Full wwPDB EM Validation Report ⓘ

Oct 8, 2022 – 05:24 PM EDT

PDB ID	:	7SQK
EMDB ID	:	EMD-25387
Title	:	Cryo-EM structure of the human augmin complex
Authors	:	Gabel, C.A.; Chang, L.
Deposited on	:	2021-11-05
Resolution	:	8.00 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

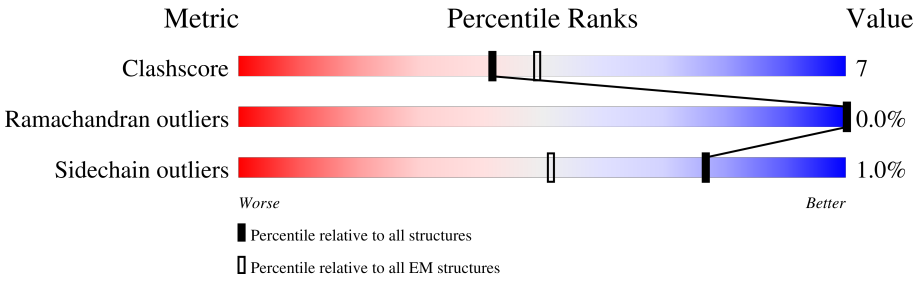
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 8.00 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=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 <=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	278	12% 82% 18%
2	B	284	8% 58% 16% 24%
3	C	603	18% 80% 19%
4	D	318	16% 73% 19% 8%
5	E	633	10% 75% 21%
6	F	432	72% 17% 11%
7	G	368	9% 79% 14% 7%
8	H	410	37% 12% 51%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 23600 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 HAUS augmin-like complex subunit 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	278	2235	1397	387	443	8	0	0

- Molecule 2 is a protein called HAUS augmin-like complex subunit 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	B	215	1731	1100	302	316	13	0	0

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-48	MET	-	expression tag	UNP Q9NVX0
B	-47	HIS	-	expression tag	UNP Q9NVX0
B	-46	HIS	-	expression tag	UNP Q9NVX0
B	-45	HIS	-	expression tag	UNP Q9NVX0
B	-44	HIS	-	expression tag	UNP Q9NVX0
B	-43	HIS	-	expression tag	UNP Q9NVX0
B	-42	HIS	-	expression tag	UNP Q9NVX0
B	-41	HIS	-	expression tag	UNP Q9NVX0
B	-40	HIS	-	expression tag	UNP Q9NVX0
B	-39	PRO	-	expression tag	UNP Q9NVX0
B	-38	GLN	-	expression tag	UNP Q9NVX0
B	-37	LEU	-	expression tag	UNP Q9NVX0
B	-36	ALA	-	expression tag	UNP Q9NVX0
B	-35	MET	-	expression tag	UNP Q9NVX0
B	-34	TRP	-	expression tag	UNP Q9NVX0
B	-33	SER	-	expression tag	UNP Q9NVX0
B	-32	HIS	-	expression tag	UNP Q9NVX0
B	-31	PRO	-	expression tag	UNP Q9NVX0
B	-30	GLN	-	expression tag	UNP Q9NVX0
B	-29	PHE	-	expression tag	UNP Q9NVX0
B	-28	GLU	-	expression tag	UNP Q9NVX0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-27	LYS	-	expression tag	UNP Q9NVX0
B	-26	GLY	-	expression tag	UNP Q9NVX0
B	-25	GLY	-	expression tag	UNP Q9NVX0
B	-24	GLY	-	expression tag	UNP Q9NVX0
B	-23	SER	-	expression tag	UNP Q9NVX0
B	-22	GLY	-	expression tag	UNP Q9NVX0
B	-21	GLY	-	expression tag	UNP Q9NVX0
B	-20	GLY	-	expression tag	UNP Q9NVX0
B	-19	SER	-	expression tag	UNP Q9NVX0
B	-18	GLY	-	expression tag	UNP Q9NVX0
B	-17	GLY	-	expression tag	UNP Q9NVX0
B	-16	GLY	-	expression tag	UNP Q9NVX0
B	-15	SER	-	expression tag	UNP Q9NVX0
B	-14	TRP	-	expression tag	UNP Q9NVX0
B	-13	SER	-	expression tag	UNP Q9NVX0
B	-12	HIS	-	expression tag	UNP Q9NVX0
B	-11	PRO	-	expression tag	UNP Q9NVX0
B	-10	GLN	-	expression tag	UNP Q9NVX0
B	-9	PHE	-	expression tag	UNP Q9NVX0
B	-8	GLU	-	expression tag	UNP Q9NVX0
B	-7	LYS	-	expression tag	UNP Q9NVX0
B	-6	GLU	-	expression tag	UNP Q9NVX0
B	-5	ASN	-	expression tag	UNP Q9NVX0
B	-4	LEU	-	expression tag	UNP Q9NVX0
B	-3	TYR	-	expression tag	UNP Q9NVX0
B	-2	PHE	-	expression tag	UNP Q9NVX0
B	-1	GLN	-	expression tag	UNP Q9NVX0
B	0	SER	-	expression tag	UNP Q9NVX0

- Molecule 3 is a protein called HAUS augmin-like complex subunit 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	600	Total	C	N	O	S	0	0
			4862	3054	826	961	21		

- Molecule 4 is a protein called Isoform 4 of HAUS augmin-like complex subunit 4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	294	Total	C	N	O	S	0	0
			2435	1538	424	462	11		

- Molecule 5 is a protein called HAUS augmin-like complex subunit 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	610	Total	C	N	O	S	0	0
			4867	3030	924	893	20		

- Molecule 6 is a protein called HAUS augmin-like complex subunit 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	385	Total	C	N	O	S	0	0
			3171	2030	556	564	21		

- Molecule 7 is a protein called HAUS augmin-like complex subunit 7.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	344	Total	C	N	O	S	0	0
			2689	1682	449	534	24		

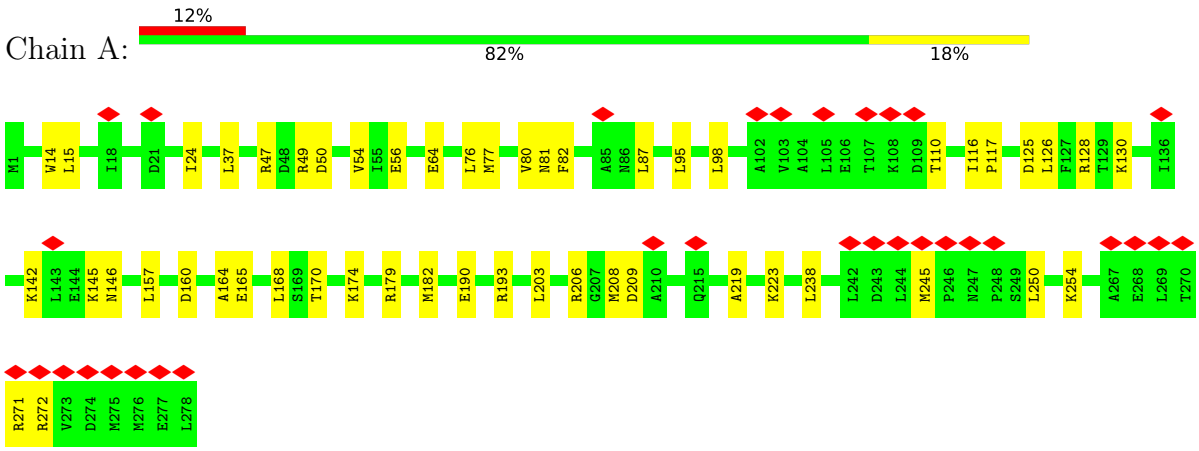
- Molecule 8 is a protein called HAUS augmin-like complex subunit 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	201	Total	C	N	O	S	0	0
			1610	1001	281	321	7		

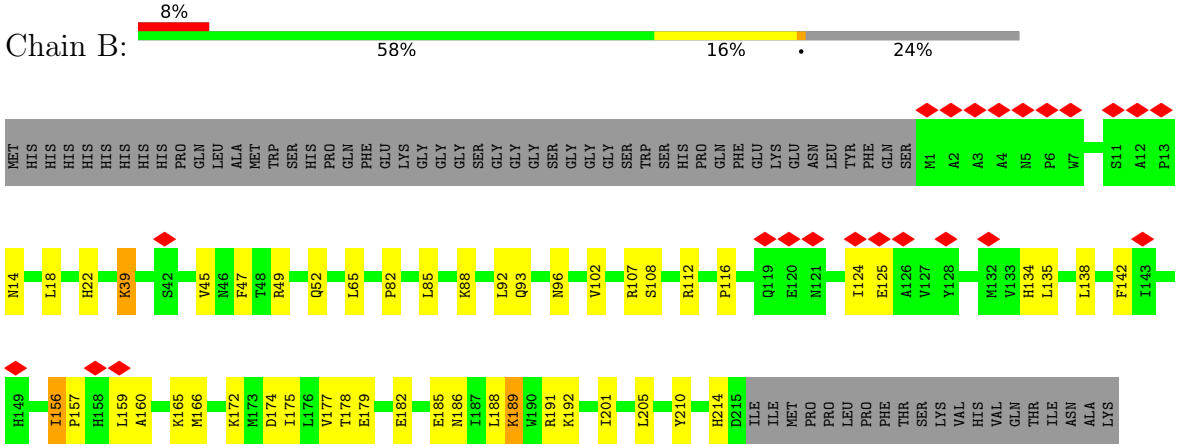
3 Residue-property plots (i)

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

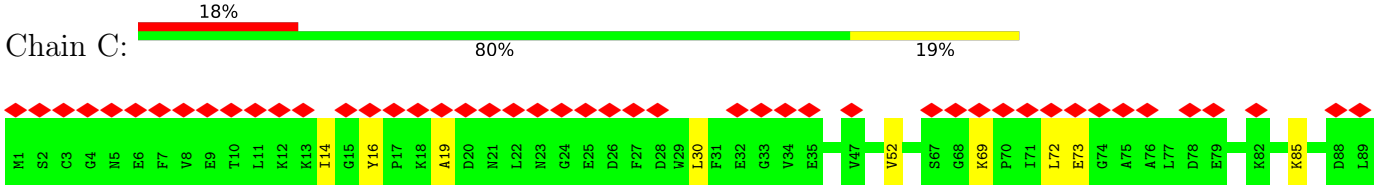
• Molecule 1: HAUS augmin-like complex subunit 1

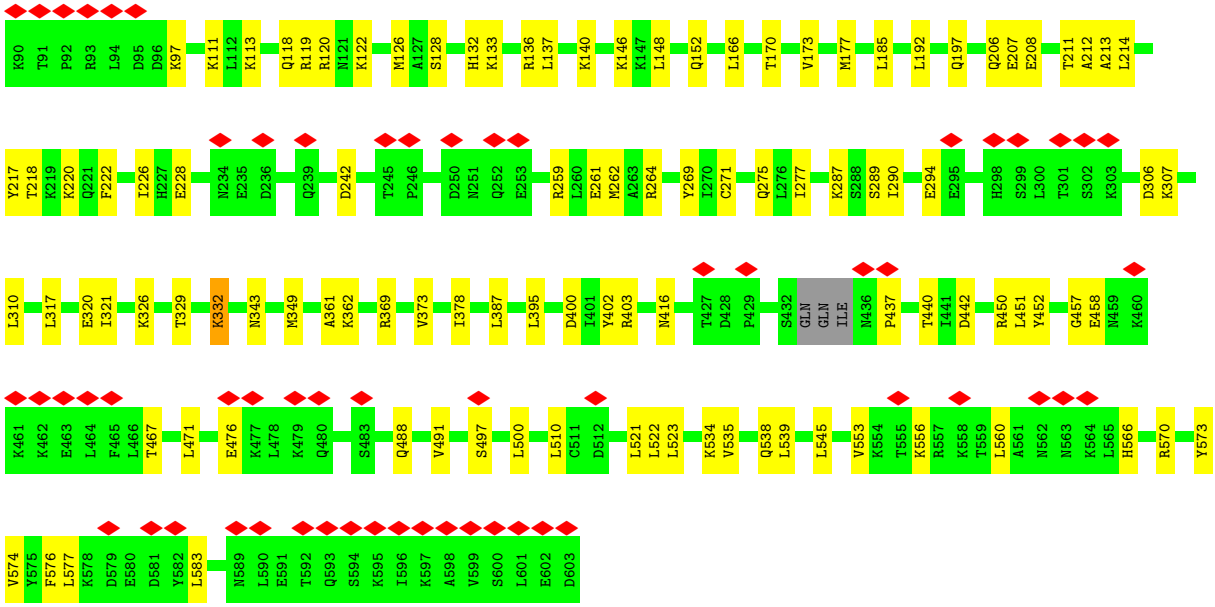


• Molecule 2: HAUS augmin-like complex subunit 2



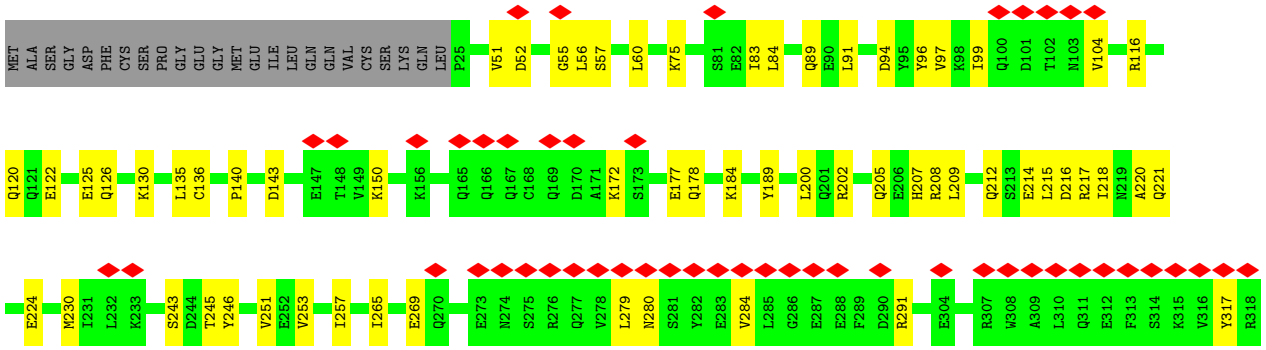
• Molecule 3: HAUS augmin-like complex subunit 3





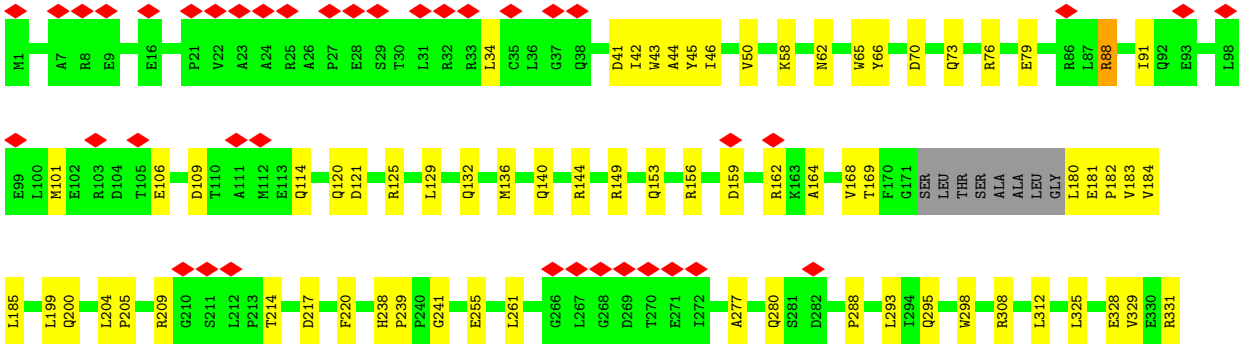
• Molecule 4: Isoform 4 of HAUS augmin-like complex subunit 4

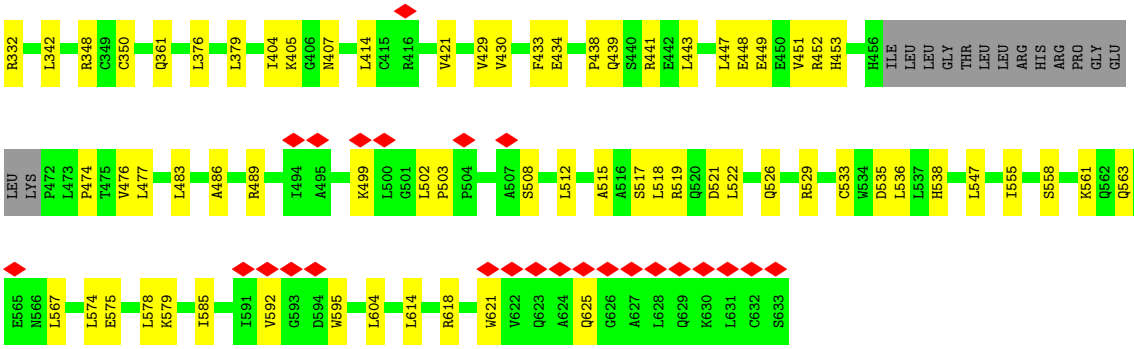
Chain D:



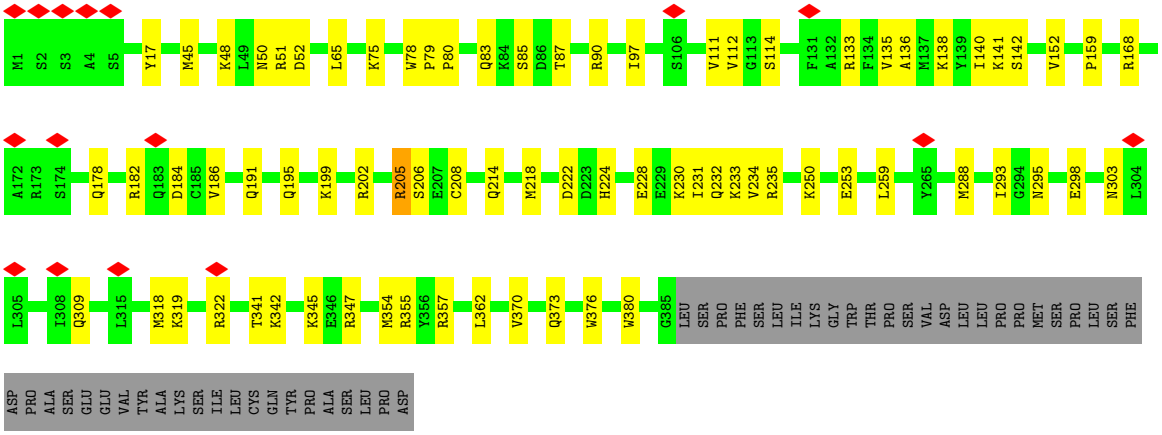
• Molecule 5: HAUS augmin-like complex subunit 5

Chain E:

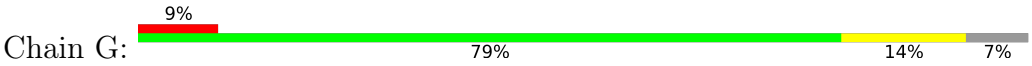


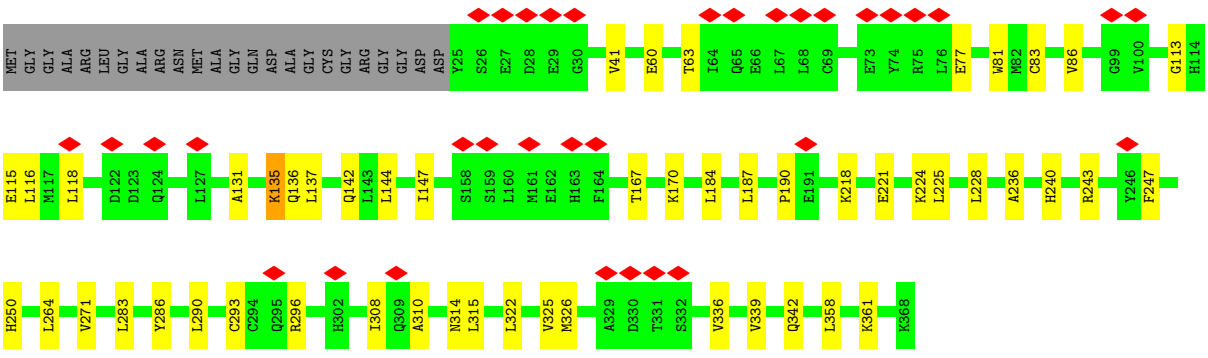


• Molecule 6: HAUS augmin-like complex subunit 6

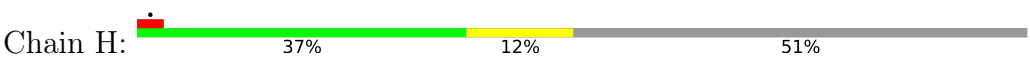


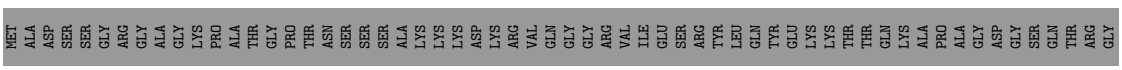
• Molecule 7: HAUS augmin-like complex subunit 7

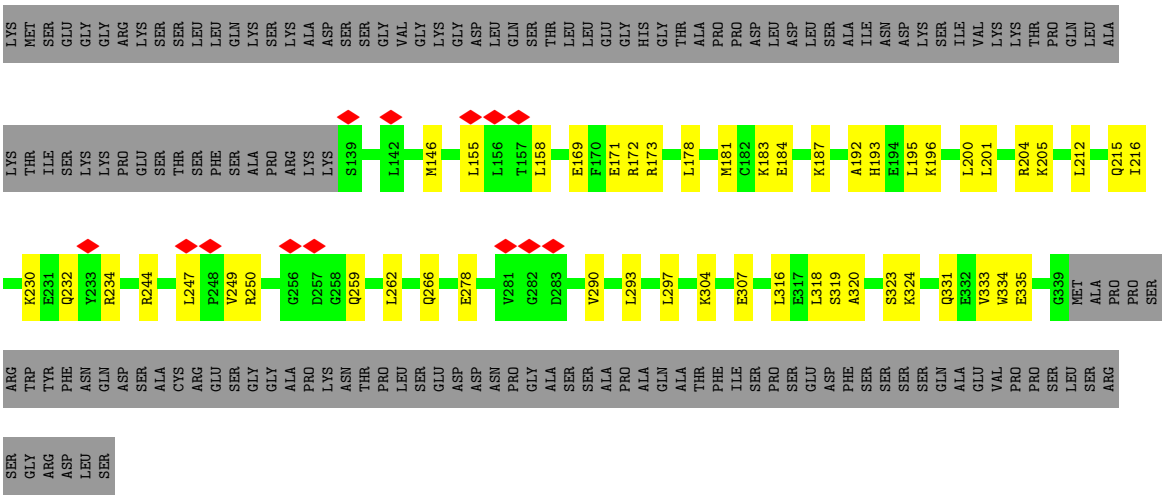




• Molecule 8: HAUS augmin-like complex subunit 8






LYS MET SER GLU GLY GLY ARG LYS SER SER LEU LEU GLN LYS SER LYS ALA ASP SER SER GLY VAL GLY LYS GLY ASP LEU GLN SER THR LEU LEU GLU GLY HIS GLY THR ALA PRO PRO ASP LEU ASP LEU SER ALA ILE ASN ASP LYS SER ILE VAL LYS LYS THR PRO GLN LEU ALA
LYS THR ILE SER LYS LYS PRO GLU SER THR SER PHE SER ALA PRO ARG LYS LYS S139 L142 M146 L155 L156 T157 L158 E169 F170 E171 R172 R173 L178 M181 C182 K183 E184 K187 A192 H193 E194 L195 K196 L200 L201 R204 K205 L212 Q215 I216
K230 E231 Q232 Y233 R234 R244 L247 P248 V249 R250 G256 D257 G258 Q259 L262 Q266 E278 V281 G282 D283 V290 L293 L297 K304 E307 L316 E317 L318 S319 A320 S323 K324 Q331 E332 V333 W334 E335 G339 MET ALA PRO PRO SER
ARG TRP TYR PHE ASN GLN ASP SER ALA CYS ARG GLU SER GLY GLY ALA PRO LYS ASN THR PRO LEU SER GLU ASP ASP ASN PRO GLY ALA SER SER ALA PRO ALA GLN ALA THR PHE ILE SER PRO SER GLU ASP PHE SER SER SER GLN ALA GLU VAL PRO PRO SER LEU SER ARG
SER GLY ARG ASP LEU SER

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	447000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	64000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.193	Depositor
Minimum map value	0.000	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	664.31995, 664.31995, 664.31995	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.384, 1.384, 1.384	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	0.25	0/2263	0.52	0/3044
2	B	0.33	0/1762	0.67	0/2381
3	C	0.25	0/4924	0.49	0/6619
4	D	0.26	0/2470	0.48	0/3325
5	E	0.25	0/4949	0.55	0/6695
6	F	0.28	0/3243	0.55	0/4362
7	G	0.27	0/2739	0.61	0/3706
8	H	0.30	0/1624	0.67	0/2182
All	All	0.27	0/23974	0.56	0/32314

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2235	0	2277	41	0
2	B	1731	0	1771	38	0
3	C	4862	0	4907	98	0
4	D	2435	0	2482	49	0
5	E	4867	0	4968	105	0
6	F	3171	0	3188	52	0
7	G	2689	0	2634	47	0
8	H	1610	0	1638	46	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	23600	0	23865	345	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 7.

All (345) 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)
7:G:283:LEU:HD23	8:H:232:GLN:NE2	1.75	1.00
2:B:135:LEU:CD1	7:G:322:LEU:HD12	2.02	0.90
2:B:135:LEU:HD13	7:G:322:LEU:HD12	1.66	0.77
6:F:168:ARG:HH21	7:G:115:GLU:HG2	1.50	0.77
6:F:373:GLN:HE22	8:H:324:LYS:HE2	1.49	0.76
3:C:120:ARG:NH2	5:E:101:MET:SD	2.65	0.70
7:G:286:TYR:HA	7:G:290:LEU:HB2	1.75	0.67
1:A:179:ARG:HA	1:A:182:MET:HG2	1.75	0.67
3:C:289:SER:OG	5:E:350:CYS:SG	2.53	0.67
5:E:204:LEU:HB3	5:E:209:ARG:HH21	1.61	0.65
3:C:577:LEU:HD11	5:E:604:LEU:HD11	1.78	0.64
4:D:214:GLU:HG3	4:D:217:ARG:HH21	1.63	0.64
2:B:65:LEU:HD22	8:H:200:LEU:HD21	1.81	0.62
3:C:361:ALA:HB1	5:E:280:GLN:HE22	1.65	0.62
5:E:182:PRO:HB2	5:E:184:VAL:HG12	1.81	0.62
1:A:110:THR:HG21	4:D:83:ILE:HG12	1.81	0.62
2:B:135:LEU:CD1	7:G:322:LEU:CD1	2.77	0.62
3:C:128:SER:O	3:C:132:HIS:ND1	2.28	0.62
2:B:166:MET:HG3	7:G:342:GLN:HG3	1.82	0.62
6:F:191:GLN:O	6:F:195:GLN:NE2	2.33	0.62
3:C:261:GLU:OE1	8:H:324:LYS:NZ	2.33	0.61
1:A:54:VAL:HG22	5:E:512:LEU:HG	1.83	0.61
2:B:14:ASN:ND2	6:F:184:ASP:OD1	2.33	0.61
1:A:168:LEU:HD11	4:D:207:HIS:HA	1.83	0.61
4:D:212:GLN:HA	4:D:215:LEU:HD12	1.82	0.61
2:B:49:ARG:HD2	7:G:221:GLU:HB3	1.83	0.60
3:C:387:LEU:HD23	5:E:414:LEU:HD13	1.82	0.60
5:E:288:PRO:HB2	5:E:293:LEU:HG	1.83	0.60
6:F:228:GLU:HA	6:F:231:ILE:HD12	1.83	0.60
5:E:526:GLN:O	5:E:529:ARG:HB2	2.01	0.60
5:E:522:LEU:HG	5:E:526:GLN:HE22	1.67	0.60
7:G:283:LEU:HD23	8:H:232:GLN:HE22	1.60	0.60
1:A:179:ARG:HH21	4:D:218:ILE:HG12	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:535:ASP:O	5:E:538:HIS:HB2	2.02	0.59
3:C:442:ASP:H	5:E:489:ARG:HH12	1.50	0.59
8:H:169:GLU:OE1	8:H:173:ARG:NH1	2.35	0.59
3:C:217:TYR:OH	3:C:369:ARG:NH1	2.36	0.58
6:F:168:ARG:HD2	7:G:116:LEU:HD23	1.85	0.58
2:B:201:ILE:HG12	5:E:312:LEU:HD11	1.86	0.58
7:G:293:CYS:O	7:G:296:ARG:NH1	2.38	0.57
8:H:192:ALA:HA	8:H:195:LEU:HD12	1.85	0.57
1:A:49:ARG:HH12	3:C:457:GLY:HA2	1.70	0.57
2:B:205:LEU:HD11	5:E:308:ARG:HH21	1.69	0.57
2:B:142:PHE:HE1	7:G:326:MET:HG2	1.70	0.57
3:C:476:GLU:HB2	5:E:499:LYS:HD3	1.87	0.57
3:C:16:TYR:HB3	3:C:19:ALA:HB2	1.87	0.56
3:C:451:LEU:HA	5:E:512:LEU:HD13	1.87	0.56
7:G:358:LEU:HA	7:G:361:LYS:HE2	1.86	0.56
6:F:380:TRP:NE1	8:H:335:GLU:OE2	2.38	0.56
1:A:125:ASP:HA	1:A:128:ARG:HB2	1.87	0.56
4:D:216:ASP:OD2	5:E:563:GLN:NE2	2.39	0.56
5:E:449:GLU:O	5:E:453:HIS:ND1	2.36	0.56
3:C:416:ASN:ND2	5:E:439:GLN:OE1	2.38	0.55
5:E:295:GLN:HG2	8:H:320:ALA:HB2	1.88	0.55
3:C:69:LYS:NZ	5:E:70:ASP:OD2	2.40	0.55
1:A:126:LEU:O	1:A:130:LYS:NZ	2.39	0.55
3:C:14:ILE:HA	3:C:52:VAL:HG21	1.88	0.55
8:H:181:MET:HA	8:H:184:GLU:HG2	1.88	0.55
7:G:322:LEU:HA	7:G:325:VAL:HG22	1.89	0.55
4:D:51:VAL:HG13	4:D:55:GLY:HA2	1.89	0.55
2:B:18:LEU:O	2:B:22:HIS:ND1	2.40	0.55
5:E:448:GLU:HB3	5:E:452:ARG:HH12	1.72	0.55
3:C:218:THR:HA	3:C:222:PHE:HB2	1.89	0.54
5:E:169:THR:HA	5:E:182:PRO:HA	1.88	0.54
3:C:522:LEU:O	4:D:208:ARG:NH1	2.41	0.54
5:E:106:GLU:HA	5:E:109:ASP:HB2	1.90	0.54
7:G:283:LEU:HA	8:H:232:GLN:HE22	1.73	0.54
7:G:315:LEU:HG	8:H:250:ARG:HH21	1.73	0.54
1:A:206:ARG:HB3	4:D:251:VAL:HG21	1.89	0.54
5:E:159:ASP:HA	5:E:162:ARG:HB2	1.90	0.54
3:C:206:GLN:NE2	5:E:255:GLU:OE1	2.40	0.54
3:C:228:GLU:OE1	3:C:362:LYS:NZ	2.38	0.54
3:C:307:LYS:HA	3:C:310:LEU:HD12	1.89	0.54
6:F:205:ARG:NH1	6:F:206:SER:OG	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:72:LEU:HD12	5:E:62:ASN:HA	1.90	0.53
3:C:306:ASP:O	3:C:310:LEU:N	2.40	0.53
3:C:510:LEU:HB3	4:D:200:LEU:HD22	1.90	0.53
4:D:205:GLN:HA	4:D:209:LEU:HB2	1.90	0.53
1:A:206:ARG:NH1	4:D:246:TYR:O	2.41	0.53
3:C:538:GLN:HE22	5:E:578:LEU:HB3	1.74	0.53
3:C:185:LEU:HD12	3:C:197:GLN:HB2	1.90	0.53
5:E:153:GLN:OE1	5:E:156:ARG:NH1	2.41	0.53
1:A:82:PHE:HA	4:D:116:ARG:HH21	1.73	0.53
3:C:220:LYS:NZ	5:E:261:LEU:O	2.42	0.53
3:C:259:ARG:NH1	3:C:262:MET:SD	2.82	0.53
5:E:517:SER:O	5:E:521:ASP:N	2.39	0.53
7:G:310:ALA:O	7:G:314:ASN:ND2	2.42	0.53
6:F:295:ASN:HB3	6:F:298:GLU:HG3	1.91	0.53
7:G:283:LEU:HD23	8:H:232:GLN:CD	2.28	0.53
5:E:430:VAL:HA	5:E:433:PHE:HB2	1.91	0.52
7:G:41:VAL:HG21	7:G:137:LEU:HD22	1.90	0.52
5:E:41:ASP:O	5:E:44:ALA:HB3	2.09	0.52
7:G:144:LEU:HA	7:G:147:ILE:HD12	1.90	0.52
2:B:201:ILE:HG22	8:H:333:VAL:HG11	1.92	0.52
3:C:458:GLU:OE1	5:E:519:ARG:NH2	2.43	0.52
6:F:362:LEU:HB2	8:H:318:LEU:HD12	1.91	0.52
1:A:203:LEU:HD22	1:A:208:MET:HG3	1.91	0.52
7:G:77:GLU:OE2	7:G:81:TRP:NE1	2.43	0.52
2:B:165:LYS:HD2	7:G:339:VAL:HG22	1.90	0.52
2:B:210:TYR:O	2:B:214:HIS:ND1	2.40	0.52
1:A:49:ARG:NH1	1:A:50:ASP:OD1	2.43	0.52
3:C:140:LYS:HA	4:D:96:TYR:CZ	2.45	0.52
3:C:440:THR:HA	3:C:467:THR:HA	1.91	0.52
1:A:116:ILE:HG13	1:A:117:PRO:HD3	1.91	0.51
3:C:133:LYS:HA	3:C:136:ARG:HD3	1.93	0.51
4:D:57:SER:HB2	4:D:60:LEU:HB2	1.92	0.51
5:E:114:GLN:NE2	5:E:486:ALA:O	2.43	0.51
7:G:184:LEU:HG	7:G:187:LEU:HD12	1.92	0.51
6:F:182:ARG:HE	6:F:186:VAL:HG23	1.74	0.51
2:B:52:GLN:HE22	7:G:225:LEU:HD13	1.75	0.51
3:C:137:LEU:HA	3:C:140:LYS:HD2	1.93	0.51
5:E:533:CYS:O	5:E:536:LEU:HB3	2.09	0.51
6:F:79:PRO:HB2	6:F:85:SER:HB2	1.91	0.51
3:C:577:LEU:HD13	4:D:257:ILE:HD11	1.93	0.51
3:C:136:ARG:HE	4:D:97:VAL:HG21	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:138:LYS:NZ	6:F:142:SER:OG	2.44	0.51
4:D:217:ARG:HH11	4:D:221:GLN:HE22	1.59	0.51
8:H:212:LEU:O	8:H:216:ILE:HG12	2.11	0.51
1:A:245:MET:HG3	1:A:250:LEU:HD23	1.93	0.51
1:A:206:ARG:NH1	4:D:243:SER:O	2.39	0.50
3:C:170:THR:OG1	5:E:441:ARG:NH1	2.44	0.50
3:C:437:PRO:O	5:E:489:ARG:NH2	2.43	0.50
4:D:177:GLU:OE2	4:D:178:GLN:NE2	2.44	0.50
8:H:234:ARG:O	8:H:234:ARG:NH1	2.45	0.50
3:C:535:VAL:HG22	5:E:575:GLU:HG2	1.93	0.50
3:C:73:GLU:HG2	5:E:58:LYS:HG3	1.94	0.50
5:E:169:THR:HG22	5:E:180:LEU:HD23	1.93	0.50
7:G:247:PHE:HA	7:G:250:HIS:HB3	1.93	0.50
5:E:204:LEU:HD12	5:E:205:PRO:HD2	1.93	0.50
8:H:259:GLN:HA	8:H:262:LEU:HD12	1.92	0.50
5:E:121:ASP:HB3	5:E:125:ARG:HH21	1.76	0.49
3:C:320:GLU:OE1	5:E:348:ARG:NH1	2.45	0.49
3:C:452:TYR:HD1	3:C:471:LEU:HD13	1.77	0.49
1:A:190:GLU:OE2	1:A:193:ARG:NH1	2.45	0.49
3:C:166:LEU:HD21	5:E:443:LEU:HD23	1.93	0.49
7:G:118:LEU:HD22	7:G:142:GLN:HE21	1.78	0.49
3:C:395:LEU:HD13	5:E:421:VAL:HG22	1.94	0.49
2:B:125:GLU:HG3	8:H:247:LEU:HD13	1.93	0.49
1:A:98:LEU:HB3	4:D:83:ILE:HD13	1.94	0.49
2:B:39:LYS:HE2	6:F:178:GLN:HE22	1.77	0.49
3:C:119:ARG:HH22	4:D:140:PRO:HG3	1.78	0.48
6:F:199:LYS:HD2	6:F:202:ARG:HH21	1.78	0.48
3:C:269:TYR:HE2	3:C:343:ASN:HB3	1.79	0.48
2:B:185:GLU:HA	2:B:188:LEU:HG	1.95	0.48
5:E:329:VAL:HG13	5:E:342:LEU:HD13	1.95	0.48
3:C:277:ILE:HG12	5:E:361:GLN:HB3	1.95	0.48
6:F:319:LYS:NZ	8:H:278:GLU:OE1	2.45	0.48
7:G:190:PRO:O	8:H:173:ARG:NH2	2.45	0.48
5:E:474:PRO:HB2	5:E:476:VAL:HG23	1.96	0.48
6:F:45:MET:O	6:F:50:ASN:ND2	2.47	0.48
3:C:553:VAL:HG22	3:C:556:LYS:HZ1	1.78	0.48
5:E:298:TRP:HB3	8:H:323:SER:HB2	1.96	0.48
5:E:376:LEU:HD12	5:E:379:LEU:HD12	1.95	0.48
6:F:341:THR:HG22	8:H:297:LEU:HD21	1.96	0.48
1:A:15:LEU:HB3	1:A:24:ILE:HD13	1.96	0.47
4:D:220:ALA:HB3	5:E:567:LEU:HD22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:191:ARG:HH21	8:H:319:SER:HB2	1.79	0.47
6:F:112:VAL:HG12	6:F:114:SER:H	1.78	0.47
2:B:186:ASN:O	2:B:189:LYS:HG3	2.14	0.47
5:E:181:GLU:HG3	5:E:185:LEU:HD23	1.96	0.47
2:B:108:SER:O	2:B:112:ARG:HG2	2.15	0.47
2:B:179:GLU:HA	2:B:182:GLU:HB3	1.96	0.47
4:D:89:GLN:OE1	5:E:120:GLN:NE2	2.47	0.47
5:E:164:ALA:HB1	5:E:239:PRO:HB3	1.96	0.47
5:E:515:ALA:O	5:E:518:LEU:HB2	2.15	0.47
7:G:131:ALA:O	7:G:136:GLN:NE2	2.48	0.47
5:E:88:ARG:HA	5:E:91:ILE:HD12	1.96	0.47
1:A:50:ASP:OD2	5:E:519:ARG:NH1	2.48	0.47
3:C:400:ASP:OD1	3:C:403:ARG:NH1	2.47	0.47
5:E:73:GLN:HA	5:E:76:ARG:HG2	1.96	0.47
6:F:293:ILE:HG12	6:F:309:GLN:HB3	1.97	0.47
7:G:224:LYS:O	7:G:228:LEU:HB2	2.15	0.47
7:G:60:GLU:OE1	7:G:63:THR:N	2.41	0.46
4:D:91:LEU:HB2	4:D:126:GLN:HG3	1.96	0.46
1:A:164:ALA:HB1	3:C:523:LEU:HD11	1.98	0.46
3:C:545:LEU:HD13	5:E:585:ILE:HG21	1.97	0.46
5:E:42:ILE:O	5:E:45:TYR:HB3	2.15	0.46
6:F:52:ASP:N	6:F:52:ASP:OD1	2.48	0.46
6:F:250:LYS:O	6:F:253:GLU:HB3	2.16	0.46
3:C:177:MET:SD	5:E:433:PHE:HB3	2.56	0.46
5:E:404:ILE:HD12	5:E:407:ASN:HB2	1.98	0.46
2:B:85:LEU:HA	2:B:88:LYS:HZ2	1.80	0.46
3:C:208:GLU:O	3:C:212:ALA:N	2.45	0.46
5:E:328:GLU:OE2	5:E:332:ARG:NH1	2.48	0.46
6:F:87:THR:HA	6:F:90:ARG:HE	1.81	0.45
6:F:205:ARG:HA	6:F:208:CYS:HB2	1.98	0.45
6:F:231:ILE:O	6:F:234:VAL:HB	2.17	0.45
2:B:157:PRO:HB2	2:B:160:ALA:HB3	1.99	0.45
3:C:213:ALA:HB2	5:E:255:GLU:HG3	1.97	0.45
3:C:488:GLN:HA	3:C:491:VAL:HG12	1.98	0.45
6:F:355:ARG:HH21	8:H:307:GLU:HG3	1.81	0.45
1:A:238:LEU:HD13	4:D:279:LEU:HG	1.98	0.45
3:C:192:LEU:HD13	5:E:241:GLY:HA3	1.99	0.45
1:A:87:LEU:HD23	4:D:120:GLN:HG3	1.98	0.45
6:F:65:LEU:HD13	6:F:135:VAL:HG23	1.98	0.45
8:H:244:ARG:O	8:H:244:ARG:NH1	2.40	0.45
3:C:275:GLN:HG2	8:H:334:TRP:CG	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:122:GLU:HA	4:D:125:GLU:HB3	1.99	0.45
5:E:621:TRP:NE1	5:E:625:GLN:OE1	2.50	0.45
1:A:56:GLU:OE1	3:C:450:ARG:NE	2.50	0.45
3:C:576:PHE:HB2	3:C:583:LEU:HD22	1.99	0.45
6:F:78:TRP:O	6:F:80:PRO:HD3	2.17	0.45
1:A:77:MET:HA	1:A:81:ASN:HA	1.98	0.45
3:C:539:LEU:HD11	4:D:230:MET:HE3	1.99	0.45
6:F:17:TYR:HE1	8:H:155:LEU:HG	1.80	0.45
8:H:212:LEU:O	8:H:215:GLN:NE2	2.50	0.45
8:H:290:VAL:HA	8:H:293:LEU:HG	1.98	0.45
1:A:14:TRP:HZ3	1:A:37:LEU:HD13	1.82	0.44
6:F:75:LYS:HE2	6:F:75:LYS:HB3	1.77	0.44
6:F:342:LYS:HA	6:F:345:LYS:HG2	1.98	0.44
1:A:76:LEU:HD22	1:A:82:PHE:HB3	1.99	0.44
2:B:124:ILE:HG22	8:H:249:VAL:HG13	1.98	0.44
5:E:614:LEU:HD21	5:E:618:ARG:HH21	1.82	0.44
3:C:152:GLN:HB2	5:E:129:LEU:HD13	1.99	0.44
5:E:518:LEU:O	5:E:522:LEU:N	2.47	0.44
6:F:376:TRP:NE1	8:H:335:GLU:OE2	2.51	0.44
2:B:177:VAL:HG21	6:F:347:ARG:HD3	2.00	0.44
5:E:277:ALA:HB3	5:E:280:GLN:HB2	2.00	0.44
1:A:157:LEU:HA	1:A:160:ASP:HB2	1.99	0.44
3:C:207:GLU:O	3:C:211:THR:N	2.43	0.44
3:C:271:CYS:HB2	8:H:331:GLN:HG3	2.00	0.44
1:A:56:GLU:OE2	3:C:450:ARG:NH2	2.51	0.43
2:B:92:LEU:O	2:B:96:ASN:ND2	2.51	0.43
2:B:142:PHE:CE2	7:G:322:LEU:HD22	2.53	0.43
6:F:136:ALA:O	6:F:140:ILE:HG12	2.18	0.43
6:F:230:LYS:HA	6:F:233:LYS:HE2	2.00	0.43
6:F:232:GLN:O	6:F:235:ARG:HG3	2.18	0.43
7:G:240:HIS:HD2	7:G:243:ARG:HH22	1.66	0.43
8:H:171:GLU:OE2	8:H:172:ARG:NH1	2.51	0.43
3:C:192:LEU:HB2	5:E:239:PRO:HB2	2.00	0.43
5:E:217:ASP:HA	5:E:220:PHE:HB2	2.01	0.43
7:G:131:ALA:HB1	7:G:135:LYS:HE3	2.01	0.43
1:A:80:VAL:HG23	1:A:82:PHE:HB2	2.00	0.43
1:A:146:ASN:HB3	4:D:189:TYR:CZ	2.54	0.43
2:B:102:VAL:HG22	6:F:259:LEU:HD12	1.99	0.43
6:F:159:PRO:HG2	8:H:146:MET:HB3	2.00	0.43
6:F:288:MET:SD	6:F:288:MET:N	2.91	0.43
8:H:183:LYS:HE3	8:H:187:LYS:HE3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:201:LEU:HB3	8:H:205:LYS:NZ	2.34	0.43
8:H:262:LEU:O	8:H:266:GLN:HG2	2.18	0.43
5:E:558:SER:HA	5:E:561:LYS:HG2	2.01	0.43
7:G:308:ILE:HD12	8:H:247:LEU:H	1.83	0.43
5:E:66:TYR:O	5:E:70:ASP:N	2.45	0.43
7:G:218:LYS:HA	7:G:218:LYS:HD2	1.86	0.43
3:C:497:SER:HA	3:C:500:LEU:HD12	2.01	0.43
6:F:214:GLN:O	6:F:218:MET:HG3	2.18	0.43
1:A:209:ASP:OD1	1:A:209:ASP:N	2.50	0.43
3:C:113:LYS:HE3	5:E:91:ILE:HG12	2.01	0.43
3:C:173:VAL:O	3:C:177:MET:HG2	2.19	0.43
5:E:404:ILE:HA	5:E:407:ASN:HB2	2.00	0.43
6:F:318:MET:HB3	6:F:322:ARG:HH12	1.84	0.43
2:B:47:PHE:CD1	8:H:178:LEU:HB3	2.54	0.42
3:C:264:ARG:HH22	6:F:370:VAL:HG22	1.84	0.42
3:C:402:TYR:HB2	5:E:429:VAL:HG13	2.01	0.42
3:C:521:LEU:HD13	3:C:523:LEU:HG	2.00	0.42
4:D:52:ASP:OD1	4:D:56:LEU:N	2.51	0.42
4:D:130:LYS:HB3	4:D:130:LYS:HE3	1.83	0.42
6:F:354:MET:HA	6:F:357:ARG:HG2	2.01	0.42
8:H:193:HIS:HA	8:H:196:LYS:HE2	2.01	0.42
6:F:51:ARG:HH12	6:F:83:GLN:HE22	1.67	0.42
3:C:118:GLN:OE1	3:C:119:ARG:NH1	2.53	0.42
3:C:271:CYS:HB2	8:H:331:GLN:HE21	1.85	0.42
4:D:265:ILE:HG13	4:D:269:GLU:OE1	2.19	0.42
1:A:272:ARG:HH22	4:D:317:TYR:HB2	1.83	0.42
2:B:93:GLN:HE21	7:G:271:VAL:HG21	1.84	0.42
3:C:566:HIS:O	3:C:570:ARG:HG2	2.20	0.42
5:E:200:GLN:O	5:E:204:LEU:N	2.53	0.42
6:F:140:ILE:HD11	8:H:158:LEU:HA	2.01	0.42
6:F:295:ASN:O	6:F:303:ASN:ND2	2.37	0.42
7:G:167:THR:HA	7:G:170:LYS:HG2	2.02	0.42
7:G:236:ALA:O	7:G:240:HIS:ND1	2.39	0.42
1:A:170:THR:HG22	1:A:174:LYS:HE3	2.02	0.42
3:C:294:GLU:HG3	5:E:325:LEU:HD21	2.00	0.42
3:C:560:LEU:HD21	3:C:570:ARG:HH21	1.84	0.42
4:D:99:ILE:HG23	4:D:104:VAL:HG13	2.00	0.42
7:G:361:LYS:NZ	8:H:316:LEU:HD21	2.35	0.42
3:C:148:LEU:HD12	5:E:129:LEU:HD11	2.02	0.42
5:E:502:LEU:HD12	5:E:503:PRO:HD2	2.02	0.42
1:A:95:LEU:HD22	4:D:84:LEU:HD21	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:136:ARG:NH2	4:D:94:ASP:OD1	2.53	0.42
5:E:76:ARG:HA	5:E:79:GLU:HG3	2.02	0.42
5:E:434:GLU:O	5:E:438:PRO:HD2	2.18	0.42
3:C:52:VAL:HG22	5:E:50:VAL:HG13	2.02	0.42
4:D:245:THR:HA	5:E:595:TRP:CD1	2.55	0.42
1:A:165:GLU:OE2	4:D:202:ARG:NH2	2.53	0.42
3:C:349:MET:SD	3:C:349:MET:N	2.93	0.42
4:D:135:LEU:HD23	4:D:150:LYS:HG2	2.02	0.42
6:F:222:ASP:OD1	6:F:224:HIS:ND1	2.42	0.41
6:F:228:GLU:OE2	6:F:232:GLN:NE2	2.42	0.41
4:D:280:ASN:O	4:D:284:VAL:HG23	2.19	0.41
2:B:134:HIS:O	2:B:138:LEU:HG	2.20	0.41
5:E:140:GLN:O	5:E:144:ARG:HB2	2.20	0.41
5:E:183:VAL:HB	5:E:238:HIS:CE1	2.55	0.41
3:C:329:THR:HG23	3:C:332:LYS:HE3	2.02	0.41
3:C:287:LYS:HE2	3:C:290:ILE:HD12	2.03	0.41
5:E:328:GLU:HA	5:E:331:ARG:HE	1.86	0.41
7:G:113:GLY:HA2	7:G:116:LEU:HD12	2.03	0.41
1:A:47:ARG:NE	4:D:55:GLY:O	2.54	0.41
3:C:72:LEU:HD11	5:E:65:TRP:HD1	1.85	0.41
4:D:75:LYS:HE3	4:D:75:LYS:HB3	1.91	0.41
2:B:82:PRO:HB3	7:G:264:LEU:HD23	2.03	0.41
2:B:174:ASP:O	2:B:178:THR:HG23	2.20	0.41
3:C:97:LYS:HA	3:C:97:LYS:HD2	1.91	0.41
3:C:218:THR:O	3:C:222:PHE:N	2.54	0.41
5:E:209:ARG:HH11	5:E:214:THR:H	1.67	0.41
5:E:483:LEU:HD22	5:E:508:SER:HB2	2.02	0.41
6:F:141:LYS:HD3	6:F:152:VAL:HG11	2.02	0.41
2:B:142:PHE:HE2	7:G:322:LEU:HD22	1.86	0.41
3:C:222:PHE:O	3:C:226:ILE:N	2.37	0.41
3:C:574:VAL:HA	4:D:253:VAL:HG21	2.03	0.41
4:D:60:LEU:HD12	4:D:60:LEU:HA	1.85	0.41
4:D:209:LEU:HD23	4:D:209:LEU:HA	1.88	0.41
5:E:547:LEU:HD12	5:E:555:ILE:HD11	2.02	0.41
6:F:97:ILE:HG12	6:F:111:VAL:HG21	2.03	0.41
3:C:30:LEU:HD22	5:E:34:LEU:HD23	2.03	0.41
3:C:442:ASP:HB2	5:E:489:ARG:HH22	1.86	0.41
6:F:234:VAL:HG22	8:H:215:GLN:HE22	1.86	0.41
1:A:219:ALA:O	1:A:223:LYS:HG2	2.21	0.40
4:D:224:GLU:HA	5:E:574:LEU:HD21	2.02	0.40
5:E:168:VAL:HG12	5:E:183:VAL:HG21	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:LYS:HE2	1:A:142:LYS:HB3	1.91	0.40
2:B:172:LYS:HA	2:B:175:ILE:HG12	2.03	0.40
3:C:85:LYS:HA	3:C:85:LYS:HD3	1.80	0.40
3:C:214:LEU:HD11	3:C:373:VAL:HG22	2.02	0.40
3:C:556:LYS:HZ2	5:E:592:VAL:HG13	1.86	0.40
1:A:37:LEU:HD23	1:A:37:LEU:HA	1.89	0.40
2:B:45:VAL:HG13	7:G:218:LYS:HZ3	1.86	0.40
3:C:122:LYS:O	3:C:126:MET:HG2	2.20	0.40
3:C:137:LEU:HD23	3:C:140:LYS:HD2	2.04	0.40
3:C:378:ILE:HG23	5:E:199:LEU:HB2	2.04	0.40
3:C:573:TYR:HA	3:C:576:PHE:HB3	2.04	0.40
4:D:172:LYS:HD2	4:D:172:LYS:HA	1.87	0.40
5:E:447:LEU:O	5:E:451:VAL:HG23	2.22	0.40
6:F:259:LEU:HD23	6:F:259:LEU:HA	1.93	0.40
7:G:240:HIS:CD2	7:G:243:ARG:HH12	2.40	0.40
7:G:361:LYS:HZ1	8:H:316:LEU:HD21	1.87	0.40
1:A:64:GLU:HG2	5:E:477:LEU:HD11	2.02	0.40
3:C:317:LEU:O	3:C:321:ILE:HG13	2.22	0.40
3:C:378:ILE:HD13	5:E:200:GLN:HG3	2.03	0.40
5:E:132:GLN:O	5:E:136:MET:HG3	2.21	0.40
2:B:156:ILE:HG13	7:G:336:VAL:HG22	2.04	0.40
3:C:242:ASP:N	3:C:242:ASP:OD1	2.54	0.40
4:D:136:CYS:HA	4:D:143:ASP:HA	2.03	0.40
5:E:43:TRP:CD1	5:E:46:ILE:HD12	2.57	0.40
7:G:83:CYS:HA	7:G:86:VAL:HG22	2.02	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	276/278 (99%)	270 (98%)	6 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	213/284 (75%)	204 (96%)	8 (4%)	1 (0%)	29 69
3	C	596/603 (99%)	583 (98%)	13 (2%)	0	100 100
4	D	292/318 (92%)	289 (99%)	3 (1%)	0	100 100
5	E	604/633 (95%)	590 (98%)	14 (2%)	0	100 100
6	F	383/432 (89%)	368 (96%)	15 (4%)	0	100 100
7	G	342/368 (93%)	323 (94%)	19 (6%)	0	100 100
8	H	199/410 (48%)	196 (98%)	3 (2%)	0	100 100
All	All	2905/3326 (87%)	2823 (97%)	81 (3%)	1 (0%)	100 100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	116	PRO

5.3.2 Protein sidechains (i)

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	251/251 (100%)	248 (99%)	3 (1%)	71 83
2	B	192/250 (77%)	186 (97%)	6 (3%)	40 62
3	C	554/557 (100%)	549 (99%)	5 (1%)	78 87
4	D	273/293 (93%)	271 (99%)	2 (1%)	84 90
5	E	529/547 (97%)	525 (99%)	4 (1%)	81 89
6	F	353/396 (89%)	350 (99%)	3 (1%)	81 89
7	G	301/313 (96%)	300 (100%)	1 (0%)	92 95
8	H	178/348 (51%)	175 (98%)	3 (2%)	60 78
All	All	2631/2955 (89%)	2604 (99%)	27 (1%)	77 86

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	145	LYS
1	A	254	LYS
1	A	271	ARG
2	B	39	LYS
2	B	107	ARG
2	B	156	ILE
2	B	159	LEU
2	B	189	LYS
2	B	192	LYS
3	C	111	LYS
3	C	146	LYS
3	C	326	LYS
3	C	332	LYS
3	C	534	LYS
4	D	184	LYS
4	D	291	ARG
5	E	88	ARG
5	E	149	ARG
5	E	405	LYS
5	E	579	LYS
6	F	48	LYS
6	F	133	ARG
6	F	205	ARG
7	G	135	LYS
8	H	204	ARG
8	H	230	LYS
8	H	304	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	51	GLN
2	B	52	GLN
3	C	416	ASN
6	F	195	GLN
6	F	373	GLN
8	H	232	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

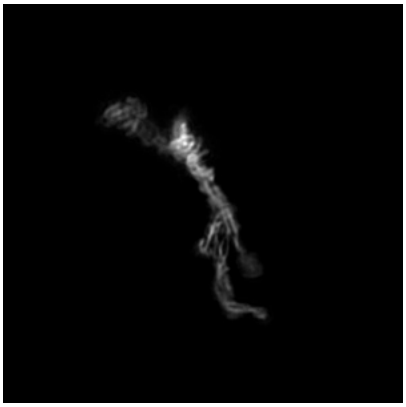
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-25387. These allow visual inspection of the internal detail of the map and identification of artifacts.

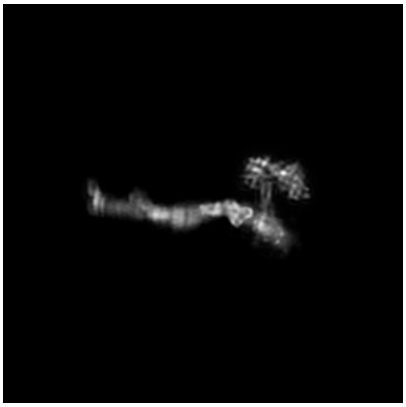
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

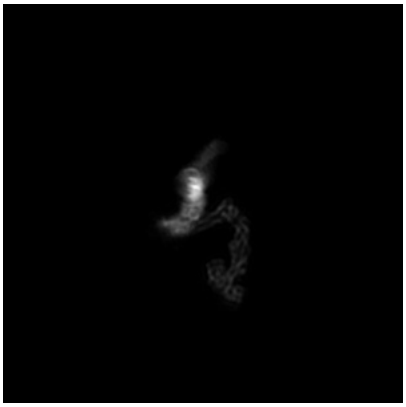
6.1.1 Primary map



X



Y



Z

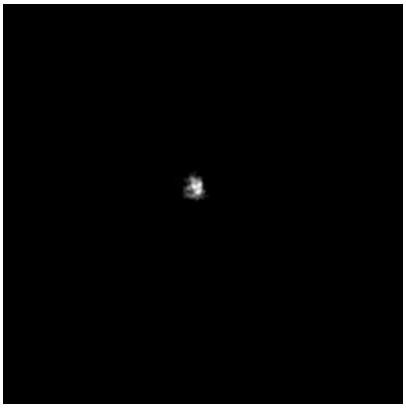
The images above show the map projected in three orthogonal directions.

6.2 Central slices

6.2.1 Primary map

X Index: 240

Y Index: 240

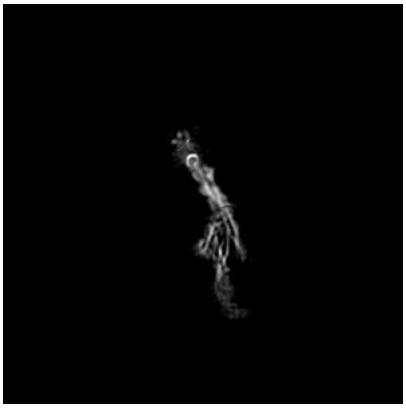


Z Index: 240

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: 228

Y Index: 249

Z Index: 312

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map

X

Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

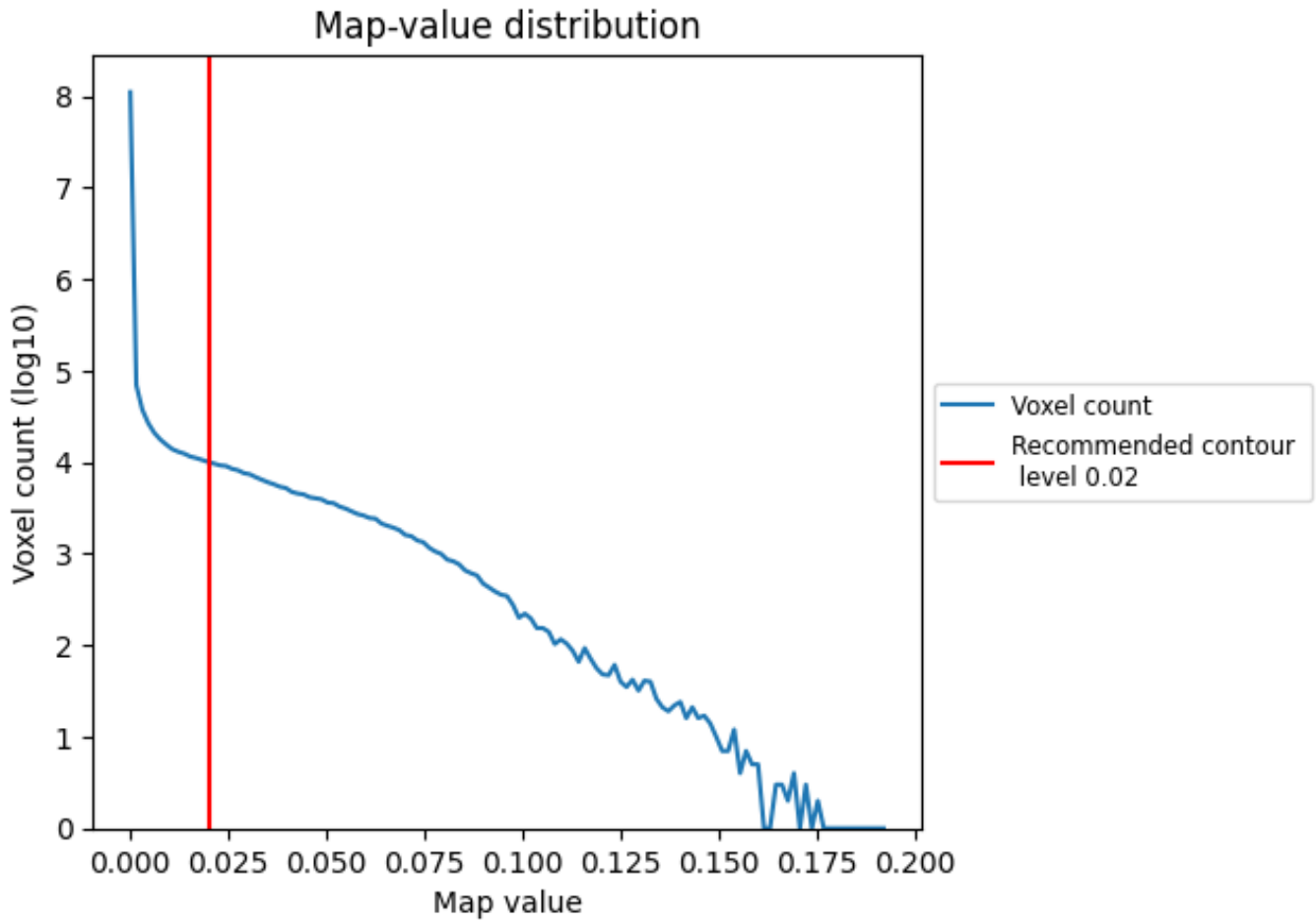
6.5 Mask visualisation (i)

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

7 Map analysis

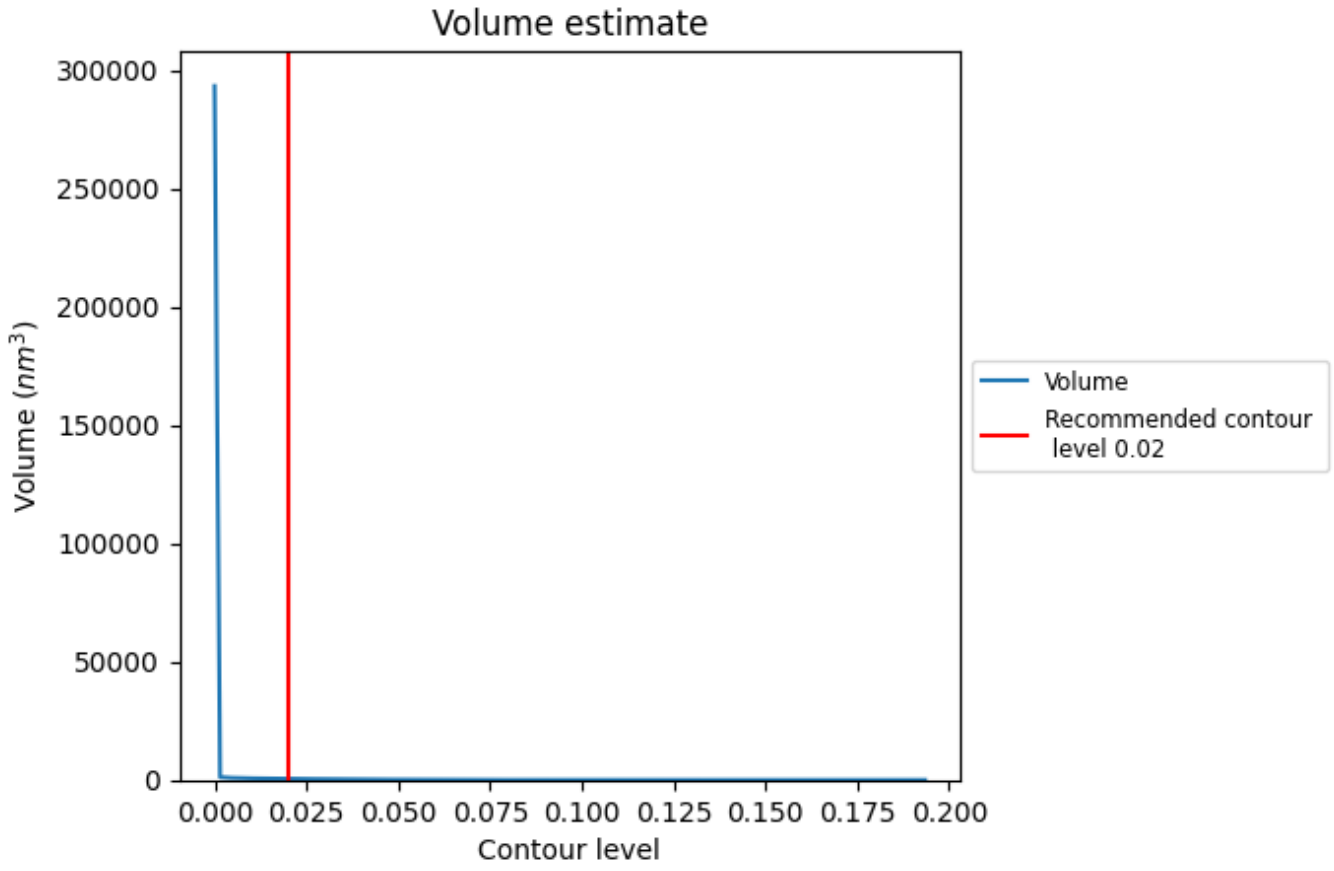
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

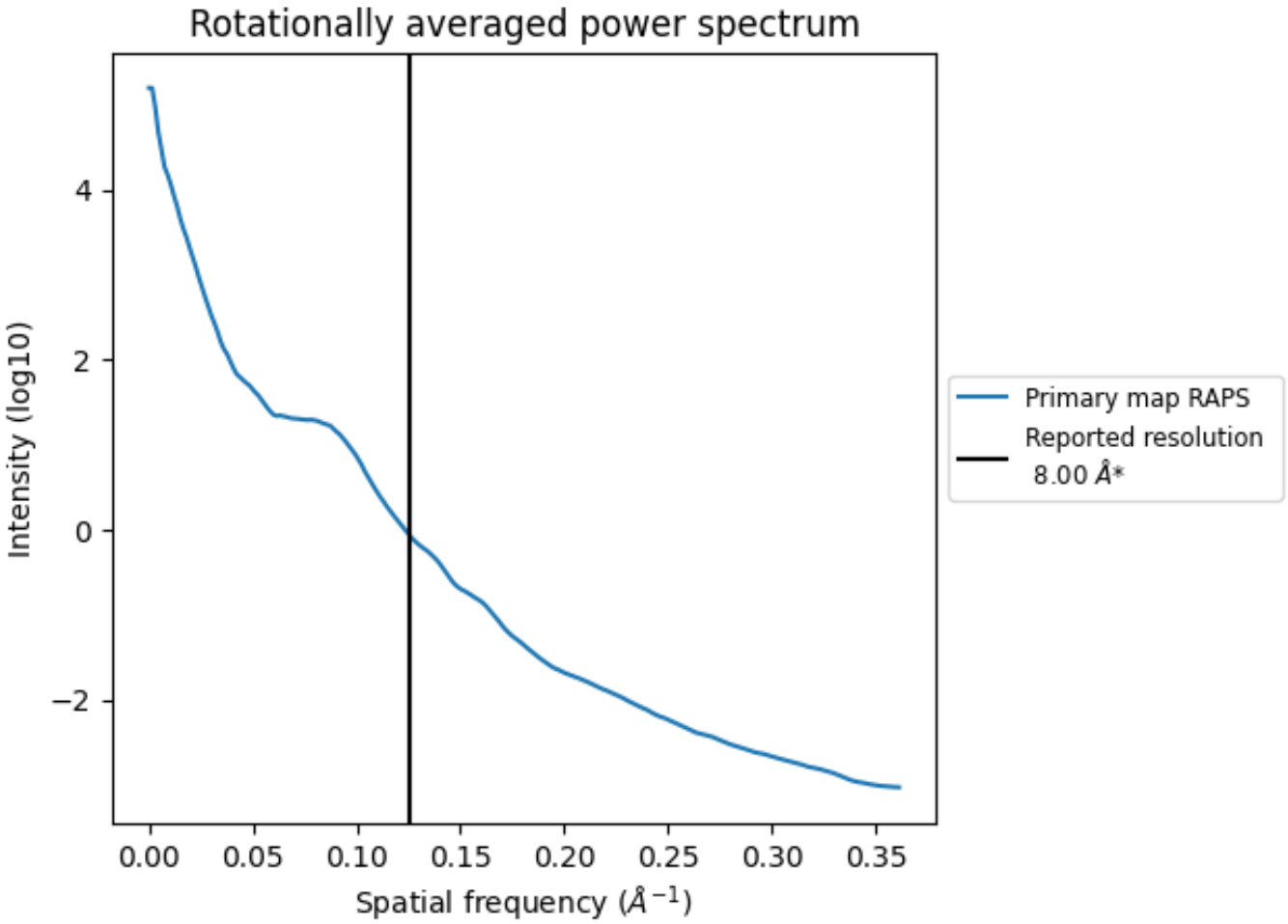
7.2 Volume estimate



The volume at the recommended contour level is 484 nm^3; this corresponds to an approximate mass of 437 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 (i)



*Reported resolution corresponds to spatial frequency of 0.125 Å^{-1}

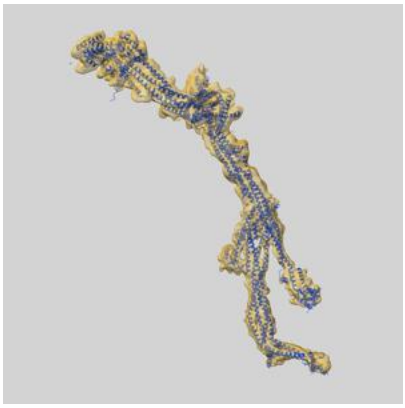
8 Fourier-Shell correlation (i)

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

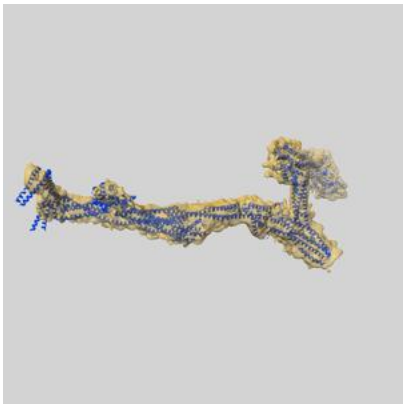
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-25387 and PDB model 7SQK. Per-residue inclusion information can be found in section 3 on page 6.

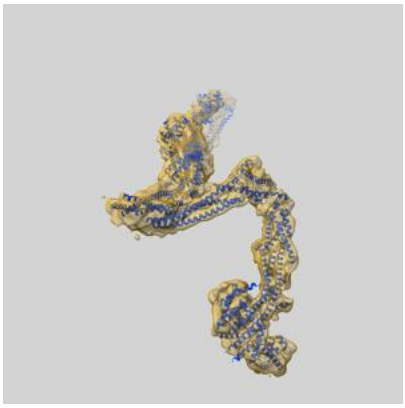
9.1 Map-model overlay



X



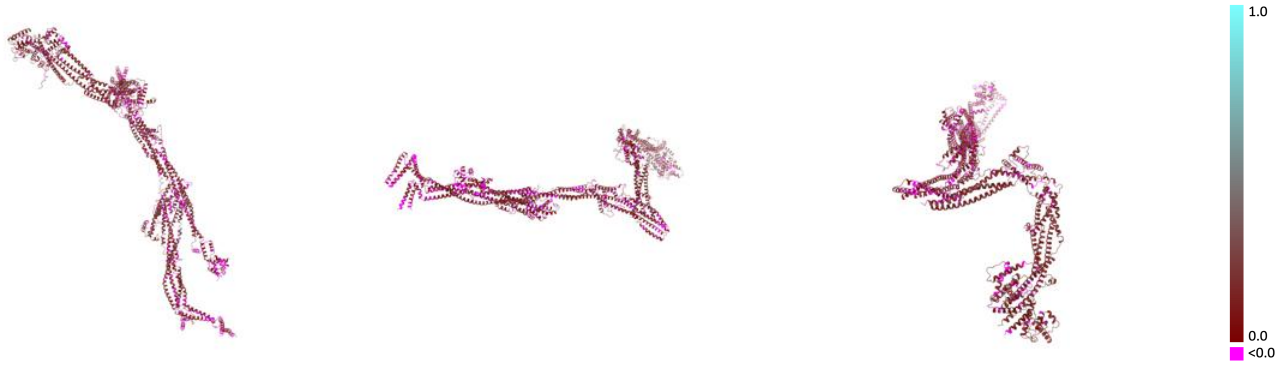
Y



Z

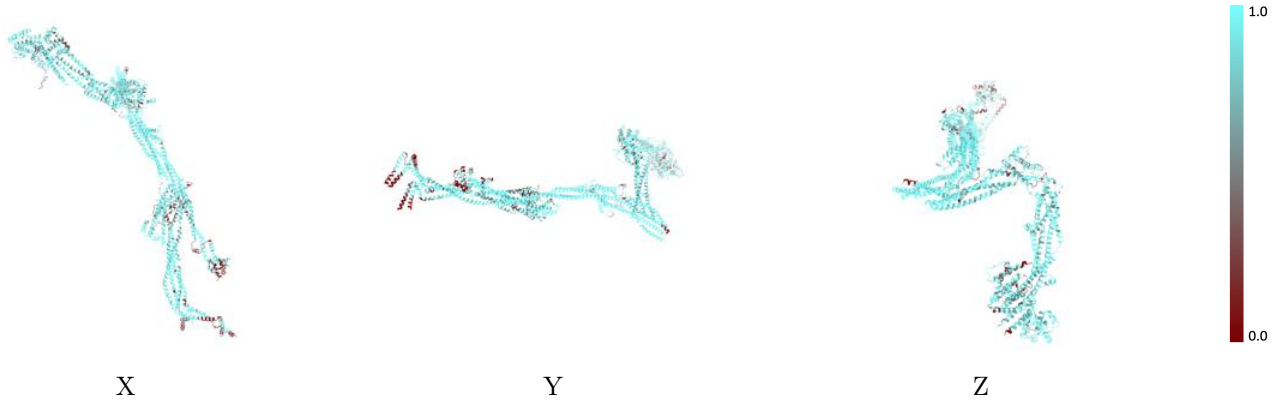
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



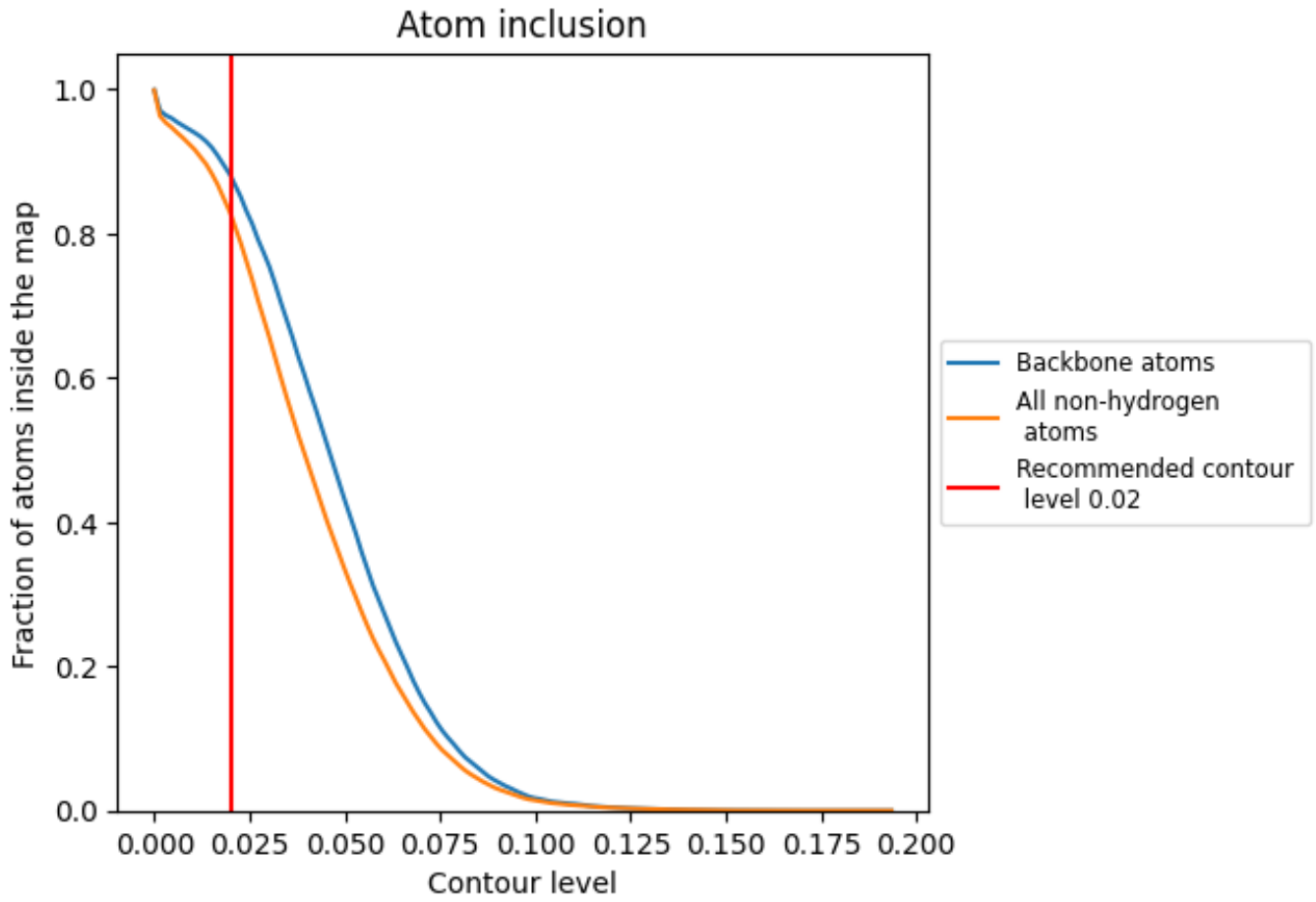
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.02).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 83% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8279	0.1190
A	0.8473	0.1290
B	0.7816	0.1460
C	0.7973	0.0780
D	0.7790	0.0840
E	0.8795	0.1000
F	0.8655	0.1740
G	0.8054	0.1520
H	0.8274	0.1440