



## wwPDB EM Validation Summary Report ⓘ

Apr 1, 2025 – 06:24 pm BST

PDB ID : 6ZYM / pdb\_00006zym  
EMDB ID : EMD-11569  
Title : Human C Complex Spliceosome - High-resolution CORE  
Authors : Bertram, K.; Kastner, B.  
Deposited on : 2020-08-02  
Resolution : 3.40 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.dev117  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

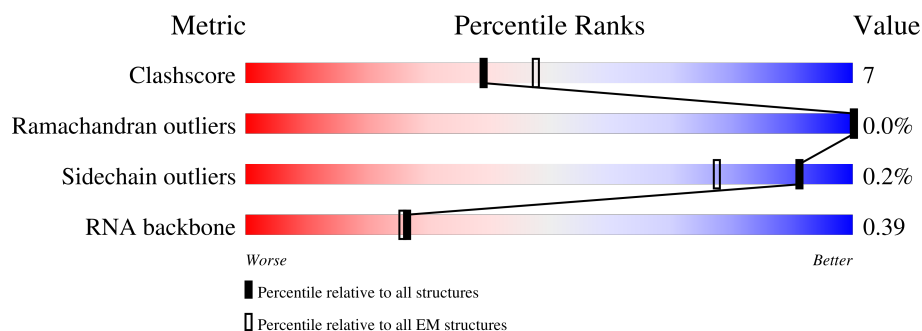
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*




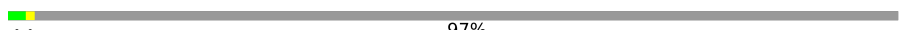



The reported resolution of this entry is 3.40 Å.

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.



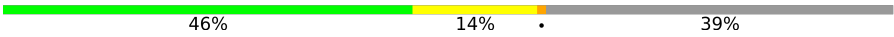







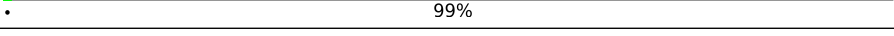


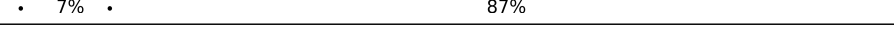
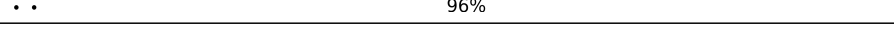
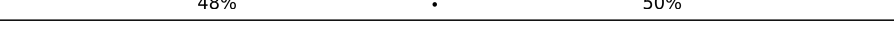
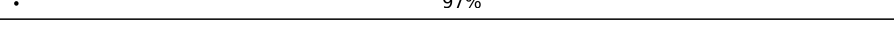
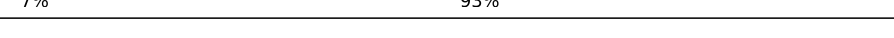
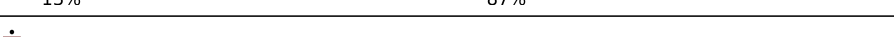

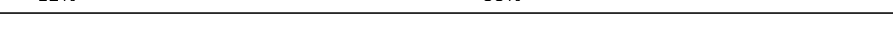
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	2	188	
2	5	116	
3	6	79	
4	9	450	
5	A	1755	
6	B	952	
7	C	536	

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Mol	Chain	Length	Quality of chain
8	D	514	
9	E	579	
10	F	357	
11	L	802	
12	O	848	
13	P	218	
14	Q	144	
15	R	229	
16	S	2752	
17	T	908	
18	V	166	
19	Y	324	
19	Z	324	
20	p	654	
21	r	1227	
22	s	285	
23	t	425	
24	u	178	
25	x	258	

## 2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 48271 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 U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	27	Total	C	N	O	P	0	0
			575	257	99	192	27		

- Molecule 2 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	74	Total	C	N	O	P	0	0
			1548	693	256	525	74		

- Molecule 3 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	6	79	Total	C	N	O	P	0	0
			1690	756	312	543	79		

- Molecule 4 is a protein called Corepressor interacting with RBPJ 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	9	14	Total	C	N	O	S	0	0
			112	68	21	22	1		

- Molecule 5 is a protein called Pre-mRNA-processing-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	1722	Total	C	N	O	S	0	0
			14270	9190	2521	2494	65		

- Molecule 6 is a protein called 116 kDa U5 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	895	Total	C	N	O	S	0	0
			6953	4447	1163	1309	34		

- Molecule 7 is a protein called SNW domain-containing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	224	Total	C	N	O	S	0	0
			1703	1074	308	312	9		

- Molecule 8 is a protein called Pleiotropic regulator 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	315	Total	C	N	O	S	0	0
			2481	1565	451	458	7		

- Molecule 9 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	78	Total	C	N	O	S	0	0
			629	400	107	118	4		

- Molecule 10 is a protein called U5 small nuclear ribonucleoprotein 40 kDa protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	299	Total	C	N	O	S	0	0
			2230	1407	381	430	12		

- Molecule 11 is a protein called Cell division cycle 5-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	202	Total	C	N	O	S	0	0
			1611	1012	297	296	6		

- Molecule 12 is a protein called Crooked neck-like protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	252	Total	C	N	O	S	0	0
			2108	1345	381	377	5		

- Molecule 13 is a protein called Pre-mRNA-splicing factor RBM22.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	195	Total	C	N	O	S	0	0
			1577	991	279	290	17		

- Molecule 14 is a protein called Protein BUD31 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	142	Total	C	N	O	S	0	0
			1162	733	216	202	11		

- Molecule 15 is a protein called Spliceosome-associated protein CWC15 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	87	Total	C	N	O	S	0	0
			681	421	134	125	1		

- Molecule 16 is a protein called Serine/arginine repetitive matrix protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	30	Total	C	N	O	S	0	0
			230	140	49	40	1		

- Molecule 17 is a protein called Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	203	Total	C	N	O	S	0	0
			1669	1071	278	307	13		

- Molecule 18 is a protein called Peptidyl-prolyl cis-trans isomerase-like 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	163	Total	C	N	O	S	0	0
			1081	677	200	199	5		

- Molecule 19 is a RNA chain called pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Y	41	Total	C	N	O	P	0	0
			873	391	155	286	41		
19	Z	13	Total	C	N	O	P	0	0
			276	123	50	90	13		

- Molecule 20 is a protein called WD repeat-containing protein 70.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	p	325	Total	C	N	O	S	0	0
			2372	1493	421	442	16		

- Molecule 21 is a protein called Pre-mRNA-splicing factor ATP-dependent RNA helicase

PRP16.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	r	35	Total	C	N	O	S	0	0
			259	157	50	51	1		

- Molecule 22 is a protein called Pre-mRNA-splicing factor ISY1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	s	20	Total	C	N	O	S	0	0
			158	96	33	28	1		

- Molecule 23 is a protein called Pre-mRNA-splicing factor CWC25 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	t	56	Total	C	N	O		0	0
			418	259	80	79			

- Molecule 24 is a protein called Splicing factor YJU2.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	u	157	Total	C	N	O	S	0	0
			1286	819	226	231	10		

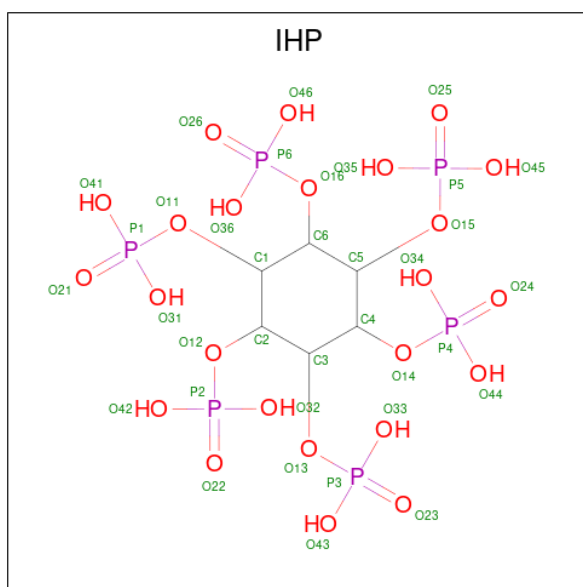
- Molecule 25 is a protein called Protein FRG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	x	30	Total	C	N	O	S	0	0
			239	149	49	40	1		

- Molecule 26 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

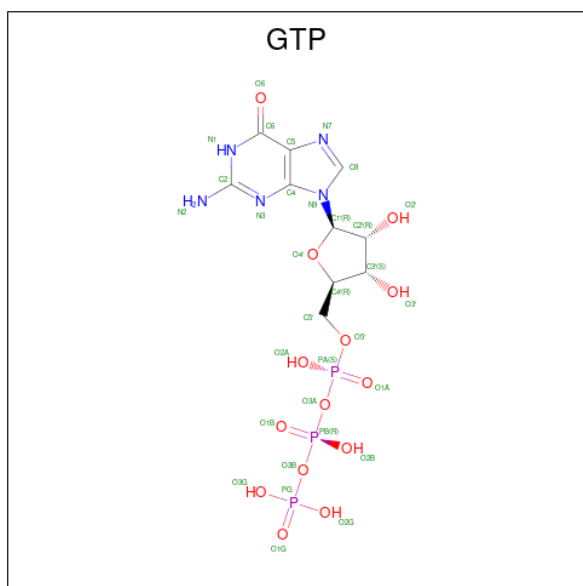
Mol	Chain	Residues	Atoms		AltConf
26	6	5	Total	Mg	0
			5	5	

- Molecule 27 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: C<sub>6</sub>H<sub>18</sub>O<sub>24</sub>P<sub>6</sub>).



Mol	Chain	Residues	Atoms				AltConf
27	A	1	Total	C	O	P	0
			36	6	24	6	

- Molecule 28 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula:  $C_{10}H_{16}N_5O_{14}P_3$ ).



Mol	Chain	Residues	Atoms					AltConf
28	B	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 29 is ZINC ION (CCD ID: ZN) (formula:  $Zn$ ).

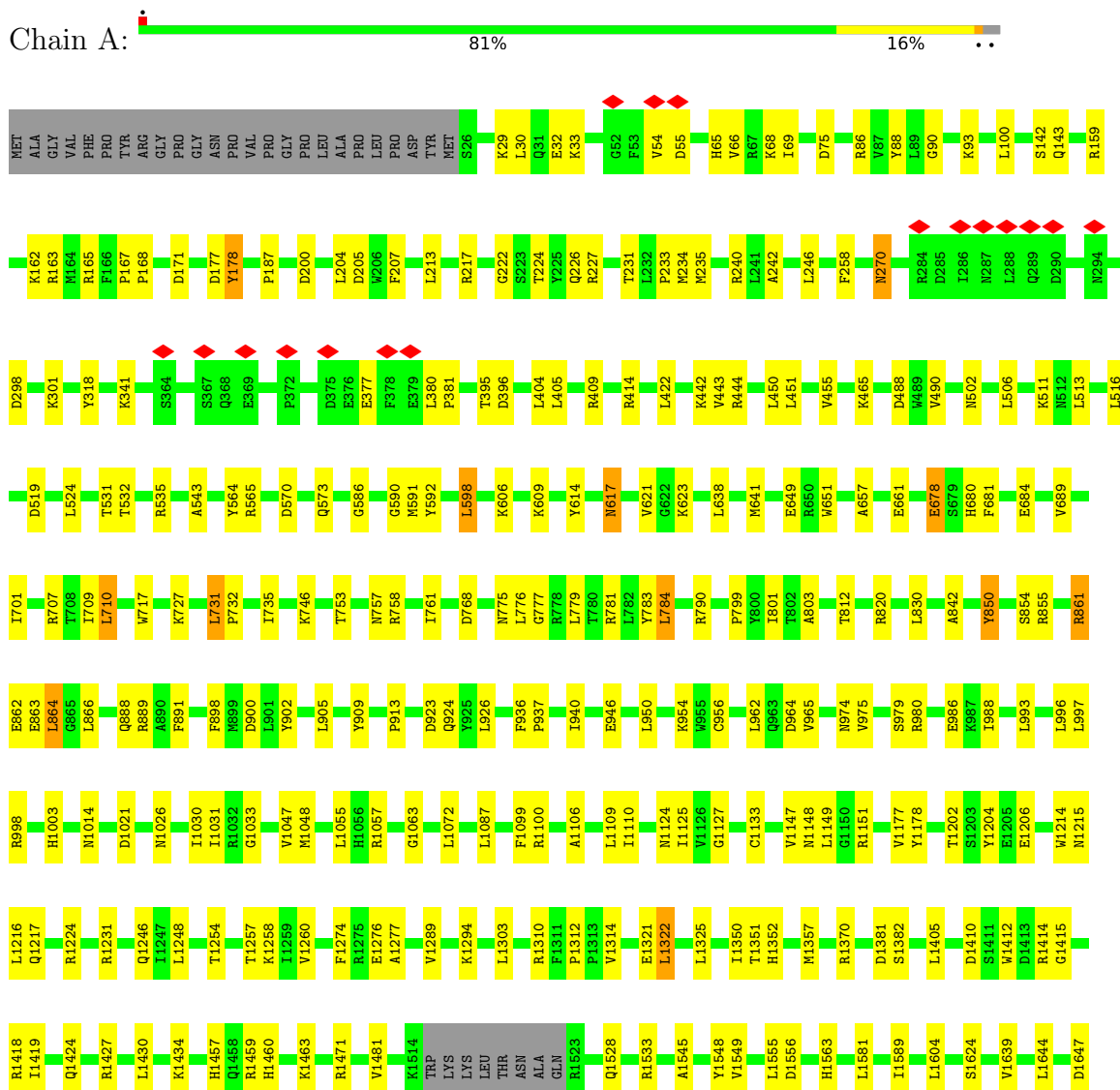


Mol	Chain	Residues	Atoms		AltConf
29	P	3	Total 3	Zn 3	0
29	Q	3	Total 3	Zn 3	0
29	u	1	Total 1	Zn 1	0



[illegible]

- Molecule 5: Pre-mRNA-processing-splicing factor 8





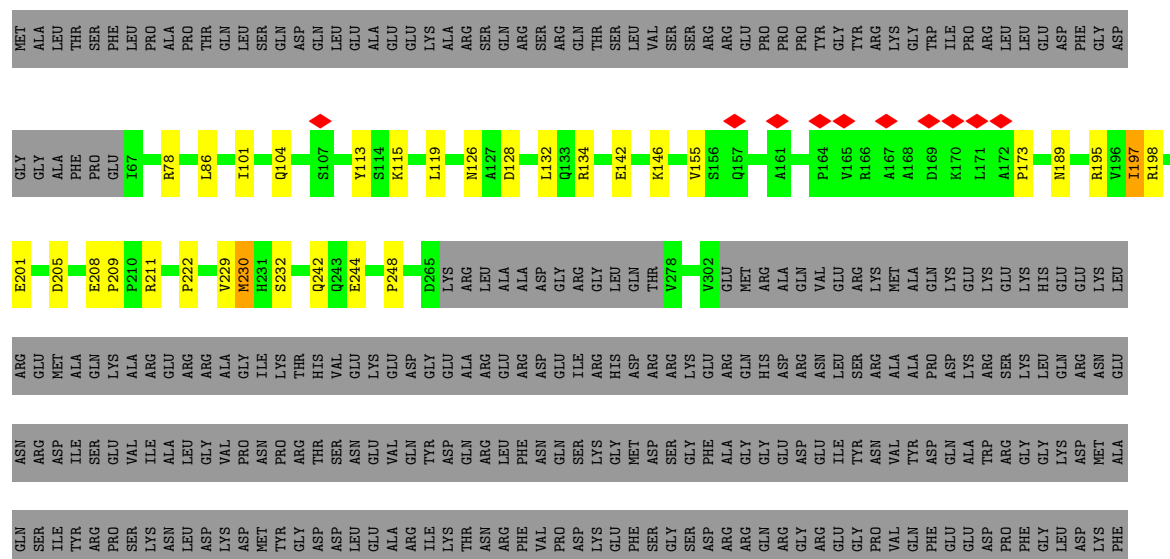
- Molecule 6: 116 kDa U5 small nuclear ribonucleoprotein component

Chain B: 75% 18% 6%



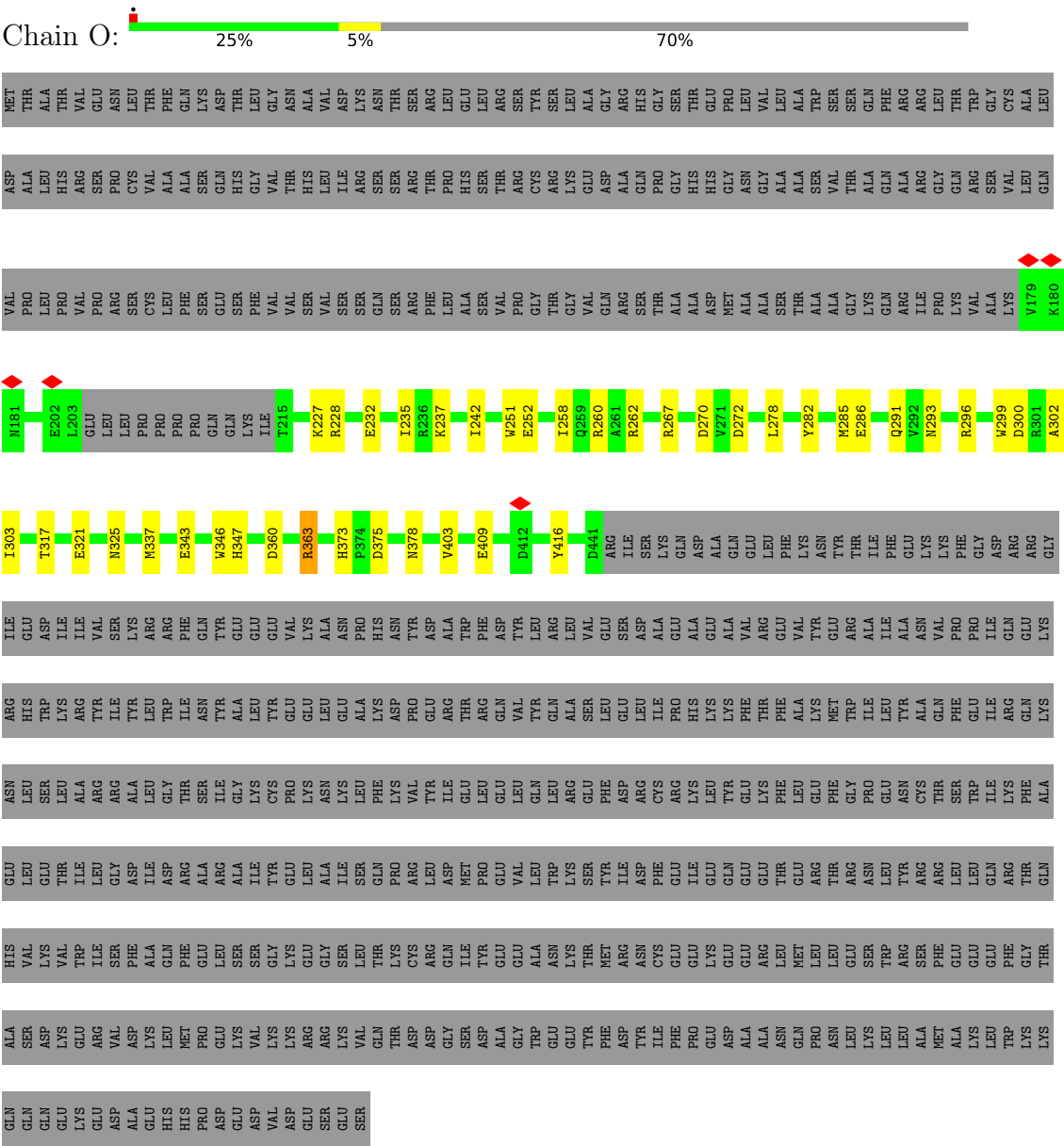
- Molecule 7: SNW domain-containing protein 1

Chain C: 36% 5% 58%

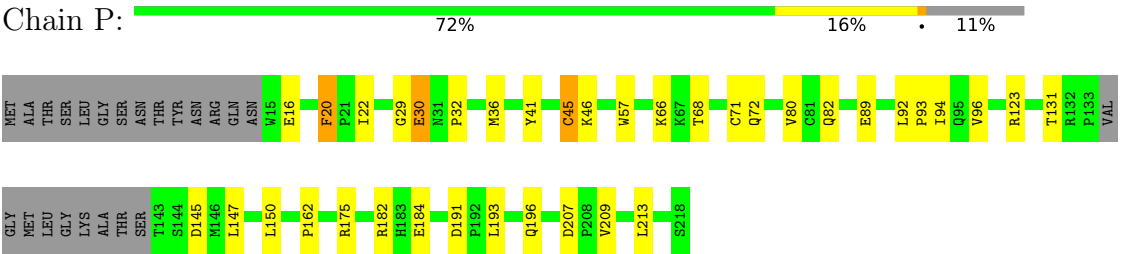








● Molecule 13: Pre-mRNA-splicing factor RBM22



● Molecule 14: Protein BUD31 homolog

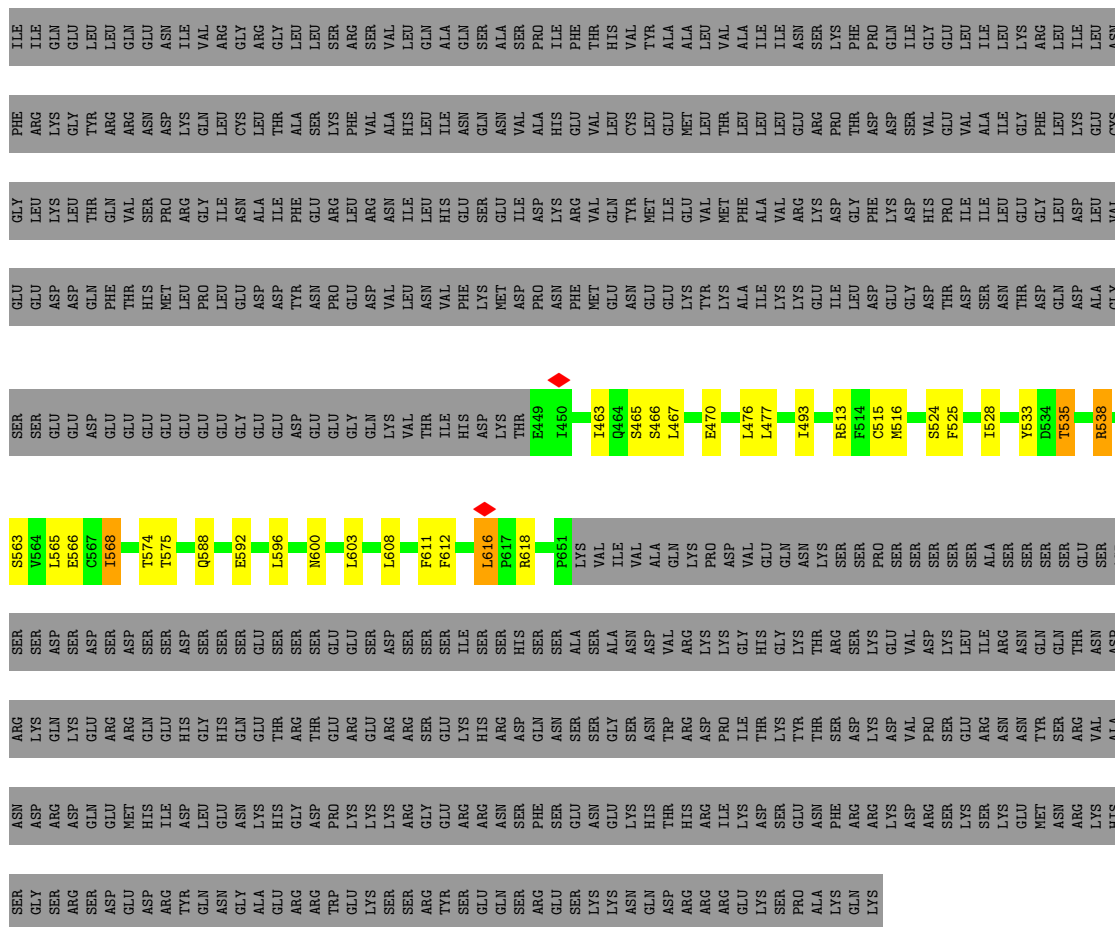




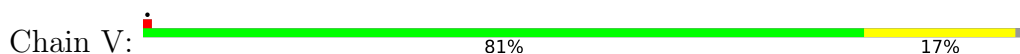




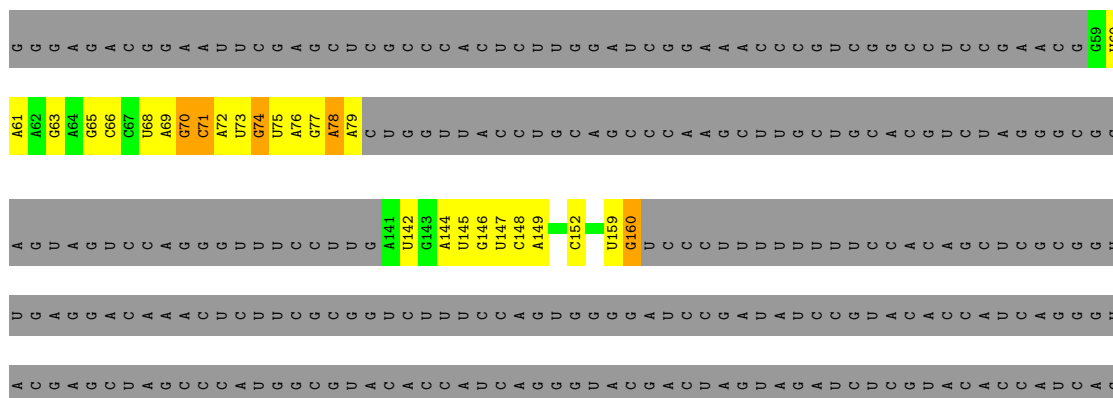




- Molecule 18: Peptidyl-prolyl cis-trans isomerase-like 1



- Molecule 19: pre-mRNA





- Molecule 22: Pre-mRNA-splicing factor ISY1 homolog

Chain s:  7% 93%

MET	A2	R3	N4	E21	GLU	GLY	LVS	VAL	LVS	GLU	ARG	ARG	PRO	PHE	LEU	ALA	SER	GLU	CYS	THR	GLU	LEU	PRO	ALA	GLY	GLU	VAL	LVS	TRP	ARG	ARG	GLN	ILE	ILE	GLY	GLY	ILE	SER	SER	LVS	LVS	VAL	ALA	GLN	ILE	GLN	GLN	ASP	ILE	ARG	ARG	PHE	GLY	GLY	GLU	PHE	ARG	LVS	ASP	LEU	LEU	ASP	SER
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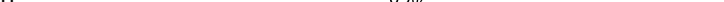
[illegible]

- Molecule 23: Pre-mRNA-splicing factor CWC25 homolog

Chain t:  13% 87%

[illegible]

- Molecule 24: Splicing factor YJU2

Chain u:  83% 5% 12%

Sequence logo for the 1000bp upstream region of the HET gene. The y-axis represents information content in bits, ranging from 0 to 1.5. The x-axis shows positions from -1000 to +1000. The HET gene is indicated by a red arrow at position 0. The sequence logo shows a strong enrichment of the TATA box (TATAAT) around position -30. Other notable features include a GC-rich region around position +100 and a T-rich region around position +200.

- Molecule 25: Protein FRG1

Chain x:  12% 88%

[illegible]

ARG	SER	CYS	ALA	GLU	ARG	GLU	THR	LYS	LYS	LYS	ASP	ASP	ILE	PRO	GLU	GLU	ASP	LYS	GLY	ASN	VAL	LYS	GLN	CYS	GLU	ILE	ASN	TYR	VAL	LYS	LYS	PHE	GLN	SER	PHE	GLN	ASP	HIS	LYS	LEU	LYS	ILE	SER	LYS	GLU	ASP	SER	K229	D237	K258
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	411539	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 ( $e^-/\text{\AA}^2$ )	120	Depositor
Minimum defocus (nm)	-1	Depositor
Maximum defocus (nm)	-3	Depositor
Magnification	132000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.336	Depositor
Minimum map value	-0.185	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	466.39996, 466.39996, 466.39996	wwPDB
Map dimensions	440, 440, 440	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	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: GTP, MG, IHP, 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	2	0.84	1/642 (0.2%)	1.08	3/998 (0.3%)
2	5	0.77	0/1725	1.04	5/2681 (0.2%)
3	6	0.86	0/1892	0.96	2/2947 (0.1%)
4	9	0.26	0/113	0.45	0/148
5	A	0.55	4/14669 (0.0%)	0.70	23/19894 (0.1%)
6	B	0.47	2/7112 (0.0%)	0.67	9/9681 (0.1%)
7	C	0.48	1/1738 (0.1%)	0.69	4/2353 (0.2%)
8	D	0.68	2/2547 (0.1%)	0.76	4/3471 (0.1%)
9	E	0.39	0/650	0.64	1/886 (0.1%)
10	F	0.47	1/2282 (0.0%)	0.76	9/3109 (0.3%)
11	L	0.46	0/1641	0.65	1/2208 (0.0%)
12	O	0.45	0/2160	0.65	4/2920 (0.1%)
13	P	0.60	2/1613 (0.1%)	0.71	1/2174 (0.0%)
14	Q	0.81	7/1187 (0.6%)	0.96	10/1591 (0.6%)
15	R	0.55	0/690	0.71	0/922
16	S	0.56	0/233	0.70	0/312
17	T	0.50	1/1704 (0.1%)	1.08	10/2291 (0.4%)
18	V	0.33	0/1105	0.58	0/1511
19	Y	0.67	0/975	1.14	9/1514 (0.6%)
19	Z	0.89	0/307	0.87	0/476
20	p	0.48	1/2424 (0.0%)	0.77	5/3295 (0.2%)
21	r	0.36	0/262	0.55	0/356
22	s	0.38	0/158	0.50	0/209
23	t	0.59	0/424	0.74	1/570 (0.2%)
24	u	0.91	9/1312 (0.7%)	1.10	9/1764 (0.5%)
25	x	0.36	0/240	0.58	0/317
All	All	0.58	31/49805 (0.1%)	0.78	110/68598 (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	A	0	2
6	B	0	1
20	p	0	3
24	u	0	1
All	All	0	7

The worst 5 of 31 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	u	136	VAL	CB-CG1	-15.50	1.20	1.52
14	Q	137	CYS	CB-SG	-12.19	1.61	1.82
24	u	136	VAL	CB-CG2	-9.93	1.31	1.52
24	u	46	CYS	CB-SG	9.92	1.99	1.82
14	Q	134	CYS	CB-SG	-9.87	1.65	1.82

The worst 5 of 110 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	T	538	ARG	NE-CZ-NH2	-32.07	104.27	120.30
5	A	506	LEU	CB-CG-CD1	-24.98	68.54	111.00
17	T	538	ARG	NE-CZ-NH1	20.37	130.49	120.30
24	u	140	ARG	NE-CZ-NH2	-18.29	111.16	120.30
24	u	136	VAL	CG1-CB-CG2	-17.26	83.29	110.90

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	A	1649	LYS	Peptide
5	A	380	LEU	Peptide
6	B	366	GLN	Peptide
20	p	227	CYS	Peptide
20	p	352	GLN	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	575	0	288	7	0
2	5	1548	0	785	3	0
3	6	1690	0	855	12	0
4	9	112	0	109	3	0
5	A	14270	0	14118	188	0
6	B	6953	0	6837	109	0
7	C	1703	0	1692	28	0
8	D	2481	0	2431	52	0
9	E	629	0	572	13	0
10	F	2230	0	2087	52	0
11	L	1611	0	1588	16	0
12	O	2108	0	1963	26	0
13	P	1577	0	1543	30	0
14	Q	1162	0	1163	12	0
15	R	681	0	635	9	0
16	S	230	0	238	3	0
17	T	1669	0	1662	20	0
18	V	1081	0	929	20	0
19	Y	873	0	440	9	0
19	Z	276	0	143	2	0
20	p	2372	0	2209	0	0
21	r	259	0	213	0	0
22	s	158	0	162	0	0
23	t	418	0	379	0	0
24	u	1286	0	1274	0	0
25	x	239	0	252	0	0
26	6	5	0	0	0	0
27	A	36	0	6	4	0
28	B	32	0	12	0	0
29	P	3	0	0	0	0
29	Q	3	0	0	0	0
29	u	1	0	0	0	0
All	All	48271	0	44585	541	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 7.

The worst 5 of 541 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)
5:A:75:ASP:HA	5:A:502:ASN:HD22	1.45	0.80
13:P:96:VAL:HG21	13:P:213:LEU:HD23	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:591:MET:HG3	5:A:598:LEU:HD21	1.64	0.78
5:A:993:LEU:O	5:A:997:LEU:HB2	1.83	0.77
18:V:53:PHE:HB3	18:V:56:ILE:HD11	1.67	0.75

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	
4	9	12/450 (3%)	10 (83%)	2 (17%)	0	100	100
5	A	1718/1755 (98%)	1567 (91%)	150 (9%)	1 (0%)	48	78
6	B	893/952 (94%)	809 (91%)	84 (9%)	0	100	100
7	C	220/536 (41%)	187 (85%)	33 (15%)	0	100	100
8	D	313/514 (61%)	277 (88%)	36 (12%)	0	100	100
9	E	76/579 (13%)	66 (87%)	10 (13%)	0	100	100
10	F	297/357 (83%)	262 (88%)	35 (12%)	0	100	100
11	L	198/802 (25%)	176 (89%)	22 (11%)	0	100	100
12	O	248/848 (29%)	229 (92%)	19 (8%)	0	100	100
13	P	191/218 (88%)	175 (92%)	16 (8%)	0	100	100
14	Q	140/144 (97%)	126 (90%)	14 (10%)	0	100	100
15	R	83/229 (36%)	77 (93%)	6 (7%)	0	100	100
16	S	28/2752 (1%)	23 (82%)	5 (18%)	0	100	100
17	T	201/908 (22%)	184 (92%)	17 (8%)	0	100	100
18	V	161/166 (97%)	149 (92%)	12 (8%)	0	100	100
20	p	321/654 (49%)	273 (85%)	48 (15%)	0	100	100
21	r	33/1227 (3%)	30 (91%)	3 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	s	18/285 (6%)	16 (89%)	2 (11%)	0	100	100
23	t	54/425 (13%)	54 (100%)	0	0	100	100
24	u	153/178 (86%)	131 (86%)	22 (14%)	0	100	100
25	x	28/258 (11%)	26 (93%)	2 (7%)	0	100	100
All	All	5386/14237 (38%)	4847 (90%)	538 (10%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	A	803	ALA

### 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	
4	9	11/411 (3%)	11 (100%)	0	100	100
5	A	1528/1584 (96%)	1524 (100%)	4 (0%)	91	95
6	B	756/847 (89%)	756 (100%)	0	100	100
7	C	173/459 (38%)	173 (100%)	0	100	100
8	D	271/441 (62%)	271 (100%)	0	100	100
9	E	65/502 (13%)	65 (100%)	0	100	100
10	F	231/300 (77%)	231 (100%)	0	100	100
11	L	158/709 (22%)	158 (100%)	0	100	100
12	O	201/751 (27%)	201 (100%)	0	100	100
13	P	175/197 (89%)	175 (100%)	0	100	100
14	Q	125/130 (96%)	125 (100%)	0	100	100
15	R	64/203 (32%)	64 (100%)	0	100	100
16	S	24/2432 (1%)	24 (100%)	0	100	100
17	T	186/838 (22%)	186 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
18	V	87/134 (65%)	87 (100%)	0	100	100
20	p	234/572 (41%)	234 (100%)	0	100	100
21	r	23/1074 (2%)	22 (96%)	1 (4%)	25	50
22	s	14/240 (6%)	13 (93%)	1 (7%)	12	37
23	t	36/381 (9%)	36 (100%)	0	100	100
24	u	139/167 (83%)	138 (99%)	1 (1%)	81	88
25	x	23/223 (10%)	23 (100%)	0	100	100
All	All	4524/12595 (36%)	4517 (100%)	7 (0%)	91	96

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	A	617	ASN
21	r	380	ASN
24	u	136	VAL
22	s	4	ASN
5	A	409	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
20	p	480	HIS
12	O	325	ASN
8	D	287	HIS
6	B	903	HIS
9	E	128	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	26/188 (13%)	13 (50%)	2 (7%)
19	Y	39/324 (12%)	23 (58%)	0
19	Z	12/324 (3%)	1 (8%)	0
2	5	73/116 (62%)	11 (15%)	1 (1%)
3	6	78/79 (98%)	22 (28%)	0
All	All	228/1031 (22%)	70 (30%)	3 (1%)

5 of 70 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	19	G
1	2	22	U
1	2	24	A
1	2	25	G
1	2	29	A

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	28	C
1	2	39	U
2	5	23	C

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 12 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
28	GTP	B	1001	6	26,34,34	1.35	2 (7%)	32,54,54	1.86	8 (25%)
27	IHP	A	3001	-	36,36,36	0.85	0	54,60,60	1.38	6 (11%)

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
28	GTP	B	1001	6	-	8/18/38/38	0/3/3/3
27	IHP	A	3001	-	-	7/30/54/54	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	B	1001	GTP	C5-C6	-4.92	1.37	1.47
28	B	1001	GTP	C5-C4	-2.08	1.37	1.43

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	B	1001	GTP	C3'-C2'-C1'	4.66	108.00	100.98
27	A	3001	IHP	C6-C1-C2	3.80	118.72	110.41
28	B	1001	GTP	C5-C6-N1	3.54	120.20	113.95
28	B	1001	GTP	C2-N1-C6	-3.45	118.75	125.10
27	A	3001	IHP	C5-C6-C1	3.20	117.42	110.41

There are no chirality outliers.

5 of 15 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
27	A	3001	IHP	C1-O11-P1-O21
27	A	3001	IHP	C2-O12-P2-O22
27	A	3001	IHP	C4-O14-P4-O24
27	A	3001	IHP	C5-O15-P5-O25
28	B	1001	GTP	C5'-O5'-PA-O3A

There are no ring outliers.

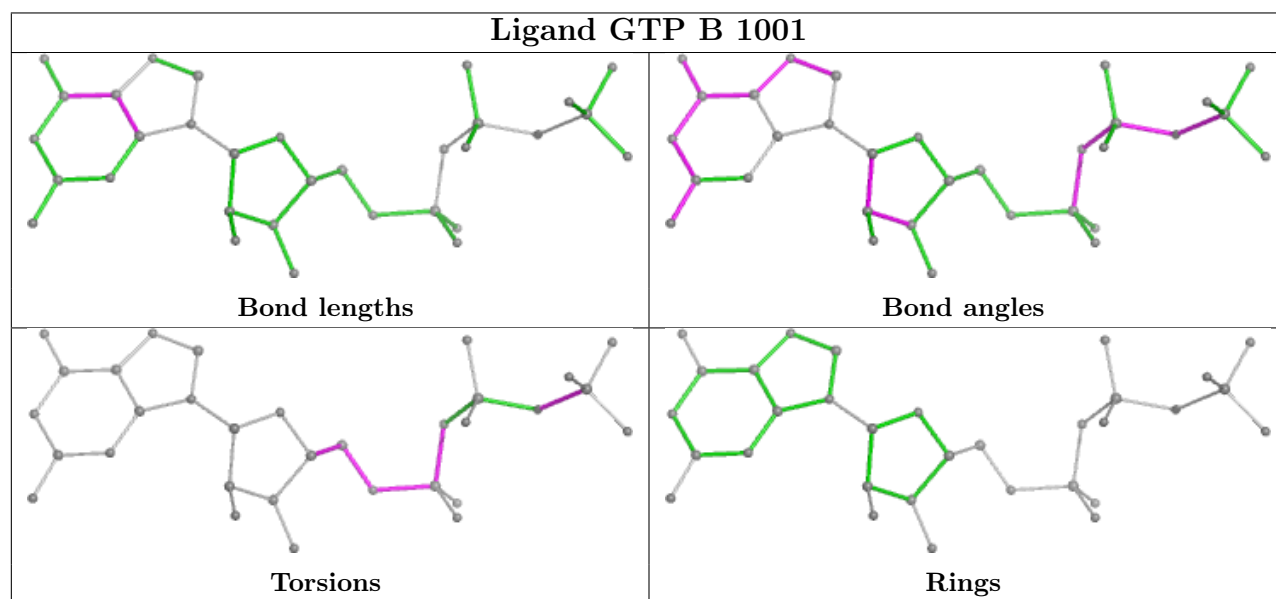
1 monomer is involved in 4 short contacts:

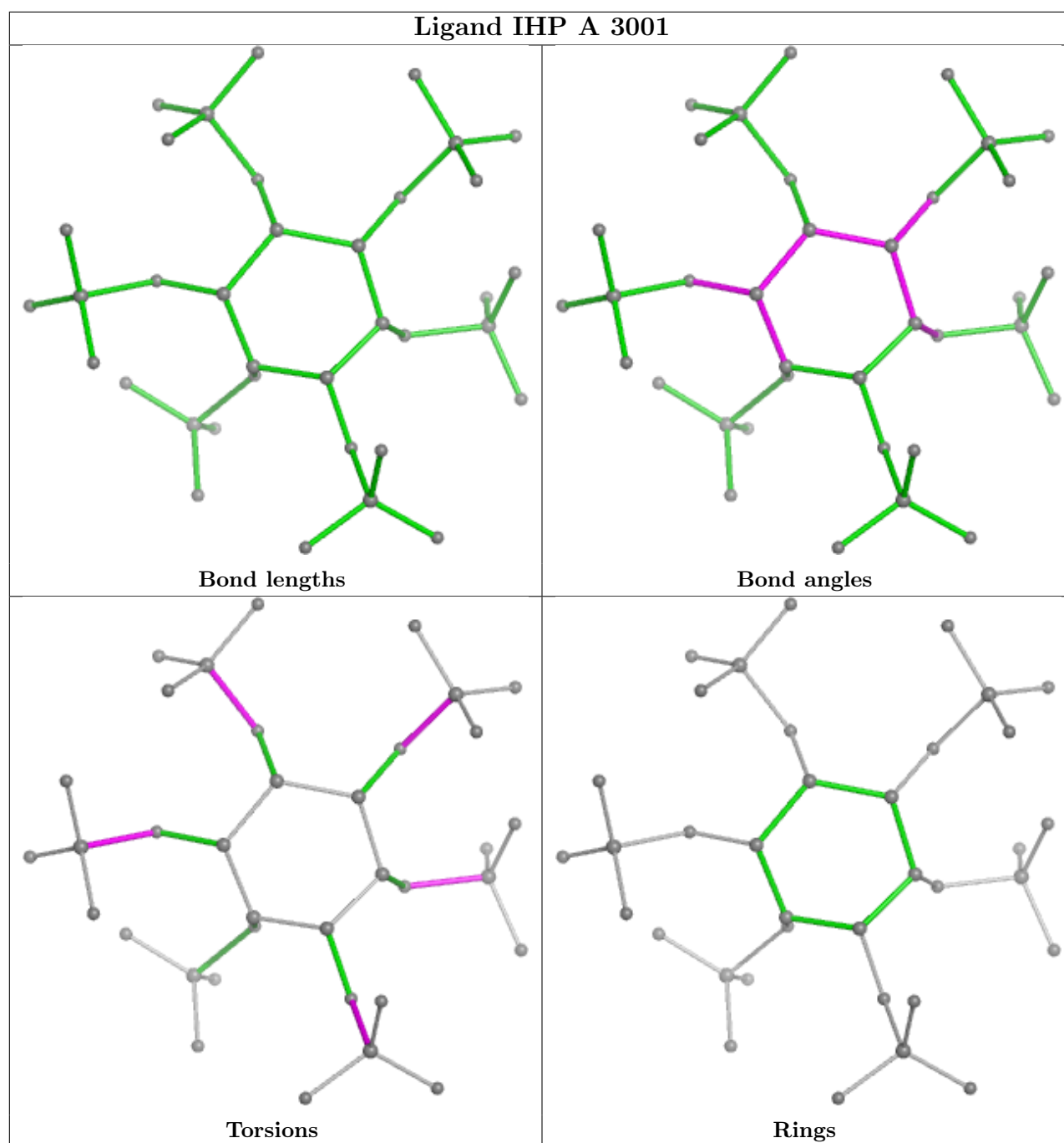
Mol	Chain	Res	Type	Clashes	Symm-Clashes
27	A	3001	IHP	4	0

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.

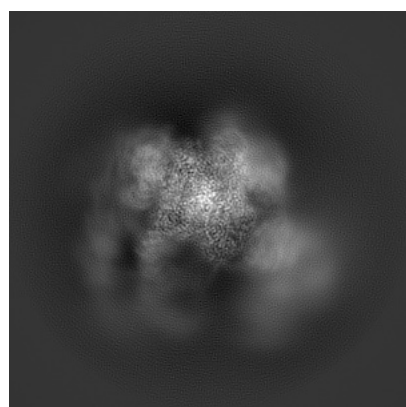
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11569. These allow visual inspection of the internal detail of the map and identification of artifacts.

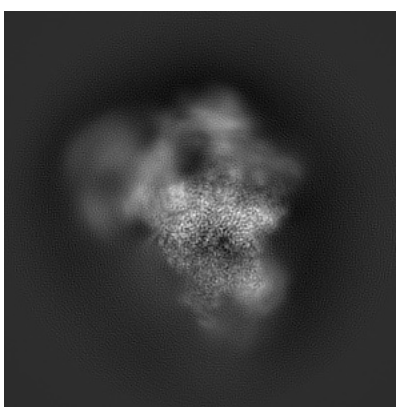
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

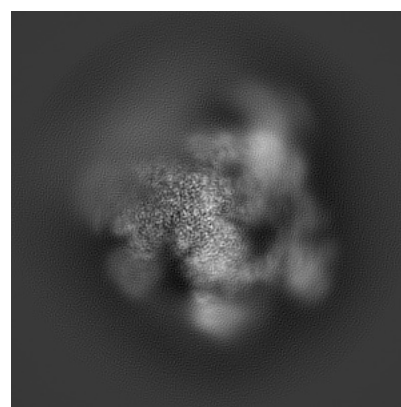
#### 6.1.1 Primary map



X



Y

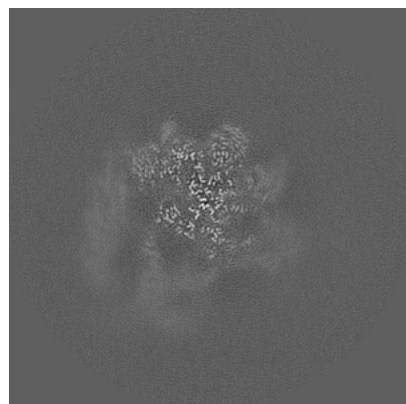


Z

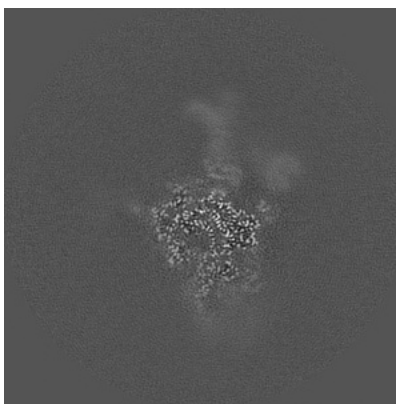
The images above show the map projected in three orthogonal directions.

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

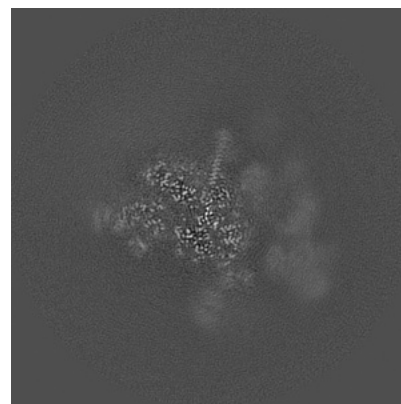
#### 6.2.1 Primary map



X Index: 220



Y Index: 220

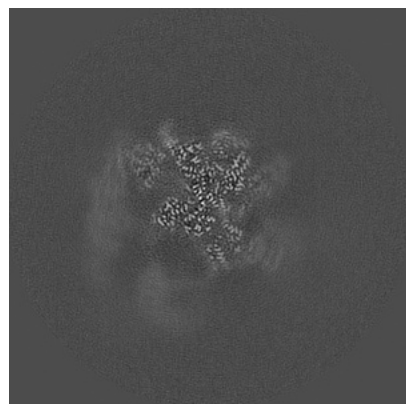


Z Index: 220

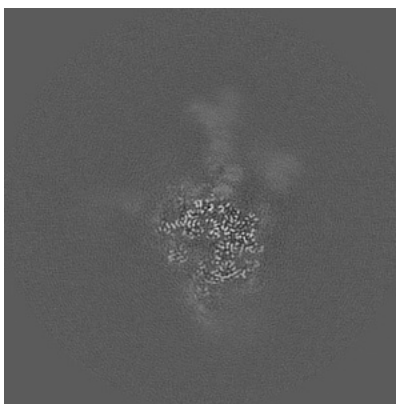
The images above show central slices of the map in three orthogonal directions.

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

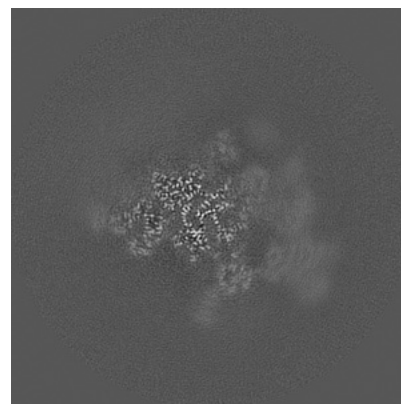
### 6.3.1 Primary map



X Index: 213



Y Index: 216

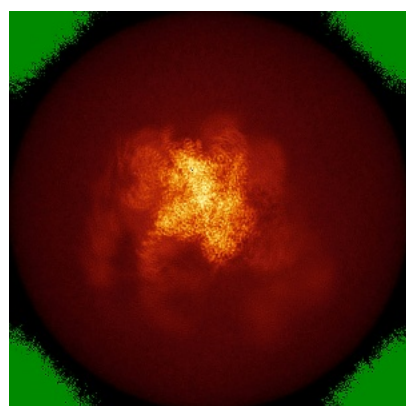


Z Index: 227

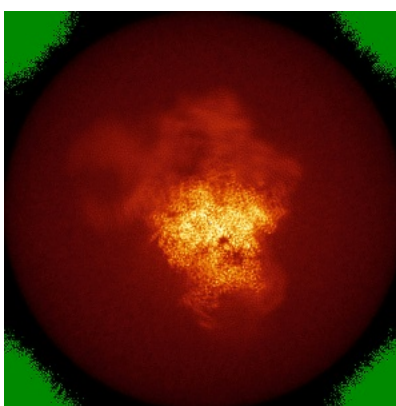
The images above show the largest variance slices of the map in three orthogonal directions.

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

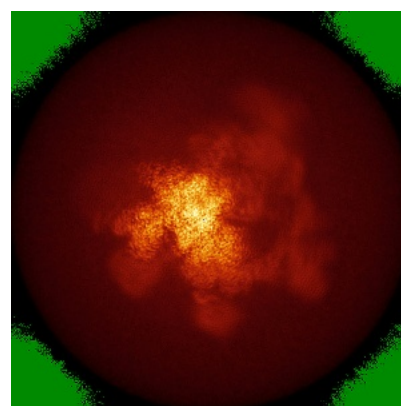
### 6.4.1 Primary map



X



Y

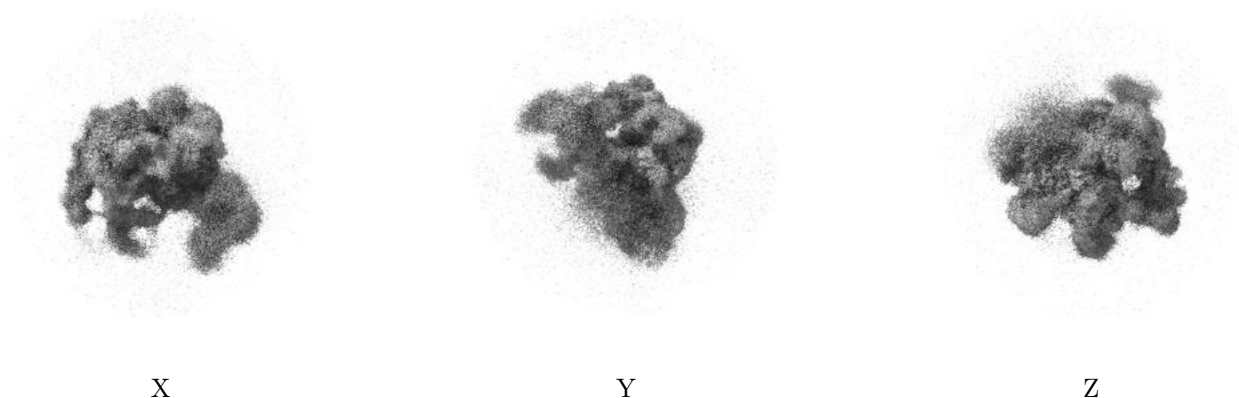


Z

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

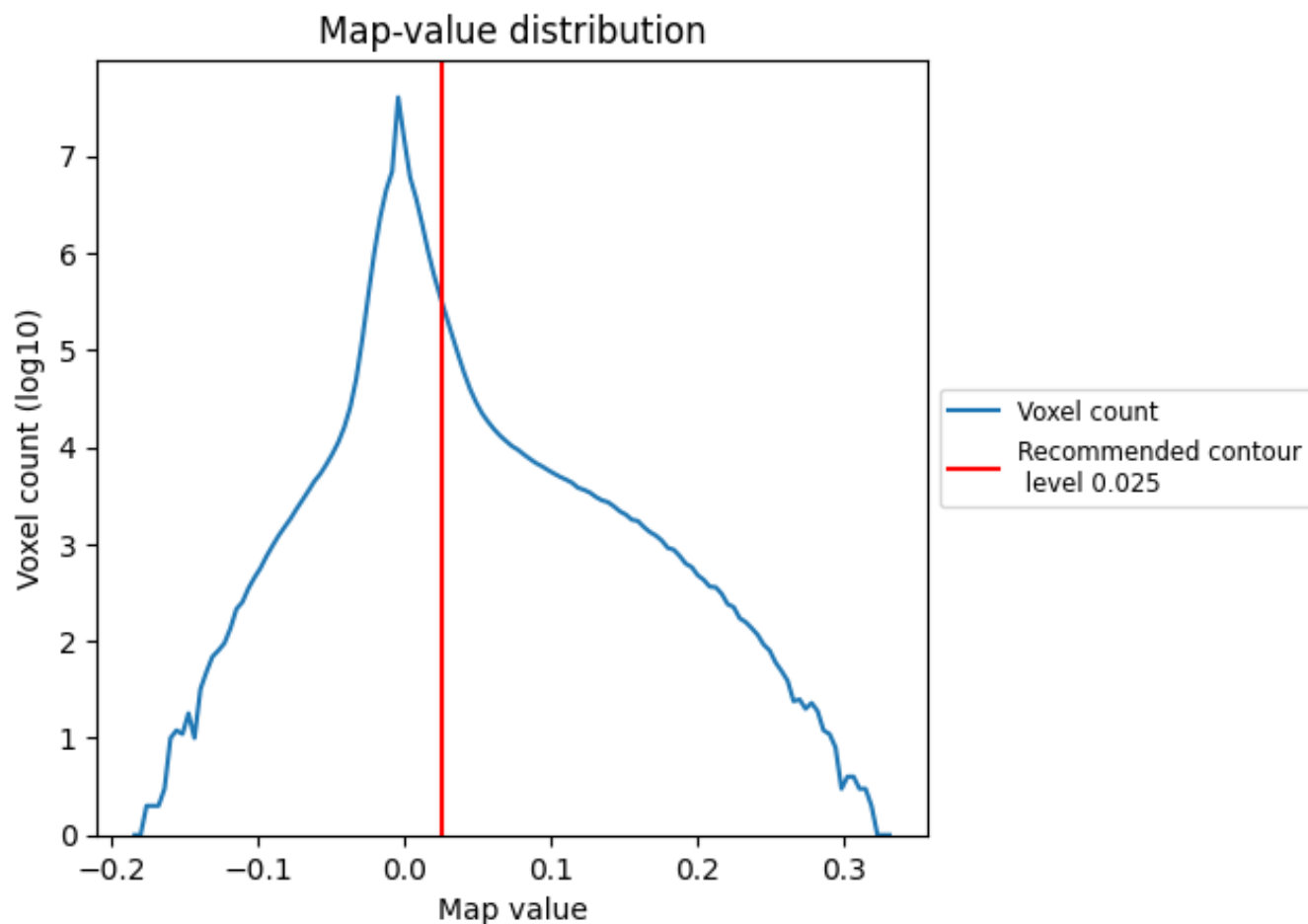
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

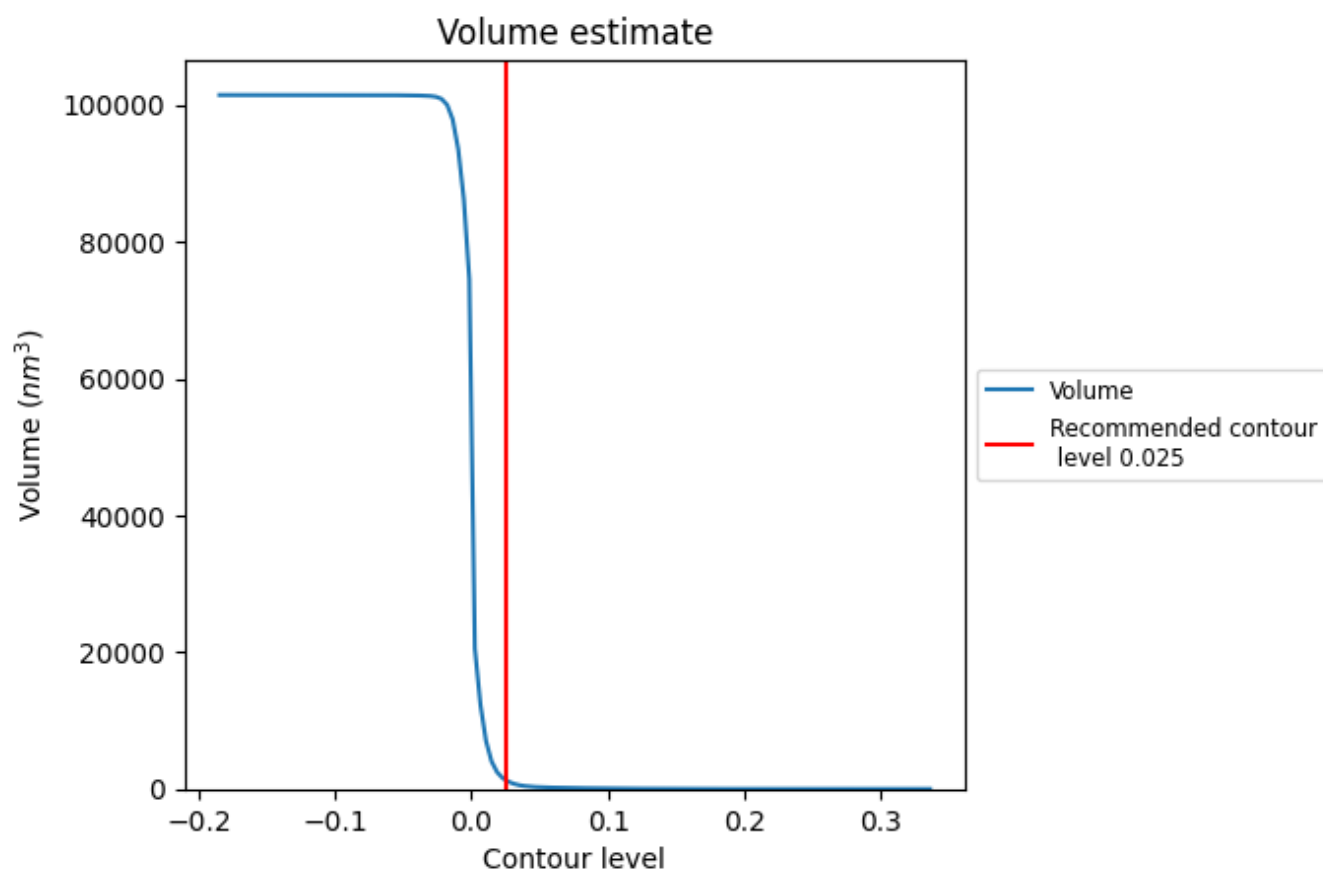
This section contains the results of statistical analysis of the map.

### 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.

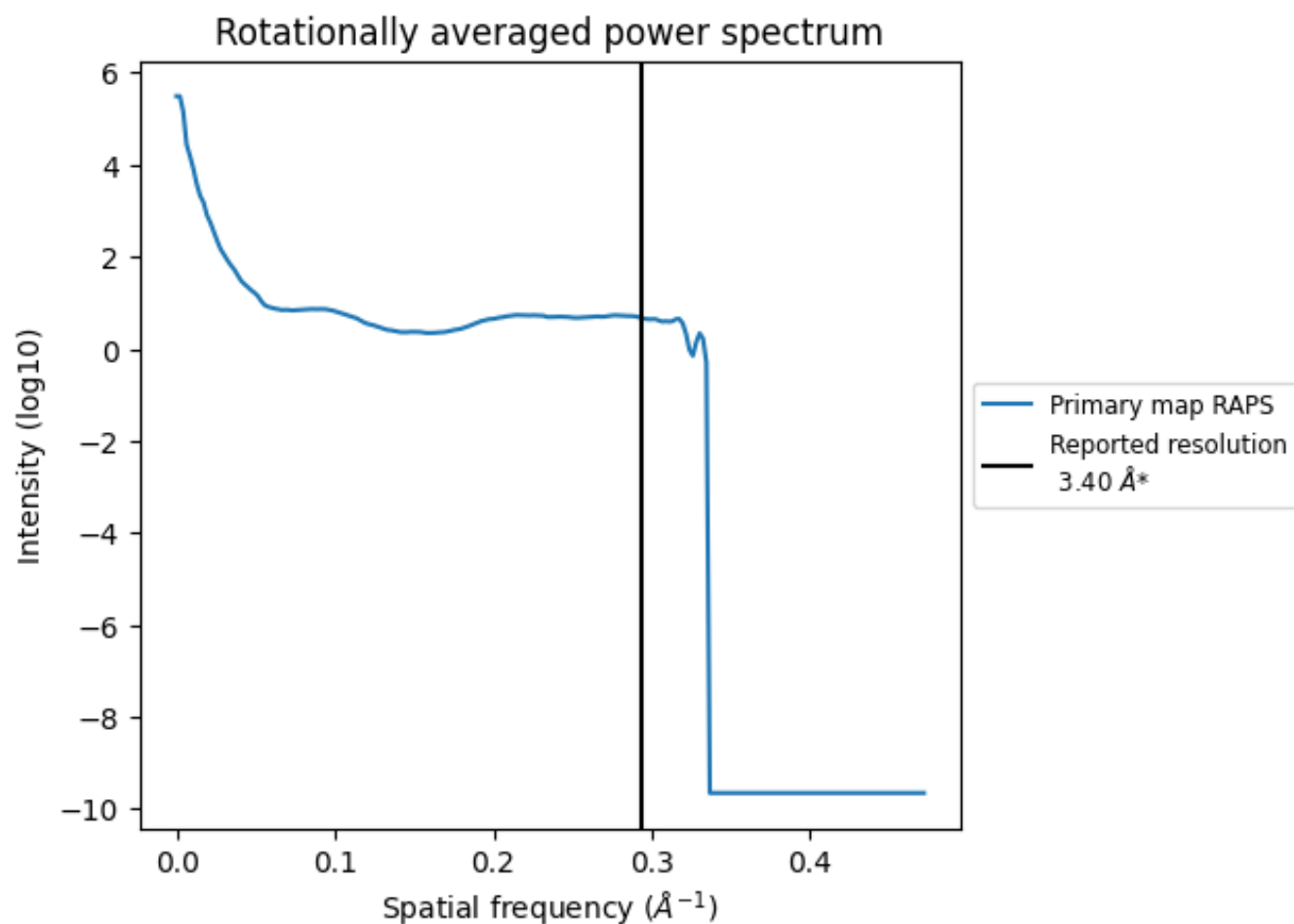
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1311  $\text{nm}^3$ ; this corresponds to an approximate mass of 1184 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 0.294 Å<sup>-1</sup>



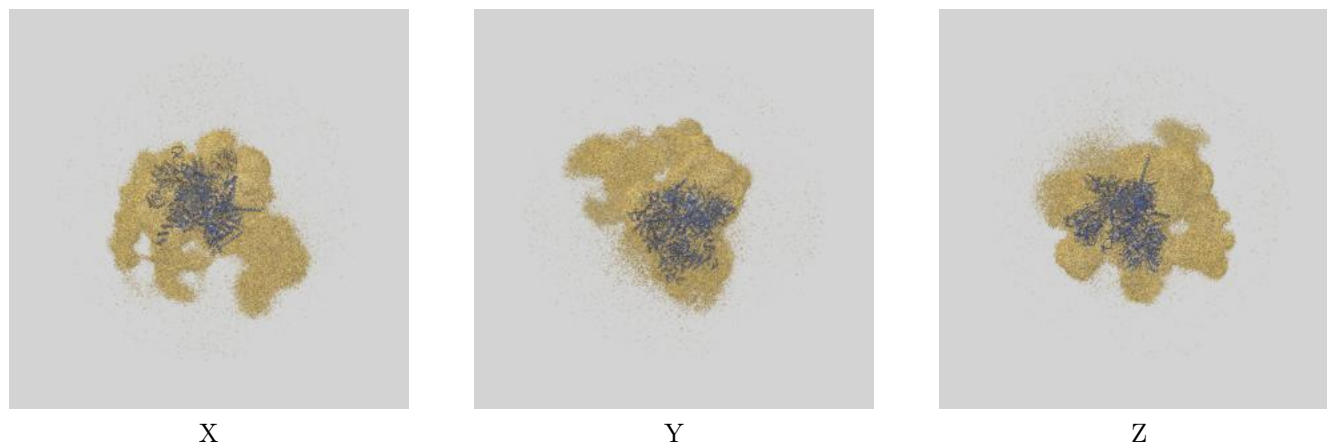
## 8 Fourier-Shell correlation ⓘ

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

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

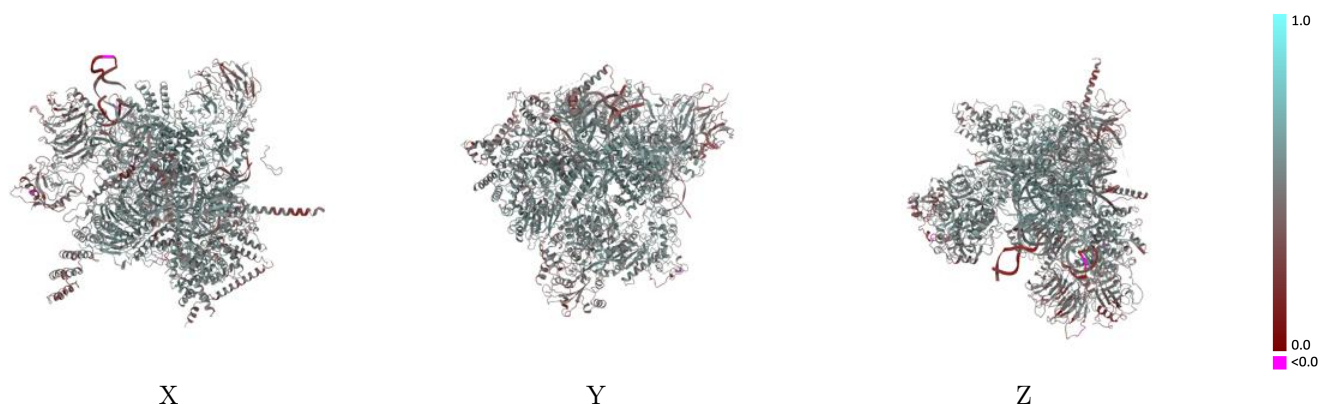
This section contains information regarding the fit between EMDB map EMD-11569 and PDB model 6ZYM. Per-residue inclusion information can be found in [section 3](#) on [page 10](#).

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



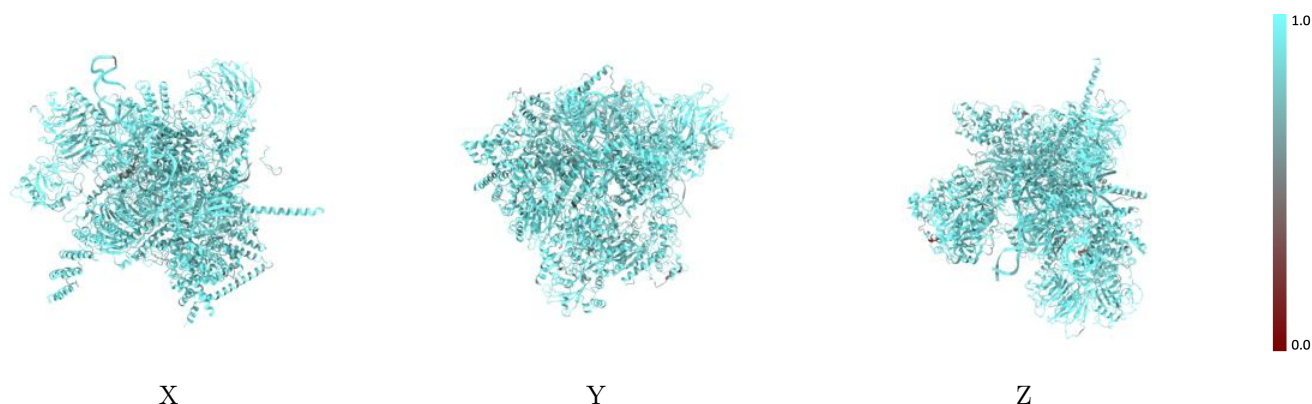
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



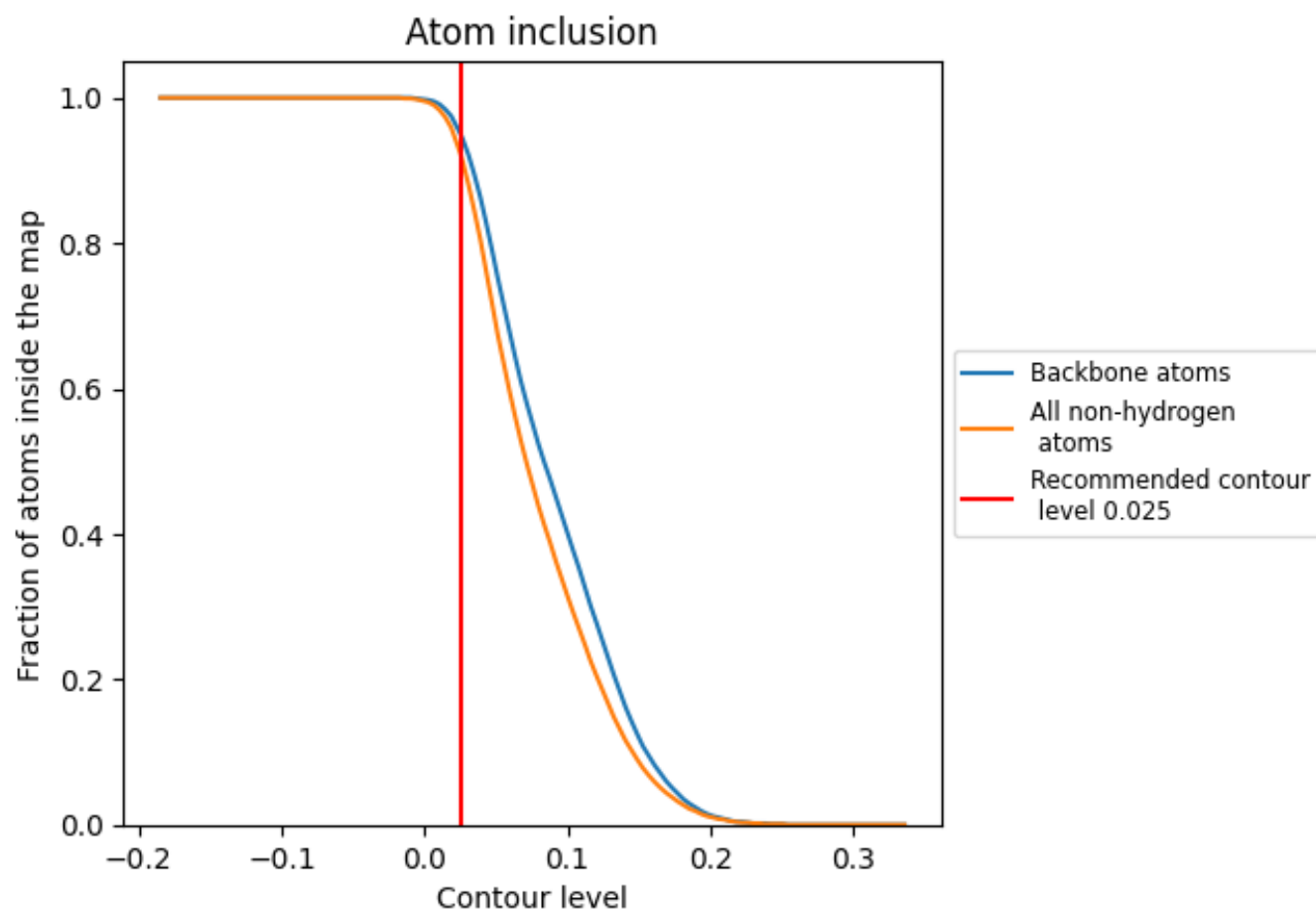
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.025).























































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.025) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9240	 0.4980
2	 0.9040	 0.4570
5	 0.9350	 0.4550
6	 0.9500	 0.4720
9	 0.6790	 0.4240
A	 0.9350	 0.5390
B	 0.9220	 0.4880
C	 0.8900	 0.4710
D	 0.9570	 0.5520
E	 0.9060	 0.4900
F	 0.9260	 0.4340
L	 0.8910	 0.4840
O	 0.9080	 0.4660
P	 0.9150	 0.5070
Q	 0.9490	 0.5260
R	 0.8840	 0.4980
S	 0.9080	 0.5290
T	 0.9030	 0.4820
V	 0.9290	 0.4170
Y	 0.9270	 0.4580
Z	 0.9460	 0.5490
p	 0.9350	 0.4540
r	 0.8330	 0.4610
s	 0.9340	 0.5570
t	 0.8910	 0.4500
u	 0.8930	 0.4830
x	 0.8960	 0.5330

