



Full wwPDB EM Validation Report ⓘ

Jul 28, 2024 – 12:20 AM JST

PDB ID : 8YH9
EMDB ID : EMD-39285
Title : Type I-FHNN Cascade complex
Authors : Li, Z.
Deposited on : 2024-02-27
Resolution : 3.35 Å (reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

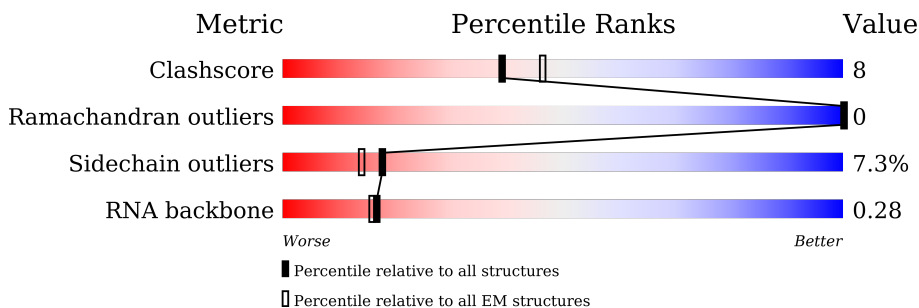
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.37.1

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 3.35 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.



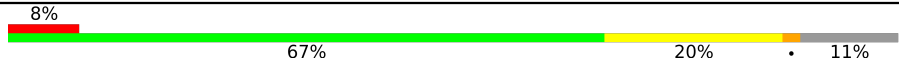
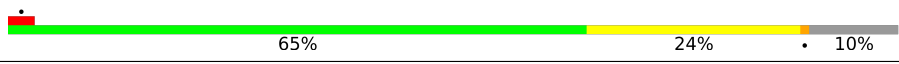
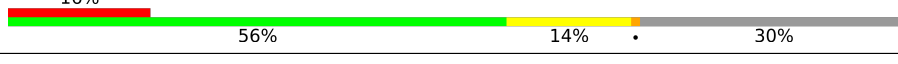
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	255	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">8%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: left;">72%</div> <div style="text-align: right;">22%</div> </div>
2	B	181	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">79%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: left;">70%</div> <div style="text-align: right;">25%</div> </div>
3	C	60	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">30%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: left;">42%</div> <div style="text-align: right;">47%</div> </div>
4	D	335	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">19%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: left;">70%</div> <div style="text-align: right;">15%</div> </div>
4	E	335	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">8%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: left;">59%</div> <div style="text-align: right;">26%</div> </div>
4	F	335	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">7%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: left;">71%</div> <div style="text-align: right;">17%</div> </div>
4	G	335	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: right;">7%</div> <div style="width: 100%; height: 15px; background: linear-gradient(to right, red, orange, yellow, green, grey);"></div> <div style="text-align: left;">71%</div> <div style="text-align: right;">19%</div> </div>

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Mol	Chain	Length	Quality of chain
4	H	335	
4	I	335	
5	J	344	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 21153 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 Cas5f.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	245	1934	1235	324	361	14	0	0

- Molecule 2 is a protein called Cas6f.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	175	1415	913	239	258	5	0	0

- Molecule 3 is a RNA chain called 60-nt crRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	C	60	1287	577	240	411	59	0	0

- Molecule 4 is a protein called Cas7f.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	I	302	2467	1581	407	466	13	0	0
4	H	297	2423	1553	399	458	13	0	0
4	G	302	2461	1576	407	465	13	0	0
4	F	300	2447	1570	403	461	13	0	0
4	E	294	2397	1539	393	452	13	0	0
4	D	293	2393	1534	393	453	13	0	0

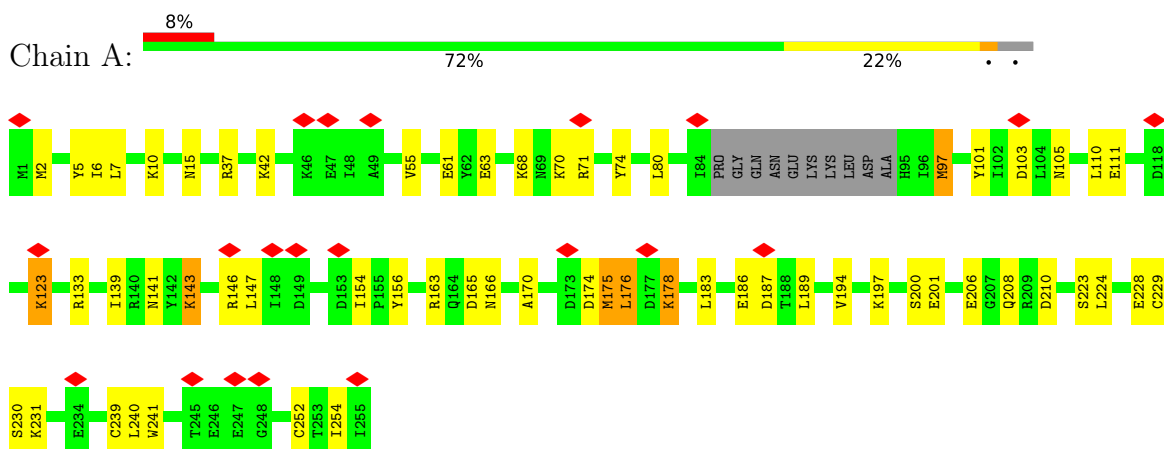
- Molecule 5 is a protein called Cas8f fusion with HNH.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	J	242	1929	1229	334	360	6	0	0

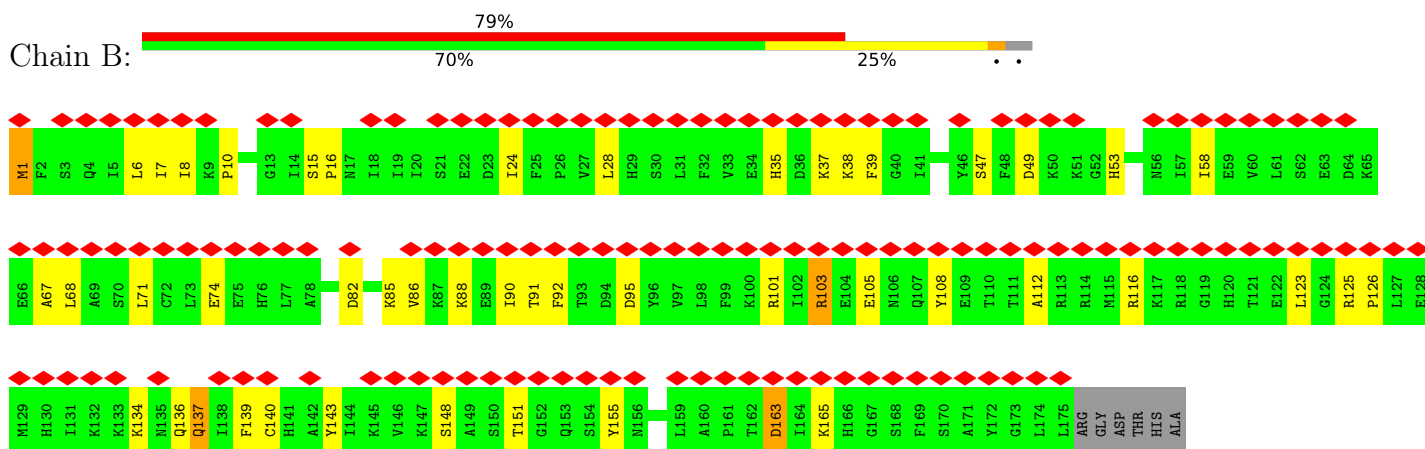
3 Residue-property plots [i](#)

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.

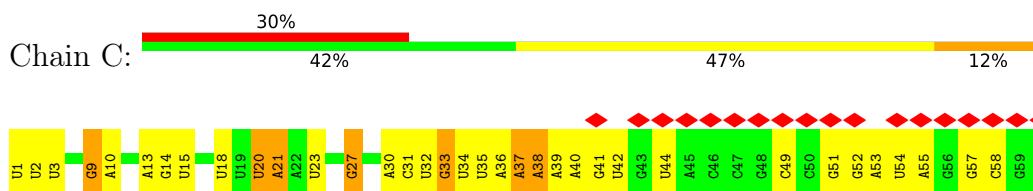
- Molecule 1: Cas5f



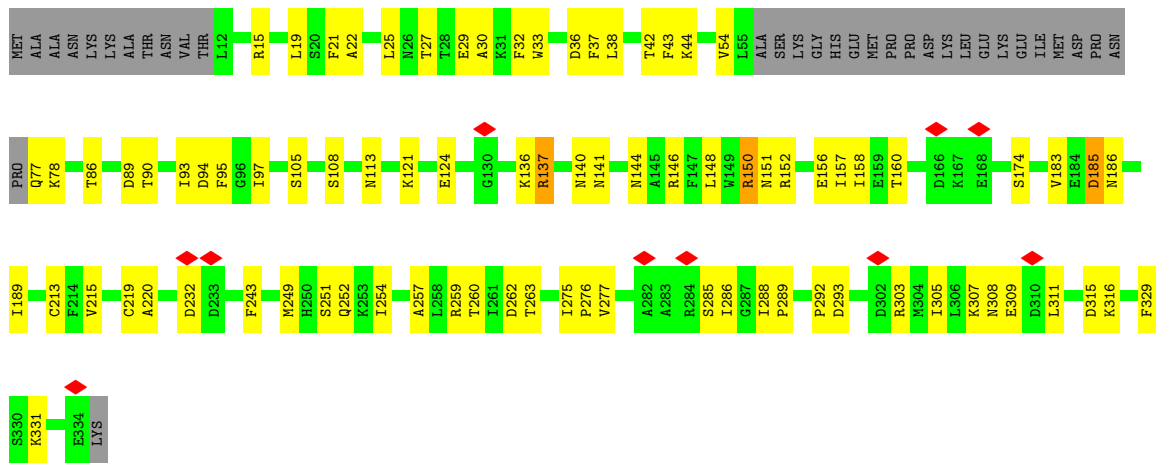
- Molecule 2: Cas6f



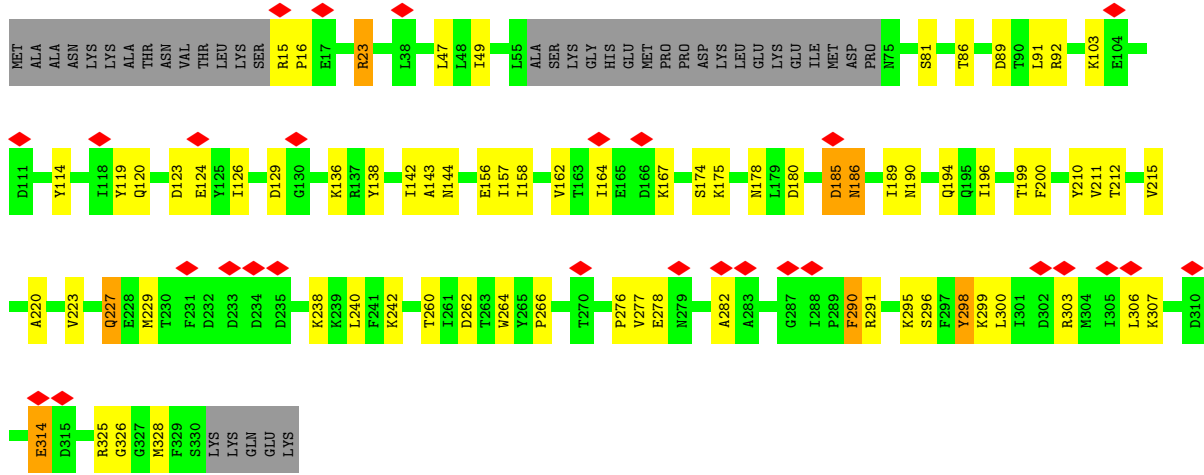
- Molecule 3: 60-nt crRNA



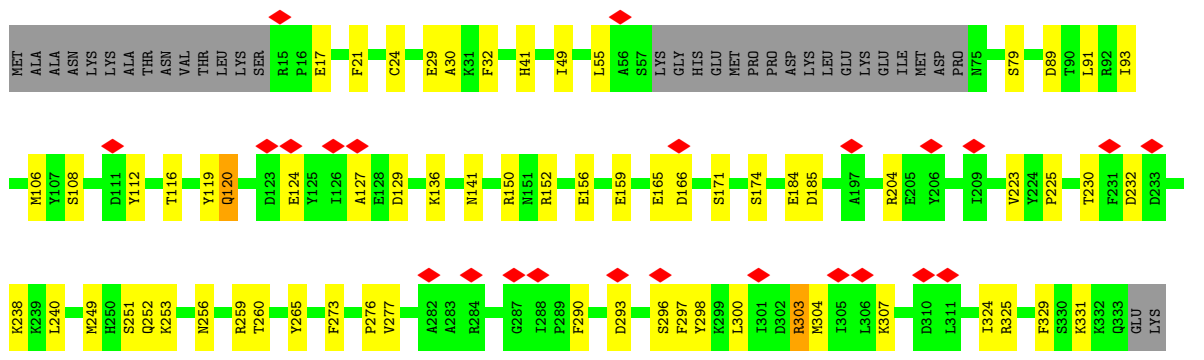
- Molecule 4: Cas7f



• Molecule 4: Cas7f

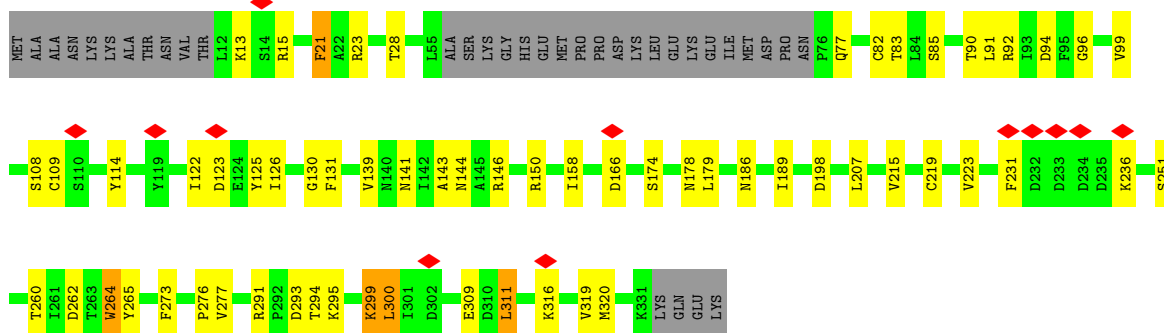


• Molecule 4: Cas7f



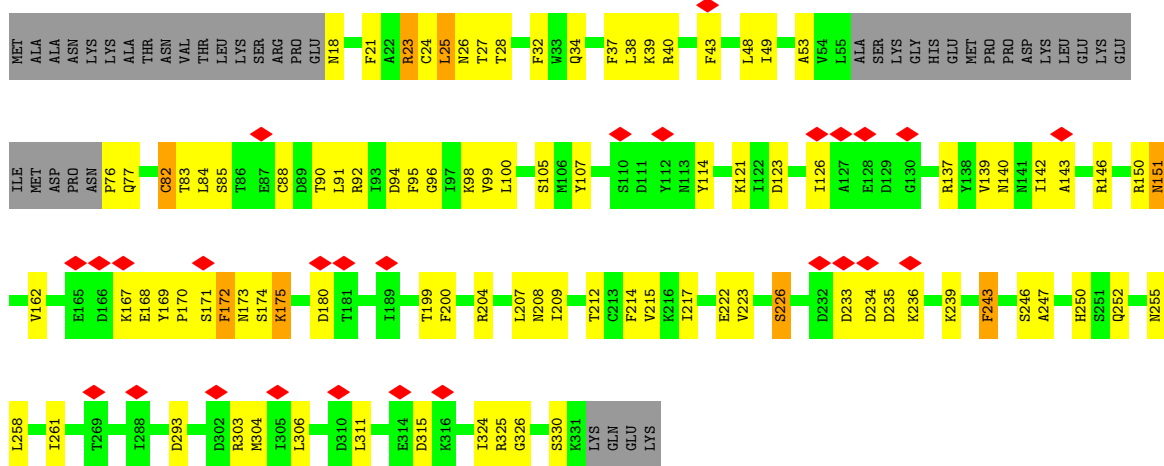
• Molecule 4: Cas7f

Chain F: 



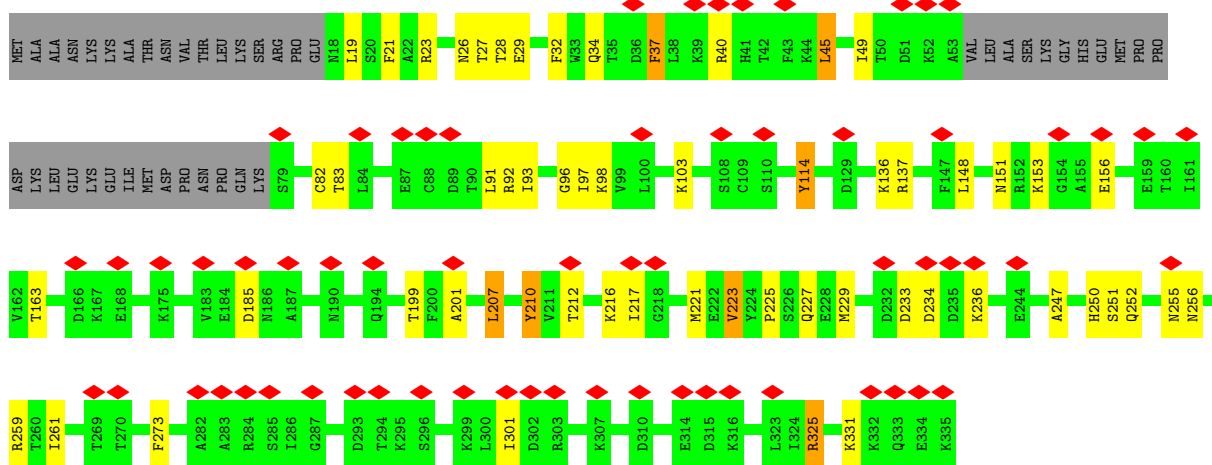
• Molecule 4: Cas7f

Chain E: 

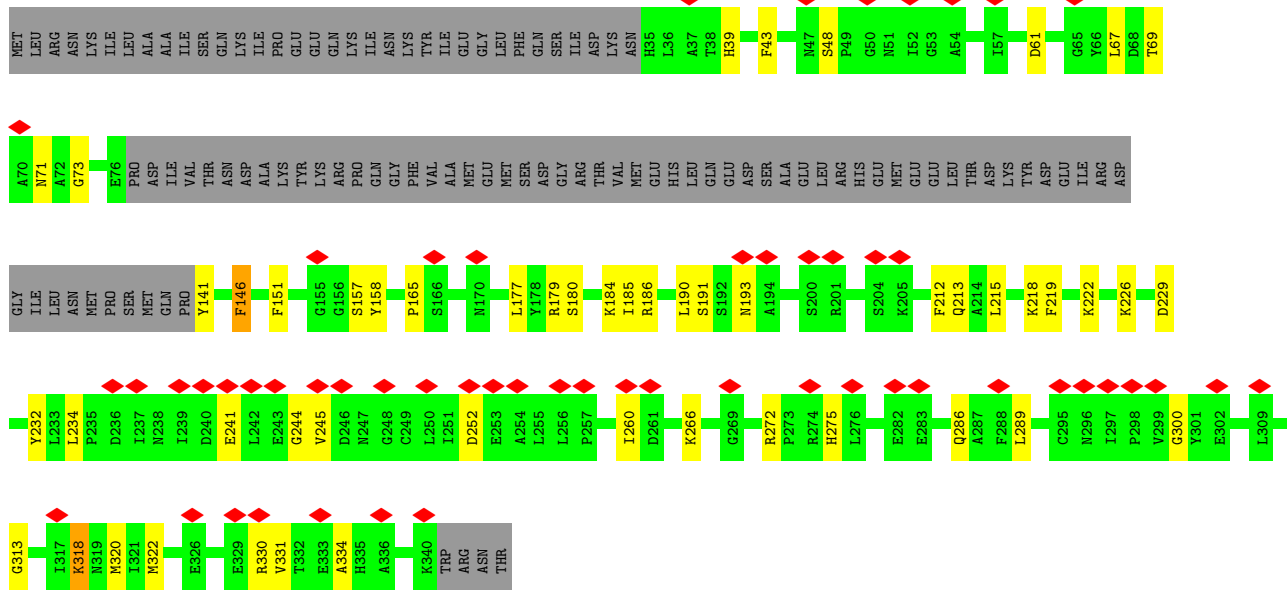


• Molecule 4: Cas7f

Chain D: 



• Molecule 5: Cas8f fusion with HNH



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	110316	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 ($e^-/\text{\AA}^2$)	54	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	2.135	Depositor
Minimum map value	-1.352	Depositor
Average map value	-0.001	Depositor
Map value standard deviation	0.066	Depositor
Recommended contour level	0.25	Depositor
Map size (\AA)	255.0, 255.0, 255.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.85, 0.85, 0.85	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.28	0/1967	0.58	0/2650
2	B	0.26	0/1446	0.51	0/1945
3	C	0.30	0/1443	0.89	0/2250
4	D	0.26	0/2445	0.52	0/3299
4	E	0.29	0/2450	0.55	0/3308
4	F	0.30	0/2501	0.54	0/3376
4	G	0.28	0/2515	0.56	0/3396
4	H	0.27	0/2477	0.55	0/3347
4	I	0.28	0/2520	0.54	0/3400
5	J	0.26	0/1972	0.59	0/2668
All	All	0.28	0/21736	0.58	0/29639

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1934	0	1953	39	0
2	B	1415	0	1437	25	0
3	C	1287	0	645	23	0
4	D	2393	0	2359	33	0
4	E	2397	0	2368	59	0
4	F	2447	0	2423	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	G	2461	0	2430	36	0
4	H	2423	0	2386	35	0
4	I	2467	0	2442	42	0
5	J	1929	0	1921	29	0
All	All	21153	0	20364	322	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.

All (322) 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)
4:F:300:LEU:HD11	4:F:319:VAL:HG11	1.55	0.88
4:E:139:VAL:HG22	4:E:172:PHE:HZ	1.42	0.85
4:D:91:LEU:HD22	4:D:223:VAL:HG21	1.63	0.80
4:F:300:LEU:HD21	4:F:319:VAL:HG12	1.74	0.69
4:I:150:ARG:HH22	4:H:23:ARG:HH21	1.44	0.66
4:H:156:GLU:HG3	4:H:157:ILE:HG12	1.79	0.65
1:A:63:GLU:HB2	1:A:103:ASP:HB2	1.77	0.65
4:E:23:ARG:HD2	4:E:255:ASN:HD21	1.62	0.65
4:E:49:ILE:HG12	4:E:82:CYS:HB2	1.80	0.64
4:I:156:GLU:HG2	4:I:157:ILE:HG12	1.79	0.63
4:G:116:THR:O	4:G:120:GLN:NE2	2.32	0.63
4:G:303:ARG:NH1	4:G:304:MET:SD	2.73	0.62
1:A:176:LEU:HD12	5:J:73:GLY:HA3	1.81	0.61
3:C:21:A:N6	4:G:230:THR:O	2.35	0.60
4:I:141:ASN:HD21	4:I:260:THR:H	1.49	0.60
4:D:156:GLU:H	4:D:217:ILE:HG21	1.67	0.60
4:E:34:GLN:NE2	4:E:88:CYS:SG	2.75	0.60
2:B:137:GLN:HG2	5:J:300:GLY:HA3	1.84	0.59
4:I:77:GLN:N	4:H:229:MET:SD	2.76	0.59
4:I:260:THR:HA	4:I:276:PRO:HA	1.83	0.59
4:E:28:THR:HB	4:E:96:GLY:H	1.68	0.59
4:I:286:ILE:HG22	4:I:288:ILE:H	1.68	0.59
3:C:38:A:OP2	4:D:256:ASN:ND2	2.36	0.59
4:G:30:ALA:HB3	4:G:249:MET:HB3	1.84	0.58
3:C:20:U:O2	4:G:253:LYS:NZ	2.35	0.58
4:I:160:THR:HG1	4:I:213:CYS:HG	1.50	0.58
4:G:260:THR:HG22	4:G:276:PRO:HG3	1.86	0.58
1:A:229:CYS:SG	1:A:230:SER:N	2.78	0.57
4:I:148:LEU:HB3	4:I:151:ASN:HB3	1.84	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:23:U:OP1	4:G:150:ARG:NH1	2.38	0.57
5:J:222:LYS:HA	5:J:226:LYS:HD2	1.85	0.57
4:E:83:THR:HG23	4:E:222:GLU:HA	1.86	0.57
4:I:186:ASN:HB3	4:I:189:ILE:HB	1.87	0.57
4:E:121:LYS:NZ	4:E:304:MET:SD	2.79	0.56
4:G:17:GLU:HA	4:G:331:LYS:HG2	1.88	0.56
4:I:32:PHE:HE1	4:I:93:ILE:HD12	1.70	0.56
4:E:23:ARG:HG2	4:E:25:LEU:O	2.05	0.56
4:E:18:ASN:N	4:E:330:SER:HG	2.04	0.56
1:A:6:ILE:HG22	1:A:110:LEU:HB2	1.88	0.56
4:I:19:LEU:HD22	4:I:329:PHE:HB2	1.88	0.56
4:D:185:ASP:OD1	4:D:185:ASP:N	2.39	0.55
4:I:140:ASN:ND2	4:I:183:VAL:O	2.38	0.55
4:G:293:ASP:HA	4:G:296:SER:HB3	1.89	0.55
4:F:300:LEU:HD21	4:F:319:VAL:CG1	2.37	0.55
4:H:185:ASP:OD1	4:H:185:ASP:N	2.37	0.55
4:I:185:ASP:N	4:I:185:ASP:OD1	2.37	0.55
4:G:259:ARG:NH1	4:G:277:VAL:O	2.39	0.55
4:D:225:PRO:HG3	4:D:247:ALA:HB1	1.88	0.55
4:I:137:ARG:HA	4:I:140:ASN:HB2	1.87	0.54
4:D:236:LYS:NZ	5:J:330:ARG:O	2.40	0.54
1:A:175:MET:HG2	5:J:67:LEU:HB3	1.87	0.54
1:A:7:LEU:HD23	1:A:146:ARG:HB2	1.89	0.54
4:F:264:TRP:O	4:F:291:ARG:NH2	2.40	0.54
3:C:20:U:OP2	4:G:259:ARG:NH2	2.41	0.54
4:H:49:ILE:HD13	4:H:240:LEU:HB2	1.90	0.54
4:E:23:ARG:HD2	4:E:255:ASN:ND2	2.22	0.54
2:B:1:MET:SD	2:B:1:MET:N	2.76	0.54
4:I:54:VAL:O	4:I:77:GLN:N	2.40	0.54
4:G:296:SER:OG	4:G:297:PHE:N	2.41	0.54
4:E:25:LEU:HD11	4:E:200:PHE:HE1	1.73	0.54
4:D:82:CYS:SG	4:D:83:THR:N	2.80	0.54
1:A:97:MET:HA	5:J:190:LEU:HD13	1.90	0.53
4:I:262:ASP:HB3	4:I:275:ILE:HG13	1.89	0.53
4:G:232:ASP:OD1	4:G:232:ASP:N	2.41	0.53
4:E:90:THR:OG1	4:E:91:LEU:N	2.42	0.53
4:H:227:GLN:HG3	4:H:238:LYS:HZ2	1.74	0.53
1:A:80:LEU:HD13	3:C:9:G:H5''	1.90	0.53
1:A:175:MET:HB3	5:J:67:LEU:HD22	1.90	0.53
1:A:37:ARG:NH2	5:J:158:TYR:OH	2.41	0.53
4:G:32:PHE:HD2	4:G:91:LEU:HD11	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:158:ILE:HG23	4:F:215:VAL:HG12	1.90	0.53
4:I:86:THR:HA	4:I:220:ALA:HB2	1.89	0.53
4:F:291:ARG:HG2	4:F:295:LYS:HB2	1.91	0.53
1:A:15:ASN:HA	1:A:101:TYR:HB3	1.90	0.53
4:H:49:ILE:HD12	4:H:242:LYS:HG3	1.91	0.53
4:E:151:ASN:HB3	4:E:217:ILE:HD11	1.91	0.53
4:F:77:GLN:HG2	4:F:236:LYS:HB2	1.90	0.52
4:E:76:PRO:O	4:E:77:GLN:NE2	2.41	0.52
1:A:194:VAL:HG21	1:A:223:SER:HB2	1.91	0.52
2:B:148:SER:OG	2:B:151:THR:O	2.27	0.52
4:I:158:ILE:HD12	4:I:215:VAL:HG22	1.92	0.52
4:E:91:LEU:HB3	4:E:215:VAL:O	2.10	0.52
4:G:165:GLU:OE2	4:G:204:ARG:NH2	2.43	0.52
4:G:223:VAL:HG23	4:G:225:PRO:HD3	1.91	0.52
4:F:291:ARG:NH1	4:F:295:LYS:O	2.42	0.52
4:I:140:ASN:O	4:I:144:ASN:ND2	2.43	0.52
4:E:170:PRO:O	4:E:174:SER:HB3	2.10	0.52
4:H:129:ASP:OD1	4:H:129:ASP:N	2.43	0.51
1:A:174:ASP:O	1:A:178:LYS:HB3	2.09	0.51
4:F:262:ASP:HB2	4:F:277:VAL:HG22	1.92	0.51
1:A:133:ARG:O	3:C:2:U:N3	2.42	0.51
1:A:74:TYR:HB2	5:J:185:ILE:HD12	1.93	0.51
4:I:303:ARG:HE	4:I:311:LEU:HD21	1.75	0.51
4:F:90:THR:HA	4:F:215:VAL:O	2.11	0.51
3:C:27:G:H5'	4:G:55:LEU:HB2	1.92	0.51
4:H:282:ALA:HB2	4:H:290:PHE:HB2	1.93	0.51
3:C:37:A:OP1	4:D:255:ASN:ND2	2.44	0.50
4:F:300:LEU:HD11	4:F:319:VAL:CG1	2.33	0.50
4:E:27:THR:OG1	4:E:28:THR:N	2.44	0.50
4:G:185:ASP:N	4:G:185:ASP:OD1	2.44	0.50
4:G:141:ASN:ND2	4:G:260:THR:OG1	2.44	0.50
4:E:311:LEU:HB3	4:E:315:ASP:HB3	1.93	0.50
1:A:165:ASP:OD1	1:A:165:ASP:N	2.39	0.49
2:B:47:SER:O	2:B:53:HIS:ND1	2.45	0.49
4:G:136:LYS:NZ	4:G:184:GLU:O	2.45	0.49
3:C:34:U:O3'	4:E:150:ARG:NH1	2.40	0.49
4:E:139:VAL:HG22	4:E:172:PHE:CZ	2.33	0.49
4:I:146:ARG:HB3	4:I:257:ALA:HB1	1.93	0.49
4:E:226:SER:HG	4:E:250:HIS:CE1	2.30	0.49
2:B:7:ILE:HG22	2:B:85:LYS:HB3	1.93	0.49
1:A:163:ARG:NH2	1:A:228:GLU:OE1	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:CYS:HA	1:A:254:ILE:HD13	1.95	0.49
3:C:21:A:H62	4:G:230:THR:H	1.61	0.49
4:G:24:CYS:HB3	4:G:324:ILE:HG23	1.93	0.49
4:D:93:ILE:O	4:D:212:THR:HA	2.13	0.49
5:J:39:HIS:HE1	5:J:69:THR:HG21	1.76	0.49
1:A:111:GLU:HB2	1:A:240:LEU:HD23	1.95	0.49
4:F:82:CYS:SG	4:F:83:THR:N	2.86	0.49
3:C:33:G:OP1	4:E:226:SER:OG	2.31	0.49
4:D:259:ARG:HD2	4:D:325:ARG:HG3	1.95	0.49
4:I:22:ALA:HB3	4:I:105:SER:HB3	1.95	0.49
4:D:28:THR:O	4:D:251:SER:OG	2.28	0.49
3:C:20:U:H5'	4:G:256:ASN:HB2	1.95	0.48
4:F:311:LEU:HD21	4:F:316:LYS:HB2	1.95	0.48
4:I:305:ILE:O	4:I:308:ASN:ND2	2.45	0.48
4:F:143:ALA:O	4:F:174:SER:OG	2.27	0.48
4:F:146:ARG:NH2	4:F:179:LEU:O	2.44	0.48
4:D:26:ASN:HB2	4:D:98:LYS:HB3	1.96	0.48
3:C:1:U:H2'	5:J:151:PHE:HD2	1.78	0.48
4:H:92:ARG:HH21	4:H:212:THR:HG21	1.77	0.48
1:A:6:ILE:HD12	1:A:147:LEU:HD13	1.96	0.48
4:I:137:ARG:HH12	4:I:263:THR:HG23	1.78	0.48
4:H:262:ASP:HB2	4:H:277:VAL:HG22	1.96	0.48
2:B:24:ILE:O	2:B:28:LEU:HB2	2.13	0.48
2:B:136:GLN:O	2:B:139:PHE:HB3	2.14	0.48
4:D:49:ILE:HD11	4:D:247:ALA:HB2	1.95	0.48
4:F:126:ILE:HA	4:F:130:GLY:HA2	1.95	0.48
4:D:234:ASP:N	4:D:234:ASP:OD1	2.46	0.48
4:F:141:ASN:ND2	4:F:260:THR:OG1	2.40	0.48
3:C:51:G:N2	3:C:55:A:OP1	2.47	0.47
3:C:51:G:O2'	3:C:55:A:N6	2.47	0.47
4:F:99:VAL:HG22	4:F:207:LEU:HB3	1.95	0.47
4:E:94:ASP:HA	4:E:212:THR:HA	1.96	0.47
5:J:244:GLY:HA2	5:J:252:ASP:HB2	1.97	0.47
4:I:307:LYS:HG3	4:I:309:GLU:HB2	1.96	0.47
4:G:124:GLU:O	4:G:127:ALA:HB3	2.14	0.47
3:C:31:C:H5''	4:E:252:GLN:HG2	1.95	0.47
4:H:325:ARG:NH1	4:H:326:GLY:O	2.48	0.47
4:F:91:LEU:HD13	4:F:223:VAL:HG11	1.95	0.47
4:F:139:VAL:HG13	4:F:189:ILE:HG13	1.96	0.47
3:C:30:A:H5''	4:E:23:ARG:HD3	1.96	0.47
4:H:303:ARG:HA	4:H:307:LYS:HE2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:199:THR:HA	4:E:204:ARG:HB2	1.97	0.47
1:A:2:MET:SD	1:A:2:MET:N	2.88	0.47
1:A:208:GLN:NE2	1:A:210:ASP:O	2.47	0.47
2:B:148:SER:HB3	2:B:155:TYR:HE1	1.80	0.47
4:E:235:ASP:O	4:E:239:LYS:NZ	2.48	0.47
5:J:48:SER:HB3	5:J:146:PHE:HB3	1.96	0.47
5:J:177:LEU:HD12	5:J:184:LYS:HD3	1.97	0.47
1:A:200:SER:OG	1:A:201:GLU:N	2.47	0.47
4:I:121:LYS:HA	4:I:121:LYS:HD2	1.75	0.47
4:E:25:LEU:HG	4:E:99:VAL:HA	1.97	0.47
2:B:39:PHE:HE1	2:B:67:ALA:HB1	1.80	0.46
2:B:91:THR:OG1	2:B:92:PHE:N	2.47	0.46
4:I:124:GLU:OE2	4:I:316:LYS:NZ	2.48	0.46
4:I:152:ARG:NH1	4:I:174:SER:OG	2.48	0.46
2:B:74:GLU:HA	2:B:86:VAL:HG11	1.98	0.46
4:H:164:ILE:HB	4:H:210:TYR:H	1.81	0.46
4:D:28:THR:OG1	4:D:96:GLY:N	2.46	0.46
4:G:91:LEU:HD13	4:G:223:VAL:HG11	1.97	0.46
4:E:39:LYS:HB3	4:E:43:PHE:HB2	1.97	0.46
4:E:174:SER:OG	4:E:175:LYS:N	2.48	0.46
2:B:35:HIS:O	2:B:38:LYS:NZ	2.49	0.46
3:C:31:C:OP1	4:E:255:ASN:ND2	2.41	0.46
4:G:265:TYR:OH	4:G:273:PHE:O	2.33	0.46
4:E:25:LEU:HD11	4:E:99:VAL:HG13	1.98	0.46
4:E:325:ARG:NH1	4:E:326:GLY:O	2.49	0.46
4:G:156:GLU:N	4:G:156:GLU:OE2	2.49	0.46
4:E:169:TYR:HD2	4:E:171:SER:HB3	1.79	0.46
5:J:43:PHE:HB3	5:J:165:PRO:HG3	1.98	0.46
1:A:230:SER:OG	1:A:231:LYS:NZ	2.49	0.46
4:D:199:THR:HG21	4:D:207:LEU:HB2	1.98	0.46
2:B:108:TYR:O	2:B:112:ALA:HB2	2.16	0.46
4:D:40:ARG:O	4:D:92:ARG:NH1	2.49	0.46
1:A:170:ALA:HB3	1:A:178:LYS:HE2	1.97	0.45
5:J:229:ASP:HB2	5:J:272:ARG:HD3	1.97	0.45
4:F:260:THR:HG22	4:F:276:PRO:HG3	1.98	0.45
4:G:129:ASP:N	4:G:129:ASP:OD1	2.49	0.45
4:D:103:LYS:NZ	4:D:201:ALA:O	2.42	0.45
1:A:186:GLU:HG3	1:A:189:LEU:HB2	1.99	0.45
1:A:10:LYS:HB2	1:A:143:LYS:HB3	1.97	0.45
4:D:26:ASN:O	4:D:97:ILE:HA	2.17	0.45
4:D:27:THR:HB	4:D:251:SER:HB3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:E:23:ARG:HB3	4:E:26:ASN:ND2	2.31	0.45
4:E:303:ARG:HH12	4:E:311:LEU:HD11	1.81	0.45
4:F:92:ARG:NE	4:F:94:ASP:OD1	2.45	0.45
4:F:265:TYR:HB3	4:F:291:ARG:HE	1.82	0.45
4:E:171:SER:HA	4:E:174:SER:OG	2.16	0.45
5:J:213:GLN:HE22	5:J:215:LEU:HG	1.82	0.45
1:A:187:ASP:OD1	1:A:187:ASP:N	2.49	0.45
4:E:236:LYS:HB2	4:E:236:LYS:HE2	1.78	0.45
5:J:177:LEU:HD13	5:J:180:SER:HB3	1.98	0.45
5:J:331:VAL:HA	5:J:334:ALA:HB3	1.99	0.45
4:E:123:ASP:HA	4:E:126:ILE:HD12	1.98	0.44
5:J:234:LEU:O	5:J:266:LYS:NZ	2.43	0.44
4:E:105:SER:O	4:E:105:SER:OG	2.34	0.44
5:J:232:TYR:HB3	5:J:313:GLY:H	1.82	0.44
3:C:20:U:H5'	4:G:252:GLN:HB2	1.98	0.44
5:J:260:ILE:HD11	5:J:334:ALA:HB1	2.00	0.44
3:C:35:U:O2'	4:D:21:PHE:O	2.33	0.44
5:J:241:GLU:OE1	5:J:245:VAL:HG22	2.16	0.44
3:C:37:A:H2'	4:D:252:GLN:HE21	1.82	0.44
2:B:7:ILE:HD12	2:B:7:ILE:HA	1.82	0.44
4:H:143:ALA:O	4:H:174:SER:OG	2.29	0.44
1:A:154:ILE:HB	1:A:230:SER:HB2	1.99	0.44
2:B:37:LYS:HB2	2:B:37:LYS:HE3	1.80	0.44
4:F:294:THR:OG1	4:F:295:LYS:N	2.51	0.43
2:B:103:ARG:HH11	2:B:105:GLU:HG3	1.84	0.43
4:E:258:LEU:HD23	4:E:258:LEU:HA	1.85	0.43
4:H:120:GLN:O	4:H:124:GLU:HG2	2.18	0.43
4:F:122:ILE:HG23	4:F:131:PHE:HE2	1.83	0.43
4:F:186:ASN:HB2	4:F:189:ILE:HG22	1.98	0.43
4:E:24:CYS:HB2	4:E:324:ILE:HA	2.00	0.43
4:D:37:PHE:O	4:D:216:LYS:NZ	2.46	0.43
1:A:42:LYS:HD3	1:A:42:LYS:HA	1.77	0.43
1:A:175:MET:SD	1:A:175:MET:N	2.92	0.43
4:D:301:ILE:HD12	4:D:301:ILE:HA	1.86	0.43
5:J:191:SER:OG	5:J:193:ASN:OD1	2.35	0.43
4:E:199:THR:HG21	4:E:207:LEU:HB2	2.00	0.43
4:G:49:ILE:HD13	4:G:240:LEU:HB2	2.00	0.43
1:A:55:VAL:O	1:A:241:TRP:N	2.52	0.43
2:B:163:ASP:OD1	2:B:165:LYS:NZ	2.45	0.43
4:F:293:ASP:O	4:F:299:LYS:NZ	2.52	0.43
1:A:139:ILE:HD13	1:A:139:ILE:HA	1.89	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:H:260:THR:HA	4:H:276:PRO:HA	2.01	0.43
4:I:42:THR:OG1	4:I:43:PHE:N	2.52	0.42
4:H:175:LYS:HD2	4:H:175:LYS:HA	1.81	0.42
4:G:159:GLU:OE1	4:G:171:SER:OG	2.36	0.42
4:E:32:PHE:N	4:E:247:ALA:O	2.52	0.42
4:I:25:LEU:HD12	4:I:25:LEU:HA	1.90	0.42
5:J:218:LYS:HA	5:J:218:LYS:HD2	1.80	0.42
1:A:37:ARG:HA	1:A:37:ARG:HD2	1.82	0.42
5:J:219:PHE:O	5:J:226:LYS:NZ	2.39	0.42
1:A:141:ASN:OD1	1:A:141:ASN:N	2.51	0.42
2:B:68:LEU:HB3	2:B:90:ILE:HG21	2.02	0.42
3:C:23:U:O2'	4:F:21:PHE:O	2.32	0.42
4:I:38:LEU:HD23	4:I:38:LEU:HA	1.90	0.42
4:H:15:ARG:HH22	4:H:298:TYR:HA	1.84	0.42
4:G:30:ALA:HB1	4:G:93:ILE:HG23	2.01	0.42
4:D:114:TYR:HE2	4:D:331:LYS:HZ1	1.66	0.42
4:D:163:THR:HG23	4:D:210:TYR:HD2	1.85	0.42
5:J:286:GLN:HA	5:J:289:LEU:HB2	2.01	0.42
4:I:27:THR:HG22	4:I:97:ILE:HG12	2.01	0.42
4:H:91:LEU:HD13	4:H:223:VAL:HG11	2.01	0.42
4:H:266:PRO:HD2	4:H:291:ARG:HD3	2.01	0.42
4:H:123:ASP:HA	4:H:126:ILE:HG12	2.02	0.42
4:H:196:ILE:HA	4:H:199:THR:HG22	2.01	0.42
4:E:40:ARG:HG3	4:E:214:PHE:CE2	2.55	0.42
2:B:68:LEU:HA	2:B:71:LEU:HD12	2.01	0.42
4:H:314:GLU:H	4:H:314:GLU:HG3	1.68	0.42
4:H:162:VAL:HG22	4:H:211:VAL:HG22	2.02	0.42
4:E:172:PHE:O	4:E:173:ASN:HB2	2.20	0.42
1:A:61:GLU:OE1	1:A:105:ASN:ND2	2.43	0.42
2:B:134:LYS:HE3	2:B:134:LYS:HB2	1.78	0.42
4:H:86:THR:HA	4:H:220:ALA:HB2	2.02	0.42
4:G:29:GLU:OE1	4:G:251:SER:N	2.53	0.42
4:F:166:ASP:OD1	4:F:166:ASP:N	2.51	0.42
4:E:137:ARG:HB3	4:E:261:ILE:HG21	2.02	0.42
4:D:23:ARG:NH1	4:D:26:ASN:OD1	2.53	0.42
4:H:186:ASN:HB2	4:H:189:ILE:HB	2.01	0.41
4:D:32:PHE:CG	4:D:91:LEU:HD11	2.54	0.41
4:I:289:PRO:HB2	4:I:292:PRO:HG3	2.02	0.41
1:A:70:LYS:HE2	1:A:70:LYS:HB2	1.85	0.41
4:H:299:LYS:HD3	4:H:299:LYS:HA	1.87	0.41
4:D:148:LEU:HB3	4:D:151:ASN:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:259:ARG:NH1	4:I:277:VAL:O	2.53	0.41
4:H:47:LEU:HD12	4:H:47:LEU:HA	1.89	0.41
4:H:16:PRO:HG3	4:H:114:TYR:CZ	2.56	0.41
4:F:108:SER:OG	4:F:109:CYS:N	2.53	0.41
4:E:53:ALA:H	4:D:250:HIS:CE1	2.39	0.41
4:I:15:ARG:H	4:I:331:LYS:HE2	1.85	0.41
4:I:251:SER:HA	4:I:254:ILE:HG22	2.03	0.41
4:I:307:LYS:HA	4:I:307:LYS:HD2	1.85	0.41
4:F:28:THR:HB	4:F:96:GLY:H	1.84	0.41
4:E:34:GLN:HE22	4:E:85:SER:HB2	1.84	0.41
4:E:212:THR:O	4:E:212:THR:OG1	2.30	0.41
4:I:37:PHE:HD1	4:I:90:THR:HG21	1.86	0.41
4:H:138:TYR:O	4:H:142:ILE:HD12	2.20	0.41
2:B:6:LEU:HB3	2:B:58:ILE:HG23	2.03	0.41
4:I:29:GLU:HG3	4:I:251:SER:HB3	2.03	0.41
4:E:208:ASN:OD1	4:E:208:ASN:N	2.51	0.41
1:A:183:LEU:HD21	1:A:224:LEU:HD11	2.02	0.41
2:B:8:ILE:HG23	2:B:10:PRO:HD3	2.02	0.41
2:B:88:LYS:HA	2:B:88:LYS:HD2	1.79	0.41
2:B:140:CYS:HB3	5:J:300:GLY:HA2	2.03	0.41
4:I:78:LYS:HD2	4:I:78:LYS:HA	1.75	0.41
4:H:158:ILE:HG12	4:H:215:VAL:HG13	2.03	0.41
4:H:242:LYS:HB2	4:H:242:LYS:HE2	1.90	0.41
4:G:79:SER:HB2	4:G:238:LYS:H	1.86	0.41
4:F:260:THR:HA	4:F:276:PRO:HA	2.02	0.41
4:E:162:VAL:HB	4:E:209:ILE:HD12	2.03	0.41
4:E:243:PHE:N	4:E:246:SER:O	2.52	0.41
4:D:137:ARG:HB3	4:D:261:ILE:HG21	2.02	0.41
4:I:30:ALA:HB2	4:I:95:PHE:HB3	2.03	0.41
4:G:112:TYR:O	4:G:116:THR:OG1	2.30	0.40
4:F:236:LYS:HA	4:F:236:LYS:HD3	1.85	0.40
4:E:140:ASN:HA	4:E:143:ALA:HB3	2.02	0.40
4:H:264:TRP:HB3	4:H:314:GLU:HB2	2.03	0.40
4:E:304:MET:O	4:E:306:LEU:N	2.54	0.40
4:D:34:GLN:O	4:D:45:LEU:HD12	2.20	0.40
2:B:8:ILE:HG21	2:B:16:PRO:HG3	2.03	0.40
4:H:136:LYS:HZ1	4:H:190:ASN:HA	1.86	0.40
4:F:144:ASN:HA	4:F:174:SER:HA	2.04	0.40
4:E:142:ILE:HG22	4:E:172:PHE:CE2	2.56	0.40
4:E:217:ILE:HD12	4:E:223:VAL:HG22	2.03	0.40
5:J:318:LYS:HA	5:J:318:LYS:HD3	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:LYS:HE2	1:A:123:LYS:HB2	1.81	0.40
4:I:33:TRP:CD2	4:I:44:LYS:HE2	2.56	0.40
4:G:252:GLN:H	4:G:252:GLN:HG2	1.66	0.40
4:E:234:ASP:N	4:E:234:ASP:OD1	2.54	0.40
4:D:227:GLN:HG3	4:D:229:MET:H	1.87	0.40
4:E:311:LEU:HD13	4:E:311:LEU:HA	1.95	0.40

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	A	241/255 (94%)	206 (86%)	35 (14%)	0	100	100
2	B	173/181 (96%)	155 (90%)	18 (10%)	0	100	100
4	D	289/335 (86%)	271 (94%)	18 (6%)	0	100	100
4	E	290/335 (87%)	261 (90%)	29 (10%)	0	100	100
4	F	296/335 (88%)	278 (94%)	18 (6%)	0	100	100
4	G	298/335 (89%)	276 (93%)	22 (7%)	0	100	100
4	H	293/335 (88%)	275 (94%)	18 (6%)	0	100	100
4	I	298/335 (89%)	281 (94%)	17 (6%)	0	100	100
5	J	238/344 (69%)	212 (89%)	26 (11%)	0	100	100
All	All	2416/2790 (87%)	2215 (92%)	201 (8%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	211/219 (96%)	197 (93%)	14 (7%)	16	47
2	B	156/160 (98%)	142 (91%)	14 (9%)	9	33
4	D	262/299 (88%)	248 (95%)	14 (5%)	22	54
4	E	263/299 (88%)	238 (90%)	25 (10%)	8	31
4	F	269/299 (90%)	248 (92%)	21 (8%)	12	40
4	G	270/299 (90%)	253 (94%)	17 (6%)	18	49
4	H	266/299 (89%)	243 (91%)	23 (9%)	10	36
4	I	271/299 (91%)	253 (93%)	18 (7%)	16	47
5	J	211/304 (69%)	199 (94%)	12 (6%)	20	52
All	All	2179/2477 (88%)	2021 (93%)	158 (7%)	18	43

All (158) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	TYR
1	A	68	LYS
1	A	71	ARG
1	A	97	MET
1	A	123	LYS
1	A	143	LYS
1	A	156	TYR
1	A	166	ASN
1	A	175	MET
1	A	176	LEU
1	A	178	LYS
1	A	197	LYS
1	A	206	GLU
1	A	252	CYS
2	B	1	MET
2	B	15	SER
2	B	49	ASP
2	B	82	ASP

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Mol	Chain	Res	Type
2	B	95	ASP
2	B	101	ARG
2	B	103	ARG
2	B	116	ARG
2	B	123	LEU
2	B	125	ARG
2	B	126	PRO
2	B	137	GLN
2	B	143	TYR
2	B	163	ASP
4	I	21	PHE
4	I	36	ASP
4	I	89	ASP
4	I	94	ASP
4	I	108	SER
4	I	113	ASN
4	I	136	LYS
4	I	137	ARG
4	I	150	ARG
4	I	185	ASP
4	I	219	CYS
4	I	232	ASP
4	I	243	PHE
4	I	249	MET
4	I	252	GLN
4	I	285	SER
4	I	293	ASP
4	I	315	ASP
4	H	23	ARG
4	H	81	SER
4	H	89	ASP
4	H	103	LYS
4	H	119	TYR
4	H	144	ASN
4	H	167	LYS
4	H	178	ASN
4	H	180	ASP
4	H	185	ASP
4	H	186	ASN
4	H	194	GLN
4	H	200	PHE
4	H	227	GLN

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Mol	Chain	Res	Type
4	H	278	GLU
4	H	290	PHE
4	H	295	LYS
4	H	296	SER
4	H	298	TYR
4	H	300	LEU
4	H	306	LEU
4	H	314	GLU
4	H	328	MET
4	G	21	PHE
4	G	41	HIS
4	G	89	ASP
4	G	106	MET
4	G	108	SER
4	G	119	TYR
4	G	120	GLN
4	G	152	ARG
4	G	166	ASP
4	G	174	SER
4	G	290	PHE
4	G	298	TYR
4	G	300	LEU
4	G	303	ARG
4	G	307	LYS
4	G	325	ARG
4	G	329	PHE
4	F	13	LYS
4	F	15	ARG
4	F	21	PHE
4	F	23	ARG
4	F	85	SER
4	F	114	TYR
4	F	123	ASP
4	F	125	TYR
4	F	150	ARG
4	F	178	ASN
4	F	198	ASP
4	F	219	CYS
4	F	231	PHE
4	F	251	SER
4	F	264	TRP
4	F	273	PHE

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Mol	Chain	Res	Type
4	F	299	LYS
4	F	300	LEU
4	F	309	GLU
4	F	311	LEU
4	F	320	MET
4	E	21	PHE
4	E	23	ARG
4	E	25	LEU
4	E	37	PHE
4	E	38	LEU
4	E	48	LEU
4	E	82	CYS
4	E	84	LEU
4	E	92	ARG
4	E	95	PHE
4	E	98	LYS
4	E	100	LEU
4	E	107	TYR
4	E	114	TYR
4	E	146	ARG
4	E	151	ASN
4	E	167	LYS
4	E	168	GLU
4	E	172	PHE
4	E	175	LYS
4	E	180	ASP
4	E	226	SER
4	E	233	ASP
4	E	243	PHE
4	E	293	ASP
4	D	19	LEU
4	D	29	GLU
4	D	37	PHE
4	D	45	LEU
4	D	114	TYR
4	D	136	LYS
4	D	153	LYS
4	D	207	LEU
4	D	210	TYR
4	D	221	MET
4	D	223	VAL
4	D	233	ASP

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Mol	Chain	Res	Type
4	D	273	PHE
4	D	325	ARG
5	J	61	ASP
5	J	71	ASN
5	J	141	TYR
5	J	146	PHE
5	J	157	SER
5	J	179	ARG
5	J	186	ARG
5	J	212	PHE
5	J	275	HIS
5	J	318	LYS
5	J	320	MET
5	J	322	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
4	I	141	ASN
4	G	120	GLN
4	E	26	ASN
4	E	141	ASN
5	J	328	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	C	59/60 (98%)	26 (44%)	0

All (26) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	C	3	U
3	C	9	G
3	C	10	A
3	C	13	A
3	C	14	G
3	C	15	U
3	C	18	U
3	C	20	U

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Mol	Chain	Res	Type
3	C	21	A
3	C	27	G
3	C	32	U
3	C	33	G
3	C	36	A
3	C	37	A
3	C	38	A
3	C	39	A
3	C	40	A
3	C	41	G
3	C	42	U
3	C	44	U
3	C	49	C
3	C	52	G
3	C	53	A
3	C	54	U
3	C	57	G
3	C	58	C

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 monosaccharides 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

There are no chain breaks in this entry.

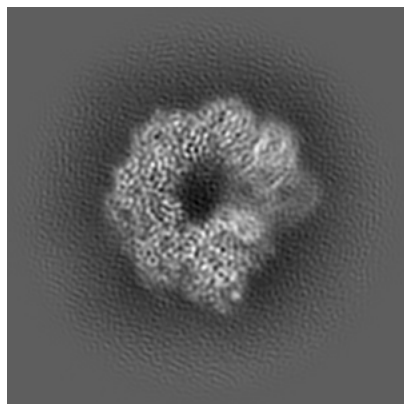
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-39285. These allow visual inspection of the internal detail of the map and identification of artifacts.

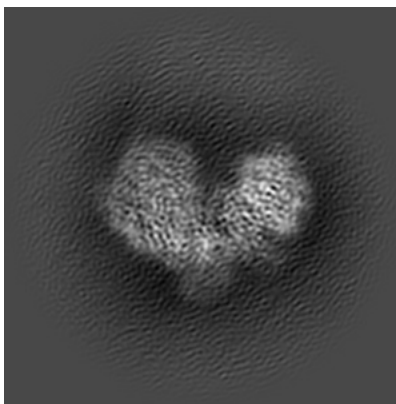
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

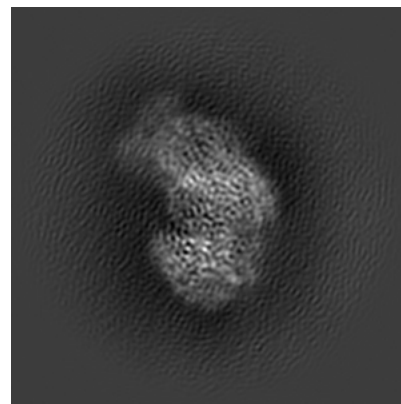
6.1.1 Primary map



X

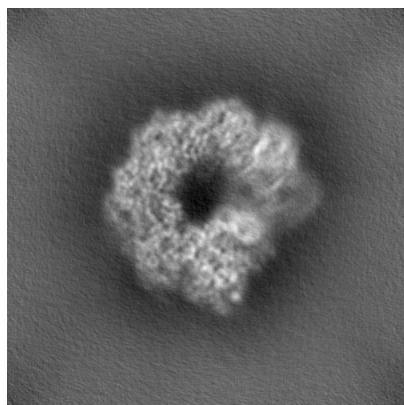


Y

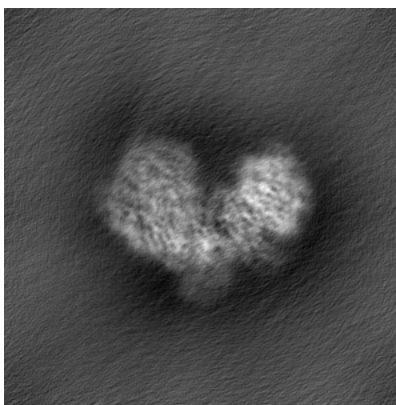


Z

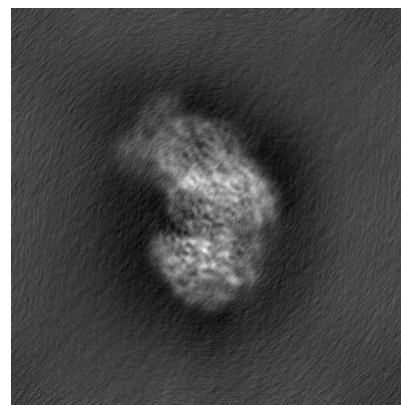
6.1.2 Raw map



X



Y

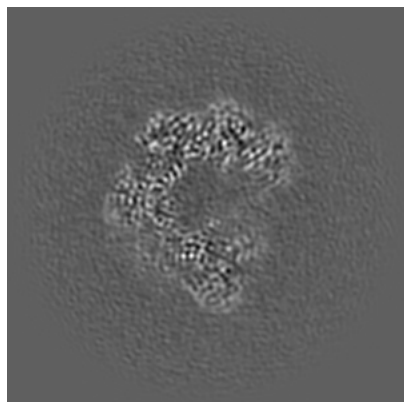


Z

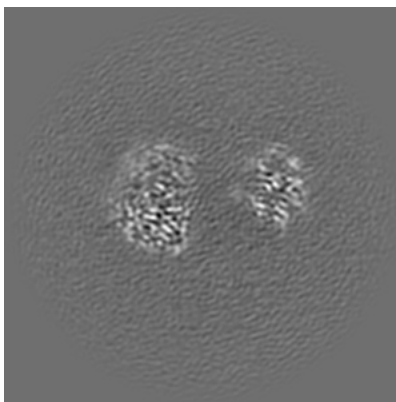
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

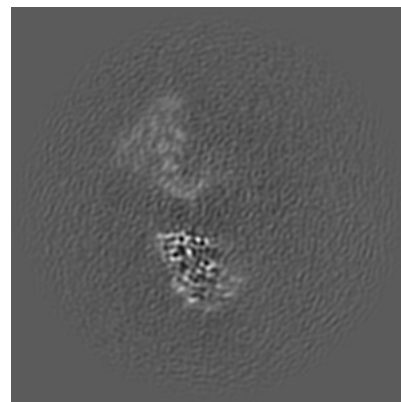
6.2.1 Primary map



X Index: 150

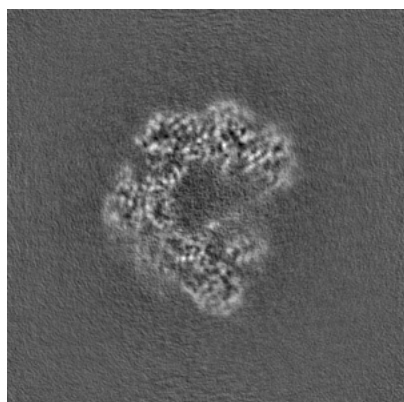


Y Index: 150

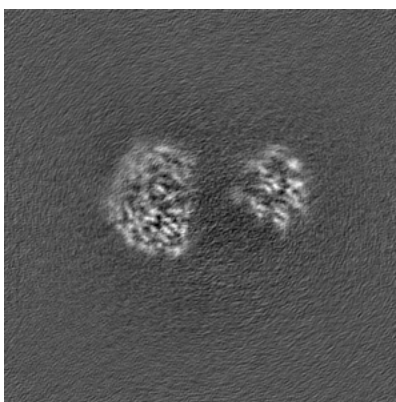


Z Index: 150

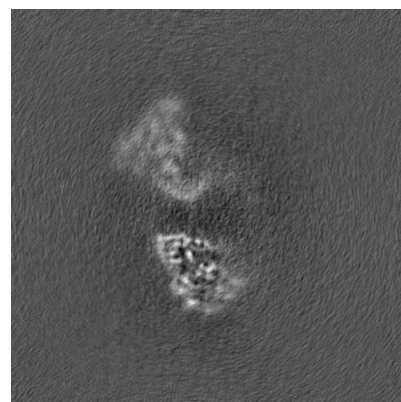
6.2.2 Raw map



X Index: 150



Y Index: 150

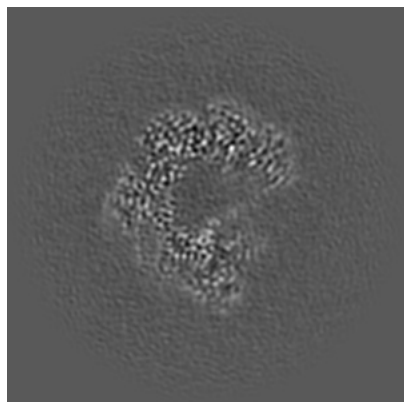


Z Index: 150

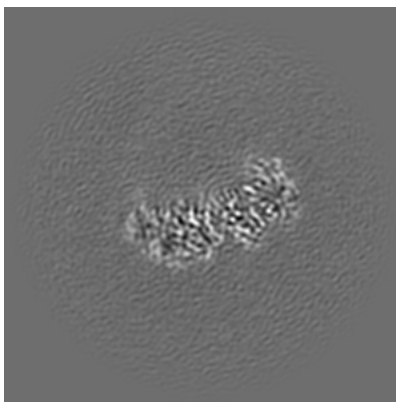
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

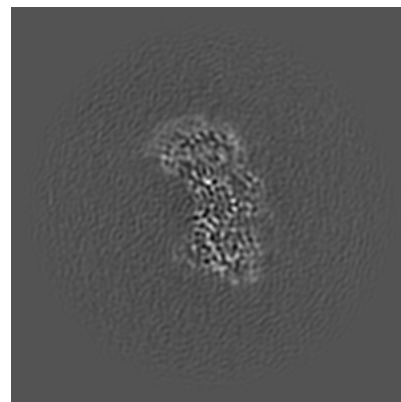
6.3.1 Primary map



X Index: 148

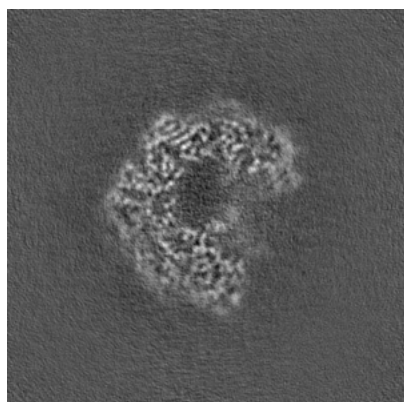


Y Index: 119

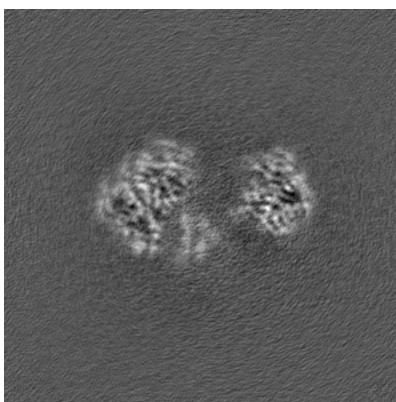


Z Index: 194

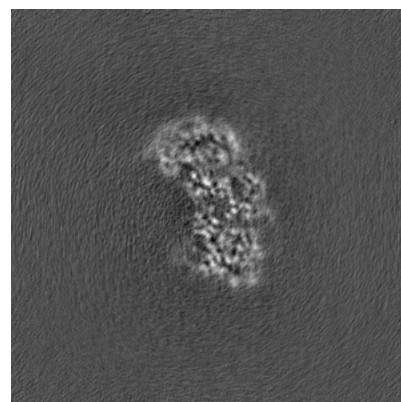
6.3.2 Raw map



X Index: 144



Y Index: 163

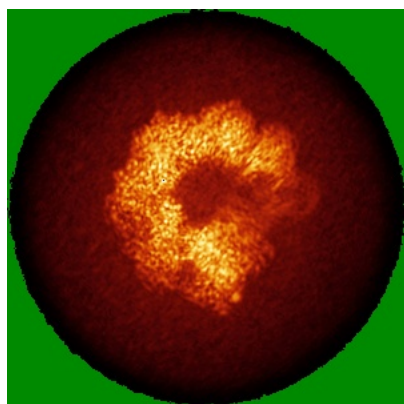


Z Index: 195

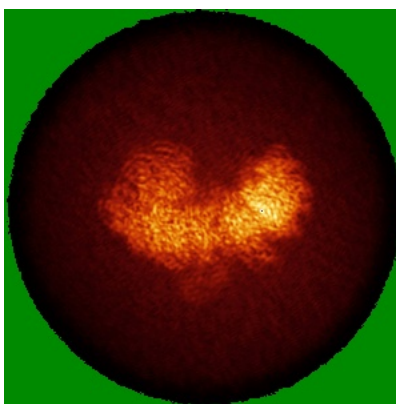
The images above show the largest variance slices of the map in three orthogonal directions.

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

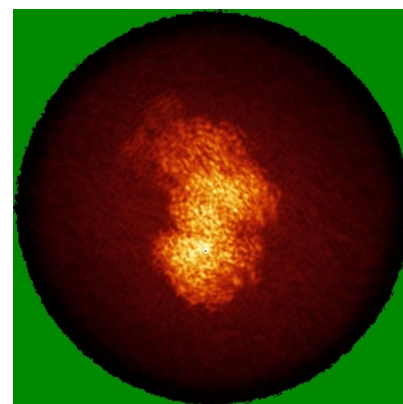
6.4.1 Primary map



X

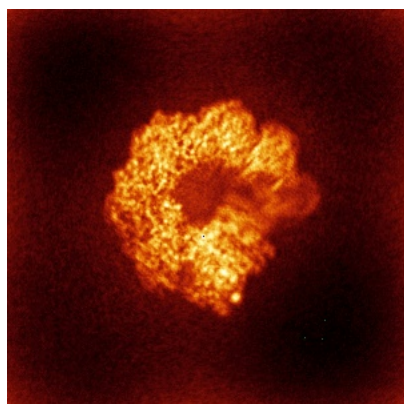


Y

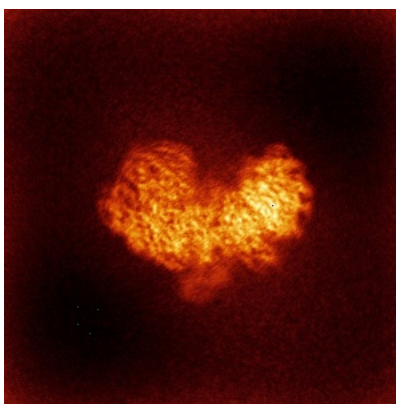


Z

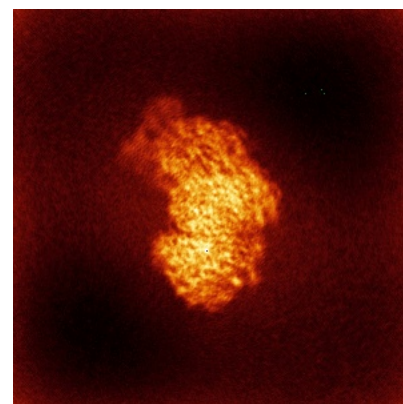
6.4.2 Raw map



X



Y

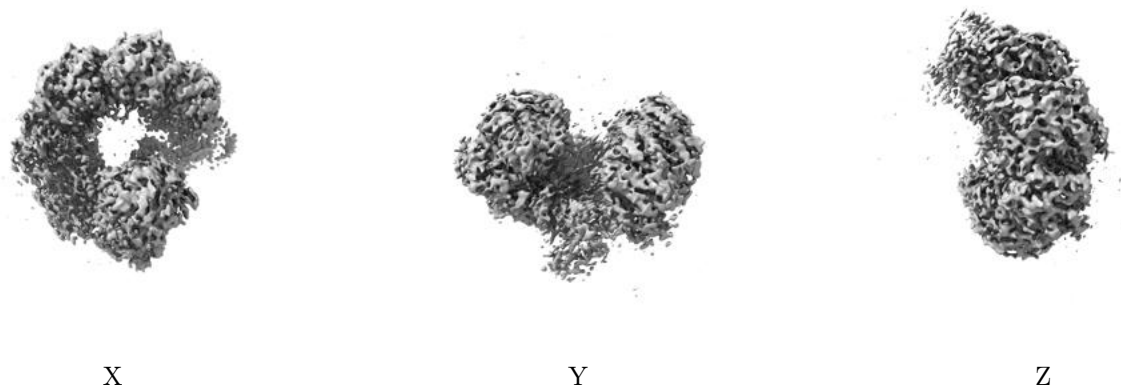


Z

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.

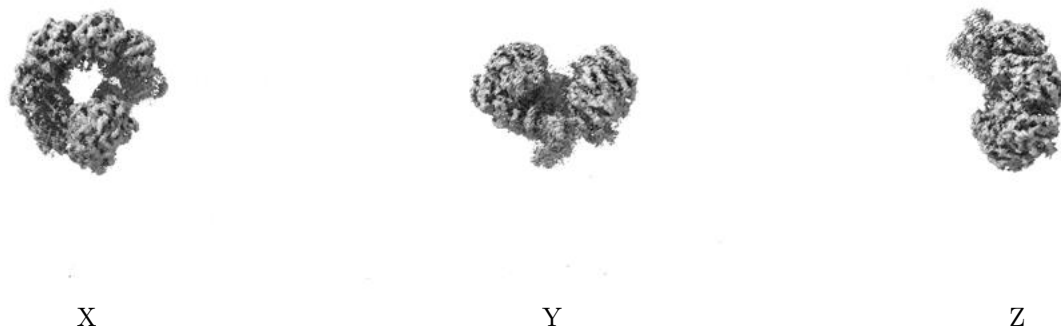
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. 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.

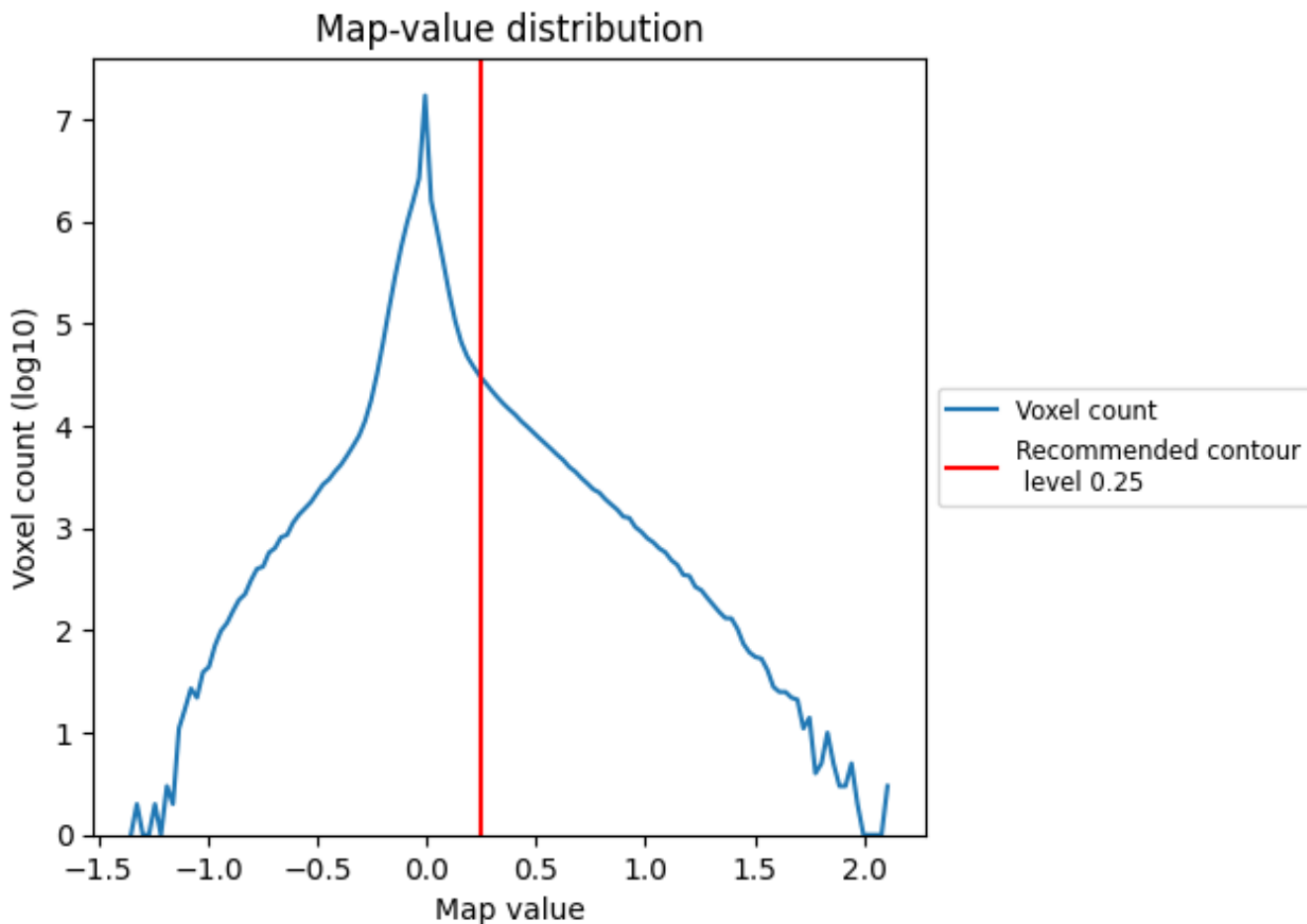
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

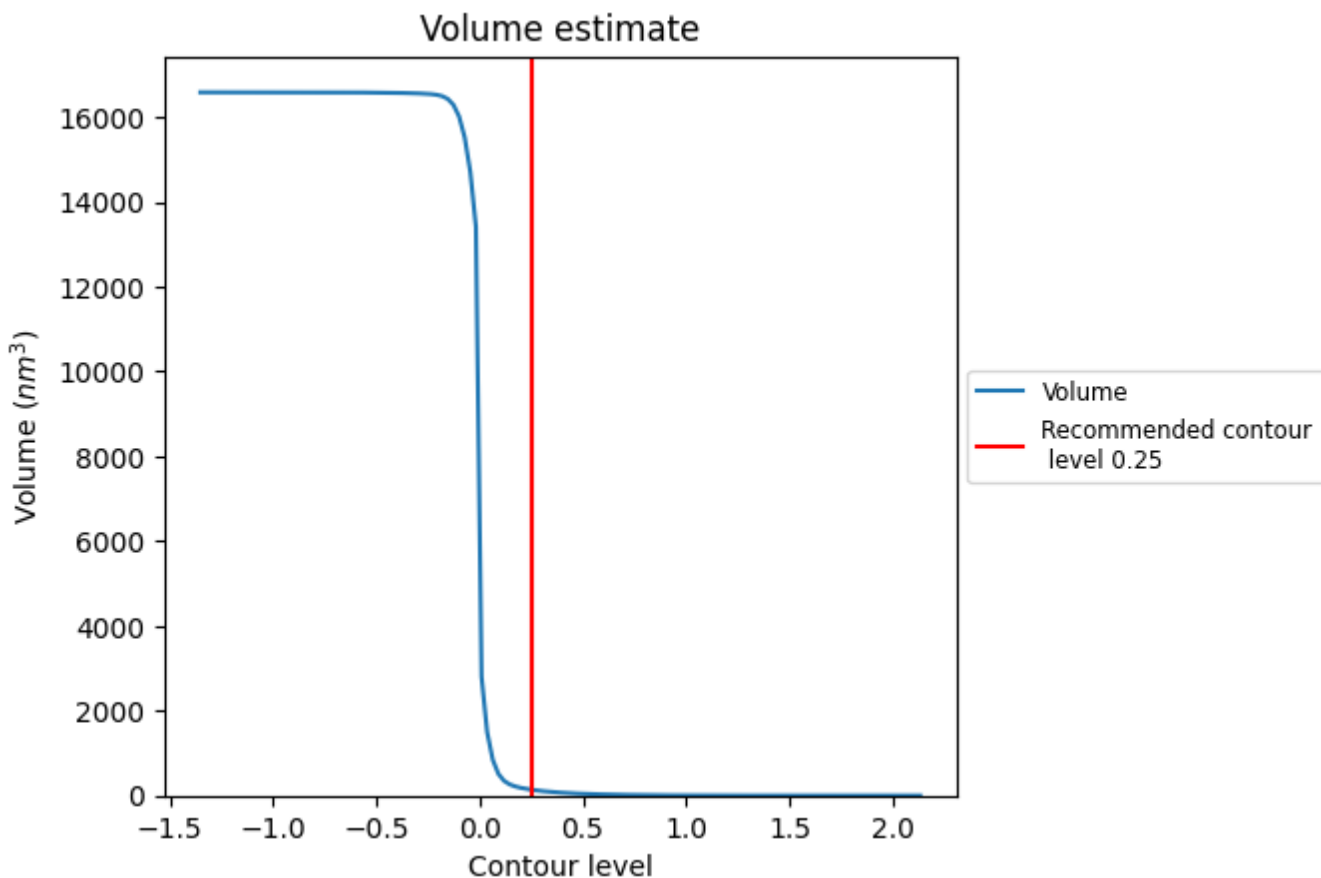
This section contains the results of statistical analysis of the map.

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.

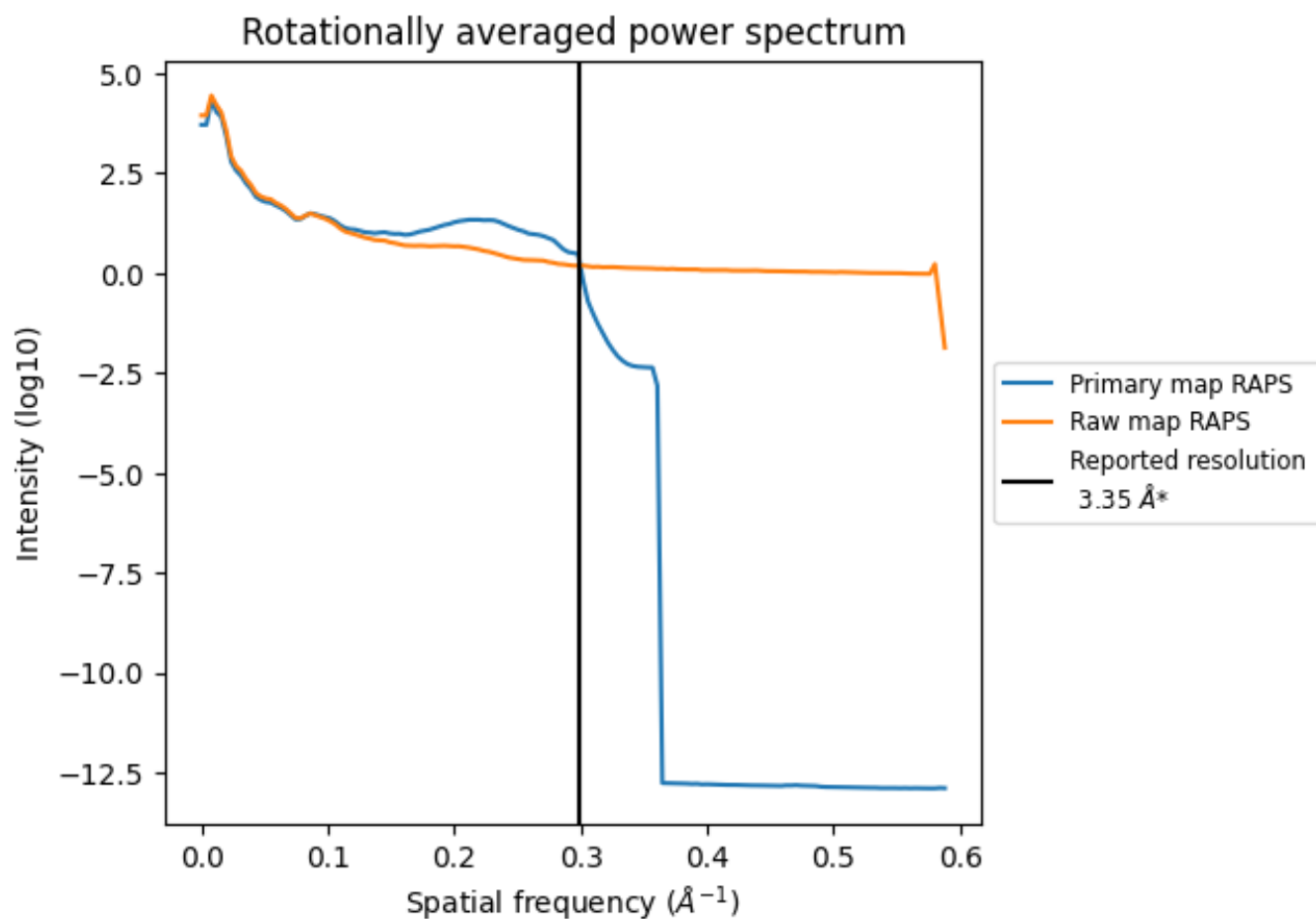
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 139 nm³; this corresponds to an approximate mass of 126 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 [i](#)

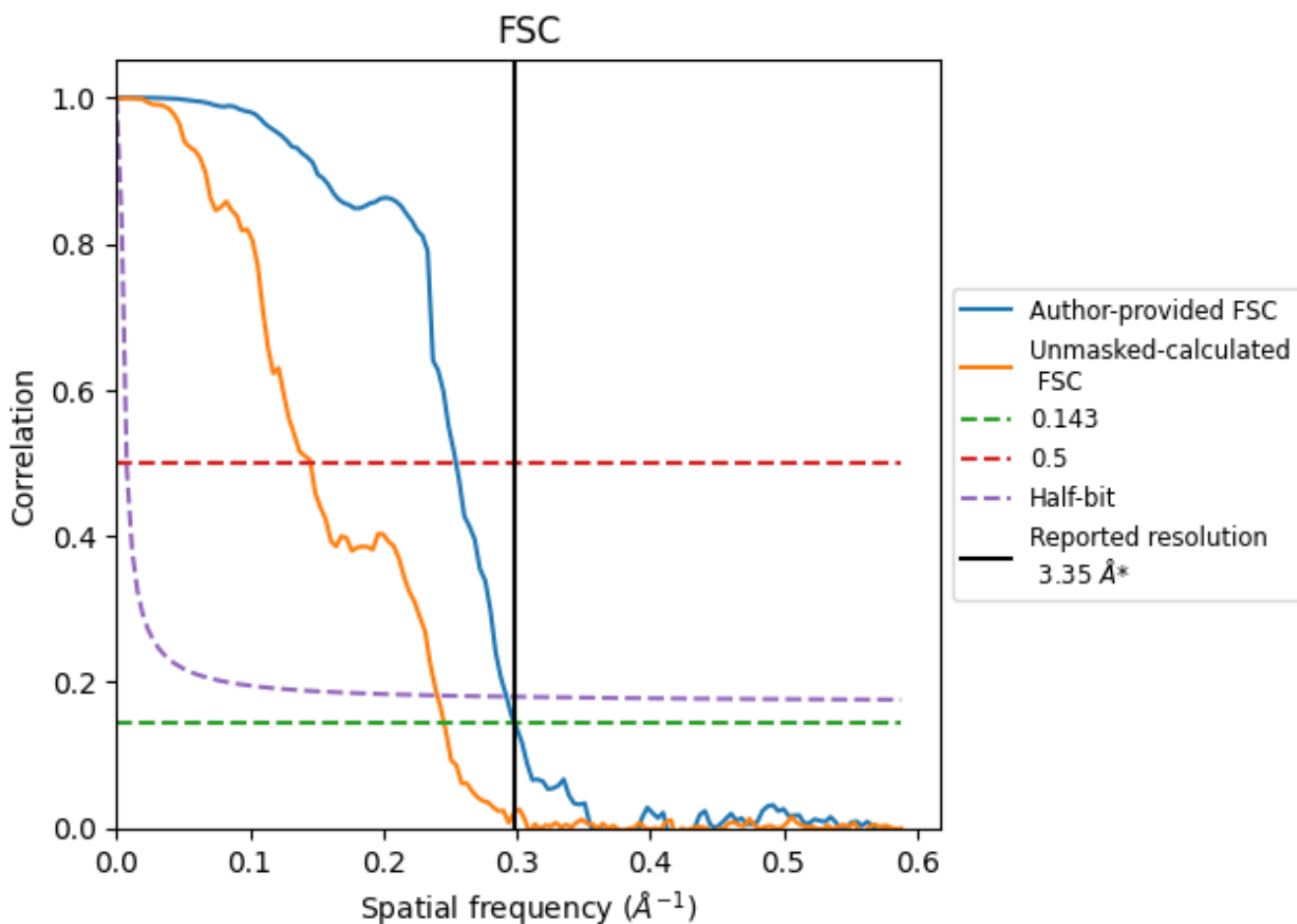


*Reported resolution corresponds to spatial frequency of 0.299 Å⁻¹

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 0.299 Å⁻¹

8.2 Resolution estimates [i](#)

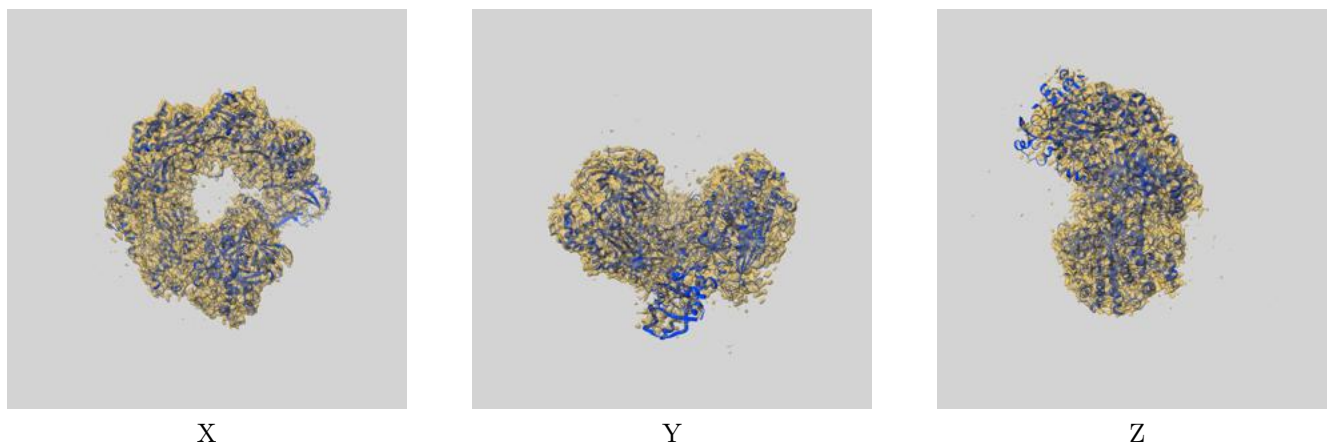
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.35	-	-
Author-provided FSC curve	3.35	3.93	3.42
Unmasked-calculated*	4.07	6.88	4.16

*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 4.07 differs from the reported value 3.35 by more than 10 %

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-39285 and PDB model 8YH9. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



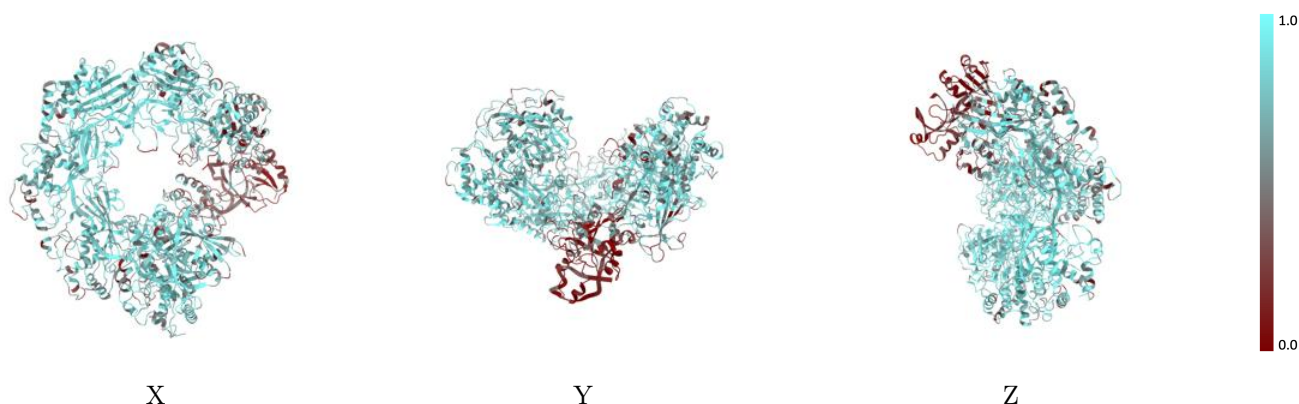
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



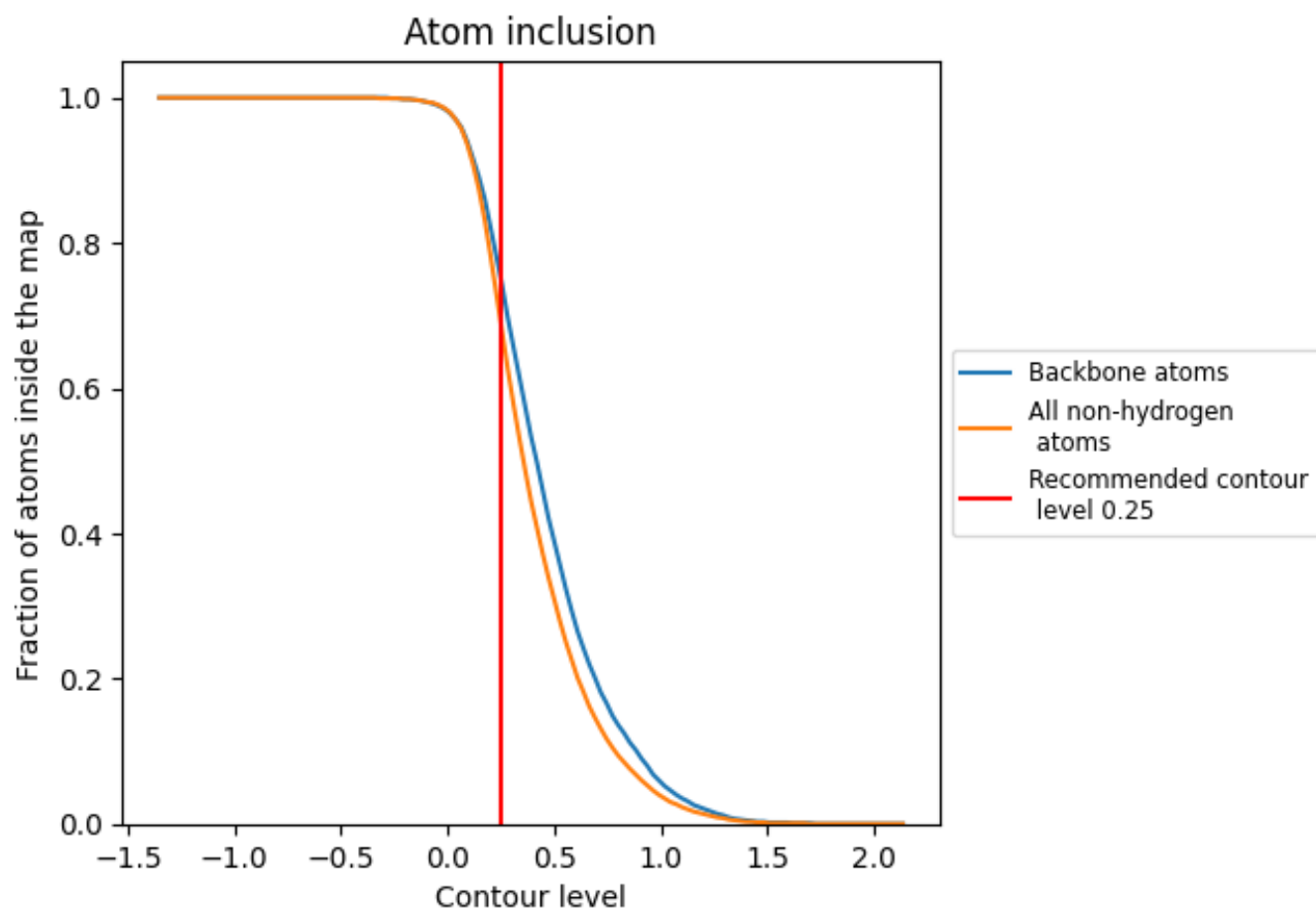
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).























9.4 Atom inclusion [i](#)



At the recommended contour level, 75% of all backbone atoms, 69% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6870	 0.4060
A	 0.7100	 0.4200
B	 0.2280	 0.2750
C	 0.6120	 0.3600
D	 0.6150	 0.3630
E	 0.7420	 0.3980
F	 0.8120	 0.4610
G	 0.7650	 0.4410
H	 0.7490	 0.4360
I	 0.7960	 0.4600
J	 0.6000	 0.3590

