



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:43 AM UTC

PDB ID : 3NM1 / pdb\_00003nm1  
Title : The Crystal Structure of Candida glabrata THI6, a Bifunctional Enzyme involved in Thiamin Biosynthesis of Eukaryotes  
Authors : Paul, D.; Chatterjee, A.; Begley, T.P.; Ealick, S.E.  
Deposited on : 2010-06-21  
Resolution : 3.21 Å (reported)

This is a wwPDB X-ray Structure 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/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 : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

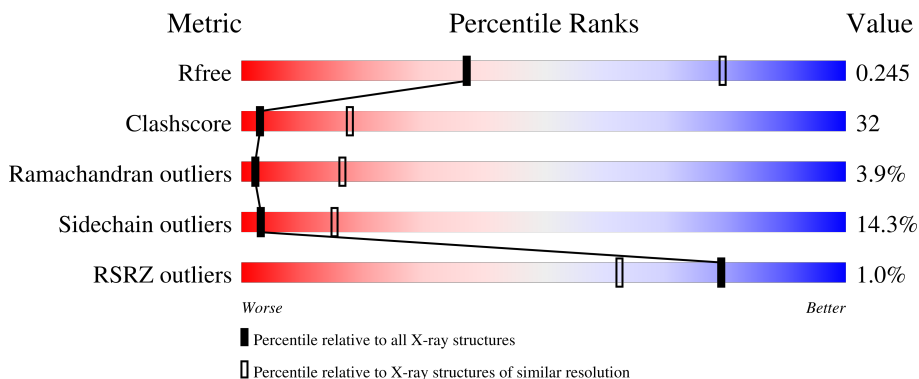
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.21 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))
$R_{free}$	180053	1768 (3.24-3.20)
Clashscore	190562	1879 (3.24-3.20)
Ramachandran outliers	187476	1844 (3.24-3.20)
Sidechain outliers	187428	1843 (3.24-3.20)
RSRZ outliers	180081	1768 (3.24-3.20)

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	540	
1	B	540	
1	C	540	
1	D	540	
1	E	540	

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Mol	Chain	Length	Quality of chain
1	F	540	 <p>A horizontal bar chart showing the quality distribution of chain F. The bar is divided into four segments: a green segment representing 47%, a yellow segment representing 37%, an orange segment representing 9%, and a grey segment representing 6%. A small red square is at the beginning of the bar, and a '%' symbol is above it.</p>

## 2 Entry composition [i](#)

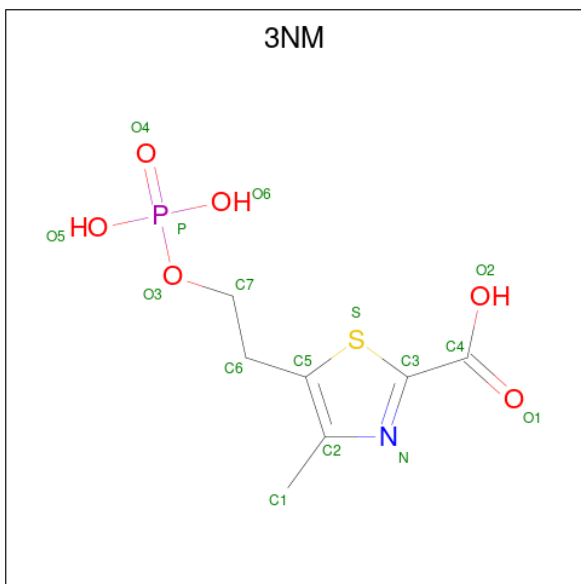
There are 5 unique types of molecules in this entry. The entry contains 22801 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Thiamine biosynthetic bifunctional enzyme.

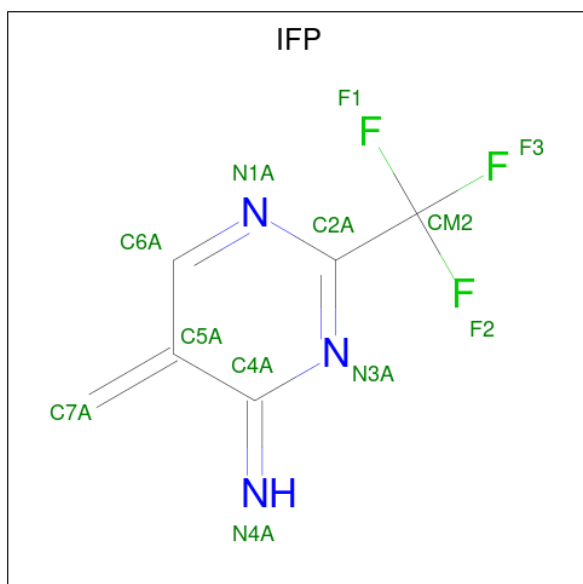
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	507	Total 3765	C 2386	N 632	O 726	S 21	0	0	0
1	B	507	Total 3765	C 2386	N 632	O 726	S 21	0	0	0
1	C	507	Total 3765	C 2386	N 632	O 726	S 21	0	0	0
1	D	507	Total 3765	C 2386	N 632	O 726	S 21	0	0	0
1	E	505	Total 3748	C 2375	N 629	O 723	S 21	0	0	0
1	F	507	Total 3765	C 2386	N 632	O 726	S 21	0	0	0

- Molecule 2 is 4-methyl-5-[2-(phosphonoxy)ethyl]-1,3-thiazole-2-carboxylic acid (CCD ID: 3NM) (formula: C<sub>7</sub>H<sub>10</sub>NO<sub>6</sub>PS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	N	O	P			S
2	A	1	Total 16	C 7	N 1	O 6	P 1	S 1	0	0
2	B	1	Total 16	C 7	N 1	O 6	P 1	S 1	0	0
2	C	1	Total 16	C 7	N 1	O 6	P 1	S 1	0	0
2	D	1	Total 16	C 7	N 1	O 6	P 1	S 1	0	0
2	E	1	Total 16	C 7	N 1	O 6	P 1	S 1	0	0
2	F	1	Total 16	C 7	N 1	O 6	P 1	S 1	0	0

- Molecule 3 is 2-TRIFLUOROMETHYL-5-METHYLENE-5H-PYRIMIDIN-4-YLIDENEA MINE (CCD ID: IFP) (formula: C<sub>6</sub>H<sub>4</sub>F<sub>3</sub>N<sub>3</sub>).



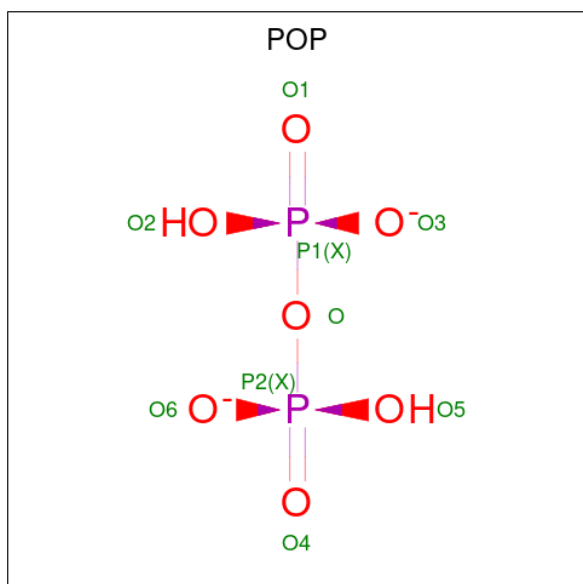
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	F			N
3	A	1	Total 12	C 6	F 3	N 3	0	0
3	B	1	Total 12	C 6	F 3	N 3	0	0
3	C	1	Total 12	C 6	F 3	N 3	0	0
3	D	1	Total 12	C 6	F 3	N 3	0	0
3	E	1	Total 12	C 6	F 3	N 3	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	F	1	Total	C	F	N	0	0
			12	6	3	3		

- Molecule 4 is PYROPHOSPHATE 2- (CCD ID: POP) (formula:  $H_2O_7P_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			9	7	2		
4	B	1	Total	O	P	0	0
			9	7	2		
4	C	1	Total	O	P	0	0
			9	7	2		
4	D	1	Total	O	P	0	0
			9	7	2		
4	E	1	Total	O	P	0	0
			9	7	2		
4	F	1	Total	O	P	0	0
			9	7	2		

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

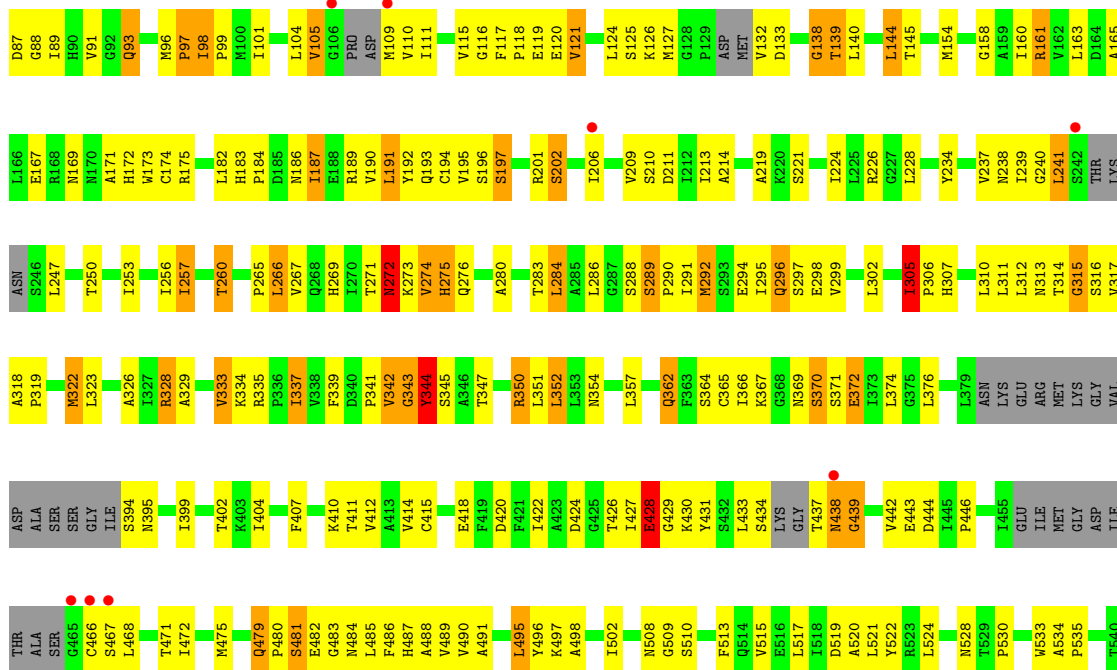
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		
5	B	1	Total	Mg	0	0
			1	1		

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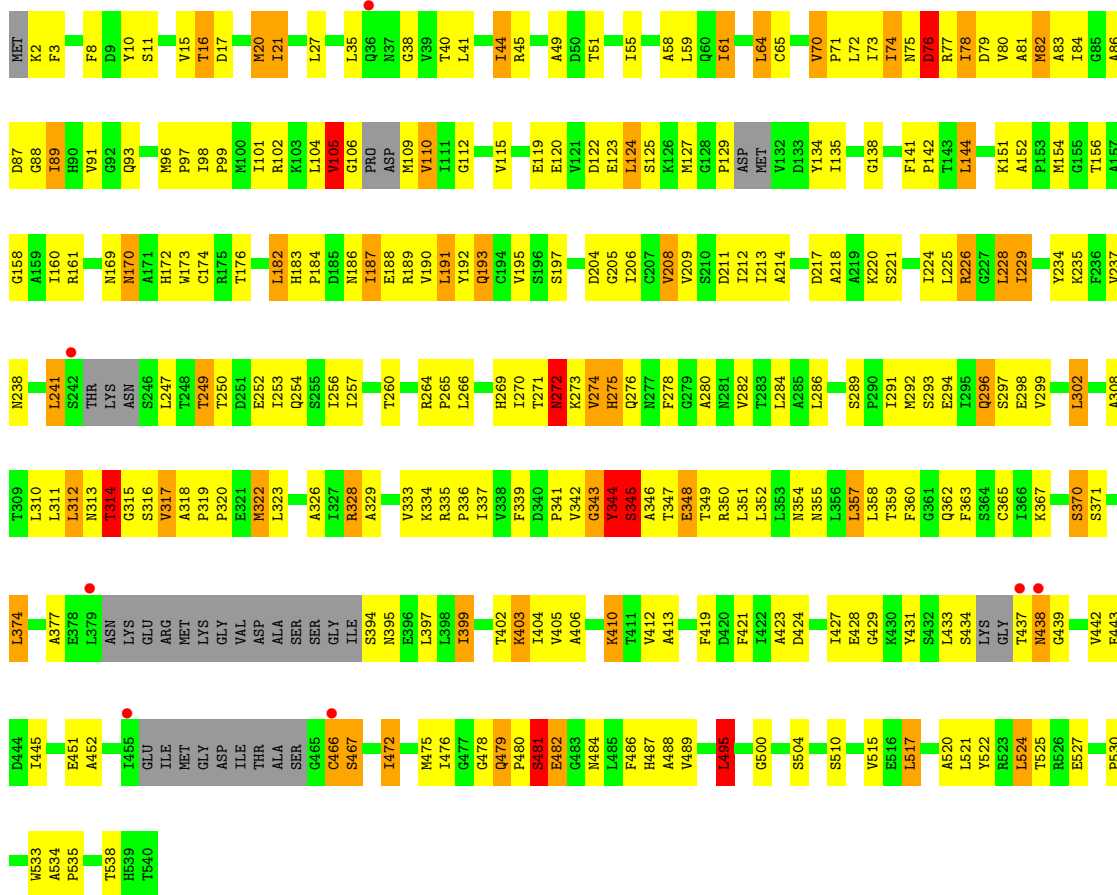
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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
5	C	1	Total 1	Mg 1	0	0
5	D	1	Total 1	Mg 1	0	0
5	E	1	Total 1	Mg 1	0	0
5	F	1	Total 1	Mg 1	0	0





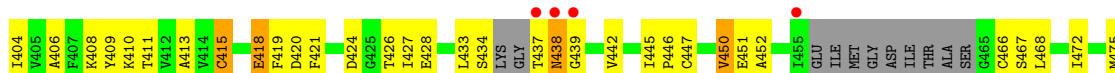
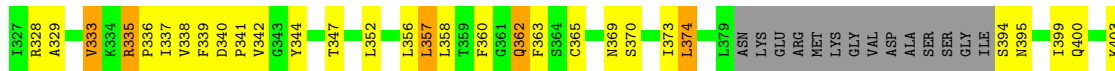
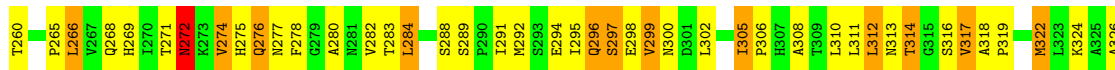
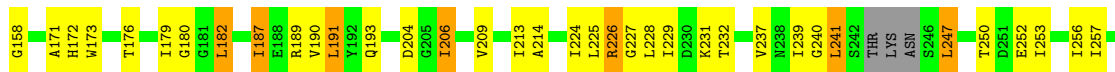
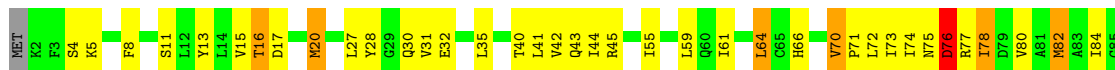
• Molecule 1: Thiamine biosynthetic bifunctional enzyme







● Molecule 1: Thiamine biosynthetic bifunctional enzyme



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.94Å 154.21Å 148.70Å 90.00° 102.10° 90.00°	Depositor
Resolution (Å)	38.55 – 3.21 38.55 – 3.21	Depositor EDS
% Data completeness (in resolution range)	97.8 (38.55-3.21) 97.9 (38.55-3.21)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.65 (at 3.18Å)	Xtrriage
Refinement program	PHENIX 1.5_2	Depositor
R, $R_{free}$	0.201 , 0.232 0.193 , 0.245	Depositor DCC
$R_{free}$ test set	3731 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	72.8	Xtrriage
Anisotropy	0.553	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 53.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	22801	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	78.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.82% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, POP, IFP, 3NM

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	0.61	0/3824	1.02	17/5190 (0.3%)
1	B	0.59	0/3824	1.01	12/5190 (0.2%)
1	C	0.63	0/3824	1.02	9/5190 (0.2%)
1	D	0.63	0/3824	1.06	12/5190 (0.2%)
1	E	0.61	0/3806	1.02	10/5164 (0.2%)
1	F	0.60	0/3824	0.99	7/5190 (0.1%)
All	All	0.61	0/22926	1.02	67/31114 (0.2%)

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	B	1	0
1	D	0	1
All	All	1	1

There are no bond length outliers.

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	317	VAL	CB-CA-C	-18.45	81.02	111.29
1	E	344	TYR	CB-CA-C	12.73	135.76	110.42
1	C	344	TYR	CB-CA-C	12.37	135.03	110.42
1	C	345	SER	N-CA-CB	-11.83	90.49	110.49
1	A	344	TYR	CB-CA-C	11.60	132.58	116.34

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	344	TYR	CA

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	317	VAL	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	3765	0	3750	280	0
1	B	3765	0	3750	244	0
1	C	3765	0	3750	236	0
1	D	3765	0	3750	233	0
1	E	3748	0	3730	234	0
1	F	3765	0	3750	243	0
2	A	16	0	7	3	0
2	B	16	0	7	3	0
2	C	16	0	7	0	0
2	D	16	0	7	1	0
2	E	16	0	7	2	0
2	F	16	0	7	2	0
3	A	12	0	4	1	0
3	B	12	0	4	1	0
3	C	12	0	4	0	0
3	D	12	0	4	0	0
3	E	12	0	4	2	0
3	F	12	0	4	0	0
4	A	9	0	0	1	0
4	B	9	0	0	2	0
4	C	9	0	0	0	0
4	D	9	0	0	0	0
4	E	9	0	0	0	0
4	F	9	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
All	All	22801	0	22546	1431	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 32.

The worst 5 of 1431 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:B:343:GLY:HA3	1:B:350:ARG:HD3	1.29	1.09
1:F:78:ILE:HG21	1:F:96:MET:HE1	1.36	1.07
1:F:8:PHE:CE2	1:F:110:VAL:HG21	1.91	1.06
1:A:313:ASN:ND2	1:A:342:VAL:HG21	1.71	1.06
1:E:77:ARG:HH11	1:E:77:ARG:HG2	1.18	1.04

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	493/540 (91%)	398 (81%)	78 (16%)	17 (3%)	3	19
1	B	493/540 (91%)	423 (86%)	49 (10%)	21 (4%)	2	15
1	C	493/540 (91%)	430 (87%)	42 (8%)	21 (4%)	2	15
1	D	493/540 (91%)	411 (83%)	61 (12%)	21 (4%)	2	15
1	E	489/540 (91%)	418 (86%)	49 (10%)	22 (4%)	2	14
1	F	493/540 (91%)	411 (83%)	70 (14%)	12 (2%)	4	26
All	All	2954/3240 (91%)	2491 (84%)	349 (12%)	114 (4%)	2	17

5 of 114 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	20	MET
1	A	76	ASP
1	A	247	LEU
1	A	317	VAL
1	B	20	MET

### 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	405/449 (90%)	351 (87%)	54 (13%)	4 18
1	B	405/449 (90%)	343 (85%)	62 (15%)	3 13
1	C	405/449 (90%)	338 (84%)	67 (16%)	2 10
1	D	405/449 (90%)	353 (87%)	52 (13%)	4 19
1	E	403/449 (90%)	347 (86%)	56 (14%)	3 16
1	F	405/449 (90%)	349 (86%)	56 (14%)	3 17
All	All	2428/2694 (90%)	2081 (86%)	347 (14%)	3 15

5 of 347 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	495	LEU
1	E	495	LEU
1	E	63	GLU
1	E	249	THR
1	F	91	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 75 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	281	ASN
1	F	355	ASN

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Mol	Chain	Res	Type
1	E	355	ASN
1	F	169	ASN
1	B	514	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 24 ligands modelled in this entry, 6 are monoatomic - leaving 18 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
4	POP	E	543	5	6,8,8	0.58	0	12,13,13	0.73	0
2	3NM	C	541	-	15,16,16	5.05	5 (33%)	19,23,23	7.55	7 (36%)
3	IFP	F	542	-	9,12,12	3.11	3 (33%)	11,18,18	3.58	4 (36%)
3	IFP	D	542	-	9,12,12	3.22	3 (33%)	11,18,18	3.69	6 (54%)
4	POP	B	543	5	6,8,8	0.74	0	12,13,13	0.87	0
3	IFP	A	542	-	9,12,12	3.18	3 (33%)	11,18,18	3.74	5 (45%)
4	POP	C	543	5	6,8,8	0.62	0	12,13,13	0.99	1 (8%)
3	IFP	C	542	-	9,12,12	3.28	3 (33%)	11,18,18	3.56	3 (27%)
3	IFP	E	542	-	9,12,12	3.41	3 (33%)	11,18,18	3.43	4 (36%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	POP	D	543	5	6,8,8	0.68	0	12,13,13	0.92	0
3	IFP	B	542	-	9,12,12	3.35	3 (33%)	11,18,18	3.42	3 (27%)
2	3NM	E	541	-	15,16,16	5.00	5 (33%)	19,23,23	7.77	7 (36%)
4	POP	A	543	5	6,8,8	0.55	0	12,13,13	1.13	1 (8%)
4	POP	F	543	5	6,8,8	0.67	0	12,13,13	0.92	0
2	3NM	D	541	-	15,16,16	5.08	5 (33%)	19,23,23	8.28	8 (42%)
2	3NM	F	541	-	15,16,16	4.94	5 (33%)	19,23,23	7.11	8 (42%)
2	3NM	A	541	-	15,16,16	5.01	6 (40%)	19,23,23	7.70	7 (36%)
2	3NM	B	541	-	15,16,16	4.98	5 (33%)	19,23,23	7.30	6 (31%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	POP	E	543	5	-	0/6/6/6	-
2	3NM	C	541	-	-	5/10/11/11	0/1/1/1
3	IFP	F	542	-	-	0/6/19/19	0/1/1/1
3	IFP	D	542	-	-	0/6/19/19	0/1/1/1
4	POP	B	543	5	-	0/6/6/6	-
3	IFP	A	542	-	-	0/6/19/19	0/1/1/1
4	POP	C	543	5	-	3/6/6/6	-
3	IFP	C	542	-	-	0/6/19/19	0/1/1/1
3	IFP	E	542	-	-	0/6/19/19	0/1/1/1
4	POP	D	543	5	-	0/6/6/6	-
3	IFP	B	542	-	-	0/6/19/19	0/1/1/1
2	3NM	E	541	-	-	6/10/11/11	0/1/1/1
4	POP	A	543	5	-	0/6/6/6	-
4	POP	F	543	5	-	1/6/6/6	-
2	3NM	D	541	-	-	7/10/11/11	0/1/1/1
2	3NM	F	541	-	-	4/10/11/11	0/1/1/1
2	3NM	A	541	-	-	3/10/11/11	0/1/1/1
2	3NM	B	541	-	-	7/10/11/11	0/1/1/1

The worst 5 of 49 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	541	3NM	C5-S	-11.84	1.50	1.74

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	541	3NM	C5-S	-11.83	1.50	1.74
2	B	541	3NM	C5-S	-11.80	1.50	1.74
2	D	541	3NM	C2-N	11.75	1.61	1.38
2	C	541	3NM	C2-N	11.70	1.61	1.38

The worst 5 of 70 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	541	3NM	C5-S-C3	34.03	108.95	91.34
2	E	541	3NM	C5-S-C3	31.90	107.85	91.34
2	A	541	3NM	C5-S-C3	31.53	107.66	91.34
2	C	541	3NM	C5-S-C3	30.92	107.34	91.34
2	B	541	3NM	C5-S-C3	29.78	106.75	91.34

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	541	3NM	C5-C6-C7-O3
2	B	541	3NM	C7-O3-P-O5
2	B	541	3NM	C7-O3-P-O6
2	B	541	3NM	C5-C6-C7-O3
2	C	541	3NM	N-C3-C4-O1

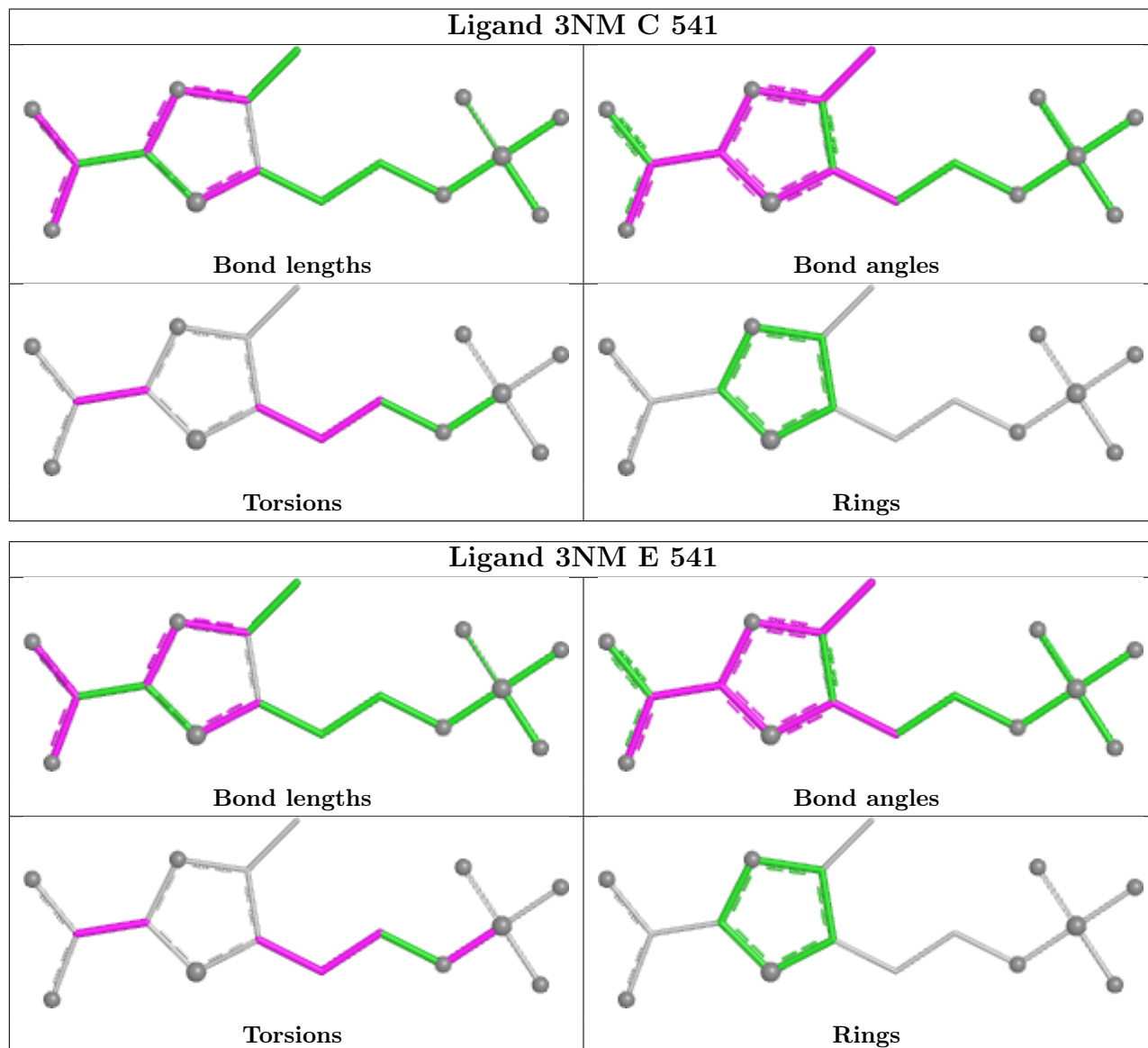
There are no ring outliers.

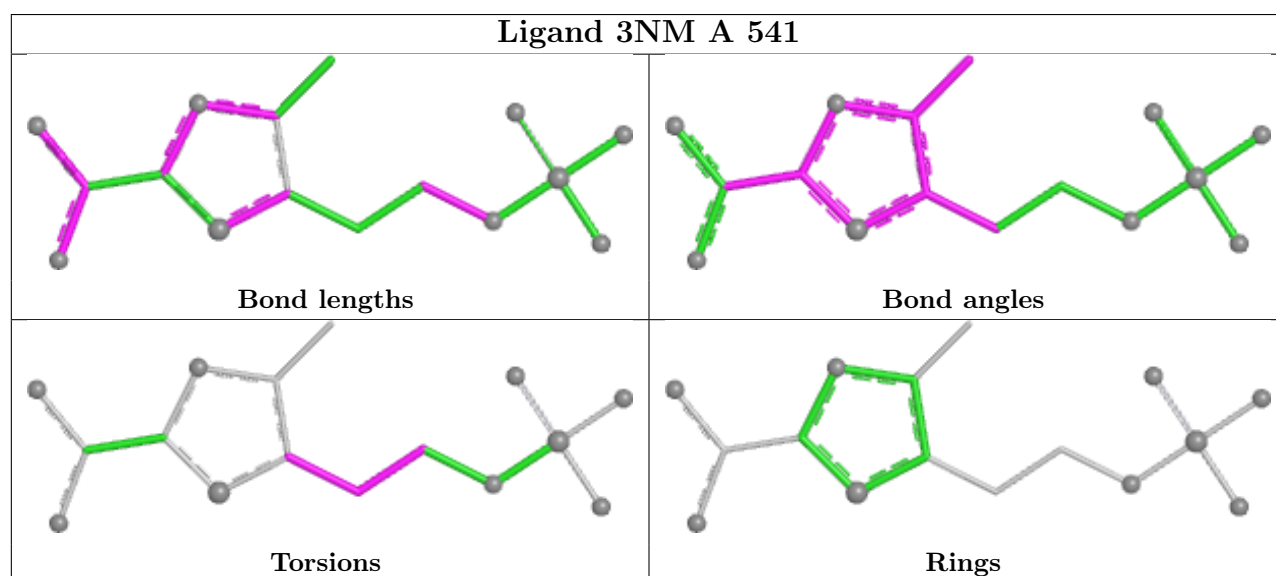
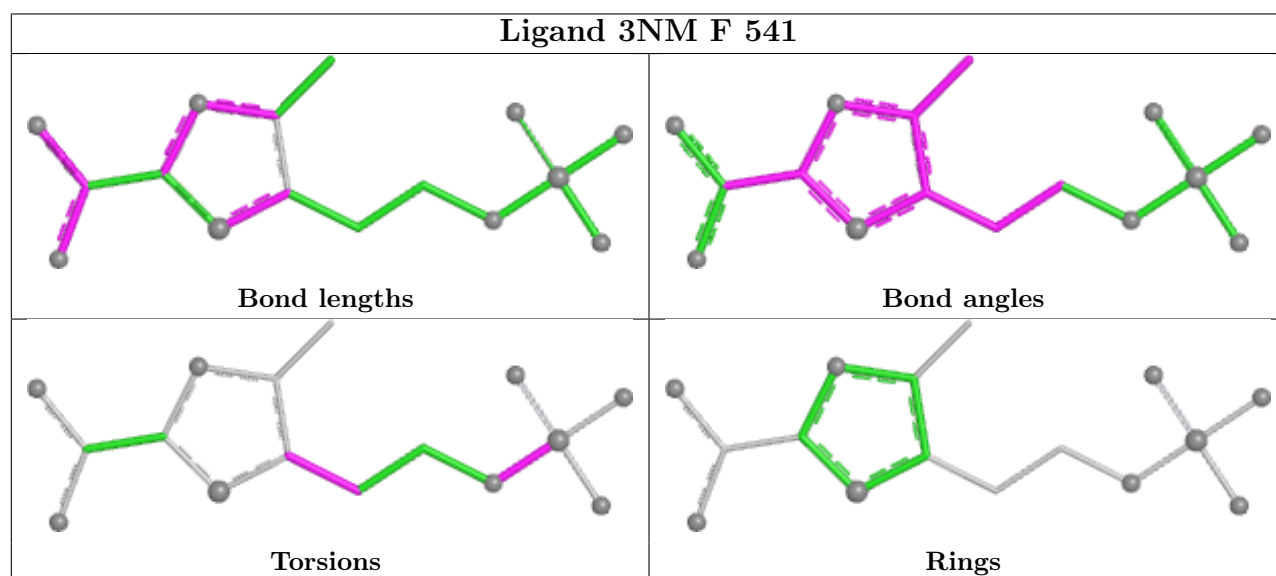
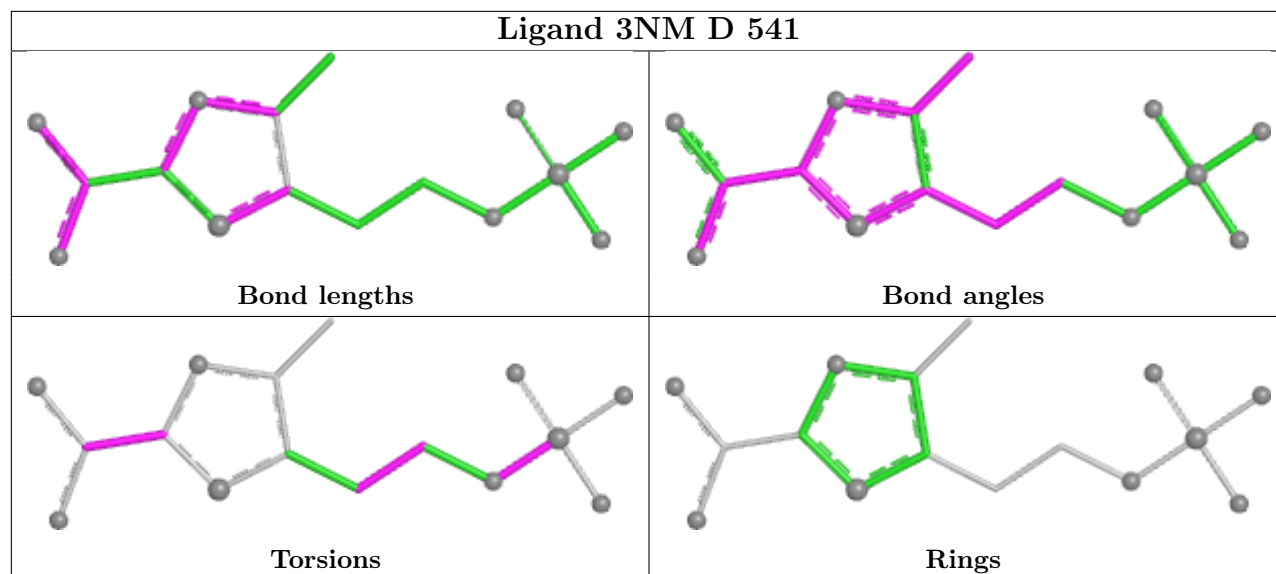
10 monomers are involved in 15 short contacts:

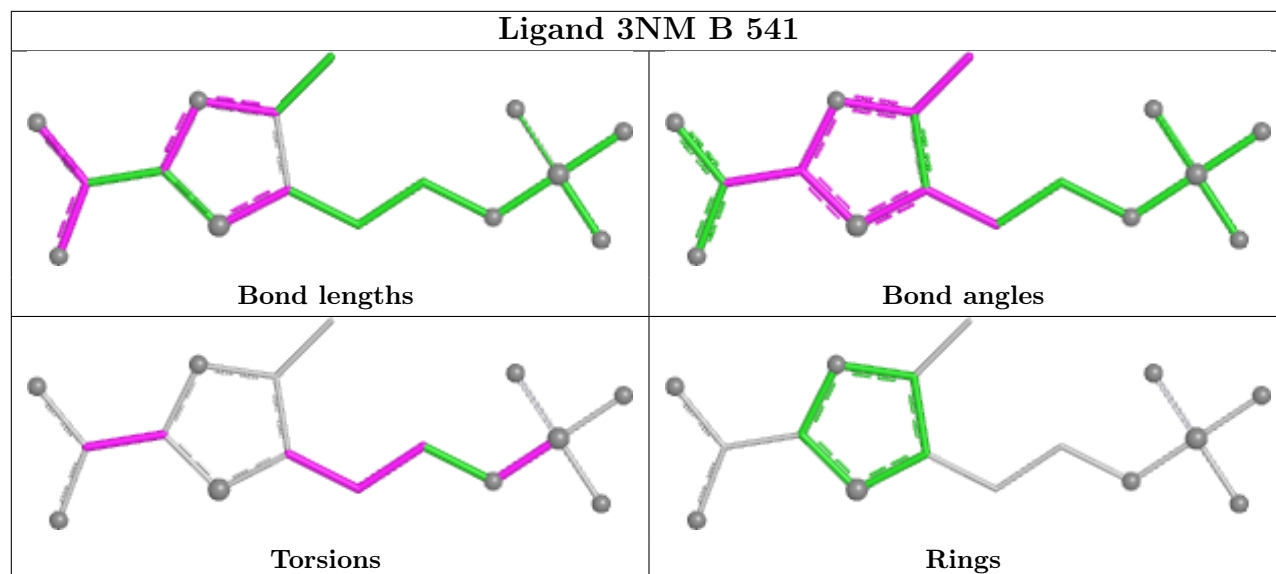
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	543	POP	2	0
3	A	542	IFP	1	0
3	E	542	IFP	2	0
3	B	542	IFP	1	0
2	E	541	3NM	2	0
4	A	543	POP	1	0
2	D	541	3NM	1	0
2	F	541	3NM	2	0
2	A	541	3NM	3	0
2	B	541	3NM	3	0

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 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	507/540 (93%)	-0.27	5 (0%) 79 62	30, 79, 99, 120	0
1	B	507/540 (93%)	-0.22	8 (1%) 70 51	41, 81, 103, 127	0
1	C	507/540 (93%)	-0.33	7 (1%) 73 54	41, 74, 96, 117	0
1	D	507/540 (93%)	-0.33	2 (0%) 88 79	39, 75, 99, 120	0
1	E	505/540 (93%)	-0.28	5 (0%) 79 62	42, 80, 101, 124	0
1	F	507/540 (93%)	-0.32	4 (0%) 82 67	42, 78, 100, 119	0
All	All	3040/3240 (93%)	-0.29	31 (1%) 79 62	30, 78, 101, 127	0

The worst 5 of 31 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	438	ASN	3.8
1	B	438	ASN	3.6
1	E	455	ILE	3.5
1	D	438	ASN	3.3
1	B	109	MET	3.3

### 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 oligosaccharides in this entry.

## 6.4 Ligands

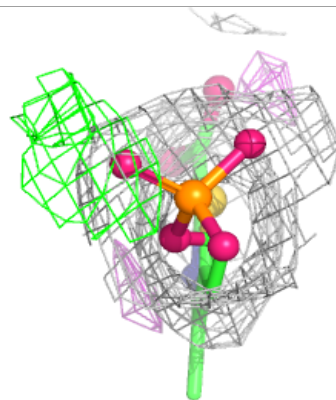
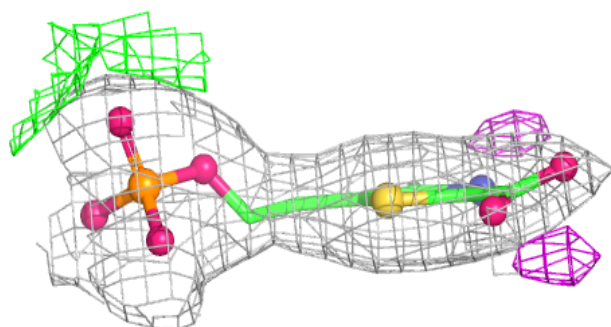
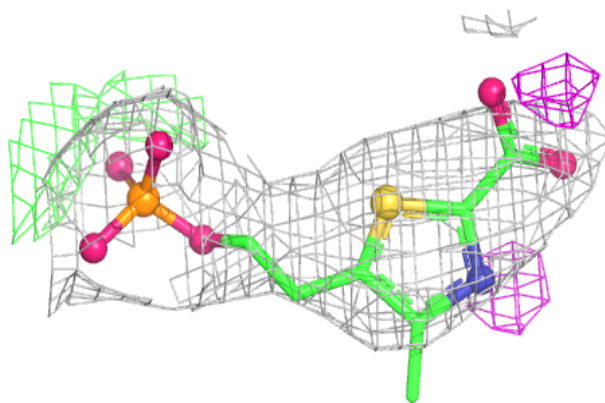
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
5	MG	A	544	1/1	0.89	0.15	66,66,66,66	0
4	POP	E	543	9/9	0.92	0.08	64,79,88,90	0
5	MG	E	544	1/1	0.92	0.13	61,61,61,61	0
2	3NM	B	541	16/16	0.93	0.11	76,78,85,88	0
4	POP	F	543	9/9	0.93	0.08	68,79,86,86	0
2	3NM	D	541	16/16	0.94	0.09	70,75,81,83	0
5	MG	B	544	1/1	0.94	0.18	56,56,56,56	0
3	IFP	B	542	12/12	0.94	0.08	75,77,81,83	0
4	POP	B	543	9/9	0.95	0.08	70,78,81,87	0
5	MG	C	544	1/1	0.95	0.14	56,56,56,56	0
5	MG	D	544	1/1	0.95	0.14	61,61,61,61	0
3	IFP	A	542	12/12	0.95	0.08	70,73,77,77	0
2	3NM	E	541	16/16	0.96	0.09	69,76,79,83	0
5	MG	F	544	1/1	0.96	0.18	60,60,60,60	0
2	3NM	F	541	16/16	0.97	0.08	69,78,87,88	0
3	IFP	C	542	12/12	0.97	0.08	62,66,71,74	0
3	IFP	E	542	12/12	0.97	0.06	68,73,80,80	0
3	IFP	F	542	12/12	0.97	0.07	70,74,78,79	0
4	POP	A	543	9/9	0.97	0.06	64,80,89,91	0
2	3NM	A	541	16/16	0.97	0.07	71,77,84,87	0
4	POP	C	543	9/9	0.97	0.06	62,72,80,82	0
4	POP	D	543	9/9	0.97	0.07	61,72,74,74	0
2	3NM	C	541	16/16	0.98	0.07	65,69,75,77	0
3	IFP	D	542	12/12	0.98	0.07	65,69,72,74	0

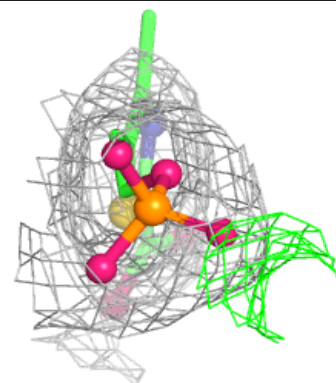
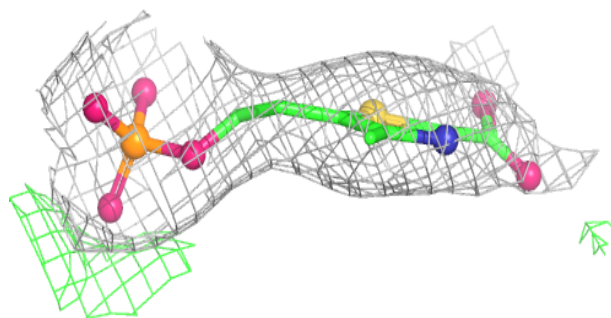
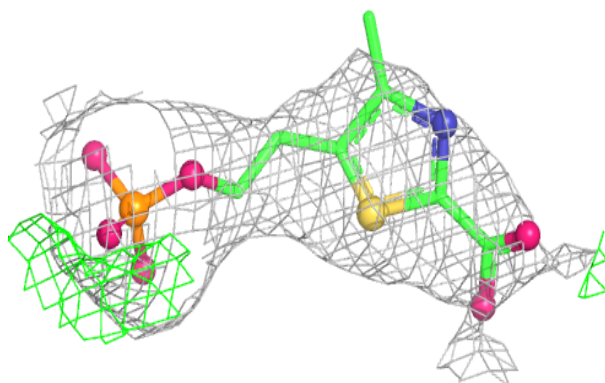
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around 3NM B 541:**

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

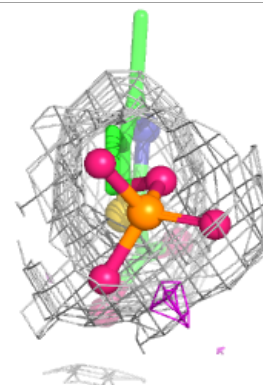
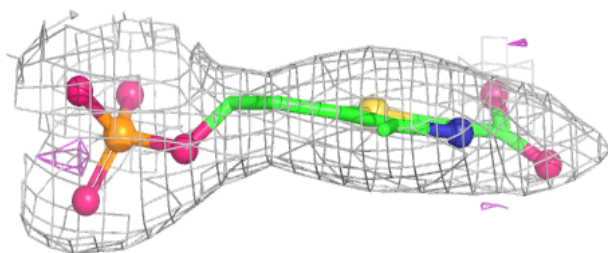
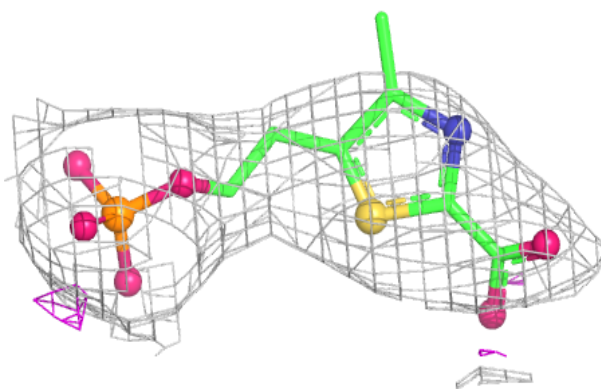
**Electron density around 3NM D 541:**

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

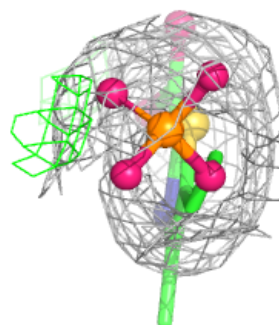
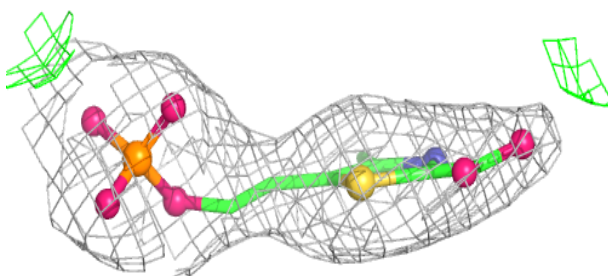
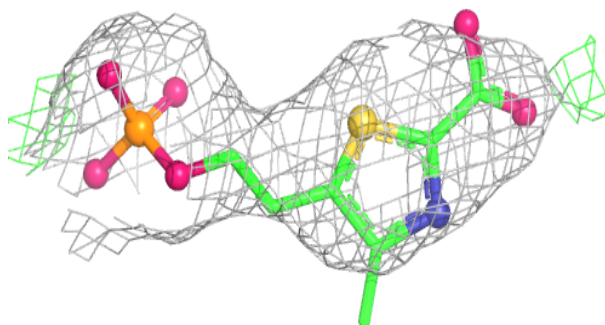


**Electron density around 3NM E 541:**

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

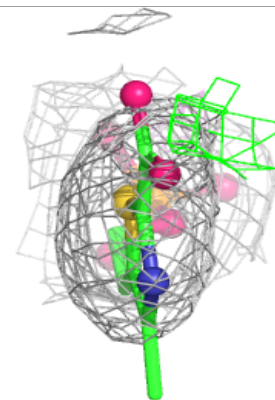
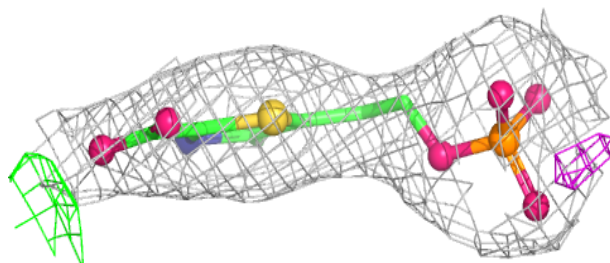
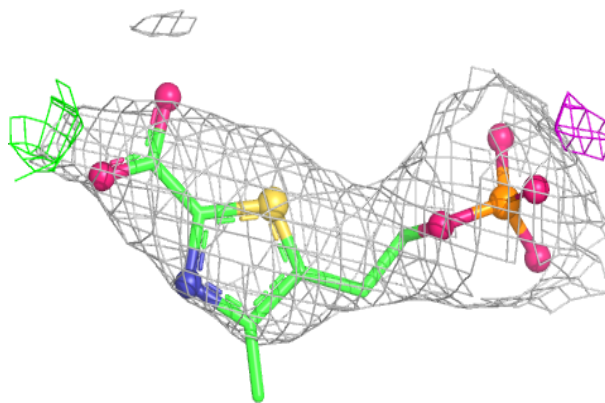
**Electron density around 3NM F 541:**

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

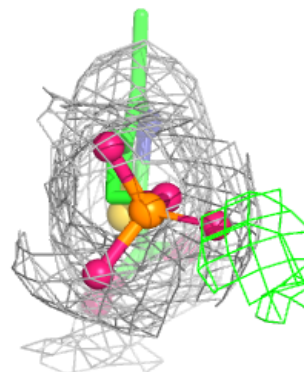
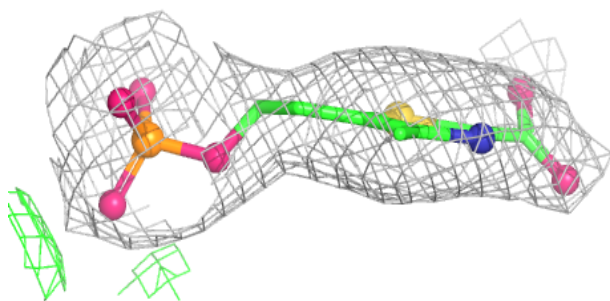
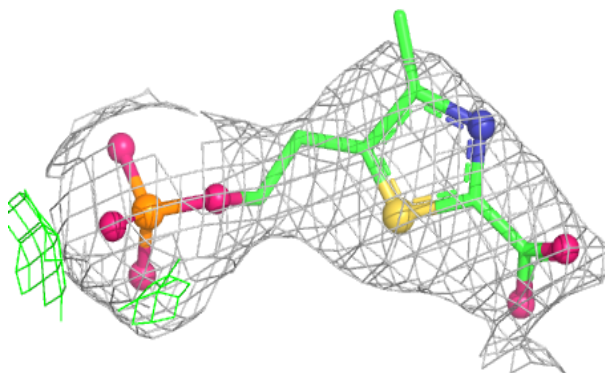


**Electron density around 3NM A 541:**

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

**Electron density around 3NM C 541:**

$2mF_o-DF_c$  (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.