wwPDB EM Validation Summary Report ⓘ

Nov 9, 2026 – 06:12 pm GMT

PDB ID	:	9T5G / pdb_00009t5g
EMDB ID	:	EMD-55577
Title	:	Structure of a stalled E. coli 70S RNC-NuoK-86 in complex with the SecYEG translocon
Authors	:	Rosales-Hernandez, C.; Busch, M.; Kamel, M.; Kedrov, A.; Beckmann, R.
Deposited on	:	2025-11-05
Resolution	:	2.55 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

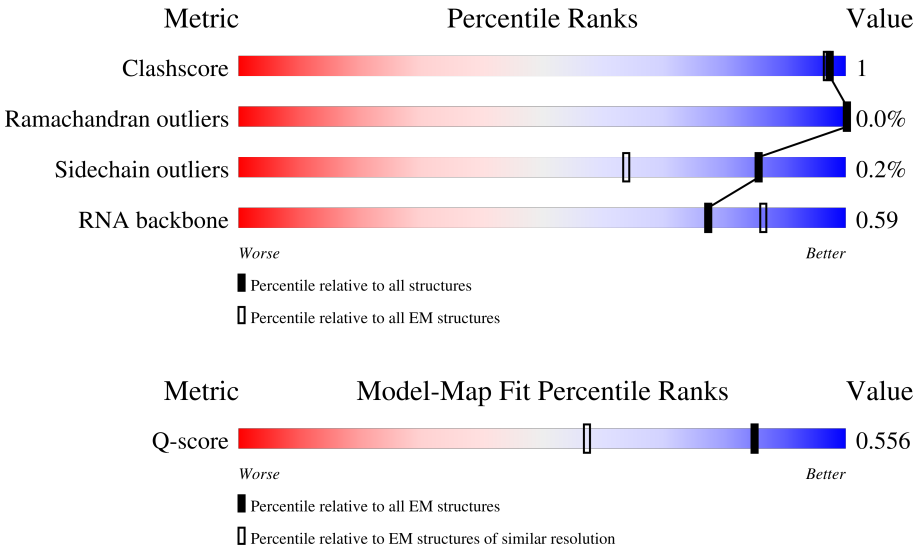
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.2
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.51

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.55 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.



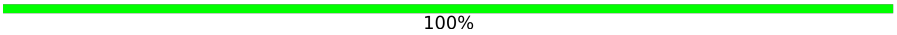
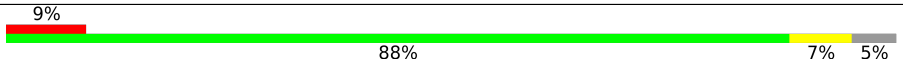
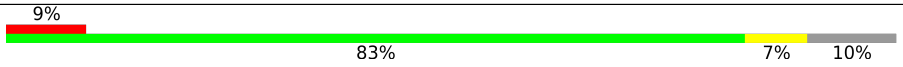
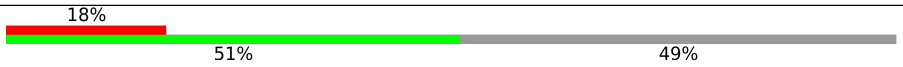
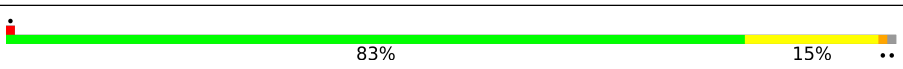
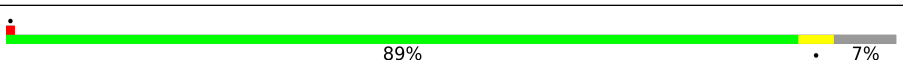
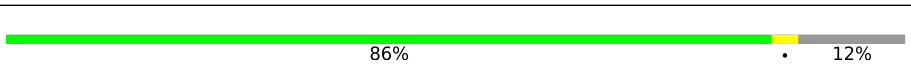
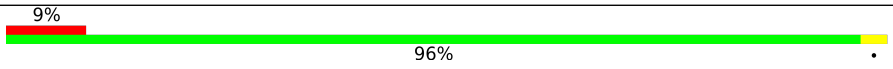
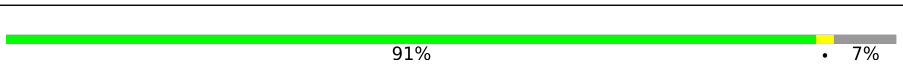
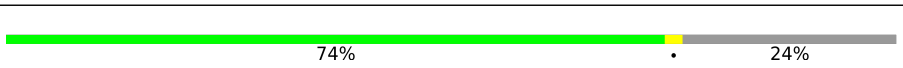
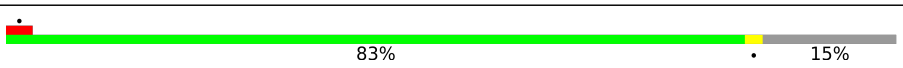
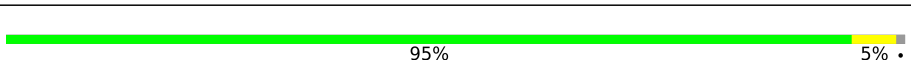
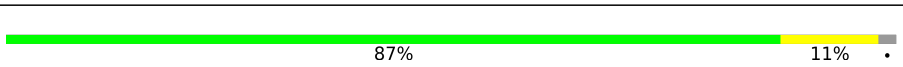
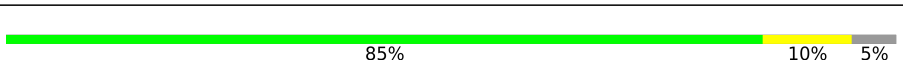
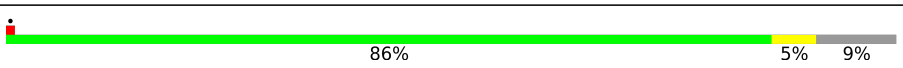
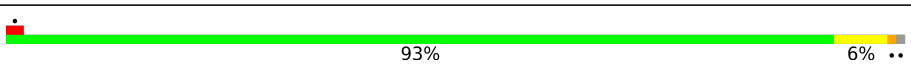
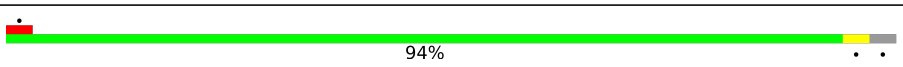
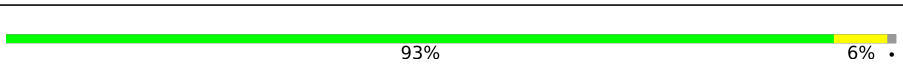
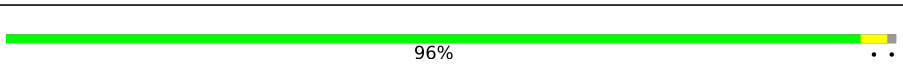
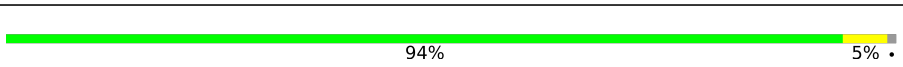
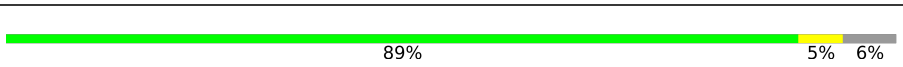
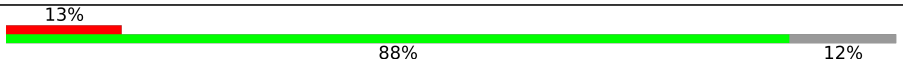
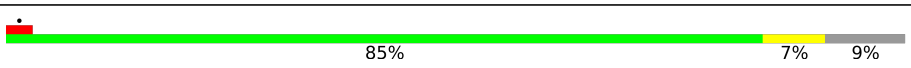
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7475 (2.05 - 3.05)

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 <=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	0	55	93% 7%
2	1	46	100%
3	2	65	94%

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Mol	Chain	Length	Quality of chain
4	3	38	
5	4	70	
6	5	2	
7	6	443	
8	7	127	
9	8	110	
10	A	1542	
11	B	241	
12	C	233	
13	D	206	
14	E	167	
15	F	135	
16	G	179	
17	H	130	
18	I	130	
19	J	103	
20	K	129	
21	L	124	
22	M	118	
23	N	101	
24	O	89	
25	P	82	
26	Q	84	
27	R	75	
28	S	92	

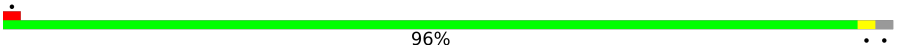
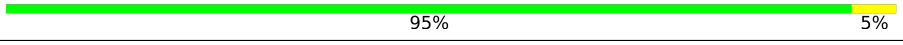
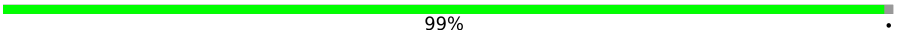
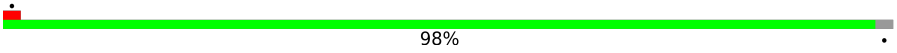
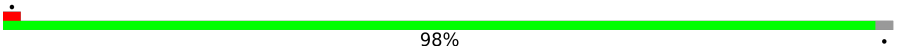
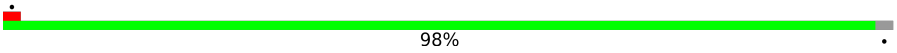
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Mol	Chain	Length	Quality of chain
29	T	87	97%
30	U	71	73% 96%
31	V	120	16% 38% 61%
32	X	9	89% 11%
33	Y	77	10% 83% 17%
34	Z	77	82% 16%
35	a	2904	83% 11% 5%
36	b	120	88% 11%
37	c	273	99%
38	d	209	99%
39	e	201	99%
40	f	179	93% 6%
41	g	177	94% 5%
42	h	149	25% 72%
43	i	142	98%
44	j	123	98%
45	k	144	97%
46	l	136	98%
47	m	127	93% 7%
48	n	117	99%
49	o	115	98%
50	p	118	98%
51	q	103	100%
52	r	110	98%
53	s	100	93% 7%

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Mol	Chain	Length	Quality of chain
54	t	104	
55	u	94	
56	v	85	
57	w	78	
58	x	63	
59	y	59	
60	z	57	

2 Entry composition (i)

There are 64 unique types of molecules in this entry. The entry contains 146815 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	51	Total	C	N	O	0	0
			417	269	76	72		

- Molecule 2 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 3 is a protein called Large ribosomal subunit protein bL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 4 is a protein called Large ribosomal subunit protein bL36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 5 is a protein called Large ribosomal subunit protein bL31A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	60	Total	C	N	O	S	0	0
			480	299	90	85	6		

- Molecule 6 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	2	Total	C	N	O	P	0	0
			42	19	8	13	2		

- Molecule 7 is a protein called Protein translocase subunit SecY.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	421	Total	C	N	O	S	0	0
			3260	2158	535	550	17		

- Molecule 8 is a protein called Protein translocase subunit SecE.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	114	Total	C	N	O	S	0	0
			874	579	149	143	3		

- Molecule 9 is a protein called Protein-export membrane protein SecG.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	56	Total	C	N	O	S	0	0
			431	287	68	72	4		

- Molecule 10 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	1519	Total	C	N	O	P	0	0
			32612	14552	5986	10555	1519		

- Molecule 11 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	224	Total	C	N	O	S	0	0
			1753	1109	315	321	8		

- Molecule 12 is a protein called Small ribosomal subunit protein uS3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 13 is a protein called Small ribosomal subunit protein uS4.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 14 is a protein called Small ribosomal subunit protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 15 is a protein called Small ribosomal subunit protein bS6, fully modified isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F	103	Total	C	N	O	S	0	0
			839	530	151	151	7		

- Molecule 16 is a protein called Small ribosomal subunit protein uS7.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	153	Total	C	N	O	S	0	0
			1203	750	231	218	4		

- Molecule 17 is a protein called Small ribosomal subunit protein uS8.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 18 is a protein called Small ribosomal subunit protein uS9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	I	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 19 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	J	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 20 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	K	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 21 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 22 is a protein called Small ribosomal subunit protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

- Molecule 23 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	N	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 24 is a protein called Small ribosomal subunit protein uS15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	O	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 25 is a protein called Small ribosomal subunit protein bS16.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	81	Total	C	N	O	S	0	0
			643	403	127	112	1		

- Molecule 26 is a protein called Small ribosomal subunit protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

- Molecule 27 is a protein called Small ribosomal subunit protein bS18.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	R	66	Total	C	N	O	S	0	0
			544	345	102	96	1		

- Molecule 28 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

- Molecule 29 is a protein called Small ribosomal subunit protein bS20.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

- Molecule 30 is a protein called Small ribosomal subunit protein bS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 31 is a protein called NADH-quinone oxidoreductase subunit K.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	V	47	Total	C	N	O	0	0
			336	222	57	57		

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	1	MET	-	initiating methionine	UNP P0AFE4
V	2	SER	-	expression tag	UNP P0AFE4
V	3	THR	-	expression tag	UNP P0AFE4
V	89	PRO	-	expression tag	UNP P0AFE4
V	90	GLY	-	expression tag	UNP P0AFE4
V	91	TYR	-	expression tag	UNP P0AFE4
V	92	PRO	-	expression tag	UNP P0AFE4
V	93	TYR	-	expression tag	UNP P0AFE4
V	94	ASP	-	expression tag	UNP P0AFE4
V	95	VAL	-	expression tag	UNP P0AFE4
V	96	PRO	-	expression tag	UNP P0AFE4
V	97	ASP	-	expression tag	UNP P0AFE4
V	98	TYR	-	expression tag	UNP P0AFE4
V	99	ALA	-	expression tag	UNP P0AFE4
V	100	GLY	-	expression tag	UNP P0AFE4
V	101	GLY	-	expression tag	UNP P0AFE4
V	102	SER	-	expression tag	UNP P0AFE4
V	103	GLY	-	expression tag	UNP P0AFE4
V	104	PHE	-	expression tag	UNP P0AFE4

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Chain	Residue	Modelled	Actual	Comment	Reference
V	105	SER	-	expression tag	UNP P0AFE4
V	106	THR	-	expression tag	UNP P0AFE4
V	107	PRO	-	expression tag	UNP P0AFE4
V	108	VAL	-	expression tag	UNP P0AFE4
V	109	TRP	-	expression tag	UNP P0AFE4
V	110	ILE	-	expression tag	UNP P0AFE4
V	111	TRP	-	expression tag	UNP P0AFE4
V	112	TRP	-	expression tag	UNP P0AFE4
V	113	TRP	-	expression tag	UNP P0AFE4
V	114	PRO	-	expression tag	UNP P0AFE4
V	115	ARG	-	expression tag	UNP P0AFE4
V	116	ILE	-	expression tag	UNP P0AFE4
V	117	ARG	-	expression tag	UNP P0AFE4
V	118	GLY	-	expression tag	UNP P0AFE4
V	119	PRO	-	expression tag	UNP P0AFE4
V	120	PRO	-	expression tag	UNP P0AFE4

- Molecule 32 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	X	9	Total	C	N	O	P	0	0
			189	84	31	65	9		

- Molecule 33 is a RNA chain called A-site tRNA-Pro.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Y	77	Total	C	N	O	P	0	0
			1646	734	297	539	76		

- Molecule 34 is a RNA chain called P-site tRNA-Pro.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Z	77	Total	C	N	O	P	0	0
			1644	733	295	540	76		

- Molecule 35 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	a	2753	Total	C	N	O	P	0	0
			59127	26381	10897	19096	2753		

- Molecule 36 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 37 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	c	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 38 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	d	209	Total	C	N	O	S	0	0
			1566	980	288	294	4		

- Molecule 39 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	e	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 40 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	f	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 41 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	g	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 42 is a protein called Large ribosomal subunit protein bL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 43 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	i	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 44 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 45 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	k	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 46 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	l	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 47 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 48 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	n	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 49 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	o	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 50 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	p	117	Total 947	C 604	N 192	O 151	0	0

- Molecule 51 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	q	103	Total 816	C 516	N 153	O 145	S 2	0	0

- Molecule 52 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	r	110	Total 857	C 532	N 166	O 156	S 3	0	0

- Molecule 53 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	s	93	Total 738	C 466	N 139	O 131	S 2	0	0

- Molecule 54 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	t	102	Total 779	C 492	N 146	O 141	0	0

- Molecule 55 is a protein called Large ribosomal subunit protein bL25.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	u	94	Total 753	C 479	N 137	O 134	S 3	0	0

- Molecule 56 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	v	78	Total 592	C 365	N 119	O 107	S 1	0	0

- Molecule 57 is a protein called Large ribosomal subunit protein bL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	w	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 58 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	x	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 59 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	y	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 60 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	z	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 61 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
61	3	1	Total	Zn	0
			1	1	
61	4	1	Total	Zn	0
			1	1	

- Molecule 62 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

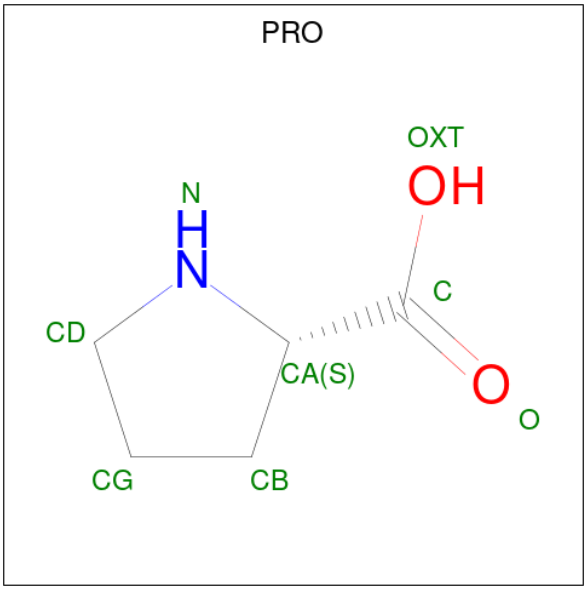
Mol	Chain	Residues	Atoms		AltConf
62	A	92	Total	Mg	0
			92	92	
62	Q	1	Total	Mg	0
			1	1	
62	V	1	Total	Mg	0
			1	1	
62	a	207	Total	Mg	0
			207	207	
62	b	5	Total	Mg	0
			5	5	

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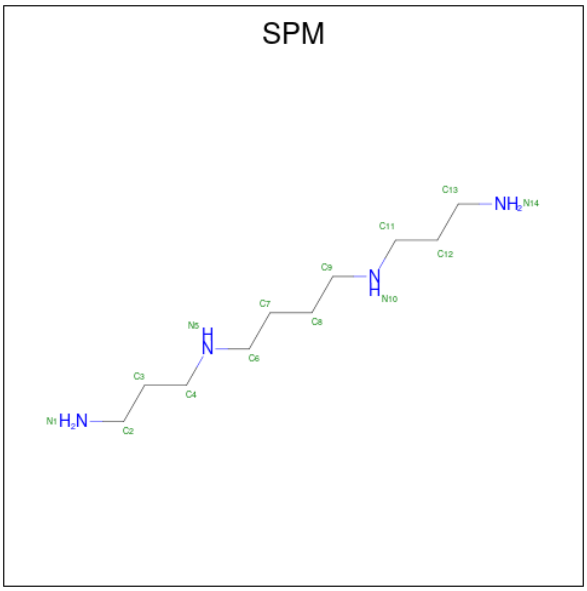
Mol	Chain	Residues	Atoms	AltConf
62	c	1	Total Mg 1 1	0
62	d	1	Total Mg 1 1	0
62	z	1	Total Mg 1 1	0

- Molecule 63 is PROLINE (CCD ID: PRO) (formula: $C_5H_9NO_2$).



Mol	Chain	Residues	Atoms	AltConf
63	Y	1	Total C N O 7 5 1 1	0

- Molecule 64 is SPERMINE (CCD ID: SPM) (formula: $C_{10}H_{26}N_4$).



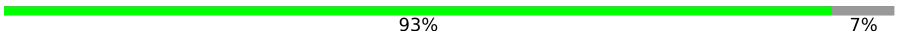
Mol	Chain	Residues	Atoms			AltConf
64	a	1	Total	C	N	0
			14	10	4	

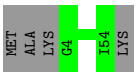
3 Residue-property plots (i)

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: Large ribosomal subunit protein bL33

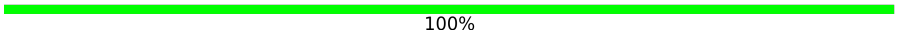
Chain 0:





• Molecule 2: Large ribosomal subunit protein bL34

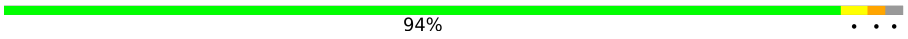
Chain 1:

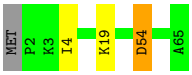


There are no outlier residues recorded for this chain.

• Molecule 3: Large ribosomal subunit protein bL35

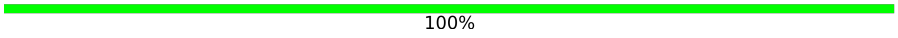
Chain 2:





• Molecule 4: Large ribosomal subunit protein bL36A

Chain 3:

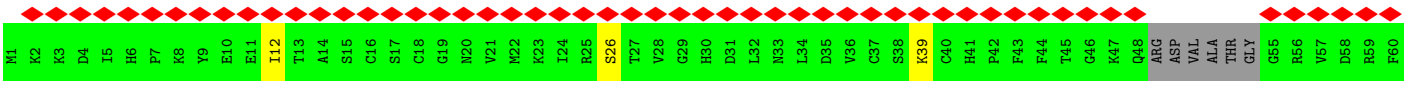


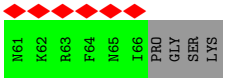
There are no outlier residues recorded for this chain.

• Molecule 5: Large ribosomal subunit protein bL31A

Chain 4:







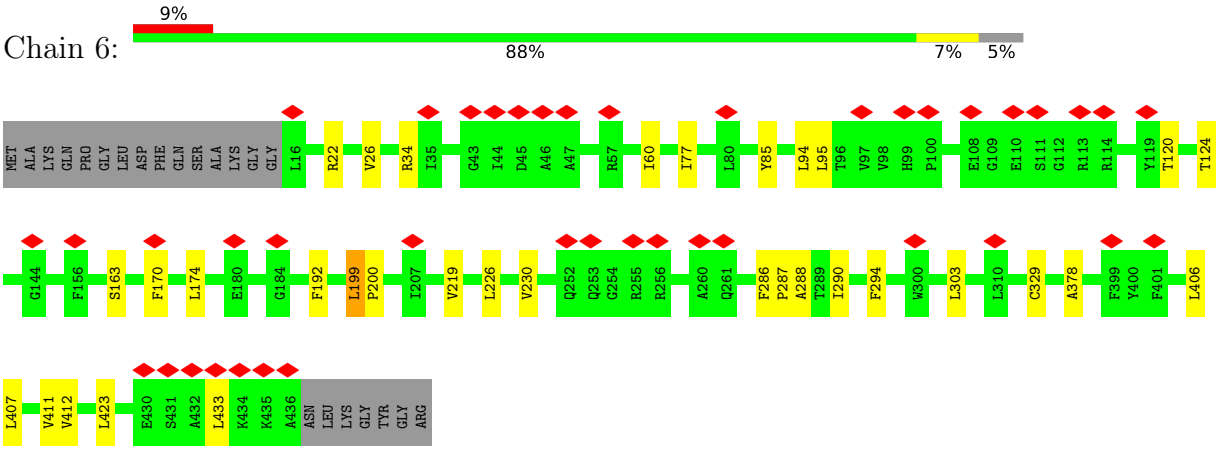
• Molecule 6: E-site tRNA

Chain 5:



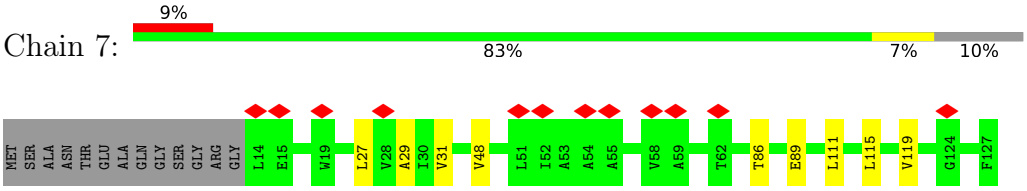
• Molecule 7: Protein translocase subunit SecY

Chain 6:



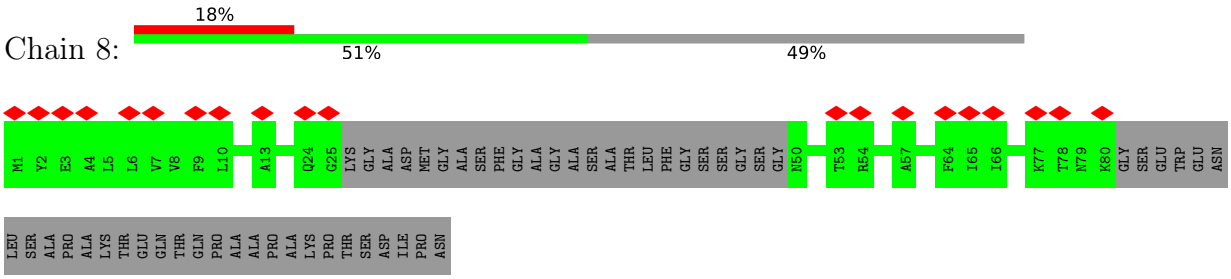
• Molecule 8: Protein translocase subunit SecE

Chain 7:



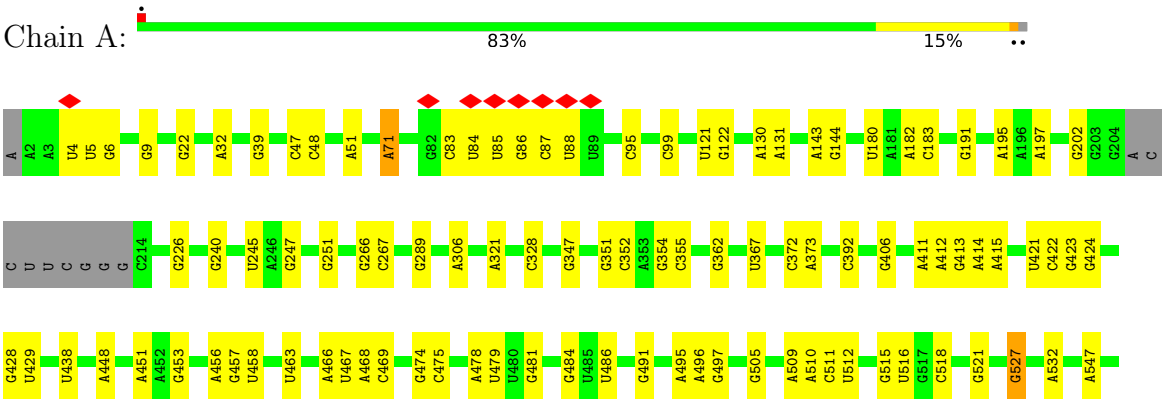
• Molecule 9: Protein-export membrane protein SecG

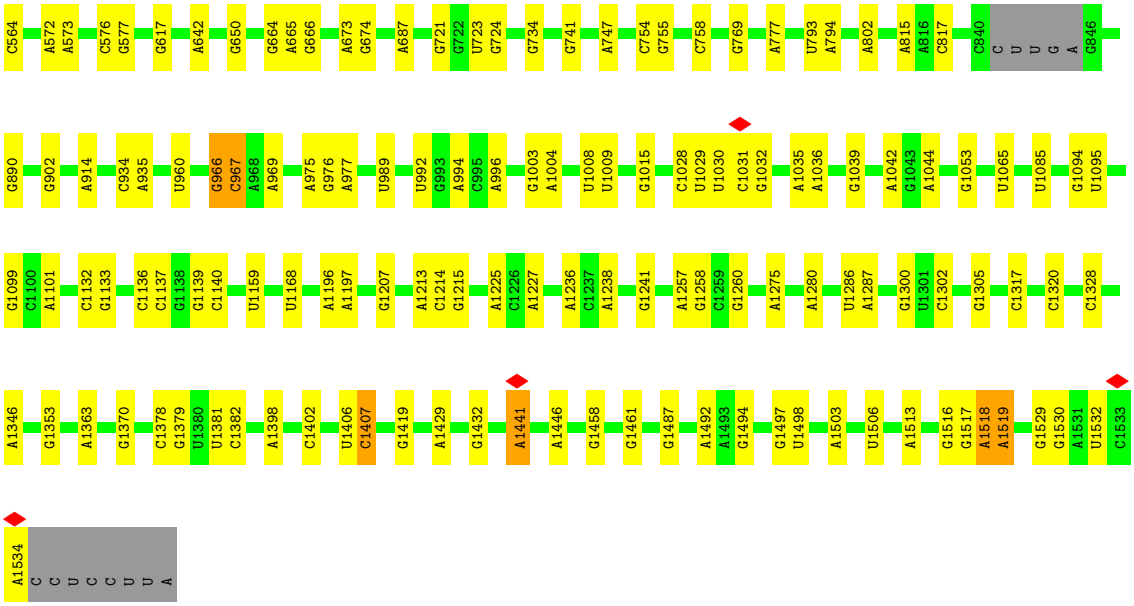
Chain 8:



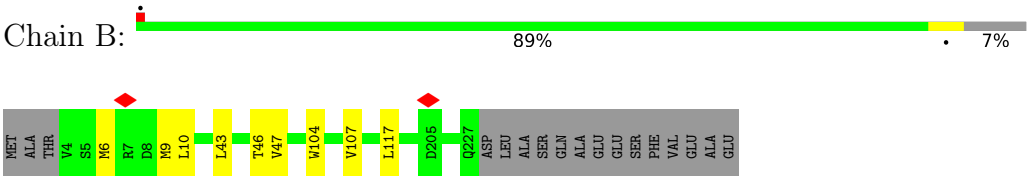
• Molecule 10: 16S rRNA

Chain A:

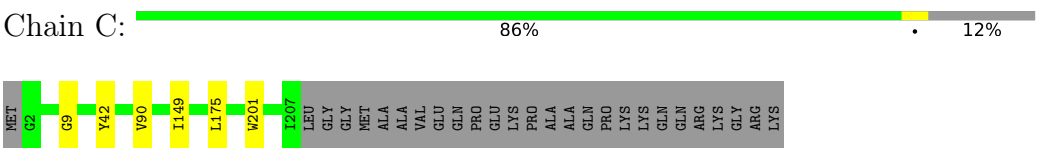




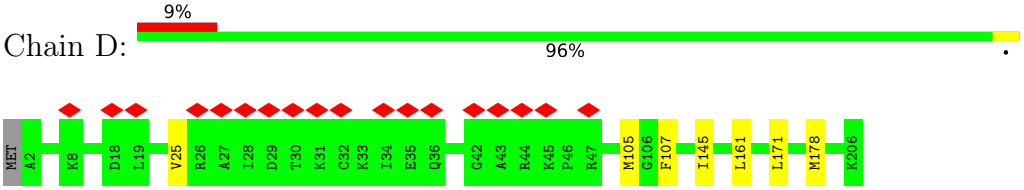
• Molecule 11: Small ribosomal subunit protein uS2



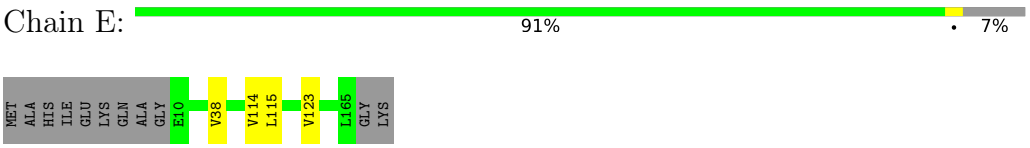
• Molecule 12: Small ribosomal subunit protein uS3



• Molecule 13: Small ribosomal subunit protein uS4



• Molecule 14: Small ribosomal subunit protein uS5



• Molecule 15: Small ribosomal subunit protein bS6, fully modified isoform

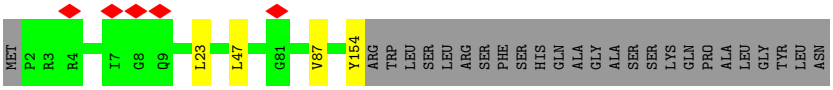




• Molecule 16: Small ribosomal subunit protein uS7

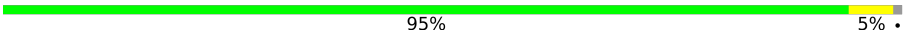
Chain G:

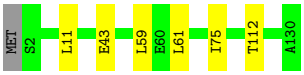




• Molecule 17: Small ribosomal subunit protein uS8

Chain H:

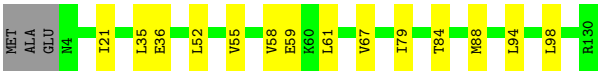




• Molecule 18: Small ribosomal subunit protein uS9

Chain I:

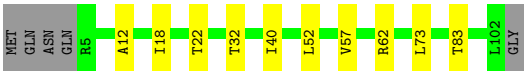




• Molecule 19: Small ribosomal subunit protein uS10

Chain J:

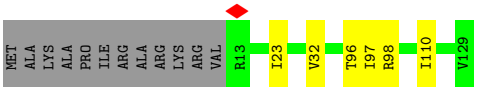




• Molecule 20: Small ribosomal subunit protein uS11

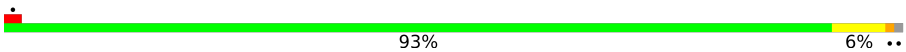
Chain K:

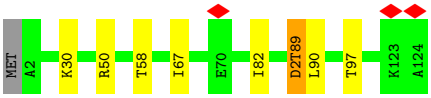




• Molecule 21: Small ribosomal subunit protein uS12

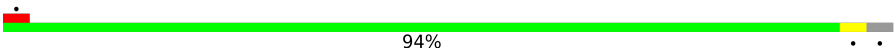
Chain L:

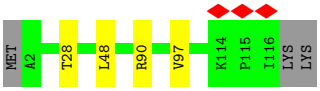




• Molecule 22: Small ribosomal subunit protein uS13

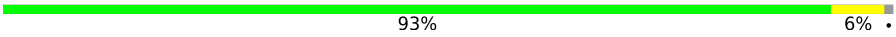
Chain M:





• Molecule 23: Small ribosomal subunit protein uS14

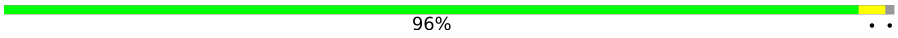
Chain N:





• Molecule 24: Small ribosomal subunit protein uS15

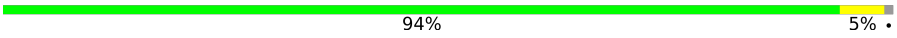
Chain O:





• Molecule 25: Small ribosomal subunit protein bS16

Chain P:

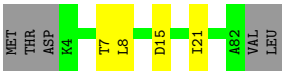




• Molecule 26: Small ribosomal subunit protein uS17

Chain Q:

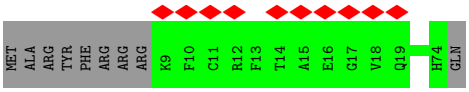




• Molecule 27: Small ribosomal subunit protein bS18

Chain R:

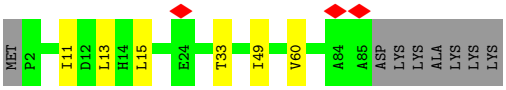




• Molecule 28: Small ribosomal subunit protein uS19

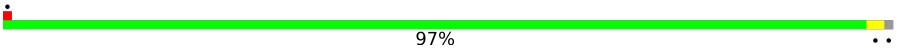
Chain S:





• Molecule 29: Small ribosomal subunit protein bS20

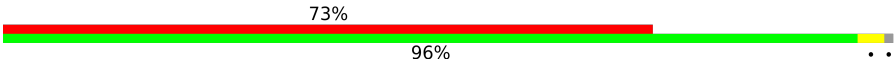
Chain T:

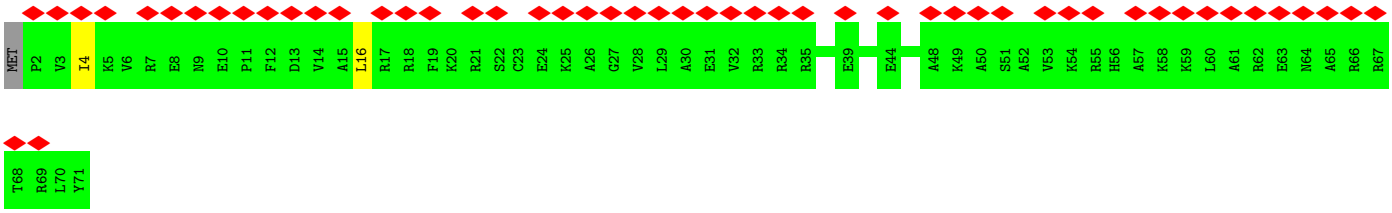




• Molecule 30: Small ribosomal subunit protein bS21

Chain U:

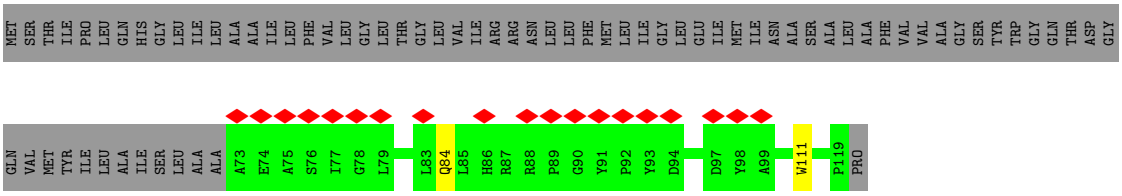




• Molecule 31: NADH-quinone oxidoreductase subunit K

Chain V:





• Molecule 32: mRNA

Chain X:

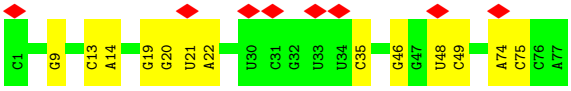




• Molecule 33: A-site tRNA-Pro

Chain Y:

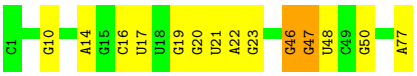




• Molecule 34: P-site tRNA-Pro

Chain Z:

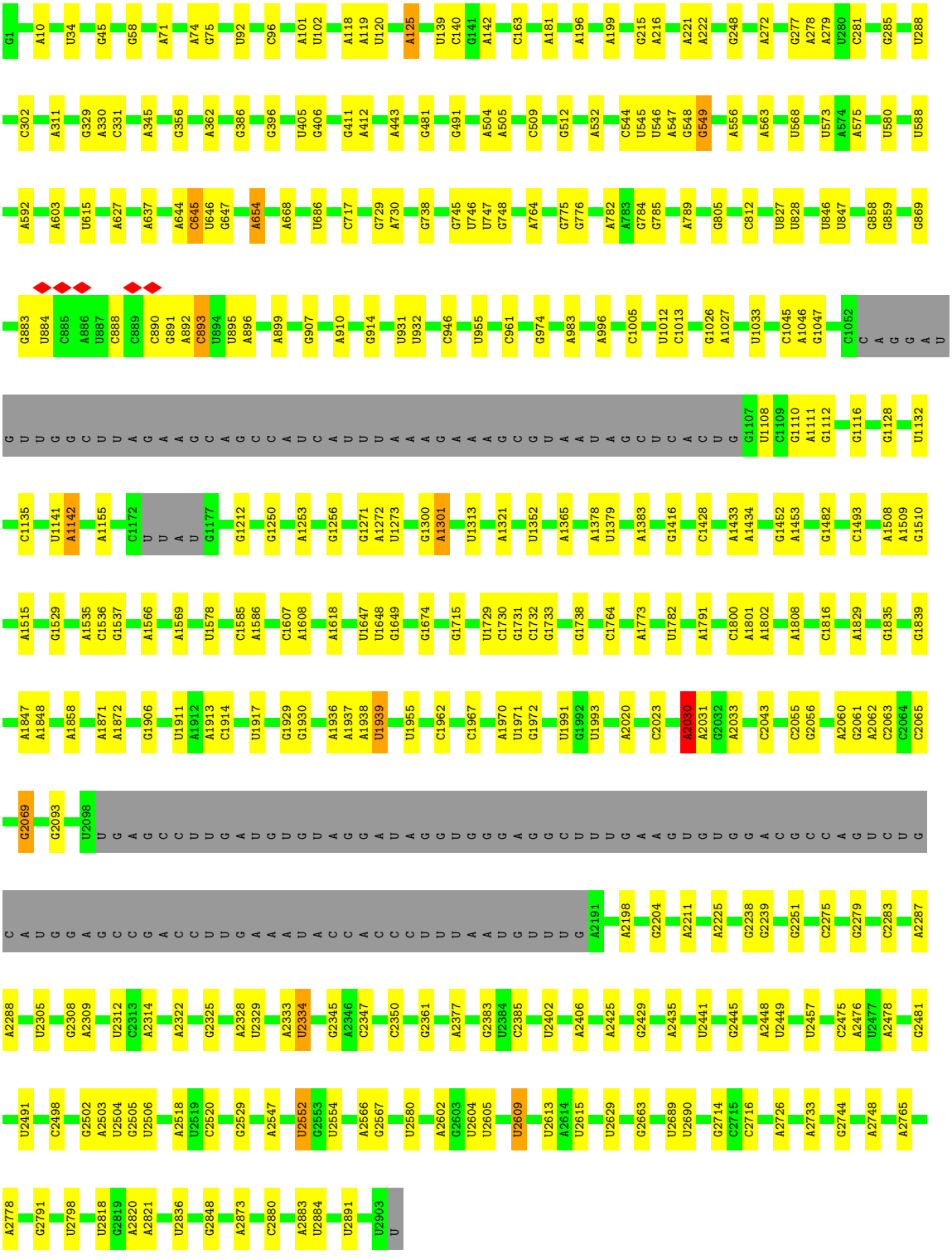




• Molecule 35: 23S rRNA

Chain a:

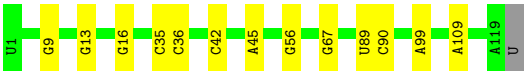




• Molecule 36: 5S rRNA

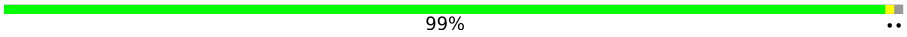
Chain b:





• Molecule 37: Large ribosomal subunit protein uL2

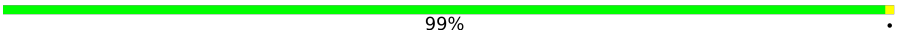
Chain c:





• Molecule 38: Large ribosomal subunit protein uL3

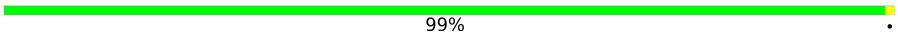
Chain d:





• Molecule 39: Large ribosomal subunit protein uL4

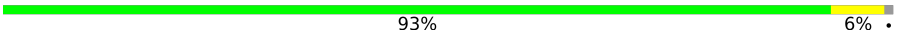
Chain e:

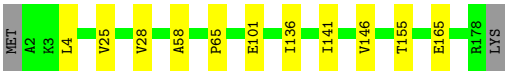




• Molecule 40: Large ribosomal subunit protein uL5

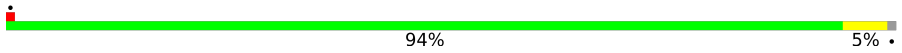
Chain f:





• Molecule 41: Large ribosomal subunit protein uL6

Chain g:

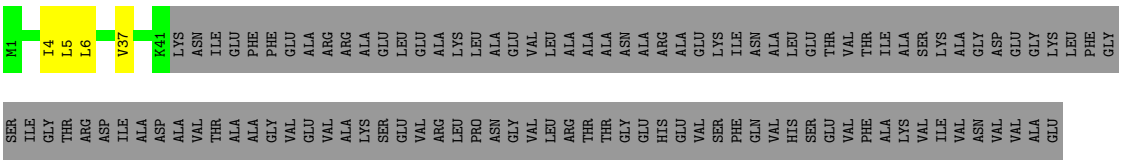




• Molecule 42: Large ribosomal subunit protein bL9

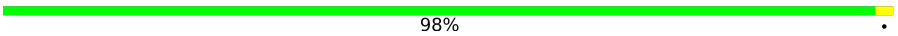
Chain h:

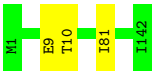




• Molecule 43: Large ribosomal subunit protein uL13

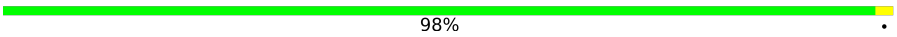
Chain i:





• Molecule 44: Large ribosomal subunit protein uL14

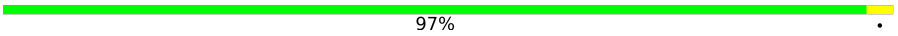
Chain j:





• Molecule 45: Large ribosomal subunit protein uL15

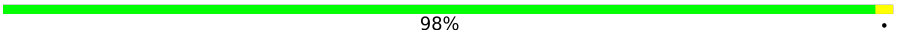
Chain k:





• Molecule 46: 50S ribosomal protein L16

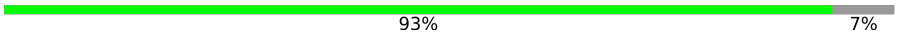
Chain l:

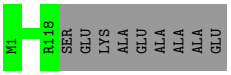




• Molecule 47: Large ribosomal subunit protein bL17

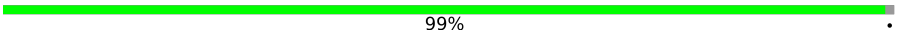
Chain m:





• Molecule 48: Large ribosomal subunit protein uL18

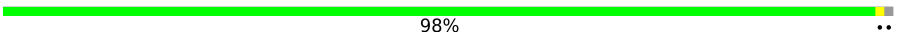
Chain n:





• Molecule 49: Large ribosomal subunit protein bL19

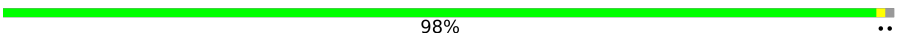
Chain o:

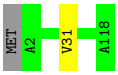




• Molecule 50: Large ribosomal subunit protein bL20

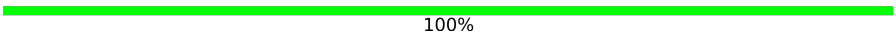
Chain p:





• Molecule 51: Large ribosomal subunit protein bL21

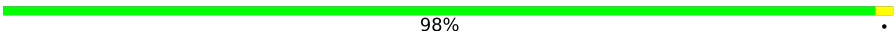
Chain q:



There are no outlier residues recorded for this chain.

• Molecule 52: Large ribosomal subunit protein uL22

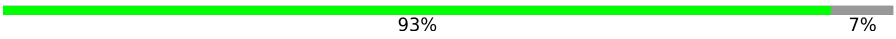
Chain r:

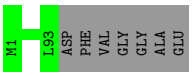




• Molecule 53: Large ribosomal subunit protein uL23

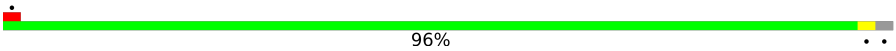
Chain s:

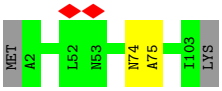




• Molecule 54: Large ribosomal subunit protein uL24

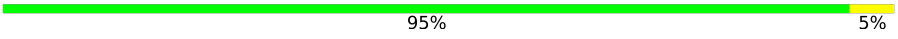
Chain t:

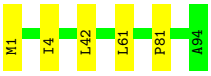




• Molecule 55: Large ribosomal subunit protein bL25

Chain u:

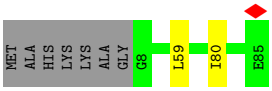




• Molecule 56: Large ribosomal subunit protein bL27

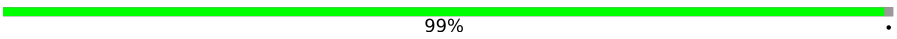
Chain v:





• Molecule 57: Large ribosomal subunit protein bL28

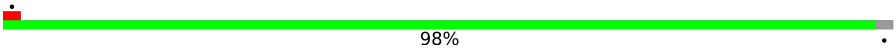
Chain w:





• Molecule 58: Large ribosomal subunit protein uL29

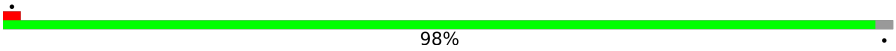
Chain x:





• Molecule 59: Large ribosomal subunit protein uL30

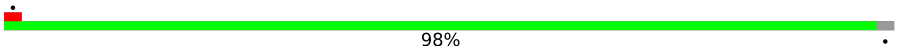
Chain y:





• Molecule 60: Large ribosomal subunit protein bL32

Chain z:





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	57156	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.999	Depositor
Minimum map value	-0.372	Depositor
Average map value	0.011	Depositor
Map value standard deviation	0.059	Depositor
Recommended contour level	0.175	Depositor
Map size (Å)	494.36, 494.36, 494.36	wwPDB
Map dimensions	680, 680, 680	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	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, 5MC, OMU, 2MG, 6MZ, MG, 2MA, 1MG, 4OC, SPM, MA6, D2T, OMC, G7M, OMG, PSU, MEQ, UR3, H2U

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	0	0.22	0/424	0.31	0/565
2	1	0.43	0/380	0.32	0/498
3	2	0.37	0/513	0.35	0/676
4	3	0.36	0/303	0.34	0/397
5	4	0.20	0/488	0.39	0/649
6	5	0.52	0/46	0.70	0/69
7	6	0.17	0/3335	0.37	0/4526
8	7	0.16	0/887	0.35	0/1209
9	8	0.16	0/434	0.30	0/584
10	A	0.60	0/36236	0.75	2/56520 (0.0%)
11	B	0.18	0/1784	0.33	0/2403
12	C	0.19	0/1651	0.29	0/2225
13	D	0.18	0/1665	0.31	0/2227
14	E	0.25	0/1165	0.35	0/1568
15	F	0.20	0/858	0.31	0/1160
16	G	0.18	0/1219	0.34	0/1635
17	H	0.23	0/989	0.29	0/1326
18	I	0.17	0/1034	0.35	0/1375
19	J	0.17	0/796	0.33	0/1077
20	K	0.18	0/893	0.32	0/1205
21	L	0.19	0/960	0.35	0/1286
22	M	0.15	0/900	0.34	0/1204
23	N	0.18	0/817	0.33	0/1088
24	O	0.21	0/722	0.30	0/964
25	P	0.21	0/653	0.34	0/877
26	Q	0.19	0/650	0.38	0/871
27	R	0.20	0/553	0.29	0/742
28	S	0.14	0/685	0.29	0/922
29	T	0.22	0/676	0.34	0/895
30	U	0.15	0/597	0.30	0/792
31	V	0.20	0/353	0.36	0/491

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
32	X	0.44	0/209	0.66	0/323
33	Y	0.37	0/1840	0.70	0/2869
34	Z	0.45	0/1837	0.72	0/2864
35	a	0.99	0/65718	0.79	16/102519 (0.0%)
36	b	0.76	0/2850	0.73	0/4444
37	c	0.38	0/2121	0.35	0/2852
38	d	0.39	0/1576	0.34	0/2119
39	e	0.36	0/1571	0.33	0/2113
40	f	0.22	0/1434	0.35	0/1926
41	g	0.24	0/1343	0.33	0/1816
42	h	0.26	0/306	0.36	0/413
43	i	0.38	0/1152	0.31	0/1551
44	j	0.36	0/955	0.33	0/1279
45	k	0.36	0/1062	0.32	0/1413
46	l	0.37	0/1093	0.33	0/1460
47	m	0.41	0/958	0.34	0/1281
48	n	0.27	0/902	0.33	0/1209
49	o	0.35	0/929	0.33	0/1242
50	p	0.42	0/960	0.36	0/1278
51	q	0.36	0/829	0.32	0/1107
52	r	0.38	0/864	0.33	0/1156
53	s	0.34	0/744	0.33	0/994
54	t	0.31	0/787	0.33	0/1051
55	u	0.30	0/766	0.34	0/1025
56	v	0.34	0/599	0.34	0/792
57	w	0.36	0/635	0.35	0/848
58	x	0.28	0/502	0.33	0/667
59	y	0.34	0/453	0.36	0/605
60	z	0.38	0/450	0.31	0/599
All	All	0.73	0/158111	0.68	18/235841 (0.0%)

There are no bond length outliers.

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
35	a	893	C	N3-C2-O2	-6.76	117.17	121.90
35	a	2506	U	C2-N1-C1'	6.70	125.74	117.70
35	a	512	G	O4'-C1'-N9	6.70	113.56	108.20
35	a	1313	U	C2-N1-C1'	6.64	125.67	117.70
35	a	1301	A	O5'-C5'-C4'	6.16	114.33	109.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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	0	417	0	451	0	0
2	1	377	0	418	0	0
3	2	504	0	572	3	0
4	3	302	0	340	0	0
5	4	480	0	478	1	0
6	5	42	0	23	0	0
7	6	3260	0	3416	21	0
8	7	874	0	966	5	0
9	8	431	0	475	0	0
10	A	32612	0	16426	16	0
11	B	1753	0	1780	8	0
12	C	1624	0	1696	3	0
13	D	1643	0	1707	4	0
14	E	1152	0	1196	2	0
15	F	839	0	833	1	0
16	G	1203	0	1254	2	0
17	H	979	0	1031	3	0
18	I	1022	0	1070	10	0
19	J	786	0	828	6	0
20	K	877	0	887	6	0
21	L	957	0	1017	6	0
22	M	891	0	952	3	0
23	N	805	0	844	6	0
24	O	714	0	734	1	0
25	P	643	0	661	3	0
26	Q	641	0	682	3	0
27	R	544	0	565	0	0
28	S	668	0	693	4	0
29	T	670	0	719	1	0
30	U	589	0	629	5	0
31	V	336	0	269	2	0
32	X	189	0	98	0	0
33	Y	1646	0	832	0	0
34	Z	1644	0	832	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
35	a	59127	0	29763	12	0
36	b	2549	0	1291	0	0
37	c	2082	0	2154	1	0
38	d	1566	0	1618	1	0
39	e	1552	0	1619	1	0
40	f	1410	0	1444	8	0
41	g	1323	0	1371	5	0
42	h	303	0	327	2	0
43	i	1129	0	1162	2	0
44	j	946	0	1023	1	0
45	k	1053	0	1129	4	0
46	l	1074	0	1157	2	0
47	m	945	0	989	0	0
48	n	892	0	923	0	0
49	o	917	0	962	2	0
50	p	947	0	1019	1	0
51	q	816	0	839	0	0
52	r	857	0	922	1	0
53	s	738	0	807	0	0
54	t	779	0	831	1	0
55	u	753	0	780	4	0
56	v	592	0	607	1	0
57	w	625	0	652	0	0
58	x	501	0	531	0	0
59	y	449	0	488	0	0
60	z	444	0	458	0	0
61	3	1	0	0	0	0
61	4	1	0	0	0	0
62	A	92	0	0	0	0
62	Q	1	0	0	0	0
62	V	1	0	0	0	0
62	a	207	0	0	0	0
62	b	5	0	0	0	0
62	c	1	0	0	0	0
62	d	1	0	0	0	0
62	z	1	0	0	0	0
63	Y	7	0	7	0	0
64	a	14	0	26	0	0
All	All	146815	0	100273	156	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 1.

The worst 5 of 156 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)
10:A:1441:A:H62	10:A:1461:G:H21	1.03	0.99
20:K:97:ILE:HD13	30:U:16:LEU:HD11	1.45	0.97
10:A:1441:A:N6	10:A:1461:G:H21	1.63	0.96
10:A:1441:A:H62	10:A:1461:G:N2	1.70	0.89
18:I:88:MET:HE3	18:I:98:LEU:HD12	1.59	0.84

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	49/55 (89%)	49 (100%)	0	0	100	100
2	1	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
3	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
4	3	36/38 (95%)	36 (100%)	0	0	100	100
5	4	56/70 (80%)	52 (93%)	4 (7%)	0	100	100
7	6	419/443 (95%)	404 (96%)	15 (4%)	0	100	100
8	7	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
9	8	52/110 (47%)	52 (100%)	0	0	100	100
11	B	222/241 (92%)	214 (96%)	8 (4%)	0	100	100
12	C	204/233 (88%)	195 (96%)	9 (4%)	0	100	100
13	D	203/206 (98%)	194 (96%)	9 (4%)	0	100	100
14	E	154/167 (92%)	150 (97%)	4 (3%)	0	100	100
15	F	101/135 (75%)	95 (94%)	6 (6%)	0	100	100
16	G	151/179 (84%)	143 (95%)	8 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	H	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
18	I	125/130 (96%)	115 (92%)	10 (8%)	0	100	100
19	J	96/103 (93%)	89 (93%)	6 (6%)	1 (1%)	12	17
20	K	115/129 (89%)	109 (95%)	6 (5%)	0	100	100
21	L	120/124 (97%)	110 (92%)	10 (8%)	0	100	100
22	M	113/118 (96%)	107 (95%)	6 (5%)	0	100	100
23	N	98/101 (97%)	97 (99%)	1 (1%)	0	100	100
24	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100
25	P	79/82 (96%)	72 (91%)	7 (9%)	0	100	100
26	Q	77/84 (92%)	70 (91%)	7 (9%)	0	100	100
27	R	64/75 (85%)	61 (95%)	3 (5%)	0	100	100
28	S	82/92 (89%)	79 (96%)	3 (4%)	0	100	100
29	T	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
30	U	68/71 (96%)	67 (98%)	1 (2%)	0	100	100
31	V	45/120 (38%)	42 (93%)	3 (7%)	0	100	100
37	c	269/273 (98%)	260 (97%)	9 (3%)	0	100	100
38	d	206/209 (99%)	198 (96%)	7 (3%)	1 (0%)	24	34
39	e	199/201 (99%)	193 (97%)	6 (3%)	0	100	100
40	f	175/179 (98%)	168 (96%)	7 (4%)	0	100	100
41	g	174/177 (98%)	163 (94%)	11 (6%)	0	100	100
42	h	39/149 (26%)	35 (90%)	4 (10%)	0	100	100
43	i	140/142 (99%)	139 (99%)	1 (1%)	0	100	100
44	j	121/123 (98%)	116 (96%)	5 (4%)	0	100	100
45	k	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
46	l	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
47	m	116/127 (91%)	112 (97%)	4 (3%)	0	100	100
48	n	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
49	o	112/115 (97%)	109 (97%)	3 (3%)	0	100	100
50	p	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
51	q	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
52	r	108/110 (98%)	106 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
53	s	91/100 (91%)	88 (97%)	3 (3%)	0	100	100
54	t	100/104 (96%)	94 (94%)	6 (6%)	0	100	100
55	u	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
56	v	76/85 (89%)	73 (96%)	3 (4%)	0	100	100
57	w	75/78 (96%)	75 (100%)	0	0	100	100
58	x	60/63 (95%)	59 (98%)	1 (2%)	0	100	100
59	y	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
60	z	54/57 (95%)	54 (100%)	0	0	100	100
All	All	6113/6713 (91%)	5882 (96%)	229 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
19	J	57	VAL
38	d	149	ASN

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	0	46/49 (94%)	46 (100%)	0	100	100
2	1	38/38 (100%)	38 (100%)	0	100	100
3	2	51/52 (98%)	50 (98%)	1 (2%)	48	67
4	3	34/34 (100%)	34 (100%)	0	100	100
5	4	55/62 (89%)	54 (98%)	1 (2%)	51	70
7	6	344/359 (96%)	343 (100%)	1 (0%)	86	92
8	7	91/99 (92%)	91 (100%)	0	100	100
9	8	48/84 (57%)	48 (100%)	0	100	100
11	B	186/199 (94%)	186 (100%)	0	100	100
12	C	170/190 (90%)	169 (99%)	1 (1%)	78	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	D	172/173 (99%)	172 (100%)	0	100	100
14	E	119/126 (94%)	119 (100%)	0	100	100
15	F	90/116 (78%)	89 (99%)	1 (1%)	65	79
16	G	126/147 (86%)	126 (100%)	0	100	100
17	H	104/105 (99%)	104 (100%)	0	100	100
18	I	105/107 (98%)	105 (100%)	0	100	100
19	J	86/90 (96%)	86 (100%)	0	100	100
20	K	90/99 (91%)	90 (100%)	0	100	100
21	L	102/103 (99%)	102 (100%)	0	100	100
22	M	93/96 (97%)	92 (99%)	1 (1%)	65	79
23	N	83/84 (99%)	83 (100%)	0	100	100
24	O	76/77 (99%)	75 (99%)	1 (1%)	61	76
25	P	65/65 (100%)	65 (100%)	0	100	100
26	Q	73/78 (94%)	73 (100%)	0	100	100
27	R	57/65 (88%)	57 (100%)	0	100	100
28	S	72/79 (91%)	71 (99%)	1 (1%)	59	75
29	T	65/66 (98%)	65 (100%)	0	100	100
30	U	60/61 (98%)	60 (100%)	0	100	100
31	V	25/94 (27%)	25 (100%)	0	100	100
37	c	216/218 (99%)	216 (100%)	0	100	100
38	d	163/163 (100%)	163 (100%)	0	100	100
39	e	165/165 (100%)	165 (100%)	0	100	100
40	f	148/150 (99%)	147 (99%)	1 (1%)	76	85
41	g	137/138 (99%)	136 (99%)	1 (1%)	76	85
42	h	32/114 (28%)	32 (100%)	0	100	100
43	i	116/116 (100%)	116 (100%)	0	100	100
44	j	104/104 (100%)	103 (99%)	1 (1%)	68	80
45	k	103/103 (100%)	103 (100%)	0	100	100
46	l	109/109 (100%)	109 (100%)	0	100	100
47	m	98/103 (95%)	98 (100%)	0	100	100
48	n	86/87 (99%)	86 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
49	o	99/100 (99%)	99 (100%)	0	100 100
50	p	89/90 (99%)	89 (100%)	0	100 100
51	q	84/84 (100%)	84 (100%)	0	100 100
52	r	93/93 (100%)	93 (100%)	0	100 100
53	s	80/84 (95%)	80 (100%)	0	100 100
54	t	83/85 (98%)	83 (100%)	0	100 100
55	u	78/78 (100%)	77 (99%)	1 (1%)	61 76
56	v	59/63 (94%)	59 (100%)	0	100 100
57	w	67/68 (98%)	67 (100%)	0	100 100
58	x	54/55 (98%)	54 (100%)	0	100 100
59	y	48/49 (98%)	48 (100%)	0	100 100
60	z	47/48 (98%)	47 (100%)	0	100 100
All	All	5084/5464 (93%)	5072 (100%)	12 (0%)	85 93

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	S	60	VAL
40	f	165	GLU
55	u	61	LEU
41	g	48	ASN
12	C	149	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
43	i	138	GLN
49	o	10	GLN
48	n	29	HIS
49	o	15	GLN
19	J	70	HIS

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	1516/1542 (98%)	206 (13%)	2 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
32	X	8/9 (88%)	1 (12%)	0
33	Y	76/77 (98%)	11 (14%)	2 (2%)
34	Z	76/77 (98%)	12 (15%)	0
35	a	2749/2904 (94%)	298 (10%)	0
36	b	118/120 (98%)	13 (11%)	0
6	5	1/2 (50%)	1 (100%)	0
All	All	4544/4731 (96%)	542 (11%)	4 (0%)

5 of 542 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	5	76	A
10	A	4	U
10	A	5	U
10	A	6	G
10	A	9	G

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	A	428	G
10	A	1035	A
33	Y	13	C
33	Y	48	U

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

34 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
35	G7M	a	2069	35	23,26,27	2.82	9 (39%)	35,39,42	2.21	10 (28%)
10	PSU	A	516	10	18,21,22	2.41	7 (38%)	22,30,33	1.88	4 (18%)
21	D2T	L	89	21	7,9,10	1.27	1 (14%)	6,11,13	1.61	1 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
35	2MA	a	2503	62,35	22,25,26	1.58	4 (18%)	33,37,40	4.43	12 (36%)
35	2MG	a	1835	35	23,26,27	2.61	8 (34%)	32,38,41	2.30	11 (34%)
10	MA6	A	1518	10	23,26,27	1.59	4 (17%)	34,38,41	3.55	11 (32%)
10	G7M	A	527	10	23,26,27	2.89	10 (43%)	35,39,42	2.14	10 (28%)
35	6MZ	a	1618	35	22,25,26	2.52	5 (22%)	30,36,39	2.55	11 (36%)
10	5MC	A	967	10	18,22,23	3.57	7 (38%)	26,32,35	1.03	2 (7%)
35	1MG	a	745	35	22,26,27	2.59	7 (31%)	33,39,42	1.84	9 (27%)
35	H2U	a	2449	35	18,21,22	2.57	5 (27%)	21,30,33	1.93	5 (23%)
10	UR3	A	1498	10	19,22,23	2.73	6 (31%)	26,32,35	1.34	2 (7%)
35	2MG	a	2445	35	23,26,27	2.56	8 (34%)	32,38,41	2.22	14 (43%)
35	PSU	a	2504	35	18,21,22	2.50	8 (44%)	22,30,33	1.88	4 (18%)
35	OMC	a	2498	62,35	19,22,23	2.69	8 (42%)	26,31,34	0.71	0
10	4OC	A	1402	10	20,23,24	3.34	8 (40%)	26,32,35	0.90	1 (3%)
38	MEQ	d	150	38	8,9,10	0.94	0	5,10,12	1.20	1 (20%)
35	PSU	a	1917	35	18,21,22	2.47	7 (38%)	22,30,33	1.83	3 (13%)
10	2MG	A	966	10	23,26,27	2.87	9 (39%)	32,38,41	2.55	11 (34%)
10	MA6	A	1519	10	23,26,27	1.59	4 (17%)	34,38,41	3.67	11 (32%)
35	PSU	a	2580	35	18,21,22	2.59	9 (50%)	22,30,33	1.96	5 (22%)
35	PSU	a	2604	35	18,21,22	2.45	7 (38%)	22,30,33	1.92	4 (18%)
10	2MG	A	1207	10	23,26,27	2.75	9 (39%)	32,38,41	2.41	11 (34%)
35	PSU	a	746	62,35	18,21,22	2.56	8 (44%)	22,30,33	1.72	4 (18%)
10	5MC	A	1407	10	18,22,23	3.45	7 (38%)	26,32,35	0.94	2 (7%)
35	PSU	a	955	35	18,21,22	2.50	8 (44%)	22,30,33	1.98	4 (18%)
35	PSU	a	1911	35	18,21,22	2.45	6 (33%)	22,30,33	1.87	4 (18%)
35	PSU	a	2605	35	18,21,22	2.49	7 (38%)	22,30,33	1.92	4 (18%)
35	6MZ	a	2030	35	22,25,26	2.46	6 (27%)	30,36,39	2.84	12 (40%)
10	2MG	A	1516	10	23,26,27	2.69	9 (39%)	32,38,41	2.45	13 (40%)
35	OMU	a	2552	35	19,22,23	2.97	8 (42%)	26,31,34	1.81	5 (19%)
35	PSU	a	2457	35	18,21,22	2.50	9 (50%)	22,30,33	1.96	4 (18%)
35	5MC	a	1962	35	18,22,23	3.41	7 (38%)	26,32,35	1.10	2 (7%)
35	OMG	a	2251	34,35	23,26,27	2.32	7 (30%)	33,38,41	1.90	9 (27%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
35	G7M	a	2069	35	-	1/7/25/26	0/3/3/3
10	PSU	A	516	10	-	1/7/25/26	0/2/2/2
21	D2T	L	89	21	-	0/7/12/14	-
35	2MA	a	2503	62,35	-	1/7/25/26	0/3/3/3
35	2MG	a	1835	35	-	0/9/27/28	0/3/3/3
10	MA6	A	1518	10	-	0/11/29/30	0/3/3/3
10	G7M	A	527	10	-	3/7/25/26	0/3/3/3
35	6MZ	a	1618	35	-	1/9/27/28	0/3/3/3
10	5MC	A	967	10	-	2/7/25/26	0/2/2/2
35	1MG	a	745	35	-	0/7/25/26	0/3/3/3
35	H2U	a	2449	35	-	0/7/38/39	0/2/2/2
10	UR3	A	1498	10	-	0/7/25/26	0/2/2/2
35	2MG	a	2445	35	-	0/9/27/28	0/3/3/3
35	PSU	a	2504	35	-	2/7/25/26	0/2/2/2
35	OMC	a	2498	62,35	-	0/9/27/28	0/2/2/2
10	4OC	A	1402	10	-	2/9/29/30	0/2/2/2
38	MEQ	d	150	38	-	3/8/9/11	-
35	PSU	a	1917	35	-	0/7/25/26	0/2/2/2
10	2MG	A	966	10	-	0/9/27/28	0/3/3/3
10	MA6	A	1519	10	-	5/11/29/30	0/3/3/3
35	PSU	a	2580	35	-	1/7/25/26	0/2/2/2
35	PSU	a	2604	35	-	0/7/25/26	0/2/2/2
10	2MG	A	1207	10	-	0/9/27/28	0/3/3/3
35	PSU	a	746	62,35	-	1/7/25/26	0/2/2/2
10	5MC	A	1407	10	-	0/7/25/26	0/2/2/2
35	PSU	a	955	35	-	0/7/25/26	0/2/2/2
35	PSU	a	1911	35	-	0/7/25/26	0/2/2/2
35	PSU	a	2605	35	-	0/7/25/26	0/2/2/2
35	6MZ	a	2030	35	-	2/9/27/28	0/3/3/3
10	2MG	A	1516	10	-	0/9/27/28	0/3/3/3
35	OMU	a	2552	35	-	0/9/27/28	0/2/2/2
35	PSU	a	2457	35	-	0/7/25/26	0/2/2/2
35	5MC	a	1962	35	-	0/7/25/26	0/2/2/2
35	OMG	a	2251	34,35	-	0/9/27/28	0/3/3/3

The worst 5 of 232 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	a	1618	6MZ	C6-N6	9.74	1.44	1.34
35	a	2030	6MZ	C6-N6	9.13	1.44	1.34
10	A	1407	5MC	C6-C5	8.77	1.49	1.34
10	A	967	5MC	C6-C5	8.67	1.48	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
35	a	1962	5MC	C6-C5	8.17	1.48	1.34

The worst 5 of 216 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
35	a	2503	2MA	CM2-C2-N3	17.23	144.06	117.15
10	A	1519	MA6	N1-C6-N6	-15.21	100.45	117.08
10	A	1518	MA6	N1-C6-N6	-14.63	101.09	117.08
35	a	2503	2MA	CM2-C2-N1	-13.23	96.49	117.15
10	A	1519	MA6	C5-C6-N6	8.36	139.85	125.30

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	527	G7M	C3'-C4'-C5'-O5'
10	A	967	5MC	O4'-C4'-C5'-O5'
10	A	967	5MC	C3'-C4'-C5'-O5'
10	A	1519	MA6	C5-C6-N6-C9
10	A	1519	MA6	C5-C6-N6-C10

There are no ring outliers.

6 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
21	L	89	D2T	1	0
10	A	1518	MA6	1	0
10	A	1519	MA6	1	0
10	A	1407	5MC	1	0
35	a	2030	6MZ	1	0
35	a	2552	OMU	1	0

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 313 ligands modelled in this entry, 311 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
64	SPM	a	6208	-	13,13,13	0.35	0	12,12,12	0.85	0
63	PRO	Y	101	33	5,7,8	0.66	0	7,8,10	1.21	1 (14%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
64	SPM	a	6208	-	-	4/11/11/11	-
63	PRO	Y	101	33	-	0/0/9/11	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
63	Y	101	PRO	O-C-CA	-2.14	119.16	124.78

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
64	a	6208	SPM	C7-C8-C9-N10
64	a	6208	SPM	N10-C11-C12-C13
64	a	6208	SPM	C8-C9-N10-C11
64	a	6208	SPM	C2-C3-C4-N5

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)

There are no chain breaks in this entry.

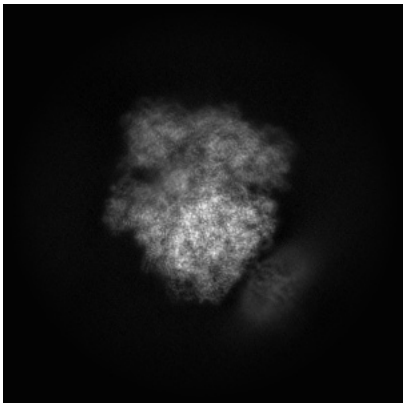
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-55577. These allow visual inspection of the internal detail of the map and identification of artifacts.

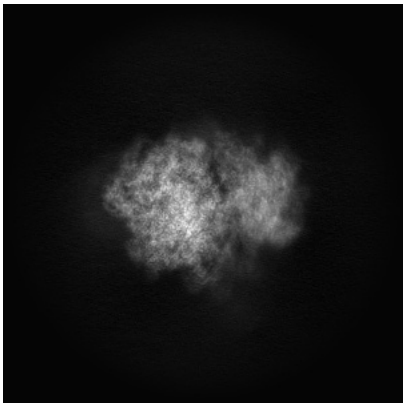
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

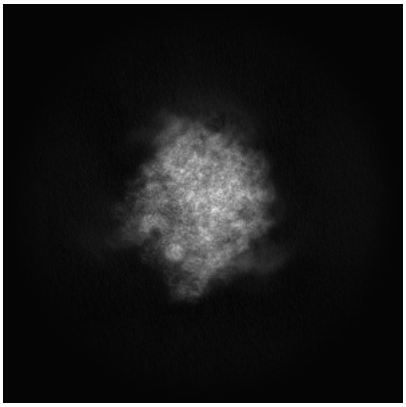
6.1.1 Primary map



X



Y

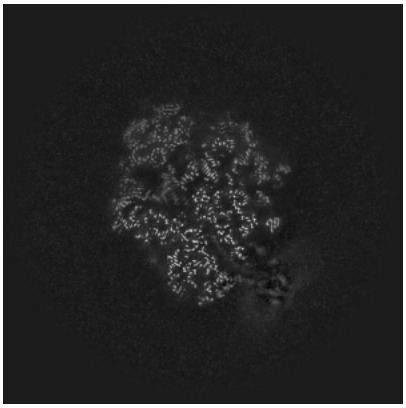


Z

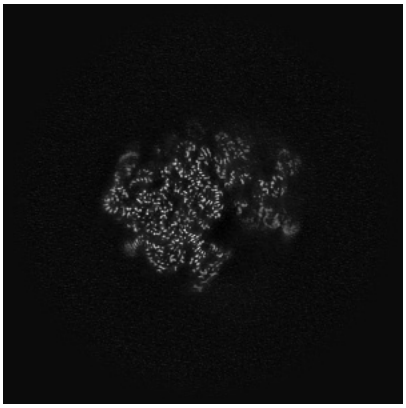
The images above show the map projected in three orthogonal directions.

6.2 Central slices

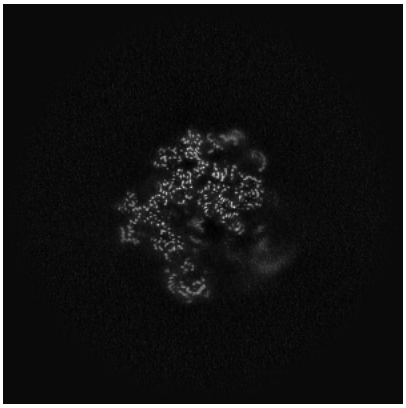
6.2.1 Primary map



X Index: 340



Y Index: 340

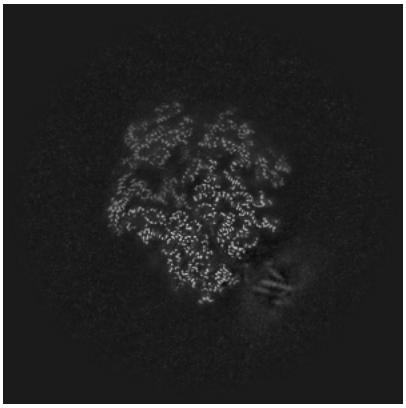


Z Index: 340

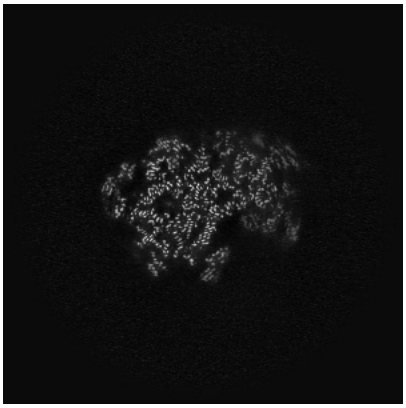
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

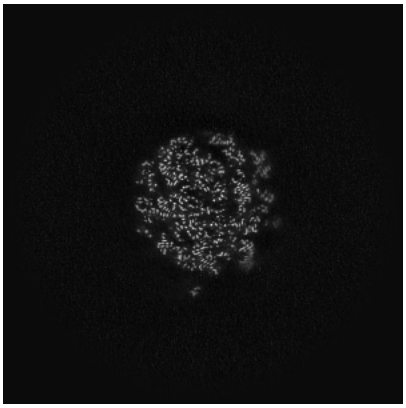
6.3.1 Primary map



X Index: 334



Y Index: 358

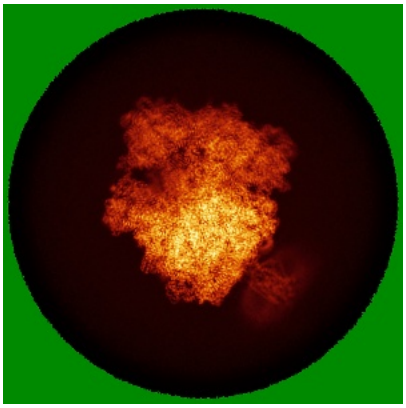


Z Index: 288

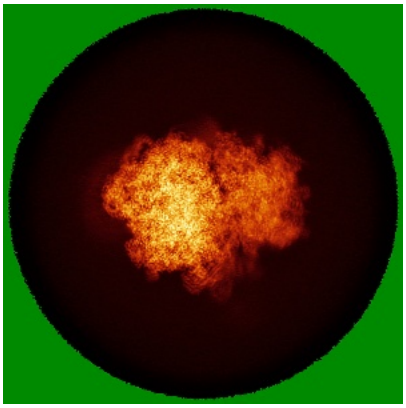
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

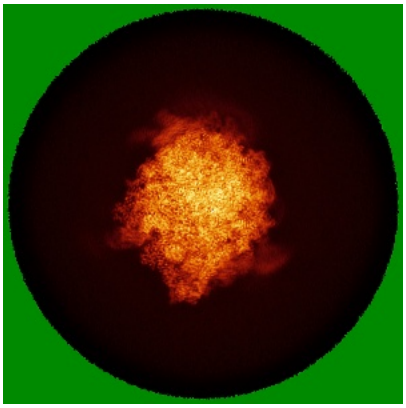
6.4.1 Primary map



X



Y

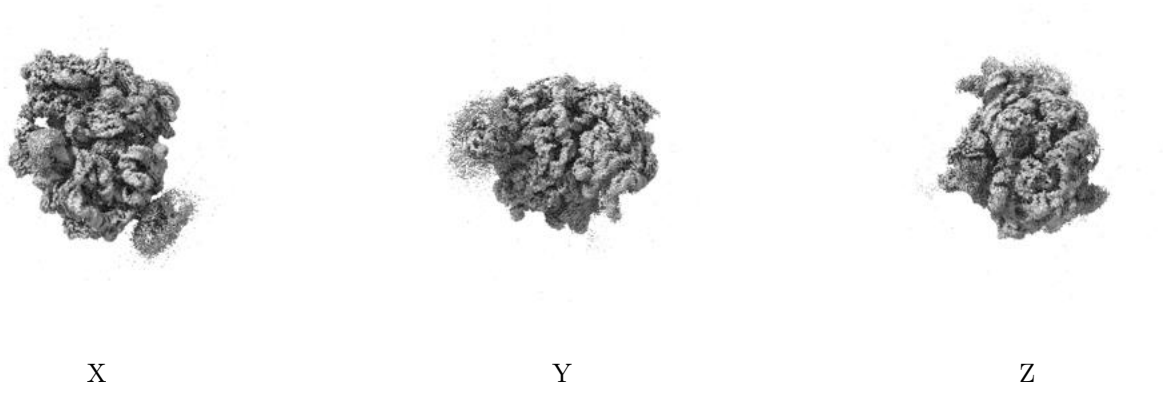


Z

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 0.175. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

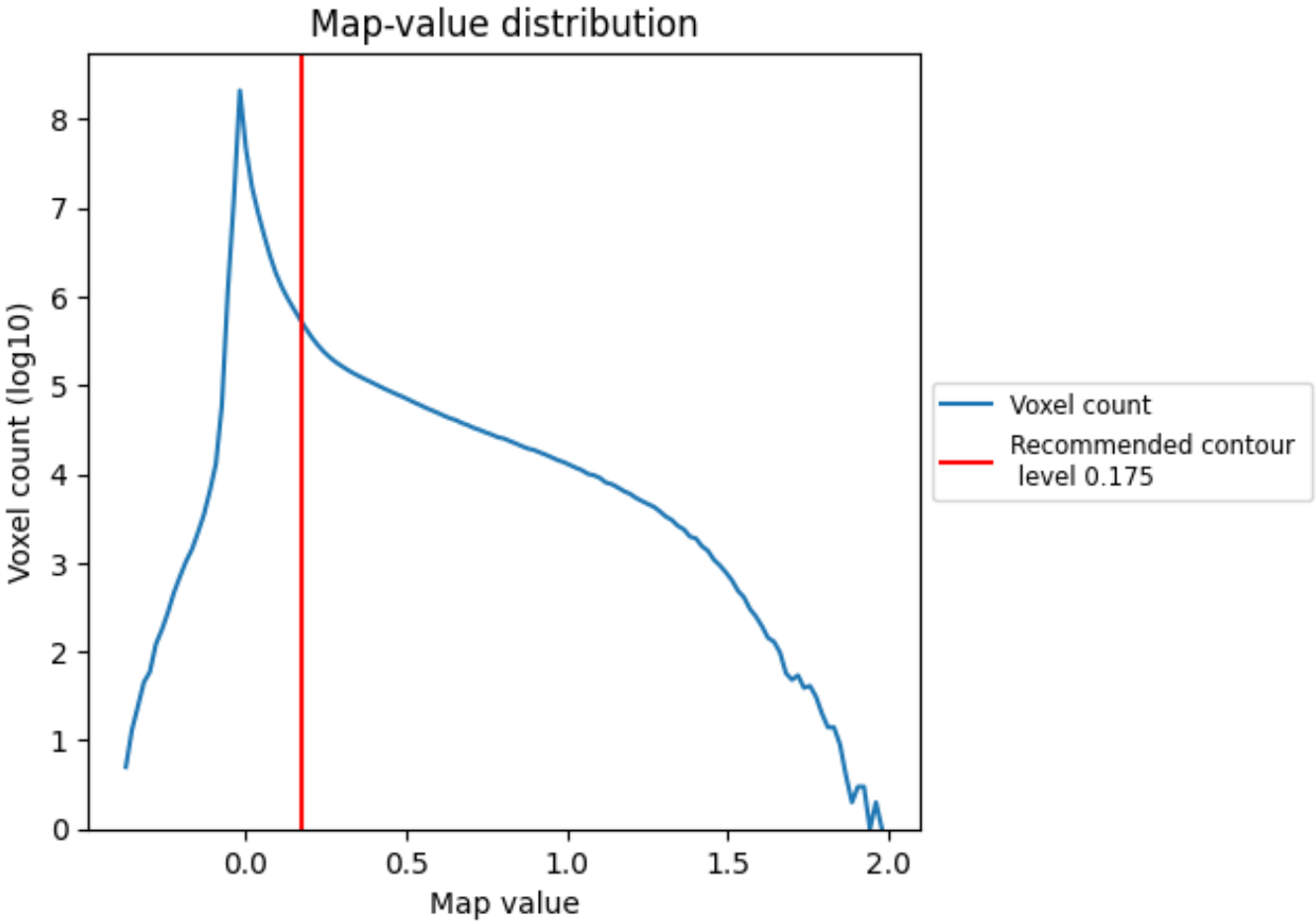
6.6 Mask visualisation (i)

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

7 Map analysis

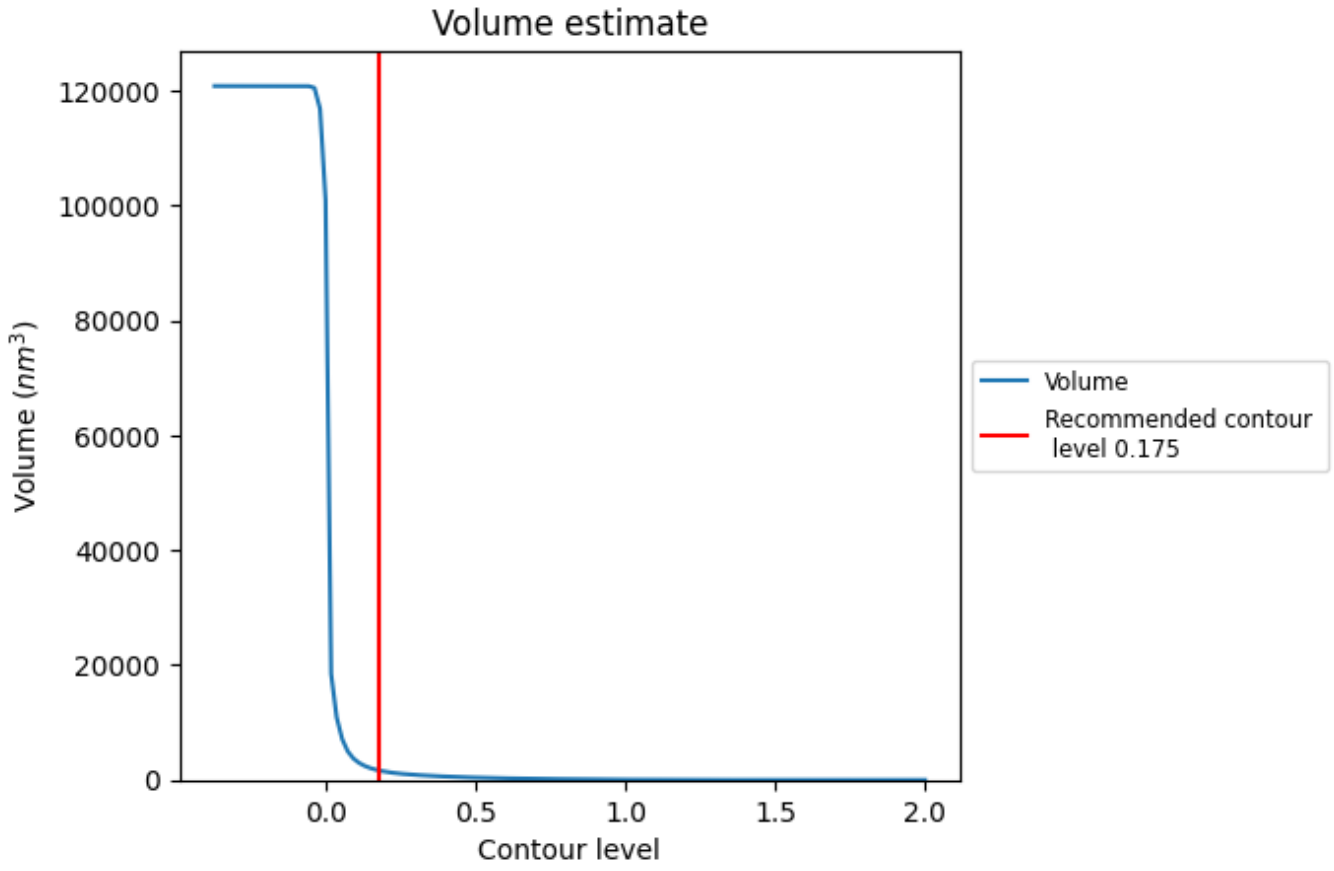
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

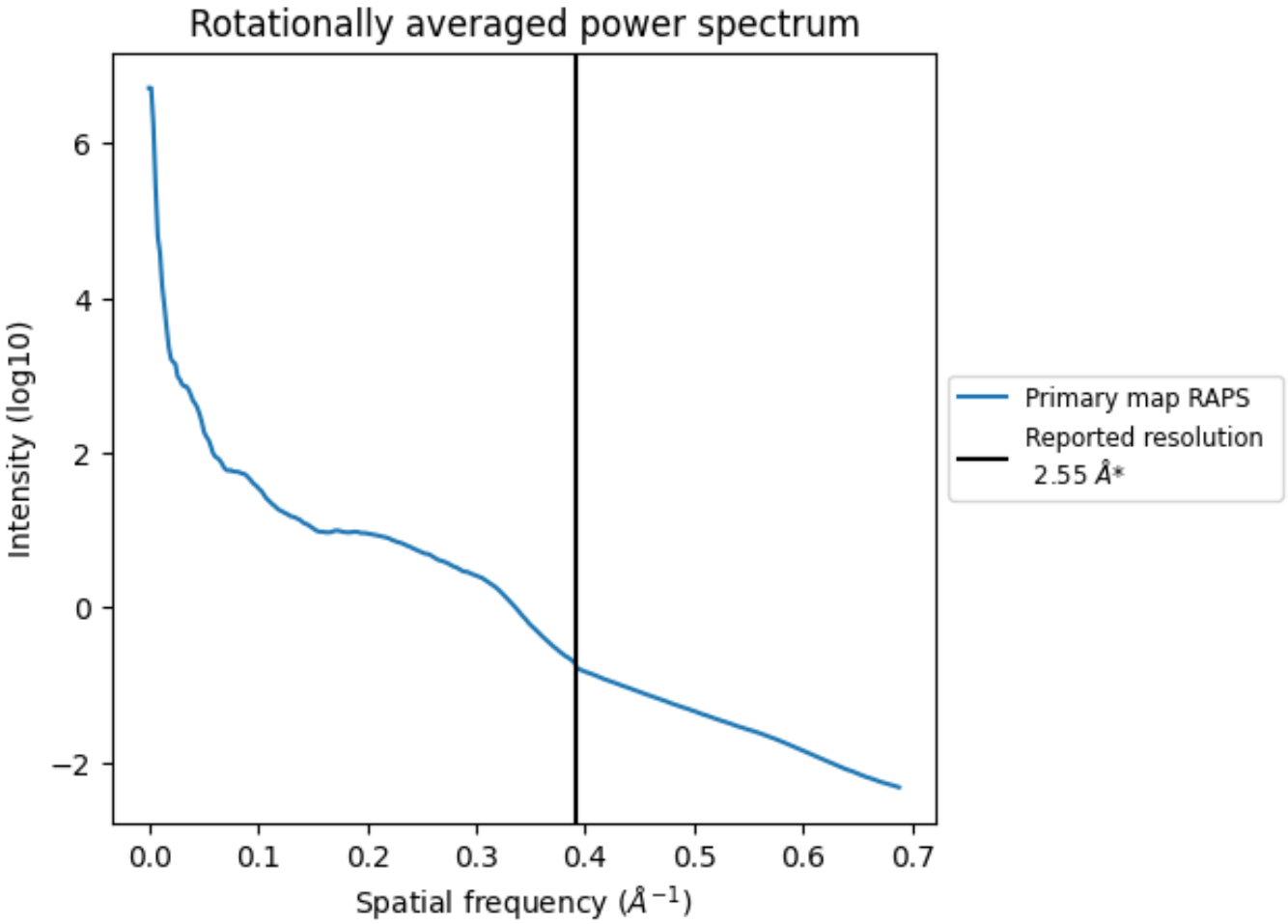
7.2 Volume estimate (i)



The volume at the recommended contour level is 1674 nm^3; this corresponds to an approximate mass of 1512 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 0.392 Å^{-1}

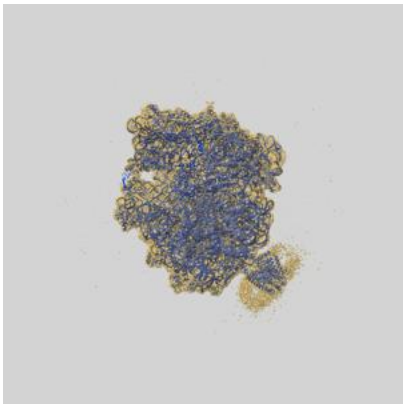
8 Fourier-Shell correlation

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

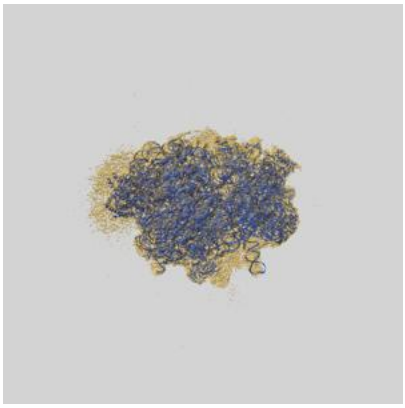
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-55577 and PDB model 9T5G. Per-residue inclusion information can be found in section 3 on page 18.

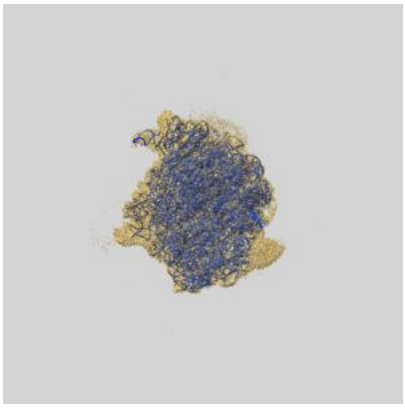
9.1 Map-model overlay



X



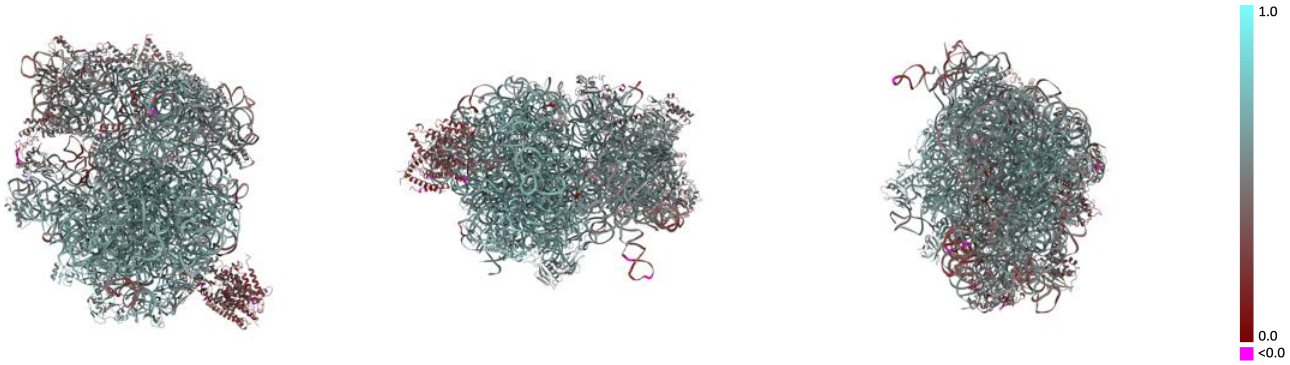
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.175 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.

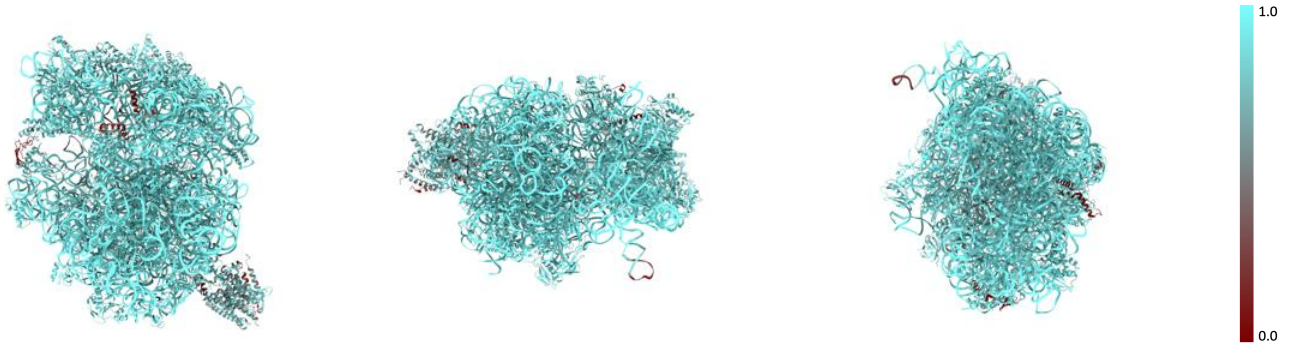
9.2 Q-score mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according 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.

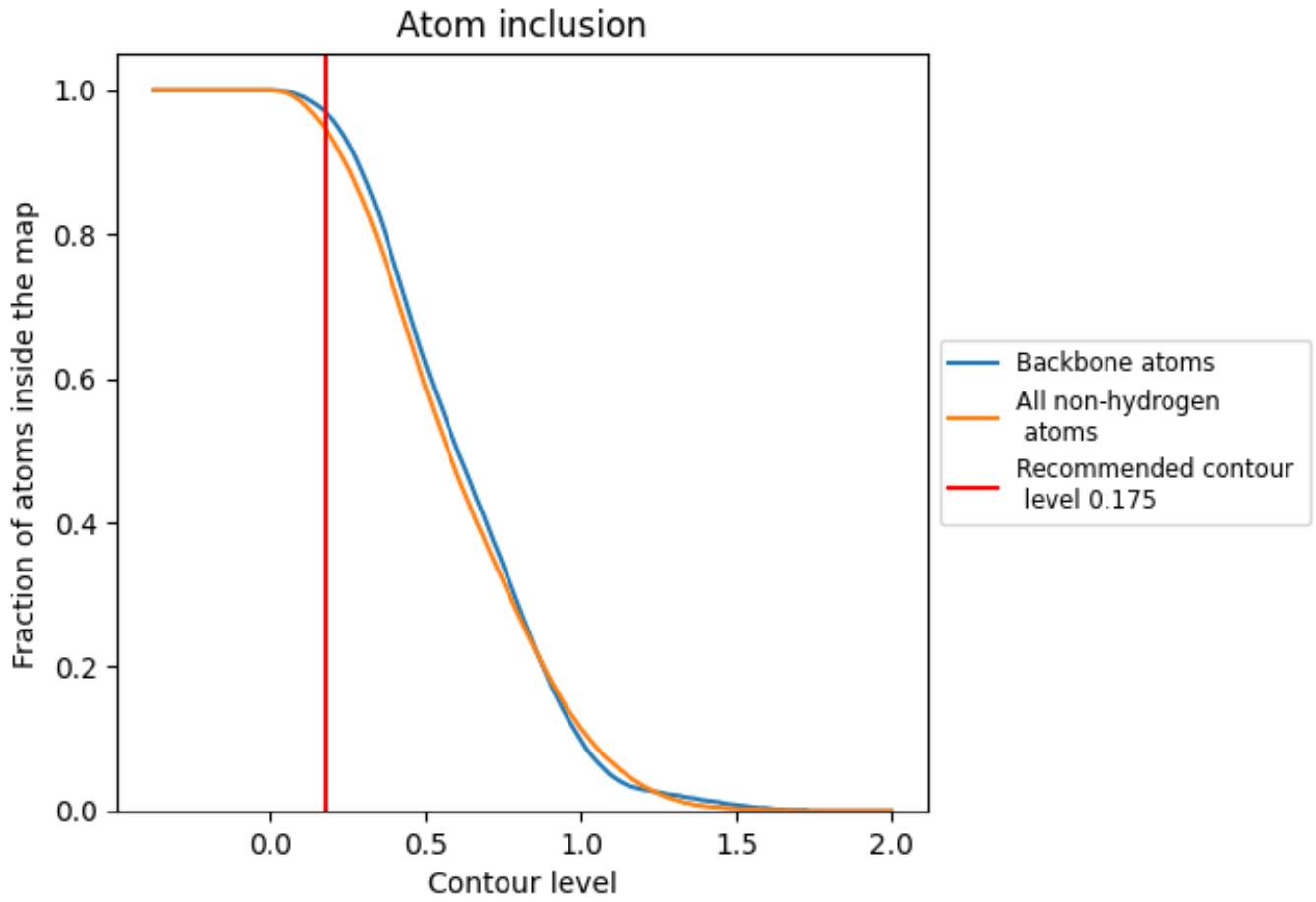
9.3 Atom inclusion mapped to coordinate model



X Y Z

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 (0.175).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.175) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9480	0.5560
0	0.8800	0.5560
1	0.9830	0.6400
2	0.9780	0.6290
3	0.9800	0.6120
4	0.0340	0.1080
5	0.7380	0.4960
6	0.6760	0.3040
7	0.6660	0.2680
8	0.5190	0.1850
A	0.9810	0.5270
B	0.8590	0.4640
C	0.8870	0.4870
D	0.7840	0.4640
E	0.9320	0.5530
F	0.8950	0.5030
G	0.8230	0.4120
H	0.9340	0.5450
I	0.8980	0.4320
J	0.8700	0.4380
K	0.8910	0.4960
L	0.8250	0.4800
M	0.8300	0.4200
N	0.9210	0.4830
O	0.9260	0.5170
P	0.8920	0.5120
Q	0.8830	0.4890
R	0.7950	0.4620
S	0.8300	0.4170
T	0.8950	0.4830
U	0.2430	0.2790
V	0.5710	0.3710
X	0.8520	0.4890
Y	0.7080	0.4760
Z	0.9470	0.4870



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Chain	Atom inclusion	Q-score
a	0.9940	0.6120
b	0.9980	0.5750
c	0.9820	0.6350
d	0.9680	0.6250
e	0.9630	0.6010
f	0.8810	0.4720
g	0.9250	0.5250
h	0.9300	0.5420
i	0.9630	0.6130
j	0.9710	0.6180
k	0.9710	0.6140
l	0.9670	0.6140
m	0.9920	0.6410
n	0.9500	0.5520
o	0.9470	0.6110
p	0.9840	0.6340
q	0.9560	0.6070
r	0.9650	0.6090
s	0.9390	0.5770
t	0.9350	0.5590
u	0.9470	0.5740
v	0.9530	0.6140
w	0.9670	0.5970
x	0.9180	0.5070
y	0.9520	0.6000
z	0.9650	0.6200