



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:46 PM UTC

PDB ID : 2YGD / pdb_00002ygd
EMDB ID : EMD-1894
Title : Molecular architectures of the 24meric eye lens chaperone alphaB- crystallin elucidated by a triple hybrid approach
Authors : Braun, N.; Zacharias, M.; Peschek, J.; Kastenmueller, A.; Zou, J.; Hanzlik, M.; Haslbeck, M.; Rappsilber, J.; Buchner, J.; Weinkauff, S.
Deposited on : 2011-04-13
Resolution : 9.40 Å (reported)
Based on initial model : 2KLR

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:

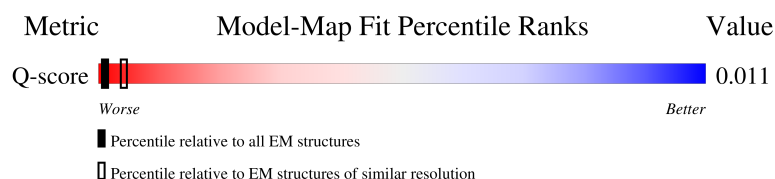
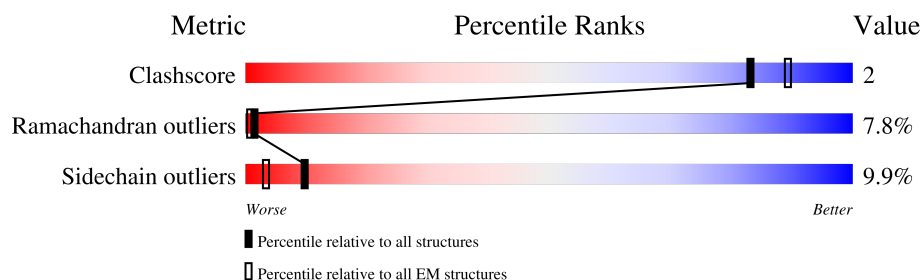
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 9.40 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	224 (8.90 - 9.90)

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	175	9% 74% 20% 5%
1	B	175	10% 78% 18% ..
1	C	175	9% 76% 20% ..
1	D	175	8% 77% 19% ..

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Mol	Chain	Length	Quality of chain
1	E	175	
1	F	175	
1	G	175	
1	H	175	
1	I	175	
1	J	175	
1	K	175	
1	L	175	
1	M	175	
1	N	175	
1	O	175	
1	P	175	
1	Q	175	
1	R	175	
1	S	175	
1	T	175	
1	U	175	
1	V	175	
1	W	175	
1	X	175	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 34296 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 ALPHA-CRYSTALLIN B CHAIN.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	B	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	C	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	D	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	E	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	F	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	G	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	H	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	I	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	J	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	K	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	L	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	M	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	N	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	O	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	P	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		
1	Q	175	Total	C	N	O	S	0	0
			1429	916	252	259	2		

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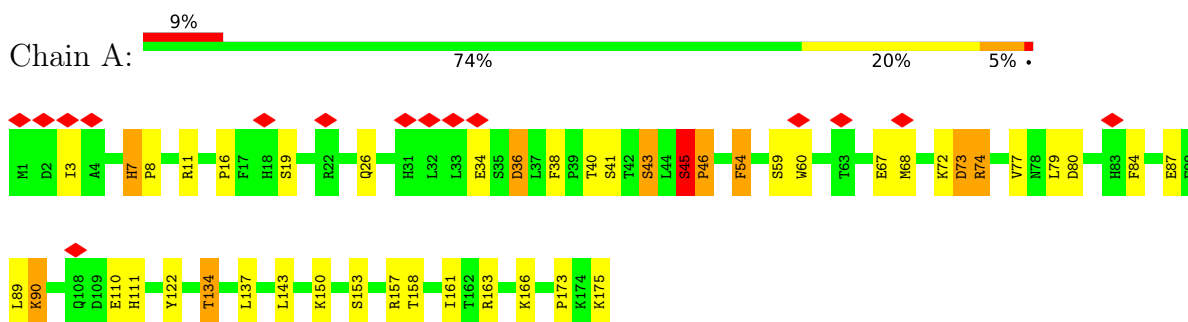
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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	175	Total 1429	C 916	N 252	O 259	S 2	0	0
1	S	175	Total 1429	C 916	N 252	O 259	S 2	0	0
1	T	175	Total 1429	C 916	N 252	O 259	S 2	0	0
1	U	175	Total 1429	C 916	N 252	O 259	S 2	0	0
1	V	175	Total 1429	C 916	N 252	O 259	S 2	0	0
1	W	175	Total 1429	C 916	N 252	O 259	S 2	0	0
1	X	175	Total 1429	C 916	N 252	O 259	S 2	0	0

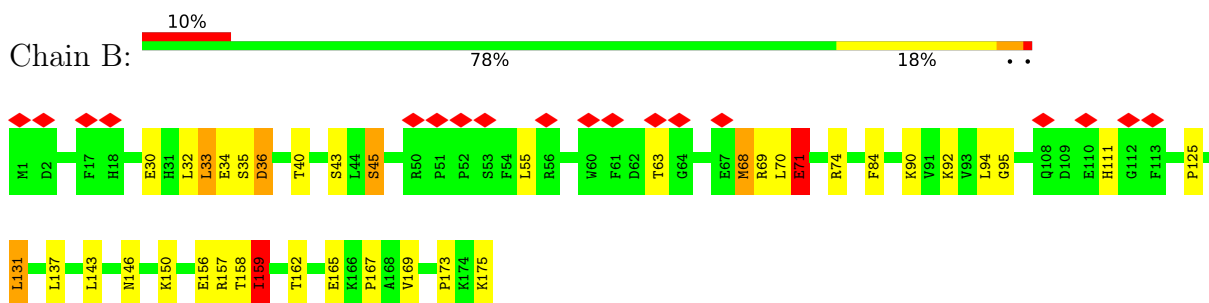
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

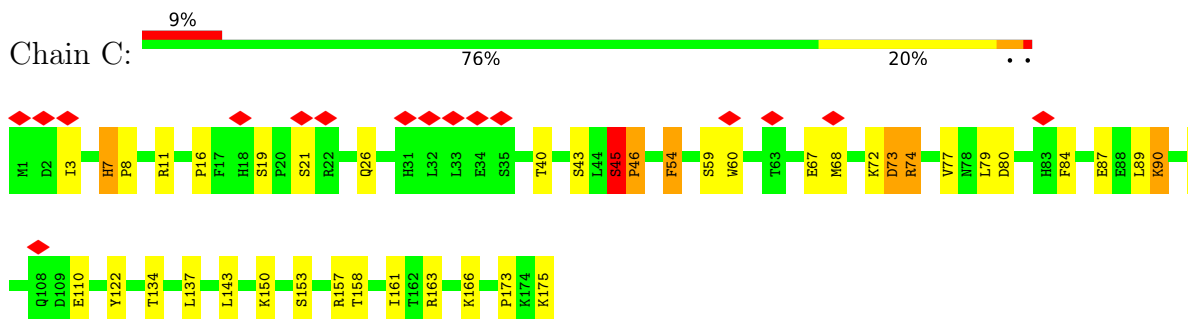
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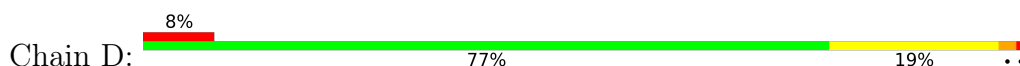
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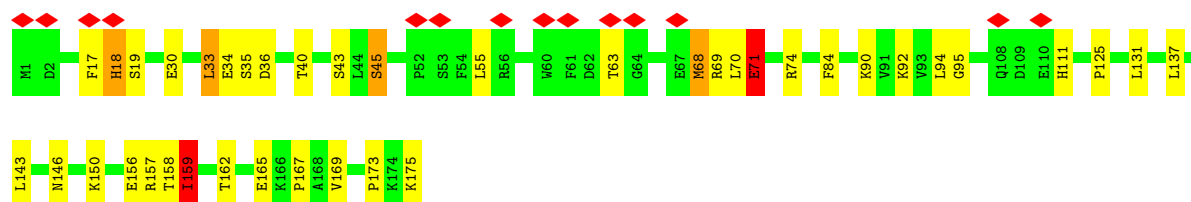


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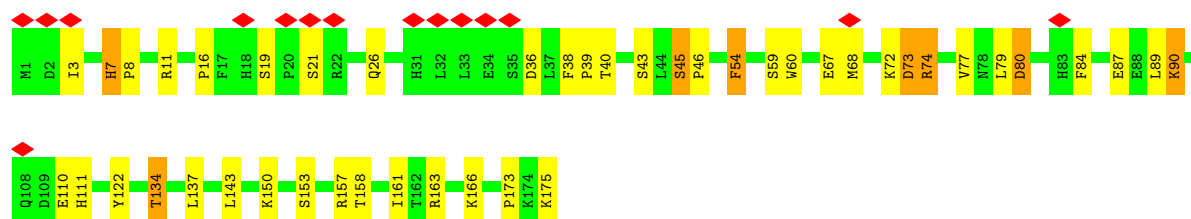
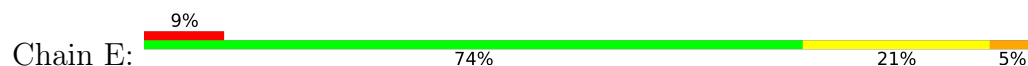


• Molecule 1: ALPHA-CRYSTALLIN B CHAIN

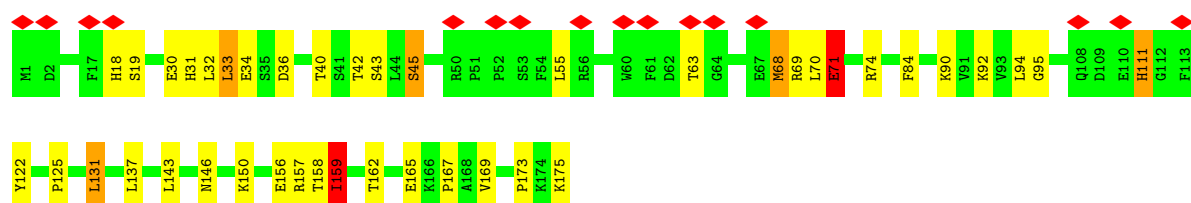
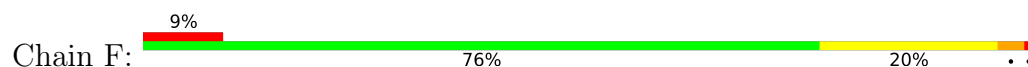




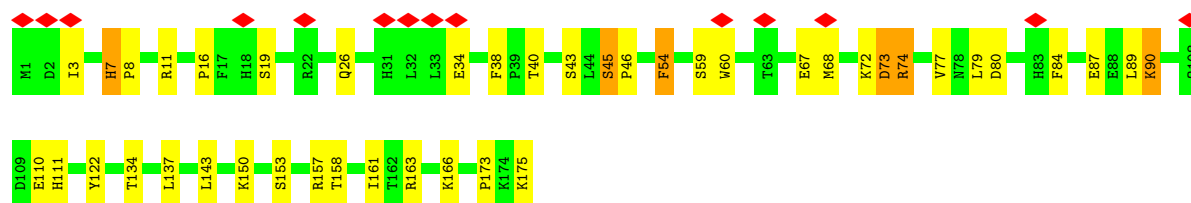
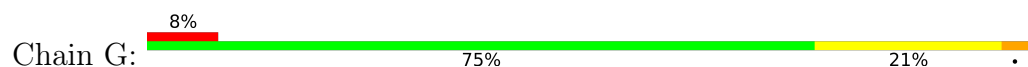
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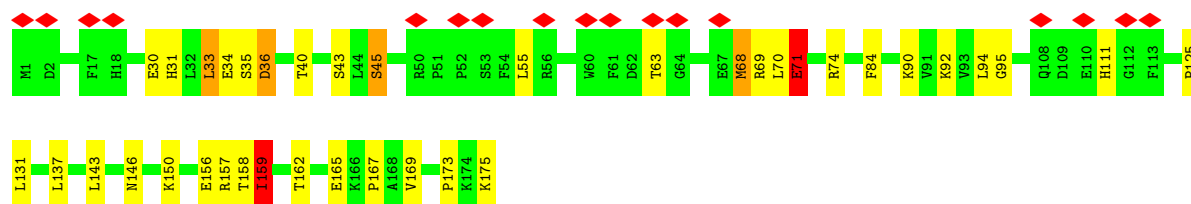
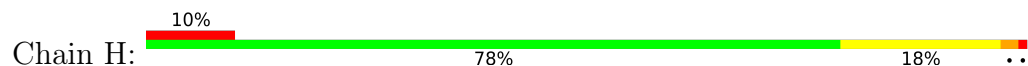
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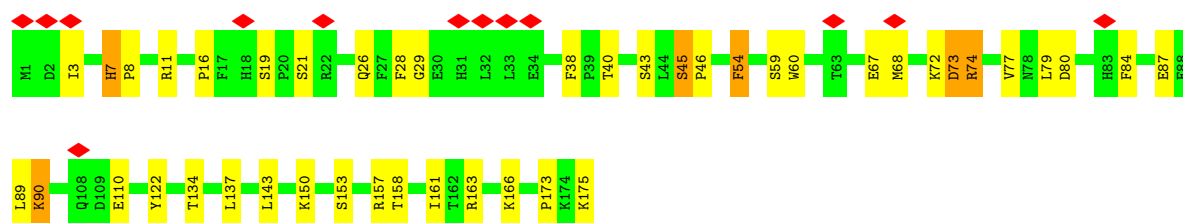
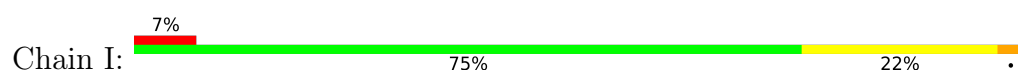
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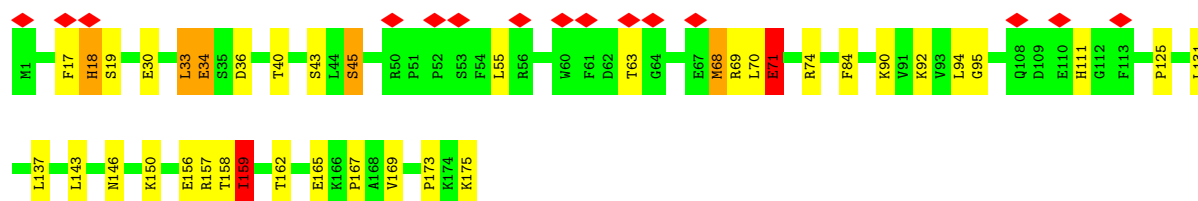
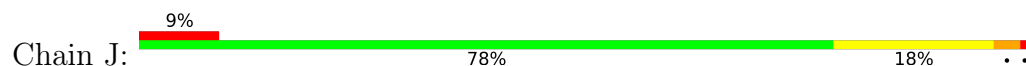
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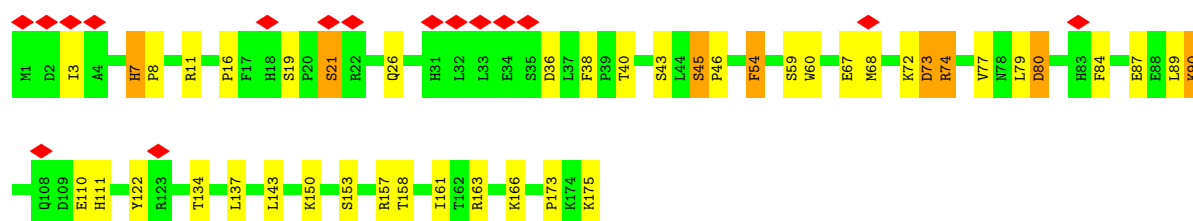
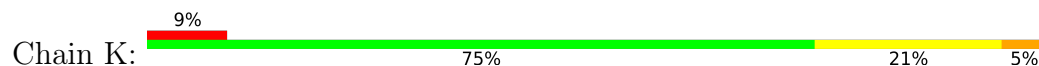
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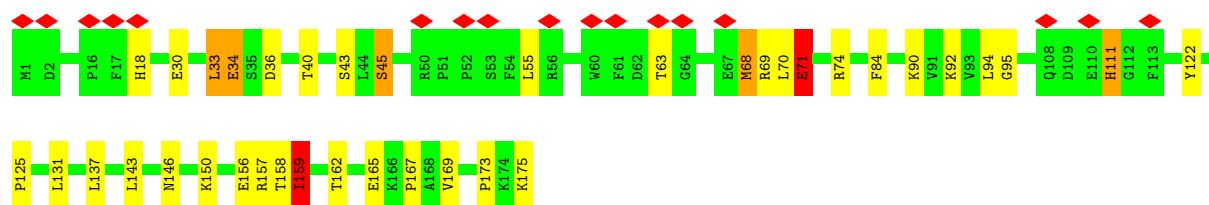
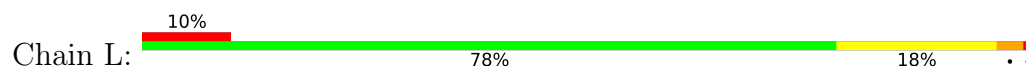
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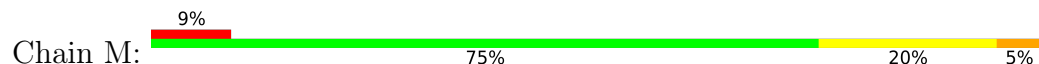
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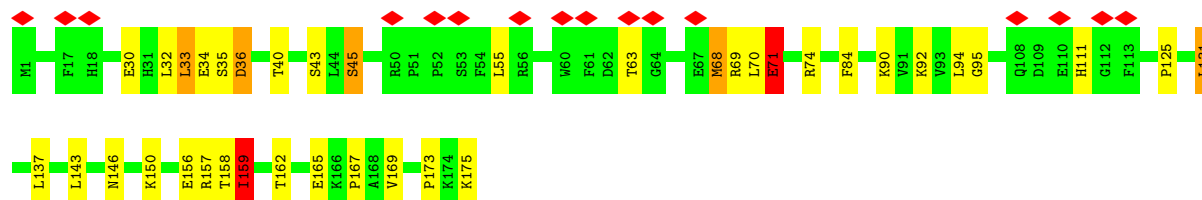
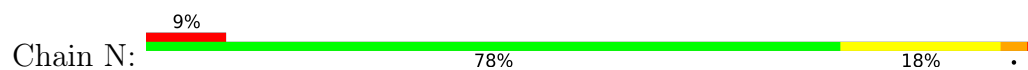


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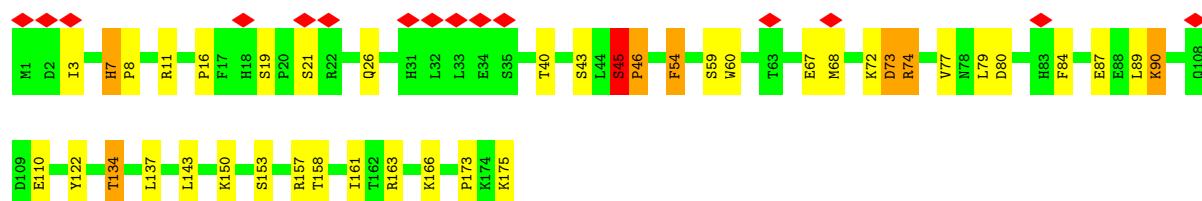
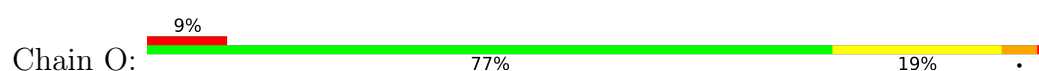




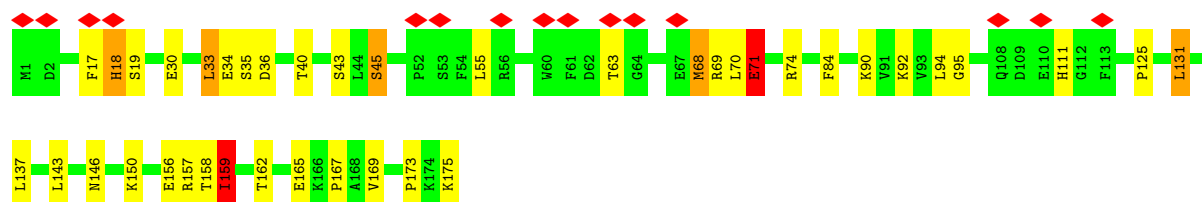
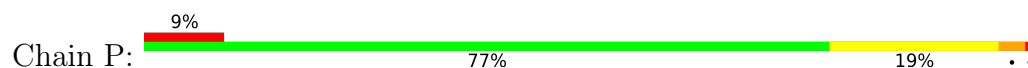
• Molecule 1: ALPHA-CRYSTALLIN B CHAIN



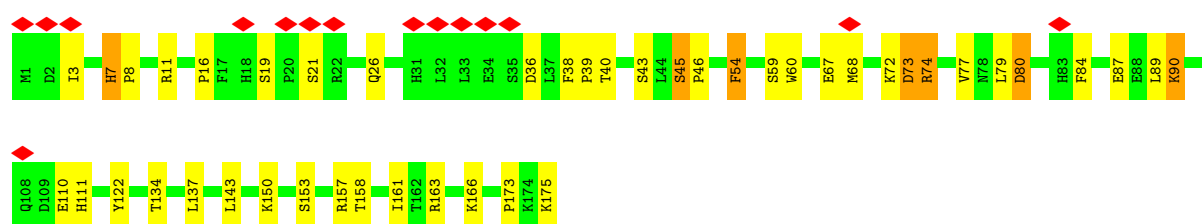
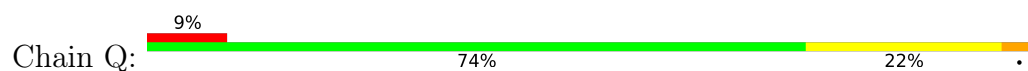
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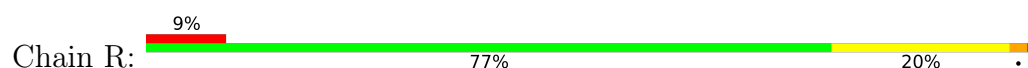
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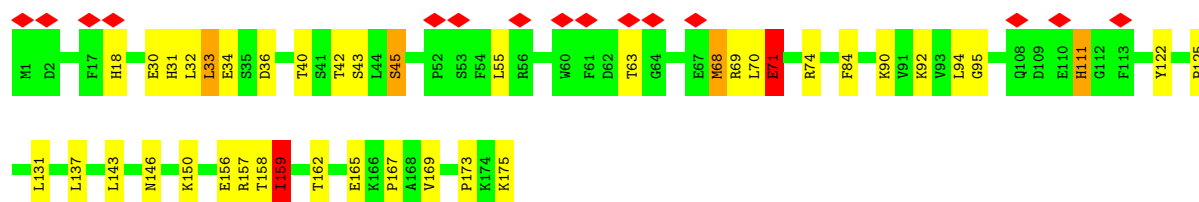


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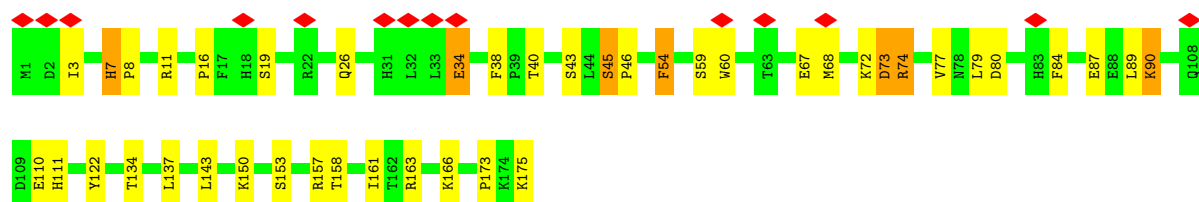
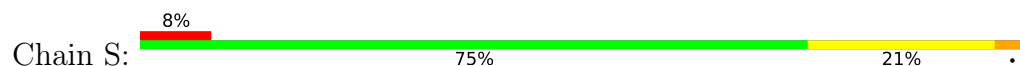


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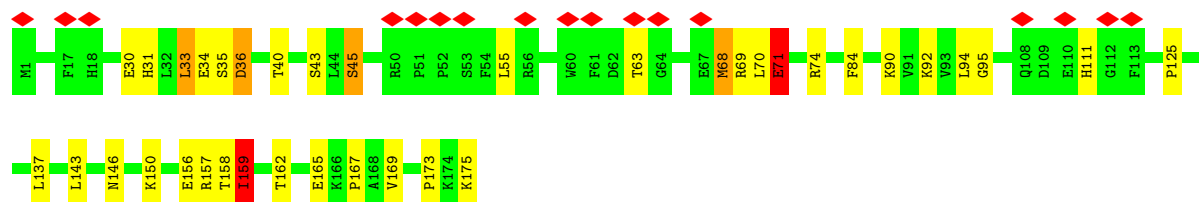
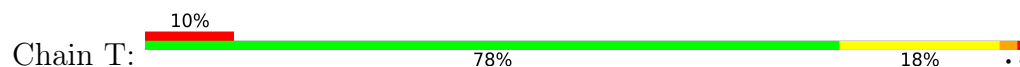




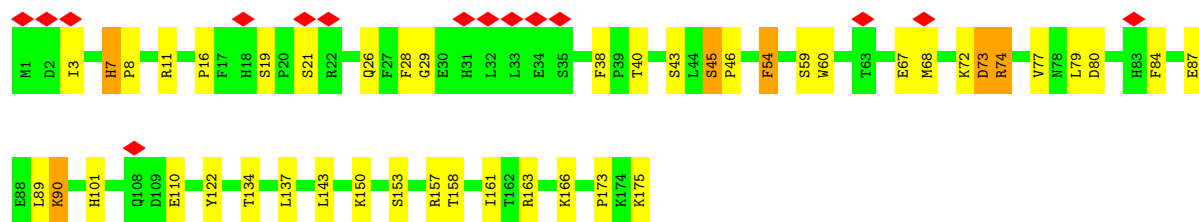
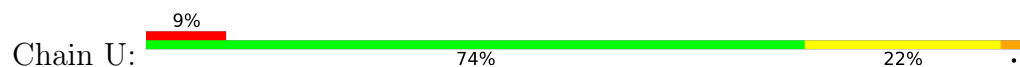
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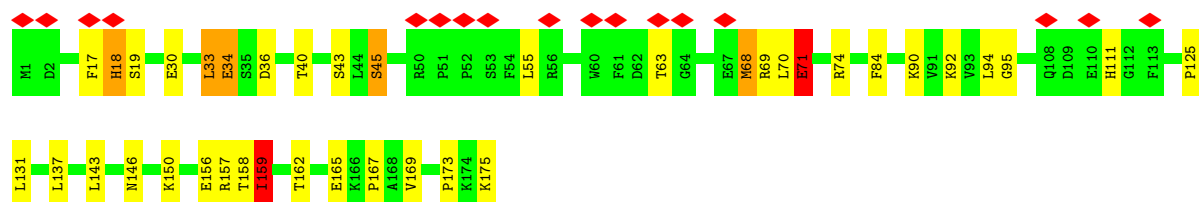
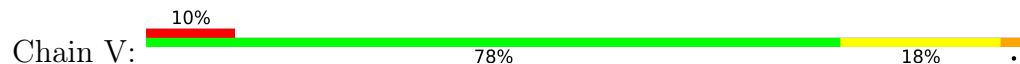
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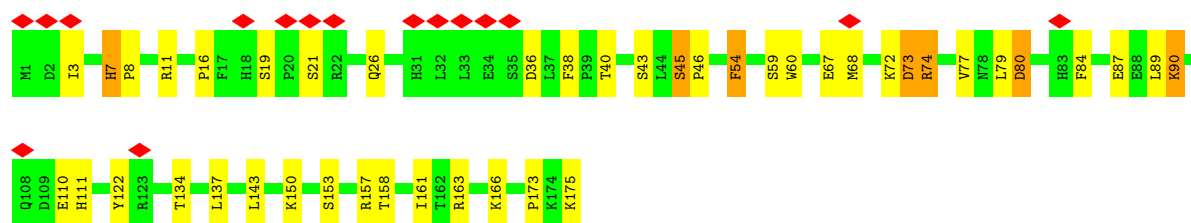
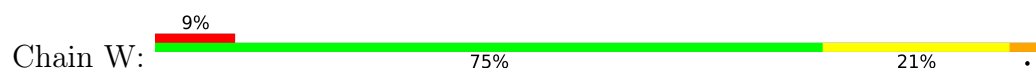
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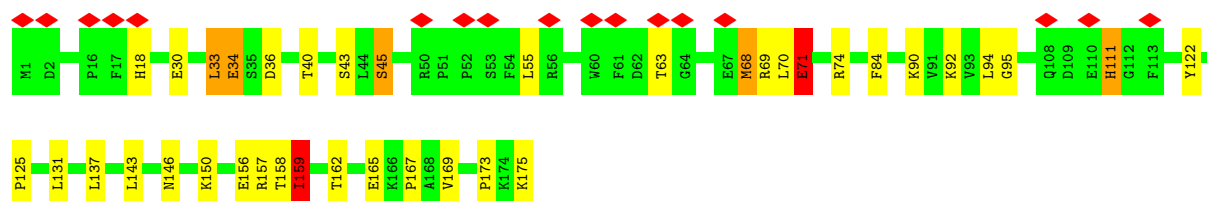
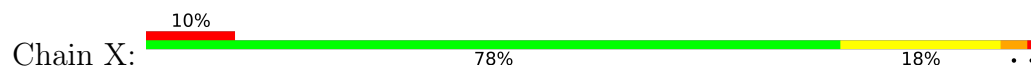
• Molecule 1: ALPHA-CRYSTALLIN B CHAIN



• Molecule 1: ALPHA-CRYSTALLIN B CHAIN



• Molecule 1: ALPHA-CRYSTALLIN B CHAIN



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	17560	Depositor
Resolution determination method	Not provided	
CTF correction method	EACH MICROGRAPH, PHASE FLIPPING	Depositor
Microscope	JEOL 2010HT	Depositor
Voltage (kV)	120	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	47000	Depositor
Image detector	Not provided	
Maximum map value	0.080	Depositor
Minimum map value	0.000	Depositor
Average map value	0.005	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.004	Depositor
Map size ($\text{\AA}$)	230.4, 230.4, 230.4	wwPDB
Map dimensions	128, 128, 128	wwPDB
Map angles ($^\circ$)	90, 90, 90	wwPDB
Pixel spacing ($\text{\AA}$)	1.8, 1.8, 1.8	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	0.85	0/1474	1.56	10/1997 (0.5%)
1	B	0.86	0/1474	1.54	8/1997 (0.4%)
1	C	0.86	0/1474	1.55	9/1997 (0.5%)
1	D	0.86	0/1474	1.53	6/1997 (0.3%)
1	E	0.86	0/1474	1.56	10/1997 (0.5%)
1	F	0.86	0/1474	1.55	11/1997 (0.6%)
1	G	0.86	0/1474	1.55	9/1997 (0.5%)
1	H	0.86	0/1474	1.53	6/1997 (0.3%)
1	I	0.86	0/1474	1.55	7/1997 (0.4%)
1	J	0.86	0/1474	1.53	6/1997 (0.3%)
1	K	0.86	0/1474	1.55	10/1997 (0.5%)
1	L	0.87	0/1474	1.54	7/1997 (0.4%)
1	M	0.86	0/1474	1.56	10/1997 (0.5%)
1	N	0.86	0/1474	1.54	8/1997 (0.4%)
1	O	0.86	0/1474	1.55	7/1997 (0.4%)
1	P	0.86	0/1474	1.53	6/1997 (0.3%)
1	Q	0.86	0/1474	1.56	10/1997 (0.5%)
1	R	0.86	0/1474	1.55	9/1997 (0.5%)
1	S	0.86	0/1474	1.55	9/1997 (0.5%)
1	T	0.86	0/1474	1.53	6/1997 (0.3%)
1	U	0.86	0/1474	1.55	9/1997 (0.5%)
1	V	0.86	0/1474	1.53	6/1997 (0.3%)
1	W	0.85	0/1474	1.55	10/1997 (0.5%)
1	X	0.87	0/1474	1.54	7/1997 (0.4%)
All	All	0.86	0/35376	1.55	196/47928 (0.4%)

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	10

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	3
1	C	0	9
1	D	0	3
1	E	0	10
1	F	0	3
1	G	0	10
1	H	0	3
1	I	0	10
1	J	0	2
1	K	0	10
1	L	0	3
1	M	0	10
1	N	0	3
1	O	0	9
1	P	0	3
1	Q	0	10
1	R	0	3
1	S	0	10
1	T	0	3
1	U	0	10
1	V	0	2
1	W	0	10
1	X	0	3
All	All	0	152

There are no bond length outliers.

All (196) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	36	ASP	CA-CB-CG	9.17	121.77	112.60
1	M	36	ASP	CA-CB-CG	9.11	121.71	112.60
1	I	54	PHE	CA-CB-CG	8.44	122.24	113.80
1	C	54	PHE	CA-CB-CG	8.43	122.23	113.80
1	K	54	PHE	CA-CB-CG	8.42	122.22	113.80
1	W	54	PHE	CA-CB-CG	8.40	122.20	113.80
1	Q	54	PHE	CA-CB-CG	8.39	122.19	113.80
1	U	54	PHE	CA-CB-CG	8.38	122.18	113.80
1	O	54	PHE	CA-CB-CG	8.38	122.18	113.80
1	E	54	PHE	CA-CB-CG	8.38	122.18	113.80
1	M	54	PHE	CA-CB-CG	8.33	122.13	113.80
1	A	54	PHE	CA-CB-CG	8.29	122.09	113.80
1	G	54	PHE	CA-CB-CG	8.23	122.03	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	54	PHE	CA-CB-CG	8.23	122.03	113.80
1	G	84	PHE	CA-CB-CG	7.18	120.98	113.80
1	K	84	PHE	CA-CB-CG	7.17	120.97	113.80
1	E	84	PHE	CA-CB-CG	7.17	120.97	113.80
1	Q	84	PHE	CA-CB-CG	7.16	120.96	113.80
1	A	84	PHE	CA-CB-CG	7.15	120.95	113.80
1	M	84	PHE	CA-CB-CG	7.13	120.93	113.80
1	W	84	PHE	CA-CB-CG	7.12	120.92	113.80
1	S	84	PHE	CA-CB-CG	7.12	120.92	113.80
1	U	84	PHE	CA-CB-CG	7.06	120.86	113.80
1	I	84	PHE	CA-CB-CG	7.04	120.84	113.80
1	C	84	PHE	CA-CB-CG	7.03	120.83	113.80
1	O	84	PHE	CA-CB-CG	7.01	120.81	113.80
1	E	36	ASP	CA-CB-CG	6.97	119.57	112.60
1	Q	36	ASP	CA-CB-CG	6.97	119.57	112.60
1	S	111	HIS	CA-C-N	6.76	127.26	122.33
1	S	111	HIS	C-N-CA	6.76	127.26	122.33
1	A	111	HIS	CA-C-N	6.70	127.22	122.33
1	A	111	HIS	C-N-CA	6.70	127.22	122.33
1	M	111	HIS	CA-C-N	6.70	127.22	122.33
1	M	111	HIS	C-N-CA	6.70	127.22	122.33
1	G	111	HIS	CA-C-N	6.63	127.17	122.33
1	G	111	HIS	C-N-CA	6.63	127.17	122.33
1	W	68	MET	CA-C-N	6.40	133.22	121.70
1	W	68	MET	C-N-CA	6.40	133.22	121.70
1	E	68	MET	CA-C-N	6.39	133.21	121.70
1	E	68	MET	C-N-CA	6.39	133.21	121.70
1	U	68	MET	CA-C-N	6.39	133.21	121.70
1	U	68	MET	C-N-CA	6.39	133.21	121.70
1	K	68	MET	CA-C-N	6.39	133.20	121.70
1	K	68	MET	C-N-CA	6.39	133.20	121.70
1	A	68	MET	CA-C-N	6.38	133.19	121.70
1	A	68	MET	C-N-CA	6.38	133.19	121.70
1	I	68	MET	CA-C-N	6.38	133.19	121.70
1	I	68	MET	C-N-CA	6.38	133.19	121.70
1	O	68	MET	CA-C-N	6.38	133.19	121.70
1	O	68	MET	C-N-CA	6.38	133.19	121.70
1	C	68	MET	CA-C-N	6.38	133.18	121.70
1	C	68	MET	C-N-CA	6.38	133.18	121.70
1	M	68	MET	CA-C-N	6.37	133.17	121.70
1	M	68	MET	C-N-CA	6.37	133.17	121.70
1	G	68	MET	CA-C-N	6.37	133.16	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	68	MET	C-N-CA	6.37	133.16	121.70
1	Q	68	MET	CA-C-N	6.36	133.15	121.70
1	Q	68	MET	C-N-CA	6.36	133.15	121.70
1	S	68	MET	CA-C-N	6.36	133.14	121.70
1	S	68	MET	C-N-CA	6.36	133.14	121.70
1	W	36	ASP	CA-CB-CG	6.18	118.78	112.60
1	K	36	ASP	CA-CB-CG	6.17	118.77	112.60
1	B	32	LEU	CA-C-N	6.01	130.76	120.72
1	B	32	LEU	C-N-CA	6.01	130.76	120.72
1	E	111	HIS	CA-C-N	6.00	126.71	122.33
1	E	111	HIS	C-N-CA	6.00	126.71	122.33
1	N	32	LEU	CA-C-N	5.99	130.72	120.72
1	N	32	LEU	C-N-CA	5.99	130.72	120.72
1	K	111	HIS	CA-C-N	5.96	126.68	122.33
1	K	111	HIS	C-N-CA	5.96	126.68	122.33
1	Q	111	HIS	CA-C-N	5.96	126.68	122.33
1	Q	111	HIS	C-N-CA	5.96	126.68	122.33
1	W	111	HIS	CA-C-N	5.96	126.68	122.33
1	W	111	HIS	C-N-CA	5.96	126.68	122.33
1	L	68	MET	CA-C-N	5.64	131.85	121.70
1	L	68	MET	C-N-CA	5.64	131.85	121.70
1	R	111	HIS	CA-CB-CG	5.61	119.41	113.80
1	X	111	HIS	CA-CB-CG	5.61	119.41	113.80
1	B	68	MET	CA-C-N	5.61	131.79	121.70
1	B	68	MET	C-N-CA	5.61	131.79	121.70
1	D	68	MET	CA-C-N	5.60	131.79	121.70
1	D	68	MET	C-N-CA	5.60	131.79	121.70
1	P	68	MET	CA-C-N	5.60	131.79	121.70
1	P	68	MET	C-N-CA	5.60	131.79	121.70
1	J	68	MET	CA-C-N	5.60	131.78	121.70
1	J	68	MET	C-N-CA	5.60	131.78	121.70
1	V	68	MET	CA-C-N	5.60	131.78	121.70
1	V	68	MET	C-N-CA	5.60	131.78	121.70
1	X	68	MET	CA-C-N	5.60	131.78	121.70
1	X	68	MET	C-N-CA	5.60	131.78	121.70
1	T	68	MET	CA-C-N	5.60	131.78	121.70
1	T	68	MET	C-N-CA	5.60	131.78	121.70
1	F	68	MET	CA-C-N	5.60	131.77	121.70
1	F	68	MET	C-N-CA	5.60	131.77	121.70
1	L	111	HIS	CA-CB-CG	5.59	119.39	113.80
1	N	68	MET	CA-C-N	5.59	131.76	121.70
1	N	68	MET	C-N-CA	5.59	131.76	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	68	MET	CA-C-N	5.58	131.75	121.70
1	R	68	MET	C-N-CA	5.58	131.75	121.70
1	F	111	HIS	CA-CB-CG	5.58	119.38	113.80
1	H	68	MET	CA-C-N	5.58	131.74	121.70
1	H	68	MET	C-N-CA	5.58	131.74	121.70
1	N	69	ARG	CA-C-N	5.55	132.14	121.54
1	N	69	ARG	C-N-CA	5.55	132.14	121.54
1	J	69	ARG	CA-C-N	5.55	132.13	121.54
1	J	69	ARG	C-N-CA	5.55	132.13	121.54
1	D	69	ARG	CA-C-N	5.54	132.12	121.54
1	D	69	ARG	C-N-CA	5.54	132.12	121.54
1	H	69	ARG	CA-C-N	5.54	132.12	121.54
1	H	69	ARG	C-N-CA	5.54	132.12	121.54
1	L	69	ARG	CA-C-N	5.54	132.12	121.54
1	L	69	ARG	C-N-CA	5.54	132.12	121.54
1	F	69	ARG	CA-C-N	5.54	132.11	121.54
1	F	69	ARG	C-N-CA	5.54	132.11	121.54
1	R	69	ARG	CA-C-N	5.54	132.11	121.54
1	R	69	ARG	C-N-CA	5.54	132.11	121.54
1	V	69	ARG	CA-C-N	5.53	132.11	121.54
1	V	69	ARG	C-N-CA	5.53	132.11	121.54
1	X	69	ARG	CA-C-N	5.53	132.11	121.54
1	X	69	ARG	C-N-CA	5.53	132.11	121.54
1	B	69	ARG	CA-C-N	5.53	132.09	121.54
1	B	69	ARG	C-N-CA	5.53	132.09	121.54
1	T	69	ARG	CA-C-N	5.52	132.09	121.54
1	T	69	ARG	C-N-CA	5.52	132.09	121.54
1	P	69	ARG	CA-C-N	5.52	132.09	121.54
1	P	69	ARG	C-N-CA	5.52	132.09	121.54
1	K	161	ILE	CA-C-N	5.45	128.34	120.38
1	K	161	ILE	C-N-CA	5.45	128.34	120.38
1	U	161	ILE	CA-C-N	5.45	128.33	120.38
1	U	161	ILE	C-N-CA	5.45	128.33	120.38
1	E	161	ILE	CA-C-N	5.44	128.33	120.38
1	E	161	ILE	C-N-CA	5.44	128.33	120.38
1	O	161	ILE	CA-C-N	5.44	128.33	120.38
1	O	161	ILE	C-N-CA	5.44	128.33	120.38
1	M	161	ILE	CA-C-N	5.44	128.32	120.38
1	M	161	ILE	C-N-CA	5.44	128.32	120.38
1	G	161	ILE	CA-C-N	5.44	128.32	120.38
1	G	161	ILE	C-N-CA	5.44	128.32	120.38
1	S	161	ILE	CA-C-N	5.43	128.31	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	161	ILE	C-N-CA	5.43	128.31	120.38
1	W	161	ILE	CA-C-N	5.43	128.32	120.38
1	W	161	ILE	C-N-CA	5.43	128.32	120.38
1	C	161	ILE	CA-C-N	5.43	128.31	120.38
1	C	161	ILE	C-N-CA	5.43	128.31	120.38
1	A	161	ILE	CA-C-N	5.43	128.31	120.38
1	A	161	ILE	C-N-CA	5.43	128.31	120.38
1	Q	161	ILE	CA-C-N	5.41	128.28	120.38
1	Q	161	ILE	C-N-CA	5.41	128.28	120.38
1	I	161	ILE	CA-C-N	5.39	128.25	120.38
1	I	161	ILE	C-N-CA	5.39	128.25	120.38
1	F	32	LEU	CA-C-N	5.31	130.43	121.14
1	F	32	LEU	C-N-CA	5.31	130.43	121.14
1	N	156	GLU	CA-C-N	5.31	131.68	121.54
1	N	156	GLU	C-N-CA	5.31	131.68	121.54
1	R	32	LEU	CA-C-N	5.30	130.42	121.14
1	R	32	LEU	C-N-CA	5.30	130.42	121.14
1	T	156	GLU	CA-C-N	5.30	131.66	121.54
1	T	156	GLU	C-N-CA	5.30	131.66	121.54
1	P	156	GLU	CA-C-N	5.29	131.65	121.54
1	P	156	GLU	C-N-CA	5.29	131.65	121.54
1	V	156	GLU	CA-C-N	5.29	131.65	121.54
1	V	156	GLU	C-N-CA	5.29	131.65	121.54
1	H	156	GLU	CA-C-N	5.29	131.65	121.54
1	H	156	GLU	C-N-CA	5.29	131.65	121.54
1	L	156	GLU	CA-C-N	5.29	131.65	121.54
1	L	156	GLU	C-N-CA	5.29	131.65	121.54
1	R	156	GLU	CA-C-N	5.29	131.64	121.54
1	R	156	GLU	C-N-CA	5.29	131.64	121.54
1	F	156	GLU	CA-C-N	5.28	131.62	121.54
1	F	156	GLU	C-N-CA	5.28	131.62	121.54
1	X	156	GLU	CA-C-N	5.28	131.62	121.54
1	X	156	GLU	C-N-CA	5.28	131.62	121.54
1	B	156	GLU	CA-C-N	5.27	131.60	121.54
1	B	156	GLU	C-N-CA	5.27	131.60	121.54
1	D	156	GLU	CA-C-N	5.26	131.60	121.54
1	D	156	GLU	C-N-CA	5.26	131.60	121.54
1	J	156	GLU	CA-C-N	5.26	131.58	121.54
1	J	156	GLU	C-N-CA	5.26	131.58	121.54
1	S	68	MET	O-C-N	-5.25	116.28	122.58
1	I	68	MET	O-C-N	-5.23	116.31	122.58
1	G	68	MET	O-C-N	-5.22	116.31	122.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	68	MET	O-C-N	-5.22	116.32	122.58
1	M	68	MET	O-C-N	-5.21	116.33	122.58
1	E	68	MET	O-C-N	-5.21	116.33	122.58
1	A	68	MET	O-C-N	-5.20	116.34	122.58
1	C	68	MET	O-C-N	-5.20	116.34	122.58
1	U	68	MET	O-C-N	-5.20	116.34	122.58
1	K	68	MET	O-C-N	-5.20	116.34	122.58
1	W	68	MET	O-C-N	-5.20	116.34	122.58
1	O	68	MET	O-C-N	-5.18	116.36	122.58
1	U	101	HIS	CA-C-N	5.05	126.02	122.33
1	U	101	HIS	C-N-CA	5.05	126.02	122.33
1	F	19	SER	CA-C-N	5.02	126.02	120.45
1	F	19	SER	C-N-CA	5.02	126.02	120.45
1	C	101	HIS	CA-C-N	5.00	125.98	122.33
1	C	101	HIS	C-N-CA	5.00	125.98	122.33

There are no chirality outliers.

All (152) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	11	ARG	Sidechain
1	A	134	THR	Peptide
1	A	150	LYS	Peptide
1	A	157	ARG	Peptide
1	A	38	PHE	Peptide
1	A	45	SER	Peptide
1	A	46	PRO	Peptide
1	A	72	LYS	Peptide
1	A	74	ARG	Peptide
1	A	80	ASP	Peptide
1	B	165	GLU	Peptide
1	B	35	SER	Peptide
1	B	43	SER	Peptide
1	C	11	ARG	Sidechain
1	C	134	THR	Peptide
1	C	150	LYS	Peptide
1	C	157	ARG	Peptide
1	C	45	SER	Peptide
1	C	46	PRO	Peptide
1	C	72	LYS	Peptide
1	C	74	ARG	Peptide
1	C	80	ASP	Peptide

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Mol	Chain	Res	Type	Group
1	D	165	GLU	Peptide
1	D	35	SER	Peptide
1	D	43	SER	Peptide
1	E	11	ARG	Sidechain
1	E	134	THR	Peptide
1	E	150	LYS	Peptide
1	E	157	ARG	Peptide
1	E	38	PHE	Peptide
1	E	45	SER	Peptide
1	E	46	PRO	Peptide
1	E	72	LYS	Peptide
1	E	74	ARG	Peptide
1	E	80	ASP	Peptide
1	F	122	TYR	Sidechain
1	F	165	GLU	Peptide
1	F	43	SER	Peptide
1	G	11	ARG	Sidechain
1	G	134	THR	Peptide
1	G	150	LYS	Peptide
1	G	157	ARG	Peptide
1	G	38	PHE	Peptide
1	G	45	SER	Peptide
1	G	46	PRO	Peptide
1	G	72	LYS	Peptide
1	G	74	ARG	Peptide
1	G	80	ASP	Peptide
1	H	165	GLU	Peptide
1	H	35	SER	Peptide
1	H	43	SER	Peptide
1	I	11	ARG	Sidechain
1	I	134	THR	Peptide
1	I	150	LYS	Peptide
1	I	157	ARG	Peptide
1	I	38	PHE	Peptide
1	I	45	SER	Peptide
1	I	46	PRO	Peptide
1	I	72	LYS	Peptide
1	I	74	ARG	Peptide
1	I	80	ASP	Peptide
1	J	165	GLU	Peptide
1	J	43	SER	Peptide
1	K	11	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	K	134	THR	Peptide
1	K	150	LYS	Peptide
1	K	157	ARG	Peptide
1	K	38	PHE	Peptide
1	K	45	SER	Peptide
1	K	46	PRO	Peptide
1	K	72	LYS	Peptide
1	K	74	ARG	Peptide
1	K	80	ASP	Peptide
1	L	122	TYR	Sidechain
1	L	165	GLU	Peptide
1	L	43	SER	Peptide
1	M	11	ARG	Sidechain
1	M	134	THR	Peptide
1	M	150	LYS	Peptide
1	M	157	ARG	Peptide
1	M	38	PHE	Peptide
1	M	45	SER	Peptide
1	M	46	PRO	Peptide
1	M	72	LYS	Peptide
1	M	74	ARG	Peptide
1	M	80	ASP	Peptide
1	N	165	GLU	Peptide
1	N	35	SER	Peptide
1	N	43	SER	Peptide
1	O	11	ARG	Sidechain
1	O	134	THR	Peptide
1	O	150	LYS	Peptide
1	O	157	ARG	Peptide
1	O	45	SER	Peptide
1	O	46	PRO	Peptide
1	O	72	LYS	Peptide
1	O	74	ARG	Peptide
1	O	80	ASP	Peptide
1	P	165	GLU	Peptide
1	P	35	SER	Peptide
1	P	43	SER	Peptide
1	Q	11	ARG	Sidechain
1	Q	134	THR	Peptide
1	Q	150	LYS	Peptide
1	Q	157	ARG	Peptide
1	Q	38	PHE	Peptide

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Mol	Chain	Res	Type	Group
1	Q	45	SER	Peptide
1	Q	46	PRO	Peptide
1	Q	72	LYS	Peptide
1	Q	74	ARG	Peptide
1	Q	80	ASP	Peptide
1	R	122	TYR	Sidechain
1	R	165	GLU	Peptide
1	R	43	SER	Peptide
1	S	11	ARG	Sidechain
1	S	134	THR	Peptide
1	S	150	LYS	Peptide
1	S	157	ARG	Peptide
1	S	38	PHE	Peptide
1	S	45	SER	Peptide
1	S	46	PRO	Peptide
1	S	72	LYS	Peptide
1	S	74	ARG	Peptide
1	S	80	ASP	Peptide
1	T	165	GLU	Peptide
1	T	35	SER	Peptide
1	T	43	SER	Peptide
1	U	11	ARG	Sidechain
1	U	134	THR	Peptide
1	U	150	LYS	Peptide
1	U	157	ARG	Peptide
1	U	38	PHE	Peptide
1	U	45	SER	Peptide
1	U	46	PRO	Peptide
1	U	72	LYS	Peptide
1	U	74	ARG	Peptide
1	U	80	ASP	Peptide
1	V	165	GLU	Peptide
1	V	43	SER	Peptide
1	W	11	ARG	Sidechain
1	W	134	THR	Peptide
1	W	150	LYS	Peptide
1	W	157	ARG	Peptide
1	W	38	PHE	Peptide
1	W	45	SER	Peptide
1	W	46	PRO	Peptide
1	W	72	LYS	Peptide
1	W	74	ARG	Peptide

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Mol	Chain	Res	Type	Group
1	W	80	ASP	Peptide
1	X	122	TYR	Sidechain
1	X	165	GLU	Peptide
1	X	43	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	1429	0	1407	12	0
1	B	1429	0	1407	12	0
1	C	1429	0	1407	7	0
1	D	1429	0	1407	12	0
1	E	1429	0	1407	8	0
1	F	1429	0	1407	13	0
1	G	1429	0	1407	8	0
1	H	1429	0	1407	11	0
1	I	1429	0	1407	7	0
1	J	1429	0	1407	13	0
1	K	1429	0	1407	7	0
1	L	1429	0	1407	10	0
1	M	1429	0	1407	11	0
1	N	1429	0	1407	13	0
1	O	1429	0	1407	8	0
1	P	1429	0	1407	13	0
1	Q	1429	0	1407	7	0
1	R	1429	0	1407	13	0
1	S	1429	0	1407	9	0
1	T	1429	0	1407	10	0
1	U	1429	0	1407	7	0
1	V	1429	0	1407	13	0
1	W	1429	0	1407	6	0
1	X	1429	0	1407	10	0
All	All	34296	0	33768	165	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 2.

All (165) 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:F:33:LEU:HD12	1:F:33:LEU:H	1.60	0.66
1:R:33:LEU:H	1:R:33:LEU:HD12	1.60	0.66
1:C:122:TYR:CE2	1:F:111:HIS:HB3	2.39	0.58
1:O:122:TYR:CE2	1:R:111:HIS:HB3	2.39	0.58
1:I:122:TYR:CE2	1:L:111:HIS:HB3	2.39	0.58
1:U:122:TYR:CE2	1:X:111:HIS:HB3	2.39	0.58
1:H:71:GLU:H	1:H:167:PRO:CD	2.20	0.55
1:T:71:GLU:H	1:T:167:PRO:CD	2.20	0.55
1:D:71:GLU:H	1:D:167:PRO:CD	2.20	0.55
1:P:71:GLU:H	1:P:167:PRO:CD	2.20	0.55
1:B:71:GLU:H	1:B:167:PRO:CD	2.20	0.54
1:N:71:GLU:H	1:N:167:PRO:CD	2.20	0.54
1:L:71:GLU:H	1:L:167:PRO:CD	2.20	0.54
1:J:71:GLU:H	1:J:167:PRO:CD	2.20	0.53
1:F:71:GLU:H	1:F:167:PRO:CD	2.20	0.53
1:R:71:GLU:H	1:R:167:PRO:CD	2.20	0.53
1:X:71:GLU:H	1:X:167:PRO:CD	2.20	0.53
1:V:71:GLU:H	1:V:167:PRO:CD	2.20	0.53
1:N:33:LEU:H	1:N:33:LEU:HD12	1.75	0.52
1:B:33:LEU:HD12	1:B:33:LEU:H	1.75	0.52
1:K:90:LYS:HE3	1:L:94:LEU:HD13	1.93	0.51
1:A:90:LYS:HE3	1:B:94:LEU:HD13	1.93	0.51
1:M:90:LYS:HE3	1:N:94:LEU:HD13	1.93	0.51
1:W:90:LYS:HE3	1:X:94:LEU:HD13	1.93	0.51
1:C:90:LYS:HE3	1:D:94:LEU:HD13	1.93	0.51
1:O:90:LYS:HE3	1:P:94:LEU:HD13	1.93	0.51
1:B:111:HIS:HB3	1:E:122:TYR:CE2	2.47	0.50
1:T:111:HIS:HB3	1:W:122:TYR:CE2	2.47	0.50
1:G:90:LYS:HE3	1:H:94:LEU:HD13	1.93	0.50
1:H:111:HIS:HB3	1:K:122:TYR:CE2	2.47	0.50
1:N:111:HIS:HB3	1:Q:122:TYR:CE2	2.47	0.50
1:S:90:LYS:HE3	1:T:94:LEU:HD13	1.93	0.50
1:E:90:LYS:HE3	1:F:94:LEU:HD13	1.92	0.50
1:I:90:LYS:HE3	1:J:94:LEU:HD13	1.93	0.50
1:U:90:LYS:HE3	1:V:94:LEU:HD13	1.93	0.50
1:A:90:LYS:HE3	1:B:94:LEU:CD1	2.42	0.50
1:W:90:LYS:HE3	1:X:94:LEU:CD1	2.42	0.50
1:C:90:LYS:HE3	1:D:94:LEU:CD1	2.42	0.50
1:M:90:LYS:HE3	1:N:94:LEU:CD1	2.42	0.50
1:O:90:LYS:HE3	1:P:94:LEU:CD1	2.42	0.50
1:Q:90:LYS:HE3	1:R:94:LEU:HD13	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:90:LYS:HE3	1:L:94:LEU:CD1	2.42	0.49
1:E:90:LYS:HE3	1:F:94:LEU:CD1	2.41	0.49
1:Q:90:LYS:HE3	1:R:94:LEU:CD1	2.42	0.49
1:C:7:HIS:H	1:C:8:PRO:CD	2.25	0.49
1:O:7:HIS:H	1:O:8:PRO:CD	2.25	0.49
1:G:90:LYS:HE3	1:H:94:LEU:CD1	2.42	0.49
1:S:90:LYS:HE3	1:T:94:LEU:CD1	2.42	0.49
1:U:90:LYS:HE3	1:V:94:LEU:CD1	2.42	0.49
1:I:90:LYS:HE3	1:J:94:LEU:CD1	2.42	0.49
1:S:7:HIS:H	1:S:8:PRO:CD	2.26	0.49
1:T:33:LEU:HD12	1:T:33:LEU:H	1.78	0.49
1:H:33:LEU:HD12	1:H:33:LEU:H	1.78	0.49
1:A:7:HIS:H	1:A:8:PRO:CD	2.26	0.48
1:G:7:HIS:H	1:G:8:PRO:CD	2.26	0.48
1:M:7:HIS:H	1:M:8:PRO:CD	2.26	0.48
1:K:7:HIS:H	1:K:8:PRO:CD	2.27	0.47
1:W:7:HIS:H	1:W:8:PRO:CD	2.27	0.47
1:Q:7:HIS:H	1:Q:8:PRO:CD	2.27	0.47
1:E:7:HIS:H	1:E:8:PRO:CD	2.27	0.47
1:S:77:VAL:HG11	1:S:122:TYR:CE2	2.50	0.47
1:G:77:VAL:HG11	1:G:122:TYR:CE2	2.50	0.47
1:J:159:ILE:HD12	1:J:159:ILE:H	1.80	0.47
1:B:33:LEU:HD13	1:J:33:LEU:HD21	1.97	0.47
1:I:7:HIS:H	1:I:8:PRO:CD	2.27	0.47
1:N:33:LEU:HD13	1:V:33:LEU:HD21	1.97	0.47
1:T:159:ILE:H	1:T:159:ILE:HD12	1.80	0.47
1:V:159:ILE:HD12	1:V:159:ILE:H	1.80	0.47
1:D:159:ILE:HD12	1:D:159:ILE:H	1.80	0.47
1:P:159:ILE:H	1:P:159:ILE:HD12	1.80	0.47
1:U:7:HIS:H	1:U:8:PRO:CD	2.27	0.47
1:H:159:ILE:HD12	1:H:159:ILE:H	1.80	0.46
1:A:77:VAL:HG11	1:A:122:TYR:CE2	2.50	0.46
1:M:77:VAL:HG11	1:M:122:TYR:CE2	2.50	0.46
1:R:159:ILE:HD12	1:R:159:ILE:H	1.80	0.46
1:B:33:LEU:CD2	1:R:33:LEU:HD13	2.46	0.46
1:F:33:LEU:HD13	1:N:33:LEU:CD2	2.46	0.46
1:F:159:ILE:H	1:F:159:ILE:HD12	1.81	0.46
1:C:77:VAL:HG11	1:C:122:TYR:CE2	2.51	0.46
1:I:77:VAL:HG11	1:I:122:TYR:CE2	2.51	0.46
1:O:77:VAL:HG11	1:O:122:TYR:CE2	2.51	0.46
1:U:77:VAL:HG11	1:U:122:TYR:CE2	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:125:PRO:O	1:D:150:LYS:HE2	2.17	0.45
1:L:125:PRO:O	1:L:150:LYS:HE2	2.17	0.45
1:N:159:ILE:HD12	1:N:159:ILE:H	1.80	0.45
1:P:125:PRO:O	1:P:150:LYS:HE2	2.17	0.45
1:N:125:PRO:O	1:N:150:LYS:HE2	2.17	0.45
1:X:125:PRO:O	1:X:150:LYS:HE2	2.17	0.45
1:X:159:ILE:H	1:X:159:ILE:HD12	1.80	0.45
1:B:125:PRO:O	1:B:150:LYS:HE2	2.17	0.45
1:H:125:PRO:O	1:H:150:LYS:HE2	2.17	0.45
1:L:159:ILE:H	1:L:159:ILE:HD12	1.80	0.45
1:T:125:PRO:O	1:T:150:LYS:HE2	2.17	0.45
1:B:159:ILE:HD12	1:B:159:ILE:H	1.81	0.45
1:J:125:PRO:O	1:J:150:LYS:HE2	2.17	0.44
1:V:125:PRO:O	1:V:150:LYS:HE2	2.17	0.44
1:R:125:PRO:O	1:R:150:LYS:HE2	2.17	0.44
1:F:125:PRO:O	1:F:150:LYS:HE2	2.17	0.44
1:G:122:TYR:CE2	1:J:111:HIS:HB3	2.53	0.44
1:S:122:TYR:CE2	1:V:111:HIS:HB3	2.53	0.44
1:C:87:GLU:CD	1:D:158:THR:H	2.26	0.44
1:M:45:SER:HB3	1:M:46:PRO:CD	2.47	0.44
1:O:87:GLU:CD	1:P:158:THR:H	2.26	0.44
1:A:45:SER:HB3	1:A:46:PRO:CD	2.47	0.43
1:M:87:GLU:CD	1:N:158:THR:H	2.26	0.43
1:S:87:GLU:CD	1:T:158:THR:H	2.26	0.43
1:A:87:GLU:CD	1:B:158:THR:H	2.26	0.43
1:D:33:LEU:HD21	1:H:33:LEU:HD13	2.00	0.43
1:G:87:GLU:CD	1:H:158:THR:H	2.26	0.43
1:P:33:LEU:HD21	1:T:33:LEU:HD13	2.00	0.43
1:U:87:GLU:CD	1:V:158:THR:H	2.26	0.43
1:A:122:TYR:CE2	1:D:111:HIS:HB3	2.53	0.43
1:B:33:LEU:HD22	1:R:33:LEU:HD13	2.00	0.43
1:F:33:LEU:HD13	1:N:33:LEU:HD22	2.00	0.43
1:I:87:GLU:CD	1:J:158:THR:H	2.26	0.43
1:M:122:TYR:CE2	1:P:111:HIS:HB3	2.53	0.43
1:F:33:LEU:H	1:F:33:LEU:CD1	2.25	0.43
1:Q:77:VAL:HG11	1:Q:122:TYR:CE2	2.54	0.43
1:W:87:GLU:CD	1:X:158:THR:H	2.26	0.43
1:E:77:VAL:HG11	1:E:122:TYR:CE2	2.54	0.43
1:K:87:GLU:CD	1:L:158:THR:H	2.26	0.43
1:R:33:LEU:H	1:R:33:LEU:CD1	2.25	0.42
1:E:87:GLU:CD	1:F:158:THR:H	2.26	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:31:HIS:CD2	1:X:34:GLU:HG3	2.54	0.42
1:L:33:LEU:HD12	1:L:33:LEU:H	1.84	0.42
1:Q:87:GLU:CD	1:R:158:THR:H	2.26	0.42
1:L:34:GLU:HG3	1:T:31:HIS:CD2	2.54	0.42
1:K:77:VAL:HG11	1:K:122:TYR:CE2	2.54	0.42
1:X:33:LEU:H	1:X:33:LEU:HD12	1.84	0.42
1:A:122:TYR:CE2	1:D:111:HIS:CB	3.03	0.42
1:J:34:GLU:HG3	1:R:31:HIS:CD2	2.55	0.42
1:W:77:VAL:HG11	1:W:122:TYR:CE2	2.54	0.42
1:M:122:TYR:CE2	1:P:111:HIS:CB	3.03	0.42
1:C:45:SER:HB3	1:C:46:PRO:CD	2.49	0.42
1:F:31:HIS:CD2	1:V:34:GLU:HG3	2.55	0.42
1:O:45:SER:HB3	1:O:46:PRO:CD	2.49	0.42
1:G:122:TYR:CE2	1:J:111:HIS:CB	3.03	0.41
1:S:122:TYR:CE2	1:V:111:HIS:CB	3.03	0.41
1:J:71:GLU:H	1:J:167:PRO:HD2	1.85	0.41
1:D:71:GLU:H	1:D:167:PRO:HD2	1.85	0.41
1:L:71:GLU:H	1:L:167:PRO:HD2	1.85	0.41
1:V:71:GLU:H	1:V:167:PRO:HD2	1.85	0.41
1:P:71:GLU:H	1:P:167:PRO:HD2	1.85	0.41
1:R:71:GLU:H	1:R:167:PRO:HD2	1.85	0.41
1:X:71:GLU:H	1:X:167:PRO:HD2	1.85	0.41
1:A:122:TYR:CD2	1:D:111:HIS:HB3	2.56	0.41
1:E:39:PRO:HD3	1:M:36:ASP:HB2	2.03	0.41
1:H:71:GLU:H	1:H:167:PRO:HD2	1.85	0.41
1:K:21:SER:OG	1:S:34:GLU:OE1	2.37	0.41
1:U:28:PHE:CG	1:U:29:GLY:N	2.89	0.41
1:A:36:ASP:HB2	1:Q:39:PRO:HD3	2.03	0.40
1:I:28:PHE:CG	1:I:29:GLY:N	2.89	0.40
1:M:122:TYR:CD2	1:P:111:HIS:HB3	2.56	0.40
1:G:122:TYR:CD2	1:J:111:HIS:HB3	2.56	0.40
1:J:17:PHE:CG	1:J:18:HIS:N	2.90	0.40
1:S:122:TYR:CD2	1:V:111:HIS:HB3	2.56	0.40
1:A:134:THR:HB	1:B:131:LEU:HA	2.04	0.40
1:M:134:THR:HB	1:N:131:LEU:HA	2.04	0.40
1:V:17:PHE:CG	1:V:18:HIS:N	2.90	0.40
1:D:17:PHE:CG	1:D:18:HIS:N	2.90	0.40
1:O:134:THR:HB	1:P:131:LEU:HA	2.04	0.40
1:P:17:PHE:CG	1:P:18:HIS:N	2.90	0.40
1:A:41:SER:C	1:A:43:SER:H	2.30	0.40
1:E:134:THR:HB	1:F:131:LEU:HA	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:71:GLU:H	1:N:167:PRO:HD2	1.85	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	173/175 (99%)	130 (75%)	30 (17%)	13 (8%)	1	10
1	B	173/175 (99%)	128 (74%)	32 (18%)	13 (8%)	1	10
1	C	173/175 (99%)	131 (76%)	29 (17%)	13 (8%)	1	10
1	D	173/175 (99%)	125 (72%)	33 (19%)	15 (9%)	0	9
1	E	173/175 (99%)	132 (76%)	28 (16%)	13 (8%)	1	10
1	F	173/175 (99%)	127 (73%)	32 (18%)	14 (8%)	1	9
1	G	173/175 (99%)	129 (75%)	31 (18%)	13 (8%)	1	10
1	H	173/175 (99%)	130 (75%)	30 (17%)	13 (8%)	1	10
1	I	173/175 (99%)	131 (76%)	29 (17%)	13 (8%)	1	10
1	J	173/175 (99%)	124 (72%)	34 (20%)	15 (9%)	0	9
1	K	173/175 (99%)	132 (76%)	28 (16%)	13 (8%)	1	10
1	L	173/175 (99%)	128 (74%)	31 (18%)	14 (8%)	1	9
1	M	173/175 (99%)	130 (75%)	30 (17%)	13 (8%)	1	10
1	N	173/175 (99%)	128 (74%)	32 (18%)	13 (8%)	1	10
1	O	173/175 (99%)	131 (76%)	29 (17%)	13 (8%)	1	10
1	P	173/175 (99%)	125 (72%)	33 (19%)	15 (9%)	0	9
1	Q	173/175 (99%)	132 (76%)	28 (16%)	13 (8%)	1	10
1	R	173/175 (99%)	127 (73%)	32 (18%)	14 (8%)	1	9
1	S	173/175 (99%)	129 (75%)	31 (18%)	13 (8%)	1	10

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T	173/175 (99%)	130 (75%)	30 (17%)	13 (8%)	1	10
1	U	173/175 (99%)	131 (76%)	29 (17%)	13 (8%)	1	10
1	V	173/175 (99%)	124 (72%)	34 (20%)	15 (9%)	0	9
1	W	173/175 (99%)	132 (76%)	28 (16%)	13 (8%)	1	10
1	X	173/175 (99%)	128 (74%)	31 (18%)	14 (8%)	1	9
All	All	4152/4200 (99%)	3094 (74%)	734 (18%)	324 (8%)	1	10

All (324) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	HIS
1	A	40	THR
1	A	45	SER
1	A	74	ARG
1	A	110	GLU
1	A	158	THR
1	B	36	ASP
1	B	40	THR
1	B	45	SER
1	B	70	LEU
1	C	40	THR
1	C	45	SER
1	C	74	ARG
1	C	110	GLU
1	C	158	THR
1	D	36	ASP
1	D	45	SER
1	D	70	LEU
1	E	40	THR
1	E	45	SER
1	E	74	ARG
1	E	110	GLU
1	E	158	THR
1	F	40	THR
1	F	45	SER
1	F	70	LEU
1	G	7	HIS
1	G	40	THR
1	G	45	SER
1	G	74	ARG

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Mol	Chain	Res	Type
1	G	110	GLU
1	G	158	THR
1	H	36	ASP
1	H	40	THR
1	H	45	SER
1	H	70	LEU
1	I	40	THR
1	I	45	SER
1	I	74	ARG
1	I	110	GLU
1	I	158	THR
1	J	36	ASP
1	J	45	SER
1	J	70	LEU
1	K	40	THR
1	K	45	SER
1	K	74	ARG
1	K	110	GLU
1	K	158	THR
1	L	36	ASP
1	L	40	THR
1	L	45	SER
1	L	70	LEU
1	M	7	HIS
1	M	40	THR
1	M	45	SER
1	M	74	ARG
1	M	110	GLU
1	M	158	THR
1	N	36	ASP
1	N	40	THR
1	N	45	SER
1	N	70	LEU
1	O	40	THR
1	O	45	SER
1	O	74	ARG
1	O	110	GLU
1	O	158	THR
1	P	36	ASP
1	P	45	SER
1	P	70	LEU
1	Q	40	THR

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Mol	Chain	Res	Type
1	Q	45	SER
1	Q	74	ARG
1	Q	110	GLU
1	Q	158	THR
1	R	40	THR
1	R	45	SER
1	R	70	LEU
1	S	7	HIS
1	S	40	THR
1	S	45	SER
1	S	74	ARG
1	S	110	GLU
1	S	158	THR
1	T	36	ASP
1	T	40	THR
1	T	45	SER
1	T	70	LEU
1	U	40	THR
1	U	45	SER
1	U	74	ARG
1	U	110	GLU
1	U	158	THR
1	V	36	ASP
1	V	45	SER
1	V	70	LEU
1	W	40	THR
1	W	45	SER
1	W	74	ARG
1	W	110	GLU
1	W	158	THR
1	X	36	ASP
1	X	40	THR
1	X	45	SER
1	X	70	LEU
1	A	3	ILE
1	A	73	ASP
1	B	68	MET
1	B	71	GLU
1	B	157	ARG
1	C	7	HIS
1	C	73	ASP
1	D	40	THR

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Mol	Chain	Res	Type
1	D	68	MET
1	D	71	GLU
1	D	157	ARG
1	E	3	ILE
1	E	7	HIS
1	E	73	ASP
1	F	36	ASP
1	F	68	MET
1	F	71	GLU
1	F	157	ARG
1	G	3	ILE
1	G	43	SER
1	G	73	ASP
1	H	68	MET
1	H	71	GLU
1	H	157	ARG
1	I	3	ILE
1	I	7	HIS
1	I	73	ASP
1	J	40	THR
1	J	68	MET
1	J	71	GLU
1	J	157	ARG
1	K	3	ILE
1	K	7	HIS
1	K	73	ASP
1	L	68	MET
1	L	71	GLU
1	L	157	ARG
1	M	3	ILE
1	M	73	ASP
1	N	68	MET
1	N	71	GLU
1	N	157	ARG
1	O	7	HIS
1	O	73	ASP
1	P	40	THR
1	P	68	MET
1	P	71	GLU
1	P	157	ARG
1	Q	3	ILE
1	Q	7	HIS

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Mol	Chain	Res	Type
1	Q	73	ASP
1	R	36	ASP
1	R	68	MET
1	R	71	GLU
1	R	157	ARG
1	S	3	ILE
1	S	43	SER
1	S	73	ASP
1	T	68	MET
1	T	71	GLU
1	T	157	ARG
1	U	3	ILE
1	U	7	HIS
1	U	73	ASP
1	V	40	THR
1	V	68	MET
1	V	71	GLU
1	V	157	ARG
1	W	3	ILE
1	W	7	HIS
1	W	73	ASP
1	X	68	MET
1	X	71	GLU
1	X	157	ARG
1	A	173	PRO
1	B	84	PHE
1	C	3	ILE
1	C	43	SER
1	C	173	PRO
1	D	18	HIS
1	D	84	PHE
1	E	173	PRO
1	F	18	HIS
1	F	84	PHE
1	G	173	PRO
1	H	84	PHE
1	I	173	PRO
1	J	18	HIS
1	J	84	PHE
1	K	173	PRO
1	L	18	HIS
1	L	84	PHE

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Mol	Chain	Res	Type
1	M	173	PRO
1	N	84	PHE
1	O	3	ILE
1	O	43	SER
1	O	173	PRO
1	P	18	HIS
1	P	84	PHE
1	Q	173	PRO
1	R	18	HIS
1	R	84	PHE
1	S	173	PRO
1	T	84	PHE
1	U	173	PRO
1	V	18	HIS
1	V	84	PHE
1	W	173	PRO
1	X	18	HIS
1	X	84	PHE
1	A	16	PRO
1	A	43	SER
1	A	166	LYS
1	B	95	GLY
1	B	131	LEU
1	C	16	PRO
1	C	166	LYS
1	D	95	GLY
1	D	131	LEU
1	E	16	PRO
1	E	43	SER
1	E	166	LYS
1	F	95	GLY
1	F	131	LEU
1	G	16	PRO
1	G	166	LYS
1	H	95	GLY
1	H	131	LEU
1	I	16	PRO
1	I	43	SER
1	I	166	LYS
1	J	95	GLY
1	J	131	LEU
1	K	16	PRO

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Mol	Chain	Res	Type
1	K	166	LYS
1	L	95	GLY
1	L	131	LEU
1	M	16	PRO
1	M	43	SER
1	M	166	LYS
1	N	95	GLY
1	N	131	LEU
1	O	16	PRO
1	O	166	LYS
1	P	95	GLY
1	P	131	LEU
1	Q	16	PRO
1	Q	43	SER
1	Q	166	LYS
1	R	95	GLY
1	R	131	LEU
1	S	16	PRO
1	S	166	LYS
1	T	95	GLY
1	T	131	LEU
1	U	16	PRO
1	U	43	SER
1	U	166	LYS
1	V	95	GLY
1	V	131	LEU
1	W	16	PRO
1	W	166	LYS
1	X	95	GLY
1	X	131	LEU
1	A	60	TRP
1	B	63	THR
1	B	173	PRO
1	C	60	TRP
1	D	63	THR
1	D	173	PRO
1	E	60	TRP
1	F	63	THR
1	F	173	PRO
1	G	60	TRP
1	H	63	THR
1	H	173	PRO

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Mol	Chain	Res	Type
1	I	60	TRP
1	J	63	THR
1	J	173	PRO
1	K	43	SER
1	L	63	THR
1	L	173	PRO
1	M	60	TRP
1	N	63	THR
1	N	173	PRO
1	O	60	TRP
1	P	63	THR
1	P	173	PRO
1	Q	60	TRP
1	R	63	THR
1	R	173	PRO
1	S	60	TRP
1	T	63	THR
1	T	173	PRO
1	U	60	TRP
1	V	63	THR
1	V	173	PRO
1	W	43	SER
1	W	60	TRP
1	X	63	THR
1	X	173	PRO
1	D	19	SER
1	J	19	SER
1	K	60	TRP
1	P	19	SER
1	V	19	SER
1	B	159	ILE
1	D	159	ILE
1	F	159	ILE
1	H	159	ILE
1	J	159	ILE
1	L	159	ILE
1	N	159	ILE
1	P	159	ILE
1	R	159	ILE
1	T	159	ILE
1	V	159	ILE
1	X	159	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	161/161 (100%)	146 (91%)	15 (9%)	8	26
1	B	161/161 (100%)	144 (89%)	17 (11%)	6	21
1	C	161/161 (100%)	146 (91%)	15 (9%)	8	26
1	D	161/161 (100%)	145 (90%)	16 (10%)	7	24
1	E	161/161 (100%)	145 (90%)	16 (10%)	7	24
1	F	161/161 (100%)	144 (89%)	17 (11%)	6	21
1	G	161/161 (100%)	146 (91%)	15 (9%)	8	26
1	H	161/161 (100%)	144 (89%)	17 (11%)	6	21
1	I	161/161 (100%)	146 (91%)	15 (9%)	8	26
1	J	161/161 (100%)	145 (90%)	16 (10%)	7	24
1	K	161/161 (100%)	145 (90%)	16 (10%)	7	24
1	L	161/161 (100%)	145 (90%)	16 (10%)	7	24
1	M	161/161 (100%)	146 (91%)	15 (9%)	8	26
1	N	161/161 (100%)	144 (89%)	17 (11%)	6	21
1	O	161/161 (100%)	146 (91%)	15 (9%)	8	26
1	P	161/161 (100%)	145 (90%)	16 (10%)	7	24
1	Q	161/161 (100%)	145 (90%)	16 (10%)	7	24
1	R	161/161 (100%)	144 (89%)	17 (11%)	6	21
1	S	161/161 (100%)	146 (91%)	15 (9%)	8	26
1	T	161/161 (100%)	144 (89%)	17 (11%)	6	21
1	U	161/161 (100%)	146 (91%)	15 (9%)	8	26
1	V	161/161 (100%)	145 (90%)	16 (10%)	7	24
1	W	161/161 (100%)	145 (90%)	16 (10%)	7	24
1	X	161/161 (100%)	145 (90%)	16 (10%)	7	24
All	All	3864/3864 (100%)	3482 (90%)	382 (10%)	10	24

All (382) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	SER
1	A	26	GLN
1	A	34	GLU
1	A	54	PHE
1	A	59	SER
1	A	67	GLU
1	A	73	ASP
1	A	79	LEU
1	A	89	LEU
1	A	90	LYS
1	A	137	LEU
1	A	143	LEU
1	A	153	SER
1	A	163	ARG
1	A	175	LYS
1	B	30	GLU
1	B	33	LEU
1	B	34	GLU
1	B	36	ASP
1	B	45	SER
1	B	55	LEU
1	B	71	GLU
1	B	74	ARG
1	B	90	LYS
1	B	92	LYS
1	B	137	LEU
1	B	143	LEU
1	B	146	ASN
1	B	159	ILE
1	B	162	THR
1	B	169	VAL
1	B	175	LYS
1	C	19	SER
1	C	21	SER
1	C	26	GLN
1	C	54	PHE
1	C	59	SER
1	C	67	GLU
1	C	73	ASP
1	C	79	LEU
1	C	89	LEU
1	C	90	LYS
1	C	137	LEU

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Mol	Chain	Res	Type
1	C	143	LEU
1	C	153	SER
1	C	163	ARG
1	C	175	LYS
1	D	30	GLU
1	D	33	LEU
1	D	34	GLU
1	D	45	SER
1	D	55	LEU
1	D	71	GLU
1	D	74	ARG
1	D	90	LYS
1	D	92	LYS
1	D	137	LEU
1	D	143	LEU
1	D	146	ASN
1	D	159	ILE
1	D	162	THR
1	D	169	VAL
1	D	175	LYS
1	E	19	SER
1	E	21	SER
1	E	26	GLN
1	E	54	PHE
1	E	59	SER
1	E	67	GLU
1	E	73	ASP
1	E	79	LEU
1	E	80	ASP
1	E	89	LEU
1	E	90	LYS
1	E	137	LEU
1	E	143	LEU
1	E	153	SER
1	E	163	ARG
1	E	175	LYS
1	F	30	GLU
1	F	33	LEU
1	F	34	GLU
1	F	42	THR
1	F	45	SER
1	F	55	LEU

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Mol	Chain	Res	Type
1	F	71	GLU
1	F	74	ARG
1	F	90	LYS
1	F	92	LYS
1	F	137	LEU
1	F	143	LEU
1	F	146	ASN
1	F	159	ILE
1	F	162	THR
1	F	169	VAL
1	F	175	LYS
1	G	19	SER
1	G	26	GLN
1	G	34	GLU
1	G	54	PHE
1	G	59	SER
1	G	67	GLU
1	G	73	ASP
1	G	79	LEU
1	G	89	LEU
1	G	90	LYS
1	G	137	LEU
1	G	143	LEU
1	G	153	SER
1	G	163	ARG
1	G	175	LYS
1	H	30	GLU
1	H	33	LEU
1	H	34	GLU
1	H	36	ASP
1	H	45	SER
1	H	55	LEU
1	H	71	GLU
1	H	74	ARG
1	H	90	LYS
1	H	92	LYS
1	H	137	LEU
1	H	143	LEU
1	H	146	ASN
1	H	159	ILE
1	H	162	THR
1	H	169	VAL

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Mol	Chain	Res	Type
1	H	175	LYS
1	I	19	SER
1	I	21	SER
1	I	26	GLN
1	I	54	PHE
1	I	59	SER
1	I	67	GLU
1	I	73	ASP
1	I	79	LEU
1	I	89	LEU
1	I	90	LYS
1	I	137	LEU
1	I	143	LEU
1	I	153	SER
1	I	163	ARG
1	I	175	LYS
1	J	30	GLU
1	J	33	LEU
1	J	34	GLU
1	J	45	SER
1	J	55	LEU
1	J	71	GLU
1	J	74	ARG
1	J	90	LYS
1	J	92	LYS
1	J	137	LEU
1	J	143	LEU
1	J	146	ASN
1	J	159	ILE
1	J	162	THR
1	J	169	VAL
1	J	175	LYS
1	K	19	SER
1	K	21	SER
1	K	26	GLN
1	K	54	PHE
1	K	59	SER
1	K	67	GLU
1	K	73	ASP
1	K	79	LEU
1	K	80	ASP
1	K	89	LEU

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Mol	Chain	Res	Type
1	K	90	LYS
1	K	137	LEU
1	K	143	LEU
1	K	153	SER
1	K	163	ARG
1	K	175	LYS
1	L	30	GLU
1	L	33	LEU
1	L	34	GLU
1	L	45	SER
1	L	55	LEU
1	L	71	GLU
1	L	74	ARG
1	L	90	LYS
1	L	92	LYS
1	L	137	LEU
1	L	143	LEU
1	L	146	ASN
1	L	159	ILE
1	L	162	THR
1	L	169	VAL
1	L	175	LYS
1	M	19	SER
1	M	26	GLN
1	M	34	GLU
1	M	54	PHE
1	M	59	SER
1	M	67	GLU
1	M	73	ASP
1	M	79	LEU
1	M	89	LEU
1	M	90	LYS
1	M	137	LEU
1	M	143	LEU
1	M	153	SER
1	M	163	ARG
1	M	175	LYS
1	N	30	GLU
1	N	33	LEU
1	N	34	GLU
1	N	36	ASP
1	N	45	SER

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Mol	Chain	Res	Type
1	N	55	LEU
1	N	71	GLU
1	N	74	ARG
1	N	90	LYS
1	N	92	LYS
1	N	137	LEU
1	N	143	LEU
1	N	146	ASN
1	N	159	ILE
1	N	162	THR
1	N	169	VAL
1	N	175	LYS
1	O	19	SER
1	O	21	SER
1	O	26	GLN
1	O	54	PHE
1	O	59	SER
1	O	67	GLU
1	O	73	ASP
1	O	79	LEU
1	O	89	LEU
1	O	90	LYS
1	O	137	LEU
1	O	143	LEU
1	O	153	SER
1	O	163	ARG
1	O	175	LYS
1	P	30	GLU
1	P	33	LEU
1	P	34	GLU
1	P	45	SER
1	P	55	LEU
1	P	71	GLU
1	P	74	ARG
1	P	90	LYS
1	P	92	LYS
1	P	137	LEU
1	P	143	LEU
1	P	146	ASN
1	P	159	ILE
1	P	162	THR
1	P	169	VAL

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Mol	Chain	Res	Type
1	P	175	LYS
1	Q	19	SER
1	Q	21	SER
1	Q	26	GLN
1	Q	54	PHE
1	Q	59	SER
1	Q	67	GLU
1	Q	73	ASP
1	Q	79	LEU
1	Q	80	ASP
1	Q	89	LEU
1	Q	90	LYS
1	Q	137	LEU
1	Q	143	LEU
1	Q	153	SER
1	Q	163	ARG
1	Q	175	LYS
1	R	30	GLU
1	R	33	LEU
1	R	34	GLU
1	R	42	THR
1	R	45	SER
1	R	55	LEU
1	R	71	GLU
1	R	74	ARG
1	R	90	LYS
1	R	92	LYS
1	R	137	LEU
1	R	143	LEU
1	R	146	ASN
1	R	159	ILE
1	R	162	THR
1	R	169	VAL
1	R	175	LYS
1	S	19	SER
1	S	26	GLN
1	S	34	GLU
1	S	54	PHE
1	S	59	SER
1	S	67	GLU
1	S	73	ASP
1	S	79	LEU

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Mol	Chain	Res	Type
1	S	89	LEU
1	S	90	LYS
1	S	137	LEU
1	S	143	LEU
1	S	153	SER
1	S	163	ARG
1	S	175	LYS
1	T	30	GLU
1	T	33	LEU
1	T	34	GLU
1	T	36	ASP
1	T	45	SER
1	T	55	LEU
1	T	71	GLU
1	T	74	ARG
1	T	90	LYS
1	T	92	LYS
1	T	137	LEU
1	T	143	LEU
1	T	146	ASN
1	T	159	ILE
1	T	162	THR
1	T	169	VAL
1	T	175	LYS
1	U	19	SER
1	U	21	SER
1	U	26	GLN
1	U	54	PHE
1	U	59	SER
1	U	67	GLU
1	U	73	ASP
1	U	79	LEU
1	U	89	LEU
1	U	90	LYS
1	U	137	LEU
1	U	143	LEU
1	U	153	SER
1	U	163	ARG
1	U	175	LYS
1	V	30	GLU
1	V	33	LEU
1	V	34	GLU

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Mol	Chain	Res	Type
1	V	45	SER
1	V	55	LEU
1	V	71	GLU
1	V	74	ARG
1	V	90	LYS
1	V	92	LYS
1	V	137	LEU
1	V	143	LEU
1	V	146	ASN
1	V	159	ILE
1	V	162	THR
1	V	169	VAL
1	V	175	LYS
1	W	19	SER
1	W	21	SER
1	W	26	GLN
1	W	54	PHE
1	W	59	SER
1	W	67	GLU
1	W	73	ASP
1	W	79	LEU
1	W	80	ASP
1	W	89	LEU
1	W	90	LYS
1	W	137	LEU
1	W	143	LEU
1	W	153	SER
1	W	163	ARG
1	W	175	LYS
1	X	30	GLU
1	X	33	LEU
1	X	34	GLU
1	X	45	SER
1	X	55	LEU
1	X	71	GLU
1	X	74	ARG
1	X	90	LYS
1	X	92	LYS
1	X	137	LEU
1	X	143	LEU
1	X	146	ASN
1	X	159	ILE

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Mol	Chain	Res	Type
1	X	162	THR
1	X	169	VAL
1	X	175	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	6	HIS
1	A	146	ASN
1	B	78	ASN
1	C	6	HIS
1	C	7	HIS
1	C	146	ASN
1	D	78	ASN
1	E	6	HIS
1	E	7	HIS
1	E	146	ASN
1	G	6	HIS
1	G	146	ASN
1	H	78	ASN
1	I	7	HIS
1	I	146	ASN
1	J	78	ASN
1	K	6	HIS
1	K	7	HIS
1	K	146	ASN
1	M	6	HIS
1	M	146	ASN
1	O	6	HIS
1	O	7	HIS
1	O	146	ASN
1	P	78	ASN
1	Q	6	HIS
1	Q	7	HIS
1	Q	146	ASN
1	S	6	HIS
1	S	146	ASN
1	T	78	ASN
1	U	7	HIS
1	U	146	ASN
1	V	78	ASN
1	W	6	HIS

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Mol	Chain	Res	Type
1	W	7	HIS
1	W	146	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

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.

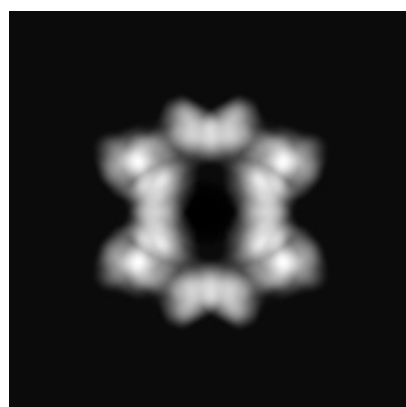
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-1894. 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](#)

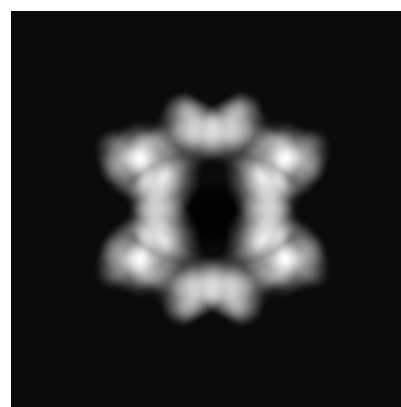
6.1.1 Primary map



X



Y

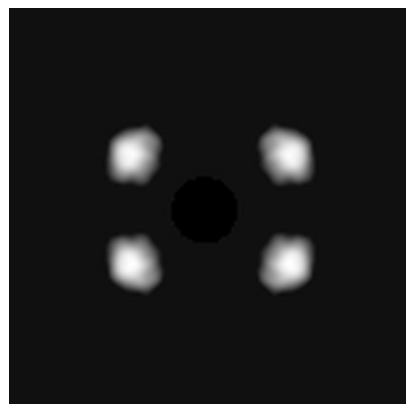


Z

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

6.2 Central slices [i](#)

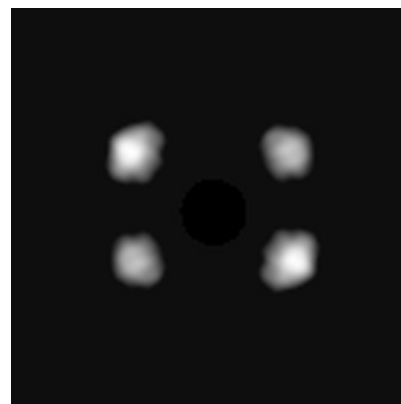
6.2.1 Primary map



X Index: 64



Y Index: 64



Z Index: 64

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: 80



Y Index: 80

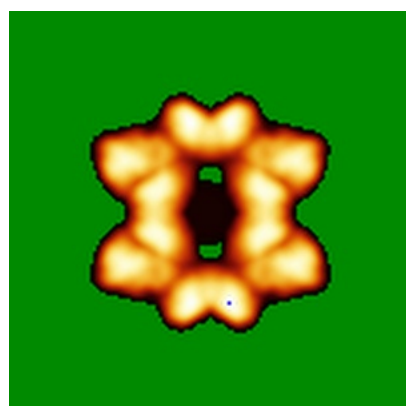


Z Index: 47

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

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

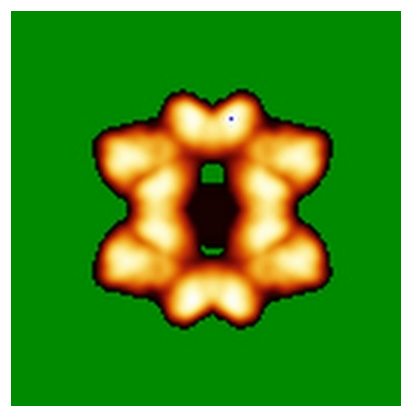
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

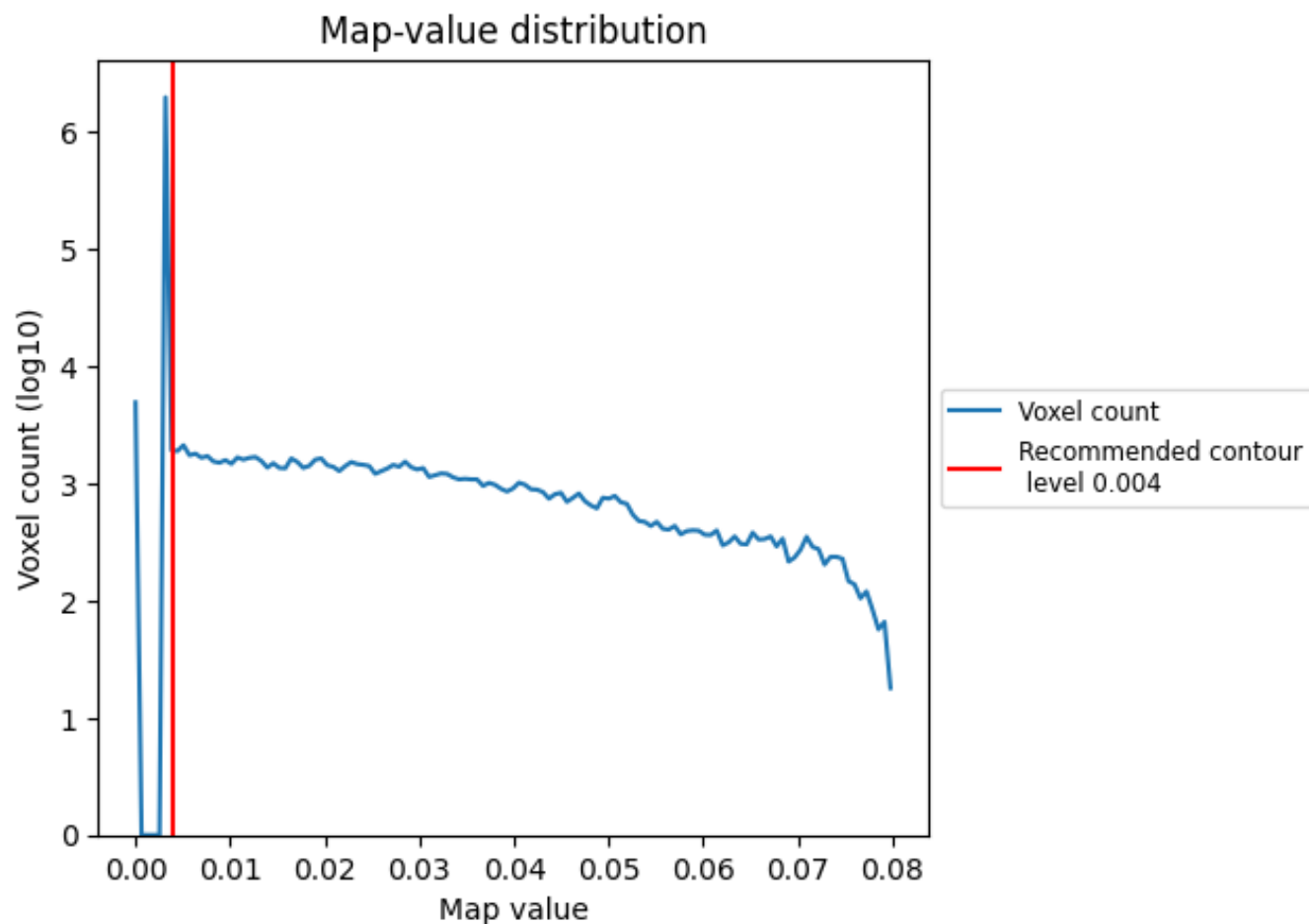
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

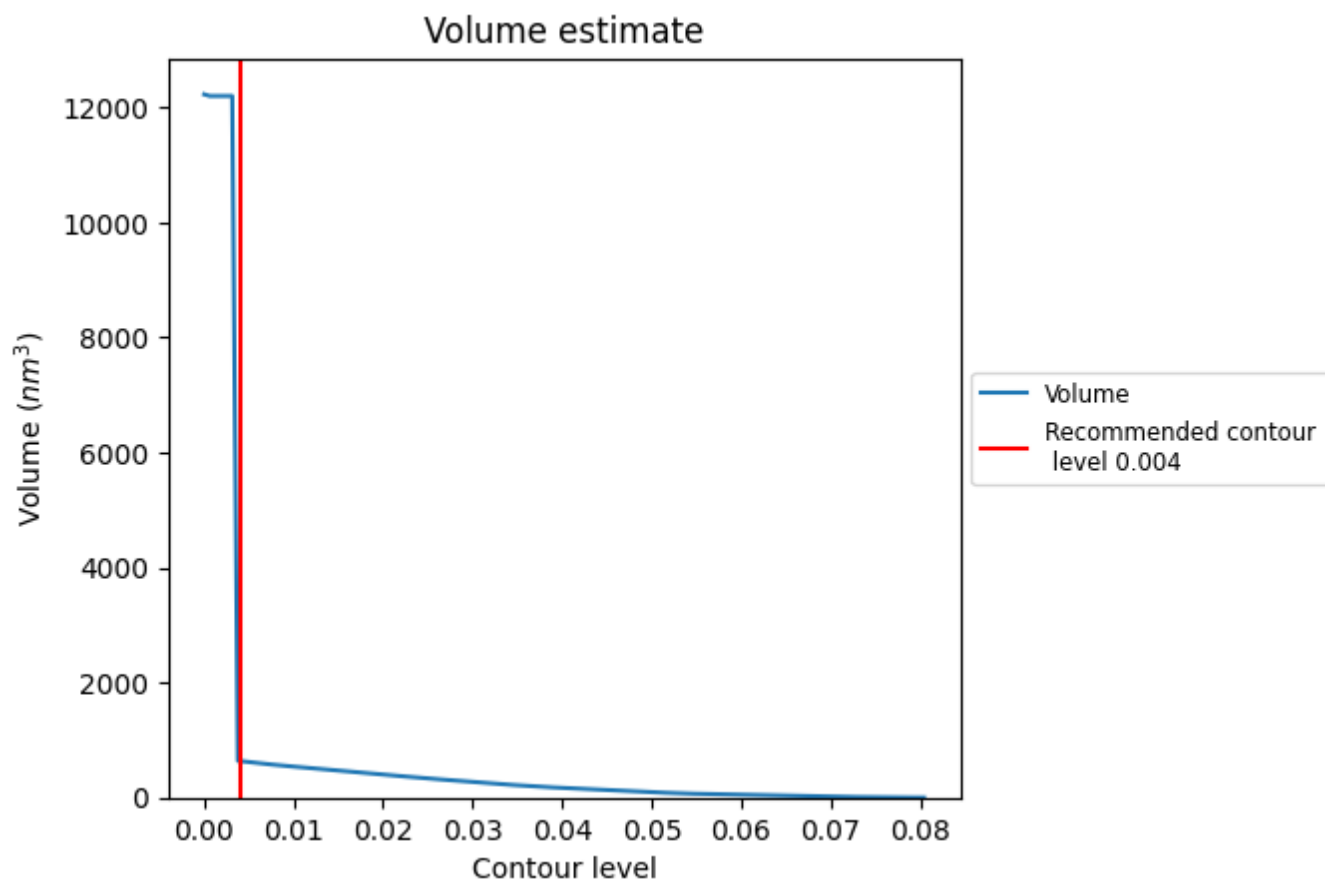
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

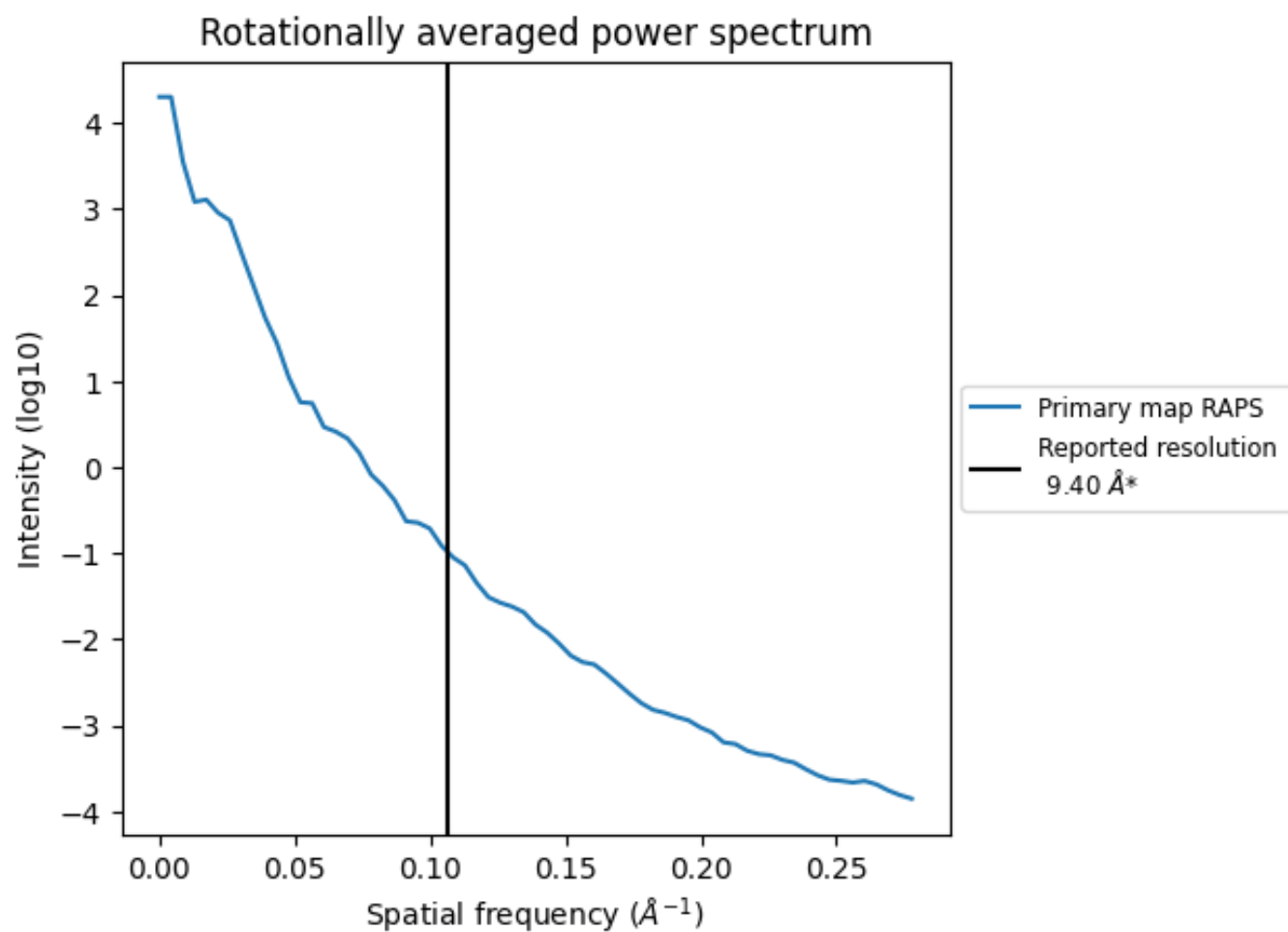
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 635 nm³; this corresponds to an approximate mass of 574 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 0.106 Å⁻¹

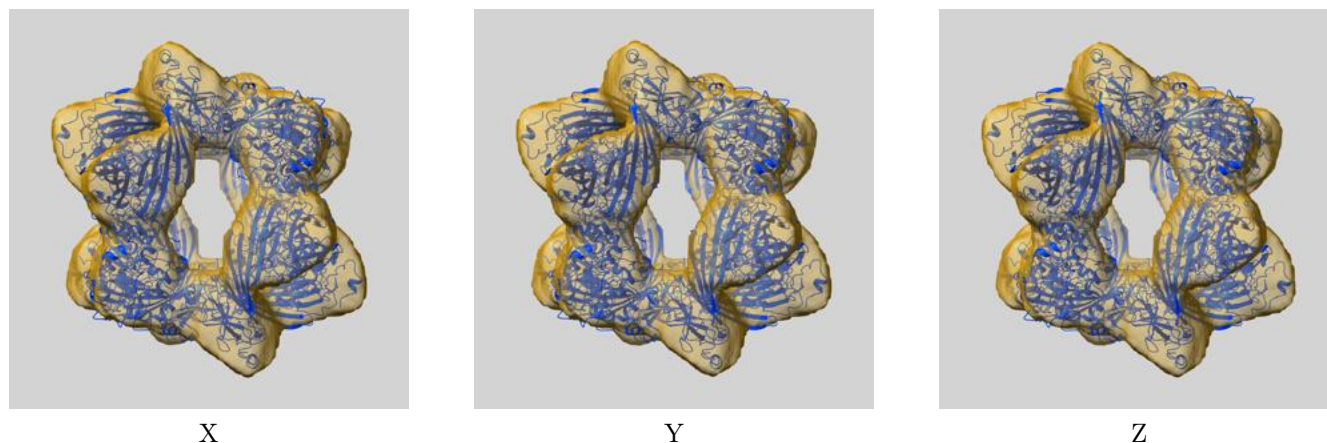
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

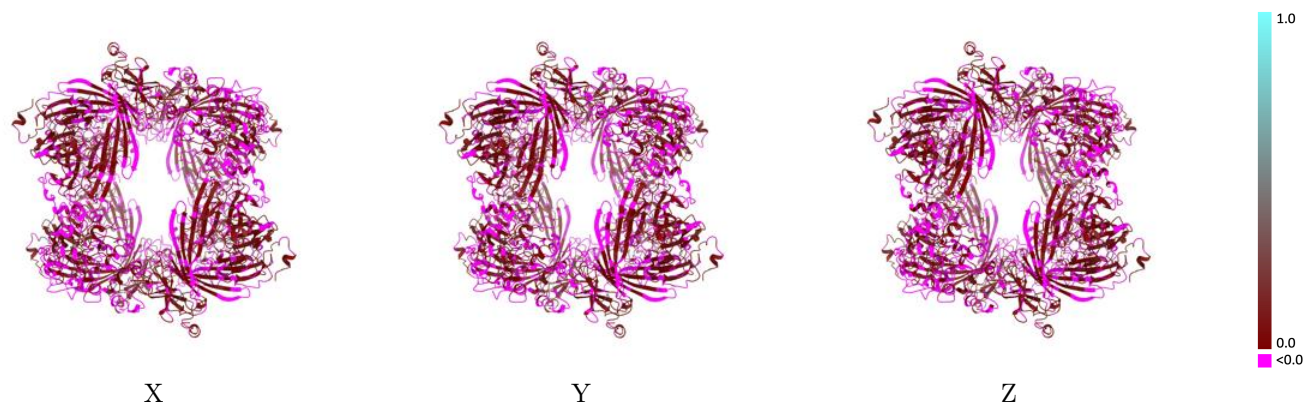
This section contains information regarding the fit between EMDB map EMD-1894 and PDB model 2YGD. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.004 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](#)

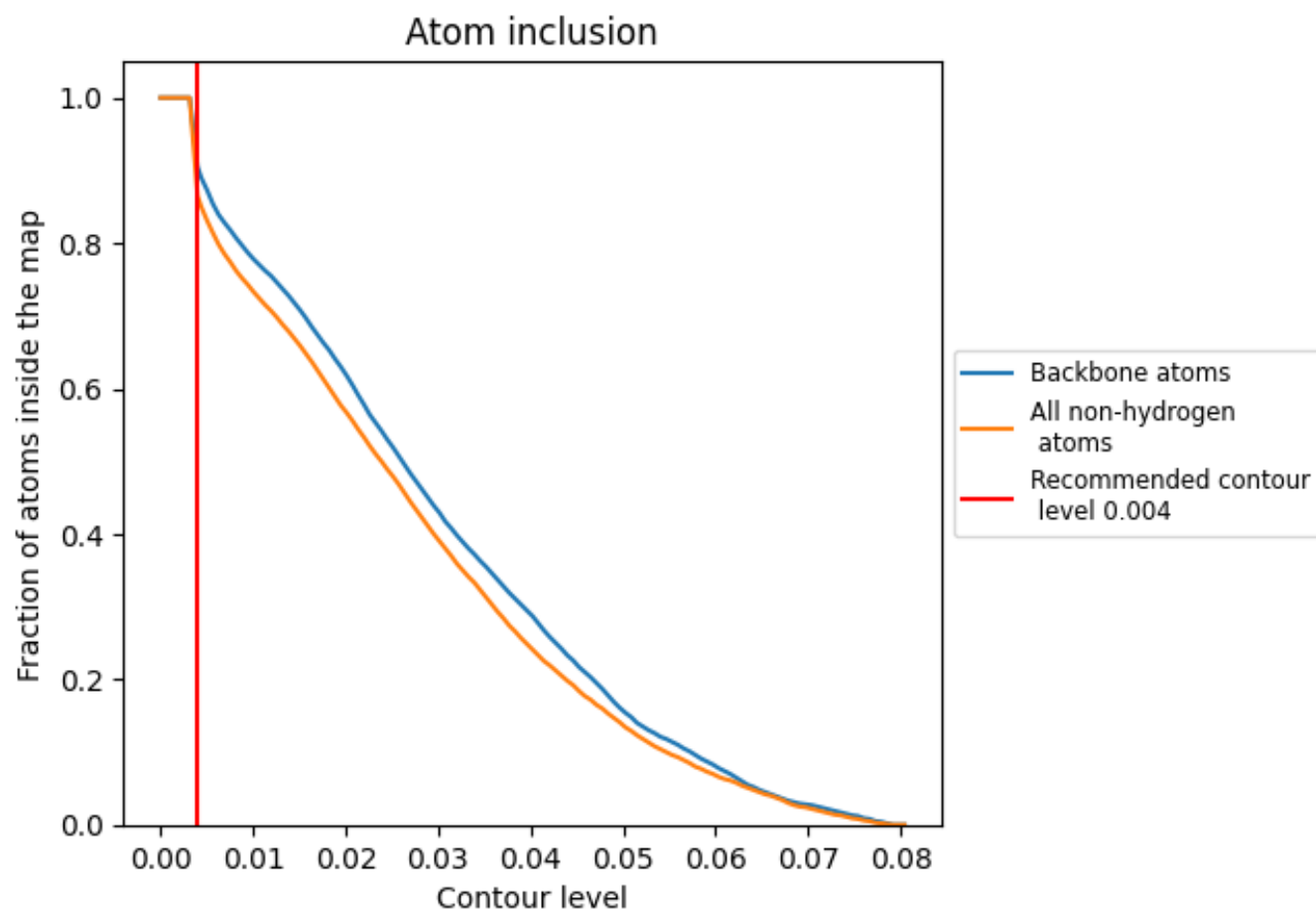


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 86% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8650	 0.0110
A	 0.8400	 -0.0020
B	 0.8730	 0.0190
C	 0.8500	 0.0010
D	 0.8880	 0.0250
E	 0.8570	 -0.0020
F	 0.8840	 0.0270
G	 0.8350	 -0.0080
H	 0.8750	 0.0210
I	 0.8540	 -0.0020
J	 0.8780	 0.0290
K	 0.8580	 0.0080
L	 0.8780	 0.0190
M	 0.8400	 -0.0060
N	 0.8800	 0.0250
O	 0.8580	 -0.0030
P	 0.8860	 0.0290
Q	 0.8580	 0.0030
R	 0.8890	 0.0260
S	 0.8410	 -0.0050
T	 0.8730	 0.0230
U	 0.8560	 0.0050
V	 0.8750	 0.0210
W	 0.8550	 -0.0020
X	 0.8840	 0.0260

