



wwPDB EM Validation Summary Report ⓘ

Mar 6, 2026 – 01:58 PM UTC

PDB ID : 8K24 / pdb_00008k24
EMDB ID : EMD-36827
Title : ICP1 Csy-dsDNA-Cas1-Cas2/3 complex (fully assembled form), C2 symmetry
Authors : Zhang, L.X.; Feng, Y.
Deposited on : 2023-07-12
Resolution : 3.72 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

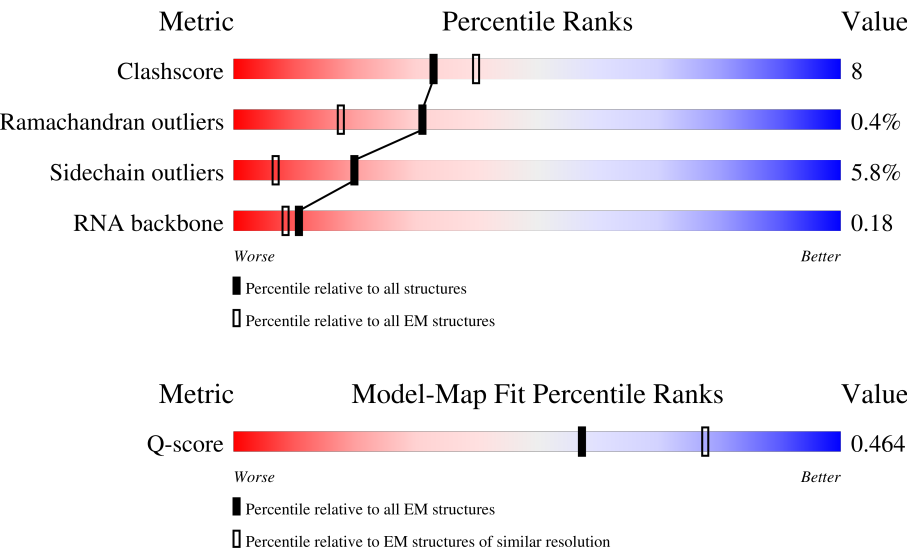
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.72 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	10474 (3.22 - 4.22)

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	930	73% 25%
1	a	930	72% 26%
2	B	179	82% 16%

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Mol	Chain	Length	Quality of chain
2	b	179	 79% 18% ..
3	C	248	 79% 18% .
3	c	248	 77% 19% .
4	D	302	 76% 17% . .
4	E	302	 76% 21% .
4	d	302	 72% 24% . .
4	e	302	 69% 25% . .
5	G	306	 76% 22% ..
5	I	306	 78% 19% ..
5	J	306	 76% 21% ..
5	K	306	 73% 25% .
5	L	306	 6% 70% 27% ..
5	M	306	 73% 25% ..
5	g	306	 77% 21% ..
5	i	306	 78% 19% ..
5	j	306	 76% 21% ..
5	k	306	 73% 25% ..
5	l	306	 6% 69% 28% ..
5	m	306	 72% 26% ..
6	H	168	 78% 18% . .
6	h	168	 77% 19% . .
7	P	60	 23% 42% 33% .
7	p	60	 22% 42% 37%
8	Q	43	 74% 23% .
8	U	43	 37% 12% 51%

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Mol	Chain	Length	Quality of chain
8	q	43	 72% 26%
9	R	31	 77% 23%
9	r	31	 77% 23%
10	V	21	 81% 19%

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 67211 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 HD Cas3-type domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	929	Total	C	N	O	S	0	0
			7252	4612	1242	1364	34		
1	A	929	Total	C	N	O	S	0	0
			7278	4632	1245	1367	34		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	834	LYS	ARG	conflict	UNP F1D5V9
A	834	LYS	ARG	conflict	UNP F1D5V9

- Molecule 2 is a protein called Csy1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	b	177	Total	C	N	O	S	0	0
			1415	896	235	274	10		
2	B	177	Total	C	N	O	S	0	0
			1415	896	235	274	10		

- Molecule 3 is a protein called Csy2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	c	247	Total	C	N	O	S	0	0
			1903	1214	320	355	14		
3	C	247	Total	C	N	O	S	0	0
			1903	1214	320	355	14		

- Molecule 4 is a protein called Cas1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	d	295	Total	C	N	O	S	2	0
			2337	1492	401	431	13		

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Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	295	Total	C	N	O	S	0	0
			2324	1489	393	429	13		
4	D	295	Total	C	N	O	S	2	0
			2319	1481	397	429	12		
4	E	295	Total	C	N	O	S	0	0
			2329	1491	394	431	13		

- Molecule 5 is a protein called Csy3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	g	302	Total	C	N	O	S	0	0
			2314	1456	392	459	7		
5	i	302	Total	C	N	O	S	0	0
			2298	1447	389	455	7		
5	j	302	Total	C	N	O	S	0	0
			2318	1459	393	459	7		
5	k	302	Total	C	N	O	S	0	0
			2318	1459	393	459	7		
5	l	302	Total	C	N	O	S	0	0
			2307	1450	391	459	7		
5	m	302	Total	C	N	O	S	0	0
			2314	1456	392	459	7		
5	G	302	Total	C	N	O	S	0	0
			2314	1456	392	459	7		
5	I	302	Total	C	N	O	S	0	0
			2298	1447	389	455	7		
5	J	302	Total	C	N	O	S	0	0
			2318	1459	393	459	7		
5	K	302	Total	C	N	O	S	0	0
			2318	1459	393	459	7		
5	L	302	Total	C	N	O	S	0	0
			2307	1450	391	459	7		
5	M	302	Total	C	N	O	S	0	0
			2314	1456	392	459	7		

- Molecule 6 is a protein called Csy4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	h	165	Total	C	N	O	S	0	0
			1290	818	221	245	6		
6	H	165	Total	C	N	O	S	0	0
			1290	818	221	245	6		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	51	ILE	VAL	conflict	UNP F1D5V5
H	51	ILE	VAL	conflict	UNP F1D5V5

- Molecule 7 is a RNA chain called RNA (60-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
7	p	60	Total	C	N	O	P	0	0
			1260	565	210	425	60		
7	P	60	Total	C	N	O	P	0	0
			1260	565	210	425	60		

- Molecule 8 is a DNA chain called DNA (43-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
8	q	43	Total	C	N	O	P	0	0
			898	425	184	246	43		
8	Q	43	Total	C	N	O	P	0	0
			898	425	184	246	43		
8	U	21	Total	C	N	O	P	0	0
			439	209	88	121	21		

- Molecule 9 is a DNA chain called DNA (31-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
9	r	31	Total	C	N	O	P	0	0
			620	299	94	196	31		
9	R	31	Total	C	N	O	P	0	0
			620	299	94	196	31		

- Molecule 10 is a DNA chain called DNA (5'-D(*AP*TP*CP*TP*TP*CP*CP*CP*TP*AP*TP*TP*TP*AP*AP*AP*TP*TP*GP*CP*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
10	V	21	Total	C	N	O	P	0	0
			419	205	65	129	20		

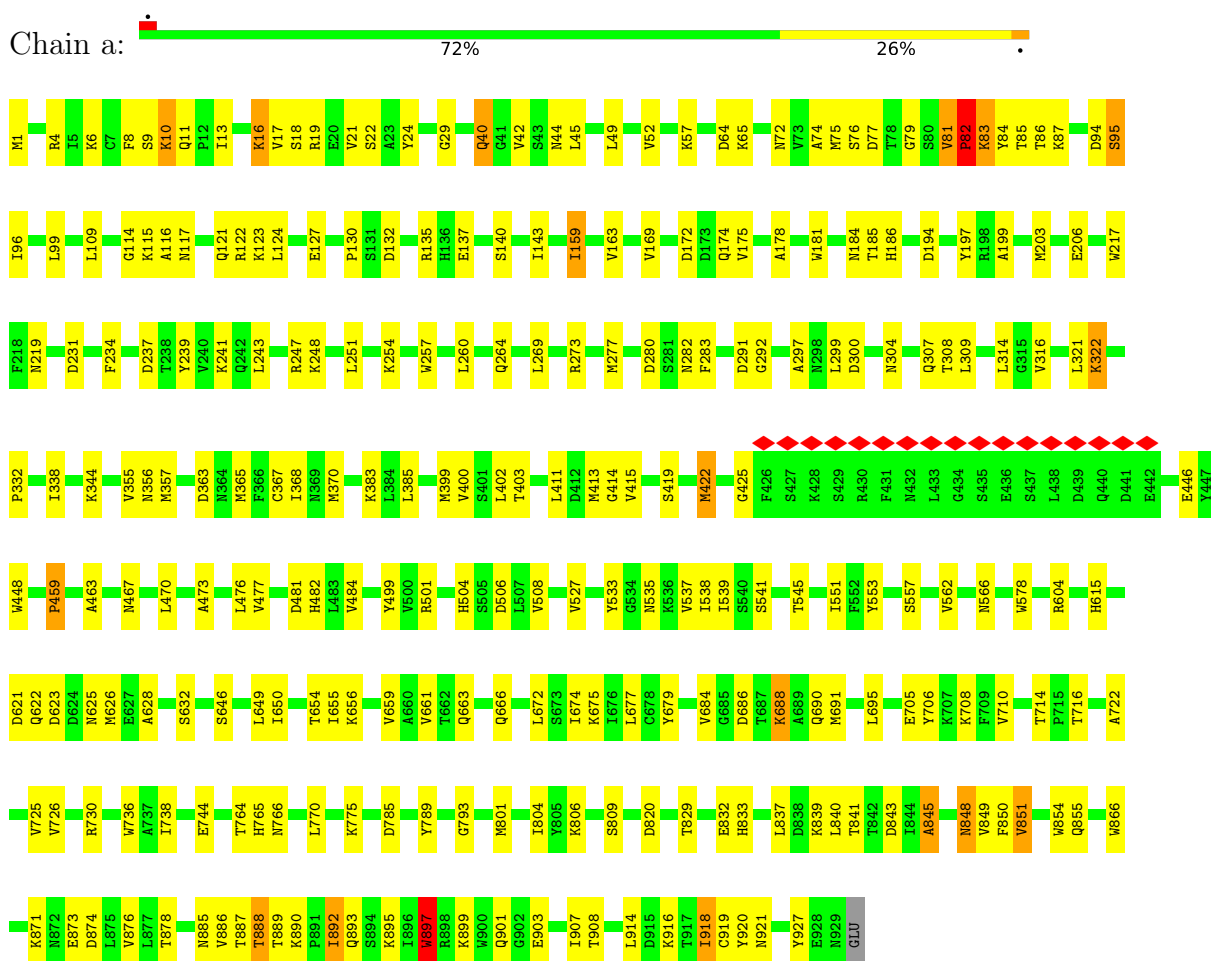
- Molecule 11 is MANGANESE (II) ION (CCD ID: MN) (formula: Mn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
11	a	2	Total 2	Mn 2	0
11	A	2	Total 2	Mn 2	0

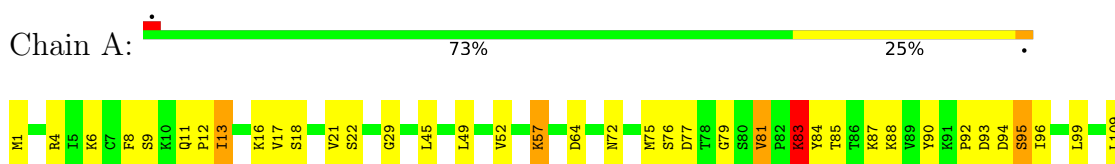
3 Residue-property plots [i](#)

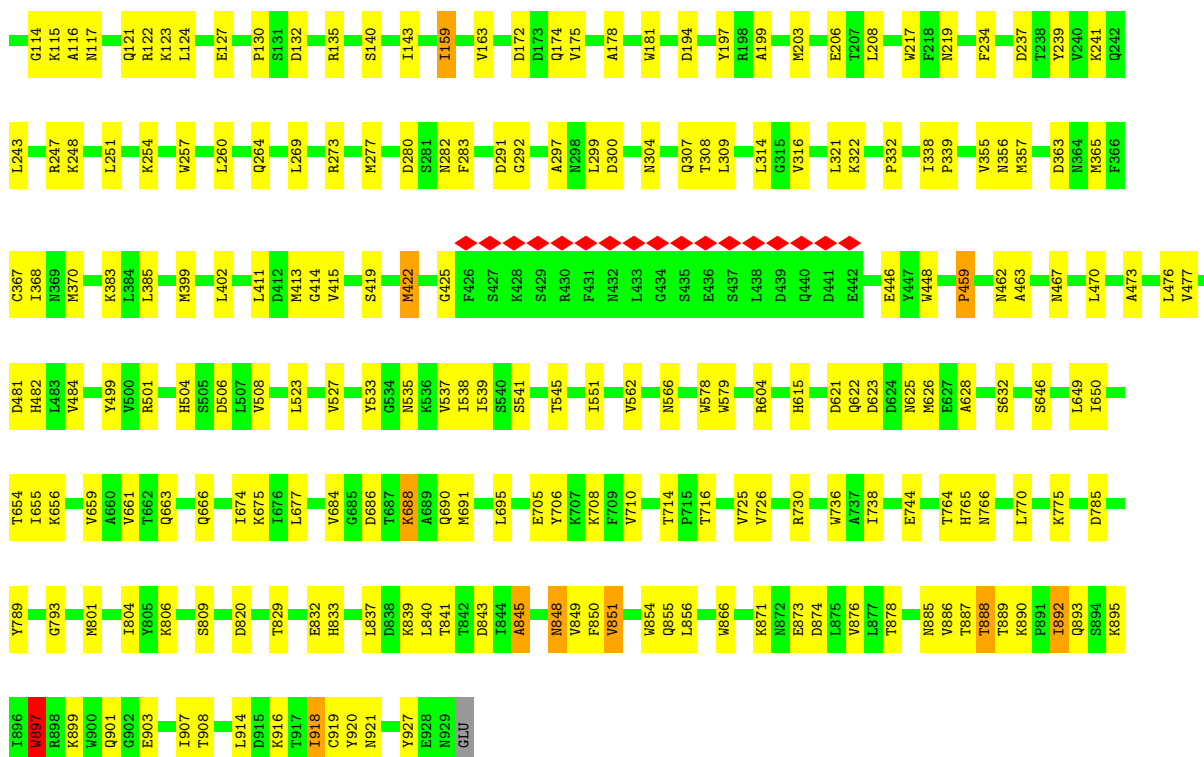
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: HD Cas3-type domain-containing protein



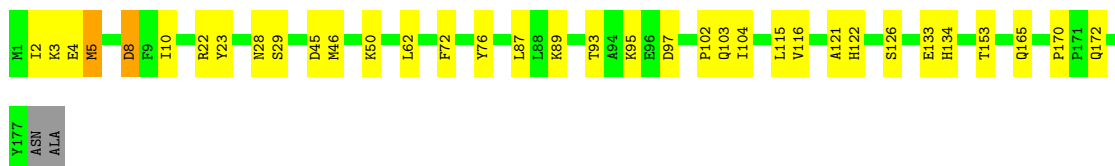
• Molecule 1: HD Cas3-type domain-containing protein



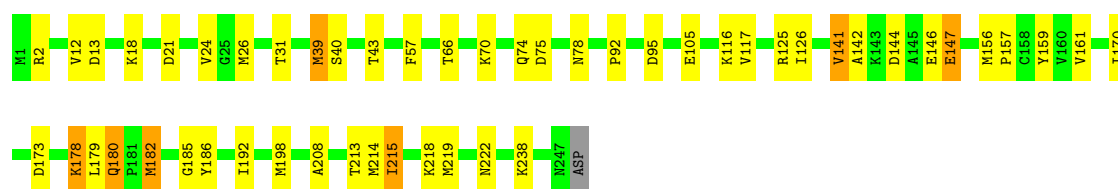


• Molecule 2: Csy1

Chain b: 79% 18% ..

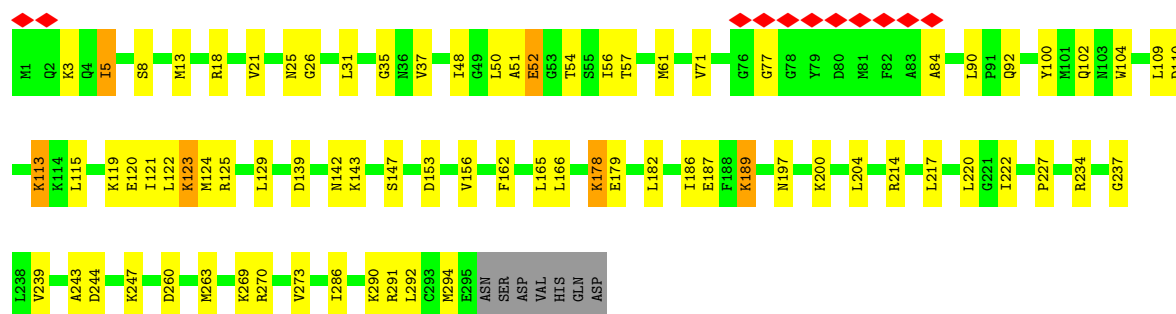


Chain C:  79% 18%



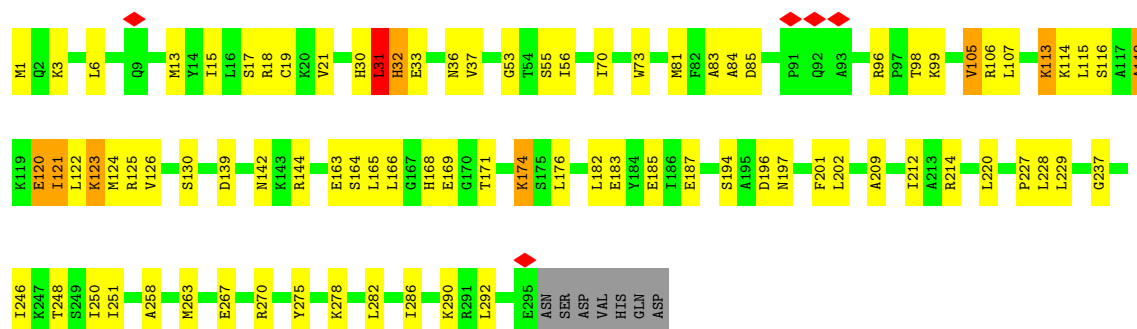
• Molecule 4: Cas1

Chain d:  72% 24%



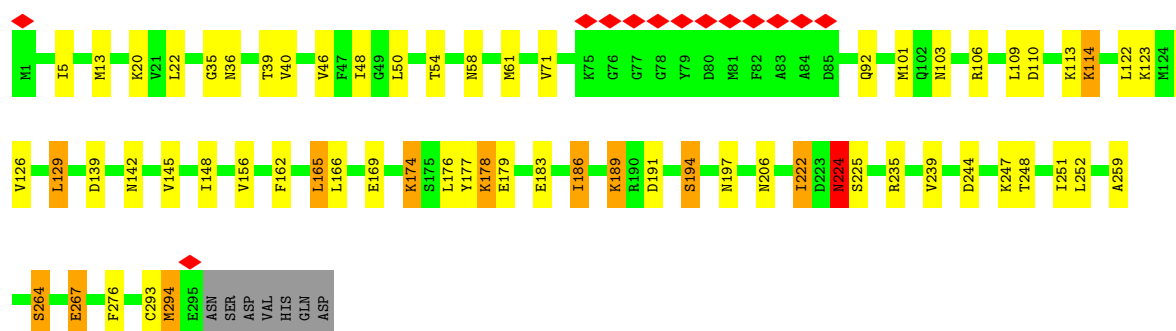
• Molecule 4: Cas1

Chain e:  69% 25%

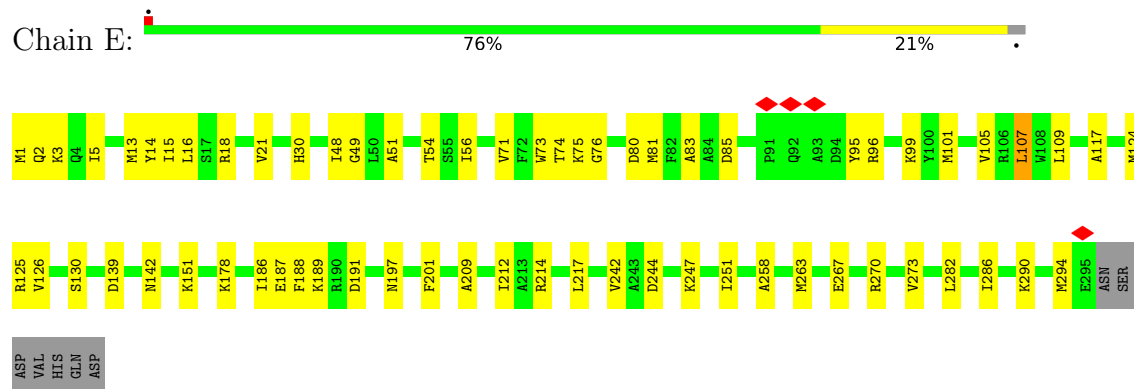


• Molecule 4: Cas1

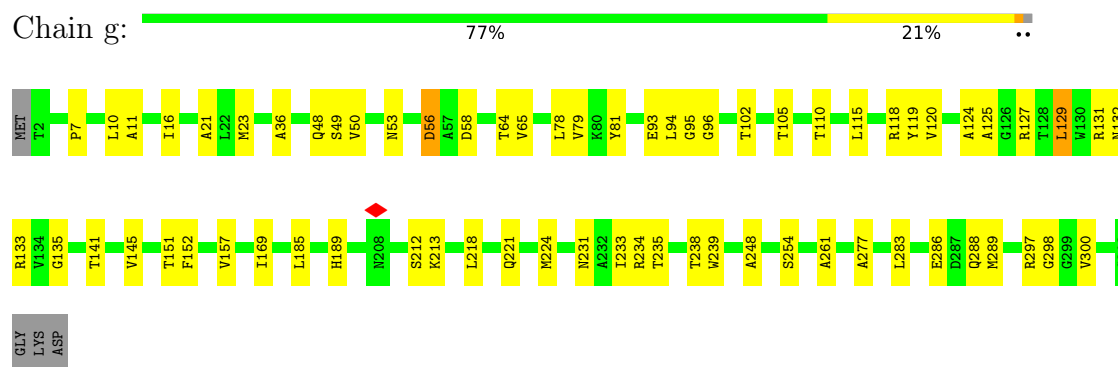
Chain D:  76% 17%



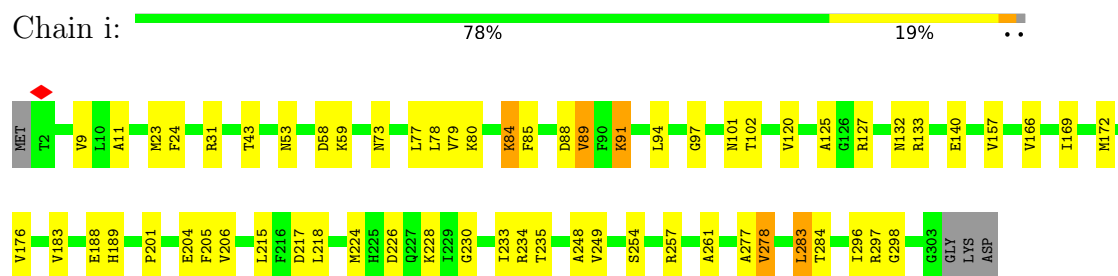
- Molecule 4: Cas1



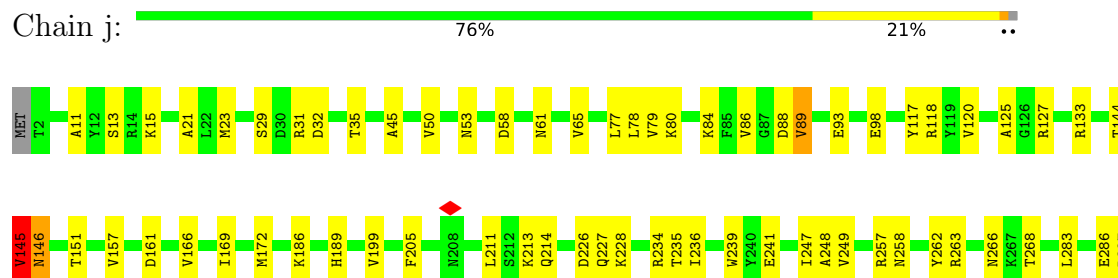
- Molecule 5: Csy3

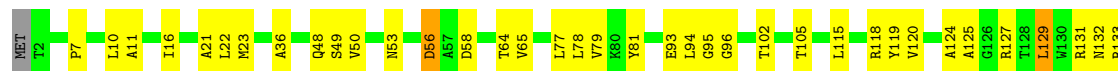


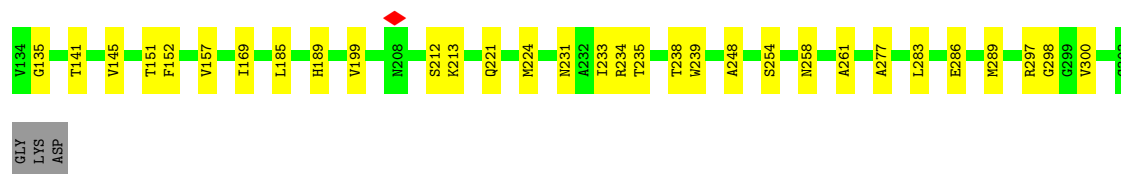
- Molecule 5: Csy3



- Molecule 5: Csy3

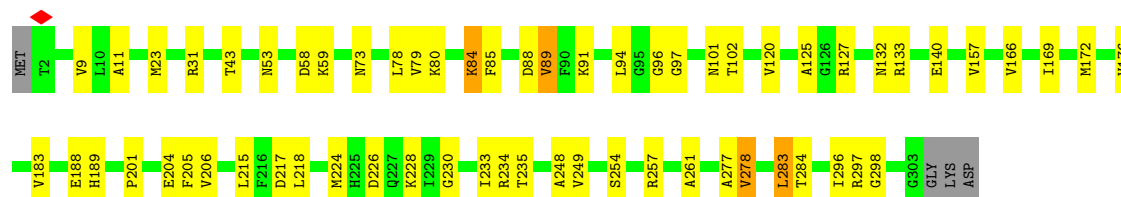






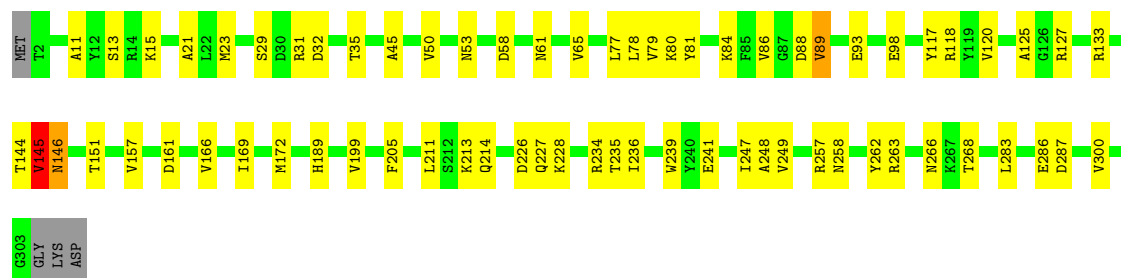
- Molecule 5: Csy3

Chain I: 78% 19% ..



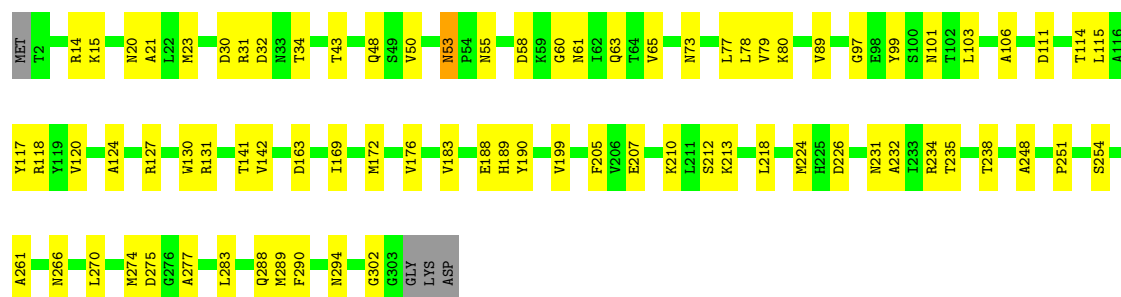
- Molecule 5: Csy3

Chain J: 76% 21% ..



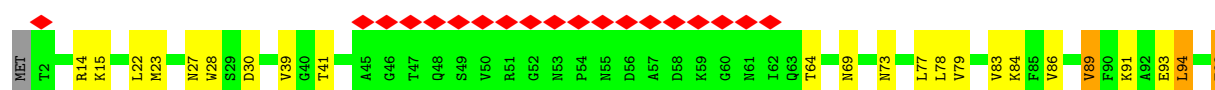
- Molecule 5: Csy3

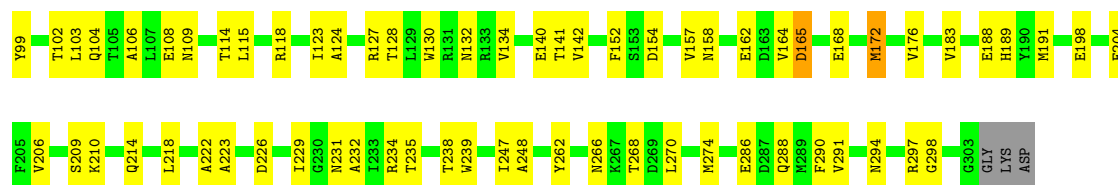
Chain K: 73% 25% .



- Molecule 5: Csy3

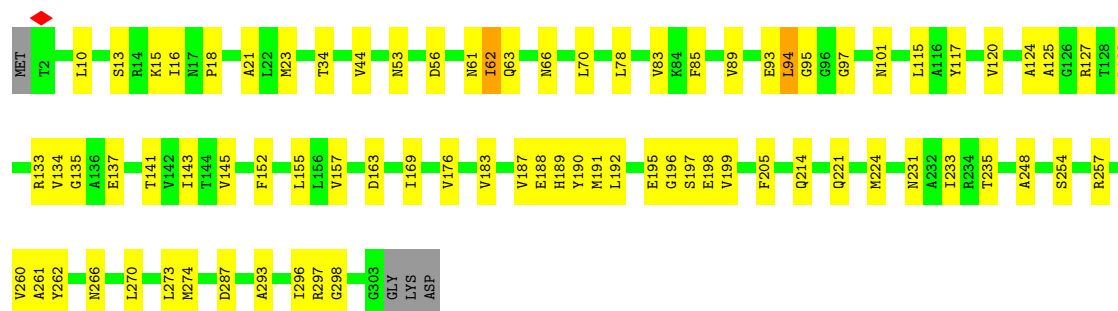
Chain L: 6% 70% 27% ..





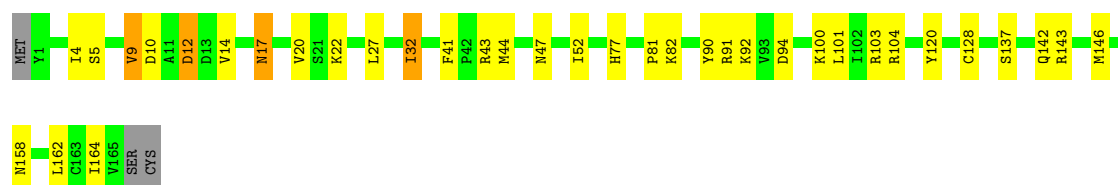
- Molecule 5: Csy3

Chain M: 73% 25% ..



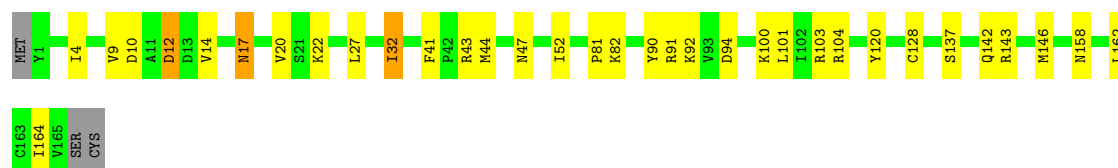
- Molecule 6: Csy4

Chain h: 77% 19% ..



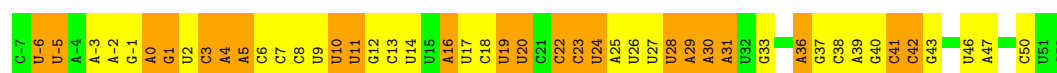
- Molecule 6: Csy4

Chain H: 78% 18% ..

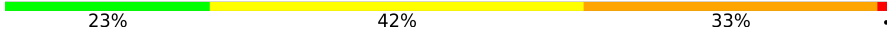


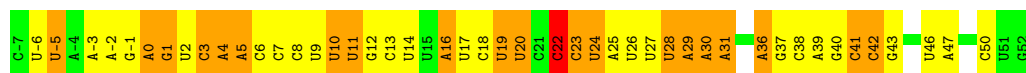
- Molecule 7: RNA (60-MER)

Chain p: 22% 42% 37%



- Molecule 7: RNA (60-MER)

Chain P:  23% 42% 33% .



• Molecule 8: DNA (43-MER)

Chain q:  72% 26% .



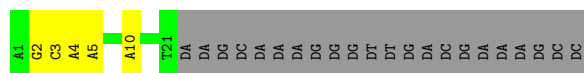
• Molecule 8: DNA (43-MER)

Chain Q:  74% 23% .



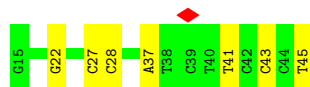
• Molecule 8: DNA (43-MER)

Chain U:  37% 12% 51%



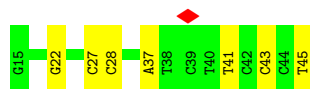
• Molecule 9: DNA (31-MER)

Chain r:  77% 23%



• Molecule 9: DNA (31-MER)

Chain R:  77% 23%



• Molecule 10: DNA (5'-D(*AP*TP*CP*TP*TP*CP*CP*CP*TP*AP*TP*TP*TP*AP*AP*AP*TP*TP*GP*CP*T)-3')

Chain V:  81% 19%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	132865	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.937	Depositor
Minimum map value	-0.354	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.015	Depositor
Map size ($\text{\AA}$)	440.0, 440.0, 440.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.1, 1.1, 1.1	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.37	1/7432 (0.0%)	0.72	14/10072 (0.1%)
1	a	0.40	1/7404 (0.0%)	0.73	15/10037 (0.1%)
2	B	0.32	0/1448	0.62	2/1956 (0.1%)
2	b	0.32	0/1448	0.61	2/1956 (0.1%)
3	C	0.33	0/1940	0.67	3/2625 (0.1%)
3	c	0.33	0/1940	0.67	3/2625 (0.1%)
4	D	0.48	0/2373	0.76	2/3211 (0.1%)
4	E	0.27	0/2377	0.62	3/3210 (0.1%)
4	d	0.35	0/2391	0.75	0/3231
4	e	0.52	2/2373 (0.1%)	0.75	7/3208 (0.2%)
5	G	0.34	0/2354	0.60	1/3198 (0.0%)
5	I	0.36	0/2338	0.65	2/3180 (0.1%)
5	J	0.35	0/2358	0.67	2/3202 (0.1%)
5	K	0.36	0/2358	0.64	0/3202
5	L	0.42	0/2347	0.78	5/3190 (0.2%)
5	M	0.29	0/2354	0.63	2/3198 (0.1%)
5	g	0.34	0/2354	0.60	1/3198 (0.0%)
5	i	0.36	0/2338	0.65	2/3180 (0.1%)
5	j	0.35	0/2358	0.67	2/3202 (0.1%)
5	k	0.36	0/2358	0.64	0/3202
5	l	0.42	0/2347	0.78	5/3190 (0.2%)
5	m	0.29	0/2354	0.63	2/3198 (0.1%)
6	H	0.38	0/1308	0.77	1/1757 (0.1%)
6	h	0.38	0/1308	0.77	1/1757 (0.1%)
7	P	0.35	0/1404	0.62	3/2181 (0.1%)
7	p	0.35	0/1404	0.62	2/2181 (0.1%)
8	Q	0.31	0/1014	0.53	1/1565 (0.1%)
8	U	0.32	0/495	0.48	0/763
8	q	0.31	0/1014	0.53	1/1565 (0.1%)
9	R	0.29	0/688	0.53	0/1057
9	r	0.29	0/688	0.53	0/1057
10	V	0.54	0/466	0.80	1/716 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
All	All	0.37	4/69133 (0.0%)	0.68	85/95070 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	e	31	LEU	CA-C	-6.95	1.44	1.53
1	a	84	TYR	N-CA	-6.30	1.38	1.46
1	A	83	LYS	CA-C	-6.21	1.44	1.52
4	e	96	ARG	C-N	5.12	1.39	1.33

The worst 5 of 85 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	l	98	GLU	N-CA-C	-10.41	100.64	113.97
5	L	98	GLU	N-CA-C	-10.37	100.69	113.97
5	j	53	ASN	CB-CA-C	10.10	118.37	111.20
5	J	53	ASN	CB-CA-C	10.04	118.33	111.20
1	A	13	ILE	N-CA-C	-9.93	103.37	112.90

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	7278	0	7186	142	0
1	a	7252	0	7131	157	0
2	B	1415	0	1353	14	0
2	b	1415	0	1353	17	0
3	C	1903	0	1916	33	0
3	c	1903	0	1916	39	0
4	D	2319	0	2283	49	0
4	E	2329	0	2300	38	0
4	d	2337	0	2318	52	0
4	e	2324	0	2296	69	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	2314	0	2249	37	0
5	I	2298	0	2216	33	0
5	J	2318	0	2260	34	0
5	K	2318	0	2260	48	0
5	L	2307	0	2229	48	0
5	M	2314	0	2249	45	0
5	g	2314	0	2249	36	0
5	i	2298	0	2216	35	0
5	j	2318	0	2260	34	0
5	k	2318	0	2260	50	0
5	l	2307	0	2229	58	0
5	m	2314	0	2249	47	0
6	H	1290	0	1336	24	0
6	h	1290	0	1336	44	0
7	P	1260	0	641	35	0
7	p	1260	0	641	35	0
8	Q	898	0	481	9	0
8	U	439	0	237	5	0
8	q	898	0	481	10	0
9	R	620	0	355	7	0
9	r	620	0	355	7	0
10	V	419	0	243	4	0
11	A	2	0	0	0	0
11	a	2	0	0	0	0
All	All	67211	0	63084	1088	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 8.

The worst 5 of 1088 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)
1:a:356:ASN:O	4:D:197:ASN:ND2	1.66	1.26
4:e:144:ARG:HH21	6:h:9:VAL:HG21	1.08	1.15
4:e:144:ARG:NH2	6:h:9:VAL:HG21	1.73	1.03
1:a:663:GLN:HG2	1:a:892:ILE:HD11	1.49	0.94
4:e:182:LEU:HD23	6:h:77:HIS:CG	2.02	0.94

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	927/930 (100%)	850 (92%)	69 (7%)	8 (1%)	14	45
1	a	927/930 (100%)	852 (92%)	66 (7%)	9 (1%)	12	43
2	B	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
2	b	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
3	C	245/248 (99%)	225 (92%)	20 (8%)	0	100	100
3	c	245/248 (99%)	225 (92%)	20 (8%)	0	100	100
4	D	295/302 (98%)	279 (95%)	14 (5%)	2 (1%)	18	49
4	E	293/302 (97%)	286 (98%)	7 (2%)	0	100	100
4	d	295/302 (98%)	278 (94%)	16 (5%)	1 (0%)	36	65
4	e	293/302 (97%)	279 (95%)	14 (5%)	0	100	100
5	G	300/306 (98%)	290 (97%)	10 (3%)	0	100	100
5	I	300/306 (98%)	284 (95%)	16 (5%)	0	100	100
5	J	300/306 (98%)	286 (95%)	11 (4%)	3 (1%)	12	43
5	K	300/306 (98%)	286 (95%)	14 (5%)	0	100	100
5	L	300/306 (98%)	285 (95%)	15 (5%)	0	100	100
5	M	300/306 (98%)	286 (95%)	13 (4%)	1 (0%)	36	65
5	g	300/306 (98%)	290 (97%)	10 (3%)	0	100	100
5	i	300/306 (98%)	284 (95%)	16 (5%)	0	100	100
5	j	300/306 (98%)	286 (95%)	11 (4%)	3 (1%)	12	43
5	k	300/306 (98%)	286 (95%)	14 (5%)	0	100	100
5	l	300/306 (98%)	285 (95%)	15 (5%)	0	100	100
5	m	300/306 (98%)	286 (95%)	13 (4%)	1 (0%)	36	65
6	H	163/168 (97%)	148 (91%)	14 (9%)	1 (1%)	21	52
6	h	163/168 (97%)	148 (91%)	14 (9%)	1 (1%)	21	52
All	All	7796/7930 (98%)	7334 (94%)	432 (6%)	30 (0%)	31	60

5 of 30 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	a	159	ILE
1	a	851	VAL
5	m	62	ILE
5	M	62	ILE
1	A	159	ILE

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	792/817 (97%)	743 (94%)	49 (6%)	16	43
1	a	785/817 (96%)	726 (92%)	59 (8%)	12	39
2	B	155/157 (99%)	146 (94%)	9 (6%)	18	45
2	b	155/157 (99%)	146 (94%)	9 (6%)	18	45
3	C	208/211 (99%)	195 (94%)	13 (6%)	16	43
3	c	208/211 (99%)	196 (94%)	12 (6%)	18	45
4	D	246/261 (94%)	223 (91%)	23 (9%)	8	32
4	E	247/261 (95%)	239 (97%)	8 (3%)	34	55
4	d	250/261 (96%)	232 (93%)	18 (7%)	13	40
4	e	247/261 (95%)	226 (92%)	21 (8%)	10	34
5	G	246/251 (98%)	238 (97%)	8 (3%)	33	55
5	I	241/251 (96%)	227 (94%)	14 (6%)	18	45
5	J	247/251 (98%)	232 (94%)	15 (6%)	17	44
5	K	247/251 (98%)	235 (95%)	12 (5%)	22	48
5	L	244/251 (97%)	225 (92%)	19 (8%)	11	37
5	M	246/251 (98%)	239 (97%)	7 (3%)	38	58
5	g	246/251 (98%)	238 (97%)	8 (3%)	33	55
5	i	241/251 (96%)	227 (94%)	14 (6%)	18	45
5	j	247/251 (98%)	232 (94%)	15 (6%)	17	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	k	247/251 (98%)	235 (95%)	12 (5%)	22	48
5	l	244/251 (97%)	225 (92%)	19 (8%)	11	37
5	m	246/251 (98%)	239 (97%)	7 (3%)	38	58
6	H	148/151 (98%)	143 (97%)	5 (3%)	32	55
6	h	148/151 (98%)	143 (97%)	5 (3%)	32	55
All	All	6531/6728 (97%)	6150 (94%)	381 (6%)	20	45

5 of 381 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	D	174	LYS
5	J	89	VAL
4	D	194	SER
6	H	9	VAL
5	K	55	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
5	J	69	ASN
1	A	36	HIS
5	J	227	GLN
5	L	66	ASN
1	A	264	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	P	59/60 (98%)	37 (62%)	3 (5%)
7	p	59/60 (98%)	37 (62%)	0
All	All	118/120 (98%)	74 (62%)	3 (2%)

5 of 74 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	p	-6	U
7	p	-5	U
7	p	-2	A

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Mol	Chain	Res	Type
7	p	0	A
7	p	1	G

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
7	P	11	U
7	P	22	C
7	P	41	C

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 [i](#)

There are no chain breaks in this entry.

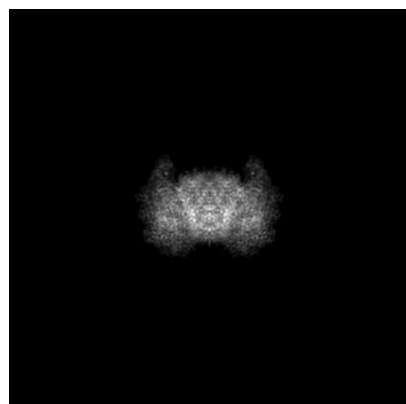
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-36827. These allow visual inspection of the internal detail of the map and identification of artifacts.

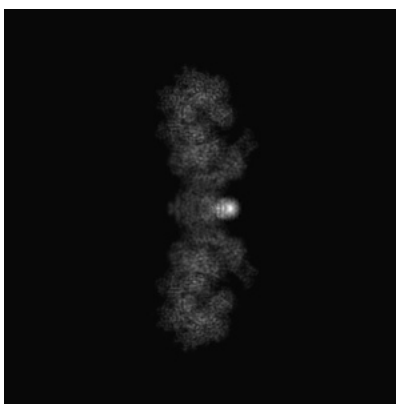
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

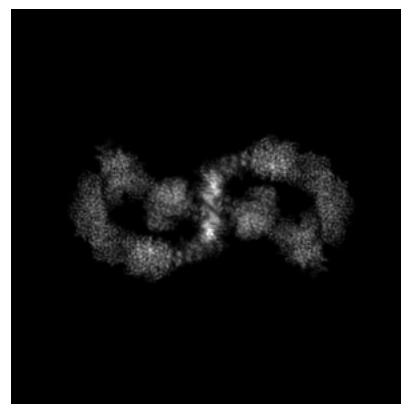
6.1.1 Primary map



X

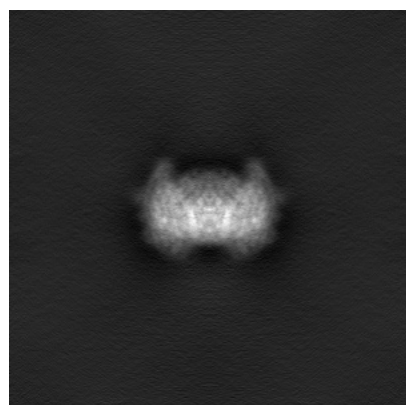


Y

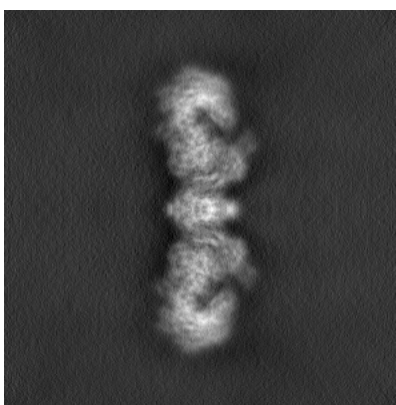


Z

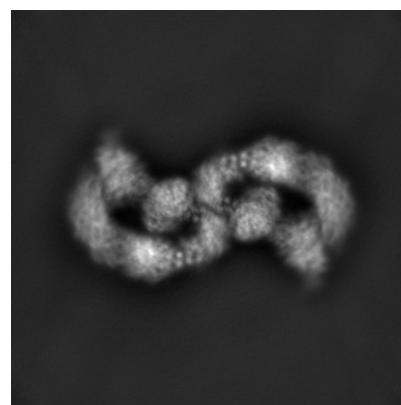
6.1.2 Raw map



X



Y

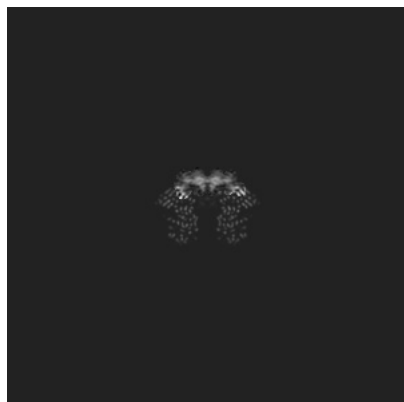


Z

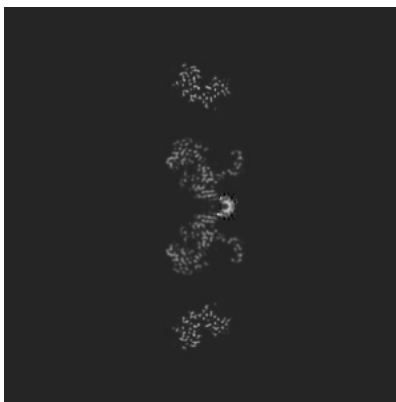
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 200

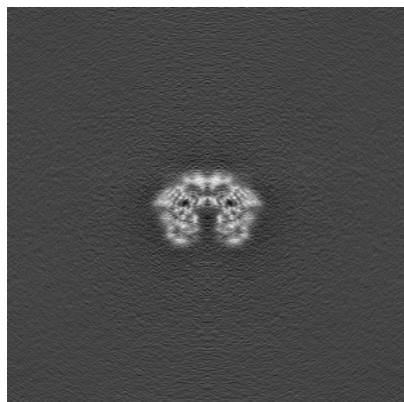


Y Index: 200

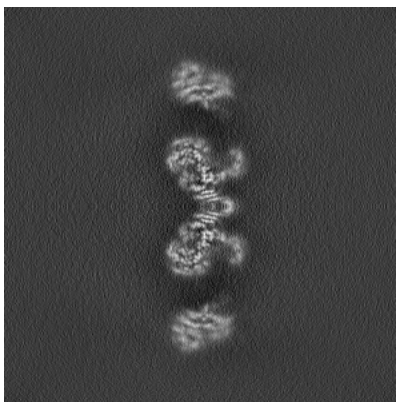


Z Index: 200

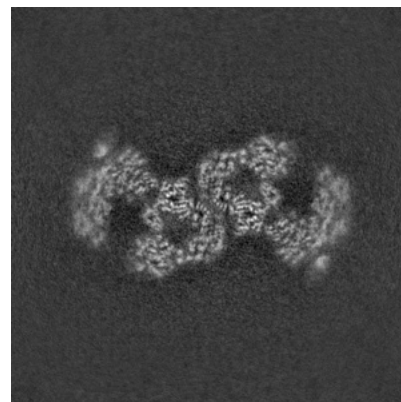
6.2.2 Raw map



X Index: 200



Y Index: 200

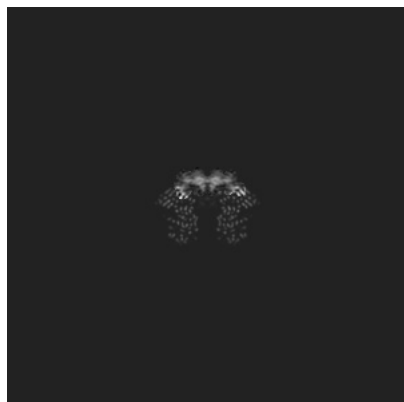


Z Index: 200

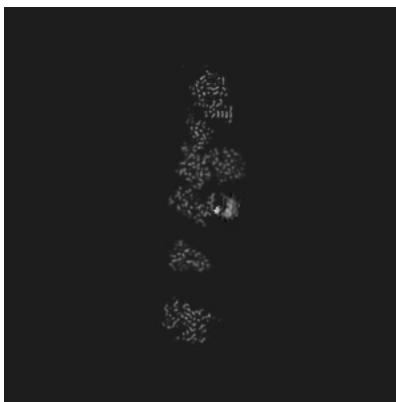
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

6.3.1 Primary map



X Index: 200

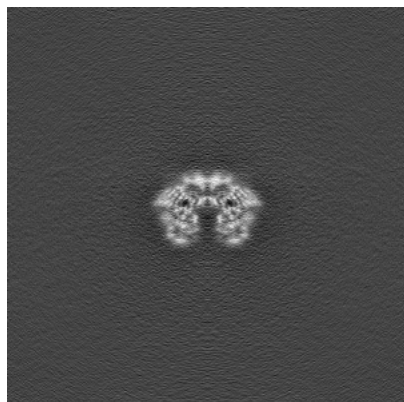


Y Index: 183

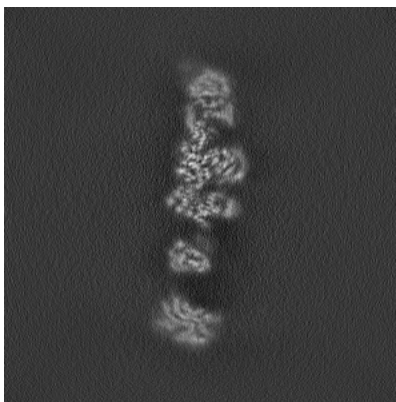


Z Index: 197

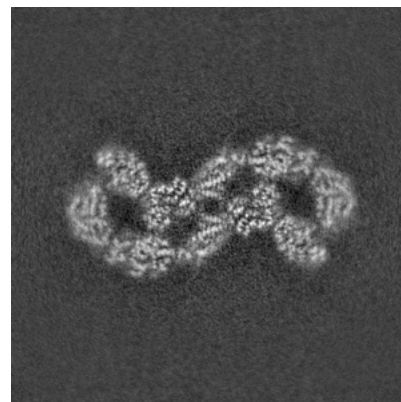
6.3.2 Raw map



X Index: 200



Y Index: 183

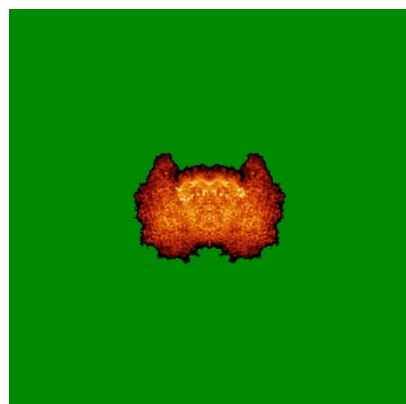


Z Index: 189

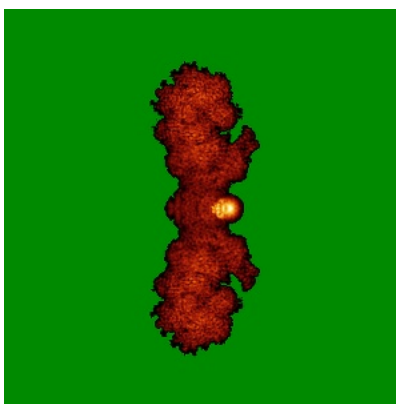
The images above show the largest variance slices of the map in three orthogonal directions.

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

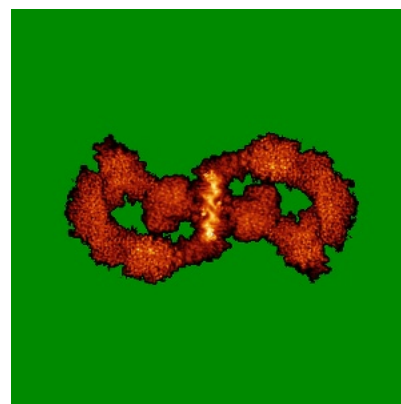
6.4.1 Primary map



X

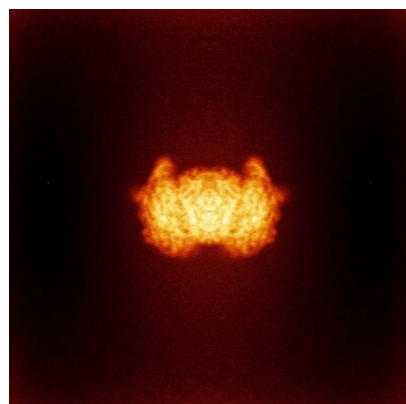


Y

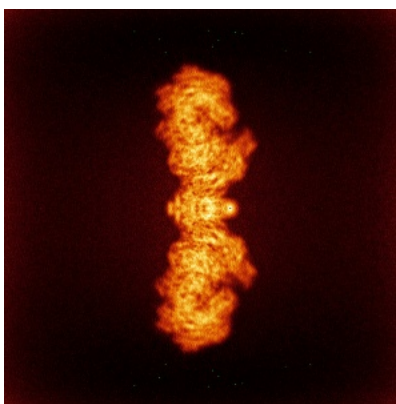


Z

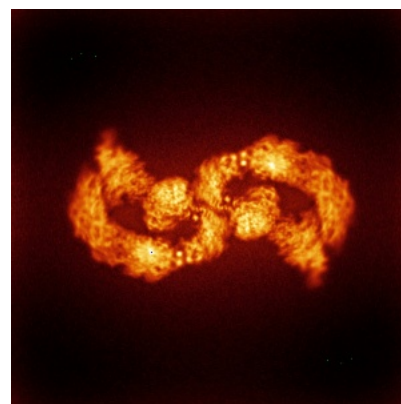
6.4.2 Raw map



X



Y

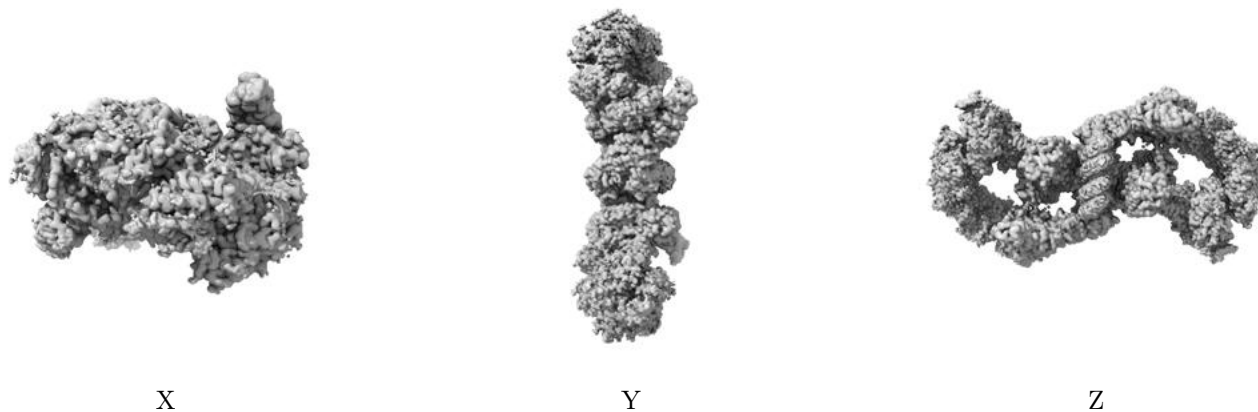


Z

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.

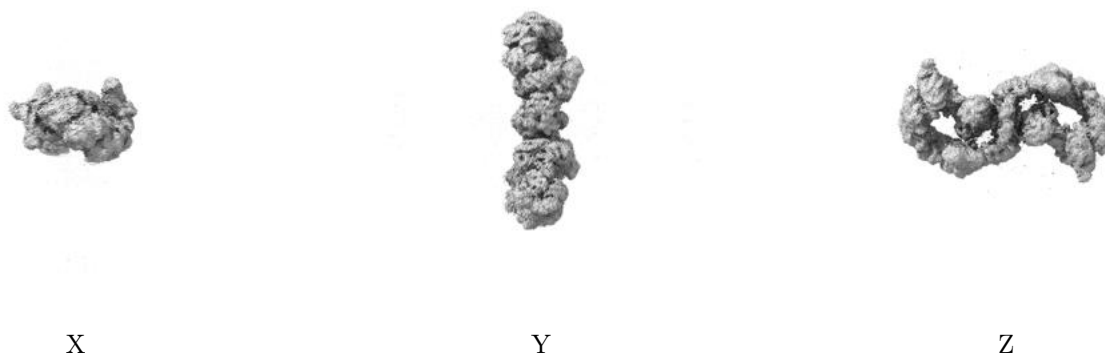
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.015. 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.

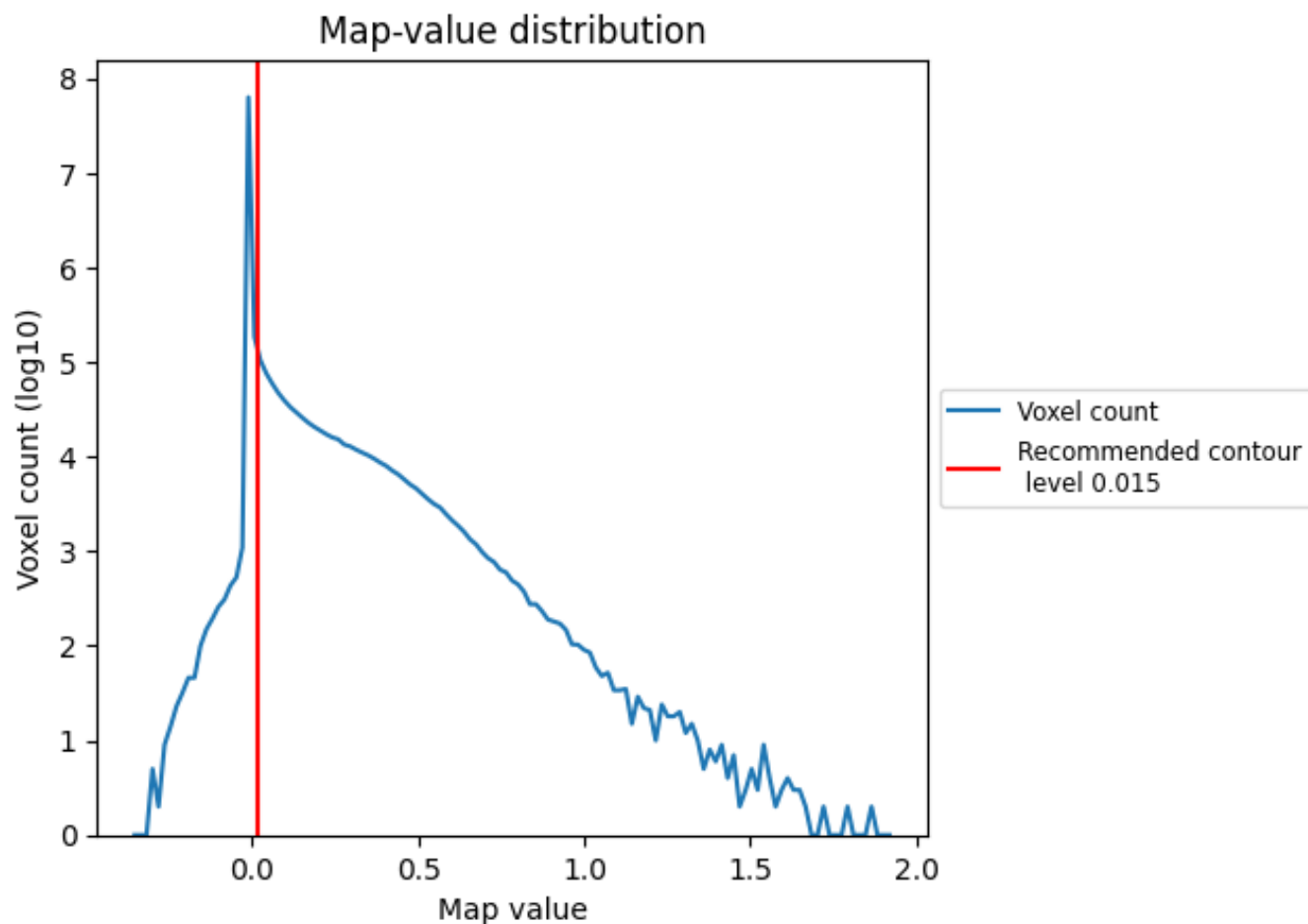
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

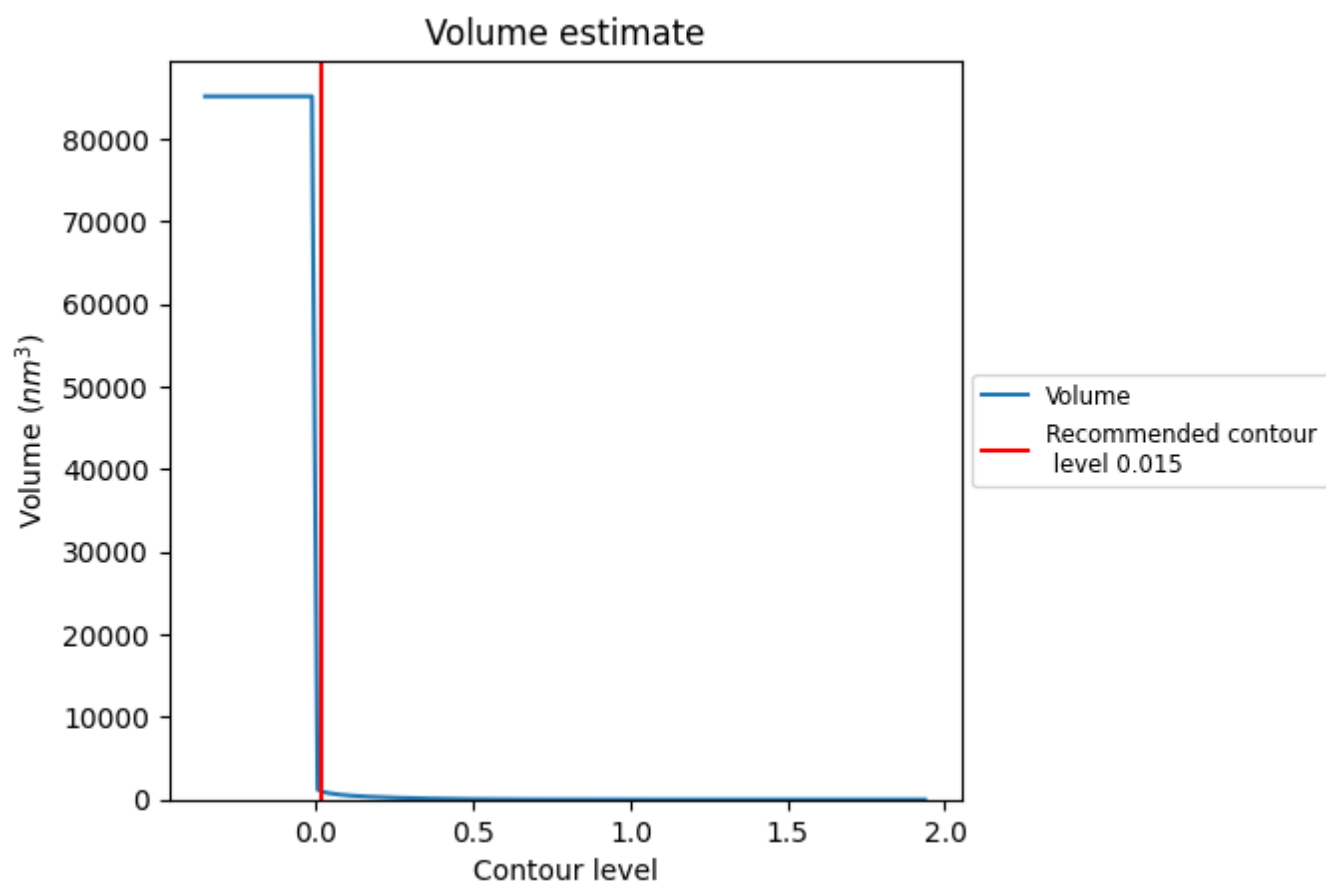
This section contains the results of statistical analysis of the map.

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.

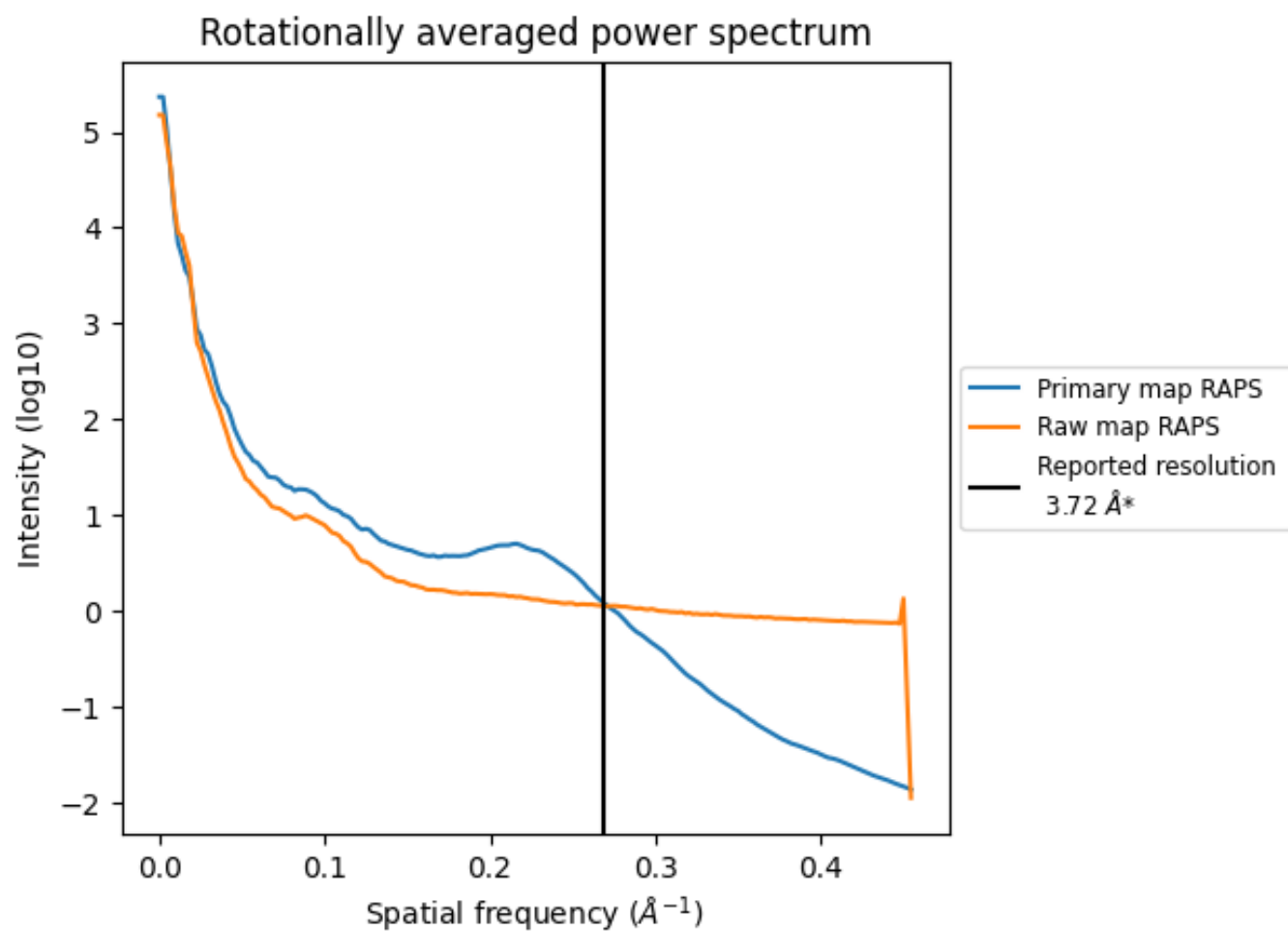
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1041 nm^3 ; this corresponds to an approximate mass of 940 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 ⓘ

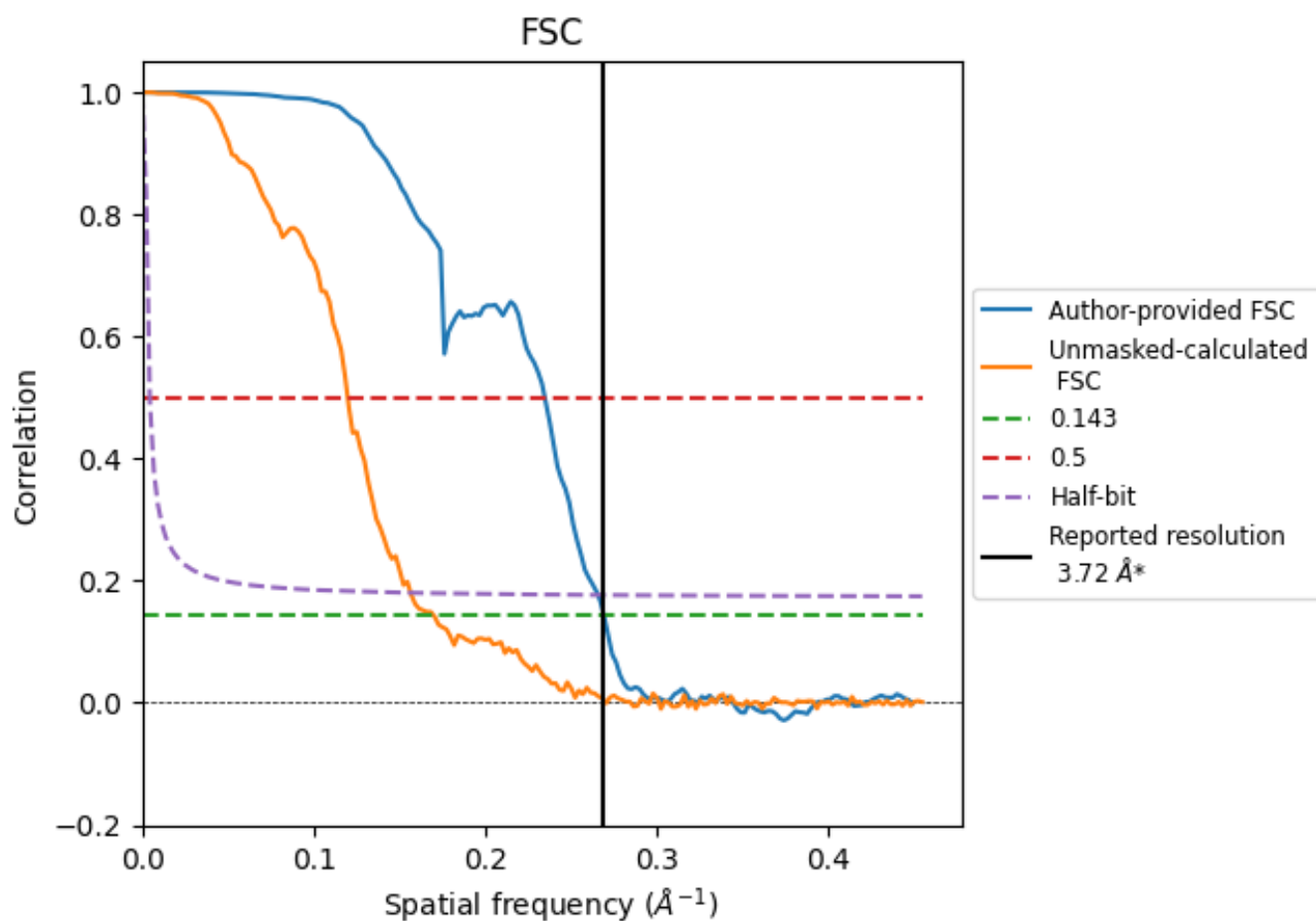


*Reported resolution corresponds to spatial frequency of $0.269 \text{ \AA}^{-1}$

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 0.269 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

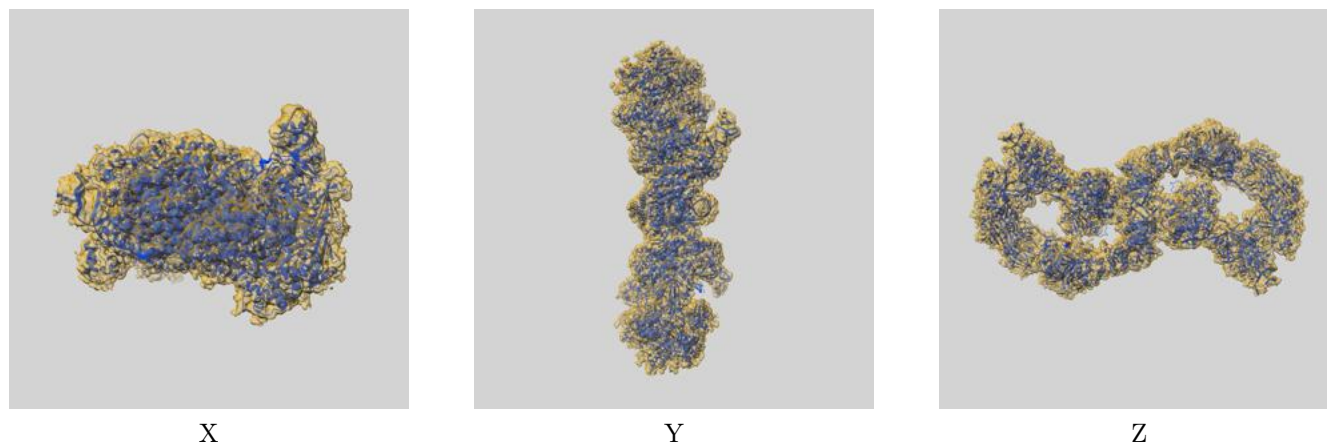
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.72	-	-
Author-provided FSC curve	3.72	4.26	3.77
Unmasked-calculated*	5.89	8.35	6.39

*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 5.89 differs from the reported value 3.72 by more than 10 %

9 Map-model fit [i](#)

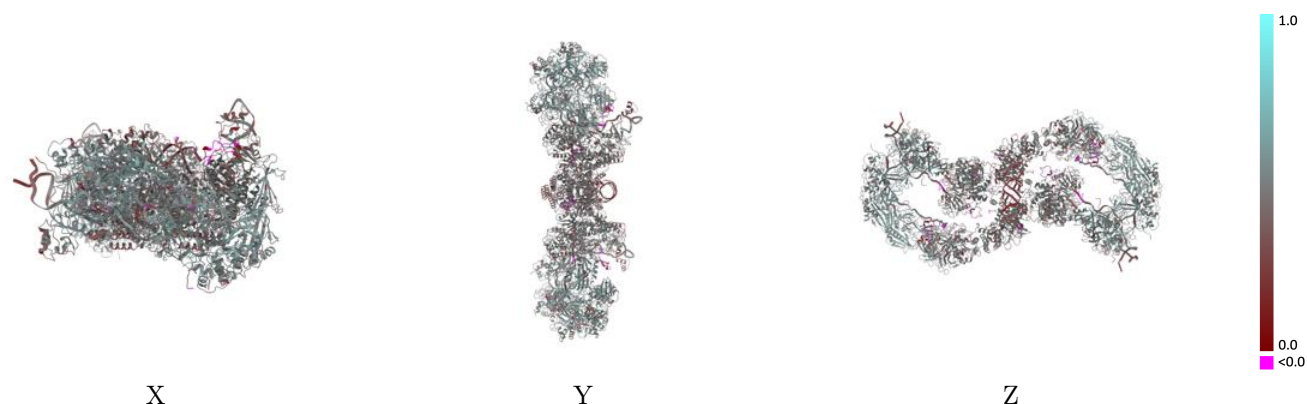
This section contains information regarding the fit between EMDB map EMD-36827 and PDB model 8K24. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

9.1 Map-model overlay [i](#)



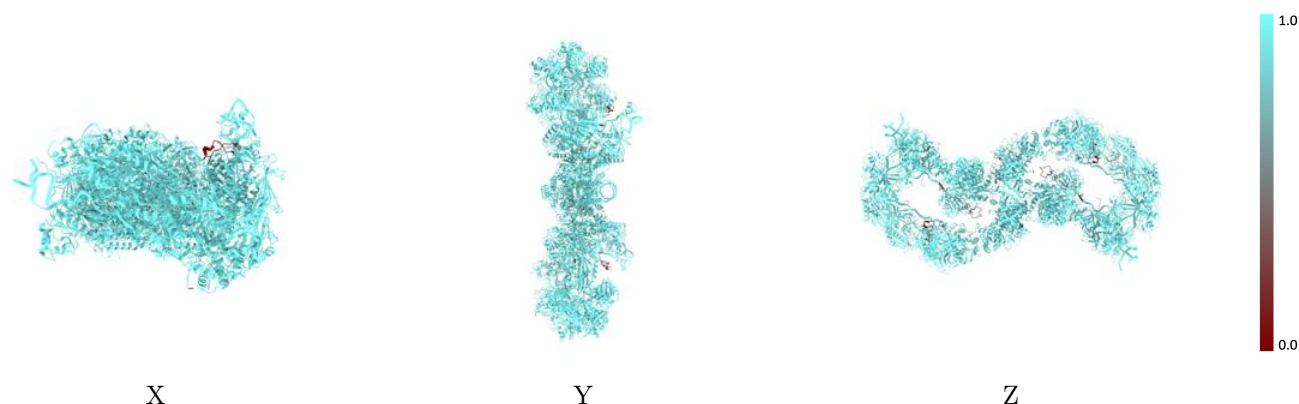
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



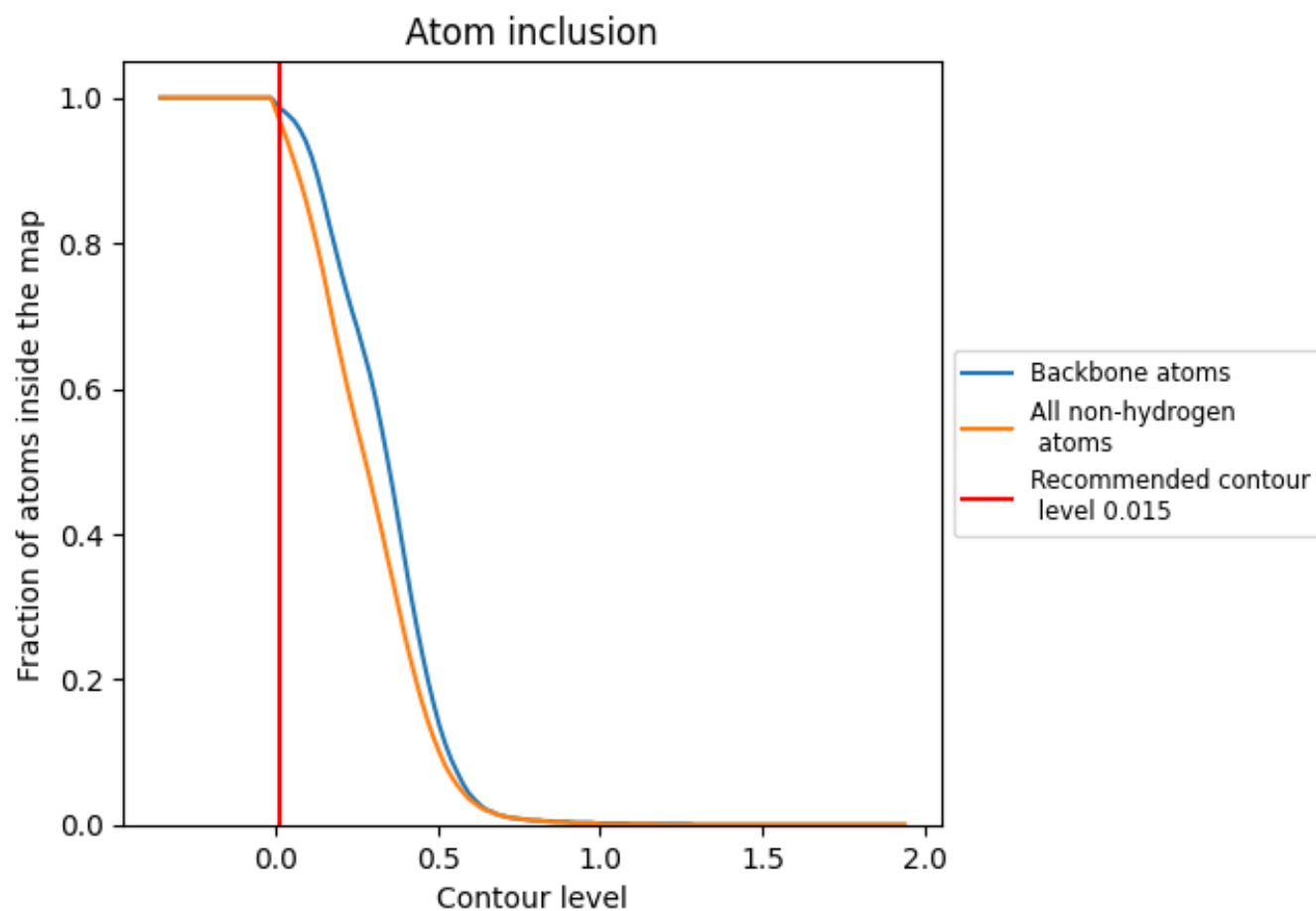
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).

9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 97% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9670	 0.4640
A	 0.9730	 0.4370
B	 0.9790	 0.4920
C	 0.9810	 0.5100
D	 0.9370	 0.4180
E	 0.9550	 0.4310
G	 0.9790	 0.5190
H	 0.9650	 0.4070
I	 0.9750	 0.5170
J	 0.9790	 0.5170
K	 0.9790	 0.5110
L	 0.9110	 0.4280
M	 0.9790	 0.5050
P	 0.9910	 0.4670
Q	 0.9760	 0.4550
R	 0.9310	 0.3780
U	 0.9980	 0.2770
V	 1.0000	 0.2700
a	 0.9750	 0.4380
b	 0.9790	 0.4930
c	 0.9790	 0.5120
d	 0.9400	 0.3920
e	 0.9480	 0.4230
g	 0.9760	 0.5190
h	 0.9650	 0.4130
i	 0.9770	 0.5140
j	 0.9770	 0.5190
k	 0.9780	 0.5140
l	 0.9150	 0.4270
m	 0.9790	 0.5040
p	 0.9910	 0.4690
q	 0.9770	 0.4480
r	 0.9340	 0.3720

