



## wwPDB EM Validation Summary Report ⓘ

Dec 25, 2023 – 04:51 PM JST

PDB ID : 8J4U  
EMDB ID : EMD-35978  
Title : Structure of HerA-Sir2 complex from Escherichia coli Nezha system  
Authors : Chen, Q.; Yu, Y.  
Deposited on : 2023-04-20  
Resolution : 2.97 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:

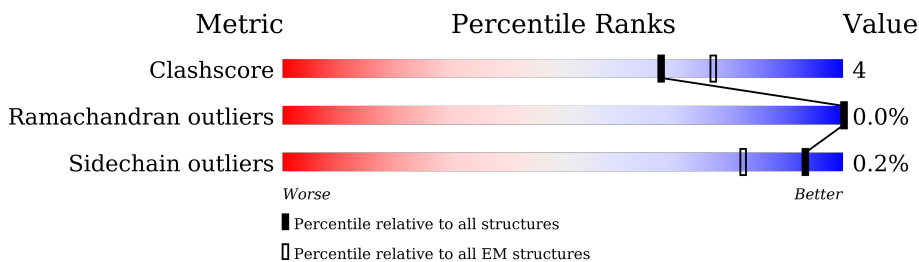
EMDB validation analysis : 0.0.1.dev70  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4.02b-467  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 2.97 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.












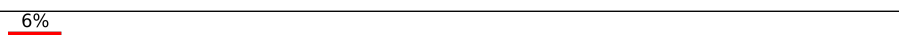
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	415	
1	B	415	
1	C	415	
1	D	415	
1	E	415	
1	F	415	
1	G	415	
1	H	415	

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Mol	Chain	Length	Quality of chain
1	I	415	 81% 13% 6%
1	J	415	 84% 12% .
1	K	415	 83% 13% .
1	L	415	 85% 11% .
2	M	610	 81% 12% 6%
2	N	610	 87% 7% 6%
2	O	610	 89% 7% .
2	P	610	 83% 9% 8%
2	Q	610	 81% 10% 9%
2	R	610	 6% 76% 10% 14%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 129090 atoms, of which 63520 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 SIR2-like domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	398	6277	2048	3092	532	599	6	0	0
1	B	401	6260	2059	3057	536	602	6	0	0
1	C	398	6283	2048	3098	532	599	6	0	0
1	D	398	6229	2050	3043	532	598	6	0	0
1	E	398	6285	2051	3098	532	597	7	1	0
1	F	400	6252	2057	3053	535	601	6	0	0
1	G	395	6220	2027	3066	527	594	6	0	0
1	H	400	6254	2057	3055	535	601	6	0	0
1	I	390	6153	2006	3034	520	587	6	0	0
1	J	400	6232	2053	3038	534	601	6	0	0
1	K	400	6179	2053	2985	534	601	6	0	0
1	L	401	6260	2059	3057	536	602	6	0	0

- Molecule 2 is a protein called Nucleoside triphosphate hydrolase.

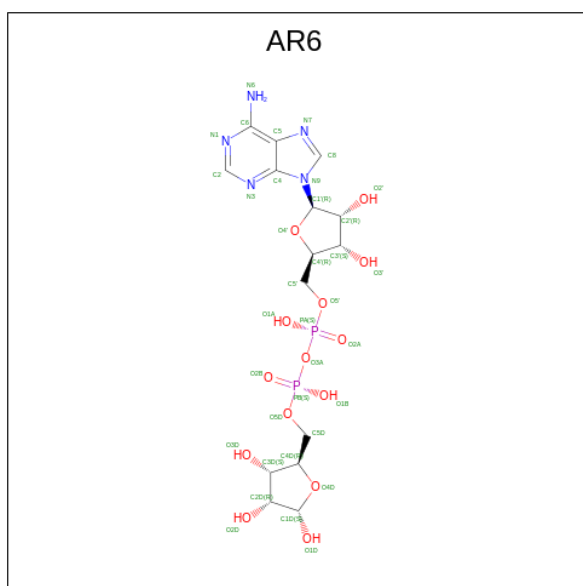
Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	M	573	9042	2887	4506	798	838	13	0	0
2	N	574	9041	2898	4493	799	839	12	0	0
2	O	585	9292	2951	4655	812	862	12	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
2	P	559	Total	C	H	N	O	S	0	0
			8832	2827	4406	763	824	12		
2	Q	557	Total	C	H	N	O	S	0	0
			8681	2829	4252	776	811	13		
2	R	527	Total	C	H	N	O	S	0	0
			8413	2677	4215	734	776	11		

- Molecule 3 is [(2R,3S,4R,5R)-5-(6-AMINOPURIN-9-YL)-3,4-DIHYDROXY-OXOLAN-2-YL]METHYL [HYDROXY-[[[(2R,3S,4R,5S)-3,4,5-TRIHYDROXYOXOLAN-2-YL]METHOXY]PHOSPHORYL] HYDROGEN PHOSPHATE (three-letter code: AR6) (formula: C<sub>15</sub>H<sub>23</sub>N<sub>5</sub>O<sub>14</sub>P<sub>2</sub>).



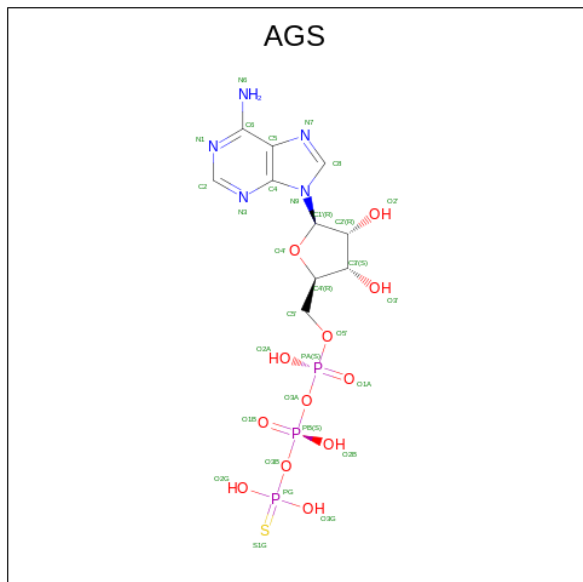
Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
3	A	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	
3	B	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	
3	C	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	
3	D	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	
3	E	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	
3	F	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	
3	G	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	

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Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
3	H	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	
3	I	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	
3	J	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	
3	K	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	
3	L	1	Total	C	H	N	O	P	0
			57	15	21	5	14	2	

- Molecule 4 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: C<sub>10</sub>H<sub>16</sub>N<sub>5</sub>O<sub>12</sub>P<sub>3</sub>S).



Mol	Chain	Residues	Atoms						AltConf	
			Total	C	H	N	O	P		S
4	M	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	
4	N	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	
4	O	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	
4	P	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	
4	Q	1	Total	C	H	N	O	P	S	0
			44	10	13	5	12	3	1	

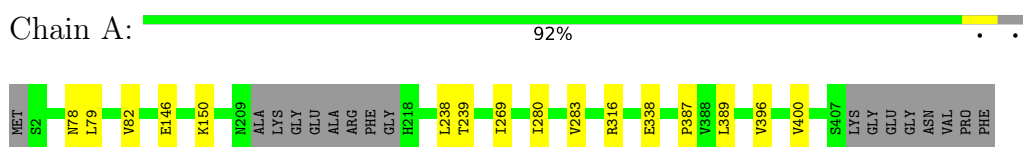
- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>AltConf</b>
5	N	1	Total	Mg	0
			1	1	

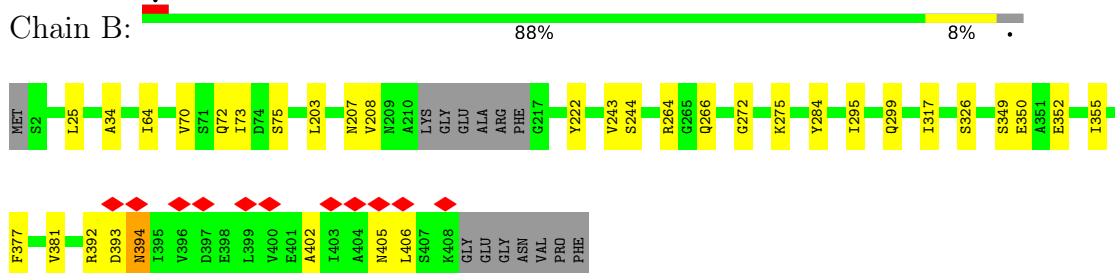
### 3 Residue-property plots [i](#)

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.

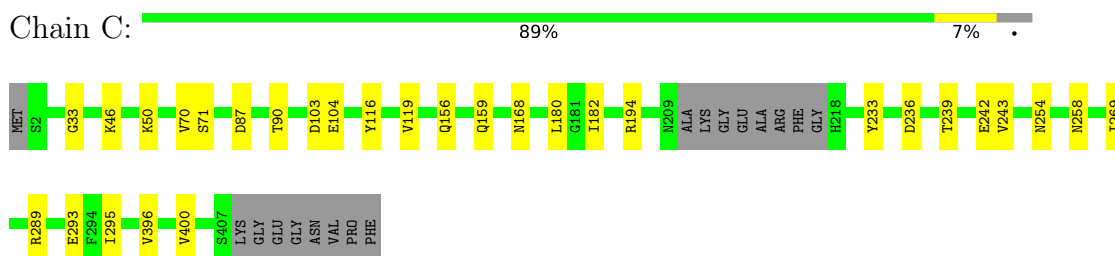
- Molecule 1: SIR2-like domain-containing protein



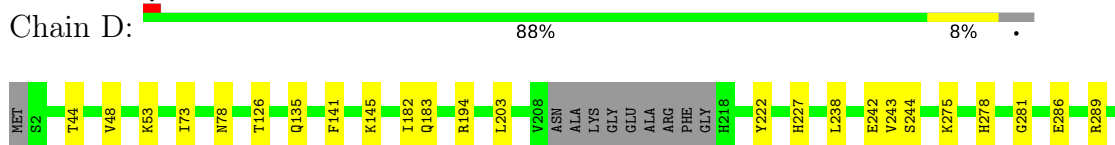
- Molecule 1: SIR2-like domain-containing protein



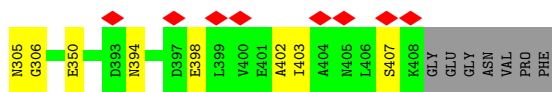
- Molecule 1: SIR2-like domain-containing protein



- Molecule 1: SIR2-like domain-containing protein

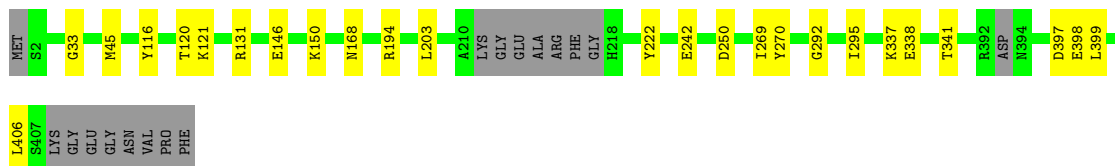






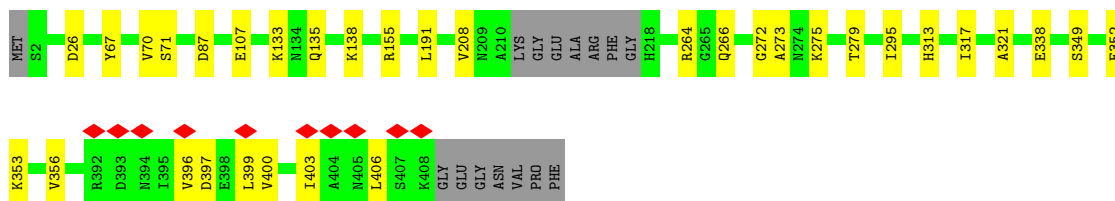
- Molecule 1: SIR2-like domain-containing protein

Chain E: 90% 6%



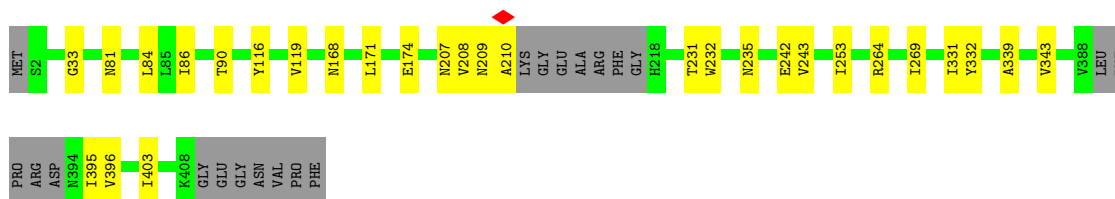
- Molecule 1: SIR2-like domain-containing protein

Chain F: 88% 8%



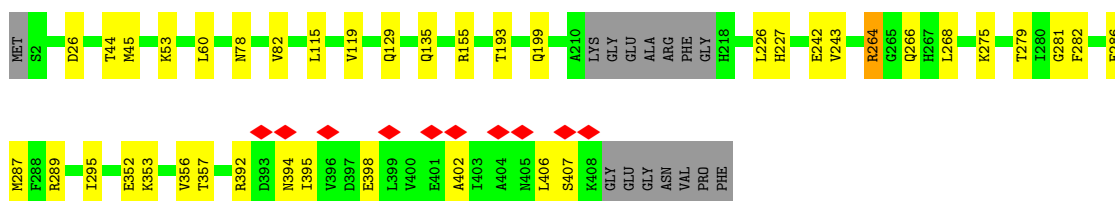
- Molecule 1: SIR2-like domain-containing protein

Chain G: 88% 7% 5%



- Molecule 1: SIR2-like domain-containing protein

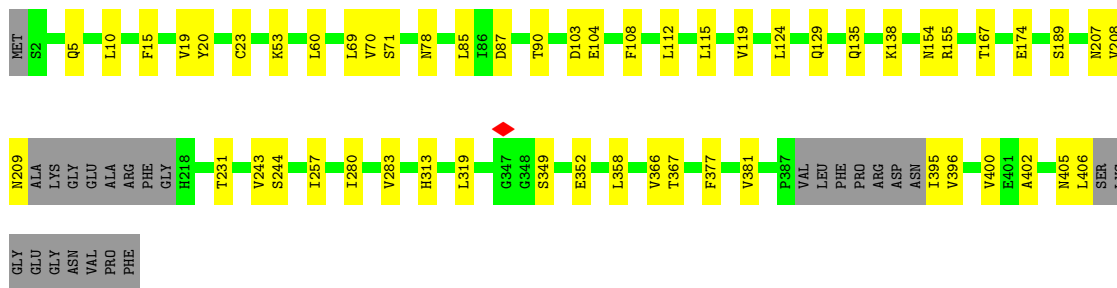
Chain H: 87% 9%



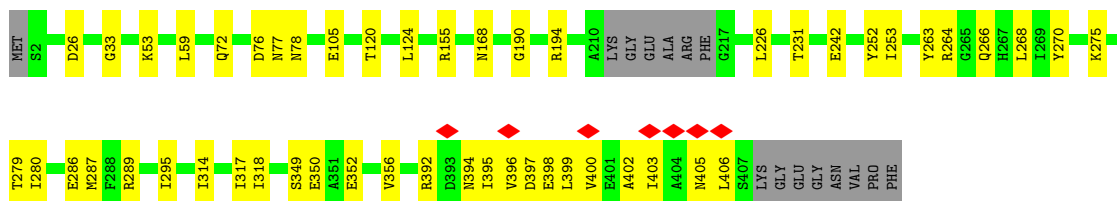
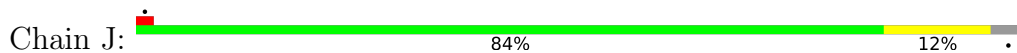
- Molecule 1: SIR2-like domain-containing protein

Chain I: 81% 13% 6%

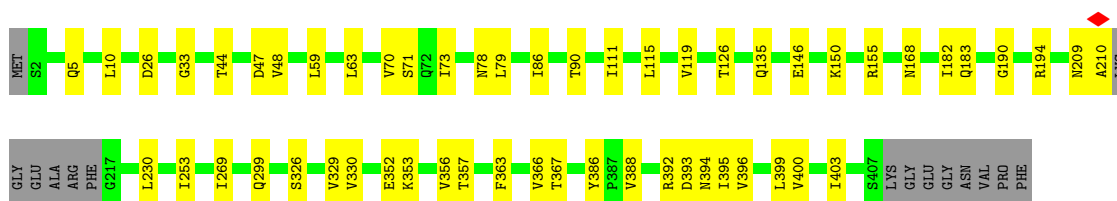
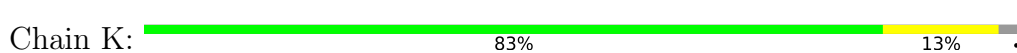




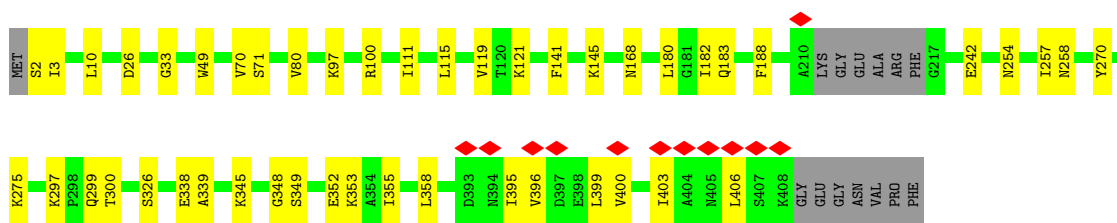
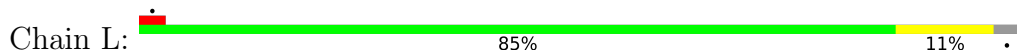
• Molecule 1: SIR2-like domain-containing protein



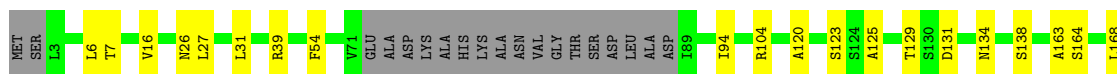
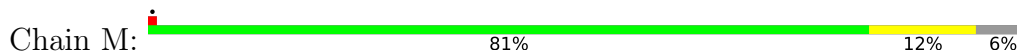
• Molecule 1: SIR2-like domain-containing protein

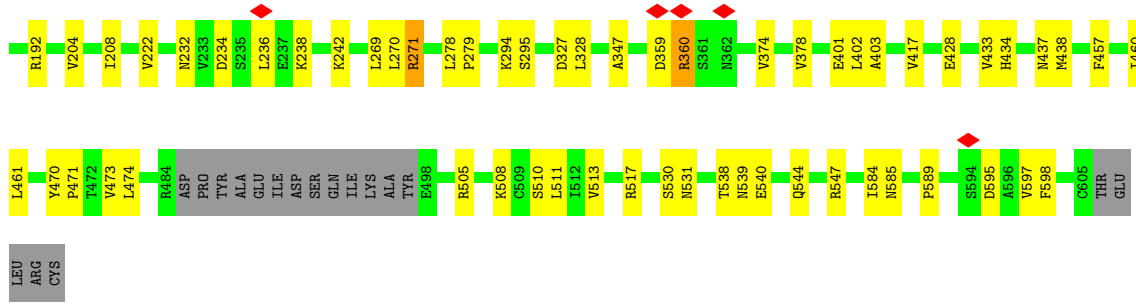


• Molecule 1: SIR2-like domain-containing protein

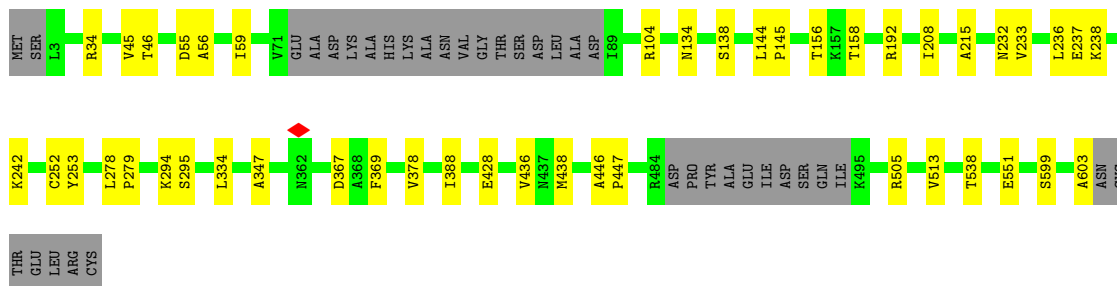
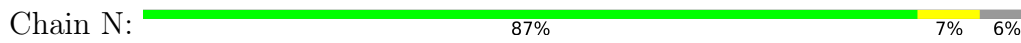


• Molecule 2: Nucleoside triphosphate hydrolase

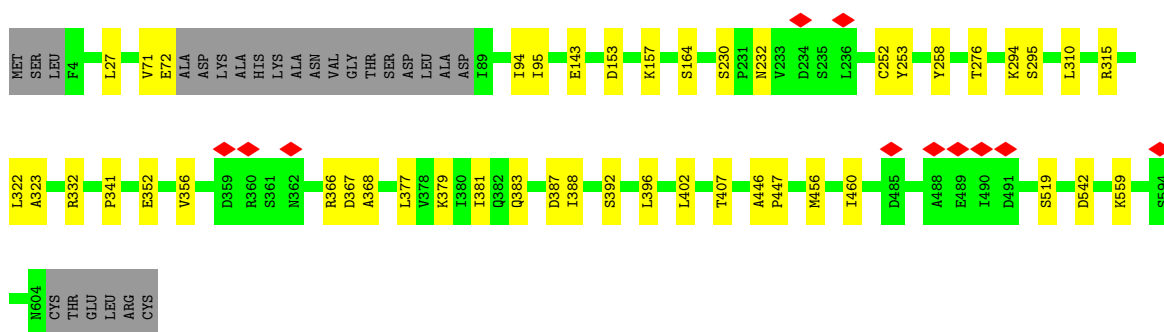
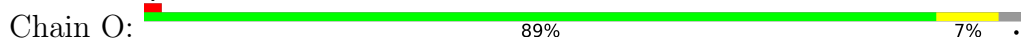




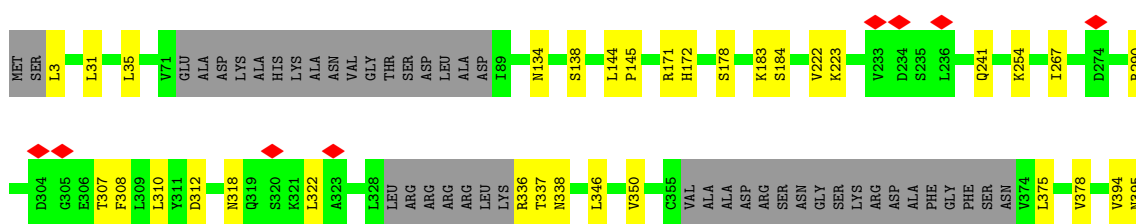
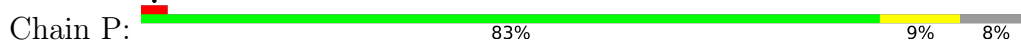
• Molecule 2: Nucleoside triphosphate hydrolase



• Molecule 2: Nucleoside triphosphate hydrolase



• Molecule 2: Nucleoside triphosphate hydrolase





## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	590454	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 ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.831	Depositor
Minimum map value	-2.150	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.086	Depositor
Recommended contour level	0.176	Depositor
Map size (Å)	355.2, 355.2, 355.2	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.11, 1.11, 1.11	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: AR6, MG, AGS

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	0.31	0/3259	0.45	0/4406
1	B	0.30	0/3277	0.46	0/4429
1	C	0.33	0/3259	0.49	0/4406
1	D	0.32	0/3260	0.47	0/4406
1	E	0.33	0/3263	0.50	3/4409 (0.1%)
1	F	0.32	0/3273	0.48	0/4424
1	G	0.31	0/3225	0.46	0/4357
1	H	0.31	0/3273	0.47	0/4424
1	I	0.27	0/3190	0.45	0/4310
1	J	0.30	0/3268	0.48	1/4418 (0.0%)
1	K	0.29	0/3268	0.45	0/4418
1	L	0.28	0/3277	0.46	0/4429
2	M	0.26	0/4624	0.48	0/6243
2	N	0.28	0/4637	0.48	0/6260
2	O	0.28	0/4729	0.50	0/6388
2	P	0.27	0/4514	0.48	0/6101
2	Q	0.25	0/4515	0.46	0/6089
2	R	0.25	0/4278	0.46	0/5774
All	All	0.29	0/66389	0.47	4/89691 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	399	LEU	CB-CG-CD2	6.02	121.23	111.00
1	E	121	LYS	C-N-CA	5.87	136.37	121.70
1	J	268	LEU	CB-CA-C	5.64	120.92	110.20
1	E	399	LEU	CB-CG-CD1	5.30	120.01	111.00

There are no chirality outliers.

There are no planarity outliers.

## 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	3185	3092	3109	12	0
1	B	3203	3057	3130	27	0
1	C	3185	3098	3109	19	0
1	D	3186	3043	3116	22	0
1	E	3187	3098	3118	12	0
1	F	3199	3053	3127	24	0
1	G	3154	3066	3082	21	0
1	H	3199	3055	3127	34	0
1	I	3119	3034	3044	35	0
1	J	3194	3038	3117	38	0
1	K	3194	2985	3117	35	0
1	L	3203	3057	3130	30	0
2	M	4536	4506	4576	52	0
2	N	4548	4493	4592	33	0
2	O	4637	4655	4664	28	0
2	P	4426	4406	4452	34	0
2	Q	4429	4252	4481	35	0
2	R	4198	4215	4233	39	0
3	A	36	21	21	0	0
3	B	36	21	21	1	0
3	C	36	21	21	0	0
3	D	36	21	21	0	0
3	E	36	21	21	0	0
3	F	36	21	21	0	0
3	G	36	21	21	0	0
3	H	36	21	21	0	0
3	I	36	21	21	0	0
3	J	36	21	21	0	0
3	K	36	21	21	0	0
3	L	36	21	21	0	0
4	M	31	13	12	0	0
4	N	31	13	12	0	0
4	O	31	13	12	1	0
4	P	31	13	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	Q	31	13	12	0	0
5	N	1	0	0	0	0
All	All	65570	63520	64636	502	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 4.

The worst 5 of 502 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:H:394:ASN:O	1:H:398:GLU:N	2.08	0.85
1:H:392:ARG:O	1:H:394:ASN:ND2	2.12	0.82
2:M:232:ASN:ND2	2:M:234:ASP:O	2.14	0.81
2:O:27:LEU:HD21	2:O:94:ILE:HD12	1.60	0.81
1:I:349:SER:OG	1:I:352:GLU:OE1	2.01	0.79

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	394/415 (95%)	371 (94%)	23 (6%)	0	100	100
1	B	397/415 (96%)	377 (95%)	19 (5%)	1 (0%)	41	74
1	C	394/415 (95%)	366 (93%)	28 (7%)	0	100	100
1	D	394/415 (95%)	373 (95%)	21 (5%)	0	100	100
1	E	393/415 (95%)	361 (92%)	32 (8%)	0	100	100
1	F	396/415 (95%)	371 (94%)	25 (6%)	0	100	100
1	G	389/415 (94%)	364 (94%)	25 (6%)	0	100	100
1	H	396/415 (95%)	380 (96%)	16 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	I	384/415 (92%)	362 (94%)	22 (6%)	0	100	100
1	J	396/415 (95%)	372 (94%)	24 (6%)	0	100	100
1	K	396/415 (95%)	363 (92%)	33 (8%)	0	100	100
1	L	397/415 (96%)	376 (95%)	21 (5%)	0	100	100
2	M	567/610 (93%)	495 (87%)	72 (13%)	0	100	100
2	N	568/610 (93%)	528 (93%)	40 (7%)	0	100	100
2	O	581/610 (95%)	529 (91%)	52 (9%)	0	100	100
2	P	551/610 (90%)	507 (92%)	44 (8%)	0	100	100
2	Q	547/610 (90%)	494 (90%)	53 (10%)	0	100	100
2	R	519/610 (85%)	471 (91%)	48 (9%)	0	100	100
All	All	8059/8640 (93%)	7460 (93%)	598 (7%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	394	ASN

### 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	340/351 (97%)	339 (100%)	1 (0%)	92	97
1	B	341/351 (97%)	341 (100%)	0	100	100
1	C	340/351 (97%)	340 (100%)	0	100	100
1	D	340/351 (97%)	340 (100%)	0	100	100
1	E	340/351 (97%)	338 (99%)	2 (1%)	86	94
1	F	341/351 (97%)	341 (100%)	0	100	100
1	G	336/351 (96%)	336 (100%)	0	100	100
1	H	341/351 (97%)	340 (100%)	1 (0%)	92	97

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	332/351 (95%)	332 (100%)	0	100	100
1	J	340/351 (97%)	340 (100%)	0	100	100
1	K	340/351 (97%)	340 (100%)	0	100	100
1	L	341/351 (97%)	340 (100%)	1 (0%)	92	97
2	M	489/519 (94%)	487 (100%)	2 (0%)	91	97
2	N	489/519 (94%)	489 (100%)	0	100	100
2	O	499/519 (96%)	497 (100%)	2 (0%)	91	97
2	P	478/519 (92%)	478 (100%)	0	100	100
2	Q	477/519 (92%)	476 (100%)	1 (0%)	93	98
2	R	451/519 (87%)	449 (100%)	2 (0%)	91	97
All	All	6955/7326 (95%)	6943 (100%)	12 (0%)	93	98

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	O	332	ARG
2	O	559	LYS
2	R	242	LYS
2	Q	333	ARG
1	H	264	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 62 such sidechains are listed below:

Mol	Chain	Res	Type
1	J	227	HIS
2	Q	221	ASN
1	L	72	GLN
2	Q	107	ASN
2	R	493	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 1 is monoatomic - leaving 17 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
3	AR6	E	501	-	34,39,39	0.80	1 (2%)	40,60,60	1.37	6 (15%)
3	AR6	L	501	-	34,39,39	0.81	1 (2%)	40,60,60	1.40	6 (15%)
3	AR6	B	501	-	34,39,39	0.81	1 (2%)	40,60,60	1.35	5 (12%)
3	AR6	D	501	-	34,39,39	0.80	1 (2%)	40,60,60	1.32	4 (10%)
3	AR6	I	501	-	34,39,39	0.81	1 (2%)	40,60,60	1.38	6 (15%)
4	AGS	N	701	5	26,33,33	1.86	3 (11%)	26,52,52	1.59	4 (15%)
4	AGS	O	701	-	26,33,33	1.88	3 (11%)	26,52,52	1.58	5 (19%)
3	AR6	F	501	-	34,39,39	0.81	1 (2%)	40,60,60	1.31	5 (12%)
3	AR6	K	501	-	34,39,39	0.80	1 (2%)	40,60,60	1.34	5 (12%)
3	AR6	C	501	-	34,39,39	0.81	1 (2%)	40,60,60	1.34	6 (15%)
3	AR6	J	501	-	34,39,39	0.81	1 (2%)	40,60,60	1.32	5 (12%)
4	AGS	M	701	-	26,33,33	1.86	2 (7%)	26,52,52	1.55	4 (15%)
4	AGS	Q	701	-	26,33,33	1.87	3 (11%)	26,52,52	1.57	4 (15%)
4	AGS	P	701	-	26,33,33	1.88	3 (11%)	26,52,52	1.56	4 (15%)
3	AR6	H	501	-	34,39,39	0.81	1 (2%)	40,60,60	1.35	6 (15%)
3	AR6	A	501	-	34,39,39	0.82	1 (2%)	40,60,60	1.34	7 (17%)
3	AR6	G	501	-	34,39,39	0.81	1 (2%)	40,60,60	1.38	6 (15%)

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
3	AR6	E	501	-	-	11/18/54/54	0/4/4/4
3	AR6	L	501	-	-	6/18/54/54	0/4/4/4
3	AR6	B	501	-	-	10/18/54/54	0/4/4/4
3	AR6	D	501	-	-	8/18/54/54	0/4/4/4
3	AR6	I	501	-	-	8/18/54/54	0/4/4/4
4	AGS	N	701	5	-	2/17/38/38	0/3/3/3
4	AGS	O	701	-	-	5/17/38/38	0/3/3/3
3	AR6	F	501	-	-	11/18/54/54	0/4/4/4
3	AR6	K	501	-	-	7/18/54/54	0/4/4/4
3	AR6	C	501	-	-	9/18/54/54	0/4/4/4
3	AR6	J	501	-	-	4/18/54/54	0/4/4/4
4	AGS	M	701	-	-	6/17/38/38	0/3/3/3
4	AGS	Q	701	-	-	0/17/38/38	0/3/3/3
4	AGS	P	701	-	-	4/17/38/38	0/3/3/3
3	AR6	H	501	-	-	4/18/54/54	0/4/4/4
3	AR6	A	501	-	-	10/18/54/54	0/4/4/4
3	AR6	G	501	-	-	6/18/54/54	0/4/4/4

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	P	701	AGS	PG-S1G	8.03	2.08	1.90
4	O	701	AGS	PG-S1G	7.99	2.08	1.90
4	M	701	AGS	PG-S1G	7.96	2.08	1.90
4	Q	701	AGS	PG-S1G	7.91	2.07	1.90
4	N	701	AGS	PG-S1G	7.88	2.07	1.90

The worst 5 of 88 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	P	701	AGS	PA-O3A-PB	-3.82	119.73	132.83
3	K	501	AR6	N3-C2-N1	-3.73	122.86	128.68
4	O	701	AGS	N3-C2-N1	-3.72	122.87	128.68
4	Q	701	AGS	N3-C2-N1	-3.71	122.88	128.68
4	P	701	AGS	N3-C2-N1	-3.69	122.91	128.68

There are no chirality outliers.

5 of 111 torsion outliers are listed below:

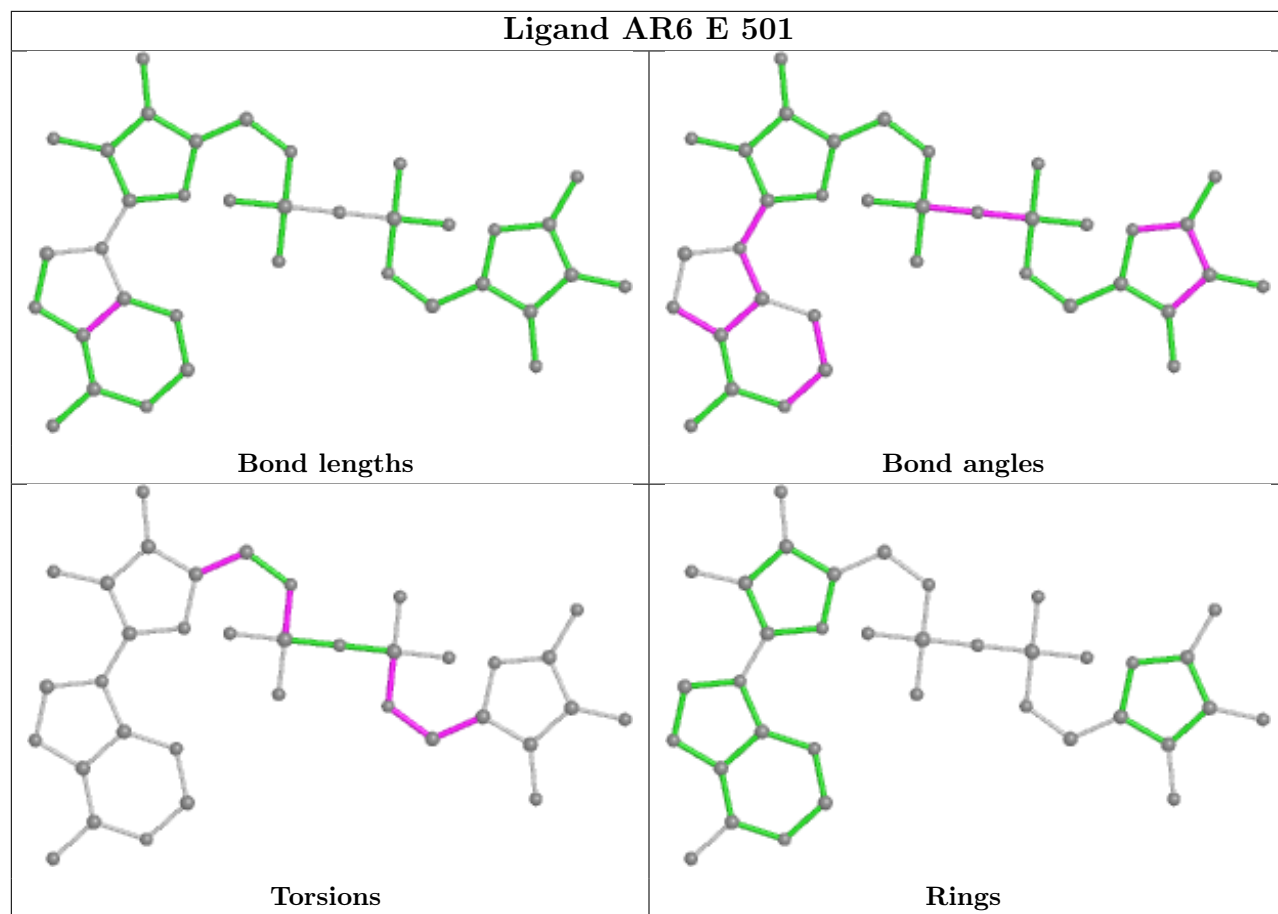
Mol	Chain	Res	Type	Atoms
3	A	501	AR6	C5'-O5'-PA-O1A
3	A	501	AR6	C5'-O5'-PA-O3A
3	A	501	AR6	C5D-O5D-PB-O2B
3	A	501	AR6	C5D-O5D-PB-O3A
3	B	501	AR6	C5'-O5'-PA-O2A

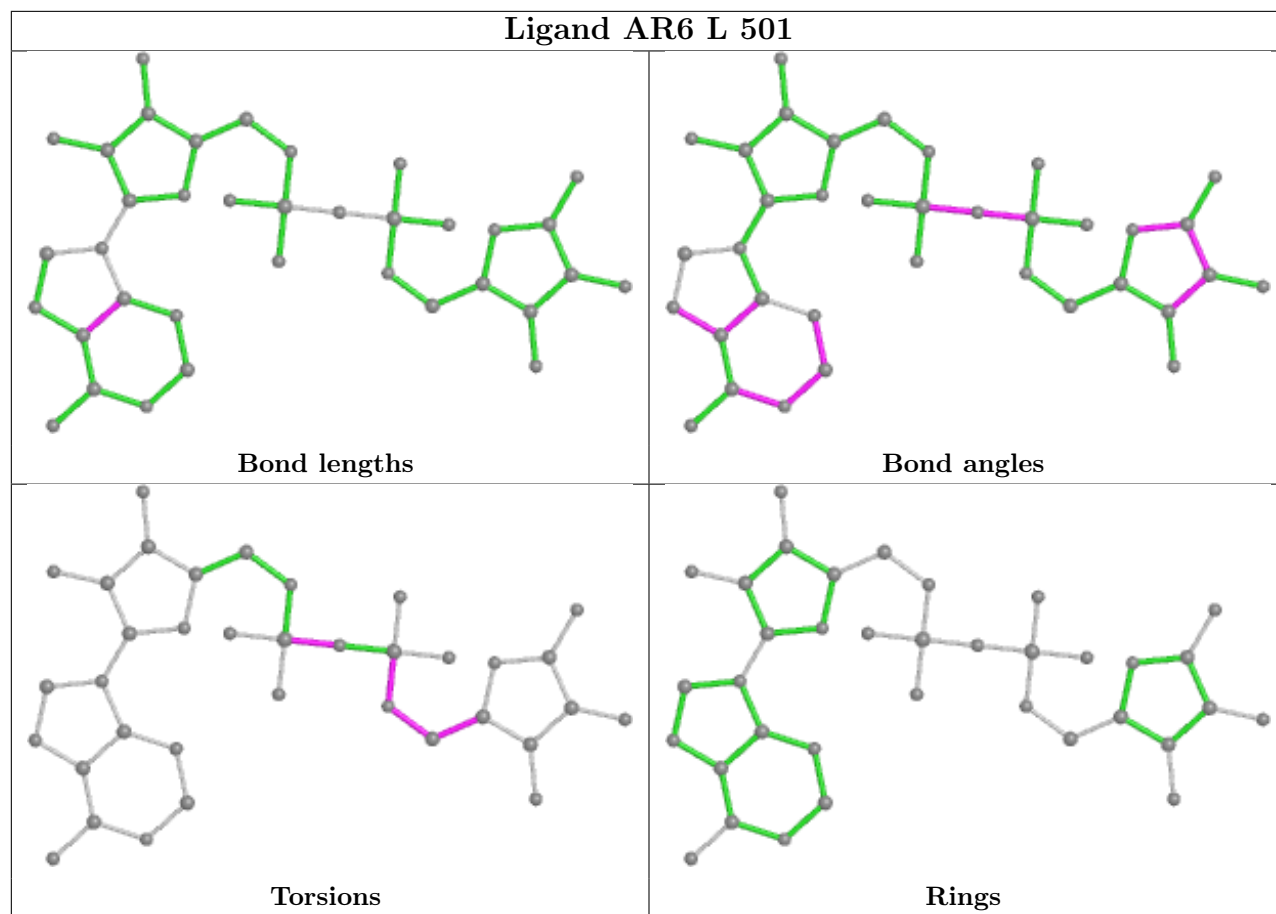
There are no ring outliers.

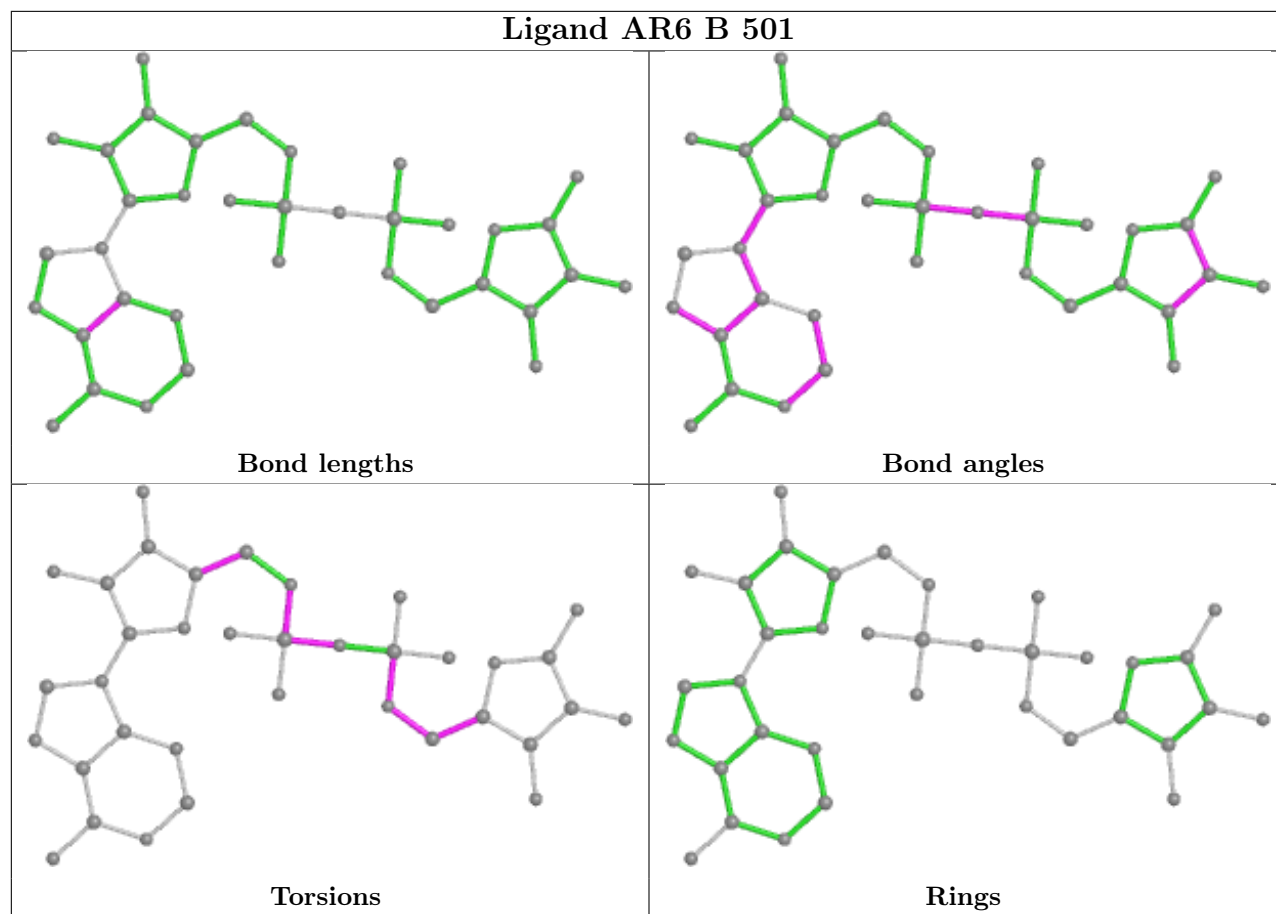
3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	501	AR6	1	0
4	O	701	AGS	1	0
4	P	701	AGS	1	0

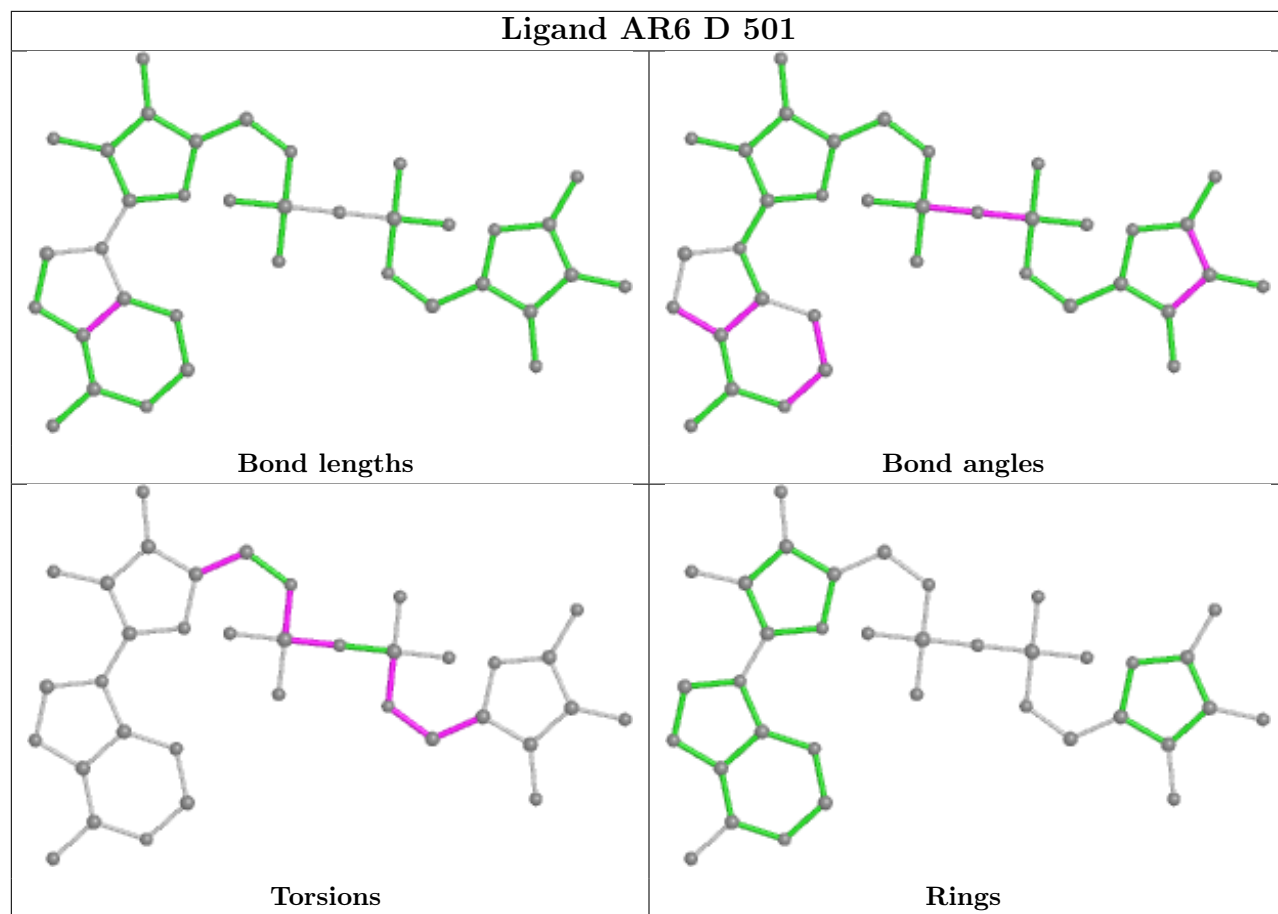
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

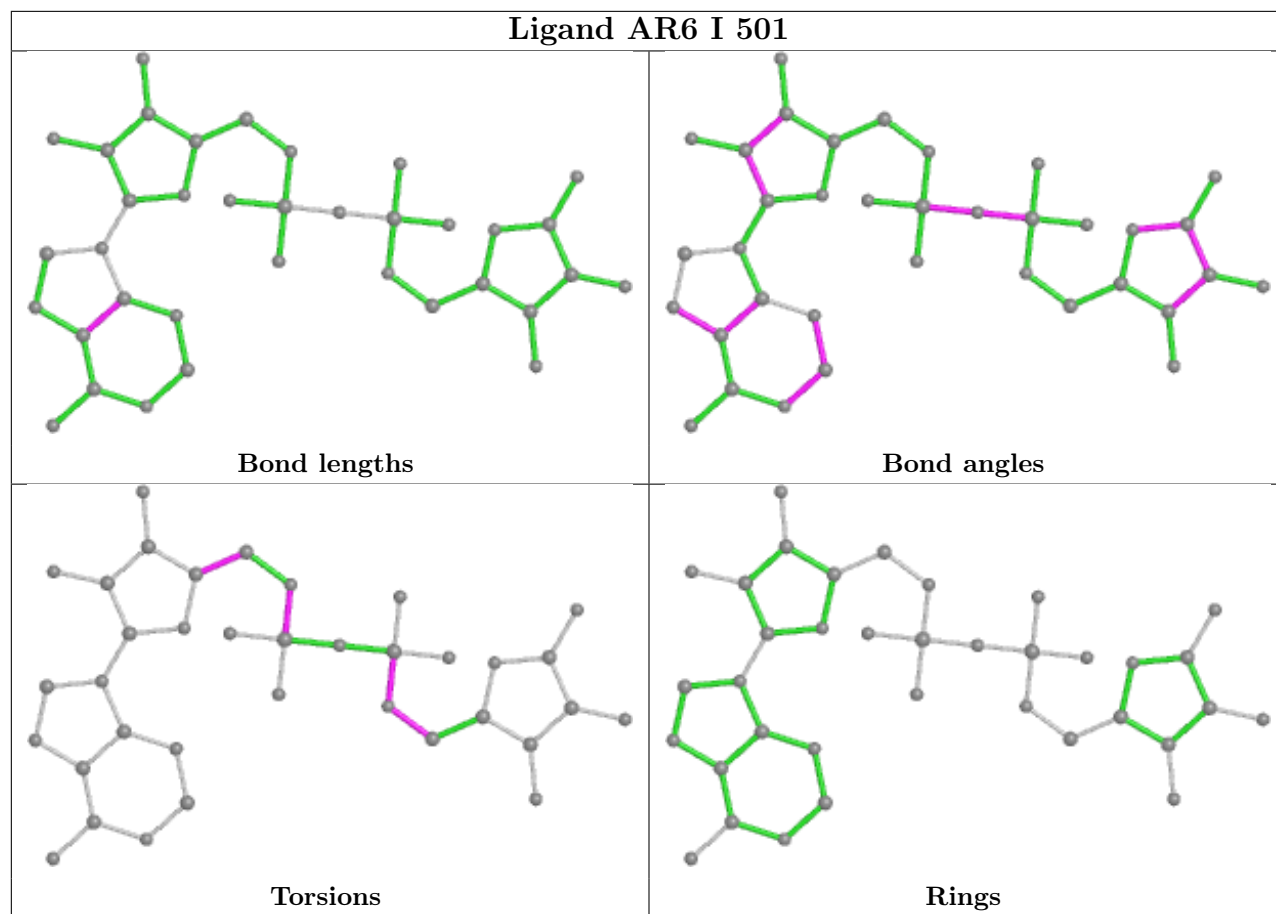


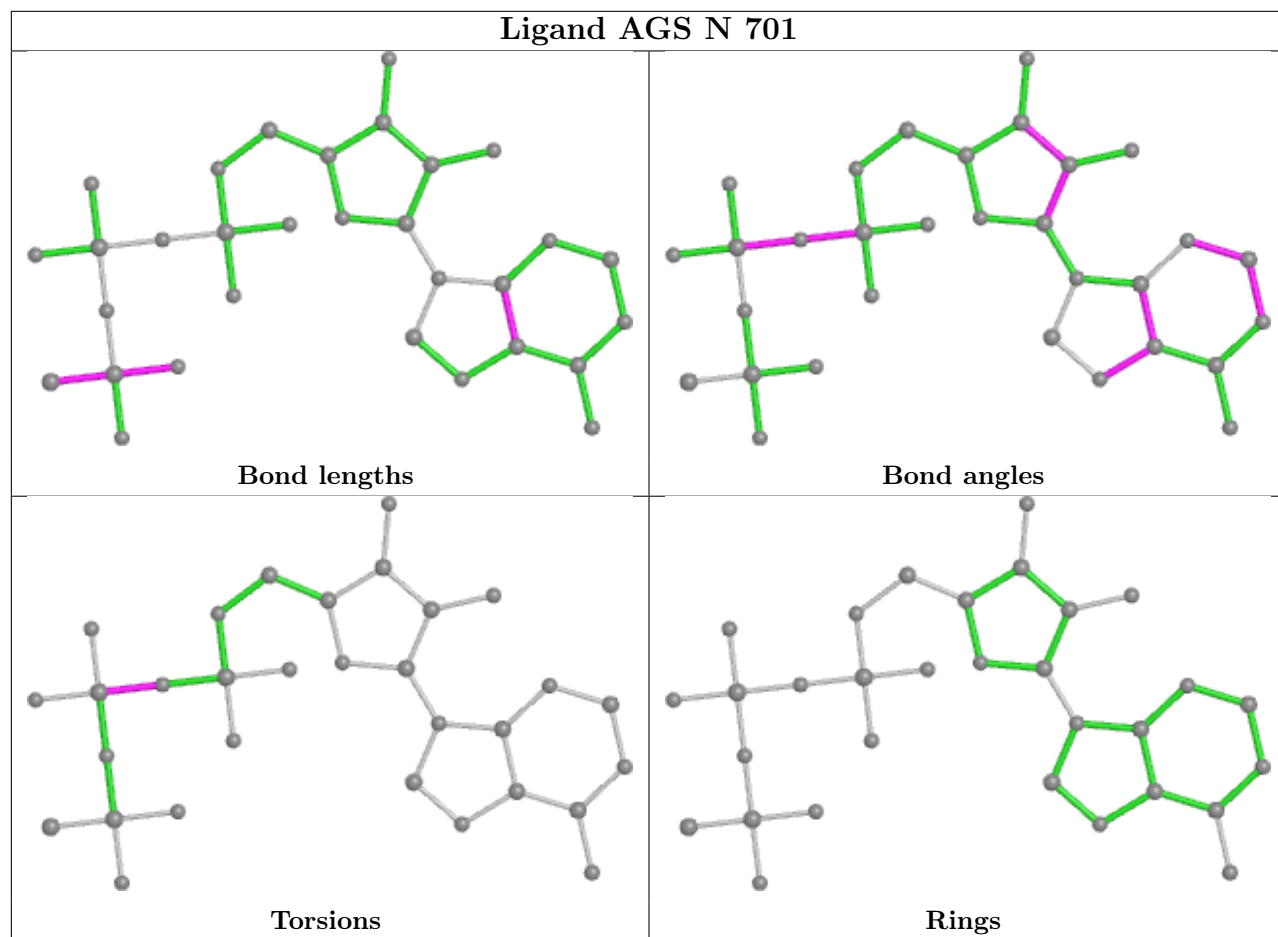


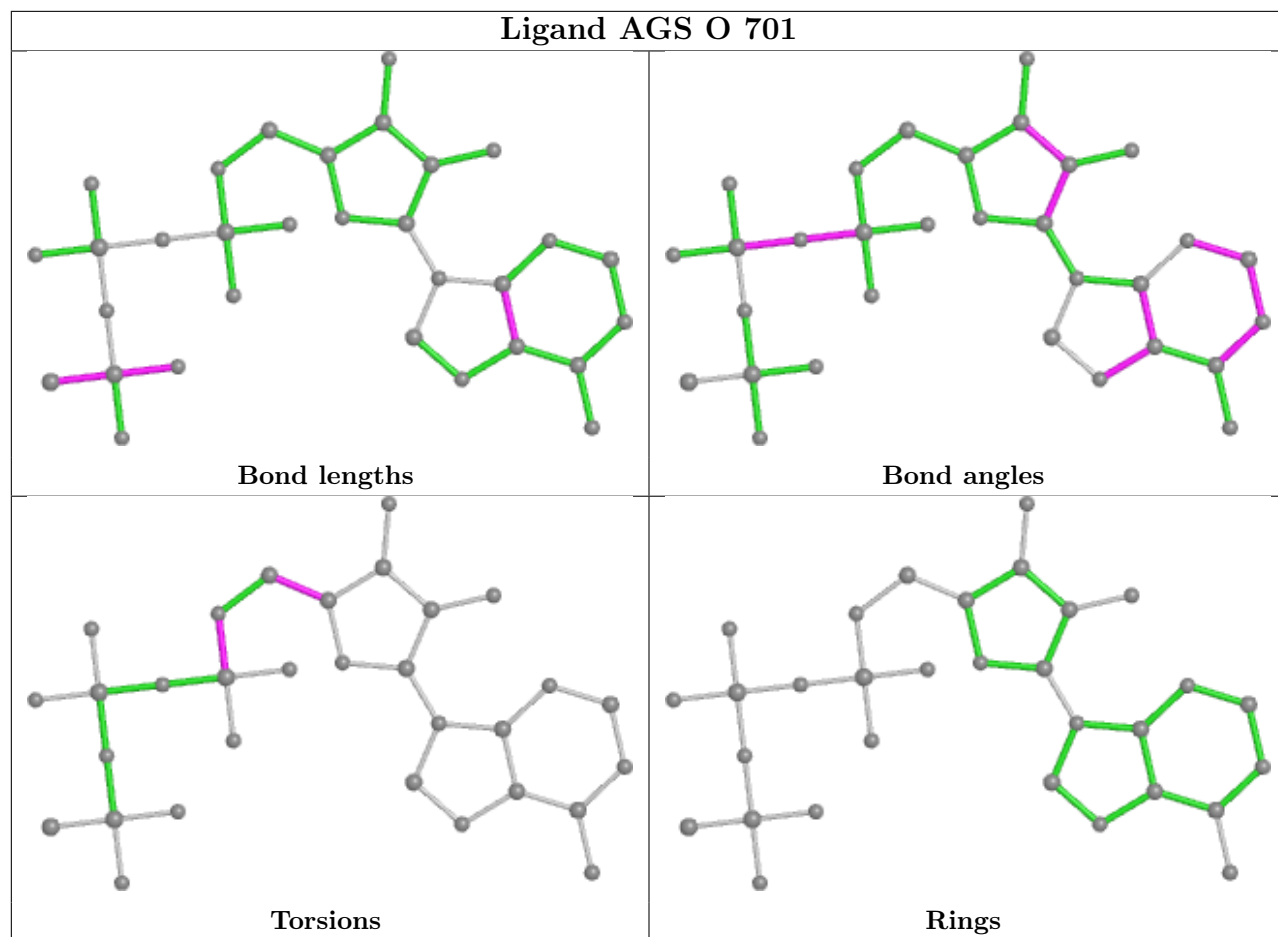


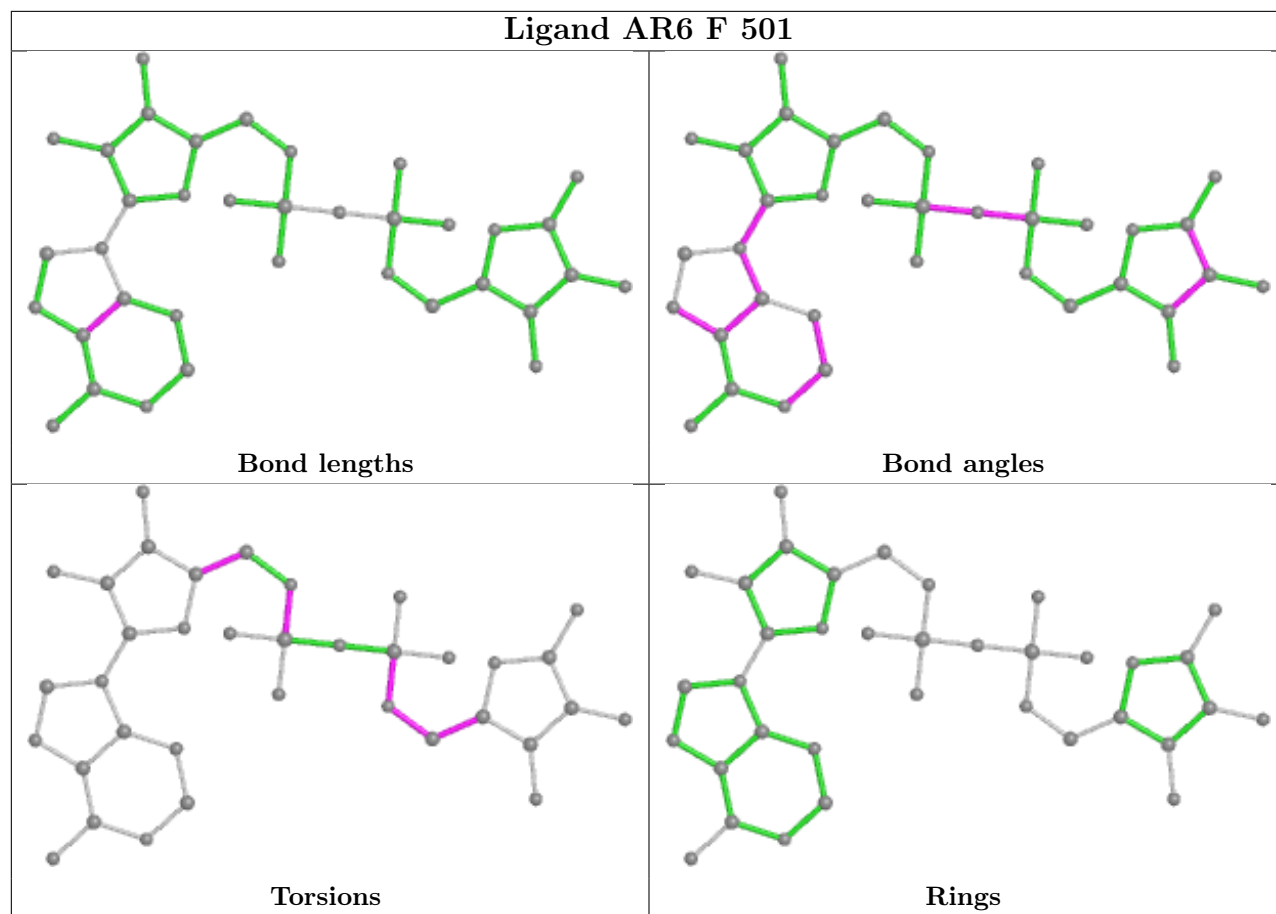


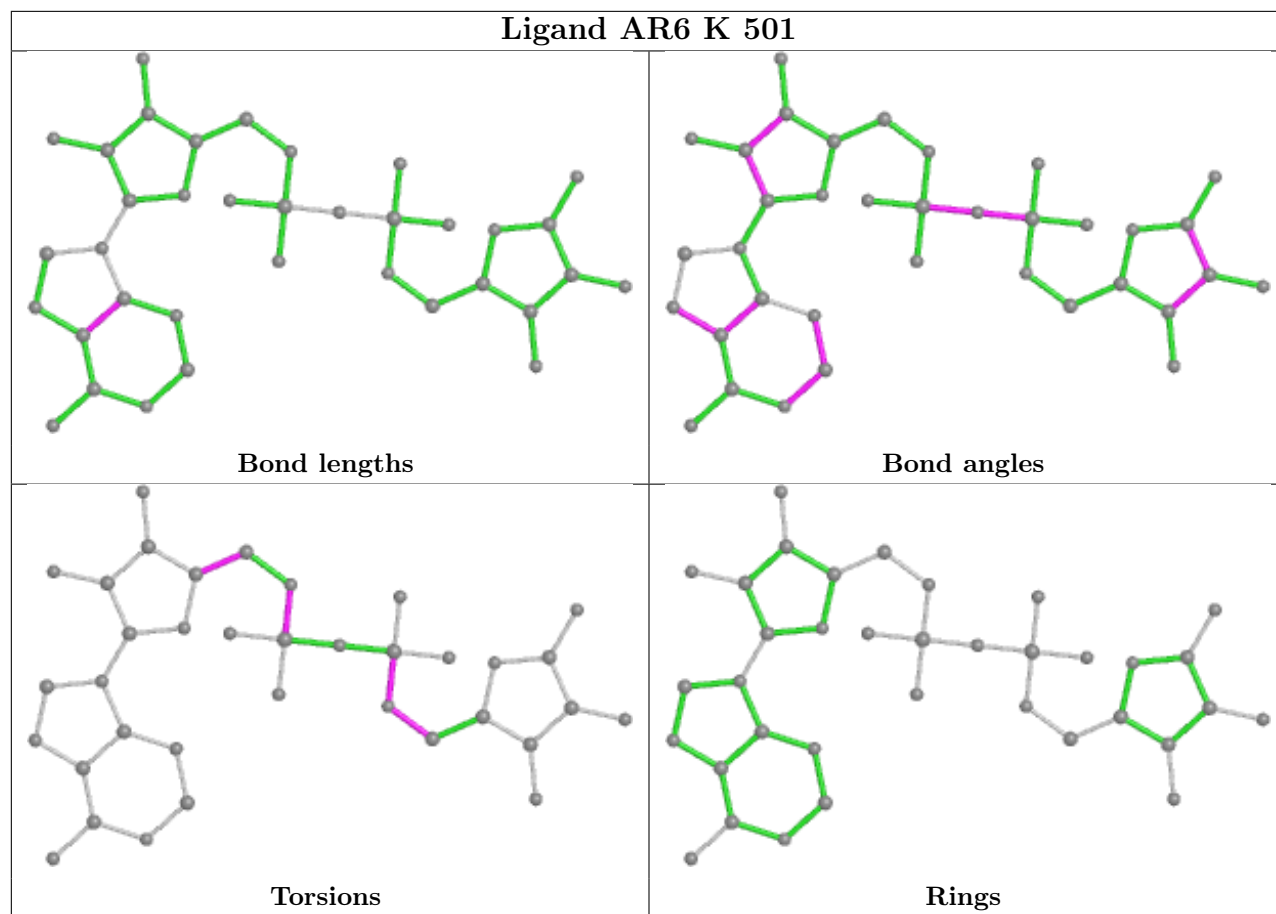


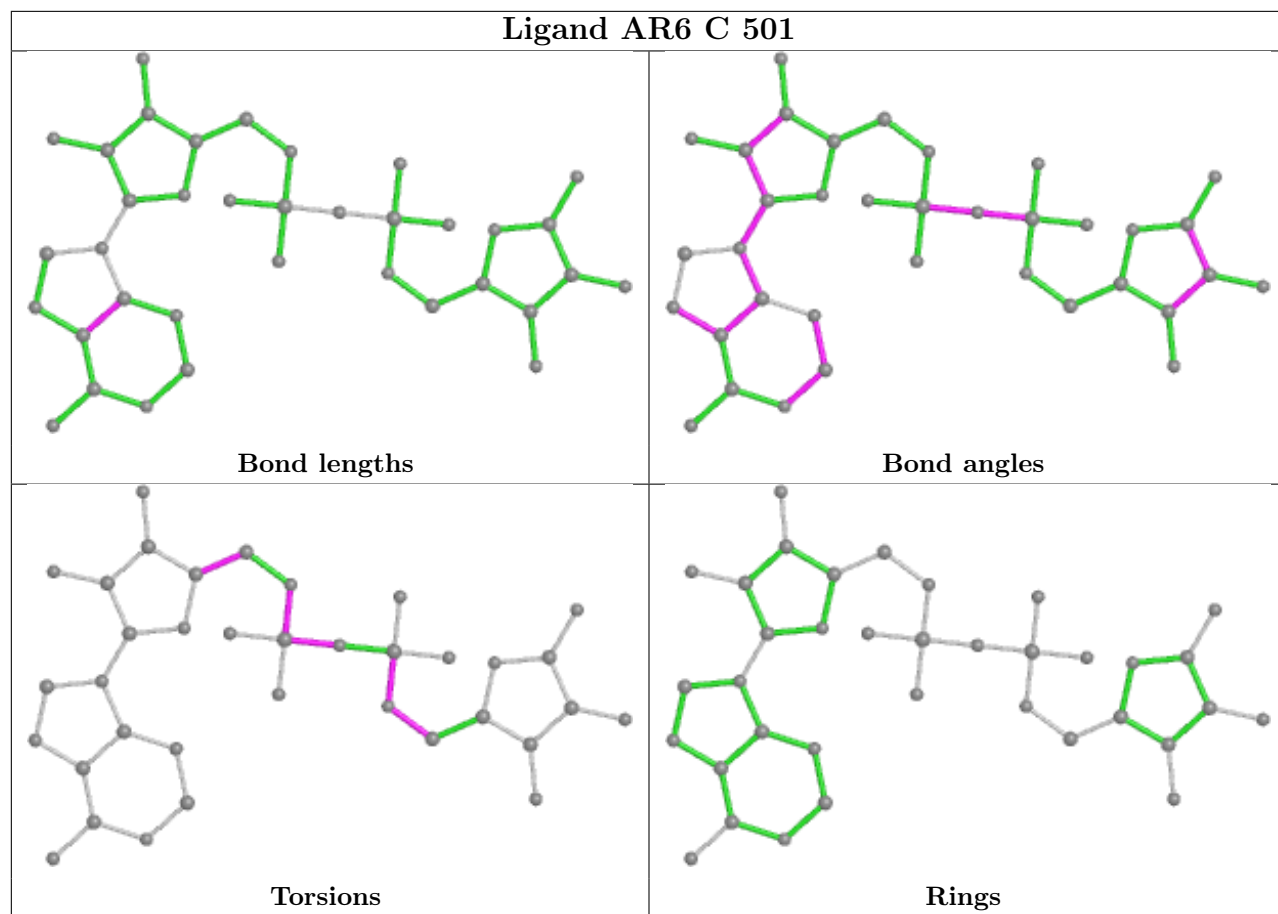


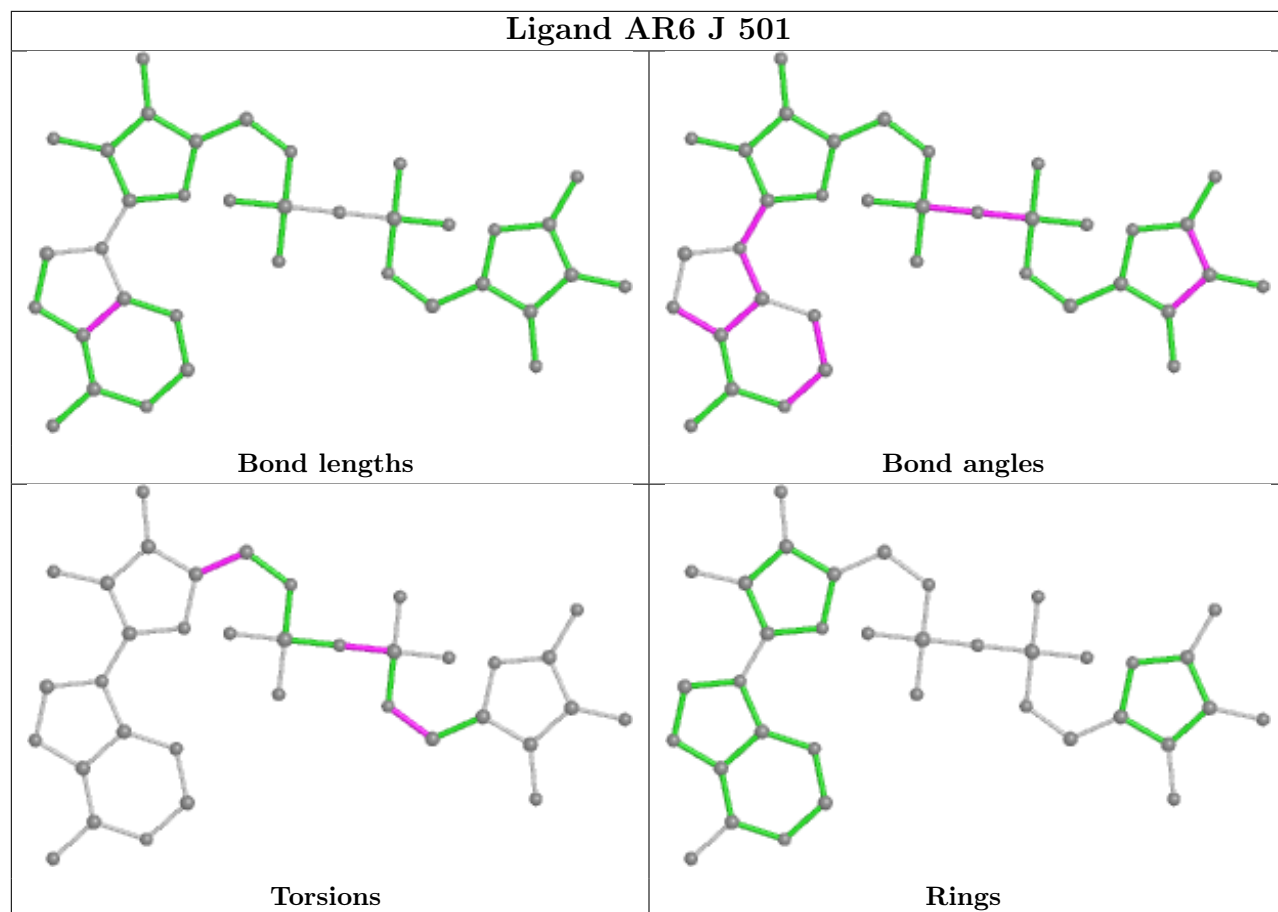




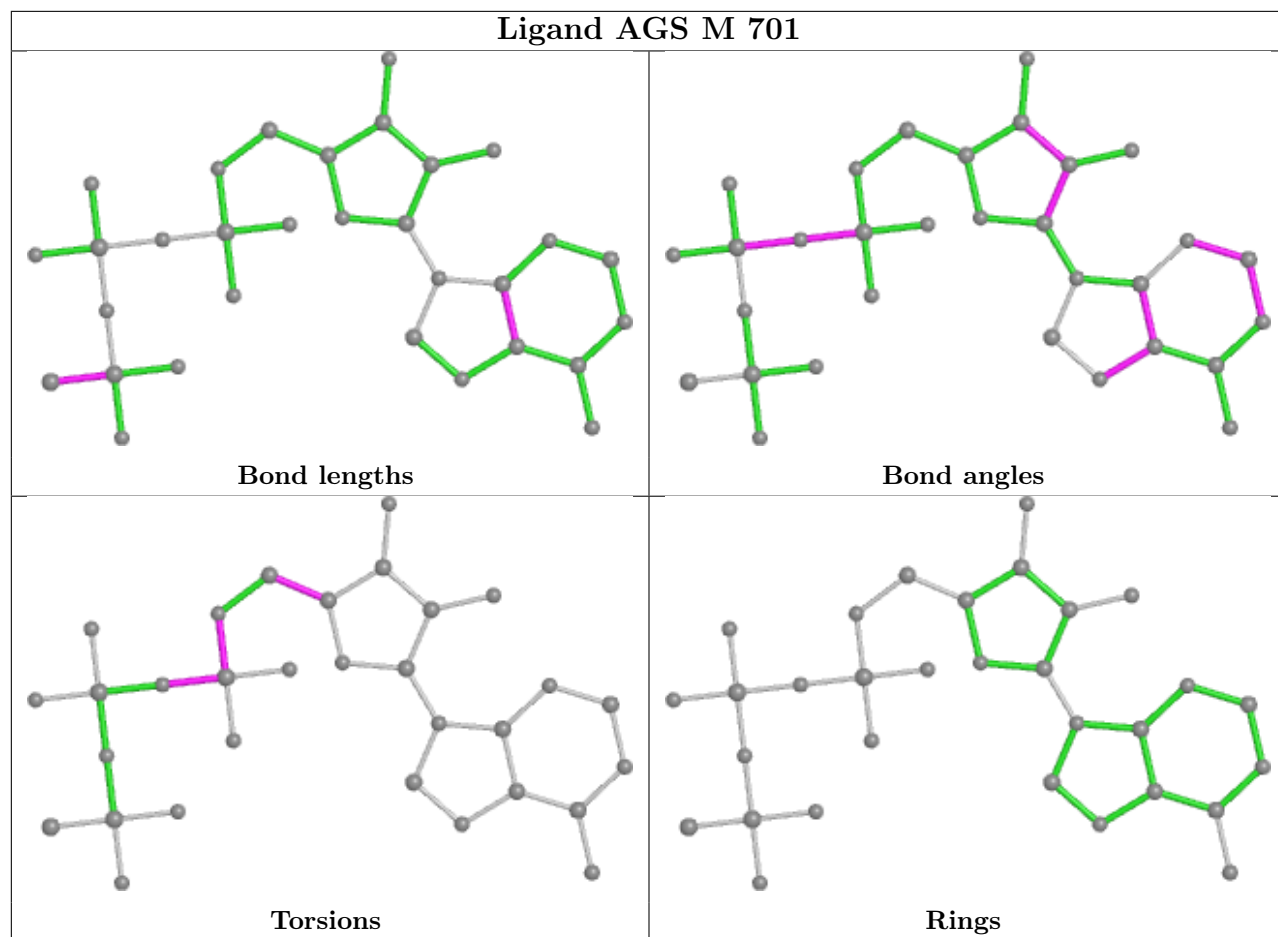


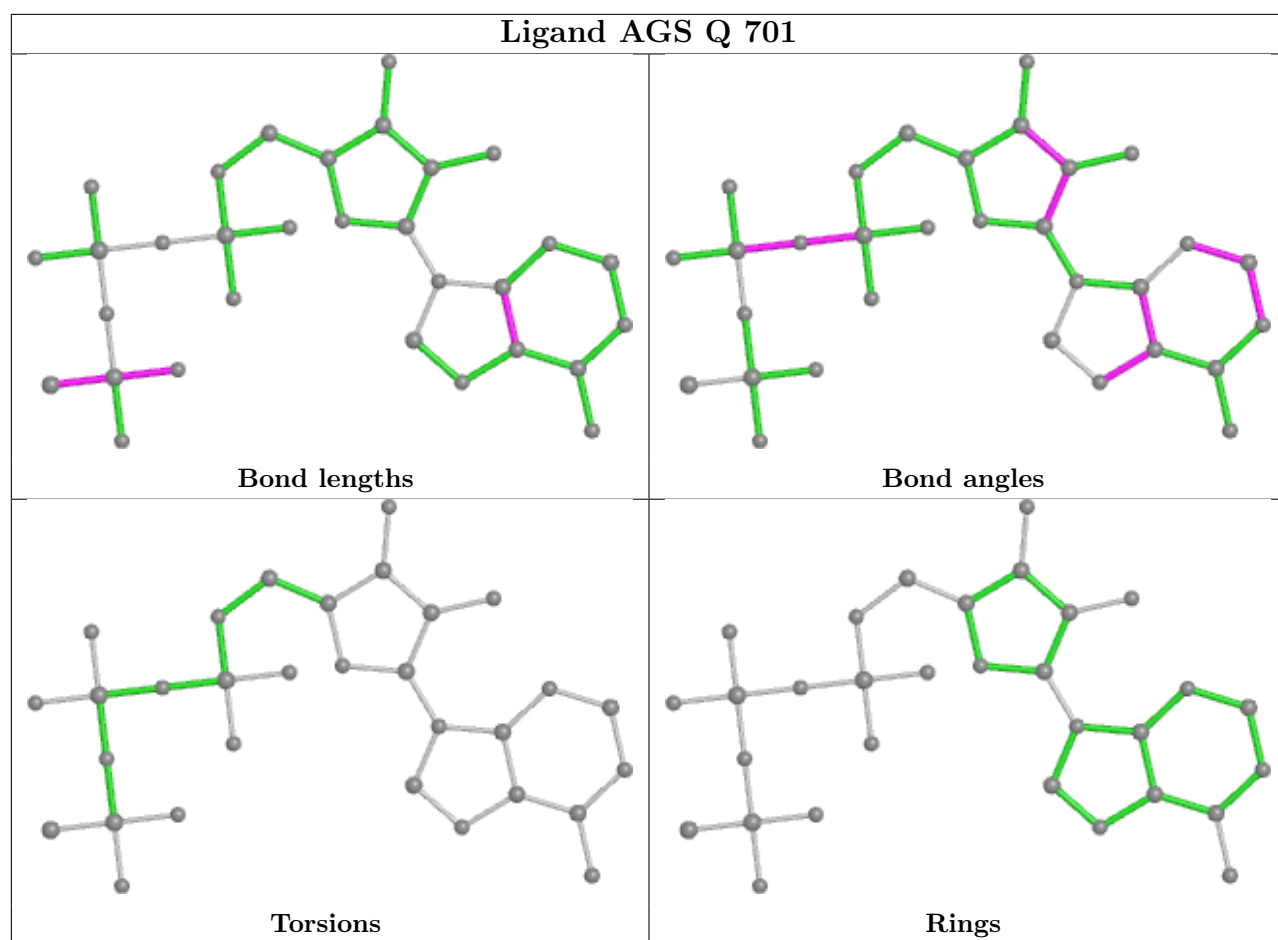


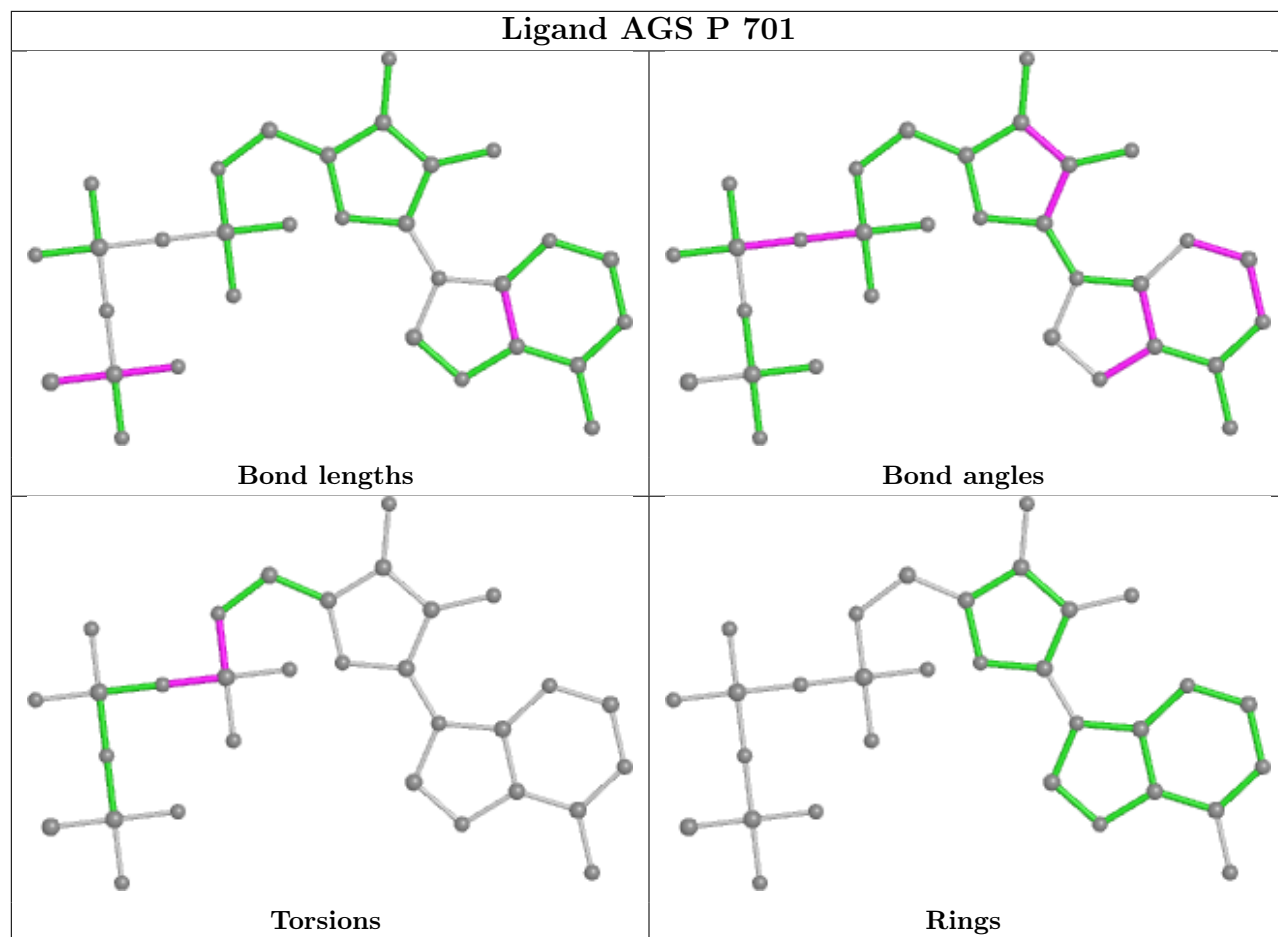


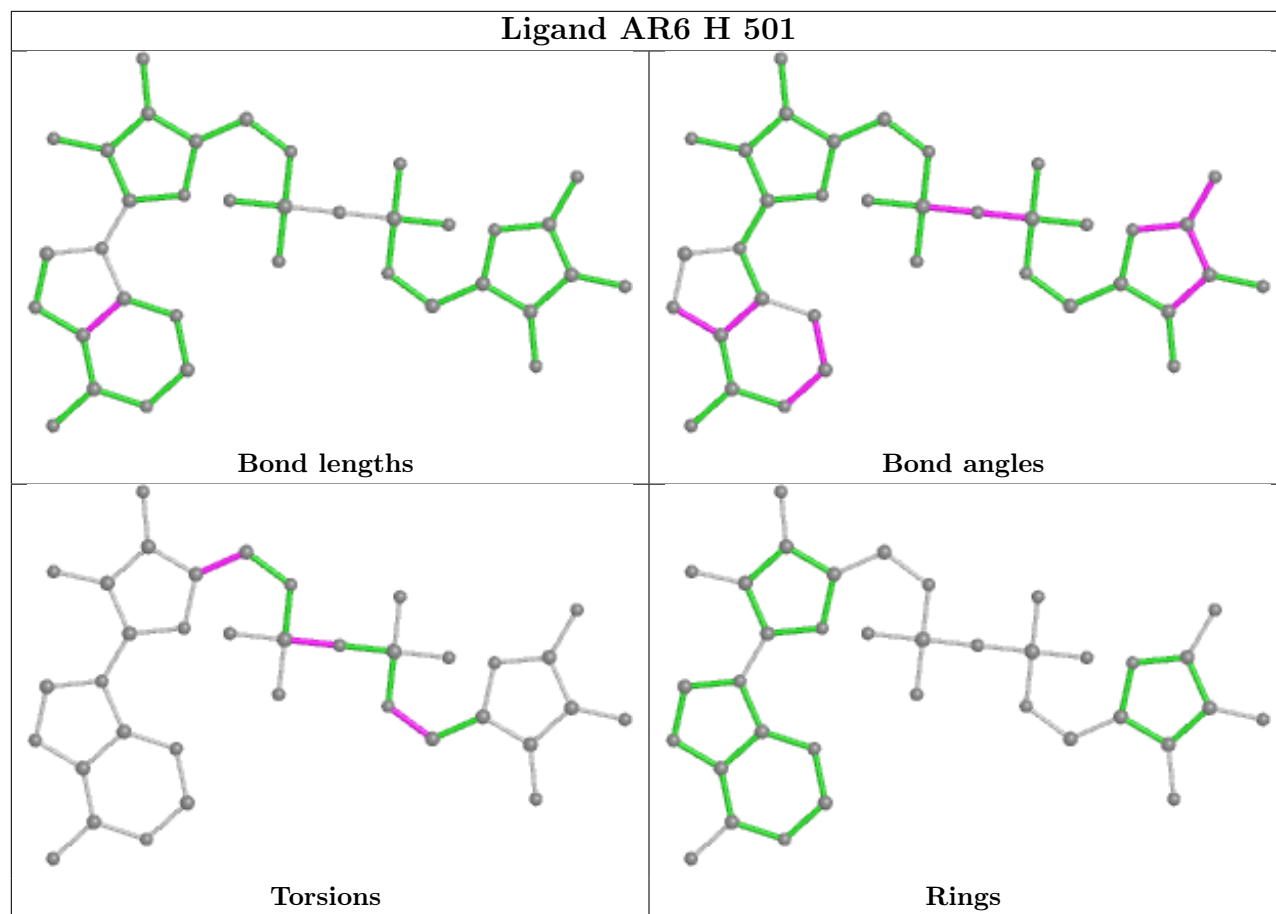


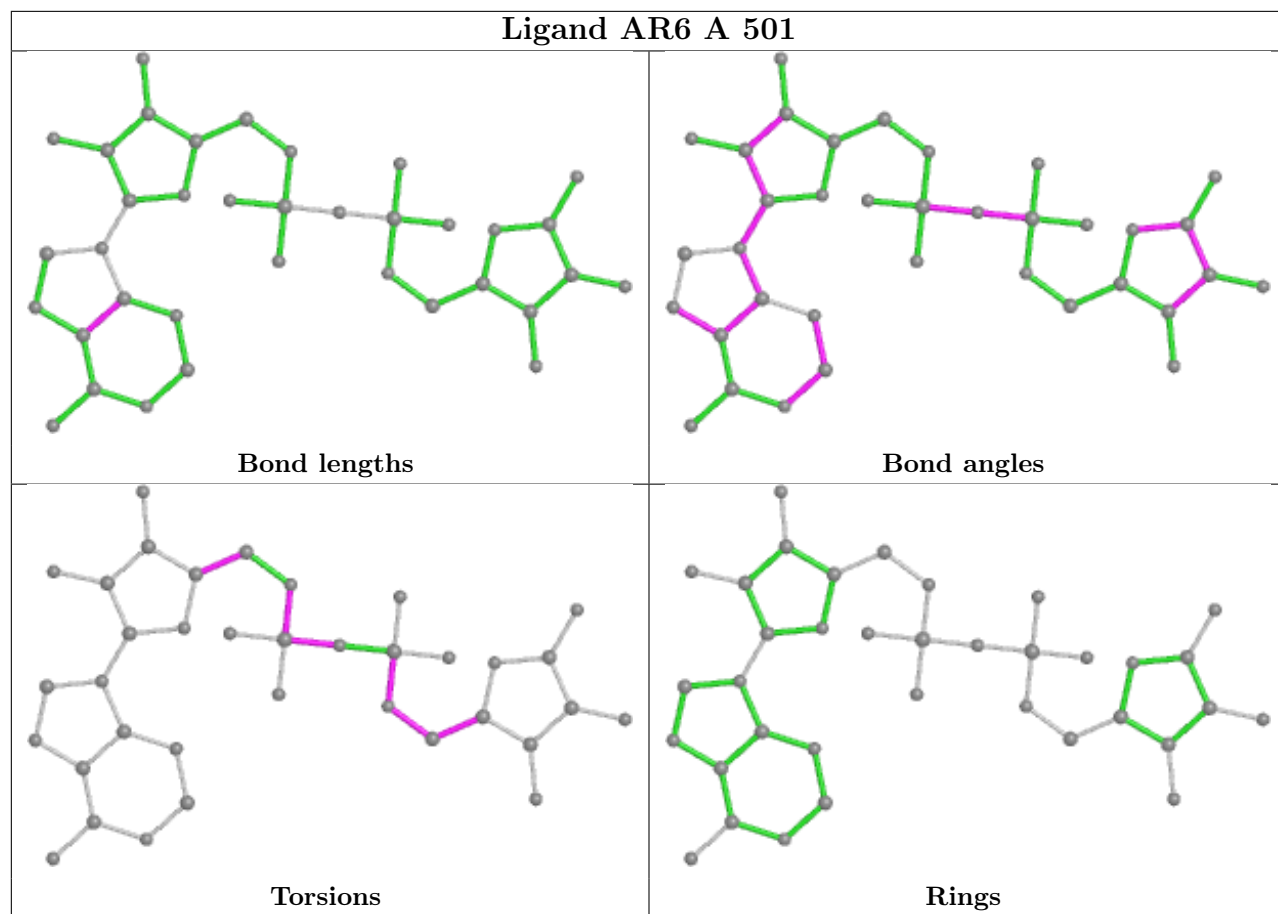


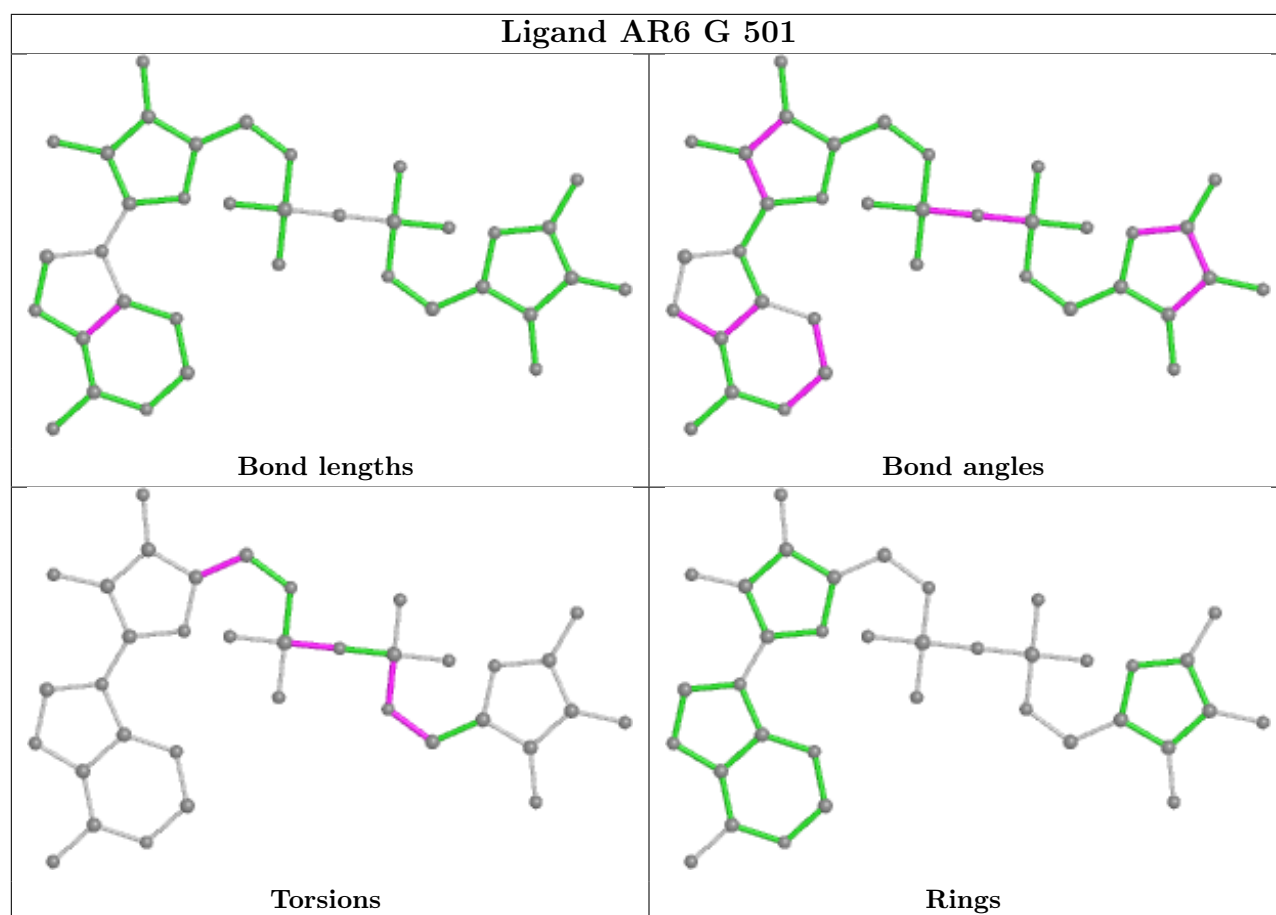












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

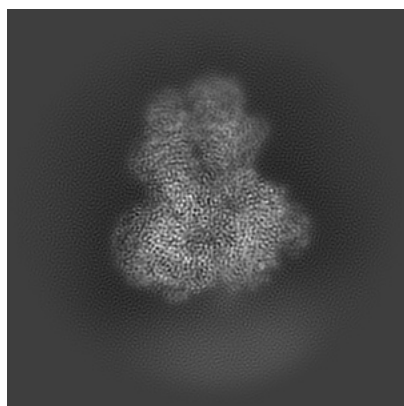
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-35978. These allow visual inspection of the internal detail of the map and identification of artifacts.

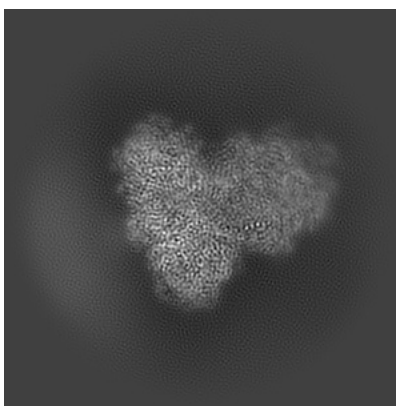
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

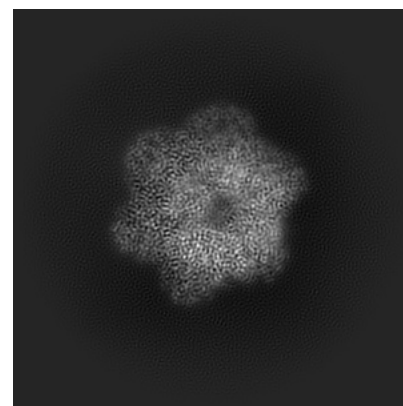
#### 6.1.1 Primary map



X

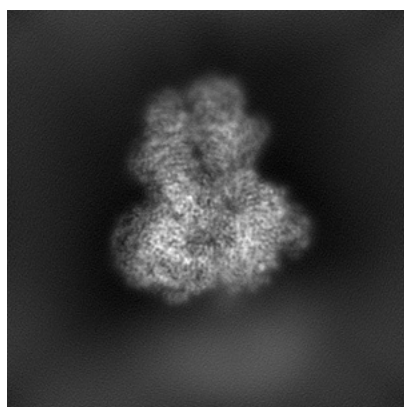


Y

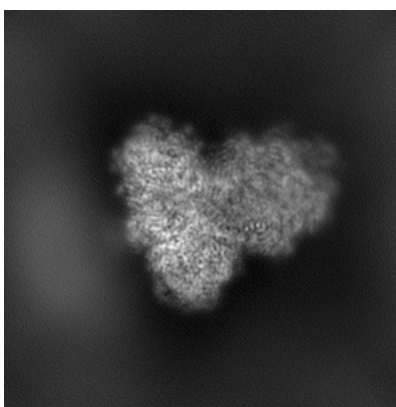


Z

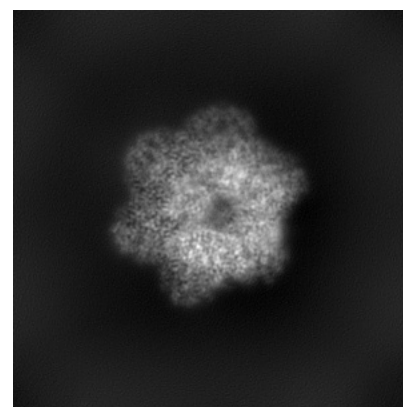
#### 6.1.2 Raw map



X



Y

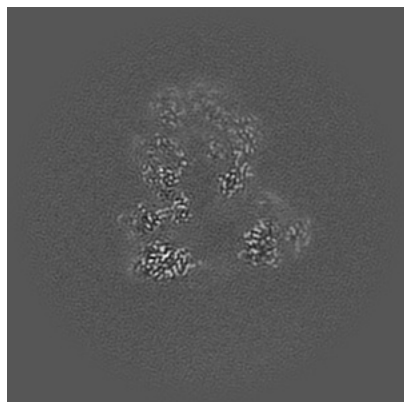


Z

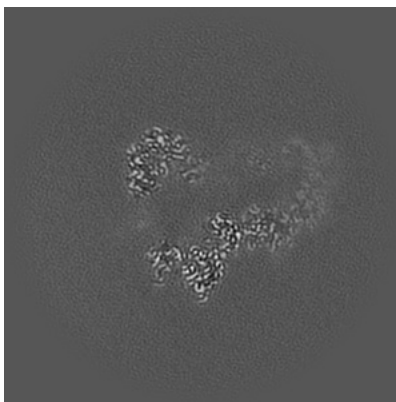
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

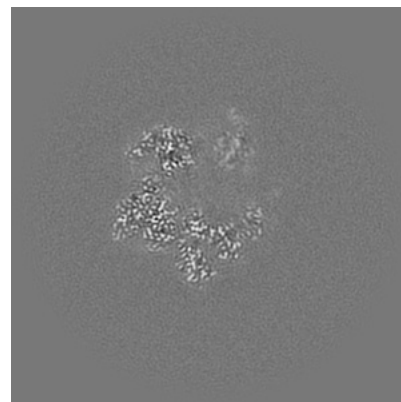
### 6.2.1 Primary map



X Index: 160

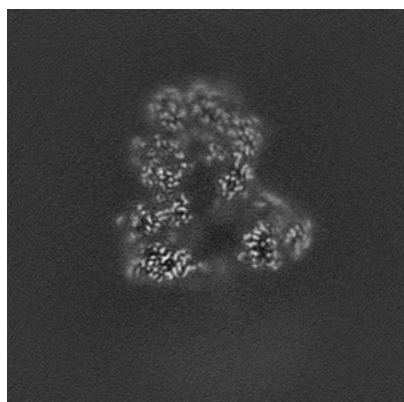


Y Index: 160

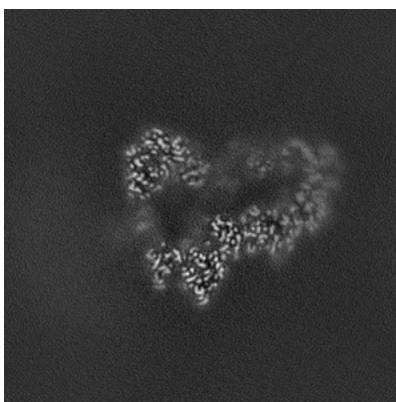


Z Index: 160

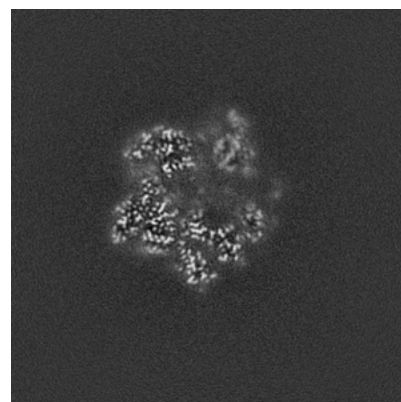
### 6.2.2 Raw map



X Index: 160



Y Index: 160



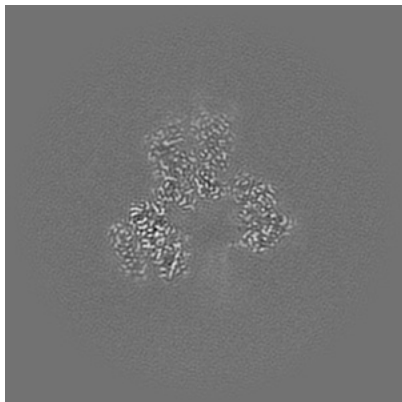
Z Index: 160

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

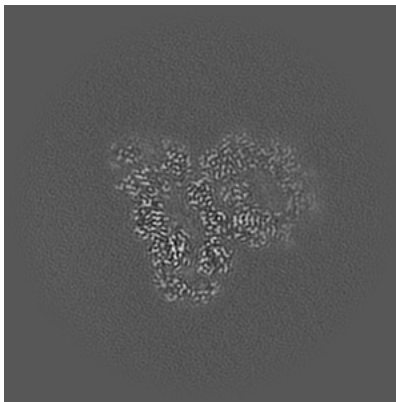


## 6.3 Largest variance slices [i](#)

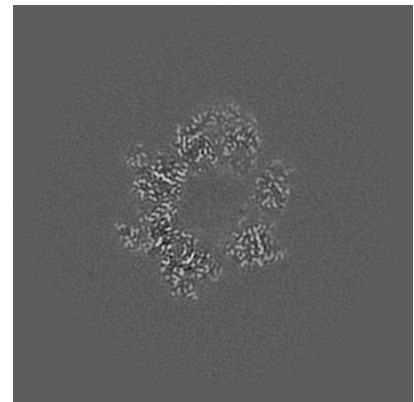
### 6.3.1 Primary map



X Index: 141

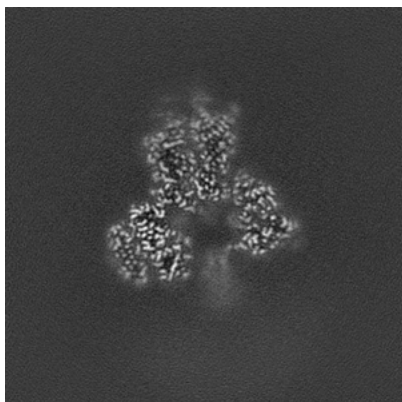


Y Index: 137

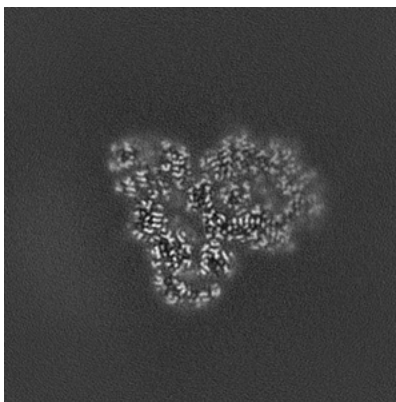


Z Index: 139

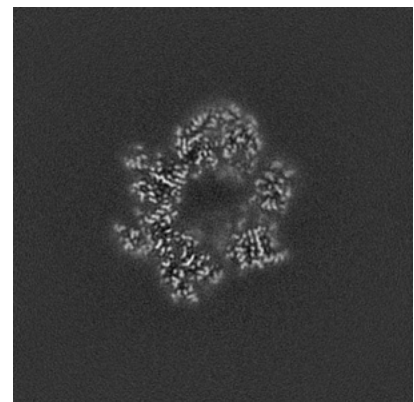
### 6.3.2 Raw map



X Index: 141



Y Index: 136

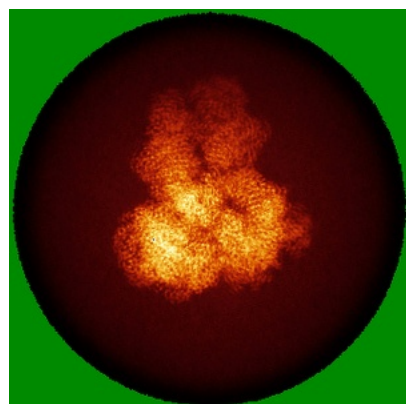


Z Index: 139

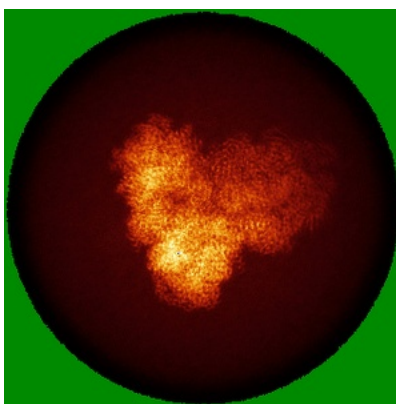
The images above show the largest variance slices of the map in three orthogonal directions.

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

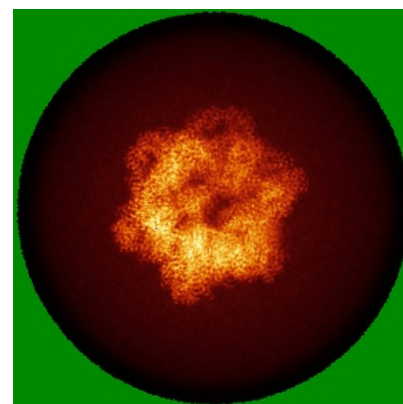
### 6.4.1 Primary map



X

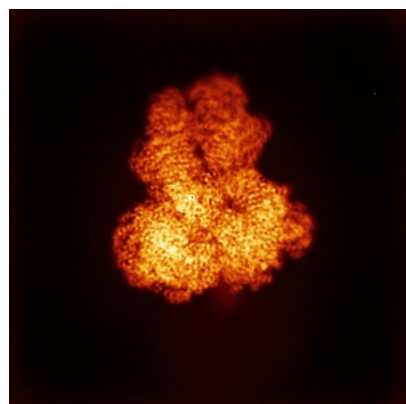


Y

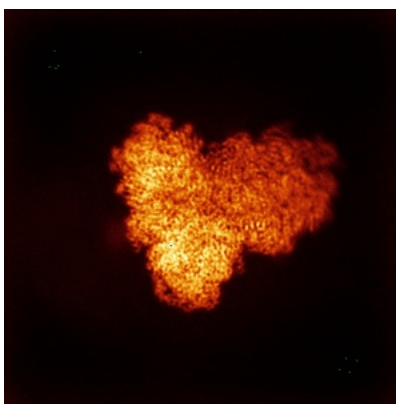


Z

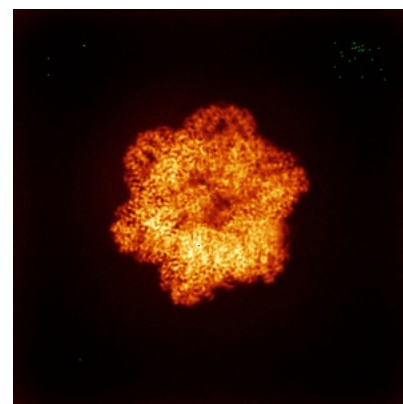
### 6.4.2 Raw map



X



Y

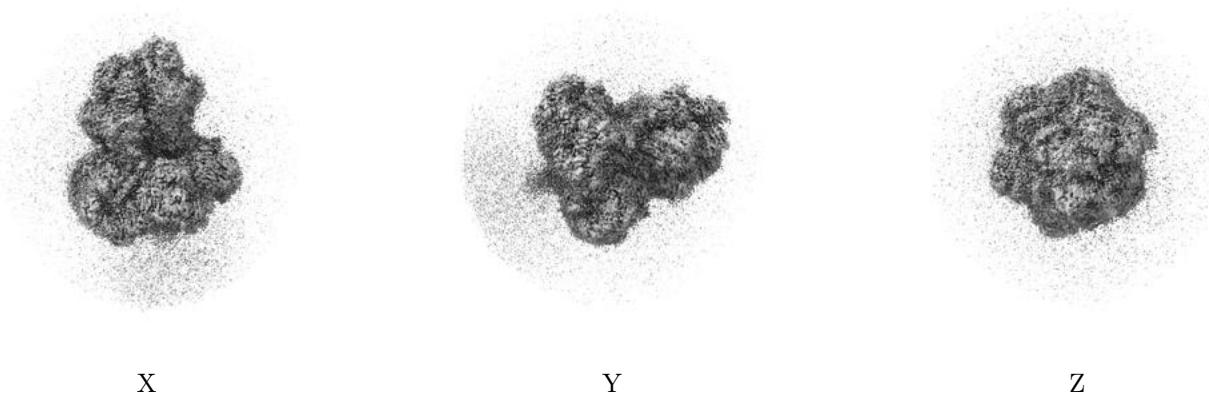


Z

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.

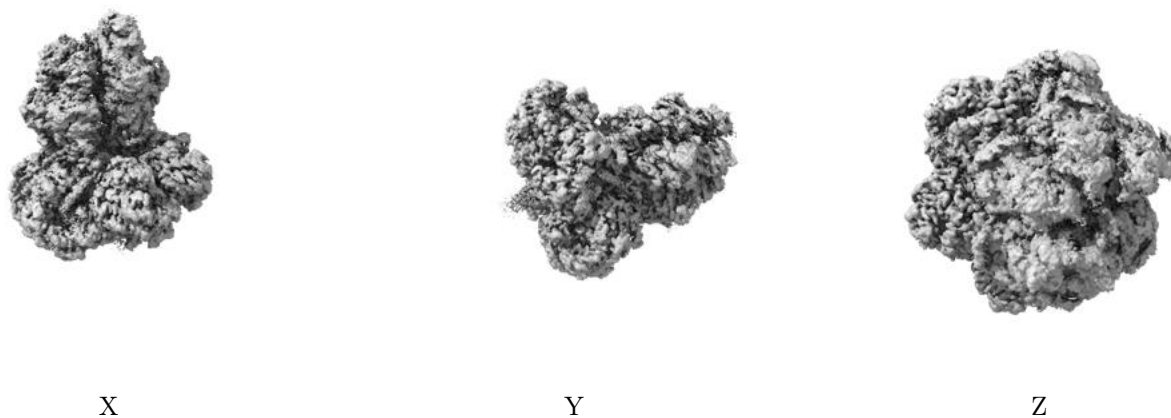
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.176. 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.

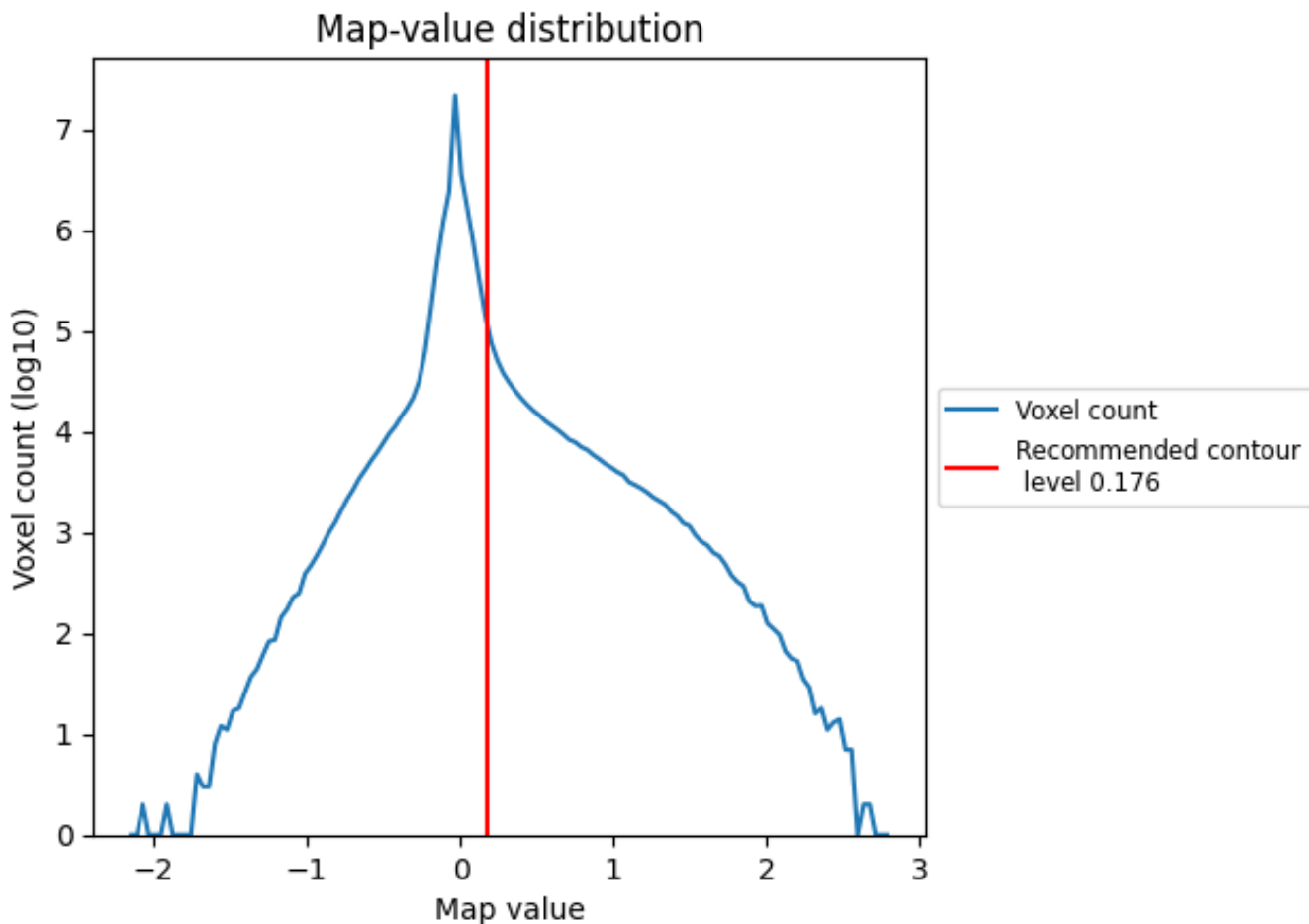
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

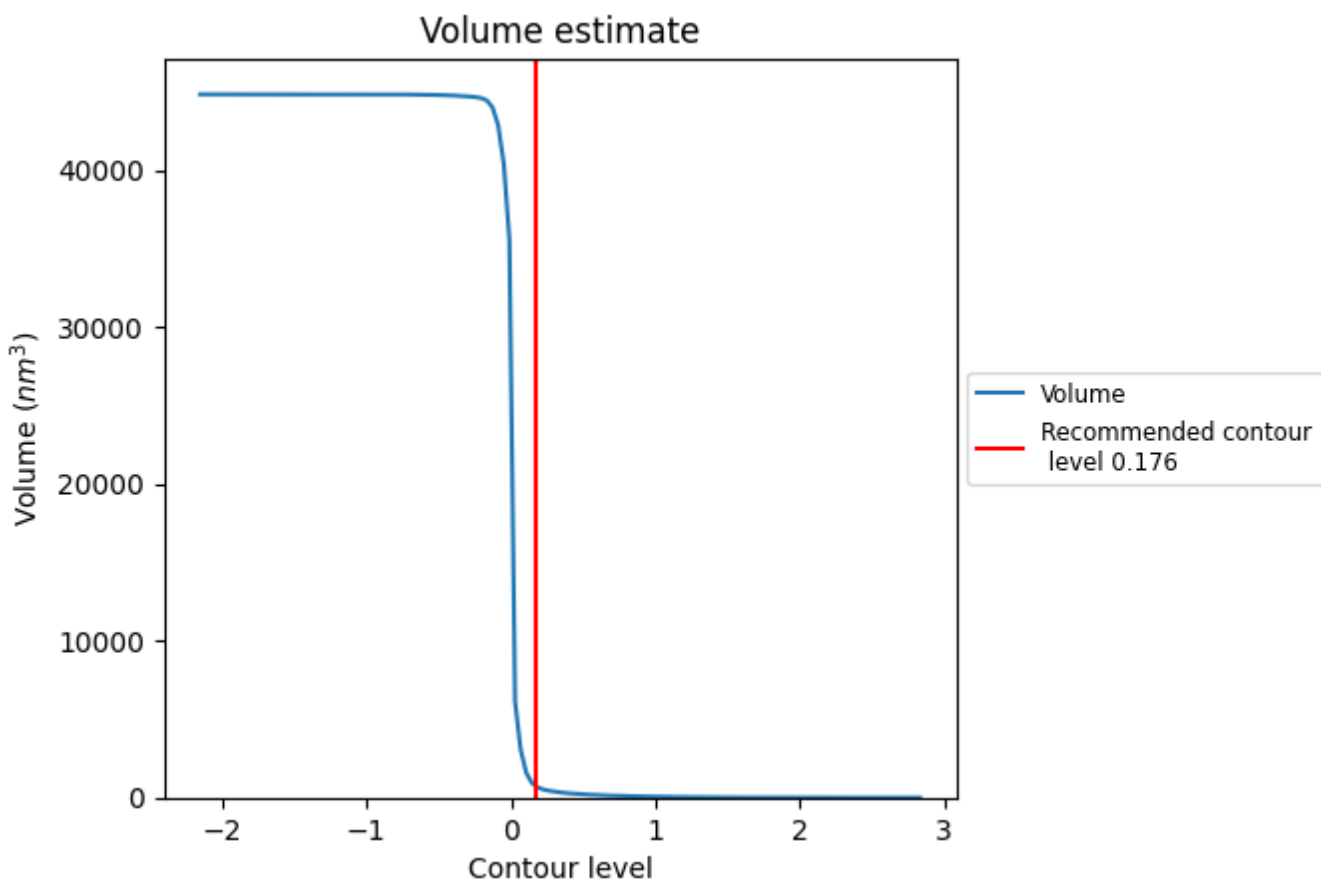
This section contains the results of statistical analysis of the map.

### 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.

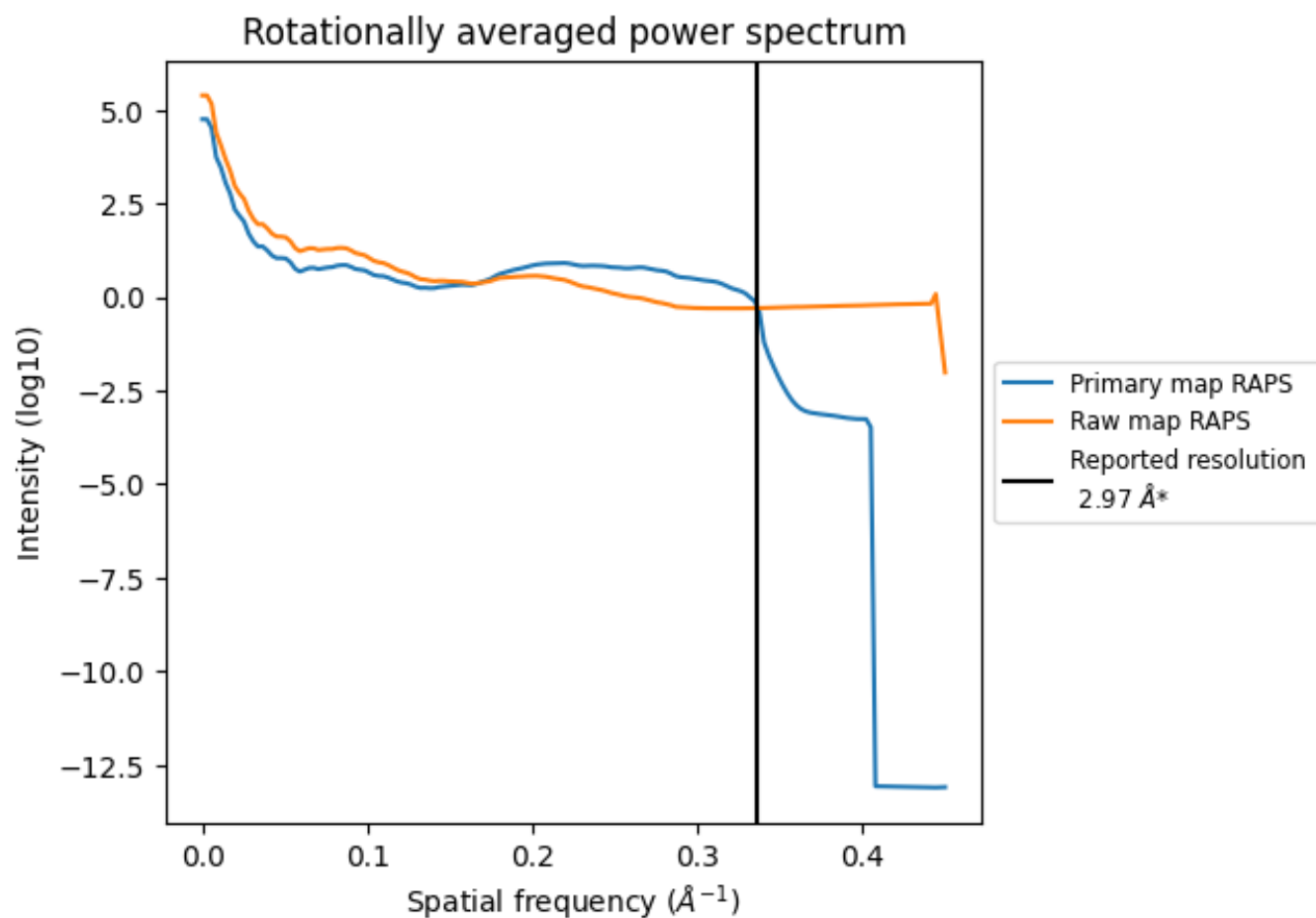
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 711 nm<sup>3</sup>; this corresponds to an approximate mass of 642 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](#)

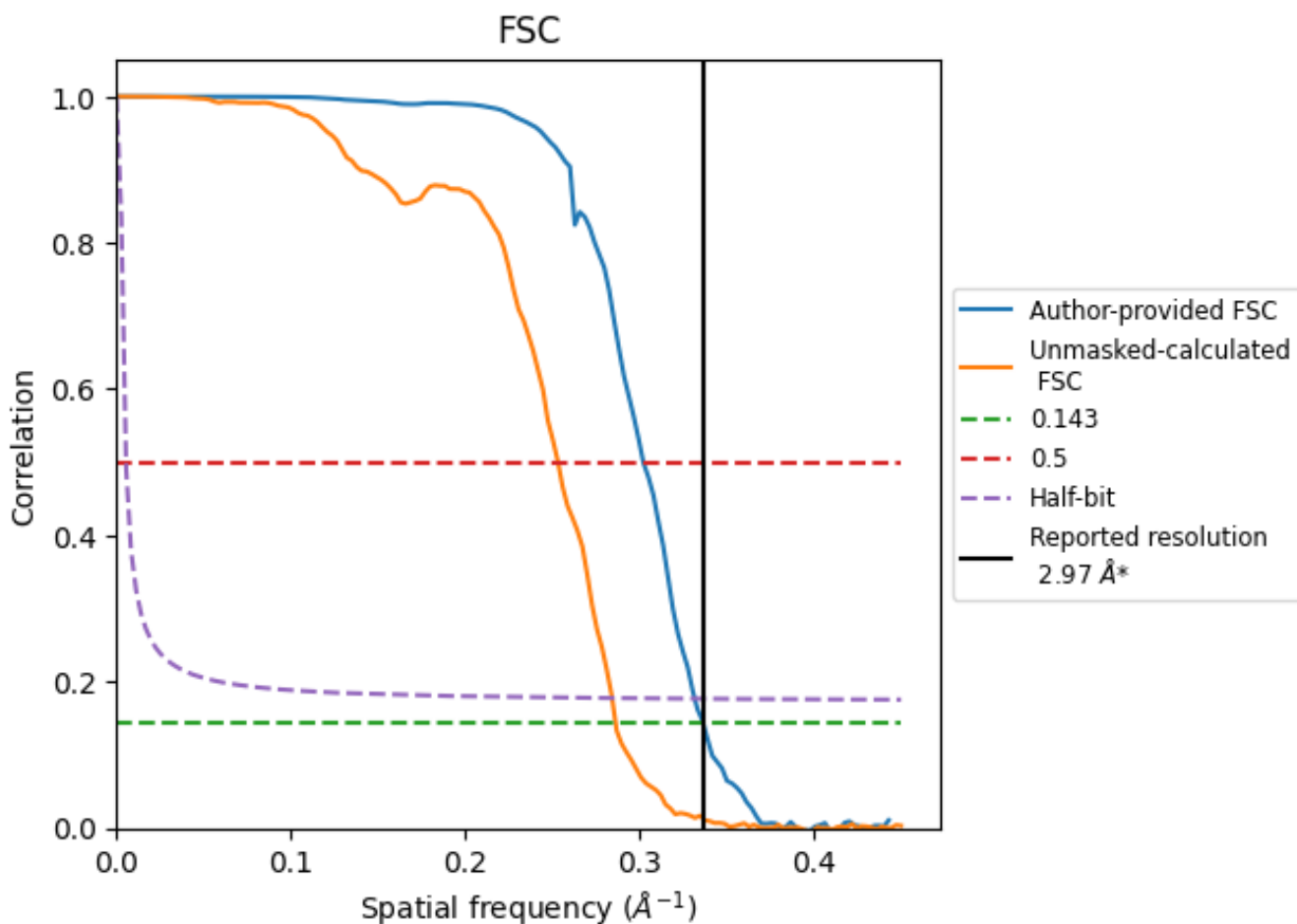


\*Reported resolution corresponds to spatial frequency of 0.337 Å<sup>-1</sup>

## 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 0.337 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	2.97	-	-
Author-provided FSC curve	2.97	3.31	3.01
Unmasked-calculated*	3.49	3.94	3.51

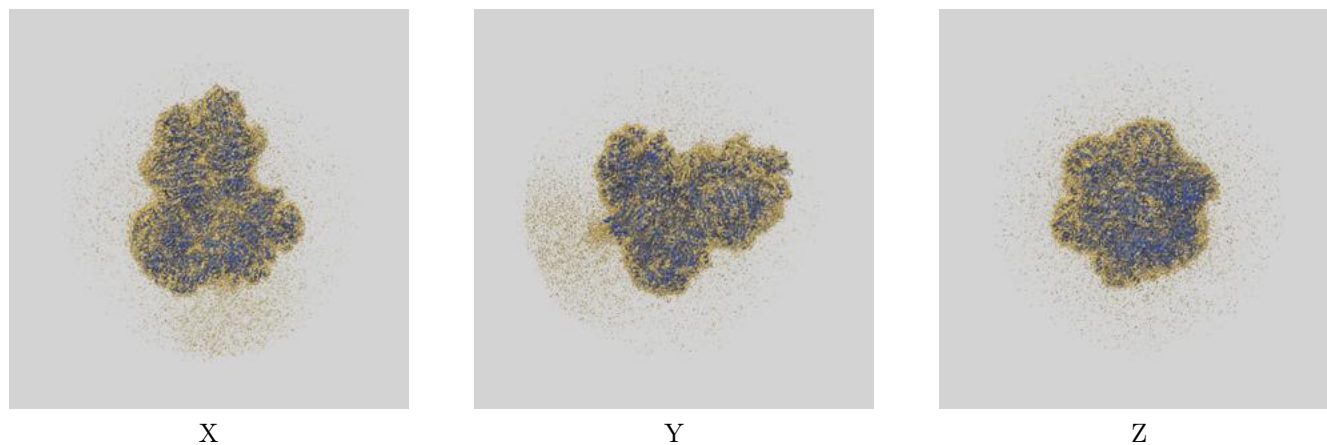
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.49 differs from the reported value 2.97 by more than 10 %



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

This section contains information regarding the fit between EMDB map EMD-35978 and PDB model 8J4U. Per-residue inclusion information can be found in section 3 on page 8.

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



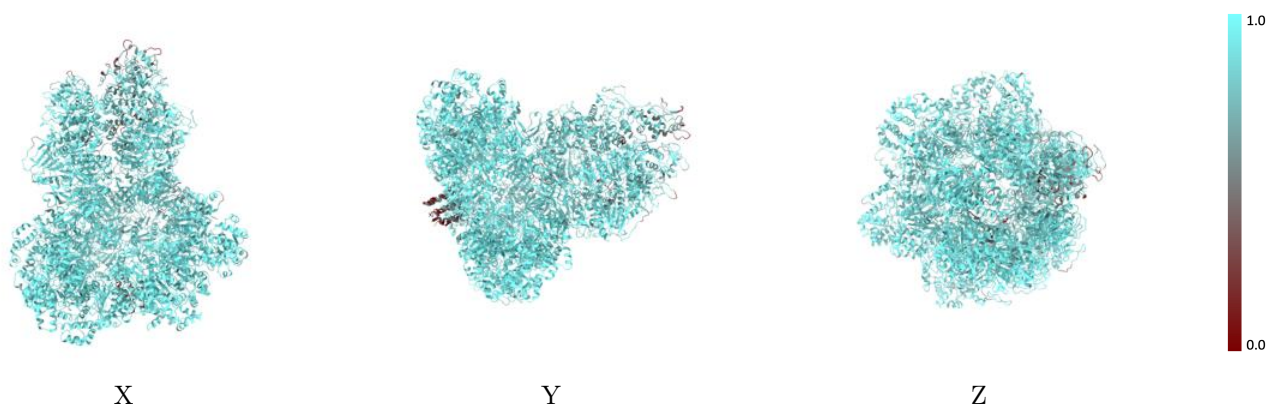
The images above show the 3D surface view of the map at the recommended contour level 0.176 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



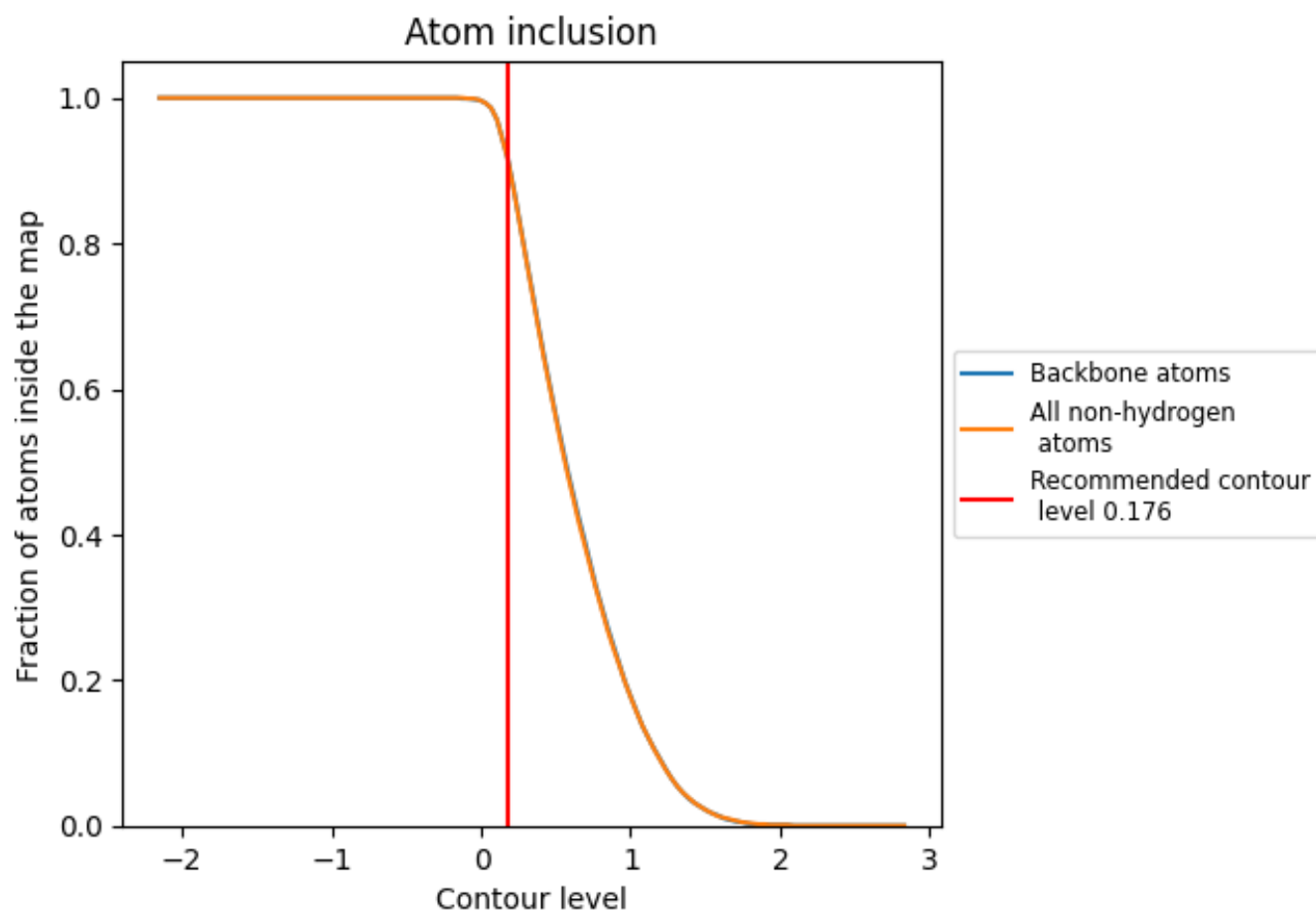
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.176).







































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 92% 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 (0.176) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9180	 0.5610
A	 0.9580	 0.5930
B	 0.9240	 0.5660
C	 0.9580	 0.6000
D	 0.9420	 0.5870
E	 0.9660	 0.6060
F	 0.9410	 0.5850
G	 0.9530	 0.5880
H	 0.9360	 0.5810
I	 0.9270	 0.5270
J	 0.9360	 0.5660
K	 0.9440	 0.5720
L	 0.9290	 0.5660
M	 0.9020	 0.5450
N	 0.9440	 0.5790
O	 0.9190	 0.5610
P	 0.8930	 0.5330
Q	 0.8830	 0.5260
R	 0.7830	 0.4720

