



wwPDB EM Validation Summary Report ⓘ

Sep 5, 2026 – 08:49 am BST

PDB ID : 9SPJ / pdb_00009spj
EMDB ID : EMD-55092
Title : CryoEM structure of the vacant Candida auris 80S ribosome
Authors : Atamas, A.; Stetsenko, A.; Incarnato, D.; Macia Valero, A.; Rogachev, A.;
Billerbeck, S.; Guskov, A.
Deposited on : 2025-09-17
Resolution : 2.13 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.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMD 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) : 2.50

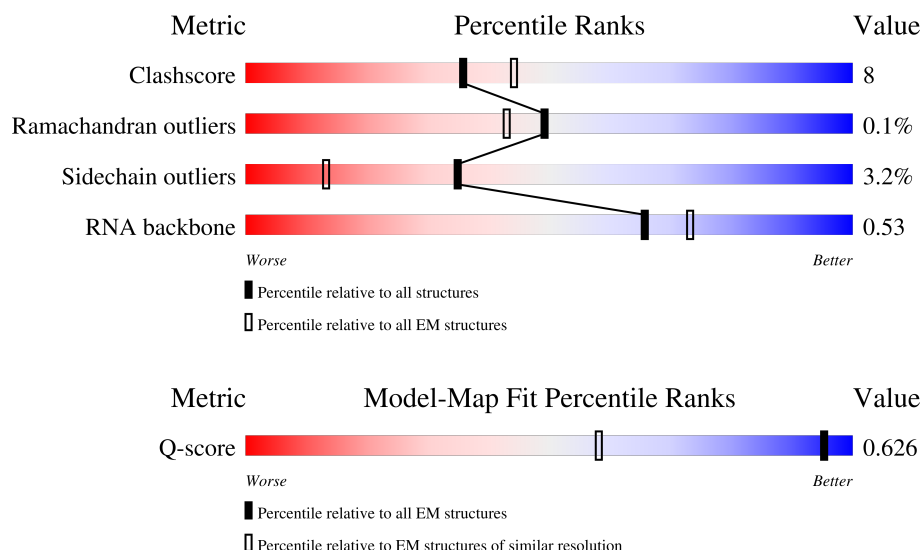
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.13 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.



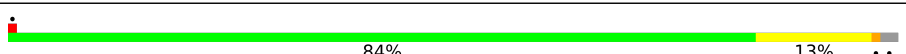
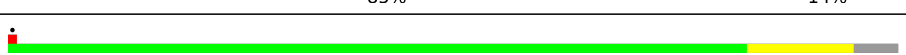
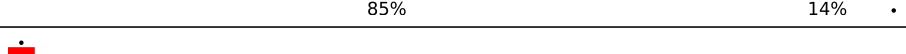
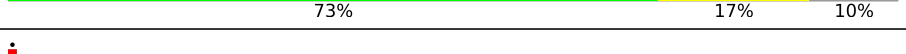
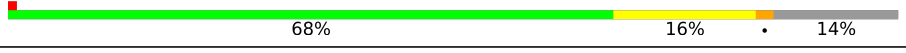
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	2439 (1.64 - 2.63)

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	A	3283	
2	B	122	
3	C	158	

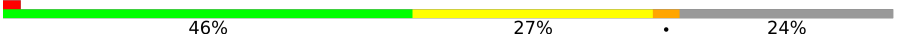
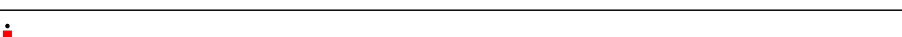
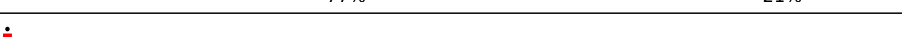
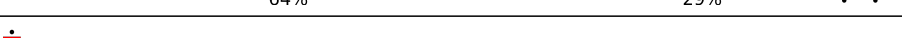
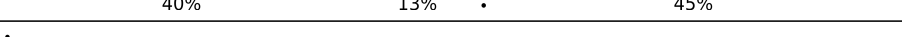
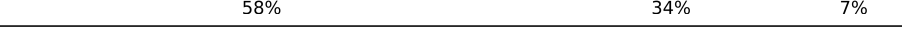
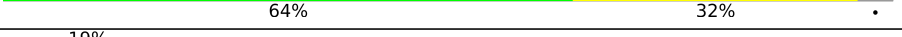
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Mol	Chain	Length	Quality of chain
4	CA	1775	
5	D	254	
6	E	389	
7	F	363	
8	G	298	
9	H	165	
10	I	241	
11	J	263	
12	K	191	
13	L	220	
14	M	172	
15	N	198	
16	O	131	
17	P	204	
18	Q	200	
19	R	185	
20	S	186	
21	T	208	
22	U	186	
23	V	160	
24	W	119	
25	X	137	
26	Y	156	
27	Z	140	
28	ZA	204	

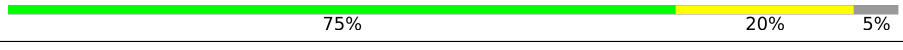
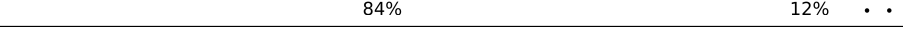
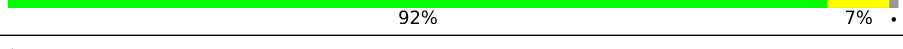
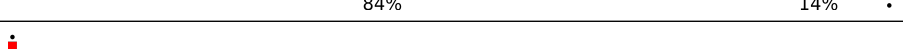
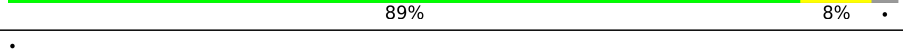
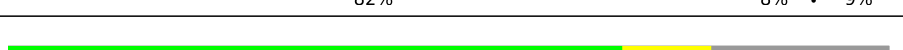
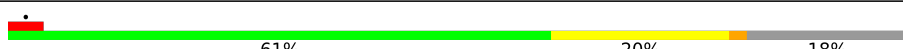
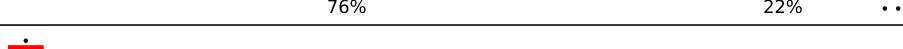
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Mol	Chain	Length	Quality of chain
29	ZB	189	
30	ZC	123	
31	ZD	155	
32	ZE	151	
33	ZF	132	
34	ZG	141	
35	ZH	142	
36	ZI	137	
37	ZJ	145	
38	ZK	145	
39	ZL	118	
40	ZM	87	
41	ZO	130	
42	ZP	145	
43	ZQ	135	
44	ZR	130	
45	ZS	182	
46	ZT	82	
47	ZU	67	
48	ZV	56	
49	ZW	63	
50	ZY	315	
51	a	127	
52	b	136	
53	c	149	

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Mol	Chain	Length	Quality of chain
54	d	76	
55	e	105	
56	f	113	
57	g	149	
58	h	107	
59	i	115	
60	j	120	
61	k	99	
62	l	85	
63	m	78	
64	n	51	
65	o	52	
66	p	25	
67	q	106	
68	r	99	
69	s	264	
70	t	256	
71	u	249	
72	v	250	
73	w	264	
74	x	223	
75	y	236	
76	z	188	

2 Entry composition

There are 79 unique types of molecules in this entry. The entry contains 192719 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	3022	Total	C	N	O	P	0	0
			64660	28869	11690	21079	3022		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	122	Total	C	N	O	P	0	0
			2609	1164	470	853	122		

- Molecule 3 is a RNA chain called 5.8S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	154	Total	C	N	O	P	0	0
			3274	1464	577	1079	154		

- Molecule 4 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	CA	1674	Total	C	N	O	P	0	0
			35746	15971	6401	11700	1674		

- Molecule 5 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	247	Total	C	N	O	S	0	0
			1873	1170	377	324	2		

- Molecule 6 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	387	Total	C	N	O	S	0	0
			3087	1957	579	544	7		

- Molecule 7 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	361	Total	C	N	O	S	0	0
			2786	1751	534	498	3		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	291	Total	C	N	O	S	0	0
			2370	1506	411	449	4		

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	150	Total	C	N	O		0	0
			1183	761	214	208			

- Molecule 10 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	237	Total	C	N	O	S	0	0
			1913	1230	345	336	2		

- Molecule 11 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	233	Total	C	N	O	S	0	0
			1847	1182	339	322	4		

- Molecule 12 is a protein called 60S ribosomal protein L9-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	190	Total	C	N	O	S	0	0
			1519	965	272	278	4		

- Molecule 13 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	211	Total	C	N	O	S	0	0
			1720	1087	327	298	8		

- Molecule 14 is a protein called 60S ribosomal protein L11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	170	Total	C	N	O	S	0	0
			1364	854	261	244	5		

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	194	Total	C	N	O	S	0	0
			1538	962	306	269	1		

- Molecule 16 is a protein called Large ribosomal subunit protein eL14 domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	129	Total	C	N	O	S	0	0
			1030	657	194	178	1		

- Molecule 17 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	203	Total	C	N	O	S	0	0
			1703	1066	356	279	2		

- Molecule 18 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	199	Total	C	N	O	S	0	0
			1587	1020	299	266	2		

- Molecule 19 is a protein called 60S ribosomal protein L17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	176	Total	C	N	O		0	0
			1418	882	286	250			

- Molecule 20 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	185	Total	C	N	O		0	0
			1456	919	293	244			

- Molecule 21 is a protein called Ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	182	Total	C	N	O	S	0	0
			1469	908	316	241	4		

- Molecule 22 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	172	Total	C	N	O	S	0	0
			1448	941	261	242	4		

- Molecule 23 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	159	Total	C	N	O	S	0	0
			1282	816	242	221	3		

- Molecule 24 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	107	Total	C	N	O		0	0
			871	566	148	157			

- Molecule 25 is a protein called 60S ribosomal protein L23-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	137	Total	C	N	O	S	0	0
			1013	636	189	179	9		

- Molecule 26 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	62	Total	C	N	O	S	0	0
			517	330	103	83	1		

- Molecule 27 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	120	Total	C	N	O		0	0
			955	607	175	173			

- Molecule 28 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	ZA	194	Total	C	N	O	S	0	0
			1545	958	309	276	2		

- Molecule 29 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	ZB	178	Total	C	N	O	S	1	0
			1470	927	291	250	2		

- Molecule 30 is a protein called 40S ribosomal protein S10-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	ZC	93	Total	C	N	O	S	0	0
			786	513	128	144	1		

- Molecule 31 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	ZD	143	Total	C	N	O	S	0	0
			1150	735	219	193	3		

- Molecule 32 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	ZE	150	Total	C	N	O	S	0	0
			1192	759	222	210	1		

- Molecule 33 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	ZF	127	Total	C	N	O	S	0	0
			945	578	188	176	3		

- Molecule 34 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	ZG	116	Total	C	N	O	S	0	0
			904	582	161	156	5		

- Molecule 35 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	ZH	141	Total	C	N	O	S	0	0
			1100	705	201	193	1		

- Molecule 36 is a protein called 40S ribosomal protein S17-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	ZI	128	Total	C	N	O	S	0	0
			1027	644	190	192	1		

- Molecule 37 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	ZJ	142	Total	C	N	O	S	0	0
			1170	733	229	204	4		

- Molecule 38 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	ZK	141	Total	C	N	O		0	0
			1101	691	208	202			

- Molecule 39 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	ZL	100	Total	C	N	O	S	0	0
			782	496	142	142	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	ZM	87	Total	C	N	O	S	0	0
			678	415	127	134	2		

- Molecule 41 is a protein called 40S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	ZO	129	Total	C	N	O	S	0	0
			1032	656	190	183	3		

- Molecule 42 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	ZP	143	Total	C	N	O	S	0	0
			1109	698	219	190	2		

- Molecule 43 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	ZQ	130	Total	C	N	O	S	0	0
			1060	670	205	185			

- Molecule 44 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	ZR	71	Total	C	N	O	S	0	0
			564	360	104	99	1		

- Molecule 45 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	ZS	100	Total	C	N	O	S	0	0
			805	496	172	131	6		

- Molecule 46 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	ZT	81	Total	C	N	O	S	0	0
			617	383	112	115	7		

- Molecule 47 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	ZU	62	Total	C	N	O	S	0	0
			488	299	98	89	2		

- Molecule 48 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	ZV	54	Total	C	N	O	S	0	0
			449	278	93	74	4		

- Molecule 49 is a protein called Small ribosomal subunit protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	ZW	54	Total	C	N	O	S	0	0
			432	270	87	73	2		

- Molecule 50 is a protein called Small ribosomal subunit protein RACK1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	ZY	308	Total	C	N	O	S	0	0
			2383	1510	405	464	4		

- Molecule 51 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	a	126	Total	C	N	O	S	0	0
			994	624	188	181	1		

- Molecule 52 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	b	135	Total	C	N	O	S	0	0
			1081	691	207	182	1		

- Molecule 53 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	c	148	Total	C	N	O	S	0	0
			1174	742	234	196	2		

- Molecule 54 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	d	60	Total	C	N	O	0	0
			498	302	114	82		

- Molecule 55 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	e	100	Total	C	N	O	S	0	0
			753	482	127	140	4		

- Molecule 56 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	f	109	Total	C	N	O	S	0	0
			895	563	173	156	3		

- Molecule 57 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	g	123	Total	C	N	O	S	0	0
			1002	629	201	170	2		

- Molecule 58 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	h	106	Total	C	N	O	S	0	0
			859	544	168	146	1		

- Molecule 59 is a protein called 60S ribosomal protein L34-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	i	113	Total	C	N	O	S	0	0
			897	558	179	156	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	j	118	Total	C	N	O	S	0	0
			956	603	191	162			

- Molecule 61 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	k	98	Total	C	N	O	S	0	0
			774	479	163	131	1		

- Molecule 62 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	l	83	Total	C	N	O	S	0	0
			654	396	142	109	7		

- Molecule 63 is a protein called Large ribosomal subunit protein eL38.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	m	77	Total	C	N	O	0	0
			617	396	112	109		

- Molecule 64 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms				AltConf	Trace
64	n	50	Total	C	N	O	0	0
			442	277	98	67		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	50	ASN	GLY	conflict	UNP A0A1D8PDT4

- Molecule 65 is a protein called Large ribosomal subunit protein eL40.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	o	52	Total	C	N	O	S	0	0
			419	260	86	67	6		

- Molecule 66 is a protein called Small ribosomal subunit protein eS32.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	p	25	Total	C	N	O	S	0	0
			236	144	63	28	1		

- Molecule 67 is a protein called 60S ribosomal protein L44.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	q	103	Total	C	N	O	S	1	0
			832	523	167	137	5		

- Molecule 68 is a protein called 60S ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	r	90	Total	C	N	O	S	0	0
			691	425	141	121	4		

- Molecule 69 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	s	210	Total	C	N	O	S	0	0
			1655	1059	288	305	3		

- Molecule 70 is a protein called Small ribosomal subunit protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	t	211	Total	C	N	O	S	0	0
			1692	1075	311	302	4		

- Molecule 71 is a protein called Rps21 ribosomal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	u	216	Total	C	N	O	S	0	0
			1636	1048	287	296	5		

- Molecule 72 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	v	209	Total	C	N	O	S	0	0
			1619	1033	297	284	5		

- Molecule 73 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	w	260	Total	C	N	O	S	0	0
			2056	1303	386	361	6		

- Molecule 74 is a protein called 40S ribosomal protein uS7 (formerly S5).

Mol	Chain	Residues	Atoms					AltConf	Trace
74	x	206	Total	C	N	O	S	0	0
			1610	1008	300	298	4		

- Molecule 75 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	y	226	Total	C	N	O	S	0	0
			1819	1128	355	331	5		

- Molecule 76 is a protein called 40S ribosomal protein eS7 (formerly S7).

Mol	Chain	Residues	Atoms				AltConf	Trace
76	z	182	Total	C	N	O	0	0
			1466	939	264	263		

- Molecule 77 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
77	A	152	Total	Mg	0
			152	152	
77	B	3	Total	Mg	0
			3	3	
77	C	1	Total	Mg	0
			1	1	
77	CA	87	Total	Mg	0
			87	87	
77	D	1	Total	Mg	0
			1	1	
77	L	2	Total	Mg	0
			2	2	
77	R	1	Total	Mg	0
			1	1	
77	X	1	Total	Mg	0
			1	1	
77	ZA	1	Total	Mg	0
			1	1	
77	h	1	Total	Mg	0
			1	1	
77	y	1	Total	Mg	0
			1	1	

- Molecule 78 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
78	ZS	1	Total	Zn	0
			1	1	
78	ZV	1	Total	Zn	0
			1	1	
78	i	1	Total	Zn	0
			1	1	
78	l	1	Total	Zn	0
			1	1	
78	o	1	Total	Zn	0
			1	1	
78	q	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
78	r	1	Total	Zn	0
			1	1	

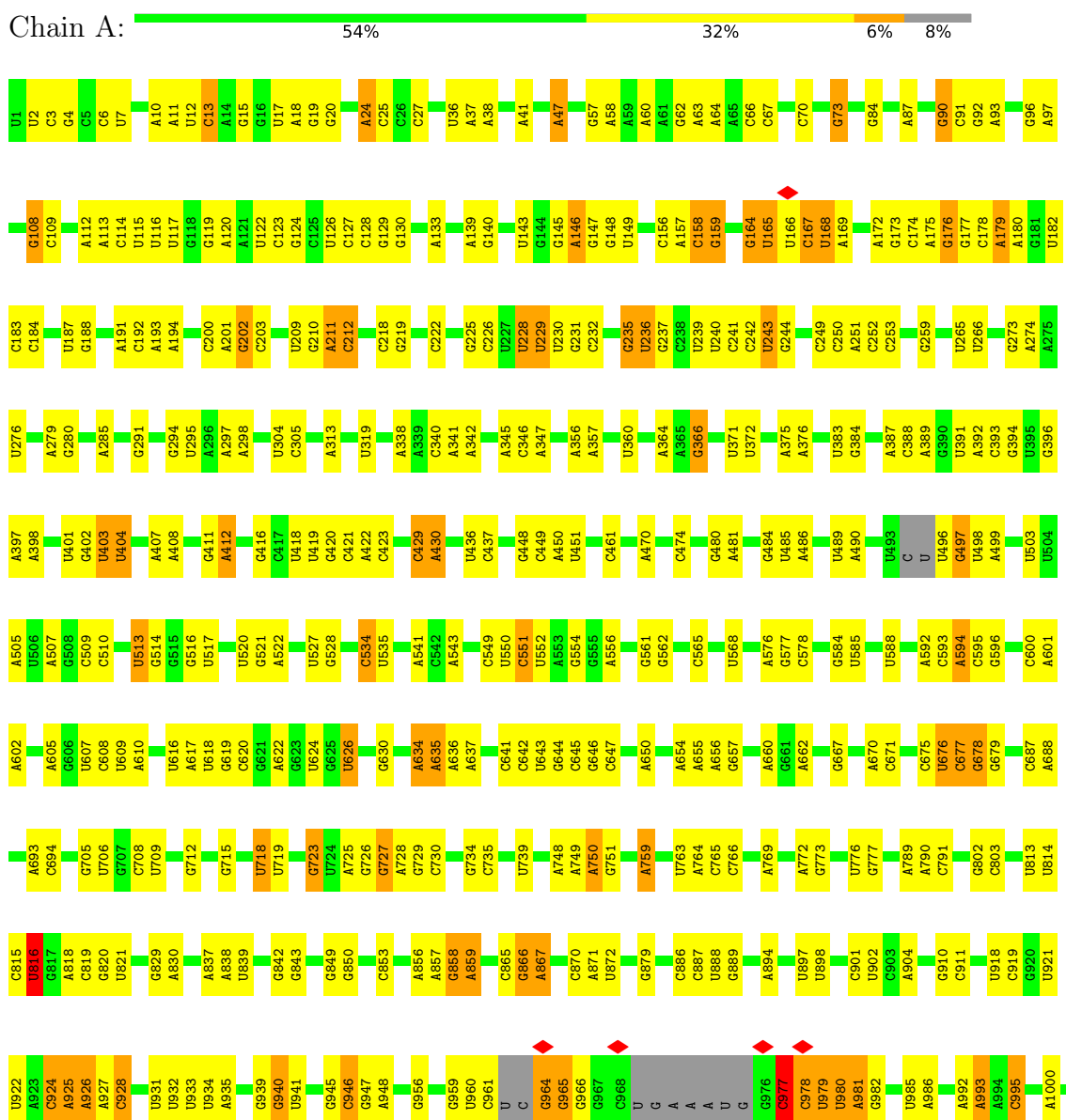
- Molecule 79 is water.

Mol	Chain	Residues	Atoms		AltConf
79	A	82	Total	O	0
			82	82	
79	B	2	Total	O	0
			2	2	
79	C	4	Total	O	0
			4	4	
79	CA	10	Total	O	0
			10	10	
79	E	2	Total	O	0
			2	2	
79	P	1	Total	O	0
			1	1	
79	ZE	2	Total	O	0
			2	2	
79	ZF	1	Total	O	0
			1	1	
79	d	1	Total	O	0
			1	1	
79	i	1	Total	O	0
			1	1	
79	q	1	Total	O	0
			1	1	

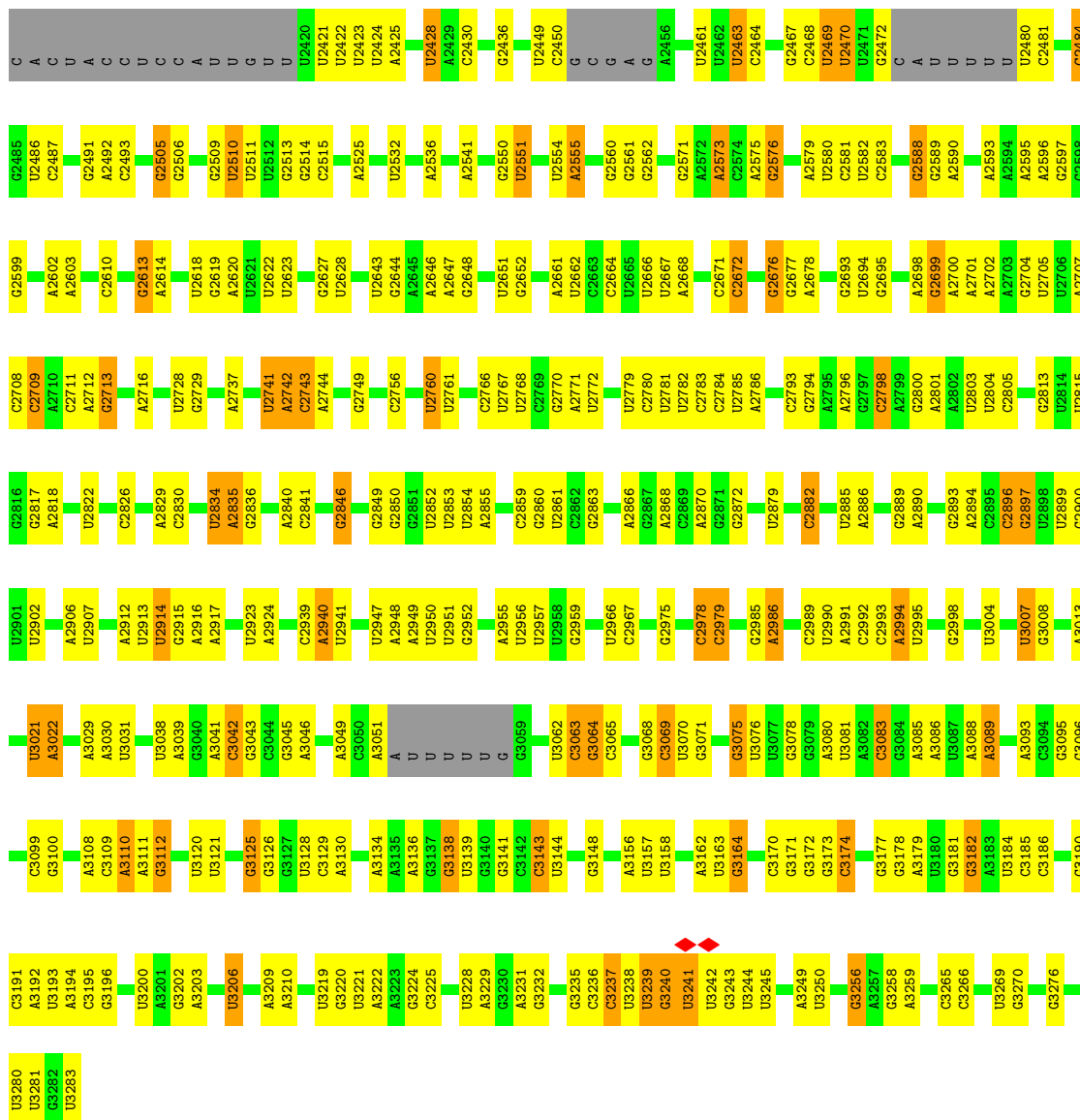
3 Residue-property plots

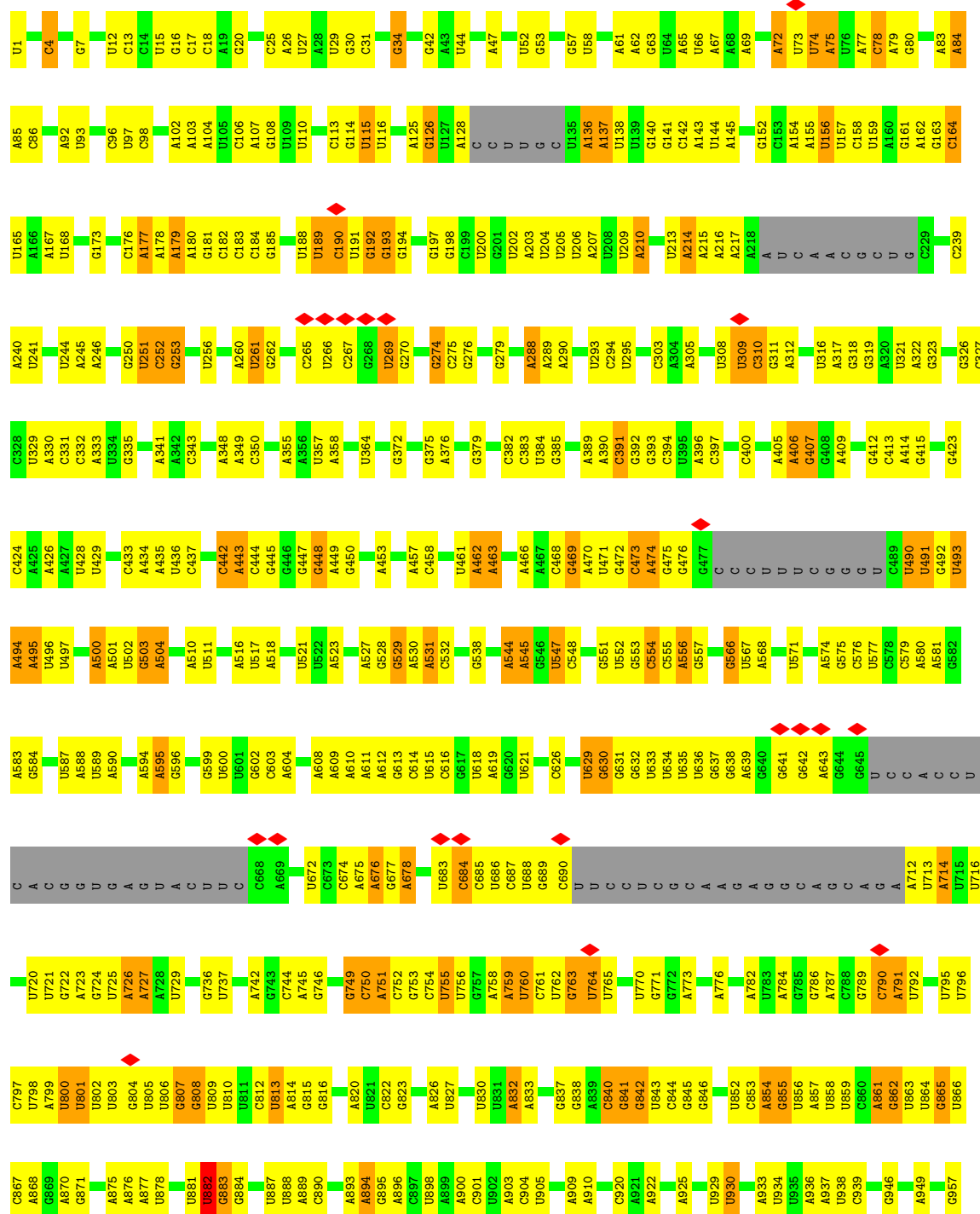
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

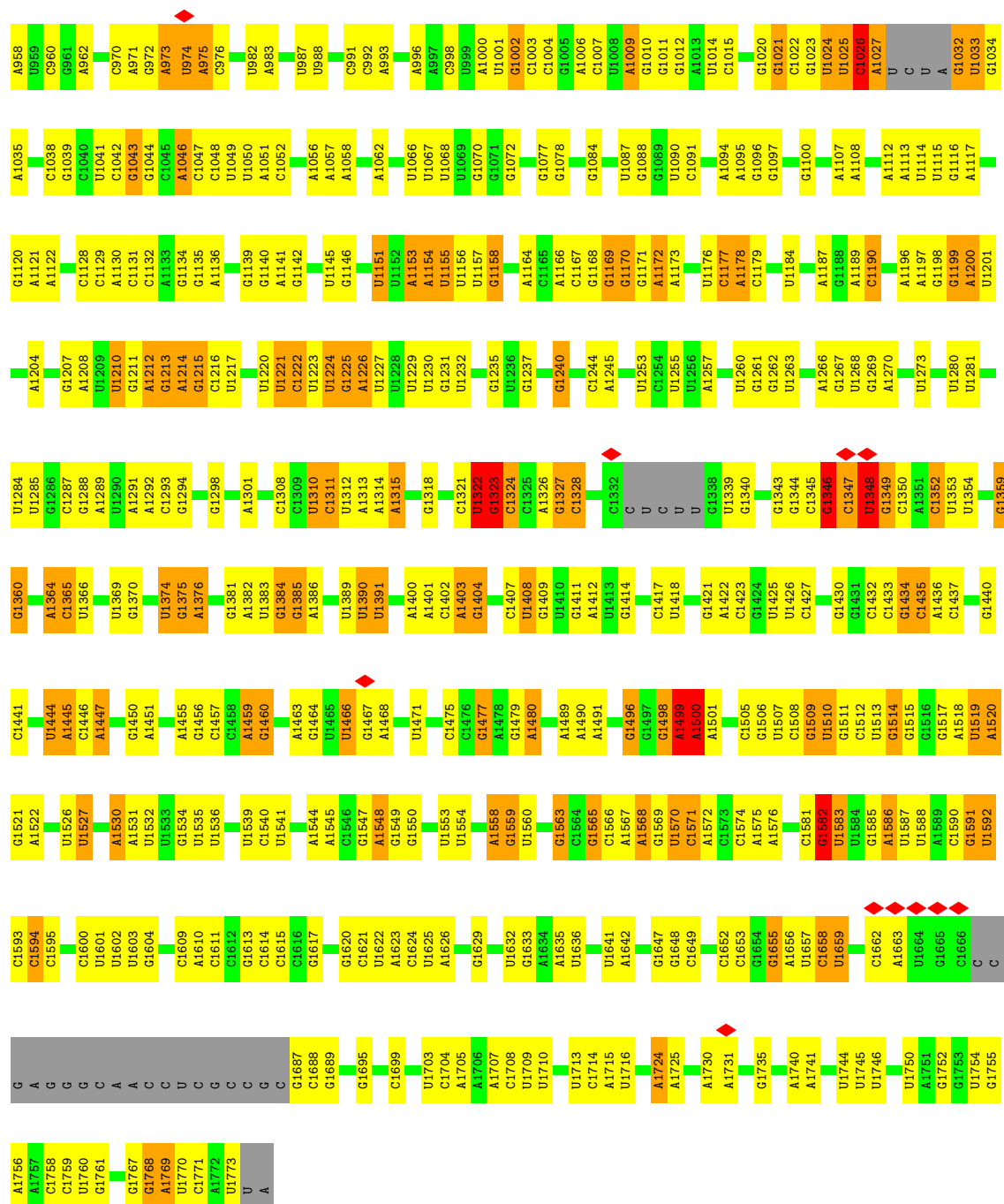
• Molecule 1: 25S rRNA





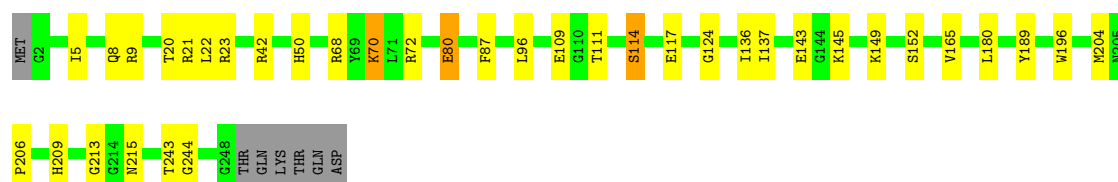






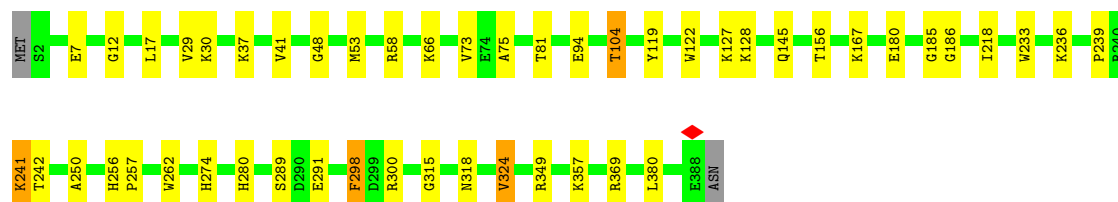
- Molecule 5: 60S ribosomal protein L2-A

Chain D: 83% 13% ..



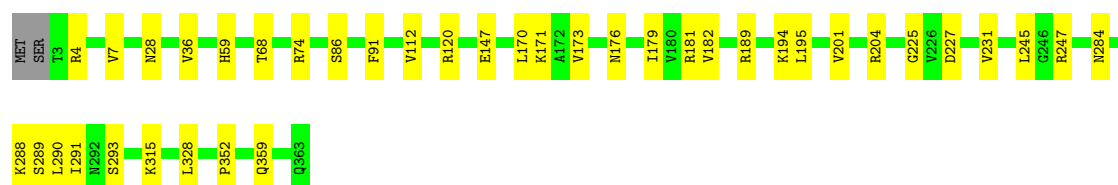
- Molecule 6: Large ribosomal subunit protein uL3

Chain E:  87% 12% ..



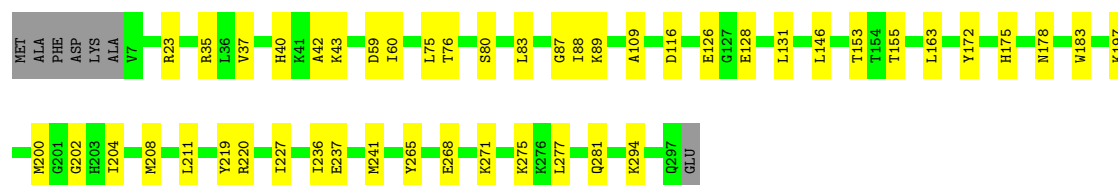
- Molecule 7: 60S ribosomal protein L4-A

Chain F:  89% 11% .



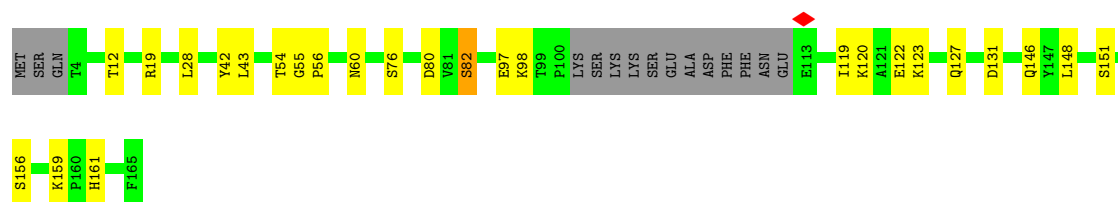
- Molecule 8: 60S ribosomal protein L5

Chain G:  82% 16% .



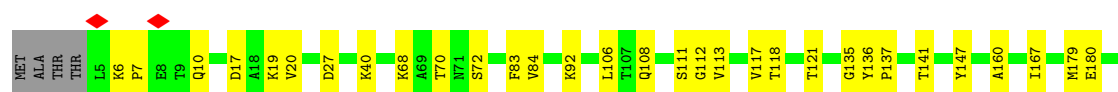
- Molecule 9: 60S ribosomal protein L6

Chain H:  75% 15% . 9%



- Molecule 10: 60S ribosomal protein L7

Chain I:  82% 16% .





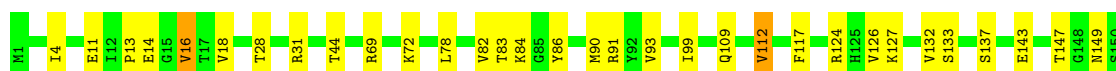
- Molecule 11: 60S ribosomal protein L8

Chain J: 75% 13% 11%



- Molecule 12: 60S ribosomal protein L9-B

Chain K: 79% 19% 2%



- Molecule 13: 60S ribosomal protein L10

Chain L: 82% 14% 4%



- Molecule 14: 60S ribosomal protein L11-A

Chain M: 76% 22% 2%



- Molecule 15: 60S ribosomal protein L13

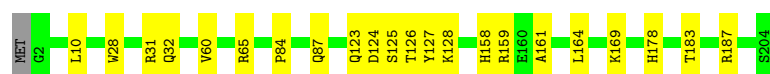
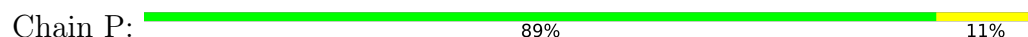
Chain N: 84% 13% 3%



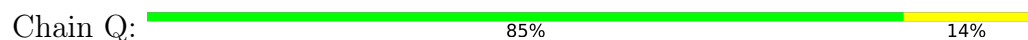
- Molecule 16: Large ribosomal subunit protein eL14 domain-containing protein



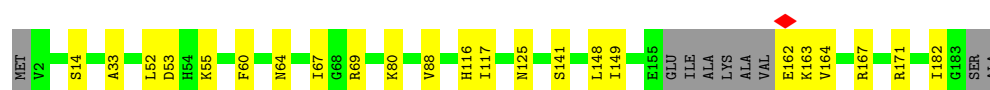
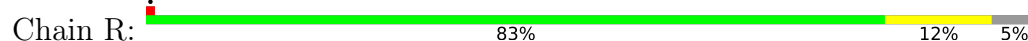
- Molecule 17: Ribosomal protein L15



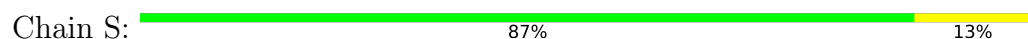
- Molecule 18: 60S ribosomal protein L16-B



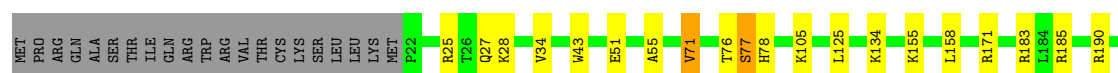
- Molecule 19: 60S ribosomal protein L17-B



- Molecule 20: 60S ribosomal protein L18-A

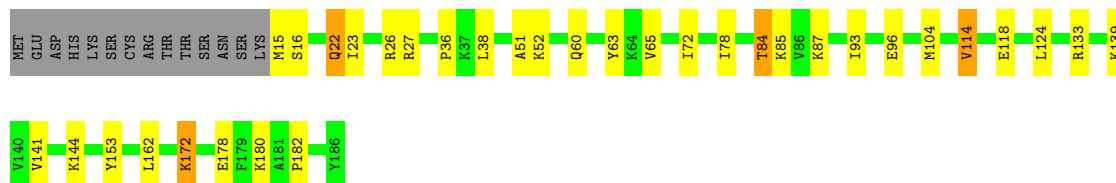


- Molecule 21: Ribosomal protein L19



- Molecule 22: 60S ribosomal protein L20-A

Chain U:  74% 16% 8%



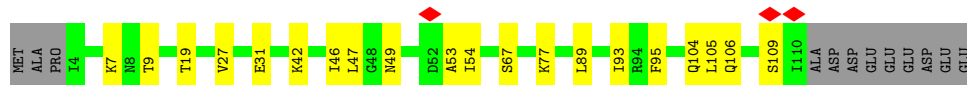
- Molecule 23: 60S ribosomal protein L21-A

Chain V:  85% 14% 1%



- Molecule 24: 60S ribosomal protein L22

Chain W:  73% 17% 10%



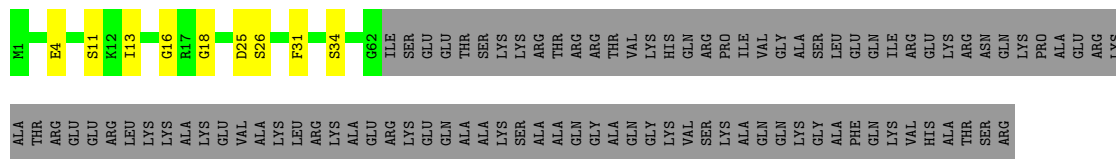
- Molecule 25: 60S ribosomal protein L23-B

Chain X:  80% 19% 1%



- Molecule 26: 60S ribosomal protein L24

Chain Y:  34% 6% 60%



- Molecule 27: Large ribosomal subunit protein uL23

Chain Z:  68% 16% 14%





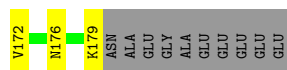
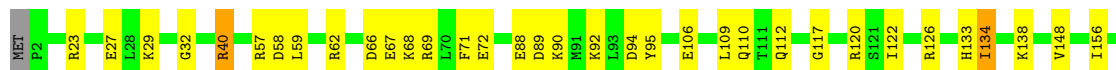
- Molecule 28: 40S ribosomal protein S8

Chain ZA: 76% 19% 5%



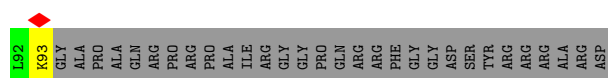
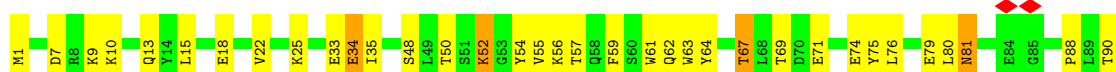
- Molecule 29: 40S ribosomal protein S9-A

Chain ZB: 75% 19% 6%



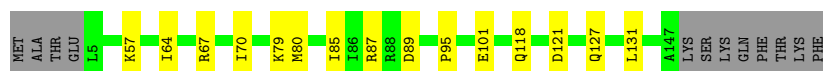
- Molecule 30: 40S ribosomal protein S10-A

Chain ZC: 46% 27% 24%



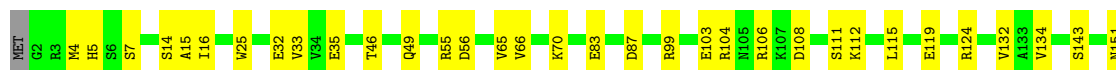
- Molecule 31: 40S ribosomal protein S11-A

Chain ZD: 83% 10% 8%



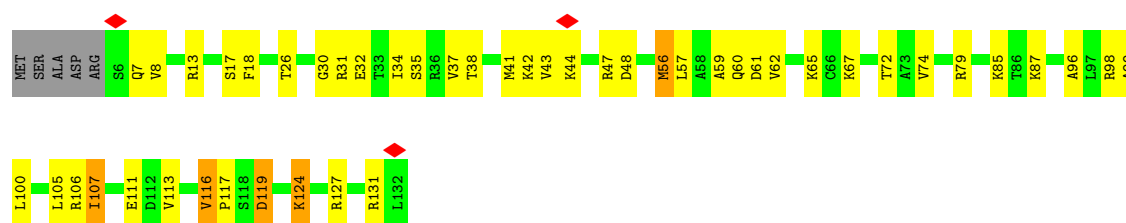
- Molecule 32: 40S ribosomal protein S13

Chain ZE: 77% 22% 1%



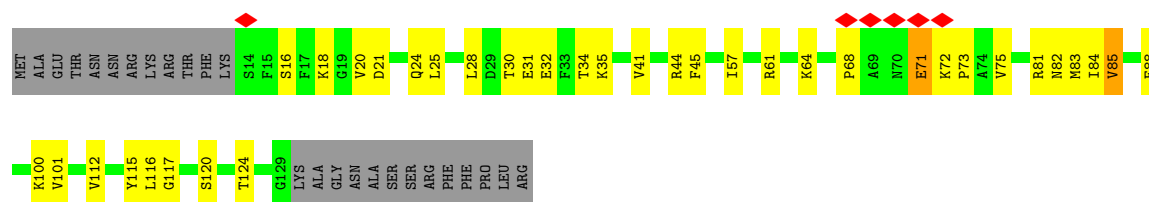
- Molecule 33: Small ribosomal subunit protein uS11

Chain ZF: 



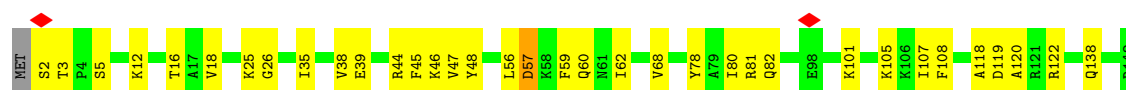
- Molecule 34: 40S ribosomal protein S15

Chain ZG: 



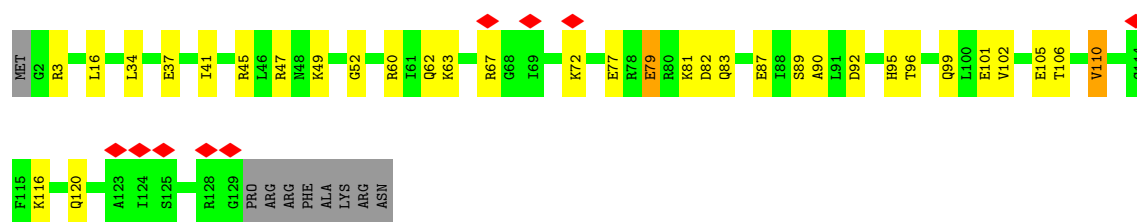
- Molecule 35: Small ribosomal subunit protein uS9

Chain ZH: 



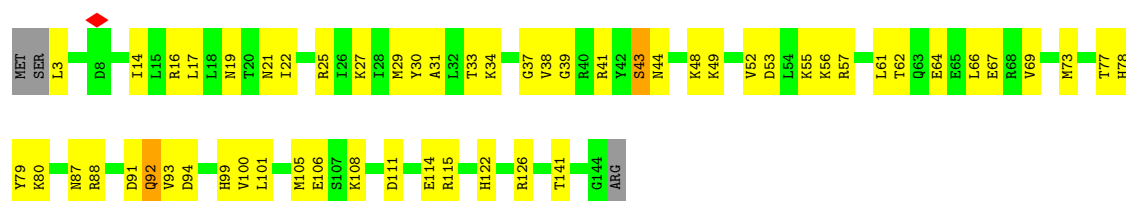
- Molecule 36: 40S ribosomal protein S17-B

Chain ZI: 



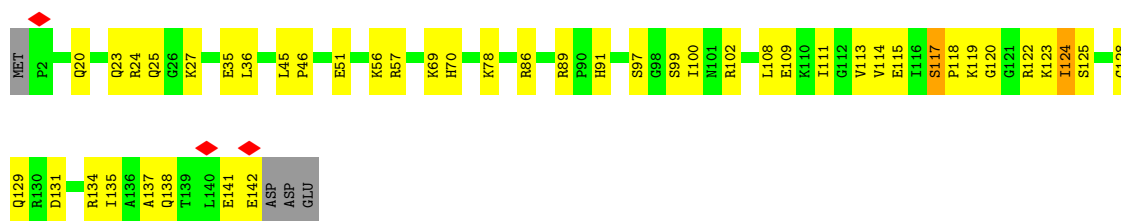
- Molecule 37: 40S ribosomal protein S18

Chain ZJ: 



- Molecule 38: 40S ribosomal protein S19-A

Chain ZK:  66% 30%



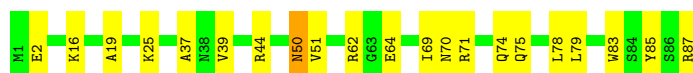
- Molecule 39: Small ribosomal subunit protein uS10

Chain ZL:  52% 31% 15%



- Molecule 40: 40S ribosomal protein S21

Chain ZM:  76% 23%



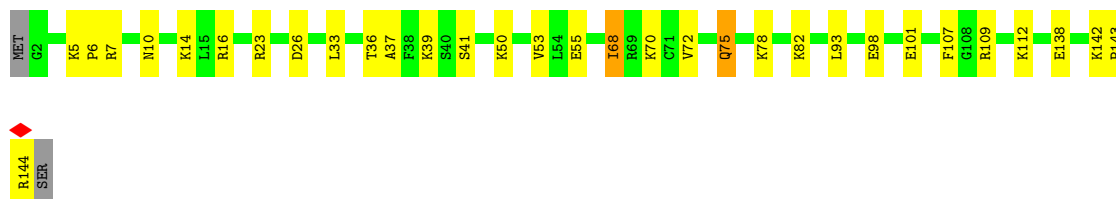
- Molecule 41: 40S ribosomal protein S22

Chain ZO:  81% 18%



- Molecule 42: 40S ribosomal protein S23

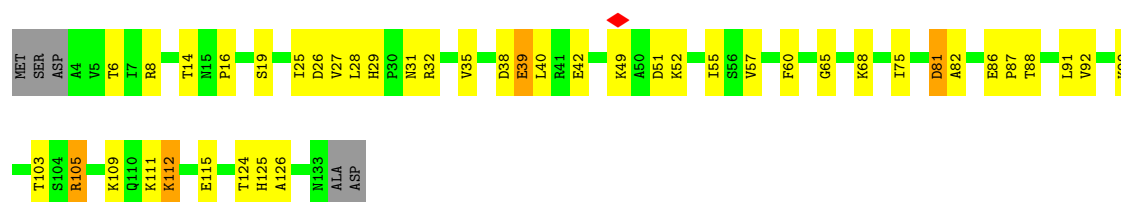
Chain ZP:  77% 21%



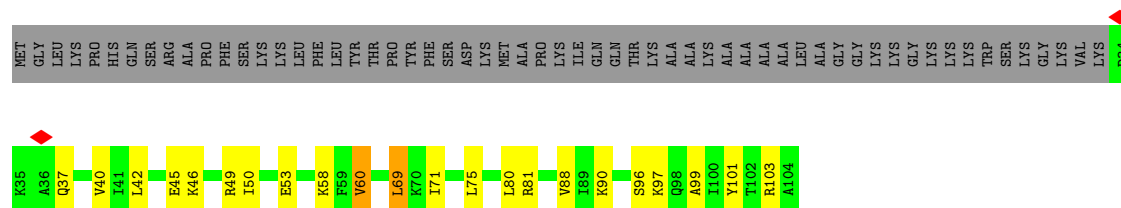
- Molecule 43: 40S ribosomal protein S24

Chain ZQ:  64% 29%

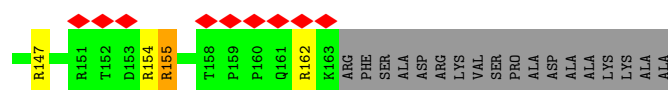
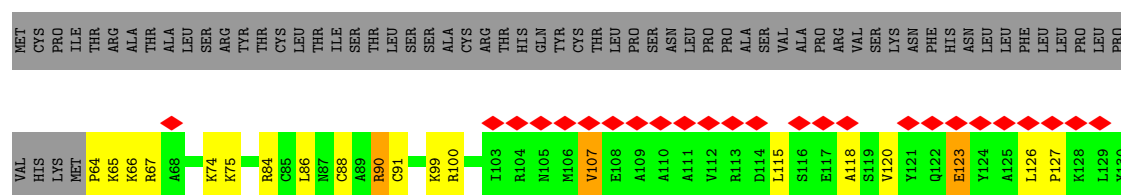
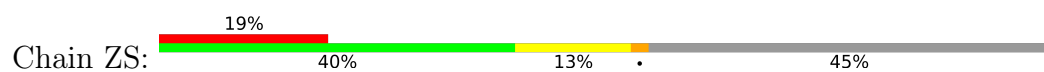




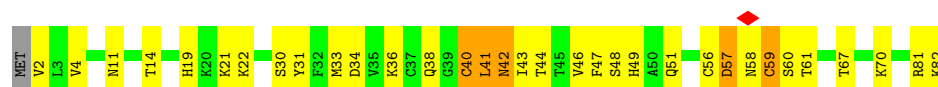
- Molecule 44: 40S ribosomal protein S25



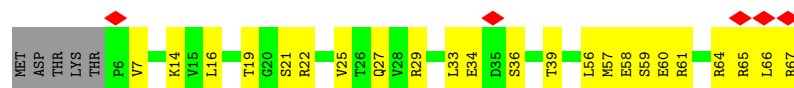
- Molecule 45: 40S ribosomal protein S26



- Molecule 46: 40S ribosomal protein S27



- Molecule 47: 40S ribosomal protein S28-A



- Molecule 48: Small ribosomal subunit protein uS14



- Molecule 53: 60S ribosomal protein L28

Chain c:  81% 18%



- Molecule 54: 60S ribosomal protein L29

Chain d:  71% 8% 21%



- Molecule 55: 60S ribosomal protein L30

Chain e:  75% 20% 5%



- Molecule 56: 60S ribosomal protein L31-A

Chain f:  84% 12% 4%



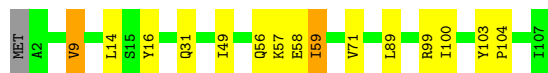
- Molecule 57: 60S ribosomal protein L32

Chain g:  68% 13% 17%



- Molecule 58: 60S ribosomal protein L33-A

Chain h:  85% 12% 3%

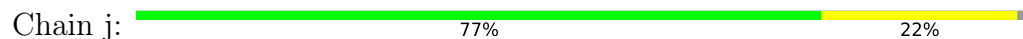


- Molecule 59: 60S ribosomal protein L34-B

Chain i:  5% 81% 17%



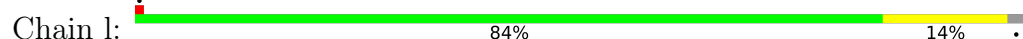
- Molecule 60: 60S ribosomal protein L35



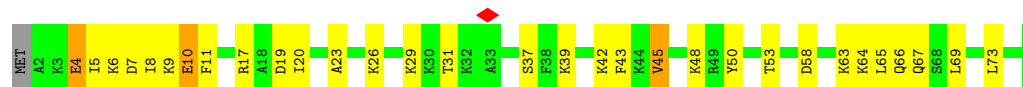
- Molecule 61: 60S ribosomal protein L36



- Molecule 62: Ribosomal protein L37



- Molecule 63: Large ribosomal subunit protein eL38



- Molecule 64: Large ribosomal subunit protein eL39

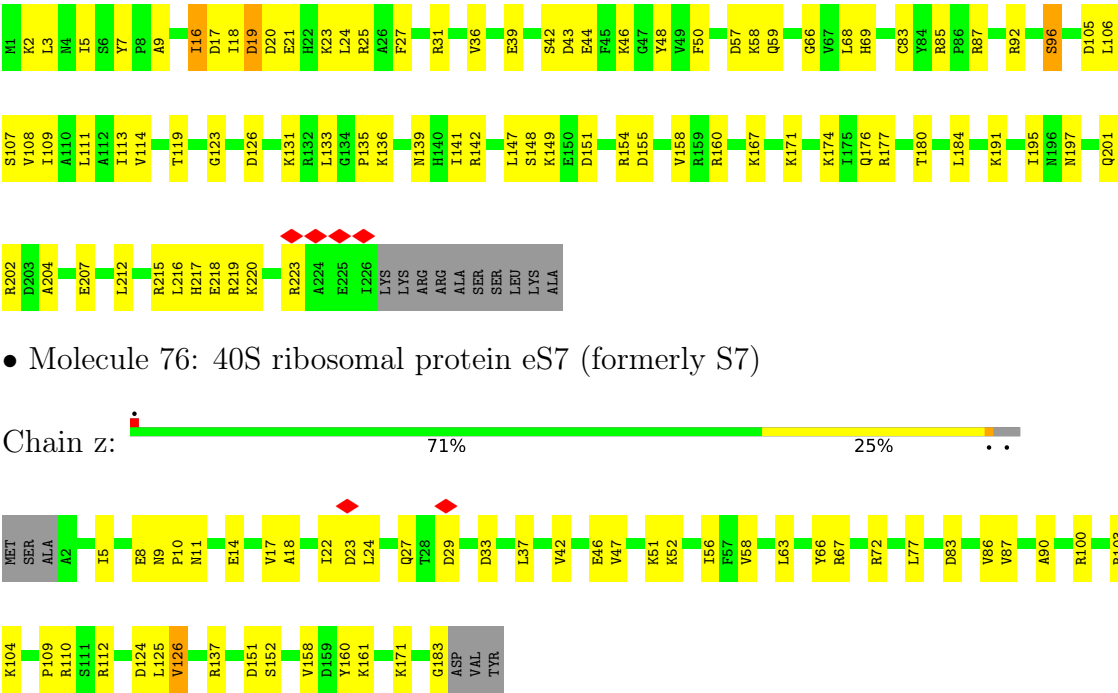


- Molecule 65: Large ribosomal subunit protein eL40



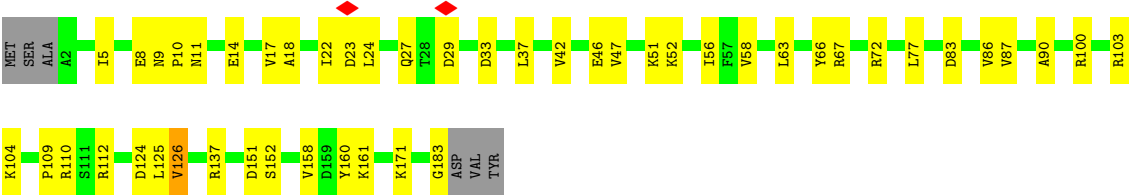
- Molecule 66: Small ribosomal subunit protein eS32





• Molecule 76: 40S ribosomal protein eS7 (formerly S7)

Chain z: 71% 25%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	383840	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.247	Depositor
Minimum map value	-0.176	Depositor
Average map value	0.013	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	376.2, 376.2, 376.2	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.836, 0.836, 0.836	Depositor

5 Model quality

5.1 Standard geometry

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

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	A	0.26	0/72363	0.43	108/112811 (0.1%)
2	B	0.19	0/2918	0.27	0/4548
3	C	0.26	0/3659	0.41	5/5698 (0.1%)
4	CA	0.20	0/39990	0.36	22/62317 (0.0%)
5	D	0.24	0/1907	0.41	0/2560
6	E	0.26	0/3155	0.42	1/4246 (0.0%)
7	F	0.21	0/2835	0.34	0/3823
8	G	0.14	0/2419	0.29	0/3253
9	H	0.17	0/1203	0.34	0/1621
10	I	0.19	0/1950	0.34	0/2621
11	J	0.28	0/1879	0.40	0/2525
12	K	0.18	0/1539	0.32	0/2068
13	L	0.16	0/1756	0.30	0/2355
14	M	0.15	0/1385	0.37	0/1854
15	N	0.17	0/1564	0.36	0/2104
16	O	0.17	0/1044	0.29	0/1410
17	P	0.19	0/1743	0.33	0/2340
18	Q	0.20	0/1618	0.34	0/2169
19	R	0.20	0/1444	0.34	0/1943
20	S	0.18	0/1479	0.30	0/1985
21	T	0.16	0/1488	0.26	0/1981
22	U	0.20	0/1483	0.32	0/1996
23	V	0.18	0/1308	0.35	0/1758
24	W	0.15	0/887	0.34	0/1194
25	X	0.26	0/1030	0.43	0/1387
26	Y	0.17	0/530	0.28	0/704
27	Z	0.40	0/970	0.57	0/1311
28	ZA	0.28	0/1571	0.48	1/2103 (0.0%)
29	ZB	0.16	0/1496	0.35	0/2005
30	ZC	0.42	0/805	0.67	0/1088
31	ZD	0.16	0/1174	0.26	0/1578
32	ZE	0.16	0/1215	0.31	0/1637

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	ZF	0.32	0/956	0.51	0/1284
34	ZG	0.17	0/922	0.35	0/1239
35	ZH	0.24	0/1119	0.45	0/1500
36	ZI	0.18	0/1039	0.45	0/1392
37	ZJ	0.19	0/1188	0.40	0/1591
38	ZK	0.19	0/1122	0.48	0/1510
39	ZL	0.16	0/791	0.41	0/1069
40	ZM	0.15	0/686	0.30	0/924
41	ZO	0.19	0/1049	0.40	0/1410
42	ZP	0.17	0/1127	0.35	0/1505
43	ZQ	0.18	0/1077	0.38	0/1439
44	ZR	0.16	0/572	0.39	0/767
45	ZS	0.13	0/817	0.34	0/1093
46	ZT	0.46	1/627 (0.2%)	0.72	3/847 (0.4%)
47	ZU	0.20	0/490	0.56	0/655
48	ZV	0.16	0/461	0.33	0/613
49	ZW	0.13	0/438	0.35	0/582
50	ZY	0.33	0/2437	0.50	0/3320
51	a	0.17	0/1005	0.31	0/1339
52	b	0.17	0/1104	0.35	0/1480
53	c	0.19	0/1203	0.34	0/1611
54	d	0.17	0/506	0.29	0/670
55	e	0.15	0/761	0.24	0/1022
56	f	0.18	0/911	0.30	0/1223
57	g	0.17	0/1019	0.31	0/1362
58	h	0.23	0/877	0.38	0/1180
59	i	0.19	0/906	0.36	0/1209
60	j	0.18	0/963	0.35	0/1284
61	k	0.19	0/780	0.36	0/1034
62	l	0.19	0/666	0.31	0/883
63	m	0.25	0/623	0.51	0/828
64	n	0.18	0/451	0.28	0/600
65	o	0.29	0/425	0.39	0/563
66	p	0.12	0/237	0.30	0/304
67	q	0.16	0/845	0.26	0/1118
68	r	0.29	0/699	0.42	0/933
69	s	0.14	0/1694	0.34	0/2311
70	t	0.14	0/1717	0.31	0/2305
71	u	0.15	0/1664	0.29	0/2253
72	v	0.16	0/1642	0.39	0/2201
73	w	0.25	0/2094	0.41	0/2816
74	x	0.13	0/1628	0.32	0/2195
75	y	0.14	0/1845	0.31	0/2467

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	z	0.16	0/1490	0.36	0/2004
All	All	0.23	1/206480 (0.0%)	0.39	140/302928 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
6	E	0	1
11	J	0	2
27	Z	0	2
28	ZA	0	2
40	ZM	0	1
50	ZY	0	1
65	o	0	1
73	w	0	1
All	All	0	11

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
46	ZT	59	CYS	CA-CB	6.93	1.64	1.53

The worst 5 of 140 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	ZT	59	CYS	CA-CB-SG	12.33	142.75	114.40
1	A	2122	A	P-O3'-C3'	-10.04	105.14	120.20
1	A	3125	G	P-O3'-C3'	-9.10	106.55	120.20
1	A	3126	G	P-O3'-C3'	-9.05	106.63	120.20
3	C	8	C	P-O3'-C3'	-8.95	106.78	120.20

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	E	300	ARG	Sidechain
11	J	172	ARG	Sidechain
11	J	231	ARG	Sidechain
27	Z	53	ARG	Sidechain

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Mol	Chain	Res	Type	Group
27	Z	54	ARG	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	A	64660	0	32534	705	0
2	B	2609	0	1315	25	0
3	C	3274	0	1654	32	0
4	CA	35746	0	17991	613	0
5	D	1873	0	1943	26	0
6	E	3087	0	3173	37	0
7	F	2786	0	2912	26	0
8	G	2370	0	2360	33	0
9	H	1183	0	1276	17	0
10	I	1913	0	1998	24	0
11	J	1847	0	1970	23	0
12	K	1519	0	1588	26	0
13	L	1720	0	1760	24	0
14	M	1364	0	1396	27	0
15	N	1538	0	1614	18	0
16	O	1030	0	1113	13	0
17	P	1703	0	1748	14	0
18	Q	1587	0	1695	26	0
19	R	1418	0	1446	14	0
20	S	1456	0	1570	21	0
21	T	1469	0	1579	17	0
22	U	1448	0	1511	28	0
23	V	1282	0	1341	20	0
24	W	871	0	903	10	0
25	X	1013	0	1057	24	0
26	Y	517	0	535	6	0
27	Z	955	0	1012	18	0
28	ZA	1545	0	1580	30	0
29	ZB	1470	0	1543	30	0
30	ZC	786	0	797	33	0
31	ZD	1150	0	1218	9	0
32	ZE	1192	0	1252	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
33	ZF	945	0	979	38	0
34	ZG	904	0	944	22	0
35	ZH	1100	0	1162	22	0
36	ZI	1027	0	1080	33	0
37	ZJ	1170	0	1213	45	0
38	ZK	1101	0	1113	35	0
39	ZL	782	0	854	26	0
40	ZM	678	0	671	15	0
41	ZO	1032	0	1072	17	0
42	ZP	1109	0	1173	22	0
43	ZQ	1060	0	1117	31	0
44	ZR	564	0	598	15	0
45	ZS	805	0	861	25	0
46	ZT	617	0	631	23	0
47	ZU	488	0	523	19	0
48	ZV	449	0	425	16	0
49	ZW	432	0	471	23	0
50	ZY	2383	0	2344	79	0
51	a	994	0	1075	18	0
52	b	1081	0	1134	21	0
53	c	1174	0	1204	18	0
54	d	498	0	517	5	0
55	e	753	0	797	12	0
56	f	895	0	927	9	0
57	g	1002	0	1062	18	0
58	h	859	0	889	9	0
59	i	897	0	970	12	0
60	j	956	0	1067	20	0
61	k	774	0	848	5	0
62	l	654	0	668	8	0
63	m	617	0	685	25	0
64	n	442	0	478	13	0
65	o	419	0	460	3	0
66	p	236	0	285	13	0
67	q	832	0	892	6	0
68	r	691	0	723	7	0
69	s	1655	0	1670	18	0
70	t	1692	0	1787	40	0
71	u	1636	0	1743	40	0
72	v	1619	0	1718	36	0
73	w	2056	0	2145	42	0
74	x	1610	0	1687	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
75	y	1819	0	1882	63	0
76	z	1466	0	1554	33	0
77	A	152	0	0	0	0
77	B	3	0	0	0	0
77	C	1	0	0	0	0
77	CA	87	0	0	0	0
77	D	1	0	0	0	0
77	L	2	0	0	0	0
77	R	1	0	0	0	0
77	X	1	0	0	0	0
77	ZA	1	0	0	0	0
77	h	1	0	0	0	0
77	y	1	0	0	0	0
78	ZS	1	0	0	0	0
78	ZV	1	0	0	0	0
78	i	1	0	0	0	0
78	l	1	0	0	0	0
78	o	1	0	0	0	0
78	q	1	0	0	0	0
78	r	1	0	0	0	0
79	A	82	0	0	4	0
79	B	2	0	0	0	0
79	C	4	0	0	0	0
79	CA	10	0	0	0	0
79	E	2	0	0	1	0
79	P	1	0	0	0	0
79	ZE	2	0	0	0	0
79	ZF	1	0	0	0	0
79	d	1	0	0	0	0
79	i	1	0	0	0	0
79	q	1	0	0	0	0
All	All	192719	0	143482	2597	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 8.

The worst 5 of 2597 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:B:19:G:H1	2:B:62:U:H3	0.98	0.97
1:A:960:U:H3	1:A:982:G:H1	1.21	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:CA:1261:G:H1	4:CA:1294:G:H22	1.20	0.89
51:a:31:MET:HB3	51:a:101:PRO:HG2	1.55	0.88
37:ZJ:111:ASP:HA	37:ZJ:114:GLU:HG3	1.56	0.87

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	D	245/254 (96%)	234 (96%)	11 (4%)	0	100	100
6	E	385/389 (99%)	373 (97%)	12 (3%)	0	100	100
7	F	359/363 (99%)	351 (98%)	8 (2%)	0	100	100
8	G	289/298 (97%)	281 (97%)	8 (3%)	0	100	100
9	H	146/165 (88%)	140 (96%)	6 (4%)	0	100	100
10	I	235/241 (98%)	228 (97%)	7 (3%)	0	100	100
11	J	231/263 (88%)	227 (98%)	4 (2%)	0	100	100
12	K	188/191 (98%)	184 (98%)	4 (2%)	0	100	100
13	L	207/220 (94%)	200 (97%)	6 (3%)	1 (0%)	24	19
14	M	168/172 (98%)	166 (99%)	2 (1%)	0	100	100
15	N	192/198 (97%)	188 (98%)	3 (2%)	1 (0%)	24	19
16	O	127/131 (97%)	122 (96%)	5 (4%)	0	100	100
17	P	201/204 (98%)	194 (96%)	7 (4%)	0	100	100
18	Q	197/200 (98%)	196 (100%)	1 (0%)	0	100	100
19	R	172/185 (93%)	169 (98%)	3 (2%)	0	100	100
20	S	183/186 (98%)	174 (95%)	9 (5%)	0	100	100
21	T	180/208 (86%)	173 (96%)	6 (3%)	1 (1%)	21	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	U	170/186 (91%)	166 (98%)	4 (2%)	0	100	100
23	V	157/160 (98%)	153 (98%)	4 (2%)	0	100	100
24	W	105/119 (88%)	98 (93%)	7 (7%)	0	100	100
25	X	135/137 (98%)	132 (98%)	3 (2%)	0	100	100
26	Y	60/156 (38%)	58 (97%)	2 (3%)	0	100	100
27	Z	118/140 (84%)	116 (98%)	2 (2%)	0	100	100
28	ZA	192/204 (94%)	188 (98%)	4 (2%)	0	100	100
29	ZB	177/189 (94%)	175 (99%)	2 (1%)	0	100	100
30	ZC	91/123 (74%)	85 (93%)	5 (6%)	1 (1%)	11	6
31	ZD	141/155 (91%)	139 (99%)	2 (1%)	0	100	100
32	ZE	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
33	ZF	125/132 (95%)	119 (95%)	6 (5%)	0	100	100
34	ZG	114/141 (81%)	111 (97%)	3 (3%)	0	100	100
35	ZH	139/142 (98%)	133 (96%)	6 (4%)	0	100	100
36	ZI	126/137 (92%)	123 (98%)	3 (2%)	0	100	100
37	ZJ	140/145 (97%)	136 (97%)	4 (3%)	0	100	100
38	ZK	139/145 (96%)	137 (99%)	2 (1%)	0	100	100
39	ZL	98/118 (83%)	91 (93%)	7 (7%)	0	100	100
40	ZM	85/87 (98%)	83 (98%)	2 (2%)	0	100	100
41	ZO	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
42	ZP	141/145 (97%)	138 (98%)	3 (2%)	0	100	100
43	ZQ	128/135 (95%)	122 (95%)	6 (5%)	0	100	100
44	ZR	69/130 (53%)	68 (99%)	1 (1%)	0	100	100
45	ZS	98/182 (54%)	97 (99%)	1 (1%)	0	100	100
46	ZT	79/82 (96%)	75 (95%)	3 (4%)	1 (1%)	9	4
47	ZU	60/67 (90%)	55 (92%)	5 (8%)	0	100	100
48	ZV	52/56 (93%)	49 (94%)	3 (6%)	0	100	100
49	ZW	52/63 (82%)	51 (98%)	1 (2%)	0	100	100
50	ZY	306/315 (97%)	282 (92%)	24 (8%)	0	100	100
51	a	124/127 (98%)	122 (98%)	2 (2%)	0	100	100
52	b	133/136 (98%)	132 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	c	146/149 (98%)	140 (96%)	6 (4%)	0	100	100
54	d	58/76 (76%)	57 (98%)	1 (2%)	0	100	100
55	e	98/105 (93%)	95 (97%)	3 (3%)	0	100	100
56	f	107/113 (95%)	107 (100%)	0	0	100	100
57	g	121/149 (81%)	120 (99%)	1 (1%)	0	100	100
58	h	104/107 (97%)	102 (98%)	2 (2%)	0	100	100
59	i	111/115 (96%)	108 (97%)	3 (3%)	0	100	100
60	j	116/120 (97%)	115 (99%)	1 (1%)	0	100	100
61	k	96/99 (97%)	92 (96%)	4 (4%)	0	100	100
62	l	81/85 (95%)	80 (99%)	1 (1%)	0	100	100
63	m	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
64	n	48/51 (94%)	47 (98%)	1 (2%)	0	100	100
65	o	50/52 (96%)	50 (100%)	0	0	100	100
66	p	23/25 (92%)	23 (100%)	0	0	100	100
67	q	102/106 (96%)	101 (99%)	1 (1%)	0	100	100
68	r	88/99 (89%)	86 (98%)	2 (2%)	0	100	100
69	s	208/264 (79%)	199 (96%)	9 (4%)	0	100	100
70	t	209/256 (82%)	206 (99%)	3 (1%)	0	100	100
71	u	214/249 (86%)	208 (97%)	6 (3%)	0	100	100
72	v	207/250 (83%)	198 (96%)	8 (4%)	1 (0%)	24	19
73	w	258/264 (98%)	252 (98%)	6 (2%)	0	100	100
74	x	204/223 (92%)	195 (96%)	8 (4%)	1 (0%)	24	19
75	y	224/236 (95%)	221 (99%)	3 (1%)	0	100	100
76	z	180/188 (96%)	174 (97%)	6 (3%)	0	100	100
All	All	10662/11662 (91%)	10353 (97%)	302 (3%)	7 (0%)	49	49

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	N	47	ALA
21	T	77	SER
30	ZC	34	GLU
72	v	85	ILE
46	ZT	57	ASP

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	D	186/193 (96%)	181 (97%)	5 (3%)	39	41
6	E	328/330 (99%)	322 (98%)	6 (2%)	51	57
7	F	298/300 (99%)	292 (98%)	6 (2%)	48	53
8	G	247/252 (98%)	244 (99%)	3 (1%)	63	69
9	H	131/145 (90%)	127 (97%)	4 (3%)	35	35
10	I	199/202 (98%)	196 (98%)	3 (2%)	57	63
11	J	196/216 (91%)	188 (96%)	8 (4%)	27	24
12	K	168/168 (100%)	161 (96%)	7 (4%)	26	23
13	L	183/189 (97%)	182 (100%)	1 (0%)	81	86
14	M	143/145 (99%)	138 (96%)	5 (4%)	32	31
15	N	156/160 (98%)	152 (97%)	4 (3%)	40	42
16	O	110/111 (99%)	109 (99%)	1 (1%)	70	77
17	P	175/176 (99%)	174 (99%)	1 (1%)	78	84
18	Q	166/167 (99%)	163 (98%)	3 (2%)	51	57
19	R	146/152 (96%)	143 (98%)	3 (2%)	47	51
20	S	153/154 (99%)	153 (100%)	0	100	100
21	T	146/170 (86%)	143 (98%)	3 (2%)	47	51
22	U	154/168 (92%)	148 (96%)	6 (4%)	28	26
23	V	138/139 (99%)	134 (97%)	4 (3%)	37	38
24	W	96/106 (91%)	92 (96%)	4 (4%)	26	23
25	X	105/105 (100%)	100 (95%)	5 (5%)	23	18
26	Y	55/131 (42%)	54 (98%)	1 (2%)	51	57
27	Z	105/118 (89%)	102 (97%)	3 (3%)	37	38
28	ZA	157/167 (94%)	155 (99%)	2 (1%)	61	67
29	ZB	156/163 (96%)	153 (98%)	3 (2%)	50	55
30	ZC	87/108 (81%)	84 (97%)	3 (3%)	32	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	ZD	127/138 (92%)	126 (99%)	1 (1%)	73	79
32	ZE	130/131 (99%)	127 (98%)	3 (2%)	44	47
33	ZF	98/102 (96%)	91 (93%)	7 (7%)	13	8
34	ZG	97/118 (82%)	91 (94%)	6 (6%)	16	11
35	ZH	115/116 (99%)	110 (96%)	5 (4%)	26	23
36	ZI	113/121 (93%)	111 (98%)	2 (2%)	51	57
37	ZJ	126/129 (98%)	118 (94%)	8 (6%)	16	11
38	ZK	114/118 (97%)	108 (95%)	6 (5%)	20	16
39	ZL	90/104 (86%)	83 (92%)	7 (8%)	11	7
40	ZM	72/72 (100%)	68 (94%)	4 (6%)	19	14
41	ZO	113/114 (99%)	111 (98%)	2 (2%)	51	57
42	ZP	117/119 (98%)	109 (93%)	8 (7%)	14	9
43	ZQ	114/118 (97%)	105 (92%)	9 (8%)	11	7
44	ZR	62/107 (58%)	56 (90%)	6 (10%)	8	3
45	ZS	87/158 (55%)	82 (94%)	5 (6%)	18	14
46	ZT	72/73 (99%)	65 (90%)	7 (10%)	8	3
47	ZU	55/60 (92%)	52 (94%)	3 (6%)	19	15
48	ZV	47/48 (98%)	45 (96%)	2 (4%)	26	23
49	ZW	47/54 (87%)	47 (100%)	0	100	100
50	ZY	261/267 (98%)	247 (95%)	14 (5%)	20	15
51	a	111/112 (99%)	104 (94%)	7 (6%)	16	11
52	b	113/114 (99%)	109 (96%)	4 (4%)	32	31
53	c	119/120 (99%)	116 (98%)	3 (2%)	42	44
54	d	50/66 (76%)	49 (98%)	1 (2%)	48	53
55	e	80/84 (95%)	78 (98%)	2 (2%)	42	44
56	f	97/100 (97%)	94 (97%)	3 (3%)	35	35
57	g	109/130 (84%)	107 (98%)	2 (2%)	51	57
58	h	92/93 (99%)	90 (98%)	2 (2%)	45	49
59	i	97/99 (98%)	92 (95%)	5 (5%)	21	16
60	j	101/102 (99%)	97 (96%)	4 (4%)	28	25
61	k	80/81 (99%)	79 (99%)	1 (1%)	61	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	l	69/70 (99%)	68 (99%)	1 (1%)	59	65
63	m	69/70 (99%)	65 (94%)	4 (6%)	18	13
64	n	47/48 (98%)	44 (94%)	3 (6%)	16	11
65	o	47/47 (100%)	46 (98%)	1 (2%)	47	51
66	p	24/24 (100%)	22 (92%)	2 (8%)	10	6
67	q	88/90 (98%)	87 (99%)	1 (1%)	65	71
68	r	70/76 (92%)	69 (99%)	1 (1%)	59	65
69	s	182/218 (84%)	179 (98%)	3 (2%)	55	61
70	t	186/223 (83%)	180 (97%)	6 (3%)	34	35
71	u	178/203 (88%)	175 (98%)	3 (2%)	53	58
72	v	165/192 (86%)	156 (94%)	9 (6%)	19	15
73	w	219/222 (99%)	212 (97%)	7 (3%)	34	35
74	x	175/192 (91%)	170 (97%)	5 (3%)	37	38
75	y	194/202 (96%)	184 (95%)	10 (5%)	21	16
76	z	163/168 (97%)	161 (99%)	2 (1%)	63	69
All	All	9166/9848 (93%)	8875 (97%)	291 (3%)	35	35

5 of 291 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
60	j	95	GLN
75	y	151	ASP
64	n	10	LYS
72	v	54	SER
32	ZE	151	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
55	e	76	ASN
69	s	83	GLN
56	f	20	HIS
60	j	19	GLN
70	t	118	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	3011/3283 (91%)	453 (15%)	27 (0%)
2	B	121/122 (99%)	15 (12%)	1 (0%)
3	C	153/158 (96%)	26 (16%)	0
4	CA	1665/1775 (93%)	420 (25%)	25 (1%)
All	All	4950/5338 (92%)	914 (18%)	53 (1%)

5 of 914 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	G
1	A	15	G
1	A	24	A
1	A	38	A
1	A	41	A

5 of 53 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	CA	61	A
4	CA	493	U
4	CA	1434	G
4	CA	136	A
4	CA	406	A

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 258 ligands modelled in this entry, 258 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

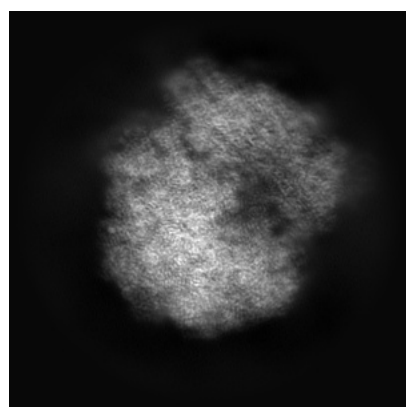
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55092. These allow visual inspection of the internal detail of the map and identification of artifacts.

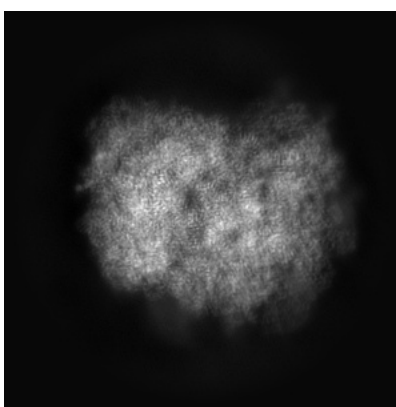
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

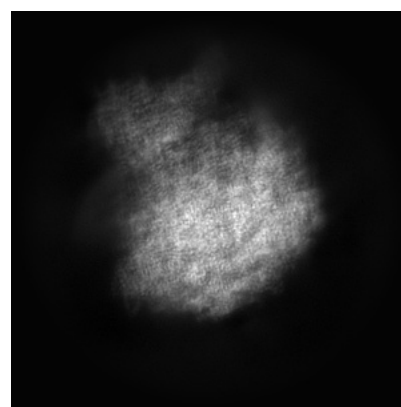
6.1.1 Primary map



X



Y

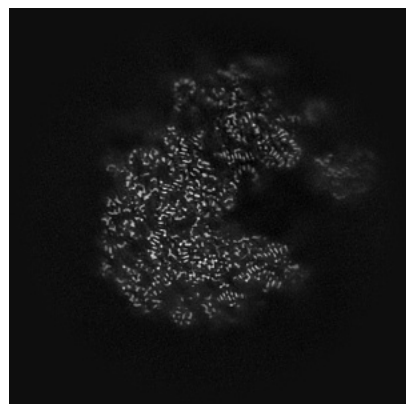


Z

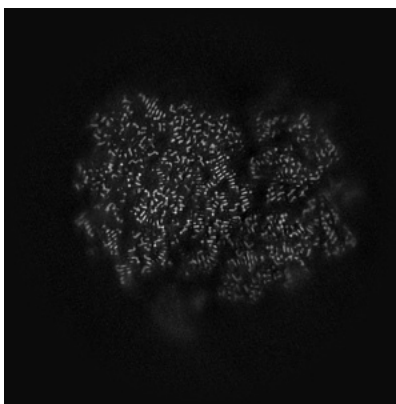
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

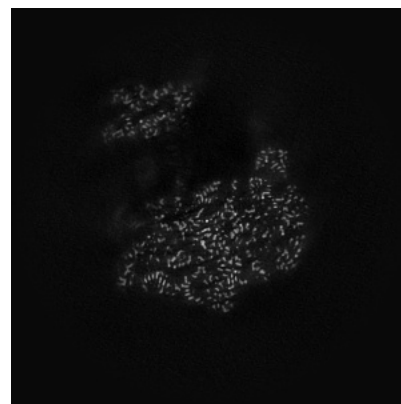
6.2.1 Primary map



X Index: 225



Y Index: 225

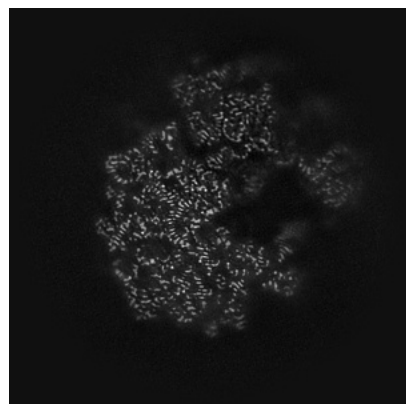


Z Index: 225

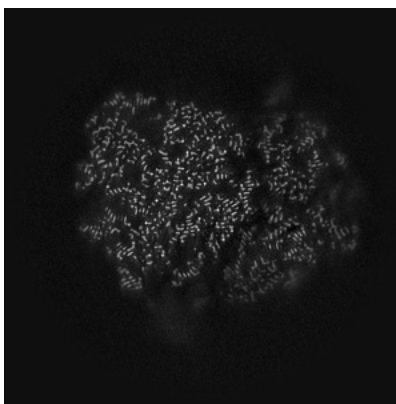
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

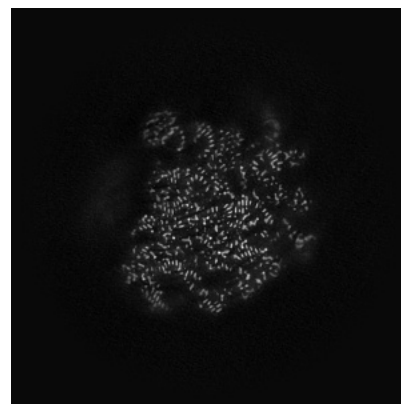
6.3.1 Primary map



X Index: 212



Y Index: 217

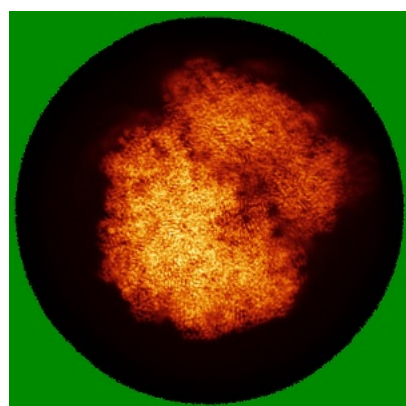


Z Index: 177

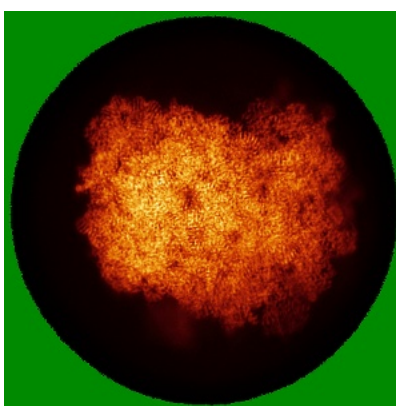
The images above show the largest variance slices of the map in three orthogonal directions.

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

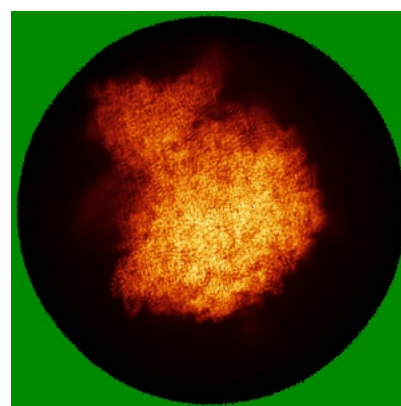
6.4.1 Primary map



X



Y

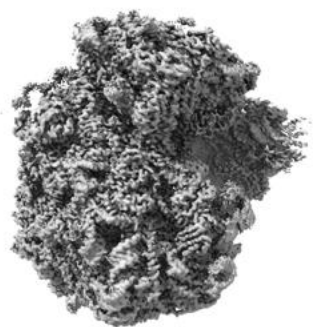


Z

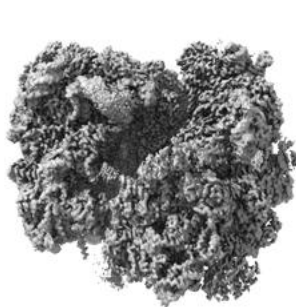
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

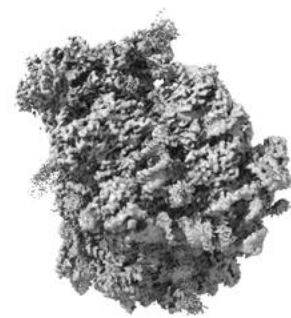
6.5.1 Primary map



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.

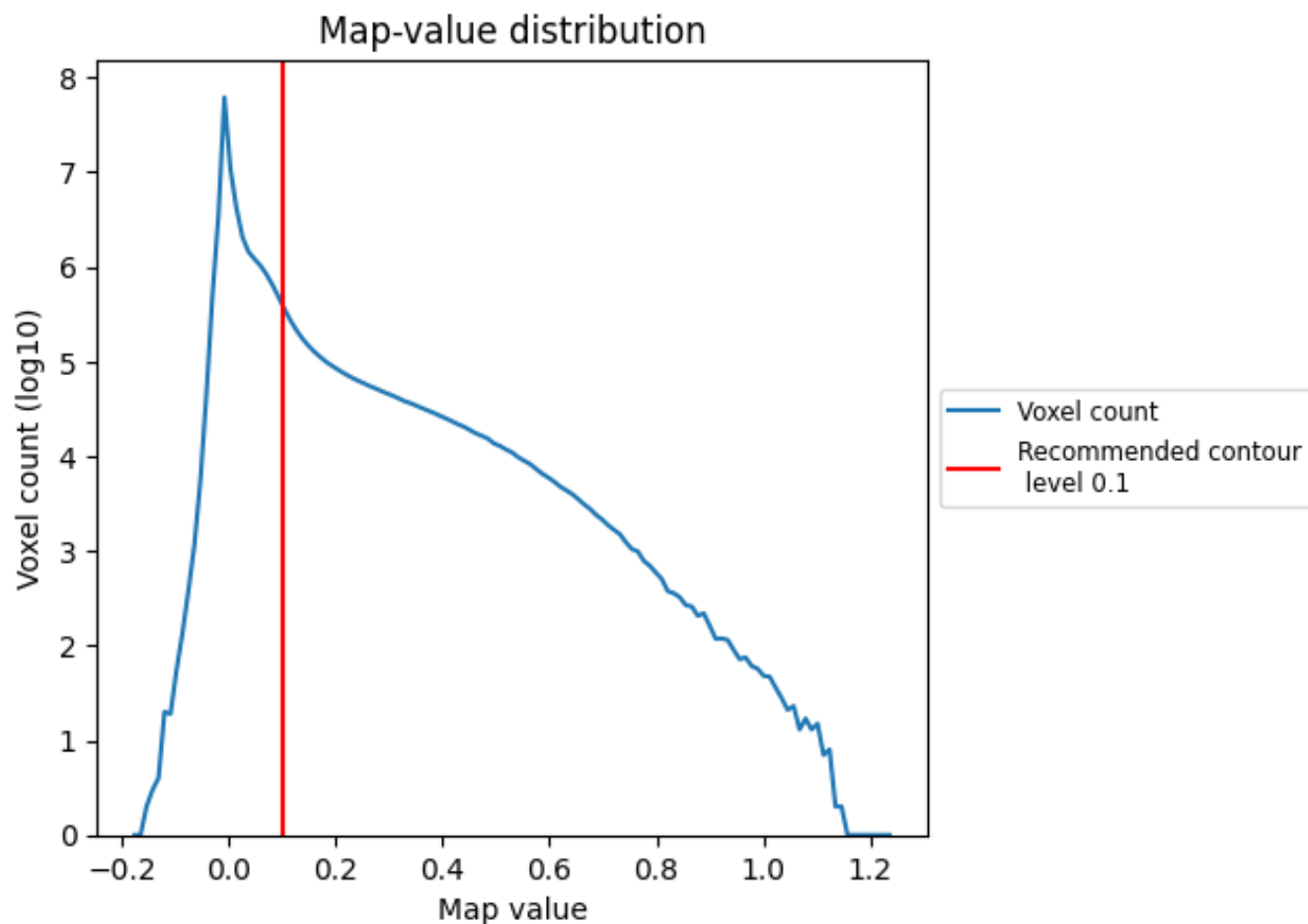
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

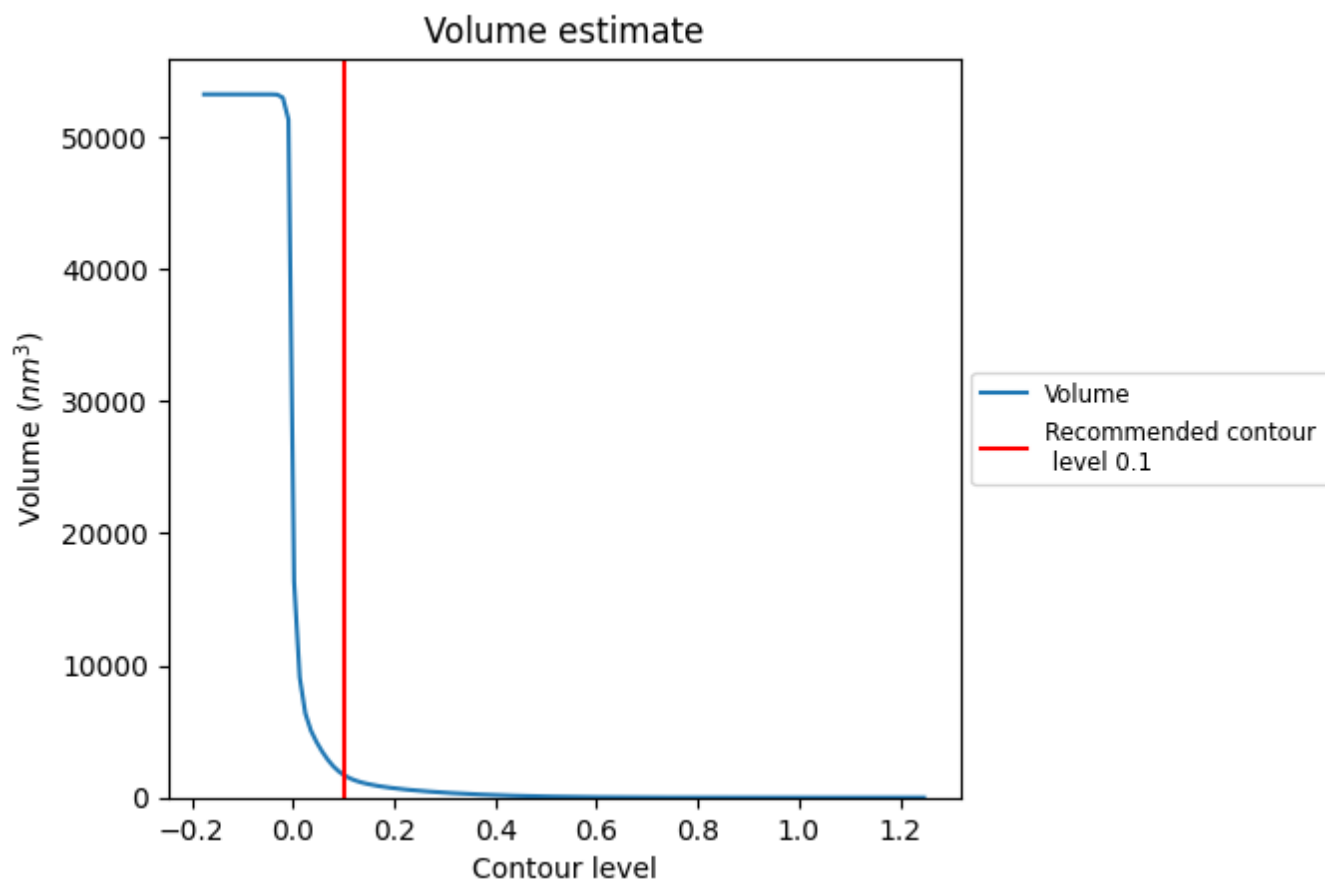
This section contains the results of statistical analysis of the map.

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.

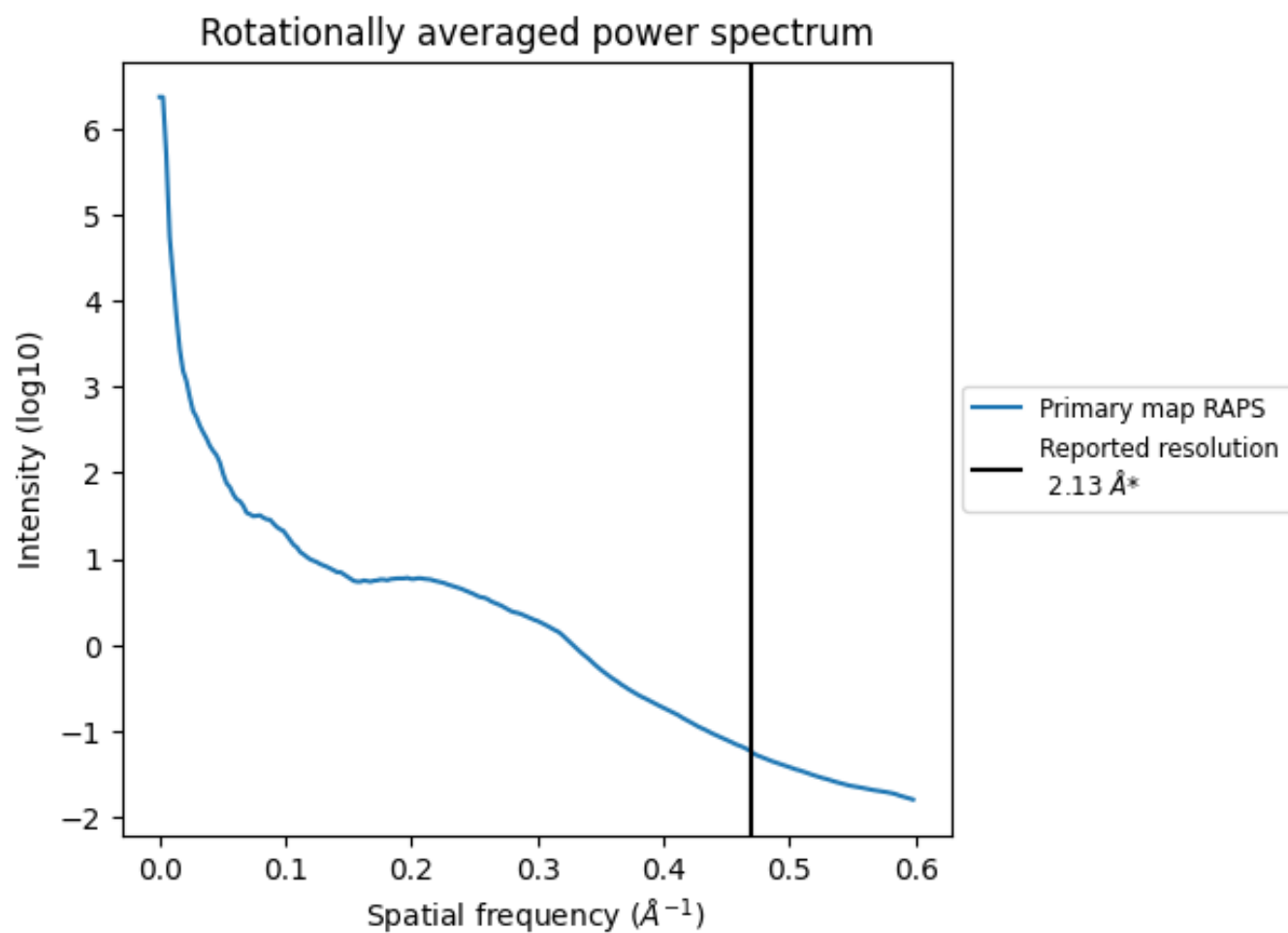
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1721 nm³; this corresponds to an approximate mass of 1555 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 0.469 Å⁻¹

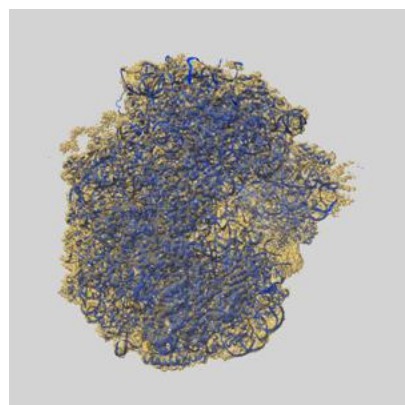
8 Fourier-Shell correlation

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

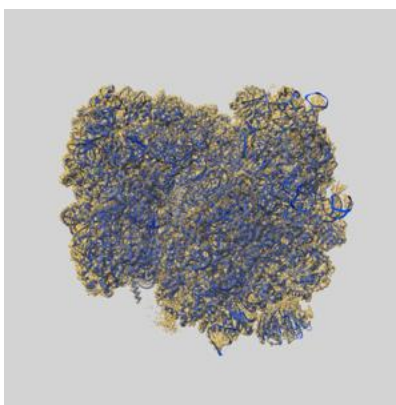
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55092 and PDB model 9SPJ. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

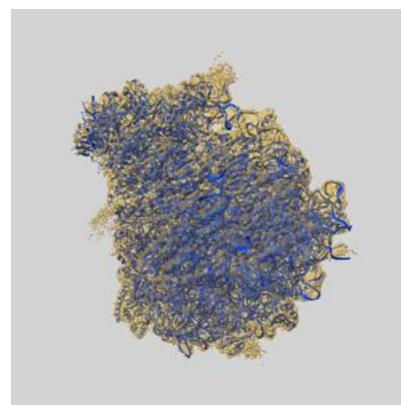
9.1 Map-model overlay [i](#)



X



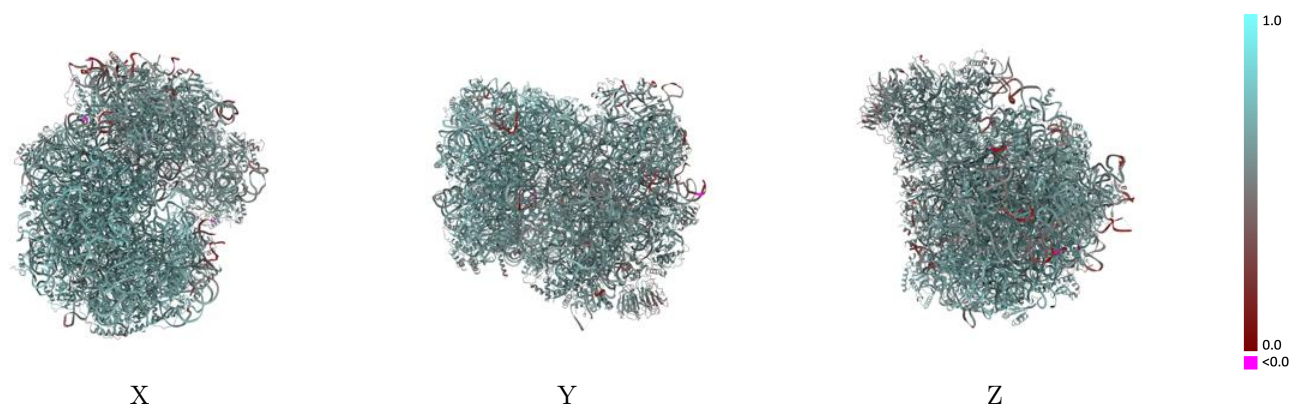
Y



Z

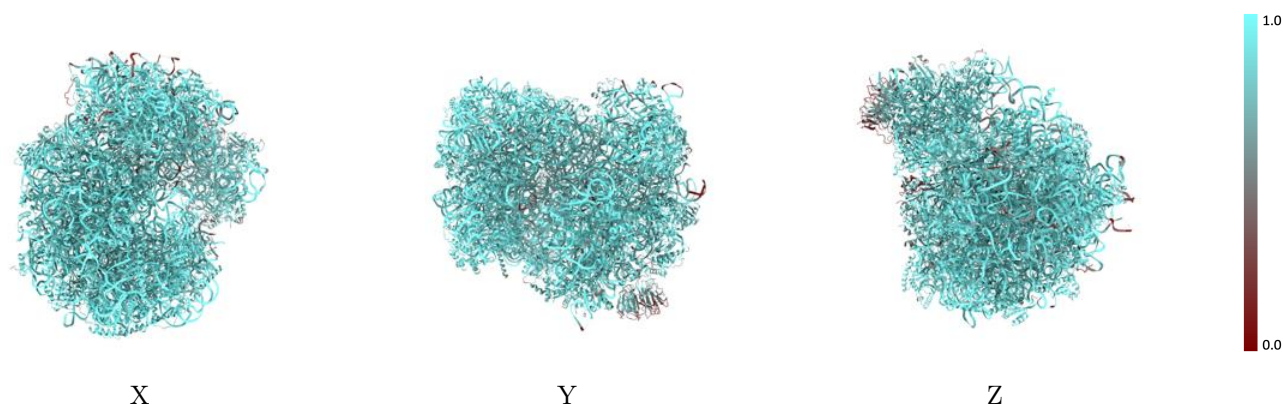
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



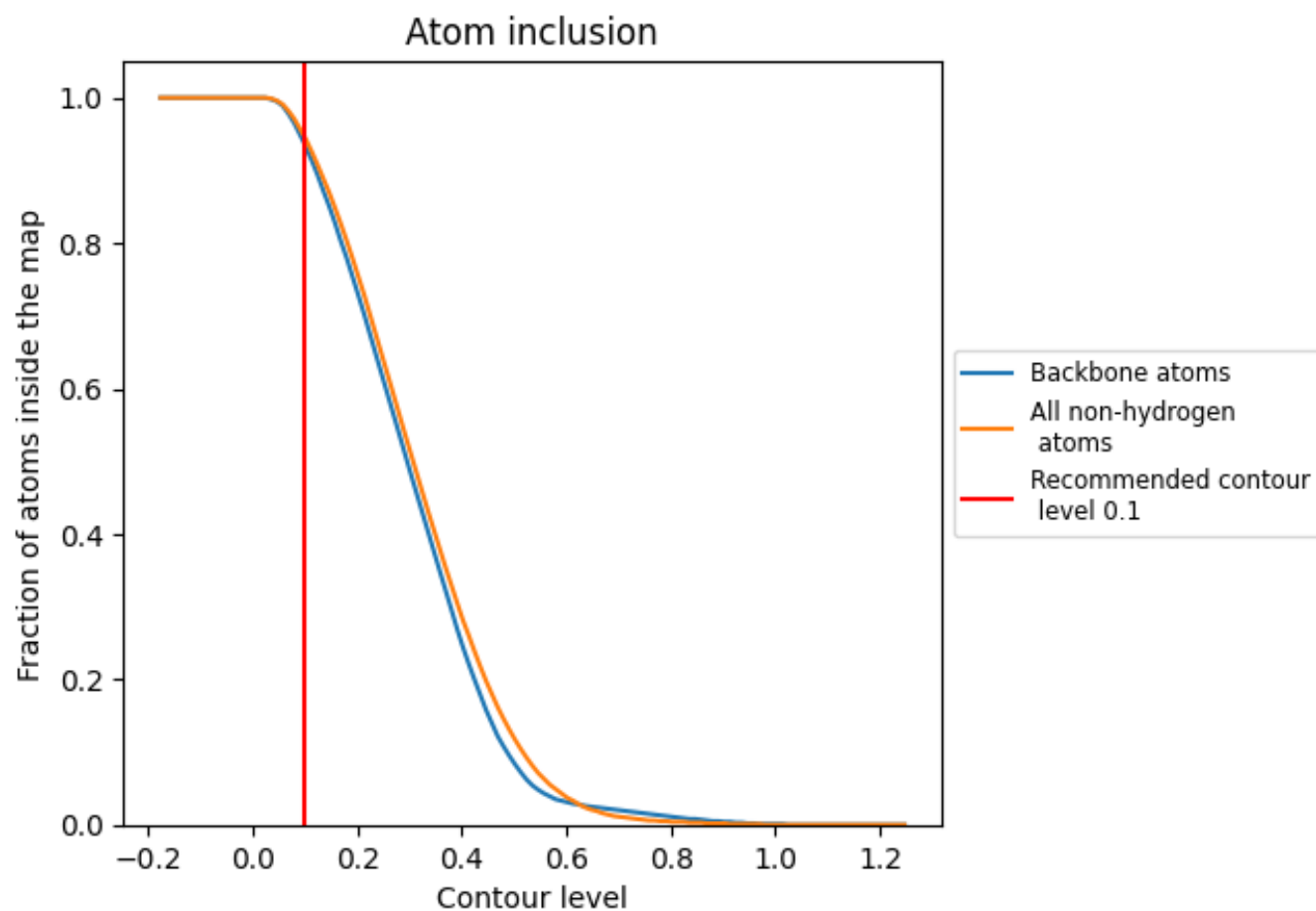
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 94% of all backbone atoms, 95% 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	 0.9460	 0.6260
A	 0.9870	 0.6510
B	 0.9950	 0.6420
C	 0.9950	 0.6620
CA	 0.9460	 0.5760
D	 0.9880	 0.6950
E	 0.9760	 0.6860
F	 0.9760	 0.6760
G	 0.9350	 0.6080
H	 0.9480	 0.6250
I	 0.9590	 0.6630
J	 0.9290	 0.6270
K	 0.9600	 0.6520
L	 0.9540	 0.6540
M	 0.8580	 0.5580
N	 0.9490	 0.6510
O	 0.9740	 0.6550
P	 0.9940	 0.7040
Q	 0.9750	 0.6820
R	 0.9720	 0.6840
S	 0.9840	 0.6800
T	 0.9570	 0.6420
U	 0.9670	 0.6740
V	 0.9640	 0.6620
W	 0.9070	 0.5770
X	 0.9570	 0.6810
Y	 0.9620	 0.6890
Z	 0.9550	 0.6600
ZA	 0.8990	 0.6120
ZB	 0.9400	 0.6020
ZC	 0.8630	 0.5540
ZD	 0.9460	 0.6480
ZE	 0.9540	 0.6120
ZF	 0.8280	 0.5620
ZG	 0.8780	 0.5740



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Chain	Atom inclusion	Q-score
ZH	 0.8920	 0.5970
ZI	 0.7980	 0.5310
ZJ	 0.8690	 0.5810
ZK	 0.8710	 0.5880
ZL	 0.8040	 0.5420
ZM	 0.9330	 0.6100
ZO	 0.9600	 0.6350
ZP	 0.9260	 0.6250
ZQ	 0.9120	 0.5960
ZR	 0.8280	 0.5600
ZS	 0.5300	 0.5530
ZT	 0.9540	 0.5920
ZU	 0.8100	 0.5260
ZV	 0.9420	 0.6230
ZW	 0.6990	 0.5170
ZY	 0.5150	 0.4960
a	 0.9530	 0.6620
b	 0.9580	 0.6270
c	 0.9830	 0.6870
d	 0.9290	 0.6410
e	 0.9580	 0.6240
f	 0.9470	 0.6600
g	 0.9720	 0.6890
h	 0.9840	 0.6980
i	 0.9280	 0.6530
j	 0.9560	 0.6470
k	 0.9360	 0.6370
l	 0.9810	 0.7020
m	 0.9010	 0.5950
n	 0.9620	 0.6550
o	 0.9700	 0.6600
p	 0.2330	 0.5050
q	 0.9430	 0.6770
r	 0.9580	 0.6700
s	 0.9350	 0.5960
t	 0.8150	 0.5780
u	 0.9410	 0.6140
v	 0.8530	 0.5750
w	 0.9350	 0.6140
x	 0.8670	 0.5720
y	 0.8580	 0.5660
z	 0.8830	 0.5560