wwPDB EM Validation Summary Report

Oct 19, 2026 – 01:08 PM EDT

PDB ID	:	9OTX / pdb_00009otx
EMDB ID	:	EMD-70861
Title	:	Cryo-EM structure of the Substrate-bound clpXP complex (clpX harbors the Q208A mutation in subunits B, D, and F), Class-III
Authors	:	Florez Ariza, A.J.; Sosa, R.; Bustamante, C.
Deposited on	:	2025-05-27
Resolution	:	3.40 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*
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:

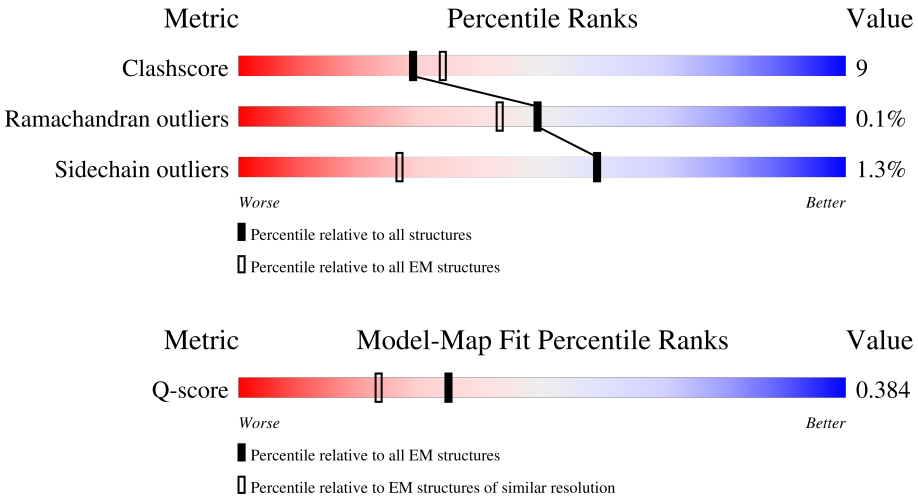
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.2
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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)	:	2.51

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 3.40 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	424	49% 25% • 23%
1	C	424	65% 18% 17%
1	E	424	65% 18% 17%
2	B	424	59% 20% • 19%

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Mol	Chain	Length	Quality of chain
2	D	424	65% 17% 17%
2	F	424	54% 24% 20%
3	G	207	76% 16% 7%
3	H	207	81% 12% 7%
3	I	207	82% 11% 7%
3	J	207	83% 10% 7%
3	K	207	82% 11% 7%
3	L	207	79% 14% 7%
3	M	207	84% 9% 7%
3	N	207	81% 11% 7%
3	O	207	79% 14% 7%
3	P	207	77% 15% 7%
3	Q	207	73% 19% 7%
3	R	207	78% 14% 7%
3	S	207	77% 15% 7%
3	T	207	81% 12% 7%
4	U	9	100%

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 74531 atoms, of which 37488 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 ATP-binding subunit ClpX.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	326	Total	C	H	N	O	S	0	0
			5065	1589	2569	414	487	6		
1	C	352	Total	C	H	N	O	S	0	0
			5450	1702	2758	457	527	6		
1	E	352	Total	C	H	N	O	S	0	0
			5449	1702	2757	457	527	6		

- Molecule 2 is a protein called ATP-dependent Clp protease ATP-binding subunit ClpX.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	B	342	Total	C	H	N	O	S	0	0
			5294	1657	2680	441	510	6		
2	D	352	Total	C	H	N	O	S	0	0
			5442	1700	2754	456	526	6		
2	F	338	Total	C	H	N	O	S	0	0
			5245	1642	2657	437	503	6		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	208	ALA	GLN	engineered mutation	UNP A7ZIJ6
D	208	ALA	GLN	engineered mutation	UNP A7ZIJ6
F	208	ALA	GLN	engineered mutation	UNP A7ZIJ6

- Molecule 3 is a protein called ATP-dependent Clp protease proteolytic subunit.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	G	192	Total	C	H	N	O	S	0	0
			3018	947	1515	261	283	12		
3	H	192	Total	C	H	N	O	S	0	0
			3018	947	1515	261	283	12		
3	I	192	Total	C	H	N	O	S	0	0
			3018	947	1515	261	283	12		

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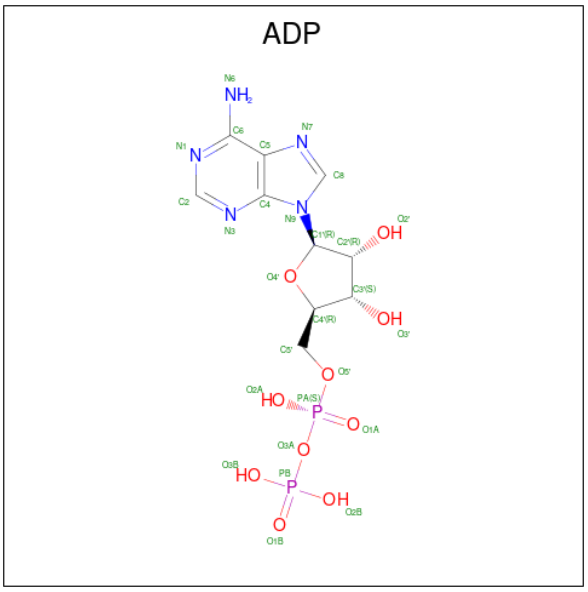
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Mol	Chain	Residues	Atoms						AltConf	Trace
3	J	192	Total	C	H	N	O	S	0	0
			3017	947	1514	261	283	12		
3	K	192	Total	C	H	N	O	S	0	0
			3017	947	1514	261	283	12		
3	L	192	Total	C	H	N	O	S	0	0
			3017	947	1514	261	283	12		
3	M	192	Total	C	H	N	O	S	0	0
			3018	947	1515	261	283	12		
3	N	192	Total	C	H	N	O	S	0	0
			3017	947	1514	261	283	12		
3	O	192	Total	C	H	N	O	S	0	0
			3018	947	1515	261	283	12		
3	P	192	Total	C	H	N	O	S	0	0
			3018	947	1515	261	283	12		
3	Q	192	Total	C	H	N	O	S	0	0
			3017	947	1514	261	283	12		
3	R	192	Total	C	H	N	O	S	0	0
			3018	947	1515	261	283	12		
3	S	192	Total	C	H	N	O	S	0	0
			3017	947	1514	261	283	12		
3	T	192	Total	C	H	N	O	S	0	0
			3017	947	1514	261	283	12		

- Molecule 4 is a protein called Substrate.

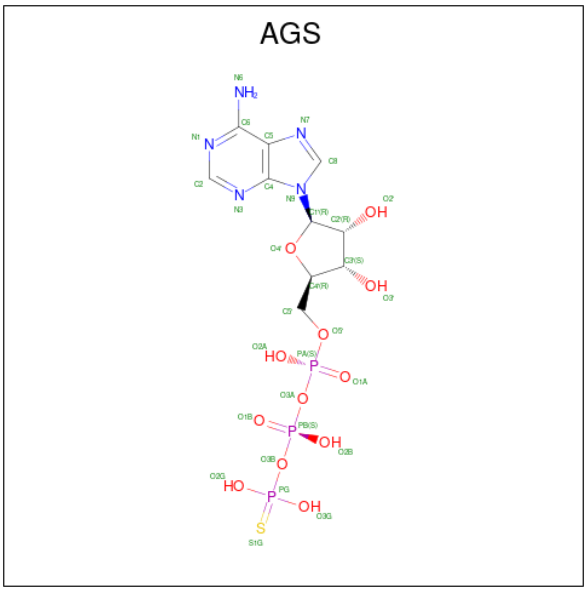
Mol	Chain	Residues	Atoms					AltConf	Trace
4	U	9	Total	C	H	N	O	0	0
			84	27	38	9	10		

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						AltConf
5	A	1	Total	C	H	N	O	P	0
			39	10	12	5	10	2	

- Molecule 6 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (CCD ID: AGS) (formula: $C_{10}H_{16}N_5O_{12}P_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							AltConf
6	B	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	
6	C	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	

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Mol	Chain	Residues	Atoms							AltConf
6	D	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	
6	E	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	
6	F	1	Total	C	H	N	O	P	S	0
			43	10	12	5	12	3	1	

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

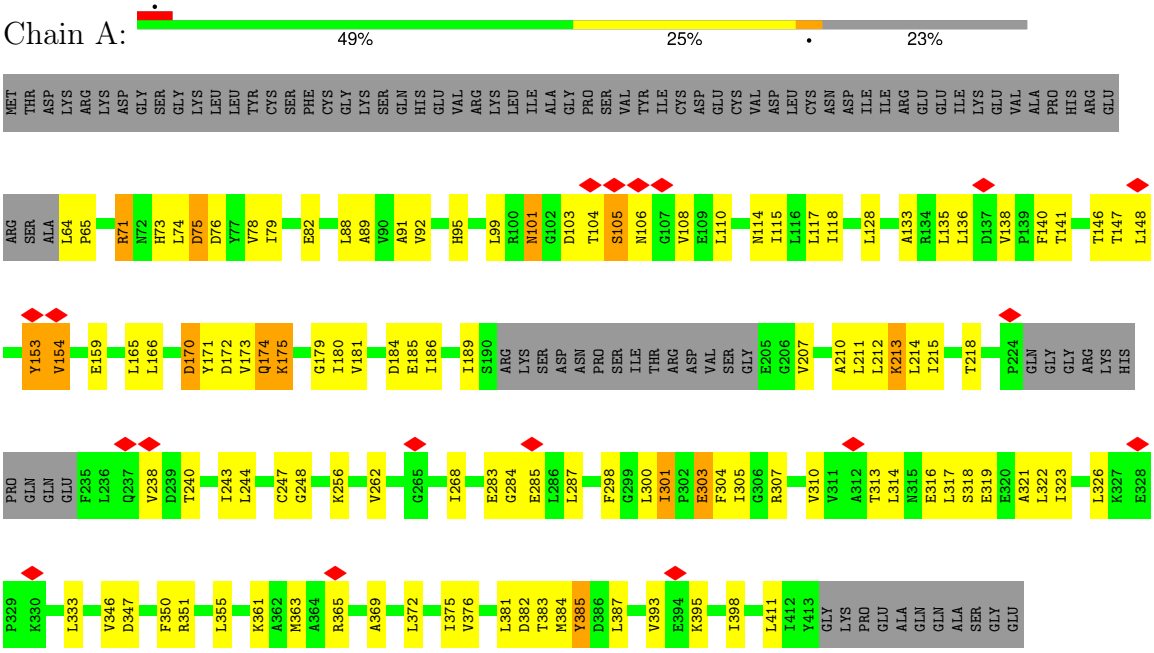
Mol	Chain	Residues	Atoms			AltConf
7	B	1	Total	Mg		0
			1	1		
7	C	1	Total	Mg		0
			1	1		
7	D	1	Total	Mg		0
			1	1		

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.

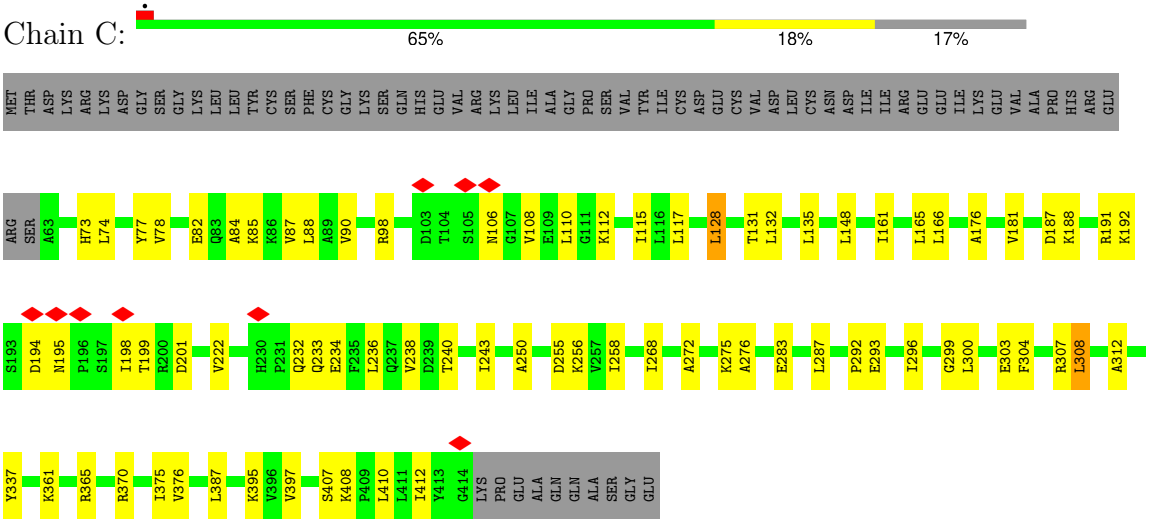
• Molecule 1: ATP-dependent Clp protease ATP-binding subunit ClpX

Chain A:



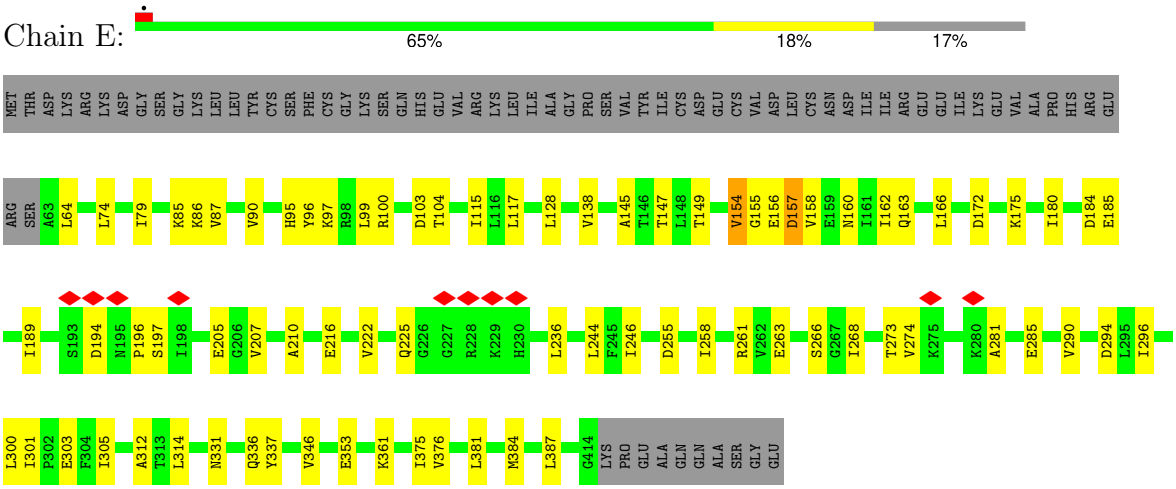
• Molecule 1: ATP-dependent Clp protease ATP-binding subunit ClpX

Chain C:



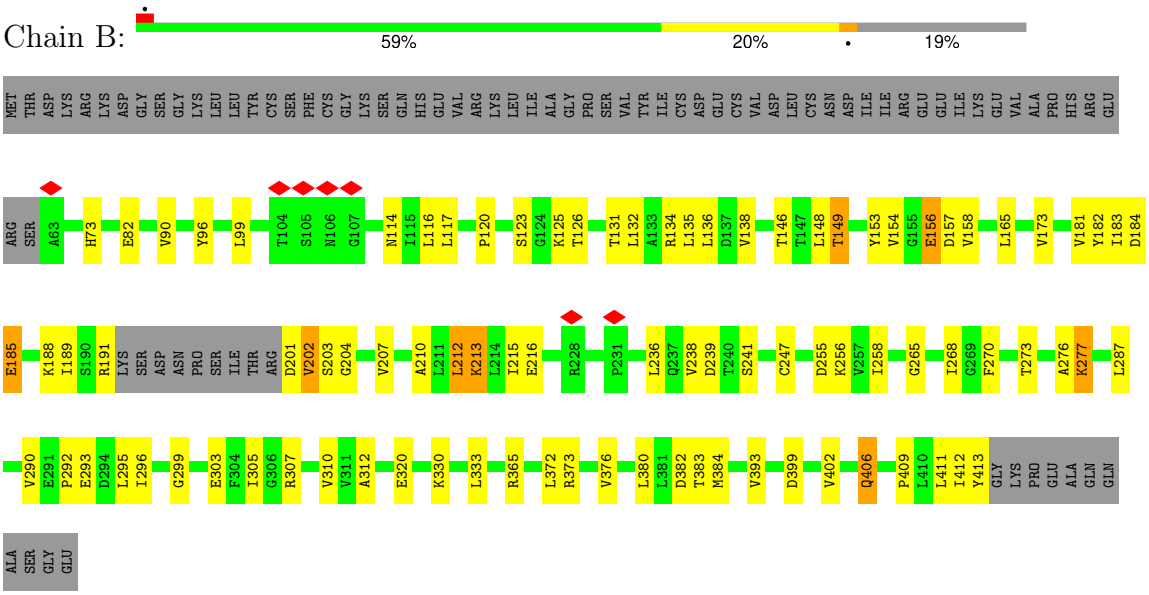
• Molecule 1: ATP-dependent Clp protease ATP-binding subunit ClpX

Chain E:



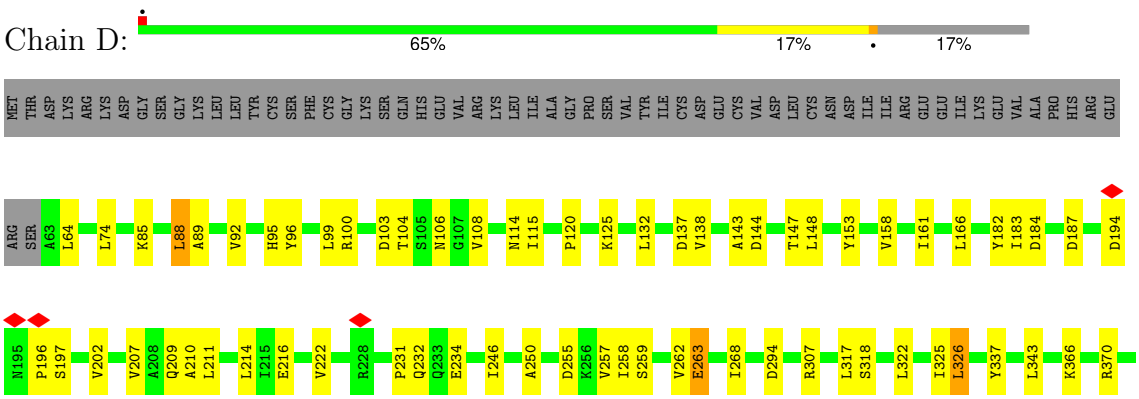
• Molecule 2: ATP-dependent Clp protease ATP-binding subunit ClpX

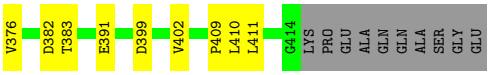
Chain B:



• Molecule 2: ATP-dependent Clp protease ATP-binding subunit ClpX

Chain D:

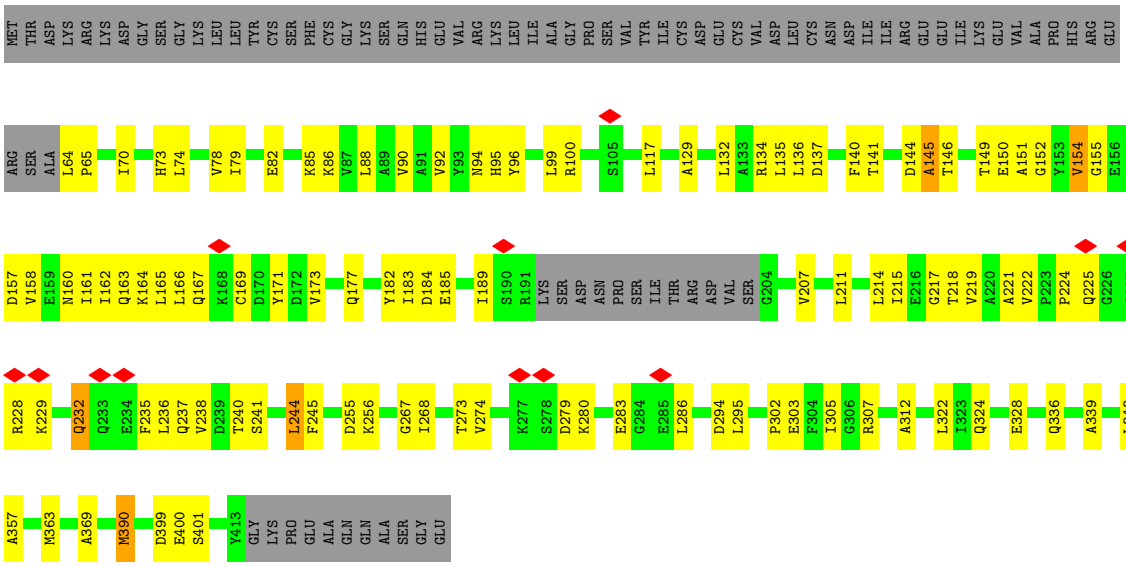




• Molecule 2: ATP-dependent Clp protease ATP-binding subunit ClpX

Chain F:

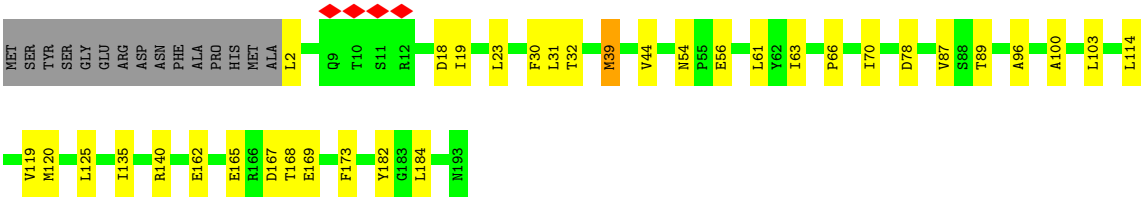




• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain G:

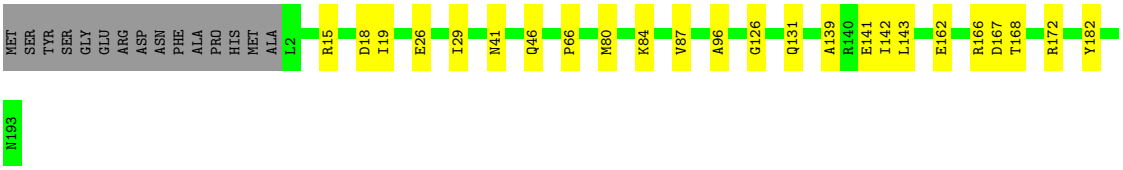




• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain H:





• Molecule 3: ATP-dependent Clp protease proteolytic subunit

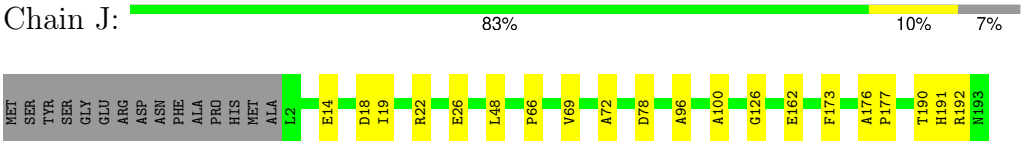
Chain I:





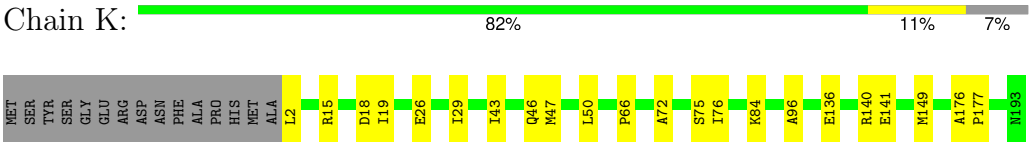
• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain J:



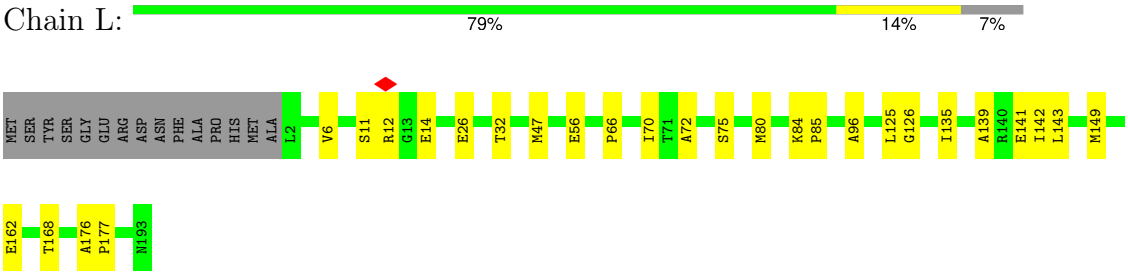
• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain K:



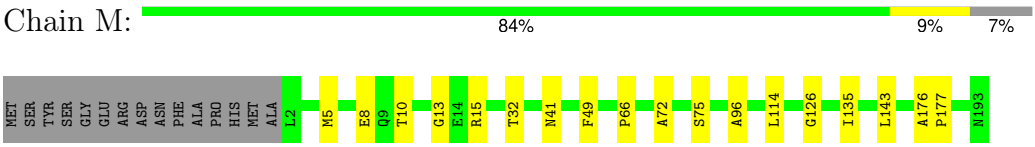
• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain L:



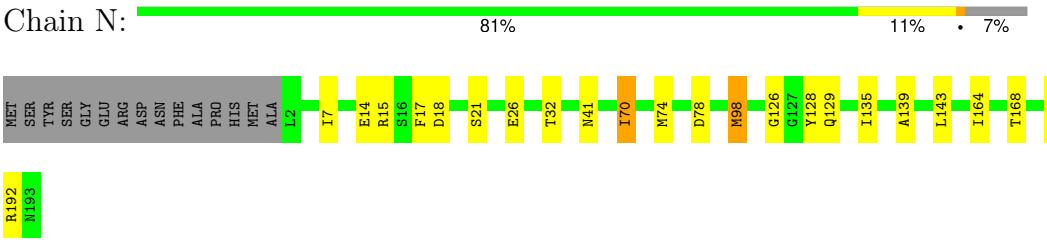
• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain M:



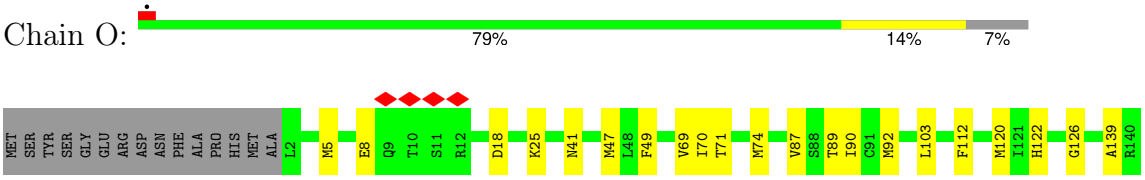
• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain N:



• Molecule 3: ATP-dependent Clp protease proteolytic subunit

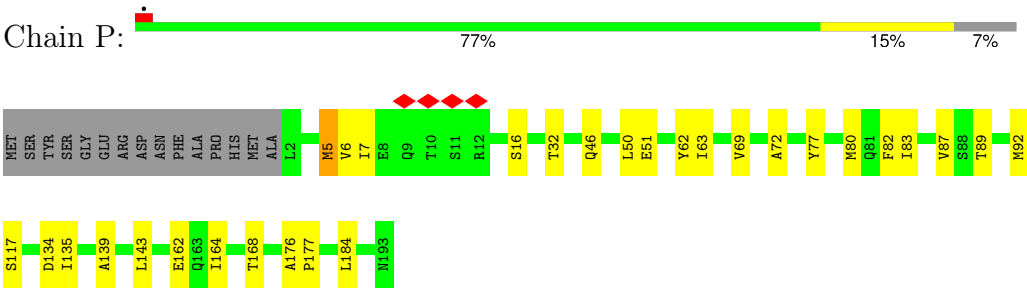
Chain O:





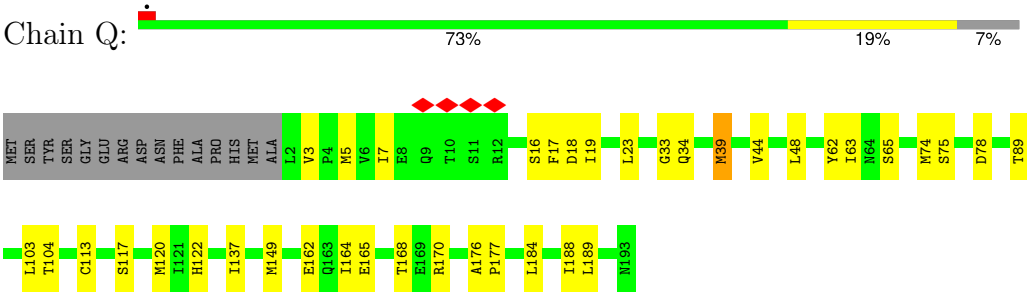
• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain P:



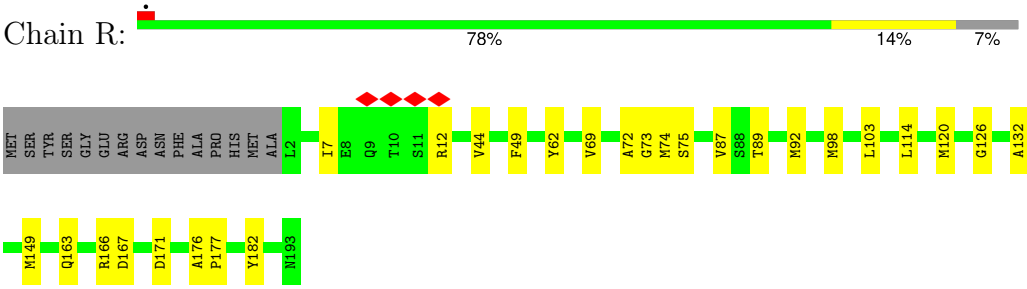
• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain Q:



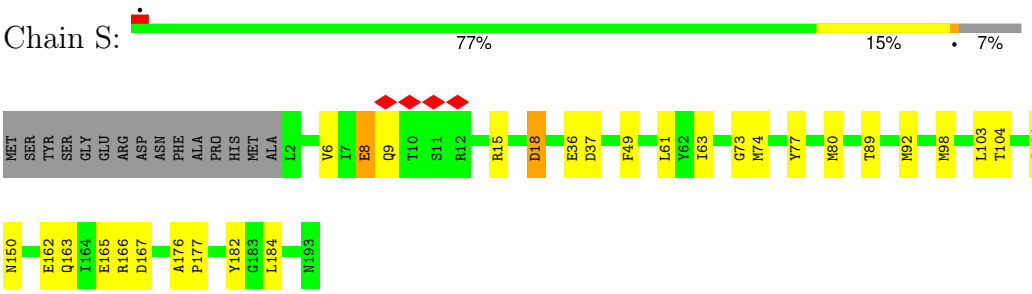
• Molecule 3: ATP-dependent Clp protease proteolytic subunit

Chain R:



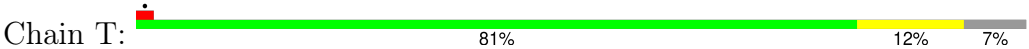
• Molecule 3: ATP-dependent Clp protease proteolytic subunit

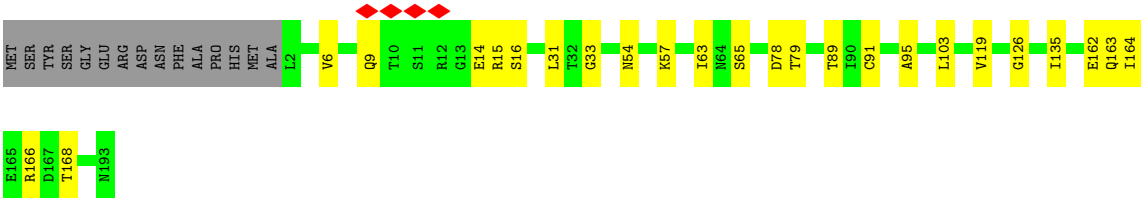
Chain S:



• Molecule 3: ATP-dependent Clp protease proteolytic subunit

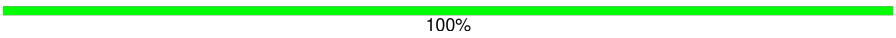
Chain T:





- Molecule 4: Substrate

Chain U:



There are no outlier residues recorded for this chain.

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	76882	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOCONTINUUM (6k x 4k)	Depositor
Maximum map value	0.413	Depositor
Minimum map value	-0.163	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.015	Depositor
Recommended contour level	0.092	Depositor
Map size (Å)	401.63202, 401.63202, 401.63202	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.141, 1.141, 1.141	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.19	0/2527	0.63	3/3416 (0.1%)
1	C	0.12	0/2728	0.36	0/3688
1	E	0.13	0/2728	0.41	0/3688
2	B	0.14	0/2648	0.45	0/3579
2	D	0.13	0/2724	0.38	0/3683
2	F	0.16	0/2622	0.54	1/3543 (0.0%)
3	G	0.15	0/1527	0.38	0/2058
3	H	0.16	0/1527	0.35	0/2058
3	I	0.15	0/1527	0.35	0/2058
3	J	0.16	0/1527	0.33	0/2058
3	K	0.16	0/1527	0.34	0/2058
3	L	0.15	0/1527	0.33	0/2058
3	M	0.16	0/1527	0.34	0/2058
3	N	0.17	0/1527	0.36	0/2058
3	O	0.15	0/1527	0.35	0/2058
3	P	0.16	0/1527	0.38	0/2058
3	Q	0.18	0/1527	0.37	0/2058
3	R	0.14	0/1527	0.35	0/2058
3	S	0.16	0/1527	0.37	0/2058
3	T	0.15	0/1527	0.37	0/2058
All	All	0.15	0/37355	0.41	4/50409 (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
2	D	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	145	ALA	N-CA-C	5.26	117.93	111.82
1	A	105	SER	N-CA-C	5.10	119.08	112.86
1	A	101	ASN	CA-C-N	-5.08	111.44	121.41
1	A	101	ASN	C-N-CA	-5.08	111.44	121.41

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	263	GLU	Sidechain

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	A	2496	2569	2565	97	0
1	C	2692	2758	2756	63	0
1	E	2692	2757	2756	63	0
2	B	2614	2680	2678	80	0
2	D	2688	2754	2753	56	0
2	F	2588	2657	2655	102	0
3	G	1503	1515	1513	28	0
3	H	1503	1515	1513	20	0
3	I	1503	1515	1513	13	0
3	J	1503	1514	1513	17	0
3	K	1503	1514	1513	16	0
3	L	1503	1514	1513	20	0
3	M	1503	1515	1513	19	0
3	N	1503	1514	1513	23	0
3	O	1503	1515	1513	20	0
3	P	1503	1515	1513	23	0
3	Q	1503	1514	1513	30	0
3	R	1503	1515	1513	22	0
3	S	1503	1514	1513	30	0
3	T	1503	1514	1513	18	0
4	U	46	38	11	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	27	12	12	2	0
6	B	31	12	12	4	0
6	C	31	12	12	2	0
6	D	31	12	12	1	0
6	E	31	12	12	2	0
6	F	31	12	12	4	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
All	All	37043	37488	37428	698	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

The worst 5 of 698 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)
2:B:393:VAL:HG13	2:B:411:LEU:HD21	1.39	1.01
1:A:141:THR:HG21	1:A:165:LEU:HD13	1.48	0.95
3:J:22:ARG:NH1	3:J:26:GLU:OE2	2.01	0.93
3:J:26:GLU:N	3:J:26:GLU:OE1	2.02	0.91
2:B:406:GLN:N	2:B:406:GLN:OE1	2.03	0.91

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	320/424 (76%)	305 (95%)	13 (4%)	2 (1%)	21 50
1	C	350/424 (82%)	342 (98%)	8 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	E	350/424 (82%)	341 (97%)	8 (2%)	1 (0%)	36 65
2	B	338/424 (80%)	333 (98%)	4 (1%)	1 (0%)	36 65
2	D	350/424 (82%)	342 (98%)	8 (2%)	0	100 100
2	F	334/424 (79%)	325 (97%)	8 (2%)	1 (0%)	36 65
3	G	190/207 (92%)	189 (100%)	1 (0%)	0	100 100
3	H	190/207 (92%)	189 (100%)	1 (0%)	0	100 100
3	I	190/207 (92%)	188 (99%)	2 (1%)	0	100 100
3	J	190/207 (92%)	189 (100%)	1 (0%)	0	100 100
3	K	190/207 (92%)	189 (100%)	1 (0%)	0	100 100
3	L	190/207 (92%)	187 (98%)	3 (2%)	0	100 100
3	M	190/207 (92%)	189 (100%)	1 (0%)	0	100 100
3	N	190/207 (92%)	189 (100%)	1 (0%)	0	100 100
3	O	190/207 (92%)	189 (100%)	1 (0%)	0	100 100
3	P	190/207 (92%)	190 (100%)	0	0	100 100
3	Q	190/207 (92%)	190 (100%)	0	0	100 100
3	R	190/207 (92%)	189 (100%)	1 (0%)	0	100 100
3	S	190/207 (92%)	189 (100%)	1 (0%)	0	100 100
3	T	190/207 (92%)	189 (100%)	1 (0%)	0	100 100
All	All	4702/5442 (86%)	4633 (98%)	64 (1%)	5 (0%)	49 78

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	154	VAL
2	B	202	VAL
2	F	154	VAL
1	E	157	ASP
1	A	170	ASP

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	A	270/354 (76%)	257 (95%)	13 (5%)	23 50
1	C	291/354 (82%)	289 (99%)	2 (1%)	76 78
1	E	291/354 (82%)	288 (99%)	3 (1%)	68 75
2	B	281/353 (80%)	273 (97%)	8 (3%)	38 60
2	D	290/353 (82%)	288 (99%)	2 (1%)	76 78
2	F	278/353 (79%)	274 (99%)	4 (1%)	59 70
3	G	163/175 (93%)	160 (98%)	3 (2%)	51 67
3	H	163/175 (93%)	161 (99%)	2 (1%)	63 72
3	I	163/175 (93%)	161 (99%)	2 (1%)	63 72
3	J	163/175 (93%)	163 (100%)	0	100 100
3	K	163/175 (93%)	160 (98%)	3 (2%)	51 67
3	L	163/175 (93%)	162 (99%)	1 (1%)	78 80
3	M	163/175 (93%)	163 (100%)	0	100 100
3	N	163/175 (93%)	161 (99%)	2 (1%)	63 72
3	O	163/175 (93%)	161 (99%)	2 (1%)	63 72
3	P	163/175 (93%)	162 (99%)	1 (1%)	78 80
3	Q	163/175 (93%)	161 (99%)	2 (1%)	63 72
3	R	163/175 (93%)	163 (100%)	0	100 100
3	S	163/175 (93%)	161 (99%)	2 (1%)	63 72
3	T	163/175 (93%)	163 (100%)	0	100 100
All	All	3983/4571 (87%)	3931 (99%)	52 (1%)	59 71

5 of 52 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	146	THR
3	H	141	GLU
3	Q	39	MET
2	F	232	GLN
3	G	39	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
3	J	46	GLN
3	L	131	GLN
3	T	138	HIS
3	R	131	GLN
3	J	123	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 for Mogul analysis.

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	$\#\|Z\| > 2$
6	AGS	B	501	7	32,33,33	0.55	1 (3%)	45,52,52	0.70	1 (2%)
5	ADP	A	501	-	28,29,29	1.36	4 (14%)	43,45,45	1.84	8 (18%)
6	AGS	C	501	7	32,33,33	0.54	1 (3%)	45,52,52	0.73	1 (2%)
6	AGS	F	501	-	32,33,33	0.51	1 (3%)	45,52,52	0.74	1 (2%)
6	AGS	D	501	7	32,33,33	0.49	1 (3%)	45,52,52	0.68	1 (2%)
6	AGS	E	501	-	32,33,33	0.51	1 (3%)	45,52,52	0.68	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
6	AGS	B	501	7	-	3/21/38/38	0/3/3/3
5	ADP	A	501	-	-	7/16/32/32	0/3/3/3
6	AGS	C	501	7	-	11/21/38/38	0/3/3/3
6	AGS	F	501	-	-	3/21/38/38	0/3/3/3
6	AGS	D	501	7	-	0/21/38/38	0/3/3/3
6	AGS	E	501	-	-	6/21/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	501	ADP	C5-C4	4.46	1.47	1.39
5	A	501	ADP	C5-N7	-2.54	1.34	1.39
5	A	501	ADP	C5-C6	2.35	1.47	1.41
6	F	501	AGS	PG-S1G	2.14	1.95	1.90
6	B	501	AGS	PG-S1G	2.13	1.95	1.90

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	501	ADP	C5-C4-N3	-5.73	118.82	126.72
5	A	501	ADP	N3-C4-N9	5.03	135.73	127.17
6	B	501	AGS	PB-O3B-PG	-3.94	118.75	133.17
6	F	501	AGS	PB-O3B-PG	-3.77	119.36	133.17
6	C	501	AGS	PB-O3B-PG	-3.75	119.44	133.17

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	501	ADP	C5'-O5'-PA-O1A
5	A	501	ADP	C5'-O5'-PA-O2A
5	A	501	ADP	C5'-O5'-PA-O3A
5	A	501	ADP	C3'-C4'-C5'-O5'
6	B	501	AGS	C5'-O5'-PA-O1A

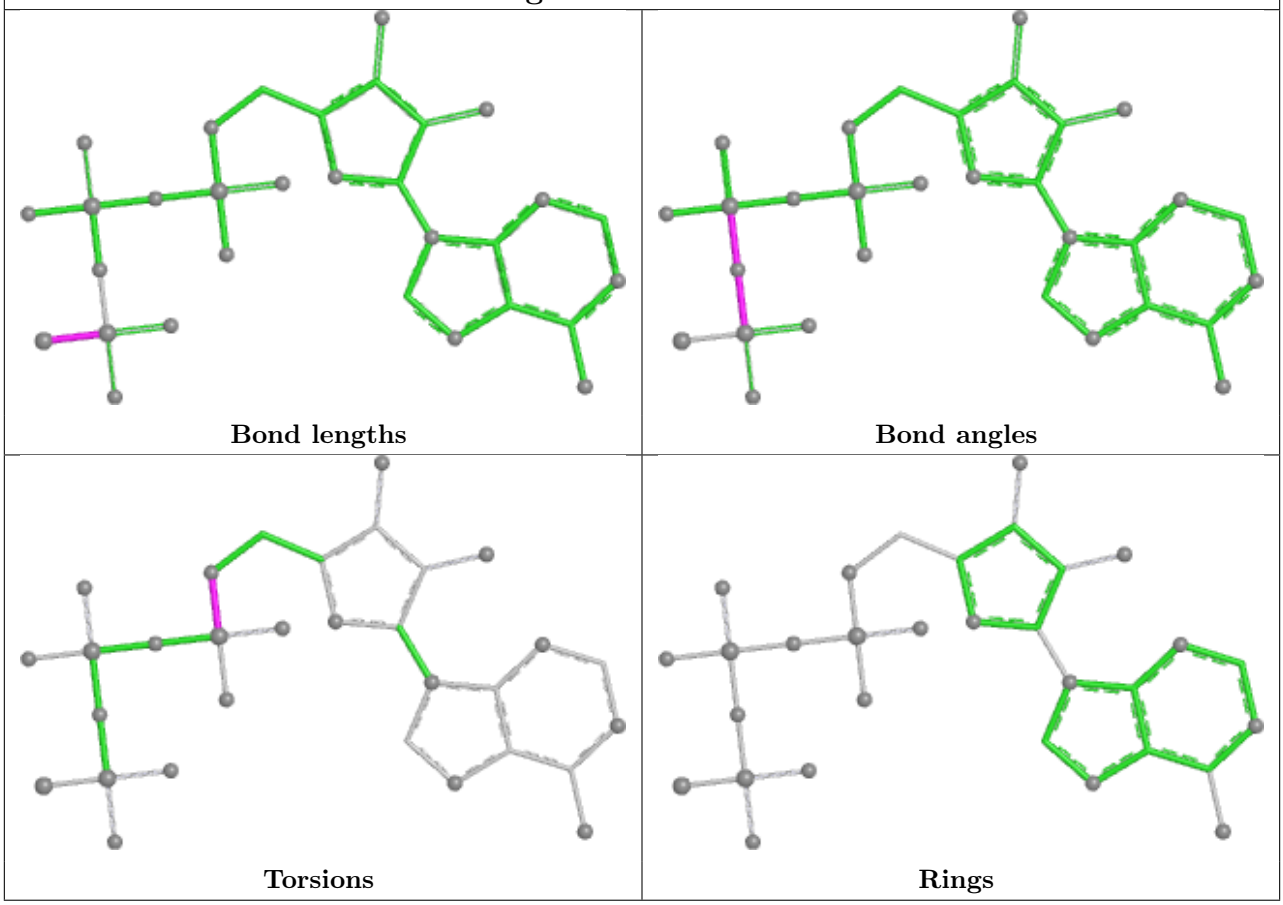
There are no ring outliers.

6 monomers are involved in 15 short contacts:

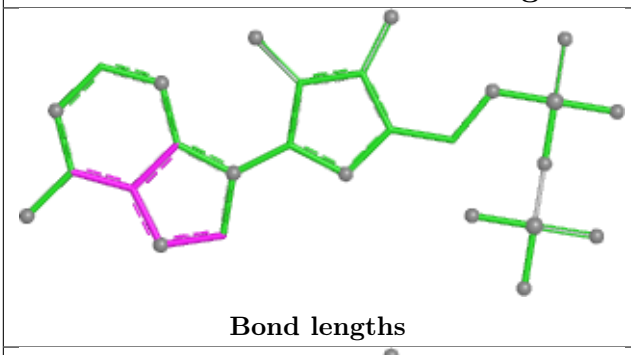
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	501	AGS	4	0
5	A	501	ADP	2	0
6	C	501	AGS	2	0
6	F	501	AGS	4	0
6	D	501	AGS	1	0
6	E	501	AGS	2	0

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 then 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.

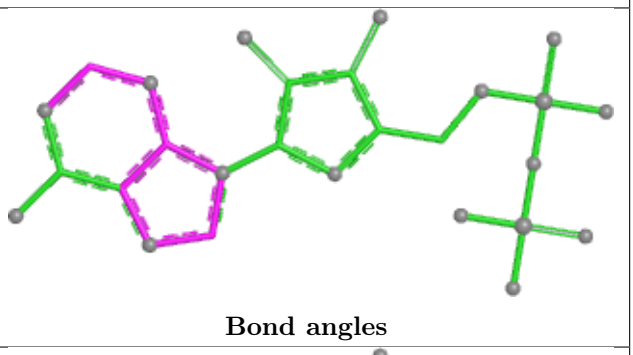
Ligand AGS B 501



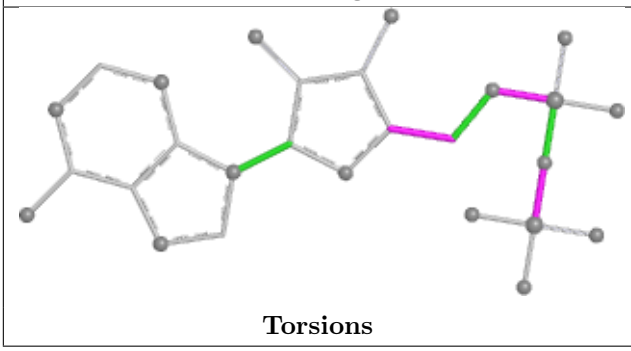
Ligand ADP A 501



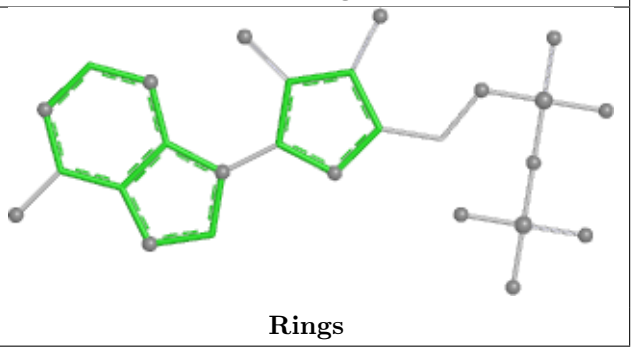
Bond lengths



Bond angles

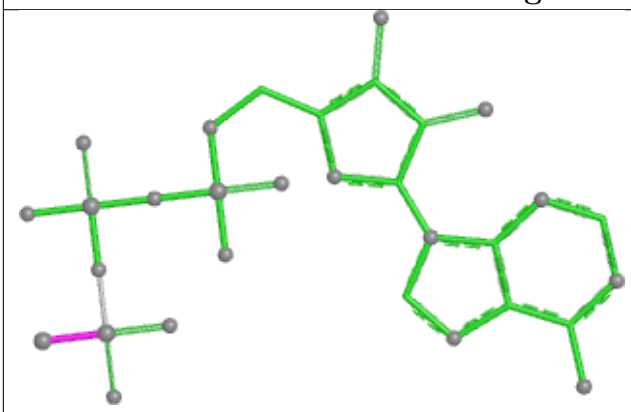


Torsions

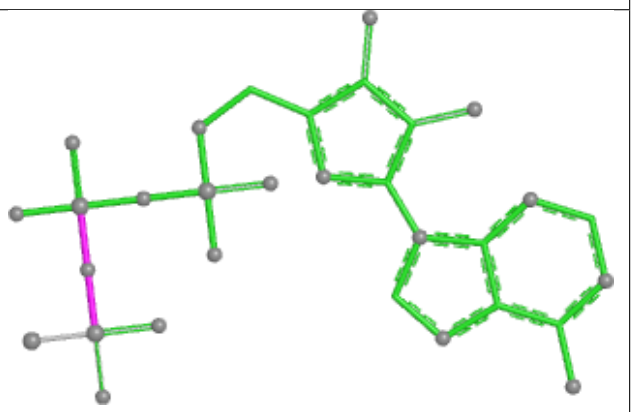


Rings

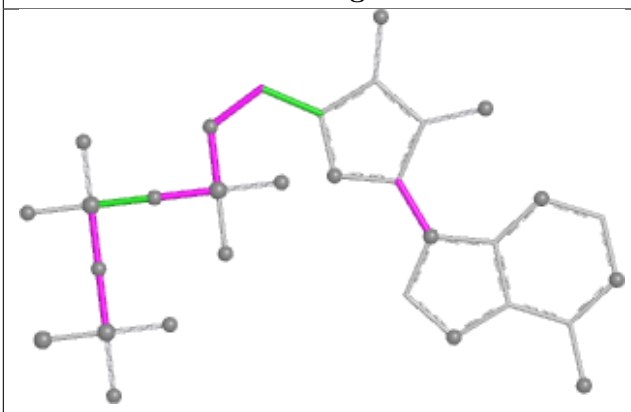
Ligand AGS C 501



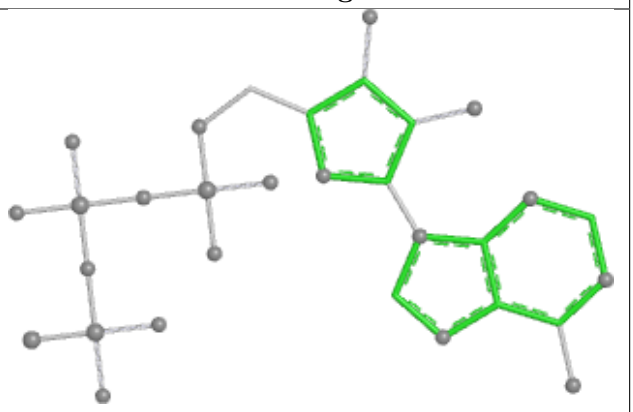
Bond lengths



Bond angles

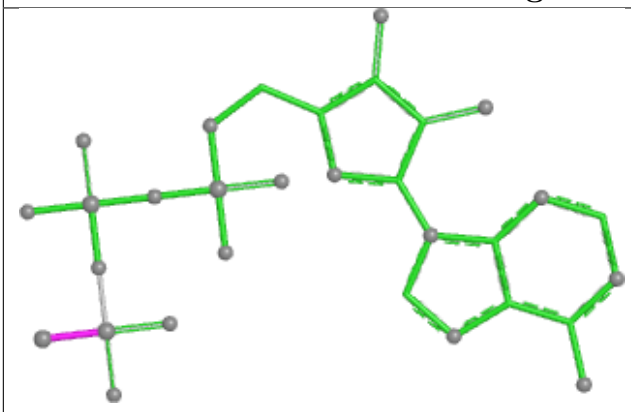


Torsions

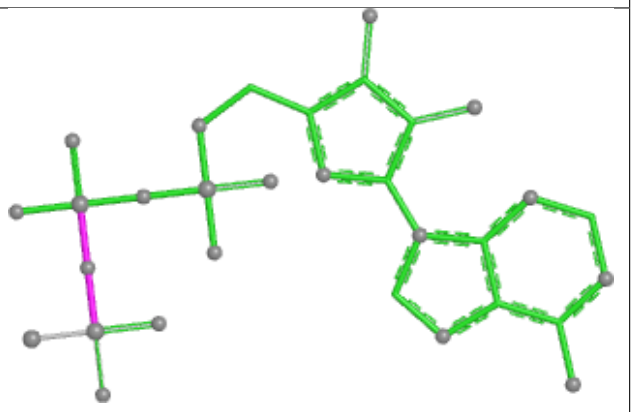


Rings

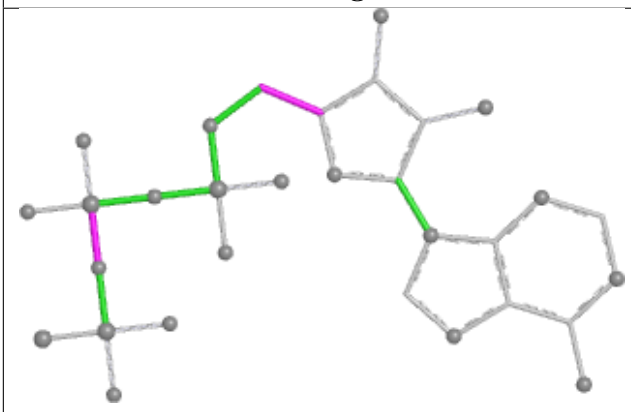
Ligand AGS F 501



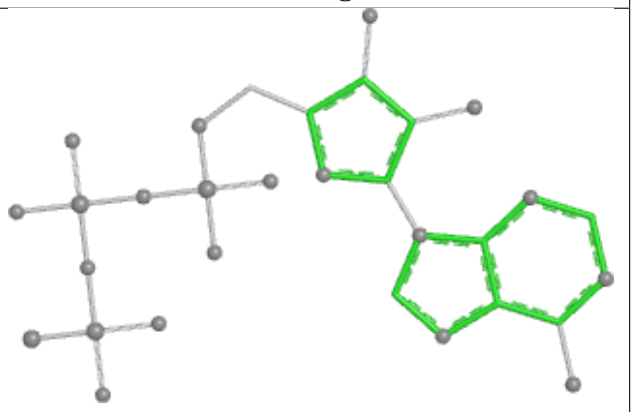
Bond lengths



Bond angles

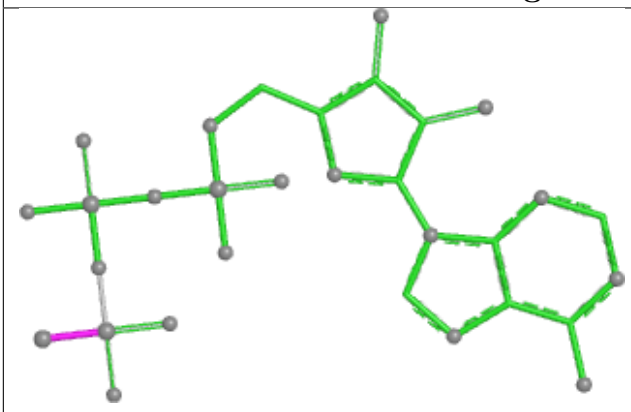


Torsions

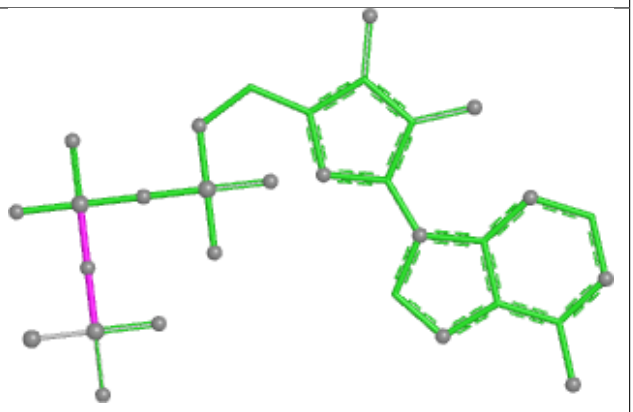


Rings

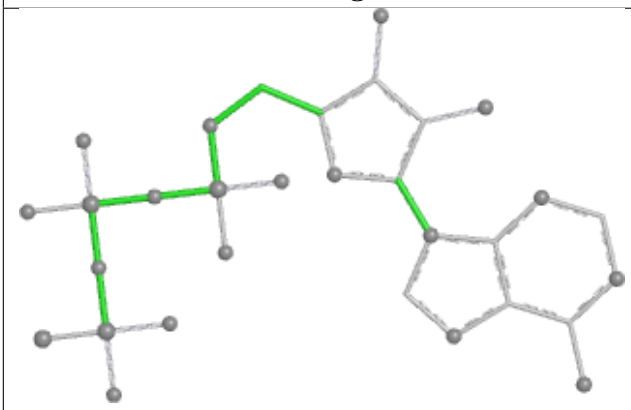
Ligand AGS D 501



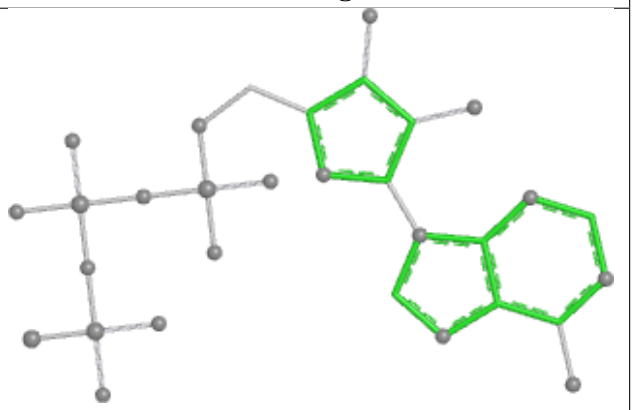
Bond lengths



Bond angles

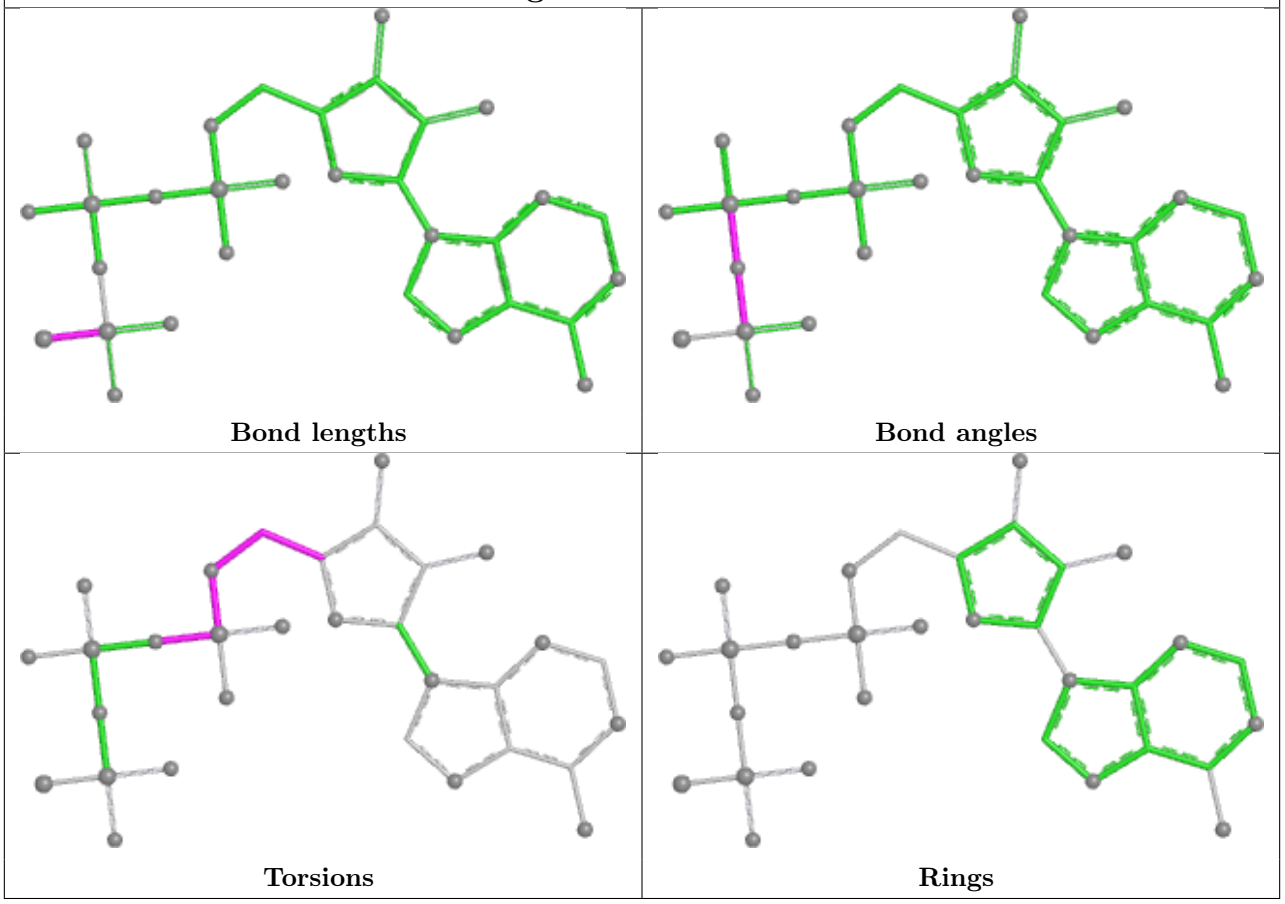


Torsions



Rings

Ligand AGS E 501



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.

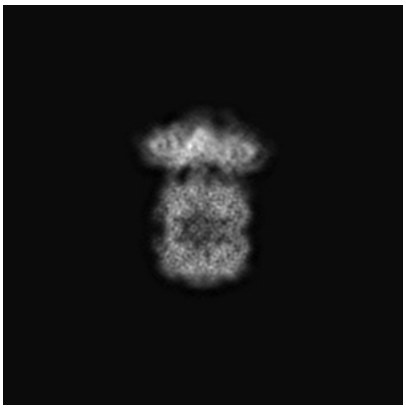
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-70861. These allow visual inspection of the internal detail of the map and identification of artifacts.

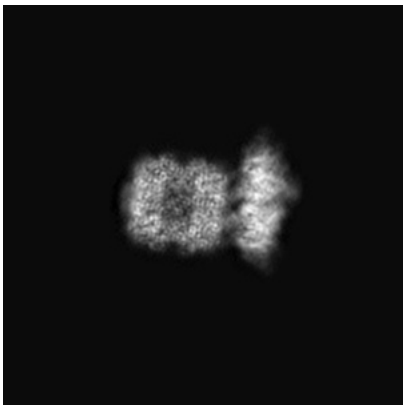
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

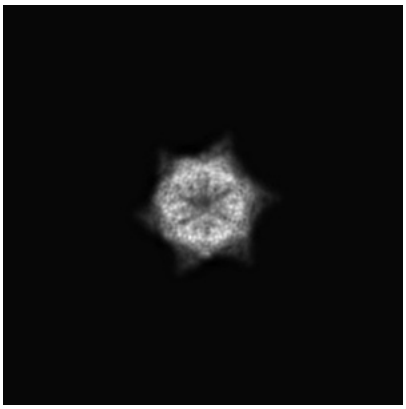
6.1.1 Primary map



X

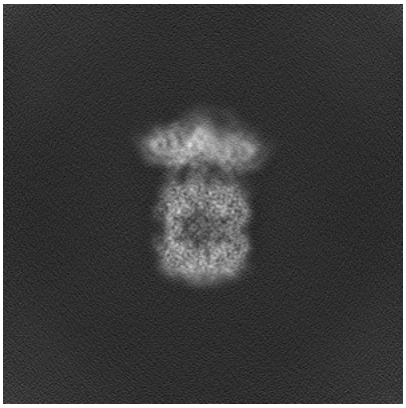


Y

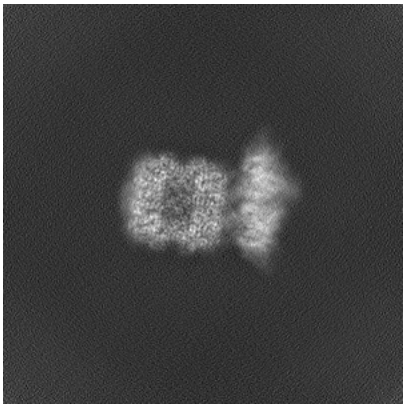


Z

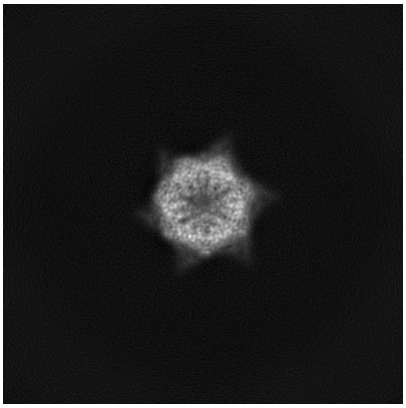
6.1.2 Raw map



X



Y



Z

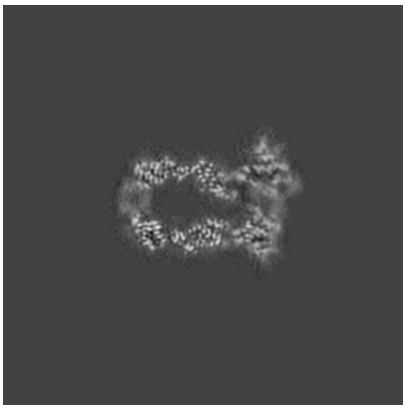
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

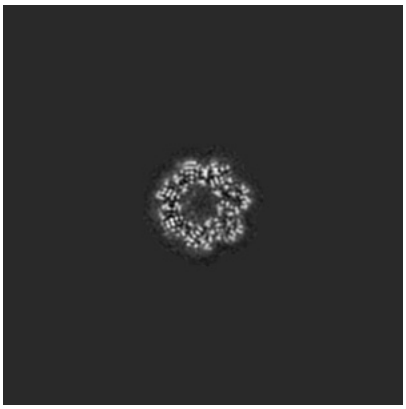
6.2.1 Primary map



X Index: 176

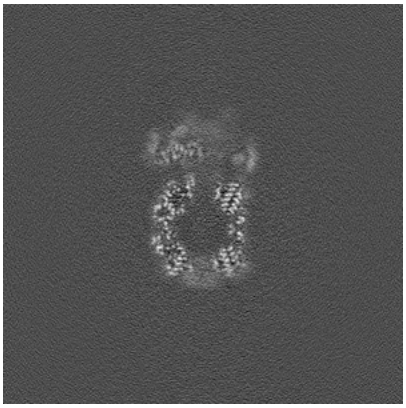


Y Index: 176

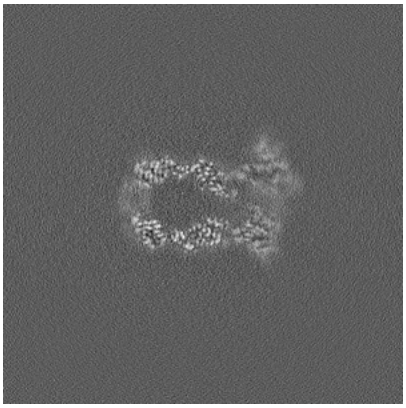


Z Index: 176

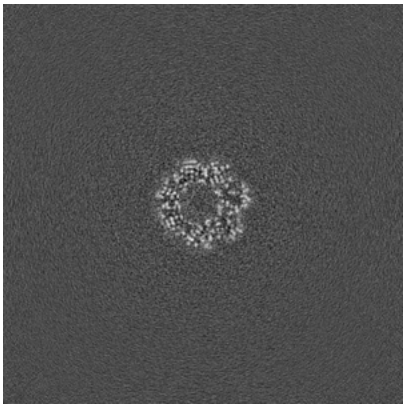
6.2.2 Raw map



X Index: 176



Y Index: 176



Z Index: 176

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: 184

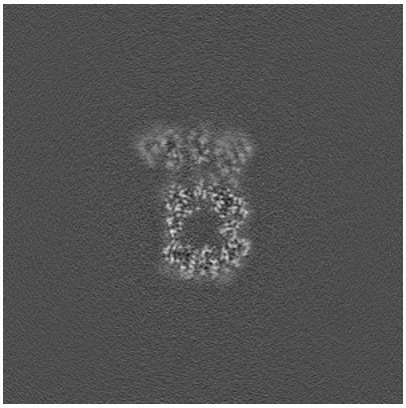


Y Index: 153

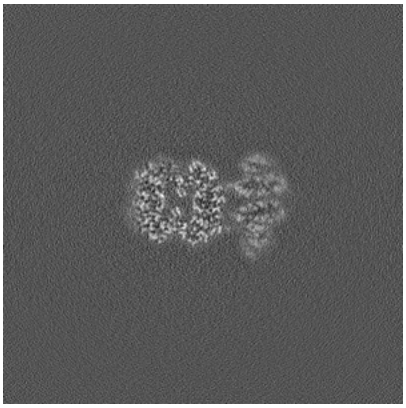


Z Index: 223

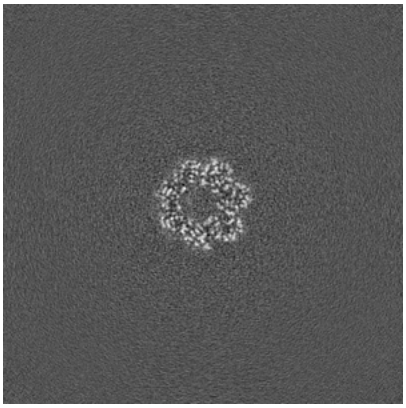
6.3.2 Raw map



X Index: 160



Y Index: 153

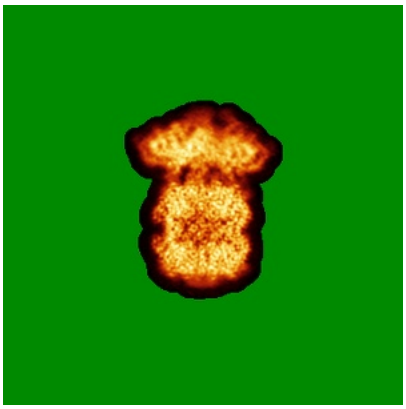


Z Index: 175

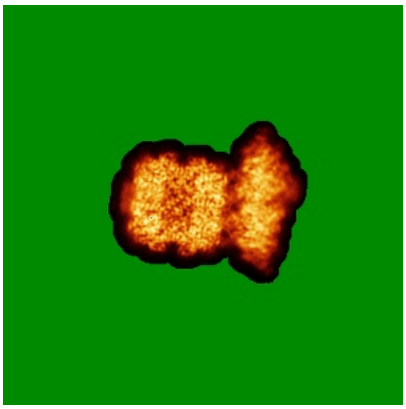
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

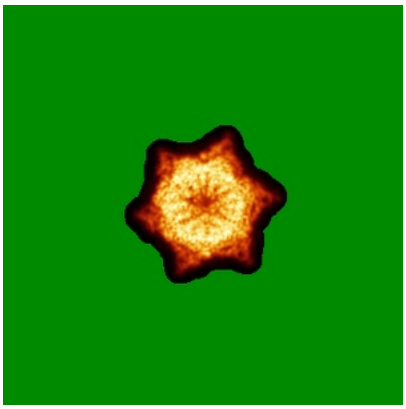
6.4.1 Primary map



X

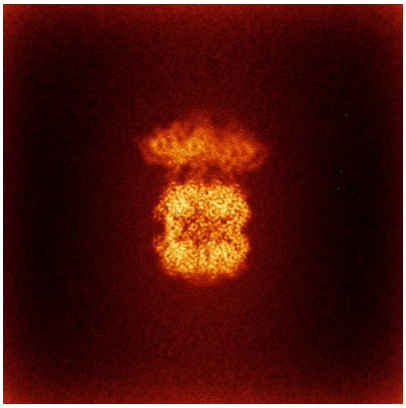


Y

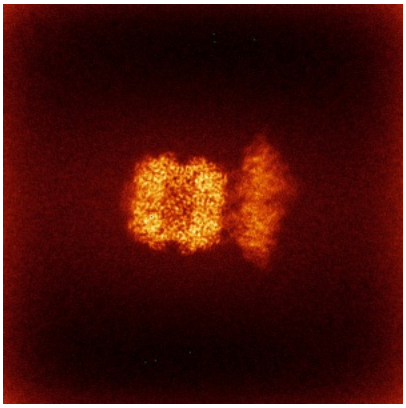


Z

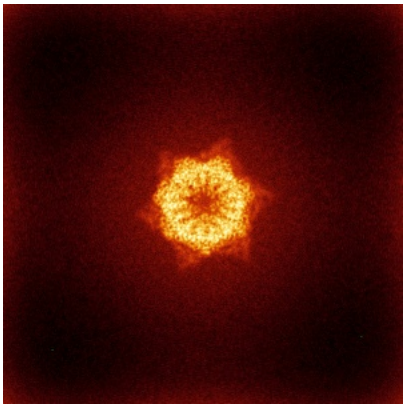
6.4.2 Raw map



X



Y

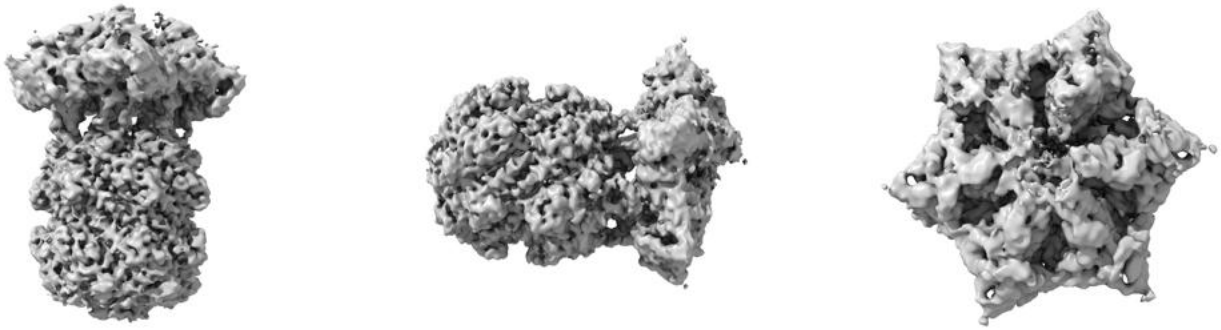


Z

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)

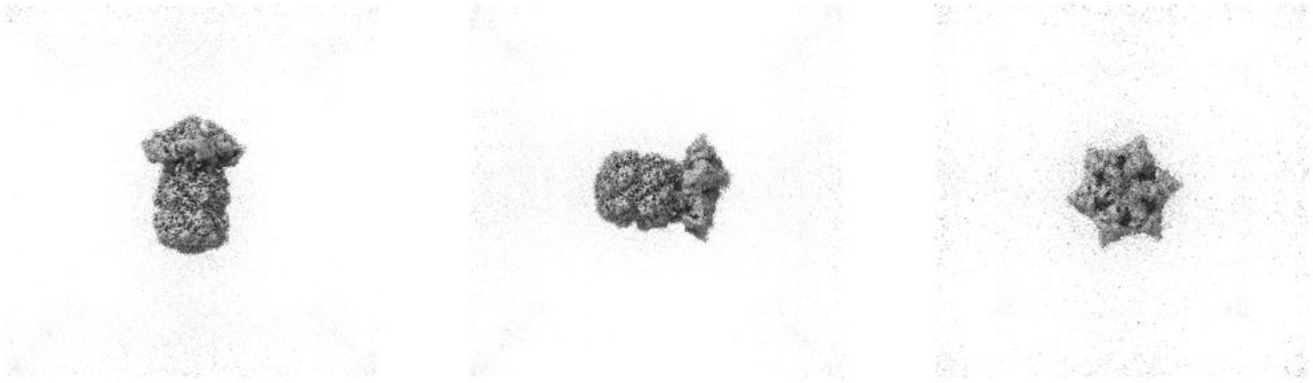
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.092. 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.

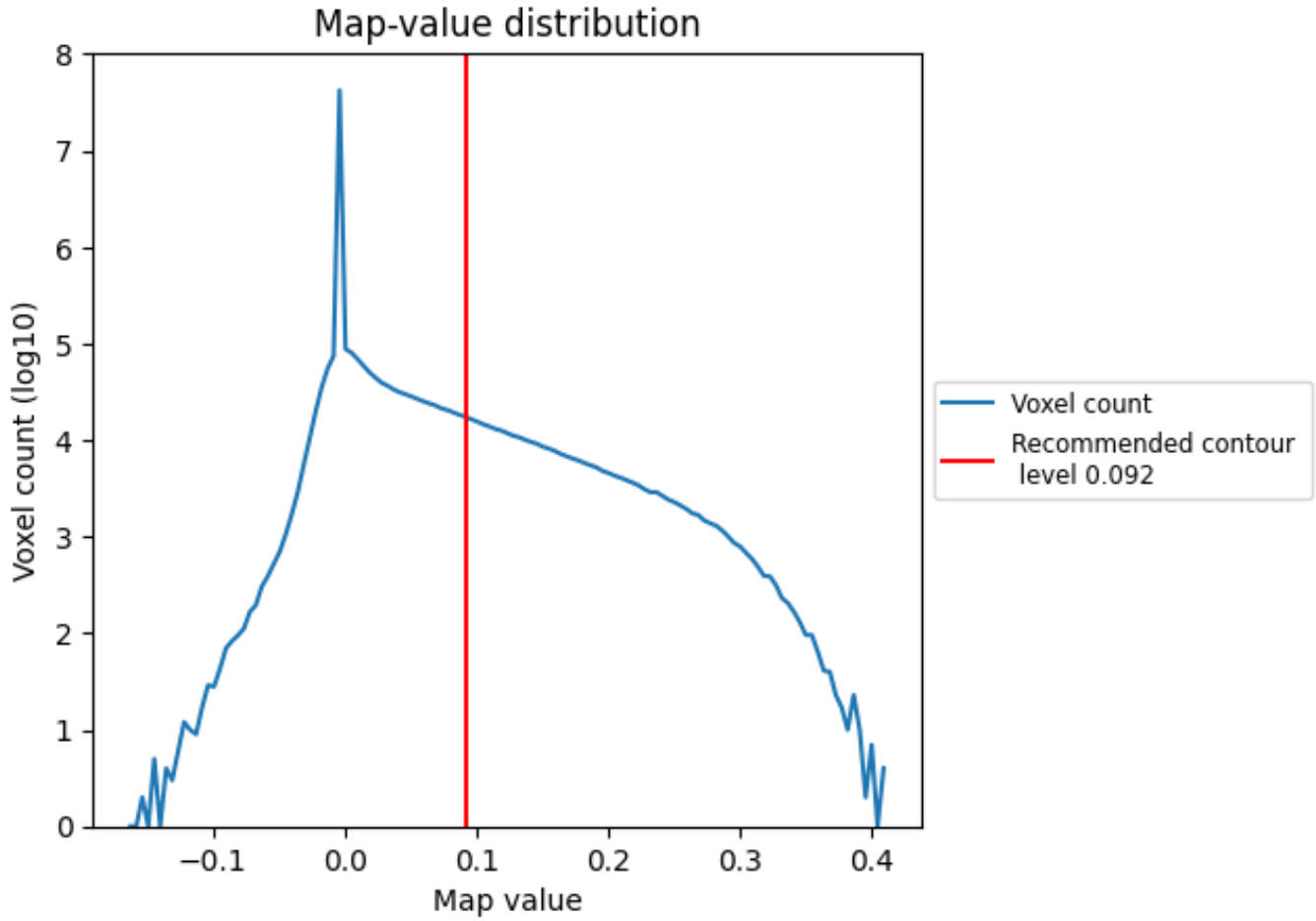
6.6 Mask visualisation (i)

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

7 Map analysis

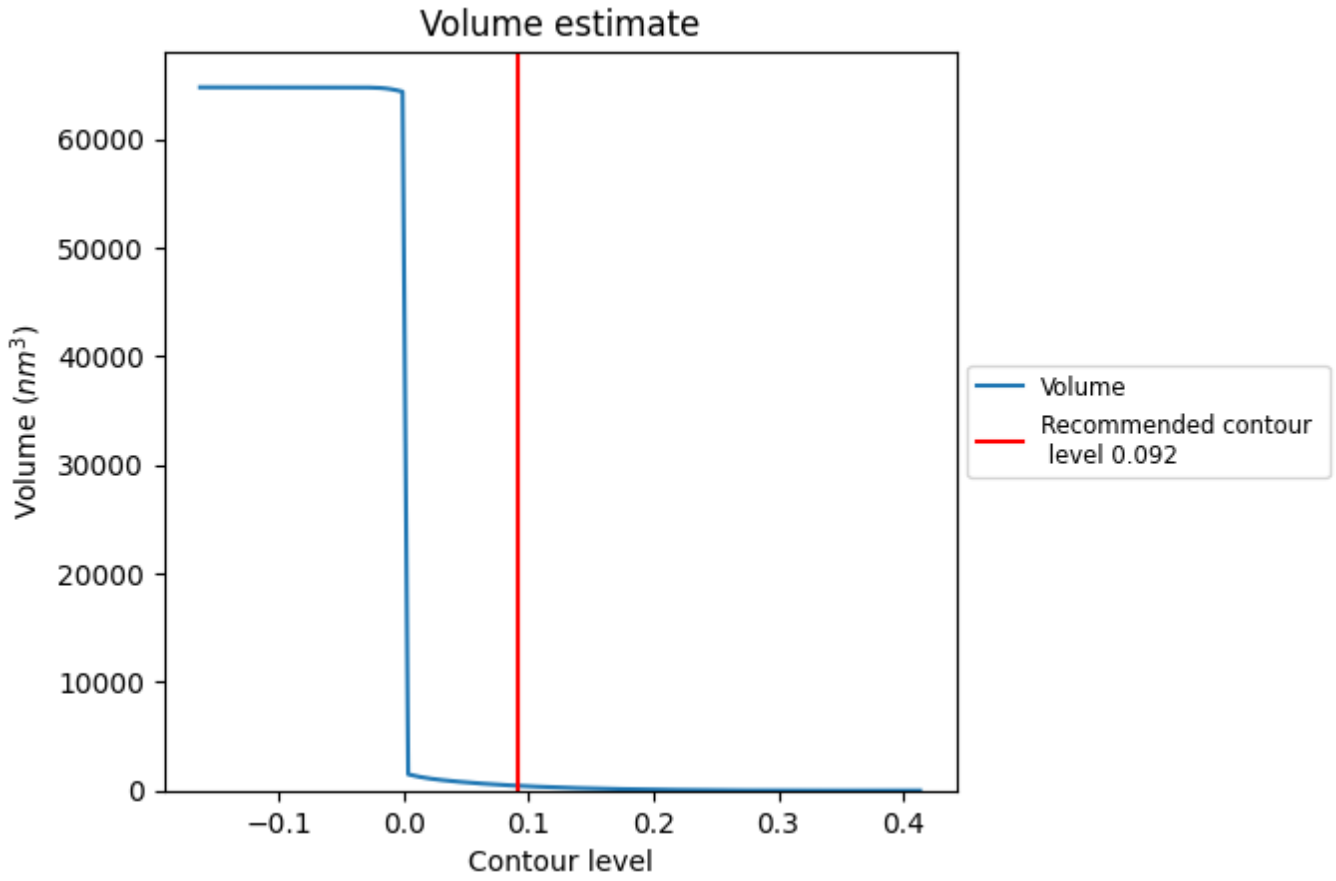
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

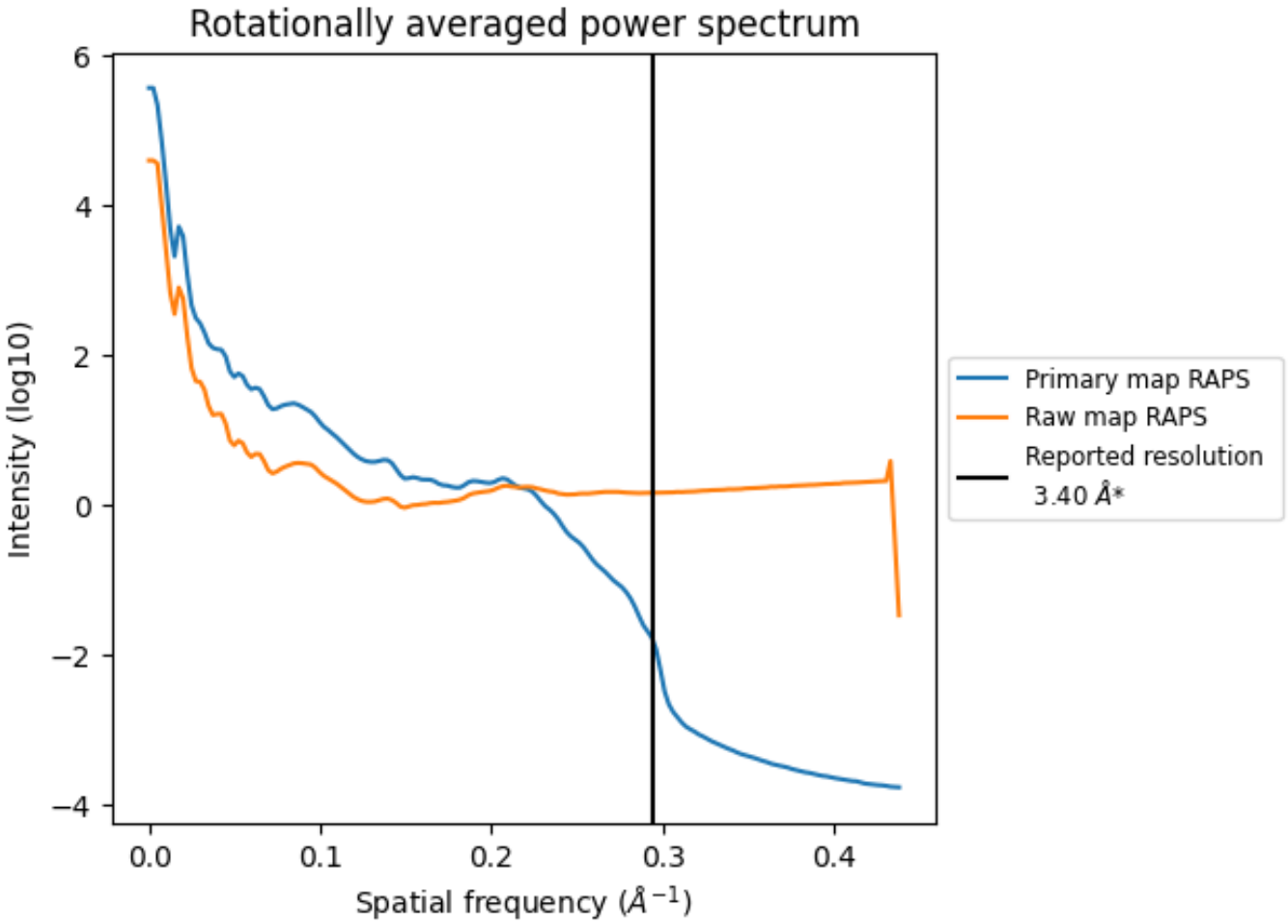
7.2 Volume estimate (i)



The volume at the recommended contour level is 440 nm^3; this corresponds to an approximate mass of 397 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)

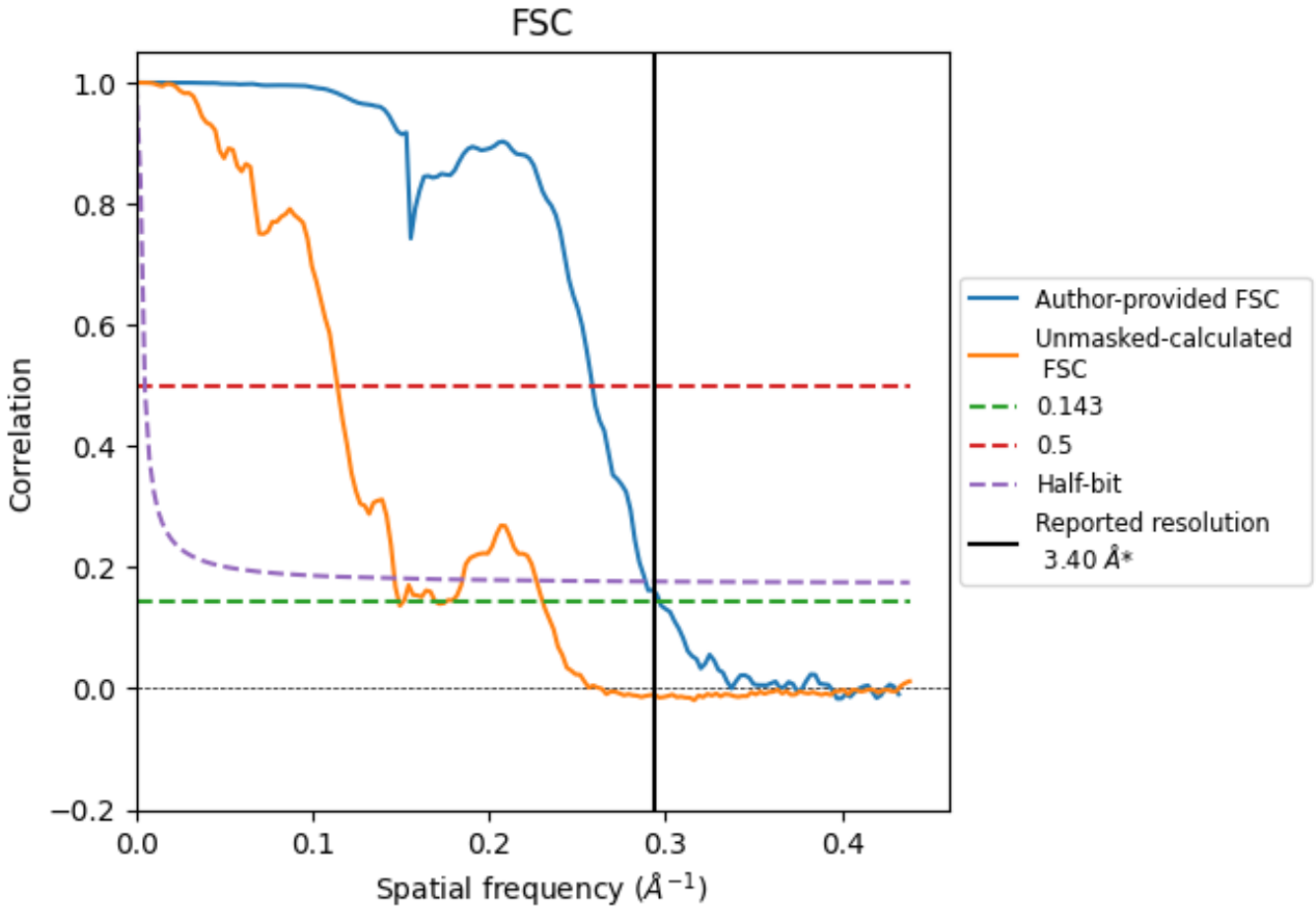


*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8.2 Resolution estimates (i)

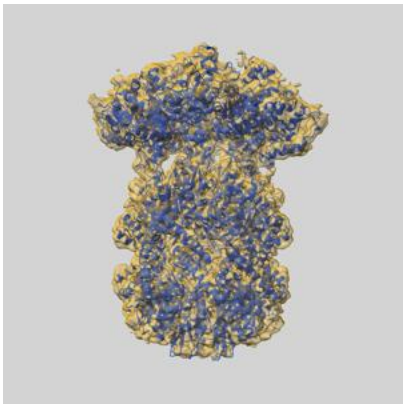
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.37	3.87	3.47
Unmasked-calculated*	6.72	8.76	6.83

*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 6.72 differs from the reported value 3.4 by more than 10 %

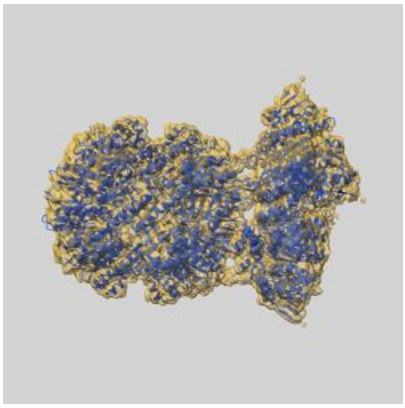
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-70861 and PDB model 9OTX. Per-residue inclusion information can be found in section 3 on page 8.

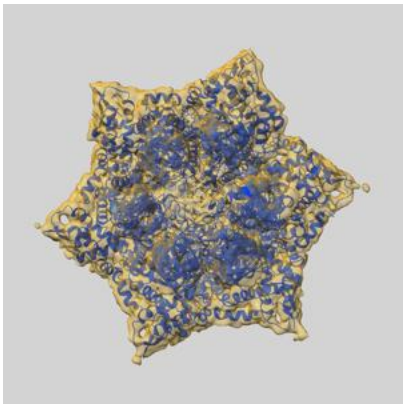
9.1 Map-model overlay



X



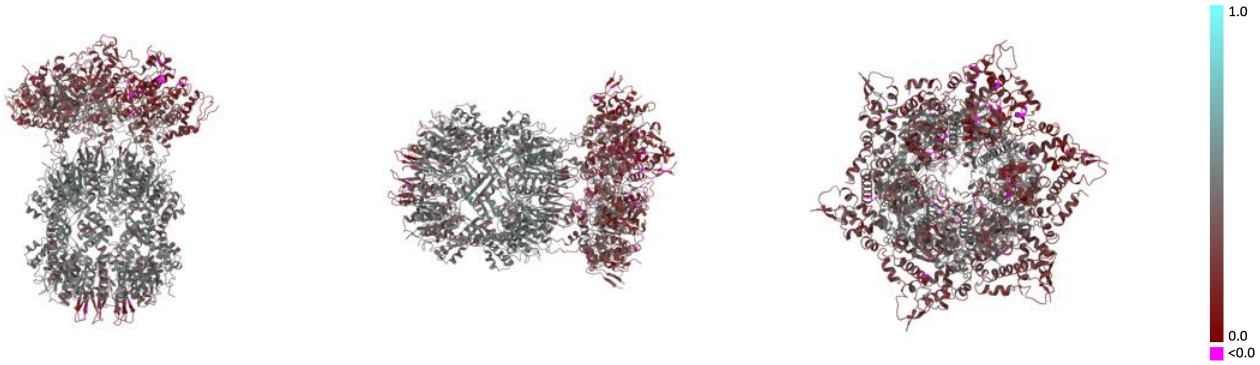
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.092 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.

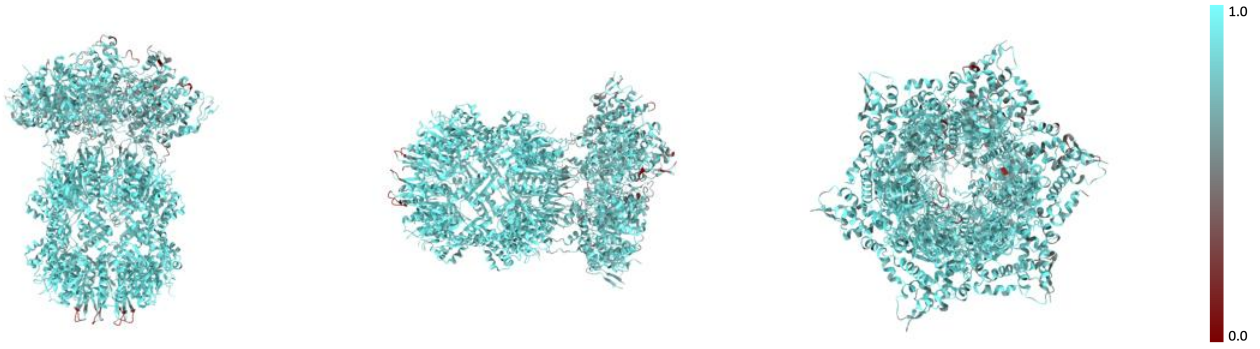
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

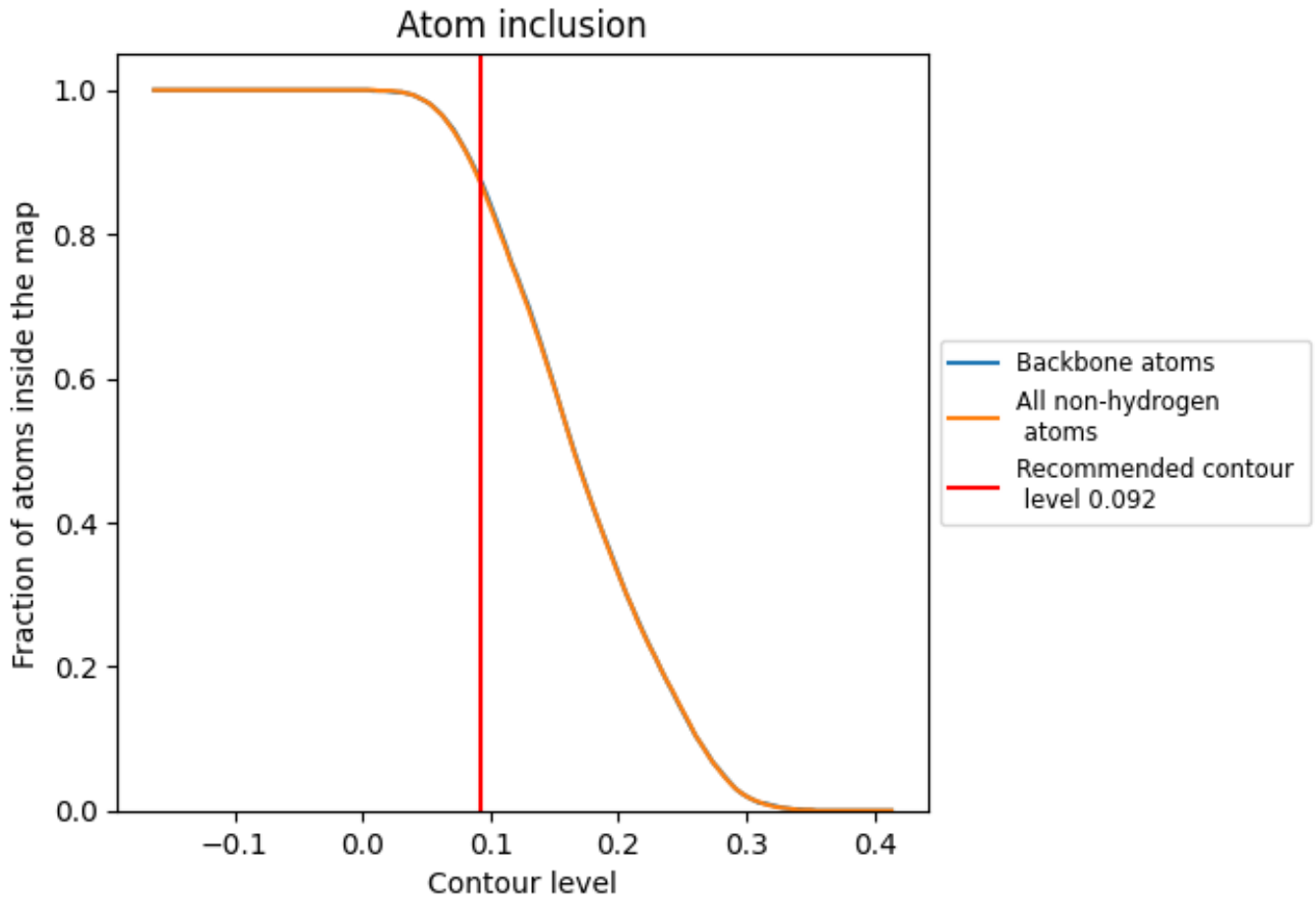
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.092).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 87% 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 (0.092) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8720	0.3840
A	0.7520	0.2040
B	0.8050	0.2790
C	0.8520	0.3220
D	0.8540	0.3350
E	0.8380	0.3310
F	0.8030	0.2550
G	0.9250	0.4380
H	0.9330	0.4660
I	0.9350	0.4820
J	0.9420	0.4780
K	0.9560	0.4870
L	0.9460	0.4840
M	0.9300	0.4780
N	0.9400	0.4720
O	0.9250	0.4370
P	0.9150	0.4420
Q	0.9050	0.4330
R	0.9120	0.4360
S	0.8760	0.4210
T	0.9060	0.4320
U	0.9570	0.4130

