



wwPDB EM Validation Summary Report ⓘ

Nov 6, 2022 – 12:10 PM EST

PDB ID : 7TUT
EMDB ID : EMD-26133
Title : Structure of the rabbit 80S ribosome stalled on a 4-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 : 2022-02-03
Resolution : 3.88 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

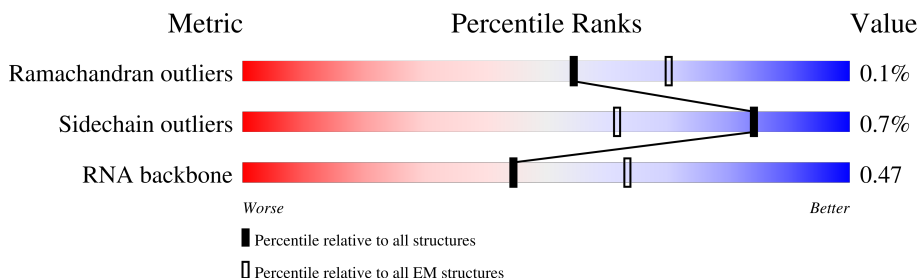
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 3.88 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.



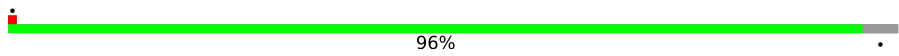
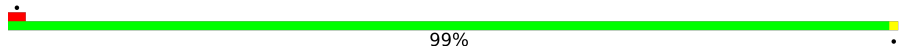

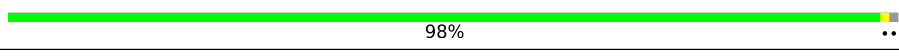
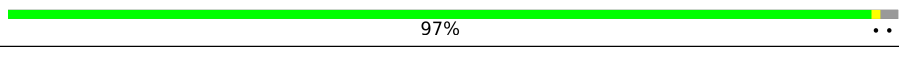

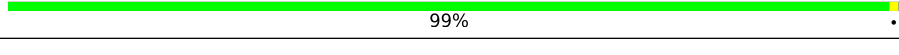

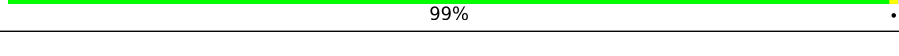
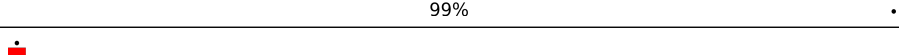
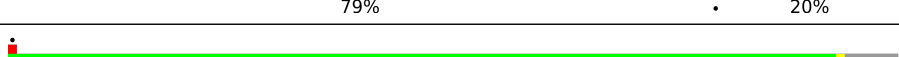
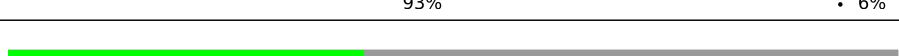

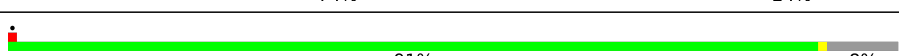
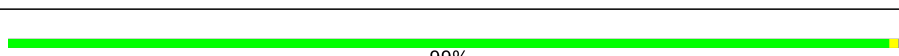
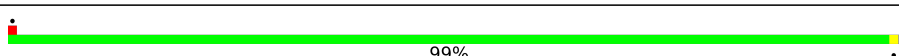
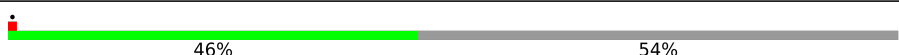


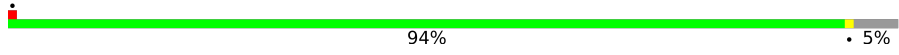
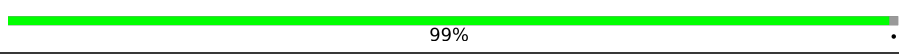
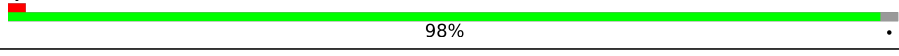
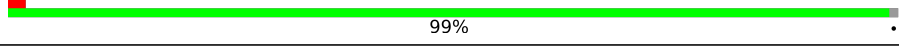
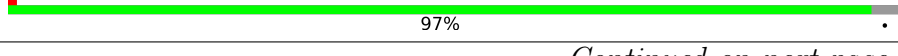

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	
2	C	413	
3	D	297	
4	E	291	
5	F	247	
6	G	319	
7	H	192	
8	I	214	


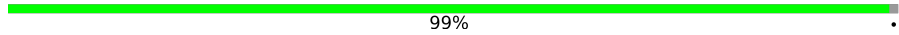
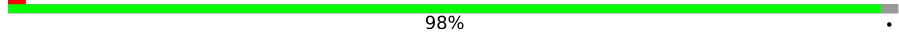
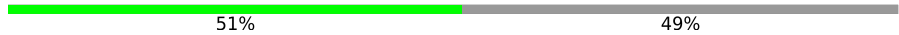
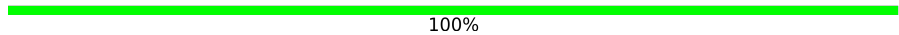
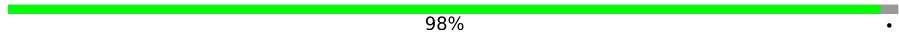
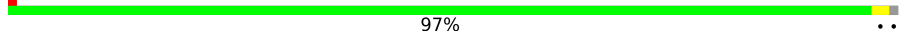




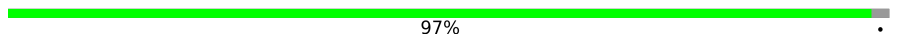

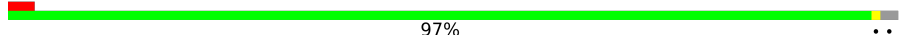

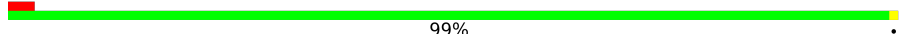



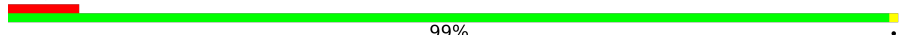
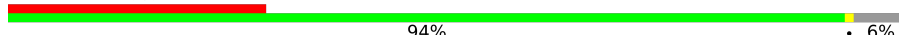


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Mol	Chain	Length	Quality of chain
9	J	178	 96%
10	L	211	 99%
11	M	218	 63% 37%
12	N	204	 98%
13	O	203	 97%
14	P	184	 82% 17%
15	Q	188	 99%
16	R	196	 79% 21%
17	S	176	 99%
18	T	160	 99%
19	U	128	 79% 20%
20	V	140	 93% 6%
21	W	157	 40% 60%
22	X	156	 74% 24%
23	Y	145	 91% 8%
24	Z	136	 99%
25	a	148	 99%
26	b	226	 46% 54%
27	c	115	 84% 15%
28	d	125	 84% 14%
29	e	135	 94% 5%
30	f	110	 99%
31	g	116	 98%
32	h	123	 99%
33	i	105	 97%

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Mol	Chain	Length	Quality of chain
34	j	97	 87% 11%
35	k	70	 99%
36	l	51	 98%
37	m	102	 51% 49%
38	n	25	 100%
39	o	106	 98%
40	p	92	 97%
41	q	77	 78% 19%
42	r	137	 91% 9%
43	u	120	 88% 12%
44	v	156	 76% 24%
45	w	403	 97%
46	B	273	 25% 74%
47	1	476	 97%
48	2	96	 30% 70%
49	3	68	 99%
50	4	483	 5% 70% 29%
51	5	106	 8% 85% 15%
52	7	563	 80% 93% 7%
53	6	224	 8% 99%
54	8	188	 29% 94% 6%
55	K	3543	 76% 24%
56	9	129	 26% 82% 16%

2 Entry composition i

There are 58 unique types of molecules in this entry. The entry contains 267107 atoms, of which 114508 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 uL4.

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

- Molecule 3 is a protein called uL18.

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

- Molecule 4 is a protein called eL6.

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

- Molecule 5 is a protein called uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
5	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

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Chain	Residue	Modelled	Actual	Comment	Reference
F	153	ILE	VAL	conflict	UNP G1TUB1

- Molecule 6 is a protein called eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
6	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 7 is a protein called uL6.

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

- Molecule 8 is a protein called uL16.

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

- Molecule 9 is a protein called uL5.

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

- Molecule 10 is a protein called eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
10	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 11 is a protein called eL14.

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

- Molecule 12 is a protein called eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
12	N	202	3441	1069	1745	358	265	4	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	2	GLY	ALA	conflict	UNP G1T0C1

- Molecule 13 is a protein called uL13.

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

- Molecule 14 is a protein called uL22.

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

- Molecule 15 is a protein called eL18.

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

- Molecule 16 is a protein called eL19.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
16	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 17 is a protein called eL20.

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

- Molecule 18 is a protein called eL21.

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

- Molecule 19 is a protein called eL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
19	U	102	1690	534	856	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

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Chain	Residue	Modelled	Actual	Comment	Reference
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 20 is a protein called uL14.

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

- Molecule 21 is a protein called eL24.

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

- Molecule 22 is a protein called eL23.

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

- Molecule 23 is a protein called uL24.

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

- Molecule 24 is a protein called eL27.

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

- Molecule 25 is a protein called uL15.

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

- Molecule 26 is a protein called eL29.

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

- Molecule 27 is a protein called eL30.

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

- Molecule 28 is a protein called eL31.

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

- Molecule 29 is a protein called eL32.

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

- Molecule 30 is a protein called eL33.

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

- Molecule 31 is a protein called eL34.

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

- Molecule 32 is a protein called eL35.

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

- Molecule 33 is a protein called eL36.

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

- Molecule 34 is a protein called eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
34	j	86	1443	434	738	155	111	5	0	0

- Molecule 35 is a protein called eL38.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
35	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 36 is a protein called eL39.

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

- Molecule 37 is a protein called eL40.

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

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
m	1	MET	-	initiating methionine	UNP A0A2K5PSA0

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Chain	Residue	Modelled	Actual	Comment	Reference
m	2	GLY	-	expression tag	UNP A0A2K5PSA0
m	3	ASP	-	expression tag	UNP A0A2K5PSA0
m	4	PRO	-	expression tag	UNP A0A2K5PSA0
m	5	GLU	-	expression tag	UNP A0A2K5PSA0
m	6	SER	-	expression tag	UNP A0A2K5PSA0
m	7	GLY	-	expression tag	UNP A0A2K5PSA0
m	8	GLY	-	expression tag	UNP A0A2K5PSA0
m	9	CYS	-	expression tag	UNP A0A2K5PSA0

- Molecule 38 is a protein called eL41.

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

- Molecule 39 is a protein called eL42.

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

- Molecule 40 is a protein called eL43.

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

- Molecule 41 is a RNA chain called P-site tRNA.

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

- Molecule 42 is a protein called eL28.

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

- Molecule 43 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			P
43	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 44 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 45 is a protein called uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
45	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 46 is a protein called Nascent chain.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
46	B	70	1054	349	528	84	87	6	0	0

- 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	5595	1738	2817	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 protein called Calcium load-activated calcium channel.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
54	8	177	2884	900	1478	242	252	12	0	0

- Molecule 55 is a RNA chain called 28S ribosomal RNA.

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

- Molecule 56 is a protein called Obligate partner of TMCO1 insertase.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
56	9	109	1784	610	881	134	156	3	0	0

- Molecule 57 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	C	1	Total	Mg	0
			1	1	
57	D	1	Total	Mg	0
			1	1	
57	I	2	Total	Mg	0
			2	2	
57	J	1	Total	Mg	0
			1	1	
57	P	1	Total	Mg	0
			1	1	
57	V	1	Total	Mg	0
			1	1	
57	a	1	Total	Mg	0
			1	1	
57	u	4	Total	Mg	0
			4	4	
57	v	6	Total	Mg	0
			6	6	
57	K	202	Total	Mg	0
			202	202	

- Molecule 58 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
58	g	1	Total	Zn	0
			1	1	
58	j	1	Total	Zn	0
			1	1	
58	m	1	Total	Zn	0
			1	1	

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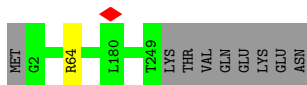
Mol	Chain	Residues	Atoms		AltConf
58	o	1	Total 1	Zn 1	0
58	p	1	Total 1	Zn 1	0

3 Residue-property plots [i](#)

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.

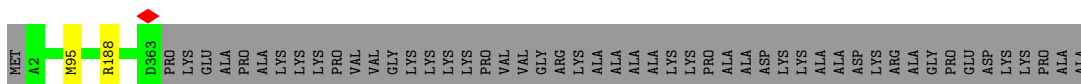
- Molecule 1: uL2

Chain A:  96%



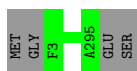
- Molecule 2: uL4

Chain C:  87%




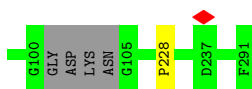
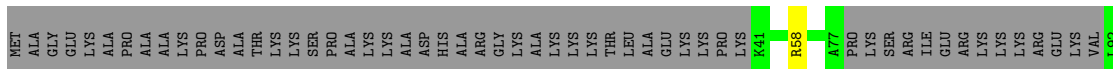
- Molecule 3: uL18

Chain D:  99%




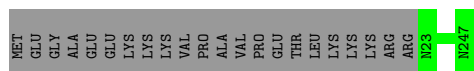
- Molecule 4: eL6

Chain E:  79%

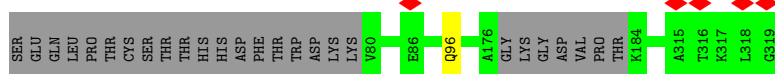
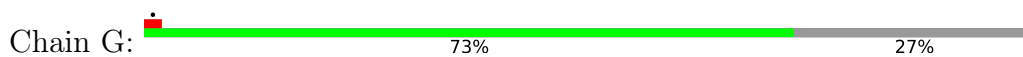


- Molecule 5: uL30

Chain F:  91%



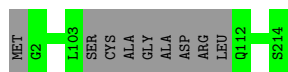
• Molecule 6: eL8



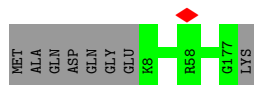
• Molecule 7: uL6



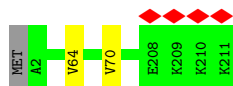
• Molecule 8: uL16



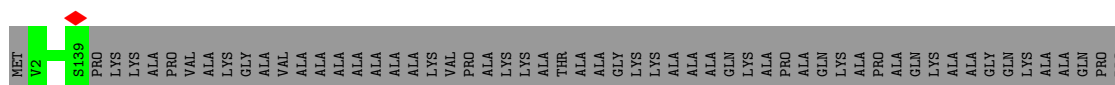
• Molecule 9: uL5



• Molecule 10: eL13



• Molecule 11: eL14



LYS
ALA
GLN
LYS
GLY
GLN
LYS
PRO
ALA
GLN
LYS
ALA
PRO
ALA
LYS
SER
GLY
LYS
LYS
ALA

• Molecule 12: eL15



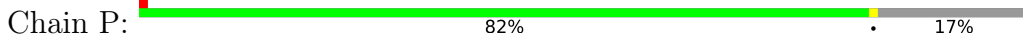
MET
GLY
G2
R26
P76
T80
R204

• Molecule 13: uL13



MET
ALA
GLU
GLY
Q5
Q173
Q180
V203

• Molecule 14: uL22



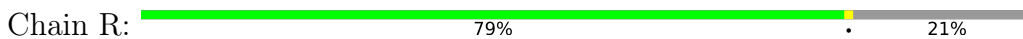
MET
V2
N97
Q118
E154
GLN
ILE
VAL
PRO
LYS
PRO
GLU
GLU
VAL
ALA
GLN
LYS
LYS
ILE
SER
GLN
LYS
LYS
LEU
LYS
GLN
LYS
LEU
MET
ALA
ARG
GLU

• Molecule 15: eL18



G2
M8
N188
UNK

• Molecule 16: eL19



MET
G2
R71
A156
ASP
GLN
ALA
GLU
ALA
ARG
ARG
SER
LYS
THR
LYS
GLU
ALA
ARG
LYS
ARG
ARG
GLU
GLU
LEU
GLN
ALA
LYS
GLU
GLU
ILE
ILE
LYS
THR
LEU
SER
LYS
GLU
GLU
THR
LYS
LYS

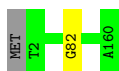
• Molecule 17: eL20



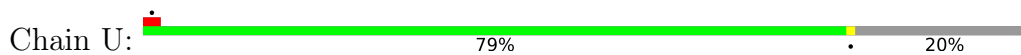
M1
V67
T90
F176

• Molecule 18: eL21

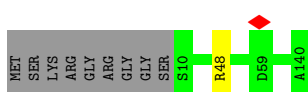




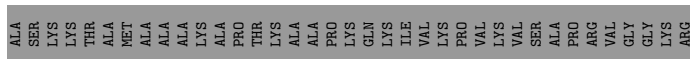
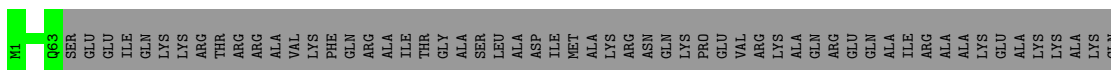
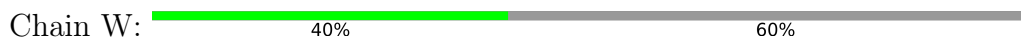
• Molecule 19: eL22



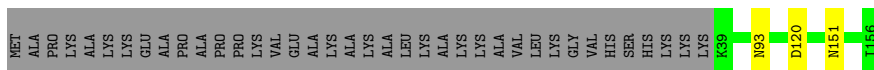
• Molecule 20: uL14



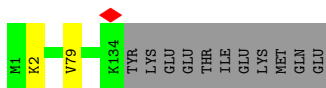
• Molecule 21: eL24



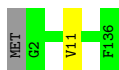
• Molecule 22: eL23



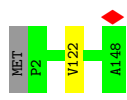
• Molecule 23: uL24



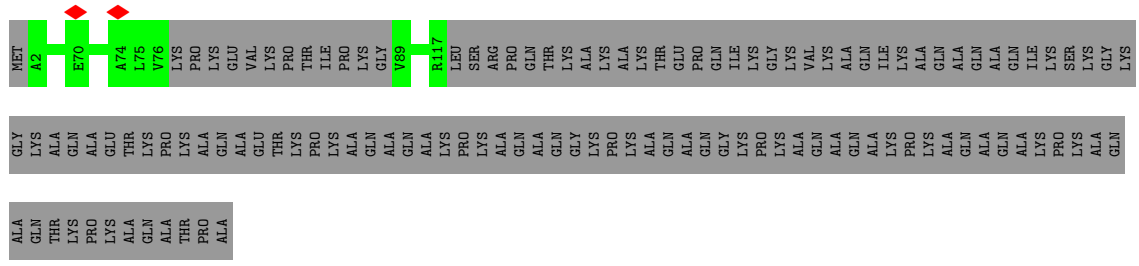
• Molecule 24: eL27



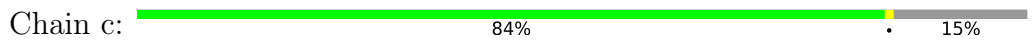
• Molecule 25: uL15



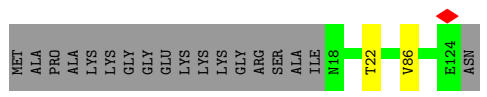
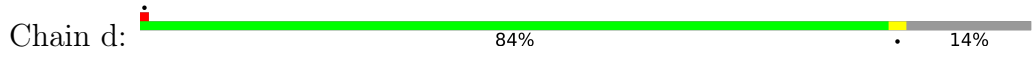
• Molecule 26: eL29



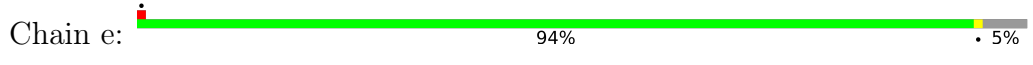
• Molecule 27: eL30



• Molecule 28: eL31



• Molecule 29: eL32

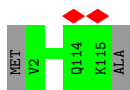


• Molecule 30: eL33



• Molecule 31: eL34

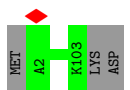




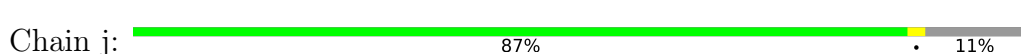
• Molecule 32: eL35



• Molecule 33: eL36



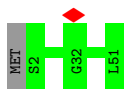
• Molecule 34: eL37



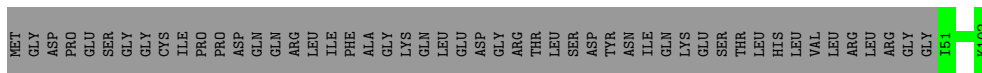
• Molecule 35: eL38



• Molecule 36: eL39



• Molecule 37: eL40



• Molecule 38: eL41



There are no outlier residues recorded for this chain.

- Molecule 39: eL42

Chain o:  98%




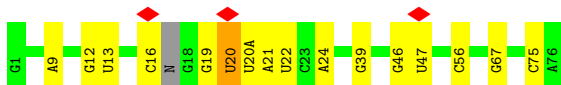
- Molecule 40: eL43

Chain p:  97%



- Molecule 41: P-site tRNA

Chain q:  78% 19%




- Molecule 42: eL28

Chain r:  91% 9%




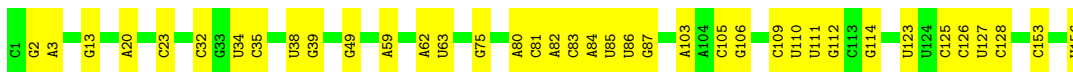
- Molecule 43: 5S ribosomal RNA

Chain u:  88% 12%



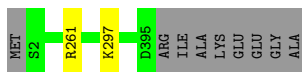
- Molecule 44: 5.8S ribosomal RNA

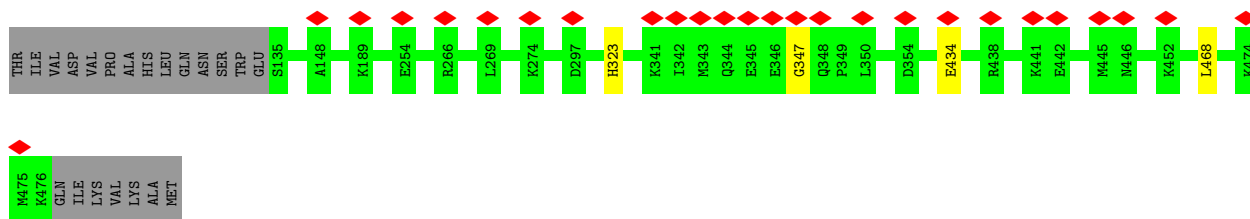
Chain v:  76% 24%



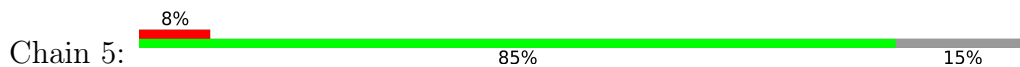
- Molecule 45: uL3

Chain w:  97%

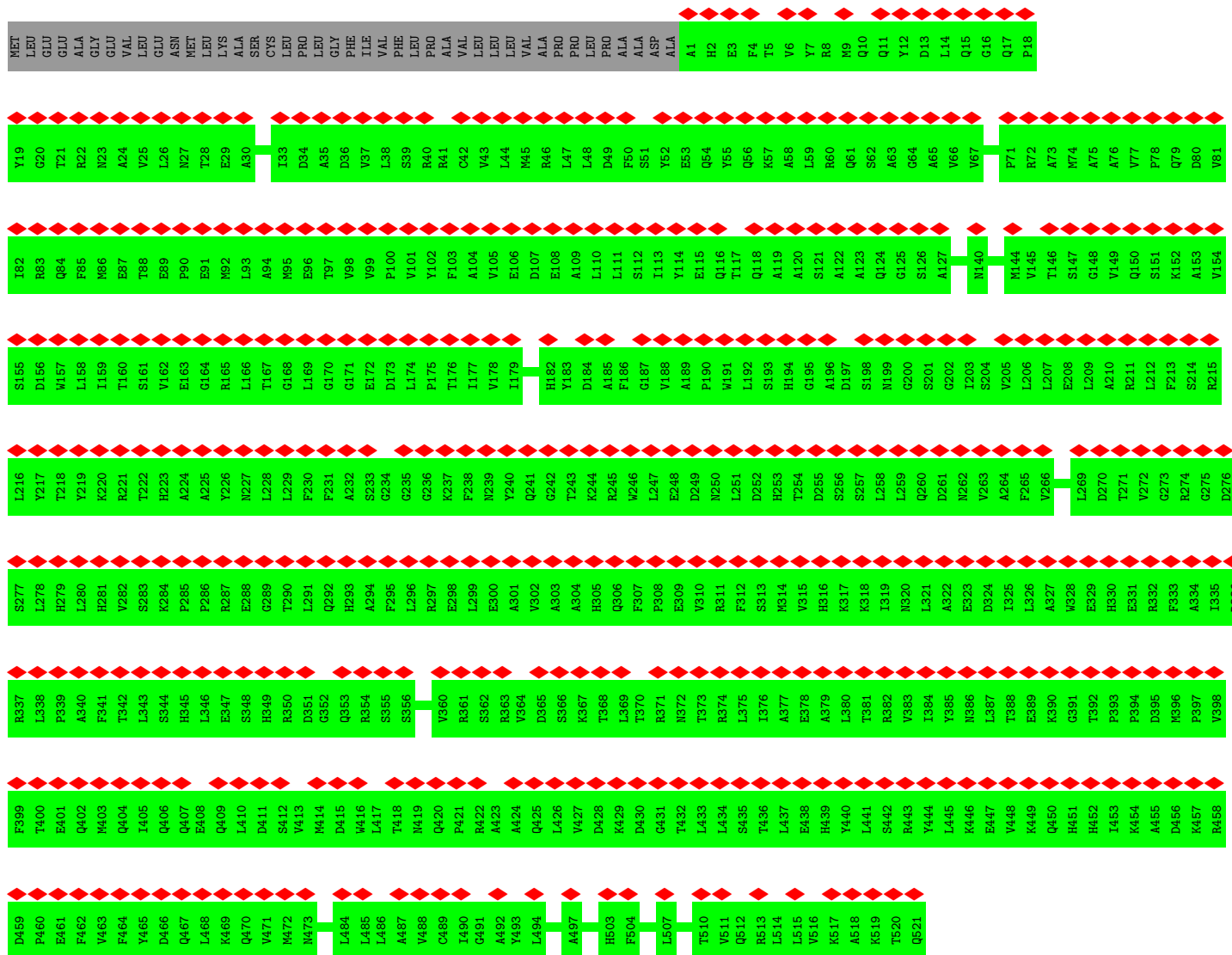
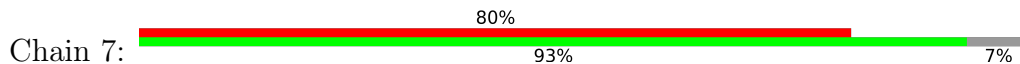




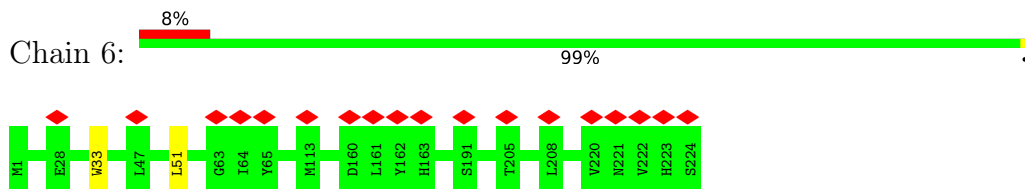
• Molecule 51: PAT complex subunit Asterix



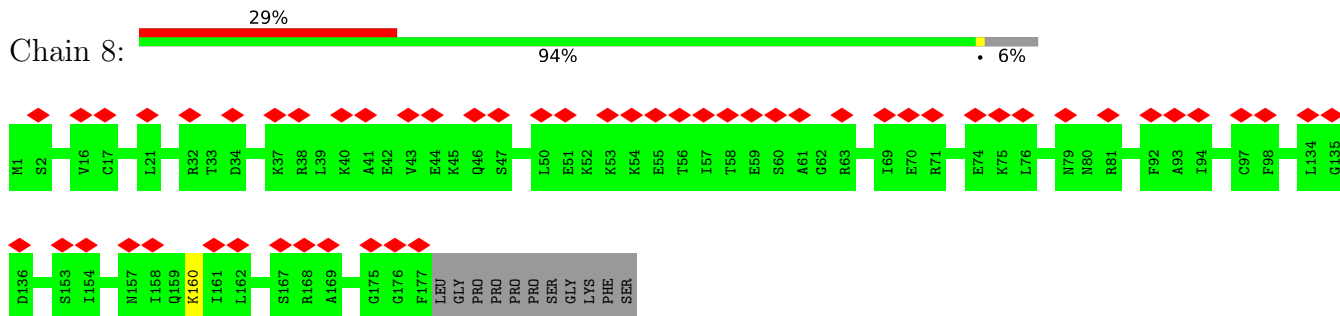
• Molecule 52: Nicalin



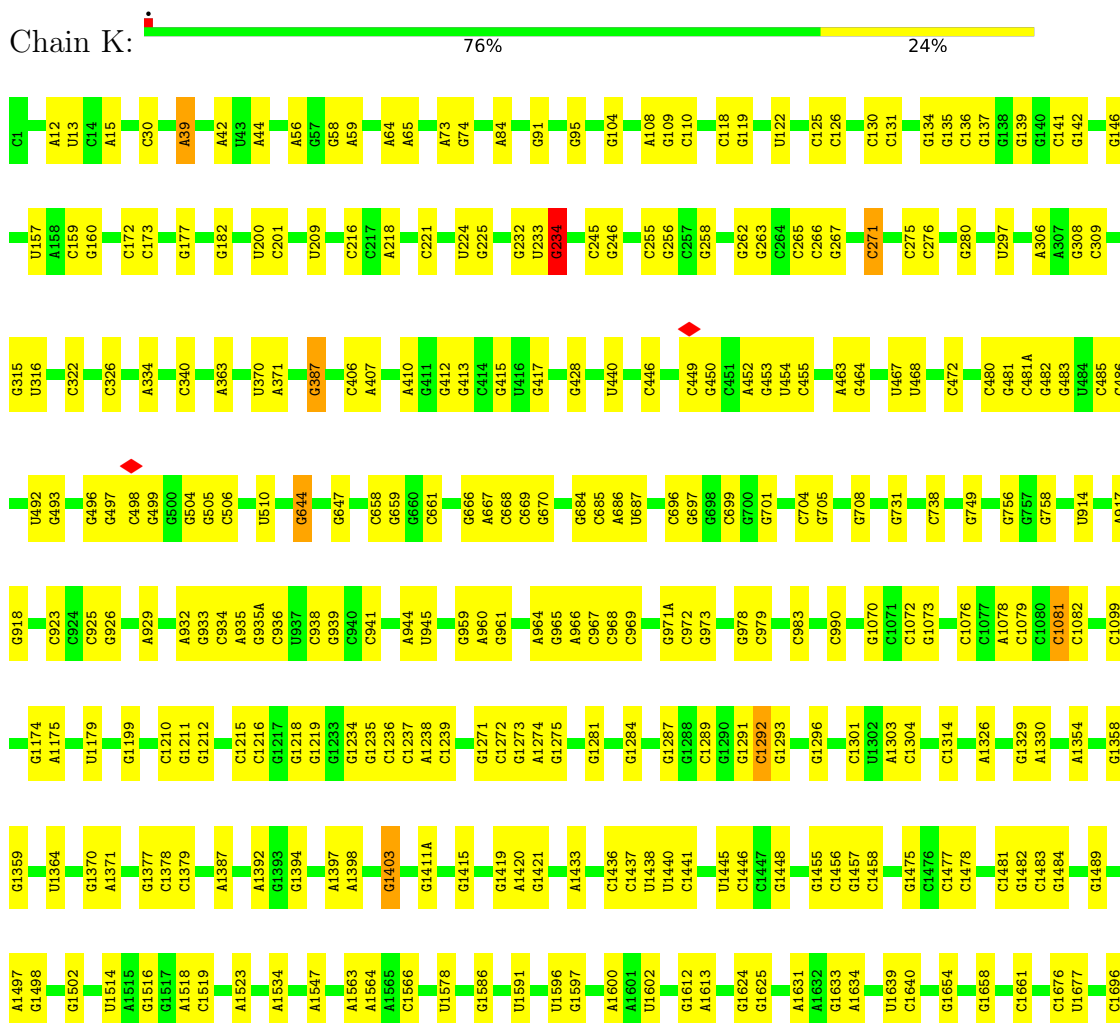
• Molecule 53: Transmembrane protein 147

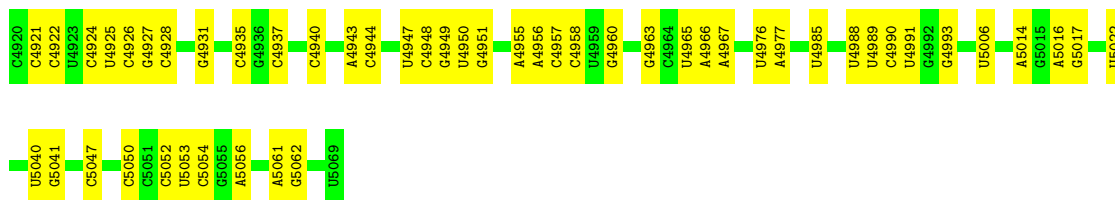


• Molecule 54: Calcium load-activated calcium channel

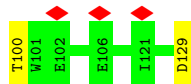
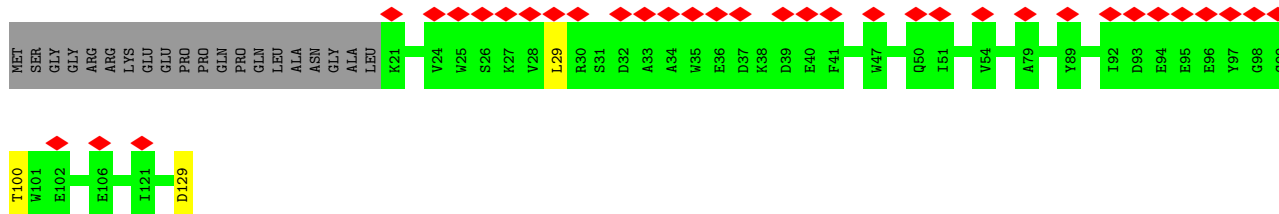
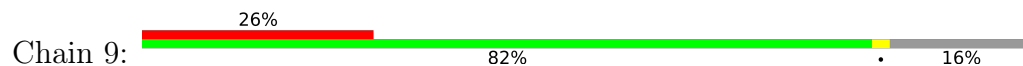


• Molecule 55: 28S ribosomal RNA





- Molecule 56: Obligate partner of TMCO1 insertase



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	136812	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	3.210	Depositor
Minimum map value	-1.145	Depositor
Average map value	0.019	Depositor
Map value standard deviation	0.183	Depositor
Recommended contour level	0.5	Depositor
Map size (\AA)	552.08, 552.08, 552.08	wwPDB
Map dimensions	412, 412, 412	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.34, 1.34, 1.34	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.25	0/1936	0.57	0/2596
2	C	0.25	0/2937	0.57	0/3946
3	D	0.26	0/2437	0.53	0/3264
4	E	0.26	0/1914	0.55	0/2566
5	F	0.25	0/1911	0.53	0/2549
6	G	0.25	0/1910	0.55	0/2569
7	H	0.25	0/1535	0.55	0/2063
8	I	0.25	0/1702	0.55	0/2272
9	J	0.26	0/1385	0.55	0/1852
10	L	0.25	0/1733	0.60	0/2316
11	M	0.26	0/1158	0.56	0/1547
12	N	0.25	0/1741	0.60	0/2331
13	O	0.26	0/1662	0.55	0/2222
14	P	0.27	0/1268	0.55	0/1700
15	Q	0.25	0/1538	0.61	0/2054
16	R	0.24	0/1310	0.60	0/1734
17	S	0.26	0/1501	0.58	0/2012
18	T	0.25	0/1326	0.53	0/1770
19	U	0.26	0/848	0.51	0/1138
20	V	0.26	0/993	0.53	0/1332
21	W	0.26	0/541	0.53	0/720
22	X	0.26	0/984	0.54	0/1323
23	Y	0.25	0/1132	0.57	0/1504
24	Z	0.26	0/1130	0.54	0/1507
25	a	0.25	0/1191	0.55	0/1590
26	b	0.24	0/861	0.56	0/1138
27	c	0.26	0/771	0.49	0/1034
28	d	0.25	0/903	0.58	0/1216
29	e	0.24	0/1071	0.56	0/1429
30	f	0.27	0/895	0.58	0/1198
31	g	0.25	0/916	0.60	0/1220
32	h	0.25	0/1017	0.55	0/1344

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.25	0/841	0.58	0/1112
34	j	0.24	0/720	0.61	0/952
35	k	0.25	0/575	0.54	0/761
36	l	0.24	0/459	0.65	0/608
37	m	0.24	0/435	0.55	0/575
38	n	0.26	0/240	0.73	0/305
39	o	0.26	0/864	0.55	0/1140
40	p	0.25	0/718	0.54	0/953
41	q	0.24	0/1805	0.86	1/2809 (0.0%)
42	r	0.25	0/1010	0.59	0/1354
43	u	0.25	0/2858	0.80	0/4455
44	v	0.26	0/3701	0.82	1/5766 (0.0%)
45	w	0.25	0/3240	0.51	0/4339
46	B	0.28	0/541	0.59	0/738
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	0.25	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	8	0.25	0/1426	0.46	0/1908
55	K	0.29	0/84979	0.87	44/132532 (0.0%)
56	9	0.24	0/932	0.43	0/1268
All	All	0.27	0/163576	0.76	46/239659 (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
55	K	0	1

There are no bond length outliers.

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	K	234	G	C8-N9-C4	-10.19	102.32	106.40
44	v	39	G	O4'-C1'-N9	8.19	114.75	108.20
55	K	271	C	C2-N1-C1'	7.38	126.92	118.80
55	K	1219	G	N3-C4-N9	-7.09	121.75	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	K	139	G	N3-C4-N9	-6.82	121.91	126.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
55	K	234	G	Sidechain

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%)	220 (89%)	26 (11%)	0	100	100
2	C	360/413 (87%)	336 (93%)	24 (7%)	0	100	100
3	D	291/297 (98%)	270 (93%)	21 (7%)	0	100	100
4	E	227/291 (78%)	218 (96%)	8 (4%)	1 (0%)	34	71
5	F	223/247 (90%)	208 (93%)	15 (7%)	0	100	100
6	G	229/319 (72%)	214 (93%)	15 (7%)	0	100	100
7	H	188/192 (98%)	176 (94%)	12 (6%)	0	100	100
8	I	201/214 (94%)	182 (90%)	19 (10%)	0	100	100
9	J	168/178 (94%)	158 (94%)	10 (6%)	0	100	100
10	L	208/211 (99%)	194 (93%)	13 (6%)	1 (0%)	29	67
11	M	136/218 (62%)	126 (93%)	10 (7%)	0	100	100
12	N	200/204 (98%)	185 (92%)	14 (7%)	1 (0%)	29	67

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	O	197/203 (97%)	187 (95%)	10 (5%)	0	100	100
14	P	151/184 (82%)	143 (95%)	8 (5%)	0	100	100
15	Q	185/188 (98%)	171 (92%)	14 (8%)	0	100	100
16	R	153/196 (78%)	144 (94%)	9 (6%)	0	100	100
17	S	174/176 (99%)	160 (92%)	14 (8%)	0	100	100
18	T	157/160 (98%)	139 (88%)	17 (11%)	1 (1%)	25	63
19	U	100/128 (78%)	90 (90%)	10 (10%)	0	100	100
20	V	129/140 (92%)	121 (94%)	8 (6%)	0	100	100
21	W	61/157 (39%)	55 (90%)	6 (10%)	0	100	100
22	X	116/156 (74%)	106 (91%)	10 (9%)	0	100	100
23	Y	132/145 (91%)	125 (95%)	7 (5%)	0	100	100
24	Z	133/136 (98%)	122 (92%)	11 (8%)	0	100	100
25	a	145/148 (98%)	132 (91%)	13 (9%)	0	100	100
26	b	100/226 (44%)	95 (95%)	5 (5%)	0	100	100
27	c	96/115 (84%)	92 (96%)	4 (4%)	0	100	100
28	d	105/125 (84%)	94 (90%)	11 (10%)	0	100	100
29	e	126/135 (93%)	118 (94%)	8 (6%)	0	100	100
30	f	107/110 (97%)	101 (94%)	6 (6%)	0	100	100
31	g	112/116 (97%)	106 (95%)	6 (5%)	0	100	100
32	h	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
33	i	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
34	j	84/97 (87%)	81 (96%)	3 (4%)	0	100	100
35	k	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
36	l	48/51 (94%)	39 (81%)	9 (19%)	0	100	100
37	m	50/102 (49%)	47 (94%)	3 (6%)	0	100	100
38	n	23/25 (92%)	23 (100%)	0	0	100	100
39	o	102/106 (96%)	93 (91%)	9 (9%)	0	100	100
40	p	89/92 (97%)	81 (91%)	8 (9%)	0	100	100
42	r	122/137 (89%)	112 (92%)	10 (8%)	0	100	100
45	w	392/403 (97%)	361 (92%)	31 (8%)	0	100	100
46	B	68/273 (25%)	56 (82%)	11 (16%)	1 (2%)	10	45

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	336 (99%)	3 (1%)	1 (0%)	41	75
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
54	8	175/188 (93%)	174 (99%)	1 (1%)	0	100	100
56	9	107/129 (83%)	101 (94%)	6 (6%)	0	100	100
All	All	8428/9902 (85%)	7941 (94%)	481 (6%)	6 (0%)	54	84

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
12	N	76	PRO
10	L	64	VAL
50	4	347	GLY
18	T	82	GLY
46	B	242	PRO

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	C	302/337 (90%)	300 (99%)	2 (1%)	84	90
3	D	247/250 (99%)	247 (100%)	0	100	100
4	E	206/251 (82%)	205 (100%)	1 (0%)	88	93
5	F	196/215 (91%)	196 (100%)	0	100	100
6	G	200/272 (74%)	199 (100%)	1 (0%)	88	93
7	H	169/171 (99%)	169 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	I	175/181 (97%)	175 (100%)	0	100	100
9	J	143/149 (96%)	143 (100%)	0	100	100
10	L	175/176 (99%)	174 (99%)	1 (1%)	86	91
11	M	117/161 (73%)	117 (100%)	0	100	100
12	N	171/172 (99%)	169 (99%)	2 (1%)	71	83
13	O	171/173 (99%)	169 (99%)	2 (1%)	71	83
14	P	134/163 (82%)	132 (98%)	2 (2%)	65	80
15	Q	164/164 (100%)	163 (99%)	1 (1%)	86	91
16	R	138/175 (79%)	137 (99%)	1 (1%)	84	90
17	S	157/157 (100%)	155 (99%)	2 (1%)	69	81
18	T	139/140 (99%)	139 (100%)	0	100	100
19	U	92/114 (81%)	91 (99%)	1 (1%)	73	84
20	V	101/107 (94%)	100 (99%)	1 (1%)	76	86
21	W	55/126 (44%)	55 (100%)	0	100	100
22	X	106/134 (79%)	103 (97%)	3 (3%)	43	66
23	Y	124/135 (92%)	122 (98%)	2 (2%)	62	79
24	Z	117/118 (99%)	116 (99%)	1 (1%)	78	87
25	a	119/120 (99%)	118 (99%)	1 (1%)	81	89
26	b	84/172 (49%)	84 (100%)	0	100	100
27	c	84/98 (86%)	83 (99%)	1 (1%)	71	83
28	d	98/110 (89%)	96 (98%)	2 (2%)	55	74
29	e	114/121 (94%)	113 (99%)	1 (1%)	78	87
30	f	88/89 (99%)	88 (100%)	0	100	100
31	g	98/99 (99%)	98 (100%)	0	100	100
32	h	108/110 (98%)	108 (100%)	0	100	100
33	i	86/89 (97%)	86 (100%)	0	100	100
34	j	73/80 (91%)	71 (97%)	2 (3%)	44	67
35	k	64/65 (98%)	64 (100%)	0	100	100
36	l	47/48 (98%)	47 (100%)	0	100	100
37	m	48/90 (53%)	48 (100%)	0	100	100
38	n	24/24 (100%)	24 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
39	o	92/94 (98%)	92 (100%)	0	100	100
40	p	74/75 (99%)	72 (97%)	2 (3%)	44	67
42	r	108/121 (89%)	108 (100%)	0	100	100
45	w	342/348 (98%)	340 (99%)	2 (1%)	86	91
46	B	54/207 (26%)	54 (100%)	0	100	100
47	1	390/398 (98%)	386 (99%)	4 (1%)	76	86
48	2	26/74 (35%)	26 (100%)	0	100	100
49	3	59/59 (100%)	58 (98%)	1 (2%)	60	78
50	4	306/435 (70%)	303 (99%)	3 (1%)	76	86
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
54	8	155/164 (94%)	154 (99%)	1 (1%)	86	91
56	9	93/108 (86%)	90 (97%)	3 (3%)	39	63
All	All	7336/8400 (87%)	7287 (99%)	49 (1%)	84	90

5 of 49 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
29	e	48	ARG
47	1	18	GLU
34	j	67	LEU
40	p	52	VAL
47	1	130	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
7	H	76	HIS
16	R	58	HIS
45	w	322	HIS
47	1	294	GLN
52	7	452	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
41	q	74/77 (96%)	16 (21%)	0
43	u	119/120 (99%)	14 (11%)	0
44	v	155/156 (99%)	37 (23%)	0
55	K	3519/3543 (99%)	818 (23%)	58 (1%)
All	All	3867/3896 (99%)	885 (22%)	58 (1%)

5 of 885 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
41	q	9	A
41	q	12	G
41	q	13	U
41	q	16	C
41	q	19	G

5 of 58 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
55	K	1455	G
55	K	4925	U
55	K	2266	C
55	K	4921	C
55	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
55	K	24

The worst 5 of 24 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	40.45
1	K	1252:C	O3'	1271:G	P	37.04
1	K	1219:G	O3'	1233:G	P	18.73
1	K	3948:C	O3'	4065:G	P	18.66
1	K	4138:C	O3'	4146:G	P	17.71

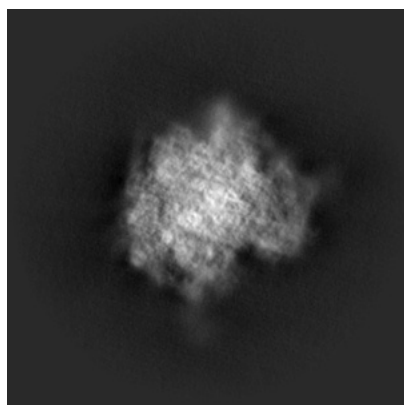
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26133. These allow visual inspection of the internal detail of the map and identification of artifacts.

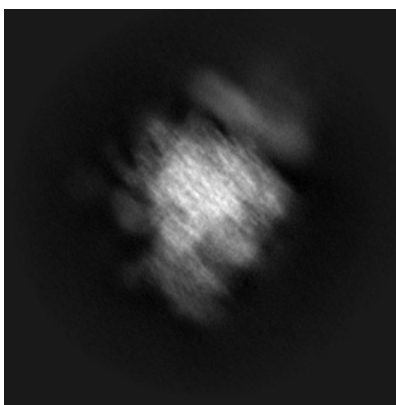
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

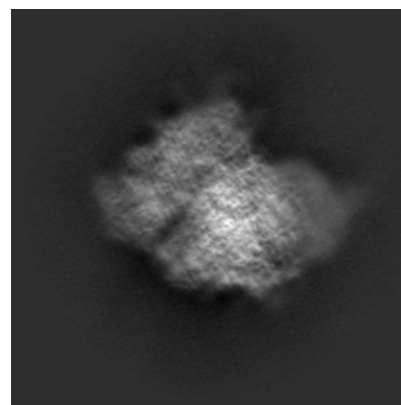
6.1.1 Primary map



X



Y

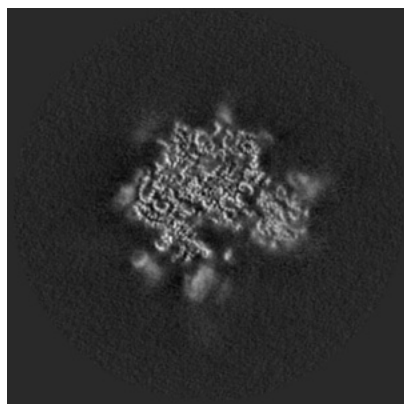


Z

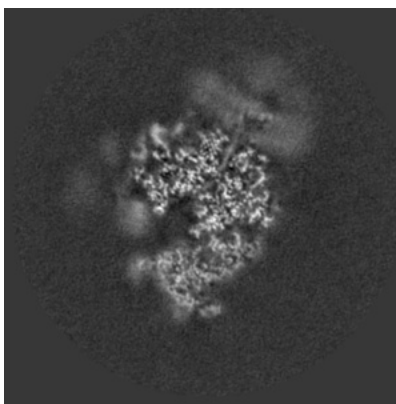
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

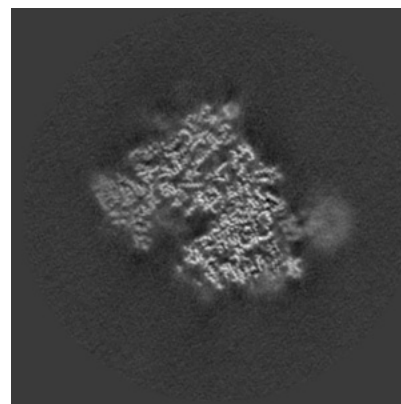
6.2.1 Primary map



X Index: 206



Y Index: 206

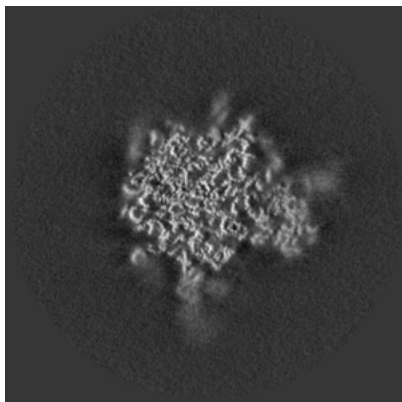


Z Index: 206

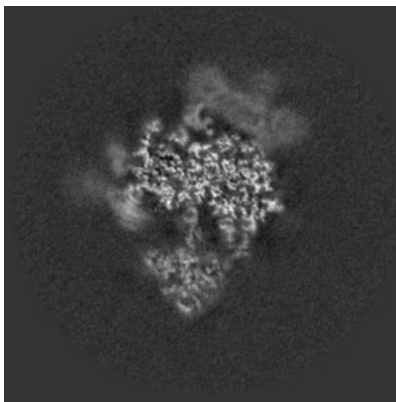
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

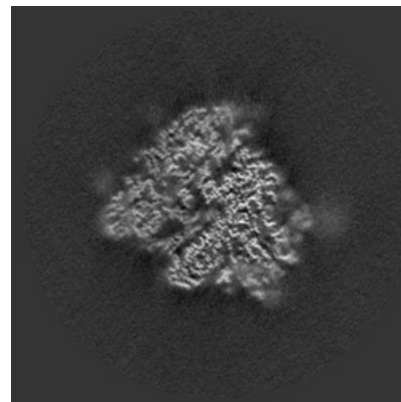
6.3.1 Primary map



X Index: 218



Y Index: 194

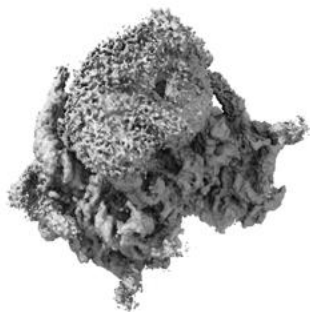


Z Index: 192

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

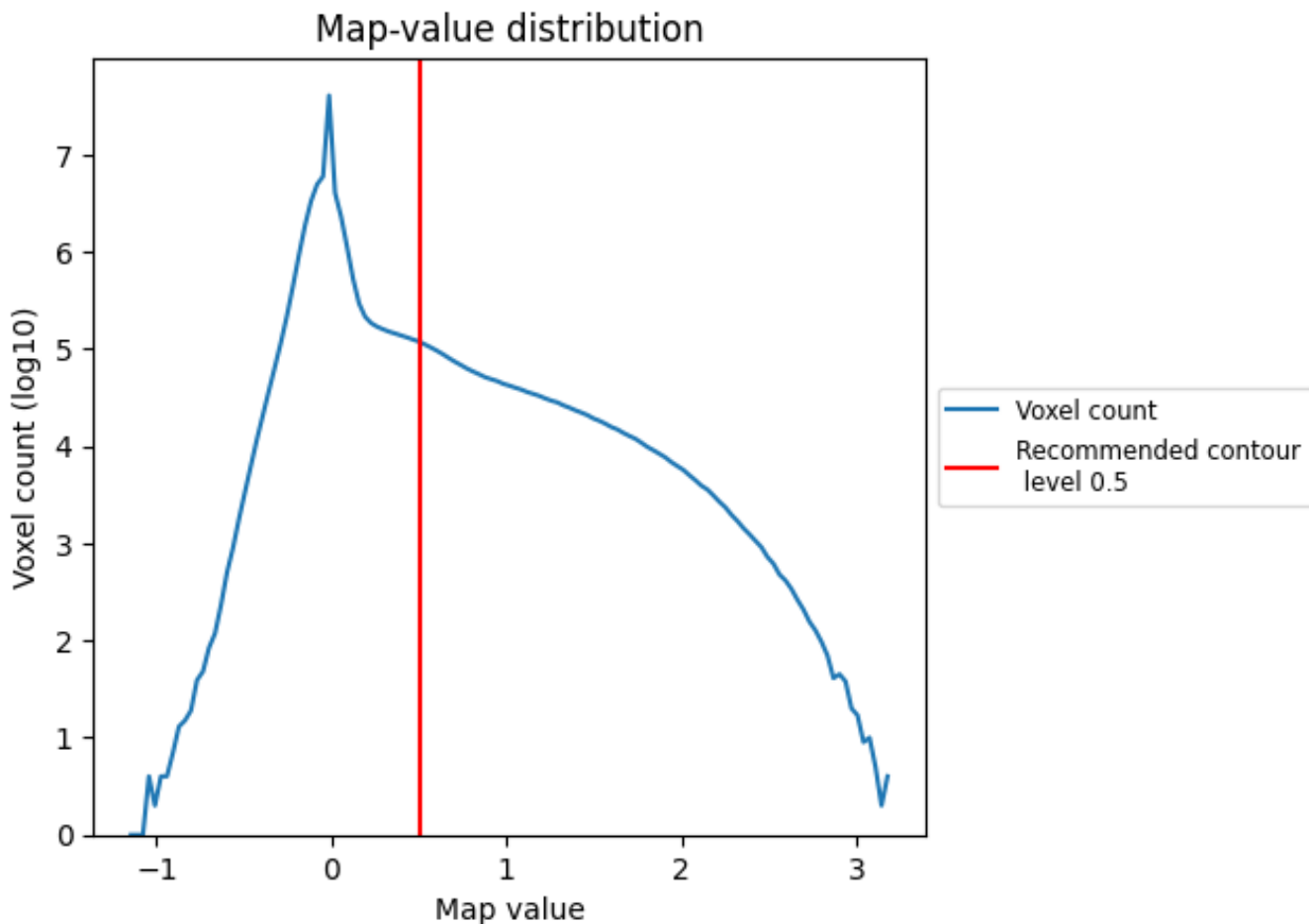
6.5 Mask visualisation

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

7 Map analysis [i](#)

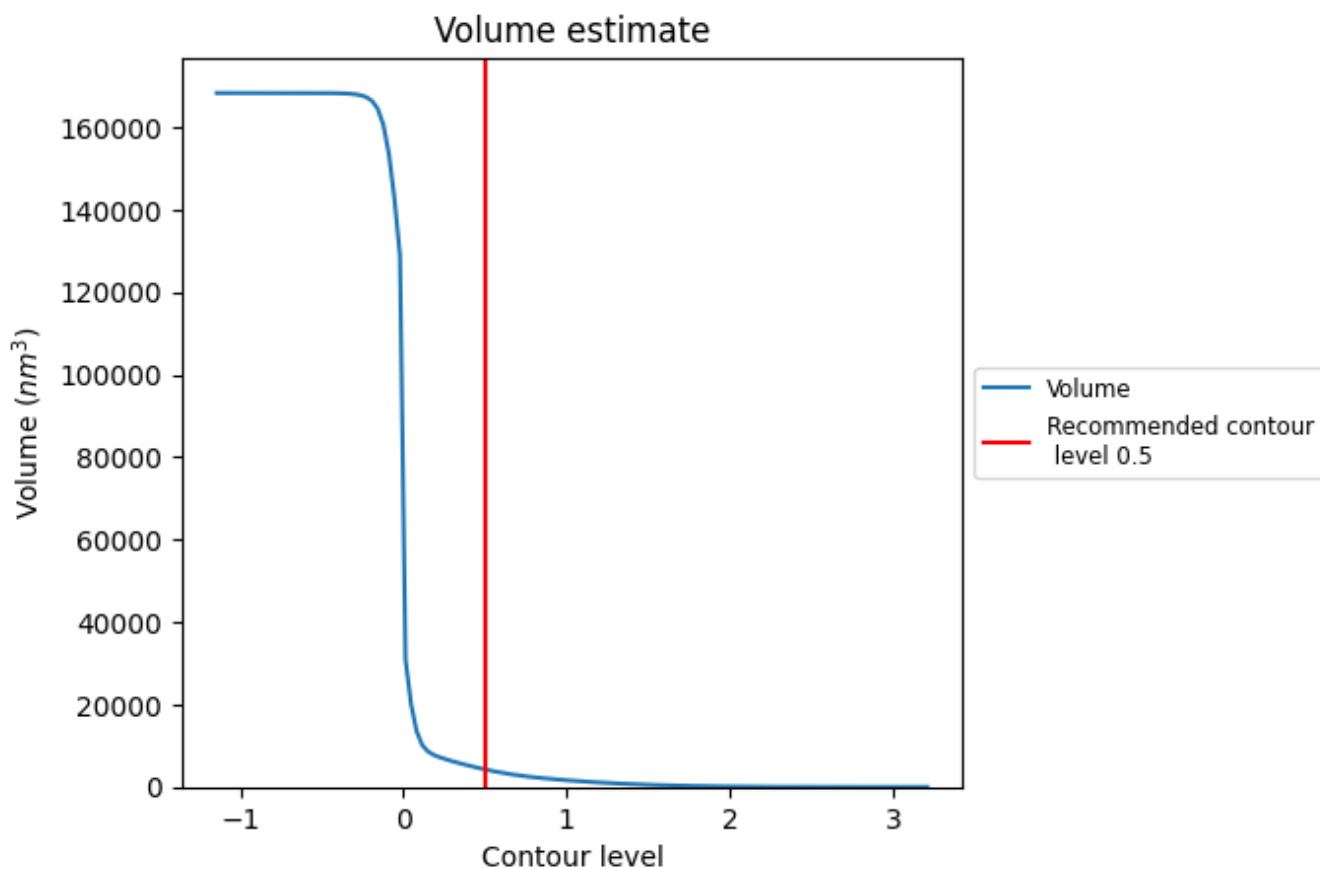
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

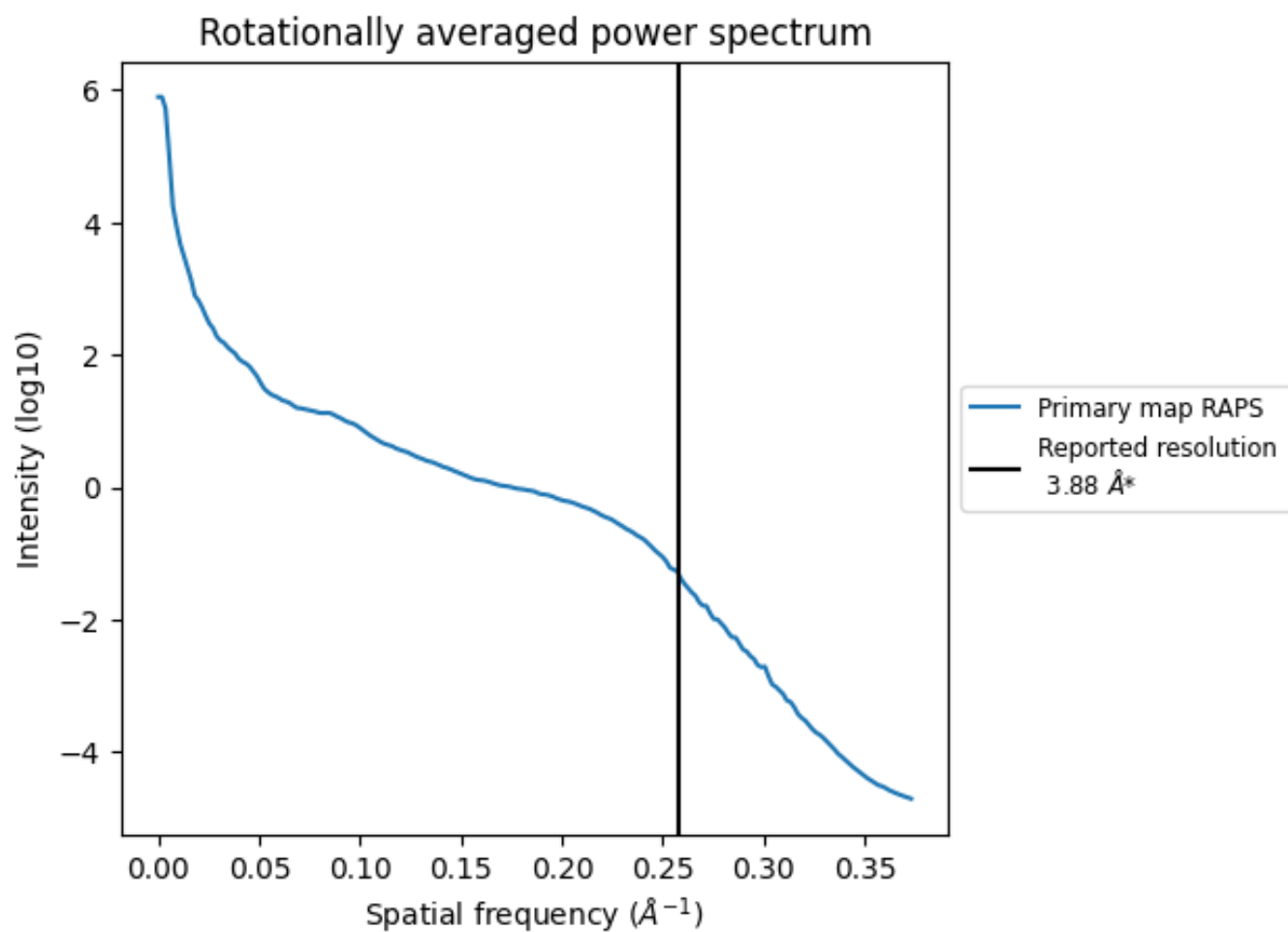
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 4244 nm^3 ; this corresponds to an approximate mass of 3834 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 0.258 Å⁻¹

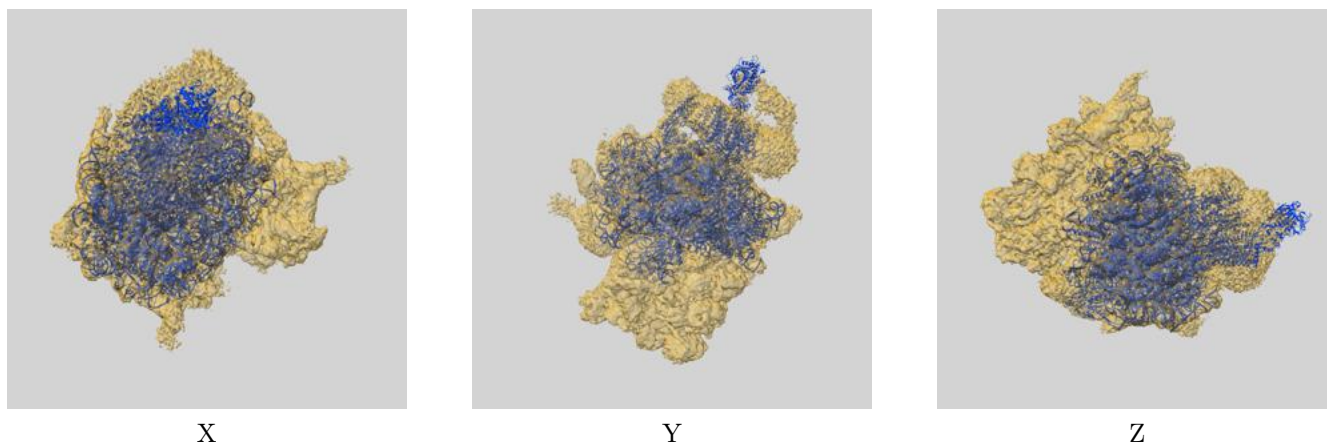
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

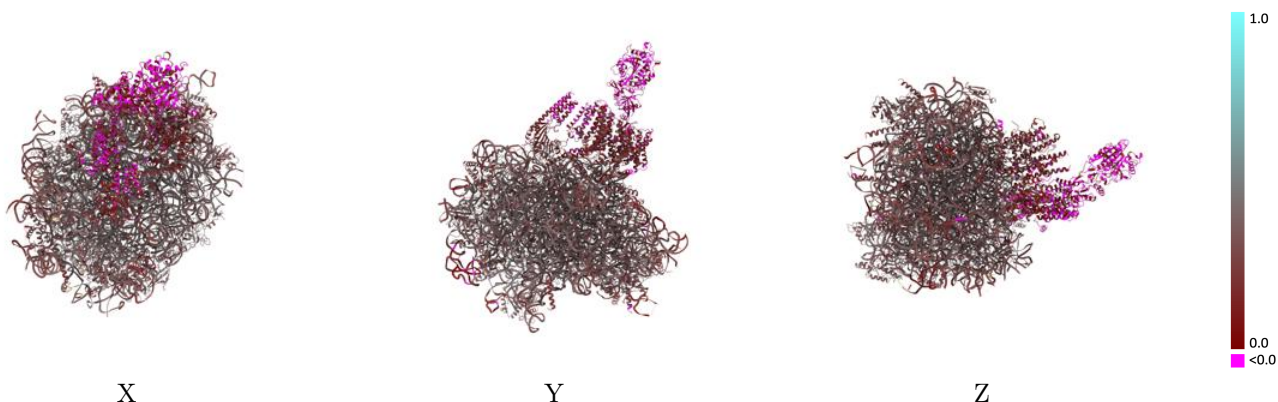
This section contains information regarding the fit between EMDB map EMD-26133 and PDB model 7TUT. Per-residue inclusion information can be found in section 3 on page 17.

9.1 Map-model overlay [i](#)



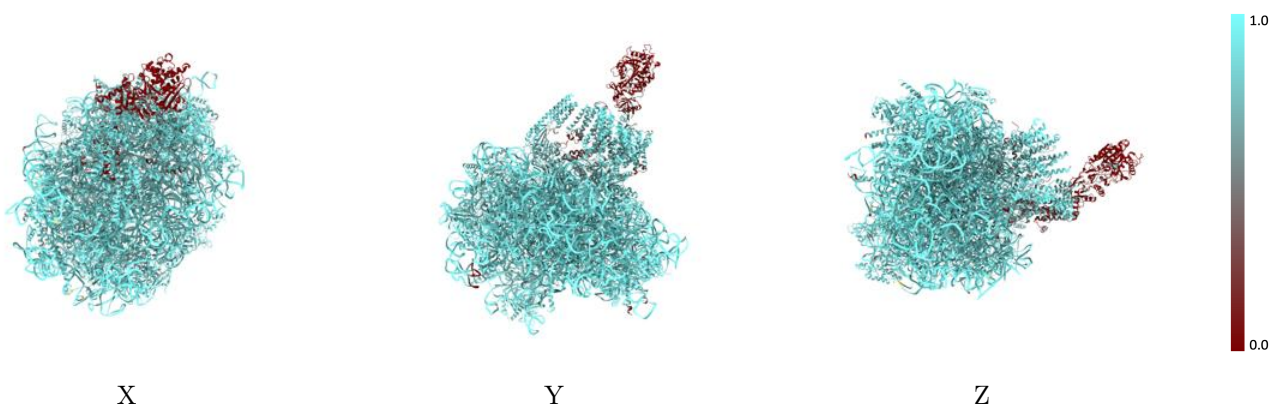
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



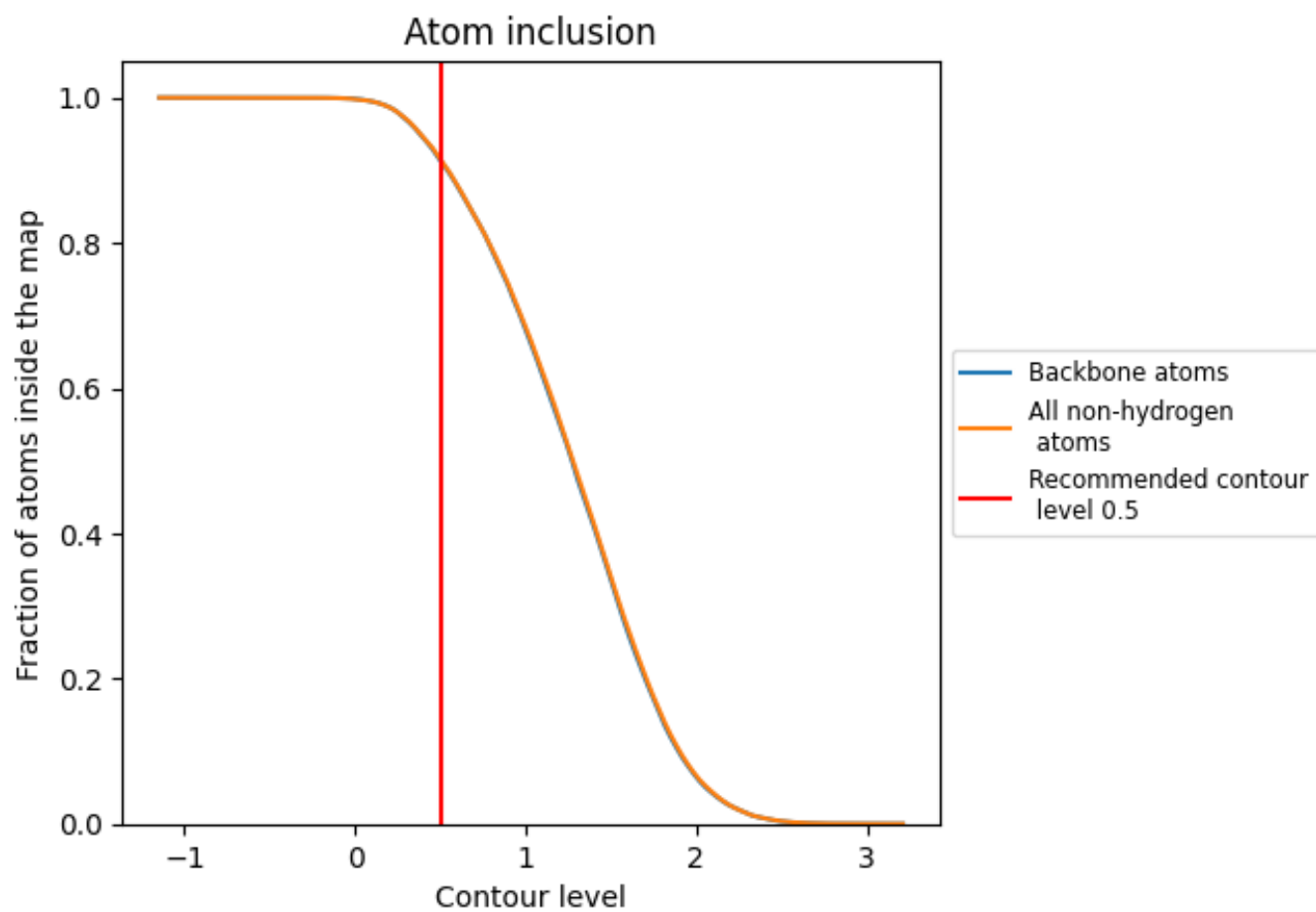
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary













































The table lists the average atom inclusion at the recommended contour level (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9156	 0.3250
1	 0.8125	 0.2120
2	 0.8584	 0.1580
3	 0.7682	 0.1660
4	 0.7566	 0.1820
5	 0.8207	 0.0900
6	 0.8013	 0.1400
7	 0.1386	 0.0200
8	 0.6010	 0.1030
9	 0.6233	 0.0320
A	 0.9221	 0.3700
B	 0.7842	 0.2490
C	 0.9196	 0.3570
D	 0.9379	 0.3220
E	 0.9188	 0.3340
F	 0.9057	 0.3420
G	 0.8756	 0.3020
H	 0.8951	 0.3520
I	 0.9121	 0.3640
J	 0.9138	 0.3220
K	 0.9877	 0.3510
L	 0.8960	 0.3290
M	 0.9090	 0.3450
N	 0.9164	 0.3470
O	 0.8922	 0.3470
P	 0.8865	 0.3480
Q	 0.9386	 0.3670
R	 0.8838	 0.3280
S	 0.9226	 0.3740
T	 0.8963	 0.3620
U	 0.8578	 0.3010
V	 0.9113	 0.3820
W	 0.9077	 0.3630
X	 0.8904	 0.3420
Y	 0.8534	 0.3400



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Chain	Atom inclusion	Q-score
Z	 0.9152	 0.3380
a	 0.9345	 0.3580
b	 0.8736	 0.2900
c	 0.9341	 0.3320
d	 0.9277	 0.3540
e	 0.8977	 0.3730
f	 0.9133	 0.3800
g	 0.8885	 0.3390
h	 0.8728	 0.3120
i	 0.9083	 0.3200
j	 0.9346	 0.3480
k	 0.8564	 0.3050
l	 0.8946	 0.3240
m	 0.9279	 0.3500
n	 0.8486	 0.2300
o	 0.9249	 0.3640
p	 0.8911	 0.3330
q	 0.8892	 0.3160
r	 0.9310	 0.3650
u	 0.9953	 0.3740
v	 0.9855	 0.3500
w	 0.9170	 0.3710