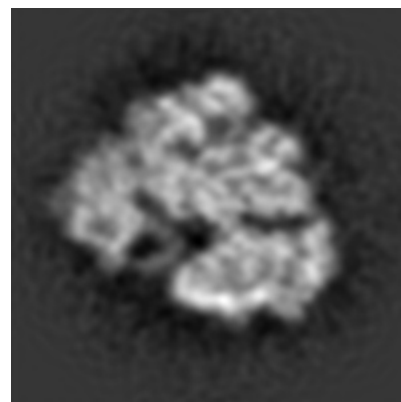
6.2.1 Primary map



X Index: 125



Y Index: 125

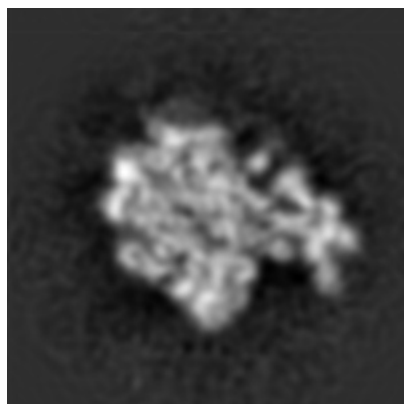


Z Index: 125

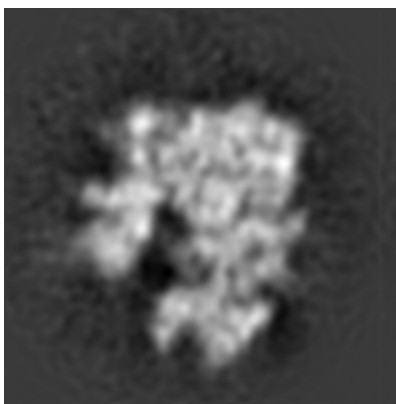
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

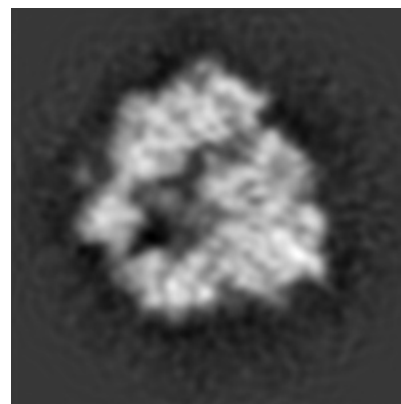
6.3.1 Primary map



X Index: 130



Y Index: 130

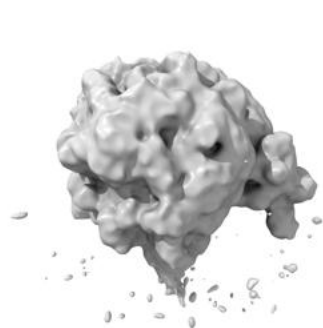


Z Index: 114

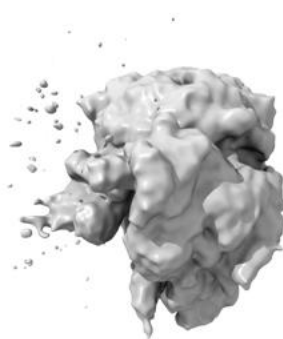
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

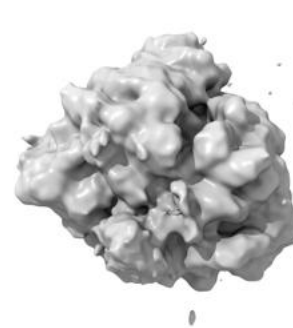
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

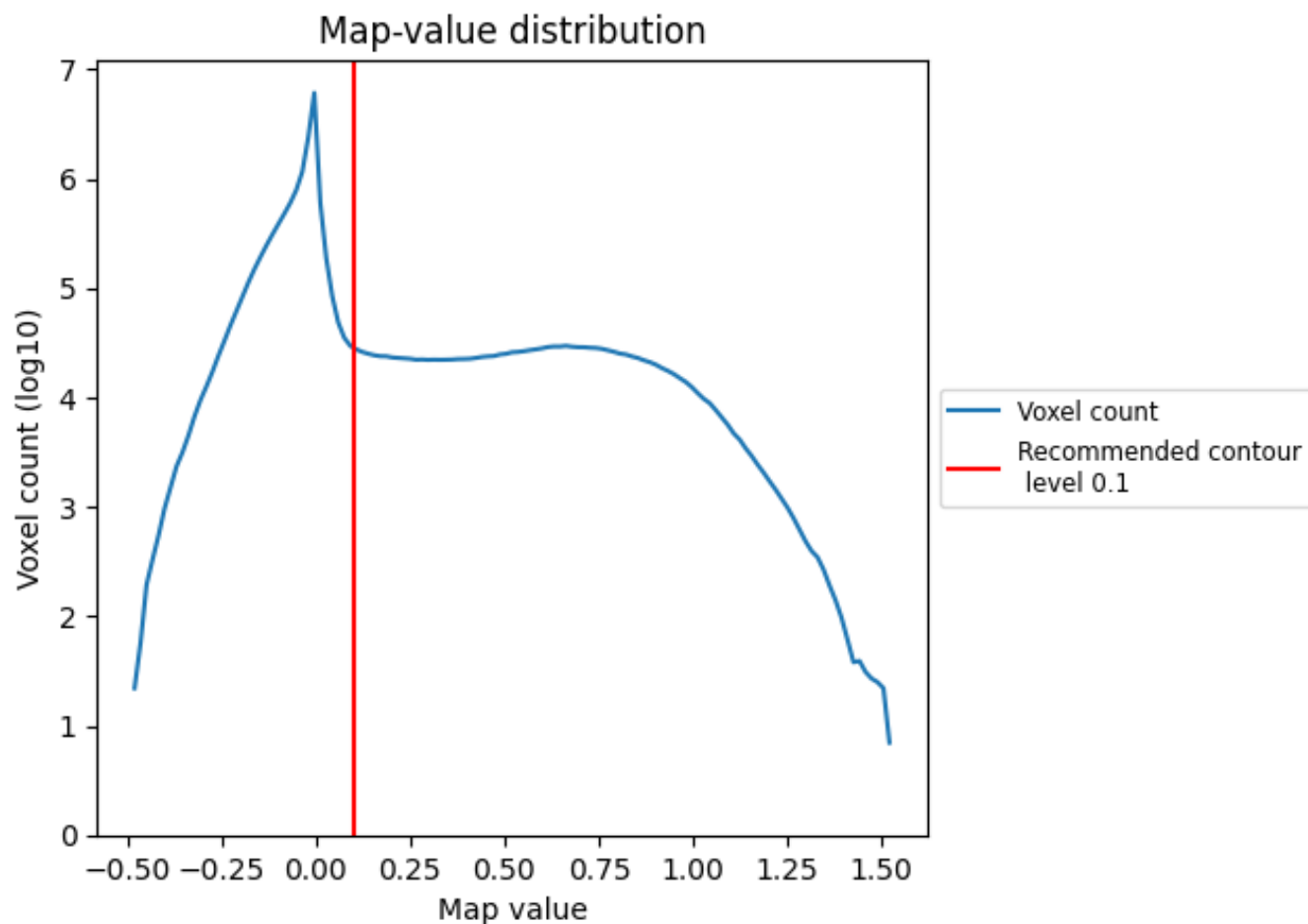
6.5 Mask visualisation

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

7 Map analysis [i](#)

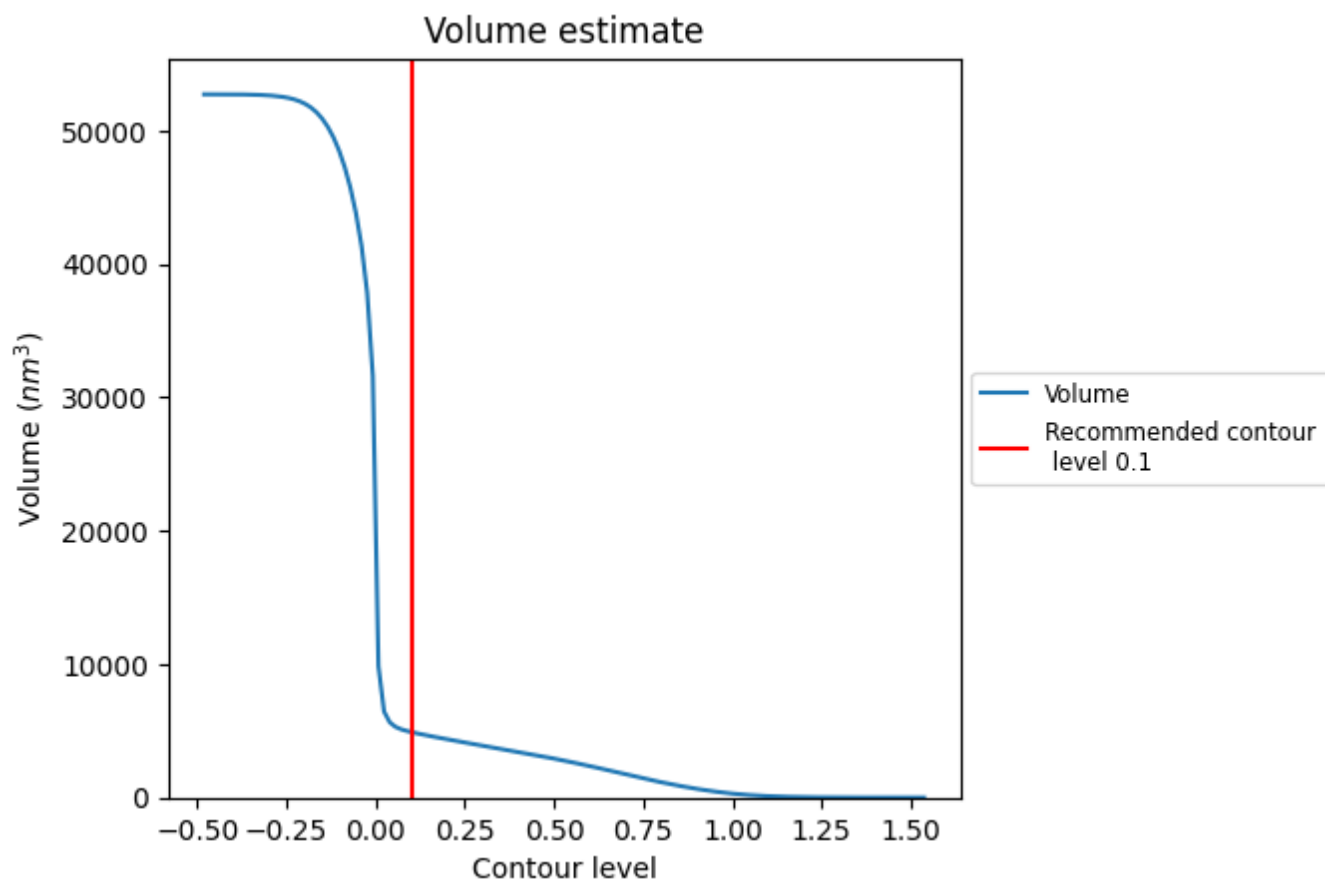
This section contains the results of statistical analysis of the map.

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.

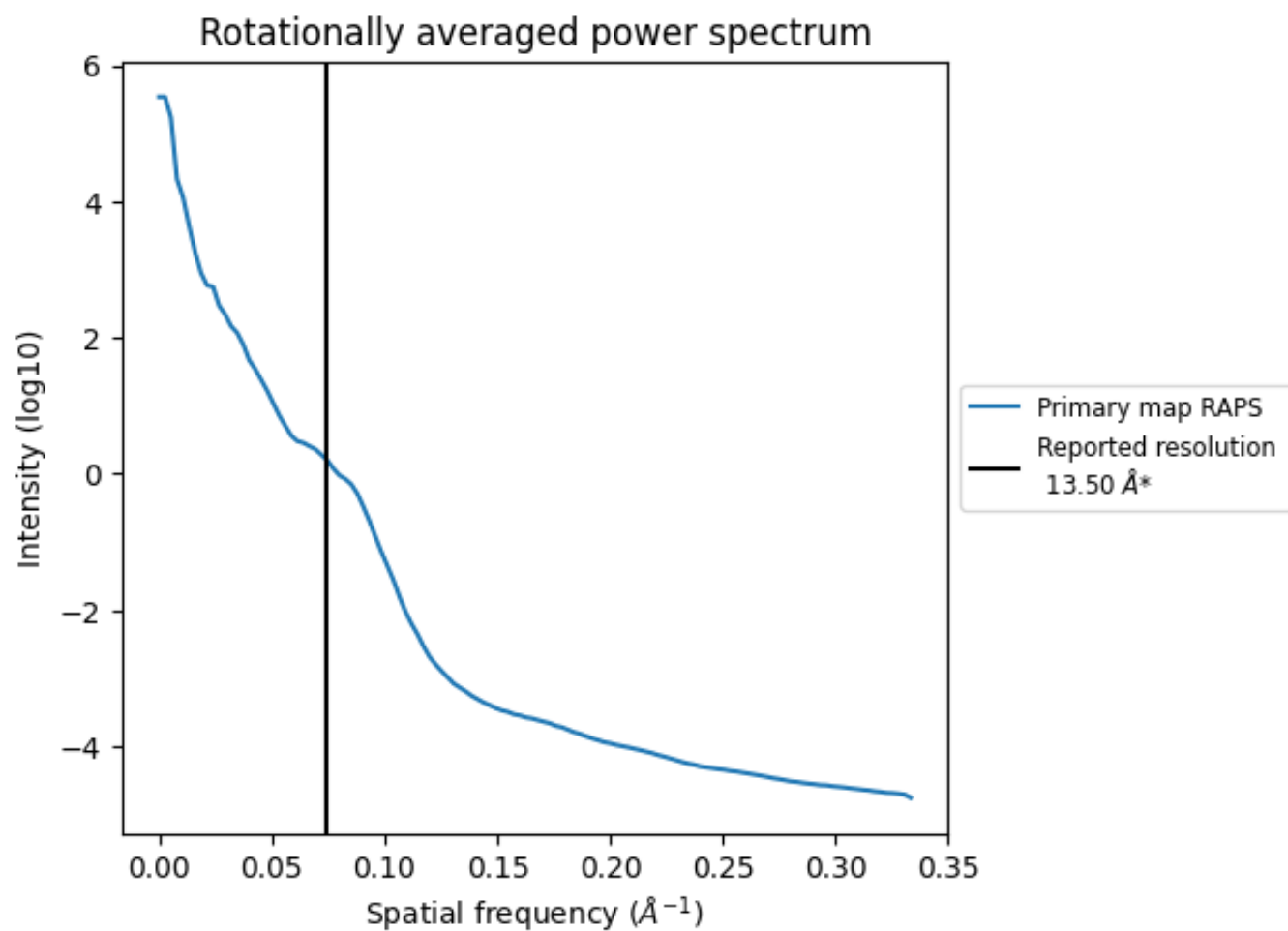
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4913 nm³; this corresponds to an approximate mass of 4438 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 0.074 Å⁻¹

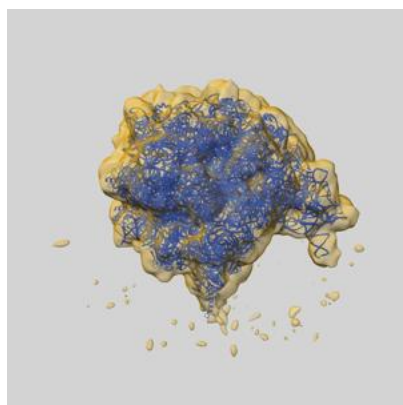
8 Fourier-Shell correlation

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

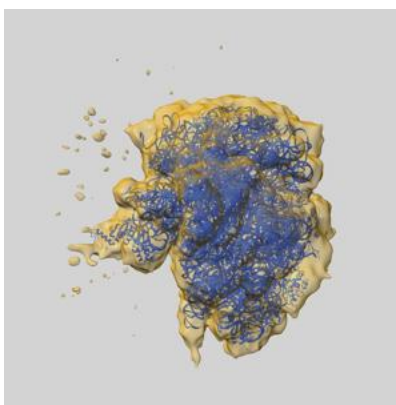
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5364 and PDB model 4V6P. Per-residue inclusion information can be found in section [3](#) on page [15](#).

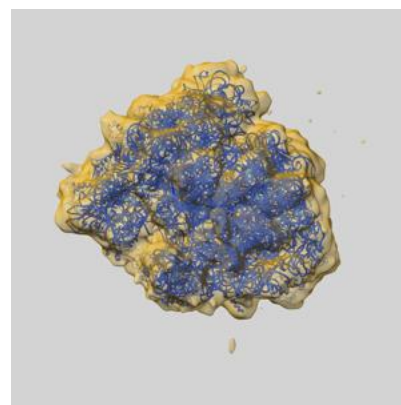
9.1 Map-model overlay [i](#)



X



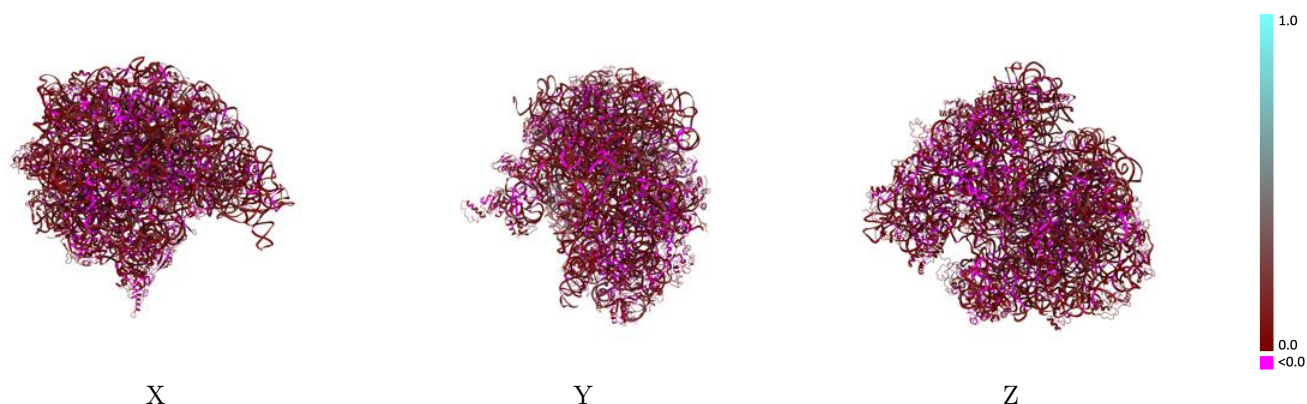
Y



Z

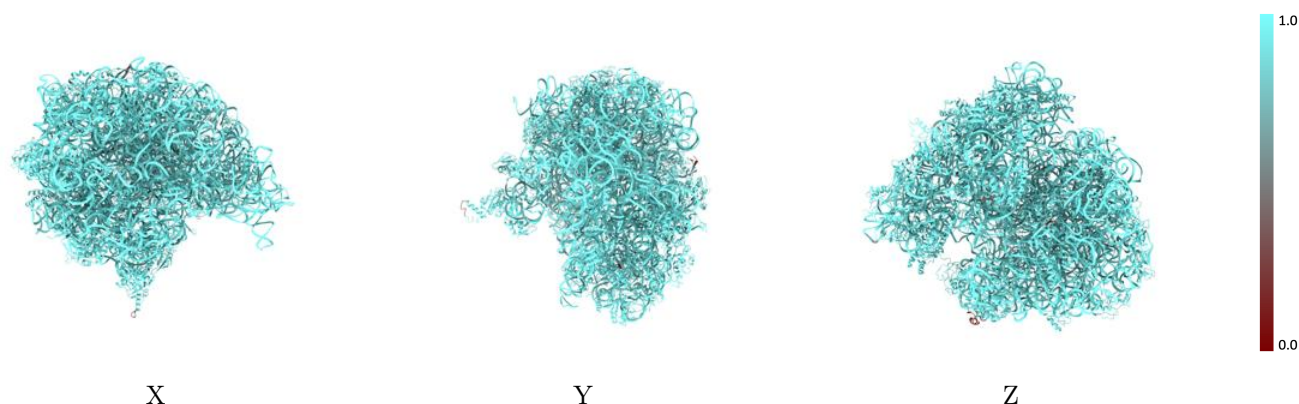
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



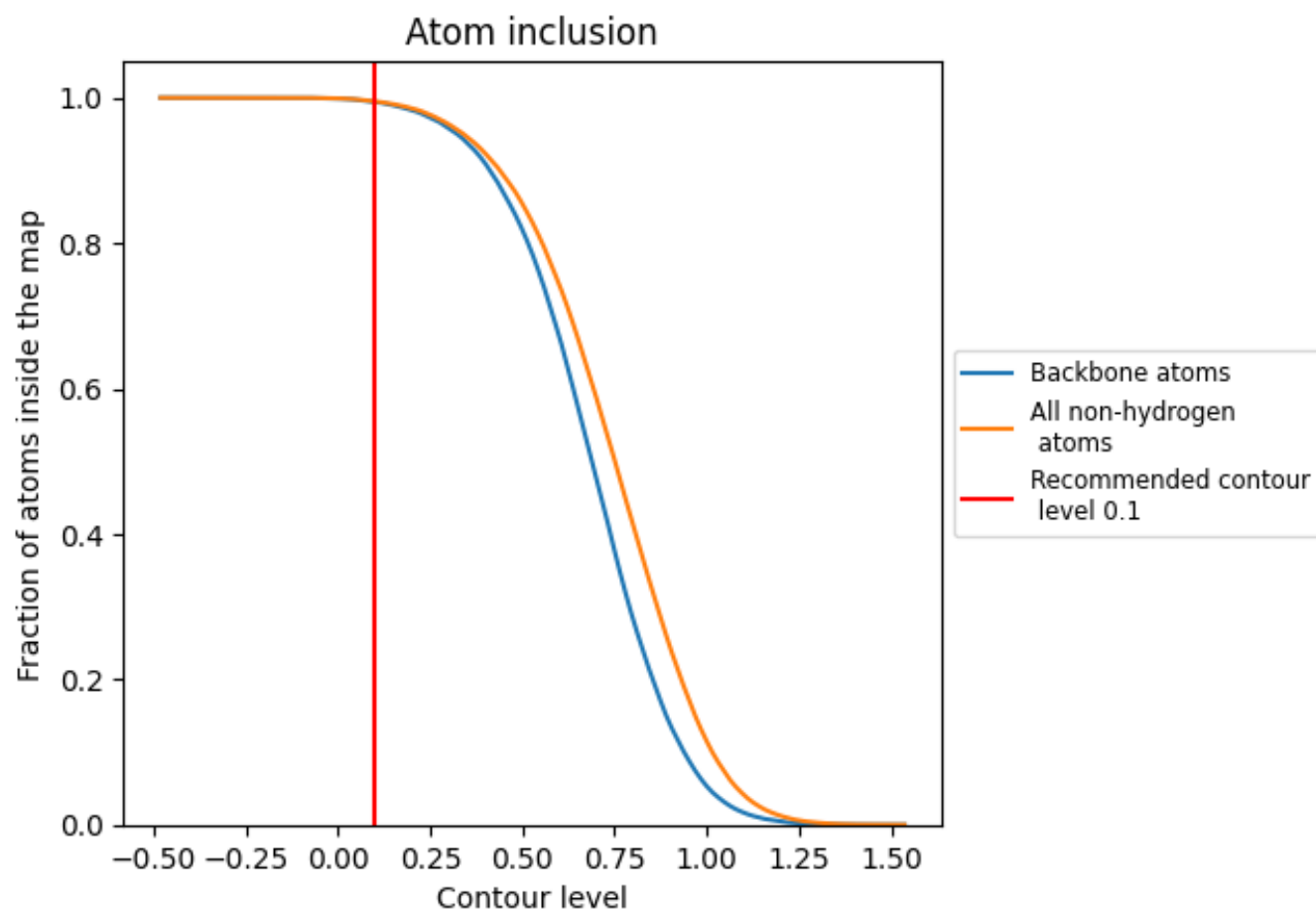
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 100% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9951	 0.0640
AA	 0.9993	 0.0780
AB	 0.9573	 0.0490
AC	 0.9194	 -0.0060
AD	 0.9464	 0.0460
AE	 0.9902	 0.0400
AF	 0.9989	 0.0530
AG	 1.0000	 0.0350
AH	 1.0000	 0.0530
AI	 0.9776	 0.0440
AJ	 1.0000	 0.0500
AK	 0.9958	 0.0360
AL	 0.9990	 0.0480
AM	 1.0000	 0.0260
AN	 1.0000	 0.0430
AO	 0.9913	 0.0130
AP	 1.0000	 0.0490
AQ	 1.0000	 0.0080
AR	 1.0000	 0.0430
AS	 1.0000	 0.0320
AT	 1.0000	 0.0420
AU	 1.0000	 0.0630
AV	 0.9564	 0.0190
AW	 1.0000	 0.0310
AX	 0.9839	 0.0110
B0	 1.0000	 0.0200
B1	 1.0000	 0.0440
B2	 0.9981	 0.0410
B3	 1.0000	 0.0340
B4	 1.0000	 0.0440
B5	 1.0000	 0.0120
B6	 1.0000	 -0.0200
B7	 1.0000	 0.0490
BA	 1.0000	 0.0900
BB	 0.9991	 0.0820



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Chain	Atom inclusion	Q-score
BC	 0.9239	 0.0270
BD	 1.0000	 0.0120
BE	 1.0000	 0.0220
BF	 1.0000	 0.0580
BG	 1.0000	 0.0490
BH	 1.0000	 0.0260
BI	 0.9261	 0.0230
BJ	 0.9486	 0.0530
BK	 0.9795	 0.0350
BL	 1.0000	 0.0110
BM	 0.9957	 0.0340
BN	 1.0000	 0.0120
BO	 1.0000	 0.0240
BP	 1.0000	 0.0150
BQ	 0.9977	 0.0620
BR	 0.9944	 0.0170
BS	 0.9923	 0.0070
BT	 1.0000	 0.0430
BU	 1.0000	 0.0100
BV	 1.0000	 0.0120
BW	 0.9936	 0.0540
BX	 1.0000	 0.0680
BY	 0.9806	 -0.0030
BZ	 1.0000	 0.0140