



wwPDB EM Validation Summary Report ⓘ

Mar 10, 2026 – 12:47 PM UTC

PDB ID : 7ELN / pdb_00007eln
EMDB ID : EMD-31186
Title : Structure of Csy-AcrIF24-dsDNA
Authors : Zhang, L.; Feng, Y.
Deposited on : 2021-04-12
Resolution : 3.00 Å(reported)

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

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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:

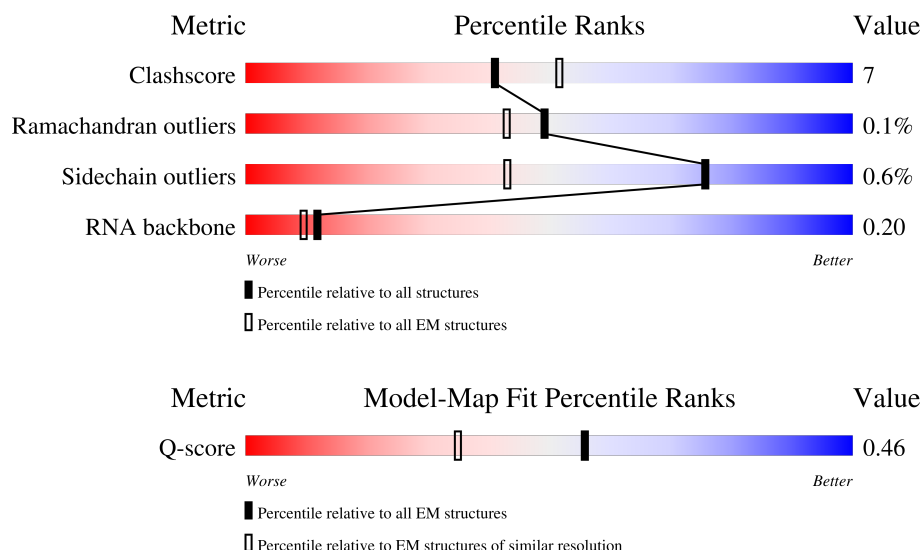
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.00 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.





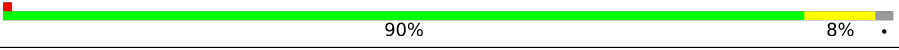



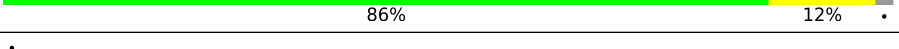
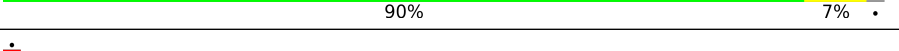
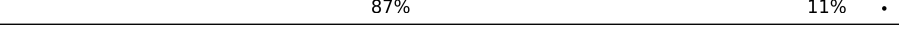
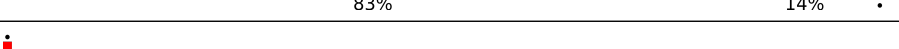




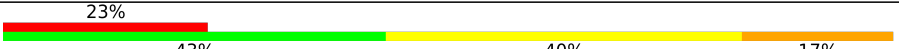
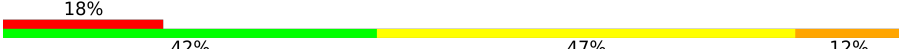







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14081 (2.50 - 3.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	327	
1	L	327	
2	C	342	

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Mol	Chain	Length	Quality of chain
2	D	342	
2	E	342	
2	F	342	
2	G	342	
2	H	342	
2	M	342	
2	N	342	
2	O	342	
2	P	342	
2	Q	342	
2	R	342	
3	I	187	
3	S	187	
4	U	228	
4	V	228	
5	J	60	
5	T	60	
6	A	434	
6	X	434	
7	K	54	
7	Y	54	
8	W	54	
8	Z	54	

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 48906 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 CRISPR type I-F/YPEST-associated protein Csy2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	305	Total	C	N	O	S	0	0
			2198	1386	400	409	3		
1	L	305	Total	C	N	O	S	0	0
			2321	1471	431	414	5		

- Molecule 2 is a protein called CRISPR-associated protein Csy3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	293	Total	C	N	O	S	0	0
			2144	1350	379	413	2		
2	D	334	Total	C	N	O	S	0	0
			2531	1590	454	485	2		
2	E	337	Total	C	N	O	S	0	0
			2587	1626	469	490	2		
2	F	335	Total	C	N	O	S	0	0
			2577	1619	470	486	2		
2	G	329	Total	C	N	O	S	0	0
			2523	1586	459	476	2		
2	H	332	Total	C	N	O	S	0	0
			2487	1555	452	478	2		
2	M	293	Total	C	N	O	S	0	0
			2227	1406	396	423	2		
2	N	335	Total	C	N	O	S	0	0
			2571	1613	468	488	2		
2	O	334	Total	C	N	O	S	0	0
			2562	1611	467	482	2		
2	P	335	Total	C	N	O	S	0	0
			2581	1622	471	486	2		
2	Q	333	Total	C	N	O	S	0	0
			2552	1605	465	480	2		
2	R	333	Total	C	N	O	S	0	0
			2529	1588	461	479	1		

- Molecule 3 is a protein called type I-F CRISPR-associated endoribonuclease Cas6/Csy4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	I	187	Total	C	N	O	S	0	0
			1445	919	264	258	4		
3	S	187	Total	C	N	O	S	1	0
			1445	918	264	258	5		

- Molecule 4 is a protein called AcrIF24.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	U	227	Total	C	N	O	S	0	0
			1758	1124	308	323	3		
4	V	227	Total	C	N	O	S	0	0
			1758	1124	308	323	3		

- Molecule 5 is a RNA chain called RNA (60-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	60	Total	C	N	O	P	0	0
			1271	569	223	420	59		
5	T	60	Total	C	N	O	P	0	0
			1271	569	223	420	59		

- Molecule 6 is a protein called Type I-F CRISPR-associated protein Csy1.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	A	424	Total	C	N	O	0	0
			2251	1290	491	470		
6	X	424	Total	C	N	O	0	0
			2251	1290	491	470		

- Molecule 7 is a DNA chain called 54-MER DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	K	13	Total	C	N	O	P	0	0
			269	127	50	79	13		
7	Y	13	Total	C	N	O	P	0	0
			269	127	50	79	13		

- Molecule 8 is a DNA chain called 54-MER DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	W	13	Total	C	N	O	P	0	0
			264	125	49	77	13		

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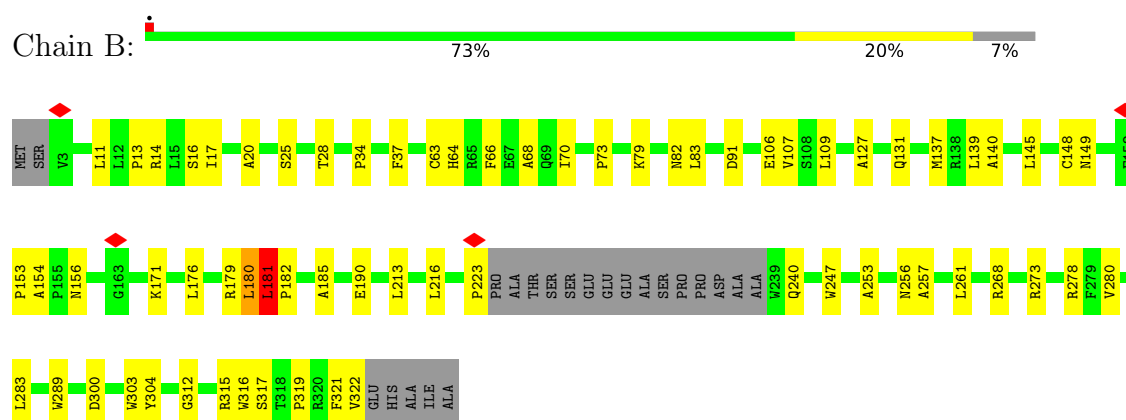
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Mol	Chain	Residues	Atoms					AltConf	Trace
8	Z	13	Total 264	C 125	N 49	O 77	P 13	0	0

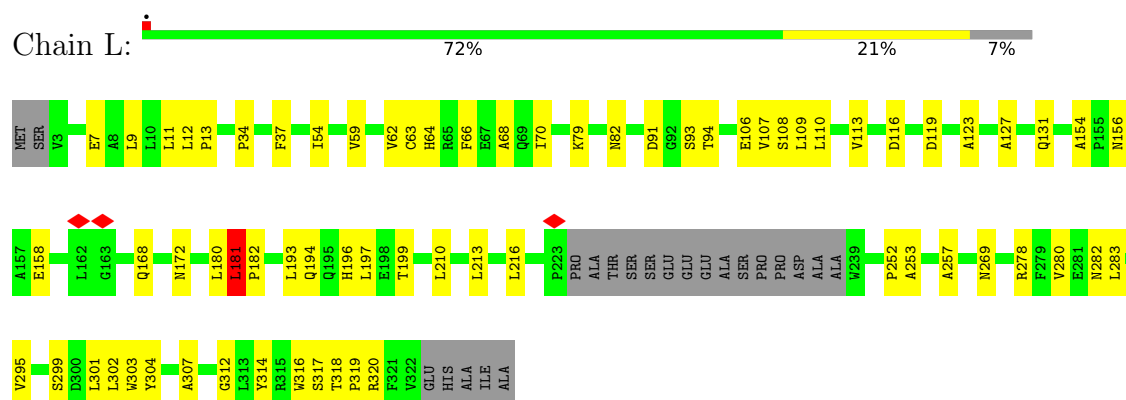
3 Residue-property plots [i](#)

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.

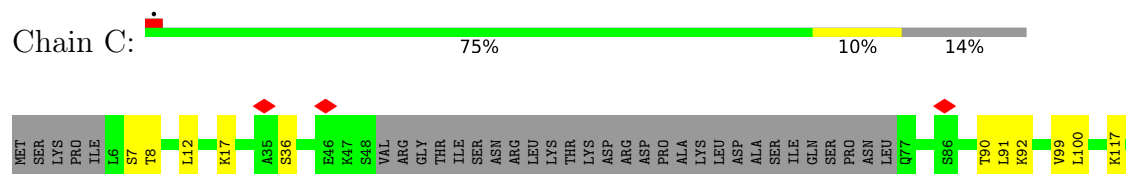
- Molecule 1: CRISPR type I-F/YPEST-associated protein Csy2

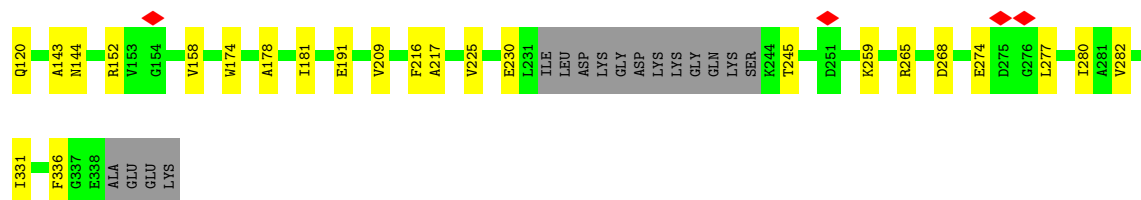


- Molecule 1: CRISPR type I-F/YPEST-associated protein Csy2

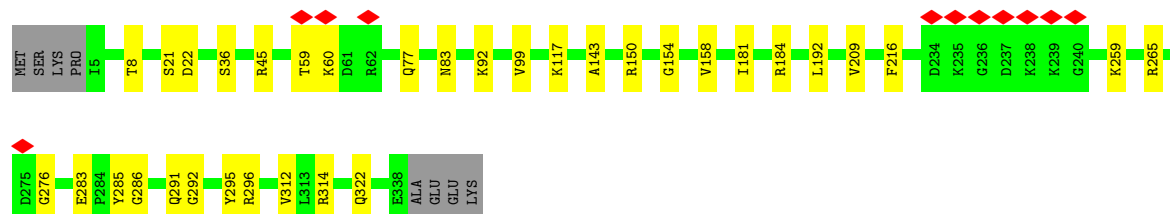
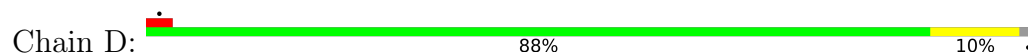


- Molecule 2: CRISPR-associated protein Csy3

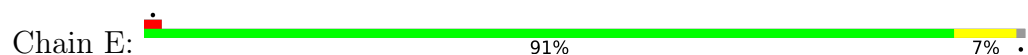




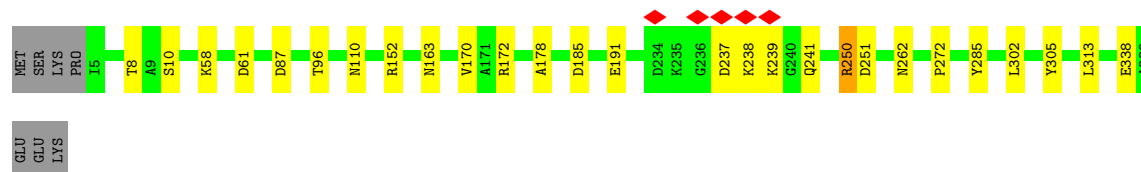
- Molecule 2: CRISPR-associated protein Csy3



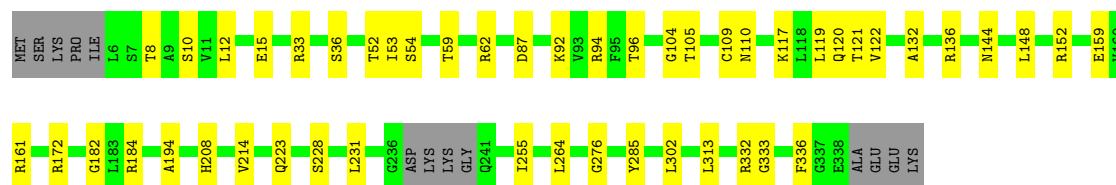
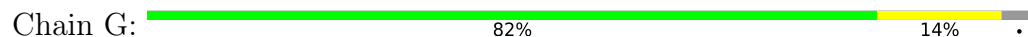
- Molecule 2: CRISPR-associated protein Csy3



- Molecule 2: CRISPR-associated protein Csy3



- Molecule 2: CRISPR-associated protein Csy3



- Molecule 2: CRISPR-associated protein Csy3

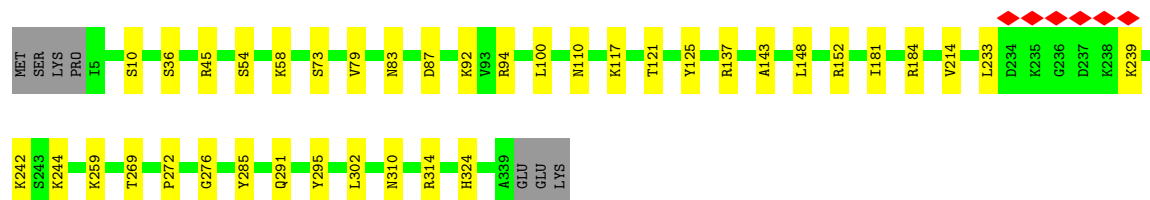
E338		MET
ALA		SER
GLU		LYS
GLU		PRO
LYS		ILE
		LEU
		S7
		R16
		D19
		R50
		G51
		T52
		I53
		L57
		R62
		D63
		K66
		D67
		D111
		Y125
		L134
		N144
		R152
		R184
		Q223
		E230
		L231
		Q241
		D275
		G276
		D303
		P318
		Q323
		H324
		Y325
		V326
		I327
		A328
		N329

- | Gene | Protein |
|------|---------|
| E283 | V99 |
| G286 | L119 |
| S287 | E133 |
| V288 | R137 |
| K293 | M141 |
| Q297 | L142 |
| D303 | A143 |
| F304 | M144 |
| Y305 | A145 |
| T306 | R146 |
| L307 | R152 |
| N310 | V158 |
| R314 | M163 |
| E338 | V170 |
| ALA | A178 |
| GLU | L179 |
| GIJ | V209 |
| LYS | A217 |
| | E230 |
| | L231 |
| | ILE |
| | LEU |
| | ASP |
| | LYS |
| | GLY |
| | ASP |
| | PRO |
| | LYS |
| | ALA |
| | GLY |
| | GLN |
| | LYS |
| | SER |
| | K244 |
| | T245 |
| | V249 |
| | A254 |
| | I255 |
| | H256 |
| | R265 |
| | D275 |
| | C276 |
| | P280 |
| | S281 |
| | D22 |
| | A23 |
| | L24 |
| | K25 |
| | S26 |
| | A41 |
| | V44 |
| | S48 |
| | VAL |
| | ARG |
| | GLY |
| | THR |
| | ILE |
| | SER |
| | ASN |
| | ARG |
| | LEU |
| | LYS |
| | THR |
| | LYS |
| | ASP |
| | ARG |
| | ASP |
| | PRO |
| | LYS |
| | ALA |
| | LEU |
| | ASP |
| | ALA |
| | SER |
| | ILE |
| | GLN |
| | SER |
| | PRO |
| | ASN |
| | LEU |
| | Q77 |
| | A82 |
| | T90 |
| | Y93 |
| | T96 |

- [illegible]

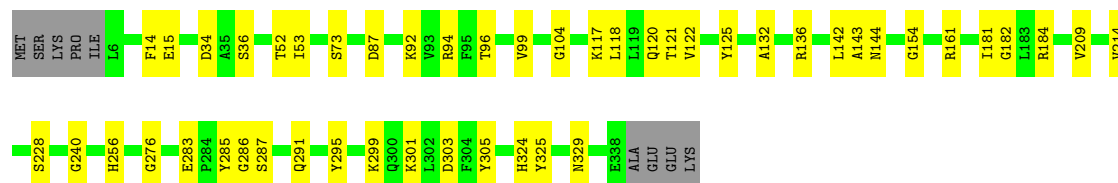
- [illegible]

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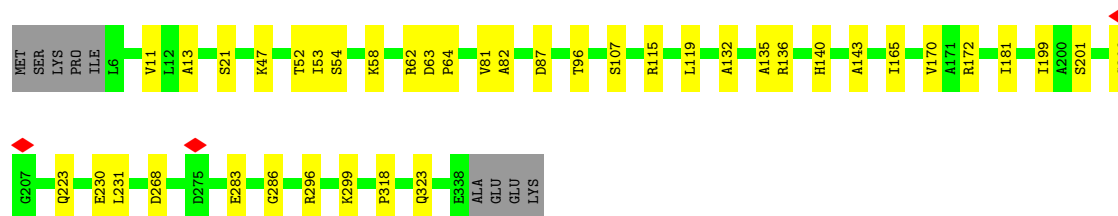
• Molecule 2: CRISPR-associated protein Csy3

Chain Q: 83% 14%



• Molecule 2: CRISPR-associated protein Csy3

Chain R: 86% 12%



• Molecule 3: type I-F CRISPR-associated endoribonuclease Cas6/Csy4

Chain I: 88% 81% 19%



• Molecule 3: type I-F CRISPR-associated endoribonuclease Cas6/Csy4

Chain S: 75% 81% 19%





• Molecule 4: AcrIF24

Chain U: 87% 13%



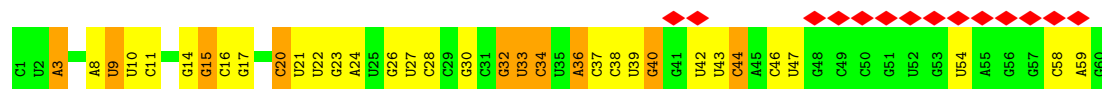
• Molecule 4: AcrIF24

Chain V: 87% 13%



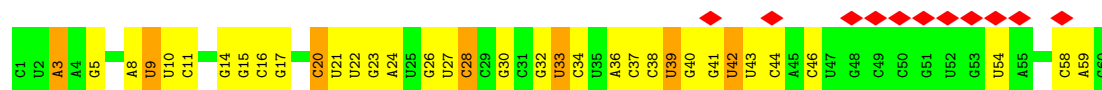
• Molecule 5: RNA (60-MER)

Chain J: 23% 43% 40% 17%



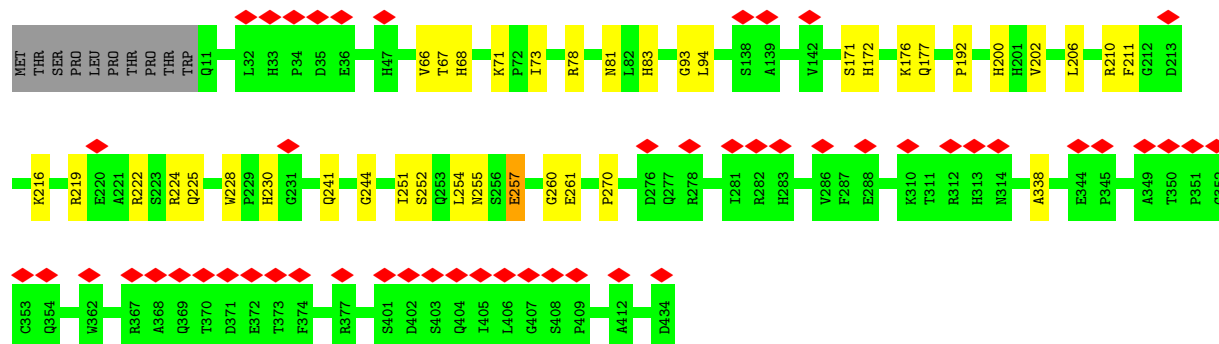
• Molecule 5: RNA (60-MER)

Chain T: 18% 42% 47% 12%

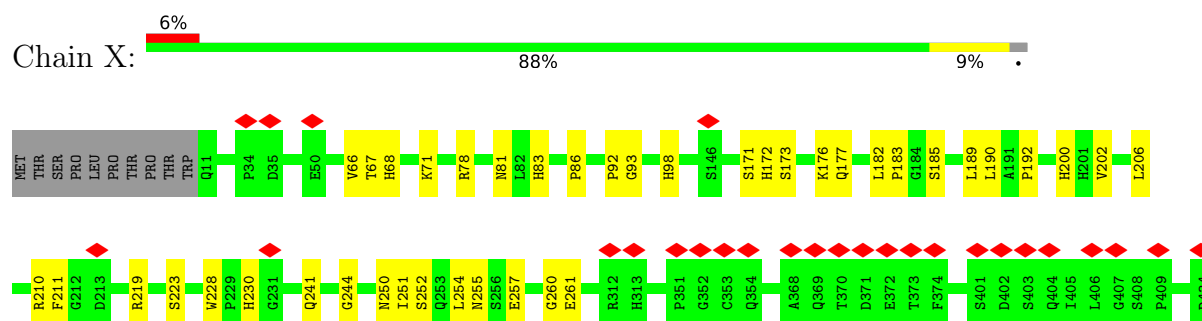


• Molecule 6: Type I-F CRISPR-associated protein Csy1

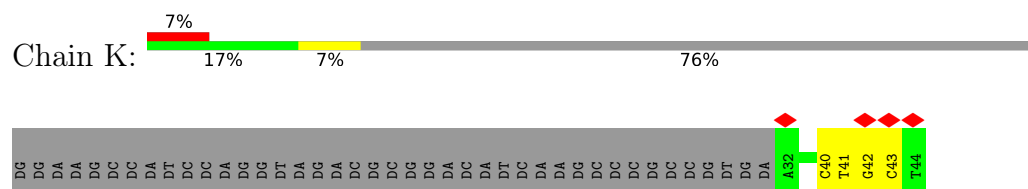
Chain A: 12% 89% 9%



- Molecule 6: Type I-F CRISPR-associated protein Csy1



- Molecule 7: 54-MER DNA



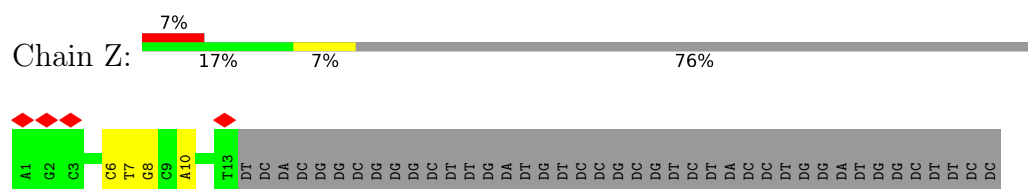
- Molecule 7: 54-MER DNA



- Molecule 8: 54-MER DNA



- Molecule 8: 54-MER DNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	364290	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	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	0.104	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.008	Depositor
Map size (\AA)	343.74402, 343.74402, 343.74402	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.0742, 1.0742, 1.0742	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	B	0.25	0/2248	0.53	0/3077
1	L	0.29	0/2378	0.58	1/3246 (0.0%)
2	C	0.22	0/2182	0.48	0/2977
2	D	0.33	0/2578	0.50	0/3507
2	E	0.39	0/2634	0.53	0/3575
2	F	0.39	0/2624	0.50	0/3561
2	G	0.36	0/2569	0.49	0/3488
2	H	0.28	0/2530	0.50	0/3440
2	M	0.24	0/2269	0.44	0/3087
2	N	0.36	0/2618	0.49	0/3555
2	O	0.42	0/2609	0.50	0/3542
2	P	0.42	0/2628	0.50	0/3565
2	Q	0.38	0/2599	0.49	0/3528
2	R	0.32	0/2576	0.48	0/3502
3	I	0.23	0/1484	0.53	0/2016
3	S	0.24	0/1487	0.54	0/2020
4	U	0.41	0/1809	0.53	0/2474
4	V	0.41	0/1809	0.52	0/2474
5	J	0.37	0/1419	0.41	0/2208
5	T	0.37	0/1419	0.42	0/2208
6	A	0.23	0/2292	0.53	0/3000
6	X	0.24	0/2292	0.57	0/3000
7	K	0.30	0/301	0.61	0/463
7	Y	0.29	0/301	0.69	0/463
8	W	0.36	0/295	0.67	0/452
8	Z	0.35	0/295	0.67	0/452
All	All	0.33	0/50245	0.51	1/68880 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	L	181	LEU	N-CA-C	6.64	121.25	112.35

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	B	2198	0	2017	74	0
1	L	2321	0	2248	50	0
2	C	2144	0	2026	22	0
2	D	2531	0	2464	20	0
2	E	2587	0	2563	17	0
2	F	2577	0	2562	18	0
2	G	2523	0	2492	39	0
2	H	2487	0	2405	23	0
2	M	2227	0	2167	33	0
2	N	2571	0	2537	31	0
2	O	2562	0	2540	17	0
2	P	2581	0	2573	23	0
2	Q	2552	0	2531	32	0
2	R	2529	0	2471	36	0
3	I	1445	0	1387	21	0
3	S	1445	0	1383	37	0
4	U	1758	0	1720	21	0
4	V	1758	0	1720	22	0
5	J	1271	0	647	23	0
5	T	1271	0	647	17	0
6	A	2251	0	1413	31	0
6	X	2251	0	1413	34	0
7	K	269	0	147	34	0
7	Y	269	0	147	35	0
8	W	264	0	146	8	0
8	Z	264	0	146	11	0
All	All	48906	0	44512	638	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 7.

The worst 5 of 638 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:L:181:LEU:HD12	1:L:182:PRO:CD	1.24	1.64
1:L:181:LEU:CD1	1:L:182:PRO:HD3	1.23	1.60
1:B:321:PHE:CD1	1:B:322:VAL:HG13	1.47	1.46
3:S:146:LEU:HD12	3:S:147:ARG:N	1.31	1.40
7:K:41:DT:C2'	7:K:42:DG:H5''	1.61	1.29

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	301/327 (92%)	274 (91%)	25 (8%)	2 (1%)	18	53
1	L	301/327 (92%)	276 (92%)	25 (8%)	0	100	100
2	C	287/342 (84%)	275 (96%)	12 (4%)	0	100	100
2	D	332/342 (97%)	313 (94%)	19 (6%)	0	100	100
2	E	335/342 (98%)	320 (96%)	14 (4%)	1 (0%)	36	70
2	F	333/342 (97%)	314 (94%)	18 (5%)	1 (0%)	36	70
2	G	325/342 (95%)	309 (95%)	16 (5%)	0	100	100
2	H	330/342 (96%)	310 (94%)	20 (6%)	0	100	100
2	M	287/342 (84%)	270 (94%)	17 (6%)	0	100	100
2	N	333/342 (97%)	317 (95%)	16 (5%)	0	100	100
2	O	332/342 (97%)	317 (96%)	15 (4%)	0	100	100
2	P	333/342 (97%)	313 (94%)	20 (6%)	0	100	100
2	Q	331/342 (97%)	314 (95%)	17 (5%)	0	100	100
2	R	331/342 (97%)	316 (96%)	15 (4%)	0	100	100
3	I	185/187 (99%)	177 (96%)	8 (4%)	0	100	100
3	S	186/187 (100%)	178 (96%)	8 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	U	225/228 (99%)	211 (94%)	14 (6%)	0	100	100
4	V	225/228 (99%)	211 (94%)	14 (6%)	0	100	100
6	A	422/434 (97%)	398 (94%)	24 (6%)	0	100	100
6	X	422/434 (97%)	398 (94%)	24 (6%)	0	100	100
All	All	6156/6456 (95%)	5811 (94%)	341 (6%)	4 (0%)	49	80

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	14	ARG
2	F	250	ARG
2	E	240	GLY
1	B	181	LEU

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	203/270 (75%)	201 (99%)	2 (1%)	68	84
1	L	232/270 (86%)	231 (100%)	1 (0%)	84	90
2	C	202/274 (74%)	202 (100%)	0	100	100
2	D	253/274 (92%)	251 (99%)	2 (1%)	73	86
2	E	262/274 (96%)	261 (100%)	1 (0%)	84	90
2	F	262/274 (96%)	261 (100%)	1 (0%)	84	90
2	G	255/274 (93%)	253 (99%)	2 (1%)	73	86
2	H	244/274 (89%)	243 (100%)	1 (0%)	84	90
2	M	221/274 (81%)	221 (100%)	0	100	100
2	N	260/274 (95%)	257 (99%)	3 (1%)	63	82
2	O	259/274 (94%)	257 (99%)	2 (1%)	73	86
2	P	263/274 (96%)	262 (100%)	1 (0%)	84	90

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	Q	258/274 (94%)	257 (100%)	1 (0%)	84	90
2	R	251/274 (92%)	250 (100%)	1 (0%)	84	90
3	I	145/160 (91%)	145 (100%)	0	100	100
3	S	145/160 (91%)	144 (99%)	1 (1%)	76	86
4	U	181/182 (100%)	180 (99%)	1 (1%)	78	88
4	V	181/182 (100%)	180 (99%)	1 (1%)	78	88
6	A	117/365 (32%)	114 (97%)	3 (3%)	40	72
6	X	117/365 (32%)	116 (99%)	1 (1%)	70	85
All	All	4311/5242 (82%)	4286 (99%)	25 (1%)	76	88

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	O	285	TYR
2	R	172	ARG
6	X	211	PHE
2	Q	285	TYR
3	S	146	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
6	A	273	GLN
6	X	68	HIS
2	H	329	ASN
2	H	323	GLN
6	X	177	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	J	59/60 (98%)	28 (47%)	1 (1%)
5	T	59/60 (98%)	27 (45%)	1 (1%)
All	All	118/120 (98%)	55 (46%)	2 (1%)

5 of 55 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	J	3	A
5	J	8	A
5	J	9	U
5	J	10	U
5	J	14	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	J	16	C
5	T	16	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](#)

There are no ligands in this entry.

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.

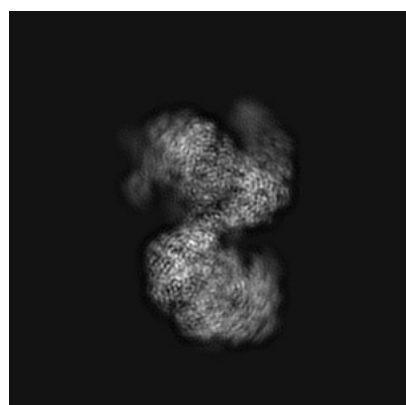
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31186. These allow visual inspection of the internal detail of the map and identification of artifacts.

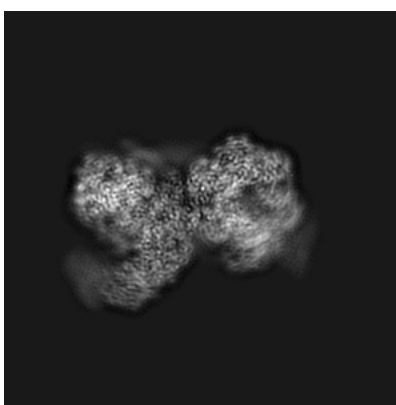
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

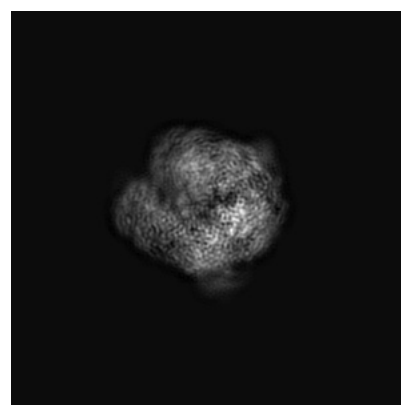
6.1.1 Primary map



X



Y

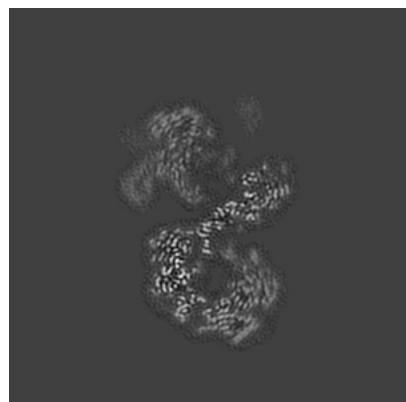


Z

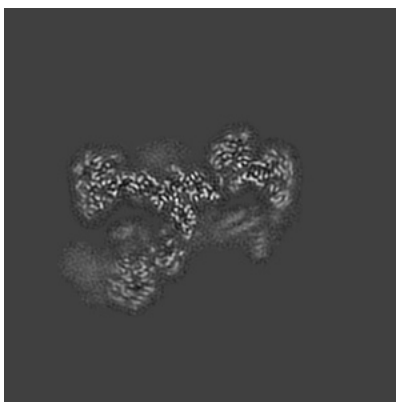
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

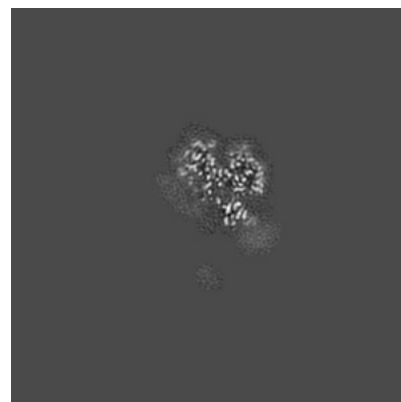
6.2.1 Primary map



X Index: 160



Y Index: 160

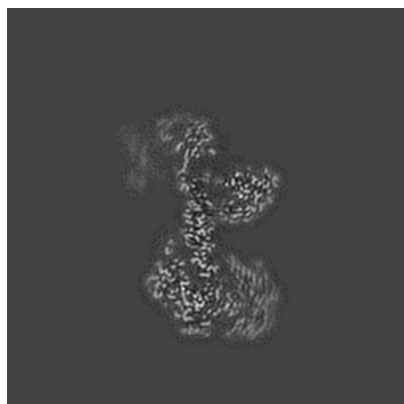


Z Index: 160

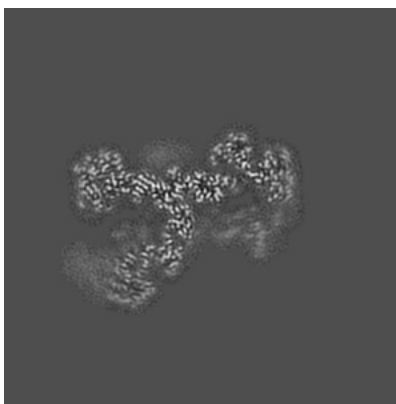
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

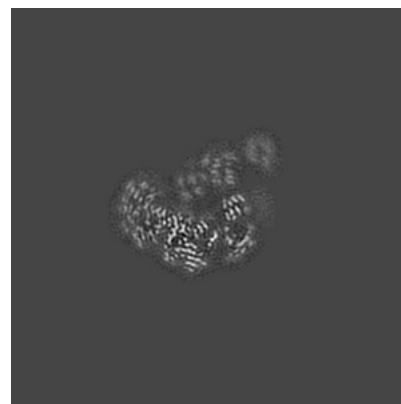
6.3.1 Primary map



X Index: 176



Y Index: 157

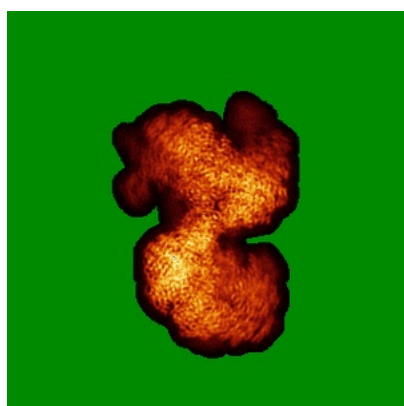


Z Index: 113

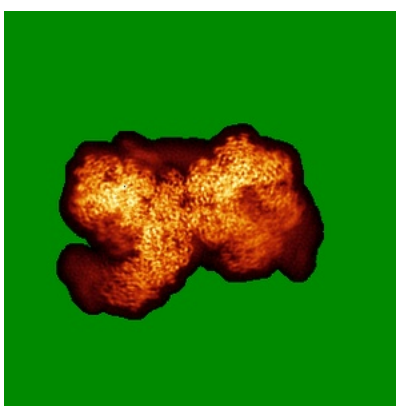
The images above show the largest variance slices of the map in three orthogonal directions.

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

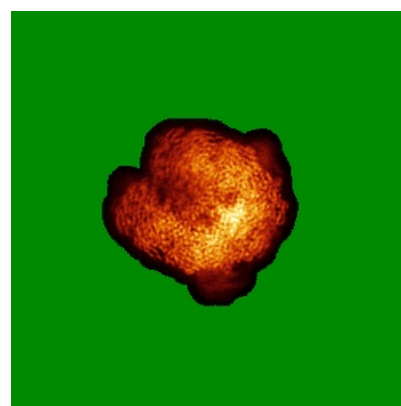
6.4.1 Primary map



X



Y

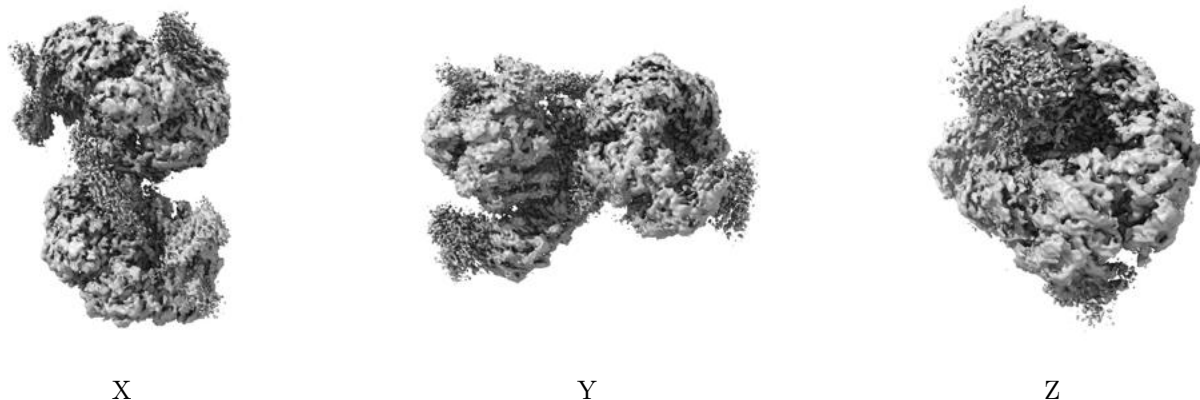


Z

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

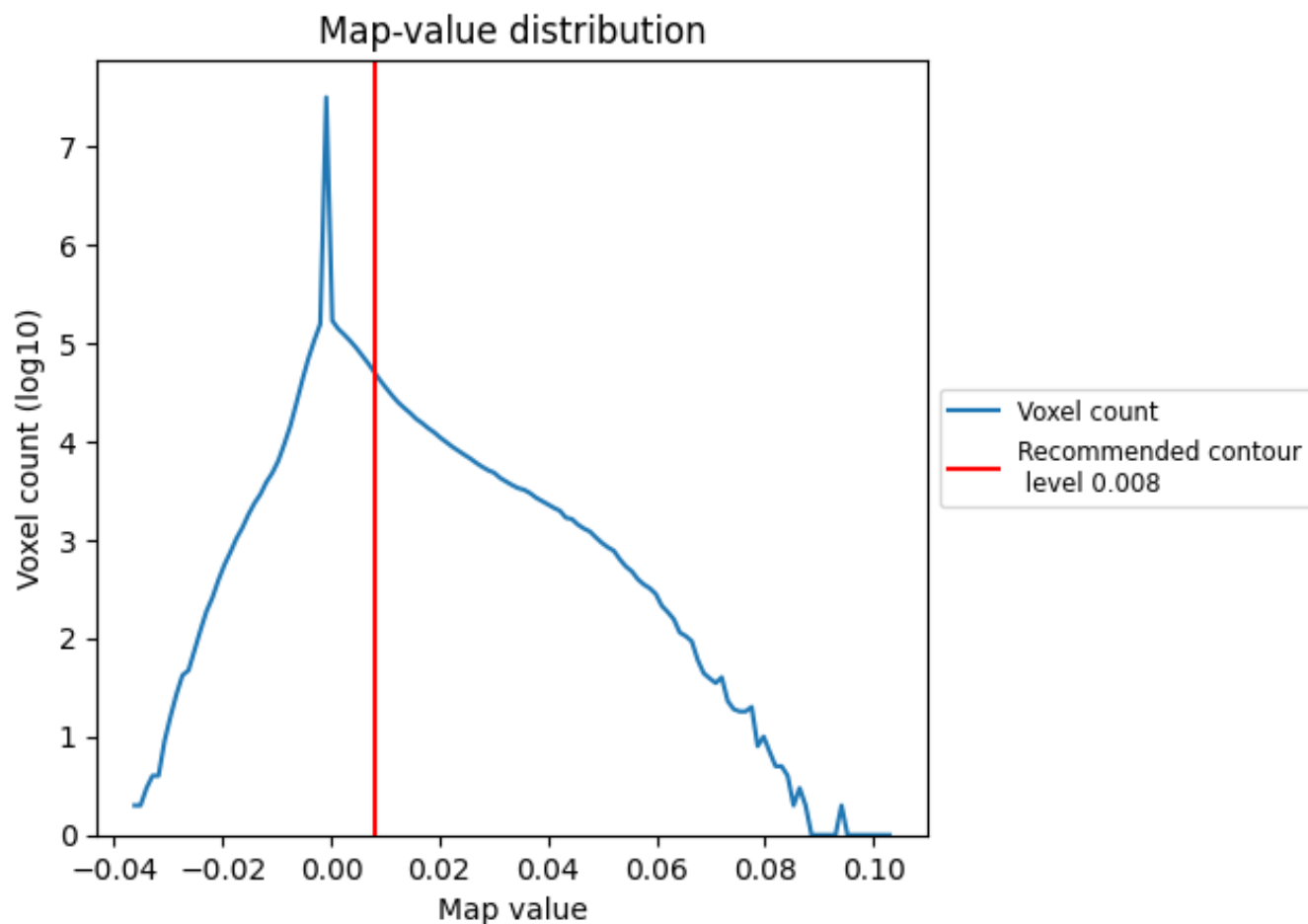
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

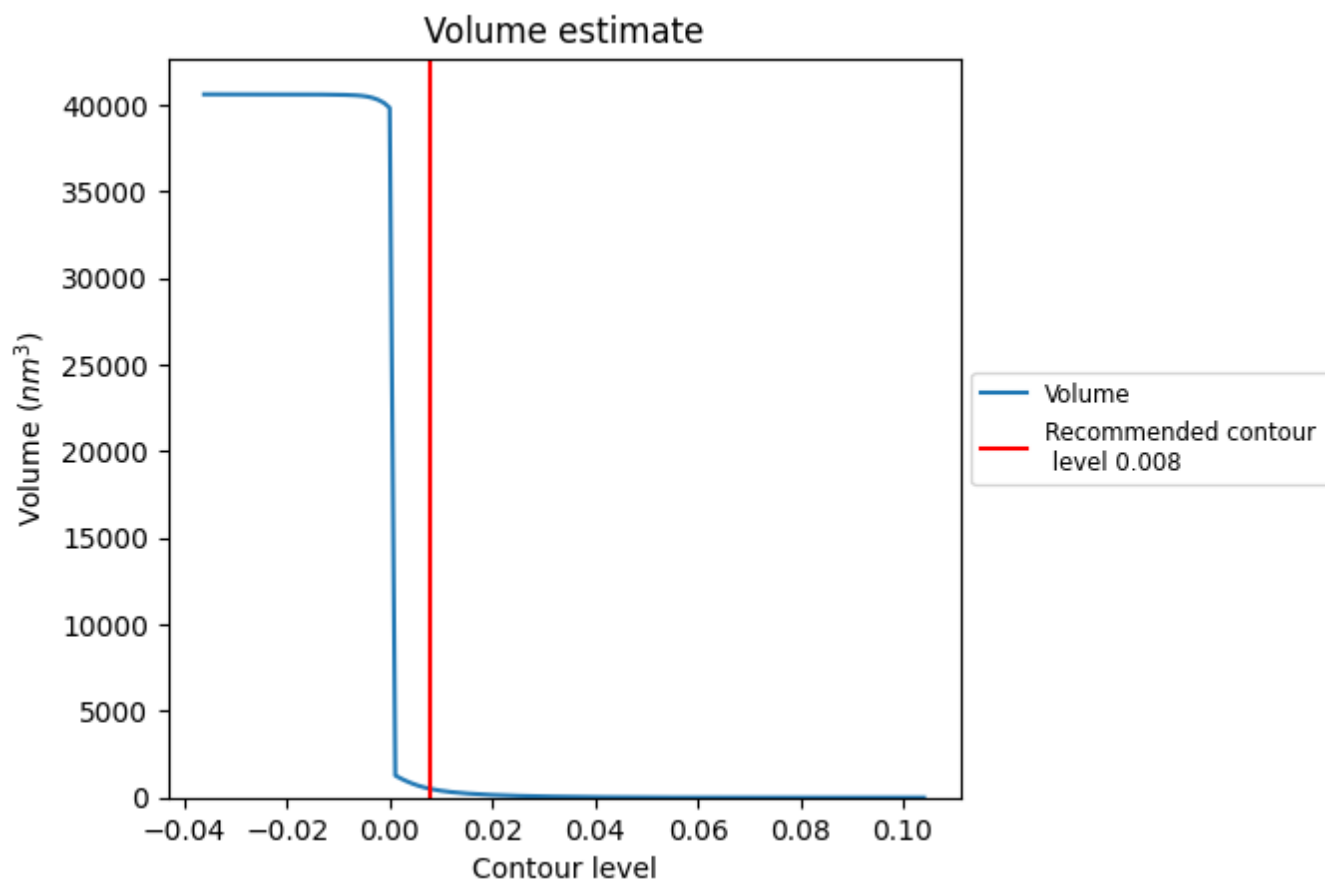
This section contains the results of statistical analysis of the map.

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.

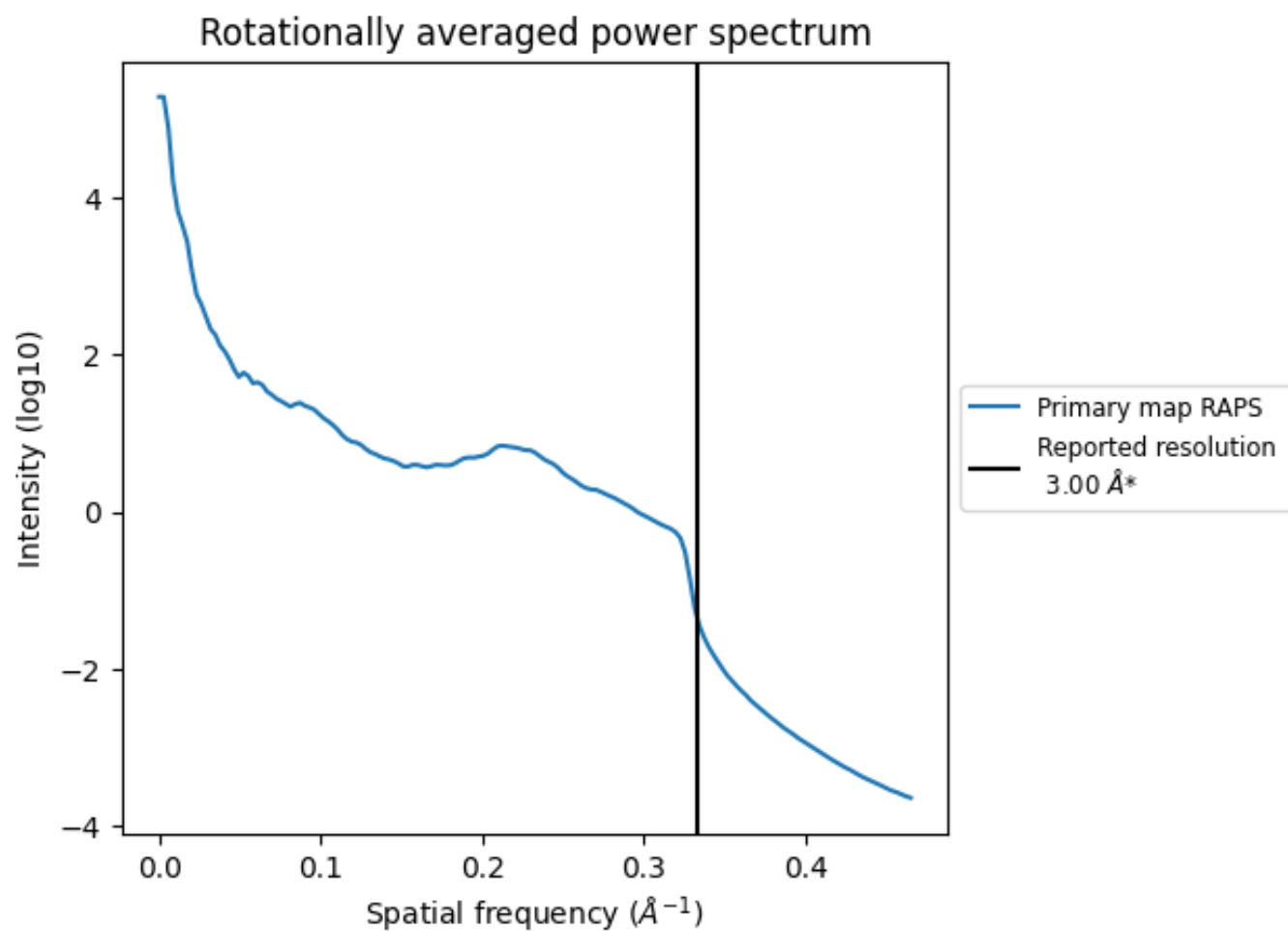
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 496 nm^3 ; this corresponds to an approximate mass of 448 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 ⓘ

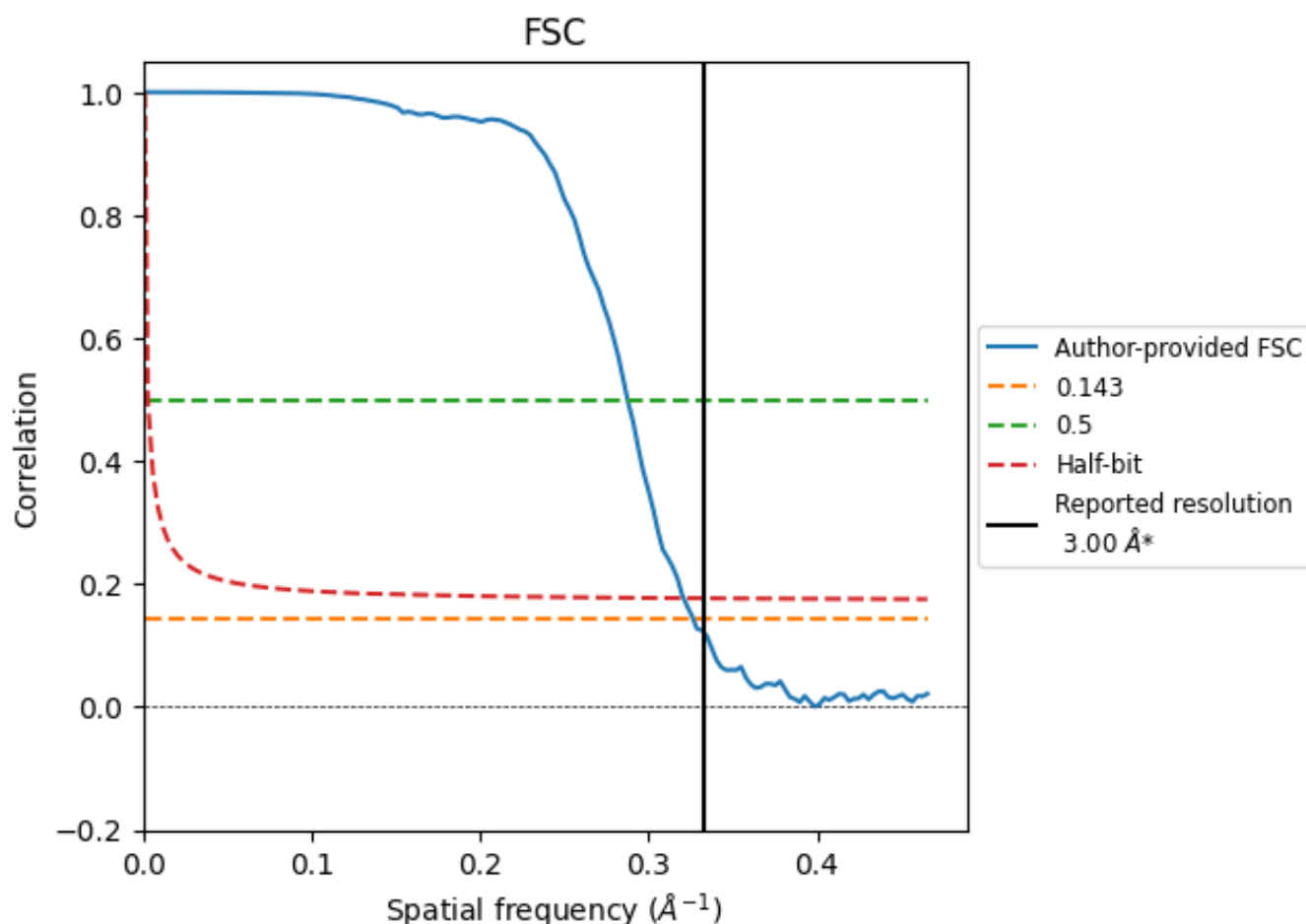


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

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 0.333 Å⁻¹

8.2 Resolution estimates [i](#)

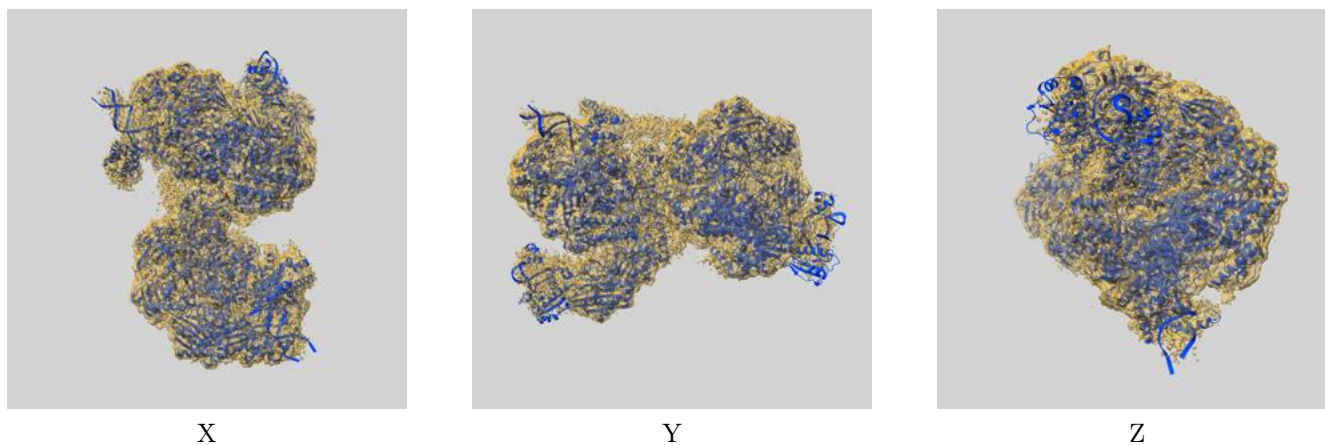
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	3.06	3.48	3.12
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

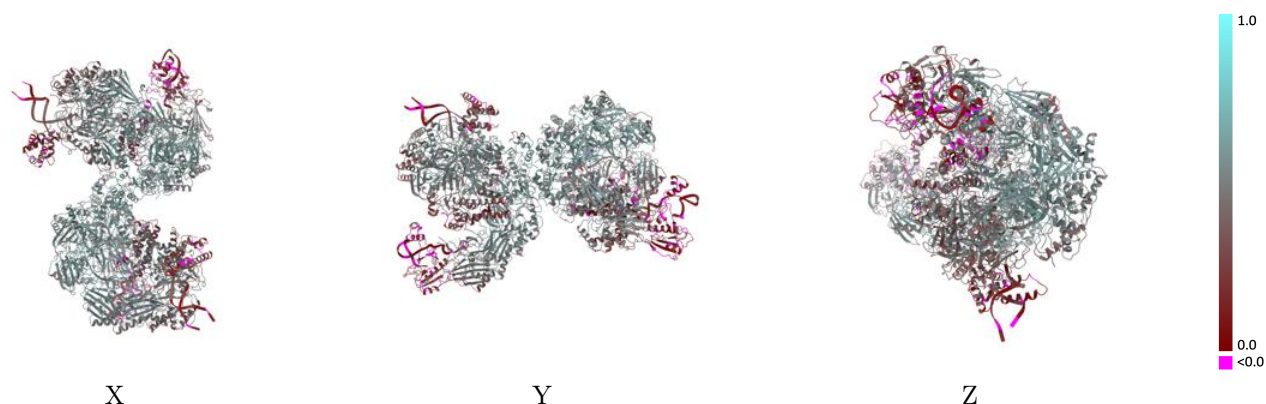
This section contains information regarding the fit between EMDB map EMD-31186 and PDB model 7ELN. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



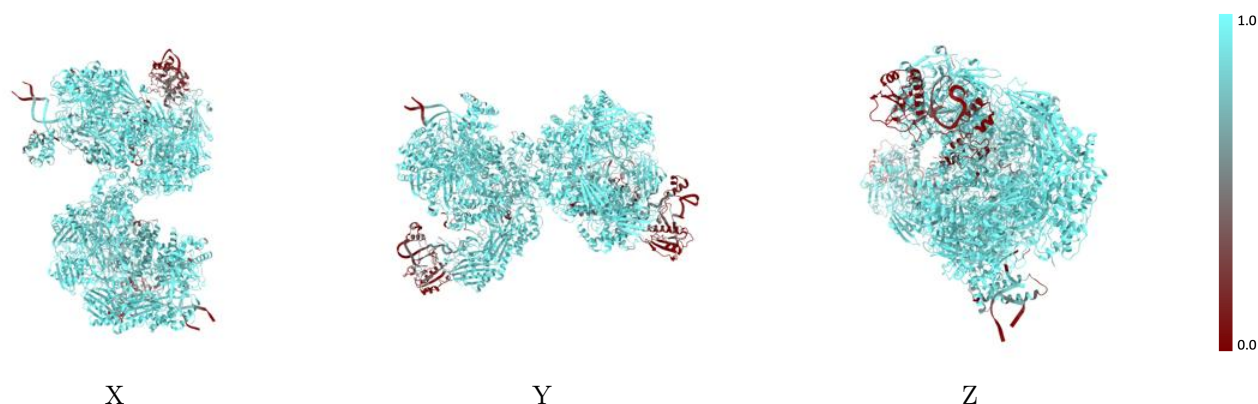
The images above show the 3D surface view of the map at the recommended contour level 0.008 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



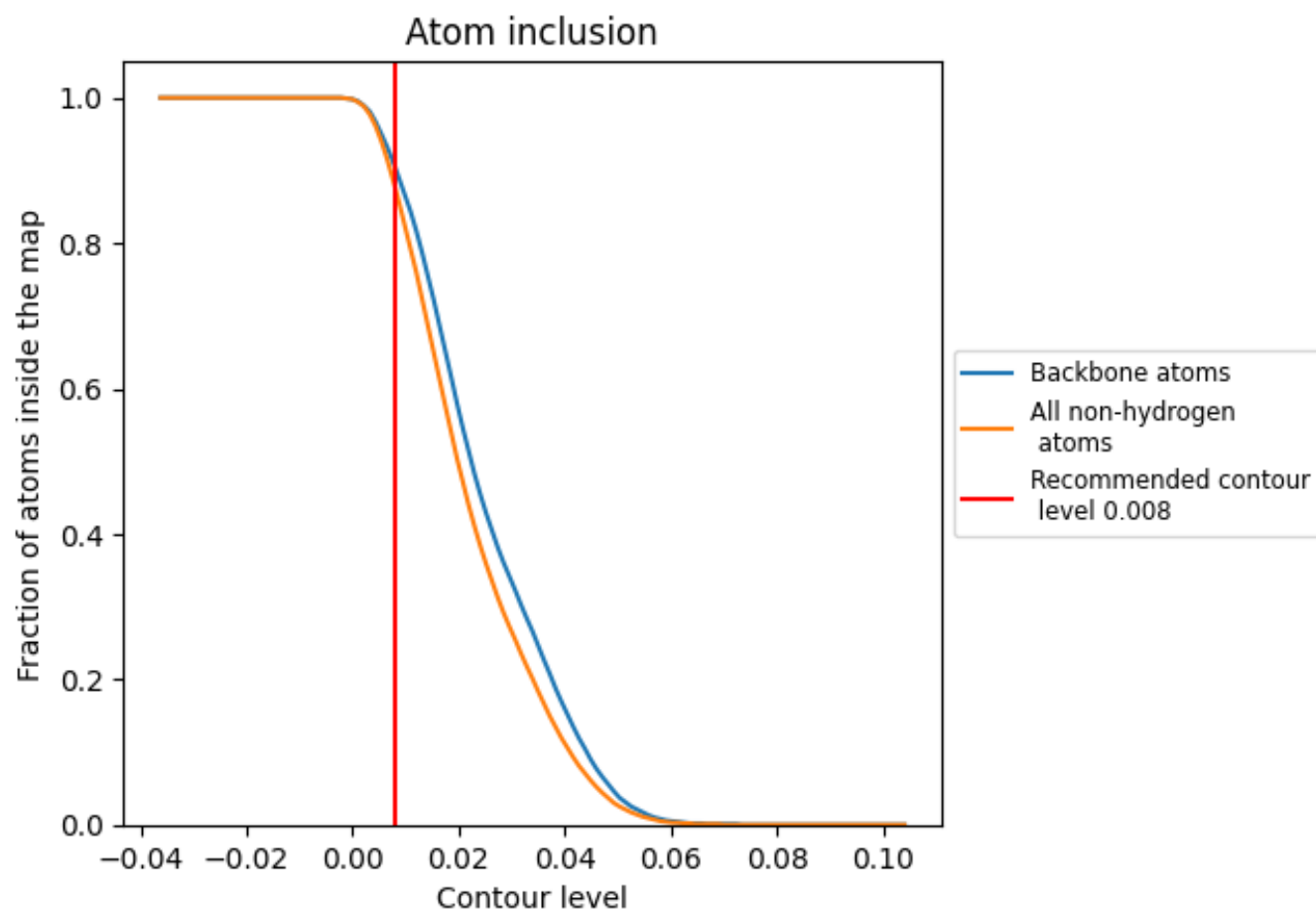
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.008).























































9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 88% 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 (0.008) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8770	 0.4600
A	 0.8070	 0.3210
B	 0.9110	 0.4110
C	 0.8930	 0.4230
D	 0.9360	 0.5130
E	 0.9620	 0.5490
F	 0.9600	 0.5510
G	 0.9680	 0.5350
H	 0.9360	 0.4550
I	 0.1490	 0.1020
J	 0.7250	 0.3700
K	 0.6060	 0.2680
L	 0.9260	 0.4430
M	 0.9140	 0.4570
N	 0.9540	 0.5330
O	 0.9640	 0.5600
P	 0.9670	 0.5620
Q	 0.9740	 0.5520
R	 0.9590	 0.4920
S	 0.2680	 0.1600
T	 0.7730	 0.3860
U	 0.9710	 0.5670
V	 0.9670	 0.5670
W	 0.5420	 0.1780
X	 0.8850	 0.3720
Y	 0.6430	 0.2340
Z	 0.5870	 0.1850

