



Full wwPDB EM Validation Report ⓘ

Nov 16, 2022 – 04:23 PM JST

PDB ID : 7BOZ
EMDB ID : EMD-30137
Title : N-terminal of mature bacteriophage T7 tail fiber protein gp17
Authors : Chen, W.Y.; Xiao, H.
Deposited on : 2020-03-20
Resolution : 3.80 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

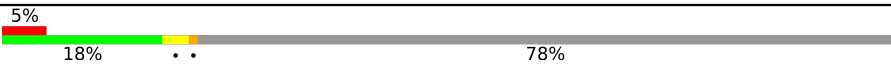
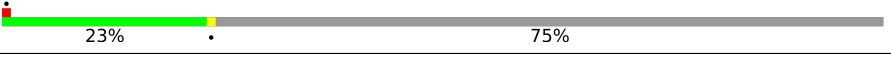

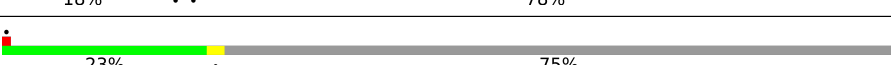



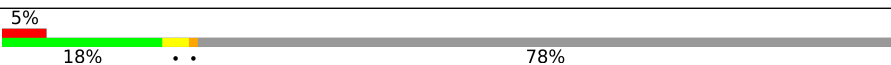


The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

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Mol	Chain	Length	Quality of chain
1	i	553	
1	j	553	
1	k	553	
1	l	553	
1	m	553	
1	n	553	
1	o	553	
1	p	553	
1	q	553	
1	r	553	

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 18516 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 N-terminal of mature bacteriophage T7 tail fiber protein gp17.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	138	Total	C	N	O	S	0	0
			1093	686	196	210	1		
1	b	131	Total	C	N	O	S	0	0
			1045	656	187	201	1		
1	c	119	Total	C	N	O	S	0	0
			948	598	164	185	1		
1	d	138	Total	C	N	O	S	0	0
			1093	686	196	210	1		
1	e	131	Total	C	N	O	S	0	0
			1045	656	187	201	1		
1	f	119	Total	C	N	O	S	0	0
			948	598	164	185	1		
1	g	138	Total	C	N	O	S	0	0
			1093	686	196	210	1		
1	h	131	Total	C	N	O	S	0	0
			1045	656	187	201	1		
1	i	119	Total	C	N	O	S	0	0
			948	598	164	185	1		
1	j	138	Total	C	N	O	S	0	0
			1093	686	196	210	1		
1	k	131	Total	C	N	O	S	0	0
			1045	656	187	201	1		
1	l	119	Total	C	N	O	S	0	0
			948	598	164	185	1		
1	m	138	Total	C	N	O	S	0	0
			1093	686	196	210	1		
1	n	131	Total	C	N	O	S	0	0
			1045	656	187	201	1		
1	o	119	Total	C	N	O	S	0	0
			948	598	164	185	1		
1	p	138	Total	C	N	O	S	0	0
			1093	686	196	210	1		
1	q	131	Total	C	N	O	S	0	0
			1045	656	187	201	1		

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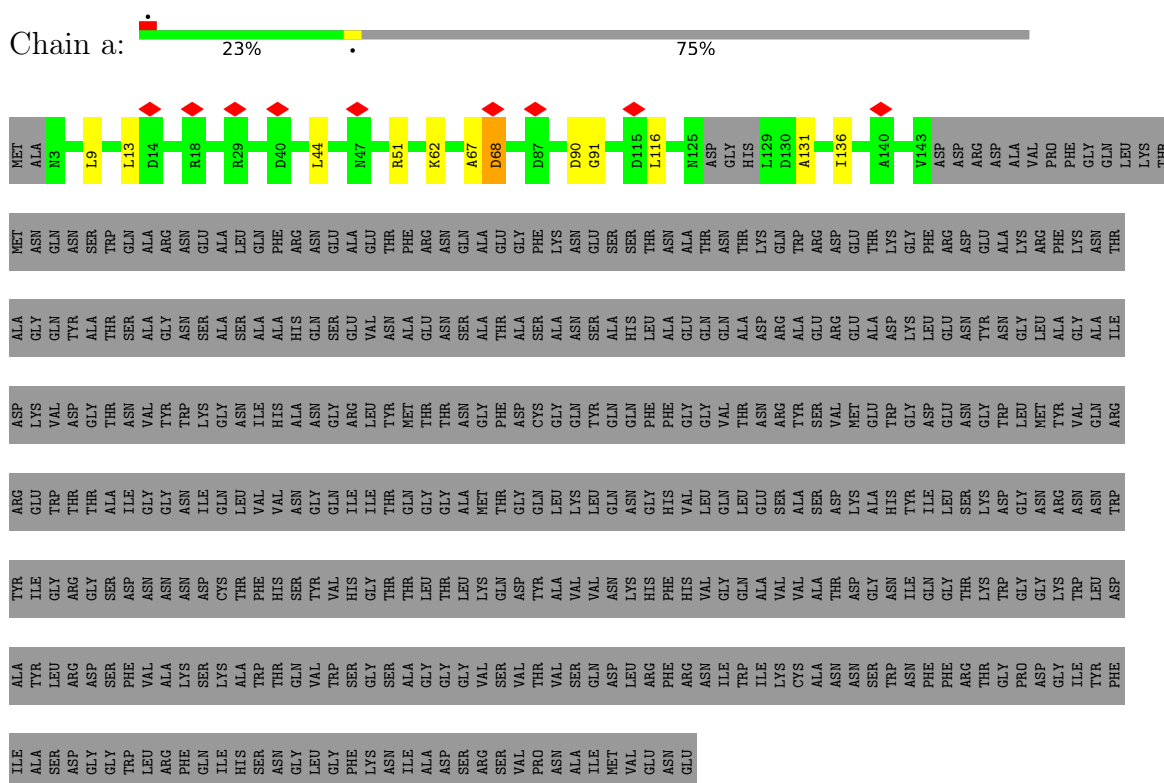
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	r	119	Total	C	N	O	S	0	0
			948	598	164	185	1		

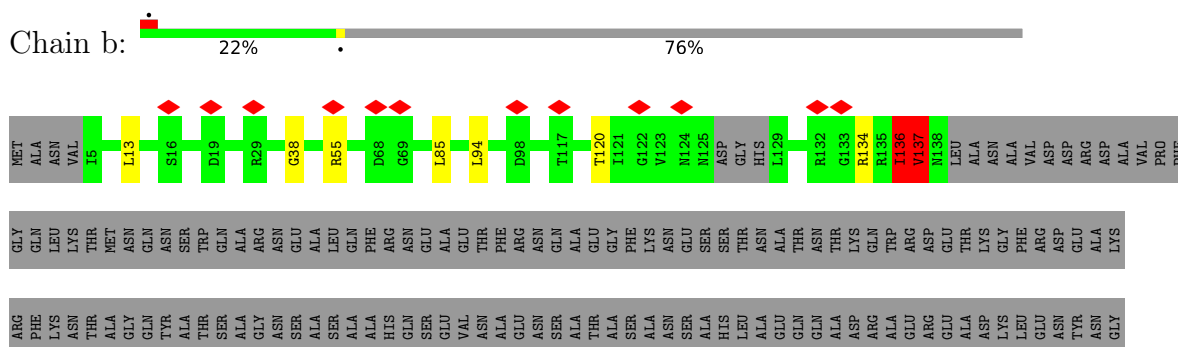
3 Residue-property plots [i](#)

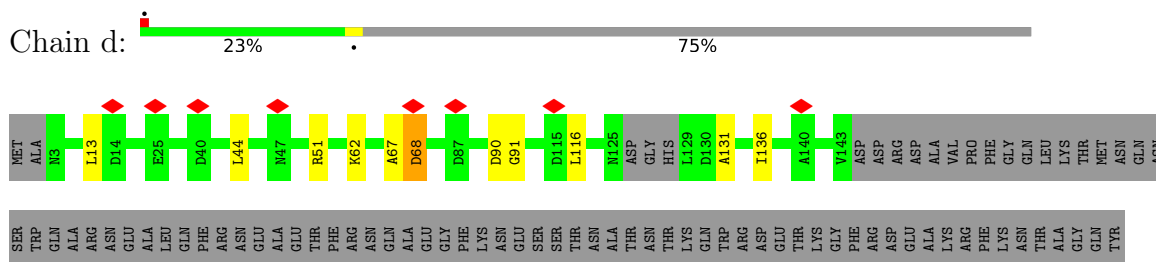
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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.

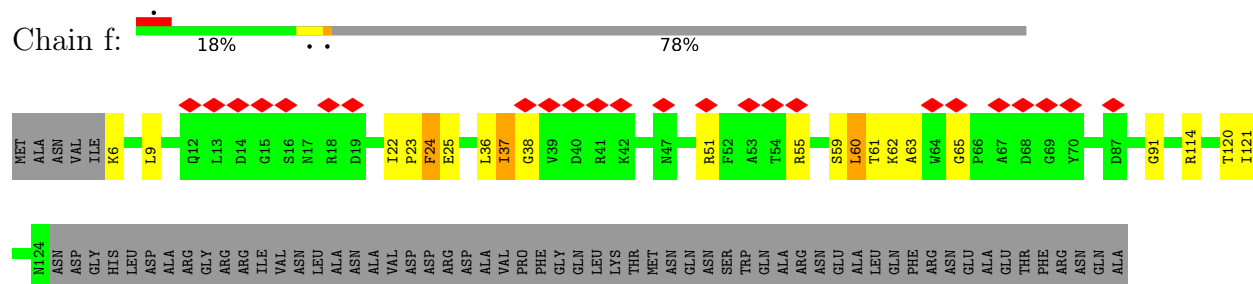
- Molecule 1: N-terminal of mature bacteriophage T7 tail fiber protein gp17



- Molecule 1: N-terminal of mature bacteriophage T7 tail fiber protein gp17

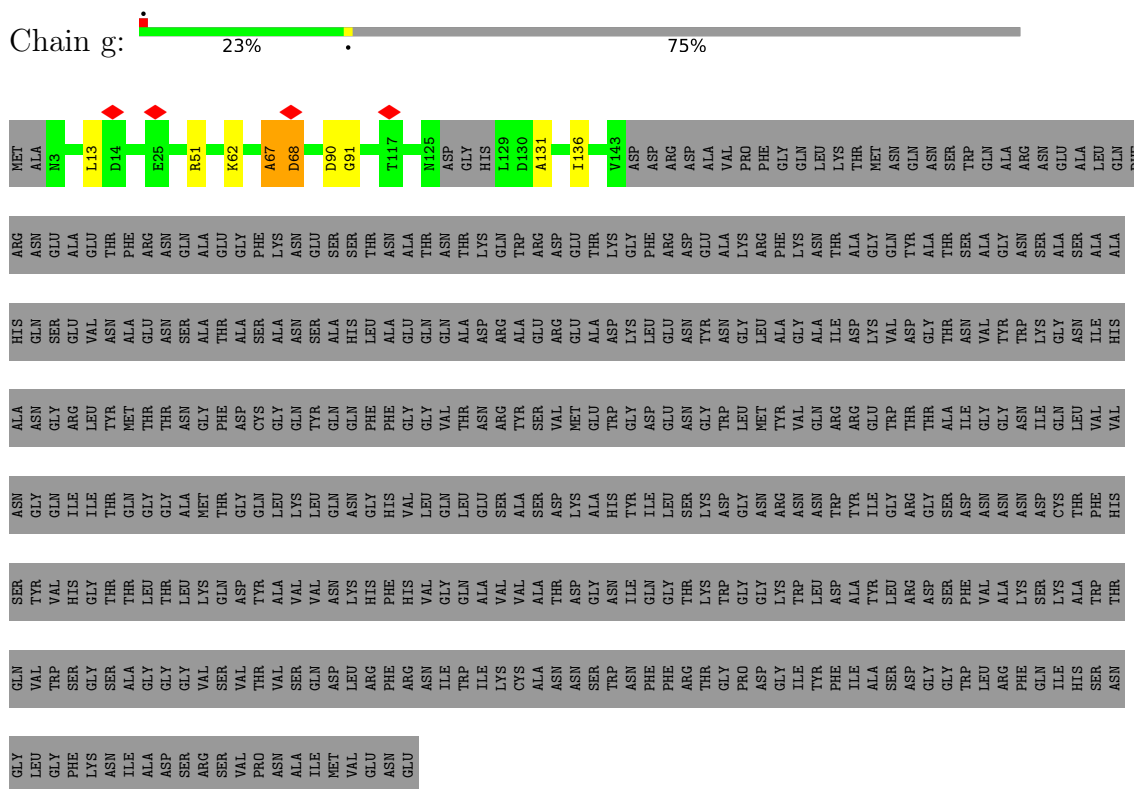




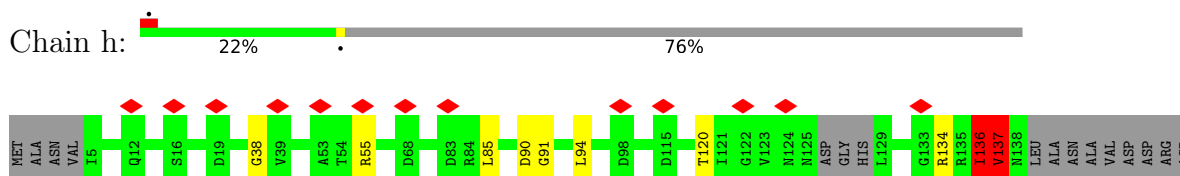


[illegible]

- Molecule 1: N-terminal of mature bacteriophage T7 tail fiber protein gp17

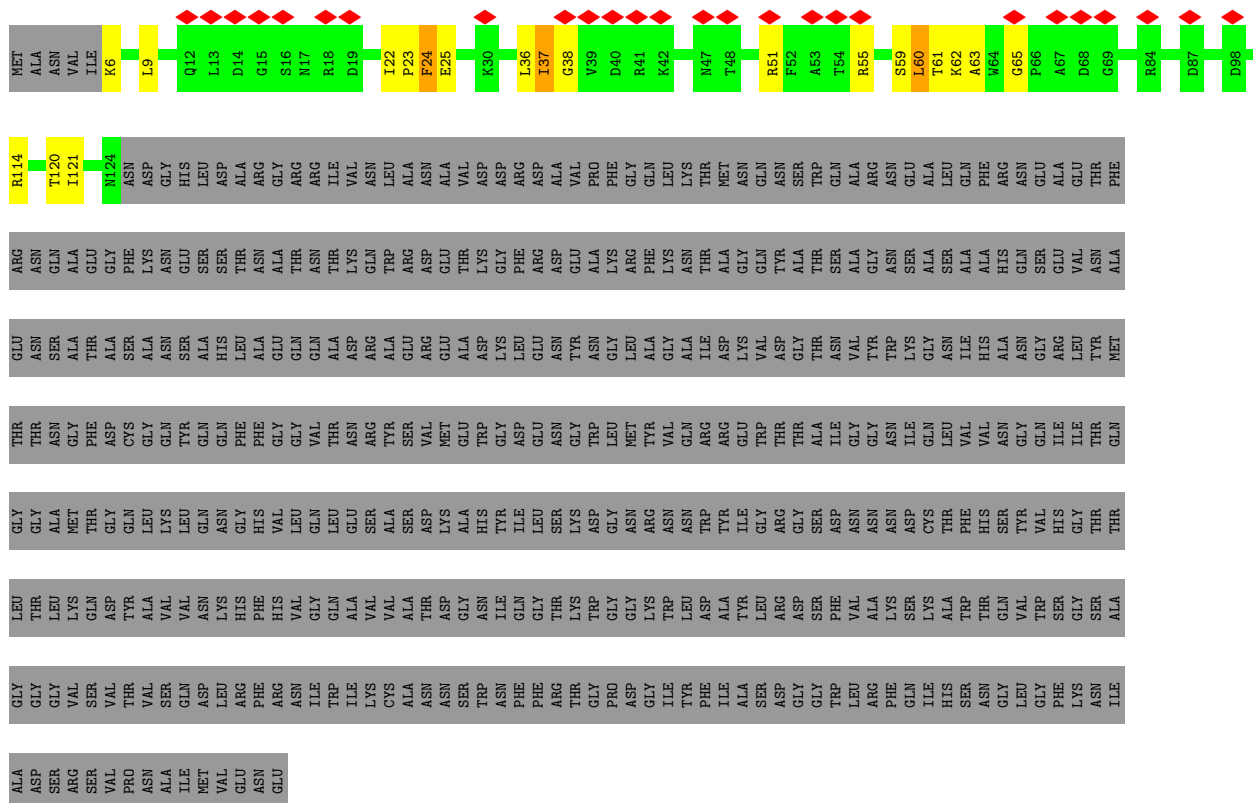


- Molecule 1: N-terminal of mature bacteriophage T7 tail fiber protein gp17



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- Molecule 1: N-terminal of mature bacteriophage T7 tail fiber protein gp17



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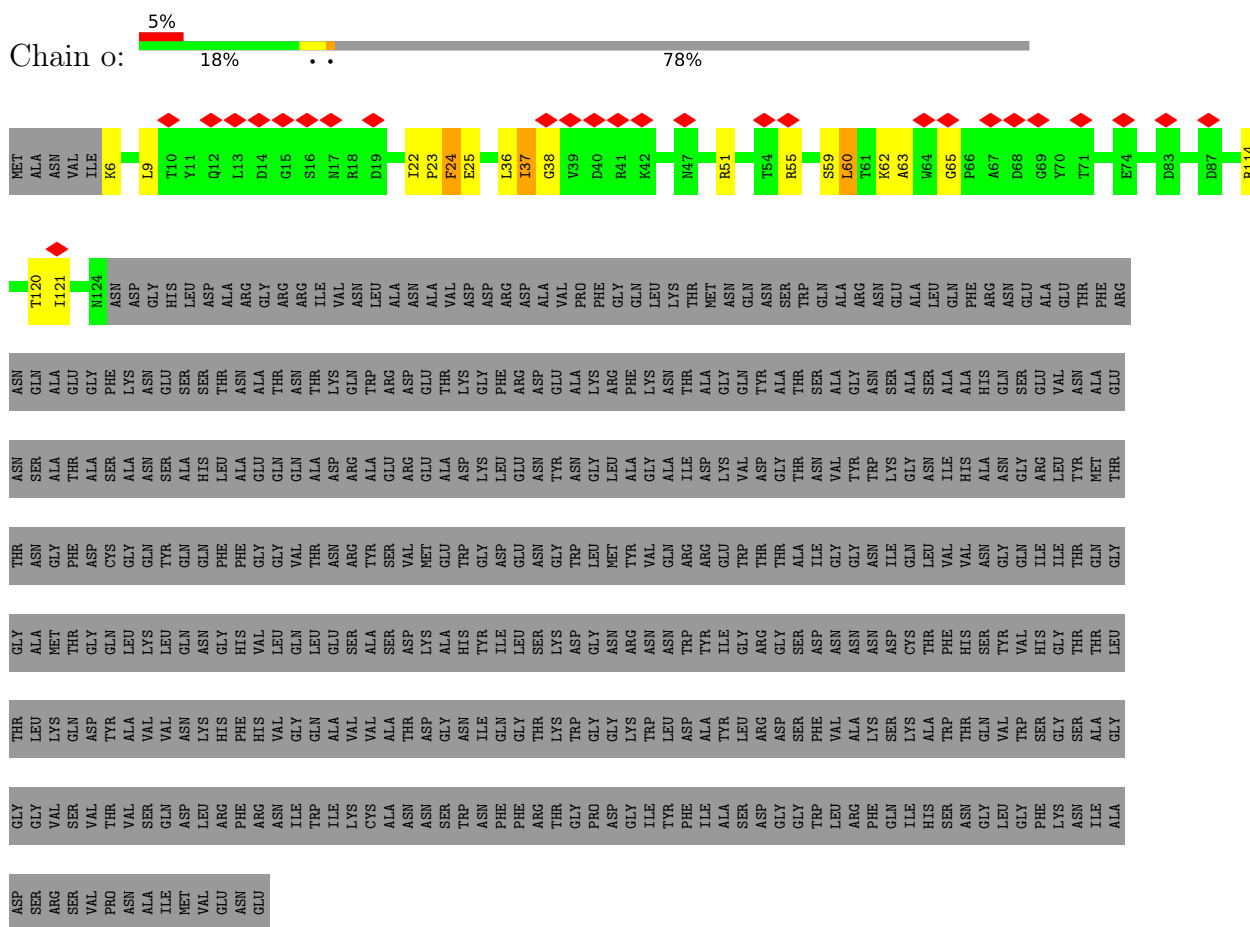


- Molecule 1: N-terminal of mature bacteriophage T7 tail fiber protein gp17

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- Molecule 1: N-terminal of mature bacteriophage T7 tail fiber protein gp17



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55212	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	24	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	27.532	Depositor
Minimum map value	-14.838	Depositor
Average map value	-0.319	Depositor
Map value standard deviation	0.994	Depositor
Recommended contour level	7.0	Depositor
Map size (Å)	447.03998, 447.03998, 447.03998	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.27, 1.27, 1.27	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	a	0.45	0/1106	0.90	7/1504 (0.5%)
1	b	0.46	0/1058	0.93	5/1437 (0.3%)
1	c	0.46	0/962	0.98	5/1310 (0.4%)
1	d	0.45	0/1106	0.90	5/1504 (0.3%)
1	e	0.46	0/1058	0.94	5/1437 (0.3%)
1	f	0.47	0/962	0.98	6/1310 (0.5%)
1	g	0.45	0/1106	0.90	4/1504 (0.3%)
1	h	0.46	0/1058	0.93	5/1437 (0.3%)
1	i	0.48	0/962	0.97	5/1310 (0.4%)
1	j	0.44	0/1106	0.88	4/1504 (0.3%)
1	k	0.47	0/1058	0.90	5/1437 (0.3%)
1	l	0.46	0/962	0.96	4/1310 (0.3%)
1	m	0.44	0/1106	0.89	5/1504 (0.3%)
1	n	0.47	0/1058	0.89	2/1437 (0.1%)
1	o	0.45	0/962	0.97	4/1310 (0.3%)
1	p	0.45	0/1106	0.89	6/1504 (0.4%)
1	q	0.47	0/1058	0.93	3/1437 (0.2%)
1	r	0.45	0/962	0.97	5/1310 (0.4%)
All	All	0.46	0/18756	0.93	85/25506 (0.3%)

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	0	6
1	b	0	5
1	c	0	11
1	d	0	7
1	e	0	6
1	f	0	10
1	g	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	h	0	6
1	i	0	10
1	j	0	6
1	k	0	7
1	l	0	10
1	m	0	7
1	n	0	5
1	o	0	10
1	p	0	7
1	q	0	5
1	r	0	11
All	All	0	136

There are no bond length outliers.

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	f	60	LEU	CA-CB-CG	11.19	141.03	115.30
1	c	60	LEU	CA-CB-CG	10.87	140.31	115.30
1	i	60	LEU	CA-CB-CG	10.68	139.86	115.30
1	r	60	LEU	CA-CB-CG	9.83	137.91	115.30
1	l	60	LEU	CA-CB-CG	9.55	137.25	115.30
1	o	60	LEU	CA-CB-CG	9.27	136.61	115.30
1	o	60	LEU	CB-CG-CD1	-7.94	97.50	111.00
1	q	94	LEU	CA-CB-CG	7.59	132.75	115.30
1	l	60	LEU	CB-CG-CD1	-7.54	98.18	111.00
1	r	60	LEU	CB-CG-CD1	-7.36	98.49	111.00
1	b	94	LEU	CA-CB-CG	7.26	131.99	115.30
1	m	13	LEU	CA-CB-CG	7.26	131.99	115.30
1	e	94	LEU	CA-CB-CG	7.17	131.79	115.30
1	p	13	LEU	CA-CB-CG	6.95	131.28	115.30
1	c	60	LEU	CB-CG-CD1	-6.86	99.35	111.00
1	f	60	LEU	CB-CG-CD1	-6.74	99.53	111.00
1	i	60	LEU	CB-CG-CD1	-6.70	99.61	111.00
1	e	85	LEU	CB-CG-CD2	-6.55	99.86	111.00
1	h	94	LEU	CA-CB-CG	6.45	130.14	115.30
1	h	85	LEU	CB-CG-CD2	-6.42	100.08	111.00
1	j	13	LEU	CA-CB-CG	6.35	129.91	115.30
1	n	94	LEU	CA-CB-CG	6.29	129.76	115.30
1	a	13	LEU	CA-CB-CG	6.24	129.64	115.30
1	g	68	ASP	CB-CG-OD1	6.20	123.88	118.30
1	j	68	ASP	CB-CG-OD1	6.09	123.78	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	d	68	ASP	CB-CG-OD1	6.05	123.74	118.30
1	p	68	ASP	CB-CG-OD1	6.01	123.71	118.30
1	a	68	ASP	CB-CG-OD1	6.01	123.71	118.30
1	m	68	ASP	CB-CG-OD1	6.00	123.70	118.30
1	k	94	LEU	CA-CB-CG	5.84	128.73	115.30
1	b	85	LEU	CB-CG-CD2	-5.83	101.09	111.00
1	d	13	LEU	CA-CB-CG	5.74	128.49	115.30
1	o	37	ILE	C-N-CA	5.69	134.26	122.30
1	r	37	ILE	C-N-CA	5.68	134.24	122.30
1	k	136	ILE	C-N-CA	5.63	135.78	121.70
1	g	13	LEU	CA-CB-CG	5.63	128.25	115.30
1	h	136	ILE	C-N-CA	5.63	135.78	121.70
1	i	37	ILE	C-N-CA	5.61	134.08	122.30
1	n	136	ILE	C-N-CA	5.59	135.67	121.70
1	e	136	ILE	C-N-CA	5.55	135.56	121.70
1	l	37	ILE	C-N-CA	5.54	133.94	122.30
1	k	85	LEU	CB-CG-CD2	-5.51	101.63	111.00
1	q	136	ILE	C-N-CA	5.51	135.48	121.70
1	b	136	ILE	C-N-CA	5.50	135.46	121.70
1	a	9	LEU	CB-CG-CD2	-5.49	101.67	111.00
1	c	37	ILE	C-N-CA	5.42	133.68	122.30
1	r	24	PHE	C-N-CA	5.37	135.13	121.70
1	f	37	ILE	C-N-CA	5.33	133.50	122.30
1	o	24	PHE	C-N-CA	5.33	135.02	121.70
1	p	44	LEU	CA-CB-CG	5.30	127.49	115.30
1	k	91	GLY	C-N-CA	5.29	134.93	121.70
1	f	24	PHE	C-N-CA	5.26	134.86	121.70
1	c	24	PHE	C-N-CA	5.26	134.84	121.70
1	d	116	LEU	CA-CB-CG	5.25	127.38	115.30
1	h	91	GLY	C-N-CA	5.25	134.81	121.70
1	f	91	GLY	C-N-CA	5.24	134.80	121.70
1	b	13	LEU	CA-CB-CG	5.21	127.29	115.30
1	e	13	LEU	CA-CB-CG	5.20	127.26	115.30
1	a	44	LEU	CA-CB-CG	5.18	127.21	115.30
1	l	24	PHE	C-N-CA	5.17	134.62	121.70
1	i	24	PHE	C-N-CA	5.16	134.60	121.70
1	c	91	GLY	C-N-CA	5.16	134.60	121.70
1	m	91	GLY	C-N-CA	5.15	134.59	121.70
1	m	44	LEU	CA-CB-CG	5.15	127.15	115.30
1	d	44	LEU	CA-CB-CG	5.15	127.14	115.30
1	g	91	GLY	C-N-CA	5.15	134.57	121.70
1	j	91	GLY	C-N-CA	5.14	134.54	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	q	85	LEU	CB-CG-CD2	-5.13	102.28	111.00
1	e	91	GLY	C-N-CA	5.12	134.51	121.70
1	d	91	GLY	C-N-CA	5.11	134.49	121.70
1	r	91	GLY	C-N-CA	5.11	134.48	121.70
1	p	91	GLY	C-N-CA	5.09	134.44	121.70
1	m	67	ALA	C-N-CA	5.08	134.41	121.70
1	a	91	GLY	C-N-CA	5.07	134.38	121.70
1	a	67	ALA	C-N-CA	5.06	134.36	121.70
1	k	137	VAL	N-CA-CB	-5.06	100.36	111.50
1	h	137	VAL	N-CA-CB	-5.06	100.38	111.50
1	p	67	ALA	C-N-CA	5.05	134.34	121.70
1	j	67	ALA	C-N-CA	5.05	134.32	121.70
1	p	9	LEU	CB-CG-CD2	-5.03	102.44	111.00
1	b	137	VAL	N-CA-CB	-5.03	100.43	111.50
1	f	61	THR	C-N-CA	5.03	134.27	121.70
1	a	116	LEU	CA-CB-CG	5.02	126.84	115.30
1	i	61	THR	C-N-CA	5.02	134.24	121.70
1	g	67	ALA	C-N-CA	5.01	134.22	121.70

There are no chirality outliers.

All (136) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	a	131	ALA	Peptide
1	a	136	ILE	Peptide
1	a	51	ARG	Peptide
1	a	62	LYS	Peptide
1	a	68	ASP	Peptide
1	a	90	ASP	Peptide
1	b	120	THR	Peptide
1	b	134	ARG	Peptide
1	b	136	ILE	Peptide
1	b	137	VAL	Peptide
1	b	38	GLY	Peptide
1	c	120	THR	Peptide
1	c	22	ILE	Peptide
1	c	23	PRO	Peptide
1	c	24	PHE	Peptide
1	c	36	LEU	Peptide
1	c	37	ILE	Peptide
1	c	59	SER	Peptide
1	c	62	LYS	Peptide

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Mol	Chain	Res	Type	Group
1	c	63	ALA	Peptide
1	c	65	GLY	Peptide
1	c	90	ASP	Peptide
1	d	131	ALA	Peptide
1	d	136	ILE	Peptide
1	d	51	ARG	Peptide
1	d	62	LYS	Peptide
1	d	67	ALA	Peptide
1	d	68	ASP	Peptide
1	d	90	ASP	Peptide
1	e	120	THR	Peptide
1	e	134	ARG	Peptide
1	e	136	ILE	Peptide
1	e	137	VAL	Peptide
1	e	38	GLY	Peptide
1	e	90	ASP	Peptide
1	f	120	THR	Peptide
1	f	22	ILE	Peptide
1	f	23	PRO	Peptide
1	f	24	PHE	Peptide
1	f	36	LEU	Peptide
1	f	37	ILE	Peptide
1	f	59	SER	Peptide
1	f	62	LYS	Peptide
1	f	63	ALA	Peptide
1	f	65	GLY	Peptide
1	g	131	ALA	Peptide
1	g	136	ILE	Peptide
1	g	51	ARG	Peptide
1	g	62	LYS	Peptide
1	g	67	ALA	Peptide
1	g	68	ASP	Peptide
1	g	90	ASP	Peptide
1	h	120	THR	Peptide
1	h	134	ARG	Peptide
1	h	136	ILE	Peptide
1	h	137	VAL	Peptide
1	h	38	GLY	Peptide
1	h	90	ASP	Peptide
1	i	120	THR	Peptide
1	i	22	ILE	Peptide
1	i	23	PRO	Peptide

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Mol	Chain	Res	Type	Group
1	i	24	PHE	Peptide
1	i	36	LEU	Peptide
1	i	37	ILE	Peptide
1	i	59	SER	Peptide
1	i	62	LYS	Peptide
1	i	63	ALA	Peptide
1	i	65	GLY	Peptide
1	j	131	ALA	Peptide
1	j	136	ILE	Peptide
1	j	51	ARG	Peptide
1	j	62	LYS	Peptide
1	j	68	ASP	Peptide
1	j	90	ASP	Peptide
1	k	120	THR	Peptide
1	k	134	ARG	Peptide
1	k	136	ILE	Peptide
1	k	137	VAL	Peptide
1	k	38	GLY	Peptide
1	k	45	THR	Peptide
1	k	90	ASP	Peptide
1	l	120	THR	Peptide
1	l	22	ILE	Peptide
1	l	23	PRO	Peptide
1	l	24	PHE	Peptide
1	l	36	LEU	Peptide
1	l	37	ILE	Peptide
1	l	59	SER	Peptide
1	l	62	LYS	Peptide
1	l	63	ALA	Peptide
1	l	65	GLY	Peptide
1	m	131	ALA	Peptide
1	m	136	ILE	Peptide
1	m	38	GLY	Peptide
1	m	51	ARG	Peptide
1	m	62	LYS	Peptide
1	m	68	ASP	Peptide
1	m	90	ASP	Peptide
1	n	120	THR	Peptide
1	n	134	ARG	Peptide
1	n	136	ILE	Peptide
1	n	137	VAL	Peptide
1	n	38	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	o	120	THR	Peptide
1	o	22	ILE	Peptide
1	o	23	PRO	Peptide
1	o	24	PHE	Peptide
1	o	36	LEU	Peptide
1	o	37	ILE	Peptide
1	o	59	SER	Peptide
1	o	62	LYS	Peptide
1	o	63	ALA	Peptide
1	o	65	GLY	Peptide
1	p	131	ALA	Peptide
1	p	136	ILE	Peptide
1	p	38	GLY	Peptide
1	p	51	ARG	Peptide
1	p	62	LYS	Peptide
1	p	68	ASP	Peptide
1	p	90	ASP	Peptide
1	q	120	THR	Peptide
1	q	134	ARG	Peptide
1	q	136	ILE	Peptide
1	q	137	VAL	Peptide
1	q	38	GLY	Peptide
1	r	120	THR	Peptide
1	r	22	ILE	Peptide
1	r	23	PRO	Peptide
1	r	24	PHE	Peptide
1	r	36	LEU	Peptide
1	r	37	ILE	Peptide
1	r	59	SER	Peptide
1	r	62	LYS	Peptide
1	r	63	ALA	Peptide
1	r	65	GLY	Peptide
1	r	90	ASP	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	1093	0	1107	0	0
1	b	1045	0	1056	0	0
1	c	948	0	952	0	0
1	d	1093	0	1107	0	0
1	e	1045	0	1056	0	0
1	f	948	0	952	0	0
1	g	1093	0	1107	0	0
1	h	1045	0	1056	0	0
1	i	948	0	952	0	0
1	j	1093	0	1107	0	0
1	k	1045	0	1056	0	0
1	l	948	0	952	0	0
1	m	1093	0	1107	0	0
1	n	1045	0	1056	0	0
1	o	948	0	952	0	0
1	p	1093	0	1107	0	0
1	q	1045	0	1056	0	0
1	r	948	0	952	0	0
All	All	18516	0	18690	0	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 11.

There are no clashes within the asymmetric unit.

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	134/553 (24%)	115 (86%)	19 (14%)	0	100	100
1	b	127/553 (23%)	111 (87%)	14 (11%)	2 (2%)	9	44
1	c	117/553 (21%)	97 (83%)	16 (14%)	4 (3%)	3	31
1	d	134/553 (24%)	115 (86%)	19 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	e	127/553 (23%)	110 (87%)	15 (12%)	2 (2%)	9	44
1	f	117/553 (21%)	96 (82%)	17 (14%)	4 (3%)	3	31
1	g	134/553 (24%)	114 (85%)	20 (15%)	0	100	100
1	h	127/553 (23%)	111 (87%)	14 (11%)	2 (2%)	9	44
1	i	117/553 (21%)	97 (83%)	16 (14%)	4 (3%)	3	31
1	j	134/553 (24%)	115 (86%)	19 (14%)	0	100	100
1	k	127/553 (23%)	112 (88%)	13 (10%)	2 (2%)	9	44
1	l	117/553 (21%)	97 (83%)	16 (14%)	4 (3%)	3	31
1	m	134/553 (24%)	115 (86%)	19 (14%)	0	100	100
1	n	127/553 (23%)	111 (87%)	14 (11%)	2 (2%)	9	44
1	o	117/553 (21%)	97 (83%)	16 (14%)	4 (3%)	3	31
1	p	134/553 (24%)	115 (86%)	19 (14%)	0	100	100
1	q	127/553 (23%)	110 (87%)	16 (13%)	1 (1%)	19	57
1	r	117/553 (21%)	97 (83%)	16 (14%)	4 (3%)	3	31
All	All	2268/9954 (23%)	1935 (85%)	298 (13%)	35 (2%)	14	46

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	137	VAL
1	c	60	LEU
1	c	121	ILE
1	e	137	VAL
1	f	60	LEU
1	f	121	ILE
1	h	137	VAL
1	i	60	LEU
1	i	121	ILE
1	k	137	VAL
1	l	60	LEU
1	l	121	ILE
1	n	137	VAL
1	o	60	LEU
1	o	121	ILE
1	q	137	VAL
1	r	60	LEU
1	r	121	ILE

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Mol	Chain	Res	Type
1	c	38	GLY
1	f	38	GLY
1	i	38	GLY
1	l	38	GLY
1	o	38	GLY
1	r	38	GLY
1	c	25	GLU
1	l	25	GLU
1	o	25	GLU
1	r	25	GLU
1	f	25	GLU
1	i	25	GLU
1	b	136	ILE
1	e	136	ILE
1	h	136	ILE
1	k	136	ILE
1	n	136	ILE

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	120/451 (27%)	120 (100%)	0	100	100
1	b	115/451 (26%)	114 (99%)	1 (1%)	78	88
1	c	105/451 (23%)	100 (95%)	5 (5%)	25	56
1	d	120/451 (27%)	120 (100%)	0	100	100
1	e	115/451 (26%)	114 (99%)	1 (1%)	78	88
1	f	105/451 (23%)	100 (95%)	5 (5%)	25	56
1	g	120/451 (27%)	120 (100%)	0	100	100
1	h	115/451 (26%)	114 (99%)	1 (1%)	78	88
1	i	105/451 (23%)	100 (95%)	5 (5%)	25	56
1	j	120/451 (27%)	120 (100%)	0	100	100
1	k	115/451 (26%)	113 (98%)	2 (2%)	60	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	l	105/451 (23%)	100 (95%)	5 (5%)	25	56
1	m	120/451 (27%)	120 (100%)	0	100	100
1	n	115/451 (26%)	113 (98%)	2 (2%)	60	78
1	o	105/451 (23%)	100 (95%)	5 (5%)	25	56
1	p	120/451 (27%)	120 (100%)	0	100	100
1	q	115/451 (26%)	114 (99%)	1 (1%)	78	88
1	r	105/451 (23%)	100 (95%)	5 (5%)	25	56
All	All	2040/8118 (25%)	2002 (98%)	38 (2%)	59	76

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	b	55	ARG
1	c	6	LYS
1	c	9	LEU
1	c	51	ARG
1	c	55	ARG
1	c	114	ARG
1	e	55	ARG
1	f	6	LYS
1	f	9	LEU
1	f	51	ARG
1	f	55	ARG
1	f	114	ARG
1	h	55	ARG
1	i	6	LYS
1	i	9	LEU
1	i	51	ARG
1	i	55	ARG
1	i	114	ARG
1	k	9	LEU
1	k	55	ARG
1	l	6	LYS
1	l	9	LEU
1	l	51	ARG
1	l	55	ARG
1	l	114	ARG
1	n	9	LEU
1	n	55	ARG
1	o	6	LYS

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Mol	Chain	Res	Type
1	o	9	LEU
1	o	51	ARG
1	o	55	ARG
1	o	114	ARG
1	q	55	ARG
1	r	6	LYS
1	r	9	LEU
1	r	51	ARG
1	r	55	ARG
1	r	114	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	a	103	GLN
1	a	105	GLN
1	a	108	HIS
1	b	108	HIS
1	d	103	GLN
1	d	105	GLN
1	d	108	HIS
1	e	108	HIS
1	g	103	GLN
1	g	105	GLN
1	g	108	HIS
1	h	108	HIS
1	j	103	GLN
1	j	105	GLN
1	k	108	HIS
1	m	103	GLN
1	m	105	GLN
1	m	108	HIS
1	n	108	HIS
1	p	103	GLN
1	p	105	GLN
1	p	108	HIS
1	q	108	HIS

5.3.3 RNA ⓘ

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

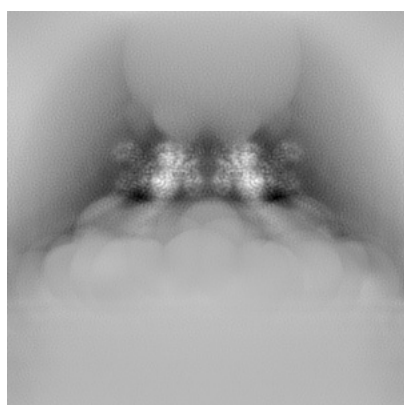
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30137. These allow visual inspection of the internal detail of the map and identification of artifacts.

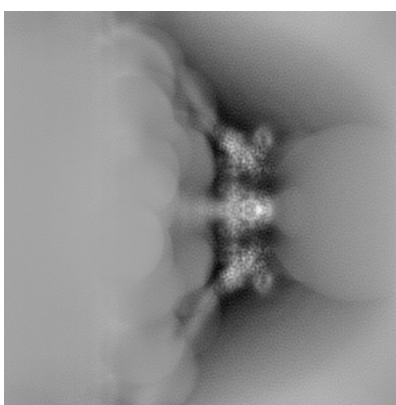
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

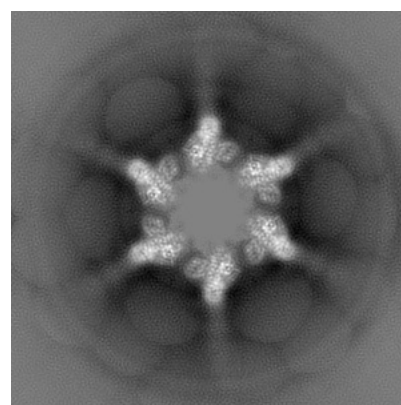
6.1.1 Primary map



X



Y

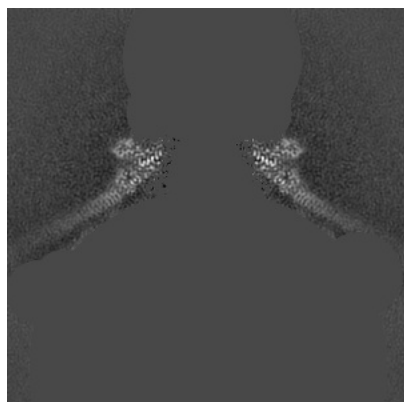


Z

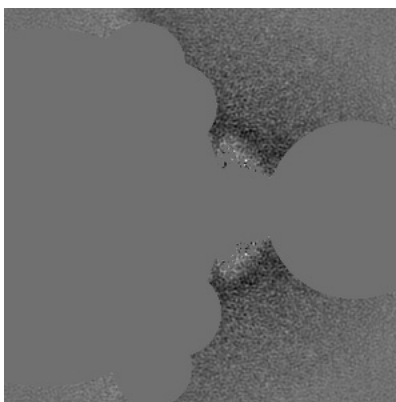
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

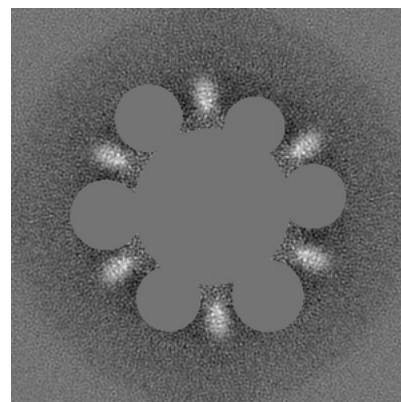
6.2.1 Primary map



X Index: 176



Y Index: 176

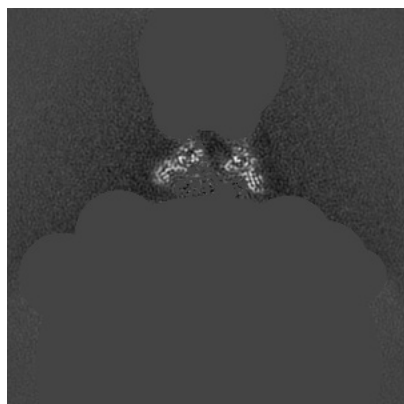


Z Index: 176

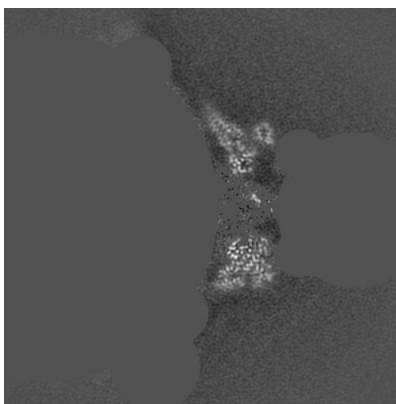
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

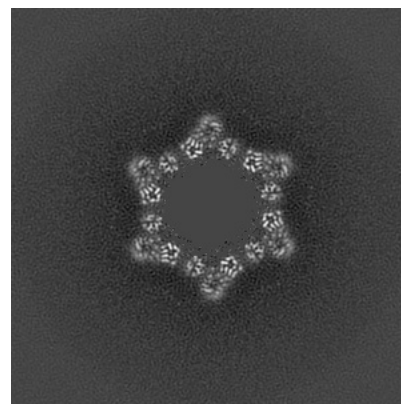
6.3.1 Primary map



X Index: 218



Y Index: 141

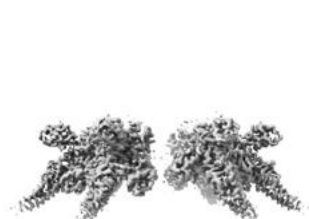


Z Index: 202

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

6.4 Orthogonal surface views [i](#)

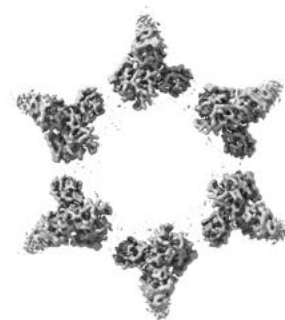
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 7.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

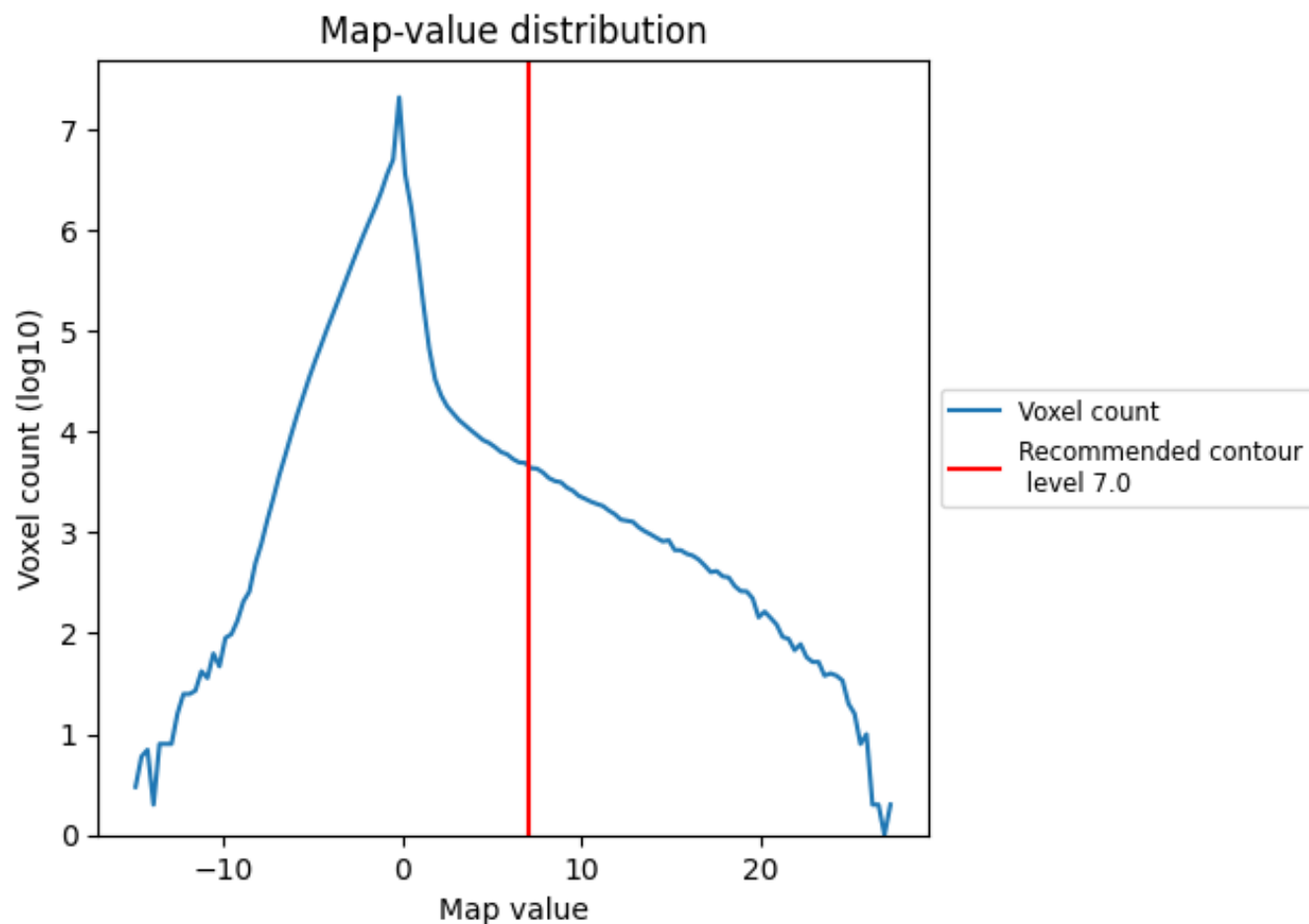
6.5 Mask visualisation

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

7 Map analysis [i](#)

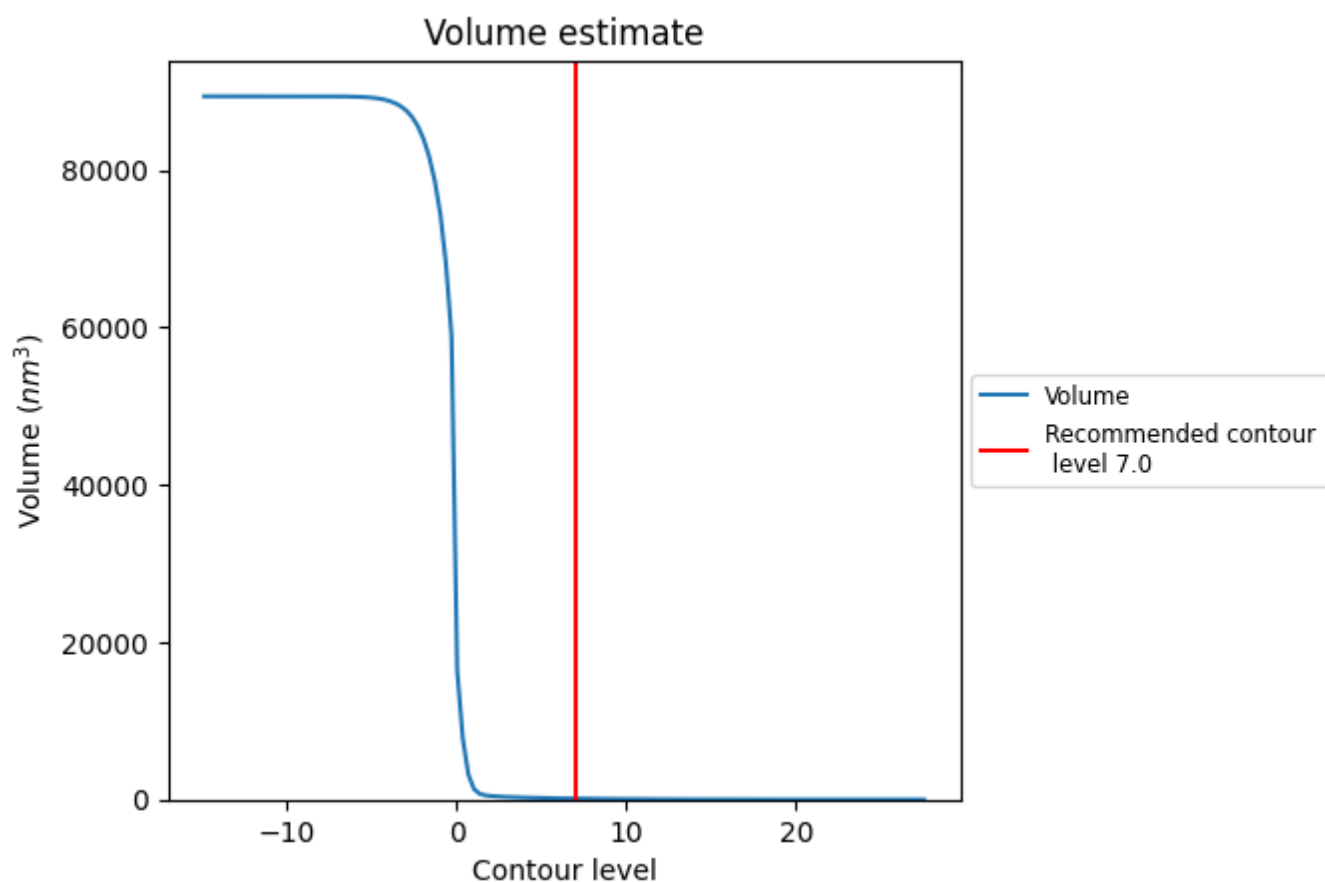
This section contains the results of statistical analysis of the map.

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.

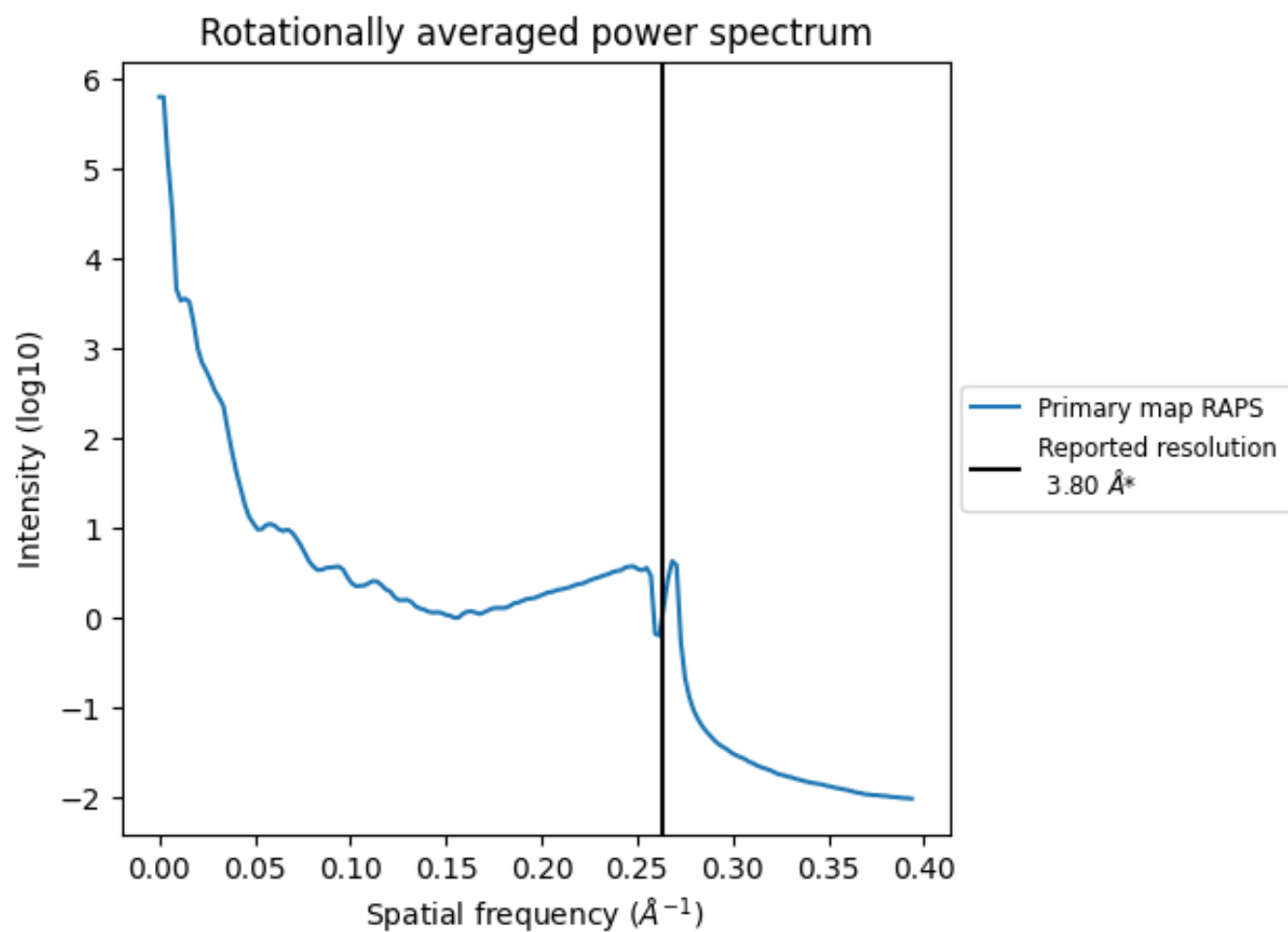
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 124 nm^3 ; this corresponds to an approximate mass of 112 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 0.263 Å⁻¹

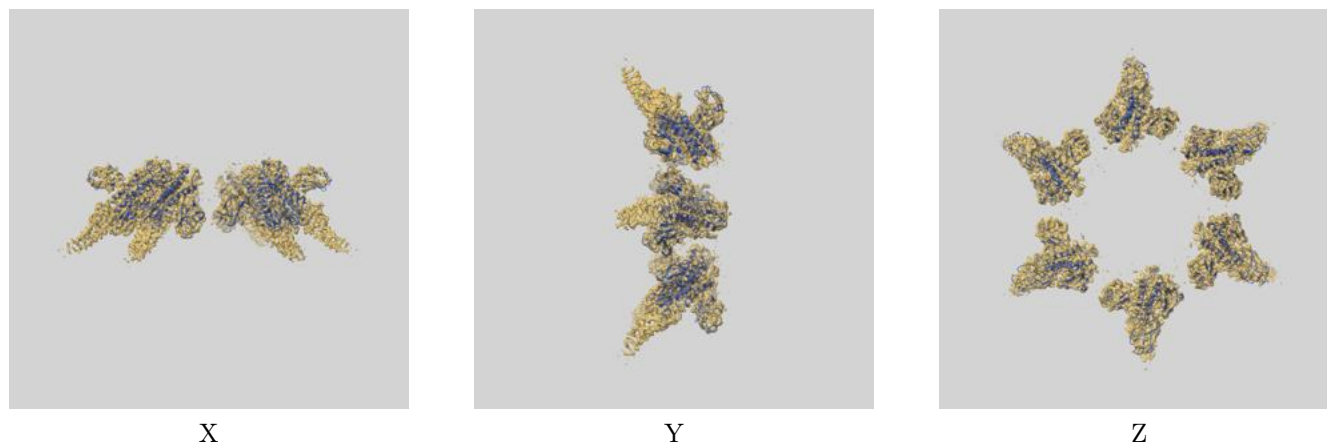
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

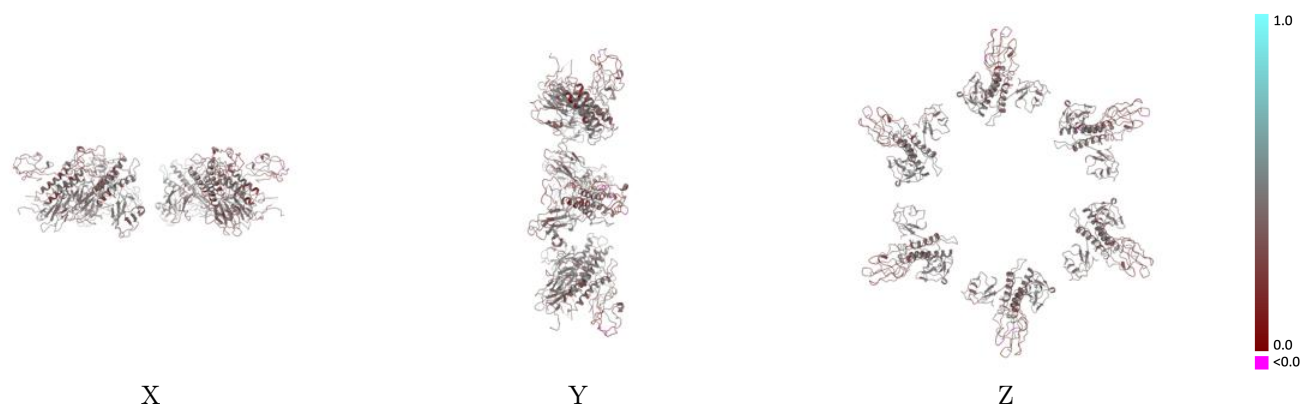
This section contains information regarding the fit between EMDB map EMD-30137 and PDB model 7BOZ. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



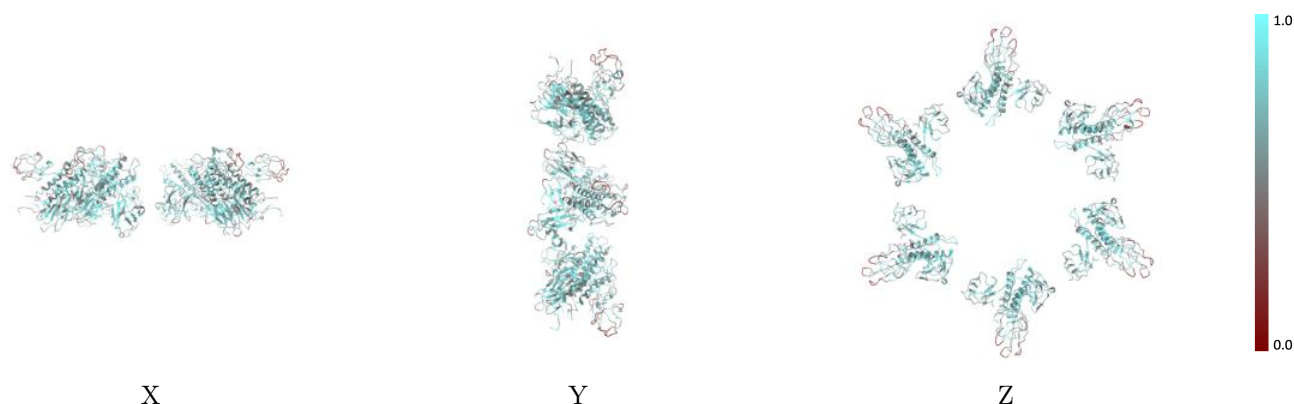
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



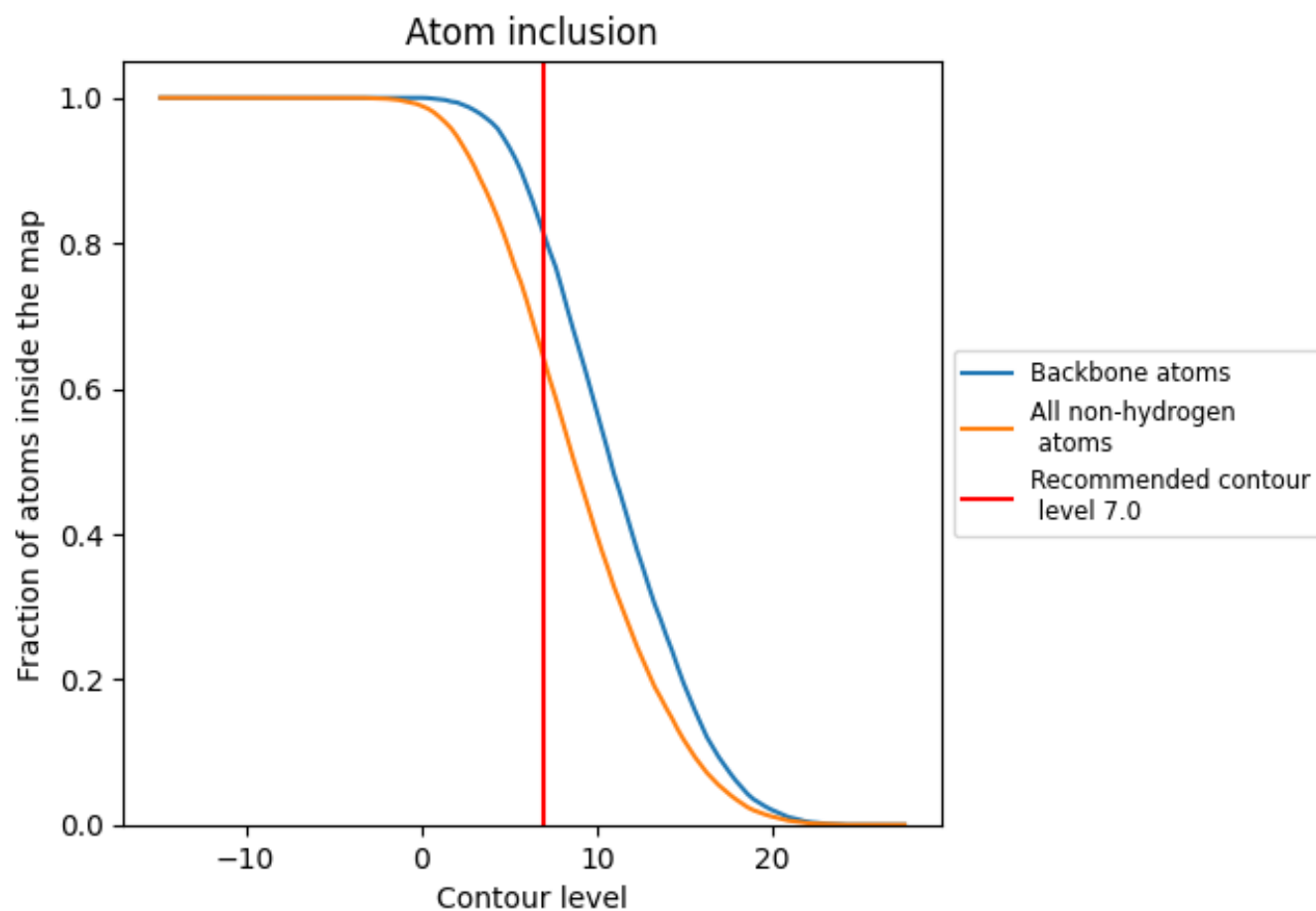
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (7.0).







































9.4 Atom inclusion [i](#)



At the recommended contour level, 81% of all backbone atoms, 64% 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 (7.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6397	 0.3930
a	 0.6927	 0.4230
b	 0.6505	 0.4190
c	 0.5727	 0.3560
d	 0.6993	 0.4230
e	 0.6535	 0.4120
f	 0.5607	 0.3450
g	 0.7172	 0.4320
h	 0.6555	 0.4210
i	 0.5629	 0.3510
j	 0.7116	 0.4370
k	 0.6476	 0.4150
l	 0.5705	 0.3580
m	 0.6927	 0.4080
n	 0.6338	 0.3900
o	 0.5521	 0.3130
p	 0.6890	 0.4010
q	 0.6387	 0.3990
r	 0.5542	 0.3260

