



Full wwPDB EM Validation Report ⓘ

Apr 11, 2024 – 11:23 am BST

PDB ID : 9EOJ
EMDB ID : EMD-19861
Title : Vertebrate microtubule-capping gamma-tubulin ring complex
Authors : Vermeulen, B.J.A.; Pfeffer, S.
Deposited on : 2024-03-15
Resolution : 17.00 Å (reported)
Based on initial models : 6TF9, .

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:

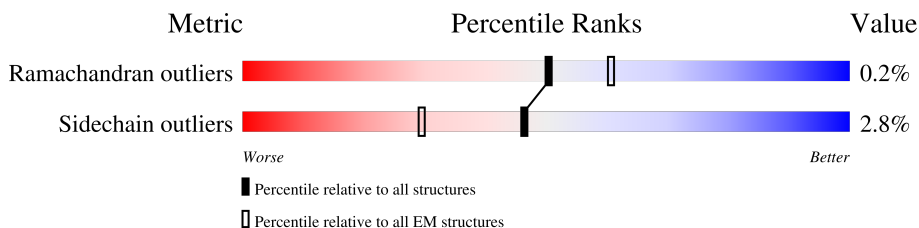
EMDB validation analysis : 0.0.1.dev92
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

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 17.00 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	B	72	65% (red), 76% (orange), 22% (grey)
1	D	72	31% (red), 71% (orange), 28% (grey)
2	Q	906	16% (red), 66% (orange), 31% (grey)
2	c	906	11% (red), 68% (orange), 31% (grey)
2	d	906	11% (red), 67% (orange), 31% (grey)
2	e	906	14% (red), 77% (orange), 21% (grey)
2	f	906	40% (red), 67% (orange), 31% (grey)
3	R	896	20% (red), 61% (orange), 38% (grey)
3	Y	896	7% (red), 60% (orange), 38% (grey)

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Mol	Chain	Length	Quality of chain
3	Z	896	6% 60% 39%
3	a	896	21% 61% 39%
3	b	896	6% 61% 38%
4	S	1698	9% 37% 61%
5	T	451	33% 92% ..
5	h	451	28% 92% ..
5	i	451	18% 92% ..
5	k	451	12% 92% ..
5	l	451	18% 92% ..
5	m	451	25% 92% ..
5	n	451	13% 92% ..
5	o	451	12% 92% ..
5	p	451	13% 92% ..
5	q	451	16% 92% ..
5	r	451	20% 92% ..
5	s	451	12% 92% ..
5	t	451	16% 92% ..
5	w	451	32% 92% ..
6	U	1019	5% 54% 44%
7	V	666	15% 81% 5% 14%
7	W	666	9% 81% 14%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 117778 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 Mitotic-spindle organizing protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	B	56	Total	C	N	O	S	0	0
			429	263	73	89	4		
1	D	52	Total	C	N	O	S	0	0
			403	248	71	79	5		

- Molecule 2 is a protein called Gamma-tubulin complex component 3 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	Q	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		
2	c	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		
2	d	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		
2	e	718	Total	C	N	O	S	0	0
			5871	3756	1017	1070	28		
2	f	625	Total	C	N	O	S	0	0
			5118	3276	880	936	26		

- Molecule 3 is a protein called Gamma-tubulin complex component.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	R	553	Total	C	N	O	S	0	0
			4519	2904	742	841	32		
3	Y	553	Total	C	N	O	S	0	0
			4519	2904	742	841	32		
3	Z	551	Total	C	N	O	S	0	0
			4508	2898	740	838	32		
3	a	551	Total	C	N	O	S	0	0
			4503	2894	739	838	32		
3	b	553	Total	C	N	O	S	0	0
			4519	2904	742	841	32		

- Molecule 4 is a protein called Gamma-tubulin complex component 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	S	661	5380	3507	877	968	28	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S	392	ASP	GLU	conflict	UNP A0A974HT83
S	394	VAL	ILE	conflict	UNP A0A974HT83

- Molecule 5 is a protein called Tubulin gamma-1 chain.

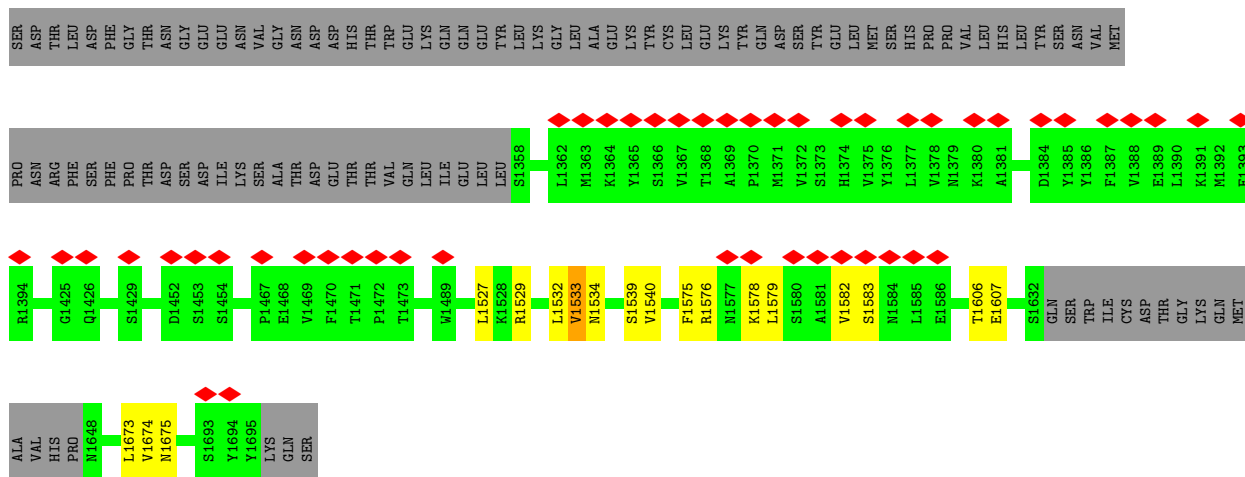
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	T	436	3479	2188	615	662	14	0	0
5	h	436	3479	2188	615	662	14	0	0
5	i	436	3479	2188	615	662	14	0	0
5	k	436	3479	2188	615	662	14	0	0
5	l	436	3479	2188	615	662	14	0	0
5	m	436	3479	2188	615	662	14	0	0
5	n	436	3479	2188	615	662	14	0	0
5	o	436	3479	2188	615	662	14	0	0
5	p	436	3479	2188	615	662	14	0	0
5	q	436	3479	2188	615	662	14	0	0
5	r	436	3479	2188	615	662	14	0	0
5	s	436	3479	2188	615	662	14	0	0
5	t	436	3479	2188	615	662	14	0	0
5	w	436	3479	2188	615	662	14	0	0

- Molecule 6 is a protein called Gamma-tubulin complex component.

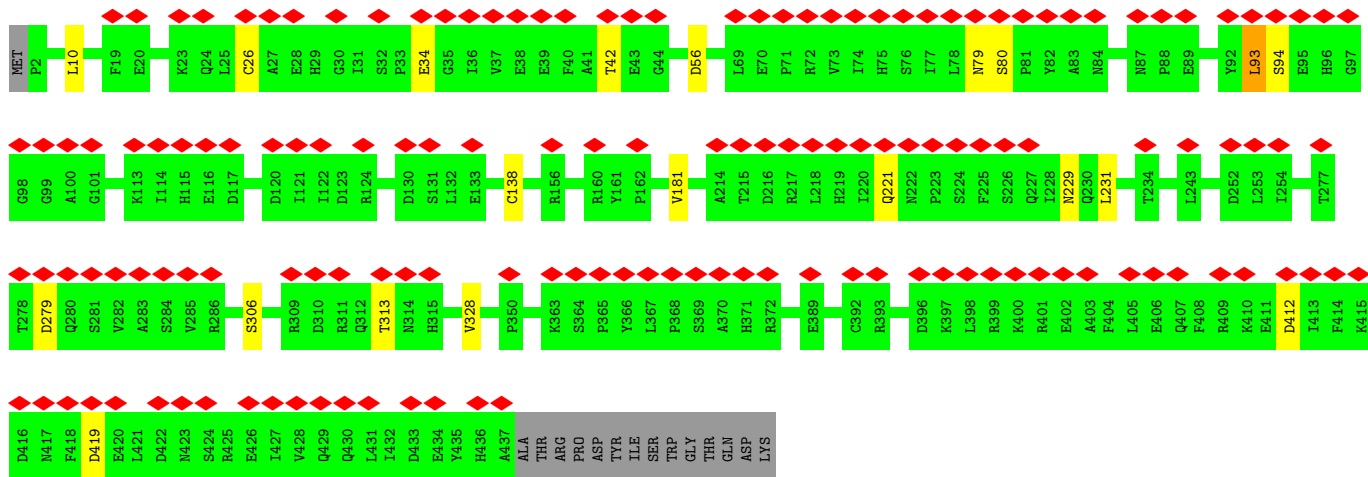
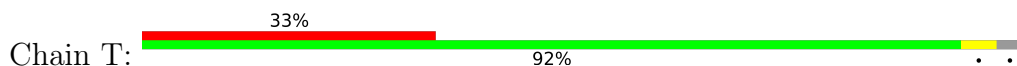
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	U	569	4679	3041	787	825	26	0	0

- Molecule 7 is a protein called Gamma-tubulin complex component.

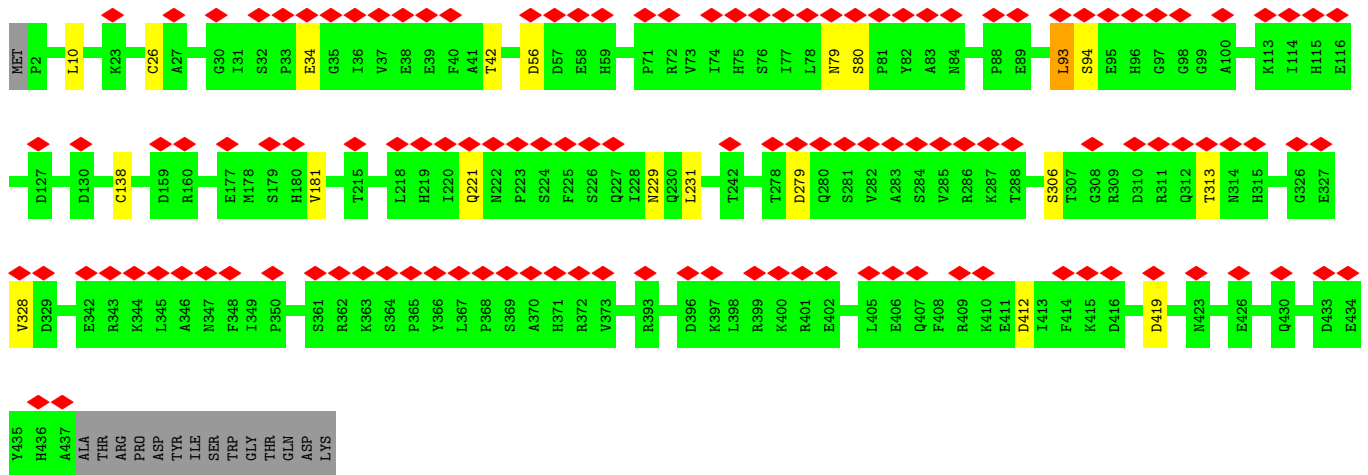
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	V	571	4635	2993	790	831	21	0	0
7	W	571	4635	2993	790	831	21	0	0



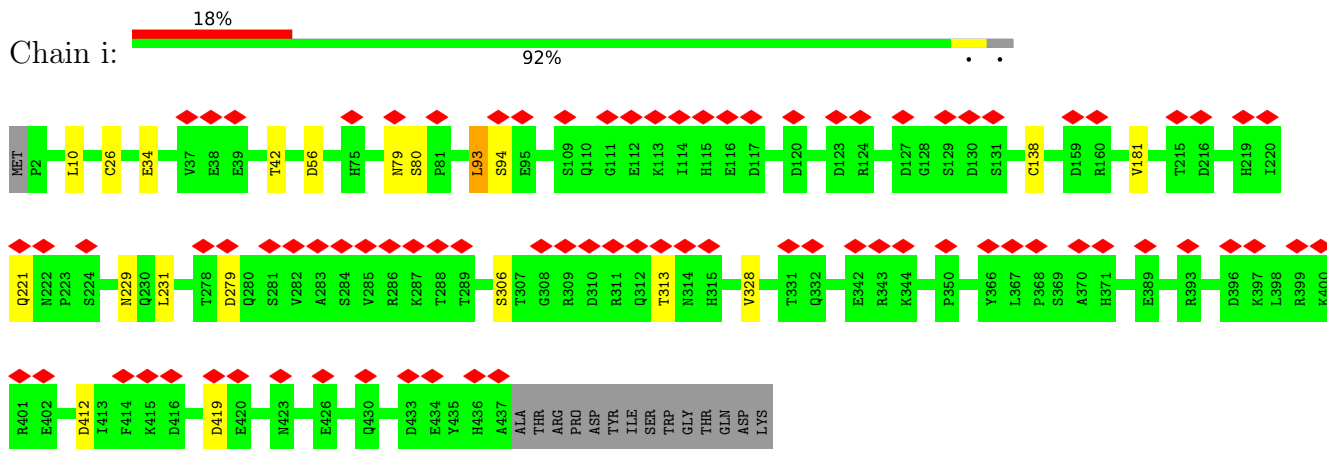
• Molecule 5: Tubulin gamma-1 chain



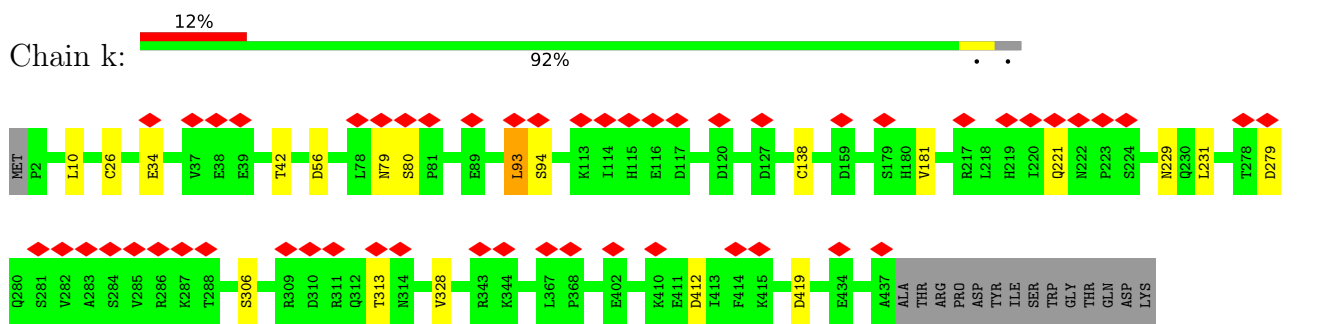
• Molecule 5: Tubulin gamma-1 chain



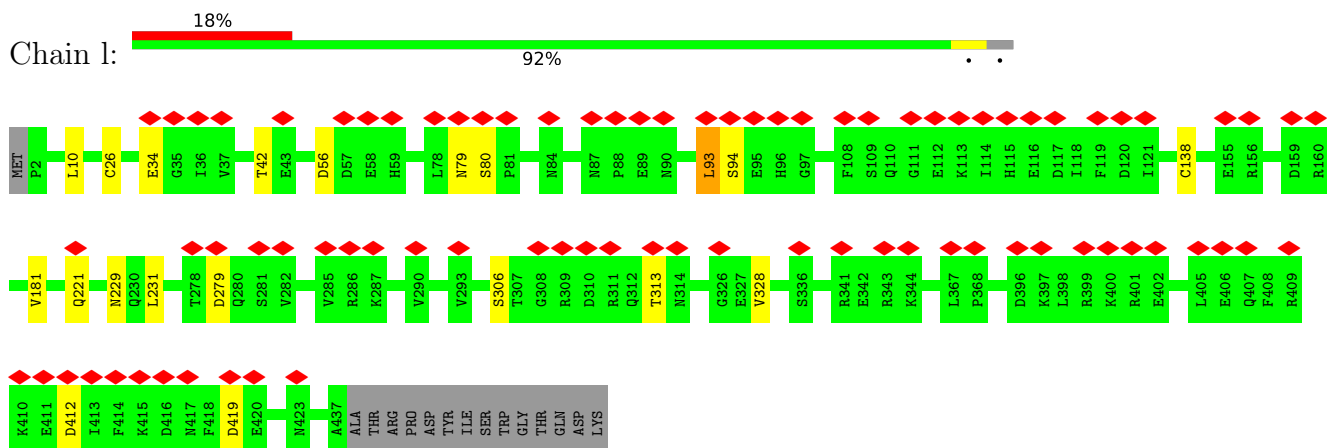
• Molecule 5: Tubulin gamma-1 chain



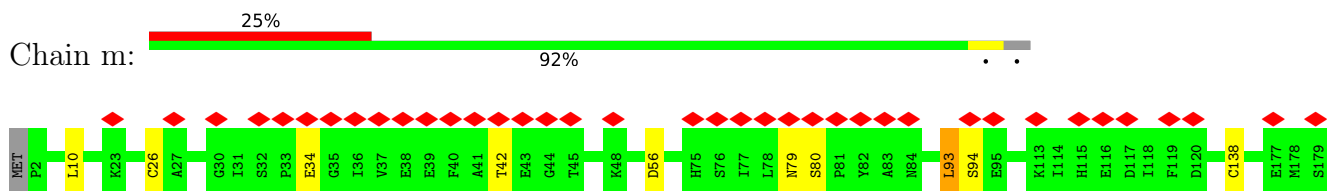
• Molecule 5: Tubulin gamma-1 chain

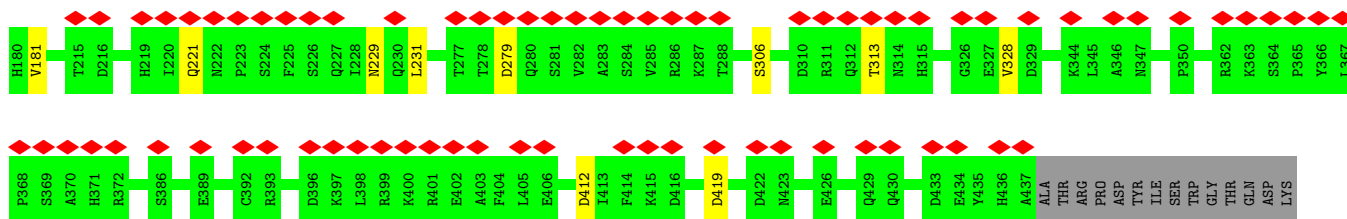


• Molecule 5: Tubulin gamma-1 chain

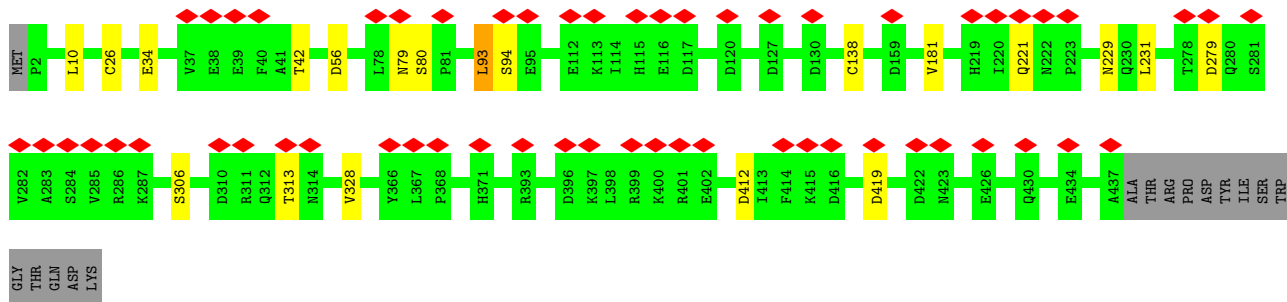


• Molecule 5: Tubulin gamma-1 chain

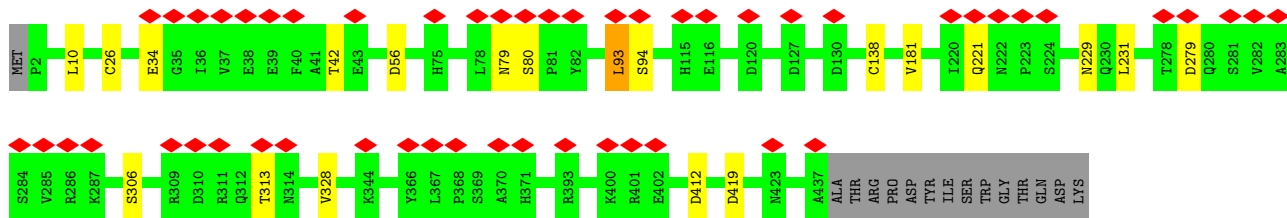
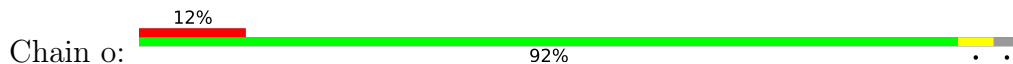




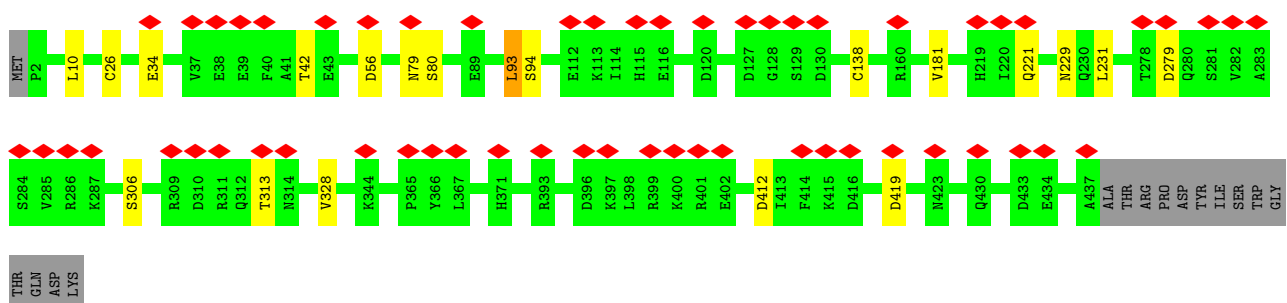
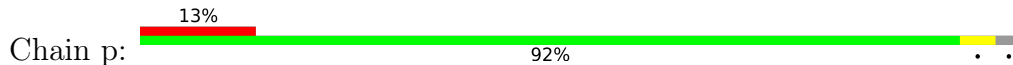
• Molecule 5: Tubulin gamma-1 chain



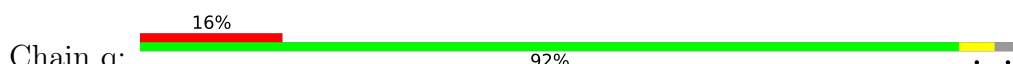
• Molecule 5: Tubulin gamma-1 chain

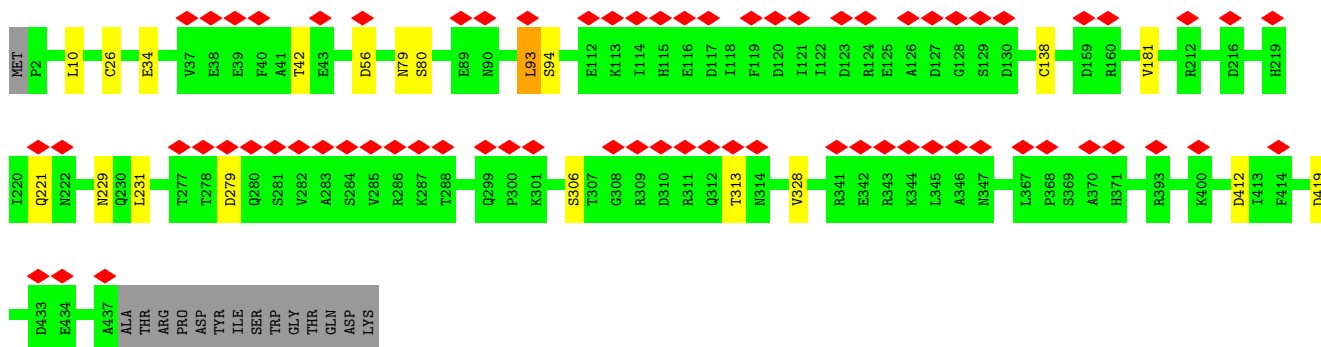


• Molecule 5: Tubulin gamma-1 chain

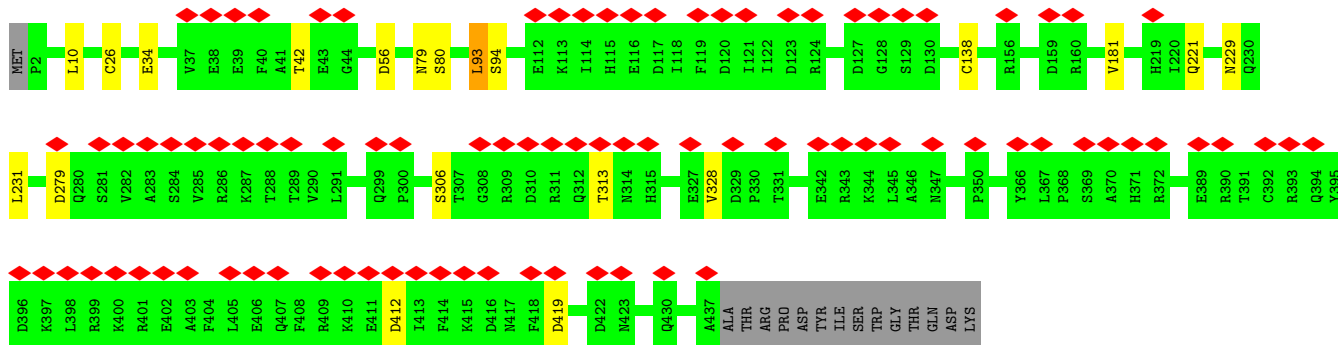


• Molecule 5: Tubulin gamma-1 chain

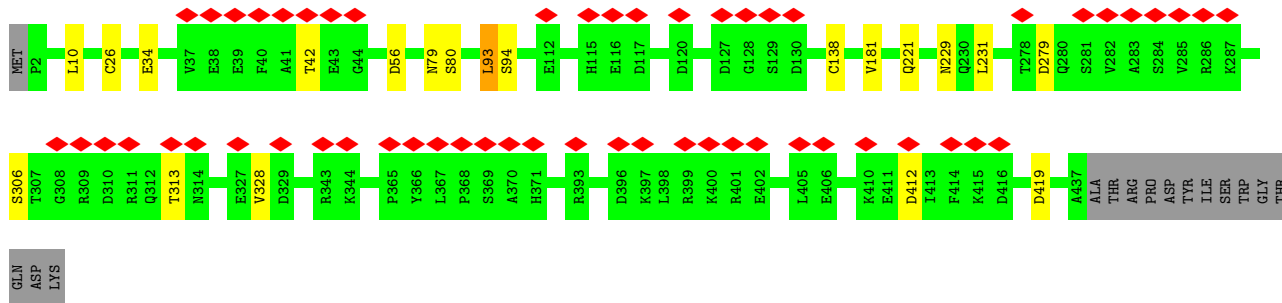




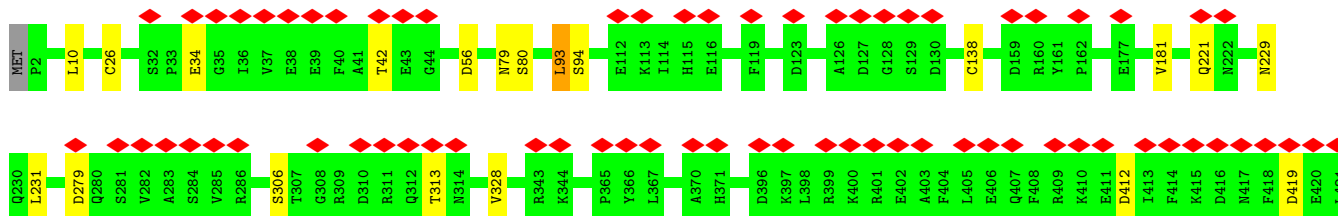
• Molecule 5: Tubulin gamma-1 chain

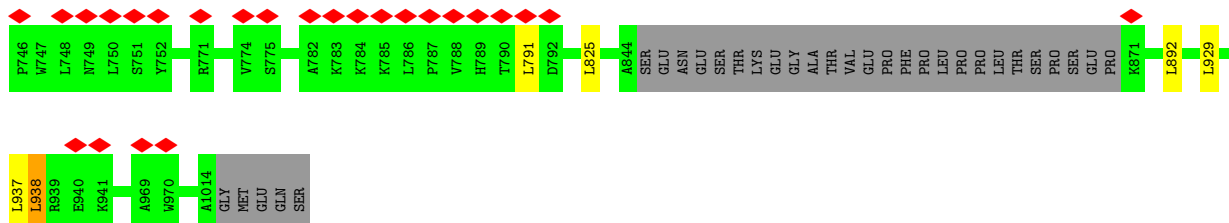


• Molecule 5: Tubulin gamma-1 chain

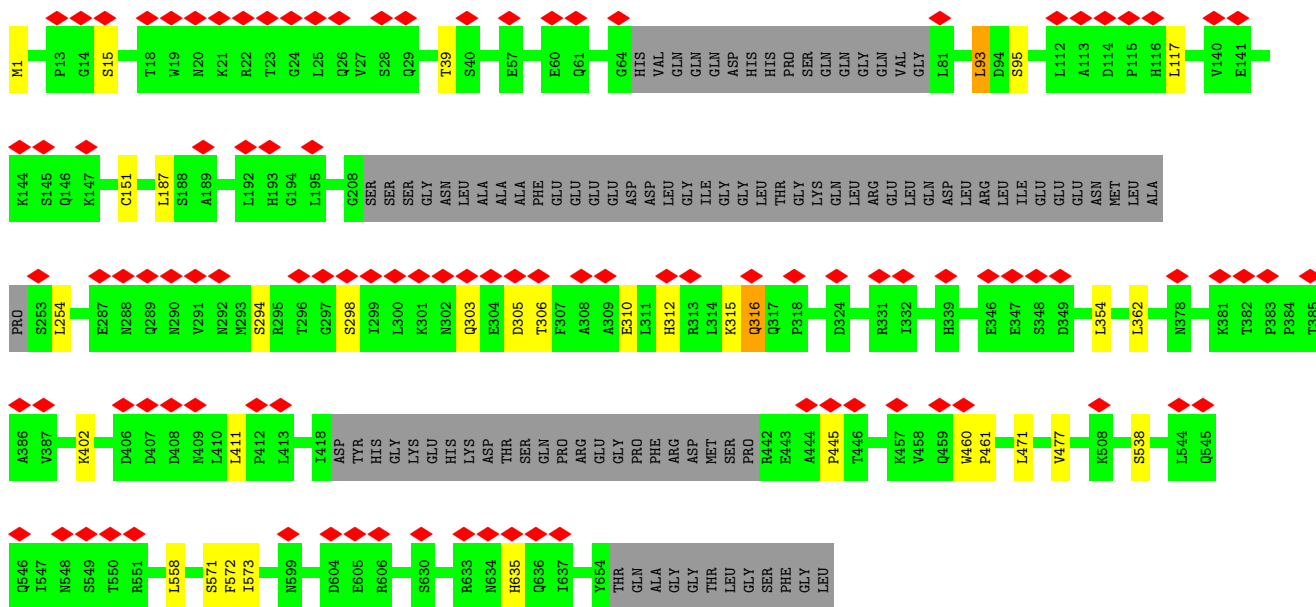
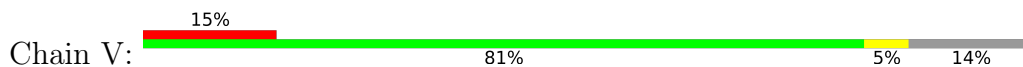


• Molecule 5: Tubulin gamma-1 chain

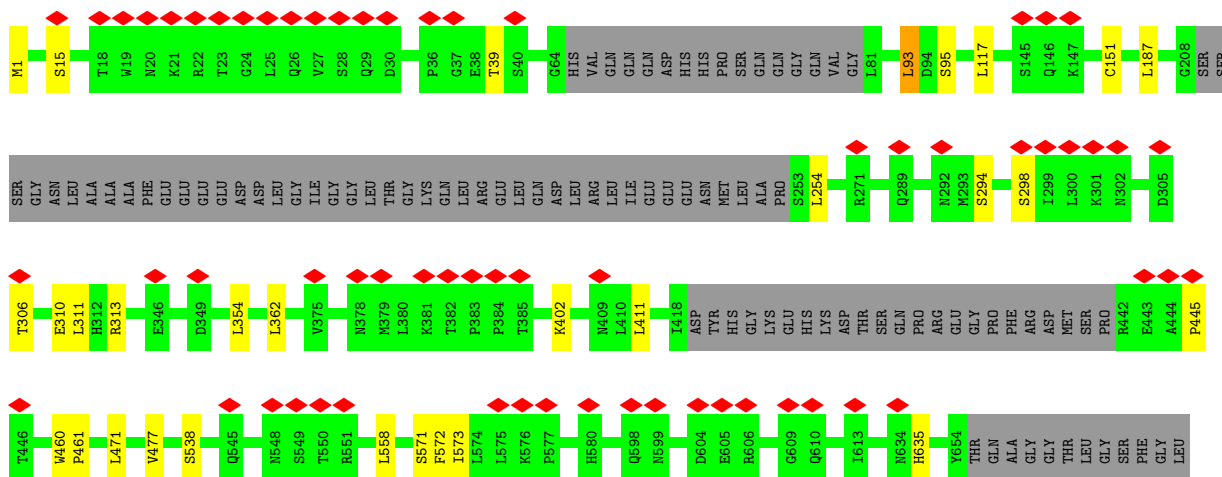
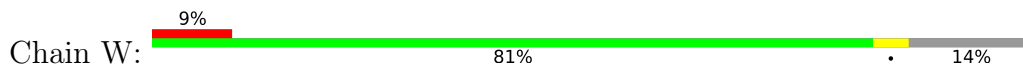




• Molecule 7: Gamma-tubulin complex component



• Molecule 7: Gamma-tubulin complex component



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	8497	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 ($e^-/\text{\AA}^2$)	43	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	33000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.050	Depositor
Minimum map value	-0.015	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.006	Depositor
Recommended contour level	0.0192	Depositor
Map size (Å)	513.024, 513.024, 513.024	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.004, 2.004, 2.004	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	B	0.56	0/429	0.84	1/577 (0.2%)
1	D	0.56	0/403	0.87	1/541 (0.2%)
2	Q	0.33	0/5227	0.65	7/7060 (0.1%)
2	c	0.31	0/5227	0.62	6/7060 (0.1%)
2	d	0.30	0/5227	0.65	7/7060 (0.1%)
2	e	0.36	0/5991	0.66	7/8086 (0.1%)
2	f	0.31	0/5227	0.63	8/7060 (0.1%)
3	R	0.36	0/4614	0.68	4/6236 (0.1%)
3	Y	0.35	0/4614	0.66	6/6236 (0.1%)
3	Z	0.32	0/4603	0.63	4/6221 (0.1%)
3	a	0.31	0/4598	0.60	2/6215 (0.0%)
3	b	0.31	0/4614	0.62	8/6236 (0.1%)
4	S	0.38	0/5500	0.72	6/7442 (0.1%)
5	T	0.28	0/3551	0.54	2/4815 (0.0%)
5	h	0.29	0/3551	0.54	2/4815 (0.0%)
5	i	0.29	0/3551	0.55	2/4815 (0.0%)
5	k	0.28	0/3551	0.54	2/4815 (0.0%)
5	l	0.29	0/3551	0.54	2/4815 (0.0%)
5	m	0.29	0/3551	0.55	2/4815 (0.0%)
5	n	0.29	0/3551	0.55	2/4815 (0.0%)
5	o	0.29	0/3551	0.54	2/4815 (0.0%)
5	p	0.29	0/3551	0.54	2/4815 (0.0%)
5	q	0.29	0/3551	0.55	2/4815 (0.0%)
5	r	0.29	0/3551	0.54	2/4815 (0.0%)
5	s	0.28	0/3551	0.54	2/4815 (0.0%)
5	t	0.29	0/3551	0.55	2/4815 (0.0%)
5	w	0.29	0/3551	0.54	2/4815 (0.0%)
6	U	0.31	0/4778	0.68	9/6459 (0.1%)
7	V	0.33	0/4738	0.68	7/6416 (0.1%)
7	W	0.33	0/4738	0.68	7/6416 (0.1%)
All	All	0.32	0/120242	0.61	118/162731 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected

by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	Q	0	3
2	c	0	2
2	d	0	2
2	e	0	5
2	f	0	3
3	R	0	1
3	Y	0	2
3	Z	0	5
3	a	0	3
3	b	0	2
4	S	0	11
6	U	0	5
7	V	0	3
7	W	0	3
All	All	0	50

There are no bond length outliers.

All (118) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	d	544	LEU	CB-CG-CD2	-9.70	94.51	111.00
3	b	556	LEU	CA-CB-CG	8.41	134.64	115.30
6	U	791	LEU	CA-CB-CG	8.32	134.43	115.30
3	R	263	LEU	CA-CB-CG	7.90	133.48	115.30
2	e	67	ARG	NE-CZ-NH1	7.84	124.22	120.30
6	U	937	LEU	CA-CB-CG	7.75	133.12	115.30
2	Q	254	LEU	CB-CG-CD1	-7.74	97.83	111.00
3	Z	491	TYR	CB-CG-CD1	7.72	125.63	121.00
3	b	743	LEU	CB-CG-CD2	7.46	123.67	111.00
2	Q	426	LEU	CA-CB-CG	7.39	132.29	115.30
2	f	293	LEU	CB-CG-CD2	7.17	123.18	111.00
2	f	426	LEU	CA-CB-CG	7.16	131.77	115.30
3	R	274	ARG	NE-CZ-NH1	7.13	123.86	120.30
2	Q	521	LEU	CA-CB-CG	7.11	131.65	115.30
3	R	478	LEU	CA-CB-CG	7.10	131.63	115.30
2	c	525	LEU	CA-CB-CG	7.08	131.59	115.30
3	R	460	ARG	NE-CZ-NH2	7.01	123.81	120.30
3	Z	491	TYR	CB-CG-CD2	-6.95	116.83	121.00
7	W	93	LEU	CA-CB-CG	6.85	131.05	115.30
7	V	93	LEU	CA-CB-CG	6.79	130.93	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	c	426	LEU	CA-CB-CG	6.71	130.73	115.30
3	Z	442	LEU	CA-CB-CG	6.69	130.68	115.30
4	S	607	LEU	CA-CB-CG	6.67	130.64	115.30
2	c	268	CYS	CA-CB-SG	6.62	125.91	114.00
3	Y	334	MET	CG-SD-CE	6.60	110.76	100.20
3	b	849	ASP	CB-CG-OD1	6.59	124.23	118.30
6	U	432	LEU	CA-CB-CG	6.58	130.43	115.30
3	Z	331	LEU	CA-CB-CG	6.58	130.43	115.30
6	U	432	LEU	CB-CG-CD2	6.51	122.07	111.00
2	e	426	LEU	CA-CB-CG	6.50	130.25	115.30
5	q	412	ASP	CB-CG-OD1	6.48	124.13	118.30
2	d	426	LEU	CA-CB-CG	6.47	130.18	115.30
5	i	412	ASP	CB-CG-OD1	6.44	124.09	118.30
1	D	58	ARG	NE-CZ-NH1	6.43	123.52	120.30
5	w	412	ASP	CB-CG-OD1	6.42	124.08	118.30
5	t	412	ASP	CB-CG-OD1	6.38	124.04	118.30
2	f	576	LEU	CA-CB-CG	6.38	129.96	115.30
5	l	412	ASP	CB-CG-OD1	6.37	124.03	118.30
5	m	412	ASP	CB-CG-OD1	6.36	124.03	118.30
5	k	412	ASP	CB-CG-OD1	6.28	123.95	118.30
4	S	458	LEU	CB-CG-CD1	-6.25	100.38	111.00
7	V	362	LEU	CA-CB-CG	6.25	129.66	115.30
2	f	293	LEU	CB-CG-CD1	-6.24	100.39	111.00
5	s	412	ASP	CB-CG-OD1	6.23	123.91	118.30
5	T	412	ASP	CB-CG-OD1	6.23	123.90	118.30
5	n	412	ASP	CB-CG-OD1	6.22	123.90	118.30
7	W	362	LEU	CA-CB-CG	6.20	129.55	115.30
5	h	412	ASP	CB-CG-OD1	6.17	123.86	118.30
3	b	556	LEU	CB-CG-CD1	6.17	121.48	111.00
5	p	412	ASP	CB-CG-OD1	6.13	123.82	118.30
5	r	412	ASP	CB-CG-OD1	6.12	123.81	118.30
5	o	412	ASP	CB-CG-OD1	6.08	123.77	118.30
3	Y	323	LEU	CA-CB-CG	6.06	129.23	115.30
4	S	596	TYR	CB-CG-CD1	-6.05	117.37	121.00
4	S	80	ARG	NE-CZ-NH1	6.01	123.30	120.30
7	W	354	LEU	CA-CB-CG	5.90	128.87	115.30
1	B	58	ARG	NE-CZ-NH1	5.89	123.25	120.30
3	Y	223	ILE	CG1-CB-CG2	-5.88	98.45	111.40
7	V	354	LEU	CA-CB-CG	5.85	128.75	115.30
6	U	723	LEU	CA-CB-CG	5.79	128.62	115.30
2	Q	253	LEU	CA-CB-CG	5.77	128.58	115.30
7	W	411	LEU	CA-CB-CG	5.71	128.43	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	d	515	PRO	CA-N-CD	-5.71	103.51	111.50
2	e	515	PRO	CA-N-CD	-5.67	103.57	111.50
7	V	411	LEU	CA-CB-CG	5.66	128.32	115.30
3	Y	331	LEU	CA-CB-CG	5.63	128.25	115.30
5	t	93	LEU	CA-CB-CG	5.60	128.18	115.30
4	S	1527	LEU	CA-CB-CG	5.59	128.16	115.30
3	Y	263	LEU	CB-CG-CD2	5.58	120.48	111.00
5	o	93	LEU	CA-CB-CG	5.58	128.13	115.30
5	T	93	LEU	CA-CB-CG	5.58	128.12	115.30
5	i	93	LEU	CA-CB-CG	5.57	128.11	115.30
5	k	93	LEU	CA-CB-CG	5.57	128.11	115.30
5	p	93	LEU	CA-CB-CG	5.57	128.10	115.30
2	f	515	PRO	CA-N-CD	-5.56	103.71	111.50
5	w	93	LEU	CA-CB-CG	5.56	128.09	115.30
5	r	93	LEU	CA-CB-CG	5.56	128.09	115.30
5	n	93	LEU	CA-CB-CG	5.55	128.06	115.30
5	h	93	LEU	CA-CB-CG	5.54	128.05	115.30
2	f	293	LEU	CA-CB-CG	5.53	128.01	115.30
5	m	93	LEU	CA-CB-CG	5.52	128.00	115.30
5	s	93	LEU	CA-CB-CG	5.52	127.99	115.30
6	U	568	LEU	CA-CB-CG	5.51	127.98	115.30
5	l	93	LEU	CA-CB-CG	5.51	127.98	115.30
2	c	576	LEU	CA-CB-CG	5.51	127.97	115.30
5	q	93	LEU	CA-CB-CG	5.51	127.97	115.30
2	Q	458	LEU	CA-CB-CG	5.50	127.96	115.30
2	Q	515	PRO	CA-N-CD	-5.46	103.85	111.50
2	f	840	PRO	CA-N-CD	-5.45	103.87	111.50
7	V	254	LEU	CA-CB-CG	5.44	127.82	115.30
7	W	254	LEU	CA-CB-CG	5.39	127.70	115.30
2	e	496	CYS	CA-CB-SG	5.39	123.70	114.00
2	e	90	ARG	NE-CZ-NH1	5.38	122.99	120.30
3	b	331	LEU	CA-CB-CG	5.37	127.65	115.30
2	c	515	PRO	CA-N-CD	-5.36	103.99	111.50
3	Y	334	MET	CB-CG-SD	5.36	128.48	112.40
7	V	471	LEU	CA-CB-CG	5.36	127.62	115.30
7	W	471	LEU	CA-CB-CG	5.35	127.60	115.30
6	U	929	LEU	CA-CB-CG	5.33	127.57	115.30
2	d	345	LEU	CA-CB-CG	5.25	127.38	115.30
6	U	892	LEU	CA-CB-CG	5.24	127.36	115.30
7	W	558	LEU	CA-CB-CG	5.24	127.36	115.30
3	a	374	LEU	CA-CB-CG	5.24	127.34	115.30
3	b	220	LEU	CA-CB-CG	5.23	127.34	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	b	556	LEU	CB-CG-CD2	-5.22	102.13	111.00
2	e	458	LEU	CA-CB-CG	5.21	127.27	115.30
2	d	544	LEU	CA-CB-CG	5.20	127.27	115.30
2	Q	496	CYS	CA-CB-SG	5.19	123.34	114.00
7	V	558	LEU	CA-CB-CG	5.18	127.21	115.30
2	d	690	LEU	CA-CB-CG	5.17	127.19	115.30
2	d	458	LEU	CA-CB-CG	5.17	127.18	115.30
2	c	458	LEU	CA-CB-CG	5.14	127.12	115.30
3	a	861	LEU	CA-CB-CG	5.14	127.11	115.30
4	S	586	VAL	C-N-CA	5.12	134.49	121.70
2	f	458	LEU	CA-CB-CG	5.06	126.94	115.30
2	e	327	LEU	CB-CG-CD2	5.06	119.60	111.00
6	U	825	LEU	CA-CB-CG	5.04	126.89	115.30
3	b	348	GLU	CA-CB-CG	5.04	124.48	113.40

There are no chirality outliers.

All (50) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Q	271	GLU	Peptide
2	Q	311	SER	Peptide
2	Q	318	LEU	Peptide
3	R	485	GLU	Sidechain
4	S	1529	ARG	Peptide
4	S	1533	VAL	Peptide
4	S	1539	SER	Peptide
4	S	1540	VAL	Peptide
4	S	1673	LEU	Peptide
4	S	1674	VAL	Peptide
4	S	385	TYR	Peptide
4	S	512	ASN	Peptide
4	S	575	LEU	Peptide
4	S	582	ASP	Peptide
4	S	585	PRO	Peptide
6	U	276	GLY	Peptide
6	U	277	VAL	Peptide
6	U	424	ARG	Peptide
6	U	677	SER	Peptide
6	U	938	LEU	Peptide
7	V	460	TRP	Peptide
7	V	572	PHE	Peptide
7	V	635	HIS	Peptide

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Mol	Chain	Res	Type	Group
7	W	460	TRP	Peptide
7	W	572	PHE	Peptide
7	W	635	HIS	Peptide
3	Y	472	LYS	Peptide
3	Y	480	GLU	Peptide
3	Z	282	PHE	Peptide
3	Z	432	THR	Peptide
3	Z	433	ILE	Peptide
3	Z	515	ILE	Peptide
3	Z	520	LEU	Peptide
3	a	428	ASP	Peptide
3	a	473	GLU	Peptide
3	a	479	LYS	Peptide
3	b	348	GLU	Peptide
3	b	403	TYR	Peptide
2	c	266	LYS	Peptide
2	c	313	ASP	Peptide
2	d	271	GLU	Peptide
2	d	313	ASP	Peptide
2	e	19	ARG	Sidechain
2	e	271	GLU	Peptide
2	e	313	ASP	Peptide
2	e	522	PHE	Peptide
2	e	523	THR	Peptide
2	f	271	GLU	Peptide
2	f	500	THR	Peptide
2	f	839	ILE	Peptide

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	B	54/72 (75%)	54 (100%)	0	0	100	100
1	D	50/72 (69%)	50 (100%)	0	0	100	100
2	Q	619/906 (68%)	580 (94%)	37 (6%)	2 (0%)	41	77
2	c	619/906 (68%)	579 (94%)	38 (6%)	2 (0%)	41	77
2	d	619/906 (68%)	580 (94%)	39 (6%)	0	100	100
2	e	710/906 (78%)	670 (94%)	39 (6%)	1 (0%)	51	86
2	f	619/906 (68%)	585 (94%)	33 (5%)	1 (0%)	47	81
3	R	543/896 (61%)	511 (94%)	32 (6%)	0	100	100
3	Y	543/896 (61%)	504 (93%)	36 (7%)	3 (1%)	25	66
3	Z	541/896 (60%)	508 (94%)	31 (6%)	2 (0%)	34	72
3	a	541/896 (60%)	499 (92%)	39 (7%)	3 (1%)	25	66
3	b	543/896 (61%)	518 (95%)	25 (5%)	0	100	100
4	S	645/1698 (38%)	583 (90%)	50 (8%)	12 (2%)	8	38
5	T	434/451 (96%)	409 (94%)	25 (6%)	0	100	100
5	h	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
5	i	434/451 (96%)	409 (94%)	25 (6%)	0	100	100
5	k	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
5	l	434/451 (96%)	409 (94%)	25 (6%)	0	100	100
5	m	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
5	n	434/451 (96%)	409 (94%)	25 (6%)	0	100	100
5	o	434/451 (96%)	409 (94%)	25 (6%)	0	100	100
5	p	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
5	q	434/451 (96%)	409 (94%)	25 (6%)	0	100	100
5	r	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
5	s	434/451 (96%)	409 (94%)	25 (6%)	0	100	100
5	t	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
5	w	434/451 (96%)	410 (94%)	24 (6%)	0	100	100
6	U	559/1019 (55%)	516 (92%)	41 (7%)	2 (0%)	34	72
7	V	563/666 (84%)	520 (92%)	39 (7%)	4 (1%)	22	63
7	W	563/666 (84%)	521 (92%)	39 (7%)	3 (0%)	29	69
All	All	14407/19517 (74%)	13511 (94%)	861 (6%)	35 (0%)	50	81

All (35) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	S	586	VAL
4	S	1533	VAL
4	S	1534	ASN
4	S	1583	SER
4	S	1606	THR
6	U	490	ILE
3	Y	473	GLU
3	Y	482	ALA
2	Q	319	VAL
4	S	1532	LEU
3	Y	481	GLN
3	Z	433	ILE
3	a	480	GLU
4	S	585	PRO
4	S	1575	PHE
6	U	938	LEU
7	V	316	GLN
7	V	445	PRO
7	W	445	PRO
2	c	267	MET
2	c	268	CYS
2	f	840	PRO
4	S	386	ILE
4	S	1582	VAL
7	V	461	PRO
7	W	461	PRO
3	Z	432	THR
2	e	523	THR
2	Q	861	LEU
4	S	1675	ASN
3	a	474	ILE
3	a	496	LYS
4	S	1607	GLU
7	V	573	ILE
7	W	573	ILE

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	51/62 (82%)	51 (100%)	0	100	100
1	D	48/62 (77%)	48 (100%)	0	100	100
2	Q	561/798 (70%)	543 (97%)	18 (3%)	39	61
2	c	561/798 (70%)	558 (100%)	3 (0%)	88	93
2	d	561/798 (70%)	554 (99%)	7 (1%)	71	83
2	e	643/798 (81%)	637 (99%)	6 (1%)	78	87
2	f	561/798 (70%)	547 (98%)	14 (2%)	47	68
3	R	507/824 (62%)	502 (99%)	5 (1%)	76	86
3	Y	507/824 (62%)	504 (99%)	3 (1%)	86	92
3	Z	506/824 (61%)	500 (99%)	6 (1%)	71	83
3	a	505/824 (61%)	505 (100%)	0	100	100
3	b	507/824 (62%)	506 (100%)	1 (0%)	93	96
4	S	605/1539 (39%)	601 (99%)	4 (1%)	84	90
5	T	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	h	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	i	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	k	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	l	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	m	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	n	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	o	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	p	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	q	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	r	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	s	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	t	387/400 (97%)	368 (95%)	19 (5%)	25	50
5	w	387/400 (97%)	368 (95%)	19 (5%)	25	50
6	U	523/933 (56%)	523 (100%)	0	100	100
7	V	518/595 (87%)	497 (96%)	21 (4%)	30	55
7	W	518/595 (87%)	500 (96%)	18 (4%)	36	59
All	All	13100/17496 (75%)	12728 (97%)	372 (3%)	46	65

All (372) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	Q	254	LEU
2	Q	314	ARG
2	Q	337	LEU
2	Q	363	LEU
2	Q	365	ARG
2	Q	366	LEU
2	Q	367	LEU
2	Q	369	TRP
2	Q	508	VAL
2	Q	510	LYS
2	Q	511	SER
2	Q	515	PRO
2	Q	516	LYS
2	Q	517	ASP
2	Q	862	VAL
2	Q	863	LEU
2	Q	864	LEU
2	Q	866	THR
3	R	754	CYS
3	R	756	MET
3	R	761	LEU
3	R	762	GLN
3	R	763	ARG
4	S	19	PHE
4	S	1576	ARG
4	S	1578	LYS
4	S	1579	LEU
5	T	10	LEU
5	T	26	CYS
5	T	34	GLU
5	T	42	THR
5	T	56	ASP
5	T	79	ASN
5	T	80	SER
5	T	93	LEU
5	T	94	SER
5	T	138	CYS
5	T	181	VAL
5	T	221	GLN
5	T	229	ASN
5	T	231	LEU
5	T	279	ASP
5	T	306	SER

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Mol	Chain	Res	Type
5	T	313	THR
5	T	328	VAL
5	T	419	ASP
7	V	1	MET
7	V	15	SER
7	V	39	THR
7	V	93	LEU
7	V	95	SER
7	V	117	LEU
7	V	151	CYS
7	V	187	LEU
7	V	294	SER
7	V	298	SER
7	V	303	GLN
7	V	305	ASP
7	V	306	THR
7	V	310	GLU
7	V	312	HIS
7	V	315	LYS
7	V	316	GLN
7	V	402	LYS
7	V	477	VAL
7	V	538	SER
7	V	571	SER
7	W	1	MET
7	W	15	SER
7	W	39	THR
7	W	93	LEU
7	W	95	SER
7	W	117	LEU
7	W	151	CYS
7	W	187	LEU
7	W	294	SER
7	W	298	SER
7	W	306	THR
7	W	310	GLU
7	W	311	LEU
7	W	313	ARG
7	W	402	LYS
7	W	477	VAL
7	W	538	SER
7	W	571	SER

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Mol	Chain	Res	Type
3	Y	262	ILE
3	Y	540	LYS
3	Y	720	ASP
3	Z	491	TYR
3	Z	516	LYS
3	Z	652	ARG
3	Z	655	CYS
3	Z	658	TRP
3	Z	659	ILE
3	b	503	MET
2	c	510	LYS
2	c	515	PRO
2	c	516	LYS
2	d	484	LEU
2	d	508	VAL
2	d	510	LYS
2	d	511	SER
2	d	515	PRO
2	d	517	ASP
2	d	540	THR
2	e	91	TRP
2	e	390	ARG
2	e	510	LYS
2	e	511	SER
2	e	515	PRO
2	e	516	LYS
2	f	293	LEU
2	f	508	VAL
2	f	510	LYS
2	f	511	SER
2	f	515	PRO
2	f	516	LYS
2	f	517	ASP
2	f	825	GLU
2	f	826	ASP
2	f	829	ASN
2	f	830	LYS
2	f	836	GLN
2	f	837	GLU
2	f	840	PRO
5	h	10	LEU
5	h	26	CYS

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Mol	Chain	Res	Type
5	h	34	GLU
5	h	42	THR
5	h	56	ASP
5	h	79	ASN
5	h	80	SER
5	h	93	LEU
5	h	94	SER
5	h	138	CYS
5	h	181	VAL
5	h	221	GLN
5	h	229	ASN
5	h	231	LEU
5	h	279	ASP
5	h	306	SER
5	h	313	THR
5	h	328	VAL
5	h	419	ASP
5	i	10	LEU
5	i	26	CYS
5	i	34	GLU
5	i	42	THR
5	i	56	ASP
5	i	79	ASN
5	i	80	SER
5	i	93	LEU
5	i	94	SER
5	i	138	CYS
5	i	181	VAL
5	i	221	GLN
5	i	229	ASN
5	i	231	LEU
5	i	279	ASP
5	i	306	SER
5	i	313	THR
5	i	328	VAL
5	i	419	ASP
5	k	10	LEU
5	k	26	CYS
5	k	34	GLU
5	k	42	THR
5	k	56	ASP
5	k	79	ASN

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Mol	Chain	Res	Type
5	k	80	SER
5	k	93	LEU
5	k	94	SER
5	k	138	CYS
5	k	181	VAL
5	k	221	GLN
5	k	229	ASN
5	k	231	LEU
5	k	279	ASP
5	k	306	SER
5	k	313	THR
5	k	328	VAL
5	k	419	ASP
5	l	10	LEU
5	l	26	CYS
5	l	34	GLU
5	l	42	THR
5	l	56	ASP
5	l	79	ASN
5	l	80	SER
5	l	93	LEU
5	l	94	SER
5	l	138	CYS
5	l	181	VAL
5	l	221	GLN
5	l	229	ASN
5	l	231	LEU
5	l	279	ASP
5	l	306	SER
5	l	313	THR
5	l	328	VAL
5	l	419	ASP
5	m	10	LEU
5	m	26	CYS
5	m	34	GLU
5	m	42	THR
5	m	56	ASP
5	m	79	ASN
5	m	80	SER
5	m	93	LEU
5	m	94	SER
5	m	138	CYS

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Mol	Chain	Res	Type
5	m	181	VAL
5	m	221	GLN
5	m	229	ASN
5	m	231	LEU
5	m	279	ASP
5	m	306	SER
5	m	313	THR
5	m	328	VAL
5	m	419	ASP
5	n	10	LEU
5	n	26	CYS
5	n	34	GLU
5	n	42	THR
5	n	56	ASP
5	n	79	ASN
5	n	80	SER
5	n	93	LEU
5	n	94	SER
5	n	138	CYS
5	n	181	VAL
5	n	221	GLN
5	n	229	ASN
5	n	231	LEU
5	n	279	ASP
5	n	306	SER
5	n	313	THR
5	n	328	VAL
5	n	419	ASP
5	o	10	LEU
5	o	26	CYS
5	o	34	GLU
5	o	42	THR
5	o	56	ASP
5	o	79	ASN
5	o	80	SER
5	o	93	LEU
5	o	94	SER
5	o	138	CYS
5	o	181	VAL
5	o	221	GLN
5	o	229	ASN
5	o	231	LEU

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Mol	Chain	Res	Type
5	o	279	ASP
5	o	306	SER
5	o	313	THR
5	o	328	VAL
5	o	419	ASP
5	p	10	LEU
5	p	26	CYS
5	p	34	GLU
5	p	42	THR
5	p	56	ASP
5	p	79	ASN
5	p	80	SER
5	p	93	LEU
5	p	94	SER
5	p	138	CYS
5	p	181	VAL
5	p	221	GLN
5	p	229	ASN
5	p	231	LEU
5	p	279	ASP
5	p	306	SER
5	p	313	THR
5	p	328	VAL
5	p	419	ASP
5	q	10	LEU
5	q	26	CYS
5	q	34	GLU
5	q	42	THR
5	q	56	ASP
5	q	79	ASN
5	q	80	SER
5	q	93	LEU
5	q	94	SER
5	q	138	CYS
5	q	181	VAL
5	q	221	GLN
5	q	229	ASN
5	q	231	LEU
5	q	279	ASP
5	q	306	SER
5	q	313	THR
5	q	328	VAL

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Mol	Chain	Res	Type
5	q	419	ASP
5	r	10	LEU
5	r	26	CYS
5	r	34	GLU
5	r	42	THR
5	r	56	ASP
5	r	79	ASN
5	r	80	SER
5	r	93	LEU
5	r	94	SER
5	r	138	CYS
5	r	181	VAL
5	r	221	GLN
5	r	229	ASN
5	r	231	LEU
5	r	279	ASP
5	r	306	SER
5	r	313	THR
5	r	328	VAL
5	r	419	ASP
5	s	10	LEU
5	s	26	CYS
5	s	34	GLU
5	s	42	THR
5	s	56	ASP
5	s	79	ASN
5	s	80	SER
5	s	93	LEU
5	s	94	SER
5	s	138	CYS
5	s	181	VAL
5	s	221	GLN
5	s	229	ASN
5	s	231	LEU
5	s	279	ASP
5	s	306	SER
5	s	313	THR
5	s	328	VAL
5	s	419	ASP
5	t	10	LEU
5	t	26	CYS
5	t	34	GLU

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Mol	Chain	Res	Type
5	t	42	THR
5	t	56	ASP
5	t	79	ASN
5	t	80	SER
5	t	93	LEU
5	t	94	SER
5	t	138	CYS
5	t	181	VAL
5	t	221	GLN
5	t	229	ASN
5	t	231	LEU
5	t	279	ASP
5	t	306	SER
5	t	313	THR
5	t	328	VAL
5	t	419	ASP
5	w	10	LEU
5	w	26	CYS
5	w	34	GLU
5	w	42	THR
5	w	56	ASP
5	w	79	ASN
5	w	80	SER
5	w	93	LEU
5	w	94	SER
5	w	138	CYS
5	w	181	VAL
5	w	221	GLN
5	w	229	ASN
5	w	231	LEU
5	w	279	ASP
5	w	306	SER
5	w	313	THR
5	w	328	VAL
5	w	419	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (171) such sidechains are listed below:

Mol	Chain	Res	Type
2	Q	575	HIS
2	Q	593	GLN
2	Q	594	HIS

Continued on next page...

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Mol	Chain	Res	Type
2	Q	702	GLN
3	R	437	GLN
3	R	457	ASN
3	R	649	HIS
3	R	661	ASN
3	R	717	ASN
3	R	731	ASN
3	R	762	GLN
3	R	864	ASN
4	S	70	ASN
4	S	431	GLN
4	S	517	ASN
4	S	557	ASN
4	S	571	HIS
4	S	593	ASN
4	S	1535	GLN
4	S	1553	GLN
4	S	1566	GLN
5	T	15	ASN
5	T	198	ASN
5	T	357	GLN
5	T	429	GLN
6	U	284	GLN
6	U	493	ASN
6	U	554	GLN
6	U	754	ASN
6	U	813	GLN
6	U	817	ASN
6	U	909	GLN
7	V	3	HIS
7	V	98	GLN
7	V	102	GLN
7	V	186	GLN
7	V	207	GLN
7	V	317	GLN
7	V	377	GLN
7	V	390	HIS
7	V	409	ASN
7	V	621	GLN
7	V	635	HIS
7	W	102	GLN
7	W	186	GLN

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Mol	Chain	Res	Type
7	W	207	GLN
7	W	312	HIS
7	W	317	GLN
7	W	377	GLN
7	W	621	GLN
7	W	635	HIS
3	Y	260	ASN
3	Y	328	GLN
3	Y	564	ASN
3	Y	638	GLN
3	Y	740	ASN
3	Y	830	ASN
3	Z	241	GLN
3	Z	279	ASN
3	Z	345	ASN
3	Z	400	ASN
3	Z	457	ASN
3	Z	683	GLN
3	Z	687	ASN
3	Z	690	GLN
3	Z	691	ASN
3	Z	693	GLN
3	Z	830	ASN
3	Z	834	HIS
3	Z	864	ASN
3	a	268	ASN
3	a	286	GLN
3	a	311	HIS
3	a	321	GLN
3	a	517	HIS
3	a	690	GLN
3	a	717	ASN
3	a	731	ASN
3	a	825	ASN
3	b	691	ASN
3	b	830	ASN
3	b	864	ASN
2	c	258	GLN
2	c	342	HIS
2	d	321	GLN
2	d	400	HIS
2	d	551	ASN

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Mol	Chain	Res	Type
2	d	569	GLN
2	d	593	GLN
2	d	804	GLN
2	e	10	ASN
2	e	14	GLN
2	e	33	GLN
2	e	321	GLN
2	e	388	GLN
2	e	493	HIS
2	e	575	HIS
2	e	594	HIS
2	f	309	GLN
2	f	594	HIS
2	f	801	GLN
2	f	829	ASN
2	f	833	GLN
5	h	15	ASN
5	h	198	ASN
5	h	221	GLN
5	h	357	GLN
5	h	429	GLN
5	i	15	ASN
5	i	198	ASN
5	i	251	ASN
5	i	322	ASN
5	i	357	GLN
5	i	429	GLN
5	k	15	ASN
5	k	198	ASN
5	k	299	GLN
5	k	357	GLN
5	k	429	GLN
5	l	15	ASN
5	l	59	HIS
5	l	198	ASN
5	l	250	ASN
5	l	357	GLN
5	l	429	GLN
5	m	15	ASN
5	m	198	ASN
5	m	334	HIS
5	m	338	GLN

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Mol	Chain	Res	Type
5	m	357	GLN
5	m	429	GLN
5	n	15	ASN
5	n	198	ASN
5	n	251	ASN
5	n	322	ASN
5	n	357	GLN
5	n	429	GLN
5	o	15	ASN
5	o	198	ASN
5	o	299	GLN
5	o	357	GLN
5	o	429	GLN
5	p	15	ASN
5	p	198	ASN
5	p	251	ASN
5	p	338	GLN
5	p	357	GLN
5	p	429	GLN
5	q	15	ASN
5	q	198	ASN
5	q	251	ASN
5	q	322	ASN
5	q	357	GLN
5	q	429	GLN
5	r	15	ASN
5	r	357	GLN
5	r	429	GLN
5	s	15	ASN
5	s	198	ASN
5	s	338	GLN
5	s	357	GLN
5	s	429	GLN
5	t	15	ASN
5	t	198	ASN
5	t	299	GLN
5	t	357	GLN
5	t	429	GLN
5	w	15	ASN
5	w	198	ASN
5	w	357	GLN
5	w	429	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

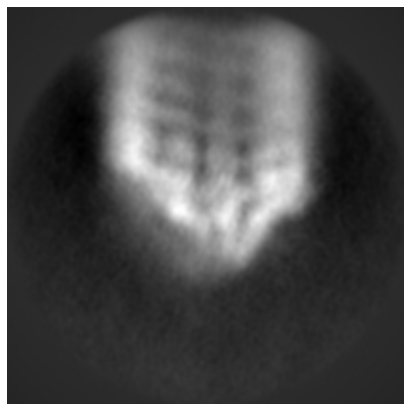
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19861. These allow visual inspection of the internal detail of the map and identification of artifacts.

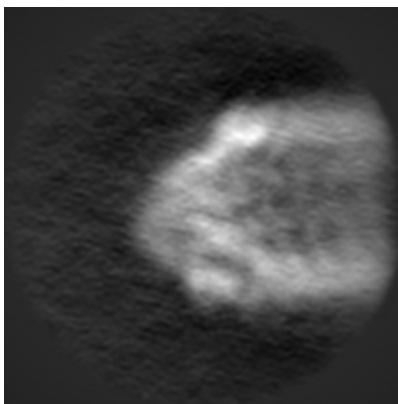
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

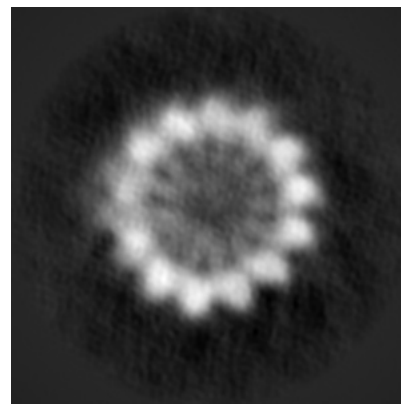
6.1.1 Primary map



X

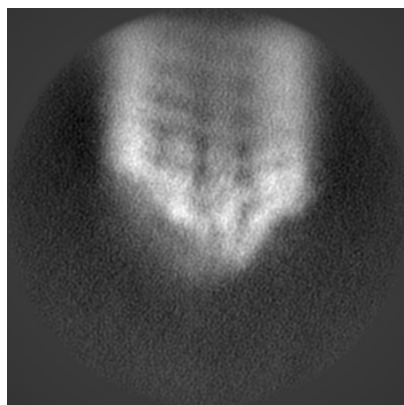


Y

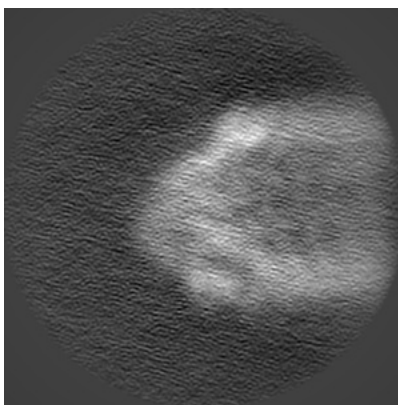


Z

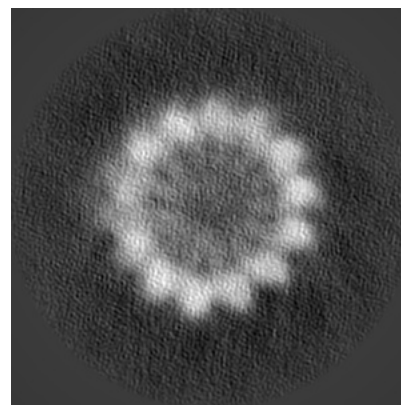
6.1.2 Raw map



X



Y

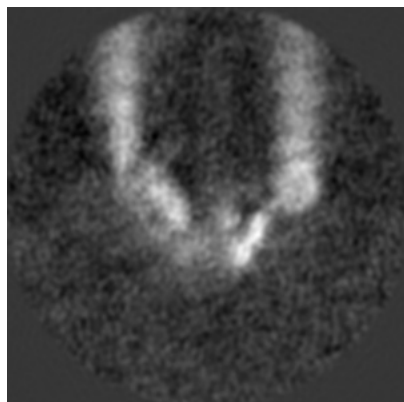


Z

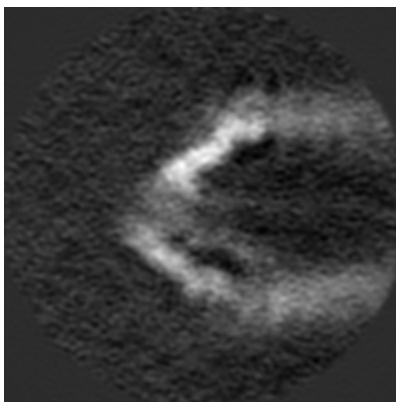
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

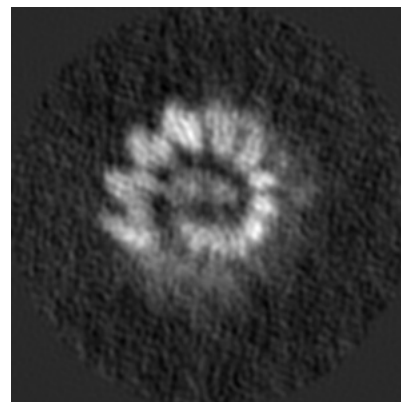
6.2.1 Primary map



X Index: 128

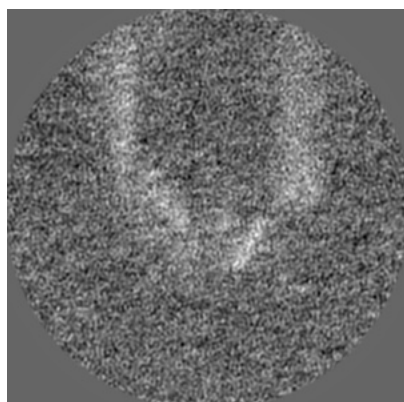


Y Index: 128

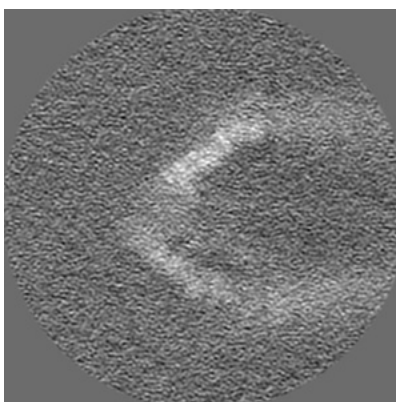


Z Index: 128

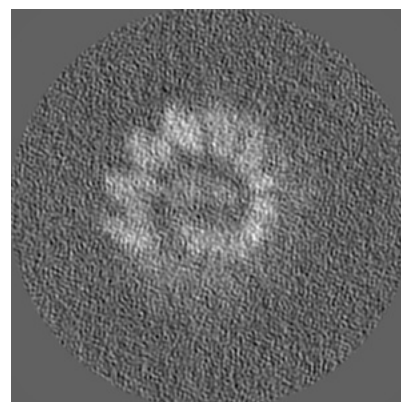
6.2.2 Raw map



X Index: 128



Y Index: 128

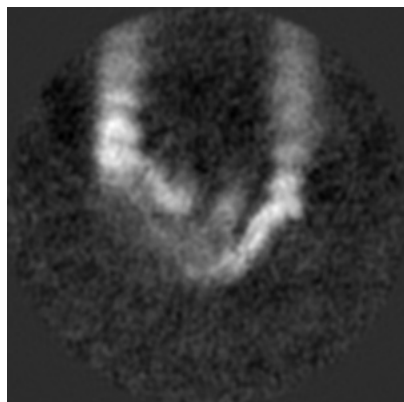


Z Index: 128

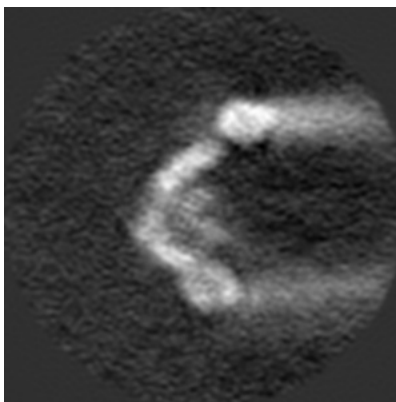
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

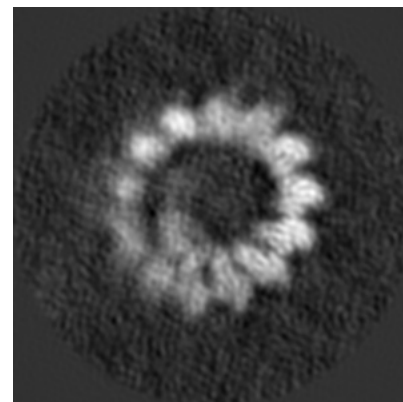
6.3.1 Primary map



X Index: 116

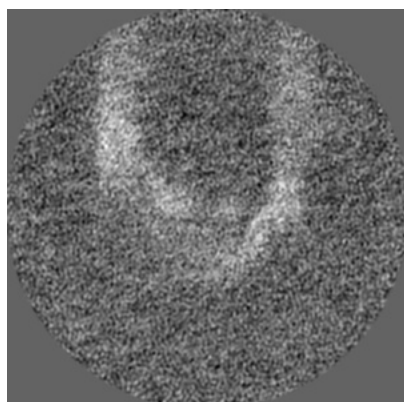


Y Index: 141

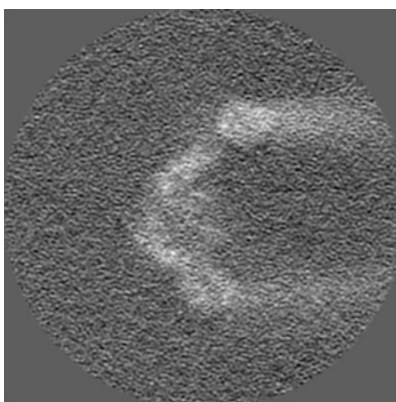


Z Index: 148

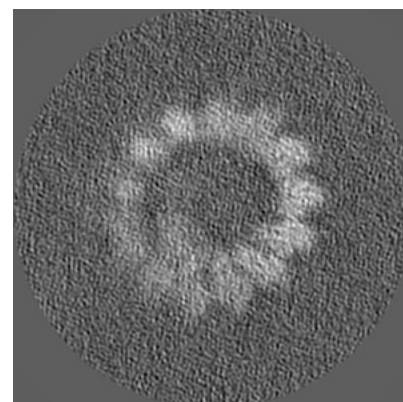
6.3.2 Raw map



X Index: 116



Y Index: 140

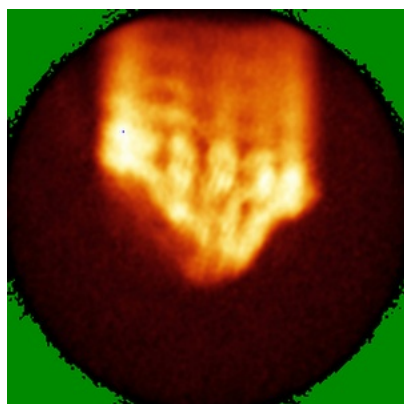


Z Index: 148

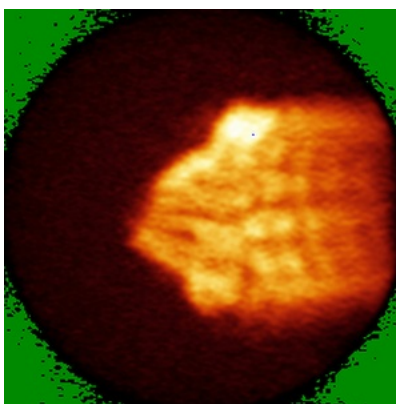
The images above show the largest variance slices of the map in three orthogonal directions.

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

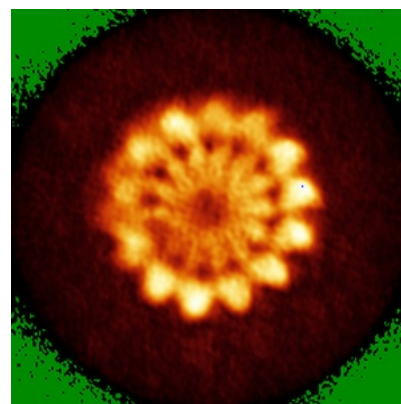
6.4.1 Primary map



X

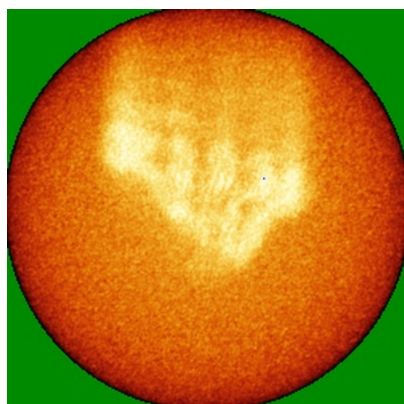


Y

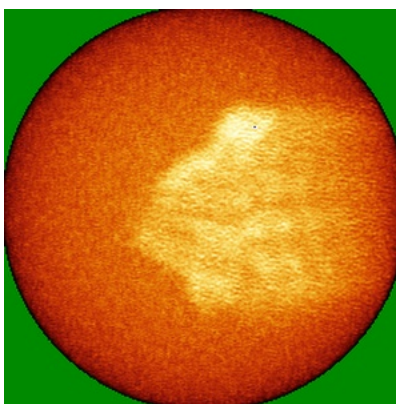


Z

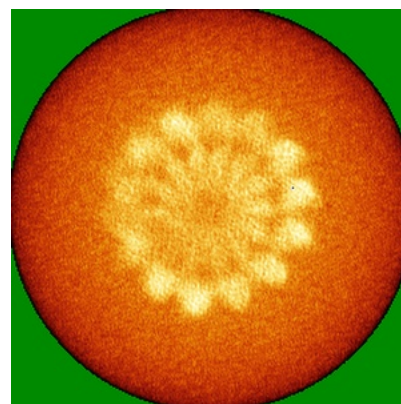
6.4.2 Raw map



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.

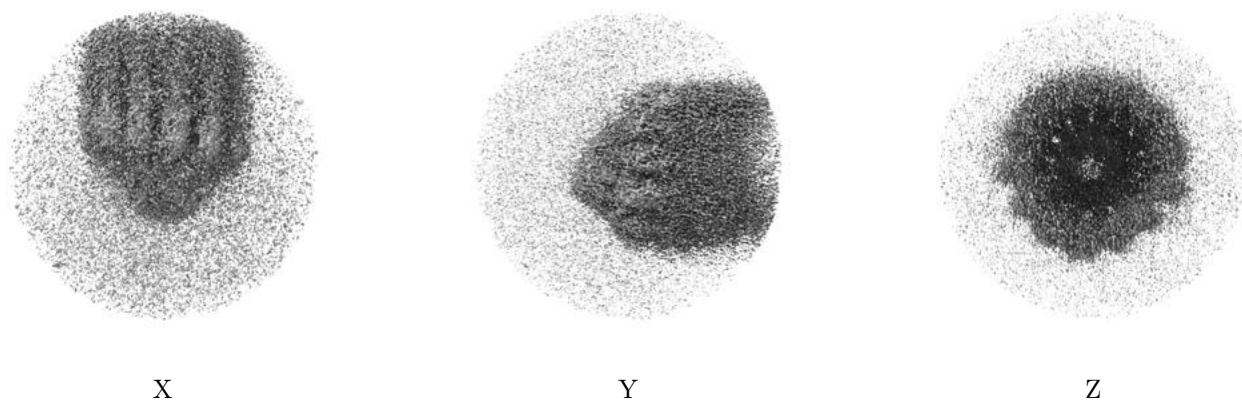
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0192. 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.

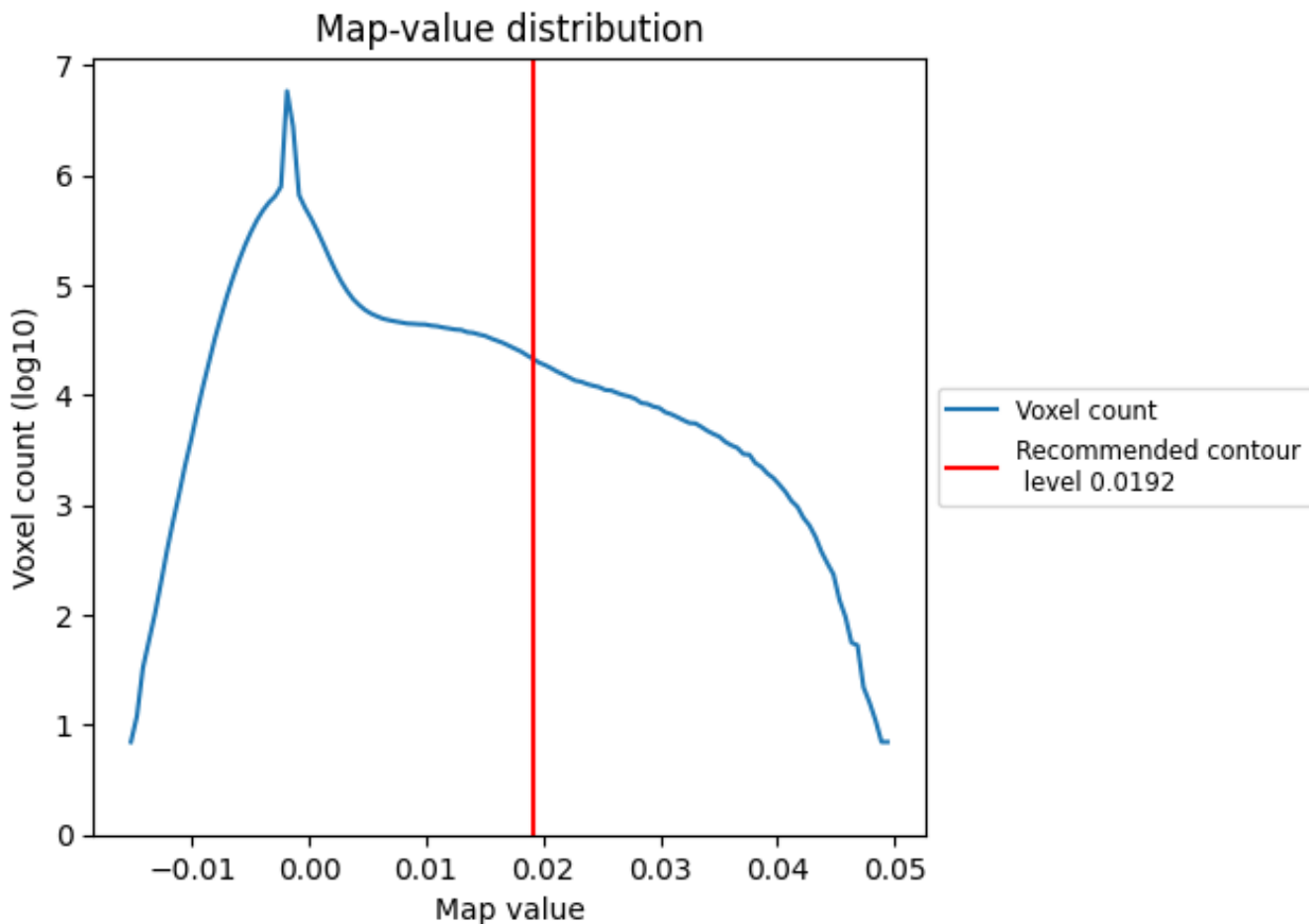
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

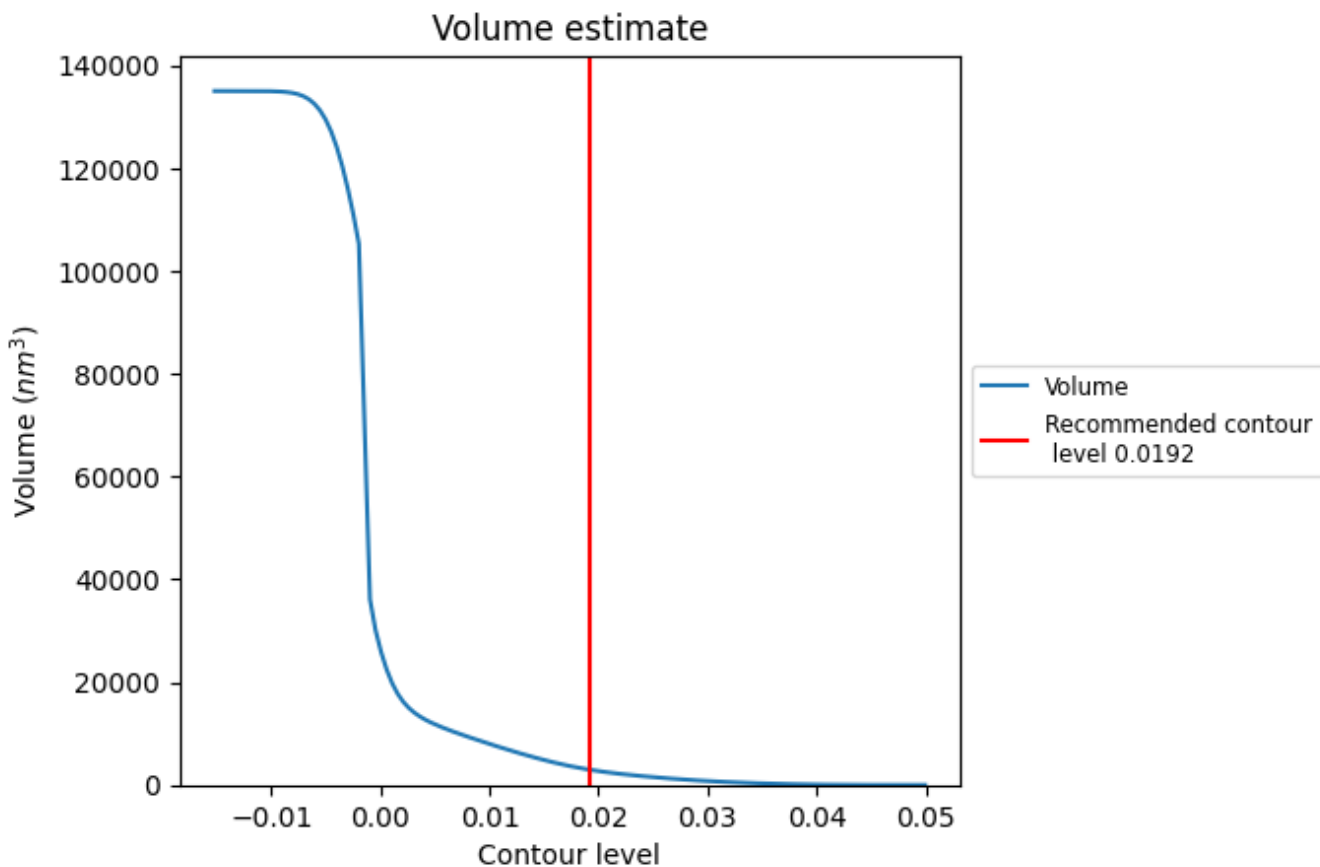
This section contains the results of statistical analysis of the map.

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.

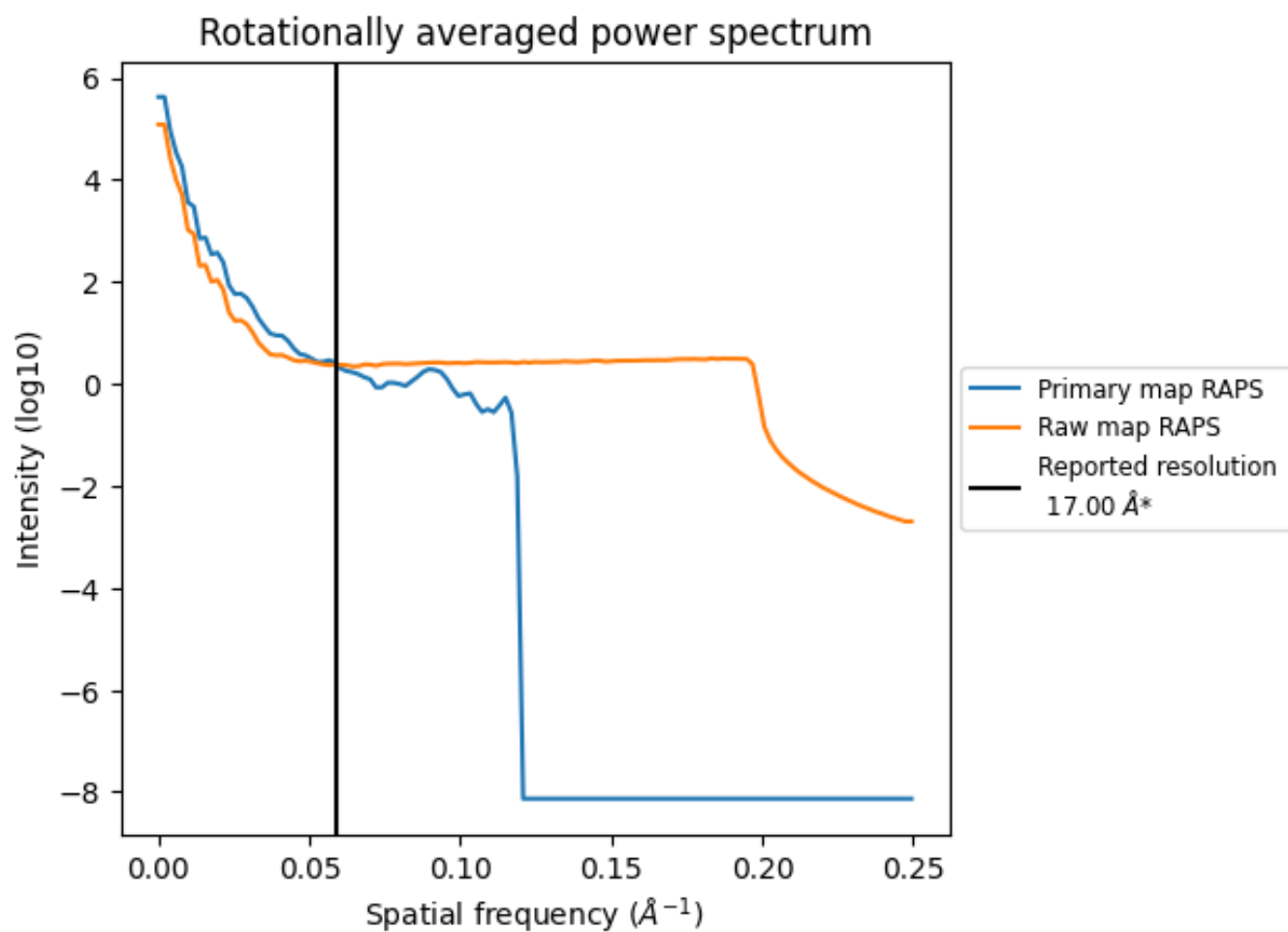
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 2960 nm³; this corresponds to an approximate mass of 2674 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum i

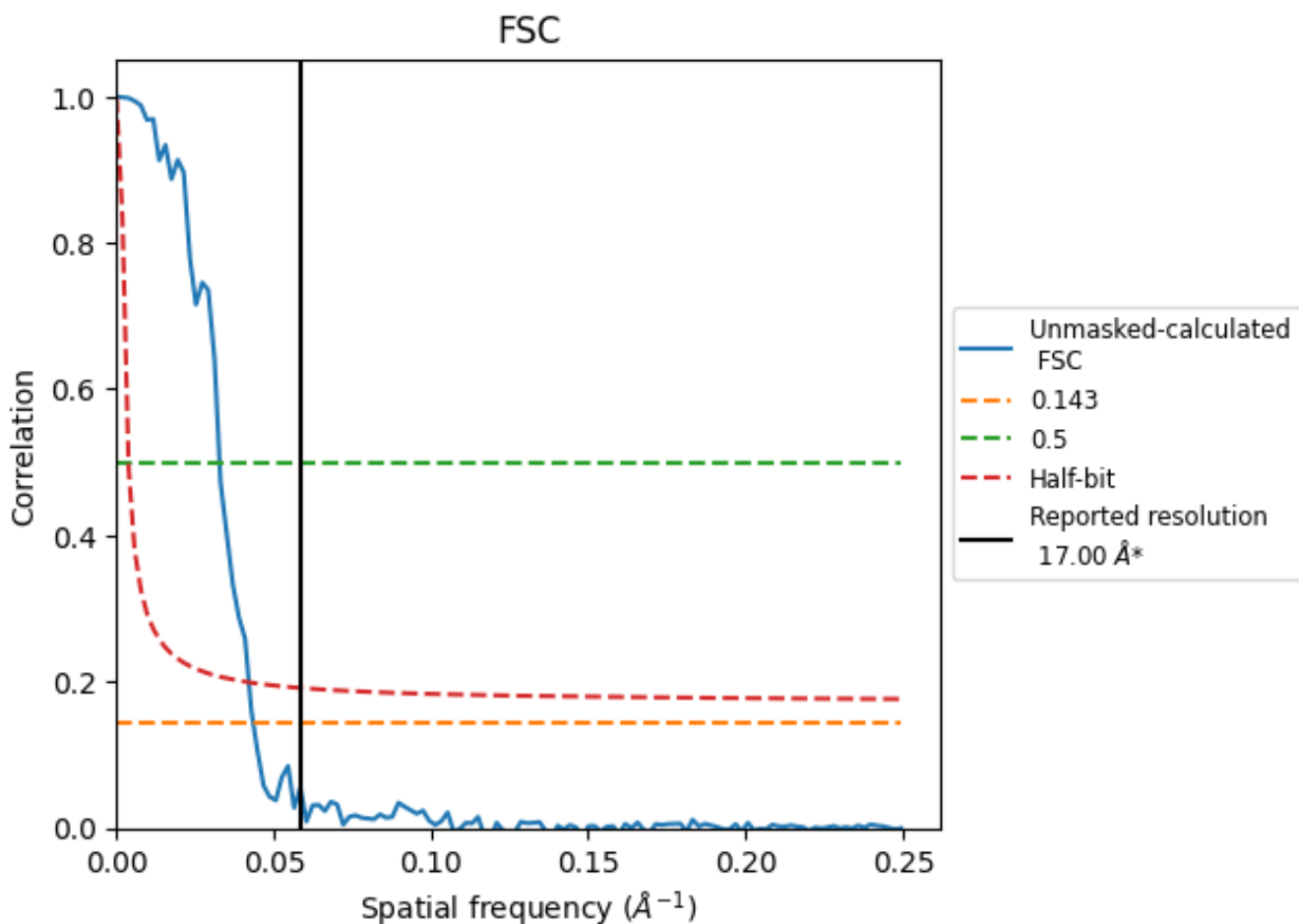


*Reported resolution corresponds to spatial frequency of 0.059 Å⁻¹

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 0.059 Å⁻¹

8.2 Resolution estimates [i](#)

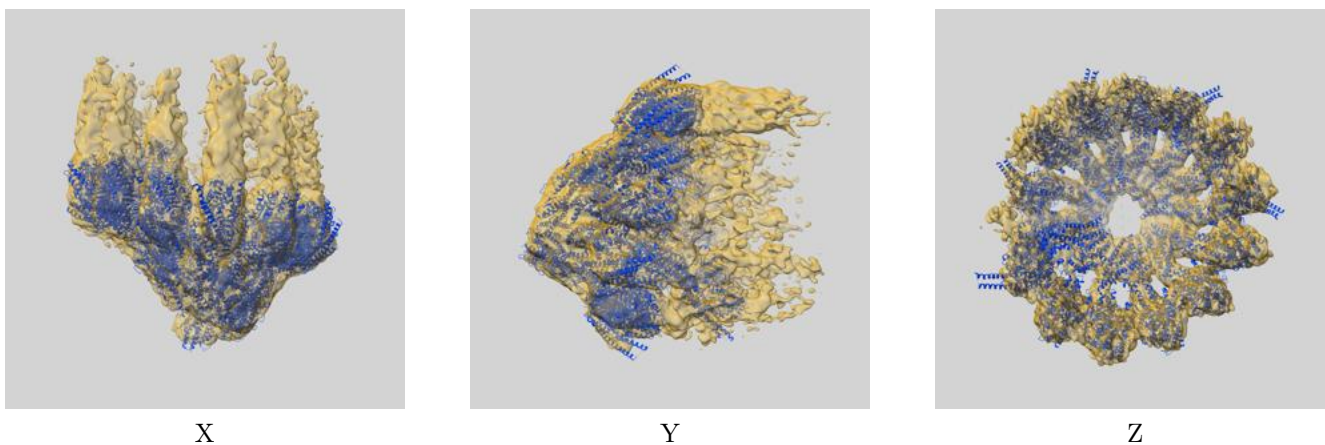
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	17.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	22.99	30.49	23.75

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 22.99 differs from the reported value 17.0 by more than 10 %

9 Map-model fit [i](#)

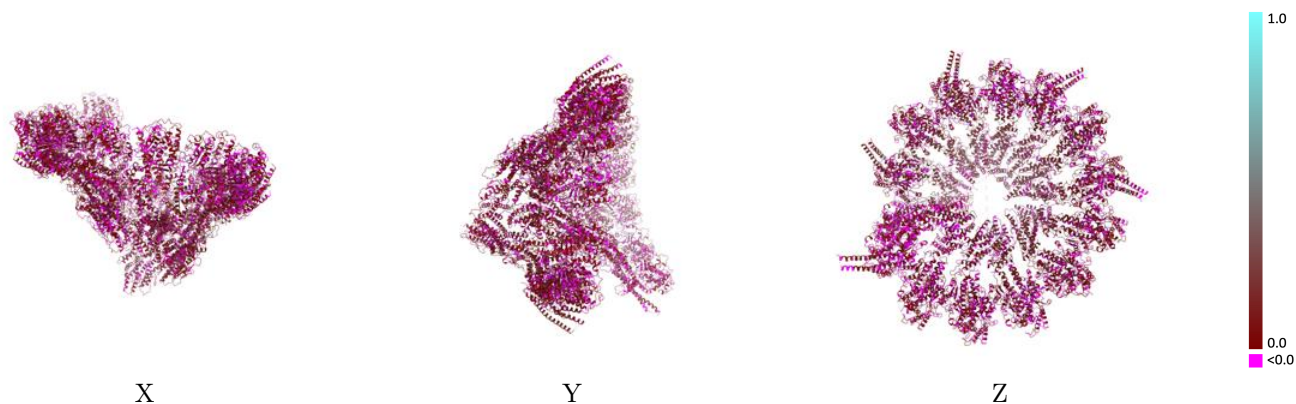
This section contains information regarding the fit between EMDB map EMD-19861 and PDB model 9EOJ. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



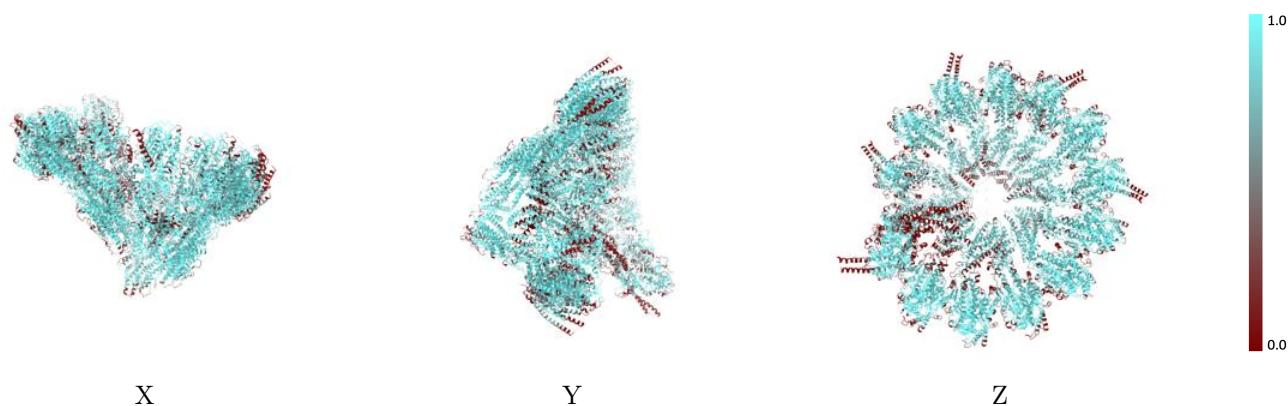
The images above show the 3D surface view of the map at the recommended contour level 0.0192 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



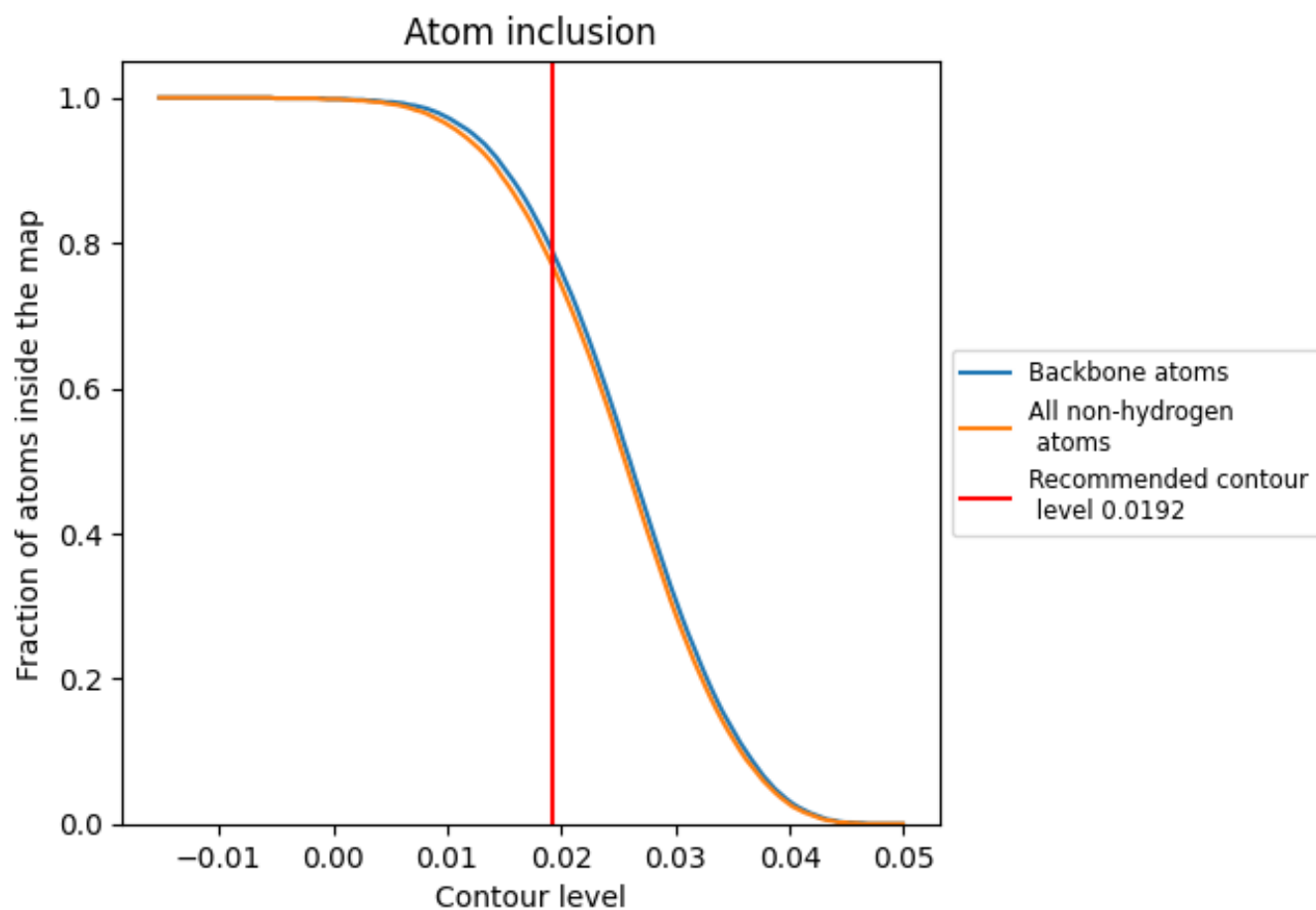
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0192).































































9.4 Atom inclusion [i](#)



At the recommended contour level, 79% of all backbone atoms, 77% 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 (0.0192) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7700	 0.0560
B	 0.1400	 0.0890
D	 0.4560	 0.1070
Q	 0.7500	 0.0820
R	 0.6620	 0.0520
S	 0.7330	 0.0660
T	 0.6270	 0.0240
U	 0.8740	 0.0800
V	 0.7910	 0.0650
W	 0.8610	 0.0690
Y	 0.8590	 0.0850
Z	 0.8680	 0.0680
a	 0.6350	 0.0470
b	 0.9290	 0.0790
c	 0.8220	 0.0780
d	 0.8240	 0.0700
e	 0.8110	 0.0690
f	 0.4130	 0.0400
h	 0.6840	 0.0400
i	 0.7770	 0.0360
k	 0.8470	 0.0450
l	 0.7700	 0.0330
m	 0.7130	 0.0330
n	 0.8490	 0.0490
o	 0.8640	 0.0440
p	 0.8400	 0.0440
q	 0.8140	 0.0520
r	 0.7550	 0.0380
s	 0.8440	 0.0350
t	 0.8060	 0.0360
w	 0.6480	 0.0250

