



wwPDB EM Validation Summary Report ⓘ

Apr 15, 2026 – 12:51 AM UTC

PDB ID : 9ZE3 / pdb_00009ze3
EMDB ID : EMD-74090
Title : Cryo-EM structure of the endogenous U2/branchpoint spliceosomal complex (Distal DHX15 state)
Authors : Liu, S.; Su, T.; Zhou, Z.H.
Deposited on : 2025-11-27
Resolution : 3.93 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

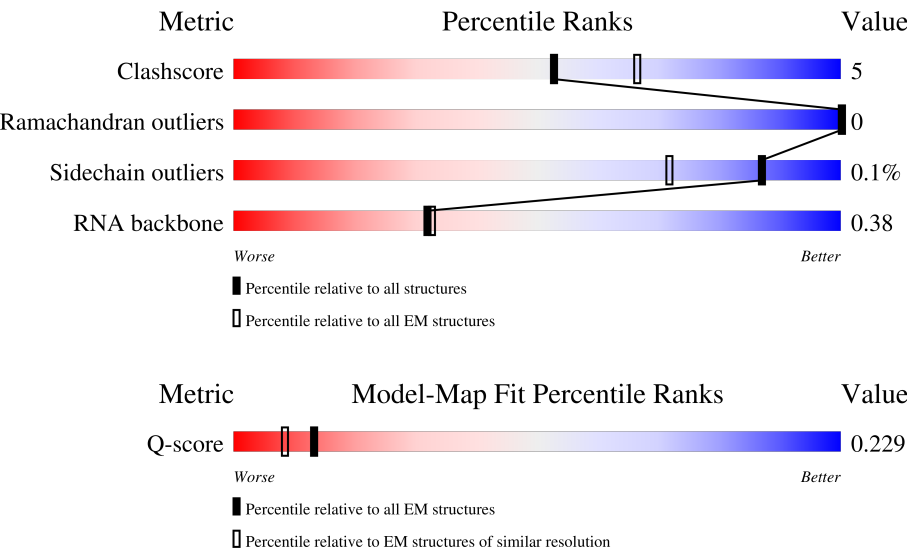
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.93 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	7811 (3.43 - 4.43)

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	A	824	<div><div>16% 14% 83%</div></div>
2	B	795	<div><div>85% 72% 13% 15%</div></div>
3	C	1029	<div><div>15% 12% 85%</div></div>

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Mol	Chain	Length	Quality of chain
4	2	37	
5	H	110	
6	R	44	
7	B1	1304	
8	B2	895	
9	B3	1217	
10	B4	424	
11	B5	86	
12	B6	125	
13	A1	793	
14	A2	464	
15	A3	501	

2 Entry composition

There are 16 unique types of molecules in this entry. The entry contains 37987 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 RNA-binding protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	137	Total	C	N	O	S	0	0
			1113	687	219	197	10		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	816	MET	-	expression tag	UNP P52756
A	817	ASP	-	expression tag	UNP P52756
A	818	TYR	-	expression tag	UNP P52756
A	819	LYS	-	expression tag	UNP P52756
A	820	ASP	-	expression tag	UNP P52756
A	821	ASP	-	expression tag	UNP P52756
A	822	ASP	-	expression tag	UNP P52756
A	823	ASP	-	expression tag	UNP P52756
A	824	LYS	-	expression tag	UNP P52756

- Molecule 2 is a protein called ATP-dependent RNA helicase DHX15.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	672	Total	C	N	O	S	0	0
			5409	3433	933	1008	35		

- Molecule 3 is a protein called U2 snRNP-associated SURP motif-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	152	Total	C	N	O	S	0	0
			1234	794	208	226	6		

- Molecule 4 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	2	37	Total	C	N	O	P	0	0
			781	352	127	265	37		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	H	103	Total	C	N	O	S	0	0
			794	490	142	148	14		

- Molecule 6 is a RNA chain called Pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	R	44	Total	C	N	O	P	0	0
			882	397	93	348	44		

- Molecule 7 is a protein called Splicing factor 3B subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B1	895	Total	C	N	O	S	0	0
			7142	4581	1225	1295	41		

- Molecule 8 is a protein called Splicing factor 3B subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B2	250	Total	C	N	O	S	0	0
			1960	1260	348	345	7		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B3	1198	Total	C	N	O	S	0	0
			9396	5959	1598	1794	45		

- Molecule 10 is a protein called Splicing factor 3B subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	B4	205	Total	C	N	O	S	0	0
			1593	1011	270	305	7		

- Molecule 11 is a protein called Splicing factor 3B subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B5	75	Total	C	N	O	S	0	0
			616	390	108	113	5		

- Molecule 12 is a protein called Splicing factor 3B subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	B6	98	Total	C	N	O	S	0	0
			805	515	144	142	4		

- Molecule 13 is a protein called Splicing factor 3A subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	A1	159	Total	C	N	O	S	0	0
			1344	864	229	249	2		

- Molecule 14 is a protein called Splicing factor 3A subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	A2	197	Total	C	N	O	S	0	0
			1645	1042	300	295	8		

- Molecule 15 is a protein called Splicing factor 3A subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	A3	388	Total	C	N	O	S	0	0
			3270	2068	570	618	14		

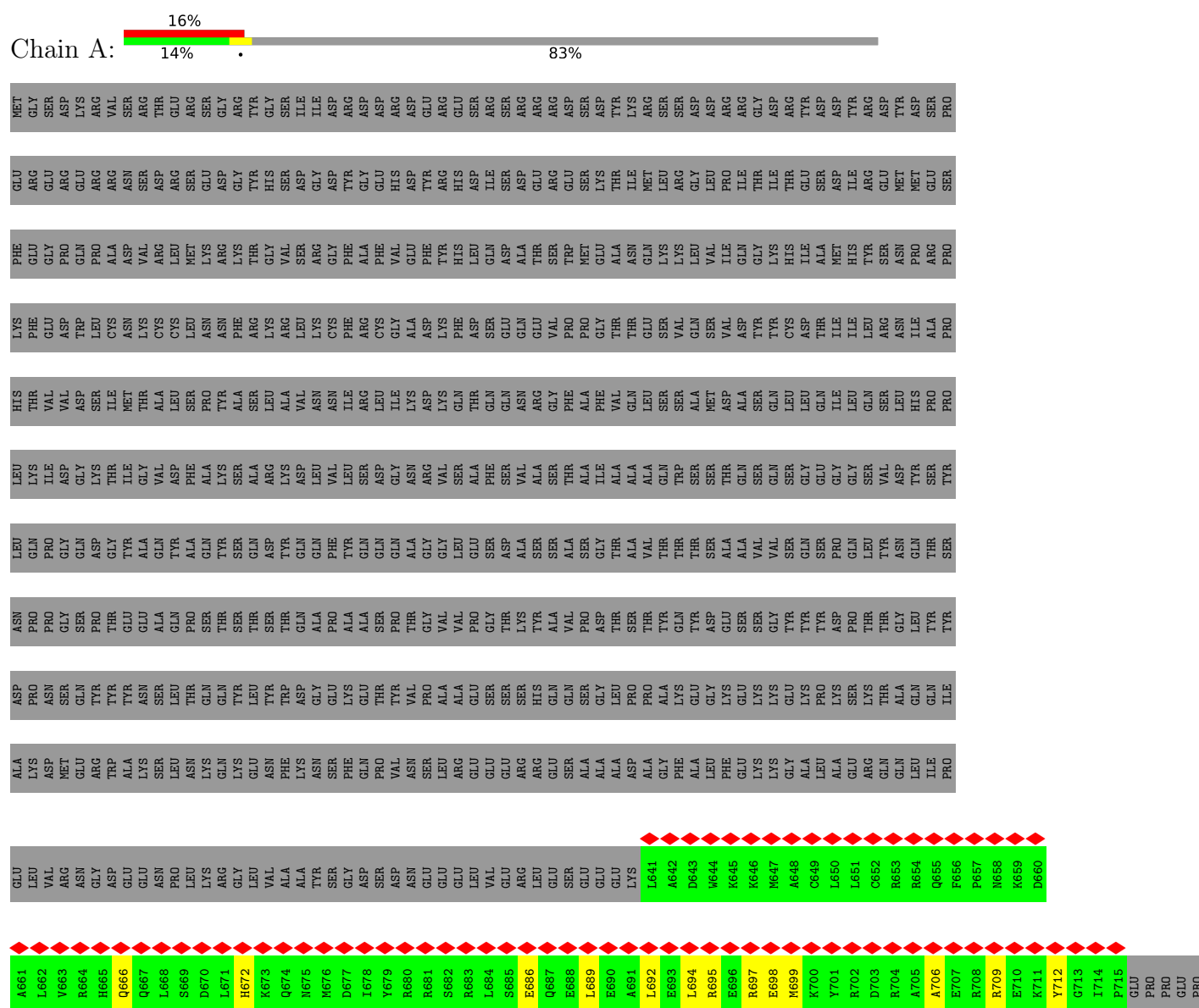
- Molecule 16 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

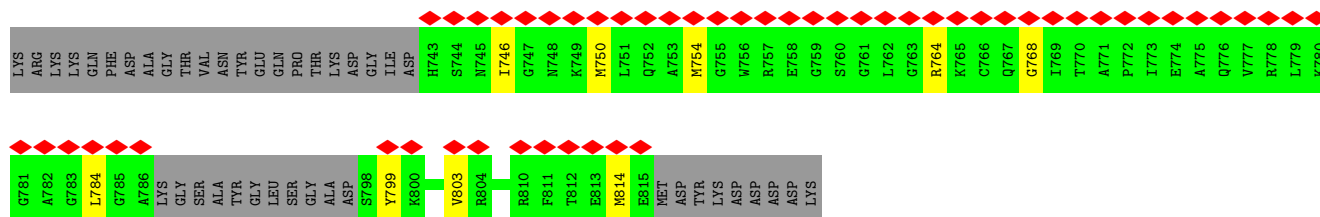
Mol	Chain	Residues	Atoms		AltConf
16	H	3	Total	Zn	0
			3	3	

3 Residue-property plots

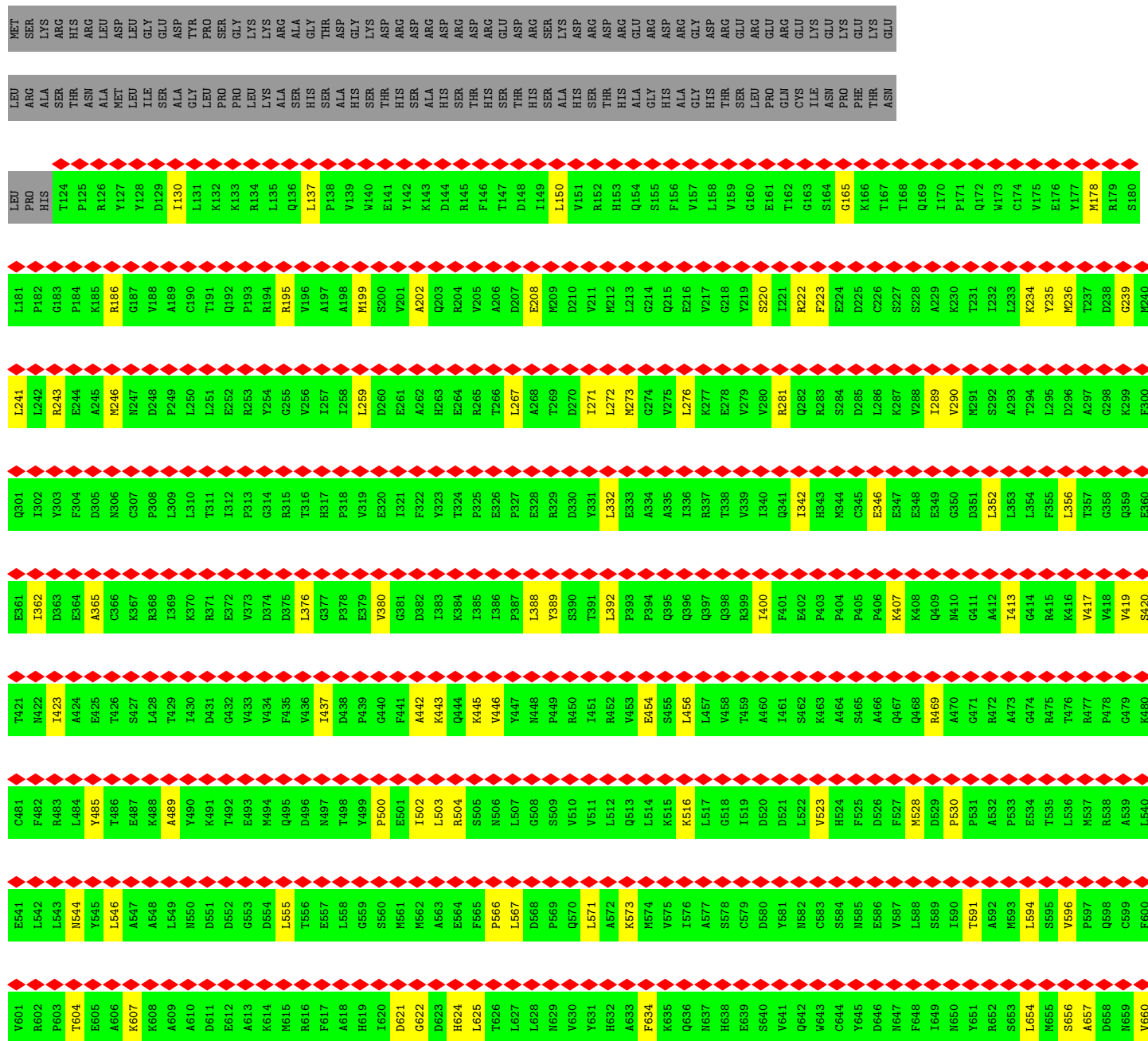
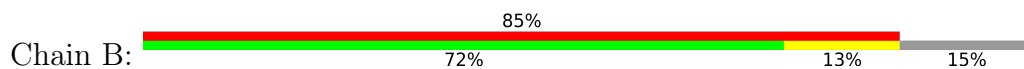
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

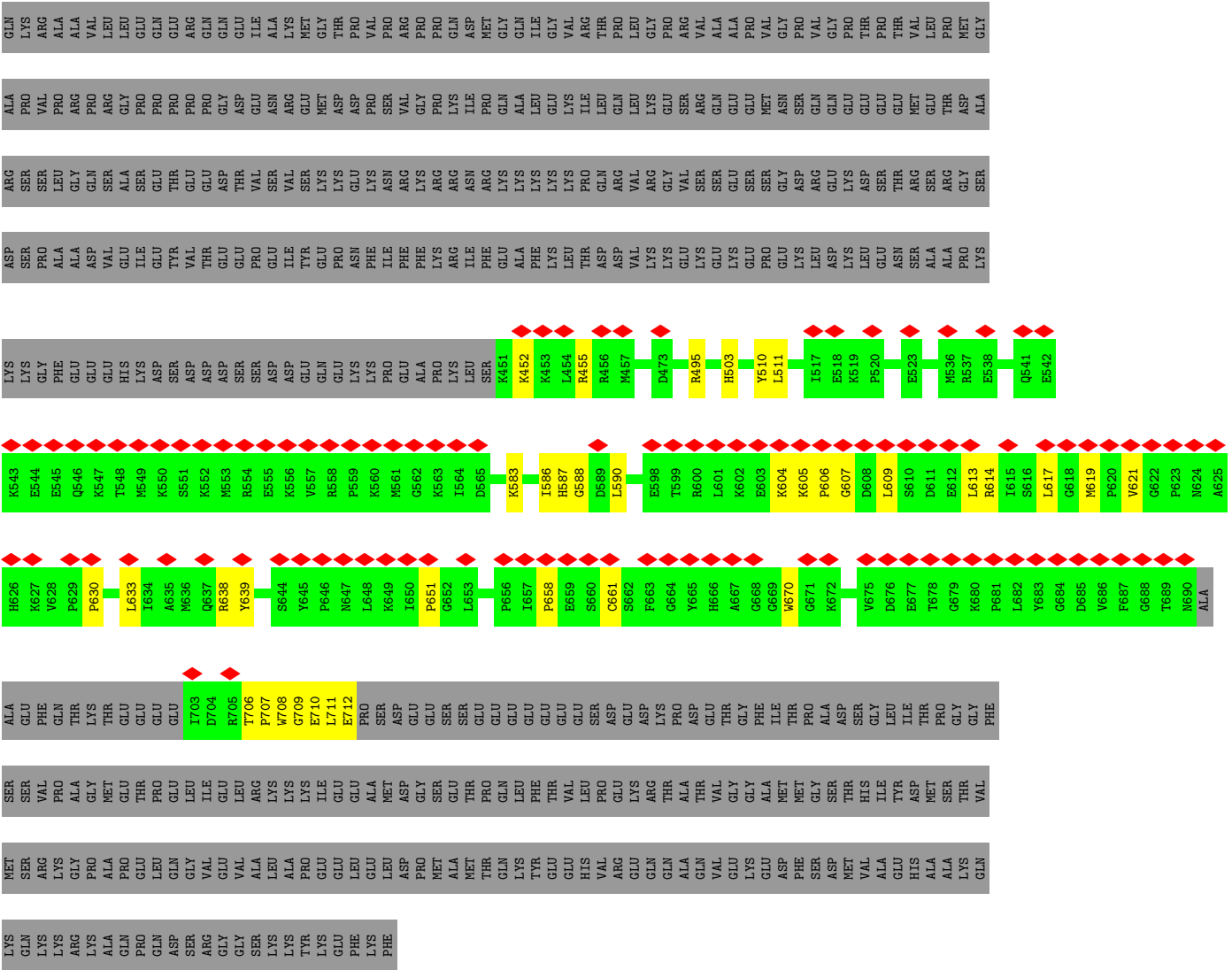
• Molecule 1: RNA-binding protein 5



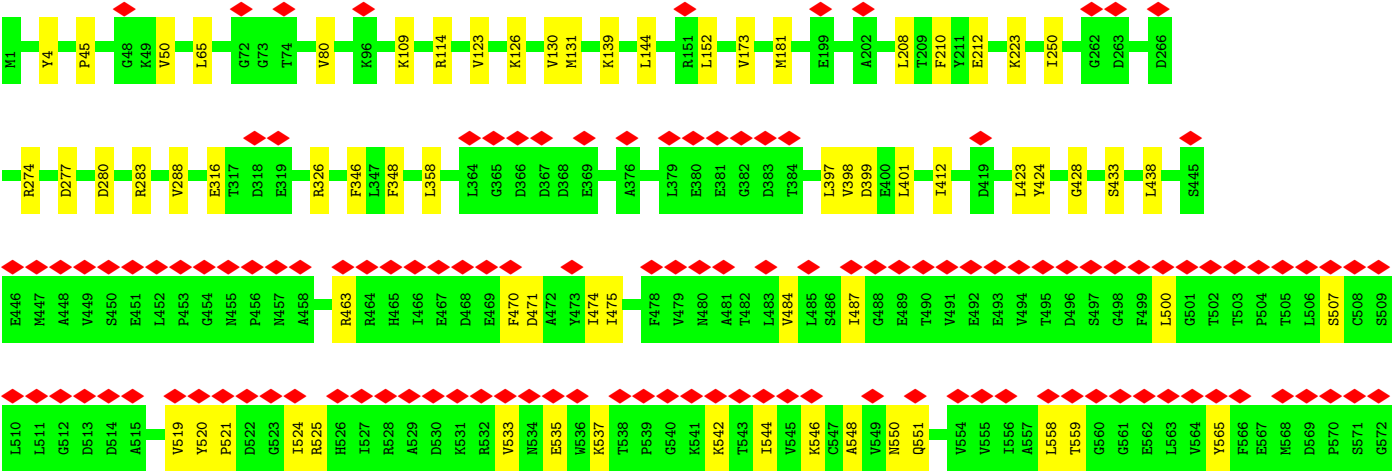
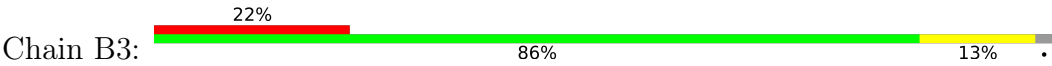


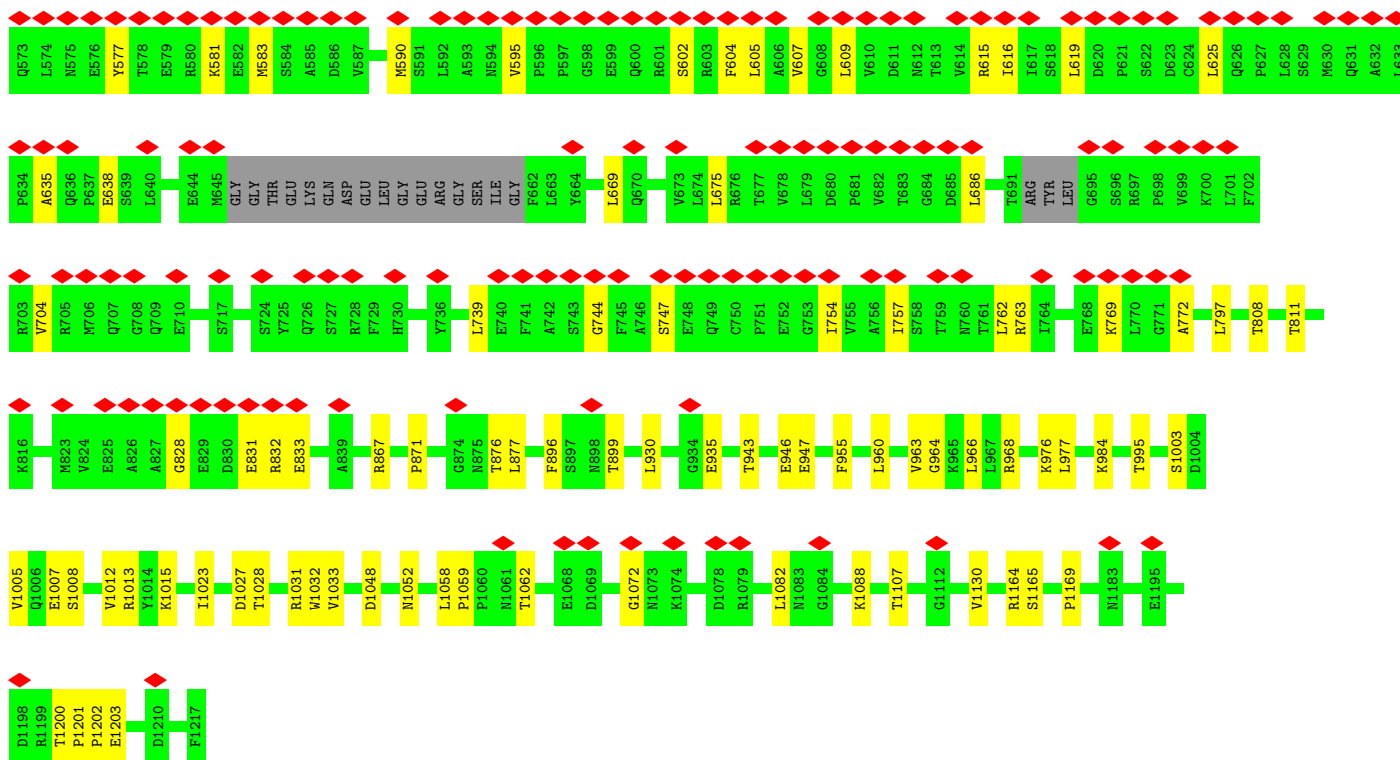
• Molecule 2: ATP-dependent RNA helicase DHX15



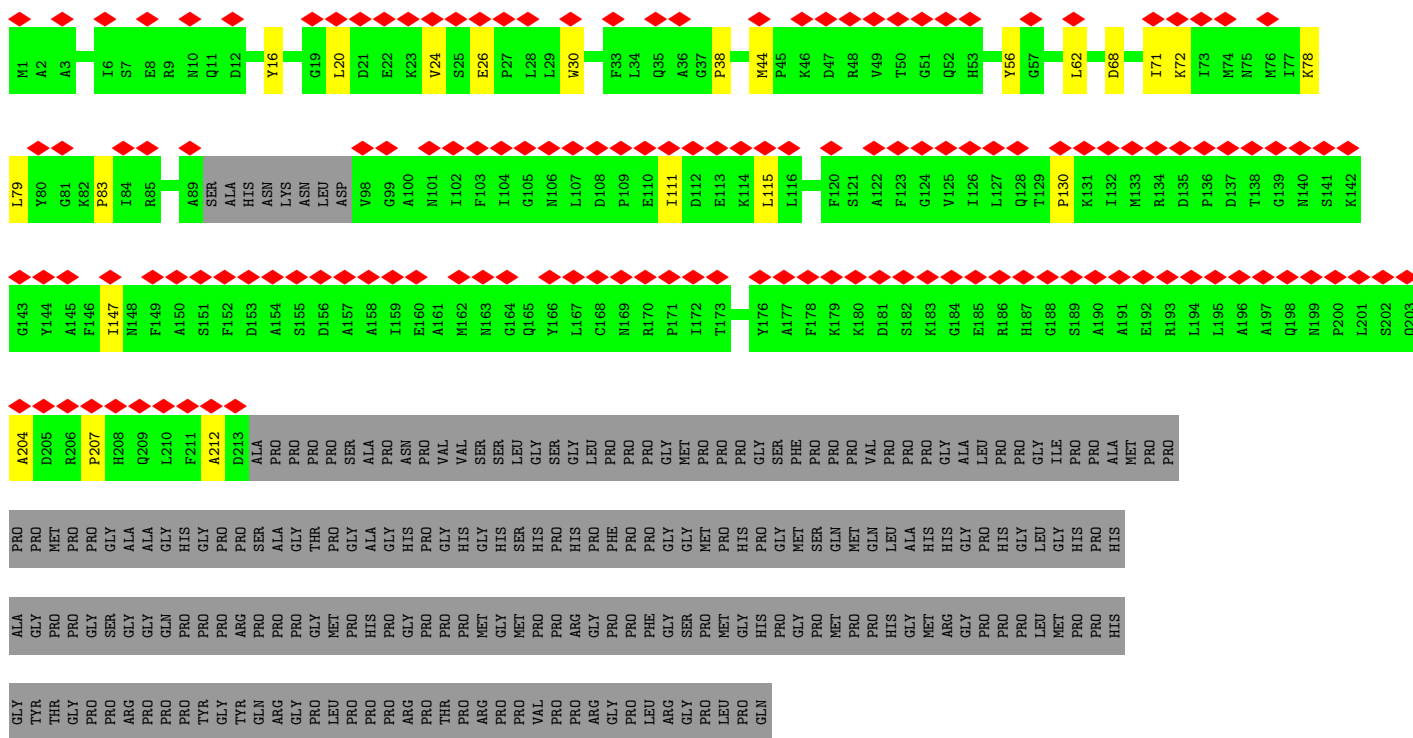
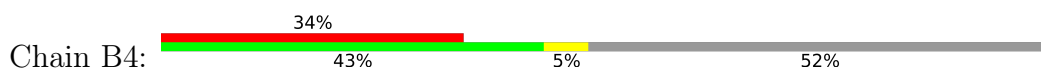


● Molecule 9: Splicing factor 3B subunit 3





• Molecule 10: Splicing factor 3B subunit 4



• Molecule 11: Splicing factor 3B subunit 5

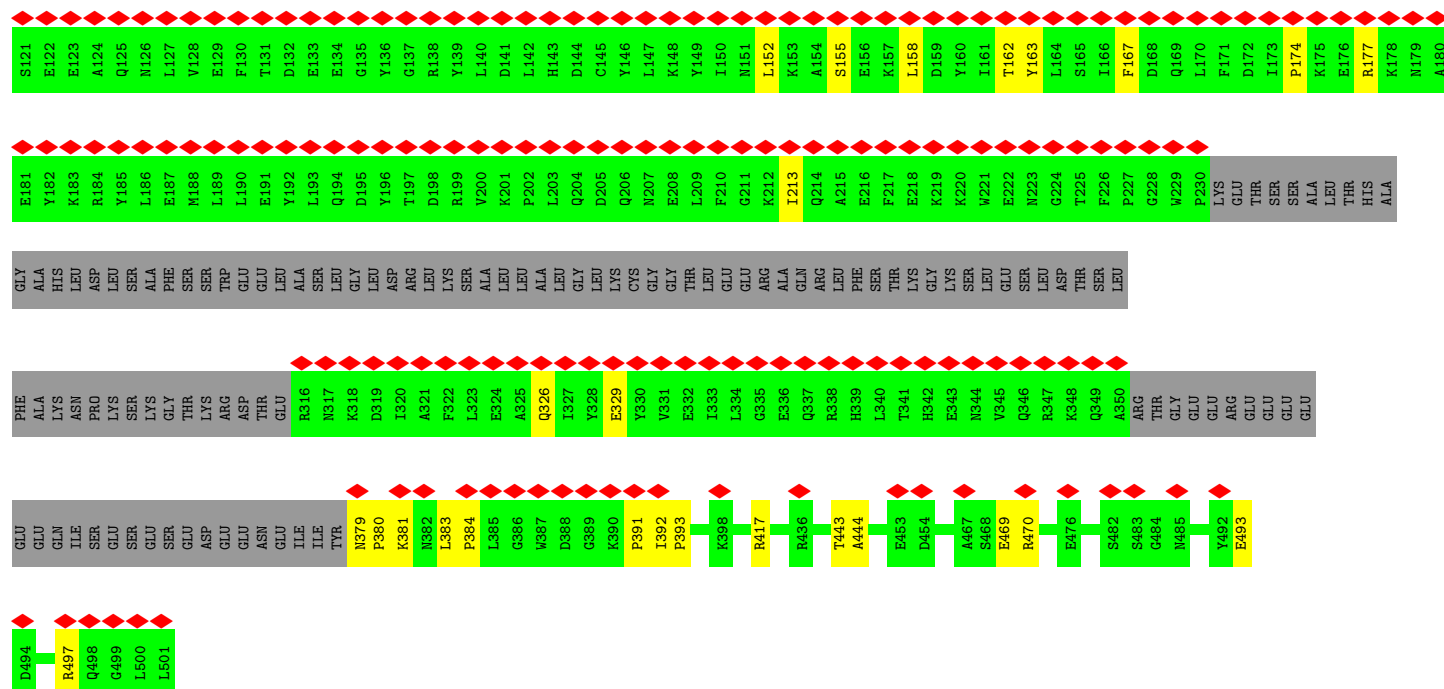
Chain B5:

Chain B6:

Chain A1:







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	49971	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	81000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.340	Depositor
Minimum map value	-1.398	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.45	Depositor
Map size (\AA)	422.40002, 422.40002, 422.40002	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.08	0/1127	0.23	0/1496
2	B	0.08	0/5521	0.23	0/7479
3	C	0.08	0/1257	0.20	0/1696
4	2	0.09	0/625	0.21	0/972
5	H	0.15	0/807	0.36	0/1082
6	R	0.09	0/970	0.24	0/1497
7	B1	0.13	0/7284	0.33	0/9868
8	B2	0.18	0/2017	0.40	0/2735
9	B3	0.14	0/9590	0.33	0/13015
10	B4	0.09	0/1627	0.24	0/2200
11	B5	0.13	0/634	0.27	0/857
12	B6	0.09	0/823	0.25	0/1114
13	A1	0.08	0/1377	0.20	0/1857
14	A2	0.09	0/1686	0.23	0/2264
15	A3	0.08	0/3345	0.21	0/4503
All	All	0.12	0/38690	0.29	0/52635

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

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	A	1113	0	1128	20	0
2	B	5409	0	5433	66	0
3	C	1234	0	1257	20	0
4	2	781	0	398	17	0
5	H	794	0	775	9	0
6	R	882	0	444	10	0
7	B1	7142	0	7319	92	0
8	B2	1960	0	1911	28	0
9	B3	9396	0	9309	96	0
10	B4	1593	0	1556	15	0
11	B5	616	0	579	9	0
12	B6	805	0	802	10	0
13	A1	1344	0	1309	14	0
14	A2	1645	0	1629	21	0
15	A3	3270	0	3163	21	0
16	H	3	0	0	0	0
All	All	37987	0	37012	399	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 5.

The worst 5 of 399 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)
2:B:243:ARG:HA	2:B:246:MET:HG3	1.59	0.83
9:B3:704:VAL:HG11	9:B3:754:ILE:HG22	1.65	0.78
5:H:58:CYS:HB3	5:H:62:GLY:H	1.47	0.78
2:B:443:LYS:HB3	2:B:456:LEU:HD11	1.67	0.77
5:H:1:MET:HA	5:H:34:ASP:OD2	1.87	0.74

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	A	131/824 (16%)	130 (99%)	1 (1%)	0	100	100
2	B	670/795 (84%)	662 (99%)	8 (1%)	0	100	100
3	C	150/1029 (15%)	149 (99%)	1 (1%)	0	100	100
5	H	101/110 (92%)	92 (91%)	9 (9%)	0	100	100
7	B1	891/1304 (68%)	862 (97%)	29 (3%)	0	100	100
8	B2	246/895 (28%)	232 (94%)	14 (6%)	0	100	100
9	B3	1192/1217 (98%)	1128 (95%)	64 (5%)	0	100	100
10	B4	201/424 (47%)	197 (98%)	4 (2%)	0	100	100
11	B5	73/86 (85%)	70 (96%)	3 (4%)	0	100	100
12	B6	96/125 (77%)	94 (98%)	2 (2%)	0	100	100
13	A1	157/793 (20%)	154 (98%)	3 (2%)	0	100	100
14	A2	195/464 (42%)	188 (96%)	7 (4%)	0	100	100
15	A3	382/501 (76%)	378 (99%)	4 (1%)	0	100	100
All	All	4485/8567 (52%)	4336 (97%)	149 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	113/704 (16%)	113 (100%)	0	100	100
2	B	599/704 (85%)	599 (100%)	0	100	100
3	C	135/934 (14%)	135 (100%)	0	100	100
5	H	89/95 (94%)	89 (100%)	0	100	100
7	B1	775/1104 (70%)	775 (100%)	0	100	100
8	B2	201/776 (26%)	200 (100%)	1 (0%)	81	82
9	B3	1037/1051 (99%)	1036 (100%)	1 (0%)	88	90
10	B4	167/336 (50%)	167 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	B5	66/77 (86%)	66 (100%)	0	100	100
12	B6	84/109 (77%)	84 (100%)	0	100	100
13	A1	144/709 (20%)	144 (100%)	0	100	100
14	A2	174/382 (46%)	174 (100%)	0	100	100
15	A3	350/446 (78%)	350 (100%)	0	100	100
All	All	3934/7427 (53%)	3932 (100%)	2 (0%)	87	90

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
8	B2	712	GLU
9	B3	144	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
9	B3	861	GLN
11	B5	8	HIS
15	A3	8	GLN
11	B5	36	HIS
9	B3	1160	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	2	36/37 (97%)	7 (19%)	1 (2%)
6	R	43/44 (97%)	21 (48%)	1 (2%)
All	All	79/81 (97%)	28 (35%)	2 (2%)

5 of 28 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	2	30	A
4	2	31	G
4	2	43	PSU
4	2	44	PSU
4	2	46	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	2	44	PSU
6	R	18	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	PSU	2	37	4	18,21,22	1.09	1 (5%)	21,30,33	1.98	5 (23%)
4	OMC	2	47	4	19,22,23	0.51	0	25,31,34	1.02	2 (8%)
4	PSU	2	58	4	18,21,22	1.09	1 (5%)	21,30,33	1.73	4 (19%)
4	PSU	2	54	4	18,21,22	1.14	1 (5%)	21,30,33	1.93	4 (19%)
4	PSU	2	44	4	18,21,22	1.11	1 (5%)	21,30,33	1.76	4 (19%)
4	PSU	2	39	4,6	18,21,22	1.11	1 (5%)	21,30,33	1.89	4 (19%)
4	OMC	2	40	4,6	19,22,23	0.50	0	25,31,34	0.72	0
4	PSU	2	41	4,6	18,21,22	1.09	1 (5%)	21,30,33	1.92	4 (19%)
4	OMC	2	61	4	19,22,23	0.49	0	25,31,34	0.69	0
4	PSU	2	43	4	18,21,22	1.11	1 (5%)	21,30,33	1.70	4 (19%)
4	PSU	2	34	4,6	18,21,22	1.10	1 (5%)	21,30,33	1.87	4 (19%)

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
4	PSU	2	37	4	-	0/7/25/26	0/2/2/2
4	OMC	2	47	4	-	6/9/27/28	0/2/2/2
4	PSU	2	58	4	-	3/7/25/26	0/2/2/2
4	PSU	2	54	4	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PSU	2	44	4	-	3/7/25/26	0/2/2/2
4	PSU	2	39	4,6	-	0/7/25/26	0/2/2/2
4	OMC	2	40	4,6	-	0/9/27/28	0/2/2/2
4	PSU	2	41	4,6	-	0/7/25/26	0/2/2/2
4	OMC	2	61	4	-	0/9/27/28	0/2/2/2
4	PSU	2	43	4	-	6/7/25/26	0/2/2/2
4	PSU	2	34	4,6	-	0/7/25/26	0/2/2/2

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	2	43	PSU	C6-C5	3.91	1.39	1.35
4	2	44	PSU	C6-C5	3.84	1.39	1.35
4	2	58	PSU	C6-C5	3.74	1.39	1.35
4	2	54	PSU	C6-C5	3.70	1.39	1.35
4	2	39	PSU	C6-C5	3.66	1.39	1.35

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	2	37	PSU	C4-N3-C2	-4.97	119.52	126.37
4	2	37	PSU	N1-C2-N3	4.88	120.32	115.17
4	2	54	PSU	N1-C2-N3	4.82	120.25	115.17
4	2	54	PSU	C4-N3-C2	-4.81	119.75	126.37
4	2	41	PSU	N1-C2-N3	4.79	120.22	115.17

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	2	43	PSU	C2'-C1'-C5-C4
4	2	43	PSU	O4'-C1'-C5-C4
4	2	43	PSU	O4'-C1'-C5-C6
4	2	43	PSU	C3'-C4'-C5'-O5'
4	2	43	PSU	O4'-C4'-C5'-O5'

There are no ring outliers.

8 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	2	37	PSU	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	2	47	OMC	1	0
4	2	58	PSU	1	0
4	2	39	PSU	2	0
4	2	40	OMC	4	0
4	2	41	PSU	3	0
4	2	43	PSU	1	0
4	2	34	PSU	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

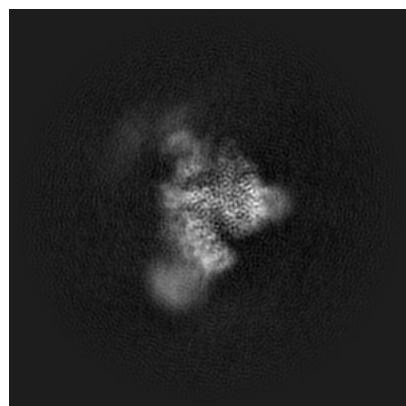
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-74090. These allow visual inspection of the internal detail of the map and identification of artifacts.

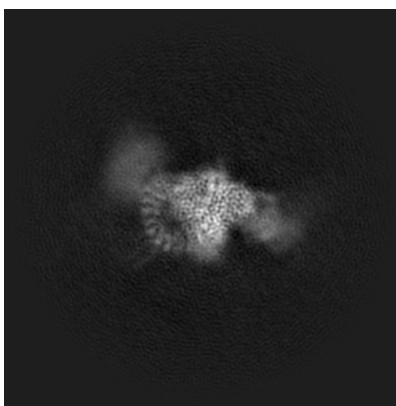
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

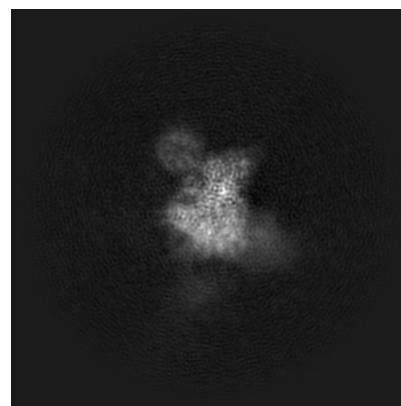
6.1.1 Primary map



X

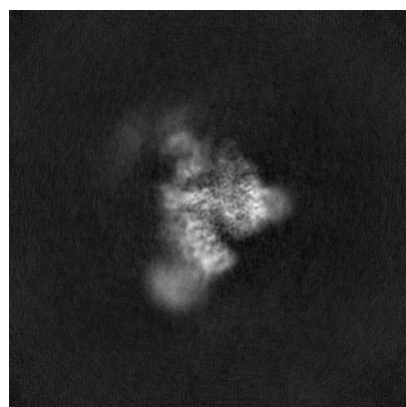


Y

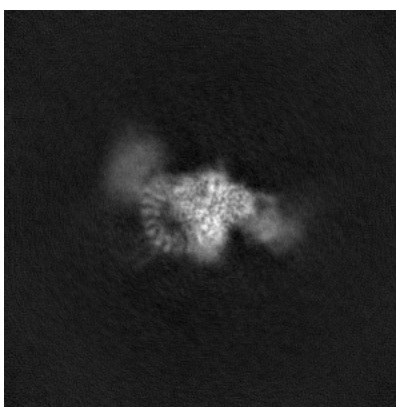


Z

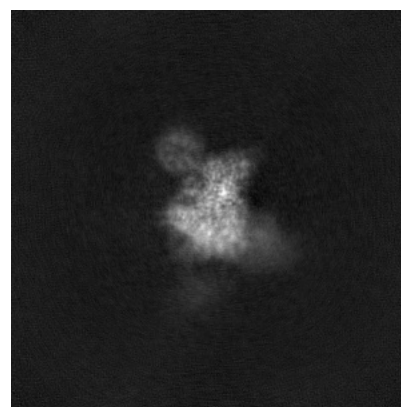
6.1.2 Raw map



X



Y

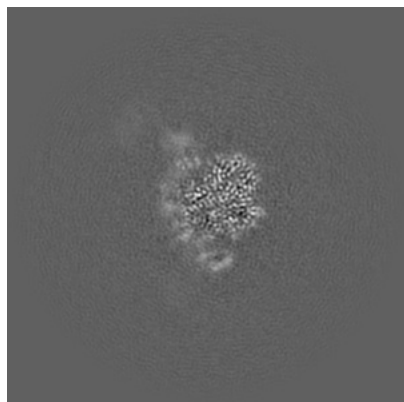


Z

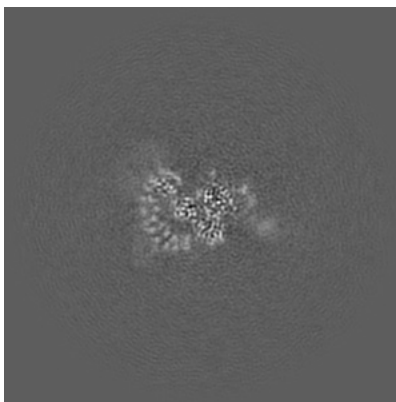
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

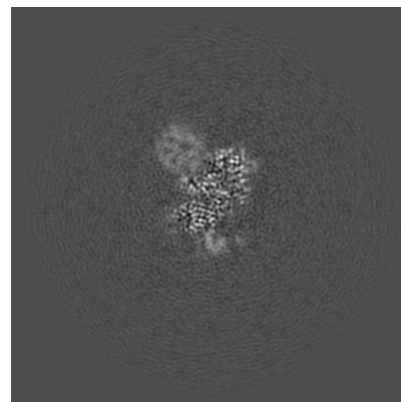
6.2.1 Primary map



X Index: 192

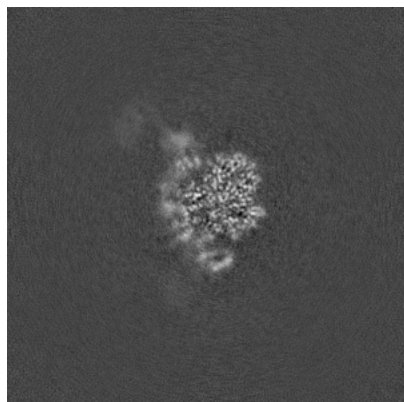


Y Index: 192

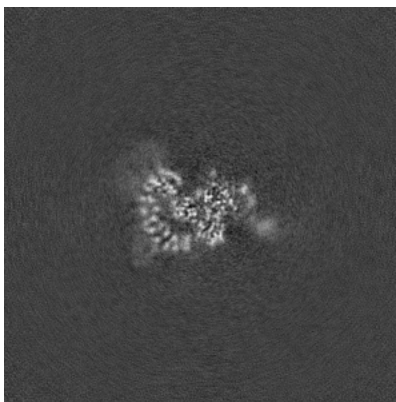


Z Index: 192

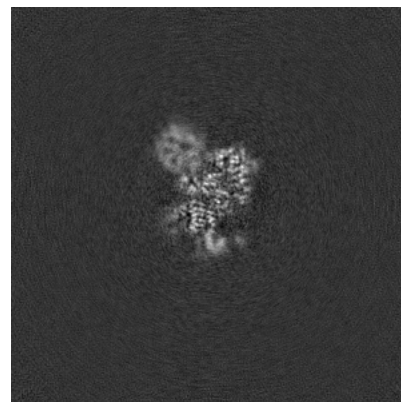
6.2.2 Raw map



X Index: 192



Y Index: 192

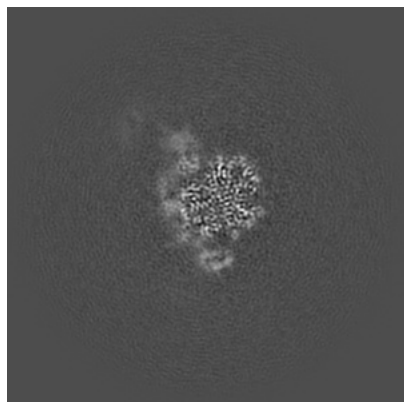


Z Index: 192

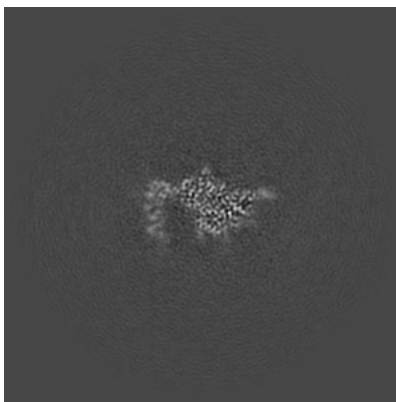
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

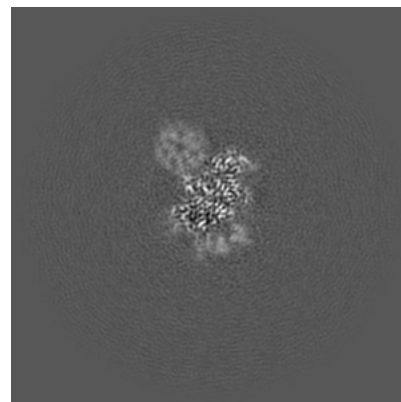
6.3.1 Primary map



X Index: 190

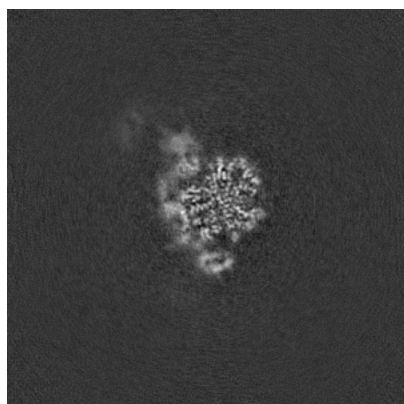


Y Index: 208

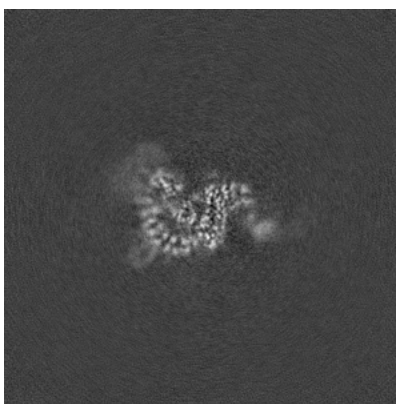


Z Index: 197

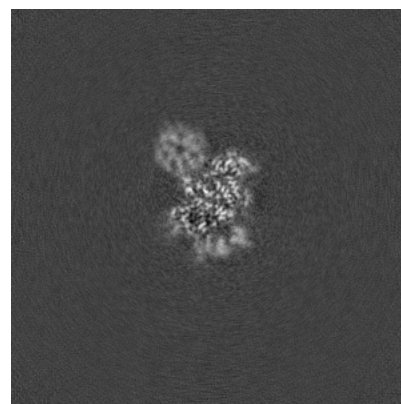
6.3.2 Raw map



X Index: 190



Y Index: 189

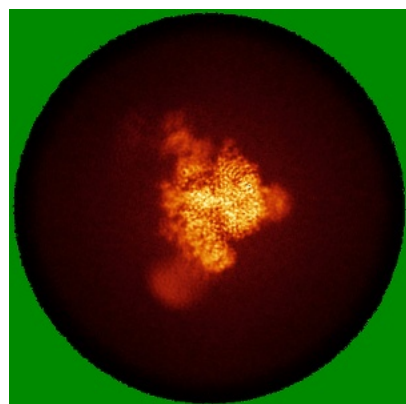


Z Index: 197

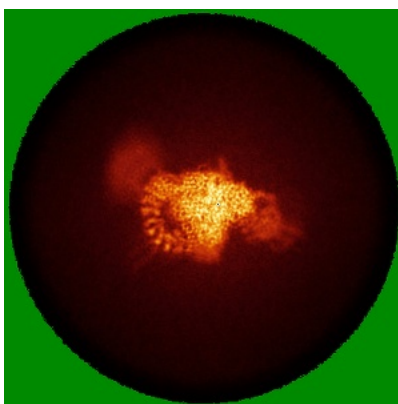
The images above show the largest variance slices of the map in three orthogonal directions.

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

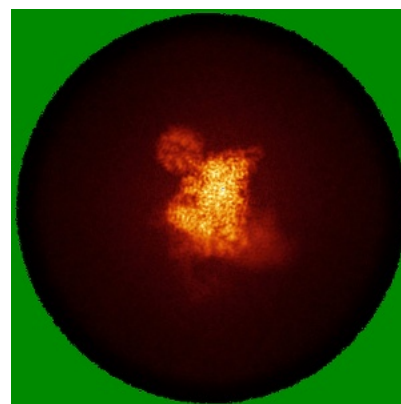
6.4.1 Primary map



X

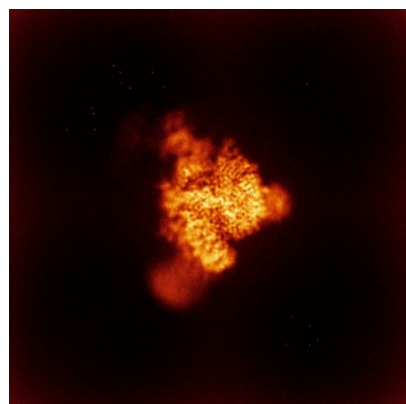


Y

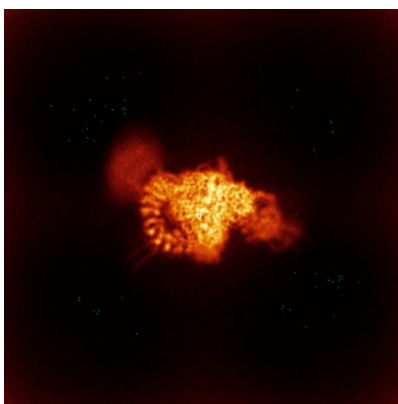


Z

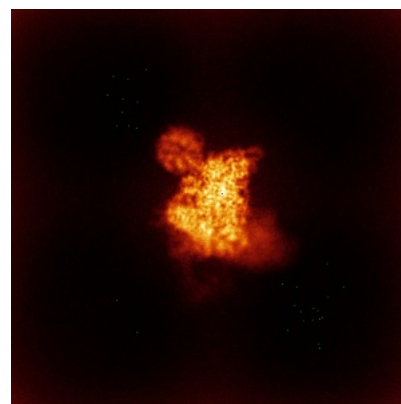
6.4.2 Raw map



X



Y

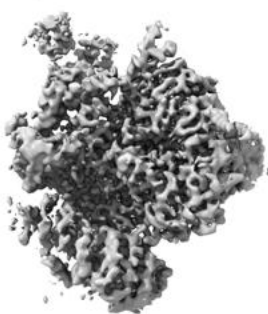


Z

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

6.5 Orthogonal surface views [i](#)

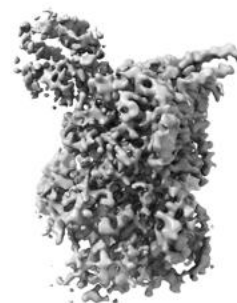
6.5.1 Primary map



X



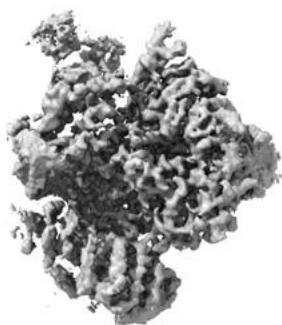
Y



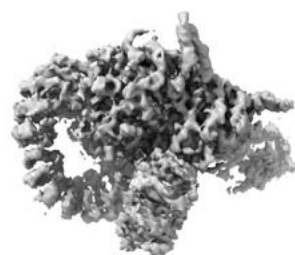
Z

The images above show the 3D surface view of the map at the recommended contour level 0.45. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

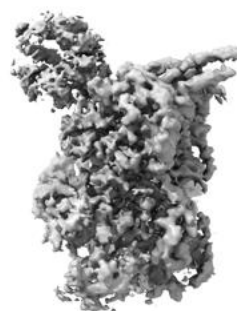
6.5.2 Raw map



X



Y



Z

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

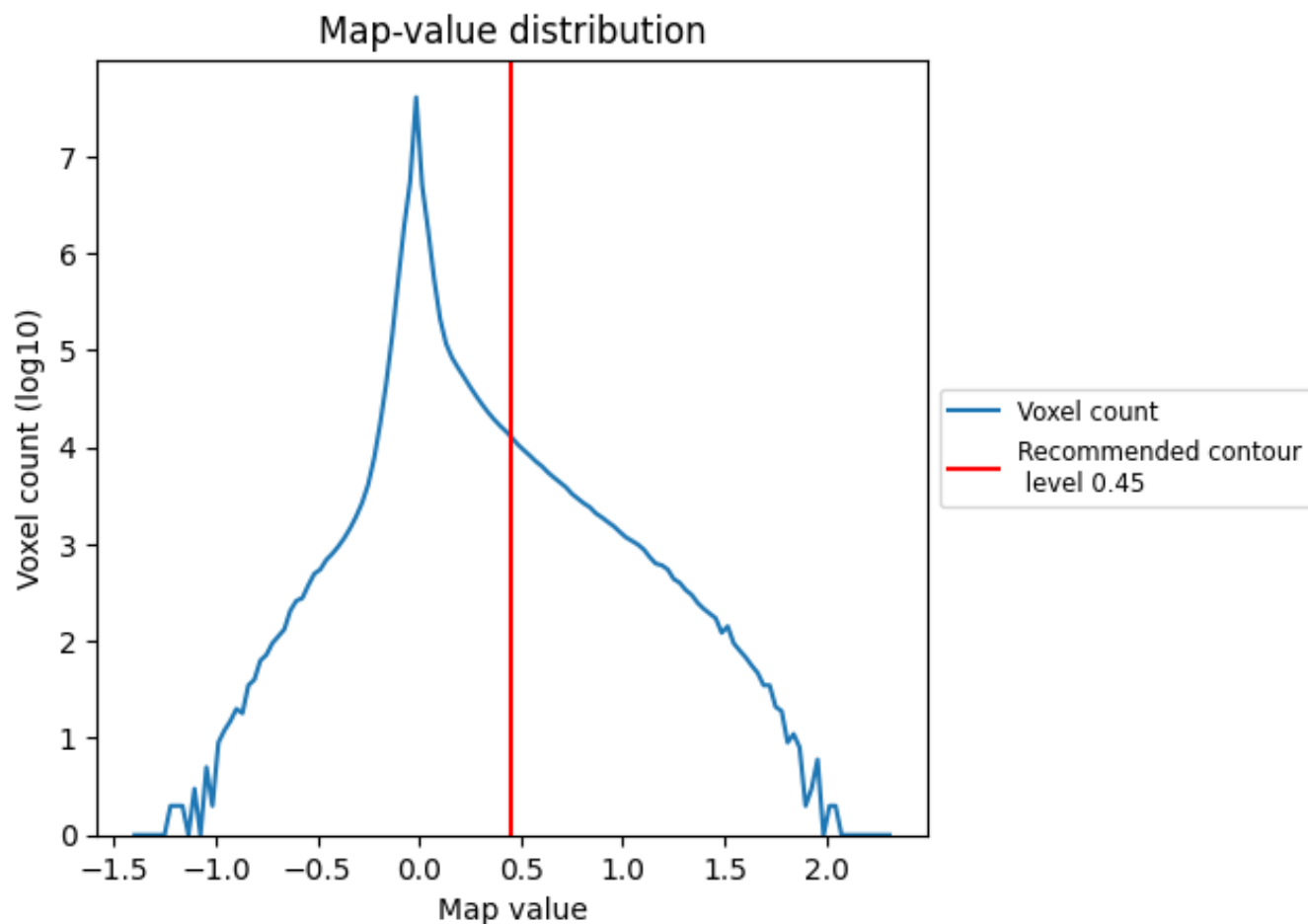
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

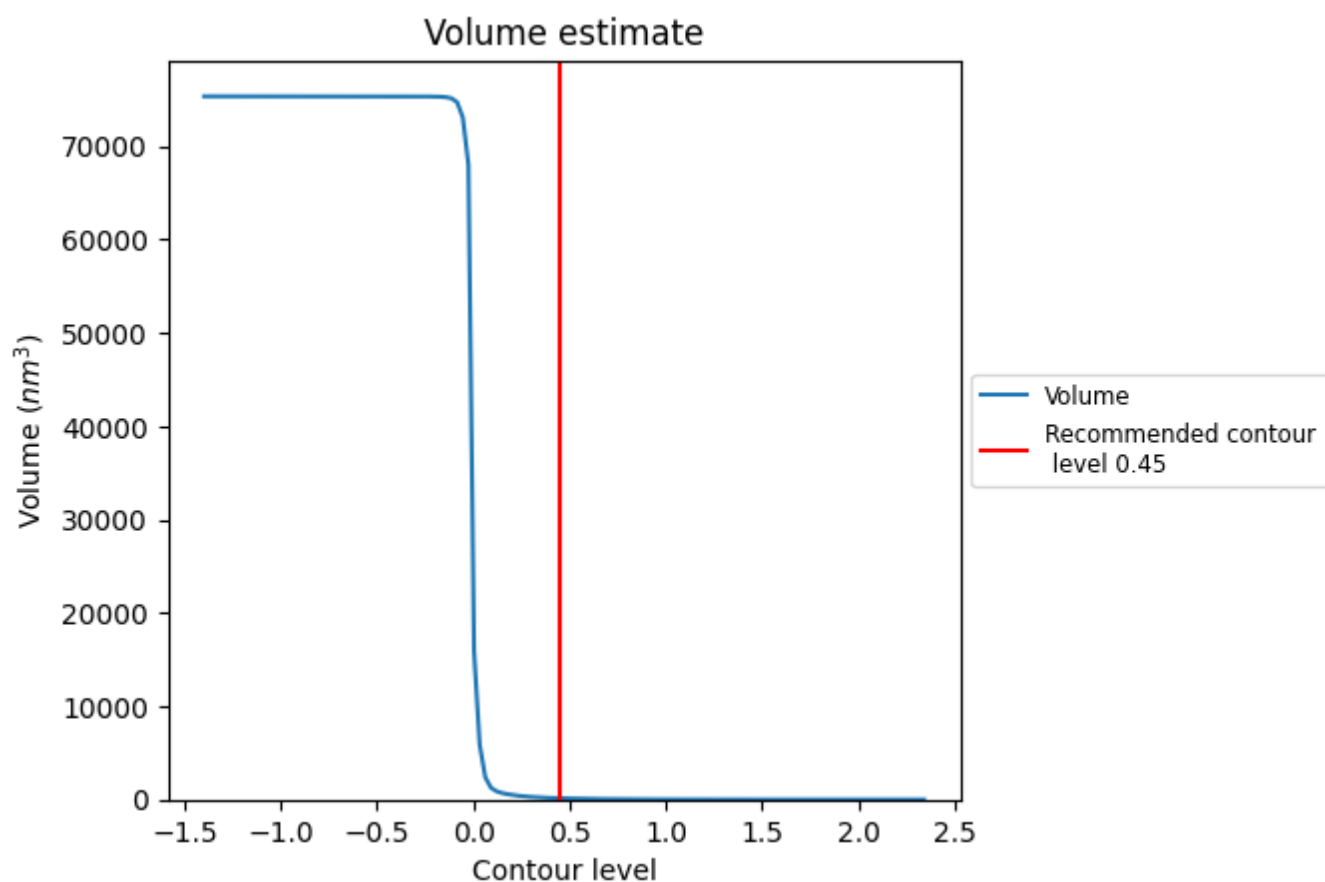
This section contains the results of statistical analysis of the map.

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.

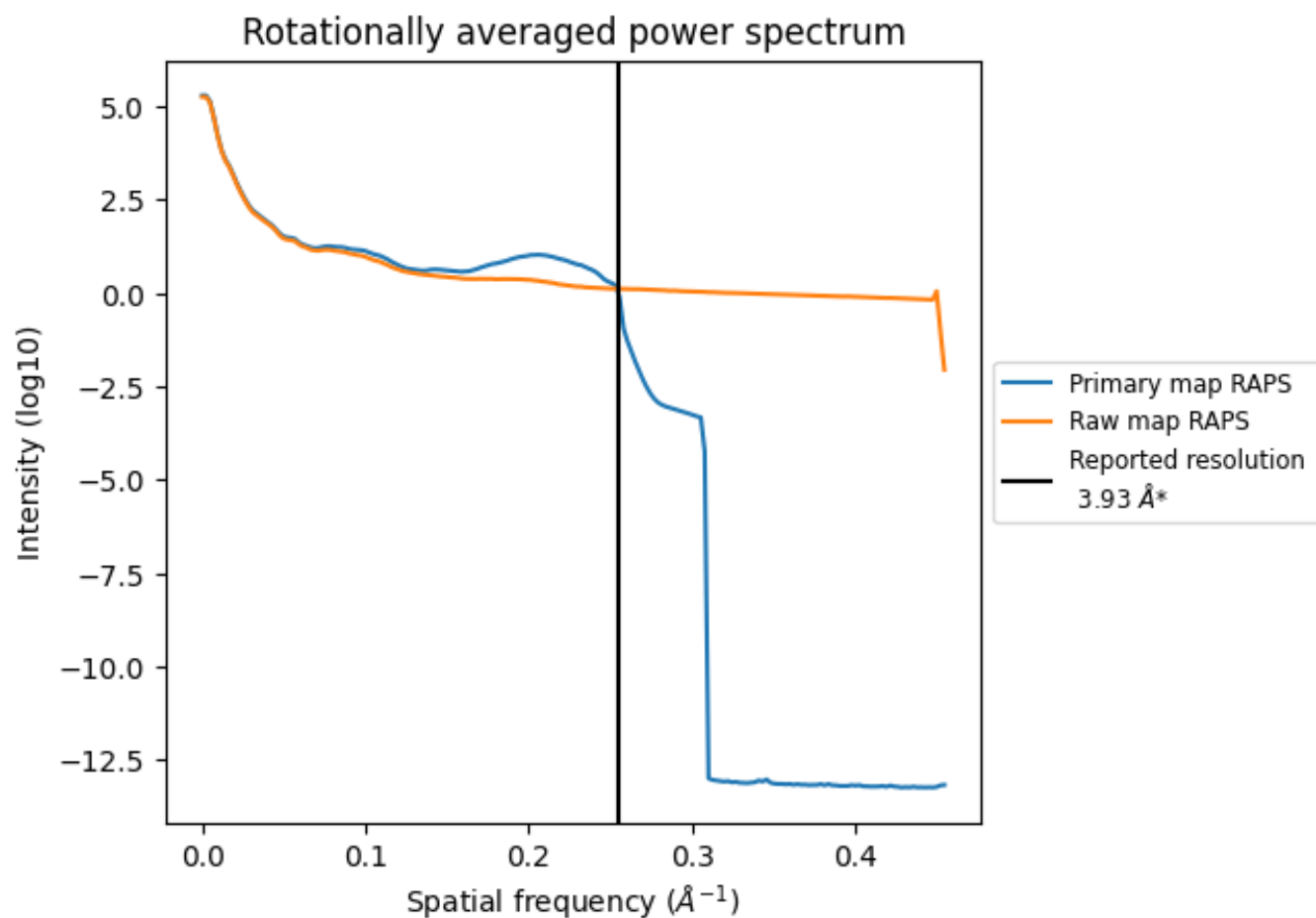
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 140 nm³; this corresponds to an approximate mass of 126 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 ⓘ

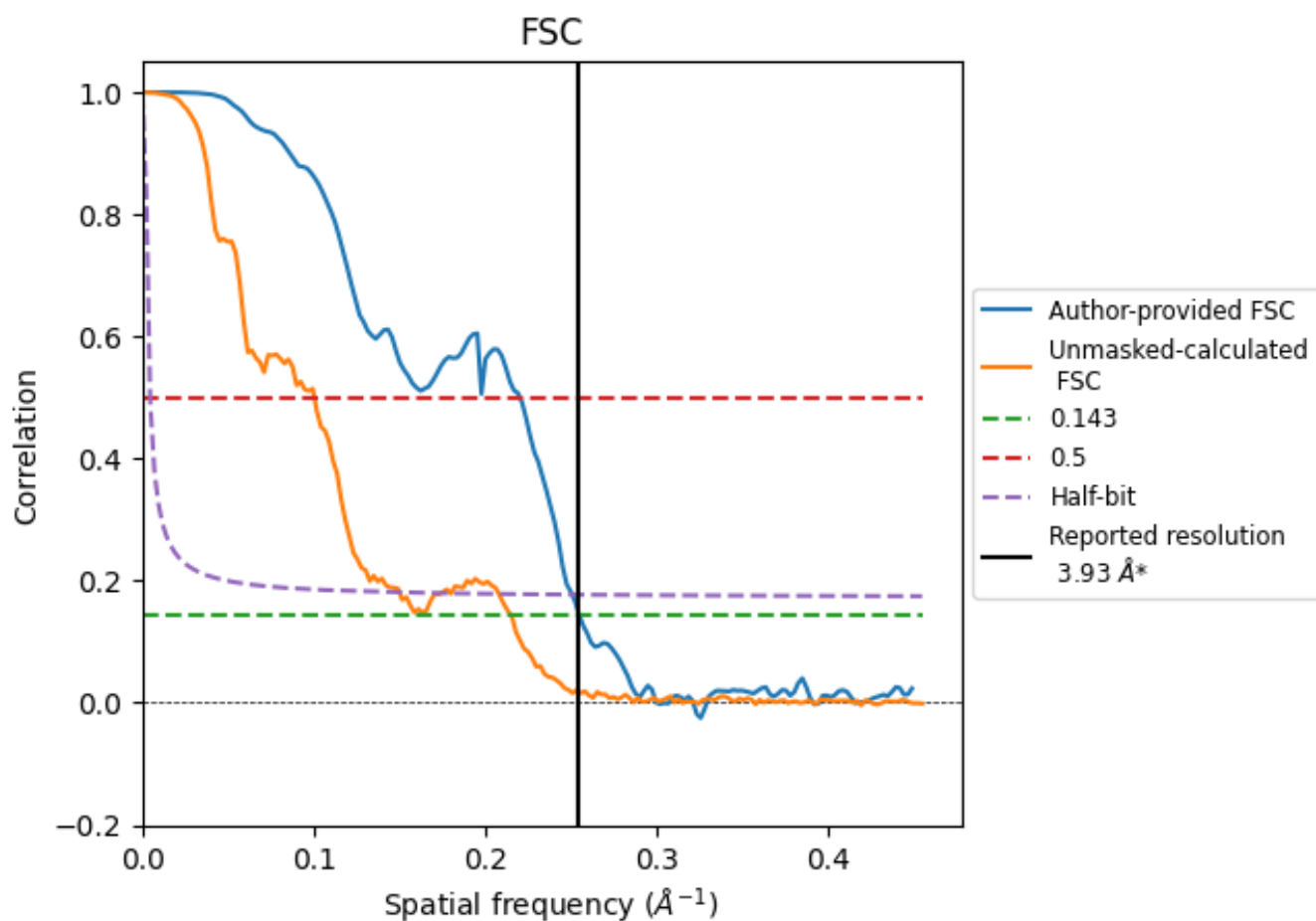


*Reported resolution corresponds to spatial frequency of 0.254 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.254 Å⁻¹

8.2 Resolution estimates

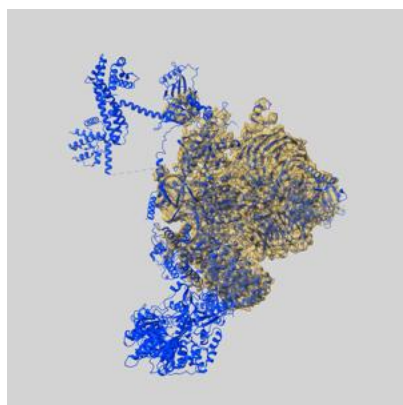
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.93	-	-
Author-provided FSC curve	3.93	4.54	3.99
Unmasked-calculated*	4.65	9.97	6.67

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.65 differs from the reported value 3.93 by more than 10 %

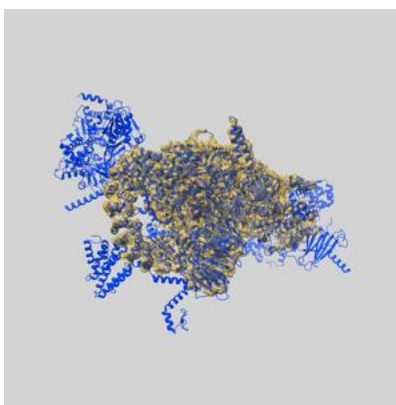
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-74090 and PDB model 9ZE3. Per-residue inclusion information can be found in section [3](#) on page [7](#).

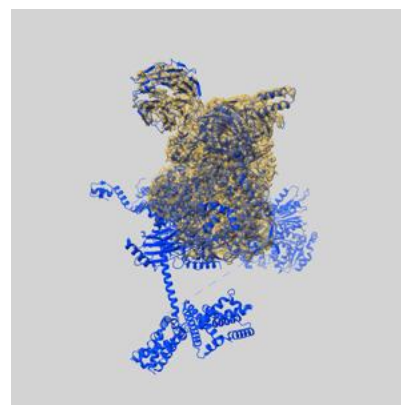
9.1 Map-model overlay [i](#)



X



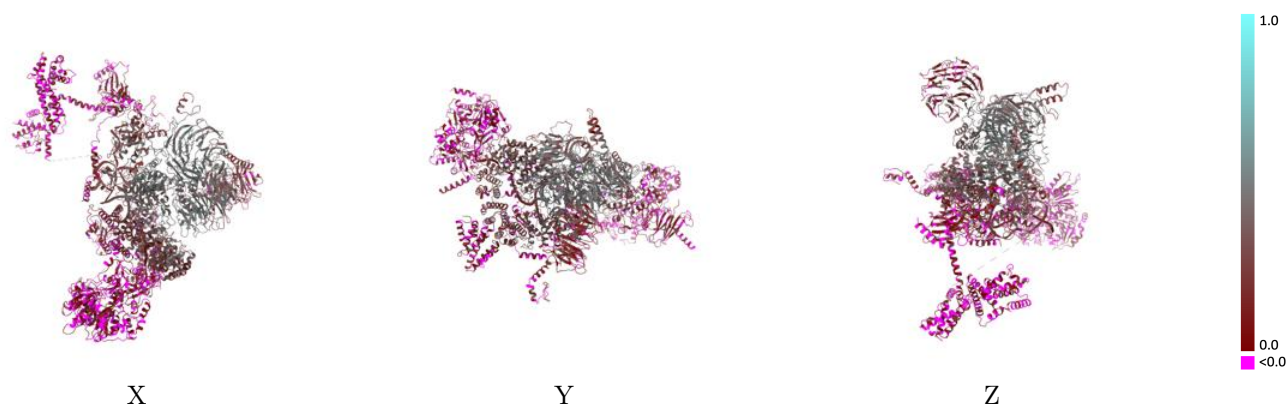
Y



Z

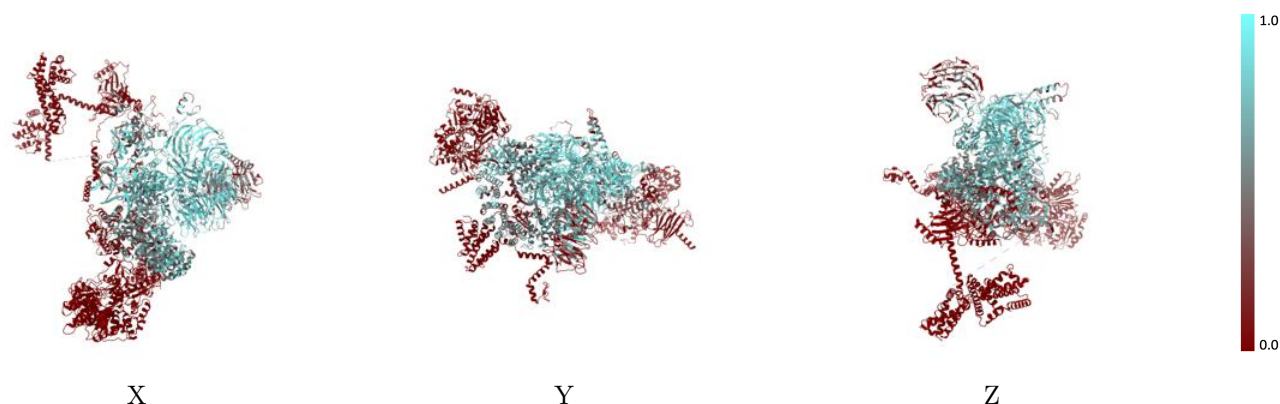
The images above show the 3D surface view of the map at the recommended contour level 0.45 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



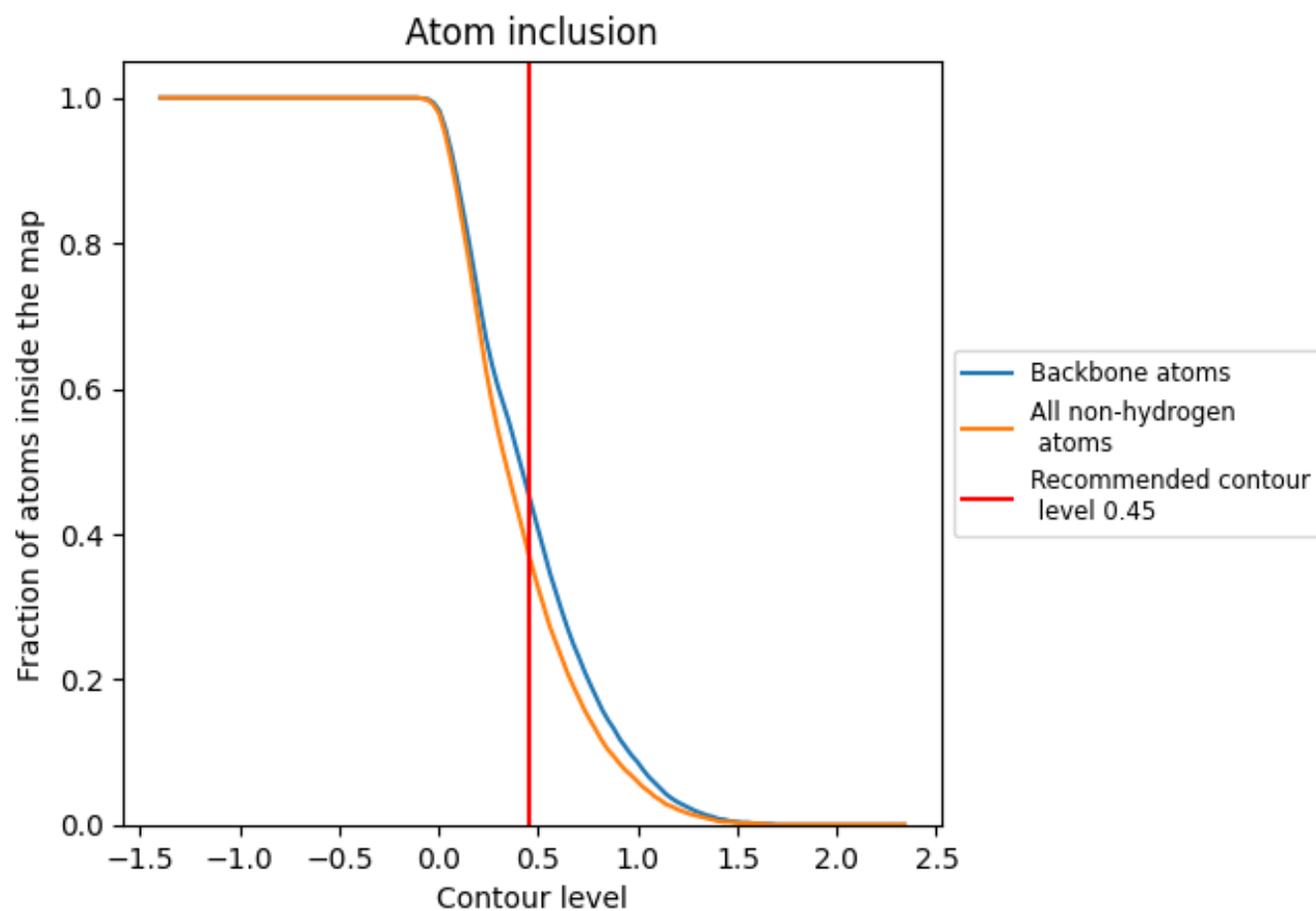
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.45).

9.4 Atom inclusion [i](#)



At the recommended contour level, 46% of all backbone atoms, 37% 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 (0.45) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.3740	<div></div> 0.2290
2	<div></div> 0.6670	<div></div> 0.2830
A	<div></div> 0.0470	<div></div> 0.0630
A1	<div></div> 0.0010	<div></div> 0.0460
A2	<div></div> 0.0600	<div></div> 0.1230
A3	<div></div> 0.1880	<div></div> 0.1130
B	<div></div> 0.0000	<div></div> 0.0270
B1	<div></div> 0.5740	<div></div> 0.3160
B2	<div></div> 0.4830	<div></div> 0.2980
B3	<div></div> 0.6400	<div></div> 0.3740
B4	<div></div> 0.2510	<div></div> 0.1910
B5	<div></div> 0.7710	<div></div> 0.4560
B6	<div></div> 0.0080	<div></div> 0.0910
C	<div></div> 0.0030	<div></div> 0.0790
H	<div></div> 0.7540	<div></div> 0.4360
R	<div></div> 0.4080	<div></div> 0.2090

