



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 10:45 PM UTC

PDB ID : 7VTP / pdb_00007vtp
EMDB ID : EMD-32119
Title : Cryo-EM structure of PYD-deleted human NLRP3 hexamer
Authors : Ohto, U.; Shimizu, T.
Deposited on : 2021-10-30
Resolution : 3.23 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:

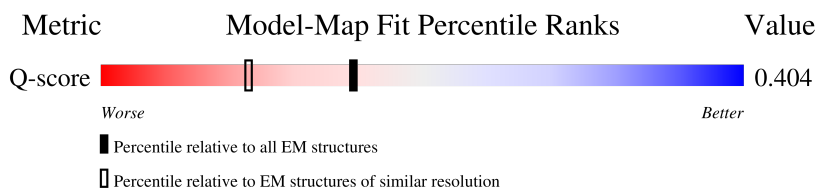
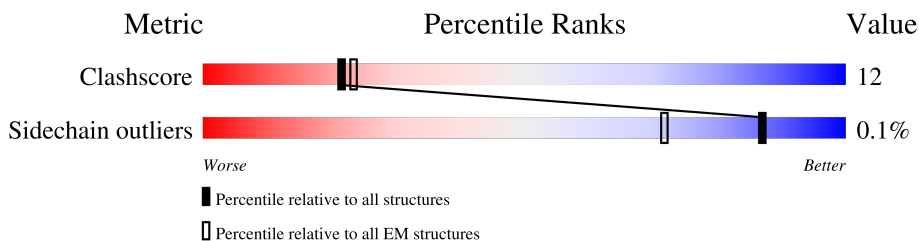
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.23 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.



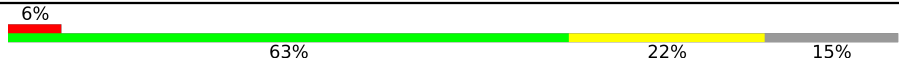
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashescore	229148	23984	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14612 (2.73 - 3.73)

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

Mol	Chain	Length	Quality of chain
1	A	931	
1	B	931	
1	C	931	
1	D	931	
1	E	931	

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Mol	Chain	Length	Quality of chain
1	F	931	 <p>6% 63% 22% 15%</p>

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 38358 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called NACHT, LRR and PYD domains-containing protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	795	6338	4051	1071	1161	55	0	0
1	B	795	6338	4051	1071	1161	55	0	0
1	C	795	6338	4051	1071	1161	55	0	0
1	D	795	6338	4051	1071	1161	55	0	0
1	E	795	6338	4051	1071	1161	55	0	0
1	F	795	6338	4051	1071	1161	55	0	0

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	106	HIS	-	expression tag	UNP Q96P20
A	107	HIS	-	expression tag	UNP Q96P20
A	108	HIS	-	expression tag	UNP Q96P20
A	109	HIS	-	expression tag	UNP Q96P20
A	110	HIS	-	expression tag	UNP Q96P20
A	111	HIS	-	expression tag	UNP Q96P20
A	112	ASP	-	expression tag	UNP Q96P20
A	113	TYR	-	expression tag	UNP Q96P20
A	114	LYS	-	expression tag	UNP Q96P20
A	115	ASP	-	expression tag	UNP Q96P20
A	116	ASP	-	expression tag	UNP Q96P20
A	117	ASP	-	expression tag	UNP Q96P20
A	118	ASP	-	expression tag	UNP Q96P20
A	119	LYS	-	expression tag	UNP Q96P20
A	120	LEU	-	expression tag	UNP Q96P20
A	121	GLU	-	expression tag	UNP Q96P20
A	122	VAL	-	expression tag	UNP Q96P20
A	123	LEU	-	expression tag	UNP Q96P20

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Chain	Residue	Modelled	Actual	Comment	Reference
A	124	PHE	-	expression tag	UNP Q96P20
A	125	GLN	-	expression tag	UNP Q96P20
A	126	GLY	-	expression tag	UNP Q96P20
A	127	PRO	-	expression tag	UNP Q96P20
A	128	GLU	-	expression tag	UNP Q96P20
A	129	PHE	-	expression tag	UNP Q96P20
B	106	HIS	-	expression tag	UNP Q96P20
B	107	HIS	-	expression tag	UNP Q96P20
B	108	HIS	-	expression tag	UNP Q96P20
B	109	HIS	-	expression tag	UNP Q96P20
B	110	HIS	-	expression tag	UNP Q96P20
B	111	HIS	-	expression tag	UNP Q96P20
B	112	ASP	-	expression tag	UNP Q96P20
B	113	TYR	-	expression tag	UNP Q96P20
B	114	LYS	-	expression tag	UNP Q96P20
B	115	ASP	-	expression tag	UNP Q96P20
B	116	ASP	-	expression tag	UNP Q96P20
B	117	ASP	-	expression tag	UNP Q96P20
B	118	ASP	-	expression tag	UNP Q96P20
B	119	LYS	-	expression tag	UNP Q96P20
B	120	LEU	-	expression tag	UNP Q96P20
B	121	GLU	-	expression tag	UNP Q96P20
B	122	VAL	-	expression tag	UNP Q96P20
B	123	LEU	-	expression tag	UNP Q96P20
B	124	PHE	-	expression tag	UNP Q96P20
B	125	GLN	-	expression tag	UNP Q96P20
B	126	GLY	-	expression tag	UNP Q96P20
B	127	PRO	-	expression tag	UNP Q96P20
B	128	GLU	-	expression tag	UNP Q96P20
B	129	PHE	-	expression tag	UNP Q96P20
C	106	HIS	-	expression tag	UNP Q96P20
C	107	HIS	-	expression tag	UNP Q96P20
C	108	HIS	-	expression tag	UNP Q96P20
C	109	HIS	-	expression tag	UNP Q96P20
C	110	HIS	-	expression tag	UNP Q96P20
C	111	HIS	-	expression tag	UNP Q96P20
C	112	ASP	-	expression tag	UNP Q96P20
C	113	TYR	-	expression tag	UNP Q96P20
C	114	LYS	-	expression tag	UNP Q96P20
C	115	ASP	-	expression tag	UNP Q96P20
C	116	ASP	-	expression tag	UNP Q96P20
C	117	ASP	-	expression tag	UNP Q96P20

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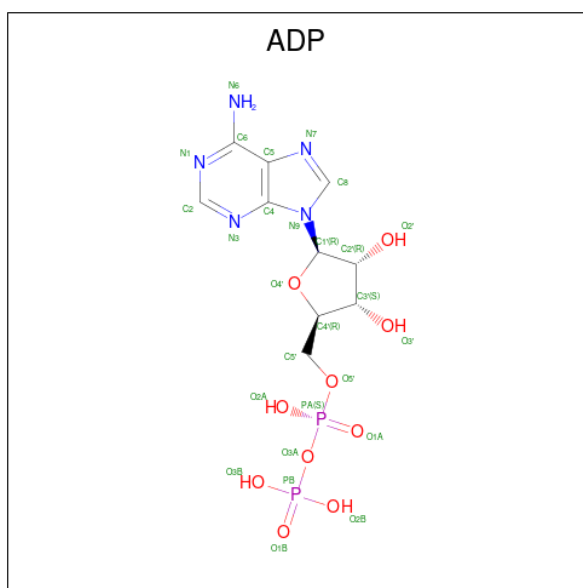
Chain	Residue	Modelled	Actual	Comment	Reference
C	118	ASP	-	expression tag	UNP Q96P20
C	119	LYS	-	expression tag	UNP Q96P20
C	120	LEU	-	expression tag	UNP Q96P20
C	121	GLU	-	expression tag	UNP Q96P20
C	122	VAL	-	expression tag	UNP Q96P20
C	123	LEU	-	expression tag	UNP Q96P20
C	124	PHE	-	expression tag	UNP Q96P20
C	125	GLN	-	expression tag	UNP Q96P20
C	126	GLY	-	expression tag	UNP Q96P20
C	127	PRO	-	expression tag	UNP Q96P20
C	128	GLU	-	expression tag	UNP Q96P20
C	129	PHE	-	expression tag	UNP Q96P20
D	106	HIS	-	expression tag	UNP Q96P20
D	107	HIS	-	expression tag	UNP Q96P20
D	108	HIS	-	expression tag	UNP Q96P20
D	109	HIS	-	expression tag	UNP Q96P20
D	110	HIS	-	expression tag	UNP Q96P20
D	111	HIS	-	expression tag	UNP Q96P20
D	112	ASP	-	expression tag	UNP Q96P20
D	113	TYR	-	expression tag	UNP Q96P20
D	114	LYS	-	expression tag	UNP Q96P20
D	115	ASP	-	expression tag	UNP Q96P20
D	116	ASP	-	expression tag	UNP Q96P20
D	117	ASP	-	expression tag	UNP Q96P20
D	118	ASP	-	expression tag	UNP Q96P20
D	119	LYS	-	expression tag	UNP Q96P20
D	120	LEU	-	expression tag	UNP Q96P20
D	121	GLU	-	expression tag	UNP Q96P20
D	122	VAL	-	expression tag	UNP Q96P20
D	123	LEU	-	expression tag	UNP Q96P20
D	124	PHE	-	expression tag	UNP Q96P20
D	125	GLN	-	expression tag	UNP Q96P20
D	126	GLY	-	expression tag	UNP Q96P20
D	127	PRO	-	expression tag	UNP Q96P20
D	128	GLU	-	expression tag	UNP Q96P20
D	129	PHE	-	expression tag	UNP Q96P20
E	106	HIS	-	expression tag	UNP Q96P20
E	107	HIS	-	expression tag	UNP Q96P20
E	108	HIS	-	expression tag	UNP Q96P20
E	109	HIS	-	expression tag	UNP Q96P20
E	110	HIS	-	expression tag	UNP Q96P20
E	111	HIS	-	expression tag	UNP Q96P20

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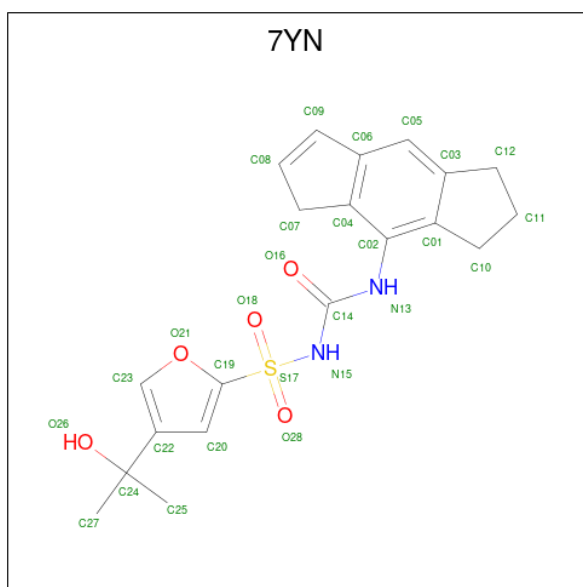
Chain	Residue	Modelled	Actual	Comment	Reference
E	112	ASP	-	expression tag	UNP Q96P20
E	113	TYR	-	expression tag	UNP Q96P20
E	114	LYS	-	expression tag	UNP Q96P20
E	115	ASP	-	expression tag	UNP Q96P20
E	116	ASP	-	expression tag	UNP Q96P20
E	117	ASP	-	expression tag	UNP Q96P20
E	118	ASP	-	expression tag	UNP Q96P20
E	119	LYS	-	expression tag	UNP Q96P20
E	120	LEU	-	expression tag	UNP Q96P20
E	121	GLU	-	expression tag	UNP Q96P20
E	122	VAL	-	expression tag	UNP Q96P20
E	123	LEU	-	expression tag	UNP Q96P20
E	124	PHE	-	expression tag	UNP Q96P20
E	125	GLN	-	expression tag	UNP Q96P20
E	126	GLY	-	expression tag	UNP Q96P20
E	127	PRO	-	expression tag	UNP Q96P20
E	128	GLU	-	expression tag	UNP Q96P20
E	129	PHE	-	expression tag	UNP Q96P20
F	106	HIS	-	expression tag	UNP Q96P20
F	107	HIS	-	expression tag	UNP Q96P20
F	108	HIS	-	expression tag	UNP Q96P20
F	109	HIS	-	expression tag	UNP Q96P20
F	110	HIS	-	expression tag	UNP Q96P20
F	111	HIS	-	expression tag	UNP Q96P20
F	112	ASP	-	expression tag	UNP Q96P20
F	113	TYR	-	expression tag	UNP Q96P20
F	114	LYS	-	expression tag	UNP Q96P20
F	115	ASP	-	expression tag	UNP Q96P20
F	116	ASP	-	expression tag	UNP Q96P20
F	117	ASP	-	expression tag	UNP Q96P20
F	118	ASP	-	expression tag	UNP Q96P20
F	119	LYS	-	expression tag	UNP Q96P20
F	120	LEU	-	expression tag	UNP Q96P20
F	121	GLU	-	expression tag	UNP Q96P20
F	122	VAL	-	expression tag	UNP Q96P20
F	123	LEU	-	expression tag	UNP Q96P20
F	124	PHE	-	expression tag	UNP Q96P20
F	125	GLN	-	expression tag	UNP Q96P20
F	126	GLY	-	expression tag	UNP Q96P20
F	127	PRO	-	expression tag	UNP Q96P20
F	128	GLU	-	expression tag	UNP Q96P20
F	129	PHE	-	expression tag	UNP Q96P20

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
2	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
2	B	1	Total	C	N	O	P	0
			27	10	5	10	2	
2	C	1	Total	C	N	O	P	0
			27	10	5	10	2	
2	D	1	Total	C	N	O	P	0
			27	10	5	10	2	
2	E	1	Total	C	N	O	P	0
			27	10	5	10	2	
2	F	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 3 is 1-[4-(2-oxidanylpropan-2-yl)furan-2-yl]sulfonyl-3-(1,2,3,5-tetrahydro-s-indacen-4-yl)urea (CCD ID: 7YN) (formula: $C_{20}H_{22}N_2O_5S$) (labeled as "Ligand of Interest" by depositor).

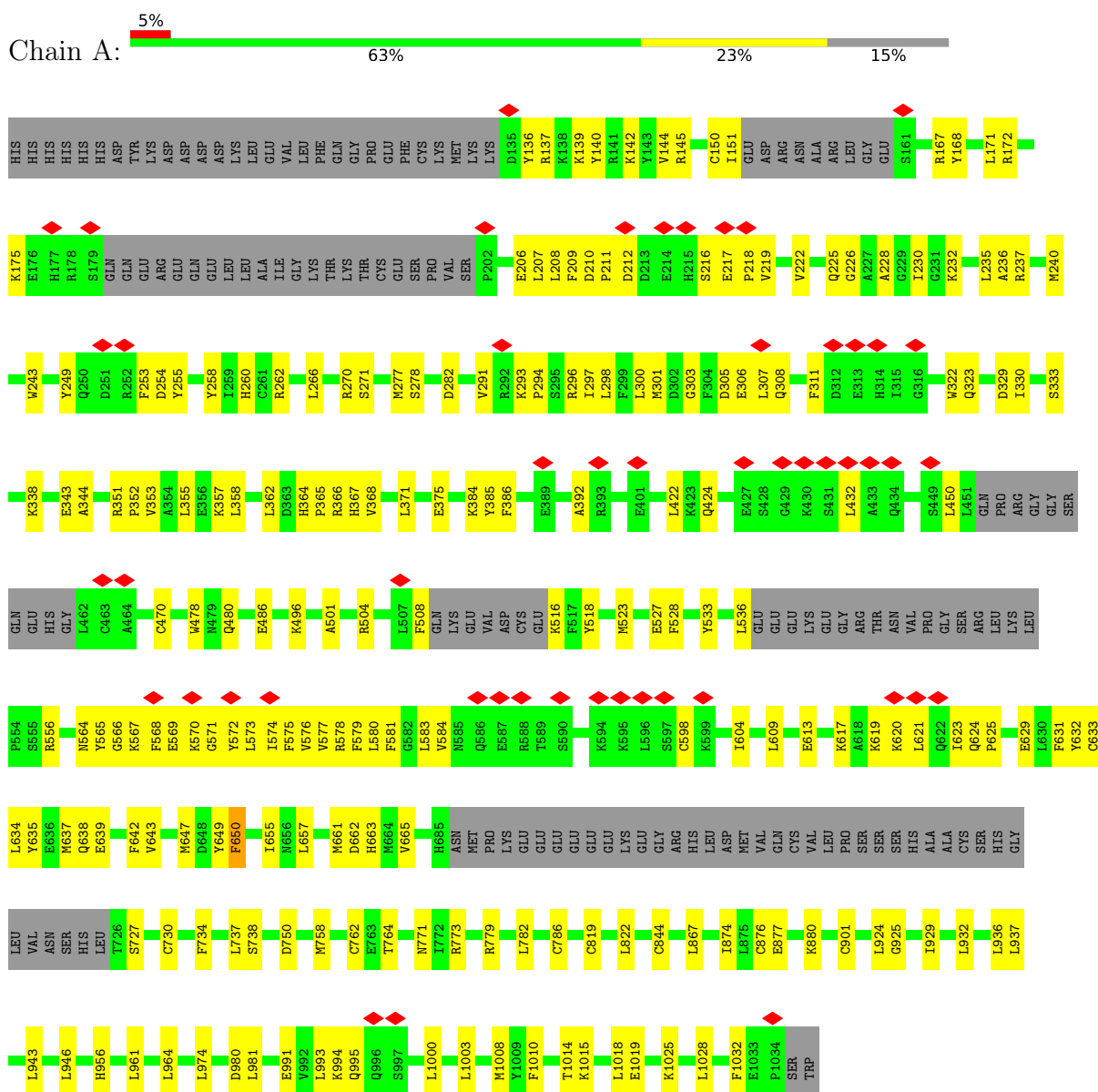


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	S	
3	A	1	Total	C	N	O	S	0
			28	20	2	5	1	
3	B	1	Total	C	N	O	S	0
			28	20	2	5	1	
3	C	1	Total	C	N	O	S	0
			28	20	2	5	1	
3	D	1	Total	C	N	O	S	0
			28	20	2	5	1	
3	E	1	Total	C	N	O	S	0
			28	20	2	5	1	
3	F	1	Total	C	N	O	S	0
			28	20	2	5	1	

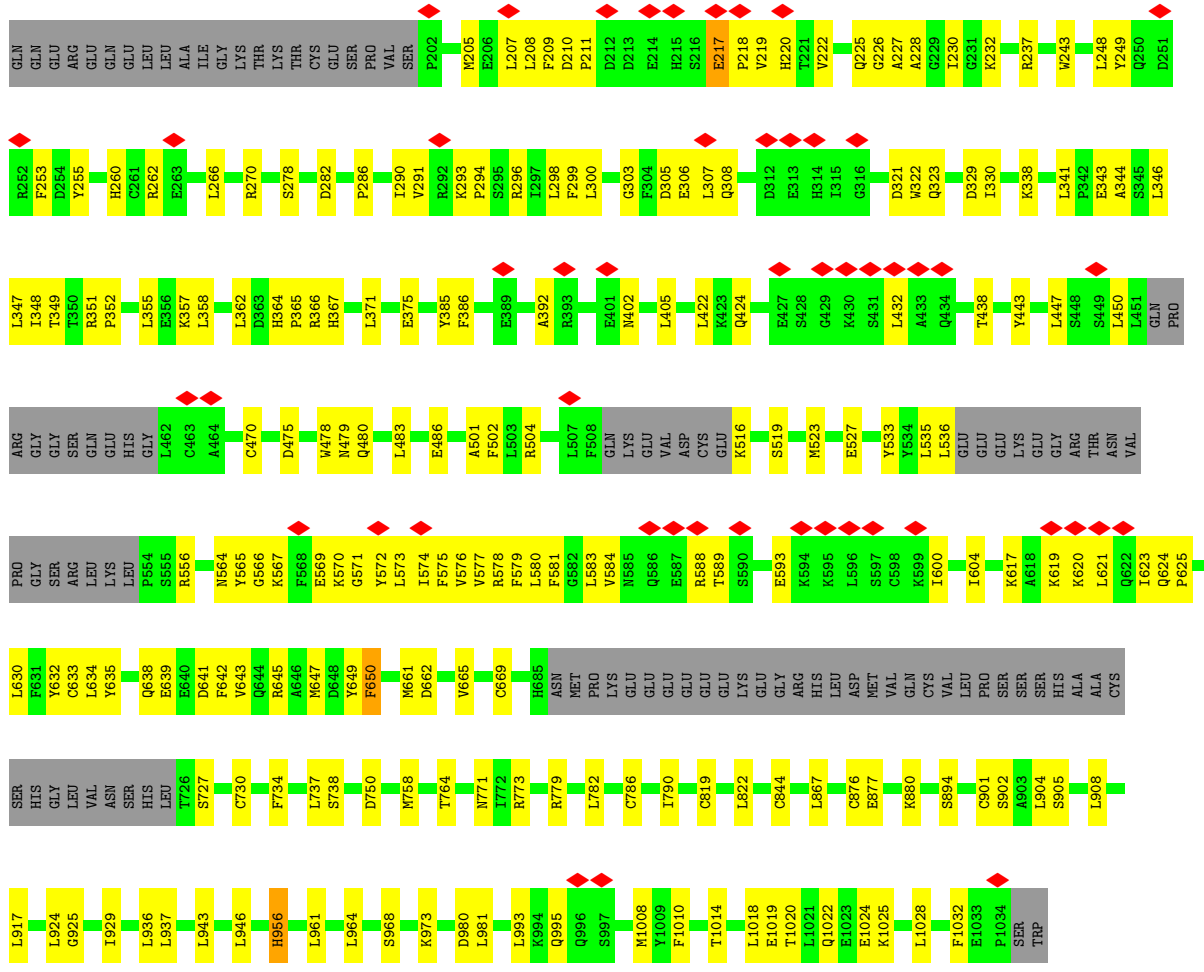
3 Residue-property plots [i](#)

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: NACHT, LRR and PYD domains-containing protein 3



- Molecule 1: NACHT, LRR and PYD domains-containing protein 3



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D3	Depositor
Number of particles used	105139	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	68	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.074	Depositor
Minimum map value	-0.026	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.015	Depositor
Map size (\AA)	249.0, 249.0, 249.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.245, 1.245, 1.245	Depositor

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ADP, 7YN

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.13	0/6457	0.39	2/8704 (0.0%)
1	B	0.15	0/6457	0.36	2/8704 (0.0%)
1	C	0.13	0/6457	0.34	0/8704
1	D	0.13	0/6457	0.39	2/8704 (0.0%)
1	E	0.13	0/6457	0.34	0/8704
1	F	0.13	0/6457	0.34	0/8704
All	All	0.13	0/38742	0.36	6/52224 (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
1	A	0	1
1	B	0	2
1	C	0	2
1	D	0	1
1	E	0	2
1	F	0	2
All	All	0	10

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	216	SER	CA-C-N	13.11	140.61	120.68
1	A	216	SER	C-N-CA	13.11	140.61	120.68
1	D	216	SER	CA-C-N	13.11	140.61	120.68
1	D	216	SER	C-N-CA	13.11	140.61	120.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	218	PRO	CA-N-CD	-6.86	102.40	112.00

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	650	PHE	Peptide
1	B	217	GLU	Peptide
1	B	650	PHE	Peptide
1	C	217	GLU	Peptide
1	C	650	PHE	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6338	0	6401	154	0
1	B	6338	0	6401	145	0
1	C	6338	0	6401	144	0
1	D	6338	0	6401	154	0
1	E	6338	0	6401	145	0
1	F	6338	0	6401	153	0
2	A	27	0	12	1	0
2	B	27	0	12	1	0
2	C	27	0	12	1	0
2	D	27	0	12	1	0
2	E	27	0	12	1	0
2	F	27	0	12	1	0
3	A	28	0	0	0	0
3	B	28	0	0	1	0
3	C	28	0	0	1	0
3	D	28	0	0	0	0
3	E	28	0	0	1	0
3	F	28	0	0	1	0
All	All	38358	0	38478	895	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 12.

The worst 5 of 895 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:A:357:LYS:HE3	1:A:567:LYS:HG2	1.52	0.90
1:D:357:LYS:HE3	1:D:567:LYS:HG2	1.52	0.90
1:F:357:LYS:HE3	1:F:567:LYS:HG2	1.56	0.84
1:B:240:MET:HE2	1:B:258:TYR:HB2	1.61	0.81
1:E:240:MET:HE2	1:E:258:TYR:HB2	1.62	0.80

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	720/843 (85%)	719 (100%)	1 (0%)	88	90
1	B	720/843 (85%)	720 (100%)	0	100	100
1	C	720/843 (85%)	719 (100%)	1 (0%)	88	90
1	D	720/843 (85%)	719 (100%)	1 (0%)	88	90
1	E	720/843 (85%)	720 (100%)	0	100	100
1	F	720/843 (85%)	719 (100%)	1 (0%)	88	90
All	All	4320/5058 (85%)	4316 (100%)	4 (0%)	87	90

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	956	HIS
1	C	956	HIS
1	D	956	HIS
1	F	956	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	220	HIS
1	F	480	GLN
1	F	225	GLN
1	F	323	GLN
1	C	308	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](#)

12 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ADP	D	1501	-	28,29,29	1.39	4 (14%)	43,45,45	1.83	8 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ADP	C	1501	-	28,29,29	1.39	4 (14%)	43,45,45	1.84	8 (18%)
2	ADP	E	1501	-	28,29,29	1.39	4 (14%)	43,45,45	1.83	8 (18%)
3	7YN	A	1502	-	28,31,31	1.95	5 (17%)	33,48,48	2.06	10 (30%)
3	7YN	B	1502	-	28,31,31	1.91	5 (17%)	33,48,48	2.05	11 (33%)
3	7YN	C	1502	-	28,31,31	1.87	5 (17%)	33,48,48	2.08	11 (33%)
2	ADP	B	1501	-	28,29,29	1.39	4 (14%)	43,45,45	1.83	8 (18%)
3	7YN	F	1502	-	28,31,31	1.89	5 (17%)	33,48,48	2.07	12 (36%)
3	7YN	D	1502	-	28,31,31	1.95	5 (17%)	33,48,48	2.07	10 (30%)
3	7YN	E	1502	-	28,31,31	1.88	5 (17%)	33,48,48	2.05	11 (33%)
2	ADP	A	1501	-	28,29,29	1.40	4 (14%)	43,45,45	1.84	8 (18%)
2	ADP	F	1501	-	28,29,29	1.39	4 (14%)	43,45,45	1.84	8 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ADP	D	1501	-	-	3/16/32/32	0/3/3/3
2	ADP	C	1501	-	-	2/16/32/32	0/3/3/3
2	ADP	E	1501	-	-	3/16/32/32	0/3/3/3
3	7YN	A	1502	-	-	5/19/33/33	0/4/4/4
3	7YN	B	1502	-	-	5/19/33/33	0/4/4/4
3	7YN	C	1502	-	-	5/19/33/33	0/4/4/4
2	ADP	B	1501	-	-	2/16/32/32	0/3/3/3
3	7YN	F	1502	-	-	5/19/33/33	0/4/4/4
3	7YN	D	1502	-	-	5/19/33/33	0/4/4/4
3	7YN	E	1502	-	-	5/19/33/33	0/4/4/4
2	ADP	A	1501	-	-	2/16/32/32	0/3/3/3
2	ADP	F	1501	-	-	3/16/32/32	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1502	7YN	S17-N15	6.28	1.70	1.64
3	A	1502	7YN	S17-N15	6.21	1.70	1.64
3	B	1502	7YN	S17-N15	5.96	1.69	1.64

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	1502	7YN	S17-N15	5.90	1.69	1.64
3	E	1502	7YN	S17-N15	5.84	1.69	1.64

The worst 5 of 113 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1501	ADP	C5-C4-N3	-5.94	118.54	126.72
2	C	1501	ADP	C5-C4-N3	-5.90	118.59	126.72
2	F	1501	ADP	C5-C4-N3	-5.90	118.59	126.72
2	D	1501	ADP	C5-C4-N3	-5.89	118.61	126.72
2	E	1501	ADP	C5-C4-N3	-5.88	118.62	126.72

There are no chirality outliers.

5 of 45 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1501	ADP	C5'-O5'-PA-O1A
2	E	1501	ADP	C5'-O5'-PA-O1A
2	F	1501	ADP	C5'-O5'-PA-O1A
3	A	1502	7YN	C20-C19-S17-N15
3	B	1502	7YN	C20-C19-S17-N15

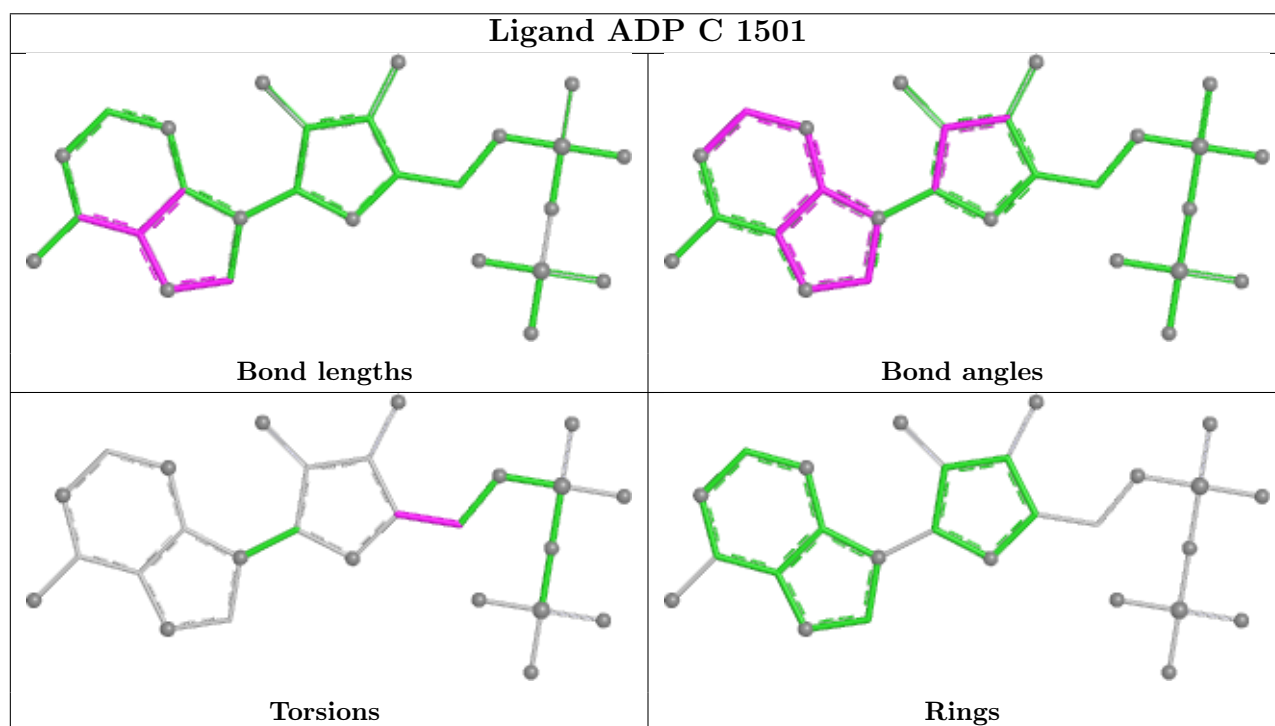
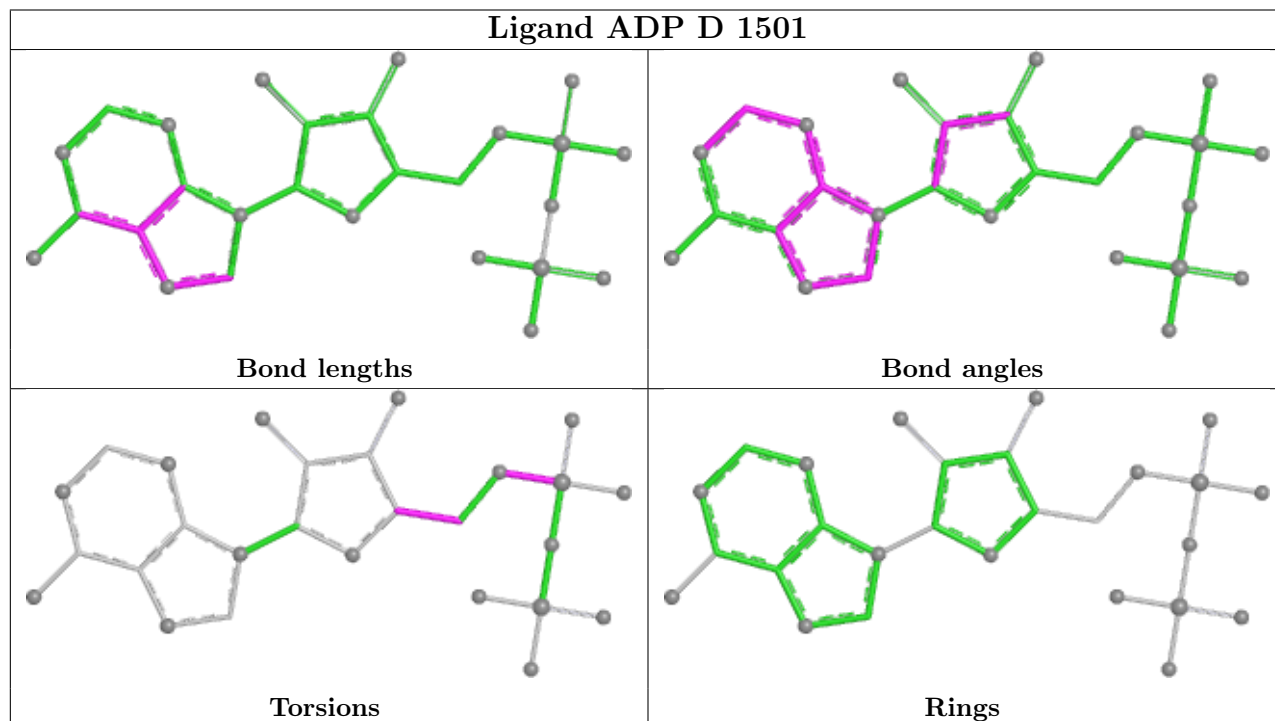
There are no ring outliers.

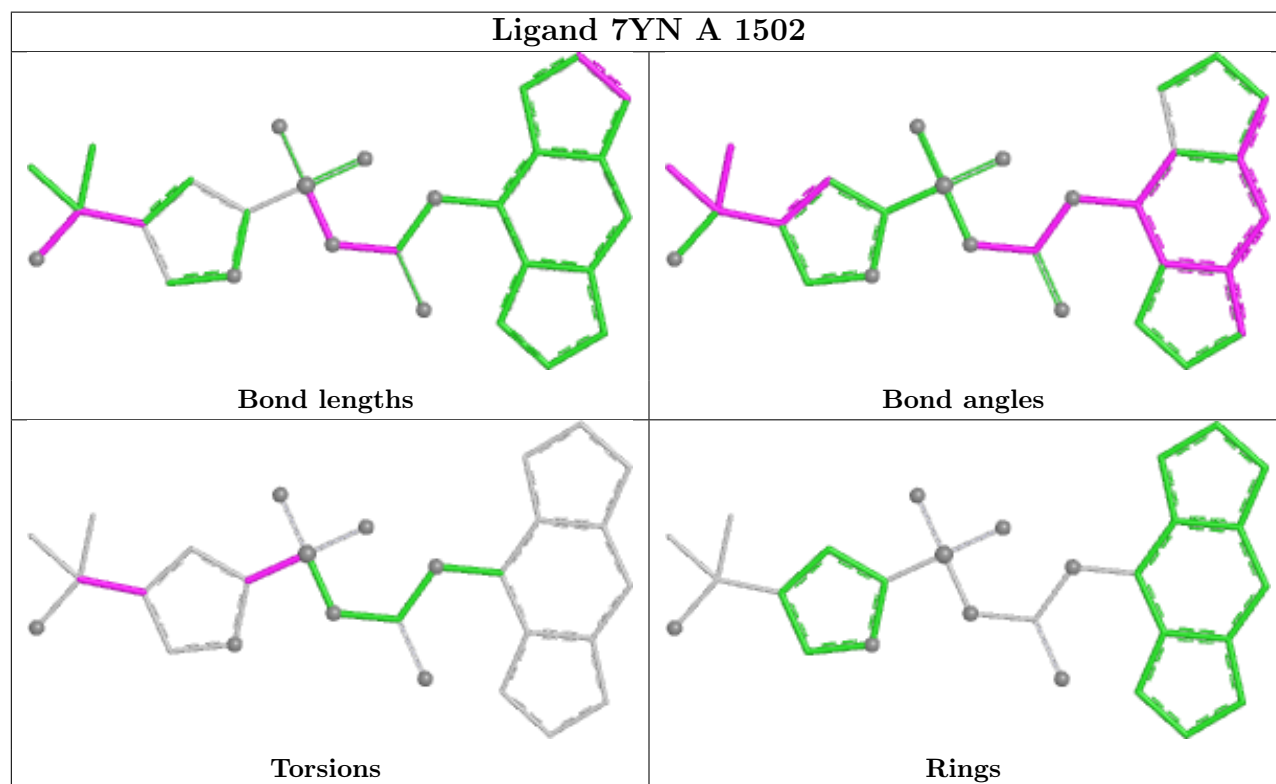
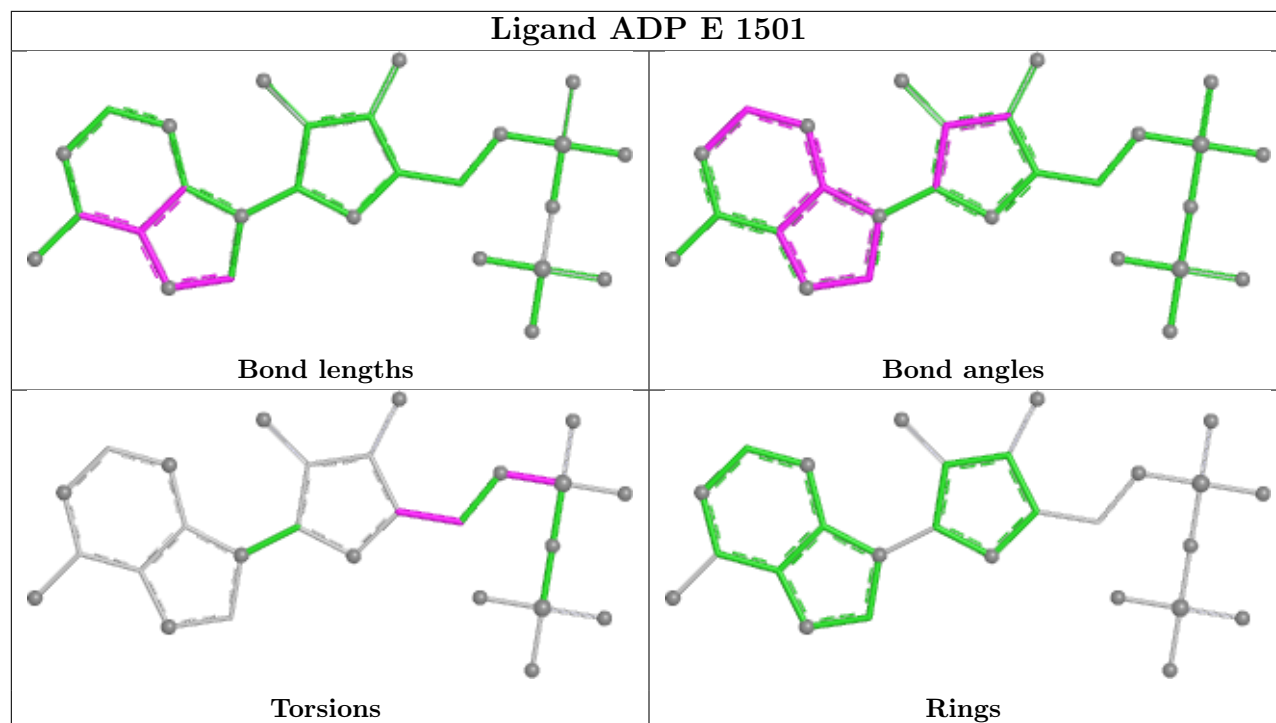
10 monomers are involved in 10 short contacts:

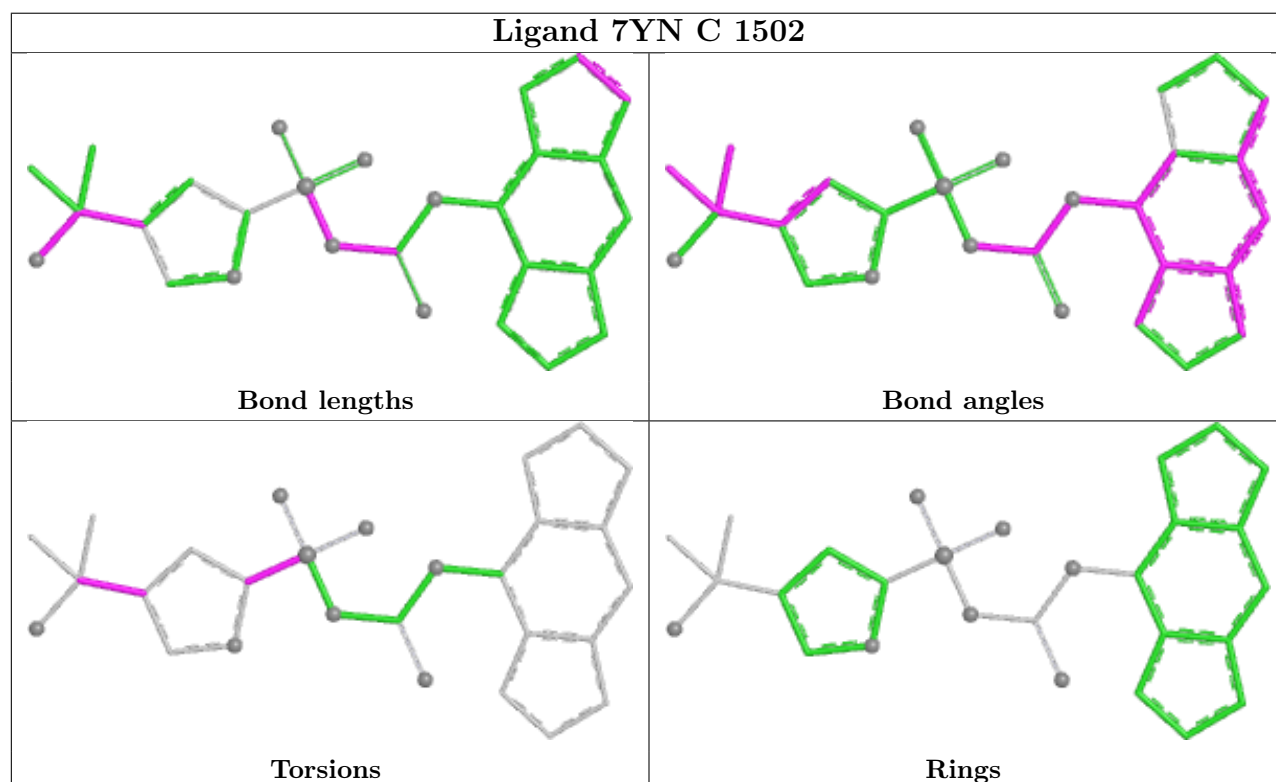
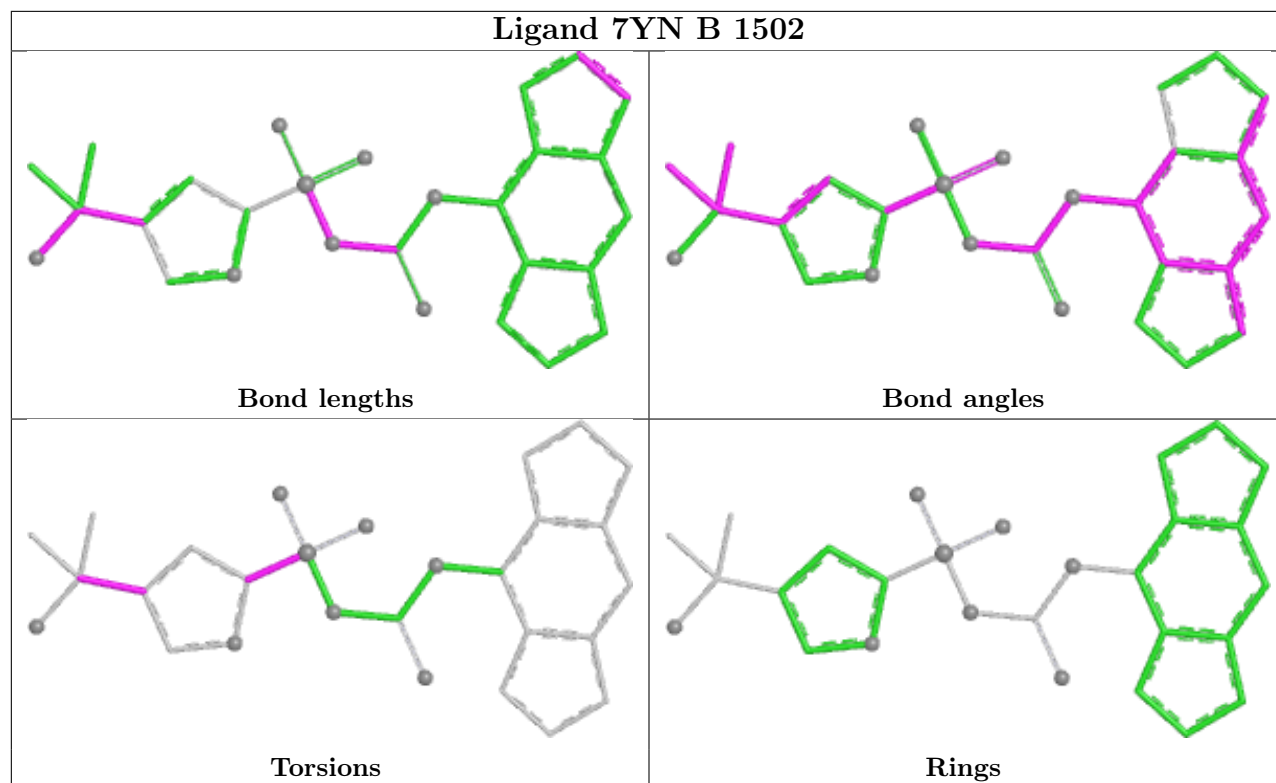
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1501	ADP	1	0
2	C	1501	ADP	1	0
2	E	1501	ADP	1	0
3	B	1502	7YN	1	0
3	C	1502	7YN	1	0
2	B	1501	ADP	1	0
3	F	1502	7YN	1	0
3	E	1502	7YN	1	0
2	A	1501	ADP	1	0
2	F	1501	ADP	1	0

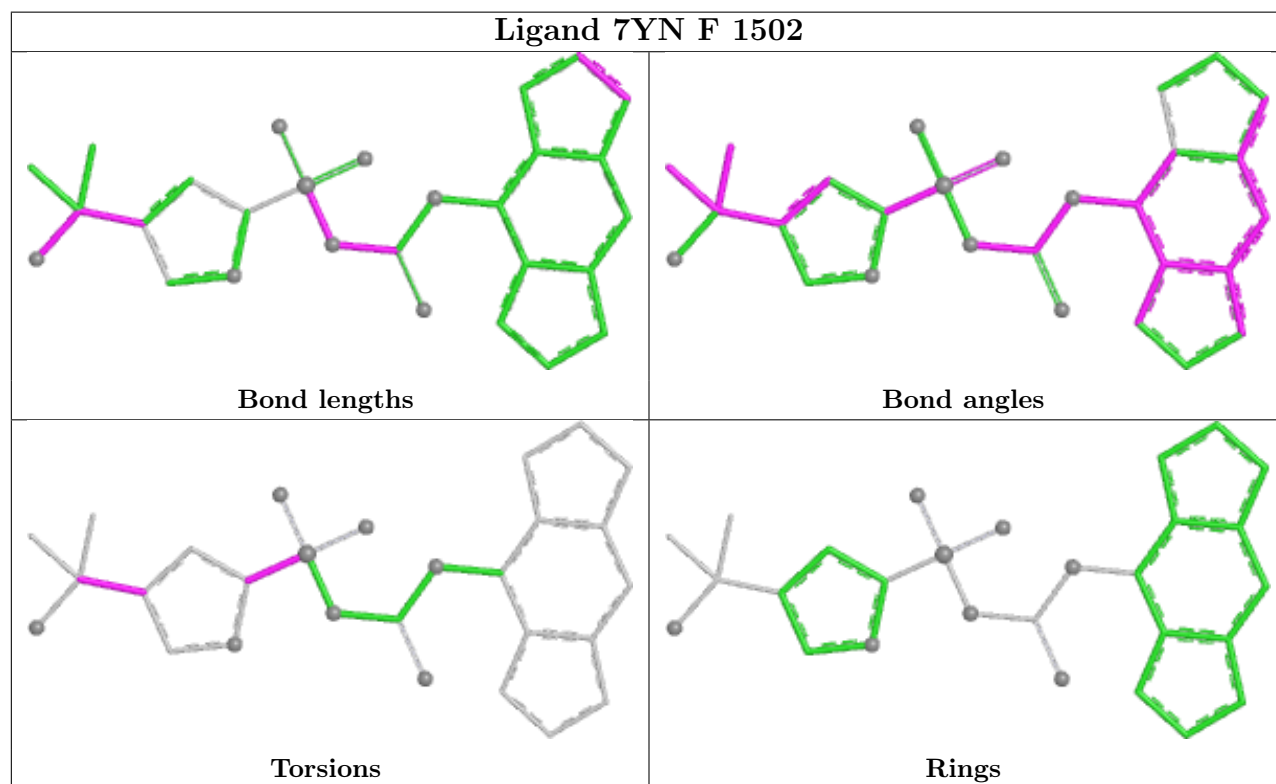
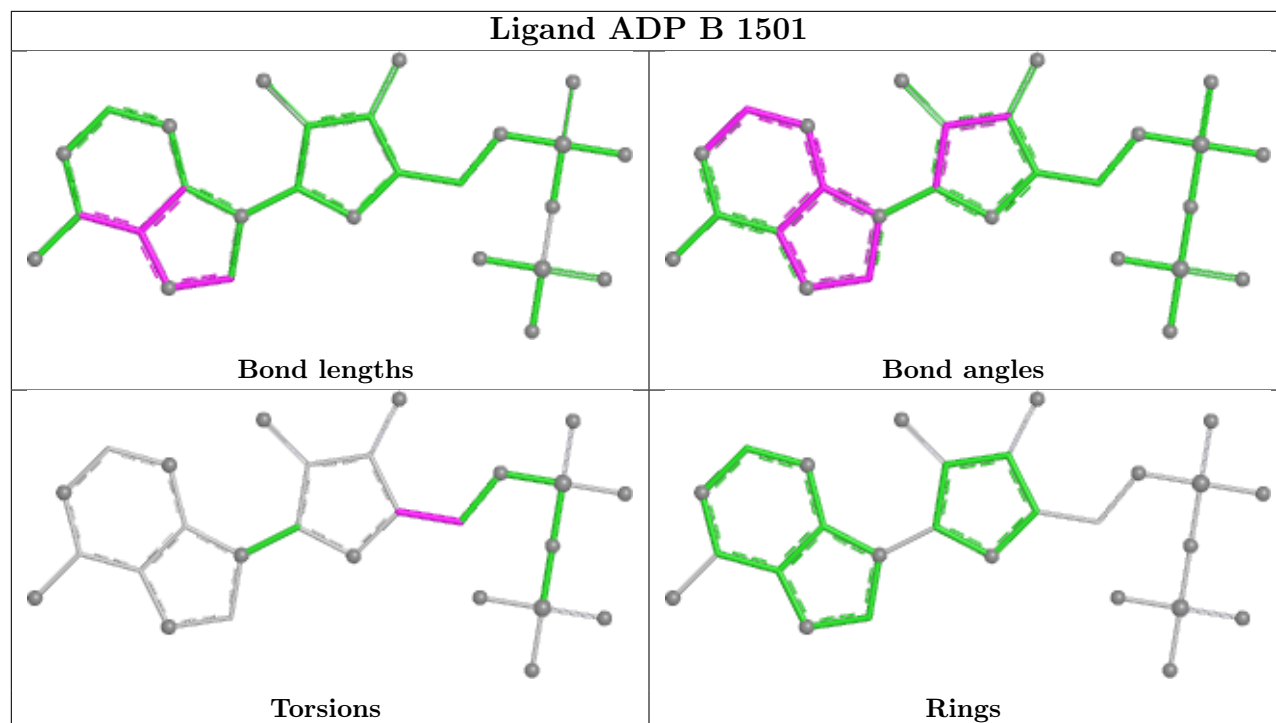
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

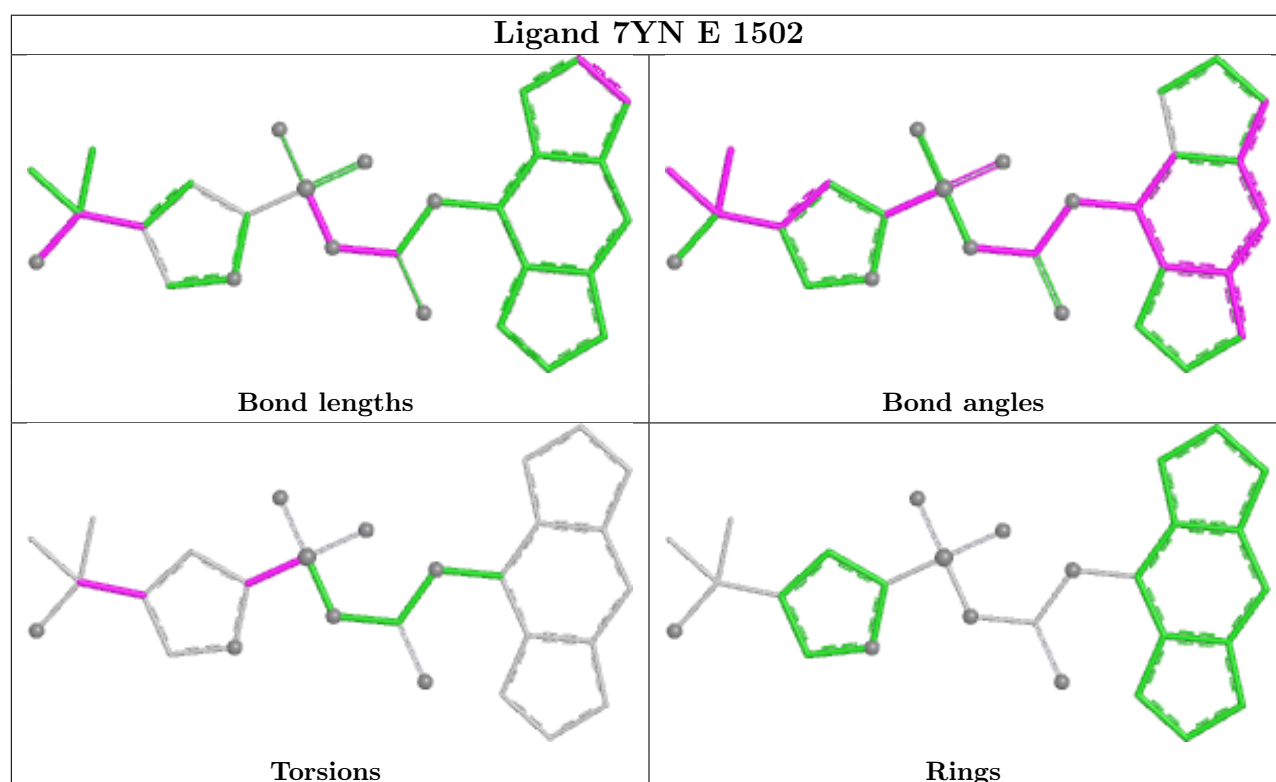
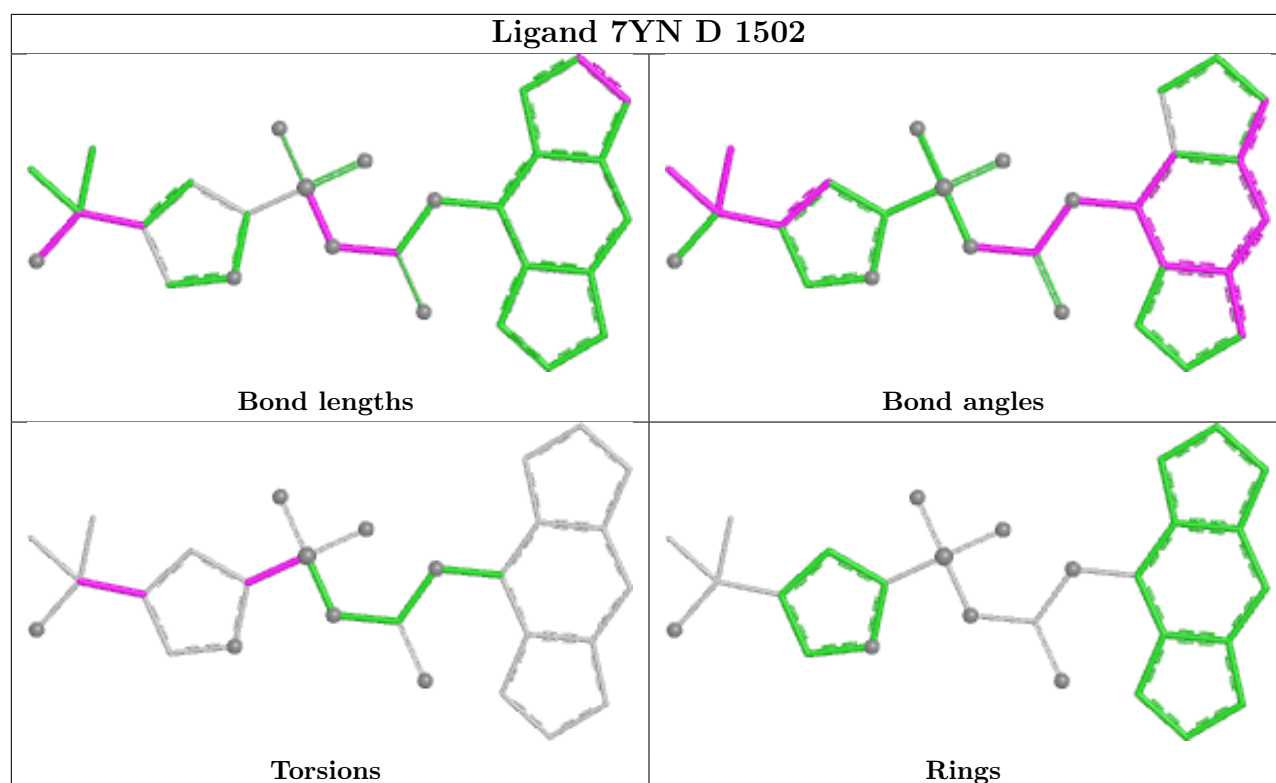
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

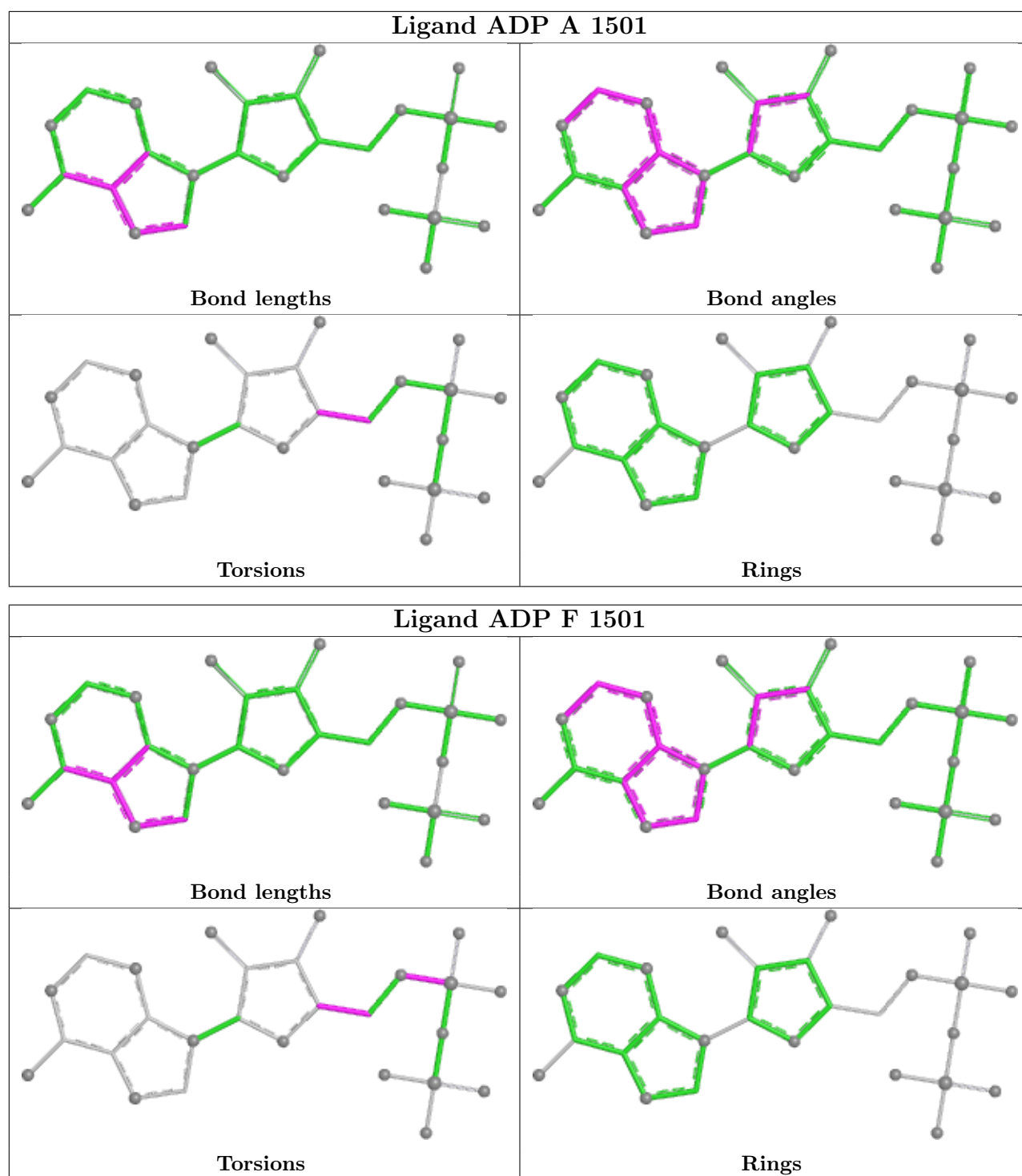












5.7 Other polymers [\(i\)](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

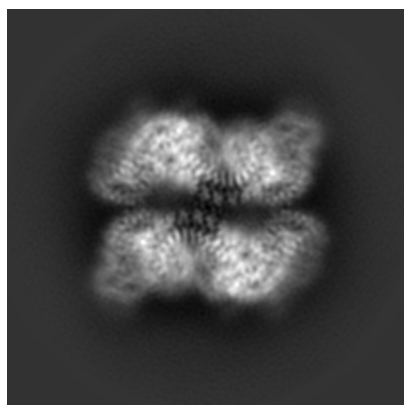
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32119. These allow visual inspection of the internal detail of the map and identification of artifacts.

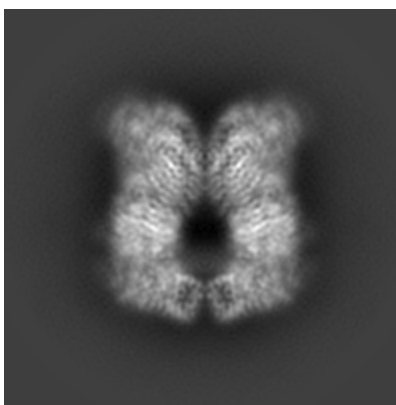
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

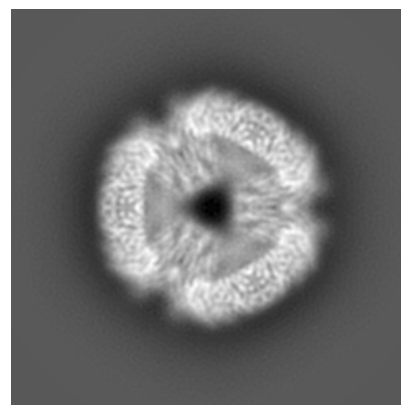
6.1.1 Primary map



X



Y

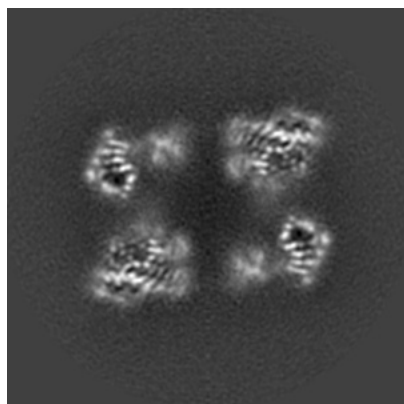


Z

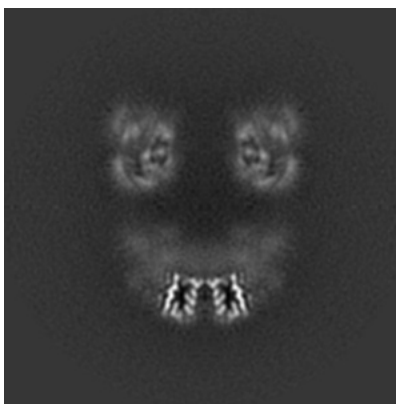
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

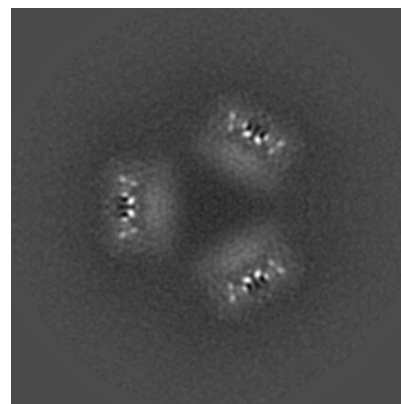
6.2.1 Primary map



X Index: 100



Y Index: 100

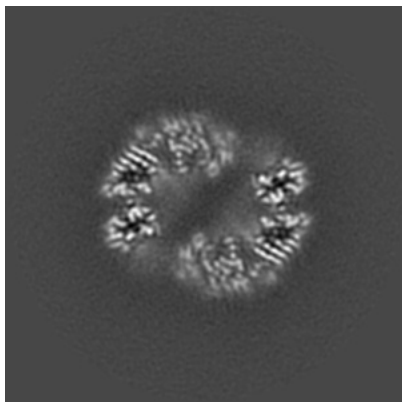


Z Index: 100

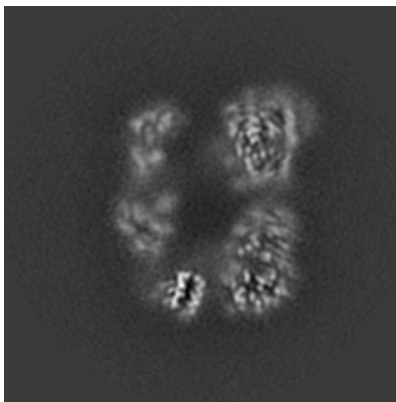
The images above show central slices of the map in three orthogonal directions.

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

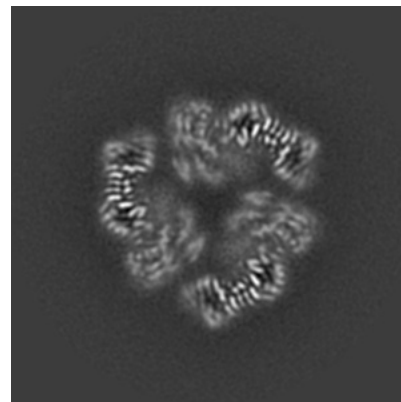
6.3.1 Primary map



X Index: 126



Y Index: 88

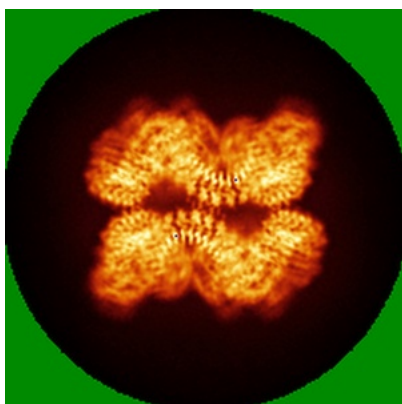


Z Index: 117

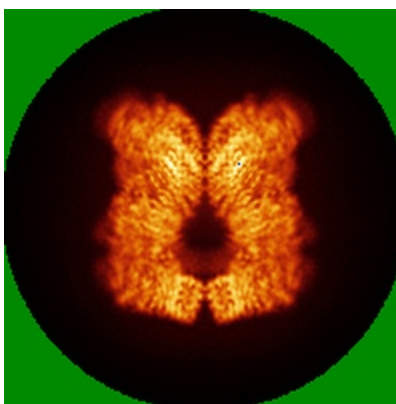
The images above show the largest variance slices of the map in three orthogonal directions.

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

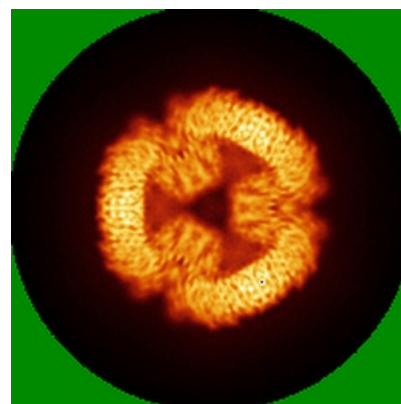
6.4.1 Primary map



X



Y

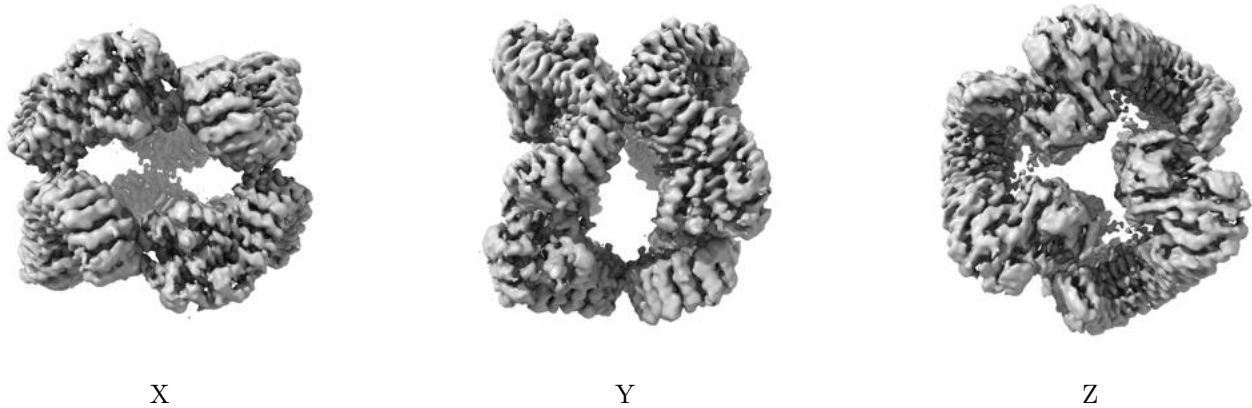


Z

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 0.015. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

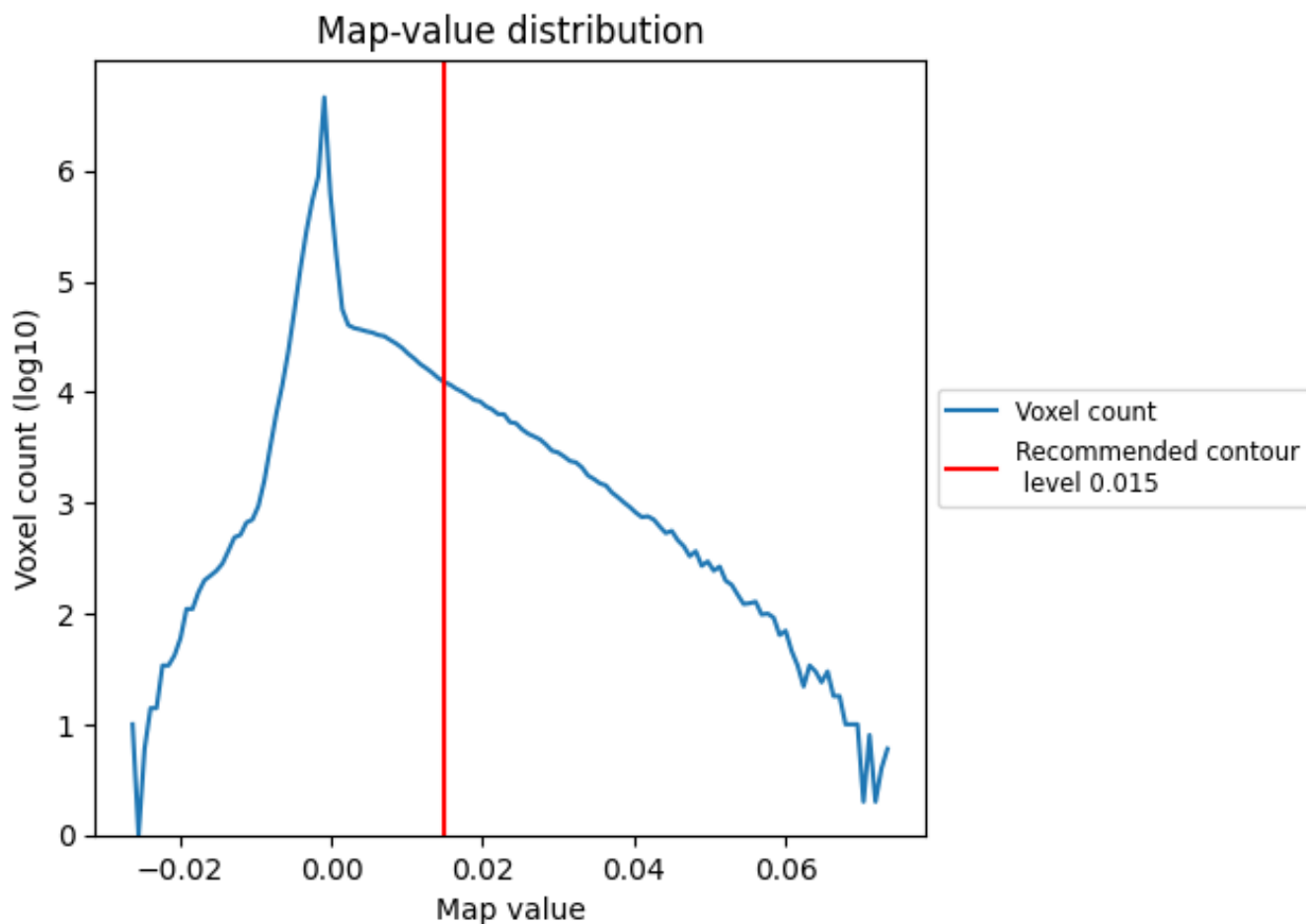
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

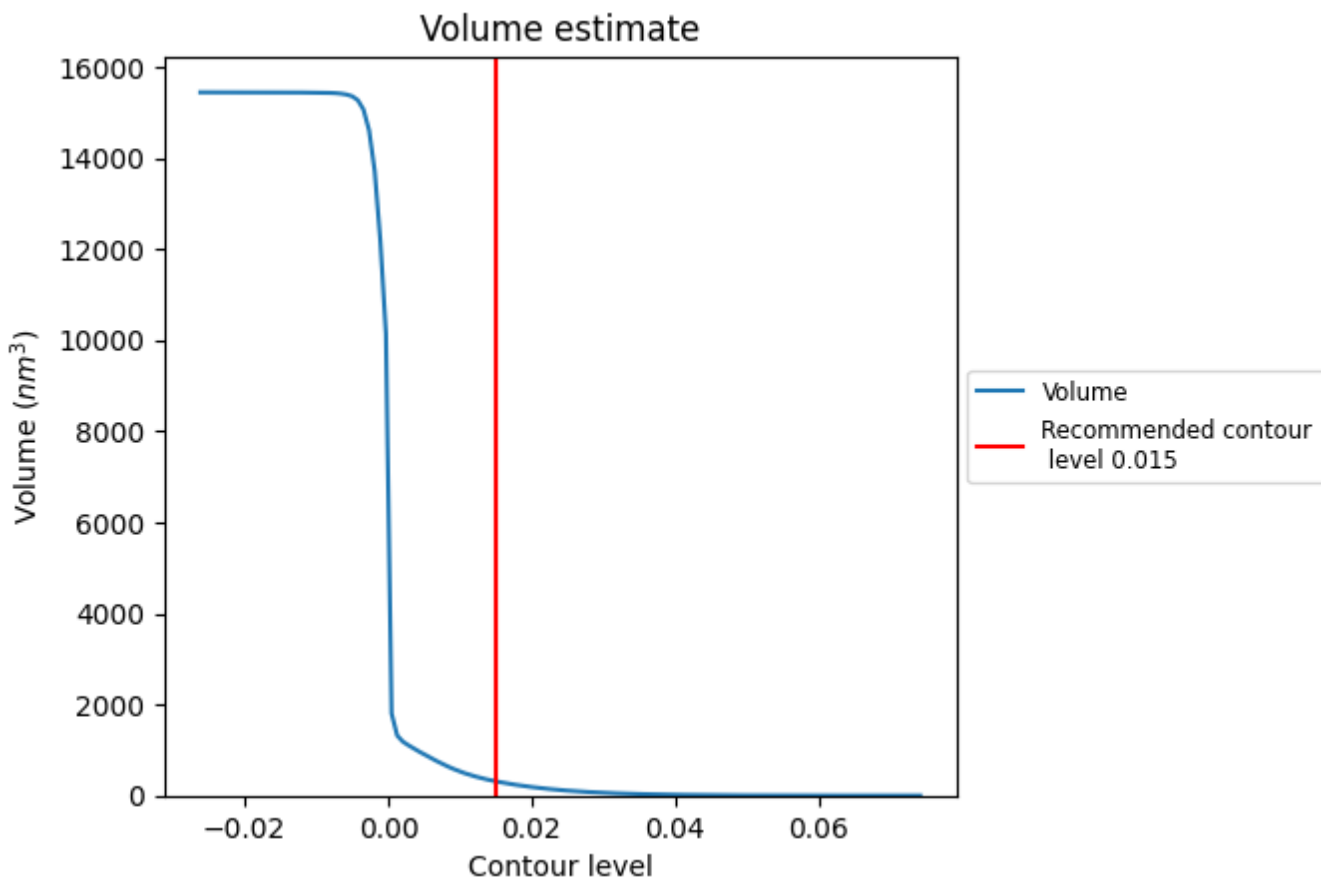
This section contains the results of statistical analysis of the map.

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.

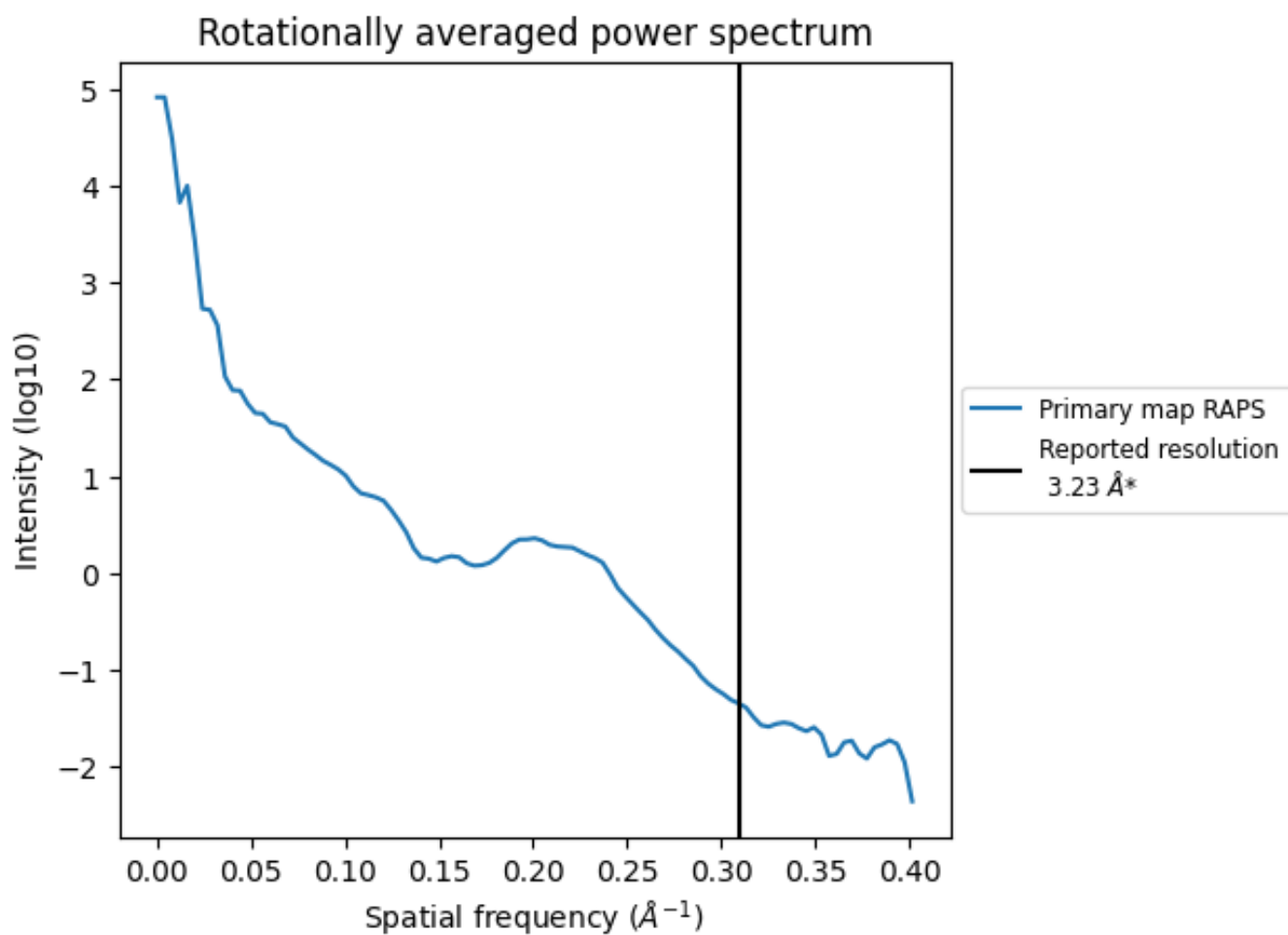
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 313 nm³; this corresponds to an approximate mass of 283 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 0.310 Å⁻¹

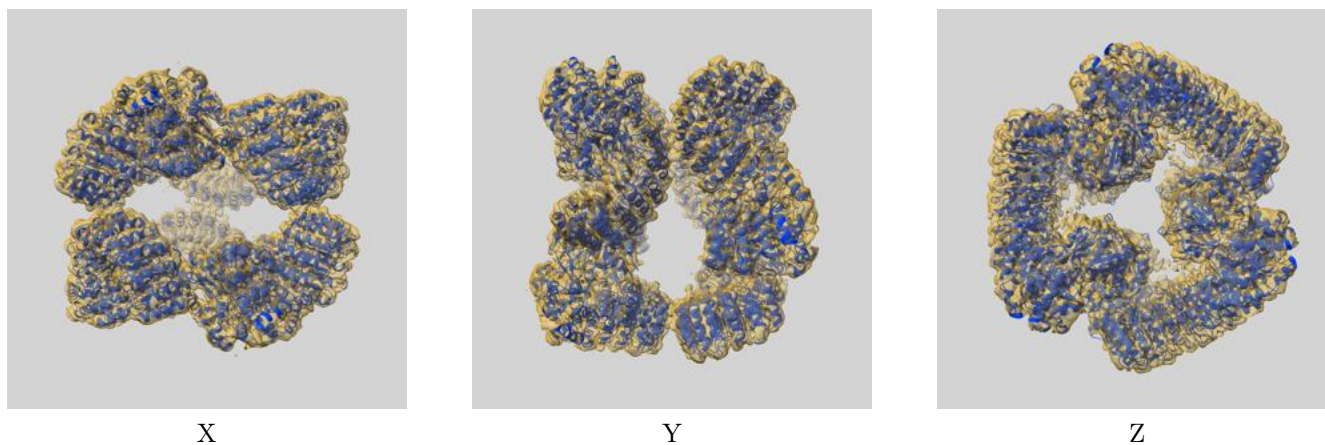
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

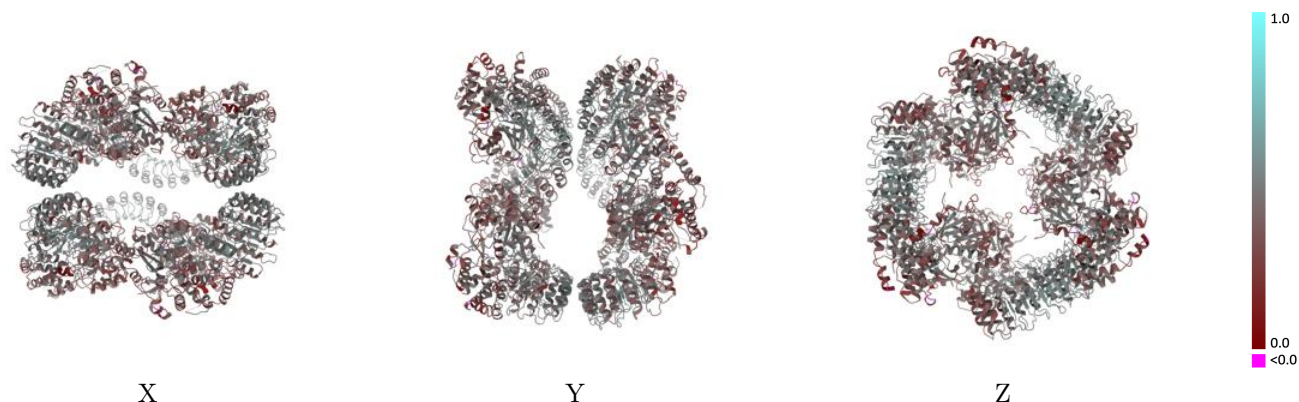
This section contains information regarding the fit between EMDB map EMD-32119 and PDB model 7VTP. Per-residue inclusion information can be found in section 3 on page 10.

9.1 Map-model overlay [i](#)



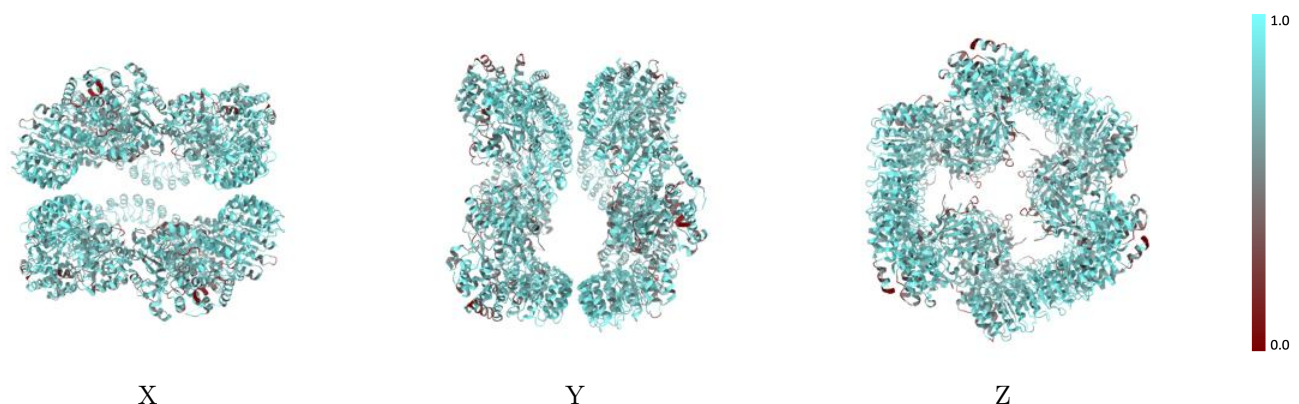
The images above show the 3D surface view of the map at the recommended contour level 0.015 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



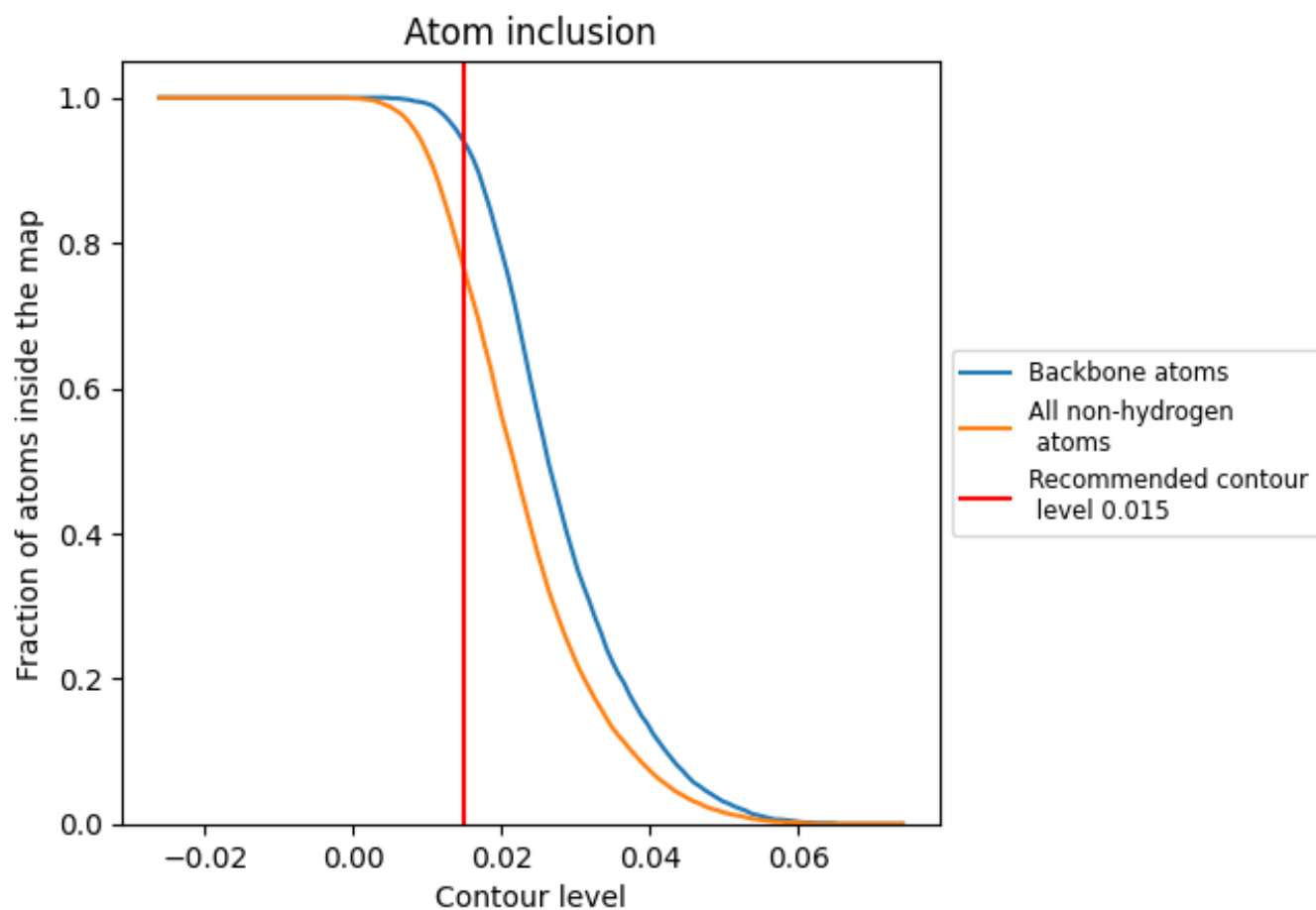
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.015).















9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 76% 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 (0.015) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7620	 0.4040
A	 0.7620	 0.4040
B	 0.7640	 0.4040
C	 0.7620	 0.4040
D	 0.7620	 0.4040
E	 0.7620	 0.4040
F	 0.7600	 0.4040

