



## wwPDB EM Validation Summary Report ⓘ

Apr 16, 2026 – 04:51 pm BST

PDB ID : 29HB / pdb\_000029hb  
EMDB ID : EMD-57170  
Title : Cryo-EM structure of the ClpE/ClpP degradation complex from E.faecalis  
Authors : Carroni, M.; Mogk, A.  
Deposited on : 2026-03-11  
Resolution : 2.80 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:

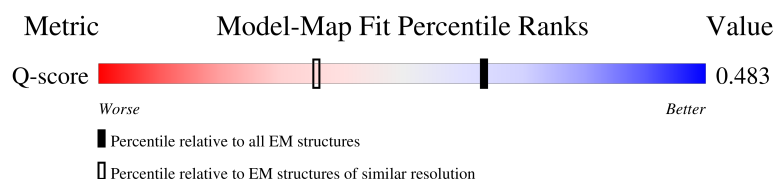
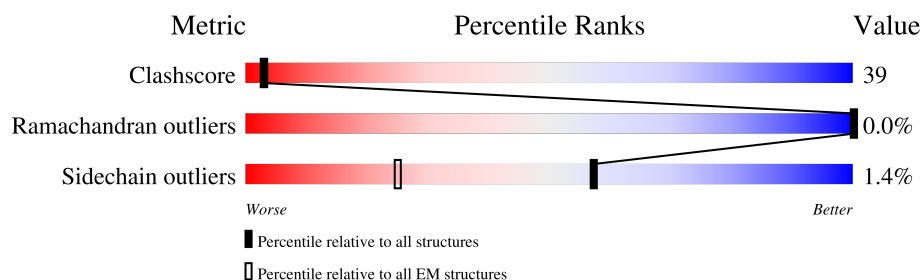
EMDB validation analysis : 0.0.1.dev132  
Mogul : 1.8.4, CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using 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 2.80 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.





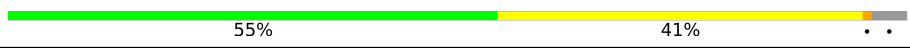

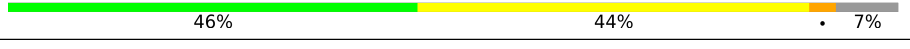


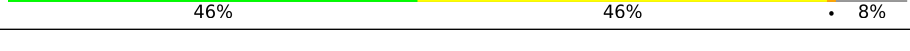
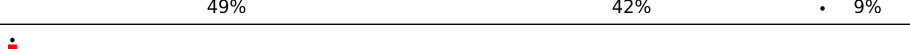
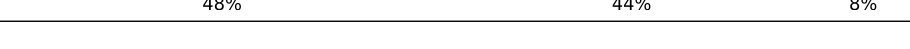
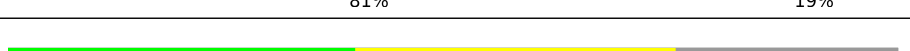
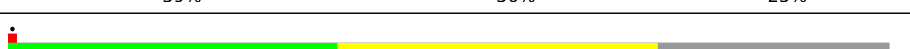
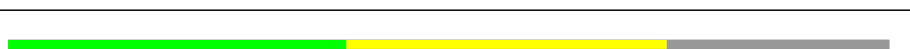
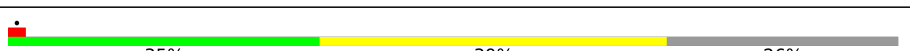
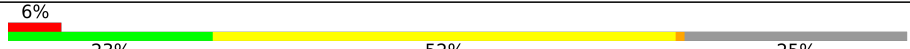
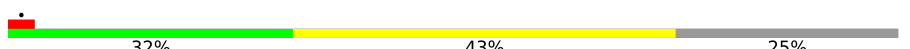

Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11806 ( 2.30 - 3.30 )

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

Mol	Chain	Length	Quality of chain
1	A	197	
1	B	197	
1	C	197	
1	D	197	

*Continued on next page...*

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Mol	Chain	Length	Quality of chain
1	E	197	
1	F	197	
1	G	197	
1	I	197	
1	K	197	
1	L	197	
1	M	197	
1	N	197	
1	S	197	
1	T	197	
2	H	16	
3	a	746	
3	b	746	
3	c	746	
3	d	746	
3	e	746	
3	f	746	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ATP	f	801	-	-	X	-
4	ATP	f	802	-	-	X	-

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 46198 atoms, of which 28 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 ATP-dependent Clp protease proteolytic subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	189	Total	C	N	O	S	0	0
			1449	908	248	286	7		
1	B	189	Total	C	N	O	S	0	0
			1438	900	247	285	6		
1	C	189	Total	C	N	O	S	0	0
			1433	895	244	287	7		
1	D	189	Total	C	N	O	S	0	0
			1443	903	245	288	7		
1	E	189	Total	C	N	O	S	0	0
			1443	900	249	287	7		
1	F	189	Total	C	N	O	S	0	0
			1427	893	243	285	6		
1	G	189	Total	C	N	O	S	0	0
			1430	892	244	287	7		
1	I	185	Total	C	N	O	S	0	0
			1385	868	236	275	6		
1	K	183	Total	C	N	O	S	0	0
			1395	877	236	275	7		
1	L	180	Total	C	N	O	S	0	0
			1367	860	230	270	7		
1	M	181	Total	C	N	O	S	0	0
			1377	865	237	269	6		
1	N	182	Total	C	N	O	S	0	0
			1387	872	235	274	6		
1	S	180	Total	C	N	O	S	0	0
			1363	859	229	269	6		
1	T	181	Total	C	N	O	S	0	0
			1354	847	231	269	7		

- Molecule 2 is a protein called unknown substrate bound to ClpE/ClpP.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	H	16	Total	C	H	N	O	0	0
			108	48	28	16	16		

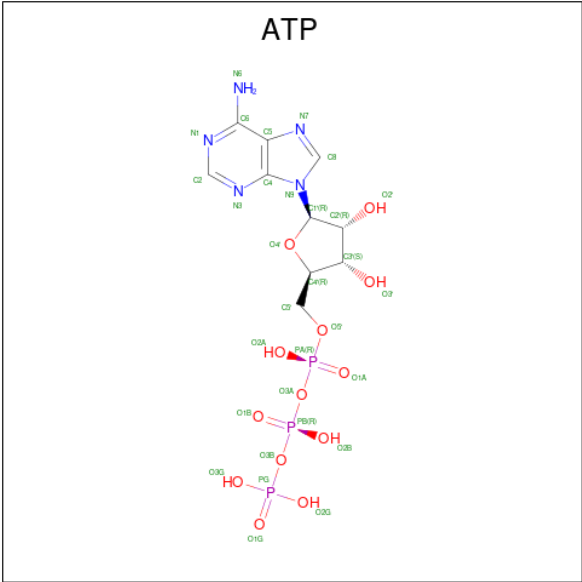
- Molecule 3 is a protein called ATP-dependent Clp protease, ATP-binding subunit ClpE.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	b	553	Total	C	N	O	S	0	0
			4304	2708	747	837	12		
3	c	561	Total	C	N	O	S	0	0
			4360	2744	756	848	12		
3	d	555	Total	C	N	O	S	0	0
			4321	2723	748	838	12		
3	a	563	Total	C	N	O	S	0	0
			4368	2748	758	850	12		
3	e	563	Total	C	N	O	S	0	0
			4368	2748	758	850	12		
3	f	563	Total	C	N	O	S	0	0
			4368	2748	758	850	12		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
b	550	VAL	ILE	conflict	UNP Q837W9
b	656	SER	GLY	conflict	UNP Q837W9
c	550	VAL	ILE	conflict	UNP Q837W9
c	656	SER	GLY	conflict	UNP Q837W9
d	550	VAL	ILE	conflict	UNP Q837W9
d	656	SER	GLY	conflict	UNP Q837W9
a	550	VAL	ILE	conflict	UNP Q837W9
a	656	SER	GLY	conflict	UNP Q837W9
e	550	VAL	ILE	conflict	UNP Q837W9
e	656	SER	GLY	conflict	UNP Q837W9
f	550	VAL	ILE	conflict	UNP Q837W9
f	656	SER	GLY	conflict	UNP Q837W9

- Molecule 4 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ) (labeled as "Ligand of Interest" by depositor).

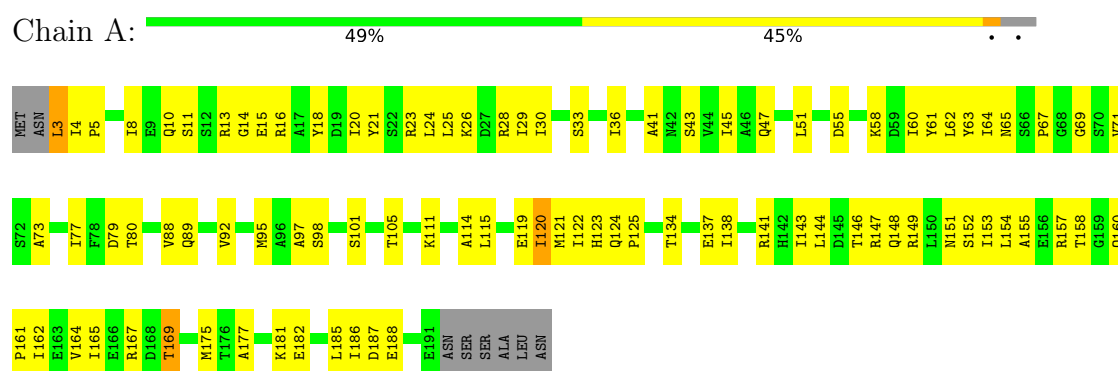


Mol	Chain	Residues	Atoms					AltConf
4	b	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	c	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	c	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	d	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	d	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	d	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	a	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	a	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	f	1	Total	C	N	O	P	0
			31	10	5	13	3	
4	f	1	Total	C	N	O	P	0
			31	10	5	13	3	

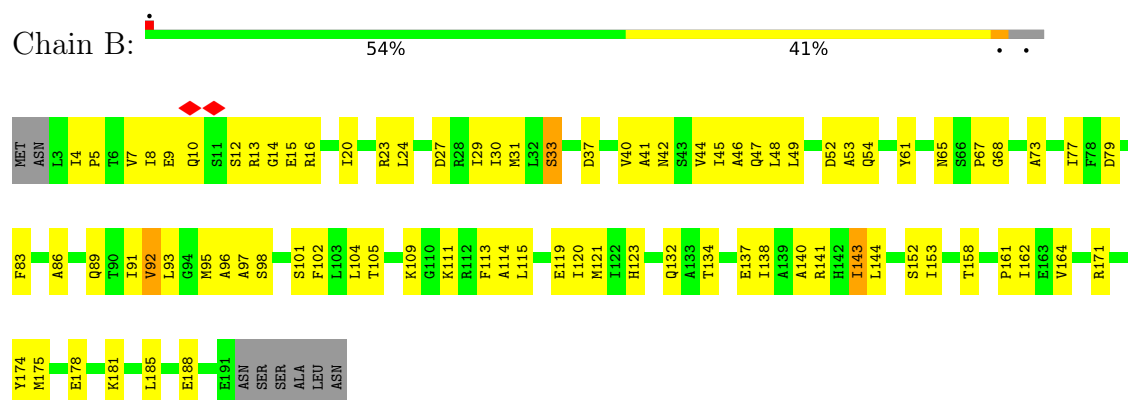
### 3 Residue-property plots [i](#)

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.

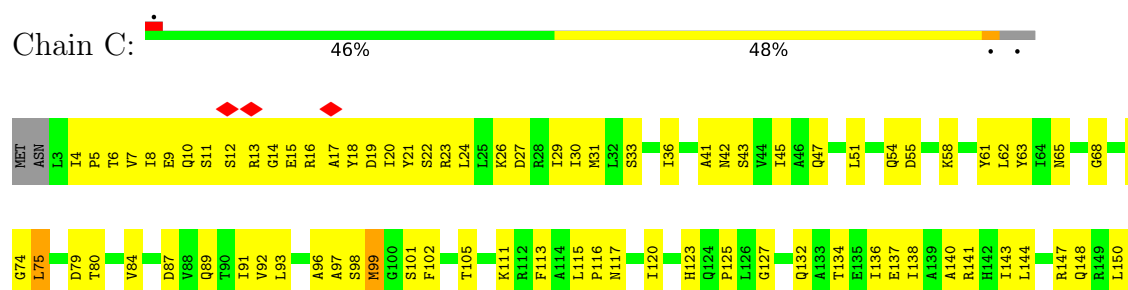
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



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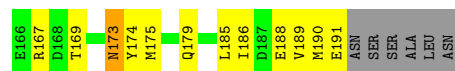




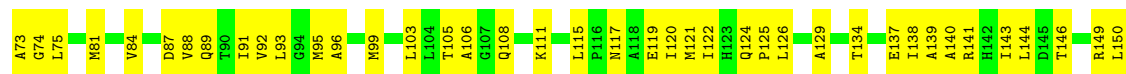
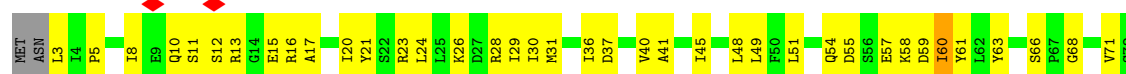
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



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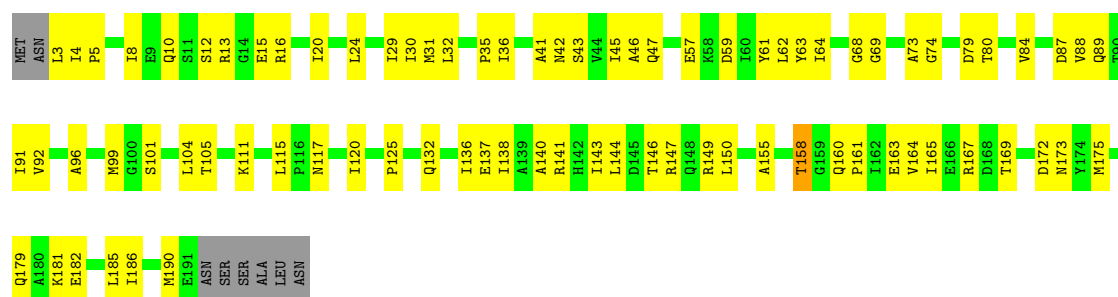
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



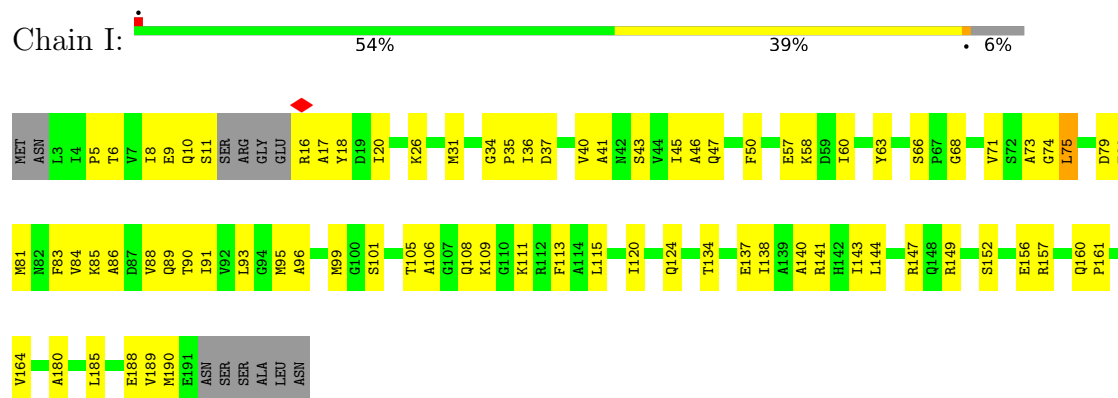
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



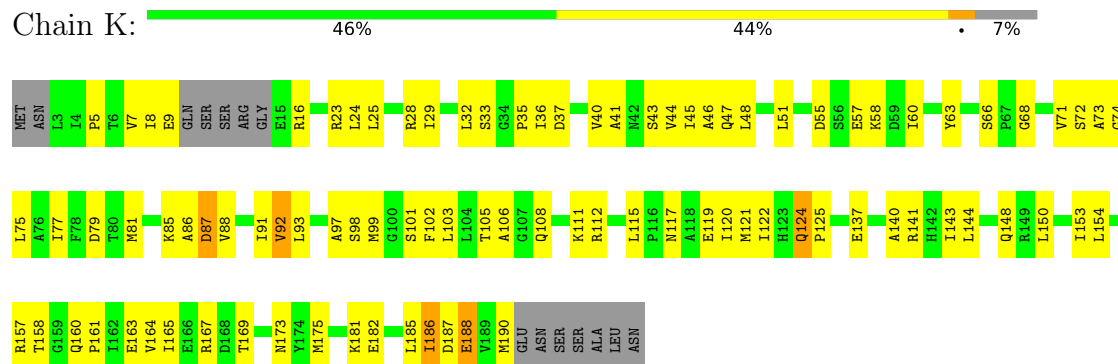




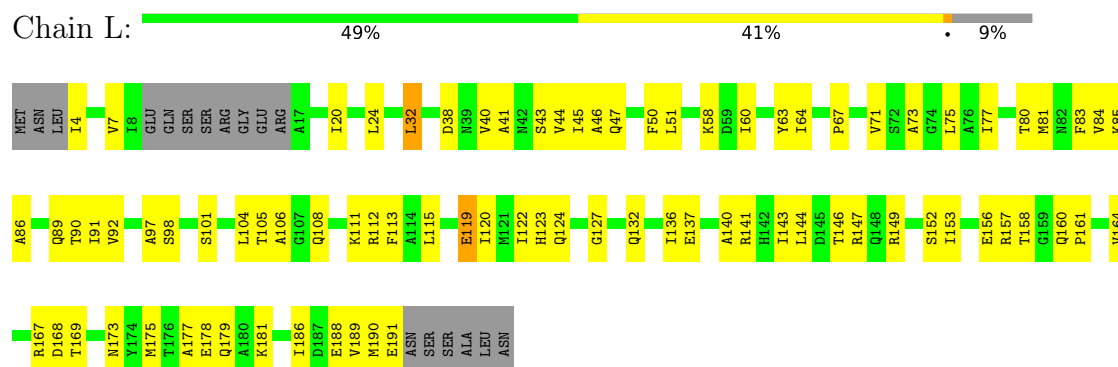
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



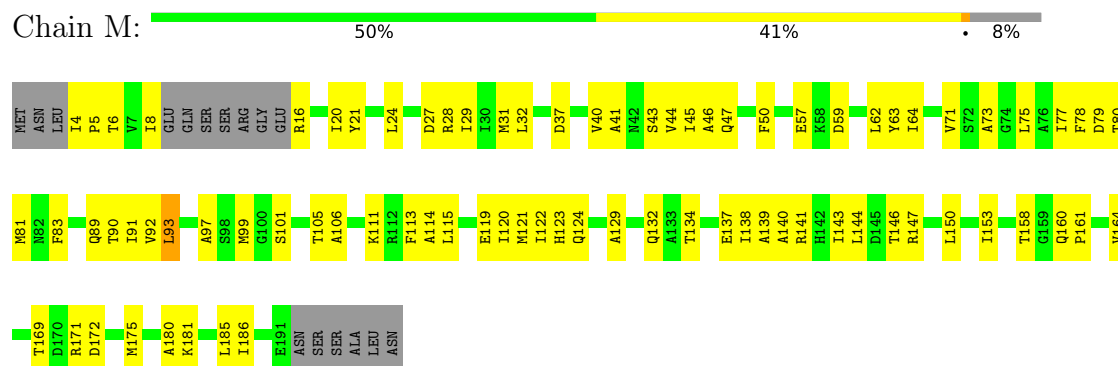
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



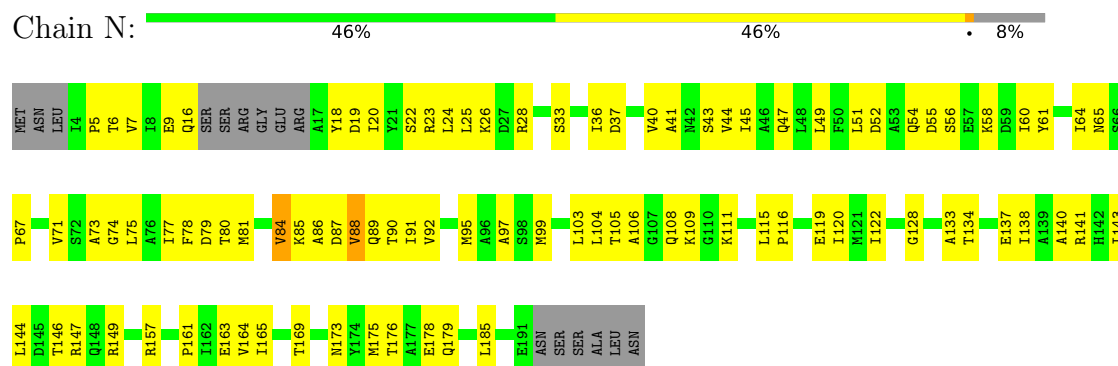
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



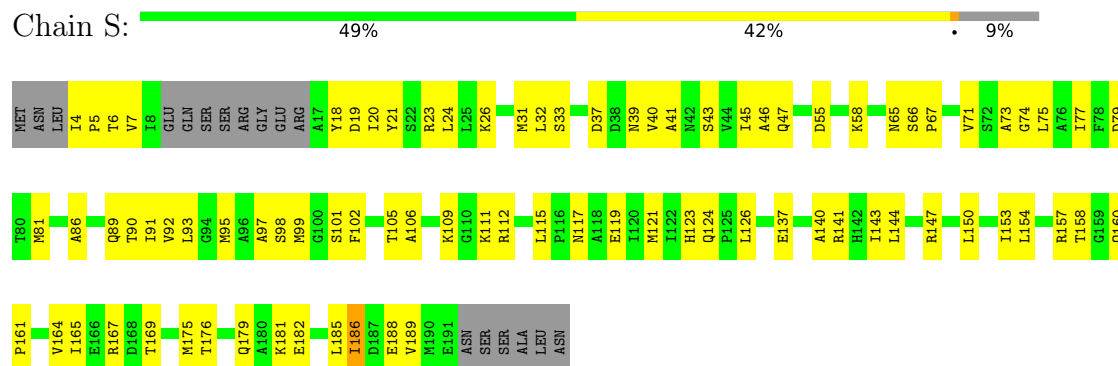
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



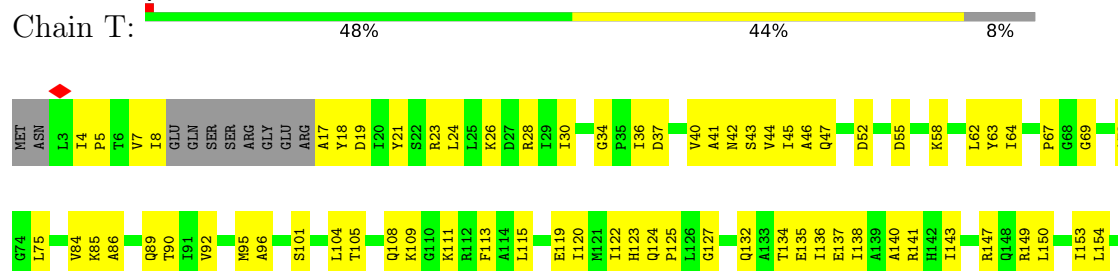
- Molecule 1: ATP-dependent Clp protease proteolytic subunit



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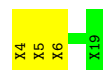
- Molecule 1: ATP-dependent Clp protease proteolytic subunit





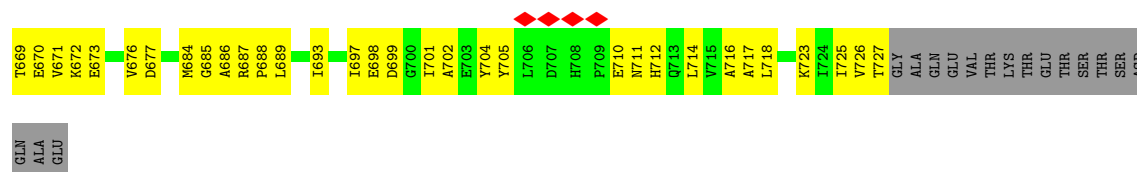
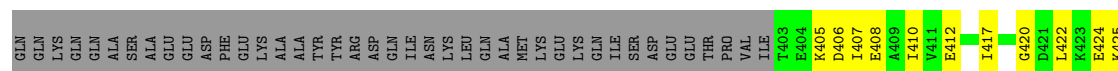
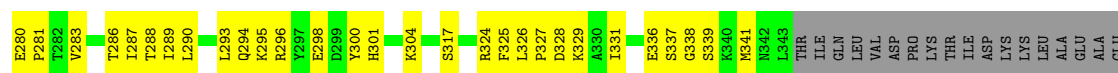
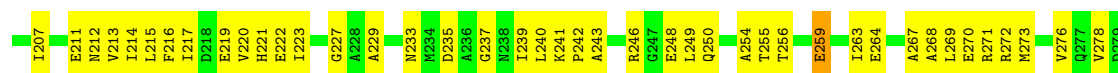
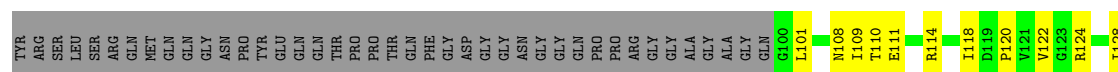
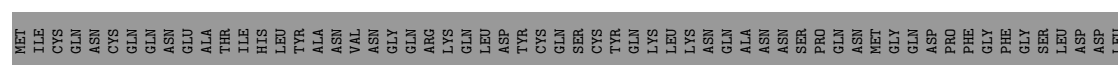
- Molecule 2: unknown substrate bound to ClpE/ClpP

Chain H: 81% 19%

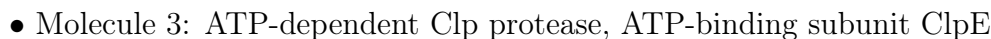


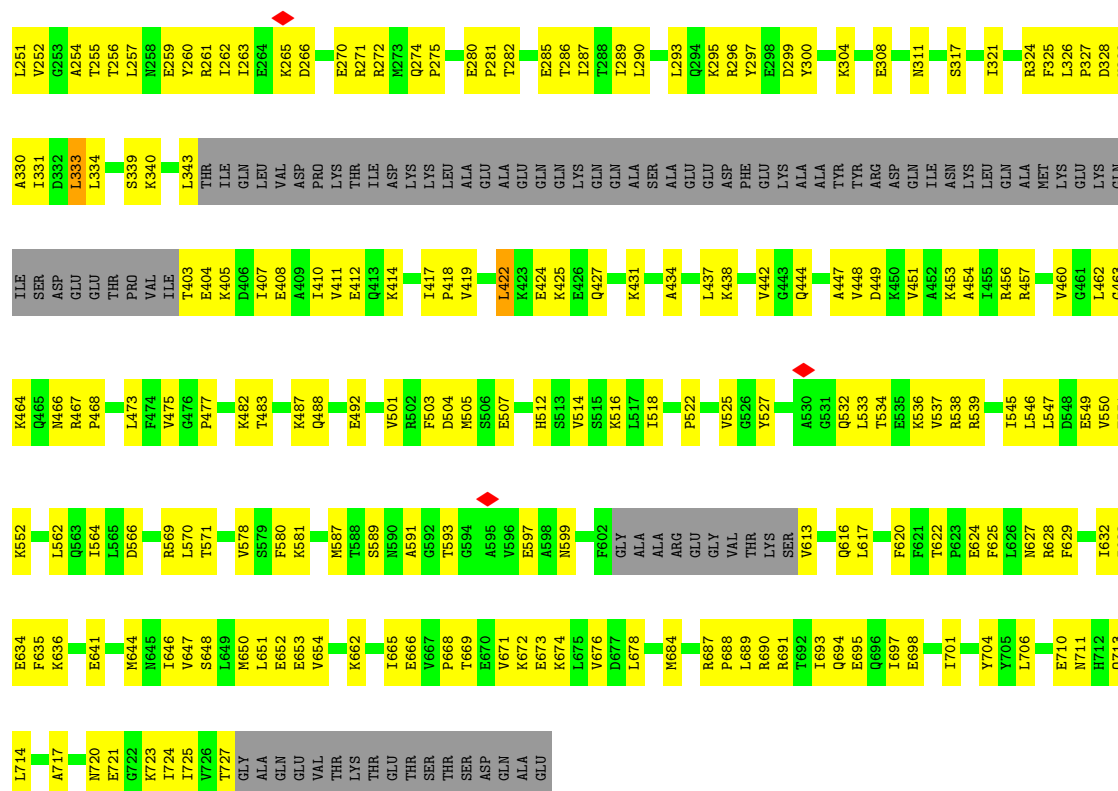
- Molecule 3: ATP-dependent Clp protease, ATP-binding subunit ClpE

Chain b: 37% 36% 26%



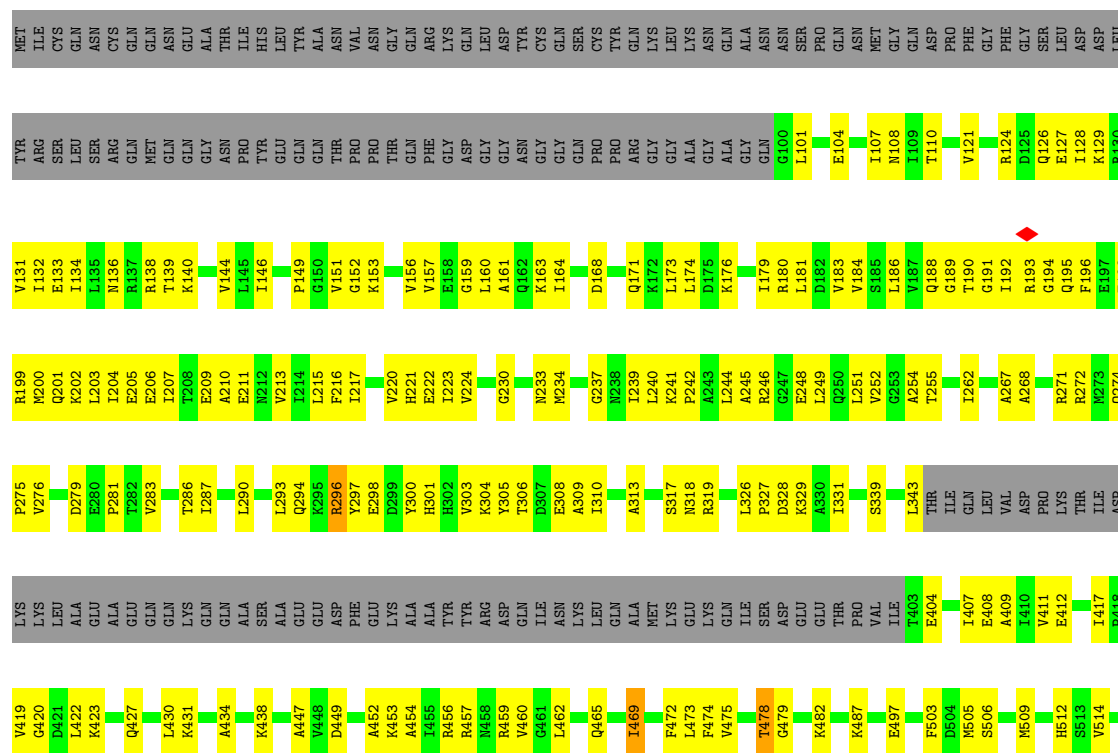
- Molecule 3: ATP-dependent Clp protease, ATP-binding subunit ClpE



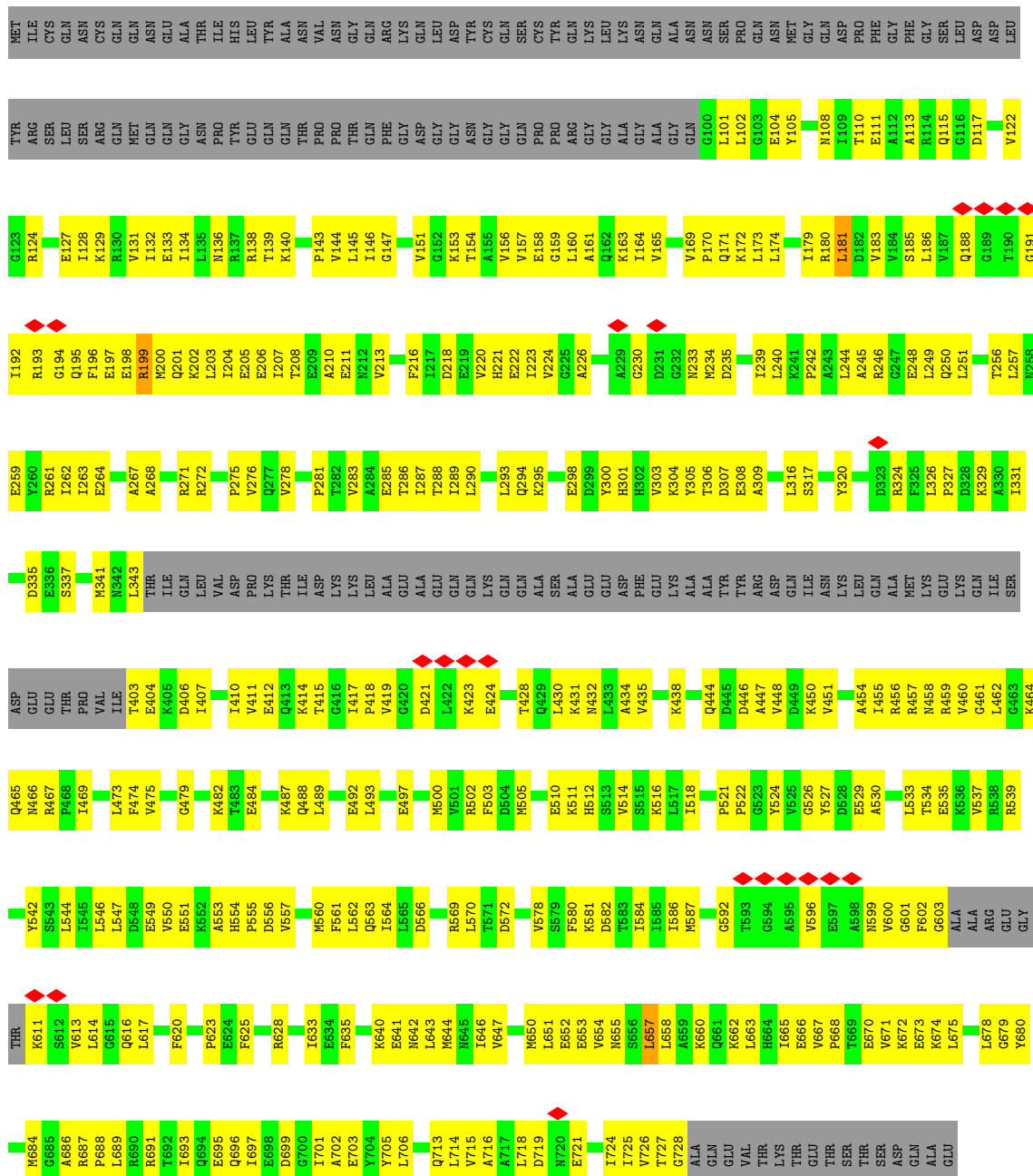


• Molecule 3: ATP-dependent Clp protease, ATP-binding subunit ClpE

Chain a:







## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	556680	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	40	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	0.471	Depositor
Minimum map value	-0.191	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.063	Depositor
Map size (Å)	396.0, 396.0, 396.0	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.825, 0.825, 0.825	Depositor



## 5 Model quality

### 5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	A	0.13	0/1467	0.34	0/1983
1	B	0.13	0/1456	0.40	0/1972
1	C	0.13	0/1451	0.38	0/1965
1	D	0.13	0/1461	0.34	0/1978
1	E	0.14	0/1460	0.38	0/1974
1	F	0.15	0/1444	0.37	0/1956
1	G	0.14	0/1447	0.40	1/1960 (0.1%)
1	I	0.12	0/1401	0.35	0/1897
1	K	0.14	0/1411	0.37	0/1908
1	L	0.12	0/1383	0.35	0/1871
1	M	0.13	0/1393	0.35	0/1884
1	N	0.13	0/1404	0.39	0/1901
1	S	0.13	0/1380	0.34	0/1870
1	T	0.14	0/1368	0.39	0/1852
3	a	0.14	0/4425	0.39	0/5973
3	b	0.13	0/4359	0.38	0/5882
3	c	0.13	0/4416	0.38	0/5960
3	d	0.14	0/4376	0.39	0/5906
3	e	0.15	0/4425	0.46	2/5973 (0.0%)
3	f	0.14	0/4425	0.42	0/5973
All	All	0.14	0/46352	0.39	3/62638 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	e	271	ARG	CA-CB-CG	6.58	127.27	114.10
1	G	158	THR	N-CA-C	-5.30	108.07	114.75
3	e	683	ALA	N-CA-C	-5.12	108.30	114.75

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1449	0	1449	101	0
1	B	1438	0	1422	101	0
1	C	1433	0	1404	131	0
1	D	1443	0	1428	113	0
1	E	1443	0	1434	99	0
1	F	1427	0	1410	117	0
1	G	1430	0	1406	102	0
1	I	1385	0	1358	95	0
1	K	1395	0	1396	111	0
1	L	1367	0	1366	97	0
1	M	1377	0	1379	101	0
1	N	1387	0	1376	113	0
1	S	1363	0	1351	96	0
1	T	1354	0	1331	100	0
2	H	80	28	21	4	0
3	a	4368	0	4414	315	0
3	b	4304	0	4358	327	0
3	c	4360	0	4407	314	0
3	d	4321	0	4372	401	0
3	e	4368	0	4415	580	0
3	f	4368	0	4417	434	0
4	a	62	0	22	1	0
4	b	31	0	12	4	0
4	c	62	0	24	5	0
4	d	93	0	35	12	0
4	f	62	0	24	26	0
All	All	46170	28	46031	3554	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 39.

The worst 5 of 3554 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:89:GLN:HB3	1:F:111:LYS:HB3	1.25	1.14
3:e:538:ARG:HG3	3:e:578:VAL:HG12	1.26	1.13
1:I:11:SER:HB2	1:T:8:ILE:HB	1.24	1.12
1:F:10:GLN:HB3	1:F:15:GLU:HB3	1.17	1.12
3:c:723:LYS:HA	3:c:723:LYS:HE3	1.31	1.11

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	187/197 (95%)	180 (96%)	7 (4%)	0	100	100
1	B	187/197 (95%)	181 (97%)	6 (3%)	0	100	100
1	C	187/197 (95%)	174 (93%)	13 (7%)	0	100	100
1	D	187/197 (95%)	180 (96%)	7 (4%)	0	100	100
1	E	187/197 (95%)	179 (96%)	8 (4%)	0	100	100
1	F	187/197 (95%)	176 (94%)	11 (6%)	0	100	100
1	G	187/197 (95%)	180 (96%)	7 (4%)	0	100	100
1	I	181/197 (92%)	173 (96%)	8 (4%)	0	100	100
1	K	179/197 (91%)	174 (97%)	4 (2%)	1 (1%)	21	51
1	L	176/197 (89%)	172 (98%)	4 (2%)	0	100	100
1	M	177/197 (90%)	175 (99%)	2 (1%)	0	100	100
1	N	178/197 (90%)	170 (96%)	8 (4%)	0	100	100
1	S	176/197 (89%)	174 (99%)	2 (1%)	0	100	100
1	T	175/197 (89%)	167 (95%)	8 (5%)	0	100	100
3	a	557/746 (75%)	541 (97%)	16 (3%)	0	100	100
3	b	545/746 (73%)	524 (96%)	21 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	c	553/746 (74%)	539 (98%)	13 (2%)	1 (0%)	43	72
3	d	545/746 (73%)	528 (97%)	17 (3%)	0	100	100
3	e	557/746 (75%)	532 (96%)	25 (4%)	0	100	100
3	f	557/746 (75%)	534 (96%)	23 (4%)	0	100	100
All	All	5865/7234 (81%)	5653 (96%)	210 (4%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	K	87	ASP
3	c	101	LEU

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	154/163 (94%)	151 (98%)	3 (2%)	50	81
1	B	151/163 (93%)	147 (97%)	4 (3%)	40	75
1	C	150/163 (92%)	146 (97%)	4 (3%)	39	74
1	D	153/163 (94%)	150 (98%)	3 (2%)	48	80
1	E	153/163 (94%)	149 (97%)	4 (3%)	40	75
1	F	150/163 (92%)	148 (99%)	2 (1%)	61	86
1	G	150/163 (92%)	149 (99%)	1 (1%)	76	91
1	I	143/163 (88%)	141 (99%)	2 (1%)	59	85
1	K	148/163 (91%)	143 (97%)	5 (3%)	32	68
1	L	145/163 (89%)	143 (99%)	2 (1%)	59	85
1	M	145/163 (89%)	144 (99%)	1 (1%)	76	91
1	N	146/163 (90%)	142 (97%)	4 (3%)	39	74
1	S	143/163 (88%)	141 (99%)	2 (1%)	59	85
1	T	140/163 (86%)	139 (99%)	1 (1%)	76	91

*Continued on next page...*

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	a	471/625 (75%)	466 (99%)	5 (1%)	65	87
3	b	466/625 (75%)	461 (99%)	5 (1%)	65	87
3	c	471/625 (75%)	465 (99%)	6 (1%)	61	86
3	d	467/625 (75%)	462 (99%)	5 (1%)	65	87
3	e	471/625 (75%)	466 (99%)	5 (1%)	65	87
3	f	471/625 (75%)	467 (99%)	4 (1%)	73	90
All	All	4888/6032 (81%)	4820 (99%)	68 (1%)	57	85

5 of 68 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	a	469	ILE
3	e	263	ILE
3	f	199	ARG
1	K	124	GLN
1	K	92	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
3	a	427	GLN
3	e	294	GLN
3	a	574	GLN
3	a	711	ASN
3	e	440	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry

10 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$
4	ATP	d	803	-	29,33,33	0.28	0	44,52,52	0.53	1 (2%)
4	ATP	f	801	-	29,33,33	0.37	0	44,52,52	0.51	1 (2%)
4	ATP	d	802	-	29,33,33	0.26	0	44,52,52	0.50	1 (2%)
4	ATP	d	801	-	29,33,33	0.29	0	44,52,52	0.52	1 (2%)
4	ATP	a	802	-	29,33,33	0.29	0	44,52,52	0.52	1 (2%)
4	ATP	c	801	-	29,33,33	0.27	0	44,52,52	0.50	0
4	ATP	c	802	-	29,33,33	0.29	0	44,52,52	0.49	1 (2%)
4	ATP	b	801	-	29,33,33	0.28	0	44,52,52	0.48	1 (2%)
4	ATP	a	801	-	29,33,33	0.28	0	44,52,52	0.51	1 (2%)
4	ATP	f	802	-	29,33,33	0.28	0	44,52,52	0.49	1 (2%)

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
4	ATP	d	803	-	-	6/22/38/38	0/3/3/3
4	ATP	f	801	-	-	11/22/38/38	0/3/3/3
4	ATP	d	802	-	-	3/22/38/38	0/3/3/3
4	ATP	d	801	-	-	4/22/38/38	0/3/3/3
4	ATP	a	802	-	-	7/22/38/38	0/3/3/3
4	ATP	c	801	-	-	1/22/38/38	0/3/3/3
4	ATP	c	802	-	-	0/22/38/38	0/3/3/3
4	ATP	b	801	-	-	6/22/38/38	0/3/3/3
4	ATP	a	801	-	-	5/22/38/38	0/3/3/3
4	ATP	f	802	-	-	11/22/38/38	0/3/3/3

There are no bond length outliers.

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	f	802	ATP	PB-O3B-PG	2.11	140.07	132.83
4	f	801	ATP	PB-O3B-PG	2.10	140.05	132.83
4	d	801	ATP	PB-O3B-PG	2.07	139.92	132.83
4	d	803	ATP	PB-O3B-PG	2.07	139.92	132.83
4	a	801	ATP	PB-O3B-PG	2.06	139.90	132.83

There are no chirality outliers.

5 of 54 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	b	801	ATP	PB-O3B-PG-O2G
4	b	801	ATP	PB-O3B-PG-O3G
4	d	801	ATP	O4'-C4'-C5'-O5'
4	d	801	ATP	C3'-C4'-C5'-O5'
4	d	802	ATP	PB-O3B-PG-O2G

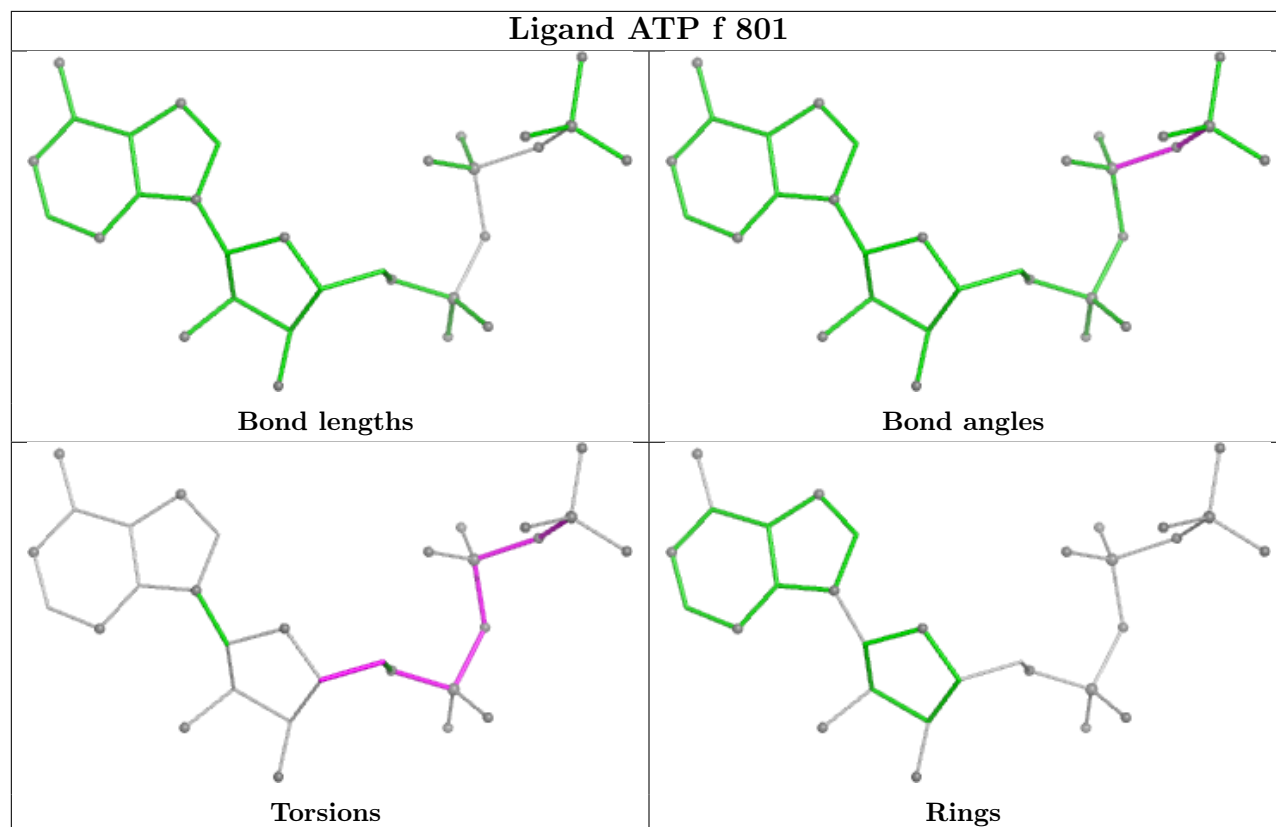
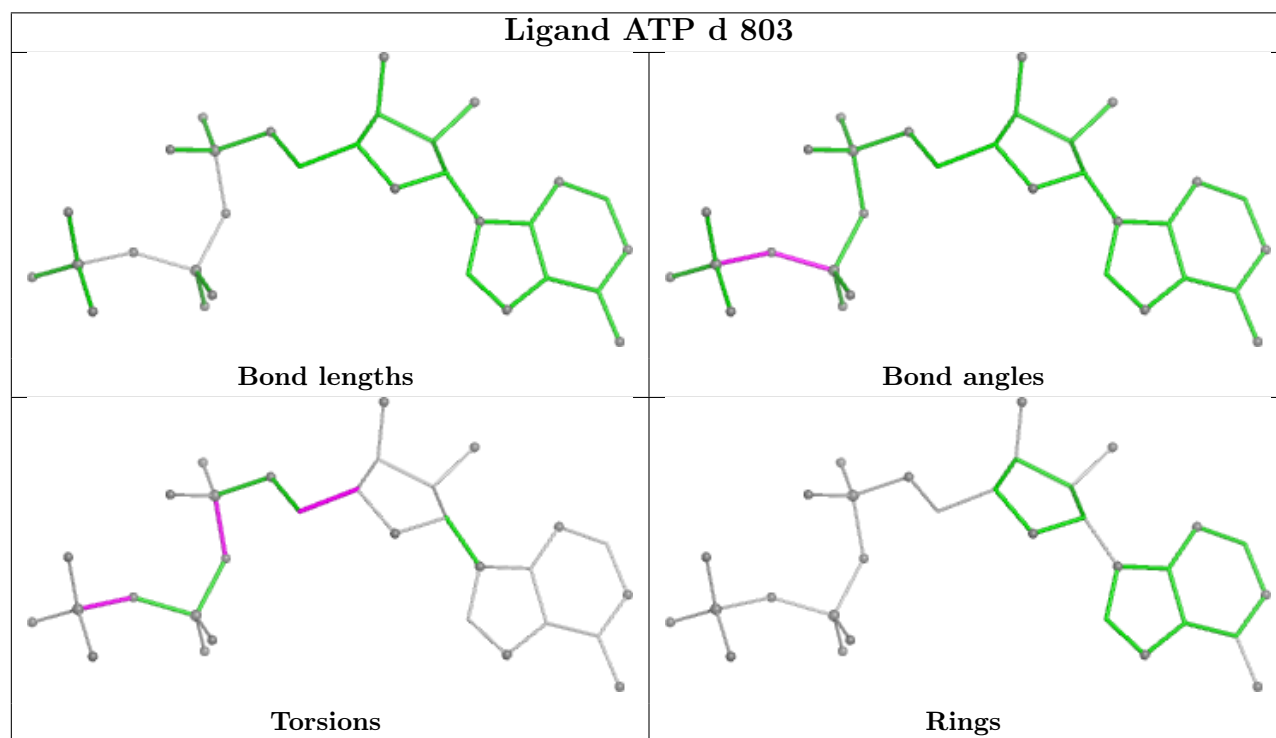
There are no ring outliers.

9 monomers are involved in 48 short contacts:

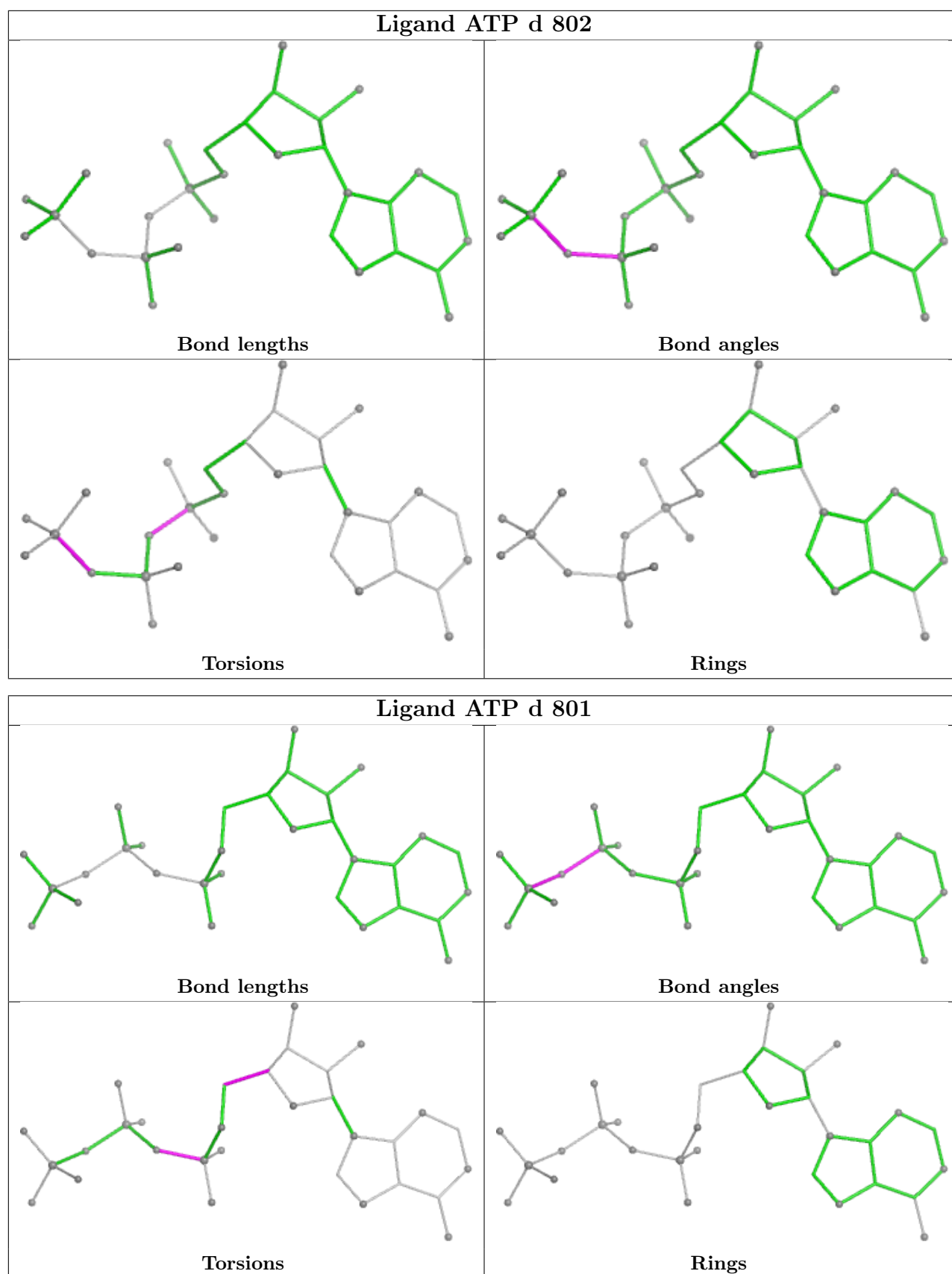
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	d	803	ATP	1	0
4	f	801	ATP	15	0
4	d	802	ATP	5	0
4	d	801	ATP	6	0
4	a	802	ATP	1	0
4	c	801	ATP	4	0
4	c	802	ATP	1	0
4	b	801	ATP	4	0
4	f	802	ATP	11	0

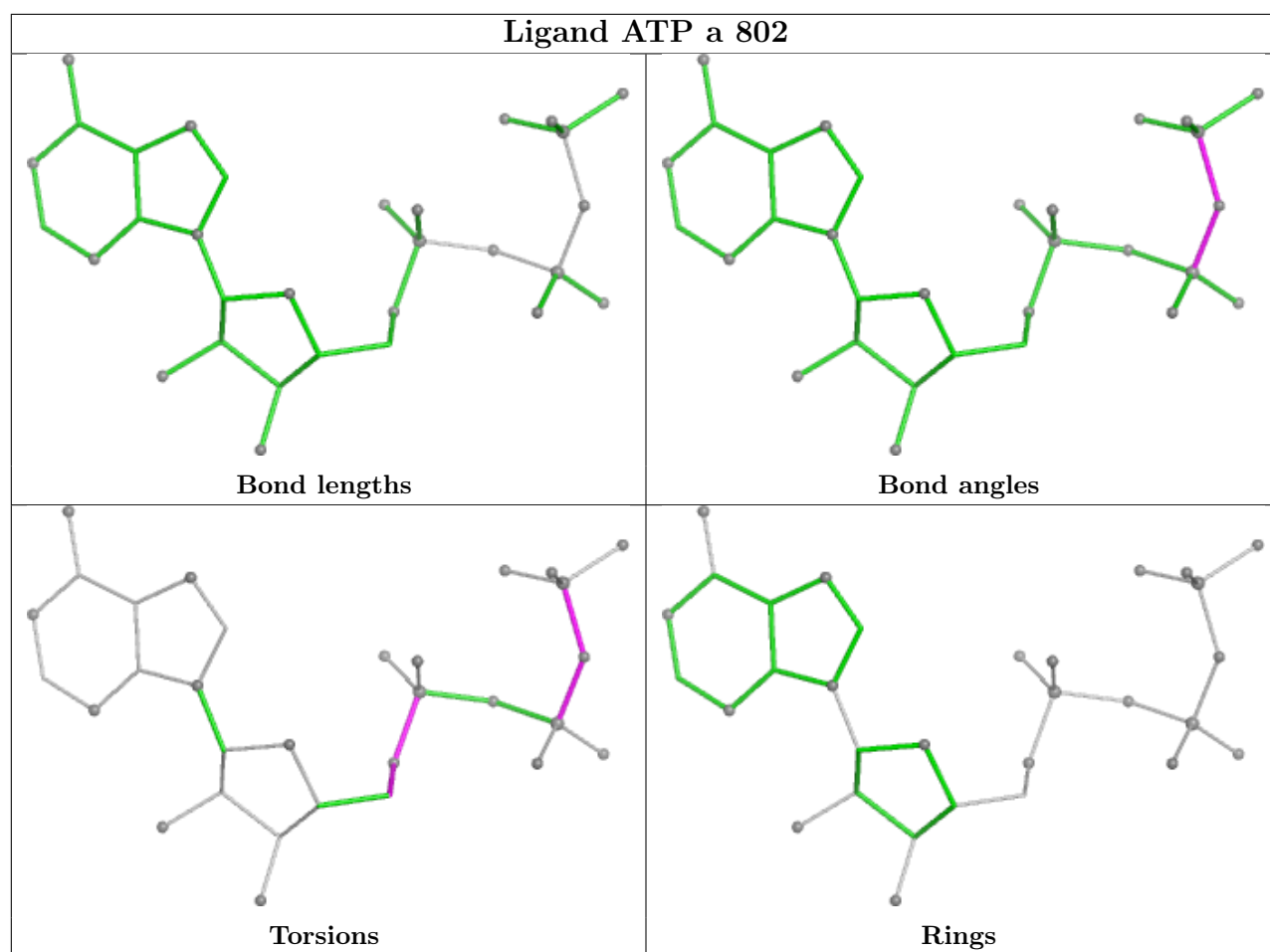
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

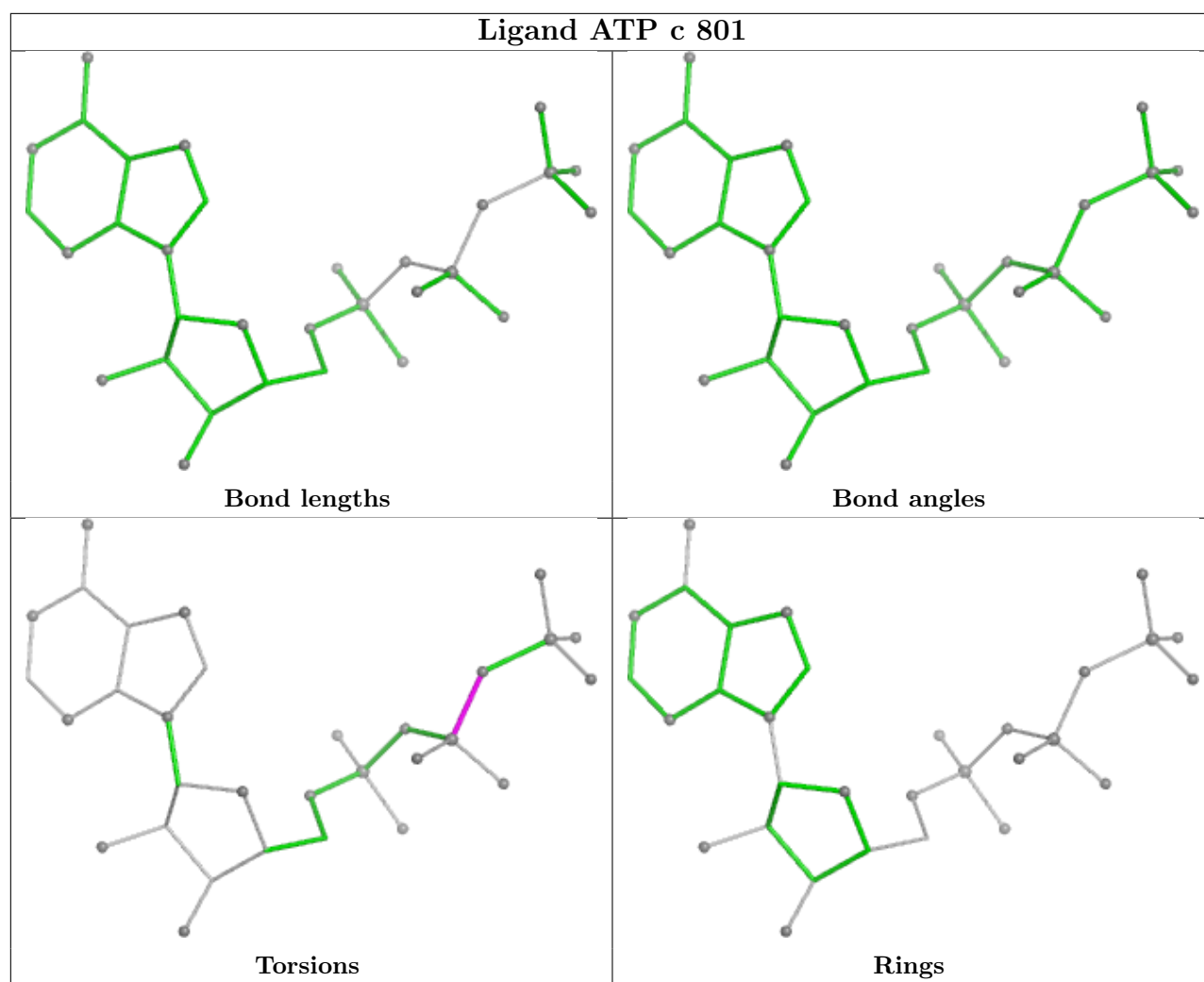
The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

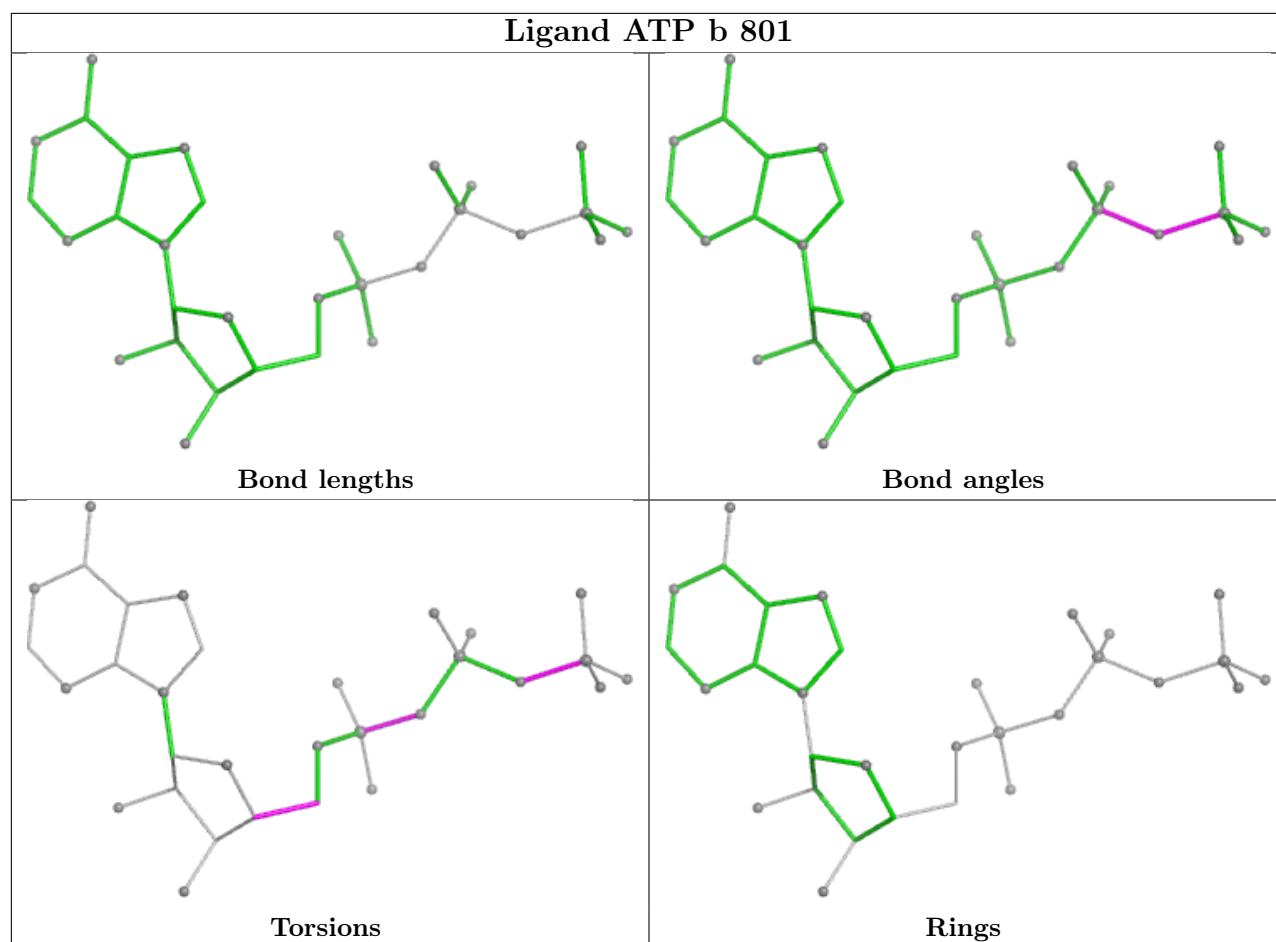
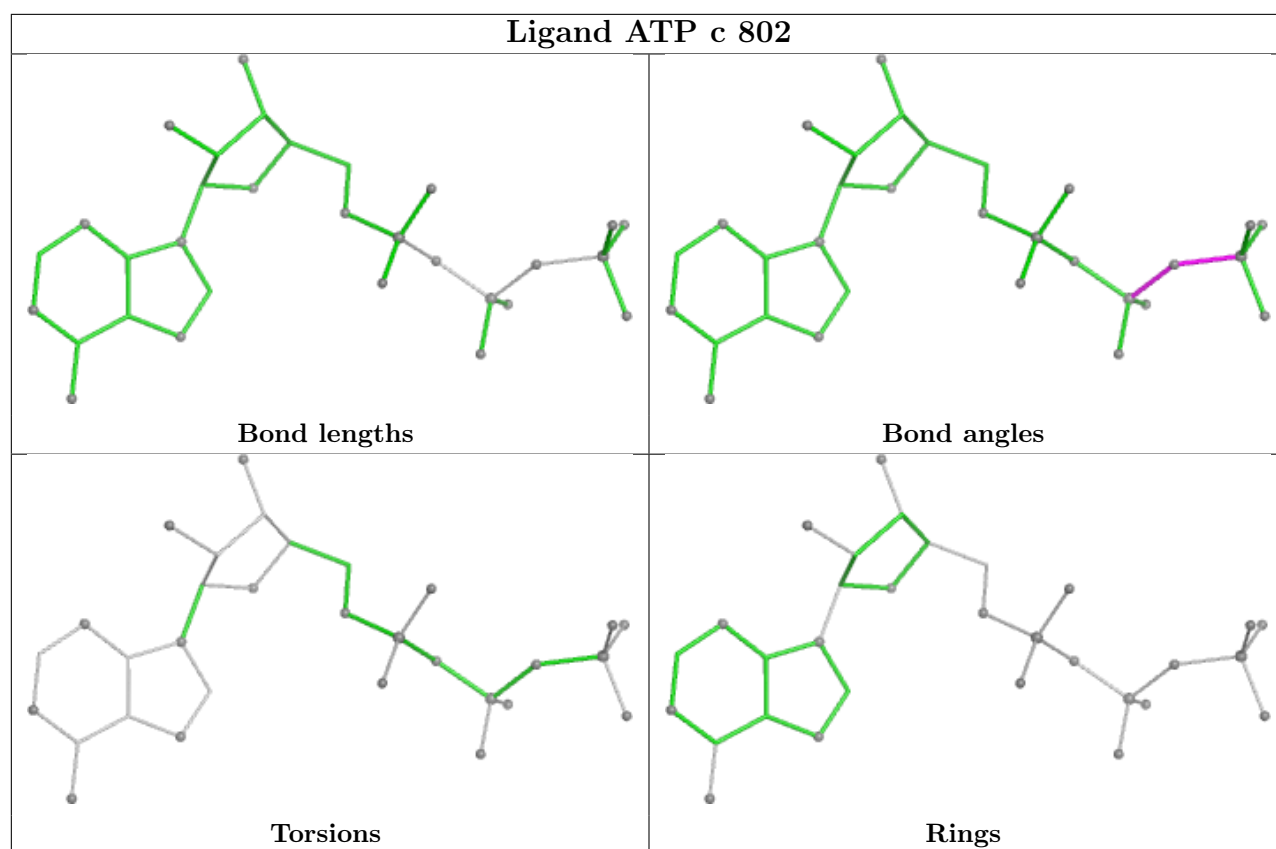


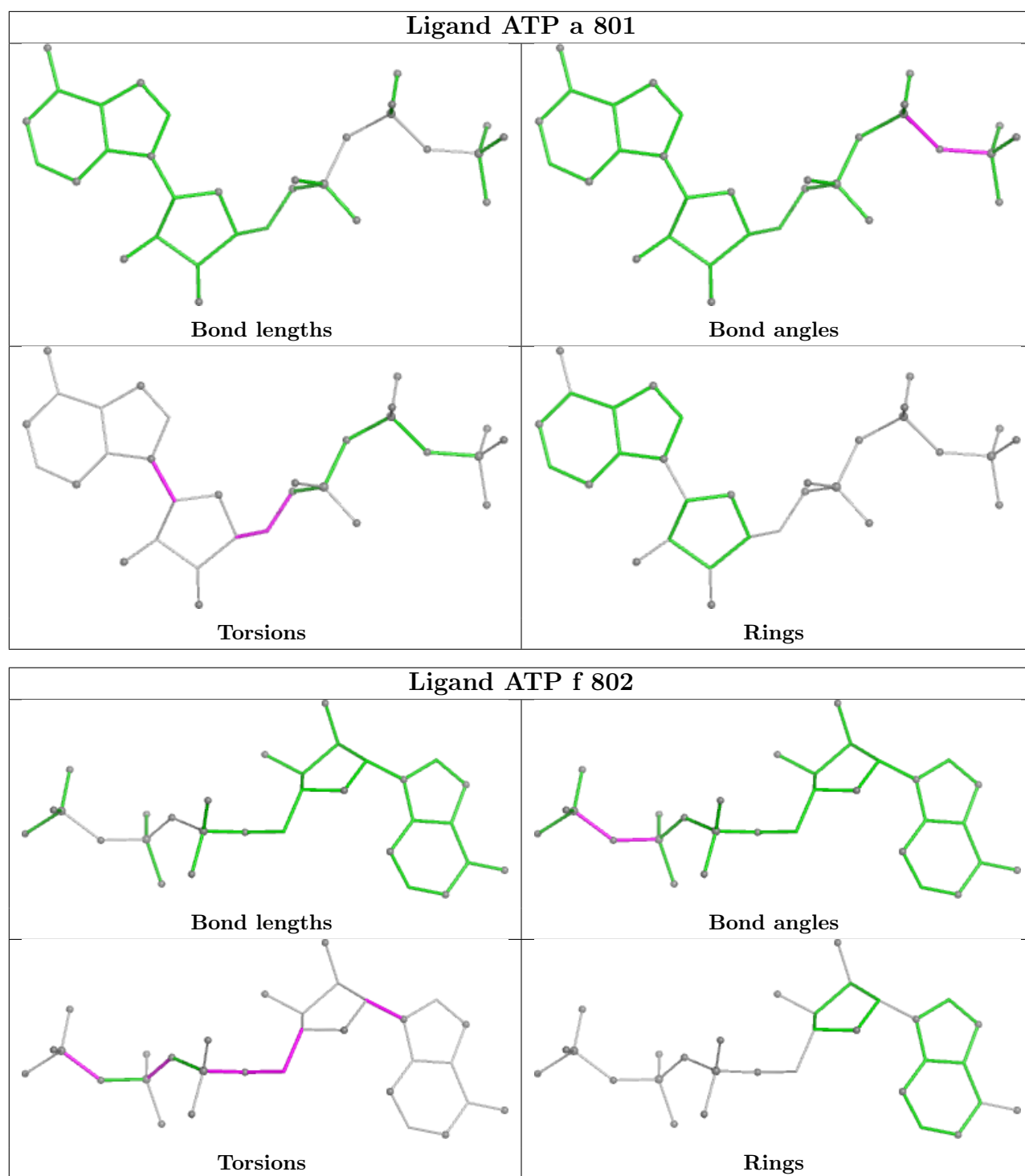












## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	N	1
3	c	1
3	b	1
1	T	1
3	d	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	N	9:GLU	C	16:GLN	N	6.47
1	c	718:LEU	C	719:ASP	N	5.42
1	b	716:ALA	C	717:ALA	N	4.15
1	T	34:GLY	C	35:PRO	N	3.13
1	d	711:ASN	C	712:HIS	N	3.12

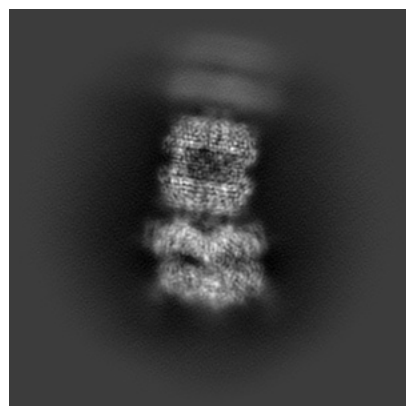
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-57170. These allow visual inspection of the internal detail of the map and identification of artifacts.

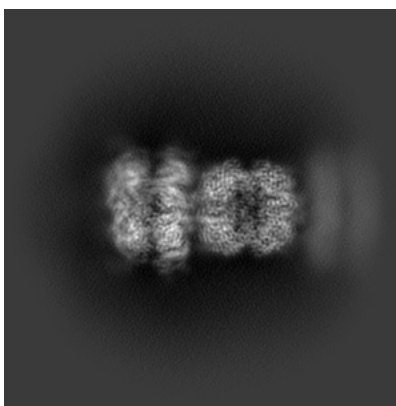
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

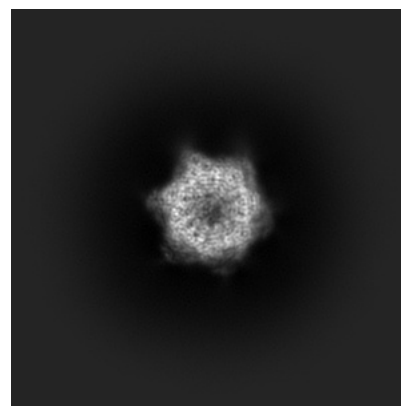
#### 6.1.1 Primary map



X

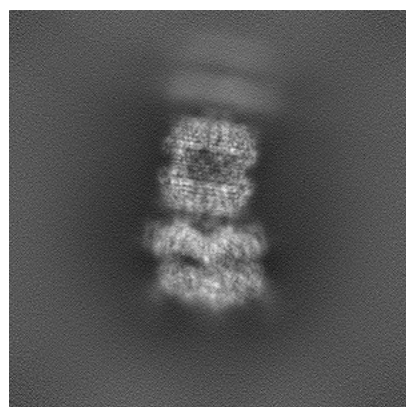


Y

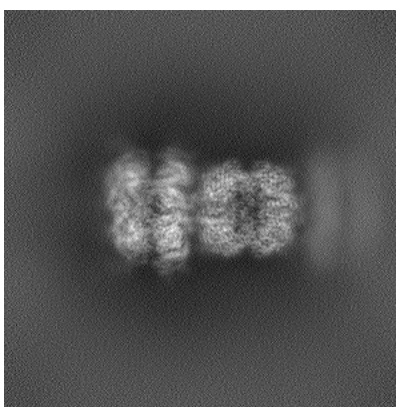


Z

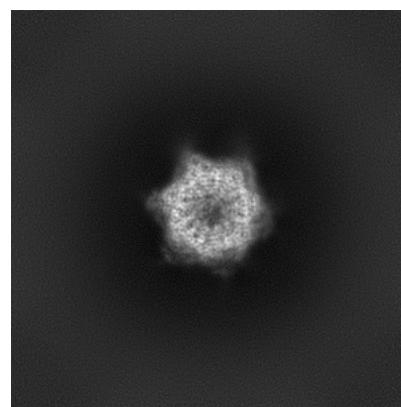
#### 6.1.2 Raw map



X



Y

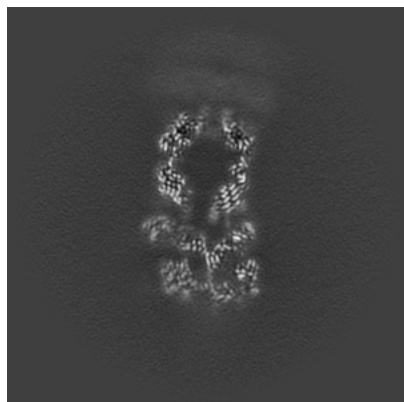


Z

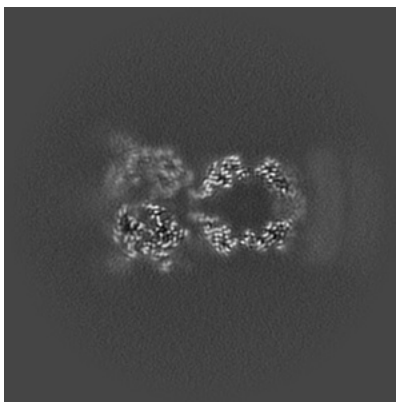
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

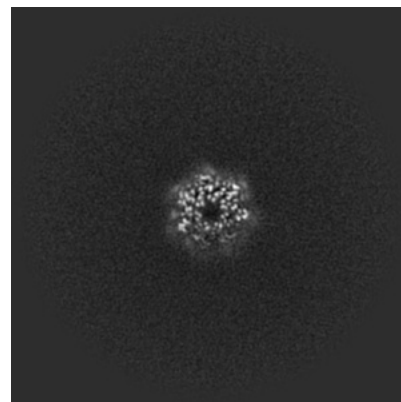
### 6.2.1 Primary map



X Index: 240

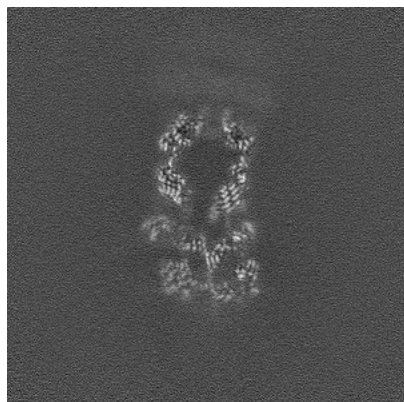


Y Index: 240

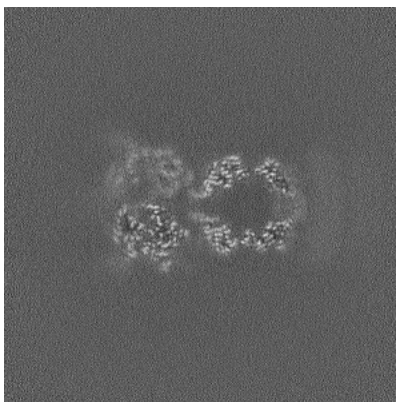


Z Index: 240

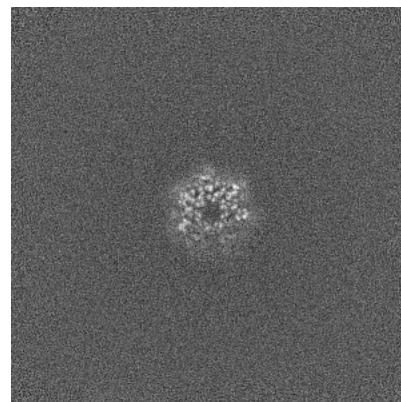
### 6.2.2 Raw map



X Index: 240



Y Index: 240



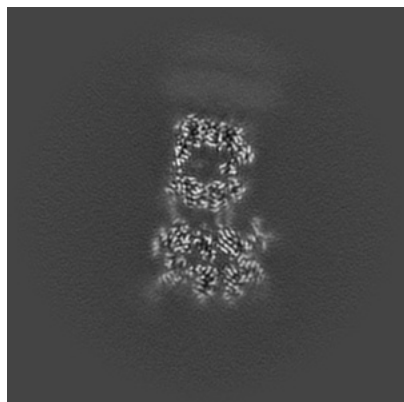
Z Index: 240

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

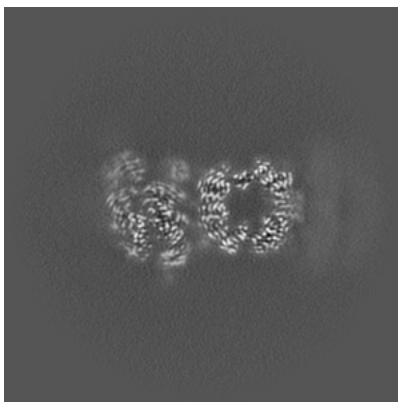


## 6.3 Largest variance slices [i](#)

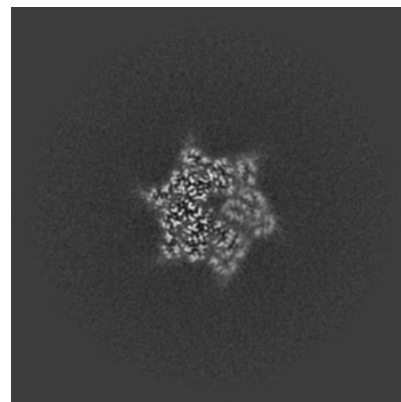
### 6.3.1 Primary map



X Index: 214

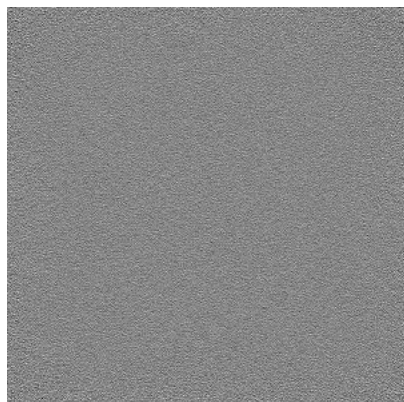


Y Index: 260

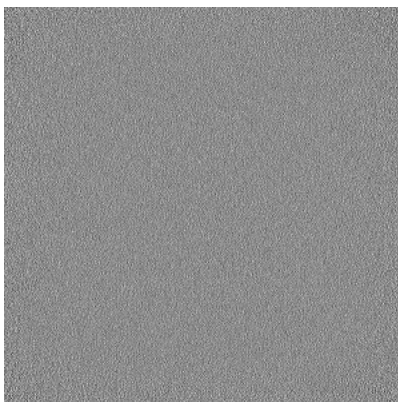


Z Index: 201

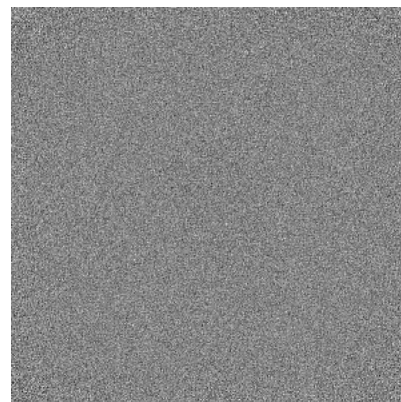
### 6.3.2 Raw map



X Index: 0



Y Index: 0

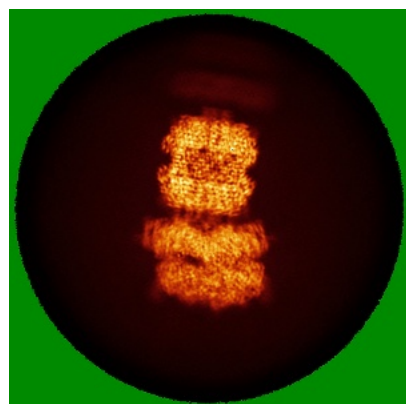


Z Index: 0

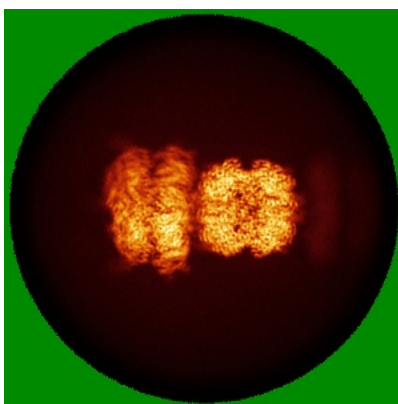
The images above show the largest variance slices of the map in three orthogonal directions.

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

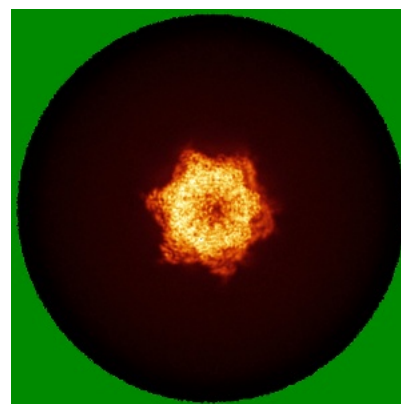
### 6.4.1 Primary map



X

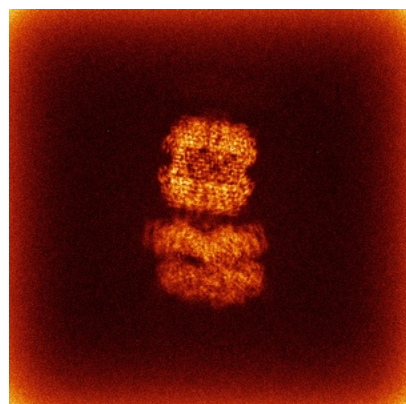


Y

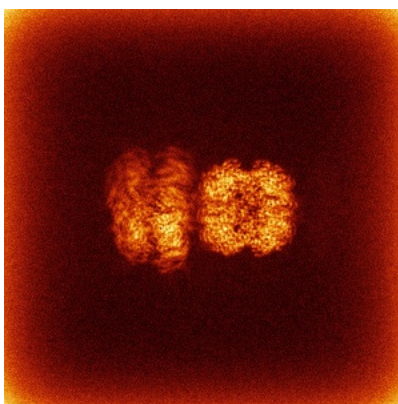


Z

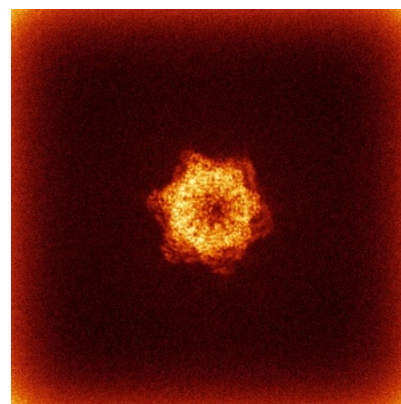
### 6.4.2 Raw map



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](#)

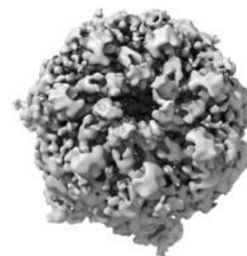
### 6.5.1 Primary map



X



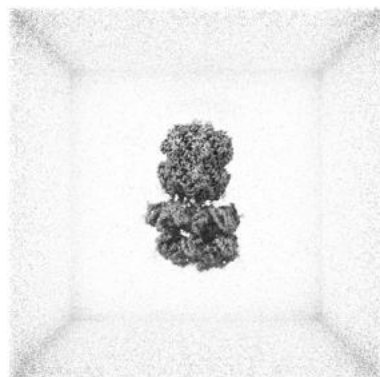
Y



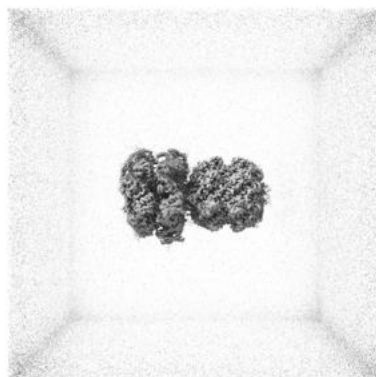
Z

The images above show the 3D surface view of the map at the recommended contour level 0.063. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

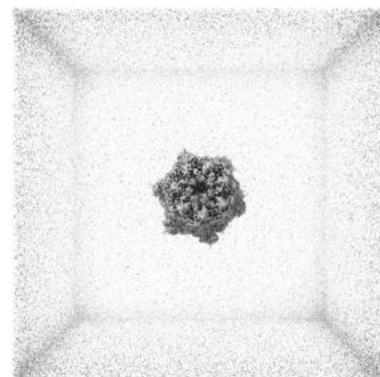
### 6.5.2 Raw map



X



Y



Z

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

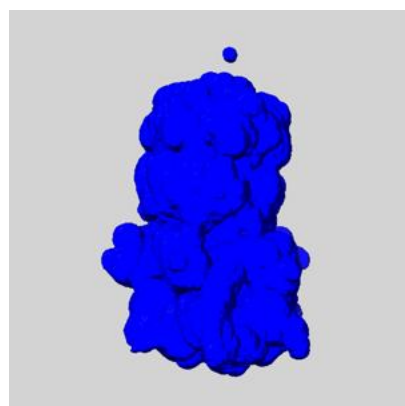
## 6.6 Mask visualisation [i](#)

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

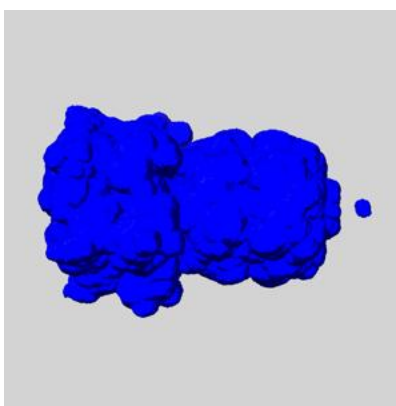
A mask typically either:

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

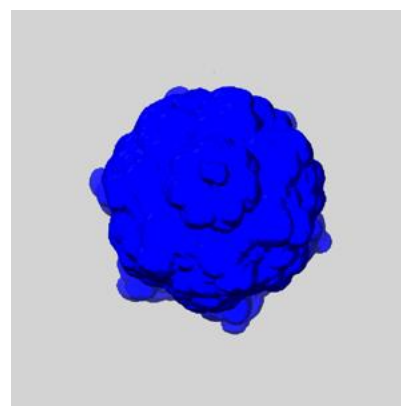
### 6.6.1 emd\_57170\_msk\_1.map [i](#)



X



Y

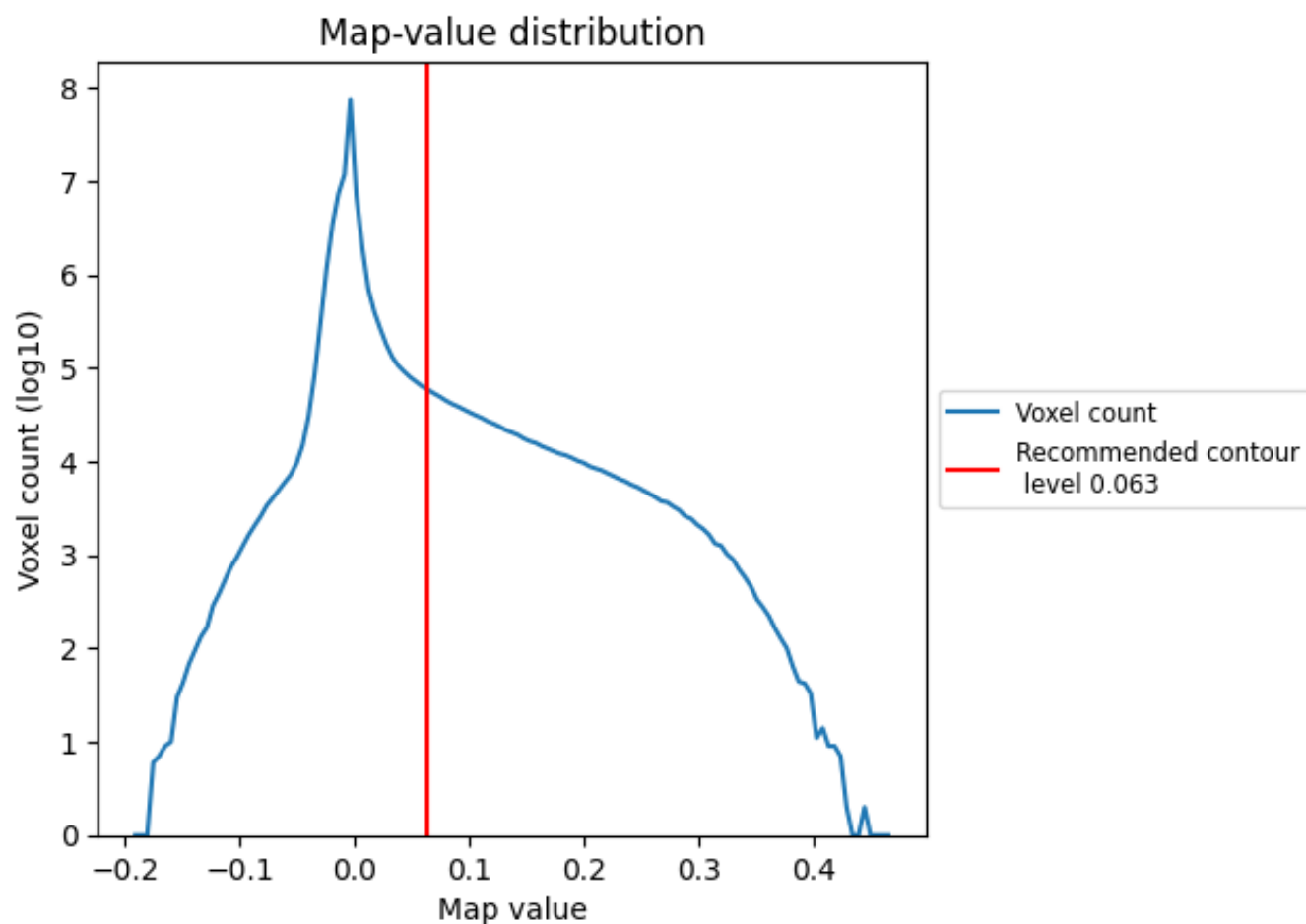


Z

## 7 Map analysis [i](#)

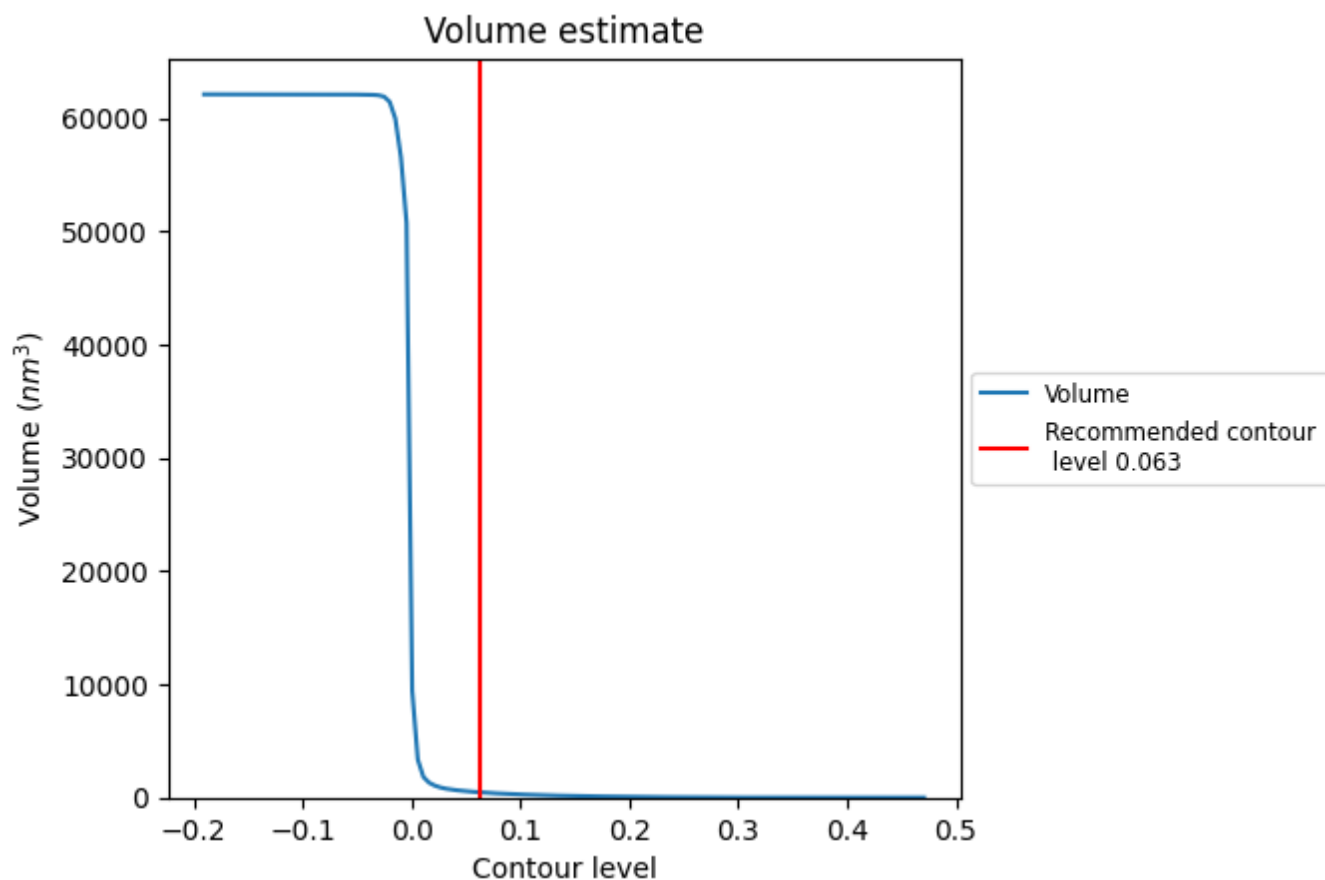
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

## 7.2 Volume estimate [i](#)

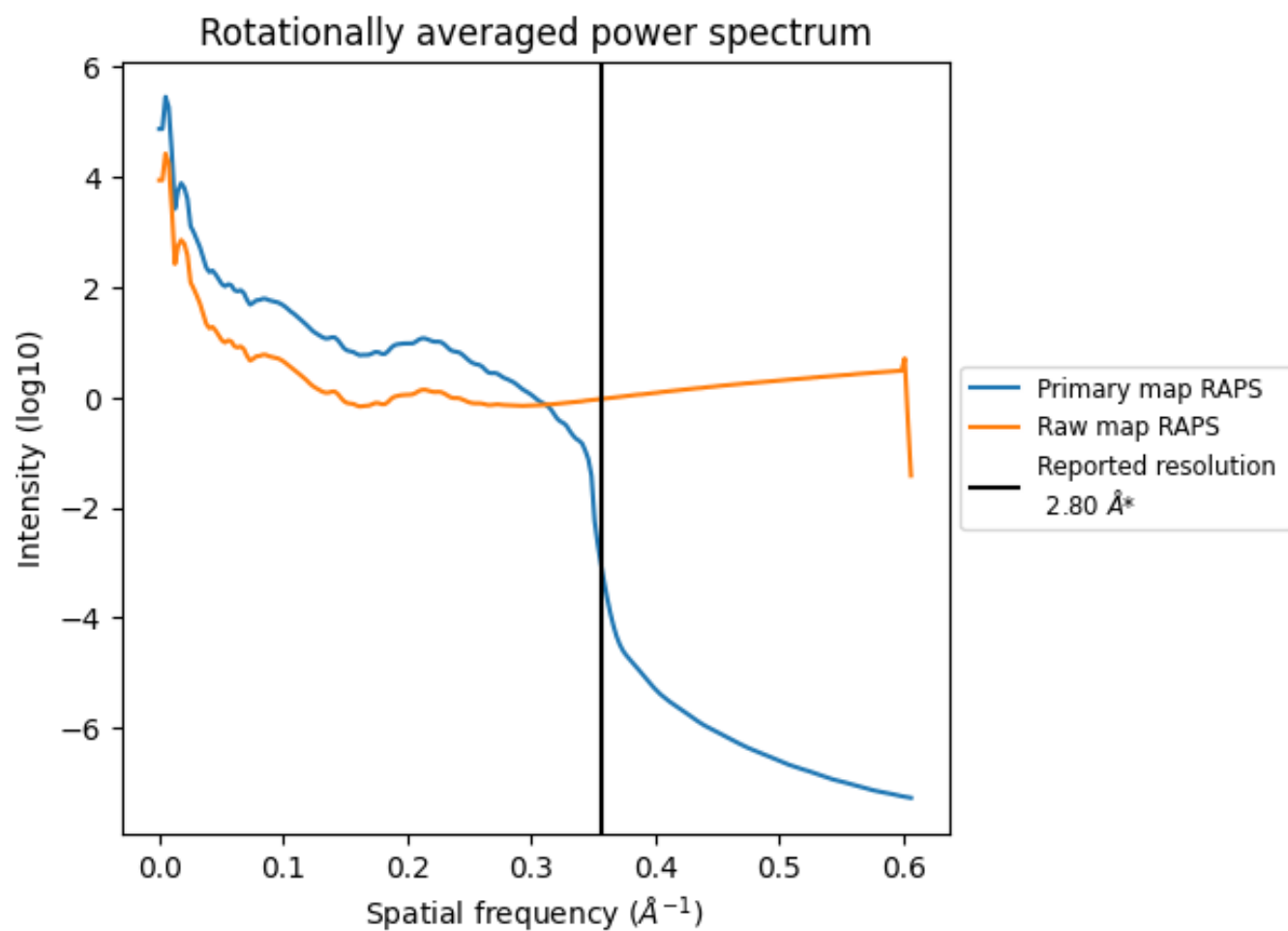


The volume at the recommended contour level is 460  $\text{nm}^3$ ; this corresponds to an approximate mass of 416 kDa.

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



### 7.3 Rotationally averaged power spectrum ⓘ

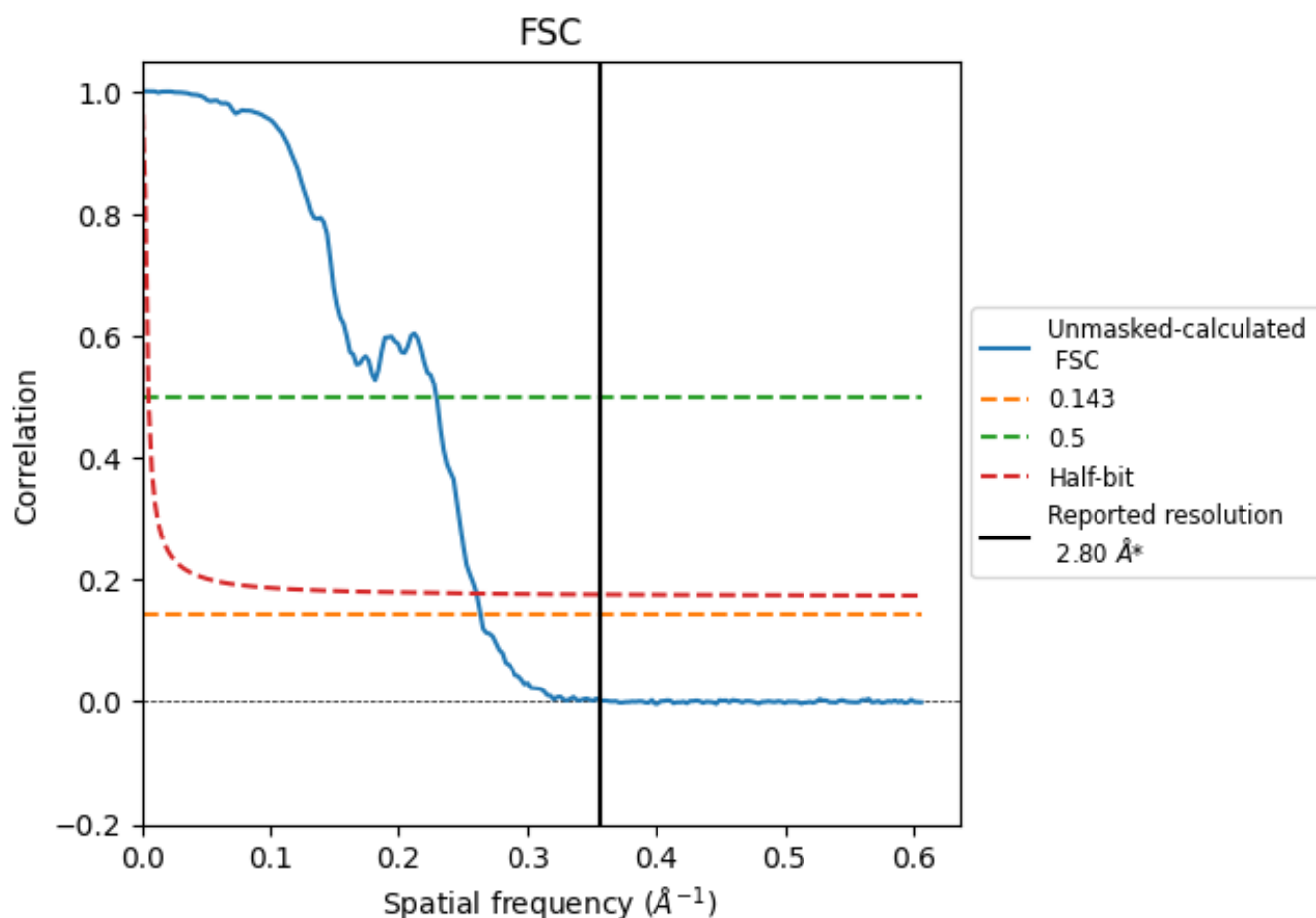


\*Reported resolution corresponds to spatial frequency of 0.357 Å<sup>-1</sup>

## 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 0.357 Å<sup>-1</sup>



## 8.2 Resolution estimates [i](#)

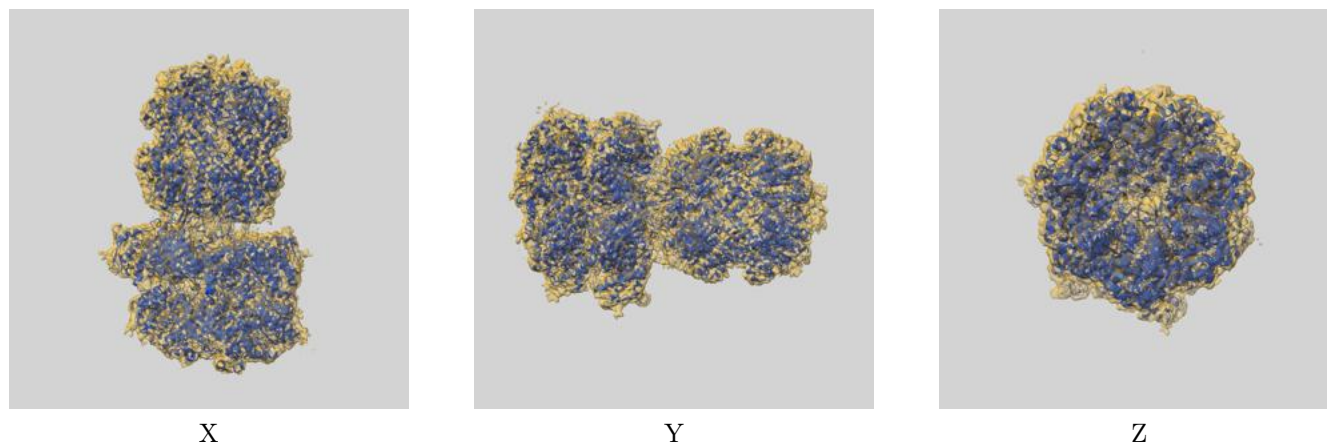
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.80	4.36	3.84

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.80 differs from the reported value 2.8 by more than 10 %

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

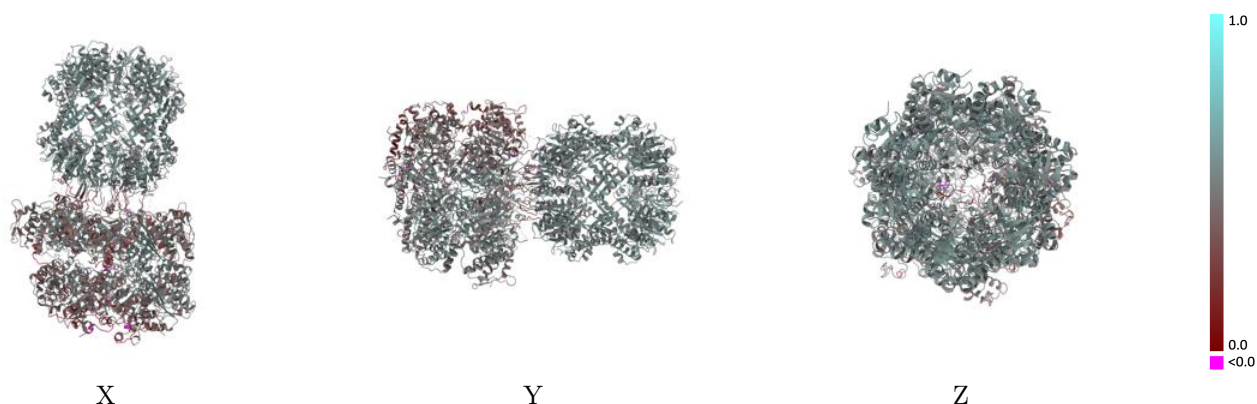
This section contains information regarding the fit between EMDB map EMD-57170 and PDB model 29HB. Per-residue inclusion information can be found in section [3](#) on page [7](#).

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



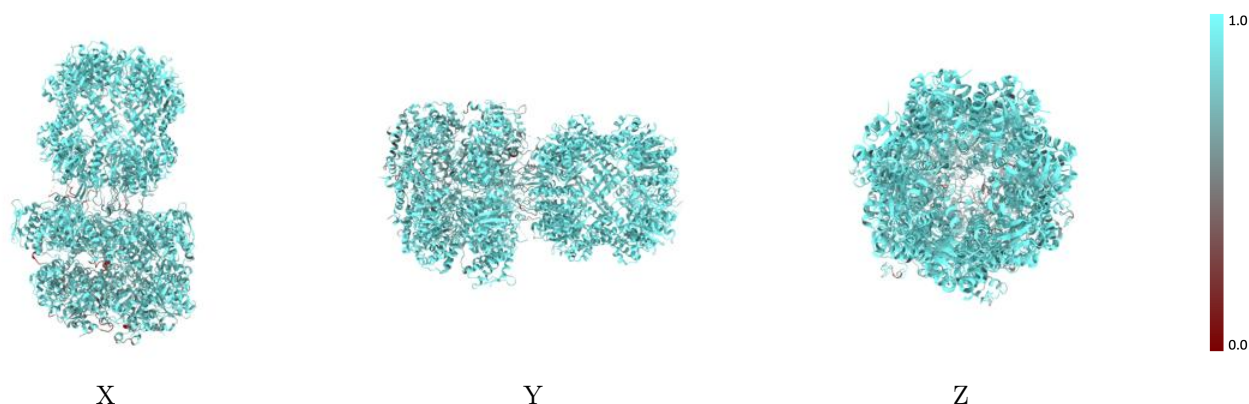
The images above show the 3D surface view of the map at the recommended contour level 0.063 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



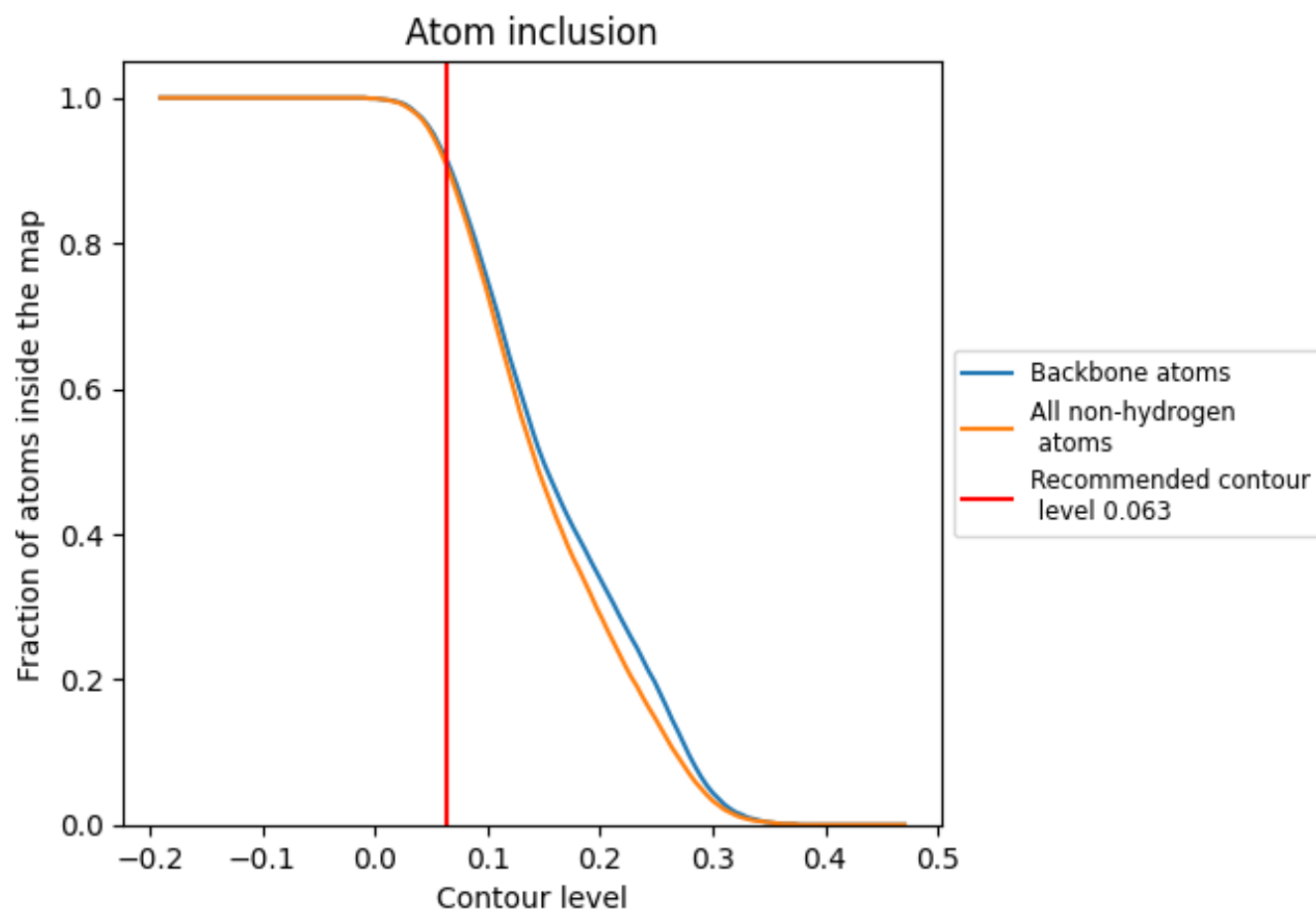
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.063).













































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 91% 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 (0.063) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9090	 0.4830
A	 0.9680	 0.5320
B	 0.9550	 0.5200
C	 0.9490	 0.5170
D	 0.9530	 0.5130
E	 0.9540	 0.5080
F	 0.9480	 0.5090
G	 0.9530	 0.5230
H	 0.9380	 0.5030
I	 0.9460	 0.5200
K	 0.9510	 0.5300
L	 0.9640	 0.5400
M	 0.9630	 0.5360
N	 0.9560	 0.5340
S	 0.9610	 0.5340
T	 0.9520	 0.5290
a	 0.9190	 0.4910
b	 0.9220	 0.4990
c	 0.9200	 0.4980
d	 0.8730	 0.4360
e	 0.7840	 0.3570
f	 0.8560	 0.4330

