



Full wwPDB EM Validation Report ⓘ

Mar 6, 2026 – 09:02 PM UTC

PDB ID : 6NIJ / pdb_00006nij
EMDB ID : EMD-9378
Title : PGT145 Fab in complex with full length AMC011 HIV-1 Env
Authors : Cottrell, C.A.; Torrents de la Pena, A.; Rantalainen, K.; Torres, J.L.; Ward, A.B.
Deposited on : 2018-12-29
Resolution : 5.70 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:

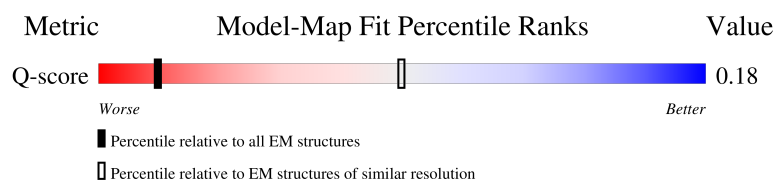
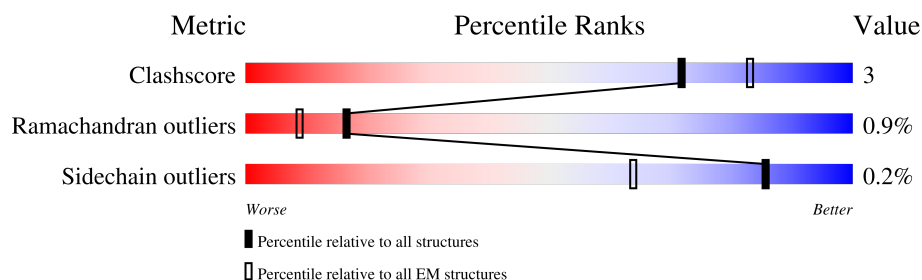
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 5.70 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.



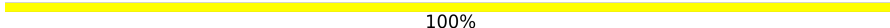
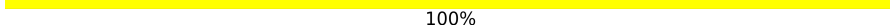
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	503 (5.20 - 6.20)

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	H	140	 89% 10% •
2	L	113	 87% 12% •
3	A	473	 82% 11% • 5%
3	C	473	 81% 12% • 6%

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Mol	Chain	Length	Quality of chain
3	E	473	
4	B	345	
4	D	345	
4	F	345	
5	G	2	
6	I	3	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 15939 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 PGT145 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	H	140	Total	C	N	O	S	0	0
			1095	685	191	214	5		

- Molecule 2 is a protein called PGT145 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	112	Total	C	N	O	S	0	0
			860	542	153	161	4		

- Molecule 3 is a protein called AMC011 Glycoprotein 120.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	449	Total	C	N	O	S	0	0
			3535	2229	618	662	26		
3	C	445	Total	C	N	O	S	0	0
			3507	2214	612	655	26		
3	E	444	Total	C	N	O	S	0	0
			3495	2205	612	652	26		

- Molecule 4 is a protein called AMC011 Glycoprotein 41.

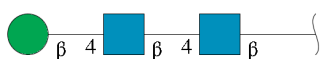
Mol	Chain	Residues	Atoms					AltConf	Trace
4	B	140	Total	C	N	O	S	0	0
			1124	714	191	213	6		
4	D	133	Total	C	N	O	S	0	0
			1067	676	180	205	6		
4	F	139	Total	C	N	O	S	0	0
			1119	711	190	212	6		

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



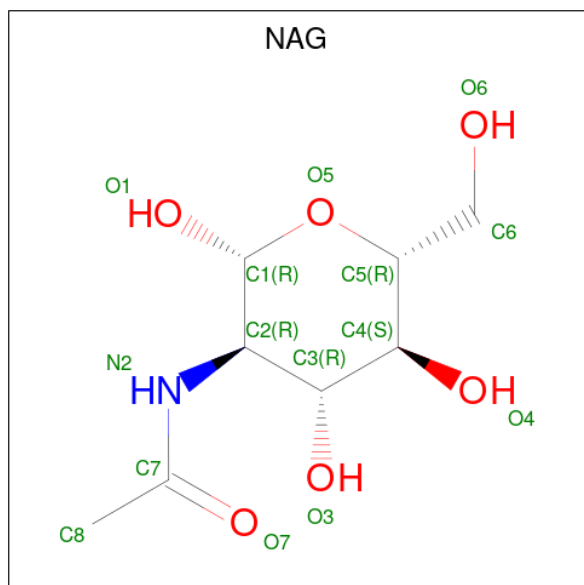
Mol	Chain	Residues	Atoms				AltConf	Trace
5	G	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 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
6	I	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).

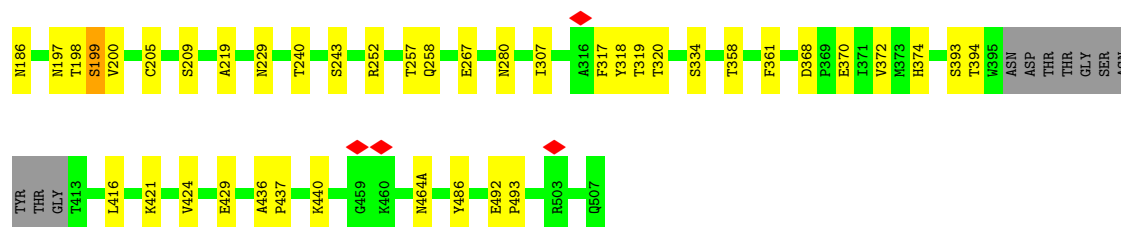


Mol	Chain	Residues	Atoms				AltConf
7	A	1	Total	C	N	O	0
			14	8	1	5	
7	C	1	Total	C	N	O	0
			14	8	1	5	

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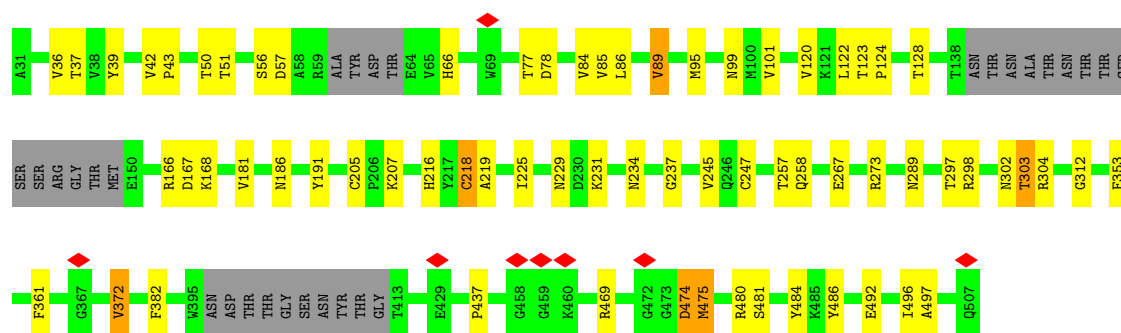
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Mol	Chain	Residues	Atoms				AltConf
7	C	1	Total	C	N	O	0
			14	8	1	5	
7	C	1	Total	C	N	O	0
			14	8	1	5	
7	E	1	Total	C	N	O	0
			14	8	1	5	



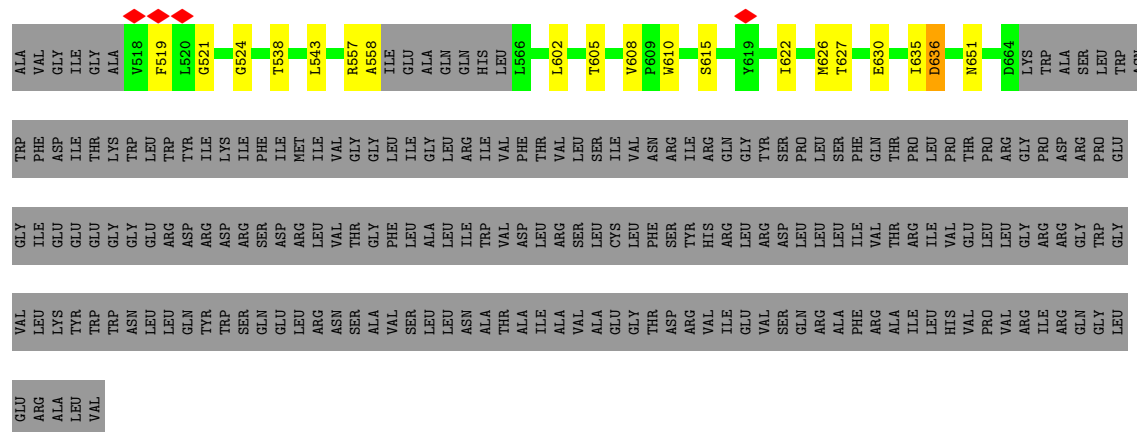
• Molecule 3: AMC011 Glycoprotein 120

Chain E: 79% 13% 6%



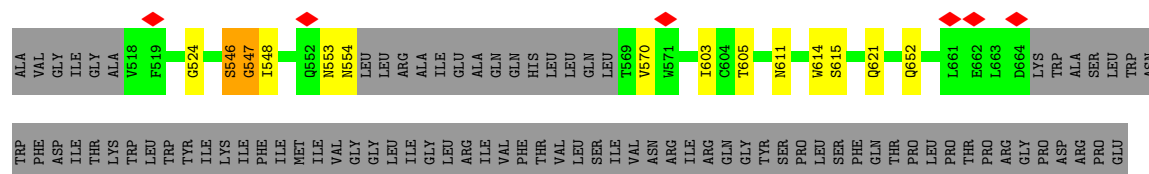
• Molecule 4: AMC011 Glycoprotein 41

Chain B: 35% 5% 59%

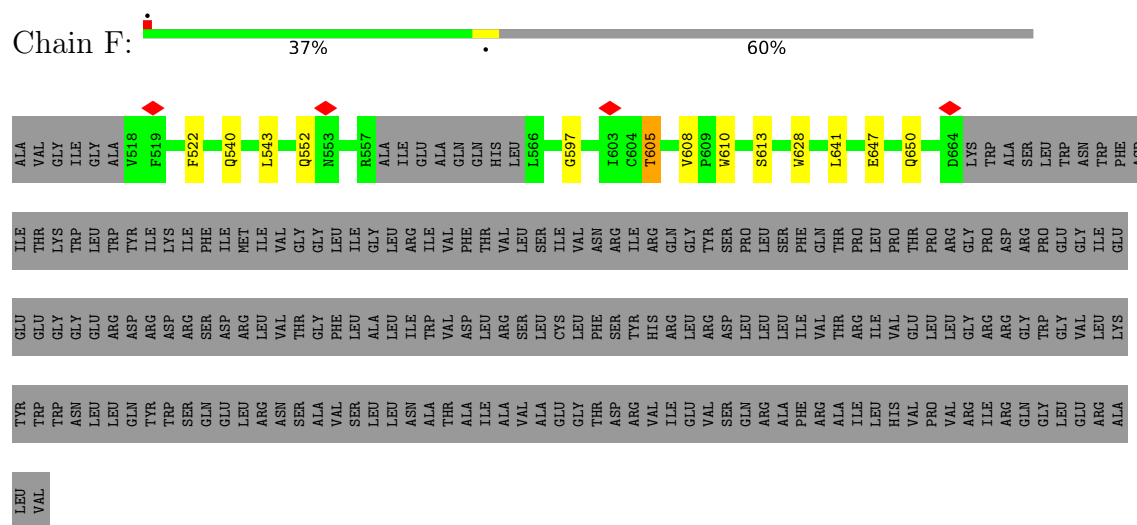


• Molecule 4: AMC011 Glycoprotein 41

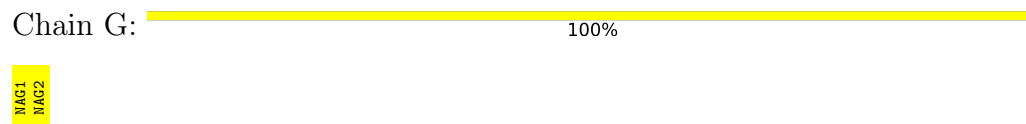
Chain D: 34% 61% 5%



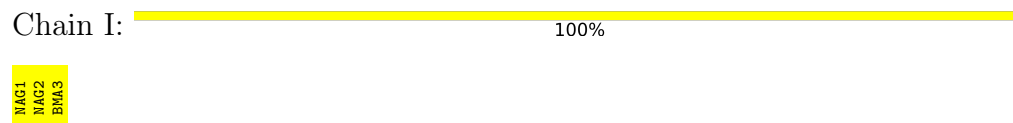
- Molecule 4: AMC011 Glycoprotein 41



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



- Molecule 6: beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	51588	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.533	Depositor
Minimum map value	-0.505	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.062	Depositor
Recommended contour level	0.4	Depositor
Map size (Å)	368.0, 368.0, 368.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.15, 1.15, 1.15	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

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	H	1.10	1/1122 (0.1%)	1.35	12/1519 (0.8%)
2	L	1.07	0/883	1.40	11/1199 (0.9%)
3	A	0.98	2/3609 (0.1%)	1.44	56/4899 (1.1%)
3	C	0.95	0/3581	1.57	50/4860 (1.0%)
3	E	0.98	0/3567	1.41	48/4839 (1.0%)
4	B	1.00	0/1143	1.25	12/1551 (0.8%)
4	D	1.01	0/1086	1.19	7/1474 (0.5%)
4	F	1.03	0/1138	1.27	7/1544 (0.5%)
All	All	1.00	3/16129 (0.0%)	1.42	203/21885 (0.9%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	452	LEU	CA-C	-6.16	1.50	1.53
1	H	37	VAL	CB-CG1	-5.93	1.32	1.52
3	A	35	TRP	NE1-CE2	-5.50	1.31	1.37

All (203) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	440	LYS	CA-C-O	-36.91	80.59	121.19
3	C	440	LYS	O-C-N	31.82	162.01	122.87
1	H	106	ASP	N-CA-C	10.70	125.66	109.62
2	L	76	PHE	CA-CB-CG	9.74	123.54	113.80
4	F	613	SER	N-CA-C	-9.54	101.76	113.97
1	H	37	VAL	CB-CA-C	-8.34	99.76	111.19
4	B	608	VAL	CA-C-N	8.34	128.22	120.21
4	B	608	VAL	C-N-CA	8.34	128.22	120.21
3	A	49	THR	N-CA-C	-8.24	99.89	110.53
4	B	538	THR	N-CA-C	-7.92	104.50	114.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	469	ARG	CA-C-N	7.92	127.87	120.03
3	A	469	ARG	C-N-CA	7.92	127.87	120.03
3	C	492	GLU	CA-C-N	7.90	128.09	119.87
3	C	492	GLU	C-N-CA	7.90	128.09	119.87
3	E	219	ALA	CA-C-N	7.83	128.27	120.52
3	E	219	ALA	C-N-CA	7.83	128.27	120.52
3	A	34	LEU	N-CA-C	7.78	121.58	110.14
3	E	303	THR	N-CA-C	7.73	118.19	108.45
3	E	205	CYS	CA-C-N	7.63	129.38	119.84
3	E	205	CYS	C-N-CA	7.63	129.38	119.84
3	E	492	GLU	CA-C-N	7.59	127.55	120.03
3	E	492	GLU	C-N-CA	7.59	127.55	120.03
3	A	245	VAL	N-CA-C	7.39	118.54	107.75
3	C	437	PRO	CA-C-N	7.39	127.55	120.31
3	C	437	PRO	C-N-CA	7.39	127.55	120.31
3	C	199	SER	CB-CA-C	-7.36	108.08	116.54
3	C	307	ILE	CB-CA-C	-7.36	101.43	110.99
3	A	319	THR	N-CA-C	7.32	121.11	110.28
3	C	317	PHE	N-CA-C	7.31	118.85	108.54
3	A	59	ARG	N-CA-C	-7.21	106.40	114.62
3	C	240	THR	N-CA-C	7.15	123.12	113.97
3	A	446	SER	N-CA-C	7.12	119.68	108.79
3	A	98	ASN	N-CA-C	7.05	125.82	110.80
3	A	205	CYS	CA-C-N	7.04	126.67	119.56
3	A	205	CYS	C-N-CA	7.04	126.67	119.56
3	A	298	ARG	CA-C-N	7.01	127.00	119.78
3	A	298	ARG	C-N-CA	7.01	127.00	119.78
2	L	31	HIS	N-CA-C	-6.95	99.99	110.28
3	C	42	VAL	CA-C-N	6.93	128.50	119.84
3	C	42	VAL	C-N-CA	6.93	128.50	119.84
4	B	627	THR	N-CA-C	-6.92	99.58	109.96
3	E	382	PHE	N-CA-C	6.91	119.94	108.96
3	A	97	LYS	N-CA-C	6.90	119.66	109.24
3	C	199	SER	N-CA-C	6.84	118.71	108.31
3	E	122	LEU	N-CA-C	6.79	119.47	108.41
4	F	641	LEU	N-CA-C	-6.78	103.97	111.36
3	A	72	HIS	N-CA-C	-6.71	103.89	111.14
3	E	437	PRO	CA-C-N	6.68	126.66	119.78
3	E	437	PRO	C-N-CA	6.68	126.66	119.78
3	A	71	THR	N-CA-C	-6.67	105.29	113.50
3	A	255	VAL	N-CA-C	6.63	117.84	108.36
3	E	120	VAL	N-CA-C	6.58	118.05	108.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	478	ASN	CA-CB-CG	6.54	119.14	112.60
3	E	42	VAL	N-CA-C	-6.50	94.84	108.88
3	E	166	ARG	N-CA-C	6.45	119.13	111.71
1	H	37	VAL	N-CA-C	6.43	118.09	108.96
1	H	106	ASP	CA-C-N	-6.41	112.83	121.80
1	H	106	ASP	C-N-CA	-6.41	112.83	121.80
3	C	205	CYS	CA-C-N	6.40	126.89	119.47
3	C	205	CYS	C-N-CA	6.40	126.89	119.47
3	C	219	ALA	CA-C-N	6.40	126.36	120.03
3	C	219	ALA	C-N-CA	6.40	126.36	120.03
3	A	237	GLY	CA-C-N	6.39	126.34	119.76
3	A	237	GLY	C-N-CA	6.39	126.34	119.76
4	B	630	GLU	N-CA-C	-6.37	105.53	113.55
3	C	182	VAL	CA-C-N	6.36	126.31	119.76
3	C	182	VAL	C-N-CA	6.36	126.31	119.76
3	A	80	ASN	CA-C-N	6.35	126.32	119.78
3	A	80	ASN	C-N-CA	6.35	126.32	119.78
3	A	117	LYS	CA-C-N	6.32	126.44	119.87
3	A	117	LYS	C-N-CA	6.32	126.44	119.87
3	E	474	ASP	CA-CB-CG	6.30	118.90	112.60
3	C	318	TYR	N-CA-C	6.28	119.73	109.24
4	D	652	GLN	N-CA-C	6.26	118.19	111.36
4	F	608	VAL	CA-C-N	6.25	126.21	119.78
4	F	608	VAL	C-N-CA	6.25	126.21	119.78
4	B	615	SER	N-CA-C	-6.23	101.55	110.59
3	E	36	VAL	N-CA-C	6.21	117.09	108.89
3	E	216	HIS	CA-CB-CG	6.20	120.00	113.80
3	A	123	THR	CA-C-N	6.17	125.87	119.82
3	A	123	THR	C-N-CA	6.17	125.87	119.82
3	A	211	GLU	CA-C-N	6.16	126.12	119.78
3	A	211	GLU	C-N-CA	6.16	126.12	119.78
3	C	334	SER	CA-C-N	6.16	126.93	120.03
3	C	334	SER	C-N-CA	6.16	126.93	120.03
1	H	35	HIS	CA-CB-CG	6.16	119.96	113.80
4	B	636	ASP	CA-CB-CG	6.14	118.74	112.60
3	C	486	TYR	N-CA-C	6.11	118.36	109.07
3	C	50	THR	N-CA-C	6.06	118.34	108.76
3	A	75	VAL	N-CA-C	6.06	114.64	107.73
1	H	50	TRP	N-CA-C	6.06	119.07	109.50
3	C	267	GLU	N-CA-C	6.05	117.95	111.36
3	C	372	VAL	N-CA-C	6.04	117.98	111.58
4	F	605	THR	N-CA-C	6.02	118.20	108.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	186	ASN	N-CA-C	6.02	119.94	112.24
2	L	48	THR	N-CA-C	-5.98	101.33	110.07
3	A	273	ARG	N-CA-C	5.96	119.19	109.24
3	C	416	LEU	CA-C-N	5.94	125.88	119.76
3	C	416	LEU	C-N-CA	5.94	125.88	119.76
3	A	78	ASP	CA-C-N	5.91	125.58	119.56
3	A	78	ASP	C-N-CA	5.91	125.58	119.56
3	A	191	TYR	N-CA-C	5.86	119.03	109.24
3	E	361	PHE	N-CA-C	5.82	119.02	109.76
2	L	75	ASP	CA-CB-CG	5.81	118.41	112.60
2	L	12	PRO	N-CA-C	-5.80	102.08	111.19
3	A	284	ILE	N-CA-C	5.74	116.57	108.36
1	H	101	TYR	N-CA-C	5.70	122.93	110.80
3	C	209	SER	N-CA-C	-5.68	102.35	110.59
3	E	497	ALA	CA-C-N	5.66	125.57	119.85
3	E	497	ALA	C-N-CA	5.66	125.57	119.85
3	E	218	CYS	N-CA-C	5.66	116.86	108.60
3	A	99	ASN	N-CA-C	5.66	122.85	110.80
3	E	496	ILE	N-CA-C	5.66	117.47	108.87
3	A	63	THR	N-CA-C	5.63	117.80	109.69
2	L	102	THR	O-C-N	5.63	125.00	120.83
3	E	486	TYR	N-CA-C	5.62	117.62	109.07
2	L	6	GLN	N-CA-C	5.61	117.75	108.49
3	E	42	VAL	CA-C-N	5.60	126.08	120.14
3	E	42	VAL	C-N-CA	5.60	126.08	120.14
3	E	437	PRO	N-CA-C	-5.57	104.62	110.58
1	H	96	SER	N-CA-C	5.55	117.23	108.96
3	C	368	ASP	CA-C-N	5.55	125.91	119.47
3	C	368	ASP	C-N-CA	5.55	125.91	119.47
3	C	374	HIS	CA-CB-CG	5.55	119.35	113.80
3	E	475	MET	N-CA-C	-5.53	105.41	111.82
3	C	125	LEU	CA-C-N	-5.52	113.22	122.17
3	C	125	LEU	C-N-CA	-5.52	113.22	122.17
3	C	123	THR	CA-C-N	5.51	125.22	119.82
3	C	123	THR	C-N-CA	5.51	125.22	119.82
3	A	358	THR	CA-C-N	5.51	128.57	120.91
3	A	358	THR	C-N-CA	5.51	128.57	120.91
3	A	375	SER	N-CA-C	5.51	118.58	110.59
2	L	14	THR	N-CA-C	-5.50	102.72	109.65
3	E	312	GLY	CA-C-N	5.50	125.33	119.28
3	E	312	GLY	C-N-CA	5.50	125.33	119.28
3	E	89	VAL	N-CA-C	5.49	115.79	108.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	610	TRP	N-CA-C	5.48	116.30	108.74
3	E	297	THR	CA-C-N	5.47	127.99	120.39
3	E	297	THR	C-N-CA	5.47	127.99	120.39
3	E	120	VAL	N-CA-CB	-5.45	104.78	110.72
4	D	546	SER	N-CA-C	5.44	116.41	108.14
3	A	497	ALA	CA-C-N	5.41	125.17	119.76
3	A	497	ALA	C-N-CA	5.41	125.17	119.76
3	A	41	GLY	N-CA-C	-5.40	107.75	115.64
4	D	570	VAL	CA-C-N	5.39	128.04	120.28
4	D	570	VAL	C-N-CA	5.39	128.04	120.28
4	B	610	TRP	CB-CA-C	-5.38	101.86	110.79
3	C	120	VAL	N-CA-C	5.36	120.50	109.34
3	E	298	ARG	N-CA-C	5.36	116.45	109.64
3	E	372	VAL	CB-CA-C	-5.36	106.16	111.30
3	C	317	PHE	CB-CA-C	-5.36	103.77	111.70
4	D	621	GLN	N-CA-C	-5.36	105.52	111.36
3	C	436	ALA	CA-C-N	5.34	123.50	119.66
3	C	436	ALA	C-N-CA	5.34	123.50	119.66
3	E	128	THR	N-CA-C	5.32	117.55	110.53
3	A	436	ALA	CA-C-N	5.30	125.84	120.38
3	A	436	ALA	C-N-CA	5.30	125.84	120.38
3	A	452	LEU	N-CA-C	5.30	113.84	108.75
2	L	75	ASP	N-CA-C	5.30	116.33	108.60
4	B	651	ASN	CA-CB-CG	-5.29	107.31	112.60
3	C	424	VAL	N-CA-C	5.29	117.68	108.95
3	A	42	VAL	N-CA-C	-5.28	104.11	109.02
2	L	63	VAL	CA-C-N	5.28	125.74	120.52
2	L	63	VAL	C-N-CA	5.28	125.74	120.52
4	F	597	GLY	N-CA-C	-5.27	107.99	115.43
3	C	89	VAL	N-CA-C	5.27	115.49	108.11
3	E	101	VAL	N-CA-C	-5.25	104.53	111.09
3	E	237	GLY	CA-C-N	5.24	125.16	119.76
3	E	237	GLY	C-N-CA	5.24	125.16	119.76
3	A	84	VAL	N-CA-C	5.23	115.39	107.75
3	A	42	VAL	CA-C-N	5.23	126.38	119.84
3	A	42	VAL	C-N-CA	5.23	126.38	119.84
1	H	56	GLY	N-CA-C	-5.21	105.62	112.82
3	E	219	ALA	N-CA-C	5.20	116.44	109.83
3	C	131	CYS	N-CA-C	5.20	116.42	108.52
3	E	191	TYR	N-CA-C	5.19	117.70	109.50
3	A	417	PRO	N-CA-C	-5.19	103.13	111.38
4	B	602	LEU	N-CA-C	-5.16	104.59	111.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	80	ASN	CA-C-N	5.13	125.06	119.78
3	C	80	ASN	C-N-CA	5.13	125.06	119.78
1	H	35	HIS	N-CA-C	-5.11	100.01	108.75
3	E	273	ARG	N-CA-C	5.11	117.15	109.23
4	B	524	GLY	N-CA-C	5.09	121.54	114.92
3	A	414	ILE	CA-C-N	-5.09	116.34	123.10
3	A	414	ILE	C-N-CA	-5.09	116.34	123.10
3	A	467	ILE	CA-C-N	-5.09	115.66	122.42
3	A	467	ILE	C-N-CA	-5.09	115.66	122.42
3	E	85	VAL	N-CA-C	5.08	115.29	108.17
3	E	229	ASN	N-CA-C	-5.06	106.42	112.59
3	E	43	PRO	CA-C-N	5.06	129.87	122.69
3	E	43	PRO	C-N-CA	5.06	129.87	122.69
3	A	120	VAL	N-CA-C	5.05	116.10	109.58
3	A	158	SER	N-CA-C	5.04	116.85	109.24
4	D	547	GLY	CA-C-N	5.03	131.03	121.97
4	D	547	GLY	C-N-CA	5.03	131.03	121.97
3	E	43	PRO	N-CA-C	5.03	120.08	111.68
1	H	16	SER	N-CA-C	5.02	117.11	109.63
3	C	64	GLU	N-CA-C	-5.02	105.51	111.69
3	C	252	ARG	CA-C-N	5.02	124.92	119.85
3	C	252	ARG	C-N-CA	5.02	124.92	119.85
3	E	353	PHE	N-CA-C	-5.01	107.56	113.97
4	B	521	GLY	N-CA-C	-5.01	101.31	113.18
3	C	493	PRO	N-CA-C	5.00	120.18	114.03

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	H	1095	0	1033	6	0
2	L	860	0	841	2	0
3	A	3535	0	3500	16	0
3	C	3507	0	3475	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	3495	0	3468	29	0
4	B	1124	0	1114	6	0
4	D	1067	0	1044	12	0
4	F	1119	0	1109	29	0
5	G	28	0	25	0	0
6	I	39	0	33	0	0
7	A	14	0	13	0	0
7	C	42	0	39	1	0
7	E	14	0	13	0	0
All	All	15939	0	15707	108	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 3.

All (108) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:522:PHE:CD2	4:F:543:LEU:HD21	1.27	1.70
4:F:522:PHE:CD2	4:F:543:LEU:CD2	1.91	1.51
4:D:605:THR:HG22	3:E:37:THR:CG2	1.41	1.50
4:F:540:GLN:CD	4:F:543:LEU:HD12	1.46	1.40
4:F:540:GLN:NE2	4:F:543:LEU:CD1	2.06	1.19
4:F:540:GLN:OE1	4:F:543:LEU:HD12	1.42	1.17
4:F:522:PHE:CG	4:F:543:LEU:HD21	1.82	1.14
4:D:605:THR:CG2	3:E:37:THR:HG22	1.78	1.12
4:F:540:GLN:CD	4:F:543:LEU:CD1	2.24	1.10
4:F:540:GLN:HE22	4:F:543:LEU:HD11	1.13	1.09
4:F:540:GLN:NE2	4:F:543:LEU:HD11	1.65	1.09
4:D:605:THR:CG2	3:E:37:THR:CG2	2.30	1.08
4:D:605:THR:HG22	3:E:37:THR:HG23	1.40	1.01
4:D:605:THR:HG22	3:E:37:THR:HG22	1.03	0.99
4:F:522:PHE:CE2	4:F:543:LEU:CD2	2.48	0.96
4:F:540:GLN:HE22	4:F:543:LEU:CD1	1.71	0.96
4:F:540:GLN:OE1	4:F:543:LEU:CD1	2.13	0.95
4:F:522:PHE:CD2	4:F:543:LEU:HD23	2.03	0.93
4:F:522:PHE:HD2	4:F:543:LEU:HD21	1.13	0.90
4:F:522:PHE:CD2	4:F:543:LEU:CG	2.57	0.87
4:F:540:GLN:NE2	4:F:543:LEU:HD12	1.80	0.87
4:F:522:PHE:CE2	4:F:543:LEU:HD23	2.08	0.86
4:F:522:PHE:HD2	4:F:543:LEU:CG	1.94	0.80
4:F:522:PHE:HD2	4:F:543:LEU:CD2	1.70	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:160:ASN:N	3:A:160:ASN:OD1	2.32	0.63
4:F:522:PHE:CD2	4:F:543:LEU:HG	2.35	0.61
3:A:66:HIS:NE2	3:A:115:SER:HB2	2.15	0.61
3:A:35:TRP:CD2	4:B:605:THR:HG23	2.40	0.57
3:A:35:TRP:CE3	4:B:605:THR:HG23	2.40	0.56
1:H:100(A):ARG:HB3	1:H:100(P):TRP:HB3	1.88	0.56
4:D:553:ASN:O	4:D:554:ASN:C	2.48	0.56
3:A:66:HIS:CE1	3:A:115:SER:HB2	2.42	0.55
4:F:522:PHE:CE2	4:F:543:LEU:HG	2.43	0.53
3:E:231:LYS:NZ	3:E:267:GLU:OE1	2.41	0.53
3:E:167:ASP:OD2	3:E:168:LYS:NZ	2.42	0.53
3:E:289:ASN:OD1	3:E:289:ASN:N	2.40	0.52
3:C:123:THR:N	3:C:124:PRO:HD2	2.25	0.52
3:A:63:THR:OG1	3:A:64:GLU:N	2.44	0.51
4:B:519:PHE:CD2	4:B:543:LEU:HD21	2.45	0.51
4:F:522:PHE:CB	4:F:543:LEU:HD21	2.37	0.51
3:C:197:ASN:OD1	3:C:197:ASN:N	2.43	0.51
4:F:628:TRP:H	4:F:628:TRP:CD1	2.29	0.51
4:D:546:SER:OG	4:D:547:GLY:N	2.43	0.50
1:H:108:TRP:CG	1:H:109:GLY:H	2.29	0.50
4:F:522:PHE:CE2	4:F:543:LEU:CG	2.91	0.50
4:B:557:ARG:O	4:B:558:ALA:C	2.53	0.49
3:C:163:THR:OG1	3:C:164:SER:N	2.43	0.49
3:E:123:THR:N	3:E:124:PRO:CD	2.76	0.49
4:F:605:THR:O	4:F:605:THR:HG23	2.12	0.49
3:E:474:ASP:OD1	3:E:475:MET:N	2.45	0.49
4:F:540:GLN:HA	4:F:543:LEU:HD12	1.93	0.49
3:E:225:ILE:HB	3:E:245:VAL:HB	1.94	0.48
3:E:56:SER:OG	3:E:57:ASP:N	2.46	0.48
1:H:16:SER:OG	1:H:17:SER:N	2.47	0.48
3:E:303:THR:OG1	3:E:304:ARG:N	2.46	0.48
2:L:112:LYS:NZ	2:L:113:ARG:OXT	2.40	0.47
3:C:199:SER:OG	3:C:200:VAL:N	2.47	0.47
3:C:370:GLU:OE2	3:C:421:LYS:NZ	2.47	0.47
4:B:622:ILE:O	4:B:626:MET:N	2.47	0.47
3:A:198:THR:OG1	3:A:199:SER:N	2.47	0.47
3:C:62:ASP:O	3:C:66:HIS:CD2	2.68	0.47
3:E:257:THR:OG1	3:E:258:GLN:N	2.46	0.47
3:E:66:HIS:NE2	3:E:207:LYS:HE2	2.30	0.47
3:C:198:THR:HB	7:C:603:NAG:H82	1.97	0.46
4:D:614:TRP:CG	4:D:615:SER:H	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:95:MET:HB3	3:E:484:TYR:CD2	2.50	0.46
3:A:77:THR:OG1	3:A:78:ASP:N	2.47	0.46
3:C:77:THR:OG1	3:C:78:ASP:N	2.48	0.46
3:C:160:ASN:OD1	3:C:160:ASN:N	2.48	0.46
3:E:99:ASN:OD1	3:E:99:ASN:N	2.47	0.46
3:C:162:THR:OG1	3:C:163:THR:N	2.47	0.46
4:D:614:TRP:CG	4:D:615:SER:N	2.85	0.45
4:F:540:GLN:OE1	4:F:543:LEU:HD13	2.13	0.45
3:A:283:ILE:HG12	3:A:454:LEU:HB3	1.99	0.45
4:D:611:ASN:OD1	4:D:611:ASN:N	2.50	0.45
3:E:258:GLN:NE2	3:E:372:VAL:O	2.50	0.45
3:C:358:THR:OG1	3:C:464(A):ASN:O	2.34	0.44
3:E:77:THR:OG1	3:E:78:ASP:N	2.50	0.44
3:C:229:ASN:ND2	3:C:243:SER:OG	2.50	0.44
3:E:123:THR:N	3:E:124:PRO:HD2	2.33	0.43
3:C:62:ASP:OD1	3:C:62:ASP:N	2.50	0.43
1:H:100(J):GLY:N	1:H:100(K):PRO:CD	2.81	0.43
3:A:362:ASN:HB3	3:A:467:ILE:HG23	2.01	0.43
4:F:647:GLU:O	4:F:650:GLN:HG2	2.20	0.42
3:E:480:ARG:HB3	3:E:484:TYR:CE2	2.54	0.42
2:L:40:TRP:HE1	2:L:91:TYR:HB3	1.84	0.42
4:B:635:ILE:O	4:B:636:ASP:C	2.63	0.42
3:A:122:LEU:O	3:A:123:THR:C	2.62	0.42
3:C:280:ASN:OD1	3:C:280:ASN:N	2.47	0.42
4:D:603:ILE:HB	3:E:39:TYR:CZ	2.54	0.42
3:C:393:SER:OG	3:C:394:THR:N	2.53	0.42
4:D:524:GLY:H	3:E:86:LEU:HD23	1.84	0.42
3:E:186:ASN:OD1	3:E:186:ASN:N	2.53	0.42
1:H:108:TRP:CG	1:H:109:GLY:N	2.87	0.41
3:A:36:VAL:O	3:A:37:THR:CB	2.68	0.41
3:E:480:ARG:O	3:E:481:SER:C	2.63	0.41
3:C:319:THR:OG1	3:C:320:THR:N	2.53	0.41
3:E:86:LEU:HB3	3:E:89:VAL:HB	2.02	0.41
1:H:93:LEU:HD12	1:H:106:ASP:HB3	2.02	0.41
3:A:123:THR:N	3:A:124:PRO:CD	2.84	0.41
4:F:552:GLN:OE1	4:F:552:GLN:N	2.48	0.41
3:E:50:THR:OG1	3:E:51:THR:N	2.53	0.41
3:E:218:CYS:HB3	3:E:247:CYS:HA	2.02	0.41
3:E:234:ASN:N	3:E:234:ASN:OD1	2.52	0.41
3:A:133:ASP:OD1	3:A:155:LYS:NZ	2.53	0.40
3:A:211:GLU:HA	3:A:212:PRO:HD3	1.96	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:469:ARG:HB2	3:A:470:PRO:HD2	2.03	0.40
3:C:257:THR:OG1	3:C:258:GLN:N	2.46	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	138/140 (99%)	134 (97%)	4 (3%)	0	100	100
2	L	110/113 (97%)	102 (93%)	7 (6%)	1 (1%)	14	50
3	A	443/473 (94%)	419 (95%)	18 (4%)	6 (1%)	9	39
3	C	439/473 (93%)	413 (94%)	19 (4%)	7 (2%)	7	37
3	E	436/473 (92%)	415 (95%)	18 (4%)	3 (1%)	18	55
4	B	136/345 (39%)	133 (98%)	3 (2%)	0	100	100
4	D	129/345 (37%)	122 (95%)	6 (5%)	1 (1%)	16	53
4	F	135/345 (39%)	130 (96%)	5 (4%)	0	100	100
All	All	1966/2707 (73%)	1868 (95%)	80 (4%)	18 (1%)	16	50

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	100	PRO
3	A	37	THR
3	A	501	ALA
3	C	163	THR
3	C	165	MET
3	A	98	ASN
3	A	305	LYS
3	A	205	CYS

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Mol	Chain	Res	Type
3	C	72	HIS
3	C	361	PHE
3	A	230	ASP
3	C	429	GLU
3	E	84	VAL
3	E	302	ASN
3	C	51	THR
4	D	548	ILE
3	E	181	VAL
3	C	120	VAL

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	H	115/115 (100%)	115 (100%)	0	100	100
2	L	95/96 (99%)	95 (100%)	0	100	100
3	A	400/420 (95%)	399 (100%)	1 (0%)	86	85
3	C	397/420 (94%)	396 (100%)	1 (0%)	86	85
3	E	396/420 (94%)	395 (100%)	1 (0%)	86	85
4	B	122/298 (41%)	122 (100%)	0	100	100
4	D	116/298 (39%)	116 (100%)	0	100	100
4	F	122/298 (41%)	122 (100%)	0	100	100
All	All	1763/2365 (74%)	1760 (100%)	3 (0%)	85	86

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	A	160	ASN
3	C	160	ASN
3	E	469	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	35	HIS
1	H	110	HIS
2	L	31	HIS
2	L	58	HIS
3	A	82	GLN
3	A	428	GLN
3	A	507	GLN
3	C	66	HIS
3	C	92	ASN
3	C	229	ASN
3	C	425	ASN
3	E	114	GLN
3	E	425	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	$\# Z > 2$
5	NAG	G	1	5,3	14,14,15	2.13	3 (21%)	17,19,21	1.09	0
5	NAG	G	2	5	14,14,15	2.07	2 (14%)	17,19,21	0.94	0
6	NAG	I	1	6,3	14,14,15	2.06	2 (14%)	17,19,21	0.80	1 (5%)
6	NAG	I	2	6	14,14,15	2.09	4 (28%)	17,19,21	0.79	0
6	BMA	I	3	6	11,11,12	1.76	2 (18%)	15,15,17	0.92	1 (6%)

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
5	NAG	G	1	5,3	-	2/6/23/26	0/1/1/1
5	NAG	G	2	5	-	1/6/23/26	0/1/1/1
6	NAG	I	1	6,3	-	0/6/23/26	0/1/1/1
6	NAG	I	2	6	-	1/6/23/26	0/1/1/1
6	BMA	I	3	6	-	1/2/19/22	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	1	NAG	O5-C1	6.94	1.55	1.43
5	G	2	NAG	O5-C1	6.90	1.55	1.43
6	I	1	NAG	O5-C1	6.58	1.54	1.43
6	I	2	NAG	O5-C1	6.44	1.54	1.43
6	I	3	BMA	O2-C2	-4.17	1.34	1.43
5	G	1	NAG	C3-C2	-2.52	1.47	1.52
6	I	1	NAG	C3-C2	-2.35	1.47	1.52
6	I	2	NAG	C4-C3	2.25	1.58	1.52
6	I	2	NAG	C1-C2	-2.12	1.49	1.52
6	I	2	NAG	C3-C2	-2.04	1.48	1.52
5	G	1	NAG	C4-C3	2.04	1.57	1.52
5	G	2	NAG	C3-C2	-2.02	1.48	1.52
6	I	3	BMA	C2-C3	-2.01	1.49	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	I	3	BMA	C2-C3-C4	-2.36	106.71	110.86
6	I	1	NAG	C3-C4-C5	-2.17	106.30	110.23

There are no chirality outliers.

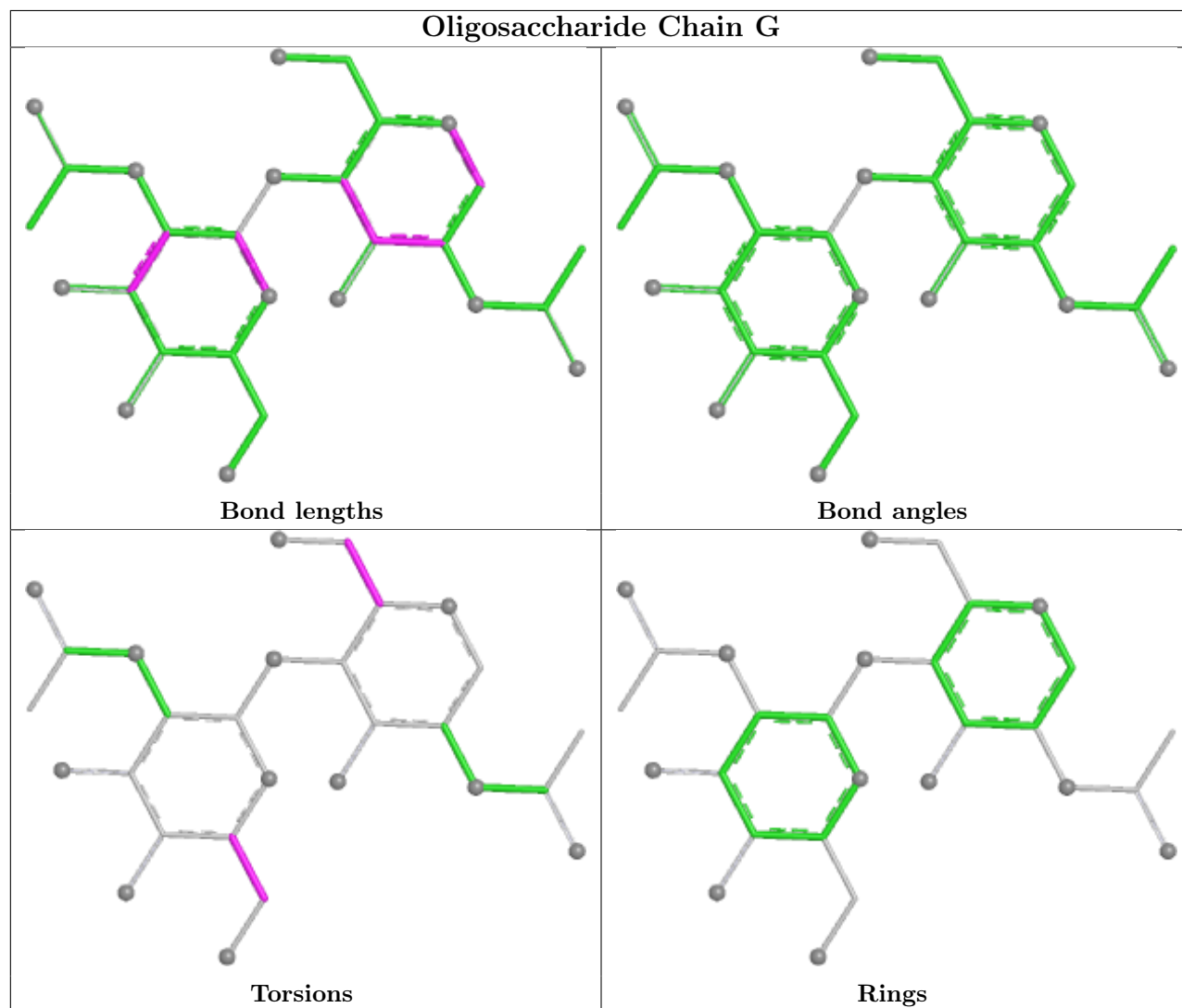
All (5) torsion outliers are listed below:

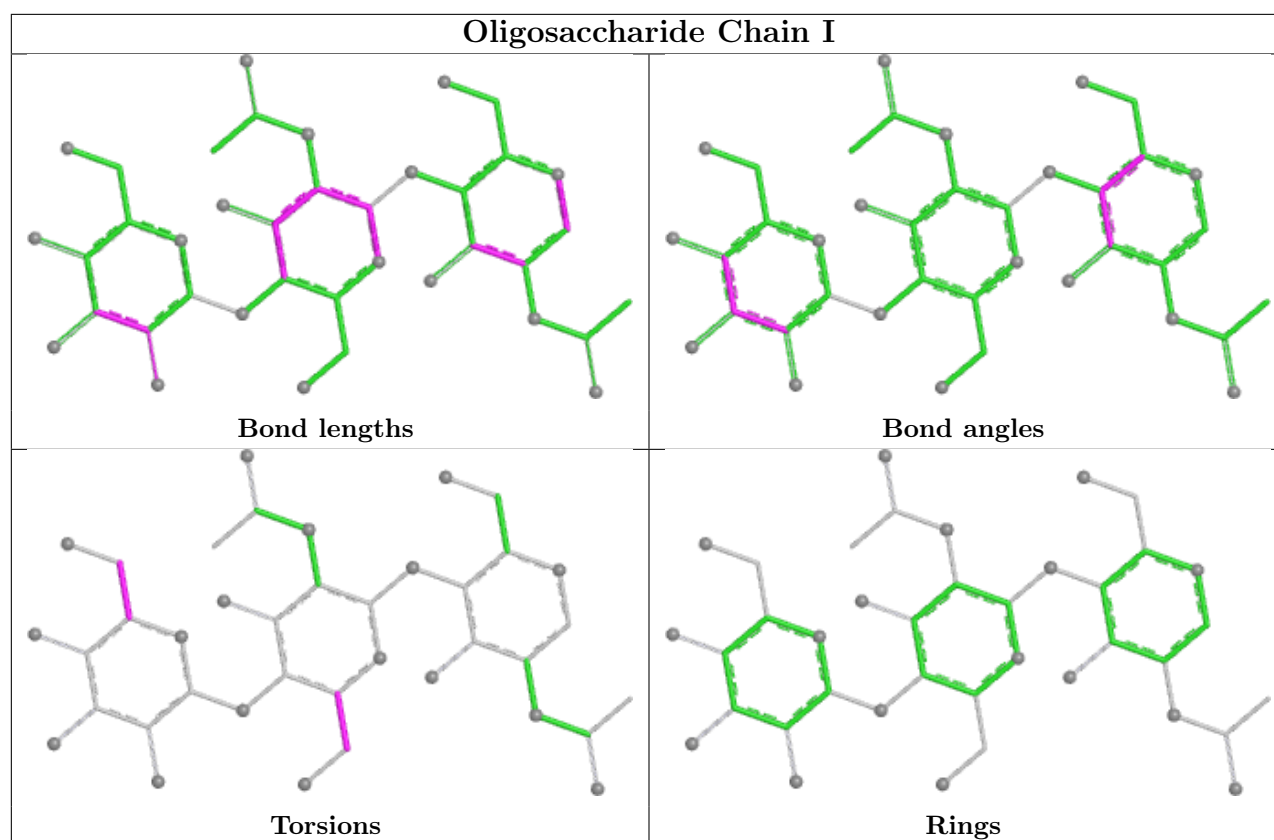
Mol	Chain	Res	Type	Atoms
5	G	2	NAG	O5-C5-C6-O6
6	I	3	BMA	O5-C5-C6-O6
5	G	1	NAG	O5-C5-C6-O6
6	I	2	NAG	O5-C5-C6-O6
5	G	1	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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





5.6 Ligand geometry [i](#)

5 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	$\# Z > 2$
7	NAG	C	603	3	14,14,15	2.10	2 (14%)	17,19,21	0.86	1 (5%)
7	NAG	C	601	3	14,14,15	2.05	2 (14%)	17,19,21	1.13	2 (11%)
7	NAG	A	603	3	14,14,15	2.05	2 (14%)	17,19,21	1.13	1 (5%)
7	NAG	E	604	3	14,14,15	2.08	2 (14%)	17,19,21	0.87	1 (5%)
7	NAG	C	602	3	14,14,15	2.06	1 (7%)	17,19,21	0.97	1 (5%)

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
7	NAG	C	603	3	-	1/6/23/26	0/1/1/1
7	NAG	C	601	3	-	1/6/23/26	0/1/1/1
7	NAG	A	603	3	-	4/6/23/26	0/1/1/1
7	NAG	E	604	3	-	2/6/23/26	0/1/1/1
7	NAG	C	602	3	-	1/6/23/26	0/1/1/1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	C	602	NAG	O5-C1	6.87	1.55	1.43
7	C	603	NAG	O5-C1	6.80	1.55	1.43
7	E	604	NAG	O5-C1	6.78	1.55	1.43
7	A	603	NAG	O5-C1	6.75	1.55	1.43
7	C	601	NAG	O5-C1	6.52	1.54	1.43
7	E	604	NAG	C3-C2	-2.27	1.47	1.52
7	A	603	NAG	C3-C2	-2.20	1.47	1.52
7	C	603	NAG	C3-C2	-2.18	1.47	1.52
7	C	601	NAG	C3-C2	-2.01	1.48	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	C	601	NAG	C1-O5-C5	-3.24	107.84	112.19
7	A	603	NAG	C8-C7-N2	2.94	121.00	116.12
7	C	601	NAG	C4-C3-C2	-2.64	107.15	111.02
7	C	603	NAG	C4-C3-C2	-2.36	107.55	111.02
7	E	604	NAG	C4-C3-C2	-2.34	107.59	111.02
7	C	602	NAG	C2-N2-C7	2.07	125.68	122.90

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	E	604	NAG	O5-C5-C6-O6
7	A	603	NAG	O5-C5-C6-O6
7	A	603	NAG	C8-C7-N2-C2
7	A	603	NAG	O7-C7-N2-C2
7	C	603	NAG	O5-C5-C6-O6
7	C	602	NAG	O5-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
7	C	601	NAG	O5-C5-C6-O6
7	E	604	NAG	C4-C5-C6-O6
7	A	603	NAG	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	C	603	NAG	1	0

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.

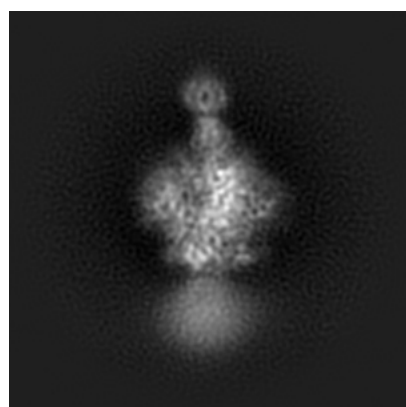
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9378. These allow visual inspection of the internal detail of the map and identification of artifacts.

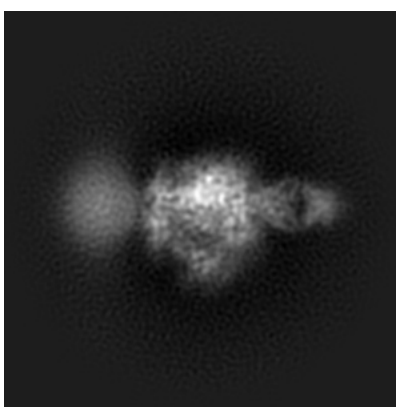
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

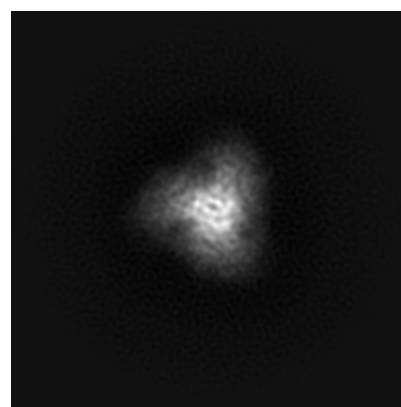
6.1.1 Primary map



X



Y

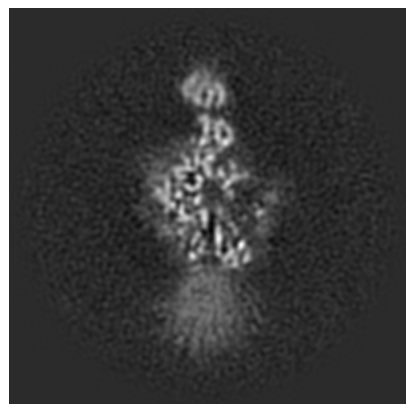


Z

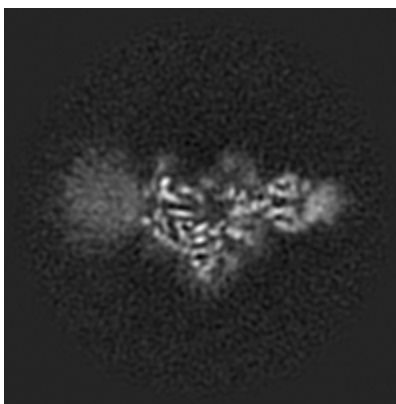
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

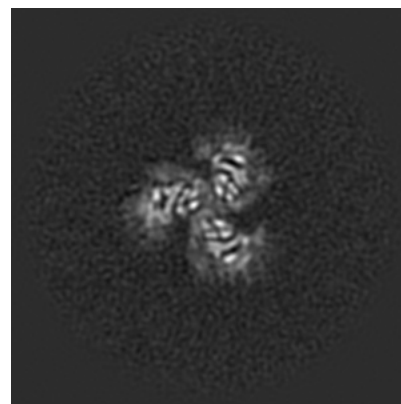
6.2.1 Primary map



X Index: 160



Y Index: 160

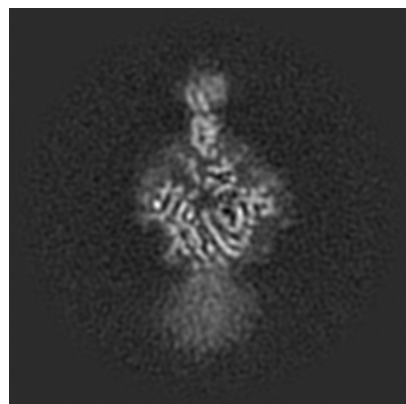


Z Index: 160

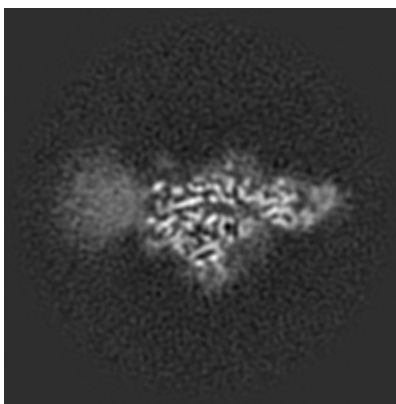
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

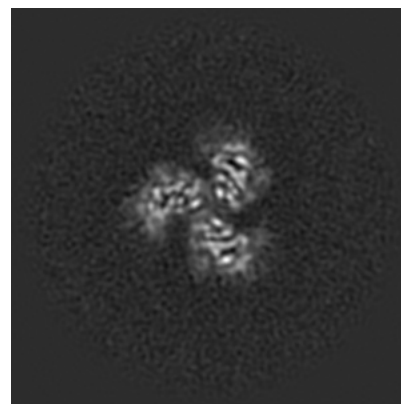
6.3.1 Primary map



X Index: 172



Y Index: 165

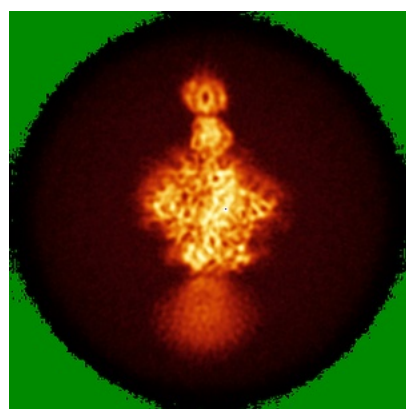


Z Index: 162

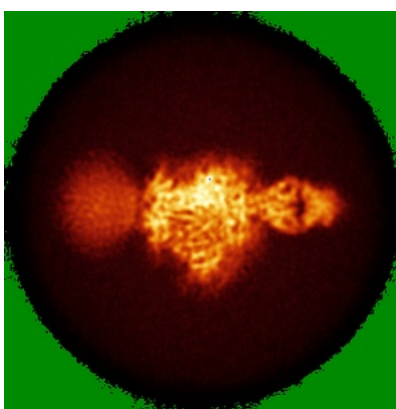
The images above show the largest variance slices of the map in three orthogonal directions.

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

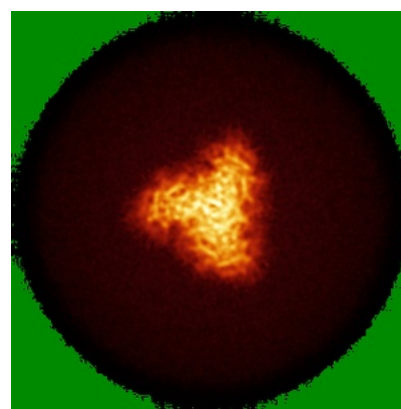
6.4.1 Primary map



X



Y

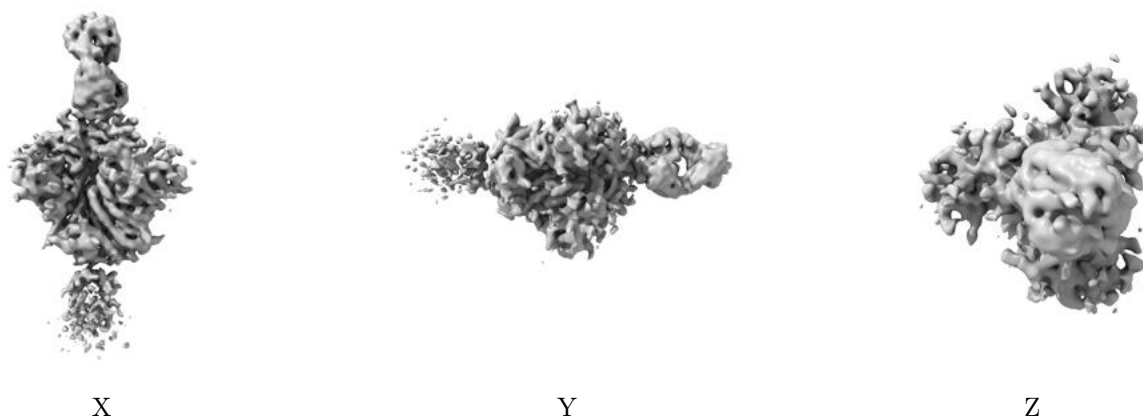


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.4. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

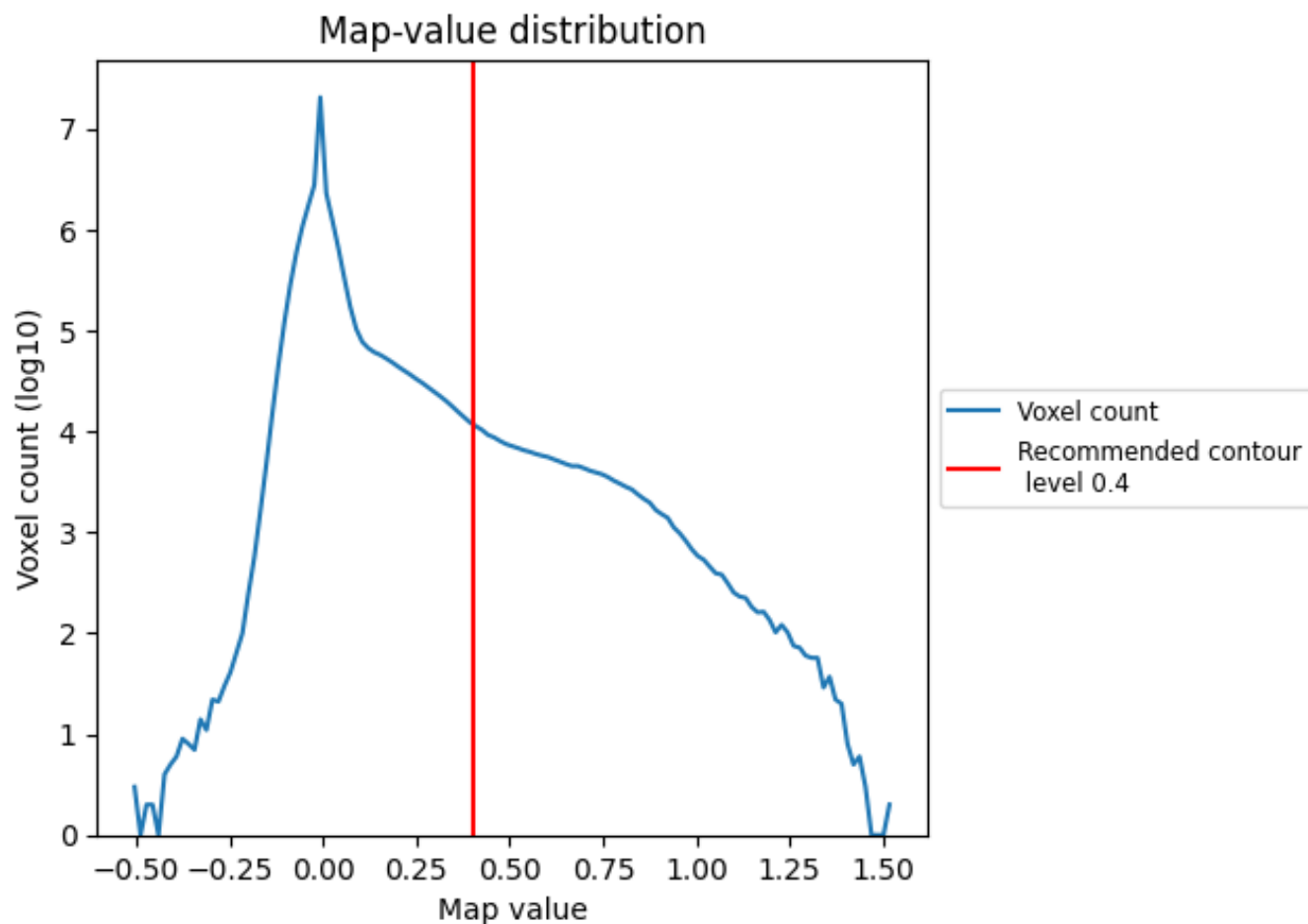
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

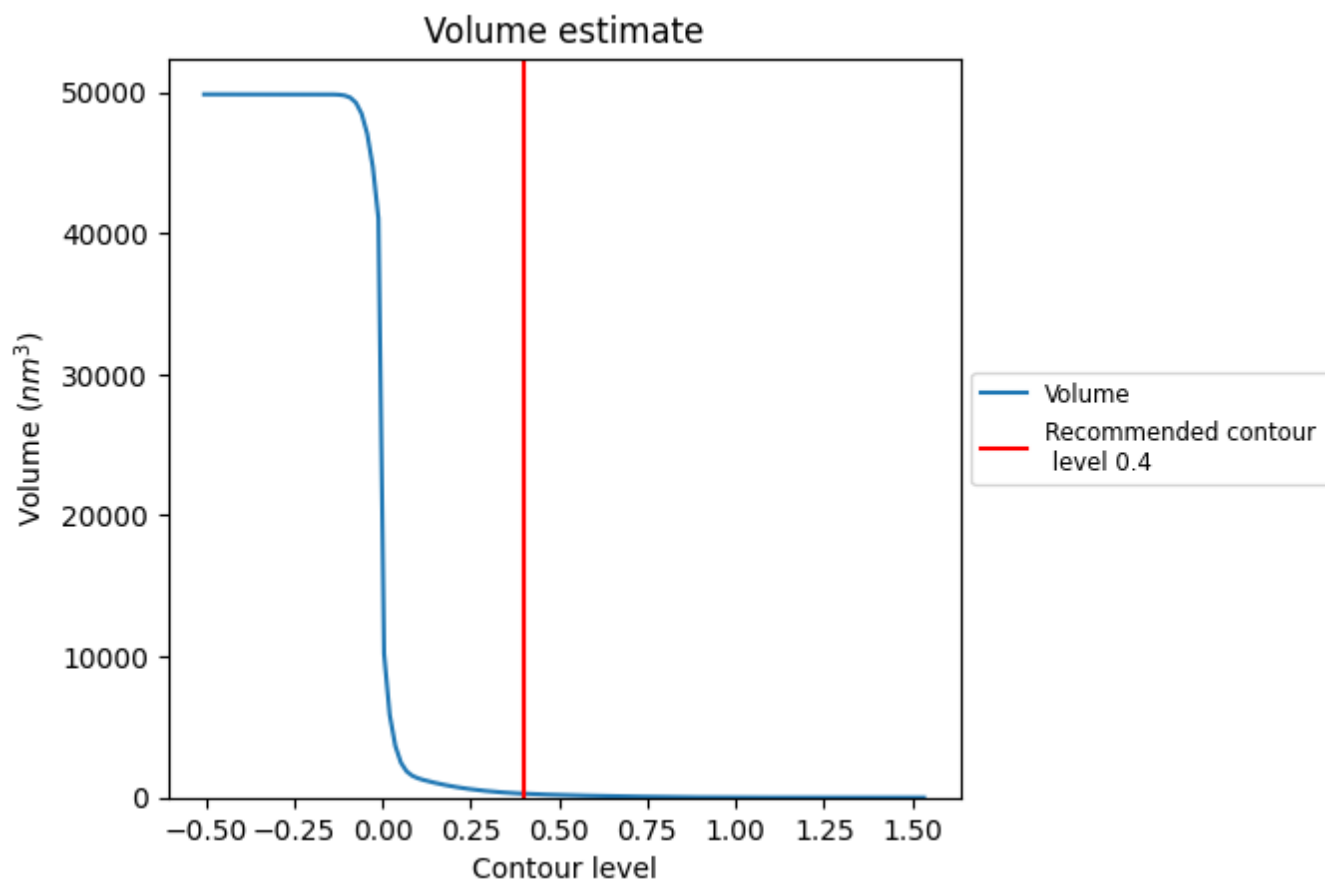
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

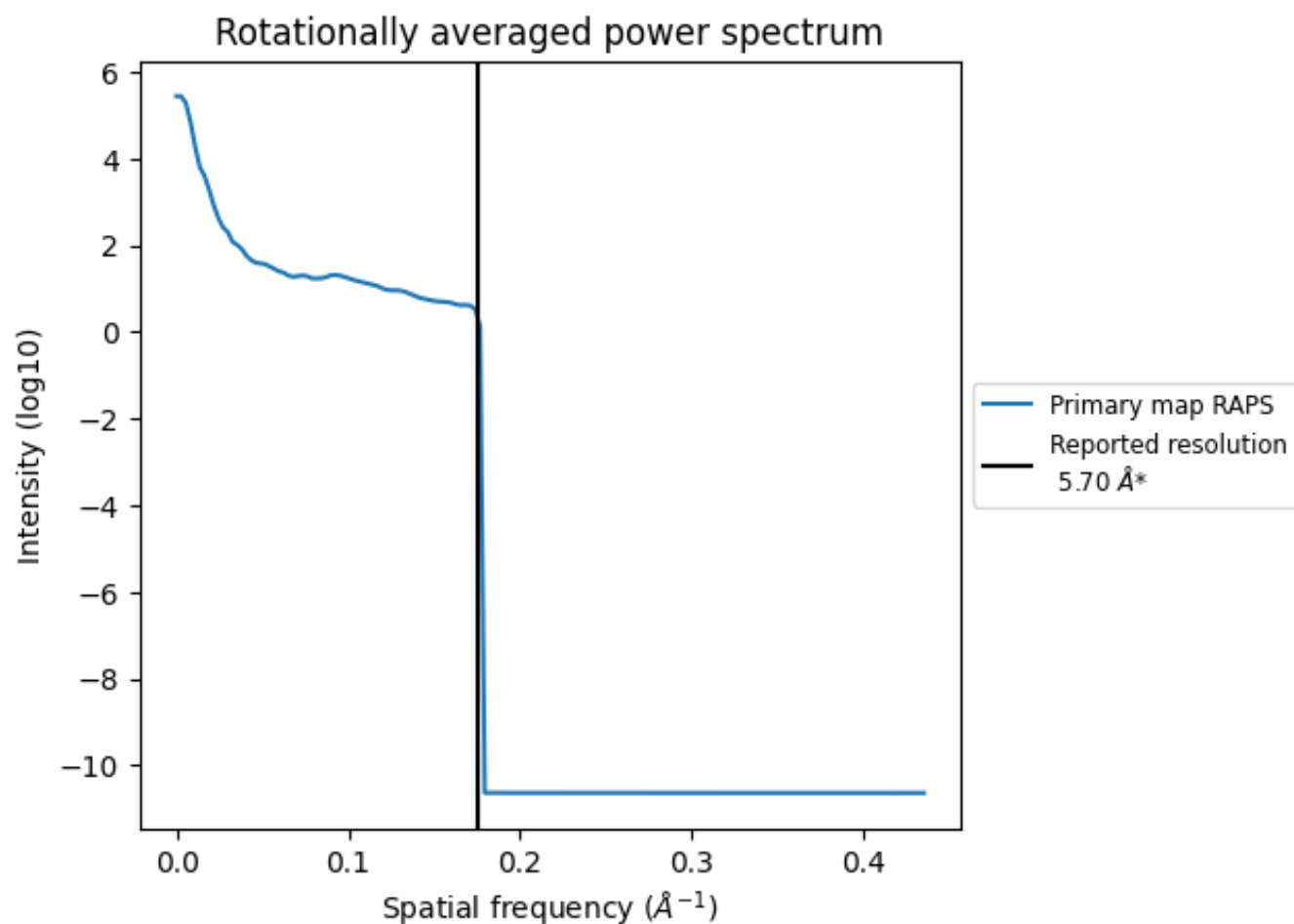
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 276 nm³; this corresponds to an approximate mass of 250 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 0.175 Å⁻¹

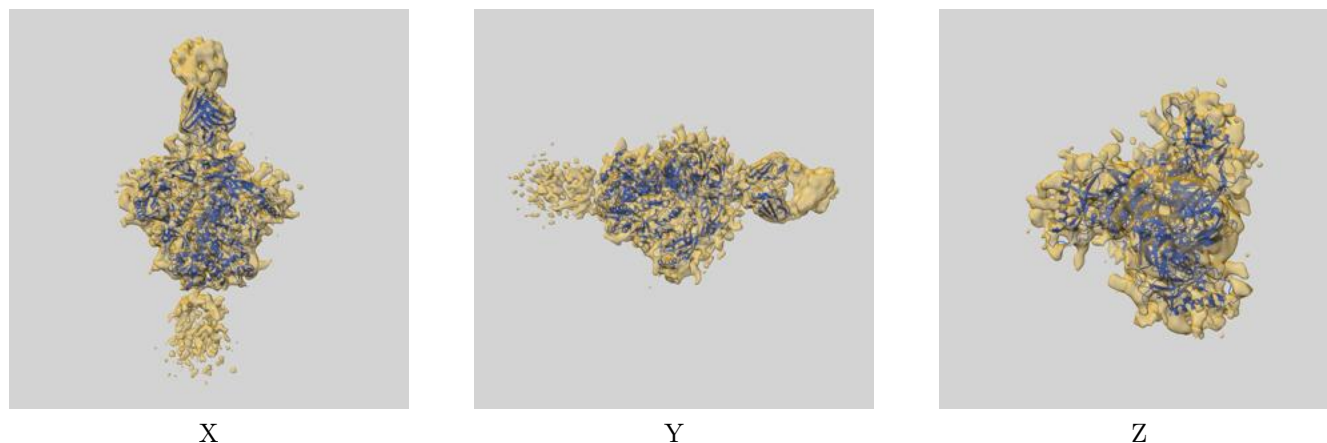
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9378 and PDB model 6NIJ. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



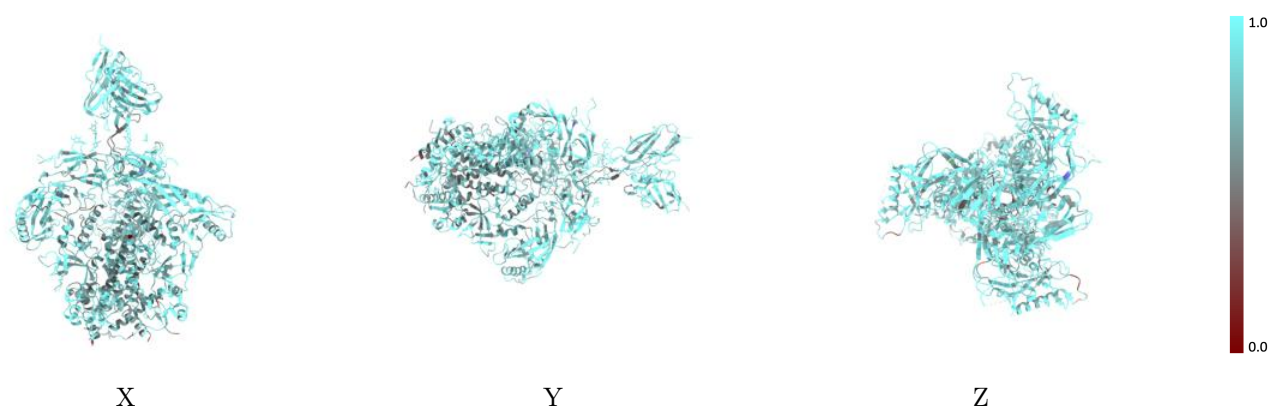
The images above show the 3D surface view of the map at the recommended contour level 0.4 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



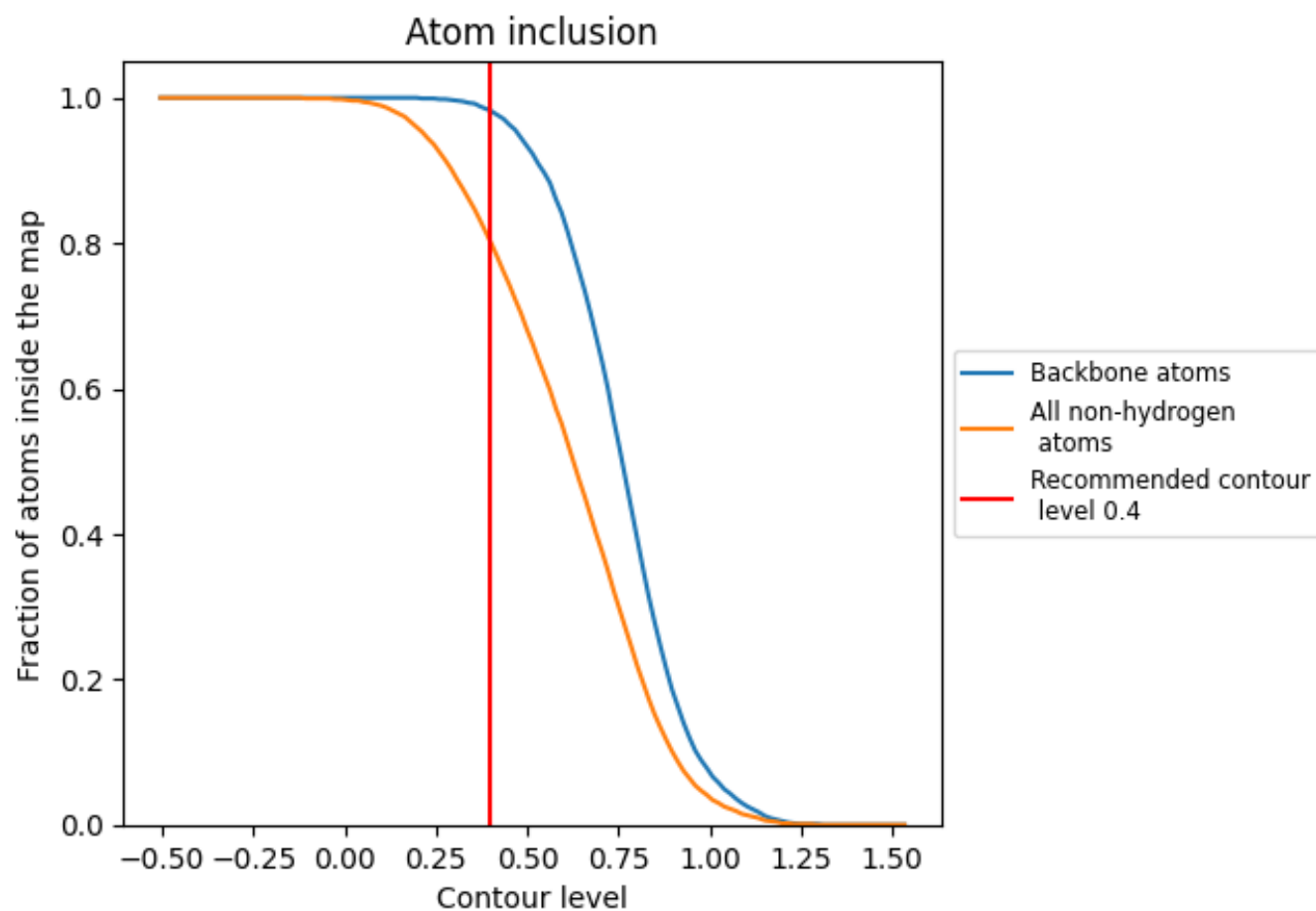
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 80% 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 (0.4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8010	0.1800
A	0.8160	0.1900
B	0.7540	0.1560
C	0.8040	0.1830
D	0.7230	0.1610
E	0.8120	0.1860
F	0.7240	0.1620
G	1.0000	0.3190
H	0.8570	0.1720
I	0.9230	0.3560
L	0.8550	0.1750

1.0

0.0

<0.0