



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 03:24 AM UTC

PDB ID : 7JOA / pdb_00007joa
EMDB ID : EMD-22409
Title : 2:1 cGAS-nucleosome complex
Authors : Boyer, J.A.; Spangler, C.J.; Strauss, J.D.; Cesmat, A.P.; Liu, P.; McGinty, R.K.; Zhang, Q.
Deposited on : 2020-08-06
Resolution : 3.30 Å(reported)
Based on initial models : 4K8V, 6FQ5

This is a Full wwPDB EM Validation 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:

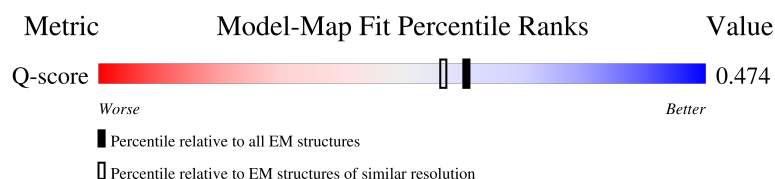
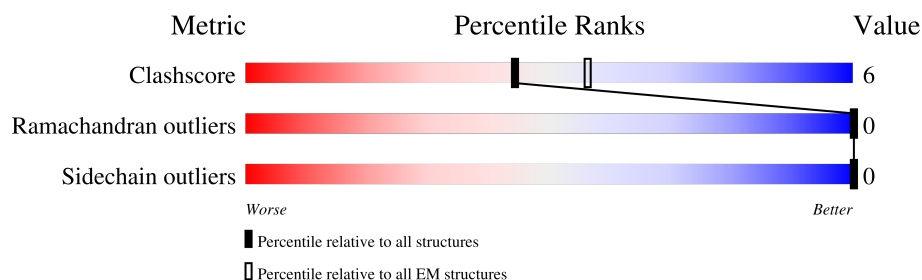
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.30 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.



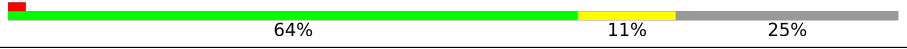
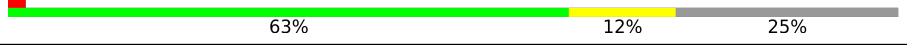
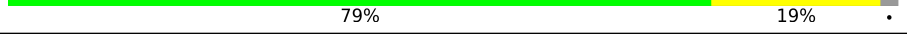
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	136	
1	E	136	
2	B	103	
2	F	103	

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Mol	Chain	Length	Quality of chain
3	C	129	
3	G	129	
4	D	125	
4	H	125	
5	I	147	
6	J	147	
7	K	366	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14994 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 H3.2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	98	Total	C	N	O	S	0	0
			810	511	157	139	3		
1	E	97	Total	C	N	O	S	0	0
			801	505	155	138	3		

- Molecule 2 is a protein called Histone H4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	81	Total	C	N	O	S	0	0
			648	410	126	111	1		
2	F	85	Total	C	N	O	S	0	0
			683	430	136	116	1		

- Molecule 3 is a protein called Histone H2A type 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	109	Total	C	N	O		0	0
			837	529	164	144			
3	G	109	Total	C	N	O		0	0
			837	529	164	144			

- Molecule 4 is a protein called Histone H2B type 1-C/E/F/G/I.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	94	Total	C	N	O	S	0	0
			736	461	134	139	2		
4	H	94	Total	C	N	O	S	0	0
			736	461	134	139	2		

- Molecule 5 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	I	145	Total	C	N	O	P	0	0
			2990	1415	559	871	145		

- Molecule 6 is a DNA chain called DNA (145-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	J	145	Total	C	N	O	P	0	0
			2955	1403	538	869	145		

- Molecule 7 is a protein called Cyclic GMP-AMP synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	358	Total	C	N	O	S	0	0
			2960	1902	504	541	13		

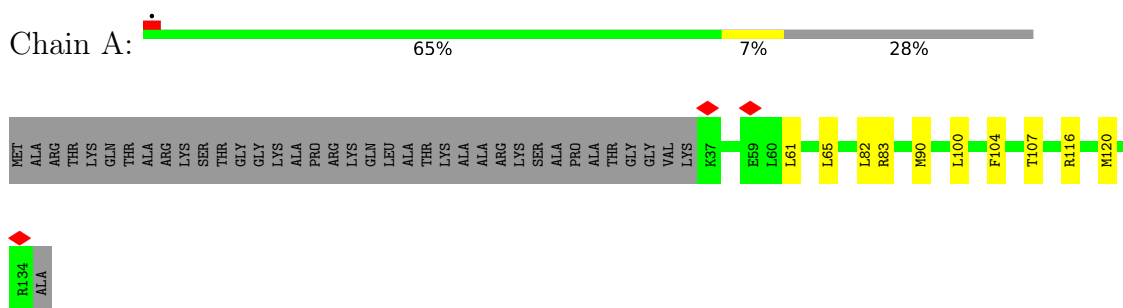
- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
8	K	1	Total	Zn	0
			1	1	

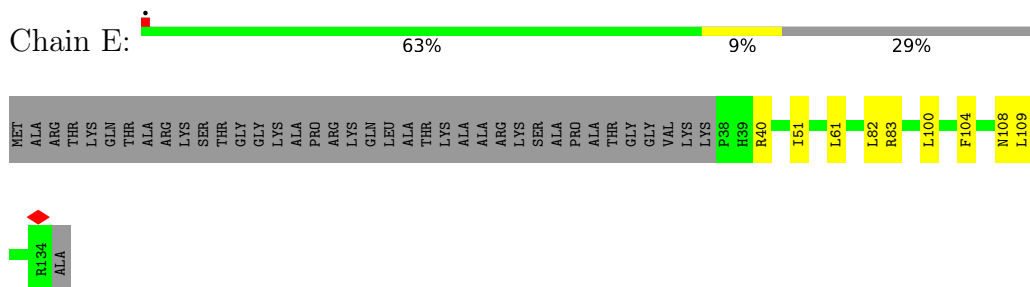
3 Residue-property plots [i](#)

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.

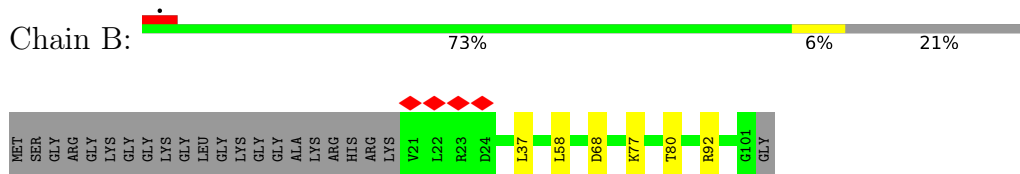
- Molecule 1: Histone H3.2



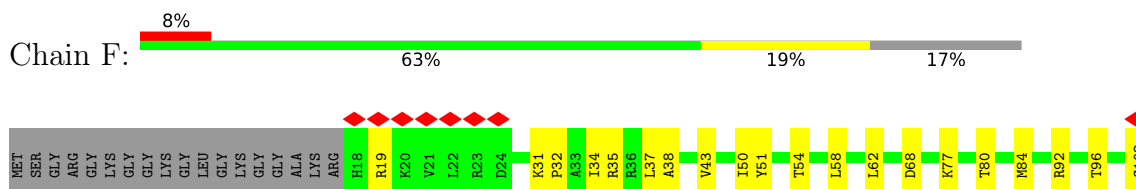
- Molecule 1: Histone H3.2



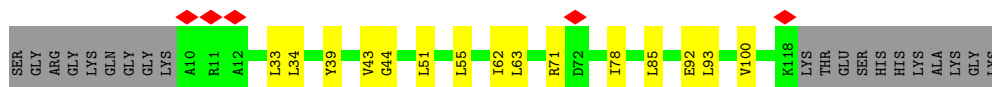
- Molecule 2: Histone H4



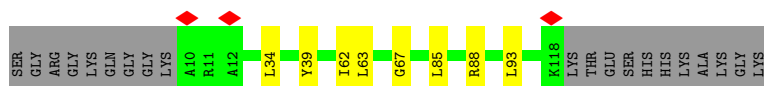
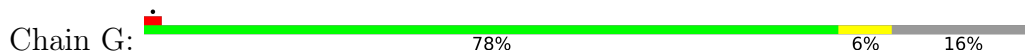
- Molecule 2: Histone H4



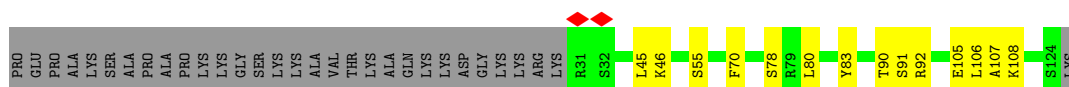
- Molecule 3: Histone H2A type 1



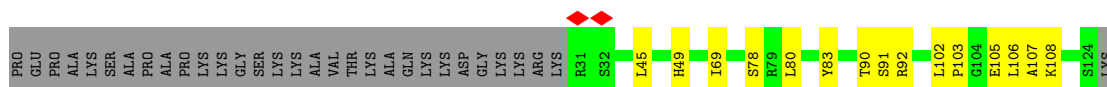
• Molecule 3: Histone H2A type 1



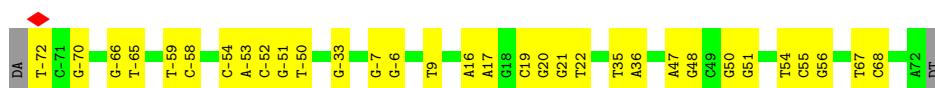
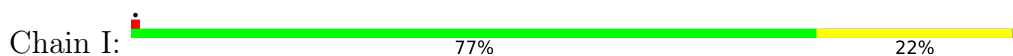
• Molecule 4: Histone H2B type 1-C/E/F/G/I



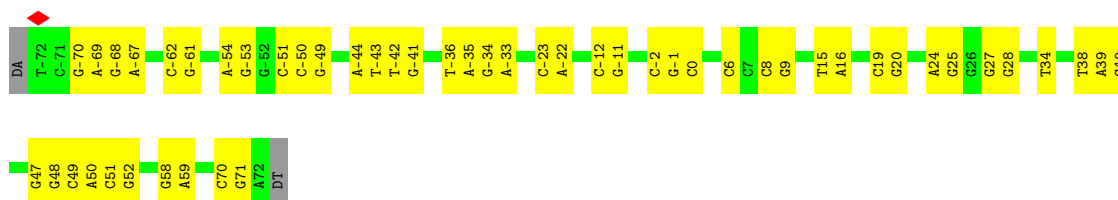
• Molecule 4: Histone H2B type 1-C/E/F/G/I



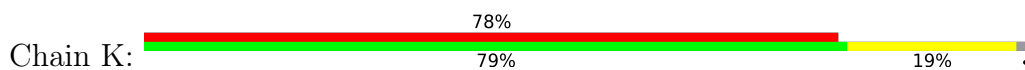
• Molecule 5: DNA (145-MER)



• Molecule 6: DNA (145-MER)



• Molecule 7: Cyclic GMP-AMP synthase



K472	E411	K350	E272	E202	GLY
F473	F412	N351	E273	H203	SER
N474	Q413	A352	V274	V204	ARG
L475	E414	K353	K275	K205	LYS
F476	L415	D354	E276	I206	GLU
S477	D416	G355	I277	S207	PRO
Q478	A417	N356	K278	A208	D148
E479	F418	K357	I279	P209	K149
L480	C419	F358	I280	N210	L150
I481	S420	Q359	D281	E211	K151
D482	Y421	C360	V282	F212	K152
R483	H422	E361	S283	D213	V153
K484	V423	K364	V284	I214	L154
S485	K424	L365	E285	M215	D155
K486	T425	K366	K286	K216	K156
E487	A426	F367	E287	F217	L157
F488	I427	S368	K288	L218	R158
L489	F428	H369	P289	E219	L159
S490	H429	T370	G290	I223	K160
K491	M430	E371	S291	K239	R161
K492	W431	K372	P292	F240	K162
I493	T432	I373	A293	K241	D163
E494	Q433	I374	V294	Y228	I164
Y495	D434	L375	T295	Y229	S165
E496	P435	N376	L296	E230	E166
E497	Q436	N377	L297	T231	A167
N498	D437	H378	I298	G232	A168
N499	S438	C379	R299	A233	E169
G500	Q439	I380	N300	K239	T170
F501	W440	E381	P301	F240	V171
P502	D441	K382	E302	K241	N172
I503	P442	T383	E303	R244	K173
F504	K443	C384	I304	G245	V174
D505	N444	C385	S305	G246	V175
LYS	L445	E386	V306	I247	E176
LEU	S446	S387	D307	L248	R177
	A447	S388	I308	S249	L178
	C448	C389	I309	H250	L179
	F449	A390	L310	F251	R180
	D450	K391	A311	L252	R181
	K451	C392	L312	E253	M182
	L452	C393	E313	G254	Q183
	L453	R394	G316	E255	K184
	A454	K395	S317	S258	R185
	F455	E396	T322	A259	E186
	F456	C397	K323	T260	A187
	L457	L398	G325	L263	E188
	E458	K399	E324	S264	F189
	C459	L400	L326	K265	K190
	L460	M401	I328	F266	G191
	R461	K402	G329	R267	E192
	T462	Y403	K330	K268	E193
	E463	L404	W331	T269	Q194
	K464	L405	L332	I270	L195
	L465	E406	G333	K271	N196
	D466	Q407	T334		T197
	H467	L408			G198
	Y468	K409			S199
	P471	K410			Y200
					Y201

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of particles used	45587	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	53	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.111	Depositor
Minimum map value	-0.051	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	300.30002, 300.30002, 300.30002	wwPDB
Map dimensions	330, 330, 330	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.91, 0.91, 0.91	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.44	0/822	0.55	0/1102
1	E	0.44	0/813	0.54	0/1090
2	B	0.45	0/655	0.52	0/878
2	F	0.46	0/691	0.53	0/923
3	C	0.44	0/847	0.47	0/1142
3	G	0.44	0/847	0.47	0/1142
4	D	0.45	0/747	0.50	0/1004
4	H	0.45	0/747	0.50	0/1004
5	I	0.35	0/3357	0.47	0/5184
6	J	0.36	0/3311	0.43	0/5103
7	K	0.21	0/3024	0.50	0/4060
All	All	0.37	0/15861	0.48	0/22632

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 [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	810	0	851	9	0
1	E	801	0	839	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	648	0	693	6	0
2	F	683	0	729	18	0
3	C	837	0	902	15	0
3	G	837	0	902	8	0
4	D	736	0	756	12	0
4	H	736	0	756	11	0
5	I	2990	0	1628	22	0
6	J	2955	0	1627	40	0
7	K	2960	0	3003	50	0
8	K	1	0	0	0	0
All	All	14994	0	12686	176	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.

All (176) 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)
3:C:71:ARG:HH22	7:K:317:SER:HA	1.41	0.83
3:C:92:GLU:OE1	7:K:241:ARG:NH1	2.21	0.73
1:E:129:ARG:O	1:E:129:ARG:NH1	2.23	0.71
7:K:274:VAL:HG11	7:K:284:VAL:HG23	1.72	0.71
7:K:427:ILE:HG23	7:K:431:TRP:CZ3	2.27	0.70
7:K:494:GLU:OE2	7:K:498:ASN:ND2	2.24	0.70
2:F:19:ARG:NH2	6:J:-22:DA:OP1	2.25	0.69
5:I:21:DG:H2''	5:I:22:DT:H5''	1.75	0.68
1:A:116:ARG:HH12	1:A:120:MET:HG3	1.60	0.67
5:I:-66:DG:H2'	5:I:-65:DT:H71	1.79	0.64
6:J:-12:DC:H2''	6:J:-11:DG:H8	1.65	0.62
7:K:247:PRO:HG2	7:K:248:LEU:HD12	1.82	0.61
5:I:-7:DG:H2''	5:I:-6:DG:N7	2.17	0.60
1:A:116:ARG:NH1	1:A:120:MET:HG3	2.16	0.59
6:J:8:DC:H2''	6:J:9:DG:C8	2.38	0.58
2:F:84:MET:HE1	2:F:102:GLY:HA2	1.84	0.58
7:K:185:ARG:NH2	7:K:269:ILE:HG23	2.19	0.57
7:K:161:ARG:HA	7:K:164:ILE:HG12	1.86	0.57
6:J:8:DC:H2''	6:J:9:DG:H8	1.68	0.57
6:J:39:DA:H2''	6:J:40:DG:H8	1.69	0.57
7:K:185:ARG:HH21	7:K:269:ILE:HG23	1.70	0.57
5:I:-72:DT:C6	5:I:-72:DT:H5'	2.39	0.57
2:F:68:ASP:OD2	2:F:92:ARG:NH2	2.27	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:108:ASN:HB2	2:F:43:VAL:HG12	1.88	0.55
5:I:-51:DG:H2'	5:I:-50:DT:H71	1.87	0.55
1:A:104:PHE:HA	1:A:107:THR:HG22	1.87	0.55
7:K:280:ILE:HG23	7:K:282:VAL:HG23	1.88	0.55
7:K:459:CYS:SG	7:K:465:LEU:HB2	2.47	0.54
3:G:62:ILE:HD11	3:G:93:LEU:HD22	1.89	0.54
3:C:62:ILE:HD11	3:C:93:LEU:HD22	1.89	0.53
7:K:407:GLN:HB3	7:K:503:ILE:HG12	1.90	0.53
7:K:421:TYR:OH	7:K:467:HIS:NE2	2.34	0.53
3:C:100:VAL:HG22	2:F:96:THR:HB	1.89	0.53
1:E:61:LEU:HD12	2:F:37:LEU:HD23	1.89	0.52
1:E:40:ARG:NH2	5:I:9:DT:O2	2.35	0.52
2:F:31:LYS:HB3	2:F:32:PRO:HD3	1.92	0.52
6:J:58:DG:H2''	6:J:59:DA:C8	2.45	0.52
7:K:178:LEU:HD11	7:K:296:LEU:HD11	1.92	0.52
2:B:77:LYS:HE2	4:D:92:ARG:HH12	1.75	0.51
5:I:67:DT:H2''	5:I:68:DC:C5	2.45	0.51
5:I:35:DT:H2''	5:I:36:DA:C8	2.46	0.51
7:K:383:THR:O	7:K:389:GLY:HA3	2.11	0.51
6:J:-68:DG:H2''	6:J:-67:DA:C8	2.46	0.51
6:J:49:DC:H2''	6:J:50:DA:C8	2.46	0.50
7:K:394:ARG:NH2	7:K:437:ASP:OD1	2.25	0.50
6:J:-23:DC:H2''	6:J:-22:DA:H8	1.75	0.50
5:I:16:DA:H1'	5:I:17:DA:C8	2.47	0.50
6:J:-62:DC:H2''	6:J:-61:DG:H8	1.77	0.50
6:J:-2:DC:H2''	6:J:-1:DG:H8	1.76	0.50
6:J:19:DC:H2''	6:J:20:DG:H8	1.77	0.49
7:K:229:TYR:HD2	7:K:233:ALA:HB3	1.77	0.49
7:K:217:LYS:HA	7:K:311:ALA:O	2.12	0.49
7:K:327:PRO:HD2	7:K:468:TYR:CZ	2.47	0.49
2:F:38:ALA:HB1	2:F:43:VAL:HG21	1.94	0.49
7:K:428:PHE:HD2	7:K:431:TRP:HZ3	1.60	0.49
5:I:-59:DT:H2''	5:I:-58:DC:O5'	2.12	0.49
7:K:213:ASP:OD1	7:K:307:ASP:HB2	2.13	0.49
7:K:424:LYS:HA	7:K:427:ILE:HG22	1.95	0.49
6:J:-62:DC:H2''	6:J:-61:DG:C8	2.48	0.48
7:K:182:MET:HE1	7:K:269:ILE:HG21	1.94	0.48
1:A:90:MET:HE3	1:A:90:MET:HA	1.94	0.48
5:I:-7:DG:O6	6:J:6:DC:N4	2.47	0.48
3:C:78:ILE:O	4:D:55:SER:OG	2.25	0.48
1:A:83:ARG:O	2:B:80:THR:HA	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:428:PHE:HA	7:K:431:TRP:HE3	1.78	0.48
5:I:55:DC:H2''	5:I:56:DG:N7	2.29	0.48
6:J:-49:DG:H5''	6:J:-49:DG:C8	2.49	0.47
5:I:-52:DC:H2''	5:I:-51:DG:C8	2.49	0.47
7:K:223:ILE:HG22	7:K:239:PHE:HE1	1.78	0.47
7:K:239:PHE:HD2	7:K:246:ASN:HD21	1.63	0.47
7:K:482:ASP:OD2	7:K:484:LYS:HG2	2.15	0.47
7:K:153:VAL:O	7:K:157:LEU:HG	2.14	0.47
7:K:448:CYS:O	7:K:451:LYS:HG2	2.14	0.46
3:G:63:LEU:HA	3:G:63:LEU:HD23	1.61	0.46
5:I:-59:DT:H4'	5:I:-58:DC:OP1	2.15	0.46
6:J:51:DC:H2''	6:J:52:DG:C8	2.51	0.46
1:E:83:ARG:O	2:F:80:THR:HA	2.16	0.45
1:E:104:PHE:HD2	2:F:38:ALA:HA	1.82	0.45
6:J:27:DG:H2''	6:J:28:DG:C8	2.52	0.45
7:K:351:ASN:OD1	7:K:360:GLY:N	2.38	0.45
1:A:61:LEU:HD12	2:B:37:LEU:HD23	1.98	0.45
7:K:297:LEU:HD23	7:K:297:LEU:HA	1.85	0.45
2:F:62:LEU:HD23	2:F:62:LEU:HA	1.61	0.45
2:F:77:LYS:NZ	4:H:92:ARG:HH12	2.15	0.45
3:G:63:LEU:HD13	4:H:45:LEU:HB2	1.99	0.45
7:K:429:HIS:NE2	7:K:466:ASP:OD1	2.50	0.45
4:D:106:LEU:O	4:D:107:ALA:C	2.61	0.44
5:I:50:DG:C6	5:I:51:DG:C6	3.05	0.44
2:F:34:ILE:HD12	2:F:54:THR:HG21	2.00	0.44
7:K:229:TYR:CD2	7:K:233:ALA:HB3	2.52	0.44
7:K:428:PHE:CD2	7:K:431:TRP:HZ3	2.36	0.43
6:J:24:DA:H2''	6:J:25:DG:C8	2.53	0.43
4:D:105:GLU:O	4:D:106:LEU:C	2.61	0.43
6:J:58:DG:H2''	6:J:59:DA:H8	1.81	0.43
7:K:466:ASP:OD1	7:K:466:ASP:N	2.50	0.43
3:C:34:LEU:HD23	3:C:34:LEU:HA	1.77	0.43
5:I:47:DA:H2''	5:I:48:DG:C8	2.54	0.43
7:K:223:ILE:HG22	7:K:239:PHE:CE1	2.53	0.43
2:B:37:LEU:HD23	2:B:37:LEU:HA	1.87	0.43
4:H:105:GLU:O	4:H:106:LEU:C	2.61	0.43
7:K:434:ASP:O	7:K:440:TRP:CH2	2.71	0.43
3:C:39:TYR:HB3	4:D:78:SER:HB2	2.00	0.43
7:K:499:ASN:O	7:K:502:PRO:HD3	2.19	0.43
3:G:88:ARG:HA	3:G:88:ARG:HD3	1.81	0.43
6:J:47:DG:H2''	6:J:48:DG:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:K:367:PHE:HB3	7:K:370:THR:HG22	2.01	0.43
4:H:69:ILE:HD13	4:H:69:ILE:HA	1.90	0.42
6:J:38:DT:H2''	6:J:39:DA:C8	2.54	0.42
3:C:33:LEU:HD23	3:C:33:LEU:HA	1.79	0.42
3:G:34:LEU:HD23	3:G:34:LEU:HA	1.77	0.42
6:J:15:DT:H2''	6:J:16:DA:C8	2.54	0.42
7:K:394:ARG:HG2	7:K:431:TRP:HE1	1.83	0.42
4:H:106:LEU:O	4:H:107:ALA:C	2.61	0.42
2:B:58:LEU:HD12	2:B:58:LEU:HA	1.84	0.42
4:D:80:LEU:HA	4:D:83:TYR:HD1	1.85	0.42
6:J:-34:DG:C2	6:J:-33:DA:C5	3.07	0.42
1:A:100:LEU:HA	1:A:100:LEU:HD23	1.79	0.42
6:J:-50:DC:C6	6:J:-50:DC:H5'	2.55	0.42
7:K:189:PHE:O	7:K:192:VAL:HG23	2.20	0.42
3:C:63:LEU:HD13	4:D:45:LEU:HB2	2.02	0.42
2:B:68:ASP:OD2	2:B:92:ARG:NH2	2.26	0.42
2:F:32:PRO:HA	2:F:35:ARG:HB3	2.02	0.42
7:K:169:GLU:HG3	7:K:173:LYS:NZ	2.35	0.42
3:G:67:GLY:HA3	4:H:49:HIS:CD2	2.55	0.42
4:H:102:LEU:HA	4:H:103:PRO:HD3	1.81	0.42
6:J:70:DC:H6	6:J:70:DC:H2'	1.72	0.42
1:E:118:THR:HG22	1:E:119:ILE:N	2.35	0.42
2:F:50:ILE:HD13	2:F:50:ILE:HA	1.89	0.41
6:J:-54:DA:C6	6:J:-53:DG:C6	3.08	0.41
6:J:-51:DC:H5'	6:J:-51:DC:H6	1.83	0.41
3:C:85:LEU:HD23	3:C:85:LEU:HA	1.87	0.41
4:D:90:THR:HG22	4:D:91:SER:N	2.35	0.41
6:J:19:DC:H2''	6:J:20:DG:C8	2.55	0.41
4:H:90:THR:HG22	4:H:91:SER:N	2.35	0.41
3:C:55:LEU:HD11	4:D:70:PHE:HB2	2.02	0.41
4:H:80:LEU:HA	4:H:83:TYR:HD1	1.85	0.41
5:I:-54:DC:H1'	5:I:-53:DA:C8	2.56	0.41
5:I:19:DC:H2''	5:I:20:DG:C8	2.56	0.41
6:J:-1:DG:C4	6:J:0:DC:C5	3.09	0.41
7:K:271:LYS:O	7:K:274:VAL:HG12	2.19	0.41
7:K:394:ARG:HD3	7:K:431:TRP:NE1	2.35	0.41
3:G:39:TYR:HB3	4:H:78:SER:HB2	2.03	0.41
6:J:-36:DT:H2''	6:J:-35:DA:C8	2.56	0.41
3:C:63:LEU:HA	3:C:63:LEU:HD23	1.62	0.41
4:D:46:LYS:HD3	4:D:46:LYS:HA	1.79	0.41
1:E:109:LEU:HA	1:E:109:LEU:HD23	1.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:85:LEU:HD23	3:G:85:LEU:HA	1.86	0.41
7:K:394:ARG:CG	7:K:431:TRP:HE1	2.34	0.41
7:K:282:VAL:HG22	7:K:298:ILE:HG12	2.02	0.41
3:C:51:LEU:HD21	4:D:70:PHE:CD1	2.55	0.41
3:C:71:ARG:HH12	7:K:316:GLY:C	2.29	0.41
1:E:100:LEU:HD23	1:E:100:LEU:HA	1.79	0.41
5:I:70:DG:C2	6:J:71:DG:N2	2.89	0.41
5:I:33:DG:N2	6:J:34:DT:O2	2.54	0.41
7:K:398:LEU:HD13	7:K:427:ILE:HG21	2.02	0.40
3:C:43:VAL:HG12	3:C:44:GLY:O	2.21	0.40
4:H:107:ALA:O	4:H:108:LYS:C	2.64	0.40
6:J:-49:DG:H5''	6:J:-49:DG:H8	1.86	0.40
6:J:-12:DC:H2''	6:J:-11:DG:C8	2.49	0.40
6:J:50:DA:C4	6:J:51:DC:C5	3.08	0.40
1:A:82:LEU:HA	1:A:82:LEU:HD23	1.90	0.40
2:F:31:LYS:HD2	2:F:51:TYR:CE2	2.56	0.40
5:I:21:DG:C8	5:I:22:DT:H72	2.56	0.40
6:J:-70:DG:H2''	6:J:-69:DA:C8	2.56	0.40
6:J:-51:DC:H5'	6:J:-51:DC:C6	2.56	0.40
6:J:-42:DT:O4	6:J:-41:DG:O6	2.39	0.40
6:J:-42:DT:C4	6:J:-41:DG:O6	2.74	0.40
7:K:322:THR:HG22	7:K:322:THR:O	2.21	0.40
1:A:65:LEU:HA	1:A:65:LEU:HD23	1.77	0.40
4:D:107:ALA:O	4:D:108:LYS:C	2.63	0.40
2:F:58:LEU:HD12	2:F:58:LEU:HA	1.81	0.40
5:I:54:DT:H2''	5:I:55:DC:C6	2.56	0.40
6:J:-44:DA:H1'	6:J:-43:DT:H5'	2.04	0.40
1:E:51:ILE:HD11	2:F:43:VAL:O	2.21	0.40
1:E:82:LEU:HD23	1:E:82:LEU:HA	1.84	0.40
7:K:266:PHE:CZ	7:K:270:ILE:HD11	2.57	0.40

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	A	96/136 (71%)	91 (95%)	5 (5%)	0	100	100
1	E	95/136 (70%)	89 (94%)	6 (6%)	0	100	100
2	B	79/103 (77%)	69 (87%)	10 (13%)	0	100	100
2	F	83/103 (81%)	73 (88%)	10 (12%)	0	100	100
3	C	107/129 (83%)	102 (95%)	5 (5%)	0	100	100
3	G	107/129 (83%)	102 (95%)	5 (5%)	0	100	100
4	D	92/125 (74%)	83 (90%)	9 (10%)	0	100	100
4	H	92/125 (74%)	83 (90%)	9 (10%)	0	100	100
7	K	356/366 (97%)	343 (96%)	13 (4%)	0	100	100
All	All	1107/1352 (82%)	1035 (94%)	72 (6%)	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	86/111 (78%)	86 (100%)	0	100	100
1	E	85/111 (77%)	85 (100%)	0	100	100
2	B	67/79 (85%)	67 (100%)	0	100	100
2	F	70/79 (89%)	70 (100%)	0	100	100
3	C	84/98 (86%)	84 (100%)	0	100	100
3	G	84/98 (86%)	84 (100%)	0	100	100
4	D	81/105 (77%)	81 (100%)	0	100	100
4	H	81/105 (77%)	81 (100%)	0	100	100
7	K	331/338 (98%)	331 (100%)	0	100	100
All	All	969/1124 (86%)	969 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	HIS
4	D	49	HIS
4	D	82	HIS
4	D	84	ASN
1	E	113	HIS
4	H	82	HIS
4	H	84	ASN
7	K	196	ASN
7	K	439	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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 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.

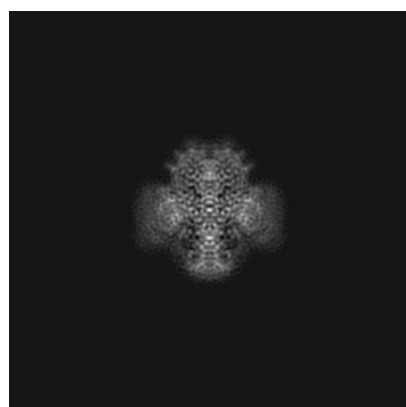
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22409. These allow visual inspection of the internal detail of the map and identification of artifacts.

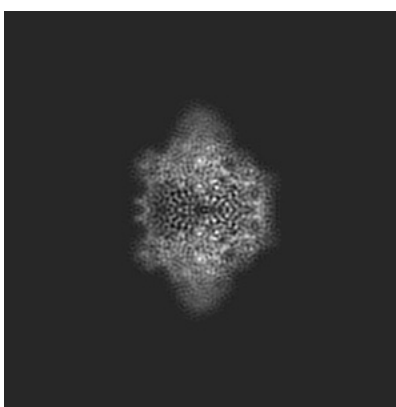
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

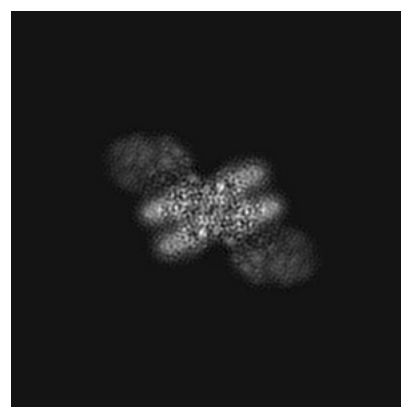
6.1.1 Primary map



X



Y



Z

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

6.2 Central slices [i](#)

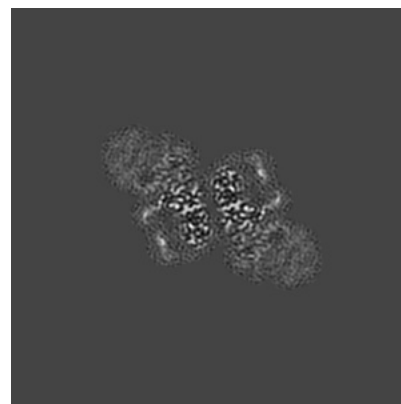
6.2.1 Primary map



X Index: 165



Y Index: 165

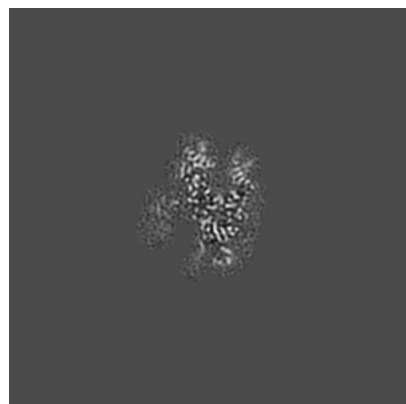


Z Index: 165

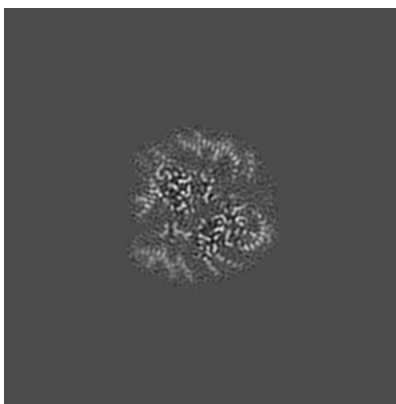
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

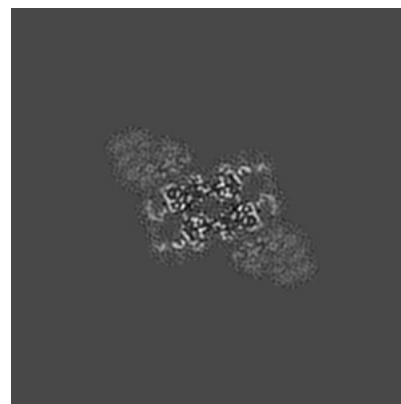
6.3.1 Primary map



X Index: 187



Y Index: 170

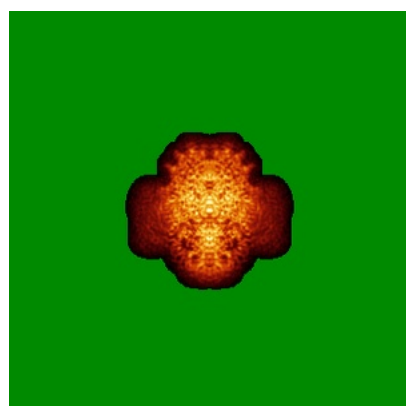


Z Index: 173

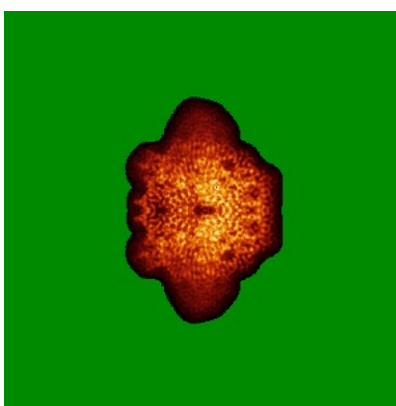
The images above show the largest variance slices of the map in three orthogonal directions.

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

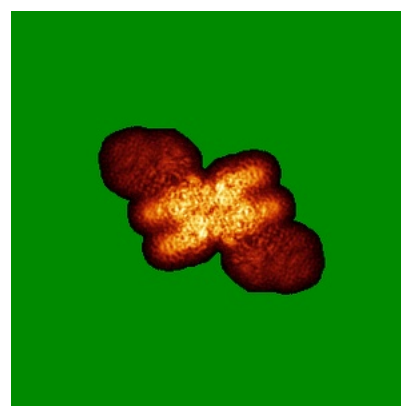
6.4.1 Primary map



X



Y

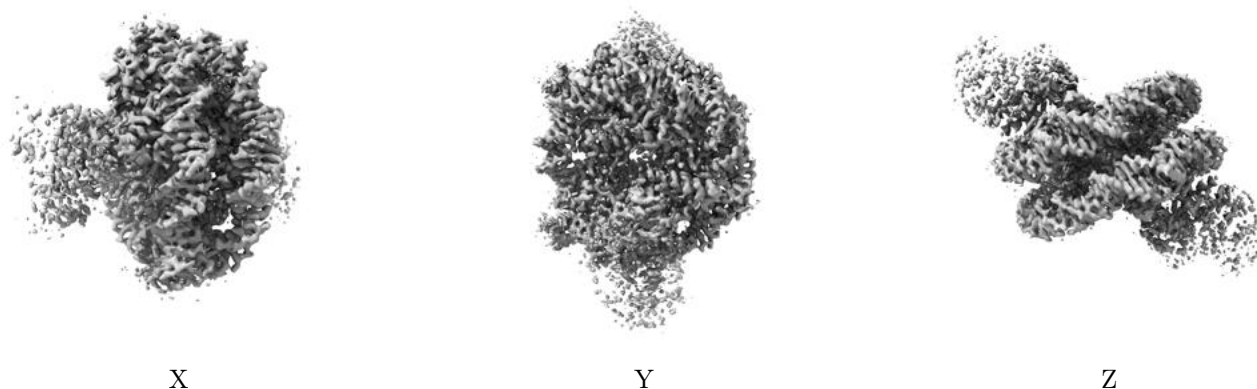


Z

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

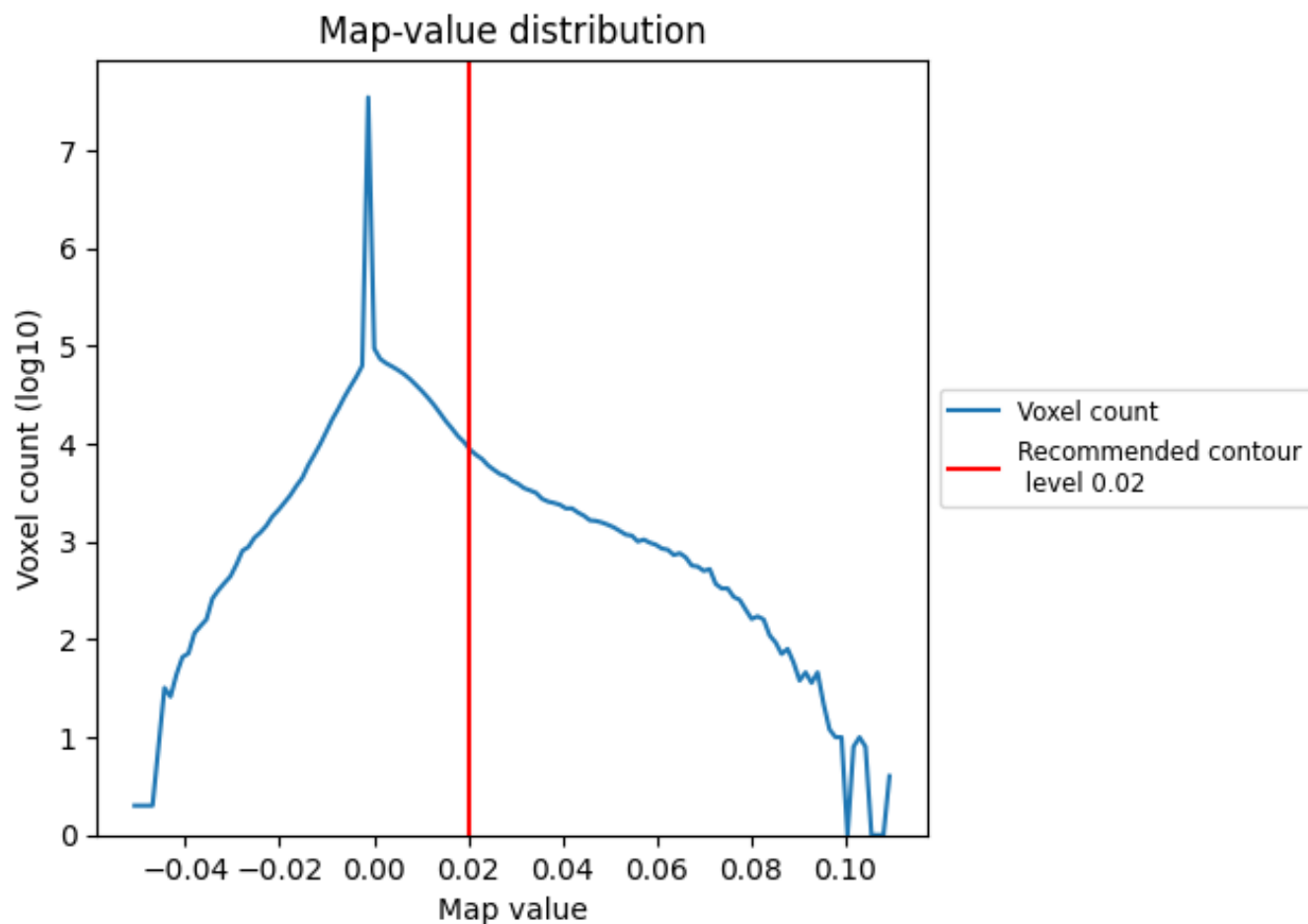
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

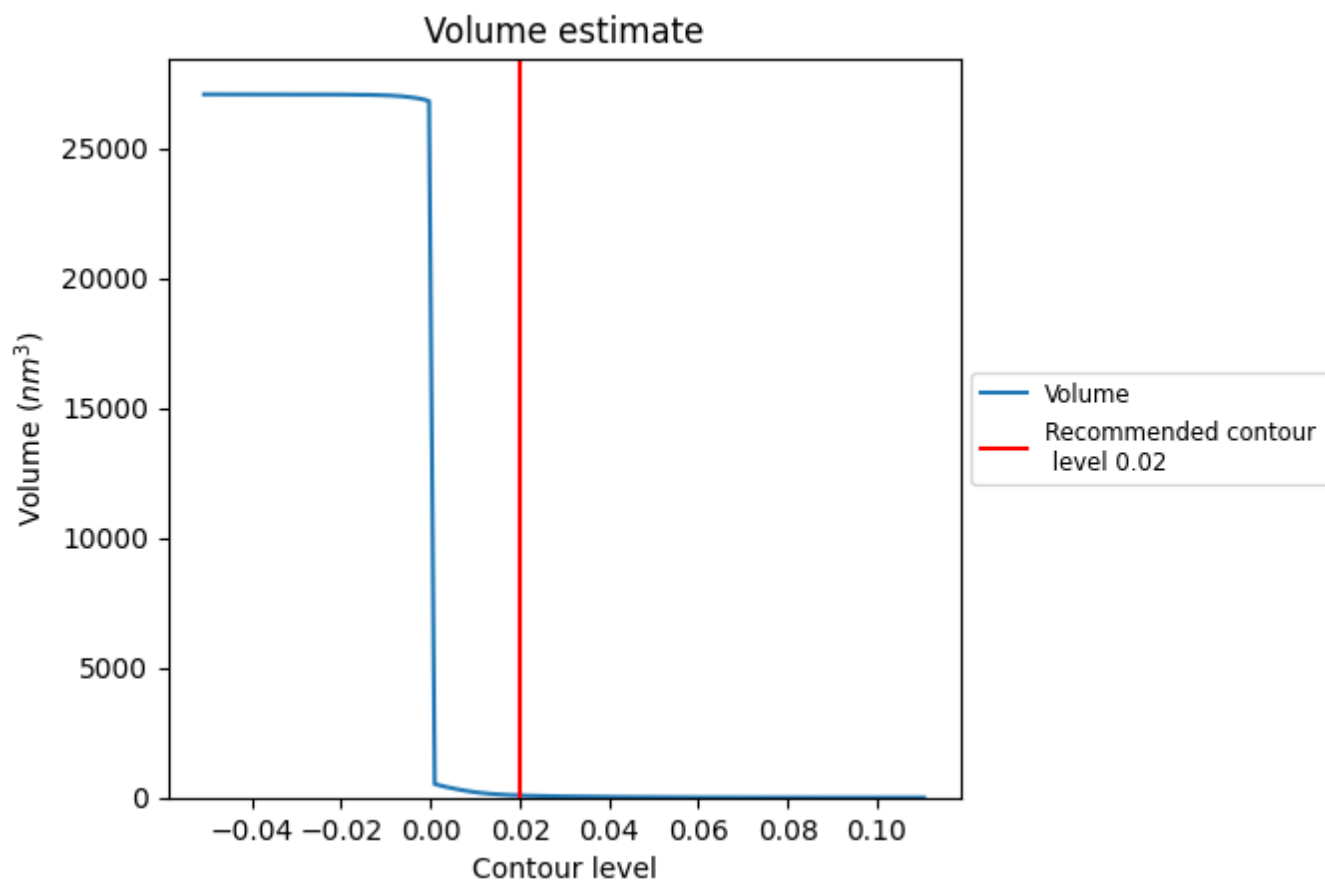
This section contains the results of statistical analysis of the map.

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.

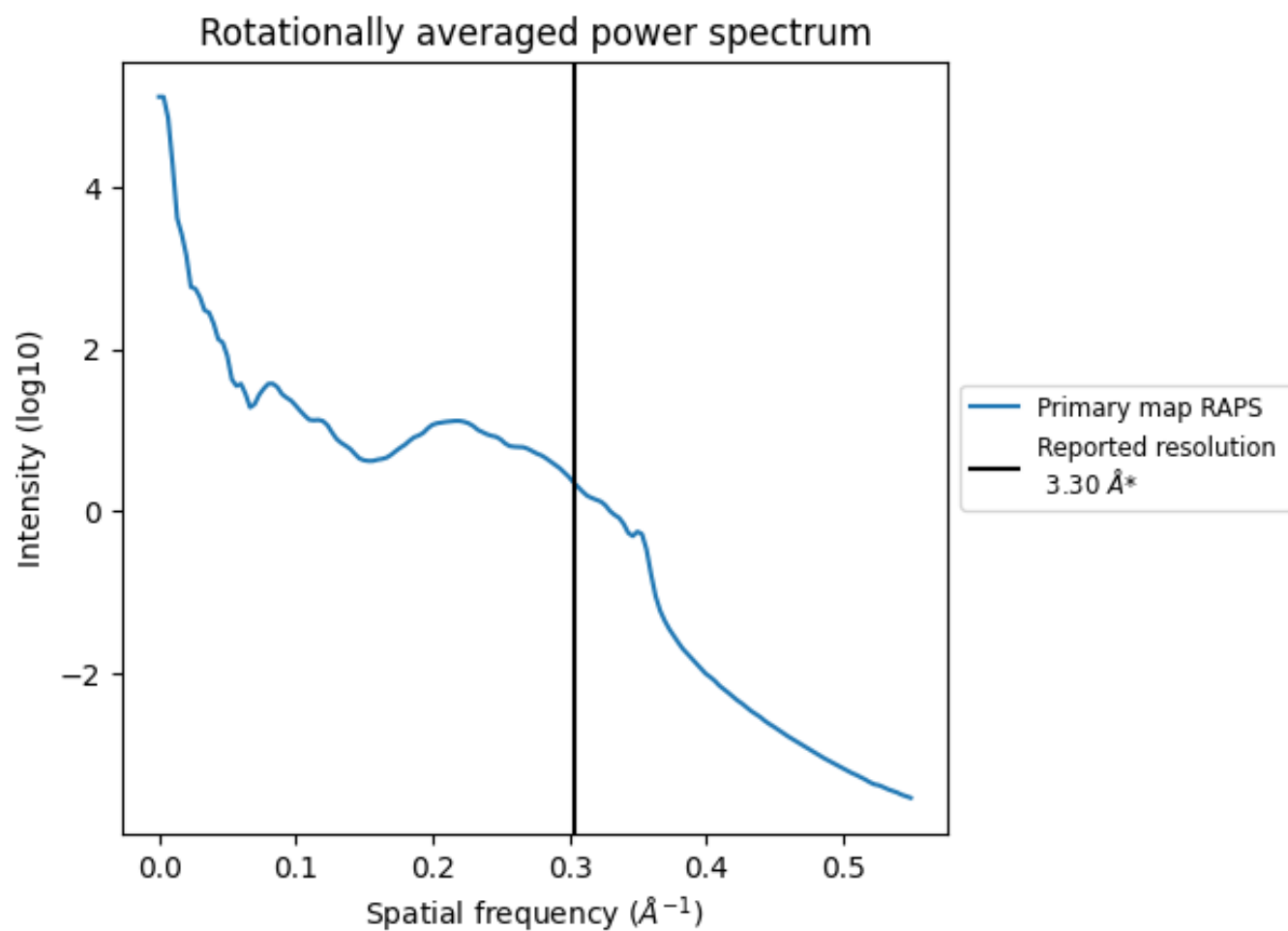
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 82 nm^3 ; this corresponds to an approximate mass of 74 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 ⓘ

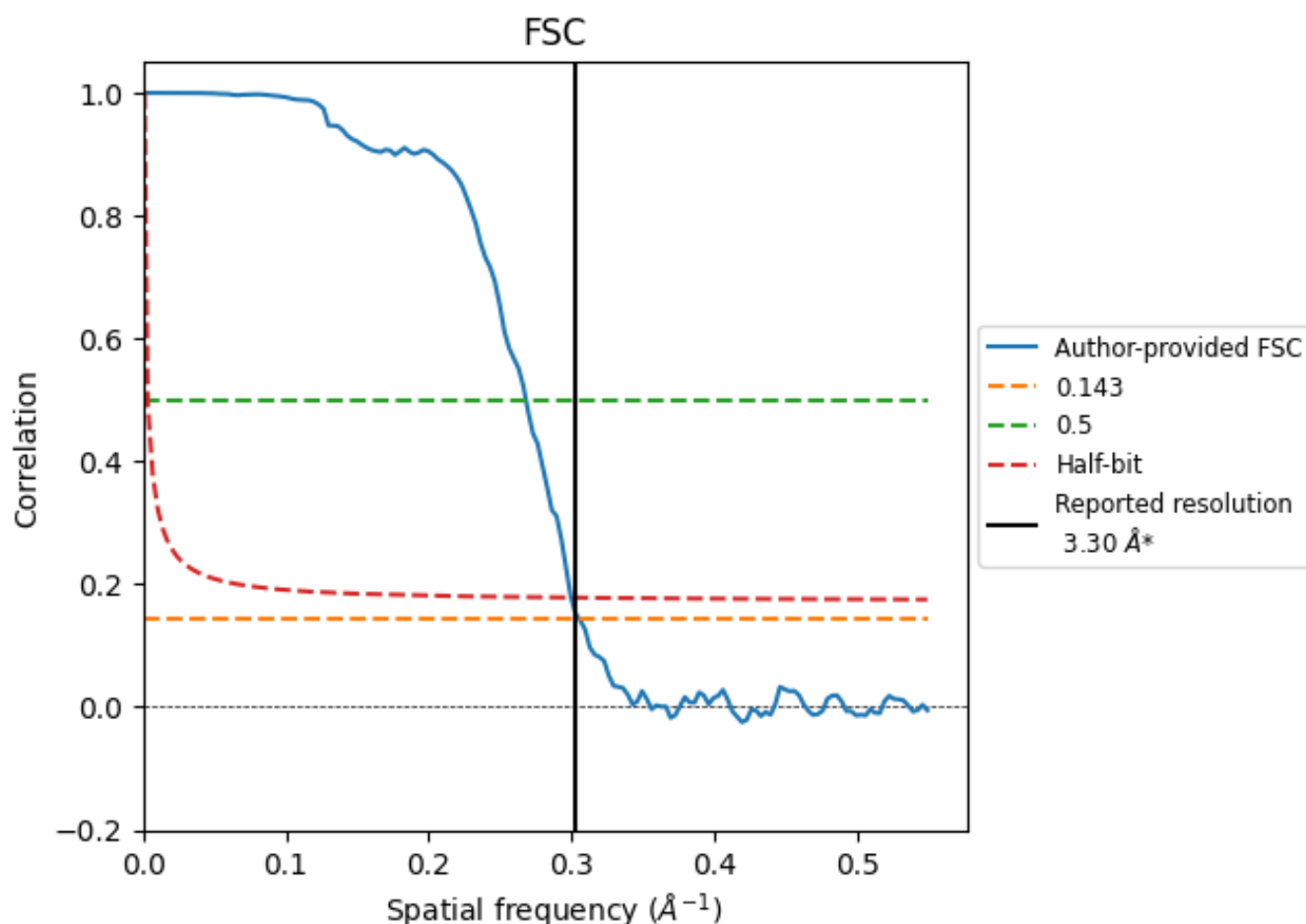


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 $0.303 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

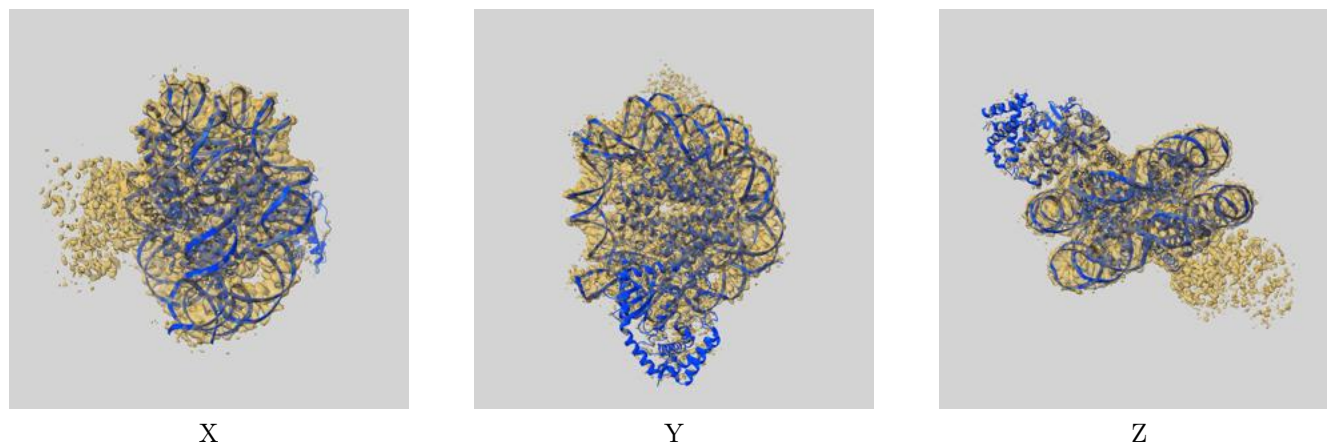
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.27	3.73	3.34
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

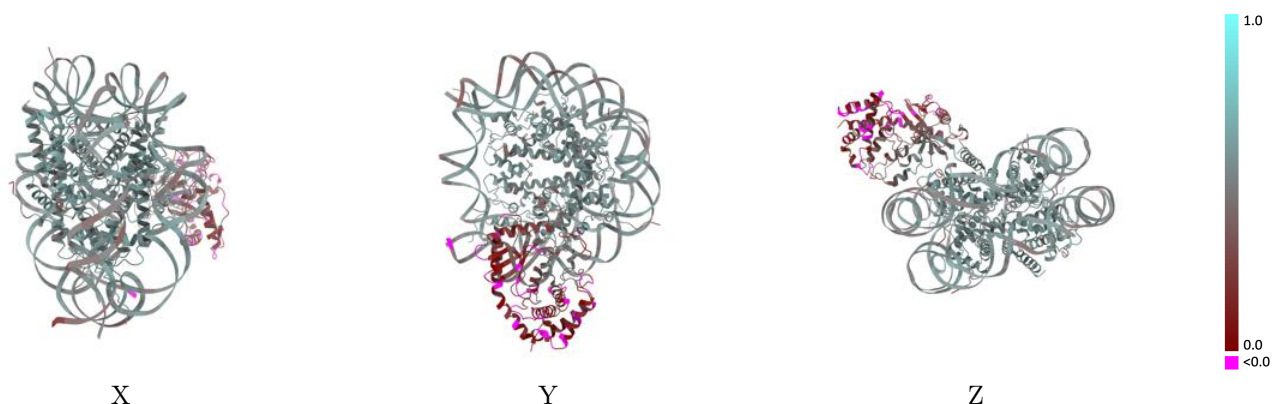
This section contains information regarding the fit between EMDB map EMD-22409 and PDB model 7JOA. Per-residue inclusion information can be found in section [3](#) on page [6](#).

9.1 Map-model overlay [i](#)



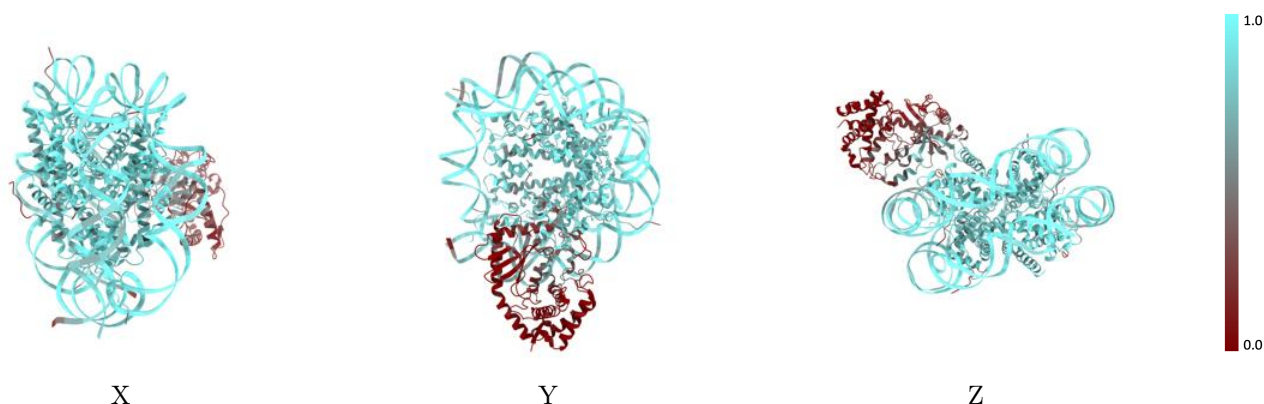
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



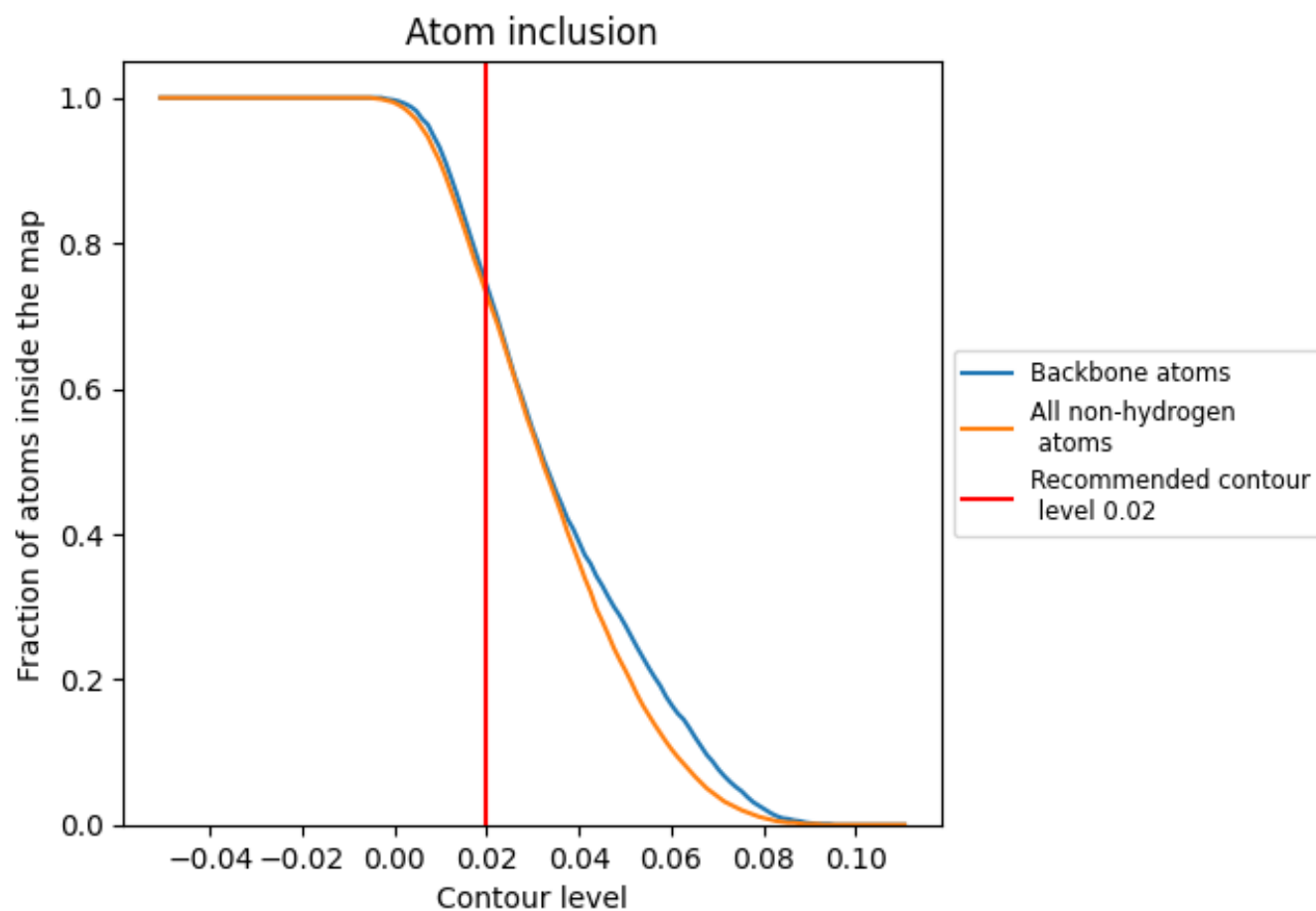
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 74% of all backbone atoms, 73% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7290	0.4740
A	0.8560	0.5620
B	0.8490	0.5610
C	0.8560	0.5460
D	0.8580	0.5420
E	0.8640	0.5670
F	0.8090	0.5350
G	0.8530	0.5540
H	0.8590	0.5380
I	0.8670	0.5230
J	0.8590	0.5050
K	0.2060	0.2360

1.0

0.0

<0.0