



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 08:48 PM UTC

PDB ID : 6N7P / pdb_00006n7p
EMDB ID : EMD-0360
Title : S. cerevisiae spliceosomal E complex (UBC4)
Authors : Liu, S.; Li, X.; Zhou, Z.H.; Zhao, R.
Deposited on : 2018-11-27
Resolution : 3.60 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:

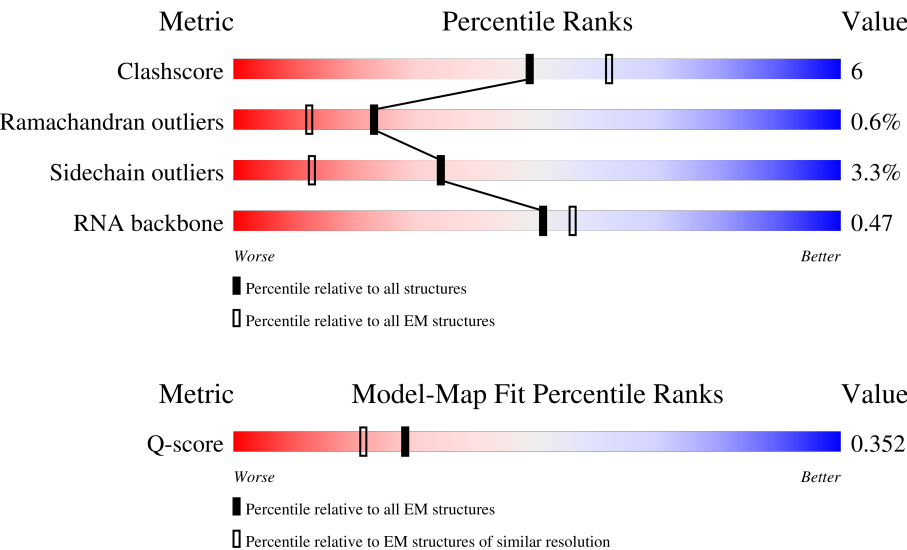
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.60 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	12797 (3.10 - 4.10)

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	300	33% 57% 38%
2	B	231	10% 70% 13% 16%
3	C	350	7% 30% 7% 62%

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Mol	Chain	Length	Quality of chain
4	D	544	
5	E	629	
6	F	523	
7	G	492	
8	H	105	
9	I	261	
10	J	583	
11	K	196	
12	L	146	
13	M	110	
14	N	101	
15	O	94	
16	P	86	
17	Q	77	
18	R	568	
19	r	253	
20	X	861	
21	Y	208	

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 41488 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 U1 small nuclear ribonucleoprotein 70 kDa homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	186	Total	C	N	O	S	0	0
			1207	745	228	233	1		

- Molecule 2 is a protein called U1 small nuclear ribonucleoprotein C.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	195	Total	C	N	O	S	0	0
			1570	976	301	288	5		

- Molecule 3 is a protein called U1 small nuclear ribonucleoprotein A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	132	Total	C	N	O	S	0	0
			1058	674	193	187	4		

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	299	GLY	-	expression tag	UNP P32605
C	300	ARG	-	expression tag	UNP P32605
C	301	ARG	-	expression tag	UNP P32605
C	302	ILE	-	expression tag	UNP P32605
C	303	PRO	-	expression tag	UNP P32605
C	304	GLY	-	expression tag	UNP P32605
C	305	LEU	-	expression tag	UNP P32605
C	306	ILE	-	expression tag	UNP P32605
C	307	ASN	-	expression tag	UNP P32605
C	308	PRO	-	expression tag	UNP P32605
C	309	TRP	-	expression tag	UNP P32605
C	310	LYS	-	expression tag	UNP P32605
C	311	ARG	-	expression tag	UNP P32605
C	312	ARG	-	expression tag	UNP P32605
C	313	TRP	-	expression tag	UNP P32605

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Chain	Residue	Modelled	Actual	Comment	Reference
C	314	LYS	-	expression tag	UNP P32605
C	315	LYS	-	expression tag	UNP P32605
C	316	ASN	-	expression tag	UNP P32605
C	317	PHE	-	expression tag	UNP P32605
C	318	ILE	-	expression tag	UNP P32605
C	319	ALA	-	expression tag	UNP P32605
C	320	VAL	-	expression tag	UNP P32605
C	321	SER	-	expression tag	UNP P32605
C	322	ALA	-	expression tag	UNP P32605
C	323	ALA	-	expression tag	UNP P32605
C	324	ASN	-	expression tag	UNP P32605
C	325	ARG	-	expression tag	UNP P32605
C	326	PHE	-	expression tag	UNP P32605
C	327	LYS	-	expression tag	UNP P32605
C	328	LYS	-	expression tag	UNP P32605
C	329	ILE	-	expression tag	UNP P32605
C	330	SER	-	expression tag	UNP P32605
C	331	SER	-	expression tag	UNP P32605
C	332	SER	-	expression tag	UNP P32605
C	333	GLY	-	expression tag	UNP P32605
C	334	ALA	-	expression tag	UNP P32605
C	335	LEU	-	expression tag	UNP P32605
C	336	ASP	-	expression tag	UNP P32605
C	337	TYR	-	expression tag	UNP P32605
C	338	ASP	-	expression tag	UNP P32605
C	339	ILE	-	expression tag	UNP P32605
C	340	PRO	-	expression tag	UNP P32605
C	341	THR	-	expression tag	UNP P32605
C	342	THR	-	expression tag	UNP P32605
C	343	ALA	-	expression tag	UNP P32605
C	344	SER	-	expression tag	UNP P32605
C	345	GLU	-	expression tag	UNP P32605
C	346	ASN	-	expression tag	UNP P32605
C	347	LEU	-	expression tag	UNP P32605
C	348	TYR	-	expression tag	UNP P32605
C	349	PHE	-	expression tag	UNP P32605
C	350	GLN	-	expression tag	UNP P32605

- Molecule 4 is a protein called U1 small nuclear ribonucleoprotein component PRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	544	Total	C	N	O	S	0	0
			4561	2990	723	828	20		

- Molecule 5 is a protein called Pre-mRNA-processing factor 39.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	576	Total	C	N	O	S	0	0
			3981	2527	693	752	9		

- Molecule 6 is a protein called Protein NAM8.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	267	Total	C	N	O	S	0	0
			1818	1128	326	353	11		

- Molecule 7 is a protein called 56 kDa U1 small nuclear ribonucleoprotein component.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	239	Total	C	N	O	S	0	0
			1954	1267	321	354	12		

- Molecule 8 is a protein called U1 small nuclear ribonucleoprotein component SNU71,U1 small nuclear ribonucleoprotein component SNU71,Snu71.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	105	Total	C	N	O	S	0	0
			685	425	127	132	1		

- Molecule 9 is a protein called Protein LUC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	192	Total	C	N	O	S	0	0
			1409	878	262	258	11		

- Molecule 10 is a protein called Pre-mRNA-processing protein PRP40.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	198	Total	C	N	O	S	0	0
			984	588	198	198			

- Molecule 11 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	123	Total	C	N	O	S	0	0
			1008	636	191	178	3		

- Molecule 12 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	119	Total	C	N	O	S	0	0
			921	578	164	176	3		

- Molecule 13 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	107	Total	C	N	O	S	0	0
			858	545	159	150	4		

- Molecule 14 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	93	Total	C	N	O	S	0	0
			710	450	122	134	4		

- Molecule 15 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	74	Total	C	N	O	S	0	0
			563	375	90	95	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	74	Total	C	N	O	S	0	0
			584	377	103	103	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	71	Total	C	N	O	S	0	0
			543	344	95	103	1		

- Molecule 18 is a RNA chain called U1 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	558	Total	C	N	O	P	0	0
			11822	5287	2003	3974	558		

- Molecule 19 is a RNA chain called UBC4 pre-mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	r	22	Total	C	N	O	P	0	0
			471	211	85	153	22		

- Molecule 20 is a protein called Nuclear cap-binding protein complex subunit 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	X	826	Total	C	N	O	0	0
			4101	2449	826	826		

- Molecule 21 is a protein called Nuclear cap-binding protein subunit 2.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	Y	138	Total	C	N	O	0	0
			677	401	138	138		

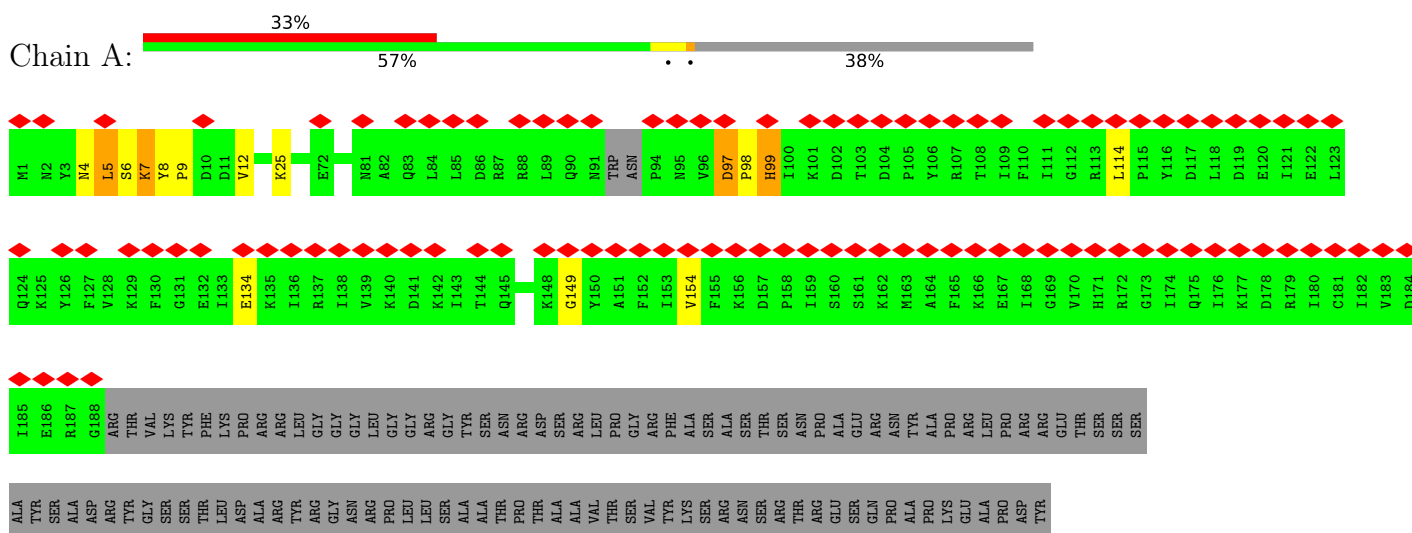
- Molecule 22 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
22	B	1	Total	Zn	0
			1	1	
22	I	2	Total	Zn	0
			2	2	

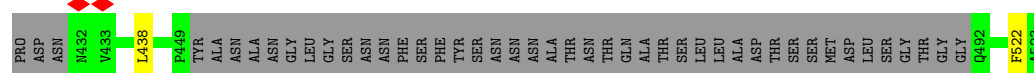
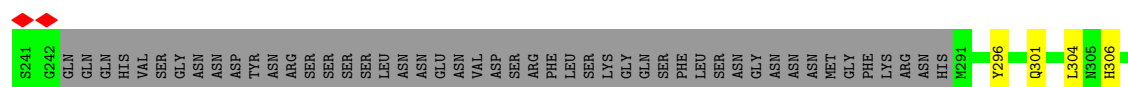
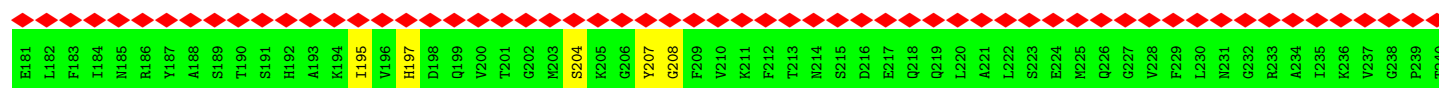
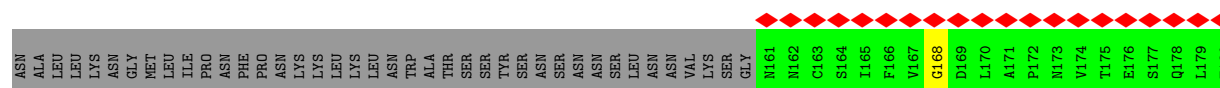
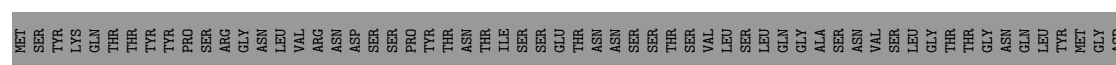
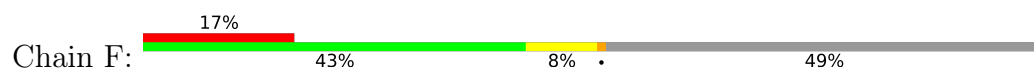
3 Residue-property plots

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.

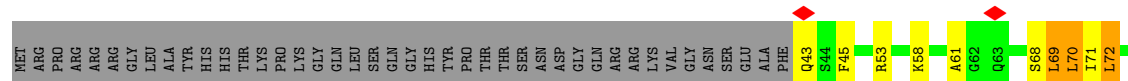
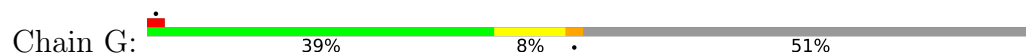
- Molecule 1: U1 small nuclear ribonucleoprotein 70 kDa homolog

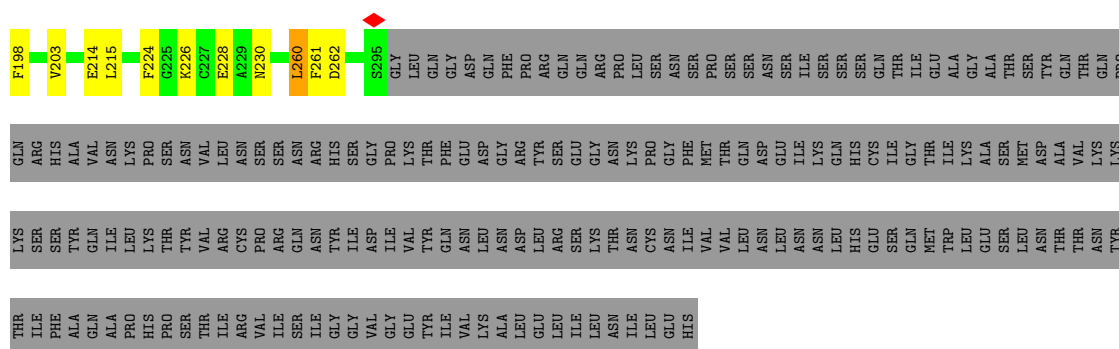


- Molecule 6: Protein NAM8



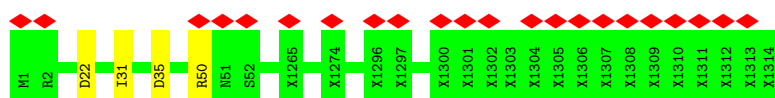
- Molecule 7: 56 kDa U1 small nuclear ribonucleoprotein component





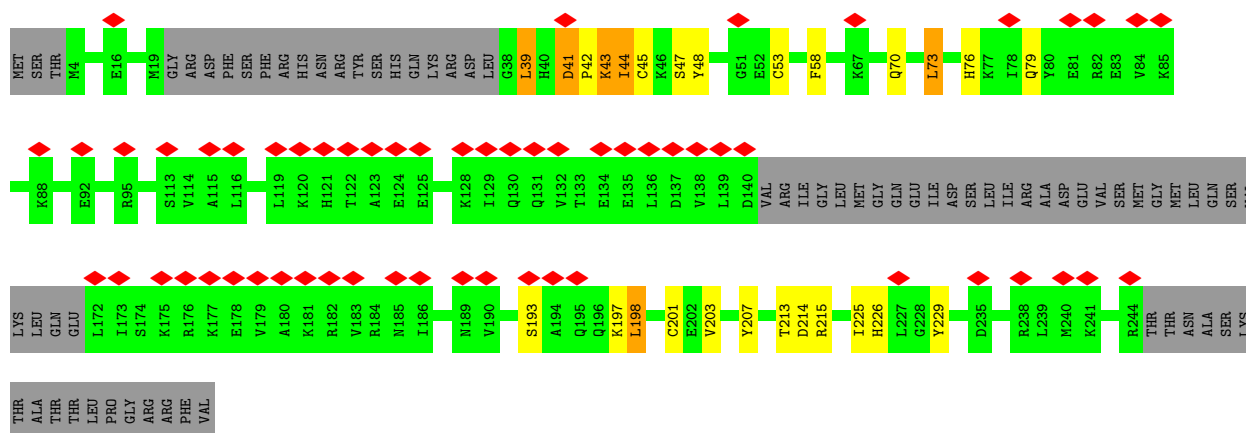
- Molecule 8: U1 small nuclear ribonucleoprotein component SNU71, U1 small nuclear ribonucleoprotein component SNU71, Snu71

Chain H: 21% 96%



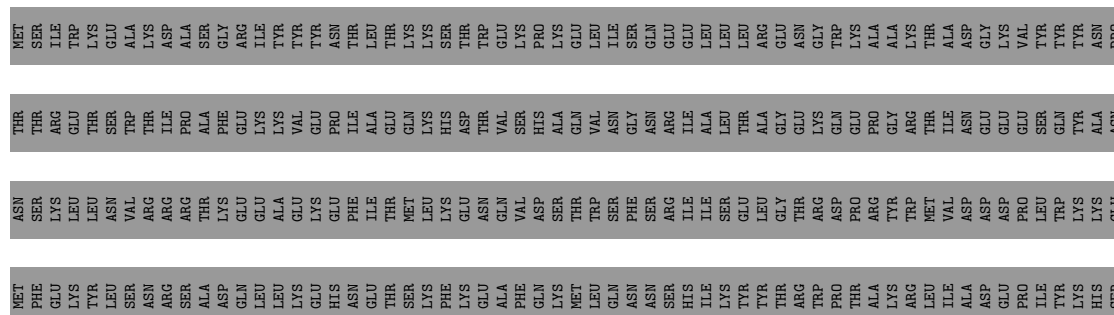
- Molecule 9: Protein LUC7

Chain I: 22% 64% 8% 26%

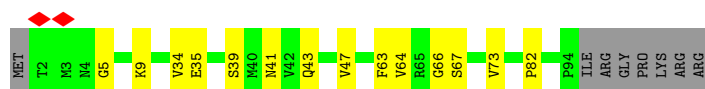


- Molecule 10: Pre-mRNA-processing protein PRP40

Chain J: 34% 33% 66%

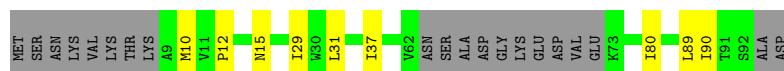


Chain N:  78% 14% 8%



• Molecule 15: Small nuclear ribonucleoprotein E

Chain O:  69% 10% 21%



• Molecule 16: Small nuclear ribonucleoprotein F

Chain P:  69% 17% 14%

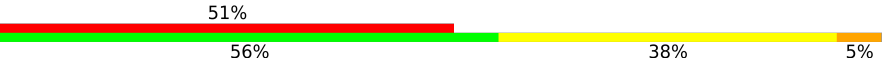


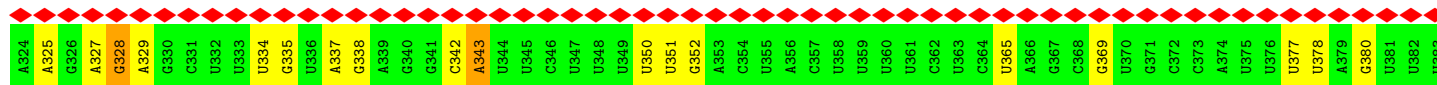
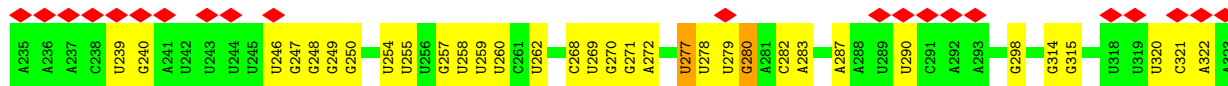
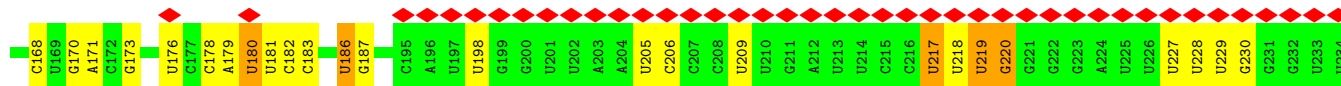
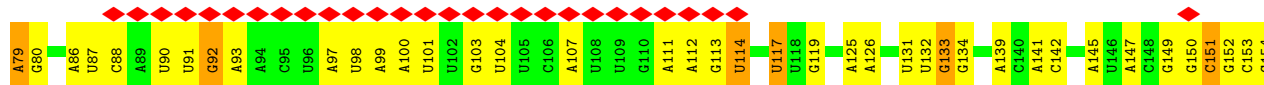
• Molecule 17: Small nuclear ribonucleoprotein G

Chain Q:  75% 12% 5% 8%



• Molecule 18: U1 snRNA

Chain R:  51% 56% 38% 5%





P301	D361	T421	L481	P541	T601	L661	F721	D781	A841
S302	L362	I422	D482	Q542	H602	K662	N722	E782	T842
V303	V363	L423	W483	E543	K603	E663	E723	D783	P843
D304	E364	G424	F484	F544	A604	D664	T724	I784	H844
D305	S365	L425	S485	T545	N605	L665	G725	E785	E845
L306	L366	L426	I486	K546	N606	K666	L726	I786	S846
K307	E367	F427	Q487	Y547	S607	T667	K727	P787	T847
S308	F368	K428	M488	L548	R608	I668	N728	K788	R848
F309	N369	L429	S489	D549	E609	F669	N729	V789	R849
V310	N370	P430	M490	T550	V610	A670	G730	N790	T850
R311	K371	S431	F491	S551	T611	K671	L731	G791	I851
L312	E372	V432	M492	Y552	E612	I672	I732	E792	S852
N313	V373	S433	F493	I553	L613	E673	E733	M793	N853
K314	A374	Q434	S494	P554	E614	L674	A734	D794	W854
N315	R375	P435	W495	R555	S615	D675	T735	I795	I855
F316	Q376	F436	K496	D556	I616	I676	A736	D796	Q856
G317	I377	A437	W497	Q557	L617	E677	I737	D797	E857
S318	I378	Y438	M498	L558	G618	T678	E738	I798	T858
V319	T379	F439	E499	I559	E619	K679	A739	E799	K859
D320	L380	Y440	W500	N560	L620	E680	V740	D800	E860
S321	D381	T441	E501	Y561	K621	I681	F741	D801	W861
M322	L382	L442	D502	Y562	N622	I682	R742	K802	
W323	F383	L443	D503	Q563	E623	I683	N743	L803	
K324	F384	V444	S504	S564	Y624	L684	L744	D804	
T325	K385	D445	I505	L565	G625	E685	S745	L805	
P326	A386	I446	K506	F566	S626	A686	Q746	K806	
R327	G387	C447	F507	T567	I627	V687	Q747	W807	
Y328	I388	Q448	G508	G568	E628	L688	I748	K808	
A329	F389	N449	K509	Y569	S629	T689	S749	Y809	
F330	T390	S450	Y510	T570	D630	F690	E750	F810	
H331	E391	P451	F511	V571	F631	W691	E751	T811	
V332	P392	K452	Y512	E572	N632	N692	N752	W812	
V333	G393	A453	N513	E573	K633	A693	E753	L813	
L334	E394	I454	P514	D574	F634	N694	F754	G814	
P335	S395	A455	K515	S575	V635	P695	G755	F815	
N336	I396	P456	V516	V576	I636	Q696	N756	L816	
S337	A397	V457	N517	R577	I637	T697	N757	K817	
A338	Q398	F458	F518	K378	L638	G698	F758	S818	
G339	L399	G459	A519	N579	L639	F699	E759	L819	
N340	I400	R460	K520	D580	V640	L700	F760	R820	
F341	A401	A461	N521	L581	Q641	V701	V761	R821	
E342	T402	F462	I522	F583	A642	A702	F762	R822	
T343	Y403	R463	I523	F583	V643	D703	E763	E823	
V344	E404	F464	Q524	R584	T644	A704	R764	S824	
V345	E405	F465	K525	Q585	D645	F705	L765	H825	
P346	N406	Y466	E526	E586	S646	K706	C766	E826	
I347	P407	S467	L527	G587	G647	Y707	T767	Y827	
S348	L408	H468	R528	V588	S648	A708	I768	R828	
T349	A409	L469	L529	F589	R649	G709	A769	E829	
Y350	P410	D470	T530	N590	S650	L710	N770	L830	
A351	T411	S471	S531	E591	L651	L711	S771	A831	
G352	F412	L472	N532	N592	S652	T712	T772	D832	
Q353	K413	D473	F533	T593	H653	R713	I773	K833	
L354	I414	F474	S534	V594	A654	S714	D774	F834	
F355	E415	E475	E535	R595	N655	T715	L775	I835	
N356	D416	L476	V536	K596	K656	I716	L776	A836	
D357	L417	K477	E537	I597	Y657	F717	D777	N837	
I358	A418	L478	D538	L598	T658	T718	V778	L838	
I359	I419	R479	S539	D599	N659	F719	N779	D839	
I360	E420	Y480	L540	Y600	D660	I720	A780	N840	

● Molecule 21: Nuclear cap-binding protein subunit 2



MET	SER	LEU	GLU	GLU	PHE	ASP	GLU	GLU	VAL	LYS	TYR	ASP	HIS	SER	THR	LYS	ARG	LEU																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	</
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	124825	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.371	Depositor
Minimum map value	-0.206	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.065	Depositor
Map size ($\text{\AA}$)	522.24, 522.24, 522.24	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.36, 1.36, 1.36	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.49	0/1224	0.73	0/1675
2	B	0.54	0/1601	0.77	0/2154
3	C	0.43	0/1072	0.73	0/1437
4	D	0.68	0/4676	0.77	2/6320 (0.0%)
5	E	0.50	0/4046	0.74	4/5539 (0.1%)
6	F	0.58	0/1844	0.80	2/2511 (0.1%)
7	G	0.57	0/1996	0.77	0/2682
8	H	0.45	0/428	0.52	0/575
9	I	0.38	0/1428	0.66	0/1924
10	J	0.47	0/983	0.80	1/1371 (0.1%)
11	K	0.62	0/1014	0.74	0/1350
12	L	0.58	0/930	0.72	0/1261
13	M	0.51	0/872	0.63	0/1174
14	N	0.67	0/722	0.76	2/979 (0.2%)
15	O	0.55	0/573	0.64	0/778
16	P	0.61	0/597	0.80	0/809
17	Q	0.65	0/546	0.84	0/735
18	R	0.33	0/13201	0.49	4/20553 (0.0%)
19	r	0.31	0/527	0.49	0/819
20	X	0.28	0/4100	0.94	22/5721 (0.4%)
21	Y	0.26	0/676	0.78	0/937
All	All	0.47	0/43056	0.69	37/61304 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	C	0	2
20	X	0	24

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	26

There are no bond length outliers.

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	X	281	TRP	N-CA-C	8.95	121.80	110.61
20	X	673	GLU	CA-C-N	8.63	138.02	121.54
20	X	673	GLU	C-N-CA	8.63	138.02	121.54
18	R	442	U	OP2-P-O3'	-8.61	82.18	108.00
18	R	442	U	OP1-P-O3'	-8.60	82.20	108.00

There are no chirality outliers.

5 of 26 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	12	ARG	Sidechain,Peptide
20	X	281	TRP	Peptide
20	X	284	LEU	Peptide
20	X	69	GLY	Peptide
20	X	70	HIS	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	A	1207	0	927	13	0
2	B	1570	0	1553	35	0
3	C	1058	0	1118	26	0
4	D	4561	0	4549	74	0
5	E	3981	0	3282	35	0
6	F	1818	0	1567	29	0
7	G	1954	0	1961	44	0
8	H	685	0	477	4	0
9	I	1409	0	1285	24	0
10	J	984	0	416	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	K	1008	0	1109	9	0
12	L	921	0	972	10	0
13	M	858	0	882	13	0
14	N	710	0	730	17	0
15	O	563	0	594	6	0
16	P	584	0	586	11	0
17	Q	543	0	560	7	0
18	R	11822	0	5939	99	0
19	r	471	0	236	6	0
20	X	4101	0	1779	14	0
21	Y	677	0	298	1	0
22	B	1	0	0	0	0
22	I	2	0	0	0	0
All	All	41488	0	30820	421	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 6.

The worst 5 of 421 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)
4:D:303:LEU:CD1	4:D:312:VAL:HG11	1.70	1.21
2:B:8:TYR:CE1	14:N:82:PRO:HG3	1.80	1.15
3:C:13:PRO:HD2	3:C:19:TYR:CD1	1.82	1.14
2:B:136:LEU:HD23	2:B:137:PRO:HD2	1.11	1.09
2:B:8:TYR:HE1	14:N:82:PRO:CG	1.64	1.09

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	182/300 (61%)	162 (89%)	17 (9%)	3 (2%)	7	36
2	B	193/231 (84%)	180 (93%)	10 (5%)	3 (2%)	7	36
3	C	126/350 (36%)	120 (95%)	6 (5%)	0	100	100
4	D	542/544 (100%)	515 (95%)	27 (5%)	0	100	100
5	E	570/629 (91%)	532 (93%)	38 (7%)	0	100	100
6	F	259/523 (50%)	240 (93%)	19 (7%)	0	100	100
7	G	235/492 (48%)	218 (93%)	17 (7%)	0	100	100
8	H	50/105 (48%)	47 (94%)	3 (6%)	0	100	100
9	I	186/261 (71%)	174 (94%)	11 (6%)	1 (0%)	24	57
10	J	196/583 (34%)	185 (94%)	10 (5%)	1 (0%)	24	57
11	K	119/196 (61%)	111 (93%)	8 (7%)	0	100	100
12	L	117/146 (80%)	111 (95%)	6 (5%)	0	100	100
13	M	105/110 (96%)	103 (98%)	2 (2%)	0	100	100
14	N	91/101 (90%)	84 (92%)	7 (8%)	0	100	100
15	O	70/94 (74%)	68 (97%)	2 (3%)	0	100	100
16	P	72/86 (84%)	68 (94%)	4 (6%)	0	100	100
17	Q	67/77 (87%)	62 (92%)	5 (8%)	0	100	100
20	X	824/861 (96%)	727 (88%)	80 (10%)	17 (2%)	5	31
21	Y	136/208 (65%)	120 (88%)	15 (11%)	1 (1%)	18	51
All	All	4140/5897 (70%)	3827 (92%)	287 (7%)	26 (1%)	23	54

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	98	PRO
2	B	139	ARG
10	J	370	PRO
20	X	71	GLU
20	X	284	LEU

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	82/265 (31%)	80 (98%)	2 (2%)	43	63
2	B	171/214 (80%)	165 (96%)	6 (4%)	32	57
3	C	117/317 (37%)	112 (96%)	5 (4%)	26	52
4	D	508/519 (98%)	490 (96%)	18 (4%)	32	57
5	E	316/603 (52%)	310 (98%)	6 (2%)	50	67
6	F	157/451 (35%)	148 (94%)	9 (6%)	18	46
7	G	218/448 (49%)	203 (93%)	15 (7%)	14	41
8	H	48/48 (100%)	48 (100%)	0	100	100
9	I	130/234 (56%)	125 (96%)	5 (4%)	29	55
11	K	114/176 (65%)	114 (100%)	0	100	100
12	L	107/129 (83%)	107 (100%)	0	100	100
13	M	95/103 (92%)	94 (99%)	1 (1%)	65	74
14	N	81/89 (91%)	80 (99%)	1 (1%)	63	73
15	O	62/83 (75%)	62 (100%)	0	100	100
16	P	64/77 (83%)	62 (97%)	2 (3%)	35	59
17	Q	59/66 (89%)	51 (86%)	8 (14%)	3	20
All	All	2329/3822 (61%)	2251 (97%)	78 (3%)	34	58

5 of 78 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	G	122	ILE
17	Q	17	LEU
7	G	203	VAL
9	I	198	LEU
17	Q	63	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
5	E	617	ASN
16	P	47	ASN
6	F	497	GLN
16	P	24	ASN
13	M	86	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
18	R	556/568 (97%)	134 (24%)	18 (3%)
19	r	21/253 (8%)	6 (28%)	0
All	All	577/821 (70%)	140 (24%)	18 (3%)

5 of 140 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
18	R	10	U
18	R	11	U
18	R	12	A
18	R	13	A
18	R	17	A

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
18	R	277	U
18	R	505	U
18	R	399	A
18	R	133	G
18	R	268	C

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
8	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	52:SER	C	1262:UNK	N	64.87

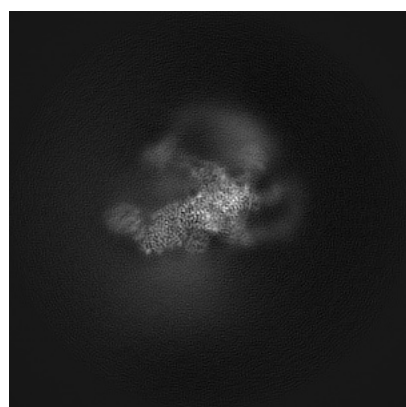
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0360. These allow visual inspection of the internal detail of the map and identification of artifacts.

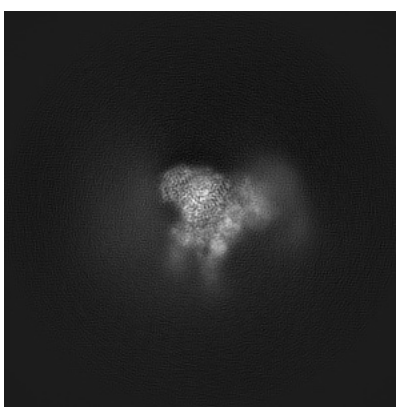
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

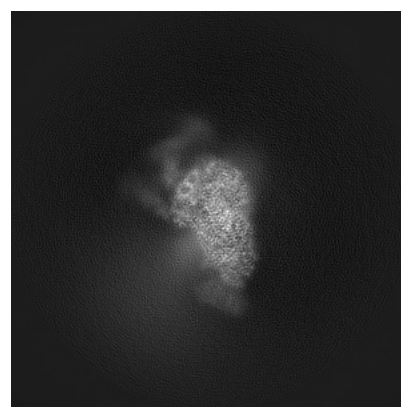
6.1.1 Primary map



X



Y

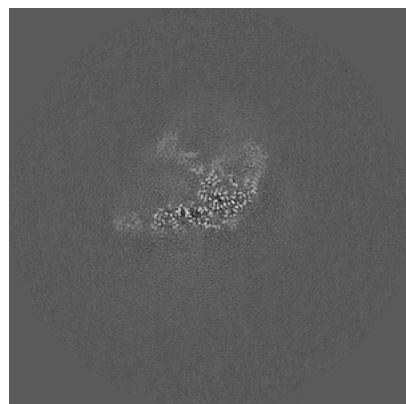


Z

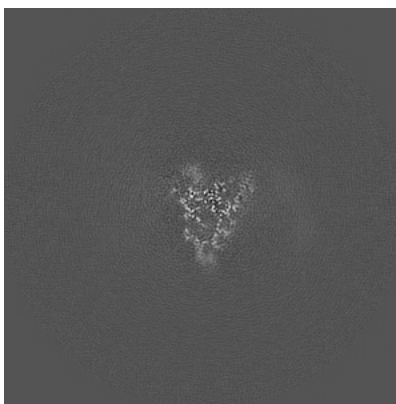
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

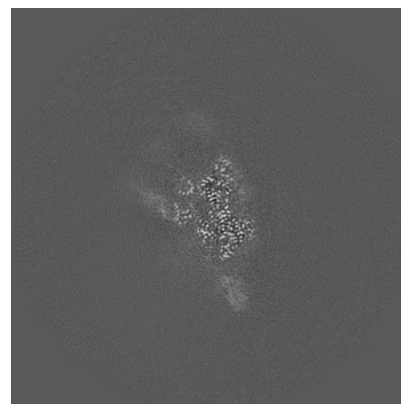
6.2.1 Primary map



X Index: 192



Y Index: 192

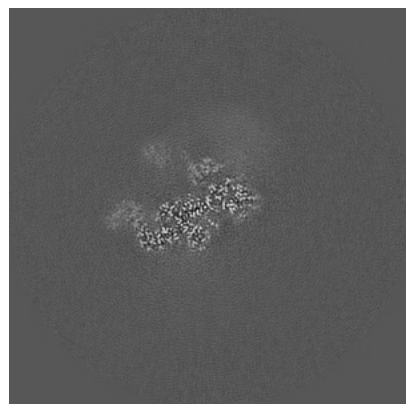


Z Index: 192

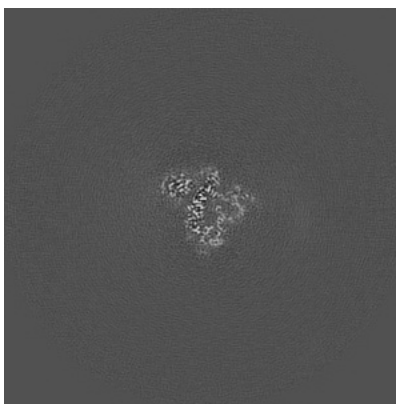
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

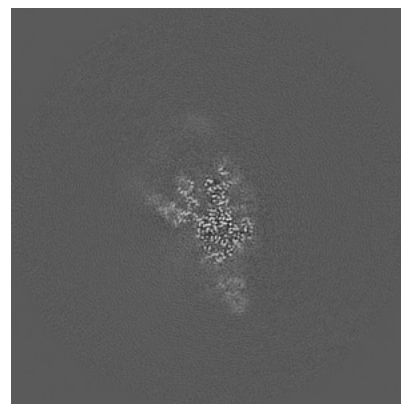
6.3.1 Primary map



X Index: 208



Y Index: 182

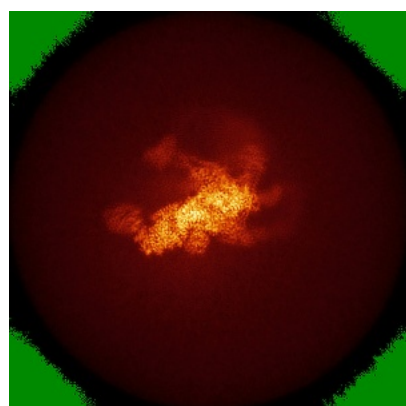


Z Index: 189

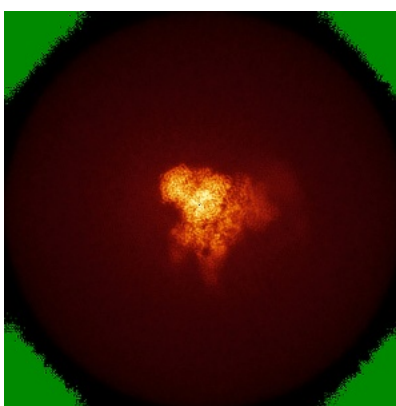
The images above show the largest variance slices of the map in three orthogonal directions.

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

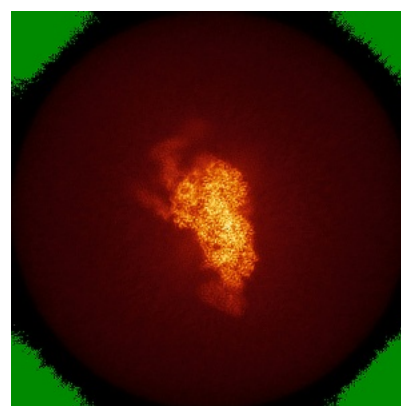
6.4.1 Primary map



X



Y

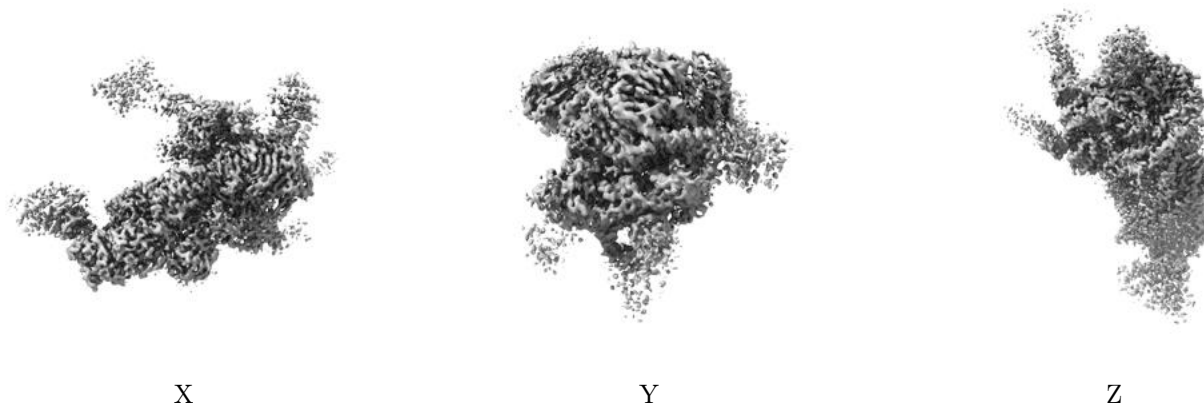


Z

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

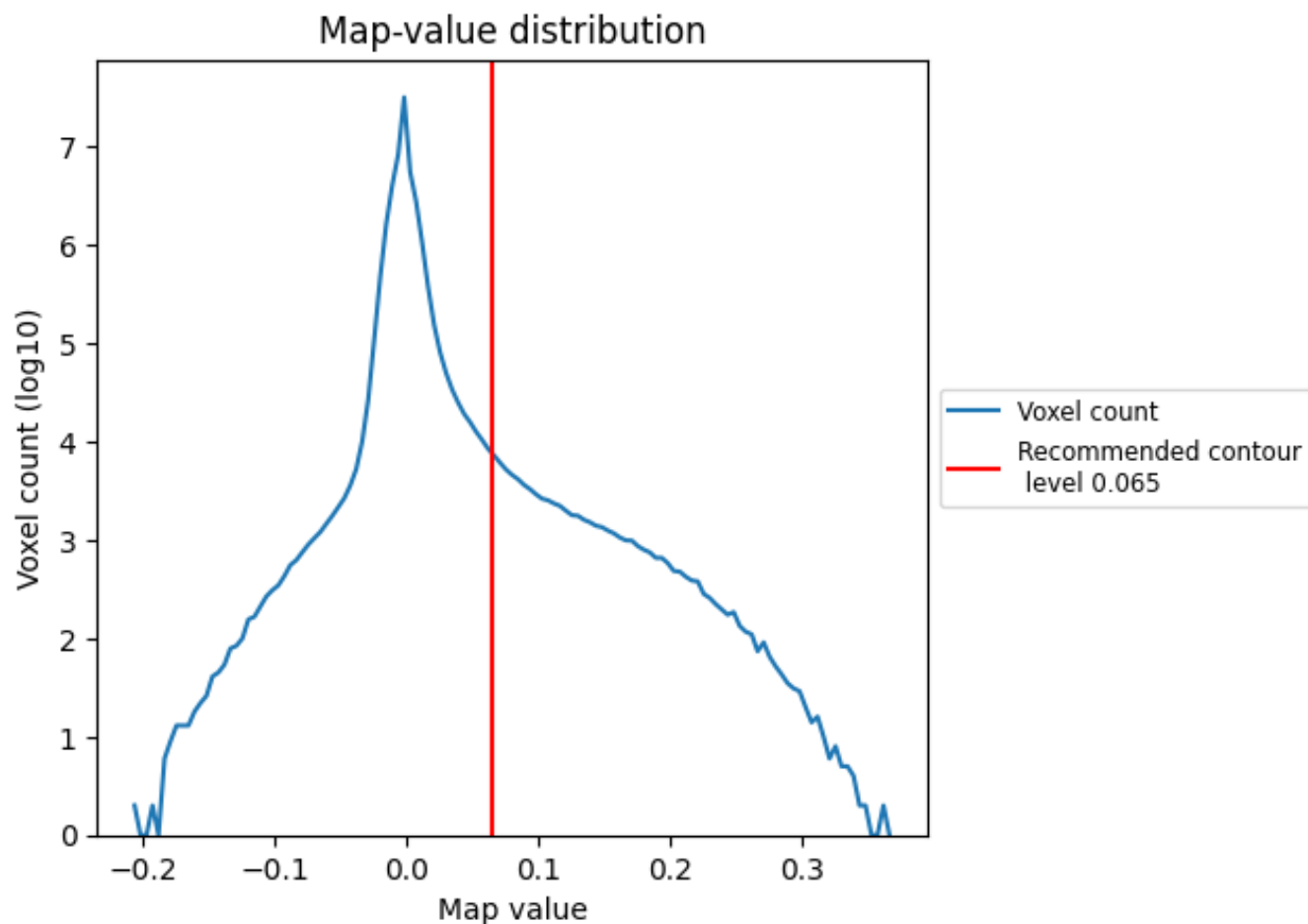
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

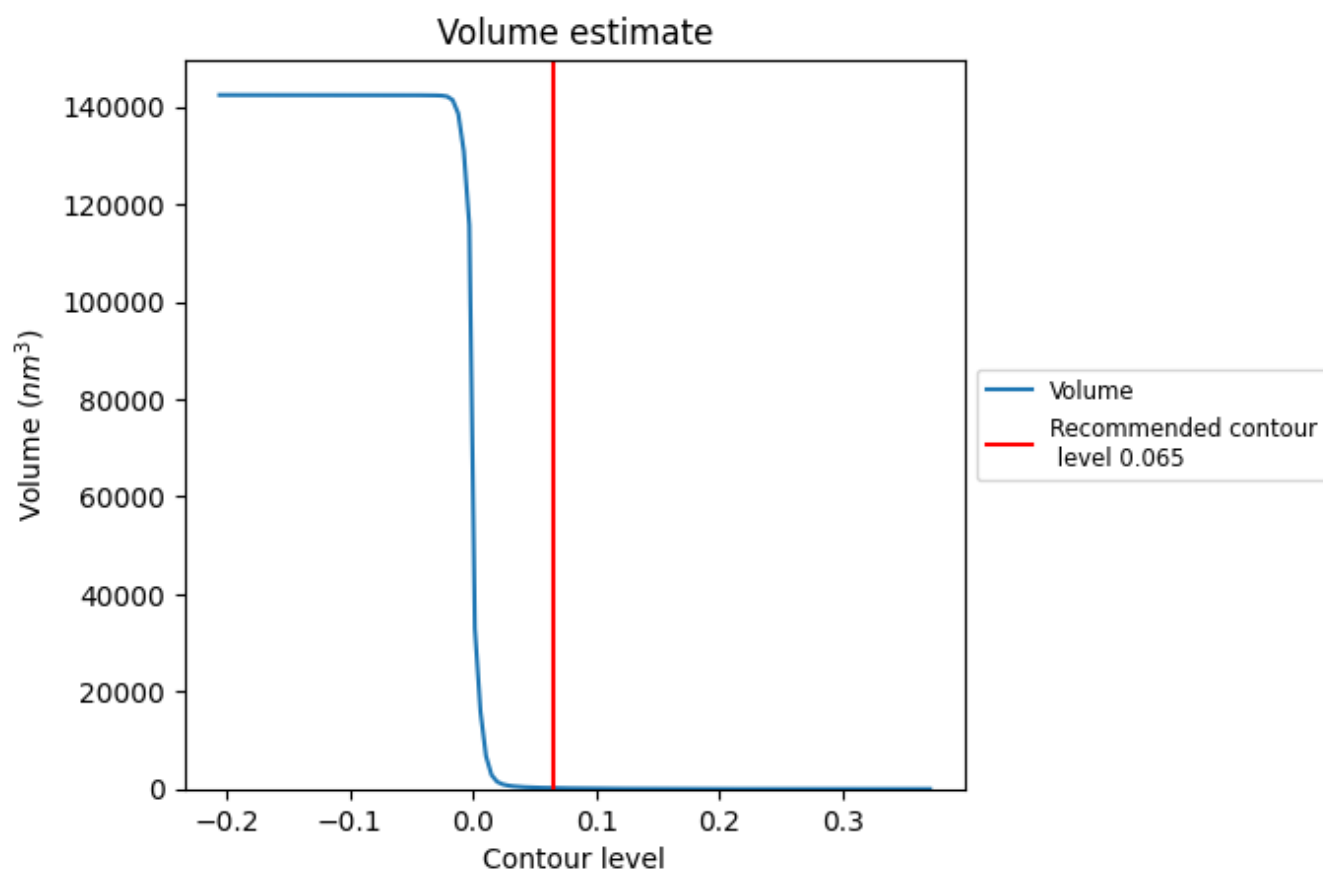
This section contains the results of statistical analysis of the map.

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.

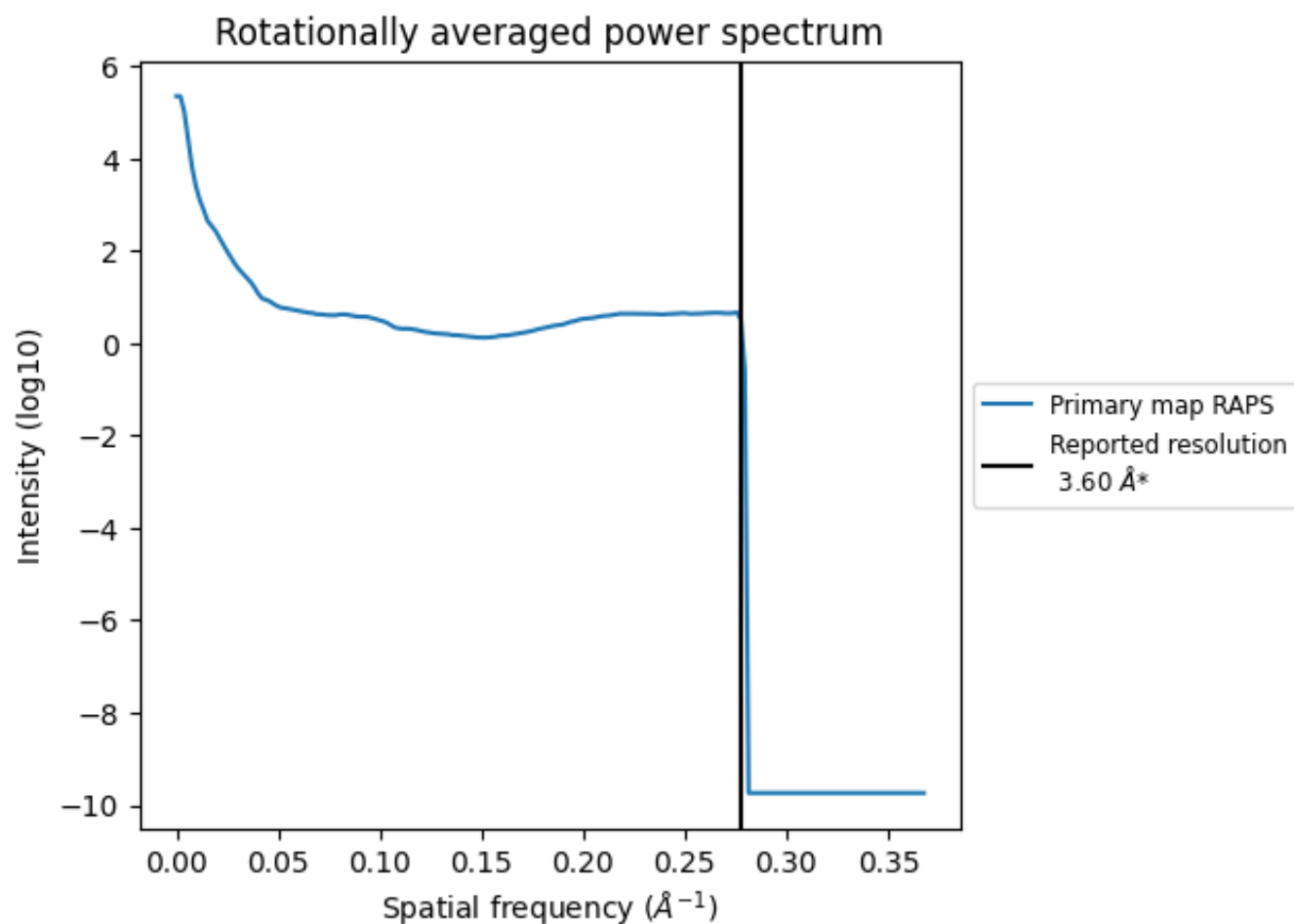
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 190 nm^3 ; this corresponds to an approximate mass of 171 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 ⓘ

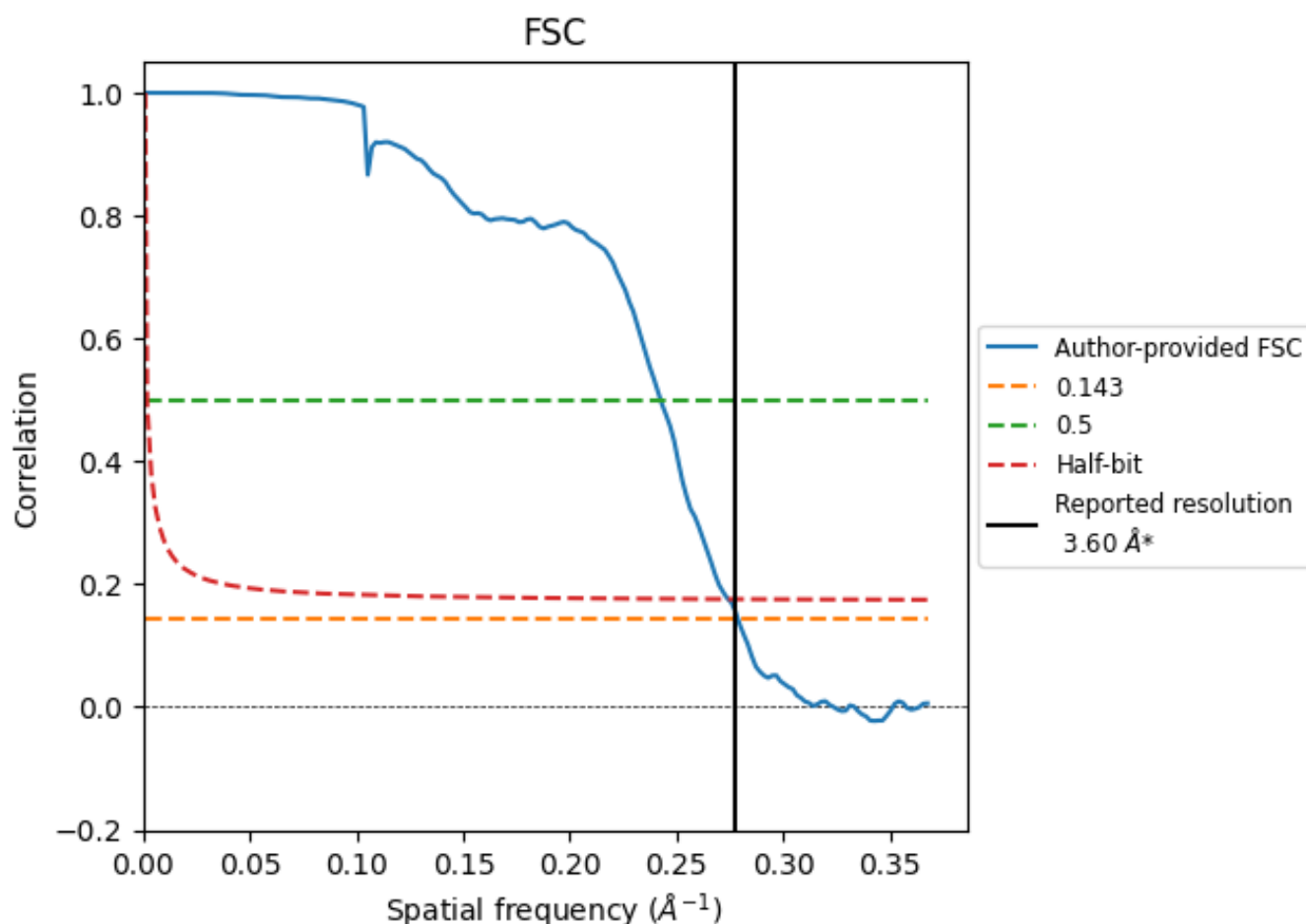


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

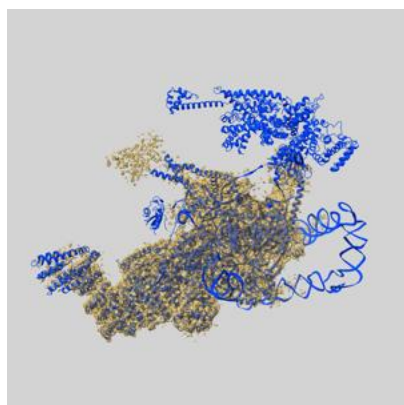
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.59	4.12	3.65
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

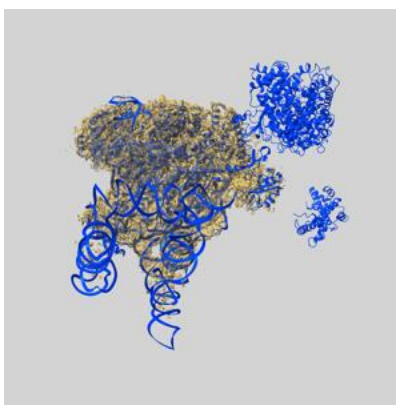
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0360 and PDB model 6N7P. Per-residue inclusion information can be found in section [3](#) on page [9](#).

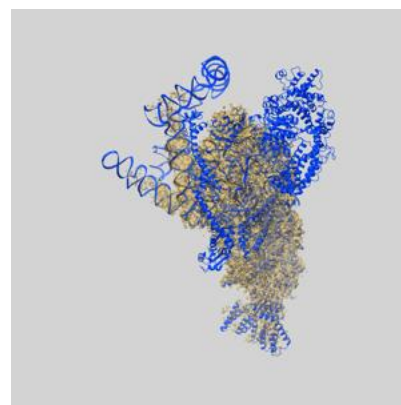
9.1 Map-model overlay [i](#)



X



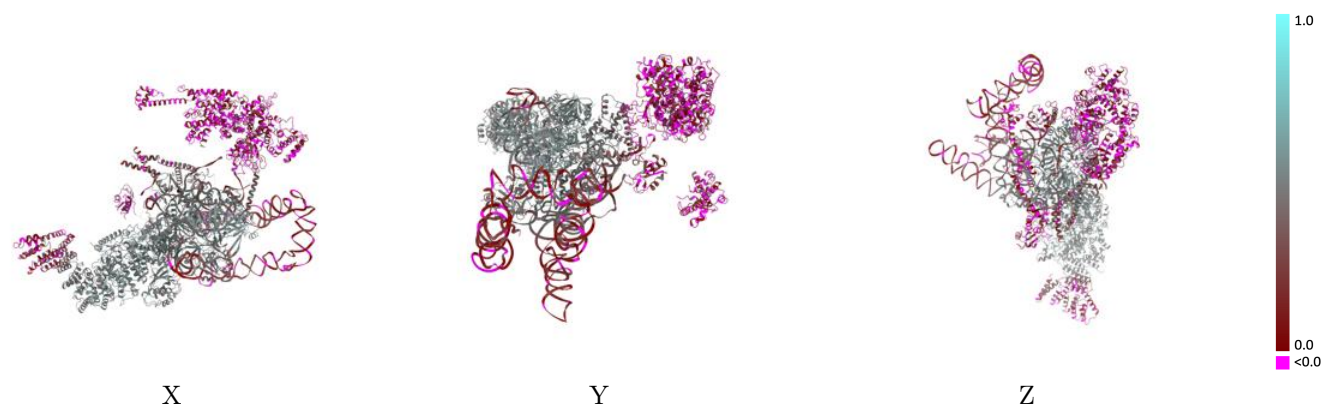
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.065 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](#)

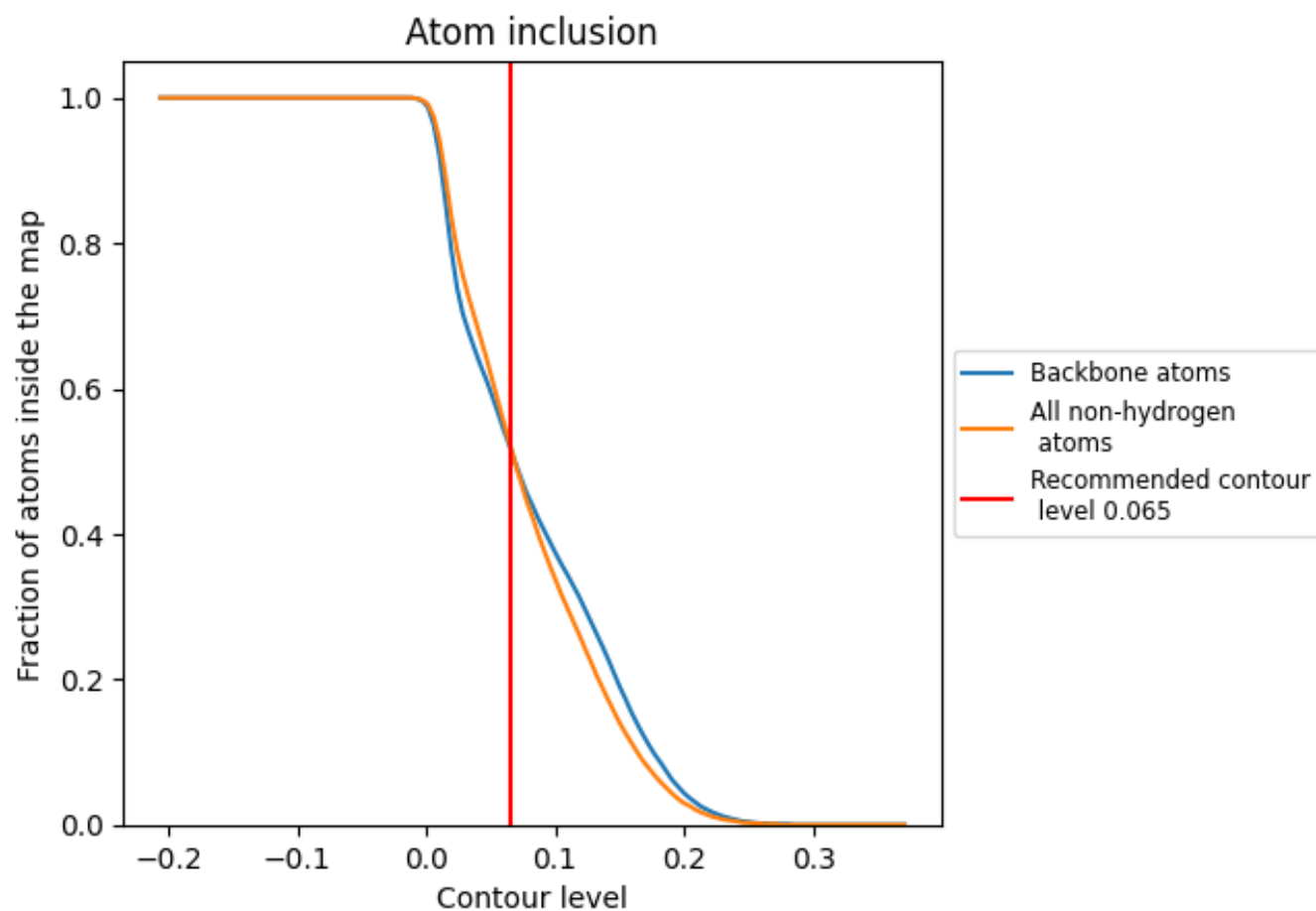


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 52% of all backbone atoms, 52% 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 (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5230	 0.3520
A	 0.4790	 0.3590
B	 0.7210	 0.4940
C	 0.6150	 0.4190
D	 0.8350	 0.5290
E	 0.5890	 0.3960
F	 0.6130	 0.4260
G	 0.7570	 0.5030
H	 0.6720	 0.4630
I	 0.5690	 0.4080
J	 0.0000	 0.0480
K	 0.7590	 0.5120
L	 0.7970	 0.5130
M	 0.7630	 0.5140
N	 0.7880	 0.5370
O	 0.8070	 0.5180
P	 0.8310	 0.5250
Q	 0.8020	 0.5270
R	 0.4330	 0.2710
X	 0.0000	 0.0480
Y	 0.0000	 0.0440
r	 0.4310	 0.2910

