WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB EM Validation Report ⓘ

Nov 27, 2022 – 03:41 PM EST

PDB ID	:	6W6L
EMDB ID	:	EMD-21435
Title	:	Cryo-EM structure of the human ribosome-TMCO1 translocon
Authors	:	Keenan, R.J.; McGilvray, P.T.
Deposited on	:	2020-03-17
Resolution	:	3.84 Å(reported)
Based on initial models	:	5A63, 6OM0, 6FTI

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

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

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

The following versions of software and data (see references ⓘ) were used in the production of this report:
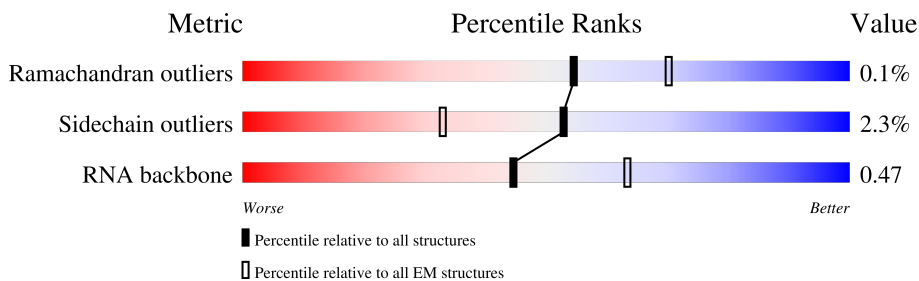
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance ⓘ

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

The reported resolution of this entry is 3.84 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	Percentile Ranks	Value
Ramachandran outliers		0.1%
Sidechain outliers		2.3%
RNA backbone		0.47

Worse → *Better*

▮ Percentile relative to all structures
◨ Percentile relative to all EM structures

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

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

Mol	Chain	Length	Quality of chain
1	A	257	96% ·
2	B	403	98% ·
3	C	427	85% 15%
4	D	157	57% 36% 7%
5	E	119	88% 11% ·
6	F	297	82% · 16%
7	G	288	75% · 24%
8	H	248	89% · 9%
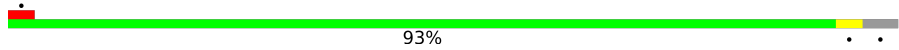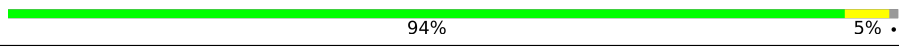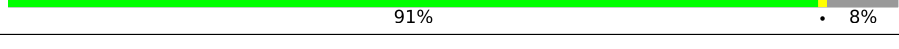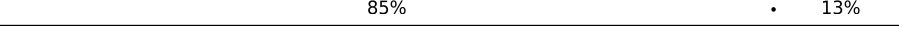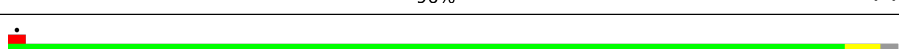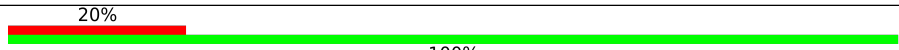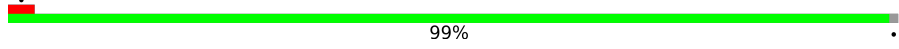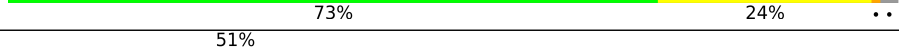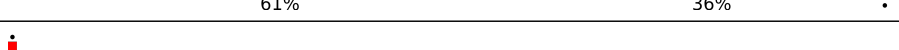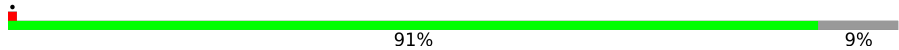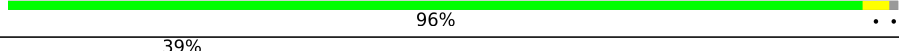
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Mol	Chain	Length	Quality of chain
9	I	266	88% 12%
10	J	192	99%
11	K	214	30% 71% 29%
12	L	178	8% 95% 5%
13	M	211	96%
14	N	215	64% 36%
15	O	204	98%
16	P	203	94%
17	Q	184	82% 17%
18	R	188	98%
19	S	196	79% 20%
20	T	176	98%
21	U	160	98%
22	V	128	14% 76% 23%
23	W	140	92% 8%
24	X	157	39% 61%
25	Y	156	74% 25%
26	Z	145	90% 8%
27	a	136	98%
28	b	148	98%
29	c	159	60% 40%
30	d	115	81% 17%
31	e	125	84% 15%
32	f	135	95%
33	g	110	98%

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Mol	Chain	Length	Quality of chain
34	h	117	93%
35	i	123	94% 5%
36	j	105	91% 8%
37	k	97	85% 13%
38	l	70	96%
39	m	51	94%
40	o	25	20% 100%
41	p	106	6% 92% 7%
42	q	92	99%
43	r	137	88% 11%
44	t	3579	73% 24%
45	u	76	51% 61% 36%
46	v	76	58% 38%
47	y	27	19% 100%
48	1	476	88% 11%
49	2	68	91% 9%
50	3	96	29% 70%
51	4	224	96%
52	5	563	39% 84% 8% 8%
53	7	483	17% 56% 40%
54	6	188	7% 87% 5% 7%

2 Entity composition ⓘ

There are 57 unique types of molecules in this entry. The entry contains 259082 atoms, of which 110309 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 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	246	Total	C	H	N	O	S	0	0
			3870	1183	1983	387	311	6		

- Molecule 2 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	396	Total	C	H	N	O	S	0	0
			6535	2036	3338	601	546	14		

- Molecule 3 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	C	363	Total	C	H	N	O	S	0	0
			5952	1817	3064	577	480	14		

- Molecule 4 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	157	Total	C	H	N	O	P	0	0
			5029	1489	1692	587	1104	157		

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

Mol	Chain	Residues	Atoms						AltConf	Trace
5	E	119	Total	C	H	N	O	P	0	0
			3825	1132	1284	454	836	119		

- Molecule 6 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	F	248	Total	C	H	N	O	S	0	0
			4010	1271	1998	358	370	13		

- Molecule 7 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	G	220	Total	C	H	N	O	S	0	0
			3689	1138	1917	335	295	4		

- Molecule 8 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	H	225	Total	C	H	N	O	S	0	0
			3866	1202	1996	358	301	9		

- Molecule 9 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	I	234	Total	C	H	N	O	S	0	0
			3898	1197	2018	362	317	4		

- Molecule 10 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	J	191	Total	C	H	N	O	S	0	0
			3131	960	1605	285	275	6		

- Molecule 11 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	K	152	Total	C	H	N	O	S	0	0
			2508	789	1270	233	208	8		

- Molecule 12 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	L	169	Total	C	H	N	O	S	0	0
			2739	855	1386	252	240	6		

- Molecule 13 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms						AltConf	Trace
13	M	205	Total	C	H	N	O	S	0	0
			3421	1036	1764	344	273	4		

- Molecule 14 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms						AltConf	Trace
14	N	138	Total	C	H	N	O	S	0	0
			2328	725	1197	217	182	7		

- Molecule 15 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms						AltConf	Trace
15	O	203	Total	C	H	N	O	S	0	0
			3450	1072	1749	359	266	4		

- Molecule 16 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms						AltConf	Trace
16	P	195	Total	C	H	N	O	S	0	0
			3352	1034	1746	315	252	5		

- Molecule 17 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms						AltConf	Trace
17	Q	153	Total	C	H	N	O	S	0	0
			2511	776	1269	241	216	9		

- Molecule 18 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms						AltConf	Trace
18	R	187	Total	C	H	N	O	S	0	0
			3141	944	1628	314	250	5		

- Molecule 19 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms						AltConf	Trace
19	S	156	Total	C	H	N	O	S	0	0
			2750	816	1439	278	209	8		

- Molecule 20 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms						AltConf	Trace
20	T	175	Total	C	H	N	O	S	0	0
			2942	921	1493	283	234	11		

- Molecule 21 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms						AltConf	Trace
21	U	157	Total 2636	C 815	H 1352	N 250	O 214	S 5	0	0

- Molecule 22 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms						AltConf	Trace
22	V	99	Total 1639	C 518	H 831	N 141	O 147	S 2	0	0

- Molecule 23 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms						AltConf	Trace
23	W	129	Total 2000	C 613	H 1031	N 182	O 169	S 5	0	0

- Molecule 24 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms						AltConf	Trace
24	X	61	Total 1032	C 327	H 521	N 100	O 82	S 2	0	0

- Molecule 25 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms						AltConf	Trace
25	Y	117	Total 1987	C 612	H 1029	N 180	O 165	S 1	0	0

- Molecule 26 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms						AltConf	Trace
26	Z	133	Total 2298	C 694	H 1192	N 224	O 185	S 3	0	0

- Molecule 27 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms						AltConf	Trace
27	a	134	Total 2282	C 712	H 1179	N 207	O 181	S 3	0	0

- Molecule 28 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms						AltConf	Trace
28	b	147	Total	C	H	N	O	S	0	0
			2375	736	1213	237	186	3		

- Molecule 29 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms						AltConf	Trace
29	c	96	Total	C	H	N	O	S	0	0
			1641	489	854	174	121	3		

- Molecule 30 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms						AltConf	Trace
30	d	95	Total	C	H	N	O	S	0	0
			1512	468	774	131	133	6		

- Molecule 31 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms						AltConf	Trace
31	e	106	Total	C	H	N	O	S	0	0
			1803	555	924	170	152	2		

- Molecule 32 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms						AltConf	Trace
32	f	129	Total	C	H	N	O	S	0	0
			2224	673	1160	220	166	5		

- Molecule 33 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms						AltConf	Trace
33	g	109	Total	C	H	N	O	S	0	0
			1788	555	912	174	144	3		

- Molecule 34 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms						AltConf	Trace
34	h	112	Total	C	H	N	O	S	0	0
			1867	555	979	183	144	6		

- Molecule 35 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms						AltConf	Trace
35	i	122	Total 2163	C 641	H 1148	N 205	O 168	S 1	0	0

- Molecule 36 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms						AltConf	Trace
36	j	97	Total 1664	C 497	H 870	N 168	O 124	S 5	0	0

- Molecule 37 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms						AltConf	Trace
37	k	84	Total 1407	C 423	H 718	N 152	O 109	S 5	0	0

- Molecule 38 is a protein called 60S ribosomal protein L38.

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

- Molecule 39 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms						AltConf	Trace
39	m	50	Total 927	C 281	H 483	N 98	O 64	S 1	0	0

- Molecule 40 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms						AltConf	Trace
40	o	25	Total 529	C 145	H 289	N 64	O 28	S 3	0	0

- Molecule 41 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms						AltConf	Trace
41	p	99	Total 1696	C 510	H 882	N 167	O 131	S 6	0	0

- Molecule 42 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms						AltConf	Trace
42	q	91	Total	C	H	N	O	S	0	0
			1464	445	756	136	120	7		

- Molecule 43 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms						AltConf	Trace
43	r	122	Total	C	H	N	O	S	0	0
			2021	607	1041	204	165	4		

- Molecule 44 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
44	t	3510	Total	C	H	N	O	P	0	0
			113261	33507	38018	13757	24469	3510		

- Molecule 45 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
45	u	75	Total	C	H	N	O	P	0	0
			2402	710	809	278	530	75		

- Molecule 46 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
46	v	76	Total	C	H	N	O	P	0	0
			2440	721	822	287	534	76		

- Molecule 47 is a protein called Nascent chain mixture.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	y	27	Total	C	H	N	O	0	0
			245	81	110	27	27		

- Molecule 48 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
48	1	426	Total	C	H	N	O	S	0	0
			6775	2189	3452	535	578	21		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	145	SER	ALA	conflict	UNP P61619
1	343	HIS	TYR	conflict	UNP P61619

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

Mol	Chain	Residues	Atoms						AltConf	Trace
49	2	62	Total 1021	C 326	H 527	N 86	O 79	S 3	0	0

- Molecule 50 is a protein called Protein transport protein Sec61 subunit beta.

Mol	Chain	Residues	Atoms						AltConf	Trace
50	3	29	Total 474	C 157	H 245	N 36	O 34	S 2	0	0

- Molecule 51 is a protein called Transmembrane protein 147.

Mol	Chain	Residues	Atoms						AltConf	Trace
51	4	221	Total 3526	C 1175	H 1769	N 272	O 294	S 16	0	0

- Molecule 52 is a protein called Nicalin.

Mol	Chain	Residues	Atoms						AltConf	Trace
52	5	516	Total 8173	C 2595	H 4083	N 722	O 756	S 17	0	0

- Molecule 53 is a protein called Coiled-coil domain-containing protein 47.

Mol	Chain	Residues	Atoms						AltConf	Trace
53	7	290	Total 4775	C 1475	H 2400	N 435	O 447	S 18	0	0

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

Mol	Chain	Residues	Atoms						AltConf	Trace
54	6	174	Total 2850	C 887	H 1463	N 239	O 249	S 12	0	0

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

Mol	Chain	Residues	Atoms		AltConf
55	B	1	Total 1	Mg 1	0
55	D	6	Total 6	Mg 6	0
55	E	9	Total 9	Mg 9	0
55	k	1	Total 1	Mg 1	0
55	o	1	Total 1	Mg 1	0
55	t	10	Total 10	Mg 10	0

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

Mol	Chain	Residues	Atoms		AltConf
56	k	1	Total 1	Zn 1	0
56	p	1	Total 1	Zn 1	0
56	q	1	Total 1	Zn 1	0

- Molecule 57 is water.

Mol	Chain	Residues	Atoms		AltConf
57	u	1	Total 1	O 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.
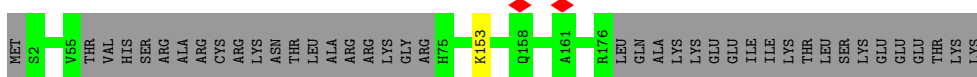
• Molecule 1: 60S ribosomal protein L8
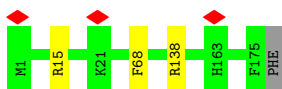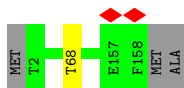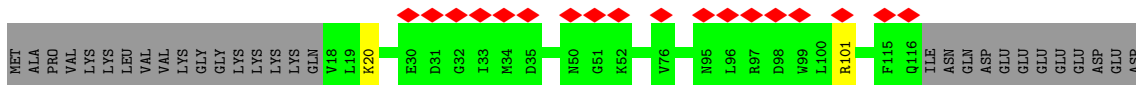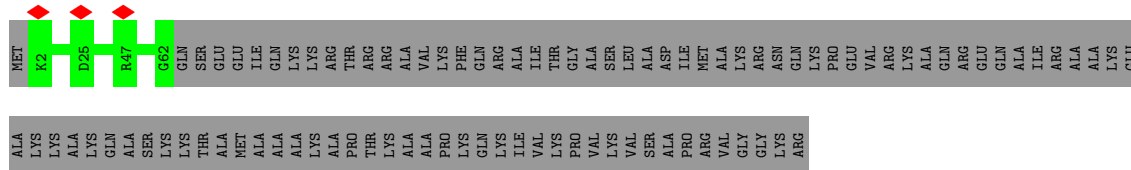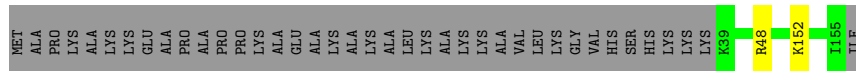
Chain A:
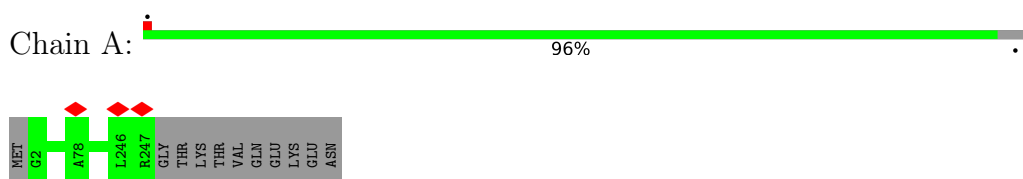
• Molecule 2: 60S ribosomal protein L3

Chain B:
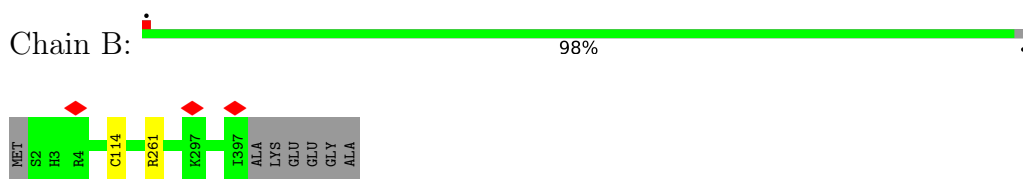
• Molecule 3: 60S ribosomal protein L4

Chain C:
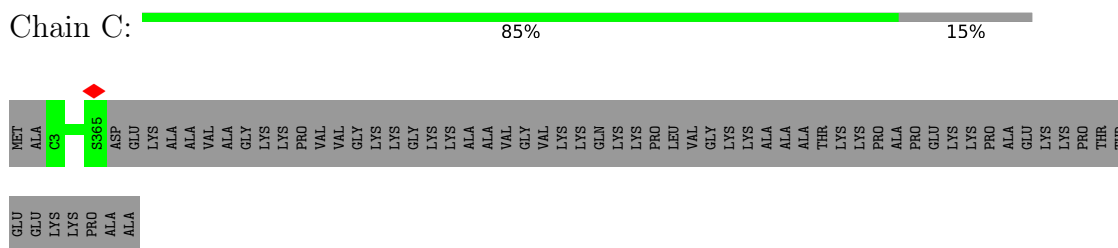
• Molecule 4: 5.8S ribosomal RNA

Chain D:
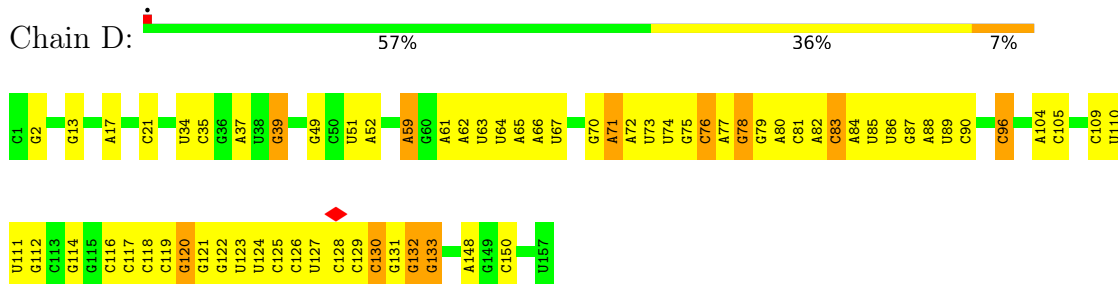
• Molecule 5: 5S ribosomal RNA

Chain E:

88%   11%

G1 G7 A11 A22 A23 C24 U33 C34 U35 U40 G48 A49 U53 G64 U96 G110 U119
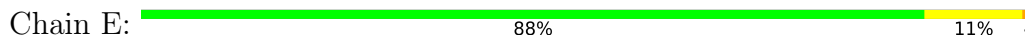
• Molecule 6: 60S ribosomal protein L5

Chain F:

82%   16%

MET GLY PHE VAL LYS VAL VAL LYS N9 K10 V55 E186 S187 K188 R196 K256 PRO LYS LYS GLU VAL LYS LYS ARG TRP ASN ARG PRO LYS MET SER LEU ALA GLN LYS LYS ASP ARG VAL ALA GLN LYS LYS ALA SER PHE LEU ARG ALA GLN ARG ALA ALA GLU
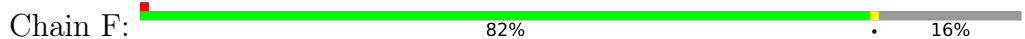
SER

• Molecule 7: 60S ribosomal protein L6

Chain G:

75%   24%

MET ALA GLY LYS VAL GLU LYS PRO ASP THR LYS GLU LYS LYS PRO GLU ALA LYS LYS VAL ASP ALA GLY LYS GLY LYS VAL LYS LYS GLY ASN LEU LYS ALA LYS LYS PRO LYS GLY LYS P42 R52 A76 LYS SER LYS VAL GLU LYS LYS LYS LYS GLU LYS VAL LEU ALA

THR VAL T93 S127 H128 N205 L222 ARG LYS PRO ARG HIS GLN GLU GLY GLU ILE PHE D234 F288
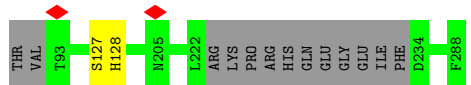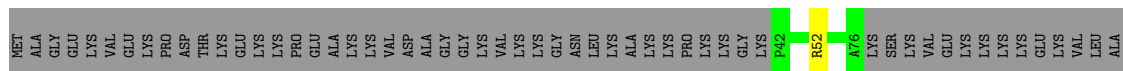
• Molecule 8: 60S ribosomal protein L7

Chain H:

89%   9%

MET GLU GLY VAL GLU GLU LYS LYS LYS GLU VAL PRO ALA VAL PRO GLU THR LEU LYS LYS LYS ARG ARG N24 F25 R106 L169 L174 I194 T225 R245 N248
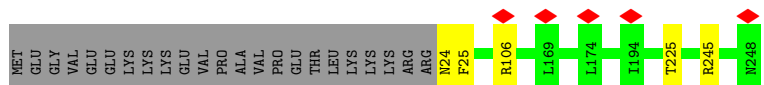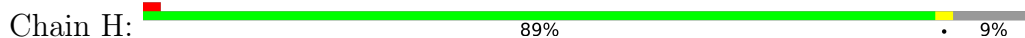
• Molecule 9: 60S ribosomal protein L7a

Chain I:

88%   12%

MET PRO LYS GLY LYS LYS ALA LYS GLY LYS LYS VAL ALA PRO ALA PRO ALA VAL VAL LYS LYS GLN GLU ALA LYS LYS VAL VAL N29 L70 A123 G124 K125 G126 D127 V128 P129 L261 A262 THR LYS LEU GLY
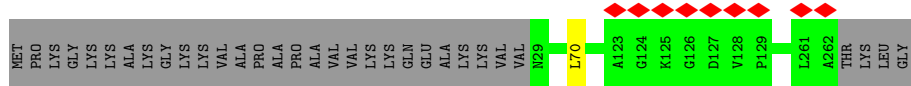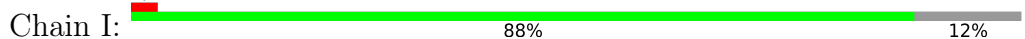
• Molecule 10: 60S ribosomal protein L9

Chain J:

99%

M1 K21 I41 Q138 A139 A190 D191 GLU
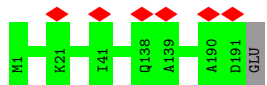
• Molecule 11: 60S ribosomal protein L10

Chain K:

30%

71%   29%

MET GLY ARG ARG PRO ALA ARG CYS TYR ARG TYR CYS K13 N14 K15 P16 K19 S20 R21 F22 C23 R24 G25 V26 P27 D28 A29 K30 I31 R32 I33 D55 E56 Y57 E58 Q59 L60 L65 R69 P93 F94 H95 V96 I97 R98 ILE ASN LYS MET LEU SER CYS ALA GLY ALA

ASP ARG LEU GLN THR GLY MET ARG GLY ALA PHE GLY LYS P122 Q123 G124 T125 V126 A127 R128 V129 H130 I131 G132 I135 E146 H147 V148 I149 R153 P160 G161 R162 H166 I167 S168 K169 K175 F176 N177 A178 D179 E180 F181 E182 D183 M184 V185 A186 E187 LYS ARG LEU ILE

PRO ASP GLY CYS VAL GLY TYR ILE PRO ASN ARG GLY PRO LEU ASP LYS TRP ARG ALA LEU HIS SER

• Molecule 12: 60S ribosomal protein L11

Chain L:

8%

95%   5%

MET ALA GLN ASP GLN GLY GLU LYS E9 S29 G30 D31 G45 R58 S59 F60 G61 D101 P121 S122 I123 G124 I125 G177 LYS
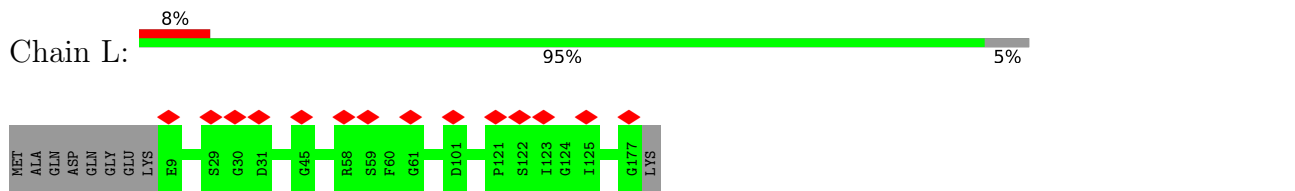
• Molecule 13: 60S ribosomal protein L13

Chain M:

96%

MET A2 R21 R102 R198 A199 K200 E201 A202 A203 E204 Q205 D206 VAL GLU LYS LYS LYS
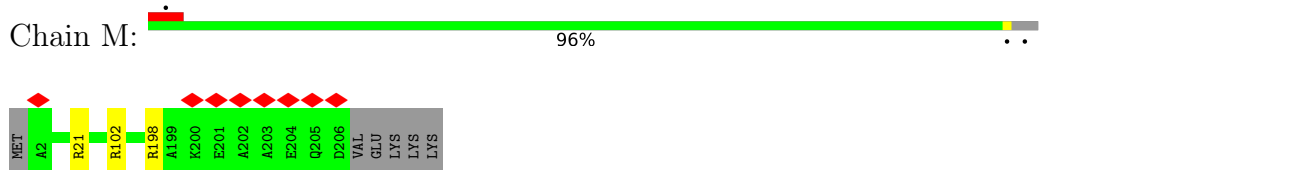
• Molecule 14: 60S ribosomal protein L14

Chain N:

64%   36%

MET V2 V127 A138 S139 PRO LYS LYS ALA PRO GLY THR LYS GLY THR ALA ALA ALA ALA ALA ALA ALA LYS VAL PRO ALA LYS LYS ILE THR ALA ALA SER LYS LYS ALA PRO ALA GLN LYS VAL PRO ALA GLN LYS ALA THR GLY GLN LYS ALA ALA PRO ALA PRO

LYS ALA GLN LYS GLY GLN LYS ALA PRO ALA GLN LYS ALA PRO ALA PRO LYS ALA SER GLY LYS LYS ALA
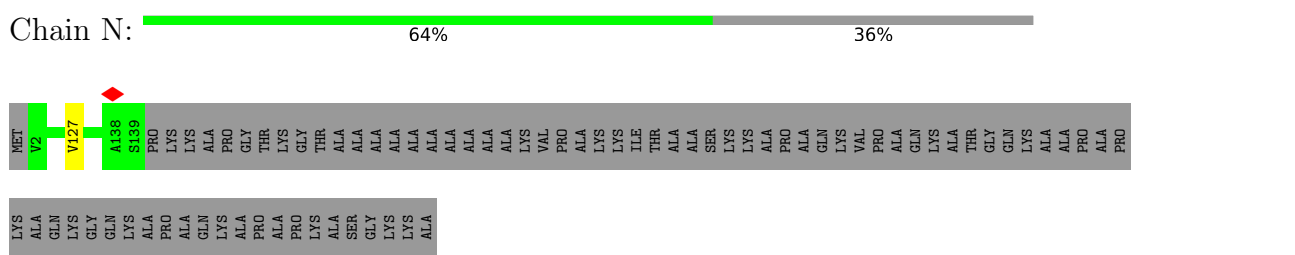
• Molecule 15: 60S ribosomal protein L15

Chain O:

98%

MET G2 R63 N90 I133 R204
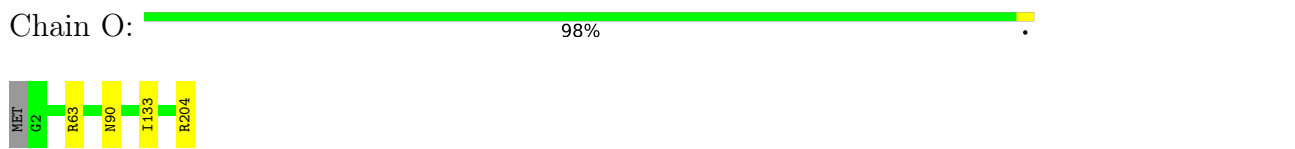
• Molecule 16: 60S ribosomal protein L13a

Chain P:

94%

MET ALA GLU VAL Q5 D10 R94 R101 L141 R169 R178 H199 GLY LEU LEU VAL

• Molecule 17: 60S ribosomal protein L17

Chain Q:

82% 17%

MET V2 R127 Y139 I146 E154 GLN ILE VAL PRO LYS PRO GLU GLU GLU VAL ALA GLN LYS LYS LYS ILE SER GLN LYS LYS LEU LYS LYS LYS GLN LYS LEU MET ALA ARG GLU

• Molecule 18: 60S ribosomal protein L18

Chain R:

98%

MET G2 R37 R91 R168 N188

• Molecule 19: 60S ribosomal protein L19

Chain S:

79% 20%

MET S2 V55 THR VAL HIS SER ARG ALA ARG CYS ARG LYS ASN THR LEU ALA ARG ARG LYS GLY ARG H75 K153 Q158 A161 R176 LEU GLN ALA LYS LYS GLU GLU ILE ILE LYS THR LEU SER LYS GLU GLU THR LYS LYS

• Molecule 20: 60S ribosomal protein L18a

Chain T:

98%

M1 R15 K21 F68 R138 H163 F175 PHE

• Molecule 21: 60S ribosomal protein L21

Chain U:

98%

MET T2 T68 E157 F158 MET ALA

• Molecule 22: 60S ribosomal protein L22

Chain V:

14%

76% 23%

MET ALA PRO VAL LYS LYS LEU VAL VAL LYS GLY GLY LYS LYS LYS LYS GLN V18 L19 K20 E30 D31 G32 I33 M34 D35 N50 G51 K52 V76 N95 L96 R97 D98 W99 L100 R101 F115 Q116 ILE ASN GLN ASP GLU GLU GLU GLU ASP GLU ASP
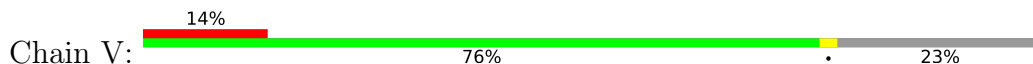
• Molecule 23: 60S ribosomal protein L23

Chain W:

92% 8%

MET SER LYS ARG GLY ARG GLY GLY SER SER GLY A12 I139 A140
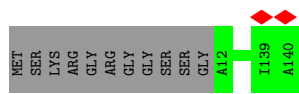
• Molecule 24: 60S ribosomal protein L24

Chain X:

39% 61%

MET K2 D25 R47 G62 GLN SER GLU GLU ILE GLN LYS LYS ARG THR ARG ARG ALA VAL LYS PHE GLN ARG ALA ILE THR GLY ALA SER LEU ALA ASP ILE MET ALA LYS ARG ASN GLN LYS PRO GLU VAL ARG LYS ALA GLN ARG GLU GLN ALA ILE ARG ALA ALA LYS GLU

ALA LYS LYS ALA LYS GLN ALA SER LYS LYS THR ALA MET ALA ALA ALA LYS ALA PRO THR LYS ALA ALA PRO LYS GLN LYS ILE VAL LYS PRO VAL LYS VAL SER ALA PRO ARG VAL GLY GLY LYS ARG

• Molecule 25: 60S ribosomal protein L23a

Chain Y:

74% 25%

MET ALA PRO LYS ALA LYS LYS GLU ALA PRO ALA PRO PRO LYS ALA GLU ALA LYS ALA LYS ALA LEU LYS ALA LYS LYS ALA VAL LEU LYS GLY VAL HIS SER HIS LYS LYS LYS K39 R48 K152 I155 ILE

• Molecule 26: 60S ribosomal protein L26

Chain Z:

90% 8%

M1 K28 L38 K132 G133 LYS TYR LYS GLU GLU THR ILE GLU GLU LYS MET GLN GLU
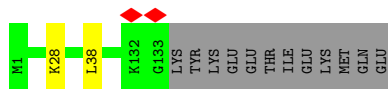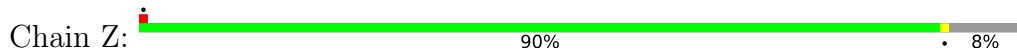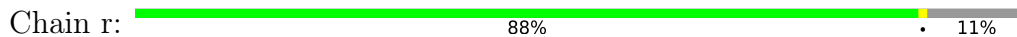
• Molecule 27: 60S ribosomal protein L27

Chain a:

98%

MET GLY K3 R17 F136
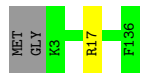
• Molecule 28: 60S ribosomal protein L27a

Chain b:

98%

MET P2 R87 R105 A148

• Molecule 29: 60S ribosomal protein L29

Chain c:

60% 40%

MET A2 K3 K22 R68 A69 GLU ALA ILE LYS ALA LEU VAL LYS PRO LYS GLU VAL LYS PRO LYS ILE PRO LYS GLY VAL SER R91 L116 R117 L118 CYS ARG PRO LYS ALA LYS ALA LYS ALA LYS ASP GLN THR LYS ALA GLN ALA ALA PRO ALA SER VAL PRO

ALA GLN ALA PRO LYS ARG THR GLN ALA PRO THR LYS ALA SER GLU
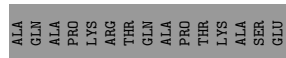
• Molecule 30: 60S ribosomal protein L30

Chain d: 81% 17%

MET VAL ALA ALA LYS LYS THR LYS LYS SER LEU GLU S13 L20 L55 S107 MET PRO GLN THR GLY GLU LYS
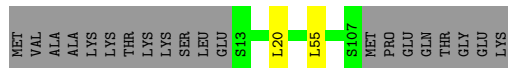
• Molecule 31: 60S ribosomal protein L31

Chain e: 84% 15%

MET ALA PRO ALA LYS LYS GLY GLY GLU LYS LYS LYS GLY ARG SER ALA ILE N18 D97 D123 GLU ASN
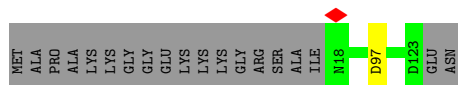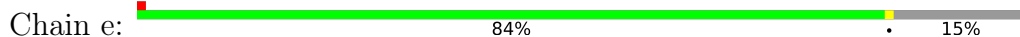
• Molecule 32: 60S ribosomal protein L32

Chain f: 95%

MET A2 R33 R130 SER GLU GLU ASN GLU
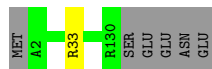
• Molecule 33: 60S ribosomal protein L35a

Chain g: 98%

MET S2 D37 H99 I110
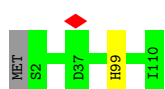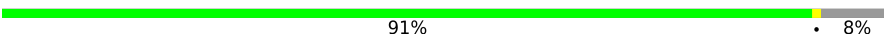
• Molecule 34: 60S ribosomal protein L34

Chain h: 93%

MET V2 R54 K105 Q110 A111 Q112 S113 GLN LYS ALA LYS
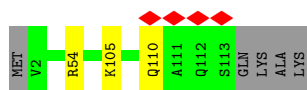
• Molecule 35: 60S ribosomal protein L35

Chain i: 94% 5%

MET A2 R70 K86 R93 K97 R109 R112 A123

• Molecule 36: 60S ribosomal protein L36

Chain j:

91%   8%

MET ALA LEU ARG Y5 D66 A101 ALA LYS LYS ASP

• Molecule 37: 60S ribosomal protein L37

Chain k:

85%   13%

MET T2 R12 R56 K85 PRO LYS ARG ALA ALA VAL ALA ALA SER SER SER SER
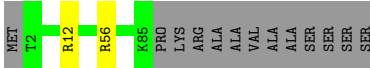
• Molecule 38: 60S ribosomal protein L38

Chain l:

96%

MET P2 K9 R17 K70

• Molecule 39: 60S ribosomal protein L39

Chain m:

94%

MET S2 S3 H4 R21 L51
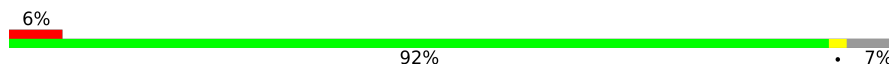
• Molecule 40: 60S ribosomal protein L41

Chain o:

20%
100%

M1 K16 Q22 R23 S24 K25
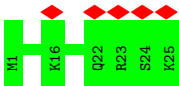
• Molecule 41: 60S ribosomal protein L36a

Chain p:

6%
92%   7%

MET V2 K28 R69 R81 G95 D96 K97 K98 R99 K100 GLY GLN VAL ILE GLN PHE
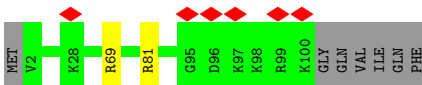
• Molecule 42: 60S ribosomal protein L37a

Chain q:

99%

MET A2 K3 D91 Q92
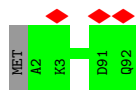
• Molecule 43: 60S ribosomal protein L28

Chain r: 88% 11%

MET S2 L5 L17 P123 VAL MET VAL LYS ARG LYS ARG THR ARG PRO THR LYS SER SER
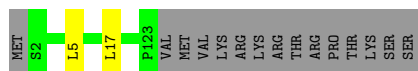
• Molecule 44: 28S ribosomal RNA

Chain t: 73% 24%
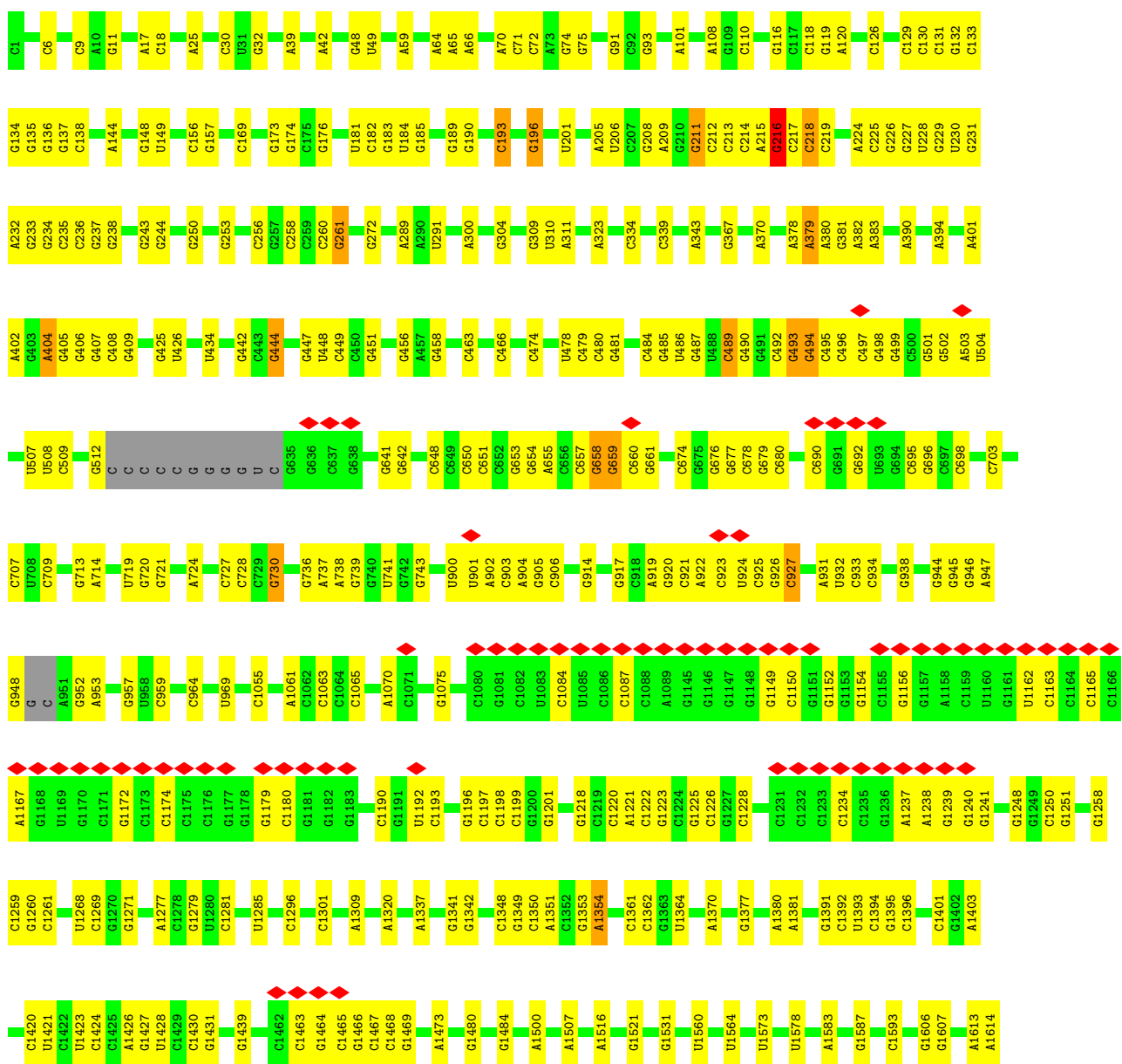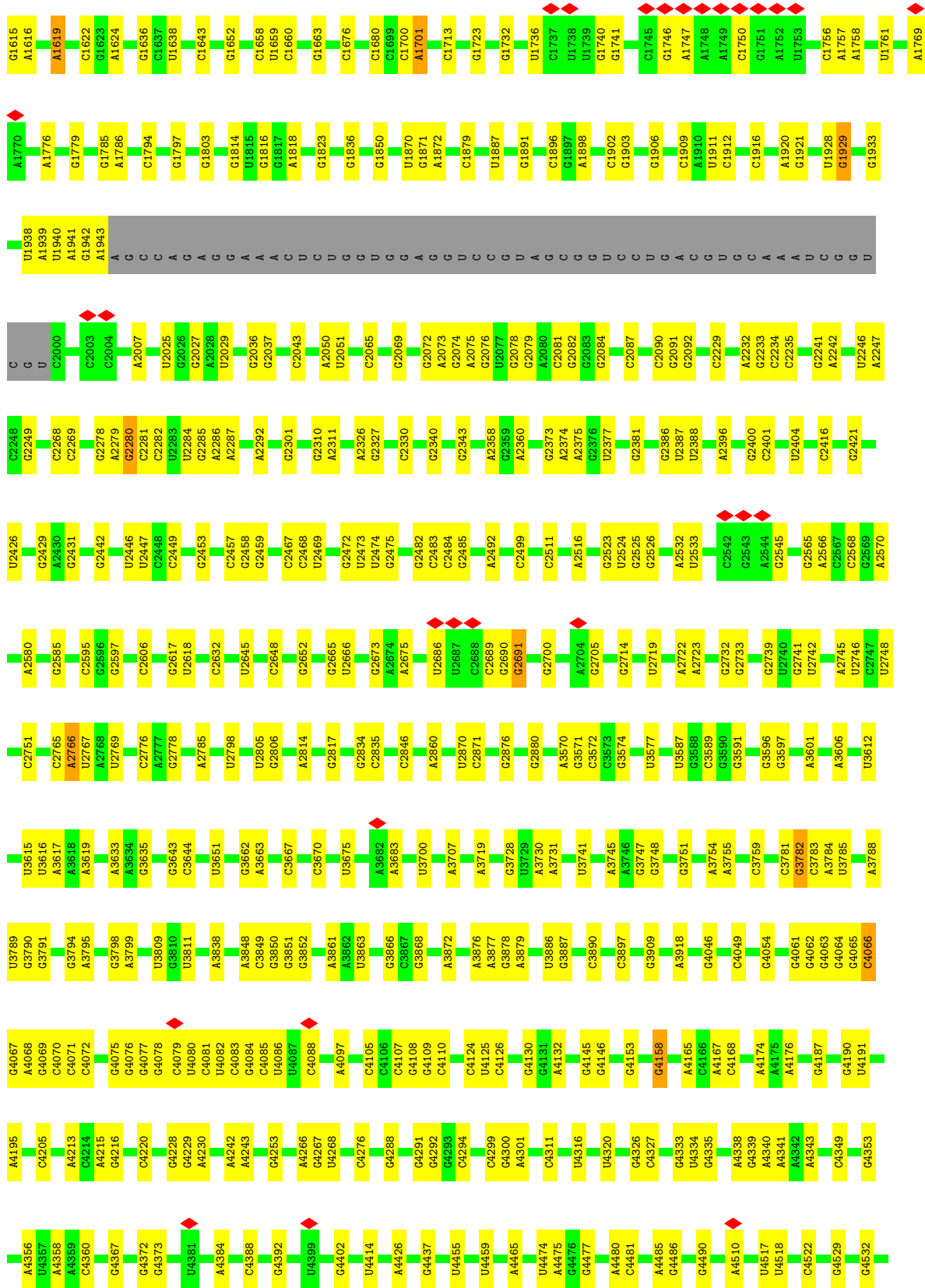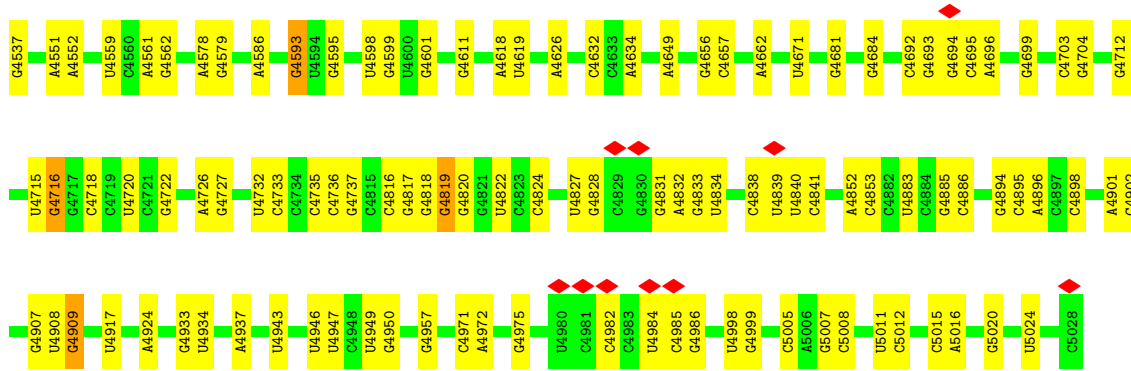
• Molecule 45: tRNA
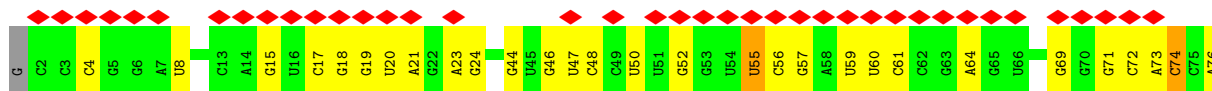
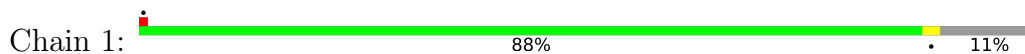Chain u:

• Molecule 46: tRNA
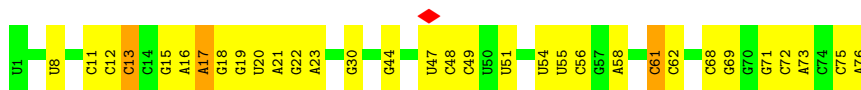
Chain v:
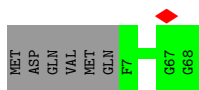

• Molecule 47: Nascent chain mixture

Chain y:
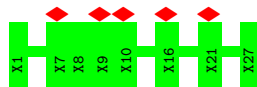
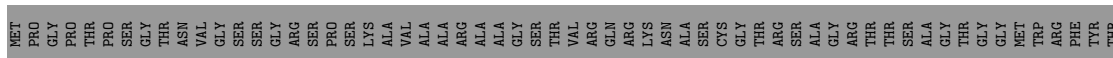• Molecule 48: Protein transport protein Sec61 subunit alpha isoform 1

Chain 1:
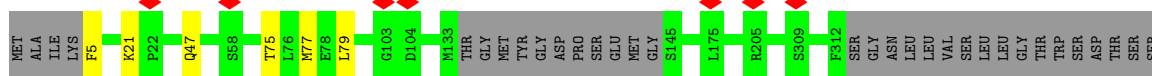
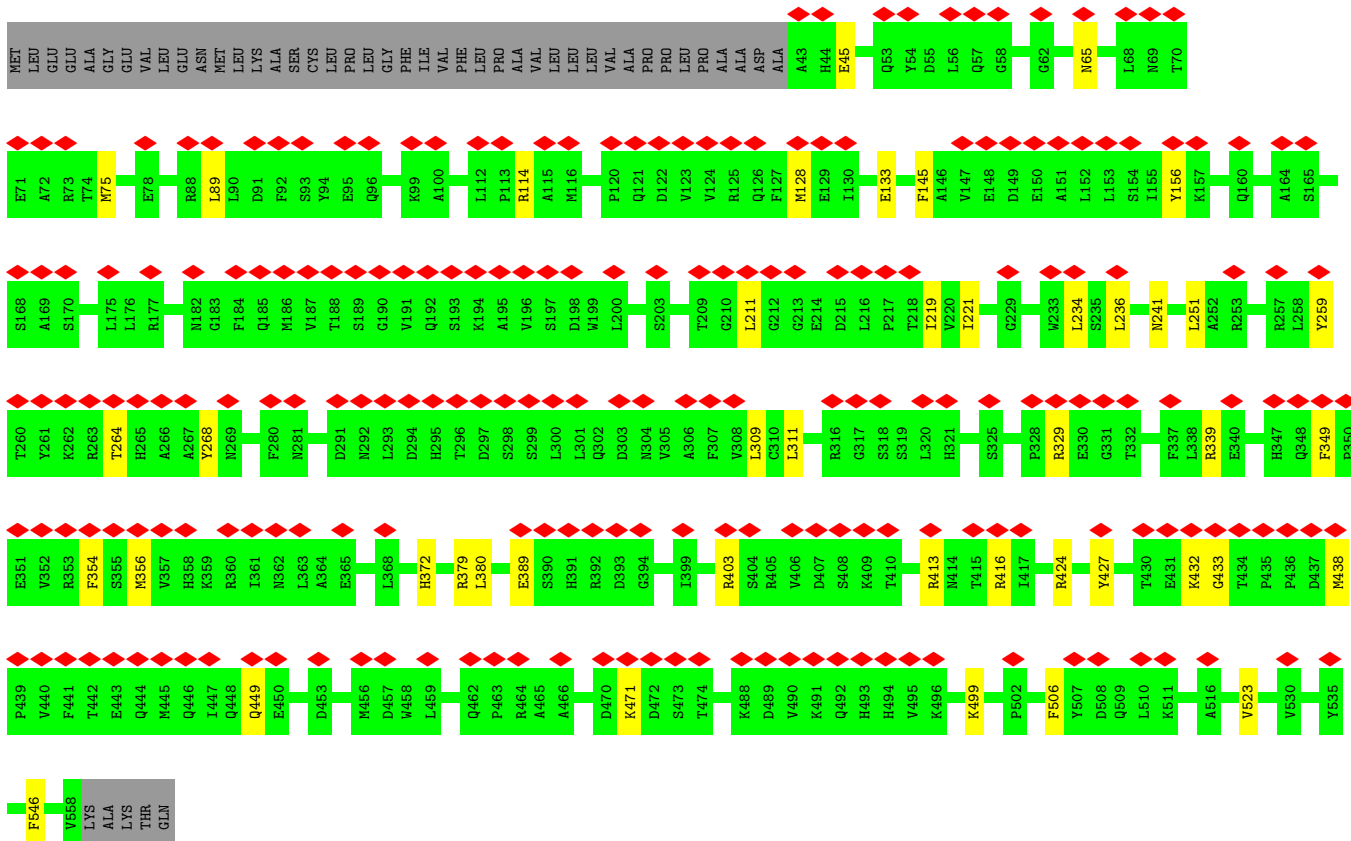• Molecule 49: Protein transport protein Sec61 subunit gamma
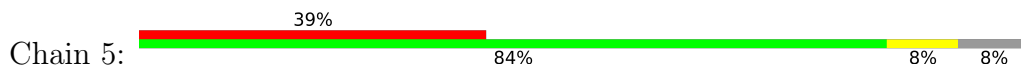
Chain 2:

• Molecule 50: Protein transport protein Sec61 subunit beta

Chain 3:

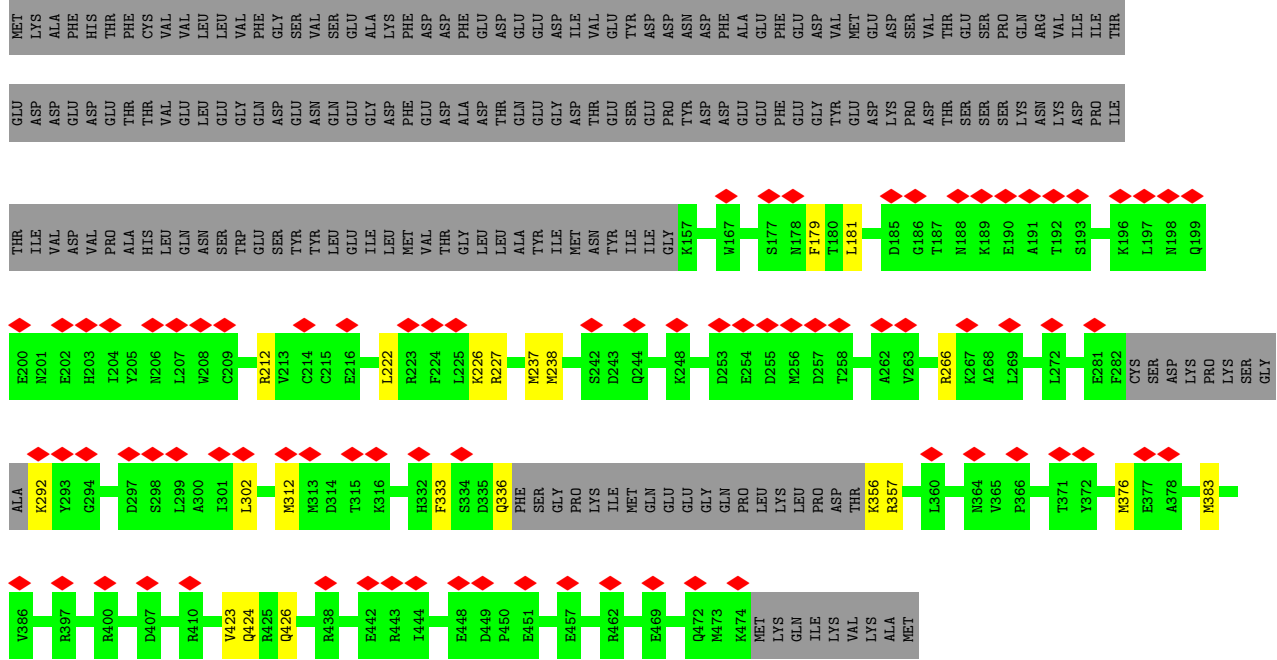

• Molecule 51: Transmembrane protein 147
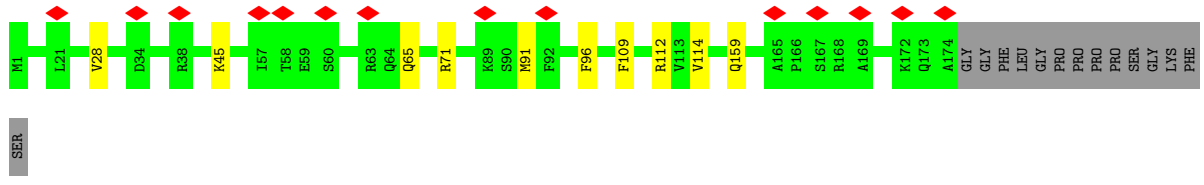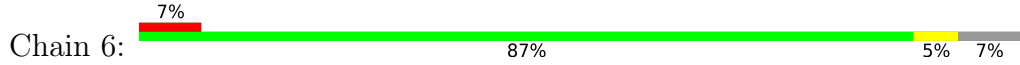
Chain 4:

• Molecule 52: Nicalin

Chain 5:

• Molecule 53: Coiled-coil domain-containing protein 47

Chain 7:

• Molecule 54: Calcium load-activated calcium channel

Chain 6:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	82684	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.047	Depositor
Minimum map value	-0.019	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0073	Depositor
Map size (Å)	680.0, 680.0, 680.0	wwPDB
Map dimensions	500, 500, 500	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.36, 1.36, 1.36	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	0.42	0/1925	0.52	0/2581
2	B	0.37	0/3265	0.50	0/4370
3	C	0.54	0/2942	0.55	0/3951
4	D	1.50	12/3726 (0.3%)	1.27	17/5804 (0.3%)
5	E	0.49	0/2839	0.90	1/4425 (0.0%)
6	F	0.30	0/2052	0.47	0/2755
7	G	0.32	0/1806	0.48	0/2421
8	H	0.37	0/1905	0.49	0/2539
9	I	0.34	0/1913	0.46	0/2576
10	J	0.30	0/1545	0.48	0/2077
11	K	0.26	0/1265	0.46	0/1688
12	L	0.28	0/1376	0.47	0/1841
13	M	0.39	0/1688	0.52	0/2260
14	N	0.32	0/1153	0.45	0/1542
15	O	0.47	0/1746	0.54	0/2338
16	P	0.37	0/1638	0.49	0/2191
17	Q	0.68	0/1268	0.60	0/1701
18	R	0.40	0/1537	0.53	0/2052
19	S	0.43	0/1325	0.52	0/1750
20	T	0.33	0/1488	0.51	0/1997
21	U	0.32	0/1312	0.45	0/1753
22	V	0.28	0/822	0.45	0/1103
23	W	0.33	0/983	0.47	0/1319
24	X	0.38	0/524	0.45	0/698
25	Y	0.76	0/975	0.58	0/1312
26	Z	0.75	0/1123	0.56	0/1493
27	a	0.36	0/1126	0.48	0/1502
28	b	0.41	0/1191	0.51	0/1591
29	c	0.31	0/799	0.48	0/1053
30	d	0.36	0/748	0.49	0/1004
31	e	0.45	0/894	0.52	0/1204
32	f	0.58	0/1082	0.56	0/1443

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
33	g	0.42	0/895	0.51	0/1198
34	h	0.48	0/898	0.54	0/1197
35	i	0.61	0/1023	0.58	0/1351
36	j	0.32	0/805	0.46	0/1065
37	k	0.75	0/703	0.61	0/929
38	l	0.41	0/575	0.50	0/761
39	m	0.64	0/454	0.59	0/599
40	o	0.28	0/241	0.46	0/305
41	p	0.37	0/827	0.47	0/1090
42	q	0.41	0/718	0.51	0/953
43	r	0.51	0/995	0.56	0/1334
44	t	0.91	40/84165 (0.0%)	1.02	105/131283 (0.1%)
45	u	0.32	0/1777	1.00	5/2767 (0.2%)
46	v	0.48	0/1806	1.28	4/2813 (0.1%)
48	1	0.40	0/3394	0.49	0/4598
49	2	0.42	0/504	0.50	0/673
50	3	0.29	0/236	0.43	0/321
51	4	0.36	0/1808	0.49	0/2459
52	5	0.25	0/4174	0.45	0/5661
53	7	0.30	0/2406	0.48	1/3214 (0.0%)
54	6	0.31	0/1406	0.45	0/1882
All	All	0.76	52/159791 (0.0%)	0.88	133/234787 (0.1%)

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
44	t	0	1

All (52) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	t	238	G	N9-C4	-7.20	1.32	1.38
4	D	62	A	N9-C4	-6.49	1.33	1.37
44	t	224	A	N9-C4	-6.43	1.33	1.37
44	t	235	C	N1-C2	-6.38	1.33	1.40
44	t	193	C	N3-C4	-6.28	1.29	1.33
44	t	1281	C	C2-O2	-6.22	1.18	1.24
44	t	226	G	N9-C4	-6.17	1.33	1.38
44	t	404	A	N9-C4	-6.15	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	118	C	C2-O2	-6.07	1.19	1.24
44	t	402	A	N3-C4	-5.92	1.31	1.34
44	t	2286	A	N9-C4	-5.86	1.34	1.37
44	t	378	A	N9-C4	-5.72	1.34	1.37
44	t	234	G	N7-C5	-5.66	1.35	1.39
4	D	37	A	N9-C4	-5.66	1.34	1.37
4	D	59	A	N9-C4	-5.64	1.34	1.37
44	t	225	C	N1-C6	-5.64	1.33	1.37
44	t	383	A	N9-C4	-5.60	1.34	1.37
4	D	62	A	N3-C4	-5.56	1.31	1.34
44	t	238	G	N3-C4	-5.50	1.31	1.35
44	t	402	A	N9-C4	-5.46	1.34	1.37
44	t	4716	G	N9-C4	-5.46	1.33	1.38
4	D	21	C	N1-C6	-5.42	1.33	1.37
44	t	2360	A	N9-C4	-5.41	1.34	1.37
44	t	236	C	N3-C4	-5.40	1.30	1.33
44	t	201	U	N1-C2	-5.38	1.33	1.38
44	t	2287	A	N9-C4	-5.37	1.34	1.37
44	t	218	C	N1-C6	-5.33	1.33	1.37
44	t	231	G	N3-C4	-5.31	1.31	1.35
4	D	96	C	N1-C6	-5.26	1.33	1.37
44	t	2766	A	N3-C4	-5.24	1.31	1.34
44	t	394	A	N3-C4	-5.23	1.31	1.34
4	D	76	C	N1-C6	-5.20	1.34	1.37
44	t	494	G	N9-C4	-5.20	1.33	1.38
44	t	401	A	N9-C4	-5.19	1.34	1.37
44	t	1619	A	N9-C4	-5.18	1.34	1.37
44	t	217	C	N1-C6	-5.17	1.34	1.37
4	D	59	A	N3-C4	-5.17	1.31	1.34
44	t	211	G	C6-N1	-5.16	1.35	1.39
44	t	401	A	N3-C4	-5.16	1.31	1.34
44	t	382	A	N9-C4	-5.15	1.34	1.37
44	t	1484	G	N9-C4	-5.15	1.33	1.38
44	t	2281	C	N1-C6	-5.14	1.34	1.37
44	t	380	A	N9-C4	-5.13	1.34	1.37
44	t	379	A	C5-C4	-5.12	1.35	1.38
4	D	17	A	N9-C4	-5.09	1.34	1.37
4	D	90	C	N1-C6	-5.08	1.34	1.37
44	t	2511	C	N1-C6	-5.08	1.34	1.37
44	t	196	G	N9-C4	-5.08	1.33	1.38
44	t	394	A	N9-C4	-5.06	1.34	1.37
44	t	390	A	N9-C4	-5.03	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
44	t	2280	G	N7-C5	-5.02	1.36	1.39
4	D	71	A	N9-C4	-5.00	1.34	1.37

All (133) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
44	t	494	G	N3-C4-N9	-9.37	120.38	126.00
46	v	61	C	C2-N1-C1'	9.27	129.00	118.80
44	t	4716	G	N3-C4-N9	-9.19	120.49	126.00
44	t	494	G	N3-C4-C5	8.86	133.03	128.60
44	t	444	G	O4'-C1'-N9	8.84	115.27	108.20
44	t	1281	C	C2-N3-C4	-8.68	115.56	119.90
45	u	55	U	N3-C2-O2	-8.67	116.13	122.20
4	D	83	C	C2-N1-C1'	8.62	128.28	118.80
44	t	1484	G	N3-C4-N9	-8.49	120.90	126.00
44	t	4716	G	N3-C4-C5	8.30	132.75	128.60
44	t	1484	G	C4-N9-C1'	-8.24	115.79	126.50
44	t	1281	C	N1-C2-N3	8.13	124.89	119.20
44	t	227	G	C6-C5-N7	-8.01	125.59	130.40
44	t	481	G	N3-C4-N9	-7.88	121.27	126.00
4	D	83	C	C6-N1-C2	-7.70	117.22	120.30
4	D	83	C	N3-C2-O2	-7.67	116.53	121.90
44	t	227	G	N1-C2-N2	-7.61	109.35	116.20
44	t	1484	G	C8-N9-C1'	7.60	136.88	127.00
44	t	227	G	C2-N3-C4	-7.60	108.10	111.90
46	v	61	C	C6-N1-C1'	-7.58	111.70	120.80
44	t	493	G	C4-N9-C1'	7.39	136.11	126.50
44	t	225	C	C2-N3-C4	-7.37	116.22	119.90
4	D	133	G	C2-N3-C4	-7.32	108.24	111.90
4	D	39	G	O4'-C1'-N9	7.12	113.90	108.20
44	t	1484	G	N3-C2-N2	-7.10	114.93	119.90
44	t	1756	C	N1-C2-O2	-7.09	114.65	118.90
4	D	78	G	O4'-C1'-N9	7.00	113.80	108.20
44	t	1281	C	N3-C2-O2	-7.00	117.00	121.90
44	t	493	G	C8-N9-C1'	-6.92	118.00	127.00
4	D	83	C	N1-C2-O2	6.89	123.03	118.90
44	t	2459	G	N3-C4-N9	-6.87	121.88	126.00
44	t	226	G	N3-C4-C5	6.84	132.02	128.60
45	u	55	U	N1-C2-O2	6.83	127.58	122.80
44	t	226	G	C2-N3-C4	-6.71	108.54	111.90
44	t	236	C	C2-N3-C4	-6.64	116.58	119.90
45	u	55	U	C2-N1-C1'	6.61	125.64	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
44	t	4158	G	C8-N9-C1'	-6.49	118.57	127.00
4	D	133	G	O4'-C1'-N9	-6.44	103.05	108.20
44	t	235	C	C2-N1-C1'	-6.43	111.72	118.80
44	t	238	G	N3-C4-C5	6.43	131.82	128.60
44	t	927	C	C2-N1-C1'	6.35	125.79	118.80
44	t	216	G	C8-N9-C4	-6.35	103.86	106.40
44	t	490	G	O4'-C1'-N9	6.33	113.26	108.20
44	t	234	G	N3-C2-N2	6.28	124.30	119.90
44	t	235	C	N1-C2-O2	-6.28	115.13	118.90
44	t	4158	G	N3-C4-N9	6.25	129.75	126.00
44	t	493	G	N3-C4-N9	6.25	129.75	126.00
44	t	1484	G	N1-C2-N2	6.25	121.82	116.20
44	t	238	G	C2-N3-C4	-6.24	108.78	111.90
44	t	243	G	N3-C4-N9	-6.19	122.28	126.00
44	t	1701	A	C8-N9-C4	-6.19	103.32	105.80
44	t	4158	G	C5-C6-O6	-6.18	124.89	128.60
44	t	4733	C	N3-C2-O2	-6.14	117.61	121.90
44	t	1756	C	C2-N1-C1'	-6.08	112.11	118.80
44	t	1484	G	C6-C5-N7	6.08	134.05	130.40
4	D	130	C	C6-N1-C2	6.00	122.70	120.30
44	t	4158	G	C4-N9-C1'	5.97	134.26	126.50
44	t	1484	G	N3-C4-C5	5.95	131.58	128.60
44	t	481	G	N3-C4-C5	5.89	131.55	128.60
44	t	3791	G	C2-N3-C4	-5.85	108.97	111.90
4	D	96	C	C6-N1-C2	5.80	122.62	120.30
44	t	4909	G	N3-C2-N2	5.78	123.95	119.90
44	t	730	G	N3-C4-N9	-5.77	122.53	126.00
44	t	653	G	N1-C6-O6	-5.77	116.44	119.90
44	t	3782	G	N3-C2-N2	-5.76	115.86	119.90
44	t	227	G	C5-C6-N1	-5.75	108.63	111.50
44	t	227	G	N3-C2-N2	5.73	123.91	119.90
44	t	659	G	C4-N9-C1'	5.73	133.95	126.50
44	t	494	G	C2-N3-C4	-5.69	109.05	111.90
44	t	190	G	N3-C4-N9	-5.66	122.61	126.00
44	t	226	G	N3-C4-N9	-5.65	122.61	126.00
4	D	132	G	C8-N9-C1'	-5.63	119.69	127.00
44	t	227	G	N9-C4-C5	-5.62	103.15	105.40
44	t	232	A	C4-C5-N7	5.55	113.47	110.70
44	t	4909	G	N1-C2-N2	-5.54	111.21	116.20
44	t	653	G	C5-C6-O6	5.53	131.92	128.60
44	t	659	G	C8-N9-C1'	-5.53	119.82	127.00
44	t	1241	G	N3-C4-N9	5.50	129.30	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
44	t	489	C	C2-N1-C1'	-5.48	112.77	118.80
44	t	1354	A	O4'-C1'-N9	5.48	112.58	108.20
44	t	4158	G	C6-C5-N7	-5.47	127.12	130.40
44	t	442	G	N3-C4-N9	5.44	129.26	126.00
44	t	235	C	C6-N1-C1'	5.42	127.31	120.80
44	t	651	C	N1-C2-O2	5.41	122.15	118.90
44	t	261	G	N3-C4-C5	5.41	131.30	128.60
4	D	62	A	C2-N3-C4	-5.39	107.91	110.60
44	t	236	C	N3-C2-O2	-5.37	118.14	121.90
44	t	189	G	N3-C4-N9	-5.35	122.79	126.00
53	7	356	LYS	N-CA-C	-5.33	96.60	111.00
44	t	261	G	C2-N3-C4	-5.32	109.24	111.90
44	t	225	C	O4'-C1'-N1	5.30	112.44	108.20
44	t	236	C	N3-C4-C5	5.30	124.02	121.90
44	t	4593	G	C4-N9-C1'	5.29	133.38	126.50
44	t	2459	G	C8-N9-C1'	5.29	133.88	127.00
44	t	227	G	C4-C5-C6	5.28	121.97	118.80
4	D	120	G	N9-C4-C5	-5.26	103.30	105.40
44	t	4392	G	N9-C4-C5	-5.25	103.30	105.40
4	D	83	C	C6-N1-C1'	-5.25	114.50	120.80
44	t	235	C	N3-C4-N4	-5.23	114.34	118.00
44	t	2459	G	N3-C4-C5	5.23	131.21	128.60
44	t	707	C	C2-N1-C1'	-5.23	113.05	118.80
45	u	55	U	C6-N1-C2	-5.22	117.87	121.00
45	u	74	C	N1-C2-O2	5.22	122.03	118.90
44	t	481	G	C8-N9-C1'	5.19	133.74	127.00
44	t	485	G	N3-C4-N9	-5.18	122.89	126.00
44	t	2386	G	C4-N9-C1'	5.18	133.24	126.50
44	t	658	G	C4-N9-C1'	-5.18	119.77	126.50
44	t	238	G	N1-C6-O6	5.18	123.00	119.90
44	t	1929	G	N3-C2-N2	-5.17	116.28	119.90
46	v	17	A	P-O3'-C3'	5.17	125.90	119.70
46	v	13	C	C2-N1-C1'	-5.16	113.13	118.80
44	t	4593	G	C8-N9-C1'	-5.16	120.30	127.00
44	t	3794	G	C2-N3-C4	-5.15	109.32	111.90
44	t	4819	G	N3-C4-N9	5.15	129.09	126.00
44	t	658	G	N3-C4-N9	-5.12	122.92	126.00
44	t	244	G	C2-N3-C4	-5.12	109.34	111.90
44	t	2459	G	C4-N9-C1'	-5.12	119.85	126.50
44	t	2765	C	C6-N1-C2	5.11	122.34	120.30
4	D	132	G	C4-N9-C1'	5.10	133.13	126.50
4	D	66	A	N9-C1'-C2'	-5.09	106.40	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
44	t	232	A	C5-N7-C8	-5.09	101.35	103.90
44	t	2691	G	C8-N9-C1'	-5.08	120.39	127.00
44	t	1761	U	C2-N1-C1'	5.08	123.80	117.70
44	t	493	G	N3-C4-C5	-5.08	126.06	128.60
44	t	261	G	N3-C4-N9	-5.07	122.96	126.00
4	D	120	G	C4-C5-N7	5.07	112.83	110.80
44	t	208	G	C4-N9-C1'	5.07	133.09	126.50
44	t	4066	C	P-O3'-C3'	5.05	125.77	119.70
44	t	707	C	N1-C2-O2	-5.05	115.87	118.90
44	t	493	G	C6-C5-N7	-5.04	127.38	130.40
5	E	64	G	O4'-C1'-N9	-5.01	104.20	108.20
44	t	2373	G	O4'-C1'-N9	5.00	112.20	108.20
44	t	713	G	N3-C4-N9	-5.00	123.00	126.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
44	t	216	G	Sidechain

5.2　Too-close contacts　ⓘ

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

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	244/257 (95%)	224 (92%)	20 (8%)	0	100	100
2	B	394/403 (98%)	363 (92%)	31 (8%)	0	100	100
3	C	361/427 (84%)	337 (93%)	24 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	F	246/297 (83%)	235 (96%)	11 (4%)	0	100	100
7	G	214/288 (74%)	186 (87%)	26 (12%)	2 (1%)	17	53
8	H	223/248 (90%)	207 (93%)	16 (7%)	0	100	100
9	I	232/266 (87%)	221 (95%)	11 (5%)	0	100	100
10	J	189/192 (98%)	173 (92%)	16 (8%)	0	100	100
11	K	148/214 (69%)	141 (95%)	7 (5%)	0	100	100
12	L	167/178 (94%)	155 (93%)	12 (7%)	0	100	100
13	M	203/211 (96%)	180 (89%)	23 (11%)	0	100	100
14	N	136/215 (63%)	127 (93%)	9 (7%)	0	100	100
15	O	201/204 (98%)	181 (90%)	19 (10%)	1 (0%)	29	66
16	P	193/203 (95%)	187 (97%)	6 (3%)	0	100	100
17	Q	151/184 (82%)	147 (97%)	4 (3%)	0	100	100
18	R	185/188 (98%)	175 (95%)	10 (5%)	0	100	100
19	S	152/196 (78%)	146 (96%)	6 (4%)	0	100	100
20	T	173/176 (98%)	165 (95%)	8 (5%)	0	100	100
21	U	155/160 (97%)	146 (94%)	9 (6%)	0	100	100
22	V	97/128 (76%)	95 (98%)	2 (2%)	0	100	100
23	W	127/140 (91%)	123 (97%)	4 (3%)	0	100	100
24	X	59/157 (38%)	57 (97%)	2 (3%)	0	100	100
25	Y	115/156 (74%)	107 (93%)	8 (7%)	0	100	100
26	Z	131/145 (90%)	126 (96%)	5 (4%)	0	100	100
27	a	132/136 (97%)	121 (92%)	11 (8%)	0	100	100
28	b	145/148 (98%)	128 (88%)	17 (12%)	0	100	100
29	c	92/159 (58%)	85 (92%)	7 (8%)	0	100	100
30	d	93/115 (81%)	91 (98%)	2 (2%)	0	100	100
31	e	104/125 (83%)	97 (93%)	7 (7%)	0	100	100
32	f	127/135 (94%)	115 (91%)	12 (9%)	0	100	100
33	g	107/110 (97%)	100 (94%)	7 (6%)	0	100	100
34	h	110/117 (94%)	105 (96%)	5 (4%)	0	100	100
35	i	120/123 (98%)	115 (96%)	5 (4%)	0	100	100
36	j	95/105 (90%)	94 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	k	82/97 (84%)	79 (96%)	3 (4%)	0	100	100
38	l	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
39	m	48/51 (94%)	48 (100%)	0	0	100	100
40	o	23/25 (92%)	23 (100%)	0	0	100	100
41	p	97/106 (92%)	94 (97%)	3 (3%)	0	100	100
42	q	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
43	r	120/137 (88%)	106 (88%)	14 (12%)	0	100	100
48	1	420/476 (88%)	403 (96%)	16 (4%)	1 (0%)	47	78
49	2	60/68 (88%)	59 (98%)	1 (2%)	0	100	100
50	3	27/96 (28%)	25 (93%)	2 (7%)	0	100	100
51	4	219/224 (98%)	206 (94%)	13 (6%)	0	100	100
52	5	514/563 (91%)	472 (92%)	39 (8%)	3 (1%)	25	62
53	7	286/483 (59%)	273 (96%)	13 (4%)	0	100	100
54	6	172/188 (92%)	165 (96%)	7 (4%)	0	100	100
All	All	7845/9182 (85%)	7357 (94%)	481 (6%)	7 (0%)	54	83

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	G	127	SER
48	1	75	THR
7	G	128	HIS
52	5	432	LYS
15	O	90	ASN
52	5	523	VAL
52	5	433	GLY

5.3.2   Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	189/199 (95%)	189 (100%)	0	100	100
2	B	345/349 (99%)	343 (99%)	2 (1%)	86	92
3	C	302/348 (87%)	302 (100%)	0	100	100
6	F	208/250 (83%)	205 (99%)	3 (1%)	67	81
7	G	195/252 (77%)	194 (100%)	1 (0%)	88	94
8	H	194/215 (90%)	189 (97%)	5 (3%)	46	69
9	I	199/223 (89%)	198 (100%)	1 (0%)	88	94
10	J	170/171 (99%)	170 (100%)	0	100	100
11	K	132/181 (73%)	131 (99%)	1 (1%)	81	89
12	L	142/149 (95%)	142 (100%)	0	100	100
13	M	171/177 (97%)	168 (98%)	3 (2%)	59	77
14	N	117/161 (73%)	116 (99%)	1 (1%)	78	88
15	O	171/172 (99%)	168 (98%)	3 (2%)	59	77
16	P	168/174 (97%)	163 (97%)	5 (3%)	41	66
17	Q	134/163 (82%)	131 (98%)	3 (2%)	52	72
18	R	164/165 (99%)	161 (98%)	3 (2%)	59	77
19	S	139/175 (79%)	138 (99%)	1 (1%)	84	91
20	T	156/157 (99%)	153 (98%)	3 (2%)	57	76
21	U	138/140 (99%)	137 (99%)	1 (1%)	84	91
22	V	89/115 (77%)	87 (98%)	2 (2%)	52	72
23	W	100/107 (94%)	100 (100%)	0	100	100
24	X	53/126 (42%)	53 (100%)	0	100	100
25	Y	105/133 (79%)	103 (98%)	2 (2%)	57	76
26	Z	123/135 (91%)	121 (98%)	2 (2%)	62	79
27	a	117/118 (99%)	116 (99%)	1 (1%)	78	88
28	b	120/121 (99%)	118 (98%)	2 (2%)	60	78
29	c	79/126 (63%)	78 (99%)	1 (1%)	69	82
30	d	80/97 (82%)	78 (98%)	2 (2%)	47	70
31	e	97/110 (88%)	96 (99%)	1 (1%)	76	86
32	f	115/121 (95%)	114 (99%)	1 (1%)	78	88
33	g	88/89 (99%)	87 (99%)	1 (1%)	73	85
34	h	96/100 (96%)	93 (97%)	3 (3%)	40	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
35	i	109/110 (99%)	103 (94%)	6 (6%)	21	53
36	j	83/89 (93%)	82 (99%)	1 (1%)	71	84
37	k	71/80 (89%)	69 (97%)	2 (3%)	43	67
38	l	64/65 (98%)	62 (97%)	2 (3%)	40	65
39	m	47/48 (98%)	45 (96%)	2 (4%)	29	57
40	o	24/24 (100%)	24 (100%)	0	100	100
41	p	88/94 (94%)	86 (98%)	2 (2%)	50	71
42	q	74/75 (99%)	74 (100%)	0	100	100
43	r	106/121 (88%)	104 (98%)	2 (2%)	57	76
48	1	362/399 (91%)	355 (98%)	7 (2%)	57	76
49	2	53/59 (90%)	53 (100%)	0	100	100
50	3	26/74 (35%)	25 (96%)	1 (4%)	33	60
51	4	183/186 (98%)	177 (97%)	6 (3%)	38	64
52	5	438/475 (92%)	397 (91%)	41 (9%)	8	34
53	7	261/436 (60%)	241 (92%)	20 (8%)	13	42
54	6	154/164 (94%)	144 (94%)	10 (6%)	17	48
All	All	6839/7818 (88%)	6683 (98%)	156 (2%)	53	71

All (156) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	114	CYS
2	B	261	ARG
6	F	9	ASN
6	F	10	LYS
6	F	196	ARG
7	G	52	ARG
8	H	24	ASN
8	H	25	PHE
8	H	106	ARG
8	H	225	THR
8	H	245	ARG
9	I	70	LEU
11	K	69	ARG
13	M	21	ARG
13	M	102	ARG

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Mol	Chain	Res	Type
13	M	198	ARG
14	N	127	VAL
15	O	63	ARG
15	O	133	ILE
15	O	204	ARG
16	P	94	ARG
16	P	101	ARG
16	P	141	LEU
16	P	169	ARG
16	P	178	ARG
17	Q	127	ARG
17	Q	139	TYR
17	Q	146	ILE
18	R	37	ARG
18	R	91	ARG
18	R	168	ARG
19	S	153	LYS
20	T	15	ARG
20	T	68	PHE
20	T	138	ARG
21	U	68	THR
22	V	20	LYS
22	V	101	ARG
25	Y	48	ARG
25	Y	152	LYS
26	Z	28	LYS
26	Z	38	LEU
27	a	17	ARG
28	b	87	ARG
28	b	105	ARG
29	c	116	LEU
30	d	20	LEU
30	d	55	LEU
31	e	97	ASP
32	f	33	ARG
33	g	99	HIS
34	h	54	ARG
34	h	105	LYS
34	h	110	GLN
35	i	70	ARG
35	i	86	LYS
35	i	93	ARG

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Mol	Chain	Res	Type
35	i	97	LYS
35	i	109	ARG
35	i	112	ARG
36	j	66	ASP
37	k	12	ARG
37	k	56	ARG
38	l	9	LYS
38	l	17	ARG
39	m	4	HIS
39	m	21	ARG
41	p	69	ARG
41	p	81	ARG
43	r	5	LEU
43	r	17	LEU
48	1	5	PHE
48	1	21	LYS
48	1	47	GLN
48	1	77	MET
48	1	79	LEU
48	1	436	ASP
48	1	441	ILE
50	3	87	LEU
51	4	6	PHE
51	4	35	CYS
51	4	145	HIS
51	4	154	TRP
51	4	158	ARG
51	4	188	HIS
52	5	45	GLU
52	5	65	ASN
52	5	75	MET
52	5	89	LEU
52	5	114	ARG
52	5	128	MET
52	5	133	GLU
52	5	145	PHE
52	5	156	TYR
52	5	211	LEU
52	5	219	ILE
52	5	221	ILE
52	5	234	LEU
52	5	236	LEU

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Mol	Chain	Res	Type
52	5	241	ASN
52	5	251	LEU
52	5	259	TYR
52	5	264	THR
52	5	268	TYR
52	5	309	LEU
52	5	311	LEU
52	5	329	ARG
52	5	339	ARG
52	5	349	PHE
52	5	354	PHE
52	5	356	MET
52	5	372	HIS
52	5	379	ARG
52	5	380	LEU
52	5	389	GLU
52	5	403	ARG
52	5	413	ARG
52	5	416	ARG
52	5	424	ARG
52	5	427	TYR
52	5	438	MET
52	5	449	GLN
52	5	471	LYS
52	5	499	LYS
52	5	506	PHE
52	5	546	PHE
53	7	179	PHE
53	7	181	LEU
53	7	212	ARG
53	7	222	LEU
53	7	226	LYS
53	7	227	ARG
53	7	237	MET
53	7	238	MET
53	7	266	ARG
53	7	292	LYS
53	7	302	LEU
53	7	312	MET
53	7	333	PHE
53	7	336	GLN
53	7	357	ARG

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Mol	Chain	Res	Type
53	7	376	MET
53	7	383	MET
53	7	423	VAL
53	7	424	GLN
53	7	426	GLN
54	6	28	VAL
54	6	45	LYS
54	6	65	GLN
54	6	71	ARG
54	6	91	MET
54	6	96	PHE
54	6	109	PHE
54	6	112	ARG
54	6	114	VAL
54	6	159	GLN

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

Mol	Chain	Res	Type
19	S	39	GLN
48	1	456	GLN

5.3.3　RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	D	156/157 (99%)	60 (38%)	20 (12%)
44	t	3495/3579 (97%)	849 (24%)	0
45	u	74/76 (97%)	29 (39%)	0
46	v	75/76 (98%)	32 (42%)	0
5	E	118/119 (99%)	14 (11%)	0
All	All	3918/4007 (97%)	984 (25%)	20 (0%)

All (984) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	D	2	G
4	D	13	G
4	D	34	U
4	D	35	C
4	D	39	G

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Mol	Chain	Res	Type
4	D	49	G
4	D	51	U
4	D	52	A
4	D	59	A
4	D	61	A
4	D	63	U
4	D	64	U
4	D	65	A
4	D	67	U
4	D	71	A
4	D	72	A
4	D	73	U
4	D	74	U
4	D	75	G
4	D	76	C
4	D	77	A
4	D	78	G
4	D	79	G
4	D	80	A
4	D	81	C
4	D	82	A
4	D	83	C
4	D	84	A
4	D	85	U
4	D	86	U
4	D	87	G
4	D	88	A
4	D	89	U
4	D	96	C
4	D	104	A
4	D	105	C
4	D	109	C
4	D	110	U
4	D	111	U
4	D	112	G
4	D	114	G
4	D	116	C
4	D	117	C
4	D	119	C
4	D	120	G
4	D	121	G
4	D	122	G

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Mol	Chain	Res	Type
4	D	123	U
4	D	124	U
4	D	125	C
4	D	126	C
4	D	127	U
4	D	128	C
4	D	129	C
4	D	130	C
4	D	131	G
4	D	132	G
4	D	133	G
4	D	148	A
4	D	150	C
5	E	7	G
5	E	11	A
5	E	22	A
5	E	23	A
5	E	24	C
5	E	33	U
5	E	35	U
5	E	40	U
5	E	48	G
5	E	49	A
5	E	53	U
5	E	64	G
5	E	96	U
5	E	110	G
44	t	6	C
44	t	9	C
44	t	11	G
44	t	17	A
44	t	18	C
44	t	25	A
44	t	30	C
44	t	32	G
44	t	39	A
44	t	42	A
44	t	48	G
44	t	49	U
44	t	59	A
44	t	64	A
44	t	65	A

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Mol	Chain	Res	Type
44	t	66	A
44	t	70	A
44	t	71	C
44	t	72	C
44	t	74	G
44	t	75	G
44	t	91	G
44	t	93	G
44	t	101	A
44	t	108	A
44	t	110	C
44	t	116	G
44	t	118	C
44	t	119	G
44	t	120	A
44	t	126	C
44	t	129	C
44	t	130	C
44	t	131	C
44	t	132	G
44	t	133	C
44	t	134	G
44	t	135	G
44	t	136	G
44	t	137	G
44	t	138	C
44	t	144	A
44	t	148	G
44	t	149	U
44	t	156	C
44	t	157	G
44	t	169	C
44	t	173	G
44	t	174	G
44	t	176	G
44	t	181	U
44	t	182	C
44	t	183	G
44	t	184	U
44	t	185	G
44	t	193	C
44	t	196	G

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Mol	Chain	Res	Type
44	t	205	A
44	t	206	U
44	t	209	A
44	t	211	G
44	t	212	C
44	t	213	C
44	t	214	C
44	t	215	A
44	t	216	G
44	t	218	C
44	t	219	C
44	t	228	U
44	t	229	G
44	t	230	U
44	t	233	G
44	t	237	G
44	t	250	G
44	t	253	G
44	t	256	C
44	t	258	C
44	t	260	C
44	t	261	G
44	t	272	G
44	t	289	A
44	t	291	U
44	t	300	A
44	t	304	G
44	t	309	G
44	t	310	U
44	t	311	A
44	t	323	A
44	t	334	C
44	t	339	C
44	t	343	A
44	t	367	G
44	t	370	A
44	t	379	A
44	t	381	G
44	t	404	A
44	t	405	G
44	t	406	G
44	t	407	G

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Mol	Chain	Res	Type
44	t	408	C
44	t	409	G
44	t	425	G
44	t	426	U
44	t	434	U
44	t	444	G
44	t	447	G
44	t	448	U
44	t	449	C
44	t	451	G
44	t	456	G
44	t	458	G
44	t	463	C
44	t	466	C
44	t	474	C
44	t	478	U
44	t	479	C
44	t	480	C
44	t	484	C
44	t	486	U
44	t	487	G
44	t	489	C
44	t	492	C
44	t	493	G
44	t	494	G
44	t	495	C
44	t	496	C
44	t	497	C
44	t	498	G
44	t	499	G
44	t	501	G
44	t	502	G
44	t	503	A
44	t	504	U
44	t	507	U
44	t	508	U
44	t	509	C
44	t	512	G
44	t	641	G
44	t	642	G
44	t	648	C
44	t	650	C

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Mol	Chain	Res	Type
44	t	654	G
44	t	655	A
44	t	657	C
44	t	658	G
44	t	659	G
44	t	660	C
44	t	661	G
44	t	674	C
44	t	676	G
44	t	677	G
44	t	678	C
44	t	679	G
44	t	680	C
44	t	690	C
44	t	692	G
44	t	695	C
44	t	696	G
44	t	698	C
44	t	703	C
44	t	709	C
44	t	714	A
44	t	719	U
44	t	720	G
44	t	721	G
44	t	724	A
44	t	727	C
44	t	728	C
44	t	730	G
44	t	736	G
44	t	737	A
44	t	738	A
44	t	739	G
44	t	741	U
44	t	743	G
44	t	900	U
44	t	901	U
44	t	902	A
44	t	903	C
44	t	904	A
44	t	905	G
44	t	906	C
44	t	914	G

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Mol	Chain	Res	Type
44	t	917	G
44	t	919	A
44	t	920	G
44	t	921	C
44	t	922	A
44	t	923	C
44	t	924	U
44	t	925	C
44	t	926	G
44	t	927	C
44	t	931	A
44	t	932	U
44	t	933	C
44	t	934	C
44	t	938	G
44	t	944	G
44	t	945	G
44	t	946	G
44	t	947	A
44	t	948	G
44	t	952	G
44	t	953	A
44	t	957	G
44	t	959	C
44	t	964	C
44	t	969	U
44	t	1055	C
44	t	1061	A
44	t	1063	C
44	t	1065	C
44	t	1070	A
44	t	1075	G
44	t	1084	C
44	t	1087	C
44	t	1149	G
44	t	1150	C
44	t	1152	G
44	t	1154	G
44	t	1156	G
44	t	1162	U
44	t	1163	C
44	t	1165	C

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Mol	Chain	Res	Type
44	t	1167	A
44	t	1172	G
44	t	1174	C
44	t	1179	G
44	t	1180	C
44	t	1190	C
44	t	1192	U
44	t	1193	C
44	t	1196	G
44	t	1197	C
44	t	1198	C
44	t	1199	C
44	t	1201	G
44	t	1218	G
44	t	1220	C
44	t	1221	A
44	t	1222	C
44	t	1223	G
44	t	1225	G
44	t	1226	C
44	t	1228	C
44	t	1234	C
44	t	1237	A
44	t	1238	A
44	t	1239	G
44	t	1240	G
44	t	1248	G
44	t	1250	C
44	t	1251	G
44	t	1258	G
44	t	1259	C
44	t	1260	G
44	t	1261	C
44	t	1268	U
44	t	1269	C
44	t	1271	G
44	t	1277	A
44	t	1279	G
44	t	1285	U
44	t	1296	C
44	t	1301	C
44	t	1309	A

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Mol	Chain	Res	Type
44	t	1320	A
44	t	1337	A
44	t	1341	G
44	t	1342	G
44	t	1348	C
44	t	1349	G
44	t	1350	C
44	t	1351	A
44	t	1353	G
44	t	1354	A
44	t	1361	C
44	t	1362	C
44	t	1364	U
44	t	1370	A
44	t	1377	G
44	t	1380	A
44	t	1381	A
44	t	1391	G
44	t	1392	C
44	t	1393	U
44	t	1394	C
44	t	1395	G
44	t	1396	C
44	t	1401	C
44	t	1403	A
44	t	1420	C
44	t	1421	U
44	t	1423	U
44	t	1424	C
44	t	1426	A
44	t	1427	G
44	t	1428	U
44	t	1430	C
44	t	1431	G
44	t	1439	G
44	t	1463	C
44	t	1464	G
44	t	1465	C
44	t	1466	G
44	t	1467	C
44	t	1468	C
44	t	1469	G

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Mol	Chain	Res	Type
44	t	1473	A
44	t	1480	G
44	t	1500	A
44	t	1507	A
44	t	1516	A
44	t	1521	G
44	t	1531	G
44	t	1560	U
44	t	1564	U
44	t	1573	U
44	t	1578	U
44	t	1583	A
44	t	1587	G
44	t	1593	C
44	t	1606	G
44	t	1607	G
44	t	1613	A
44	t	1614	A
44	t	1615	G
44	t	1616	A
44	t	1619	A
44	t	1622	C
44	t	1624	A
44	t	1636	G
44	t	1638	U
44	t	1643	C
44	t	1652	G
44	t	1658	C
44	t	1659	U
44	t	1660	C
44	t	1663	G
44	t	1676	C
44	t	1680	C
44	t	1700	C
44	t	1701	A
44	t	1713	C
44	t	1723	G
44	t	1732	G
44	t	1736	U
44	t	1740	G
44	t	1741	G
44	t	1746	G

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Mol	Chain	Res	Type
44	t	1747	A
44	t	1750	C
44	t	1757	A
44	t	1758	A
44	t	1769	A
44	t	1776	A
44	t	1779	G
44	t	1785	G
44	t	1786	A
44	t	1794	C
44	t	1797	G
44	t	1803	G
44	t	1814	G
44	t	1816	G
44	t	1818	A
44	t	1823	G
44	t	1836	G
44	t	1850	G
44	t	1870	U
44	t	1871	G
44	t	1872	A
44	t	1879	C
44	t	1887	U
44	t	1891	G
44	t	1896	C
44	t	1898	A
44	t	1902	C
44	t	1903	G
44	t	1906	G
44	t	1909	C
44	t	1911	U
44	t	1912	C
44	t	1916	C
44	t	1920	A
44	t	1921	G
44	t	1928	U
44	t	1929	G
44	t	1933	G
44	t	1938	U
44	t	1939	A
44	t	1940	U
44	t	1941	A

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Mol	Chain	Res	Type
44	t	1942	G
44	t	1943	A
44	t	2007	A
44	t	2025	U
44	t	2027	G
44	t	2029	U
44	t	2036	G
44	t	2037	G
44	t	2043	C
44	t	2050	A
44	t	2051	U
44	t	2065	C
44	t	2069	G
44	t	2072	G
44	t	2073	A
44	t	2074	G
44	t	2075	A
44	t	2076	G
44	t	2078	G
44	t	2079	G
44	t	2081	C
44	t	2082	G
44	t	2084	G
44	t	2087	C
44	t	2090	C
44	t	2091	G
44	t	2092	G
44	t	2229	C
44	t	2232	A
44	t	2233	G
44	t	2234	C
44	t	2235	C
44	t	2241	G
44	t	2242	A
44	t	2246	U
44	t	2247	A
44	t	2249	G
44	t	2268	C
44	t	2269	C
44	t	2278	G
44	t	2279	A
44	t	2280	G

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Mol	Chain	Res	Type
44	t	2282	C
44	t	2284	U
44	t	2285	G
44	t	2292	A
44	t	2301	G
44	t	2310	G
44	t	2311	A
44	t	2326	A
44	t	2327	G
44	t	2330	C
44	t	2340	G
44	t	2343	G
44	t	2358	A
44	t	2374	A
44	t	2375	A
44	t	2377	U
44	t	2381	G
44	t	2387	U
44	t	2388	U
44	t	2396	A
44	t	2400	G
44	t	2401	C
44	t	2404	U
44	t	2416	C
44	t	2421	G
44	t	2426	U
44	t	2429	G
44	t	2431	G
44	t	2442	G
44	t	2446	U
44	t	2447	U
44	t	2449	C
44	t	2453	G
44	t	2457	C
44	t	2458	G
44	t	2467	C
44	t	2468	C
44	t	2469	U
44	t	2472	G
44	t	2473	U
44	t	2474	U
44	t	2475	G

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Mol	Chain	Res	Type
44	t	2482	G
44	t	2483	C
44	t	2484	C
44	t	2485	G
44	t	2492	A
44	t	2499	C
44	t	2516	A
44	t	2523	G
44	t	2524	U
44	t	2525	G
44	t	2526	G
44	t	2532	A
44	t	2533	U
44	t	2545	G
44	t	2565	G
44	t	2566	A
44	t	2568	C
44	t	2570	A
44	t	2580	A
44	t	2585	G
44	t	2595	C
44	t	2597	G
44	t	2606	C
44	t	2617	G
44	t	2618	U
44	t	2632	C
44	t	2645	U
44	t	2648	C
44	t	2652	G
44	t	2665	G
44	t	2666	U
44	t	2673	G
44	t	2675	A
44	t	2686	U
44	t	2689	C
44	t	2690	G
44	t	2691	G
44	t	2700	G
44	t	2705	G
44	t	2714	G
44	t	2719	U
44	t	2722	A

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Mol	Chain	Res	Type
44	t	2723	A
44	t	2732	G
44	t	2733	G
44	t	2739	G
44	t	2741	G
44	t	2742	U
44	t	2745	A
44	t	2746	U
44	t	2748	U
44	t	2751	C
44	t	2766	A
44	t	2767	U
44	t	2769	U
44	t	2776	C
44	t	2778	G
44	t	2785	A
44	t	2798	U
44	t	2805	U
44	t	2806	G
44	t	2814	A
44	t	2817	G
44	t	2834	G
44	t	2835	C
44	t	2846	C
44	t	2860	A
44	t	2870	U
44	t	2871	C
44	t	2876	G
44	t	2880	G
44	t	3570	A
44	t	3571	G
44	t	3572	C
44	t	3574	G
44	t	3577	U
44	t	3587	U
44	t	3589	C
44	t	3591	G
44	t	3596	G
44	t	3597	G
44	t	3601	A
44	t	3606	A
44	t	3612	U

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Mol	Chain	Res	Type
44	t	3615	U
44	t	3616	U
44	t	3617	A
44	t	3619	A
44	t	3633	A
44	t	3635	G
44	t	3643	G
44	t	3644	C
44	t	3651	U
44	t	3662	G
44	t	3663	A
44	t	3667	C
44	t	3670	C
44	t	3675	U
44	t	3683	A
44	t	3700	U
44	t	3707	A
44	t	3719	A
44	t	3728	G
44	t	3730	A
44	t	3731	A
44	t	3741	U
44	t	3745	A
44	t	3747	G
44	t	3748	G
44	t	3751	G
44	t	3754	A
44	t	3755	A
44	t	3759	C
44	t	3781	C
44	t	3782	G
44	t	3783	C
44	t	3784	A
44	t	3785	U
44	t	3788	A
44	t	3789	U
44	t	3790	G
44	t	3795	A
44	t	3798	G
44	t	3799	A
44	t	3809	U
44	t	3811	U

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Mol	Chain	Res	Type
44	t	3838	A
44	t	3848	A
44	t	3849	C
44	t	3850	G
44	t	3851	G
44	t	3852	G
44	t	3861	A
44	t	3863	U
44	t	3866	G
44	t	3868	G
44	t	3872	A
44	t	3876	A
44	t	3877	A
44	t	3878	G
44	t	3879	A
44	t	3886	U
44	t	3887	G
44	t	3890	C
44	t	3897	C
44	t	3909	G
44	t	3918	A
44	t	4046	G
44	t	4049	C
44	t	4054	G
44	t	4061	G
44	t	4062	G
44	t	4063	G
44	t	4064	G
44	t	4065	G
44	t	4066	C
44	t	4067	G
44	t	4068	A
44	t	4069	G
44	t	4070	C
44	t	4071	C
44	t	4072	C
44	t	4075	G
44	t	4076	G
44	t	4077	G
44	t	4078	G
44	t	4079	C
44	t	4080	U

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Mol	Chain	Res	Type
44	t	4081	C
44	t	4082	U
44	t	4083	C
44	t	4084	G
44	t	4085	C
44	t	4086	U
44	t	4088	C
44	t	4097	A
44	t	4105	C
44	t	4107	C
44	t	4108	G
44	t	4109	G
44	t	4110	C
44	t	4124	C
44	t	4125	U
44	t	4126	C
44	t	4130	G
44	t	4132	A
44	t	4145	G
44	t	4146	G
44	t	4153	G
44	t	4158	G
44	t	4165	A
44	t	4167	A
44	t	4168	C
44	t	4174	A
44	t	4176	A
44	t	4187	G
44	t	4190	G
44	t	4191	U
44	t	4195	A
44	t	4205	C
44	t	4213	A
44	t	4215	A
44	t	4216	G
44	t	4220	C
44	t	4228	G
44	t	4229	G
44	t	4230	A
44	t	4242	A
44	t	4243	A
44	t	4253	G

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Mol	Chain	Res	Type
44	t	4266	A
44	t	4267	G
44	t	4268	U
44	t	4276	C
44	t	4288	G
44	t	4291	G
44	t	4292	G
44	t	4294	C
44	t	4299	C
44	t	4300	G
44	t	4301	A
44	t	4311	C
44	t	4316	U
44	t	4320	U
44	t	4326	G
44	t	4327	C
44	t	4333	G
44	t	4334	U
44	t	4335	G
44	t	4338	A
44	t	4339	G
44	t	4340	A
44	t	4341	A
44	t	4343	A
44	t	4349	C
44	t	4353	G
44	t	4356	A
44	t	4358	A
44	t	4360	C
44	t	4367	G
44	t	4372	G
44	t	4373	G
44	t	4384	A
44	t	4388	C
44	t	4402	G
44	t	4414	U
44	t	4426	A
44	t	4437	G
44	t	4455	U
44	t	4459	U
44	t	4465	A
44	t	4474	U

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Mol	Chain	Res	Type
44	t	4475	A
44	t	4477	G
44	t	4480	A
44	t	4481	C
44	t	4485	A
44	t	4486	G
44	t	4490	G
44	t	4510	A
44	t	4517	U
44	t	4518	U
44	t	4522	C
44	t	4529	G
44	t	4532	G
44	t	4537	G
44	t	4551	A
44	t	4552	A
44	t	4559	U
44	t	4561	A
44	t	4562	G
44	t	4578	A
44	t	4579	G
44	t	4586	A
44	t	4593	G
44	t	4595	G
44	t	4598	U
44	t	4599	G
44	t	4601	G
44	t	4611	G
44	t	4618	A
44	t	4619	U
44	t	4626	A
44	t	4632	C
44	t	4634	A
44	t	4649	A
44	t	4656	G
44	t	4657	C
44	t	4662	A
44	t	4671	U
44	t	4681	G
44	t	4684	G
44	t	4692	C
44	t	4693	G

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Mol	Chain	Res	Type
44	t	4694	G
44	t	4695	C
44	t	4696	A
44	t	4699	G
44	t	4703	C
44	t	4704	G
44	t	4712	G
44	t	4715	U
44	t	4716	G
44	t	4718	C
44	t	4720	U
44	t	4722	G
44	t	4726	A
44	t	4727	G
44	t	4732	U
44	t	4735	C
44	t	4736	C
44	t	4737	G
44	t	4816	C
44	t	4817	G
44	t	4818	G
44	t	4819	G
44	t	4820	G
44	t	4822	U
44	t	4824	C
44	t	4827	U
44	t	4828	G
44	t	4831	G
44	t	4832	A
44	t	4833	G
44	t	4834	U
44	t	4838	C
44	t	4839	U
44	t	4840	U
44	t	4841	C
44	t	4852	A
44	t	4853	C
44	t	4883	U
44	t	4885	G
44	t	4886	C
44	t	4894	G
44	t	4895	C

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Mol	Chain	Res	Type
44	t	4896	A
44	t	4898	C
44	t	4901	A
44	t	4902	C
44	t	4907	G
44	t	4908	U
44	t	4909	G
44	t	4917	U
44	t	4924	A
44	t	4933	G
44	t	4934	U
44	t	4937	A
44	t	4943	U
44	t	4946	U
44	t	4947	U
44	t	4949	U
44	t	4950	G
44	t	4957	G
44	t	4971	C
44	t	4972	A
44	t	4975	G
44	t	4982	C
44	t	4984	U
44	t	4985	C
44	t	4986	G
44	t	4998	U
44	t	4999	G
44	t	5005	C
44	t	5007	G
44	t	5008	C
44	t	5011	U
44	t	5012	C
44	t	5015	C
44	t	5016	A
44	t	5020	G
44	t	5024	U
45	u	4	C
45	u	8	U
45	u	15	G
45	u	17	C
45	u	18	G
45	u	19	G

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Mol	Chain	Res	Type
45	u	20	U
45	u	21	A
45	u	23	A
45	u	24	G
45	u	44	G
45	u	46	G
45	u	47	U
45	u	48	C
45	u	50	U
45	u	52	G
45	u	55	U
45	u	56	C
45	u	57	G
45	u	59	U
45	u	60	U
45	u	61	C
45	u	64	A
45	u	69	G
45	u	71	G
45	u	72	C
45	u	73	A
45	u	74	C
45	u	76	A
46	v	8	U
46	v	11	C
46	v	12	C
46	v	13	C
46	v	15	G
46	v	16	A
46	v	17	A
46	v	18	G
46	v	19	G
46	v	20	U
46	v	21	A
46	v	22	G
46	v	23	A
46	v	30	G
46	v	44	G
46	v	47	U
46	v	48	C
46	v	49	C
46	v	51	U

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Mol	Chain	Res	Type
46	v	54	U
46	v	55	U
46	v	56	C
46	v	58	A
46	v	61	C
46	v	62	C
46	v	68	C
46	v	69	G
46	v	71	G
46	v	72	C
46	v	73	A
46	v	75	C
46	v	76	A

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	D	70	G
4	D	72	A
4	D	73	U
4	D	75	G
4	D	76	C
4	D	77	A
4	D	78	G
4	D	79	G
4	D	80	A
4	D	81	C
4	D	82	A
4	D	83	C
4	D	84	A
4	D	85	U
4	D	86	U
4	D	87	G
4	D	123	U
4	D	125	C
4	D	126	C
4	D	129	C

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 31 ligands modelled in this entry, 31 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
44	t	11

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	t	750:G	O3'	890:C	P	20.30
1	t	3919:C	O3'	4035:G	P	19.55
1	t	976:U	O3'	1047:G	P	16.16
1	t	1680:C	O3'	1699:C	P	15.85
1	t	1089:A	O3'	1145:G	P	15.56
1	t	2881:G	O3'	3569:C	P	15.47
1	t	2093:C	O3'	2228:C	P	14.21
1	t	1253:A	O3'	1256:G	P	12.99
1	t	4737:G	O3'	4815:C	P	12.48
1	t	4853:C	O3'	4882:C	P	11.15
1	t	1202:G	O3'	1216:G	P	9.86

6 Map visualisation ⓘ

This section contains visualisations of the EMDB entry EMD-21435. These allow visual inspection of the internal detail of the map and identification of artifacts.

Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections ⓘ
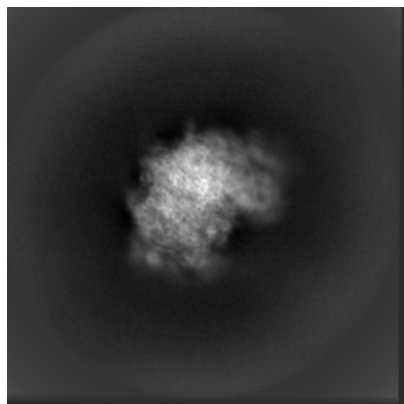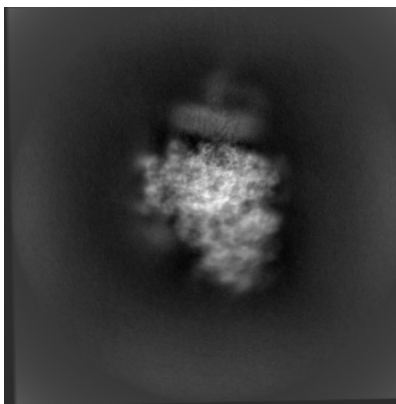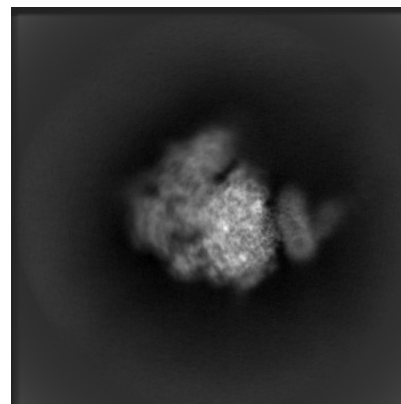
6.1.1 Primary map

X	Y	Z

6.1.2 Raw map

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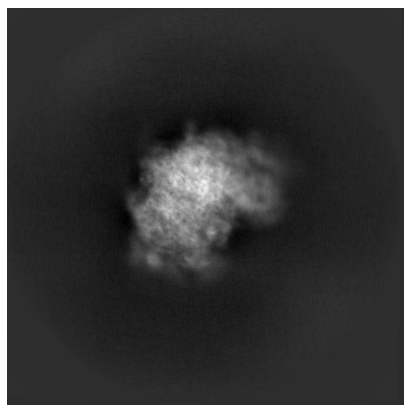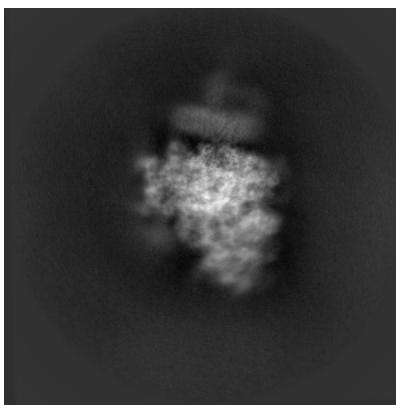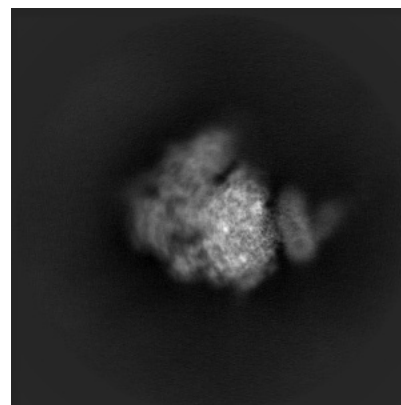
The images above show the map projected in three orthogonal directions.

6.2　Central slices　ⓘ
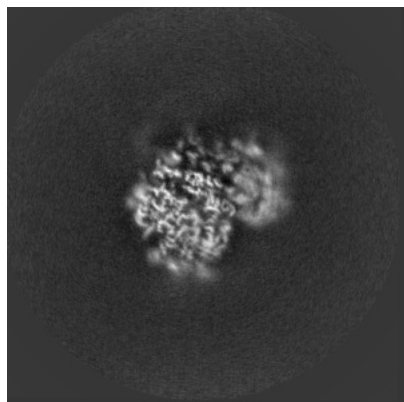
6.2.1　Primary map
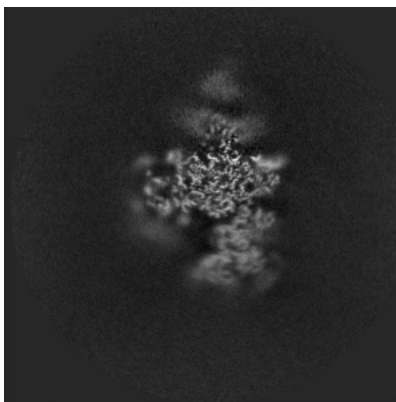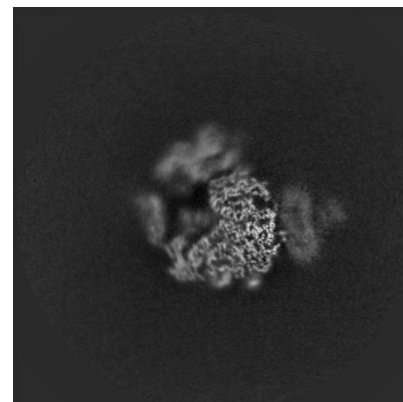
| X Index: 250 | Y Index: 250 | Z Index: 250 |

6.2.2　Raw map
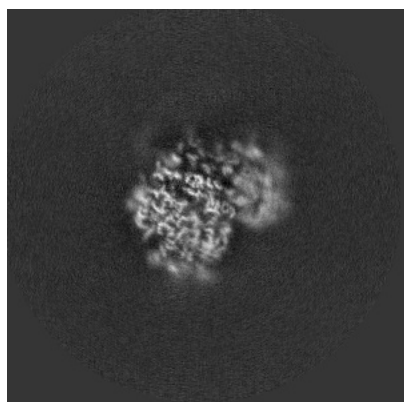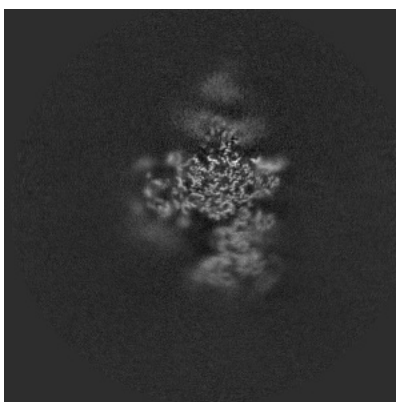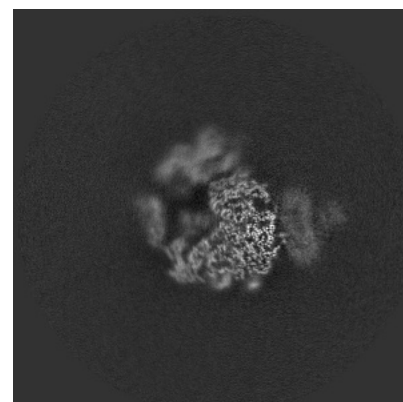
| X Index: 250 | Y Index: 250 | Z Index: 250 |

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

6.3   Largest variance slices ⓘ
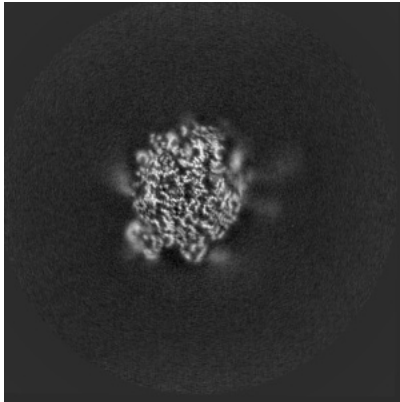
6.3.1   Primary map
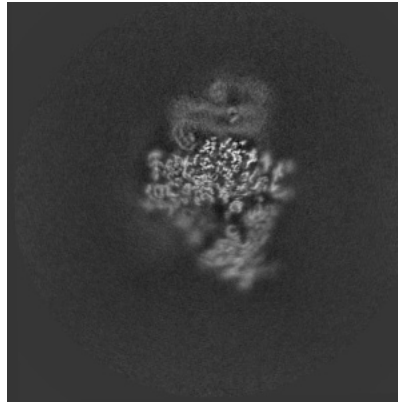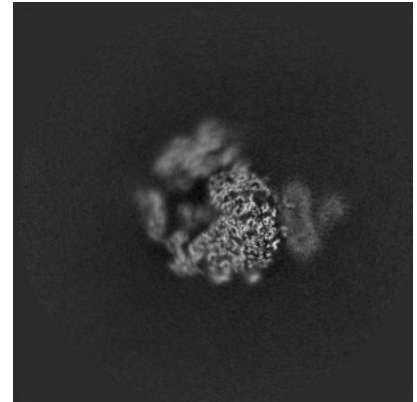
X Index: 285   Y Index: 225   Z Index: 252

6.3.2   Raw map
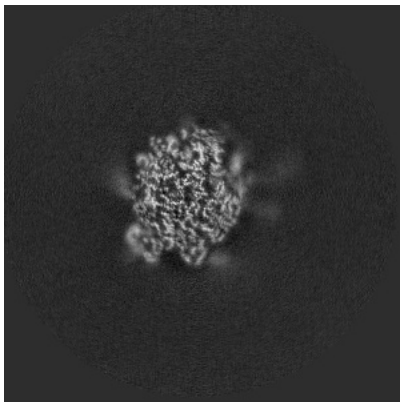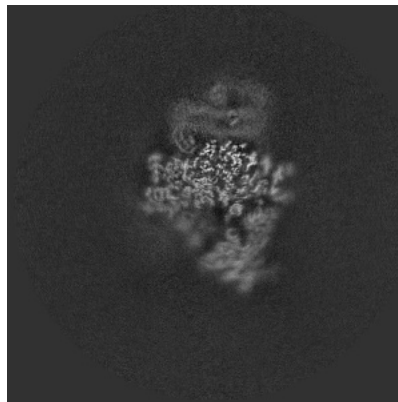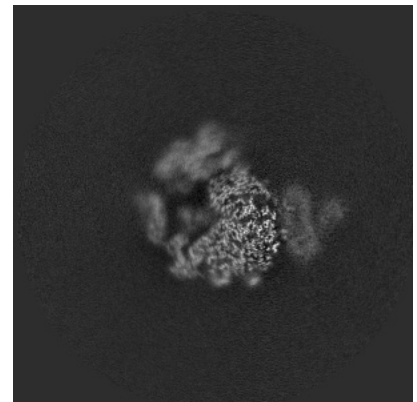
X Index: 285   Y Index: 225   Z Index: 252

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

6.4 Orthogonal surface views ⓘ

6.4.1 Primary map

| X | Y | Z |
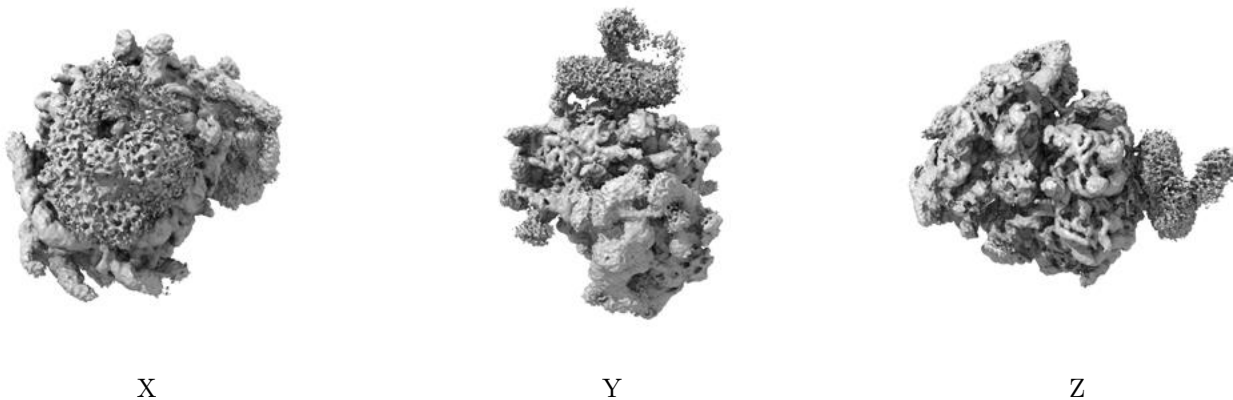
The images above show the 3D surface view of the map at the recommended contour level 0.0073. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map

| X | Y | Z |
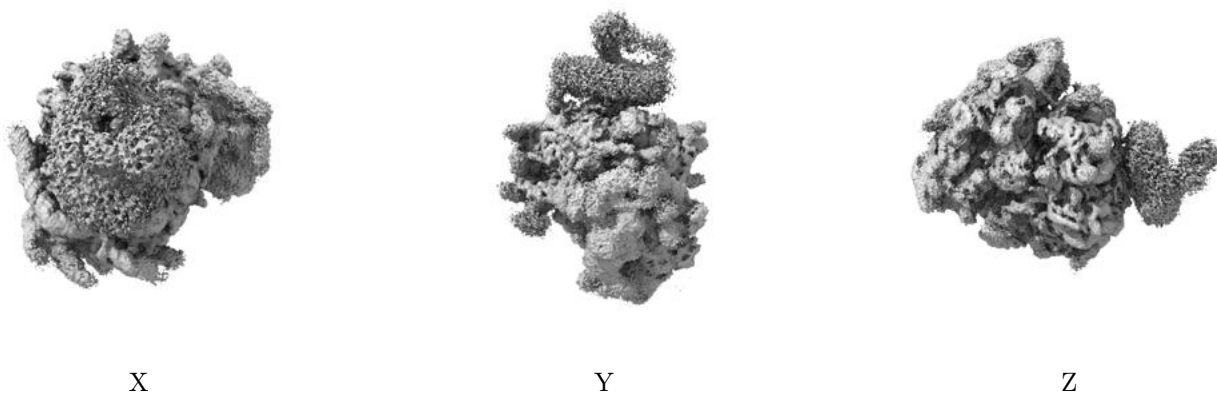
These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

6.5 Mask visualisation (i)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

A mask typically either:

- Encompasses the whole structure

- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

6.5.1 emd_21435_msk_1.map (i)
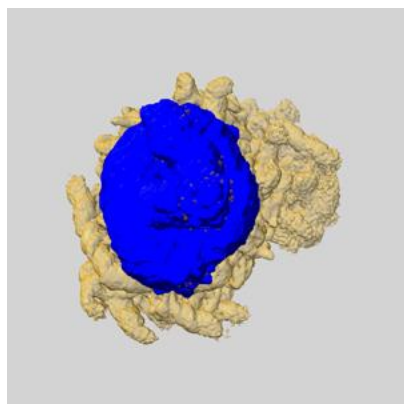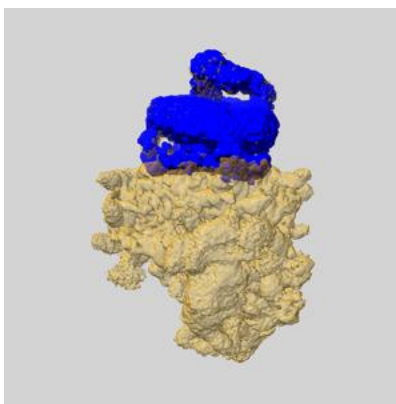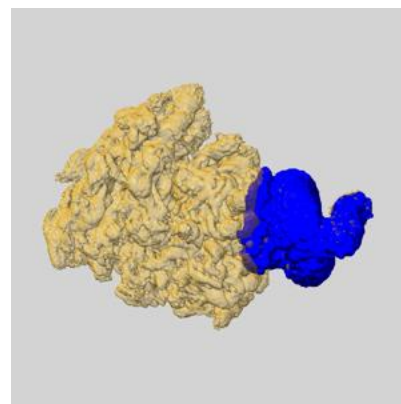
X   Y   Z

7 Map analysis (i)

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

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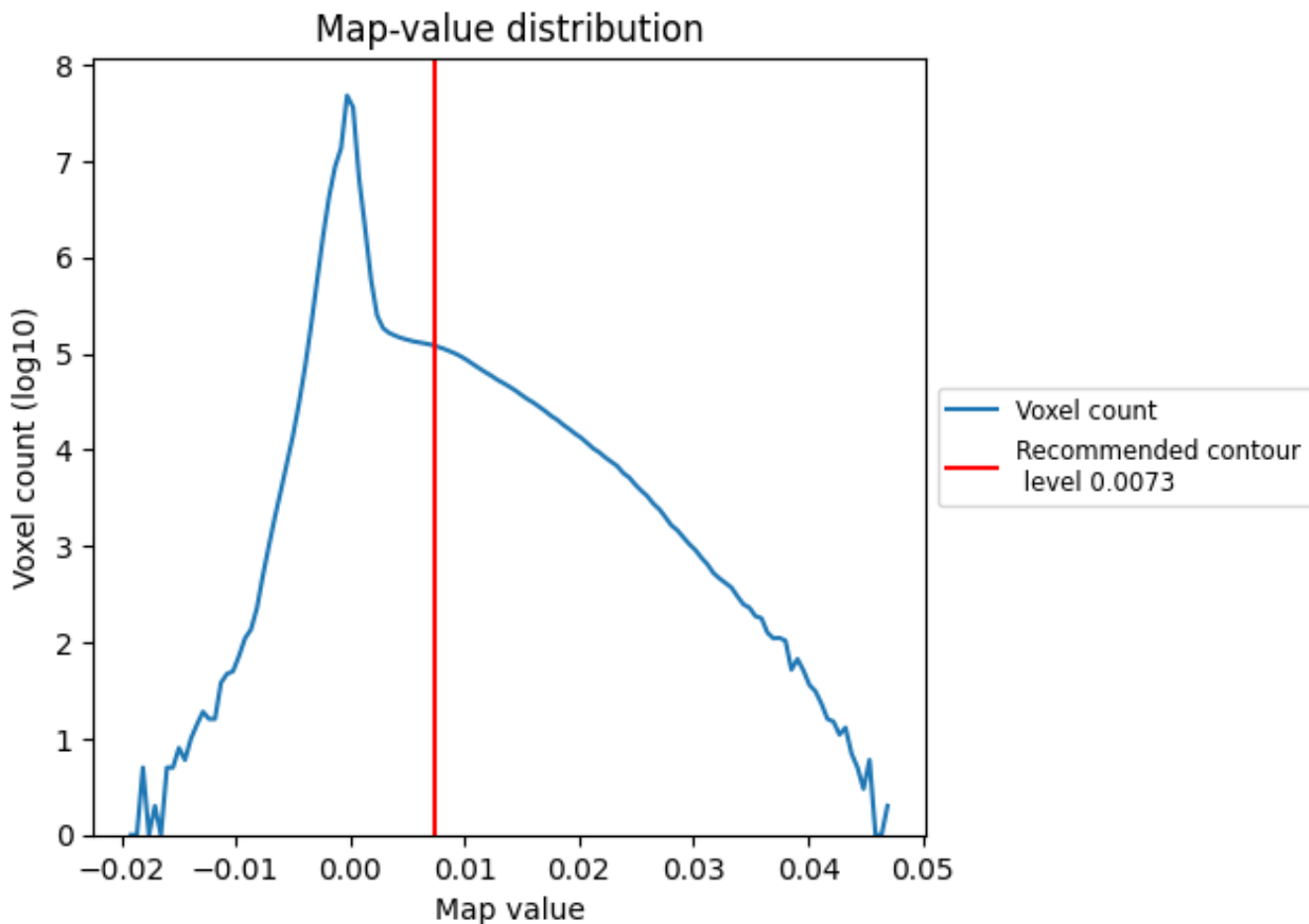
The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2　Volume estimate ⓘ
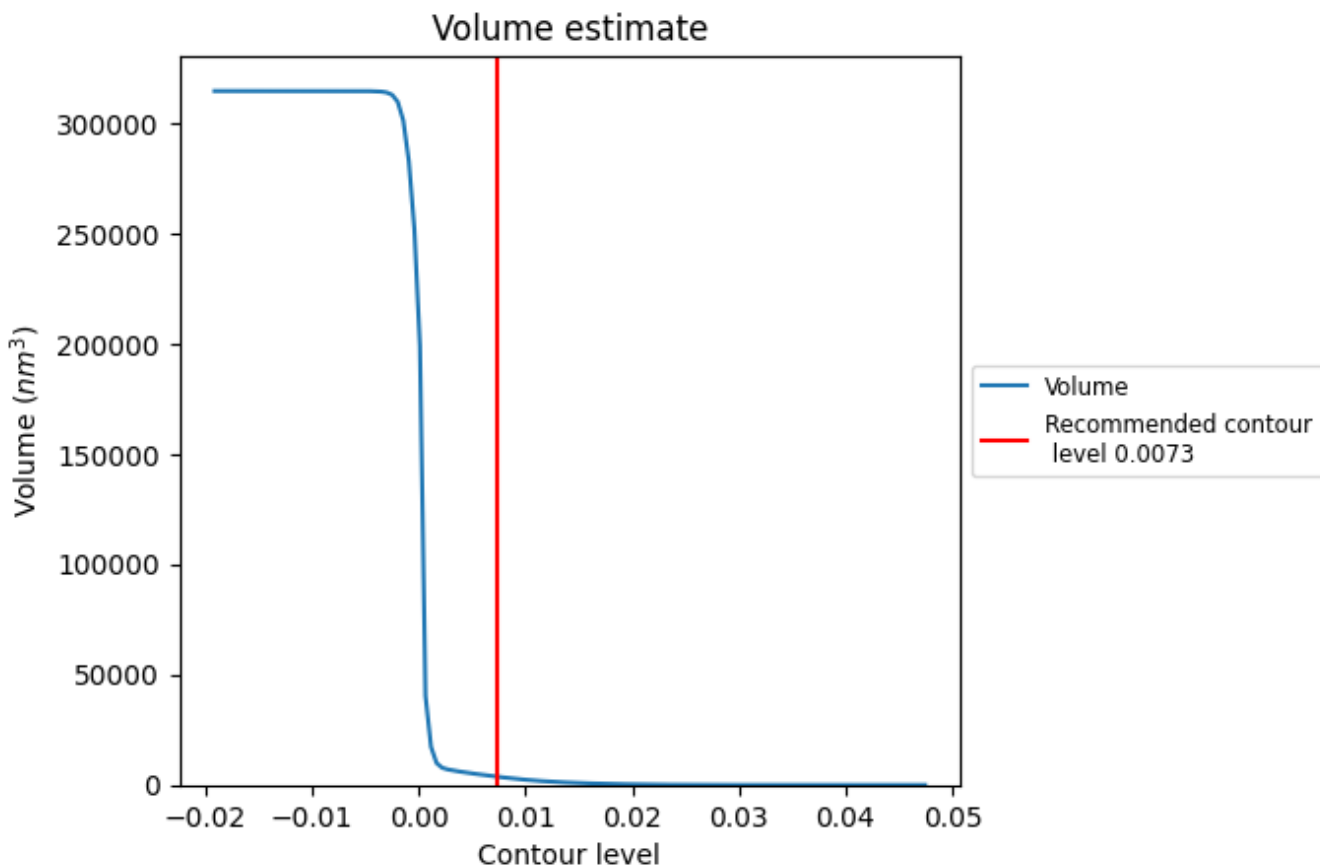
The volume at the recommended contour level is 3776 nm^3; this corresponds to an approximate mass of 3411 kDa.

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 ⓘ
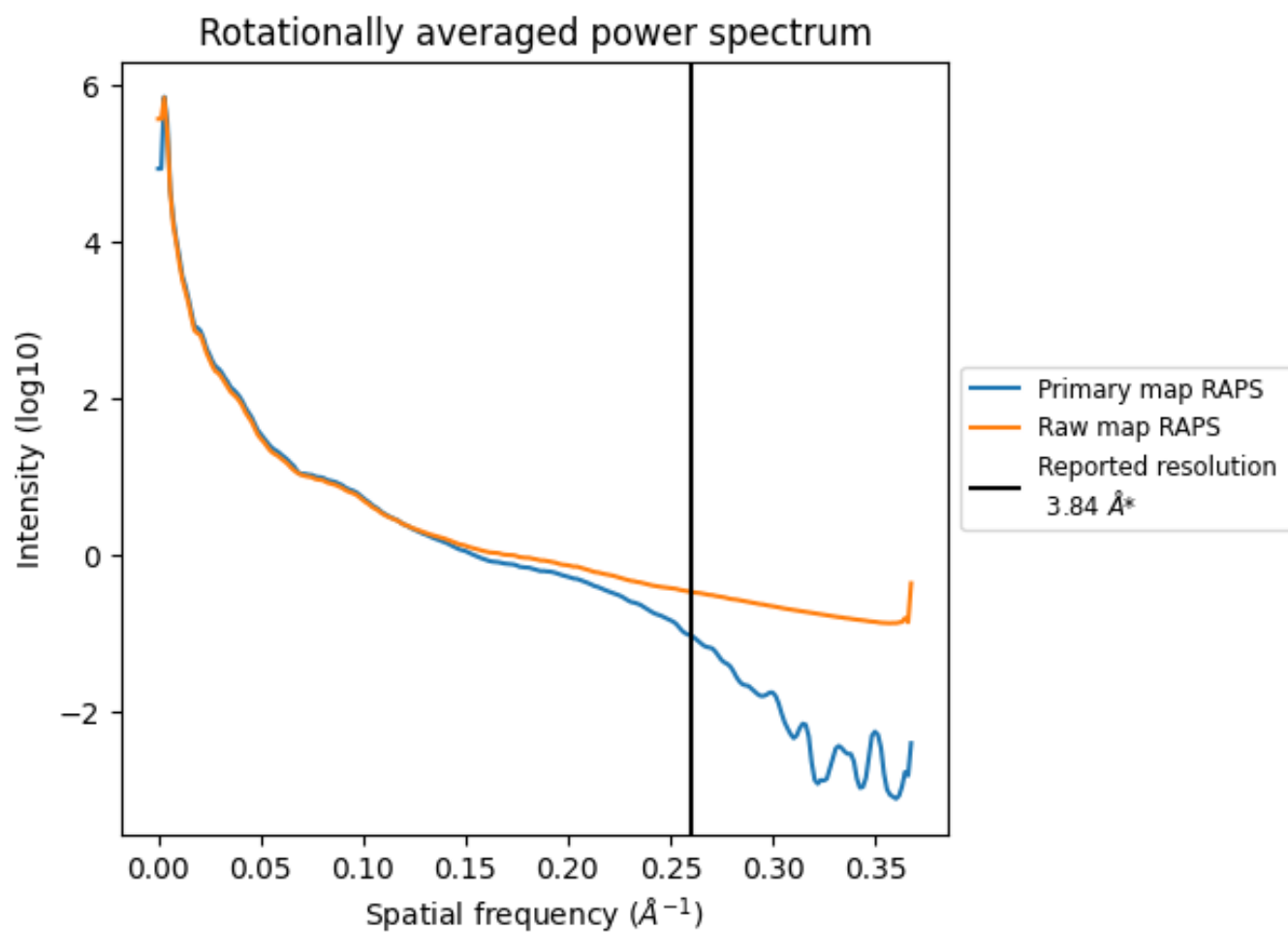
*Reported resolution corresponds to spatial frequency of 0.260 Å^{-1}

8 Fourier-Shell correlation (i)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC (i)
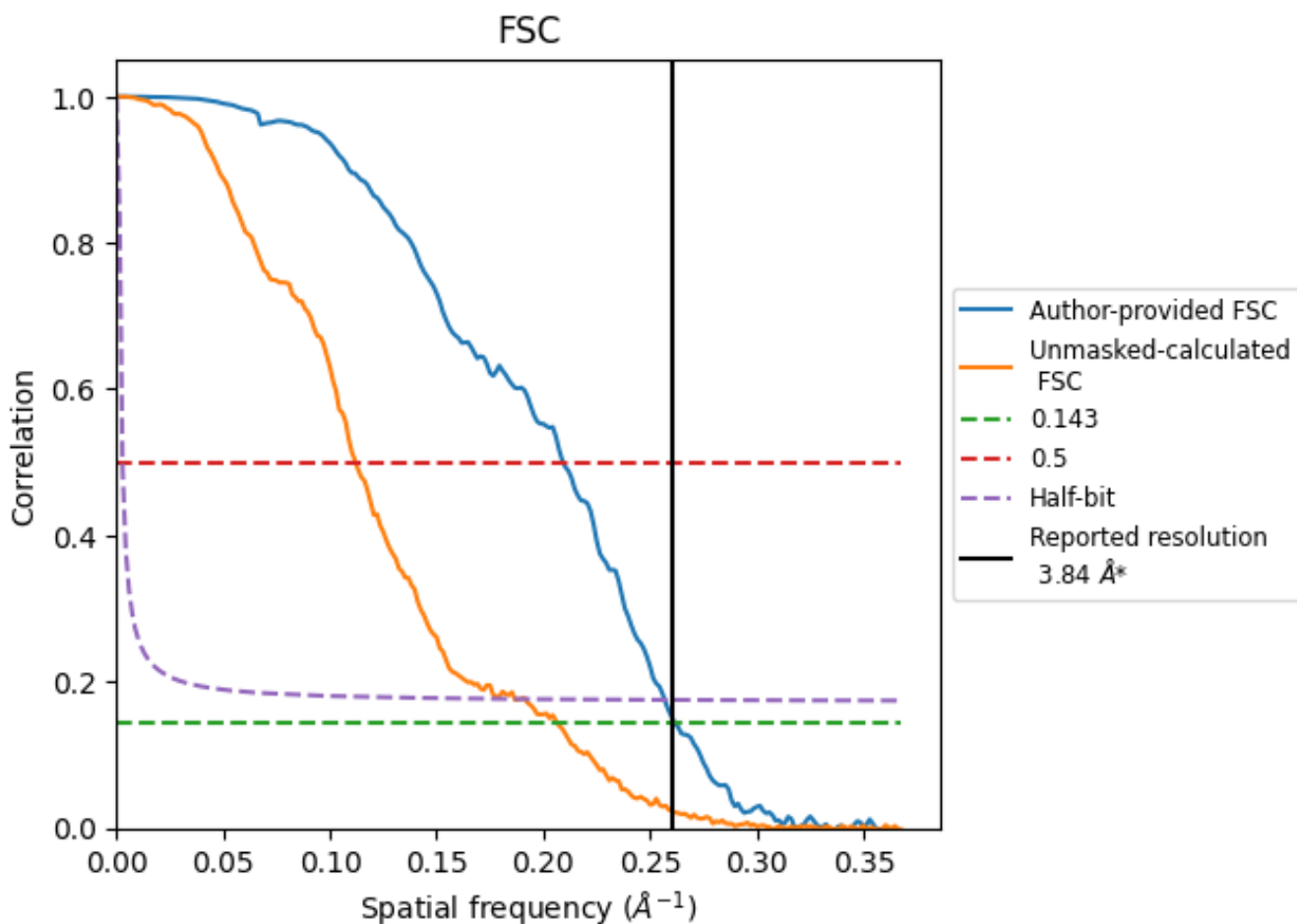
*Reported resolution corresponds to spatial frequency of 0.260 Å^{-1}

8.2   Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.84	-	-
Author-provided FSC curve	3.82	4.78	3.89
Unmasked-calculated*	4.84	8.93	5.36

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.84 differs from the reported value 3.84 by more than 10 %

9   Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-21435 and PDB model 6W6L. Per-residue inclusion information can be found in section 3 on page 14.

9.1   Map-model overlay ⓘ
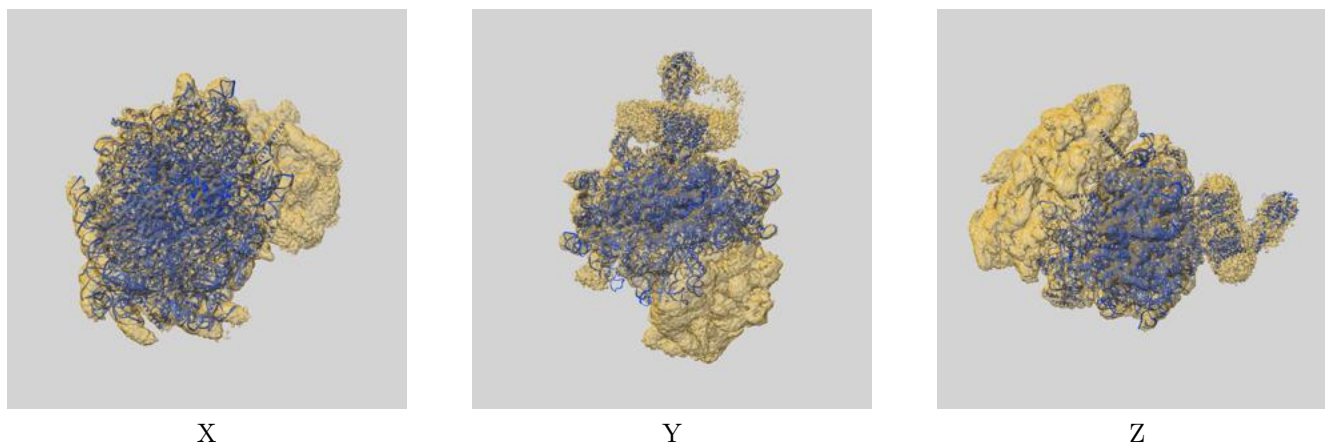
| X | Y | Z |

The images above show the 3D surface view of the map at the recommended contour level 0.0073 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)

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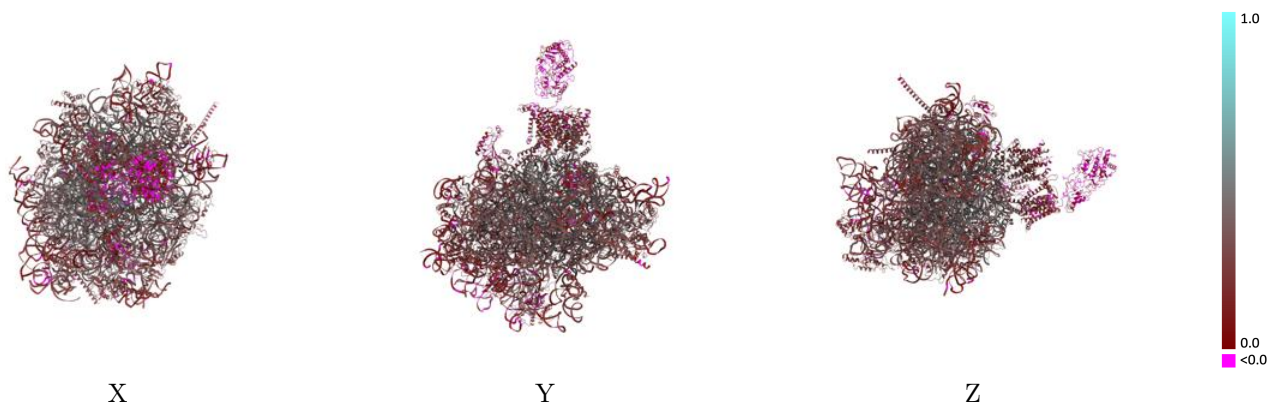
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

X   Y   Z
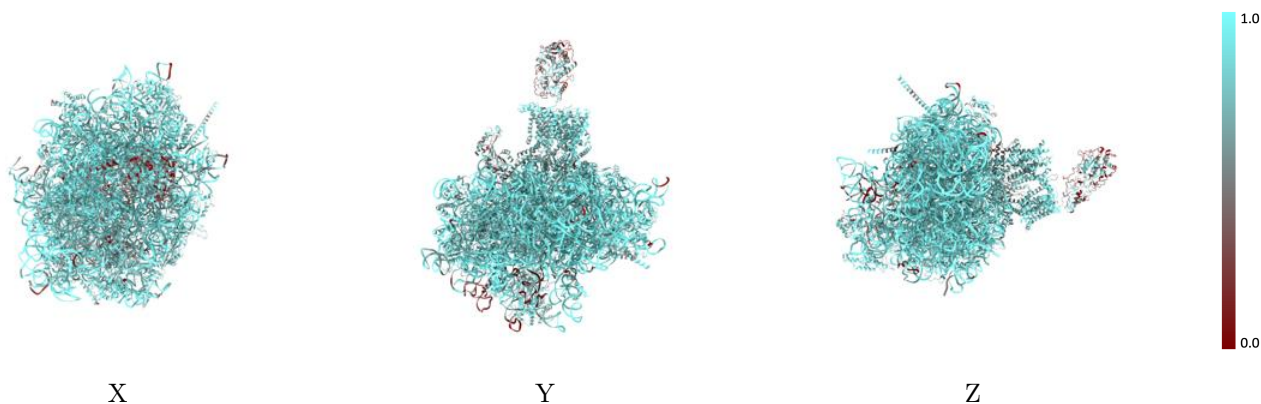
The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0073).

9.4 Atom inclusion ⓘ
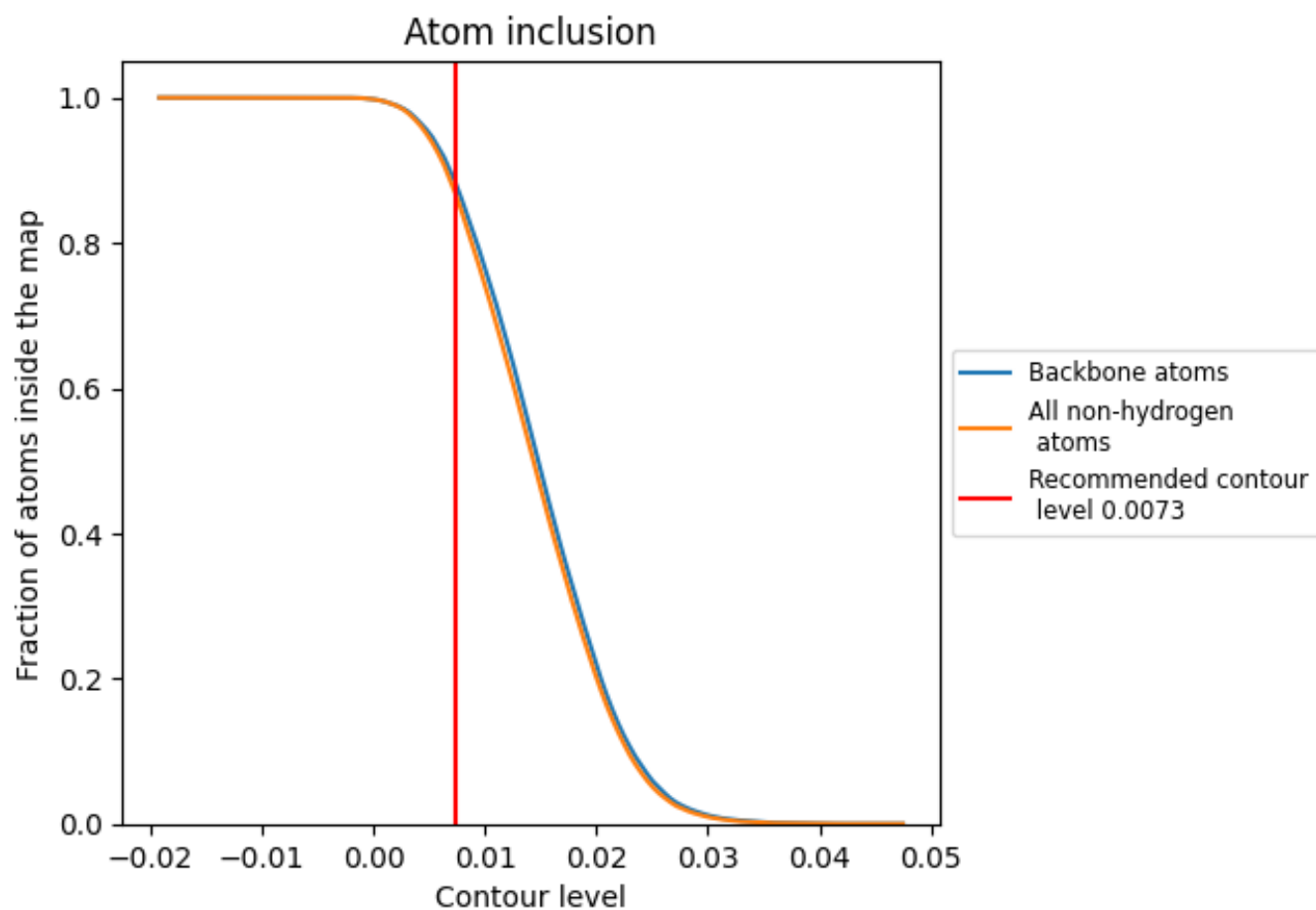
At the recommended contour level, 89% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.0073) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8714	0.2910
1	0.7882	0.2400
2	0.7819	0.2730
3	0.7556	0.1440
4	0.8209	0.1830
5	0.4940	0.0340
6	0.7636	0.1550
7	0.5226	0.1630
A	0.8394	0.3420
B	0.8623	0.3090
C	0.8925	0.3840
D	0.9835	0.3990
E	0.9937	0.2630
F	0.8961	0.1970
G	0.8856	0.2800
H	0.8218	0.2760
I	0.8434	0.2960
J	0.8306	0.2060
K	0.5281	0.0810
L	0.7782	0.1730
M	0.8340	0.3220
N	0.8818	0.2330
O	0.9062	0.3690
P	0.8454	0.2920
Q	0.8955	0.4140
R	0.8867	0.3530
S	0.8455	0.3000
T	0.8754	0.2450
U	0.8423	0.2700
V	0.7177	0.1210
W	0.7899	0.3020
X	0.8333	0.2910
Y	0.8679	0.4090
Z	0.8634	0.4170
a	0.8840	0.2930

1.0

0.0
<0.0

Continued from previous page...

Chain	Atom inclusion	Q-score
b	0.9230	0.3400
c	0.8232	0.2050
d	0.8710	0.2620
e	0.9021	0.3670
f	0.8606	0.4040
g	0.8634	0.3580
h	0.8637	0.3570
i	0.8318	0.3590
j	0.8609	0.2760
k	0.9225	0.4330
l	0.8366	0.3220
m	0.8913	0.4240
o	0.6636	0.1890
p	0.7959	0.2550
q	0.7997	0.3020
r	0.9107	0.3860
t	0.9506	0.3110
u	0.3949	0.1160
v	0.8300	0.2100
y	0.7259	0.3850