



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:39 AM UTC

PDB ID : 3FBC / pdb\_00003fbc  
Title : Crystal structure of the Mimivirus NDK N62L-R107G double mutant complexed with dTDP  
Authors : Jeudy, S.; Lartigue, A.; Claverie, J.M.; Abergel, C.  
Deposited on : 2008-11-19  
Resolution : 2.60 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

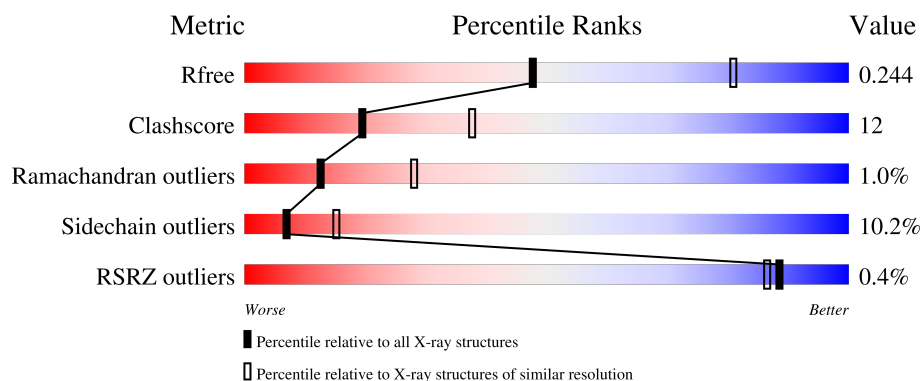
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	142	
1	B	142	
1	C	142	
1	D	142	
1	E	142	

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Mol	Chain	Length	Quality of chain
1	F	142	<div> <div>%</div> <div> <div></div> <div>58%</div> <div>26%</div> <div>7%</div> <div>9%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PO4	D	139	-	-	X	-

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6555 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 Nucleoside diphosphate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	131	Total	C	N	O	S	0	0	0
			1046	664	178	200	4			
1	B	130	Total	C	N	O	S	0	0	0
			1042	662	177	199	4			
1	C	132	Total	C	N	O	S	0	0	0
			1053	668	179	202	4			
1	D	131	Total	C	N	O	S	0	0	0
			1046	664	178	200	4			
1	E	130	Total	C	N	O	S	0	0	0
			1042	662	177	199	4			
1	F	129	Total	C	N	O	S	0	0	0
			1033	657	176	196	4			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	TYR	-	expression tag	UNP Q5UQL3
A	-3	LYS	-	expression tag	UNP Q5UQL3
A	-2	LYS	-	expression tag	UNP Q5UQL3
A	-1	ALA	-	expression tag	UNP Q5UQL3
A	0	GLY	-	expression tag	UNP Q5UQL3
A	1	LEU	-	expression tag	UNP Q5UQL3
A	62	LEU	ASN	engineered mutation	UNP Q5UQL3
A	107	GLY	ARG	engineered mutation	UNP Q5UQL3
B	-4	TYR	-	expression tag	UNP Q5UQL3
B	-3	LYS	-	expression tag	UNP Q5UQL3
B	-2	LYS	-	expression tag	UNP Q5UQL3
B	-1	ALA	-	expression tag	UNP Q5UQL3
B	0	GLY	-	expression tag	UNP Q5UQL3
B	1	LEU	-	expression tag	UNP Q5UQL3
B	62	LEU	ASN	engineered mutation	UNP Q5UQL3
B	107	GLY	ARG	engineered mutation	UNP Q5UQL3
C	-4	TYR	-	expression tag	UNP Q5UQL3

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	LYS	-	expression tag	UNP Q5UQL3
C	-2	LYS	-	expression tag	UNP Q5UQL3
C	-1	ALA	-	expression tag	UNP Q5UQL3
C	0	GLY	-	expression tag	UNP Q5UQL3
C	1	LEU	-	expression tag	UNP Q5UQL3
C	62	LEU	ASN	engineered mutation	UNP Q5UQL3
C	107	GLY	ARG	engineered mutation	UNP Q5UQL3
D	-4	TYR	-	expression tag	UNP Q5UQL3
D	-3	LYS	-	expression tag	UNP Q5UQL3
D	-2	LYS	-	expression tag	UNP Q5UQL3
D	-1	ALA	-	expression tag	UNP Q5UQL3
D	0	GLY	-	expression tag	UNP Q5UQL3
D	1	LEU	-	expression tag	UNP Q5UQL3
D	62	LEU	ASN	engineered mutation	UNP Q5UQL3
D	107	GLY	ARG	engineered mutation	UNP Q5UQL3
E	-4	TYR	-	expression tag	UNP Q5UQL3
E	-3	LYS	-	expression tag	UNP Q5UQL3
E	-2	LYS	-	expression tag	UNP Q5UQL3
E	-1	ALA	-	expression tag	UNP Q5UQL3
E	0	GLY	-	expression tag	UNP Q5UQL3
E	1	LEU	-	expression tag	UNP Q5UQL3
E	62	LEU	ASN	engineered mutation	UNP Q5UQL3
E	107	GLY	ARG	engineered mutation	UNP Q5UQL3
F	-4	TYR	-	expression tag	UNP Q5UQL3
F	-3	LYS	-	expression tag	UNP Q5UQL3
F	-2	LYS	-	expression tag	UNP Q5UQL3
F	-1	ALA	-	expression tag	UNP Q5UQL3
F	0	GLY	-	expression tag	UNP Q5UQL3
F	1	LEU	-	expression tag	UNP Q5UQL3
F	62	LEU	ASN	engineered mutation	UNP Q5UQL3
F	107	GLY	ARG	engineered mutation	UNP Q5UQL3

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

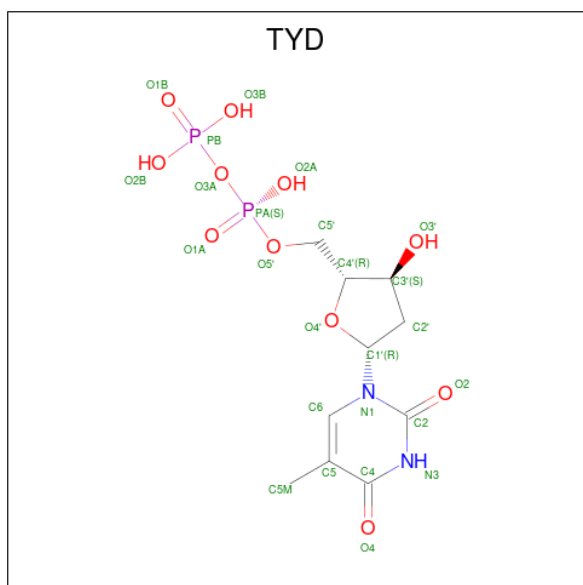
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	1	Total	Mg	0	0
			1	1		
2	F	1	Total	Mg	0	0
			1	1		

- Molecule 3 is THYMIDINE-5'-DIPHOSPHATE (CCD ID: TYD) (formula:  $C_{10}H_{16}N_2O_{11}P_2$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
3	B	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
3	C	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
3	D	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
3	E	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
3	F	1	Total	C	N	O	P	0	0
			25	10	2	11	2		

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula:  $O_4P$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		
4	B	1	Total	O	P	0	0
			5	4	1		
4	C	1	Total	O	P	0	0
			5	4	1		
4	D	1	Total	O	P	0	0
			5	4	1		
4	E	1	Total	O	P	0	0
			5	4	1		
4	F	1	Total	O	P	0	0
			5	4	1		

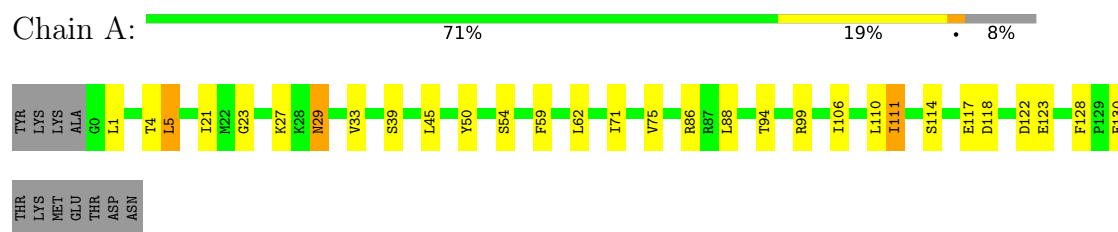
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	19	Total	O	0	0
			19	19		
5	B	13	Total	O	0	0
			13	13		
5	C	24	Total	O	0	0
			24	24		
5	D	18	Total	O	0	0
			18	18		
5	E	18	Total	O	0	0
			18	18		
5	F	15	Total	O	0	0
			15	15		

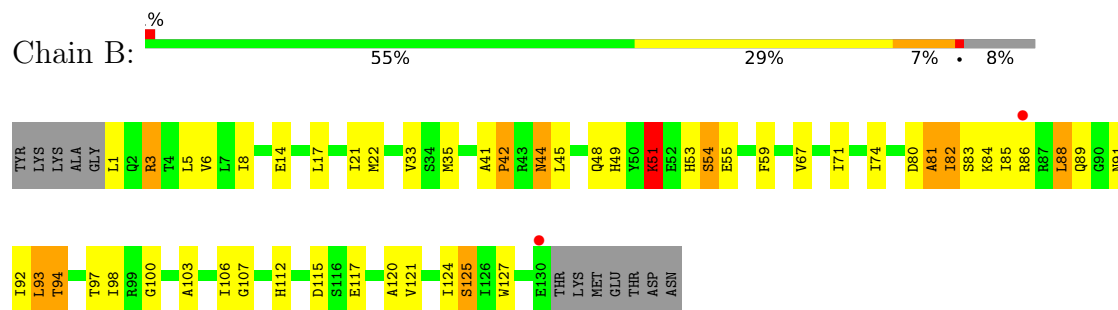
### 3 Residue-property plots

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.

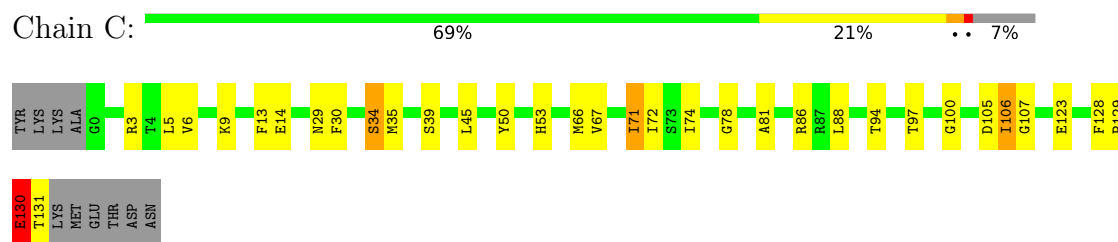
- Molecule 1: Nucleoside diphosphate kinase



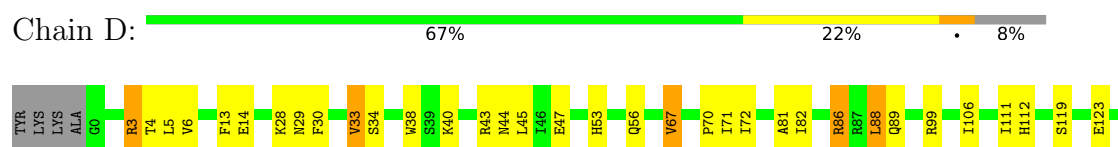
- Molecule 1: Nucleoside diphosphate kinase



- Molecule 1: Nucleoside diphosphate kinase



- Molecule 1: Nucleoside diphosphate kinase





P129
E130
THR
LYS
LYS
GLU
THR
ASP
ASN

● Molecule 1: Nucleoside diphosphate kinase



TYR	LYS	LYS	LYS	ALA	GLY	L1	G2	R3	T4	L5	V6	F13	K28	N29	V33	S34	H35	R43	M44	L45	I46	E47	Q48	K51	E52	H53	S54	E55	F59	D64	F65	M66	I72	S73	I74	G78	T79	D80	A81	I82	S83	K84	I85	R86	H112	E123	E130	THR
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LYS
MET
GLU
THR
ASP
ASN

● Molecule 1: Nucleoside diphosphate kinase



TYR	LYS	LYS	ALA	GLY	L1	L5	V6	L7	I8	K9	P10	E14	I21	R24	N29	V33	S39	R43	M44	L45	H49	E52	E55	D56	S57	Y58	F59	N60	D64	F65	M66	V67	I71	I82	R86	R87	L88	I92	L93	T94	P95	G96	T97
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I98	R99	G100	A103	I106	G107	E108	I111	H112	D115	S116	E117	A120	V121	I124	P129	GLU	THR	LYS	MET	GLU	THR	ASP	ASN
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## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.39Å 153.34Å 185.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.11 – 2.60 48.11 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.11-2.60) 99.6 (48.11-2.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.40 (at 2.61Å)	Xtriage
Refinement program	PHENIX, REFMAC 5.2	Depositor
R, $R_{free}$	0.189 , 0.247 0.188 , 0.244	Depositor DCC
$R_{free}$ test set	1753 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	53.0	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 39.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	6555	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.12% 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: PO4, MG, TYD

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	0/1066	0.85	1/1438 (0.1%)
1	B	0.49	0/1062	0.89	0/1433
1	C	0.54	0/1073	0.87	0/1448
1	D	0.49	0/1066	0.84	0/1438
1	E	0.50	0/1062	0.86	0/1433
1	F	0.51	0/1053	0.85	1/1421 (0.1%)
All	All	0.51	0/6382	0.86	2/8611 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	111	ILE	N-CA-C	5.54	115.66	108.35
1	F	111	ILE	N-CA-C	5.46	115.56	108.35

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	1046	0	1043	14	0
1	B	1042	0	1040	38	0
1	C	1053	0	1050	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1046	0	1043	21	0
1	E	1042	0	1040	18	0
1	F	1033	0	1034	29	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
3	A	25	0	13	1	0
3	B	25	0	13	2	0
3	C	25	0	13	1	0
3	D	25	0	13	2	0
3	E	25	0	13	1	0
3	F	25	0	13	2	0
4	A	5	0	0	1	0
4	B	5	0	0	0	0
4	C	5	0	0	0	0
4	D	5	0	0	2	0
4	E	5	0	0	0	0
4	F	5	0	0	0	0
5	A	19	0	0	1	0
5	B	13	0	0	0	0
5	C	24	0	0	0	0
5	D	18	0	0	3	0
5	E	18	0	0	1	0
5	F	15	0	0	1	0
All	All	6555	0	6328	148	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 148 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)
3:A:138:TYD:H6	3:A:138:TYD:O5'	1.67	0.95
1:A:5:LEU:HD22	1:A:123:GLU:HB3	1.57	0.87
1:B:120:ALA:O	1:B:124:ILE:HG13	1.75	0.86
3:C:138:TYD:H6	3:C:138:TYD:O5'	1.80	0.80
1:B:86:ARG:NH1	1:B:115:ASP:HB3	1.97	0.78

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	129/142 (91%)	122 (95%)	7 (5%)	0	100	100
1	B	128/142 (90%)	113 (88%)	10 (8%)	5 (4%)	2	3
1	C	130/142 (92%)	124 (95%)	5 (4%)	1 (1%)	16	34
1	D	129/142 (91%)	120 (93%)	9 (7%)	0	100	100
1	E	128/142 (90%)	121 (94%)	7 (6%)	0	100	100
1	F	127/142 (89%)	119 (94%)	6 (5%)	2 (2%)	7	16
All	All	771/852 (90%)	719 (93%)	44 (6%)	8 (1%)	12	28

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	82	ILE
1	B	51	LYS
1	B	54	SER
1	B	81	ALA
1	C	130	GLU

### 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	116/126 (92%)	104 (90%)	12 (10%)	7	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	116/126 (92%)	104 (90%)	12 (10%)	7	15
1	C	117/126 (93%)	106 (91%)	11 (9%)	8	18
1	D	116/126 (92%)	104 (90%)	12 (10%)	7	15
1	E	116/126 (92%)	108 (93%)	8 (7%)	14	32
1	F	115/126 (91%)	99 (86%)	16 (14%)	3	7
All	All	696/756 (92%)	625 (90%)	71 (10%)	7	15

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	29	ASN
1	F	39	SER
1	F	71	ILE
1	C	3	ARG
1	B	125	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	29	ASN
1	F	2	GLN
1	D	2	GLN
1	E	89	GLN
1	C	48	GLN

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry

Of 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 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	TYD	A	138	-	25,26,26	1.45	5 (20%)	38,40,40	1.81	7 (18%)
3	TYD	E	138	-	25,26,26	1.46	5 (20%)	38,40,40	1.83	6 (15%)
4	PO4	A	139	-	4,4,4	0.87	0	6,6,6	0.62	0
4	PO4	F	139	-	4,4,4	0.86	0	6,6,6	0.55	0
3	TYD	B	138	-	25,26,26	1.50	5 (20%)	38,40,40	1.81	7 (18%)
3	TYD	D	138	-	25,26,26	1.55	5 (20%)	38,40,40	1.80	8 (21%)
4	PO4	B	139	-	4,4,4	0.85	0	6,6,6	0.53	0
4	PO4	D	139	-	4,4,4	0.86	0	6,6,6	0.69	0
3	TYD	F	138	-	25,26,26	1.51	5 (20%)	38,40,40	1.74	6 (15%)
4	PO4	E	139	-	4,4,4	0.80	0	6,6,6	0.40	0
3	TYD	C	138	2	25,26,26	1.42	4 (16%)	38,40,40	1.85	7 (18%)
4	PO4	C	139	-	4,4,4	0.87	0	6,6,6	0.72	0

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	TYD	A	138	-	-	2/16/28/28	0/2/2/2
3	TYD	E	138	-	-	0/16/28/28	0/2/2/2
3	TYD	B	138	-	-	1/16/28/28	0/2/2/2
3	TYD	D	138	-	-	0/16/28/28	0/2/2/2
3	TYD	F	138	-	-	4/16/28/28	0/2/2/2
3	TYD	C	138	2	-	2/16/28/28	0/2/2/2

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	138	TYD	PA-O3A	3.72	1.63	1.59
3	E	138	TYD	PA-O3A	3.53	1.63	1.59
3	F	138	TYD	C6-C5	3.50	1.40	1.34
3	F	138	TYD	PA-O3A	3.42	1.63	1.59
3	B	138	TYD	PA-O3A	3.40	1.63	1.59

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	138	TYD	N3-C2-N1	5.17	121.62	114.89
3	E	138	TYD	C4-N3-C2	-5.00	120.78	127.34
3	A	138	TYD	N3-C2-N1	4.96	121.35	114.89
3	B	138	TYD	C4-N3-C2	-4.94	120.86	127.34
3	C	138	TYD	C4-N3-C2	-4.89	120.92	127.34

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	138	TYD	PA-O3A-PB-O2B
3	C	138	TYD	PA-O3A-PB-O2B
3	C	138	TYD	PA-O3A-PB-O3B
3	F	138	TYD	PA-O3A-PB-O2B
3	F	138	TYD	PA-O3A-PB-O3B

There are no ring outliers.

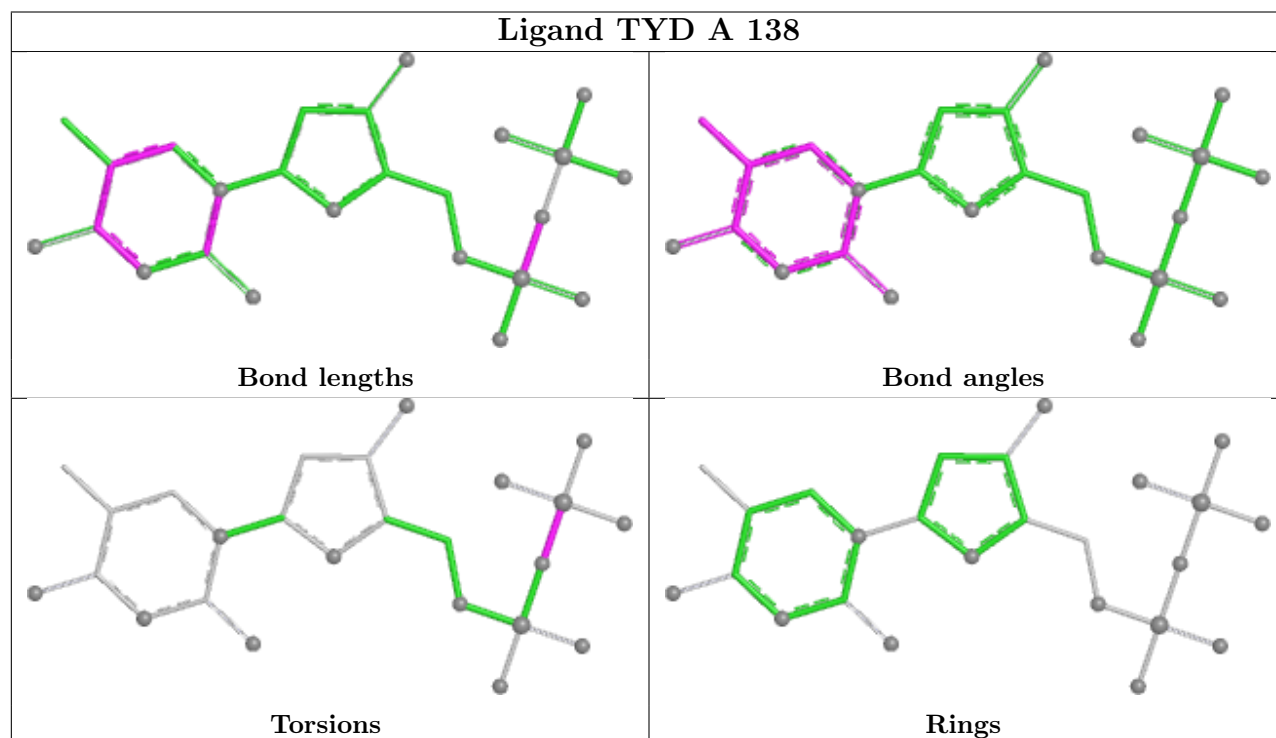
8 monomers are involved in 12 short contacts:

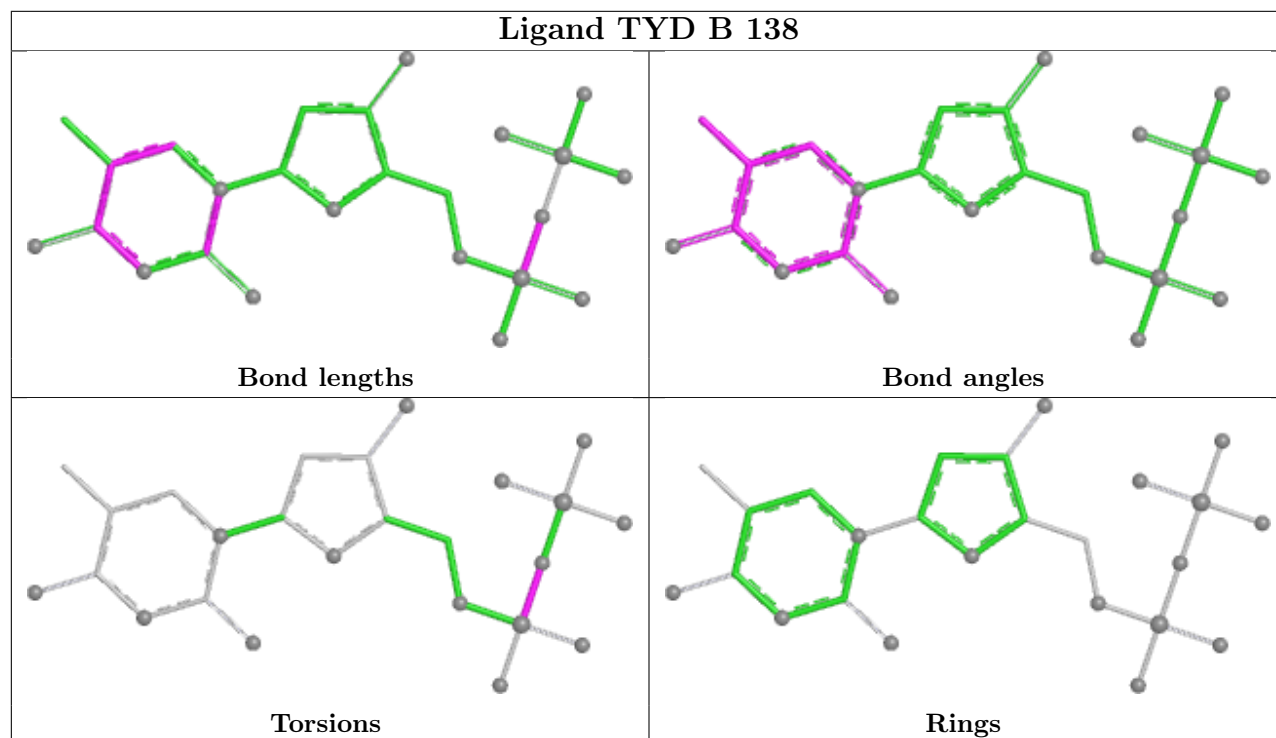
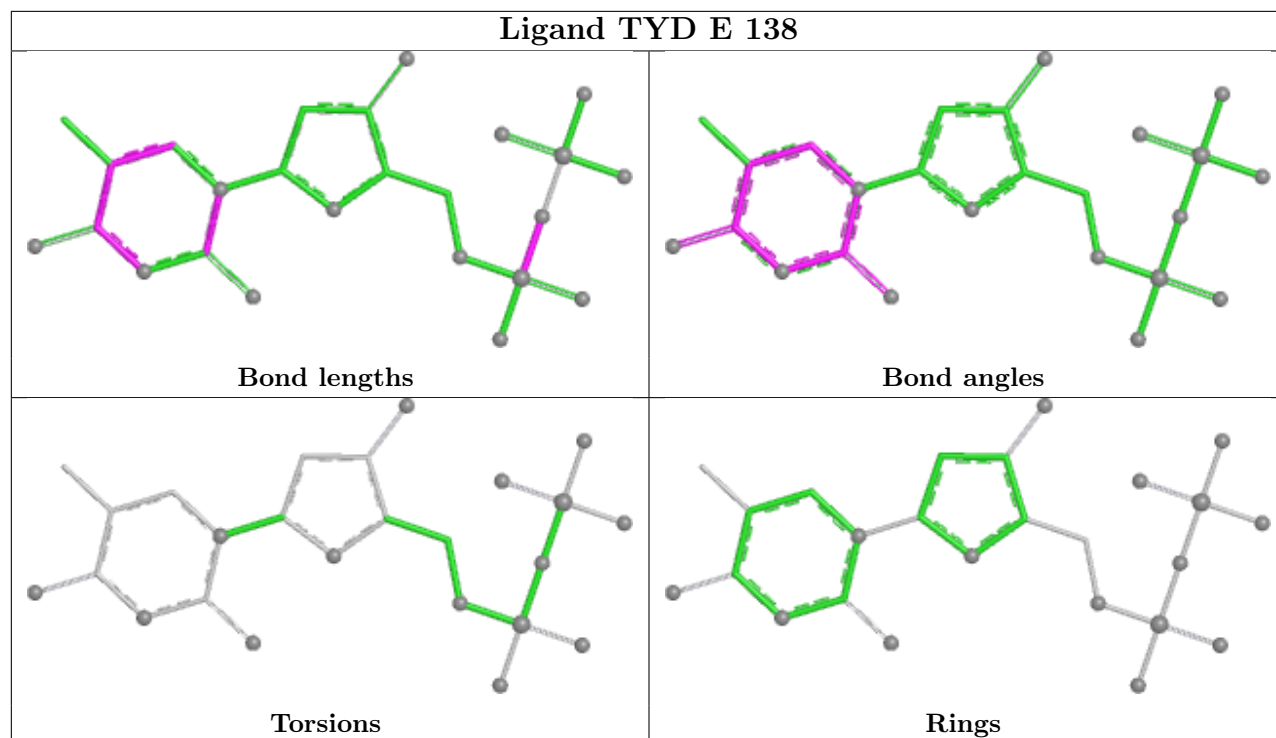
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	138	TYD	1	0
3	E	138	TYD	1	0
4	A	139	PO4	1	0
3	B	138	TYD	2	0
3	D	138	TYD	2	0
4	D	139	PO4	2	0
3	F	138	TYD	2	0
3	C	138	TYD	1	0

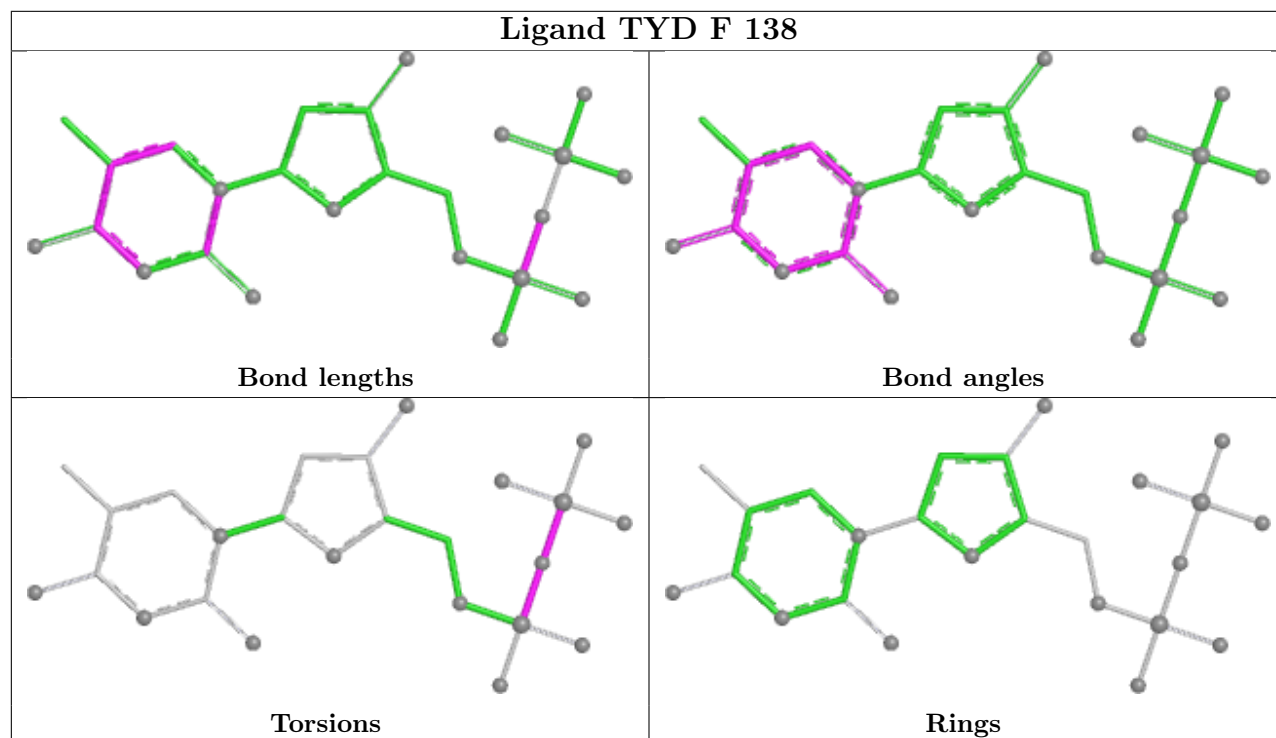
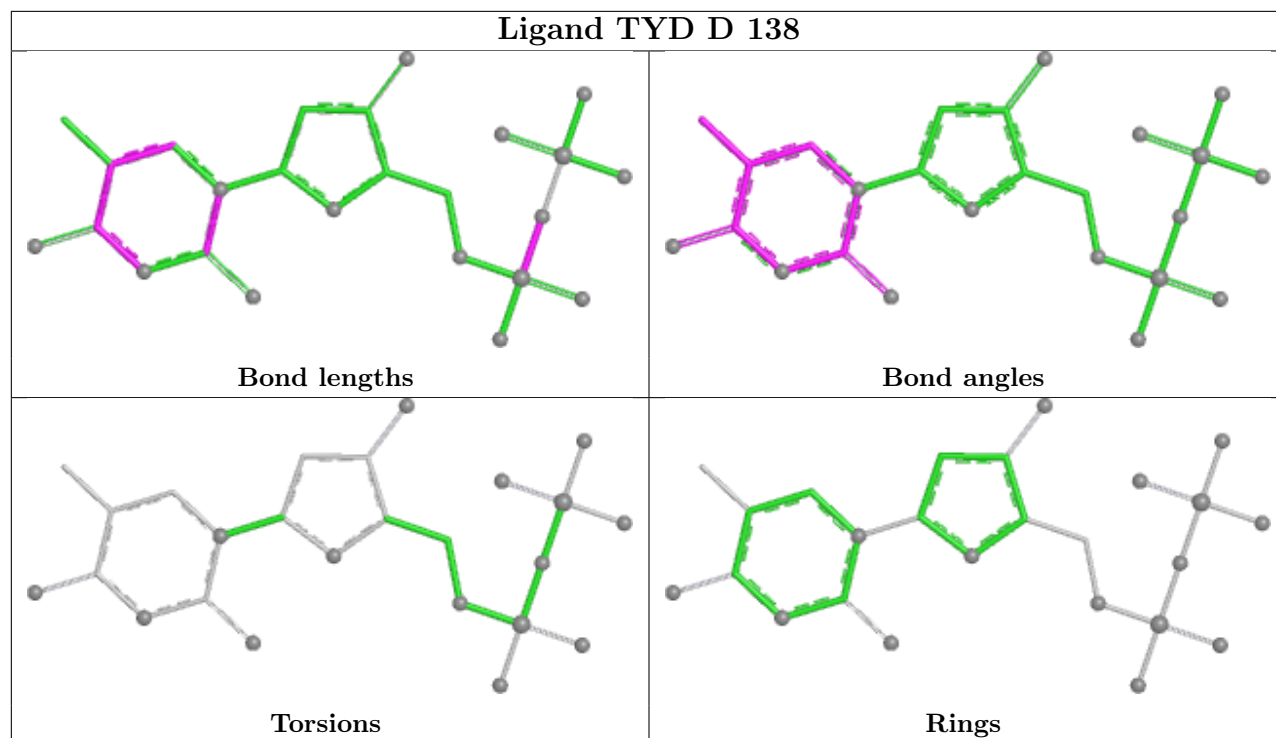
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

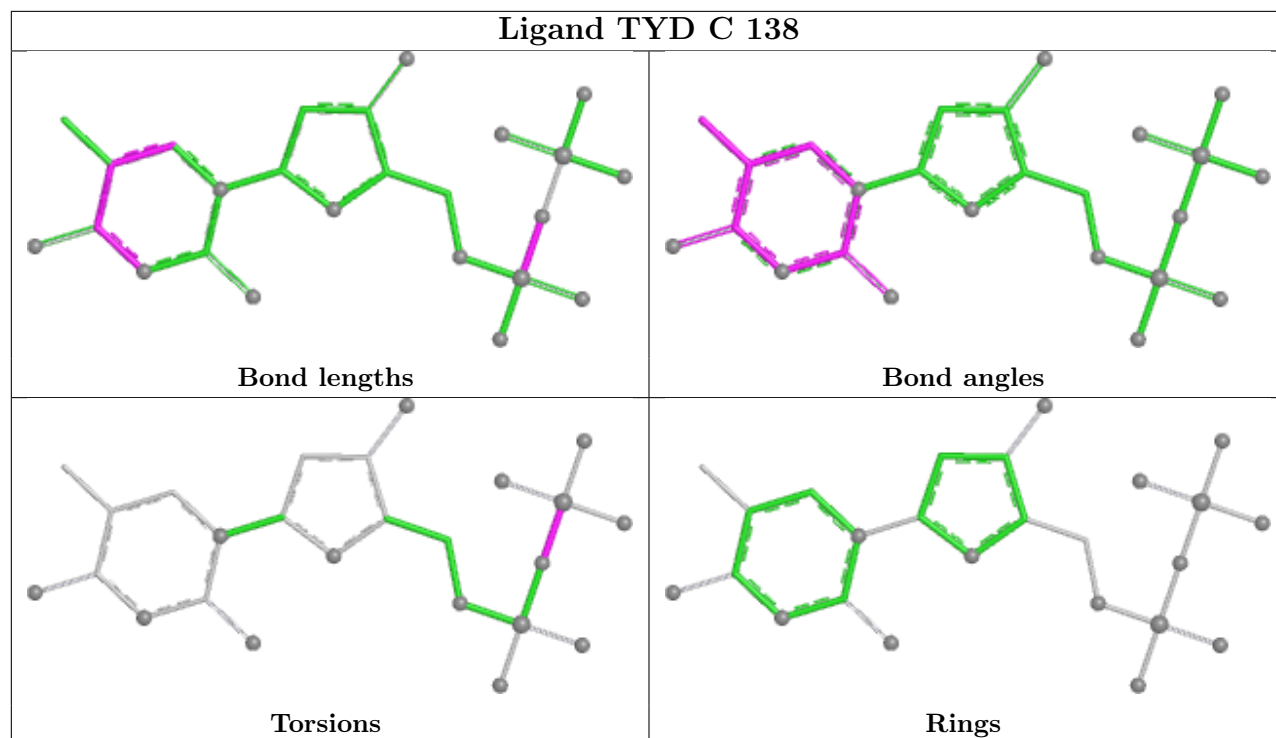


within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question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









## 5.7 Other polymers [i](#)

There are no such residues in this entry.

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

There are no chain breaks in this entry.

## 6 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	131/142 (92%)	-0.50	0 <b>100</b> <b>100</b>	33, 47, 70, 80	0
1	B	130/142 (91%)	0.01	2 (1%) 72 68	32, 52, 79, 95	0
1	C	132/142 (92%)	-0.55	0 <b>100</b> <b>100</b>	33, 45, 62, 78	0
1	D	131/142 (92%)	-0.35	0 <b>100</b> <b>100</b>	35, 52, 72, 82	0
1	E	130/142 (91%)	-0.42	0 <b>100</b> <b>100</b>	35, 49, 77, 97	0
1	F	129/142 (90%)	-0.38	1 (0%) 82 80	35, 49, 74, 97	0
All	All	783/852 (91%)	-0.37	3 (0%) <b>88</b> <b>86</b>	32, 49, 73, 97	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	86	ARG	3.0
1	B	130	GLU	2.6
1	F	58	TYR	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 oligosaccharides 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,

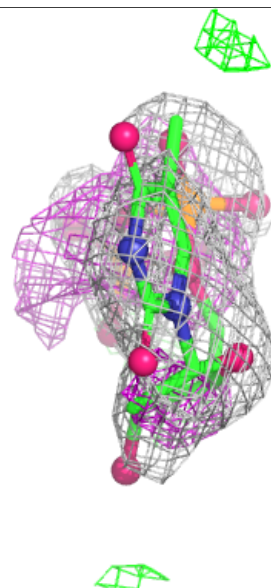
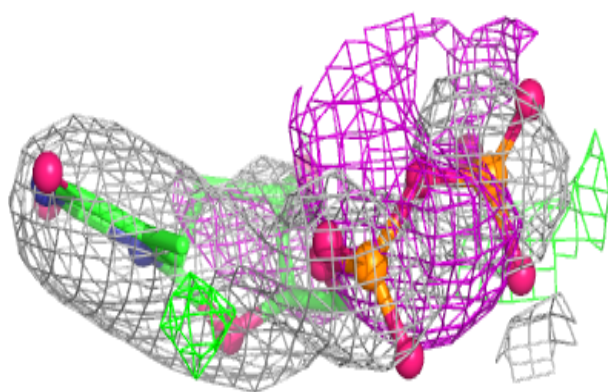
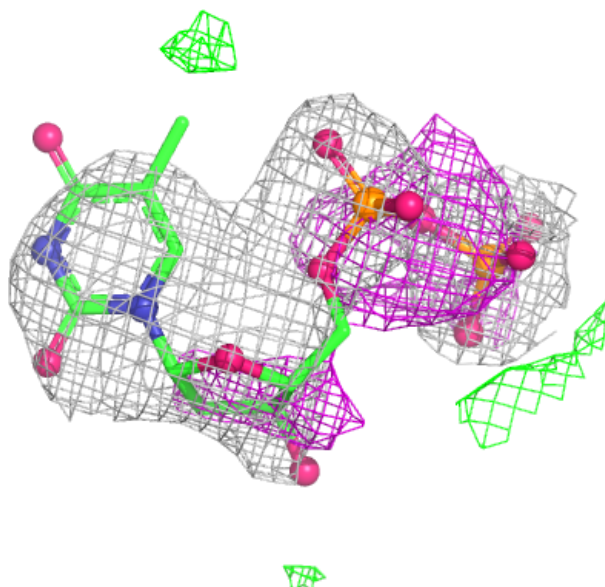
median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	TYD	E	138	25/25	0.71	0.16	76,100,116,122	0
2	MG	B	161	1/1	0.75	0.28	94,94,94,94	0
3	TYD	B	138	25/25	0.76	0.16	75,101,116,124	0
3	TYD	D	138	25/25	0.81	0.13	67,79,91,97	0
2	MG	C	162	1/1	0.81	0.15	72,72,72,72	0
3	TYD	F	138	25/25	0.81	0.13	74,97,103,113	0
4	PO4	D	139	5/5	0.81	0.24	68,77,86,87	0
2	MG	A	160	1/1	0.83	0.21	83,83,83,83	0
3	TYD	A	138	25/25	0.84	0.12	59,77,89,94	0
2	MG	D	163	1/1	0.85	0.17	78,78,78,78	0
2	MG	E	164	1/1	0.85	0.19	84,84,84,84	0
3	TYD	C	138	25/25	0.86	0.12	68,75,88,96	0
2	MG	F	165	1/1	0.87	0.11	75,75,75,75	0
4	PO4	A	139	5/5	0.92	0.14	59,60,70,74	0
4	PO4	B	139	5/5	0.94	0.17	65,65,78,82	0
4	PO4	C	139	5/5	0.96	0.14	49,52,69,75	0
4	PO4	E	139	5/5	0.96	0.13	60,60,75,76	0
4	PO4	F	139	5/5	0.96	0.09	57,59,71,72	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 TYD E 138:**

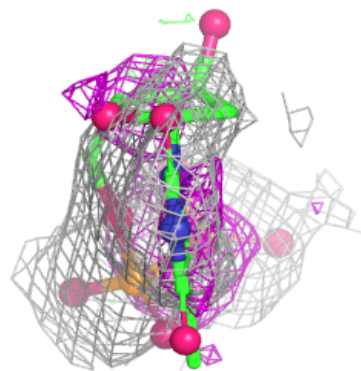
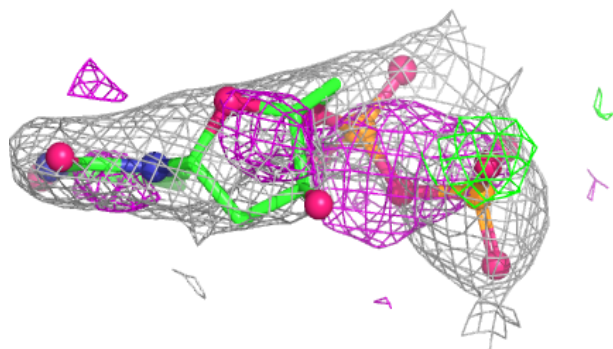
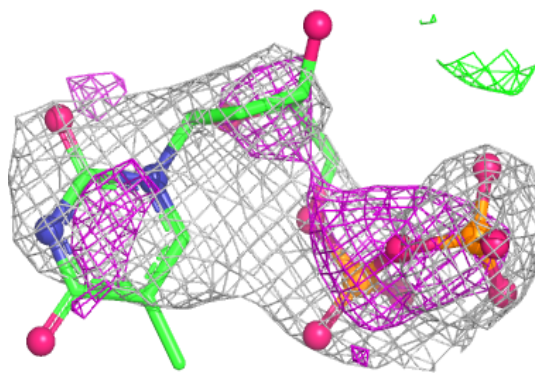
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



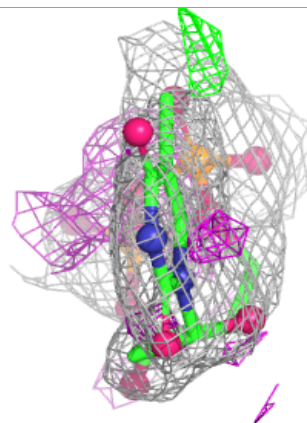
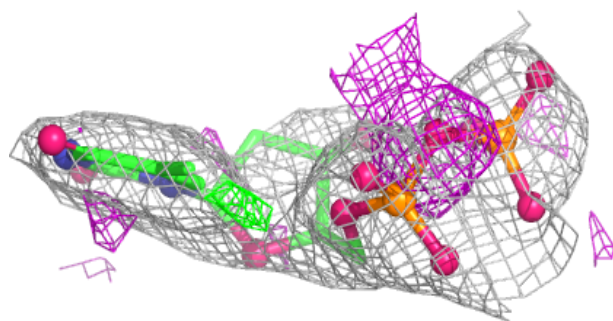
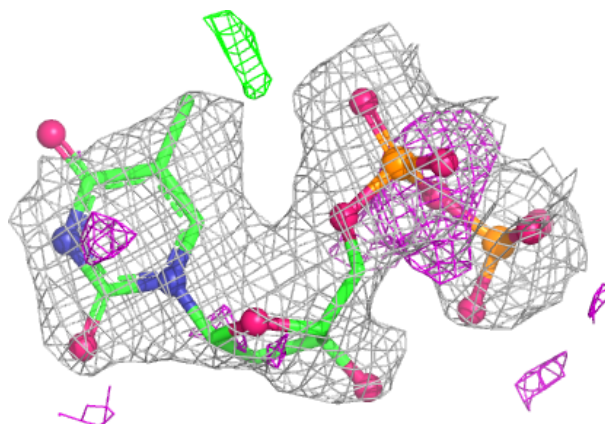


**Electron density around TYD B 138:**

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

**Electron density around TYD D 138:**

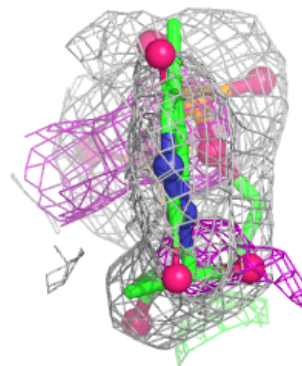
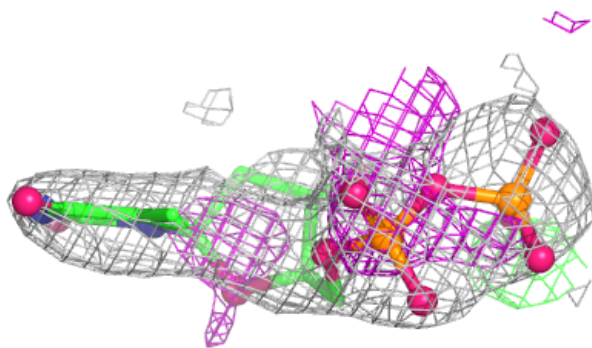
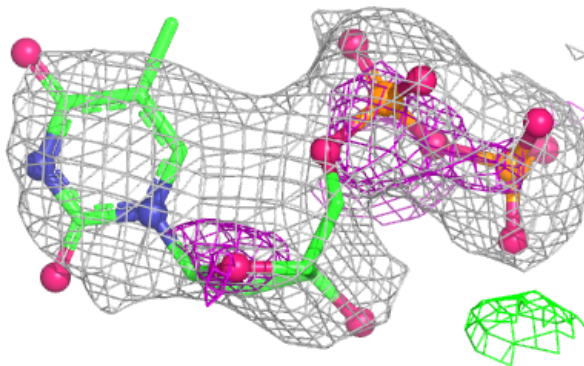
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



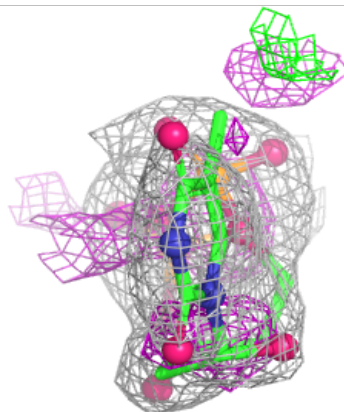
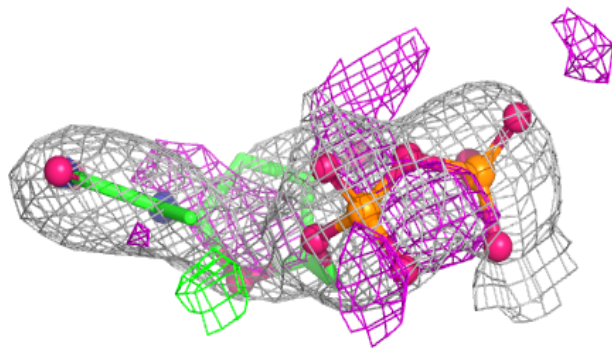
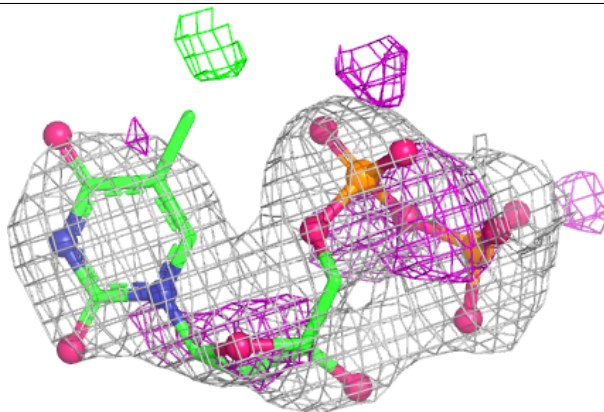


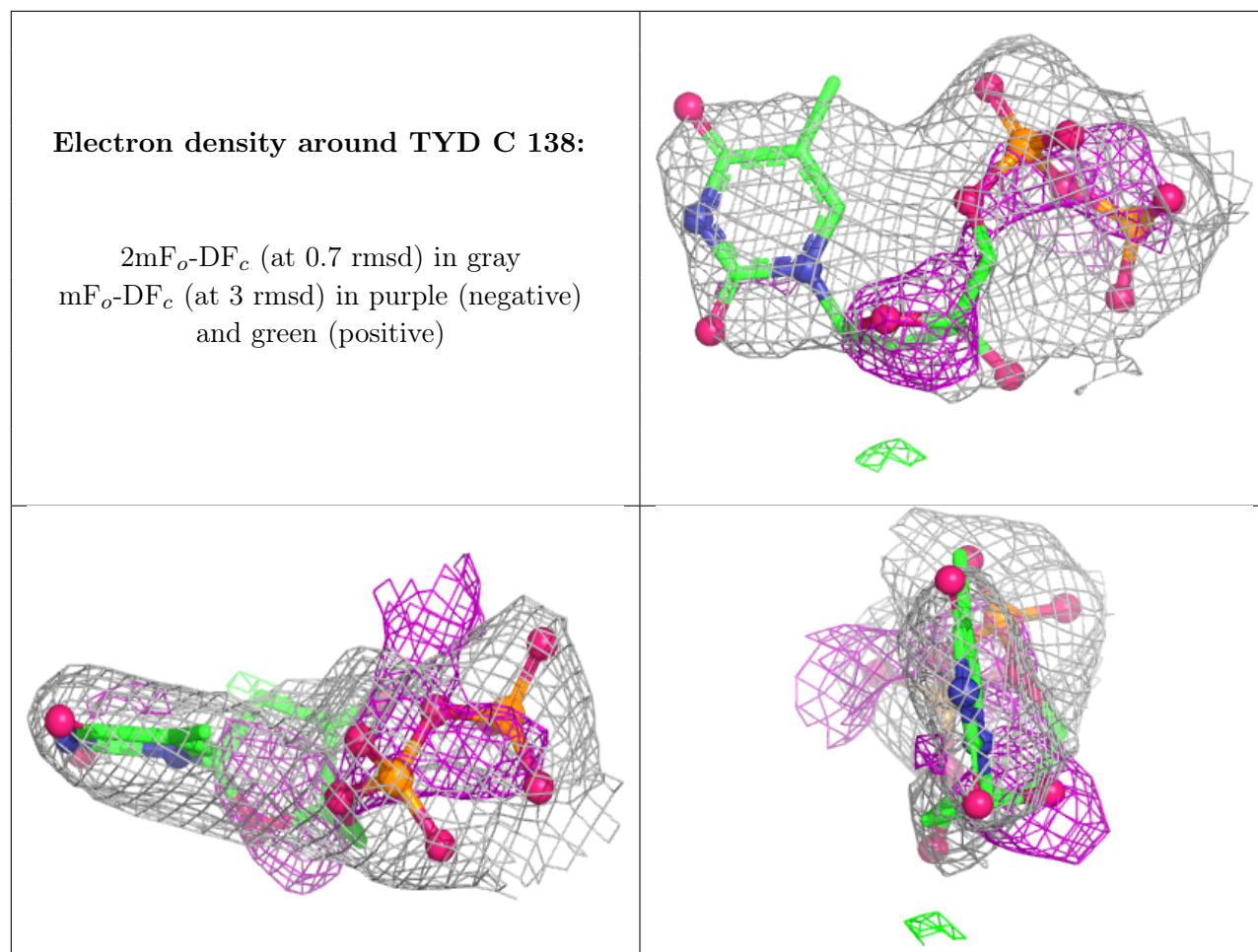
**Electron density around TYD F 138:**

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

**Electron density around TYD A 138:**

$2mF_o-DF_c$  (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.