



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 10:21 AM UTC

PDB ID : 7SSO / pdb_00007sso
EMDB ID : EMD-25411
Title : Pre translocation 70S ribosome with A/A and P/E tRNA (Structure II-A)
Authors : Carbone, C.E.; Korostelev, A.A.
Deposited on : 2021-11-11
Resolution : 3.20 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

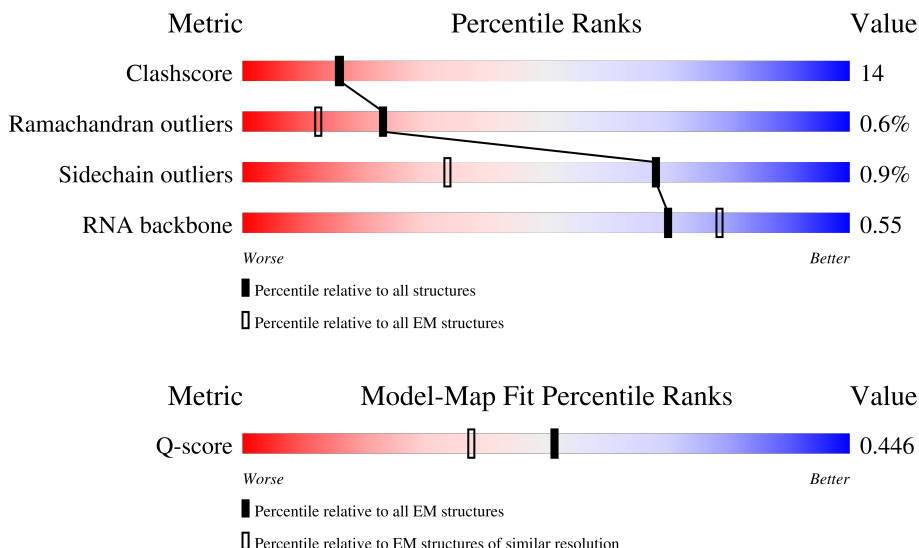
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 Å.

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



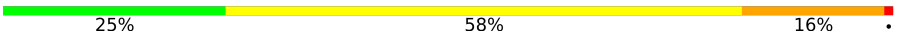
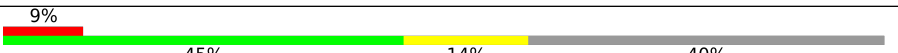
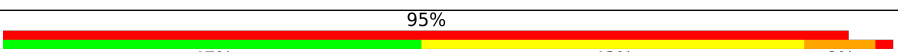
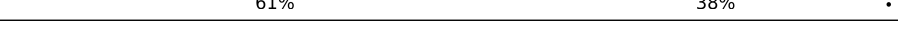
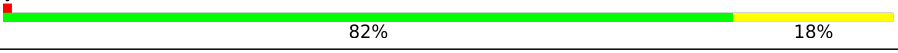
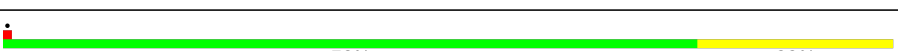
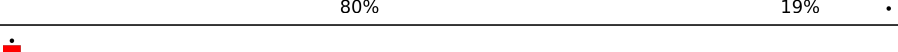
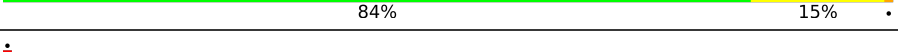
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15020 (2.70 - 3.70)

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	3	1539	
2	1	2903	
3	2	120	

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Mol	Chain	Length	Quality of chain
4	5	77	
5	b	271	
6	c	209	
7	d	201	
8	e	177	
9	f	176	
10	g	149	
11	a	223	
12	h	131	
13	i	141	
14	j	142	
15	k	122	
16	l	143	
17	m	136	
18	n	120	
19	o	116	
20	p	114	
21	q	117	
22	r	103	
23	s	110	
24	t	93	
25	u	102	
26	v	94	
27	w	75	
28	x	77	

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Mol	Chain	Length	Quality of chain
29	y	63	
30	z	58	
31	A	66	
32	B	56	
33	C	50	
34	D	46	
35	E	64	
36	F	38	
37	4	35	
38	6	77	
39	G	225	
40	H	206	
41	I	205	
42	J	157	
43	K	100	
44	L	151	
45	M	129	
46	N	127	
47	O	98	
48	P	116	
49	Q	123	
50	R	114	
51	S	100	
52	T	88	
53	U	82	

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Mol	Chain	Length	Quality of chain
54	V	80	 72% 25% .
55	W	65	 83% 17%
56	X	79	 8% 62% 38%
57	Y	85	 72% 27% .
58	Z	65	 69% 28% .

2 Entry composition [i](#)

There are 60 unique types of molecules in this entry. The entry contains 148980 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 rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 3 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 4 is a RNA chain called tRNA Pro.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 9 is a protein called 50S ribosomal protein L6.

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

- Molecule 10 is a protein called 50S ribosomal protein L9.

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

- Molecule 11 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 12 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

- Molecule 13 is a protein called 50S ribosomal protein L11.

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

- Molecule 14 is a protein called 50S ribosomal protein L13.

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

- Molecule 15 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 16 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 17 is a protein called 50S ribosomal protein L16.

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

- Molecule 18 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 19 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	o	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 20 is a protein called 50S ribosomal protein L19.

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

- Molecule 21 is a protein called 50S ribosomal protein L20.

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

- Molecule 22 is a protein called 50S ribosomal protein L21.

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

- Molecule 23 is a protein called 50S ribosomal protein L22.

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

- Molecule 24 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	t	93	Total	C	N	O	S	0
			739	466	139	132	2	0

- Molecule 25 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	u	102	Total	C	N	O		0
			780	492	146	142		0

- Molecule 26 is a protein called 50S ribosomal protein L25.

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

- Molecule 27 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 28 is a protein called 50S ribosomal protein L28.

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

- Molecule 29 is a protein called 50S ribosomal protein L29.

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

- Molecule 30 is a protein called 50S ribosomal protein L30.

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

- Molecule 31 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A	45	Total	C	N	O	S	0	0
			351	219	61	65	6		

- Molecule 32 is a protein called 50S ribosomal protein L32.

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

- Molecule 33 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 34 is a protein called 50S ribosomal protein L34.

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

- Molecule 35 is a protein called 50S ribosomal protein L35.

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

- Molecule 36 is a protein called 50S ribosomal protein L36.

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

- Molecule 37 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	4	19	Total	C	N	O	P	0	0
			413	186	85	124	18		

- Molecule 38 is a RNA chain called tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 39 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	G	225	Total	C	N	O	S	0	0
			1757	1111	315	323	8		

- Molecule 40 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 41 is a protein called 30S ribosomal protein S4.

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

- Molecule 42 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 43 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 44 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 45 is a protein called 30S ribosomal protein S8.

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

- Molecule 46 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	N	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 47 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 48 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 49 is a protein called 30S ribosomal protein S12.

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

- Molecule 50 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 51 is a protein called 30S ribosomal protein S14.

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

- Molecule 52 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	T	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 53 is a protein called 30S ribosomal protein S16.

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

- Molecule 54 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 55 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 56 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 57 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 58 is a protein called 30S ribosomal protein S21.

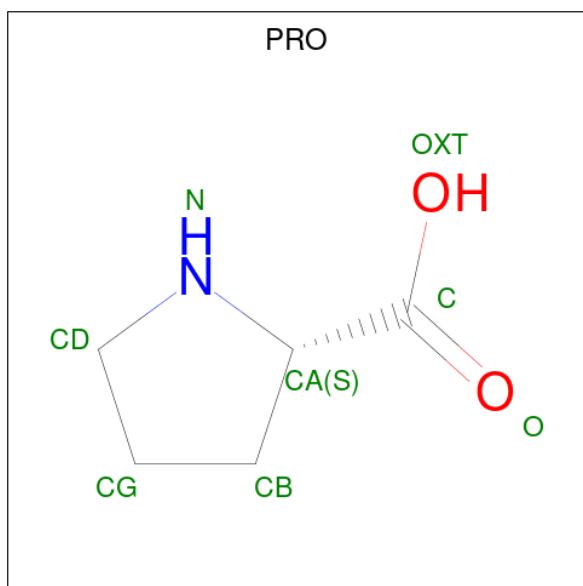
Mol	Chain	Residues	Atoms					AltConf	Trace
58	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 59 is N-FORMYLMETHIONINE (CCD ID: FME) (formula: C₆H₁₁NO₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
59	1	1	Total	C	N	O	S	0
			8	5	1	1	1	

- Molecule 60 is PROLINE (CCD ID: PRO) (formula: $C_5H_9NO_2$).

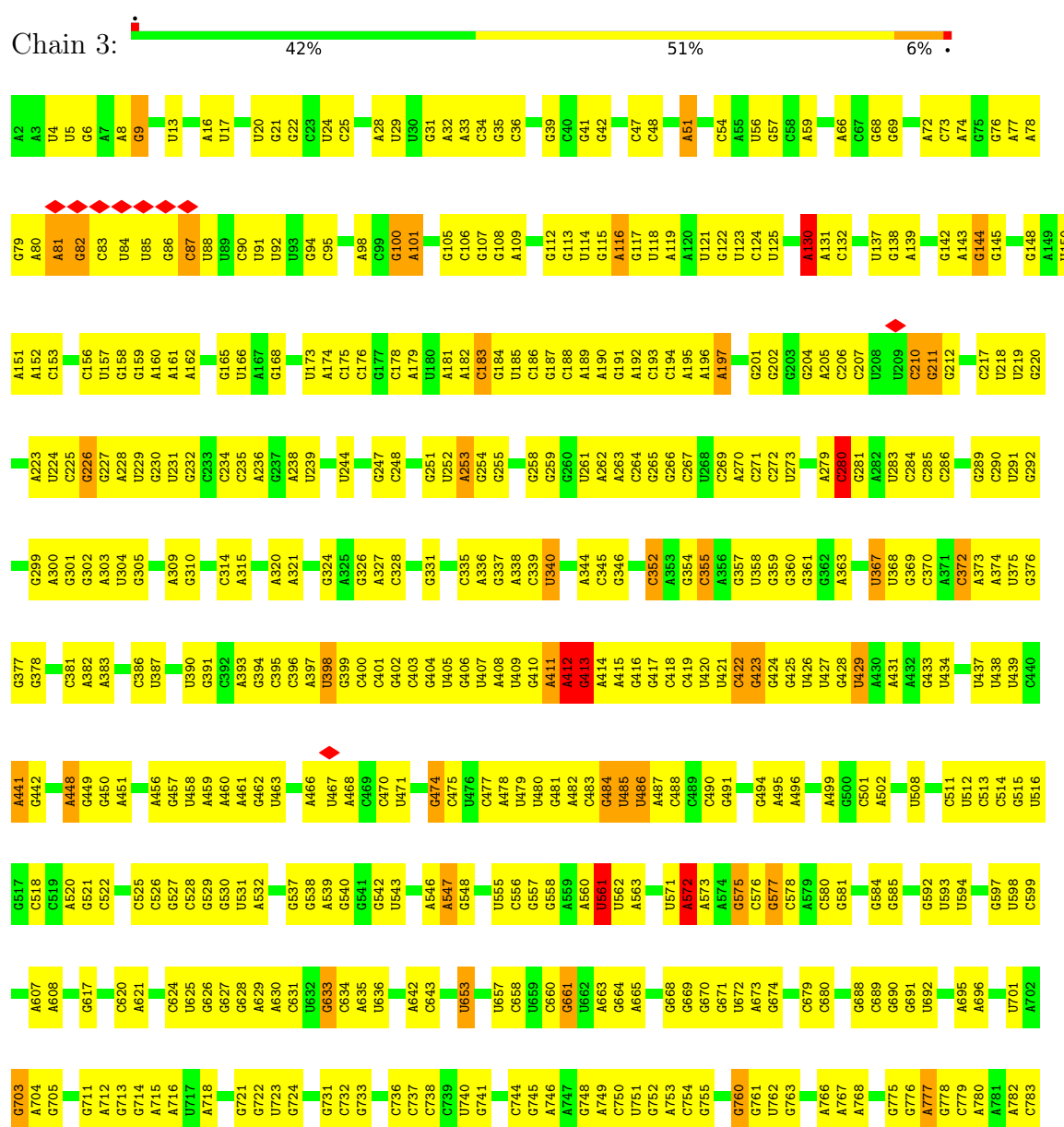


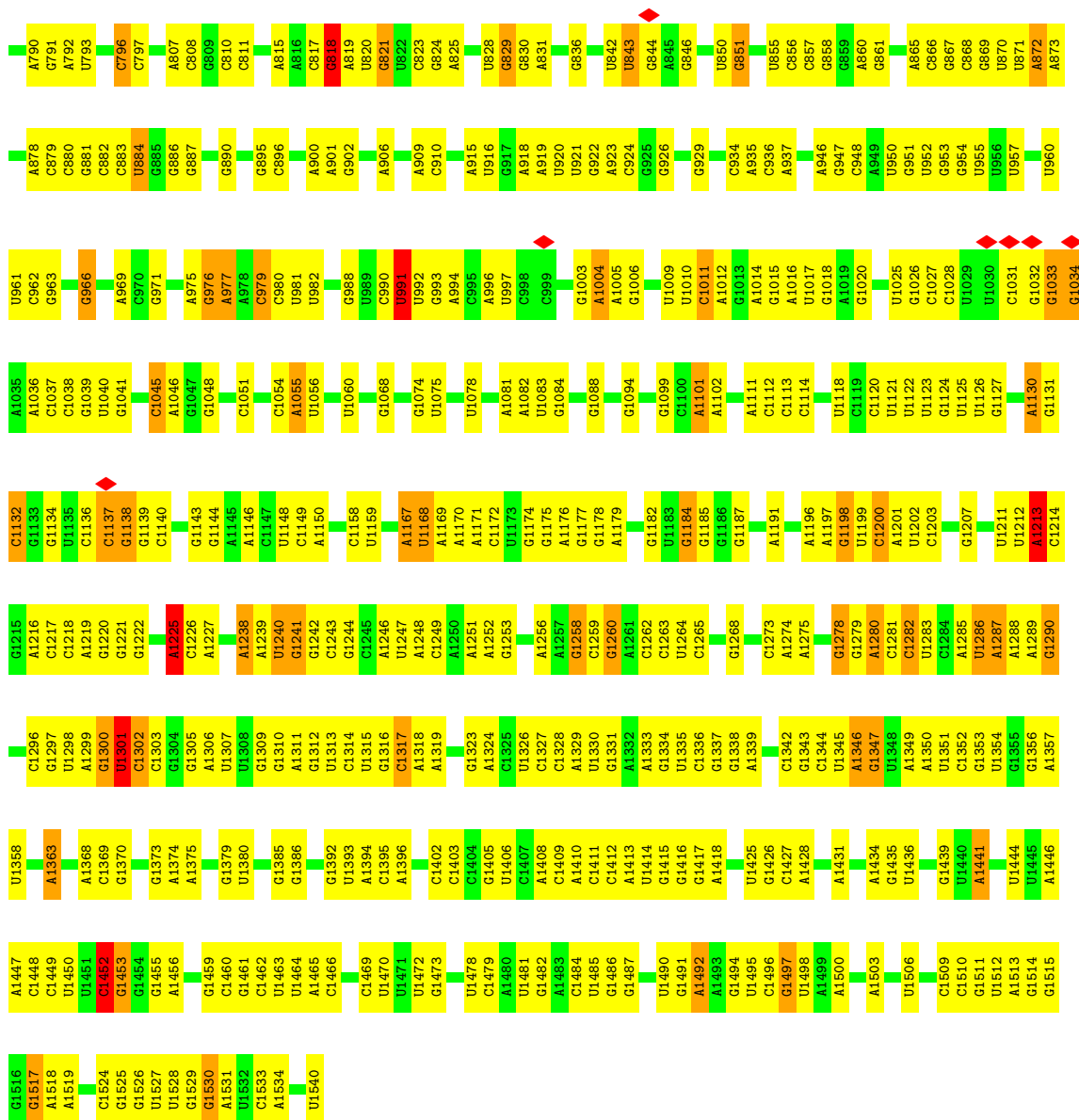
Mol	Chain	Residues	Atoms					AltConf
60	5	1	Total	C	N	O		0
			7	5	1	1		

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.

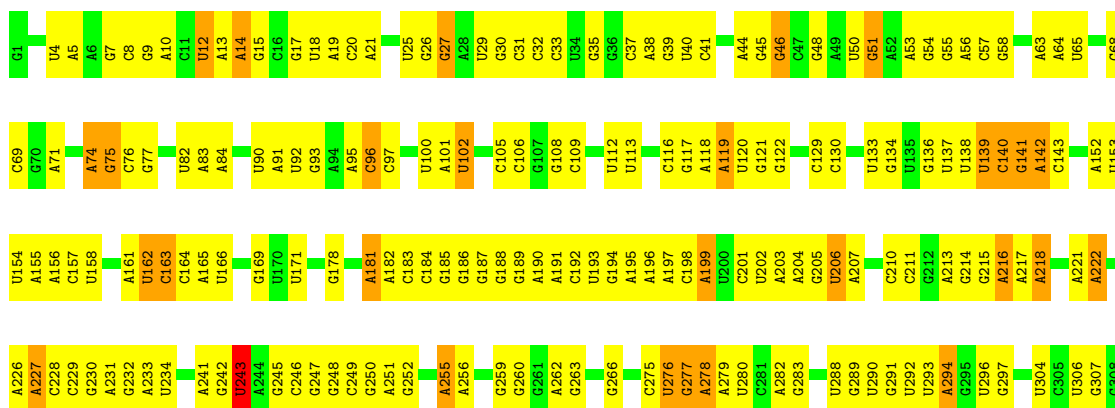
• Molecule 1: 16S rRNA





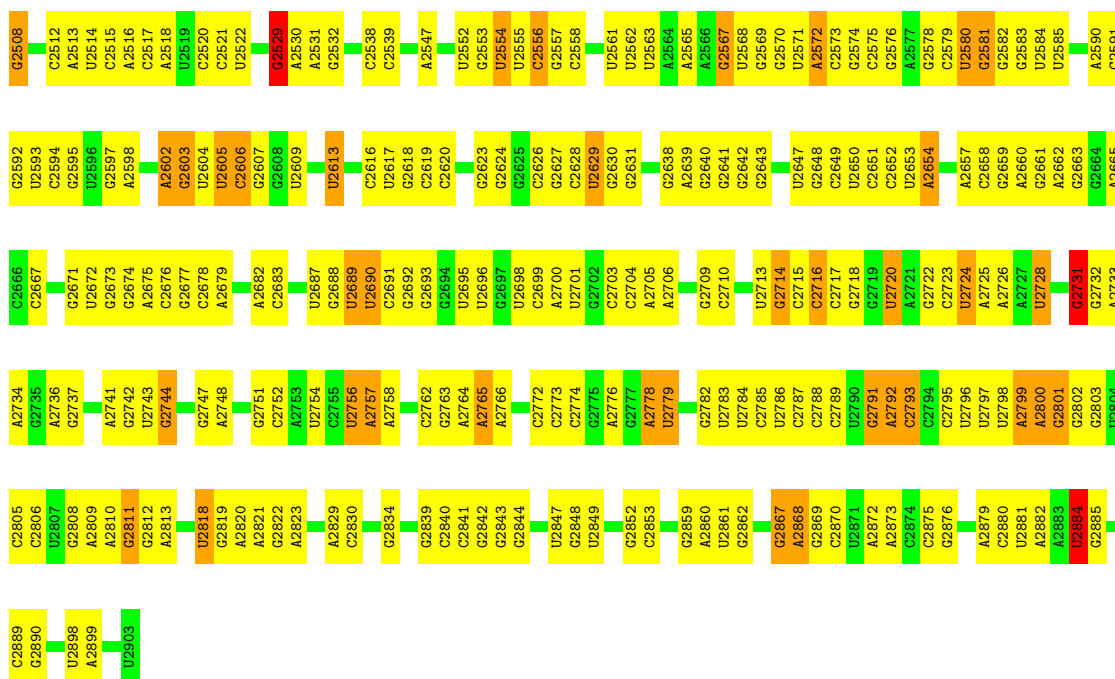
• Molecule 2: 23S rRNA

Chain 1: 38% 51% 10%

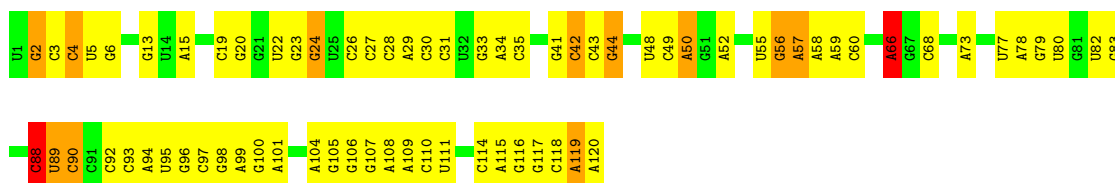


A1403	A1297	A1214	G1071	G1002	U850	G778	A693	C623	U546	A471	A382	A309
A1404	C1298	G1215	C1072	C1005	C851	U779	U694	C624	A547	A472	G386	A310
U1405	G1299	G1216	A1073	C1006	U852	G780	G695	A627	G548	G473	G387	A311
U1406	G1300	U1217	G1074	C1007	C853	A781			G549	G474		G312
G1407	A1301	G1225	C1075	C1008	G854	A782	G700	A633	C550	C475	C394	C318
A1302	A1302	A1226	C1076	A1009	G855	G783	U702	C634	G555	A476	U395	G319
G1303	A1303	G1227	U1077	A1010	G857	G785	U703	C635	A556	A477	U396	G320
A1304	G1304	G1228	C1078	G1011	G858	G786	G704	C636	C557	A478	G396	A320
C1305	C1305	A1229	C1079	U1012	G859	C787	A705	A637	U558	A479		U321
A1413	A1230	A1230	A1080	C1013	U860	A788	A706	A638	G559	A480	A401	A322
	U1231	U1231	U1081		A861	A789	G707	U639	C560	G481		C323
		A1151	U1082	C945	G862		G708	C640		G488	A404	A324
		C1152	U1083	C946	A863	A792	U709	U641	A563	G489	U405	G329
	G1238	C1153	U1019	A947	A865	A793	U710	U642	C564	G490	G406	A330
	G1239	U1154	A1020	C948	G864		U711	A643	C565	G407	G408	A331
	U1240	A1155	A1021	G949	C865		G712	A644	U566	A492		
	A1241	A1096	G1022	G950	A866	G797	G713	C645		G493	G411	C335
	U1242	G1087	G1025	C951	C867	G798	U714	U646	U571		A412	C336
	C1243	A1088	G1026	G952	U870	G799	A715	G647	A572	A497	C413	C337
		A1089	A1027	G953	U871	A800	A716	G648	U573	A498	C414	G338
	G1248	A1090	A1028	G954	U872	A802	C717	G649	A574	U499	A415	U339
	U1249	C1091	A1029	U955	U877	U803	A718	C650	A575	G500	U416	A340
	G1250	C1092	A1029	G956	A878	A804	C719		U576	A501	C417	C341
		G1093		C957	A879	G805	U720	A654	G577	A502	C418	A342
		U1094	A1032	U958		C806	A721	A655	C578	A503		C343
		A1095	U1033			U807	A722	U657	G579	A504	A423	A344
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		A1097	G1036	G962	A896	G809		C660	C581	G506		A346
		U1098	G1037	U963	U887	U810	G728	A661	A582	A507	A432	A347
		U1099	G1038	C964	C888	U811	G729	G662	G583	A508	A433	A348
		U1176	A1039	C965	C889	C812	A730	G663	C584	A509	C433	U349
	G1259	G1177	A1040	G966	C890	U813	C731	G664	G585	C510	U494	G350
	A1260	C1178	A1041	U967	C891	C814	G732	A666	C587	U511	C435	A351
	C1261	G1179	G1042	C968		C815	G733	U665	U588	G512	C436	A352
	U1262	U1180				C816		A667	A513	U513		C353
	A1263	A1181	C1045	G971	U894	C817	C740	U667	A514	A441	U441	A354
		G1182	A1046	A972	U895	G818	U741	A668	A515	G442		U355
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	A1269	U1190	C1052	G978	U907	U826	G745	C672		C523	U451	G361
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	A1272	G1193	G1055			A829			C601	A529	G367	A368
		A1194	G1056	A983	G914	G830	U753	A677	A602	A529	A454	A371
			A1057		C915	G831	U754	C678	A603	A529	C455	G372
	G1276	G1197	U1058	G989	G916	U832	A755	C679	A603	A529	A457	U373
	G1277	U1198	G1059	A990	A917	A833	G757	C680	C610	A532	U459	A374
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	G1280	C1200	U1061	C992	U919	C840	G759	U683	G612	G535	G465	G376
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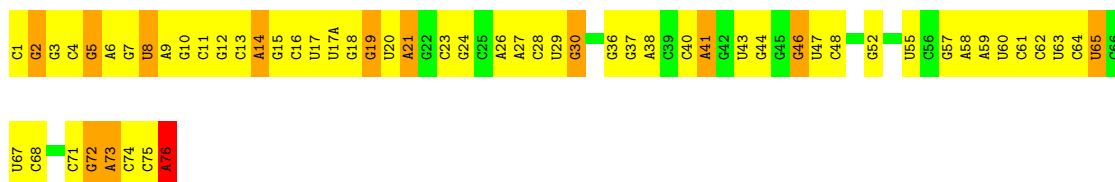
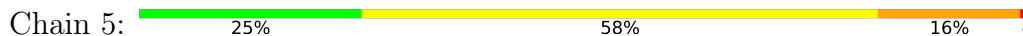
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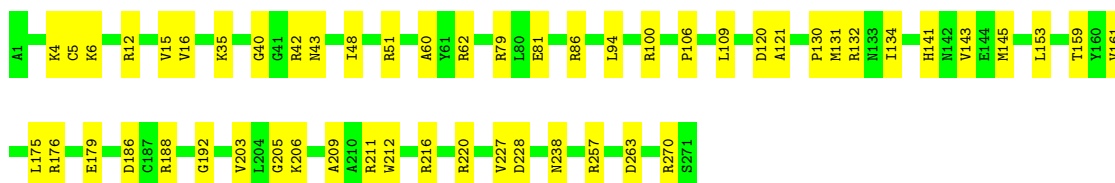
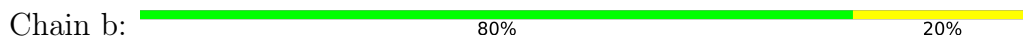
• Molecule 3: 5S rRNA



• Molecule 4: tRNA Pro

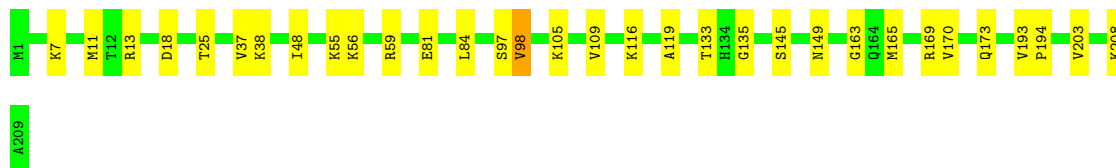


• Molecule 5: 50S ribosomal protein L2



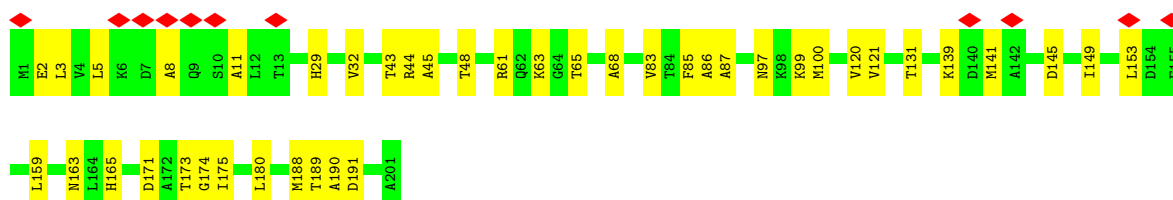
- Molecule 6: 50S ribosomal protein L3

Chain c:  85% 15%



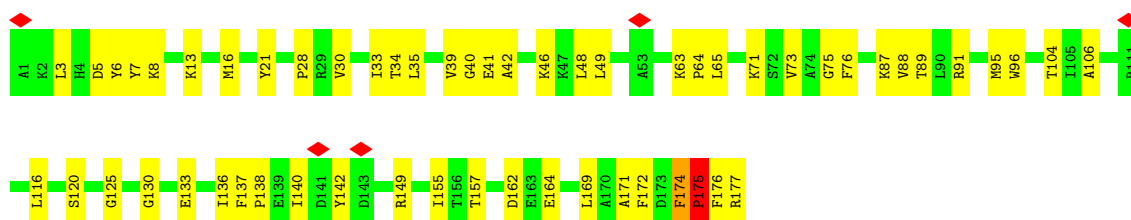
- Molecule 7: 50S ribosomal protein L4

Chain d:  5% 79% 21%



- Molecule 8: 50S ribosomal protein L5

Chain e:  68% 31% ..



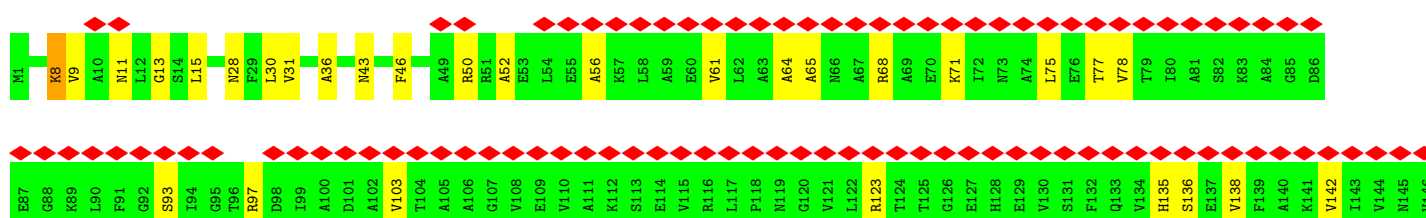
- Molecule 9: 50S ribosomal protein L6

Chain f:  81% 18% .



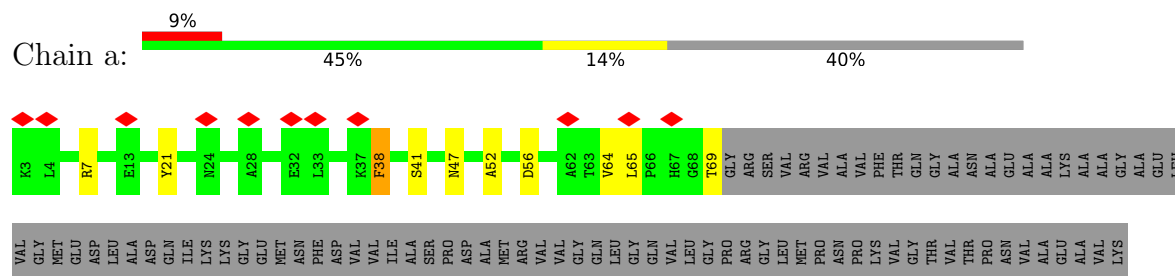
- Molecule 10: 50S ribosomal protein L9

Chain g:  66% 80% 19% .

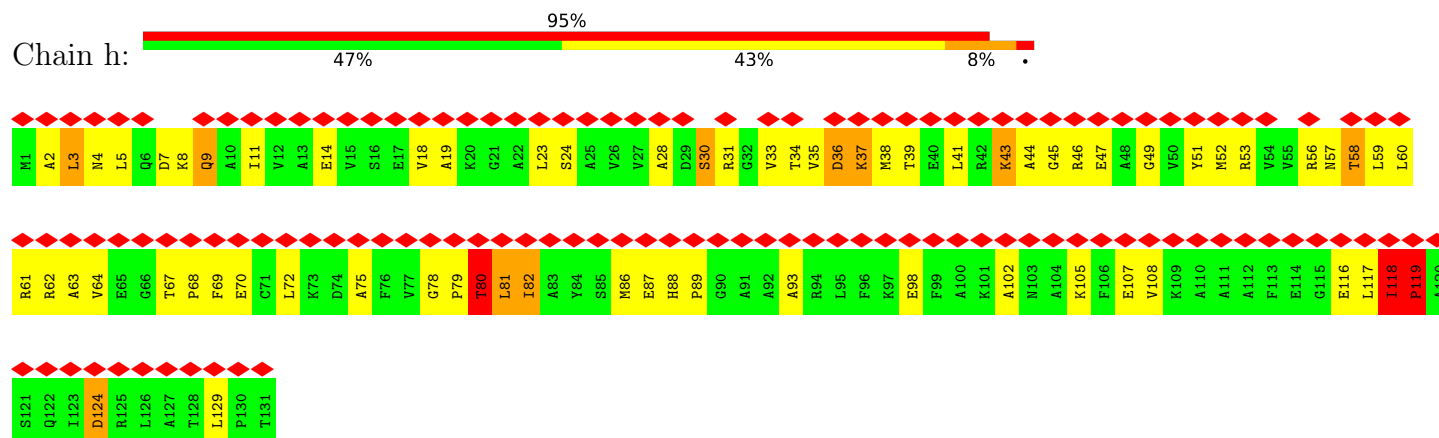




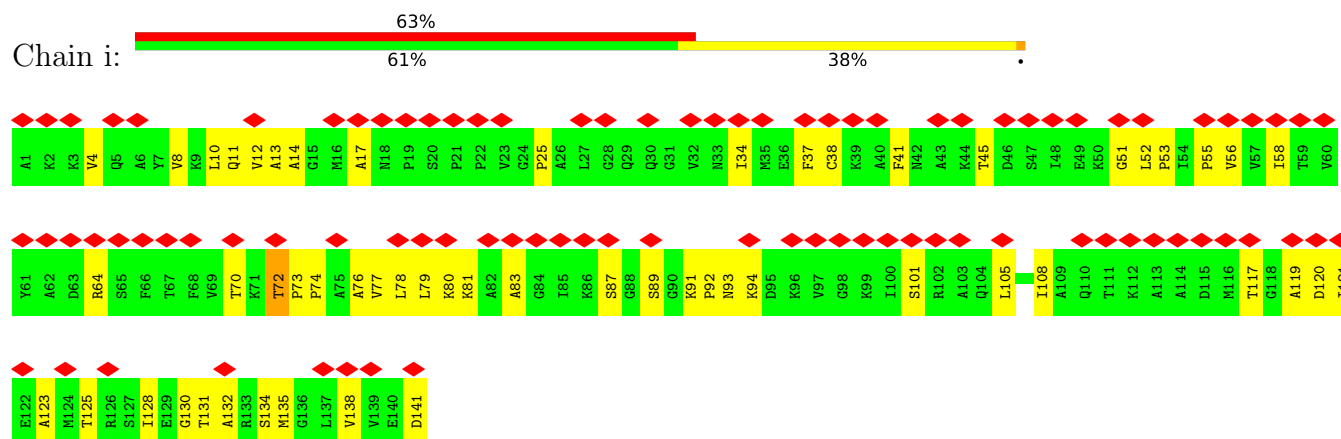
• Molecule 11: 50S ribosomal protein L1



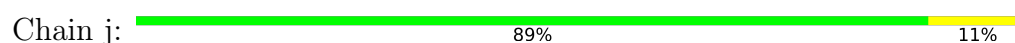
• Molecule 12: 50S ribosomal protein L10



• Molecule 13: 50S ribosomal protein L11



• Molecule 14: 50S ribosomal protein L13





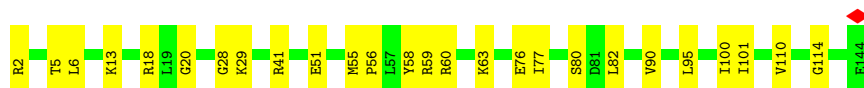
- Molecule 15: 50S ribosomal protein L14

Chain k: 74% 25%



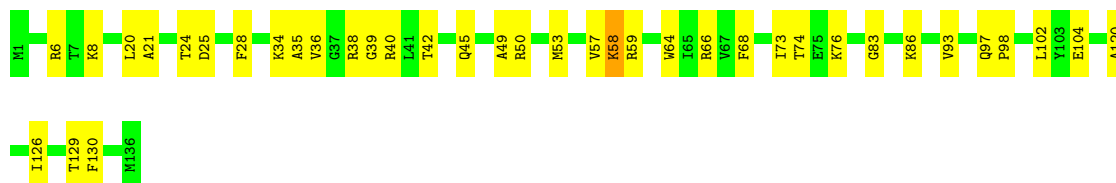
- Molecule 16: 50S ribosomal protein L15

Chain l: 82% 18%



- Molecule 17: 50S ribosomal protein L16

Chain m: 72% 27%



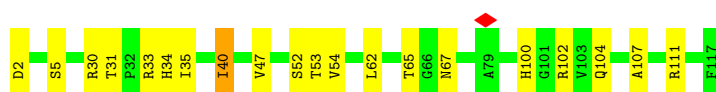
- Molecule 18: 50S ribosomal protein L17

Chain n: 78% 22%



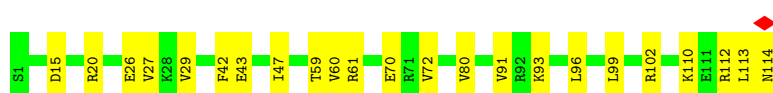
- Molecule 19: 50S ribosomal protein L18

Chain o: 83% 16%

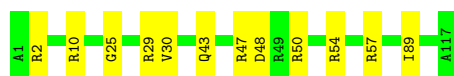


- Molecule 20: 50S ribosomal protein L19

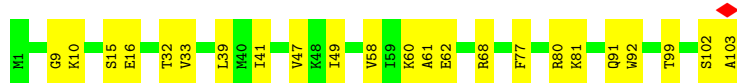
Chain p: 80% 20%



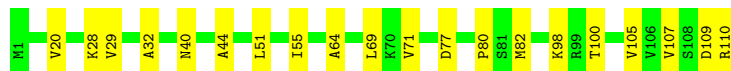
• Molecule 21: 50S ribosomal protein L20

Chain q:  90% 10%

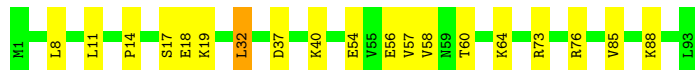
• Molecule 22: 50S ribosomal protein L21

Chain r:  78% 22%

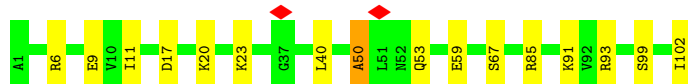
• Molecule 23: 50S ribosomal protein L22

Chain s:  82% 18%

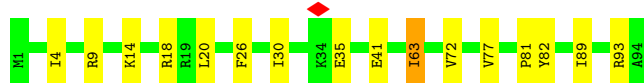
• Molecule 24: 50S ribosomal protein L23

Chain t:  80% 19%

• Molecule 25: 50S ribosomal protein L24

Chain u:  84% 15%

• Molecule 26: 50S ribosomal protein L25

Chain v:  83% 16%

• Molecule 27: 50S ribosomal protein L27

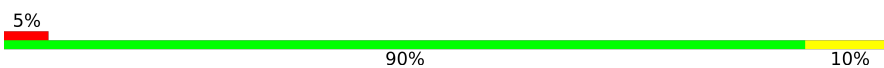
Chain w:  83% 17%

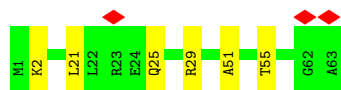
- Molecule 28: 50S ribosomal protein L28

Chain x:  82% 18%



- Molecule 29: 50S ribosomal protein L29

Chain y:  5% 90% 10%



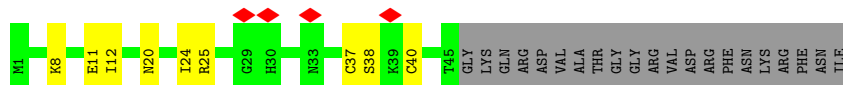
- Molecule 30: 50S ribosomal protein L30

Chain z:  88% 12%



- Molecule 31: 50S ribosomal protein L31

Chain A:  6% 55% 14% 32%



- Molecule 32: 50S ribosomal protein L32

Chain B:  84% 16%



- Molecule 33: 50S ribosomal protein L33

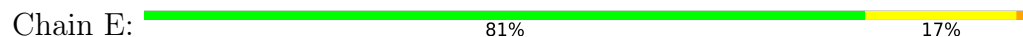
Chain C:  70% 28% .



- Molecule 34: 50S ribosomal protein L34

Chain D:  78% 22%

- Molecule 35: 50S ribosomal protein L35



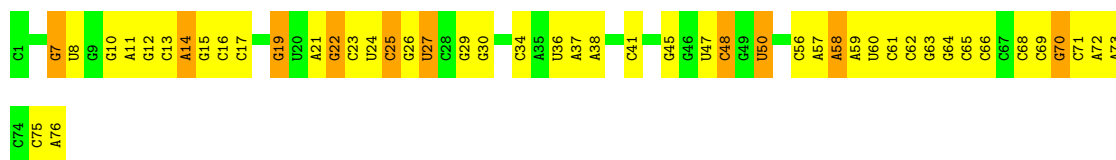
- Molecule 36: 50S ribosomal protein L36



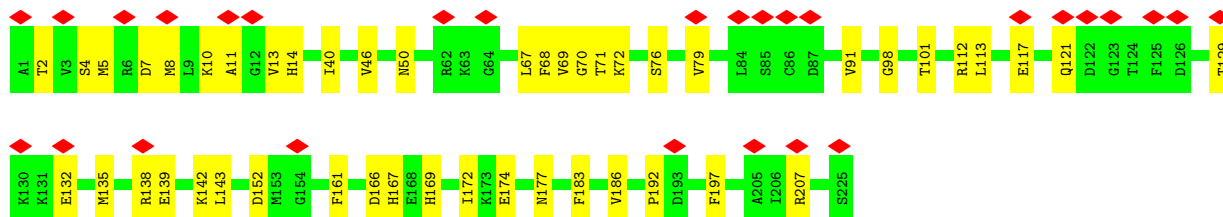
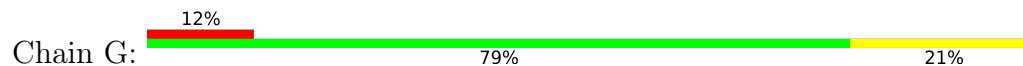
- Molecule 37: mRNA



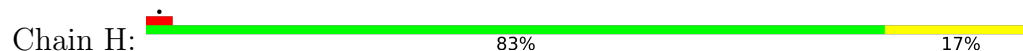
- Molecule 38: tRNA fMet

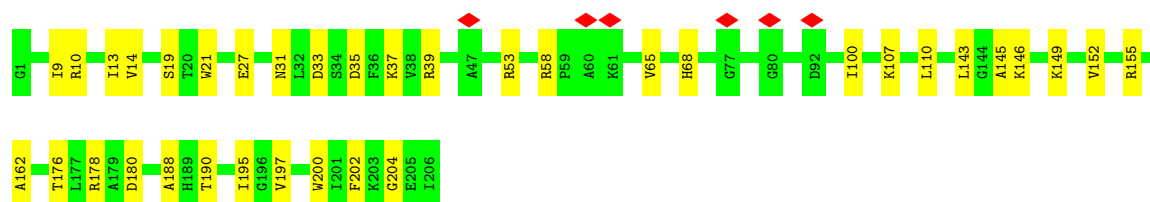


- Molecule 39: 30S ribosomal protein S2

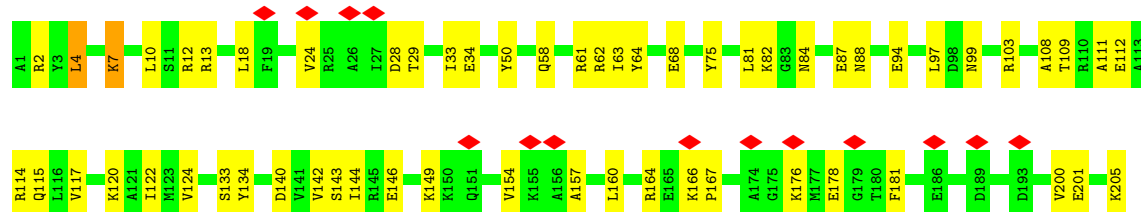


- Molecule 40: 30S ribosomal protein S3

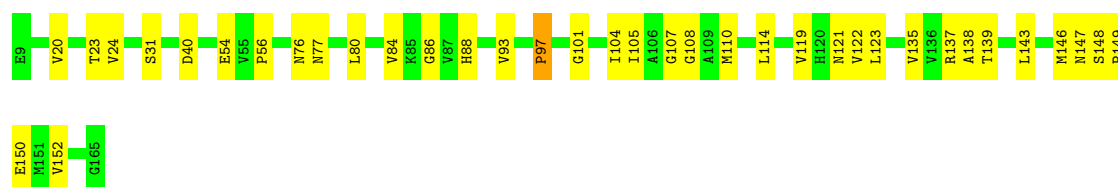




- Molecule 41: 30S ribosomal protein S4



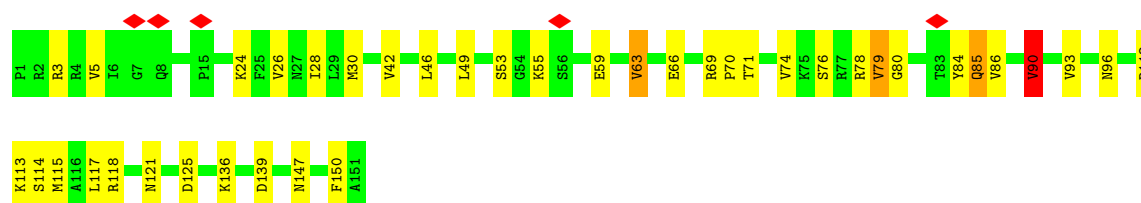
- Molecule 42: 30S ribosomal protein S5



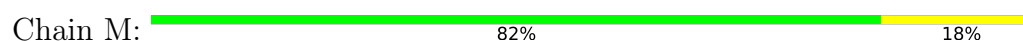
- Molecule 43: 30S ribosomal protein S6



- Molecule 44: 30S ribosomal protein S7

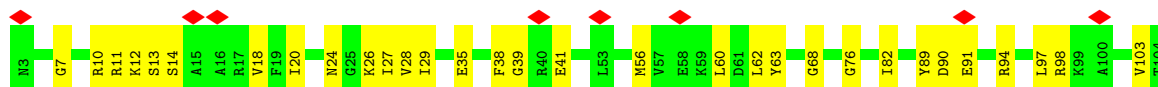


- Molecule 45: 30S ribosomal protein S8

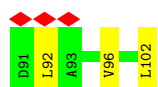
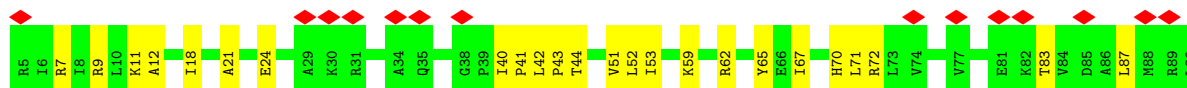




- Molecule 46: 30S ribosomal protein S9



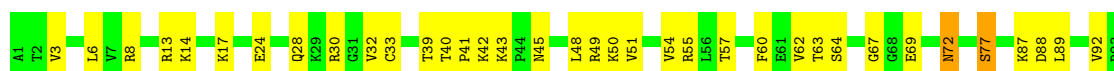
- Molecule 47: 30S ribosomal protein S10



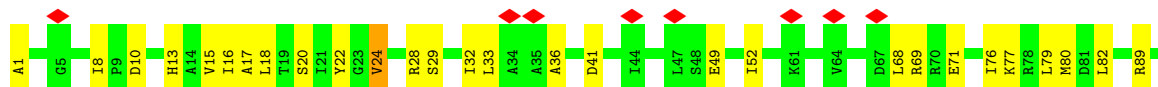
- Molecule 48: 30S ribosomal protein S11



- Molecule 49: 30S ribosomal protein S12

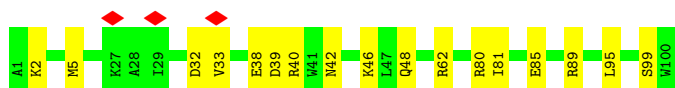
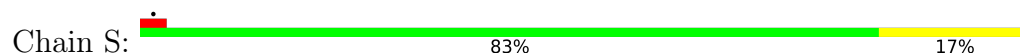


- Molecule 50: 30S ribosomal protein S13





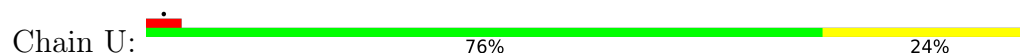
- Molecule 51: 30S ribosomal protein S14



- Molecule 52: 30S ribosomal protein S15



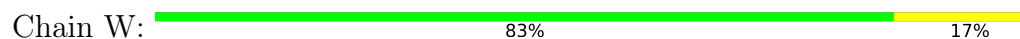
- Molecule 53: 30S ribosomal protein S16



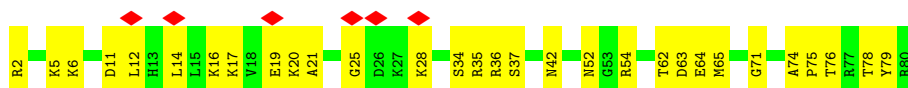
- Molecule 54: 30S ribosomal protein S17



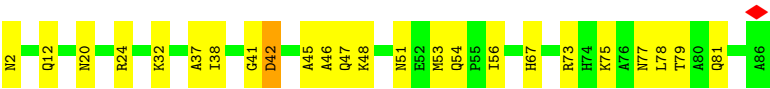
- Molecule 55: 30S ribosomal protein S18



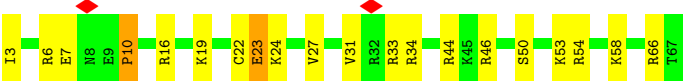
- Molecule 56: 30S ribosomal protein S19



- Molecule 57: 30S ribosomal protein S20



• Molecule 58: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	7257	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	19.960	Depositor
Minimum map value	-7.347	Depositor
Average map value	-0.020	Depositor
Map value standard deviation	1.142	Depositor
Recommended contour level	2.3	Depositor
Map size (Å)	381.8, 381.8, 381.8	wwPDB
Map dimensions	460, 460, 460	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: FME

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	3	0.61	0/36963	0.59	16/57662 (0.0%)
2	1	0.61	4/69796 (0.0%)	0.63	44/108888 (0.0%)
3	2	0.62	0/2872	0.60	2/4479 (0.0%)
4	5	0.67	0/1840	0.65	2/2868 (0.1%)
5	b	0.54	0/2122	0.77	0/2852
6	c	0.47	0/1586	0.78	0/2134
7	d	0.43	1/1571 (0.1%)	0.76	2/2113 (0.1%)
8	e	0.31	0/1435	0.75	0/1926
9	f	0.36	0/1343	0.74	0/1816
10	g	0.33	0/1122	0.89	4/1515 (0.3%)
11	a	0.29	0/1034	0.84	1/1387 (0.1%)
12	h	0.36	0/1002	1.14	12/1350 (0.9%)
13	i	0.36	0/1046	0.90	2/1410 (0.1%)
14	j	0.46	1/1152 (0.1%)	0.69	1/1551 (0.1%)
15	k	0.51	0/948	0.80	0/1268
16	l	0.45	0/1054	0.83	0/1403
17	m	0.45	0/1093	0.71	1/1460 (0.1%)
18	n	0.48	0/974	0.76	0/1301
19	o	0.32	0/902	0.81	4/1209 (0.3%)
20	p	0.42	0/929	0.71	0/1242
21	q	0.48	0/960	0.66	0/1278
22	r	0.41	0/829	0.68	0/1107
23	s	0.44	0/864	0.70	0/1156
24	t	0.39	0/745	0.72	0/994
25	u	0.34	0/788	0.76	3/1051 (0.3%)
26	v	0.39	0/766	0.68	0/1025
27	w	0.46	0/582	0.66	0/769
28	x	0.47	0/635	0.72	0/848
29	y	0.29	0/510	0.65	0/677
30	z	0.37	0/453	0.63	0/605
31	A	0.26	0/358	0.72	0/480
32	B	0.43	0/450	0.71	0/599

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	C	0.36	0/417	0.68	0/554
34	D	0.55	0/380	0.78	0/498
35	E	0.48	0/513	0.70	0/676
36	F	0.46	0/303	0.75	0/397
37	4	0.64	0/465	0.58	0/725
38	6	0.68	0/1832	0.65	0/2855
39	G	0.32	0/1788	0.69	0/2408
40	H	0.34	0/1652	0.66	0/2225
41	I	0.32	0/1665	0.78	2/2227 (0.1%)
42	J	0.44	0/1170	0.86	2/1573 (0.1%)
43	K	0.39	0/836	0.92	4/1128 (0.4%)
44	L	0.48	0/1196	0.86	4/1602 (0.2%)
45	M	0.40	0/989	0.67	0/1326
46	N	0.33	0/1034	0.83	2/1375 (0.1%)
47	O	0.33	0/797	0.79	0/1077
48	P	0.42	0/886	0.82	1/1195 (0.1%)
49	Q	0.44	0/969	0.87	0/1300
50	R	0.31	0/893	0.84	2/1193 (0.2%)
51	S	0.33	0/817	0.75	0/1088
52	T	0.38	0/722	0.69	0/964
53	U	0.34	0/659	0.68	0/884
54	V	0.37	0/658	0.87	2/881 (0.2%)
55	W	0.35	0/545	0.75	2/731 (0.3%)
56	X	0.36	0/653	0.79	1/877 (0.1%)
57	Y	0.35	0/671	0.76	2/888 (0.2%)
58	Z	0.38	0/551	1.17	4/728 (0.5%)
All	All	0.56	6/161785 (0.0%)	0.66	122/241798 (0.1%)

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	3	0	6
2	1	0	43
3	2	0	1
4	5	0	2
5	b	0	1
8	e	0	3
10	g	0	2
11	a	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
13	i	0	1
15	k	0	2
17	m	0	2
35	E	0	1
36	F	0	1
42	J	0	1
43	K	0	1
44	L	0	1
46	N	0	1
47	O	0	1
48	P	0	1
49	Q	0	1
58	Z	0	1
All	All	0	74

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1	870	U	C3'-O3'	8.96	1.55	1.42
2	1	870	U	O3'-P	8.67	1.74	1.61
2	1	906	U	O3'-P	5.82	1.69	1.61
7	d	43	THR	CA-CB	-5.68	1.45	1.53
2	1	1057	A	C3'-O3'	5.50	1.50	1.42

The worst 5 of 122 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	V	63	CYS	CA-C-N	10.63	135.17	120.39
54	V	63	CYS	C-N-CA	10.63	135.17	120.39
2	1	1057	A	C3'-C2'-O2'	9.35	124.72	110.70
2	1	1105	U	C4'-C3'-O3'	-8.55	96.58	109.40
12	h	44	ALA	N-CA-C	-7.67	103.71	113.23

There are no chirality outliers.

5 of 74 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	3	1167	A	Sidechain
1	3	130	A	Sidechain
1	3	760	G	Sidechain
1	3	818	G	Sidechain

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Mol	Chain	Res	Type	Group
1	3	884	U	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	3	33012	0	16618	758	0
2	1	62317	0	31346	1875	0
3	2	2568	0	1303	74	0
4	5	1647	0	831	78	0
5	b	2083	0	2157	41	0
6	c	1565	0	1616	27	0
7	d	1552	0	1619	27	0
8	e	1411	0	1447	42	0
9	f	1323	0	1374	28	0
10	g	1111	0	1148	15	0
11	a	1027	0	1092	23	0
12	h	989	0	1025	185	0
13	i	1032	0	1088	39	0
14	j	1129	0	1162	8	0
15	k	939	0	1012	23	0
16	l	1045	0	1117	23	0
17	m	1074	0	1157	41	0
18	n	961	0	1000	21	0
19	o	892	0	923	12	0
20	p	917	0	965	18	0
21	q	947	0	1022	10	0
22	r	816	0	839	18	0
23	s	857	0	922	13	0
24	t	739	0	807	13	0
25	u	780	0	834	9	0
26	v	753	0	780	14	0
27	w	575	0	592	8	0
28	x	625	0	655	11	0
29	y	509	0	543	5	0
30	z	449	0	491	4	0
31	A	351	0	350	7	0
32	B	444	0	461	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	C	410	0	440	10	0
34	D	377	0	418	8	0
35	E	504	0	574	8	0
36	F	302	0	343	7	0
37	4	413	0	209	14	0
38	6	1640	0	837	60	0
39	G	1757	0	1787	26	0
40	H	1625	0	1699	22	0
41	I	1643	0	1710	44	0
42	J	1157	0	1199	29	0
43	K	818	0	808	19	0
44	L	1182	0	1240	34	0
45	M	979	0	1034	18	0
46	N	1022	0	1070	27	0
47	O	787	0	828	20	0
48	P	870	0	878	25	0
49	Q	955	0	1019	41	0
50	R	884	0	944	31	0
51	S	805	0	847	14	0
52	T	714	0	737	20	0
53	U	649	0	666	19	0
54	V	649	0	691	14	0
55	W	536	0	552	7	0
56	X	638	0	665	25	0
57	Y	665	0	714	17	0
58	Z	545	0	579	26	0
59	1	8	0	8	0	0
60	5	7	0	7	0	0
All	All	148980	0	100799	3572	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 14.

The worst 5 of 3572 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1057:A:C2'	12:h:34:THR:CG2	1.76	1.60
2:1:1057:A:H2'	12:h:34:THR:CG2	1.19	1.58
2:1:1057:A:C3'	12:h:34:THR:HG21	1.25	1.56
2:1:1046:A:H1'	12:h:8:LYS:NZ	1.11	1.42
2:1:871:U:H4'	17:m:68:PHE:CE1	1.61	1.35

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	b	269/271 (99%)	235 (87%)	33 (12%)	1 (0%)	30	62
6	c	207/209 (99%)	188 (91%)	19 (9%)	0	100	100
7	d	199/201 (99%)	184 (92%)	15 (8%)	0	100	100
8	e	175/177 (99%)	158 (90%)	15 (9%)	2 (1%)	11	43
9	f	174/176 (99%)	156 (90%)	17 (10%)	1 (1%)	21	56
10	g	147/149 (99%)	121 (82%)	24 (16%)	2 (1%)	9	39
11	a	130/223 (58%)	109 (84%)	20 (15%)	1 (1%)	16	50
12	h	129/131 (98%)	92 (71%)	27 (21%)	10 (8%)	1	5
13	i	139/141 (99%)	116 (84%)	22 (16%)	1 (1%)	18	52
14	j	140/142 (99%)	126 (90%)	13 (9%)	1 (1%)	18	52
15	k	120/122 (98%)	99 (82%)	21 (18%)	0	100	100
16	l	141/143 (99%)	120 (85%)	21 (15%)	0	100	100
17	m	134/136 (98%)	120 (90%)	14 (10%)	0	100	100
18	n	118/120 (98%)	104 (88%)	14 (12%)	0	100	100
19	o	114/116 (98%)	105 (92%)	9 (8%)	0	100	100
20	p	112/114 (98%)	104 (93%)	8 (7%)	0	100	100
21	q	115/117 (98%)	111 (96%)	4 (4%)	0	100	100
22	r	101/103 (98%)	85 (84%)	16 (16%)	0	100	100
23	s	108/110 (98%)	104 (96%)	3 (3%)	1 (1%)	14	47
24	t	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
25	u	100/102 (98%)	88 (88%)	12 (12%)	0	100	100
26	v	92/94 (98%)	88 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	w	73/75 (97%)	68 (93%)	5 (7%)	0	100	100
28	x	75/77 (97%)	68 (91%)	7 (9%)	0	100	100
29	y	61/63 (97%)	56 (92%)	5 (8%)	0	100	100
30	z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
31	A	43/66 (65%)	34 (79%)	9 (21%)	0	100	100
32	B	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
33	C	48/50 (96%)	43 (90%)	5 (10%)	0	100	100
34	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
35	E	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	7	36
36	F	36/38 (95%)	27 (75%)	9 (25%)	0	100	100
39	G	223/225 (99%)	207 (93%)	16 (7%)	0	100	100
40	H	204/206 (99%)	185 (91%)	19 (9%)	0	100	100
41	I	203/205 (99%)	174 (86%)	28 (14%)	1 (0%)	24	59
42	J	155/157 (99%)	133 (86%)	21 (14%)	1 (1%)	21	56
43	K	98/100 (98%)	71 (72%)	26 (26%)	1 (1%)	12	45
44	L	149/151 (99%)	134 (90%)	14 (9%)	1 (1%)	18	52
45	M	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
46	N	125/127 (98%)	108 (86%)	16 (13%)	1 (1%)	16	50
47	O	96/98 (98%)	81 (84%)	15 (16%)	0	100	100
48	P	114/116 (98%)	97 (85%)	15 (13%)	2 (2%)	6	34
49	Q	121/123 (98%)	100 (83%)	20 (16%)	1 (1%)	16	50
50	R	112/114 (98%)	98 (88%)	13 (12%)	1 (1%)	14	47
51	S	98/100 (98%)	84 (86%)	14 (14%)	0	100	100
52	T	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	42
53	U	80/82 (98%)	71 (89%)	9 (11%)	0	100	100
54	V	78/80 (98%)	65 (83%)	13 (17%)	0	100	100
55	W	63/65 (97%)	61 (97%)	2 (3%)	0	100	100
56	X	77/79 (98%)	72 (94%)	5 (6%)	0	100	100
57	Y	83/85 (98%)	81 (98%)	2 (2%)	0	100	100
58	Z	63/65 (97%)	40 (64%)	21 (33%)	2 (3%)	3	21
All	All	5962/6178 (96%)	5252 (88%)	677 (11%)	33 (1%)	23	56

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	h	80	THR
12	h	108	VAL
12	h	118	ILE
50	R	104	ASN
52	T	46	LYS

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	b	216/216 (100%)	216 (100%)	0	100	100
6	c	164/164 (100%)	163 (99%)	1 (1%)	78	84
7	d	165/165 (100%)	164 (99%)	1 (1%)	78	84
8	e	148/148 (100%)	148 (100%)	0	100	100
9	f	137/137 (100%)	135 (98%)	2 (2%)	57	76
10	g	114/114 (100%)	110 (96%)	4 (4%)	32	64
11	a	110/174 (63%)	110 (100%)	0	100	100
12	h	100/100 (100%)	94 (94%)	6 (6%)	17	50
13	i	109/109 (100%)	106 (97%)	3 (3%)	38	68
14	j	116/116 (100%)	116 (100%)	0	100	100
15	k	103/103 (100%)	100 (97%)	3 (3%)	37	67
16	l	102/102 (100%)	102 (100%)	0	100	100
17	m	109/109 (100%)	109 (100%)	0	100	100
18	n	100/100 (100%)	99 (99%)	1 (1%)	68	80
19	o	86/86 (100%)	86 (100%)	0	100	100
20	p	99/99 (100%)	98 (99%)	1 (1%)	68	80
21	q	89/89 (100%)	88 (99%)	1 (1%)	65	79
22	r	84/84 (100%)	83 (99%)	1 (1%)	63	79
23	s	93/93 (100%)	92 (99%)	1 (1%)	65	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
24	t	80/80 (100%)	79 (99%)	1 (1%)	61	78
25	u	83/83 (100%)	82 (99%)	1 (1%)	63	79
26	v	78/78 (100%)	77 (99%)	1 (1%)	61	78
27	w	57/57 (100%)	57 (100%)	0	100	100
28	x	67/67 (100%)	67 (100%)	0	100	100
29	y	55/55 (100%)	55 (100%)	0	100	100
30	z	48/48 (100%)	48 (100%)	0	100	100
31	A	42/59 (71%)	42 (100%)	0	100	100
32	B	47/47 (100%)	47 (100%)	0	100	100
33	C	45/45 (100%)	44 (98%)	1 (2%)	45	71
34	D	38/38 (100%)	38 (100%)	0	100	100
35	E	51/51 (100%)	51 (100%)	0	100	100
36	F	34/34 (100%)	34 (100%)	0	100	100
39	G	186/186 (100%)	185 (100%)	1 (0%)	81	85
40	H	170/170 (100%)	169 (99%)	1 (1%)	78	84
41	I	172/172 (100%)	172 (100%)	0	100	100
42	J	119/119 (100%)	119 (100%)	0	100	100
43	K	87/87 (100%)	87 (100%)	0	100	100
44	L	124/124 (100%)	121 (98%)	3 (2%)	43	70
45	M	104/104 (100%)	104 (100%)	0	100	100
46	N	105/105 (100%)	104 (99%)	1 (1%)	68	80
47	O	86/86 (100%)	85 (99%)	1 (1%)	63	79
48	P	89/89 (100%)	88 (99%)	1 (1%)	65	79
49	Q	103/103 (100%)	101 (98%)	2 (2%)	50	73
50	R	92/92 (100%)	90 (98%)	2 (2%)	45	71
51	S	83/83 (100%)	83 (100%)	0	100	100
52	T	76/76 (100%)	74 (97%)	2 (3%)	40	69
53	U	65/65 (100%)	65 (100%)	0	100	100
54	V	74/74 (100%)	71 (96%)	3 (4%)	27	60
55	W	56/56 (100%)	56 (100%)	0	100	100
56	X	70/70 (100%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	Y	65/65 (100%)	65 (100%)	0	100	100
58	Z	55/55 (100%)	55 (100%)	0	100	100
All	All	4950/5031 (98%)	4904 (99%)	46 (1%)	68	81

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	C	22	THR
47	O	67	ILE
39	G	69	VAL
44	L	85	GLN
49	Q	60	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 98 such sidechains are listed below:

Mol	Chain	Res	Type
40	H	139	ASN
44	L	85	GLN
41	I	70	GLN
42	J	76	ASN
46	N	30	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	1538/1539 (99%)	184 (11%)	4 (0%)
2	1	2902/2903 (99%)	422 (14%)	19 (0%)
3	2	119/120 (99%)	16 (13%)	1 (0%)
37	4	18/35 (51%)	4 (22%)	0
38	6	76/77 (98%)	14 (18%)	0
4	5	76/77 (98%)	15 (19%)	0
All	All	4729/4751 (99%)	655 (13%)	24 (0%)

5 of 655 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	4	U
1	3	5	U
1	3	6	G

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Mol	Chain	Res	Type
1	3	9	G
1	3	13	U

5 of 24 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	1156	A
2	1	2311	A
2	1	2296	U
2	1	2326	C
2	1	760	G

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	$\# Z > 2$
59	FME	1	3001	60	6,7,10	0.86	0	2,7,11	1.32	0
60	PRO	5	101	4,59	6,7,8	4.47	4 (66%)	7,8,10	1.56	1 (14%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	FME	1	3001	60	-	4/5/6/11	-
60	PRO	5	101	4,59	-	0/0/9/11	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	5	101	PRO	CA-N	7.21	1.61	1.48
60	5	101	PRO	CD-N	-5.57	1.29	1.49
60	5	101	PRO	O-C	5.20	1.39	1.20
60	5	101	PRO	CB-CA	-2.66	1.31	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	5	101	PRO	O-C-CA	-3.52	115.71	124.77

There are no chirality outliers.

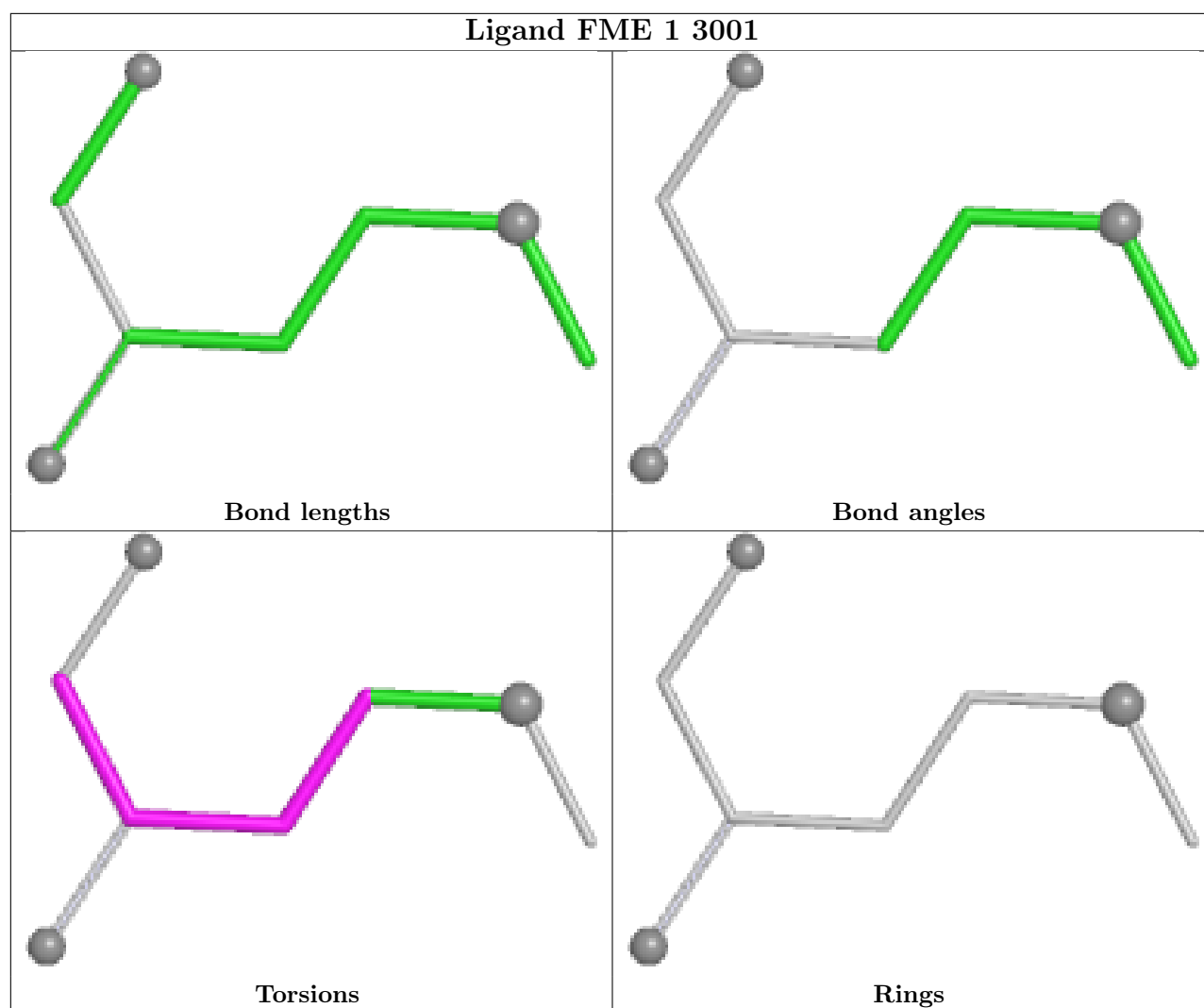
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
59	1	3001	FME	N-CA-CB-CG
59	1	3001	FME	C-CA-CB-CG
59	1	3001	FME	O-C-CA-CB
59	1	3001	FME	CA-CB-CG-SD

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

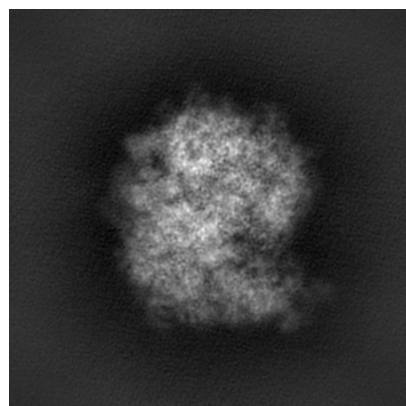
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25411. These allow visual inspection of the internal detail of the map and identification of artifacts.

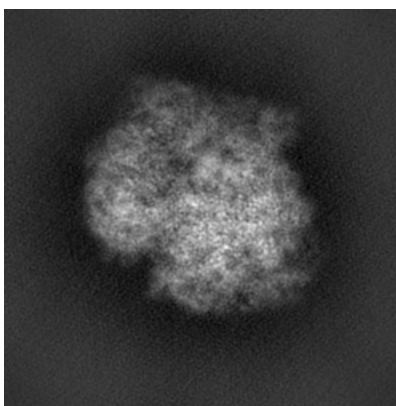
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

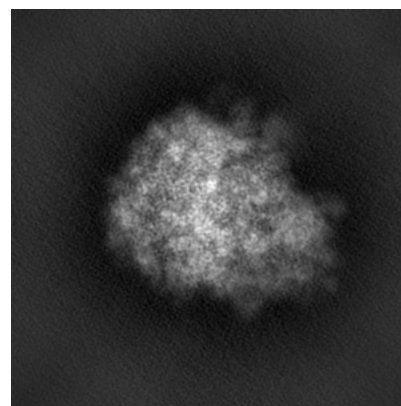
6.1.1 Primary map



X

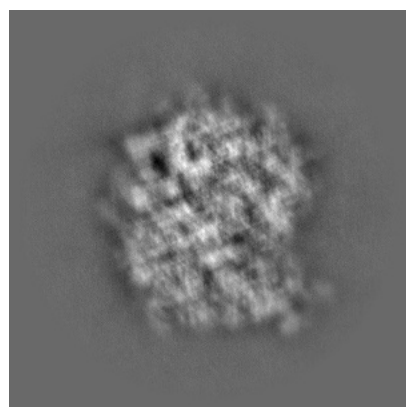


Y

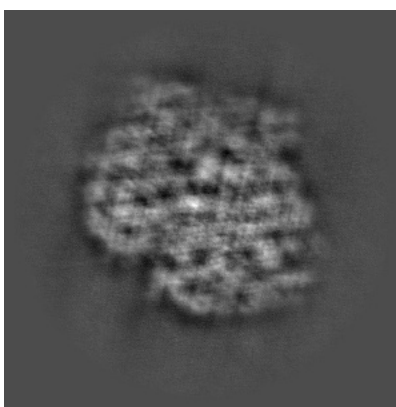


Z

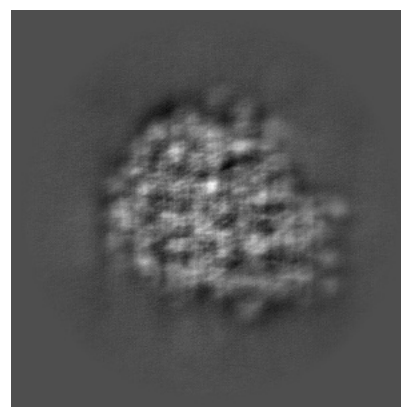
6.1.2 Raw map



X



Y

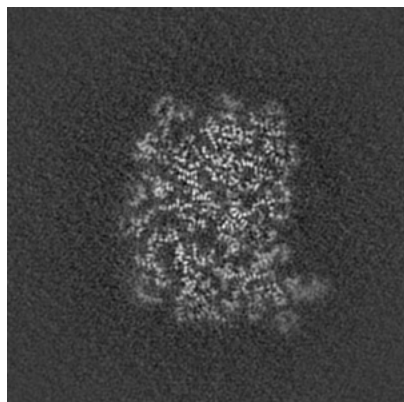


Z

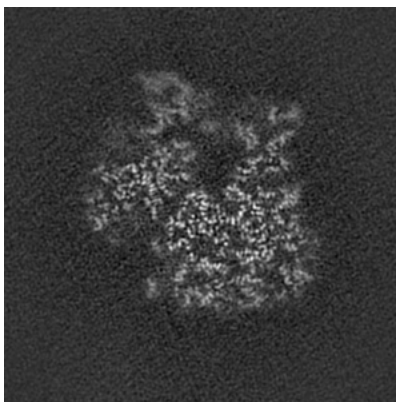
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

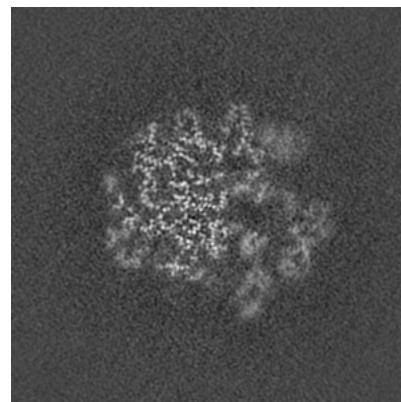
6.2.1 Primary map



X Index: 230

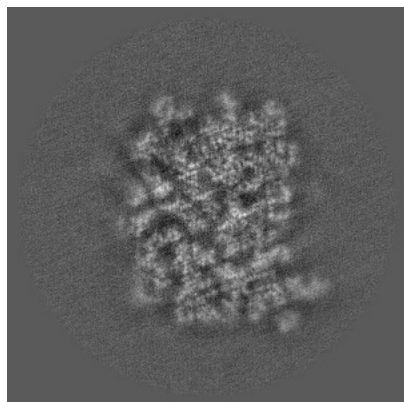


Y Index: 230

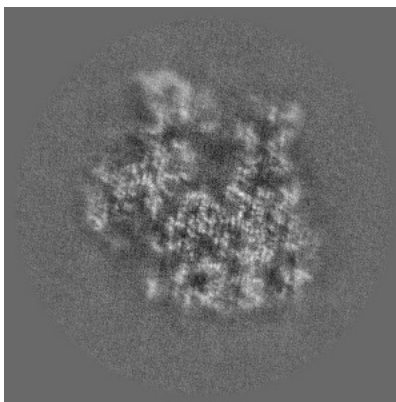


Z Index: 230

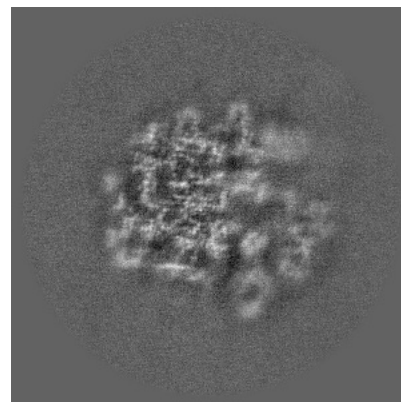
6.2.2 Raw map



X Index: 230



Y Index: 230

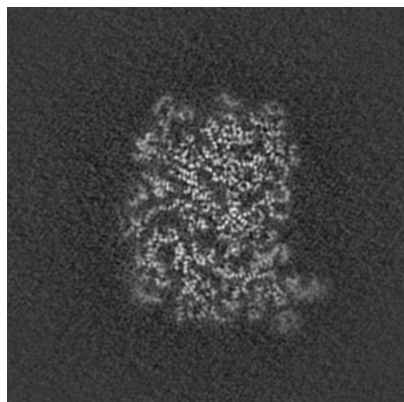


Z Index: 230

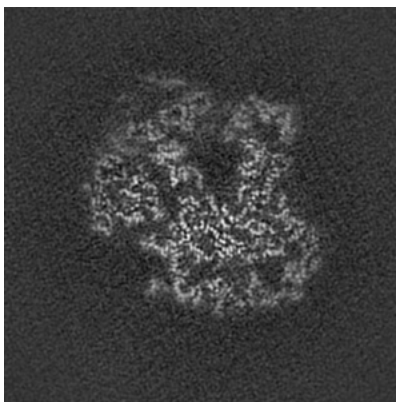
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

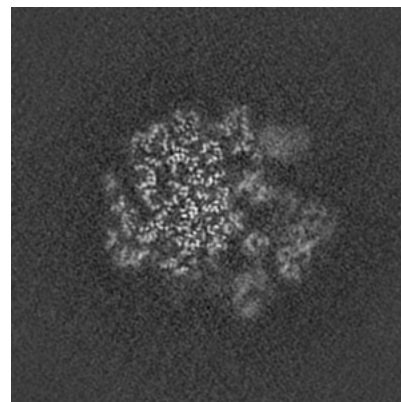
6.3.1 Primary map



X Index: 229

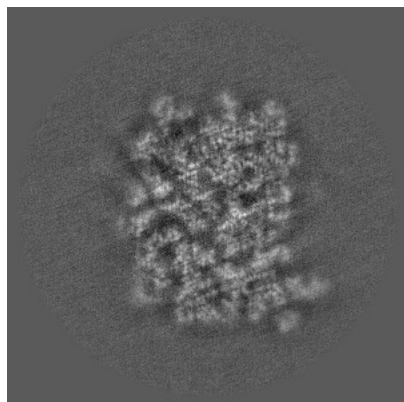


Y Index: 222

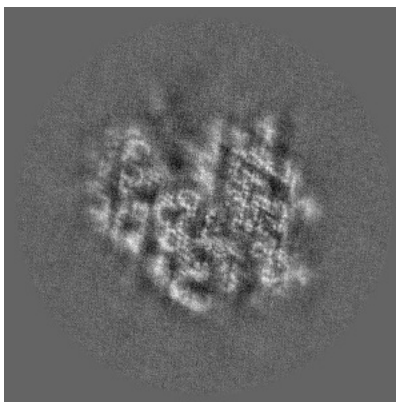


Z Index: 227

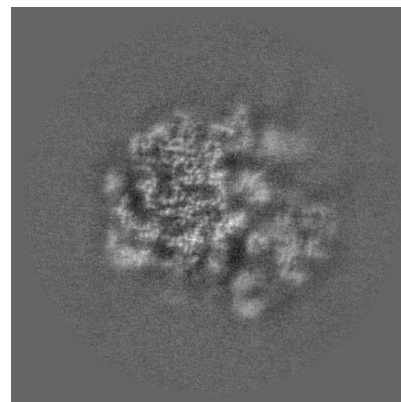
6.3.2 Raw map



X Index: 230



Y Index: 253

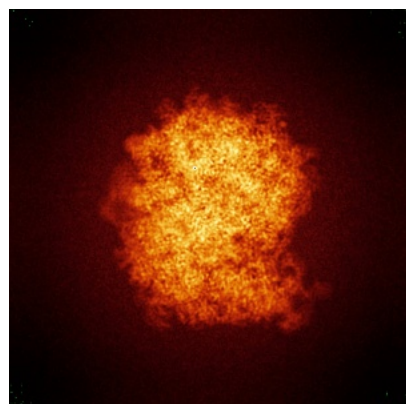


Z Index: 224

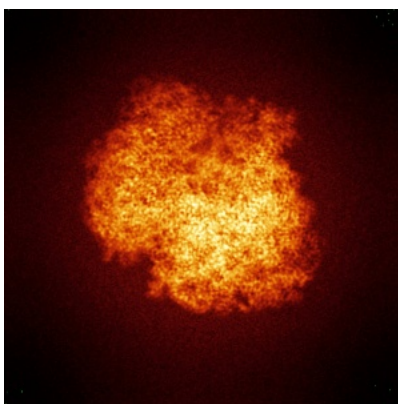
The images above show the largest variance slices of the map in three orthogonal directions.

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

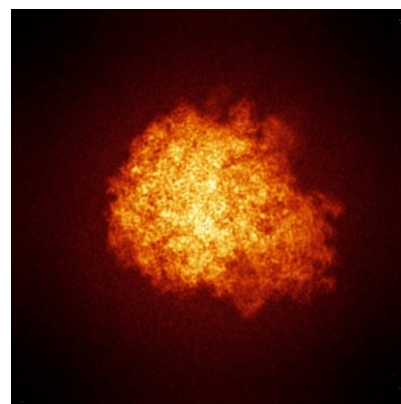
6.4.1 Primary map



X

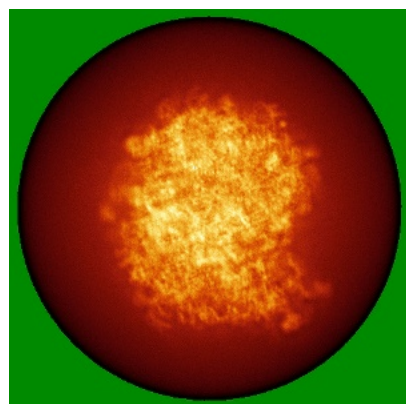


Y

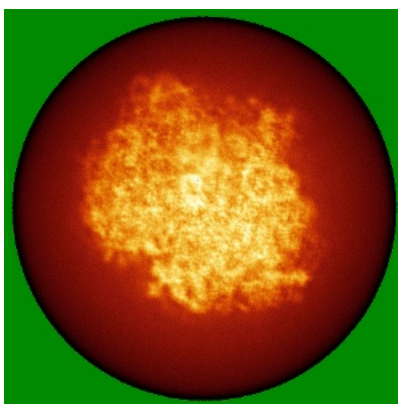


Z

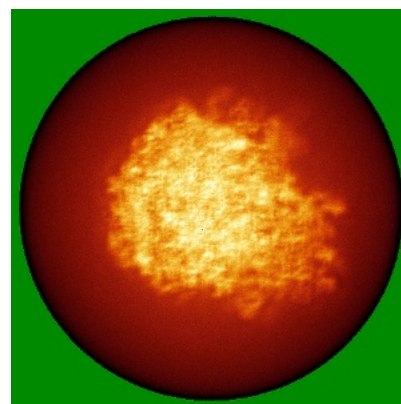
6.4.2 Raw map



X



Y

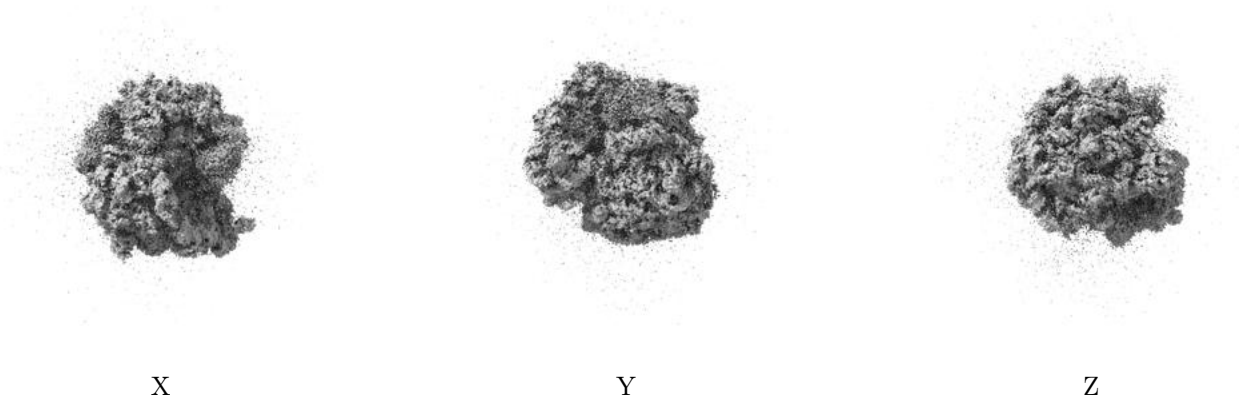


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

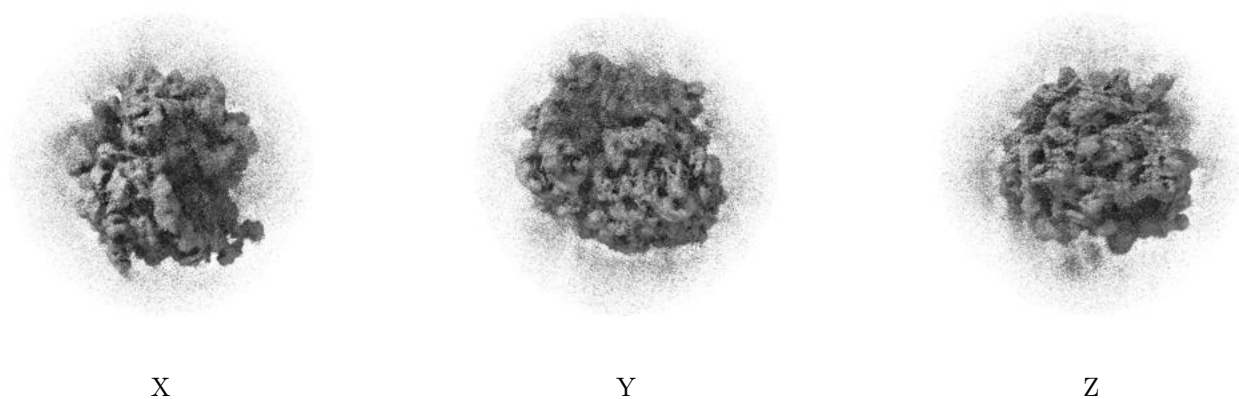
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 2.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

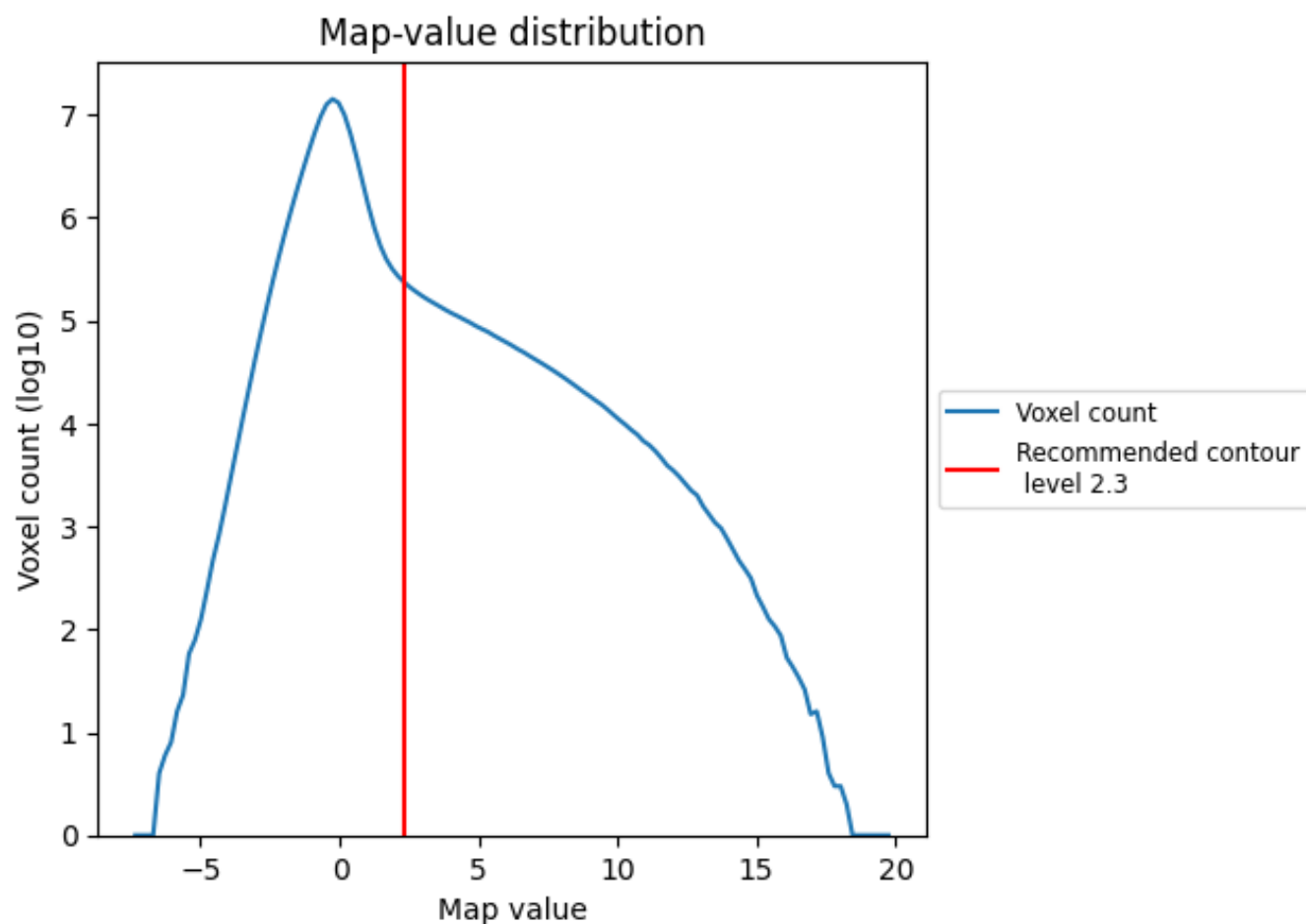
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

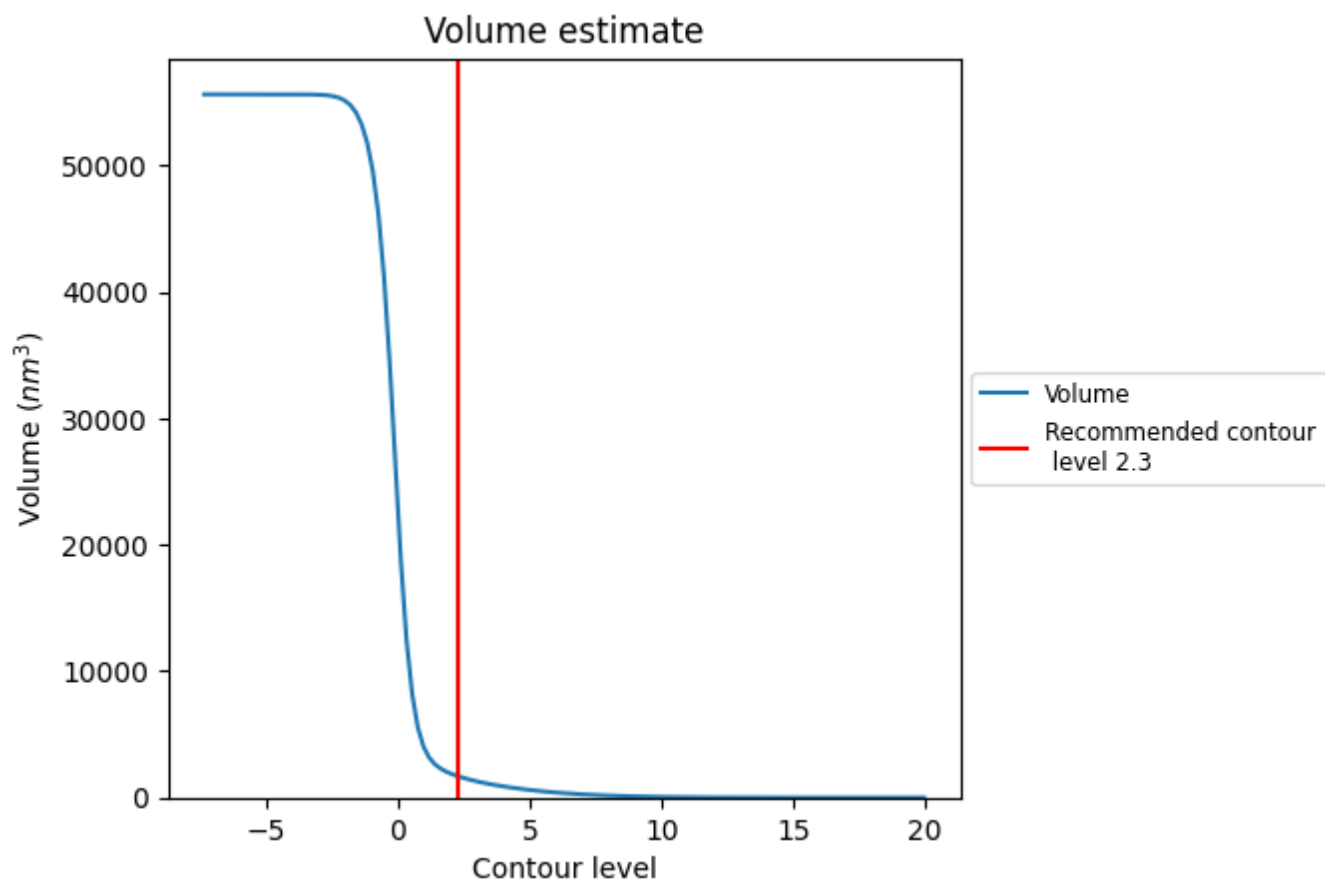
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

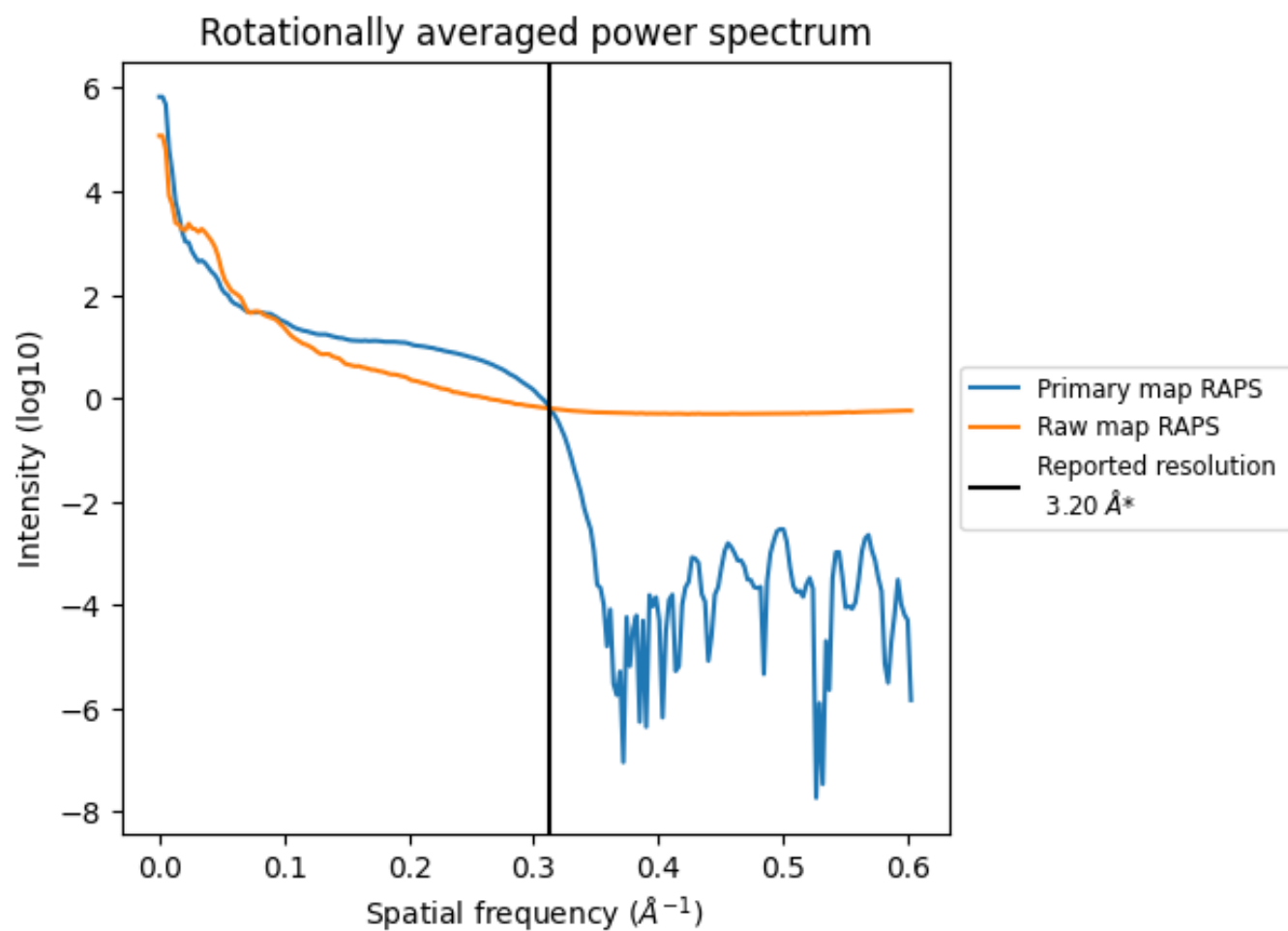
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1677 nm^3 ; this corresponds to an approximate mass of 1515 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 ⓘ

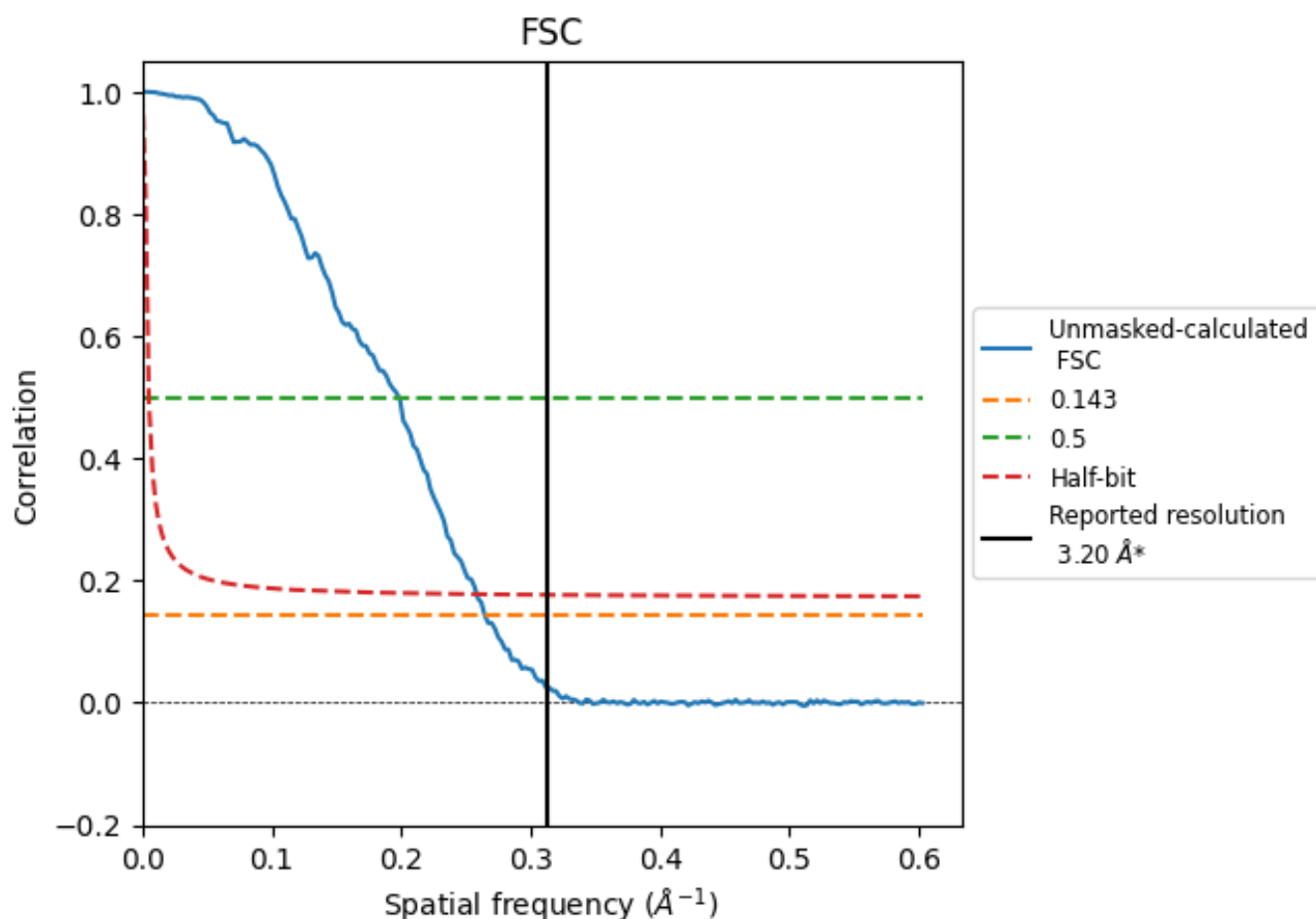


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

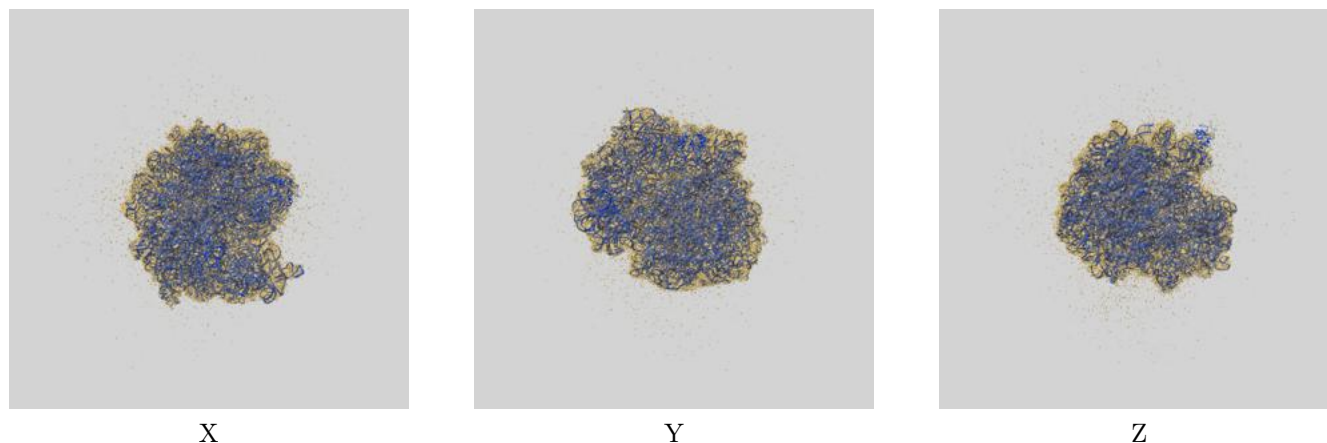
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.78	5.05	3.87

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.78 differs from the reported value 3.2 by more than 10 %

9 Map-model fit [i](#)

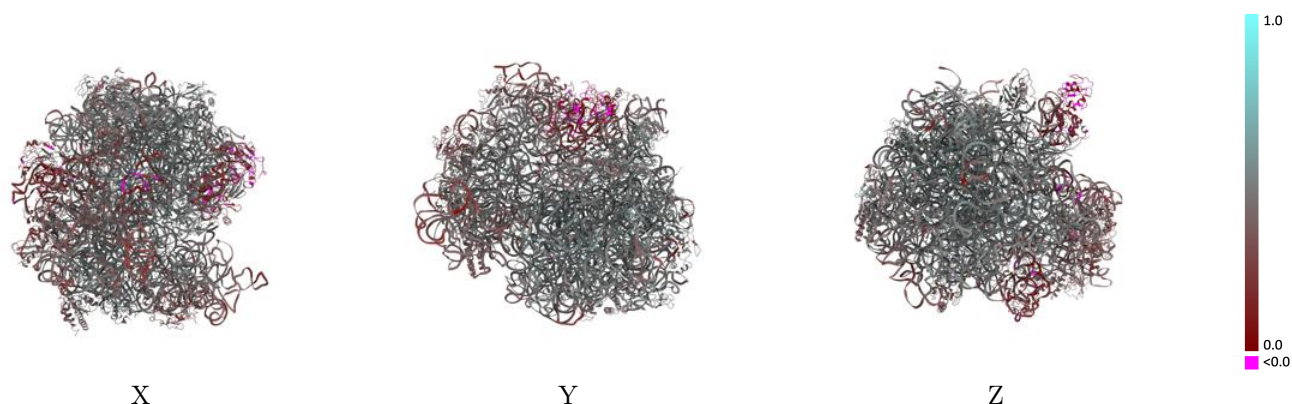
This section contains information regarding the fit between EMDB map EMD-25411 and PDB model 7SSO. Per-residue inclusion information can be found in section [3](#) on page [16](#).

9.1 Map-model overlay [i](#)



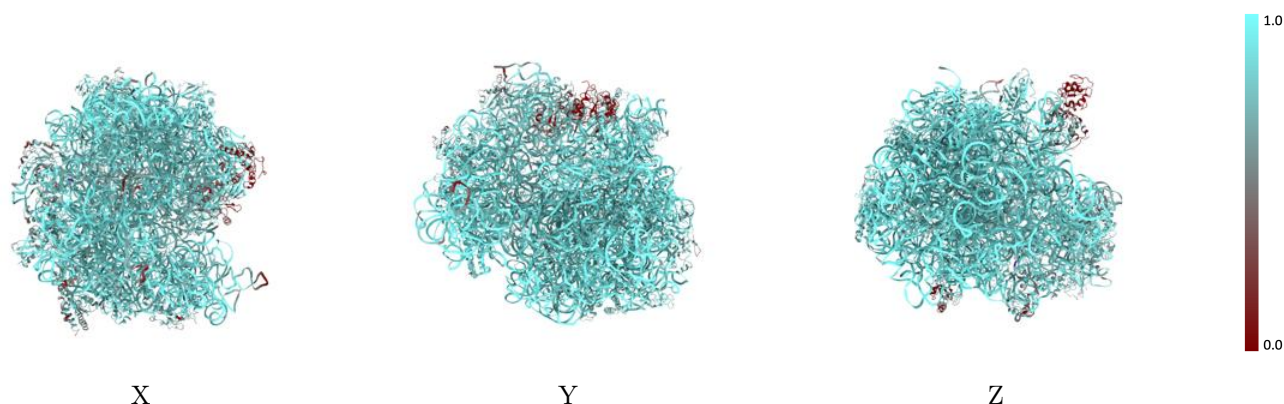
The images above show the 3D surface view of the map at the recommended contour level 2.3 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



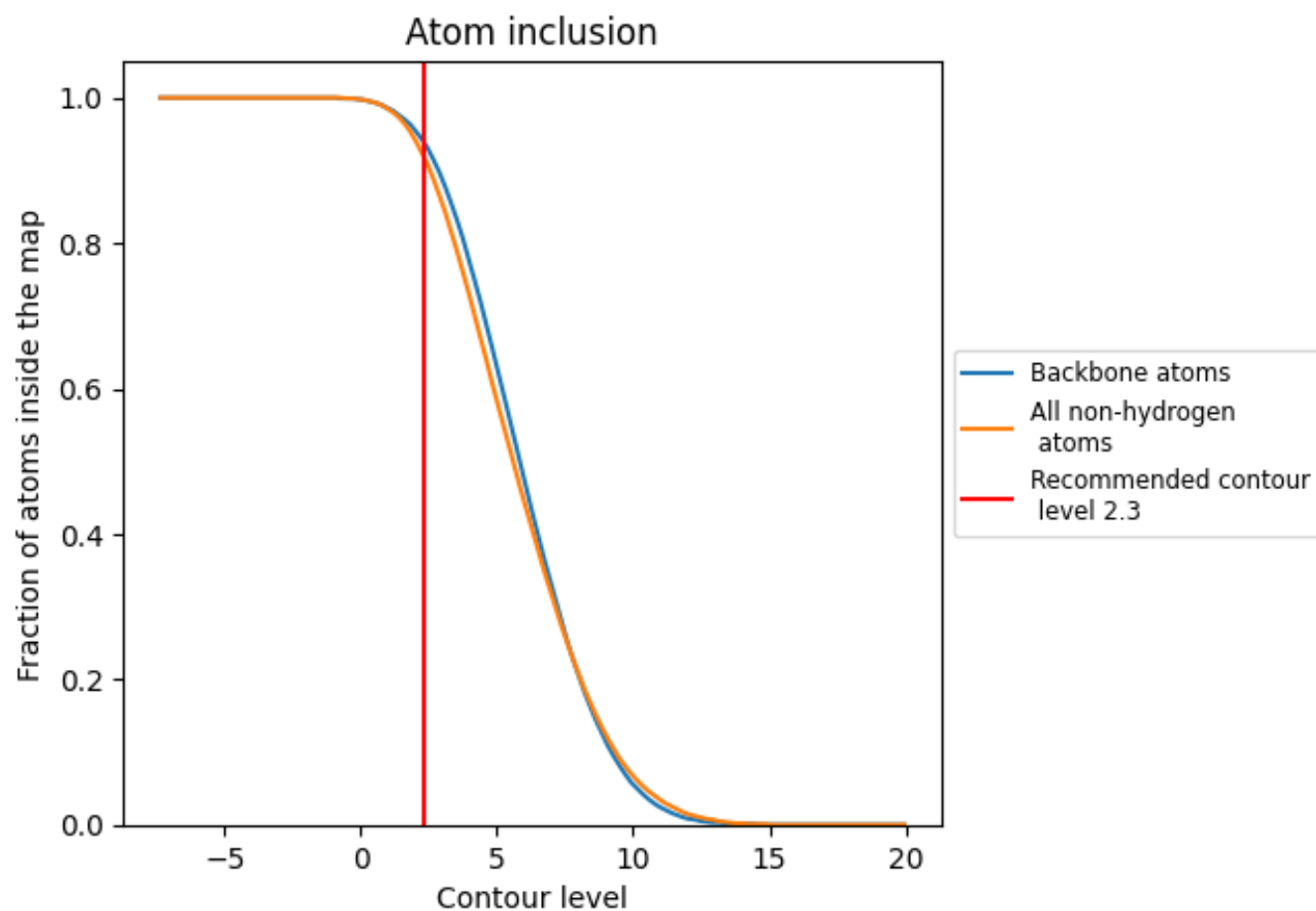
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.3).

9.4 Atom inclusion ⓘ



At the recommended contour level, 94% of all backbone atoms, 92% 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 (2.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9200	 0.4460
1	 0.9760	 0.4670
2	 0.9680	 0.4370
3	 0.9550	 0.4360
4	 0.8230	 0.2980
5	 0.9760	 0.3960
6	 0.9620	 0.3490
A	 0.7440	 0.2950
B	 0.9230	 0.4840
C	 0.8560	 0.4700
D	 0.9470	 0.5180
E	 0.9530	 0.5220
F	 0.9280	 0.5100
G	 0.6860	 0.4110
H	 0.8120	 0.4430
I	 0.7650	 0.3900
J	 0.8980	 0.4730
K	 0.8720	 0.4210
L	 0.7720	 0.3560
M	 0.8810	 0.4840
N	 0.7840	 0.4140
O	 0.6430	 0.4050
P	 0.9080	 0.4570
Q	 0.9070	 0.4620
R	 0.7660	 0.3600
S	 0.8050	 0.4070
T	 0.9260	 0.4640
U	 0.8880	 0.4600
V	 0.8880	 0.4480
W	 0.9130	 0.4730
X	 0.7880	 0.3620
Y	 0.8450	 0.4010
Z	 0.7720	 0.3790
a	 0.6600	 0.3070
b	 0.9630	 0.5200



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Chain	Atom inclusion	Q-score
c	 0.9170	 0.4980
d	 0.8220	 0.4620
e	 0.8060	 0.3520
f	 0.8690	 0.4380
g	 0.3140	 0.3340
h	 0.0900	 0.0500
i	 0.3540	 0.2350
j	 0.9290	 0.4990
k	 0.9400	 0.5110
l	 0.9050	 0.4880
m	 0.9190	 0.4980
n	 0.9200	 0.4940
o	 0.8670	 0.4370
p	 0.8960	 0.4880
q	 0.9440	 0.5130
r	 0.8780	 0.4950
s	 0.9130	 0.5020
t	 0.8750	 0.4710
u	 0.8270	 0.4530
v	 0.8710	 0.4780
w	 0.9520	 0.5230
x	 0.9420	 0.5080
y	 0.8110	 0.4110
z	 0.8830	 0.4910