



## wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 04:44 AM UTC

PDB ID : 8IAH / pdb\_00008iah  
EMDB ID : EMD-35301  
Title : Structure of mammalian spectrin-actin junctional complex of membrane skeleton, State I, Global map  
Authors : Li, N.; Chen, S.; Gao, N.  
Deposited on : 2023-02-08  
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

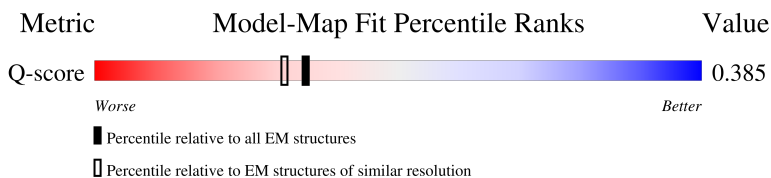
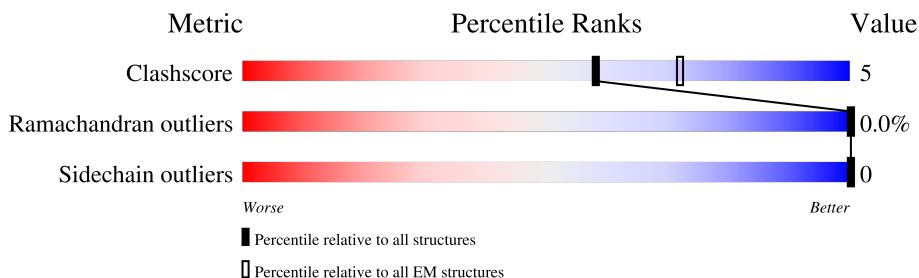
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance

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

The reported resolution of this entry is 3.60 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	-
Q-score	-	25397	12797 ( 3.10 - 4.10 )

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

Mol	Chain	Length	Quality of chain
1	0	744	
1	1	744	
1	2	744	
2	3	724	

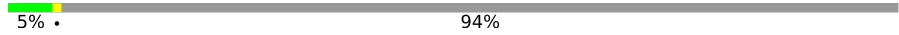


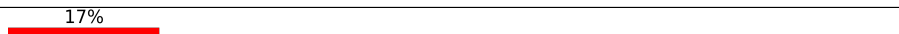
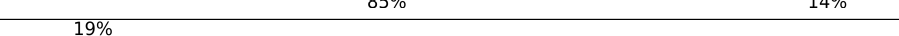


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Mol	Chain	Length	Quality of chain
2	4	724	33% 6% 61%
2	9	724	6% 93%
3	5	405	28% 70%
3	6	405	7% 28% 69%
3	7	405	6% 25% 70%
4	8	2417	15% 13% 84%
5	A	375	84% 16%
5	B	375	87% 13%
5	C	375	93% 6%
5	D	375	89% 11%
5	E	375	90% 10%
5	F	375	91% 8%
5	G	375	89% 11%
5	H	375	90% 10%
5	I	375	88% 11%
5	J	375	88% 11%
5	K	375	88% 12%
5	L	375	91% 9%
6	M	2148	5% 94%
6	N	2148	5% 94%
6	O	2148	5% 94%
6	P	2148	5% 95%
6	Q	2148	5% 94%
6	R	2148	5% 95%
6	S	2148	14% 19% 77%

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Mol	Chain	Length	Quality of chain
6	T	2148	 5% • 94%
7	U	248	 21% 86% 13% •
8	V	248	 26% 81% 18% •
8	W	248	 17% 85% 14%
8	X	248	 19% 80% 16% • •
9	Y	359	 7% 79% 14% 7%
10	Z	107	 • 7% 79% 11% • 8%

## 2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 74320 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 Adducin 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	0	54	453	280	80	87	6	0	0
1	1	334	2585	1647	448	478	12	0	0
1	2	294	2263	1444	391	418	10	0	0

- Molecule 2 is a protein called Beta-adducin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	3	365	2870	1812	500	538	20	0	0
2	4	280	2157	1369	369	403	16	0	0
2	9	54	455	280	84	88	3	0	0

- Molecule 3 is a protein called Dematin actin binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	5	123	1008	649	175	182	2	0	0
3	6	125	963	619	163	179	2	0	0
3	7	121	976	624	173	177	2	0	0

- Molecule 4 is a protein called Spectrin alpha, erythrocytic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	8	379	2799	1749	488	553	9	0	0

- Molecule 5 is a protein called Actin, cytoplasmic 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	374	Total	C	N	O	S	0	0
			2907	1837	490	560	20		
5	B	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
5	C	373	Total	C	N	O	S	0	0
			2909	1841	489	557	22		
5	D	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
5	E	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
5	F	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
5	G	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
5	H	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
5	I	373	Total	C	N	O	S	0	0
			2909	1841	489	557	22		
5	J	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
5	K	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		
5	L	374	Total	C	N	O	S	0	0
			2917	1845	490	560	22		

- Molecule 6 is a protein called Spectrin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	130	Total	C	N	O	S	0	0
			1065	671	200	188	6		
6	N	122	Total	C	N	O	S	0	0
			1004	638	189	171	6		
6	O	131	Total	C	N	O	S	0	0
			1073	675	201	191	6		
6	P	117	Total	C	N	O	S	0	0
			960	609	181	164	6		
6	Q	129	Total	C	N	O	S	0	0
			1057	667	199	185	6		
6	R	117	Total	C	N	O	S	0	0
			960	609	181	164	6		
6	S	486	Total	C	N	O	S	0	0
			3983	2511	721	739	12		

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Mol	Chain	Residues	Atoms					AltConf	Trace
6	T	128	Total	C	N	O	S	0	0
			1048	660	197	185	6		

- Molecule 7 is a protein called Tropomyosin-1.9.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	U	246	Total	C	N	O	S	0	0
			1992	1208	357	421	6		

- Molecule 8 is a protein called Tropomyosin 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	V	246	Total	C	N	O	S	0	0
			2011	1218	362	421	10		
8	W	248	Total	C	N	O	S	0	0
			2017	1222	364	421	10		
8	X	241	Total	C	N	O	S	0	0
			1974	1196	356	413	9		

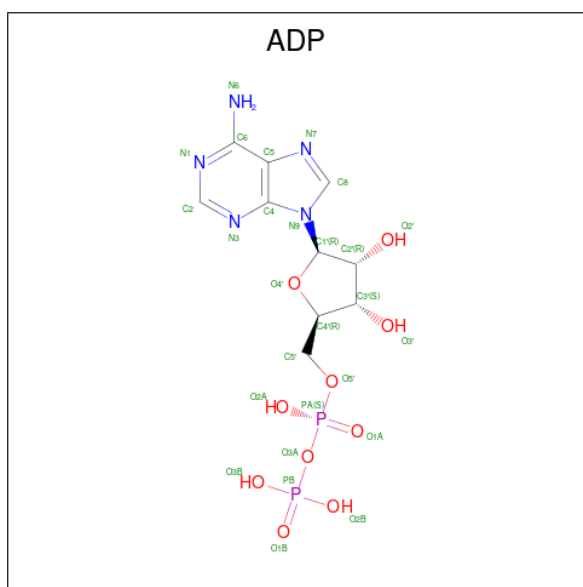
- Molecule 9 is a protein called Tropomodulin-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Y	333	Total	C	N	O	S	0	0
			2547	1599	443	496	9		

- Molecule 10 is a protein called SH3 domain-binding glutamic acid-rich-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Z	98	Total	C	N	O	S	0	0
			798	513	131	151	3		

- Molecule 11 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



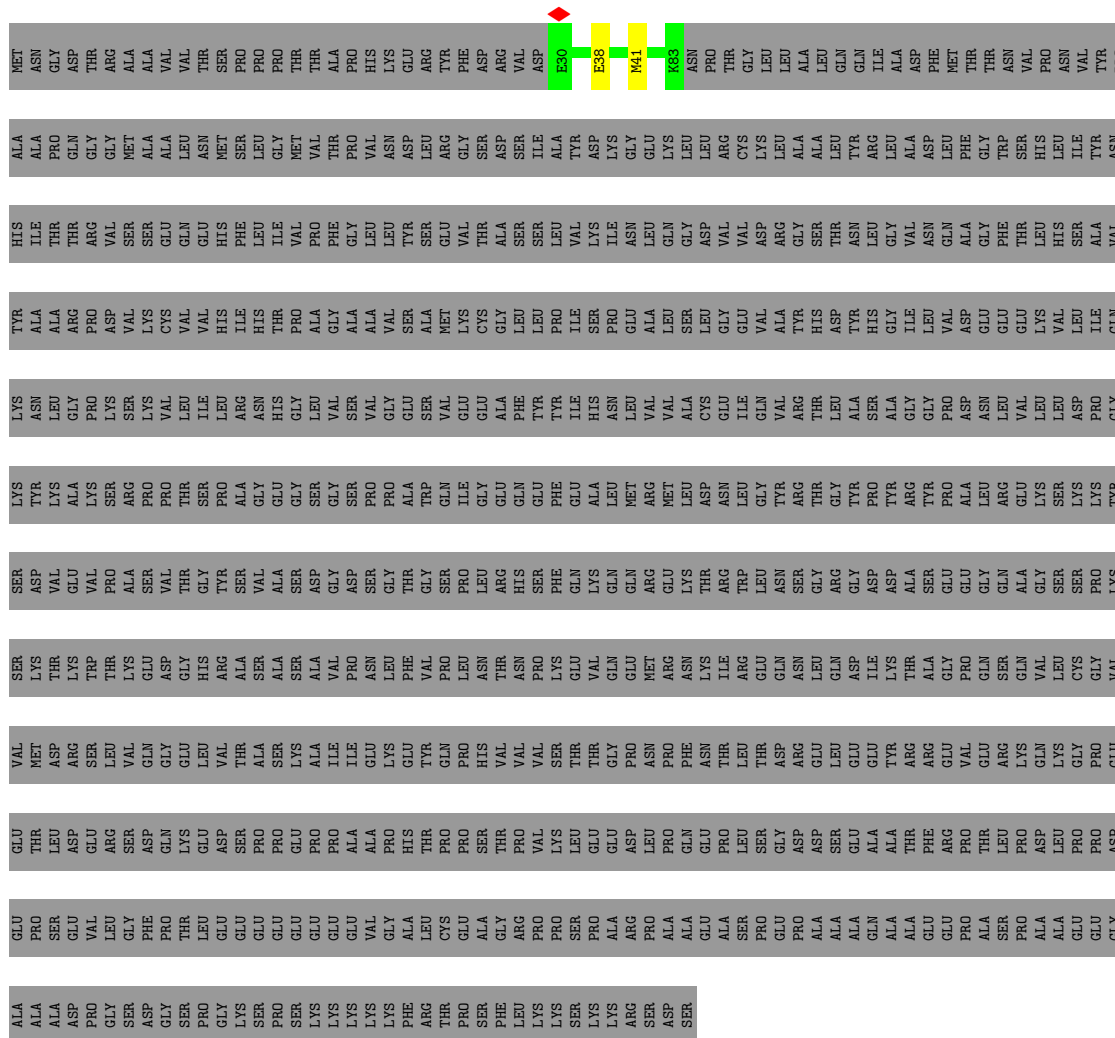
Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
11	A	1	Total 27	10	5	10	2	0
11	B	1	Total 27	10	5	10	2	0
11	C	1	Total 27	10	5	10	2	0
11	D	1	Total 27	10	5	10	2	0
11	E	1	Total 27	10	5	10	2	0
11	F	1	Total 27	10	5	10	2	0
11	G	1	Total 27	10	5	10	2	0
11	H	1	Total 27	10	5	10	2	0
11	I	1	Total 27	10	5	10	2	0
11	J	1	Total 27	10	5	10	2	0
11	K	1	Total 27	10	5	10	2	0
11	L	1	Total 27	10	5	10	2	0

### 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: Adducin 1

Chain 0:  7% 93%

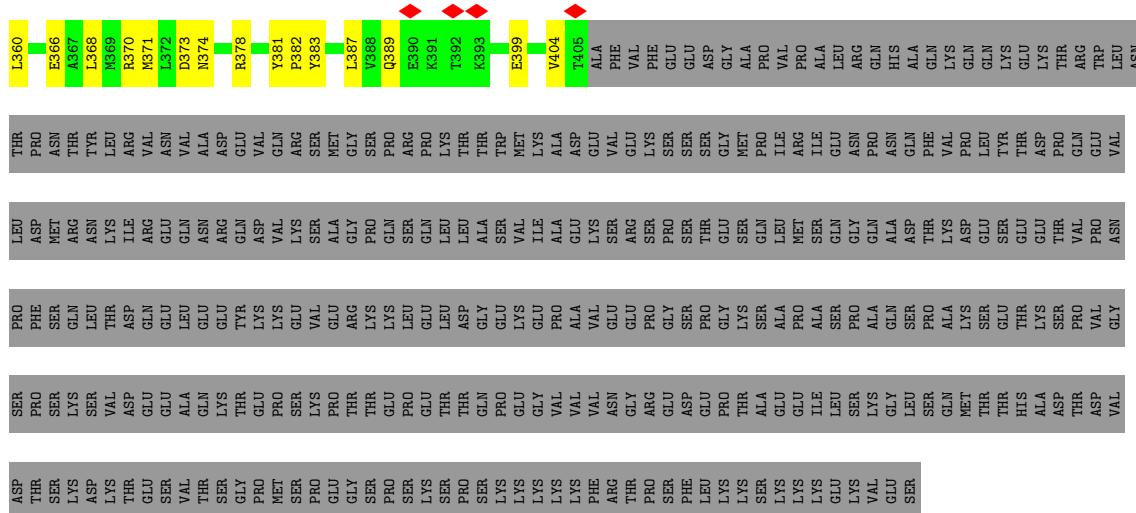


- Molecule 1: Adducin 1

Chain 1:  40% 5% 55%







● Molecule 2: Beta-adducin

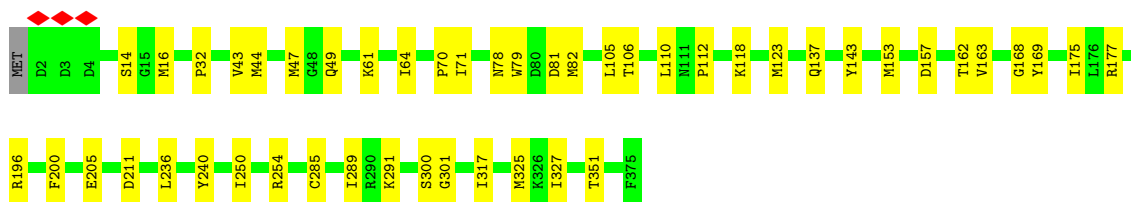












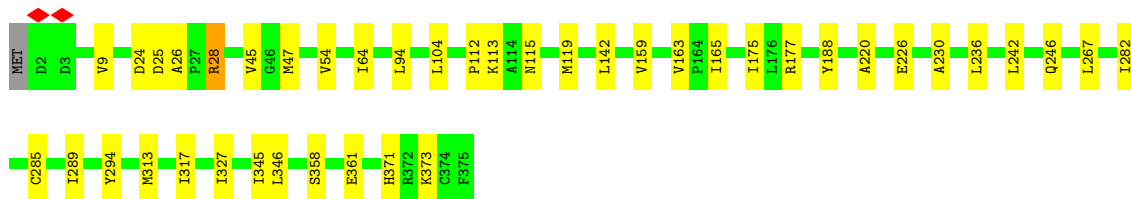
- Molecule 5: Actin, cytoplasmic 1

Chain C: 93% 6%



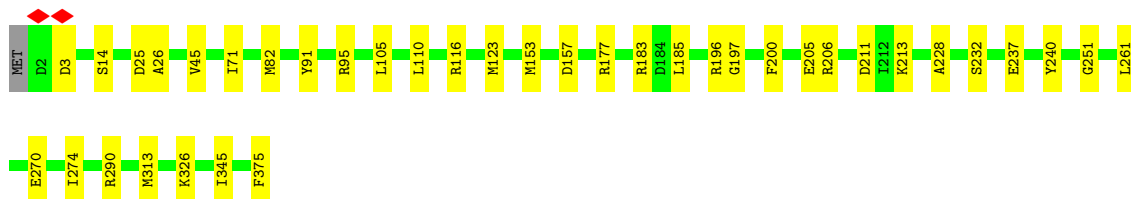
- Molecule 5: Actin, cytoplasmic 1

Chain D: 89% 11%



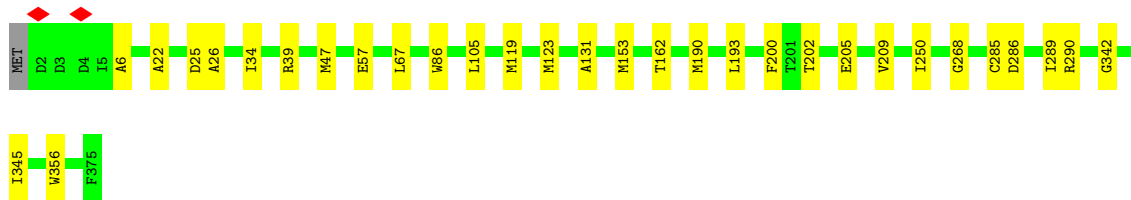
- Molecule 5: Actin, cytoplasmic 1

Chain E: 90% 10%



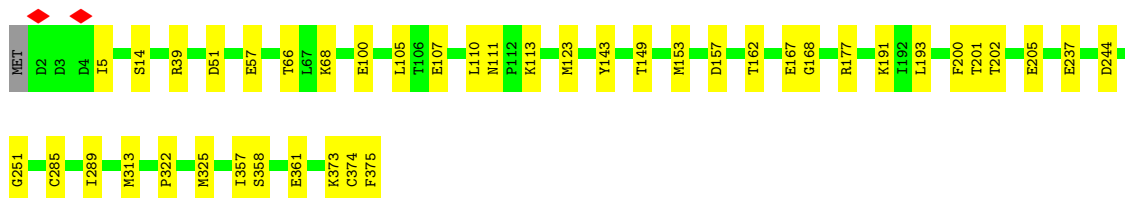
- Molecule 5: Actin, cytoplasmic 1

Chain F: 91% 8%

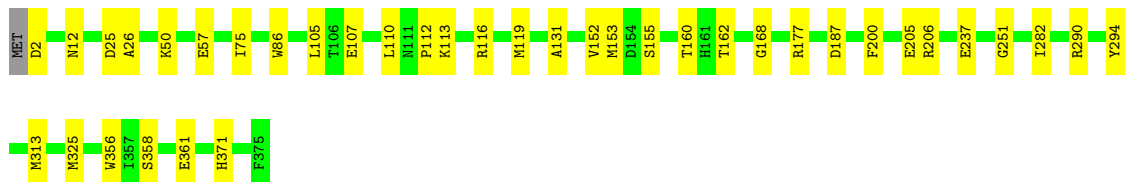
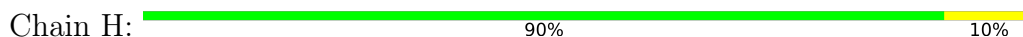


- Molecule 5: Actin, cytoplasmic 1

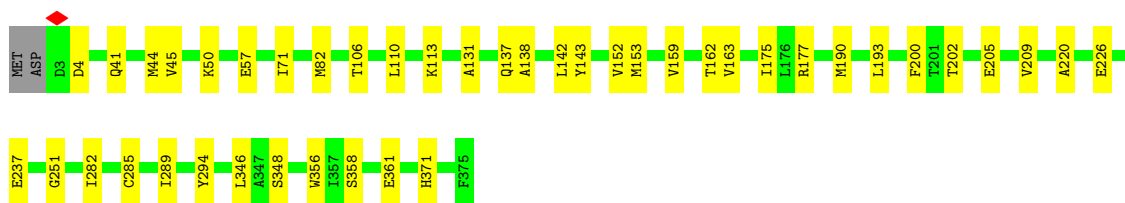
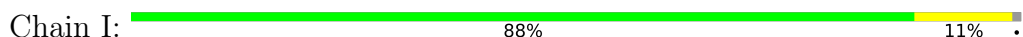
Chain G: 89% 11%



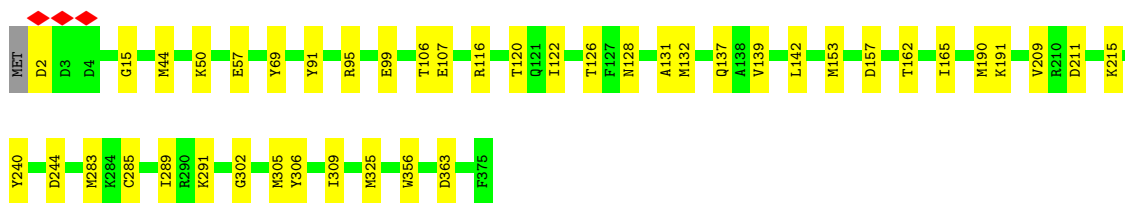
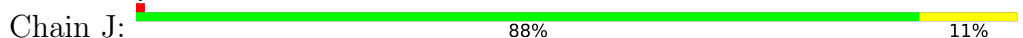
• Molecule 5: Actin, cytoplasmic 1



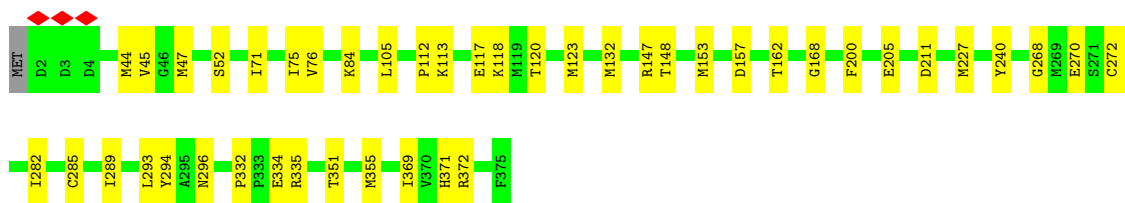
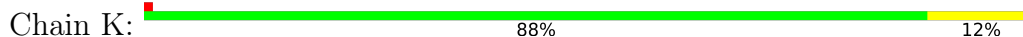
• Molecule 5: Actin, cytoplasmic 1



• Molecule 5: Actin, cytoplasmic 1



• Molecule 5: Actin, cytoplasmic 1



• Molecule 5: Actin, cytoplasmic 1





















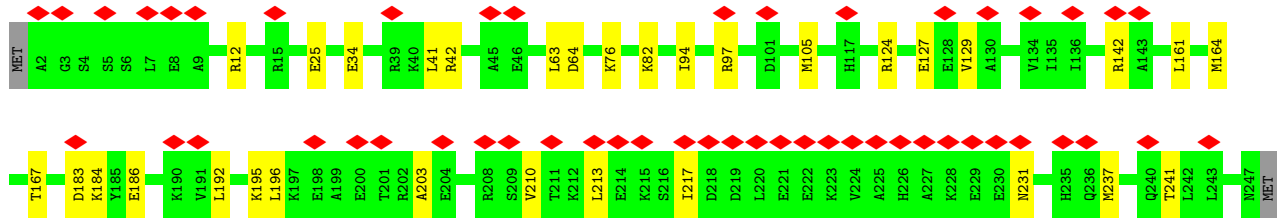




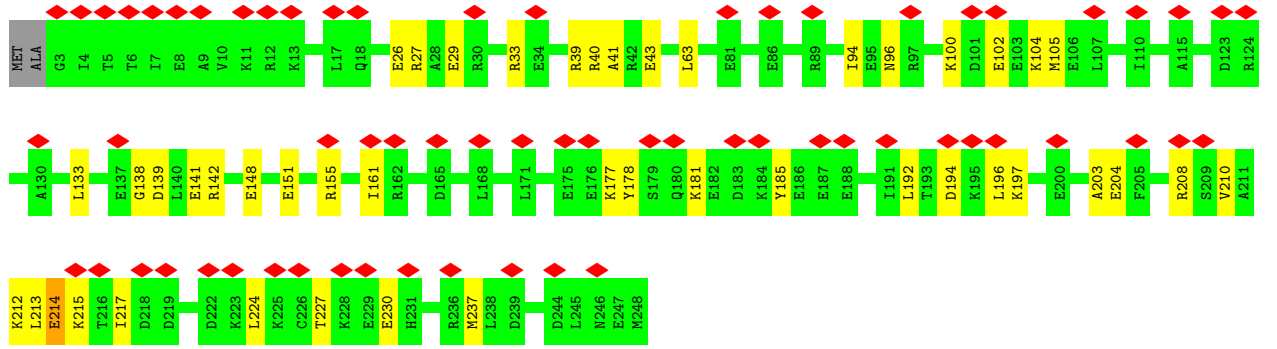
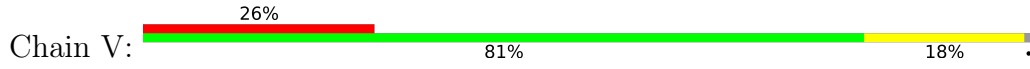




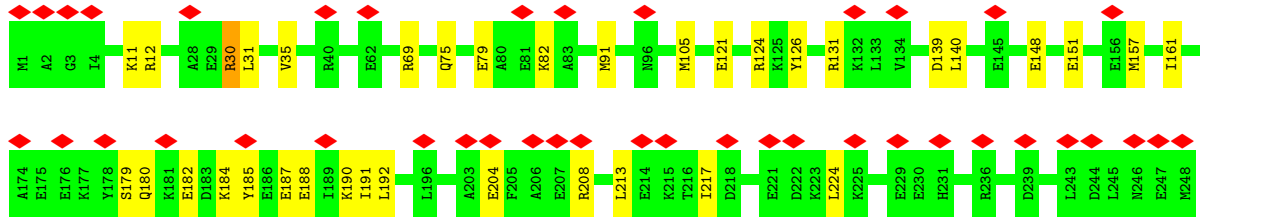
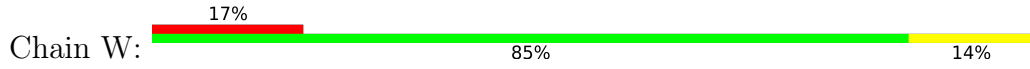




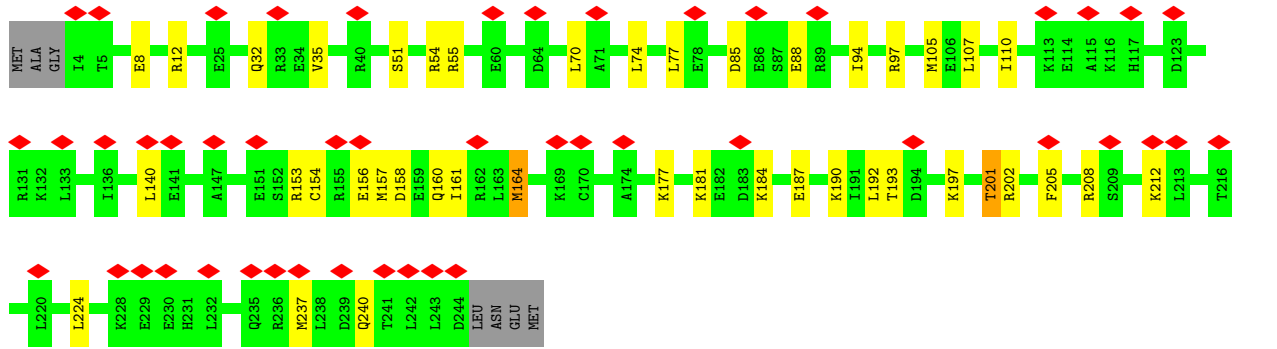
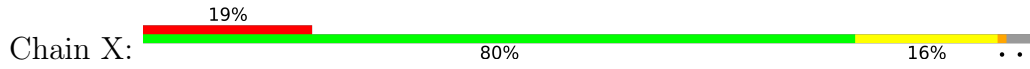
• Molecule 8: Tropomyosin 3



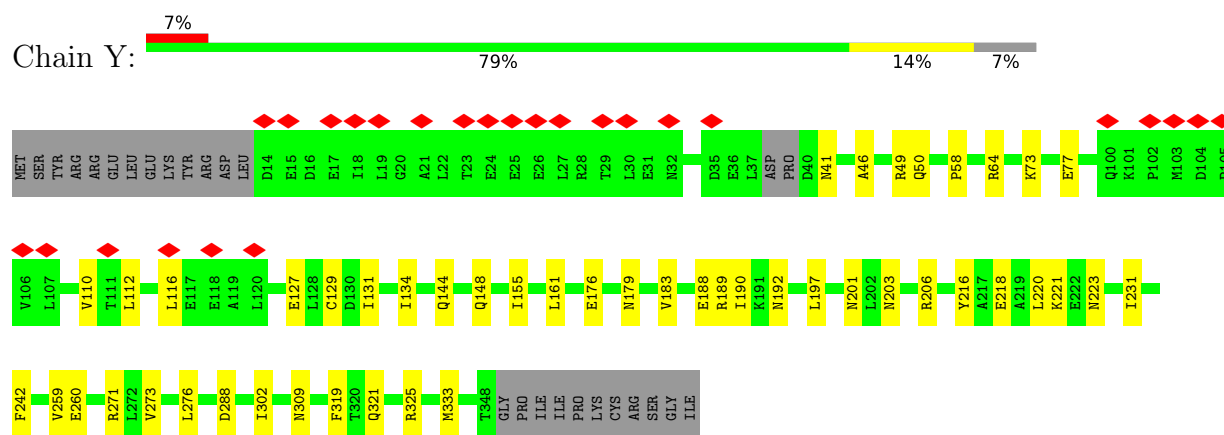
• Molecule 8: Tropomyosin 3



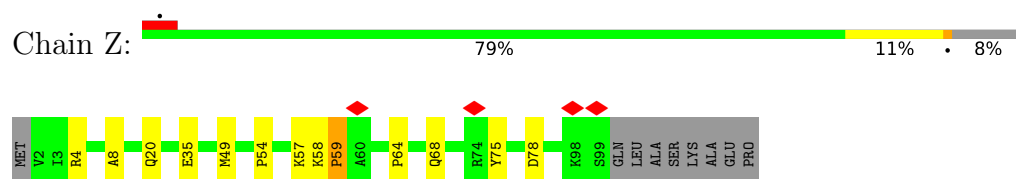
• Molecule 8: Tropomyosin 3



• Molecule 9: Tropomodulin-1



- Molecule 10: SH3 domain-binding glutamic acid-rich-like protein



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	43000	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 ( $e^-/\text{\AA}^2$ )	34.4	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	2.839	Depositor
Minimum map value	-1.150	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.071	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	657.6, 657.6, 657.6	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.37, 1.37, 1.37	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

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	0	0.24	0/459	0.66	0/609
1	1	0.17	0/2638	0.44	0/3579
1	2	0.14	0/2312	0.38	0/3139
2	3	0.18	0/2924	0.47	0/3956
2	4	0.16	0/2198	0.43	0/2978
2	9	0.29	0/459	0.77	1/610 (0.2%)
3	5	0.21	0/1040	0.58	0/1415
3	6	0.20	0/992	0.44	0/1358
3	7	0.19	0/1006	0.50	0/1369
4	8	0.26	0/2843	0.70	1/3851 (0.0%)
5	A	0.17	0/2970	0.40	0/4023
5	B	0.16	0/2980	0.35	0/4035
5	C	0.19	0/2972	0.37	0/4024
5	D	0.21	0/2980	0.42	2/4035 (0.0%)
5	E	0.20	0/2980	0.36	0/4035
5	F	0.19	0/2980	0.37	0/4035
5	G	0.18	0/2980	0.35	0/4035
5	H	0.19	0/2980	0.37	0/4035
5	I	0.20	0/2972	0.37	0/4024
5	J	0.21	0/2980	0.41	0/4035
5	K	0.19	0/2980	0.39	0/4035
5	L	0.16	0/2980	0.36	0/4035
6	M	0.19	0/1080	0.53	0/1448
6	N	0.18	0/1019	0.44	0/1365
6	O	0.20	0/1088	0.43	1/1459 (0.1%)
6	P	0.20	0/974	0.53	0/1305
6	Q	0.18	0/1072	0.40	0/1437
6	R	0.19	0/974	0.40	0/1305
6	S	0.24	0/4050	0.64	2/5458 (0.0%)
6	T	0.20	0/1063	0.42	0/1425
7	U	0.36	0/1999	0.68	1/2667 (0.0%)
8	V	0.37	0/2016	0.79	4/2687 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
8	W	0.47	0/2022	0.77	1/2696 (0.0%)
8	X	0.45	0/1979	0.79	5/2638 (0.2%)
9	Y	0.17	0/2584	0.46	0/3501
10	Z	0.51	1/817 (0.1%)	0.83	3/1099 (0.3%)
All	All	0.23	1/75342 (0.0%)	0.50	21/101740 (0.0%)

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
6	S	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	Z	59	PRO	CG-CD	-12.16	1.09	1.50

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	Z	59	PRO	N-CD-CG	-15.33	80.20	103.20
10	Z	59	PRO	CA-CB-CG	-9.20	87.02	104.50
8	X	55	ARG	CB-CG-CD	7.82	129.27	111.30
10	Z	59	PRO	CA-N-CD	-6.68	102.65	112.00
8	X	164	MET	CB-CA-C	6.46	120.87	110.09

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
6	S	405	ARG	Peptide

## 5.2 Too-close contacts [i](#)

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	0	453	0	446	1	0
1	1	2585	0	2610	22	0
1	2	2263	0	2279	40	0
2	3	2870	0	2884	34	0
2	4	2157	0	2149	33	0
2	9	455	0	456	10	0
3	5	1008	0	1009	10	0
3	6	963	0	914	9	0
3	7	976	0	965	16	0
4	8	2799	0	2478	45	0
5	A	2907	0	2851	37	0
5	B	2917	0	2879	32	0
5	C	2909	0	2875	18	0
5	D	2917	0	2879	32	0
5	E	2917	0	2879	26	0
5	F	2917	0	2879	22	0
5	G	2917	0	2879	30	0
5	H	2917	0	2879	28	0
5	I	2909	0	2875	28	0
5	J	2917	0	2879	29	0
5	K	2917	0	2879	30	0
5	L	2917	0	2879	25	0
6	M	1065	0	1109	11	0
6	N	1004	0	1060	9	0
6	O	1073	0	1113	15	0
6	P	960	0	1016	14	0
6	Q	1057	0	1105	10	0
6	R	960	0	1016	4	0
6	S	3983	0	4009	52	0
6	T	1048	0	1090	8	0
7	U	1992	0	1988	29	0
8	V	2011	0	2017	32	0
8	W	2017	0	2023	31	0
8	X	1974	0	1982	33	0
9	Y	2547	0	2527	34	0
10	Z	798	0	781	7	0
11	A	27	0	12	2	0
11	B	27	0	12	0	0
11	C	27	0	12	2	0
11	D	27	0	12	0	0
11	E	27	0	12	0	0
11	F	27	0	12	0	0
11	G	27	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	H	27	0	12	0	0
11	I	27	0	12	0	0
11	J	27	0	12	1	0
11	K	27	0	12	1	0
11	L	27	0	12	0	0
All	All	74320	0	73682	700	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 5.

The worst 5 of 700 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)
6:O:31:ASP:N	6:O:34:ASN:HD22	1.46	1.12
4:8:2206:ALA:O	4:8:2209:ARG:HB3	1.48	1.11
8:W:157:MET:HE1	8:X:158:ASP:HA	1.51	0.93
2:3:167:HIS:HA	2:3:188:VAL:O	1.81	0.80
5:I:159:VAL:HG21	5:I:177:ARG:HE	1.50	0.77

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	52/744 (7%)	50 (96%)	2 (4%)	0	100	100
1	1	328/744 (44%)	317 (97%)	11 (3%)	0	100	100
1	2	290/744 (39%)	278 (96%)	12 (4%)	0	100	100
2	3	357/724 (49%)	335 (94%)	21 (6%)	1 (0%)	36	65
2	4	276/724 (38%)	262 (95%)	14 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	9	52/724 (7%)	50 (96%)	2 (4%)	0	100	100
3	5	117/405 (29%)	114 (97%)	3 (3%)	0	100	100
3	6	119/405 (29%)	112 (94%)	7 (6%)	0	100	100
3	7	115/405 (28%)	105 (91%)	10 (9%)	0	100	100
4	8	377/2417 (16%)	356 (94%)	19 (5%)	2 (0%)	24	57
5	A	372/375 (99%)	355 (95%)	17 (5%)	0	100	100
5	B	372/375 (99%)	365 (98%)	7 (2%)	0	100	100
5	C	371/375 (99%)	363 (98%)	8 (2%)	0	100	100
5	D	372/375 (99%)	360 (97%)	12 (3%)	0	100	100
5	E	372/375 (99%)	361 (97%)	11 (3%)	0	100	100
5	F	372/375 (99%)	359 (96%)	13 (4%)	0	100	100
5	G	372/375 (99%)	363 (98%)	9 (2%)	0	100	100
5	H	372/375 (99%)	360 (97%)	12 (3%)	0	100	100
5	I	371/375 (99%)	359 (97%)	11 (3%)	1 (0%)	36	65
5	J	372/375 (99%)	363 (98%)	9 (2%)	0	100	100
5	K	372/375 (99%)	358 (96%)	14 (4%)	0	100	100
5	L	372/375 (99%)	360 (97%)	12 (3%)	0	100	100
6	M	128/2148 (6%)	124 (97%)	4 (3%)	0	100	100
6	N	120/2148 (6%)	119 (99%)	1 (1%)	0	100	100
6	O	129/2148 (6%)	127 (98%)	2 (2%)	0	100	100
6	P	115/2148 (5%)	112 (97%)	3 (3%)	0	100	100
6	Q	127/2148 (6%)	124 (98%)	3 (2%)	0	100	100
6	R	115/2148 (5%)	110 (96%)	5 (4%)	0	100	100
6	S	482/2148 (22%)	473 (98%)	9 (2%)	0	100	100
6	T	126/2148 (6%)	124 (98%)	2 (2%)	0	100	100
7	U	244/248 (98%)	242 (99%)	2 (1%)	0	100	100
8	V	244/248 (98%)	243 (100%)	1 (0%)	0	100	100
8	W	246/248 (99%)	243 (99%)	3 (1%)	0	100	100
8	X	239/248 (96%)	239 (100%)	0	0	100	100
9	Y	329/359 (92%)	318 (97%)	11 (3%)	0	100	100
10	Z	96/107 (90%)	94 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	9285/31178 (30%)	8997 (97%)	284 (3%)	4 (0%)	100	100

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	8	2068	VAL
5	I	4	ASP
4	8	2226	VAL
2	3	360	LEU

### 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	0	51/626 (8%)	51 (100%)	0	100	100
1	1	280/626 (45%)	280 (100%)	0	100	100
1	2	243/626 (39%)	243 (100%)	0	100	100
2	3	320/637 (50%)	320 (100%)	0	100	100
2	4	235/637 (37%)	235 (100%)	0	100	100
2	9	50/637 (8%)	50 (100%)	0	100	100
3	5	113/364 (31%)	113 (100%)	0	100	100
3	6	101/364 (28%)	101 (100%)	0	100	100
3	7	107/364 (29%)	107 (100%)	0	100	100
4	8	257/2118 (12%)	257 (100%)	0	100	100
5	A	313/318 (98%)	313 (100%)	0	100	100
5	B	317/318 (100%)	317 (100%)	0	100	100
5	C	316/318 (99%)	316 (100%)	0	100	100
5	D	317/318 (100%)	317 (100%)	0	100	100
5	E	317/318 (100%)	317 (100%)	0	100	100
5	F	317/318 (100%)	317 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	G	317/318 (100%)	317 (100%)	0	100	100
5	H	317/318 (100%)	317 (100%)	0	100	100
5	I	316/318 (99%)	316 (100%)	0	100	100
5	J	317/318 (100%)	317 (100%)	0	100	100
5	K	317/318 (100%)	317 (100%)	0	100	100
5	L	317/318 (100%)	317 (100%)	0	100	100
6	M	119/1870 (6%)	119 (100%)	0	100	100
6	N	111/1870 (6%)	111 (100%)	0	100	100
6	O	120/1870 (6%)	120 (100%)	0	100	100
6	P	107/1870 (6%)	107 (100%)	0	100	100
6	Q	118/1870 (6%)	118 (100%)	0	100	100
6	R	107/1870 (6%)	107 (100%)	0	100	100
6	S	429/1870 (23%)	429 (100%)	0	100	100
6	T	117/1870 (6%)	117 (100%)	0	100	100
7	U	212/214 (99%)	212 (100%)	0	100	100
8	V	215/216 (100%)	215 (100%)	0	100	100
8	W	214/216 (99%)	214 (100%)	0	100	100
8	X	211/216 (98%)	211 (100%)	0	100	100
9	Y	271/318 (85%)	271 (100%)	0	100	100
10	Z	89/96 (93%)	89 (100%)	0	100	100
All	All	7995/27051 (30%)	7995 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
6	S	447	GLN
7	U	53	ASN
9	Y	223	ASN
5	C	296	ASN
5	C	115	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

12 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
11	ADP	B	401	-	28,29,29	1.40	4 (14%)	43,45,45	1.83	11 (25%)
11	ADP	E	401	-	28,29,29	1.37	4 (14%)	43,45,45	1.86	8 (18%)
11	ADP	D	401	-	28,29,29	1.39	5 (17%)	43,45,45	1.83	8 (18%)
11	ADP	H	401	-	28,29,29	1.37	5 (17%)	43,45,45	1.84	8 (18%)
11	ADP	G	401	-	28,29,29	1.38	4 (14%)	43,45,45	1.83	9 (20%)
11	ADP	A	401	-	28,29,29	1.39	4 (14%)	43,45,45	1.83	10 (23%)
11	ADP	I	401	-	28,29,29	1.37	5 (17%)	43,45,45	1.83	8 (18%)
11	ADP	C	401	-	28,29,29	1.38	5 (17%)	43,45,45	1.84	10 (23%)
11	ADP	L	401	-	28,29,29	1.40	5 (17%)	43,45,45	1.85	11 (25%)
11	ADP	K	401	-	28,29,29	1.37	5 (17%)	43,45,45	1.84	9 (20%)
11	ADP	J	401	-	28,29,29	1.36	4 (14%)	43,45,45	1.85	8 (18%)
11	ADP	F	401	-	28,29,29	1.39	4 (14%)	43,45,45	1.84	8 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
11	ADP	B	401	-	-	6/16/32/32	0/3/3/3
11	ADP	E	401	-	-	3/16/32/32	0/3/3/3
11	ADP	D	401	-	-	5/16/32/32	0/3/3/3
11	ADP	H	401	-	-	5/16/32/32	0/3/3/3
11	ADP	G	401	-	-	5/16/32/32	0/3/3/3
11	ADP	A	401	-	-	7/16/32/32	0/3/3/3
11	ADP	I	401	-	-	5/16/32/32	0/3/3/3
11	ADP	C	401	-	-	6/16/32/32	0/3/3/3
11	ADP	L	401	-	-	3/16/32/32	0/3/3/3
11	ADP	K	401	-	-	5/16/32/32	0/3/3/3
11	ADP	J	401	-	-	5/16/32/32	0/3/3/3
11	ADP	F	401	-	-	5/16/32/32	0/3/3/3

The worst 5 of 54 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	401	ADP	C5-C4	4.66	1.47	1.39
11	F	401	ADP	C5-C4	4.62	1.47	1.39
11	L	401	ADP	C5-C4	4.62	1.47	1.39
11	B	401	ADP	C5-C4	4.62	1.47	1.39
11	D	401	ADP	C5-C4	4.59	1.47	1.39

The worst 5 of 108 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	E	401	ADP	C5-C4-N3	-6.10	118.31	126.72
11	H	401	ADP	C5-C4-N3	-5.94	118.53	126.72
11	J	401	ADP	C5-C4-N3	-5.88	118.63	126.72
11	I	401	ADP	C5-C4-N3	-5.87	118.64	126.72
11	F	401	ADP	C5-C4-N3	-5.86	118.65	126.72

There are no chirality outliers.

5 of 60 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
11	A	401	ADP	PA-O3A-PB-O3B
11	A	401	ADP	C5'-O5'-PA-O1A

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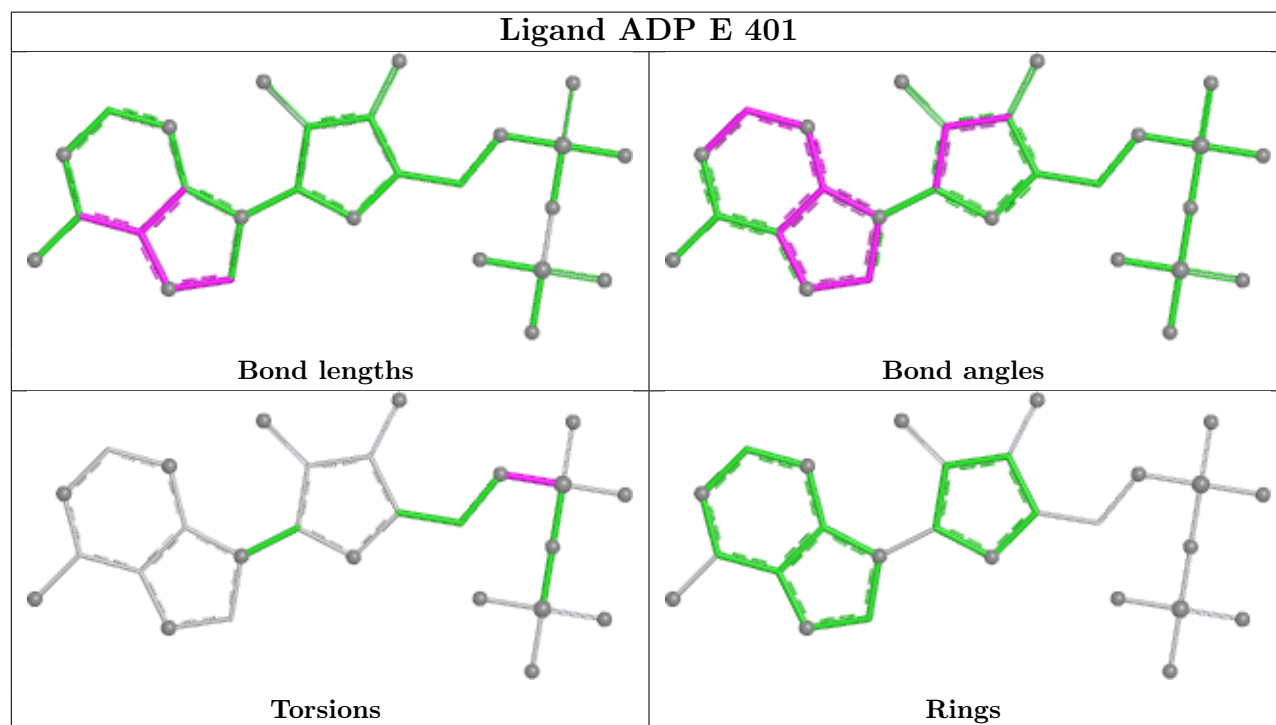
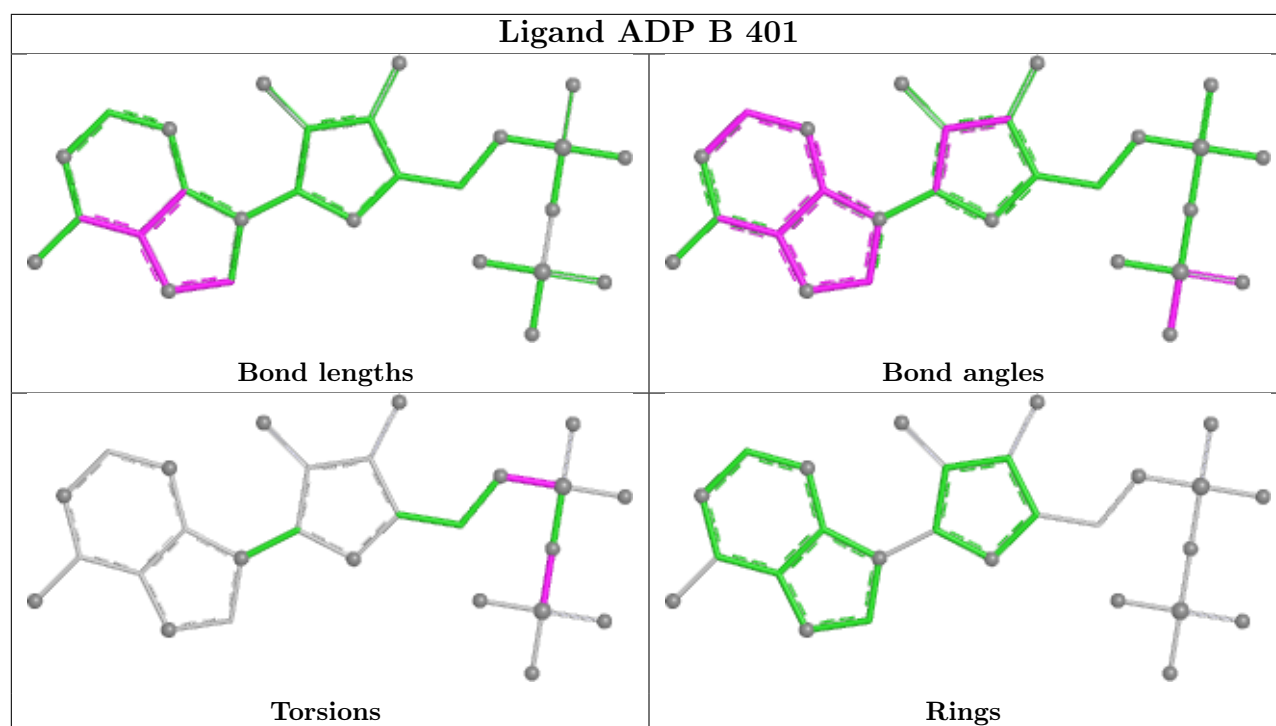
Mol	Chain	Res	Type	Atoms
11	A	401	ADP	C5'-O5'-PA-O2A
11	A	401	ADP	C5'-O5'-PA-O3A
11	B	401	ADP	PA-O3A-PB-O3B

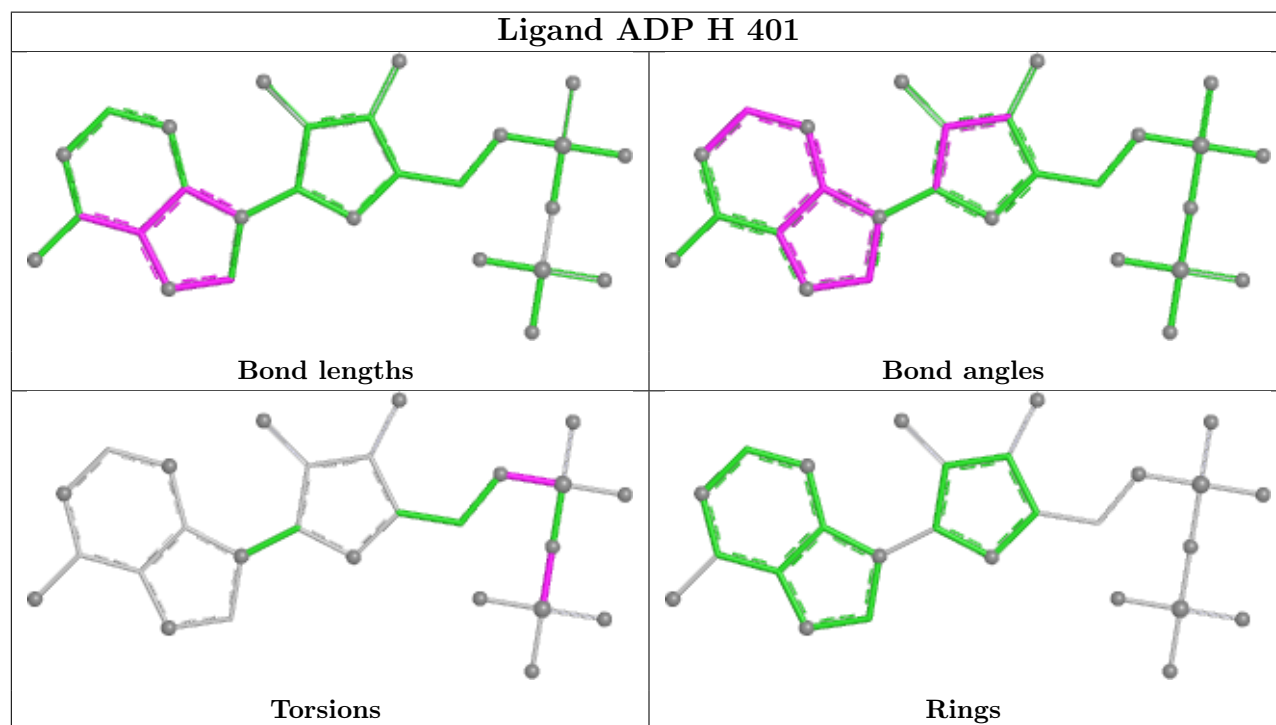
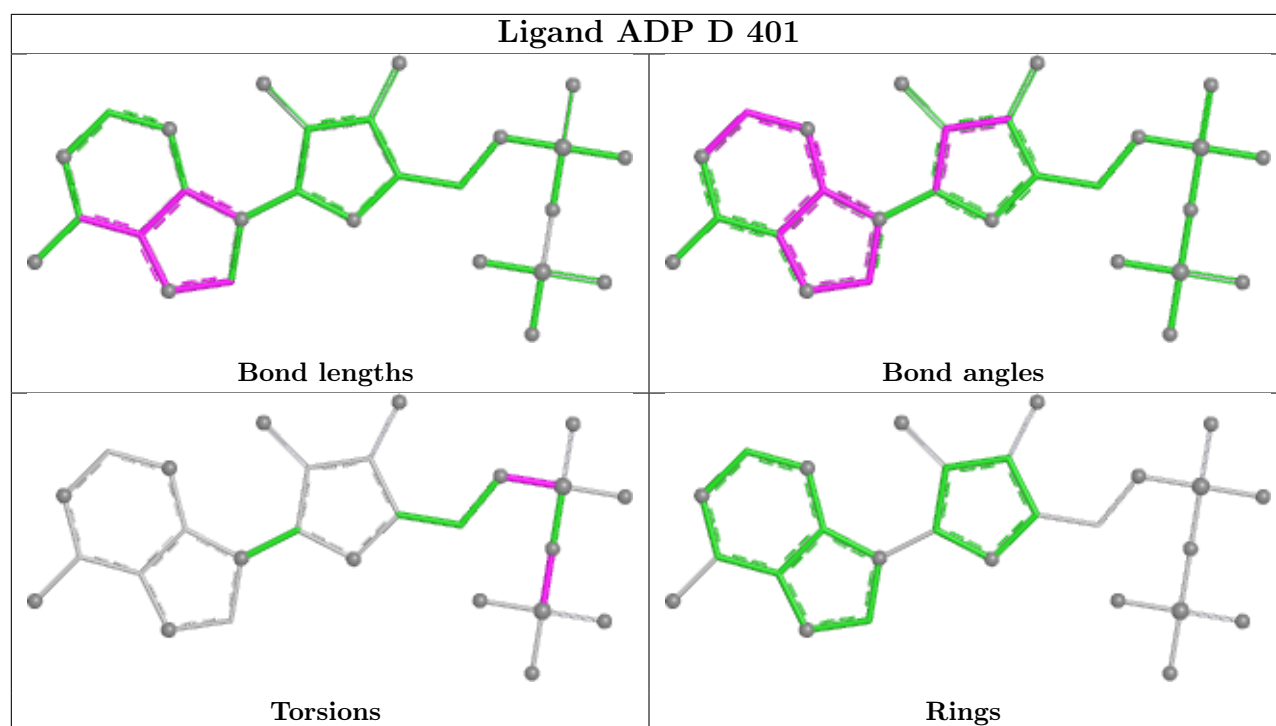
There are no ring outliers.

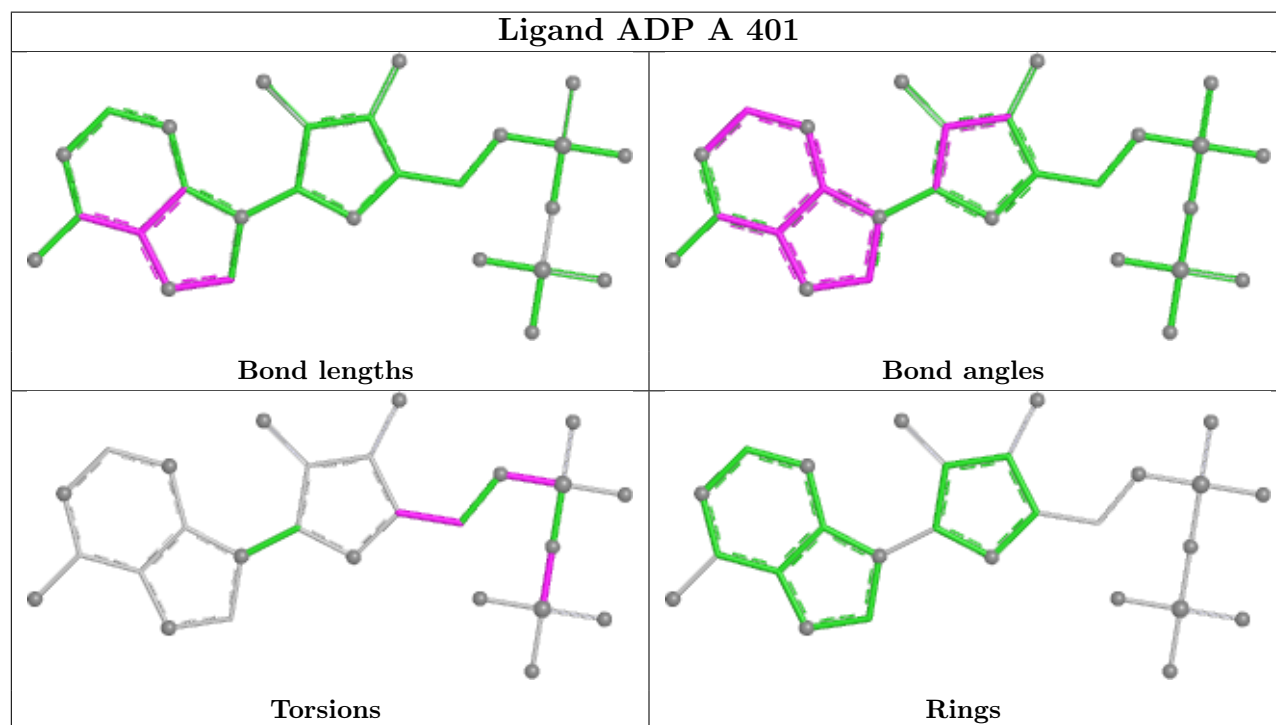
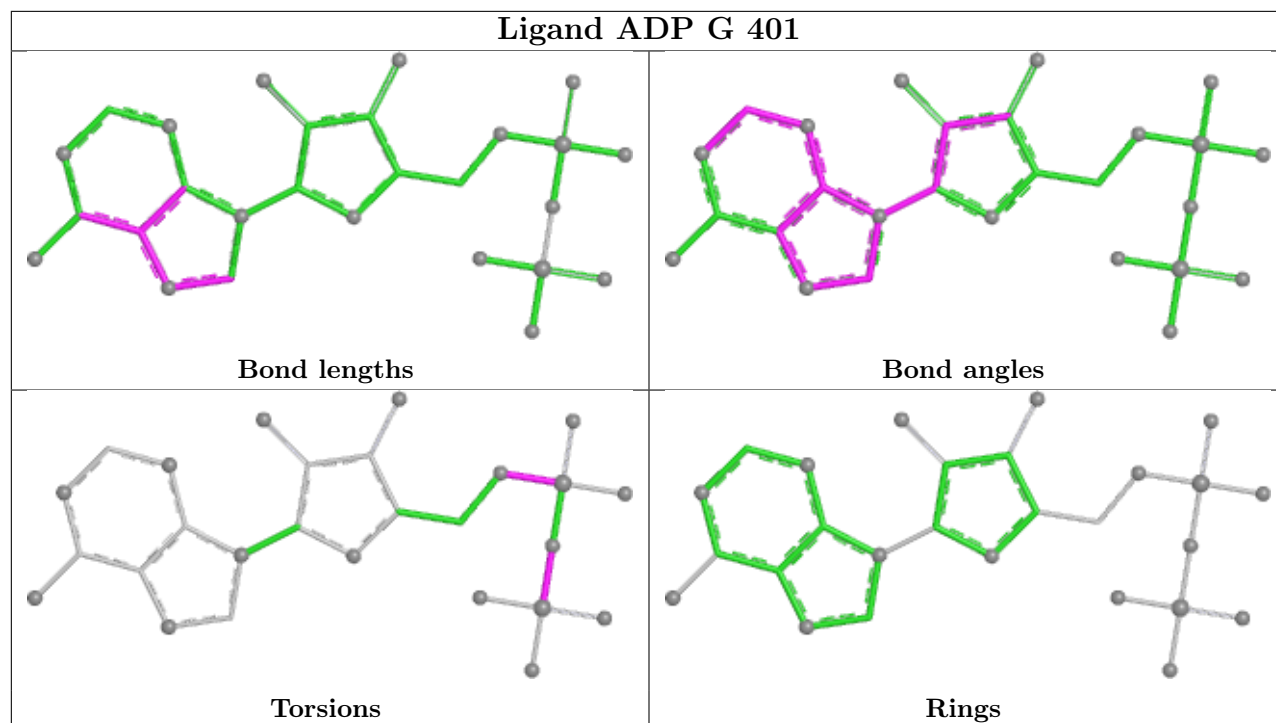
5 monomers are involved in 7 short contacts:

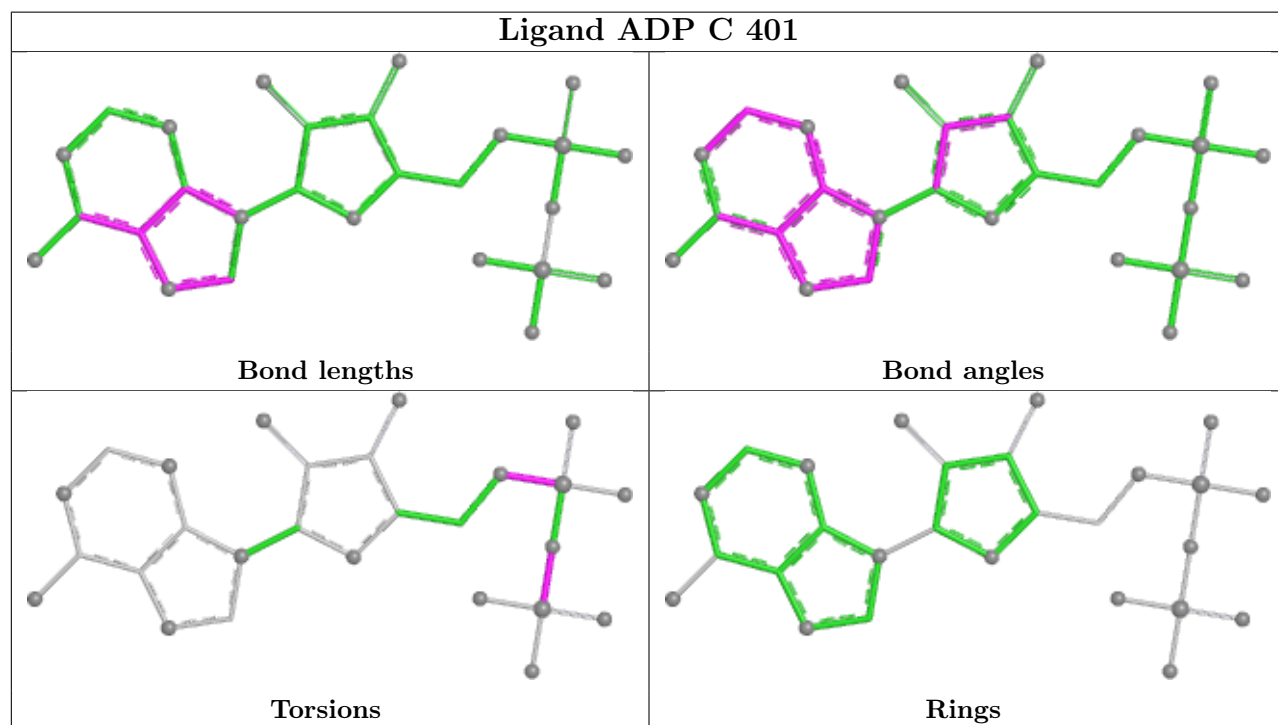
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	G	401	ADP	1	0
11	A	401	ADP	2	0
11	C	401	ADP	2	0
11	K	401	ADP	1	0
11	J	401	ADP	1	0

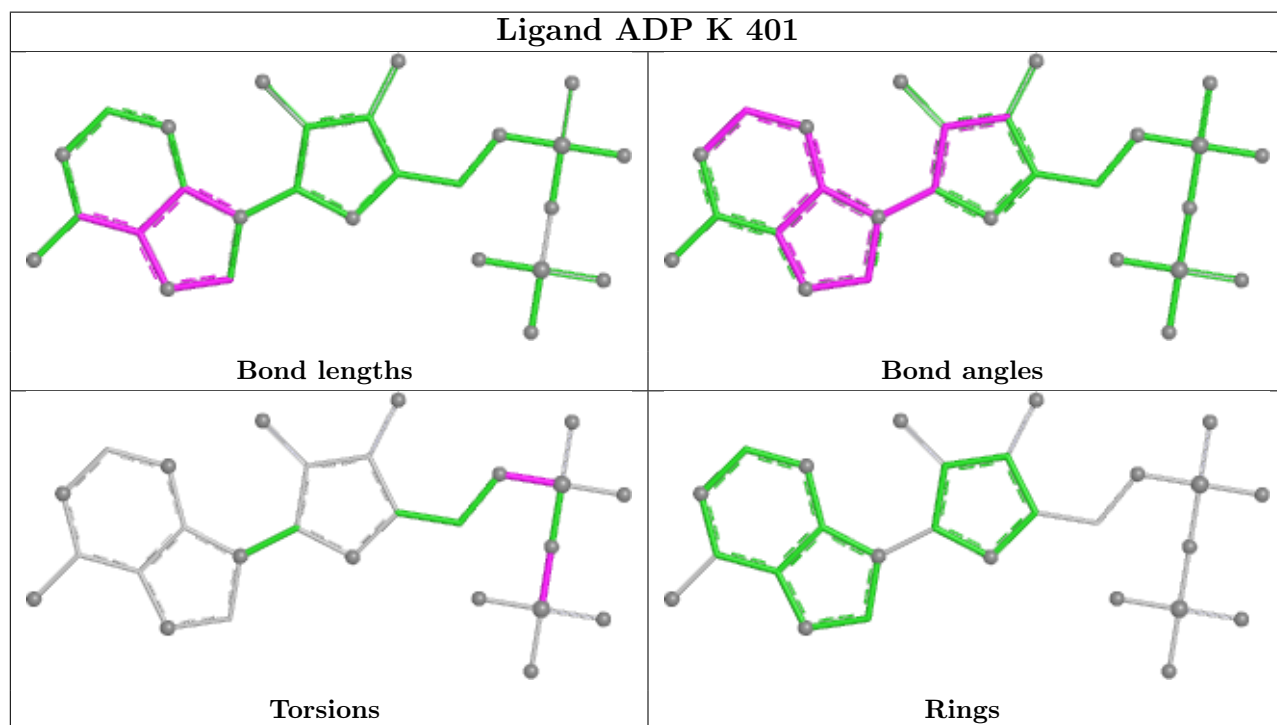
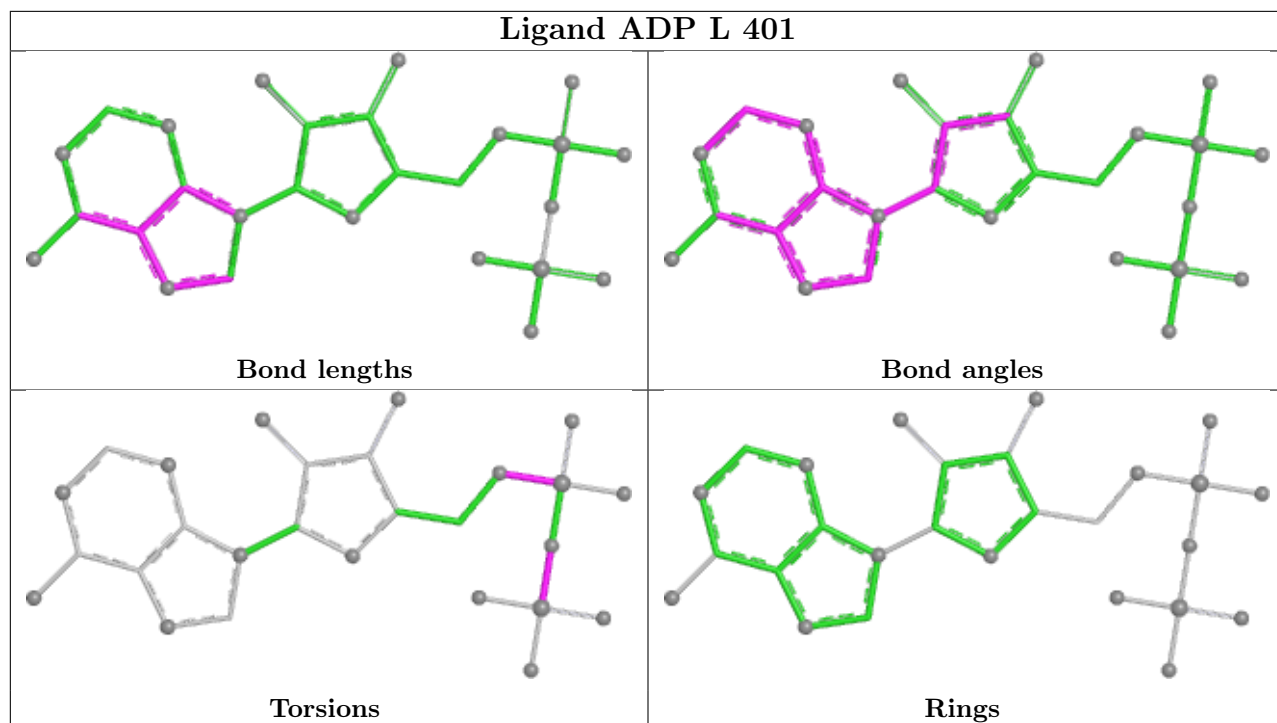
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

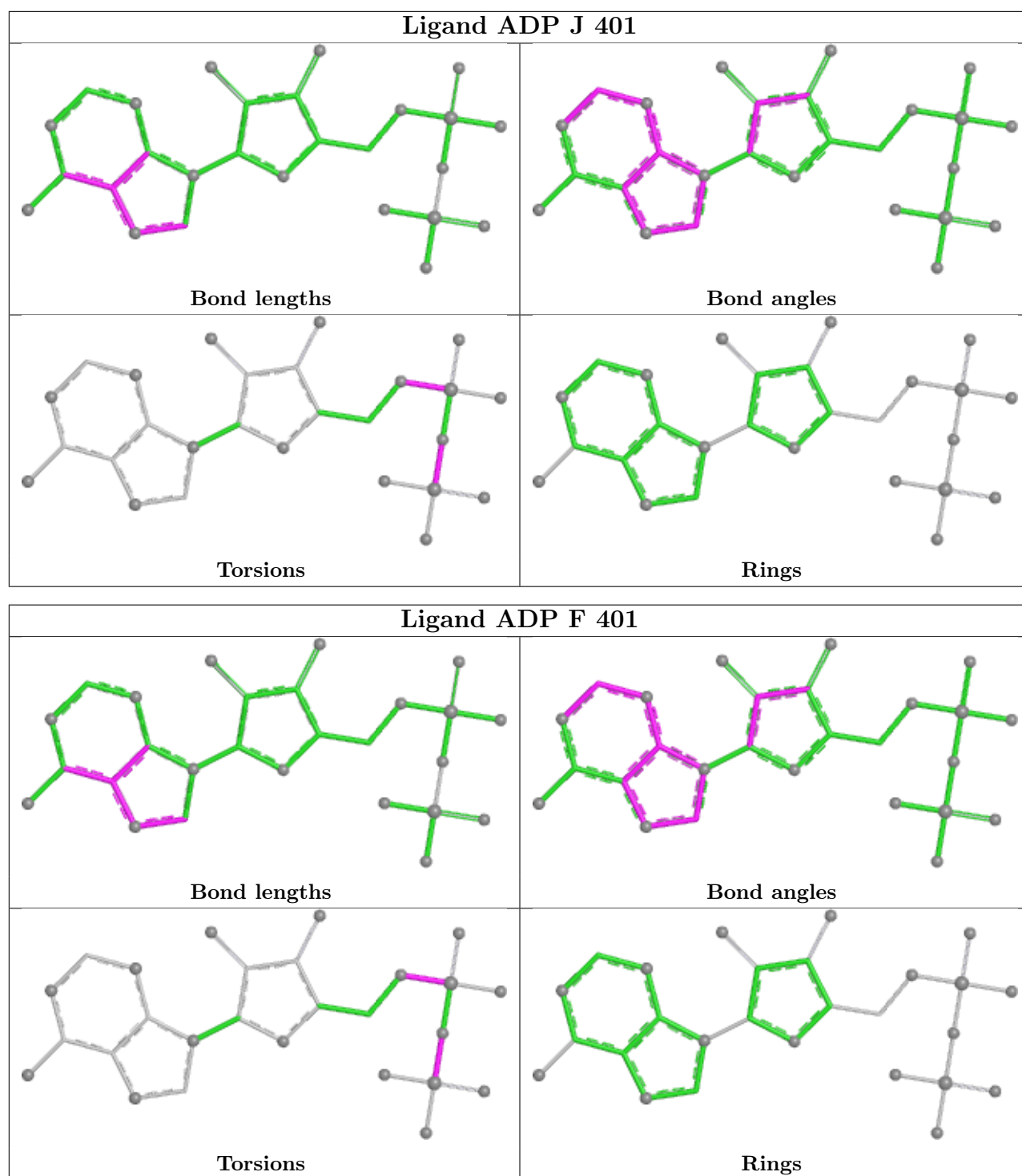












## 5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

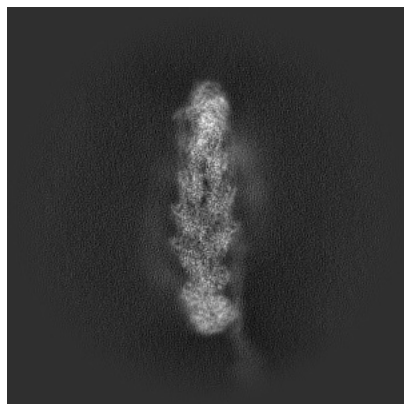
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35301. These allow visual inspection of the internal detail of the map and identification of artifacts.

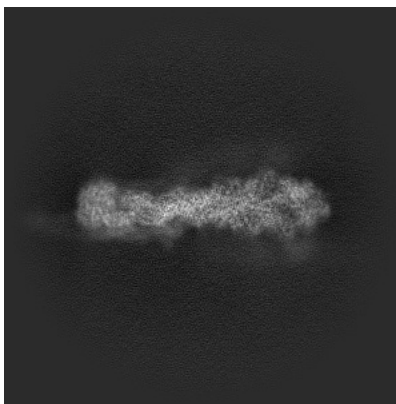
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

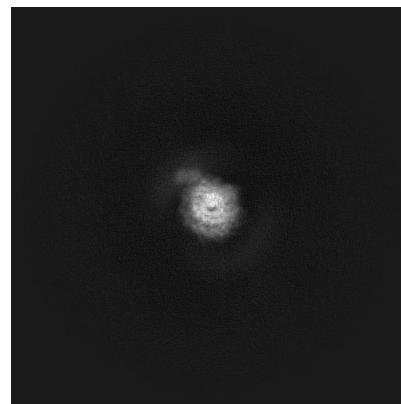
#### 6.1.1 Primary map



X

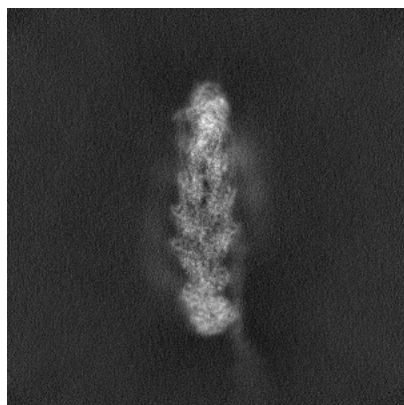


Y

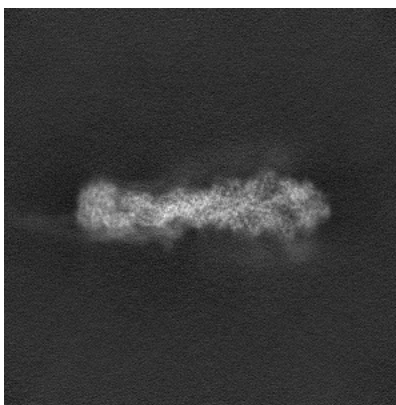


Z

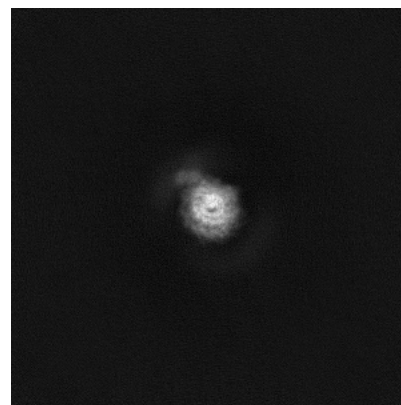
#### 6.1.2 Raw map



X



Y

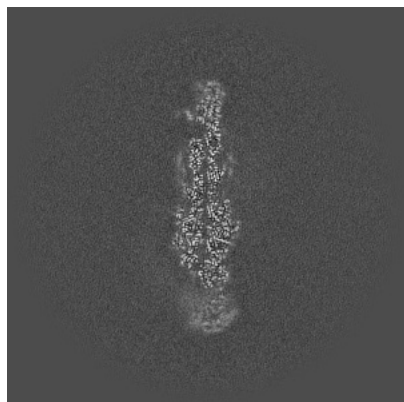


Z

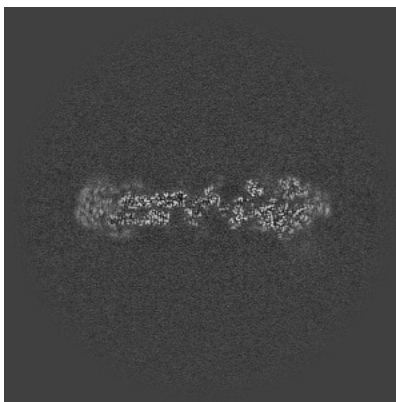
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

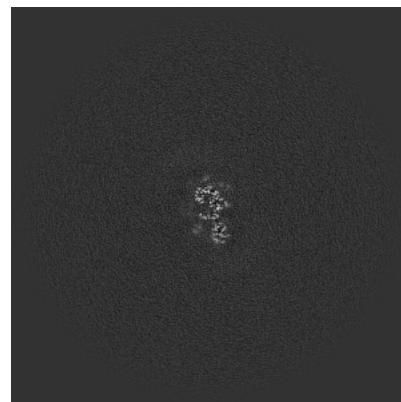
### 6.2.1 Primary map



X Index: 240

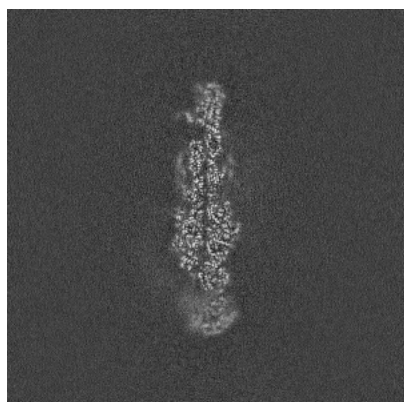


Y Index: 240

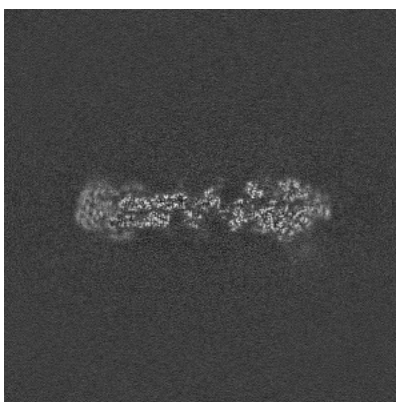


Z Index: 240

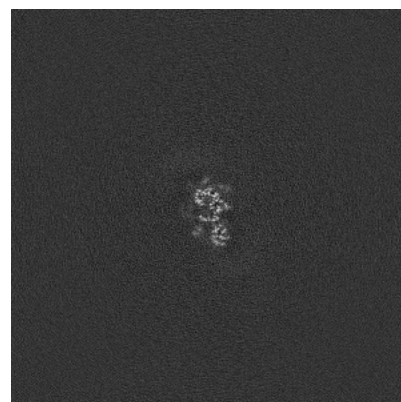
### 6.2.2 Raw map



X Index: 240



Y Index: 240

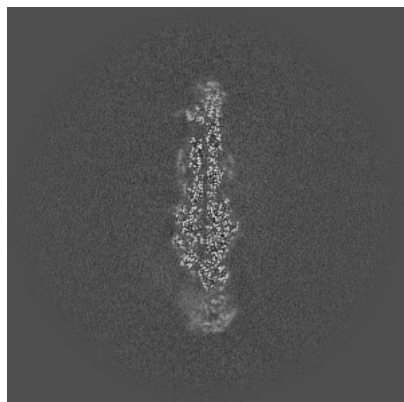


Z Index: 240

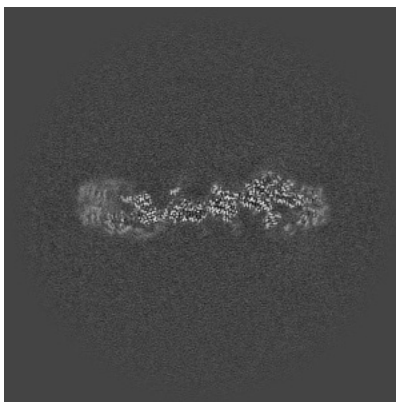
The images above show central slices of the map in three orthogonal directions.

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

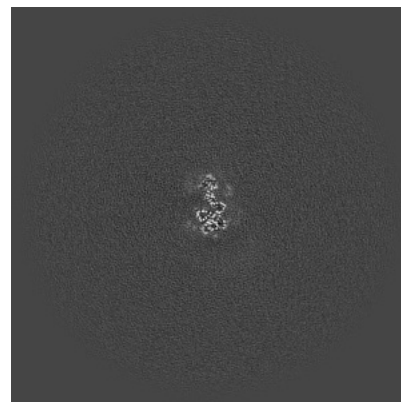
### 6.3.1 Primary map



X Index: 241

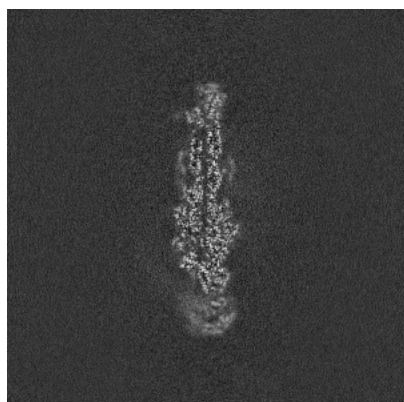


Y Index: 231

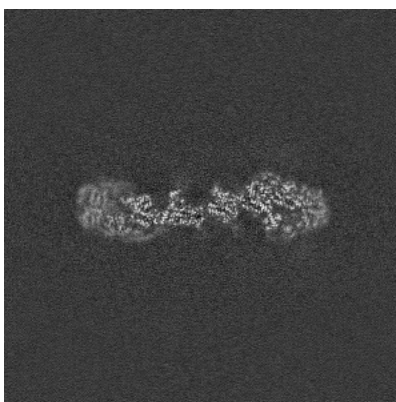


Z Index: 214

### 6.3.2 Raw map



X Index: 242



Y Index: 232

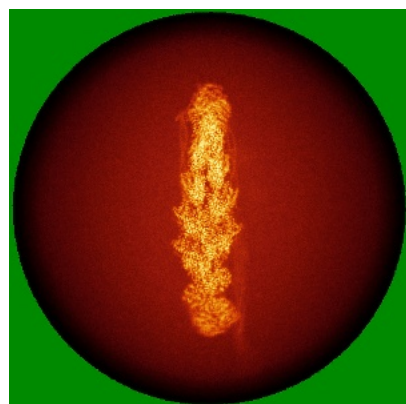


Z Index: 249

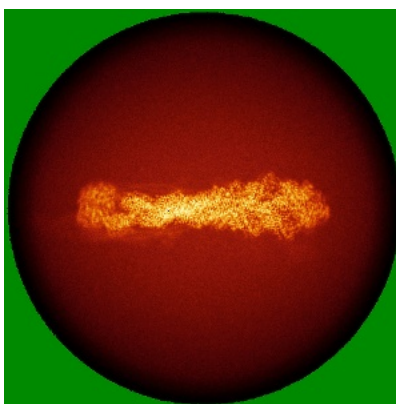
The images above show the largest variance slices of the map in three orthogonal directions.

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

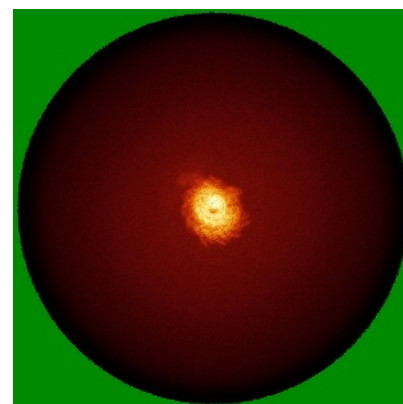
### 6.4.1 Primary map



X

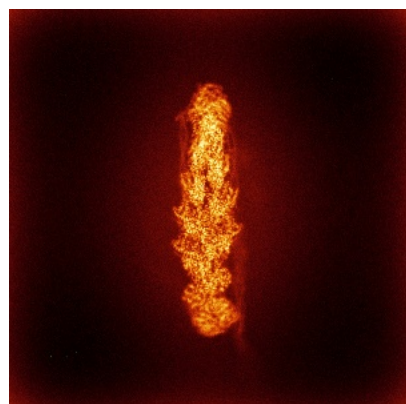


Y

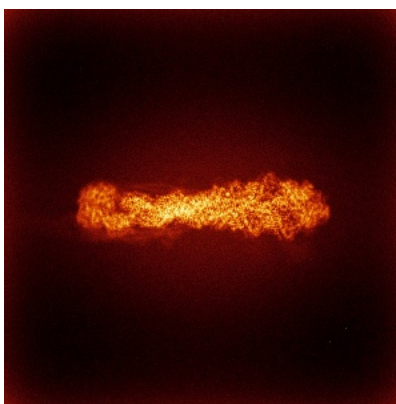


Z

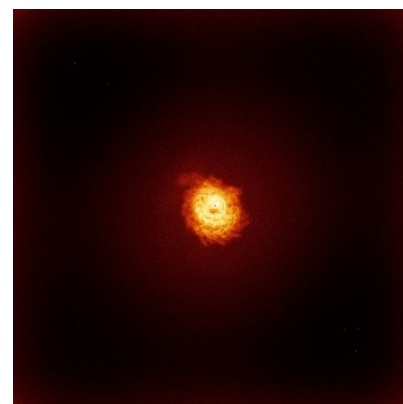
### 6.4.2 Raw map



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 0.35. 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.

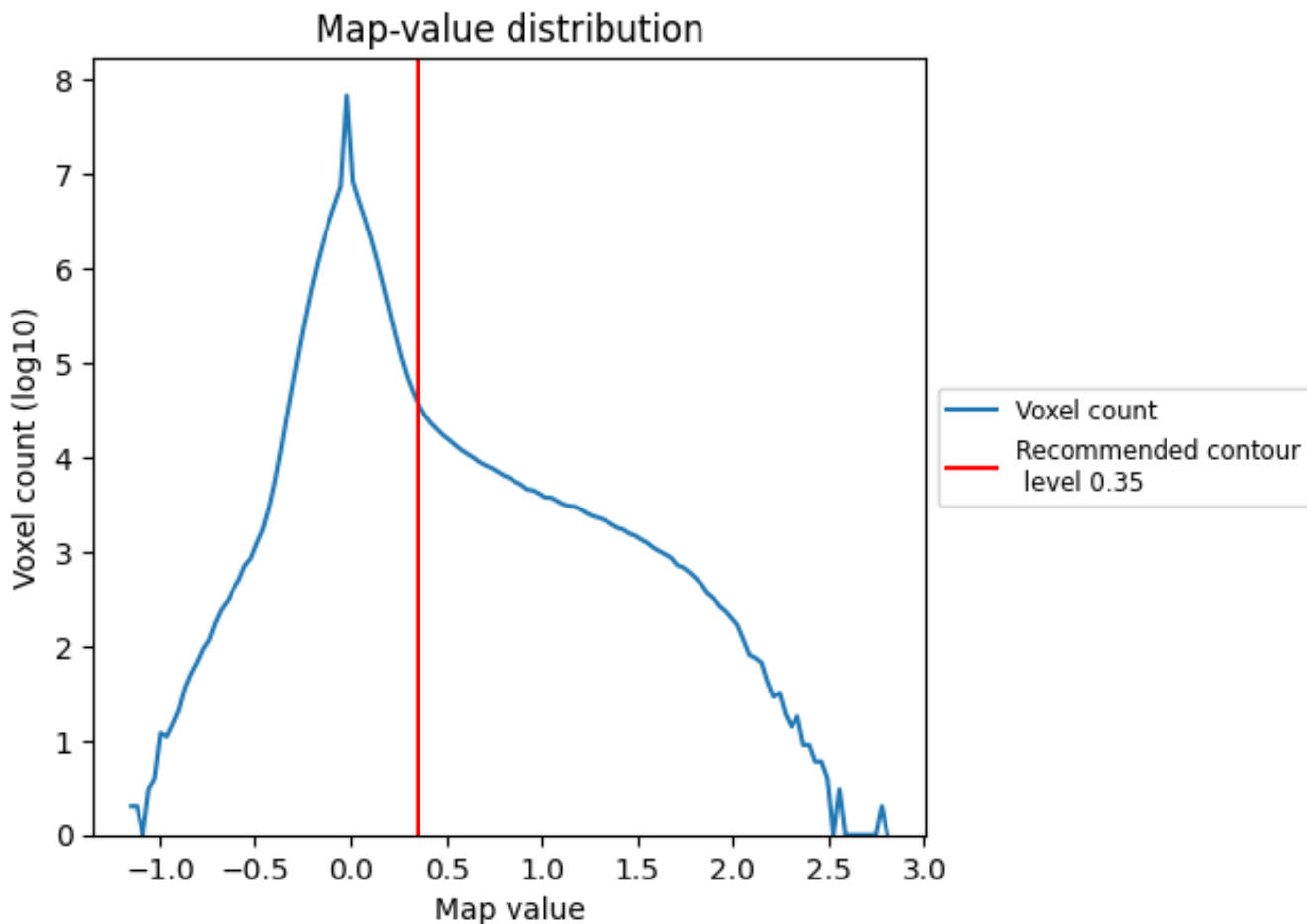
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

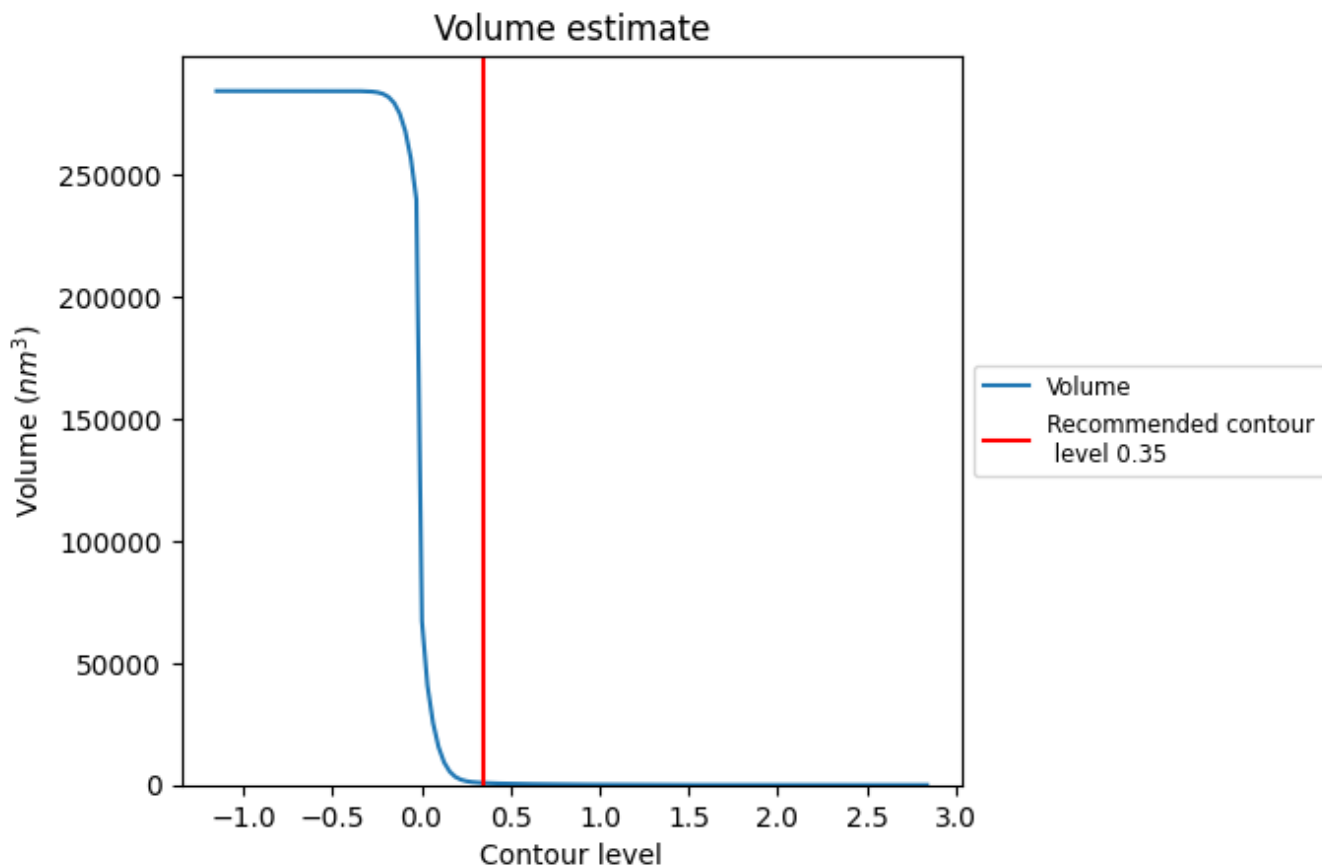
This section contains the results of statistical analysis of the map.

### 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.

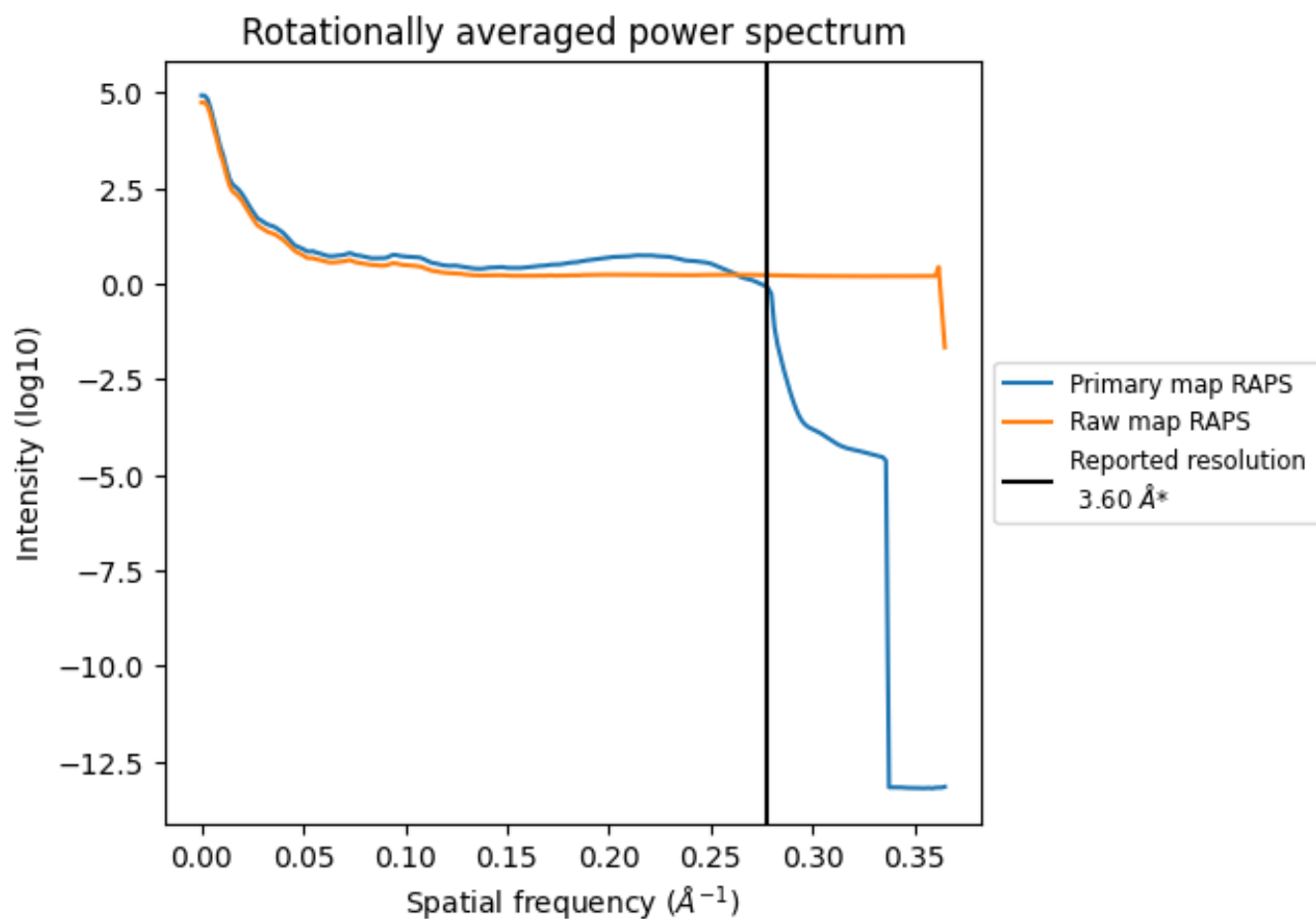
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is  $817 \text{ nm}^3$ ; this corresponds to an approximate mass of 738 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](#)

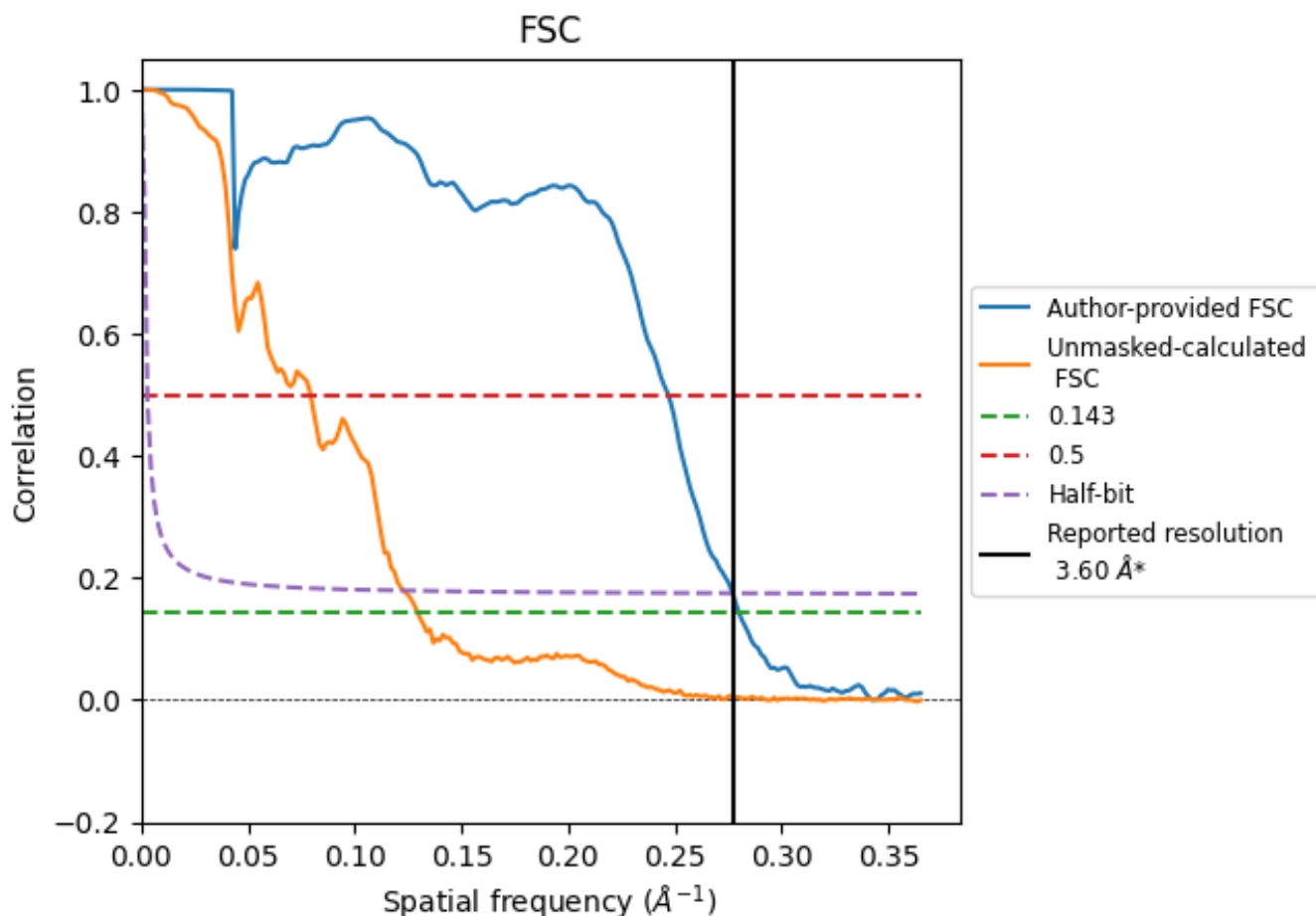


\*Reported resolution corresponds to spatial frequency of 0.278 Å<sup>-1</sup>

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

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.278 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

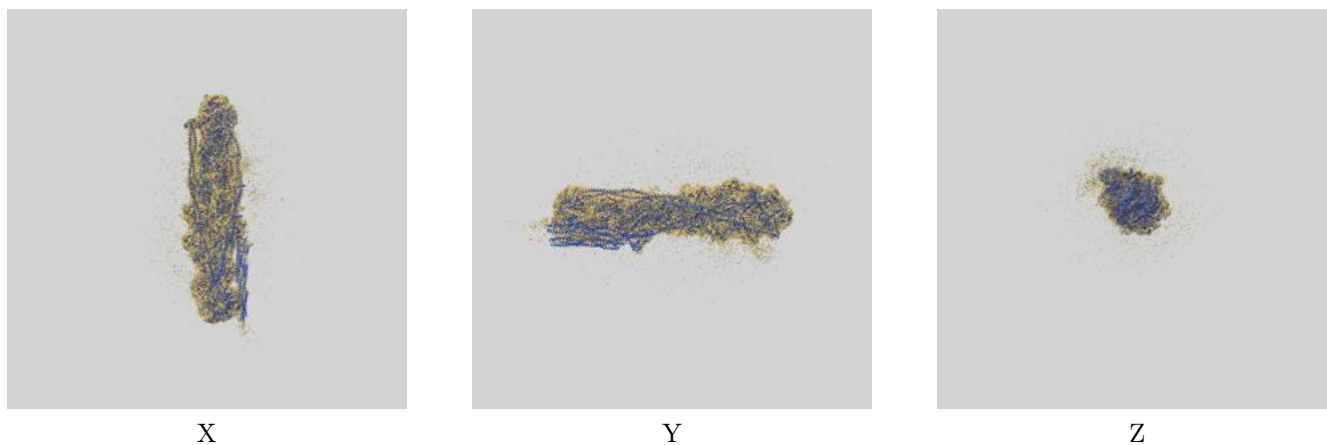
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.57	4.05	3.61
Unmasked-calculated*	7.73	12.61	8.13

\*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 7.73 differs from the reported value 3.6 by more than 10 %

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

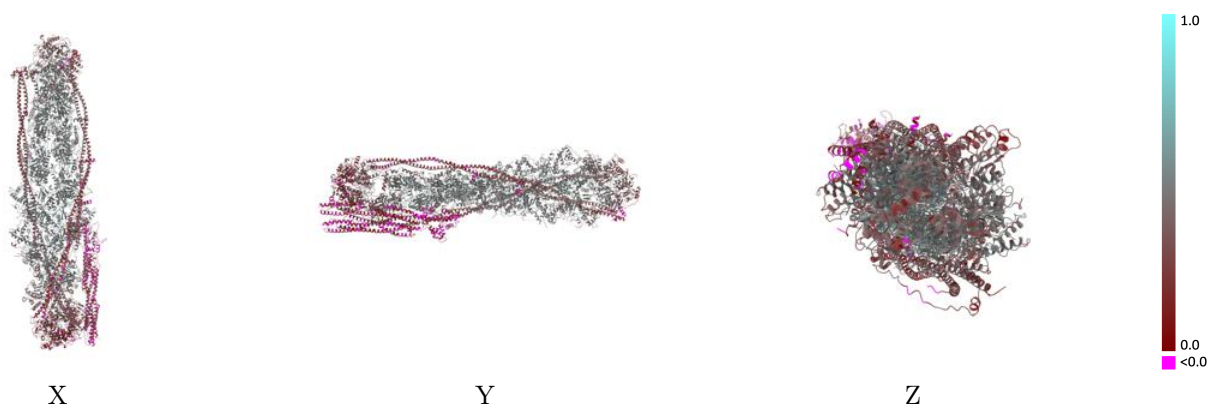
This section contains information regarding the fit between EMDB map EMD-35301 and PDB model 8IAH. Per-residue inclusion information can be found in section [3](#) on page [9](#).

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



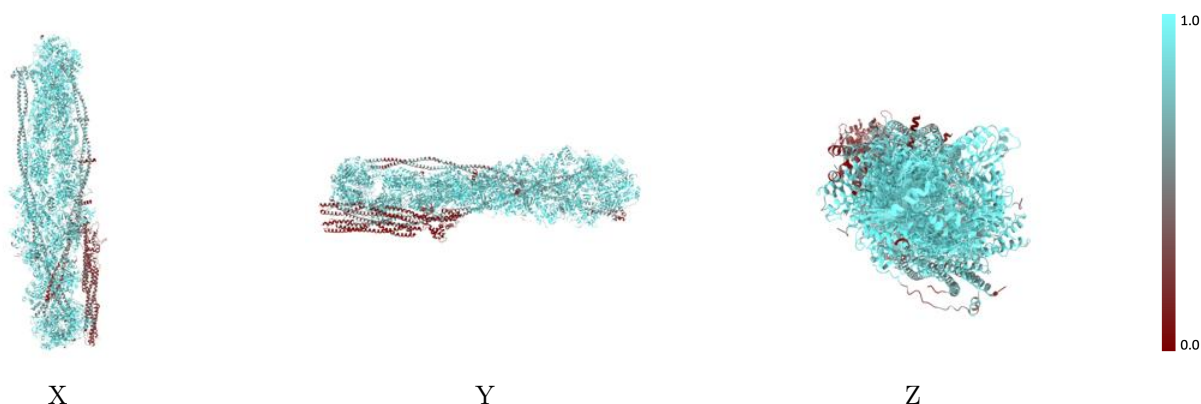
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



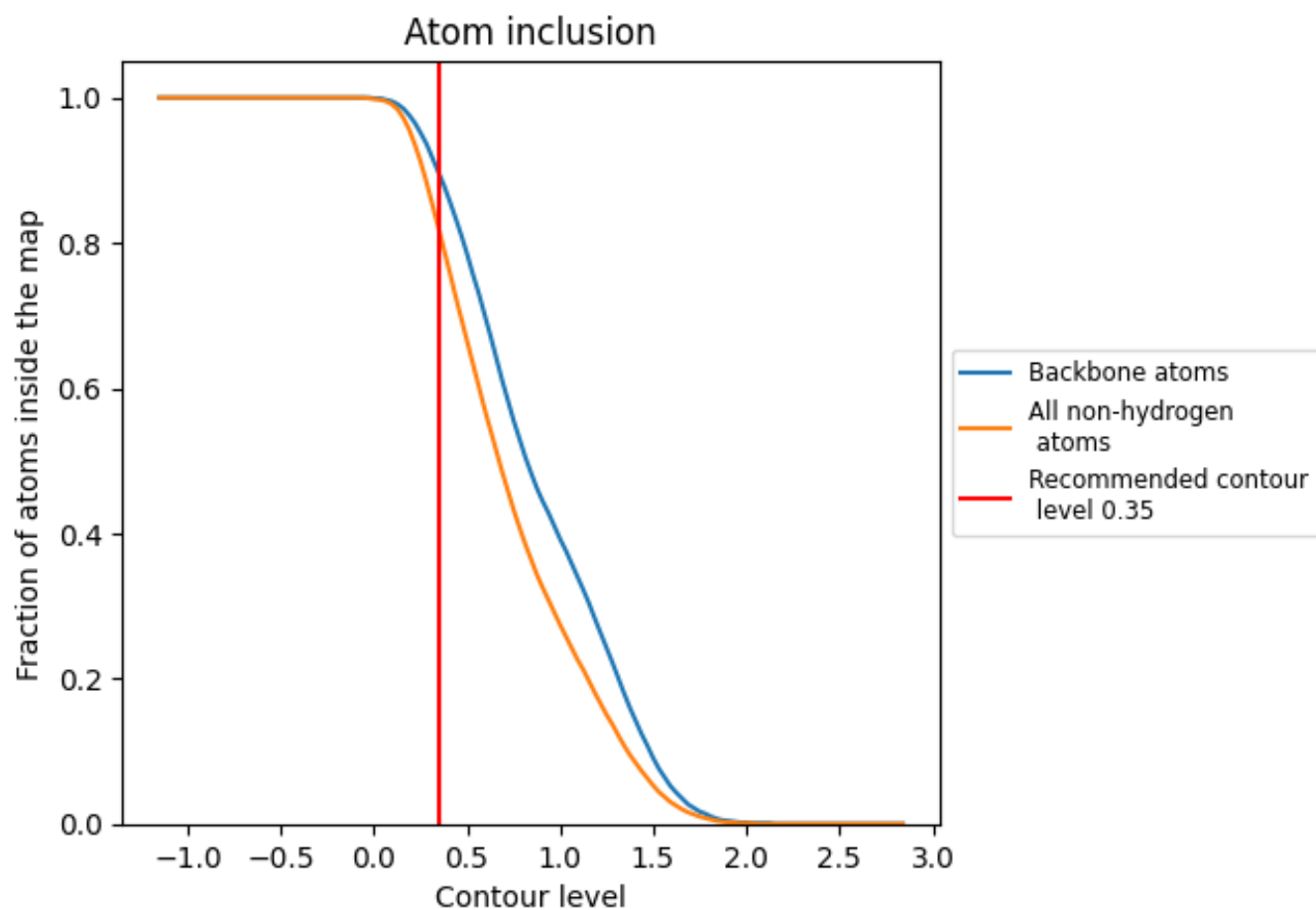
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.35).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 82% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8180	 0.3850
0	 0.8490	 0.2980
1	 0.8800	 0.3370
2	 0.8640	 0.2550
3	 0.8300	 0.2810
4	 0.8390	 0.2770
5	 0.7780	 0.3820
6	 0.6920	 0.3810
7	 0.7140	 0.3650
8	 0.1040	 0.0700
9	 0.8150	 0.3460
A	 0.9340	 0.4030
B	 0.9500	 0.4640
C	 0.9550	 0.4970
D	 0.9520	 0.4980
E	 0.9600	 0.5090
F	 0.9550	 0.5030
G	 0.9640	 0.5080
H	 0.9580	 0.5040
I	 0.9570	 0.5030
J	 0.9500	 0.5010
K	 0.9490	 0.4800
L	 0.9270	 0.4330
M	 0.9340	 0.4210
N	 0.8710	 0.4340
O	 0.9470	 0.4680
P	 0.9370	 0.4610
Q	 0.9610	 0.4690
R	 0.9520	 0.4720
S	 0.3960	 0.2030
T	 0.9450	 0.4540
U	 0.5690	 0.2710
V	 0.5340	 0.2430
W	 0.5970	 0.2320
X	 0.5750	 0.2260



*Continued on next page...*

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Chain	Atom inclusion	Q-score
Y	 0.8280	 0.3220
Z	 0.8400	 0.3540