



Full wwPDB EM Validation Report ⓘ

Jun 17, 2026 – 04:15 pm BST

PDB ID : 8RG0 / pdb_00008rg0
EMDB ID : EMD-19128
Title : Structure of human eIF3 core from closed 48S translation initiation complex
Authors : Petrychenko, V.; Yi, S.-H.; Liedtke, D.; Peng, B.Z.; Rodnina, M.V.; Fischer, N.
Deposited on : 2023-12-13
Resolution : 3.40 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:

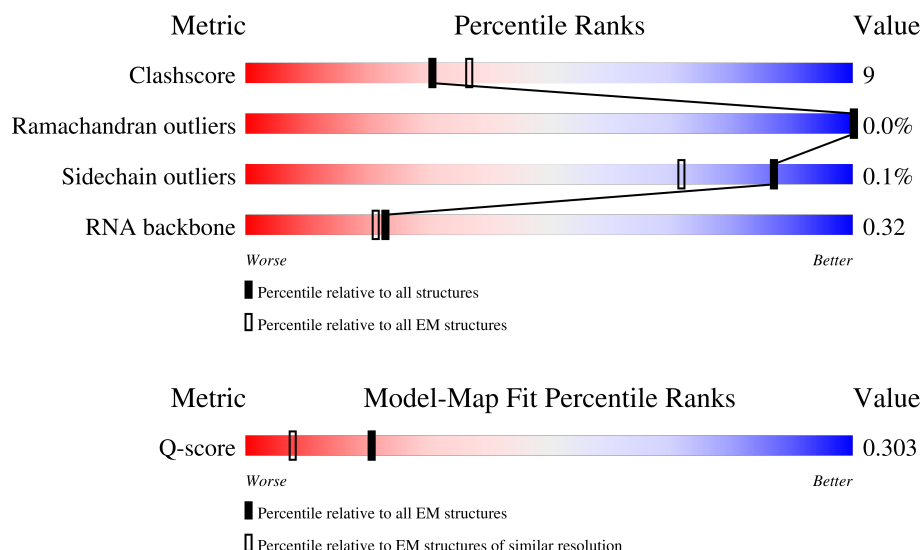
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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

Mol	Chain	Length	Quality of chain
1	3	218	71% 95% ..
2	4	357	17% 70% 28%
3	5	564	71% 79% 13% 8%

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Mol	Chain	Length	Quality of chain
4	6	374	
5	7	255	
6	8	352	
7	A	1869	
8	H	84	
9	I	151	
10	M	135	
11	N	295	
12	O	264	
13	P	151	
14	Q	115	
15	n	69	
16	u	1382	
17	v	445	
18	x	548	
19	y	913	

2 Entry composition

There are 21 unique types of molecules in this entry. The entry contains 31348 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 Eukaryotic translation initiation factor 3 subunit K.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	3	213	Total	C	N	O	0	0
			1057	631	213	213		

- Molecule 2 is a protein called Eukaryotic translation initiation factor 3 subunit F.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	4	257	Total	C	N	O	0	0
			1272	757	257	258		

- Molecule 3 is a protein called Eukaryotic translation initiation factor 3 subunit L.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5	520	Total	C	N	O	S	0	0
			4347	2814	721	793	19		

- Molecule 4 is a protein called Eukaryotic translation initiation factor 3 subunit M.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	362	Total	C	N	O	S	0	0
			2196	1348	414	427	7		

- Molecule 5 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	31	Total	C	N	O	P	0	0
			663	299	132	201	31		

- Molecule 6 is a protein called Eukaryotic translation initiation factor 3 subunit H.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	8	317	Total	C	N	O	0	0
			1574	937	318	319		

- Molecule 7 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	121	Total	C	N	O	P	0	0
			2594	1154	467	852	121		

- Molecule 8 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	71	Total	C	N	O	S	0	0
			555	347	103	98	7		

- Molecule 9 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	I	95	Total	C	N	O	0	0
			753	484	139	130		

- Molecule 10 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	M	32	Total	C	N	O	S	0	0
			257	161	43	51	2		

- Molecule 11 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	32	Total	C	N	O	S	0	0
			255	163	43	48	1		

- Molecule 12 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	O	178	Total	C	N	O	S	0	0
			1455	925	260	256	14		

- Molecule 13 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	P	88	Total	C	N	O	S	0	0
			651	404	120	124	3		

- Molecule 14 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	96	Total	C	N	O	S	0	0
			767	476	160	126	5		

- Molecule 15 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	n	58	Total	C	N	O	S	0	0
			455	275	91	87	2		

- Molecule 16 is a protein called Eukaryotic translation initiation factor 3 subunit A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	u	603	Total	C	N	O	S	1	0
			4869	3071	879	896	23		

- Molecule 17 is a protein called Eukaryotic translation initiation factor 3 subunit E.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	v	405	Total	C	N	O	S	0	0
			2740	1720	498	510	12		

- Molecule 18 is a protein called Eukaryotic translation initiation factor 3 subunit D.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	x	63	Total	C	N	O	S	0	0
			525	331	88	104	2		

- Molecule 19 is a protein called Eukaryotic translation initiation factor 3 subunit C.

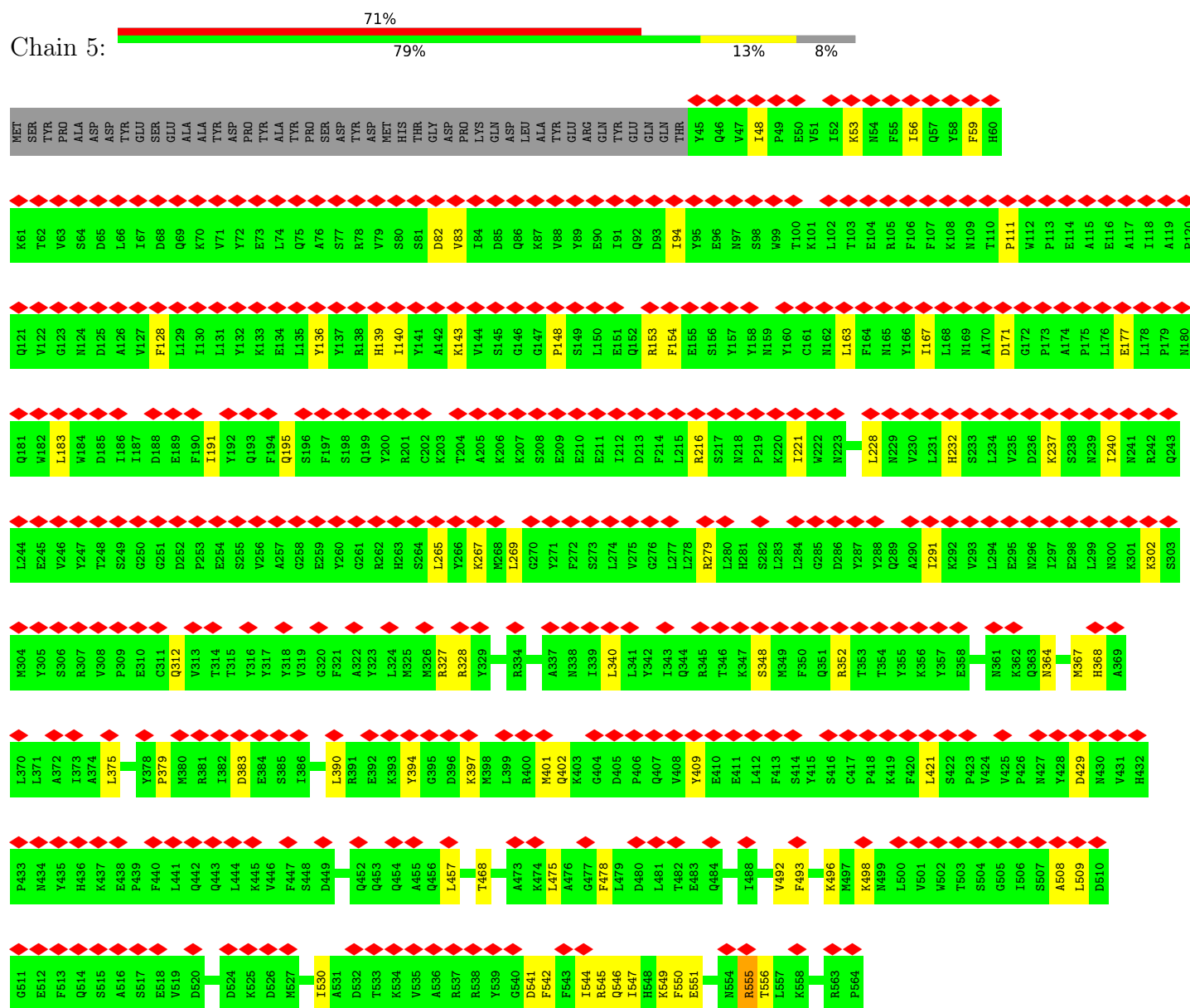
Mol	Chain	Residues	Atoms					AltConf	Trace
19	y	543	Total	C	N	O	S	0	0
			4361	2743	776	809	33		

- Molecule 20 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

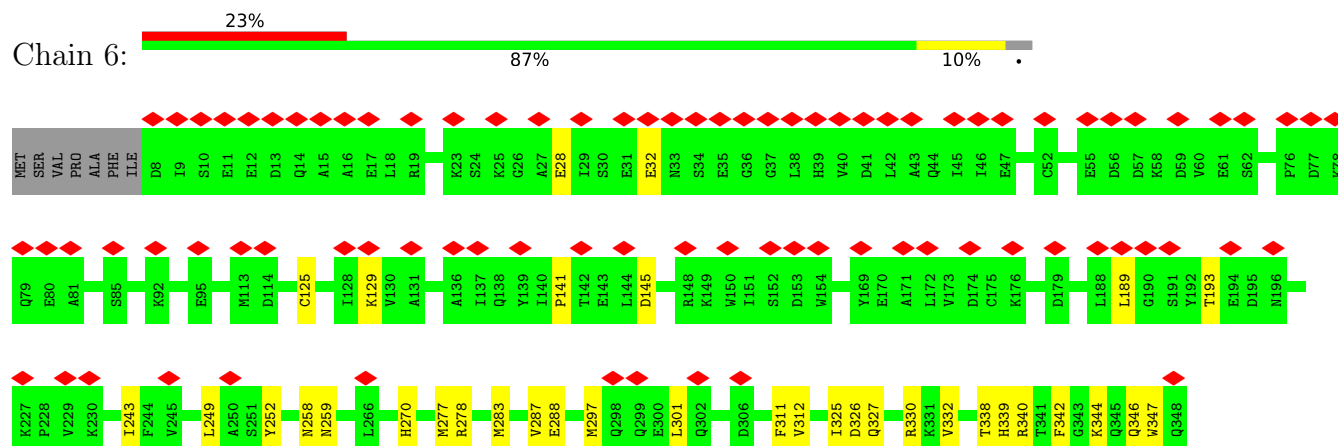
Mol	Chain	Residues	Atoms		AltConf
20	A	1	Total	Mg	0
			1	1	

- Molecule 21 is ZINC ION (CCD ID: ZN) (formula: Zn).

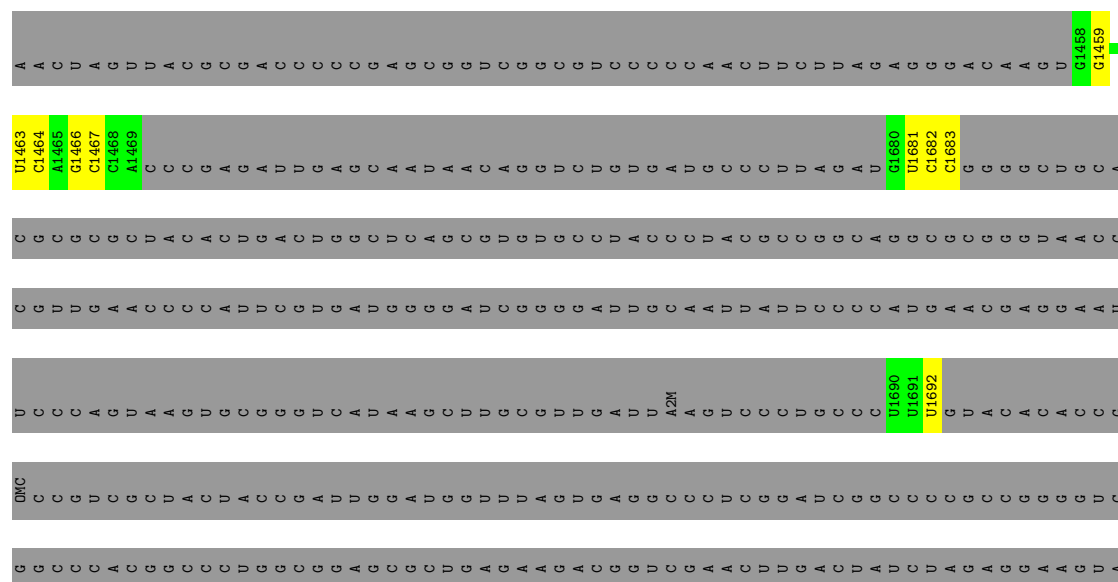
Mol	Chain	Residues	Atoms		AltConf
21	Q	1	Total	Zn	0
			1	1	



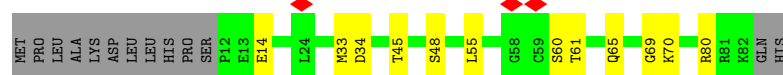
• Molecule 4: Eukaryotic translation initiation factor 3 subunit M



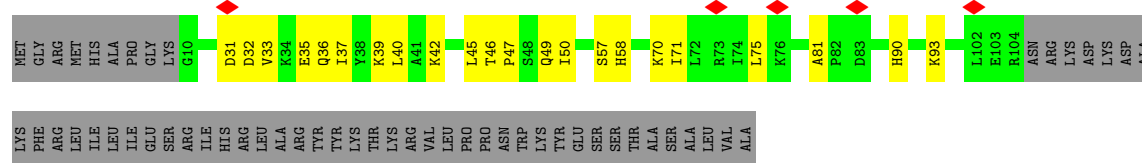




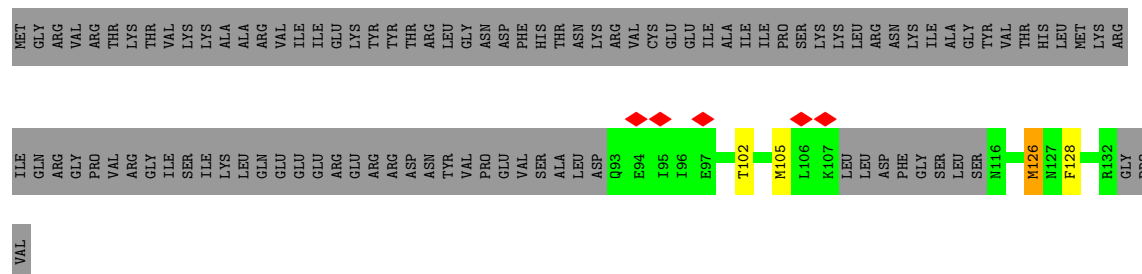
• Molecule 8: 40S ribosomal protein S27



• Molecule 9: 40S ribosomal protein S13



• Molecule 10: 40S ribosomal protein S17



R846	P849	A856	L857	F874	D875	HIS	LYS	GLN	GLY	THR	TYR	GLY	GLY	TYR	PHE	ARG	ASP	GLN	LYS	LYS	ASP	GLY	TYR	ARG	LYS	ASN	GLU	GLY	TYR	MET	ARG	ARG	GLY	GLY	TYR	ARG	GLN	GLN	GLN	SER	GLN	THR	ALA	TYR
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	356632	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 ($e^-/\text{\AA}^2$)	45	Depositor
Minimum defocus (nm)	200	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	34.833	Depositor
Minimum map value	-15.718	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	4	Depositor
Map size (Å)	278.4, 278.4, 278.4	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.16, 1.16, 1.16	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ZN

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	3	0.14	0/1055	0.39	0/1469
2	4	0.12	0/1269	0.37	0/1762
3	5	0.20	0/4458	0.52	1/6027 (0.0%)
4	6	0.21	0/2212	0.58	2/3034 (0.1%)
5	7	0.52	5/744 (0.7%)	0.48	1/1156 (0.1%)
6	8	0.17	0/1572	0.46	0/2187
7	A	0.27	0/2889	0.47	0/4479
8	H	0.30	0/565	0.81	0/755
9	I	0.33	0/766	0.82	0/1032
10	M	0.30	0/259	0.79	1/348 (0.3%)
11	N	0.41	0/259	1.01	2/347 (0.6%)
12	O	0.33	0/1475	0.84	3/1968 (0.2%)
13	P	0.28	0/661	0.77	0/891
14	Q	0.31	0/780	0.76	0/1047
15	n	0.32	0/456	0.92	1/610 (0.2%)
16	u	0.44	4/4961 (0.1%)	0.79	13/6713 (0.2%)
17	v	0.28	0/2778	0.70	1/3797 (0.0%)
18	x	0.36	0/539	0.71	0/727
19	y	0.30	0/4436	0.73	4/5989 (0.1%)
All	All	0.30	9/32134 (0.0%)	0.66	29/44338 (0.1%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
16	u	350	GLU	C-N	10.53	1.47	1.33
16	u	347	ILE	C-N	-9.24	1.22	1.33
16	u	366	THR	C-N	-8.11	1.22	1.33
5	7	-34	C	C1'-N1	6.19	1.57	1.48
5	7	-25	C	C1'-N1	6.11	1.57	1.48
5	7	-31	C	C1'-N1	5.87	1.57	1.48
5	7	-22	C	C1'-N1	5.80	1.57	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	7	-28	C	C1'-N1	5.66	1.55	1.47
16	u	333	PRO	CA-C	-5.21	1.46	1.52

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
16	u	342	LEU	N-CA-C	-13.79	85.46	108.76
16	u	369	GLY	N-CA-C	-11.54	98.53	112.49
16	u	366	THR	O-C-N	-10.54	112.75	123.29
16	u	341	LEU	N-CA-C	-8.64	100.59	113.72
16	u	506	PRO	CA-N-CD	-7.54	101.44	112.00
16	u	332	THR	CA-C-N	-7.50	111.89	119.92
16	u	332	THR	C-N-CA	-7.50	111.89	119.92
16	u	350	GLU	CA-C-N	-7.31	110.49	120.28
16	u	350	GLU	C-N-CA	-7.31	110.49	120.28
16	u	351	LYS	N-CA-C	-6.74	103.93	111.28
16	u	344	MET	N-CA-C	6.42	119.55	110.50
3	5	555	ARG	CB-CG-CD	6.40	126.01	111.30
10	M	126	MET	CA-CB-CG	6.05	126.19	114.10
12	O	168	MET	CB-CG-SD	-5.74	95.47	112.70
17	v	247	GLN	CA-CB-CG	5.70	125.51	114.10
16	u	347	ILE	N-CA-C	5.63	116.69	111.45
19	y	726	LEU	CA-CB-CG	5.51	135.60	116.30
19	y	744	MET	CB-CG-SD	-5.34	96.68	112.70
19	y	744	MET	CA-CB-CG	5.29	124.68	114.10
4	6	326	ASP	CA-C-N	5.29	131.63	121.54
4	6	326	ASP	C-N-CA	5.29	131.63	121.54
12	O	168	MET	CA-CB-CG	5.28	124.67	114.10
11	N	30	LEU	N-CA-C	5.24	117.49	107.75
15	n	31	ARG	CG-CD-NE	5.24	123.52	112.00
5	7	-21	A	P-O3'-C3'	5.24	128.05	120.20
16	u	244	GLU	CA-CB-CG	5.22	124.54	114.10
11	N	33	GLN	CA-CB-CG	5.21	124.53	114.10
12	O	213	ARG	CB-CG-CD	5.16	123.17	111.30
19	y	705	ALA	N-CA-C	5.11	115.12	108.07

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	3	1057	0	475	3	0
2	4	1272	0	564	4	0
3	5	4347	0	4294	52	0
4	6	2196	0	1547	25	0
5	7	663	0	341	3	0
6	8	1574	0	687	4	0
7	A	2594	0	1317	23	0
8	H	555	0	576	10	0
9	I	753	0	814	15	0
10	M	257	0	262	3	0
11	N	255	0	250	6	0
12	O	1455	0	1519	33	0
13	P	651	0	644	20	0
14	Q	767	0	808	18	0
15	n	455	0	475	11	0
16	u	4869	0	4861	188	0
17	v	2740	0	2251	51	0
18	x	525	0	476	10	0
19	y	4361	0	4335	100	0
20	A	1	0	0	0	0
21	Q	1	0	0	0	0
All	All	31348	0	26496	514	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 9.

All (514) 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)
16:u:340:ARG:HG3	19:y:722:GLU:OE1	1.26	1.31
16:u:340:ARG:CZ	16:u:348:ILE:HG12	1.59	1.29
16:u:340:ARG:HE	16:u:347:ILE:CG2	1.56	1.17
16:u:340:ARG:CG	19:y:722:GLU:OE1	1.94	1.15
16:u:340:ARG:NE	16:u:347:ILE:HG22	1.62	1.14
16:u:340:ARG:HE	16:u:347:ILE:HG22	0.95	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:u:340:ARG:NH1	16:u:348:ILE:CG1	2.15	1.09
16:u:340:ARG:CZ	16:u:348:ILE:CG1	2.31	1.08
16:u:340:ARG:CD	16:u:348:ILE:HD11	1.89	1.02
16:u:340:ARG:HD3	16:u:348:ILE:HD11	1.40	1.02
16:u:331:ILE:HD13	16:u:438:ARG:HH21	1.20	1.00
16:u:340:ARG:NH2	16:u:345:ASP:O	1.96	0.97
16:u:337:ASP:HA	16:u:341:LEU:HB2	1.47	0.94
16:u:531:ALA:O	16:u:535:GLU:HB2	1.68	0.94
16:u:340:ARG:NE	16:u:347:ILE:CG2	2.23	0.93
16:u:340:ARG:NH2	16:u:348:ILE:HG12	1.85	0.90
16:u:340:ARG:NH1	16:u:348:ILE:HG13	1.85	0.88
19:y:568:ALA:O	19:y:572:HIS:HB2	1.73	0.88
16:u:331:ILE:CD1	16:u:438:ARG:NH2	2.39	0.85
19:y:504:LEU:HD11	19:y:567:CYS:HB3	1.60	0.83
16:u:331:ILE:CD1	16:u:438:ARG:HH21	1.92	0.83
16:u:331:ILE:CG2	16:u:507:ILE:HG13	2.08	0.83
16:u:331:ILE:HD13	16:u:438:ARG:NH2	1.92	0.83
16:u:331:ILE:HG21	16:u:507:ILE:HD11	1.63	0.80
16:u:340:ARG:C	16:u:342:LEU:H	1.84	0.80
17:v:405:ILE:HG22	17:v:409:LYS:HE2	1.63	0.78
19:y:701:HIS:CE1	19:y:702:GLU:HG2	2.18	0.78
16:u:205:LEU:HD11	16:u:233:ARG:HH12	1.49	0.77
16:u:338:ILE:HG12	19:y:746:MET:CE	2.17	0.74
19:y:405:ILE:HG21	19:y:451:MET:HE1	1.70	0.74
16:u:340:ARG:CD	19:y:722:GLU:OE1	2.35	0.73
17:v:243:LEU:HA	17:v:247:GLN:HB3	1.67	0.73
16:u:331:ILE:HG21	16:u:507:ILE:CD1	2.17	0.73
16:u:407:VAL:HG21	16:u:435:THR:HG21	1.71	0.73
16:u:472:VAL:HG23	19:y:798:VAL:HG11	1.71	0.73
16:u:335:ARG:HB2	16:u:338:ILE:HD13	1.70	0.73
16:u:336:THR:HB	16:u:340:ARG:HH11	1.54	0.72
19:y:571:CYS:SG	19:y:608:LEU:HD21	2.30	0.72
3:5:478:PHE:O	17:v:369:ARG:NH1	2.23	0.72
17:v:342:GLU:HG3	17:v:346:ARG:HH22	1.55	0.72
16:u:340:ARG:CZ	16:u:347:ILE:HG22	2.20	0.71
16:u:340:ARG:CZ	16:u:348:ILE:CD1	2.69	0.71
17:v:406:GLU:HA	17:v:409:LYS:HD2	1.70	0.71
19:y:568:ALA:O	19:y:572:HIS:CB	2.38	0.71
7:A:925:G:H1	7:A:1017:U:H3	1.39	0.70
13:P:75:MET:HG2	13:P:118:ALA:HB2	1.73	0.70
10:M:102:THR:HA	10:M:105:MET:HG2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:y:394:LYS:HB3	19:y:397:MET:HG2	1.73	0.69
3:5:348:SER:HA	17:v:420:MET:HE2	1.72	0.69
16:u:331:ILE:HD11	16:u:438:ARG:NH2	2.07	0.69
16:u:340:ARG:CD	16:u:348:ILE:CD1	2.70	0.69
19:y:835:LEU:HB2	19:y:840:GLN:O	1.94	0.68
18:x:39:LEU:HG	19:y:613:MET:HE1	1.75	0.68
16:u:397:GLU:OE1	16:u:399:ASN:ND2	2.26	0.68
16:u:191:LYS:NZ	16:u:248:GLU:OE2	2.27	0.67
16:u:321:ARG:HE	16:u:423:GLU:HG3	1.59	0.67
16:u:331:ILE:CG2	16:u:507:ILE:CD1	2.73	0.67
16:u:366:THR:HG23	16:u:368:ILE:HB	1.77	0.67
16:u:335:ARG:HB2	16:u:338:ILE:CD1	2.25	0.66
18:x:30:TYR:HA	19:y:591:MET:HE1	1.77	0.66
12:O:217:MET:SD	12:O:217:MET:N	2.68	0.66
3:5:556:THR:OG1	17:v:416:GLN:NE2	2.29	0.66
19:y:683:GLU:HG3	19:y:733:MET:HE3	1.78	0.66
16:u:331:ILE:O	16:u:332:THR:C	2.37	0.66
16:u:366:THR:C	16:u:368:ILE:H	2.04	0.65
12:O:190:PRO:HA	16:u:14[B]:ARG:HH21	1.60	0.65
18:x:80:PHE:HB2	19:y:662:GLN:HE21	1.62	0.65
16:u:340:ARG:C	16:u:342:LEU:N	2.46	0.64
16:u:17:GLU:HA	16:u:20:GLU:HG3	1.78	0.64
3:5:48:ILE:HB	3:5:53:LYS:HE3	1.80	0.64
19:y:687:LEU:HD12	19:y:733:MET:HE1	1.79	0.64
16:u:336:THR:HB	16:u:340:ARG:NH1	2.13	0.63
16:u:405:GLU:HA	16:u:408:THR:HG22	1.78	0.63
16:u:338:ILE:HG12	19:y:746:MET:HE1	1.80	0.63
16:u:414:VAL:O	16:u:425:GLN:NE2	2.32	0.63
19:y:651:LEU:HD11	19:y:667:ARG:HD2	1.80	0.63
16:u:369:GLY:HA2	16:u:372:ASN:OD1	1.99	0.63
3:5:327:ARG:HH22	3:5:496:LYS:HG2	1.64	0.63
13:P:44:VAL:HG13	13:P:93:LEU:HD11	1.79	0.63
16:u:340:ARG:NH1	16:u:348:ILE:CD1	2.61	0.63
11:N:41:ARG:HE	11:N:45:GLY:HA2	1.63	0.63
13:P:101:GLY:HA3	13:P:134:PRO:HG2	1.80	0.63
4:6:344:LYS:HA	4:6:347:TRP:HD1	1.64	0.62
17:v:398:VAL:HA	19:y:846:ARG:HH21	1.63	0.62
17:v:212:THR:OG1	17:v:247:GLN:NE2	2.32	0.62
12:O:129:THR:OG1	12:O:179:ASN:O	2.18	0.61
16:u:368:ILE:HG23	16:u:371:ILE:HG13	1.81	0.61
16:u:331:ILE:CG2	16:u:507:ILE:CG1	2.77	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:u:338:ILE:O	16:u:339:ALA:HB3	2.00	0.61
16:u:372:ASN:HA	16:u:375:VAL:HG22	1.82	0.61
3:5:394:TYR:HB3	3:5:397:LYS:HB2	1.81	0.61
14:Q:38:LYS:HB3	14:Q:71:LEU:HB2	1.82	0.61
4:6:249:LEU:HA	4:6:277:MET:HE1	1.83	0.61
17:v:298:CYS:HA	17:v:301:VAL:HG12	1.82	0.61
7:A:1018:U:H5''	9:I:70:LYS:HZ1	1.65	0.60
9:I:35:GLU:OE2	9:I:36:GLN:NE2	2.34	0.60
15:n:34:PHE:HB2	15:n:40:ARG:HB2	1.83	0.60
19:y:410:ASP:OD1	19:y:485:ARG:NH2	2.35	0.60
14:Q:74:CYS:HB2	14:Q:77:CYS:HB2	1.82	0.60
11:N:41:ARG:NH1	11:N:47:TYR:OH	2.35	0.60
16:u:324:LEU:HD22	16:u:424:LEU:HD22	1.82	0.60
4:6:243:ILE:O	4:6:340:ARG:NH1	2.35	0.60
16:u:468:GLU:HA	16:u:471:ILE:HD12	1.84	0.60
14:Q:5:ARG:HB2	14:Q:8:ASN:HA	1.83	0.59
16:u:233:ARG:NH1	16:u:255:ASP:OD2	2.35	0.59
3:5:183:LEU:HD22	3:5:269:LEU:HD13	1.84	0.59
17:v:320:VAL:HG12	17:v:329:LEU:HD11	1.84	0.59
19:y:788:LEU:HD11	19:y:818:VAL:HG23	1.84	0.59
7:A:1869:A:N6	12:O:114:VAL:O	2.36	0.58
16:u:368:ILE:HG23	16:u:371:ILE:CG1	2.33	0.58
16:u:340:ARG:HD2	19:y:722:GLU:OE1	2.02	0.58
12:O:192:SER:HA	12:O:195:LYS:HG2	1.85	0.58
18:x:42:VAL:HG11	19:y:636:ILE:HB	1.86	0.58
16:u:498:ASN:HA	16:u:518:GLN:HE22	1.68	0.58
16:u:135:GLU:OE2	19:y:465:HIS:ND1	2.36	0.58
16:u:340:ARG:NH1	16:u:348:ILE:HD11	2.19	0.58
16:u:352:GLN:O	16:u:353:ARG:C	2.45	0.58
4:6:327:GLN:O	4:6:330:ARG:NH2	2.37	0.58
18:x:82:LEU:HD21	19:y:665:VAL:HG11	1.86	0.58
11:N:25:LEU:HD13	11:N:48:ILE:HG22	1.86	0.58
19:y:375:LYS:HA	19:y:378:ILE:HD12	1.86	0.58
3:5:352:ARG:NH2	17:v:420:MET:SD	2.76	0.58
4:6:327:GLN:HE21	16:u:450:ILE:HA	1.69	0.58
9:I:46:THR:OG1	9:I:49:GLN:OE1	2.22	0.58
16:u:340:ARG:NE	16:u:348:ILE:HD11	2.19	0.57
17:v:373:ASN:O	17:v:377:ASN:ND2	2.37	0.57
16:u:340:ARG:CZ	16:u:348:ILE:HD11	2.35	0.57
3:5:167:ILE:O	3:5:237:LYS:NZ	2.30	0.57
3:5:216:ARG:NH2	3:5:429:ASP:OD1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:N:38:ILE:HG22	11:N:49:ILE:HA	1.87	0.57
16:u:342:LEU:O	16:u:343:ASP:HB2	2.04	0.57
4:6:312:VAL:HG11	4:6:325:ILE:HG21	1.86	0.57
19:y:673:PHE:HA	19:y:676:HIS:CD2	2.39	0.57
16:u:340:ARG:NH2	16:u:345:ASP:C	2.63	0.57
19:y:452:ASP:OD1	19:y:509:HIS:NE2	2.38	0.57
9:I:75:LEU:HB3	9:I:81:ALA:HB2	1.86	0.56
13:P:95:ILE:HB	13:P:129:ILE:HG13	1.87	0.56
16:u:332:THR:O	16:u:333:PRO:C	2.45	0.56
16:u:345:ASP:C	16:u:347:ILE:H	2.12	0.56
16:u:132:VAL:O	19:y:678:ASN:ND2	2.38	0.56
13:P:121:ARG:HD3	15:n:40:ARG:HH12	1.69	0.56
3:5:544:ILE:HA	3:5:547:ILE:HD12	1.87	0.56
6:8:315:ASP:O	6:8:319:ILE:N	2.37	0.56
17:v:279:LYS:O	17:v:283:GLN:NE2	2.37	0.55
16:u:340:ARG:NE	16:u:348:ILE:CD1	2.69	0.55
2:4:118:GLY:N	2:4:173:TYR:O	2.40	0.55
10:M:105:MET:HE1	11:N:39:TYR:HB3	1.88	0.55
16:u:208:ILE:O	16:u:212:HIS:ND1	2.38	0.55
19:y:573:ILE:HG21	19:y:589:MET:HE2	1.89	0.55
9:I:40:LEU:HD21	9:I:50:ILE:HG23	1.88	0.55
4:6:312:VAL:HG11	4:6:325:ILE:HD13	1.89	0.54
19:y:373:LYS:O	19:y:377:ASN:ND2	2.40	0.54
4:6:325:ILE:HG12	16:u:446:ILE:HG13	1.89	0.54
14:Q:12:LYS:HG3	14:Q:15:ARG:HB2	1.90	0.54
12:O:193:ILE:O	12:O:197:ILE:HG12	2.08	0.54
13:P:96:LYS:HG2	13:P:132:VAL:HG21	1.89	0.54
16:u:462:VAL:HG13	16:u:466:GLN:HG2	1.89	0.54
7:A:1364:U:H5	7:A:1375:G:H21	1.56	0.54
6:8:311:PRO:O	6:8:315:ASP:N	2.38	0.54
19:y:420:VAL:HG13	19:y:440:VAL:HG13	1.90	0.54
2:4:302:ASN:O	2:4:306:ARG:N	2.39	0.54
19:y:476:GLU:OE2	19:y:509:HIS:ND1	2.32	0.54
3:5:59:PHE:HD1	3:5:94:ILE:HD13	1.73	0.53
13:P:94:HIS:ND1	13:P:128:ARG:HB2	2.22	0.53
3:5:457:LEU:HD11	3:5:492:VAL:HG12	1.90	0.53
12:O:125:VAL:O	12:O:136:ARG:HA	2.08	0.53
16:u:331:ILE:HG21	16:u:507:ILE:CG1	2.37	0.53
19:y:758:ASN:HB3	19:y:761:MET:HG2	1.90	0.53
16:u:563:LYS:HA	16:u:567:ARG:HB2	1.89	0.53
3:5:195:GLN:HG2	3:5:421:LEU:HD21	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:6:28:GLU:O	4:6:32:GLU:N	2.40	0.53
16:u:340:ARG:NH2	16:u:347:ILE:HG22	2.24	0.53
4:6:258:ASN:OD1	4:6:259:ASN:N	2.42	0.53
17:v:401:TYR:H	19:y:846:ARG:HH22	1.54	0.53
17:v:255:ARG:NH2	17:v:322:ASP:OD2	2.41	0.53
16:u:340:ARG:CG	19:y:722:GLU:CD	2.80	0.53
16:u:394:LEU:HD12	16:u:403:LEU:HD11	1.91	0.53
7:A:1864:U:OP2	14:Q:5:ARG:NH2	2.42	0.52
12:O:38:MET:SD	12:O:38:MET:N	2.82	0.52
16:u:19:LEU:HD11	16:u:53:LYS:HD2	1.90	0.52
3:5:177:GLU:HA	3:5:265:LEU:HD22	1.90	0.52
16:u:368:ILE:HG22	16:u:368:ILE:O	2.09	0.52
19:y:596:ASP:OD1	19:y:596:ASP:N	2.43	0.52
7:A:1004:U:H2'	7:A:1005:G:H8	1.74	0.52
16:u:281:THR:OG1	16:u:285:LYS:NZ	2.42	0.52
17:v:256:TYR:O	17:v:259:THR:OG1	2.27	0.52
17:v:263:THR:HG21	17:v:328:CYS:HB3	1.91	0.52
4:6:278:ARG:HD3	4:6:311:PHE:HE2	1.75	0.52
5:7:-8:A:H62	14:Q:47:ALA:HB2	1.75	0.52
7:A:1010:G:H2'	7:A:1011:A:H8	1.75	0.52
7:A:928:G:H2'	7:A:929:G:C8	2.45	0.51
12:O:187:LYS:HD3	12:O:193:ILE:HD11	1.92	0.51
16:u:340:ARG:HE	16:u:347:ILE:HG21	1.65	0.51
17:v:197:ASP:HA	17:v:211:ARG:HH21	1.75	0.51
3:5:547:ILE:HA	3:5:550:PHE:CE1	2.44	0.51
19:y:738:VAL:O	19:y:741:SER:OG	2.20	0.51
12:O:38:MET:HB2	12:O:186:ASN:HD21	1.75	0.51
19:y:627:LYS:HA	19:y:693:LEU:HD21	1.93	0.51
16:u:289:ALA:O	16:u:290:LEU:C	2.52	0.51
17:v:261:VAL:HG11	17:v:274:LEU:HD13	1.92	0.51
9:I:36:GLN:HA	9:I:39:LYS:HZ3	1.76	0.51
19:y:745:LYS:HA	19:y:790:THR:HG21	1.93	0.51
16:u:340:ARG:HG2	19:y:722:GLU:HG2	1.93	0.51
13:P:117:ARG:NH2	14:Q:46:GLU:OE2	2.44	0.51
16:u:438:ARG:HD3	16:u:510:HIS:CE1	2.46	0.50
9:I:33:VAL:O	9:I:37:ILE:HD12	2.11	0.50
17:v:282:GLN:NE2	17:v:287:THR:HA	2.26	0.50
16:u:336:THR:O	16:u:338:ILE:N	2.45	0.50
17:v:384:ILE:HG22	17:v:391:VAL:HG13	1.91	0.50
17:v:402:GLN:O	17:v:406:GLU:HG2	2.12	0.50
16:u:374:MET:HE1	16:u:380:LEU:HD22	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:u:523:LEU:HD12	16:u:526:MET:HB2	1.93	0.50
16:u:109:GLN:HA	16:u:112:VAL:HG22	1.92	0.50
16:u:440:LEU:HA	16:u:443:VAL:HG12	1.94	0.50
1:3:43:ASP:O	1:3:47:ASN:N	2.43	0.50
7:A:990:A:OP2	14:Q:37:LYS:NZ	2.44	0.50
16:u:366:THR:C	16:u:368:ILE:N	2.66	0.50
13:P:42:VAL:HG11	13:P:78:ALA:HA	1.93	0.50
16:u:135:GLU:OE1	16:u:140:ARG:NH1	2.45	0.50
8:H:60:SER:OG	8:H:61:THR:N	2.45	0.50
14:Q:90:GLU:N	14:Q:90:GLU:OE2	2.44	0.50
3:5:191:ILE:HD13	3:5:279:ARG:HE	1.77	0.49
17:v:315:CYS:O	17:v:319:LEU:HB2	2.12	0.49
17:v:363:THR:OG1	17:v:365:GLU:OE1	2.27	0.49
2:4:336:MET:HA	3:5:546:GLN:HE21	1.77	0.49
3:5:468:THR:O	3:5:530:ILE:N	2.37	0.49
16:u:336:THR:O	16:u:337:ASP:C	2.56	0.49
19:y:664:LYS:HD2	19:y:667:ARG:HH21	1.76	0.49
12:O:190:PRO:HG2	12:O:192:SER:H	1.77	0.49
16:u:398:PHE:HB3	16:u:511:LEU:HD13	1.94	0.49
16:u:347:ILE:HG23	16:u:348:ILE:N	2.26	0.49
19:y:698:MET:O	19:y:702:GLU:HB2	2.13	0.49
3:5:82:ASP:OD1	3:5:83:VAL:N	2.45	0.49
14:Q:51:ARG:HH22	15:n:39:SER:HB3	1.77	0.49
7:A:941:C:H2'	7:A:942:G:C8	2.48	0.49
12:O:124:HIS:HA	12:O:137:LEU:O	2.13	0.49
16:u:518:GLN:HE21	16:u:522:GLN:HE21	1.59	0.49
3:5:154:PHE:HD1	3:5:221:ILE:HG21	1.78	0.49
3:5:541:ASP:O	3:5:545:ARG:HG2	2.13	0.49
3:5:302:LYS:NZ	3:5:312:GLN:OE1	2.45	0.49
16:u:323:LEU:O	16:u:327:LEU:HG	2.11	0.49
4:6:297:MET:HG3	4:6:301:LEU:HD12	1.95	0.49
16:u:181:ALA:O	16:u:184:PHE:HB3	2.13	0.48
3:5:291:ILE:HG23	3:5:508:ALA:HB3	1.95	0.48
16:u:52:LEU:HD22	16:u:89:VAL:HG23	1.94	0.48
16:u:298:ARG:HA	16:u:301:HIS:CE1	2.49	0.48
19:y:611:ARG:NH2	19:y:675:LEU:O	2.30	0.48
16:u:384:VAL:O	16:u:388:LYS:N	2.44	0.48
16:u:535:GLU:HG3	16:u:538:LYS:HD2	1.95	0.48
17:v:266:ASP:O	17:v:268:ARG:NE	2.44	0.48
16:u:369:GLY:O	16:u:370:LEU:C	2.54	0.48
16:u:384:VAL:HB	16:u:387:VAL:HG22	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:y:697:TYR:C	19:y:701:HIS:HD1	2.21	0.48
19:y:757:ILE:HD11	19:y:776:ARG:HD2	1.95	0.48
16:u:403:LEU:HD23	16:u:439:LEU:HD13	1.96	0.48
18:x:32:PRO:O	19:y:593:HIS:NE2	2.33	0.48
19:y:695:ILE:HD11	19:y:744:MET:HE2	1.93	0.48
13:P:113:GLN:NE2	14:Q:44:ILE:O	2.46	0.48
19:y:702:GLU:OE1	19:y:707:ARG:HA	2.14	0.48
17:v:248:THR:OG1	17:v:249:MET:N	2.46	0.48
3:5:148:PRO:HG2	3:5:153:ARG:HE	1.78	0.47
16:u:327:LEU:HD23	16:u:370:LEU:HD21	1.95	0.47
19:y:628:ASP:OD1	19:y:629:ALA:N	2.47	0.47
7:A:1010:G:H2'	7:A:1011:A:C8	2.49	0.47
9:I:32:ASP:O	9:I:35:GLU:HG3	2.14	0.47
16:u:199:ASP:HA	16:u:202:ARG:HG2	1.96	0.47
17:v:347:ILE:HG23	19:y:826:ILE:HD11	1.96	0.47
3:5:383:ASP:HA	3:5:545:ARG:NH2	2.29	0.47
16:u:321:ARG:NE	16:u:423:GLU:HG3	2.28	0.47
16:u:440:LEU:HD21	16:u:471:ILE:HG12	1.97	0.47
17:v:404:VAL:O	17:v:407:LYS:HG3	2.14	0.47
19:y:342:LYS:O	19:y:345:THR:OG1	2.32	0.47
12:O:78:GLU:OE2	16:u:6:GLN:N	2.44	0.47
16:u:292:HIS:O	16:u:295:THR:OG1	2.28	0.47
12:O:225:LEU:O	12:O:229:MET:N	2.44	0.47
13:P:98:ARG:HH21	13:P:134:PRO:HG3	1.78	0.47
17:v:292:ILE:HG13	17:v:315:CYS:HB2	1.95	0.47
17:v:305:PHE:O	17:v:309:GLN:N	2.47	0.47
3:5:59:PHE:HD2	3:5:128:PHE:HE1	1.62	0.47
12:O:133:TYR:HD1	12:O:221:PRO:HD2	1.80	0.47
16:u:536:VAL:HB	16:u:543:LEU:HD22	1.96	0.47
17:v:161:THR:HA	17:v:165:ALA:HB2	1.97	0.47
19:y:704:ASP:OD2	19:y:856:ALA:HB3	2.15	0.47
9:I:45:LEU:HD23	9:I:49:GLN:HB3	1.96	0.47
14:Q:51:ARG:NH2	15:n:40:ARG:H	2.12	0.47
16:u:312:GLN:HA	16:u:315:MET:HG3	1.96	0.47
19:y:667:ARG:HH22	19:y:668:ARG:NH2	2.12	0.47
16:u:172:ARG:HH21	16:u:176:ASP:HB2	1.80	0.47
3:5:457:LEU:HD13	3:5:493:PHE:HA	1.97	0.47
4:6:325:ILE:HG22	4:6:332:VAL:HG12	1.97	0.47
16:u:340:ARG:O	16:u:342:LEU:N	2.47	0.46
7:A:1101:U:H2'	7:A:1102:G:C8	2.50	0.46
12:O:137:LEU:HG	12:O:215:VAL:HG22	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:v:50:MET:O	17:v:54:ALA:N	2.47	0.46
16:u:171:GLU:HG2	16:u:228:MET:HE1	1.97	0.46
16:u:336:THR:C	16:u:338:ILE:N	2.72	0.46
17:v:315:CYS:HA	17:v:318:VAL:HG12	1.96	0.46
17:v:349:GLN:OE1	17:v:393:MET:N	2.45	0.46
10:M:126:MET:HB2	10:M:128:PHE:HE2	1.80	0.46
17:v:161:THR:HA	17:v:165:ALA:CB	2.46	0.46
9:I:36:GLN:HE21	9:I:39:LYS:HZ1	1.61	0.46
16:u:175:HIS:ND1	16:u:228:MET:HE3	2.30	0.46
18:x:76:ASP:OD1	18:x:77:GLU:N	2.49	0.46
12:O:147:ASN:OD1	12:O:148:ASN:N	2.49	0.46
16:u:334:GLU:HG2	16:u:335:ARG:H	1.81	0.46
3:5:397:LYS:O	3:5:401:MET:HG3	2.16	0.46
16:u:332:THR:HG22	16:u:333:PRO:O	2.15	0.46
19:y:440:VAL:HG12	19:y:443:CYS:H	1.80	0.46
19:y:753:HIS:O	19:y:757:ILE:HG22	2.15	0.46
16:u:340:ARG:NH2	16:u:348:ILE:H	2.14	0.46
16:u:345:ASP:C	16:u:347:ILE:N	2.74	0.46
18:x:41:LYS:HB2	19:y:595:GLN:HG3	1.98	0.46
12:O:219:LYS:HG3	12:O:221:PRO:HD3	1.98	0.46
13:P:94:HIS:ND1	13:P:127:GLY:O	2.40	0.46
14:Q:25:ASN:HB3	14:Q:77:CYS:SG	2.56	0.46
12:O:88:THR:HA	12:O:98:THR:HA	1.97	0.46
13:P:39:ASP:OD1	13:P:40:THR:N	2.48	0.46
16:u:112:VAL:HA	16:u:115:ILE:HD12	1.97	0.46
16:u:367:ARG:O	16:u:368:ILE:HD13	2.16	0.46
19:y:633:LEU:HD11	19:y:682:LEU:HD11	1.98	0.46
12:O:40:ASN:O	12:O:42:ARG:N	2.49	0.45
12:O:97:LEU:HB3	12:O:232:HIS:CE1	2.51	0.45
19:y:468:GLU:O	19:y:472:HIS:ND1	2.48	0.45
15:n:32:VAL:O	15:n:41:SER:HA	2.16	0.45
16:u:293:ALA:HB3	16:u:329:ILE:HD11	1.99	0.45
3:5:136:TYR:CZ	3:5:140:ILE:HD11	2.51	0.45
3:5:240:ILE:HD11	3:5:267:LYS:HA	1.99	0.45
16:u:340:ARG:HG3	19:y:722:GLU:CD	2.24	0.45
16:u:347:ILE:CG2	16:u:348:ILE:N	2.79	0.45
19:y:448:VAL:HG11	19:y:486:VAL:HG21	1.97	0.45
7:A:1013:U:OP1	7:A:1129:G:O2'	2.35	0.45
12:O:104:ASP:OD1	12:O:105:LEU:N	2.50	0.45
16:u:331:ILE:HG22	16:u:507:ILE:CD1	2.45	0.45
16:u:332:THR:HA	16:u:478:CYS:SG	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:u:198:CYS:HG	16:u:202:ARG:HH21	1.61	0.45
19:y:551:LEU:O	19:y:555:ILE:HG12	2.17	0.45
17:v:401:TYR:HB3	19:y:846:ARG:HH22	1.82	0.45
4:6:352:ASP:OD1	4:6:353:THR:N	2.50	0.45
12:O:40:ASN:HB2	12:O:41:ILE:HD12	1.99	0.45
17:v:401:TYR:H	19:y:846:ARG:NH2	2.15	0.45
19:y:504:LEU:HD12	19:y:507:ILE:HD11	1.98	0.45
19:y:762:ASN:OD1	19:y:776:ARG:NH1	2.49	0.45
19:y:780:VAL:HA	19:y:783:ILE:HG12	1.98	0.45
3:5:545:ARG:O	3:5:549:LYS:HD2	2.16	0.45
19:y:555:ILE:HG23	19:y:564:ILE:HG22	1.97	0.45
19:y:635:ASP:OD1	19:y:636:ILE:N	2.50	0.45
19:y:801:SER:HB2	19:y:842:VAL:HG12	1.99	0.45
15:n:36:ASP:OD1	15:n:37:ASP:N	2.49	0.45
17:v:298:CYS:SG	17:v:299:LEU:N	2.90	0.45
3:5:328:ARG:NH2	3:5:509:LEU:O	2.49	0.45
16:u:492:SER:OG	16:u:493:PHE:N	2.50	0.45
16:u:336:THR:CB	16:u:340:ARG:HH11	2.28	0.44
17:v:51:VAL:O	17:v:54:ALA:HB3	2.16	0.44
19:y:686:TYR:HH	19:y:711:SER:HG	1.59	0.44
3:5:111:PRO:HA	3:5:139:HIS:CD2	2.52	0.44
16:u:246:TRP:NE1	19:y:731:GLU:OE2	2.50	0.44
19:y:801:SER:HA	19:y:842:VAL:HA	1.99	0.44
19:y:846:ARG:HD2	19:y:846:ARG:O	2.17	0.44
1:3:145:VAL:O	3:5:498:LYS:NZ	2.50	0.44
8:H:55:LEU:HD11	19:y:340:ARG:HH22	1.81	0.44
13:P:34:PHE:HD1	13:P:98:ARG:HG3	1.82	0.44
15:n:31:ARG:NH2	15:n:41:SER:O	2.50	0.44
16:u:340:ARG:HH21	16:u:347:ILE:HG22	1.82	0.44
16:u:463:ASP:H	16:u:466:GLN:NE2	2.15	0.44
3:5:364:ASN:O	3:5:368:HIS:ND1	2.50	0.44
16:u:340:ARG:HH12	16:u:348:ILE:HG13	1.75	0.44
3:5:56:ILE:HG23	3:5:128:PHE:HZ	1.82	0.44
12:O:39:PHE:CD1	12:O:74:LEU:HD23	2.52	0.44
12:O:144:LYS:HE2	12:O:208:HIS:HB3	1.99	0.44
17:v:295:PHE:CD1	17:v:311:LYS:HE3	2.53	0.44
19:y:788:LEU:HD23	19:y:792:LEU:HD23	1.99	0.44
2:4:308:LEU:HA	16:u:535:GLU:OE1	2.18	0.44
19:y:744:MET:HB2	19:y:752:CYS:SG	2.58	0.44
7:A:1004:U:H2'	7:A:1005:G:C8	2.50	0.44
12:O:160:GLN:O	12:O:164:ILE:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:P:27:VAL:N	13:P:91:THR:OG1	2.51	0.44
16:u:333:PRO:HD3	16:u:478:CYS:SG	2.57	0.44
14:Q:51:ARG:HH22	15:n:40:ARG:H	1.66	0.44
16:u:336:THR:OG1	16:u:337:ASP:N	2.51	0.44
16:u:228:MET:HA	16:u:231:GLU:HG3	1.99	0.44
16:u:336:THR:O	16:u:340:ARG:HB2	2.18	0.44
19:y:358:VAL:HG21	19:y:378:ILE:HD11	2.00	0.44
6:8:225:ALA:O	6:8:229:GLU:N	2.49	0.43
7:A:1103:C:H2'	7:A:1104:G:C8	2.53	0.43
17:v:254:LEU:O	17:v:257:LEU:HB2	2.17	0.43
4:6:125:CYS:O	4:6:129:LYS:N	2.48	0.43
19:y:691:MET:O	19:y:695:ILE:HG12	2.18	0.43
4:6:287:VAL:HG23	4:6:288:GLU:OE1	2.18	0.43
9:I:90:HIS:HA	9:I:93:LYS:HZ3	1.82	0.43
11:N:44:ASP:OD1	11:N:46:ILE:HG12	2.17	0.43
13:P:95:ILE:HD12	13:P:126:ILE:HD11	2.00	0.43
16:u:347:ILE:O	16:u:348:ILE:C	2.55	0.43
16:u:519:ILE:O	16:u:523:LEU:HB3	2.19	0.43
19:y:616:LEU:HA	19:y:616:LEU:HD23	1.81	0.43
7:A:936:G:C2'	7:A:937:C:H5'	2.48	0.43
7:A:930:C:H2'	7:A:931:C:C6	2.53	0.43
14:Q:52:ASP:OD1	14:Q:52:ASP:N	2.40	0.43
14:Q:100:ARG:HG3	14:Q:100:ARG:HH11	1.84	0.43
4:6:252:TYR:HH	4:6:270:HIS:HD1	1.54	0.43
16:u:430:GLN:O	16:u:431:LEU:C	2.61	0.43
19:y:548:MET:HE1	19:y:575:HIS:HB3	2.01	0.43
8:H:14:GLU:OE1	8:H:14:GLU:N	2.46	0.43
15:n:51:ARG:N	15:n:54:ASP:OD2	2.49	0.43
16:u:338:ILE:CD1	19:y:746:MET:HE1	2.48	0.43
16:u:564:GLU:HG2	16:u:572:ARG:NH2	2.34	0.43
17:v:366:GLU:HA	17:v:369:ARG:HB3	2.01	0.43
3:5:542:PHE:O	3:5:546:GLN:HG2	2.19	0.43
16:u:87:GLU:HG2	16:u:170:VAL:HG23	2.01	0.43
16:u:323:LEU:O	16:u:326:THR:HG22	2.19	0.43
16:u:366:THR:HG23	16:u:368:ILE:H	1.84	0.43
3:5:327:ARG:HH12	3:5:496:LYS:HZ3	1.67	0.43
3:5:402:GLN:OE1	17:v:379:ARG:NH1	2.40	0.43
4:6:342:PHE:HB2	4:6:346:GLN:HG3	2.01	0.43
7:A:1105:G:O3'	8:H:69:GLY:HA3	2.18	0.43
8:H:33:MET:HE1	8:H:48:SER:HA	2.01	0.43
13:P:34:PHE:HB3	13:P:41:PHE:HB2	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:u:316:GLN:O	16:u:320:THR:HG23	2.18	0.43
17:v:221:VAL:HB	17:v:324:PHE:HE1	1.84	0.43
17:v:294:GLU:HA	17:v:297:GLU:HG3	2.01	0.43
3:5:327:ARG:NH2	3:5:496:LYS:HG2	2.33	0.43
12:O:121:ILE:O	12:O:140:VAL:HA	2.18	0.43
13:P:121:ARG:HD3	15:n:40:ARG:NH1	2.34	0.43
16:u:338:ILE:O	16:u:339:ALA:CB	2.67	0.43
16:u:351:LYS:O	16:u:355:LEU:HG	2.18	0.43
16:u:431:LEU:HD13	16:u:431:LEU:HA	1.70	0.42
5:7:-21:A:N6	16:u:192:ALA:HB1	2.33	0.42
12:O:165:ARG:O	12:O:169:MET:HG2	2.18	0.42
16:u:293:ALA:CB	16:u:329:ILE:HD11	2.49	0.42
16:u:526:MET:HA	16:u:529:VAL:HG12	2.00	0.42
19:y:375:LYS:HB3	19:y:408:LEU:HD13	2.00	0.42
7:A:991:G:C6	7:A:1134:G:H4'	2.53	0.42
12:O:117:TRP:HB3	12:O:153:THR:HA	2.00	0.42
16:u:96:MET:HA	16:u:99:GLU:HG2	2.00	0.42
16:u:451:GLU:HA	16:u:490:THR:HA	2.00	0.42
14:Q:52:ASP:HA	14:Q:55:GLU:HG3	2.00	0.42
16:u:340:ARG:HH21	16:u:345:ASP:C	2.24	0.42
19:y:670:GLN:H	19:y:670:GLN:HG2	1.61	0.42
19:y:823:SER:O	19:y:827:ILE:HG12	2.19	0.42
3:5:228:LEU:O	3:5:232:HIS:ND1	2.53	0.42
7:A:933:G:H21	7:A:1000:C:H3'	1.84	0.42
9:I:57:SER:OG	9:I:58:HIS:N	2.52	0.42
16:u:485:ASP:OD1	19:y:801:SER:OG	2.37	0.42
3:5:143:LYS:HA	3:5:143:LYS:HD2	1.90	0.42
12:O:189:ILE:O	16:u:14[B]:ARG:NH2	2.53	0.42
16:u:489:ARG:HH12	19:y:806:THR:HG21	1.83	0.42
3:5:475:LEU:HD23	3:5:478:PHE:HD2	1.85	0.42
4:6:283:MET:HE1	4:6:338:THR:H	1.85	0.42
12:O:103:MET:HE3	12:O:215:VAL:HG23	2.00	0.42
16:u:316:GLN:O	16:u:319:SER:OG	2.28	0.42
16:u:320:THR:HG22	16:u:383:VAL:HB	2.02	0.42
16:u:431:LEU:O	16:u:432:GLN:C	2.63	0.42
19:y:799:TYR:CE1	19:y:802:ILE:HD13	2.55	0.42
3:5:163:LEU:HD12	3:5:163:LEU:HA	1.93	0.42
3:5:375:LEU:HD12	3:5:379:PRO:HA	2.02	0.42
7:A:1211:G:H2'	7:A:1212:G:C8	2.54	0.42
16:u:389:ASP:O	16:u:393:TRP:CB	2.68	0.42
17:v:331:ASP:OD1	17:v:331:ASP:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:y:326:HIS:HB2	19:y:366:LEU:HD13	2.02	0.42
16:u:315:MET:HA	16:u:318:MET:HG3	2.02	0.41
16:u:328:SER:O	16:u:329:ILE:C	2.60	0.41
3:5:340:LEU:HG	3:5:367:MET:HE1	2.02	0.41
3:5:368:HIS:HD2	3:5:390:LEU:HD21	1.84	0.41
3:5:551:GLU:HB3	3:5:555:ARG:NH1	2.36	0.41
14:Q:44:ILE:HD13	14:Q:67:LEU:HB2	2.01	0.41
17:v:291:PRO:HA	17:v:294:GLU:OE2	2.20	0.41
4:6:189:LEU:O	4:6:193:THR:N	2.53	0.41
16:u:43:TRP:O	16:u:47:HIS:ND1	2.53	0.41
16:u:389:ASP:O	16:u:393:TRP:HB3	2.19	0.41
19:y:604:PRO:O	19:y:607:ILE:HG12	2.19	0.41
19:y:684:CYS:SG	19:y:765:VAL:HG21	2.60	0.41
3:5:401:MET:HE2	3:5:409:TYR:CZ	2.56	0.41
4:6:141:PRO:O	4:6:145:ASP:N	2.47	0.41
16:u:171:GLU:HA	16:u:174:TYR:HB3	2.02	0.41
4:6:342:PHE:HD2	4:6:346:GLN:HB2	1.85	0.41
6:8:213:VAL:HA	16:u:565:HIS:ND1	2.36	0.41
12:O:107:ARG:NH1	13:P:133:THR:O	2.39	0.41
12:O:189:ILE:HG13	12:O:190:PRO:HD3	2.02	0.41
17:v:348:HIS:ND1	19:y:836:ASP:HB2	2.35	0.41
19:y:464:PRO:HG2	19:y:465:HIS:CD2	2.56	0.41
4:6:278:ARG:HB3	4:6:311:PHE:CE2	2.56	0.41
4:6:325:ILE:HG13	16:u:447:TYR:CD1	2.56	0.41
8:H:34:ASP:OD1	8:H:80:ARG:HB2	2.21	0.41
16:u:205:LEU:O	16:u:208:ILE:HG22	2.20	0.41
17:v:252:HIS:HB2	17:v:286:TYR:CZ	2.55	0.41
9:I:47:PRO:HB3	9:I:71:ILE:HD11	2.03	0.41
15:n:22:GLY:HA2	15:n:67:ARG:HH12	1.86	0.41
16:u:266:PRO:HA	16:u:267:PRO:HD3	1.92	0.41
1:3:37:ALA:HA	1:3:41:ALA:HB3	2.02	0.41
8:H:80:ARG:HD3	18:x:77:GLU:O	2.21	0.41
9:I:39:LYS:HA	9:I:42:LYS:HD2	2.03	0.41
16:u:369:GLY:O	16:u:371:ILE:N	2.54	0.41
17:v:255:ARG:HB2	17:v:286:TYR:OH	2.21	0.41
4:6:287:VAL:HG11	4:6:339:HIS:HA	2.02	0.41
7:A:1107:G:OP1	8:H:70:LYS:NZ	2.43	0.41
8:H:65:GLN:NE2	19:y:341:GLY:O	2.54	0.41
13:P:66:ARG:N	13:P:68:GLU:OE1	2.54	0.41
16:u:19:LEU:HD21	16:u:57:LEU:HD11	2.02	0.41
19:y:499:VAL:HA	19:y:502:ILE:HG22	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:y:700:ALA:HB2	19:y:793:PHE:CG	2.56	0.41
8:H:34:ASP:HA	8:H:45:THR:HA	2.03	0.40
9:I:31:ASP:OD1	9:I:32:ASP:N	2.54	0.40
16:u:517:GLU:OE1	16:u:517:GLU:N	2.53	0.40
19:y:445:LEU:HA	19:y:448:VAL:HG22	2.03	0.40
19:y:830:GLU:OE2	19:y:832:MET:HB2	2.21	0.40
7:A:931:C:H2'	7:A:932:G:C8	2.57	0.40
16:u:359:LEU:O	16:u:361:LEU:N	2.52	0.40
3:5:191:ILE:HG21	3:5:279:ARG:HE	1.86	0.40
16:u:249:ALA:O	16:u:253:VAL:HG23	2.22	0.40
16:u:274:ASN:O	16:u:278:LYS:HG2	2.21	0.40
16:u:296:LEU:HD11	16:u:321:ARG:HH11	1.86	0.40
3:5:171:ASP:OD1	3:5:171:ASP:N	2.55	0.40
5:7:-21:A:H62	16:u:192:ALA:HB1	1.85	0.40
16:u:142:ASP:O	16:u:146:LEU:N	2.55	0.40
18:x:50:TYR:HD1	18:x:53:LYS:HG3	1.87	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	3	209/218 (96%)	202 (97%)	7 (3%)	0	100	100
2	4	251/357 (70%)	235 (94%)	16 (6%)	0	100	100
3	5	518/564 (92%)	501 (97%)	17 (3%)	0	100	100
4	6	360/374 (96%)	339 (94%)	21 (6%)	0	100	100
6	8	313/352 (89%)	289 (92%)	24 (8%)	0	100	100
8	H	69/84 (82%)	67 (97%)	2 (3%)	0	100	100
9	I	93/151 (62%)	87 (94%)	6 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
10	M	28/135 (21%)	27 (96%)	1 (4%)	0	100	100
11	N	30/295 (10%)	28 (93%)	2 (7%)	0	100	100
12	O	172/264 (65%)	163 (95%)	9 (5%)	0	100	100
13	P	82/151 (54%)	77 (94%)	5 (6%)	0	100	100
14	Q	94/115 (82%)	89 (95%)	5 (5%)	0	100	100
15	n	56/69 (81%)	51 (91%)	5 (9%)	0	100	100
16	u	602/1382 (44%)	552 (92%)	49 (8%)	1 (0%)	43	71
17	v	403/445 (91%)	367 (91%)	36 (9%)	0	100	100
18	x	59/548 (11%)	52 (88%)	7 (12%)	0	100	100
19	y	539/913 (59%)	513 (95%)	26 (5%)	0	100	100
All	All	3878/6417 (60%)	3639 (94%)	238 (6%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	u	337	ASP

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	
3	5	477/515 (93%)	477 (100%)	0	100	100
4	6	112/335 (33%)	112 (100%)	0	100	100
6	8	1/310 (0%)	1 (100%)	0	100	100
8	H	64/76 (84%)	64 (100%)	0	100	100
9	I	83/131 (63%)	83 (100%)	0	100	100
10	M	31/122 (25%)	31 (100%)	0	100	100
11	N	26/243 (11%)	26 (100%)	0	100	100
12	O	164/231 (71%)	164 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	P	69/119 (58%)	69 (100%)	0	100	100
14	Q	83/98 (85%)	83 (100%)	0	100	100
15	n	51/62 (82%)	51 (100%)	0	100	100
16	u	528/1259 (42%)	526 (100%)	2 (0%)	84	83
17	v	206/406 (51%)	206 (100%)	0	100	100
18	x	55/494 (11%)	55 (100%)	0	100	100
19	y	472/811 (58%)	472 (100%)	0	100	100
All	All	2422/5212 (46%)	2420 (100%)	2 (0%)	87	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
16	u	349	VAL
16	u	431	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
3	5	60	HIS
3	5	225	HIS
3	5	263	HIS
3	5	427	ASN
3	5	453	GLN
8	H	19	HIS
8	H	65	GLN
9	I	36	GLN
9	I	62	GLN
12	O	95	ASN
12	O	124	HIS
12	O	179	ASN
14	Q	8	ASN
16	u	179	GLN
16	u	430	GLN
16	u	442	GLN
16	u	522	GLN
17	v	239	GLN
17	v	247	GLN
17	v	282	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
17	v	377	ASN
17	v	396	ASN
17	v	416	GLN
18	x	51	GLN
18	x	68	GLN
19	y	334	ASN
19	y	520	GLN
19	y	575	HIS
19	y	597	ASN
19	y	631	ASN
19	y	648	GLN
19	y	659	ASN
19	y	662	GLN
19	y	676	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	7	30/255 (11%)	17 (56%)	2 (6%)
7	A	109/1869 (5%)	34 (31%)	1 (0%)
All	All	139/2124 (6%)	51 (36%)	3 (2%)

All (51) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	7	-33	A
5	7	-30	A
5	7	-28	C
5	7	-27	A
5	7	-26	A
5	7	-23	A
5	7	-22	C
5	7	-21	A
5	7	-20	A
5	7	-17	A
5	7	-16	U
5	7	-13	A
5	7	-12	A
5	7	-11	A
5	7	-9	C
5	7	-8	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
5	7	-5	C
7	A	928	G
7	A	931	C
7	A	933	G
7	A	934	G
7	A	935	G
7	A	937	C
7	A	941	C
7	A	942	G
7	A	986	G
7	A	990	A
7	A	991	G
7	A	992	A
7	A	1001	A
7	A	1017	U
7	A	1108	G
7	A	1109	C
7	A	1122	A
7	A	1126	G
7	A	1128	C
7	A	1133	A
7	A	1210	G
7	A	1377	U
7	A	1459	G
7	A	1463	U
7	A	1464	C
7	A	1466	G
7	A	1467	C
7	A	1681	U
7	A	1682	C
7	A	1683	C
7	A	1692	U
7	A	1864	U
7	A	1865	C
7	A	1868	U

All (3) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	7	-21	A
5	7	-10	A
7	A	1682	C

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](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.

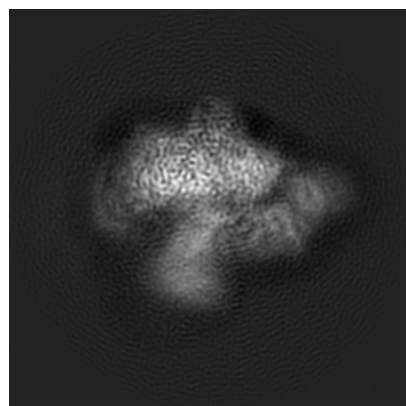
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19128. These allow visual inspection of the internal detail of the map and identification of artifacts.

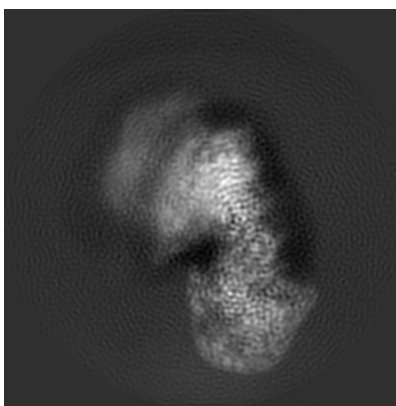
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

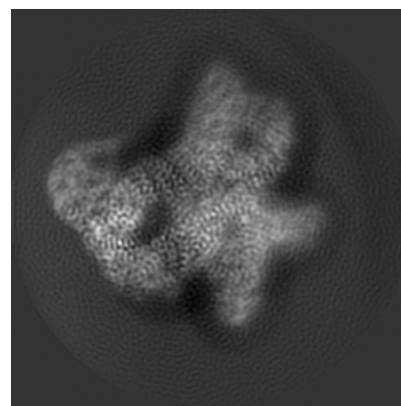
6.1.1 Primary map



X

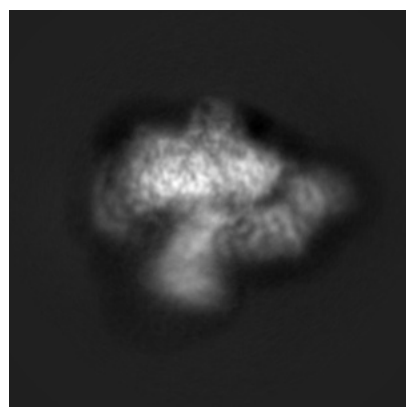


Y

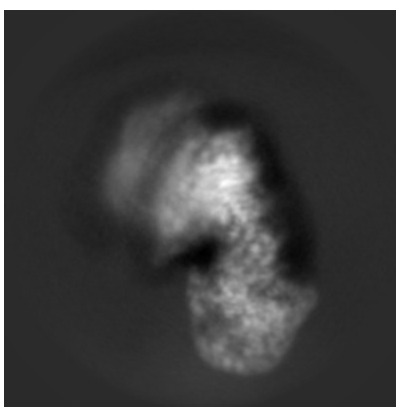


Z

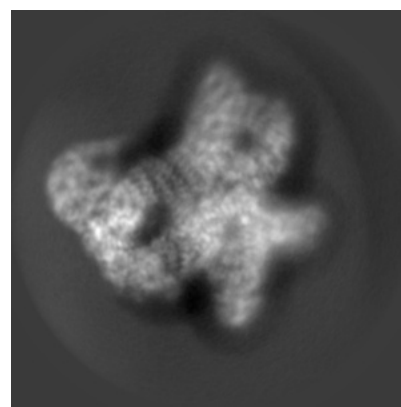
6.1.2 Raw map



X



Y

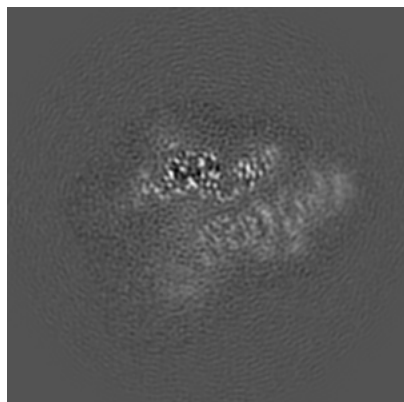


Z

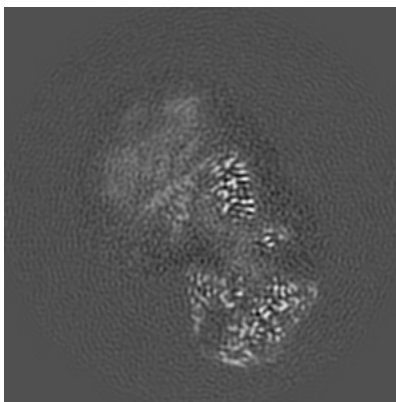
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

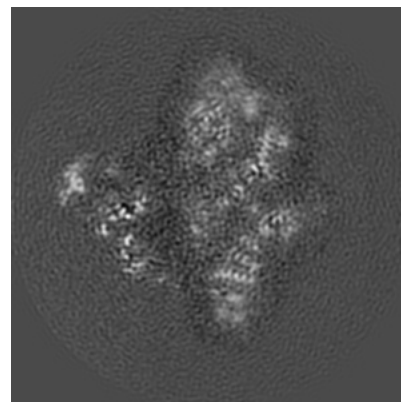
6.2.1 Primary map



X Index: 120

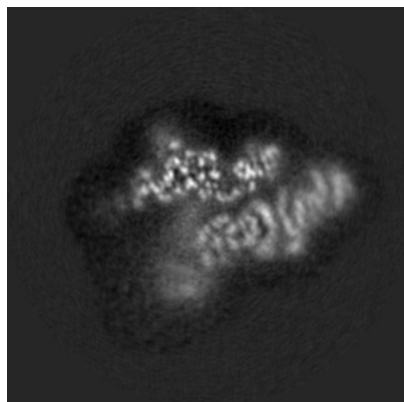


Y Index: 120

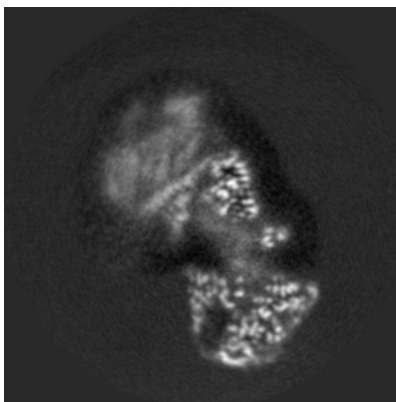


Z Index: 120

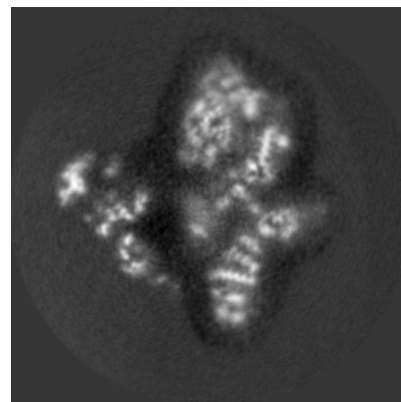
6.2.2 Raw map



X Index: 120



Y Index: 120

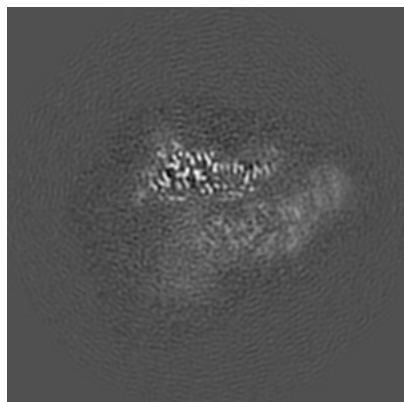


Z Index: 120

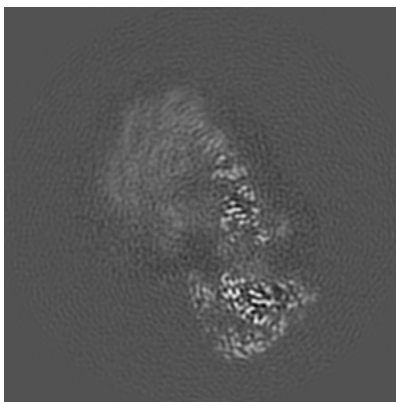
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

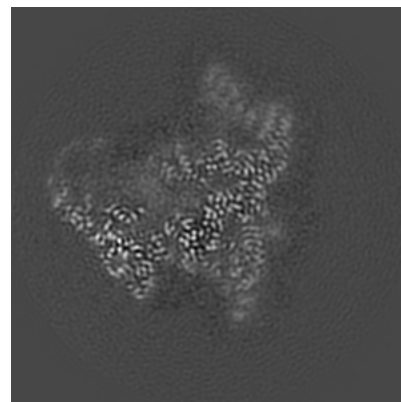
6.3.1 Primary map



X Index: 118

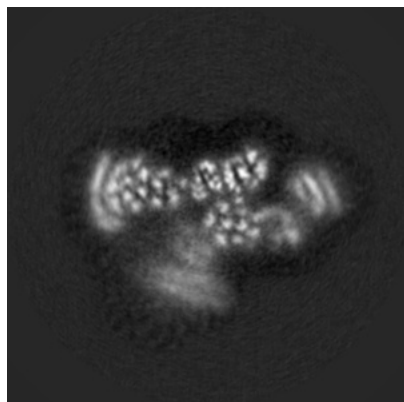


Y Index: 114

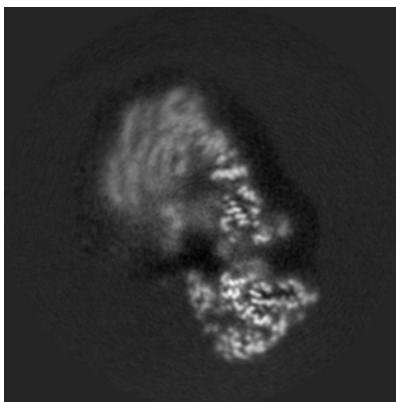


Z Index: 137

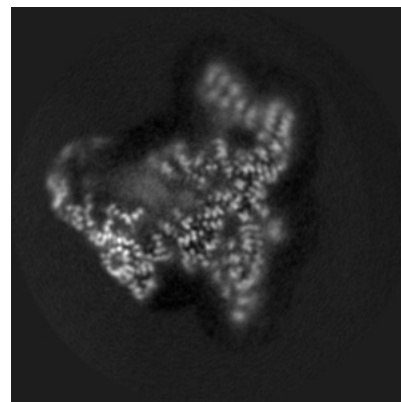
6.3.2 Raw map



X Index: 137



Y Index: 114

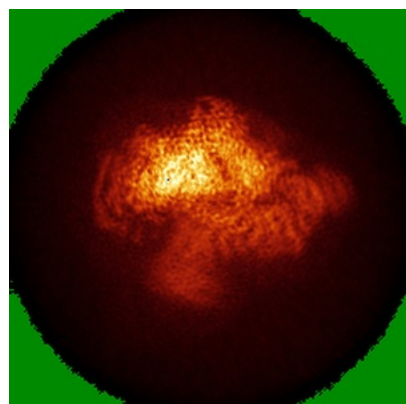


Z Index: 136

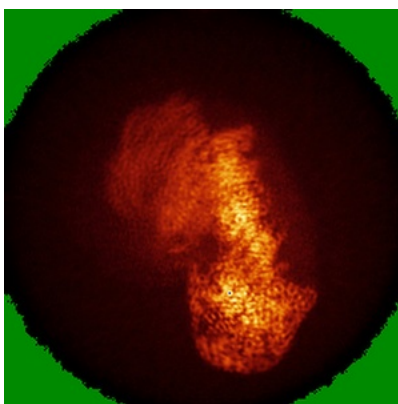
The images above show the largest variance slices of the map in three orthogonal directions.

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

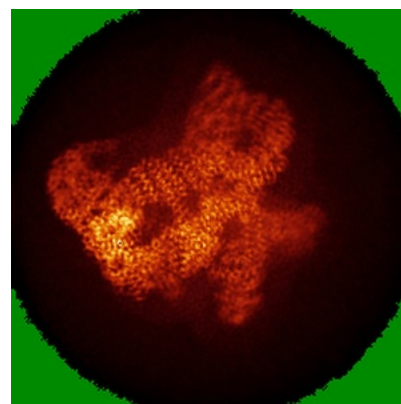
6.4.1 Primary map



X

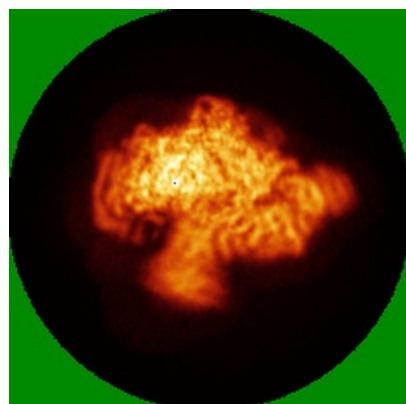


Y

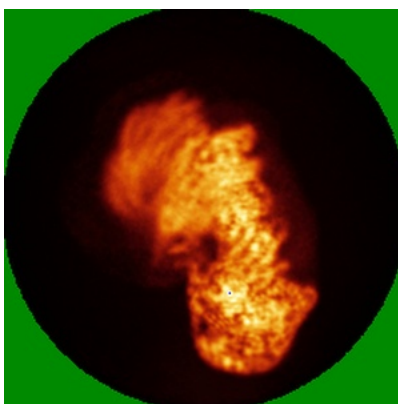


Z

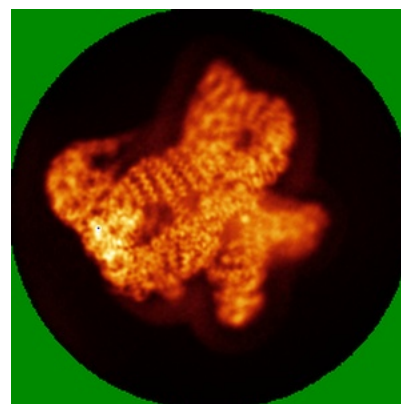
6.4.2 Raw map



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.

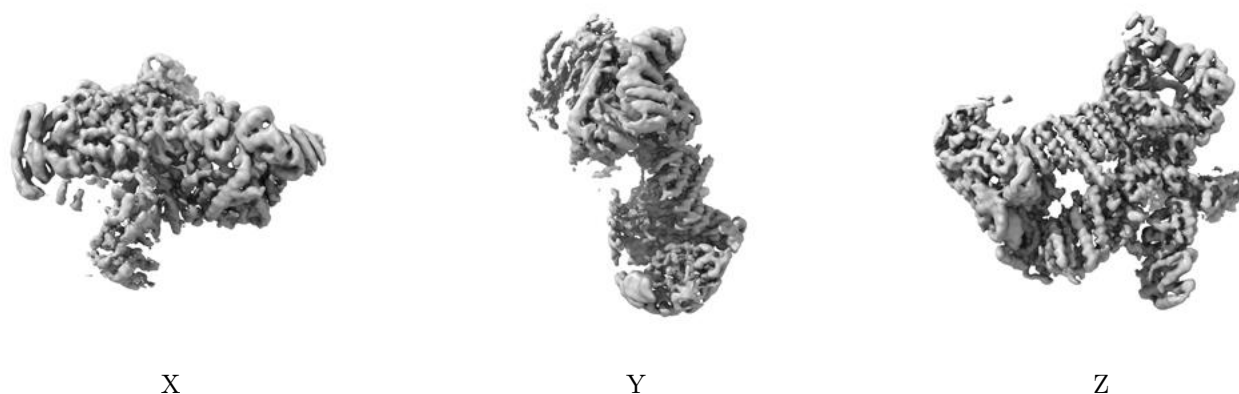
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 4.0. 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.

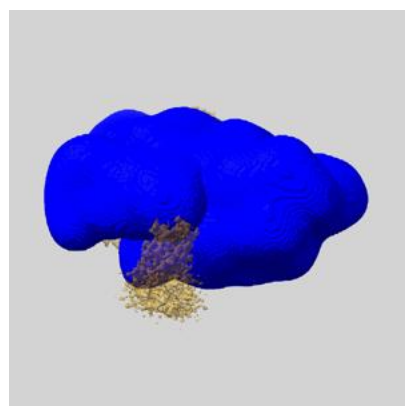
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

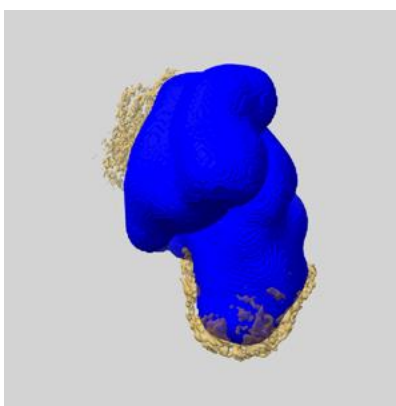
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

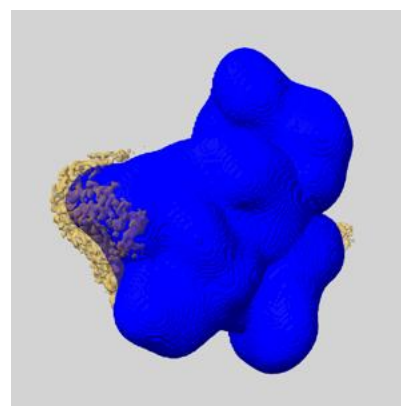
6.6.1 emd_19128_msk_1.map [i](#)



X



Y

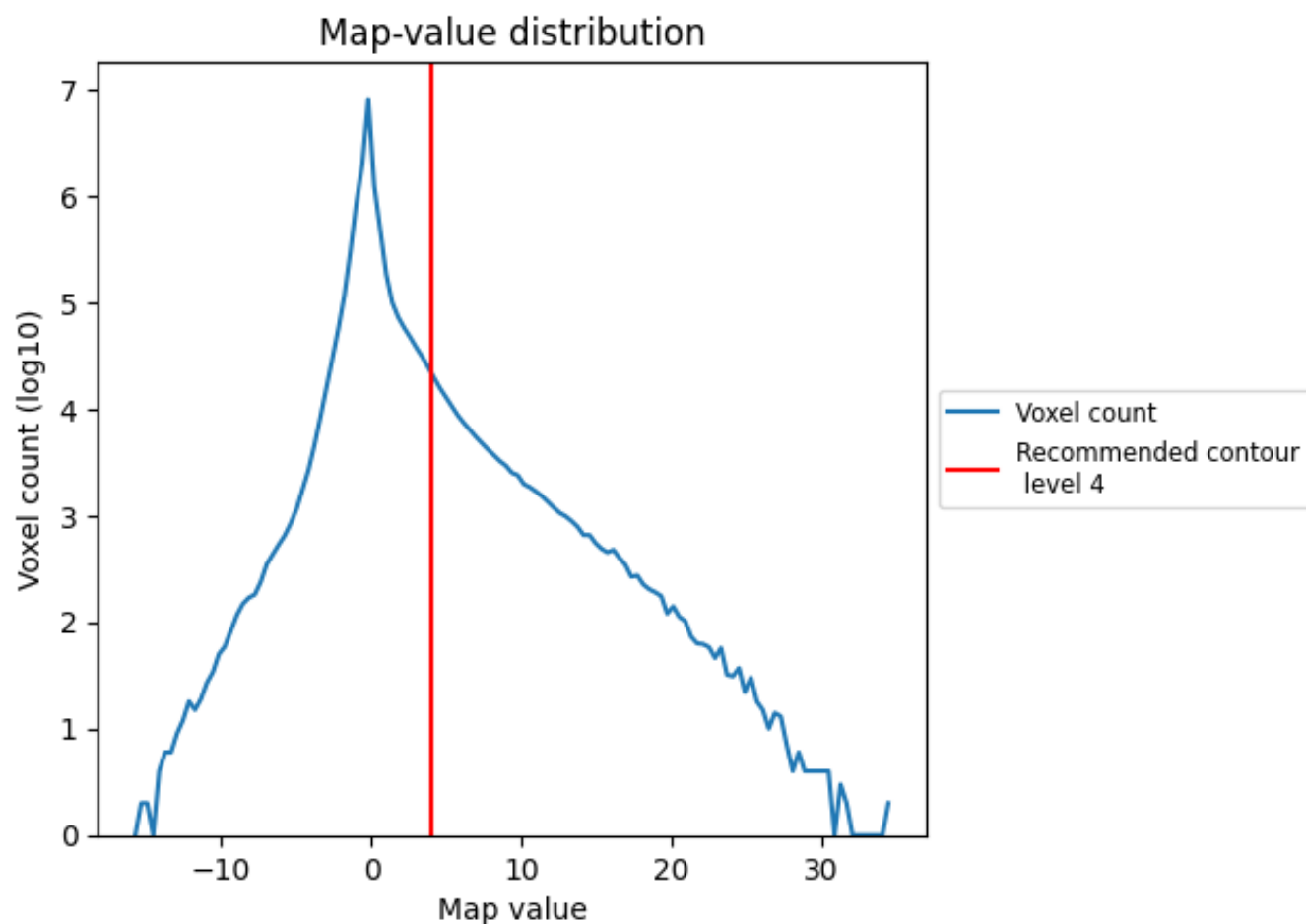


Z

7 Map analysis [i](#)

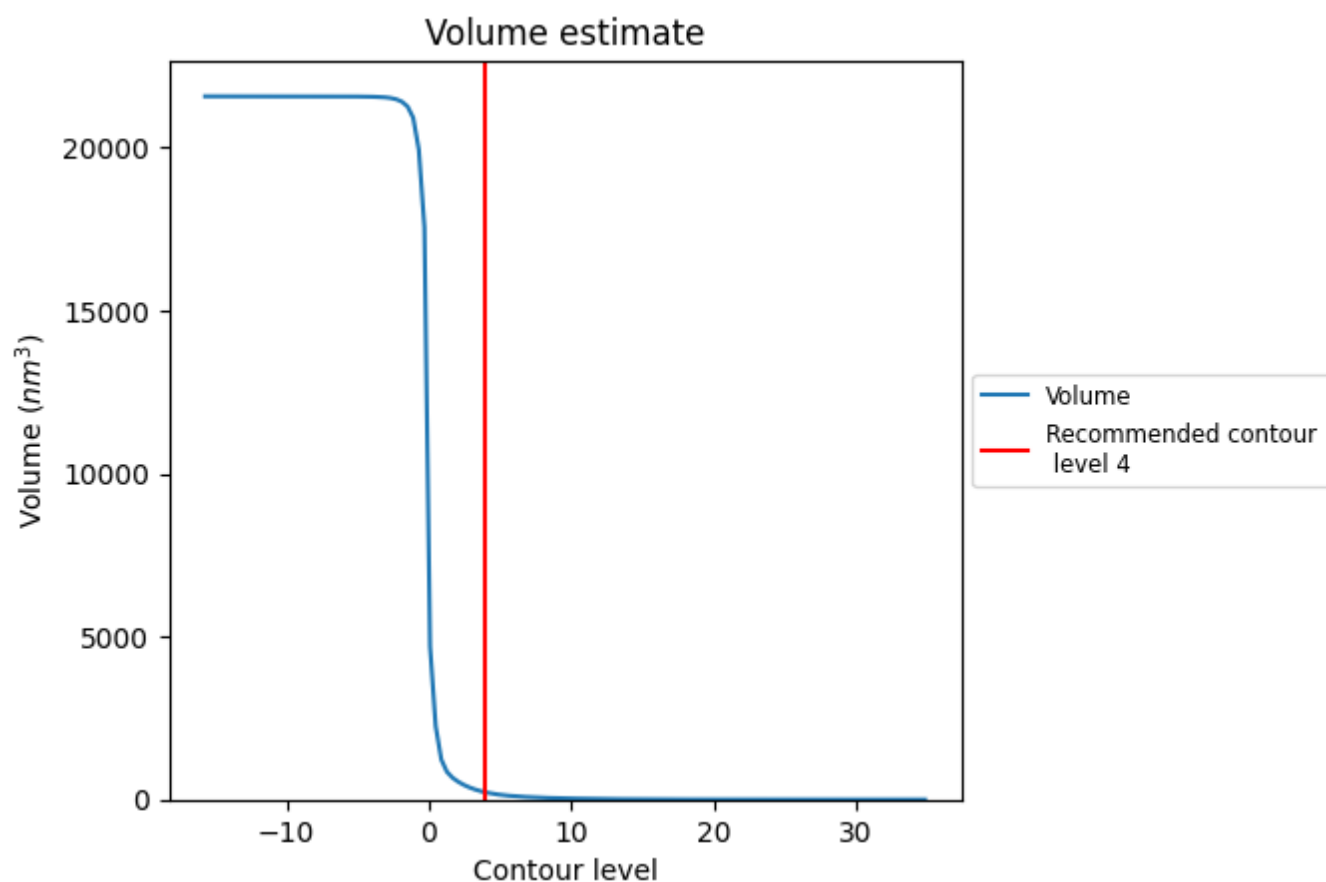
This section contains the results of statistical analysis of the map.

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.

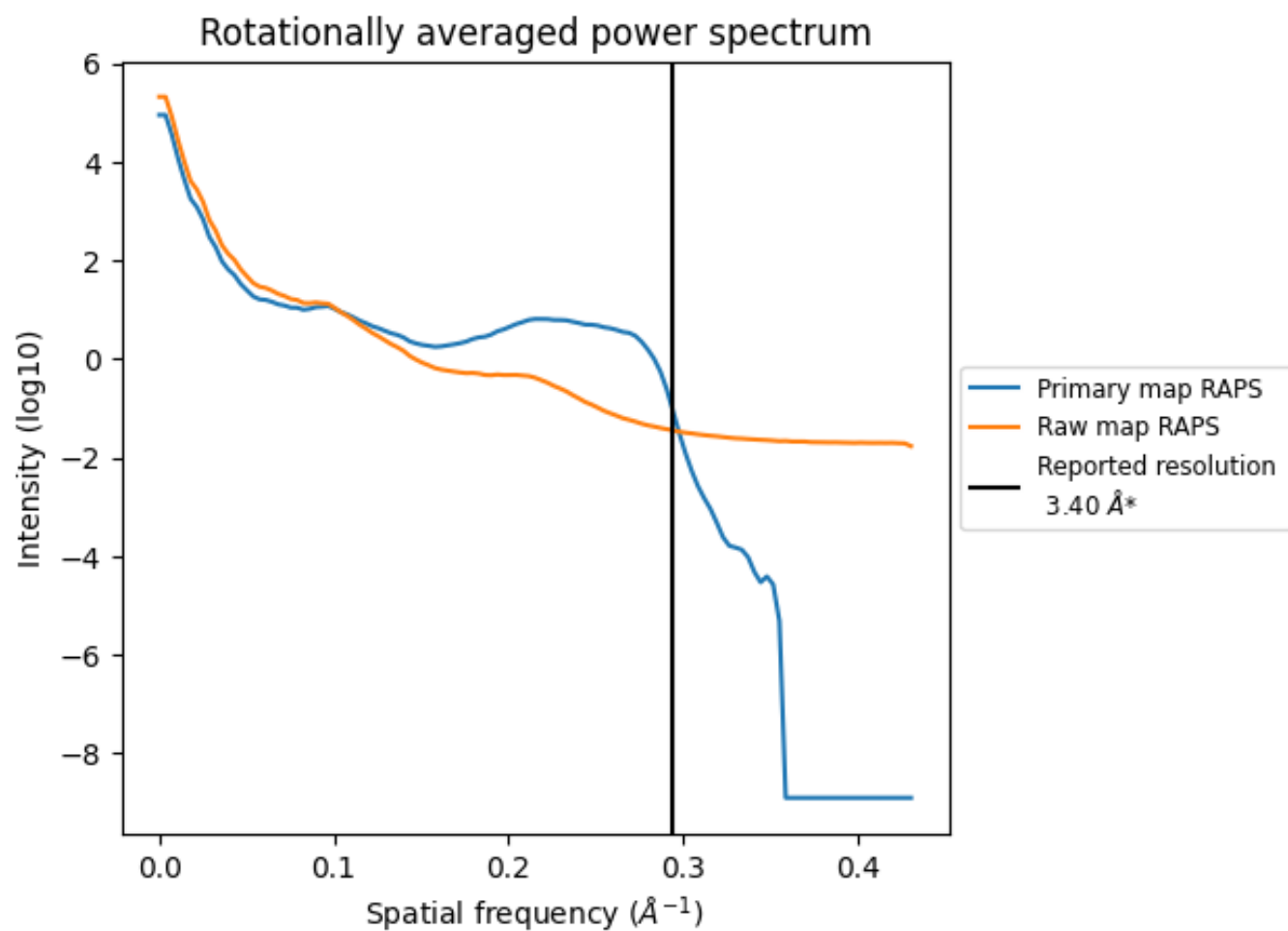
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 219 nm³; this corresponds to an approximate mass of 198 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 ⓘ

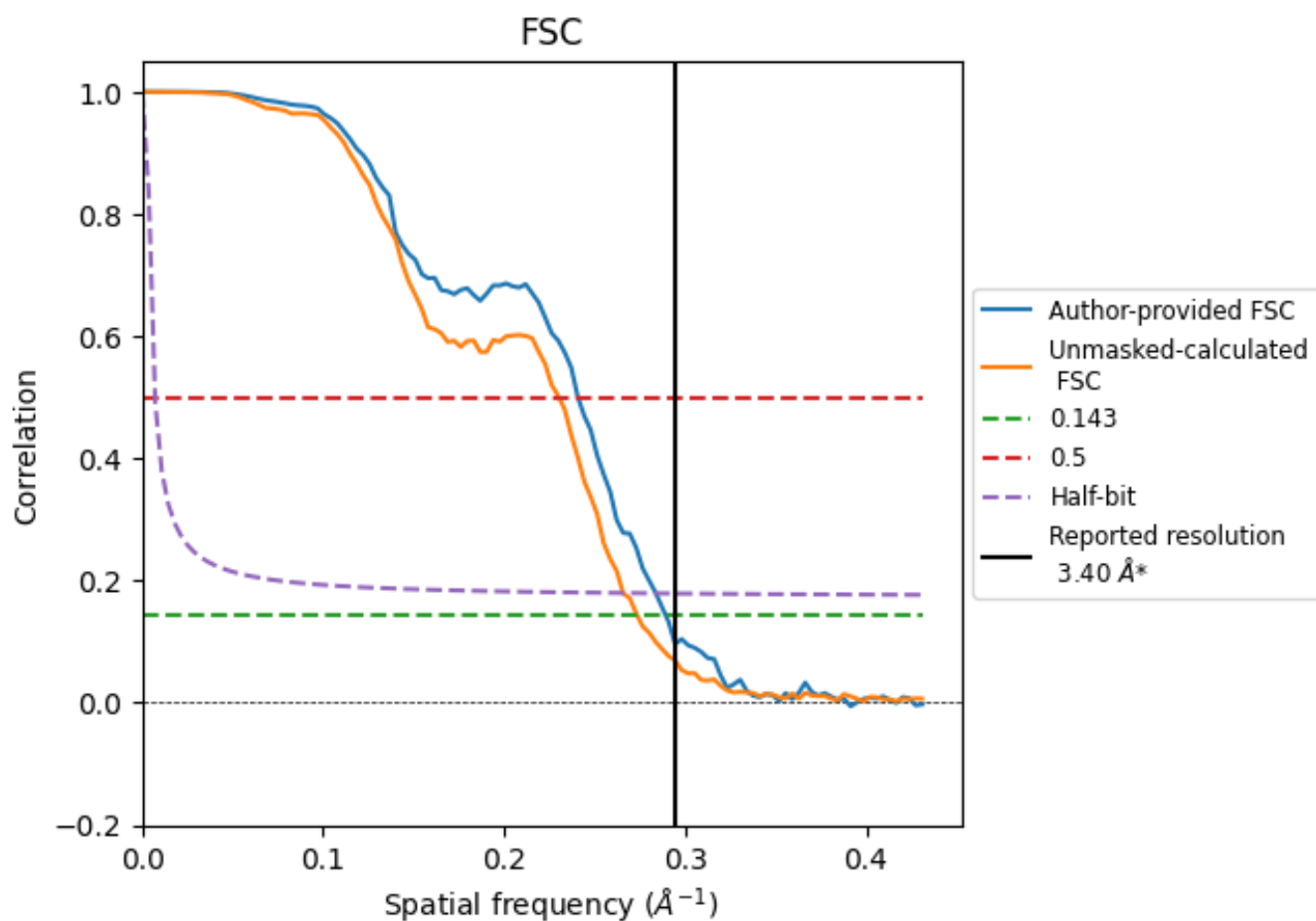


*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

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 $0.294 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

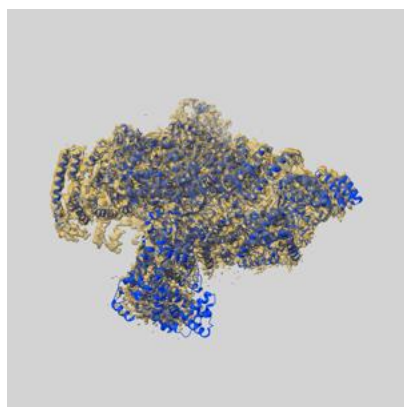
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.46	4.15	3.52
Unmasked-calculated*	3.66	4.34	3.76

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

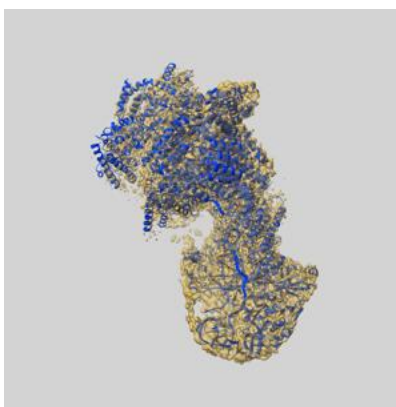
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19128 and PDB model 8RG0. Per-residue inclusion information can be found in section [3](#) on page [8](#).

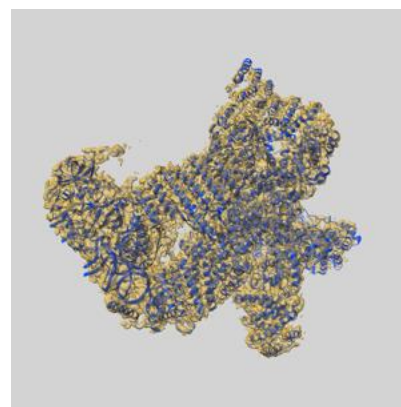
9.1 Map-model overlay [i](#)



X



Y



Z

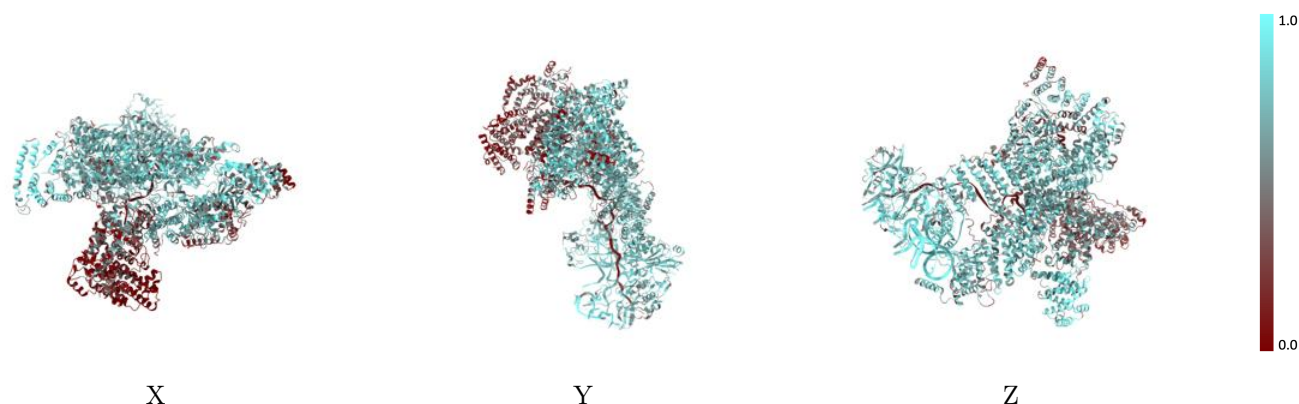
The images above show the 3D surface view of the map at the recommended contour level 4.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



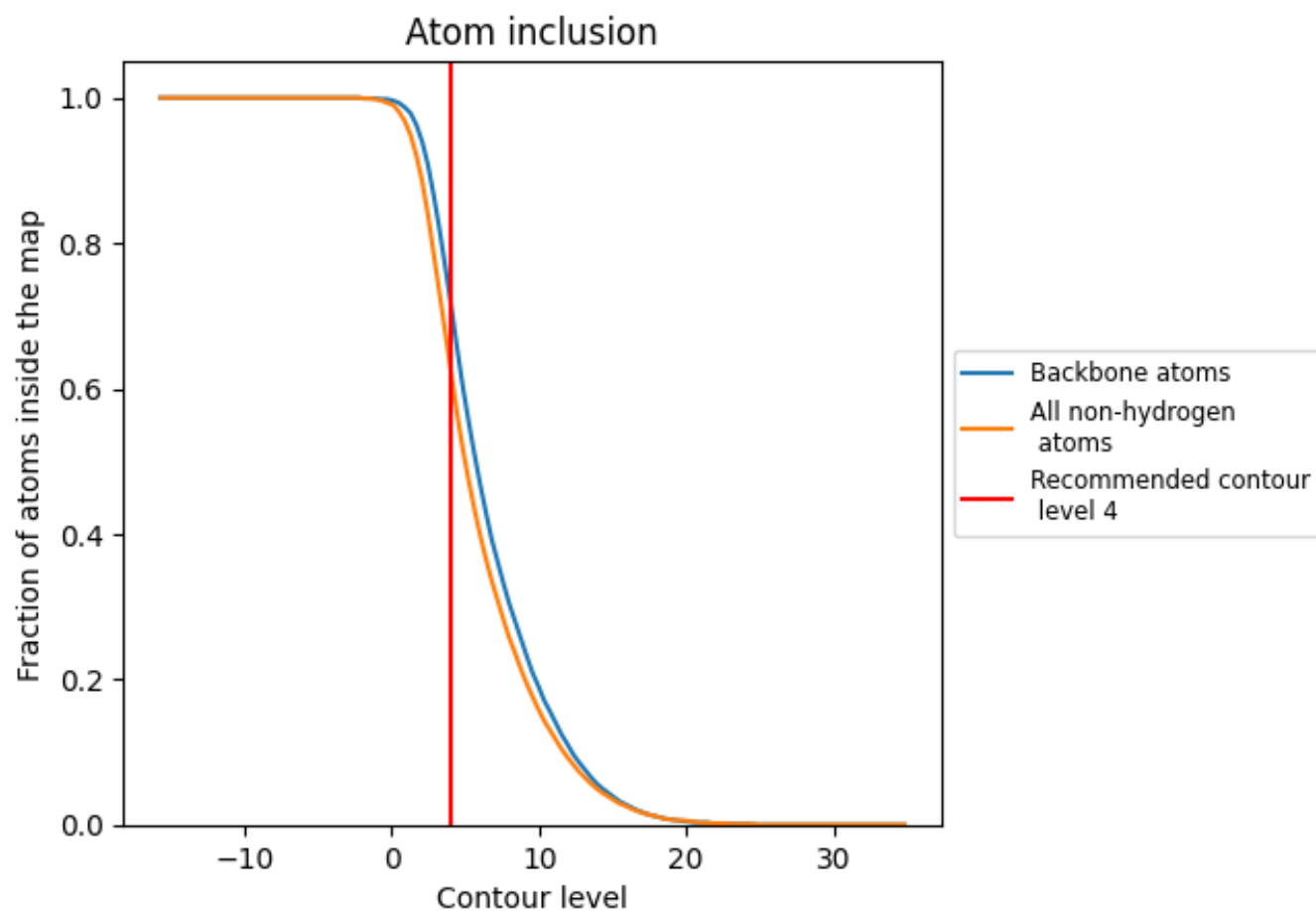
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4).

9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 62% 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 (4) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6240	 0.3030
3	 0.3170	 0.1290
4	 0.6930	 0.2850
5	 0.2280	 0.0850
6	 0.6530	 0.2700
7	 0.1820	 0.1020
8	 0.5900	 0.2470
A	 0.9080	 0.4280
H	 0.7840	 0.4270
I	 0.7550	 0.3900
M	 0.6590	 0.3480
N	 0.6880	 0.3580
O	 0.8010	 0.4400
P	 0.7480	 0.3970
Q	 0.7690	 0.4170
n	 0.5450	 0.3240
u	 0.6820	 0.3490
v	 0.6730	 0.2950
x	 0.6530	 0.3260
y	 0.7270	 0.3920

