



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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

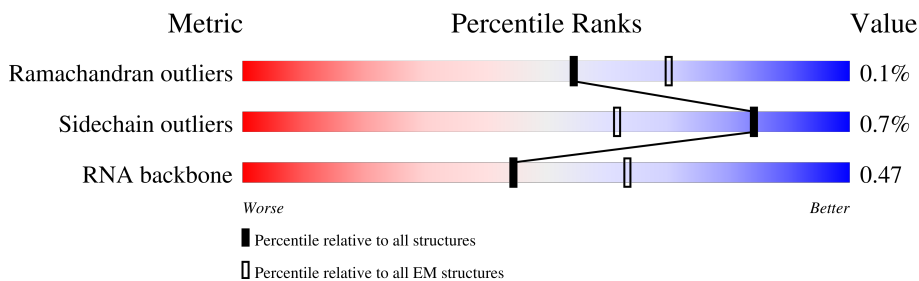
EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 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.



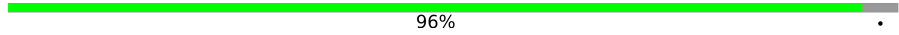
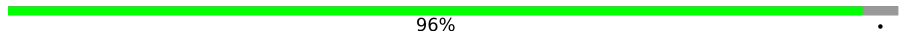
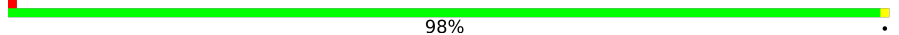

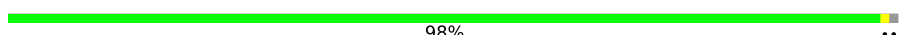
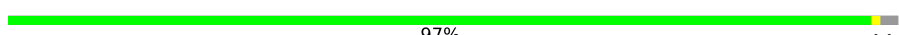





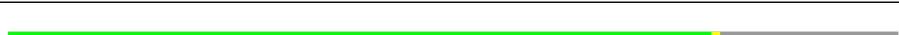

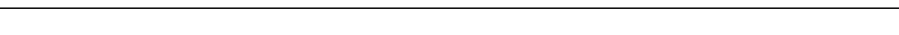
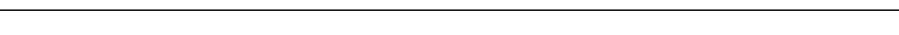
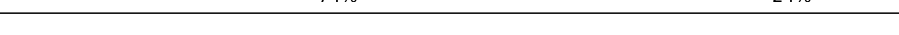
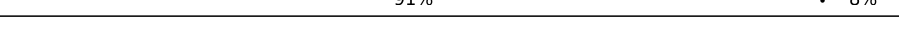
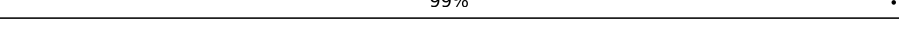
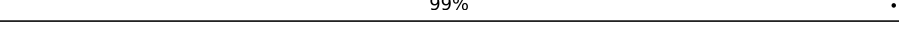



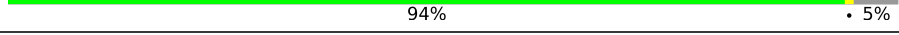
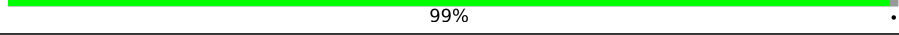
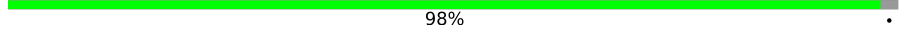
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	
2	B	229	
3	C	425	
4	D	297	
5	E	291	
6	F	247	
7	G	319	
8	H	192	

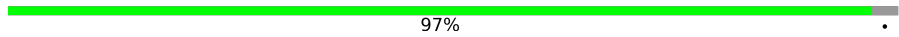

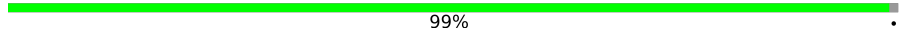
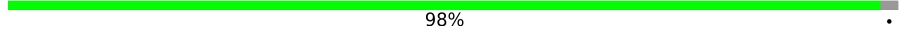

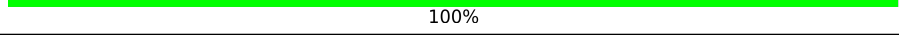
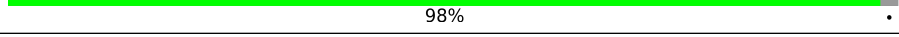
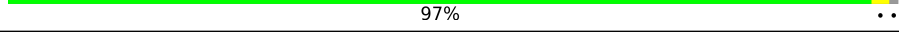
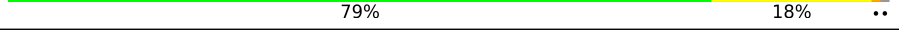
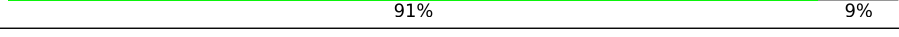
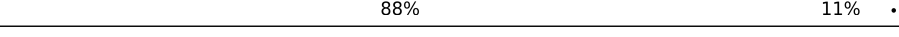

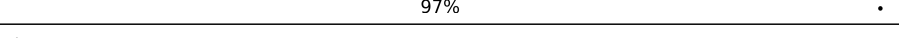
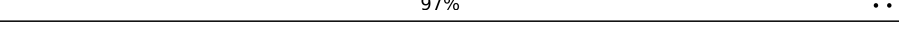
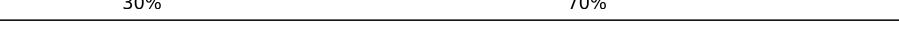
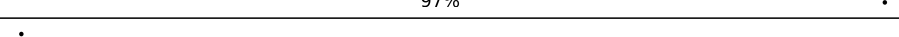


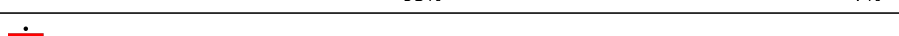


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Mol	Chain	Length	Quality of chain
9	I	214	 96%
10	J	178	 96%
11	L	211	 98%
12	M	218	 63% 37%
13	N	204	 98%
14	O	203	 97%
15	P	184	 83% 17%
16	Q	188	 99%
17	R	196	 79% 21%
18	S	176	 99%
19	T	160	 99%
20	U	128	 79% 20%
21	V	140	 93% 6%
22	W	157	 40% 60%
23	X	156	 74% 24%
24	Y	145	 91% 8%
25	Z	136	 99%
26	a	148	 99%
27	b	226	 46% 54%
28	c	115	 84% 15%
29	d	125	 83% 14%
30	e	135	 94% 5%
31	f	110	 99%
32	g	116	 98%
33	h	123	 99%

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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	
			Total	C	H	N	O			S
1	A	248	3891	1189	1993	389	314	6	0	0

- Molecule 2 is a protein called Nascent chain.

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

- Molecule 3 is a protein called uL4.

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

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
			Total	C	H	N	O	S		
4	D	293	4815	1512	2424	438	427	14	0	0

- Molecule 5 is a protein called eL6.

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

- Molecule 6 is a protein called uL30.

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

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
			Total	C	H	N	O	S		
7	G	233	3906	1199	2027	361	315	4	0	0

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
			Total	C	H	N	O	S		
8	H	190	3113	954	1597	284	272	6	0	0

- Molecule 9 is a protein called uL16.

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

- Molecule 10 is a protein called uL5.

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

- Molecule 11 is a protein called eL13.

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

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	
			Total	C	H	N	O			S
12	M	138	2348	727	1211	221	182	7	0	0

- Molecule 13 is a protein called eL15.

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

- Molecule 14 is a protein called uL13.

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

- Molecule 15 is a protein called uL22.

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

- Molecule 16 is a protein called eL18.

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

- Molecule 17 is a protein called eL19.

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

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
			Total	C	H	N	O	S		
18	S	176	2970	930	1508	285	236	11	0	0

- Molecule 19 is a protein called eL21.

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

- Molecule 20 is a protein called eL22.



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

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	
			Total	C	H	N	O			S
21	V	131	2018	618	1039	184	172	5	0	0

- Molecule 22 is a protein called eL24.

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

- Molecule 23 is a protein called uL23.

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

- Molecule 24 is a protein called uL24.

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

- Molecule 25 is a protein called eL27.

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

- Molecule 26 is a protein called uL15.

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

- Molecule 27 is a protein called eL29.

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

- Molecule 28 is a protein called eL30.

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

- Molecule 29 is a protein called eL31.

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

- Molecule 30 is a protein called eL32.

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

- Molecule 31 is a protein called eL33.

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

- Molecule 32 is a protein called eL34.

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

- Molecule 33 is a protein called uL29.

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

- Molecule 34 is a protein called eL36.

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

- Molecule 35 is a protein called eL37.

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

- Molecule 36 is a protein called eL38.

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

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	
			Total	C	H	N	O			S
37	l	50	927	286	480	96	64	1	0	0

- Molecule 38 is a protein called eL40.

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

- Molecule 39 is a protein called eL41.

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

- Molecule 40 is a protein called eL42.

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

- Molecule 41 is a protein called eL43.

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

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

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

- Molecule 43 is a protein called eL28.

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

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

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

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
			Total	C	H	N	O	P		
45	v	156	4997	1480	1683	585	1094	155	0	0

- Molecule 46 is a protein called uL3.

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

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
			Total	C	H	N	O	S		
47	1	465	7320	2360	3722	580	634	24	0	0

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

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

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

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

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

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

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

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

- Molecule 52 is a protein called Nicalin.

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

- Molecule 53 is a protein called Transmembrane protein 147.

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

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

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

- 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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*Continued from previous page...*

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).

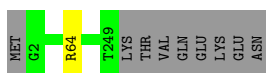
Mol	Chain	Residues	Atoms		AltConf
56	g	1	Total 1	Zn 1	0
56	j	1	Total 1	Zn 1	0
56	m	1	Total 1	Zn 1	0
56	o	1	Total 1	Zn 1	0
56	p	1	Total 1	Zn 1	0

### 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.

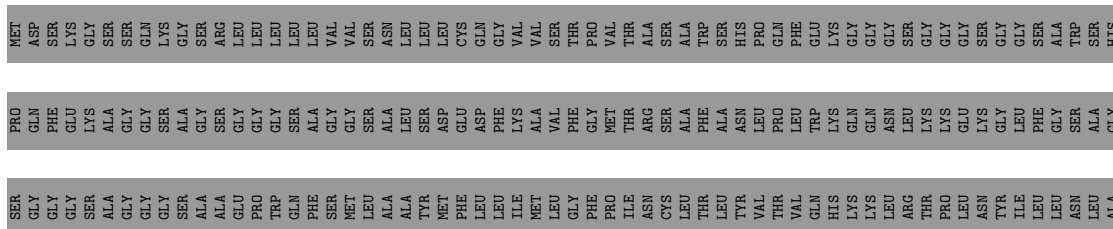
- Molecule 1: uL2

Chain A:  96%




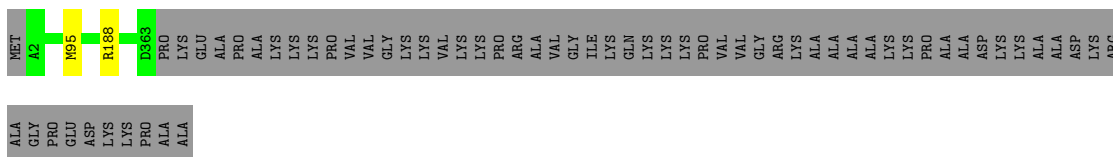
- Molecule 2: Nascent chain

Chain B:  11% 88%



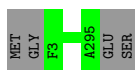
- Molecule 3: uL4

Chain C:  85% 15%



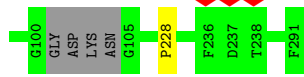
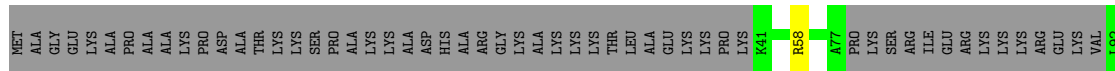
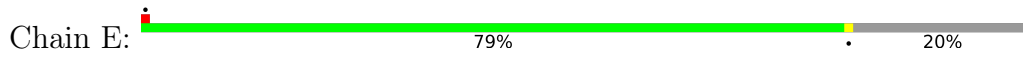
- Molecule 4: uL18

Chain D:  99%

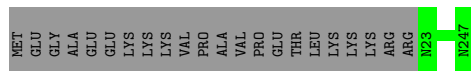
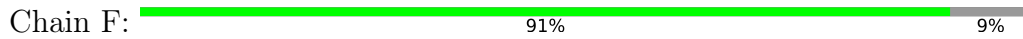




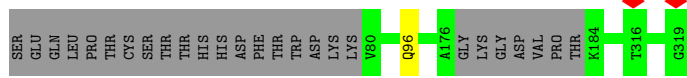
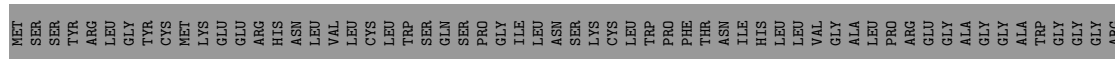
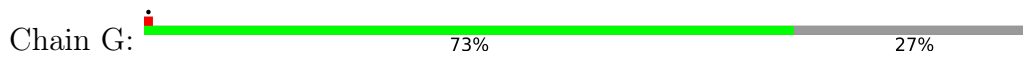
• Molecule 5: eL6



• Molecule 6: uL30



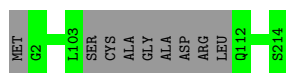
• Molecule 7: eL8



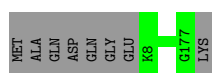
• Molecule 8: uL6



• Molecule 9: uL16



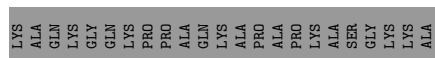
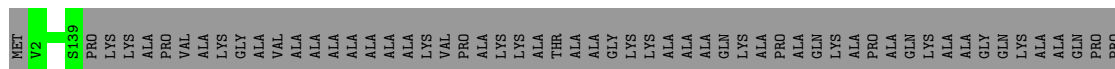
• Molecule 10: uL5



• Molecule 11: eL13



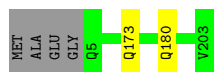
• Molecule 12: eL14



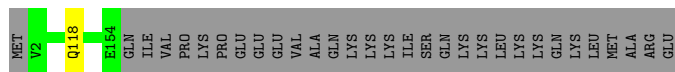
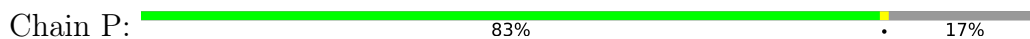
• Molecule 13: eL15



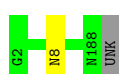
• Molecule 14: uL13



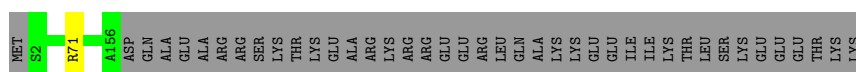
• Molecule 15: uL22



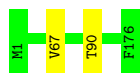
• Molecule 16: eL18



• Molecule 17: eL19



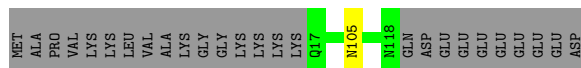
• Molecule 18: eL20



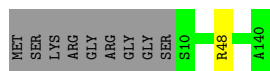
• Molecule 19: eL21



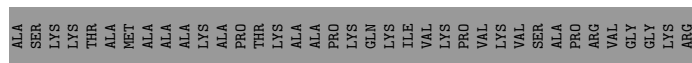
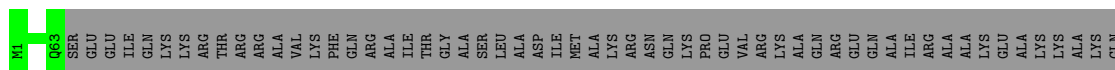
• Molecule 20: eL22



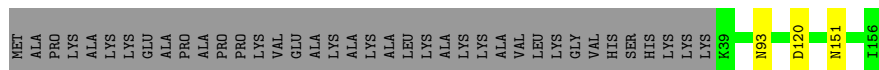
• Molecule 21: uL14



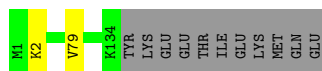
• Molecule 22: eL24



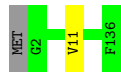
• Molecule 23: uL23



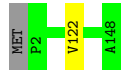
• Molecule 24: uL24



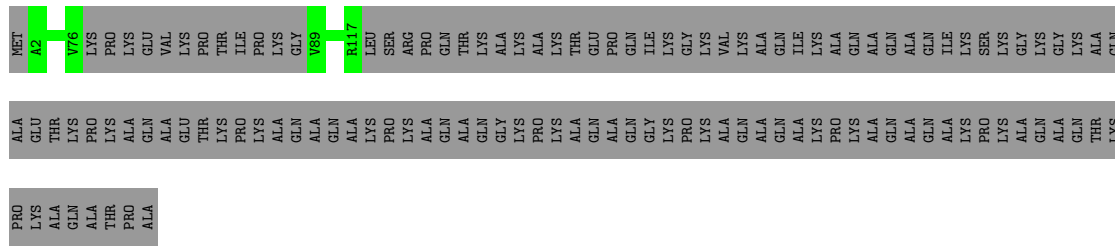
• Molecule 25: eL27



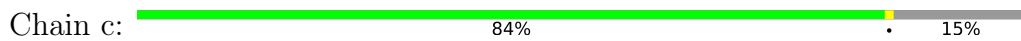
• Molecule 26: uL15



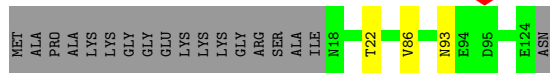
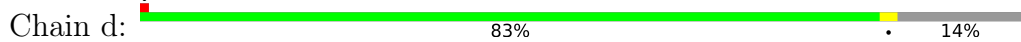
• Molecule 27: eL29



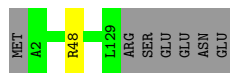
• Molecule 28: eL30



• Molecule 29: eL31



• Molecule 30: eL32



• Molecule 31: eL33





• Molecule 32: eL34



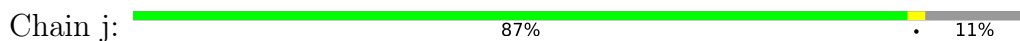
• Molecule 33: uL29



• Molecule 34: eL36



• Molecule 35: eL37



• Molecule 36: eL38

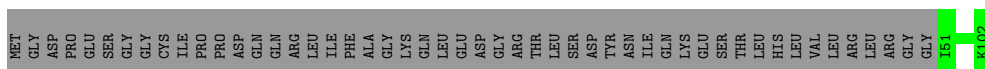


• Molecule 37: eL39



• Molecule 38: eL40





- 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%



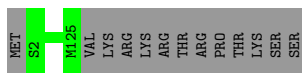
- Molecule 42: P-site tRNA

Chain q: 79% 18%



- Molecule 43: eL28

Chain r: 91% 9%



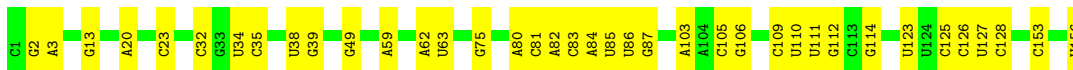
- Molecule 44: 5S ribosomal RNA

Chain u: 88% 11%



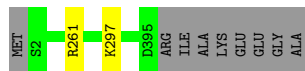
- Molecule 45: 5.8S ribosomal RNA

Chain v: 76% 24%



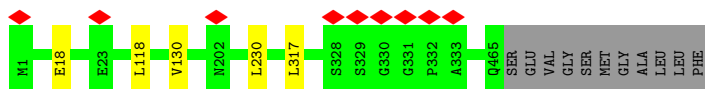
• Molecule 46: uL3

Chain w:  97%



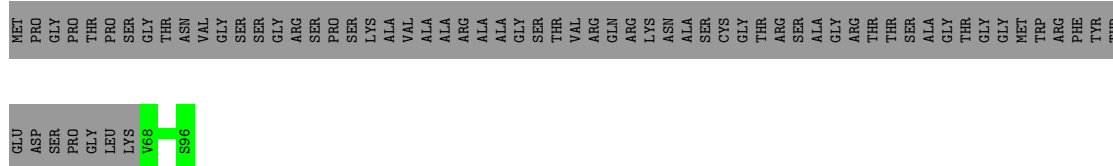
• Molecule 47: Protein transport protein Sec61 subunit alpha isoform 1

Chain 1:  97%



• Molecule 48: Protein transport protein Sec61 subunit beta

Chain 2:  30% 70%



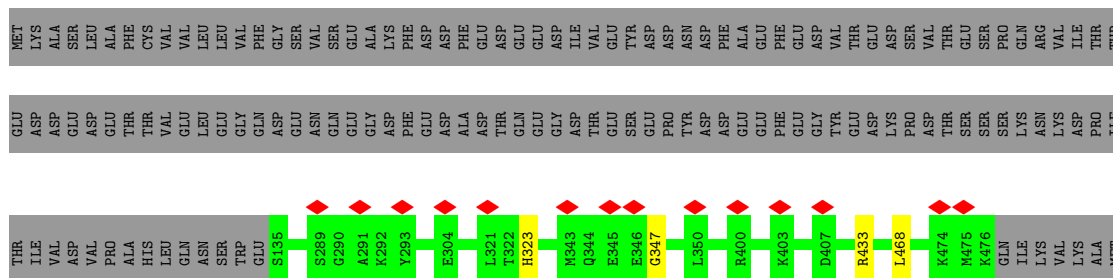
• Molecule 49: Protein transport protein Sec61 gamma

Chain 3:  97%




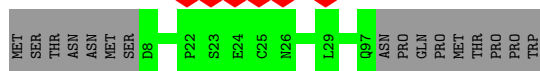
• Molecule 50: Coiled-coil domain containing 47

Chain 4:  70% 29%

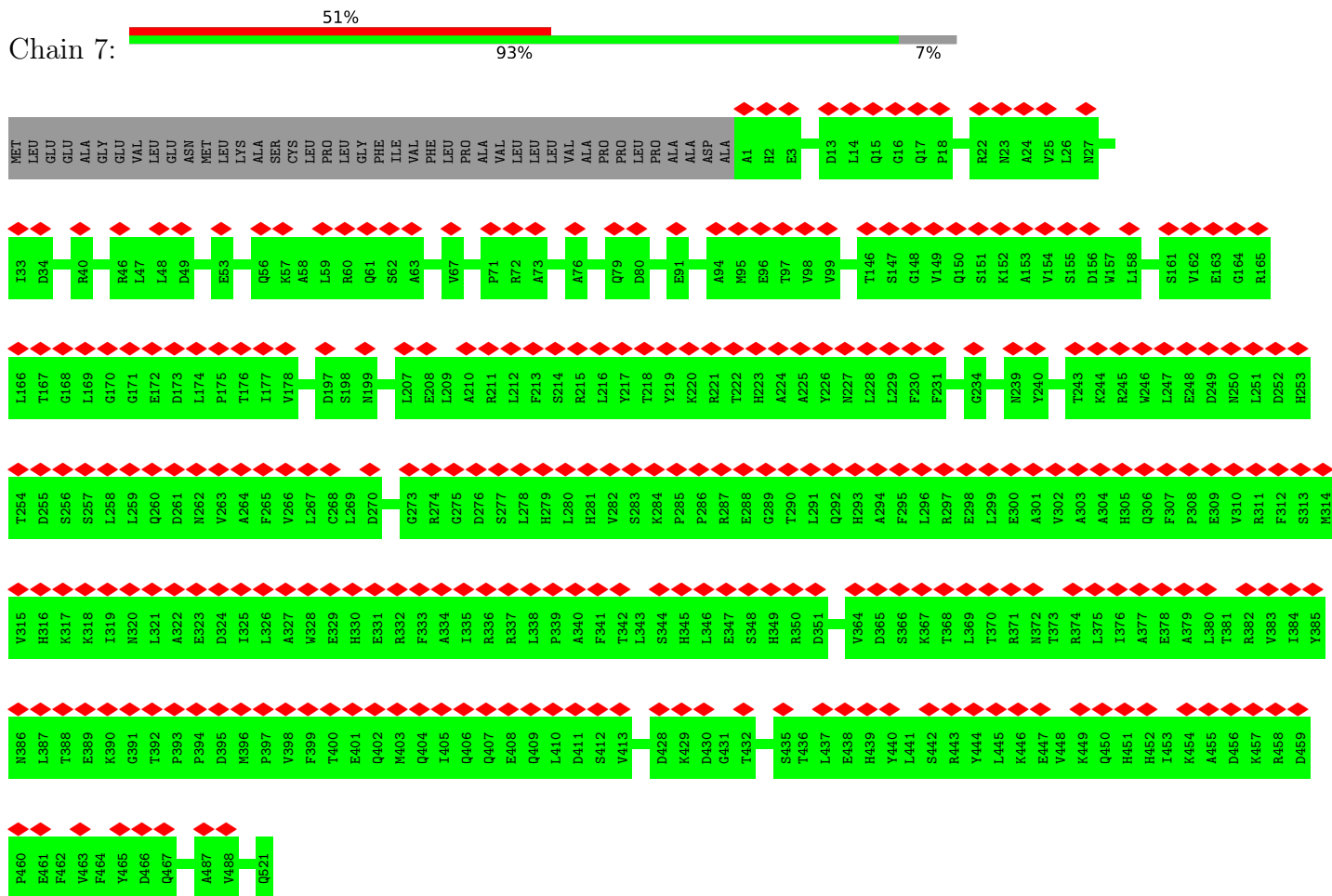


• Molecule 51: PAT complex subunit Asterix

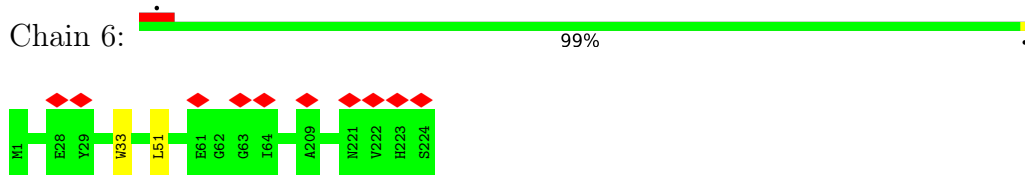
Chain 5:  6% 85% 15%



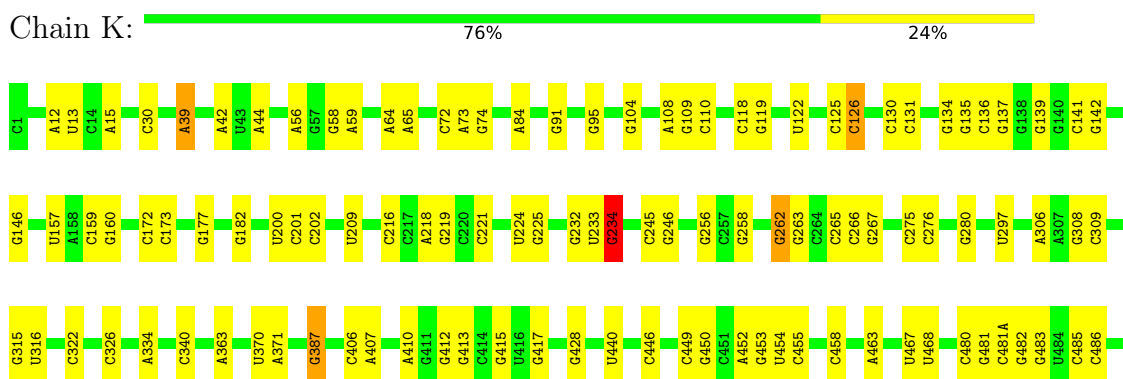
• Molecule 52: Nicalin



• Molecule 53: Transmembrane protein 147



• Molecule 54: 28S ribosomal RNA





U492	G493	C923	C924	G496	G497	G498	G499	G500	G504	G505	C506	U510	G644	C1097	C1098	C1099	G1174	A1175	U1179	A932	A933	C934	C934	A935	G935A	U936	C1210	G1211	G1212	U937	C1215	C938	C938	G1216	C1217	C940	G658	G659	G660	C661	G666	A667	C668	C669	G670	G684	C965	A686	U687	C696	G697	G698	C699	G700	C704	G705	G708	C990	G1070	C738	G749	G756	G757	G758	U914	A917	C1080	C1081	C1082	A1354	G1358	G1359	U1364	G1370	A1371	G1377	C1378	C1379	A1387	A1392	G1393	G1394	A1397	A1398	G1403	U1411A	G1415	G1419	A1420	G1421	A1433	U1436	C1437	U1438	U1440	C1441	U1445	C1446	C1447	G1448	G1455	C1456	G1457	C1458	G1475	C1476	C1477	C1478	C1481	G1482	C1483	G1484	G1489	A1497	G1498	G1502	U1514	A1515	G1516	G1517	C1518	C1519	A1523	A1534	A1547	A1563	A1564	A1565	C1566	U1578	G1586	U1591	U1596	G1597	A1600	A1601	U1602	G1612	A1613	U1624	G1625	A1631	A1632	G1633	A1634	U1639	C1640	G1654	G1658	C1661	C1676	U1677	C1696	C1731	G1732	G1733	G1741	A1742	G1750	U1756	G1760	G1761	G1764	A1767	C1768	G1769	C1772	U1773	A1774	A1775	A1780	A1787	G1798	G1799	A1804	C1807	C1808	C1809	G1810	G1811	G1815	G1818	G1819	U1820	U1821	U1822	C1828	U1834	G1835	G1836	A1837	G1842	A1843	C1847	G1855	G1869	U1882	U1889	A1892	A1897	C1898	G1916	A1917	U1918	C1920	C1921	G1922	C1931	A1932	C1935	G1940	G1945	G1946	U1947	G1948	U1957	A1958	U1959	G1961	A1962	C1963	A1964	G1965	G1968	G1969	A1970	U1971	U1974	G1975	G1976	C1977	C1978	A1979	U1980	G1981	G1982	A1984	C1987	G1988	A1990	A1991	U1997	A1998	A1999	G2000	G2001	A2002	G2003	U2004	G2005	U2006	G2007	U2008	A2009	A2010	C2011	C2018	C2019	U2020	C2022	C2023	G2024	A2025	A2026	A2043	G2046	A2047	U2048	G2052	C2053	U2054	G2055	G2056	G2063	C2064	A2069	U2070	A2071	U2084	G2089	U2090	C2091	G2092	C2094	A2095	G2096	C2098	C2099	A2107	G2102	A2103	A2105	G2106	A2107	G2108	A2109	G2110	G2259	C2260	C2266	U2267	A2268	C2269	G2275	A2276	C2277	G2278	A2279	C2289	C2289	G2294	G2299	A2300	G2301	C2306	A2313	G2314	G2315	G2316	G2331	A2332	C2333	C2335	G2348	C2351	G2364	A2382	A2395	A2396	G2397	U2398	A2417	C2422	A2423	G2424	U2425	A2431	U2432	G2433	C2441	G2599	A2600	A2601	G2602	G2618	U2619	A2621	C2627	G2638	C2653	C2653	G2662	C2669	C2673	A2674	G2675	G2676	G2677	G2686	U2687	A2695	A2696	G2705	U2706	U2707	U2708	C2709	C2710	C2711	G2714	G2721	A2725	G2726	U2740	A2743	G2760	U2761	G2762	A2764	A2769	C2772	A2787	U2788	A2789	U2790	C2794	A2798	U2803	A2807	G2808	G2822	U2826	G2827	U2828	C2834	G2842	A2850	G2855	G2855	C2867	C2875	A2879	A2895	G2898	C3598	G3603	A3604	C3605	U3616	G3617	C3618	C3622	G3625	G3626	A3630	A3635	A3784	A3785	U3644	A3646	A3648	A3649	U3657	A3662	A3663	C3664	C3667	G3672	C3673	G3674	A3682	A3692	C3696	A3702	A3711	G3714	A3728	U3729	G3743	A3748	A3906	C3749	G3750	G3753	A3756	A3760	A3763	C3767	U3772	U3773	G3776	G3777	G3780	A3783	A3784	A3785	G3786	G3787	G3809	C3810	G3811	U3814	A3817	U3818	G3819	U3822	G3823	A3824	U3838	G3839	U3840	A3876	A3877	C3878	G3879	G3880	G3888	G3889	G3897	A3901	G3904	A3905	A3906	C3907	A3908	U3915
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U5022	G4919	U4709	U4512	G4354	G4183	G3916
U5040	C4920	C4719	A4513	G4355	G4184	A3917
U5041	C4921	C4720	G4514	G4356	G4189	A3923
C5047	U4923	G4721	G4515	G4364	G4191	C3926
C5050	U4925	G4722	C4519	G4373	A4203	G3938
C5051	C4926	U4728	G4522	A4376	A4212	G3939
C5052	G4927	C4736	A4523	G4377	G4377	U3940
U5053	C4928	C4737	G4524	A4378	A4378	G3941
C5054	G4931	G4738	G4528	A4379	A4379	A3942
G5055	U4935	C4738	A4535	A4380	A4380	A3943
A5056	G4936	A4744	A4548	C4387	C4387	G3946
C5057	C4937	G4745	G4549	G4391	G4391	A3947
A5058	C4940	G4750	C4560	G4392	G4392	C3948
A5061	A4943	U4752	C4561	G4393	G4393	G4065
G5062	C4944	G4753	C4562	A4394	A4394	U4066
U5069	G4947	G4754	G4567	U4395	U4395	U4069
	C4948	C4757	G4570	C4398	C4398	U4070
	G4949	U4758	G4573	G4401	G4401	G4076
	U4950	C4759	C4574	U4419	U4419	G4084
	G4951	G4761	C4575	U4420	U4420	A4085
	A4955	A4764	U4584	A4421	A4421	G4086
	C4956	C4765	U4585	A4422	A4422	G4087
	C4957	G4771	U4586	G4430	G4430	C4088
	C4958	C4772	G4587	U4437	U4437	G4097
	U4959	G4772	G4590	U4438	U4438	U4111
	G4960	U4868	A4605	U4438	U4438	U4111
	G4963	G4869	U4605	C4444	C4444	C4114
	C4964	G4870	U4636	G4448	G4448	G4115
	U4965	C4871	U4657	A4449	A4449	C4116
	A4966	C4875	G4637	U4452	U4452	U4117
	A4967	U4882	U4638	C4453	C4453	U4118
	U4976	C4883	G4639	U4463	U4463	C4119
	A4977	G4884	G4652	A4464	A4464	U4120
	U4985	U4885	A4656	U4466	U4466	G4121
	U4988	C4895	U4657	C4466	C4466	A4127
	U4989	G4897	U4661	U4471	U4471	A4128
	C4990	G4898	C4670	G4472	G4472	C4133
	U4991	C4898	A4672	A4473	A4473	G4136
	G4992	C4903	A4671	G4475	G4475	C4158
	G4993	A4909	A4672	U4488	U4488	C4162
	U5006	G4910	U4677	G4489	G4489	U4163
	A5014	G4911	A4687	U4500	U4500	C4166
	G5015	G4912	G4694			A4170
	A5016	C4913				A4171
	G5017					C4350

## 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 ( $\text{\AA}$ )	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 ( $\text{\AA}$ )	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.

The worst 5 of 50 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
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

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
9	I	201/214 (94%)	181 (90%)	20 (10%)	0	100	100
10	J	168/178 (94%)	158 (94%)	10 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
40	o	102/106 (96%)	90 (88%)	12 (12%)	0	100	100
41	p	89/92 (97%)	83 (93%)	6 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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 [i](#)

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
5	E	206/251 (82%)	205 (100%)	1 (0%)	88	93
6	F	196/215 (91%)	196 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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
36	k	64/65 (98%)	64 (100%)	0	100	100
37	l	47/48 (98%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	d	93	ASN
46	w	297	LYS
30	e	48	ARG
41	p	4	ARG
47	1	118	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 [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
42	q	74/77 (96%)	15 (20%)	0
44	u	119/120 (99%)	14 (11%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
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%)

5 of 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

5 of 58 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
54	K	1455	G
54	K	4925	U
54	K	2266	C
54	K	4921	C
54	K	4354	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 [i](#)

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 [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
54	K	25

The worst 5 of 25 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

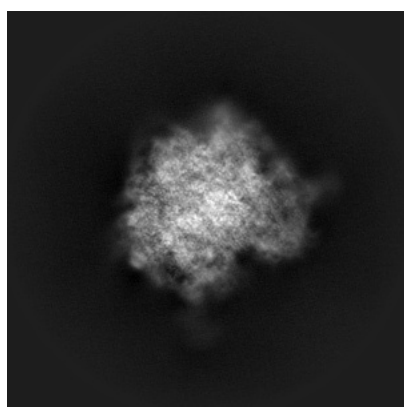
## 6 Map visualisation [i](#)

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.

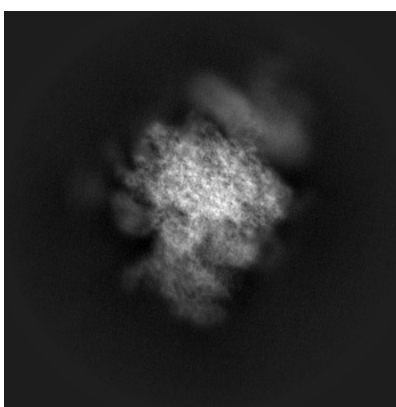
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

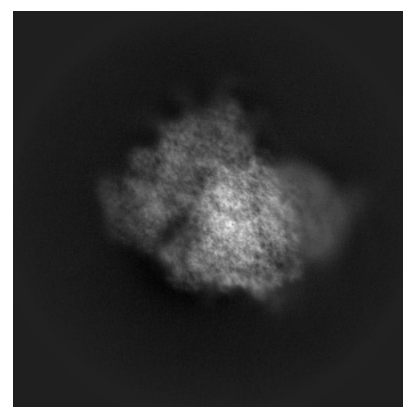
#### 6.1.1 Primary map



X



Y

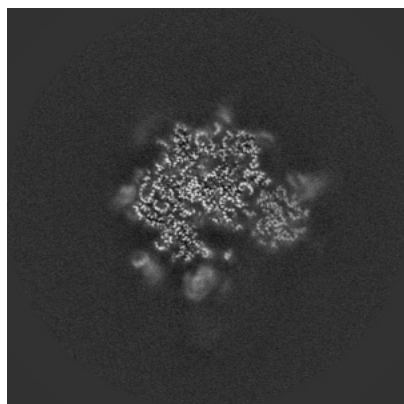


Z

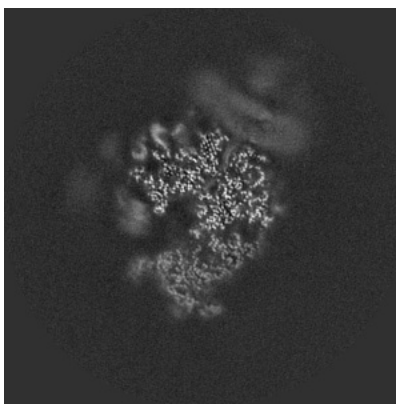
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

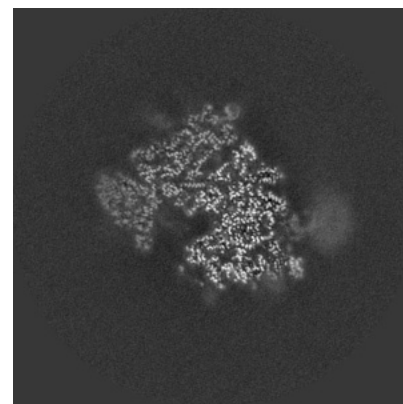
#### 6.2.1 Primary map



X Index: 206



Y Index: 206

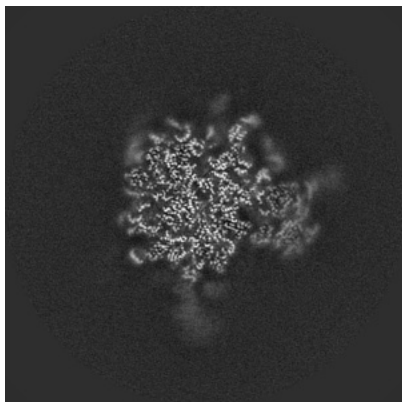


Z Index: 206

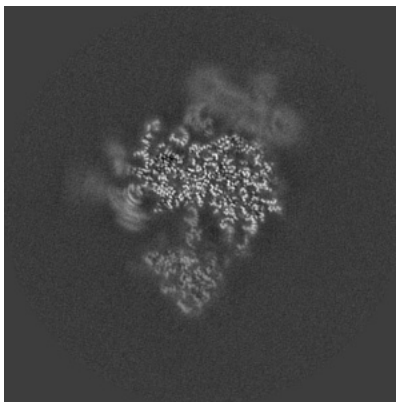
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

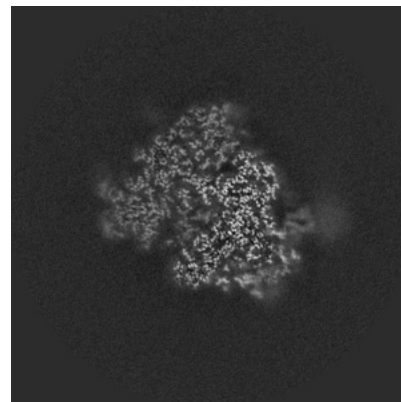
### 6.3.1 Primary map



X Index: 224



Y Index: 193

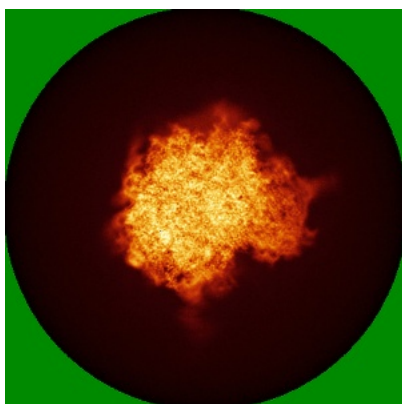


Z Index: 196

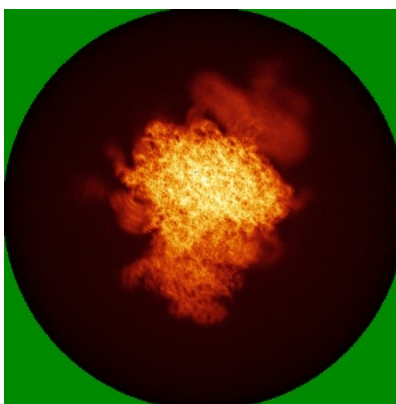
The images above show the largest variance slices of the map in three orthogonal directions.

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

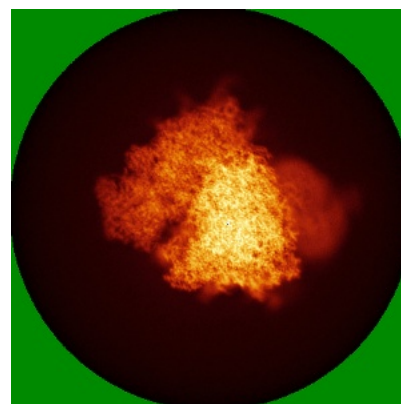
### 6.4.1 Primary map



X



Y

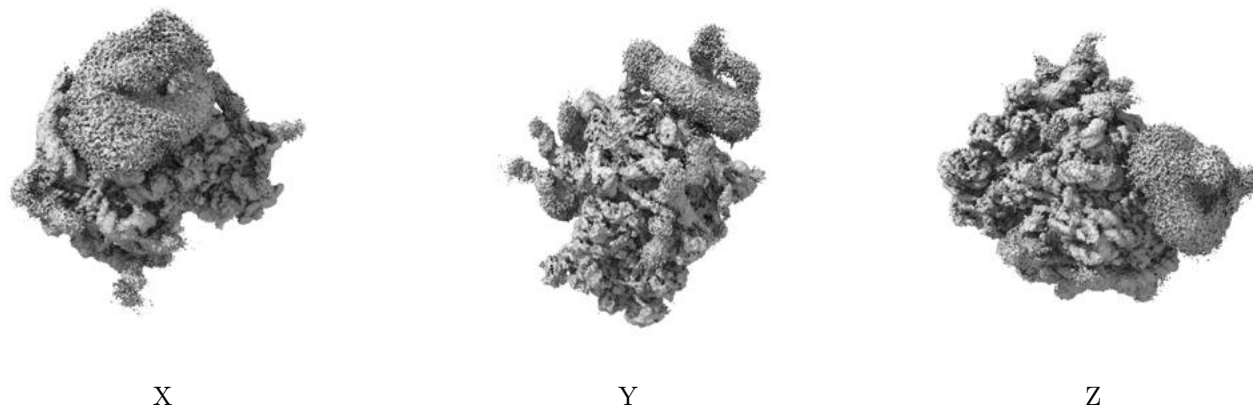


Z

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.

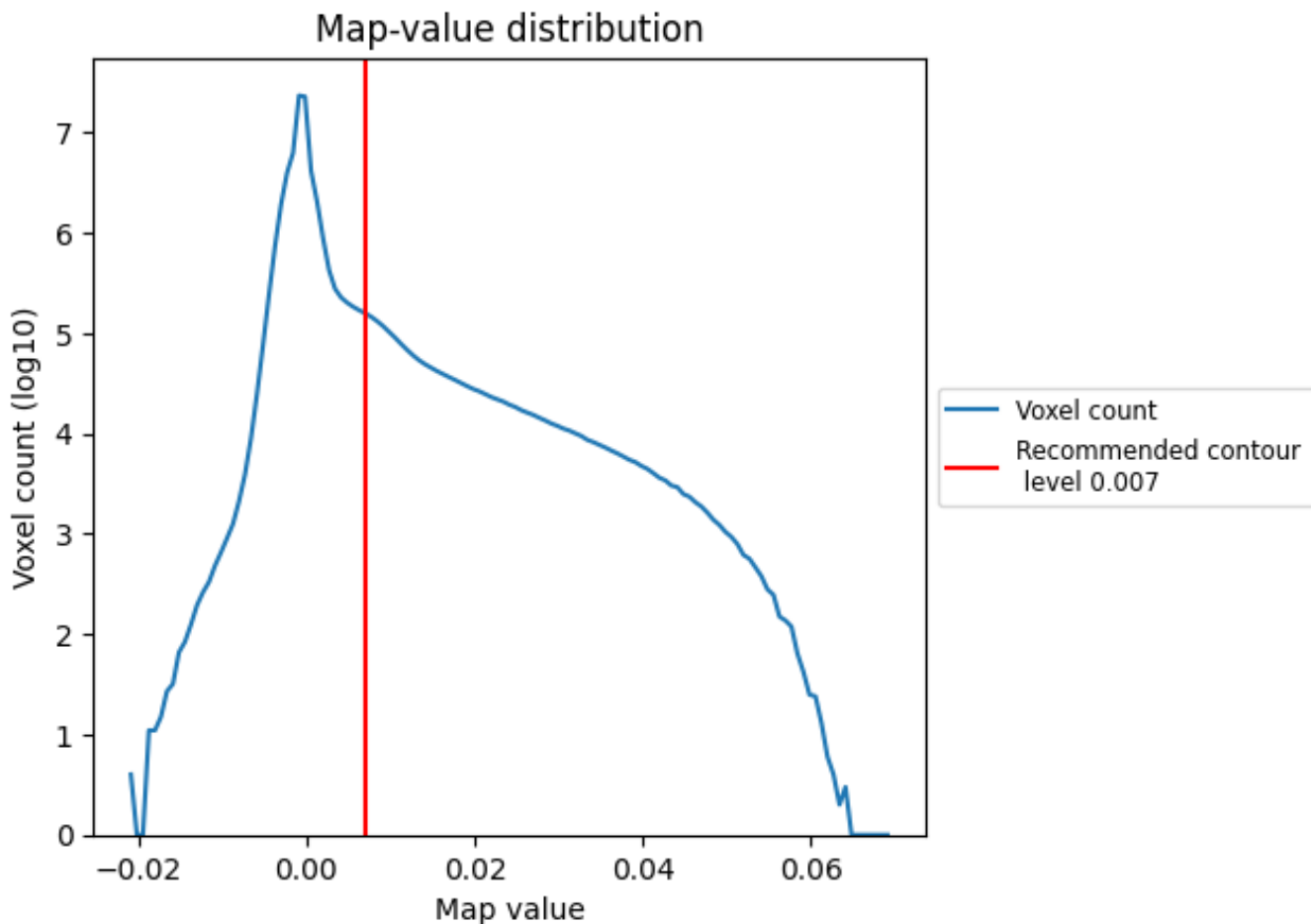
## 6.6 Mask visualisation [i](#)

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.

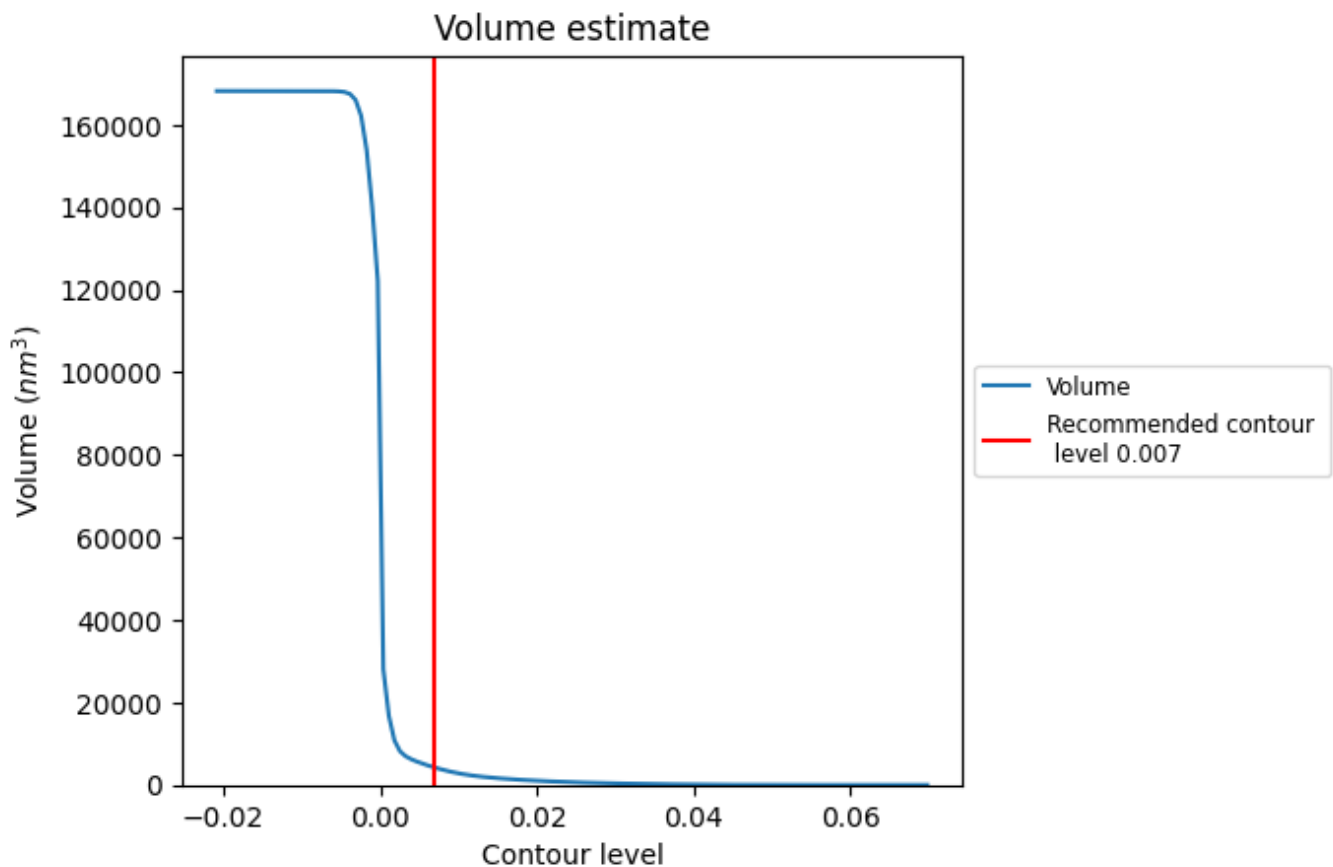
### 7.1 Map-value distribution [i](#)



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.



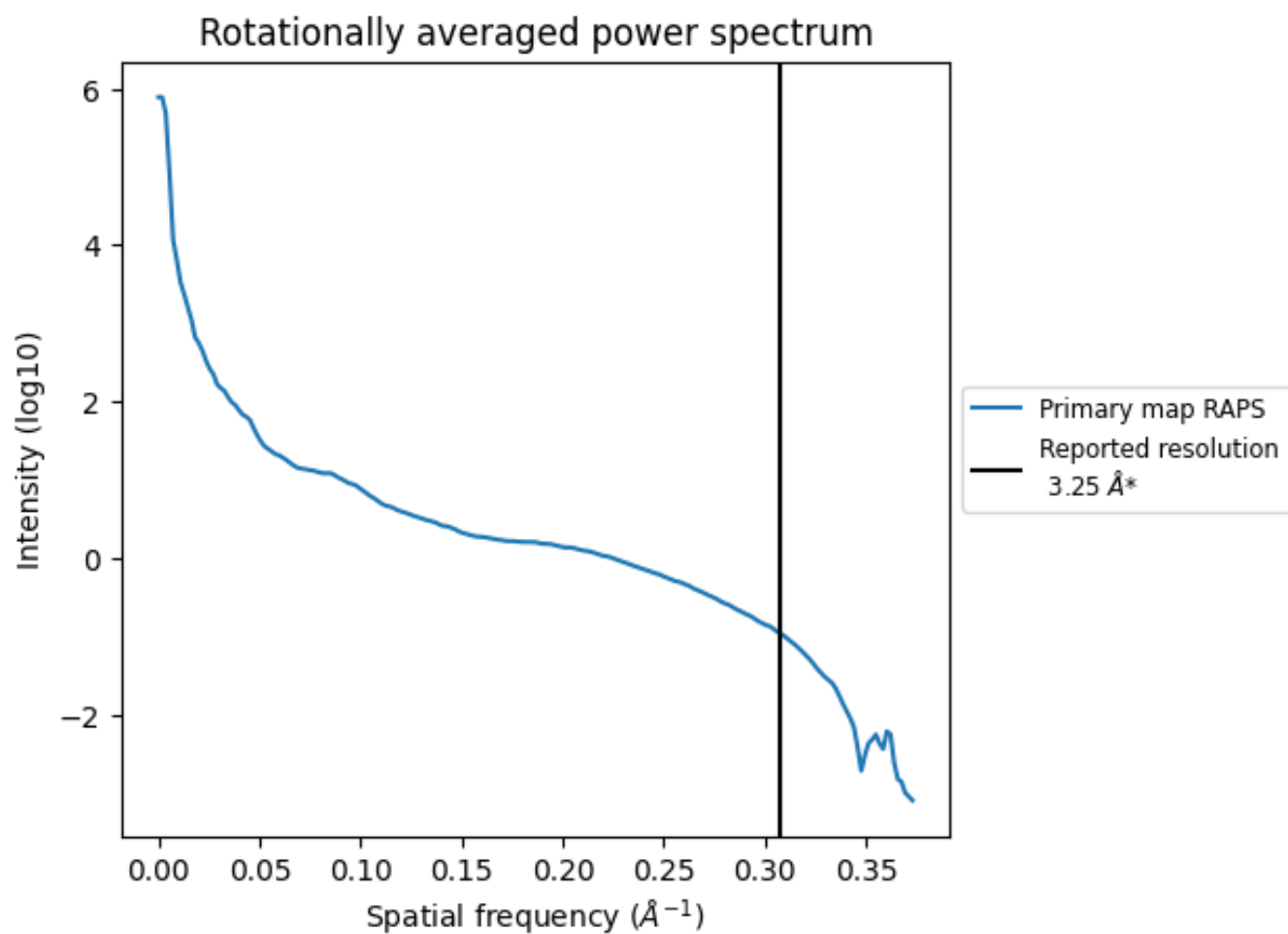
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4210 nm<sup>3</sup>; 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 [i](#)



\*Reported resolution corresponds to spatial frequency of  $0.308 \text{ \AA}^{-1}$

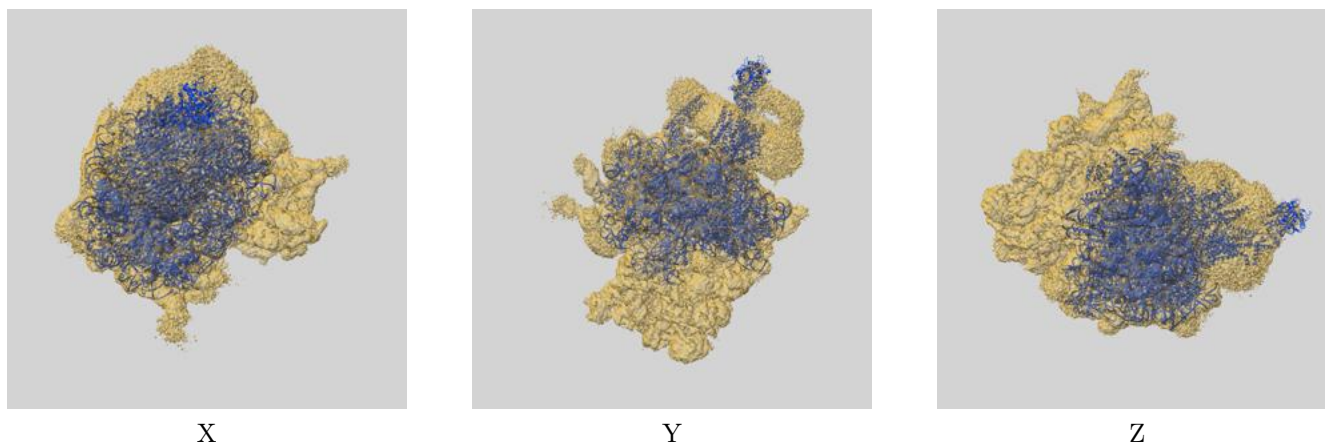
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

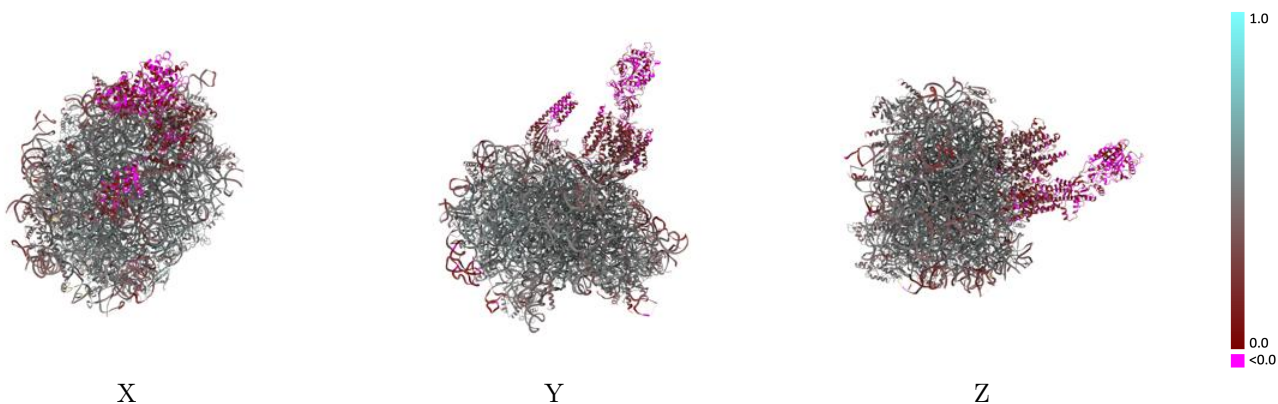
This section contains information regarding the fit between EMDB map EMD-25994 and PDB model 7TM3. Per-residue inclusion information can be found in section 3 on page 16.

### 9.1 Map-model overlay [i](#)



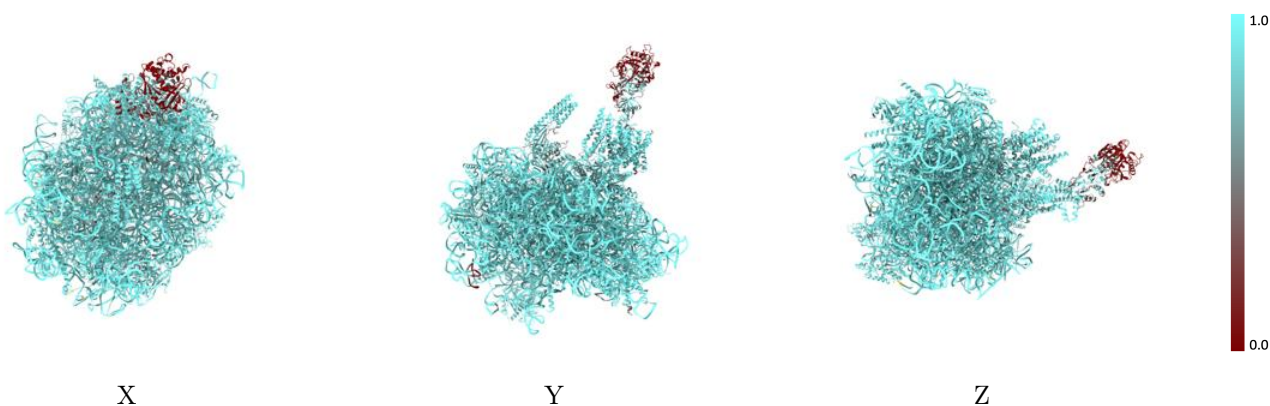
The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



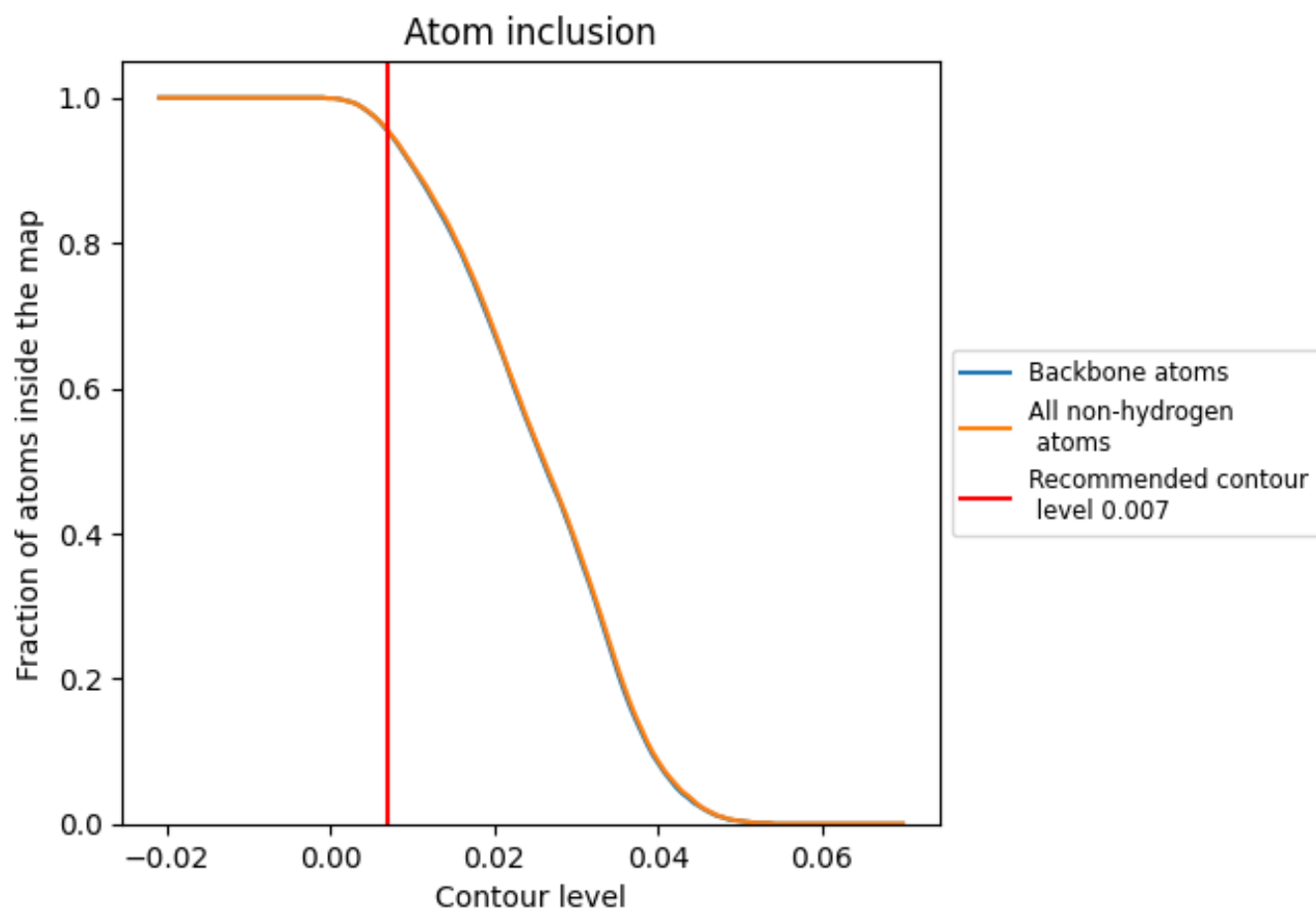
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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