



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 09:29 AM UTC

PDB ID : 7U5E / pdb_00007u5e
EMDB ID : EMD-26349
Title : I-F3b Cascade-TniQ partial R-loop complex
Authors : Park, J.U.; Mehrotra, E.; Kellogg, E.H.
Deposited on : 2022-03-02
Resolution : 4.03 Å(reported)
Based on initial model : 6PIF

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

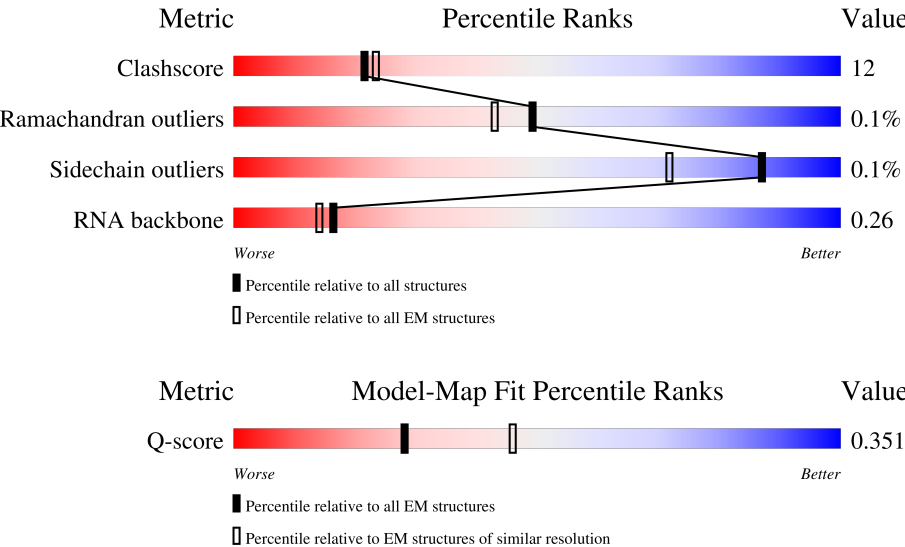
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.03 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	6618 (3.54 - 4.53)

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	1	60	20% 47% 33%
2	2	116	11% 17% 72%
3	3	116	94%

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Mol	Chain	Length	Quality of chain
4	A	704	
5	B	347	
5	C	347	
5	D	347	
5	E	347	
5	F	347	
5	G	347	
6	H	206	
7	I	410	
7	J	410	

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 29651 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 RNA chain called crRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	60	Total	C	N	O	P	0	0
			1285	576	239	411	59		

- Molecule 2 is a DNA chain called Target strand DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	33	Total	C	N	O	P	0	0
			670	321	114	202	33		

- Molecule 3 is a DNA chain called Non-target strand DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	7	Total	C	N	O	P	0	0
			138	67	20	44	7		

- Molecule 4 is a protein called Cas8/5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	501	Total	C	N	O	S	0	0
			3918	2506	685	709	18		

- Molecule 5 is a protein called Cas7.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	342	Total	C	N	O	S	0	0
			2711	1722	467	510	12		
5	C	342	Total	C	N	O	S	0	0
			2711	1722	467	510	12		
5	D	342	Total	C	N	O	S	0	0
			2711	1722	467	510	12		
5	E	342	Total	C	N	O	S	0	0
			2711	1722	467	510	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	342	Total	C	N	O	S	0	0
			2711	1722	467	510	12		
5	G	300	Total	C	N	O	S	0	0
			2390	1526	410	443	11		

- Molecule 6 is a protein called Cas6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	H	202	Total	C	N	O	S	0	0
			1631	1032	301	292	6		

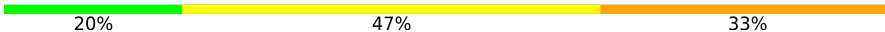
- Molecule 7 is a protein called TniQ.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	I	387	Total	C	N	O	S	0	0
			3084	1946	574	548	16		
7	J	374	Total	C	N	O	S	0	0
			2980	1886	548	530	16		

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.

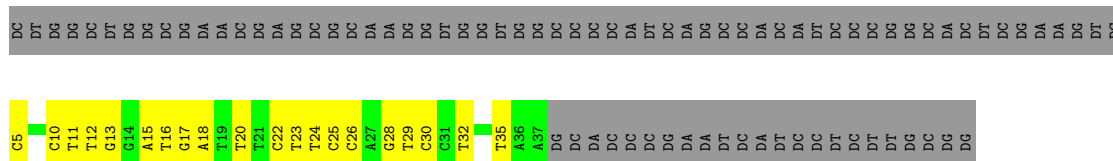
- Molecule 1: crRNA

Chain 1: 



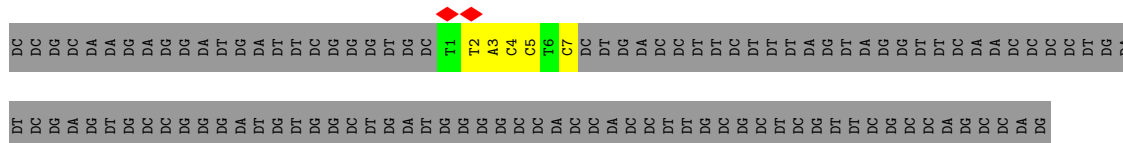
- Molecule 2: Target strand DNA

Chain 2: 



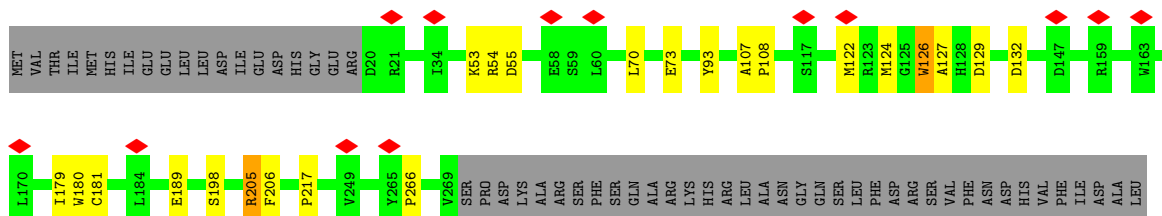
- Molecule 3: Non-target strand DNA

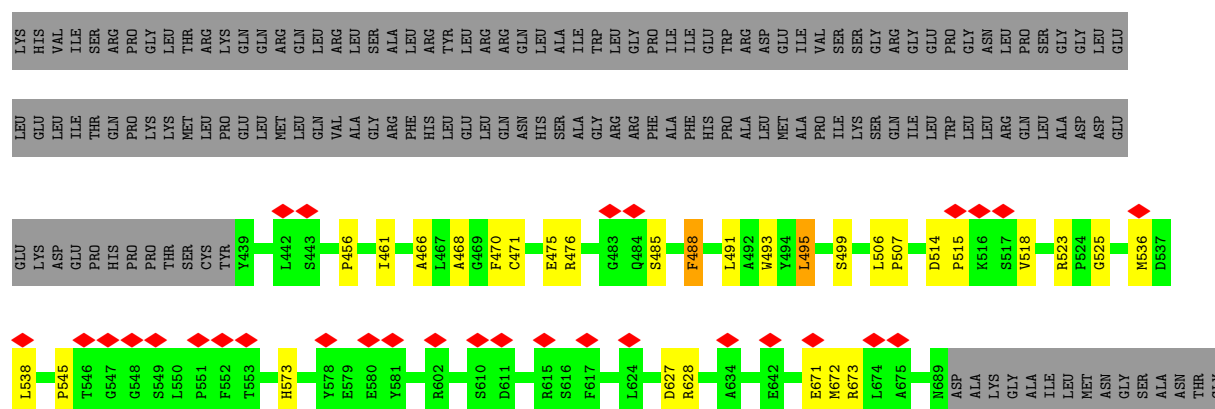
Chain 3: 



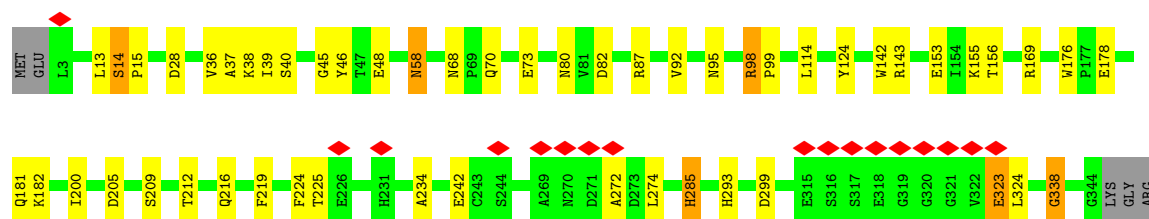
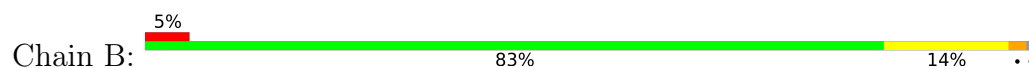
- Molecule 4: Cas8/5

Chain A: 

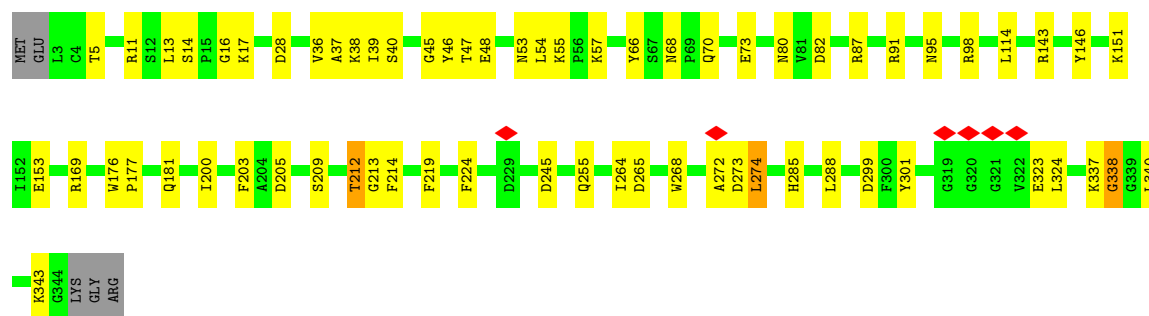
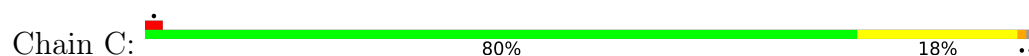




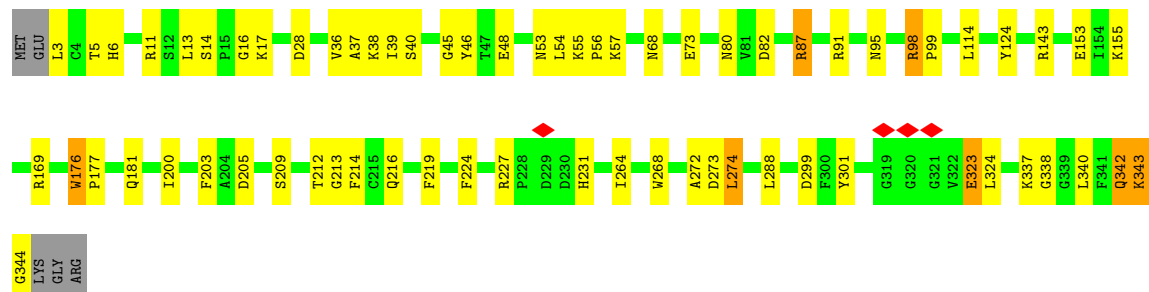
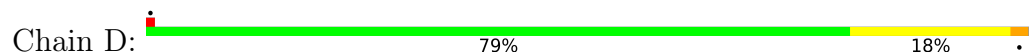
• Molecule 5: Cas7



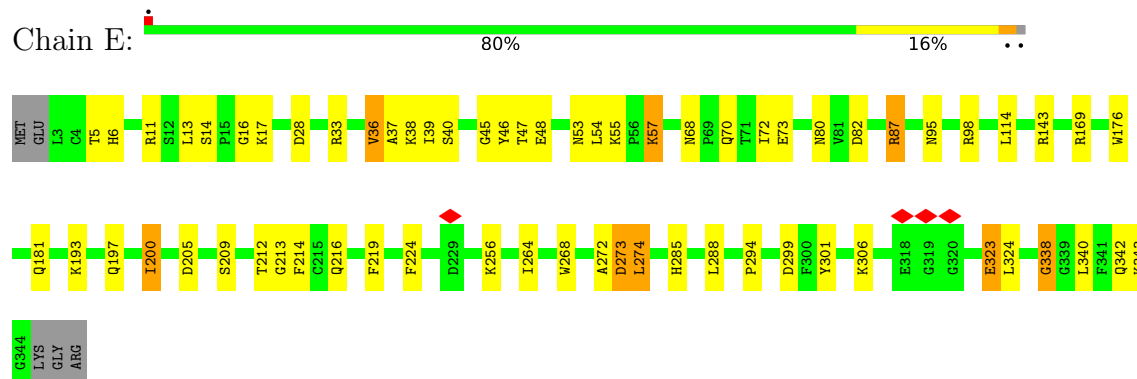
• Molecule 5: Cas7



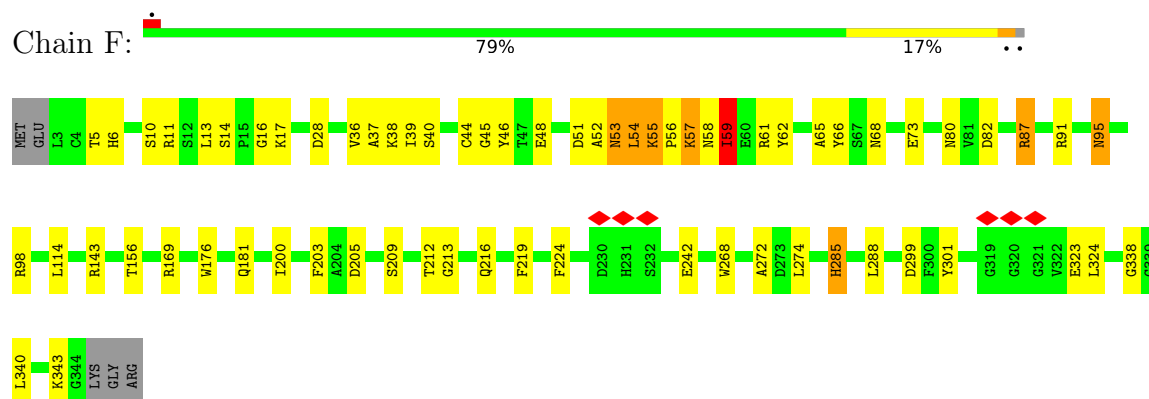
• Molecule 5: Cas7



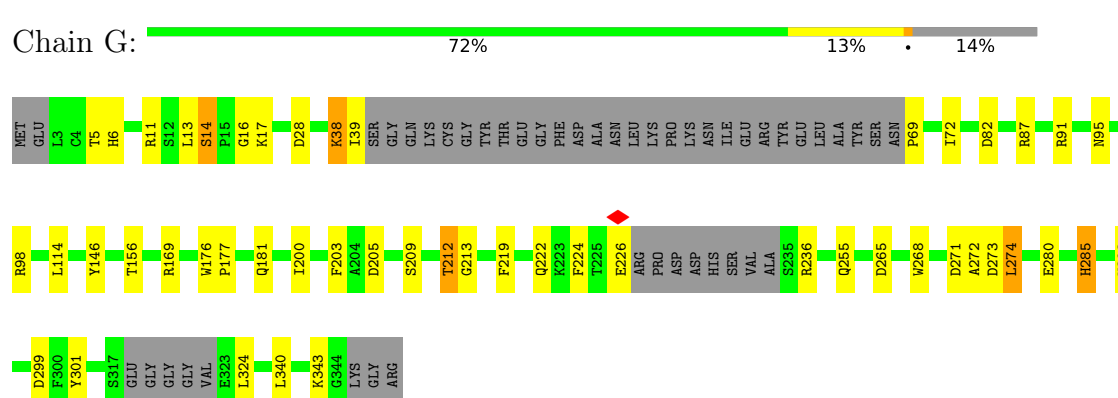
- Molecule 5: Cas7



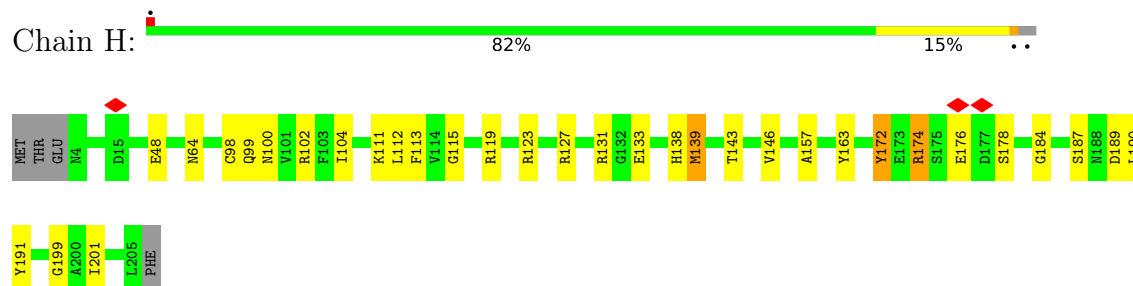
- Molecule 5: Cas7



- Molecule 5: Cas7



- Molecule 6: Cas6



Chain I:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	34800	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.055	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.007	Depositor
Map size ($\text{\AA}$)	366.66, 366.66, 366.66	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.873, 0.873, 0.873	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	1	0.21	0/1440	0.39	1/2244 (0.0%)
2	2	0.18	0/748	0.40	0/1151
3	3	0.15	0/152	0.37	0/231
4	A	0.88	0/4015	1.33	26/5465 (0.5%)
5	B	0.93	0/2778	1.23	38/3771 (1.0%)
5	C	0.92	0/2778	1.20	37/3771 (1.0%)
5	D	0.92	0/2778	1.21	39/3771 (1.0%)
5	E	0.92	0/2778	1.22	40/3771 (1.1%)
5	F	0.92	0/2778	1.23	39/3771 (1.0%)
5	G	0.93	0/2447	1.18	28/3319 (0.8%)
6	H	0.69	0/1668	1.06	12/2246 (0.5%)
7	I	1.04	2/3164 (0.1%)	1.38	57/4292 (1.3%)
7	J	1.09	2/3054 (0.1%)	1.42	58/4141 (1.4%)
All	All	0.90	4/30578 (0.0%)	1.22	375/41944 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	A	0	1
5	C	0	1
5	D	0	1
5	E	0	1
5	F	0	1
5	G	0	1
All	All	0	6

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	J	316	ILE	CA-C	-6.11	1.45	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	I	316	ILE	CA-C	-6.02	1.45	1.52
7	J	315	LEU	CA-C	-5.05	1.46	1.52
7	I	315	LEU	CA-C	-5.01	1.46	1.52

All (375) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	J	6	ARG	CA-C-N	13.18	133.57	120.52
7	J	6	ARG	C-N-CA	13.18	133.57	120.52
7	J	129	CYS	CA-C-N	12.11	133.52	119.47
7	J	129	CYS	C-N-CA	12.11	133.52	119.47
5	B	176	TRP	CA-C-N	11.13	131.25	119.89
5	B	176	TRP	C-N-CA	11.13	131.25	119.89
5	F	176	TRP	CA-C-N	11.03	131.15	119.90
5	F	176	TRP	C-N-CA	11.03	131.15	119.90
6	H	139	MET	CA-C-N	10.83	132.57	120.98
6	H	139	MET	C-N-CA	10.83	132.57	120.98
4	A	127	ALA	N-CA-C	10.57	126.94	107.60
7	I	364	LEU	CA-C-N	10.54	130.50	119.85
7	I	364	LEU	C-N-CA	10.54	130.50	119.85
7	J	66	SER	N-CA-C	10.28	122.44	111.03
4	A	179	ILE	N-CA-C	10.22	121.05	110.72
7	J	364	LEU	CA-C-N	10.21	130.63	120.52
7	J	364	LEU	C-N-CA	10.21	130.63	120.52
7	I	306	THR	N-CA-C	9.91	122.08	111.28
4	A	468	ALA	N-CA-C	-9.56	100.86	111.28
7	J	367	SER	N-CA-C	9.49	121.71	111.36
7	J	55	LEU	N-CA-C	9.12	122.40	111.82
4	A	127	ALA	CB-CA-C	-8.78	98.35	111.70
5	G	28	ASP	N-CA-C	8.44	121.61	111.82
5	C	17	LYS	N-CA-C	8.43	121.92	110.55
5	D	28	ASP	N-CA-C	8.42	121.59	111.82
7	I	62	ILE	N-CA-C	8.42	119.21	110.62
6	H	176	GLU	N-CA-C	8.41	121.10	108.31
4	A	671	GLU	N-CA-C	8.34	120.37	111.28
5	F	48	GLU	N-CA-C	-8.26	102.35	111.36
5	E	176	TRP	CA-C-N	8.25	128.28	119.78
5	E	176	TRP	C-N-CA	8.25	128.28	119.78
5	G	272	ALA	N-CA-C	8.25	120.27	111.28
5	F	272	ALA	N-CA-C	8.23	120.25	111.28
5	E	272	ALA	N-CA-C	8.19	120.20	111.28
7	J	240	HIS	N-CA-C	-8.18	101.62	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	272	ALA	N-CA-C	8.18	120.19	111.28
5	B	272	ALA	N-CA-C	8.18	120.19	111.28
5	D	272	ALA	N-CA-C	8.16	120.18	111.28
7	I	244	ARG	N-CA-C	-8.16	100.36	110.65
7	J	53	PHE	CA-C-N	8.16	128.19	119.78
7	J	53	PHE	C-N-CA	8.16	128.19	119.78
7	J	162	CYS	CA-C-N	8.15	128.62	119.32
7	J	162	CYS	C-N-CA	8.15	128.62	119.32
5	F	68	ASN	CA-C-N	-8.09	111.68	119.85
5	F	68	ASN	C-N-CA	-8.09	111.68	119.85
5	C	68	ASN	CA-C-N	-8.08	111.69	119.85
5	C	68	ASN	C-N-CA	-8.08	111.69	119.85
5	E	68	ASN	CA-C-N	-8.08	111.69	119.85
5	E	68	ASN	C-N-CA	-8.08	111.69	119.85
5	D	68	ASN	CA-C-N	-8.07	111.70	119.85
5	D	68	ASN	C-N-CA	-8.07	111.70	119.85
5	B	68	ASN	CA-C-N	-7.99	111.78	119.85
5	B	68	ASN	C-N-CA	-7.99	111.78	119.85
7	J	86	ALA	CA-C-N	7.99	128.67	120.04
7	J	86	ALA	C-N-CA	7.99	128.67	120.04
7	I	220	GLY	N-CA-C	7.96	121.89	111.70
7	I	162	CYS	N-CA-C	7.96	127.39	109.81
4	A	126	TRP	N-CA-C	7.91	122.13	108.76
7	I	382	VAL	N-CA-C	7.83	125.63	109.34
6	H	178	SER	N-CA-C	7.80	121.61	110.14
5	G	17	LYS	N-CA-C	7.71	121.94	110.52
5	B	225	THR	N-CA-C	7.71	121.12	109.41
5	G	38	LYS	N-CA-C	7.70	121.77	112.38
5	E	17	LYS	N-CA-C	7.70	121.91	110.52
5	F	17	LYS	N-CA-C	7.68	121.88	110.52
5	D	17	LYS	N-CA-C	7.66	122.01	110.14
5	D	48	GLU	N-CA-C	-7.63	102.31	111.69
7	I	143	TRP	N-CA-C	-7.60	103.97	113.55
5	E	48	GLU	N-CA-C	-7.57	102.37	111.69
7	J	238	SER	N-CA-C	7.57	121.61	112.38
7	I	67	ARG	N-CA-C	7.51	119.55	111.36
5	C	48	GLU	N-CA-C	-7.47	102.28	111.40
5	F	28	ASP	N-CA-C	7.45	121.62	112.54
5	E	28	ASP	N-CA-C	7.41	121.58	112.54
5	B	28	ASP	N-CA-C	7.40	121.57	112.54
4	A	673	ARG	N-CA-C	-7.40	103.22	111.28
4	A	181	CYS	N-CA-C	-7.38	103.24	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	212	THR	N-CA-C	7.27	120.16	109.69
5	F	16	GLY	N-CA-C	-7.26	102.62	112.57
5	C	16	GLY	N-CA-C	-7.25	102.64	112.57
5	B	274	LEU	CA-C-N	7.24	127.16	119.85
5	B	274	LEU	C-N-CA	7.24	127.16	119.85
5	E	16	GLY	N-CA-C	-7.24	102.66	112.57
7	I	210	PHE	N-CA-C	7.23	121.45	109.95
5	D	219	PHE	CA-C-N	7.22	127.67	120.52
5	D	219	PHE	C-N-CA	7.22	127.67	120.52
7	J	352	VAL	N-CA-C	7.22	117.98	110.62
5	F	274	LEU	CA-C-N	7.21	127.13	119.85
5	F	274	LEU	C-N-CA	7.21	127.13	119.85
7	I	352	VAL	N-CA-C	7.21	117.97	110.62
5	F	219	PHE	CA-C-N	7.21	127.65	120.52
5	F	219	PHE	C-N-CA	7.21	127.65	120.52
5	G	16	GLY	N-CA-C	-7.19	102.72	112.57
5	C	274	LEU	CA-C-N	7.16	127.08	119.85
5	C	274	LEU	C-N-CA	7.16	127.08	119.85
5	B	212	THR	N-CA-C	7.13	120.21	109.95
5	D	274	LEU	CA-C-N	7.12	127.08	120.03
5	D	274	LEU	C-N-CA	7.12	127.08	120.03
5	G	212	THR	N-CA-C	7.11	120.19	109.95
7	I	159	ILE	N-CA-C	-7.11	100.41	109.58
5	G	274	LEU	CA-C-N	7.10	127.03	119.85
5	G	274	LEU	C-N-CA	7.10	127.03	119.85
5	G	219	PHE	CA-C-N	7.10	127.55	120.52
5	G	219	PHE	C-N-CA	7.10	127.55	120.52
7	I	259	TRP	CA-C-N	-7.09	111.25	119.47
7	I	259	TRP	C-N-CA	-7.09	111.25	119.47
5	D	212	THR	N-CA-C	7.08	120.14	109.95
7	I	394	ALA	N-CA-C	7.08	119.08	111.36
5	E	274	LEU	CA-C-N	7.07	126.99	119.85
5	E	274	LEU	C-N-CA	7.07	126.99	119.85
5	C	212	THR	N-CA-C	7.06	120.12	109.95
7	I	94	ALA	N-CA-C	7.05	119.93	110.35
5	G	169	ARG	N-CA-C	7.03	121.17	112.59
7	J	394	ALA	N-CA-C	7.03	119.02	111.36
7	I	233	GLN	N-CA-C	7.02	118.58	111.07
5	B	169	ARG	N-CA-C	7.01	121.14	112.59
7	J	396	MET	N-CA-C	7.01	121.54	112.92
5	E	212	THR	N-CA-C	6.98	120.00	109.95
7	I	177	ILE	N-CA-C	6.98	117.94	111.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	174	ARG	N-CA-C	6.94	120.99	109.46
5	C	28	ASP	N-CA-C	6.93	121.58	113.20
5	F	169	ARG	N-CA-C	6.92	121.20	111.30
5	E	169	ARG	N-CA-C	6.91	121.18	111.30
7	J	160	TYR	N-CA-C	6.89	119.86	110.55
5	D	169	ARG	N-CA-C	6.89	121.15	111.30
5	D	16	GLY	N-CA-C	-6.88	102.64	112.55
5	B	14	SER	CA-C-N	6.87	128.42	119.84
5	B	14	SER	C-N-CA	6.87	128.42	119.84
7	I	367	SER	N-CA-C	6.86	121.65	113.28
4	A	124	MET	CA-C-N	6.85	128.26	122.17
4	A	124	MET	C-N-CA	6.85	128.26	122.17
5	B	234	ALA	N-CA-C	6.84	120.15	110.23
5	F	82	ASP	N-CA-C	6.84	118.82	111.36
4	A	495	LEU	N-CA-C	6.83	120.08	107.99
7	I	109	VAL	N-CA-C	6.83	117.73	108.17
4	A	488	PHE	N-CA-C	6.82	120.00	107.99
5	D	82	ASP	N-CA-C	6.82	118.80	111.36
5	B	14	SER	N-CA-C	6.79	120.27	109.40
7	I	396	MET	N-CA-C	6.73	121.56	112.88
7	I	271	VAL	N-CA-C	-6.70	104.32	110.82
5	B	37	ALA	N-CA-C	6.70	119.51	108.99
5	E	95	ASN	N-CA-C	6.68	120.74	112.59
5	B	95	ASN	N-CA-C	6.68	120.74	112.59
5	E	37	ALA	N-CA-C	6.68	119.48	108.99
5	G	95	ASN	N-CA-C	6.68	120.74	112.59
5	C	37	ALA	N-CA-C	6.68	119.47	108.99
5	F	37	ALA	N-CA-C	6.63	119.39	108.99
5	D	37	ALA	N-CA-C	6.61	119.37	108.99
5	C	169	ARG	N-CA-C	6.58	121.14	111.87
7	J	61	ASN	N-CA-C	6.58	120.02	110.28
7	J	214	ASN	CA-C-N	6.57	126.55	119.78
7	J	214	ASN	C-N-CA	6.57	126.55	119.78
4	A	180	TRP	N-CA-C	6.53	118.40	111.28
7	I	187	ARG	N-CA-C	-6.53	99.34	108.54
7	I	172	LEU	N-CA-C	6.52	121.36	113.41
7	J	259	TRP	N-CA-C	6.51	124.19	109.81
5	F	95	ASN	N-CA-C	6.50	120.84	112.26
7	I	258	ALA	N-CA-C	-6.50	103.97	112.41
7	I	57	LEU	N-CA-C	6.49	118.35	111.28
7	I	110	HIS	N-CA-C	6.49	119.31	108.73
5	G	209	SER	N-CA-C	6.47	119.48	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	573	HIS	CA-C-N	6.46	127.03	120.38
4	A	573	HIS	C-N-CA	6.46	127.03	120.38
7	I	235	ARG	N-CA-C	6.45	118.39	111.36
7	I	253	ILE	N-CA-C	6.44	117.19	110.62
5	C	95	ASN	N-CA-C	6.42	120.92	111.87
7	I	331	VAL	N-CA-C	-6.35	99.33	108.53
7	I	261	ASP	N-CA-C	6.33	121.05	112.88
5	D	95	ASN	N-CA-C	6.33	120.80	111.87
7	J	242	ALA	N-CA-C	6.30	118.43	108.79
5	C	80	ASN	N-CA-C	6.29	120.30	112.24
5	F	80	ASN	N-CA-C	6.29	120.30	112.24
4	A	198	SER	CA-C-N	6.29	125.97	119.56
4	A	198	SER	C-N-CA	6.29	125.97	119.56
6	H	172	TYR	N-CA-C	6.29	119.58	110.28
5	E	80	ASN	N-CA-C	6.28	120.28	112.24
4	A	122	MET	N-CA-C	6.27	119.30	109.96
5	D	80	ASN	N-CA-C	6.26	120.25	112.24
6	H	143	THR	N-CA-C	6.26	119.10	108.90
5	E	219	PHE	CA-C-N	6.25	127.67	120.98
5	E	219	PHE	C-N-CA	6.25	127.67	120.98
5	B	80	ASN	N-CA-C	6.25	120.24	112.24
7	J	241	GLU	N-CA-C	6.24	121.06	113.38
5	C	219	PHE	CA-C-N	6.24	127.66	120.98
5	C	219	PHE	C-N-CA	6.24	127.66	120.98
7	I	173	ALA	N-CA-C	-6.23	105.68	113.28
5	B	219	PHE	CA-C-N	6.21	127.63	120.98
5	B	219	PHE	C-N-CA	6.21	127.63	120.98
5	F	114	LEU	N-CA-C	6.20	117.83	111.14
5	E	273	ASP	CB-CA-C	-6.17	109.44	116.54
5	C	209	SER	N-CA-C	6.17	119.52	109.59
5	D	209	SER	N-CA-C	6.16	119.51	109.59
5	E	209	SER	N-CA-C	6.15	119.50	109.59
5	F	209	SER	N-CA-C	6.15	119.50	109.59
5	C	57	LYS	CB-CA-C	-6.15	108.47	115.79
5	D	342	GLN	N-CA-C	6.14	120.01	108.65
5	E	57	LYS	CB-CA-C	-6.13	108.49	115.79
7	J	213	SER	N-CA-C	6.12	117.54	108.60
5	B	209	SER	N-CA-C	6.12	119.51	109.72
5	D	57	LYS	CB-CA-C	-6.11	108.52	115.79
7	I	328	GLN	N-CA-C	6.08	119.05	110.23
5	C	324	LEU	CA-C-N	6.08	126.27	120.31
5	C	324	LEU	C-N-CA	6.08	126.27	120.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	I	222	LEU	N-CA-C	6.08	117.91	111.28
5	E	324	LEU	CA-C-N	6.06	126.25	120.31
5	E	324	LEU	C-N-CA	6.06	126.25	120.31
7	I	132	CYS	N-CA-C	-6.05	106.44	113.88
5	G	114	LEU	N-CA-C	6.05	117.95	111.36
5	B	324	LEU	CA-C-N	6.04	126.23	120.31
5	B	324	LEU	C-N-CA	6.04	126.23	120.31
7	J	137	ALA	N-CA-C	6.04	118.99	109.39
5	B	114	LEU	N-CA-C	6.03	117.86	111.28
5	F	36	VAL	O-C-N	-6.03	116.75	123.26
5	G	324	LEU	CA-C-N	6.03	126.22	120.31
5	G	324	LEU	C-N-CA	6.03	126.22	120.31
5	C	114	LEU	N-CA-C	6.02	117.92	111.36
7	J	310	PHE	N-CA-C	6.01	119.72	112.38
5	B	87	ARG	N-CA-C	6.01	118.20	109.07
5	F	324	LEU	CA-C-N	6.01	126.19	120.31
5	F	324	LEU	C-N-CA	6.01	126.19	120.31
5	D	114	LEU	N-CA-C	6.00	117.82	111.28
7	I	310	PHE	N-CA-C	5.99	119.69	112.38
5	E	82	ASP	N-CA-C	5.98	118.75	111.82
5	C	36	VAL	O-C-N	-5.97	116.81	123.26
5	D	36	VAL	O-C-N	-5.97	116.73	123.18
7	I	369	ARG	CA-C-N	5.97	126.16	120.31
7	I	369	ARG	C-N-CA	5.97	126.16	120.31
7	J	328	GLN	N-CA-C	5.97	118.99	110.10
5	E	114	LEU	N-CA-C	5.96	117.86	111.36
5	E	36	VAL	O-C-N	-5.95	116.75	123.18
7	I	382	VAL	CB-CA-C	-5.94	101.54	111.29
5	B	36	VAL	O-C-N	-5.94	116.76	123.18
5	D	324	LEU	CA-C-N	5.94	126.13	120.31
5	D	324	LEU	C-N-CA	5.94	126.13	120.31
7	J	99	ALA	N-CA-C	5.94	118.54	111.71
7	I	28	PHE	N-CA-C	-5.92	100.73	109.62
6	H	176	GLU	CB-CA-C	-5.90	109.76	116.54
5	E	14	SER	N-CA-C	5.90	120.57	107.95
5	F	14	SER	N-CA-C	5.89	120.57	107.95
7	I	85	GLY	N-CA-C	5.89	121.04	112.55
5	C	14	SER	N-CA-C	5.89	120.56	107.95
5	C	98	ARG	CA-C-N	5.82	125.84	119.90
5	C	98	ARG	C-N-CA	5.82	125.84	119.90
5	D	98	ARG	CA-C-N	5.81	125.82	119.90
5	D	98	ARG	C-N-CA	5.81	125.82	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	98	ARG	CA-C-N	5.80	125.82	119.90
5	E	98	ARG	C-N-CA	5.80	125.82	119.90
5	D	87	ARG	N-CA-C	5.80	118.22	109.23
5	B	73	GLU	N-CA-C	-5.76	101.50	110.42
5	G	87	ARG	N-CA-C	5.75	118.14	109.23
5	F	58	ASN	N-CA-C	5.73	119.38	112.38
5	F	87	ARG	N-CA-C	5.73	118.11	109.23
5	B	82	ASP	N-CA-C	5.73	118.73	111.69
5	F	285	HIS	N-CA-C	5.73	117.60	111.36
5	D	73	GLU	N-CA-C	-5.72	101.55	110.42
5	E	87	ARG	N-CA-C	5.72	118.10	109.23
7	J	62	ILE	N-CA-C	5.71	116.45	110.62
5	G	285	HIS	N-CA-C	5.71	117.58	111.36
7	J	388	VAL	N-CA-C	5.69	115.88	110.53
5	C	82	ASP	N-CA-C	5.68	118.68	111.69
7	J	204	LEU	N-CA-C	5.65	119.65	112.87
5	G	5	THR	N-CA-C	5.64	117.23	111.14
7	J	177	ILE	N-CA-C	5.64	116.69	111.45
5	E	5	THR	N-CA-C	5.60	117.19	111.14
7	J	88	PHE	N-CA-C	5.60	118.22	108.76
5	C	5	THR	N-CA-C	5.59	117.18	111.14
7	J	47	HIS	N-CA-C	5.59	117.37	111.28
4	A	70	LEU	N-CA-C	5.58	118.13	111.71
5	G	14	SER	CA-C-N	5.57	126.73	120.66
5	G	14	SER	C-N-CA	5.57	126.73	120.66
5	C	14	SER	CA-C-N	5.57	126.73	120.66
5	C	14	SER	C-N-CA	5.57	126.73	120.66
5	E	14	SER	CA-C-N	5.56	126.72	120.66
5	E	14	SER	C-N-CA	5.56	126.72	120.66
5	F	98	ARG	CA-C-N	5.56	125.88	119.93
5	F	98	ARG	C-N-CA	5.56	125.88	119.93
5	C	73	GLU	N-CA-C	-5.54	101.55	110.14
7	I	251	LYS	N-CA-C	5.53	119.28	112.54
7	I	295	VAL	CB-CA-C	-5.52	104.90	111.97
5	G	98	ARG	CA-C-N	5.52	125.83	119.93
5	G	98	ARG	C-N-CA	5.52	125.83	119.93
7	J	271	VAL	N-CA-C	5.52	117.99	111.09
5	C	200	ILE	N-CA-C	-5.52	100.45	108.17
5	F	14	SER	CA-C-N	5.51	126.81	120.85
5	F	14	SER	C-N-CA	5.51	126.81	120.85
5	E	73	GLU	N-CA-C	-5.51	101.60	110.14
7	I	61	ASN	N-CA-C	5.51	118.27	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	98	ARG	CA-C-N	5.50	125.81	119.93
5	B	98	ARG	C-N-CA	5.50	125.81	119.93
7	I	301	ILE	N-CA-C	-5.49	103.91	108.63
7	J	57	LEU	N-CA-C	5.47	117.95	111.33
4	A	672	MET	N-CA-C	5.47	119.67	112.89
5	B	58	ASN	N-CA-C	5.46	117.61	107.99
5	D	200	ILE	N-CA-C	-5.45	100.54	108.17
5	F	200	ILE	N-CA-C	-5.45	100.54	108.17
5	G	200	ILE	N-CA-C	-5.44	100.49	108.11
6	H	184	GLY	N-CA-C	-5.44	106.70	115.08
5	D	14	SER	CA-C-N	5.43	126.71	120.85
5	D	14	SER	C-N-CA	5.43	126.71	120.85
5	E	200	ILE	N-CA-C	-5.42	100.53	108.11
5	C	87	ARG	N-CA-C	5.40	118.24	109.06
7	J	302	PRO	N-CA-C	5.40	120.61	113.86
5	B	200	ILE	N-CA-C	-5.39	100.56	108.11
5	F	73	GLU	N-CA-C	-5.39	101.49	110.17
5	F	56	PRO	N-CA-C	-5.39	102.73	111.19
7	J	84	ASP	N-CA-C	5.38	117.67	110.35
7	I	264	TRP	N-CA-C	5.38	117.90	111.71
7	J	100	ILE	N-CA-C	5.38	119.59	112.76
5	D	5	THR	N-CA-C	5.37	117.21	111.36
7	I	100	ILE	N-CA-C	5.37	115.83	107.99
5	F	5	THR	N-CA-C	5.36	117.20	111.36
7	J	224	ALA	N-CA-C	5.33	117.09	111.28
5	D	124	TYR	N-CA-C	-5.30	106.07	112.54
5	C	57	LYS	N-CA-C	5.29	119.06	109.32
5	B	124	TYR	N-CA-C	-5.29	106.08	112.54
5	D	57	LYS	N-CA-C	5.29	119.06	109.32
7	I	302	PRO	N-CA-C	5.29	120.54	114.03
7	J	306	THR	N-CA-C	5.28	122.04	110.80
7	J	282	LEU	N-CA-C	5.27	117.02	111.28
5	E	57	LYS	N-CA-C	5.25	118.98	109.32
1	1	19	G	O4'-C1'-N9	5.24	116.07	108.20
7	J	94	ALA	N-CA-C	5.23	117.14	109.24
7	I	178	ASN	N-CA-C	5.23	117.89	111.82
4	A	266	PRO	CA-C-N	5.23	123.42	119.66
4	A	266	PRO	C-N-CA	5.23	123.42	119.66
7	I	186	LEU	N-CA-C	5.22	117.61	108.52
7	J	36	GLY	N-CA-C	-5.22	106.44	112.50
5	G	82	ASP	N-CA-C	5.22	118.81	112.23
5	B	323	GLU	N-CA-C	5.21	118.90	112.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	323	GLU	N-CA-C	5.21	118.89	112.54
5	E	323	GLU	N-CA-C	5.20	118.89	112.54
7	I	169	LEU	N-CA-C	5.18	118.19	109.95
7	I	36	GLY	N-CA-C	5.17	125.44	113.18
5	C	323	GLU	N-CA-C	5.17	118.85	112.54
4	A	205	ARG	N-CA-C	5.16	117.86	109.24
5	D	323	GLU	N-CA-C	5.16	118.83	112.54
7	J	205	ALA	N-CA-C	-5.16	105.78	111.71
7	J	118	LEU	N-CA-C	5.15	117.63	111.71
5	E	338	GLY	N-CA-C	5.15	117.85	111.93
7	J	301	ILE	N-CA-C	-5.15	103.91	108.95
7	I	388	VAL	N-CA-C	5.14	115.91	110.72
6	H	100	ASN	N-CA-C	5.12	118.42	110.17
7	J	218	ALA	N-CA-C	-5.12	104.33	110.88
5	G	156	THR	N-CA-C	5.11	117.44	109.52
4	A	189	GLU	N-CA-C	5.10	119.20	112.92
4	A	73	GLU	CA-C-N	5.10	125.60	119.94
4	A	73	GLU	C-N-CA	5.10	125.60	119.94
5	D	176	TRP	CA-C-N	5.09	125.37	119.92
5	D	176	TRP	C-N-CA	5.09	125.37	119.92
5	G	181	GLN	N-CA-C	-5.09	105.73	111.28
5	B	181	GLN	N-CA-C	-5.08	105.74	111.28
5	G	236	ARG	N-CA-C	5.08	117.41	110.55
7	J	237	LEU	N-CA-C	-5.08	102.01	109.62
7	J	181	GLN	N-CA-C	5.07	118.73	112.54
5	E	181	GLN	N-CA-C	-5.06	105.77	111.28
7	I	326	HIS	CA-C-N	5.06	125.04	120.03
7	I	326	HIS	C-N-CA	5.06	125.04	120.03
5	B	156	THR	N-CA-C	5.05	117.35	109.52
5	B	285	HIS	N-CA-C	5.05	117.68	111.82
5	F	156	THR	N-CA-C	5.05	117.34	109.52
5	D	343	LYS	N-CA-C	5.04	118.54	111.74
5	B	338	GLY	N-CA-C	5.04	117.72	111.93
5	C	338	GLY	N-CA-C	5.04	117.72	111.93
7	J	49	ALA	CA-C-N	5.02	127.01	120.28
7	J	49	ALA	C-N-CA	5.02	127.01	120.28
6	H	138	HIS	N-CA-C	5.02	116.95	108.02
5	C	181	GLN	N-CA-C	-5.01	105.81	111.28
6	H	199	GLY	N-CA-C	-5.01	108.75	115.32
7	I	250	THR	N-CA-C	5.01	117.39	111.33
5	C	285	HIS	N-CA-C	5.01	117.63	111.82
5	F	181	GLN	N-CA-C	-5.01	105.82	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	181	GLN	N-CA-C	-5.01	105.82	111.28
5	E	285	HIS	N-CA-C	5.01	117.63	111.82
7	J	326	HIS	CA-C-N	5.00	125.01	120.21
7	J	326	HIS	C-N-CA	5.00	125.01	120.21

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	A	93	TYR	Sidechain
5	C	205	ASP	Mainchain
5	D	205	ASP	Mainchain
5	E	205	ASP	Mainchain
5	F	205	ASP	Mainchain
5	G	205	ASP	Mainchain

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	1	1285	0	643	193	0
2	2	670	0	371	32	0
3	3	138	0	81	5	0
4	A	3918	0	3909	77	0
5	B	2711	0	2645	62	0
5	C	2711	0	2645	76	0
5	D	2711	0	2643	66	0
5	E	2711	0	2645	81	0
5	F	2711	0	2644	104	0
5	G	2390	0	2346	90	0
6	H	1631	0	1596	75	0
7	I	3084	0	3005	106	0
7	J	2980	0	2907	77	0
All	All	29651	0	28080	675	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 12.

All (675) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:13:C:C5	5:B:39:ILE:HD12	1.13	1.60
1:1:13:C:C5	5:B:39:ILE:CD1	1.80	1.56
5:F:62:TYR:CE1	7:I:370:PRO:HG2	1.40	1.52
2:2:22:DC:N4	5:C:70:GLN:CD	1.68	1.49
1:1:13:C:H5	5:B:39:ILE:CD1	1.10	1.47
5:G:39:ILE:HD13	6:H:146:VAL:CG2	1.45	1.45
5:G:39:ILE:CD1	6:H:146:VAL:HG21	1.44	1.43
1:1:52:U:H4'	6:H:131:ARG:NH2	1.18	1.42
5:F:62:TYR:CZ	7:I:370:PRO:HG2	1.54	1.39
1:1:51:G:C5	6:H:127:ARG:NH1	1.89	1.38
7:J:366:LEU:CD1	7:J:368:ILE:O	1.70	1.37
2:2:22:DC:N4	5:C:70:GLN:CG	1.88	1.36
2:2:35:DT:C4'	4:A:129:ASP:OD1	1.71	1.35
1:1:2:C:N4	4:A:470:PHE:CD1	1.95	1.34
1:1:31:G:O6	5:E:70:GLN:HG3	1.25	1.34
7:J:239:ASP:OD1	7:J:244:ARG:NE	1.62	1.32
1:1:33:U:N3	5:F:224:PHE:CE1	1.98	1.31
5:G:72:ILE:CD1	6:H:112:LEU:HB3	1.59	1.31
1:1:33:U:C4	5:F:224:PHE:CE1	2.20	1.29
5:G:39:ILE:HA	6:H:146:VAL:CG2	1.61	1.27
1:1:31:G:O6	5:E:70:GLN:CG	1.83	1.26
1:1:8:A:C2	5:B:142:TRP:CH2	2.22	1.26
5:G:146:TYR:CE2	7:J:47:HIS:CE1	2.26	1.24
1:1:25:A:OP2	5:E:11:ARG:HD3	1.10	1.22
2:2:22:DC:N4	5:C:70:GLN:OE1	1.71	1.22
1:1:52:U:C4'	6:H:131:ARG:NH2	2.01	1.22
4:A:461:ILE:CG2	4:A:493:TRP:CH2	2.25	1.20
2:2:22:DC:N4	5:C:70:GLN:HG3	1.52	1.18
7:I:130:PRO:HD2	7:I:160:TYR:CD2	1.77	1.18
7:J:366:LEU:HD13	7:J:368:ILE:O	1.29	1.18
5:G:39:ILE:HD12	6:H:146:VAL:HG21	1.22	1.17
1:1:2:C:N3	4:A:470:PHE:HB2	1.60	1.17
1:1:50:C:OP2	6:H:123:ARG:NH2	1.78	1.16
1:1:13:C:N4	5:B:70:GLN:HB2	1.61	1.16
4:A:461:ILE:CG2	4:A:493:TRP:HH2	1.55	1.16
1:1:13:C:C6	5:B:39:ILE:HD12	1.82	1.14
7:J:249:LEU:HD13	7:J:249:LEU:O	1.45	1.14
5:F:62:TYR:CZ	7:I:370:PRO:CG	2.29	1.13
7:I:213:SER:HB2	7:I:219:ILE:HD11	1.31	1.12
5:F:62:TYR:CE1	7:I:370:PRO:CG	2.33	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:72:ILE:CD1	6:H:112:LEU:HD13	1.78	1.12
4:A:461:ILE:HG23	4:A:493:TRP:CH2	1.84	1.11
5:G:146:TYR:CE2	7:J:47:HIS:ND1	2.19	1.10
7:I:88:PHE:HE2	7:J:363:PHE:CE2	1.69	1.10
5:G:39:ILE:CD1	6:H:146:VAL:CG2	2.12	1.10
1:1:1:C:H5	4:A:205:ARG:NE	1.51	1.09
1:1:19:G:N7	5:C:39:ILE:HD12	1.65	1.09
1:1:25:A:OP2	5:E:11:ARG:CD	1.99	1.09
5:G:39:ILE:HD13	6:H:146:VAL:HG22	1.24	1.09
1:1:15:G:OP2	5:B:40:SER:HB3	1.52	1.09
5:G:39:ILE:HA	6:H:146:VAL:HG22	1.16	1.08
4:A:461:ILE:HG23	4:A:493:TRP:HH2	1.12	1.08
5:G:72:ILE:HD12	6:H:112:LEU:HB3	1.17	1.07
1:1:19:G:N7	5:C:39:ILE:CD1	2.17	1.07
1:1:2:C:C4	4:A:470:PHE:HD1	1.73	1.07
2:2:35:DT:H4'	4:A:129:ASP:CG	1.79	1.06
1:1:13:C:H5	5:B:39:ILE:CG1	1.69	1.06
1:1:12:A:H4'	5:C:338:GLY:O	1.54	1.05
1:1:2:C:C2	4:A:470:PHE:HB2	1.90	1.05
1:1:51:G:N7	6:H:127:ARG:NH1	2.05	1.05
1:1:2:C:N4	4:A:470:PHE:HD1	1.41	1.05
1:1:60:G:O3'	6:H:157:ALA:HB3	1.57	1.05
7:I:130:PRO:CD	7:I:160:TYR:CD2	2.41	1.04
5:G:72:ILE:CD1	6:H:112:LEU:CB	2.36	1.03
7:I:132:CYS:HB3	7:I:154:HIS:HE1	1.20	1.03
5:F:51:ASP:OD1	5:F:57:LYS:HD2	1.58	1.02
1:1:13:C:H41	5:B:70:GLN:HB2	1.14	1.02
1:1:21:A:OP2	5:C:40:SER:HB3	1.59	1.02
1:1:2:C:N3	4:A:470:PHE:CB	2.23	1.01
5:G:38:LYS:HG3	5:G:69:PRO:HG3	1.41	1.01
5:G:72:ILE:HD11	6:H:112:LEU:HD13	1.43	1.01
1:1:33:U:C4	5:F:224:PHE:CD1	2.49	1.00
2:2:35:DT:H4'	4:A:129:ASP:OD1	0.83	1.00
7:I:213:SER:CB	7:I:219:ILE:HD11	1.89	1.00
5:B:216:GLN:HE21	5:C:91:ARG:NH1	1.59	1.00
7:I:88:PHE:CE2	7:J:363:PHE:CE2	2.50	0.99
1:1:7:A:C2	4:A:507:PRO:CB	2.45	0.99
1:1:13:C:C5	5:B:39:ILE:HD11	1.92	0.99
5:F:38:LYS:NZ	5:G:226:GLU:HG2	1.78	0.98
1:1:52:U:C4'	6:H:131:ARG:HH21	1.66	0.98
1:1:31:G:C6	5:E:70:GLN:HG3	1.99	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:288:LEU:CD1	5:D:6:HIS:CD2	2.47	0.97
5:E:214:PHE:CE1	5:F:87:ARG:NH2	2.32	0.97
1:1:8:A:H2	5:B:142:TRP:CH2	1.67	0.97
5:B:216:GLN:NE2	5:C:91:ARG:NH1	2.13	0.97
1:1:33:U:C4	5:F:224:PHE:CZ	2.53	0.96
7:I:132:CYS:HB3	7:I:154:HIS:CE1	1.99	0.96
1:1:31:G:O6	5:E:70:GLN:CB	2.13	0.96
1:1:51:G:C8	6:H:127:ARG:NH2	2.34	0.96
5:G:91:ARG:HG2	5:G:203:PHE:CE2	2.00	0.96
5:G:39:ILE:HA	6:H:146:VAL:HG23	1.48	0.96
7:I:54:PRO:HG3	7:I:59:ARG:NE	1.80	0.96
4:A:491:LEU:HD12	4:A:491:LEU:O	1.65	0.96
5:G:72:ILE:HD11	6:H:112:LEU:HB3	1.44	0.96
1:1:1:C:C5	4:A:205:ARG:CZ	2.48	0.95
5:G:91:ARG:HD3	5:G:203:PHE:HE2	1.30	0.95
7:I:130:PRO:HD2	7:I:160:TYR:HD2	1.27	0.94
1:1:2:C:N3	4:A:470:PHE:CD1	2.36	0.94
7:J:239:ASP:OD1	7:J:244:ARG:CG	2.15	0.94
5:G:72:ILE:HD11	6:H:112:LEU:CG	1.98	0.94
5:F:38:LYS:HZ2	5:G:226:GLU:HG2	1.29	0.94
7:I:130:PRO:CD	7:I:160:TYR:HD2	1.79	0.93
5:G:72:ILE:HD13	6:H:112:LEU:HD13	1.49	0.93
2:2:22:DC:H42	5:C:70:GLN:HG3	1.21	0.93
5:G:72:ILE:HD11	6:H:112:LEU:CD1	1.98	0.92
5:D:343:LYS:O	5:D:343:LYS:HG3	1.67	0.92
1:1:33:U:O4	5:F:224:PHE:CZ	2.23	0.92
5:C:288:LEU:HD11	5:D:6:HIS:CD2	2.05	0.91
7:J:214:ASN:N	7:J:215:PRO:HD2	1.85	0.91
1:1:25:A:N7	5:D:39:ILE:CD1	2.33	0.91
5:E:38:LYS:HE2	5:F:224:PHE:CE2	2.05	0.91
1:1:2:C:N3	4:A:470:PHE:HD1	1.69	0.91
7:I:130:PRO:HD2	7:I:160:TYR:CE2	2.06	0.91
1:1:1:C:H5	4:A:205:ARG:HE	1.15	0.90
2:2:22:DC:C4	5:C:70:GLN:CD	2.49	0.90
1:1:1:C:C5	4:A:205:ARG:NE	2.38	0.90
7:I:88:PHE:CE2	7:J:363:PHE:HE2	1.87	0.90
5:G:39:ILE:CA	6:H:146:VAL:HG22	2.02	0.90
1:1:2:C:C4	4:A:470:PHE:CD1	2.51	0.90
1:1:8:A:N1	5:B:142:TRP:CH2	2.41	0.89
1:1:7:A:C2	4:A:507:PRO:HB2	2.07	0.89
1:1:25:A:N7	5:D:39:ILE:HD12	1.88	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:33:U:C5	5:F:224:PHE:CD1	2.60	0.89
1:1:2:C:C4	4:A:470:PHE:HA	2.08	0.89
5:E:33:ARG:NH2	5:F:242:GLU:OE1	2.06	0.89
7:J:213:SER:C	7:J:215:PRO:HD2	1.98	0.89
1:1:1:C:C5	4:A:205:ARG:NH2	2.40	0.89
7:J:366:LEU:HD12	7:J:368:ILE:O	1.72	0.89
5:G:72:ILE:CD1	6:H:112:LEU:CD1	2.50	0.88
1:1:31:G:OP2	5:F:11:ARG:HD3	1.71	0.88
5:G:91:ARG:HG2	5:G:203:PHE:CD2	2.08	0.88
1:1:13:C:H42	5:B:70:GLN:HG3	1.39	0.87
7:J:239:ASP:OD1	7:J:244:ARG:CD	2.21	0.87
4:A:126:TRP:CZ2	4:A:132:ASP:HB2	2.10	0.87
5:G:72:ILE:HD11	6:H:112:LEU:CB	2.00	0.87
7:J:16:GLU:N	7:J:16:GLU:OE1	2.06	0.87
7:J:214:ASN:N	7:J:215:PRO:CD	2.38	0.86
7:I:54:PRO:HG3	7:I:59:ARG:HE	1.35	0.86
1:1:13:C:N4	5:B:70:GLN:CB	2.38	0.86
1:1:13:C:H42	5:B:70:GLN:CG	1.88	0.86
5:E:264:ILE:HG13	5:E:264:ILE:O	1.76	0.86
5:G:91:ARG:HD3	5:G:203:PHE:CE2	2.10	0.85
1:1:7:A:C2	4:A:507:PRO:CA	2.52	0.85
5:G:39:ILE:CA	6:H:146:VAL:CG2	2.52	0.85
7:I:188:THR:HG22	7:I:188:THR:O	1.76	0.85
1:1:31:G:O6	5:E:70:GLN:HB2	1.75	0.85
1:1:46:C:OP2	6:H:115:GLY:HA3	1.78	0.84
5:D:264:ILE:HG13	5:D:264:ILE:O	1.75	0.84
7:I:77:GLN:HE22	7:J:395:ARG:NH2	1.73	0.84
1:1:31:G:P	5:F:11:ARG:HD3	2.18	0.83
1:1:51:G:C6	6:H:127:ARG:NH1	2.46	0.83
1:1:1:C:N4	4:A:205:ARG:HH21	1.74	0.83
5:D:288:LEU:CD1	5:E:6:HIS:CD2	2.61	0.83
5:B:13:LEU:CD1	5:B:92:VAL:HG22	2.08	0.83
7:I:54:PRO:HB2	7:I:59:ARG:HD3	1.60	0.83
5:B:38:LYS:HD3	5:C:224:PHE:O	1.78	0.83
1:1:33:U:N3	5:F:224:PHE:HE1	1.72	0.82
7:I:128:CYS:HA	7:I:143:TRP:CZ3	2.14	0.82
5:G:11:ARG:NE	5:G:14:SER:HB3	1.94	0.82
7:J:366:LEU:HD12	7:J:366:LEU:O	1.78	0.82
5:G:91:ARG:CG	5:G:203:PHE:CE2	2.62	0.82
7:I:102:PHE:CD2	7:I:102:PHE:O	2.33	0.81
1:1:1:C:N3	4:A:476:ARG:NH2	2.25	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:146:TYR:HE2	7:J:47:HIS:ND1	1.78	0.81
5:G:91:ARG:CD	5:G:203:PHE:CE2	2.63	0.81
5:D:38:LYS:HD3	5:E:224:PHE:O	1.80	0.80
1:1:19:G:C8	5:C:39:ILE:HD12	2.16	0.80
1:1:19:G:OP1	5:D:11:ARG:HD3	1.81	0.80
1:1:23:U:OP1	5:D:143:ARG:NH1	2.14	0.80
1:1:19:G:O6	5:C:70:GLN:HG3	1.80	0.80
5:G:72:ILE:HD12	6:H:112:LEU:CB	2.03	0.80
1:1:33:U:C2	5:F:224:PHE:CE1	2.70	0.80
1:1:7:A:H2	4:A:507:PRO:HB2	1.45	0.79
4:A:518:VAL:O	5:B:293:HIS:NE2	2.15	0.79
7:I:54:PRO:CB	7:I:59:ARG:HD3	2.12	0.79
1:1:52:U:C3'	6:H:131:ARG:NH2	2.46	0.79
1:1:52:U:H4'	6:H:131:ARG:HH22	1.44	0.79
1:1:25:A:P	5:E:11:ARG:HD3	2.22	0.79
5:G:146:TYR:CD2	7:J:47:HIS:CE1	2.70	0.78
7:J:249:LEU:HD13	7:J:249:LEU:C	2.08	0.78
1:1:52:U:C4'	6:H:131:ARG:HH22	1.95	0.78
1:1:60:G:O3'	6:H:157:ALA:CB	2.31	0.78
5:F:216:GLN:HE22	5:G:91:ARG:HE	1.29	0.78
5:C:264:ILE:HG13	5:C:264:ILE:O	1.81	0.78
1:1:51:G:N7	6:H:127:ARG:CZ	2.47	0.78
3:3:7:DC:OP1	4:A:54:ARG:NH1	2.14	0.78
4:A:485:SER:O	4:A:545:PRO:HD2	1.84	0.77
5:B:216:GLN:HE21	5:C:91:ARG:HH12	1.28	0.77
1:1:19:G:N7	5:C:39:ILE:HD11	1.97	0.77
1:1:8:A:C2	5:B:142:TRP:CZ3	2.73	0.77
7:I:213:SER:CB	7:I:219:ILE:CD1	2.62	0.77
5:C:214:PHE:CE1	5:D:87:ARG:NH2	2.53	0.77
1:1:13:C:C4	5:B:39:ILE:CD1	2.67	0.76
2:2:18:DA:O4'	5:E:342:GLN:OE1	2.03	0.76
5:E:45:GLY:HA2	5:F:301:TYR:OH	1.86	0.76
5:E:288:LEU:CD1	5:F:6:HIS:CD2	2.69	0.76
1:1:15:G:C6	5:C:224:PHE:CE1	2.74	0.76
1:1:60:G:HO3'	6:H:157:ALA:HB3	1.47	0.76
5:F:62:TYR:OH	7:I:371:ALA:O	2.02	0.76
7:J:239:ASP:CG	7:J:244:ARG:HG2	2.11	0.76
1:1:55:A:OP1	6:H:111:LYS:NZ	2.14	0.75
2:2:22:DC:C4	5:C:70:GLN:OE1	2.38	0.75
5:D:214:PHE:CE1	5:E:87:ARG:NH2	2.55	0.74
1:1:25:A:OP2	5:E:11:ARG:NH1	2.20	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:216:GLN:NE2	5:C:91:ARG:HH11	1.84	0.74
5:G:343:LYS:O	5:G:343:LYS:HG3	1.87	0.74
5:E:38:LYS:HD3	5:F:224:PHE:HD2	1.52	0.74
5:F:213:GLY:H	5:F:216:GLN:HG3	1.52	0.74
7:I:54:PRO:HG3	7:I:59:ARG:CD	2.18	0.74
1:1:25:A:N7	5:D:39:ILE:HD11	2.01	0.74
7:J:239:ASP:OD1	7:J:244:ARG:HG2	1.87	0.73
5:F:216:GLN:HE22	5:G:91:ARG:NE	1.86	0.73
6:H:187:SER:HB3	6:H:191:TYR:HB2	1.71	0.73
1:1:8:A:N7	5:B:285:HIS:ND1	2.37	0.72
5:F:91:ARG:HD3	5:F:203:PHE:HE2	1.53	0.72
1:1:52:U:C3'	6:H:131:ARG:HH22	2.02	0.72
5:E:213:GLY:HA3	5:E:216:GLN:HE21	1.52	0.72
7:I:85:GLY:HA2	7:I:89:ARG:NH1	2.03	0.72
2:2:22:DC:H2'	2:2:23:DT:H71	1.71	0.72
5:D:45:GLY:HA2	5:E:301:TYR:OH	1.89	0.72
7:I:127:PRO:HB2	7:I:159:ILE:HG22	1.71	0.72
5:G:91:ARG:CD	5:G:203:PHE:HE2	2.02	0.72
7:I:54:PRO:CG	7:I:59:ARG:CD	2.67	0.72
1:1:13:C:C4	5:B:39:ILE:HD11	2.24	0.71
5:G:146:TYR:HE2	7:J:47:HIS:HD1	1.36	0.71
5:G:39:ILE:HD13	6:H:146:VAL:HG21	1.15	0.71
1:1:27:C:C5	5:E:224:PHE:HA	2.25	0.71
2:2:22:DC:C5	5:C:70:GLN:CD	2.67	0.71
5:C:343:LYS:HG3	5:C:343:LYS:O	1.89	0.71
1:1:8:A:C2	5:B:142:TRP:CZ2	2.79	0.70
4:A:461:ILE:CG2	4:A:493:TRP:CZ3	2.74	0.70
1:1:33:U:C6	5:F:224:PHE:CD1	2.79	0.70
5:E:214:PHE:HE1	5:F:87:ARG:NH2	1.88	0.70
7:I:88:PHE:HE2	7:J:363:PHE:CD2	2.09	0.70
1:1:1:C:C4	4:A:205:ARG:NH2	2.59	0.70
1:1:33:U:N3	5:F:224:PHE:CD1	2.57	0.70
4:A:461:ILE:HG21	4:A:493:TRP:CZ3	2.26	0.70
5:D:343:LYS:O	5:D:343:LYS:CG	2.39	0.70
7:I:88:PHE:CE2	7:J:363:PHE:CD2	2.79	0.70
1:1:1:C:H5	4:A:205:ARG:CZ	1.92	0.70
1:1:1:C:H41	4:A:205:ARG:HH21	1.40	0.70
5:F:91:ARG:HD3	5:F:203:PHE:CE2	2.27	0.69
5:D:91:ARG:HD3	5:D:203:PHE:HE2	1.57	0.69
7:I:88:PHE:HD1	7:J:394:ALA:O	1.75	0.69
1:1:8:A:H2	5:B:142:TRP:CZ3	2.07	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:216:GLN:OE1	5:F:91:ARG:CZ	2.41	0.69
7:J:239:ASP:CG	7:J:244:ARG:CG	2.65	0.69
1:1:31:G:OP2	5:F:11:ARG:CD	2.41	0.69
4:A:461:ILE:HG21	4:A:493:TRP:CH2	2.24	0.69
5:E:213:GLY:H	5:E:216:GLN:HG3	1.58	0.69
1:1:33:U:C5	5:F:224:PHE:CG	2.80	0.69
5:G:72:ILE:HD11	6:H:112:LEU:CD2	2.22	0.69
1:1:51:G:C8	6:H:127:ARG:CZ	2.76	0.68
5:F:216:GLN:NE2	5:G:91:ARG:HE	1.92	0.68
4:A:506:LEU:HD13	5:B:224:PHE:CE1	2.29	0.68
5:G:72:ILE:HD11	6:H:112:LEU:HD22	1.75	0.68
5:E:214:PHE:CD1	5:F:87:ARG:NH2	2.61	0.68
1:1:18:A:H4'	5:D:338:GLY:O	1.94	0.68
7:I:54:PRO:CG	7:I:59:ARG:HE	2.07	0.68
1:1:7:A:C2	4:A:507:PRO:HA	2.29	0.67
1:1:13:C:C5	5:B:39:ILE:CG1	2.58	0.67
5:F:91:ARG:HG2	5:F:203:PHE:CE2	2.29	0.67
1:1:33:U:OP2	5:E:40:SER:HB2	1.95	0.67
5:E:343:LYS:O	5:E:343:LYS:HG3	1.92	0.67
7:J:125:GLN:N	7:J:125:GLN:OE1	2.28	0.67
1:1:39:C:N3	5:G:224:PHE:HE1	1.93	0.67
1:1:52:U:O3'	6:H:131:ARG:NH2	2.25	0.67
4:A:506:LEU:HD13	5:B:224:PHE:HE1	1.60	0.67
1:1:39:C:N3	5:G:224:PHE:CE1	2.63	0.67
5:E:38:LYS:CE	5:F:224:PHE:CE2	2.77	0.67
4:A:126:TRP:CH2	4:A:132:ASP:HB2	2.29	0.66
5:E:38:LYS:HE2	5:F:224:PHE:CD2	2.30	0.66
5:F:343:LYS:O	5:F:343:LYS:HG3	1.94	0.66
2:2:32:DT:H2''	4:A:523:ARG:HB2	1.76	0.66
1:1:51:G:C8	6:H:127:ARG:NH1	2.63	0.66
5:D:91:ARG:HD3	5:D:203:PHE:CE2	2.31	0.66
6:H:190:LEU:O	6:H:191:TYR:CD2	2.48	0.66
7:I:127:PRO:HB2	7:I:159:ILE:CG2	2.26	0.66
7:I:87:PRO:CB	7:J:395:ARG:NH2	2.50	0.65
5:F:91:ARG:HG2	5:F:203:PHE:CD2	2.32	0.65
1:1:2:C:N3	4:A:470:PHE:CG	2.63	0.65
1:1:31:G:N7	5:E:39:ILE:CD1	2.59	0.65
1:1:33:U:C2	5:F:224:PHE:CD1	2.85	0.65
1:1:8:A:H2	5:B:142:TRP:CZ2	2.13	0.65
1:1:40:U:OP2	5:G:222:GLN:HB2	1.96	0.65
5:B:38:LYS:HE3	5:C:224:PHE:CD2	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2:C:C2	4:A:470:PHE:CB	2.76	0.64
5:G:146:TYR:CZ	7:J:47:HIS:ND1	2.64	0.64
1:1:13:C:OP2	5:C:11:ARG:HD3	1.97	0.64
7:I:54:PRO:CG	7:I:59:ARG:HD3	2.28	0.64
1:1:15:G:C5	5:C:224:PHE:CE1	2.86	0.64
7:J:239:ASP:OD2	7:J:244:ARG:CG	2.46	0.64
5:D:3:LEU:HB2	5:D:344:GLY:HA3	1.79	0.63
5:B:13:LEU:HD12	5:B:92:VAL:HG22	1.79	0.63
1:1:8:A:N1	5:B:142:TRP:HH2	1.95	0.63
5:F:62:TYR:CD1	7:I:370:PRO:HG2	2.25	0.63
1:1:28:C:P	5:E:256:LYS:HZ1	2.21	0.62
1:1:21:A:OP2	5:C:40:SER:CB	2.43	0.62
5:F:61:ARG:HG3	7:I:360:HIS:CE1	2.35	0.62
2:2:24:DT:H5'	5:D:342:GLN:NE2	2.15	0.62
7:I:219:ILE:HG22	7:I:220:GLY:N	2.14	0.62
6:H:131:ARG:HG2	6:H:133:GLU:HG3	1.82	0.62
7:J:199:ILE:HD12	7:J:249:LEU:HG	1.82	0.62
1:1:39:C:C4	5:G:224:PHE:CE1	2.88	0.61
5:E:193:LYS:HE2	5:E:200:ILE:CD1	2.30	0.61
1:1:13:C:H42	5:B:70:GLN:CB	2.09	0.61
4:A:514:ASP:OD1	4:A:515:PRO:HD2	2.01	0.61
5:F:38:LYS:HE2	5:G:224:PHE:HD2	1.65	0.61
1:1:24:C:O2'	5:E:338:GLY:O	2.19	0.61
1:1:19:G:OP1	5:D:11:ARG:CD	2.49	0.61
5:F:44:CYS:HB2	5:G:280:GLU:OE1	2.01	0.61
5:G:72:ILE:HD13	6:H:112:LEU:CD1	2.23	0.61
1:1:13:C:N4	5:B:70:GLN:CG	2.60	0.60
1:1:58:C:OP1	6:H:187:SER:OG	2.16	0.60
5:F:62:TYR:CE2	7:I:370:PRO:CG	2.84	0.60
7:I:218:ALA:O	7:I:219:ILE:HD13	2.00	0.60
2:2:10:DC:H1'	2:2:11:DT:H71	1.83	0.60
4:A:491:LEU:HD12	4:A:491:LEU:C	2.27	0.60
1:1:18:A:H5''	5:D:11:ARG:HB2	1.83	0.60
7:I:188:THR:O	7:I:188:THR:CG2	2.49	0.60
7:I:142:CYS:SG	7:I:206:TYR:CB	2.90	0.60
7:J:249:LEU:C	7:J:249:LEU:CD1	2.74	0.60
5:G:11:ARG:CZ	5:G:14:SER:HB3	2.31	0.60
7:I:128:CYS:HB2	7:I:133:LEU:HD11	1.84	0.60
1:1:31:G:N7	5:E:39:ILE:HD12	2.17	0.60
1:1:35:G:N3	5:G:340:LEU:HD21	2.17	0.59
4:A:507:PRO:HG3	4:A:525:GLY:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:11:ARG:CZ	5:G:14:SER:CB	2.81	0.59
1:1:36:G:H1	2:2:5:DC:H42	1.47	0.59
5:E:38:LYS:HD3	5:F:224:PHE:CD2	2.36	0.59
2:2:22:DC:C5	5:C:70:GLN:NE2	2.70	0.59
7:J:239:ASP:OD2	7:J:244:ARG:HG2	2.01	0.59
2:2:17:DG:C8	2:2:17:DG:H5'	2.38	0.59
7:I:142:CYS:SG	7:I:206:TYR:HB2	2.43	0.59
2:2:22:DC:H5	5:C:70:GLN:NE2	2.01	0.59
7:I:364:LEU:HD12	7:I:364:LEU:O	2.03	0.59
5:G:146:TYR:CZ	7:J:47:HIS:CE1	2.88	0.58
4:A:485:SER:O	4:A:545:PRO:CD	2.50	0.58
7:I:54:PRO:CG	7:I:59:ARG:NE	2.60	0.58
5:E:213:GLY:HA3	5:E:216:GLN:NE2	2.17	0.58
5:G:39:ILE:CA	6:H:146:VAL:HG23	2.25	0.58
1:1:33:U:O4	5:F:224:PHE:CE2	2.56	0.58
4:A:499:SER:HB2	5:B:242:GLU:OE1	2.03	0.58
5:F:216:GLN:HE22	5:G:91:ARG:CD	2.16	0.58
7:I:364:LEU:HD12	7:I:364:LEU:C	2.28	0.58
1:1:12:A:C2	5:C:340:LEU:HD12	2.38	0.58
1:1:23:U:C2	5:E:340:LEU:HD21	2.39	0.58
5:E:38:LYS:CE	5:F:224:PHE:CD2	2.87	0.58
5:F:91:ARG:CD	5:F:203:PHE:CE2	2.87	0.58
1:1:31:G:N7	5:E:39:ILE:HD11	2.19	0.57
2:2:15:DA:H2''	5:D:231:HIS:CE1	2.38	0.57
5:F:216:GLN:NE2	5:G:91:ARG:NE	2.50	0.57
7:J:366:LEU:HD12	7:J:366:LEU:C	2.27	0.57
2:2:11:DT:H3	5:F:340:LEU:HD12	1.69	0.57
5:C:146:TYR:CD2	5:D:91:ARG:HD2	2.40	0.57
7:I:88:PHE:CD1	7:J:394:ALA:C	2.83	0.57
7:I:398:SER:HB3	7:J:99:ALA:HB3	1.87	0.57
1:1:2:C:C4	4:A:470:PHE:CA	2.85	0.57
7:J:300:GLN:HA	7:J:300:GLN:OE1	2.05	0.57
1:1:12:A:H2	5:C:340:LEU:HD12	1.69	0.57
1:1:14:U:H5''	5:C:255:GLN:HB2	1.85	0.57
7:J:366:LEU:HD11	7:J:368:ILE:O	1.95	0.57
1:1:54:U:C4	6:H:139:MET:HB3	2.40	0.56
1:1:25:A:C8	5:D:39:ILE:HD12	2.41	0.56
1:1:28:C:OP1	5:E:256:LYS:NZ	2.34	0.56
5:D:213:GLY:H	5:D:216:GLN:HG3	1.70	0.56
6:H:172:TYR:CE2	6:H:174:ARG:HB2	2.40	0.56
7:I:139:VAL:HG23	7:I:177:ILE:HD12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:I:165:CYS:SG	7:I:167:GLU:OE2	2.64	0.56
4:A:471:CYS:SG	4:A:491:LEU:HD22	2.46	0.56
1:I:17:A:N3	5:D:340:LEU:HD21	2.20	0.56
5:C:146:TYR:CE2	5:D:91:ARG:HD2	2.41	0.56
7:I:142:CYS:SG	7:I:206:TYR:HA	2.45	0.56
5:D:91:ARG:HG2	5:D:203:PHE:CD2	2.39	0.56
5:F:38:LYS:NZ	5:G:226:GLU:CG	2.62	0.56
4:A:461:ILE:HG22	4:A:493:TRP:HH2	1.59	0.56
1:I:53:A:OP2	6:H:127:ARG:CZ	2.55	0.55
5:F:61:ARG:HD3	5:G:293:HIS:CD2	2.41	0.55
7:J:282:LEU:C	7:J:282:LEU:HD23	2.31	0.55
2:2:22:DC:C5	5:C:70:GLN:OE1	2.60	0.55
7:J:239:ASP:H	7:J:244:ARG:HH21	1.54	0.55
5:F:213:GLY:CA	5:F:216:GLN:HG2	2.37	0.55
1:I:15:G:C6	5:C:224:PHE:CZ	2.95	0.55
1:I:39:C:H5"	5:F:40:SER:OG	2.07	0.55
7:I:198:GLU:N	7:I:198:GLU:OE1	2.40	0.55
7:I:88:PHE:HD1	7:J:394:ALA:C	2.15	0.55
1:I:2:C:N3	4:A:470:PHE:CA	2.69	0.54
7:J:239:ASP:OD2	7:J:244:ARG:HG3	2.06	0.54
1:I:13:C:P	5:C:11:ARG:HD3	2.47	0.54
5:E:193:LYS:HE2	5:E:200:ILE:HD11	1.87	0.54
1:I:13:C:C5	5:B:39:ILE:HG13	2.43	0.54
1:I:15:G:OP2	5:B:40:SER:CB	2.41	0.54
1:I:24:C:OP1	5:E:11:ARG:N	2.40	0.54
6:H:48:GLU:HG2	6:H:48:GLU:O	2.08	0.54
7:I:54:PRO:CB	7:I:59:ARG:CD	2.84	0.54
1:I:13:C:N4	5:B:39:ILE:HD11	2.22	0.54
1:I:24:C:OP2	5:D:143:ARG:NH2	2.40	0.54
5:F:62:TYR:CE2	7:I:370:PRO:HG3	2.42	0.54
5:C:45:GLY:HA2	5:D:301:TYR:OH	2.08	0.54
7:I:10:PHE:HB2	7:I:13:GLU:HB2	1.89	0.53
1:I:9:A:C6	5:B:224:PHE:CE1	2.96	0.53
5:F:91:ARG:CG	5:F:203:PHE:CE2	2.91	0.53
5:E:288:LEU:HD11	5:F:6:HIS:CD2	2.42	0.53
5:C:288:LEU:HD11	5:D:6:HIS:CG	2.43	0.53
5:F:62:TYR:CD1	7:I:370:PRO:CG	2.89	0.53
5:C:143:ARG:O	5:C:143:ARG:HG2	2.09	0.53
5:F:52:ALA:C	5:F:54:LEU:H	2.16	0.53
5:F:38:LYS:HE2	5:G:224:PHE:CD2	2.42	0.53
4:A:493:TRP:CE2	4:A:495:LEU:HD11	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:39:ILE:O	6:H:146:VAL:O	2.27	0.53
5:G:146:TYR:CD2	7:J:47:HIS:HE1	2.22	0.53
5:E:268:TRP:CD1	5:E:268:TRP:H	2.27	0.53
5:F:65:ALA:O	5:G:285:HIS:CE1	2.62	0.53
5:F:216:GLN:NE2	5:G:91:ARG:HD3	2.24	0.53
5:F:45:GLY:HA2	5:G:301:TYR:OH	2.08	0.52
5:F:288:LEU:CD2	5:G:6:HIS:CD2	2.92	0.52
7:I:130:PRO:CG	7:I:160:TYR:CD2	2.92	0.52
7:I:242:ALA:O	7:I:243:VAL:HG12	2.10	0.52
1:1:13:C:OP2	5:C:11:ARG:NH1	2.43	0.52
7:I:87:PRO:HB3	7:J:395:ARG:NH2	2.23	0.52
1:1:3:A:C2	4:A:217:PRO:HG2	2.45	0.52
5:F:216:GLN:NE2	5:G:91:ARG:CD	2.73	0.52
1:1:3:A:N6	4:A:456:PRO:CD	2.72	0.52
5:G:271:ASP:HB2	7:J:67:ARG:HH12	1.73	0.52
5:C:268:TRP:CD1	5:C:268:TRP:H	2.26	0.52
5:D:288:LEU:HD12	5:E:6:HIS:CD2	2.45	0.52
1:1:39:C:C2	5:G:224:PHE:CE1	2.98	0.52
1:1:47:U:OP2	6:H:119:ARG:HD3	2.10	0.52
6:H:190:LEU:O	6:H:191:TYR:CG	2.63	0.52
7:I:88:PHE:CE1	7:J:395:ARG:N	2.78	0.52
7:I:167:GLU:O	7:I:169:LEU:HD12	2.10	0.51
5:D:91:ARG:CD	5:D:203:PHE:CE2	2.92	0.51
5:D:213:GLY:CA	5:D:216:GLN:HG2	2.40	0.51
1:1:12:A:C2	5:C:340:LEU:CD1	2.93	0.51
1:1:52:U:H4'	6:H:131:ARG:HH21	0.69	0.51
2:2:35:DT:C5'	4:A:129:ASP:OD1	2.54	0.51
4:A:461:ILE:HG22	4:A:493:TRP:CH2	2.35	0.51
5:C:46:TYR:OH	5:C:53:ASN:N	2.43	0.51
7:I:87:PRO:HB3	7:J:395:ARG:HH21	1.75	0.51
5:F:143:ARG:O	5:F:143:ARG:HG2	2.10	0.51
1:1:2:C:O2	4:A:466:ALA:O	2.28	0.51
1:1:15:G:H5''	5:B:40:SER:CB	2.41	0.51
1:1:1:C:O5'	4:A:206:PHE:HA	2.11	0.51
5:B:143:ARG:O	5:B:143:ARG:HG2	2.11	0.51
5:E:38:LYS:CD	5:F:224:PHE:CD2	2.94	0.51
1:1:2:C:O2	4:A:470:PHE:HB2	2.08	0.50
5:G:146:TYR:HE2	7:J:43:HIS:ND1	2.09	0.50
5:F:46:TYR:OH	5:F:53:ASN:N	2.44	0.50
7:J:204:LEU:C	7:J:204:LEU:HD12	2.37	0.50
1:1:3:A:H62	4:A:456:PRO:HD2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:491:LEU:O	4:A:491:LEU:CD1	2.51	0.50
7:J:46:ASP:C	7:J:46:ASP:OD2	2.53	0.50
5:D:143:ARG:HG2	5:D:143:ARG:O	2.11	0.50
5:F:10:SER:OG	5:F:95:ASN:ND2	2.45	0.50
7:I:130:PRO:HD3	7:I:160:TYR:HD2	1.69	0.50
7:J:241:GLU:OE1	7:J:241:GLU:N	2.39	0.50
3:3:7:DC:OP1	4:A:54:ARG:NH2	2.45	0.50
7:J:5:VAL:N	7:J:84:ASP:OD2	2.45	0.50
1:1:17:A:OP1	5:C:143:ARG:NH1	2.44	0.49
5:F:39:ILE:C	5:F:39:ILE:HD12	2.37	0.49
5:F:52:ALA:C	5:F:54:LEU:N	2.71	0.49
7:I:88:PHE:CD1	7:J:395:ARG:N	2.70	0.49
1:1:8:A:N1	5:B:142:TRP:CZ3	2.78	0.49
5:B:153:GLU:OE2	5:B:155:LYS:NZ	2.45	0.49
1:1:46:C:C4	6:H:163:TYR:HB3	2.47	0.49
5:F:66:TYR:OH	7:I:369:ARG:HB3	2.12	0.49
7:I:102:PHE:O	7:I:102:PHE:CG	2.65	0.49
7:I:128:CYS:HA	7:I:143:TRP:CH2	2.48	0.49
7:I:334:VAL:O	7:I:334:VAL:HG13	2.13	0.49
5:E:213:GLY:H	5:E:216:GLN:CG	2.24	0.49
2:2:12:DT:H4'	2:2:13:DG:OP1	2.13	0.49
5:D:268:TRP:H	5:D:268:TRP:CD1	2.30	0.49
5:D:288:LEU:HD11	5:E:6:HIS:CD2	2.46	0.49
7:I:391:LEU:HD23	7:I:391:LEU:C	2.38	0.48
1:1:33:U:C5	5:F:224:PHE:HA	2.48	0.48
1:1:39:C:C2	5:G:224:PHE:HE1	2.31	0.48
6:H:172:TYR:OH	6:H:174:ARG:HG3	2.13	0.48
5:E:306:LYS:HE2	5:E:306:LYS:HA	1.94	0.48
1:1:3:A:H62	4:A:456:PRO:CD	2.27	0.48
5:B:45:GLY:HA2	5:C:301:TYR:OH	2.14	0.48
5:D:38:LYS:HE3	5:E:224:PHE:CD2	2.48	0.48
5:E:213:GLY:CA	5:E:216:GLN:HG2	2.43	0.48
5:F:57:LYS:NZ	5:F:59:ILE:HD11	2.29	0.48
7:J:249:LEU:O	7:J:249:LEU:CD1	2.39	0.48
7:J:364:LEU:H	7:J:364:LEU:HD23	1.79	0.48
5:D:91:ARG:HG2	5:D:203:PHE:CE2	2.48	0.48
5:E:214:PHE:CD1	5:F:87:ARG:CZ	2.97	0.48
7:I:53:PHE:HD2	7:I:53:PHE:O	1.97	0.48
7:I:243:VAL:HG13	7:I:243:VAL:O	2.13	0.48
7:J:82:LEU:HD12	7:J:82:LEU:C	2.38	0.48
5:B:323:GLU:CD	5:B:323:GLU:H	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:146:TYR:OH	7:J:47:HIS:CG	2.67	0.48
5:D:46:TYR:OH	5:D:53:ASN:N	2.46	0.47
5:D:56:PRO:HG3	5:E:294:PRO:HB2	1.96	0.47
7:I:139:VAL:HG11	7:I:171:TYR:CE1	2.50	0.47
2:2:16:DT:H5''	5:D:227:ARG:HH21	1.78	0.47
5:D:323:GLU:CD	5:D:323:GLU:H	2.22	0.47
5:C:299:ASP:OD1	5:C:299:ASP:C	2.57	0.47
1:1:2:C:C4	4:A:470:PHE:CB	2.96	0.47
5:E:299:ASP:OD1	5:E:299:ASP:C	2.56	0.47
1:1:1:C:N4	4:A:205:ARG:NH2	2.53	0.47
5:C:214:PHE:CD1	5:D:87:ARG:NH2	2.82	0.47
5:E:264:ILE:O	5:E:264:ILE:CG1	2.52	0.47
6:H:64:ASN:OD1	6:H:64:ASN:C	2.57	0.47
6:H:201:ILE:HG13	6:H:201:ILE:O	2.13	0.47
7:J:364:LEU:HD23	7:J:364:LEU:N	2.29	0.47
1:1:23:U:O2	5:E:340:LEU:HD21	2.15	0.47
5:B:299:ASP:OD1	5:B:299:ASP:C	2.56	0.47
5:F:213:GLY:HA3	5:F:216:GLN:HG2	1.97	0.47
1:1:21:A:H5''	5:C:40:SER:CB	2.45	0.47
5:E:13:LEU:C	5:E:13:LEU:HD23	2.40	0.47
1:1:30:A:OP1	5:F:11:ARG:N	2.42	0.47
5:B:58:ASN:C	5:B:58:ASN:OD1	2.58	0.47
7:I:219:ILE:CG2	7:I:220:GLY:N	2.76	0.47
7:I:88:PHE:CD1	7:J:394:ALA:O	2.63	0.46
7:I:243:VAL:O	7:I:243:VAL:HG22	2.14	0.46
5:E:193:LYS:HE2	5:E:200:ILE:HD13	1.97	0.46
5:F:285:HIS:O	5:F:288:LEU:HD12	2.14	0.46
7:I:363:PHE:CE2	7:J:67:ARG:HG2	2.50	0.46
5:G:39:ILE:HD11	6:H:112:LEU:CD1	2.45	0.46
5:G:255:GLN:OE1	5:G:255:GLN:N	2.30	0.46
7:I:261:ASP:O	7:I:265:ARG:NH1	2.48	0.46
5:E:54:LEU:O	5:E:55:LYS:C	2.59	0.46
7:I:259:TRP:O	7:I:260:PRO:C	2.54	0.46
1:1:58:C:OP1	6:H:189:ASP:O	2.34	0.46
5:E:72:ILE:C	5:E:72:ILE:HD12	2.40	0.46
7:I:242:ALA:C	7:I:243:VAL:HG12	2.40	0.46
5:G:268:TRP:H	5:G:268:TRP:CD1	2.34	0.46
7:I:95:LEU:HD11	7:I:111:ARG:HD2	1.96	0.46
5:F:299:ASP:C	5:F:299:ASP:OD1	2.58	0.46
1:1:27:C:OP2	5:D:40:SER:HB3	2.16	0.46
2:2:16:DT:C5'	5:D:227:ARG:HH21	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:143:ARG:O	5:E:143:ARG:HG2	2.16	0.46
5:F:38:LYS:HZ1	5:G:226:GLU:CD	2.23	0.46
5:F:57:LYS:HZ2	5:F:57:LYS:CB	2.29	0.46
5:G:72:ILE:CD1	6:H:112:LEU:CG	2.75	0.46
7:I:175:GLU:OE1	7:I:175:GLU:N	2.34	0.46
5:D:13:LEU:C	5:D:13:LEU:HD23	2.41	0.45
5:E:323:GLU:CD	5:E:323:GLU:H	2.24	0.45
3:3:7:DC:OP1	4:A:54:ARG:CZ	2.65	0.45
3:3:2:DT:H2'	3:3:3:DA:C8	2.51	0.45
5:D:214:PHE:CD1	5:E:87:ARG:NH2	2.84	0.45
5:D:299:ASP:C	5:D:299:ASP:OD1	2.59	0.45
7:J:53:PHE:HD1	7:J:53:PHE:O	1.98	0.45
7:J:263:PHE:N	7:J:263:PHE:CD1	2.84	0.45
7:I:54:PRO:CG	7:I:59:ARG:HG2	2.47	0.45
5:B:38:LYS:CE	5:C:224:PHE:HD2	2.29	0.45
5:D:213:GLY:HA3	5:D:216:GLN:HE21	1.81	0.45
5:F:55:LYS:HA	5:F:55:LYS:HD2	1.45	0.45
7:I:138:TYR:CE1	7:I:140:ARG:HG2	2.52	0.45
1:1:29:A:H5''	5:E:143:ARG:NH1	2.32	0.45
5:G:38:LYS:HG3	5:G:69:PRO:CG	2.30	0.45
7:I:139:VAL:HG23	7:I:177:ILE:CD1	2.47	0.45
7:I:242:ALA:O	7:I:243:VAL:CG1	2.65	0.45
7:J:89:ARG:NE	7:J:89:ARG:HA	2.32	0.45
5:E:288:LEU:HD13	5:F:6:HIS:CD2	2.51	0.45
4:A:536:MET:CE	4:A:538:LEU:HD21	2.46	0.45
5:B:178:GLU:OE1	5:B:182:LYS:NZ	2.49	0.45
5:E:38:LYS:NZ	5:F:224:PHE:HE2	2.15	0.45
5:G:39:ILE:HG23	6:H:146:VAL:HG23	1.99	0.45
6:H:190:LEU:C	6:H:191:TYR:CD2	2.94	0.45
4:A:53:LYS:NZ	4:A:55:ASP:OD2	2.49	0.44
5:C:146:TYR:CD2	5:D:91:ARG:NH1	2.83	0.44
5:F:13:LEU:C	5:F:13:LEU:HD23	2.42	0.44
5:G:39:ILE:HD11	6:H:112:LEU:HD13	1.98	0.44
7:J:263:PHE:N	7:J:263:PHE:HD1	2.15	0.44
1:1:31:G:N1	5:E:70:GLN:HG3	2.29	0.44
3:3:4:DC:H2''	3:3:5:DC:H5''	1.98	0.44
5:B:46:TYR:C	5:B:48:GLU:H	2.26	0.44
7:I:130:PRO:HG2	7:I:160:TYR:CD2	2.51	0.44
1:1:6:A:H4'	5:B:338:GLY:O	2.17	0.44
1:1:33:U:C4	5:F:224:PHE:CG	3.03	0.44
5:F:213:GLY:HA3	5:F:216:GLN:CG	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:I:213:SER:HB3	7:I:219:ILE:CD1	2.47	0.44
5:C:13:LEU:HD23	5:C:13:LEU:C	2.43	0.44
5:G:299:ASP:OD1	5:G:299:ASP:C	2.59	0.44
4:A:485:SER:HB2	4:A:545:PRO:HG2	1.99	0.44
5:C:212:THR:OG1	5:C:213:GLY:N	2.51	0.44
5:C:288:LEU:HD12	5:D:6:HIS:CD2	2.46	0.44
5:G:13:LEU:C	5:G:13:LEU:HD23	2.43	0.44
5:G:273:ASP:CG	5:G:274:LEU:H	2.26	0.44
7:J:146:LYS:N	7:J:147:PRO:CD	2.80	0.44
5:B:38:LYS:CE	5:C:224:PHE:CD2	2.99	0.43
5:B:205:ASP:OD2	5:B:205:ASP:C	2.61	0.43
5:C:143:ARG:O	5:C:143:ARG:CG	2.66	0.43
5:E:216:GLN:OE1	5:F:91:ARG:NE	2.51	0.43
5:F:57:LYS:NZ	5:F:57:LYS:CB	2.80	0.43
1:1:19:G:P	5:D:11:ARG:HD3	2.57	0.43
5:F:62:TYR:OH	7:I:370:PRO:HB2	2.17	0.43
4:A:475:GLU:HB2	4:A:488:PHE:CE2	2.53	0.43
5:D:213:GLY:HA3	5:D:216:GLN:HG2	1.98	0.43
5:C:151:LYS:NZ	5:C:153:GLU:OE2	2.51	0.43
1:1:19:G:O6	5:C:70:GLN:CG	2.60	0.43
7:I:88:PHE:HZ	7:J:391:LEU:CD1	2.30	0.43
5:C:255:GLN:OE1	5:C:255:GLN:N	2.33	0.43
1:1:15:G:H5"	5:B:40:SER:HB2	2.01	0.43
5:G:176:TRP:HA	5:G:177:PRO:HD3	1.87	0.43
5:C:214:PHE:HE1	5:D:87:ARG:NH2	2.13	0.43
1:1:2:C:C5	4:A:470:PHE:HA	2.51	0.43
1:1:30:A:O2'	5:F:338:GLY:O	2.30	0.43
1:1:25:A:OP2	5:E:11:ARG:CZ	2.67	0.42
5:B:143:ARG:O	5:B:143:ARG:CG	2.67	0.42
5:C:54:LEU:O	5:C:55:LYS:C	2.57	0.42
5:F:143:ARG:O	5:F:143:ARG:CG	2.67	0.42
7:I:246:ASP:OD1	7:I:247:ARG:N	2.50	0.42
5:B:98:ARG:HA	5:B:99:PRO:HD3	1.96	0.42
5:D:38:LYS:CE	5:E:224:PHE:CD2	3.03	0.42
7:J:5:VAL:HG22	7:J:5:VAL:O	2.19	0.42
5:C:265:ASP:OD2	5:C:265:ASP:C	2.59	0.42
5:D:153:GLU:OE2	5:D:155:LYS:NZ	2.52	0.42
5:D:176:TRP:HA	5:D:177:PRO:HD3	1.84	0.42
5:D:273:ASP:CG	5:D:274:LEU:H	2.28	0.42
7:I:364:LEU:CD1	7:I:383:PHE:CE2	3.03	0.42
5:D:54:LEU:O	5:D:55:LYS:C	2.58	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:46:TYR:OH	5:E:53:ASN:N	2.52	0.42
5:E:273:ASP:CG	5:E:274:LEU:H	2.28	0.42
7:J:53:PHE:O	7:J:53:PHE:CD1	2.73	0.42
7:J:171:TYR:CD2	7:J:171:TYR:C	2.97	0.42
1:1:21:A:H5''	5:C:40:SER:HB2	2.01	0.42
4:A:627:ASP:OD1	4:A:628:ARG:N	2.50	0.42
5:D:337:LYS:O	5:D:337:LYS:HG2	2.20	0.42
2:2:28:DG:H2'	2:2:29:DT:C5	2.55	0.42
7:I:87:PRO:HB2	7:J:395:ARG:NE	2.34	0.42
7:I:148:TYR:CE2	7:I:159:ILE:HD11	2.55	0.42
5:G:39:ILE:HD12	6:H:146:VAL:CG2	2.11	0.42
7:I:53:PHE:CD2	7:I:53:PHE:C	2.97	0.42
5:C:337:LYS:O	5:C:337:LYS:HG2	2.19	0.41
1:1:33:U:C4	5:F:224:PHE:CE2	3.05	0.41
5:E:55:LYS:NZ	5:E:57:LYS:O	2.52	0.41
6:H:131:ARG:HD3	6:H:133:GLU:OE1	2.21	0.41
2:2:29:DT:H2''	2:2:30:DC:C6	2.55	0.41
5:B:38:LYS:HE3	5:C:224:PHE:HD2	1.80	0.41
5:C:38:LYS:HG2	5:D:224:PHE:CD2	2.55	0.41
5:E:143:ARG:O	5:E:143:ARG:CG	2.69	0.41
5:E:193:LYS:HE3	5:E:197:GLN:OE1	2.20	0.41
7:I:53:PHE:O	7:I:53:PHE:CD2	2.74	0.41
7:I:259:TRP:CD1	7:I:259:TRP:C	2.98	0.41
7:I:327:PRO:HG3	7:J:81:ARG:HH12	1.85	0.41
1:1:29:A:H5''	5:E:143:ARG:HH12	1.85	0.41
5:F:268:TRP:CD1	5:F:268:TRP:H	2.38	0.41
7:J:310:PHE:CD1	7:J:310:PHE:C	2.98	0.41
2:2:25:DC:H2''	2:2:26:DC:O4'	2.20	0.41
5:C:176:TRP:HA	5:C:177:PRO:HD3	1.88	0.41
6:H:98:CYS:SG	6:H:99:GLN:N	2.93	0.41
5:B:14:SER:HA	5:B:15:PRO:HD3	1.83	0.41
5:C:273:ASP:CG	5:C:274:LEU:H	2.28	0.41
5:G:265:ASP:OD2	5:G:265:ASP:C	2.62	0.41
6:H:102:ARG:HB3	6:H:104:ILE:HG13	2.02	0.41
1:1:33:U:C6	5:F:224:PHE:HA	2.55	0.41
5:D:98:ARG:HA	5:D:99:PRO:HD3	1.97	0.41
5:D:143:ARG:O	5:D:143:ARG:CG	2.69	0.41
5:E:46:TYR:C	5:E:47:THR:HG23	2.46	0.41
7:I:130:PRO:CD	7:I:160:TYR:CE2	2.88	0.41
7:J:53:PHE:CD1	7:J:53:PHE:C	2.99	0.41
1:1:12:A:C2	5:C:340:LEU:HG	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:91:ARG:HG2	5:C:203:PHE:CD2	2.56	0.41
5:F:213:GLY:CA	5:F:216:GLN:CG	2.98	0.41
5:G:212:THR:OG1	5:G:213:GLY:N	2.54	0.41
7:I:54:PRO:HG3	7:I:59:ARG:CG	2.51	0.41
5:B:13:LEU:HD13	5:B:92:VAL:HG22	1.96	0.40
7:I:216:LEU:HD12	7:I:259:TRP:CD1	2.56	0.40
5:E:214:PHE:CE1	5:F:87:ARG:CZ	3.01	0.40
7:J:338:LEU:N	7:J:338:LEU:HD22	2.36	0.40
1:I:45:U:N3	6:H:113:PHE:CZ	2.90	0.40
2:2:17:DG:H5'	2:2:17:DG:H8	1.84	0.40
5:D:213:GLY:HA3	5:D:216:GLN:CG	2.51	0.40
5:E:36:VAL:HG13	5:E:36:VAL:O	2.21	0.40
5:F:57:LYS:HZ2	5:F:59:ILE:HD11	1.86	0.40
2:2:20:DT:H1'	5:C:66:TYR:HB3	2.02	0.40
4:A:107:ALA:HA	4:A:108:PRO:HD3	1.95	0.40
7:I:54:PRO:CB	7:I:59:ARG:HE	2.33	0.40
5:C:46:TYR:C	5:C:47:THR:HG23	2.46	0.40
5:C:245:ASP:OD1	5:C:245:ASP:C	2.65	0.40
5:F:59:ILE:H	5:F:59:ILE:HG12	1.48	0.40
7:I:286:ASP:O	7:I:287:PHE:C	2.63	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	
4	A	497/704 (71%)	493 (99%)	4 (1%)	0	100	100
5	B	340/347 (98%)	328 (96%)	12 (4%)	0	100	100
5	C	340/347 (98%)	324 (95%)	16 (5%)	0	100	100
5	D	340/347 (98%)	326 (96%)	14 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	E	340/347 (98%)	330 (97%)	10 (3%)	0	100	100
5	F	340/347 (98%)	325 (96%)	13 (4%)	2 (1%)	21	57
5	G	292/347 (84%)	284 (97%)	8 (3%)	0	100	100
6	H	200/206 (97%)	196 (98%)	4 (2%)	0	100	100
7	I	383/410 (93%)	360 (94%)	22 (6%)	1 (0%)	36	69
7	J	368/410 (90%)	359 (98%)	8 (2%)	1 (0%)	36	69
All	All	3440/3812 (90%)	3325 (97%)	111 (3%)	4 (0%)	49	80

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	F	53	ASN
5	F	59	ILE
7	I	144	HIS
7	J	208	CYS

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	
4	A	423/597 (71%)	423 (100%)	0	100	100
5	B	289/293 (99%)	289 (100%)	0	100	100
5	C	289/293 (99%)	289 (100%)	0	100	100
5	D	289/293 (99%)	289 (100%)	0	100	100
5	E	289/293 (99%)	289 (100%)	0	100	100
5	F	289/293 (99%)	285 (99%)	4 (1%)	59	71
5	G	256/293 (87%)	256 (100%)	0	100	100
6	H	172/176 (98%)	172 (100%)	0	100	100
7	I	331/351 (94%)	331 (100%)	0	100	100
7	J	319/351 (91%)	319 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	2946/3233 (91%)	2942 (100%)	4 (0%)	87 89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	F	54	LEU
5	F	55	LYS
5	F	57	LYS
5	F	59	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
4	A	155	GLN
5	B	163	HIS
5	B	216	GLN
5	B	329	HIS
5	D	6	HIS
5	D	231	HIS
5	D	329	HIS
5	E	6	HIS
5	F	6	HIS
5	F	95	ASN
5	F	216	GLN
5	F	329	HIS
5	F	342	GLN
5	G	6	HIS
6	H	100	ASN
6	H	136	GLN
6	H	166	HIS
6	H	188	ASN
7	I	43	HIS
7	I	77	GLN
7	I	359	HIS
7	J	179	HIS
7	J	234	GLN
7	J	255	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	59/60 (98%)	28 (47%)	0

All (28) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	3	A
1	1	9	A
1	1	13	C
1	1	14	U
1	1	15	G
1	1	20	A
1	1	21	A
1	1	22	A
1	1	24	C
1	1	25	A
1	1	26	U
1	1	27	C
1	1	30	A
1	1	31	G
1	1	32	U
1	1	33	U
1	1	34	G
1	1	36	G
1	1	39	C
1	1	40	U
1	1	41	A
1	1	42	U
1	1	43	U
1	1	44	U
1	1	45	U
1	1	46	C
1	1	55	A
1	1	60	G

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

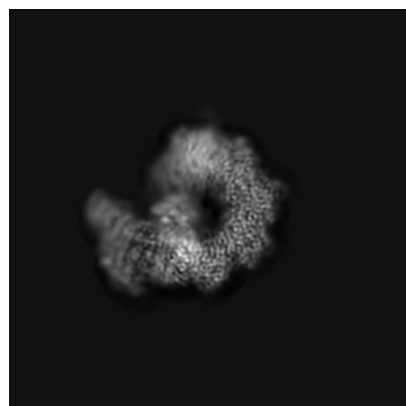
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26349. These allow visual inspection of the internal detail of the map and identification of artifacts.

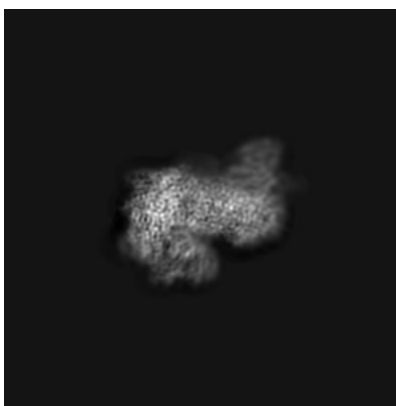
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

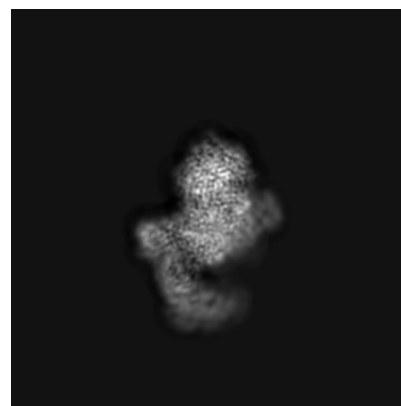
6.1.1 Primary map



X

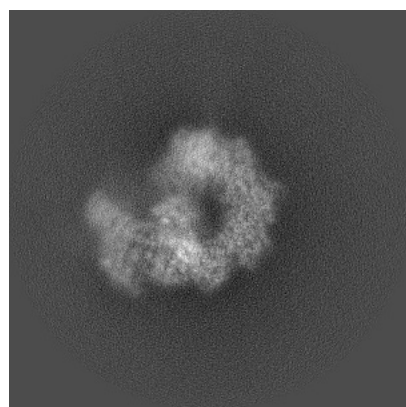


Y

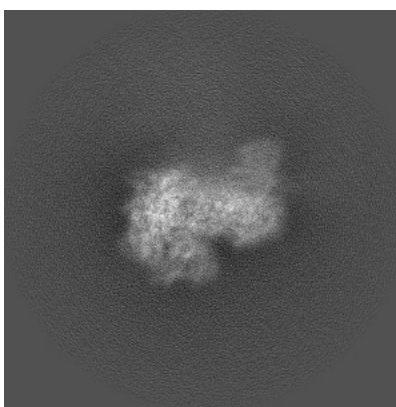


Z

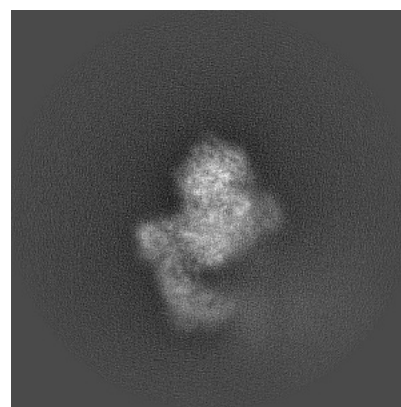
6.1.2 Raw map



X



Y

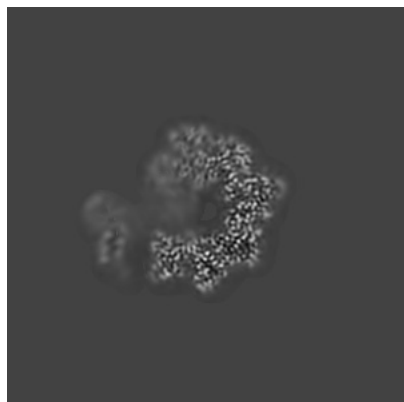


Z

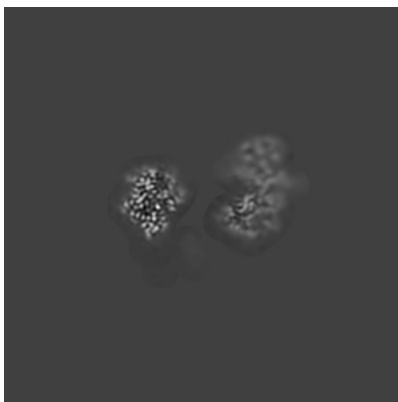
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

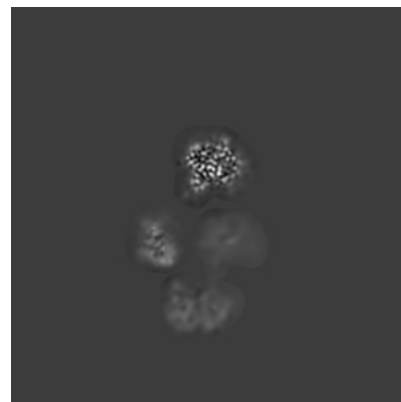
6.2.1 Primary map



X Index: 210

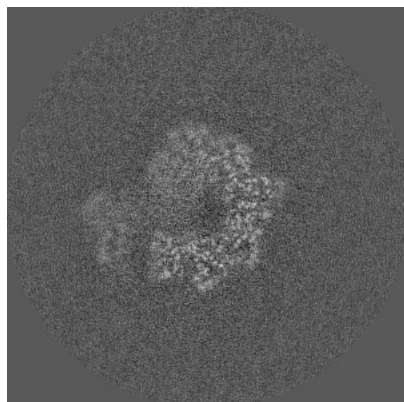


Y Index: 210

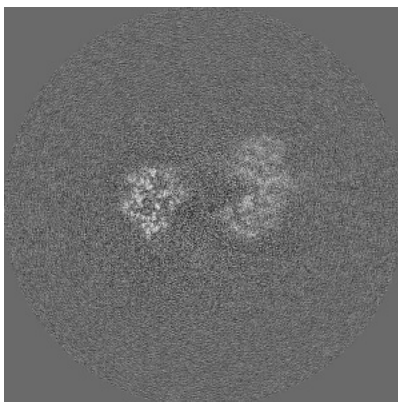


Z Index: 210

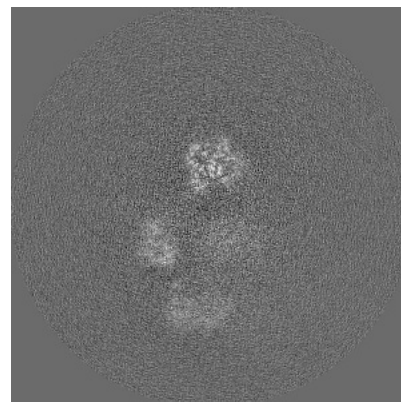
6.2.2 Raw map



X Index: 210



Y Index: 210

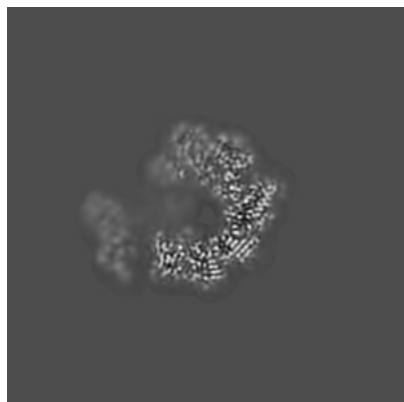


Z Index: 210

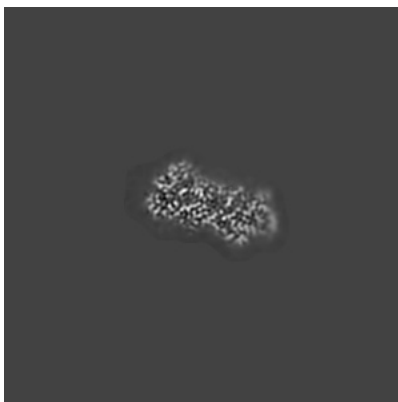
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

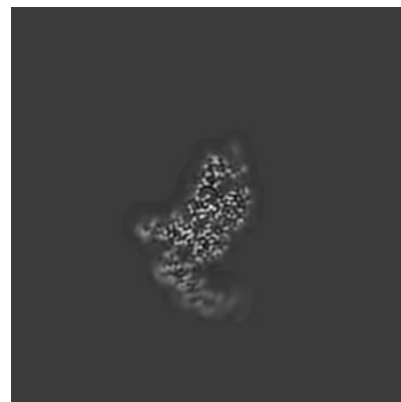
6.3.1 Primary map



X Index: 204

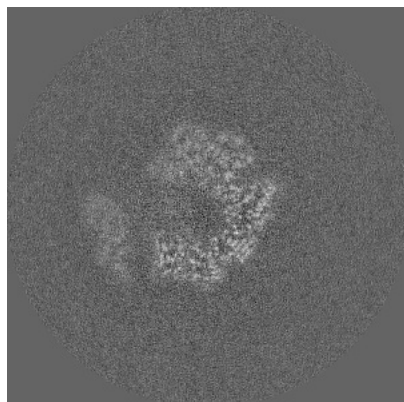


Y Index: 243

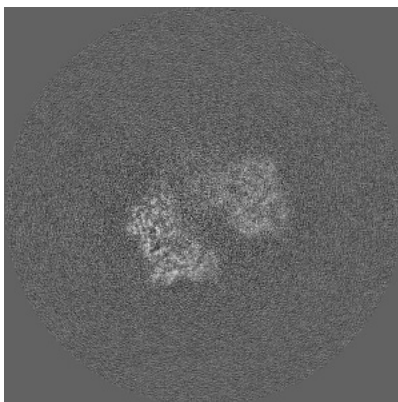


Z Index: 161

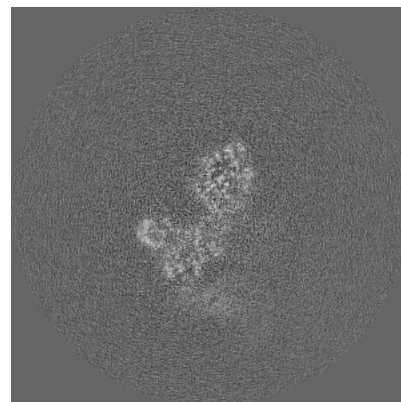
6.3.2 Raw map



X Index: 204



Y Index: 183

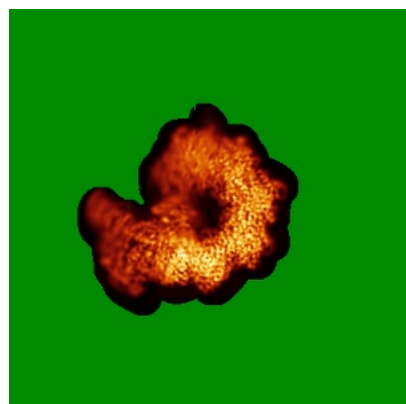


Z Index: 176

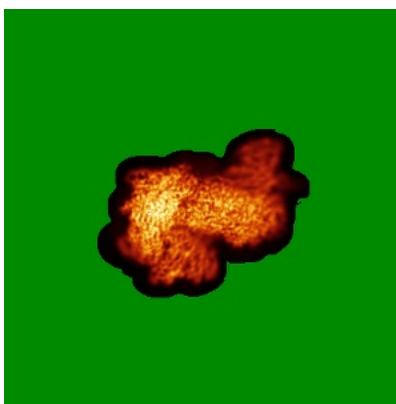
The images above show the largest variance slices of the map in three orthogonal directions.

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

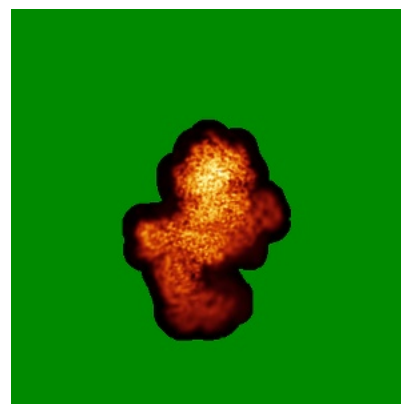
6.4.1 Primary map



X

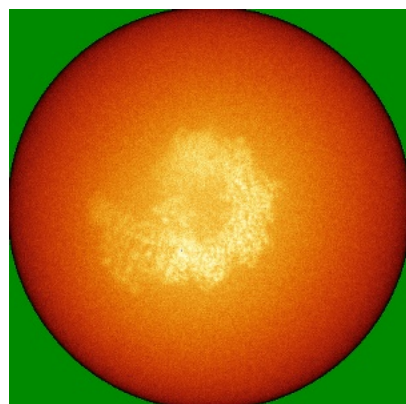


Y

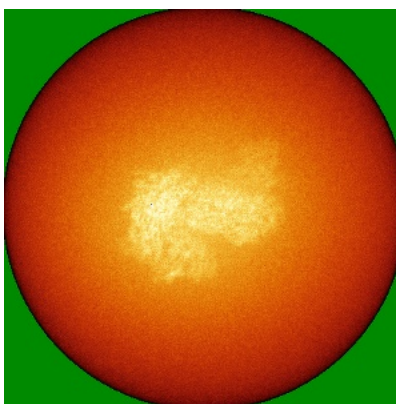


Z

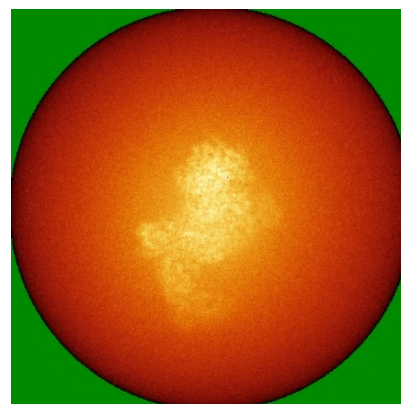
6.4.2 Raw map



X



Y

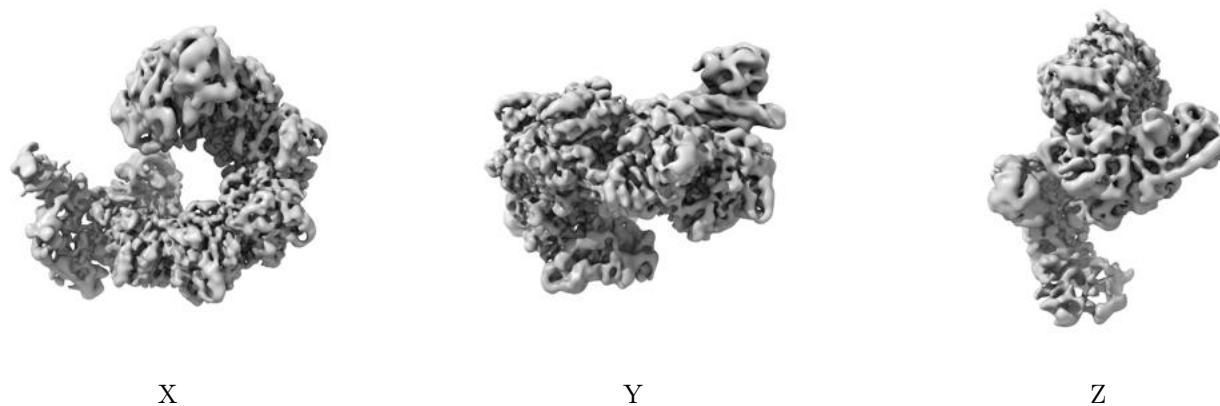


Z

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.

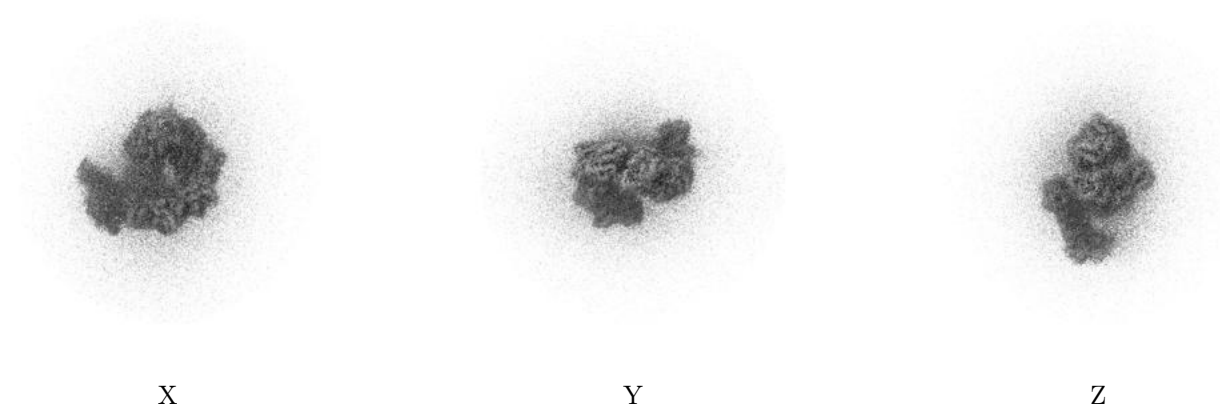
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.007. 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.

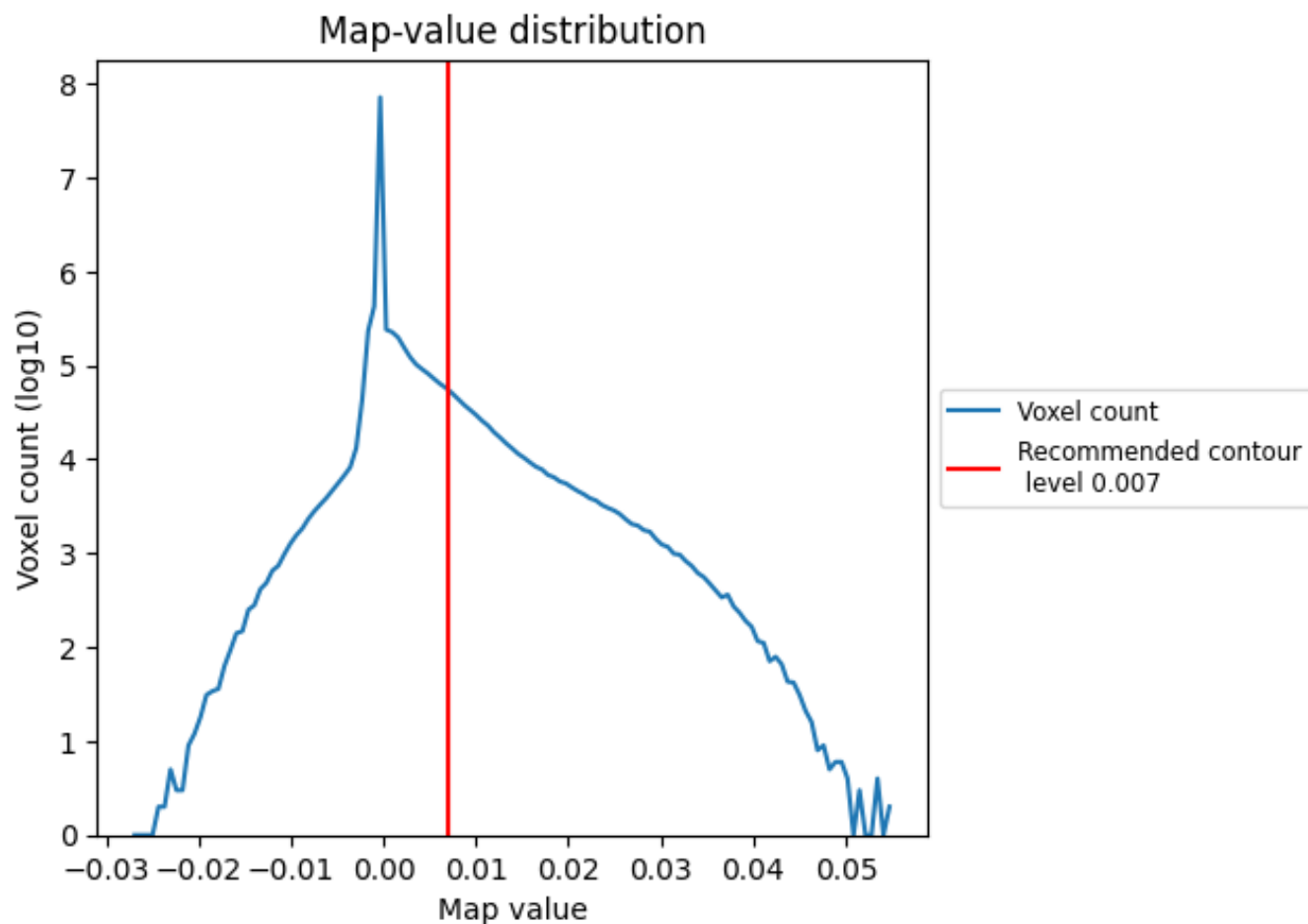
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

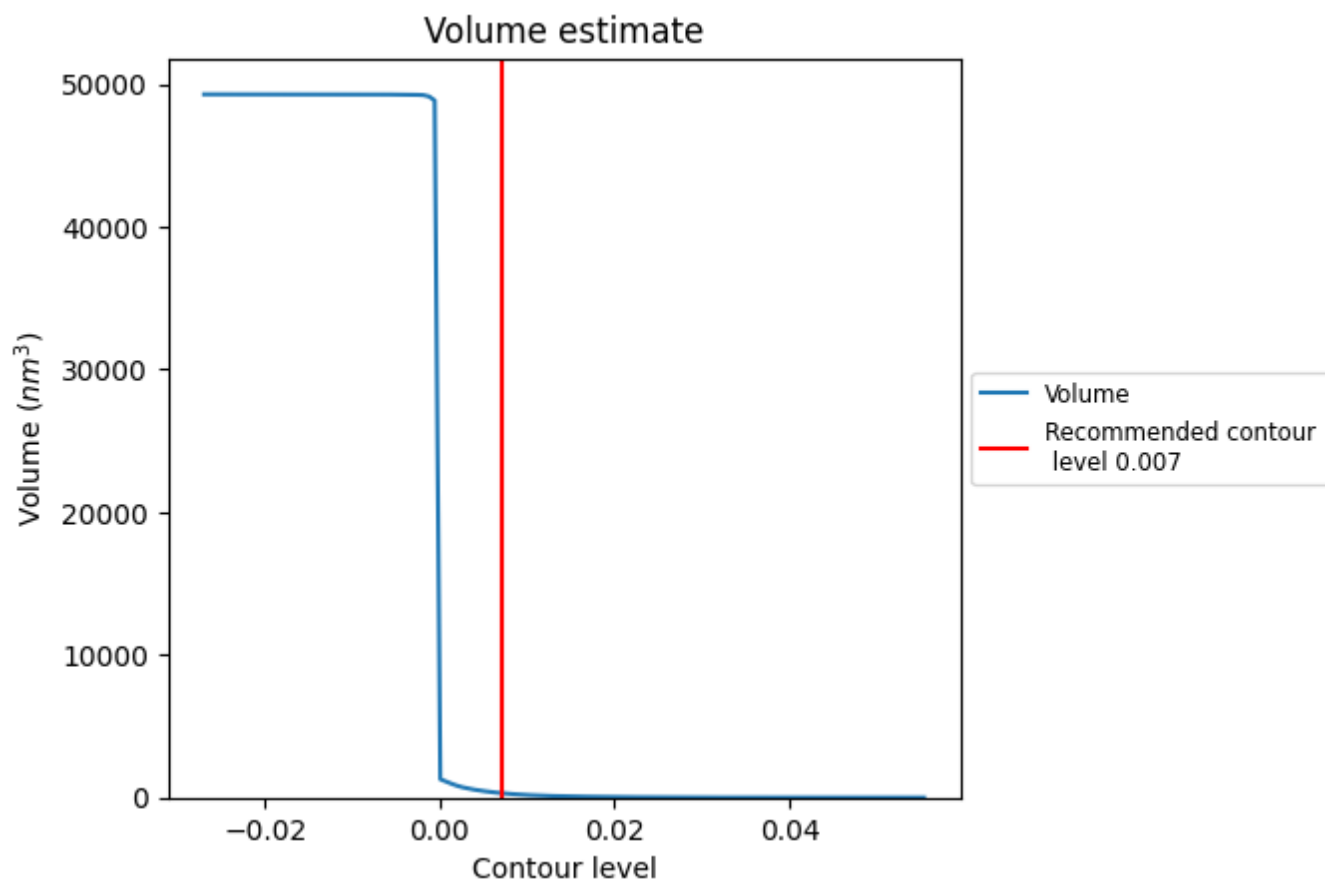
This section contains the results of statistical analysis of the map.

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.

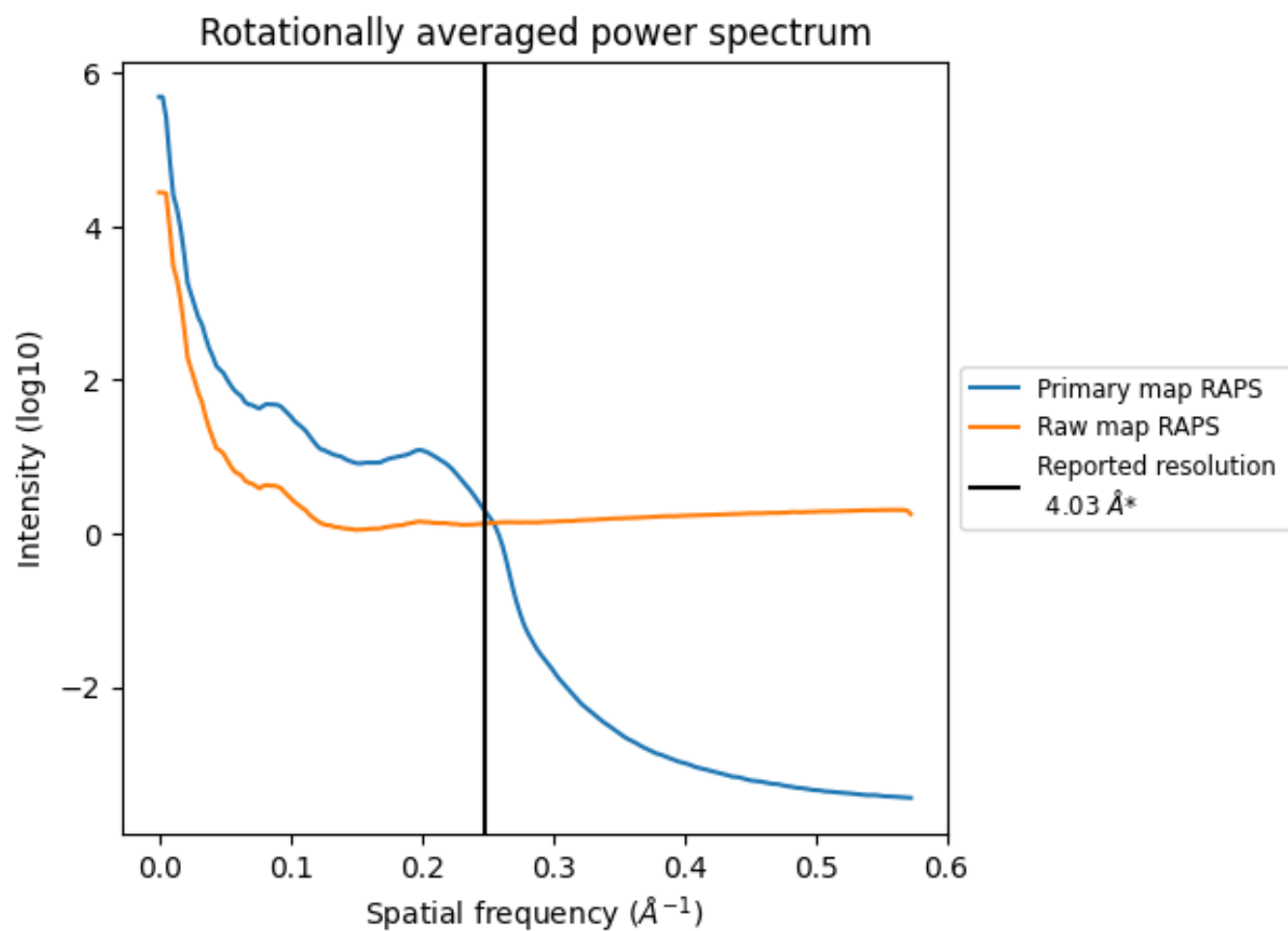
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 314 nm³; this corresponds to an approximate mass of 283 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 0.248 $\text{\AA}^{-1}$

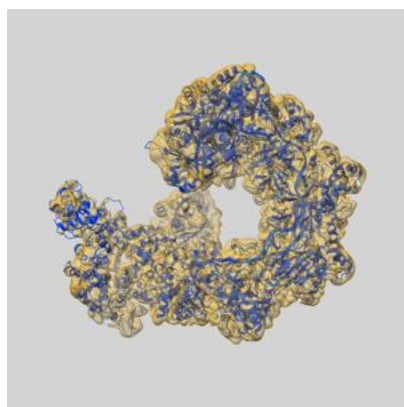
8 Fourier-Shell correlation ⓘ

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

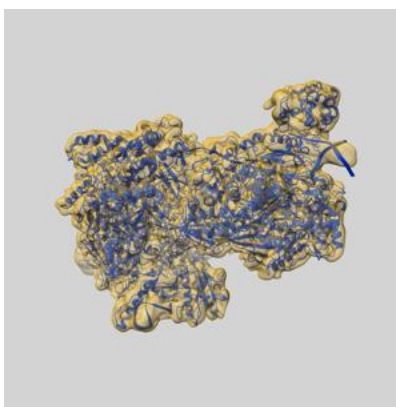
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26349 and PDB model 7U5E. Per-residue inclusion information can be found in section [3](#) on page [6](#).

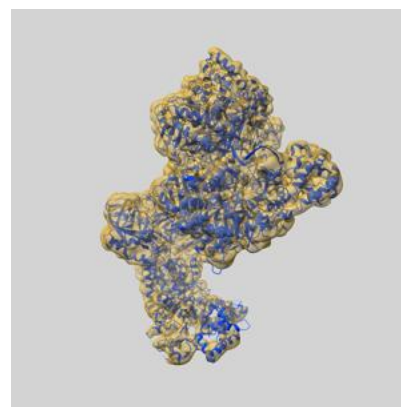
9.1 Map-model overlay [i](#)



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.007 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

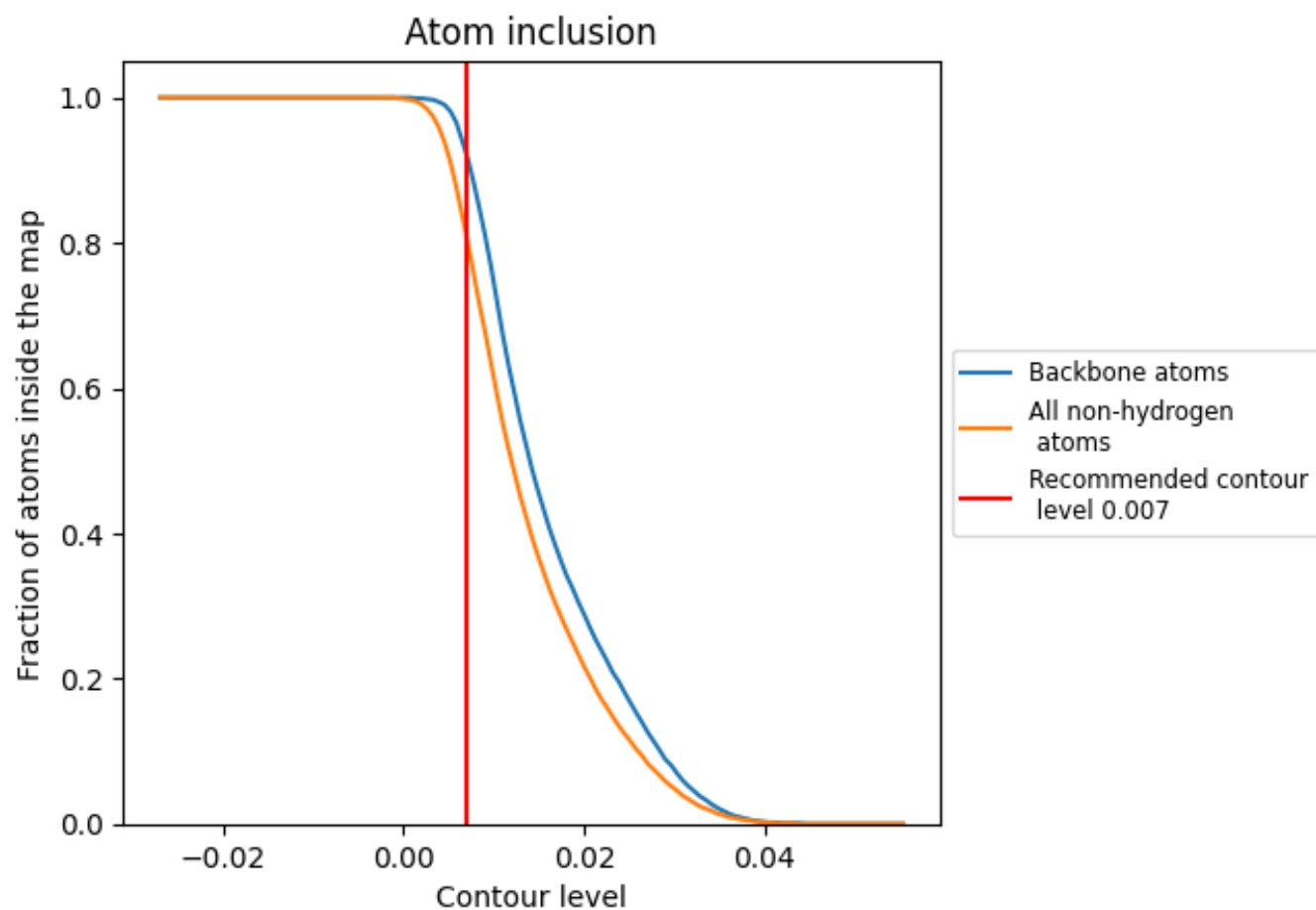


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 81% 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 (0.007) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8100	 0.3510
1	 0.9710	 0.4240
2	 0.9210	 0.3870
3	 0.7390	 0.2500
A	 0.7090	 0.2060
B	 0.8030	 0.3210
C	 0.8990	 0.4240
D	 0.9110	 0.4520
E	 0.9090	 0.4590
F	 0.9020	 0.4530
G	 0.8990	 0.4390
H	 0.8630	 0.3180
I	 0.5770	 0.2520
J	 0.6430	 0.2390

