



# wwPDB EM Validation Summary Report ⓘ

May 14, 2024 – 12:43 AM JST

PDB ID : 7VPX  
EMDB ID : EMD-32074  
Title : The cryo-EM structure of the human pre-A complex  
Authors : Zhang, X.; Zhan, X.; Shi, Y.  
Deposited on : 2021-10-18  
Resolution : 3.00 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

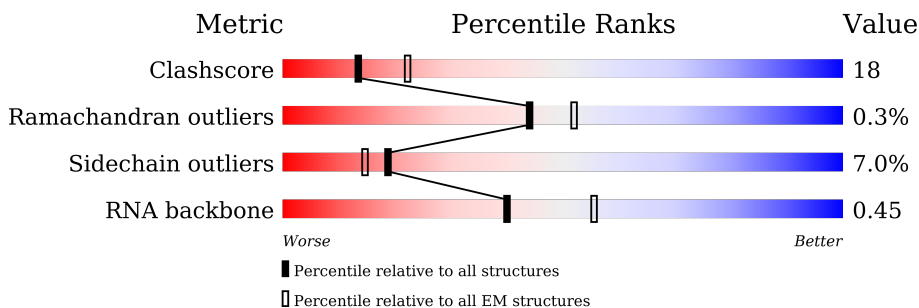
EMDB validation analysis : 0.0.1.dev92  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

# 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)
Clashscore	158937	4297
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  $\geq 3$ , 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	B	464	
2	D	639	
3	J	253	
4	H	188	
5	1	1304	
6	2	895	
7	3	1217	

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Mol	Chain	Length	Quality of chain
8	4	424	
9	5	86	
10	A	793	
11	C	501	
12	E	1031	
13	F	255	
14	G	225	
15	a	118	
15	i	118	
16	b	86	
16	m	86	
17	c	92	
17	l	92	
18	d	76	
18	n	76	
19	e	126	
19	j	126	
20	f	240	
20	k	240	
21	g	119	
21	h	119	
22	I	259	
23	K	10	
24	L	164	
25	O	437	

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Mol	Chain	Length	Quality of chain
26	M	282	
27	N	159	
28	6	110	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
30	SJT	6	204	X	-	-	-

## 2 Entry composition i

There are 30 unique types of molecules in this entry. The entry contains 43240 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	147	799	455	173	168	3	0	0

- Molecule 2 is a protein called Splicing factor 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	D	122	604	360	122	122	0	0

- Molecule 3 is a protein called DnaJ homolog subfamily C member 8.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	J	54	369	224	73	72	0	0

- Molecule 4 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	H	130	2754	1233	478	915	128	0	0

- Molecule 5 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	1	815	6487	4163	1121	1164	39	0	0

- Molecule 6 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	2	187	1325	835	245	243	2	0	0

- Molecule 7 is a protein called Splicing factor 3B subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	3	1180	9247	5872	1571	1759	45	0	0

- Molecule 8 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	4	160	664	344	160	160	0	0

- Molecule 9 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	5	66	539	342	93	99	5	0	0

- Molecule 10 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	A	123	504	258	123	123	0	0

- Molecule 11 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	C	425	2127	1191	470	462	4	0	0

- Molecule 12 is a protein called Probable ATP-dependent RNA helicase DDX46.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	E	455	2153	1157	487	507	2	0	0

- Molecule 13 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	F	162	666	342	162	162	0	0

- Molecule 14 is a protein called U2 small nuclear ribonucleoprotein B'.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	G	166	Total	C	N	O	0	0
			685	353	166	166		

- Molecule 15 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	a	90	Total	C	N	O	0	0	
			372	192	90	90			
15	i	94	Total	C	N	O	S	0	0
			764	478	139	141	6		

- Molecule 16 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	b	74	Total	C	N	O	0	0	
			308	160	74	74			
16	m	74	Total	C	N	O	S	0	0
			576	373	95	103	5		

- Molecule 17 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	c	79	Total	C	N	O	0	0	
			319	161	79	79			
17	l	77	Total	C	N	O	S	0	0
			638	405	113	115	5		

- Molecule 18 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	d	74	Total	C	N	O	0	0	
			305	157	74	74			
18	n	73	Total	C	N	O	S	0	0
			568	358	102	102	6		

- Molecule 19 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	e	83	Total	C	N	O	0	0	
			341	175	83	83			
19	j	81	Total	C	N	O	S	0	0
			637	400	112	119	6		

- Molecule 20 is a protein called Small nuclear ribonucleoprotein-associated proteins B and B'.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	f	71	Total	C	N	O			
			293	151	71	71	0	0	
20	k	86	Total	C	N	O	S		
			692	435	126	124	7	0	

- Molecule 21 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	g	82	Total	C	N	O			
			337	173	82	82	0	0	
21	h	81	Total	C	N	O	S		
			641	408	112	118	3	0	

- Molecule 22 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	I	15	Total	C	N	O	P		
			314	141	51	107	15	0	

- Molecule 23 is a RNA chain called 5SS.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	K	10	Total	C	N	O	P		
			216	97	42	68	9	0	

- Molecule 24 is a RNA chain called U1 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	L	164	Total	C	N	O	P		
			3485	1555	607	1159	164	0	

- Molecule 25 is a protein called U1 small nuclear ribonucleoprotein 70 kDa.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	O	201	Total	C	N	O	S		
			1643	1030	317	291	5	0	

- Molecule 26 is a protein called U1 small nuclear ribonucleoprotein A.



Mol	Chain	Residues	Atoms					AltConf	Trace
26	M	98	Total	C	N	O	S	0	0
			787	506	134	143	4		

- Molecule 27 is a protein called U1 small nuclear ribonucleoprotein C.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	N	50	Total	C	N	O	S	0	0
			425	266	73	82	4		

- Molecule 28 is a protein called PHD finger-like domain-containing protein 5A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	6	81	Total	C	N	O	S	0	0
			613	376	109	115	13		

- Molecule 29 is ZINC ION (three-letter code: ZN) (formula: Zn).

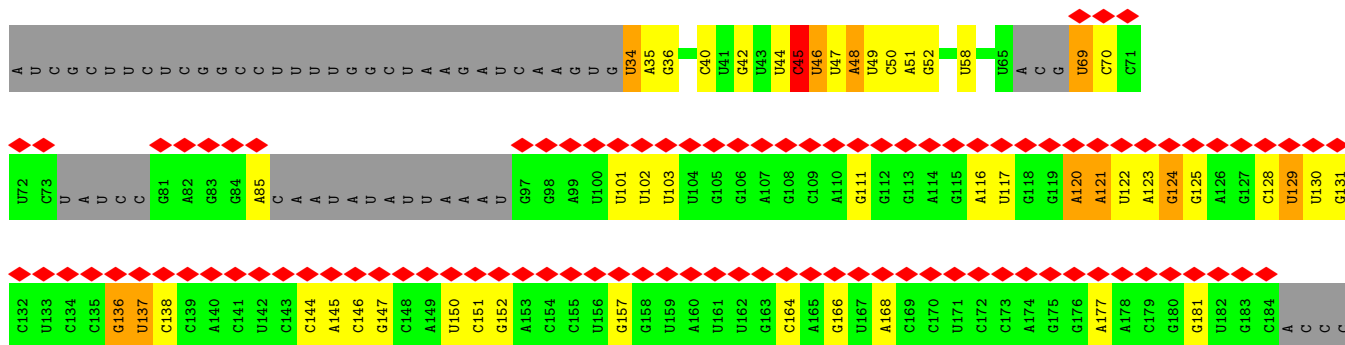
Mol	Chain	Residues	Atoms		AltConf
29	B	1	Total	Zn	0
			1	1	
29	C	1	Total	Zn	0
			1	1	
29	N	1	Total	Zn	0
			1	1	
29	6	3	Total	Zn	0
			3	3	

- Molecule 30 is spliceostatin A (form II) (three-letter code: SJT) (formula: C<sub>28</sub>H<sub>45</sub>NO<sub>8</sub>) (labeled as "Ligand of Interest" by depositor).

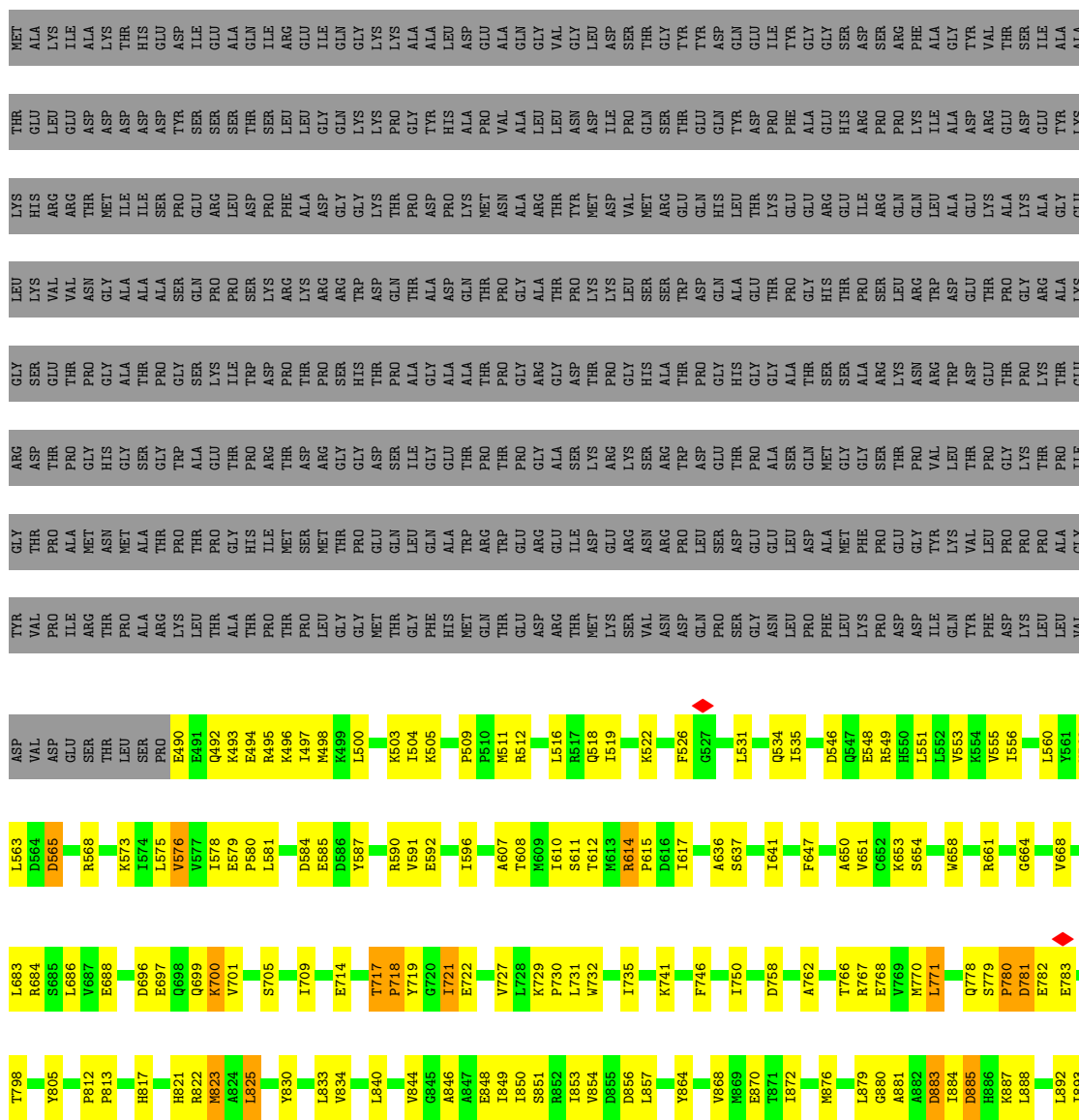








• Molecule 5: Splicing factor 3B subunit 1



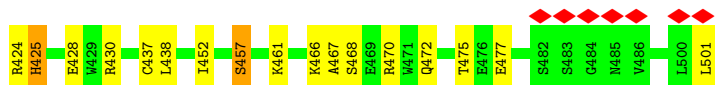
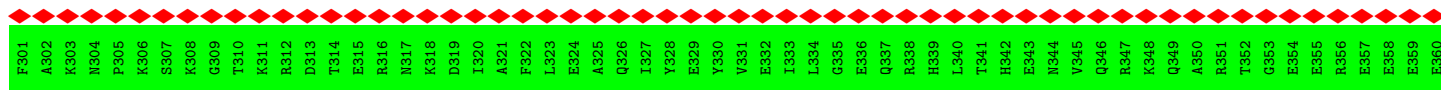




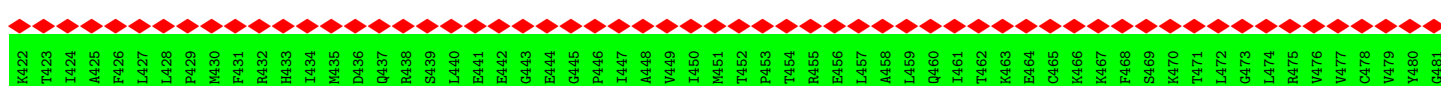
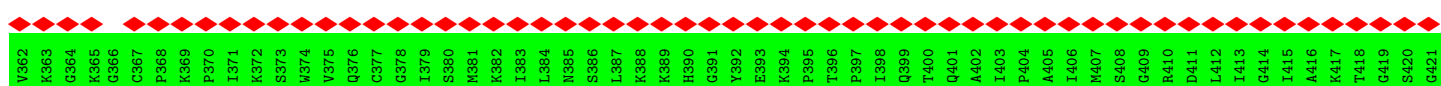
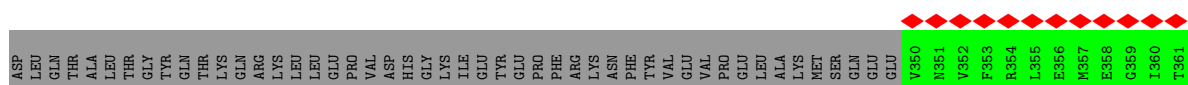
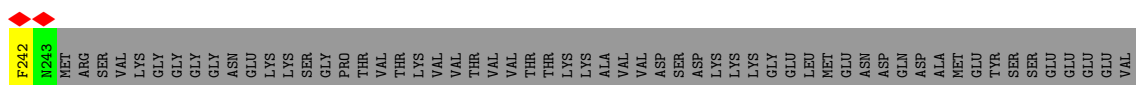
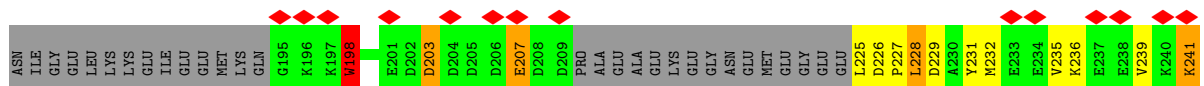
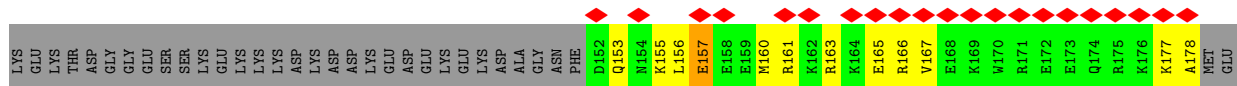
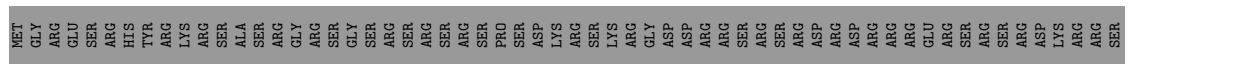




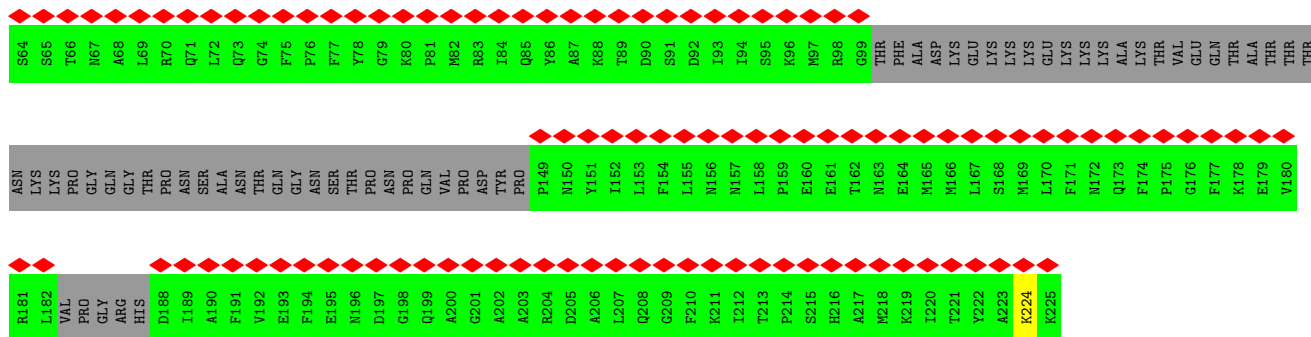




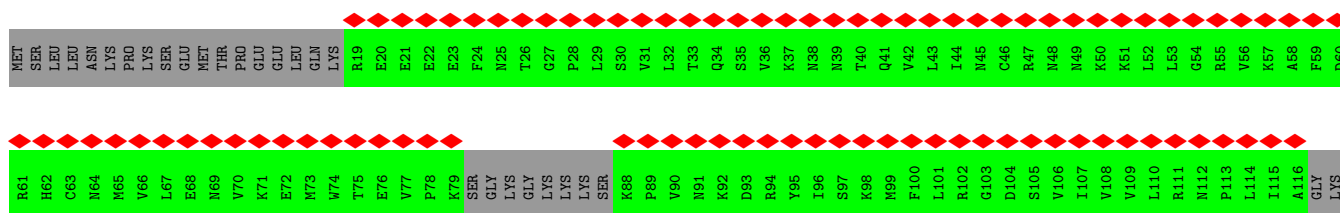
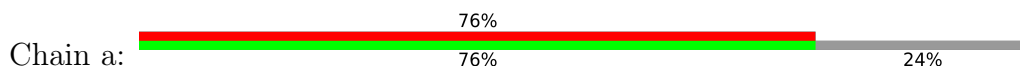
● Molecule 12: Probable ATP-dependent RNA helicase DDX46



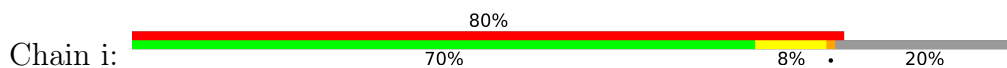




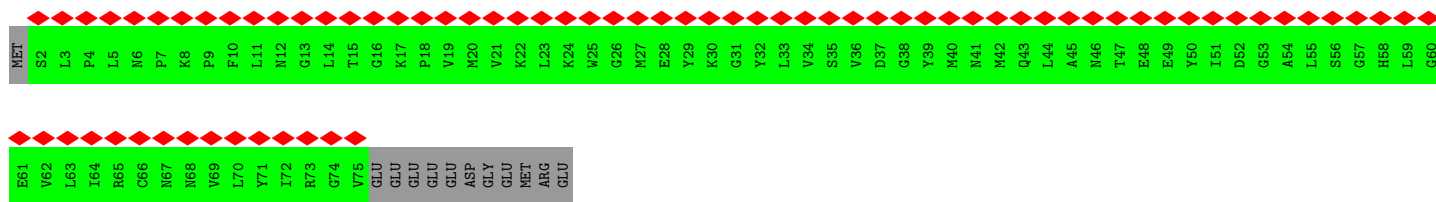
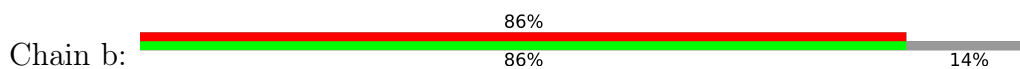
• Molecule 15: Small nuclear ribonucleoprotein Sm D2



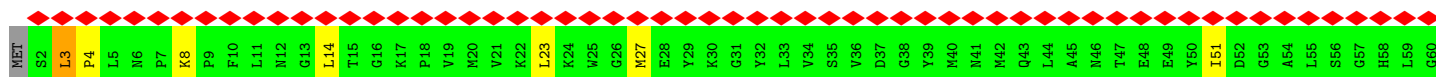
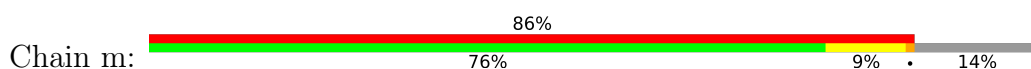
• Molecule 15: Small nuclear ribonucleoprotein Sm D2

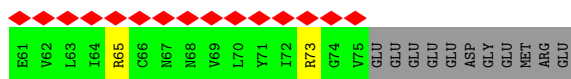


• Molecule 16: Small nuclear ribonucleoprotein F

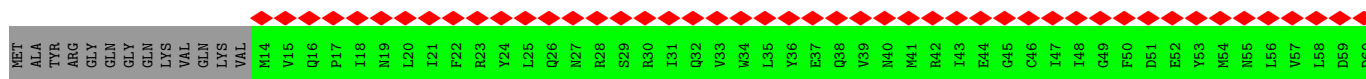
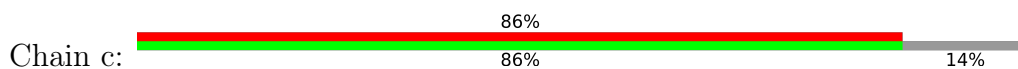


• Molecule 16: Small nuclear ribonucleoprotein F

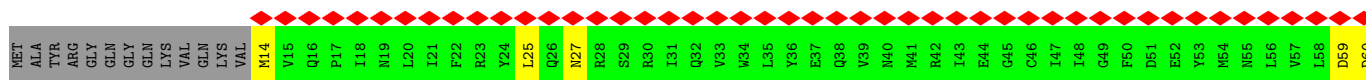
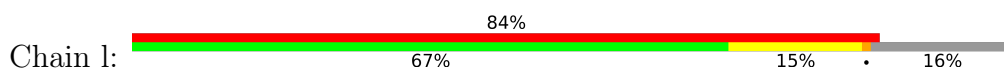




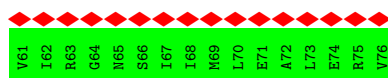
- Molecule 17: Small nuclear ribonucleoprotein E



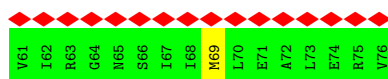
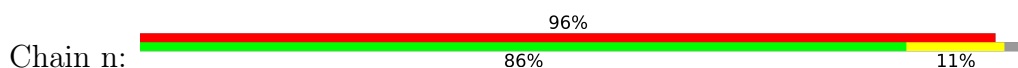
- Molecule 17: Small nuclear ribonucleoprotein E



- Molecule 18: Small nuclear ribonucleoprotein G

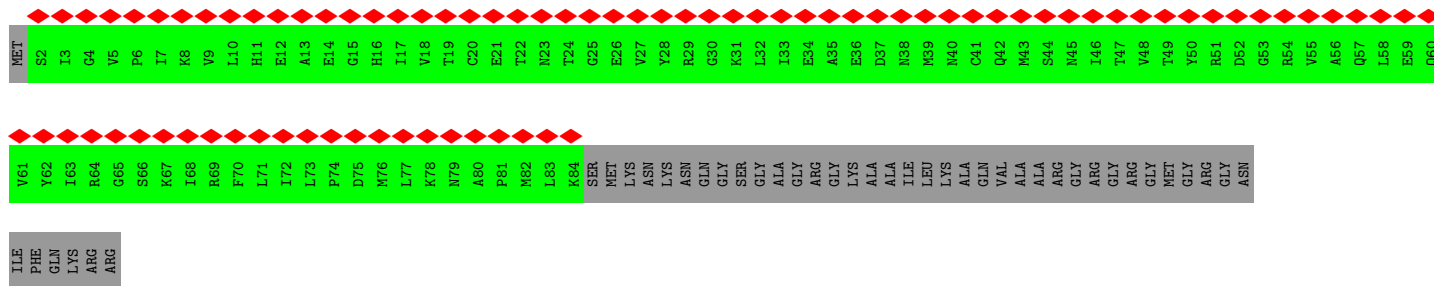


- Molecule 18: Small nuclear ribonucleoprotein G

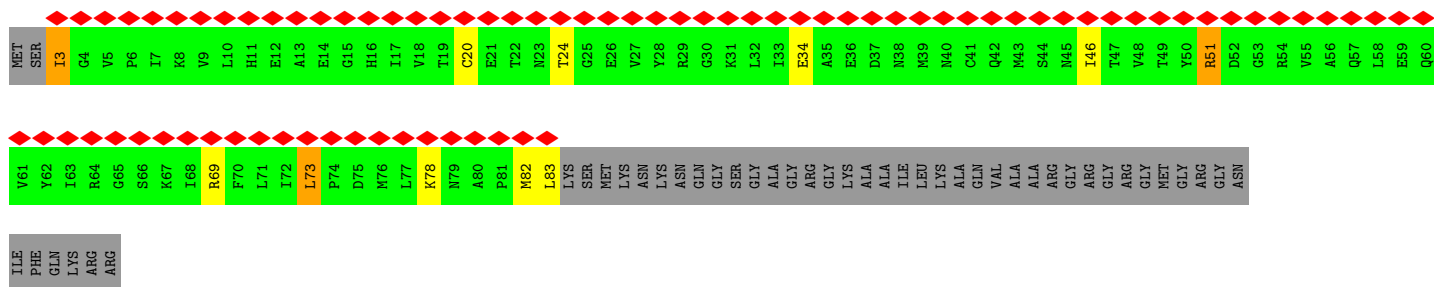


- Molecule 19: Small nuclear ribonucleoprotein Sm D3

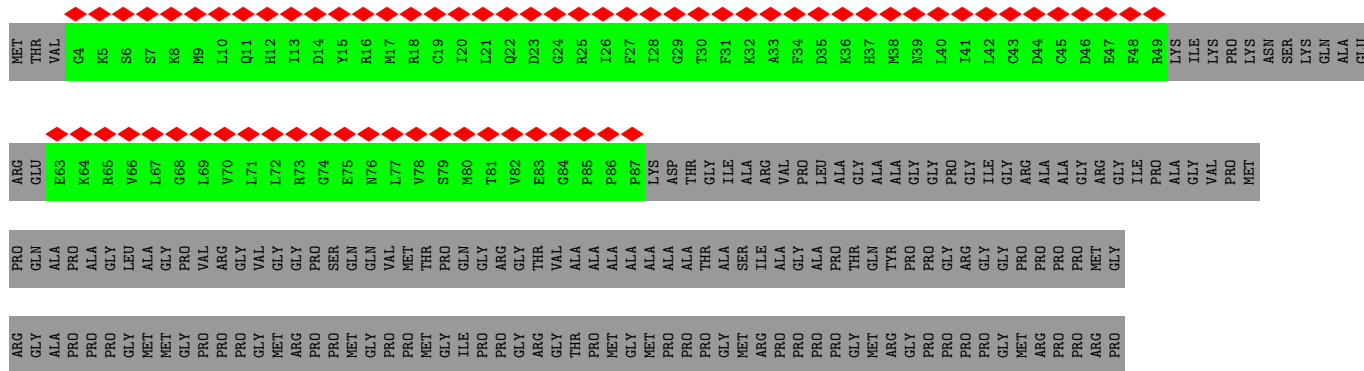




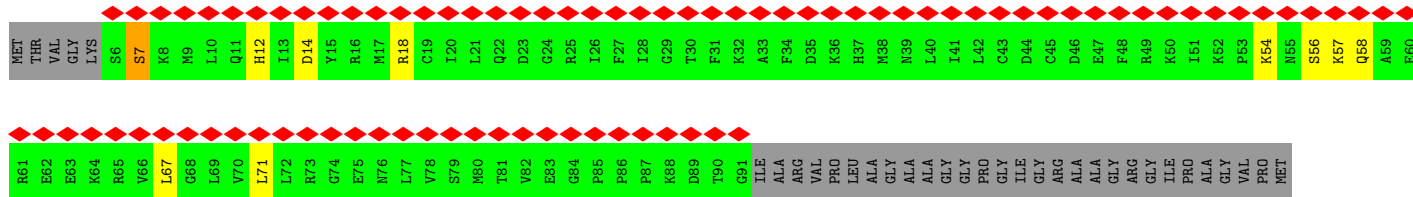
• Molecule 19: Small nuclear ribonucleoprotein Sm D3



• Molecule 20: Small nuclear ribonucleoprotein-associated proteins B and B'



• Molecule 20: Small nuclear ribonucleoprotein-associated proteins B and B'











## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	419522	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	3.684	Depositor
Minimum map value	-2.084	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.043	Depositor
Recommended contour level	0.25	Depositor
Map size ( $\text{\AA}$ )	521.76, 521.76, 521.76	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.087, 1.087, 1.087	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

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	B	0.31	0/812	0.52	0/1060
2	D	0.33	0/600	0.61	0/830
3	J	0.70	0/374	0.66	0/507
4	H	0.34	0/3073	1.09	26/4779 (0.5%)
5	1	0.38	2/6609 (0.0%)	0.57	9/8946 (0.1%)
6	2	0.44	0/1364	0.52	0/1831
7	3	0.27	0/9435	0.52	3/12802 (0.0%)
8	4	0.24	0/670	0.45	0/850
9	5	0.49	1/555 (0.2%)	0.52	0/750
10	A	0.24	0/507	0.41	0/640
11	C	0.43	2/2158 (0.1%)	0.51	1/2808 (0.0%)
12	E	0.42	1/2171 (0.0%)	0.55	1/2779 (0.0%)
13	F	0.24	0/671	0.49	0/849
14	G	0.24	0/689	0.46	0/869
15	a	0.24	0/374	0.50	0/472
15	i	0.69	0/773	1.15	3/1039 (0.3%)
16	b	0.25	0/311	0.51	0/395
16	m	0.65	1/588 (0.2%)	1.18	4/795 (0.5%)
17	c	0.24	0/319	0.49	0/399
17	l	0.62	0/646	1.27	5/867 (0.6%)
18	d	0.25	0/307	0.51	0/388
18	n	0.58	0/575	1.17	4/768 (0.5%)
19	e	0.25	0/343	0.51	0/433
19	j	0.53	0/645	1.19	6/870 (0.7%)
20	f	0.24	0/294	0.49	0/370
20	k	0.64	0/702	1.16	3/936 (0.3%)
21	g	0.24	0/339	0.51	0/428
21	h	0.68	0/649	1.24	7/878 (0.8%)
22	I	0.52	1/349 (0.3%)	1.19	5/540 (0.9%)
23	K	0.67	0/242	1.09	0/377
24	L	0.62	7/3891 (0.2%)	0.90	12/6061 (0.2%)
25	O	1.14	2/1688 (0.1%)	1.19	16/2279 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
26	M	1.04	0/801	1.02	2/1074 (0.2%)
27	N	0.56	0/437	1.16	4/587 (0.7%)
28	6	0.68	2/621 (0.3%)	1.10	5/833 (0.6%)
All	All	0.49	19/44582 (0.0%)	0.78	116/61089 (0.2%)

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
5	1	0	1
15	i	0	1
25	O	0	1
All	All	0	3

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	C	419	PRO	N-CA	13.18	1.69	1.47
5	1	718	PRO	N-CA	11.30	1.66	1.47
28	6	38	ARG	C-N	9.43	1.52	1.34
9	5	78	PRO	C-N	8.70	1.50	1.34
24	L	35	A	O3'-P	-7.27	1.52	1.61

The worst 5 of 116 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	3	1064	ASP	N-CA-CB	17.17	141.51	110.60
27	N	28	ARG	NE-CZ-NH1	12.38	126.49	120.30
24	L	3	A	N9-C1'-C2'	-10.85	99.89	114.00
19	j	73	LEU	CB-CG-CD2	10.23	128.39	111.00
16	m	73	ARG	NE-CZ-NH1	-10.09	115.26	120.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	1	1002	ASN	Mainchain
25	O	56	PRO	Peptide
15	i	17	GLN	Peptide

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	799	0	514	31	0
2	D	604	0	261	2	0
3	J	369	0	275	22	0
4	H	2754	0	1398	21	0
5	1	6487	0	6699	498	0
6	2	1325	0	1184	131	0
7	3	9247	0	9179	197	0
8	4	664	0	230	0	0
9	5	539	0	505	38	0
10	A	504	0	150	0	0
11	C	2127	0	1138	76	0
12	E	2153	0	1054	143	0
13	F	666	0	209	0	0
14	G	685	0	226	7	0
15	a	372	0	118	0	0
15	i	764	0	783	0	0
16	b	308	0	115	0	0
16	m	576	0	589	0	0
17	c	319	0	92	0	0
17	l	638	0	657	0	0
18	d	305	0	105	0	0
18	n	568	0	590	0	0
19	e	341	0	112	0	0
19	j	637	0	652	0	0
20	f	293	0	99	0	0
20	k	692	0	717	0	0
21	g	337	0	110	0	0
21	h	641	0	680	0	0
22	I	314	0	160	33	0
23	K	216	0	110	6	0
24	L	3485	0	1759	257	0
25	O	1643	0	1605	145	0
26	M	787	0	797	7	0
27	N	425	0	392	20	0
28	6	613	0	596	20	0
29	6	3	0	0	0	0
29	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	C	1	0	0	0	0
29	N	1	0	0	0	0
30	6	37	0	0	16	0
All	All	43240	0	33860	1223	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

The worst 5 of 1223 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:2:574:ALA:HA	6:2:578:TRP:CE3	1.40	1.51
5:1:1114:VAL:HG21	30:6:204:SJT:C1	1.40	1.51
25:O:61:GLU:CB	25:O:65:GLU:HG2	1.41	1.50
24:L:92:C:H2'	24:L:93:G:C8	1.44	1.48
24:L:32:A:N3	25:O:135:VAL:HG22	1.22	1.47

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	141/464 (30%)	139 (99%)	2 (1%)	0	100	100
2	D	114/639 (18%)	113 (99%)	1 (1%)	0	100	100
3	J	52/253 (21%)	51 (98%)	1 (2%)	0	100	100
5	1	813/1304 (62%)	776 (95%)	33 (4%)	4 (0%)	29	68
6	2	177/895 (20%)	162 (92%)	14 (8%)	1 (1%)	25	64
7	3	1168/1217 (96%)	1119 (96%)	47 (4%)	2 (0%)	47	82
8	4	156/424 (37%)	153 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	5	64/86 (74%)	63 (98%)	1 (2%)	0	100	100
10	A	121/793 (15%)	121 (100%)	0	0	100	100
11	C	419/501 (84%)	397 (95%)	20 (5%)	2 (0%)	29	68
12	E	447/1031 (43%)	430 (96%)	16 (4%)	1 (0%)	47	82
13	F	160/255 (63%)	160 (100%)	0	0	100	100
14	G	160/225 (71%)	158 (99%)	2 (1%)	0	100	100
15	a	86/118 (73%)	84 (98%)	2 (2%)	0	100	100
15	i	90/118 (76%)	84 (93%)	6 (7%)	0	100	100
16	b	72/86 (84%)	71 (99%)	1 (1%)	0	100	100
16	m	72/86 (84%)	69 (96%)	3 (4%)	0	100	100
17	c	77/92 (84%)	77 (100%)	0	0	100	100
17	l	75/92 (82%)	70 (93%)	5 (7%)	0	100	100
18	d	72/76 (95%)	72 (100%)	0	0	100	100
18	n	71/76 (93%)	69 (97%)	2 (3%)	0	100	100
19	e	81/126 (64%)	79 (98%)	2 (2%)	0	100	100
19	j	79/126 (63%)	75 (95%)	4 (5%)	0	100	100
20	f	67/240 (28%)	67 (100%)	0	0	100	100
20	k	84/240 (35%)	82 (98%)	2 (2%)	0	100	100
21	g	80/119 (67%)	79 (99%)	1 (1%)	0	100	100
21	h	79/119 (66%)	77 (98%)	2 (2%)	0	100	100
25	O	199/437 (46%)	182 (92%)	13 (6%)	4 (2%)	7	34
26	M	96/282 (34%)	94 (98%)	2 (2%)	0	100	100
27	N	48/159 (30%)	47 (98%)	1 (2%)	0	100	100
28	6	79/110 (72%)	71 (90%)	5 (6%)	3 (4%)	3	18
All	All	5499/10789 (51%)	5291 (96%)	191 (4%)	17 (0%)	44	76

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	1	969	LYS
5	1	1052	ALA
5	1	1053	ARG
7	3	1064	ASP
25	O	59	ARG

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	47/382 (12%)	47 (100%)	0	100	100
3	J	24/226 (11%)	22 (92%)	2 (8%)	11	39
5	1	701/1104 (64%)	653 (93%)	48 (7%)	16	48
6	2	124/776 (16%)	118 (95%)	6 (5%)	25	62
7	3	1022/1051 (97%)	963 (94%)	59 (6%)	20	55
8	4	8/336 (2%)	8 (100%)	0	100	100
9	5	57/77 (74%)	56 (98%)	1 (2%)	59	85
10	A	4/709 (1%)	4 (100%)	0	100	100
11	C	83/446 (19%)	73 (88%)	10 (12%)	5	22
12	E	73/892 (8%)	65 (89%)	8 (11%)	6	25
13	F	6/218 (3%)	6 (100%)	0	100	100
14	G	7/195 (4%)	7 (100%)	0	100	100
15	a	4/110 (4%)	4 (100%)	0	100	100
15	i	89/110 (81%)	81 (91%)	8 (9%)	9	35
16	b	4/74 (5%)	4 (100%)	0	100	100
16	m	63/74 (85%)	56 (89%)	7 (11%)	6	25
17	c	1/84 (1%)	1 (100%)	0	100	100
17	l	72/84 (86%)	61 (85%)	11 (15%)	2	13
18	d	3/66 (4%)	3 (100%)	0	100	100
18	n	63/66 (96%)	57 (90%)	6 (10%)	8	32
19	e	3/101 (3%)	3 (100%)	0	100	100
19	j	71/101 (70%)	61 (86%)	10 (14%)	3	16
20	f	3/177 (2%)	3 (100%)	0	100	100
20	k	78/177 (44%)	70 (90%)	8 (10%)	7	28
21	g	3/101 (3%)	3 (100%)	0	100	100
21	h	76/101 (75%)	72 (95%)	4 (5%)	22	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	O	169/373 (45%)	160 (95%)	9 (5%)	22	58
26	M	85/240 (35%)	82 (96%)	3 (4%)	36	71
27	N	48/135 (36%)	42 (88%)	6 (12%)	4	20
28	6	69/95 (73%)	62 (90%)	7 (10%)	7	29
All	All	3060/8681 (35%)	2847 (93%)	213 (7%)	19	47

5 of 213 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	5	48	ASP
16	m	3	LEU
19	j	34	GLU
11	C	425	HIS
12	E	225	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 45 such sidechains are listed below:

Mol	Chain	Res	Type
7	3	594	ASN
7	3	916	ASN
7	3	612	ASN
7	3	805	ASN
7	3	983	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
22	I	15/259 (5%)	7 (46%)	4 (26%)
23	K	9/10 (90%)	2 (22%)	0
24	L	163/164 (99%)	51 (31%)	6 (3%)
4	H	126/188 (67%)	29 (23%)	2 (1%)
All	All	313/621 (50%)	89 (28%)	12 (3%)

5 of 89 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	H	35	A
4	H	36	G

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Mol	Chain	Res	Type
4	H	45	C
4	H	46	U
4	H	47	U

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
24	L	90	U
24	L	92	C
24	L	128	U
24	L	123	A
22	I	28	G

#### 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 7 ligands modelled in this entry, 6 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
30	SJT	6	204	-	37,38,38	1.24	6 (16%)	42,55,55	1.56	7 (16%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	SJT	6	204	-	5/5/12/18	19/26/63/63	0/2/2/2

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	6	204	SJT	C17-C16	-3.16	1.44	1.50
30	6	204	SJT	C1-C	-3.11	1.41	1.48
30	6	204	SJT	O1-C3	-2.66	1.44	1.47
30	6	204	SJT	O1-C5	-2.45	1.29	1.35
30	6	204	SJT	C18-C16	-2.13	1.41	1.45

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	6	204	SJT	C2-C1-C	-5.55	108.80	122.69
30	6	204	SJT	C26-C25-C24	-3.87	109.69	113.37
30	6	204	SJT	O7-C25-C26	-3.43	111.01	113.61
30	6	204	SJT	C13-C7-N	3.06	115.59	110.86
30	6	204	SJT	C13-C7-C8	2.50	114.03	109.34

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
30	6	204	SJT	C10
30	6	204	SJT	C22
30	6	204	SJT	C25
30	6	204	SJT	C3
30	6	204	SJT	C8

5 of 19 torsion outliers are listed below:

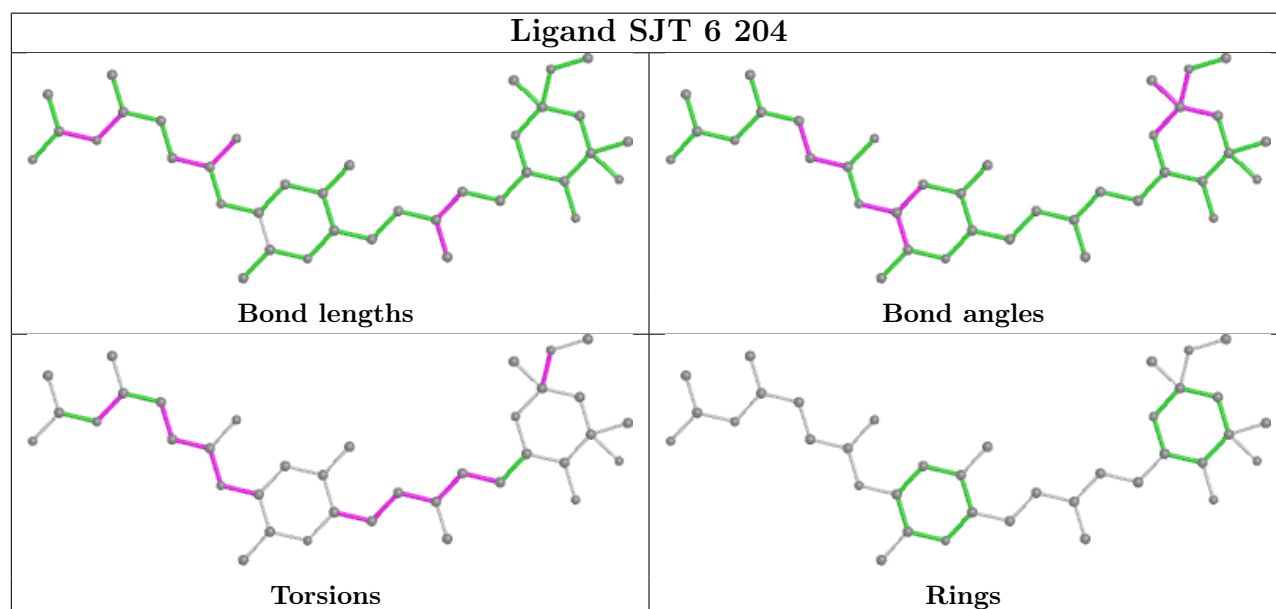
Mol	Chain	Res	Type	Atoms
30	6	204	SJT	C-C1-C2-C3
30	6	204	SJT	O-C-N-C7
30	6	204	SJT	C1-C-N-C7
30	6	204	SJT	C13-C7-N-C
30	6	204	SJT	C11-C10-C14-C15

There are no ring outliers.

1 monomer is involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	6	204	SJT	16	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



## 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.

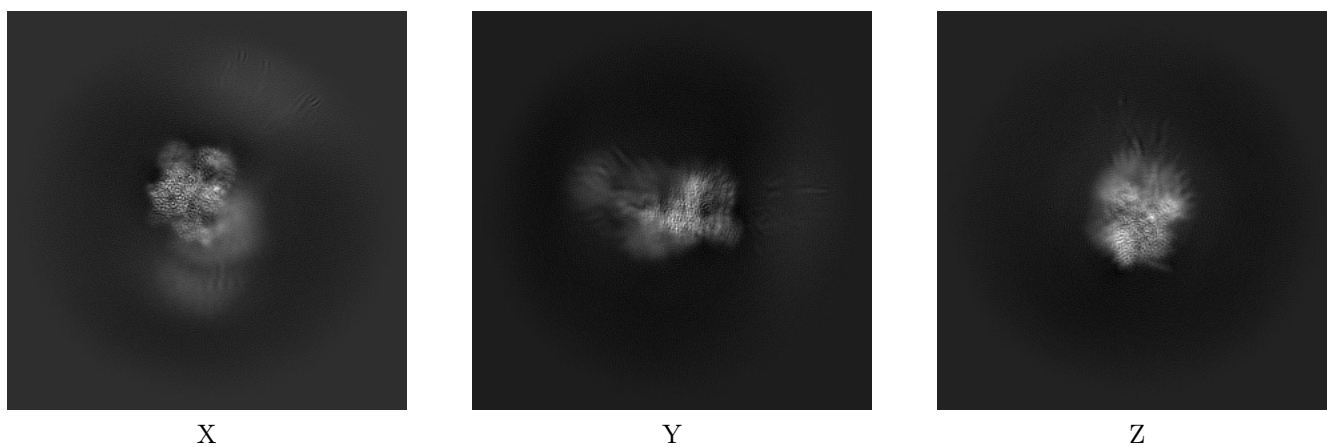
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32074. 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](#)

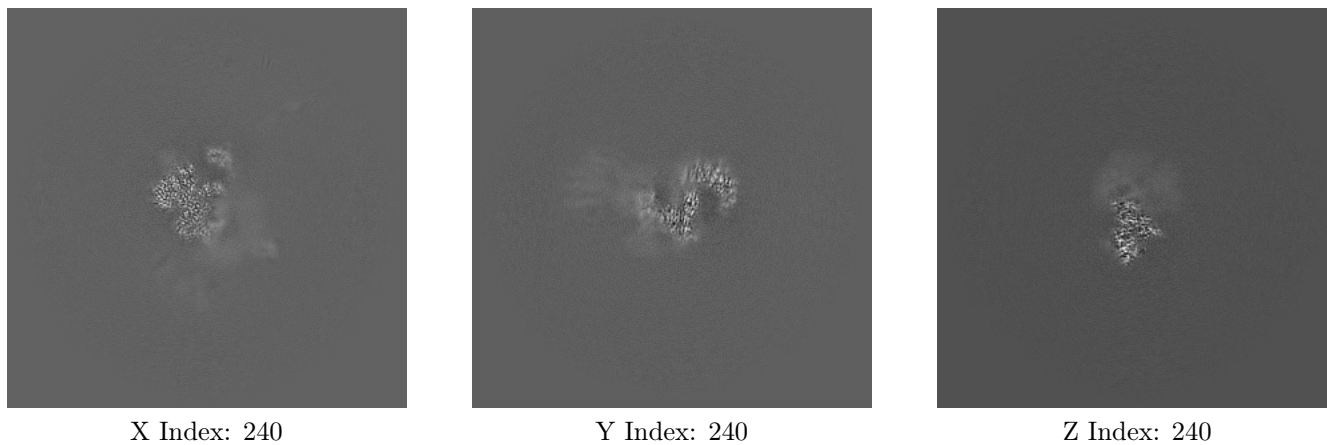
#### 6.1.1 Primary map



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

### 6.2 Central slices [i](#)

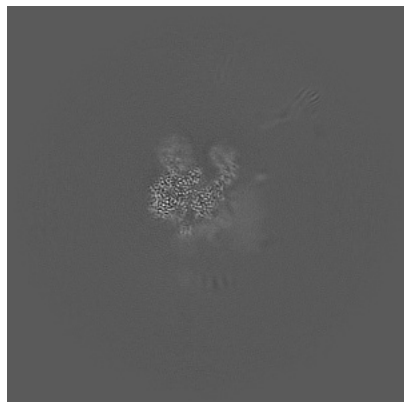
#### 6.2.1 Primary map



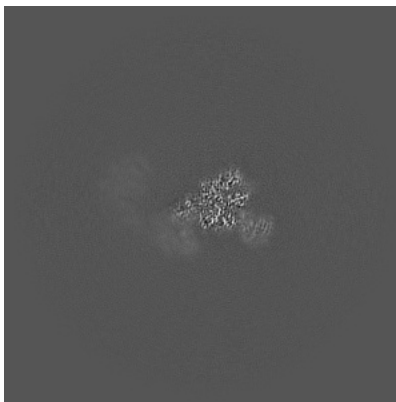
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

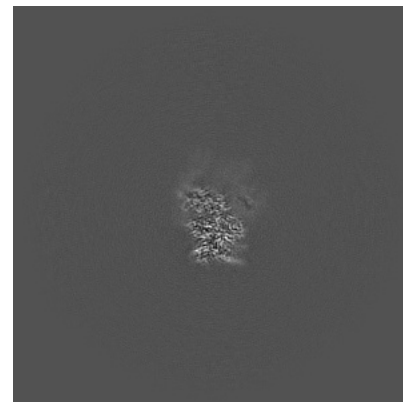
### 6.3.1 Primary map



X Index: 226



Y Index: 211

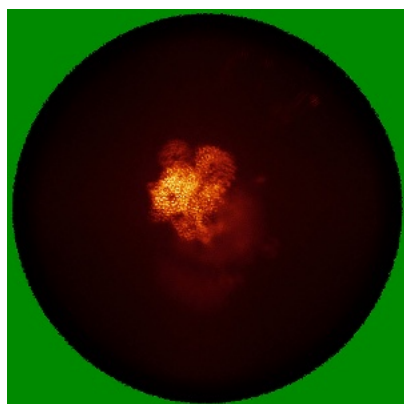


Z Index: 260

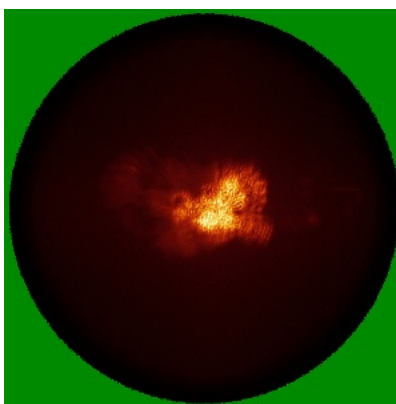
The images above show the largest variance slices of the map in three orthogonal directions.

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

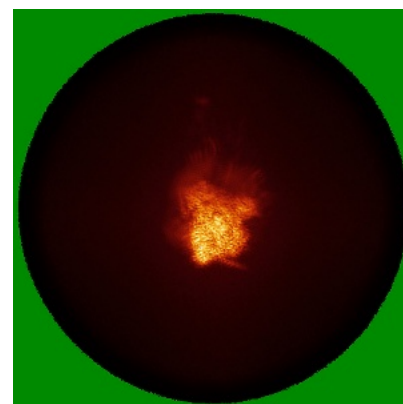
### 6.4.1 Primary map



X



Y



Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

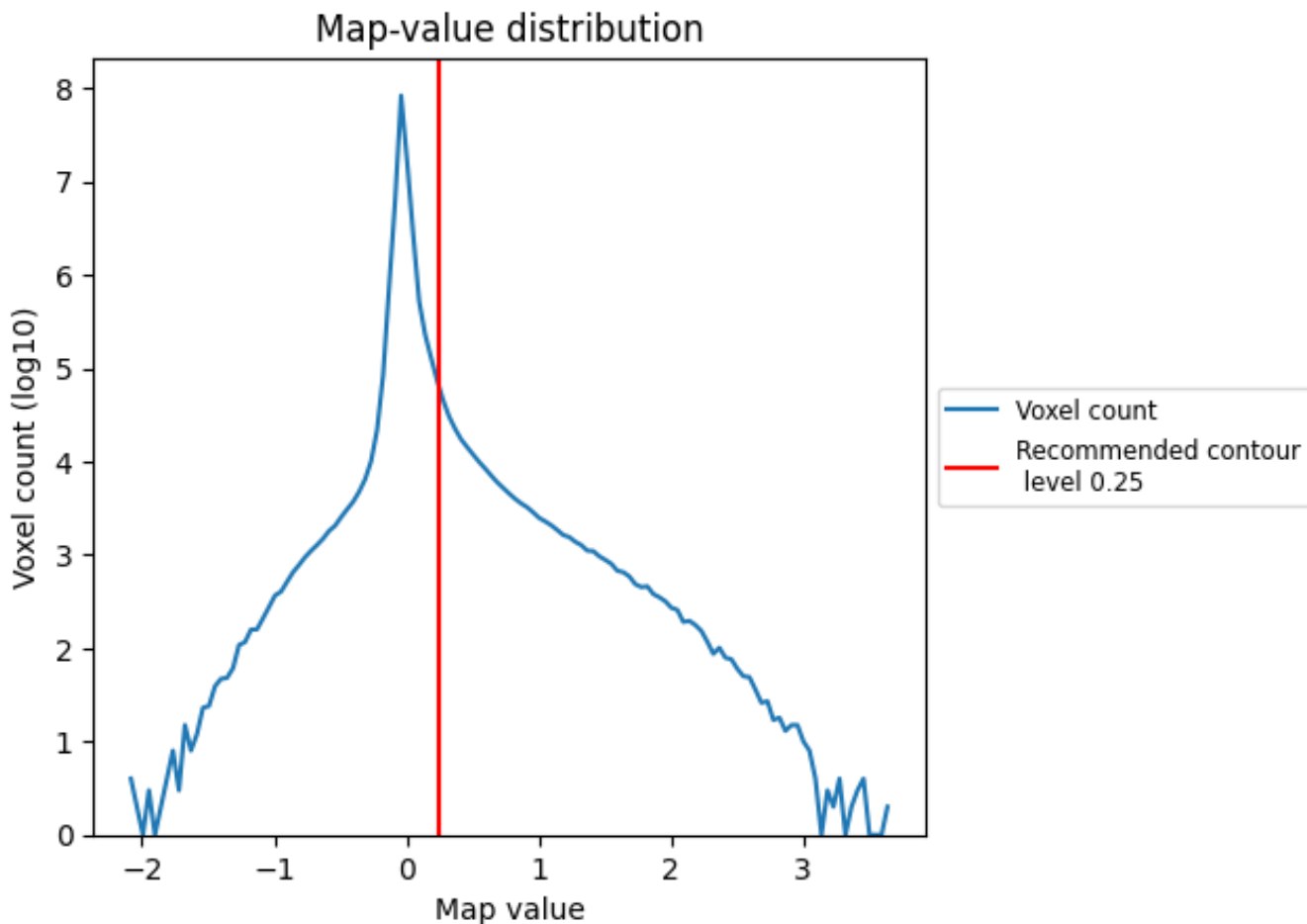
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

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

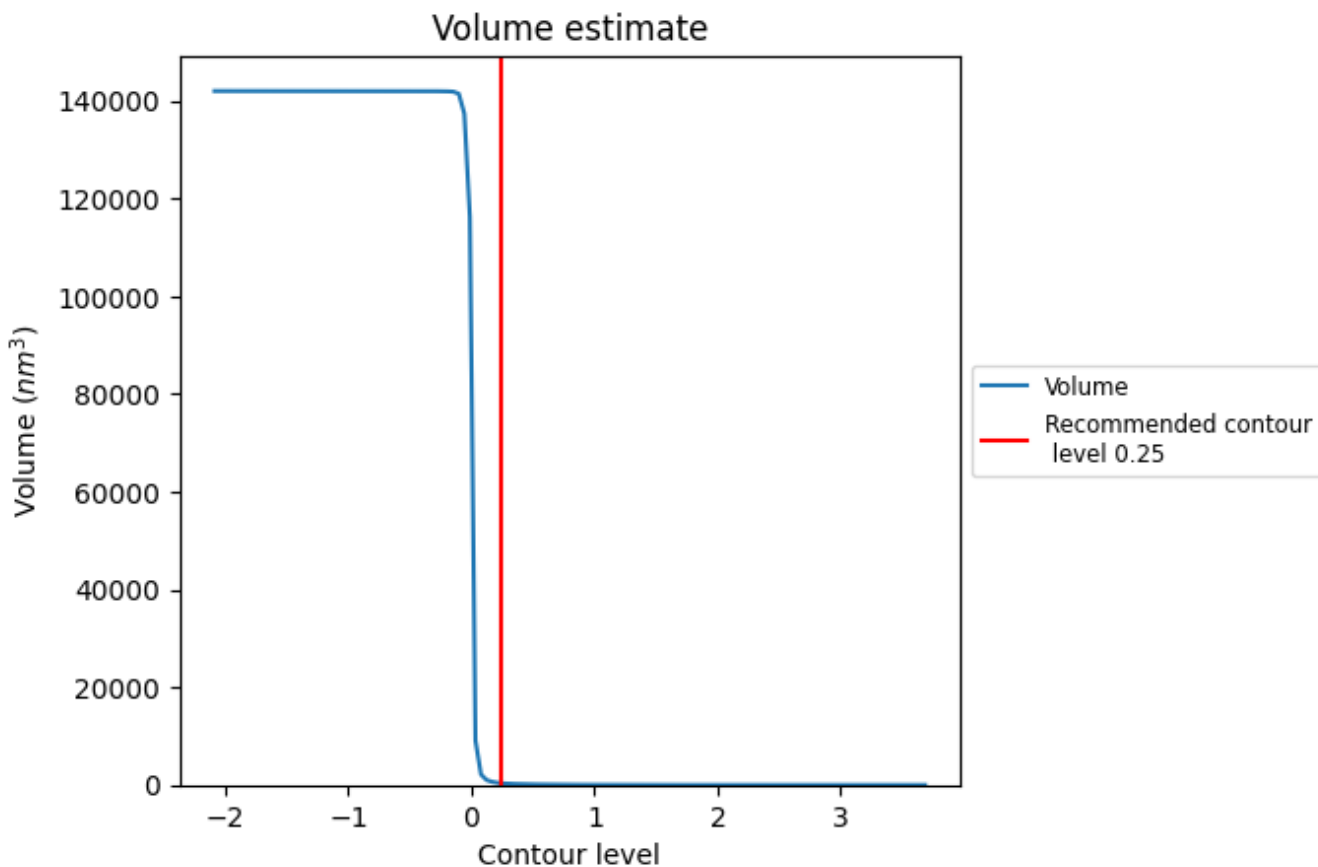
### 7.1 Map-value distribution [i](#)



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



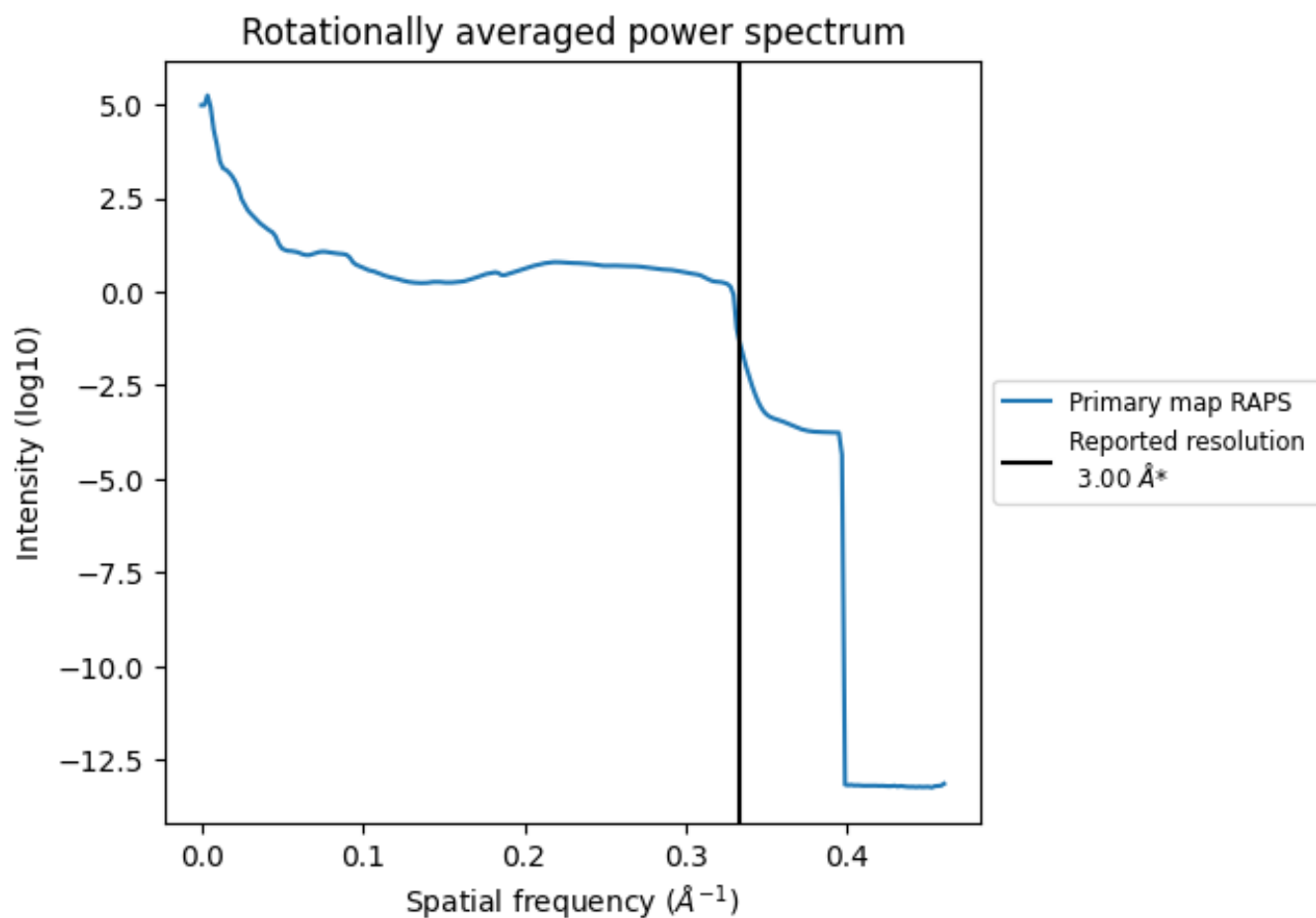
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 341  $\text{nm}^3$ ; this corresponds to an approximate mass of 308 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 Å<sup>-1</sup>

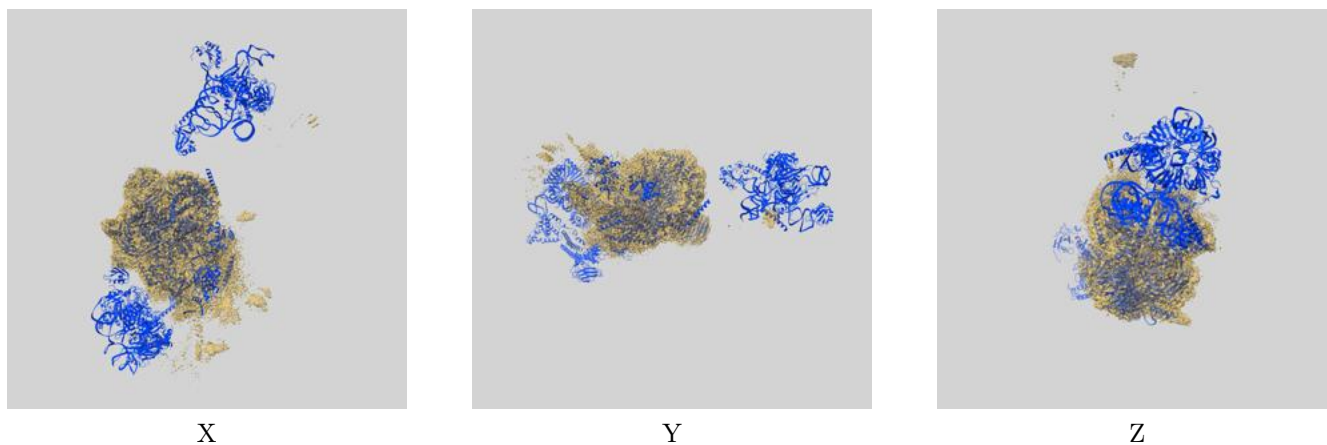
## 8 Fourier-Shell correlation

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

## 9 Map-model fit [i](#)

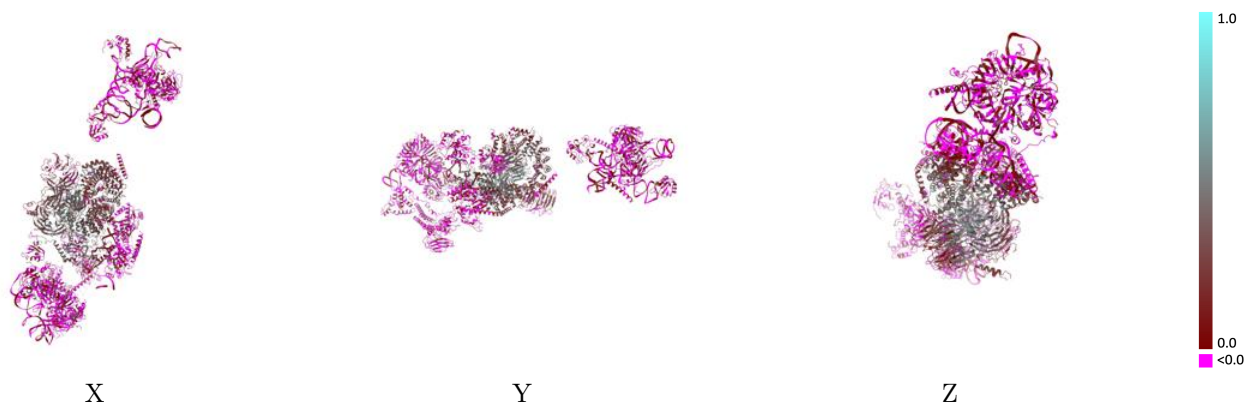
This section contains information regarding the fit between EMDB map EMD-32074 and PDB model 7VPX. Per-residue inclusion information can be found in section 3 on page 11.

### 9.1 Map-model overlay [i](#)



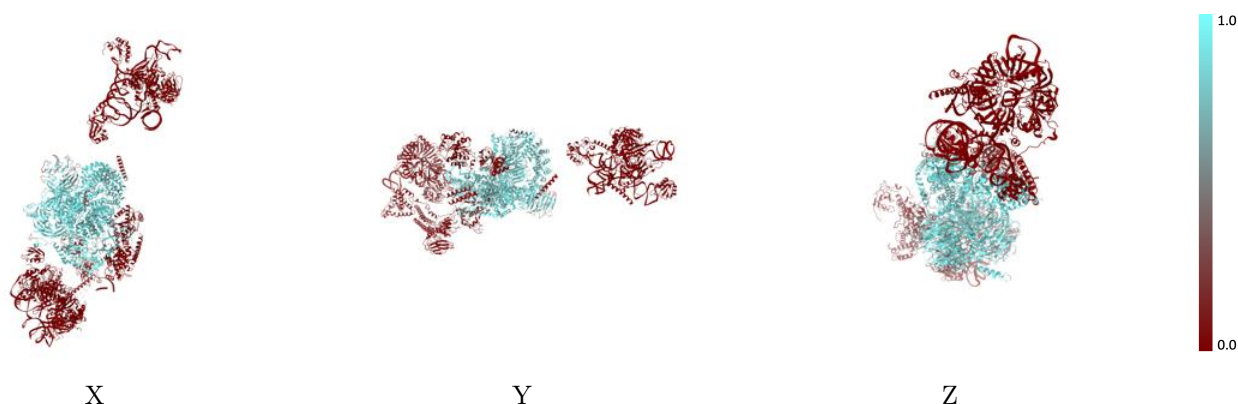
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



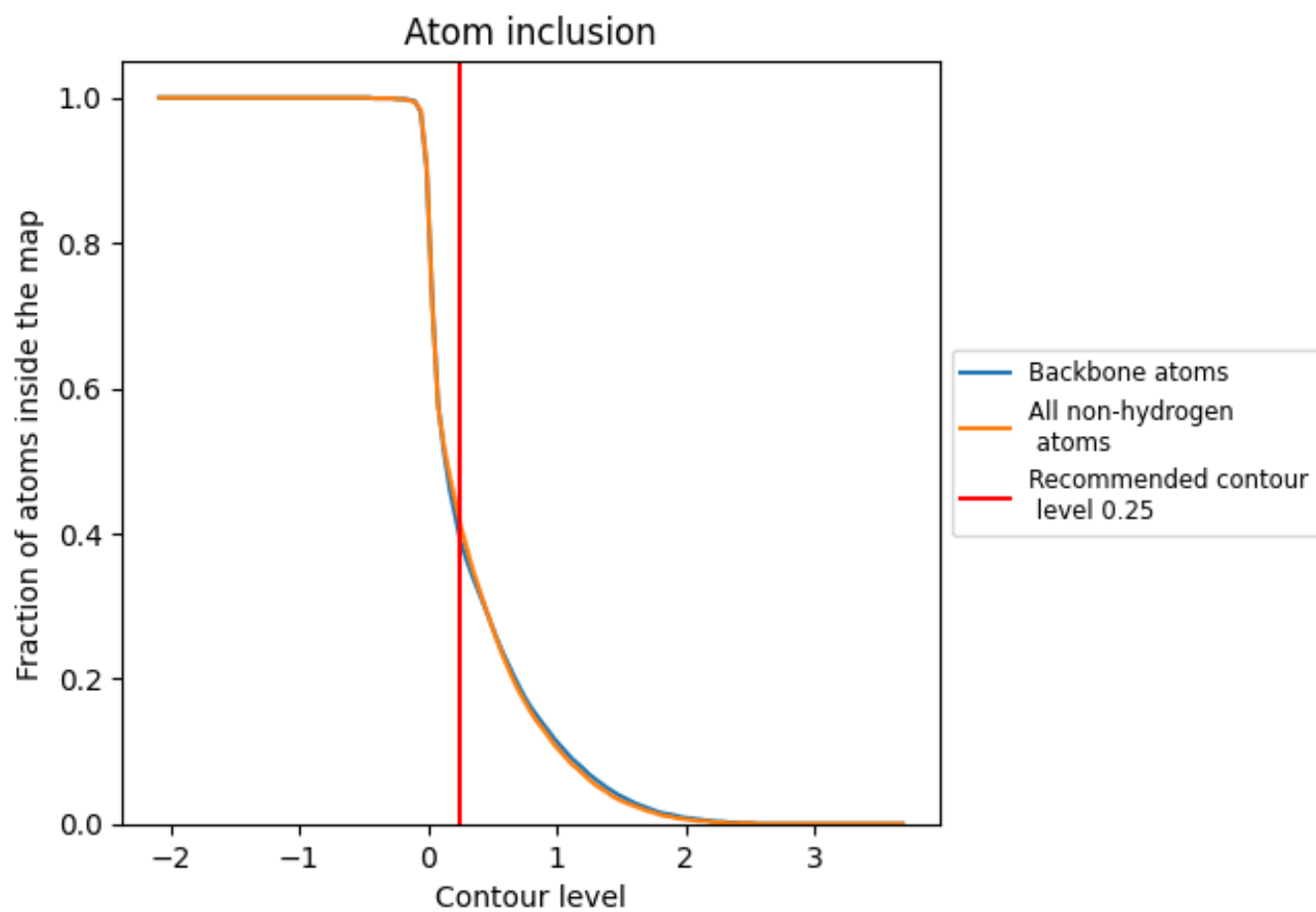
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).









































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 39% of all backbone atoms, 41% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4130	 0.1550
1	 0.8560	 0.3180
2	 0.6680	 0.2780
3	 0.8360	 0.3320
4	 0.1820	 -0.0130
5	 0.9150	 0.4810
6	 0.9070	 0.4080
A	 0.0000	 -0.0220
B	 0.3050	 0.0340
C	 0.3410	 0.1190
D	 0.3080	 0.0390
E	 0.1050	 0.0210
F	 0.0000	 0.0170
G	 0.0000	 -0.0200
H	 0.2320	 0.0690
I	 0.8540	 0.1490
J	 0.7150	 0.1100
K	 0.0000	 0.0440
L	 0.0000	 0.0100
M	 0.0000	 0.0120
N	 0.0000	 0.0110
O	 0.0000	 0.0030
a	 0.0000	 0.0040
b	 0.0000	 0.0060
c	 0.0000	 -0.0130
d	 0.0000	 0.0090
e	 0.0000	 0.0120
f	 0.0030	 -0.0260
g	 0.0030	 -0.0450
h	 0.0000	 -0.0010
i	 0.0000	 0.0050
j	 0.0000	 0.0260
k	 0.0000	 0.0060
l	 0.0000	 0.0120
m	 0.0000	 -0.0060
n	 0.0000	 -0.0180

