



Full wwPDB EM Validation Report ⓘ

May 27, 2024 – 09:40 AM EDT

PDB ID : 7TM3
EMDB ID : EMD-25994
Title : Structure of the rabbit 80S ribosome stalled on a 2-TMD Rhodopsin intermediate in complex with the multipass translocon
Authors : Kim, M.K.; Lewis, A.J.O.; Keenan, R.J.; Hegde, R.S.
Deposited on : 2022-01-19
Resolution : 3.25 Å(reported)

This is a Full wwPDB EM Validation 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.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36.2

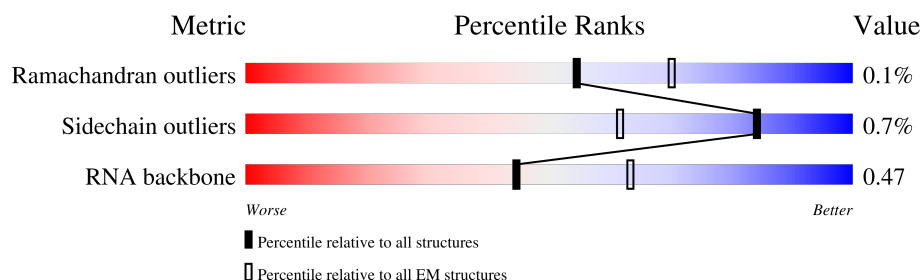
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

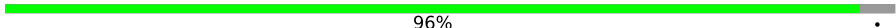


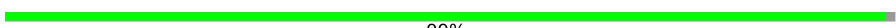



The reported resolution of this entry is 3.25 Å.

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



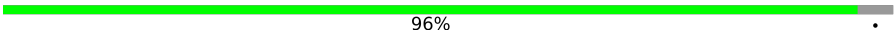
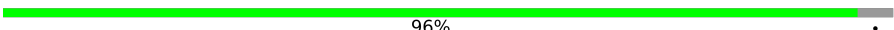
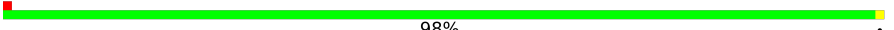

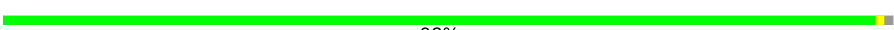





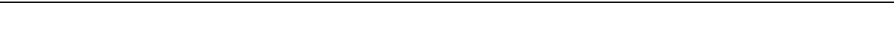

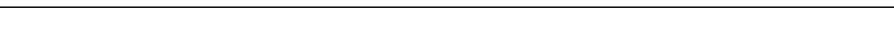
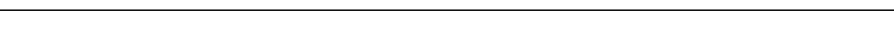



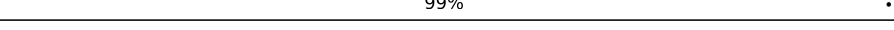
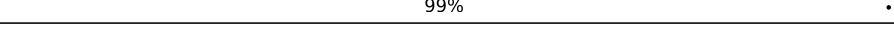



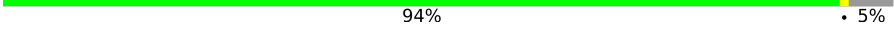
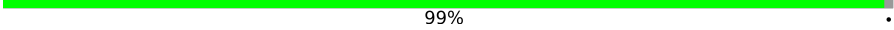
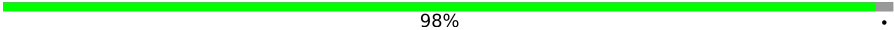
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	257	 96% .
2	B	229	 11% 88%
3	C	425	 85% 15%
4	D	297	 99% .
5	E	291	 79% . 20%
6	F	247	 91% 9%
7	G	319	 73% 27%
8	H	192	 99% .

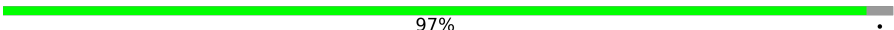

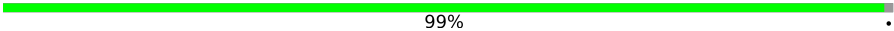
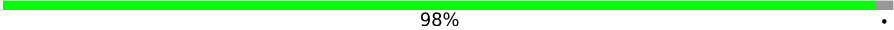

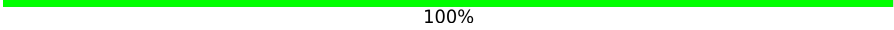
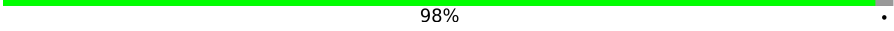
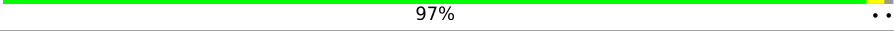

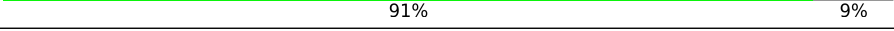


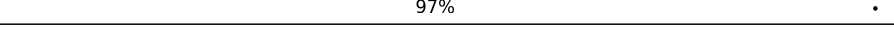
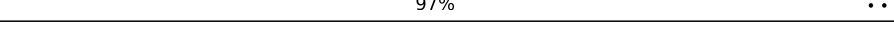

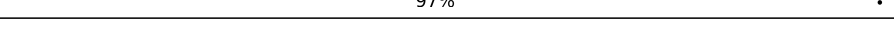


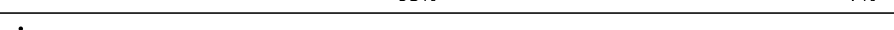


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Mol	Chain	Length	Quality of chain
9	I	214	
10	J	178	
11	L	211	
12	M	218	
13	N	204	
14	O	203	
15	P	184	
16	Q	188	
17	R	196	
18	S	176	
19	T	160	
20	U	128	
21	V	140	
22	W	157	
23	X	156	
24	Y	145	
25	Z	136	
26	a	148	
27	b	226	
28	c	115	
29	d	125	
30	e	135	
31	f	110	
32	g	116	
33	h	123	

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Mol	Chain	Length	Quality of chain
34	i	105	 97% .
35	j	97	 87% . 11%
36	k	70	 99% .
37	l	51	 98% .
38	m	102	 51% 49%
39	n	25	 100%
40	o	106	 98% .
41	p	92	 97% ..
42	q	77	 79% 18% ..
43	r	137	 91% 9%
44	u	120	 88% 11% .
45	v	156	 76% 24%
46	w	403	 97% .
47	1	476	 97% ..
48	2	96	 30% 70%
49	3	68	 97% .
50	4	483	 70% . 29%
51	5	106	 6% 85% 15%
52	7	563	 51% 93% 7%
53	6	224	 99% .
54	K	3543	 76% 24%

2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 261738 atoms, of which 111794 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called uL2.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	248	Total	C	H	N	O	S	0	0
			3891	1189	1993	389	314	6		

- Molecule 2 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	27	Total	C	H	N	O	S	0	0
			351	112	171	31	36	1		

- Molecule 3 is a protein called uL4.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	362	Total	C	H	N	O	S	0	0
			5936	1812	3053	577	480	14		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	378	LYS	-	insertion	UNP G1SVW5
C	379	VAL	-	insertion	UNP G1SVW5
C	380	LYS	-	insertion	UNP G1SVW5
C	381	LYS	-	insertion	UNP G1SVW5
C	382	PRO	-	insertion	UNP G1SVW5
C	383	ARG	-	insertion	UNP G1SVW5
C	384	ALA	-	insertion	UNP G1SVW5
C	385	VAL	-	insertion	UNP G1SVW5
C	386	GLY	-	insertion	UNP G1SVW5
C	387	ILE	-	insertion	UNP G1SVW5
C	388	LYS	-	insertion	UNP G1SVW5
C	389	GLN	-	insertion	UNP G1SVW5

- Molecule 4 is a protein called uL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	293	Total	C	H	N	O	S	0	0
			4815	1512	2424	438	427	14		

- Molecule 5 is a protein called eL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	233	Total	C	H	N	O	S	0	0
			3908	1206	2031	357	311	3		

- Molecule 6 is a protein called uL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	225	Total	C	H	N	O	S	0	0
			3870	1205	1995	358	303	9		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	61	ARG	GLY	conflict	UNP G1TUB1
F	93	ARG	GLY	conflict	UNP G1TUB1
F	131	MET	VAL	conflict	UNP G1TUB1
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 7 is a protein called eL8.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	233	Total	C	H	N	O	S	0	0
			3906	1199	2027	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 8 is a protein called uL6.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	190	Total	C	H	N	O	S	0	0
			3113	954	1597	284	272	6		

- Molecule 9 is a protein called uL16.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	205	Total	C	H	N	O	S	0	0
			3376	1056	1712	321	274	13		

- Molecule 10 is a protein called uL5.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	170	Total	C	H	N	O	S	0	0
			2761	861	1399	254	241	6		

- Molecule 11 is a protein called eL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	L	210	Total	C	H	N	O	S	0	0
			3522	1065	1820	354	279	4		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	46	ILE	-	insertion	UNP G1TPV0
L	47	ALA	-	insertion	UNP G1TPV0
L	48	PRO	-	insertion	UNP G1TPV0
L	49	ARG	-	insertion	UNP G1TPV0
L	50	PRO	-	insertion	UNP G1TPV0
L	51	ALA	-	insertion	UNP G1TPV0
L	52	ALA	-	insertion	UNP G1TPV0
L	53	GLY	-	insertion	UNP G1TPV0
L	54	PRO	-	insertion	UNP G1TPV0

- Molecule 12 is a protein called eL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	M	138	Total	C	H	N	O	S	0	0
			2348	727	1211	221	182	7		

- Molecule 13 is a protein called eL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	N	202	Total	C	H	N	O	S	0	0
			3440	1069	1744	358	265	4		

- Molecule 14 is a protein called uL13.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	O	199	Total	C	H	N	O	S	0	0
			3408	1051	1778	319	255	5		

- Molecule 15 is a protein called uL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	P	153	Total	C	H	N	O	S	0	0
			2516	777	1274	241	215	9		

- Molecule 16 is a protein called eL18.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	Q	187	Total	C	H	N	O	S	0	0
			3148	946	1634	315	249	4		

- Molecule 17 is a protein called eL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	R	155	Total	C	H	N	O	S	0	0
			2728	808	1434	278	199	9		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	38	ARG	CYS	conflict	UNP G1TJR3
R	64	ARG	GLN	conflict	UNP G1TJR3
R	94	THR	LYS	conflict	UNP G1TJR3

- Molecule 18 is a protein called eL20.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	S	176	Total	C	H	N	O	S	0	0
			2970	930	1508	285	236	11		

- Molecule 19 is a protein called eL21.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	T	159	Total	C	H	N	O	S	0	0
			2665	823	1367	252	217	6		

- Molecule 20 is a protein called eL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	U	102	Total	C	H	N	O	S	0	0
			1692	534	858	146	152	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1
U	60	VAL	ALA	conflict	UNP G1TSG1
U	62	SER	THR	conflict	UNP G1TSG1
U	63	LEU	ILE	conflict	UNP G1TSG1
U	97	ARG	HIS	conflict	UNP G1TSG1
U	106	THR	SER	conflict	UNP G1TSG1
U	126	GLU	ASP	conflict	UNP G1TSG1

- Molecule 21 is a protein called uL14.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	V	131	Total	C	H	N	O	S	0	0
			2018	618	1039	184	172	5		

- Molecule 22 is a protein called eL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	W	63	Total	C	H	N	O	S	0	0
			1069	337	541	103	85	3		

- Molecule 23 is a protein called uL23.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	X	118	Total	C	H	N	O	S	0	0
			2007	618	1040	181	167	1		

- Molecule 24 is a protein called uL24.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	Y	134	Total	C	H	N	O	S	0	0
			2320	700	1205	226	186	3		

- Molecule 25 is a protein called eL27.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Z	135	Total	C	H	N	O	S	0	0
			2289	714	1182	208	182	3		

- Molecule 26 is a protein called uL15.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	a	147	Total	C	H	N	O	S	0	0
			2371	734	1209	239	185	4		

- Molecule 27 is a protein called eL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	b	104	Total	C	H	N	O	S	0	0
			1768	527	920	189	129	3		

- Molecule 28 is a protein called eL30.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	c	98	Total	C	H	N	O	S	0	0
			1555	481	794	134	140	6		

- Molecule 29 is a protein called eL31.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	d	107	Total	C	H	N	O	S	0	0
			1818	560	930	171	155	2		

- Molecule 30 is a protein called eL32.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	e	128	Total	C	H	N	O	S	0	0
			2200	667	1147	216	165	5		

- Molecule 31 is a protein called eL33.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	f	109	Total	C	H	N	O	S	0	0
			1788	555	912	174	143	4		

- Molecule 32 is a protein called eL34.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	g	114	Total	C	H	N	O	S	0	0
			1904	566	998	187	147	6		

- Molecule 33 is a protein called uL29.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	h	122	Total	C	H	N	O	S	0	0
			2145	637	1136	203	168	1		

- Molecule 34 is a protein called eL36.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	i	102	Total	C	H	N	O	S	0	0
			1746	520	916	176	129	5		

- Molecule 35 is a protein called eL37.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	j	86	Total	C	H	N	O	S	0	0
			1442	434	737	155	111	5		

- Molecule 36 is a protein called eL38.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	k	69	Total	C	H	N	O	S	0	0
			1206	366	637	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called eL39.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	l	50	Total	C	H	N	O	S	0	0
			927	286	480	96	64	1		

- Molecule 38 is a protein called eL40.

Mol	Chain	Residues	Atoms						AltConf	Trace
38	m	52	Total	C	H	N	O	S	0	0
			895	266	466	90	67	6		

- Molecule 39 is a protein called eL41.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	n	25	Total	C	H	N	O	S	0	0
			528	145	289	64	27	3		

- Molecule 40 is a protein called eL42.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	o	104	Total	C	H	N	O	S	0	0
			1773	533	922	174	138	6		

- Molecule 41 is a protein called eL43.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	p	91	Total	C	H	N	O	S	0	0
			1465	445	757	136	120	7		

- Molecule 42 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	q	76	Total	C	H	N	O	P	0	0
			2439	723	823	291	527	75		

- Molecule 43 is a protein called eL28.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	r	124	Total	C	H	N	O	S	0	0
			2045	616	1051	205	167	6		

- Molecule 44 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	u	120	Total	C	H	N	O	P	0	0
			3854	1141	1296	456	842	119		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	2	U	N	conflict	GB X06789.1
u	36	C	N	conflict	GB X06789.1
u	102	U	N	conflict	GB X06789.1
u	112	U	N	conflict	GB X06789.1
u	114	U	N	conflict	GB X06789.1
u	119	U	C	conflict	GB X06789.1
u	120	U	N	conflict	GB X06789.1

- Molecule 45 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	v	156	Total	C	H	N	O	P	0	0
			4997	1480	1683	585	1094	155		

- Molecule 46 is a protein called uL3.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	w	394	Total	C	H	N	O	S	0	0
			6482	2020	3310	597	542	13		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
w	1	MET	-	insertion	UNP G1TL06

- Molecule 47 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
47	1	465	Total	C	H	N	O	S	0	0
			7320	2360	3722	580	634	24		

- Molecule 48 is a protein called Protein transport protein Sec61 subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	2	29	Total	C	H	N	O	S	0	0
			475	157	245	36	35	2		

- Molecule 49 is a protein called Protein transport protein Sec61 gamma.

Mol	Chain	Residues	Atoms						AltConf	Trace
49	3	68	Total	C	H	N	O	S	0	0
			1120	355	577	94	89	5		

- Molecule 50 is a protein called Coiled-coil domain containing 47.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	4	342	Total	C	H	N	O	S	0	0
			5597	1738	2819	495	522	23		

- Molecule 51 is a protein called PAT complex subunit Asterix.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	5	90	Total	C	H	N	O	S	0	0
			1421	456	710	115	128	12		

- Molecule 52 is a protein called Nicalin.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	7	521	Total	C	H	N	O	S	0	0
			8260	2625	4121	726	771	17		

- Molecule 53 is a protein called Transmembrane protein 147.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	6	224	Total	C	H	N	O	S	0	0
			3575	1190	1792	277	300	16		

- Molecule 54 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	K	3543	Total	C	H	N	O	P	0	0
			114330	33833	38358	13910	24686	3543		

- Molecule 55 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
55	P	2	Total	Mg	0
			2	2	
55	V	1	Total	Mg	0
			1	1	
55	a	1	Total	Mg	0
			1	1	
55	g	1	Total	Mg	0
			1	1	
55	j	1	Total	Mg	0
			1	1	

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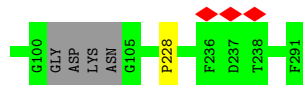
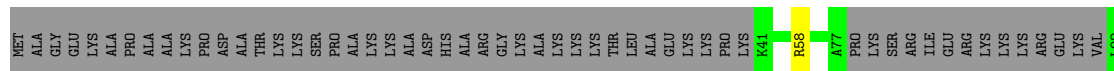
Mol	Chain	Residues	Atoms		AltConf
55	u	7	Total 7	Mg 7	0
55	v	6	Total 6	Mg 6	0
55	K	201	Total 201	Mg 201	0

- Molecule 56 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	g	1	Total 1	Zn 1	0
56	j	1	Total 1	Zn 1	0
56	m	1	Total 1	Zn 1	0
56	o	1	Total 1	Zn 1	0
56	p	1	Total 1	Zn 1	0

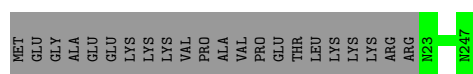
- Molecule 5: eL6

Chain E:  79% 20%



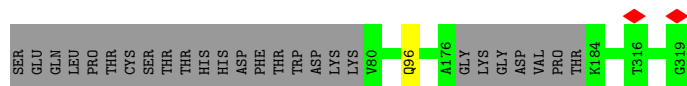
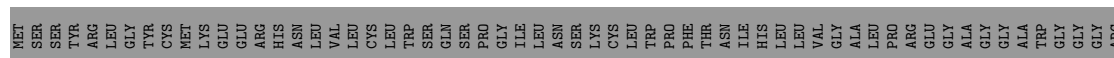
- Molecule 6: uL30

Chain F:  91% 9%



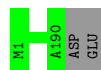
- Molecule 7: eL8

Chain G:  73% 27%



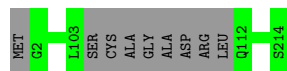
- Molecule 8: uL6

Chain H:  99%



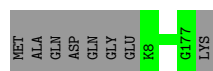
- Molecule 9: uL16

Chain I:  96%



- Molecule 10: uL5

Chain J:  96%



- Molecule 11: eL13

- Chain M:  63% 37%

[illegible]

- Chain N:  98% ..

Diagram illustrating the R204Q mutation in the RBD of SARS-CoV-2. The sequence shown is MET, G2, ALA, Y4, R26, P76, T80, and R204. The R204 is highlighted in red, indicating the site of the mutation.

- Chain 0:  97% ..

MET
ALA
GLU
GLY
Q5
Q173
Q180
V203

- Chain P: 83% 17%

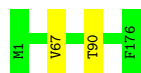
MET	V2	Q118	E154	GLN	ILE	VAL	PRO	LYS	LYS	PRO	GLU	GLU	GLU	VAL	ALA	GLN	LYS	LYS	LYS	LYS	LEU	LYS	LYS	GLN	LYS	LYS	LEU	LEU	MET	ALA	ARG	GLU
-----	----	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain Q: 99% ..

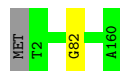
- Chain R: 79% 21%

MET
S2
R71
A156
ASP
GLN
ALA
GLU
ALA
ARG
ARG
SER
LYS
THR
LYS
GLU
ALA
ARG
LYS
ARG
ARG
GLU
GLU
ARG
LEU
GLN
ALA
LYS
LYS
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THR
LEU
SER
LYS
GLU
GLU
THR
LYS
LYS

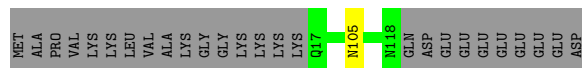
● Molecule 18: eL20

Chain S:  99%

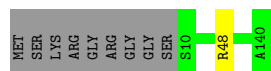
● Molecule 19: eL21

Chain T:  99%

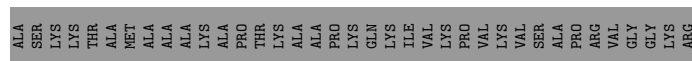
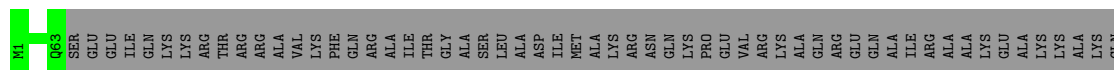
● Molecule 20: eL22

Chain U:  79% 20%

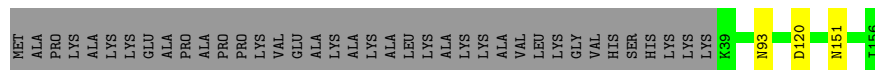
● Molecule 21: uL14

Chain V:  93% 6%

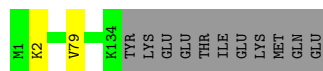
● Molecule 22: eL24

Chain W:  40% 60%

● Molecule 23: uL23

Chain X:  74% 24%

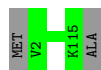
● Molecule 24: uL24

Chain Y:  91% 8%



- Molecule 32: eL34

Chain g:  98%



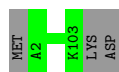
- Molecule 33: uL29

Chain h:  99%


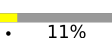


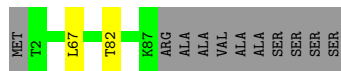
- Molecule 34: eL36

Chain i:  97%



- Molecule 35: eL37

Chain j:  87%  11%



- Molecule 36: eL38

Chain k:  99%



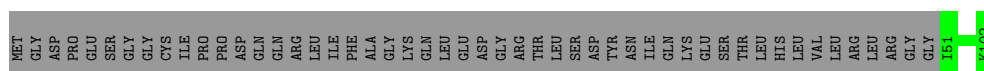
- Molecule 37: eL39

Chain l:  98%



- Molecule 38: eL40

Chain m:  51%  49%



- Molecule 39: eL41

Chain n: 100%

There are no outlier residues recorded for this chain.

- Molecule 40: eL42

Chain o: 98%



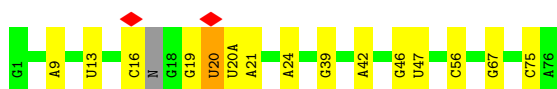
- Molecule 41: eL43

Chain p: 97%



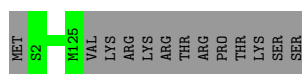
- Molecule 42: P-site tRNA

Chain q: 79%



- Molecule 43: eL28

Chain r: 91%



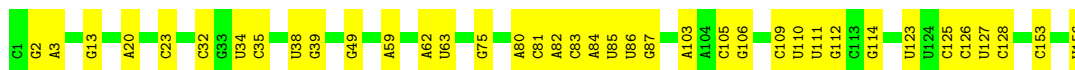
- Molecule 44: 5S ribosomal RNA

Chain u: 88%



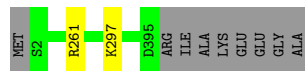
- Molecule 45: 5.8S ribosomal RNA

Chain v: 76%



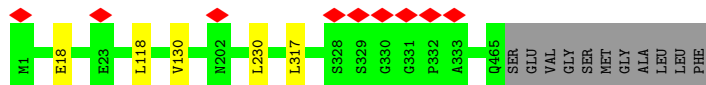
- Molecule 46: uL3

Chain w:  97%



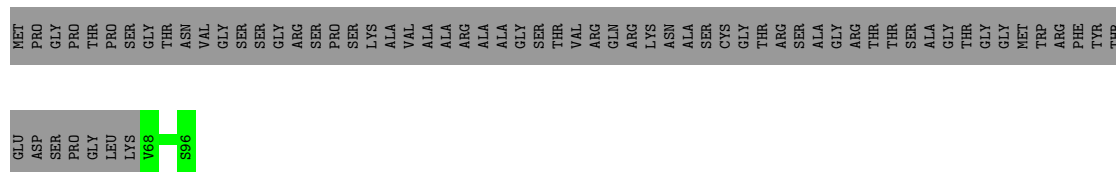
- Molecule 47: Protein transport protein Sec61 subunit alpha isoform 1

Chain 1:  97%



- Molecule 48: Protein transport protein Sec61 subunit beta

Chain 2:  30%



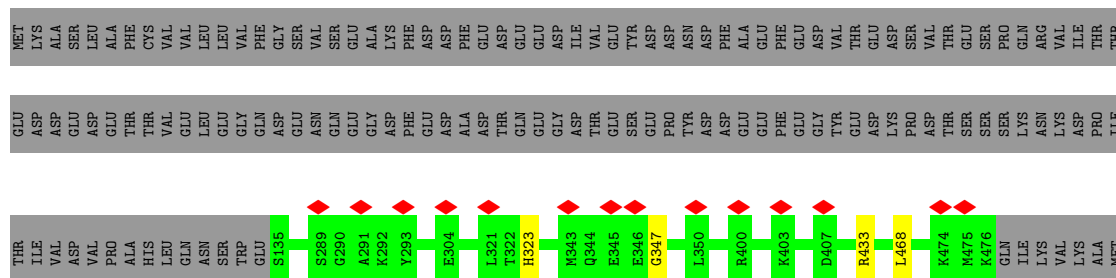
- Molecule 49: Protein transport protein Sec61 gamma

Chain 3:  97%




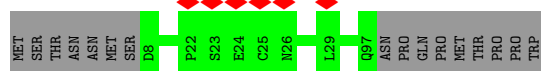
- Molecule 50: Coiled-coil domain containing 47

Chain 4:  70%



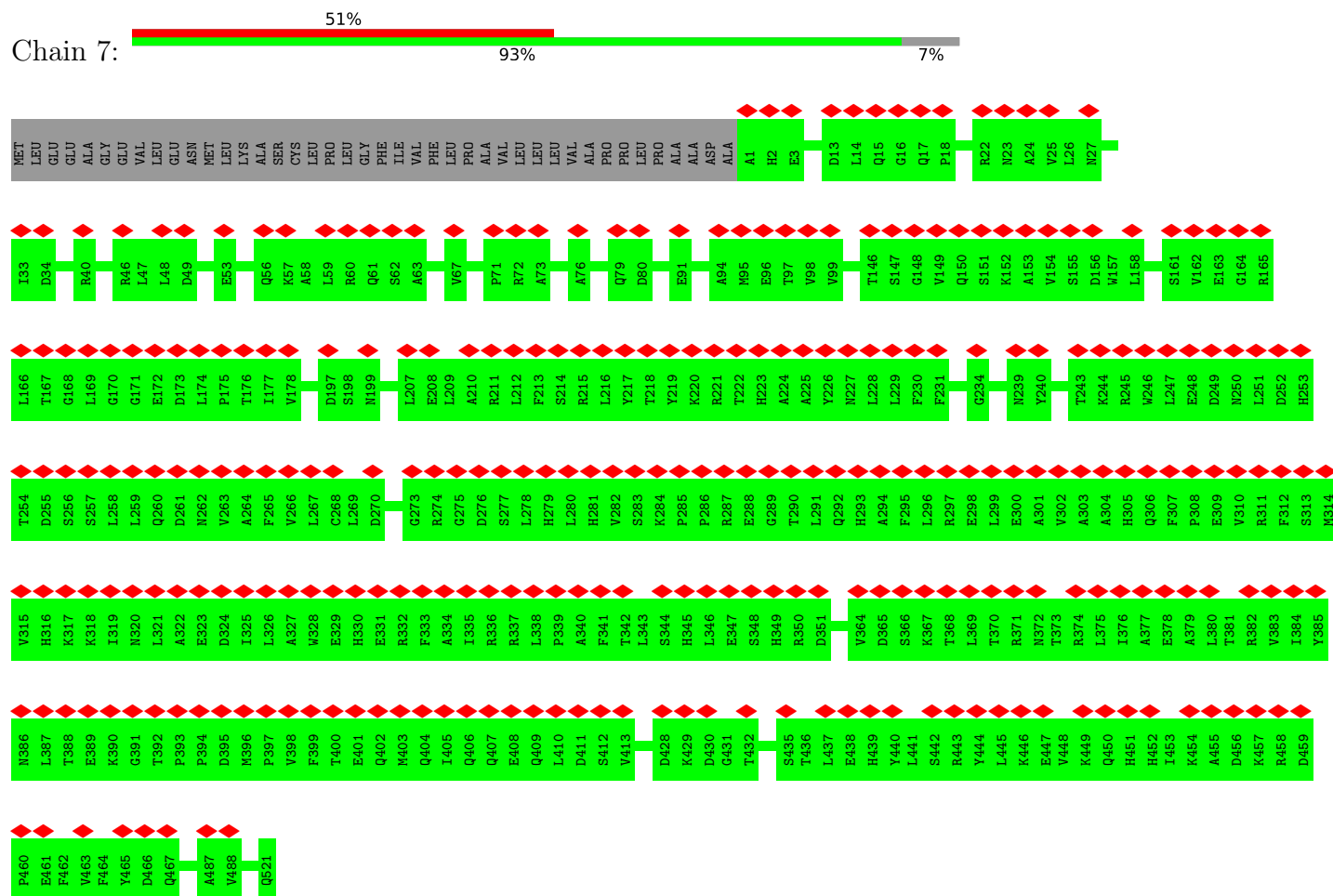
- Molecule 51: PAT complex subunit Asterix

Chain 5:  6%



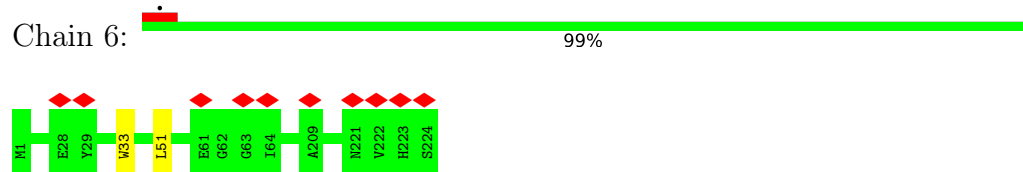
- Molecule 52: Nicalin

Chain 7:



- Molecule 53: Transmembrane protein 147

Chain 6:



- Molecule 54: 28S ribosomal RNA

Chain K:



A3756	G3603	G2714	G2546	G2092	A1843	U1677	G1489	A1354	C1097	C923	U492
A3760	A3604	G2721	G2547	G2093	A1847	C1696	A1497	G1358	G1098	C924	G493
A3763	C3605	A2725	A2553	C2094	G1855	G1731	G1498	G1359	C1099	C925	G496
C3767	U3616	G2726	G2554	A2097	G1869	G1732	G1502	U1364	G1174	G926	G497
U3772	C3617	U2740	G2566	C2098	U1882	G1733	G1514	G1370	A1175	A929	G498
U3773	C3618	A2743	G2567	C2099	U1889	G1741	U1515	A1371	U1179	G930	G500
G3776	G3622	A2743	C2568	A2101	U1889	A1742	A1516	G1377	G1199	G932	G504
G3777	G3626	C2422	U2570	C2102	U1889	G1750	G1517	G1378	G933	G933	G505
G3780	A3630	G2424	U2575	A2104	A1892	U1756	G1518	C1379	C1210	C934	C506
A3783	A3635	U2425	C2583	A2105	A1897	U1760	C1519	A1387	G1211	A935	U510
A3784	G2586	A2431	U2613	A2107	C1898	G1760	A1523	U1387	G1212	G936	G644
A3785	C2587	G2432	U2614	G2108	C1898	G1761	A1534	A1392	C1215	G937	G647
U3786	C2588	G2433	G2110	A2109	G1916	G1764	A1547	G1393	C1216	G938	G657
G3787	G2599	C2441	G2259	G2266	U1917	A1767	A1563	G1394	G1217	C940	G658
G3809	A2600	U2447	C2260	U2267	U1918	C1768	A1564	A1397	G1218	G941	G659
C3810	A2601	G2450	U2268	U2268	C1920	G1769	A1565	A1398	G1219	C944	G660
G3811	G2602	G2450	U2269	U2269	C1921	U1772	C1566	G1403	G1233	U945	G666
U3814	G2618	A2453	A2267	A2267	G1922	U1773	U1578	G1411A	G1234	A944	A667
A3817	G2619	U2468	A2268	A2268	C1935	U1774	G1586	G1415	G1235	G959	C668
A3818	A2621	G2469	C2275	C2275	C1940	A1775	U1591	G1419	G1236	A960	C669
G3819	C2627	G2475	A2276	A2276	G1945	U1780	U1596	G1420	G1237	G961	G670
U3822	G2638	G2476	G2277	G2277	U1946	A1787	G1597	G1421	G1238	A964	G684
G3823	C2653	G2487	A2278	A2278	G1948	U1798	A1600	G1436	G1281	G972	C685
A3824	C2653	C2488	G2279	G2279	G1948	G1799	U1601	C1437	G1282	G973	A686
U3838	G2662	U2490	A2294	A2294	U1957	U1804	U1602	U1440	G1287	C978	U637
G3839	C2669	C2491	G2299	G2299	A1958	C1807	G1612	U1445	G1288	C983	C696
U3840	G2673	C2492	A2300	A2300	U1959	C1808	A1631	C1447	G1289	C986	G697
A3876	C2675	A2502	G2301	G2301	G1961	C1809	G1632	G1455	G1290	C990	G698
A3877	G2676	G2503	A2306	A2306	A1962	G1810	G1633	C1456	G1291	G979	C699
C3878	G2677	G2504	G2313	G2313	C1963	G1811	G1634	G1457	C1292	C983	G701
C3879	G2686	G2506	G2314	G2314	A1964	G1815	A1631	C1458	G1293	C986	C704
G3880	U2687	A2511	G2316	G2316	G1965	G1815	A1632	U1448	G1294	C986	G705
G3888	A2695	A2512	G2331	G2331	G1968	G1818	A1633	G1458	G1296	C990	G708
G3889	A2696	A2513	G2332	G2332	G1969	G1819	G1634	C1459	G1297	C990	G731
G3897	G2705	A2527	A2334	A2334	U1970	U1820	G1654	G1475	G1301	G1070	C738
A3901	G2706	G2528	C2335	C2335	U1971	U1822	G1658	C1476	U1302	C1071	G749
G3904	U2707	U2530	G2348	G2348	G1977	U1828	G1661	C1478	A1303	C1072	G756
A3905	U2708	U2530	A2361	A2361	C1978	U1834	C1676	C1481	A1304	C1076	G757
A3906	C2709	A2536	G2364	G2364	A1979	G1835	C1676	G1482	G1314	C1077	G758
C3907	G2710	A2537	G2364	G2364	U1980	G1836	C1676	G1483	G1314	C1078	U914
A3908	G2711	A2537	G2364	G2364	U1981	A1837	C1676	G1484	A1326	C1079	A917
U3915	G2711	A2537	G2364	G2364	G1981	G1842	C1676	G1484	G1329	C1080	G918

U5022	G4919	U4709	U4512	U4354	G3916
U5040	C4920	G4719	A4513	G4355	A3917
U5041	C4921	C4720	G4514	G4364	A3923
C5047	U4923	G4721	G4515	A4373	C3926
C5050	U4924	G4722	C4519	A4376	C3938
C5051	U4925	U4728	G4522	A4377	C3939
C5052	C4926	C4736	A4523	A4378	U3940
U5053	C4927	G4737	C4524	A4379	U3941
C5054	C4928	C4738	G4528	A4380	A3942
G5055	G4931	U4738	A4535	C4387	A3943
A5056	C4935	A4744	A4548	G4389	G3946
C5057	C4936	G4745	C4549	G4391	A3947
A5058	C4937	G4750	G4560	G4392	C3948
A5061	C4940	G4751	C4561	G4393	G4065
G5062	A4943	U4752	C4562	A4394	U4066
U5069	C4944	G4753	G4567	U4395	U4069
	U4947	G4754	G4570	C4398	U4070
	C4948	C4757	G4573	G4401	G4076
	G4949	U4758	C4575	U4419	G4084
	U4950	C4759	A4584	U4420	A4085
	G4951	G4761	G4585	A4422	G4086
	A4955	A4764	G4586	G4430	G4087
	A4956	G4765	G4587	U4437	C4088
	C4957	C4771	A4590	U4438	G4097
	C4958	C4772	A4605	C4444	U4111
	U4959	G4868	U4636	G4448	C4114
	G4960	U4869	C4637	A4449	G4115
	G4963	G4870	G4638	U4452	C4116
	C4964	C4871	G4639	C4453	U4117
	U4965	C4875	G4652	U4463	C4118
	A4966	U4882	A4656	A4464	U4119
	A4967	C4883	U4657	C4466	U4120
	U4976	G4884	G4661	U4471	G4121
	A4977	U4885	C4670	G4472	A4127
	U4985	C4895	A4672	A4473	A4128
	U4988	C4896	U4677	G4474	C4133
	U4989	U4897	A4909	A4488	G4136
	C4990	G4898	A4910	G4489	C4158
	U4991	G4903	G4911	U4500	C4162
	G4992	A4909	G4912		U4163
	G4993	A4910	G4913		G4166
	U5006	G5015			A4170
	A5014	G5016			C4349
	G5015	G5017			C4350
	G5016				
	G5017				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1665551	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	1900	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.070	Depositor
Minimum map value	-0.021	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.007	Depositor
Map size (\AA)	552.0, 552.0, 552.0	wwPDB
Map dimensions	412, 412, 412	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.3398058, 1.3398058, 1.3398058	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	0/1936	0.58	0/2596
2	B	0.27	0/186	0.52	0/254
3	C	0.26	0/2937	0.57	0/3946
4	D	0.27	0/2437	0.54	0/3264
5	E	0.26	0/1914	0.56	0/2566
6	F	0.26	0/1911	0.54	0/2549
7	G	0.26	0/1910	0.55	0/2569
8	H	0.26	0/1535	0.55	0/2063
9	I	0.26	0/1702	0.55	0/2272
10	J	0.25	0/1385	0.56	0/1852
11	L	0.25	0/1733	0.61	0/2316
12	M	0.27	0/1158	0.56	0/1547
13	N	0.27	0/1740	0.60	0/2328
14	O	0.27	0/1662	0.55	0/2222
15	P	0.27	0/1268	0.56	0/1700
16	Q	0.26	0/1538	0.61	0/2054
17	R	0.25	0/1310	0.61	0/1734
18	S	0.27	0/1501	0.59	0/2012
19	T	0.26	0/1326	0.53	0/1770
20	U	0.26	0/848	0.51	0/1138
21	V	0.26	0/993	0.54	0/1332
22	W	0.27	0/541	0.54	0/720
23	X	0.26	0/984	0.54	0/1323
24	Y	0.25	0/1132	0.57	0/1504
25	Z	0.27	0/1130	0.55	0/1507
26	a	0.26	0/1191	0.55	0/1590
27	b	0.24	0/861	0.57	0/1138
28	c	0.27	0/771	0.50	0/1034
29	d	0.25	0/903	0.58	0/1216
30	e	0.25	0/1071	0.57	0/1429
31	f	0.27	0/895	0.59	0/1198
32	g	0.26	0/916	0.61	0/1220

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	h	0.25	0/1017	0.56	0/1344
34	i	0.25	0/841	0.58	0/1112
35	j	0.25	0/720	0.61	0/952
36	k	0.26	0/575	0.54	0/761
37	l	0.25	0/459	0.58	0/608
38	m	0.24	0/435	0.56	0/575
39	n	0.26	0/240	0.75	0/305
40	o	0.26	0/864	0.55	0/1140
41	p	0.26	0/718	0.54	0/953
42	q	0.24	0/1805	0.86	1/2809 (0.0%)
43	r	0.25	0/1010	0.60	0/1354
44	u	0.28	0/2858	0.82	1/4455 (0.0%)
45	v	0.27	0/3701	0.82	1/5766 (0.0%)
46	w	0.26	0/3240	0.52	0/4339
47	1	0.26	0/3677	0.47	0/4986
48	2	0.25	0/237	0.39	0/321
49	3	0.27	0/553	0.46	0/738
50	4	0.25	0/2819	0.49	0/3772
51	5	0.26	0/730	0.42	0/988
52	7	0.24	0/4224	0.47	0/5728
53	6	0.25	0/1835	0.41	0/2495
54	K	0.31	0/84978	0.88	47/132528 (0.0%)
All	All	0.29	0/160861	0.77	50/235992 (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
13	N	0	1
50	4	0	1
54	K	0	1
All	All	0	3

There are no bond length outliers.

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	K	234	G	C8-N9-C4	-13.40	101.04	106.40
54	K	139	G	N3-C4-N9	-10.38	119.77	126.00
54	K	234	G	N3-C4-N9	-8.71	120.78	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	K	234	G	C8-N9-C1'	-8.62	115.79	127.00
45	v	39	G	O4'-C1'-N9	8.60	115.08	108.20
54	K	1219	G	N3-C4-N9	-7.76	121.34	126.00
54	K	234	G	N9-C4-C5	7.42	108.37	105.40
54	K	1081	C	N3-C2-O2	-6.67	117.23	121.90
42	q	20	U	O5'-P-OP2	-6.23	100.09	105.70
54	K	139	G	N3-C4-C5	6.23	131.71	128.60
54	K	3941	G	C8-N9-C1'	-6.19	118.95	127.00
54	K	387	G	O4'-C1'-N9	6.14	113.11	108.20
54	K	1219	G	C5-C6-O6	6.14	132.28	128.60
54	K	3667	C	N1-C2-O2	-6.11	115.23	118.90
54	K	126	C	C6-N1-C2	-6.10	117.86	120.30
54	K	4573	G	O4'-C1'-N9	6.08	113.06	108.20
54	K	3941	G	C4-N9-C1'	6.05	134.37	126.50
54	K	130	C	C6-N1-C2	-6.02	117.89	120.30
54	K	234	G	C4-N9-C1'	6.02	134.32	126.50
54	K	139	G	C5-C6-O6	5.94	132.16	128.60
54	K	4350	C	N1-C2-O2	-5.82	115.41	118.90
54	K	139	G	N9-C4-C5	5.77	107.71	105.40
54	K	4114	C	N3-C2-O2	-5.77	117.86	121.90
54	K	1292	C	C2-N1-C1'	5.74	125.11	118.80
54	K	130	C	N3-C2-O2	-5.60	117.98	121.90
54	K	39	A	O4'-C1'-N9	5.53	112.62	108.20
54	K	1639	U	C2-N1-C1'	5.48	124.28	117.70
54	K	1218	G	N3-C4-N9	5.46	129.28	126.00
54	K	2898	G	C4-N9-C1'	5.39	133.51	126.50
54	K	986	C	N1-C2-O2	-5.38	115.67	118.90
54	K	2586	G	O4'-C1'-N9	-5.37	103.90	108.20
54	K	139	G	C2-N3-C4	-5.36	109.22	111.90
54	K	4922	C	N3-C2-O2	-5.30	118.19	121.90
54	K	1097	C	N1-C2-O2	-5.29	115.73	118.90
54	K	1847	C	C2-N1-C1'	5.28	124.61	118.80
54	K	2306	G	O4'-C1'-N9	5.27	112.41	108.20
54	K	262	G	C8-N9-C1'	-5.27	120.15	127.00
54	K	2898	G	C8-N9-C1'	-5.26	120.16	127.00
54	K	458	C	C6-N1-C2	-5.26	118.20	120.30
54	K	202	C	C2-N1-C1'	5.19	124.51	118.80
54	K	4898	G	N3-C4-N9	-5.17	122.90	126.00
54	K	234	G	N7-C8-N9	5.15	115.68	113.10
54	K	219	G	C4-N9-C1'	5.12	133.16	126.50
54	K	1219	G	C8-N9-C4	-5.10	104.36	106.40
54	K	1219	G	N9-C4-C5	5.09	107.44	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	K	4463	U	O4'-C1'-N1	5.09	112.28	108.20
54	K	4898	G	C8-N9-C1'	5.07	133.60	127.00
54	K	978	G	O4'-C1'-N9	5.03	112.23	108.20
44	u	31	G	C4-N9-C1'	5.00	133.00	126.50
54	K	2020	U	C5-C4-O4	-5.00	122.90	125.90

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
50	4	433	ARG	Sidechain
54	K	234	G	Sidechain
13	N	76	PRO	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	
1	A	246/257 (96%)	219 (89%)	27 (11%)	0	100	100
2	B	25/229 (11%)	22 (88%)	2 (8%)	1 (4%)	3	17
3	C	360/425 (85%)	335 (93%)	25 (7%)	0	100	100
4	D	291/297 (98%)	269 (92%)	22 (8%)	0	100	100
5	E	227/291 (78%)	217 (96%)	9 (4%)	1 (0%)	34	67
6	F	223/247 (90%)	205 (92%)	18 (8%)	0	100	100
7	G	229/319 (72%)	213 (93%)	16 (7%)	0	100	100
8	H	188/192 (98%)	176 (94%)	12 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	201/214 (94%)	181 (90%)	20 (10%)	0	100	100
10	J	168/178 (94%)	158 (94%)	10 (6%)	0	100	100
11	L	208/211 (99%)	193 (93%)	14 (7%)	1 (0%)	29	62
12	M	136/218 (62%)	125 (92%)	11 (8%)	0	100	100
13	N	199/204 (98%)	183 (92%)	16 (8%)	0	100	100
14	O	197/203 (97%)	186 (94%)	11 (6%)	0	100	100
15	P	151/184 (82%)	143 (95%)	8 (5%)	0	100	100
16	Q	185/188 (98%)	171 (92%)	14 (8%)	0	100	100
17	R	153/196 (78%)	144 (94%)	9 (6%)	0	100	100
18	S	174/176 (99%)	159 (91%)	15 (9%)	0	100	100
19	T	157/160 (98%)	139 (88%)	17 (11%)	1 (1%)	25	59
20	U	100/128 (78%)	90 (90%)	10 (10%)	0	100	100
21	V	129/140 (92%)	121 (94%)	8 (6%)	0	100	100
22	W	61/157 (39%)	55 (90%)	6 (10%)	0	100	100
23	X	116/156 (74%)	106 (91%)	10 (9%)	0	100	100
24	Y	132/145 (91%)	124 (94%)	8 (6%)	0	100	100
25	Z	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
26	a	145/148 (98%)	132 (91%)	13 (9%)	0	100	100
27	b	100/226 (44%)	96 (96%)	4 (4%)	0	100	100
28	c	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
29	d	105/125 (84%)	94 (90%)	11 (10%)	0	100	100
30	e	126/135 (93%)	118 (94%)	8 (6%)	0	100	100
31	f	107/110 (97%)	99 (92%)	8 (8%)	0	100	100
32	g	112/116 (97%)	104 (93%)	8 (7%)	0	100	100
33	h	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
34	i	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
35	j	84/97 (87%)	83 (99%)	1 (1%)	0	100	100
36	k	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
37	l	48/51 (94%)	38 (79%)	10 (21%)	0	100	100
38	m	50/102 (49%)	46 (92%)	4 (8%)	0	100	100
39	n	23/25 (92%)	23 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
40	o	102/106 (96%)	90 (88%)	12 (12%)	0	100	100
41	p	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
43	r	122/137 (89%)	112 (92%)	10 (8%)	0	100	100
46	w	392/403 (97%)	360 (92%)	32 (8%)	0	100	100
47	1	463/476 (97%)	460 (99%)	3 (1%)	0	100	100
48	2	27/96 (28%)	27 (100%)	0	0	100	100
49	3	66/68 (97%)	66 (100%)	0	0	100	100
50	4	340/483 (70%)	338 (99%)	1 (0%)	1 (0%)	41	72
51	5	88/106 (83%)	87 (99%)	1 (1%)	0	100	100
52	7	519/563 (92%)	512 (99%)	7 (1%)	0	100	100
53	6	222/224 (99%)	222 (100%)	0	0	100	100
All	All	8102/9553 (85%)	7610 (94%)	487 (6%)	5 (0%)	54	82

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	L	64	VAL
50	4	347	GLY
2	B	42	PRO
5	E	228	PRO
19	T	82	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	190/199 (96%)	189 (100%)	1 (0%)	88	93
2	B	21/172 (12%)	21 (100%)	0	100	100
3	C	302/347 (87%)	300 (99%)	2 (1%)	84	90
4	D	247/250 (99%)	247 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	206/251 (82%)	205 (100%)	1 (0%)	88	93
6	F	196/215 (91%)	196 (100%)	0	100	100
7	G	200/272 (74%)	199 (100%)	1 (0%)	88	93
8	H	169/171 (99%)	169 (100%)	0	100	100
9	I	175/181 (97%)	175 (100%)	0	100	100
10	J	143/149 (96%)	143 (100%)	0	100	100
11	L	175/176 (99%)	173 (99%)	2 (1%)	73	84
12	M	117/161 (73%)	117 (100%)	0	100	100
13	N	171/172 (99%)	169 (99%)	2 (1%)	71	83
14	O	171/173 (99%)	169 (99%)	2 (1%)	71	83
15	P	134/163 (82%)	133 (99%)	1 (1%)	84	90
16	Q	164/164 (100%)	163 (99%)	1 (1%)	86	91
17	R	138/175 (79%)	137 (99%)	1 (1%)	84	90
18	S	157/157 (100%)	155 (99%)	2 (1%)	69	82
19	T	139/140 (99%)	139 (100%)	0	100	100
20	U	92/114 (81%)	91 (99%)	1 (1%)	73	84
21	V	101/107 (94%)	100 (99%)	1 (1%)	76	85
22	W	55/126 (44%)	55 (100%)	0	100	100
23	X	106/134 (79%)	103 (97%)	3 (3%)	43	69
24	Y	124/135 (92%)	122 (98%)	2 (2%)	62	79
25	Z	117/118 (99%)	116 (99%)	1 (1%)	78	87
26	a	119/120 (99%)	118 (99%)	1 (1%)	81	89
27	b	84/172 (49%)	84 (100%)	0	100	100
28	c	84/98 (86%)	83 (99%)	1 (1%)	71	83
29	d	98/110 (89%)	95 (97%)	3 (3%)	40	67
30	e	114/121 (94%)	113 (99%)	1 (1%)	78	87
31	f	88/89 (99%)	88 (100%)	0	100	100
32	g	98/99 (99%)	98 (100%)	0	100	100
33	h	108/110 (98%)	108 (100%)	0	100	100
34	i	86/89 (97%)	86 (100%)	0	100	100
35	j	73/80 (91%)	71 (97%)	2 (3%)	44	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	k	64/65 (98%)	64 (100%)	0	100	100
37	l	47/48 (98%)	47 (100%)	0	100	100
38	m	48/90 (53%)	48 (100%)	0	100	100
39	n	24/24 (100%)	24 (100%)	0	100	100
40	o	92/94 (98%)	92 (100%)	0	100	100
41	p	74/75 (99%)	72 (97%)	2 (3%)	44	70
43	r	108/121 (89%)	108 (100%)	0	100	100
46	w	342/348 (98%)	340 (99%)	2 (1%)	86	91
47	1	390/398 (98%)	385 (99%)	5 (1%)	69	82
48	2	26/74 (35%)	26 (100%)	0	100	100
49	3	59/59 (100%)	57 (97%)	2 (3%)	37	64
50	4	306/435 (70%)	304 (99%)	2 (1%)	84	90
51	5	83/99 (84%)	83 (100%)	0	100	100
52	7	443/476 (93%)	443 (100%)	0	100	100
53	6	187/187 (100%)	185 (99%)	2 (1%)	73	84
All	All	7055/8103 (87%)	7008 (99%)	47 (1%)	84	90

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	64	ARG
3	C	95	MET
3	C	188	ARG
5	E	58	ARG
7	G	96	GLN
11	L	10	LEU
11	L	70	VAL
13	N	26	ARG
13	N	80	THR
14	O	173	GLN
14	O	180	GLN
15	P	118	GLN
16	Q	8	ASN
17	R	71	ARG
18	S	67	VAL
18	S	90	THR
20	U	105	ASN

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Mol	Chain	Res	Type
21	V	48	ARG
23	X	93	ASN
23	X	120	ASP
23	X	151	ASN
24	Y	2	LYS
24	Y	79	VAL
25	Z	11	VAL
26	a	122	VAL
28	c	17	ARG
29	d	22	THR
29	d	86	VAL
29	d	93	ASN
30	e	48	ARG
35	j	67	LEU
35	j	82	THR
41	p	4	ARG
41	p	52	VAL
46	w	261	ARG
46	w	297	LYS
47	1	18	GLU
47	1	118	LEU
47	1	130	VAL
47	1	230	LEU
47	1	317	LEU
49	3	5	MET
49	3	21	LEU
50	4	323	HIS
50	4	468	LEU
53	6	33	TRP
53	6	51	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
17	R	58	HIS
47	1	294	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
42	q	74/77 (96%)	15 (20%)	0
44	u	119/120 (99%)	14 (11%)	0
45	v	155/156 (99%)	37 (23%)	0
54	K	3518/3543 (99%)	821 (23%)	58 (1%)
All	All	3866/3896 (99%)	887 (22%)	58 (1%)

All (887) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
42	q	9	A
42	q	13	U
42	q	16	C
42	q	19	G
42	q	20	U
42	q	20(A)	U
42	q	21	A
42	q	24	A
42	q	39	G
42	q	42	A
42	q	46	G
42	q	47	U
42	q	56	C
42	q	67	G
42	q	75	C
44	u	7	G
44	u	10	C
44	u	22	A
44	u	25	G
44	u	31	G
44	u	42	A
44	u	53	U
44	u	54	A
44	u	64	G
44	u	80	U
44	u	100	A
44	u	110	G
44	u	111	C
44	u	120	U
45	v	2	G
45	v	3	A
45	v	13	G
45	v	20	A
45	v	23	C

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Mol	Chain	Res	Type
45	v	32	C
45	v	34	U
45	v	35	C
45	v	38	U
45	v	49	G
45	v	59	A
45	v	62	A
45	v	63	U
45	v	75	G
45	v	80	A
45	v	81	C
45	v	82	A
45	v	83	C
45	v	84	A
45	v	85	U
45	v	86	U
45	v	87	G
45	v	103	A
45	v	105	C
45	v	106	G
45	v	109	C
45	v	110	U
45	v	111	U
45	v	112	G
45	v	114	G
45	v	123	U
45	v	125	C
45	v	126	C
45	v	127	U
45	v	128	C
45	v	153	C
45	v	156	U
54	K	12	A
54	K	13	U
54	K	15	A
54	K	30	C
54	K	39	A
54	K	42	A
54	K	44	A
54	K	56	A
54	K	58	G
54	K	59	A

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Mol	Chain	Res	Type
54	K	64	A
54	K	65	A
54	K	72	C
54	K	73	A
54	K	74	G
54	K	84	A
54	K	91	G
54	K	95	G
54	K	104	G
54	K	108	A
54	K	109	G
54	K	110	C
54	K	118	C
54	K	119	G
54	K	122	U
54	K	126	C
54	K	131	C
54	K	134	G
54	K	135	G
54	K	136	C
54	K	137	G
54	K	141	C
54	K	142	G
54	K	146	G
54	K	157	U
54	K	159	C
54	K	160	G
54	K	172	C
54	K	173	C
54	K	177	G
54	K	182	G
54	K	200	U
54	K	201	C
54	K	209	U
54	K	216	C
54	K	218	A
54	K	221	C
54	K	224	U
54	K	225	G
54	K	232	G
54	K	233	U
54	K	234	G

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Mol	Chain	Res	Type
54	K	246	G
54	K	256	G
54	K	258	G
54	K	262	G
54	K	263	G
54	K	265	C
54	K	266	C
54	K	267	G
54	K	276	C
54	K	280	G
54	K	297	U
54	K	306	A
54	K	308	G
54	K	309	C
54	K	315	G
54	K	316	U
54	K	322	C
54	K	326	C
54	K	334	A
54	K	340	C
54	K	363	A
54	K	370	U
54	K	371	A
54	K	387	G
54	K	407	A
54	K	410	A
54	K	412	G
54	K	413	G
54	K	415	G
54	K	417	G
54	K	428	G
54	K	440	U
54	K	446	C
54	K	449	C
54	K	450	G
54	K	452	A
54	K	453	G
54	K	454	U
54	K	455	C
54	K	463	A
54	K	467	U
54	K	468	U

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Mol	Chain	Res	Type
54	K	481	G
54	K	481(A)	C
54	K	482	G
54	K	483	G
54	K	485	C
54	K	486	C
54	K	492	U
54	K	493	G
54	K	496	G
54	K	497	G
54	K	498	C
54	K	499	G
54	K	505	G
54	K	506	C
54	K	510	U
54	K	644	G
54	K	647	G
54	K	658	C
54	K	659	G
54	K	661	C
54	K	666	G
54	K	667	A
54	K	668	C
54	K	669	C
54	K	670	G
54	K	685	C
54	K	686	A
54	K	687	U
54	K	696	C
54	K	697	G
54	K	699	C
54	K	701	G
54	K	704	C
54	K	705	G
54	K	708	G
54	K	731	G
54	K	738	C
54	K	749	G
54	K	756	G
54	K	758	G
54	K	914	U
54	K	917	A

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Mol	Chain	Res	Type
54	K	918	G
54	K	923	C
54	K	925	C
54	K	926	G
54	K	929	A
54	K	930	G
54	K	932	A
54	K	933	G
54	K	934	C
54	K	935	A
54	K	935(A)	G
54	K	936	C
54	K	938	C
54	K	939	G
54	K	941	C
54	K	944	A
54	K	945	U
54	K	959	G
54	K	960	A
54	K	961	G
54	K	964	A
54	K	965	G
54	K	966	A
54	K	967	C
54	K	968	C
54	K	969	C
54	K	971(A)	G
54	K	972	C
54	K	973	G
54	K	979	C
54	K	983	C
54	K	990	C
54	K	1070	G
54	K	1072	C
54	K	1073	G
54	K	1076	C
54	K	1078	A
54	K	1079	C
54	K	1081	C
54	K	1082	C
54	K	1099	C
54	K	1175	A

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Mol	Chain	Res	Type
54	K	1179	U
54	K	1199	G
54	K	1210	C
54	K	1211	G
54	K	1212	G
54	K	1215	C
54	K	1216	C
54	K	1234	G
54	K	1235	G
54	K	1236	C
54	K	1237	C
54	K	1238	A
54	K	1239	C
54	K	1272	C
54	K	1273	G
54	K	1274	A
54	K	1275	G
54	K	1281	G
54	K	1284	G
54	K	1287	G
54	K	1289	C
54	K	1291	G
54	K	1292	C
54	K	1293	G
54	K	1296	G
54	K	1301	C
54	K	1303	A
54	K	1304	C
54	K	1314	C
54	K	1326	A
54	K	1330	A
54	K	1354	A
54	K	1358	G
54	K	1359	G
54	K	1364	U
54	K	1370	G
54	K	1371	A
54	K	1377	G
54	K	1378	C
54	K	1379	C
54	K	1387	A
54	K	1392	A

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Mol	Chain	Res	Type
54	K	1394	G
54	K	1397	A
54	K	1398	A
54	K	1403	G
54	K	1411(A)	G
54	K	1415	G
54	K	1419	G
54	K	1420	A
54	K	1421	G
54	K	1433	A
54	K	1436	C
54	K	1437	C
54	K	1438	U
54	K	1440	U
54	K	1441	C
54	K	1445	U
54	K	1446	C
54	K	1448	G
54	K	1456	C
54	K	1457	G
54	K	1458	C
54	K	1475	G
54	K	1478	C
54	K	1481	C
54	K	1482	G
54	K	1483	C
54	K	1484	G
54	K	1489	G
54	K	1497	A
54	K	1498	G
54	K	1502	G
54	K	1514	U
54	K	1516	G
54	K	1518	A
54	K	1519	C
54	K	1523	A
54	K	1534	A
54	K	1547	A
54	K	1563	A
54	K	1564	A
54	K	1566	C
54	K	1578	U

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Mol	Chain	Res	Type
54	K	1586	G
54	K	1591	U
54	K	1596	U
54	K	1597	G
54	K	1600	A
54	K	1602	U
54	K	1612	G
54	K	1613	A
54	K	1624	G
54	K	1625	G
54	K	1631	A
54	K	1633	G
54	K	1634	A
54	K	1640	C
54	K	1654	G
54	K	1658	G
54	K	1661	C
54	K	1676	C
54	K	1677	U
54	K	1696	C
54	K	1731	C
54	K	1733	G
54	K	1741	G
54	K	1742	A
54	K	1750	G
54	K	1756	U
54	K	1760	G
54	K	1761	G
54	K	1764	G
54	K	1767	A
54	K	1768	C
54	K	1769	G
54	K	1772	C
54	K	1774	C
54	K	1775	A
54	K	1780	A
54	K	1787	A
54	K	1798	G
54	K	1799	G
54	K	1804	A
54	K	1807	C
54	K	1809	C

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Mol	Chain	Res	Type
54	K	1811	G
54	K	1815	G
54	K	1818	G
54	K	1819	G
54	K	1821	G
54	K	1822	U
54	K	1828	C
54	K	1834	U
54	K	1835	G
54	K	1836	G
54	K	1837	A
54	K	1842	G
54	K	1843	A
54	K	1847	C
54	K	1855	G
54	K	1869	G
54	K	1882	U
54	K	1889	U
54	K	1892	A
54	K	1897	A
54	K	1898	C
54	K	1916	G
54	K	1918	U
54	K	1920	C
54	K	1921	C
54	K	1922	G
54	K	1931	C
54	K	1932	A
54	K	1935	C
54	K	1940	G
54	K	1945	G
54	K	1947	U
54	K	1948	G
54	K	1957	U
54	K	1958	A
54	K	1960	A
54	K	1961	G
54	K	1962	A
54	K	1963	C
54	K	1964	A
54	K	1965	G
54	K	1968	G

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Mol	Chain	Res	Type
54	K	1969	G
54	K	1971	U
54	K	1974	U
54	K	1975	G
54	K	1976	G
54	K	1978	C
54	K	1979	A
54	K	1980	U
54	K	1984	A
54	K	1987	C
54	K	1988	G
54	K	1990	A
54	K	1991	A
54	K	1997	U
54	K	1999	A
54	K	2001	G
54	K	2002	A
54	K	2003	G
54	K	2004	U
54	K	2008	U
54	K	2011	C
54	K	2018	C
54	K	2020	U
54	K	2021	G
54	K	2022	C
54	K	2024	G
54	K	2026	A
54	K	2043	A
54	K	2046	G
54	K	2047	A
54	K	2048	U
54	K	2052	G
54	K	2053	C
54	K	2055	G
54	K	2056	G
54	K	2063	G
54	K	2064	G
54	K	2069	A
54	K	2071	A
54	K	2084	U
54	K	2090	U
54	K	2092	G

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Mol	Chain	Res	Type
54	K	2093	G
54	K	2094	C
54	K	2095	A
54	K	2097	A
54	K	2098	G
54	K	2099	C
54	K	2100	G
54	K	2101	A
54	K	2102	G
54	K	2104	A
54	K	2105	A
54	K	2107	A
54	K	2108	G
54	K	2110	G
54	K	2259	G
54	K	2260	C
54	K	2267	U
54	K	2268	A
54	K	2269	C
54	K	2275	G
54	K	2277	C
54	K	2279	A
54	K	2289	C
54	K	2294	G
54	K	2299	G
54	K	2300	A
54	K	2301	G
54	K	2306	G
54	K	2313	A
54	K	2314	G
54	K	2316	G
54	K	2331	G
54	K	2333	G
54	K	2335	C
54	K	2348	G
54	K	2351	C
54	K	2364	G
54	K	2382	A
54	K	2395	A
54	K	2396	A
54	K	2398	U
54	K	2417	A

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Mol	Chain	Res	Type
54	K	2422	C
54	K	2424	G
54	K	2425	U
54	K	2431	A
54	K	2433	G
54	K	2441	C
54	K	2447	U
54	K	2450	G
54	K	2453	A
54	K	2469	C
54	K	2475	G
54	K	2476	G
54	K	2487	G
54	K	2488	C
54	K	2489	C
54	K	2490	U
54	K	2491	C
54	K	2492	C
54	K	2498	C
54	K	2503	G
54	K	2504	C
54	K	2505	C
54	K	2506	G
54	K	2511	A
54	K	2512	A
54	K	2513	A
54	K	2527	A
54	K	2529	A
54	K	2530	U
54	K	2536	A
54	K	2537	A
54	K	2546	G
54	K	2547	G
54	K	2553	A
54	K	2554	U
54	K	2566	G
54	K	2568	C
54	K	2570	U
54	K	2575	U
54	K	2583	C
54	K	2586	G
54	K	2587	A

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Mol	Chain	Res	Type
54	K	2588	C
54	K	2599	G
54	K	2600	A
54	K	2602	G
54	K	2618	G
54	K	2620	G
54	K	2621	A
54	K	2627	C
54	K	2638	G
54	K	2653	C
54	K	2662	G
54	K	2669	C
54	K	2673	G
54	K	2674	A
54	K	2676	A
54	K	2677	G
54	K	2686	G
54	K	2687	U
54	K	2695	A
54	K	2696	A
54	K	2705	G
54	K	2707	U
54	K	2708	U
54	K	2709	C
54	K	2711	G
54	K	2714	G
54	K	2721	G
54	K	2725	A
54	K	2726	G
54	K	2740	U
54	K	2743	A
54	K	2760	G
54	K	2761	U
54	K	2763	U
54	K	2764	A
54	K	2769	U
54	K	2772	C
54	K	2787	A
54	K	2788	U
54	K	2790	U
54	K	2794	C
54	K	2798	A

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Mol	Chain	Res	Type
54	K	2803	U
54	K	2807	A
54	K	2808	G
54	K	2822	G
54	K	2826	U
54	K	2827	G
54	K	2828	U
54	K	2834	C
54	K	2842	G
54	K	2850	A
54	K	2855	G
54	K	2867	C
54	K	2875	C
54	K	2879	A
54	K	2895	A
54	K	3598	C
54	K	3603	G
54	K	3604	A
54	K	3605	C
54	K	3616	U
54	K	3617	G
54	K	3618	C
54	K	3622	C
54	K	3625	G
54	K	3626	G
54	K	3630	A
54	K	3635	A
54	K	3644	U
54	K	3646	A
54	K	3648	A
54	K	3649	A
54	K	3657	U
54	K	3662	A
54	K	3664	G
54	K	3672	G
54	K	3673	C
54	K	3674	G
54	K	3682	A
54	K	3692	A
54	K	3696	C
54	K	3702	A
54	K	3711	A

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Mol	Chain	Res	Type
54	K	3714	G
54	K	3728	A
54	K	3729	U
54	K	3743	G
54	K	3748	A
54	K	3750	G
54	K	3753	G
54	K	3756	A
54	K	3760	A
54	K	3763	A
54	K	3767	C
54	K	3772	U
54	K	3773	U
54	K	3776	G
54	K	3777	G
54	K	3780	G
54	K	3783	A
54	K	3784	A
54	K	3786	U
54	K	3787	G
54	K	3809	G
54	K	3810	C
54	K	3811	G
54	K	3814	U
54	K	3817	A
54	K	3819	G
54	K	3822	U
54	K	3824	A
54	K	3838	U
54	K	3840	U
54	K	3876	A
54	K	3877	A
54	K	3878	C
54	K	3879	G
54	K	3880	G
54	K	3889	G
54	K	3897	G
54	K	3901	A
54	K	3905	A
54	K	3906	A
54	K	3907	G
54	K	3908	A

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Mol	Chain	Res	Type
54	K	3915	U
54	K	3916	G
54	K	3917	A
54	K	3923	A
54	K	3926	C
54	K	3938	G
54	K	3939	G
54	K	3943	A
54	K	3946	G
54	K	4066	U
54	K	4069	U
54	K	4070	U
54	K	4076	G
54	K	4084	G
54	K	4086	G
54	K	4088	C
54	K	4097	G
54	K	4111	U
54	K	4116	C
54	K	4118	U
54	K	4119	C
54	K	4120	U
54	K	4121	G
54	K	4127	A
54	K	4128	A
54	K	4133	C
54	K	4136	G
54	K	4158	C
54	K	4162	C
54	K	4163	U
54	K	4166	G
54	K	4170	A
54	K	4171	C
54	K	4183	G
54	K	4184	G
54	K	4191	G
54	K	4203	A
54	K	4212	A
54	K	4215	C
54	K	4225	G
54	K	4229	U
54	K	4233	A

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Mol	Chain	Res	Type
54	K	4237	C
54	K	4251	A
54	K	4254	G
54	K	4265	U
54	K	4266	G
54	K	4267	G
54	K	4268	A
54	K	4271	A
54	K	4273	A
54	K	4281	A
54	K	4282	A
54	K	4291	G
54	K	4297	G
54	K	4304	A
54	K	4305	G
54	K	4306	U
54	K	4314	C
54	K	4317	A
54	K	4324	A
54	K	4329	G
54	K	4330	G
54	K	4332	C
54	K	4339	A
54	K	4349	C
54	K	4354	U
54	K	4355	G
54	K	4364	G
54	K	4373	G
54	K	4376	A
54	K	4377	G
54	K	4378	A
54	K	4379	A
54	K	4380	A
54	K	4387	C
54	K	4391	G
54	K	4393	G
54	K	4394	A
54	K	4395	U
54	K	4398	C
54	K	4401	G
54	K	4419	U
54	K	4421	C

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Mol	Chain	Res	Type
54	K	4422	A
54	K	4430	G
54	K	4437	U
54	K	4438	U
54	K	4444	C
54	K	4448	G
54	K	4449	A
54	K	4452	U
54	K	4453	C
54	K	4464	A
54	K	4466	C
54	K	4471	U
54	K	4472	G
54	K	4473	A
54	K	4475	G
54	K	4488	A
54	K	4489	G
54	K	4500	U
54	K	4512	U
54	K	4513	A
54	K	4515	G
54	K	4519	C
54	K	4522	G
54	K	4523	A
54	K	4524	G
54	K	4528	G
54	K	4535	A
54	K	4548	A
54	K	4549	G
54	K	4560	C
54	K	4562	C
54	K	4567	G
54	K	4570	G
54	K	4573	G
54	K	4574	U
54	K	4575	G
54	K	4584	A
54	K	4585	U
54	K	4587	G
54	K	4590	A
54	K	4605	A
54	K	4636	U

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Mol	Chain	Res	Type
54	K	4637	G
54	K	4639	G
54	K	4652	G
54	K	4656	A
54	K	4657	U
54	K	4661	G
54	K	4670	C
54	K	4672	A
54	K	4677	U
54	K	4687	A
54	K	4694	G
54	K	4709	U
54	K	4719	G
54	K	4720	C
54	K	4722	G
54	K	4728	U
54	K	4736	C
54	K	4738	C
54	K	4744	A
54	K	4745	G
54	K	4750	G
54	K	4751	G
54	K	4752	U
54	K	4754	G
54	K	4757	C
54	K	4759	C
54	K	4761	G
54	K	4764	A
54	K	4765	G
54	K	4771	C
54	K	4772	C
54	K	4868	G
54	K	4870	G
54	K	4871	C
54	K	4875	G
54	K	4882	U
54	K	4883	C
54	K	4885	U
54	K	4895	C
54	K	4896	G
54	K	4897	G
54	K	4903	G

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Mol	Chain	Res	Type
54	K	4909	A
54	K	4910	A
54	K	4912	G
54	K	4913	G
54	K	4919	G
54	K	4921	C
54	K	4922	C
54	K	4924	C
54	K	4925	U
54	K	4926	C
54	K	4927	G
54	K	4928	C
54	K	4931	G
54	K	4935	C
54	K	4937	C
54	K	4940	C
54	K	4943	A
54	K	4944	C
54	K	4948	C
54	K	4949	G
54	K	4950	U
54	K	4951	G
54	K	4955	A
54	K	4956	A
54	K	4957	C
54	K	4958	C
54	K	4960	G
54	K	4963	G
54	K	4965	U
54	K	4966	A
54	K	4967	A
54	K	4976	U
54	K	4977	A
54	K	4985	U
54	K	4988	U
54	K	4989	U
54	K	4990	C
54	K	4991	U
54	K	4993	G
54	K	5006	U
54	K	5014	A
54	K	5016	A

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Mol	Chain	Res	Type
54	K	5017	G
54	K	5022	U
54	K	5040	U
54	K	5041	G
54	K	5047	C
54	K	5050	C
54	K	5052	C
54	K	5053	U
54	K	5054	C
54	K	5056	A
54	K	5058	A
54	K	5061	A
54	K	5062	G

All (58) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	K	12	A
54	K	125	C
54	K	134	G
54	K	245	C
54	K	265	C
54	K	275	C
54	K	406	C
54	K	449	C
54	K	480	C
54	K	485	C
54	K	498	C
54	K	504	G
54	K	684	G
54	K	685	C
54	K	696	C
54	K	704	C
54	K	935(A)	G
54	K	959	G
54	K	971(A)	G
54	K	1072	C
54	K	1174	G
54	K	1211	G
54	K	1236	C
54	K	1238	A
54	K	1329	G

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Mol	Chain	Res	Type
54	K	1370	G
54	K	1440	U
54	K	1445	U
54	K	1455	G
54	K	1477	C
54	K	1482	G
54	K	1633	G
54	K	1818	G
54	K	2046	G
54	K	2089	G
54	K	2266	C
54	K	2468	U
54	K	2488	C
54	K	2502	A
54	K	2546	G
54	K	2695	A
54	K	3603	G
54	K	3625	G
54	K	3876	A
54	K	3888	G
54	K	3904	G
54	K	4119	C
54	K	4170	A
54	K	4232	U
54	K	4354	U
54	K	4378	A
54	K	4448	G
54	K	4719	G
54	K	4884	G
54	K	4921	C
54	K	4925	U
54	K	4947	U
54	K	4989	U

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 225 ligands modelled in this entry, 225 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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
54	K	25

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	2113:G	O3'	2258:C	P	40.63
1	K	1252:C	O3'	1271:G	P	36.90
1	K	1219:G	O3'	1233:G	P	19.23
1	K	3948:C	O3'	4065:G	P	18.79
1	K	4138:C	O3'	4146:G	P	18.12
1	K	990:C	O3'	1064:G	P	17.54
1	K	1696:C	O3'	1720:C	P	16.44
1	K	523:C	O3'	638:G	P	16.21
1	K	4777:C	O3'	4859:C	P	16.19
1	K	5022:U	O3'	5028:G	P	16.09
1	K	1406(C):G	O3'	1411:C	P	15.82
1	K	4101:C	O3'	4107:G	P	15.03
1	K	760:G	O3'	904:C	P	13.89
1	K	1364:U	O3'	1368:A	P	13.51
1	K	182:G	O3'	189:G	P	12.54
1	K	2901:G	O3'	3597:G	P	12.45

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	K	4729:A	O3'	4735:G	P	9.07
1	K	1180:C	O3'	1183:C	P	8.56
1	K	1100:U	O3'	1168:G	P	8.11
1	K	512:U	O3'	515:C	P	6.98
1	K	500:G	O3'	504:G	P	5.70
1	K	4740:G	O3'	4743:G	P	4.85
1	K	1239:C	O3'	1244:G	P	4.61
1	K	4899:G	O3'	4902:C	P	3.31
1	K	751:G	O3'	752:G	P	2.87

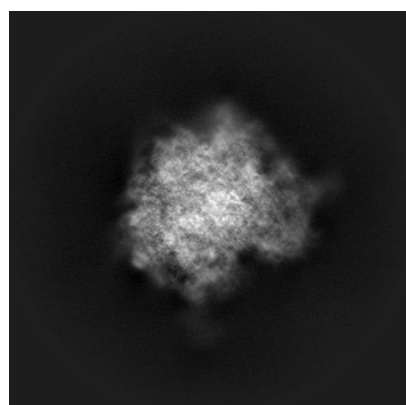
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25994. These allow visual inspection of the internal detail of the map and identification of artifacts.

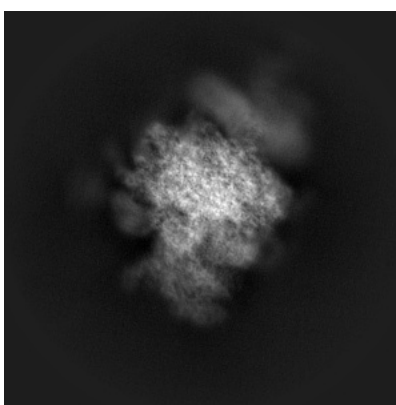
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

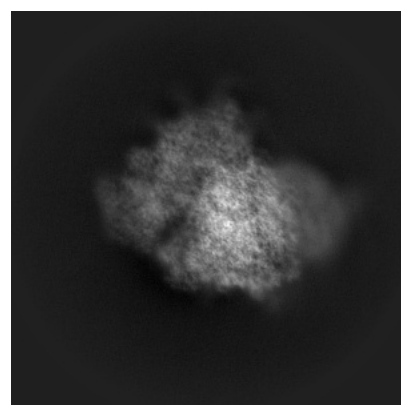
6.1.1 Primary map



X



Y

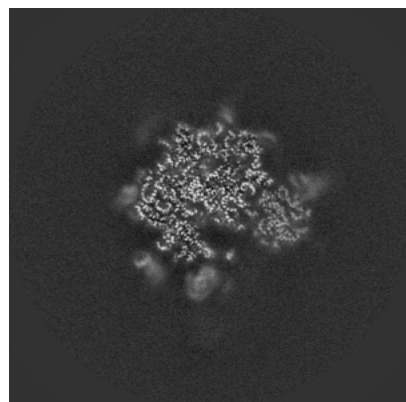


Z

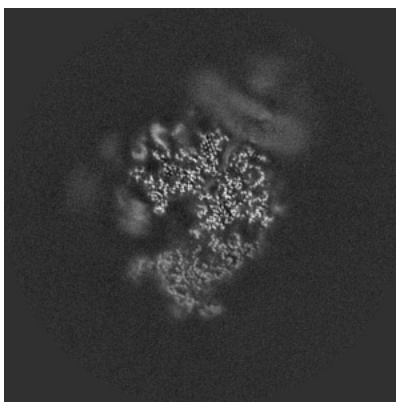
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

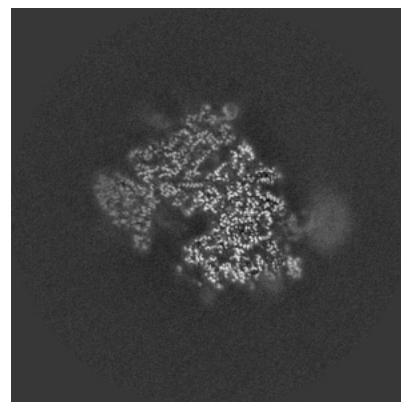
6.2.1 Primary map



X Index: 206



Y Index: 206

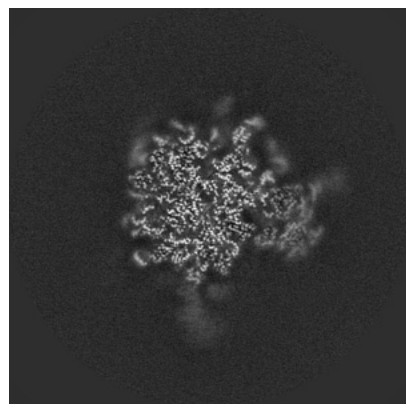


Z Index: 206

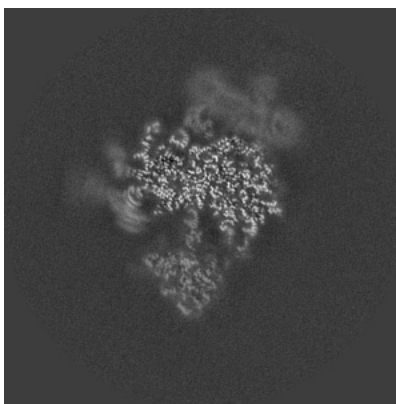
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

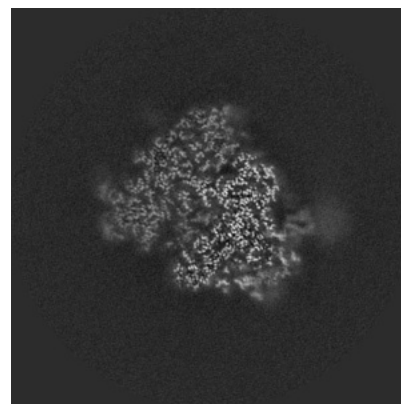
6.3.1 Primary map



X Index: 224



Y Index: 193

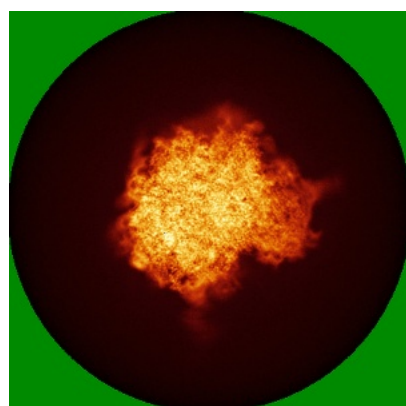


Z Index: 196

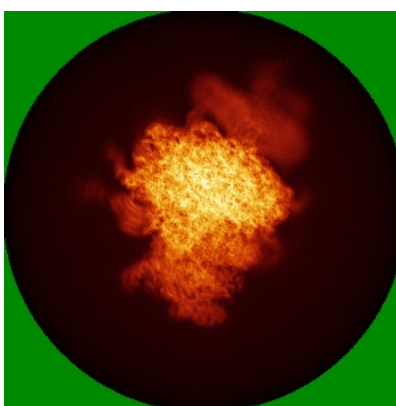
The images above show the largest variance slices of the map in three orthogonal directions.

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

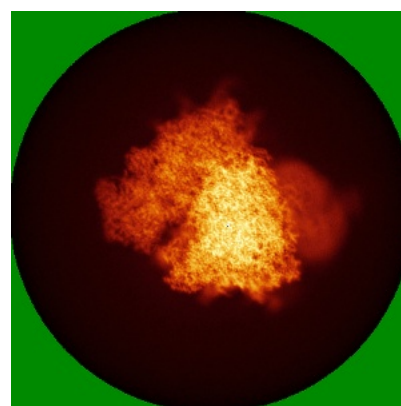
6.4.1 Primary map



X



Y

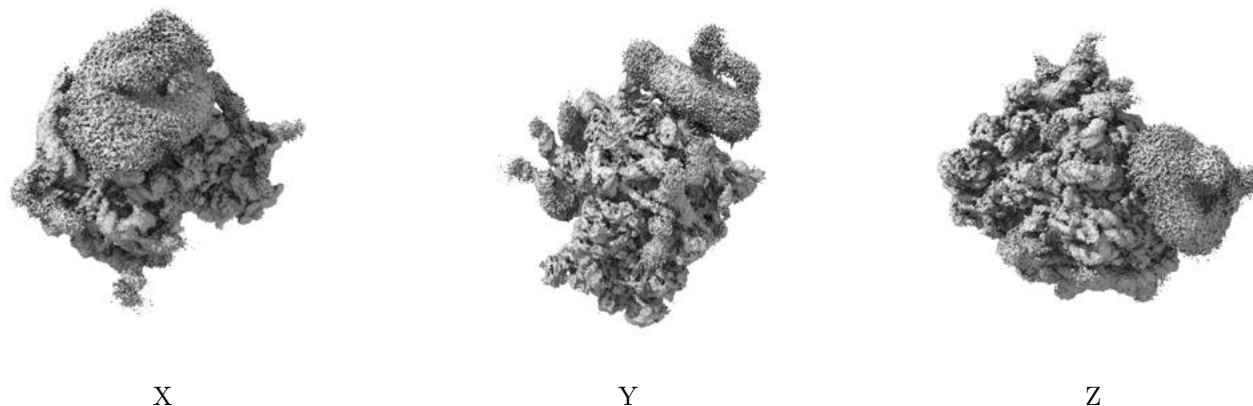


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.007. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

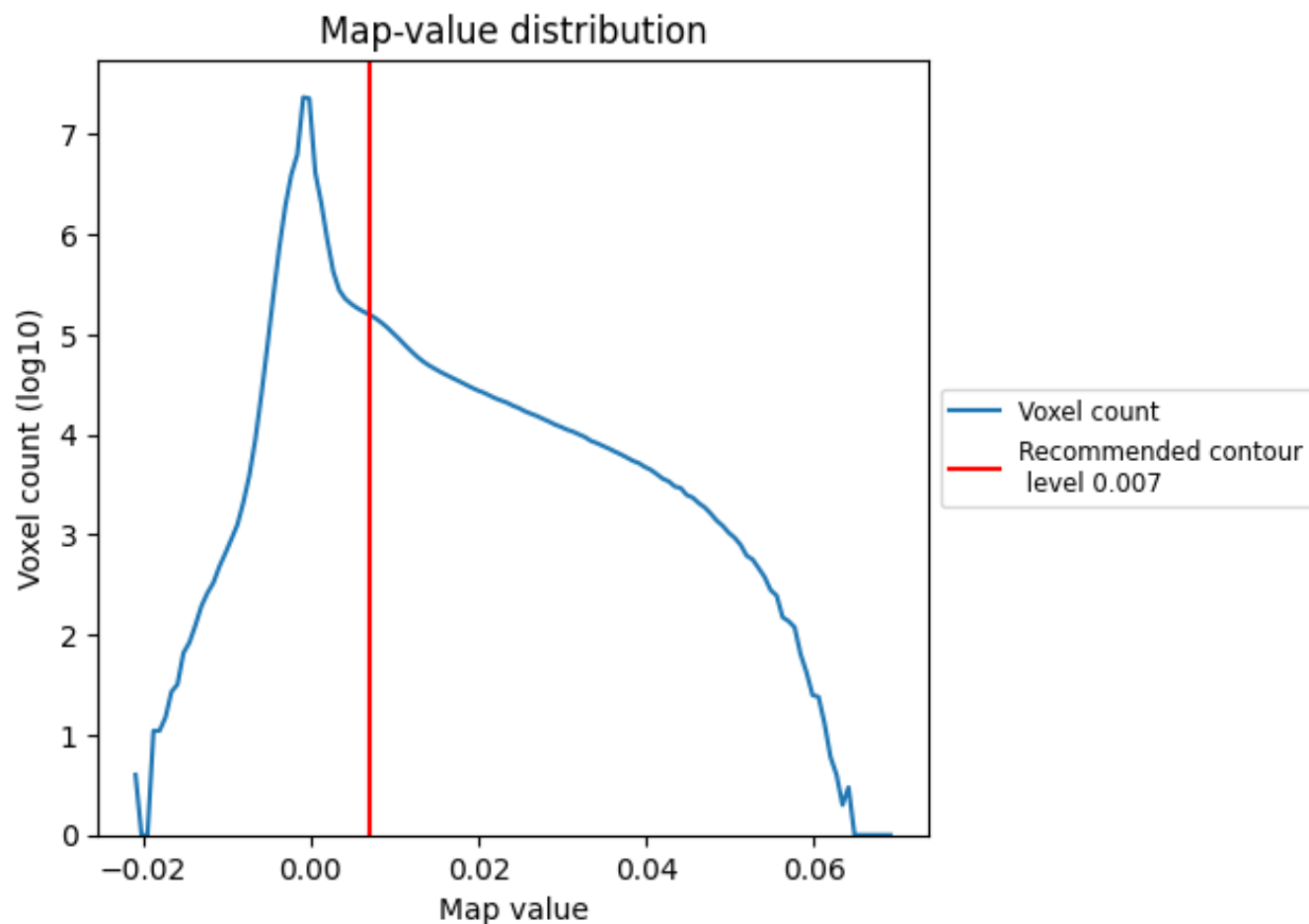
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

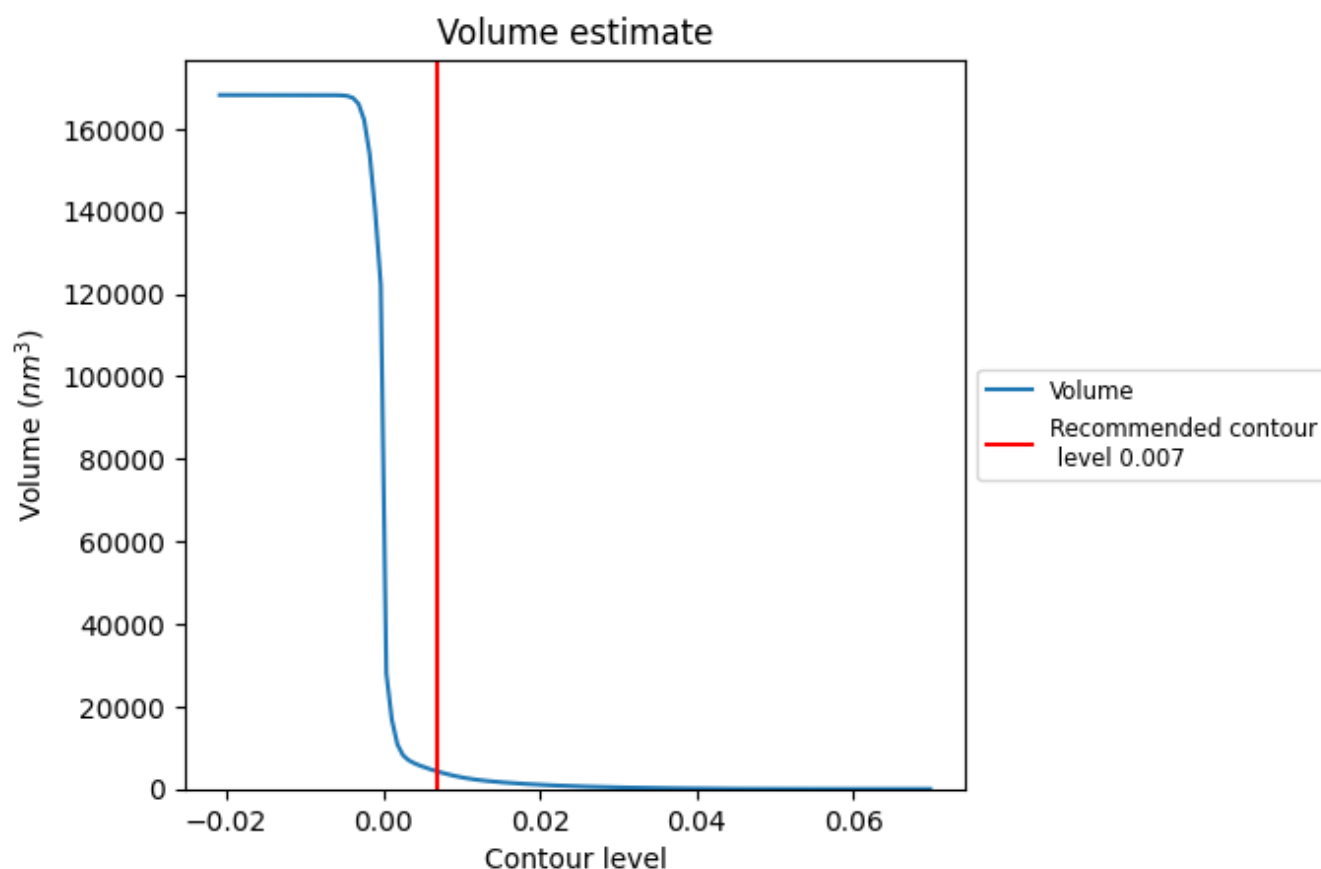
This section contains the results of statistical analysis of the map.

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.

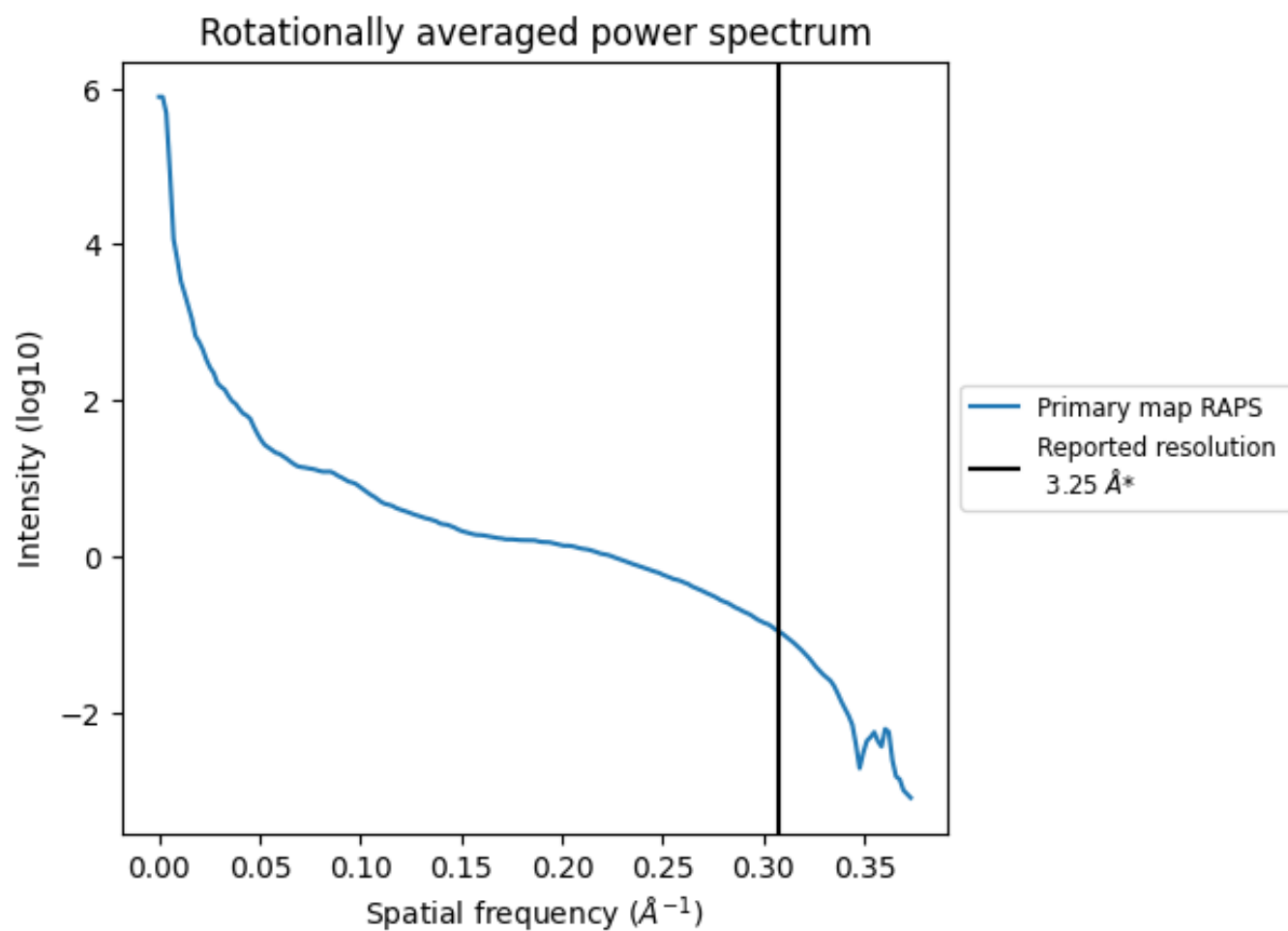
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4210 nm^3 ; this corresponds to an approximate mass of 3803 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 0.308 Å⁻¹

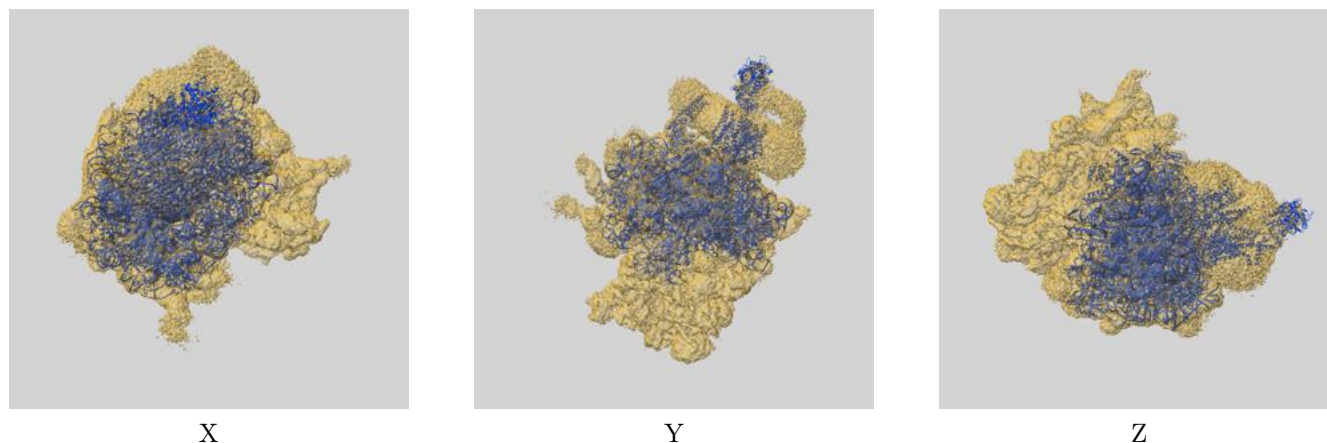
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

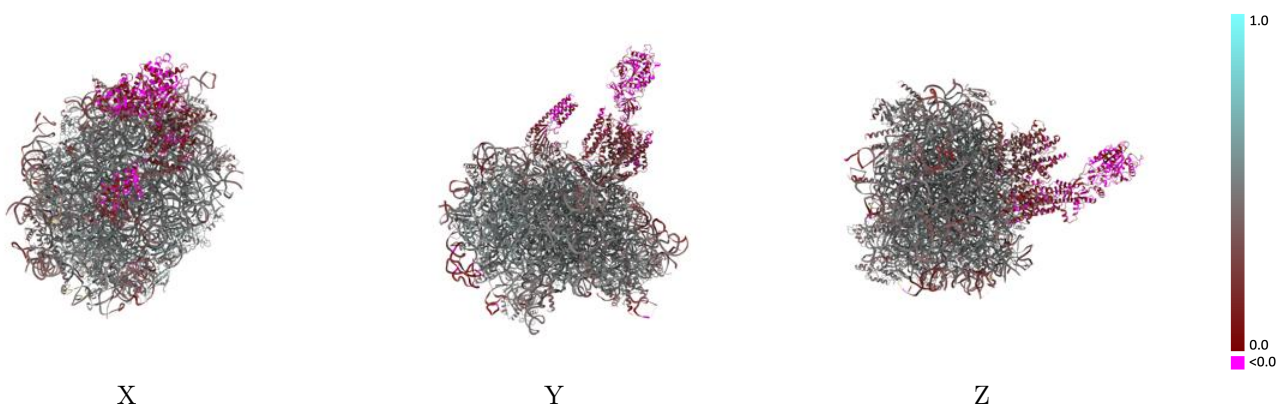
This section contains information regarding the fit between EMDB map EMD-25994 and PDB model 7TM3. Per-residue inclusion information can be found in section 3 on page 16.

9.1 Map-model overlay [i](#)



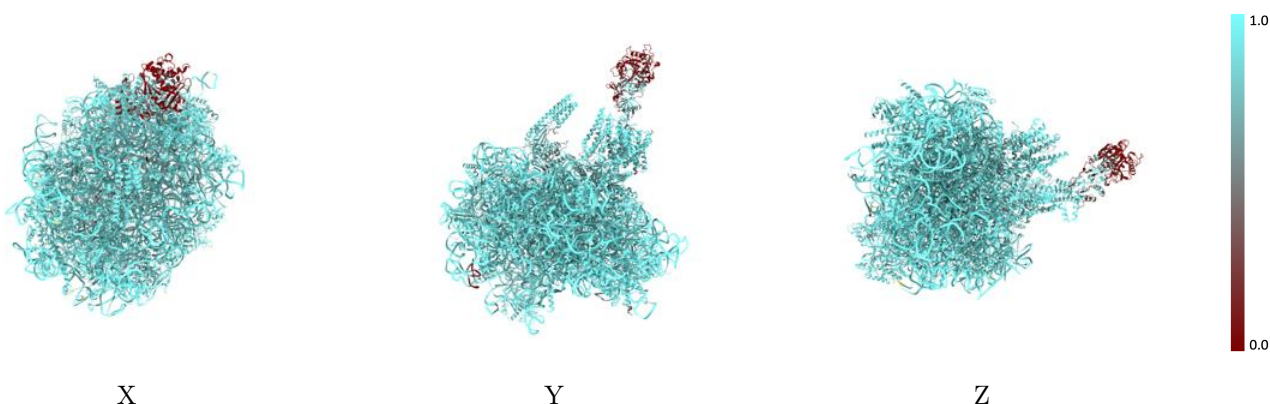
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



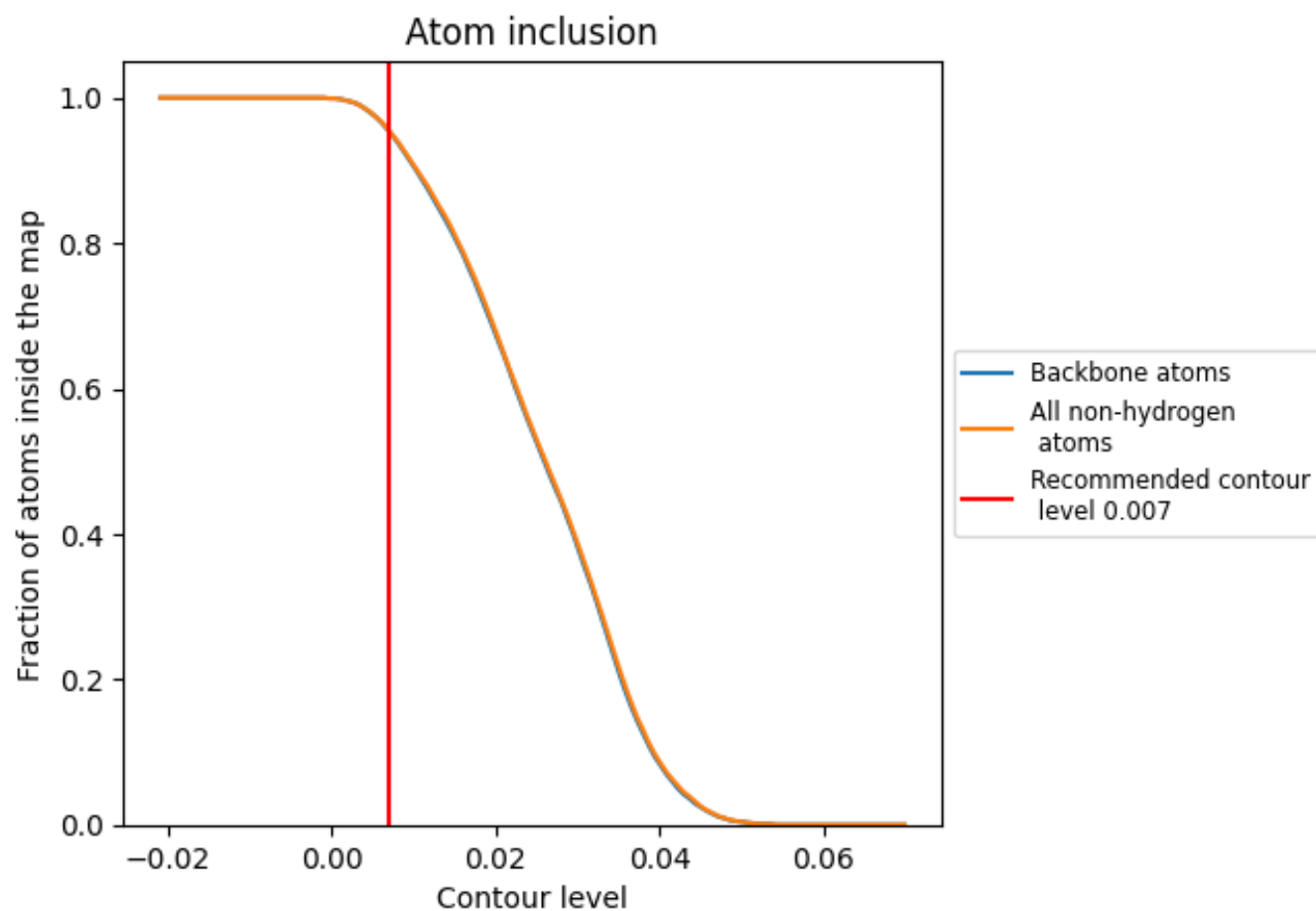
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.007).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 96% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9550	 0.4340
1	 0.8860	 0.2370
2	 0.9160	 0.1090
3	 0.8920	 0.2370
4	 0.7890	 0.2040
5	 0.8890	 0.0330
6	 0.8760	 0.1460
7	 0.3910	 0.0360
A	 0.9700	 0.5070
B	 0.9380	 0.3230
C	 0.9760	 0.4970
D	 0.9690	 0.4510
E	 0.9580	 0.4530
F	 0.9660	 0.4930
G	 0.9440	 0.4320
H	 0.9590	 0.4780
I	 0.9690	 0.4940
J	 0.9580	 0.4330
K	 0.9920	 0.4550
L	 0.9520	 0.4610
M	 0.9700	 0.4770
N	 0.9750	 0.5040
O	 0.9710	 0.4930
P	 0.9550	 0.4920
Q	 0.9770	 0.5040
R	 0.9560	 0.4660
S	 0.9760	 0.5050
T	 0.9620	 0.4830
U	 0.9350	 0.3940
V	 0.9680	 0.5100
W	 0.9610	 0.4900
X	 0.9490	 0.4690
Y	 0.9310	 0.4710
Z	 0.9680	 0.4620
a	 0.9810	 0.5030



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Chain	Atom inclusion	Q-score
b	 0.9460	 0.4210
c	 0.9490	 0.4500
d	 0.9460	 0.4690
e	 0.9710	 0.5100
f	 0.9790	 0.5240
g	 0.9530	 0.4730
h	 0.9340	 0.4560
i	 0.9520	 0.4510
j	 0.9810	 0.5080
k	 0.8890	 0.4190
l	 0.9650	 0.4830
m	 0.9710	 0.4900
n	 0.8990	 0.3970
o	 0.9650	 0.4910
p	 0.9550	 0.4660
q	 0.9480	 0.4000
r	 0.9750	 0.4960
u	 0.9970	 0.4790
v	 0.9970	 0.4530
w	 0.9720	 0.5050