



## Full wwPDB EM Validation Report ⓘ

Nov 16, 2022 – 04:32 PM JST

PDB ID : 7BP0  
EMDB ID : EMD-30138  
Title : Packing Bacteriophage T7 portal protein GP8  
Authors : Chen, W.Y.; Xiao, H.  
Deposited on : 2020-03-20  
Resolution : 4.60 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](mailto: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>.

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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

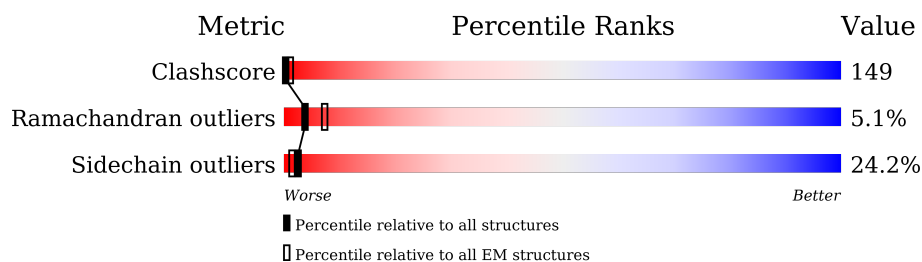
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 4.60 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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  $\geq 3$ , 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	536	 56% 22% • 18%
1	b	536	 57% 21% • 18%
1	c	536	 57% 21% • • 18%
1	d	536	 57% 21% • • 18%
1	e	536	 57% 21% • • 18%
1	f	536	 57% 21% • • 18%
1	g	536	 58% 20% • • 18%
1	h	536	 57% 21% • • 18%

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Mol	Chain	Length	Quality of chain
1	i	536	<div><div><div></div><div></div><div></div></div><div><div></div><div></div><div></div></div><div>57%21%18%</div></div>
1	j	536	<div><div><div></div><div></div><div></div></div><div><div></div><div></div><div></div></div><div>58%20%18%</div></div>
1	k	536	<div><div><div></div><div></div><div></div></div><div><div></div><div></div><div></div></div><div>57%21%18%</div></div>
1	l	536	<div><div><div></div><div></div><div></div></div><div><div></div><div></div><div></div></div><div>57%21%18%</div></div>

## 2 Entry composition

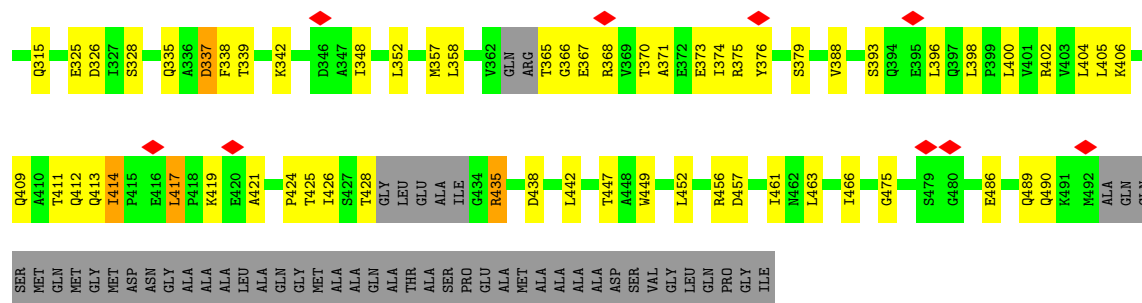
There is only 1 type of molecule in this entry. The entry contains 41388 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

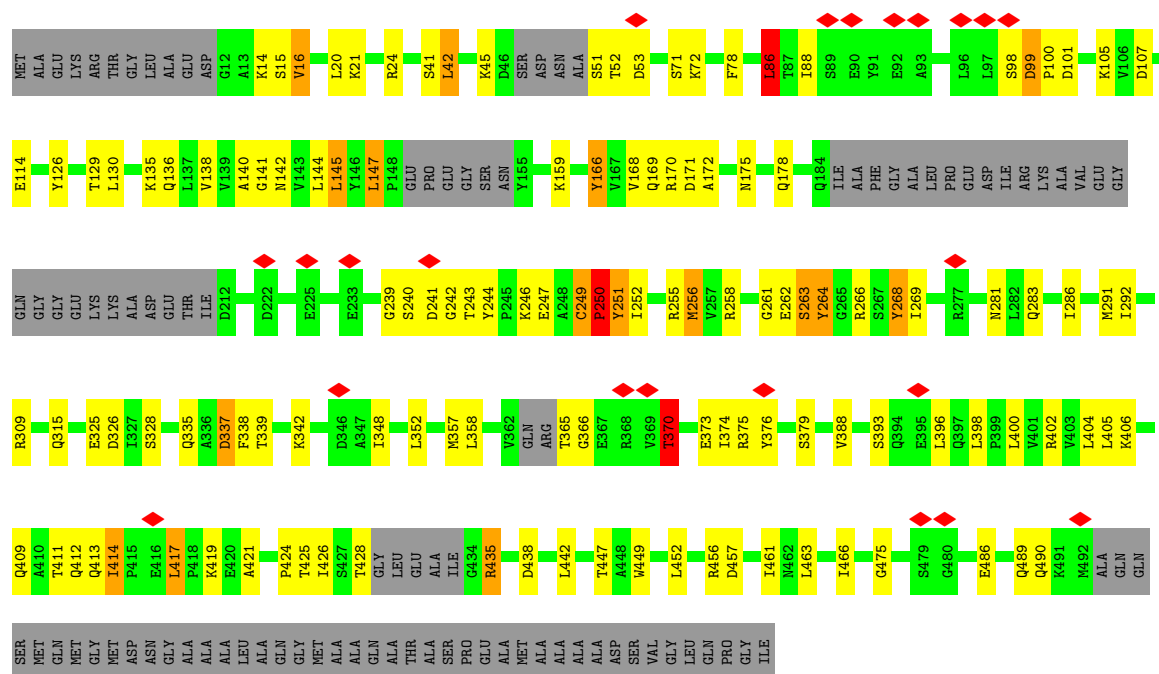
- Molecule 1 is a protein called Portal protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	a	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		
1	b	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		
1	c	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		
1	d	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		
1	e	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		
1	f	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		
1	g	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		
1	h	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		
1	i	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		
1	j	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		
1	k	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		
1	l	437	Total	C	N	O	S	0	0
			3449	2180	580	671	18		

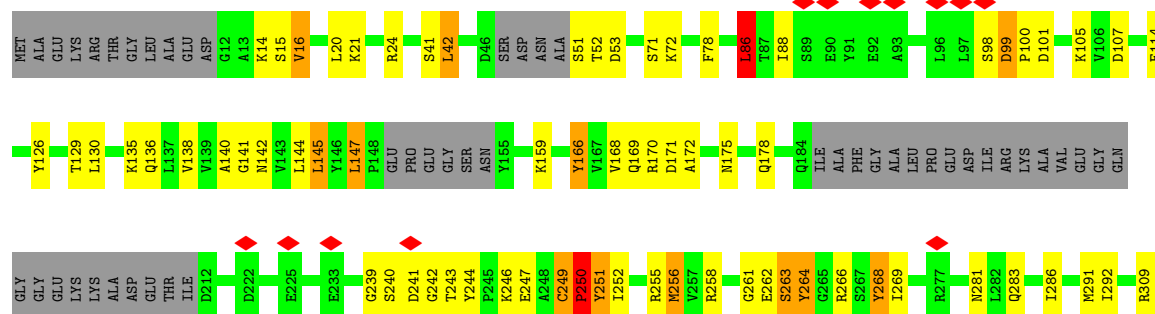




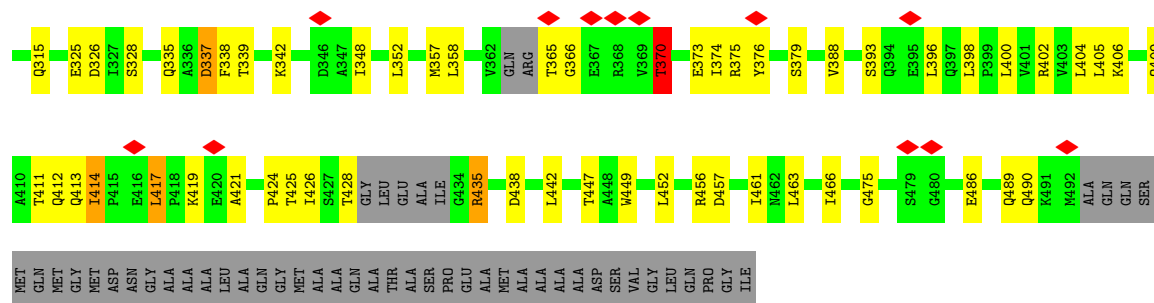
• Molecule 1: Portal protein



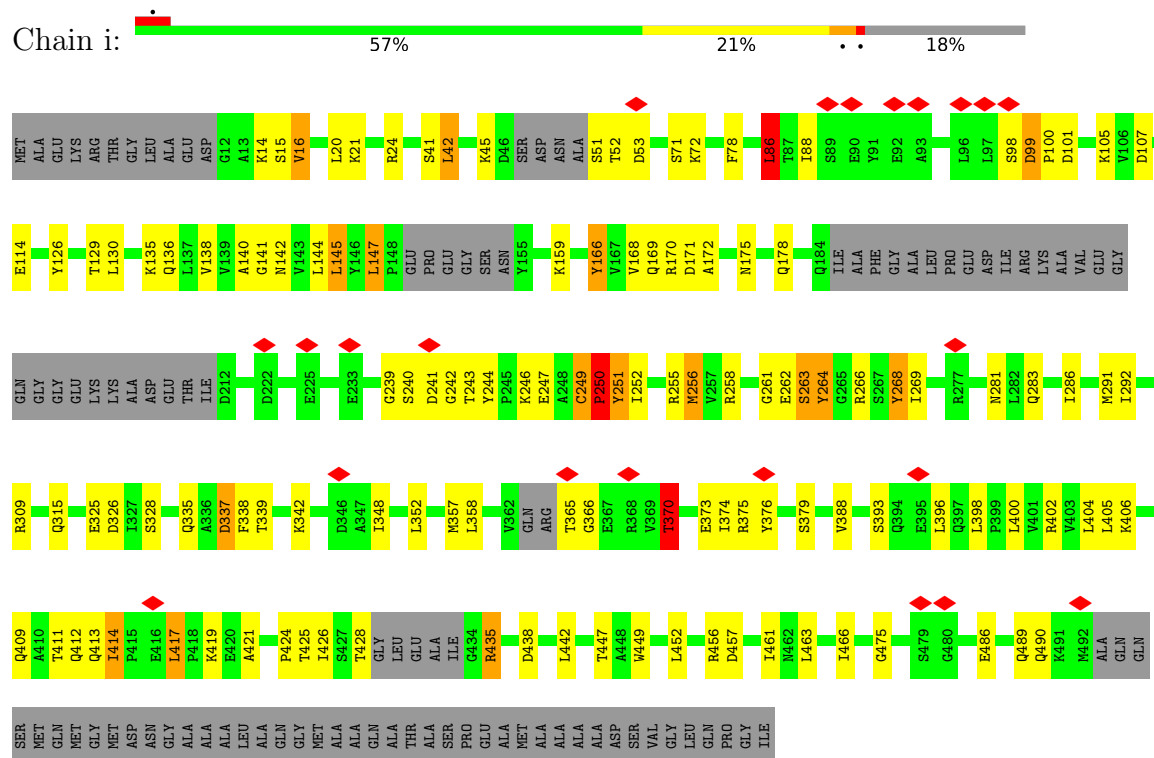




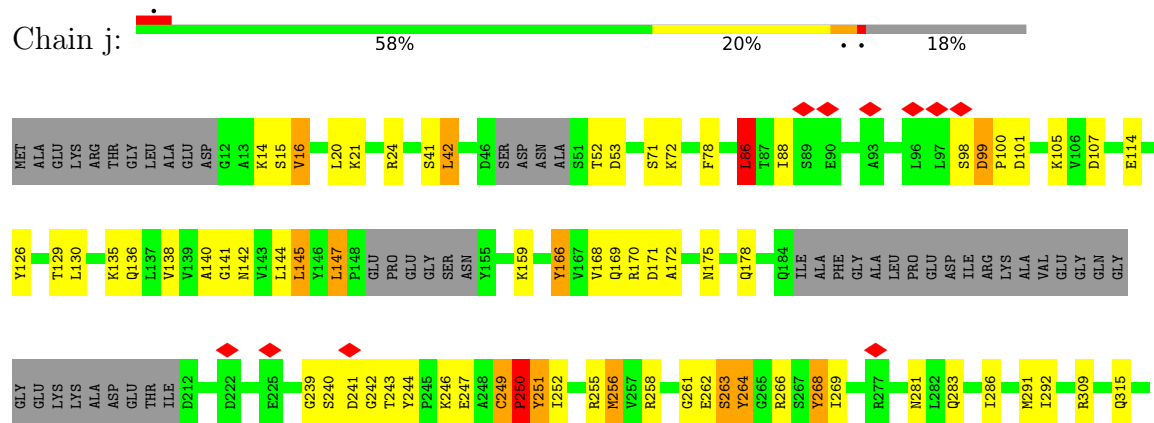




• Molecule 1: Portal protein



• Molecule 1: Portal protein







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	84318	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 ( $e^-/\text{\AA}^2$ )	27	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	34.251	Depositor
Minimum map value	-25.084	Depositor
Average map value	0.038	Depositor
Map value standard deviation	1.852	Depositor
Recommended contour level	7.0	Depositor
Map size ( $\text{\AA}$ )	406.4, 406.4, 406.4	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	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	0.67	2/3501 (0.1%)	1.12	24/4735 (0.5%)
1	b	0.66	1/3501 (0.0%)	1.12	23/4735 (0.5%)
1	c	0.66	1/3501 (0.0%)	1.12	23/4735 (0.5%)
1	d	0.66	1/3501 (0.0%)	1.12	23/4735 (0.5%)
1	e	0.66	1/3501 (0.0%)	1.12	23/4735 (0.5%)
1	f	0.66	1/3501 (0.0%)	1.12	23/4735 (0.5%)
1	g	0.66	1/3501 (0.0%)	1.12	23/4735 (0.5%)
1	h	0.66	1/3501 (0.0%)	1.12	23/4735 (0.5%)
1	i	0.66	1/3501 (0.0%)	1.12	23/4735 (0.5%)
1	j	0.66	1/3501 (0.0%)	1.12	23/4735 (0.5%)
1	k	0.66	1/3501 (0.0%)	1.12	23/4735 (0.5%)
1	l	0.66	1/3501 (0.0%)	1.12	22/4735 (0.5%)
All	All	0.66	13/42012 (0.0%)	1.12	276/56820 (0.5%)

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	17
1	b	0	18
1	c	0	17
1	d	0	17
1	e	0	17
1	f	0	17
1	g	0	17
1	h	0	17
1	i	0	17
1	j	0	17
1	k	0	18
1	l	0	18
All	All	0	207

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	a	57	PRO	N-CD	5.37	1.55	1.47
1	d	16	VAL	C-O	5.23	1.33	1.23
1	j	16	VAL	C-O	5.23	1.33	1.23
1	e	16	VAL	C-O	5.23	1.33	1.23
1	c	16	VAL	C-O	5.22	1.33	1.23
1	k	16	VAL	C-O	5.21	1.33	1.23
1	h	16	VAL	C-O	5.20	1.33	1.23
1	b	16	VAL	C-O	5.20	1.33	1.23
1	f	16	VAL	C-O	5.18	1.33	1.23
1	l	16	VAL	C-O	5.18	1.33	1.23
1	i	16	VAL	C-O	5.16	1.33	1.23
1	g	16	VAL	C-O	5.16	1.33	1.23
1	a	16	VAL	C-O	5.15	1.33	1.23

All (276) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	c	86	LEU	O-C-N	-11.89	103.67	122.70
1	j	86	LEU	O-C-N	-11.89	103.68	122.70
1	g	86	LEU	O-C-N	-11.87	103.71	122.70
1	d	86	LEU	O-C-N	-11.86	103.72	122.70
1	e	86	LEU	O-C-N	-11.86	103.73	122.70
1	i	86	LEU	O-C-N	-11.85	103.73	122.70
1	h	86	LEU	O-C-N	-11.85	103.75	122.70
1	a	86	LEU	O-C-N	-11.84	103.76	122.70
1	b	86	LEU	O-C-N	-11.84	103.76	122.70
1	f	86	LEU	O-C-N	-11.84	103.76	122.70
1	l	86	LEU	O-C-N	-11.84	103.75	122.70
1	k	86	LEU	O-C-N	-11.81	103.80	122.70
1	k	239	GLY	N-CA-C	-9.45	89.47	113.10
1	f	239	GLY	N-CA-C	-9.44	89.50	113.10
1	e	239	GLY	N-CA-C	-9.43	89.53	113.10
1	j	239	GLY	N-CA-C	-9.43	89.53	113.10
1	c	239	GLY	N-CA-C	-9.42	89.54	113.10
1	h	239	GLY	N-CA-C	-9.42	89.54	113.10
1	a	239	GLY	N-CA-C	-9.42	89.56	113.10
1	d	239	GLY	N-CA-C	-9.42	89.56	113.10
1	l	239	GLY	N-CA-C	-9.42	89.56	113.10
1	g	239	GLY	N-CA-C	-9.41	89.58	113.10
1	i	239	GLY	N-CA-C	-9.41	89.58	113.10
1	b	239	GLY	N-CA-C	-9.40	89.61	113.10
1	g	264	TYR	N-CA-C	-7.88	89.71	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	b	264	TYR	N-CA-C	-7.87	89.75	111.00
1	l	264	TYR	N-CA-C	-7.87	89.76	111.00
1	e	264	TYR	N-CA-C	-7.86	89.78	111.00
1	k	264	TYR	N-CA-C	-7.86	89.79	111.00
1	i	264	TYR	N-CA-C	-7.86	89.79	111.00
1	c	264	TYR	N-CA-C	-7.85	89.81	111.00
1	f	264	TYR	N-CA-C	-7.85	89.82	111.00
1	d	264	TYR	N-CA-C	-7.84	89.82	111.00
1	h	264	TYR	N-CA-C	-7.84	89.82	111.00
1	a	264	TYR	N-CA-C	-7.84	89.83	111.00
1	j	264	TYR	N-CA-C	-7.83	89.85	111.00
1	a	371	ALA	C-N-CA	-7.54	102.84	121.70
1	i	417	LEU	N-CA-C	-7.54	90.64	111.00
1	c	417	LEU	N-CA-C	-7.53	90.68	111.00
1	a	417	LEU	N-CA-C	-7.52	90.70	111.00
1	j	417	LEU	N-CA-C	-7.51	90.71	111.00
1	d	417	LEU	N-CA-C	-7.51	90.72	111.00
1	g	417	LEU	N-CA-C	-7.51	90.72	111.00
1	e	417	LEU	N-CA-C	-7.50	90.76	111.00
1	f	417	LEU	N-CA-C	-7.49	90.77	111.00
1	h	417	LEU	N-CA-C	-7.49	90.77	111.00
1	l	417	LEU	N-CA-C	-7.49	90.78	111.00
1	b	417	LEU	N-CA-C	-7.49	90.79	111.00
1	k	417	LEU	N-CA-C	-7.49	90.79	111.00
1	l	366	GLY	N-CA-C	6.87	130.27	113.10
1	g	16	VAL	N-CA-C	6.86	129.53	111.00
1	f	16	VAL	N-CA-C	6.86	129.51	111.00
1	c	16	VAL	N-CA-C	6.85	129.50	111.00
1	j	16	VAL	N-CA-C	6.85	129.50	111.00
1	b	16	VAL	N-CA-C	6.85	129.49	111.00
1	i	16	VAL	N-CA-C	6.85	129.49	111.00
1	k	16	VAL	N-CA-C	6.84	129.48	111.00
1	c	366	GLY	N-CA-C	6.84	130.20	113.10
1	h	16	VAL	N-CA-C	6.84	129.47	111.00
1	k	366	GLY	N-CA-C	6.84	130.20	113.10
1	d	366	GLY	N-CA-C	6.84	130.19	113.10
1	a	16	VAL	N-CA-C	6.83	129.46	111.00
1	l	16	VAL	N-CA-C	6.83	129.45	111.00
1	e	16	VAL	N-CA-C	6.83	129.45	111.00
1	i	366	GLY	N-CA-C	6.83	130.18	113.10
1	j	366	GLY	N-CA-C	6.83	130.17	113.10
1	g	366	GLY	N-CA-C	6.82	130.16	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	f	366	GLY	N-CA-C	6.82	130.16	113.10
1	d	16	VAL	N-CA-C	6.82	129.41	111.00
1	b	366	GLY	N-CA-C	6.81	130.13	113.10
1	h	366	GLY	N-CA-C	6.81	130.13	113.10
1	e	366	GLY	N-CA-C	6.80	130.11	113.10
1	a	366	GLY	N-CA-C	6.77	130.02	113.10
1	b	371	ALA	C-N-CA	-6.34	105.85	121.70
1	k	20	LEU	CA-CB-CG	-6.33	100.73	115.30
1	b	20	LEU	CA-CB-CG	-6.33	100.75	115.30
1	d	20	LEU	CA-CB-CG	-6.33	100.75	115.30
1	g	20	LEU	CA-CB-CG	-6.32	100.76	115.30
1	f	20	LEU	CA-CB-CG	-6.31	100.79	115.30
1	i	20	LEU	CA-CB-CG	-6.31	100.79	115.30
1	a	20	LEU	CA-CB-CG	-6.30	100.82	115.30
1	c	20	LEU	CA-CB-CG	-6.30	100.82	115.30
1	h	20	LEU	CA-CB-CG	-6.30	100.82	115.30
1	j	20	LEU	CA-CB-CG	-6.30	100.82	115.30
1	l	20	LEU	CA-CB-CG	-6.29	100.84	115.30
1	e	20	LEU	CA-CB-CG	-6.28	100.85	115.30
1	e	86	LEU	C-N-CA	6.21	137.22	121.70
1	c	86	LEU	C-N-CA	6.21	137.21	121.70
1	j	86	LEU	C-N-CA	6.20	137.21	121.70
1	a	86	LEU	C-N-CA	6.20	137.20	121.70
1	h	86	LEU	C-N-CA	6.20	137.19	121.70
1	d	86	LEU	C-N-CA	6.19	137.18	121.70
1	b	86	LEU	C-N-CA	6.19	137.16	121.70
1	i	86	LEU	C-N-CA	6.18	137.15	121.70
1	i	166	TYR	N-CA-C	6.17	127.67	111.00
1	l	86	LEU	C-N-CA	6.17	137.14	121.70
1	f	86	LEU	C-N-CA	6.17	137.12	121.70
1	g	86	LEU	C-N-CA	6.17	137.12	121.70
1	l	166	TYR	N-CA-C	6.17	127.65	111.00
1	k	86	LEU	C-N-CA	6.16	137.11	121.70
1	k	166	TYR	N-CA-C	6.16	127.64	111.00
1	h	166	TYR	N-CA-C	6.16	127.63	111.00
1	b	166	TYR	N-CA-C	6.16	127.62	111.00
1	e	166	TYR	N-CA-C	6.16	127.62	111.00
1	c	166	TYR	N-CA-C	6.15	127.62	111.00
1	j	166	TYR	N-CA-C	6.15	127.61	111.00
1	g	166	TYR	N-CA-C	6.14	127.59	111.00
1	f	166	TYR	N-CA-C	6.13	127.56	111.00
1	d	166	TYR	N-CA-C	6.13	127.55	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	a	166	TYR	N-CA-C	6.12	127.53	111.00
1	k	147	LEU	N-CA-C	6.10	127.47	111.00
1	f	147	LEU	N-CA-C	6.10	127.46	111.00
1	a	147	LEU	N-CA-C	6.09	127.44	111.00
1	l	147	LEU	N-CA-C	6.09	127.44	111.00
1	d	147	LEU	N-CA-C	6.09	127.43	111.00
1	c	147	LEU	N-CA-C	6.07	127.39	111.00
1	g	147	LEU	N-CA-C	6.07	127.39	111.00
1	e	147	LEU	N-CA-C	6.07	127.39	111.00
1	h	147	LEU	N-CA-C	6.07	127.39	111.00
1	b	147	LEU	N-CA-C	6.06	127.35	111.00
1	i	147	LEU	N-CA-C	6.05	127.33	111.00
1	j	147	LEU	N-CA-C	6.04	127.31	111.00
1	b	261	GLY	C-N-CA	5.97	136.63	121.70
1	e	261	GLY	C-N-CA	5.97	136.62	121.70
1	c	261	GLY	C-N-CA	5.96	136.61	121.70
1	f	261	GLY	C-N-CA	5.96	136.60	121.70
1	h	261	GLY	C-N-CA	5.95	136.57	121.70
1	j	261	GLY	C-N-CA	5.95	136.56	121.70
1	g	261	GLY	C-N-CA	5.94	136.56	121.70
1	k	261	GLY	C-N-CA	5.94	136.55	121.70
1	l	261	GLY	C-N-CA	5.94	136.54	121.70
1	i	261	GLY	C-N-CA	5.93	136.54	121.70
1	d	261	GLY	C-N-CA	5.92	136.50	121.70
1	a	261	GLY	C-N-CA	5.91	136.48	121.70
1	g	15	SER	C-N-CA	5.87	136.36	121.70
1	k	15	SER	C-N-CA	5.86	136.36	121.70
1	f	15	SER	C-N-CA	5.85	136.33	121.70
1	h	15	SER	C-N-CA	5.85	136.32	121.70
1	a	15	SER	C-N-CA	5.84	136.31	121.70
1	b	15	SER	C-N-CA	5.84	136.31	121.70
1	e	15	SER	C-N-CA	5.84	136.31	121.70
1	c	15	SER	C-N-CA	5.83	136.27	121.70
1	l	15	SER	C-N-CA	5.83	136.27	121.70
1	j	15	SER	C-N-CA	5.82	136.25	121.70
1	d	15	SER	C-N-CA	5.82	136.24	121.70
1	i	15	SER	C-N-CA	5.82	136.24	121.70
1	i	242	GLY	N-CA-C	-5.75	98.72	113.10
1	k	242	GLY	N-CA-C	-5.75	98.72	113.10
1	h	242	GLY	N-CA-C	-5.75	98.73	113.10
1	a	242	GLY	N-CA-C	-5.74	98.75	113.10
1	g	242	GLY	N-CA-C	-5.74	98.76	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	l	242	GLY	N-CA-C	-5.73	98.78	113.10
1	e	242	GLY	N-CA-C	-5.72	98.79	113.10
1	b	242	GLY	N-CA-C	-5.72	98.80	113.10
1	f	242	GLY	N-CA-C	-5.72	98.81	113.10
1	j	242	GLY	N-CA-C	-5.72	98.81	113.10
1	c	242	GLY	N-CA-C	-5.71	98.81	113.10
1	d	242	GLY	N-CA-C	-5.71	98.81	113.10
1	j	145	LEU	N-CA-C	5.67	126.31	111.00
1	e	145	LEU	N-CA-C	5.67	126.30	111.00
1	c	145	LEU	N-CA-C	5.66	126.28	111.00
1	h	145	LEU	N-CA-C	5.66	126.27	111.00
1	f	263	SER	CB-CA-C	-5.65	99.36	110.10
1	d	145	LEU	N-CA-C	5.65	126.26	111.00
1	d	263	SER	CB-CA-C	-5.65	99.37	110.10
1	d	463	LEU	CA-CB-CG	-5.65	102.31	115.30
1	c	263	SER	CB-CA-C	-5.64	99.38	110.10
1	f	145	LEU	N-CA-C	5.64	126.24	111.00
1	k	145	LEU	N-CA-C	5.64	126.23	111.00
1	l	145	LEU	N-CA-C	5.64	126.22	111.00
1	b	145	LEU	N-CA-C	5.64	126.22	111.00
1	j	365	THR	CA-C-N	5.63	127.46	116.20
1	a	145	LEU	N-CA-C	5.63	126.20	111.00
1	g	145	LEU	N-CA-C	5.63	126.20	111.00
1	i	145	LEU	N-CA-C	5.63	126.20	111.00
1	k	263	SER	CB-CA-C	-5.62	99.42	110.10
1	e	365	THR	CA-C-N	5.61	127.42	116.20
1	b	463	LEU	CA-CB-CG	-5.61	102.39	115.30
1	h	463	LEU	CA-CB-CG	-5.61	102.39	115.30
1	b	263	SER	CB-CA-C	-5.61	99.44	110.10
1	h	263	SER	CB-CA-C	-5.61	99.44	110.10
1	j	263	SER	CB-CA-C	-5.61	99.44	110.10
1	a	263	SER	CB-CA-C	-5.61	99.45	110.10
1	e	263	SER	CB-CA-C	-5.61	99.45	110.10
1	i	365	THR	CA-C-N	5.61	127.41	116.20
1	c	463	LEU	CA-CB-CG	-5.60	102.41	115.30
1	i	263	SER	CB-CA-C	-5.60	99.46	110.10
1	i	463	LEU	CA-CB-CG	-5.60	102.43	115.30
1	l	365	THR	CA-C-N	5.60	127.40	116.20
1	g	463	LEU	CA-CB-CG	-5.59	102.43	115.30
1	l	263	SER	CB-CA-C	-5.59	99.47	110.10
1	i	15	SER	CA-C-N	-5.59	104.90	117.20
1	l	463	LEU	CA-CB-CG	-5.59	102.44	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	b	365	THR	CA-C-N	5.59	127.38	116.20
1	c	365	THR	CA-C-N	5.59	127.38	116.20
1	f	463	LEU	CA-CB-CG	-5.59	102.45	115.30
1	a	463	LEU	CA-CB-CG	-5.58	102.45	115.30
1	d	15	SER	CA-C-N	-5.58	104.91	117.20
1	l	15	SER	CA-C-N	-5.58	104.91	117.20
1	k	463	LEU	CA-CB-CG	-5.58	102.47	115.30
1	f	365	THR	CA-C-N	5.58	127.36	116.20
1	a	365	THR	CA-C-N	5.58	127.35	116.20
1	j	463	LEU	CA-CB-CG	-5.58	102.47	115.30
1	f	15	SER	CA-C-N	-5.57	104.94	117.20
1	g	263	SER	CB-CA-C	-5.57	99.51	110.10
1	e	15	SER	CA-C-N	-5.57	104.95	117.20
1	k	370	THR	N-CA-C	-5.57	95.97	111.00
1	g	365	THR	CA-C-N	5.57	127.33	116.20
1	h	365	THR	CA-C-N	5.56	127.33	116.20
1	j	15	SER	CA-C-N	-5.56	104.96	117.20
1	k	365	THR	CA-C-N	5.56	127.32	116.20
1	k	15	SER	CA-C-N	-5.55	104.98	117.20
1	e	463	LEU	CA-CB-CG	-5.55	102.53	115.30
1	b	15	SER	CA-C-N	-5.55	104.99	117.20
1	g	15	SER	CA-C-N	-5.55	104.98	117.20
1	h	15	SER	CA-C-N	-5.55	104.99	117.20
1	c	15	SER	CA-C-N	-5.54	105.01	117.20
1	a	15	SER	CA-C-N	-5.52	105.05	117.20
1	d	365	THR	CA-C-N	5.50	127.20	116.20
1	a	56	THR	C-N-CD	5.48	139.91	128.40
1	i	256	MET	N-CA-C	5.48	125.80	111.00
1	k	256	MET	N-CA-C	5.48	125.79	111.00
1	h	370	THR	N-CA-C	-5.48	96.22	111.00
1	a	256	MET	N-CA-C	5.47	125.78	111.00
1	g	256	MET	N-CA-C	5.47	125.78	111.00
1	d	256	MET	N-CA-C	5.46	125.75	111.00
1	j	256	MET	N-CA-C	5.46	125.76	111.00
1	h	256	MET	N-CA-C	5.46	125.75	111.00
1	d	99	ASP	C-N-CD	5.46	139.86	128.40
1	e	256	MET	N-CA-C	5.46	125.73	111.00
1	k	255	ARG	N-CA-C	5.46	125.73	111.00
1	c	256	MET	N-CA-C	5.45	125.72	111.00
1	b	256	MET	N-CA-C	5.45	125.71	111.00
1	i	370	THR	N-CA-C	-5.45	96.29	111.00
1	l	256	MET	N-CA-C	5.45	125.70	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	i	255	ARG	N-CA-C	5.43	125.66	111.00
1	f	256	MET	N-CA-C	5.43	125.66	111.00
1	i	99	ASP	C-N-CD	5.43	139.80	128.40
1	l	370	THR	N-CA-C	-5.43	96.34	111.00
1	c	370	THR	N-CA-C	-5.43	96.35	111.00
1	d	255	ARG	N-CA-C	5.43	125.65	111.00
1	g	255	ARG	N-CA-C	5.43	125.65	111.00
1	j	255	ARG	N-CA-C	5.42	125.65	111.00
1	e	370	THR	N-CA-C	-5.42	96.36	111.00
1	b	255	ARG	N-CA-C	5.42	125.64	111.00
1	f	255	ARG	N-CA-C	5.42	125.64	111.00
1	e	255	ARG	N-CA-C	5.42	125.63	111.00
1	l	255	ARG	N-CA-C	5.41	125.61	111.00
1	j	99	ASP	C-N-CD	5.41	139.76	128.40
1	l	99	ASP	C-N-CD	5.41	139.76	128.40
1	f	99	ASP	C-N-CD	5.41	139.75	128.40
1	h	255	ARG	N-CA-C	5.40	125.59	111.00
1	k	99	ASP	C-N-CD	5.40	139.74	128.40
1	a	99	ASP	C-N-CD	5.39	139.73	128.40
1	h	99	ASP	C-N-CD	5.39	139.72	128.40
1	b	99	ASP	C-N-CD	5.38	139.71	128.40
1	a	255	ARG	N-CA-C	5.38	125.53	111.00
1	e	99	ASP	C-N-CD	5.38	139.70	128.40
1	g	99	ASP	C-N-CD	5.37	139.67	128.40
1	c	99	ASP	C-N-CD	5.36	139.66	128.40
1	f	370	THR	N-CA-C	-5.36	96.52	111.00
1	c	255	ARG	N-CA-C	5.36	125.47	111.00
1	j	370	THR	N-CA-C	-5.27	96.77	111.00
1	f	337	ASP	CB-CG-OD1	5.22	123.00	118.30
1	g	370	THR	N-CA-C	-5.14	97.11	111.00
1	d	370	THR	N-CA-C	-5.11	97.20	111.00
1	e	337	ASP	CB-CG-OD1	5.11	122.90	118.30
1	i	337	ASP	CB-CG-OD1	5.09	122.88	118.30
1	g	337	ASP	CB-CG-OD1	5.07	122.86	118.30
1	a	337	ASP	CB-CG-OD1	5.07	122.86	118.30
1	d	337	ASP	CB-CG-OD1	5.05	122.85	118.30
1	j	337	ASP	CB-CG-OD1	5.05	122.84	118.30
1	h	337	ASP	CB-CG-OD1	5.03	122.83	118.30
1	b	337	ASP	CB-CG-OD1	5.03	122.83	118.30
1	c	337	ASP	CB-CG-OD1	5.02	122.82	118.30
1	k	337	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

All (207) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	a	138	VAL	Mainchain
1	a	14	LYS	Peptide
1	a	140	ALA	Peptide
1	a	141	GLY	Peptide
1	a	159	LYS	Peptide
1	a	169	GLN	Peptide
1	a	171	ASP	Peptide
1	a	249	CYS	Peptide
1	a	250	PRO	Peptide
1	a	41	SER	Peptide
1	a	414	ILE	Peptide
1	a	421	ALA	Peptide
1	a	425	THR	Peptide
1	a	435	ARG	Peptide
1	a	86	LEU	Mainchain
1	a	88	ILE	Peptide
1	a	98	SER	Peptide
1	b	138	VAL	Mainchain
1	b	14	LYS	Peptide
1	b	140	ALA	Peptide
1	b	141	GLY	Peptide
1	b	159	LYS	Peptide
1	b	169	GLN	Peptide
1	b	171	ASP	Peptide
1	b	249	CYS	Peptide
1	b	250	PRO	Peptide
1	b	367	GLU	Mainchain
1	b	41	SER	Peptide
1	b	414	ILE	Peptide
1	b	421	ALA	Peptide
1	b	425	THR	Peptide
1	b	435	ARG	Peptide
1	b	86	LEU	Mainchain
1	b	88	ILE	Peptide
1	b	98	SER	Peptide
1	c	138	VAL	Mainchain
1	c	14	LYS	Peptide
1	c	140	ALA	Peptide
1	c	141	GLY	Peptide
1	c	159	LYS	Peptide
1	c	169	GLN	Peptide
1	c	171	ASP	Peptide

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Mol	Chain	Res	Type	Group
1	c	249	CYS	Peptide
1	c	250	PRO	Peptide
1	c	41	SER	Peptide
1	c	414	ILE	Peptide
1	c	421	ALA	Peptide
1	c	425	THR	Peptide
1	c	435	ARG	Peptide
1	c	86	LEU	Mainchain
1	c	88	ILE	Peptide
1	c	98	SER	Peptide
1	d	138	VAL	Mainchain
1	d	14	LYS	Peptide
1	d	140	ALA	Peptide
1	d	141	GLY	Peptide
1	d	159	LYS	Peptide
1	d	169	GLN	Peptide
1	d	171	ASP	Peptide
1	d	249	CYS	Peptide
1	d	250	PRO	Peptide
1	d	41	SER	Peptide
1	d	414	ILE	Peptide
1	d	421	ALA	Peptide
1	d	425	THR	Peptide
1	d	435	ARG	Peptide
1	d	86	LEU	Mainchain
1	d	88	ILE	Peptide
1	d	98	SER	Peptide
1	e	138	VAL	Mainchain
1	e	14	LYS	Peptide
1	e	140	ALA	Peptide
1	e	141	GLY	Peptide
1	e	159	LYS	Peptide
1	e	169	GLN	Peptide
1	e	171	ASP	Peptide
1	e	249	CYS	Peptide
1	e	250	PRO	Peptide
1	e	41	SER	Peptide
1	e	414	ILE	Peptide
1	e	421	ALA	Peptide
1	e	425	THR	Peptide
1	e	435	ARG	Peptide
1	e	86	LEU	Mainchain

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Mol	Chain	Res	Type	Group
1	e	88	ILE	Peptide
1	e	98	SER	Peptide
1	f	138	VAL	Mainchain
1	f	14	LYS	Peptide
1	f	140	ALA	Peptide
1	f	141	GLY	Peptide
1	f	159	LYS	Peptide
1	f	169	GLN	Peptide
1	f	171	ASP	Peptide
1	f	249	CYS	Peptide
1	f	250	PRO	Peptide
1	f	41	SER	Peptide
1	f	414	ILE	Peptide
1	f	421	ALA	Peptide
1	f	425	THR	Peptide
1	f	435	ARG	Peptide
1	f	86	LEU	Mainchain
1	f	88	ILE	Peptide
1	f	98	SER	Peptide
1	g	138	VAL	Mainchain
1	g	14	LYS	Peptide
1	g	140	ALA	Peptide
1	g	141	GLY	Peptide
1	g	159	LYS	Peptide
1	g	169	GLN	Peptide
1	g	171	ASP	Peptide
1	g	249	CYS	Peptide
1	g	250	PRO	Peptide
1	g	41	SER	Peptide
1	g	414	ILE	Peptide
1	g	421	ALA	Peptide
1	g	425	THR	Peptide
1	g	435	ARG	Peptide
1	g	86	LEU	Mainchain
1	g	88	ILE	Peptide
1	g	98	SER	Peptide
1	h	138	VAL	Mainchain
1	h	14	LYS	Peptide
1	h	140	ALA	Peptide
1	h	141	GLY	Peptide
1	h	159	LYS	Peptide
1	h	169	GLN	Peptide

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Mol	Chain	Res	Type	Group
1	h	171	ASP	Peptide
1	h	249	CYS	Peptide
1	h	250	PRO	Peptide
1	h	41	SER	Peptide
1	h	414	ILE	Peptide
1	h	421	ALA	Peptide
1	h	425	THR	Peptide
1	h	435	ARG	Peptide
1	h	86	LEU	Mainchain
1	h	88	ILE	Peptide
1	h	98	SER	Peptide
1	i	138	VAL	Mainchain
1	i	14	LYS	Peptide
1	i	140	ALA	Peptide
1	i	141	GLY	Peptide
1	i	159	LYS	Peptide
1	i	169	GLN	Peptide
1	i	171	ASP	Peptide
1	i	249	CYS	Peptide
1	i	250	PRO	Peptide
1	i	41	SER	Peptide
1	i	414	ILE	Peptide
1	i	421	ALA	Peptide
1	i	425	THR	Peptide
1	i	435	ARG	Peptide
1	i	86	LEU	Mainchain
1	i	88	ILE	Peptide
1	i	98	SER	Peptide
1	j	138	VAL	Mainchain
1	j	14	LYS	Peptide
1	j	140	ALA	Peptide
1	j	141	GLY	Peptide
1	j	159	LYS	Peptide
1	j	169	GLN	Peptide
1	j	171	ASP	Peptide
1	j	249	CYS	Peptide
1	j	250	PRO	Peptide
1	j	41	SER	Peptide
1	j	414	ILE	Peptide
1	j	421	ALA	Peptide
1	j	425	THR	Peptide
1	j	435	ARG	Peptide

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Mol	Chain	Res	Type	Group
1	j	86	LEU	Mainchain
1	j	88	ILE	Peptide
1	j	98	SER	Peptide
1	k	138	VAL	Mainchain
1	k	14	LYS	Peptide
1	k	140	ALA	Peptide
1	k	141	GLY	Peptide
1	k	15	SER	Mainchain
1	k	159	LYS	Peptide
1	k	169	GLN	Peptide
1	k	171	ASP	Peptide
1	k	249	CYS	Peptide
1	k	250	PRO	Peptide
1	k	41	SER	Peptide
1	k	414	ILE	Peptide
1	k	421	ALA	Peptide
1	k	425	THR	Peptide
1	k	435	ARG	Peptide
1	k	86	LEU	Mainchain
1	k	88	ILE	Peptide
1	k	98	SER	Peptide
1	l	138	VAL	Mainchain
1	l	14	LYS	Peptide
1	l	140	ALA	Peptide
1	l	141	GLY	Peptide
1	l	159	LYS	Peptide
1	l	169	GLN	Peptide
1	l	171	ASP	Peptide
1	l	249	CYS	Peptide
1	l	250	PRO	Peptide
1	l	369	VAL	Peptide
1	l	41	SER	Peptide
1	l	414	ILE	Peptide
1	l	421	ALA	Peptide
1	l	425	THR	Peptide
1	l	435	ARG	Peptide
1	l	86	LEU	Mainchain
1	l	88	ILE	Peptide
1	l	98	SER	Peptide

## 5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	a	3449	0	3451	0	0
1	b	3449	0	3452	0	0
1	c	3449	0	3452	0	0
1	d	3449	0	3452	0	0
1	e	3449	0	3452	0	0
1	f	3449	0	3452	0	0
1	g	3449	0	3452	0	0
1	h	3449	0	3452	0	0
1	i	3449	0	3452	0	0
1	j	3449	0	3452	0	0
1	k	3449	0	3452	0	0
1	l	3449	0	3452	0	0
All	All	41388	0	41423	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 149.

There are no clashes within the asymmetric unit.

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	a	425/536 (79%)	358 (84%)	44 (10%)	23 (5%)	2	21
1	b	425/536 (79%)	360 (85%)	43 (10%)	22 (5%)	2	22
1	c	425/536 (79%)	361 (85%)	42 (10%)	22 (5%)	2	22

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	d	425/536 (79%)	360 (85%)	44 (10%)	21 (5%)	2	23
1	e	425/536 (79%)	361 (85%)	42 (10%)	22 (5%)	2	22
1	f	425/536 (79%)	362 (85%)	41 (10%)	22 (5%)	2	22
1	g	425/536 (79%)	360 (85%)	44 (10%)	21 (5%)	2	23
1	h	425/536 (79%)	360 (85%)	43 (10%)	22 (5%)	2	22
1	i	425/536 (79%)	361 (85%)	42 (10%)	22 (5%)	2	22
1	j	425/536 (79%)	360 (85%)	44 (10%)	21 (5%)	2	23
1	k	425/536 (79%)	360 (85%)	43 (10%)	22 (5%)	2	22
1	l	425/536 (79%)	362 (85%)	42 (10%)	21 (5%)	2	23
All	All	5100/6432 (79%)	4325 (85%)	514 (10%)	261 (5%)	4	22

All (261) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	a	42	LEU
1	a	58	TRP
1	a	250	PRO
1	a	251	TYR
1	a	262	GLU
1	a	269	ILE
1	a	357	MET
1	a	370	THR
1	a	413	GLN
1	a	426	ILE
1	a	475	GLY
1	b	42	LEU
1	b	250	PRO
1	b	251	TYR
1	b	262	GLU
1	b	269	ILE
1	b	413	GLN
1	b	426	ILE
1	b	475	GLY
1	c	42	LEU
1	c	250	PRO
1	c	251	TYR
1	c	262	GLU
1	c	269	ILE
1	c	357	MET

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Mol	Chain	Res	Type
1	c	370	THR
1	c	413	GLN
1	c	426	ILE
1	c	475	GLY
1	d	42	LEU
1	d	250	PRO
1	d	251	TYR
1	d	262	GLU
1	d	269	ILE
1	d	370	THR
1	d	413	GLN
1	d	426	ILE
1	d	475	GLY
1	e	42	LEU
1	e	250	PRO
1	e	251	TYR
1	e	262	GLU
1	e	269	ILE
1	e	370	THR
1	e	413	GLN
1	e	426	ILE
1	e	475	GLY
1	f	42	LEU
1	f	250	PRO
1	f	251	TYR
1	f	262	GLU
1	f	269	ILE
1	f	357	MET
1	f	370	THR
1	f	413	GLN
1	f	426	ILE
1	f	475	GLY
1	g	42	LEU
1	g	250	PRO
1	g	251	TYR
1	g	262	GLU
1	g	269	ILE
1	g	370	THR
1	g	413	GLN
1	g	426	ILE
1	g	475	GLY
1	h	42	LEU

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Mol	Chain	Res	Type
1	h	250	PRO
1	h	251	TYR
1	h	262	GLU
1	h	269	ILE
1	h	370	THR
1	h	413	GLN
1	h	426	ILE
1	h	475	GLY
1	i	42	LEU
1	i	250	PRO
1	i	251	TYR
1	i	262	GLU
1	i	269	ILE
1	i	357	MET
1	i	370	THR
1	i	413	GLN
1	i	426	ILE
1	i	475	GLY
1	j	42	LEU
1	j	250	PRO
1	j	251	TYR
1	j	262	GLU
1	j	269	ILE
1	j	370	THR
1	j	413	GLN
1	j	426	ILE
1	j	475	GLY
1	k	42	LEU
1	k	250	PRO
1	k	251	TYR
1	k	262	GLU
1	k	269	ILE
1	k	370	THR
1	k	413	GLN
1	k	426	ILE
1	k	475	GLY
1	l	42	LEU
1	l	250	PRO
1	l	251	TYR
1	l	262	GLU
1	l	269	ILE
1	l	370	THR

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Mol	Chain	Res	Type
1	l	413	GLN
1	l	426	ILE
1	l	475	GLY
1	a	172	ALA
1	a	178	GLN
1	a	449	TRP
1	b	172	ALA
1	b	178	GLN
1	b	449	TRP
1	c	172	ALA
1	c	178	GLN
1	c	449	TRP
1	d	172	ALA
1	d	178	GLN
1	d	449	TRP
1	e	172	ALA
1	e	178	GLN
1	e	449	TRP
1	f	172	ALA
1	f	178	GLN
1	f	449	TRP
1	g	172	ALA
1	g	178	GLN
1	g	449	TRP
1	h	172	ALA
1	h	178	GLN
1	h	449	TRP
1	i	172	ALA
1	i	178	GLN
1	i	449	TRP
1	j	172	ALA
1	j	178	GLN
1	j	449	TRP
1	k	172	ALA
1	k	178	GLN
1	k	449	TRP
1	l	172	ALA
1	l	178	GLN
1	l	449	TRP
1	a	145	LEU
1	a	244	TYR
1	a	490	GLN

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Mol	Chain	Res	Type
1	b	145	LEU
1	b	244	TYR
1	b	370	THR
1	b	490	GLN
1	c	145	LEU
1	c	244	TYR
1	c	490	GLN
1	d	145	LEU
1	d	244	TYR
1	d	490	GLN
1	e	145	LEU
1	e	244	TYR
1	e	490	GLN
1	f	145	LEU
1	f	244	TYR
1	f	490	GLN
1	g	145	LEU
1	g	244	TYR
1	g	490	GLN
1	h	145	LEU
1	h	244	TYR
1	h	490	GLN
1	i	145	LEU
1	i	244	TYR
1	i	490	GLN
1	j	145	LEU
1	j	244	TYR
1	j	490	GLN
1	k	145	LEU
1	k	244	TYR
1	k	490	GLN
1	l	145	LEU
1	l	244	TYR
1	l	490	GLN
1	a	249	CYS
1	a	263	SER
1	a	268	TYR
1	b	249	CYS
1	b	263	SER
1	b	268	TYR
1	b	357	MET
1	c	249	CYS

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Mol	Chain	Res	Type
1	c	263	SER
1	c	268	TYR
1	d	249	CYS
1	d	263	SER
1	d	268	TYR
1	e	249	CYS
1	e	263	SER
1	e	268	TYR
1	e	357	MET
1	f	249	CYS
1	f	263	SER
1	f	268	TYR
1	g	249	CYS
1	g	263	SER
1	g	268	TYR
1	h	249	CYS
1	h	263	SER
1	h	268	TYR
1	h	357	MET
1	i	249	CYS
1	i	263	SER
1	i	268	TYR
1	j	249	CYS
1	j	263	SER
1	j	268	TYR
1	k	249	CYS
1	k	263	SER
1	k	268	TYR
1	k	357	MET
1	l	249	CYS
1	l	263	SER
1	l	268	TYR
1	a	424	PRO
1	b	424	PRO
1	c	424	PRO
1	d	424	PRO
1	e	424	PRO
1	f	424	PRO
1	g	424	PRO
1	h	424	PRO
1	i	424	PRO
1	j	424	PRO

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Mol	Chain	Res	Type
1	k	424	PRO
1	l	424	PRO
1	a	414	ILE
1	b	414	ILE
1	c	414	ILE
1	d	414	ILE
1	e	414	ILE
1	f	414	ILE
1	g	414	ILE
1	h	414	ILE
1	i	414	ILE
1	j	414	ILE
1	k	414	ILE
1	l	414	ILE
1	a	100	PRO
1	b	100	PRO
1	c	100	PRO
1	d	100	PRO
1	e	100	PRO
1	f	100	PRO
1	g	100	PRO
1	h	100	PRO
1	i	100	PRO
1	j	100	PRO
1	k	100	PRO
1	l	100	PRO

### 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	377/442 (85%)	285 (76%)	92 (24%)	0	4
1	b	377/442 (85%)	286 (76%)	91 (24%)	0	5
1	c	377/442 (85%)	285 (76%)	92 (24%)	0	4
1	d	377/442 (85%)	285 (76%)	92 (24%)	0	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	e	377/442 (85%)	285 (76%)	92 (24%)	0	4
1	f	377/442 (85%)	286 (76%)	91 (24%)	0	5
1	g	377/442 (85%)	286 (76%)	91 (24%)	0	5
1	h	377/442 (85%)	286 (76%)	91 (24%)	0	5
1	i	377/442 (85%)	285 (76%)	92 (24%)	0	4
1	j	377/442 (85%)	287 (76%)	90 (24%)	0	5
1	k	377/442 (85%)	285 (76%)	92 (24%)	0	4
1	l	377/442 (85%)	286 (76%)	91 (24%)	0	5
All	All	4524/5304 (85%)	3427 (76%)	1097 (24%)	2	5

All (1097) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	a	16	VAL
1	a	21	LYS
1	a	24	ARG
1	a	42	LEU
1	a	45	LYS
1	a	51	SER
1	a	52	THR
1	a	53	ASP
1	a	55	GLN
1	a	71	SER
1	a	72	LYS
1	a	78	PHE
1	a	86	LEU
1	a	99	ASP
1	a	101	ASP
1	a	105	LYS
1	a	107	ASP
1	a	114	GLU
1	a	126	TYR
1	a	129	THR
1	a	130	LEU
1	a	135	LYS
1	a	136	GLN
1	a	142	ASN
1	a	144	LEU
1	a	147	LEU

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Mol	Chain	Res	Type
1	a	166	TYR
1	a	168	VAL
1	a	170	ARG
1	a	175	ASN
1	a	240	SER
1	a	241	ASP
1	a	243	THR
1	a	246	LYS
1	a	247	GLU
1	a	250	PRO
1	a	251	TYR
1	a	252	ILE
1	a	256	MET
1	a	258	ARG
1	a	264	TYR
1	a	266	ARG
1	a	268	TYR
1	a	281	ASN
1	a	283	GLN
1	a	286	ILE
1	a	291	MET
1	a	292	ILE
1	a	309	ARG
1	a	315	GLN
1	a	325	GLU
1	a	326	ASP
1	a	328	SER
1	a	335	GLN
1	a	337	ASP
1	a	338	PHE
1	a	339	THR
1	a	342	LYS
1	a	348	ILE
1	a	352	LEU
1	a	358	LEU
1	a	373	GLU
1	a	374	ILE
1	a	375	ARG
1	a	376	TYR
1	a	379	SER
1	a	388	VAL
1	a	393	SER

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Mol	Chain	Res	Type
1	a	396	LEU
1	a	398	LEU
1	a	400	LEU
1	a	402	ARG
1	a	404	LEU
1	a	405	LEU
1	a	406	LYS
1	a	409	GLN
1	a	411	THR
1	a	412	GLN
1	a	417	LEU
1	a	419	LYS
1	a	428	THR
1	a	435	ARG
1	a	438	ASP
1	a	442	LEU
1	a	447	THR
1	a	452	LEU
1	a	456	ARG
1	a	457	ASP
1	a	461	ILE
1	a	466	ILE
1	a	486	GLU
1	a	489	GLN
1	b	16	VAL
1	b	21	LYS
1	b	24	ARG
1	b	42	LEU
1	b	51	SER
1	b	52	THR
1	b	53	ASP
1	b	71	SER
1	b	72	LYS
1	b	78	PHE
1	b	86	LEU
1	b	99	ASP
1	b	101	ASP
1	b	105	LYS
1	b	107	ASP
1	b	114	GLU
1	b	126	TYR
1	b	129	THR

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Mol	Chain	Res	Type
1	b	130	LEU
1	b	135	LYS
1	b	136	GLN
1	b	142	ASN
1	b	144	LEU
1	b	147	LEU
1	b	166	TYR
1	b	168	VAL
1	b	170	ARG
1	b	175	ASN
1	b	240	SER
1	b	241	ASP
1	b	243	THR
1	b	246	LYS
1	b	247	GLU
1	b	250	PRO
1	b	251	TYR
1	b	252	ILE
1	b	256	MET
1	b	258	ARG
1	b	264	TYR
1	b	266	ARG
1	b	268	TYR
1	b	281	ASN
1	b	283	GLN
1	b	286	ILE
1	b	291	MET
1	b	292	ILE
1	b	309	ARG
1	b	315	GLN
1	b	325	GLU
1	b	326	ASP
1	b	328	SER
1	b	335	GLN
1	b	337	ASP
1	b	338	PHE
1	b	339	THR
1	b	342	LYS
1	b	348	ILE
1	b	352	LEU
1	b	358	LEU
1	b	368	ARG

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Mol	Chain	Res	Type
1	b	373	GLU
1	b	374	ILE
1	b	375	ARG
1	b	376	TYR
1	b	379	SER
1	b	388	VAL
1	b	393	SER
1	b	396	LEU
1	b	398	LEU
1	b	400	LEU
1	b	402	ARG
1	b	404	LEU
1	b	405	LEU
1	b	406	LYS
1	b	409	GLN
1	b	411	THR
1	b	412	GLN
1	b	417	LEU
1	b	419	LYS
1	b	428	THR
1	b	435	ARG
1	b	438	ASP
1	b	442	LEU
1	b	447	THR
1	b	452	LEU
1	b	456	ARG
1	b	457	ASP
1	b	461	ILE
1	b	466	ILE
1	b	486	GLU
1	b	489	GLN
1	c	16	VAL
1	c	21	LYS
1	c	24	ARG
1	c	42	LEU
1	c	45	LYS
1	c	51	SER
1	c	52	THR
1	c	53	ASP
1	c	71	SER
1	c	72	LYS
1	c	78	PHE

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Mol	Chain	Res	Type
1	c	86	LEU
1	c	99	ASP
1	c	101	ASP
1	c	105	LYS
1	c	107	ASP
1	c	114	GLU
1	c	126	TYR
1	c	129	THR
1	c	130	LEU
1	c	135	LYS
1	c	136	GLN
1	c	142	ASN
1	c	144	LEU
1	c	147	LEU
1	c	166	TYR
1	c	168	VAL
1	c	170	ARG
1	c	175	ASN
1	c	240	SER
1	c	241	ASP
1	c	243	THR
1	c	246	LYS
1	c	247	GLU
1	c	250	PRO
1	c	251	TYR
1	c	252	ILE
1	c	256	MET
1	c	258	ARG
1	c	264	TYR
1	c	266	ARG
1	c	268	TYR
1	c	281	ASN
1	c	283	GLN
1	c	286	ILE
1	c	291	MET
1	c	292	ILE
1	c	309	ARG
1	c	315	GLN
1	c	325	GLU
1	c	326	ASP
1	c	328	SER
1	c	335	GLN

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Mol	Chain	Res	Type
1	c	337	ASP
1	c	338	PHE
1	c	339	THR
1	c	342	LYS
1	c	348	ILE
1	c	352	LEU
1	c	358	LEU
1	c	370	THR
1	c	373	GLU
1	c	374	ILE
1	c	375	ARG
1	c	376	TYR
1	c	379	SER
1	c	388	VAL
1	c	393	SER
1	c	396	LEU
1	c	398	LEU
1	c	400	LEU
1	c	402	ARG
1	c	404	LEU
1	c	405	LEU
1	c	406	LYS
1	c	409	GLN
1	c	411	THR
1	c	412	GLN
1	c	417	LEU
1	c	419	LYS
1	c	428	THR
1	c	435	ARG
1	c	438	ASP
1	c	442	LEU
1	c	447	THR
1	c	452	LEU
1	c	456	ARG
1	c	457	ASP
1	c	461	ILE
1	c	466	ILE
1	c	486	GLU
1	c	489	GLN
1	d	16	VAL
1	d	21	LYS
1	d	24	ARG

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Mol	Chain	Res	Type
1	d	42	LEU
1	d	45	LYS
1	d	52	THR
1	d	53	ASP
1	d	55	GLN
1	d	71	SER
1	d	72	LYS
1	d	78	PHE
1	d	86	LEU
1	d	99	ASP
1	d	101	ASP
1	d	105	LYS
1	d	107	ASP
1	d	114	GLU
1	d	126	TYR
1	d	129	THR
1	d	130	LEU
1	d	135	LYS
1	d	136	GLN
1	d	142	ASN
1	d	144	LEU
1	d	147	LEU
1	d	166	TYR
1	d	168	VAL
1	d	170	ARG
1	d	175	ASN
1	d	240	SER
1	d	241	ASP
1	d	243	THR
1	d	246	LYS
1	d	247	GLU
1	d	250	PRO
1	d	251	TYR
1	d	252	ILE
1	d	256	MET
1	d	258	ARG
1	d	264	TYR
1	d	266	ARG
1	d	268	TYR
1	d	281	ASN
1	d	283	GLN
1	d	286	ILE

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Mol	Chain	Res	Type
1	d	291	MET
1	d	292	ILE
1	d	309	ARG
1	d	315	GLN
1	d	325	GLU
1	d	326	ASP
1	d	328	SER
1	d	335	GLN
1	d	337	ASP
1	d	338	PHE
1	d	339	THR
1	d	342	LYS
1	d	348	ILE
1	d	352	LEU
1	d	358	LEU
1	d	370	THR
1	d	373	GLU
1	d	374	ILE
1	d	375	ARG
1	d	376	TYR
1	d	379	SER
1	d	388	VAL
1	d	393	SER
1	d	396	LEU
1	d	398	LEU
1	d	400	LEU
1	d	402	ARG
1	d	404	LEU
1	d	405	LEU
1	d	406	LYS
1	d	409	GLN
1	d	411	THR
1	d	412	GLN
1	d	417	LEU
1	d	419	LYS
1	d	428	THR
1	d	435	ARG
1	d	438	ASP
1	d	442	LEU
1	d	447	THR
1	d	452	LEU
1	d	456	ARG

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Mol	Chain	Res	Type
1	d	457	ASP
1	d	461	ILE
1	d	466	ILE
1	d	486	GLU
1	d	489	GLN
1	e	16	VAL
1	e	21	LYS
1	e	24	ARG
1	e	42	LEU
1	e	51	SER
1	e	52	THR
1	e	53	ASP
1	e	55	GLN
1	e	71	SER
1	e	72	LYS
1	e	78	PHE
1	e	86	LEU
1	e	99	ASP
1	e	101	ASP
1	e	105	LYS
1	e	107	ASP
1	e	114	GLU
1	e	126	TYR
1	e	129	THR
1	e	130	LEU
1	e	135	LYS
1	e	136	GLN
1	e	142	ASN
1	e	144	LEU
1	e	147	LEU
1	e	166	TYR
1	e	168	VAL
1	e	170	ARG
1	e	175	ASN
1	e	240	SER
1	e	241	ASP
1	e	243	THR
1	e	246	LYS
1	e	247	GLU
1	e	250	PRO
1	e	251	TYR
1	e	252	ILE

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Mol	Chain	Res	Type
1	e	256	MET
1	e	258	ARG
1	e	264	TYR
1	e	266	ARG
1	e	268	TYR
1	e	281	ASN
1	e	283	GLN
1	e	286	ILE
1	e	291	MET
1	e	292	ILE
1	e	309	ARG
1	e	315	GLN
1	e	325	GLU
1	e	326	ASP
1	e	328	SER
1	e	335	GLN
1	e	337	ASP
1	e	338	PHE
1	e	339	THR
1	e	342	LYS
1	e	348	ILE
1	e	352	LEU
1	e	358	LEU
1	e	370	THR
1	e	373	GLU
1	e	374	ILE
1	e	375	ARG
1	e	376	TYR
1	e	379	SER
1	e	388	VAL
1	e	393	SER
1	e	396	LEU
1	e	398	LEU
1	e	400	LEU
1	e	402	ARG
1	e	404	LEU
1	e	405	LEU
1	e	406	LYS
1	e	409	GLN
1	e	411	THR
1	e	412	GLN
1	e	417	LEU

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Mol	Chain	Res	Type
1	e	419	LYS
1	e	428	THR
1	e	435	ARG
1	e	438	ASP
1	e	442	LEU
1	e	447	THR
1	e	452	LEU
1	e	456	ARG
1	e	457	ASP
1	e	461	ILE
1	e	466	ILE
1	e	486	GLU
1	e	489	GLN
1	f	16	VAL
1	f	21	LYS
1	f	24	ARG
1	f	42	LEU
1	f	51	SER
1	f	52	THR
1	f	53	ASP
1	f	71	SER
1	f	72	LYS
1	f	78	PHE
1	f	86	LEU
1	f	99	ASP
1	f	101	ASP
1	f	105	LYS
1	f	107	ASP
1	f	114	GLU
1	f	126	TYR
1	f	129	THR
1	f	130	LEU
1	f	135	LYS
1	f	136	GLN
1	f	142	ASN
1	f	144	LEU
1	f	147	LEU
1	f	166	TYR
1	f	168	VAL
1	f	170	ARG
1	f	175	ASN
1	f	240	SER

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Mol	Chain	Res	Type
1	f	241	ASP
1	f	243	THR
1	f	246	LYS
1	f	247	GLU
1	f	250	PRO
1	f	251	TYR
1	f	252	ILE
1	f	256	MET
1	f	258	ARG
1	f	264	TYR
1	f	266	ARG
1	f	268	TYR
1	f	281	ASN
1	f	283	GLN
1	f	286	ILE
1	f	291	MET
1	f	292	ILE
1	f	309	ARG
1	f	315	GLN
1	f	325	GLU
1	f	326	ASP
1	f	328	SER
1	f	335	GLN
1	f	337	ASP
1	f	338	PHE
1	f	339	THR
1	f	342	LYS
1	f	348	ILE
1	f	352	LEU
1	f	358	LEU
1	f	370	THR
1	f	373	GLU
1	f	374	ILE
1	f	375	ARG
1	f	376	TYR
1	f	379	SER
1	f	388	VAL
1	f	393	SER
1	f	396	LEU
1	f	398	LEU
1	f	400	LEU
1	f	402	ARG

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Mol	Chain	Res	Type
1	f	404	LEU
1	f	405	LEU
1	f	406	LYS
1	f	409	GLN
1	f	411	THR
1	f	412	GLN
1	f	417	LEU
1	f	419	LYS
1	f	428	THR
1	f	435	ARG
1	f	438	ASP
1	f	442	LEU
1	f	447	THR
1	f	452	LEU
1	f	456	ARG
1	f	457	ASP
1	f	461	ILE
1	f	466	ILE
1	f	486	GLU
1	f	489	GLN
1	g	16	VAL
1	g	21	LYS
1	g	24	ARG
1	g	42	LEU
1	g	52	THR
1	g	53	ASP
1	g	55	GLN
1	g	71	SER
1	g	72	LYS
1	g	78	PHE
1	g	86	LEU
1	g	99	ASP
1	g	101	ASP
1	g	105	LYS
1	g	107	ASP
1	g	114	GLU
1	g	126	TYR
1	g	129	THR
1	g	130	LEU
1	g	135	LYS
1	g	136	GLN
1	g	142	ASN

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Mol	Chain	Res	Type
1	g	144	LEU
1	g	147	LEU
1	g	166	TYR
1	g	168	VAL
1	g	170	ARG
1	g	175	ASN
1	g	240	SER
1	g	241	ASP
1	g	243	THR
1	g	246	LYS
1	g	247	GLU
1	g	250	PRO
1	g	251	TYR
1	g	252	ILE
1	g	256	MET
1	g	258	ARG
1	g	264	TYR
1	g	266	ARG
1	g	268	TYR
1	g	281	ASN
1	g	283	GLN
1	g	286	ILE
1	g	291	MET
1	g	292	ILE
1	g	309	ARG
1	g	315	GLN
1	g	325	GLU
1	g	326	ASP
1	g	328	SER
1	g	335	GLN
1	g	337	ASP
1	g	338	PHE
1	g	339	THR
1	g	342	LYS
1	g	348	ILE
1	g	352	LEU
1	g	358	LEU
1	g	370	THR
1	g	373	GLU
1	g	374	ILE
1	g	375	ARG
1	g	376	TYR

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Mol	Chain	Res	Type
1	g	379	SER
1	g	388	VAL
1	g	393	SER
1	g	396	LEU
1	g	398	LEU
1	g	400	LEU
1	g	402	ARG
1	g	404	LEU
1	g	405	LEU
1	g	406	LYS
1	g	409	GLN
1	g	411	THR
1	g	412	GLN
1	g	417	LEU
1	g	419	LYS
1	g	428	THR
1	g	435	ARG
1	g	438	ASP
1	g	442	LEU
1	g	447	THR
1	g	452	LEU
1	g	456	ARG
1	g	457	ASP
1	g	461	ILE
1	g	466	ILE
1	g	486	GLU
1	g	489	GLN
1	h	16	VAL
1	h	21	LYS
1	h	24	ARG
1	h	42	LEU
1	h	51	SER
1	h	52	THR
1	h	53	ASP
1	h	71	SER
1	h	72	LYS
1	h	78	PHE
1	h	86	LEU
1	h	99	ASP
1	h	101	ASP
1	h	105	LYS
1	h	107	ASP

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Mol	Chain	Res	Type
1	h	114	GLU
1	h	126	TYR
1	h	129	THR
1	h	130	LEU
1	h	135	LYS
1	h	136	GLN
1	h	142	ASN
1	h	144	LEU
1	h	147	LEU
1	h	166	TYR
1	h	168	VAL
1	h	170	ARG
1	h	175	ASN
1	h	240	SER
1	h	241	ASP
1	h	243	THR
1	h	246	LYS
1	h	247	GLU
1	h	250	PRO
1	h	251	TYR
1	h	252	ILE
1	h	256	MET
1	h	258	ARG
1	h	264	TYR
1	h	266	ARG
1	h	268	TYR
1	h	281	ASN
1	h	283	GLN
1	h	286	ILE
1	h	291	MET
1	h	292	ILE
1	h	309	ARG
1	h	315	GLN
1	h	325	GLU
1	h	326	ASP
1	h	328	SER
1	h	335	GLN
1	h	337	ASP
1	h	338	PHE
1	h	339	THR
1	h	342	LYS
1	h	348	ILE

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Mol	Chain	Res	Type
1	h	352	LEU
1	h	358	LEU
1	h	370	THR
1	h	373	GLU
1	h	374	ILE
1	h	375	ARG
1	h	376	TYR
1	h	379	SER
1	h	388	VAL
1	h	393	SER
1	h	396	LEU
1	h	398	LEU
1	h	400	LEU
1	h	402	ARG
1	h	404	LEU
1	h	405	LEU
1	h	406	LYS
1	h	409	GLN
1	h	411	THR
1	h	412	GLN
1	h	417	LEU
1	h	419	LYS
1	h	428	THR
1	h	435	ARG
1	h	438	ASP
1	h	442	LEU
1	h	447	THR
1	h	452	LEU
1	h	456	ARG
1	h	457	ASP
1	h	461	ILE
1	h	466	ILE
1	h	486	GLU
1	h	489	GLN
1	i	16	VAL
1	i	21	LYS
1	i	24	ARG
1	i	42	LEU
1	i	45	LYS
1	i	51	SER
1	i	52	THR
1	i	53	ASP

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Mol	Chain	Res	Type
1	i	71	SER
1	i	72	LYS
1	i	78	PHE
1	i	86	LEU
1	i	99	ASP
1	i	101	ASP
1	i	105	LYS
1	i	107	ASP
1	i	114	GLU
1	i	126	TYR
1	i	129	THR
1	i	130	LEU
1	i	135	LYS
1	i	136	GLN
1	i	142	ASN
1	i	144	LEU
1	i	147	LEU
1	i	166	TYR
1	i	168	VAL
1	i	170	ARG
1	i	175	ASN
1	i	240	SER
1	i	241	ASP
1	i	243	THR
1	i	246	LYS
1	i	247	GLU
1	i	250	PRO
1	i	251	TYR
1	i	252	ILE
1	i	256	MET
1	i	258	ARG
1	i	264	TYR
1	i	266	ARG
1	i	268	TYR
1	i	281	ASN
1	i	283	GLN
1	i	286	ILE
1	i	291	MET
1	i	292	ILE
1	i	309	ARG
1	i	315	GLN
1	i	325	GLU

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Mol	Chain	Res	Type
1	i	326	ASP
1	i	328	SER
1	i	335	GLN
1	i	337	ASP
1	i	338	PHE
1	i	339	THR
1	i	342	LYS
1	i	348	ILE
1	i	352	LEU
1	i	358	LEU
1	i	370	THR
1	i	373	GLU
1	i	374	ILE
1	i	375	ARG
1	i	376	TYR
1	i	379	SER
1	i	388	VAL
1	i	393	SER
1	i	396	LEU
1	i	398	LEU
1	i	400	LEU
1	i	402	ARG
1	i	404	LEU
1	i	405	LEU
1	i	406	LYS
1	i	409	GLN
1	i	411	THR
1	i	412	GLN
1	i	417	LEU
1	i	419	LYS
1	i	428	THR
1	i	435	ARG
1	i	438	ASP
1	i	442	LEU
1	i	447	THR
1	i	452	LEU
1	i	456	ARG
1	i	457	ASP
1	i	461	ILE
1	i	466	ILE
1	i	486	GLU
1	i	489	GLN

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Mol	Chain	Res	Type
1	j	16	VAL
1	j	21	LYS
1	j	24	ARG
1	j	42	LEU
1	j	52	THR
1	j	53	ASP
1	j	71	SER
1	j	72	LYS
1	j	78	PHE
1	j	86	LEU
1	j	99	ASP
1	j	101	ASP
1	j	105	LYS
1	j	107	ASP
1	j	114	GLU
1	j	126	TYR
1	j	129	THR
1	j	130	LEU
1	j	135	LYS
1	j	136	GLN
1	j	142	ASN
1	j	144	LEU
1	j	147	LEU
1	j	166	TYR
1	j	168	VAL
1	j	170	ARG
1	j	175	ASN
1	j	240	SER
1	j	241	ASP
1	j	243	THR
1	j	246	LYS
1	j	247	GLU
1	j	250	PRO
1	j	251	TYR
1	j	252	ILE
1	j	256	MET
1	j	258	ARG
1	j	264	TYR
1	j	266	ARG
1	j	268	TYR
1	j	281	ASN
1	j	283	GLN

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Mol	Chain	Res	Type
1	j	286	ILE
1	j	291	MET
1	j	292	ILE
1	j	309	ARG
1	j	315	GLN
1	j	325	GLU
1	j	326	ASP
1	j	328	SER
1	j	335	GLN
1	j	337	ASP
1	j	338	PHE
1	j	339	THR
1	j	342	LYS
1	j	348	ILE
1	j	352	LEU
1	j	358	LEU
1	j	370	THR
1	j	373	GLU
1	j	374	ILE
1	j	375	ARG
1	j	376	TYR
1	j	379	SER
1	j	388	VAL
1	j	393	SER
1	j	396	LEU
1	j	398	LEU
1	j	400	LEU
1	j	402	ARG
1	j	404	LEU
1	j	405	LEU
1	j	406	LYS
1	j	409	GLN
1	j	411	THR
1	j	412	GLN
1	j	417	LEU
1	j	419	LYS
1	j	428	THR
1	j	435	ARG
1	j	438	ASP
1	j	442	LEU
1	j	447	THR
1	j	452	LEU

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Mol	Chain	Res	Type
1	j	456	ARG
1	j	457	ASP
1	j	461	ILE
1	j	466	ILE
1	j	486	GLU
1	j	489	GLN
1	k	16	VAL
1	k	21	LYS
1	k	24	ARG
1	k	42	LEU
1	k	45	LYS
1	k	51	SER
1	k	52	THR
1	k	53	ASP
1	k	71	SER
1	k	72	LYS
1	k	78	PHE
1	k	86	LEU
1	k	99	ASP
1	k	101	ASP
1	k	105	LYS
1	k	107	ASP
1	k	114	GLU
1	k	126	TYR
1	k	129	THR
1	k	130	LEU
1	k	135	LYS
1	k	136	GLN
1	k	142	ASN
1	k	144	LEU
1	k	147	LEU
1	k	166	TYR
1	k	168	VAL
1	k	170	ARG
1	k	175	ASN
1	k	240	SER
1	k	241	ASP
1	k	243	THR
1	k	246	LYS
1	k	247	GLU
1	k	250	PRO
1	k	251	TYR

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Mol	Chain	Res	Type
1	k	252	ILE
1	k	256	MET
1	k	258	ARG
1	k	264	TYR
1	k	266	ARG
1	k	268	TYR
1	k	281	ASN
1	k	283	GLN
1	k	286	ILE
1	k	291	MET
1	k	292	ILE
1	k	309	ARG
1	k	315	GLN
1	k	325	GLU
1	k	326	ASP
1	k	328	SER
1	k	335	GLN
1	k	337	ASP
1	k	338	PHE
1	k	339	THR
1	k	342	LYS
1	k	348	ILE
1	k	352	LEU
1	k	358	LEU
1	k	370	THR
1	k	373	GLU
1	k	374	ILE
1	k	375	ARG
1	k	376	TYR
1	k	379	SER
1	k	388	VAL
1	k	393	SER
1	k	396	LEU
1	k	398	LEU
1	k	400	LEU
1	k	402	ARG
1	k	404	LEU
1	k	405	LEU
1	k	406	LYS
1	k	409	GLN
1	k	411	THR
1	k	412	GLN

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Mol	Chain	Res	Type
1	k	417	LEU
1	k	419	LYS
1	k	428	THR
1	k	435	ARG
1	k	438	ASP
1	k	442	LEU
1	k	447	THR
1	k	452	LEU
1	k	456	ARG
1	k	457	ASP
1	k	461	ILE
1	k	466	ILE
1	k	486	GLU
1	k	489	GLN
1	l	16	VAL
1	l	21	LYS
1	l	24	ARG
1	l	42	LEU
1	l	45	LYS
1	l	51	SER
1	l	52	THR
1	l	53	ASP
1	l	71	SER
1	l	72	LYS
1	l	78	PHE
1	l	86	LEU
1	l	99	ASP
1	l	101	ASP
1	l	105	LYS
1	l	107	ASP
1	l	114	GLU
1	l	126	TYR
1	l	129	THR
1	l	130	LEU
1	l	135	LYS
1	l	136	GLN
1	l	142	ASN
1	l	144	LEU
1	l	147	LEU
1	l	166	TYR
1	l	168	VAL
1	l	170	ARG

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Mol	Chain	Res	Type
1	1	175	ASN
1	1	240	SER
1	1	241	ASP
1	1	243	THR
1	1	246	LYS
1	1	247	GLU
1	1	250	PRO
1	1	251	TYR
1	1	252	ILE
1	1	256	MET
1	1	258	ARG
1	1	264	TYR
1	1	266	ARG
1	1	268	TYR
1	1	281	ASN
1	1	283	GLN
1	1	286	ILE
1	1	291	MET
1	1	292	ILE
1	1	309	ARG
1	1	315	GLN
1	1	325	GLU
1	1	326	ASP
1	1	328	SER
1	1	335	GLN
1	1	337	ASP
1	1	338	PHE
1	1	339	THR
1	1	342	LYS
1	1	348	ILE
1	1	352	LEU
1	1	370	THR
1	1	373	GLU
1	1	374	ILE
1	1	375	ARG
1	1	376	TYR
1	1	379	SER
1	1	388	VAL
1	1	393	SER
1	1	396	LEU
1	1	398	LEU
1	1	400	LEU

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Mol	Chain	Res	Type
1	l	402	ARG
1	l	404	LEU
1	l	405	LEU
1	l	406	LYS
1	l	409	GLN
1	l	411	THR
1	l	412	GLN
1	l	417	LEU
1	l	419	LYS
1	l	428	THR
1	l	435	ARG
1	l	438	ASP
1	l	442	LEU
1	l	447	THR
1	l	452	LEU
1	l	456	ARG
1	l	457	ASP
1	l	461	ILE
1	l	466	ILE
1	l	486	GLU
1	l	489	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (114) such sidechains are listed below:

Mol	Chain	Res	Type
1	a	68	ASN
1	a	136	GLN
1	a	142	ASN
1	a	156	ASN
1	a	169	GLN
1	a	283	GLN
1	a	315	GLN
1	a	331	GLN
1	a	407	GLN
1	b	68	ASN
1	b	136	GLN
1	b	142	ASN
1	b	156	ASN
1	b	169	GLN
1	b	283	GLN
1	b	315	GLN
1	b	331	GLN

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Mol	Chain	Res	Type
1	b	407	GLN
1	c	68	ASN
1	c	136	GLN
1	c	142	ASN
1	c	156	ASN
1	c	169	GLN
1	c	283	GLN
1	c	315	GLN
1	c	331	GLN
1	c	407	GLN
1	d	68	ASN
1	d	136	GLN
1	d	142	ASN
1	d	156	ASN
1	d	169	GLN
1	d	283	GLN
1	d	315	GLN
1	d	331	GLN
1	d	335	GLN
1	d	407	GLN
1	e	68	ASN
1	e	136	GLN
1	e	142	ASN
1	e	156	ASN
1	e	169	GLN
1	e	283	GLN
1	e	315	GLN
1	e	331	GLN
1	e	335	GLN
1	e	407	GLN
1	f	68	ASN
1	f	136	GLN
1	f	142	ASN
1	f	156	ASN
1	f	169	GLN
1	f	283	GLN
1	f	315	GLN
1	f	331	GLN
1	f	335	GLN
1	f	407	GLN
1	g	68	ASN
1	g	136	GLN

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Mol	Chain	Res	Type
1	g	142	ASN
1	g	156	ASN
1	g	169	GLN
1	g	283	GLN
1	g	315	GLN
1	g	331	GLN
1	g	335	GLN
1	g	407	GLN
1	h	68	ASN
1	h	136	GLN
1	h	142	ASN
1	h	156	ASN
1	h	169	GLN
1	h	283	GLN
1	h	315	GLN
1	h	331	GLN
1	h	407	GLN
1	i	68	ASN
1	i	136	GLN
1	i	142	ASN
1	i	156	ASN
1	i	169	GLN
1	i	283	GLN
1	i	315	GLN
1	i	331	GLN
1	i	407	GLN
1	j	68	ASN
1	j	136	GLN
1	j	142	ASN
1	j	156	ASN
1	j	169	GLN
1	j	283	GLN
1	j	315	GLN
1	j	331	GLN
1	j	335	GLN
1	j	407	GLN
1	k	68	ASN
1	k	136	GLN
1	k	142	ASN
1	k	156	ASN
1	k	169	GLN
1	k	283	GLN

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Mol	Chain	Res	Type
1	k	315	GLN
1	k	331	GLN
1	k	407	GLN
1	l	68	ASN
1	l	136	GLN
1	l	142	ASN
1	l	156	ASN
1	l	169	GLN
1	l	283	GLN
1	l	315	GLN
1	l	331	GLN
1	l	335	GLN
1	l	407	GLN

### 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 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.

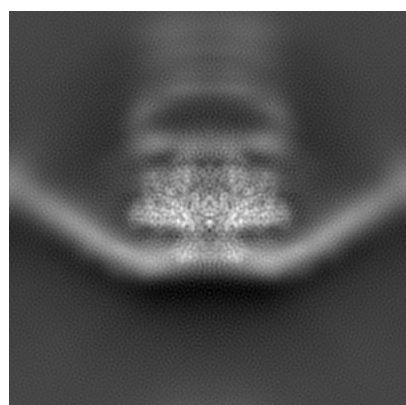
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30138. These allow visual inspection of the internal detail of the map and identification of artifacts.

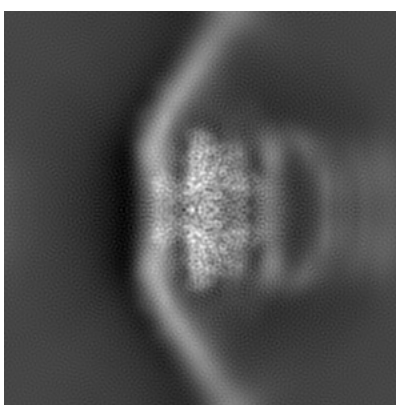
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

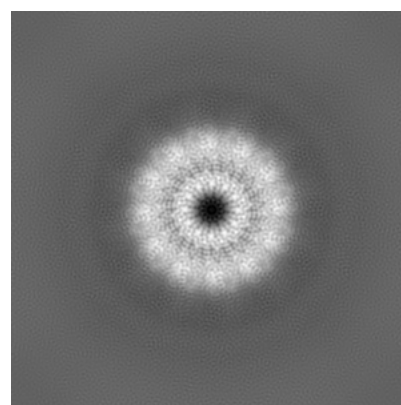
#### 6.1.1 Primary map



X



Y

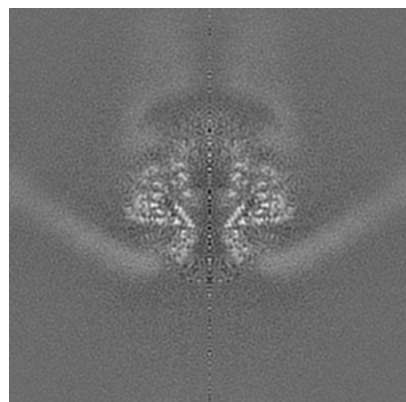


Z

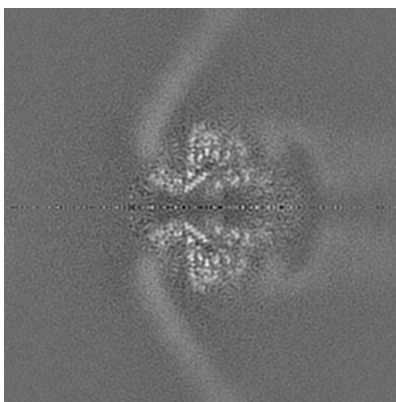
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

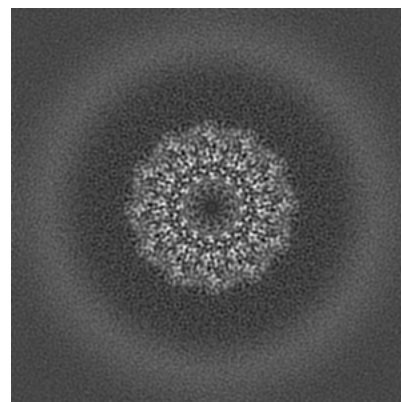
#### 6.2.1 Primary map



X Index: 160



Y Index: 160



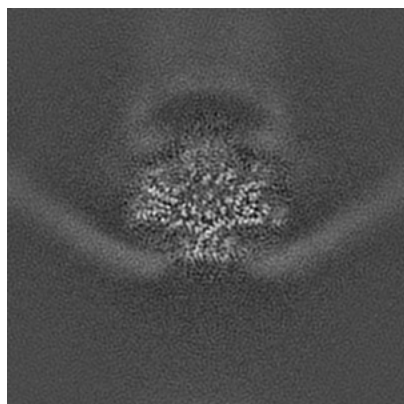
Z Index: 160



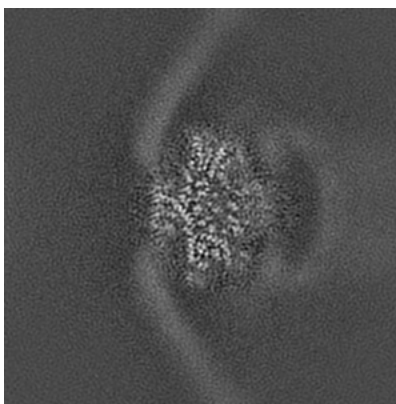
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

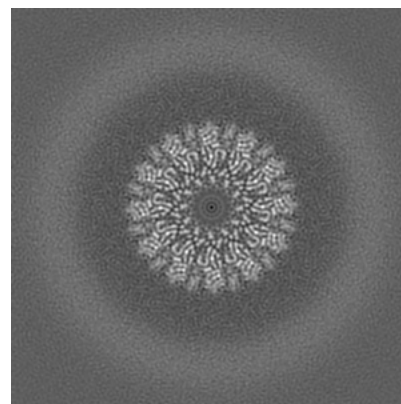
### 6.3.1 Primary map



X Index: 139



Y Index: 139

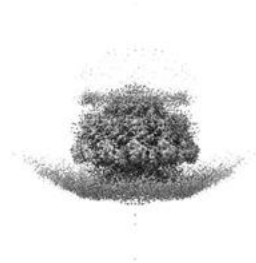


Z Index: 157

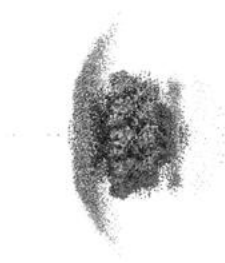
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal surface views [i](#)

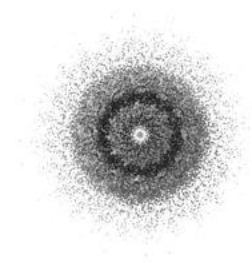
### 6.4.1 Primary map



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.

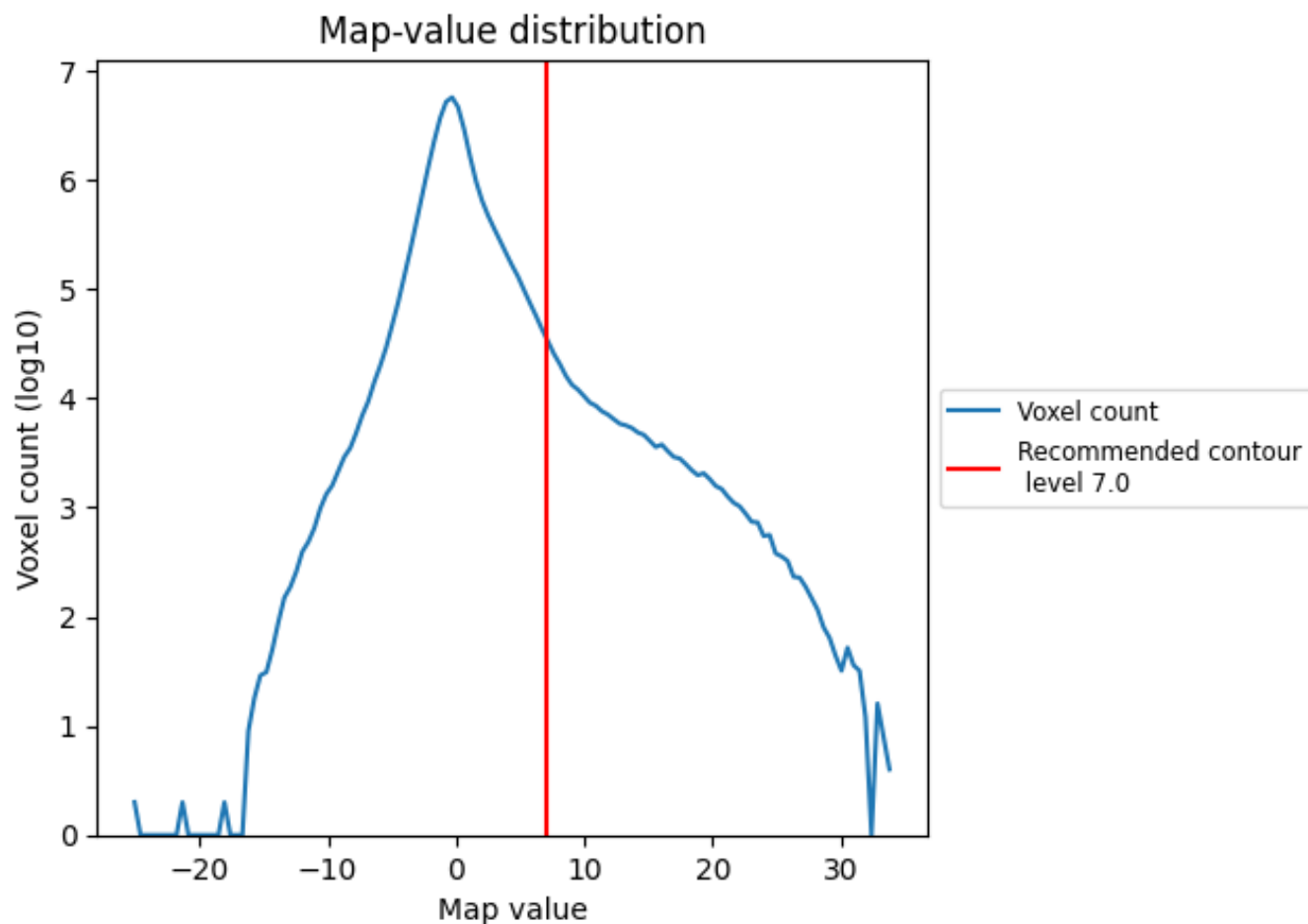
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

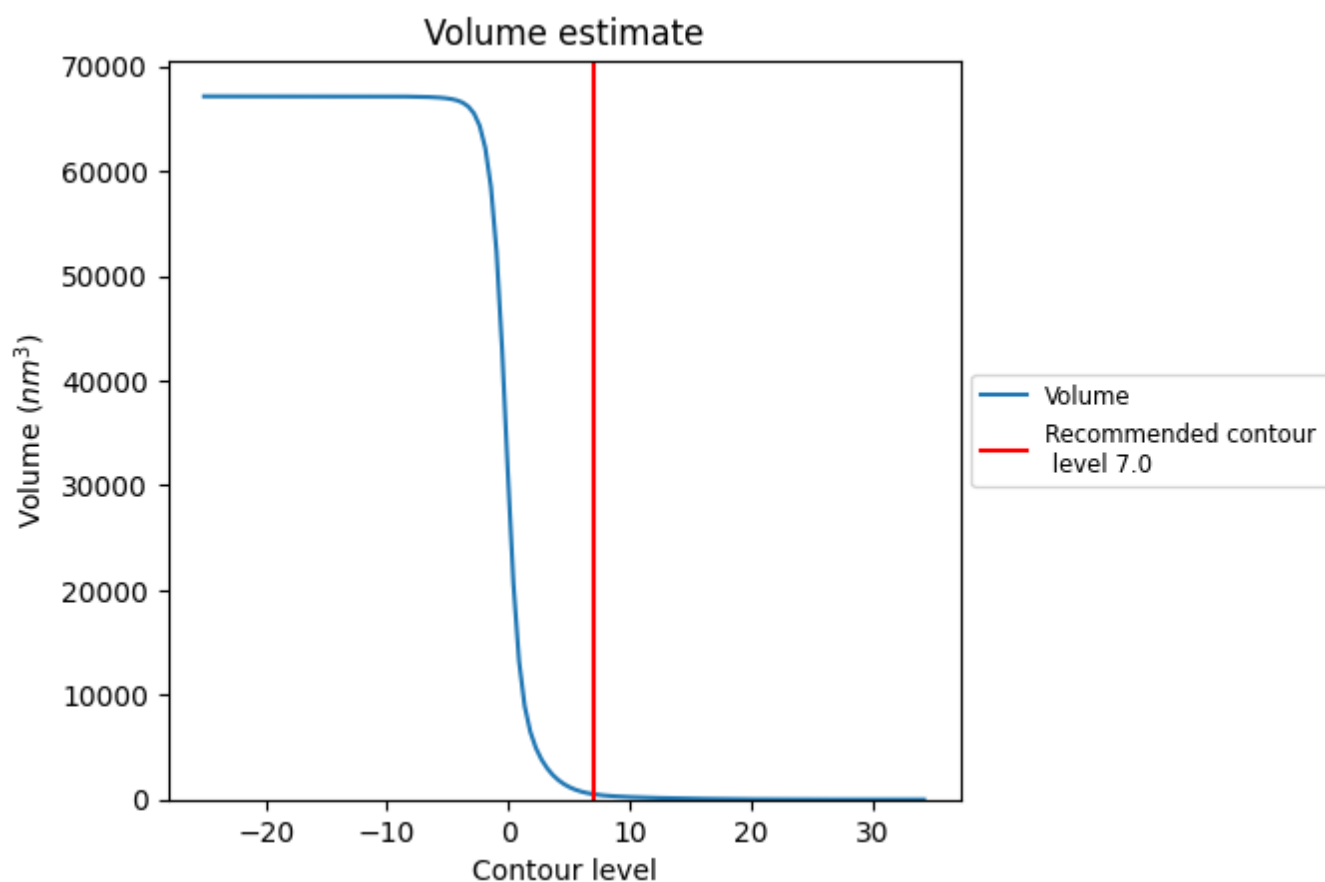
This section contains the results of statistical analysis of the map.

### 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.

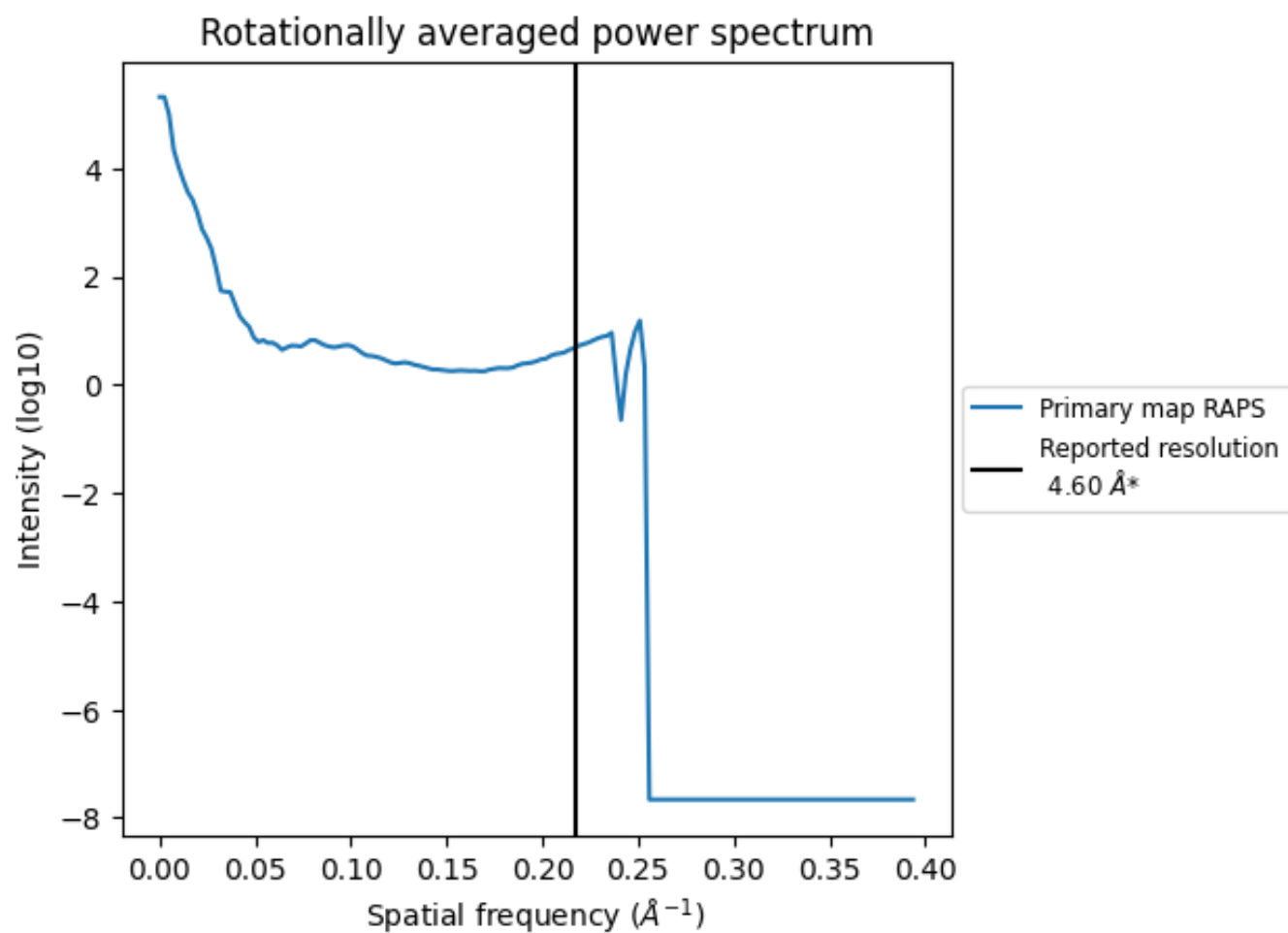
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 518 nm<sup>3</sup>; this corresponds to an approximate mass of 468 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 0.217 Å<sup>-1</sup>

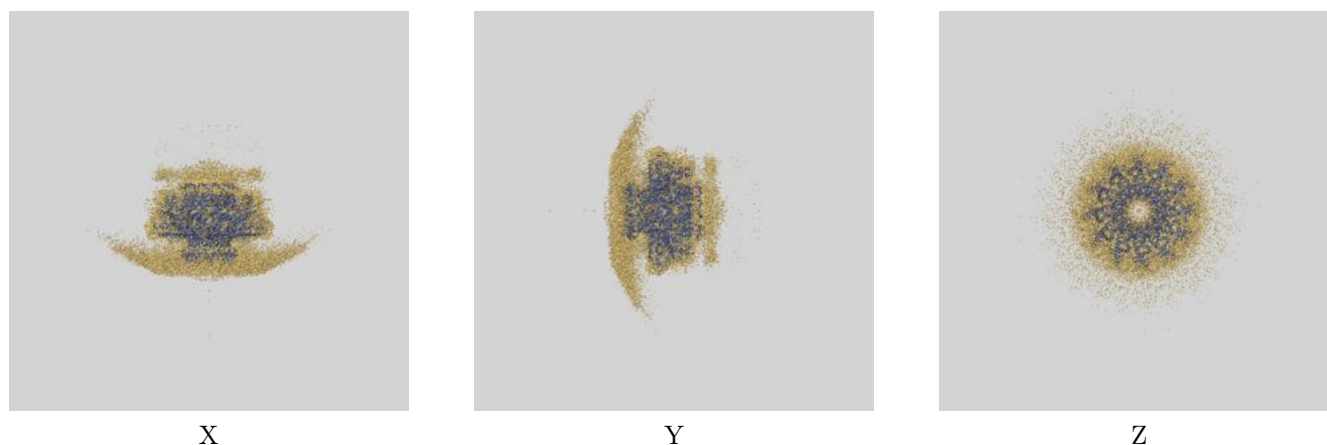
## 8 Fourier-Shell correlation ⓘ

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

## 9 Map-model fit [i](#)

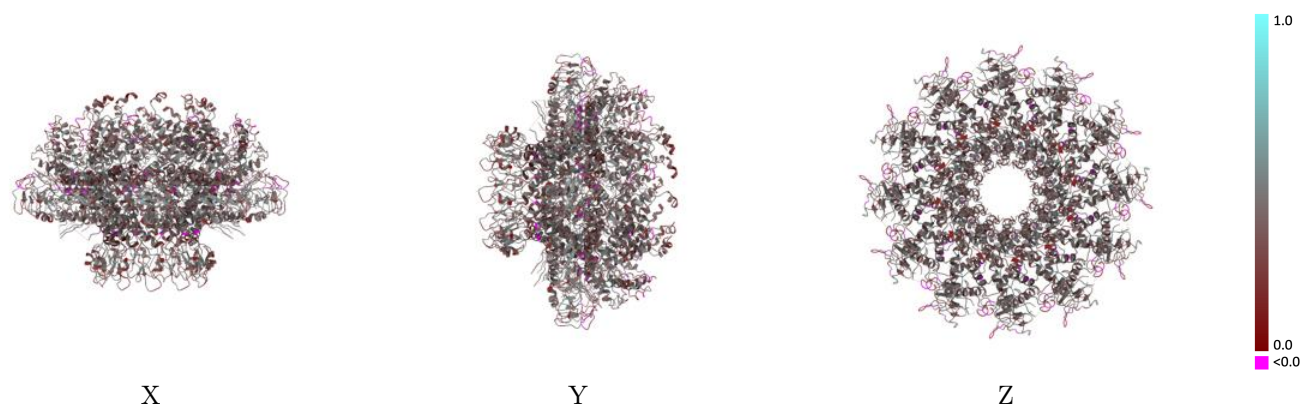
This section contains information regarding the fit between EMDB map EMD-30138 and PDB model 7BP0. Per-residue inclusion information can be found in section [3](#) on page [5](#).

### 9.1 Map-model overlay [i](#)



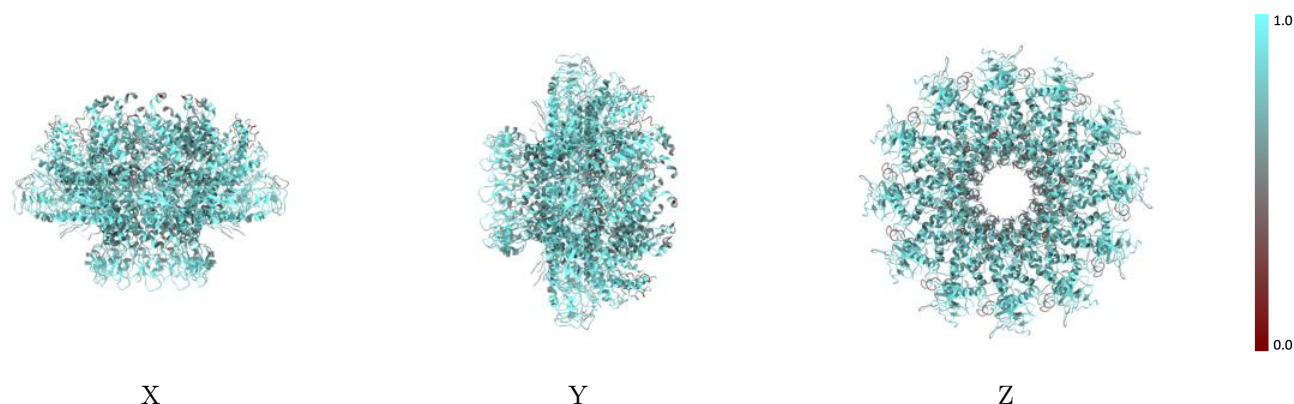
The images above show the 3D surface view of the map at the recommended contour level 7.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



The images above show the model with each residue coloured according 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.

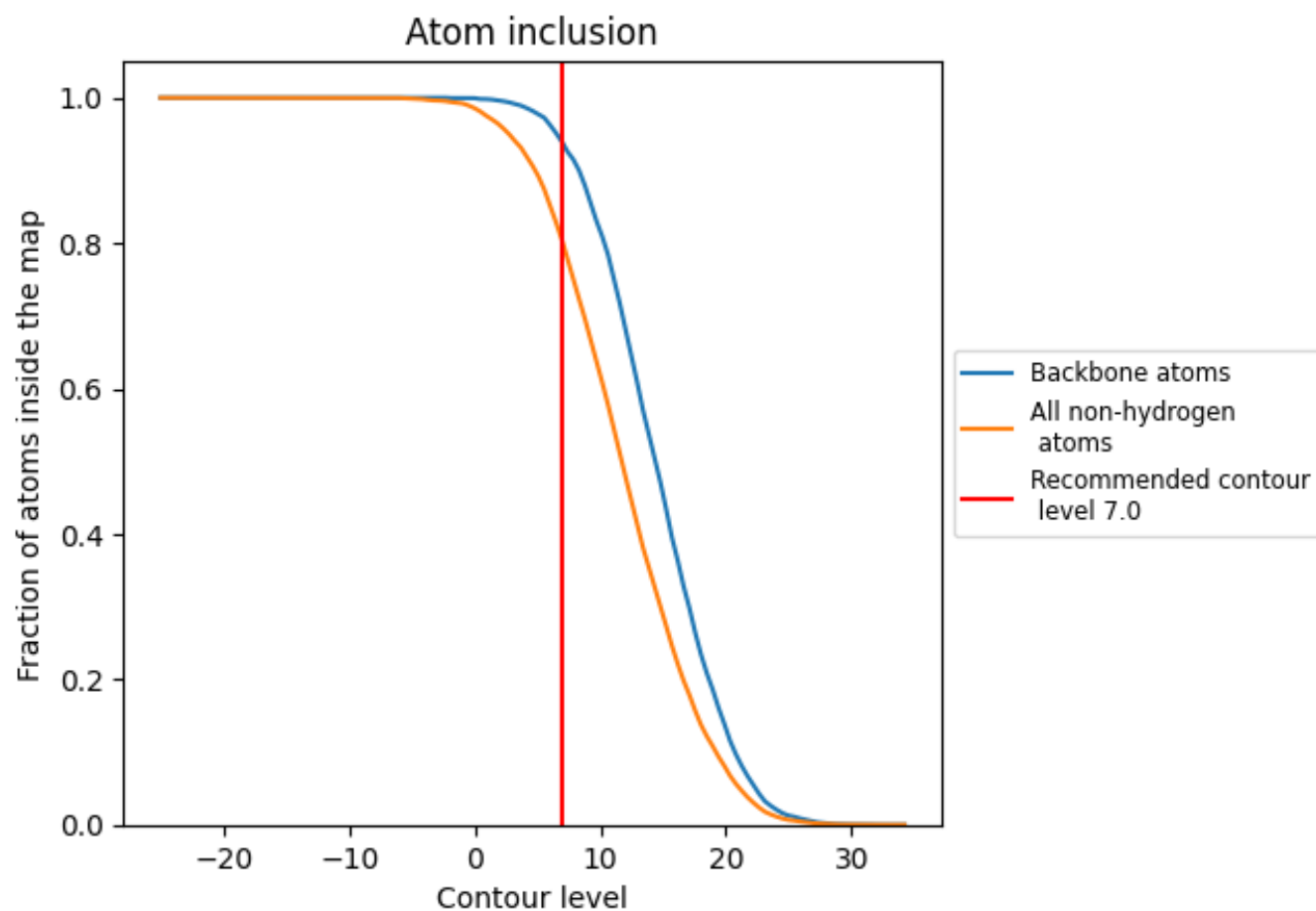
## 9.3 Atom inclusion mapped to coordinate model [i](#)



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, 94% 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 (7.0) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div><div></div>0.8006</div>	<div><div></div>0.3790</div>
a	<div><div></div>0.8010</div>	<div><div></div>0.3790</div>
b	<div><div></div>0.8025</div>	<div><div></div>0.3820</div>
c	<div><div></div>0.7998</div>	<div><div></div>0.3780</div>
d	<div><div></div>0.8016</div>	<div><div></div>0.3780</div>
e	<div><div></div>0.8007</div>	<div><div></div>0.3800</div>
f	<div><div></div>0.8001</div>	<div><div></div>0.3770</div>
g	<div><div></div>0.7995</div>	<div><div></div>0.3770</div>
h	<div><div></div>0.8004</div>	<div><div></div>0.3810</div>
i	<div><div></div>0.7995</div>	<div><div></div>0.3770</div>
j	<div><div></div>0.7995</div>	<div><div></div>0.3780</div>
k	<div><div></div>0.8022</div>	<div><div></div>0.3810</div>
l	<div><div></div>0.8001</div>	<div><div></div>0.3780</div>

1.0

0.0

<0.0