



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 02:26 PM EDT

PDB ID : 6EY2  
Title : Crystal structure of XIAP-BIR3 in complex with a cIAP1-selective SM  
Authors : Cossu, F.; Corti, A.; Milani, M.; Mastrangelo, E.  
Deposited on : 2017-11-10  
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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/XrayValidationReportHelp>

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:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.37.1  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.37.1

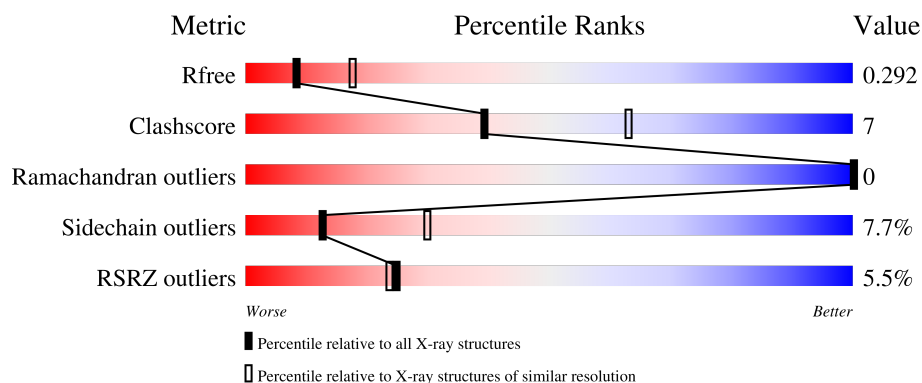
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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.



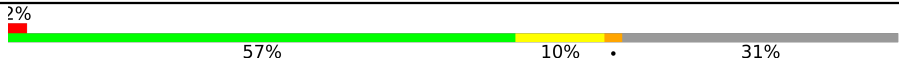
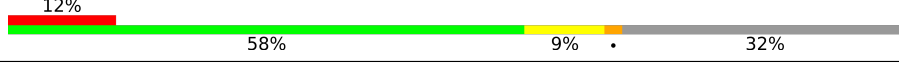
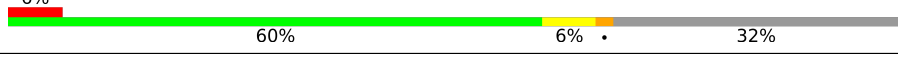
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	146	<div> <div>%</div> <div> <div></div> <div>52%</div> <div>14%</div> <div>.</div> <div>32%</div> </div> </div>
1	B	146	<div> <div>3%</div> <div> <div></div> <div>54%</div> <div>11%</div> <div>.</div> <div>33%</div> </div> </div>
1	C	146	<div> <div>3%</div> <div> <div></div> <div>52%</div> <div>14%</div> <div>.</div> <div>32%</div> </div> </div>
1	D	146	<div> <div>%</div> <div> <div></div> <div>55%</div> <div>13%</div> <div>.</div> <div>31%</div> </div> </div>
1	E	146	<div> <div>%</div> <div> <div></div> <div>56%</div> <div>10%</div> <div>.</div> <div>32%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	146	 2% 57% 10% 31%
1	G	146	 12% 58% 9% 32%
1	H	146	 6% 60% 6% 32%

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6885 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 E3 ubiquitin-protein ligase XIAP.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	99	Total	C	N	O	S	0	1	0
			815	522	139	149	5			
1	B	98	Total	C	N	O	S	0	0	0
			799	511	135	148	5			
1	C	99	Total	C	N	O	S	0	0	0
			807	517	136	149	5			
1	D	101	Total	C	N	O	S	0	1	0
			825	529	138	153	5			
1	E	100	Total	C	N	O	S	0	0	0
			813	520	137	151	5			
1	F	101	Total	C	N	O	S	0	1	0
			825	529	138	153	5			
1	G	100	Total	C	N	O	S	0	1	0
			821	527	139	150	5			
1	H	99	Total	C	N	O	S	0	0	0
			807	517	136	149	5			

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	211	HIS	-	expression tag	UNP P98170
A	212	HIS	-	expression tag	UNP P98170
A	213	HIS	-	expression tag	UNP P98170
A	214	HIS	-	expression tag	UNP P98170
A	215	HIS	-	expression tag	UNP P98170
A	216	HIS	-	expression tag	UNP P98170
A	217	SER	-	expression tag	UNP P98170
A	218	SER	-	expression tag	UNP P98170
A	219	GLY	-	expression tag	UNP P98170
A	220	LEU	-	expression tag	UNP P98170
A	221	VAL	-	expression tag	UNP P98170
A	222	PRO	-	expression tag	UNP P98170
A	223	ARG	-	expression tag	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
A	224	GLY	-	expression tag	UNP P98170
A	225	SER	-	expression tag	UNP P98170
A	226	HIS	-	expression tag	UNP P98170
A	227	MET	-	expression tag	UNP P98170
A	228	ALA	-	expression tag	UNP P98170
A	229	SER	-	expression tag	UNP P98170
A	230	MET	-	expression tag	UNP P98170
A	231	THR	-	expression tag	UNP P98170
A	232	GLY	-	expression tag	UNP P98170
A	233	GLY	-	expression tag	UNP P98170
A	234	GLN	-	expression tag	UNP P98170
A	235	GLN	-	expression tag	UNP P98170
A	236	MET	-	expression tag	UNP P98170
A	237	GLY	-	expression tag	UNP P98170
A	238	ARG	-	expression tag	UNP P98170
A	239	GLY	-	expression tag	UNP P98170
A	240	SER	-	expression tag	UNP P98170
B	211	HIS	-	expression tag	UNP P98170
B	212	HIS	-	expression tag	UNP P98170
B	213	HIS	-	expression tag	UNP P98170
B	214	HIS	-	expression tag	UNP P98170
B	215	HIS	-	expression tag	UNP P98170
B	216	HIS	-	expression tag	UNP P98170
B	217	SER	-	expression tag	UNP P98170
B	218	SER	-	expression tag	UNP P98170
B	219	GLY	-	expression tag	UNP P98170
B	220	LEU	-	expression tag	UNP P98170
B	221	VAL	-	expression tag	UNP P98170
B	222	PRO	-	expression tag	UNP P98170
B	223	ARG	-	expression tag	UNP P98170
B	224	GLY	-	expression tag	UNP P98170
B	225	SER	-	expression tag	UNP P98170
B	226	HIS	-	expression tag	UNP P98170
B	227	MET	-	expression tag	UNP P98170
B	228	ALA	-	expression tag	UNP P98170
B	229	SER	-	expression tag	UNP P98170
B	230	MET	-	expression tag	UNP P98170
B	231	THR	-	expression tag	UNP P98170
B	232	GLY	-	expression tag	UNP P98170
B	233	GLY	-	expression tag	UNP P98170
B	234	GLN	-	expression tag	UNP P98170
B	235	GLN	-	expression tag	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
B	236	MET	-	expression tag	UNP P98170
B	237	GLY	-	expression tag	UNP P98170
B	238	ARG	-	expression tag	UNP P98170
B	239	GLY	-	expression tag	UNP P98170
B	240	SER	-	expression tag	UNP P98170
C	211	HIS	-	expression tag	UNP P98170
C	212	HIS	-	expression tag	UNP P98170
C	213	HIS	-	expression tag	UNP P98170
C	214	HIS	-	expression tag	UNP P98170
C	215	HIS	-	expression tag	UNP P98170
C	216	HIS	-	expression tag	UNP P98170
C	217	SER	-	expression tag	UNP P98170
C	218	SER	-	expression tag	UNP P98170
C	219	GLY	-	expression tag	UNP P98170
C	220	LEU	-	expression tag	UNP P98170
C	221	VAL	-	expression tag	UNP P98170
C	222	PRO	-	expression tag	UNP P98170
C	223	ARG	-	expression tag	UNP P98170
C	224	GLY	-	expression tag	UNP P98170
C	225	SER	-	expression tag	UNP P98170
C	226	HIS	-	expression tag	UNP P98170
C	227	MET	-	expression tag	UNP P98170
C	228	ALA	-	expression tag	UNP P98170
C	229	SER	-	expression tag	UNP P98170
C	230	MET	-	expression tag	UNP P98170
C	231	THR	-	expression tag	UNP P98170
C	232	GLY	-	expression tag	UNP P98170
C	233	GLY	-	expression tag	UNP P98170
C	234	GLN	-	expression tag	UNP P98170
C	235	GLN	-	expression tag	UNP P98170
C	236	MET	-	expression tag	UNP P98170
C	237	GLY	-	expression tag	UNP P98170
C	238	ARG	-	expression tag	UNP P98170
C	239	GLY	-	expression tag	UNP P98170
C	240	SER	-	expression tag	UNP P98170
D	211	HIS	-	expression tag	UNP P98170
D	212	HIS	-	expression tag	UNP P98170
D	213	HIS	-	expression tag	UNP P98170
D	214	HIS	-	expression tag	UNP P98170
D	215	HIS	-	expression tag	UNP P98170
D	216	HIS	-	expression tag	UNP P98170
D	217	SER	-	expression tag	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
D	218	SER	-	expression tag	UNP P98170
D	219	GLY	-	expression tag	UNP P98170
D	220	LEU	-	expression tag	UNP P98170
D	221	VAL	-	expression tag	UNP P98170
D	222	PRO	-	expression tag	UNP P98170
D	223	ARG	-	expression tag	UNP P98170
D	224	GLY	-	expression tag	UNP P98170
D	225	SER	-	expression tag	UNP P98170
D	226	HIS	-	expression tag	UNP P98170
D	227	MET	-	expression tag	UNP P98170
D	228	ALA	-	expression tag	UNP P98170
D	229	SER	-	expression tag	UNP P98170
D	230	MET	-	expression tag	UNP P98170
D	231	THR	-	expression tag	UNP P98170
D	232	GLY	-	expression tag	UNP P98170
D	233	GLY	-	expression tag	UNP P98170
D	234	GLN	-	expression tag	UNP P98170
D	235	GLN	-	expression tag	UNP P98170
D	236	MET	-	expression tag	UNP P98170
D	237	GLY	-	expression tag	UNP P98170
D	238	ARG	-	expression tag	UNP P98170
D	239	GLY	-	expression tag	UNP P98170
D	240	SER	-	expression tag	UNP P98170
E	211	HIS	-	expression tag	UNP P98170
E	212	HIS	-	expression tag	UNP P98170
E	213	HIS	-	expression tag	UNP P98170
E	214	HIS	-	expression tag	UNP P98170
E	215	HIS	-	expression tag	UNP P98170
E	216	HIS	-	expression tag	UNP P98170
E	217	SER	-	expression tag	UNP P98170
E	218	SER	-	expression tag	UNP P98170
E	219	GLY	-	expression tag	UNP P98170
E	220	LEU	-	expression tag	UNP P98170
E	221	VAL	-	expression tag	UNP P98170
E	222	PRO	-	expression tag	UNP P98170
E	223	ARG	-	expression tag	UNP P98170
E	224	GLY	-	expression tag	UNP P98170
E	225	SER	-	expression tag	UNP P98170
E	226	HIS	-	expression tag	UNP P98170
E	227	MET	-	expression tag	UNP P98170
E	228	ALA	-	expression tag	UNP P98170
E	229	SER	-	expression tag	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
E	230	MET	-	expression tag	UNP P98170
E	231	THR	-	expression tag	UNP P98170
E	232	GLY	-	expression tag	UNP P98170
E	233	GLY	-	expression tag	UNP P98170
E	234	GLN	-	expression tag	UNP P98170
E	235	GLN	-	expression tag	UNP P98170
E	236	MET	-	expression tag	UNP P98170
E	237	GLY	-	expression tag	UNP P98170
E	238	ARG	-	expression tag	UNP P98170
E	239	GLY	-	expression tag	UNP P98170
E	240	SER	-	expression tag	UNP P98170
F	211	HIS	-	expression tag	UNP P98170
F	212	HIS	-	expression tag	UNP P98170
F	213	HIS	-	expression tag	UNP P98170
F	214	HIS	-	expression tag	UNP P98170
F	215	HIS	-	expression tag	UNP P98170
F	216	HIS	-	expression tag	UNP P98170
F	217	SER	-	expression tag	UNP P98170
F	218	SER	-	expression tag	UNP P98170
F	219	GLY	-	expression tag	UNP P98170
F	220	LEU	-	expression tag	UNP P98170
F	221	VAL	-	expression tag	UNP P98170
F	222	PRO	-	expression tag	UNP P98170
F	223	ARG	-	expression tag	UNP P98170
F	224	GLY	-	expression tag	UNP P98170
F	225	SER	-	expression tag	UNP P98170
F	226	HIS	-	expression tag	UNP P98170
F	227	MET	-	expression tag	UNP P98170
F	228	ALA	-	expression tag	UNP P98170
F	229	SER	-	expression tag	UNP P98170
F	230	MET	-	expression tag	UNP P98170
F	231	THR	-	expression tag	UNP P98170
F	232	GLY	-	expression tag	UNP P98170
F	233	GLY	-	expression tag	UNP P98170
F	234	GLN	-	expression tag	UNP P98170
F	235	GLN	-	expression tag	UNP P98170
F	236	MET	-	expression tag	UNP P98170
F	237	GLY	-	expression tag	UNP P98170
F	238	ARG	-	expression tag	UNP P98170
F	239	GLY	-	expression tag	UNP P98170
F	240	SER	-	expression tag	UNP P98170
G	211	HIS	-	expression tag	UNP P98170

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Chain	Residue	Modelled	Actual	Comment	Reference
G	212	HIS	-	expression tag	UNP P98170
G	213	HIS	-	expression tag	UNP P98170
G	214	HIS	-	expression tag	UNP P98170
G	215	HIS	-	expression tag	UNP P98170
G	216	HIS	-	expression tag	UNP P98170
G	217	SER	-	expression tag	UNP P98170
G	218	SER	-	expression tag	UNP P98170
G	219	GLY	-	expression tag	UNP P98170
G	220	LEU	-	expression tag	UNP P98170
G	221	VAL	-	expression tag	UNP P98170
G	222	PRO	-	expression tag	UNP P98170
G	223	ARG	-	expression tag	UNP P98170
G	224	GLY	-	expression tag	UNP P98170
G	225	SER	-	expression tag	UNP P98170
G	226	HIS	-	expression tag	UNP P98170
G	227	MET	-	expression tag	UNP P98170
G	228	ALA	-	expression tag	UNP P98170
G	229	SER	-	expression tag	UNP P98170
G	230	MET	-	expression tag	UNP P98170
G	231	THR	-	expression tag	UNP P98170
G	232	GLY	-	expression tag	UNP P98170
G	233	GLY	-	expression tag	UNP P98170
G	234	GLN	-	expression tag	UNP P98170
G	235	GLN	-	expression tag	UNP P98170
G	236	MET	-	expression tag	UNP P98170
G	237	GLY	-	expression tag	UNP P98170
G	238	ARG	-	expression tag	UNP P98170
G	239	GLY	-	expression tag	UNP P98170
G	240	SER	-	expression tag	UNP P98170
H	211	HIS	-	expression tag	UNP P98170
H	212	HIS	-	expression tag	UNP P98170
H	213	HIS	-	expression tag	UNP P98170
H	214	HIS	-	expression tag	UNP P98170
H	215	HIS	-	expression tag	UNP P98170
H	216	HIS	-	expression tag	UNP P98170
H	217	SER	-	expression tag	UNP P98170
H	218	SER	-	expression tag	UNP P98170
H	219	GLY	-	expression tag	UNP P98170
H	220	LEU	-	expression tag	UNP P98170
H	221	VAL	-	expression tag	UNP P98170
H	222	PRO	-	expression tag	UNP P98170
H	223	ARG	-	expression tag	UNP P98170

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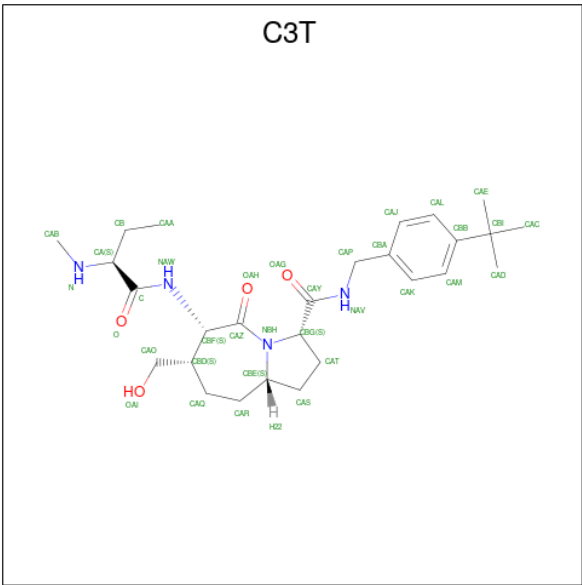
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Chain	Residue	Modelled	Actual	Comment	Reference
H	224	GLY	-	expression tag	UNP P98170
H	225	SER	-	expression tag	UNP P98170
H	226	HIS	-	expression tag	UNP P98170
H	227	MET	-	expression tag	UNP P98170
H	228	ALA	-	expression tag	UNP P98170
H	229	SER	-	expression tag	UNP P98170
H	230	MET	-	expression tag	UNP P98170
H	231	THR	-	expression tag	UNP P98170
H	232	GLY	-	expression tag	UNP P98170
H	233	GLY	-	expression tag	UNP P98170
H	234	GLN	-	expression tag	UNP P98170
H	235	GLN	-	expression tag	UNP P98170
H	236	MET	-	expression tag	UNP P98170
H	237	GLY	-	expression tag	UNP P98170
H	238	ARG	-	expression tag	UNP P98170
H	239	GLY	-	expression tag	UNP P98170
H	240	SER	-	expression tag	UNP P98170

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0
2	E	1	Total Zn 1 1	0	0
2	F	1	Total Zn 1 1	0	0
2	G	1	Total Zn 1 1	0	0
2	H	1	Total Zn 1 1	0	0

- Molecule 3 is (3 {S},6 {S},7 {S},9 {a} {S})- {N}-[(4- {tert}-butylphenyl)methyl]-7-(hydroxymethyl)-6-[[{(2 {S})-2-(methylamino)butanoyl]amino]-5-oxidanylidene-1,2,3,6,7,8,9,9 {a}-octahydropyrrolo[1,2-a]azepine-3-carboxamide (three-letter code: C3T) (formula: C<sub>27</sub>H<sub>42</sub>N<sub>4</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			35	27	4	4		
3	B	1	Total	C	N	O	0	0
			35	27	4	4		
3	C	1	Total	C	N	O	0	0
			35	27	4	4		
3	D	1	Total	C	N	O	0	0
			35	27	4	4		
3	E	1	Total	C	N	O	0	0
			35	27	4	4		
3	F	1	Total	C	N	O	0	0
			35	27	4	4		
3	G	1	Total	C	N	O	0	0
			35	27	4	4		
3	H	1	Total	C	N	O	0	0
			35	27	4	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	17	Total	O	0	0
			17	17		
4	B	7	Total	O	0	0
			7	7		
4	C	13	Total	O	0	0
			13	13		
4	D	13	Total	O	0	0
			13	13		

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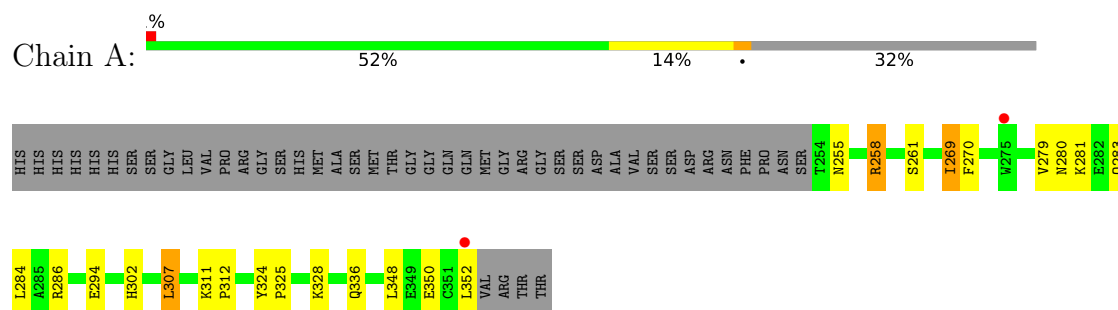
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	16	Total 16	O 16	0	0
4	F	7	Total 7	O 7	0	0
4	G	6	Total 6	O 6	0	0
4	H	6	Total 6	O 6	0	0

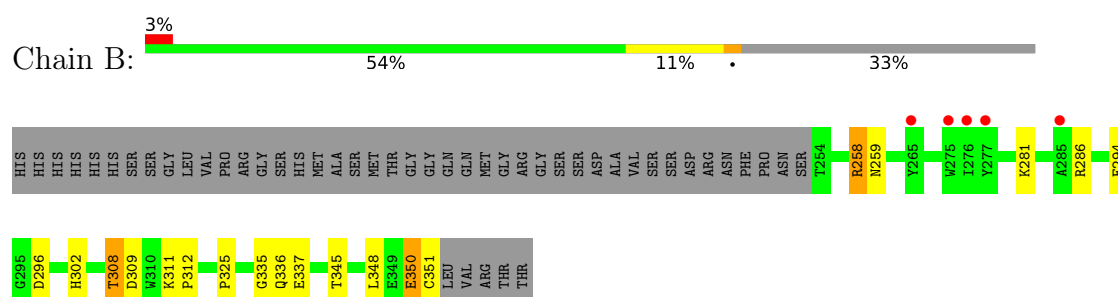
### 3 Residue-property plots [i](#)

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 electron 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 dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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.

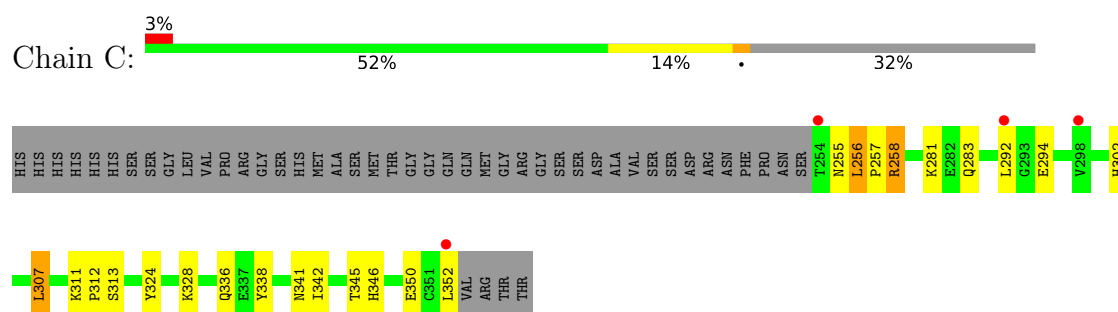
#### • Molecule 1: E3 ubiquitin-protein ligase XIAP



#### • Molecule 1: E3 ubiquitin-protein ligase XIAP

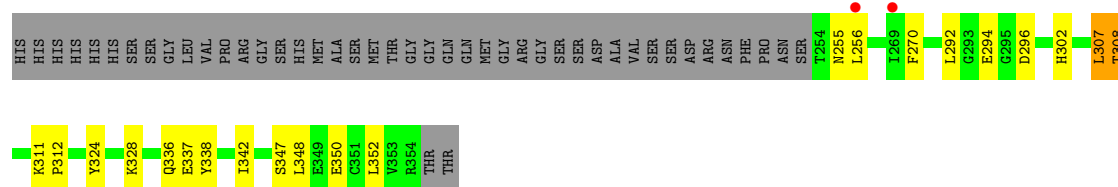


#### • Molecule 1: E3 ubiquitin-protein ligase XIAP

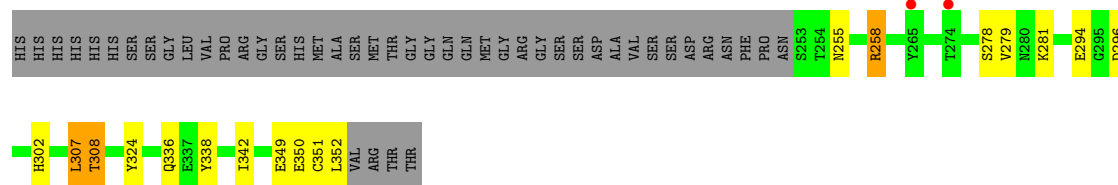


#### • Molecule 1: E3 ubiquitin-protein ligase XIAP

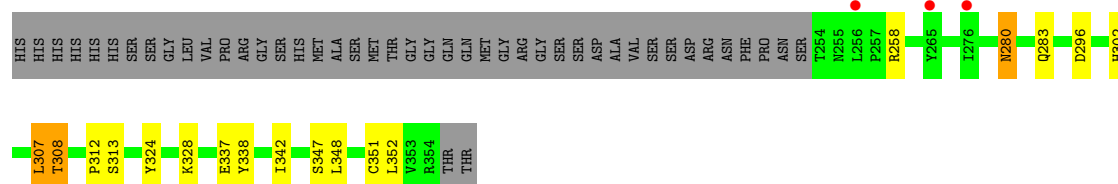




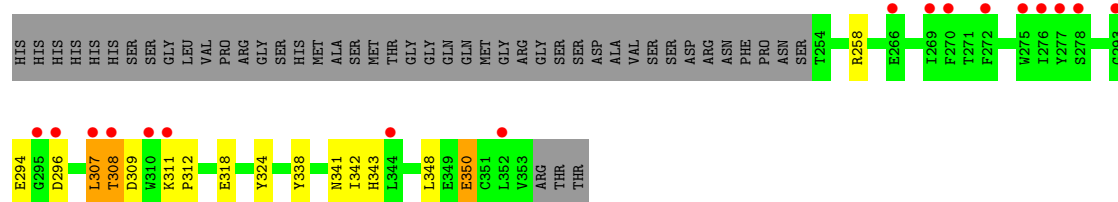
• Molecule 1: E3 ubiquitin-protein ligase XIAP



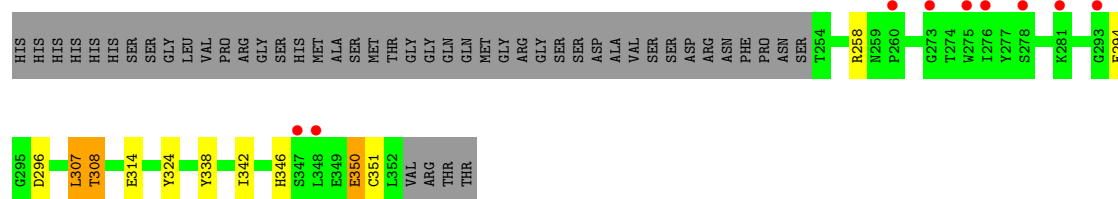
• Molecule 1: E3 ubiquitin-protein ligase XIAP



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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.23Å 97.06Å 182.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	66.50 – 2.70 66.50 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.7 (66.50-2.70) 99.7 (66.50-2.70)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.16 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, $R_{free}$	0.235 , 0.284 0.242 , 0.292	Depositor DCC
$R_{free}$ test set	1440 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	60.3	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 55.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6885	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.87% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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: C3T, ZN

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	0.52	0/844	0.66	0/1143
1	B	0.54	0/825	0.64	0/1118
1	C	0.48	0/833	0.61	0/1129
1	D	0.48	0/854	0.62	0/1158
1	E	0.47	0/839	0.64	0/1137
1	F	0.48	0/854	0.63	0/1158
1	G	0.50	0/851	0.62	0/1154
1	H	0.46	0/833	0.60	0/1129
All	All	0.49	0/6733	0.63	0/9126

There are no bond length outliers.

There are no bond angle outliers.

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	815	0	765	22	0
1	B	799	0	741	18	0
1	C	807	0	752	20	0
1	D	825	0	769	14	0
1	E	813	0	757	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	825	0	769	18	0
1	G	821	0	768	11	0
1	H	807	0	752	9	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	35	0	0	0	0
3	B	35	0	0	0	0
3	C	35	0	0	0	0
3	D	35	0	0	2	0
3	E	35	0	0	0	0
3	F	35	0	0	0	0
3	G	35	0	0	1	0
3	H	35	0	0	1	0
4	A	17	0	0	2	0
4	B	7	0	0	2	0
4	C	13	0	0	2	0
4	D	13	0	0	0	0
4	E	16	0	0	4	0
4	F	7	0	0	1	0
4	G	6	0	0	1	0
4	H	6	0	0	3	0
All	All	6885	0	6073	95	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 7.

All (95) 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:258:ARG:HH22	1:C:341:ASN:ND2	1.70	0.88
1:E:302:HIS:HD2	4:E:511:HOH:O	1.60	0.83
1:A:258:ARG:HH22	1:C:341:ASN:HD22	1.23	0.83
1:A:280:ASN:HB3	1:A:283:GLN:HE21	1.44	0.82
1:H:314:GLU:HG2	4:H:506:HOH:O	1.80	0.81
1:E:302:HIS:CD2	4:E:511:HOH:O	2.32	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:280:ASN:HB2	1:F:283:GLN:HE21	1.51	0.73
1:H:314:GLU:CG	4:H:506:HOH:O	2.34	0.73
1:A:328:LYS:H	1:B:336:GLN:HE21	1.37	0.72
1:H:350:GLU:N	1:H:350:GLU:OE1	2.24	0.71
1:E:336:GLN:HE21	1:F:328:LYS:H	1.40	0.70
1:C:292:LEU:HB3	1:F:313:SER:CB	2.22	0.69
4:A:501:HOH:O	1:C:345:THR:HG21	1.93	0.69
1:A:302:HIS:ND1	1:B:336:GLN:NE2	2.41	0.68
1:A:258:ARG:NH2	1:C:341:ASN:HD22	1.92	0.68
1:C:346:HIS:HB2	4:C:507:HOH:O	1.93	0.67
1:H:346:HIS:CE1	1:H:350:GLU:OE2	2.47	0.67
1:E:336:GLN:HE22	1:F:302:HIS:CD2	2.14	0.66
1:C:255:ASN:HD22	1:C:328:LYS:HE3	1.62	0.64
3:H:402:C3T:OAI	3:H:402:C3T:NAW	2.31	0.64
1:E:255:ASN:O	4:E:501:HOH:O	2.16	0.63
1:B:258:ARG:HH22	1:G:341:ASN:ND2	1.97	0.62
1:B:337:GLU:OE2	4:B:501:HOH:O	2.16	0.61
1:F:280:ASN:HB2	1:F:283:GLN:NE2	2.15	0.61
1:C:283:GLN:NE2	4:C:502:HOH:O	2.34	0.59
1:A:269:ILE:HD12	1:A:270:PHE:CD1	2.38	0.59
1:E:336:GLN:HE22	1:F:302:HIS:HD2	1.49	0.58
1:A:261:SER:OG	1:C:313:SER:HA	2.03	0.58
1:E:258:ARG:NH1	1:F:337[A]:GLU:OE2	2.38	0.56
1:G:350:GLU:N	1:G:350:GLU:OE2	2.40	0.54
1:G:343[B]:HIS:CE1	4:G:504:HOH:O	2.61	0.53
1:C:292:LEU:HB3	1:F:313:SER:HB3	1.88	0.53
1:A:302:HIS:CE1	1:B:336:GLN:NE2	2.75	0.53
1:E:278:SER:HB2	4:E:508:HOH:O	2.08	0.53
1:H:296:ASP:OD1	1:H:308:THR:HG22	2.08	0.53
1:B:296:ASP:OD1	1:B:308:THR:HG22	2.09	0.53
1:C:302:HIS:CE1	1:D:336:GLN:HE22	2.27	0.53
1:G:296:ASP:OD1	1:G:308:THR:HG22	2.10	0.52
1:D:296:ASP:OD1	1:D:308:THR:HG22	2.09	0.52
1:C:258:ARG:NH1	1:D:337[A]:GLU:OE2	2.43	0.52
1:B:259:ASN:HB2	4:B:506:HOH:O	2.10	0.52
1:F:296:ASP:OD1	1:F:308:THR:HG22	2.09	0.51
1:E:296:ASP:OD1	1:E:308:THR:HG22	2.10	0.51
1:A:307:LEU:HD13	1:A:324:TYR:HE2	1.74	0.50
1:D:348:LEU:HD11	1:F:347:SER:HB2	1.93	0.50
3:G:402:C3T:OAI	3:G:402:C3T:NAW	2.44	0.50
1:H:307:LEU:HD13	1:H:324:TYR:HE2	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:292:LEU:HB3	1:F:313:SER:HB2	1.92	0.50
1:H:314:GLU:HG3	4:H:506:HOH:O	2.07	0.49
1:A:328:LYS:H	1:B:336:GLN:NE2	2.08	0.49
1:A:302:HIS:CE1	1:A:328:LYS:HB3	2.48	0.48
1:A:325:PRO:HB2	1:B:325:PRO:HB2	1.95	0.48
1:D:307:LEU:HD13	1:D:324:TYR:HE2	1.78	0.48
1:E:349:GLU:O	1:E:352:LEU:HG	2.14	0.48
1:A:336:GLN:HE22	1:B:302:HIS:CE1	2.30	0.48
1:A:279:VAL:HG23	1:A:284:LEU:HD11	1.96	0.47
1:B:345:THR:HG23	3:D:402:C3T:CAL	2.45	0.47
1:C:256:LEU:HA	1:C:257:PRO:HD2	1.83	0.47
1:G:307:LEU:HD13	1:G:324:TYR:HE2	1.78	0.47
4:A:503:HOH:O	1:B:258:ARG:HD2	2.15	0.47
1:E:336:GLN:NE2	1:F:328:LYS:H	2.10	0.47
1:C:336:GLN:H	1:D:255:ASN:ND2	2.13	0.46
1:E:307:LEU:HD13	1:E:324:TYR:HE2	1.81	0.46
1:D:292:LEU:HD11	3:D:402:C3T:CAD	2.46	0.46
1:F:307:LEU:HD13	1:F:324:TYR:HE2	1.79	0.46
1:A:255:ASN:HD21	1:B:335:GLY:HA2	1.80	0.46
1:F:312:PRO:HD2	4:F:502:HOH:O	2.15	0.45
1:A:311:LYS:HB3	1:A:312:PRO:HD2	1.98	0.45
1:D:352:LEU:HD12	1:F:351:CYS:SG	2.56	0.45
1:B:258:ARG:HH22	1:G:341:ASN:HD22	1.63	0.45
1:B:350:GLU:OE2	1:B:350:GLU:HA	2.17	0.45
1:C:307:LEU:HD13	1:C:324:TYR:HE2	1.81	0.45
1:G:338:TYR:O	1:G:342:ILE:HG12	2.17	0.44
1:B:311:LYS:HB3	1:B:312:PRO:HD2	2.00	0.44
1:C:338:TYR:O	1:C:342:ILE:HG12	2.17	0.44
1:D:347:SER:HB2	1:F:348:LEU:HD11	1.99	0.44
1:E:338:TYR:O	1:E:342:ILE:HG12	2.18	0.43
1:G:311:LYS:HB3	1:G:312:PRO:HD2	1.99	0.43
1:D:338:TYR:O	1:D:342:ILE:HG12	2.17	0.43
1:G:309:ASP:O	1:G:309:ASP:CG	2.57	0.43
1:C:292:LEU:O	1:F:313:SER:HB3	2.19	0.43
1:A:286[B]:ARG:CG	1:A:286[B]:ARG:HH11	2.32	0.43
1:A:286[B]:ARG:HH11	1:A:286[B]:ARG:HG3	1.84	0.43
1:A:336:GLN:NE2	1:B:302:HIS:CE1	2.87	0.42
1:F:338:TYR:O	1:F:342:ILE:HG12	2.19	0.42
1:H:350:GLU:OE1	1:H:350:GLU:CA	2.68	0.42
1:H:338:TYR:O	1:H:342:ILE:HG12	2.19	0.42
1:B:258:ARG:HG2	1:G:318:GLU:OE1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:311:LYS:HB3	1:D:312:PRO:HD2	2.01	0.41
1:A:348:LEU:HG	1:G:348:LEU:HD13	2.01	0.41
1:C:336:GLN:H	1:D:255:ASN:HD21	1.69	0.41
1:A:286[B]:ARG:HG3	1:A:286[B]:ARG:NH1	2.35	0.40
1:D:256:LEU:HD23	1:D:256:LEU:N	2.36	0.40
1:C:311:LYS:HB3	1:C:312:PRO:HD2	2.02	0.40
1:D:302:HIS:CE1	1:D:328:LYS:HB3	2.56	0.40

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 X-ray entries followed by that with respect to entries of similar resolution.

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	98/146 (67%)	95 (97%)	3 (3%)	0	100	100
1	B	96/146 (66%)	94 (98%)	2 (2%)	0	100	100
1	C	97/146 (66%)	94 (97%)	3 (3%)	0	100	100
1	D	100/146 (68%)	96 (96%)	4 (4%)	0	100	100
1	E	98/146 (67%)	94 (96%)	4 (4%)	0	100	100
1	F	100/146 (68%)	96 (96%)	4 (4%)	0	100	100
1	G	99/146 (68%)	96 (97%)	3 (3%)	0	100	100
1	H	97/146 (66%)	94 (97%)	3 (3%)	0	100	100
All	All	785/1168 (67%)	759 (97%)	26 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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 X-ray entries followed by that with respect to entries of similar

resolution.

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	85/123 (69%)	78 (92%)	7 (8%)	11	26
1	B	83/123 (68%)	74 (89%)	9 (11%)	6	15
1	C	84/123 (68%)	77 (92%)	7 (8%)	11	25
1	D	86/123 (70%)	81 (94%)	5 (6%)	20	43
1	E	85/123 (69%)	77 (91%)	8 (9%)	8	20
1	F	86/123 (70%)	81 (94%)	5 (6%)	20	43
1	G	86/123 (70%)	81 (94%)	5 (6%)	20	43
1	H	84/123 (68%)	78 (93%)	6 (7%)	14	34
All	All	679/984 (69%)	627 (92%)	52 (8%)	13	30

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	258	ARG
1	A	269	ILE
1	A	281	LYS
1	A	294	GLU
1	A	307	LEU
1	A	350	GLU
1	A	352	LEU
1	B	258	ARG
1	B	281	LYS
1	B	286	ARG
1	B	294	GLU
1	B	308	THR
1	B	309	ASP
1	B	348	LEU
1	B	350	GLU
1	B	351	CYS
1	C	256	LEU
1	C	258	ARG
1	C	281	LYS
1	C	294	GLU
1	C	307	LEU
1	C	350	GLU
1	C	352	LEU

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Mol	Chain	Res	Type
1	D	270	PHE
1	D	294	GLU
1	D	307	LEU
1	D	308	THR
1	D	350	GLU
1	E	258	ARG
1	E	279	VAL
1	E	281	LYS
1	E	294	GLU
1	E	307	LEU
1	E	308	THR
1	E	350	GLU
1	E	351	CYS
1	F	258	ARG
1	F	280	ASN
1	F	307	LEU
1	F	308	THR
1	F	352	LEU
1	G	258	ARG
1	G	294	GLU
1	G	307	LEU
1	G	308	THR
1	G	350	GLU
1	H	258	ARG
1	H	294	GLU
1	H	307	LEU
1	H	308	THR
1	H	350	GLU
1	H	351	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	255	ASN
1	A	283	GLN
1	B	255	ASN
1	B	336	GLN
1	C	255	ASN
1	C	302	HIS
1	C	341	ASN
1	D	255	ASN
1	D	336	GLN

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Mol	Chain	Res	Type
1	E	336	GLN
1	F	283	GLN
1	F	302	HIS
1	G	341	ASN
1	H	346	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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	C3T	H	402	-	35,37,37	1.86	7 (20%)	41,53,53	1.93	9 (21%)
3	C3T	A	402	-	35,37,37	1.66	5 (14%)	41,53,53	2.18	9 (21%)
3	C3T	B	402	-	35,37,37	2.26	7 (20%)	41,53,53	2.25	9 (21%)
3	C3T	G	402	-	35,37,37	2.23	8 (22%)	41,53,53	2.75	11 (26%)
3	C3T	D	402	-	35,37,37	1.80	5 (14%)	41,53,53	2.13	11 (26%)
3	C3T	F	402	-	35,37,37	1.83	4 (11%)	41,53,53	1.83	5 (12%)
3	C3T	E	402	-	35,37,37	1.63	4 (11%)	41,53,53	1.93	9 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	C3T	C	402	-	35,37,37	1.53	6 (17%)	41,53,53	1.88	10 (24%)

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	C3T	H	402	-	-	3/29/59/59	0/3/3/3
3	C3T	A	402	-	-	2/29/59/59	0/3/3/3
3	C3T	B	402	-	-	4/29/59/59	0/3/3/3
3	C3T	G	402	-	-	13/29/59/59	0/3/3/3
3	C3T	D	402	-	-	4/29/59/59	0/3/3/3
3	C3T	F	402	-	-	7/29/59/59	0/3/3/3
3	C3T	E	402	-	-	9/29/59/59	0/3/3/3
3	C3T	C	402	-	-	7/29/59/59	0/3/3/3

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	402	C3T	CBG-NBH	6.97	1.56	1.46
3	B	402	C3T	CAP-CBA	-6.06	1.38	1.51
3	H	402	C3T	CAP-CBA	-6.00	1.38	1.51
3	B	402	C3T	CBG-NBH	5.98	1.55	1.46
3	F	402	C3T	CAP-CBA	-5.84	1.38	1.51
3	E	402	C3T	CAP-CBA	-5.71	1.39	1.51
3	B	402	C3T	CBE-NBH	5.70	1.55	1.47
3	G	402	C3T	CAP-CBA	-5.60	1.39	1.51
3	D	402	C3T	CBG-CAY	-5.45	1.40	1.52
3	C	402	C3T	CAP-CBA	-5.24	1.40	1.51
3	D	402	C3T	CAP-CBA	-5.21	1.40	1.51
3	H	402	C3T	CBG-CAY	-5.07	1.40	1.52
3	E	402	C3T	CBG-CAY	-4.98	1.41	1.52
3	F	402	C3T	CBI-CBB	-4.98	1.43	1.53
3	F	402	C3T	CBG-CAY	-4.96	1.41	1.52
3	A	402	C3T	CBI-CBB	-4.94	1.43	1.53
3	B	402	C3T	CBG-CAY	-4.73	1.41	1.52
3	D	402	C3T	CBI-CBB	-4.69	1.44	1.53
3	A	402	C3T	CAP-CBA	-4.63	1.41	1.51
3	H	402	C3T	CBI-CBB	-4.53	1.44	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	402	C3T	CBI-CBB	-4.51	1.44	1.53
3	G	402	C3T	CBE-NBH	4.33	1.53	1.47
3	G	402	C3T	CBG-CAY	-4.31	1.42	1.52
3	C	402	C3T	CBG-CAY	-4.00	1.43	1.52
3	A	402	C3T	CBG-CAY	-3.79	1.43	1.52
3	E	402	C3T	CBI-CBB	-3.70	1.46	1.53
3	D	402	C3T	CAZ-NBH	-3.29	1.31	1.35
3	A	402	C3T	CAZ-NBH	-3.09	1.32	1.35
3	C	402	C3T	CAY-NAV	2.75	1.39	1.33
3	G	402	C3T	CAZ-NBH	2.69	1.38	1.35
3	A	402	C3T	CBE-NBH	-2.63	1.44	1.47
3	H	402	C3T	CBG-NBH	2.62	1.50	1.46
3	D	402	C3T	CBG-NBH	2.62	1.50	1.46
3	G	402	C3T	CBF-NAW	2.53	1.51	1.45
3	G	402	C3T	CAY-NAV	2.50	1.39	1.33
3	C	402	C3T	CBI-CBB	-2.48	1.48	1.53
3	H	402	C3T	CAZ-NBH	-2.44	1.32	1.35
3	G	402	C3T	CAP-NAV	2.38	1.50	1.46
3	C	402	C3T	CAZ-NBH	-2.35	1.32	1.35
3	E	402	C3T	CAZ-NBH	-2.33	1.32	1.35
3	H	402	C3T	CAS-CBE	-2.22	1.47	1.53
3	B	402	C3T	CAP-NAV	2.19	1.50	1.46
3	H	402	C3T	CAM-CBB	2.17	1.42	1.39
3	C	402	C3T	CAP-NAV	2.12	1.50	1.46
3	B	402	C3T	CBF-NAW	2.08	1.50	1.45
3	F	402	C3T	CAQ-CAR	2.03	1.59	1.52

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	402	C3T	CBG-NBH-CAZ	13.10	136.30	118.60
3	B	402	C3T	CBG-NBH-CAZ	9.31	131.18	118.60
3	A	402	C3T	CBG-NBH-CAZ	8.37	129.91	118.60
3	E	402	C3T	CBG-NBH-CAZ	7.15	128.27	118.60
3	F	402	C3T	CBG-NBH-CAZ	6.71	127.67	118.60
3	H	402	C3T	OAH-CAZ-NBH	-6.63	114.34	121.69
3	D	402	C3T	OAH-CAZ-NBH	-6.51	114.48	121.69
3	B	402	C3T	OAI-CAO-CBD	-6.02	97.54	111.36
3	C	402	C3T	CBG-NBH-CAZ	5.81	126.45	118.60
3	G	402	C3T	CBG-NBH-CBE	-5.51	103.31	112.52
3	G	402	C3T	CAS-CAT-CBG	-5.34	96.49	103.84
3	D	402	C3T	CBG-NBH-CAZ	5.00	125.36	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	402	C3T	CAT-CBG-NBH	4.93	107.82	103.09
3	A	402	C3T	CAA-CB-CA	-4.68	102.46	113.44
3	A	402	C3T	OAH-CAZ-NBH	-4.59	116.60	121.69
3	H	402	C3T	CBG-NBH-CAZ	4.56	124.75	118.60
3	B	402	C3T	CBG-NBH-CBE	-4.53	104.95	112.52
3	E	402	C3T	CAT-CBG-NBH	4.47	107.38	103.09
3	E	402	C3T	OAH-CAZ-NBH	-4.35	116.87	121.69
3	D	402	C3T	CAT-CBG-NBH	4.25	107.17	103.09
3	D	402	C3T	OAI-CAO-CBD	-4.20	101.73	111.36
3	D	402	C3T	CAA-CB-CA	-3.98	104.11	113.44
3	D	402	C3T	CAS-CAT-CBG	-3.85	98.55	103.84
3	H	402	C3T	CAS-CAT-CBG	-3.84	98.56	103.84
3	F	402	C3T	OAH-CAZ-NBH	-3.66	117.64	121.69
3	H	402	C3T	CBG-NBH-CBE	-3.59	106.53	112.52
3	C	402	C3T	CAT-CBG-NBH	3.54	106.48	103.09
3	B	402	C3T	CAT-CBG-NBH	3.51	106.46	103.09
3	H	402	C3T	CAA-CB-CA	-3.46	105.33	113.44
3	C	402	C3T	OAH-CAZ-NBH	-3.32	118.02	121.69
3	H	402	C3T	CAT-CBG-NBH	3.28	106.23	103.09
3	C	402	C3T	CAP-NAV-CAY	3.24	127.00	122.34
3	G	402	C3T	OAH-CAZ-NBH	-3.24	118.11	121.69
3	E	402	C3T	CAP-NAV-CAY	3.12	126.82	122.34
3	C	402	C3T	CAA-CB-CA	-3.12	106.13	113.44
3	F	402	C3T	OAI-CAO-CBD	-3.08	104.30	111.36
3	C	402	C3T	CAS-CAT-CBG	-3.06	99.64	103.84
3	F	402	C3T	CBG-NBH-CBE	-3.04	107.44	112.52
3	G	402	C3T	OAI-CAO-CBD	-3.03	104.40	111.36
3	A	402	C3T	CAT-CBG-NBH	3.02	105.98	103.09
3	D	402	C3T	CAT-CAS-CBE	2.94	108.44	104.05
3	A	402	C3T	CAJ-CAL-CBB	2.82	124.99	121.22
3	G	402	C3T	CAL-CBB-CAM	-2.76	113.87	117.97
3	A	402	C3T	OAI-CAO-CBD	-2.72	105.11	111.36
3	E	402	C3T	CBG-NBH-CBE	-2.71	107.99	112.52
3	D	402	C3T	CB-CA-C	-2.70	104.46	110.37
3	C	402	C3T	CAL-CBB-CAM	-2.70	113.96	117.97
3	G	402	C3T	CAY-CBG-NBH	2.59	117.74	112.39
3	H	402	C3T	OAI-CAO-CBD	-2.58	105.44	111.36
3	B	402	C3T	CAS-CBE-NBH	2.56	104.57	101.70
3	A	402	C3T	CB-CA-C	-2.53	104.84	110.37
3	G	402	C3T	CAT-CBG-NBH	2.51	105.50	103.09
3	B	402	C3T	CBA-CAP-NAV	-2.50	107.70	113.05
3	G	402	C3T	C-CA-N	-2.47	104.37	112.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	402	C3T	CAL-CBB-CBI	-2.46	116.75	121.58
3	D	402	C3T	CAB-N-CA	-2.39	106.21	113.64
3	C	402	C3T	CA-C-NAW	-2.33	111.59	116.70
3	A	402	C3T	CBA-CAP-NAV	-2.26	108.20	113.05
3	G	402	C3T	CAR-CAQ-CBD	-2.21	108.36	116.42
3	A	402	C3T	CBF-NAW-C	-2.19	116.32	121.89
3	E	402	C3T	CAS-CAT-CBG	-2.17	100.86	103.84
3	H	402	C3T	CAS-CBE-NBH	-2.16	99.28	101.70
3	C	402	C3T	CAB-N-CA	-2.16	106.92	113.64
3	E	402	C3T	OAG-CAY-NAV	2.12	127.54	122.99
3	B	402	C3T	CAS-CAT-CBG	-2.10	100.95	103.84
3	H	402	C3T	CB-CA-C	-2.07	105.83	110.37
3	E	402	C3T	CAD-CBI-CBB	-2.06	105.44	110.36
3	D	402	C3T	CAE-CBI-CBB	2.05	115.28	110.36
3	C	402	C3T	CAM-CBB-CBI	2.04	125.59	121.58
3	B	402	C3T	OAH-CAZ-NBH	-2.04	119.43	121.69
3	D	402	C3T	CAM-CAK-CBA	2.03	123.82	121.03
3	G	402	C3T	CAJ-CAL-CBB	2.02	123.91	121.22
3	E	402	C3T	CAR-CAQ-CBD	-2.01	109.10	116.42

There are no chirality outliers.

All (49) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	402	C3T	C-CA-CB-CAA
3	A	402	C3T	N-CA-CB-CAA
3	B	402	C3T	OAI-CAO-CBD-CAQ
3	B	402	C3T	OAI-CAO-CBD-CBF
3	B	402	C3T	N-CA-CB-CAA
3	C	402	C3T	OAI-CAO-CBD-CAQ
3	C	402	C3T	OAI-CAO-CBD-CBF
3	C	402	C3T	C-CA-CB-CAA
3	C	402	C3T	N-CA-CB-CAA
3	D	402	C3T	OAI-CAO-CBD-CAQ
3	D	402	C3T	OAI-CAO-CBD-CBF
3	D	402	C3T	C-CA-CB-CAA
3	D	402	C3T	N-CA-CB-CAA
3	E	402	C3T	C-CA-CB-CAA
3	E	402	C3T	N-CA-CB-CAA
3	F	402	C3T	C-CA-CB-CAA
3	F	402	C3T	N-CA-CB-CAA
3	G	402	C3T	OAI-CAO-CBD-CAQ

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Mol	Chain	Res	Type	Atoms
3	G	402	C3T	OAI-CAO-CBD-CBF
3	G	402	C3T	CBD-CBF-NAW-C
3	G	402	C3T	C-CA-CB-CAA
3	G	402	C3T	N-CA-CB-CAA
3	G	402	C3T	C-CA-N-CAB
3	G	402	C3T	CB-CA-N-CAB
3	H	402	C3T	OAI-CAO-CBD-CBF
3	H	402	C3T	C-CA-CB-CAA
3	G	402	C3T	OAG-CAY-CBG-CAT
3	G	402	C3T	NAV-CAY-CBG-CAT
3	G	402	C3T	O-C-CA-CB
3	H	402	C3T	N-CA-CB-CAA
3	G	402	C3T	NAW-C-CA-CB
3	G	402	C3T	NAW-C-CA-N
3	B	402	C3T	C-CA-CB-CAA
3	G	402	C3T	O-C-CA-N
3	C	402	C3T	C-CA-N-CAB
3	C	402	C3T	O-C-CA-N
3	C	402	C3T	NAW-C-CA-N
3	E	402	C3T	CAL-CBB-CBI-CAD
3	E	402	C3T	CAM-CBB-CBI-CAD
3	F	402	C3T	CAM-CBB-CBI-CAE
3	F	402	C3T	CAL-CBB-CBI-CAE
3	E	402	C3T	CAL-CBB-CBI-CAC
3	E	402	C3T	CAL-CBB-CBI-CAE
3	E	402	C3T	CAM-CBB-CBI-CAE
3	F	402	C3T	CAM-CBB-CBI-CAC
3	E	402	C3T	CAM-CBB-CBI-CAC
3	F	402	C3T	CAL-CBB-CBI-CAC
3	E	402	C3T	CAZ-CBF-NAW-C
3	F	402	C3T	CAM-CBB-CBI-CAD

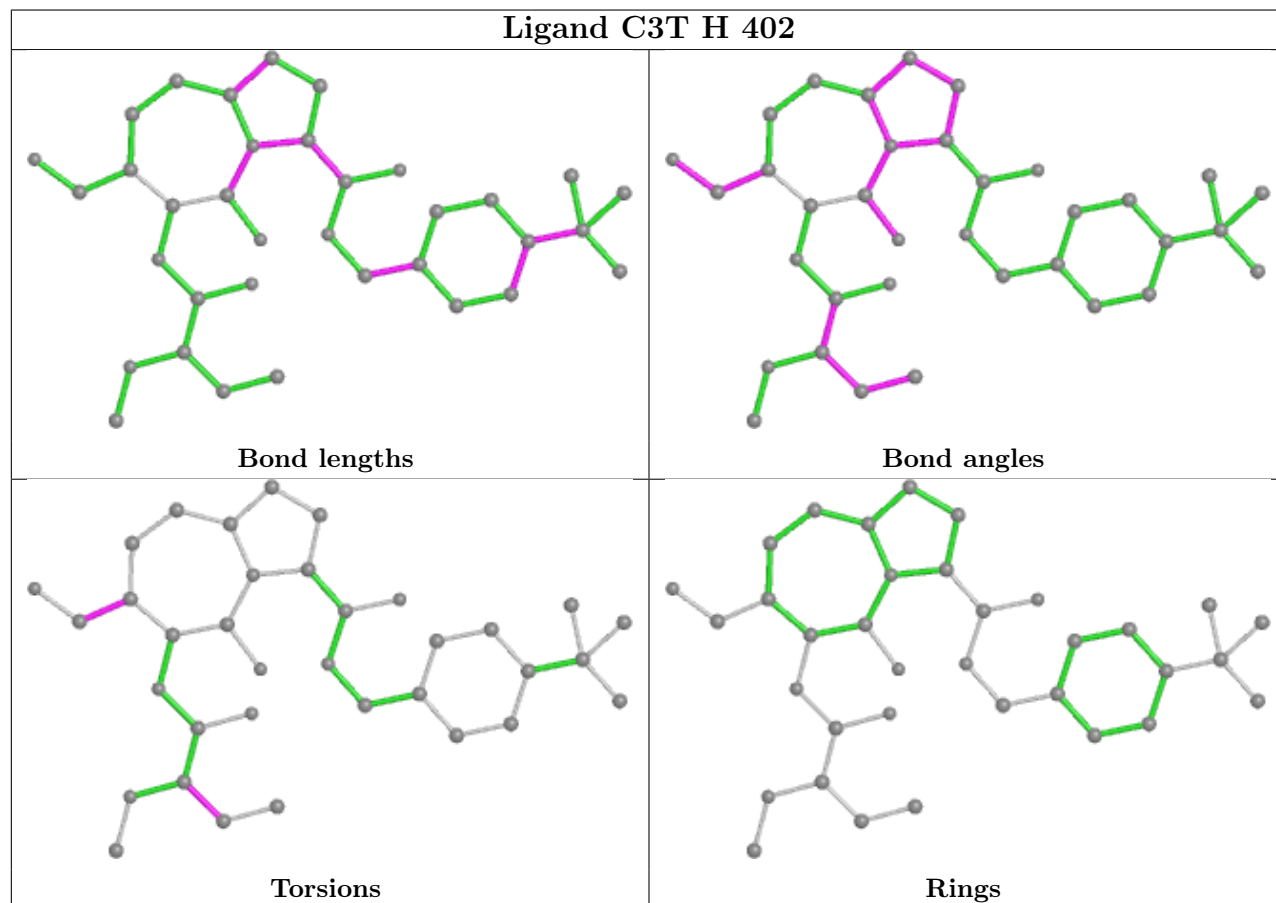
There are no ring outliers.

3 monomers are involved in 4 short contacts:

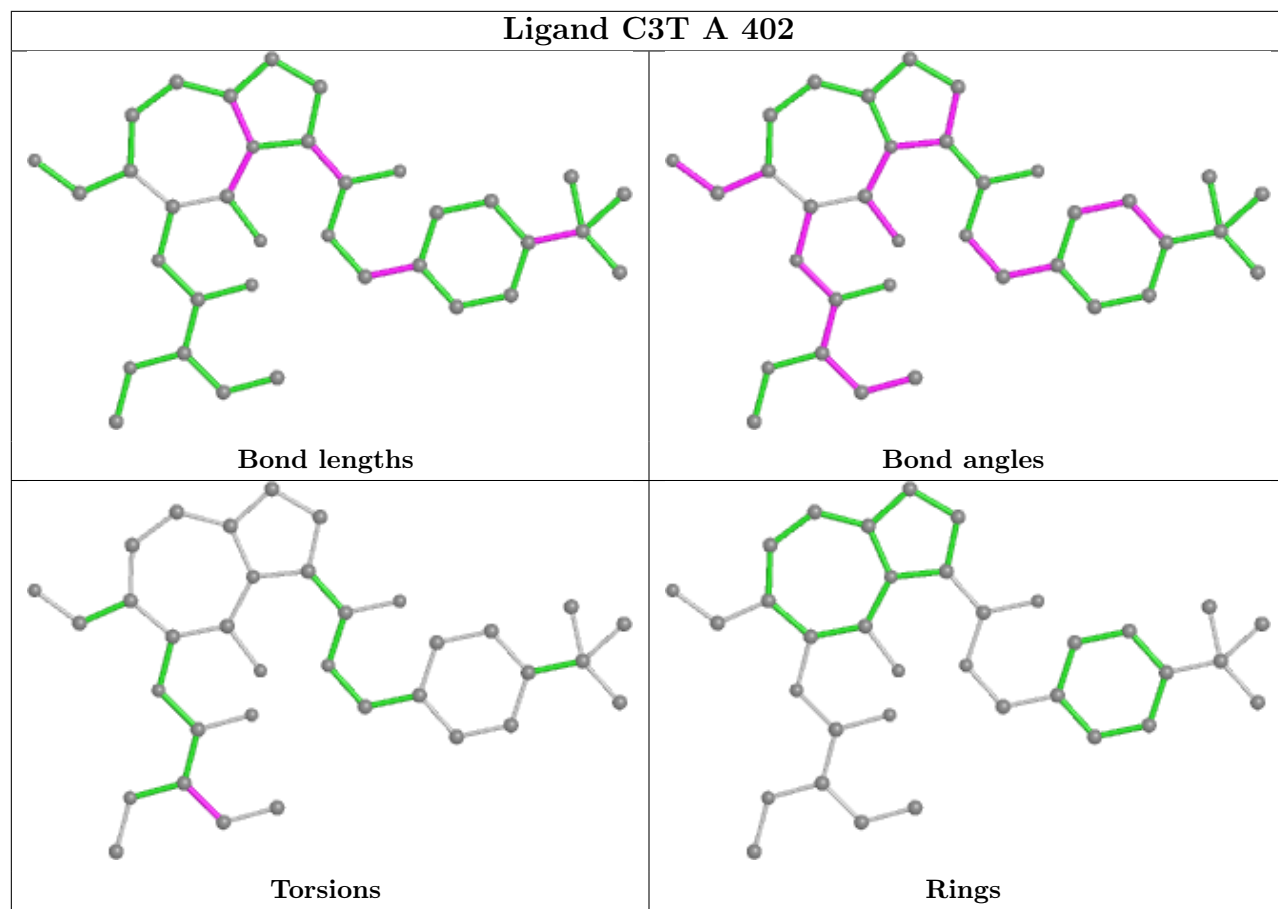
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	402	C3T	1	0
3	G	402	C3T	1	0
3	D	402	C3T	2	0

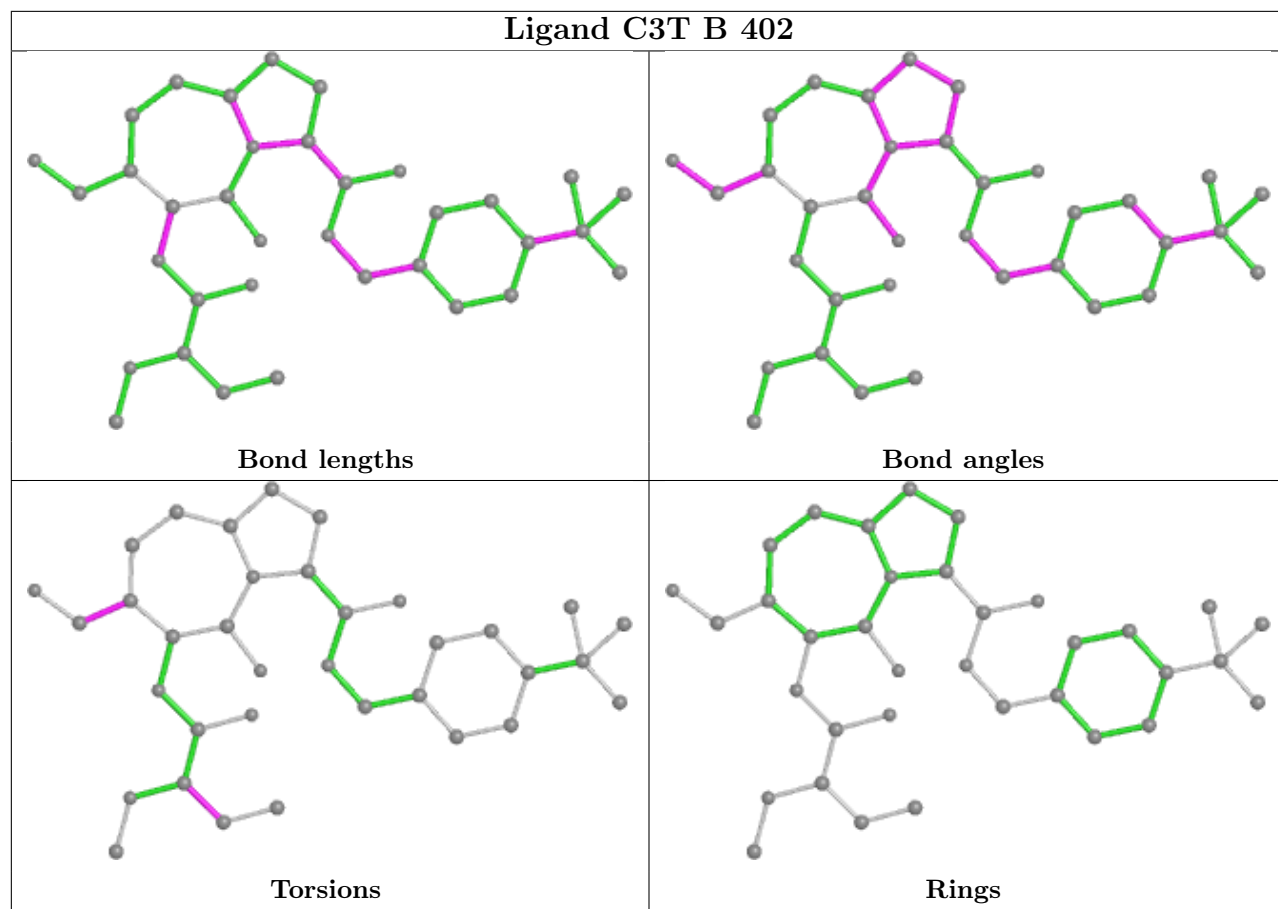
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

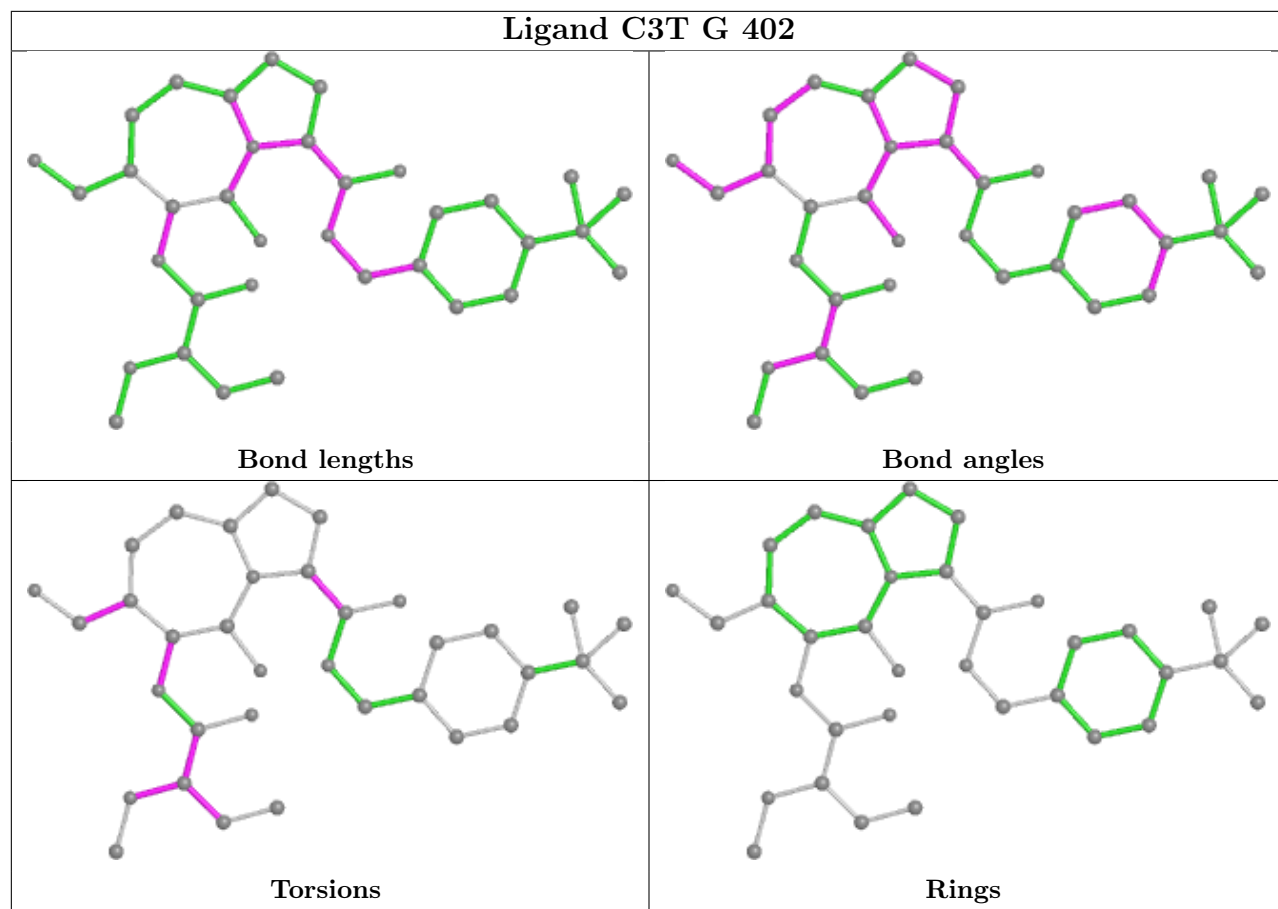
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. 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.



## Ligand C3T A 402

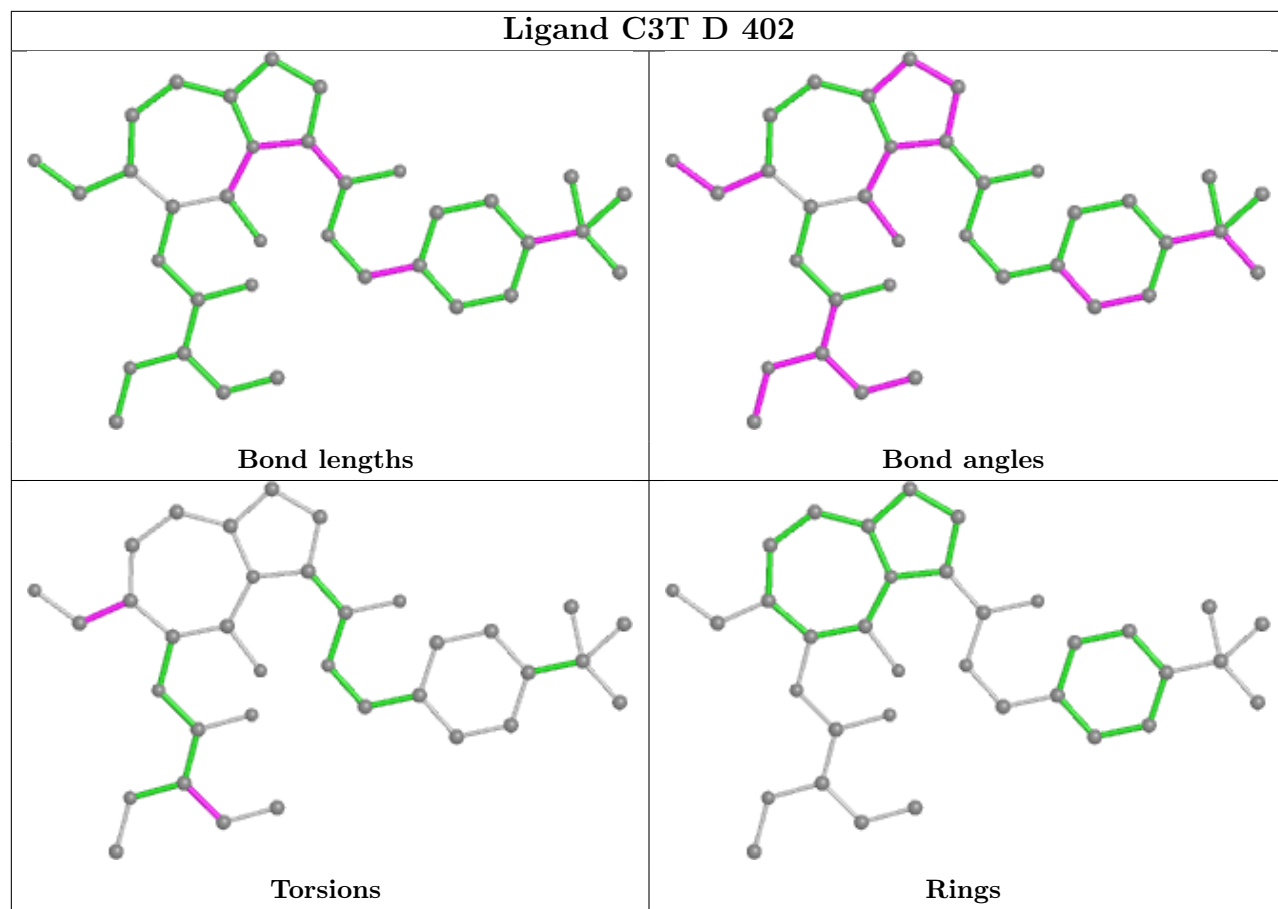




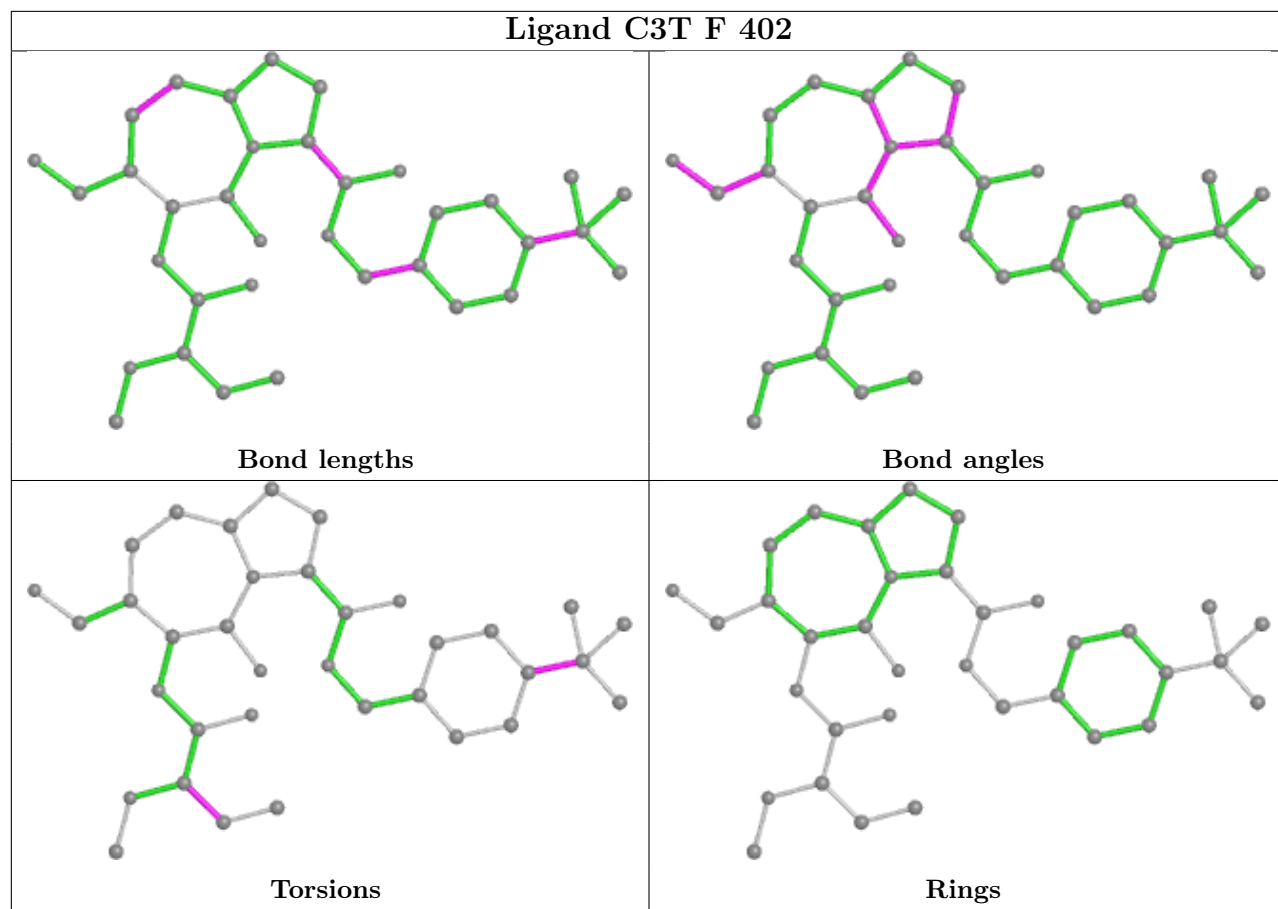




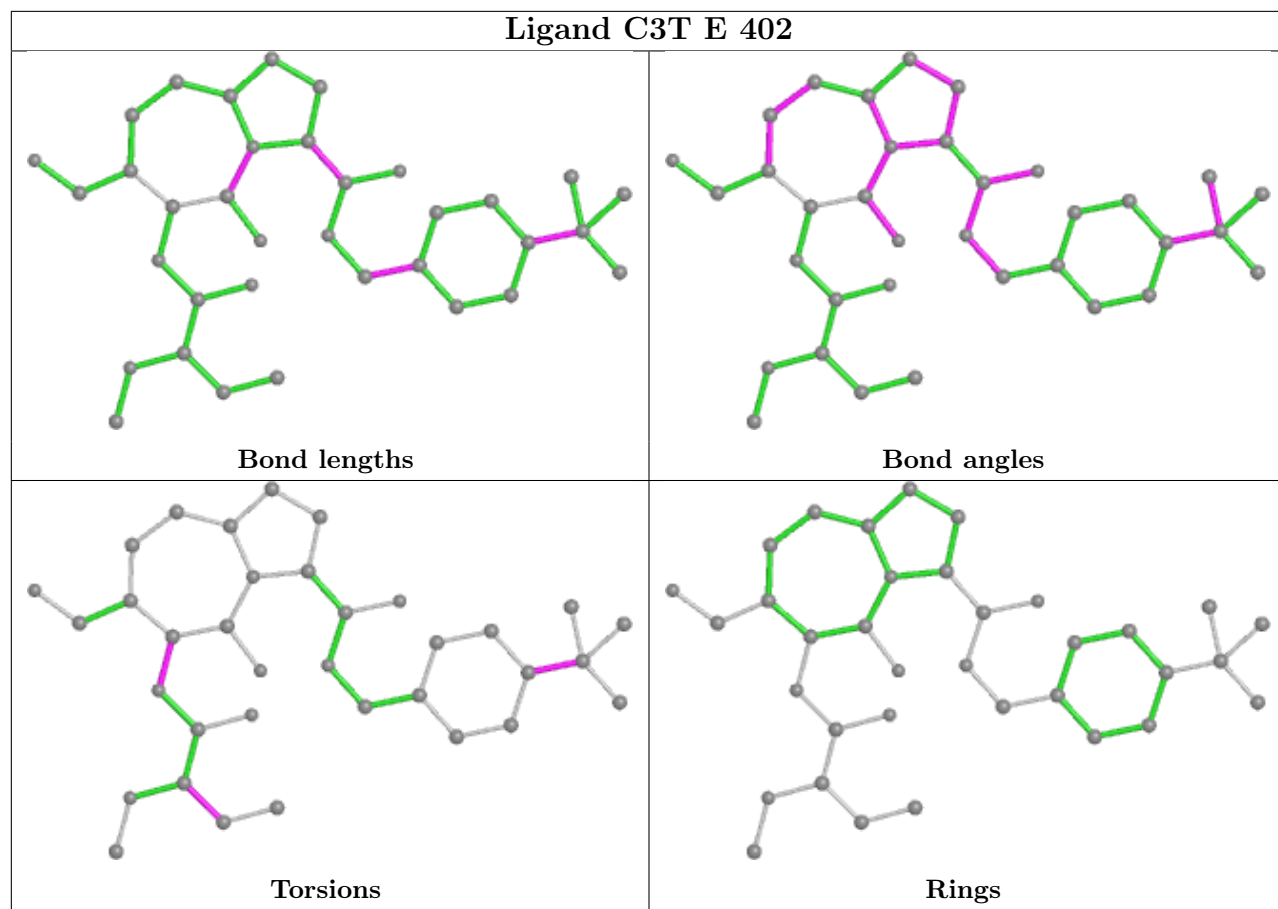
## Ligand C3T D 402

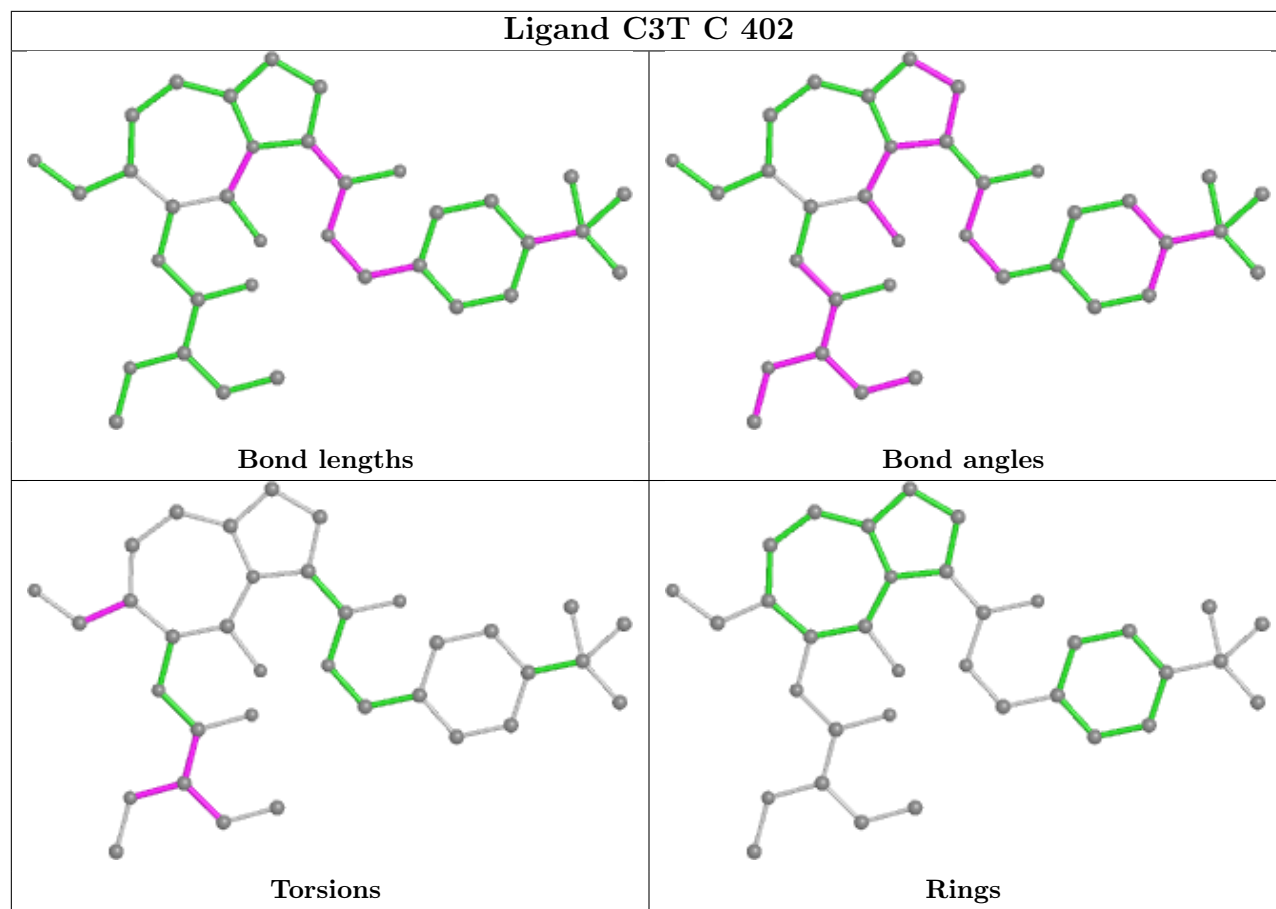


## Ligand C3T F 402



## Ligand C3T E 402





## 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 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	99/146 (67%)	0.24	2 (2%) 65 67	32, 56, 98, 133	2 (2%)
1	B	98/146 (67%)	0.51	5 (5%) 28 26	33, 73, 115, 133	2 (2%)
1	C	99/146 (67%)	0.36	4 (4%) 38 37	35, 64, 103, 132	2 (2%)
1	D	101/146 (69%)	0.29	2 (1%) 65 67	33, 67, 103, 124	2 (1%)
1	E	100/146 (68%)	0.28	2 (2%) 65 67	38, 64, 112, 120	2 (2%)
1	F	101/146 (69%)	0.32	3 (2%) 50 51	36, 63, 101, 112	2 (1%)
1	G	100/146 (68%)	0.97	17 (17%) 1 1	37, 87, 135, 150	2 (2%)
1	H	99/146 (67%)	0.59	9 (9%) 9 7	41, 82, 120, 138	2 (2%)
All	All	797/1168 (68%)	0.44	44 (5%) 25 24	32, 68, 120, 150	16 (2%)

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	310	TRP	6.1
1	G	277	TYR	5.4
1	G	272	PHE	4.5
1	G	308	THR	4.0
1	A	352	LEU	3.8
1	B	277	TYR	3.6
1	G	270	PHE	3.6
1	H	348	LEU	3.4
1	G	296	ASP	3.2
1	G	275	TRP	3.2
1	H	293	GLY	3.2
1	E	274	THR	3.1
1	G	276	ILE	3.1
1	H	347	SER	3.1
1	H	276	ILE	3.1
1	G	311	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	256	LEU	3.0
1	H	275	TRP	2.9
1	H	278	SER	2.8
1	C	352	LEU	2.8
1	C	292	LEU	2.7
1	G	266	GLU	2.7
1	H	260	PRO	2.7
1	G	307	LEU	2.7
1	H	281	LYS	2.6
1	B	275	TRP	2.5
1	A	275	TRP	2.5
1	G	269	ILE	2.5
1	H	273	GLY	2.4
1	F	256	LEU	2.4
1	C	254	THR	2.3
1	G	293	GLY	2.3
1	B	276	ILE	2.3
1	G	344	LEU	2.3
1	B	285	ALA	2.3
1	B	265	TYR	2.3
1	E	265	TYR	2.2
1	G	295	GLY	2.1
1	F	265	TYR	2.1
1	C	298	VAL	2.1
1	G	278	SER	2.1
1	D	269	ILE	2.1
1	G	352	LEU	2.1
1	F	276	ILE	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,

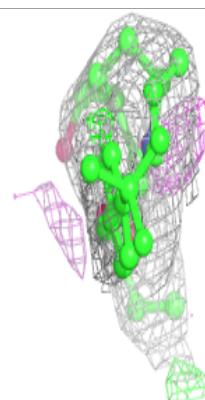
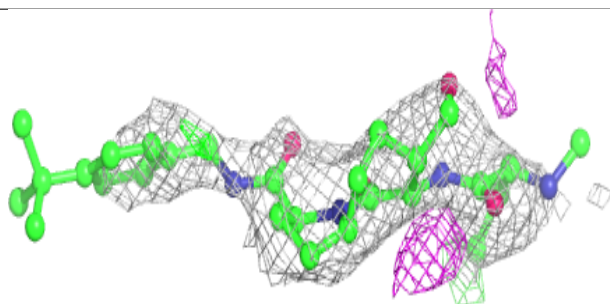
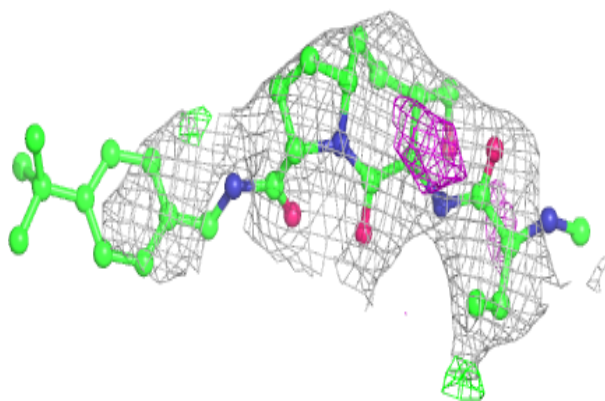
median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	C3T	G	402	35/35	0.82	0.36	73,105,157,165	0
3	C3T	H	402	35/35	0.89	0.25	84,107,143,144	0
3	C3T	B	402	35/35	0.91	0.26	53,81,129,138	0
3	C3T	F	402	35/35	0.93	0.31	59,80,105,109	0
3	C3T	E	402	35/35	0.94	0.22	52,64,84,85	0
3	C3T	C	402	35/35	0.94	0.24	51,63,97,111	0
3	C3T	A	402	35/35	0.95	0.23	39,48,56,58	0
3	C3T	D	402	35/35	0.96	0.21	40,54,78,87	0
2	ZN	F	401	1/1	0.98	0.10	49,49,49,49	0
2	ZN	D	401	1/1	0.99	0.13	42,42,42,42	0
2	ZN	A	401	1/1	0.99	0.13	36,36,36,36	0
2	ZN	G	401	1/1	0.99	0.10	50,50,50,50	0
2	ZN	H	401	1/1	0.99	0.12	46,46,46,46	0
2	ZN	B	401	1/1	0.99	0.12	51,51,51,51	0
2	ZN	C	401	1/1	0.99	0.12	48,48,48,48	0
2	ZN	E	401	1/1	1.00	0.15	42,42,42,42	0

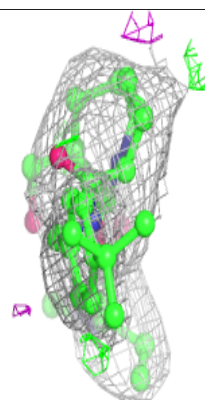
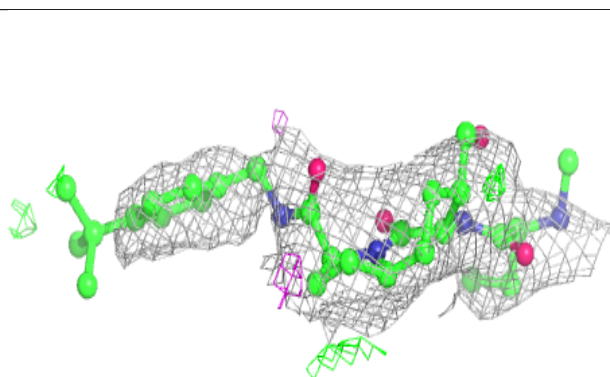
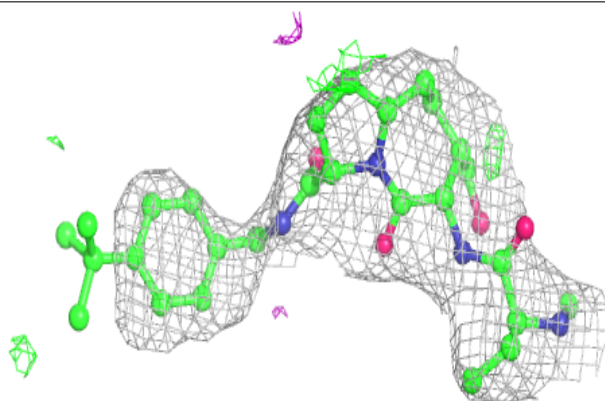
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

**Electron density around C3T G 402:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around C3T H 402:**

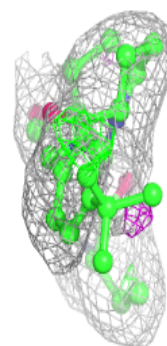
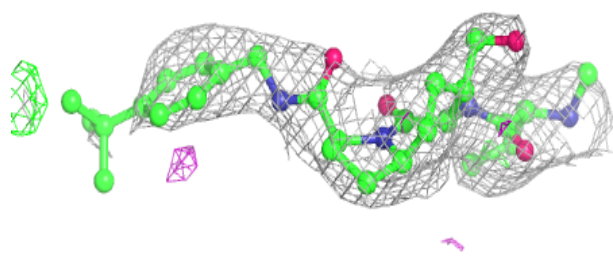
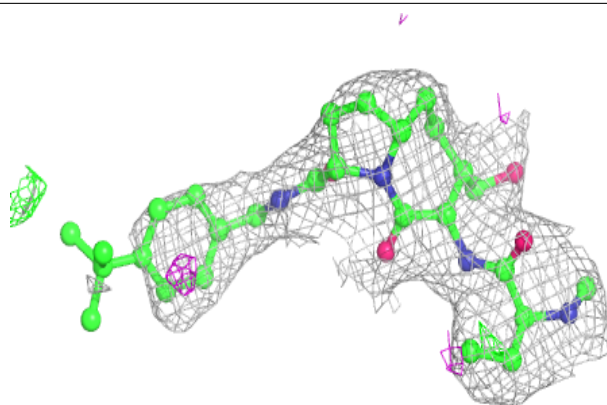
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



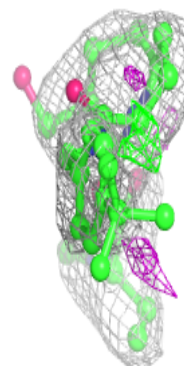
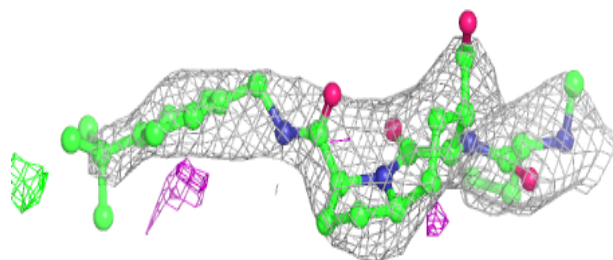
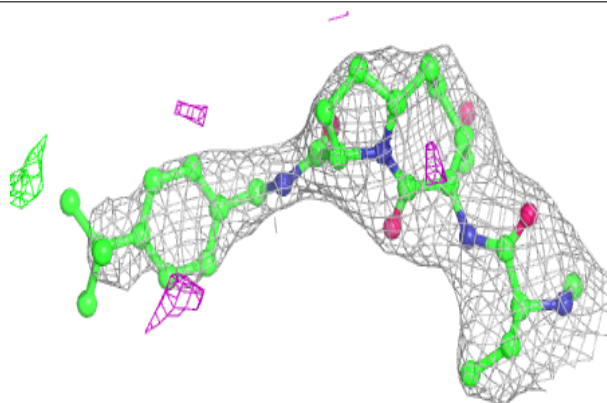


**Electron density around C3T B 402:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

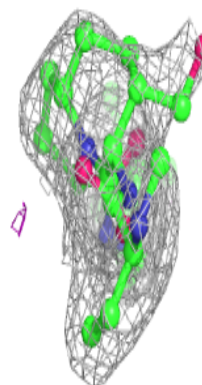
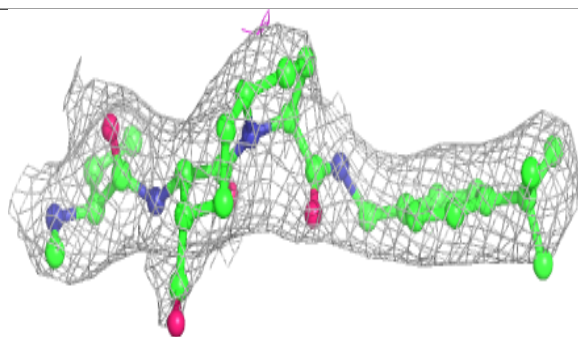
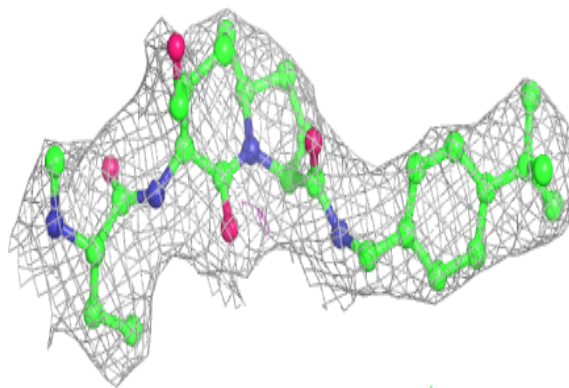
**Electron density around C3T F 402:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

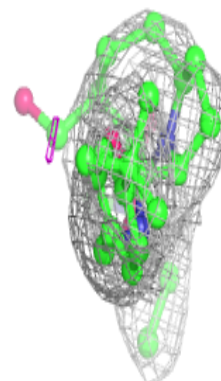
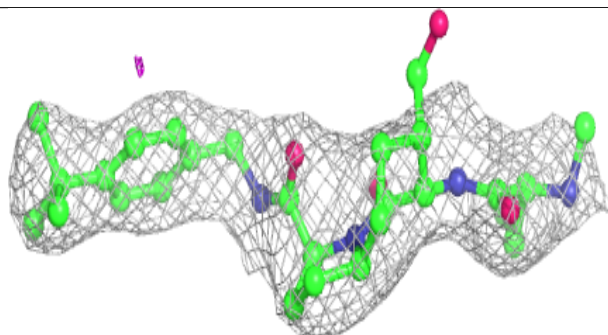
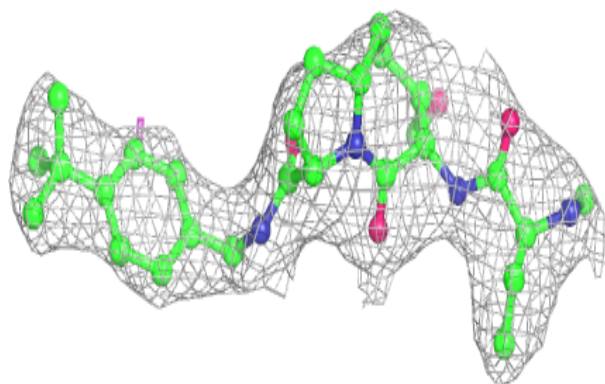


**Electron density around C3T E 402:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

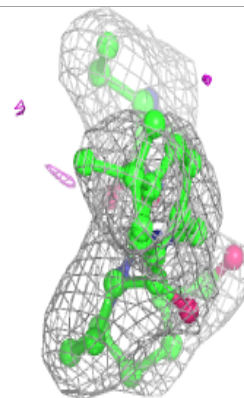
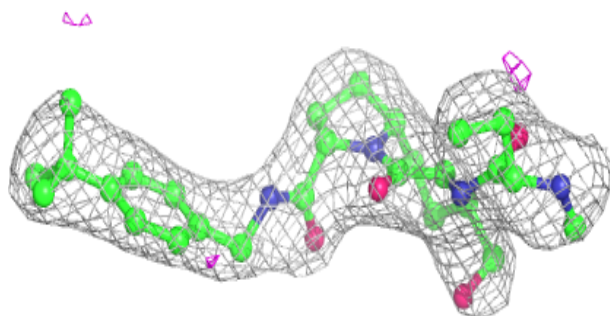
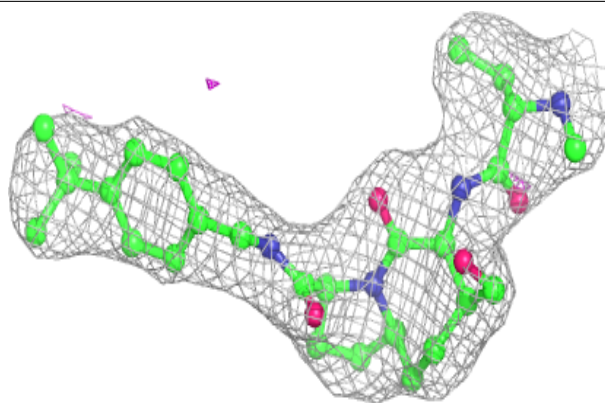
**Electron density around C3T C 402:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

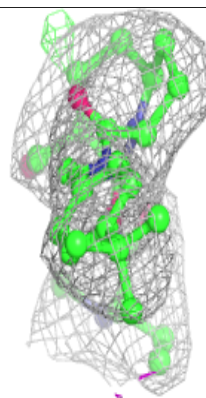
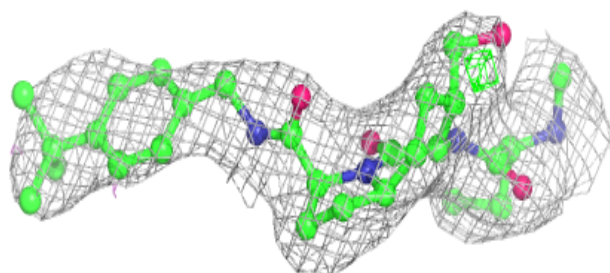
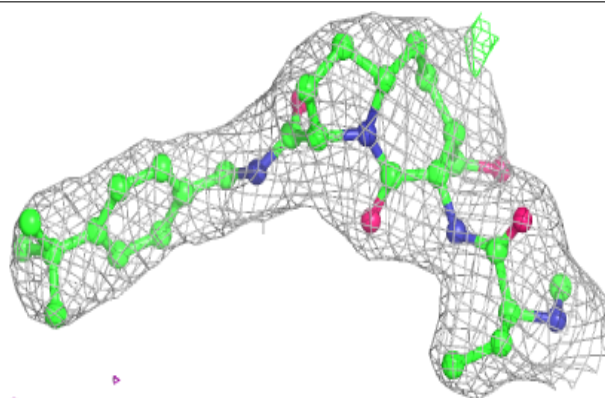


**Electron density around C3T A 402:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around C3T D 402:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.