Full wwPDB EM Validation Report

Jan 8, 2025 – 12:16 PM EST

PDB ID	:	9CQ4
EMDB ID	:	EMD-45808
Title	:	G115 gamma delta TCR/CD3 complex bound by OKT3 Fab
Authors	:	Hoque, M.; Saotome, K.; Franklin, M.C.
Deposited on	:	2024-07-19
Resolution	:	3.27 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:

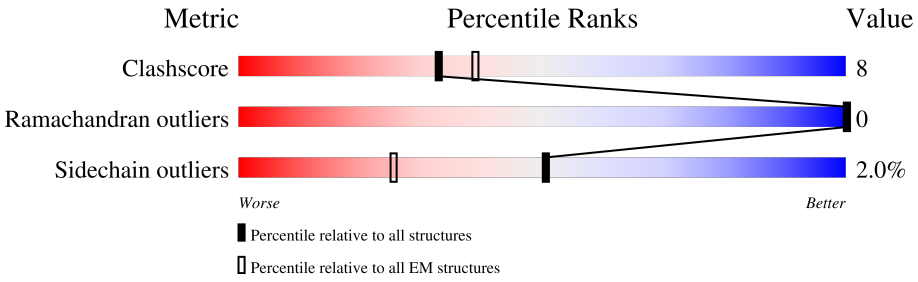
EMDB validation analysis	:	0.0.1.dev113
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

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 3.27 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 <=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	C	238	37% 13% 50%
1	H	238	5% 41% 9% 50%
2	D	213	37% 13% 50%
2	L	213	38% 12% 50%
3	A	283	11% 87%
4	B	295	12% 87%
5	K	174	8% 46% 14% 39%
6	E	210	49% 10% 41%

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Mol	Chain	Length	Quality of chain
6	F	210	7% 50% 10% 41%
7	G	185	10% 49% 13% 37%
8	Y	173	13% 84%
8	Z	173	14% 83%
9	J	3	100% 67% 33%
10	O	2	100% 100%

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 8397 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 OKT3 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	119	Total	C	N	O	S	0	0
			948	595	160	187	6		
1	H	119	Total	C	N	O	S	0	0
			948	595	160	187	6		

- Molecule 2 is a protein called OKT3 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	107	Total	C	N	O	S	0	0
			808	505	134	163	6		
2	L	106	Total	C	N	O	S	0	0
			797	499	130	162	6		

- Molecule 3 is a protein called G115 TCR delta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	37	Total	C	N	O	S	0	0
			293	197	47	46	3		

- Molecule 4 is a protein called G115 TCR gamma chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	39	Total	C	N	O	S	0	0
			318	211	49	55	3		

- Molecule 5 is a protein called T-cell surface glycoprotein CD3 delta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	K	107	Total	C	N	O	S	0	0
			831	529	139	157	6		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	172	GLY	-	expression tag	UNP P04234
K	173	SER	-	expression tag	UNP P04234
K	174	GLY	-	expression tag	UNP P04234

- Molecule 6 is a protein called T-cell surface glycoprotein CD3 epsilon chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	123	Total	C	N	O	S	0	0
			978	619	157	194	8		
6	F	124	Total	C	N	O	S	0	0
			987	625	159	195	8		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	208	GLY	-	expression tag	UNP P07766
E	209	SER	-	expression tag	UNP P07766
E	210	GLY	-	expression tag	UNP P07766
F	208	GLY	-	expression tag	UNP P07766
F	209	SER	-	expression tag	UNP P07766
F	210	GLY	-	expression tag	UNP P07766

- Molecule 7 is a protein called T-cell surface glycoprotein CD3 gamma chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	116	Total	C	N	O	S	0	0
			913	587	151	168	7		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	183	GLY	-	expression tag	UNP P09693
G	184	SER	-	expression tag	UNP P09693
G	185	GLY	-	expression tag	UNP P09693

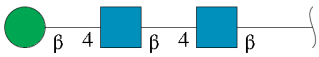
- Molecule 8 is a protein called T-cell surface glycoprotein CD3 zeta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	Y	27	Total	C	N	O	S	0	0
			221	156	32	32	1		
8	Z	30	Total	C	N	O	S	0	0
			246	169	38	38	1		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Y	165	GLY	-	expression tag	UNP P20963
Y	166	SER	-	expression tag	UNP P20963
Y	167	GLY	-	expression tag	UNP P20963
Y	168	LEU	-	expression tag	UNP P20963
Y	169	GLU	-	expression tag	UNP P20963
Y	170	VAL	-	expression tag	UNP P20963
Y	171	LEU	-	expression tag	UNP P20963
Y	172	PHE	-	expression tag	UNP P20963
Y	173	GLN	-	expression tag	UNP P20963
Z	165	GLY	-	expression tag	UNP P20963
Z	166	SER	-	expression tag	UNP P20963
Z	167	GLY	-	expression tag	UNP P20963
Z	168	LEU	-	expression tag	UNP P20963
Z	169	GLU	-	expression tag	UNP P20963
Z	170	VAL	-	expression tag	UNP P20963
Z	171	LEU	-	expression tag	UNP P20963
Z	172	PHE	-	expression tag	UNP P20963
Z	173	GLN	-	expression tag	UNP P20963

- Molecule 9 is an oligosaccharide called beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

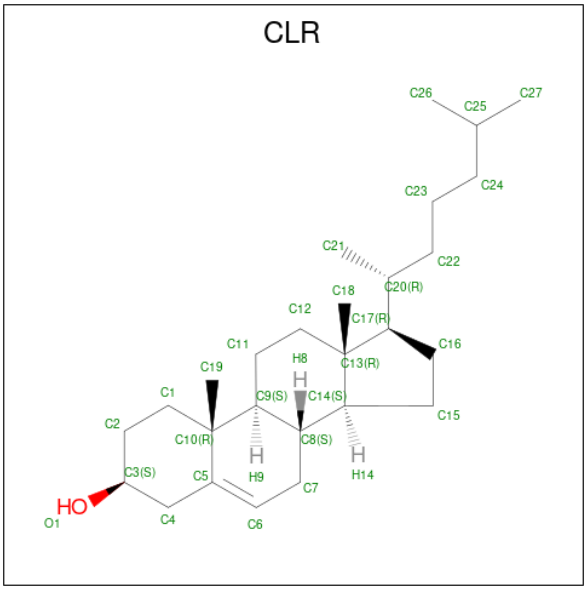


Mol	Chain	Residues	Atoms				AltConf	Trace
9	J	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 10 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

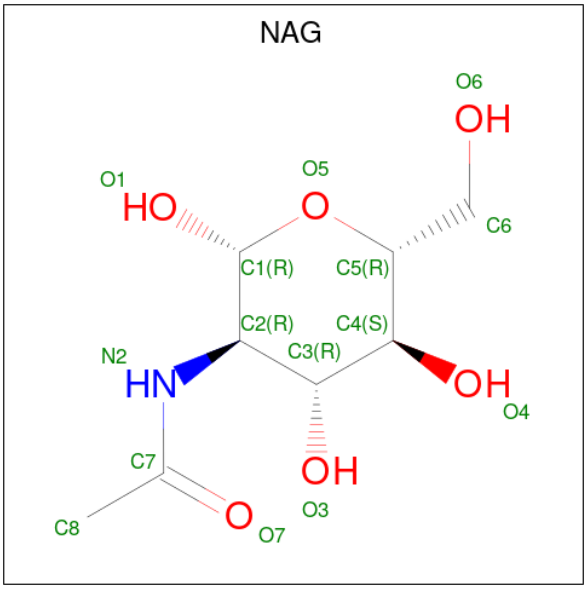
Mol	Chain	Residues	Atoms				AltConf	Trace
10	O	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 11 is CHOLESTEROL (three-letter code: CLR) (formula: $C_{27}H_{46}O$).



Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
11	A	1	28	27	1	0

- Molecule 12 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



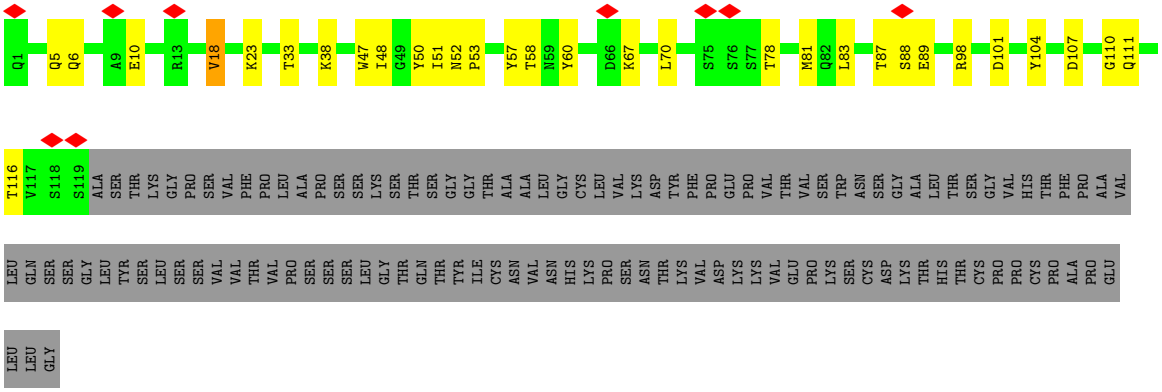
Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
12	G	1	14	8	1	5	0

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.

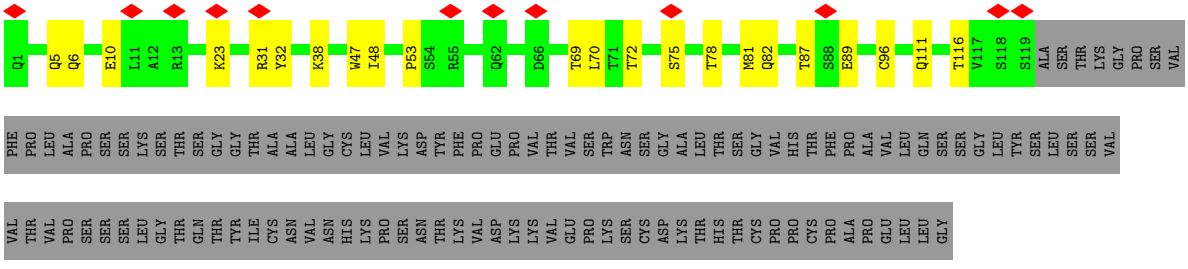
• Molecule 1: OKT3 Fab heavy chain

Chain C:



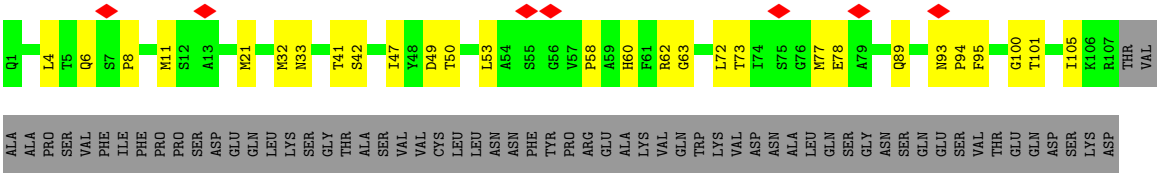
• Molecule 1: OKT3 Fab heavy chain

Chain H:



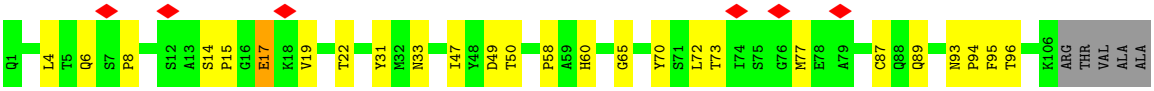
• Molecule 2: OKT3 Fab light chain

Chain D:



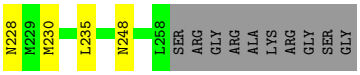
• Molecule 2: OKT3 Fab light chain

Chain L:



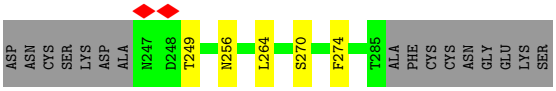
• Molecule 3: G115 TCR delta chain

Chain A:



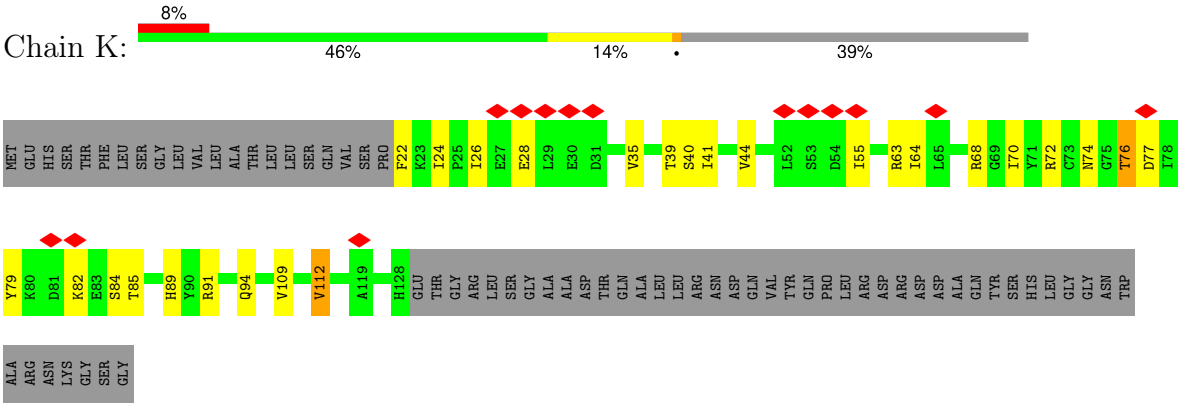
• Molecule 4: G115 TCR gamma chain

Chain B:



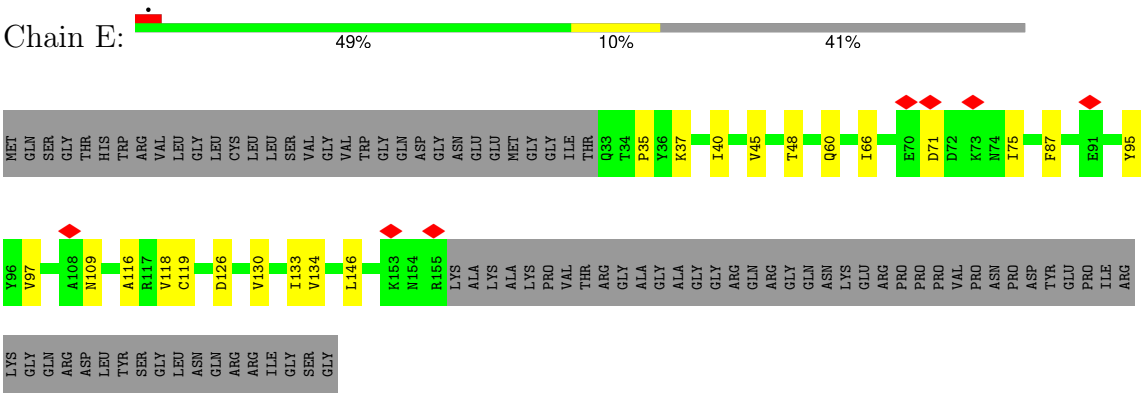
• Molecule 5: T-cell surface glycoprotein CD3 delta chain

Chain K:



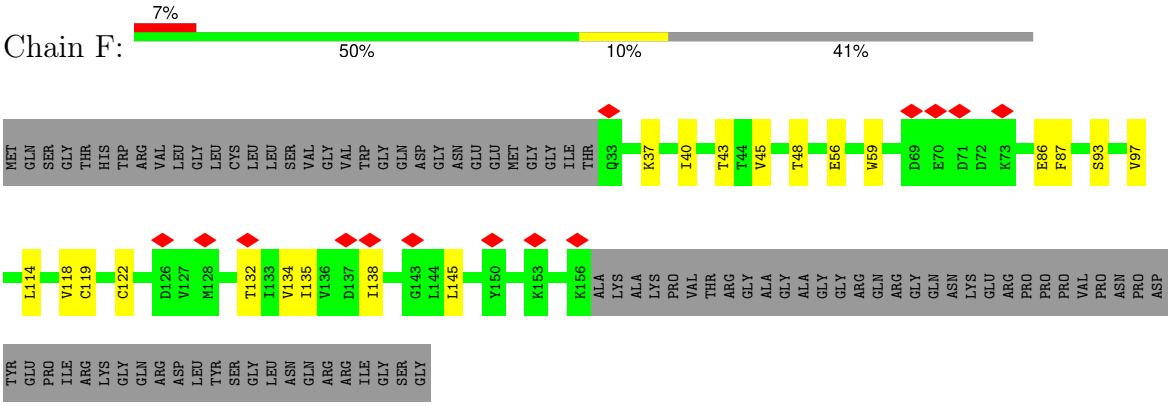
• Molecule 6: T-cell surface glycoprotein CD3 epsilon chain

Chain E:



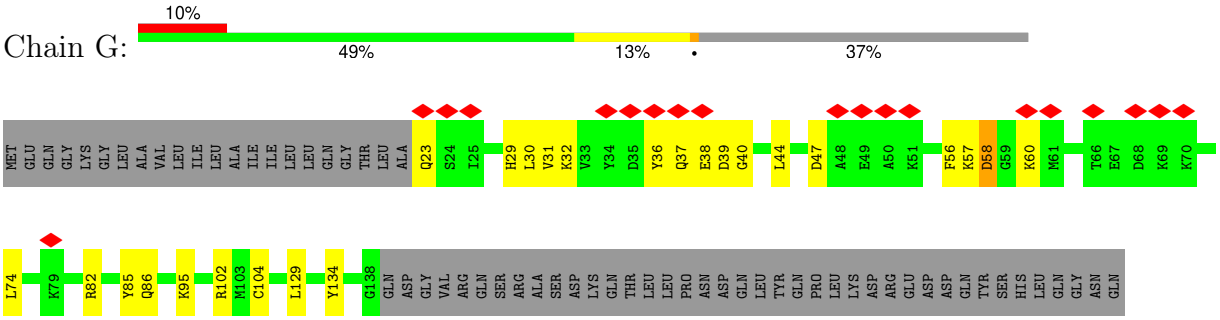
• Molecule 6: T-cell surface glycoprotein CD3 epsilon chain

Chain F:



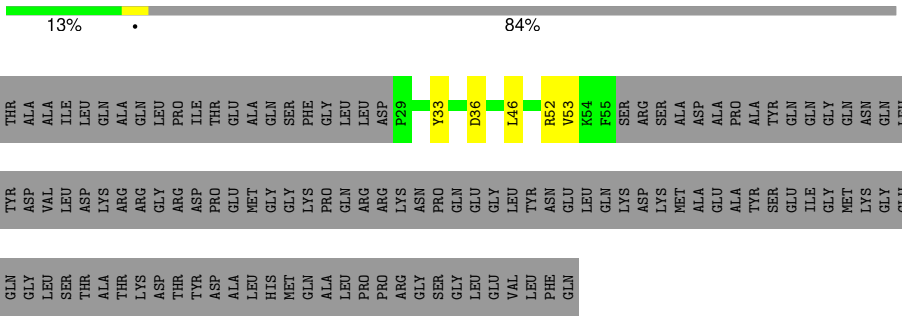
• Molecule 7: T-cell surface glycoprotein CD3 gamma chain

Chain G:



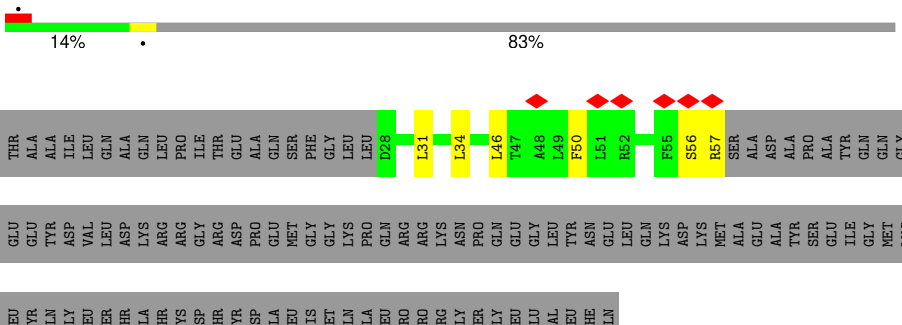
• Molecule 8: T-cell surface glycoprotein CD3 zeta chain

Chain Y:



• Molecule 8: T-cell surface glycoprotein CD3 zeta chain

Chain Z:



• Molecule 9: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:

• Molecule 10: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain O:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	290758	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	90.543	Depositor
Minimum map value	-65.905	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	7.44	Depositor
Map size (Å)	335.6, 335.6, 335.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.839, 0.839, 0.839	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, NAG, CLR

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	C	0.32	0/972	0.57	0/1317
1	H	0.29	0/972	0.53	0/1317
2	D	0.33	0/828	0.56	0/1122
2	L	0.31	0/817	0.57	0/1108
3	A	0.28	0/297	0.47	0/399
4	B	0.28	0/322	0.45	0/438
5	K	0.27	0/844	0.52	0/1147
6	E	0.28	0/999	0.48	0/1356
6	F	0.30	0/1008	0.49	0/1367
7	G	0.28	0/931	0.47	0/1252
8	Y	0.30	0/226	0.48	0/304
8	Z	0.30	0/251	0.52	0/338
All	All	0.30	0/8467	0.52	0/11465

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

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	C	948	0	897	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	H	948	0	897	12	0
2	D	808	0	771	17	0
2	L	797	0	758	17	0
3	A	293	0	323	6	0
4	B	318	0	342	5	0
5	K	831	0	836	18	0
6	E	978	0	938	15	0
6	F	987	0	951	13	0
7	G	913	0	908	16	0
8	Y	221	0	245	4	0
8	Z	246	0	266	6	0
9	J	39	0	34	1	0
10	O	28	0	25	1	0
11	A	28	0	43	7	0
12	G	14	0	13	0	0
All	All	8397	0	8247	136	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 (136) 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)
11:A:301:CLR:C9	11:A:301:CLR:C10	1.89	1.48
2:D:47:ILE:HD12	2:D:72:LEU:HD11	1.62	0.81
1:C:60:TYR:HE1	1:C:70:LEU:HD13	1.43	0.80
2:L:15:PRO:HA	2:L:77:MET:HG2	1.63	0.79
11:A:301:CLR:C10	11:A:301:CLR:C8	2.33	0.77
1:C:48:ILE:HG21	1:C:81:MET:HE3	1.68	0.76
2:D:4:LEU:HD11	2:D:89:GLN:HG3	1.70	0.72
7:G:23:GLN:HA	7:G:32:LYS:HE3	1.72	0.71
7:G:37:GLN:HB2	7:G:40:GLY:H	1.54	0.70
2:D:63:GLY:HA3	2:D:72:LEU:HD12	1.73	0.70
5:K:39:THR:HG21	5:K:74:ASN:HB2	1.74	0.69
6:F:87:PHE:HB3	6:F:118:VAL:HG21	1.75	0.68
11:A:301:CLR:C9	11:A:301:CLR:C5	2.62	0.67
11:A:301:CLR:C10	11:A:301:CLR:C11	2.73	0.66
5:K:28:GLU:OE2	5:K:63:ARG:NH2	2.25	0.66
6:F:37:LYS:HB2	6:F:48:THR:HB	1.78	0.66
7:G:44:LEU:HG	7:G:74:LEU:HD11	1.77	0.65
1:C:5:GLN:HB2	1:C:23:LYS:HB2	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:8:PRO:HB2	2:D:11:MET:SD	2.38	0.64
1:H:6:GLN:NE2	1:H:96:CYS:SG	2.71	0.64
1:C:10:GLU:N	1:C:10:GLU:OE1	2.32	0.63
2:D:6:GLN:HE21	2:D:100:GLY:H	1.48	0.61
1:H:31:ARG:NH2	1:H:32:TYR:OH	2.34	0.61
11:A:301:CLR:C9	11:A:301:CLR:C19	2.76	0.60
5:K:40:SER:HB2	5:K:55:ILE:HD12	1.82	0.60
1:H:10:GLU:OE1	1:H:10:GLU:N	2.34	0.60
2:L:17:GLU:N	2:L:17:GLU:OE1	2.35	0.60
1:C:38:LYS:HB2	1:C:48:ILE:HD11	1.85	0.59
2:D:49:ASP:O	2:D:50:THR:HG22	2.03	0.58
1:C:23:LYS:HA	1:C:78:THR:HG22	1.86	0.58
1:C:48:ILE:HD13	1:C:81:MET:HE1	1.86	0.57
7:G:30:LEU:HD22	7:G:47:ASP:HB3	1.86	0.57
1:C:87:THR:HG22	1:C:88:SER:H	1.69	0.57
1:H:23:LYS:HA	1:H:78:THR:HG22	1.86	0.57
1:H:47:TRP:CD2	2:L:95:PHE:HB3	2.39	0.57
5:K:24:ILE:O	6:E:95:TYR:OH	2.18	0.57
3:A:223:HIS:HB3	4:B:249:THR:HG21	1.87	0.56
7:G:82:ARG:NH2	7:G:102:ARG:HB3	2.22	0.55
1:C:104:TYR:O	2:D:33:ASN:ND2	2.39	0.54
1:C:60:TYR:CE1	1:C:70:LEU:HD13	2.34	0.54
2:D:78:GLU:O	2:D:105:ILE:HD11	2.07	0.54
3:A:230:MET:HG3	4:B:256:ASN:HB3	1.90	0.54
1:H:38:LYS:HB2	1:H:48:ILE:HD11	1.91	0.53
2:D:58:PRO:HB2	2:D:60:HIS:HD2	1.74	0.53
6:E:37:LYS:HB2	6:E:48:THR:OG1	2.08	0.53
1:C:6:GLN:O	1:C:111:GLN:NE2	2.41	0.53
5:K:70:ILE:HD11	6:E:35:PRO:HB3	1.91	0.52
5:K:84:SER:HA	6:E:109:ASN:HB2	1.91	0.52
1:C:50:TYR:OH	6:F:56:GLU:OE1	2.23	0.51
6:F:43:THR:O	6:F:86:GLU:N	2.42	0.51
6:F:145:LEU:HD21	7:G:129:LEU:HB3	1.93	0.51
6:F:93:SER:OG	6:F:114:LEU:O	2.27	0.51
2:L:49:ASP:O	2:L:50:THR:HG22	2.11	0.51
2:D:47:ILE:HG12	2:D:53:LEU:HD13	1.93	0.51
6:E:87:PHE:HB3	6:E:118:VAL:HG11	1.93	0.51
1:C:98:ARG:NH2	1:C:107:ASP:OD2	2.22	0.50
1:H:6:GLN:O	1:H:111:GLN:NE2	2.45	0.50
5:K:91:ARG:HB3	6:E:116:ALA:HB1	1.94	0.50
6:E:40:ILE:HG12	6:E:45:VAL:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:18:VAL:HG23	1:C:83:LEU:HB2	1.94	0.49
2:D:62:ARG:O	2:D:73:THR:OG1	2.29	0.49
5:K:35:VAL:HG12	5:K:41:ILE:HD13	1.95	0.48
11:A:301:CLR:H21	8:Y:52:ARG:HB2	1.94	0.48
5:K:44:VAL:HG21	5:K:72:ARG:HG3	1.96	0.48
7:G:31:VAL:HG21	7:G:86:GLN:HA	1.95	0.48
3:A:224:THR:O	3:A:228:ASN:ND2	2.47	0.48
1:H:5:GLN:HB2	1:H:23:LYS:HB2	1.96	0.48
2:L:58:PRO:HB2	2:L:60:HIS:CE1	2.49	0.48
5:K:76:THR:OG1	9:J:1:NAG:O7	2.28	0.47
5:K:109:VAL:O	5:K:112:VAL:HG12	2.14	0.47
2:L:47:ILE:HD12	2:L:72:LEU:HD12	1.96	0.47
1:C:47:TRP:CD2	2:D:95:PHE:HB3	2.49	0.47
1:C:57:TYR:CE2	6:F:56:GLU:HB2	2.49	0.47
6:E:126:ASP:OD1	6:E:126:ASP:N	2.47	0.47
7:G:82:ARG:HH22	7:G:102:ARG:HB3	1.78	0.47
2:L:93:ASN:HB3	2:L:94:PRO:HD3	1.96	0.47
7:G:36:TYR:CE1	7:G:38:GLU:HG3	2.50	0.46
3:A:248:ASN:ND2	4:B:270:SER:OG	2.48	0.46
2:L:65:GLY:HA3	2:L:70:TYR:HA	1.97	0.46
2:L:58:PRO:HB2	2:L:60:HIS:ND1	2.30	0.46
6:E:60:GLN:HB3	6:E:97:VAL:HG12	1.98	0.46
7:G:57:LYS:HG2	7:G:58:ASP:OD1	2.16	0.46
6:E:134:VAL:HG11	8:Z:34:LEU:HD11	1.98	0.45
2:L:6:GLN:NE2	2:L:87:CYS:SG	2.85	0.45
6:F:40:ILE:HD12	7:G:102:ARG:HD3	1.97	0.45
2:D:58:PRO:HB2	2:D:60:HIS:CD2	2.49	0.45
6:F:45:VAL:HG11	6:F:114:LEU:HD21	1.97	0.45
6:F:132:THR:HA	6:F:135:ILE:HG22	1.99	0.45
6:E:146:LEU:HD23	6:E:146:LEU:HA	1.83	0.45
2:D:21:MET:SD	2:D:101:THR:OG1	2.57	0.45
2:L:4:LEU:HD23	2:L:89:GLN:HE21	1.82	0.45
3:A:248:ASN:OD1	4:B:274:PHE:HB2	2.18	0.44
7:G:37:GLN:C	7:G:39:ASP:H	2.20	0.44
1:C:6:GLN:HE21	1:C:110:GLY:HA3	1.82	0.44
1:C:67:LYS:NZ	1:C:83:LEU:HD22	2.32	0.44
2:L:19:VAL:O	2:L:73:THR:HA	2.17	0.44
1:H:53:PRO:HA	1:H:72:THR:HG21	1.99	0.44
10:O:1:NAG:H4	10:O:2:NAG:H2	1.62	0.44
8:Y:53:VAL:HG21	8:Z:50:PHE:HE1	1.81	0.44
2:L:89:GLN:NE2	2:L:96:THR:HB	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:69:THR:OG1	1:H:82:GLN:HG2	2.17	0.43
5:K:76:THR:HG22	5:K:77:ASP:H	1.83	0.43
2:D:41:THR:OG1	2:D:42:SER:N	2.52	0.43
1:H:47:TRP:CG	2:L:95:PHE:HB3	2.54	0.43
2:D:93:ASN:HB3	2:D:94:PRO:HD3	2.00	0.43
6:E:134:VAL:HG11	8:Z:34:LEU:HD21	2.00	0.43
2:L:14:SER:HB3	2:L:17:GLU:OE2	2.19	0.43
6:E:130:VAL:HA	6:E:133:ILE:HG22	2.00	0.43
1:C:33:THR:HA	1:C:53:PRO:HD3	2.00	0.42
8:Y:33:TYR:HA	8:Y:36:ASP:OD2	2.19	0.42
11:A:301:CLR:H183	11:A:301:CLR:H20	1.75	0.42
5:K:64:ILE:CG2	5:K:94:GLN:HG3	2.49	0.42
3:A:235:LEU:HD22	8:Z:31:LEU:HB3	2.02	0.42
7:G:58:ASP:O	7:G:60:LYS:NZ	2.53	0.42
4:B:264:LEU:HD23	4:B:264:LEU:HA	1.87	0.42
6:E:66:ILE:HD12	6:E:75:ILE:HD13	2.01	0.41
6:F:59:TRP:HA	6:F:97:VAL:O	2.20	0.41
7:G:29:HIS:HA	7:G:95:LYS:HB2	2.02	0.41
1:C:47:TRP:CG	2:D:95:PHE:HB3	2.54	0.41
5:K:55:ILE:H	5:K:55:ILE:HG12	1.63	0.41
7:G:57:LYS:HE2	7:G:85:TYR:CZ	2.55	0.41
8:Z:56:SER:OG	8:Z:57:ARG:N	2.53	0.41
5:K:22:PHE:N	5:K:82:LYS:HE3	2.36	0.41
6:E:71:ASP:OD1	6:E:71:ASP:N	2.44	0.41
1:C:33:THR:HG22	1:C:52:ASN:HA	2.03	0.41
1:C:51:ILE:HG13	1:C:58:THR:HG22	2.03	0.41
5:K:68:ARG:HG2	5:K:89:HIS:HA	2.03	0.41
7:G:56:PHE:HB2	7:G:86:GLN:HG3	2.03	0.41
1:H:70:LEU:HD23	1:H:81:MET:HG3	2.01	0.40
5:K:76:THR:H	5:K:79:TYR:HB2	1.86	0.40
2:L:8:PRO:HG3	2:L:22:THR:H	1.86	0.40
2:L:31:TYR:HE2	2:L:33:ASN:HD21	1.68	0.40
5:K:26:ILE:HD12	5:K:35:VAL:HG22	2.04	0.40
6:F:119:CYS:HB2	6:F:122:CYS:HB2	1.46	0.40
6:F:134:VAL:O	6:F:138:ILE:HG23	2.21	0.40
8:Y:46:LEU:HD22	8:Z:46:LEU:HB3	2.03	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	C	117/238 (49%)	114 (97%)	3 (3%)	0	100	100
1	H	117/238 (49%)	114 (97%)	3 (3%)	0	100	100
2	D	105/213 (49%)	102 (97%)	3 (3%)	0	100	100
2	L	104/213 (49%)	101 (97%)	3 (3%)	0	100	100
3	A	35/283 (12%)	34 (97%)	1 (3%)	0	100	100
4	B	37/295 (12%)	37 (100%)	0	0	100	100
5	K	105/174 (60%)	98 (93%)	7 (7%)	0	100	100
6	E	121/210 (58%)	118 (98%)	3 (2%)	0	100	100
6	F	122/210 (58%)	116 (95%)	6 (5%)	0	100	100
7	G	114/185 (62%)	102 (90%)	12 (10%)	0	100	100
8	Y	25/173 (14%)	25 (100%)	0	0	100	100
8	Z	28/173 (16%)	27 (96%)	1 (4%)	0	100	100
All	All	1030/2605 (40%)	988 (96%)	42 (4%)	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	C	102/205 (50%)	98 (96%)	4 (4%)	27	55
1	H	102/205 (50%)	98 (96%)	4 (4%)	27	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	D	89/185 (48%)	87 (98%)	2 (2%)	47 69
2	L	88/185 (48%)	87 (99%)	1 (1%)	70 82
3	A	33/248 (13%)	33 (100%)	0	100 100
4	B	37/268 (14%)	37 (100%)	0	100 100
5	K	94/148 (64%)	91 (97%)	3 (3%)	34 60
6	E	111/178 (62%)	110 (99%)	1 (1%)	75 85
6	F	112/178 (63%)	112 (100%)	0	100 100
7	G	98/156 (63%)	95 (97%)	3 (3%)	35 61
8	Y	24/142 (17%)	24 (100%)	0	100 100
8	Z	27/142 (19%)	27 (100%)	0	100 100
All	All	917/2240 (41%)	899 (98%)	18 (2%)	50 71

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	18	VAL
1	C	89	GLU
1	C	101	ASP
1	C	116	THR
2	D	32	MET
2	D	77	MET
1	H	75	SER
1	H	87	THR
1	H	89	GLU
1	H	116	THR
2	L	17	GLU
5	K	76	THR
5	K	85	THR
5	K	112	VAL
6	E	119	CYS
7	G	58	ASP
7	G	104	CYS
7	G	134	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	6	GLN
2	D	6	GLN
1	H	6	GLN
2	L	1	GLN
2	L	89	GLN
3	A	248	ASN
6	E	65	ASN
6	F	51	GLN
6	F	121	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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)

5 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
9	NAG	J	1	5,9	14,14,15	0.70	0	17,19,21	0.64	0
9	NAG	J	2	9	14,14,15	0.70	0	17,19,21	0.67	0
9	BMA	J	3	9	11,11,12	0.86	0	15,15,17	0.74	0
10	NAG	O	1	5,10	14,14,15	0.72	0	17,19,21	0.74	0
10	NAG	O	2	10	14,14,15	0.72	0	17,19,21	0.70	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	NAG	J	1	5,9	-	2/6/23/26	0/1/1/1
9	NAG	J	2	9	-	1/6/23/26	0/1/1/1
9	BMA	J	3	9	-	0/2/19/22	0/1/1/1
10	NAG	O	1	5,10	-	4/6/23/26	0/1/1/1
10	NAG	O	2	10	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	O	1	NAG	O5-C5-C6-O6
10	O	2	NAG	C4-C5-C6-O6
10	O	2	NAG	O5-C5-C6-O6
10	O	1	NAG	C8-C7-N2-C2
10	O	1	NAG	O7-C7-N2-C2
10	O	1	NAG	C4-C5-C6-O6
9	J	2	NAG	O5-C5-C6-O6
9	J	1	NAG	C4-C5-C6-O6
9	J	1	NAG	O5-C5-C6-O6

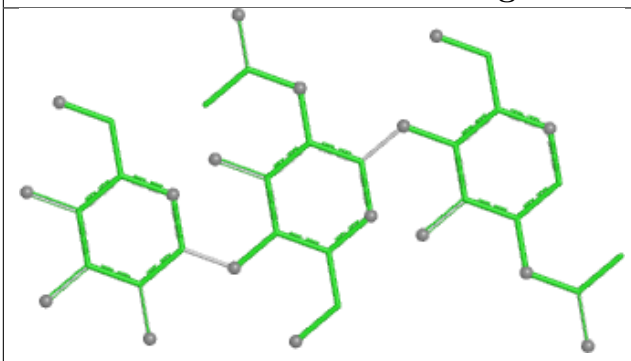
There are no ring outliers.

3 monomers are involved in 2 short contacts:

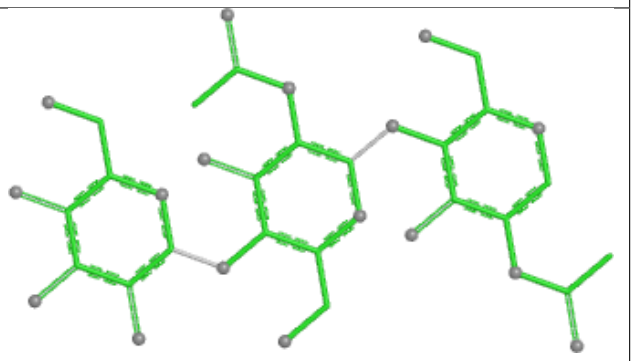
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	O	1	NAG	1	0
10	O	2	NAG	1	0
9	J	1	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

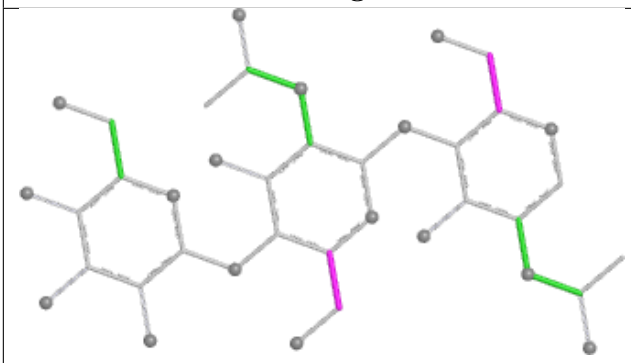
Oligosaccharide Chain J



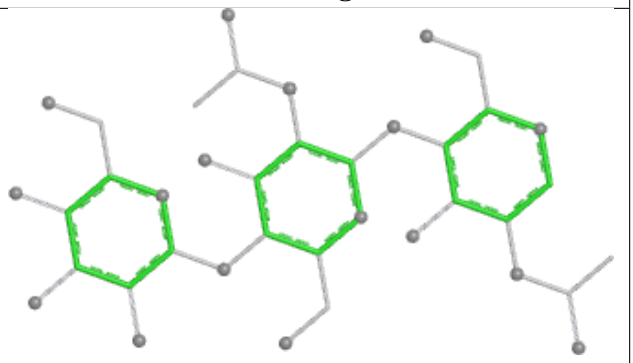
Bond lengths



Bond angles

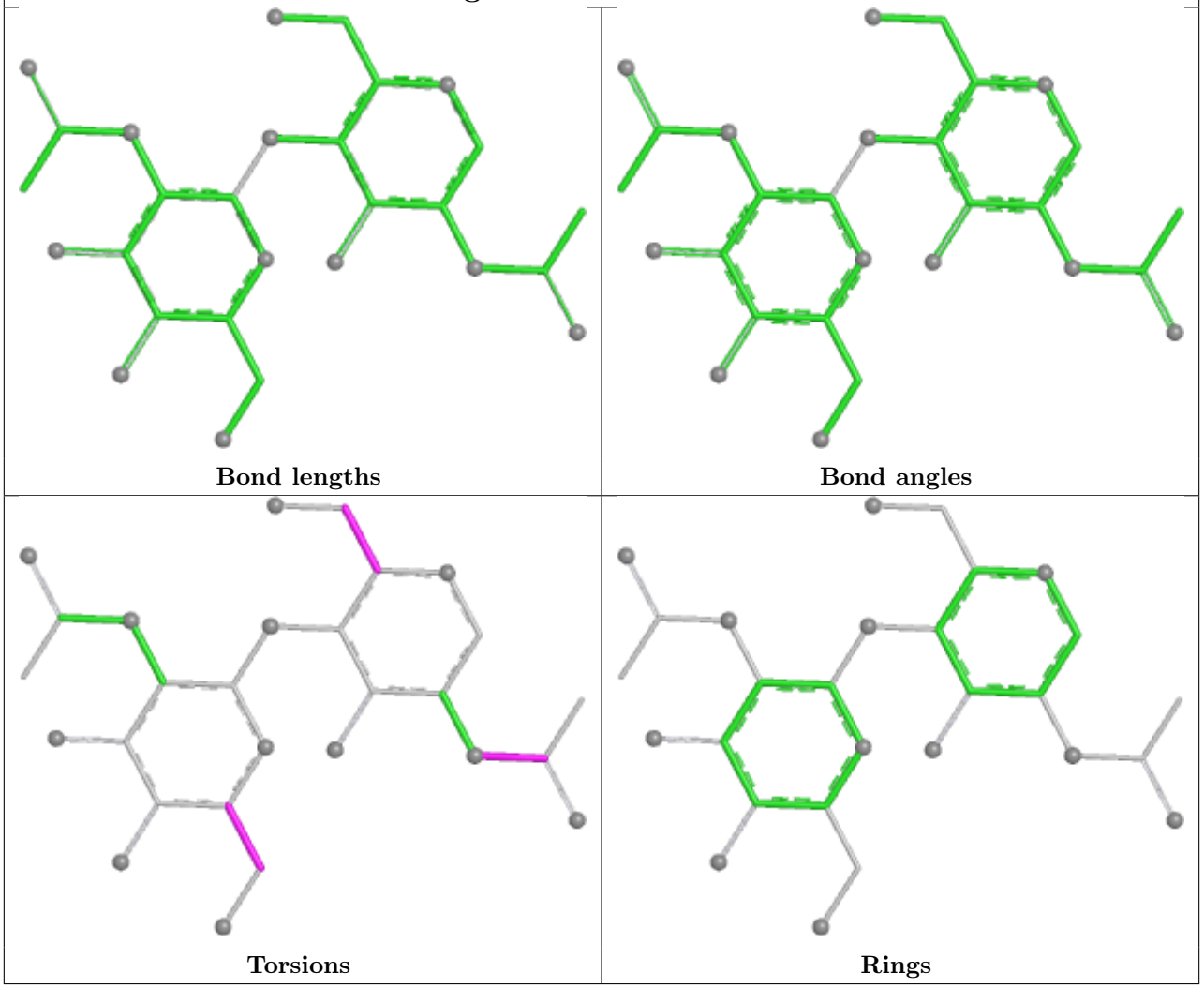


Torsions



Rings

Oligosaccharide Chain O



5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
12	NAG	G	1701	7	14,14,15	0.75	0	17,19,21	1.44	2 (11%)
11	CLR	A	301	-	31,31,31	14.20	19 (61%)	48,48,48	2.24	17 (35%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	NAG	G	1701	7	-	1/6/23/26	0/1/1/1
11	CLR	A	301	-	-	10/10/68/68	0/4/4/4

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	301	CLR	C12-C13	-56.81	0.55	1.54
11	A	301	CLR	C8-C9	-43.44	0.72	1.53
11	A	301	CLR	C10-C9	21.08	1.89	1.56
11	A	301	CLR	C8-C14	-14.70	1.26	1.53
11	A	301	CLR	C10-C5	-12.42	1.29	1.52
11	A	301	CLR	C6-C5	-9.05	1.14	1.33
11	A	301	CLR	C2-C3	-7.04	1.35	1.51
11	A	301	CLR	C12-C11	-5.83	1.41	1.53
11	A	301	CLR	C18-C13	4.80	1.62	1.54
11	A	301	CLR	C7-C8	4.33	1.60	1.53
11	A	301	CLR	C16-C17	4.28	1.63	1.54
11	A	301	CLR	C7-C6	3.74	1.57	1.50
11	A	301	CLR	C4-C5	3.58	1.58	1.51
11	A	301	CLR	C1-C10	3.31	1.60	1.54
11	A	301	CLR	C15-C14	3.25	1.61	1.54
11	A	301	CLR	C13-C17	-3.05	1.49	1.55
11	A	301	CLR	O1-C3	2.87	1.51	1.43
11	A	301	CLR	C1-C2	-2.51	1.48	1.53
11	A	301	CLR	C20-C17	-2.24	1.50	1.54

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	301	CLR	C11-C9-C10	-5.58	106.21	113.08
11	A	301	CLR	C1-C10-C9	5.35	115.82	108.74
11	A	301	CLR	C10-C9-C8	4.65	119.51	112.71
11	A	301	CLR	C15-C14-C13	4.14	108.71	103.84
12	G	1701	NAG	C2-N2-C7	4.03	128.31	122.90
11	A	301	CLR	C18-C13-C17	-3.98	104.47	111.68
11	A	301	CLR	C16-C17-C13	3.88	108.41	103.84
11	A	301	CLR	C12-C11-C9	-3.74	106.78	113.14
11	A	301	CLR	C19-C10-C9	-3.50	107.73	111.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
11	A	301	CLR	C21-C20-C17	-3.27	107.97	112.88
11	A	301	CLR	C13-C17-C20	-2.89	115.04	119.50
11	A	301	CLR	C7-C8-C9	2.88	113.06	109.72
11	A	301	CLR	C13-C14-C8	-2.74	110.52	114.41
11	A	301	CLR	C8-C7-C6	-2.59	109.18	112.76
11	A	301	CLR	C7-C8-C14	-2.53	107.34	110.93
11	A	301	CLR	C18-C13-C12	2.38	114.11	110.61
12	G	1701	NAG	C4-C3-C2	2.13	114.14	111.02
11	A	301	CLR	C1-C2-C3	2.12	113.29	110.48
11	A	301	CLR	C11-C12-C13	2.07	116.24	112.74

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	301	CLR	C13-C17-C20-C21
11	A	301	CLR	C13-C17-C20-C22
11	A	301	CLR	C16-C17-C20-C21
11	A	301	CLR	C16-C17-C20-C22
12	G	1701	NAG	C1-C2-N2-C7
11	A	301	CLR	C21-C20-C22-C23
11	A	301	CLR	C17-C20-C22-C23
11	A	301	CLR	C20-C22-C23-C24
11	A	301	CLR	C22-C23-C24-C25
11	A	301	CLR	C23-C24-C25-C26
11	A	301	CLR	C23-C24-C25-C27

There are no ring outliers.

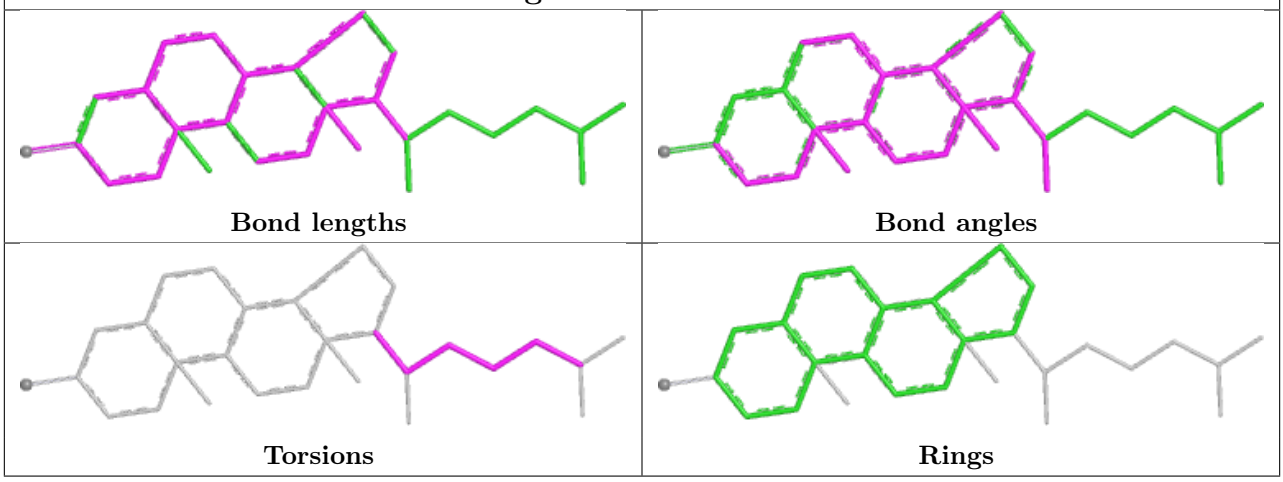
1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	A	301	CLR	7	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand CLR A 301



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.

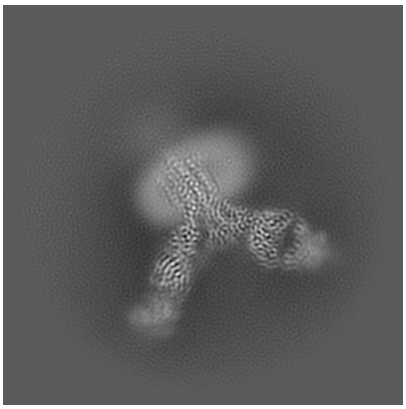
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-45808. These allow visual inspection of the internal detail of the map and identification of artifacts.

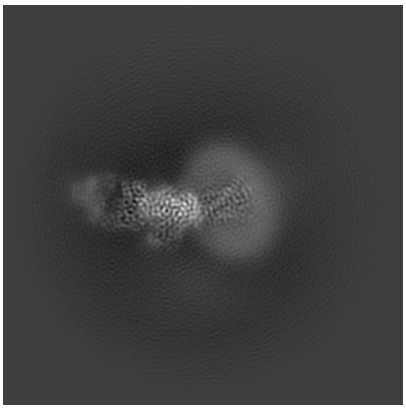
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

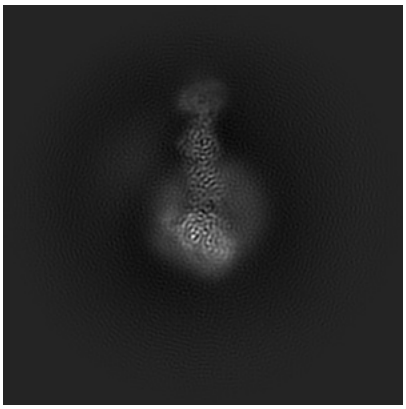
6.1.1 Primary map



X

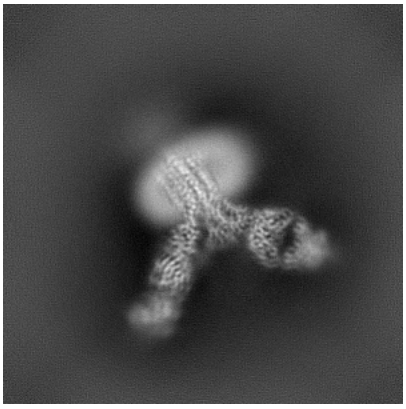


Y

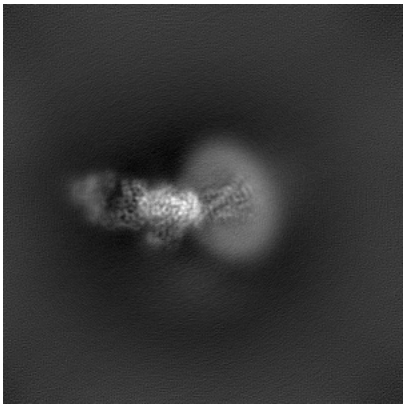


Z

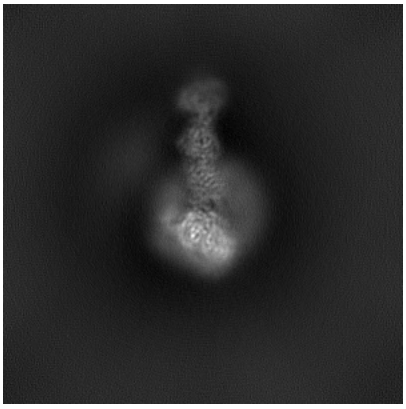
6.1.2 Raw map



X



Y

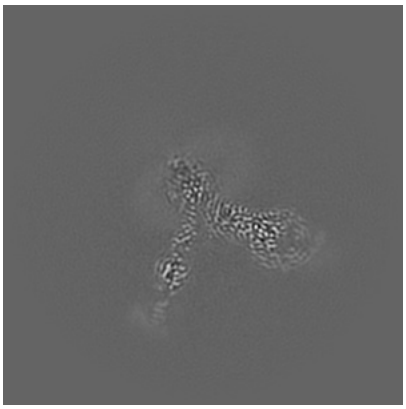


Z

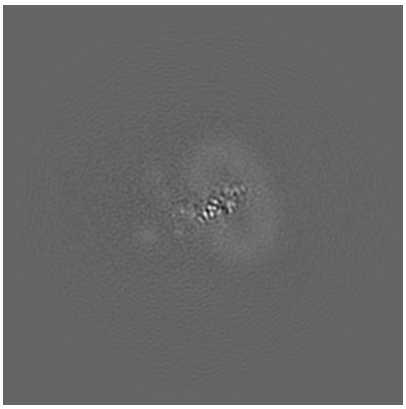
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

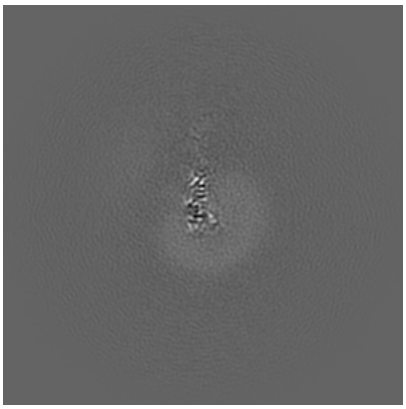
6.2.1 Primary map



X Index: 200

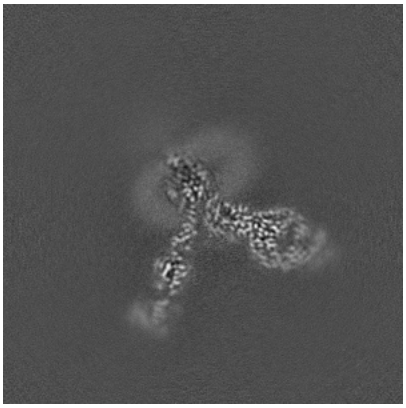


Y Index: 200

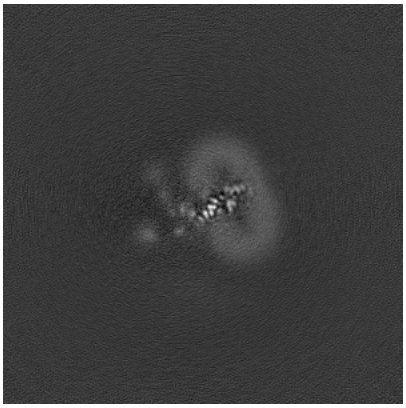


Z Index: 200

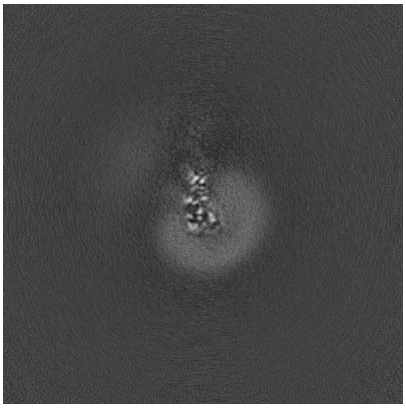
6.2.2 Raw map



X Index: 200



Y Index: 200

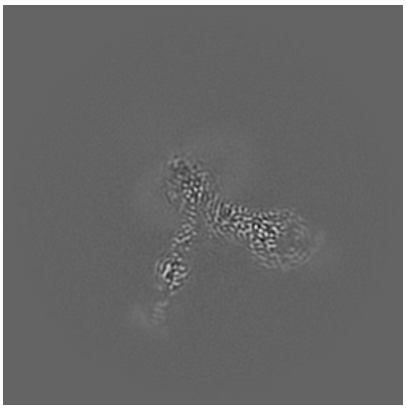


Z Index: 200

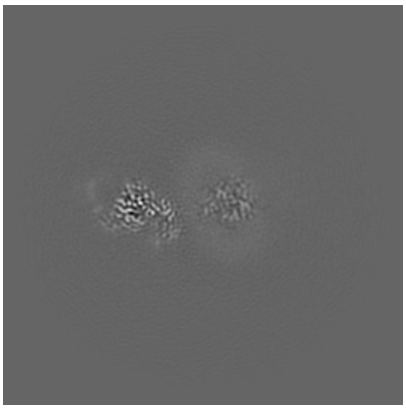
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

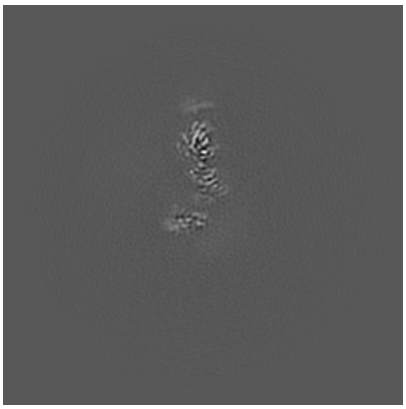
6.3.1 Primary map



X Index: 200

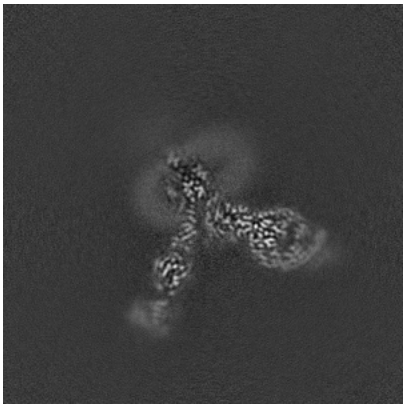


Y Index: 172

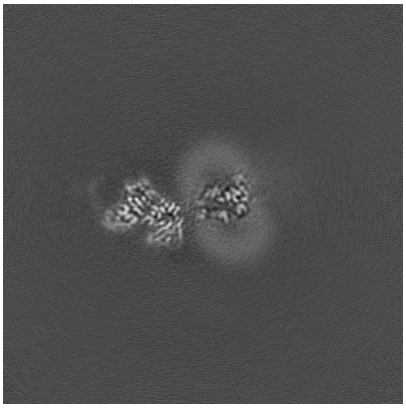


Z Index: 177

6.3.2 Raw map



X Index: 201



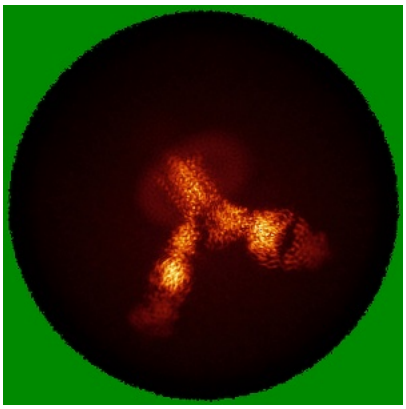
Y Index: 178

Z Index: 177

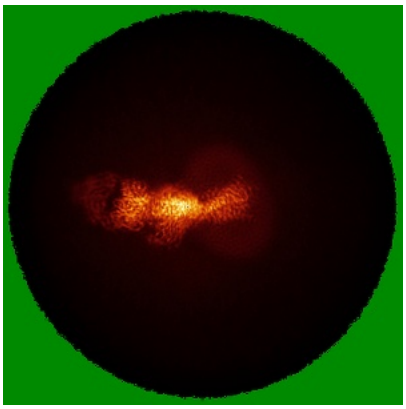
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

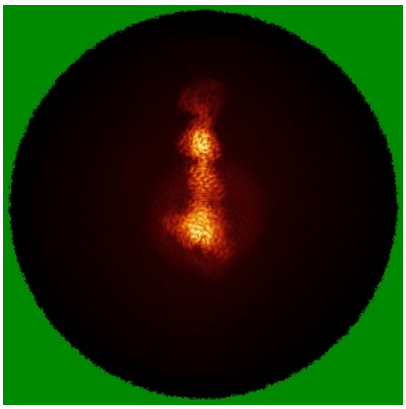
6.4.1 Primary map



X

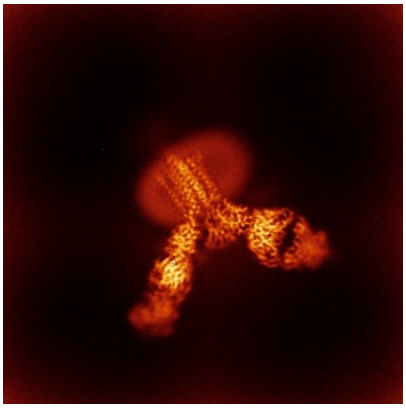


Y

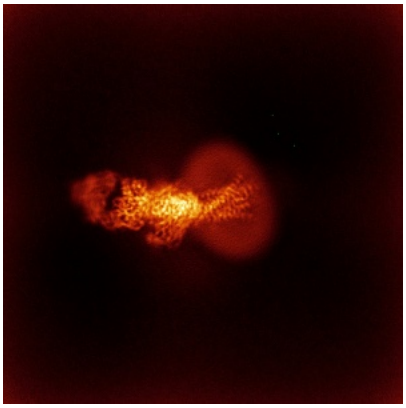


Z

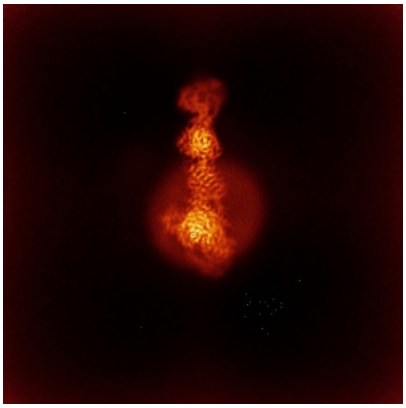
6.4.2 Raw map



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

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 7.44. 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

X Y Z

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.

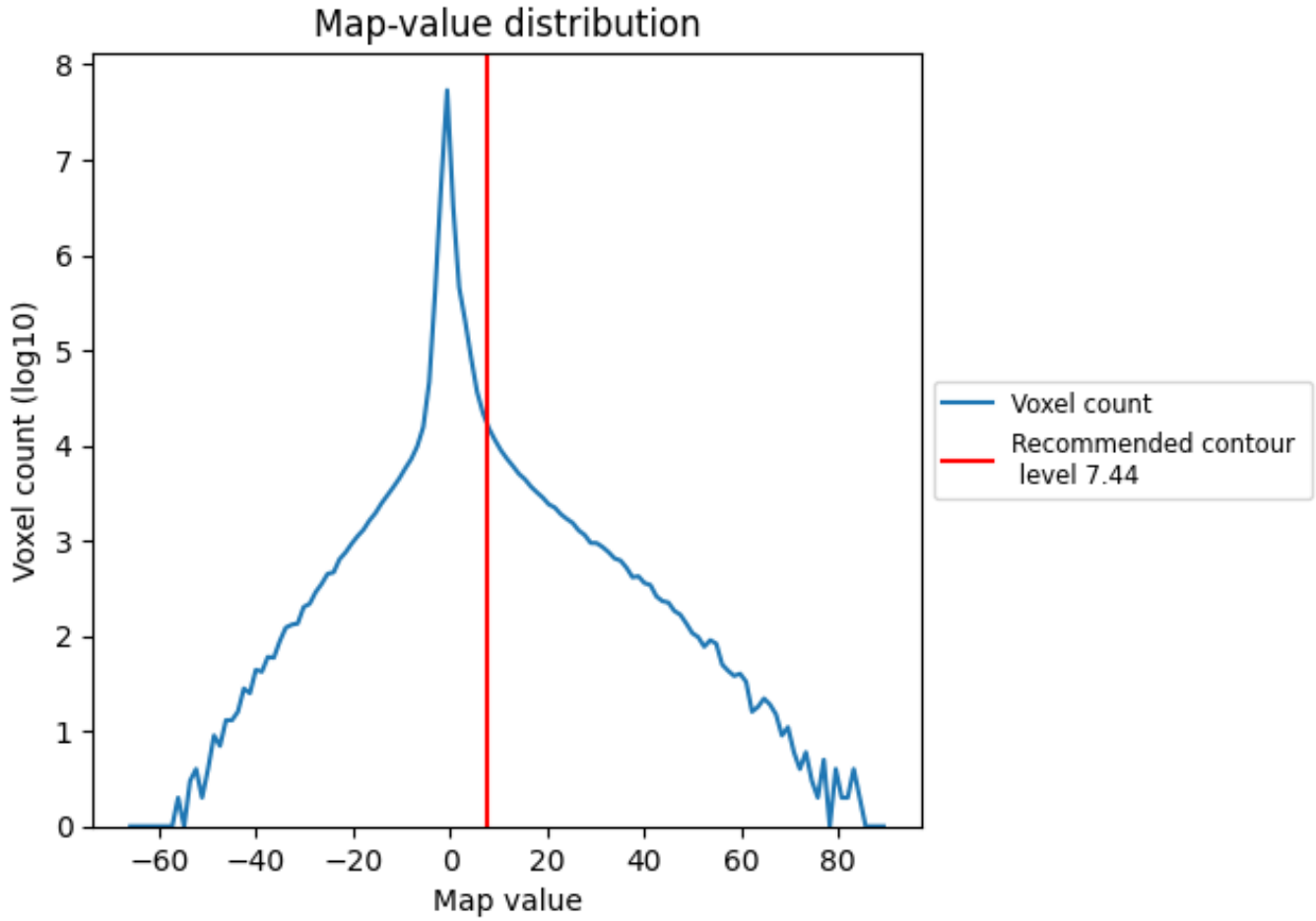
6.6 Mask visualisation (i)

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

7 Map analysis

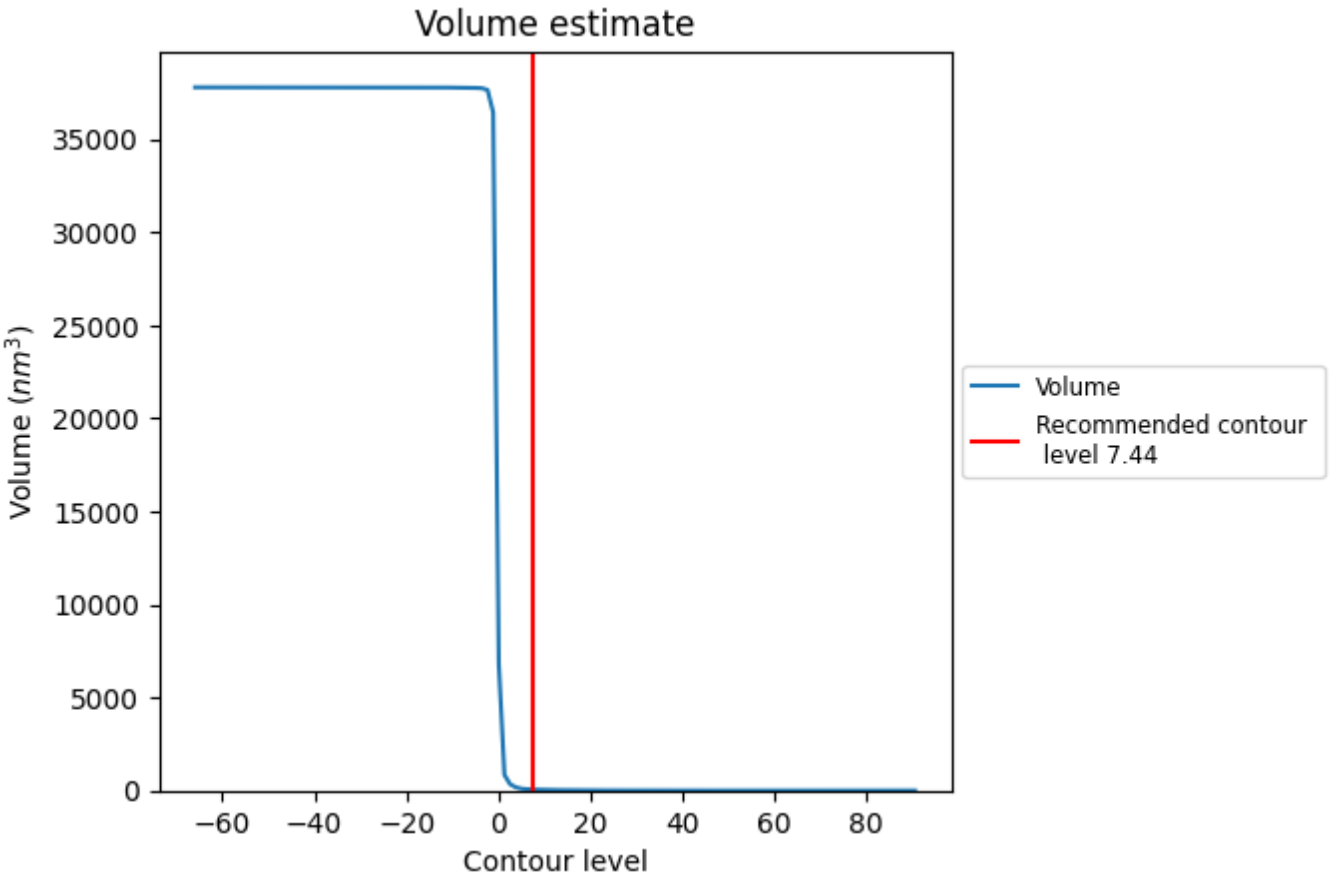
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

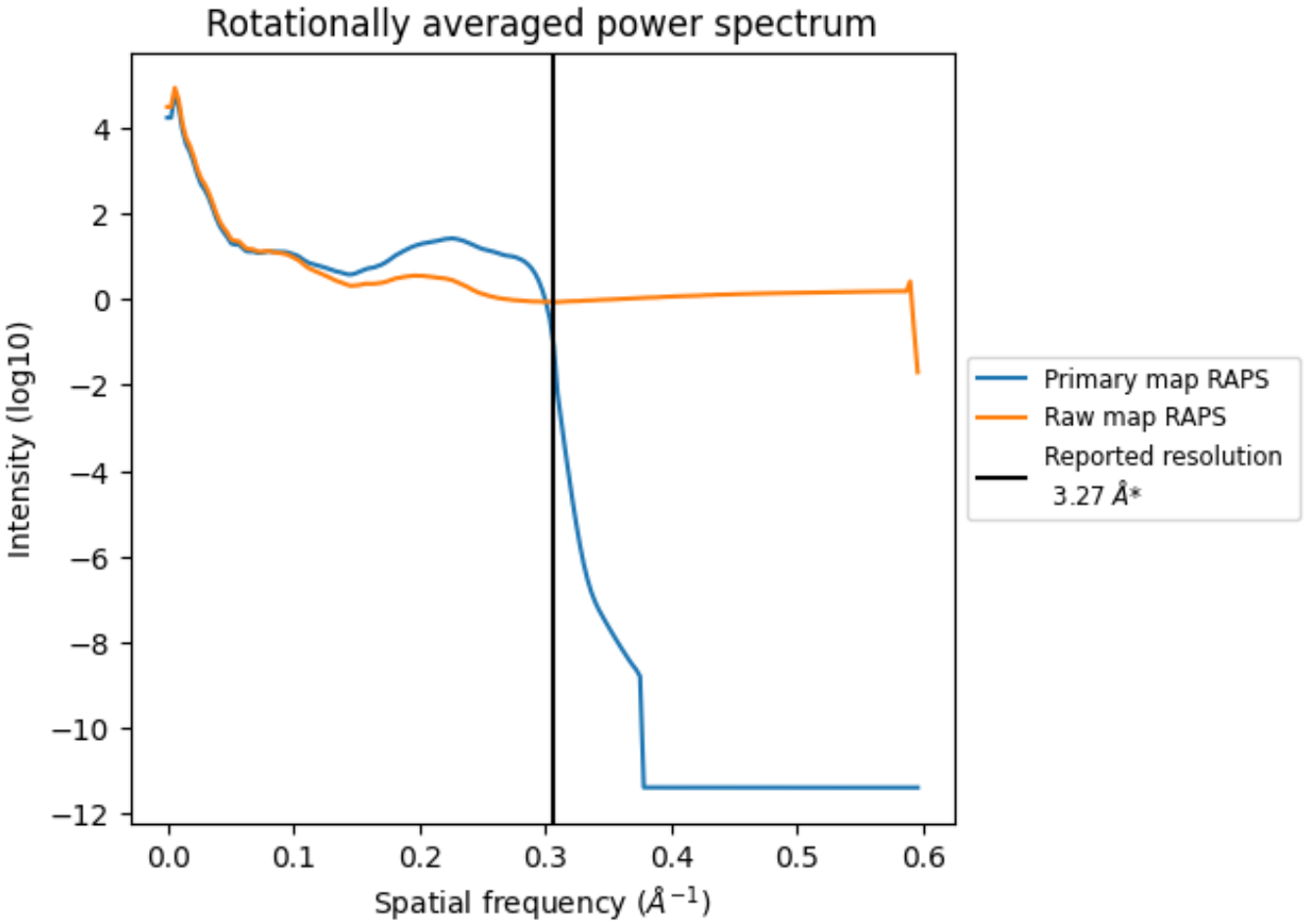
7.2 Volume estimate (i)



The volume at the recommended contour level is 58 nm^3; this corresponds to an approximate mass of 52 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)

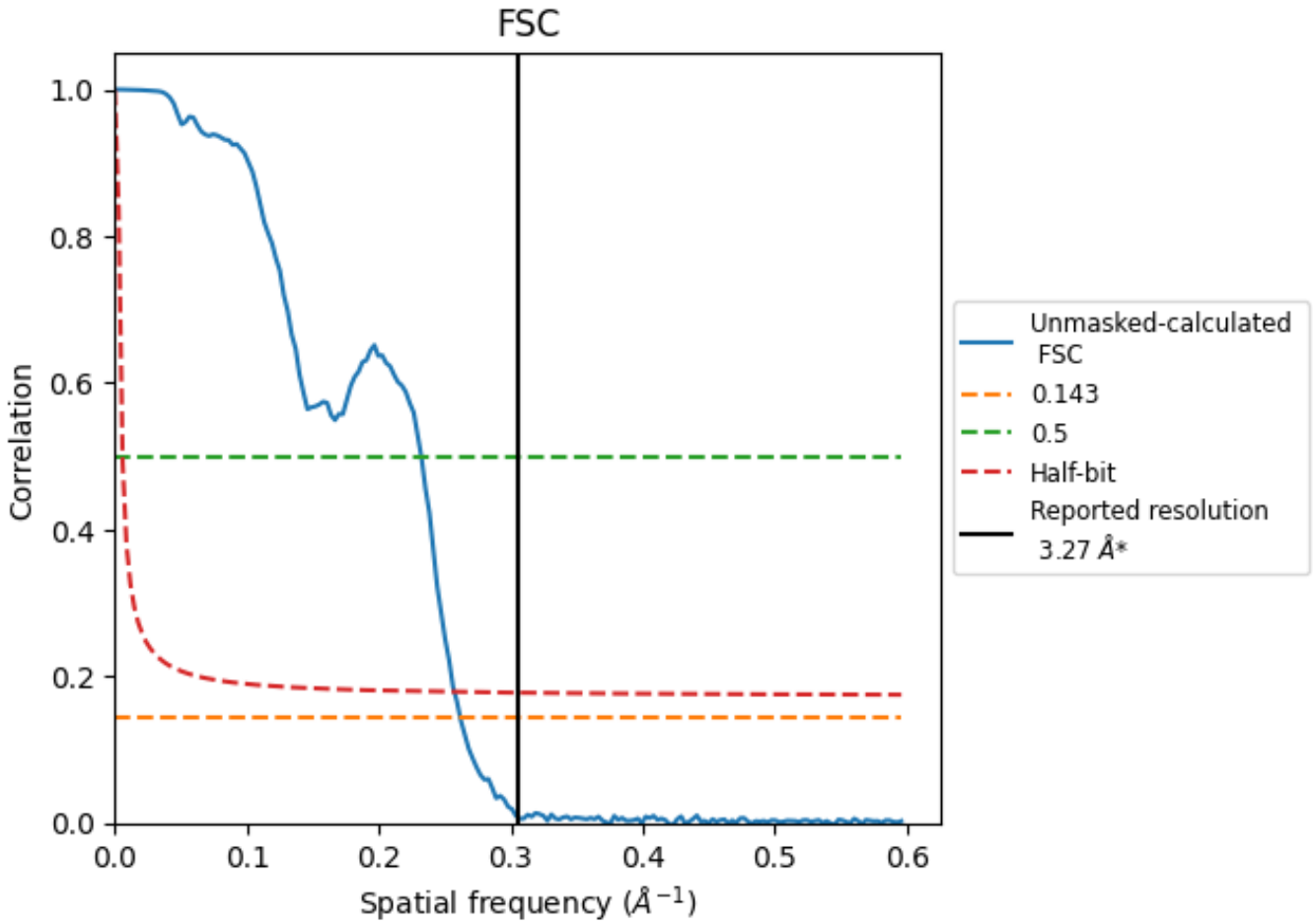


*Reported resolution corresponds to spatial frequency of 0.306 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.306 Å^{-1}

8.2 Resolution estimates (i)

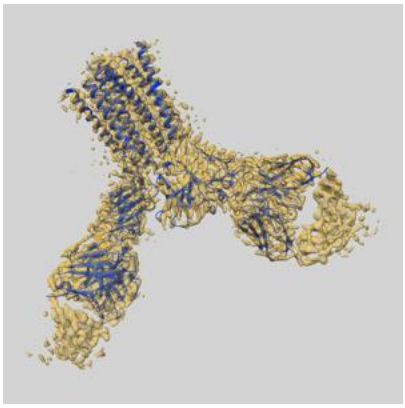
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.27	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.82	4.31	3.89

*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 3.82 differs from the reported value 3.27 by more than 10 %

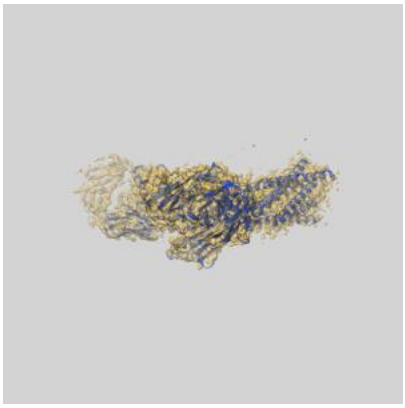
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-45808 and PDB model 9CQ4. Per-residue inclusion information can be found in section 3 on page 8.

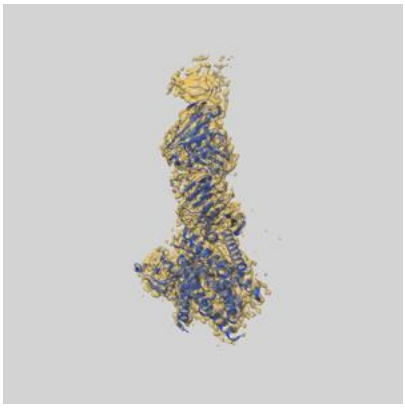
9.1 Map-model overlay



X



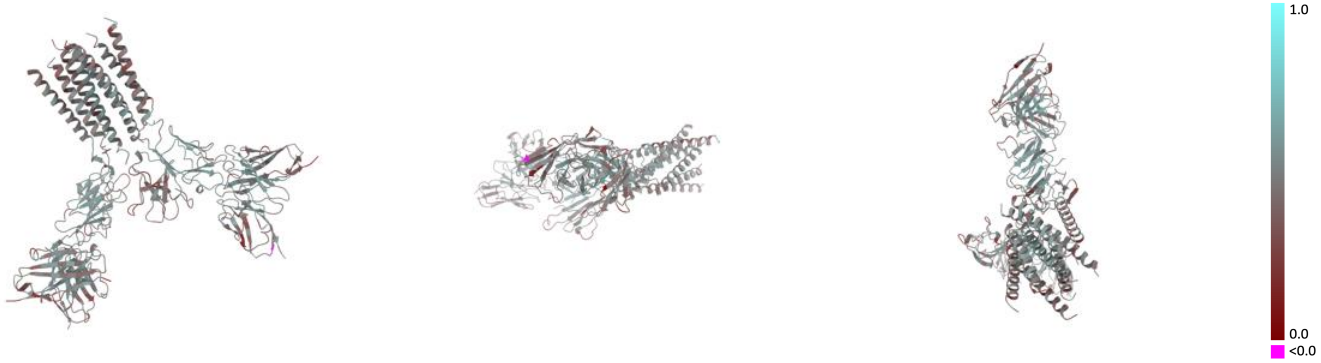
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 7.44 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.

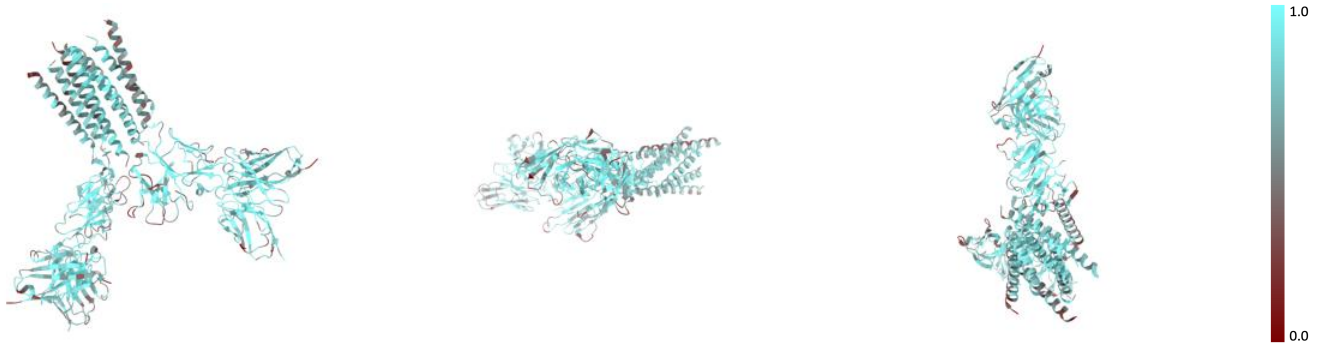
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

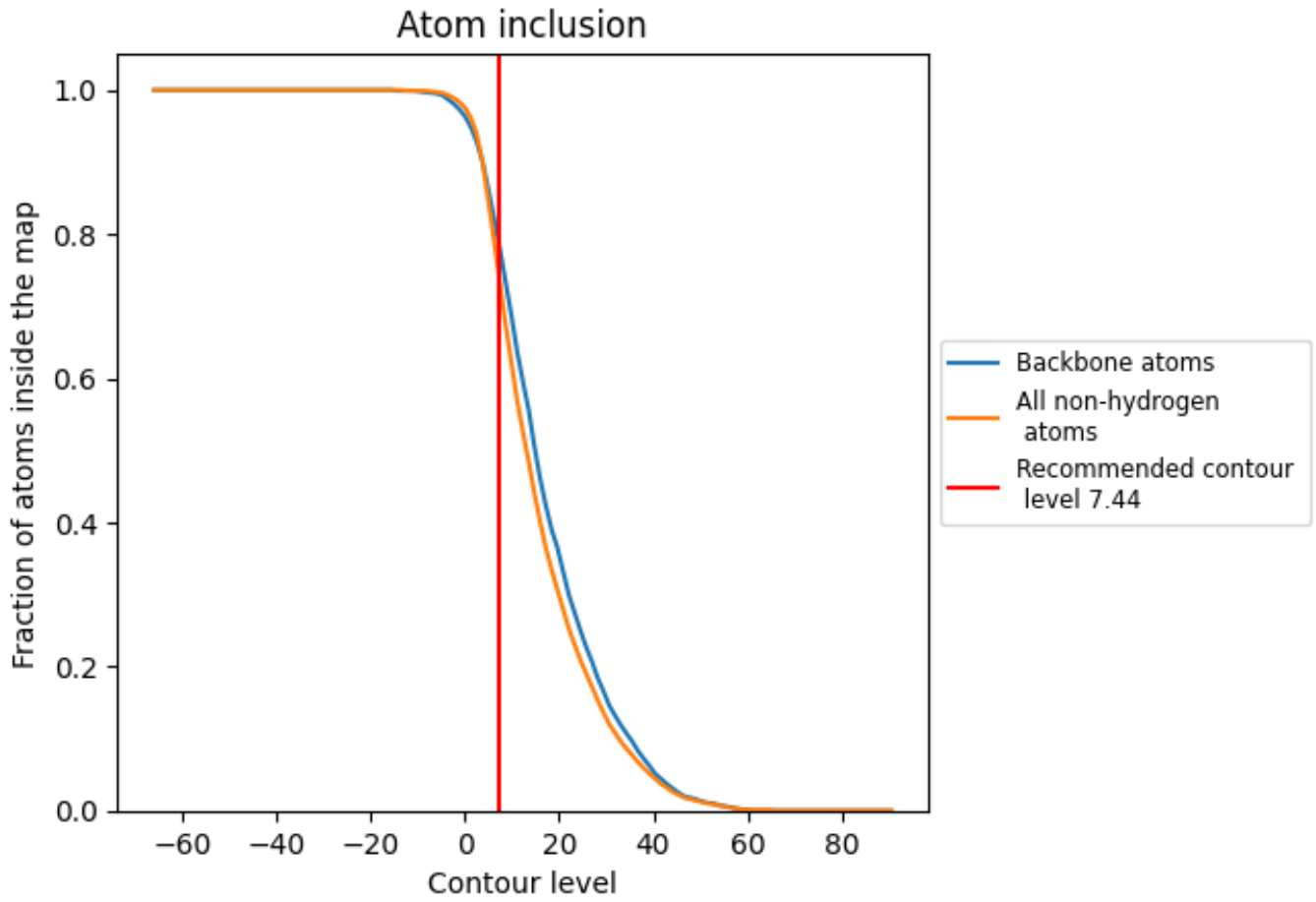
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (7.44).

9.4 Atom inclusion (i)



At the recommended contour level, 78% of all backbone atoms, 73% 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 (7.44) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7330	0.4640
A	0.8310	0.5110
B	0.7870	0.4940
C	0.7630	0.4690
D	0.7930	0.4640
E	0.7450	0.4960
F	0.7360	0.5000
G	0.6590	0.4210
H	0.7480	0.4650
J	0.1540	0.3450
K	0.6870	0.4400
L	0.7590	0.4510
O	0.1790	0.3150
Y	0.7600	0.4490
Z	0.5960	0.3990