



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 07:32 AM UTC

PDB ID : 6KW3 / pdb_00006kw3
EMDB ID : EMD-0777
Title : The ClassA RSC-Nucleosome Complex
Authors : Ye, Y.P.; Wu, H.; Chen, K.J.; Verma, N.; Cairns, B.; Gao, N.; Chen, Z.C.
Deposited on : 2019-09-05
Resolution : 7.13 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:

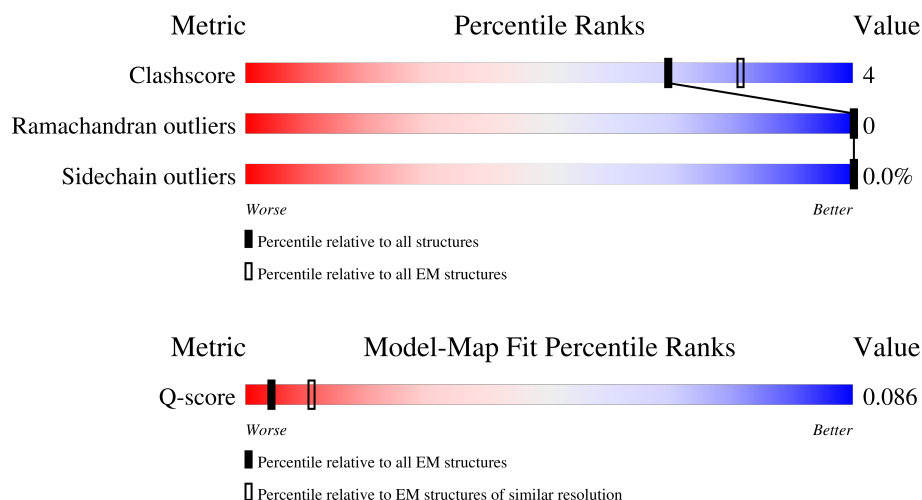
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 7.13 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	-
Q-score	-	25397	419 (6.63 - 7.61)

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	B	103	 9% 72% 8% 20%
1	R	103	 9% 72% 13% 16%
2	N	136	 65% 7% 28%
2	Q	136	 62% 8% 30%

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Mol	Chain	Length	Quality of chain
3	O	130	
3	S	130	
4	U	167	
5	V	167	
6	J	1359	
6	W	1359	
6	Y	1359	
7	f	477	
8	h	157	
9	F	435	
10	D	557	
10	H	557	
11	M	581	
12	I	483	
13	G	426	
14	A	502	
15	E	78	
16	C	883	
17	K	885	
18	X	625	
19	L	889	
20	P	126	
20	T	126	
21	g	467	

2 Entry composition

There are 22 unique types of molecules in this entry. The entry contains 45514 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 Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	82	Total	C	N	O	S	0	0
			657	416	128	112	1		
1	R	87	Total	C	N	O	S	0	0
			703	443	142	117	1		

- Molecule 2 is a protein called Histone H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	N	98	Total	C	N	O	S	0	0
			810	511	157	139	3		
2	Q	95	Total	C	N	O	S	0	0
			784	494	151	136	3		

- Molecule 3 is a protein called Histone H2A.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	O	107	Total	C	N	O	0	0
			823	519	161	143		
3	S	107	Total	C	N	O	0	0
			823	519	161	143		

- Molecule 4 is a DNA chain called DNA 167.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	U	146	Total	C	N	O	P	0	0
			2977	1414	542	875	146		

- Molecule 5 is a DNA chain called DNA 167.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	V	146	Total	C	N	O	P	0	0
			3009	1425	561	877	146		

- Molecule 6 is a protein called Nuclear protein STH1/NPS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	W	69	Total	C	N	O	S	0	0
			592	364	121	105	2		
6	J	235	Total	C	N	O	S	0	0
			1814	1136	327	349	2		
6	Y	548	Total	C	N	O	S	0	0
			4503	2873	780	832	18		

- Molecule 7 is a protein called Actin-related protein 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	f	398	Total	C	N	O	S	3	0
			3219	2075	527	602	15		

- Molecule 8 is a protein called Regulator of Ty1 transposition protein 102.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	h	54	Total	C	N	O	S	0	0
			490	313	84	92	1		

- Molecule 9 is a protein called Chromatin structure-remodeling complex subunit RSC7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	118	Total	C	N	O	S	0	0
			964	601	164	197	2		

- Molecule 10 is a protein called Chromatin structure-remodeling complex protein RSC8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	393	Total	C	N	O	S	0	0
			3215	2036	552	613	14		
10	D	305	Total	C	N	O	S	0	0
			2510	1613	416	471	10		

- Molecule 11 is a protein called Chromatin structure-remodeling complex subunit RSC9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	384	Total	C	N	O	S	0	0
			3058	1970	497	574	17		

- Molecule 12 is a protein called Chromatin structure-remodeling complex protein RSC6.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	244	Total	C	N	O	S	0	0
			1944	1234	328	377	5		

- Molecule 13 is a protein called Chromatin structure-remodeling complex subunit SFH1.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	246	Total	C	N	O	S	0	0
			1996	1271	337	380	8		

- Molecule 14 is a protein called Chromatin structure-remodeling complex protein RSC58.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	A	365	Total	C	N	O	S	0	0
			3007	1942	509	547	9		

- Molecule 15 is a protein called High temperature lethal protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E	58	Total	C	N	O	S	0	0
			477	295	86	92	4		

- Molecule 16 is a protein called Chromatin structure-remodeling complex protein RSC30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	C	33	Total	C	N	O	S	0	0
			269	177	39	52	1		

- Molecule 17 is a protein called Chromatin structure-remodeling complex protein RSC3.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	K	42	Total	C	N	O	S	0	0
			347	225	57	63	2		

- Molecule 18 is a protein called Chromatin structure-remodeling complex subunit RSC4.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	X	147	Total	C	N	O	S	0	0
			1220	776	202	234	8		

- Molecule 19 is a protein called Chromatin structure-remodeling complex subunit RSC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	85	Total	C	N	O	S	0	0
			669	428	120	119	2		

- Molecule 20 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	93	Total	C	N	O	S	0	0
			725	456	130	137	2		
20	P	93	Total	C	N	O	S	0	0
			717	450	128	137	2		

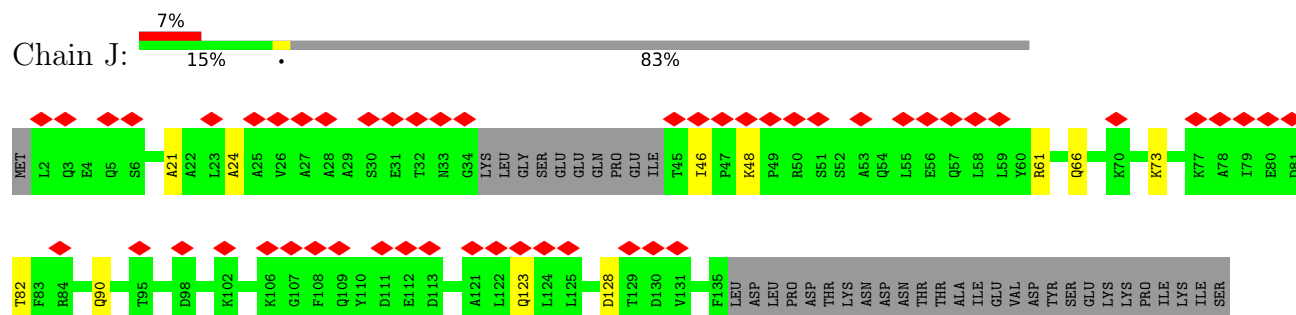
- Molecule 21 is a protein called Actin-like protein ARP9.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	g	395	Total	C	N	O	S	1	0
			3191	2048	522	614	7		

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

Mol	Chain	Residues	Atoms		AltConf
22	H	1	Total	Zn	0
			1	1	

- Molecule 6: Nuclear protein STH1/NPS1



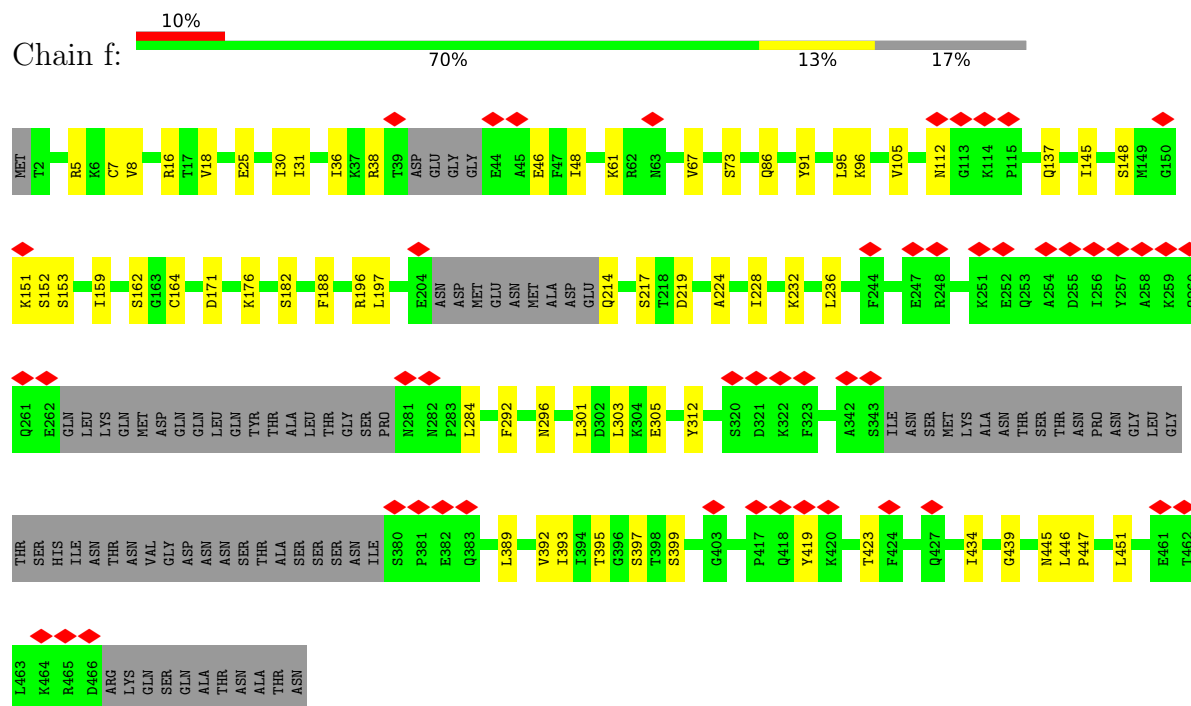


Chain Y:

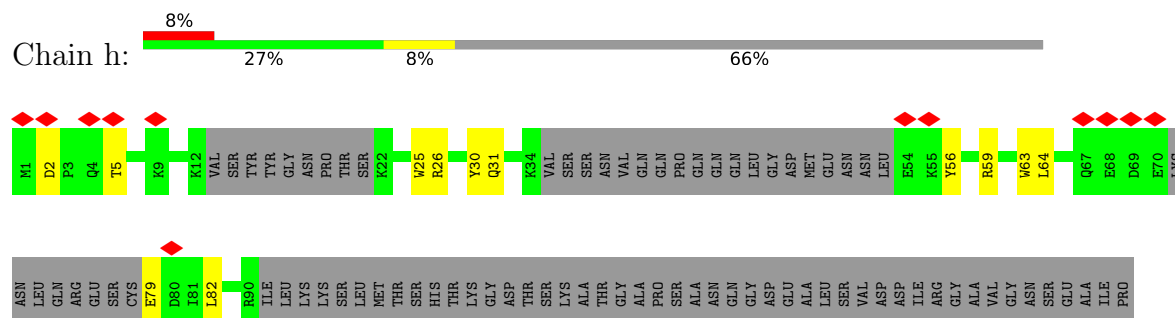




• Molecule 7: Actin-related protein 7



• Molecule 8: Regulator of Ty1 transposition protein 102



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• Molecule 9: Chromatin structure-remodeling complex subunit RSC7

Chain F:



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• Molecule 10: Chromatin structure-remodeling complex protein RSC8

Chain H:



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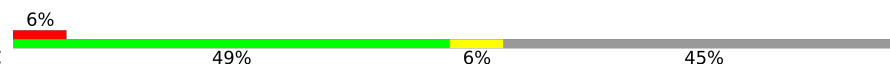
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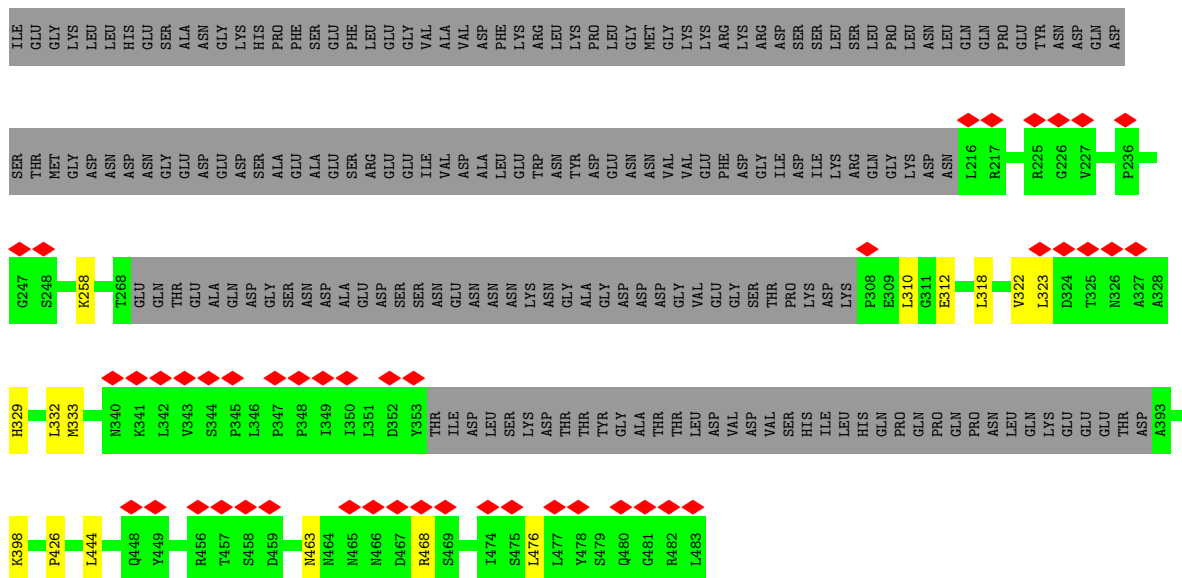
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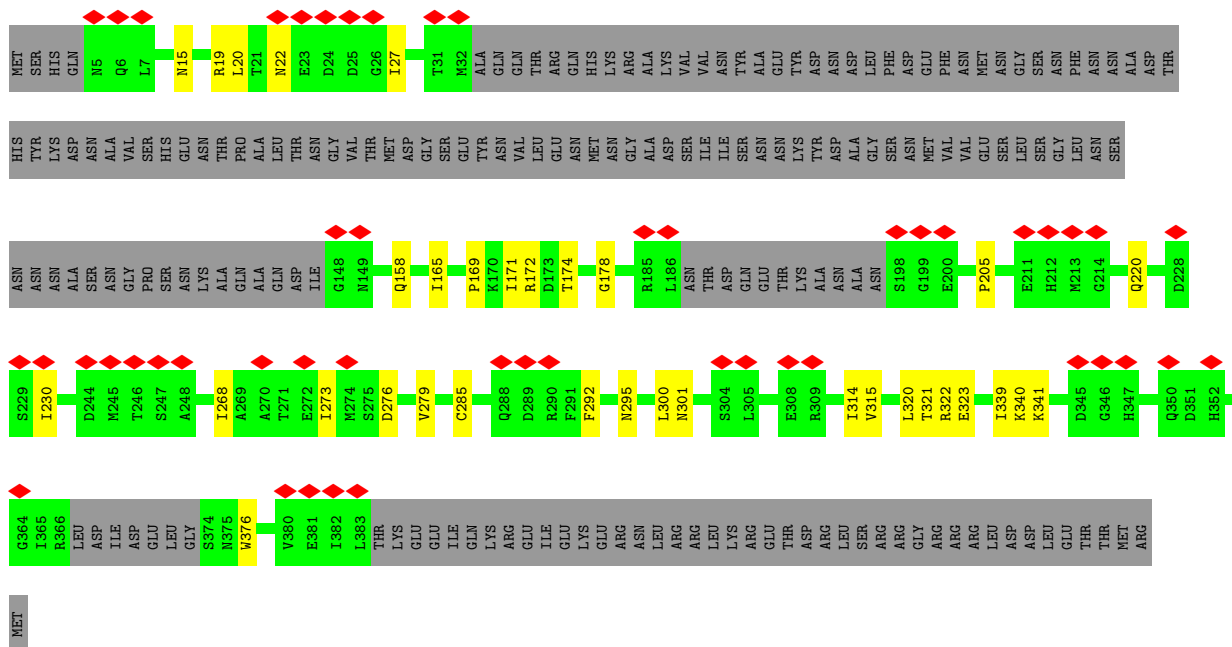
• Molecule 10: Chromatin structure-remodeling complex protein RSC8

Chain D:

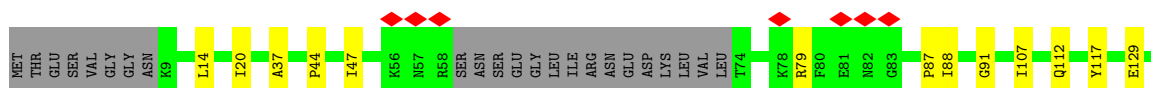


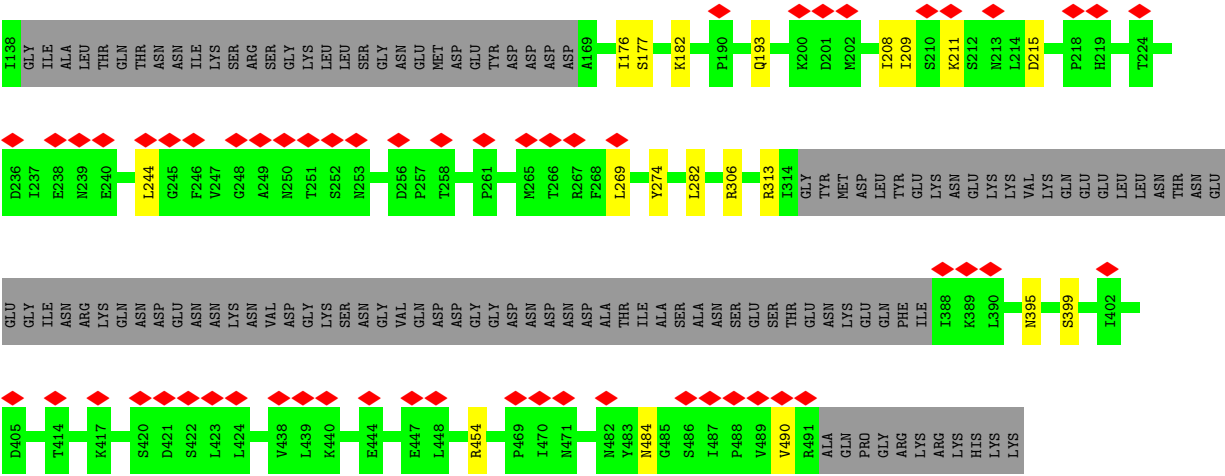


- Molecule 13: Chromatin structure-remodeling complex subunit SFH1



- Molecule 14: Chromatin structure-remodeling complex protein RSC58







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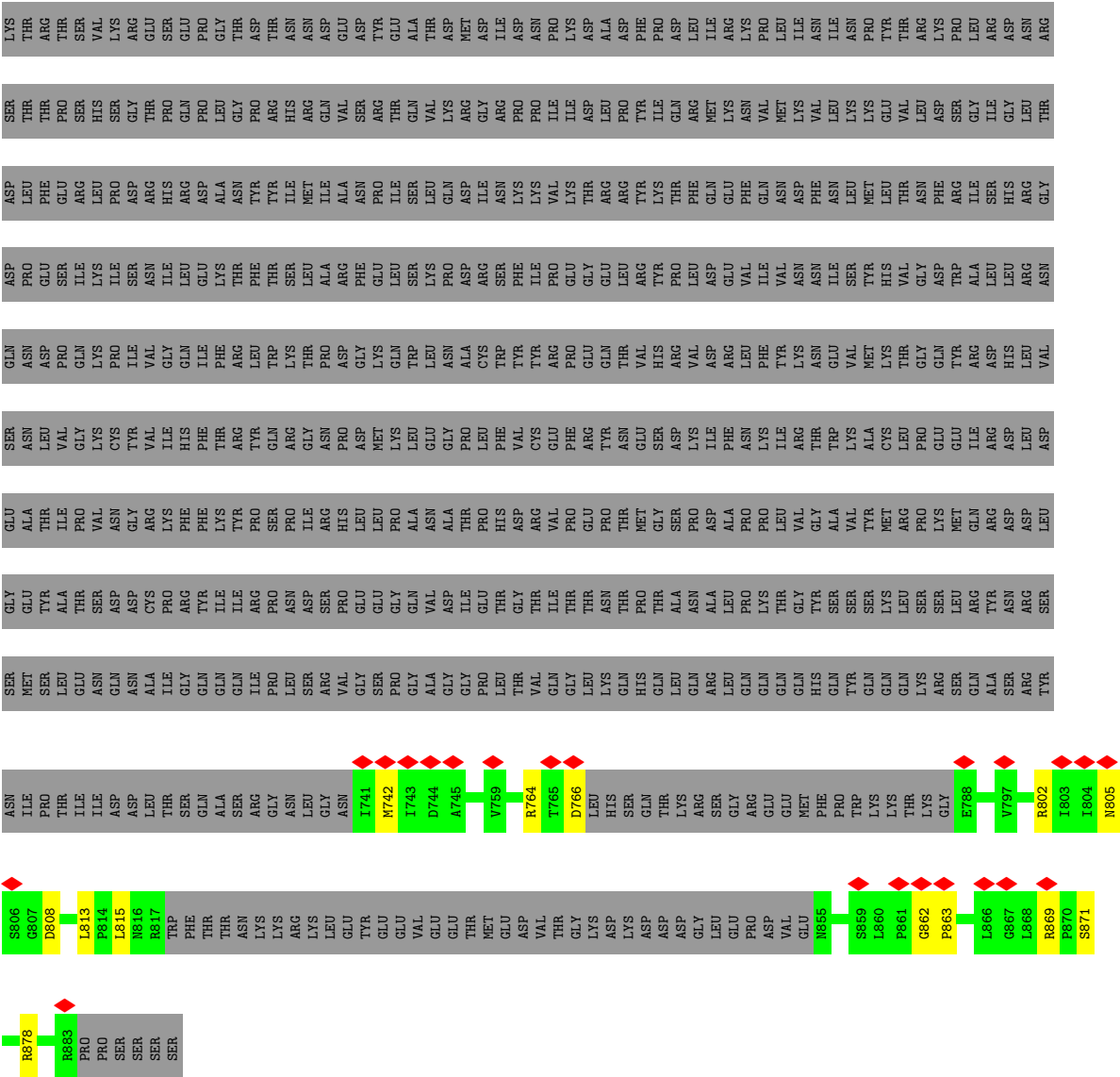
- Molecule 18: Chromatin structure-remodeling complex subunit RSC4



5596	5597	5598	5599	5600	5601	5602	6009	6100	6111	6122	6133	6144	6155	6166	6177	6188	6199	6200	6211	6222	6233	6244	6255	6266	6277	6288	6299	6300	6311	6322	6333	6344	6355	6366	6377	6388	6399	6400	6411	6422	6433	6444	6455	6466	6477	6488	6499	6500	6511	6522	6533	6544	6555	6566	6577	6588	6599	6600	6611	6622	6633	6644	6655	6666	6677	6688	6699	6700	6711	6722	6733	6744	6755	6766	6777	6788	6799	6800	6811	6822	6833	6844	6855	6866	6877	6888	6899	6900	6911	6922	6933	6944	6955	6966	6977	6988	6999	7000	7011	7022	7033	7044	7055	7066	7077	7088	7099	7100	7111	7122	7133	7144	7155	7166	7177	7188	7199	7200	7211	7222	7233	7244	7255	7266	7277	7288	7299	7300	7311	7322	7333	7344	7355	7366	7377	7388	7399	7400	7411	7422	7433	7444	7455	7466	7477	7488	7499	7500	7511	7522	7533	7544	7555	7566	7577	7588	7599	7600	7611	7622	7633	7644	7655	7666	7677	7688	7699	7700	7711	7722	7733	7744	7755	7766	7777	7788	7799	7800	7811	7822	7833	7844	7855	7866	7877	7888	7899	7900	7911	7922	7933	7944	7955	7966	7977	7988	7999	8000	8011	8022	8033	8044	8055	8066	8077	8088	8099	8100	8111	8122	8133	8144	8155	8166	8177	8188	8199	8200	8211	8222	8233	8244	8255	8266	8277	8288	8299	8300	8311	8322	8333	8344	8355	8366	8377	8388	8399	8400	8411	8422	8433	8444	8455	8466	8477	8488	8499	8500	8511	8522	8533	8544	8555	8566	8577	8588	8599	8600	8611	8622	8633	8644	8655	8666	8677	8688	8699	8700	8711	8722	8733	8744	8755	8766	8777	8788	8799	8800	8811	8822	8833	8844	8855	8866	8877	8888	8899	8900	8911	8922	8933	8944	8955	8966	8977	8988	8999	9000	9011	9022	9033	9044	9055	9066	9077	9088	9099	9100	9111	9122	9133	9144	9155	9166	9177	9188	9199	9200	9211	9222	9233	9244	9255	9266	9277	9288	9299	9300	9311	9322	9333	9344	9355	9366	9377	9388	9399	9400	9411	9422	9433	9444	9455	9466	9477	9488	9499	9500	9511	9522	9533	9544	9555	9566	9577	9588	9599	9600	9611	9622	9633	9644	9655	9666	9677	9688	9699	9700	9711	9722	9733	9744	9755	9766	9777	9788	9799	9800	9811	9822	9833	9844	9855	9866	9877	9888	9899	9900	9911	9922	9933	9944	9955	9966	9977	9988	9999	10000
5596	5597	5598	5599	5600	5601	5602	6009	6100	6111	6122	6133	6144	6155	6166	6177	6188	6199	6200	6211	6222	6233	6244	6255	6266	6277	6288	6299	6300	6311	6322	6333	6344	6355	6366	6377	6388	6399	6400	6411	6422	6433	6444	6455	6466	6477	6488	6499	6500	6511	6522	6533	6544	6555	65																																																																																																																																																																																																																																																																																																																																																								

- Molecule 19: Chromatin structure-remodeling complex subunit RSC2

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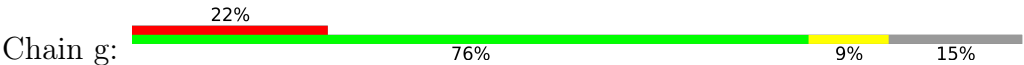
• Molecule 20: Histone H4

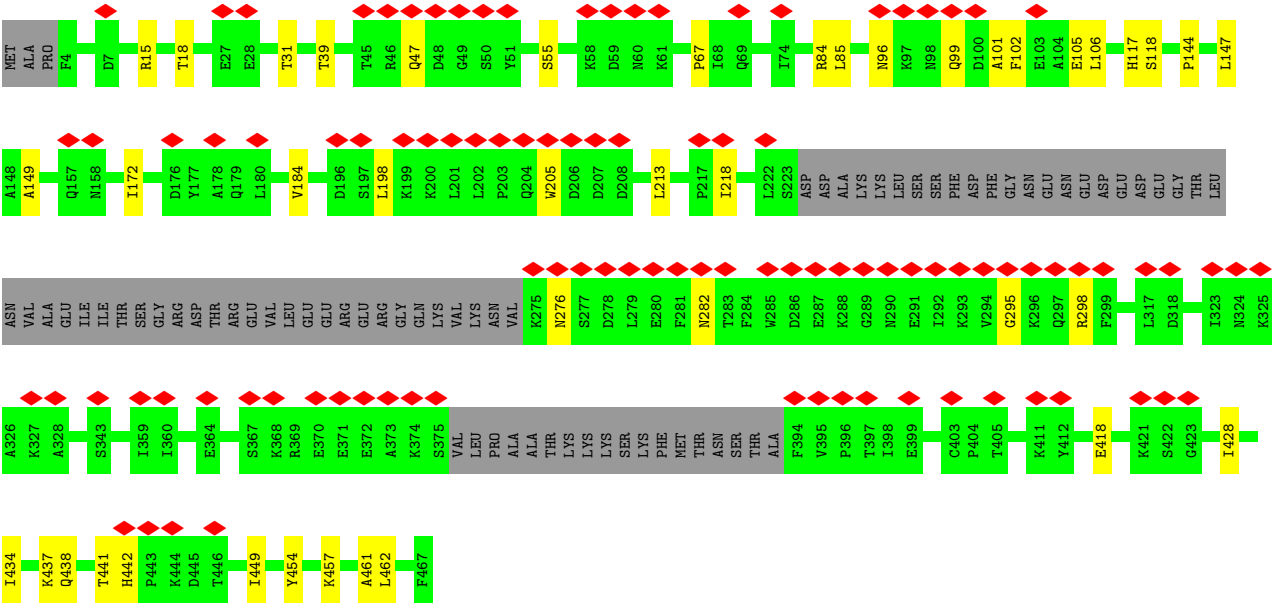


• Molecule 20: Histone H4



• Molecule 21: Actin-like protein ARP9





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45077	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 ($e^-/\text{\AA}^2$)	2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	0.119	Depositor
Minimum map value	-0.013	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.025	Depositor
Map size (Å)	385.2, 385.2, 385.2	wwPDB
Map dimensions	180, 180, 180	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.14, 2.14, 2.14	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	B	0.18	0/664	0.47	0/889
1	R	0.18	0/711	0.46	0/950
2	N	0.18	0/822	0.42	0/1102
2	Q	0.17	0/794	0.43	0/1064
3	O	0.18	0/833	0.43	0/1124
3	S	0.17	0/833	0.41	0/1124
4	U	0.19	0/3336	0.44	0/5142
5	V	0.20	0/3378	0.40	0/5216
6	J	0.18	0/1836	0.47	0/2480
6	W	0.18	0/598	0.45	0/789
6	Y	0.17	0/4580	0.45	0/6167
7	f	0.16	0/3295	0.41	0/4454
8	h	0.13	0/501	0.37	0/669
9	F	0.18	0/983	0.46	0/1337
10	D	0.15	0/2557	0.39	0/3442
10	H	0.17	0/3275	0.42	0/4409
11	M	0.19	0/3113	0.48	0/4215
12	I	0.16	0/1976	0.41	0/2685
13	G	0.19	0/2039	0.52	0/2769
14	A	0.17	0/3077	0.42	0/4169
15	E	0.18	0/480	0.47	0/643
16	C	0.14	0/272	0.34	0/366
17	K	0.12	0/356	0.35	0/483
18	X	0.14	0/1243	0.41	0/1672
19	L	0.17	0/681	0.47	0/921
20	P	0.15	0/728	0.41	0/983
20	T	0.16	0/736	0.42	0/991
21	g	0.17	0/3261	0.44	2/4421 (0.0%)
All	All	0.17	0/46958	0.43	2/64676 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
21	g	47	GLN	CA-C-N	5.96	136.69	126.32
21	g	47	GLN	C-N-CA	5.96	136.69	126.32

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	657	0	706	6	0
1	R	703	0	757	11	0
2	N	810	0	851	8	0
2	Q	784	0	824	7	0
3	O	823	0	882	7	0
3	S	823	0	882	8	0
4	U	2977	0	1639	14	0
5	V	3009	0	1640	10	0
6	J	1814	0	1777	20	0
6	W	592	0	610	9	0
6	Y	4503	0	4573	47	0
7	f	3219	0	3240	38	0
8	h	490	0	467	8	0
9	F	964	0	919	12	0
10	D	2510	0	2542	25	0
10	H	3215	0	3196	38	0
11	M	3058	0	3127	20	0
12	I	1944	0	1964	15	0
13	G	1996	0	1948	19	0
14	A	3007	0	3045	22	0
15	E	477	0	491	8	0
16	C	269	0	279	3	0
17	K	347	0	342	3	0
18	X	1220	0	1192	13	0
19	L	669	0	693	10	0
20	P	717	0	723	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	T	725	0	745	3	0
21	g	3191	0	3179	27	0
22	H	1	0	0	0	0
All	All	45514	0	43233	319	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 4.

The worst 5 of 319 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)
18:X:375:GLU:HB2	18:X:514:HIS:HB2	1.79	0.64
6:W:337:ARG:HH22	7:f:447:PRO:HD3	1.62	0.64
6:Y:760:ARG:HH21	6:Y:925:ILE:HD13	1.62	0.63
11:M:521:GLN:HE21	12:I:333:MET:HE2	1.62	0.63
10:D:193:THR:HG22	10:D:195:GLN:H	1.64	0.62

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	80/103 (78%)	78 (98%)	2 (2%)	0	100	100
1	R	85/103 (82%)	83 (98%)	2 (2%)	0	100	100
2	N	96/136 (71%)	94 (98%)	2 (2%)	0	100	100
2	Q	93/136 (68%)	93 (100%)	0	0	100	100
3	O	105/130 (81%)	105 (100%)	0	0	100	100
3	S	105/130 (81%)	105 (100%)	0	0	100	100
6	J	229/1359 (17%)	210 (92%)	19 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	W	67/1359 (5%)	67 (100%)	0	0	100	100
6	Y	536/1359 (39%)	497 (93%)	39 (7%)	0	100	100
7	f	391/477 (82%)	383 (98%)	8 (2%)	0	100	100
8	h	46/157 (29%)	44 (96%)	2 (4%)	0	100	100
9	F	116/435 (27%)	108 (93%)	8 (7%)	0	100	100
10	D	295/557 (53%)	283 (96%)	12 (4%)	0	100	100
10	H	387/557 (70%)	369 (95%)	18 (5%)	0	100	100
11	M	378/581 (65%)	362 (96%)	16 (4%)	0	100	100
12	I	236/483 (49%)	223 (94%)	13 (6%)	0	100	100
13	G	238/426 (56%)	221 (93%)	17 (7%)	0	100	100
14	A	357/502 (71%)	331 (93%)	26 (7%)	0	100	100
15	E	56/78 (72%)	55 (98%)	1 (2%)	0	100	100
16	C	31/883 (4%)	31 (100%)	0	0	100	100
17	K	40/885 (4%)	40 (100%)	0	0	100	100
18	X	139/625 (22%)	127 (91%)	12 (9%)	0	100	100
19	L	79/889 (9%)	70 (89%)	9 (11%)	0	100	100
20	P	91/126 (72%)	91 (100%)	0	0	100	100
20	T	91/126 (72%)	91 (100%)	0	0	100	100
21	g	390/467 (84%)	381 (98%)	9 (2%)	0	100	100
All	All	4757/13069 (36%)	4542 (96%)	215 (4%)	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	B	68/79 (86%)	68 (100%)	0	100	100
1	R	72/79 (91%)	72 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	N	86/111 (78%)	86 (100%)	0	100	100
2	Q	83/111 (75%)	83 (100%)	0	100	100
3	O	84/102 (82%)	84 (100%)	0	100	100
3	S	84/102 (82%)	84 (100%)	0	100	100
6	J	187/1228 (15%)	187 (100%)	0	100	100
6	W	63/1228 (5%)	63 (100%)	0	100	100
6	Y	502/1228 (41%)	502 (100%)	0	100	100
7	f	356/420 (85%)	356 (100%)	0	100	100
8	h	53/140 (38%)	53 (100%)	0	100	100
9	F	111/388 (29%)	111 (100%)	0	100	100
10	D	285/500 (57%)	285 (100%)	0	100	100
10	H	363/500 (73%)	363 (100%)	0	100	100
11	M	349/521 (67%)	349 (100%)	0	100	100
12	I	223/435 (51%)	223 (100%)	0	100	100
13	G	226/384 (59%)	225 (100%)	1 (0%)	84	84
14	A	343/462 (74%)	343 (100%)	0	100	100
15	E	56/75 (75%)	56 (100%)	0	100	100
16	C	32/824 (4%)	32 (100%)	0	100	100
17	K	39/832 (5%)	39 (100%)	0	100	100
18	X	141/578 (24%)	141 (100%)	0	100	100
19	L	77/810 (10%)	77 (100%)	0	100	100
20	P	77/105 (73%)	77 (100%)	0	100	100
20	T	79/105 (75%)	79 (100%)	0	100	100
21	g	362/423 (86%)	362 (100%)	0	100	100
All	All	4401/11770 (37%)	4400 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	G	300	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 79 such sidechains are listed below:

Mol	Chain	Res	Type
20	T	63	ASN
6	Y	687	HIS
20	P	63	ASN
6	Y	452	HIS
6	Y	808	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

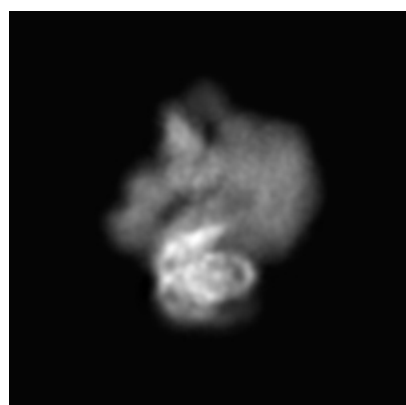
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0777. These allow visual inspection of the internal detail of the map and identification of artifacts.

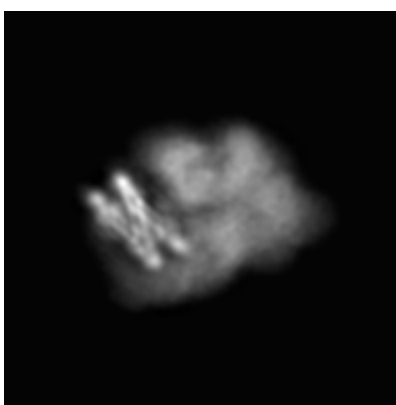
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

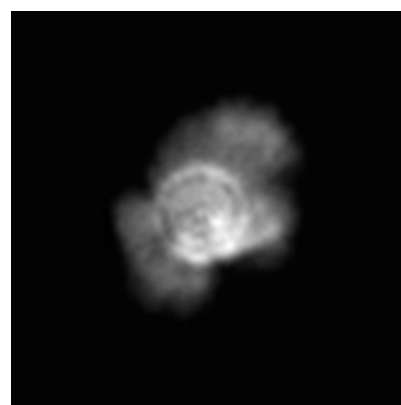
6.1.1 Primary map



X



Y

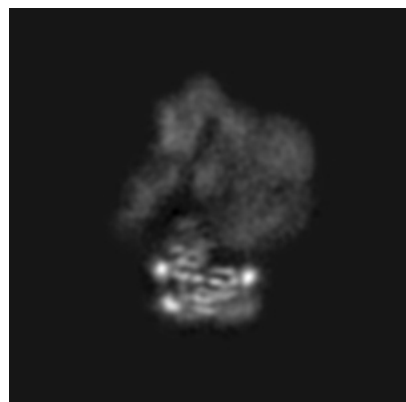


Z

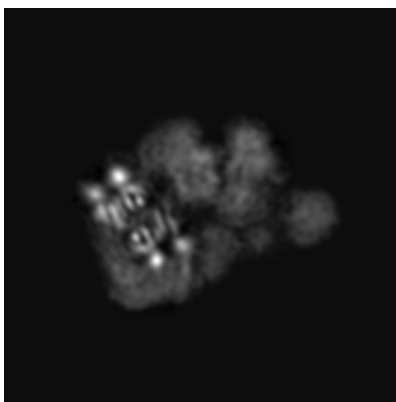
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

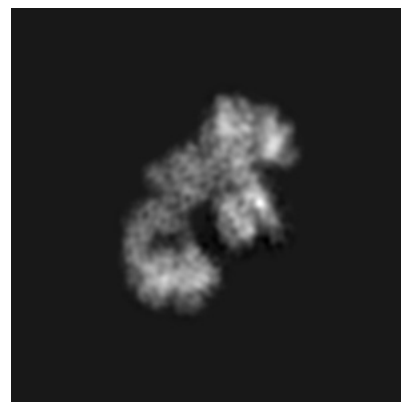
6.2.1 Primary map



X Index: 90



Y Index: 90



Z Index: 90

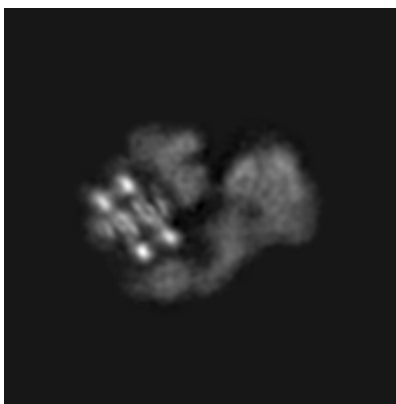
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

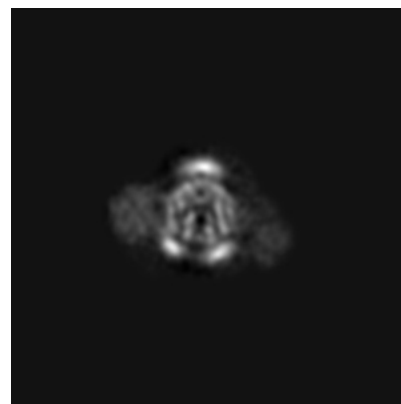
6.3.1 Primary map



X Index: 94



Y Index: 75



Z Index: 60

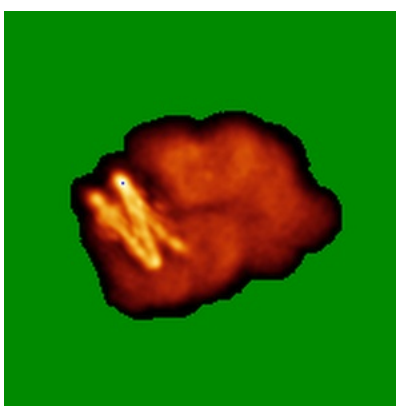
The images above show the largest variance slices of the map in three orthogonal directions.

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

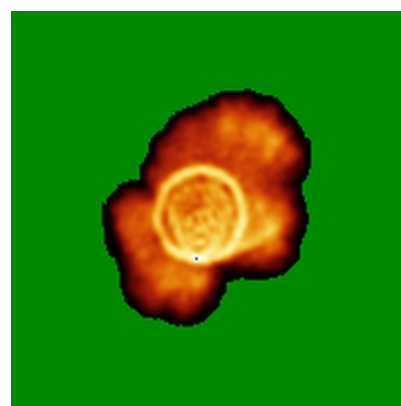
6.4.1 Primary map



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.

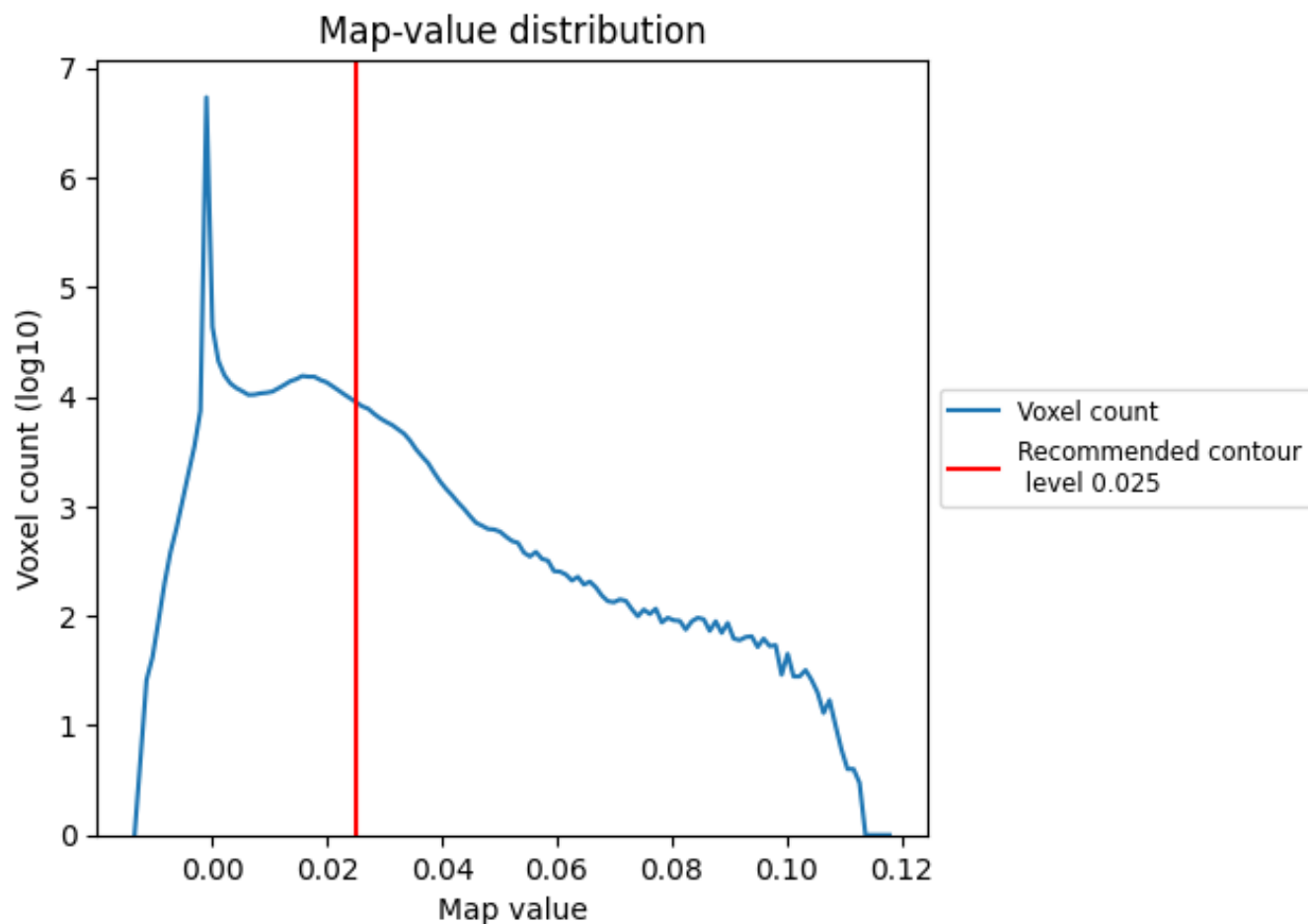
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

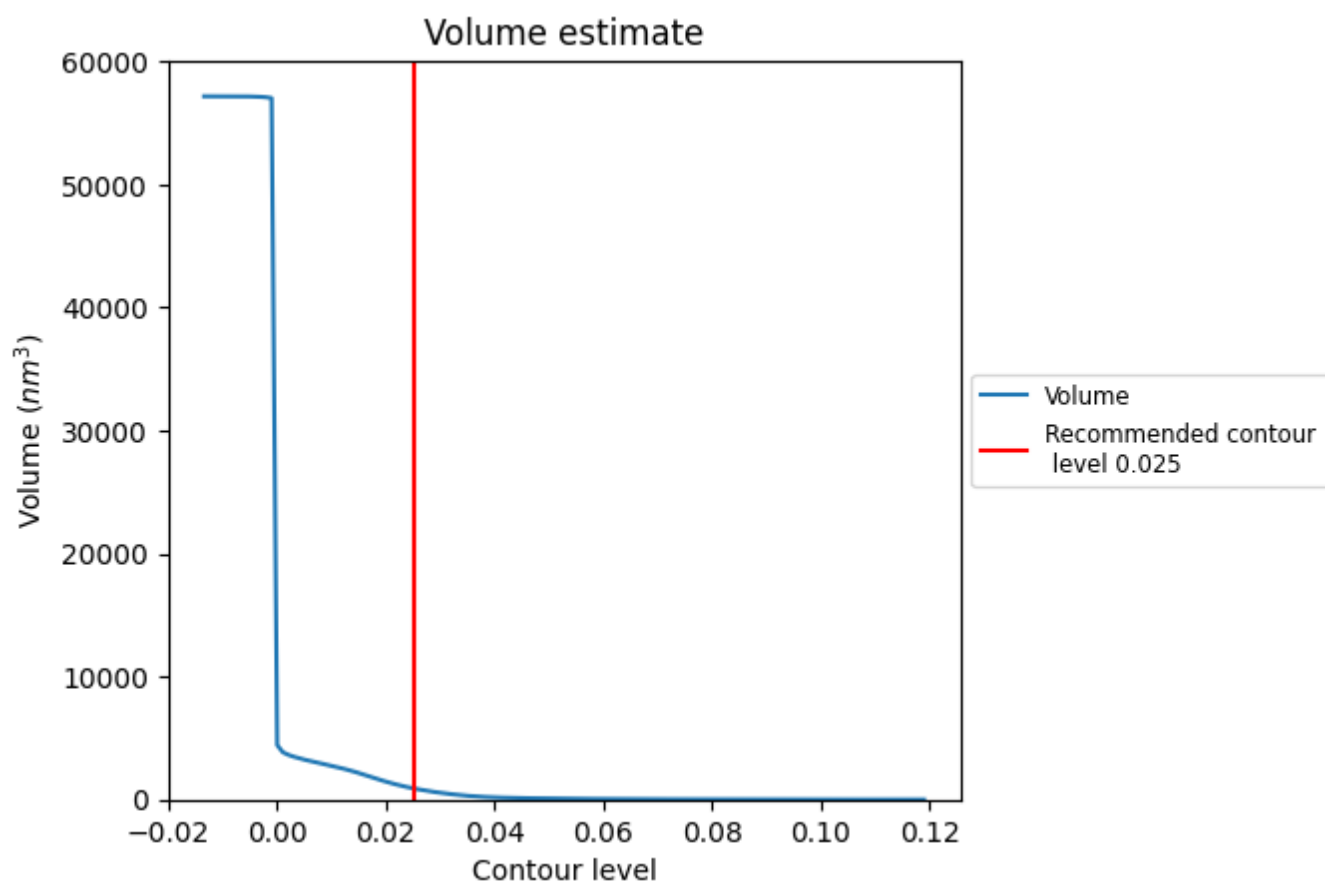
This section contains the results of statistical analysis of the map.

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.

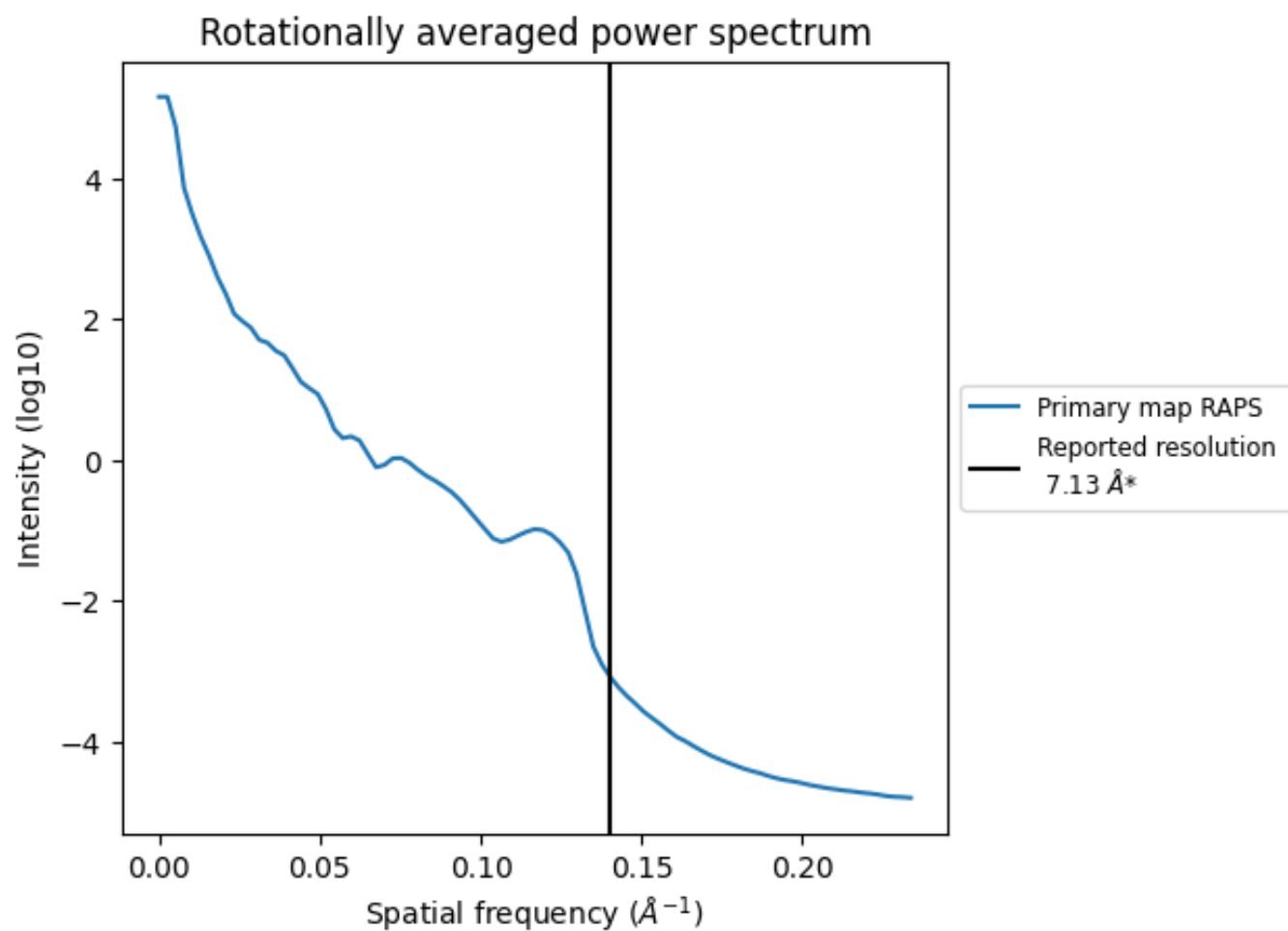
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 915 nm³; this corresponds to an approximate mass of 827 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 0.140 Å⁻¹

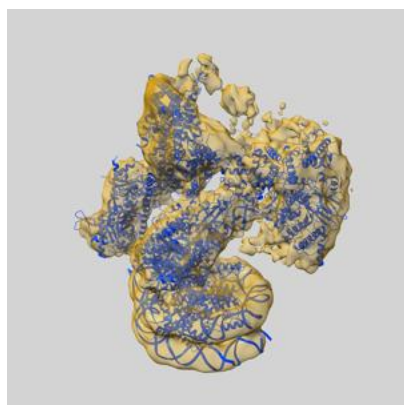
8 Fourier-Shell correlation ⓘ

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

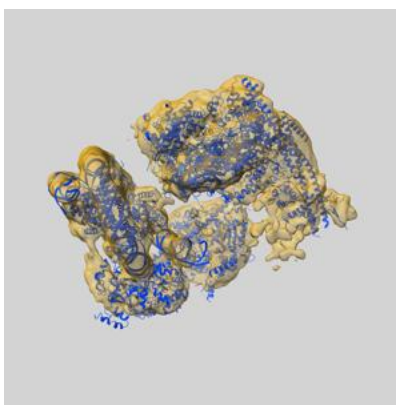
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0777 and PDB model 6KW3. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

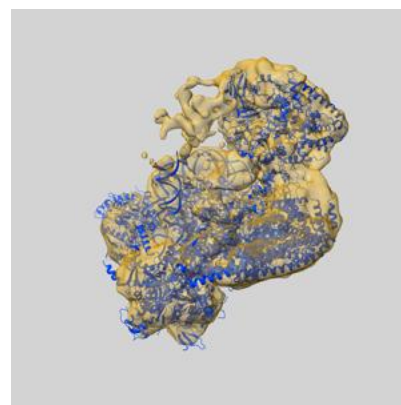
9.1 Map-model overlay [i](#)



X



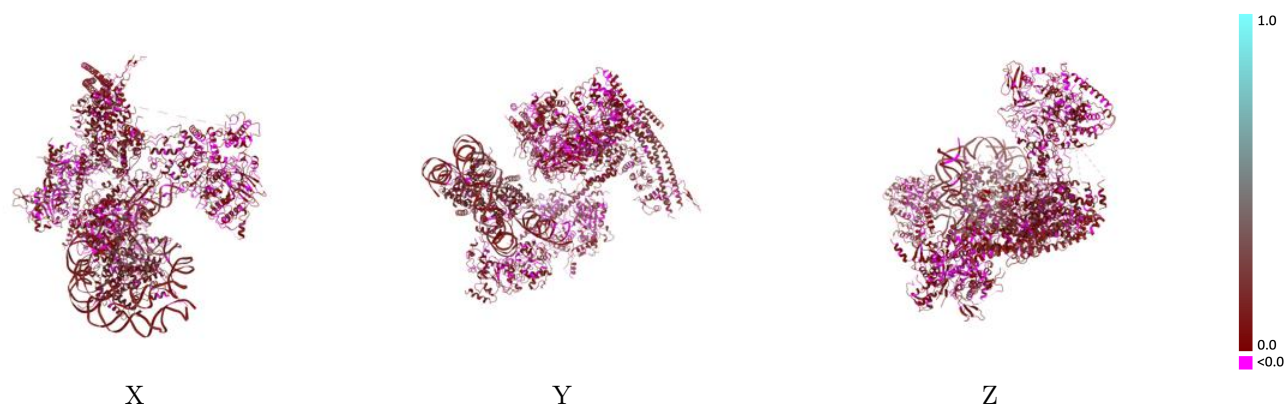
Y



Z

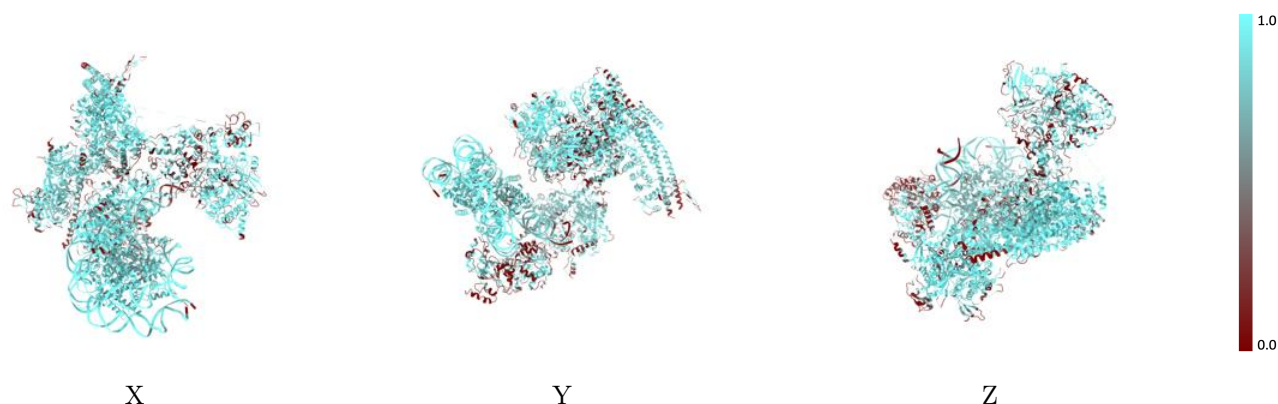
The images above show the 3D surface view of the map at the recommended contour level 0.025 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



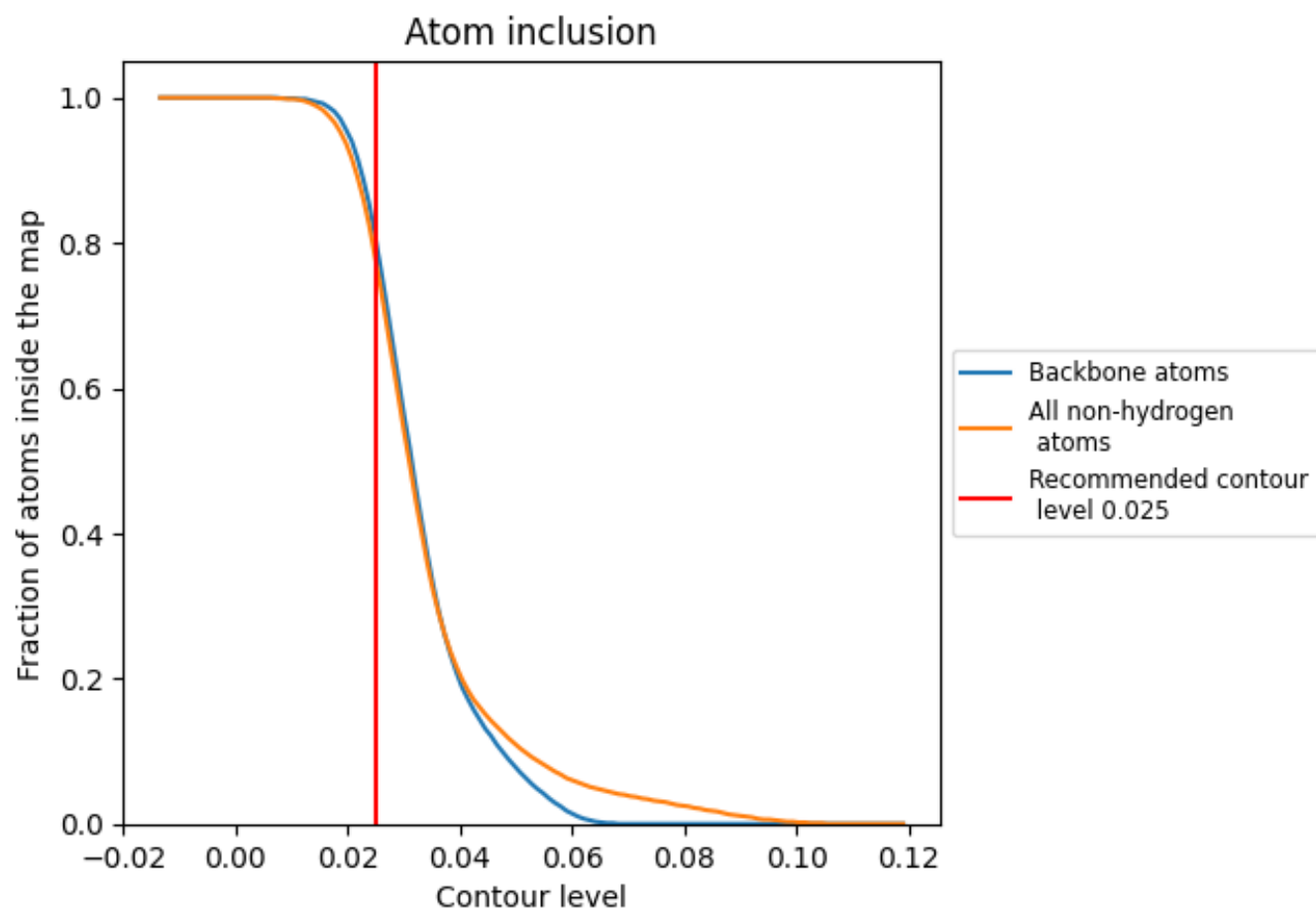
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



At the recommended contour level, 80% of all backbone atoms, 77% 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	 0.7740	 0.0860
A	 0.7840	 0.0650
B	 0.9100	 0.1200
C	 0.5170	 0.0940
D	 0.8260	 0.0890
E	 0.9270	 0.0990
F	 0.8740	 0.0960
G	 0.7560	 0.0770
H	 0.7560	 0.0820
I	 0.7620	 0.0840
J	 0.5730	 0.0520
K	 0.5010	 0.1200
L	 0.6910	 0.0260
M	 0.8140	 0.0970
N	 0.9330	 0.1350
O	 0.8210	 0.1220
P	 0.9530	 0.1470
Q	 0.9340	 0.1330
R	 0.8370	 0.1170
S	 0.9620	 0.1380
T	 0.8840	 0.1460
U	 0.9170	 0.1190
V	 0.9240	 0.1220
W	 0.5010	 0.0830
X	 0.7310	 0.0530
Y	 0.5040	 0.0690
f	 0.8540	 0.0540
g	 0.7070	 0.0420
h	 0.7380	 0.0900

