



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 11:44 AM UTC

PDB ID : 6H5I / pdb_00006h5i
EMDB ID : EMD-0140
Title : Single Particle Cryo-EM map of human Transferrin receptor 1 - H-Ferritin complex.
Authors : Testi, C.; Montemiglio, L.C.; Vallone, B.; Des Georges, A.; Boffi, A.; Mancina, F.; Baiocco, P.; Savino, C.
Deposited on : 2018-07-24
Resolution : 3.90 Å (reported)
Based on initial models : 3KAS, 3AJO

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 : **NOT EXECUTED**
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

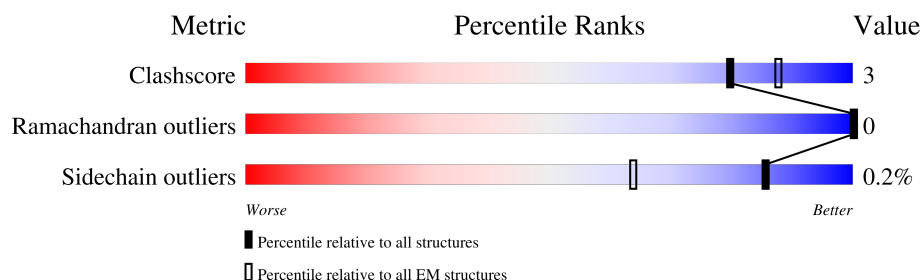
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	Aa	172	58% 92% 8%
1	Ac	172	50% 97% .
1	Ad	172	62% 93% 7%
1	Ae	172	58% 97% .
1	Af	172	35% 95% 5%
1	Ag	172	35% 94% 6%
1	Ah	172	53% 95% 5%
1	Ai	172	40% 93% 7%

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Mol	Chain	Length	Quality of chain
1	Aj	172	
1	Ak	172	
1	Al	172	
1	Am	172	
1	An	172	
1	Ao	172	
1	Ap	172	
1	Ar	172	
1	As	172	
1	At	172	
1	Au	172	
1	Av	172	
1	Aw	172	
1	Ax	172	
1	Ay	172	
1	Az	172	
2	Ab	640	
2	Aq	640	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 43900 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 Ferritin heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Aa	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ac	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ad	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ae	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Af	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ag	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ah	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ai	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Aj	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ak	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Al	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Am	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	An	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ao	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ap	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ar	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	As	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	At	171	Total	C	N	O	S	0	0
			1404	880	246	271	7		
1	Au	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Av	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Aw	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ax	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Ay	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		
1	Az	172	Total	C	N	O	S	0	0
			1413	886	248	272	7		

- Molecule 2 is a protein called Transferrin receptor protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ab	632	Total	C	N	O	S	0	0
			4993	3204	839	936	14		
2	Aq	633	Total	C	N	O	S	0	0
			5004	3210	843	937	14		

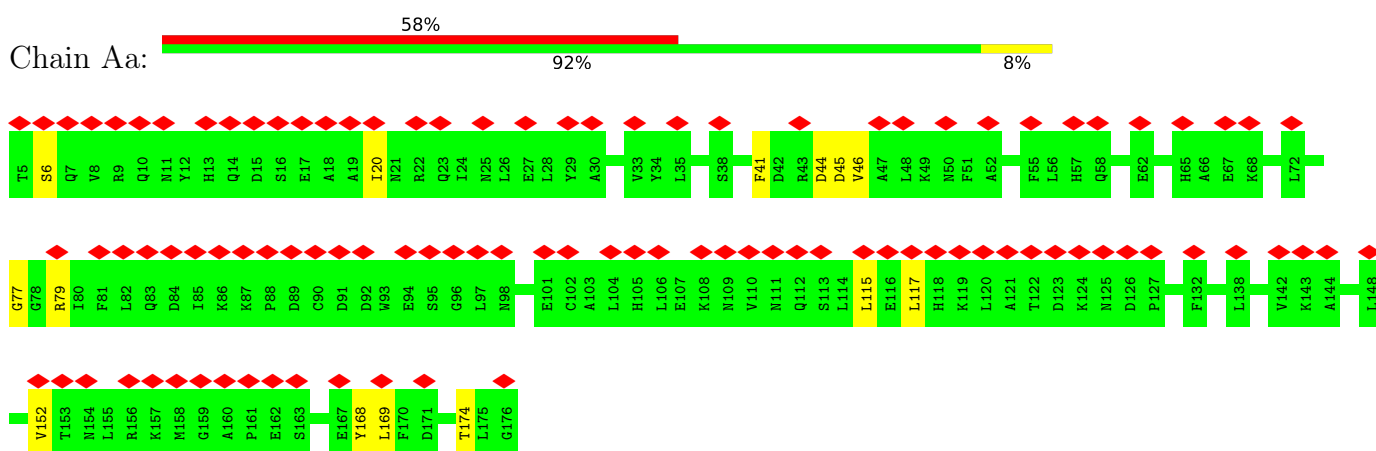
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ab	142	SER	GLY	variant	UNP P02786
Aq	142	SER	GLY	variant	UNP P02786

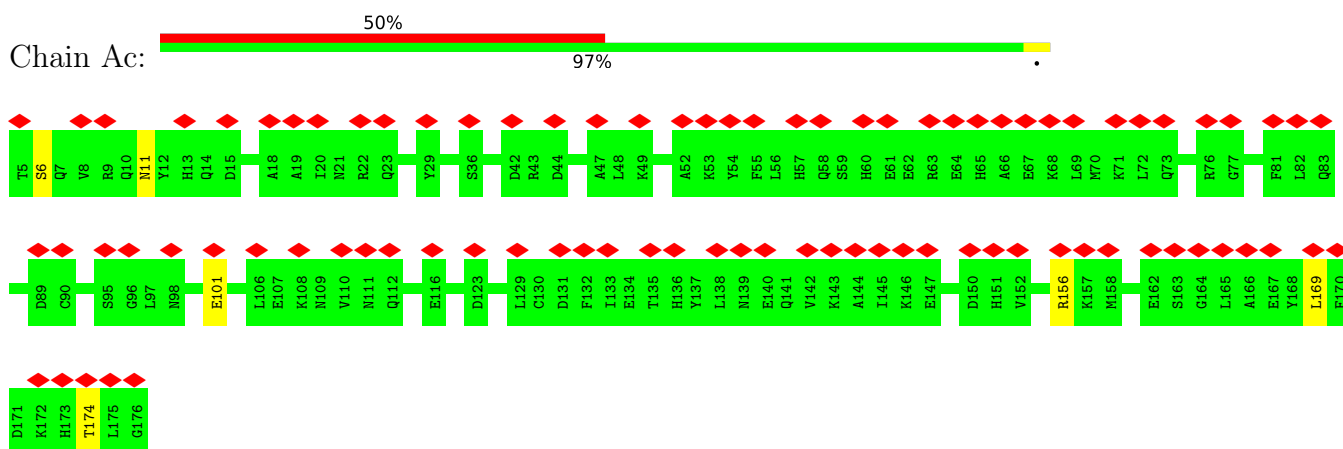
3 Residue-property plots

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

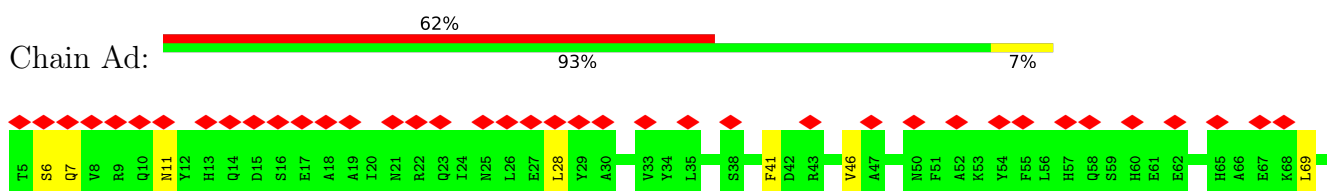
- Molecule 1: Ferritin heavy chain

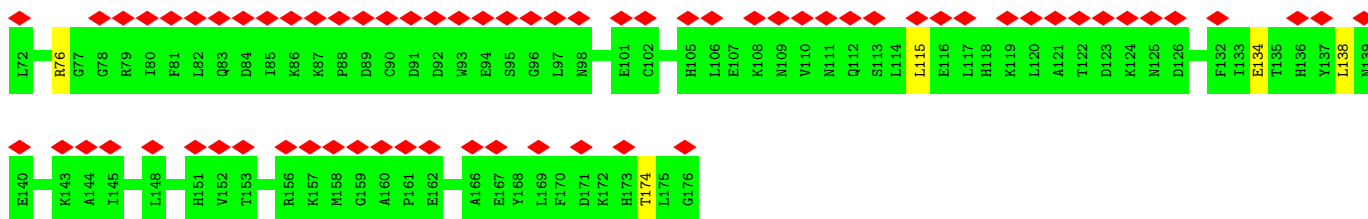


- Molecule 1: Ferritin heavy chain

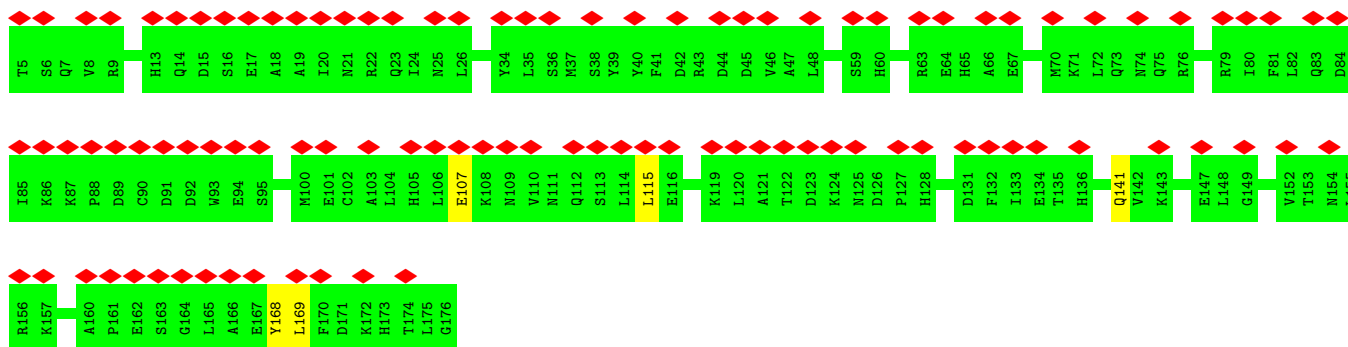


- Molecule 1: Ferritin heavy chain

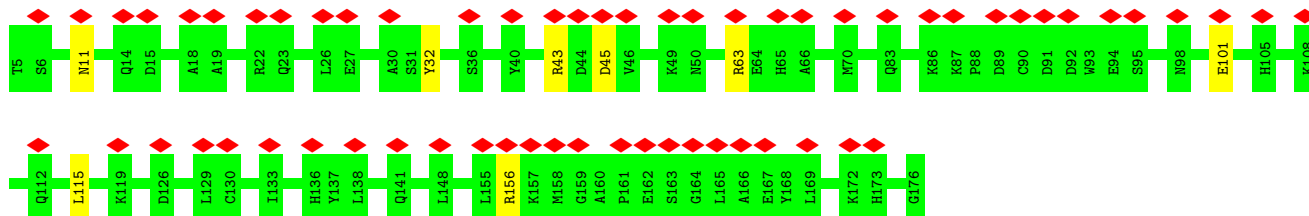




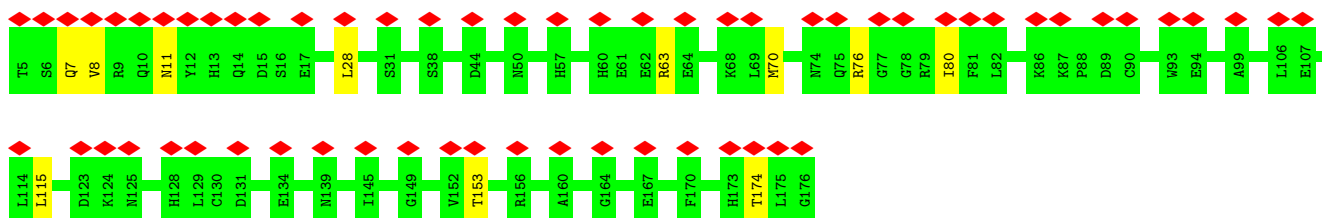
• Molecule 1: Ferritin heavy chain



• Molecule 1: Ferritin heavy chain

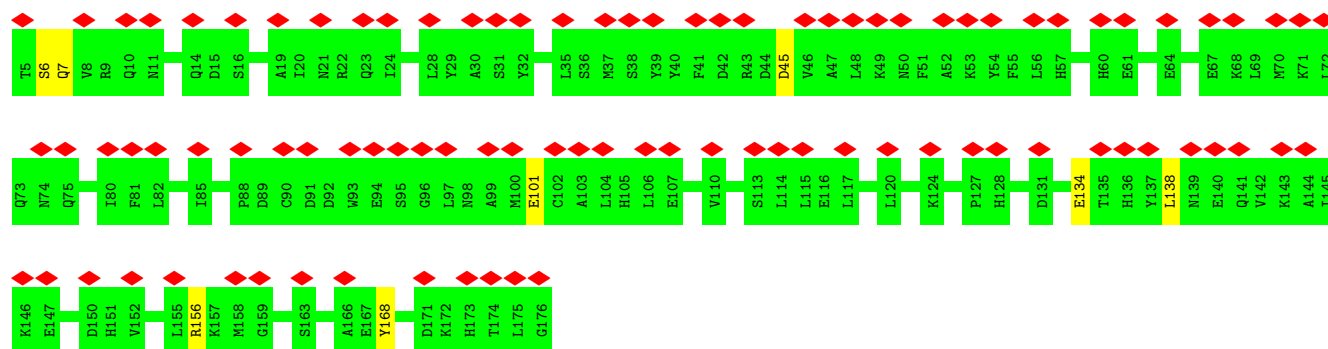


• Molecule 1: Ferritin heavy chain

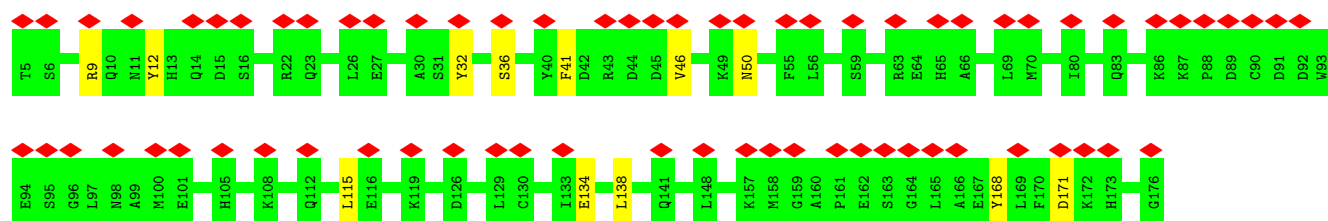


• Molecule 1: Ferritin heavy chain

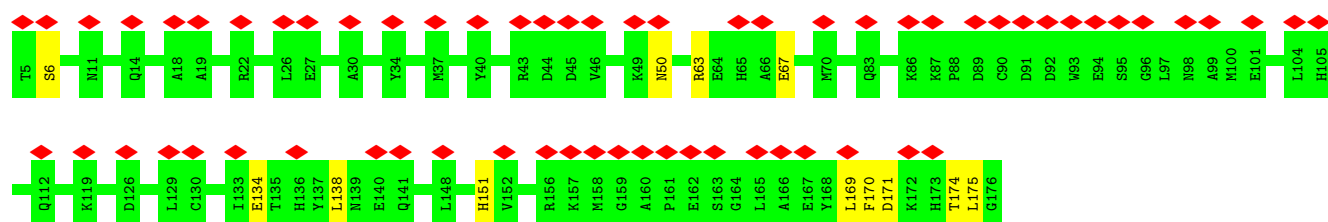
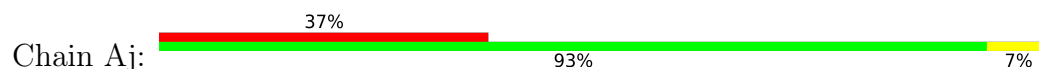




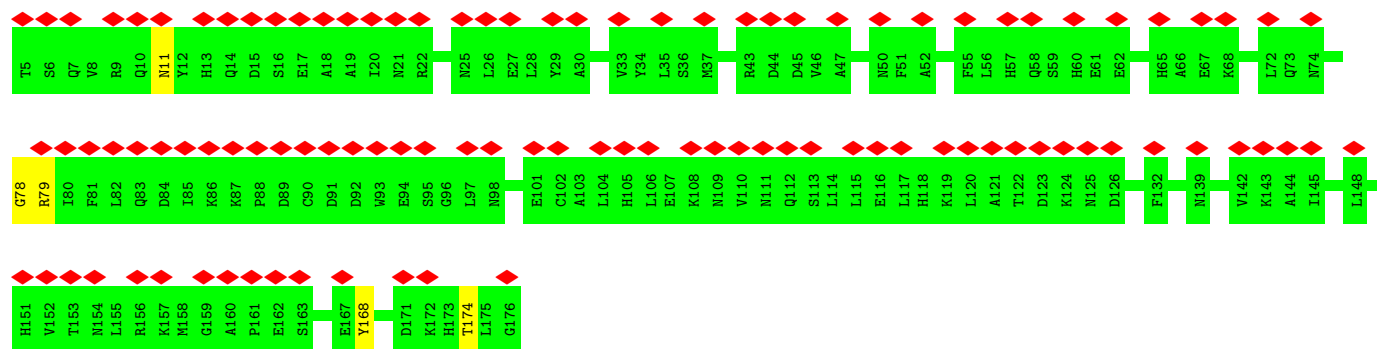
- Molecule 1: Ferritin heavy chain



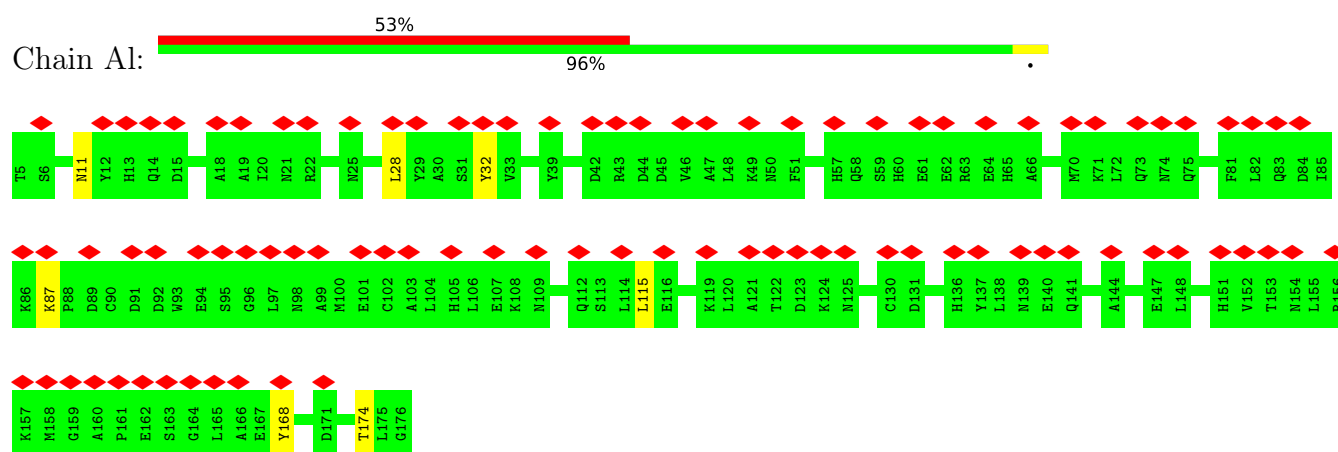
- Molecule 1: Ferritin heavy chain



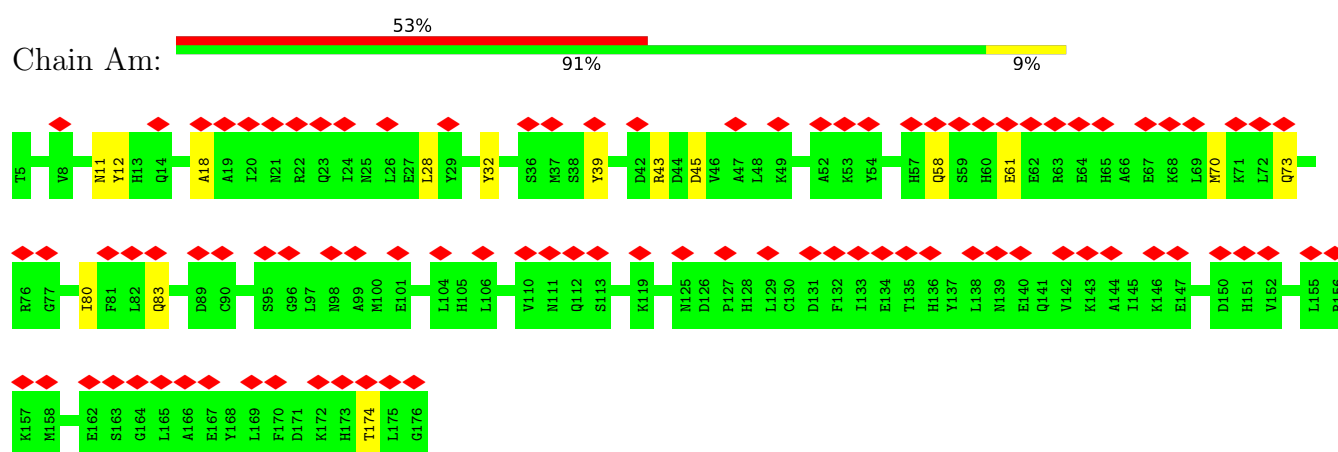
- Molecule 1: Ferritin heavy chain



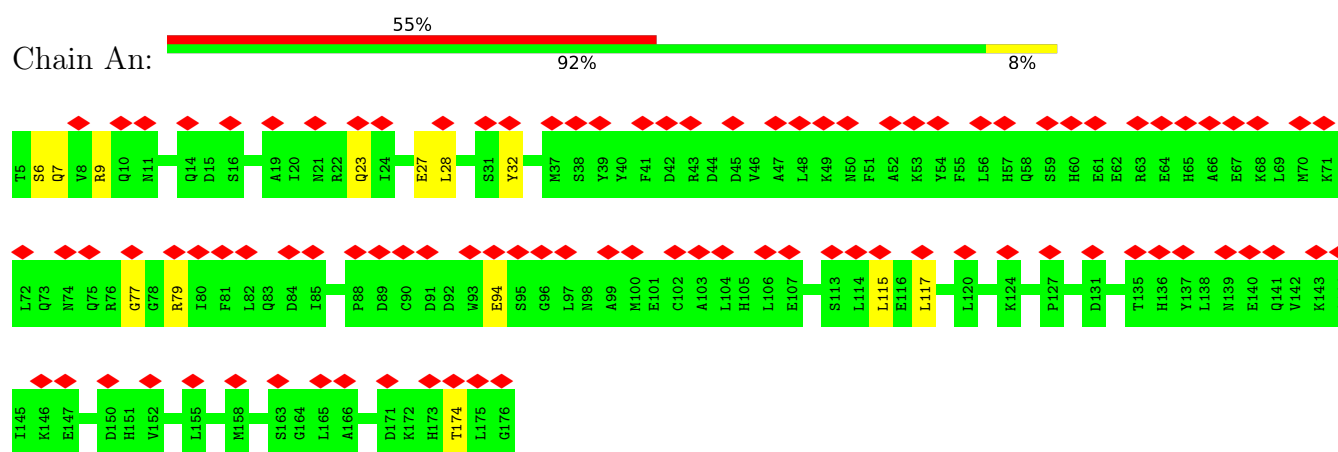
- Molecule 1: Ferritin heavy chain



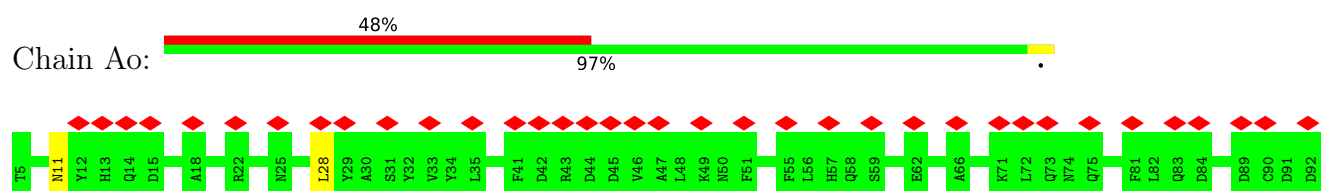
• Molecule 1: Ferritin heavy chain

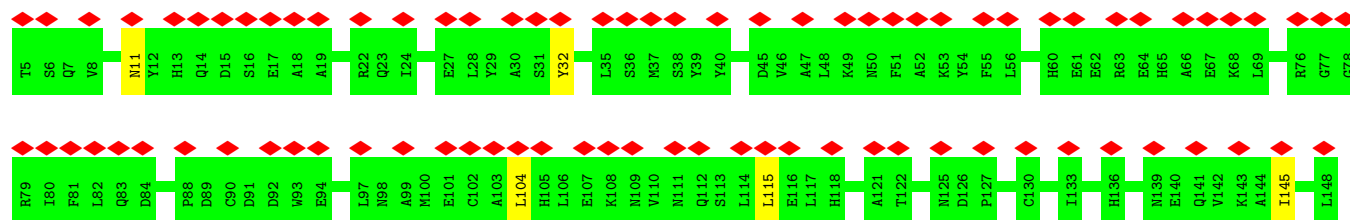


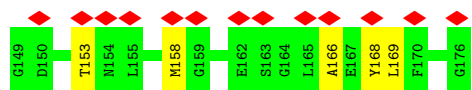
• Molecule 1: Ferritin heavy chain



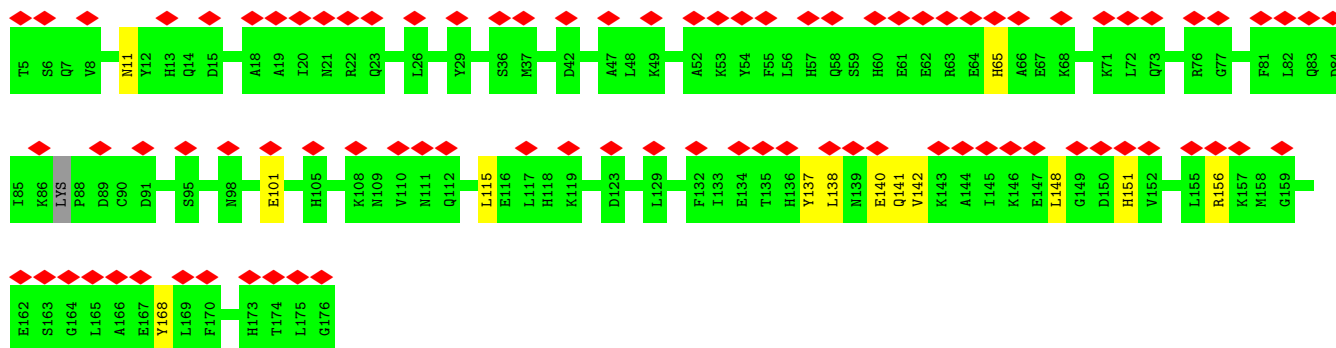
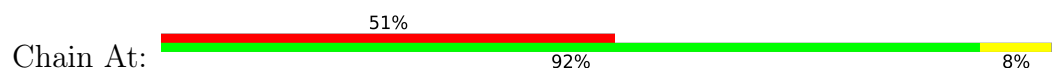
• Molecule 1: Ferritin heavy chain



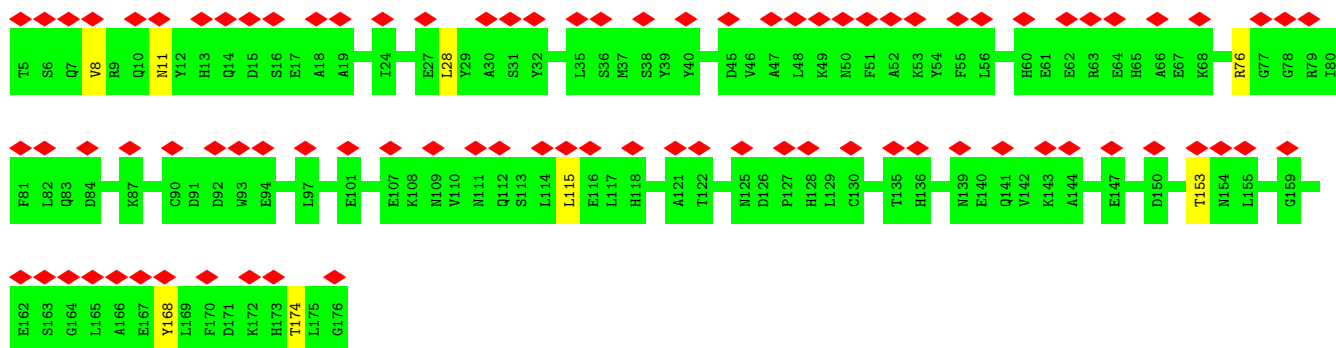




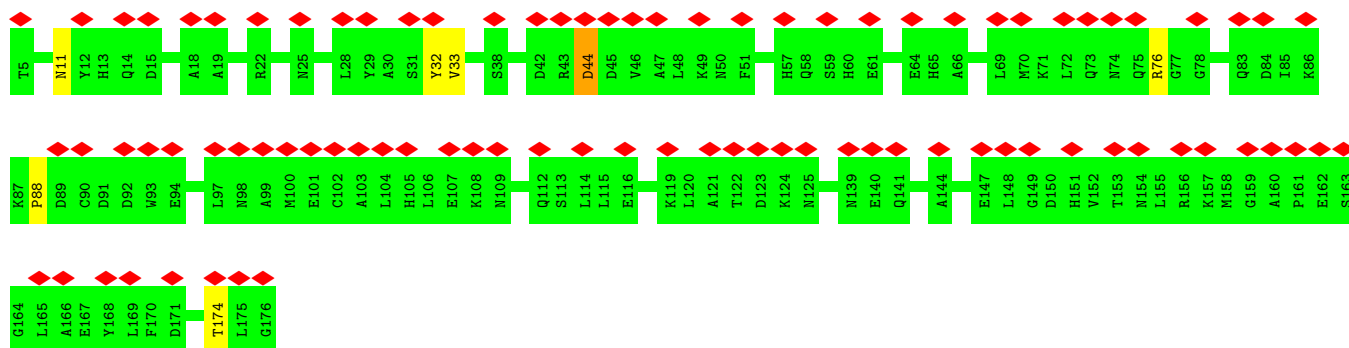
- Molecule 1: Ferritin heavy chain



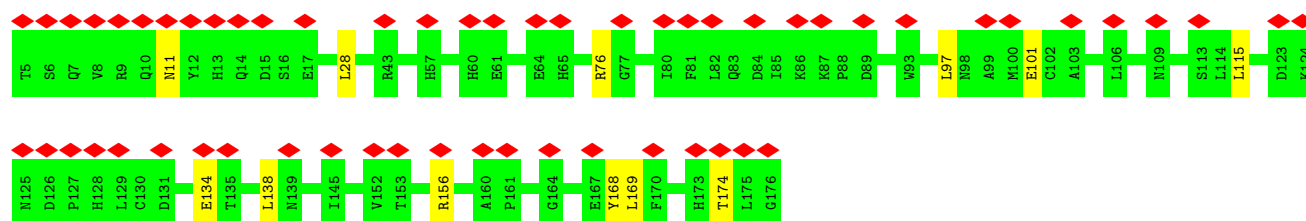
- Molecule 1: Ferritin heavy chain



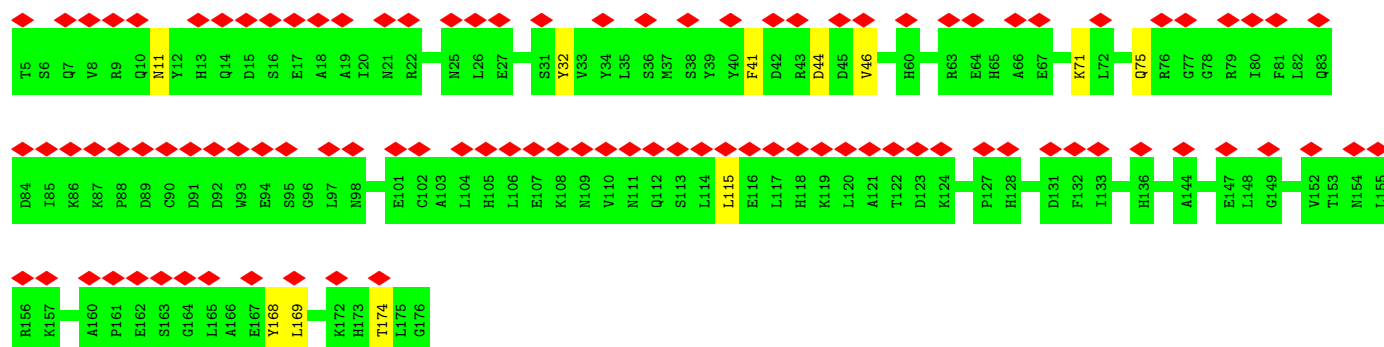
- Molecule 1: Ferritin heavy chain



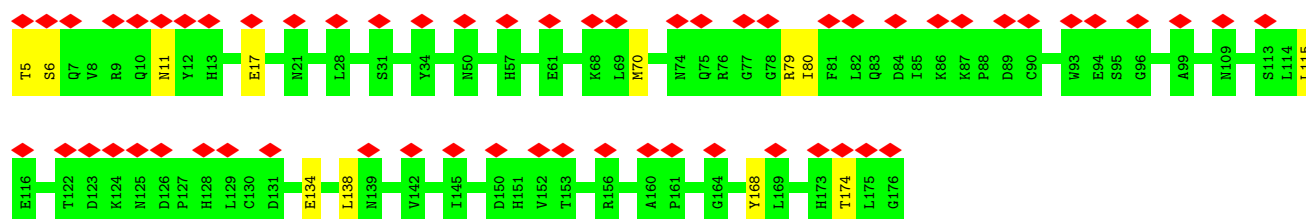
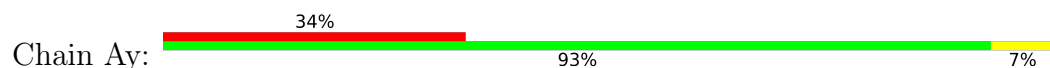
- Molecule 1: Ferritin heavy chain



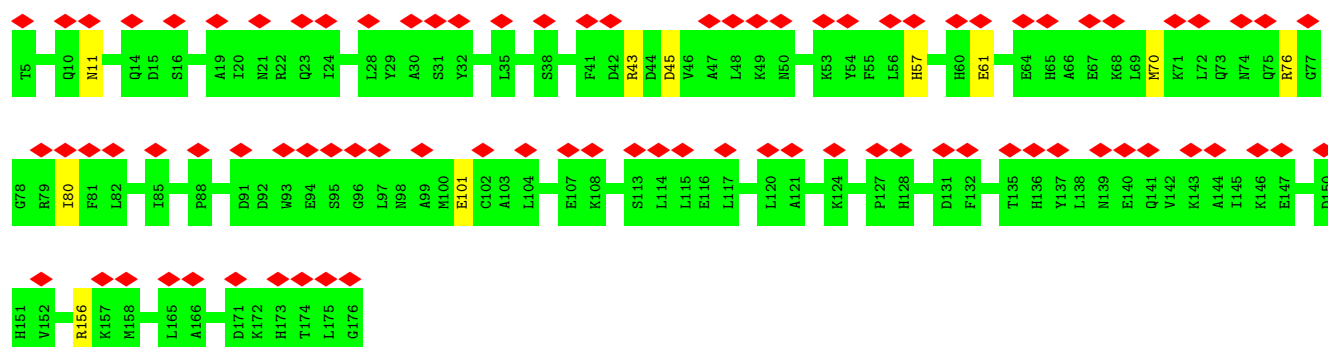
• Molecule 1: Ferritin heavy chain



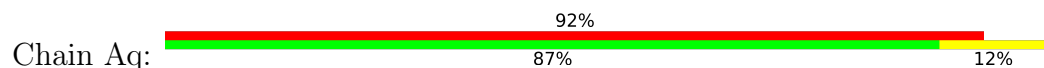
• Molecule 1: Ferritin heavy chain



• Molecule 1: Ferritin heavy chain



Chain Ab:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, O	Depositor
Number of particles used	53878	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	20.555	Depositor
Minimum map value	-11.318	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.8	Depositor
Map size ($\text{\AA}$)	340.48, 340.48, 340.48	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.33, 1.33, 1.33	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	Aa	0.26	0/1442	0.47	0/1942
1	Ac	0.27	0/1442	0.50	0/1942
1	Ad	0.27	0/1442	0.49	0/1942
1	Ae	0.32	0/1442	0.50	0/1942
1	Af	0.28	0/1442	0.48	0/1942
1	Ag	0.33	0/1442	0.48	0/1942
1	Ah	0.32	0/1442	0.46	0/1942
1	Ai	0.28	0/1442	0.47	0/1942
1	Aj	0.32	0/1442	0.49	0/1942
1	Ak	0.33	0/1442	0.49	0/1942
1	Al	0.26	0/1442	0.49	0/1942
1	Am	0.28	0/1442	0.51	0/1942
1	An	0.27	0/1442	0.50	0/1942
1	Ao	0.27	0/1442	0.50	0/1942
1	Ap	0.28	0/1442	0.48	0/1942
1	Ar	0.26	0/1442	0.47	0/1942
1	As	0.33	0/1442	0.48	0/1942
1	At	0.33	0/1432	0.51	0/1927
1	Au	0.28	0/1442	0.50	0/1942
1	Av	0.27	0/1442	0.49	0/1942
1	Aw	0.27	0/1442	0.49	0/1942
1	Ax	0.26	0/1442	0.47	0/1942
1	Ay	0.28	0/1442	0.48	0/1942
1	Az	0.27	0/1442	0.49	0/1942
2	Ab	0.21	0/5109	0.53	3/6925 (0.0%)
2	Aq	0.19	0/5121	0.51	1/6942 (0.0%)
All	All	0.27	0/44828	0.50	4/60460 (0.0%)

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
2	Ab	0	2
2	Aq	0	1
All	All	0	3

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	Aq	557	PHE	N-CA-C	-6.90	97.97	108.67
2	Ab	557	PHE	N-CA-C	-6.33	98.89	108.96
2	Ab	557	PHE	CB-CA-C	5.29	119.06	110.22
2	Ab	416	ALA	N-CA-C	5.06	116.79	111.28

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Ab	209	LEU	Peptide
2	Ab	310	THR	Peptide
2	Aq	310	THR	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	Aa	1413	0	1357	10	0
1	Ac	1413	0	1357	4	0
1	Ad	1413	0	1357	11	0
1	Ae	1413	0	1357	4	0
1	Af	1413	0	1357	6	0
1	Ag	1413	0	1357	8	0
1	Ah	1413	0	1357	5	0
1	Ai	1413	0	1357	7	0
1	Aj	1413	0	1357	10	0
1	Ak	1413	0	1357	4	0
1	Al	1413	0	1357	8	0
1	Am	1413	0	1357	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	An	1413	0	1357	11	0
1	Ao	1413	0	1357	4	0
1	Ap	1413	0	1357	5	0
1	Ar	1413	0	1357	10	0
1	As	1413	0	1357	8	0
1	At	1404	0	1344	9	0
1	Au	1413	0	1357	8	0
1	Av	1413	0	1357	8	0
1	Aw	1413	0	1357	10	0
1	Ax	1413	0	1357	9	0
1	Ay	1413	0	1357	8	0
1	Az	1413	0	1357	7	0
2	Ab	4993	0	4944	62	0
2	Aq	5004	0	4958	45	0
All	All	43900	0	42457	235	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (235) 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)
2:Ab:144:ILE:HG12	2:Ab:420:GLY:O	1.55	1.07
2:Ab:493:ASN:HB2	2:Ab:558:CYS:O	1.77	0.83
2:Ab:310:THR:HG22	2:Ab:310:THR:O	1.79	0.80
2:Ab:415:GLY:O	2:Ab:420:GLY:N	2.20	0.74
2:Ab:266:GLU:O	2:Ab:270:ASN:ND2	2.21	0.74
2:Aq:493:ASN:HB2	2:Aq:558:CYS:O	1.91	0.71
1:Aj:151:HIS:HD2	1:Aj:170:PHE:HZ	1.43	0.65
1:Af:63:ARG:HH22	1:Ag:63:ARG:HH22	1.44	0.63
1:As:115:LEU:HD13	1:At:11:ASN:HD22	1.63	0.63
1:Ag:115:LEU:HD13	1:Al:11:ASN:HD22	1.64	0.62
2:Ab:184:ASP:HB3	2:Ab:388:ASN:HB2	1.83	0.61
2:Ab:304:GLY:H	2:Ab:537:LEU:HD11	1.65	0.61
2:Aq:622:VAL:HG21	2:Aq:646:ARG:HD3	1.82	0.60
1:Al:115:LEU:HD13	1:Ap:11:ASN:HD22	1.65	0.60
2:Aq:446:ARG:NH1	2:Aq:601:LEU:O	2.35	0.60
1:Al:87:LYS:HB3	1:Ar:84:ASP:OD1	2.02	0.60
2:Ab:743:GLN:HE21	2:Ab:747:ASN:HD21	1.50	0.59
1:Aj:151:HIS:CD2	1:Aj:170:PHE:HZ	2.20	0.59
1:At:137:TYR:O	1:At:141:GLN:HG2	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ac:101:GLU:OE2	1:Ac:156:ARG:NH2	2.36	0.58
1:Ae:115:LEU:HD13	1:Ay:11:ASN:HD22	1.68	0.58
1:Aj:151:HIS:HD2	1:Aj:170:PHE:CZ	2.21	0.58
1:Aw:97:LEU:HD21	1:Aw:156:ARG:HE	1.68	0.58
2:Aq:237:PHE:O	2:Aq:267:LYS:HE3	2.04	0.58
1:Ad:174:THR:HG1	1:Ap:168:TYR:HH	1.48	0.58
2:Aq:505:LEU:O	2:Aq:509:THR:N	2.36	0.57
1:An:23:GLN:HE21	1:An:27:GLU:HG2	1.69	0.57
2:Ab:398:GLU:OE2	2:Ab:401:HIS:ND1	2.38	0.57
2:Ab:502:LEU:O	2:Ab:505:LEU:HB3	2.05	0.57
1:Aa:41:PHE:HD1	1:Aa:46:VAL:HG11	1.70	0.56
2:Ab:648:ASP:OD1	2:Ab:651:ARG:NH2	2.38	0.56
2:Ab:343:GLU:HG2	2:Ab:362:THR:HG21	1.88	0.56
1:At:138:LEU:O	1:At:142:VAL:HG23	2.05	0.56
1:Aw:11:ASN:HD22	1:Ax:115:LEU:HD13	1.70	0.56
2:Aq:147:LEU:O	2:Aq:155:ARG:NH2	2.39	0.56
2:Ab:416:ALA:O	2:Ab:420:GLY:CA	2.54	0.56
1:Av:11:ASN:O	1:Av:76:ARG:NH2	2.40	0.56
2:Ab:632:ILE:HG21	2:Ab:639:LEU:HD11	1.89	0.55
2:Aq:335:GLN:HB3	2:Aq:375:LEU:HD11	1.89	0.55
2:Aq:257:VAL:HG21	2:Aq:267:LYS:HD3	1.89	0.55
2:Ab:622:VAL:HG21	2:Ab:646:ARG:HD3	1.89	0.54
2:Ab:236:ASN:OD1	2:Ab:258:ARG:NH2	2.40	0.54
2:Aq:625:LEU:HD21	2:Aq:639:LEU:HD13	1.89	0.54
1:As:153:THR:HG21	1:Az:45:ASP:HA	1.89	0.54
2:Ab:203:VAL:HG22	2:Ab:210:VAL:HG12	1.90	0.53
2:Ab:416:ALA:O	2:Ab:420:GLY:HA3	2.08	0.53
1:Ak:168:TYR:OH	1:Al:174:THR:OG1	2.26	0.53
1:Ah:45:ASP:HA	1:Au:153:THR:HG21	1.90	0.53
2:Ab:348:ASN:HD21	1:Am:83:GLN:HE22	1.56	0.53
1:Ai:115:LEU:HD13	1:Au:11:ASN:HD22	1.74	0.53
1:Av:33:VAL:HG22	1:Av:88:PRO:HB3	1.90	0.53
1:Ay:70:MET:HE3	1:Ay:80:ILE:HG21	1.91	0.53
2:Ab:191:GLN:HG2	2:Ab:379:ASN:HB3	1.91	0.53
1:Ah:168:TYR:OH	1:Au:174:THR:OG1	2.25	0.53
2:Aq:505:LEU:HB2	2:Aq:608:ASN:HB3	1.91	0.53
2:Aq:305:THR:HG21	2:Aq:543:PRO:HG3	1.90	0.52
1:Am:11:ASN:HD22	1:Ar:115:LEU:HD13	1.72	0.52
1:An:23:GLN:O	1:An:23:GLN:NE2	2.42	0.52
1:Az:43:ARG:NH2	1:Az:45:ASP:OD2	2.42	0.52
1:Ao:101:GLU:OE2	1:Ao:156:ARG:NH2	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Aw:101:GLU:OE2	1:Aw:156:ARG:NH2	2.43	0.52
1:Ae:107:GLU:OE1	1:Ae:141:GLN:NE2	2.41	0.52
2:Ab:235:ALA:HB3	2:Ab:257:VAL:HG12	1.92	0.52
2:Aq:543:PRO:O	2:Aq:547:TYR:HB3	2.09	0.52
1:Ad:134:GLU:HA	1:Ad:138:LEU:HD12	1.92	0.51
2:Aq:126:ASP:OD1	2:Aq:129:ARG:NH2	2.43	0.51
2:Ab:483:ASN:HB2	2:Ab:553:VAL:O	2.10	0.51
1:Av:44:ASP:OD1	1:Av:44:ASP:N	2.43	0.51
1:At:101:GLU:OE2	1:At:156:ARG:NH2	2.38	0.51
1:Au:11:ASN:O	1:Au:76:ARG:NH2	2.43	0.51
1:Af:11:ASN:HD22	1:At:115:LEU:HD13	1.75	0.51
1:At:65:HIS:NE2	1:At:140:GLU:OE1	2.43	0.51
1:Au:168:TYR:HH	1:Ay:174:THR:HG1	1.57	0.51
2:Aq:535:LEU:HB3	2:Aq:542:PHE:HB2	1.93	0.51
1:Av:11:ASN:HD22	1:Ay:115:LEU:HD13	1.75	0.51
2:Ab:310:THR:O	2:Ab:310:THR:CG2	2.51	0.51
1:As:158:MET:HB3	1:As:166:ALA:HB1	1.92	0.51
1:Au:8:VAL:HG22	1:Av:44:ASP:OD2	2.11	0.51
1:An:77:GLY:O	1:An:79:ARG:NH1	2.45	0.50
2:Ab:305:THR:HG21	2:Ab:543:PRO:HG3	1.94	0.50
1:Ad:6:SER:OG	1:Ax:44:ASP:OD2	2.29	0.50
1:Ai:9:ARG:NH2	1:Ai:12:TYR:O	2.45	0.50
1:Ap:70:MET:HE3	1:Ap:80:ILE:HG21	1.94	0.50
2:Aq:263:THR:HG21	2:Aq:537:LEU:HB3	1.94	0.50
2:Ab:232:LEU:HD22	2:Ab:373:VAL:HG21	1.93	0.50
1:Ae:169:LEU:HD13	1:Aj:169:LEU:HD21	1.93	0.50
2:Aq:631:ASP:OD1	2:Aq:719:ARG:NH1	2.45	0.50
2:Aq:496:VAL:HG11	2:Aq:506:ILE:HD13	1.94	0.50
2:Aq:131:LEU:HD22	2:Aq:599:ILE:HD12	1.93	0.49
2:Ab:219:TYR:HA	2:Ab:335:GLN:HE22	1.76	0.49
2:Ab:697:PHE:HB3	2:Ab:704:SER:H	1.77	0.49
2:Aq:184:ASP:HB3	2:Aq:388:ASN:HB2	1.93	0.49
1:Au:28:LEU:HD13	1:Av:32:TYR:HE1	1.78	0.49
1:Ak:78:GLY:O	1:Ak:79:ARG:NH1	2.43	0.49
1:Af:32:TYR:HE1	1:Ag:28:LEU:HD13	1.77	0.49
1:Aa:152:VAL:HG11	1:Ad:7:GLN:HE22	1.78	0.49
2:Ab:565:TYR:HE2	2:Ab:575:GLU:HG2	1.78	0.49
2:Ab:700:VAL:HB	2:Ab:709:LEU:HG	1.93	0.49
2:Aq:268:VAL:HA	2:Aq:279:VAL:HG21	1.95	0.49
2:Aq:349:MET:HG2	2:Aq:367:THR:HG22	1.95	0.49
1:As:169:LEU:HD21	1:Aw:169:LEU:HD13	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Ab:263:THR:HG21	2:Ab:537:LEU:HB3	1.94	0.48
2:Ab:626:ASN:HD22	2:Ab:629:ARG:HD2	1.78	0.48
2:Ab:614:TYR:OH	2:Ab:682:GLU:OE1	2.32	0.48
2:Aq:201:ILE:HB	2:Aq:374:LYS:HB3	1.94	0.48
1:Af:43:ARG:NH2	1:Af:45:ASP:OD2	2.46	0.48
1:Am:43:ARG:NH2	1:Am:45:ASP:OD2	2.46	0.48
1:An:23:GLN:NE2	1:An:27:GLU:HG2	2.28	0.48
2:Aq:282:TYR:HB3	2:Aq:337:ILE:HG13	1.95	0.48
1:Az:57:HIS:NE2	1:Az:61:GLU:OE2	2.46	0.48
2:Ab:131:LEU:HD22	2:Ab:599:ILE:HD12	1.95	0.48
2:Ab:202:ILE:HD13	2:Ab:348:ASN:HD22	1.78	0.48
1:Aa:168:TYR:OH	1:Av:174:THR:OG1	2.27	0.48
1:Aa:169:LEU:HD13	1:Ax:169:LEU:HD21	1.96	0.48
1:Ay:134:GLU:HA	1:Ay:138:LEU:HD12	1.95	0.48
1:Aa:20:ILE:HD13	1:Aa:117:LEU:HD11	1.95	0.48
2:Aq:648:ASP:OD1	2:Aq:651:ARG:NH2	2.46	0.48
2:Ab:433:PHE:HD2	2:Ab:450:PHE:HZ	1.61	0.47
1:Ao:11:ASN:HD22	1:Aw:115:LEU:HD13	1.79	0.47
2:Ab:232:LEU:HD11	2:Ab:256:ILE:HB	1.96	0.47
2:Ab:173:PHE:HB3	2:Ab:181:VAL:HG11	1.96	0.47
2:Ab:147:LEU:O	2:Ab:155:ARG:NH2	2.47	0.47
2:Aq:258:ARG:NH2	2:Aq:357:TRP:O	2.38	0.47
1:Ae:168:TYR:HH	1:Ak:174:THR:HG1	1.62	0.47
1:Aj:63:ARG:NH1	1:Aj:67:GLU:OE2	2.47	0.47
1:Ag:7:GLN:HG3	1:Ag:8:VAL:HG13	1.96	0.47
1:Aj:174:THR:HG1	1:Al:168:TYR:HH	1.53	0.47
2:Aq:235:ALA:HB3	2:Aq:257:VAL:HG12	1.97	0.47
1:Aw:11:ASN:O	1:Aw:76:ARG:NH2	2.47	0.47
1:Ah:6:SER:OG	1:Ah:7:GLN:N	2.48	0.47
1:An:94:GLU:O	1:An:94:GLU:HG2	2.15	0.46
2:Aq:196:ALA:O	2:Aq:378:SER:OG	2.31	0.46
2:Ab:446:ARG:NH1	2:Ab:601:LEU:O	2.48	0.46
1:Ad:41:PHE:HD1	1:Ad:46:VAL:HG11	1.79	0.46
1:Aa:174:THR:OG1	1:Ax:168:TYR:OH	2.25	0.46
1:Ag:153:THR:HG21	1:Ar:45:ASP:HA	1.97	0.46
1:Ah:134:GLU:HA	1:Ah:138:LEU:HD12	1.96	0.46
2:Aq:232:LEU:HD11	2:Aq:256:ILE:HB	1.97	0.46
2:Ab:154:PRO:HG2	2:Ab:161:LYS:HD2	1.97	0.46
1:Ac:11:ASN:HD22	1:Au:115:LEU:HD13	1.81	0.46
1:Ar:6:SER:OG	1:Ar:7:GLN:N	2.49	0.46
2:Ab:293:ALA:HB2	2:Ab:339:ARG:HH21	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ao:115:LEU:HD13	1:Ax:11:ASN:HD22	1.80	0.46
2:Ab:124:TRP:HZ3	2:Ab:603:HIS:HB3	1.79	0.46
1:Ad:11:ASN:O	1:Ad:76:ARG:NH2	2.49	0.46
1:Am:28:LEU:HD13	1:An:32:TYR:HE1	1.80	0.45
2:Ab:308:PRO:O	2:Ab:327:SER:OG	2.31	0.45
1:Af:115:LEU:HD13	1:As:11:ASN:HD22	1.80	0.45
2:Aq:425:LEU:HD21	2:Aq:587:ALA:HB1	1.97	0.45
2:Ab:643:TYR:HD1	2:Ab:646:ARG:HH21	1.64	0.45
1:Ag:174:THR:OG1	1:Ar:168:TYR:OH	2.32	0.45
2:Aq:743:GLN:HE21	2:Aq:747:ASN:HD21	1.64	0.45
1:Az:11:ASN:O	1:Az:76:ARG:NH2	2.50	0.45
1:Af:101:GLU:OE2	1:Af:156:ARG:NH2	2.38	0.45
2:Ab:732:ARG:HH22	2:Aq:322:PRO:HD3	1.82	0.45
1:Ag:70:MET:HE3	1:Ag:80:ILE:HG21	1.98	0.45
1:Aj:151:HIS:NE2	1:Aj:175:LEU:HD21	2.32	0.45
1:Am:12:TYR:OH	1:Am:73:GLN:OE1	2.31	0.45
2:Aq:154:PRO:HG2	2:Aq:161:LYS:HD2	1.99	0.45
1:Am:174:THR:OG1	1:Ay:168:TYR:OH	2.31	0.44
1:Ar:101:GLU:OE2	1:Ar:156:ARG:NH2	2.44	0.44
2:Ab:209:LEU:HD13	2:Ab:209:LEU:HA	1.87	0.44
2:Ab:147:LEU:HD22	2:Ab:165:LEU:HD11	2.00	0.44
2:Ab:582:GLU:HB3	2:Ab:585:LYS:HB3	1.99	0.44
2:Ab:324:SER:HB2	2:Ab:329:LEU:HD11	1.99	0.44
2:Ab:626:ASN:HA	2:Ab:629:ARG:HG3	2.00	0.44
1:An:6:SER:HB3	1:An:9:ARG:HG3	1.99	0.44
1:Aw:134:GLU:HA	1:Aw:138:LEU:HD12	2.00	0.44
1:Ax:71:LYS:O	1:Ax:75:GLN:HB2	2.18	0.44
1:Am:58:GLN:NE2	1:Am:61:GLU:OE1	2.50	0.44
2:Aq:504:THR:O	2:Aq:507:GLU:HB3	2.18	0.44
2:Aq:254:ILE:HG12	2:Aq:278:GLY:HA3	1.99	0.43
1:Aj:134:GLU:HA	1:Aj:138:LEU:HD12	1.99	0.43
1:Am:32:TYR:HE1	1:An:28:LEU:HD13	1.83	0.43
1:Ap:7:GLN:HG3	1:Ap:8:VAL:HG13	2.00	0.43
1:At:148:LEU:HD23	1:At:151:HIS:HD2	1.83	0.43
2:Aq:418:LYS:O	2:Aq:418:LYS:HG2	2.17	0.43
2:Ab:232:LEU:HA	2:Ab:254:ILE:O	2.19	0.43
1:Ai:41:PHE:HD1	1:Ai:46:VAL:HG11	1.84	0.43
2:Aq:258:ARG:O	2:Aq:267:LYS:HE2	2.18	0.43
2:Ab:155:ARG:HG2	2:Ab:411:ALA:H	1.84	0.43
1:Al:32:TYR:HE1	1:Ar:28:LEU:HD13	1.84	0.43
1:Ai:32:TYR:HE1	1:Aw:28:LEU:HD13	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Az:101:GLU:OE2	1:Az:156:ARG:NH2	2.38	0.42
1:Aj:174:THR:OG1	1:Al:168:TYR:OH	2.28	0.42
1:Am:70:MET:HE3	1:Am:80:ILE:HG21	2.00	0.42
1:An:115:LEU:HD13	1:Az:11:ASN:HD22	1.84	0.42
2:Aq:681:VAL:HG22	2:Aq:749:LEU:HD13	2.01	0.42
2:Ab:403:VAL:HG13	2:Ab:480:THR:HB	2.01	0.42
1:Ai:168:TYR:OH	1:Ax:174:THR:OG1	2.25	0.42
1:Ar:23:GLN:HE22	1:Ar:26:LEU:HD23	1.85	0.42
1:As:168:TYR:OH	1:Aw:174:THR:OG1	2.26	0.42
1:Ax:41:PHE:HD1	1:Ax:46:VAL:HG11	1.84	0.42
2:Ab:212:LEU:HB2	1:Am:18:ALA:HB1	2.01	0.42
2:Ab:747:ASN:O	2:Ab:750:SER:OG	2.35	0.42
1:Ad:174:THR:OG1	1:Ap:168:TYR:OH	2.26	0.42
1:As:104:LEU:HD11	1:As:145:ILE:HG23	2.02	0.42
1:Az:70:MET:HE3	1:Az:80:ILE:HG21	2.02	0.41
1:Am:39:TYR:HD1	1:Am:39:TYR:HA	1.77	0.41
1:Ao:28:LEU:HD13	1:As:32:TYR:HE1	1.85	0.41
2:Aq:637:LEU:HD11	2:Aq:732:ARG:HH21	1.84	0.41
2:Ab:205:LYS:HB3	2:Ab:370:SER:HB2	2.01	0.41
1:Aa:115:LEU:HD13	1:Ad:11:ASN:HD22	1.84	0.41
1:Aa:168:TYR:HH	1:Av:174:THR:HG1	1.55	0.41
2:Ab:127:LEU:HD22	2:Ab:442:PHE:HD1	1.85	0.41
1:Ad:69:LEU:HD23	1:Ad:69:LEU:HA	1.93	0.41
1:Ag:11:ASN:O	1:Ag:76:ARG:NH2	2.53	0.41
2:Aq:232:LEU:HD22	2:Aq:373:VAL:HG21	2.02	0.41
2:Aq:141:THR:HA	2:Aq:144:ILE:HD12	2.01	0.41
1:At:65:HIS:O	1:At:137:TYR:OH	2.37	0.41
2:Ab:407:ALA:HB3	2:Ab:426:LEU:HD22	2.03	0.41
1:Ai:134:GLU:HA	1:Ai:138:LEU:HD12	2.02	0.41
2:Ab:234:HIS:NE2	2:Ab:282:TYR:OH	2.52	0.41
2:Ab:479:PHE:HE2	2:Ab:601:LEU:HD22	1.86	0.41
1:Ah:101:GLU:OE2	1:Ah:156:ARG:NH2	2.42	0.41
1:Aa:44:ASP:OD1	1:Aa:45:ASP:N	2.54	0.41
1:Ac:174:THR:OG1	1:Aw:168:TYR:OH	2.24	0.41
1:Ad:28:LEU:HD13	1:Ax:32:TYR:HE1	1.84	0.41
1:Ad:115:LEU:HD13	1:Ak:11:ASN:HD22	1.85	0.41
2:Aq:140:PHE:HE2	2:Aq:588:ARG:HA	1.86	0.41
1:Ar:20:ILE:HD13	1:Ar:117:LEU:HD11	2.02	0.41
2:Aq:502:LEU:HD22	2:Aq:505:LEU:HD23	2.03	0.40
1:Aa:77:GLY:O	1:Aa:79:ARG:NH1	2.54	0.40
2:Ab:499:SER:HA	2:Ab:500:PRO:HD3	1.96	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Ai:50:ASN:HB2	1:Ai:171:ASP:OD1	2.21	0.40
1:An:174:THR:OG1	1:At:168:TYR:OH	2.30	0.40
2:Aq:502:LEU:O	2:Aq:505:LEU:HB3	2.21	0.40
2:Ab:754:TRP:HE1	2:Aq:180:LYS:HD3	1.85	0.40
1:Al:28:LEU:HD13	1:Ar:32:TYR:HE1	1.87	0.40
1:Ac:169:LEU:HD23	1:Ac:169:LEU:HA	1.95	0.40
1:Aj:50:ASN:HB2	1:Aj:171:ASP:OD1	2.22	0.40
1:An:6:SER:OG	1:An:7:GLN:N	2.54	0.40
2:Aq:184:ASP:OD2	2:Aq:186:HIS:NE2	2.53	0.40
1:Ay:5:THR:OG1	1:Ay:6:SER:N	2.54	0.40
1:Ay:17:GLU:OE2	1:Ay:79:ARG:N	2.44	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	Aa	170/172 (99%)	161 (95%)	9 (5%)	0	100	100
1	Ac	170/172 (99%)	165 (97%)	5 (3%)	0	100	100
1	Ad	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
1	Ae	170/172 (99%)	164 (96%)	6 (4%)	0	100	100
1	Af	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
1	Ag	170/172 (99%)	165 (97%)	5 (3%)	0	100	100
1	Ah	170/172 (99%)	162 (95%)	8 (5%)	0	100	100
1	Ai	170/172 (99%)	162 (95%)	8 (5%)	0	100	100
1	Aj	170/172 (99%)	164 (96%)	6 (4%)	0	100	100
1	Ak	170/172 (99%)	164 (96%)	6 (4%)	0	100	100
1	Al	170/172 (99%)	164 (96%)	6 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Am	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
1	An	170/172 (99%)	167 (98%)	3 (2%)	0	100	100
1	Ao	170/172 (99%)	165 (97%)	5 (3%)	0	100	100
1	Ap	170/172 (99%)	166 (98%)	4 (2%)	0	100	100
1	Ar	170/172 (99%)	165 (97%)	5 (3%)	0	100	100
1	As	170/172 (99%)	164 (96%)	6 (4%)	0	100	100
1	At	167/172 (97%)	156 (93%)	11 (7%)	0	100	100
1	Au	170/172 (99%)	161 (95%)	9 (5%)	0	100	100
1	Av	170/172 (99%)	162 (95%)	8 (5%)	0	100	100
1	Aw	170/172 (99%)	161 (95%)	9 (5%)	0	100	100
1	Ax	170/172 (99%)	162 (95%)	8 (5%)	0	100	100
1	Ay	170/172 (99%)	163 (96%)	7 (4%)	0	100	100
1	Az	170/172 (99%)	165 (97%)	5 (3%)	0	100	100
2	Ab	626/640 (98%)	585 (94%)	41 (6%)	0	100	100
2	Aq	629/640 (98%)	600 (95%)	29 (5%)	0	100	100
All	All	5332/5408 (99%)	5102 (96%)	230 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	Aa	153/153 (100%)	152 (99%)	1 (1%)	76	78
1	Ac	153/153 (100%)	152 (99%)	1 (1%)	76	78
1	Ad	153/153 (100%)	153 (100%)	0	100	100
1	Ae	153/153 (100%)	153 (100%)	0	100	100
1	Af	153/153 (100%)	153 (100%)	0	100	100
1	Ag	153/153 (100%)	153 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	Ah	153/153 (100%)	153 (100%)	0	100	100
1	Ai	153/153 (100%)	152 (99%)	1 (1%)	76	78
1	Aj	153/153 (100%)	152 (99%)	1 (1%)	76	78
1	Ak	153/153 (100%)	153 (100%)	0	100	100
1	Al	153/153 (100%)	153 (100%)	0	100	100
1	Am	153/153 (100%)	153 (100%)	0	100	100
1	An	153/153 (100%)	152 (99%)	1 (1%)	76	78
1	Ao	153/153 (100%)	153 (100%)	0	100	100
1	Ap	153/153 (100%)	153 (100%)	0	100	100
1	Ar	153/153 (100%)	152 (99%)	1 (1%)	76	78
1	As	153/153 (100%)	153 (100%)	0	100	100
1	At	152/153 (99%)	152 (100%)	0	100	100
1	Au	153/153 (100%)	153 (100%)	0	100	100
1	Av	153/153 (100%)	152 (99%)	1 (1%)	76	78
1	Aw	153/153 (100%)	153 (100%)	0	100	100
1	Ax	153/153 (100%)	153 (100%)	0	100	100
1	Ay	153/153 (100%)	153 (100%)	0	100	100
1	Az	153/153 (100%)	153 (100%)	0	100	100
2	Ab	541/549 (98%)	540 (100%)	1 (0%)	87	87
2	Aq	542/549 (99%)	542 (100%)	0	100	100
All	All	4754/4770 (100%)	4746 (100%)	8 (0%)	85	87

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Aa	6	SER
2	Ab	310	THR
1	Ac	6	SER
1	Ai	36	SER
1	Aj	6	SER
1	An	117	LEU
1	Ar	84	ASP
1	Av	44	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (118)

such sidechains are listed below:

Mol	Chain	Res	Type
1	Aa	112	GLN
1	Aa	118	HIS
1	Aa	173	HIS
2	Ab	171	ASN
2	Ab	197	GLN
2	Ab	335	GLN
2	Ab	483	ASN
2	Ab	493	ASN
2	Ab	626	ASN
2	Ab	684	HIS
2	Ab	733	ASN
2	Ab	743	GLN
1	Ac	11	ASN
1	Ac	13	HIS
1	Ac	57	HIS
1	Ac	105	HIS
1	Ac	112	GLN
1	Ac	173	HIS
1	Ad	7	GLN
1	Ad	11	ASN
1	Ad	21	ASN
1	Ad	25	ASN
1	Ad	112	GLN
1	Ad	118	HIS
1	Ae	57	HIS
1	Ae	105	HIS
1	Ae	112	GLN
1	Ae	128	HIS
1	Ae	173	HIS
1	Af	11	ASN
1	Af	65	HIS
1	Af	141	GLN
1	Af	173	HIS
1	Ag	83	GLN
1	Ag	112	GLN
1	Ag	118	HIS
1	Ag	173	HIS
1	Ah	112	GLN
1	Ah	128	HIS
1	Ah	173	HIS
1	Ai	25	ASN
1	Ai	112	GLN

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Mol	Chain	Res	Type
1	Ai	118	HIS
1	Aj	11	ASN
1	Aj	112	GLN
1	Aj	141	GLN
1	Aj	151	HIS
1	Ak	112	GLN
1	Ak	173	HIS
1	Al	10	GLN
1	Al	11	ASN
1	Al	98	ASN
1	Al	118	HIS
1	Al	128	HIS
1	Am	11	ASN
1	Am	25	ASN
1	Am	57	HIS
1	Am	58	GLN
1	Am	83	GLN
1	Am	112	GLN
1	Am	128	HIS
1	An	25	ASN
1	An	60	HIS
1	An	112	GLN
1	An	118	HIS
1	An	173	HIS
1	Ao	11	ASN
1	Ao	60	HIS
1	Ao	112	GLN
1	Ao	173	HIS
1	Ap	7	GLN
1	Ap	11	ASN
1	Ap	65	HIS
1	Ap	112	GLN
1	Ap	136	HIS
2	Aq	160	GLN
2	Aq	171	ASN
2	Aq	483	ASN
2	Aq	524	GLN
2	Aq	596	GLN
2	Aq	608	ASN
2	Aq	640	GLN
2	Aq	715	ASN
2	Aq	733	ASN

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Mol	Chain	Res	Type
2	Aq	747	ASN
1	Ar	173	HIS
1	As	11	ASN
1	As	112	GLN
1	As	173	HIS
1	At	11	ASN
1	At	112	GLN
1	At	128	HIS
1	At	141	GLN
1	Au	11	ASN
1	Au	112	GLN
1	Au	118	HIS
1	Au	128	HIS
1	Au	173	HIS
1	Av	11	ASN
1	Av	112	GLN
1	Av	173	HIS
1	Aw	7	GLN
1	Aw	11	ASN
1	Aw	75	GLN
1	Aw	173	HIS
1	Ax	11	ASN
1	Ax	13	HIS
1	Ax	112	GLN
1	Ax	173	HIS
1	Ay	11	ASN
1	Ay	112	GLN
1	Az	10	GLN
1	Az	11	ASN
1	Az	21	ASN
1	Az	105	HIS
1	Az	112	GLN
1	Az	128	HIS
1	Az	173	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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.

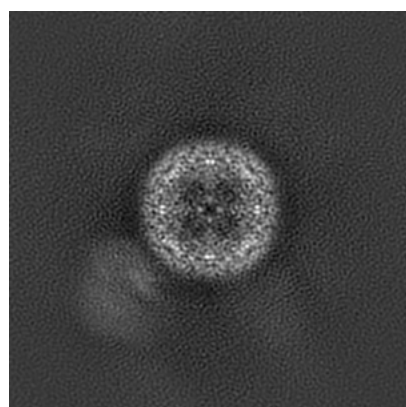
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0140. These allow visual inspection of the internal detail of the map and identification of artifacts.

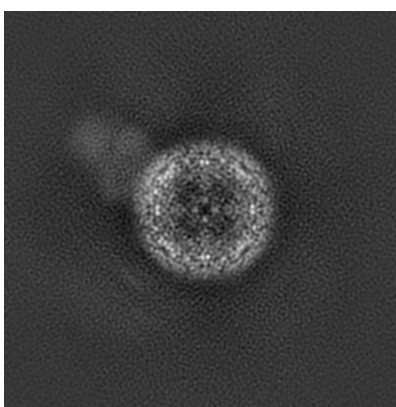
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

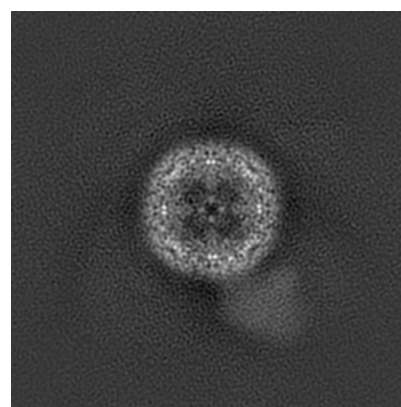
6.1.1 Primary map



X



Y

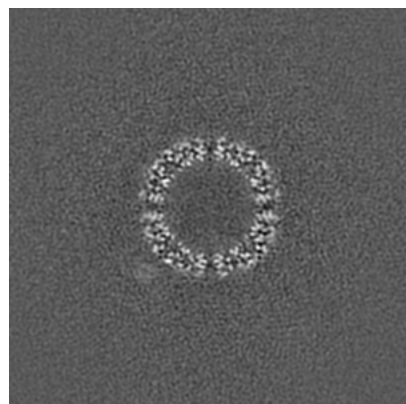


Z

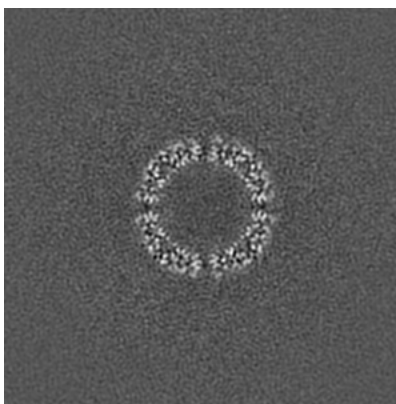
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

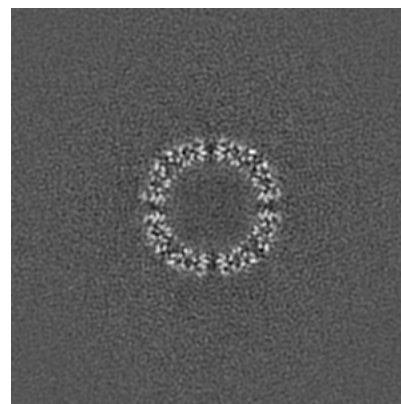
6.2.1 Primary map



X Index: 128



Y Index: 128

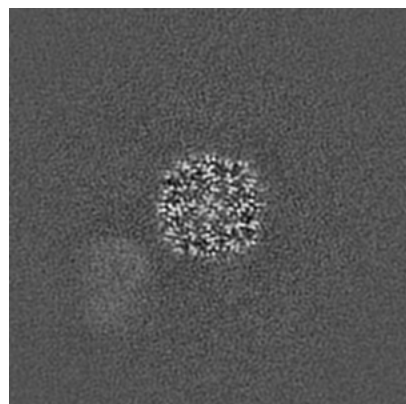


Z Index: 128

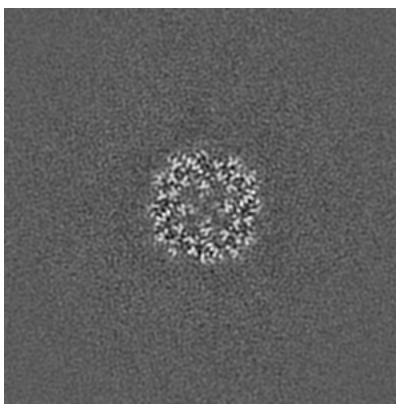
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

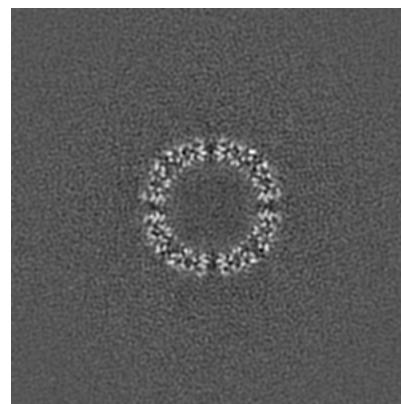
6.3.1 Primary map



X Index: 159



Y Index: 157

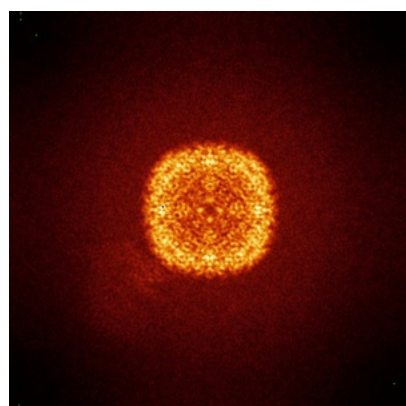


Z Index: 128

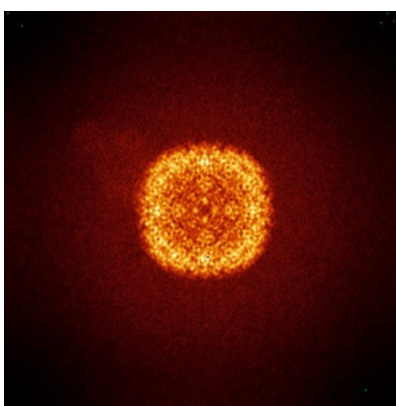
The images above show the largest variance slices of the map in three orthogonal directions.

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

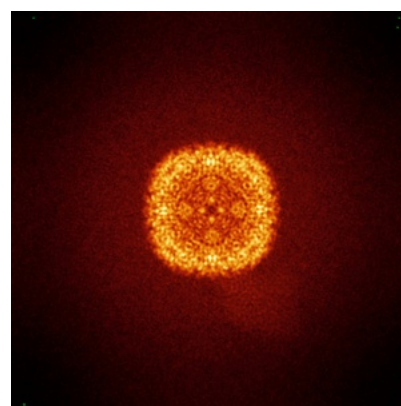
6.4.1 Primary map



X



Y

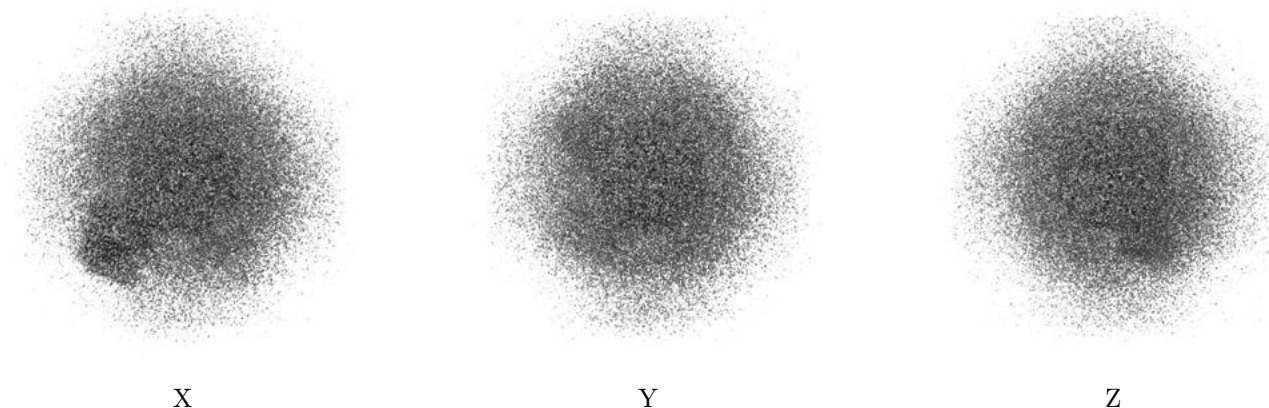


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.8. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

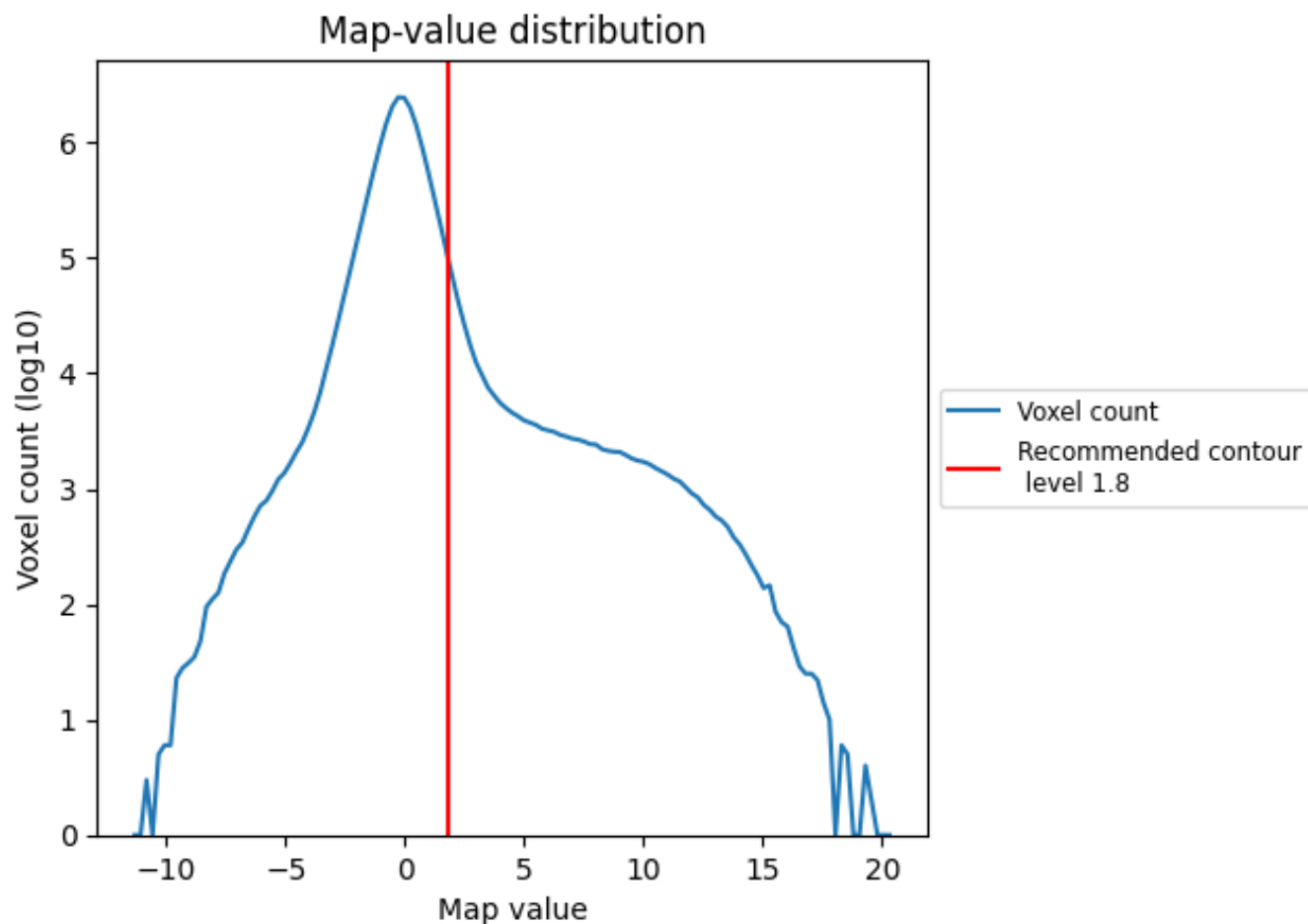
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

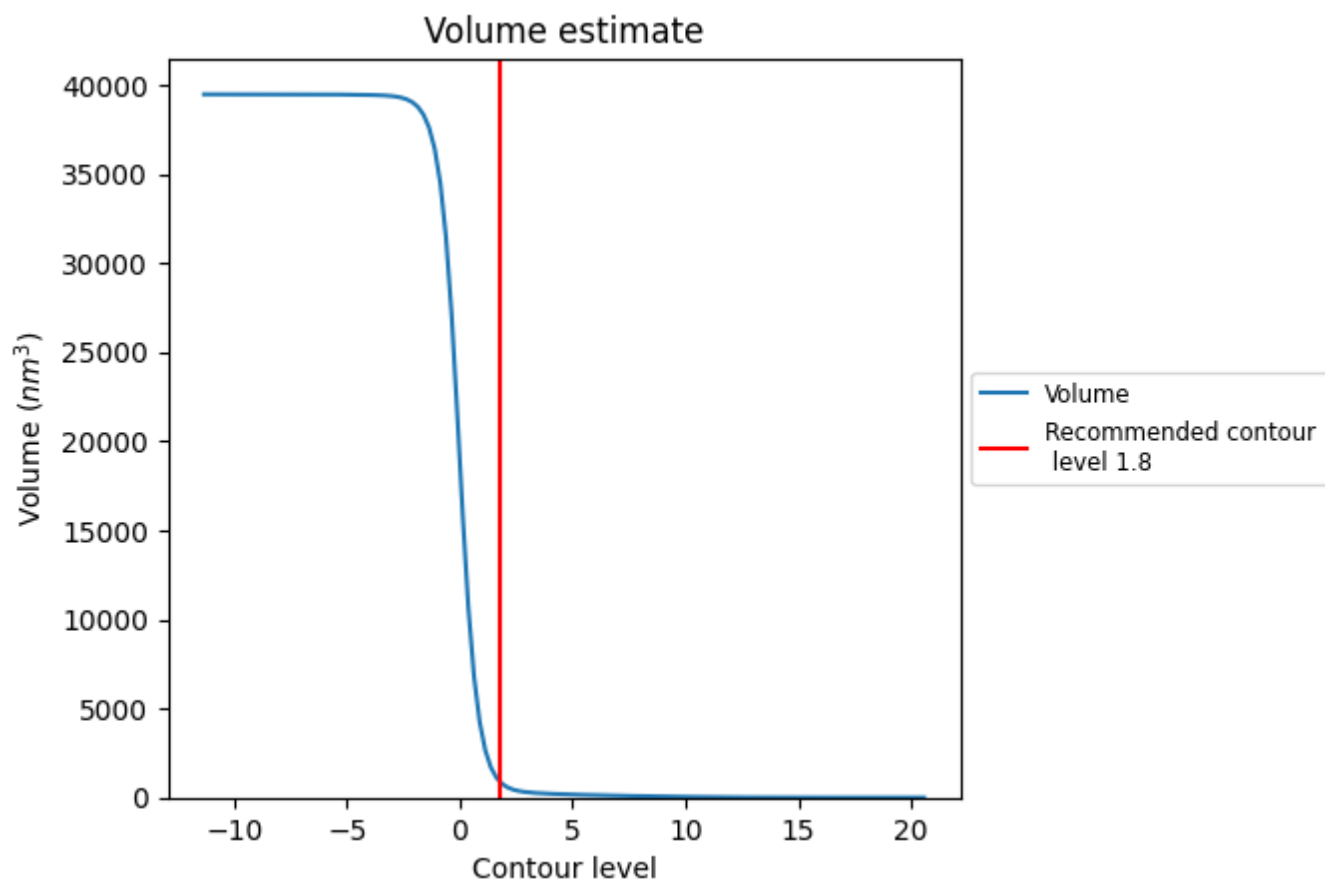
This section contains the results of statistical analysis of the map.

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.

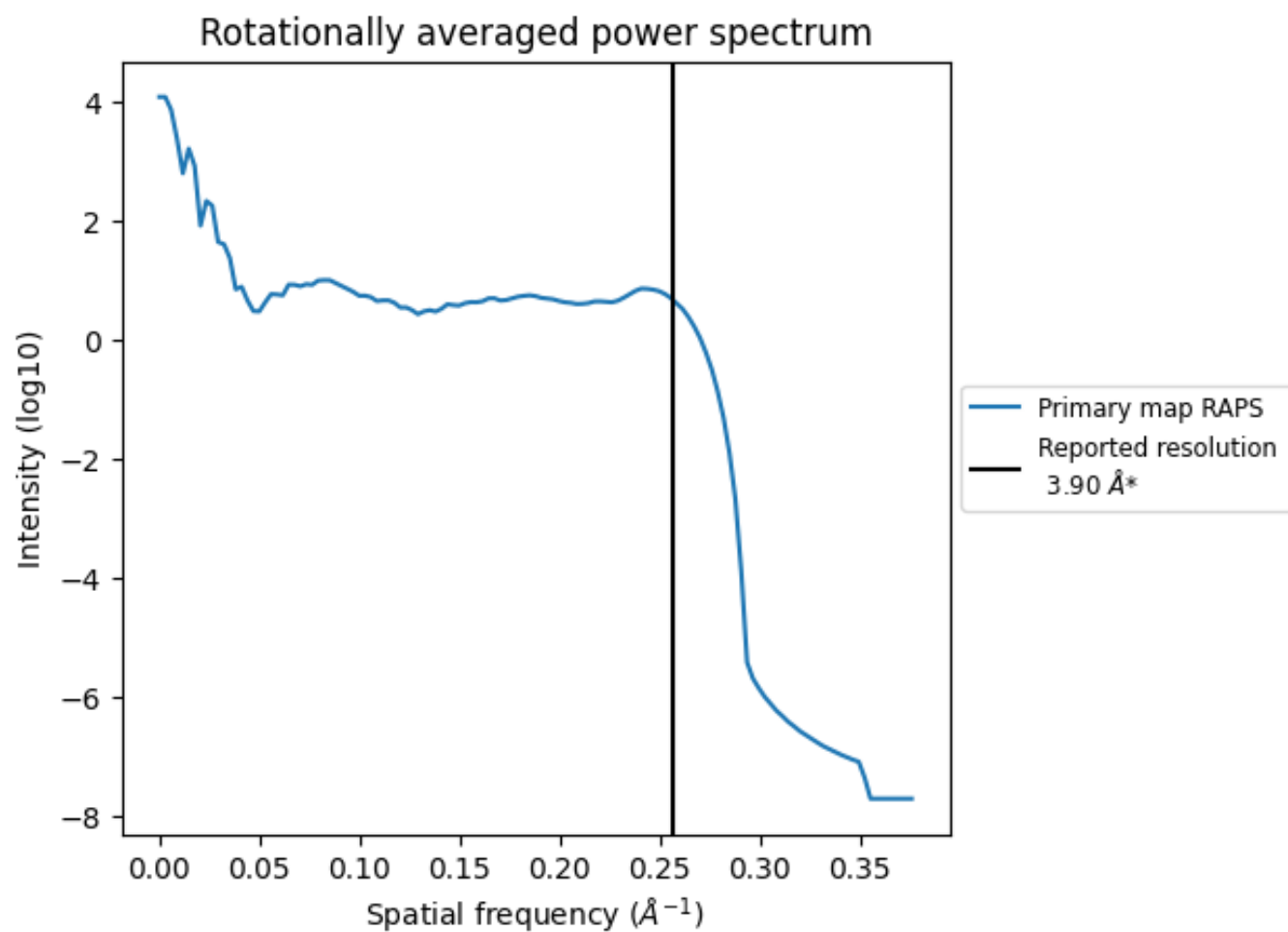
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 877 nm³; this corresponds to an approximate mass of 792 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 0.256 $\text{\AA}^{-1}$

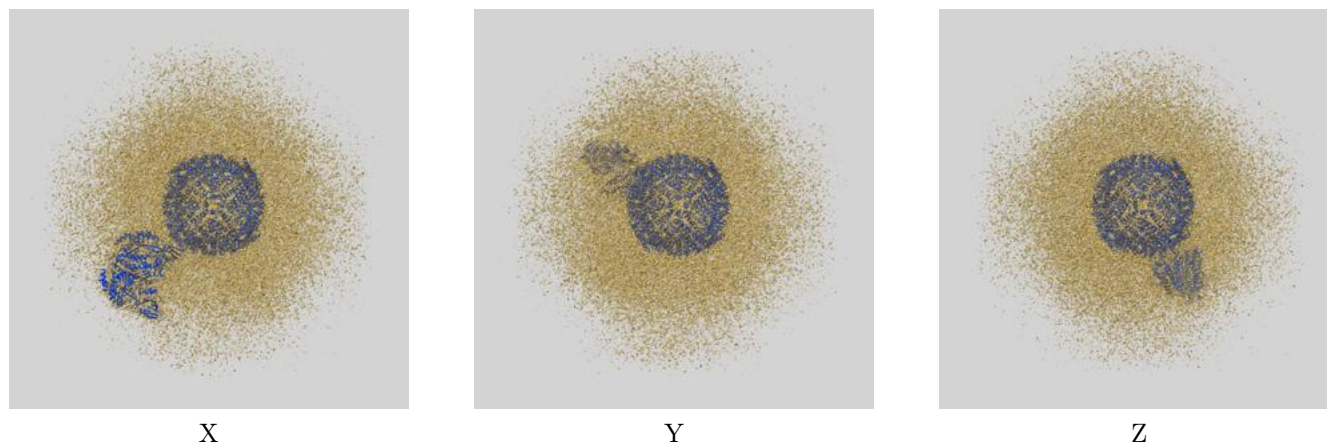
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

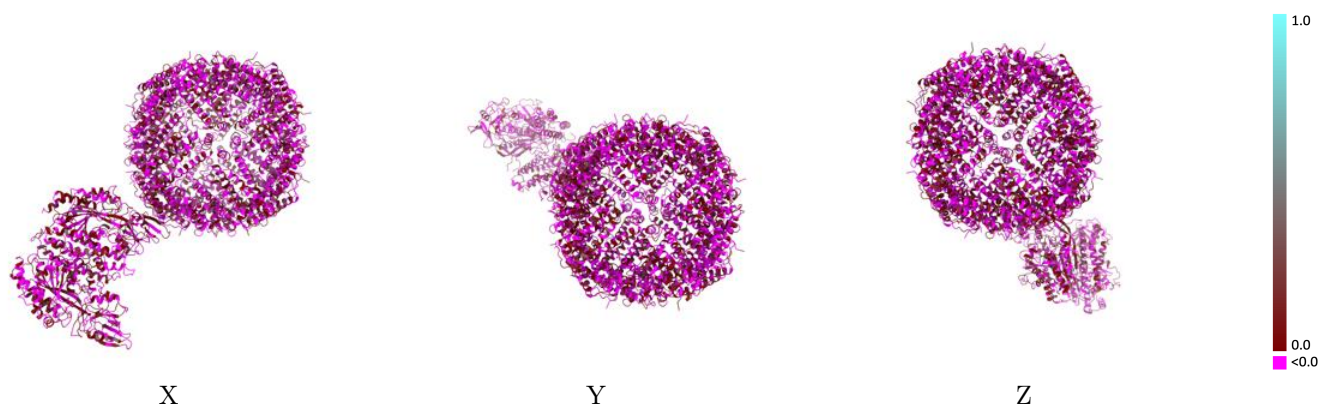
This section contains information regarding the fit between EMDB map EMD-0140 and PDB model 6H5I. Per-residue inclusion information can be found in section 3 on page 6.

9.1 Map-model overlay [i](#)



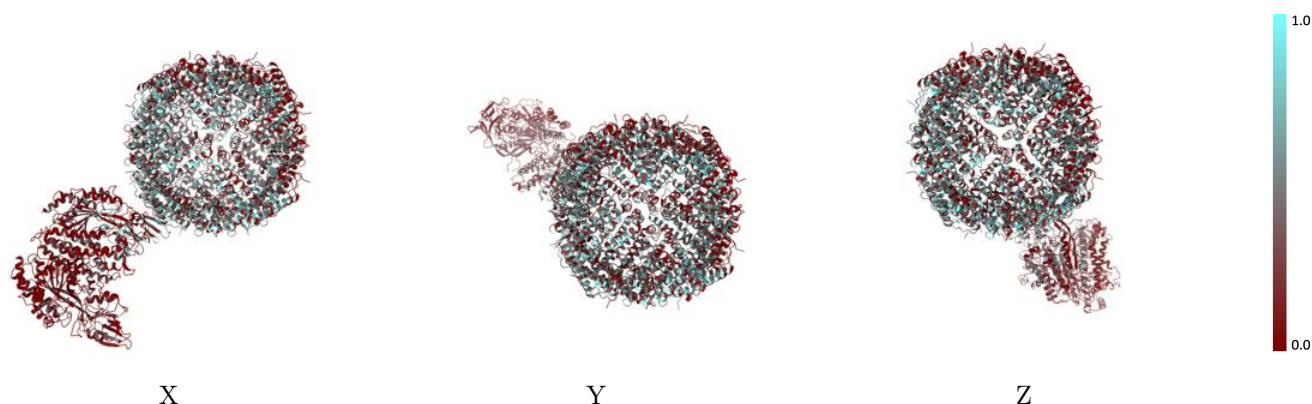
The images above show the 3D surface view of the map at the recommended contour level 1.8 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



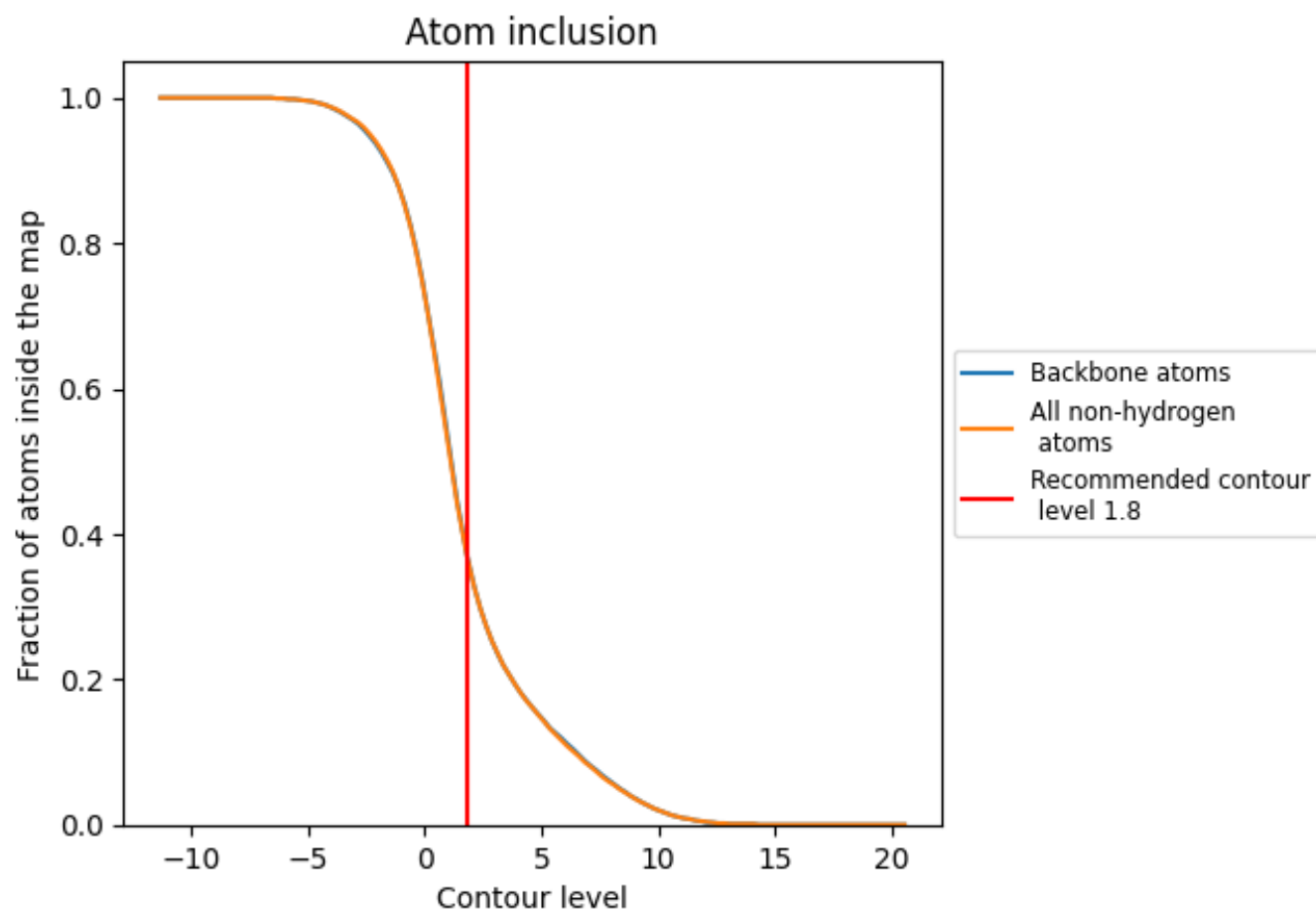
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.8).

9.4 Atom inclusion [i](#)



At the recommended contour level, 37% of all backbone atoms, 37% 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 (1.8) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3710	0.0000
Aa	0.3660	-0.0070
Ab	0.2620	0.0160
Ac	0.4240	-0.0190
Ad	0.3400	-0.0290
Ae	0.3550	-0.0260
Af	0.5230	0.0350
Ag	0.4960	0.0210
Ah	0.4070	-0.0040
Ai	0.5120	0.0250
Aj	0.5040	0.0350
Ak	0.3510	-0.0100
Al	0.4150	0.0060
Am	0.3970	-0.0200
An	0.4050	-0.0170
Ao	0.4350	0.0050
Ap	0.3410	-0.0330
Aq	0.1220	0.0040
Ar	0.4230	0.0010
As	0.4110	-0.0050
At	0.4090	-0.0210
Au	0.4380	0.0000
Av	0.4140	-0.0010
Aw	0.5160	0.0170
Ax	0.3570	-0.0510
Ay	0.5100	0.0250
Az	0.4230	0.0030

