



## Full wwPDB EM Validation Report ⓘ

Apr 24, 2025 – 02:17 PM EDT

PDB ID : 9DUM / pdb\_00009dum  
EMDB ID : EMD-47170  
Title : Human PELP1-WDR18-TEX10 complex  
Authors : Huang, J.; Tong, L.  
Deposited on : 2024-10-03  
Resolution : 3.56 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev117  
MolProbity : 4.02b-467  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.42

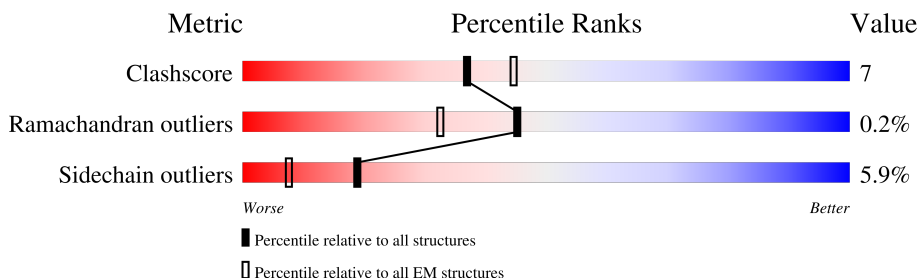
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.56 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	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	434	
1	B	434	
2	C	644	
2	D	644	
3	G	931	
3	H	931	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 22662 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 WD repeat-containing protein 18.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	358	Total	C	N	O	S	0	0
			2718	1725	468	505	20		
1	B	376	Total	C	N	O	S	0	0
			2872	1819	500	533	20		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP Q9BV38
A	0	ASN	-	expression tag	UNP Q9BV38
B	-1	SER	-	expression tag	UNP Q9BV38
B	0	ASN	-	expression tag	UNP Q9BV38

- Molecule 2 is a protein called Proline-, glutamic acid- and leucine-rich protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	481	Total	C	N	O	S	0	0
			3655	2320	646	660	29		
2	D	485	Total	C	N	O	S	0	0
			3683	2337	653	664	29		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	SER	-	expression tag	UNP Q8IZL8
C	0	ASN	-	expression tag	UNP Q8IZL8
D	-1	SER	-	expression tag	UNP Q8IZL8
D	0	ASN	-	expression tag	UNP Q8IZL8

- Molecule 3 is a protein called Testis-expressed protein 10.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	H	710	Total	C	N	O	S	0	0
			5690	3691	971	1004	24		
3	G	505	Total	C	N	O	S	0	0
			4044	2605	699	722	18		

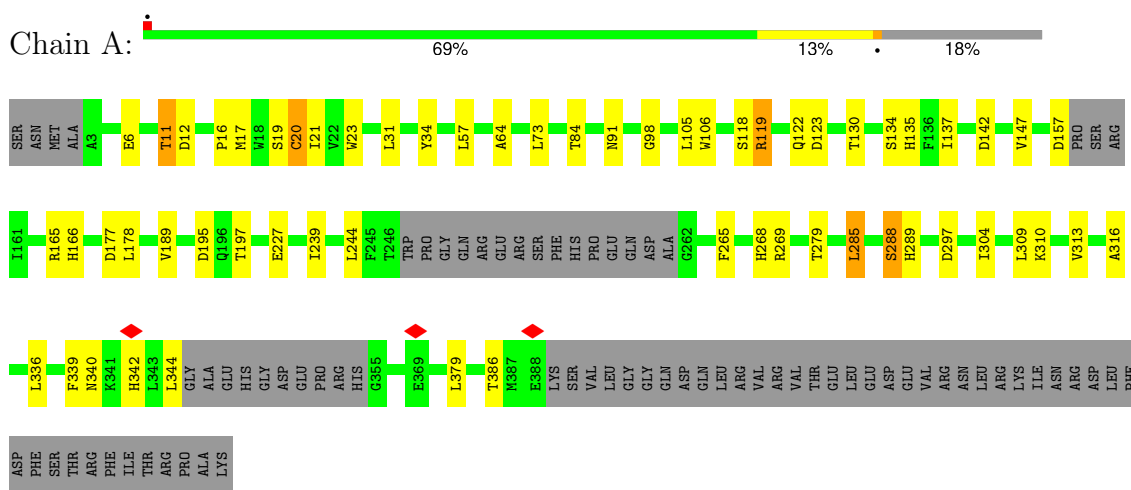
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-1	SER	-	expression tag	UNP Q9NXF1
H	0	ASN	-	expression tag	UNP Q9NXF1
G	-1	SER	-	expression tag	UNP Q9NXF1
G	0	ASN	-	expression tag	UNP Q9NXF1

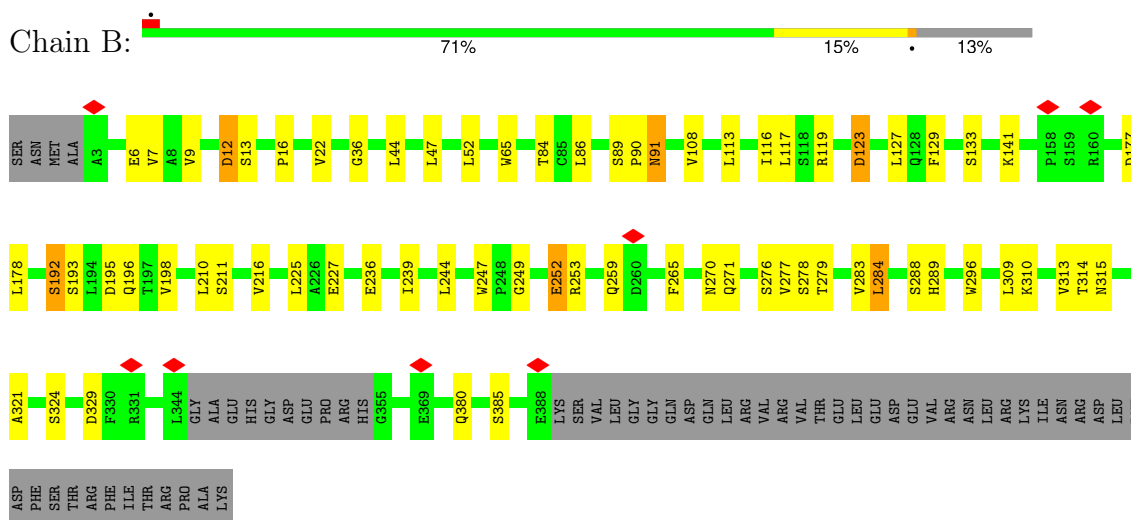
### 3 Residue-property plots

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: WD repeat-containing protein 18



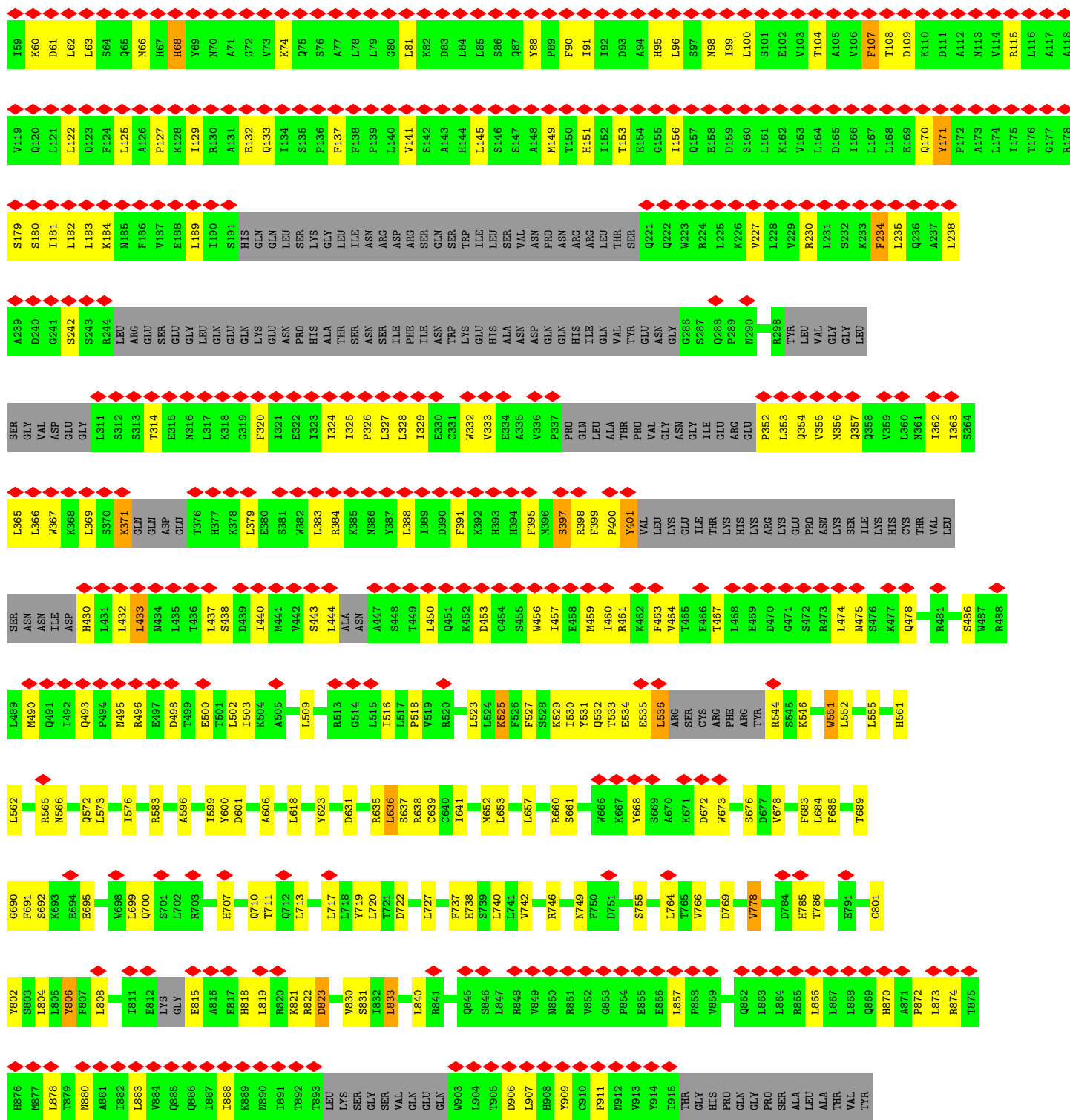
#### • Molecule 1: WD repeat-containing protein 18



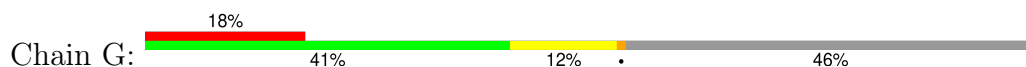
#### • Molecule 2: Proline-, glutamic acid- and leucine-rich protein 1







• Molecule 3: Testis-expressed protein 10



SER	ASN	MET	THR	LYS	LYS	ARG	LYS	ARG	LYS	GLN	HIS	ASP	ASP	GLN	LYS	VAL	LYS	LEU	LYS	VAL	GLY	LYS	LYS	LYS	LEU	PRO	LYS	LYS	GLY	SER	GLN	VAL	ALA	THR	PRO	THR	THR	ASN	PHE	LYS	LYS	THR	LYS	LYS	THR	THR	ILE	HIS	LEU	LEU	PRO	GLN	GLN	LEU	LYS	LYS	ASP	GLY	THR	THR	PRO	THR	ASN	ARG	LYS	LYS	LEU	LEU	ASN
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I887	I888	K889	N890	I891	T892	T893	L894	K895	S896	G897	S898	V899	Q900	E901	Q902	Q903	L904	T905	D906	L907	H908	Y909	C910	F911	N912	V913	Y914	I915	T916	G917	HIS	PRO	GLN	GLY	PRO	SER	ALA	ALA	THR	VAL	TTR																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
E817	H818	L819	R820	K821	R822	K824	L825	W826	G827	V828	C829	L833	P837	R841	L842	M843	L844	Q845	R848	V849	N850	R851	V852	G853	P854	E855	E856	L857	P858	V859	L863	L864	R865	L866	L867	L868	Q869	H870	A871	R874	T875	H876	M877	L878	T879	N880	A881	I882	L883	V884	Q885	Q886																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
Q710	T711	Q712	L713	S714	P715	V716	L717	L718	L727	V736	F737	Q748	I752	L753	Q754	L761	L764	T765	V766	I767	P768	D769	S770	T771	A772	G773	V778	H785	V788	S790	E791	A798	S799	C800	C801	Y802	S803	L804	L805	Y806	T810	I811	E812	L813	G814	E815	A816																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
I502	I503	K504	A505	V506	Y507	T508	L509	Y510	Q511	Q512	R513	L515	I516	L517	P518	V519	R520	T521	L522	L523	F527	Y531	Q532	T533	E534	E535	L536	ARG	SER	CYS	ARG	PHE	ARG	Y543	R544	S545	K546	S549	R550	W551	P556	N566	D575	A580	N585	K586	Q593	A594	T595																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																														
V442	S443	LEU	ALA	ASN	ALA	SER	THR	LEU	GLN	LYS	ASP	CYS	TRP	ILE	E458	M459	I460	R461	K462	F463	V464	T465	E466	T467	L468	E469	D470	G471	S472	R473	L474	N475	S476	K477	Q478	L479	N480	R481	L482	L483	G484	V485	S486	W487	R488	L489	M490	Q491	I492	Q493	P494	N495	R496	E497	D498	T499	E500	T501																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
TRP	LEU	ARG	LYS	ASN	TYR	LEU	ILE	PHE	LYS	HIS	HIS	PHE	MET	SER	ARG	PHE	PRO	TYR	VAL	LEU	LYS	GLY	ASN	GLY	THR	LYS	HIS	LYS	ARG	GLU	PRO	ASN	SER	ILE	LYS	CYS	THR	VAL	SER	ASN	ASN	ILE	D429	H430	L431	L432	L433	M434	T436	L437	S438	D439	I440	M441																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																									
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## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	268599	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	51	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.296	Depositor
Minimum map value	-1.700	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.284	Depositor
Map size (Å)	324.9, 324.9, 324.9	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.083, 1.083, 1.083	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	0.27	0/2777	0.50	0/3777
1	B	0.27	0/2940	0.51	0/4002
2	C	0.25	0/3720	0.47	0/5043
2	D	0.24	0/3748	0.47	0/5079
3	G	0.25	0/4124	0.48	0/5597
3	H	0.26	0/5799	0.50	0/7860
All	All	0.25	0/23108	0.49	0/31358

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	2718	0	2708	26	0
1	B	2872	0	2846	39	0
2	C	3655	0	3772	44	0
2	D	3683	0	3805	38	0
3	G	4044	0	4169	66	0
3	H	5690	0	5920	146	0
All	All	22662	0	23220	338	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 (338) 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)
3:H:503:ILE:HD11	3:H:530:ILE:HD11	1.29	1.13
3:H:527:PHE:HA	3:H:530:ILE:HG22	1.34	1.07
3:H:503:ILE:HD11	3:H:530:ILE:CD1	1.95	0.97
1:B:270:ASN:ND2	3:H:742:VAL:HG13	1.81	0.94
3:H:527:PHE:CA	3:H:530:ILE:HG22	1.97	0.94
3:H:527:PHE:HA	3:H:530:ILE:CG2	1.98	0.92
3:H:527:PHE:O	3:H:530:ILE:HG22	1.74	0.86
1:B:270:ASN:HD21	3:H:742:VAL:HG13	1.41	0.84
1:B:270:ASN:HD21	3:H:742:VAL:CG1	1.94	0.81
3:H:527:PHE:C	3:H:530:ILE:HG22	2.03	0.79
3:G:705:VAL:HG23	3:G:707:HIS:H	1.50	0.76
3:H:503:ILE:CD1	3:H:530:ILE:CD1	2.66	0.73
3:H:700:GLN:NE2	3:H:766:VAL:O	2.24	0.70
1:B:44:LEU:HB2	1:B:315:ASN:HD22	1.56	0.70
3:G:474:LEU:HB3	3:G:478:GLN:HB3	1.74	0.68
2:C:533:ILE:HD11	2:C:548:LEU:HD13	1.76	0.68
3:H:636:LEU:HD21	3:H:653:LEU:HD11	1.77	0.67
3:H:527:PHE:O	3:H:530:ILE:CG2	2.41	0.66
3:H:710:GLN:HG2	3:H:717:LEU:HD21	1.76	0.66
3:G:512:GLN:NE2	3:G:513:ARG:O	2.27	0.66
2:C:210:CYS:HB2	2:C:246:LEU:HD23	1.77	0.66
3:G:593:GLN:NE2	3:G:626:PRO:O	2.29	0.66
3:G:769:ASP:OD2	3:G:821:LYS:NZ	2.29	0.66
2:D:177:LEU:HD23	2:D:209:ALA:HB3	1.80	0.63
3:H:474:LEU:HB3	3:H:478:GLN:HE22	1.63	0.63
1:A:119:ARG:HH12	3:G:535:GLU:HG2	1.64	0.63
3:G:276:GLN:N	3:G:276:GLN:OE1	2.31	0.63
1:B:9:VAL:HG22	1:B:22:VAL:HG22	1.81	0.63
1:A:122:GLN:HB2	1:A:142:ASP:HB3	1.80	0.62
3:H:384:ARG:HE	3:H:388:LEU:HD22	1.65	0.62
3:G:510:TYR:O	3:G:513:ARG:NH2	2.34	0.61
1:B:211:SER:HB3	1:B:252:GLU:HG3	1.82	0.61
1:B:12:ASP:OD1	1:B:12:ASP:N	2.32	0.60
3:G:754:GLN:HE22	3:G:789:VAL:HA	1.65	0.60
3:H:804:LEU:O	3:H:808:LEU:HG	2.01	0.60
1:B:309:LEU:HD12	1:B:313:VAL:HG22	1.84	0.60
1:A:239:ILE:HB	1:A:265:PHE:HB2	1.85	0.59
3:H:722:ASP:N	3:H:722:ASP:OD1	2.34	0.59
3:G:517:LEU:HD11	3:G:566:ASN:HD21	1.67	0.59
2:D:224:ARG:HG3	2:D:224:ARG:HH11	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:239:ILE:HB	1:B:265:PHE:HB2	1.83	0.58
3:H:129:ILE:HG13	3:H:171:TYR:OH	2.03	0.58
3:G:823:ASP:OD1	3:G:823:ASP:N	2.36	0.58
3:H:438:SER:HA	3:H:460:ILE:HD11	1.86	0.58
3:H:823:ASP:N	3:H:823:ASP:OD1	2.34	0.58
1:B:16:PRO:HG3	1:B:310:LYS:HD2	1.86	0.57
3:G:470:ASP:OD1	3:G:470:ASP:N	2.37	0.57
3:G:482:LEU:O	3:G:486:SER:OG	2.22	0.57
2:C:511:ARG:NH1	2:D:121:THR:OG1	2.37	0.57
1:A:244:LEU:HD23	3:G:279:ILE:HG21	1.87	0.57
2:C:462:LEU:HD13	2:C:529:LEU:HD13	1.87	0.56
2:D:278:LEU:HD11	2:D:311:LEU:HB3	1.87	0.56
2:C:169:PHE:HD1	2:C:206:PHE:HE1	1.53	0.56
3:H:535:GLU:HB3	3:H:583:ARG:HH21	1.70	0.56
3:G:700:GLN:HA	3:G:766:VAL:HG21	1.87	0.56
2:D:514:ASP:N	2:D:514:ASP:OD1	2.38	0.56
3:H:391:PHE:HA	3:H:395:PHE:HB2	1.85	0.56
3:H:366:LEU:HA	3:H:369:LEU:HB2	1.87	0.56
3:H:717:LEU:HB2	3:H:766:VAL:HG22	1.87	0.56
1:B:177:ASP:OD1	1:B:178:LEU:N	2.38	0.56
3:H:535:GLU:HG2	3:H:536:LEU:HD22	1.88	0.56
3:G:483:LEU:HD21	3:G:523:LEU:HD23	1.86	0.56
3:H:637:SER:HB2	3:H:683:PHE:CD1	2.41	0.56
1:B:196:GLN:HE22	3:H:652:MET:HG3	1.70	0.56
3:H:880:ASN:HD21	3:H:883:LEU:HD13	1.71	0.56
3:G:684:LEU:HD22	3:G:736:VAL:HG13	1.87	0.56
2:C:192:GLU:OE2	2:C:224:ARG:NH2	2.40	0.55
1:A:137:ILE:HD13	1:A:189:VAL:HG21	1.89	0.55
1:A:309:LEU:HD12	1:A:313:VAL:HG22	1.88	0.55
3:H:60:LYS:HA	3:H:63:LEU:HD12	1.88	0.55
3:G:575:ASP:OD1	3:G:617:ARG:NH1	2.39	0.55
3:G:631:ASP:N	3:G:631:ASP:OD1	2.39	0.55
3:H:769:ASP:OD2	3:H:821:LYS:NZ	2.36	0.55
3:G:627:SER:O	3:G:629:PRO:HD3	2.07	0.55
3:H:397:SER:OG	3:H:398:ARG:N	2.39	0.55
2:C:622:GLU:OE2	2:D:531:ARG:NH1	2.40	0.54
1:A:386:THR:HG23	2:D:146:ALA:HB1	1.89	0.54
3:H:107:PHE:HE2	3:H:141:VAL:HG23	1.73	0.54
3:H:68:HIS:O	3:H:74:LYS:NZ	2.41	0.53
2:C:72:LEU:HD11	2:D:312:ARG:HH12	1.74	0.53
1:A:6:GLU:OE2	1:A:279:THR:OG1	2.20	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:503:ILE:CD1	3:H:530:ILE:HD13	2.39	0.53
1:A:297:ASP:HB2	1:A:304:ILE:HD11	1.88	0.53
2:C:542:GLU:OE2	2:C:593:ARG:NE	2.34	0.53
3:H:109:ASP:O	3:H:115:ARG:NH1	2.41	0.53
3:H:62:LEU:HD13	3:H:81:LEU:HD13	1.90	0.53
3:H:692:SER:HB2	3:H:695:GLU:HG2	1.90	0.53
2:C:102:ILE:HD13	2:C:105:ARG:HH21	1.74	0.53
3:G:761:LEU:HA	3:G:764:LEU:HD12	1.90	0.53
3:H:676:SER:O	3:H:678:VAL:N	2.42	0.53
1:B:288:SER:OG	1:B:289:HIS:N	2.41	0.52
3:G:556:PRO:HB2	3:G:595:THR:HG21	1.91	0.52
2:C:112:LEU:O	2:C:116:VAL:HG23	2.08	0.52
3:H:516:ILE:HG23	3:H:518:PRO:HD2	1.92	0.52
2:C:203:MET:HG2	2:C:246:LEU:HD21	1.92	0.52
3:H:684:LEU:HD23	3:H:740:LEU:HD13	1.92	0.52
1:B:90:PRO:HD2	1:B:133:SER:HB3	1.91	0.52
2:C:134:SER:O	2:C:138:VAL:HG23	2.10	0.52
2:C:136:GLN:HA	2:C:139:LEU:HD12	1.92	0.52
3:H:456:TRP:HA	3:H:459:MET:HG2	1.92	0.52
3:G:716:VAL:HG11	3:G:800:CYS:HA	1.92	0.52
3:H:362:ILE:HD12	3:H:363:ILE:N	2.23	0.52
1:A:11:THR:OG1	1:A:12:ASP:N	2.42	0.52
3:H:833:LEU:HD11	3:H:840:LEU:HD13	1.91	0.51
3:H:496:ARG:O	3:H:500:GLU:HG2	2.11	0.51
2:C:159:LEU:HD22	2:C:206:PHE:HE2	1.75	0.51
1:B:380:GLN:OE1	2:C:74:ARG:NH2	2.40	0.51
3:H:555:LEU:HG	3:H:573:LEU:HD22	1.91	0.50
3:H:819:LEU:HB3	3:H:822:ARG:HH21	1.75	0.50
3:G:500:GLU:HA	3:G:503:ILE:HD12	1.93	0.50
3:H:320:PHE:O	3:H:324:ILE:HG12	2.12	0.50
3:G:806:TYR:O	3:G:810:THR:HG22	2.12	0.50
2:D:115:LEU:O	2:D:119:SER:HB2	2.11	0.50
1:A:268:HIS:CE1	1:A:288:SER:HB3	2.47	0.50
1:B:196:GLN:HE22	3:H:652:MET:CG	2.25	0.50
3:H:475:ASN:O	3:H:478:GLN:NE2	2.45	0.50
3:H:503:ILE:CD1	3:H:530:ILE:HD11	2.17	0.50
3:H:870:HIS:ND1	3:H:872:PRO:HD2	2.27	0.50
3:G:646:SER:HB3	3:G:649:LEU:HD12	1.92	0.50
2:C:527:ARG:NH1	2:C:578:GLU:OE2	2.44	0.50
1:B:244:LEU:HD22	2:C:638:LEU:HD21	1.94	0.49
1:B:47:LEU:HD11	1:B:108:VAL:HG21	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:705:VAL:HG22	3:G:708:VAL:HG23	1.93	0.49
3:G:531:TYR:C	3:G:533:THR:H	2.16	0.49
1:A:177:ASP:OD1	1:A:178:LEU:N	2.45	0.49
3:H:107:PHE:CE2	3:H:141:VAL:HG23	2.46	0.49
3:H:599:ILE:HG23	3:H:600:TYR:CD1	2.47	0.49
1:B:278:SER:OG	1:B:279:THR:N	2.46	0.49
2:C:246:LEU:HD12	2:C:246:LEU:H	1.77	0.49
2:C:326:LEU:HD11	2:C:341:ILE:HD13	1.94	0.49
3:G:476:SER:HB2	3:G:516:ILE:HD11	1.94	0.48
2:D:593:ARG:HG2	2:D:593:ARG:HH11	1.78	0.48
3:H:737:PHE:HE1	3:H:778:VAL:HG23	1.78	0.48
3:G:748:GLN:O	3:G:752:ILE:HG13	2.13	0.48
2:D:98:ARG:HG2	2:D:104:THR:HB	1.94	0.48
3:H:238:LEU:O	3:H:242:SER:OG	2.29	0.48
3:G:788:VAL:HG12	3:G:788:VAL:O	2.13	0.48
1:A:84:THR:OG1	1:A:98:GLY:O	2.31	0.48
1:B:284:LEU:HD23	1:B:296:TRP:HD1	1.78	0.48
2:D:125:GLN:HG2	2:D:165:LEU:HD13	1.95	0.48
3:H:552:LEU:HD12	3:H:555:LEU:HD22	1.95	0.48
3:H:601:ASP:OD1	3:H:635:ARG:NH1	2.47	0.48
1:B:270:ASN:ND2	3:H:742:VAL:CG1	2.58	0.48
3:H:100:LEU:O	3:H:104:THR:OG1	2.28	0.48
3:H:720:LEU:HD23	3:H:818:HIS:ND1	2.28	0.48
3:H:91:ILE:HD13	3:G:913:VAL:HG13	1.96	0.48
3:H:888:ILE:HG12	3:H:907:LEU:HD21	1.95	0.48
2:D:173:SER:OG	2:D:209:ALA:HB2	2.14	0.47
3:H:495:ASN:ND2	3:H:498:ASP:OD2	2.47	0.47
3:G:708:VAL:HG12	3:G:710:GLN:H	1.79	0.47
2:D:409:TRP:CD1	2:D:427:VAL:HG11	2.49	0.47
3:H:179:SER:O	3:H:181:ILE:N	2.47	0.47
3:H:599:ILE:HG13	3:H:606:ALA:HB3	1.96	0.47
3:G:816:ALA:HA	3:G:819:LEU:HD12	1.96	0.47
2:C:221:PHE:HB3	2:C:240:TYR:HB2	1.95	0.47
3:H:88:TYR:HB2	3:H:91:ILE:HG12	1.97	0.47
3:H:179:SER:O	3:H:182:LEU:HG	2.15	0.47
3:H:183:LEU:H	3:H:183:LEU:HD12	1.79	0.47
3:H:874:ARG:O	3:H:878:LEU:HG	2.15	0.47
3:H:509:LEU:HD22	3:H:523:LEU:HD11	1.96	0.47
3:H:561:HIS:O	3:H:565:ARG:NH2	2.48	0.47
3:H:145:LEU:O	3:H:149:MET:HG3	2.15	0.47
3:G:505:ALA:O	3:G:508:THR:OG1	2.31	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:322:LEU:HD23	2:D:379:LEU:HD11	1.97	0.46
3:G:507:TYR:O	3:G:511:GLN:N	2.43	0.46
2:D:556:VAL:HG23	2:D:557:MET:HG3	1.98	0.46
1:A:130:THR:HG21	1:A:135:HIS:HB2	1.97	0.46
1:B:91:ASN:ND2	1:B:133:SER:OG	2.48	0.46
3:H:354:GLN:O	3:H:357:GLN:N	2.49	0.46
3:H:463:PHE:O	3:H:467:THR:HG22	2.15	0.46
3:H:95:HIS:O	3:H:99:ILE:HG13	2.15	0.46
2:C:312:ARG:HH12	2:D:72:LEU:HD11	1.80	0.46
1:A:137:ILE:HG12	1:A:147:VAL:HG22	1.97	0.46
3:G:691:PHE:O	3:G:696:LEU:HD13	2.15	0.46
3:H:631:ASP:O	3:H:635:ARG:HG2	2.15	0.46
3:H:746:ARG:HA	3:H:749:ASN:ND2	2.31	0.46
1:B:123:ASP:OD1	1:B:123:ASP:N	2.49	0.45
3:H:562:LEU:HD21	3:H:566:ASN:HB3	1.97	0.45
3:G:531:TYR:CE2	3:G:580:ALA:HB2	2.52	0.45
1:B:216:VAL:HG21	1:B:236:GLU:HG2	1.96	0.45
1:B:227:GLU:OE1	2:D:632:HIS:NE2	2.34	0.45
3:H:379:LEU:O	3:H:383:LEU:HG	2.16	0.45
3:H:401:TYR:OH	3:H:430:HIS:O	2.32	0.45
3:H:746:ARG:HA	3:H:749:ASN:HD21	1.81	0.45
1:B:277:VAL:HG22	1:B:284:LEU:HD12	1.97	0.45
3:G:531:TYR:O	3:G:533:THR:N	2.50	0.45
3:G:804:LEU:HD11	3:G:825:LEU:HD22	1.98	0.45
2:C:352:SER:OG	2:C:353:SER:N	2.50	0.45
3:G:874:ARG:NH2	3:G:915:ILE:HD13	2.31	0.45
1:A:344:LEU:HD23	1:A:344:LEU:HA	1.85	0.45
1:B:113:LEU:HD21	1:B:116:ILE:HG13	1.98	0.45
3:H:572:GLN:O	3:H:576:ILE:HG22	2.17	0.45
3:H:738:HIS:O	3:H:742:VAL:HG23	2.17	0.45
3:H:96:LEU:HD13	3:H:133:GLN:HG2	1.98	0.45
3:G:713:LEU:HB3	3:G:802:TYR:HE2	1.80	0.45
1:B:6:GLU:OE2	1:B:279:THR:OG1	2.33	0.45
1:B:7:VAL:HG13	1:B:321:ALA:HB2	1.98	0.45
2:C:574:ARG:O	2:C:578:GLU:HG2	2.16	0.45
3:H:397:SER:HB3	3:H:437:LEU:HD22	1.98	0.45
3:H:432:LEU:HD23	3:H:432:LEU:H	1.82	0.45
2:D:369:LEU:HD12	2:D:369:LEU:HA	1.83	0.45
3:H:362:ILE:HD12	3:H:363:ILE:HG13	2.00	0.45
3:H:637:SER:HB2	3:H:683:PHE:HD1	1.80	0.45
3:H:657:LEU:HD23	3:H:657:LEU:HA	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:717:LEU:HB2	3:G:765:THR:O	2.17	0.44
3:H:806:TYR:HD1	3:H:806:TYR:O	2.00	0.44
1:A:16:PRO:HG2	1:A:310:LYS:HD2	1.99	0.44
1:B:141:LYS:HE2	3:H:668:TYR:OH	2.17	0.44
2:D:99:LEU:HD23	2:D:134:SER:HB3	2.00	0.44
3:H:325:ILE:O	3:H:329:ILE:HG13	2.17	0.44
1:A:336:LEU:HD22	1:A:339:PHE:HE2	1.82	0.44
3:H:453:ASP:HB3	3:H:456:TRP:CE2	2.52	0.44
3:H:623:TYR:O	3:H:660:ARG:NH1	2.48	0.44
3:H:699:LEU:HD11	3:H:719:TYR:CG	2.52	0.44
3:G:618:LEU:HD23	3:G:618:LEU:HA	1.78	0.44
3:H:66:MET:O	3:H:74:LYS:NZ	2.38	0.44
3:H:367:TRP:CE2	3:H:443:SER:HB3	2.53	0.44
3:H:352:PRO:HB2	3:H:353:LEU:H	1.68	0.44
3:H:153:THR:HG22	3:H:156:ILE:H	1.82	0.44
3:H:707:HIS:O	3:H:720:LEU:HB2	2.17	0.43
3:H:830:VAL:HG23	3:H:873:LEU:HD11	1.99	0.43
2:C:70:MET:CE	2:C:114:LEU:HD12	2.48	0.43
3:H:461:ARG:HA	3:H:464:VAL:HG22	2.00	0.43
3:G:899:VAL:O	3:G:901:GLU:HG3	2.17	0.43
3:H:685:PHE:O	3:H:689:THR:HG22	2.17	0.43
3:H:711:THR:HG22	3:H:713:LEU:H	1.83	0.43
1:B:127:LEU:HD23	1:B:127:LEU:HA	1.89	0.43
3:H:329:ILE:O	3:H:333:VAL:HG23	2.18	0.43
3:H:546:LYS:H	3:H:546:LYS:HG3	1.65	0.43
3:G:718:LEU:HD23	3:G:803:SER:HB3	1.99	0.43
2:C:449:LEU:HD22	2:C:532:THR:HG21	2.00	0.43
2:D:396:ILE:H	2:D:396:ILE:HG12	1.53	0.43
1:B:195:ASP:O	1:B:196:GLN:HB2	2.18	0.43
2:C:614:LEU:HD11	2:D:441:VAL:HG12	2.00	0.43
3:H:371:LYS:HE3	3:H:371:LYS:HB3	1.66	0.43
2:C:181:LEU:HD11	2:C:210:CYS:HB3	2.01	0.43
3:H:596:ALA:HA	3:H:599:ILE:HG22	2.00	0.43
3:G:599:ILE:HG23	3:G:606:ALA:HB3	2.01	0.43
3:G:871:ALA:O	3:G:874:ARG:HG2	2.19	0.43
2:D:462:LEU:HD13	2:D:529:LEU:HD13	2.01	0.43
2:D:553:LEU:HD13	2:D:553:LEU:HA	1.82	0.43
2:D:181:LEU:HD11	2:D:210:CYS:SG	2.59	0.43
2:D:389:SER:O	2:D:389:SER:OG	2.37	0.42
3:H:525:LYS:HE2	3:H:529:LYS:HD2	2.00	0.42
3:G:893:THR:O	3:G:896:SER:OG	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:461:ARG:NH1	3:H:493:GLN:OE1	2.52	0.42
3:H:737:PHE:CE1	3:H:778:VAL:HG23	2.53	0.42
3:H:189:LEU:HD11	3:H:227:VAL:HG21	2.00	0.42
2:C:631:THR:O	2:C:633:PRO:HD3	2.19	0.42
2:C:633:PRO:HG2	2:D:635:VAL:O	2.19	0.42
3:G:527:PHE:HB3	3:G:551:TRP:CH2	2.53	0.42
2:C:275:LEU:HD12	2:C:275:LEU:HA	1.89	0.42
3:H:457:ILE:O	3:H:460:ILE:HG22	2.19	0.42
1:B:13:SER:HB2	1:B:314:THR:HG23	2.00	0.42
1:B:247:TRP:CE2	1:B:249:GLY:HA2	2.54	0.42
2:C:576:ARG:NH1	2:C:611:GLU:OE2	2.53	0.42
3:H:638:ARG:HA	3:H:641:ILE:HG22	2.02	0.42
3:H:127:PRO:HA	3:H:170:GLN:NE2	2.34	0.42
3:H:328:LEU:O	3:H:332:TRP:N	2.51	0.42
3:H:740:LEU:HD12	3:H:740:LEU:HA	1.87	0.42
3:G:633:LEU:HD12	3:G:633:LEU:HA	1.87	0.42
1:A:285:LEU:HD21	1:A:316:ALA:HB1	2.02	0.42
2:C:598:LEU:HD12	2:C:598:LEU:HA	1.94	0.42
2:D:275:LEU:HD11	2:D:279:TYR:CE2	2.55	0.42
3:G:625:LEU:O	3:G:660:ARG:NH2	2.53	0.42
1:A:227:GLU:OE1	2:C:632:HIS:NE2	2.45	0.42
3:H:433:LEU:HD12	3:H:433:LEU:H	1.85	0.42
3:G:868:LEU:HD23	3:G:868:LEU:HA	1.80	0.42
1:A:91:ASN:OD1	1:A:91:ASN:N	2.50	0.41
2:D:118:GLU:OE2	2:D:118:GLU:N	2.53	0.41
2:D:268:LEU:HD12	2:D:268:LEU:HA	1.81	0.41
3:H:235:LEU:HD13	3:H:235:LEU:HA	1.93	0.41
3:H:527:PHE:HA	3:H:530:ILE:HG21	1.92	0.41
1:A:64:ALA:O	1:A:73:LEU:HB2	2.20	0.41
2:C:402:LEU:HB2	2:C:403:PRO:HD3	2.00	0.41
3:H:713:LEU:HB3	3:H:802:TYR:HE2	1.85	0.41
3:G:478:GLN:HG2	3:G:481:ARG:HH21	1.85	0.41
3:G:517:LEU:N	3:G:518:PRO:HD2	2.35	0.41
3:G:849:VAL:HG12	3:G:850:ASN:H	1.84	0.41
1:A:165:ARG:O	1:A:166:HIS:ND1	2.53	0.41
3:H:326:PRO:HA	3:H:329:ILE:HD12	2.03	0.41
3:G:479:LEU:HA	3:G:479:LEU:HD12	1.82	0.41
2:D:112:LEU:HD11	2:D:131:TRP:CD1	2.56	0.41
2:D:271:LEU:HD23	2:D:271:LEU:HA	1.84	0.41
3:H:238:LEU:HD22	3:H:238:LEU:H	1.85	0.41
3:H:618:LEU:HA	3:H:618:LEU:HD23	1.80	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:440:ILE:H	3:G:440:ILE:HG12	1.65	0.41
3:G:602:PRO:HB2	3:G:642:MET:HE1	2.00	0.41
2:C:437:LEU:O	2:C:441:VAL:HG22	2.21	0.41
3:H:486:SER:O	3:H:490:MET:HG2	2.21	0.41
3:H:641:ILE:HG12	3:H:690:GLY:HA3	2.02	0.41
1:A:31:LEU:HD23	1:A:31:LEU:HA	1.87	0.41
1:B:210:LEU:HD11	1:B:253:ARG:NE	2.36	0.41
2:C:315:PHE:CE1	2:C:372:ILE:HG23	2.56	0.41
2:D:101:SER:OG	2:D:102:ILE:N	2.54	0.41
3:H:234:PHE:CD1	3:H:234:PHE:C	2.94	0.41
3:G:522:LEU:HD23	3:G:522:LEU:HA	1.94	0.41
2:D:274:LEU:HD23	2:D:274:LEU:HA	1.92	0.41
2:D:512:LYS:HB3	2:D:512:LYS:HE3	1.87	0.41
2:D:516:ASN:O	2:D:516:ASN:ND2	2.52	0.41
3:H:367:TRP:CZ2	3:H:443:SER:HB3	2.55	0.41
3:H:527:PHE:HB3	3:H:551:TRP:CH2	2.56	0.41
3:H:531:TYR:C	3:H:533:THR:H	2.23	0.41
2:C:112:LEU:HA	2:C:115:LEU:HD12	2.03	0.41
2:C:588:LEU:HD23	2:C:588:LEU:HA	1.90	0.41
3:H:125:LEU:O	3:H:125:LEU:HD12	2.21	0.41
3:H:440:ILE:O	3:H:444:LEU:HG	2.21	0.41
3:H:490:MET:HE3	3:H:502:LEU:HD23	2.03	0.41
3:H:866:LEU:HD13	3:H:866:LEU:HA	1.95	0.41
3:G:864:LEU:HD12	3:G:864:LEU:HA	1.81	0.41
2:C:531:ARG:HE	2:C:531:ARG:HB2	1.66	0.41
3:H:184:LYS:HD2	3:H:184:LYS:O	2.20	0.41
3:H:399:PHE:HB2	3:H:400:PRO:HD3	2.03	0.41
3:G:768:PRO:HD2	3:G:771:THR:HB	2.02	0.41
3:G:811:ILE:O	3:G:812:GLU:HG2	2.21	0.41
3:G:889:LYS:H	3:G:889:LYS:HG2	1.66	0.41
2:C:392:LEU:HD23	2:C:392:LEU:HA	1.88	0.40
2:D:577:ARG:HD2	2:D:615:GLU:OE2	2.22	0.40
3:H:573:LEU:HD23	3:H:573:LEU:HA	1.91	0.40
1:A:379:LEU:HD12	1:A:379:LEU:HA	1.93	0.40
2:C:148:MET:H	2:C:148:MET:HG2	1.67	0.40
3:H:324:ILE:O	3:H:327:LEU:N	2.49	0.40
3:H:325:ILE:HA	3:H:328:LEU:HD23	2.03	0.40
3:H:857:LEU:HD23	3:H:857:LEU:HA	1.87	0.40
1:A:20:CYS:HB3	1:A:34:TYR:HD2	1.85	0.40
2:C:401:LEU:HD23	2:C:401:LEU:HA	1.87	0.40
2:C:574:ARG:HE	2:C:574:ARG:HB3	1.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:181:LEU:HD23	2:D:181:LEU:HA	1.94	0.40
3:H:151:HIS:HD2	3:H:156:ILE:HB	1.86	0.40
3:G:737:PHE:HE1	3:G:778:VAL:HG23	1.86	0.40
3:H:815:GLU:OE1	3:H:815:GLU:N	2.55	0.40
1:B:36:GLY:HA3	1:B:65:TRP:HZ2	1.87	0.40
1:B:44:LEU:HB2	1:B:315:ASN:ND2	2.29	0.40
1:B:192:SER:HB2	1:B:198:VAL:HG22	2.02	0.40
1:B:271:GLN:H	1:B:271:GLN:HG3	1.71	0.40
3:H:115:ARG:HE	3:H:115:ARG:HB2	1.73	0.40
3:H:764:LEU:HD23	3:H:764:LEU:HA	1.95	0.40
3:G:435:LEU:HD23	3:G:435:LEU:HA	1.97	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	350/434 (81%)	325 (93%)	25 (7%)	0	100	100
1	B	372/434 (86%)	342 (92%)	30 (8%)	0	100	100
2	C	467/644 (72%)	457 (98%)	10 (2%)	0	100	100
2	D	471/644 (73%)	457 (97%)	14 (3%)	0	100	100
3	G	497/931 (53%)	447 (90%)	49 (10%)	1 (0%)	44	74
3	H	688/931 (74%)	652 (95%)	32 (5%)	4 (1%)	22	56
All	All	2845/4018 (71%)	2680 (94%)	160 (6%)	5 (0%)	45	74

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	H	180	SER

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Mol	Chain	Res	Type
3	H	355	VAL
3	H	132	GLU
3	G	532	GLN
3	H	532	GLN

### 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	303/370 (82%)	281 (93%)	22 (7%)	11	37
1	B	319/370 (86%)	298 (93%)	21 (7%)	14	42
2	C	408/528 (77%)	390 (96%)	18 (4%)	24	53
2	D	411/528 (78%)	394 (96%)	17 (4%)	26	55
3	G	458/845 (54%)	429 (94%)	29 (6%)	15	43
3	H	646/845 (76%)	603 (93%)	43 (7%)	13	41
All	All	2545/3486 (73%)	2395 (94%)	150 (6%)	19	45

All (150) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	THR
1	A	17	MET
1	A	19	SER
1	A	20	CYS
1	A	21	ILE
1	A	23	TRP
1	A	57	LEU
1	A	105	LEU
1	A	106	TRP
1	A	118	SER
1	A	119	ARG
1	A	123	ASP
1	A	134	SER
1	A	157	ASP

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Mol	Chain	Res	Type
1	A	195	ASP
1	A	197	THR
1	A	269	ARG
1	A	285	LEU
1	A	288	SER
1	A	289	HIS
1	A	340	ASN
1	A	342	HIS
1	B	12	ASP
1	B	52	LEU
1	B	84	THR
1	B	86	LEU
1	B	89	SER
1	B	91	ASN
1	B	117	LEU
1	B	119	ARG
1	B	123	ASP
1	B	129	PHE
1	B	192	SER
1	B	193	SER
1	B	225	LEU
1	B	252	GLU
1	B	259	GLN
1	B	276	SER
1	B	283	VAL
1	B	284	LEU
1	B	324	SER
1	B	329	ASP
1	B	385	SER
2	C	101	SER
2	C	114	LEU
2	C	143	ASP
2	C	175	ASN
2	C	223	SER
2	C	259	SER
2	C	313	GLN
2	C	316	SER
2	C	346	CYS
2	C	361	ASP
2	C	371	SER
2	C	375	GLU
2	C	464	SER

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Mol	Chain	Res	Type
2	C	512	LYS
2	C	518	ASN
2	C	531	ARG
2	C	573	SER
2	C	618	SER
2	D	66	LEU
2	D	101	SER
2	D	235	LEU
2	D	245	SER
2	D	328	SER
2	D	350	SER
2	D	361	ASP
2	D	396	ILE
2	D	514	ASP
2	D	516	ASN
2	D	518	ASN
2	D	541	LYS
2	D	553	LEU
2	D	561	GLN
2	D	573	SER
2	D	621	SER
2	D	634	ARG
3	H	61	ASP
3	H	68	HIS
3	H	90	PHE
3	H	98	ASN
3	H	107	PHE
3	H	108	THR
3	H	122	LEU
3	H	137	PHE
3	H	171	TYR
3	H	230	ARG
3	H	234	PHE
3	H	314	THR
3	H	356	MET
3	H	365	LEU
3	H	371	LYS
3	H	397	SER
3	H	401	TYR
3	H	433	LEU
3	H	450	LEU
3	H	525	LYS

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Mol	Chain	Res	Type
3	H	534	GLU
3	H	536	LEU
3	H	544	ARG
3	H	551	TRP
3	H	636	LEU
3	H	639	CYS
3	H	661	SER
3	H	672	ASP
3	H	673	TRP
3	H	691	PHE
3	H	727	LEU
3	H	755	SER
3	H	778	VAL
3	H	785	HIS
3	H	786	THR
3	H	801	CYS
3	H	806	TYR
3	H	823	ASP
3	H	831	SER
3	H	833	LEU
3	H	906	ASP
3	H	909	TYR
3	H	911	PHE
3	G	437	LEU
3	G	473	ARG
3	G	496	ARG
3	G	513	ARG
3	G	517	LEU
3	G	527	PHE
3	G	532	GLN
3	G	544	ARG
3	G	545	SER
3	G	549	SER
3	G	585	ASN
3	G	627	SER
3	G	631	ASP
3	G	634	SER
3	G	659	MET
3	G	686	SER
3	G	693	LYS
3	G	711	THR
3	G	718	LEU

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Mol	Chain	Res	Type
3	G	727	LEU
3	G	803	SER
3	G	805	LEU
3	G	821	LYS
3	G	829	CYS
3	G	833	LEU
3	G	849	VAL
3	G	894	LEU
3	G	909	TYR
3	G	914	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	122	GLN
1	B	196	GLN
3	H	585	ASN
3	H	880	ASN
3	G	566	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.

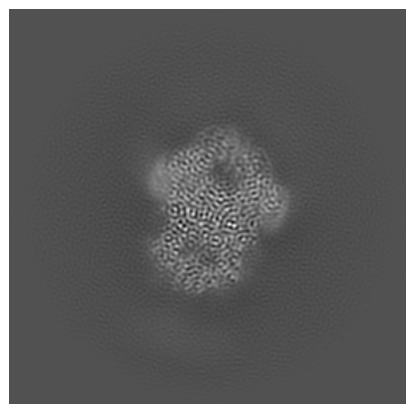
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47170. These allow visual inspection of the internal detail of the map and identification of artifacts.

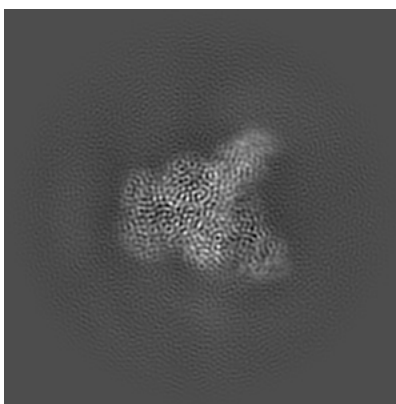
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

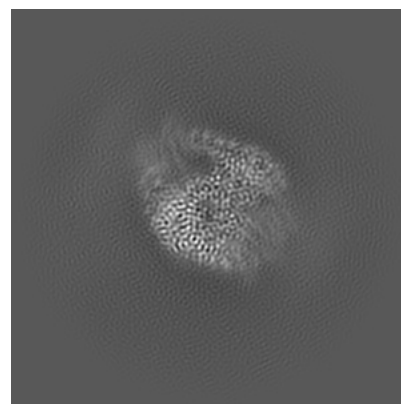
#### 6.1.1 Primary map



X

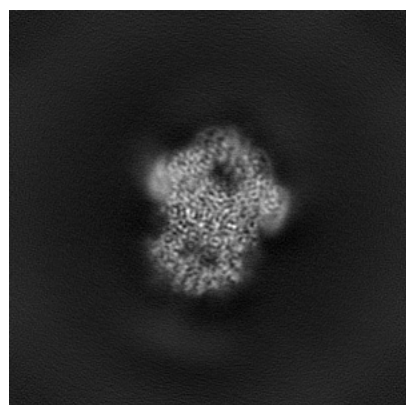


Y

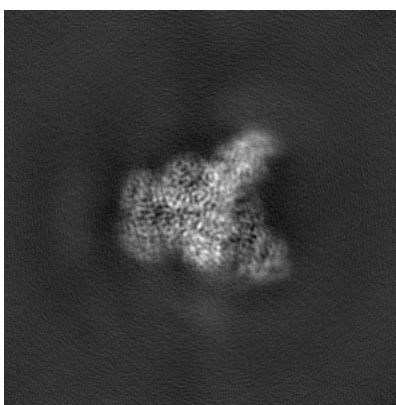


Z

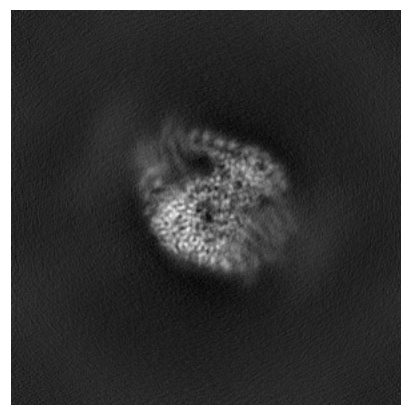
#### 6.1.2 Raw map



X



Y

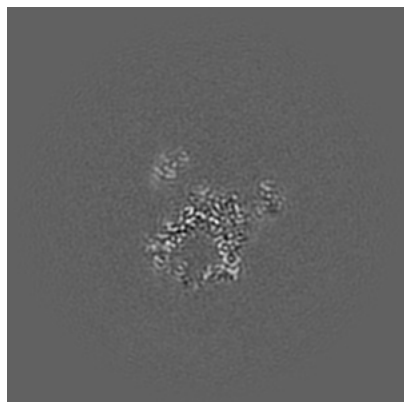


Z

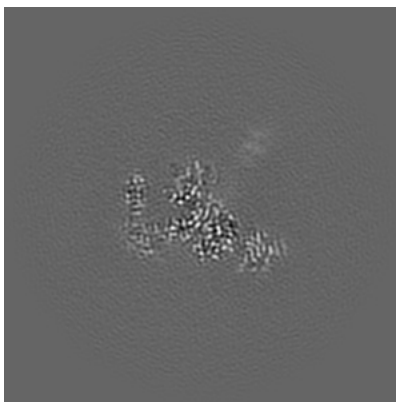
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

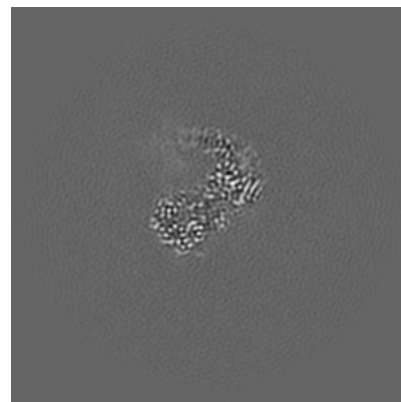
### 6.2.1 Primary map



X Index: 150

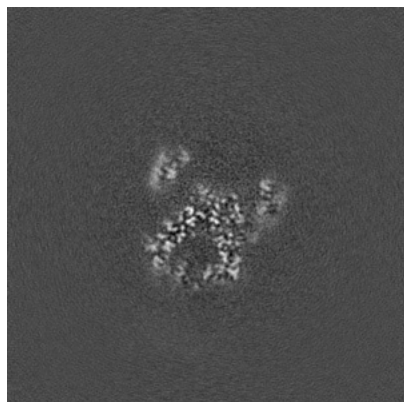


Y Index: 150

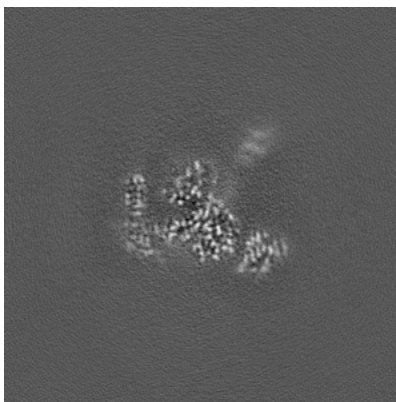


Z Index: 150

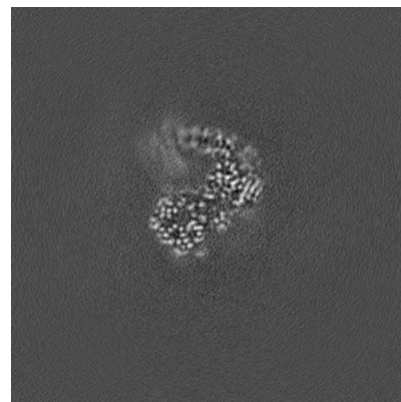
### 6.2.2 Raw map



X Index: 150



Y Index: 150

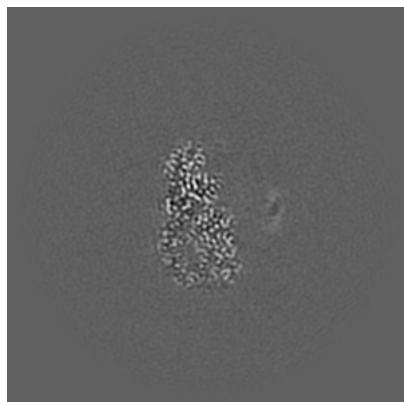


Z Index: 150

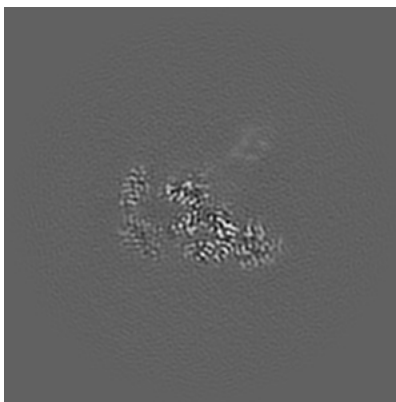
The images above show central slices of the map in three orthogonal directions.

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

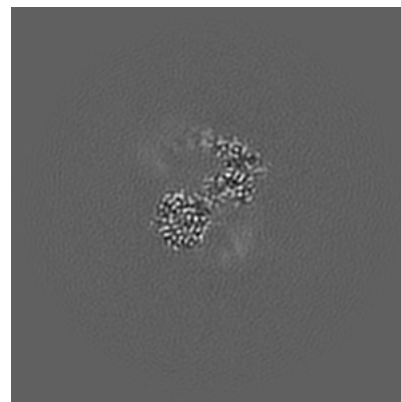
### 6.3.1 Primary map



X Index: 133

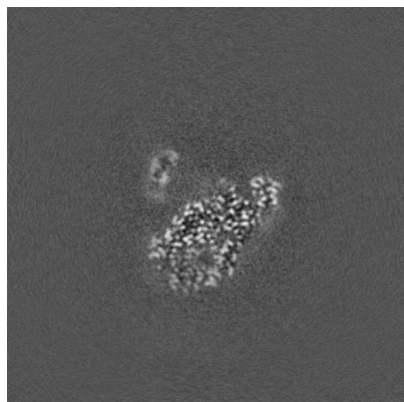


Y Index: 144

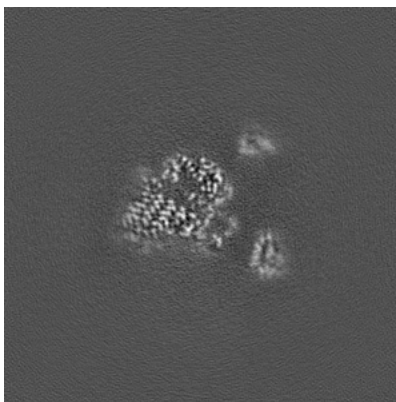


Z Index: 157

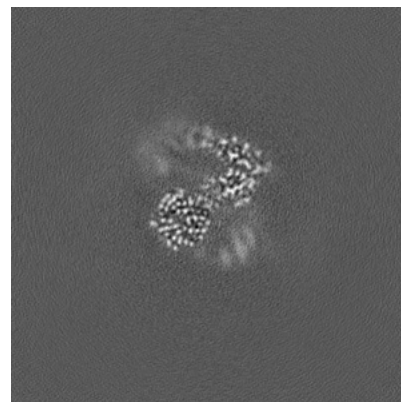
### 6.3.2 Raw map



X Index: 158



Y Index: 161

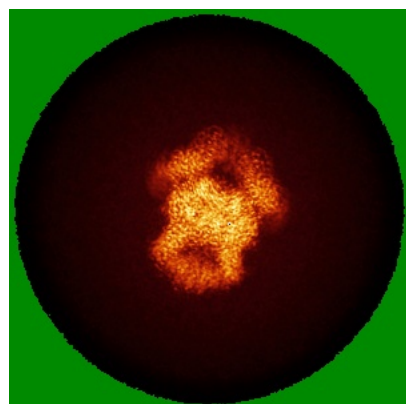


Z Index: 158

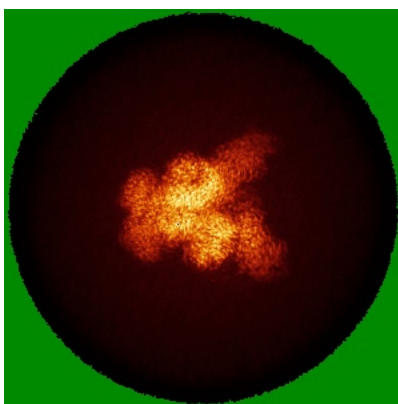
The images above show the largest variance slices of the map in three orthogonal directions.

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

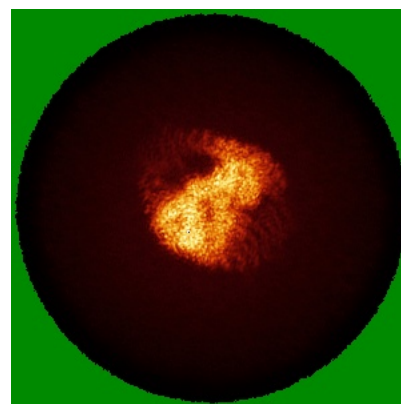
### 6.4.1 Primary map



X

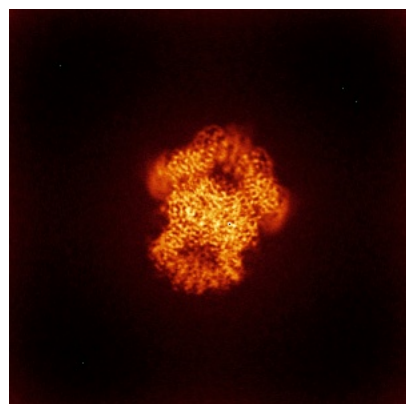


Y

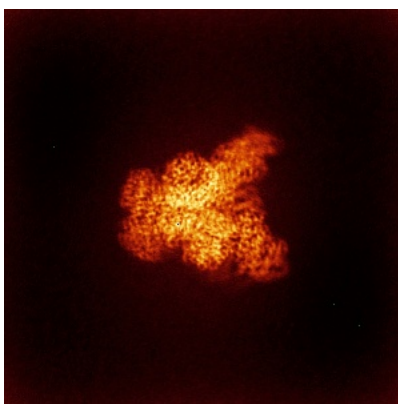


Z

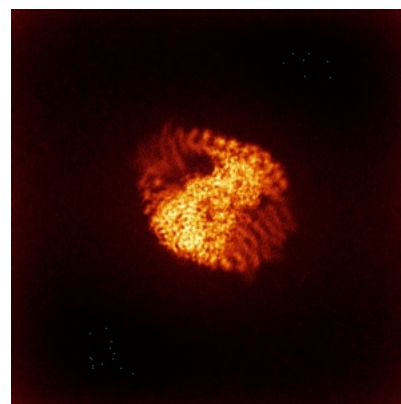
### 6.4.2 Raw map



X



Y

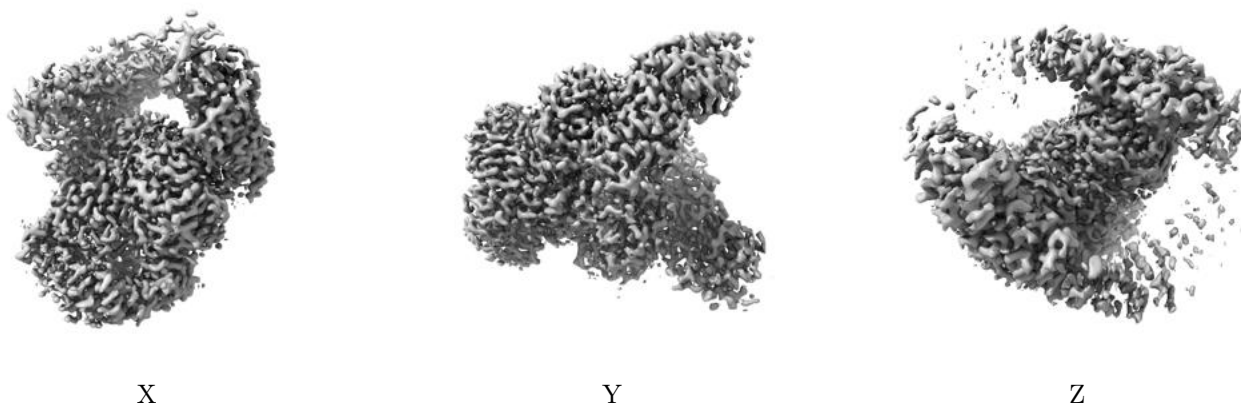


Z

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.

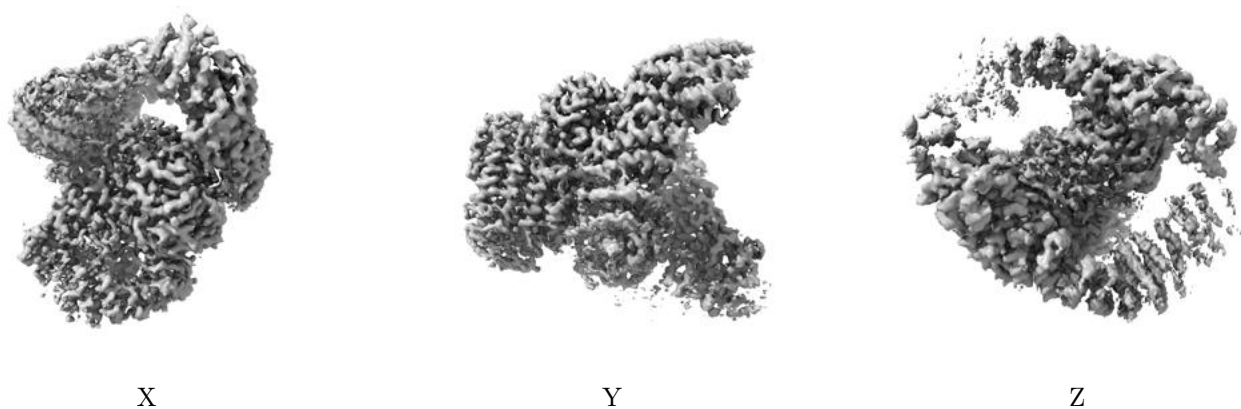
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.284. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

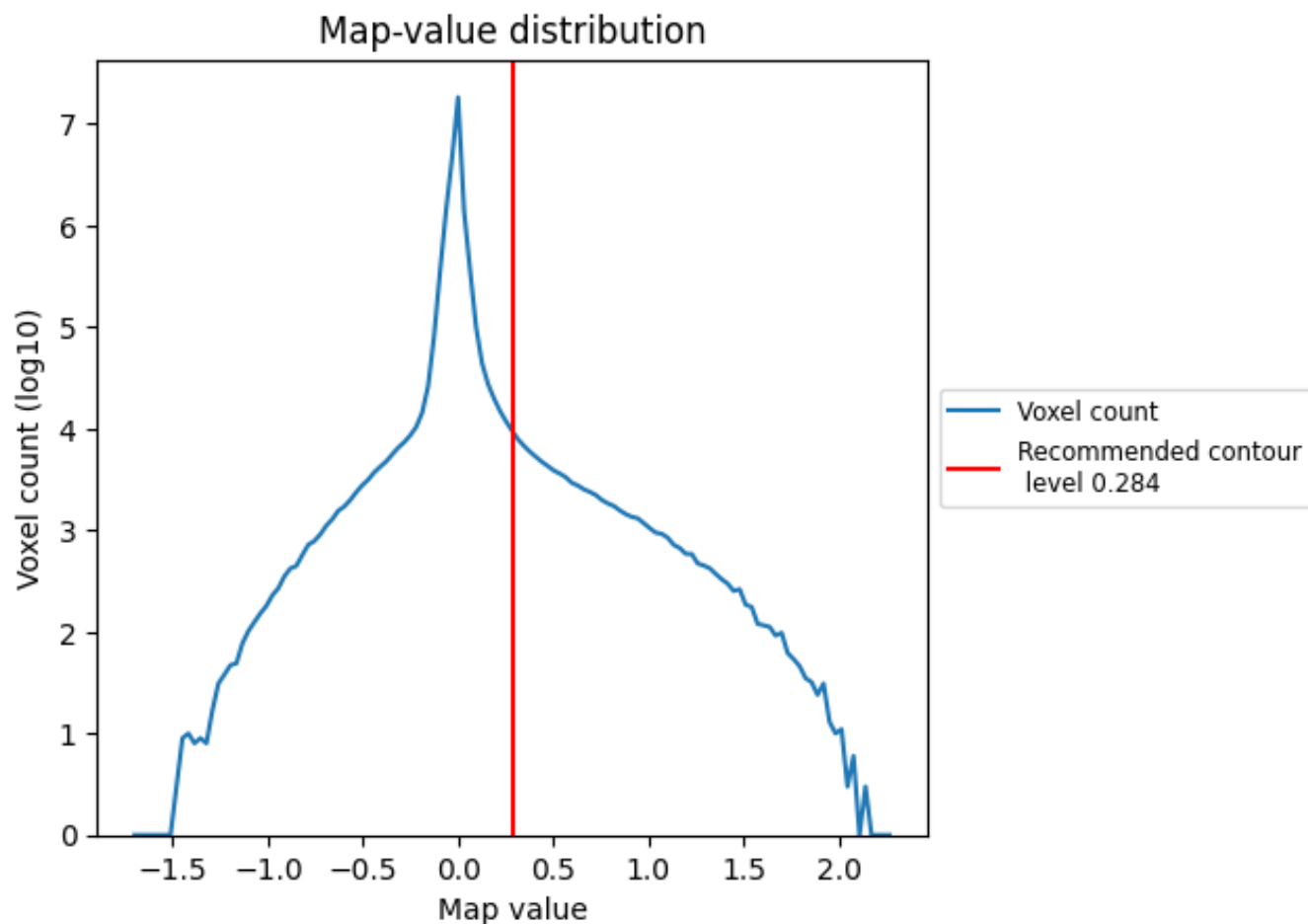
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

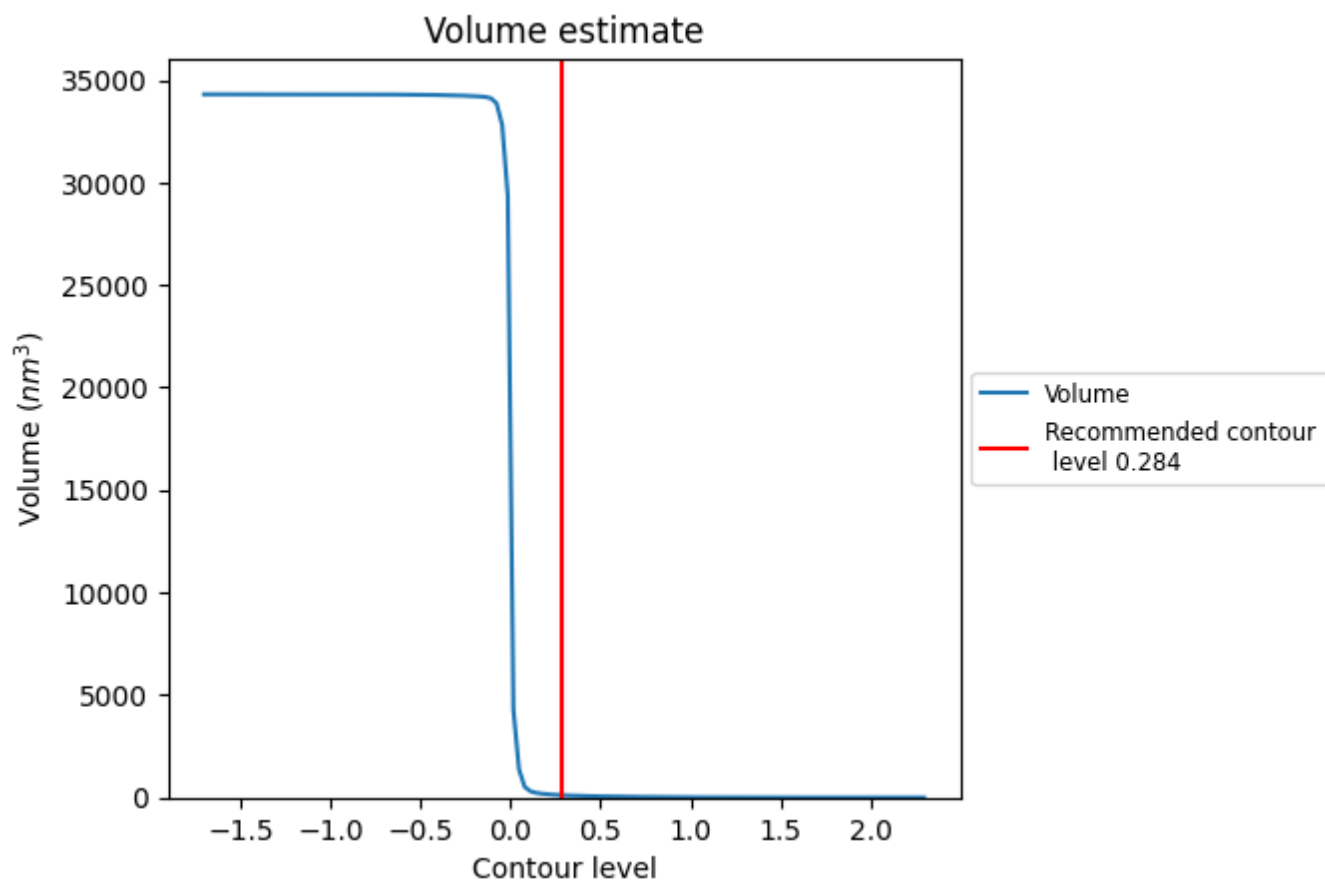
This section contains the results of statistical analysis of the map.

### 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.

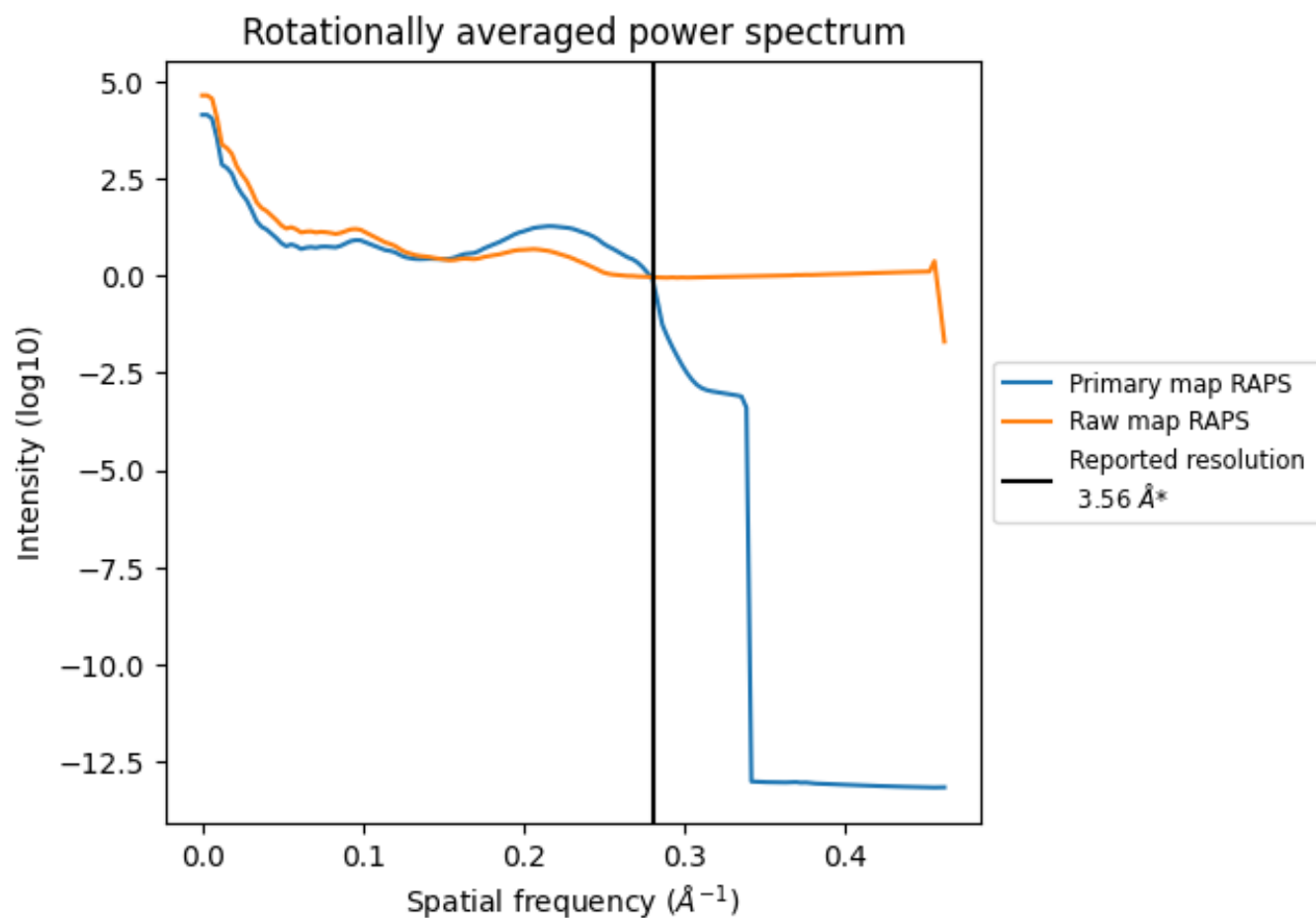
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 115 nm<sup>3</sup>; this corresponds to an approximate mass of 104 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 ⓘ

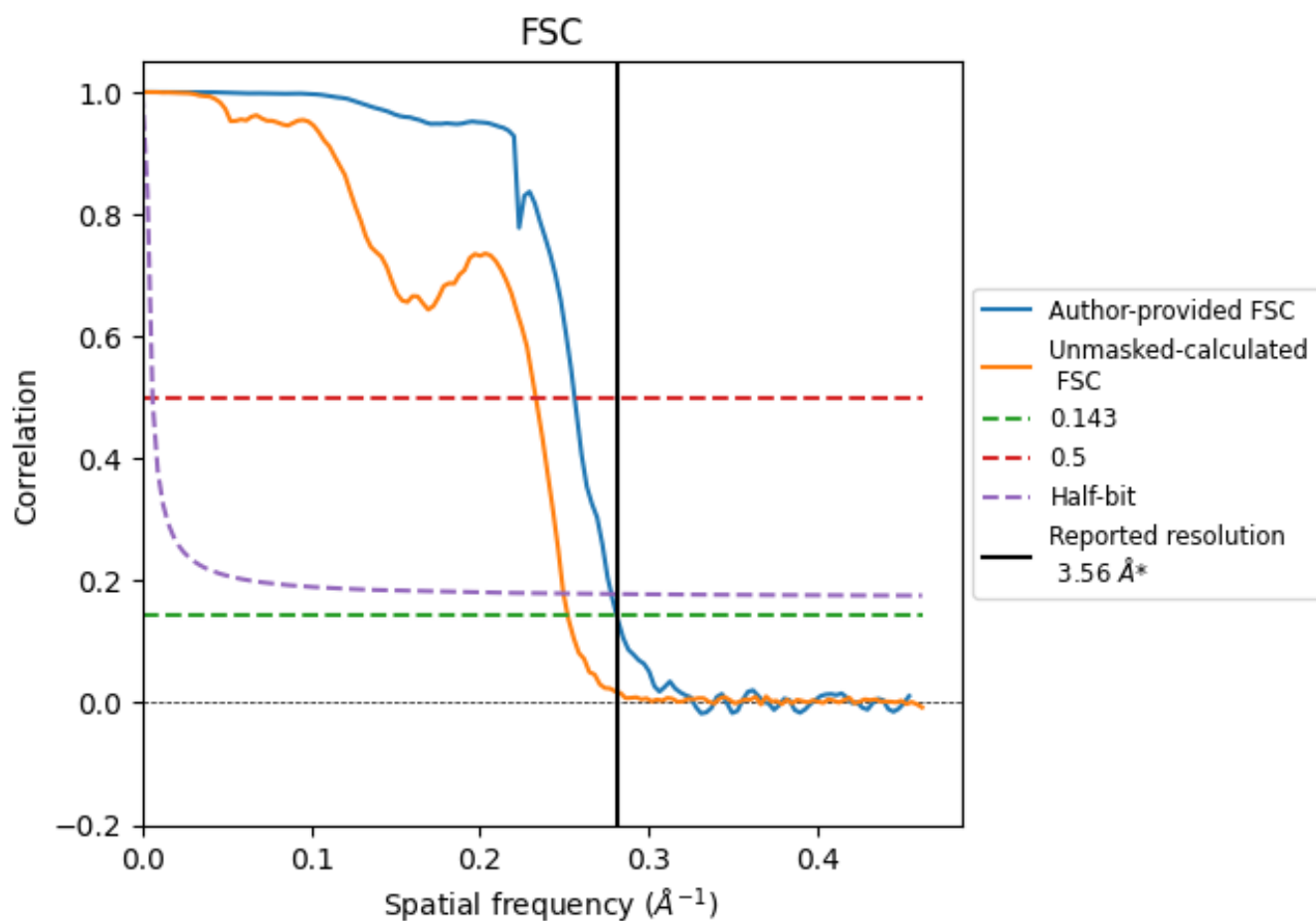


\*Reported resolution corresponds to spatial frequency of 0.281 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.281  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

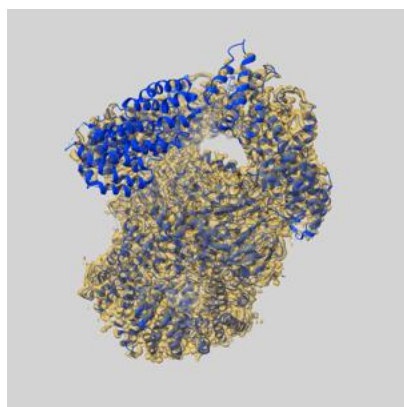
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.56	-	-
Author-provided FSC curve	3.56	3.91	3.60
Unmasked-calculated*	3.97	4.29	4.01

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.97 differs from the reported value 3.56 by more than 10 %

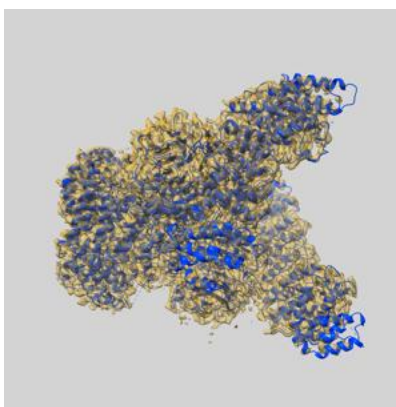
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-47170 and PDB model 9DUM. Per-residue inclusion information can be found in section [3](#) on page [5](#).

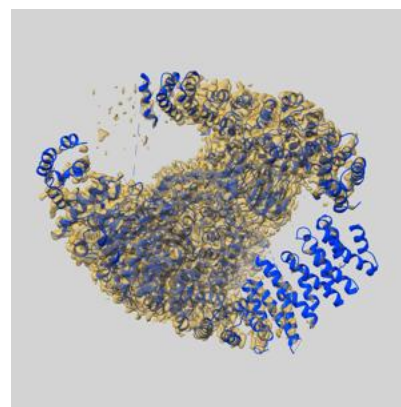
### 9.1 Map-model overlay [i](#)



X



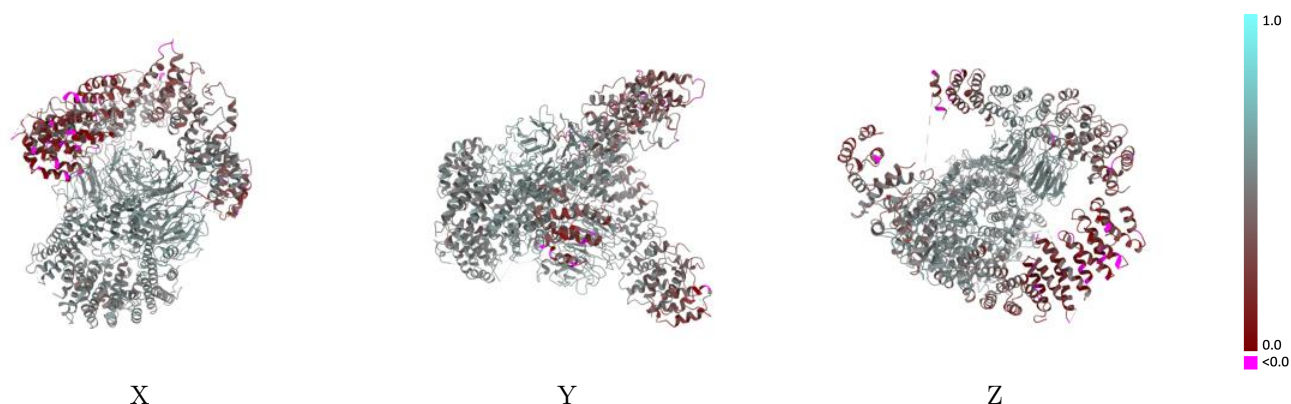
Y



Z

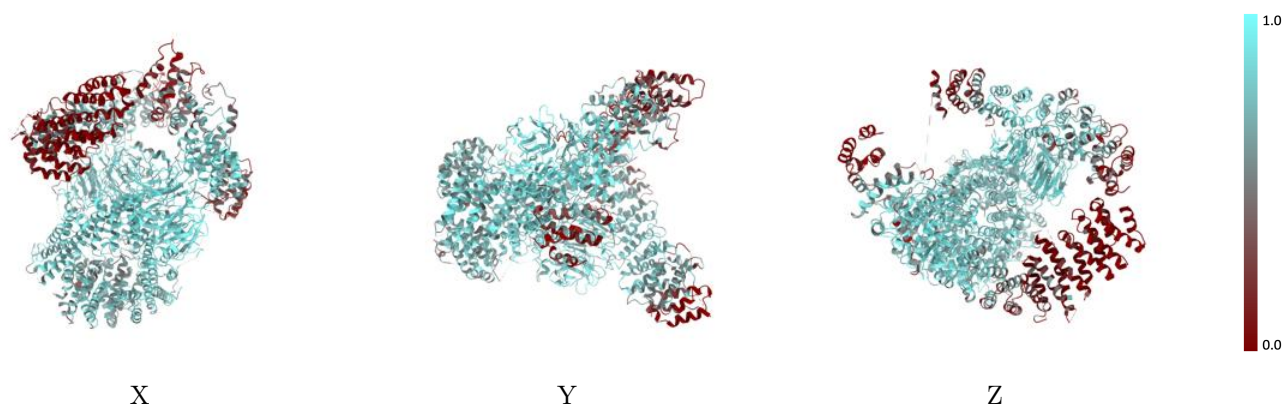
The images above show the 3D surface view of the map at the recommended contour level 0.284 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



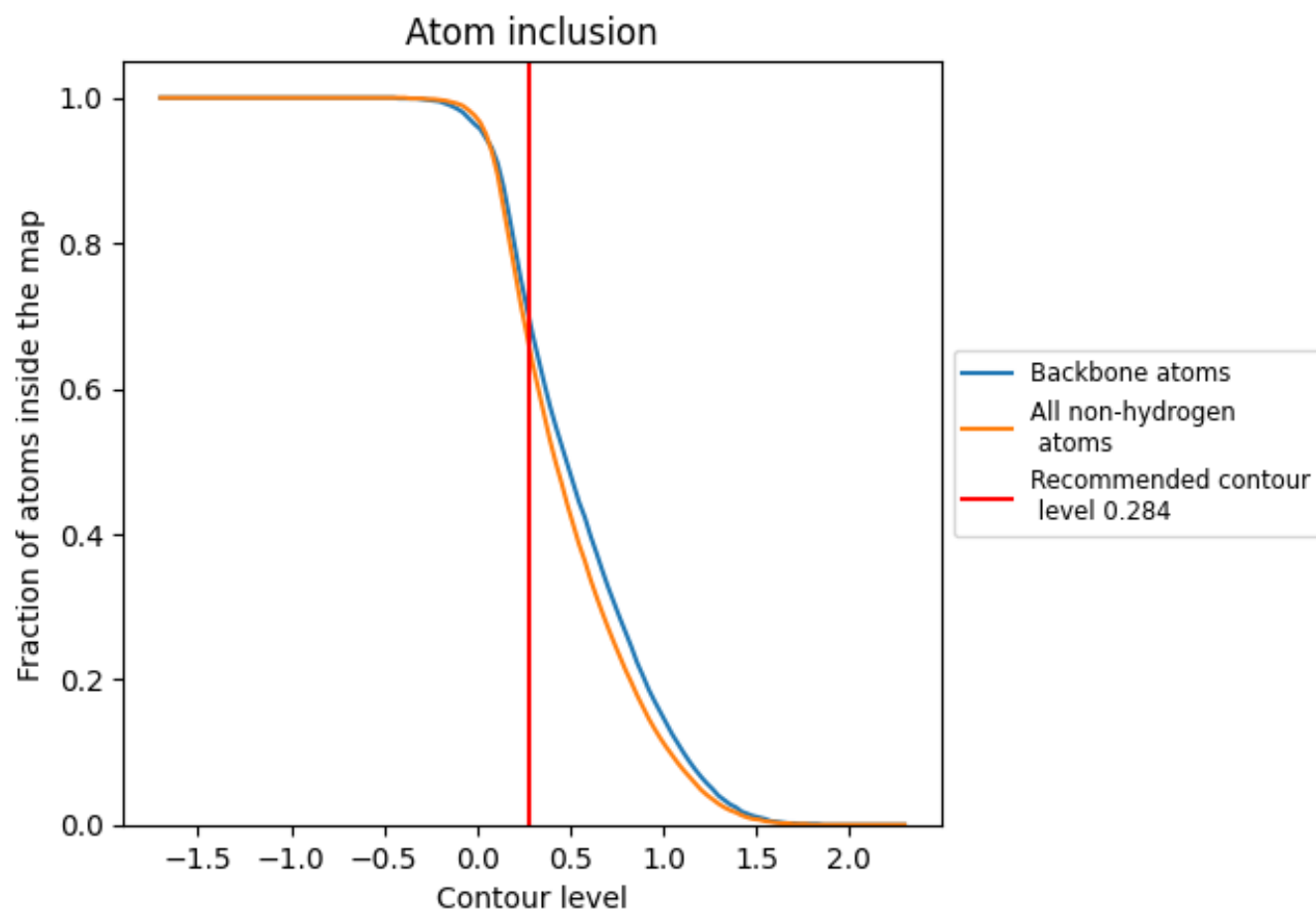
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.284).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 69% of all backbone atoms, 65% 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 (0.284) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6520	<div></div> 0.4530
A	<div></div> 0.8470	<div></div> 0.5450
B	<div></div> 0.8260	<div></div> 0.5390
C	<div></div> 0.7830	<div></div> 0.5190
D	<div></div> 0.7780	<div></div> 0.5160
G	<div></div> 0.5410	<div></div> 0.3940
H	<div></div> 0.3840	<div></div> 0.3240

1.0

0.0

<0.0