



Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 09:10 PM UTC

PDB ID : 5A6U / pdb_00005a6u
EMDB ID : EMD-3068
Title : Native mammalian ribosome-bound Sec61 protein-conducting channel in the 'non-inserting' state
Authors : Pfeffer, S.; Burbaum, L.; Unverdorben, P.; Pech, M.; Chen, Y.; Zimmermann, R.; Beckmann, R.; Foerster, F.
Deposited on : 2015-07-01
Resolution : 9.00 Å (reported)
Based on initial model : 3J7Q

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:

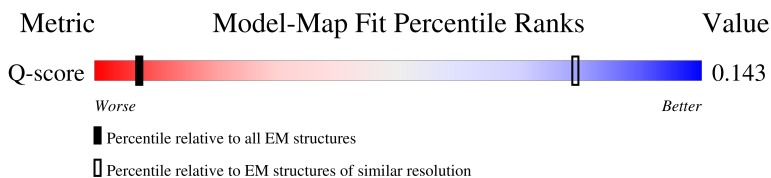
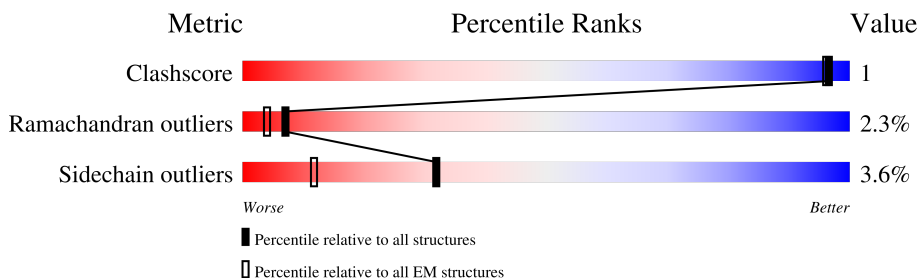
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 9.00 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	257 (8.50 - 9.50)

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

Mol	Chain	Length	Quality of chain
1	A	451	
2	B	36	
3	G	62	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7770 atoms, of which 3992 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 SEC61A.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	396	Total	C	H	N	O	S	0	4
			6180	1967	3165	497	532	19		

- Molecule 2 is a protein called SEC61B.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	36	Total	C	H	N	O	S	0	0
			576	186	297	44	47	2		

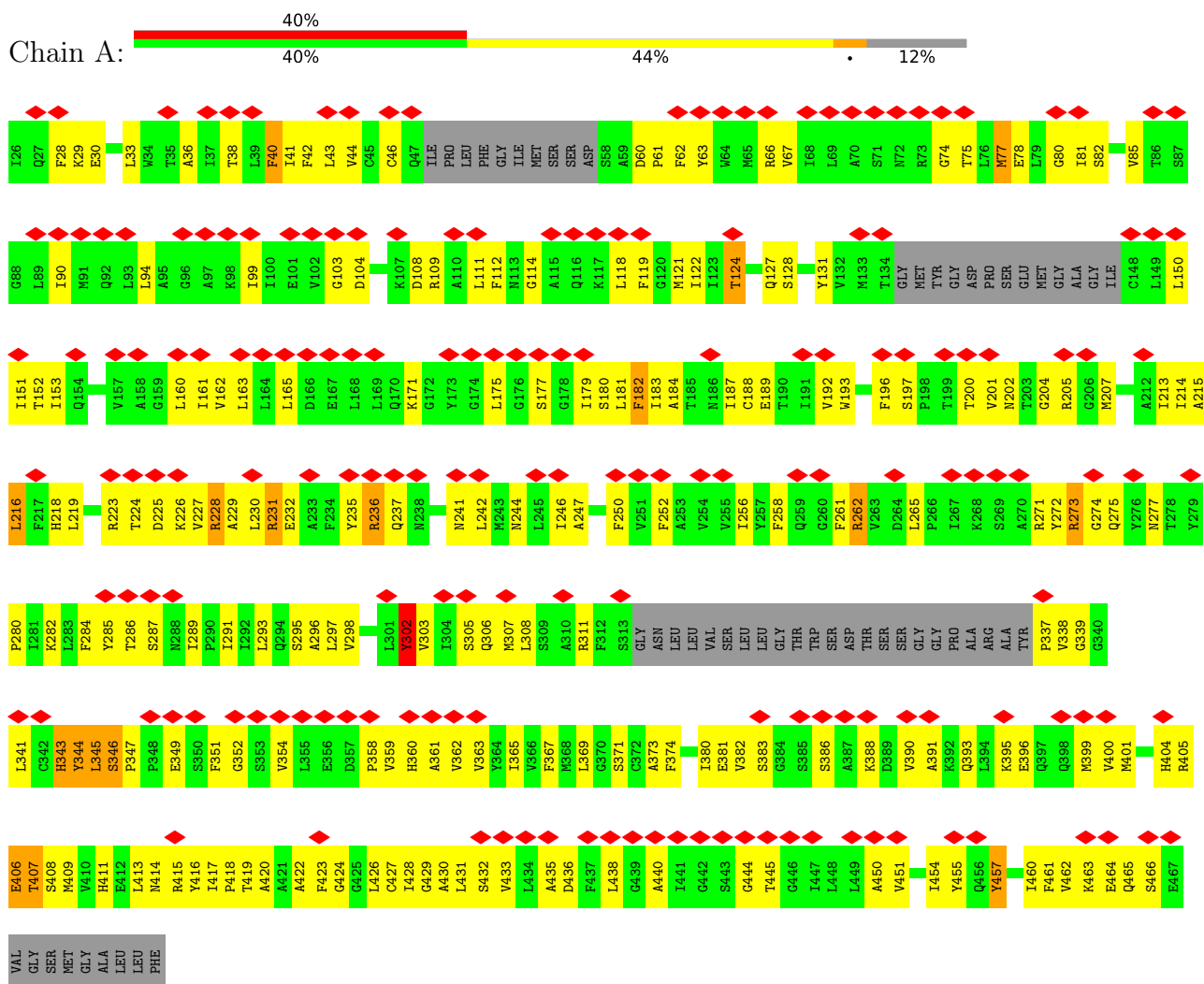
- Molecule 3 is a protein called SEC61G.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	G	62	Total	C	H	N	O	S	0	0
			1014	316	530	86	79	3		

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: SEC61A

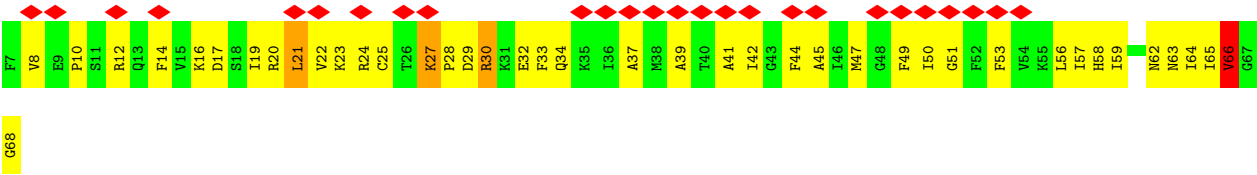


• Molecule 2: SEC61B





● Molecule 3: SEC61G



4 Experimental information

Property	Value	Source
EM reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of tilted images used	17653	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH TILT IMAGE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	3000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 (4k x 4k)	Depositor
Maximum voxel value	20.314	Depositor
Minimum voxel value	-16.746	Depositor
Average voxel value	0.000	Depositor
Voxel value standard deviation	1.000	Depositor
Recommended contour level	3	Depositor
Tomogram size ($\text{\AA}$)	576.39996, 576.39996, 576.39996	wwPDB
Tomogram dimensions	220, 220, 220	wwPDB
Tomogram angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Grid spacing ($\text{\AA}$)	2.62, 2.62, 2.62	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	2.24	111/3078 (3.6%)	2.43	197/4186 (4.7%)
2	B	2.10	6/287 (2.1%)	2.37	16/389 (4.1%)
3	G	2.31	22/494 (4.5%)	2.63	38/663 (5.7%)
All	All	2.24	139/3859 (3.6%)	2.45	251/5238 (4.8%)

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
1	A	2	11
2	B	0	2
3	G	0	1
All	All	2	14

All (139) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	215	ALA	CA-C	-9.42	1.41	1.52
1	A	189	GLU	CA-C	-8.48	1.42	1.52
1	A	354	VAL	N-CA	-8.45	1.38	1.46
3	G	39	ALA	CA-C	-8.18	1.42	1.52
1	A	152	THR	N-CA	-8.10	1.36	1.46
1	A	33	LEU	CA-C	-8.06	1.41	1.52
1	A	223	ARG	CZ-NH2	8.02	1.43	1.33
1	A	119	PHE	CA-CB	7.99	1.65	1.53
1	A	337	PRO	N-CA	7.98	1.59	1.47
1	A	258	PHE	CA-C	-7.95	1.41	1.52
1	A	242	LEU	N-CA	7.56	1.55	1.46
3	G	56	LEU	CA-CB	7.38	1.65	1.53
1	A	426	LEU	C-N	7.34	1.46	1.33
1	A	160	LEU	CA-C	-7.31	1.43	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	44	VAL	CA-C	-7.23	1.43	1.52
1	A	417	ILE	CA-CB	7.21	1.58	1.54
2	B	71	VAL	CA-CB	-7.16	1.50	1.54
1	A	296	ALA	N-CA	-7.13	1.37	1.46
3	G	12	ARG	CA-C	-7.11	1.42	1.52
3	G	20	ARG	CD-NE	7.01	1.56	1.46
1	A	341	LEU	CA-C	-6.93	1.43	1.52
1	A	228	ARG	CD-NE	6.90	1.55	1.46
1	A	30	GLU	CA-C	-6.88	1.44	1.52
1	A	66	ARG	CA-C	-6.87	1.43	1.52
2	B	62	ASP	CA-CB	6.86	1.64	1.53
1	A	80	GLY	C-N	6.82	1.42	1.33
3	G	53	PHE	C-N	6.82	1.41	1.34
1	A	28	PHE	C-N	6.72	1.43	1.33
1	A	236	ARG	NE-CZ	6.49	1.40	1.33
3	G	58	HIS	C-N	6.44	1.40	1.33
1	A	121	MET	C-N	6.42	1.42	1.34
1	A	182	PHE	N-CA	-6.40	1.38	1.46
1	A	177	SER	CA-C	-6.38	1.44	1.53
1	A	396	GLU	C-N	6.36	1.42	1.33
1	A	343	HIS	CE1-NE2	6.35	1.38	1.32
1	A	214	ILE	N-CA	-6.35	1.39	1.46
1	A	29	LYS	C-N	6.33	1.42	1.33
1	A	46	CYS	C-N	-6.29	1.24	1.33
1	A	204	GLY	CA-C	-6.24	1.43	1.51
1	A	432	SER	CA-CB	6.21	1.63	1.53
3	G	33	PHE	CA-C	-6.21	1.44	1.52
1	A	219	LEU	N-CA	-6.19	1.38	1.46
1	A	297	LEU	C-N	6.17	1.41	1.33
2	B	83	SER	N-CA	-6.14	1.39	1.46
3	G	33	PHE	CA-CB	6.10	1.62	1.53
1	A	227	VAL	CA-C	-6.09	1.47	1.52
1	A	388	LYS	CA-C	-6.09	1.45	1.52
3	G	24	ARG	CD-NE	6.06	1.54	1.46
1	A	306	GLN	CA-CB	6.05	1.63	1.53
1	A	196	PHE	N-CA	-6.01	1.40	1.46
1	A	161	ILE	C-N	6.01	1.41	1.33
1	A	60	ASP	C-O	-5.97	1.18	1.24
1	A	417	ILE	C-N	5.93	1.41	1.34
1	A	361	ALA	N-CA	-5.93	1.38	1.46
1	A	311	ARG	CZ-NH2	5.92	1.41	1.33
1	A	461	PHE	N-CA	-5.85	1.39	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	275	GLN	CA-C	-5.84	1.45	1.52
1	A	466	SER	C-N	-5.80	1.25	1.33
1	A	78	GLU	C-N	5.76	1.41	1.33
1	A	463	LYS	C-N	5.76	1.41	1.33
1	A	226	LYS	C-N	5.75	1.38	1.33
2	B	77	SER	C-N	5.66	1.41	1.33
1	A	124	THR	C-N	5.65	1.41	1.33
3	G	24	ARG	NE-CZ	5.64	1.39	1.33
1	A	285	TYR	C-N	5.64	1.40	1.33
1	A	302	TYR	C-N	5.64	1.40	1.34
3	G	27	LYS	CA-CB	5.63	1.62	1.53
1	A	365	ILE	CA-CB	5.63	1.61	1.54
1	A	428	ILE	C-N	5.60	1.40	1.33
1	A	246	ILE	CA-CB	-5.57	1.47	1.54
1	A	338	VAL	CA-CB	5.55	1.61	1.54
1	A	252	PHE	N-CA	-5.54	1.39	1.46
3	G	10	PRO	CA-CB	-5.52	1.46	1.53
1	A	63	TYR	CA-C	-5.51	1.45	1.52
1	A	284	PHE	CA-CB	5.49	1.62	1.53
1	A	193	TRP	NE1-CE2	5.46	1.43	1.37
1	A	362	VAL	CA-CB	-5.46	1.47	1.54
1	A	275	GLN	N-CA	-5.45	1.39	1.45
1	A	298	VAL	CA-CB	-5.45	1.47	1.54
1	A	189	GLU	C-N	5.44	1.41	1.33
1	A	244	ASN	N-CA	-5.42	1.39	1.46
1	A	414	ASN	C-N	5.42	1.41	1.33
1	A	187	ILE	CA-CB	-5.42	1.48	1.54
1	A	36	ALA	C-N	5.41	1.40	1.33
3	G	30	ARG	CD-NE	5.41	1.53	1.46
1	A	118	LEU	CA-CB	5.41	1.62	1.53
1	A	109	ARG	CD-NE	5.40	1.53	1.46
3	G	37	ALA	C-N	5.40	1.41	1.33
1	A	291	ILE	CA-C	-5.39	1.47	1.52
1	A	28	PHE	CA-C	-5.37	1.45	1.52
3	G	25	CYS	C-N	5.37	1.41	1.33
1	A	289	ILE	CA-C	5.36	1.58	1.52
1	A	380	ILE	CA-C	-5.32	1.46	1.52
1	A	163	LEU	N-CA	-5.31	1.40	1.46
1	A	381	GLU	N-CA	-5.31	1.39	1.46
1	A	250	PHE	N-CA	-5.30	1.39	1.46
1	A	303	VAL	CA-CB	-5.29	1.46	1.54
1	A	273	ARG	C-N	5.29	1.42	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	201	VAL	C-N	5.27	1.41	1.33
1	A	302	TYR	CA-C	-5.27	1.46	1.52
1	A	367	PHE	C-O	-5.27	1.18	1.24
3	G	50	ILE	N-CA	5.26	1.52	1.46
1	A	62	PHE	CA-C	-5.26	1.45	1.52
1	A	197	SER	CA-C	-5.26	1.46	1.52
1	A	465	GLN	C-N	5.25	1.40	1.33
1	A	225	ASP	CA-CB	5.23	1.62	1.53
3	G	29	ASP	CA-CB	5.22	1.61	1.53
1	A	346	SER	CA-C	-5.20	1.46	1.52
1	A	202	ASN	C-N	5.19	1.40	1.33
1	A	274	GLY	C-O	-5.18	1.17	1.24
1	A	180	SER	CA-C	-5.17	1.46	1.52
1	A	231	ARG	CZ-NH2	5.17	1.40	1.33
1	A	460	ILE	N-CA	-5.17	1.40	1.46
2	B	68	VAL	CA-CB	-5.16	1.46	1.54
3	G	59	ILE	CA-C	-5.16	1.47	1.52
1	A	395	LYS	C-N	5.16	1.40	1.33
1	A	430	ALA	C-N	5.15	1.41	1.33
1	A	122	ILE	CB-CG1	5.14	1.63	1.53
1	A	343	HIS	ND1-CE1	5.13	1.37	1.32
1	A	308	LEU	C-N	5.13	1.40	1.34
1	A	415	ARG	CZ-NH1	5.11	1.40	1.32
1	A	171	LYS	N-CA	-5.10	1.40	1.46
3	G	23	LYS	N-CA	-5.09	1.39	1.46
3	G	21	LEU	C-N	5.09	1.40	1.34
1	A	262	ARG	NE-CZ	5.09	1.38	1.33
2	B	81	ILE	CA-CB	-5.09	1.48	1.54
1	A	408	SER	C-N	5.08	1.41	1.33
3	G	63	ASN	CA-C	-5.08	1.46	1.52
3	G	66	VAL	CA-CB	5.08	1.61	1.54
1	A	256	ILE	CB-CG1	5.08	1.63	1.53
1	A	271	ARG	CZ-NH2	5.08	1.40	1.33
1	A	440	ALA	C-N	5.05	1.39	1.34
1	A	360	HIS	ND1-CE1	-5.05	1.27	1.32
1	A	216	LEU	CA-CB	5.04	1.61	1.53
1	A	42	PHE	N-CA	5.03	1.52	1.46
1	A	82	SER	C-N	5.03	1.40	1.33
1	A	360	HIS	CG-CD2	5.02	1.41	1.35
1	A	409	MET	N-CA	-5.02	1.40	1.46
1	A	411	HIS	CE1-NE2	5.02	1.37	1.32

All (251) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	47	MET	CA-C-N	11.83	132.84	119.94
3	G	47	MET	C-N-CA	11.83	132.84	119.94
1	A	291	ILE	N-CA-C	-11.50	102.54	111.62
1	A	128	SER	N-CA-C	9.18	122.47	111.82
1	A	407	THR	CA-CB-OG1	9.00	123.10	109.60
3	G	49	PHE	CA-C-N	8.64	132.68	120.42
3	G	49	PHE	C-N-CA	8.64	132.68	120.42
1	A	280	PRO	CA-C-N	8.09	134.11	123.11
1	A	280	PRO	C-N-CA	8.09	134.11	123.11
1	A	308	LEU	CA-C-N	7.96	131.75	120.28
1	A	308	LEU	C-N-CA	7.96	131.75	120.28
3	G	53	PHE	CA-CB-CG	-7.93	105.87	113.80
1	A	104	ASP	CA-CB-CG	-7.92	104.68	112.60
2	B	70	PRO	O-C-N	7.85	131.66	122.23
1	A	419	THR	N-CA-C	7.85	119.91	111.36
1	A	62	PHE	CA-CB-CG	7.73	121.53	113.80
1	A	401	MET	CA-C-N	7.72	130.62	120.28
1	A	401	MET	C-N-CA	7.72	130.62	120.28
1	A	393	GLN	CB-CG-CD	-7.71	99.50	112.60
3	G	27	LYS	CA-C-N	7.68	128.15	119.93
3	G	27	LYS	C-N-CA	7.68	128.15	119.93
1	A	369	LEU	CA-C-N	7.65	128.28	119.94
1	A	369	LEU	C-N-CA	7.65	128.28	119.94
1	A	67	VAL	N-CA-C	7.51	117.63	110.42
1	A	161	ILE	CA-C-N	7.47	129.97	120.56
1	A	161	ILE	C-N-CA	7.47	129.97	120.56
1	A	188	CYS	CA-C-N	7.38	131.05	120.79
1	A	188	CYS	C-N-CA	7.38	131.05	120.79
1	A	232	GLU	N-CA-C	-7.30	103.46	112.88
1	A	182	PHE	CA-C-N	7.27	129.72	120.56
1	A	182	PHE	C-N-CA	7.27	129.72	120.56
1	A	391	ALA	N-CA-C	-7.14	103.58	111.36
2	B	85	PHE	CA-CB-CG	-7.10	106.70	113.80
1	A	241	ASN	CA-CB-CG	7.07	119.67	112.60
1	A	386	SER	CA-C-N	7.07	132.43	121.19
1	A	386	SER	C-N-CA	7.07	132.43	121.19
1	A	399	MET	N-CA-CB	7.06	121.02	110.29
1	A	36	ALA	CA-C-N	7.02	129.66	120.60
1	A	36	ALA	C-N-CA	7.02	129.66	120.60
1	A	360	HIS	N-CA-CB	7.02	120.66	110.20
3	G	53	PHE	CB-CA-C	-6.98	99.92	110.88
1	A	465	GLN	N-CA-C	-6.98	103.61	111.14
1	A	427	CYS	N-CA-C	-6.97	105.40	114.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	73	VAL	O-C-N	-6.92	115.16	121.87
1	A	81	ILE	CB-CA-C	-6.90	104.15	110.91
3	G	32	GLU	CA-C-N	6.90	130.09	120.29
3	G	32	GLU	C-N-CA	6.90	130.09	120.29
1	A	354	VAL	N-CA-C	-6.87	106.53	113.47
3	G	64	ILE	N-CA-C	-6.86	105.96	113.43
1	A	363	VAL	CA-C-N	6.83	129.32	120.44
1	A	363	VAL	C-N-CA	6.83	129.32	120.44
1	A	218	HIS	ND1-CE1-NE2	6.78	115.18	108.40
1	A	463	LYS	CA-C-N	6.77	129.90	120.29
1	A	463	LYS	C-N-CA	6.77	129.90	120.29
1	A	85	VAL	O-C-N	-6.74	113.13	121.90
1	A	99	ILE	CA-CB-CG1	6.72	121.83	110.40
1	A	175	LEU	N-CA-C	-6.67	98.76	109.96
1	A	423	PHE	N-CA-CB	6.65	121.58	110.41
1	A	444	GLY	CA-C-N	6.58	134.10	121.54
1	A	444	GLY	C-N-CA	6.58	134.10	121.54
1	A	114	GLY	CA-C-N	6.57	129.08	120.28
1	A	114	GLY	C-N-CA	6.57	129.08	120.28
1	A	262	ARG	NE-CZ-NH2	-6.54	113.32	119.20
1	A	424	GLY	CA-C-N	6.54	127.19	120.00
1	A	424	GLY	C-N-CA	6.54	127.19	120.00
1	A	420	ALA	CA-C-N	6.50	128.99	120.28
1	A	420	ALA	C-N-CA	6.50	128.99	120.28
3	G	37	ALA	CA-C-N	6.50	129.28	120.44
3	G	37	ALA	C-N-CA	6.50	129.28	120.44
1	A	380	ILE	N-CA-C	6.44	117.19	110.62
1	A	63	TYR	N-CA-C	-6.43	103.78	111.69
1	A	112	PHE	N-CA-C	-6.42	104.36	111.36
1	A	414	ASN	OD1-CG-ND2	6.40	129.00	122.60
2	B	76	MET	CA-C-O	-6.40	114.10	120.82
2	B	75	VAL	O-C-N	-6.39	115.25	121.83
3	G	14	PHE	N-CA-C	-6.38	104.41	111.36
1	A	61	PRO	CA-C-N	6.38	132.97	122.07
1	A	61	PRO	C-N-CA	6.38	132.97	122.07
1	A	153	ILE	CA-C-O	6.37	127.53	120.71
3	G	58	HIS	CB-CG-ND1	-6.36	113.16	122.70
2	B	88	HIS	CA-C-N	6.34	130.90	121.77
2	B	88	HIS	C-N-CA	6.34	130.90	121.77
3	G	59	ILE	CA-CB-CG2	6.31	121.23	110.50
1	A	423	PHE	CA-C-N	6.29	126.92	120.00
1	A	423	PHE	C-N-CA	6.29	126.92	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	151	ILE	CB-CA-C	-6.29	102.78	111.65
1	A	230	LEU	N-CA-C	-6.29	104.92	112.59
1	A	293	LEU	CA-C-N	6.28	129.33	120.28
1	A	293	LEU	C-N-CA	6.28	129.33	120.28
1	A	127	GLN	N-CA-C	6.28	117.79	111.07
1	A	436	ASP	N-CA-C	-6.27	103.98	113.89
1	A	457	TYR	CA-C-N	6.27	129.19	120.29
1	A	457	TYR	C-N-CA	6.27	129.19	120.29
1	A	109	ARG	CA-C-N	6.25	129.48	120.79
1	A	109	ARG	C-N-CA	6.25	129.48	120.79
1	A	265	LEU	CA-C-O	-6.24	112.55	120.04
2	B	88	HIS	ND1-CG-CD2	6.24	112.34	106.10
1	A	391	ALA	CA-C-N	6.18	128.47	120.44
1	A	391	ALA	C-N-CA	6.18	128.47	120.44
3	G	64	ILE	O-C-N	-6.16	116.03	122.25
1	A	409	MET	N-CA-C	-6.14	104.13	111.69
1	A	38	THR	CA-C-N	6.13	128.74	120.65
1	A	38	THR	C-N-CA	6.13	128.74	120.65
2	B	64	PRO	N-CA-C	6.08	120.80	110.95
1	A	111	LEU	CA-C-N	6.07	128.92	120.29
1	A	111	LEU	C-N-CA	6.07	128.92	120.29
3	G	51	GLY	CA-C-O	5.99	126.49	120.09
1	A	247	ALA	CA-C-O	-5.98	114.08	120.42
1	A	44	VAL	N-CA-C	5.97	117.42	110.62
1	A	202	ASN	CA-CB-CG	5.97	118.57	112.60
3	G	34	GLN	N-CA-CB	5.96	118.72	110.07
1	A	343	HIS	ND1-CE1-NE2	5.94	114.34	108.40
1	A	60	ASP	O-C-N	5.93	126.18	121.55
2	B	85	PHE	CB-CA-C	-5.93	99.69	109.65
3	G	19	ILE	CB-CA-C	-5.93	104.32	111.85
2	B	68	VAL	N-CA-CB	5.93	122.43	112.47
1	A	409	MET	CA-C-N	5.92	128.57	120.46
1	A	409	MET	C-N-CA	5.92	128.57	120.46
1	A	227	VAL	CB-CA-C	-5.92	102.86	112.03
1	A	374	PHE	O-C-N	-5.91	115.00	122.27
1	A	40	PHE	O-C-N	5.90	128.87	122.15
1	A	128	SER	O-C-N	5.89	129.52	122.27
3	G	14	PHE	CA-C-N	5.89	129.78	120.47
3	G	14	PHE	C-N-CA	5.89	129.78	120.47
1	A	455	TYR	CA-C-N	5.86	128.06	120.44
1	A	455	TYR	C-N-CA	5.86	128.06	120.44
1	A	373	ALA	N-CA-C	-5.85	104.50	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	182	PHE	CA-C-O	-5.84	114.68	120.70
1	A	282	LYS	CA-C-N	5.83	128.37	120.38
1	A	282	LYS	C-N-CA	5.83	128.37	120.38
1	A	391	ALA	CA-C-O	-5.83	114.24	120.42
1	A	90	ILE	N-CA-CB	5.82	118.45	110.54
1	A	430	ALA	N-CA-C	-5.81	106.05	113.02
3	G	21	LEU	N-CA-CB	5.79	119.06	110.49
1	A	373	ALA	N-CA-CB	5.79	118.83	110.20
1	A	404	HIS	ND1-CE1-NE2	5.78	114.18	108.40
1	A	229	ALA	CA-C-N	5.78	131.86	122.67
1	A	229	ALA	C-N-CA	5.78	131.86	122.67
3	G	65	ILE	N-CA-CB	5.78	118.42	111.31
1	A	94	LEU	CA-C-N	5.77	128.01	120.28
1	A	94	LEU	C-N-CA	5.77	128.01	120.28
1	A	181	LEU	CA-C-N	5.77	128.28	120.44
1	A	181	LEU	C-N-CA	5.77	128.28	120.44
1	A	429	GLY	CA-C-O	-5.74	114.58	120.66
1	A	457	TYR	CA-CB-CG	-5.71	103.63	113.90
1	A	432	SER	CB-CA-C	-5.70	101.16	110.85
1	A	162	VAL	CA-C-N	5.65	127.85	120.28
1	A	162	VAL	C-N-CA	5.65	127.85	120.28
2	B	68	VAL	N-CA-C	-5.64	100.19	108.99
1	A	272	TYR	N-CA-C	-5.64	99.23	108.76
1	A	454	ILE	N-CA-C	-5.63	105.36	110.82
1	A	422	ALA	N-CA-C	-5.63	106.57	113.50
1	A	305	SER	N-CA-C	5.63	119.62	112.87
1	A	406	GLU	CA-C-N	5.63	132.29	121.54
1	A	406	GLU	C-N-CA	5.63	132.29	121.54
1	A	177	SER	CA-C-N	5.62	126.07	119.94
1	A	177	SER	C-N-CA	5.62	126.07	119.94
1	A	103	GLY	N-CA-C	-5.60	104.90	112.57
2	B	85	PHE	CA-C-N	5.60	128.24	120.29
2	B	85	PHE	C-N-CA	5.60	128.24	120.29
1	A	438	LEU	N-CA-C	-5.59	99.49	108.55
1	A	345	LEU	N-CA-C	-5.59	106.13	113.12
1	A	291	ILE	CA-C-N	5.58	129.48	120.55
1	A	291	ILE	C-N-CA	5.58	129.48	120.55
1	A	352	GLY	N-CA-C	-5.58	103.04	110.97
1	A	280	PRO	O-C-N	-5.57	115.12	122.64
1	A	197	SER	CA-C-N	5.56	126.00	119.99
1	A	197	SER	C-N-CA	5.56	126.00	119.99
1	A	381	GLU	O-C-N	-5.56	115.81	122.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	343	HIS	CE1-NE2-CD2	-5.55	103.45	109.00
3	G	33	PHE	N-CA-C	-5.53	105.33	111.36
1	A	413	LEU	N-CA-C	-5.53	106.54	113.72
1	A	354	VAL	CA-C-O	5.49	123.92	118.98
1	A	41	ILE	N-CA-CB	5.48	116.96	110.55
1	A	244	ASN	CA-C-N	5.47	128.63	120.31
1	A	244	ASN	C-N-CA	5.47	128.63	120.31
1	A	104	ASP	CA-C-N	5.46	128.96	120.60
1	A	104	ASP	C-N-CA	5.46	128.96	120.60
1	A	295	SER	CB-CA-C	-5.46	101.73	110.79
1	A	287	SER	N-CA-C	-5.45	102.39	113.29
1	A	75	THR	N-CA-C	-5.44	105.86	112.88
3	G	42	ILE	CA-CB-CG2	-5.44	101.26	110.50
1	A	200	THR	CA-C-O	-5.41	112.78	120.51
1	A	205	ARG	N-CA-C	-5.40	100.22	109.24
1	A	431	LEU	CA-C-N	5.39	127.94	120.29
1	A	431	LEU	C-N-CA	5.39	127.94	120.29
3	G	62	ASN	CA-CB-CG	-5.39	107.21	112.60
1	A	261	PHE	CA-CB-CG	5.38	119.18	113.80
3	G	22	VAL	CA-CB-CG1	-5.38	101.26	110.40
1	A	196	PHE	N-CA-C	-5.36	103.35	111.34
1	A	272	TYR	CA-C-O	-5.36	114.37	120.32
1	A	28	PHE	CA-C-N	5.35	127.89	120.29
1	A	28	PHE	C-N-CA	5.35	127.89	120.29
1	A	162	VAL	N-CA-C	5.35	115.55	110.42
2	B	63	SER	CA-C-O	-5.34	113.16	118.34
1	A	405	ARG	CA-C-N	5.32	131.71	121.54
1	A	405	ARG	C-N-CA	5.32	131.71	121.54
3	G	57	ILE	CA-C-O	5.32	125.51	119.92
1	A	382	VAL	CB-CA-C	-5.31	101.33	110.94
1	A	179	ILE	CB-CA-C	-5.30	105.19	111.97
1	A	183	ILE	N-CA-CB	5.29	116.74	110.55
1	A	291	ILE	N-CA-CB	5.29	115.97	111.64
3	G	44	PHE	O-C-N	-5.28	115.17	122.46
1	A	244	ASN	N-CA-C	-5.27	106.00	112.90
1	A	465	GLN	CB-CA-C	-5.24	102.62	110.90
1	A	277	ASN	CA-CB-CG	-5.22	107.38	112.60
1	A	104	ASP	CA-C-O	5.21	125.58	119.28
1	A	464	GLU	CA-C-O	-5.20	114.91	120.42
1	A	77	MET	N-CA-CB	5.20	117.86	110.16
1	A	390	VAL	CA-C-N	5.19	127.66	120.29
1	A	390	VAL	C-N-CA	5.19	127.66	120.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	118	LEU	CA-C-N	5.19	127.24	120.28
1	A	118	LEU	C-N-CA	5.19	127.24	120.28
1	A	351	PHE	N-CA-C	-5.16	105.28	112.30
1	A	405	ARG	O-C-N	5.16	129.46	122.96
1	A	242	LEU	N-CA-C	-5.15	105.75	111.36
1	A	244	ASN	CA-C-O	5.15	125.62	119.60
1	A	237	GLN	CA-C-O	-5.14	115.58	121.54
1	A	386	SER	N-CA-C	-5.14	101.14	108.23
3	G	16	LYS	CA-C-O	5.14	126.19	120.90
1	A	171	LYS	N-CA-C	-5.13	108.77	114.62
3	G	28	PRO	CB-CA-C	5.13	118.16	111.64
3	G	45	ALA	CA-C-O	-5.13	113.07	119.38
1	A	298	VAL	CA-CB-CG2	5.12	119.11	110.40
1	A	358	PRO	N-CA-C	-5.12	101.93	112.47
1	A	418	PRO	N-CA-CB	5.10	108.68	103.23
2	B	81	ILE	CA-C-O	-5.09	115.65	120.95
1	A	462	VAL	CA-CB-CG1	5.09	119.05	110.40
1	A	360	HIS	ND1-CE1-NE2	5.09	113.49	108.40
1	A	457	TYR	N-CA-C	5.09	119.20	112.89
3	G	33	PHE	O-C-N	-5.08	116.36	122.15
1	A	400	VAL	N-CA-CB	5.08	122.42	112.00
1	A	224	THR	CA-C-O	-5.08	113.02	119.31
1	A	337	PRO	CA-C-N	5.06	127.39	120.46
1	A	337	PRO	C-N-CA	5.06	127.39	120.46
1	A	43	LEU	N-CA-C	-5.06	104.76	112.04
3	G	41	ALA	CA-C-N	5.05	126.89	120.72
3	G	41	ALA	C-N-CA	5.05	126.89	120.72
1	A	347	PRO	CA-C-O	-5.05	113.23	120.56
1	A	181	LEU	N-CA-C	5.04	116.78	111.28
1	A	343	HIS	ND1-CG-CD2	5.04	111.14	106.10
3	G	22	VAL	O-C-N	5.04	127.24	122.20
1	A	371	SER	N-CA-CB	5.04	117.44	109.94
1	A	451	VAL	CA-C-O	-5.04	115.18	120.57
1	A	179	ILE	CA-C-O	-5.03	115.83	121.17
1	A	165	LEU	N-CA-C	5.03	116.76	111.28
1	A	175	LEU	CB-CA-C	5.02	117.81	109.53
3	G	25	CYS	N-CA-CB	5.02	117.92	110.29
1	A	192	VAL	CA-C-N	5.02	127.71	120.38
1	A	192	VAL	C-N-CA	5.02	127.71	120.38
1	A	150	LEU	N-CA-C	5.00	117.50	111.40

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	188	CYS	CA
1	A	447	ILE	CB

All (14) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	131	TYR	Sidechain
1	A	228	ARG	Sidechain
1	A	231	ARG	Sidechain
1	A	235	TYR	Sidechain
1	A	262	ARG	Sidechain
1	A	273	ARG	Sidechain
1	A	302	TYR	Sidechain
1	A	344	TYR	Sidechain
1	A	40	PHE	Sidechain
1	A	416	TYR	Sidechain
1	A	457	TYR	Sidechain
2	B	80	PHE	Sidechain
2	B	95	ARG	Sidechain
3	G	30	ARG	Sidechain

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	3015	3165	2959	4	0
2	B	279	297	284	1	0
3	G	484	530	477	1	0
All	All	3778	3992	3720	6	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 1.

All (6) 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:74:GLY:H	1:A:77:MET:HB3	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:80:PHE:O	2:B:84:VAL:HG23	2.12	0.49
1:A:302:TYR:CZ	1:A:345:LEU:HD13	2.49	0.48
1:A:339:GLY:O	1:A:343:HIS:CD2	2.69	0.45
1:A:184:ALA:HB2	1:A:450:ALA:CB	2.46	0.45
3:G:66:VAL:HG13	3:G:68:GLY:H	1.83	0.43

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	388/451 (86%)	338 (87%)	41 (11%)	9 (2%)	5	28
2	B	34/36 (94%)	33 (97%)	1 (3%)	0	100	100
3	G	60/62 (97%)	57 (95%)	1 (2%)	2 (3%)	3	21
All	All	482/549 (88%)	428 (89%)	43 (9%)	11 (2%)	7	28

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	213	ILE
1	A	406	GLU
1	A	407	THR
1	A	445	THR
1	A	349	GLU
1	A	435	ALA
1	A	207	MET
1	A	383	SER
3	G	27	LYS
3	G	66	VAL
1	A	236	ARG

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	290/374 (78%)	280 (97%)	10 (3%)	32	54
2	B	30/32 (94%)	30 (100%)	0	100	100
3	G	43/53 (81%)	40 (93%)	3 (7%)	14	35
All	All	363/459 (79%)	350 (96%)	13 (4%)	32	52

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	108	ASP
1	A	124	THR
1	A	182	PHE
1	A	216	LEU
1	A	286	THR
1	A	307	MET
1	A	344	TYR
1	A	346	SER
1	A	359	VAL
1	A	433	VAL
3	G	8	VAL
3	G	17	ASP
3	G	21	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	113	ASN
1	A	127	GLN
1	A	154	GLN
1	A	202	ASN
1	A	244	ASN
1	A	259	GLN
1	A	306	GLN
1	A	343	HIS

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](#)

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.

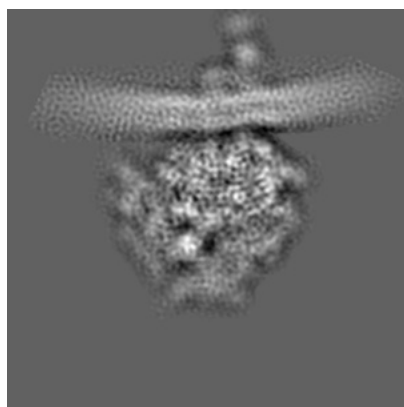
5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

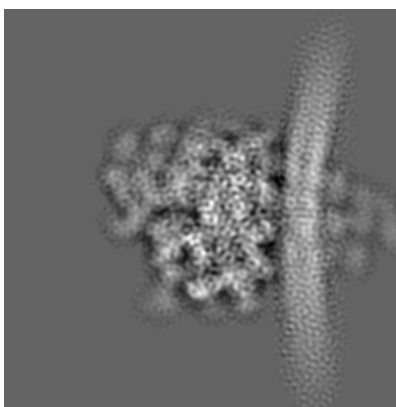
6 Tomogram visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-3068. These allow visual inspection of the internal detail of the tomogram and identification of artifacts.

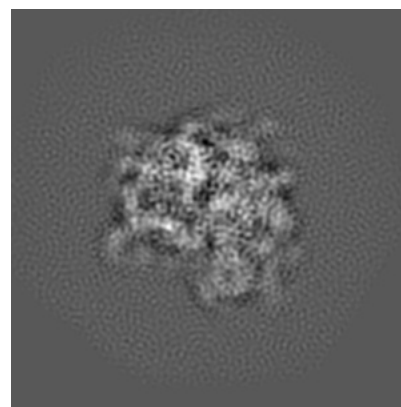
6.1 Orthogonal projections [i](#)



X



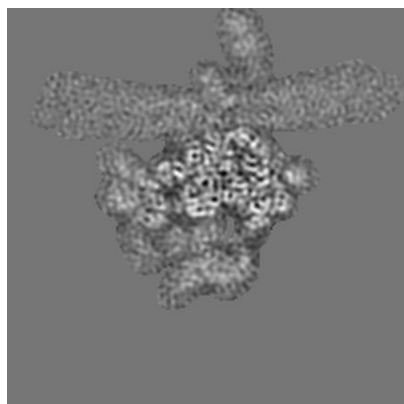
Y



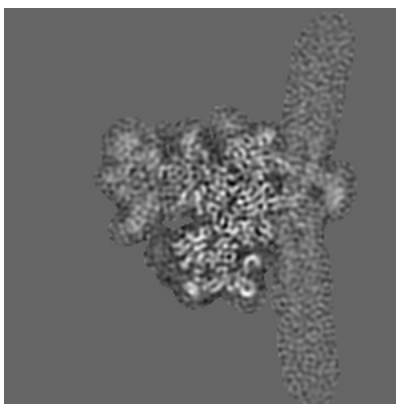
Z

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

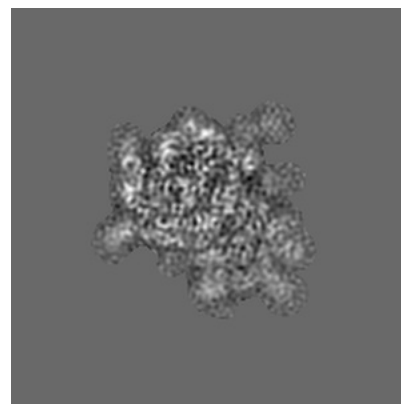
6.2 Central slices [i](#)



X Index: 110



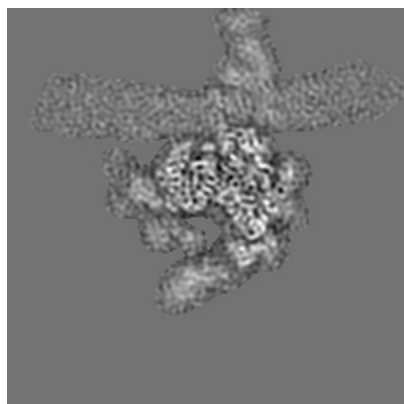
Y Index: 110



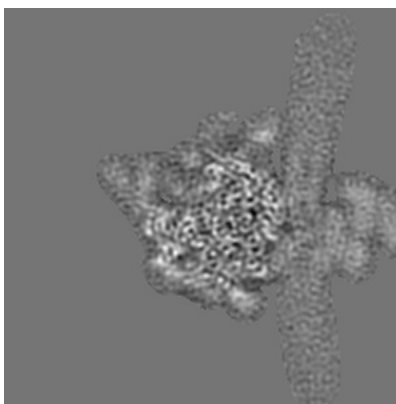
Z Index: 110

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

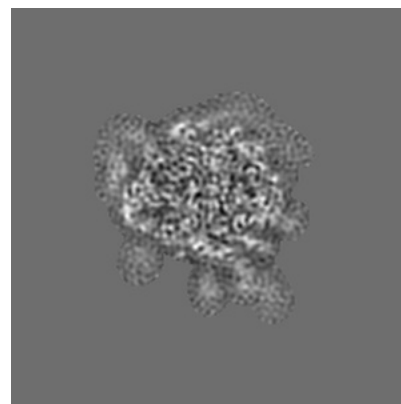
6.3 Largest variance slices [i](#)



X Index: 102



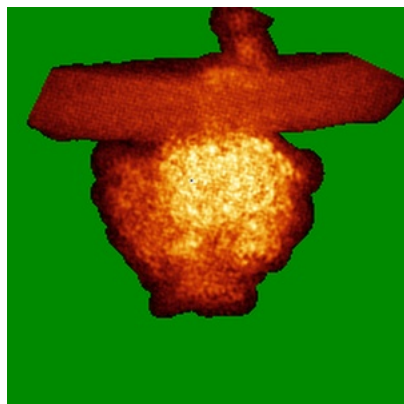
Y Index: 130



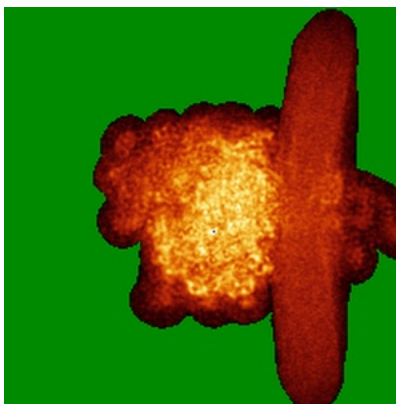
Z Index: 131

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

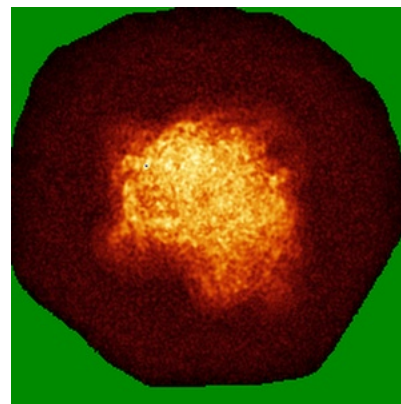
6.4 Orthogonal standard-deviation projections (False-color) [i](#)



X



Y



Z

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

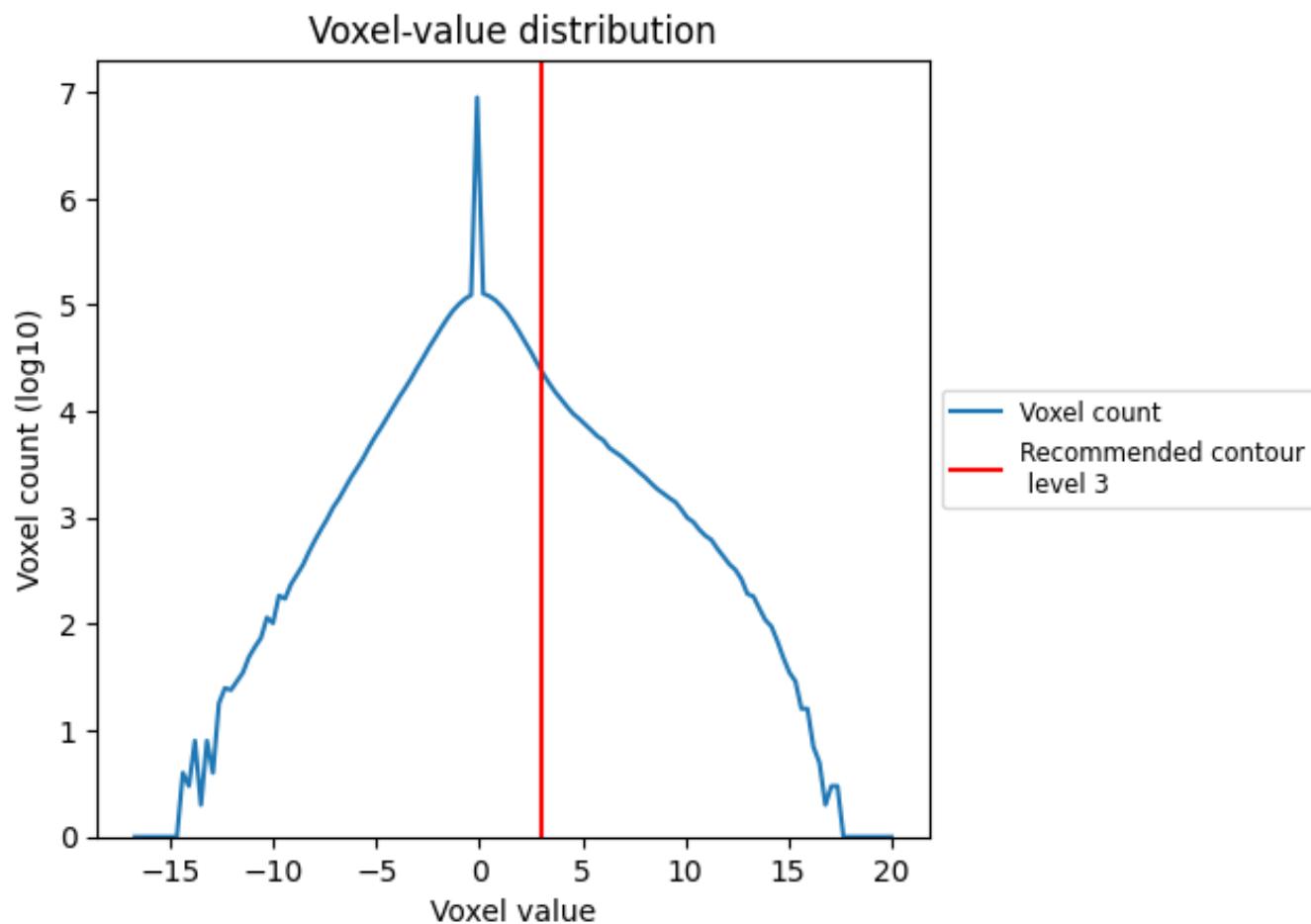
6.5 Mask visualisation [i](#)

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

7 Tomogram analysis [i](#)

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

7.1 Voxel-value distribution [i](#)



The voxel-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic.

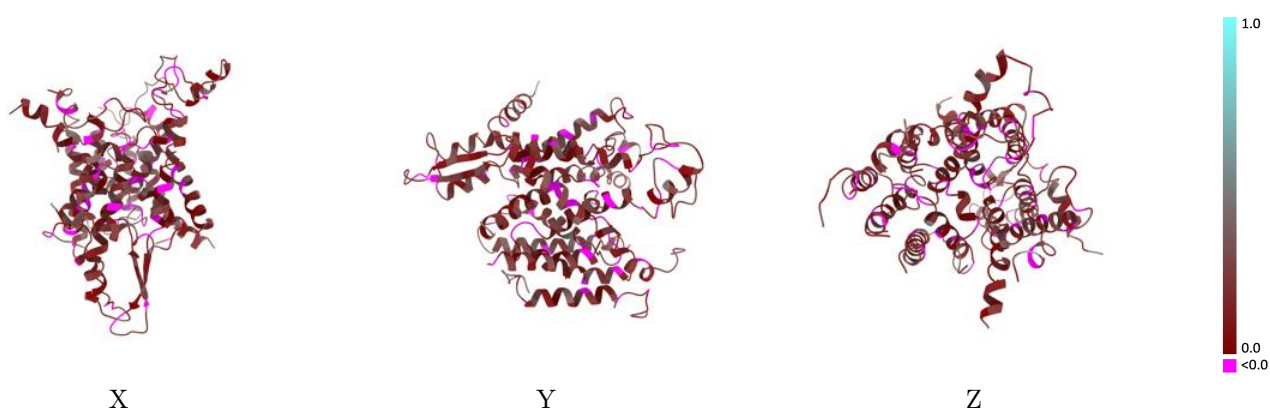
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-3068 and PDB model 5A6U. Per-residue inclusion information can be found in section 3 on page 4.

8.1 Map-model overlay [i](#)

This section was not generated.

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

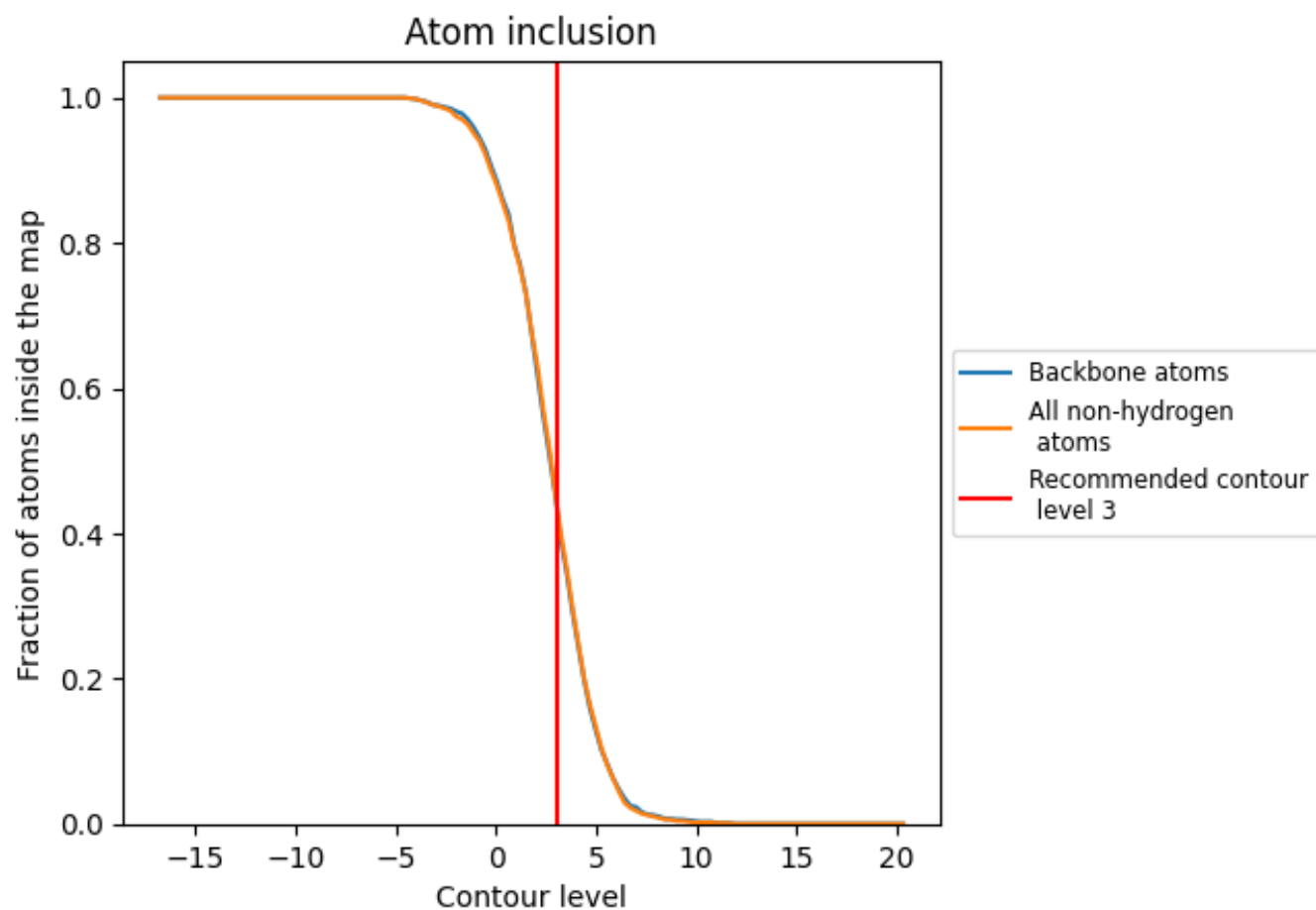


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

8.4 Atom inclusion [i](#)



At the recommended contour level, 45% of all backbone atoms, 45% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4470	0.1430
A	0.4480	0.1380
B	0.3890	0.1580
G	0.4450	0.1690

