



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 12:04 AM UTC

PDB ID : 8WA1 / pdb_00008wa1
EMDB ID : EMD-37388
Title : The cryo-EM structure of the Nicotiana tabacum PEP-PAP-TEC2
Authors : Wu, X.X.; Zhang, Y.
Deposited on : 2023-09-06
Resolution : 2.80 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

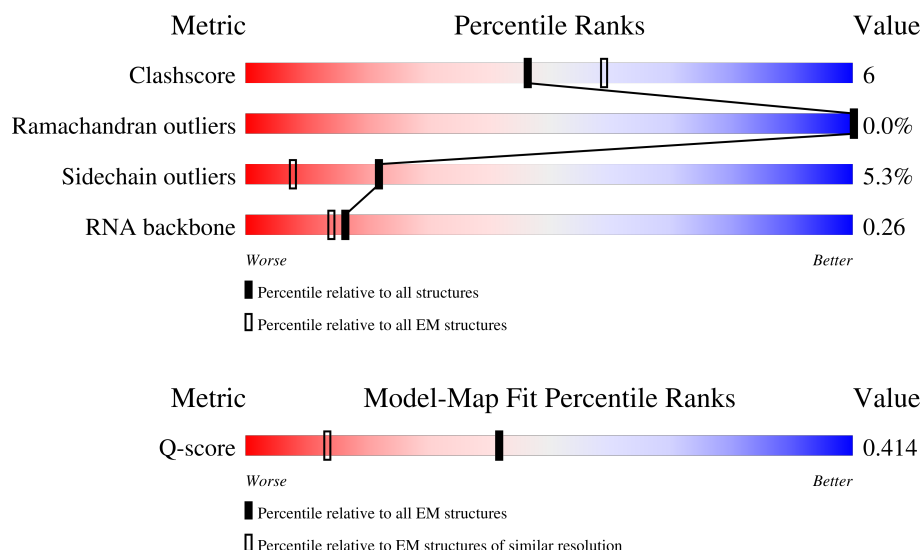
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 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.



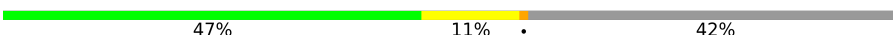
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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	337	
1	a	337	
2	B	1070	

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Mol	Chain	Length	Quality of chain
3	C	688	
4	D	892	
5	E	860	
6	F	682	
7	G	266	
8	H	531	
9	I	486	
10	J	507	
11	K	331	
12	L	303	
13	M	178	
13	m	178	
14	N	770	
15	O	167	
16	P	143	
17	Q	24	
18	R	24	
19	S	27	
20	c	1388	
21	i	648	

2 Entry composition [i](#)

There are 24 unique types of molecules in this entry. The entry contains 62699 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	288	Total	C	N	O	S	0	0
			2190	1392	378	409	11		
1	a	303	Total	C	N	O	S	0	0
			2358	1508	405	434	11		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	998	Total	C	N	O	S	0	0
			7604	4823	1367	1391	23		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	653	Total	C	N	O	S	0	0
			4899	3131	873	875	20		

- Molecule 4 is a protein called PAP1(pTAC3).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	645	Total	C	N	O	S	0	0
			5063	3202	885	950	26		

- Molecule 5 is a protein called Pentatricopeptide repeat-containing protein At1g74850, chloroplastic-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	700	Total	C	N	O	S	0	0
			4563	2840	829	872	22		

- Molecule 6 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	544	Total	C	N	O	S	0	0
			4259	2692	763	785	19		

- Molecule 7 is a protein called superoxide dismutase.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	218	Total	C	N	O	S	0	0
			1742	1134	291	310	7		

- Molecule 8 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 12-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	260	Total	C	N	O	S	0	0
			2110	1338	371	393	8		

- Molecule 9 is a protein called Fructokinase-like 1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	376	Total	C	N	O	S	0	0
			2946	1886	519	528	13		

- Molecule 10 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 14-like isoform X2.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	421	Total	C	N	O	S	0	0
			3410	2184	577	627	22		

- Molecule 11 is a protein called PAP8(pTAC6).

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	204	Total	C	N	O	S	0	0
			1705	1077	298	322	8		

- Molecule 12 is a protein called superoxide dismutase.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	229	Total	C	N	O	S	0	0
			1776	1141	306	324	5		

- Molecule 13 is a protein called Thioredoxin-like protein CITRX1, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	116	Total	C	N	O	S	0	0
			935	598	150	180	7		
13	m	109	Total	C	N	O	S	0	0
			855	548	136	164	7		

- Molecule 14 is a protein called UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2, 6-diaminopimelate ligase-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	537	Total	C	N	O	S	0	0
			2995	1825	582	582	6		

- Molecule 15 is a protein called Protein PLASTID TRANSCRIPTIONALLY ACTIVE 7-like isoform X1.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	97	Total	C	N	O	S	0	0
			780	490	140	146	4		

- Molecule 16 is a protein called PAP13(pTAC18).

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	102	Total	C	N	O	S	0	0
			843	547	142	151	3		

- Molecule 17 is a DNA chain called DNA (24-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	4	Total	C	N	O	P	0	0
			82	40	11	27	4		

- Molecule 18 is a DNA chain called DNA (24-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	14	Total	C	N	O	P	0	0
			285	136	53	82	14		

- Molecule 19 is a RNA chain called RNA (27-mer).

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	9	Total	C	N	O	P	0	0
			192	86	35	62	9		

- Molecule 20 is a protein called DNA-directed RNA polymerase subunit beta”.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	c	1176	Total	C	N	O	S	0	0
			8166	5119	1500	1517	30		

- Molecule 21 is a protein called Fructokinase-like 2, chloroplastic.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	i	375	Total	C	N	O	S	0	0
			2937	1873	500	548	16		

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

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

- Molecule 23 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
23	C	1	Total	Mg	0
			1	1	

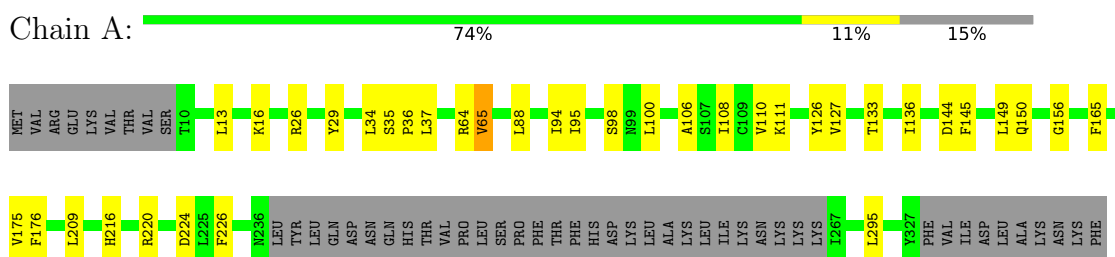
- Molecule 24 is FE (III) ION (CCD ID: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		AltConf
24	G	1	Total	Fe	0
			1	1	
24	L	1	Total	Fe	0
			1	1	

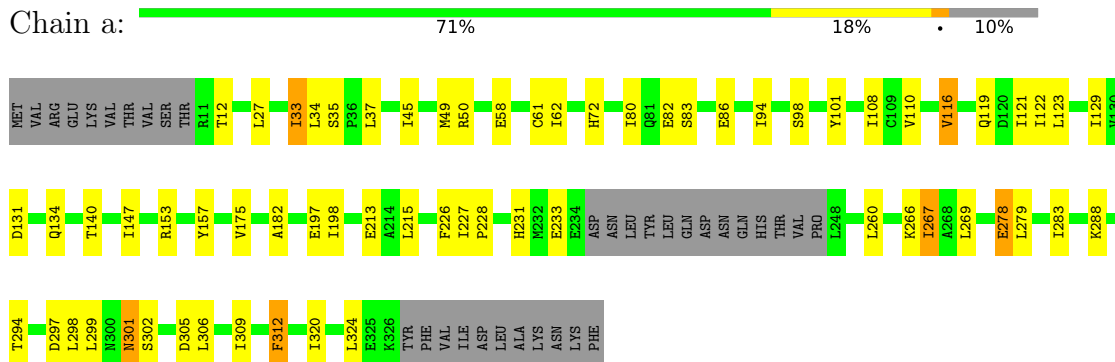
3 Residue-property plots [i](#)

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.

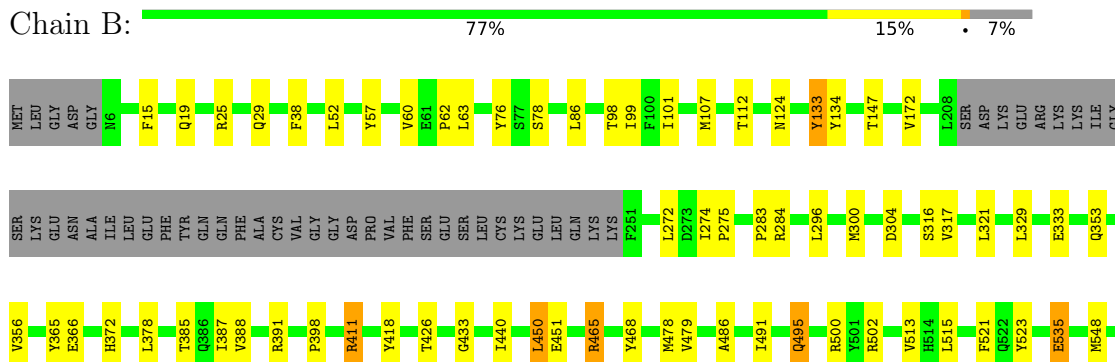
- Molecule 1: DNA-directed RNA polymerase subunit alpha

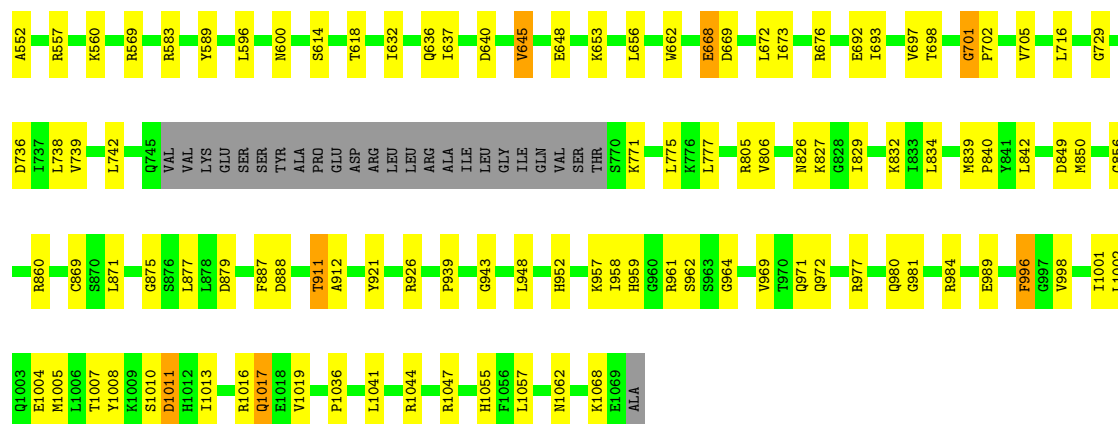


- Molecule 1: DNA-directed RNA polymerase subunit alpha



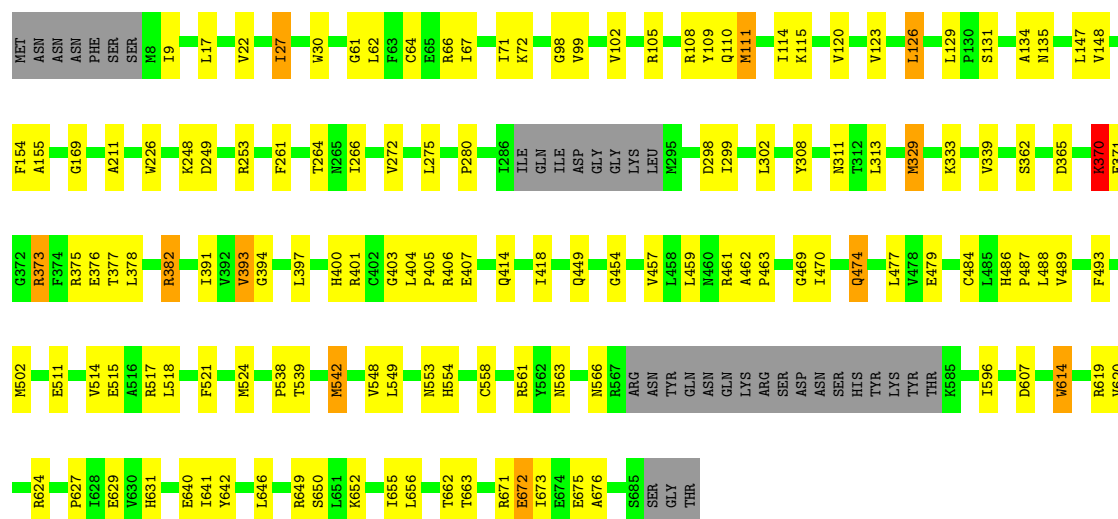
- Molecule 2: DNA-directed RNA polymerase subunit beta





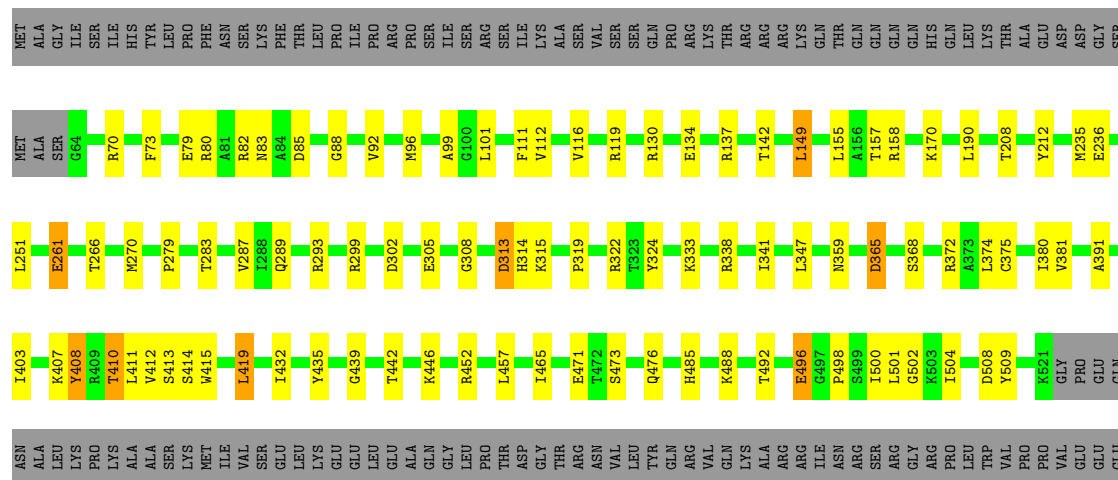
• Molecule 3: DNA-directed RNA polymerase subunit gamma

Chain C: 75% 18% 5%

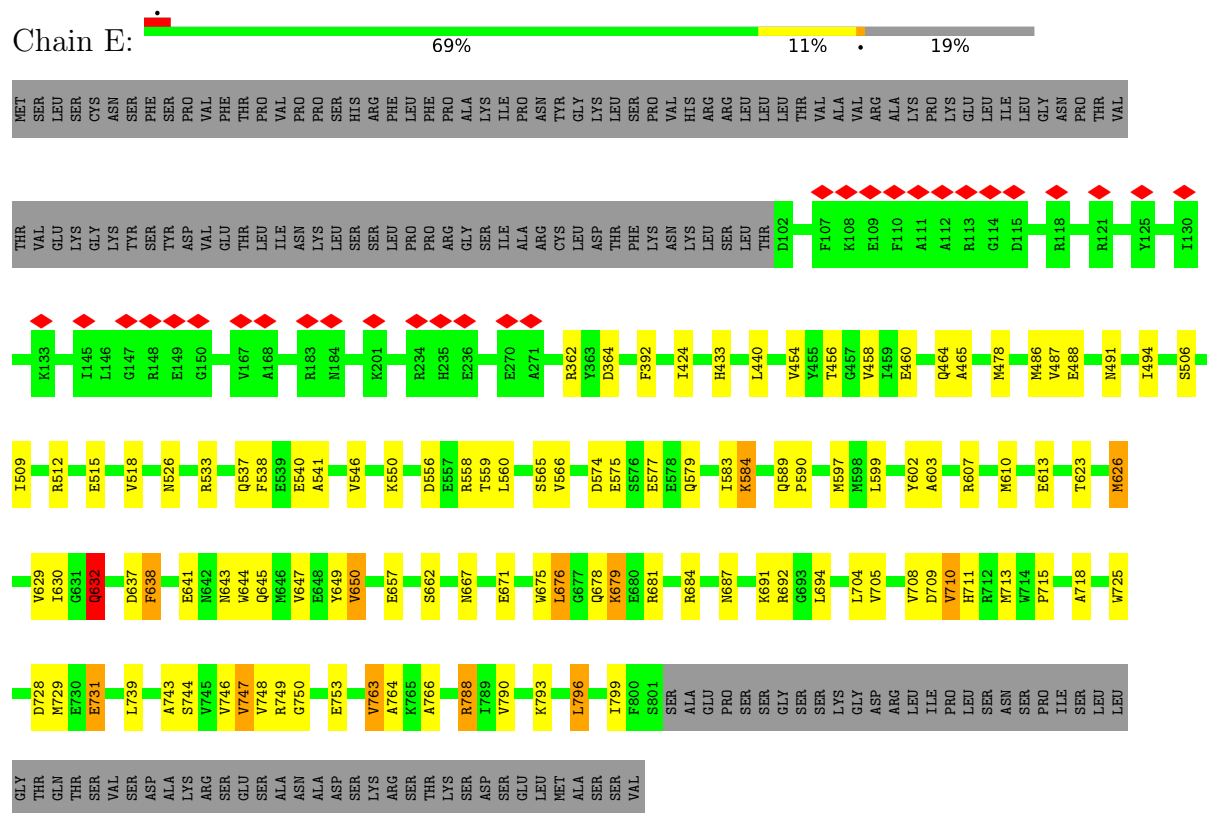


• Molecule 4: PAP1(pTAC3)

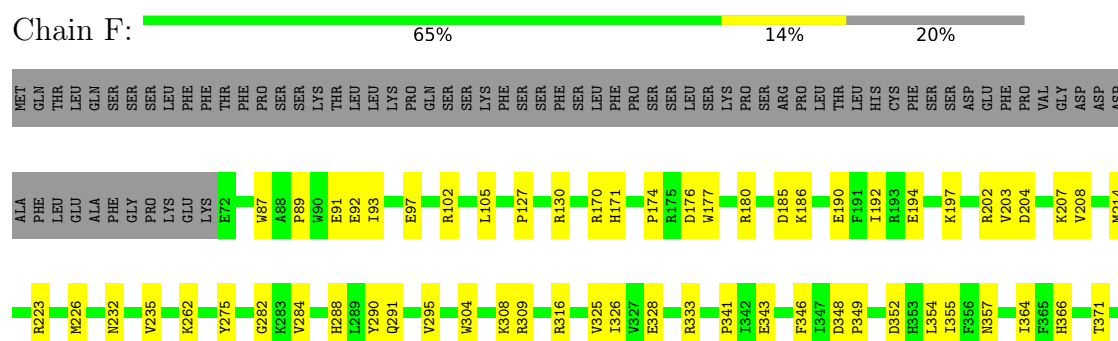
Chain D: 58% 13% 28%

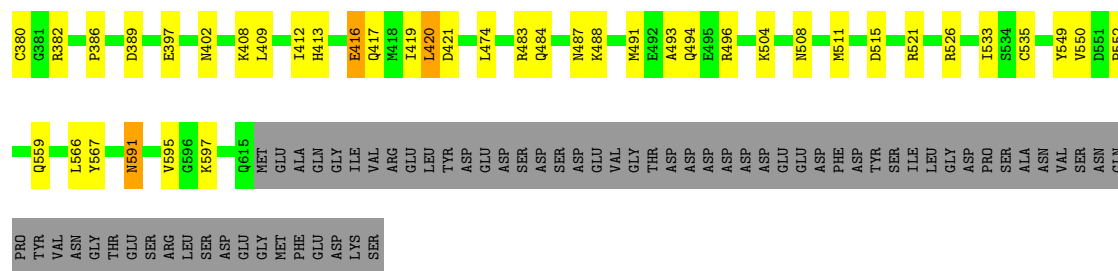


- Molecule 5: Pentatricopeptide repeat-containing protein At1g74850, chloroplastic-like

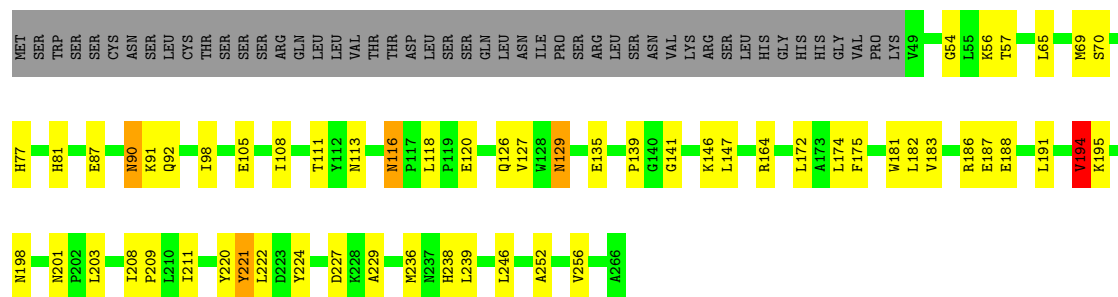


- Molecule 6: Protein PLASTID TRANSCRIPTIONALLY ACTIVE 10-like

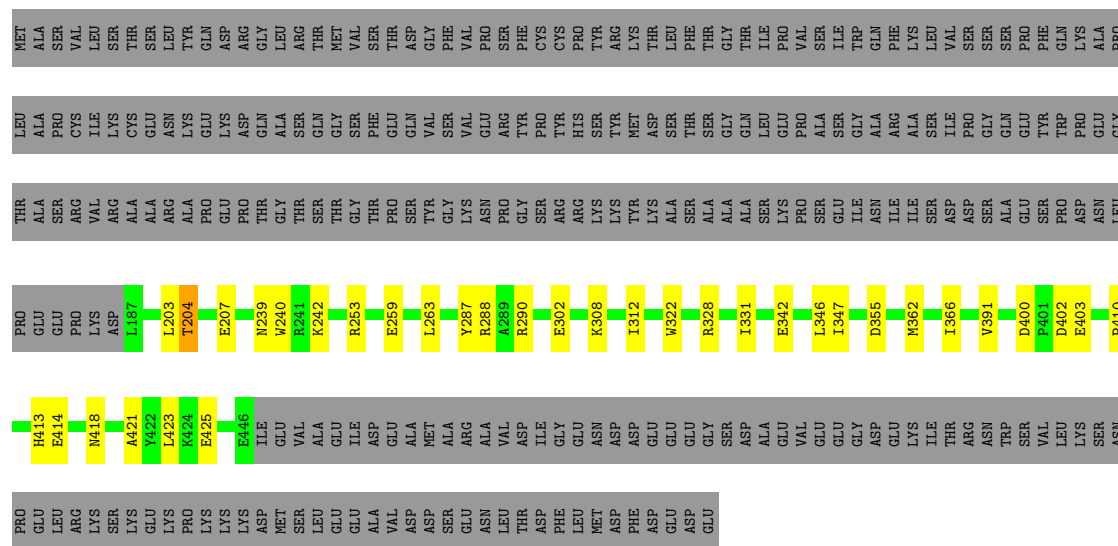




- Molecule 7: superoxide dismutase

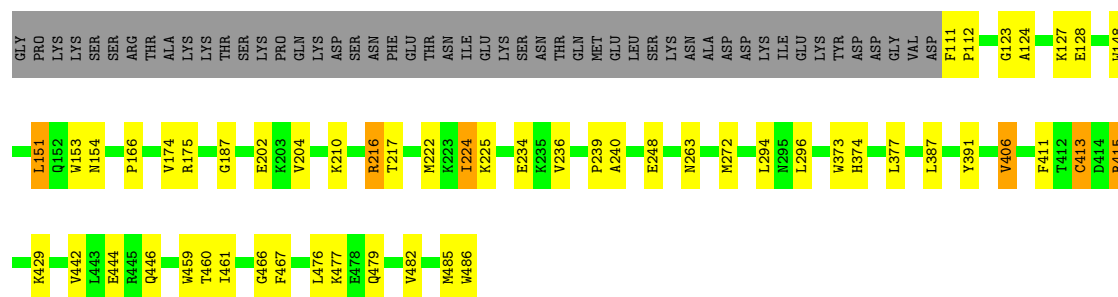


- Molecule 8: Protein PLASTID TRANSCRIPTIONALLY ACTIVE 12-like



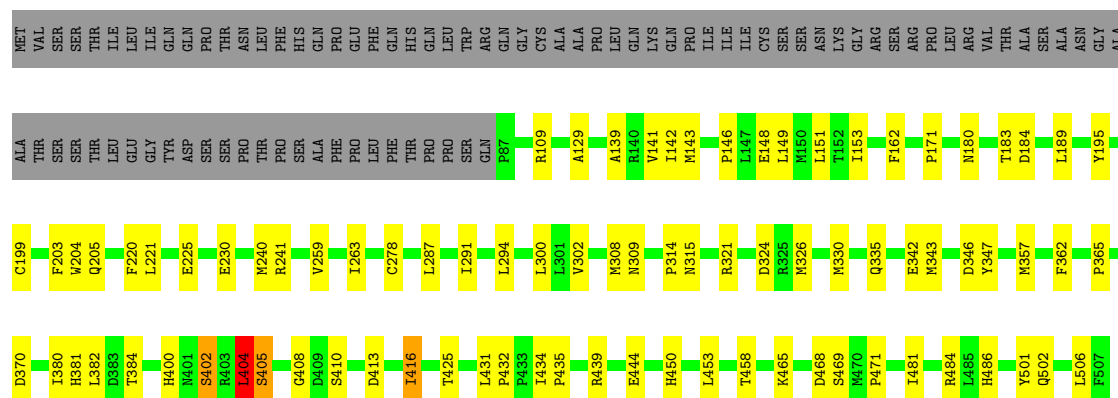
- Molecule 9: Fructokinase-like 1, chloroplastic





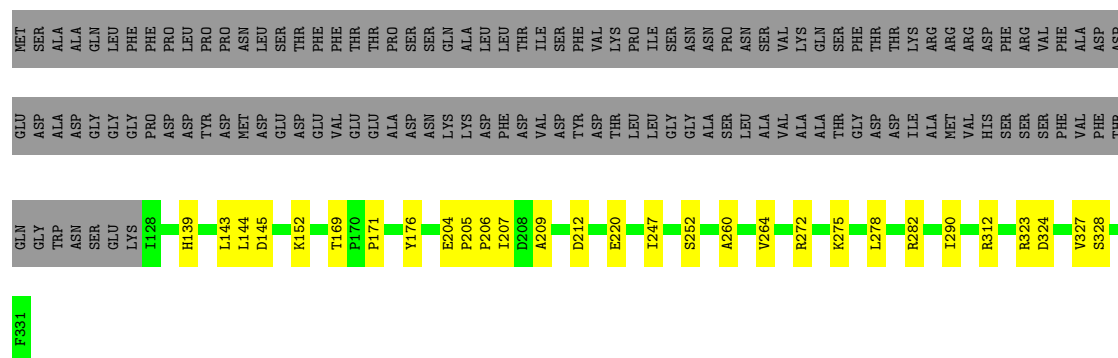
- Molecule 10: Protein PLASTID TRANSCRIPTIONALLY ACTIVE 14-like isoform X2

Chain J: 66% 16% 17%



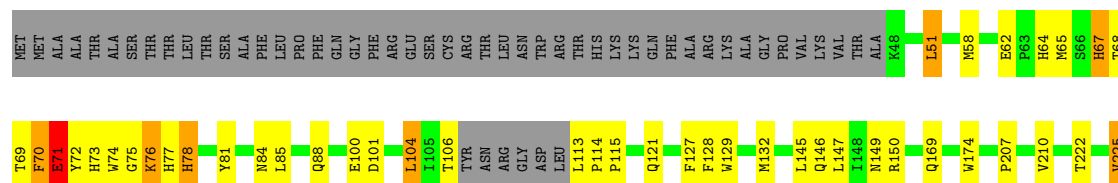
- Molecule 11: PAP8(pTAC6)

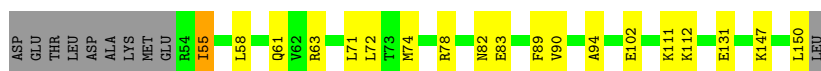
Chain K: 53% 9% 38%



- Molecule 12: superoxide dismutase

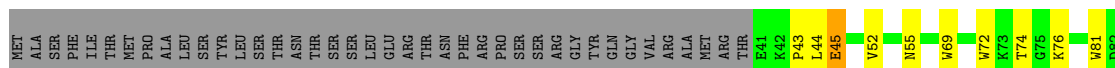
Chain L: 54% 19% 24%





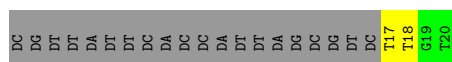
• Molecule 16: PAP13(pTAC18)

Chain P: 55% 15% 29%



• Molecule 17: DNA (24-mer)

Chain Q: 8% 8% 83%



• Molecule 18: DNA (24-mer)

Chain R: 33% 25% 42%



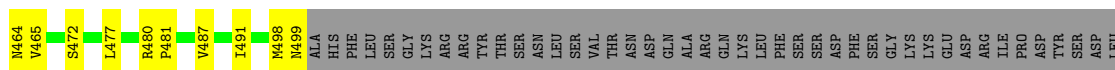
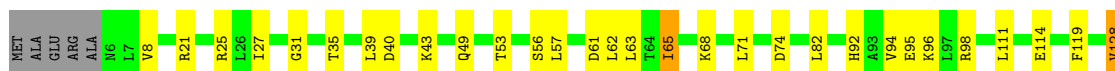
• Molecule 19: RNA (27-mer)

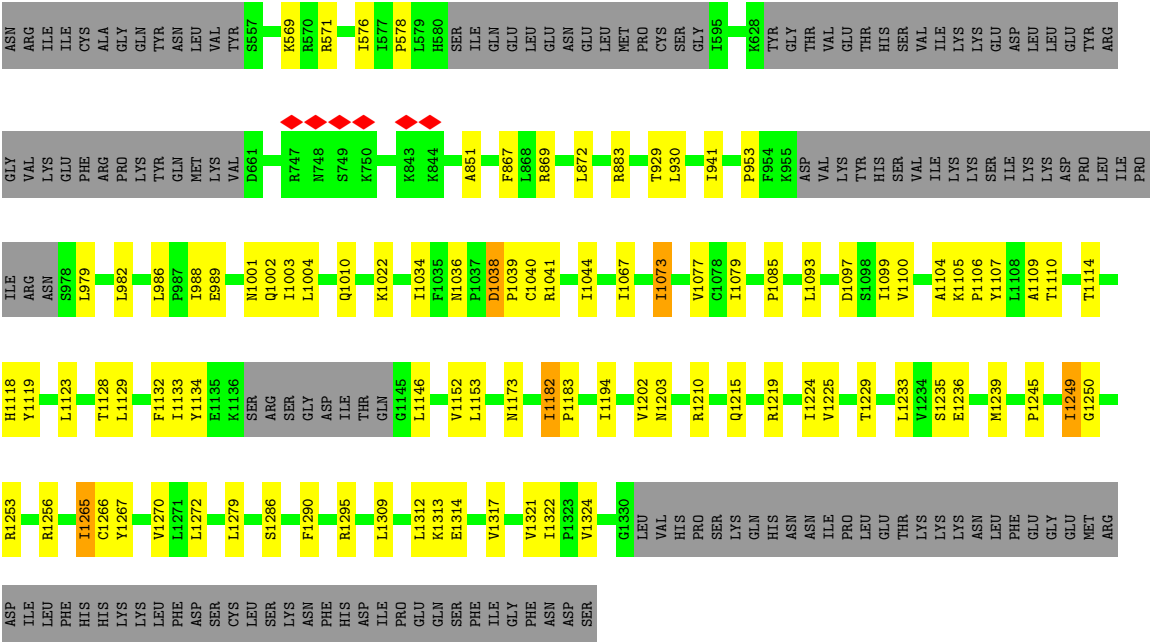
Chain S: 26% 7% 67%



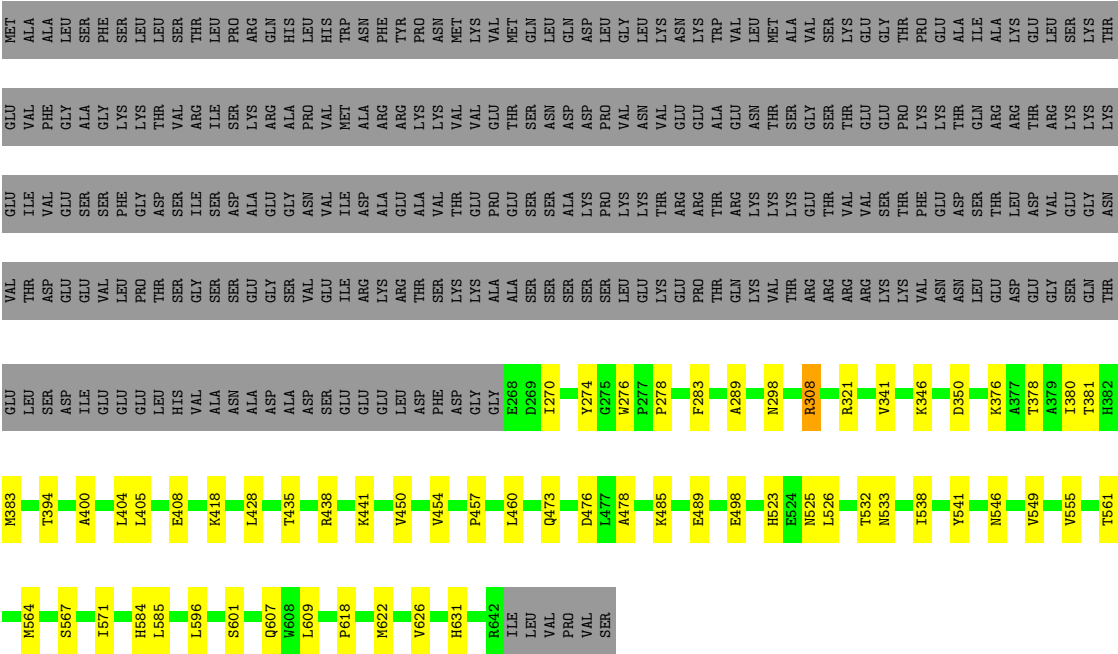
• Molecule 20: DNA-directed RNA polymerase subunit beta''

Chain c: 71% 13% 15%





● Molecule 21: Fructokinase-like 2, chloroplastic



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	88607	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 ($e^-/\text{\AA}^2$)	57.8	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.362	Depositor
Minimum map value	-0.380	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	464.8, 464.8, 464.8	wwPDB
Map dimensions	560, 560, 560	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	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, FE, MG

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	0.30	0/2227	0.40	0/3019
1	a	0.12	0/2403	0.32	1/3256 (0.0%)
2	B	0.56	3/7751 (0.0%)	0.65	6/10510 (0.1%)
3	C	0.38	1/4998 (0.0%)	0.53	7/6792 (0.1%)
4	D	0.20	0/5161	0.41	4/6986 (0.1%)
5	E	0.16	0/4633	0.39	5/6321 (0.1%)
6	F	0.22	0/4366	0.40	3/5918 (0.1%)
7	G	0.55	0/1793	0.75	8/2437 (0.3%)
8	H	0.31	0/2167	0.32	0/2942
9	I	0.20	0/3021	0.43	4/4092 (0.1%)
10	J	0.20	0/3498	0.39	2/4742 (0.0%)
11	K	0.14	0/1747	0.30	0/2362
12	L	0.62	3/1828 (0.2%)	0.82	12/2488 (0.5%)
13	M	0.52	0/951	0.63	3/1286 (0.2%)
13	m	0.42	0/869	0.54	0/1179
14	N	0.23	0/3024	0.48	8/4180 (0.2%)
15	O	0.11	0/793	0.30	0/1065
16	P	0.11	0/870	0.29	0/1182
17	Q	0.35	0/90	0.72	0/137
18	R	0.34	0/319	0.62	0/489
19	S	0.39	0/214	0.63	0/331
20	c	0.32	0/8294	0.44	4/11306 (0.0%)
21	i	0.21	0/3009	0.47	3/4078 (0.1%)
All	All	0.34	7/64026 (0.0%)	0.49	70/87098 (0.1%)

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	110	GLN	CA-C	-6.53	1.44	1.52
2	B	911	THR	CA-C	-5.65	1.45	1.52
2	B	668	GLU	CA-C	-5.57	1.48	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	L	74	TRP	CA-C	-5.52	1.45	1.52
12	L	67	HIS	C-O	-5.37	1.17	1.24

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	964	GLY	N-CA-C	21.04	136.91	112.50
20	c	1002	GLN	N-CA-C	-10.36	98.77	111.40
2	B	911	THR	N-CA-C	-10.08	92.10	108.52
14	N	683	TYR	N-CA-C	9.30	121.02	111.07
21	i	276	TRP	CA-C-N	-9.18	110.92	120.38

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2190	0	2116	20	0
1	a	2358	0	2354	35	0
2	B	7604	0	7393	92	0
3	C	4899	0	4598	81	0
4	D	5063	0	4944	71	0
5	E	4563	0	3584	61	0
6	F	4259	0	3864	70	0
7	G	1742	0	1676	30	0
8	H	2110	0	1974	22	0
9	I	2946	0	2821	31	0
10	J	3410	0	3316	52	0
11	K	1705	0	1668	16	0
12	L	1776	0	1608	36	0
13	M	935	0	934	11	0
13	m	855	0	848	12	0
14	N	2995	0	1888	17	0
15	O	780	0	754	12	0
16	P	843	0	758	16	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
17	Q	82	0	48	1	0
18	R	285	0	158	6	0
19	S	192	0	97	2	0
20	c	8166	0	7164	111	0
21	i	2937	0	2878	32	0
22	B	1	0	0	0	0
23	C	1	0	0	0	0
24	G	1	0	0	0	0
24	L	1	0	0	0	0
All	All	62699	0	57443	736	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 736 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)
10:J:402:SER:HA	10:J:405:SER:OG	1.04	1.20
4:D:137:ARG:HH22	10:J:404:LEU:CD1	1.55	1.20
10:J:402:SER:CA	10:J:405:SER:OG	1.91	1.18
4:D:137:ARG:NH2	10:J:404:LEU:HD21	1.58	1.17
4:D:137:ARG:HH21	10:J:404:LEU:HD21	1.08	1.12

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	284/337 (84%)	276 (97%)	8 (3%)	0	100	100
1	a	299/337 (89%)	291 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	992/1070 (93%)	973 (98%)	19 (2%)	0	100	100
3	C	647/688 (94%)	629 (97%)	18 (3%)	0	100	100
4	D	639/892 (72%)	627 (98%)	12 (2%)	0	100	100
5	E	698/860 (81%)	691 (99%)	7 (1%)	0	100	100
6	F	542/682 (80%)	532 (98%)	10 (2%)	0	100	100
7	G	216/266 (81%)	207 (96%)	9 (4%)	0	100	100
8	H	258/531 (49%)	256 (99%)	2 (1%)	0	100	100
9	I	374/486 (77%)	365 (98%)	9 (2%)	0	100	100
10	J	419/507 (83%)	412 (98%)	6 (1%)	1 (0%)	43	72
11	K	202/331 (61%)	200 (99%)	2 (1%)	0	100	100
12	L	225/303 (74%)	215 (96%)	10 (4%)	0	100	100
13	M	114/178 (64%)	112 (98%)	2 (2%)	0	100	100
13	m	107/178 (60%)	107 (100%)	0	0	100	100
14	N	535/770 (70%)	523 (98%)	12 (2%)	0	100	100
15	O	95/167 (57%)	93 (98%)	2 (2%)	0	100	100
16	P	100/143 (70%)	100 (100%)	0	0	100	100
20	c	1162/1388 (84%)	1129 (97%)	33 (3%)	0	100	100
21	i	373/648 (58%)	360 (96%)	13 (4%)	0	100	100
All	All	8281/10762 (77%)	8098 (98%)	182 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	J	408	GLY

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	226/308 (73%)	216 (96%)	10 (4%)	25	59
1	a	256/308 (83%)	238 (93%)	18 (7%)	14	40
2	B	767/924 (83%)	729 (95%)	38 (5%)	22	54
3	C	465/612 (76%)	433 (93%)	32 (7%)	14	41
4	D	523/770 (68%)	489 (94%)	34 (6%)	15	43
5	E	308/741 (42%)	285 (92%)	23 (8%)	12	37
6	F	401/615 (65%)	386 (96%)	15 (4%)	30	65
7	G	176/232 (76%)	166 (94%)	10 (6%)	18	49
8	H	212/472 (45%)	205 (97%)	7 (3%)	33	69
9	I	298/437 (68%)	287 (96%)	11 (4%)	30	65
10	J	368/449 (82%)	351 (95%)	17 (5%)	24	58
11	K	192/301 (64%)	188 (98%)	4 (2%)	47	79
12	L	167/258 (65%)	153 (92%)	14 (8%)	10	32
13	M	103/160 (64%)	102 (99%)	1 (1%)	68	88
13	m	93/160 (58%)	88 (95%)	5 (5%)	20	51
14	N	99/659 (15%)	90 (91%)	9 (9%)	9	28
15	O	79/144 (55%)	75 (95%)	4 (5%)	21	54
16	P	82/129 (64%)	77 (94%)	5 (6%)	17	46
20	c	697/1238 (56%)	657 (94%)	40 (6%)	18	49
21	i	316/567 (56%)	307 (97%)	9 (3%)	38	73
All	All	5828/9484 (62%)	5522 (95%)	306 (5%)	22	52

5 of 306 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	P	74	THR
20	c	1249	ILE
1	a	116	VAL
20	c	211	GLN
21	i	596	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 168 such sidechains are listed below:

Mol	Chain	Res	Type
12	L	88	GLN

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Mol	Chain	Res	Type
20	c	449	HIS
14	N	678	HIS
1	a	221	ASN
20	c	1007	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
19	S	8/27 (29%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

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 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

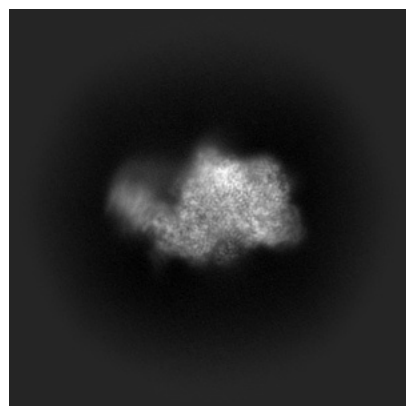
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37388. These allow visual inspection of the internal detail of the map and identification of artifacts.

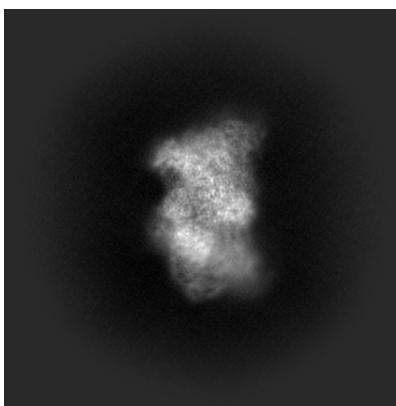
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

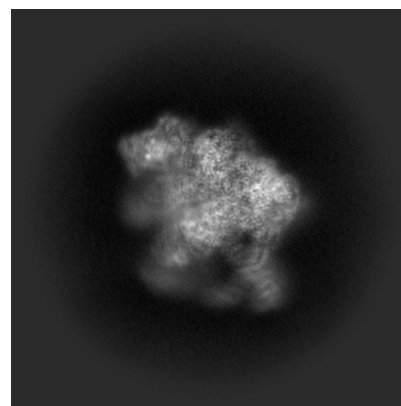
6.1.1 Primary map



X

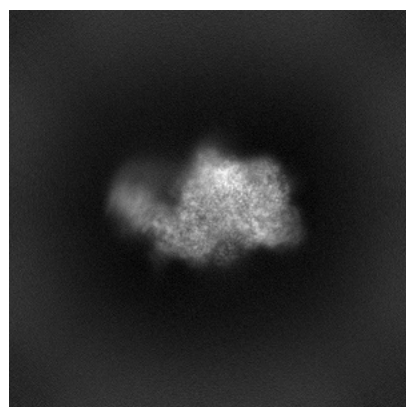


Y

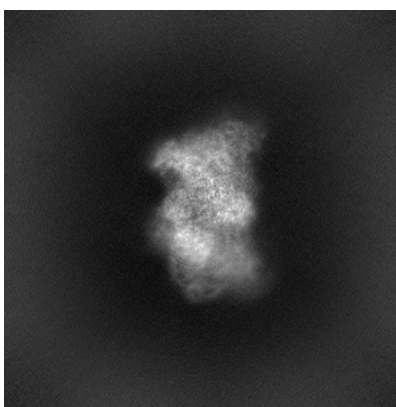


Z

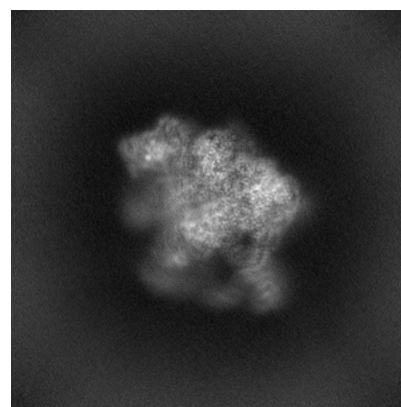
6.1.2 Raw map



X



Y

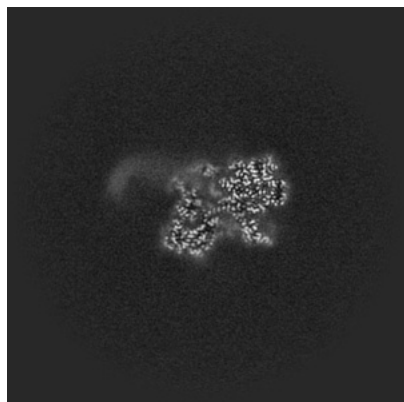


Z

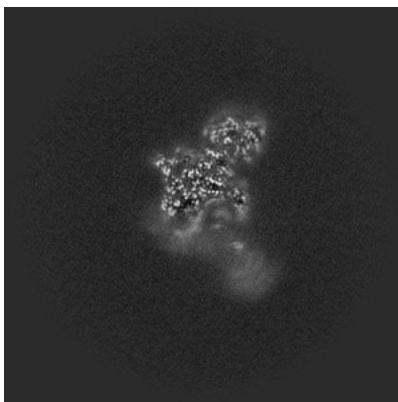
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

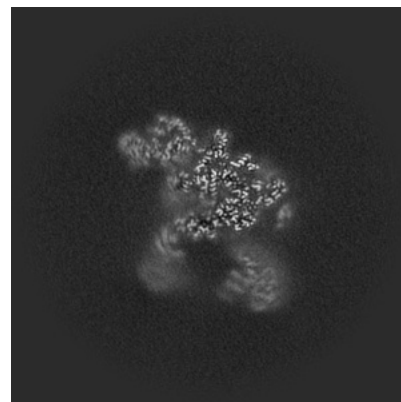
6.2.1 Primary map



X Index: 280

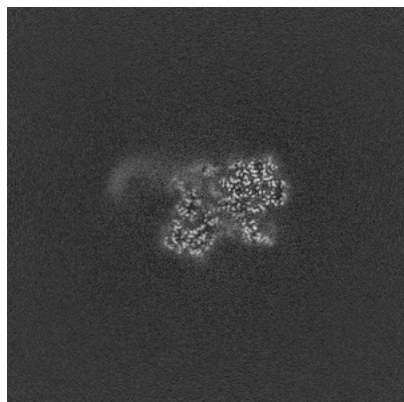


Y Index: 280

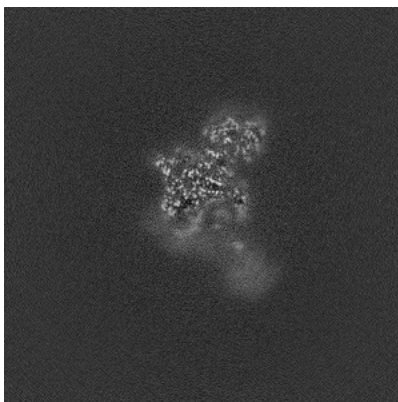


Z Index: 280

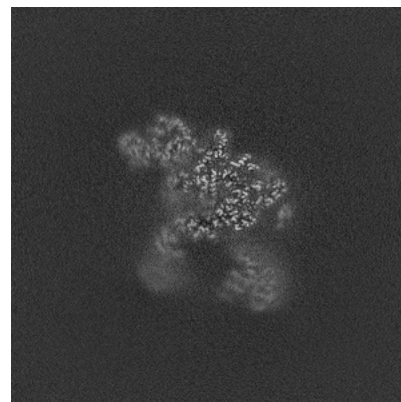
6.2.2 Raw map



X Index: 280



Y Index: 280

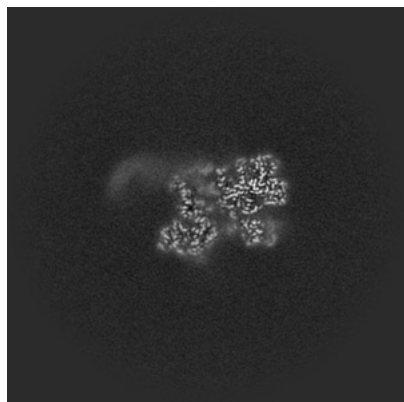


Z Index: 280

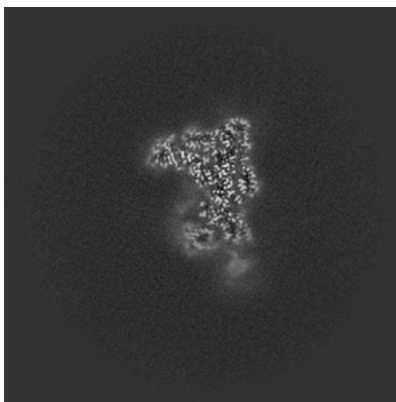
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

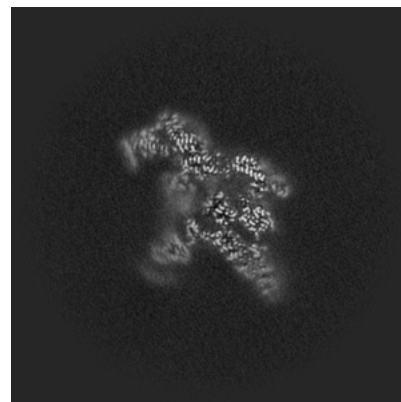
6.3.1 Primary map



X Index: 274

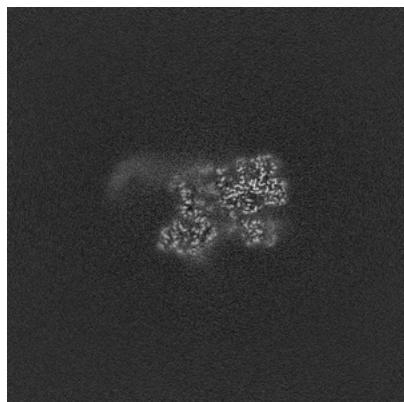


Y Index: 307

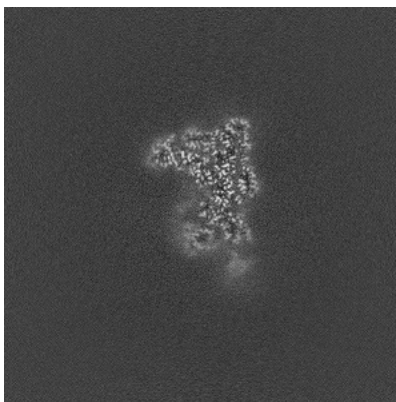


Z Index: 256

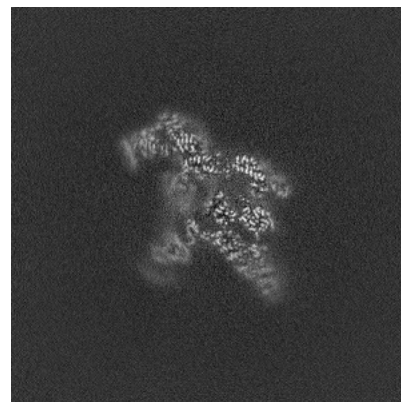
6.3.2 Raw map



X Index: 274



Y Index: 307

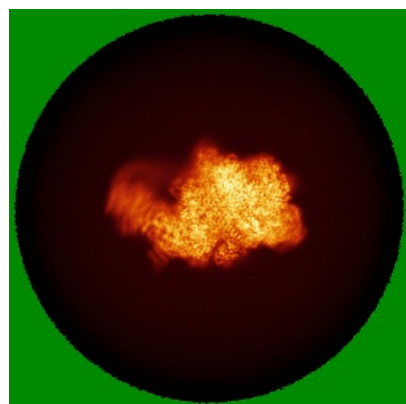


Z Index: 256

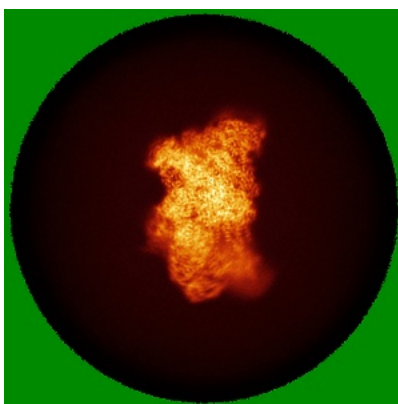
The images above show the largest variance slices of the map in three orthogonal directions.

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

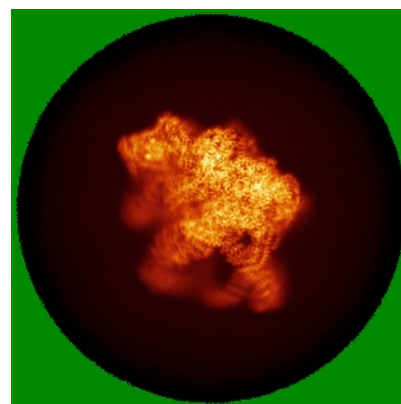
6.4.1 Primary map



X

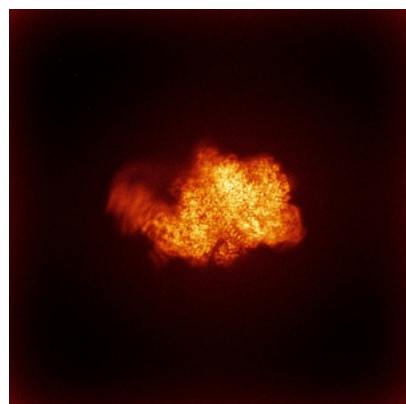


Y

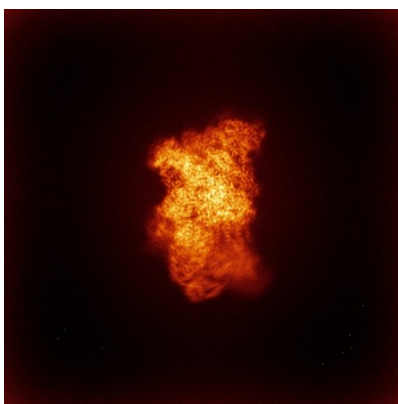


Z

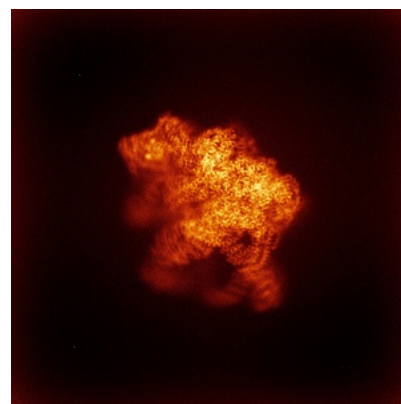
6.4.2 Raw map



X



Y

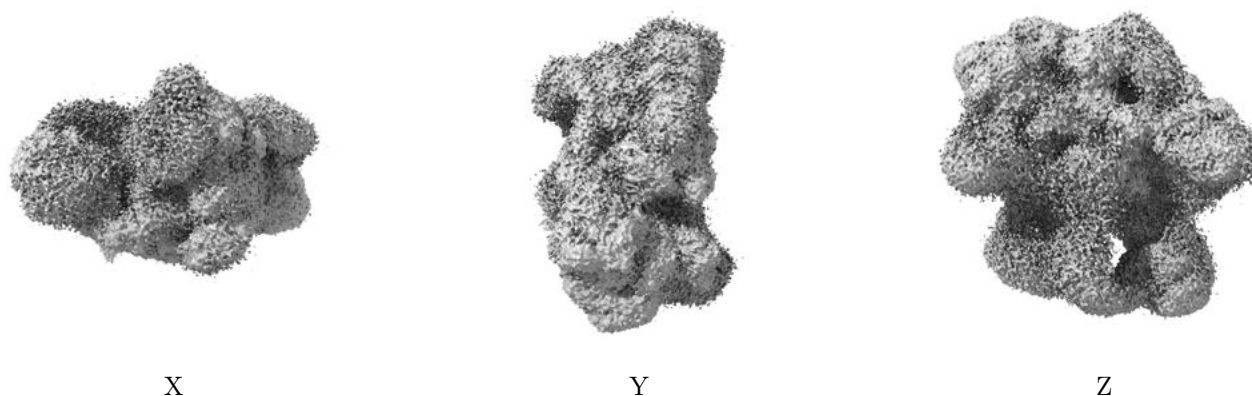


Z

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

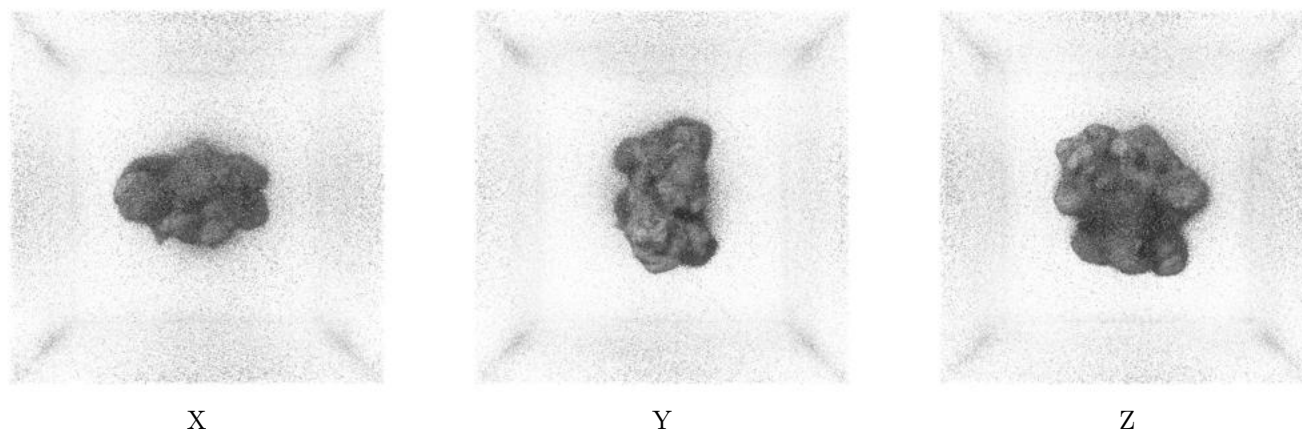
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

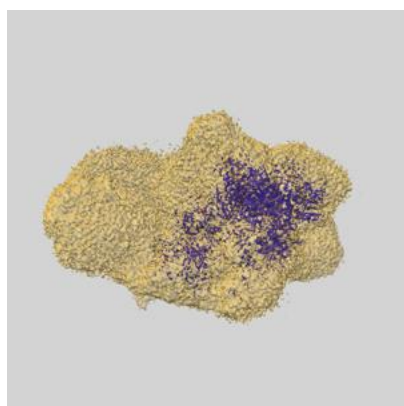
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

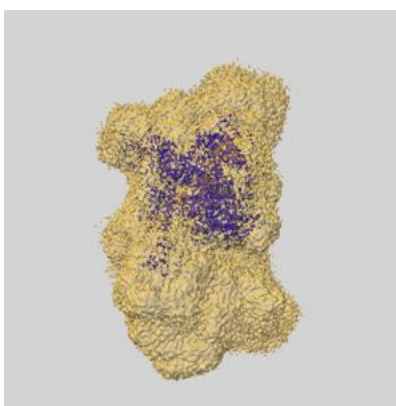
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

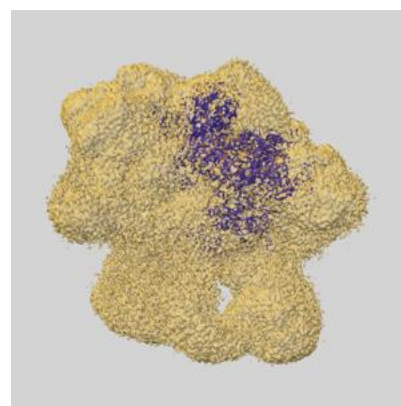
6.6.1 emd_37388_msk_1.map [i](#)



X



Y

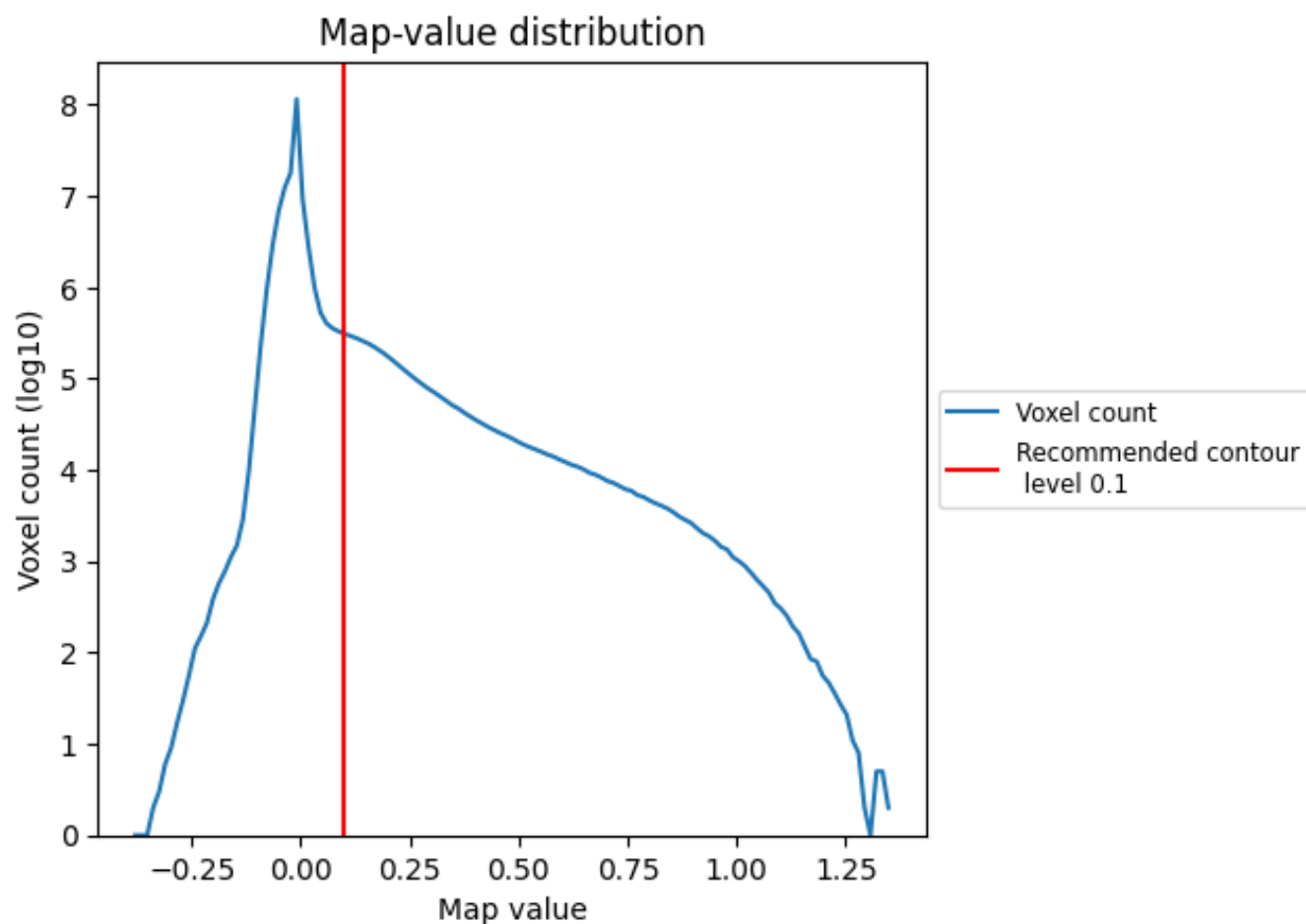


Z

7 Map analysis [i](#)

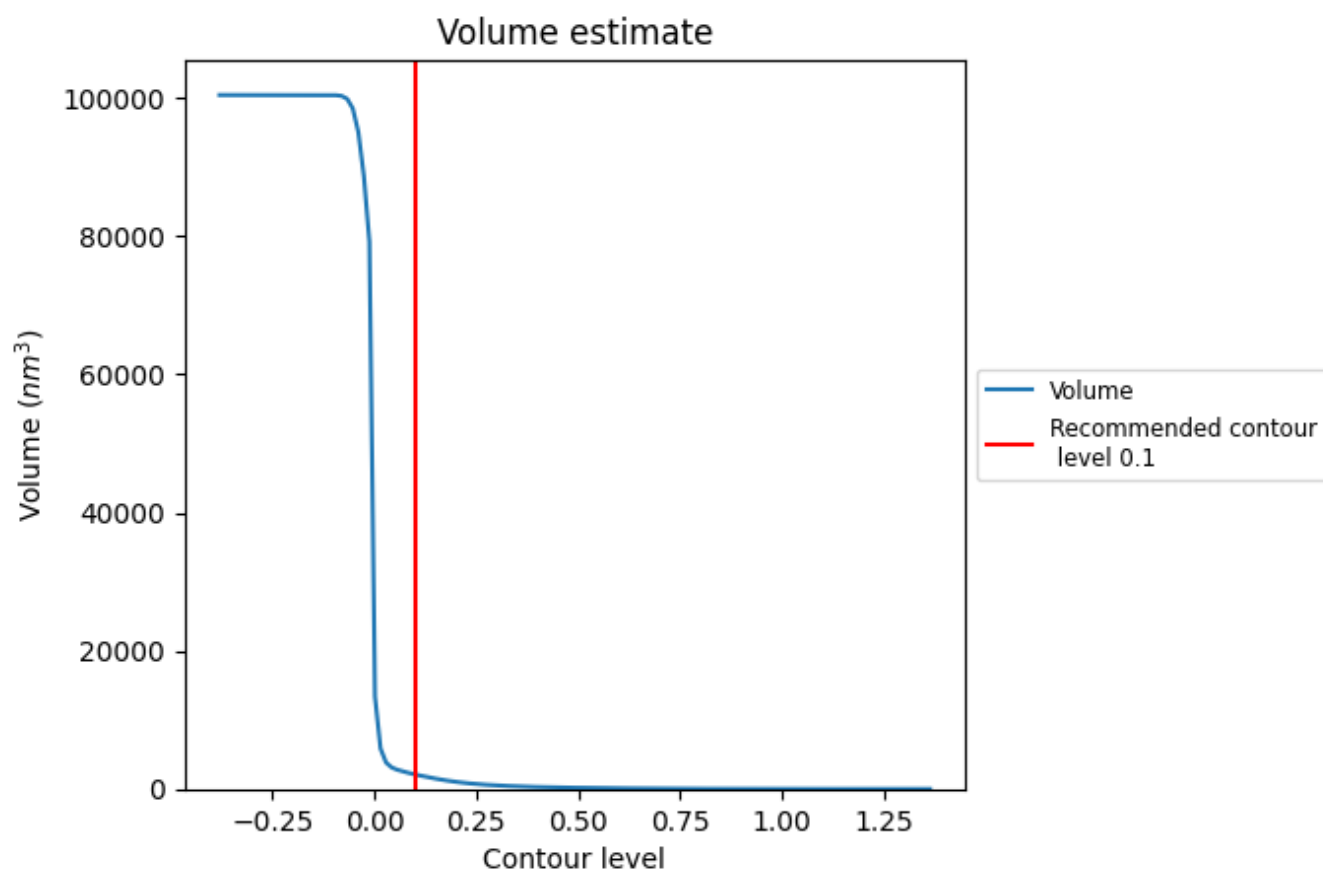
This section contains the results of statistical analysis of the map.

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.

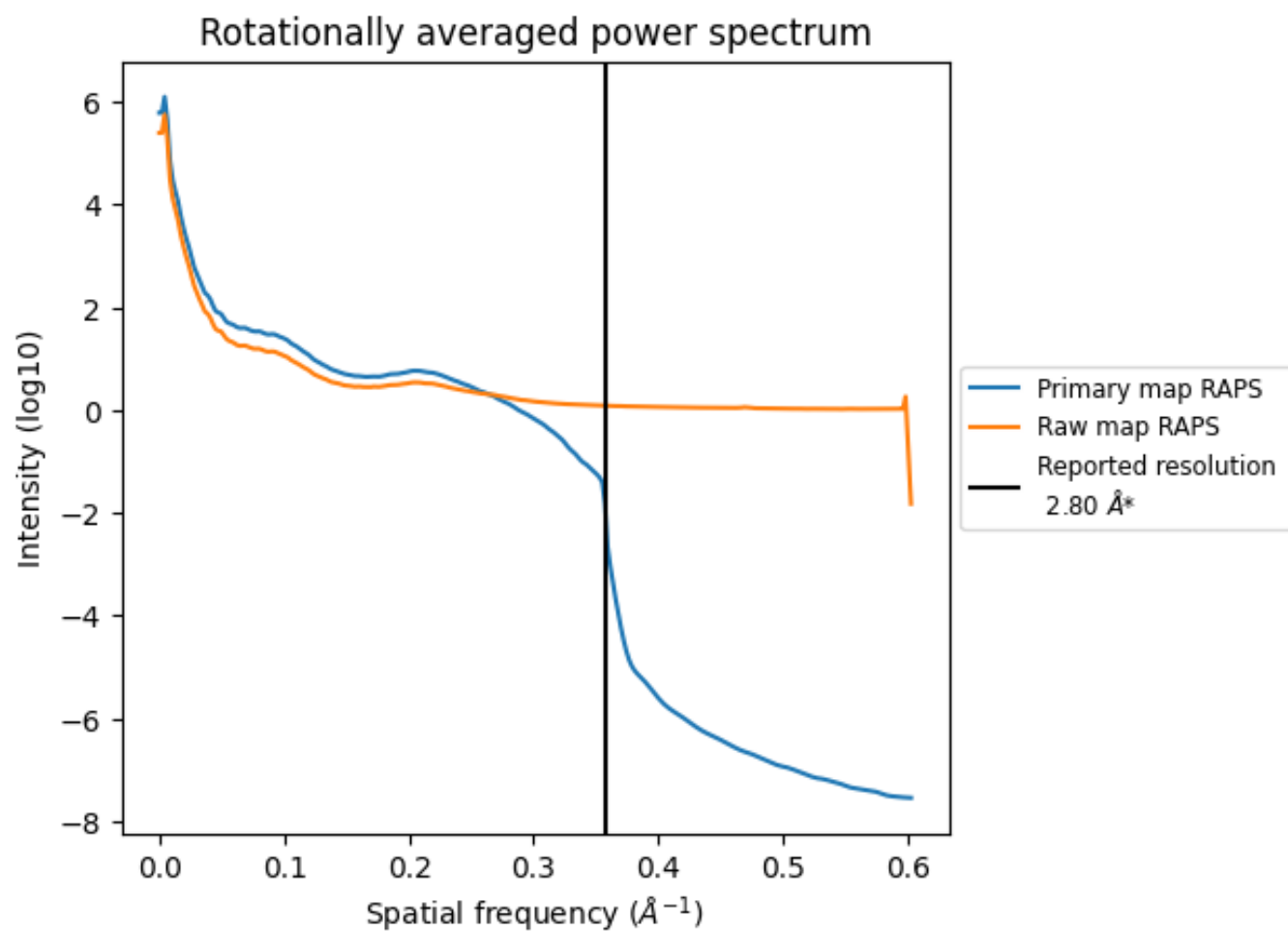
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2097 nm^3 ; this corresponds to an approximate mass of 1894 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 ⓘ

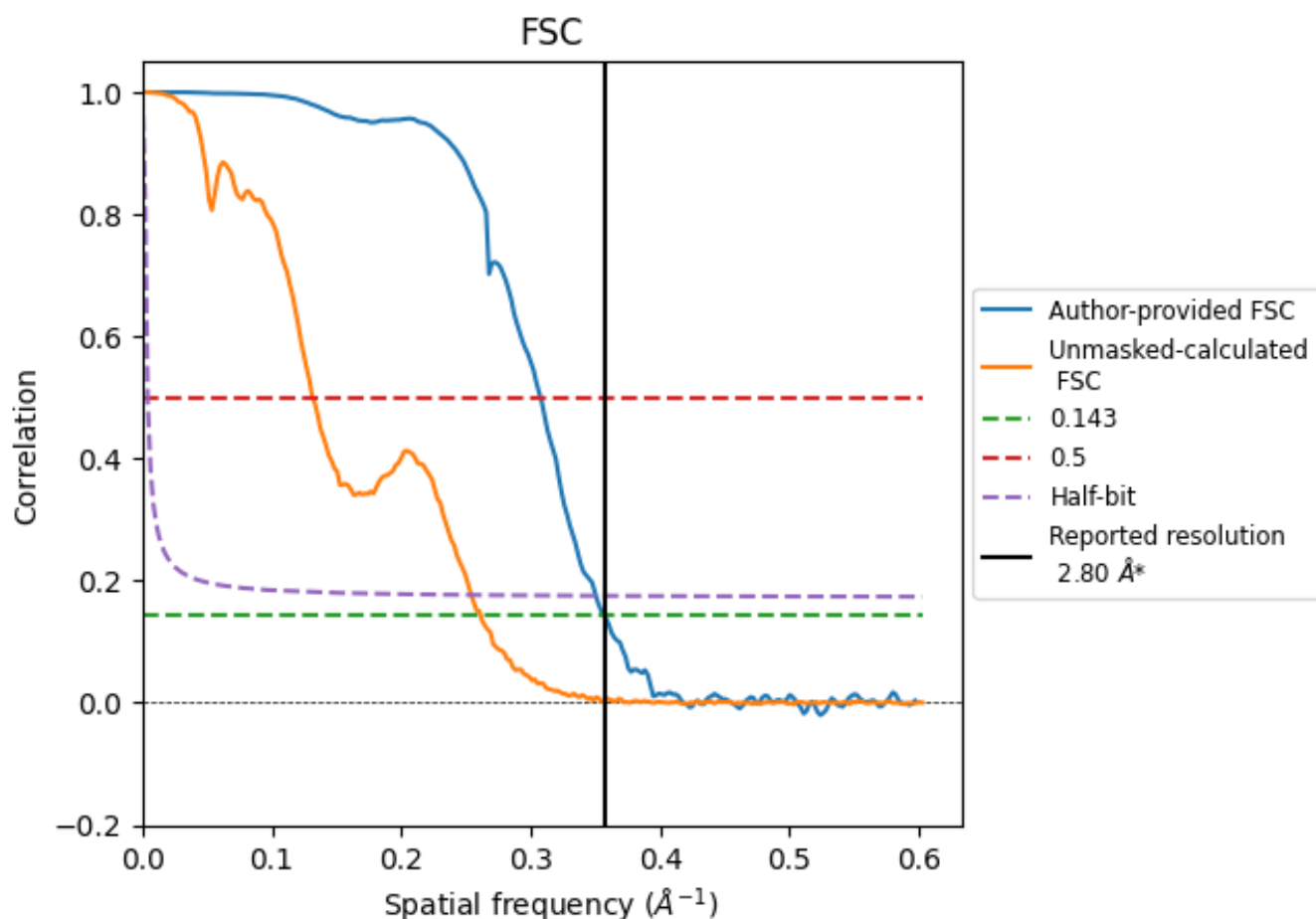


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

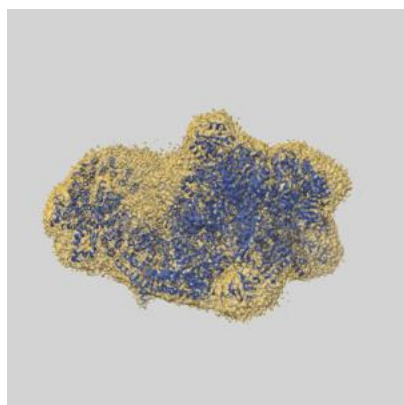
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.81	3.25	2.85
Unmasked-calculated*	3.83	7.59	3.94

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.83 differs from the reported value 2.8 by more than 10 %

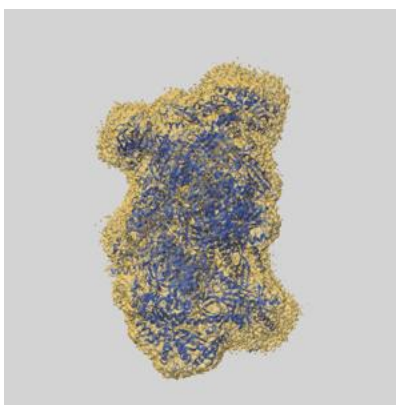
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37388 and PDB model 8WA1. Per-residue inclusion information can be found in section [3](#) on page [8](#).

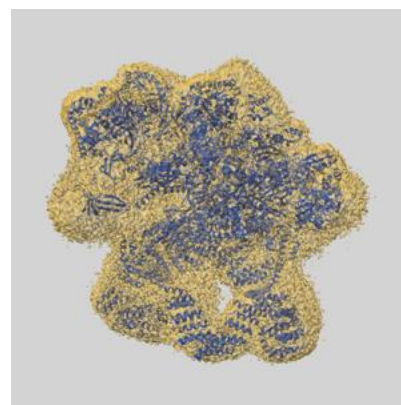
9.1 Map-model overlay [i](#)



X



Y



Z

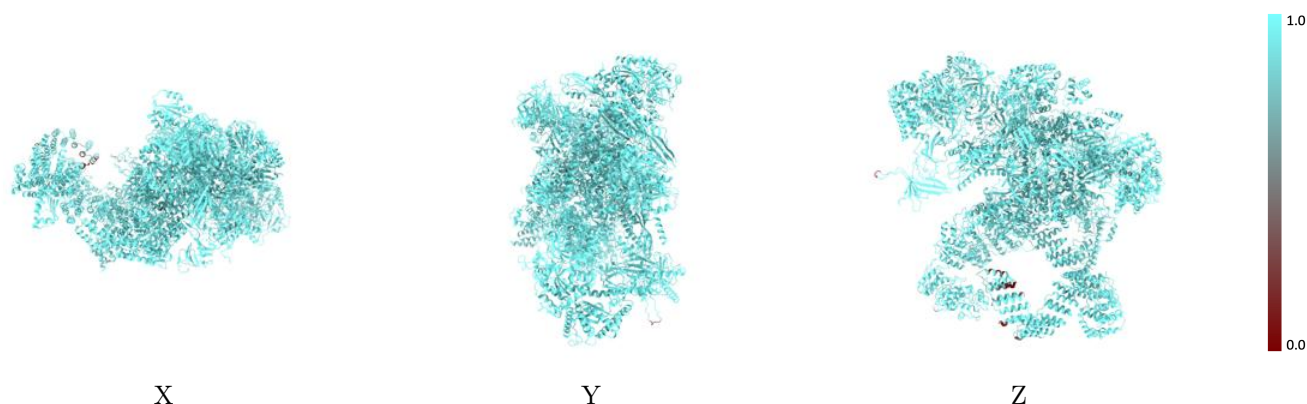
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



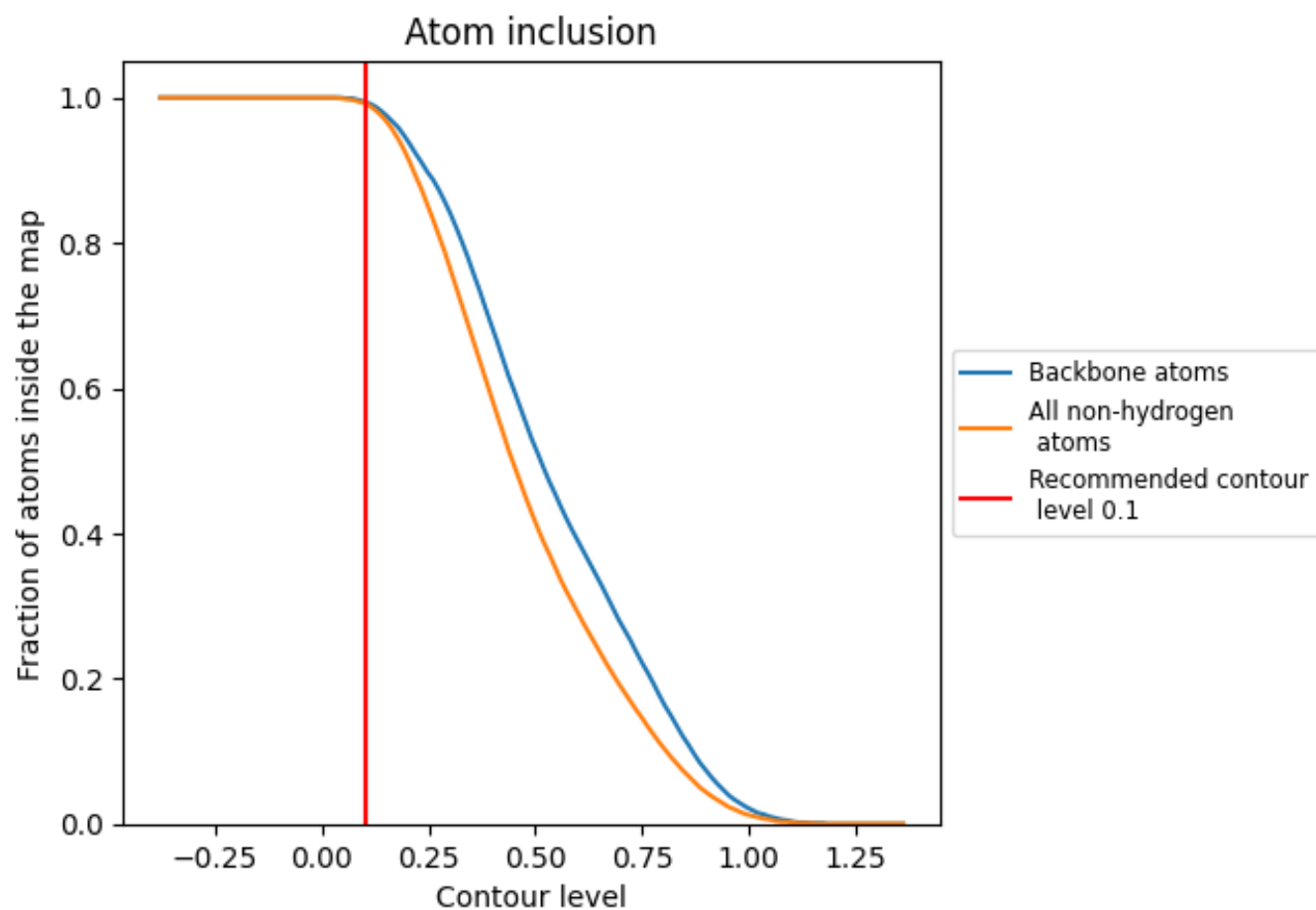
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion [i](#)



At the recommended contour level, 99% of all backbone atoms, 99% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9920	 0.4140
A	 0.9940	 0.4720
B	 0.9960	 0.4970
C	 0.9920	 0.4530
D	 0.9880	 0.3930
E	 0.9600	 0.1560
F	 0.9970	 0.3910
G	 0.9950	 0.3960
H	 0.9970	 0.5150
I	 0.9980	 0.5290
J	 0.9940	 0.4810
K	 0.9940	 0.4900
L	 0.9990	 0.2920
M	 0.9980	 0.5330
N	 0.9890	 0.1520
O	 0.9960	 0.5040
P	 0.9990	 0.3830
Q	 1.0000	 0.2810
R	 1.0000	 0.3110
S	 1.0000	 0.3220
a	 0.9970	 0.4980
c	 0.9920	 0.4130
i	 0.9970	 0.4850
m	 0.9950	 0.4610

