



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 04:09 PM UTC

PDB ID : 9IRF / pdb_00009irf
EMDB ID : EMD-60812
Title : Cryo-EM Structure of csy1-4 with crRNA
Authors : Gao, X.; Cui, S.; Zhu, H.; Zhu, K.; Shang, K.
Deposited on : 2024-07-15
Resolution : 2.80 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.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

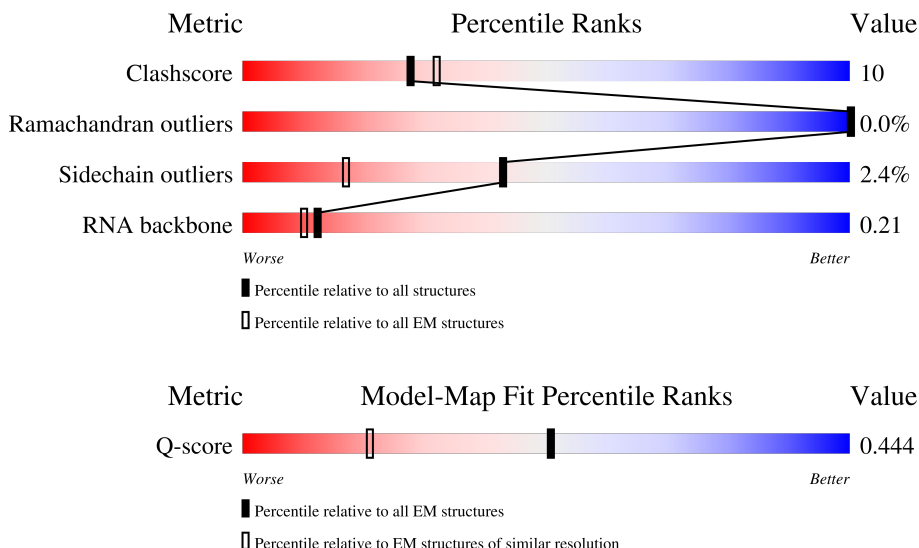
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



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

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

Mol	Chain	Length	Quality of chain
1	A	310	
2	B	184	
3	C	337	

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Mol	Chain	Length	Quality of chain
3	D	337	90% 7%
3	E	337	88% 9%
3	F	337	5% 84% 14%
3	G	337	5% 80% 17%
3	H	337	76% 13% 11%
4	I	87	22% 28% 16% 32%
5	J	443	21% 31% 24% 44%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 22171 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-associated protein Csy2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	295	Total	C	N	O	S	0	0
			2329	1469	420	427	13		

- Molecule 2 is a protein called CRISPR-associated endonuclease Cas6f/Csy4.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	184	Total	C	N	O	S	0	0
			1438	912	261	261	4		

- Molecule 3 is a protein called CRISPR-associated protein Csy3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	330	Total	C	N	O	S	0	0
			2559	1614	448	493	4		
3	D	330	Total	C	N	O	S	0	0
			2559	1614	448	493	4		
3	E	331	Total	C	N	O	S	0	0
			2566	1618	449	495	4		
3	F	331	Total	C	N	O	S	0	0
			2566	1618	449	495	4		
3	G	328	Total	C	N	O	S	0	0
			2542	1602	445	491	4		
3	H	301	Total	C	N	O	S	0	0
			2340	1480	406	450	4		

- Molecule 4 is a RNA chain called crRNA (87-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
4	I	59	Total	C	N	O	P	0	0
			1244	555	228	403	58		

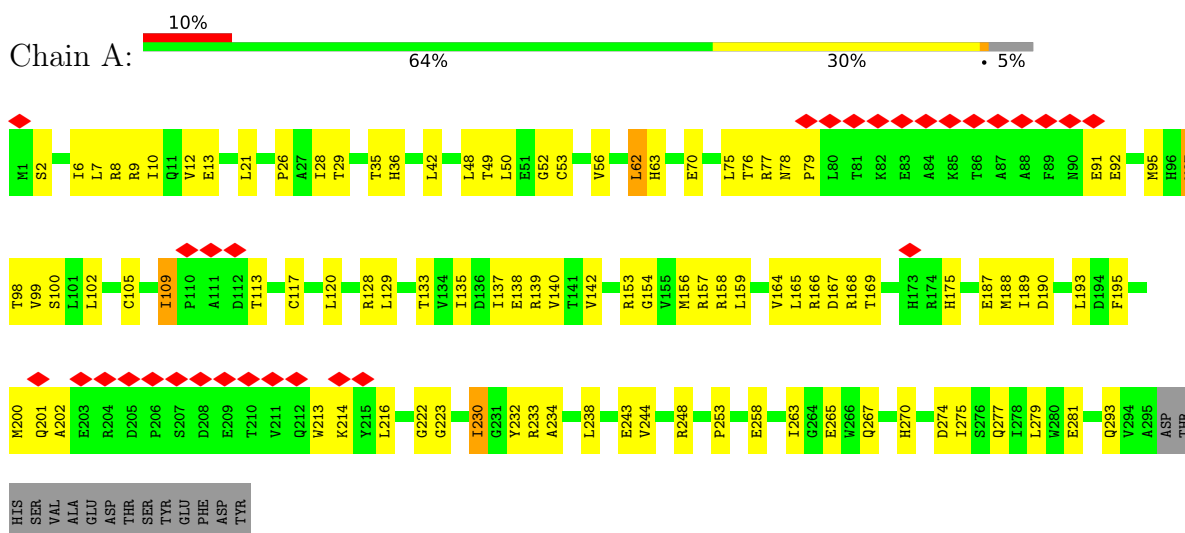
- Molecule 5 is a protein called CRISPR-associated protein Csy1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	247	Total	C	N	O	S	0	0
			2028	1272	379	373	4		

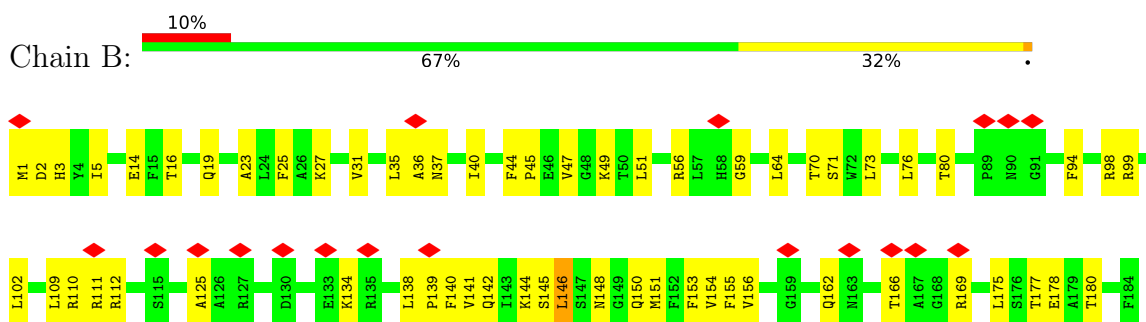
3 Residue-property plots

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.

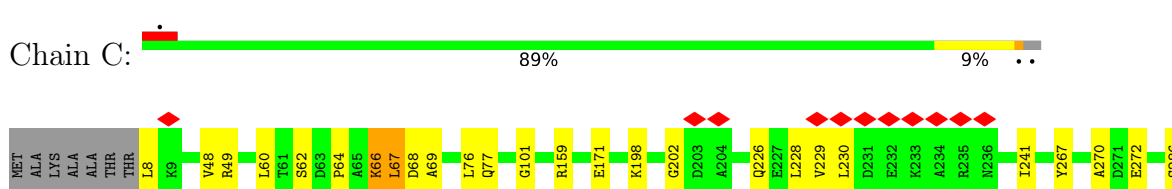
• Molecule 1: CRISPR-associated protein Csy2

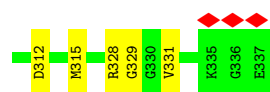


• Molecule 2: CRISPR-associated endonuclease Cas6f/Csy4



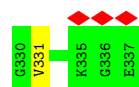
• Molecule 3: CRISPR-associated protein Csy3





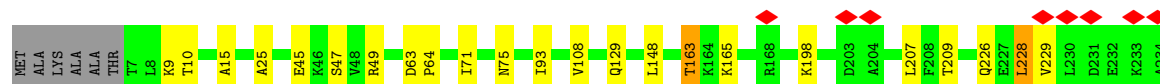
• Molecule 3: CRISPR-associated protein Csy3

Chain D: 90% 7%



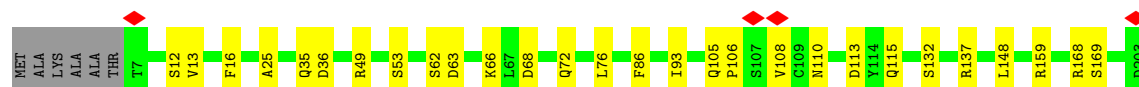
• Molecule 3: CRISPR-associated protein Csy3

Chain E: 88% 9%



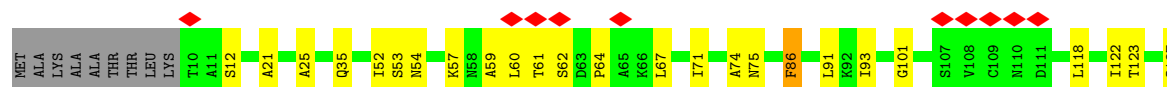
• Molecule 3: CRISPR-associated protein Csy3

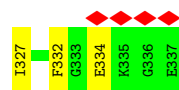
Chain F: 5% 84% 14%



• Molecule 3: CRISPR-associated protein Csy3

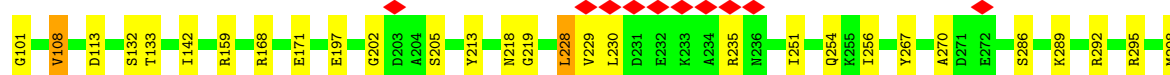
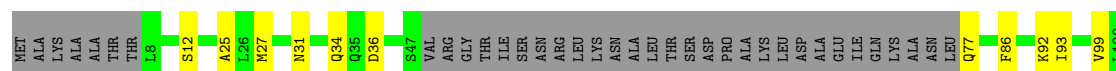
Chain G: 5% 80% 17%





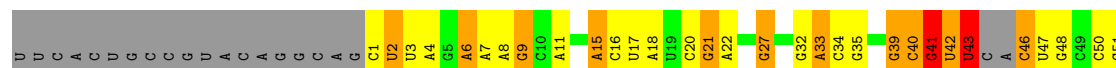
• Molecule 3: CRISPR-associated protein Csy3

Chain H: 76% 13% 11%



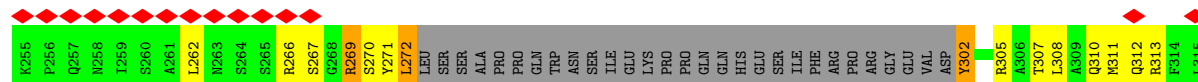
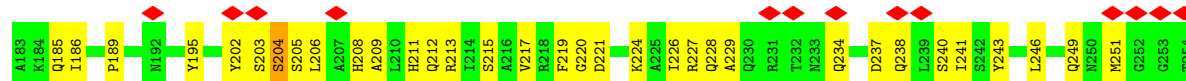
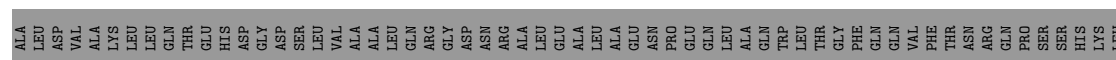
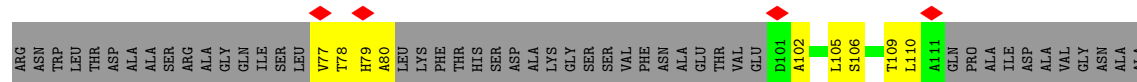
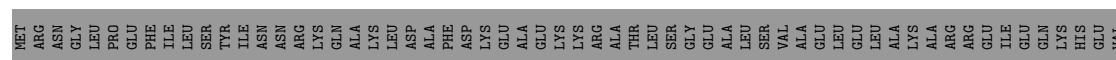
• Molecule 4: crRNA (87-MER)

Chain I: 22% 28% 16% 32%



• Molecule 5: CRISPR-associated protein Csy1

Chain J: 21% 31% 24% 44%



A387	G388	D389	W390	Q391	V394	A395	Y396	R400	W401	L402	W403	R404	R405	L406	K407	H408	E409	W410	L411	I412	F413	G414	E415	V416	E417	R418	R419	E420	W421	S422	T423	A424	A425	L426	F427	K428	R429	R430	M431	R432	E433	M434	E435	S436	A437	L438	K439	E440	E441	L442	A443
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	71806	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 ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	2500	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.987	Depositor
Minimum map value	-0.002	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.03	Depositor
Map size ($\text{\AA}$)	300.0, 300.0, 300.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.75, 0.75, 0.75	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	A	0.19	0/2385	0.54	2/3235 (0.1%)
2	B	0.15	0/1468	0.42	0/1984
3	C	0.25	0/2606	0.35	1/3532 (0.0%)
3	D	0.13	0/2606	0.33	1/3532 (0.0%)
3	E	0.13	0/2613	0.31	0/3542
3	F	0.13	0/2613	0.32	0/3542
3	G	0.21	0/2589	0.49	2/3510 (0.1%)
3	H	0.15	0/2385	0.36	1/3232 (0.0%)
4	I	0.51	2/1391 (0.1%)	0.77	12/2167 (0.6%)
5	J	0.66	6/2069 (0.3%)	0.76	7/2792 (0.3%)
All	All	0.29	8/22725 (0.0%)	0.48	26/31068 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
5	J	0	1

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	J	302	TYR	CA-C	-17.57	1.16	1.52
5	J	302	TYR	N-CA	-15.76	1.16	1.46
4	I	40	C	O3'-P	-9.78	1.46	1.61
5	J	302	TYR	CA-CB	-8.93	1.35	1.53
5	J	302	TYR	CB-CG	-7.64	1.34	1.51
5	J	302	TYR	C-N	6.54	1.43	1.33
5	J	302	TYR	C-O	-5.95	1.11	1.23
4	I	46	C	O3'-P	-5.63	1.52	1.61

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	302	TYR	CA-C-N	-16.94	91.85	121.66
5	J	302	TYR	C-N-CA	-16.94	91.85	121.66
3	G	294	PRO	CA-N-CD	-12.84	94.03	112.00
4	I	41	G	C2'-C3'-O3'	-11.27	96.80	113.70
4	I	41	G	C4'-C3'-O3'	11.18	129.77	113.00
4	I	46	C	O5'-P-OP1	-9.37	79.90	108.00
1	A	97	MET	CB-CG-SD	8.84	139.21	112.70
1	A	97	MET	CA-CB-CG	8.68	131.45	114.10
4	I	41	G	N9-C1'-C2'	-7.57	100.65	112.00
3	G	294	PRO	N-CD-CG	-7.25	92.32	103.20
4	I	46	C	C1'-C2'-O2'	7.04	118.96	108.40
4	I	46	C	P-O5'-C5'	-6.68	110.88	120.90
4	I	46	C	O5'-P-OP2	6.67	128.02	108.00
5	J	302	TYR	N-CA-C	-6.28	93.42	111.00
4	I	43	U	C3'-C2'-O2'	-6.26	105.22	114.60
5	J	302	TYR	N-CA-CB	-5.97	100.34	110.50
5	J	267	SER	N-CA-C	-5.96	105.27	113.56
5	J	302	TYR	CB-CA-C	-5.72	99.23	110.10
3	C	69	ALA	N-CA-C	-5.58	106.15	113.12
4	I	46	C	O4'-C4'-C3'	-5.49	98.52	104.00
3	H	314	PRO	CA-N-CD	-5.46	104.36	112.00
3	D	149	TRP	CB-CA-C	-5.36	110.38	116.54
4	I	46	C	C1'-O4'-C4'	-5.22	104.68	109.90
4	I	41	G	O5'-P-OP2	-5.13	92.62	108.00
5	J	302	TYR	CA-C-O	-5.12	112.09	120.80
4	I	43	U	C1'-C2'-O2'	-5.05	104.22	111.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	J	204	SER	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2329	0	2287	92	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1438	0	1462	49	0
3	C	2559	0	2531	25	0
3	D	2559	0	2531	20	0
3	E	2566	0	2538	23	0
3	F	2566	0	2538	35	0
3	G	2542	0	2507	46	0
3	H	2340	0	2296	33	0
4	I	1244	0	625	66	0
5	J	2028	0	1984	105	0
All	All	22171	0	21299	420	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 10.

All (420) 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:233:ARG:HH22	5:J:106:SER:HB2	1.38	0.88
3:G:315:MET:HE2	3:G:315:MET:H	1.40	0.87
5:J:302:TYR:HA	5:J:305:ARG:NE	1.91	0.85
5:J:302:TYR:HA	5:J:305:ARG:HE	1.41	0.82
3:H:315:MET:H	3:H:315:MET:HE2	1.42	0.81
1:A:201:GLN:HB3	1:A:216:LEU:HD21	1.62	0.80
4:I:51:G:O2'	4:I:55:A:N6	2.15	0.79
5:J:110:LEU:HD23	5:J:206:LEU:HD13	1.63	0.79
1:A:190:ASP:OD1	5:J:213:ARG:NH1	2.18	0.77
3:C:76:LEU:HD21	3:H:228:LEU:HG	1.65	0.76
3:G:261:ARG:NH2	4:I:8:A:OP2	2.18	0.76
1:A:187:GLU:HG2	1:A:189:ILE:HG22	1.66	0.76
2:B:138:LEU:HD12	2:B:139:PRO:HD2	1.68	0.76
1:A:12:VAL:HG13	1:A:97:MET:HB3	1.68	0.76
5:J:226:ILE:HD11	5:J:238:GLN:HB2	1.68	0.75
4:I:41:G:H2'	4:I:42:U:O5'	1.87	0.74
1:A:7:LEU:HD22	1:A:140:VAL:HG22	1.69	0.74
2:B:153:PHE:HZ	4:I:43:U:H2'	1.53	0.73
1:A:265:GLU:HG3	1:A:267:GLN:HE22	1.54	0.73
2:B:148:ASN:HD21	4:I:60:G:H21	1.37	0.72
1:A:158:ARG:H	1:A:158:ARG:HE	1.38	0.72
4:I:43:U:OP2	4:I:43:U:C4	2.42	0.72
3:F:49:ARG:HH11	4:I:21:G:H1'	1.55	0.72
1:A:42:LEU:HD12	1:A:50:LEU:HD11	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:MET:HE2	1:A:200:MET:HA	1.73	0.69
3:C:228:LEU:HD11	3:D:76:LEU:HB3	1.74	0.69
3:C:272:GLU:N	3:C:272:GLU:OE1	2.26	0.69
2:B:150:GLN:N	2:B:150:GLN:OE1	2.27	0.68
2:B:109:LEU:HD23	2:B:109:LEU:H	1.59	0.67
3:C:68:ASP:OD2	3:H:289:LYS:HA	1.94	0.67
5:J:305:ARG:NH1	5:J:305:ARG:HB2	2.09	0.67
3:F:12:SER:OG	3:F:110:ASN:ND2	2.29	0.66
1:A:274:ASP:HB3	1:A:277:GLN:HE22	1.58	0.66
1:A:281:GLU:OE2	1:A:281:GLU:N	2.28	0.66
3:D:165:LYS:HD2	3:D:207:LEU:HD23	1.78	0.66
4:I:40:C:C3'	4:I:41:G:H5'	2.26	0.65
3:H:315:MET:HE2	3:H:315:MET:N	2.12	0.65
5:J:302:TYR:HD1	5:J:305:ARG:HH21	1.41	0.65
5:J:364:ARG:H	5:J:364:ARG:HE	1.45	0.65
4:I:43:U:OP2	4:I:43:U:C5	2.50	0.64
3:F:285:THR:HG21	3:G:74:ALA:HB2	1.80	0.64
2:B:25:PHE:HD2	2:B:141:VAL:HG11	1.62	0.64
5:J:305:ARG:HB2	5:J:305:ARG:HH11	1.62	0.64
3:F:13:VAL:HB	3:F:110:ASN:HB3	1.79	0.64
3:H:86:PHE:O	3:H:218:ASN:ND2	2.22	0.64
3:H:228:LEU:HD11	3:H:230:LEU:HG	1.80	0.64
3:C:64:PRO:HD3	3:H:295:ARG:NH2	2.13	0.64
1:A:12:VAL:HG23	1:A:133:THR:C	2.23	0.63
1:A:277:GLN:OE1	1:A:277:GLN:N	2.21	0.63
3:G:35:GLN:OE1	3:G:159:ARG:NH2	2.32	0.63
3:G:298:MET:HA	3:G:298:MET:HE3	1.81	0.63
1:A:10:ILE:HG13	1:A:137:ILE:HG12	1.81	0.63
5:J:328:ARG:O	5:J:332:LEU:HD23	1.99	0.62
5:J:79:HIS:N	5:J:203:SER:O	2.32	0.62
1:A:154:GLY:O	1:A:158:ARG:NH2	2.32	0.62
3:G:12:SER:O	3:G:334:GLU:N	2.33	0.62
1:A:265:GLU:HG3	1:A:267:GLN:NE2	2.14	0.61
4:I:41:G:C8	4:I:42:U:C4	2.88	0.61
2:B:45:PRO:HG3	2:B:56:ARG:HE	1.66	0.61
3:E:226:GLN:HB2	4:I:22:A:OP2	2.01	0.61
5:J:431:MET:HE3	5:J:431:MET:HA	1.82	0.61
1:A:168:ARG:HB2	1:A:263:ILE:HG22	1.83	0.61
5:J:434:MET:HE3	5:J:434:MET:HA	1.81	0.61
4:I:46:C:N4	4:I:60:G:N1	2.48	0.60
1:A:274:ASP:OD1	1:A:275:ILE:N	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:428:LYS:O	5:J:432:ARG:HG2	2.02	0.60
3:H:229:VAL:O	3:H:235:ARG:NH1	2.34	0.60
1:A:42:LEU:HD11	1:A:120:LEU:HD13	1.82	0.60
1:A:92:GLU:N	1:A:92:GLU:OE2	2.34	0.60
2:B:14:GLU:N	2:B:14:GLU:OE2	2.34	0.60
2:B:156:VAL:HG23	2:B:175:LEU:HD11	1.82	0.60
3:D:315:MET:HE3	3:D:316:PRO:HD2	1.83	0.60
2:B:153:PHE:CZ	4:I:43:U:H2'	2.35	0.60
3:E:45:GLU:OE2	3:E:238:LYS:NZ	2.31	0.60
1:A:188:MET:HE2	5:J:102:ALA:HB3	1.85	0.59
3:G:61:THR:HA	3:G:67:LEU:HD22	1.85	0.59
5:J:378:ASP:HB3	5:J:381:PHE:HB2	1.83	0.59
1:A:8:ARG:NH2	1:A:158:ARG:O	2.35	0.59
1:A:2:SER:HA	1:A:105:CYS:O	2.03	0.59
3:F:108:VAL:HG13	3:G:286:SER:HB2	1.84	0.59
5:J:79:HIS:HB3	5:J:206:LEU:HB3	1.85	0.59
4:I:46:C:N4	4:I:60:G:H1	2.01	0.58
4:I:56:G:O2'	4:I:57:G:OP1	2.22	0.58
4:I:42:U:O3'	4:I:43:U:C2	2.55	0.58
1:A:258:GLU:OE1	5:J:78:THR:OG1	2.18	0.58
2:B:111:ARG:NH2	4:I:48:G:OP2	2.36	0.58
5:J:310:GLN:HG2	5:J:311:MET:HE2	1.85	0.58
5:J:311:MET:SD	5:J:334:TYR:HB3	2.43	0.58
5:J:220:GLY:O	5:J:224:LYS:HE2	2.04	0.57
5:J:362:LEU:HB3	5:J:366:GLN:HB2	1.86	0.57
2:B:111:ARG:HH22	4:I:47:U:H5'	1.68	0.57
3:F:314:PRO:HG2	3:F:319:GLN:HG2	1.85	0.57
3:G:293:GLN:HG3	3:G:294:PRO:HD3	1.85	0.57
2:B:16:THR:OG1	2:B:19:GLN:OE1	2.20	0.57
3:F:93:ILE:HD12	3:F:148:LEU:HD23	1.86	0.57
3:G:318:GLN:O	3:G:322:VAL:HG23	2.04	0.57
5:J:77:VAL:O	5:J:205:SER:HB3	2.05	0.57
5:J:209:ALA:O	5:J:213:ARG:HG2	2.05	0.57
5:J:237:ASP:OD1	5:J:237:ASP:N	2.38	0.57
1:A:167:ASP:OD1	1:A:169:THR:HG23	2.05	0.57
2:B:94:PHE:O	2:B:162:GLN:N	2.28	0.57
1:A:166:ARG:NH1	1:A:277:GLN:O	2.38	0.57
4:I:43:U:C6	4:I:43:U:O5'	2.58	0.57
1:A:157:ARG:HG3	1:A:158:ARG:HD3	1.87	0.57
1:A:166:ARG:HD3	1:A:267:GLN:HG2	1.87	0.56
2:B:71:SER:O	2:B:71:SER:OG	2.23	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:MET:SD	1:A:188:MET:N	2.78	0.56
5:J:78:THR:OG1	5:J:79:HIS:N	2.38	0.56
3:E:165:LYS:HD3	3:E:207:LEU:HD23	1.87	0.56
2:B:145:SER:OG	2:B:148:ASN:OD1	2.22	0.56
1:A:77:ARG:NH1	1:A:78:ASN:O	2.38	0.56
3:F:295:ARG:HH22	3:G:62:SER:C	2.14	0.56
4:I:41:G:H1'	4:I:42:U:O2	2.05	0.56
2:B:142:GLN:OE1	4:I:43:U:H1'	2.07	0.55
5:J:435:GLU:HA	5:J:438:LEU:HD12	1.88	0.55
2:B:1:MET:HG2	2:B:59:GLY:HA2	1.87	0.55
1:A:79:PRO:HD3	4:I:7:A:H1'	1.87	0.55
1:A:277:GLN:O	1:A:293:GLN:NE2	2.39	0.55
3:G:52:ILE:O	3:G:52:ILE:HD12	2.06	0.55
2:B:109:LEU:HD12	4:I:54:C:H5'	1.88	0.55
5:J:249:GLN:HB3	5:J:270:SER:OG	2.06	0.55
2:B:178:GLU:N	2:B:178:GLU:OE1	2.40	0.55
5:J:432:ARG:NH2	5:J:435:GLU:HG2	2.22	0.54
5:J:79:HIS:HA	5:J:204:SER:HA	1.87	0.54
3:E:163:THR:HG23	3:E:209:THR:HB	1.89	0.54
3:F:229:VAL:HG11	3:F:234:ALA:HB3	1.89	0.54
3:G:137:ARG:NH1	3:G:265:ASP:OD2	2.34	0.54
3:H:99:VAL:O	3:H:205:SER:HA	2.08	0.54
1:A:166:ARG:HG3	1:A:267:GLN:NE2	2.23	0.54
1:A:248:ARG:NH2	4:I:2:U:OP2	2.41	0.53
3:C:226:GLN:HB2	4:I:34:C:OP2	2.08	0.53
4:I:39:G:H2'	4:I:40:C:O4'	2.07	0.53
3:E:93:ILE:HD12	3:E:148:LEU:HD23	1.90	0.53
5:J:362:LEU:O	5:J:367:GLN:NE2	2.41	0.53
3:C:198:LYS:NZ	3:C:198:LYS:HB3	2.24	0.53
3:F:63:ASP:HB3	3:F:66:LYS:HG3	1.91	0.53
3:H:77:GLN:OE1	3:H:77:GLN:HA	2.09	0.53
3:F:297:LYS:HB2	3:F:297:LYS:NZ	2.23	0.53
4:I:40:C:H3'	4:I:41:G:H5'	1.90	0.53
5:J:80:ALA:HA	5:J:202:TYR:CD1	2.43	0.53
3:G:101:GLY:HA3	3:G:202:GLY:HA2	1.91	0.53
5:J:364:ARG:HD2	5:J:365:ALA:N	2.24	0.53
5:J:404:ARG:HA	5:J:407:LYS:HB2	1.91	0.53
1:A:97:MET:HE2	1:A:129:LEU:HD22	1.91	0.52
1:A:193:LEU:HD11	5:J:243:TYR:OH	2.09	0.52
3:D:228:LEU:HB3	3:E:47:SER:HB3	1.92	0.52
4:I:51:G:N2	4:I:54:C:OP2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:150:ARG:NH1	4:I:11:A:OP1	2.42	0.52
5:J:211:HIS:CG	5:J:266:ARG:HD2	2.44	0.52
5:J:342:LEU:O	5:J:346:VAL:HG23	2.10	0.52
1:A:26:PRO:HD3	1:A:95:MET:HE1	1.90	0.52
3:C:228:LEU:HD13	4:I:33:A:C5	2.45	0.52
5:J:219:PHE:HA	5:J:224:LYS:NZ	2.24	0.52
3:G:159:ARG:NH1	3:G:171:GLU:OE2	2.42	0.51
1:A:158:ARG:H	1:A:158:ARG:NE	2.07	0.51
5:J:246:LEU:HD23	5:J:271:TYR:HD2	1.75	0.51
1:A:53:CYS:HA	1:A:102:LEU:O	2.11	0.51
2:B:112:ARG:HH22	4:I:50:C:H5	1.58	0.51
5:J:213:ARG:O	5:J:217:VAL:HG23	2.11	0.51
5:J:224:LYS:HA	5:J:227:ARG:HG3	1.92	0.51
1:A:8:ARG:HH12	1:A:159:LEU:HD12	1.74	0.51
1:A:48:LEU:HD12	1:A:105:CYS:SG	2.51	0.51
3:C:66:LYS:O	3:C:67:LEU:C	2.52	0.51
3:F:228:LEU:HB2	4:I:15:A:C8	2.46	0.51
3:G:267:TYR:CZ	3:G:270:ALA:HA	2.46	0.51
5:J:329:GLN:HG2	5:J:333:HIS:NE2	2.24	0.51
5:J:425:ALA:O	5:J:429:ARG:HB2	2.10	0.51
3:F:86:PHE:O	3:F:218:ASN:ND2	2.43	0.51
5:J:352:LEU:HD22	5:J:353:PRO:HD2	1.93	0.51
5:J:418:ARG:NH1	5:J:422:SER:OG	2.44	0.51
1:A:91:GLU:HB2	5:J:249:GLN:HE21	1.76	0.51
3:C:159:ARG:NH1	3:C:171:GLU:OE2	2.44	0.51
3:F:25:ALA:HB1	3:F:93:ILE:HG23	1.93	0.50
5:J:77:VAL:HB	5:J:203:SER:HB2	1.93	0.50
5:J:400:ARG:NH2	5:J:404:ARG:HB3	2.26	0.50
1:A:243:GLU:HG3	1:A:244:VAL:HG23	1.92	0.50
2:B:166:THR:N	2:B:180:THR:OG1	2.43	0.50
3:F:337:GLU:OE2	3:G:57:LYS:NZ	2.43	0.50
5:J:307:THR:HG23	5:J:338:LEU:HD23	1.93	0.50
3:C:267:TYR:CZ	3:C:270:ALA:HA	2.46	0.50
3:G:198:LYS:HB2	3:G:198:LYS:NZ	2.25	0.50
3:G:297:LYS:O	3:G:297:LYS:HE2	2.10	0.50
1:A:36:HIS:CE1	4:I:1:C:H42	2.30	0.50
3:D:229:VAL:HG21	3:D:241:ILE:HD12	1.92	0.50
3:G:165:LYS:HB3	3:G:165:LYS:NZ	2.26	0.50
5:J:221:ASP:HA	5:J:224:LYS:HG2	1.92	0.50
3:D:328:ARG:NH1	3:D:329:GLY:O	2.44	0.50
3:H:298:MET:HE3	3:H:318:GLN:NE2	2.27	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:208:HIS:HD1	5:J:208:HIS:C	2.19	0.50
3:D:289:LYS:HB3	3:D:289:LYS:NZ	2.26	0.50
3:H:36:ASP:N	3:H:36:ASP:OD1	2.44	0.50
4:I:41:G:H1'	4:I:42:U:C2	2.47	0.50
3:C:64:PRO:HD3	3:H:295:ARG:HH22	1.75	0.49
3:E:198:LYS:NZ	3:E:198:LYS:HB3	2.27	0.49
3:F:36:ASP:OD1	3:F:36:ASP:N	2.44	0.49
1:A:223:GLY:HA2	5:J:337:GLN:HE21	1.78	0.49
5:J:368:LEU:HA	5:J:381:PHE:CZ	2.47	0.49
3:D:25:ALA:HB1	3:D:93:ILE:HG23	1.93	0.49
3:G:276:ILE:HD13	3:G:291:TYR:HD2	1.77	0.49
5:J:331:ARG:HH11	5:J:335:LEU:HB2	1.76	0.49
5:J:425:ALA:O	5:J:429:ARG:CB	2.61	0.49
1:A:233:ARG:NH2	5:J:106:SER:HB2	2.17	0.49
3:E:296:GLU:OE2	3:E:296:GLU:HA	2.13	0.49
3:G:93:ILE:HD12	3:G:148:LEU:HD23	1.94	0.49
4:I:43:U:O5'	4:I:43:U:N1	2.46	0.49
1:A:200:MET:SD	1:A:213:TRP:HB3	2.53	0.49
3:E:129:GLN:HG2	3:E:320:HIS:HE1	1.77	0.49
5:J:224:LYS:HB3	5:J:227:ARG:HH21	1.77	0.49
1:A:270:HIS:NE2	5:J:340:ASP:OD1	2.46	0.49
2:B:51:LEU:HG	2:B:139:PRO:HB2	1.94	0.49
1:A:10:ILE:HG22	1:A:99:VAL:O	2.12	0.48
4:I:43:U:C2	4:I:43:U:P	3.06	0.48
3:D:228:LEU:HD11	3:D:230:LEU:HG	1.96	0.48
3:H:197:GLU:OE2	3:H:197:GLU:HA	2.13	0.48
3:H:292:ARG:HH12	3:H:318:GLN:NE2	2.11	0.48
3:D:198:LYS:NZ	3:D:198:LYS:HB3	2.28	0.48
3:E:295:ARG:NH1	3:F:62:SER:HA	2.28	0.48
3:E:229:VAL:HB	3:E:235:ARG:HE	1.79	0.48
3:E:228:LEU:HG	3:F:76:LEU:HD22	1.95	0.48
1:A:9:ARG:H	1:A:100:SER:HB3	1.77	0.48
2:B:153:PHE:HZ	4:I:43:U:C2'	2.24	0.48
3:G:267:TYR:HD1	3:G:267:TYR:H	1.61	0.48
5:J:246:LEU:HD23	5:J:271:TYR:CD2	2.48	0.48
4:I:46:C:N4	4:I:60:G:C6	2.81	0.48
1:A:153:ARG:HH11	5:J:433:GLU:HG2	1.79	0.48
1:A:175:HIS:ND1	1:A:195:PHE:HE1	2.11	0.48
1:A:21:LEU:HA	5:J:272:LEU:HG	1.96	0.48
5:J:385:ARG:HH12	5:J:438:LEU:HD13	1.79	0.48
3:C:49:ARG:NH2	4:I:39:G:H1'	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:93:ILE:HD12	3:D:148:LEU:HD23	1.95	0.48
4:I:43:U:C6	4:I:43:U:P	3.07	0.48
3:C:66:LYS:HA	3:C:66:LYS:HD3	1.73	0.47
3:G:118:LEU:O	3:G:122:ILE:HD13	2.15	0.47
5:J:80:ALA:HA	5:J:202:TYR:CE1	2.49	0.47
3:D:128:GLU:OE1	3:D:128:GLU:HA	2.15	0.47
3:F:105:GLN:OE1	3:F:115:GLN:NE2	2.46	0.47
4:I:41:G:C8	4:I:42:U:C5	3.02	0.47
2:B:144:LYS:HG3	2:B:151:MET:HG3	1.96	0.47
3:C:228:LEU:HB3	3:D:47:SER:HB3	1.97	0.47
3:C:230:LEU:HD21	3:D:76:LEU:HB2	1.96	0.47
2:B:35:LEU:HD21	2:B:70:THR:HG21	1.95	0.47
3:F:314:PRO:HB2	3:F:318:GLN:HB2	1.97	0.47
5:J:339:ILE:HG21	5:J:430:ARG:HG3	1.97	0.47
1:A:157:ARG:HB2	5:J:437:ALA:HB1	1.96	0.47
2:B:153:PHE:CE1	4:I:43:U:O2'	2.68	0.47
3:E:9:LYS:NZ	3:E:9:LYS:HB3	2.30	0.47
3:G:91:LEU:HD13	3:G:222:VAL:HG11	1.96	0.47
5:J:227:ARG:HD2	5:J:228:GLN:N	2.29	0.47
5:J:331:ARG:HD2	5:J:421:TRP:CZ3	2.49	0.47
5:J:339:ILE:HG23	5:J:343:PHE:CE2	2.49	0.47
3:F:295:ARG:HE	3:G:64:PRO:HG3	1.78	0.47
5:J:308:LEU:HA	5:J:311:MET:HG2	1.95	0.47
1:A:75:LEU:HD23	3:G:228:LEU:HB3	1.97	0.47
1:A:133:THR:HG21	3:G:21:ALA:HB1	1.96	0.47
2:B:5:ILE:HD12	2:B:64:LEU:HD12	1.97	0.47
3:E:25:ALA:HB1	3:E:93:ILE:HG23	1.96	0.47
5:J:212:GLN:HA	5:J:212:GLN:OE1	2.14	0.47
1:A:128:ARG:NH1	4:I:6:A:OP1	2.40	0.47
2:B:23:ALA:O	2:B:27:LYS:HG2	2.15	0.47
2:B:102:LEU:HD12	2:B:134:LYS:HB2	1.96	0.47
1:A:156:MET:HE2	1:A:156:MET:HB3	1.75	0.46
2:B:111:ARG:NH2	4:I:47:U:H5'	2.30	0.46
3:G:315:MET:H	3:G:315:MET:CE	2.18	0.46
5:J:401:TRP:CD1	5:J:404:ARG:HH12	2.33	0.46
2:B:27:LYS:O	2:B:31:VAL:HG22	2.14	0.46
3:D:228:LEU:HD23	4:I:27:G:N7	2.30	0.46
3:H:305:ASP:O	3:H:309:ILE:HB	2.15	0.46
1:A:248:ARG:HD3	4:I:4:A:C2	2.50	0.46
3:F:295:ARG:NH1	3:F:295:ARG:HG3	2.31	0.46
5:J:185:GLN:C	5:J:186:ILE:HD13	2.39	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:12:SER:HA	3:F:334:GLU:HB3	1.97	0.46
4:I:34:C:O2'	4:I:35:G:O4'	2.29	0.46
1:A:166:ARG:HG3	1:A:267:GLN:HE21	1.81	0.46
2:B:44:PHE:CD2	2:B:51:LEU:HD22	2.50	0.46
1:A:113:THR:O	1:A:117:CYS:N	2.37	0.46
2:B:99:ARG:NH2	2:B:154:VAL:HA	2.31	0.46
3:G:52:ILE:HD11	3:G:71:ILE:HG23	1.98	0.46
3:G:228:LEU:HD23	4:I:9:G:C6	2.50	0.46
3:H:267:TYR:CZ	3:H:270:ALA:HA	2.51	0.46
4:I:41:G:C8	4:I:42:U:N3	2.83	0.46
5:J:400:ARG:HE	5:J:400:ARG:C	2.21	0.46
2:B:144:LYS:NZ	3:H:219:GLY:O	2.45	0.46
3:C:315:MET:HE3	3:C:315:MET:HB3	1.82	0.46
3:E:297:LYS:HE2	3:E:302:THR:HG21	1.97	0.46
4:I:46:C:O2'	4:I:47:U:O5'	2.34	0.46
5:J:251:MET:SD	5:J:251:MET:N	2.88	0.46
1:A:48:LEU:HD11	1:A:109:ILE:HG12	1.98	0.46
2:B:140:PHE:HB3	2:B:155:PHE:CE1	2.50	0.46
3:D:121:ILE:HD12	3:D:308:VAL:HG22	1.98	0.46
3:E:261:ARG:NH2	4:I:20:C:OP2	2.46	0.46
1:A:202:ALA:HB2	1:A:213:TRP:CE3	2.50	0.46
1:A:238:LEU:HD11	1:A:253:PRO:HB2	1.97	0.46
5:J:262:LEU:O	5:J:266:ARG:HG3	2.15	0.45
1:A:233:ARG:HD2	1:A:234:ALA:O	2.16	0.45
3:H:92:LYS:HG3	3:H:213:TYR:CE1	2.52	0.45
4:I:42:U:O2'	4:I:43:U:P	2.74	0.45
3:C:286:SER:HB2	3:H:108:VAL:HG12	1.98	0.45
5:J:308:LEU:HB3	5:J:312:GLN:NE2	2.32	0.45
1:A:62:LEU:HD23	1:A:63:HIS:H	1.82	0.45
1:A:258:GLU:OE2	1:A:258:GLU:HA	2.17	0.45
2:B:2:ASP:O	2:B:3:HIS:ND1	2.48	0.45
2:B:153:PHE:CZ	4:I:43:U:C2'	2.98	0.45
2:B:98:ARG:HB2	2:B:177:THR:HG22	1.99	0.45
3:C:328:ARG:NH1	3:C:329:GLY:O	2.49	0.45
3:H:25:ALA:HB2	3:H:256:ILE:HD11	1.99	0.45
4:I:42:U:HO2'	4:I:43:U:P	2.38	0.45
5:J:401:TRP:CD1	5:J:404:ARG:NH1	2.84	0.45
3:F:301:TYR:OH	3:G:53:SER:O	2.26	0.45
5:J:189:PRO:HA	5:J:195:TYR:HD1	1.82	0.45
1:A:9:ARG:HG3	1:A:9:ARG:HH11	1.81	0.45
2:B:110:ARG:HD3	2:B:125:ALA:HA	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:I:41:G:C8	4:I:42:U:C2	3.04	0.45
1:A:98:THR:HG23	1:A:98:THR:O	2.17	0.45
1:A:214:LYS:HD3	5:J:317:SER:HA	1.99	0.45
3:C:229:VAL:HG21	3:C:241:ILE:HD12	1.98	0.45
5:J:105:LEU:HA	5:J:109:THR:HG21	1.99	0.45
1:A:187:GLU:HG3	1:A:188:MET:SD	2.58	0.44
2:B:99:ARG:HE	2:B:155:PHE:H	1.65	0.44
1:A:52:GLY:HA3	1:A:279:LEU:HD23	1.98	0.44
1:A:188:MET:HE2	5:J:109:THR:HG23	1.98	0.44
2:B:45:PRO:HG3	2:B:56:ARG:NE	2.32	0.44
3:F:295:ARG:NH2	3:G:62:SER:O	2.50	0.44
3:G:86:PHE:O	3:G:218:ASN:ND2	2.50	0.44
3:G:323:ILE:HD13	3:G:323:ILE:HA	1.89	0.44
4:I:41:G:C1'	4:I:42:U:C2	3.01	0.44
1:A:12:VAL:HG13	1:A:97:MET:HG3	2.00	0.44
3:H:228:LEU:HD22	3:H:229:VAL:N	2.33	0.44
4:I:43:U:N1	4:I:43:U:P	2.91	0.44
3:C:101:GLY:HA3	3:C:202:GLY:HA2	1.98	0.44
3:F:35:GLN:HE22	3:F:159:ARG:NH2	2.16	0.44
4:I:43:U:O5'	4:I:43:U:C1'	2.66	0.44
3:G:267:TYR:CE1	3:G:270:ALA:HA	2.53	0.44
5:J:369:TRP:HE1	5:J:431:MET:HE1	1.83	0.44
3:E:305:ASP:O	3:E:309:ILE:HB	2.17	0.44
3:G:262:THR:O	3:G:262:THR:OG1	2.29	0.44
3:F:267:TYR:OH	3:F:274:GLY:O	2.30	0.43
3:H:101:GLY:HA3	3:H:202:GLY:HA2	2.00	0.43
1:A:157:ARG:HH22	5:J:434:MET:HE3	1.84	0.43
2:B:148:ASN:HD21	4:I:60:G:N2	2.12	0.43
3:E:49:ARG:HB3	4:I:27:G:H5''	2.01	0.43
3:F:228:LEU:HA	3:F:235:ARG:HH21	1.83	0.43
3:G:25:ALA:HB1	3:G:93:ILE:HG23	2.01	0.43
1:A:13:GLU:OE1	1:A:135:ILE:HD11	2.18	0.43
2:B:73:LEU:HD21	2:B:80:THR:OG1	2.18	0.43
3:H:292:ARG:HH12	3:H:318:GLN:HE22	1.66	0.43
5:J:78:THR:O	5:J:206:LEU:N	2.39	0.43
3:E:15:ALA:HB3	3:E:108:VAL:HG22	2.00	0.43
3:F:168:ARG:HG2	3:F:169:SER:H	1.83	0.43
5:J:391:GLN:HA	5:J:394:VAL:HG12	2.00	0.43
1:A:56:VAL:HG11	1:A:159:LEU:HD23	2.00	0.43
4:I:46:C:H42	4:I:60:G:H1	1.61	0.43
1:A:8:ARG:HD3	1:A:139:ARG:NH1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:229:ALA:O	5:J:234:GLN:N	2.47	0.42
5:J:310:GLN:HA	5:J:313:ARG:HB2	2.00	0.42
2:B:49:LYS:O	2:B:139:PRO:HG3	2.20	0.42
1:A:230:ILE:HD12	1:A:230:ILE:HA	1.83	0.42
1:A:275:ILE:HD13	1:A:275:ILE:HA	1.86	0.42
4:I:40:C:C5'	4:I:41:G:OP2	2.68	0.42
1:A:200:MET:HE1	1:A:214:LYS:C	2.44	0.42
3:F:271:ASP:OD1	3:F:271:ASP:C	2.61	0.42
5:J:400:ARG:HH21	5:J:404:ARG:N	2.16	0.42
3:G:60:LEU:O	3:G:67:LEU:HB2	2.20	0.42
5:J:219:PHE:HA	5:J:224:LYS:HZ1	1.84	0.42
5:J:363:LYS:HB2	5:J:366:GLN:HG2	2.00	0.42
1:A:232:TYR:HA	1:A:258:GLU:O	2.20	0.42
3:D:271:ASP:N	3:D:271:ASP:OD1	2.53	0.42
1:A:12:VAL:HG23	1:A:133:THR:O	2.19	0.42
1:A:28:ILE:HD11	1:A:165:LEU:HD23	2.01	0.42
1:A:153:ARG:NH1	5:J:433:GLU:HG2	2.34	0.42
2:B:36:ALA:HB1	2:B:40:ILE:HG12	2.02	0.42
2:B:37:ASN:O	2:B:169:ARG:NH2	2.46	0.42
3:C:60:LEU:HG	3:C:66:LYS:CG	2.49	0.42
3:E:165:LYS:HE2	3:E:165:LYS:HB2	1.94	0.42
3:F:137:ARG:NH1	3:F:265:ASP:OD1	2.44	0.42
3:G:165:LYS:HZ3	3:G:207:LEU:HD22	1.84	0.42
3:H:12:SER:O	3:H:334:GLU:N	2.51	0.42
4:I:41:G:H2'	4:I:42:U:O4'	2.20	0.42
5:J:302:TYR:HD1	5:J:305:ARG:HE	1.67	0.42
5:J:307:THR:O	5:J:311:MET:HE2	2.20	0.42
3:G:323:ILE:O	3:G:327:ILE:HG13	2.19	0.42
3:F:16:PHE:CE1	3:F:106:PRO:HB3	2.55	0.42
3:G:59:ALA:O	3:G:62:SER:OG	2.33	0.42
3:H:295:ARG:HG2	3:H:295:ARG:HH11	1.85	0.42
4:I:40:C:C5	4:I:42:U:OP2	2.73	0.42
3:G:280:PRO:HG3	3:G:332:PHE:HE1	1.85	0.41
3:C:60:LEU:HG	3:C:66:LYS:HG2	2.01	0.41
3:D:165:LYS:HB2	3:D:165:LYS:NZ	2.35	0.41
3:H:31:ASN:H	3:H:34:GLN:HE21	1.67	0.41
3:C:76:LEU:CD2	3:H:228:LEU:HG	2.44	0.41
5:J:364:ARG:HD2	5:J:365:ALA:H	1.85	0.41
1:A:70:GLU:OE2	1:A:70:GLU:HA	2.21	0.41
5:J:408:HIS:HB3	5:J:411:LEU:HB2	2.01	0.41
5:J:106:SER:H	5:J:109:THR:HB	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:76:LEU:O	2:B:80:THR:OG1	2.27	0.41
2:B:146:LEU:N	4:I:61:C:O5'	2.47	0.41
3:G:123:THR:O	3:G:127:GLN:HG2	2.20	0.41
1:A:42:LEU:HD23	1:A:42:LEU:HA	1.82	0.41
1:A:222:GLY:N	5:J:330:GLN:HE22	2.18	0.41
1:A:265:GLU:OE2	1:A:265:GLU:HA	2.21	0.41
3:D:229:VAL:O	3:D:235:ARG:NE	2.40	0.41
3:F:295:ARG:HG3	3:F:295:ARG:HH11	1.85	0.41
3:H:168:ARG:H	3:H:168:ARG:HG2	1.58	0.41
5:J:241:ILE:HD13	5:J:241:ILE:HA	1.89	0.41
5:J:385:ARG:HA	5:J:390:TRP:NE1	2.36	0.41
1:A:189:ILE:HB	5:J:105:LEU:HD11	2.03	0.41
1:A:200:MET:SD	1:A:213:TRP:HE3	2.44	0.41
3:E:49:ARG:HA	3:E:75:ASN:O	2.21	0.41
3:D:295:ARG:CZ	3:E:64:PRO:HG3	2.51	0.40
3:H:25:ALA:HB1	3:H:93:ILE:HG23	2.03	0.40
4:I:56:G:C6	4:I:57:G:C6	3.09	0.40
5:J:208:HIS:C	5:J:208:HIS:ND1	2.79	0.40
3:F:267:TYR:H	3:F:267:TYR:HD1	1.65	0.40
3:F:295:ARG:NE	3:G:64:PRO:HG3	2.36	0.40
3:H:27:MET:HE3	3:H:251:ILE:HD11	2.04	0.40
3:H:159:ARG:NH2	3:H:171:GLU:OE2	2.44	0.40
5:J:302:TYR:HD1	5:J:305:ARG:NH2	2.11	0.40
3:C:48:VAL:HG12	3:H:254:GLN:OE1	2.22	0.40
5:J:240:SER:O	5:J:241:ILE:HD13	2.21	0.40
3:E:309:ILE:HD13	3:E:309:ILE:HA	1.96	0.40
5:J:266:ARG:O	5:J:269:ARG:HG3	2.22	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	293/310 (94%)	279 (95%)	14 (5%)	0	100	100
2	B	182/184 (99%)	176 (97%)	6 (3%)	0	100	100
3	C	328/337 (97%)	319 (97%)	8 (2%)	1 (0%)	36	66
3	D	328/337 (97%)	321 (98%)	7 (2%)	0	100	100
3	E	329/337 (98%)	325 (99%)	4 (1%)	0	100	100
3	F	329/337 (98%)	321 (98%)	8 (2%)	0	100	100
3	G	326/337 (97%)	319 (98%)	7 (2%)	0	100	100
3	H	297/337 (88%)	292 (98%)	5 (2%)	0	100	100
5	J	239/443 (54%)	230 (96%)	9 (4%)	0	100	100
All	All	2651/2959 (90%)	2582 (97%)	68 (3%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	62	SER

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	244/258 (95%)	233 (96%)	11 (4%)	24	58
2	B	154/155 (99%)	152 (99%)	2 (1%)	61	86
3	C	262/266 (98%)	256 (98%)	6 (2%)	44	78
3	D	262/266 (98%)	259 (99%)	3 (1%)	65	87
3	E	263/266 (99%)	258 (98%)	5 (2%)	50	81
3	F	263/266 (99%)	254 (97%)	9 (3%)	32	68
3	G	260/266 (98%)	256 (98%)	4 (2%)	57	84
3	H	238/266 (90%)	231 (97%)	7 (3%)	37	73
5	J	211/372 (57%)	206 (98%)	5 (2%)	43	77
All	All	2157/2381 (91%)	2105 (98%)	52 (2%)	43	77

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ILE
1	A	29	THR
1	A	35	THR
1	A	49	THR
1	A	62	LEU
1	A	76	THR
1	A	109	ILE
1	A	138	GLU
1	A	142	VAL
1	A	164	VAL
1	A	230	ILE
2	B	47	VAL
2	B	146	LEU
3	C	8	LEU
3	C	66	LYS
3	C	67	LEU
3	C	77	GLN
3	C	312	ASP
3	C	331	VAL
3	D	225	SER
3	D	228	LEU
3	D	331	VAL
3	E	10	THR
3	E	63	ASP
3	E	71	ILE
3	E	163	THR
3	E	228	LEU
3	F	53	SER
3	F	68	ASP
3	F	72	GLN
3	F	113	ASP
3	F	132	SER
3	F	225	SER
3	F	228	LEU
3	F	286	SER
3	F	331	VAL
3	G	54	ASN
3	G	75	ASN
3	G	86	PHE
3	G	308	VAL
3	H	108	VAL
3	H	113	ASP

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Mol	Chain	Res	Type
3	H	132	SER
3	H	133	THR
3	H	142	ILE
3	H	228	LEU
3	H	286	SER
5	J	215	SER
5	J	269	ARG
5	J	272	LEU
5	J	339	ILE
5	J	402	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	36	HIS
1	A	46	HIS
1	A	59	GLN
1	A	267	GLN
1	A	286	ASN
2	B	162	GLN
3	E	77	GLN
3	F	31	ASN
3	F	110	ASN
3	G	31	ASN
3	G	112	GLN
3	G	218	ASN
3	H	22	ASN
3	H	318	GLN
5	J	79	HIS
5	J	249	GLN
5	J	350	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	I	56/87 (64%)	22 (39%)	2 (3%)

All (22) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	I	2	U
4	I	3	U
4	I	6	A
4	I	9	G
4	I	15	A
4	I	16	C
4	I	17	U
4	I	18	A
4	I	21	G
4	I	27	G
4	I	32	G
4	I	33	A
4	I	39	G
4	I	41	G
4	I	42	U
4	I	43	U
4	I	52	U
4	I	53	A
4	I	55	A
4	I	56	G
4	I	57	G
4	I	58	C

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	I	42	U
4	I	56	G

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.

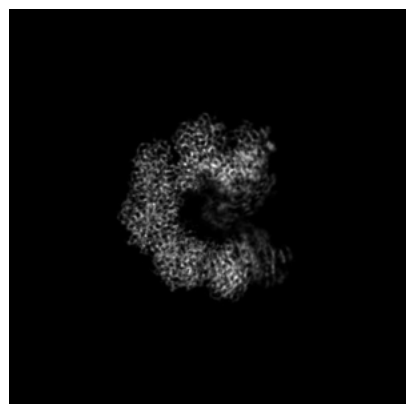
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-60812. These allow visual inspection of the internal detail of the map and identification of artifacts.

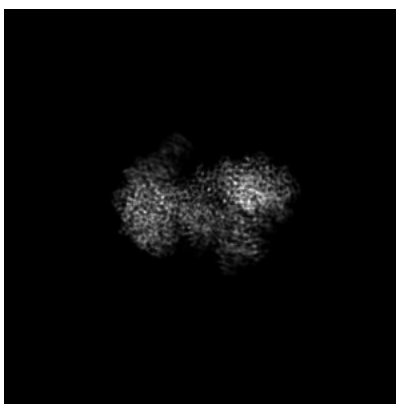
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

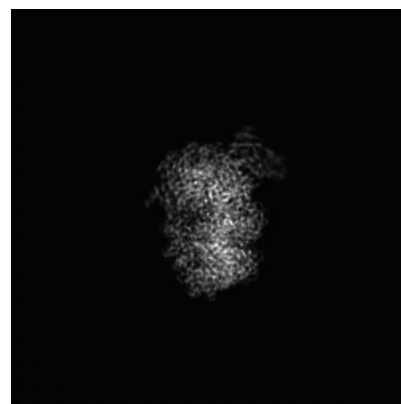
6.1.1 Primary map



X

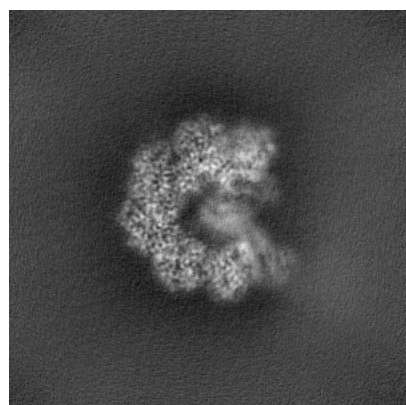


Y

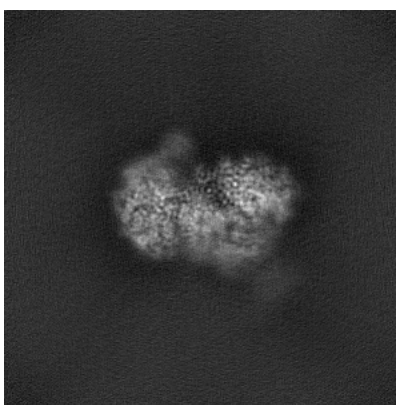


Z

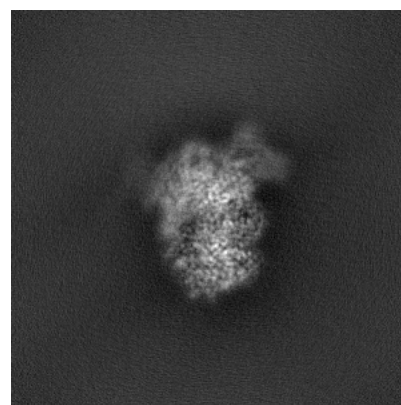
6.1.2 Raw map



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

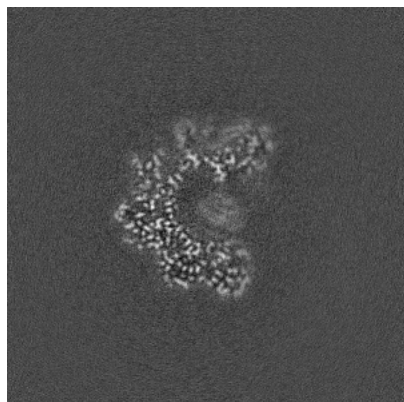


Y Index: 200

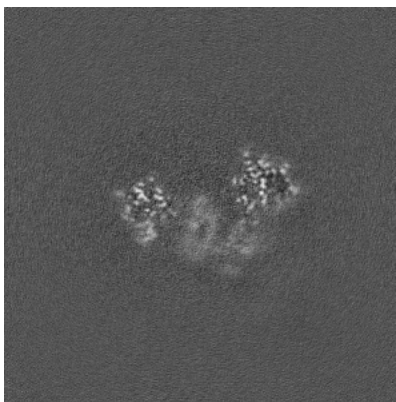


Z Index: 200

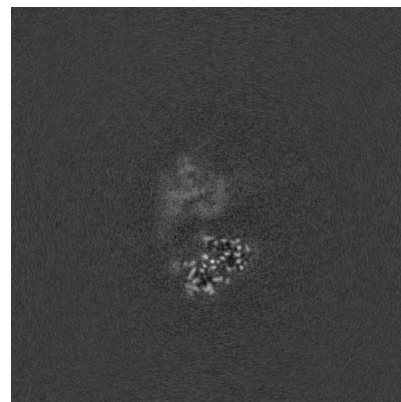
6.2.2 Raw map



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: 215

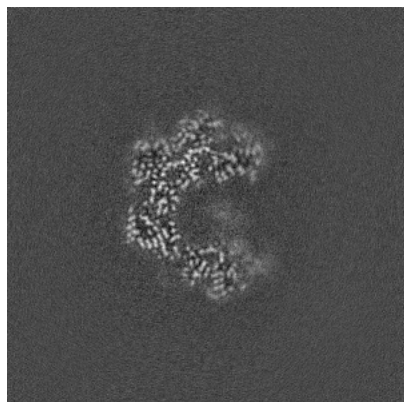


Y Index: 184

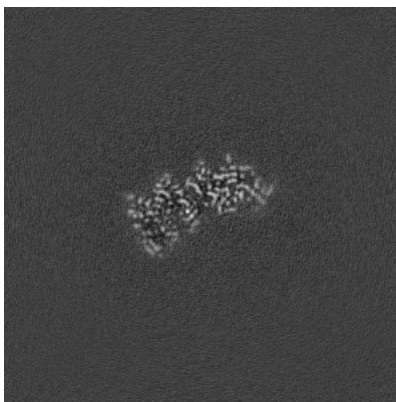


Z Index: 238

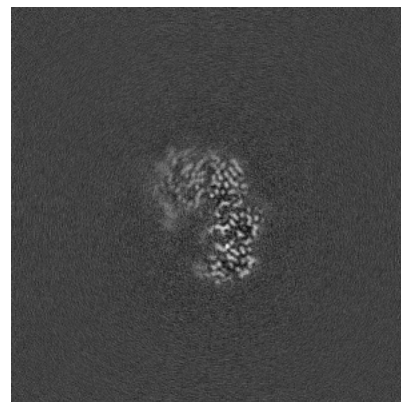
6.3.2 Raw map



X Index: 214



Y Index: 157

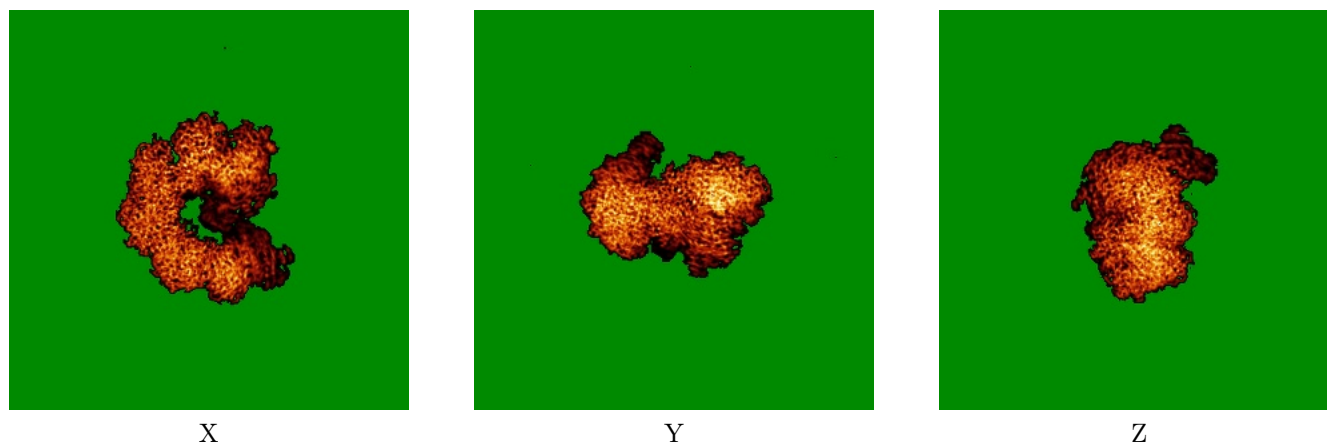


Z Index: 238

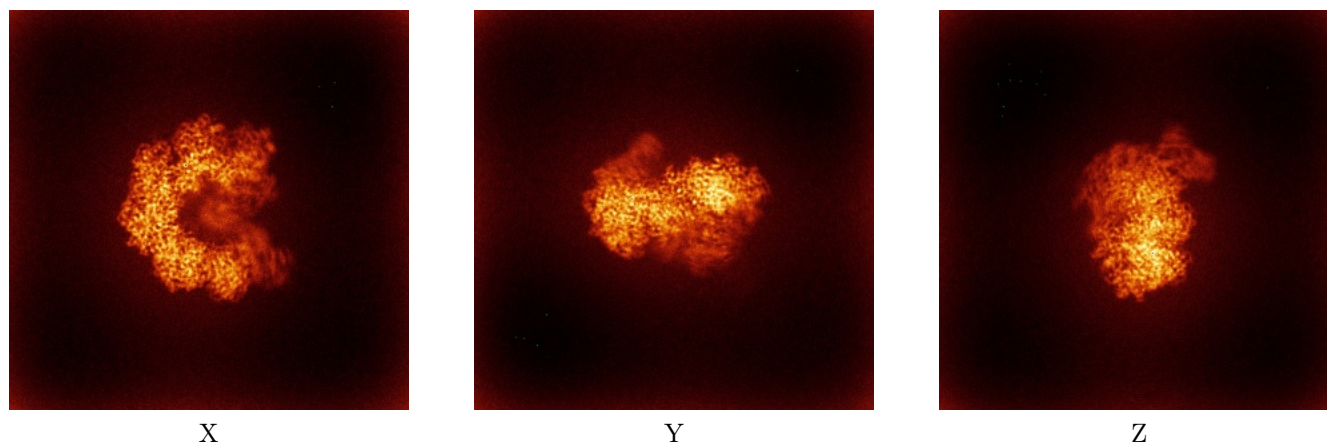
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

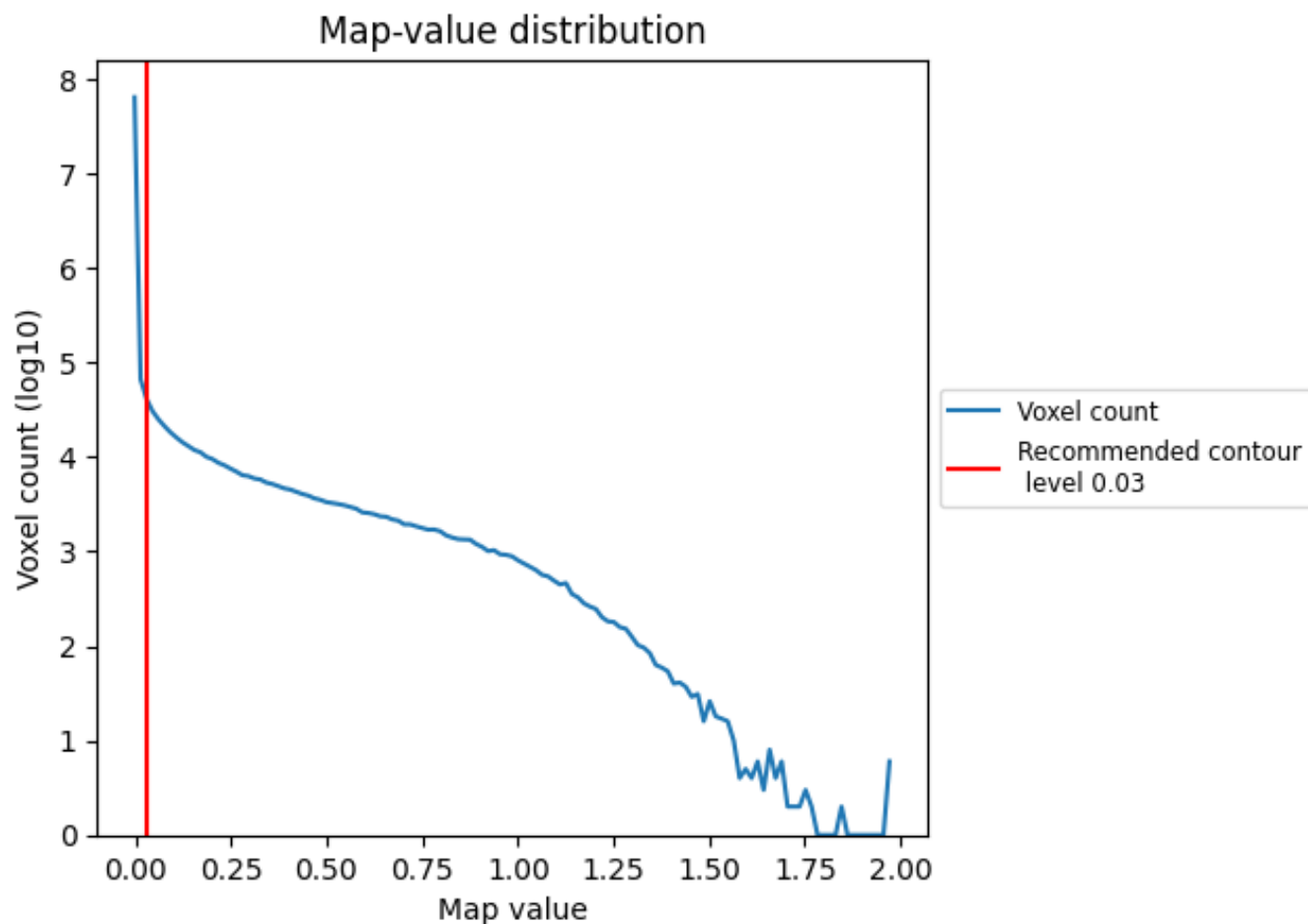
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

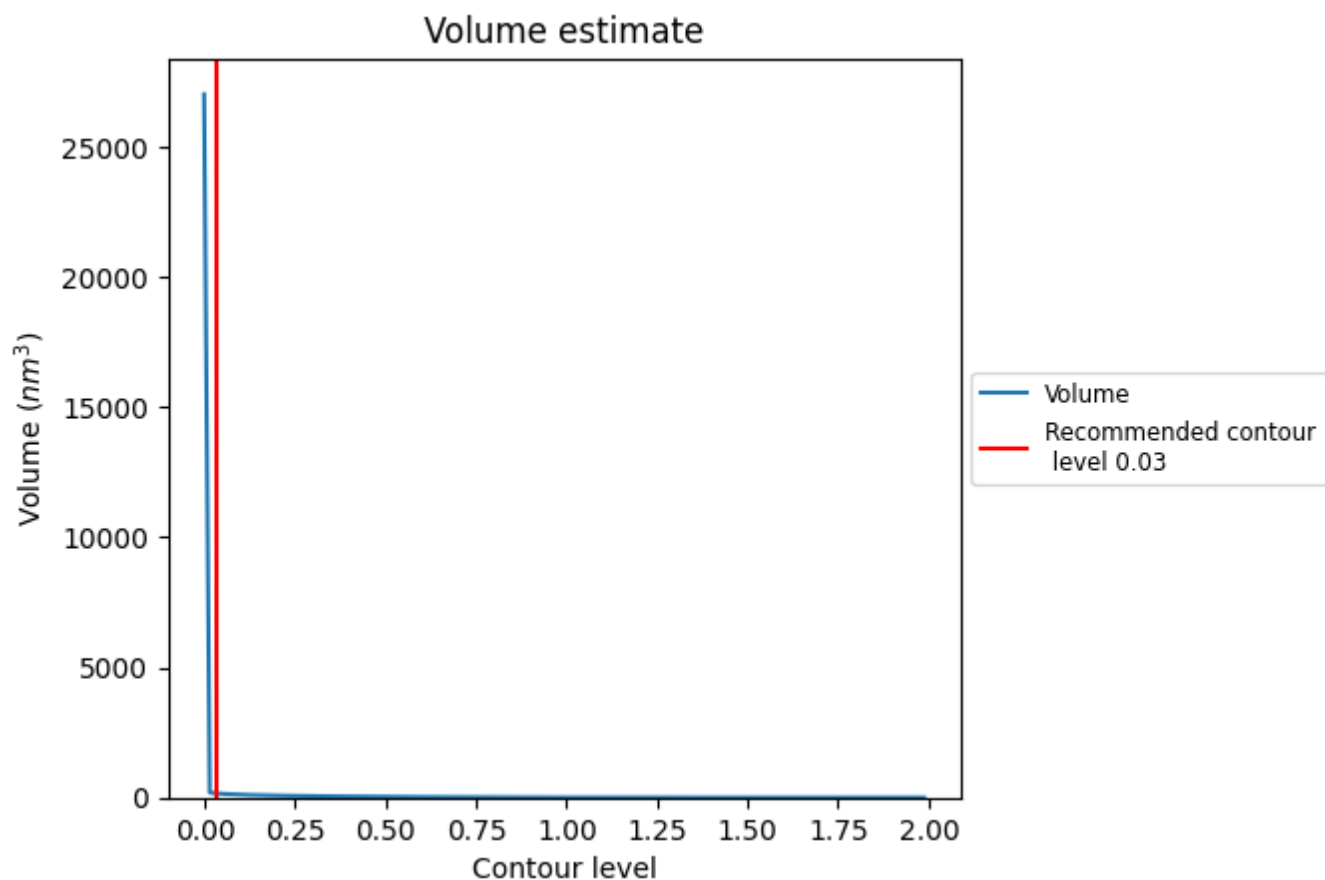
This section contains the results of statistical analysis of the map.

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.

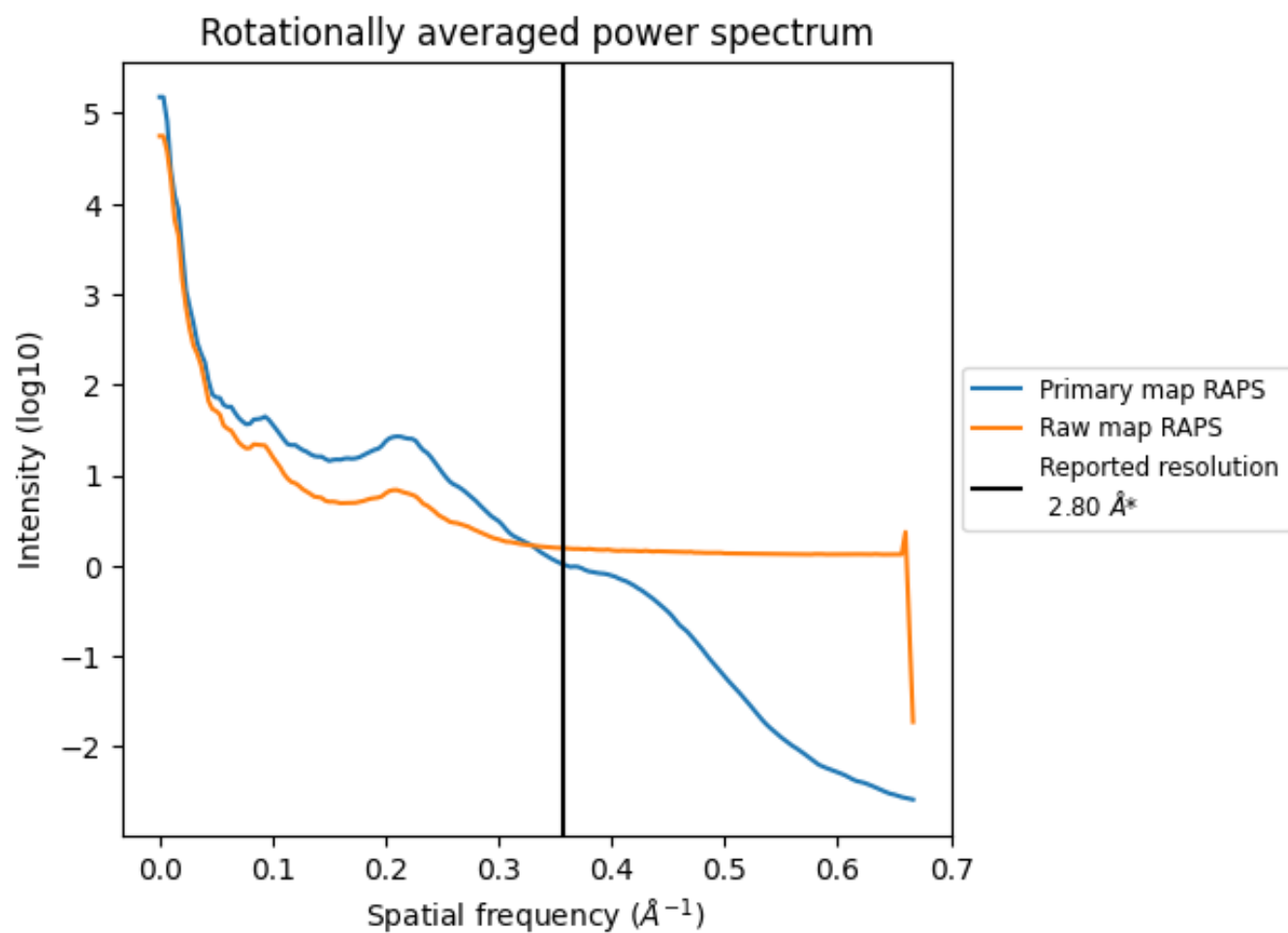
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 165 nm³; this corresponds to an approximate mass of 149 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

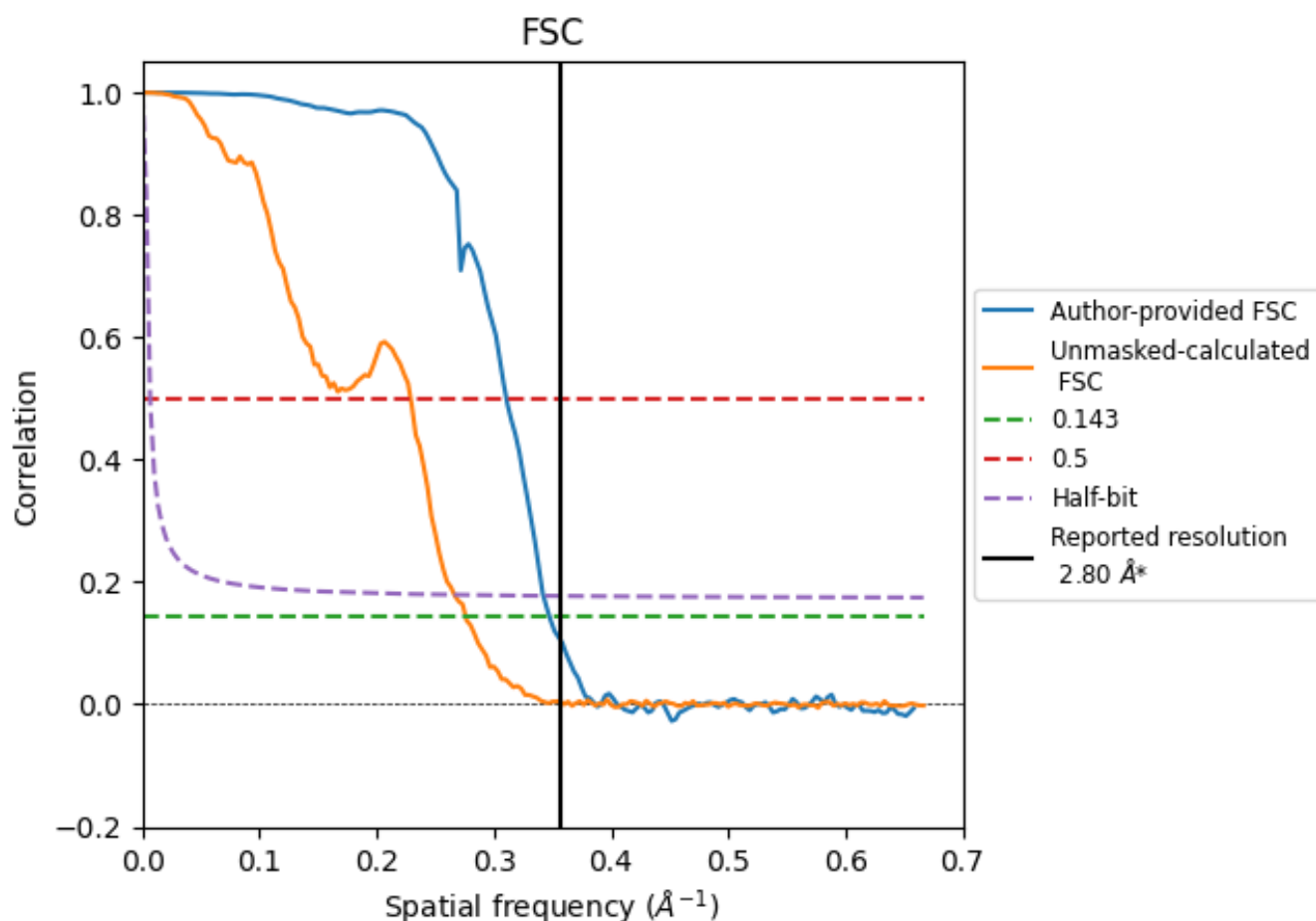


*Reported resolution corresponds to spatial frequency of $0.357 \text{ \AA}^{-1}$

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

8.2 Resolution estimates [i](#)

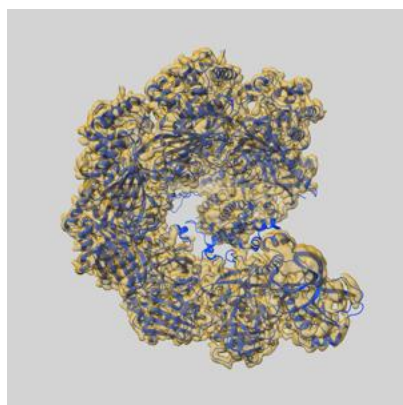
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.88	3.22	2.92
Unmasked-calculated*	3.62	4.37	3.76

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.62 differs from the reported value 2.8 by more than 10 %

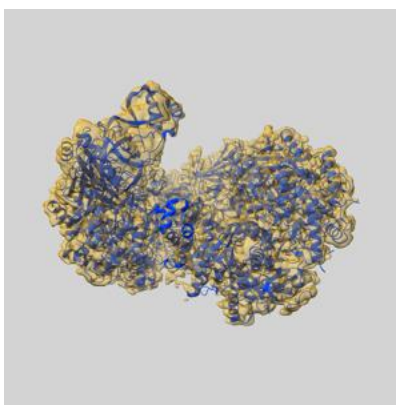
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-60812 and PDB model 9IRF. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

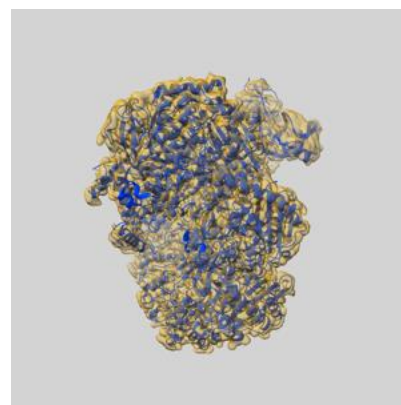
9.1 Map-model overlay [i](#)



X



Y



Z

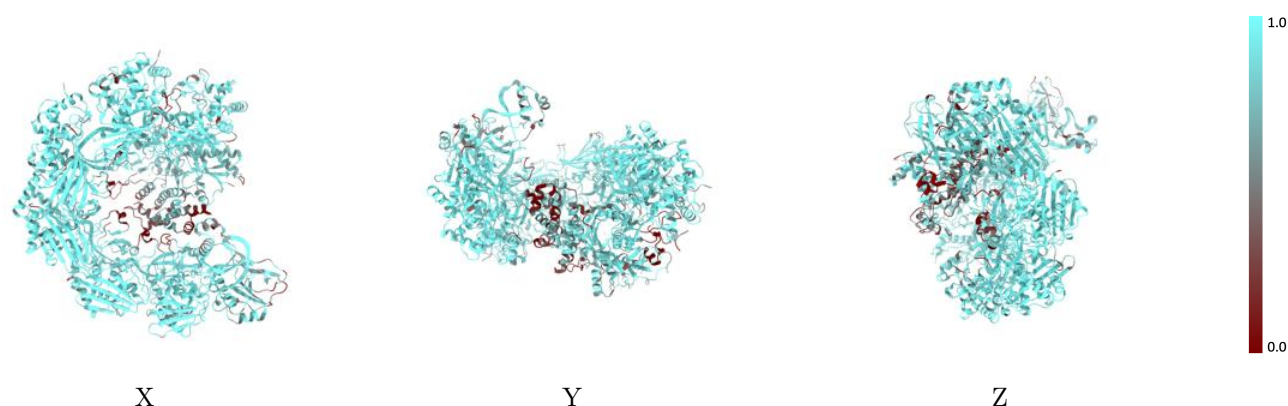
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



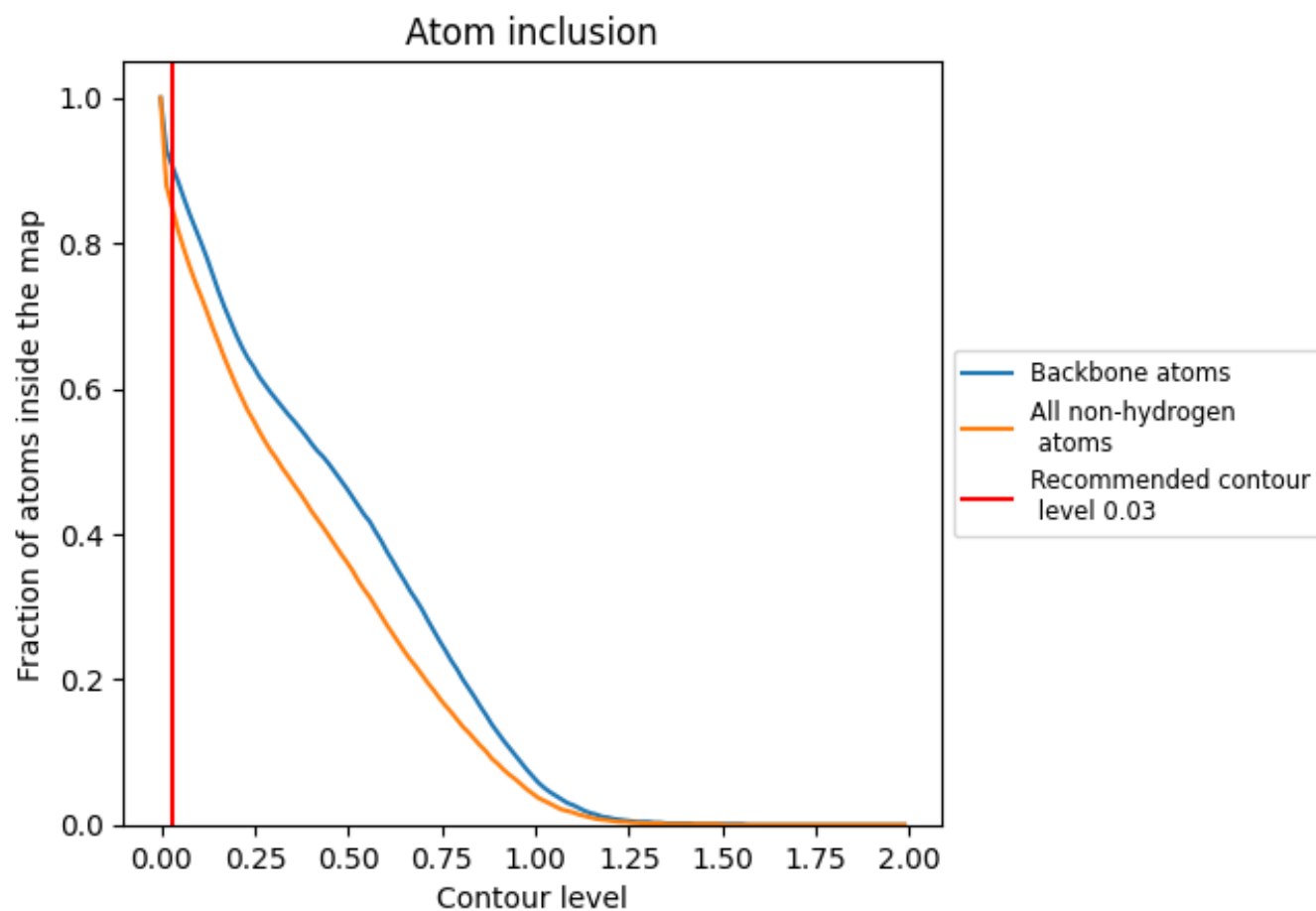
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 85% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8470	0.4440
A	0.7770	0.3370
B	0.7390	0.2450
C	0.9150	0.5370
D	0.9180	0.5440
E	0.9140	0.5360
F	0.9020	0.5180
G	0.8790	0.4650
H	0.9090	0.5050
I	0.9180	0.4410
J	0.5150	0.1570

1.0

0.0

<0.0