



Full wwPDB EM Validation Report ⓘ

Nov 21, 2022 – 04:06 PM EST

PDB ID : 8EV3
EMDB ID : EMD-24421
Title : Ytm1 associated 60S nascent ribosome (-Fkbp39) State 1B
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-19
Resolution : 3.00 Å (reported)

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:

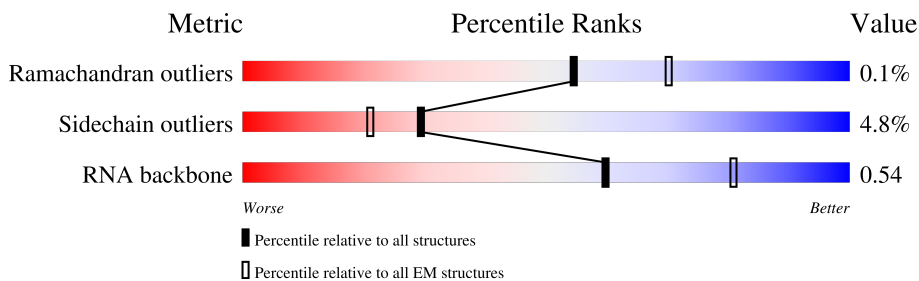
EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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 3.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



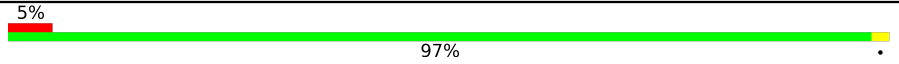
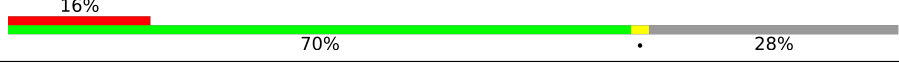
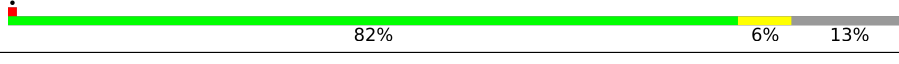
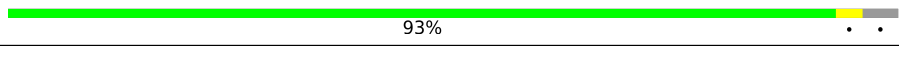

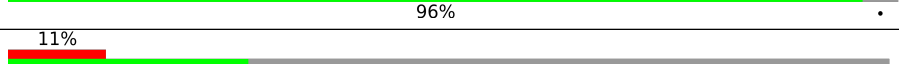
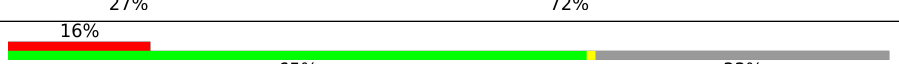
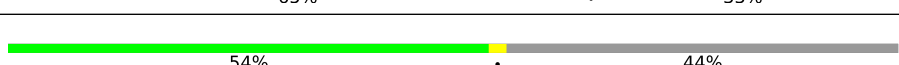
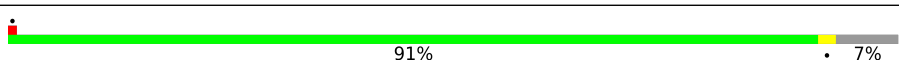

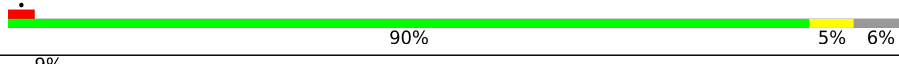
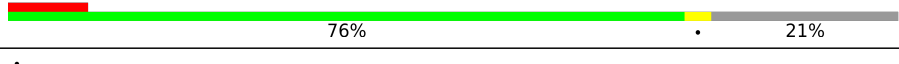
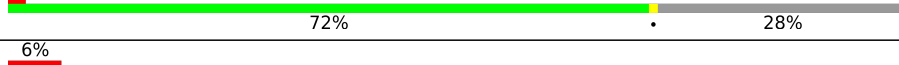

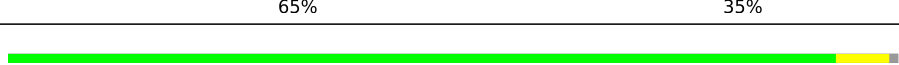
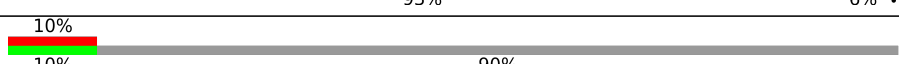
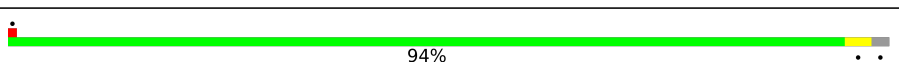
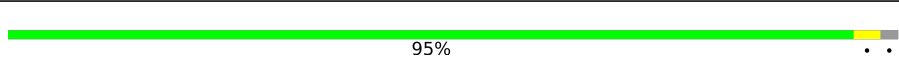
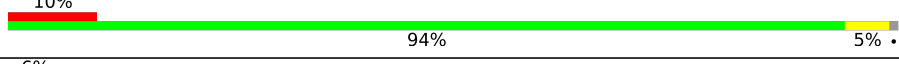
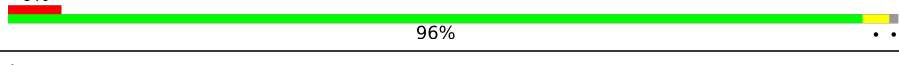

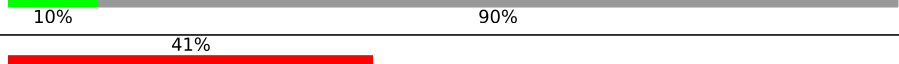



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	1	3497	
2	2	165	
3	3	302	
4	4	217	
5	5	387	
6	6	300	
7	A	295	
8	B	388	

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Mol	Chain	Length	Quality of chain
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	J	333	
16	K	373	
17	L	208	
18	M	134	
19	N	201	
20	O	197	
21	P	187	
22	Q	187	
23	S	176	
24	V	139	
25	Y	126	
26	b	642	
27	e	127	
28	f	108	
29	h	122	
30	i	99	
31	j	91	
32	m	740	
33	n	607	

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Mol	Chain	Length	Quality of chain
34	o	276	
35	r	260	
36	t	249	
37	u	192	
38	v	209	
39	x	306	
40	y	244	
41	T	19	

2 Entry composition i

There are 42 unique types of molecules in this entry. The entry contains 84746 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 RNA chain called RNA (1452-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1	1452	31076	13882	5623	10119	1452	0	0

- Molecule 2 is a RNA chain called RNA (150-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	2	150	3189	1427	564	1048	150	0	0

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	3	192	1596	1010	304	276	6	0	0

- Molecule 4 is a protein called Ribosomal RNA-processing protein 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	4	211	1776	1156	303	309	8	0	0

- Molecule 5 is a protein called Ribosome biogenesis protein nsal.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	5	340	2686	1716	468	491	11	0	0

- Molecule 6 is a RNA chain called RNA (75-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	6	75	1587	712	270	530	75	0	0

- Molecule 7 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	A	247	Total	C	N	O	S	0	0
			1999	1267	363	361	8		

- Molecule 8 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	B	332	Total	C	N	O	S	0	0
			2641	1676	488	468	9		

- Molecule 9 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	C	362	Total	C	N	O	S	0	0
			2810	1774	539	494	3		

- Molecule 10 is a protein called RNA helicase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	D	416	Total	C	N	O	S	0	0
			3186	2057	544	574	11		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	E	170	Total	C	N	O	S	0	0
			1328	854	243	228	3		

- Molecule 12 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	F	240	Total	C	N	O	S	0	0
			1944	1250	356	335	3		

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	G	164	Total	C	N	O	S	1	0
			1273	816	223	232	2		

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	H	183	902	536	183	183	0	0

- Molecule 15 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	J	92	459	275	92	92	0	0

- Molecule 16 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
16	K	249	1914	1224	328	356	6	0	0

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
17	L	116	942	592	198	151	1	0	0

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
18	M	125	1007	644	191	168	4	0	0

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
19	N	166	1406	883	291	229	3	0	0

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
20	O	186	1478	952	279	244	3	0	0

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	148	Total	C	N	O	S	0	0
			1164	743	210	208	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	135	Total	C	N	O	S	0	0
			1047	658	202	186	1		

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	168	Total	C	N	O	S	0	0
			1408	909	263	231	5		

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	91	Total	C	N	O	0	0
			446	263	91	92		

- Molecule 25 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 26 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	b	64	Total	C	N	O	0	0
			317	189	64	64		

- Molecule 27 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	e	124	Total	C	N	O	S	0	0
			995	621	202	167	5		

- Molecule 28 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	f	106	839	534	162	140	3	0	0

- Molecule 29 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	h	121	999	629	194	176		0	0

- Molecule 30 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
30	i	98	783	487	164	131	1	0	0

- Molecule 31 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
31	j	71	563	346	121	90	6	0	0

- Molecule 32 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	m	75	615	379	112	124	0	0

- Molecule 33 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
33	n	362	1791	1067	362	362	0	0

- Molecule 34 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
34	o	137	1026	655	189	176	6	0	0

- Molecule 35 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
35	r	57	283	169	57	57	0	0

- Molecule 36 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
36	t	183	1008	602	209	197	0	0

- Molecule 37 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
37	u	76	377	225	76	76	0	0

- Molecule 38 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
38	v	161	1299	818	243	235	3	0	0

- Molecule 39 is a protein called Brix domain-containing protein C4F8.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
39	x	305	2516	1578	463	467	8	0	0

- Molecule 40 is a protein called Eukaryotic translation initiation factor 6.

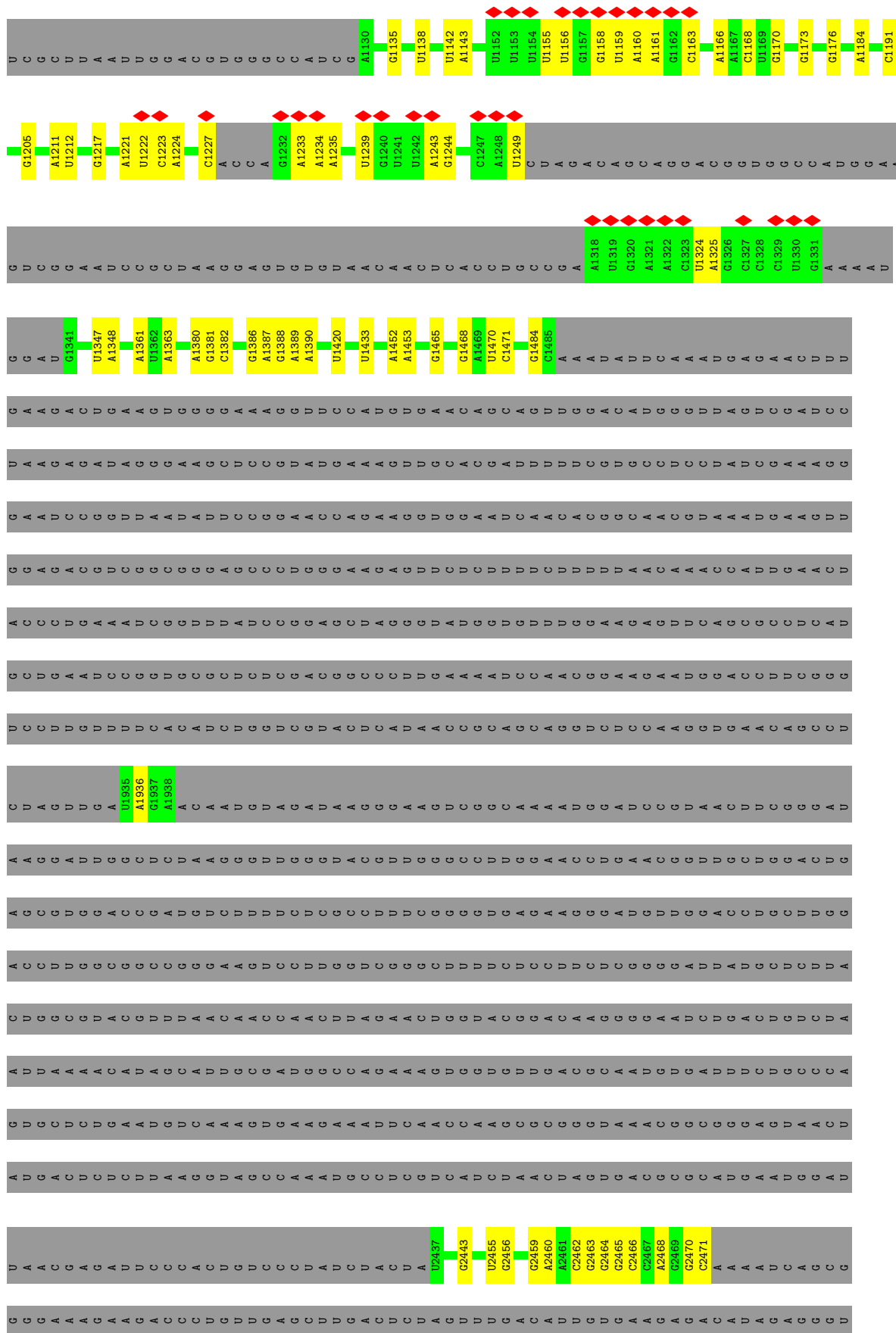
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
40	y	188	925	549	188	188	0	0

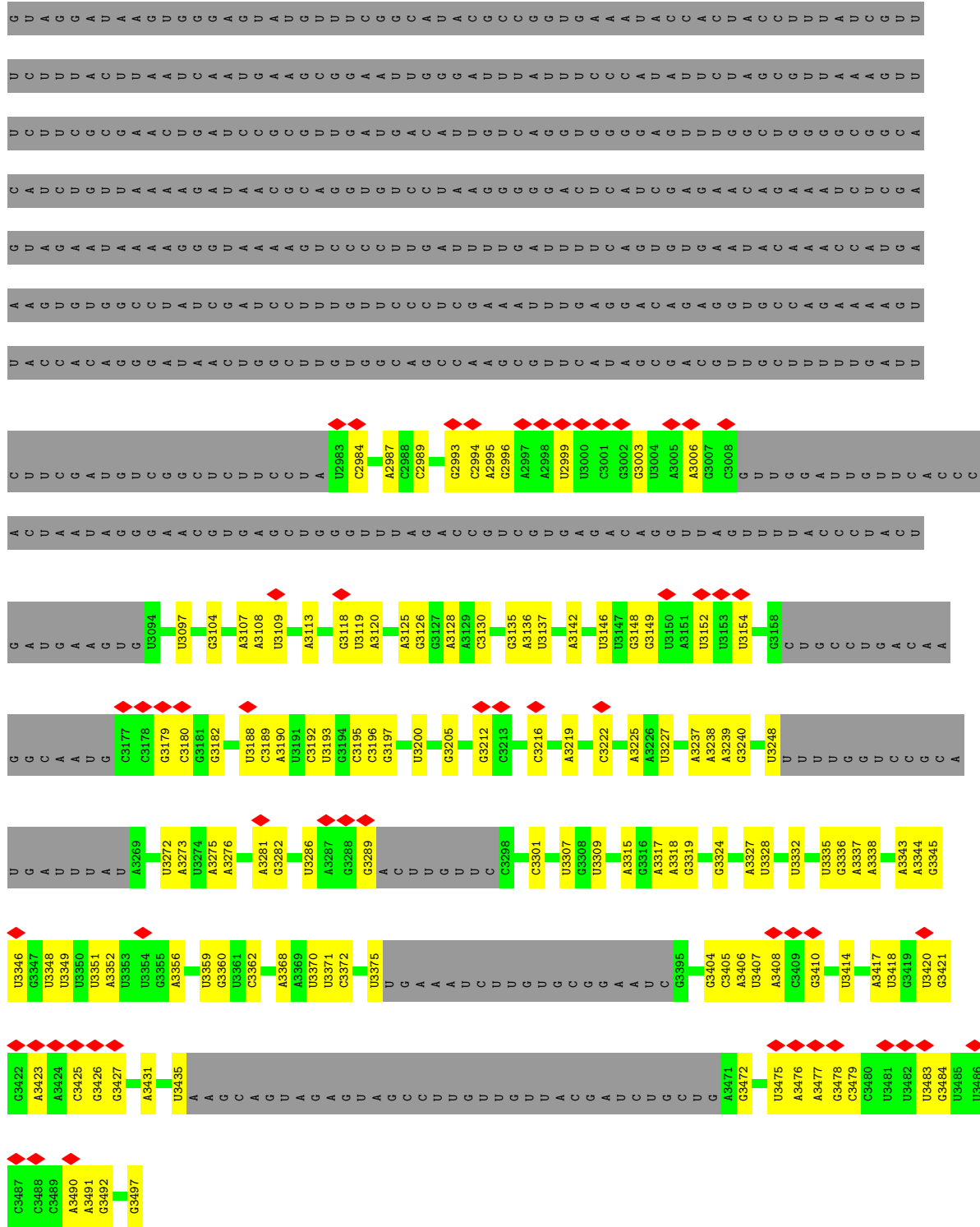
- Molecule 41 is a protein called RPL21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
41	T	19	147	93	26	28	0	0

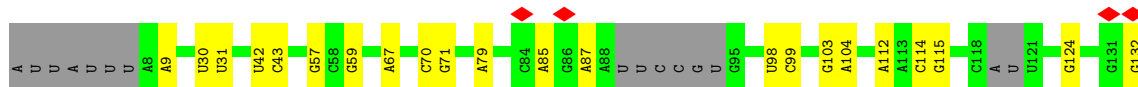
- Molecule 42 is ZINC ION (three-letter code: ZN) (formula: Zn).

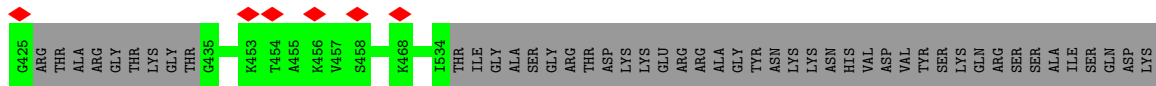
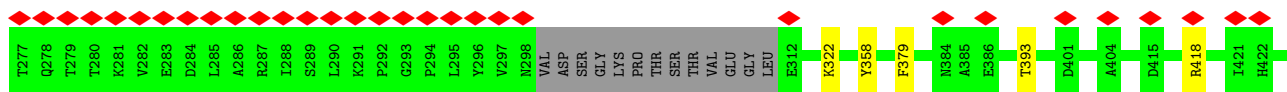
Mol	Chain	Residues	Atoms		AltConf
42	j	1	Total 1	Zn 1	0





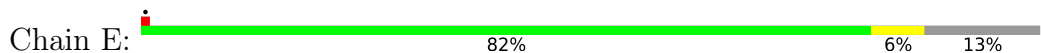
• Molecule 2: RNA (150-MER)



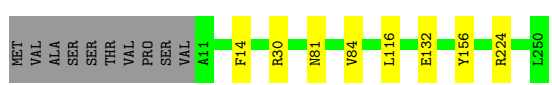


GLU ARG GLY TRP SER ARG

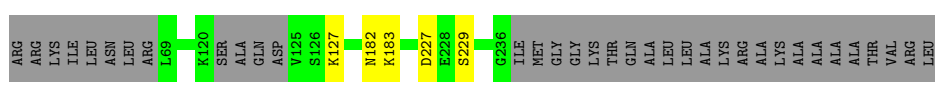
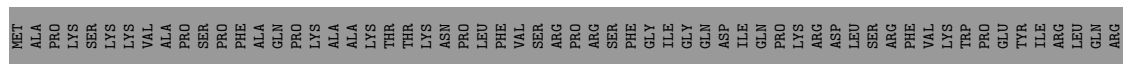
• Molecule 11: 60S ribosomal protein L6



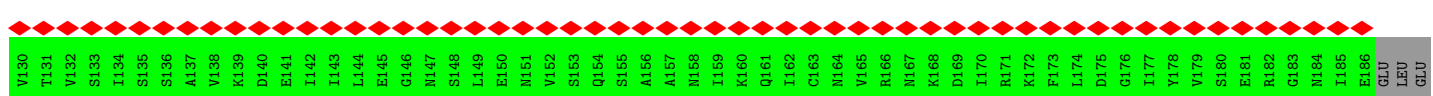
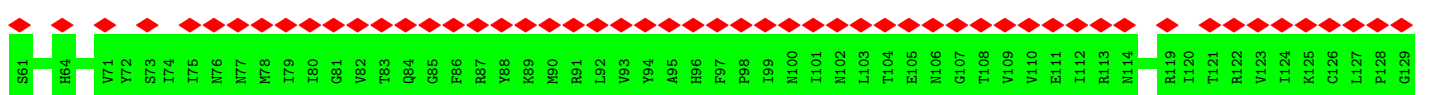
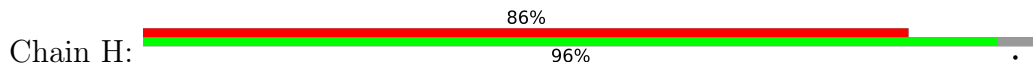
• Molecule 12: 60S ribosomal protein L7-B



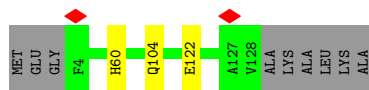
• Molecule 13: 60S ribosomal protein L8



• Molecule 14: 60S ribosomal protein L9-A

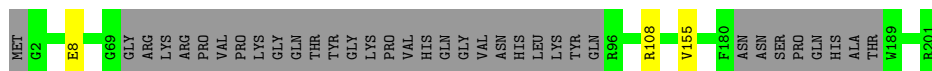


GLU



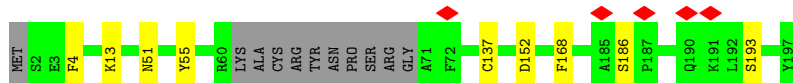
- Molecule 19: 60S ribosomal protein L15-A

Chain N: 81% 17%



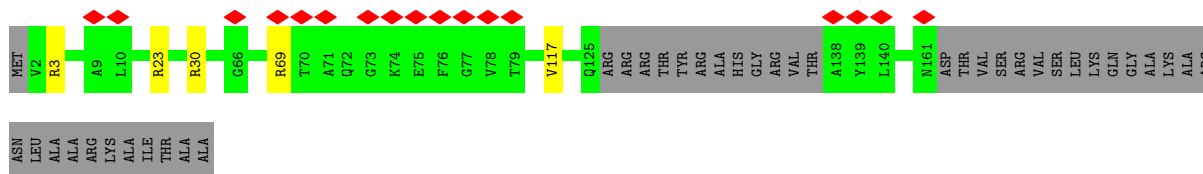
- Molecule 20: 60S ribosomal protein L16-B

Chain O: 90% 5% 6%



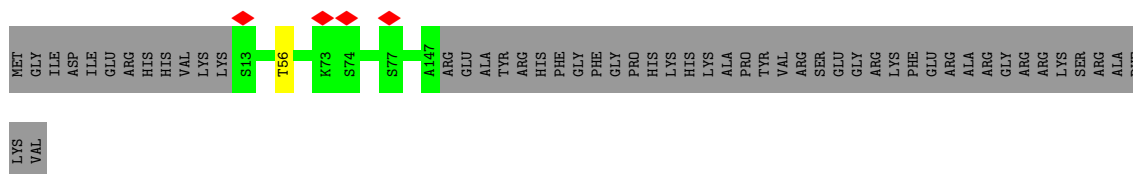
- Molecule 21: 60S ribosomal protein L17-A

Chain P: 9% 76% 21%



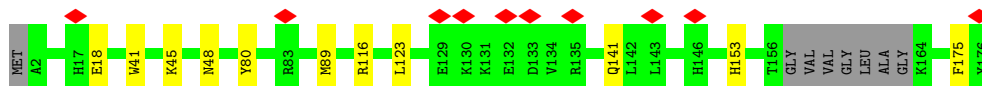
- Molecule 22: 60S ribosomal protein L18-A

Chain Q: 72% 28%



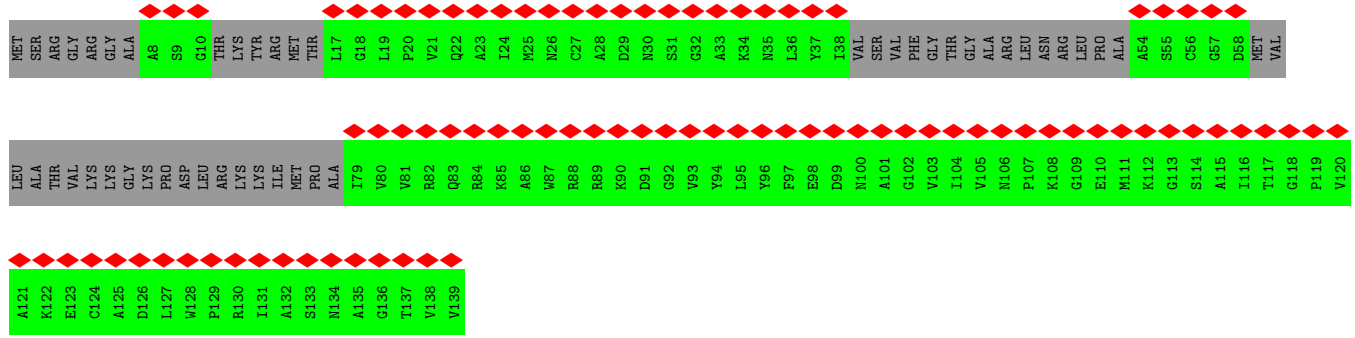
- Molecule 23: 60S ribosomal protein L20-A

Chain S: 6% 89% 6% 5%

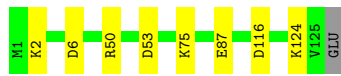


- Molecule 24: 60S ribosomal protein L23-A

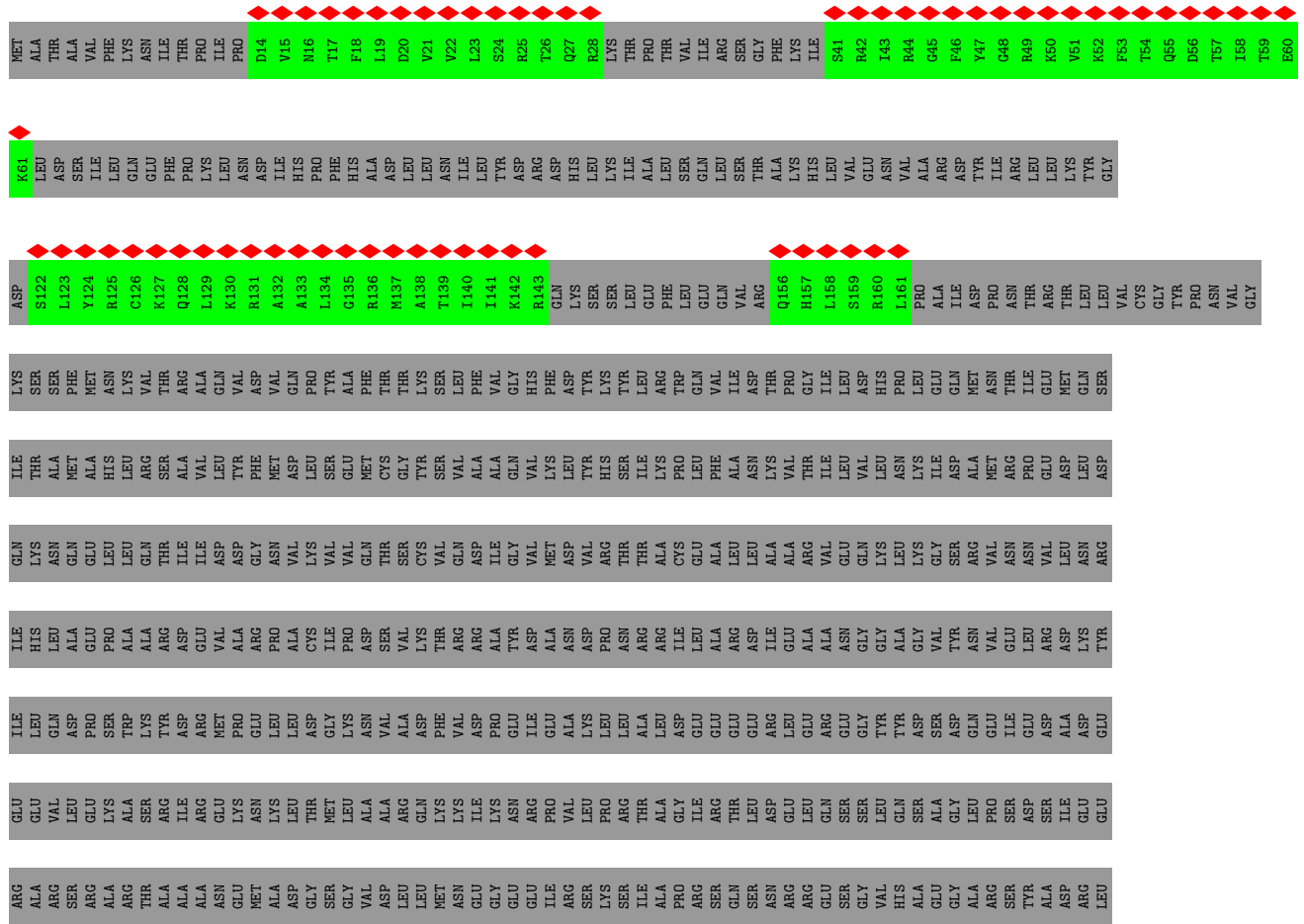
Chain V: 65% 65% 35%



● Molecule 25: Ribosomal protein L26



● Molecule 26: Probable nucleolar GTP-binding protein 1

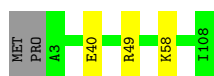


ALA ARG VAL LYS GLN ILE HIS ARG ASN ARG MET MET ALA ARG ALA SER SER SER ASP ARG HIS VAL ILE ALA ALA LYS PRO PRO LYS HIS LEU LEU SER SER GLY LYS ARG GLY ASN GLY LYS THR GLN ARG ARG

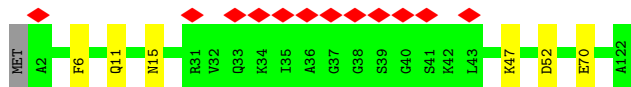
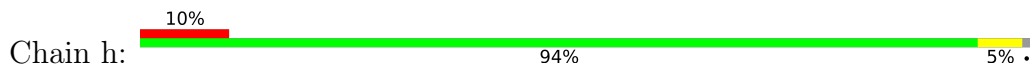
• Molecule 27: 60S ribosomal protein L32-A



• Molecule 28: 60S ribosomal protein L33-B



• Molecule 29: 60S ribosomal protein L35



• Molecule 30: 60S ribosomal protein L36-B



• Molecule 31: 60S ribosomal protein L37-B



• Molecule 32: Ribosome biogenesis protein erb1

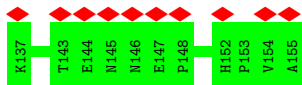


MET GLU THR GLY MET ASN ARG LYS ARG MET ARG SER LYS ARG ALA ASN SER ASN VAL GLY VAL THR PRO LYS ASP GLU LYS GLU LYS LYS ASP ASP PHE SER LYS VAL VAL THR GLU SER SER SER HIS PRO GLY LEU PRO SER PHE GLU LYS TYR ASP VAL ASP GLU LEU LEU TYR ILE PRO

SER LEU THR ALA GLU MET ASN ARG LYS ARG MET ARG SER LYS ARG ALA ASN SER ASN VAL GLY VAL THR PRO LYS ASP GLU LYS GLU LYS LYS ASP ASP PHE SER LYS VAL VAL THR GLU SER SER SER HIS PRO GLY LEU PRO SER PHE GLU LYS TYR ASP VAL ASP GLU ASN LEU TYR ILE

GLU
SER
TYR
THR

• Molecule 41: RPL21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	250000	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.756	Depositor
Minimum map value	-0.337	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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

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	1	0.36	0/34768	0.71	0/54150
2	2	0.33	0/3563	0.70	0/5543
3	3	0.32	0/1627	0.50	0/2188
4	4	0.28	0/1823	0.49	0/2462
5	5	0.27	0/2739	0.51	0/3702
6	6	0.18	0/1770	0.70	0/2745
7	A	0.26	0/2038	0.53	0/2747
8	B	0.25	0/2694	0.54	0/3619
9	C	0.31	0/2863	0.51	0/3863
10	D	0.25	0/3245	0.44	0/4396
11	E	0.29	0/1356	0.54	0/1829
12	F	0.28	0/1982	0.48	0/2658
13	G	0.29	0/1291	0.44	0/1742
14	H	0.24	0/901	0.43	0/1252
15	J	0.23	0/458	0.37	0/639
16	K	0.25	0/1948	0.46	0/2640
17	L	0.31	0/960	0.59	0/1288
18	M	0.28	0/1024	0.56	0/1375
19	N	0.32	0/1436	0.56	0/1920
20	O	0.26	0/1506	0.47	0/2017
21	P	0.27	0/1187	0.47	0/1595
22	Q	0.28	0/1058	0.55	0/1421
23	S	0.25	0/1444	0.53	0/1939
24	V	0.24	0/442	0.41	0/605
25	Y	0.28	0/1008	0.58	0/1341
26	b	0.22	0/313	0.29	0/430
27	e	0.29	0/1009	0.55	0/1345
28	f	0.29	0/859	0.52	0/1152
29	h	0.28	0/1008	0.54	0/1340
30	i	0.27	0/791	0.53	0/1050
31	j	0.27	0/575	0.56	0/761
32	m	0.28	0/627	0.54	0/844

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	n	0.24	0/1788	0.39	0/2487
34	o	0.26	0/1049	0.51	0/1419
35	r	0.22	0/282	0.29	0/392
36	t	0.25	0/1009	0.46	0/1385
37	u	0.23	0/375	0.38	0/520
38	v	0.28	0/1319	0.51	0/1769
39	x	0.27	0/2562	0.52	0/3432
40	y	0.23	0/921	0.45	0/1274
41	T	0.24	0/151	0.42	0/207
All	All	0.31	0/89769	0.61	0/129483

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3	190/302 (63%)	184 (97%)	6 (3%)	0	100	100
4	4	209/217 (96%)	205 (98%)	4 (2%)	0	100	100
5	5	336/387 (87%)	311 (93%)	25 (7%)	0	100	100
7	A	243/295 (82%)	231 (95%)	12 (5%)	0	100	100
8	B	328/388 (84%)	318 (97%)	10 (3%)	0	100	100
9	C	360/363 (99%)	342 (95%)	18 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	D	410/578 (71%)	400 (98%)	10 (2%)	0	100	100
11	E	168/195 (86%)	154 (92%)	13 (8%)	1 (1%)	25	64
12	F	238/250 (95%)	229 (96%)	9 (4%)	0	100	100
13	G	161/259 (62%)	152 (94%)	7 (4%)	2 (1%)	13	48
14	H	181/190 (95%)	180 (99%)	1 (1%)	0	100	100
15	J	90/333 (27%)	86 (96%)	3 (3%)	1 (1%)	14	50
16	K	245/373 (66%)	231 (94%)	14 (6%)	0	100	100
17	L	114/208 (55%)	110 (96%)	4 (4%)	0	100	100
18	M	123/134 (92%)	118 (96%)	5 (4%)	0	100	100
19	N	160/201 (80%)	158 (99%)	2 (1%)	0	100	100
20	O	182/197 (92%)	180 (99%)	2 (1%)	0	100	100
21	P	144/187 (77%)	136 (94%)	8 (6%)	0	100	100
22	Q	133/187 (71%)	123 (92%)	10 (8%)	0	100	100
23	S	164/176 (93%)	156 (95%)	8 (5%)	0	100	100
24	V	83/139 (60%)	78 (94%)	5 (6%)	0	100	100
25	Y	123/126 (98%)	118 (96%)	5 (4%)	0	100	100
26	b	56/642 (9%)	56 (100%)	0	0	100	100
27	e	122/127 (96%)	120 (98%)	2 (2%)	0	100	100
28	f	104/108 (96%)	100 (96%)	4 (4%)	0	100	100
29	h	119/122 (98%)	117 (98%)	2 (2%)	0	100	100
30	i	96/99 (97%)	93 (97%)	3 (3%)	0	100	100
31	j	69/91 (76%)	66 (96%)	3 (4%)	0	100	100
32	m	71/740 (10%)	69 (97%)	2 (3%)	0	100	100
33	n	356/607 (59%)	352 (99%)	4 (1%)	0	100	100
34	o	135/276 (49%)	129 (96%)	6 (4%)	0	100	100
35	r	55/260 (21%)	54 (98%)	1 (2%)	0	100	100
36	t	179/249 (72%)	172 (96%)	7 (4%)	0	100	100
37	u	72/192 (38%)	72 (100%)	0	0	100	100
38	v	157/209 (75%)	153 (98%)	3 (2%)	1 (1%)	25	64
39	x	303/306 (99%)	297 (98%)	6 (2%)	0	100	100
40	y	180/244 (74%)	173 (96%)	7 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
41	T	17/19 (90%)	16 (94%)	1 (6%)	0	100	100
All	All	6476/9976 (65%)	6239 (96%)	232 (4%)	5 (0%)	54	85

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	G	227[A]	ASP
13	G	227[B]	ASP
38	v	130	ILE
11	E	137	GLU
15	J	162	VAL

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	
3	3	169/271 (62%)	157 (93%)	12 (7%)	14	46
4	4	192/197 (98%)	185 (96%)	7 (4%)	35	70
5	5	301/345 (87%)	288 (96%)	13 (4%)	29	66
7	A	221/266 (83%)	202 (91%)	19 (9%)	10	37
8	B	282/326 (86%)	263 (93%)	19 (7%)	16	49
9	C	296/297 (100%)	287 (97%)	9 (3%)	41	75
10	D	332/505 (66%)	322 (97%)	10 (3%)	41	75
11	E	139/155 (90%)	129 (93%)	10 (7%)	14	45
12	F	201/210 (96%)	193 (96%)	8 (4%)	31	68
13	G	135/212 (64%)	131 (97%)	4 (3%)	41	75
16	K	210/333 (63%)	205 (98%)	5 (2%)	49	79
17	L	97/167 (58%)	93 (96%)	4 (4%)	30	67
18	M	108/113 (96%)	105 (97%)	3 (3%)	43	77
19	N	146/176 (83%)	143 (98%)	3 (2%)	53	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	O	153/162 (94%)	144 (94%)	9 (6%)	19	54
21	P	120/149 (80%)	115 (96%)	5 (4%)	30	66
22	Q	116/159 (73%)	115 (99%)	1 (1%)	78	92
23	S	150/154 (97%)	139 (93%)	11 (7%)	14	44
25	Y	110/111 (99%)	102 (93%)	8 (7%)	14	44
27	e	106/107 (99%)	102 (96%)	4 (4%)	33	69
28	f	89/91 (98%)	86 (97%)	3 (3%)	37	72
29	h	106/107 (99%)	100 (94%)	6 (6%)	20	56
30	i	83/84 (99%)	80 (96%)	3 (4%)	35	70
31	j	58/71 (82%)	54 (93%)	4 (7%)	15	48
32	m	67/659 (10%)	64 (96%)	3 (4%)	27	64
34	o	93/246 (38%)	81 (87%)	12 (13%)	4	19
36	t	23/223 (10%)	17 (74%)	6 (26%)	0	2
38	v	138/181 (76%)	135 (98%)	3 (2%)	52	81
39	x	272/273 (100%)	258 (95%)	14 (5%)	24	60
41	T	17/17 (100%)	17 (100%)	0	100	100
All	All	4530/6367 (71%)	4312 (95%)	218 (5%)	29	62

All (218) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	3	3	GLN
3	3	34	VAL
3	3	54	ARG
3	3	57	ASN
3	3	78	GLN
3	3	118	TYR
3	3	124	ARG
3	3	130	GLN
3	3	134	ILE
3	3	165	LEU
3	3	170	LYS
3	3	182	ASN
4	4	7	PHE
4	4	17	LYS
4	4	71	LEU

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Mol	Chain	Res	Type
4	4	85	SER
4	4	107	TYR
4	4	119	ARG
4	4	181	ASP
5	5	2	LYS
5	5	34	GLN
5	5	49	LEU
5	5	71	GLN
5	5	95	MET
5	5	103	MET
5	5	188	ASP
5	5	191	ASN
5	5	196	VAL
5	5	206	ASP
5	5	255	PRO
5	5	258	HIS
5	5	345	ARG
7	A	55	TYR
7	A	58	ARG
7	A	59	HIS
7	A	67	MET
7	A	68	MET
7	A	84	TYR
7	A	88	GLU
7	A	99	PHE
7	A	156	ASP
7	A	180	ARG
7	A	197	LYS
7	A	203	TYR
7	A	227	MET
7	A	243	TYR
7	A	245	ASN
7	A	253	MET
7	A	267	VAL
7	A	271	GLU
7	A	292	ASN
8	B	67	MET
8	B	70	ARG
8	B	90	VAL
8	B	103	THR
8	B	137	TYR
8	B	154	TYR

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Mol	Chain	Res	Type
8	B	155	CYS
8	B	179	MET
8	B	182	GLN
8	B	184	ASN
8	B	202	THR
8	B	214	MET
8	B	296	THR
8	B	308	MET
8	B	319	ASN
8	B	324	LEU
8	B	332	VAL
8	B	348	ARG
8	B	372	THR
9	C	21	THR
9	C	38	ARG
9	C	95	MET
9	C	113	VAL
9	C	122	TYR
9	C	248	ARG
9	C	291	ARG
9	C	323	ASN
9	C	341	VAL
10	D	151	LEU
10	D	152	TYR
10	D	156	PHE
10	D	196	ILE
10	D	202	ARG
10	D	322	LYS
10	D	358	TYR
10	D	379	PHE
10	D	393	THR
10	D	418	ARG
11	E	27	TYR
11	E	82	VAL
11	E	86	TYR
11	E	114	VAL
11	E	115	SER
11	E	129	ARG
11	E	147	ASN
11	E	161	ASP
11	E	188	ASP
11	E	193	MET

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Mol	Chain	Res	Type
12	F	14	PHE
12	F	30	ARG
12	F	81	ASN
12	F	84	VAL
12	F	116	LEU
12	F	132	GLU
12	F	156	TYR
12	F	224	ARG
13	G	127	LYS
13	G	182	ASN
13	G	183	LYS
13	G	229	SER
16	K	27	ARG
16	K	67	ARG
16	K	77	LYS
16	K	149	MET
16	K	191	PHE
17	L	62	THR
17	L	67	MET
17	L	115	ARG
17	L	134	LYS
18	M	60	HIS
18	M	104	GLN
18	M	122	GLU
19	N	8	GLU
19	N	108	ARG
19	N	155	VAL
20	O	4	PHE
20	O	13	LYS
20	O	51	ASN
20	O	55	TYR
20	O	137	CYS
20	O	152	ASP
20	O	168	PHE
20	O	186	SER
20	O	193	SER
21	P	3	ARG
21	P	23	ARG
21	P	30	ARG
21	P	69	ARG
21	P	117	VAL
22	Q	56	THR

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Mol	Chain	Res	Type
23	S	18	GLU
23	S	41	TRP
23	S	45	LYS
23	S	48	ASN
23	S	80	TYR
23	S	89	MET
23	S	116	ARG
23	S	123	LEU
23	S	141	GLN
23	S	153	HIS
23	S	175	PHE
25	Y	2	LYS
25	Y	6	ASP
25	Y	50	ARG
25	Y	53	ASP
25	Y	75	LYS
25	Y	87	GLU
25	Y	116	ASP
25	Y	124	LYS
27	e	5	ASN
27	e	79	VAL
27	e	100	ARG
27	e	125	SER
28	f	40	GLU
28	f	49	ARG
28	f	58	LYS
29	h	6	PHE
29	h	11	GLN
29	h	15	ASN
29	h	47	LYS
29	h	52	ASP
29	h	70	GLU
30	i	15	LEU
30	i	33	LYS
30	i	90	SER
31	j	25	ARG
31	j	30	GLN
31	j	57	ARG
31	j	58	THR
32	m	201	ASP
32	m	210	VAL
32	m	252	GLN

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Mol	Chain	Res	Type
34	o	133	ARG
34	o	141	LYS
34	o	142	THR
34	o	148	TYR
34	o	179	LYS
34	o	190	MET
34	o	191	PHE
34	o	192	LYS
34	o	198	PHE
34	o	199	LYS
34	o	203	HIS
34	o	208	ARG
36	t	52	LYS
36	t	53	ARG
36	t	60	ASN
36	t	65	GLU
36	t	67	GLU
36	t	68	ARG
38	v	119	THR
38	v	142	GLU
38	v	147	LYS
39	x	10	ARG
39	x	24	ASP
39	x	44	ARG
39	x	79	LYS
39	x	80	ASP
39	x	91	ARG
39	x	153	GLU
39	x	163	LEU
39	x	164	VAL
39	x	207	LEU
39	x	209	MET
39	x	243	ARG
39	x	255	MET
39	x	302	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
5	5	71	GLN
7	A	97	ASN
8	B	165	GLN

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Mol	Chain	Res	Type
8	B	211	GLN
8	B	279	ASN
10	D	270	GLN
16	K	78	ASN
21	P	80	GLN
21	P	97	ASN
22	Q	79	ASN
23	S	48	ASN
29	h	25	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1426/3497 (40%)	356 (24%)	16 (1%)
2	2	147/165 (89%)	31 (21%)	0
6	6	72/300 (24%)	40 (55%)	1 (1%)
All	All	1645/3962 (41%)	427 (25%)	17 (1%)

All (427) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	C
1	1	26	A
1	1	34	A
1	1	50	U
1	1	53	G
1	1	59	G
1	1	60	A
1	1	65	A
1	1	66	A
1	1	72	C
1	1	105	G
1	1	109	A
1	1	110	G
1	1	111	C
1	1	116	A
1	1	122	A
1	1	154	G
1	1	161	C
1	1	162	A
1	1	163	A

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Mol	Chain	Res	Type
1	1	177	G
1	1	197	U
1	1	198	U
1	1	207	C
1	1	217	G
1	1	218	A
1	1	225	G
1	1	226	A
1	1	227	G
1	1	239	U
1	1	240	G
1	1	244	G
1	1	259	A
1	1	276	A
1	1	277	G
1	1	303	A
1	1	305	A
1	1	306	U
1	1	331	A
1	1	337	U
1	1	338	G
1	1	341	G
1	1	346	A
1	1	347	C
1	1	359	A
1	1	360	A
1	1	383	A
1	1	384	G
1	1	399	A
1	1	406	U
1	1	411	C
1	1	428	G
1	1	430	A
1	1	432	G
1	1	433	C
1	1	437	G
1	1	445	G
1	1	446	U
1	1	448	U
1	1	449	U
1	1	450	A
1	1	451	C

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Mol	Chain	Res	Type
1	1	454	G
1	1	458	G
1	1	460	G
1	1	461	A
1	1	462	U
1	1	465	G
1	1	466	U
1	1	479	A
1	1	480	G
1	1	482	C
1	1	488	A
1	1	489	C
1	1	493	G
1	1	494	A
1	1	497	C
1	1	499	G
1	1	500	U
1	1	501	G
1	1	502	G
1	1	503	U
1	1	505	G
1	1	506	G
1	1	514	C
1	1	522	G
1	1	530	A
1	1	532	A
1	1	534	A
1	1	540	A
1	1	546	G
1	1	547	G
1	1	548	U
1	1	577	U
1	1	578	U
1	1	579	A
1	1	580	U
1	1	581	A
1	1	582	G
1	1	590	U
1	1	591	G
1	1	592	U
1	1	602	A
1	1	603	C

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Mol	Chain	Res	Type
1	1	613	A
1	1	616	A
1	1	618	U
1	1	623	C
1	1	632	A
1	1	634	G
1	1	636	A
1	1	637	U
1	1	641	G
1	1	645	U
1	1	646	A
1	1	647	A
1	1	649	G
1	1	661	C
1	1	662	C
1	1	663	C
1	1	671	A
1	1	673	C
1	1	675	C
1	1	685	A
1	1	702	A
1	1	706	U
1	1	709	G
1	1	714	A
1	1	716	G
1	1	717	A
1	1	732	A
1	1	759	C
1	1	761	U
1	1	762	U
1	1	763	G
1	1	765	G
1	1	768	G
1	1	770	G
1	1	776	U
1	1	817	G
1	1	831	G
1	1	837	G
1	1	840	A
1	1	964	U
1	1	968	A
1	1	969	G

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Mol	Chain	Res	Type
1	1	976	C
1	1	986	U
1	1	987	U
1	1	989	C
1	1	990	C
1	1	996	G
1	1	997	A
1	1	998	U
1	1	1009	C
1	1	1010	A
1	1	1011	G
1	1	1012	A
1	1	1013	U
1	1	1017	U
1	1	1023	G
1	1	1135	G
1	1	1138	U
1	1	1142	U
1	1	1143	A
1	1	1155	U
1	1	1156	U
1	1	1158	G
1	1	1159	U
1	1	1160	A
1	1	1161	A
1	1	1163	C
1	1	1166	A
1	1	1168	C
1	1	1170	G
1	1	1173	G
1	1	1176	G
1	1	1184	A
1	1	1191	C
1	1	1205	G
1	1	1211	A
1	1	1212	U
1	1	1217	G
1	1	1221	A
1	1	1222	U
1	1	1223	C
1	1	1224	A
1	1	1227	C

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Mol	Chain	Res	Type
1	1	1233	A
1	1	1234	A
1	1	1235	A
1	1	1239	U
1	1	1243	A
1	1	1244	G
1	1	1249	U
1	1	1324	U
1	1	1325	A
1	1	1347	U
1	1	1348	A
1	1	1361	A
1	1	1363	A
1	1	1380	A
1	1	1381	G
1	1	1382	C
1	1	1386	G
1	1	1387	A
1	1	1388	G
1	1	1389	A
1	1	1390	A
1	1	1420	U
1	1	1433	U
1	1	1452	A
1	1	1453	A
1	1	1465	G
1	1	1468	G
1	1	1470	U
1	1	1471	C
1	1	1484	G
1	1	1936	A
1	1	2443	G
1	1	2455	U
1	1	2456	G
1	1	2459	G
1	1	2460	A
1	1	2462	C
1	1	2463	G
1	1	2464	G
1	1	2465	G
1	1	2466	C
1	1	2468	A

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Mol	Chain	Res	Type
1	1	2470	G
1	1	2471	C
1	1	2984	C
1	1	2987	A
1	1	2989	C
1	1	2993	G
1	1	2994	C
1	1	2995	A
1	1	2996	G
1	1	2999	U
1	1	3003	G
1	1	3006	A
1	1	3097	U
1	1	3104	G
1	1	3107	A
1	1	3108	A
1	1	3109	U
1	1	3113	A
1	1	3118	G
1	1	3119	U
1	1	3120	A
1	1	3125	A
1	1	3126	G
1	1	3128	A
1	1	3130	C
1	1	3135	G
1	1	3136	A
1	1	3137	U
1	1	3142	A
1	1	3146	U
1	1	3148	G
1	1	3149	G
1	1	3152	U
1	1	3154	U
1	1	3179	G
1	1	3180	C
1	1	3182	G
1	1	3188	U
1	1	3189	C
1	1	3190	A
1	1	3192	C
1	1	3193	U

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Mol	Chain	Res	Type
1	1	3195	C
1	1	3196	C
1	1	3197	G
1	1	3200	U
1	1	3205	G
1	1	3212	G
1	1	3216	C
1	1	3219	A
1	1	3222	C
1	1	3225	A
1	1	3227	U
1	1	3237	A
1	1	3238	A
1	1	3239	A
1	1	3240	G
1	1	3248	U
1	1	3272	U
1	1	3273	A
1	1	3275	A
1	1	3276	A
1	1	3281	A
1	1	3282	G
1	1	3286	U
1	1	3289	G
1	1	3301	C
1	1	3307	U
1	1	3309	U
1	1	3315	A
1	1	3317	A
1	1	3318	A
1	1	3319	G
1	1	3324	G
1	1	3327	A
1	1	3328	U
1	1	3332	U
1	1	3335	U
1	1	3336	G
1	1	3338	A
1	1	3343	A
1	1	3344	A
1	1	3345	G
1	1	3346	U

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Mol	Chain	Res	Type
1	1	3348	U
1	1	3349	U
1	1	3351	U
1	1	3352	A
1	1	3356	A
1	1	3359	U
1	1	3360	G
1	1	3362	C
1	1	3368	A
1	1	3370	U
1	1	3371	U
1	1	3372	C
1	1	3375	U
1	1	3404	G
1	1	3405	C
1	1	3406	A
1	1	3407	U
1	1	3408	A
1	1	3410	G
1	1	3414	U
1	1	3417	A
1	1	3418	U
1	1	3420	U
1	1	3421	G
1	1	3423	A
1	1	3425	C
1	1	3426	G
1	1	3427	G
1	1	3431	A
1	1	3435	U
1	1	3472	G
1	1	3475	U
1	1	3476	A
1	1	3477	A
1	1	3478	G
1	1	3479	C
1	1	3483	U
1	1	3484	G
1	1	3490	A
1	1	3491	A
1	1	3492	G
1	1	3497	G

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Mol	Chain	Res	Type
2	2	9	A
2	2	30	U
2	2	31	U
2	2	42	U
2	2	43	C
2	2	57	G
2	2	59	G
2	2	67	A
2	2	70	C
2	2	71	G
2	2	79	A
2	2	85	A
2	2	87	A
2	2	98	U
2	2	99	C
2	2	103	G
2	2	104	A
2	2	112	A
2	2	114	C
2	2	115	G
2	2	124	G
2	2	132	G
2	2	133	U
2	2	134	U
2	2	135	C
2	2	136	U
2	2	137	A
2	2	144	G
2	2	159	U
2	2	160	G
2	2	165	U
6	6	2	C
6	6	4	A
6	6	5	U
6	6	6	C
6	6	7	U
6	6	8	U
6	6	9	C
6	6	47	U
6	6	49	U
6	6	50	U
6	6	57	A

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Mol	Chain	Res	Type
6	6	60	U
6	6	61	U
6	6	62	U
6	6	82	A
6	6	83	A
6	6	87	A
6	6	88	G
6	6	89	U
6	6	94	A
6	6	95	A
6	6	97	C
6	6	98	G
6	6	99	A
6	6	101	U
6	6	102	G
6	6	105	G
6	6	106	A
6	6	108	A
6	6	177	U
6	6	178	U
6	6	179	U
6	6	180	A
6	6	182	C
6	6	183	A
6	6	184	C
6	6	185	U
6	6	187	U
6	6	188	G
6	6	189	U

All (17) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	414	G
1	1	445	G
1	1	449	U
1	1	461	A
1	1	487	C
1	1	488	A
1	1	493	G
1	1	496	C
1	1	500	U

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Mol	Chain	Res	Type
1	1	761	U
1	1	996	G
1	1	1155	U
1	1	1159	U
1	1	1380	A
1	1	1389	A
1	1	3337	A
6	6	1	A

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

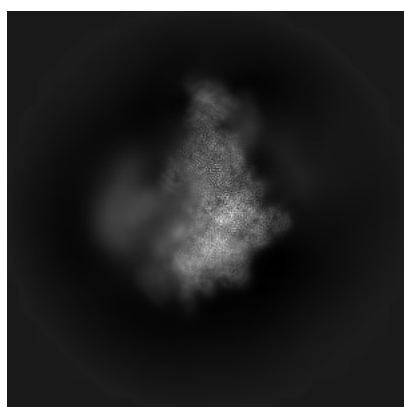
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24421. These allow visual inspection of the internal detail of the map and identification of artifacts.

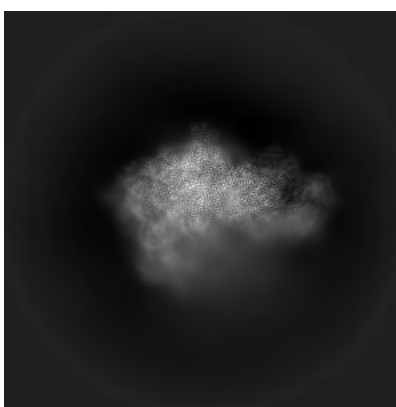
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

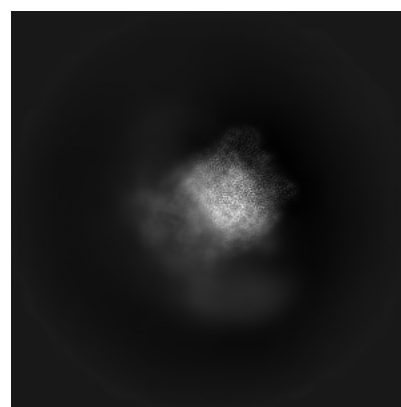
6.1.1 Primary map



X



Y

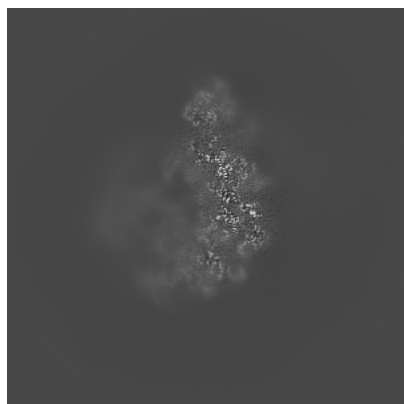


Z

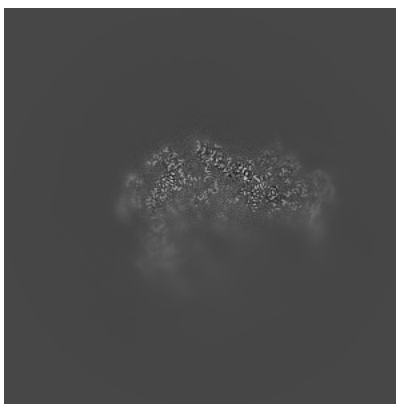
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

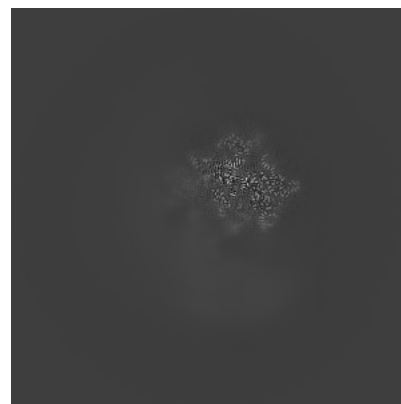
6.2.1 Primary map



X Index: 256



Y Index: 256

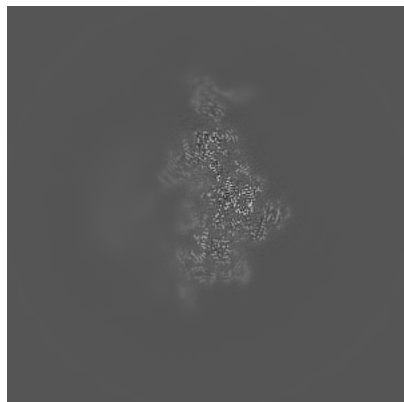


Z Index: 256

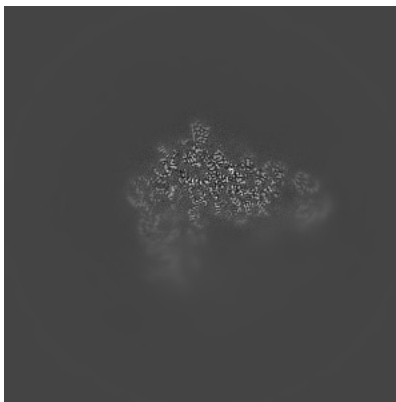
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

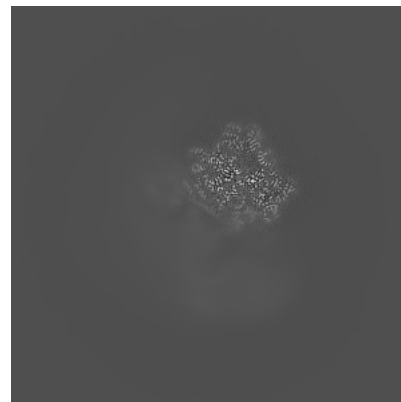
6.3.1 Primary map



X Index: 282



Y Index: 274



Z Index: 249

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

6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

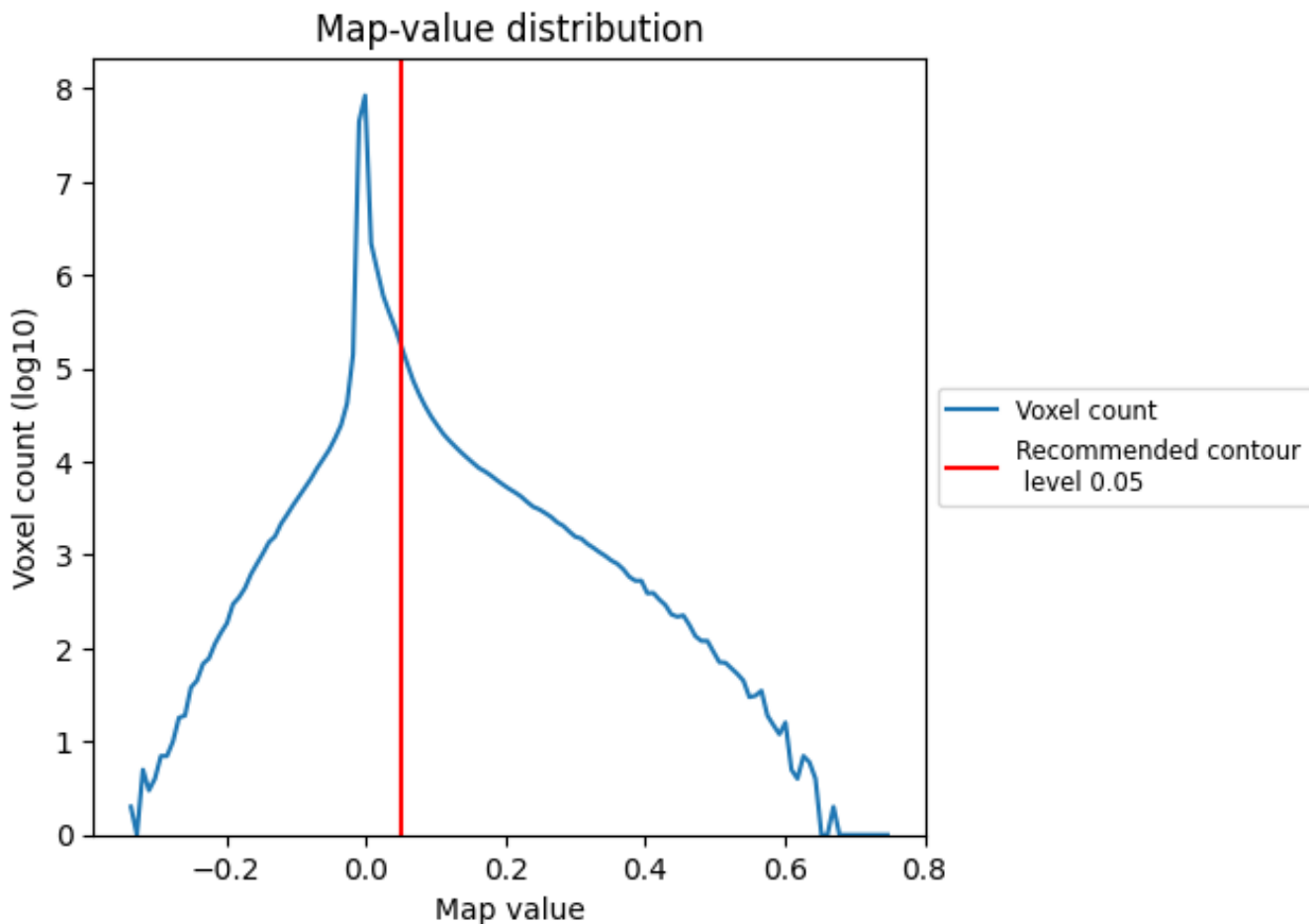
6.5 Mask visualisation

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

7 Map analysis [i](#)

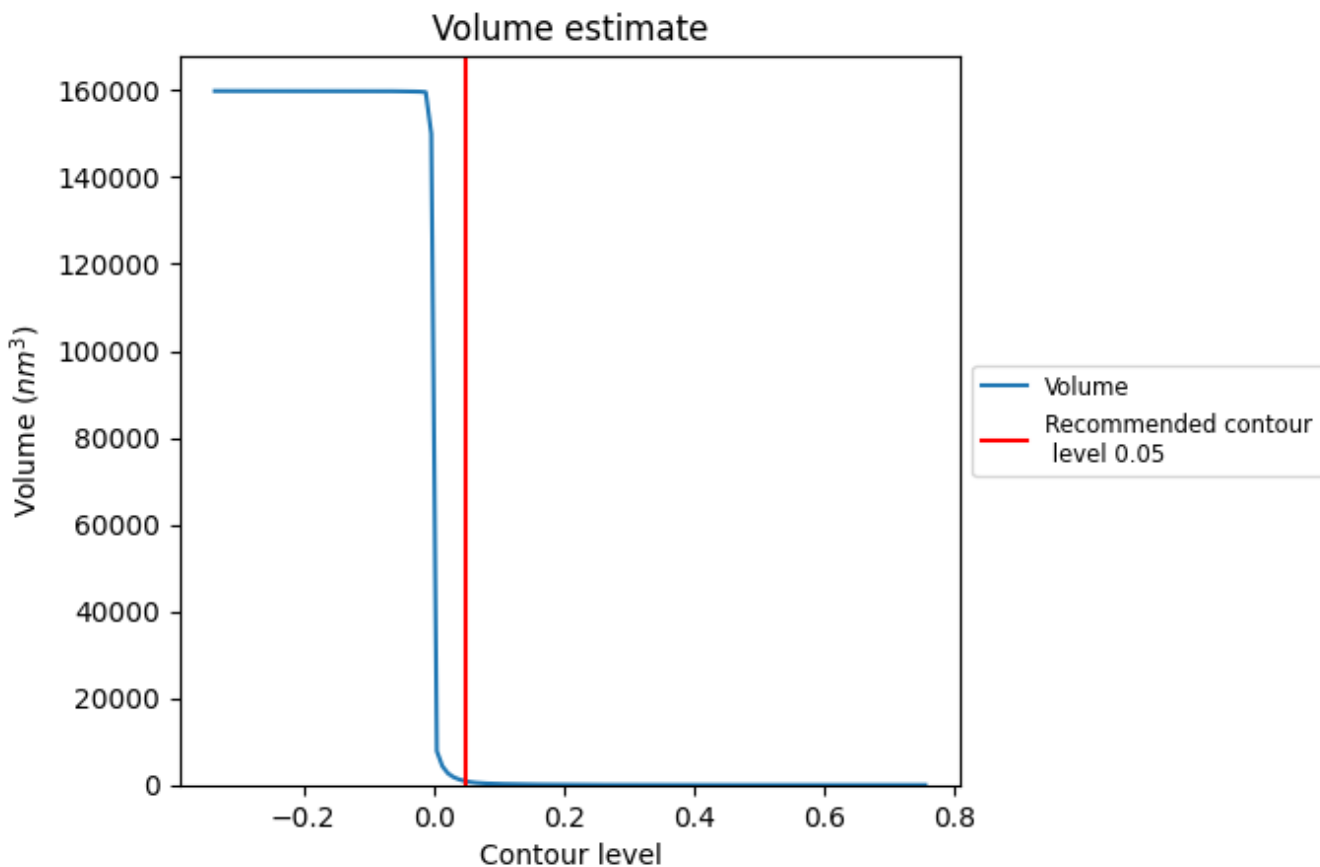
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

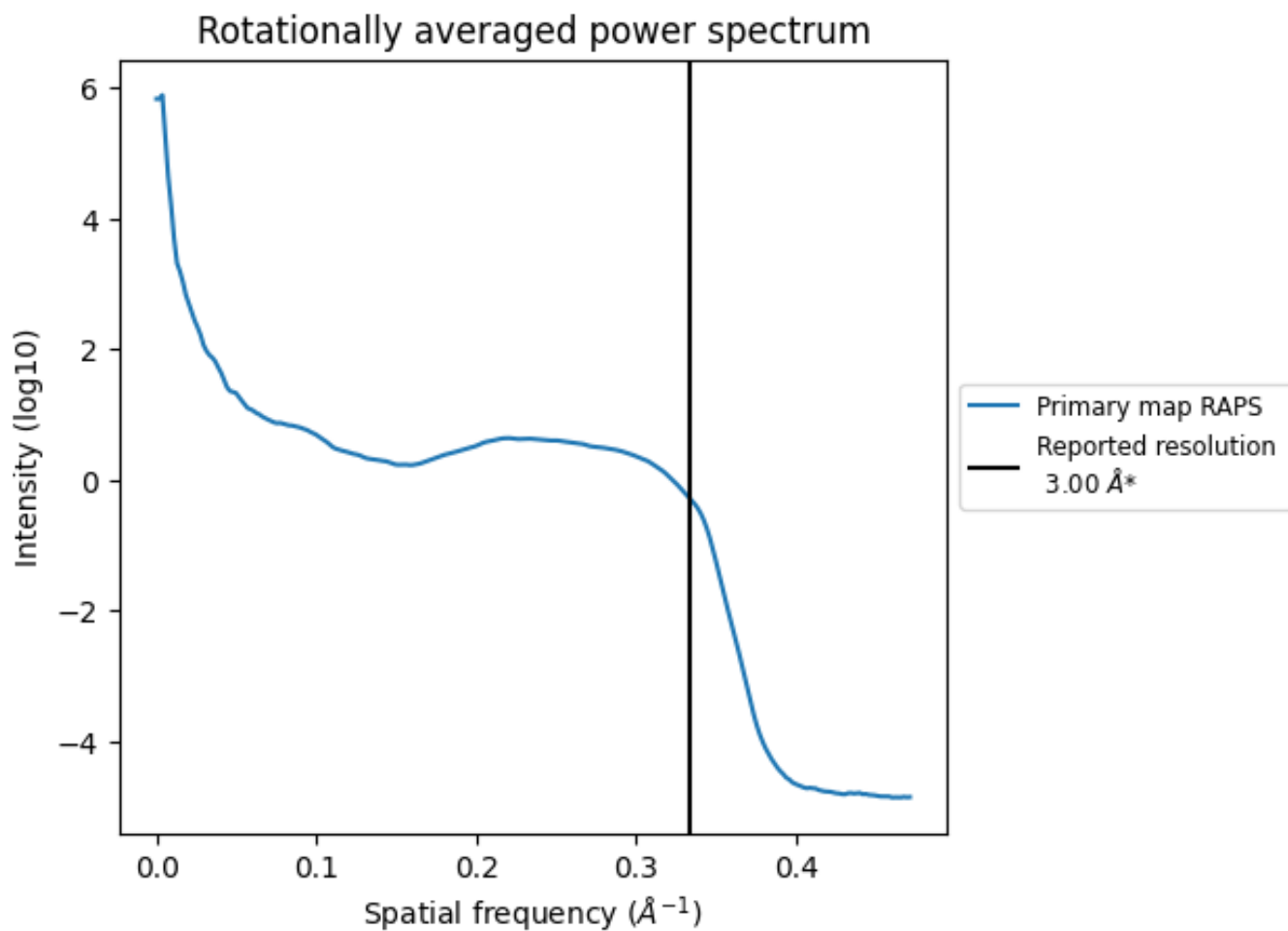
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 836 nm³; this corresponds to an approximate mass of 756 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 0.333\AA^{-1}

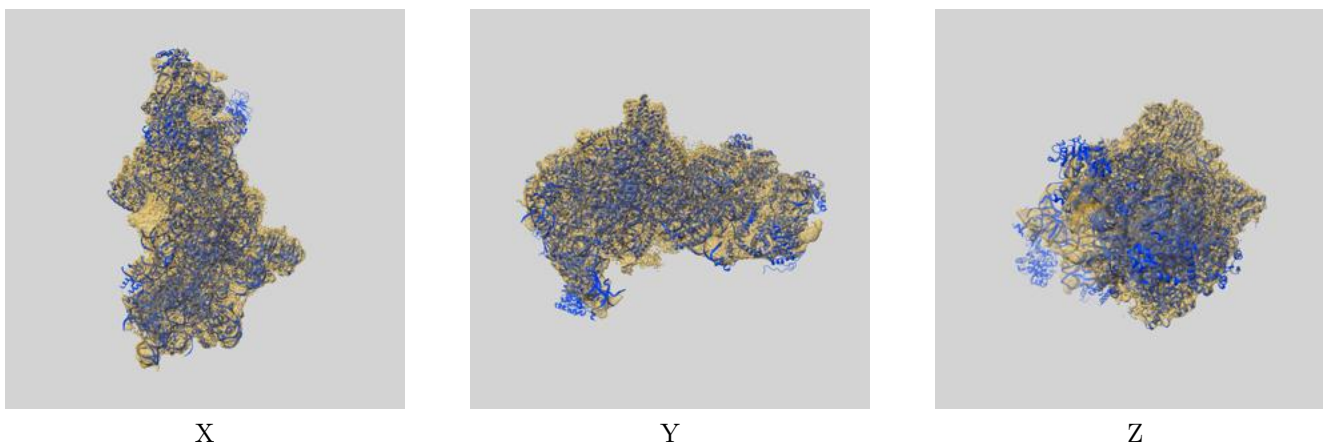
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

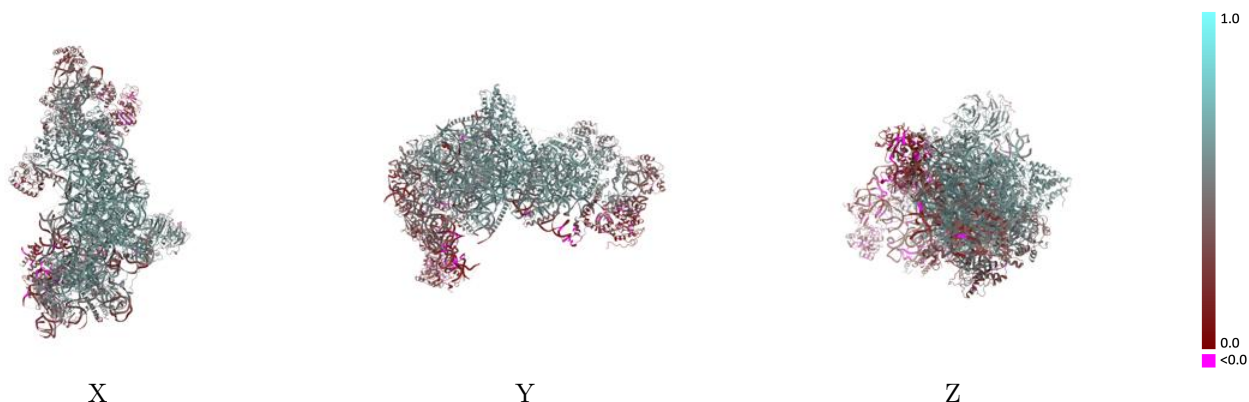
This section contains information regarding the fit between EMDB map EMD-24421 and PDB model 8EV3. Per-residue inclusion information can be found in section 3 on page 12.

9.1 Map-model overlay [i](#)



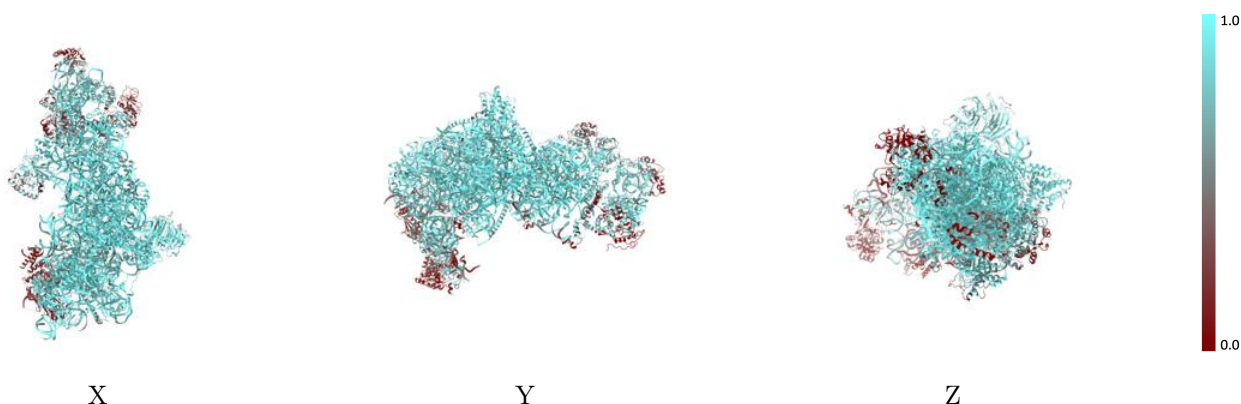
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



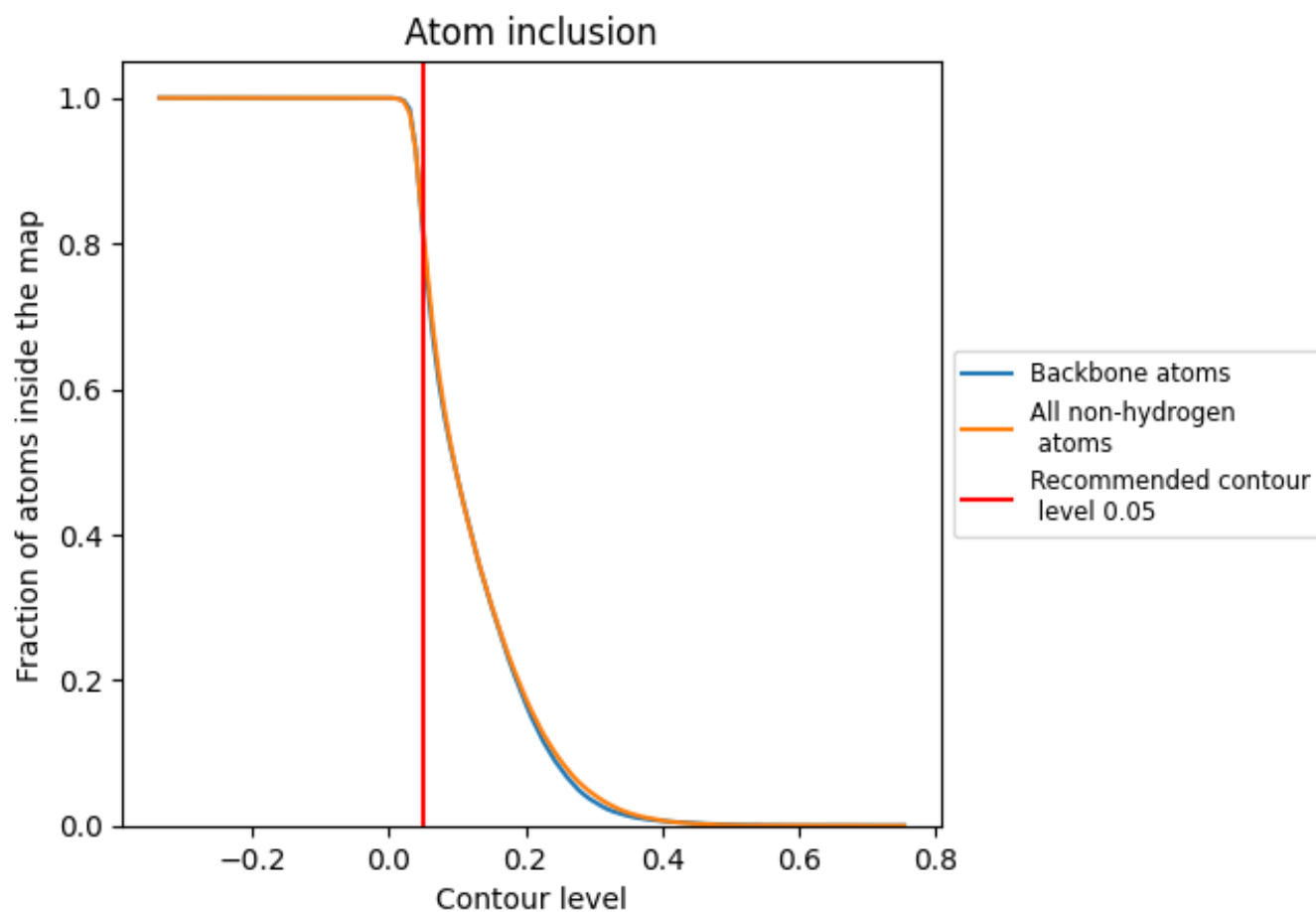
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary















The table lists the average atom inclusion at the recommended contour level (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8200	 0.4620
1	 0.8777	 0.4450
2	 0.8887	 0.4570
3	 0.9399	 0.5940
4	 0.9174	 0.5770
5	 0.8803	 0.5330
6	 0.8399	 0.3210
A	 0.7852	 0.3930
B	 0.6338	 0.2630
C	 0.9281	 0.5840
D	 0.6539	 0.4890
E	 0.9135	 0.5290
F	 0.9415	 0.5710
G	 0.9463	 0.5840
H	 0.1330	 0.2830
J	 0.5425	 0.3010
K	 0.6147	 0.3940
L	 0.9800	 0.6290
M	 0.9314	 0.4890
N	 0.9888	 0.6200
O	 0.8987	 0.4840
P	 0.8329	 0.5180
Q	 0.9558	 0.5890
S	 0.8443	 0.4560
T	 0.3673	 0.3620
V	 0.0000	 0.1100
Y	 0.9751	 0.5990
b	 0.0000	 0.2500
e	 0.9833	 0.6170
f	 0.9939	 0.6020
h	 0.8261	 0.5190
i	 0.9242	 0.5510
j	 0.9426	 0.5820
m	 0.8600	 0.5230
n	 0.3199	 0.1710



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Chain	Atom inclusion	Q-score
o	 0.7271	 0.4300
r	 0.0141	 0.1790
t	 0.7815	 0.3250
u	 0.2440	 0.1920
v	 0.9313	 0.5680
x	 0.9110	 0.5640
y	 0.0011	 0.1830