



wwPDB EM Validation Summary Report ⓘ

Mar 28, 2026 – 03:00 AM UTC

PDB ID : 7TUT / pdb_00007tut
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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

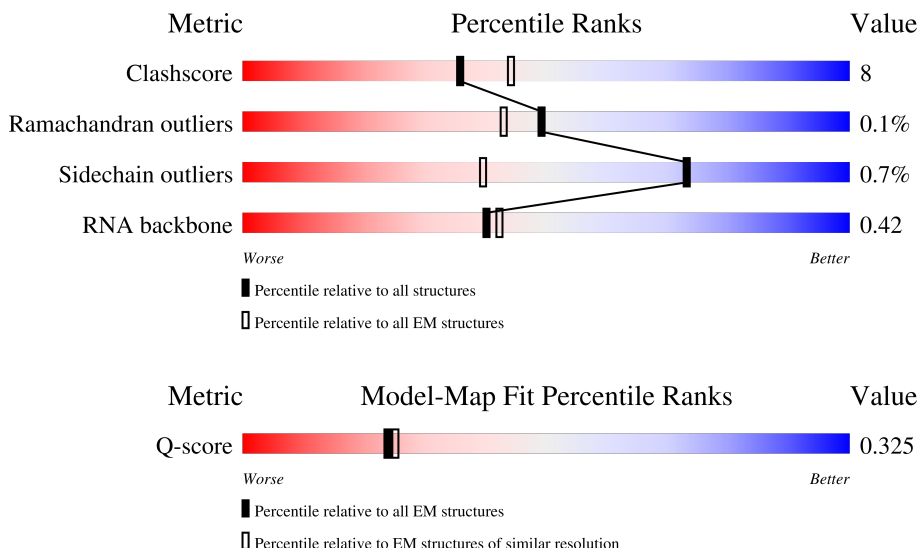
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.88 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8773 (3.38 - 4.38)

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	

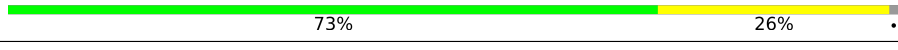
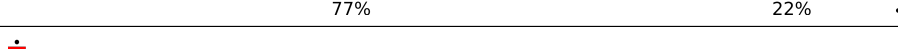
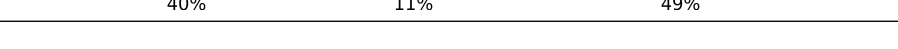
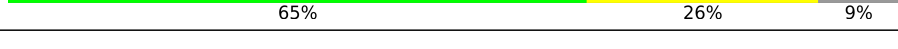
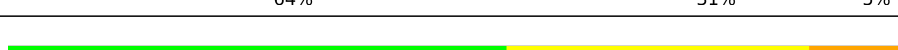
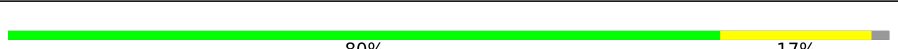
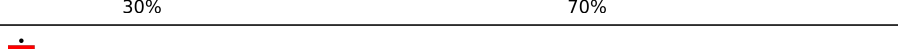
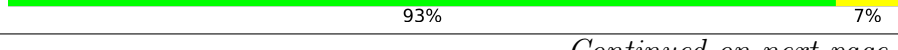
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Mol	Chain	Length	Quality of chain
4	E	291	
5	F	247	
6	G	319	
7	H	192	
8	I	214	
9	J	178	
10	L	211	
11	M	218	
12	N	204	
13	O	203	
14	P	184	
15	Q	188	
16	R	196	
17	S	176	
18	T	160	
19	U	128	
20	V	140	
21	W	157	
22	X	156	
23	Y	145	
24	Z	136	
25	a	148	
26	b	226	
27	c	115	
28	d	125	

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Mol	Chain	Length	Quality of chain
29	e	135	
30	f	110	
31	g	116	
32	h	123	
33	i	105	
34	j	97	
35	k	70	
36	l	51	
37	m	102	
38	n	25	
39	o	106	
40	p	92	
41	q	77	
42	r	137	
43	u	120	
44	v	156	
45	w	403	
46	B	273	
47	1	476	
48	2	96	
49	3	68	
50	4	483	
51	5	106	
52	7	563	
53	6	224	

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Mol	Chain	Length	Quality of chain
54	8	188	29% 77% 17% 6%
55	K	3543	51% 38% 11%
56	9	129	26% 74% 11% 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
1	A	248	Total	C	H	N	O	S	0	0
			3891	1189	1993	389	314	6		

- Molecule 2 is a protein called uL4.

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

- Molecule 3 is a protein called uL18.

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

- Molecule 4 is a protein called eL6.

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

- Molecule 5 is a protein called uL30.

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

There are 4 discrepancies between the modelled and reference sequences:

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

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 7 is a protein called uL6.

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

- Molecule 8 is a protein called uL16.

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

- Molecule 9 is a protein called uL5.

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

- Molecule 10 is a protein called eL13.

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

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	46	ILE	-	insertion	UNP G1TPV0

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

- Molecule 12 is a protein called eL15.

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

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
13	O	199	Total	C	H	N	O	S	0	0
			3408	1051	1778	319	255	5		

- Molecule 14 is a protein called uL22.

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

- Molecule 15 is a protein called eL18.

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

- Molecule 16 is a protein called eL19.

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

There are 3 discrepancies between the modelled and reference sequences:

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

- Molecule 17 is a protein called eL20.

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

- Molecule 18 is a protein called eL21.

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

- Molecule 19 is a protein called eL22.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	U	102	Total	C	H	N	O	S	0	0
			1690	534	856	146	152	2		

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	18	LEU	VAL	conflict	UNP G1TSG1
U	32	GLY	ARG	conflict	UNP G1TSG1
U	36	ALA	GLU	conflict	UNP G1TSG1
U	39	PHE	SER	conflict	UNP G1TSG1
U	54	GLY	ARG	conflict	UNP G1TSG1

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

- Molecule 21 is a protein called eL24.

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

- Molecule 22 is a protein called eL23.

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

- Molecule 23 is a protein called uL24.

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

- Molecule 24 is a protein called eL27.

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

- Molecule 25 is a protein called uL15.

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

- Molecule 26 is a protein called eL29.

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

- Molecule 27 is a protein called eL30.

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

- Molecule 28 is a protein called eL31.

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

- Molecule 29 is a protein called eL32.

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

- Molecule 30 is a protein called eL33.

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

- Molecule 31 is a protein called eL34.

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

- Molecule 32 is a protein called eL35.

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

- Molecule 33 is a protein called eL36.

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

- Molecule 34 is a protein called eL37.

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

- Molecule 35 is a protein called eL38.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 36 is a protein called eL39.

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

- Molecule 37 is a protein called eL40.

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

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
38	n	25	Total	C	H	N	O	S	0	0
			528	145	289	64	27	3		

- Molecule 39 is a protein called eL42.

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

- Molecule 40 is a protein called eL43.

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

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

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

- Molecule 42 is a protein called eL28.

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

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

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

There are 7 discrepancies between the modelled and reference sequences:

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

- Molecule 44 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 45 is a protein called uL3.

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

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 46 is a protein called Nascent chain.

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms						AltConf	Trace
50	4	342	Total	C	H	N	O	S	0	0
			5595	1738	2817	495	522	23		

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

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

- Molecule 52 is a protein called Nicalin.

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

- Molecule 53 is a protein called Transmembrane protein 147.

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

- Molecule 54 is a protein called Calcium load-activated calcium channel.

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

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

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

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

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

- Molecule 57 is MAGNESIUM ION (CCD ID: 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 (CCD ID: 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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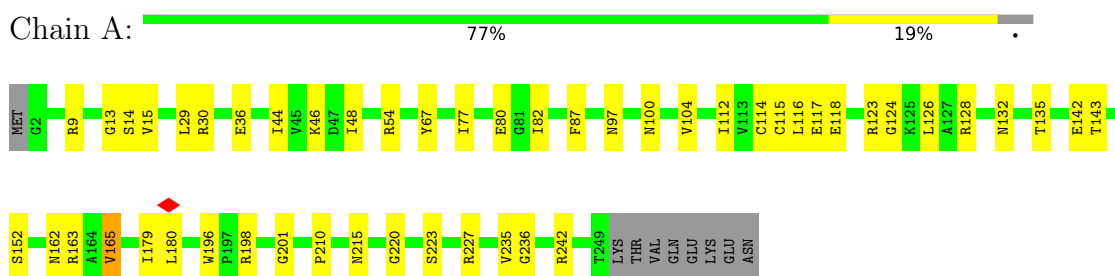
Continued from previous page...

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

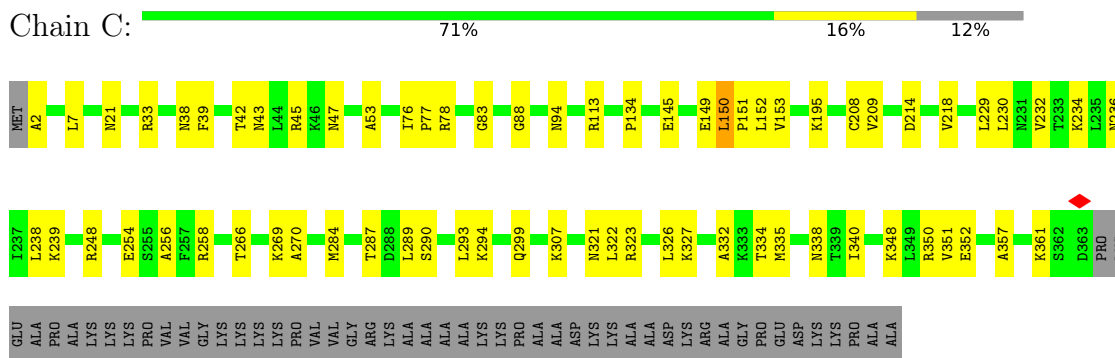
3 Residue-property plots

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.

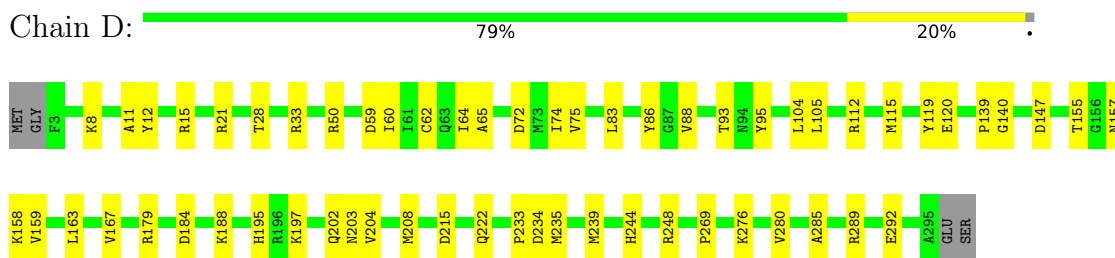
• Molecule 1: uL2



• Molecule 2: uL4

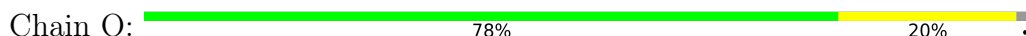


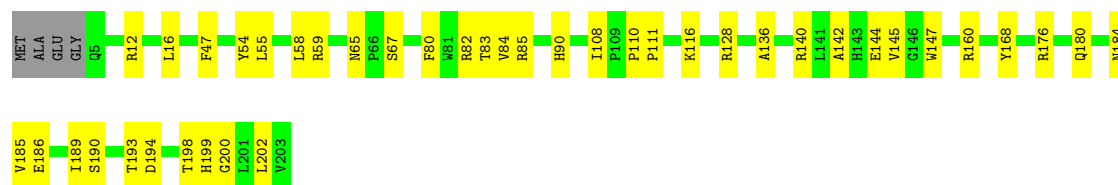
• Molecule 3: uL18



• Molecule 4: eL6

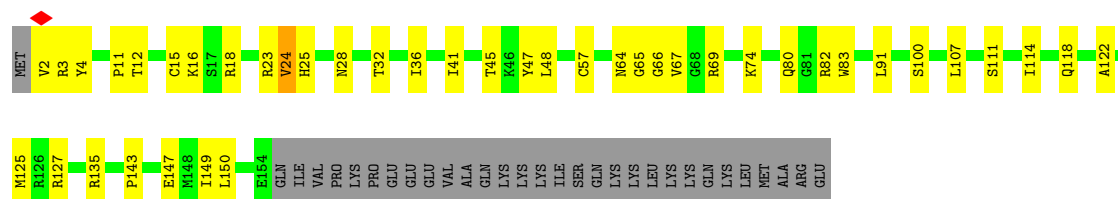






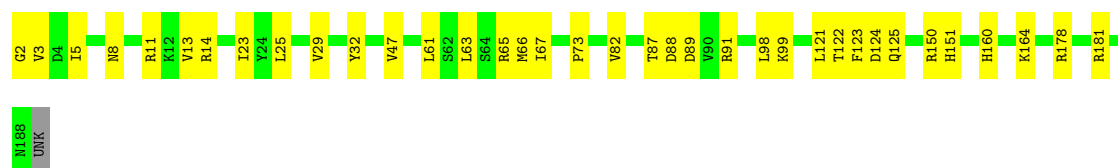
• Molecule 14: uL22

Chain P: 60% 22% 17%



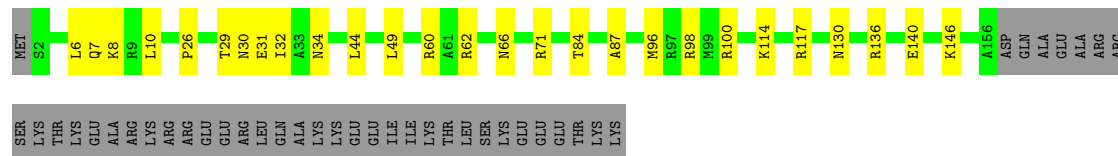
• Molecule 15: eL18

Chain Q: 80% 19%



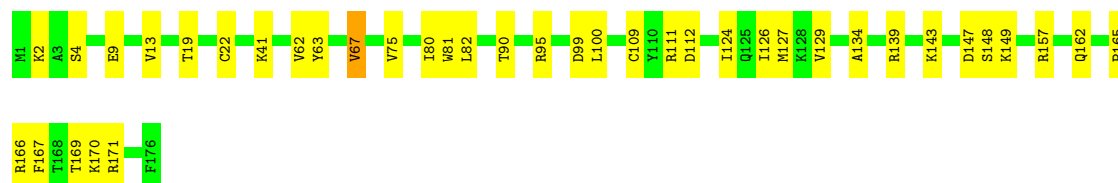
• Molecule 16: eL19

Chain R: 65% 14% 21%



• Molecule 17: eL20

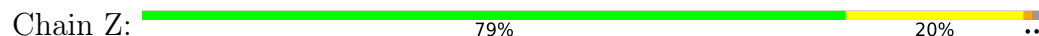
Chain S: 78% 22%



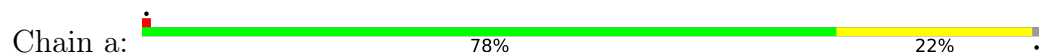
• Molecule 18: eL21

Chain T: 78% 22%

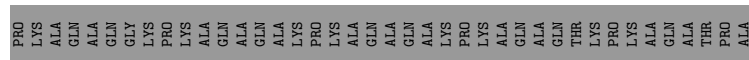
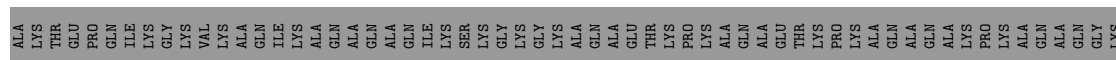
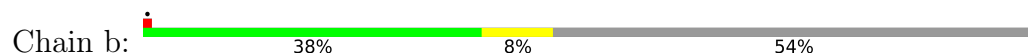
- Molecule 24: eL27



- Molecule 25: uL15



- Molecule 26: eL29



- Molecule 27: eL30

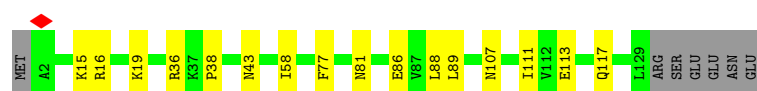


- Molecule 28: eL31



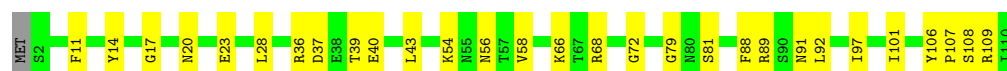
- Molecule 29: eL32

Chain e:  83% 12% 5%



- Molecule 30: eL33

Chain f:  73% 26%



- Molecule 31: eL34

Chain g:  77% 22%



- Molecule 32: eL35

Chain h:  78% 21%



- Molecule 33: eL36

Chain i:  81% 16%



- Molecule 34: eL37

Chain j:  68% 20% 11%



- Molecule 35: eL38

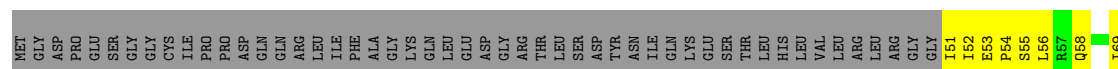
Chain k:  84% 14%



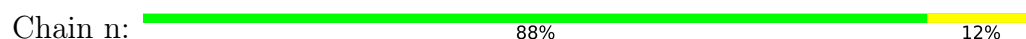
- Molecule 36: eL39



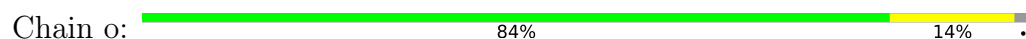
• Molecule 37: eL40



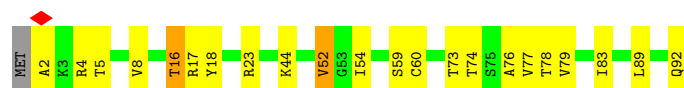
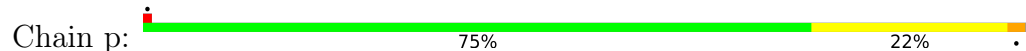
• Molecule 38: eL41



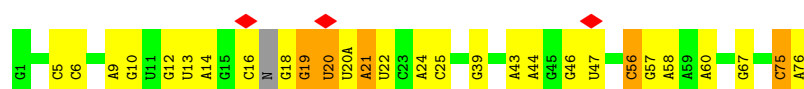
• Molecule 39: eL42



• Molecule 40: eL43

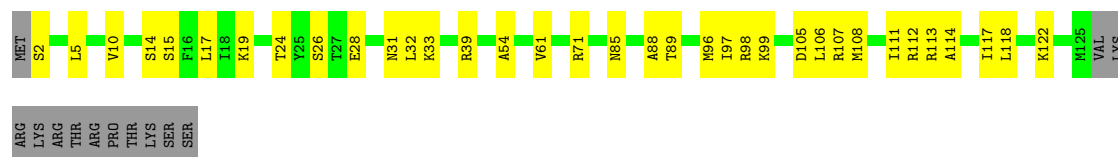


• Molecule 41: P-site tRNA

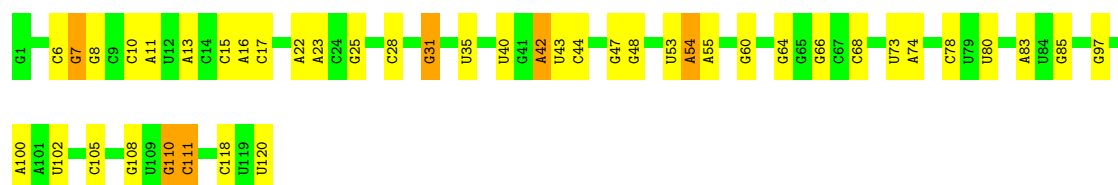


• Molecule 42: eL28

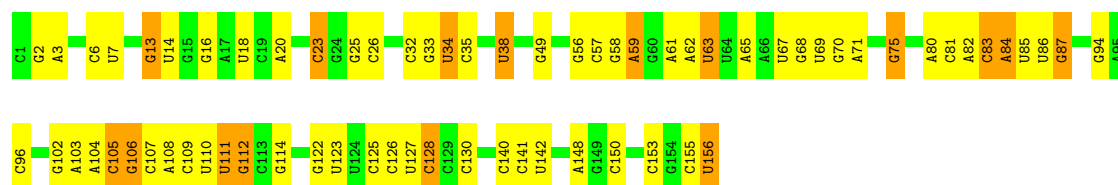




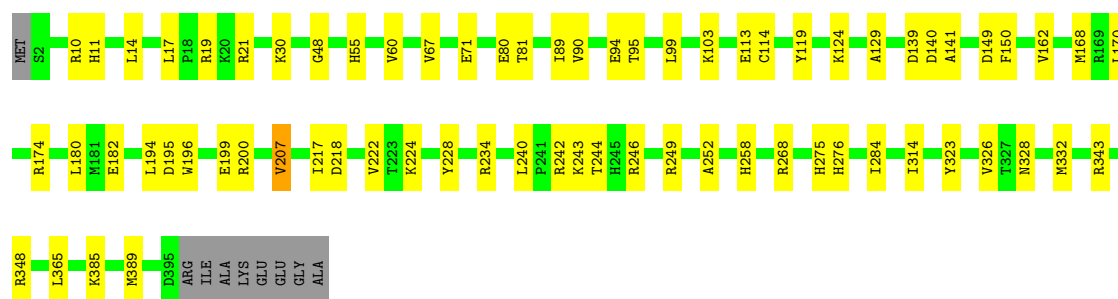
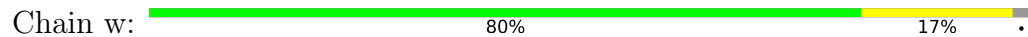
• Molecule 43: 5S ribosomal RNA



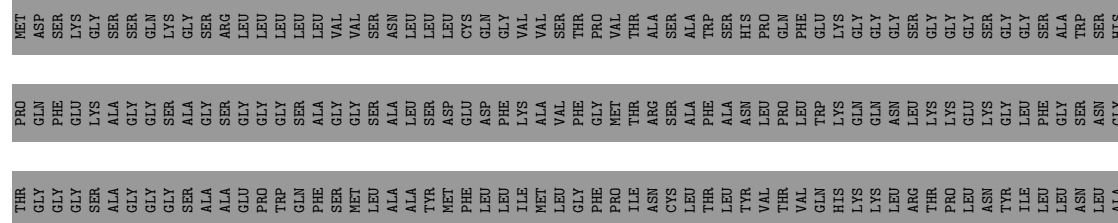
• Molecule 44: 5.8S ribosomal RNA

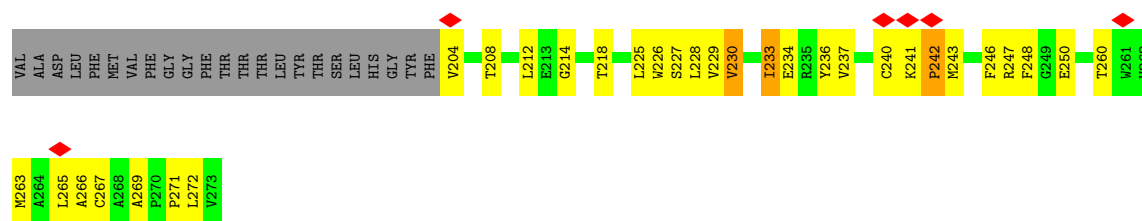


• Molecule 45: uL3



• Molecule 46: Nascent chain





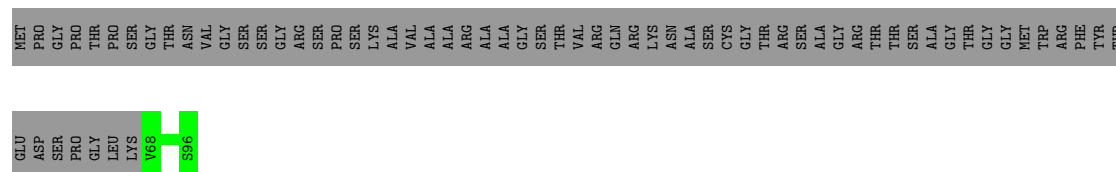
- Molecule 47: Protein transport protein Sec61 subunit alpha isoform 1

Chain 1: 82% 15%



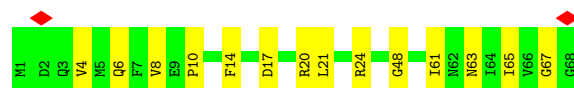
- Molecule 48: Protein transport protein Sec61 subunit beta

Chain 2: 30% 70%



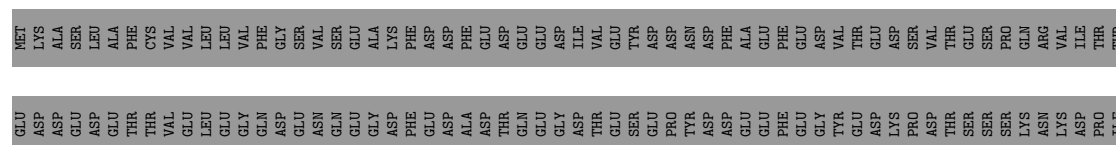
- Molecule 49: Protein transport protein Sec61 gamma

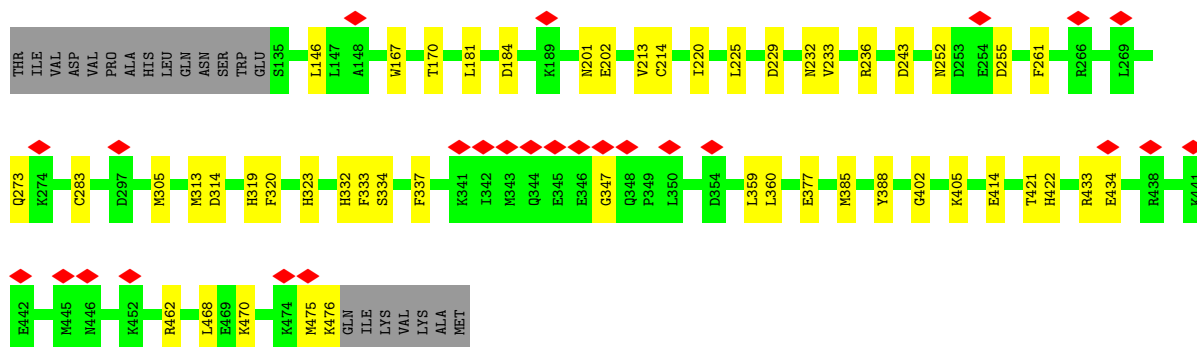
Chain 3: 79% 21%



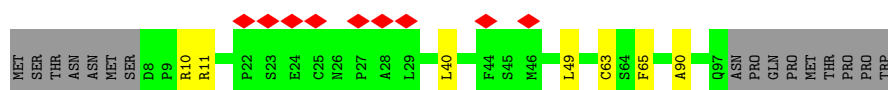
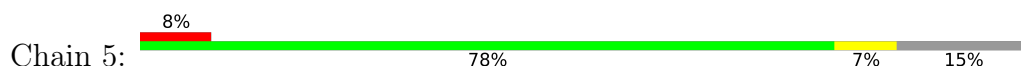
- Molecule 50: Coiled-coil domain containing 47

Chain 4: 5% 61% 10% 29%

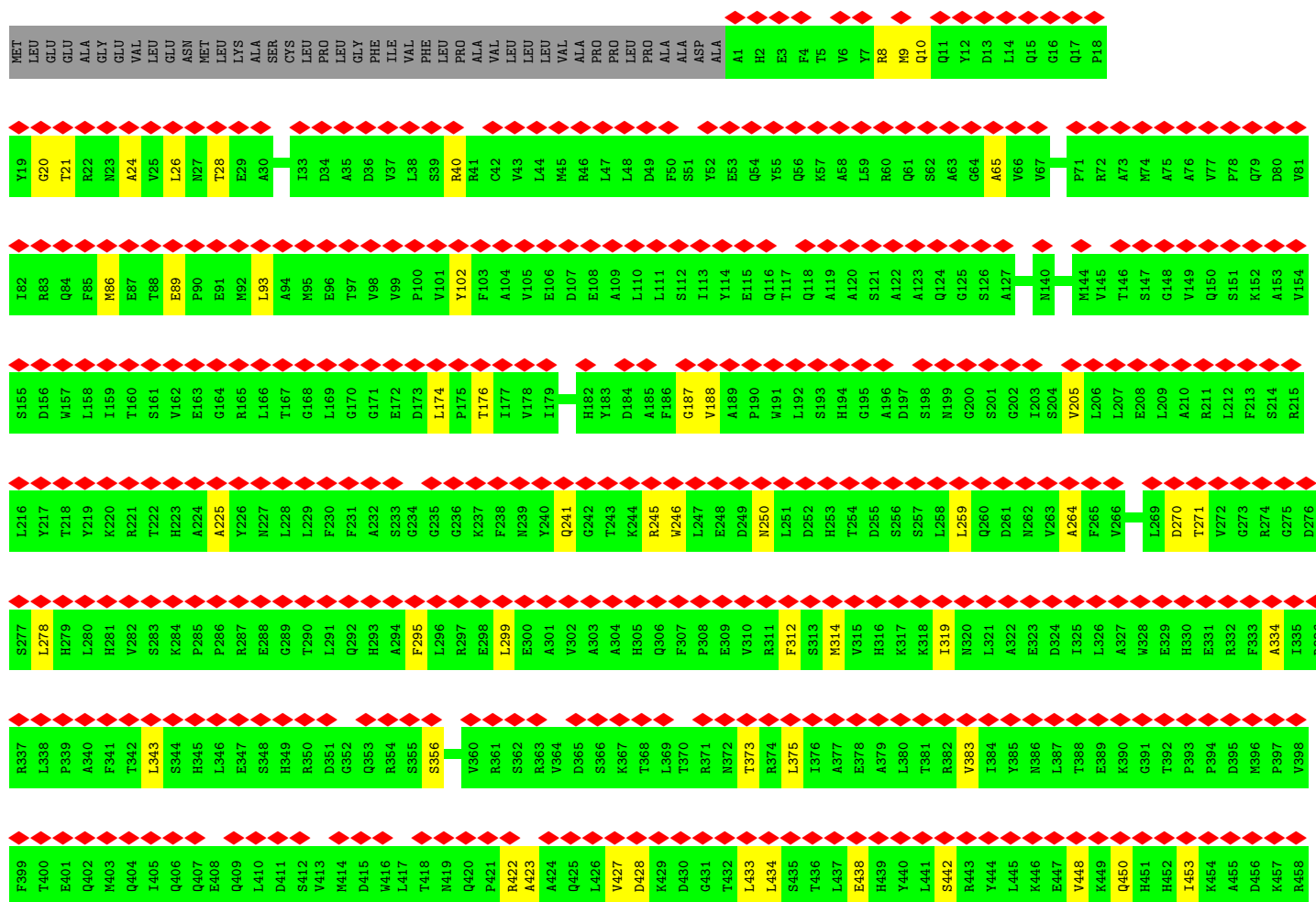
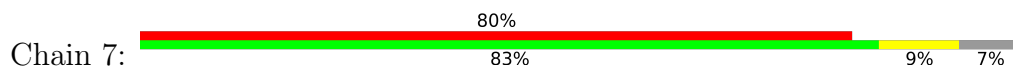


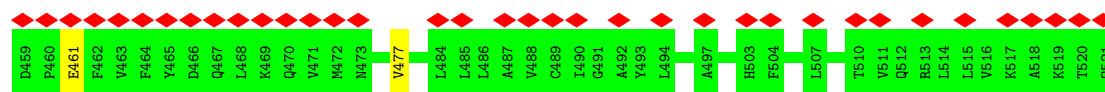


• Molecule 51: PAT complex subunit Asterix



• Molecule 52: Nicalin

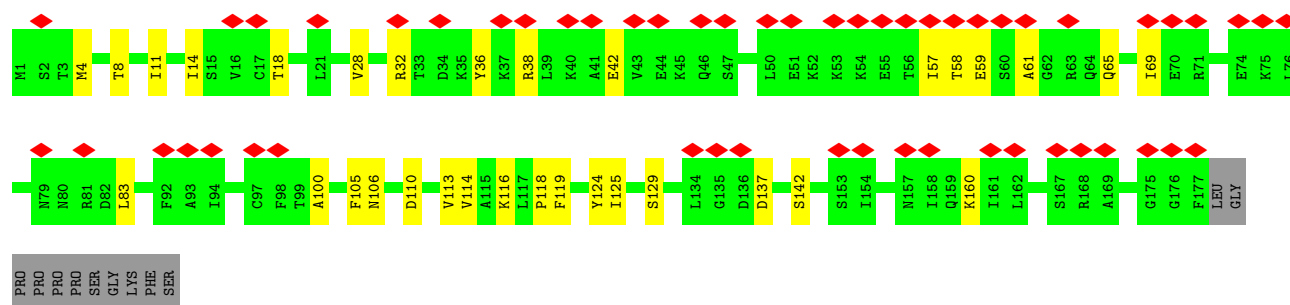




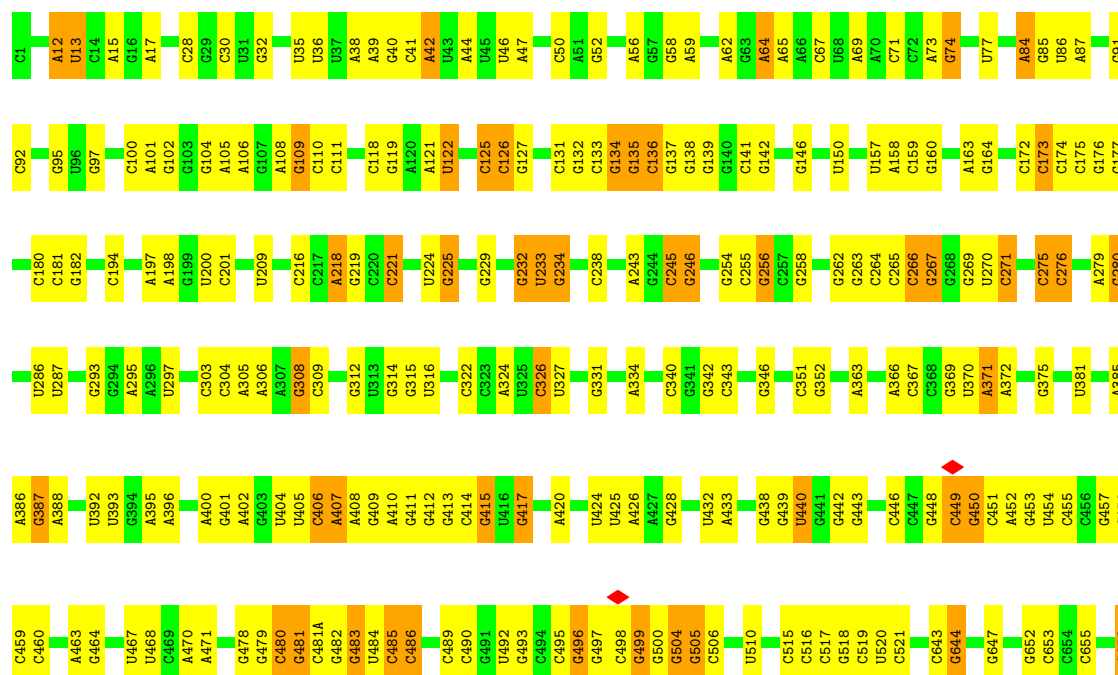
• Molecule 53: Transmembrane protein 147



• Molecule 54: Calcium load-activated calcium channel

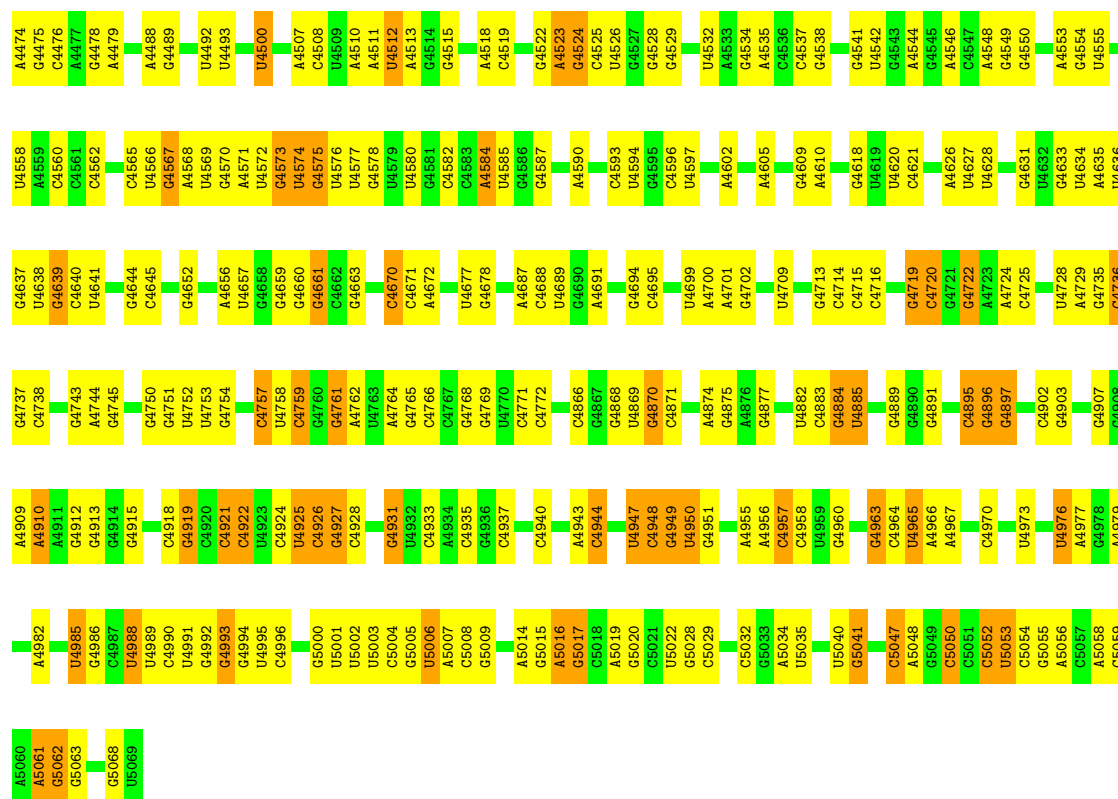


• Molecule 55: 28S ribosomal RNA

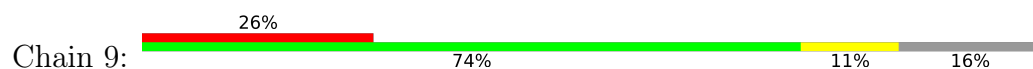


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U1997	A1998	A1999	G2000	G2001	A2002	G2003	U2004	G2005	U2006	G2007	U2008	A2009	A2010	C2011	A2017	C2018	C2019	U2020	G2021	C2022	C2023	G2024	A2025	A2026	A2029	A2030	A2040	A2041	G2045	G2046	A2047	U2048	G2052	C2053	U2054	G2055	G2056	A2057	C2062	G2063	G2064	G2065	A2069	U2070	A2071	C2072	C2073	C2074	C2077	G2078	G2079																																	
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C972	G973	C974	C975	G976	G977	G978	G979	U980	C981	U982	C983	C984	C985	C986	C987	C988	C989	C990	G1070	C1071	C1072	G1073	G1074	G1075	C1076	C1077	A929	A932	G933	C934	A935	G935A	C936	C937	C938	G939	C940	C941	G942	A943	A944	U945	G952	C953	A956	G957	G958	G959	A960	G961	C962	G963	A964	G965	A966	G967	C968	C969	C1192	C1193	G1194																							
G659	G660	C661	C666	A667	C668	C669	C670	C678	C679	G684	C685	A686	U687	C690	A691	C692	G695	C696	C697	C698	C699	C700	G701	C704	G705	C706	C707	C708	C724	G730	G731	G734	C737	C738	G739	G740	A746	A747	G748	G749	U750	G751	C752	G756	G757	G758																																						

A4390	A4302	A4213	A4306	C3812	A3728	U3845	G2842	U2747	G2683	C2568	U2485	G2399	G2296
G4391	C4303	A4214	G3907	A3913	U3729	A3646	U2842	U2747	G2684	C2569	U2486	G2400	G2299
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G4393	G4305	G4216	C3909	A3817	A3732	A3648	A2844	G2759	U2686	A2573	C2488	G2407	G2301
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A4397	A4317	A4220	U3913	U3822	G3743	A3653	A2850	U2763	G2671	G2580	C2492	G2411	U2305
A4398	U4321	G4225	U3914	A3823	A3746	A3656	G2854	U2764	G2672	U2581	G2496	A2412	U2306
G4401	G4322	U4228	U3915	A3824	A3747	U3657	G2855	A2765	G2673	A2582	C2497	U2413	G2309
G4412	A4323	G4229	A3917	C3834	A3748	C3658	G2856	U2767	G2675	C2583	C2498	G2416	G2313
C4413	A4324	U4232	A3923	C3835	G3749	G3661	C2867	U2769	G2677	G2586	C2499	A2417	G2314
A4414	A4325	U4233	C3926	U3838	C3750	A3662	U2869	G2770	G2678	C2588	C2502	A2418	G2315
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G4423	G4331	G4238	C3935	U3848	A3759	C3667	C2873	U2782	U2691	A2600	A2511	U2426	G2319
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G4430	U4340	G4250	G3938	A3856	U3764	G3673	U2880	G2786	A2695	C2607	G2516	A2429	G2330
C4431	C4341	A4251	G3939	G3859	G3765	G3674	A2881	A2787	A2696	G2608	A2517	A2431	G2331
U4434	U4344	G4254	U3940	U3860	A3766	U3680	A2882	U2788	G2697	G2616	G2518	A2432	G2332
C4435	C4345	A4258	A3942	C3866	C3767	A3681	G2883	U2789	U2699	G2617	G2519	G2433	G2333
U4437	A4347	U4259	A3943	A3867	A3770	A3682	C2884	G2791	C2702	G2618	G2520	G2434	C2334
U4438	C4349	U4260	G3946	C3870	U3771	C3683	G2885	G2792	G2705	G2619	C2526	U2440	C2335
U4442	A4349	C4261	A3947	G3873	U3772	C3684	G2886	G2793	G2706	G2620	A2527	C2441	G2336
C4443	C4350	U4265	C3948	G3874	U3773	C3685	A2887	G2794	C2707	A2621	G2528	U2447	A2341
U4445	U4354	G4266	G4065	G3875	A3774	G3686	A3599	A2798	U2708	U2627	C2531	G2448	G2348
G4448	U4359	A4268	U4066	A3876	A3775	U3688	A3599	G2799	C2710	U2628	C2532	A2449	A2349
A4449	G4364	U4271	U4067	A3877	G3776	G3689	G3600	A2799	G2711	G2629	C2533	U2350	C2351
U4450	U4371	A4272	U4069	C3878	G3780	A3692	G3603	U2803	G2714	U2632	C2534	A2453	G2348
G4451	C4372	G4273	U4070	G3879	C3781	U3695	C3605	C2804	G2715	U2633	A2535	G2457	A2341
U4452	A4373	A4274	A4073	G3880	C3782	C3696	A2806	A2807	U2718	G2634	G2536	G2458	G2348
C4453	C4374	U4275	C4074	C3881	A3783	U3616	G2808	G2809	U2719	U2635	A2537	G2459	G2348
G4454	G4375	A4281	C4075	U3882	A3784	G3617	G2809	U2810	C2720	U2636	U2538	G2462	G2348
U4457	U4377	U4282	G4076	C3883	A3785	C3618	G2810	G2721	G2722	U2637	C2539	G2463	A2368
C4458	A4378	U4283	A4077	G3886	U3786	A3702	C3622	A2811	G2723	G2640	C2540	C2464	G2378
U4459	A4379	G4284	G4084	C3887	C3787	A3707	G3625	A2812	A2725	A2647	G2546	C2465	G2379
C4461	U4380	U4285	A4085	C3888	C3788	U3708	G3626	A2813	G2726	G2651	G2550	U2467	G2380
A4462	A4381	G4291	G4086	C3889	C3789	C3708	A3630	G2822	G2732	G2652	A2551	U2468	A2391
U4463	C4382	A4292	G4087	A3893	G3792	A3711	A3635	U2826	C2733	C2653	C2552	U2469	A2392
A4464	U4203	C4204	C4088	A3894	A3795	G3714	G3636	G2827	G2739	C2654	A2553	C2470	A2392
U4465	A4205	A4205	C4096	G3897	A3796	A3717	U3637	U2828	U2740	G2658	U2554	G2471	G2397
C4466	U4208	G4297	G4097	A3901	G3806	G3722	U3641	C2834	U2741	A2659	G2559	G2475	A2395
A4467	C4209	A4298	A4098	A3901	G3809	G3725	U3644	A2835	G2742	A2660	G2566	A2477	A2396
U4471	U4210	U4299	U4111	G3904	C3810	G3726	U3644	A2836	A2743	U2661	G2567	G2478	U2398
G4472	C4211	U4300	A4112	A3905	G3811	G3726	U3644	U2837	A2744	G2662			



- 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 ($\text{\AA}$)	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 ($\text{\AA}$)	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: 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	0.10	0/1936	0.29	0/2596
2	C	0.12	0/2937	0.34	0/3946
3	D	0.12	0/2437	0.36	0/3264
4	E	0.11	0/1914	0.32	0/2566
5	F	0.12	0/1911	0.33	0/2549
6	G	0.12	0/1910	0.37	0/2569
7	H	0.11	0/1535	0.34	0/2063
8	I	0.11	0/1702	0.31	0/2272
9	J	0.12	0/1385	0.36	0/1852
10	L	0.12	0/1733	0.35	0/2316
11	M	0.13	0/1158	0.38	0/1547
12	N	0.12	0/1741	0.36	0/2331
13	O	0.13	0/1662	0.36	0/2222
14	P	0.17	0/1268	0.40	0/1700
15	Q	0.12	0/1538	0.34	0/2054
16	R	0.13	0/1310	0.37	0/1734
17	S	0.12	0/1501	0.33	0/2012
18	T	0.10	0/1326	0.29	0/1770
19	U	0.11	0/848	0.32	0/1138
20	V	0.10	0/993	0.28	0/1332
21	W	0.11	0/541	0.33	0/720
22	X	0.12	0/984	0.35	0/1323
23	Y	0.11	0/1132	0.34	0/1504
24	Z	0.11	0/1130	0.30	0/1507
25	a	0.11	0/1191	0.31	0/1590
26	b	0.11	0/861	0.35	0/1138
27	c	0.11	0/771	0.31	0/1034
28	d	0.13	0/903	0.33	0/1216
29	e	0.11	0/1071	0.32	0/1429
30	f	0.12	0/895	0.31	0/1198
31	g	0.12	0/916	0.31	0/1220
32	h	0.12	0/1017	0.37	0/1344

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	i	0.13	0/841	0.36	0/1112
34	j	0.10	0/720	0.32	0/952
35	k	0.12	0/575	0.32	0/761
36	l	0.15	0/459	0.46	0/608
37	m	0.12	0/435	0.32	0/575
38	n	0.13	0/240	0.40	0/305
39	o	0.10	0/864	0.30	0/1140
40	p	0.13	0/718	0.36	0/953
41	q	0.13	0/1805	0.37	0/2809
42	r	0.12	0/1010	0.36	0/1354
43	u	0.14	0/2858	0.33	0/4455
44	v	0.14	0/3701	0.37	0/5766
45	w	0.10	0/3240	0.28	0/4339
46	B	0.21	0/541	0.63	0/738
47	1	0.13	0/3677	0.36	0/4986
48	2	0.12	0/237	0.28	0/321
49	3	0.13	0/553	0.33	0/738
50	4	0.13	0/2819	0.36	0/3772
51	5	0.12	0/730	0.30	0/988
52	7	0.10	0/4224	0.29	0/5728
53	6	0.10	0/1835	0.30	0/2495
54	8	0.12	0/1426	0.33	0/1908
55	K	0.16	0/84979	0.41	0/132532
56	9	0.12	0/932	0.37	0/1268
All	All	0.14	0/163576	0.38	0/239659

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.

There are no bond angle outliers.

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 ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1898	1993	1993	39	0
2	C	2883	3053	3053	54	0
3	D	2391	2424	2424	38	0
4	E	1877	2031	2031	49	0
5	F	1875	1995	1995	40	0
6	G	1879	2027	2027	36	0
7	H	1516	1597	1597	33	0
8	I	1664	1712	1712	24	0
9	J	1362	1399	1399	27	0
10	L	1702	1820	1820	27	0
11	M	1137	1211	1211	19	0
12	N	1696	1745	1744	35	0
13	O	1630	1778	1778	30	0
14	P	1242	1274	1274	35	0
15	Q	1514	1634	1634	27	0
16	R	1294	1434	1434	19	0
17	S	1462	1508	1508	29	0
18	T	1298	1367	1366	30	0
19	U	834	856	858	12	0
20	V	979	1039	1039	18	0
21	W	528	541	541	2	0
22	X	967	1040	1040	28	0
23	Y	1115	1205	1205	32	0
24	Z	1107	1182	1182	17	0
25	a	1162	1209	1209	23	0
26	b	848	920	920	18	0
27	c	761	794	794	13	0
28	d	888	930	930	10	0
29	e	1053	1147	1147	12	0
30	f	876	912	912	23	0
31	g	906	998	998	19	0
32	h	1009	1136	1136	20	0
33	i	830	916	916	12	0
34	j	705	738	738	17	0
35	k	569	637	637	8	0
36	l	447	480	480	19	0
37	m	429	466	466	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	n	239	289	289	2	0
39	o	851	922	922	12	0
40	p	708	757	757	19	0
41	q	1616	823	824	13	0
42	r	994	1051	1051	29	0
43	u	2558	1296	1296	28	0
44	v	3314	1683	1683	41	0
45	w	3172	3310	3310	59	0
46	B	526	528	528	48	0
47	1	3598	3722	3722	57	0
48	2	230	245	245	0	0
49	3	543	577	577	12	0
50	4	2778	2817	2819	47	0
51	5	711	710	710	4	0
52	7	4139	4121	4123	33	0
53	6	1783	1792	1792	11	0
54	8	1406	1478	1478	26	0
55	K	75972	38358	38378	1081	0
56	9	903	881	881	9	0
57	C	1	0	0	0	0
57	D	1	0	0	0	0
57	I	2	0	0	0	0
57	J	1	0	0	0	0
57	K	202	0	0	0	0
57	P	1	0	0	0	0
57	V	1	0	0	0	0
57	a	1	0	0	0	0
57	u	4	0	0	0	0
57	v	6	0	0	0	0
58	g	1	0	0	0	0
58	j	1	0	0	0	0
58	m	1	0	0	0	0
58	o	1	0	0	0	0
58	p	1	0	0	0	0
All	All	152599	114508	114533	2031	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 2031 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:K:2638:G:N2	55:K:2697:A:N1	2.14	0.95
55:K:1442:C:O2	55:K:2112:G:N2	2.02	0.93
12:N:157:LYS:O	12:N:162:ARG:NH1	2.01	0.93
55:K:746:A:O2'	55:K:913:U:O4	1.87	0.93
55:K:1369:C:OP2	55:K:1370:G:O2'	1.87	0.92

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	30	64
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%)	24	59
11	M	136/218 (62%)	126 (93%)	10 (7%)	0	100	100
12	N	200/204 (98%)	185 (92%)	14 (7%)	1 (0%)	24	59
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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	S	174/176 (99%)	160 (92%)	14 (8%)	0	100	100
18	T	157/160 (98%)	139 (88%)	17 (11%)	1 (1%)	21	55
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%)	8	37
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%)	36	69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	49	80

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 ⓘ

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%)	81	81
2	C	302/337 (90%)	301 (100%)	1 (0%)	86	85
3	D	247/250 (99%)	247 (100%)	0	100	100
4	E	206/251 (82%)	204 (99%)	2 (1%)	68	75
5	F	196/215 (91%)	195 (100%)	1 (0%)	81	81
6	G	200/272 (74%)	199 (100%)	1 (0%)	81	81
7	H	169/171 (99%)	168 (99%)	1 (1%)	78	80
8	I	175/181 (97%)	174 (99%)	1 (1%)	78	80
9	J	143/149 (96%)	142 (99%)	1 (1%)	76	78
10	L	175/176 (99%)	172 (98%)	3 (2%)	53	67
11	M	117/161 (73%)	116 (99%)	1 (1%)	70	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	N	171/172 (99%)	170 (99%)	1 (1%)	78	80
13	O	171/173 (99%)	171 (100%)	0	100	100
14	P	134/163 (82%)	132 (98%)	2 (2%)	57	69
15	Q	164/164 (100%)	163 (99%)	1 (1%)	78	80
16	R	138/175 (79%)	138 (100%)	0	100	100
17	S	157/157 (100%)	155 (99%)	2 (1%)	61	71
18	T	139/140 (99%)	139 (100%)	0	100	100
19	U	92/114 (81%)	91 (99%)	1 (1%)	65	73
20	V	101/107 (94%)	100 (99%)	1 (1%)	68	75
21	W	55/126 (44%)	55 (100%)	0	100	100
22	X	106/134 (79%)	105 (99%)	1 (1%)	70	75
23	Y	124/135 (92%)	123 (99%)	1 (1%)	73	77
24	Z	117/118 (99%)	115 (98%)	2 (2%)	53	67
25	a	119/120 (99%)	118 (99%)	1 (1%)	73	77
26	b	84/172 (49%)	83 (99%)	1 (1%)	63	72
27	c	84/98 (86%)	83 (99%)	1 (1%)	63	72
28	d	98/110 (89%)	96 (98%)	2 (2%)	48	65
29	e	114/121 (94%)	114 (100%)	0	100	100
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%)	107 (99%)	1 (1%)	70	75
33	i	86/89 (97%)	86 (100%)	0	100	100
34	j	73/80 (91%)	71 (97%)	2 (3%)	39	59
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
39	o	92/94 (98%)	92 (100%)	0	100	100
40	p	74/75 (99%)	72 (97%)	2 (3%)	39	59
42	r	108/121 (89%)	108 (100%)	0	100	100
45	w	342/348 (98%)	340 (99%)	2 (1%)	78	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	B	54/207 (26%)	52 (96%)	2 (4%)	30	53
47	1	390/398 (98%)	386 (99%)	4 (1%)	68	75
48	2	26/74 (35%)	26 (100%)	0	100	100
49	3	59/59 (100%)	58 (98%)	1 (2%)	53	67
50	4	306/435 (70%)	303 (99%)	3 (1%)	68	75
51	5	83/99 (84%)	83 (100%)	0	100	100
52	7	443/476 (93%)	442 (100%)	1 (0%)	87	87
53	6	187/187 (100%)	186 (100%)	1 (0%)	81	81
54	8	155/164 (94%)	154 (99%)	1 (1%)	78	80
56	9	93/108 (86%)	90 (97%)	3 (3%)	34	56
All	All	7336/8400 (87%)	7283 (99%)	53 (1%)	73	78

5 of 53 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	d	22	THR
45	w	90	VAL
54	8	160	LYS
28	d	86	VAL
34	j	82	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
31	g	28	ASN
47	1	275	GLN
32	h	98	HIS
45	w	68	ASN
50	4	446	ASN

5.3.3 RNA ⓘ

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

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
55	K	3520/3543 (99%)	819 (23%)	58 (1%)
All	All	3868/3896 (99%)	886 (22%)	58 (1%)

5 of 886 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 oligosaccharides 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

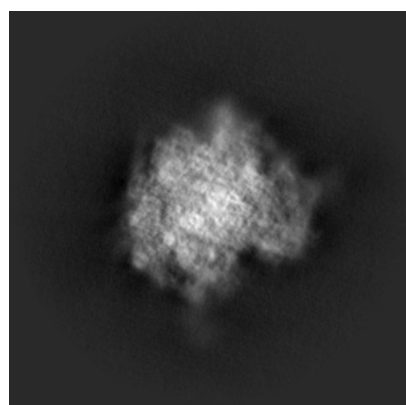
6 Map visualisation [i](#)

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.

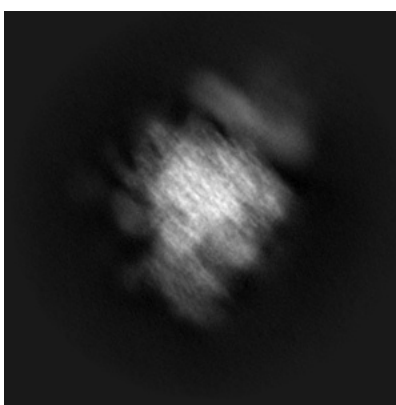
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

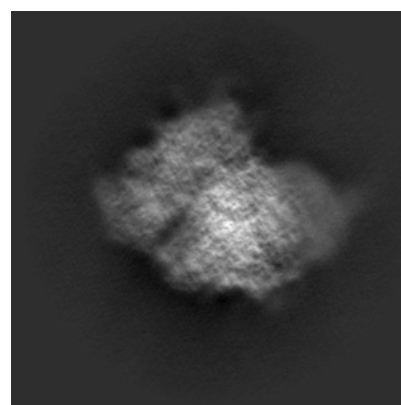
6.1.1 Primary map



X



Y

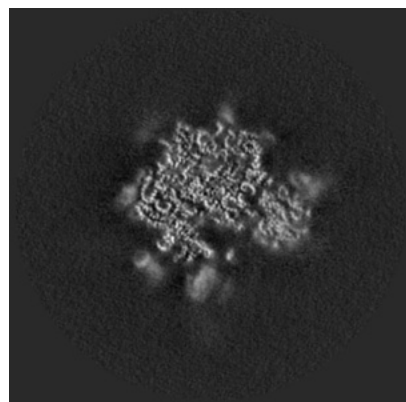


Z

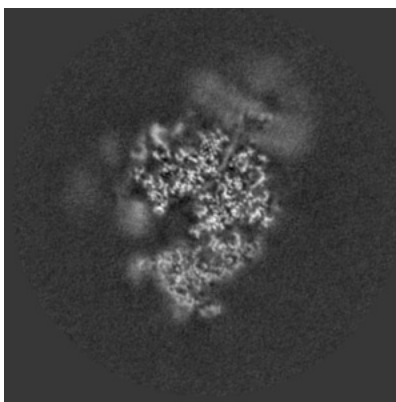
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

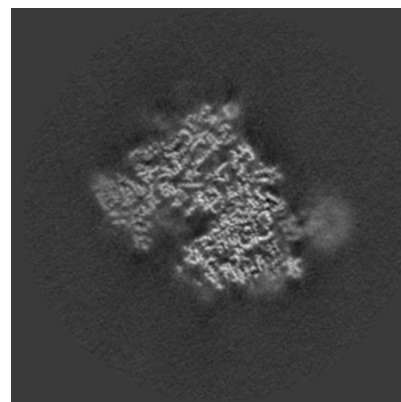
6.2.1 Primary map



X Index: 206



Y Index: 206

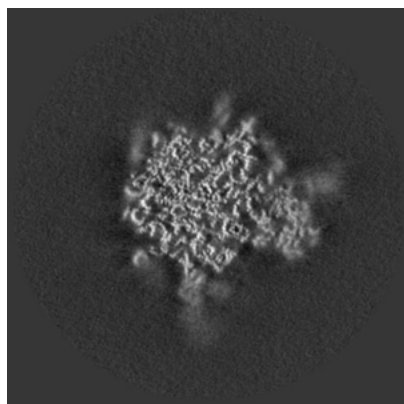


Z Index: 206

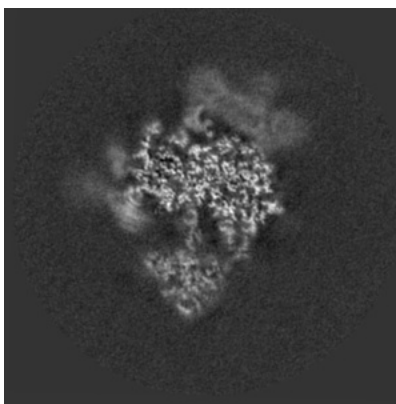
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

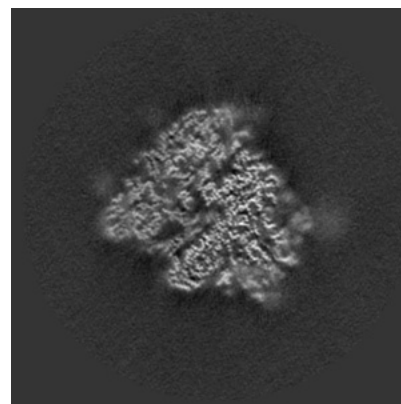
6.3.1 Primary map



X Index: 218



Y Index: 194

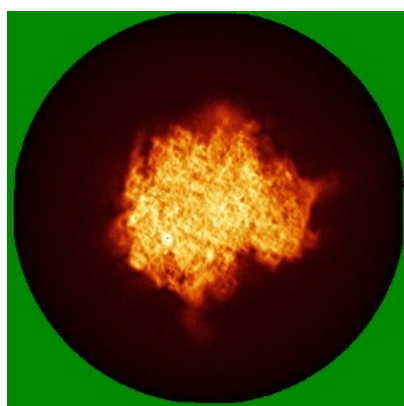


Z Index: 192

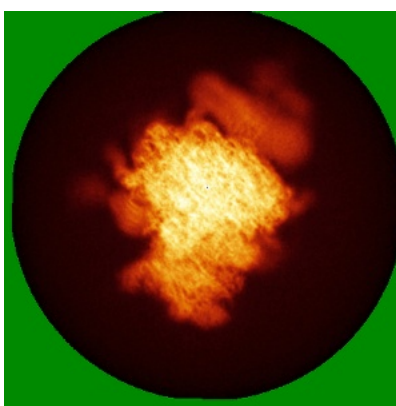
The images above show the largest variance slices of the map in three orthogonal directions.

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

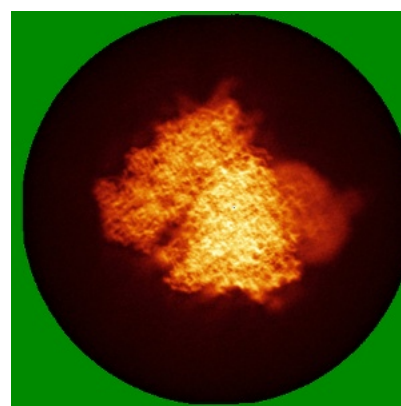
6.4.1 Primary map



X



Y

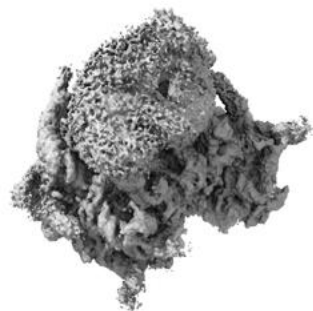


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

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

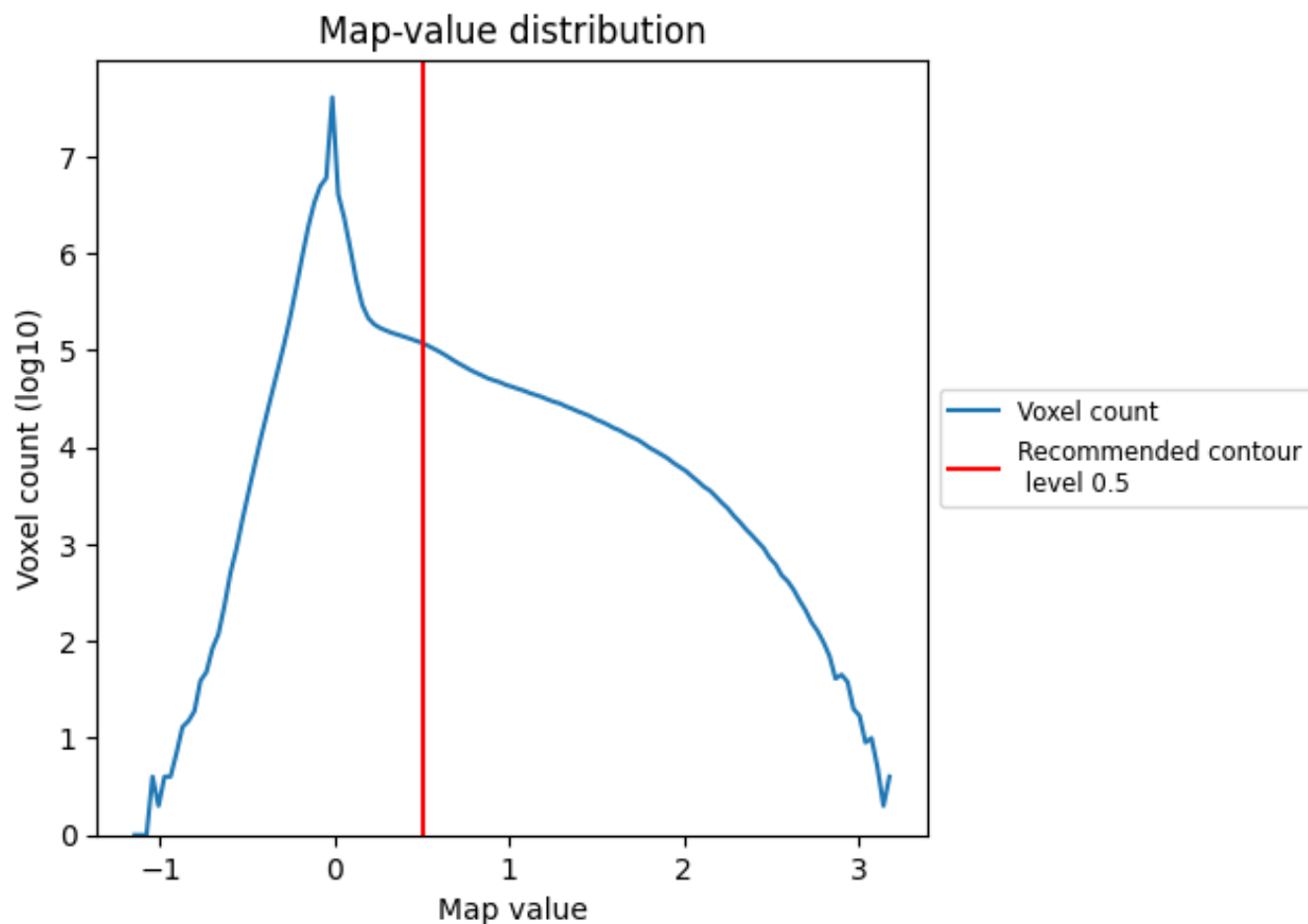
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

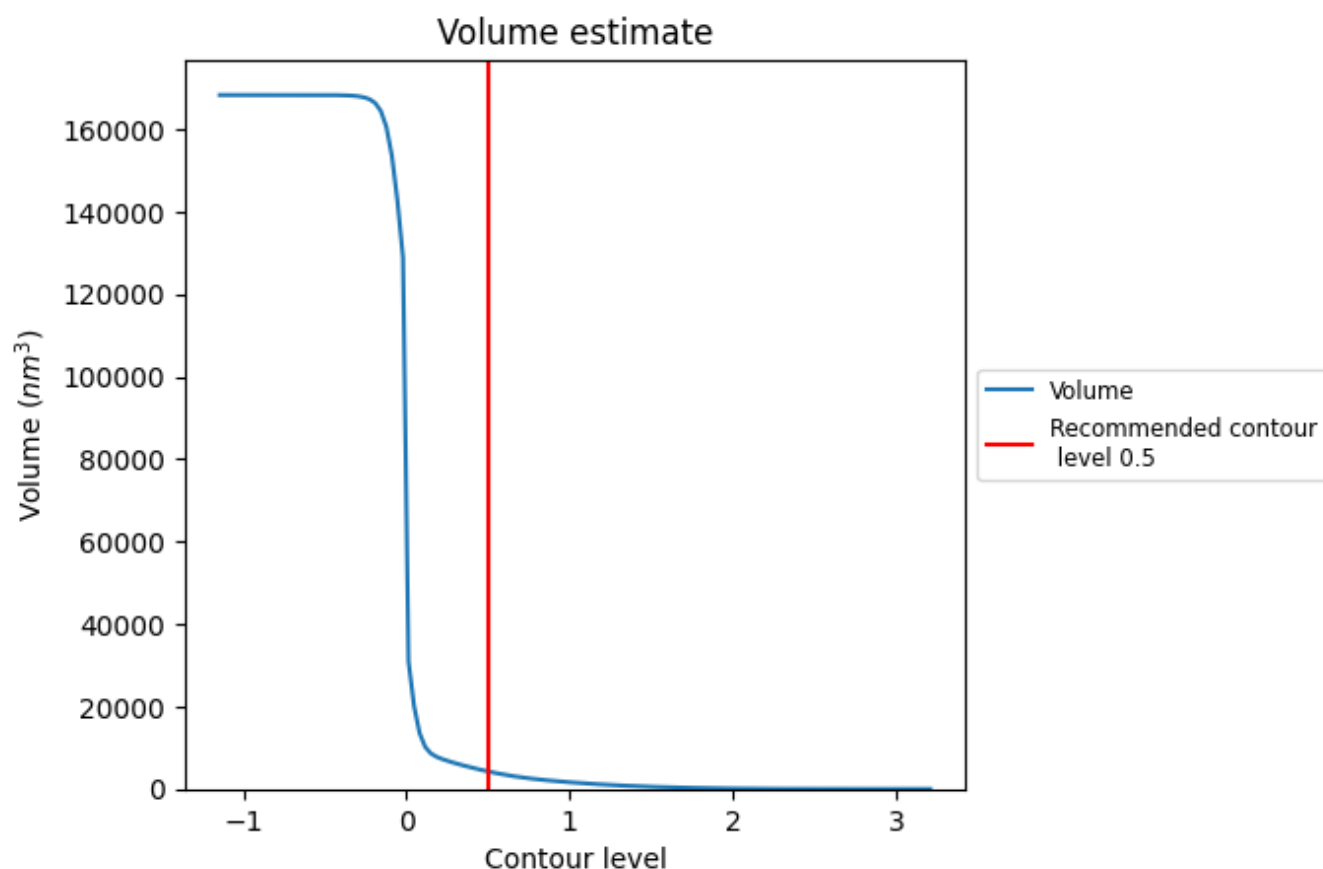
This section contains the results of statistical analysis of the map.

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.

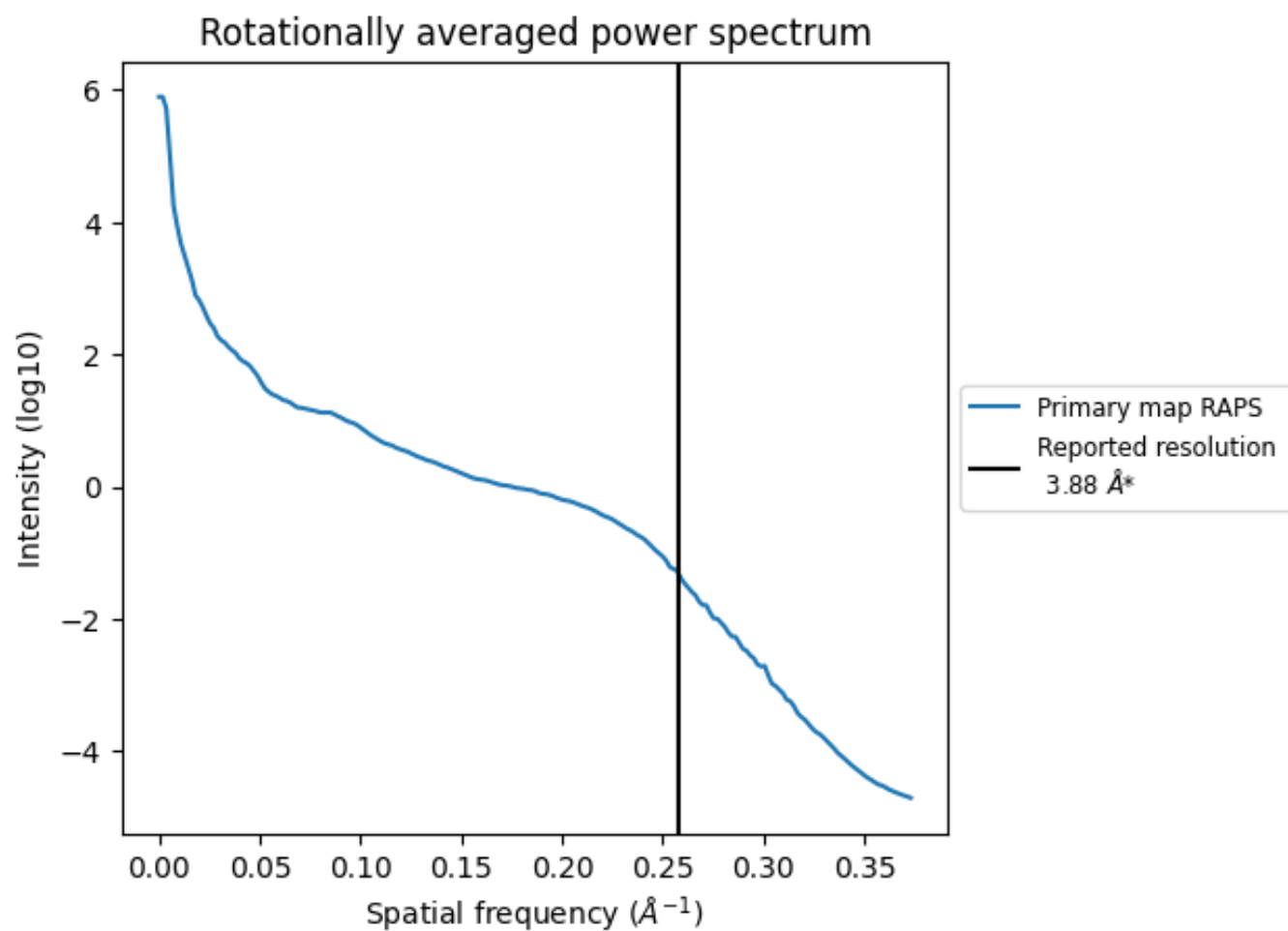
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 4244 nm³; 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.258 Å⁻¹

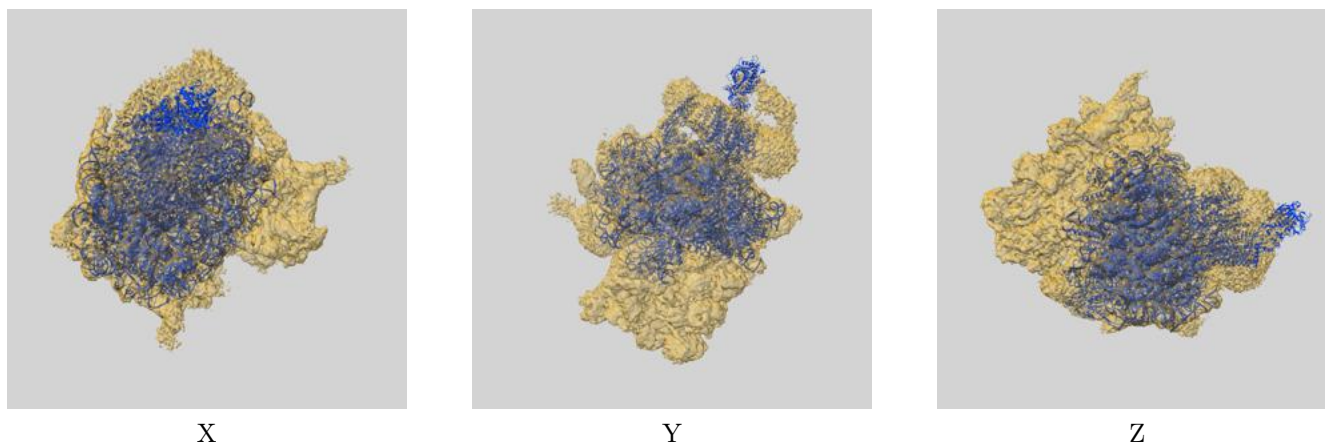
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

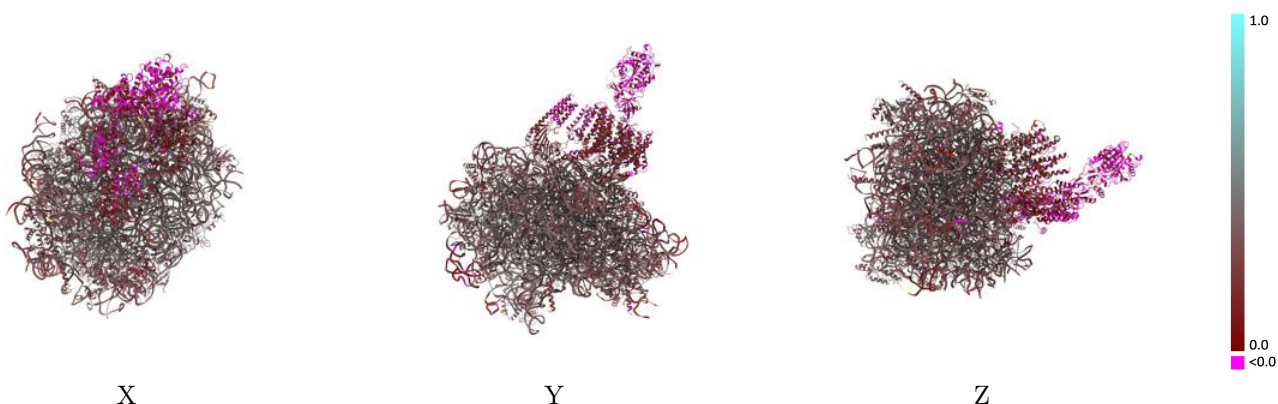
This section contains information regarding the fit between EMDB map EMD-26133 and PDB model 7TUT. Per-residue inclusion information can be found in section [3](#) on page [18](#).

9.1 Map-model overlay [i](#)



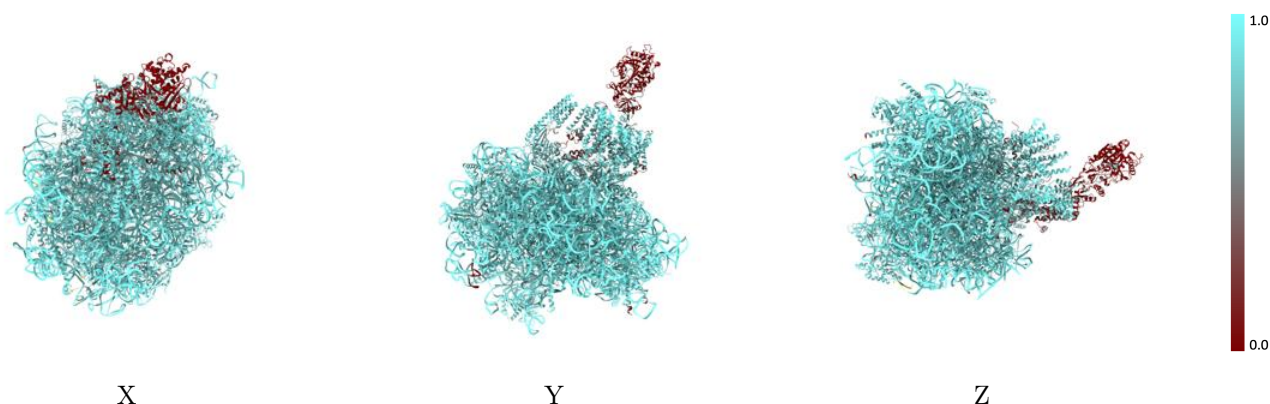
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



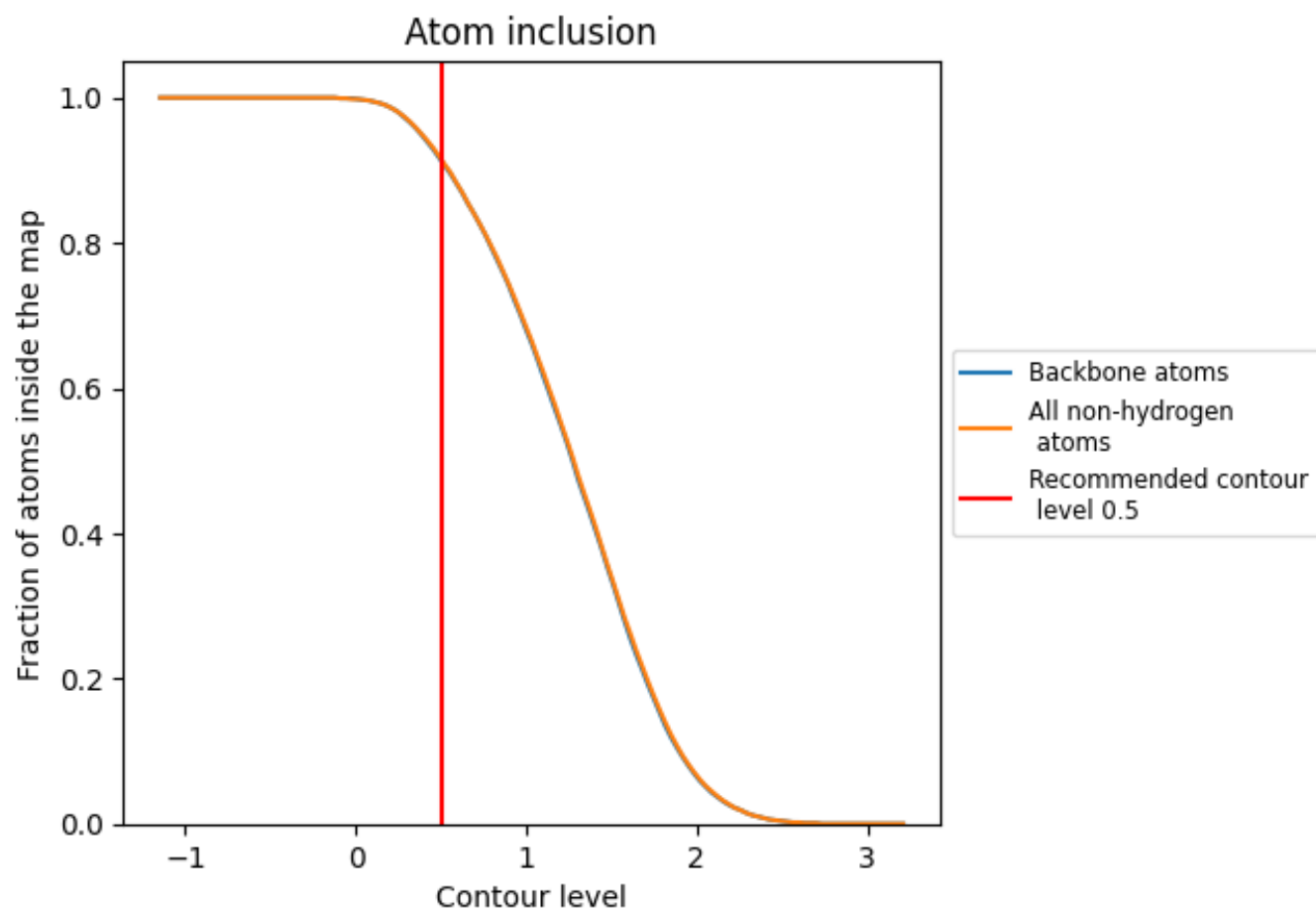
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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	 0.9160	 0.3250
1	 0.8120	 0.2120
2	 0.8580	 0.1580
3	 0.7680	 0.1660
4	 0.7570	 0.1820
5	 0.8210	 0.0900
6	 0.8010	 0.1400
7	 0.1390	 0.0200
8	 0.6010	 0.1030
9	 0.6230	 0.0320
A	 0.9220	 0.3700
B	 0.7840	 0.2490
C	 0.9200	 0.3570
D	 0.9380	 0.3220
E	 0.9190	 0.3340
F	 0.9060	 0.3420
G	 0.8760	 0.3020
H	 0.8950	 0.3520
I	 0.9120	 0.3640
J	 0.9140	 0.3220
K	 0.9880	 0.3510
L	 0.8960	 0.3290
M	 0.9090	 0.3450
N	 0.9160	 0.3470
O	 0.8920	 0.3470
P	 0.8860	 0.3480
Q	 0.9390	 0.3670
R	 0.8840	 0.3280
S	 0.9230	 0.3740
T	 0.8960	 0.3620
U	 0.8580	 0.3010
V	 0.9110	 0.3820
W	 0.9080	 0.3630
X	 0.8900	 0.3420
Y	 0.8530	 0.3400



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Chain	Atom inclusion	Q-score
Z	 0.9150	 0.3380
a	 0.9340	 0.3580
b	 0.8740	 0.2900
c	 0.9340	 0.3320
d	 0.9280	 0.3540
e	 0.8980	 0.3730
f	 0.9130	 0.3800
g	 0.8880	 0.3390
h	 0.8730	 0.3120
i	 0.9080	 0.3200
j	 0.9350	 0.3480
k	 0.8560	 0.3050
l	 0.8950	 0.3240
m	 0.9280	 0.3500
n	 0.8490	 0.2300
o	 0.9250	 0.3640
p	 0.8910	 0.3330
q	 0.8890	 0.3160
r	 0.9310	 0.3650
u	 0.9950	 0.3740
v	 0.9860	 0.3500
w	 0.9170	 0.3710