



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 26, 2024 – 04:23 PM EDT

PDB ID : 2AG1  
Title : Crystal structure of Benzaldehyde lyase (BAL)- SeMet  
Authors : Mosbacher, T.G.; Mueller, M.; Schulz, G.E.  
Deposited on : 2005-07-26  
Resolution : 2.58 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	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

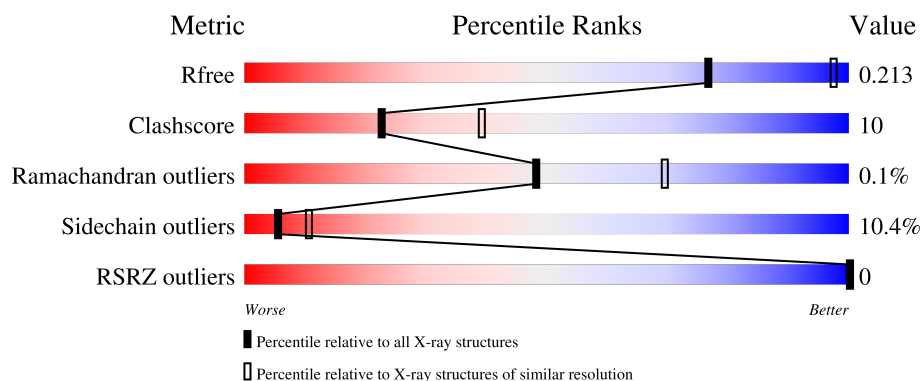
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.58 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))
$R_{free}$	164625	4456 (2.60-2.56)
Clashscore	180529	4905 (2.60-2.56)
Ramachandran outliers	177936	4847 (2.60-2.56)
Sidechain outliers	177891	4847 (2.60-2.56)
RSRZ outliers	164620	4456 (2.60-2.56)

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	563	
1	B	563	
1	C	563	
1	D	563	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16808 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 benzaldehyde lyase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	553	Total	C	N	O	S	Se	0	0	0
			4074	2573	722	763	5	11			
1	B	553	Total	C	N	O	S	Se	0	0	0
			4074	2573	722	763	5	11			
1	C	553	Total	C	N	O	S	Se	0	0	0
			4074	2573	722	763	5	11			
1	D	553	Total	C	N	O	S	Se	0	0	0
			4074	2573	722	763	5	11			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	GB 9965498
A	3	MSE	MET	modified residue	GB 9965498
A	121	MSE	MET	modified residue	GB 9965498
A	133	MSE	MET	modified residue	GB 9965498
A	143	MSE	MET	modified residue	GB 9965498
A	167	MSE	MET	modified residue	GB 9965498
A	244	MSE	MET	modified residue	GB 9965498
A	252	MSE	MET	modified residue	GB 9965498
A	275	MSE	MET	modified residue	GB 9965498
A	404	MSE	MET	modified residue	GB 9965498
A	421	MSE	MET	modified residue	GB 9965498
A	473	MSE	MET	modified residue	GB 9965498
A	559	MSE	MET	modified residue	GB 9965498
B	1	MSE	MET	modified residue	GB 9965498
B	3	MSE	MET	modified residue	GB 9965498
B	121	MSE	MET	modified residue	GB 9965498
B	133	MSE	MET	modified residue	GB 9965498
B	143	MSE	MET	modified residue	GB 9965498
B	167	MSE	MET	modified residue	GB 9965498
B	244	MSE	MET	modified residue	GB 9965498
B	252	MSE	MET	modified residue	GB 9965498

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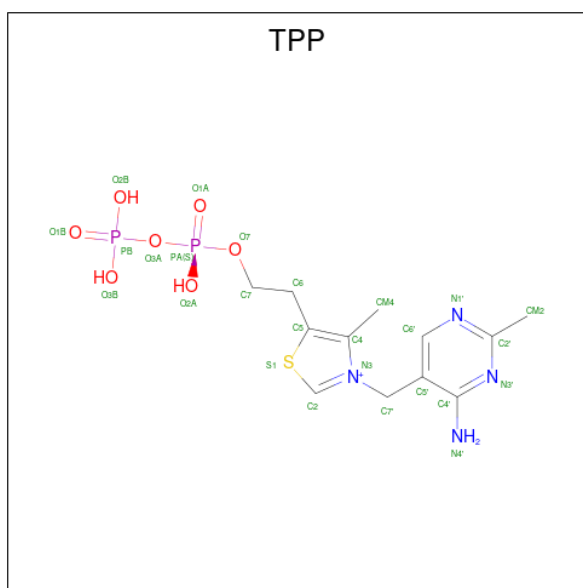
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Chain	Residue	Modelled	Actual	Comment	Reference
B	275	MSE	MET	modified residue	GB 9965498
B	404	MSE	MET	modified residue	GB 9965498
B	421	MSE	MET	modified residue	GB 9965498
B	473	MSE	MET	modified residue	GB 9965498
B	559	MSE	MET	modified residue	GB 9965498
C	1	MSE	MET	modified residue	GB 9965498
C	3	MSE	MET	modified residue	GB 9965498
C	121	MSE	MET	modified residue	GB 9965498
C	133	MSE	MET	modified residue	GB 9965498
C	143	MSE	MET	modified residue	GB 9965498
C	167	MSE	MET	modified residue	GB 9965498
C	244	MSE	MET	modified residue	GB 9965498
C	252	MSE	MET	modified residue	GB 9965498
C	275	MSE	MET	modified residue	GB 9965498
C	404	MSE	MET	modified residue	GB 9965498
C	421	MSE	MET	modified residue	GB 9965498
C	473	MSE	MET	modified residue	GB 9965498
C	559	MSE	MET	modified residue	GB 9965498
D	1	MSE	MET	modified residue	GB 9965498
D	3	MSE	MET	modified residue	GB 9965498
D	121	MSE	MET	modified residue	GB 9965498
D	133	MSE	MET	modified residue	GB 9965498
D	143	MSE	MET	modified residue	GB 9965498
D	167	MSE	MET	modified residue	GB 9965498
D	244	MSE	MET	modified residue	GB 9965498
D	252	MSE	MET	modified residue	GB 9965498
D	275	MSE	MET	modified residue	GB 9965498
D	404	MSE	MET	modified residue	GB 9965498
D	421	MSE	MET	modified residue	GB 9965498
D	473	MSE	MET	modified residue	GB 9965498
D	559	MSE	MET	modified residue	GB 9965498

- Molecule 2 is MAGNESIUM ION (three-letter code: 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

- Molecule 3 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula:  $C_{12}H_{19}N_4O_7P_2S$ ).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
3	B	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
3	C	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
3	D	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		

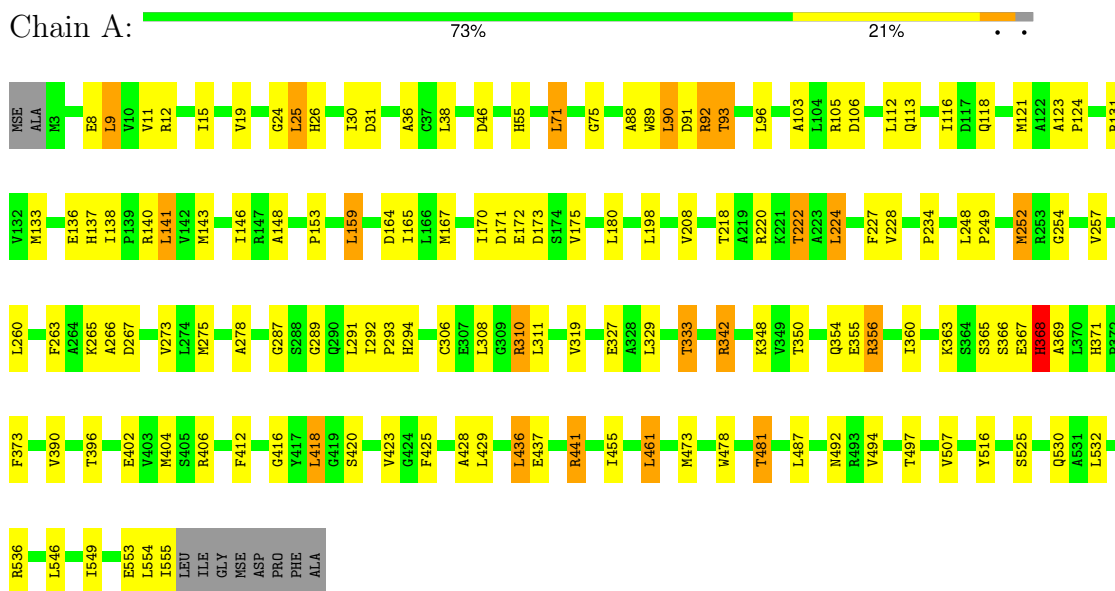
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	82	Total	O	0	0
			82	82		
4	B	62	Total	O	0	0
			62	62		
4	C	114	Total	O	0	0
			114	114		
4	D	146	Total	O	0	0
			146	146		

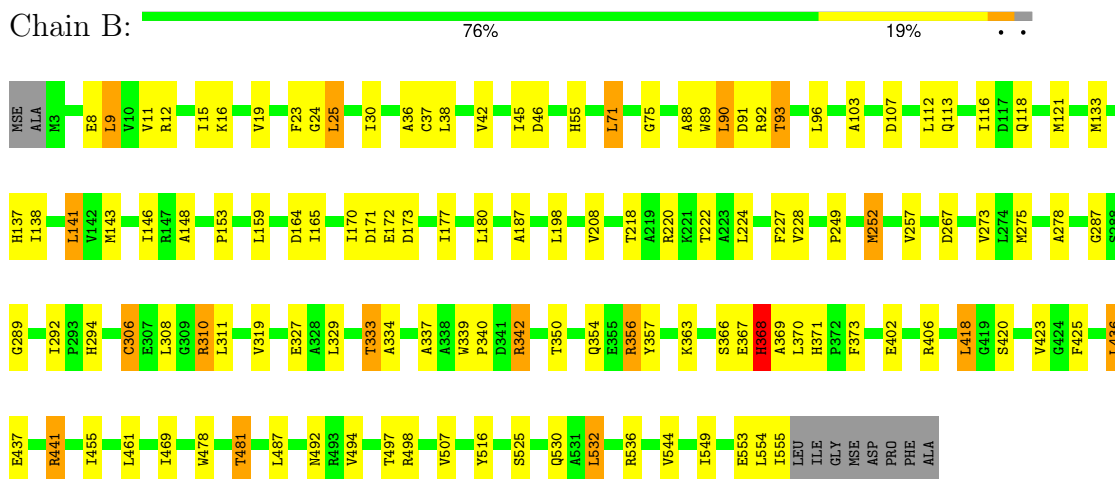
### 3 Residue-property plots

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.

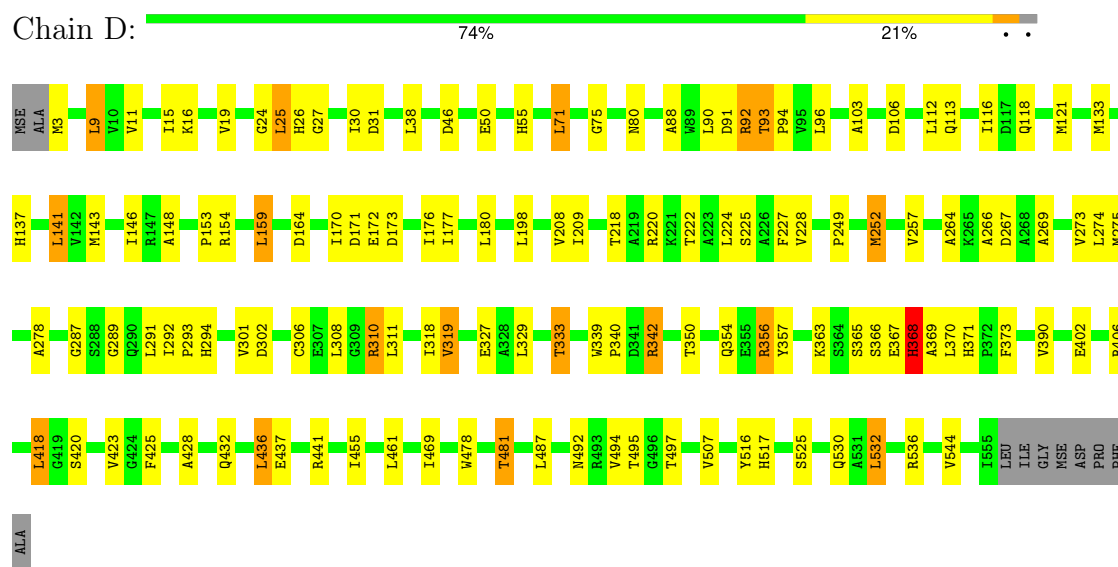
- Molecule 1: benzaldehyde lyase



- Molecule 1: benzaldehyde lyase



- Molecule 1: benzaldehyde lyase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	150.16Å 150.16Å 195.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.82 – 2.58 24.82 – 2.58	Depositor EDS
% Data completeness (in resolution range)	100.0 (24.82-2.58) 100.0 (24.82-2.58)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	127.44 (at 2.57Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.212 , 0.245 0.216 , 0.213	Depositor DCC
$R_{free}$ test set	4048 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	37.8	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 24.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.38$ , $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	0.079 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	16808	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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: TPP, MG

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	0.58	0/4147	0.71	3/5640 (0.1%)
1	B	0.57	1/4147 (0.0%)	0.72	2/5640 (0.0%)
1	C	0.65	1/4147 (0.0%)	0.76	4/5640 (0.1%)
1	D	0.70	1/4147 (0.0%)	0.76	2/5640 (0.0%)
All	All	0.63	3/16588 (0.0%)	0.74	11/22560 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
1	C	0	2
1	D	0	2
All	All	0	7

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	370	LEU	C-N	-5.94	1.20	1.34
1	D	370	LEU	C-N	-5.58	1.21	1.34
1	C	370	LEU	C-N	-5.24	1.22	1.34

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	92	ARG	NE-CZ-NH1	7.52	124.06	120.30
1	A	92	ARG	NE-CZ-NH1	6.69	123.64	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	LEU	CA-CB-CG	6.46	130.16	115.30
1	D	92	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	D	25	LEU	CA-CB-CG	5.92	128.91	115.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	365	SER	Peptide
1	A	368	HIS	Peptide
1	B	368	HIS	Peptide
1	C	365	SER	Peptide
1	C	368	HIS	Peptide

## 5.2 Too-close contacts

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	4074	0	4064	95	3
1	B	4074	0	4064	74	1
1	C	4074	0	4064	84	0
1	D	4074	0	4064	90	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
3	A	26	0	16	4	0
3	B	26	0	16	1	0
3	C	26	0	16	1	0
3	D	26	0	16	1	0
4	A	82	0	0	11	0
4	B	62	0	0	7	0
4	C	114	0	0	7	0
4	D	146	0	0	14	0
All	All	16808	0	16320	336	3

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 10.

The worst 5 of 336 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:C:167:MSE:SE	1:C:167:MSE:CE	2.14	1.45
1:D:133:MSE:SE	1:D:133:MSE:CE	2.16	1.43
1:A:133:MSE:SE	1:A:133:MSE:CE	2.19	1.40
1:A:167:MSE:SE	1:A:167:MSE:CE	2.19	1.40
1:B:133:MSE:SE	1:B:133:MSE:CE	2.18	1.39

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:265:LYS:O	1:A:265:LYS:O[6_555]	1.92	0.28
1:A:406:ARG:NH2	1:B:267:ASP:OD1[5_565]	2.09	0.11
1:A:348:LYS:CD	1:A:355:GLU:OE2[6_555]	2.10	0.10

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	551/563 (98%)	529 (96%)	21 (4%)	1 (0%)	44	64
1	B	551/563 (98%)	528 (96%)	22 (4%)	1 (0%)	44	64
1	C	551/563 (98%)	530 (96%)	20 (4%)	1 (0%)	44	64
1	D	551/563 (98%)	530 (96%)	21 (4%)	0	100	100
All	All	2204/2252 (98%)	2117 (96%)	84 (4%)	3 (0%)	48	69

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	554	LEU
1	C	554	LEU
1	B	554	LEU

### 5.3.2 Protein sidechains ⓘ

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	412/406 (102%)	370 (90%)	42 (10%)	6	11
1	B	412/406 (102%)	369 (90%)	43 (10%)	5	11
1	C	412/406 (102%)	369 (90%)	43 (10%)	5	11
1	D	412/406 (102%)	368 (89%)	44 (11%)	5	10
All	All	1648/1624 (102%)	1476 (90%)	172 (10%)	5	11

5 of 172 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	368	HIS
1	D	224	LEU
1	C	441	ARG
1	D	25	LEU
1	D	327	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 58 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	26	HIS
1	D	371	HIS
1	C	196	GLN
1	D	354	GLN
1	D	168	ASN

### 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 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	TPP	B	612	2	23,27,27	5.19	7 (30%)	30,40,40	2.19	12 (40%)
3	TPP	A	602	2	23,27,27	6.21	5 (21%)	30,40,40	2.15	12 (40%)
3	TPP	D	632	2	23,27,27	6.00	5 (21%)	30,40,40	2.06	8 (26%)
3	TPP	C	622	2	23,27,27	6.24	6 (26%)	30,40,40	1.97	9 (30%)

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	TPP	B	612	2	-	6/16/17/17	0/2/2/2
3	TPP	A	602	2	-	10/16/17/17	0/2/2/2
3	TPP	D	632	2	-	3/16/17/17	0/2/2/2
3	TPP	C	622	2	-	6/16/17/17	0/2/2/2

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	TPP	C6-C5	-27.61	1.34	1.51
3	C	622	TPP	C6-C5	-26.96	1.35	1.51
3	D	632	TPP	C6-C5	-26.28	1.35	1.51
3	B	612	TPP	C6-C5	-21.26	1.38	1.51
3	C	622	TPP	CM4-C4	-8.37	1.32	1.49

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	632	TPP	CM2-C2'-N1'	6.35	123.95	117.20
3	C	622	TPP	C7'-N3-C2	-5.20	115.96	125.35
3	A	602	TPP	N4'-C4'-N3'	4.82	123.53	117.03
3	B	612	TPP	N4'-C4'-N3'	4.42	122.99	117.03
3	C	622	TPP	C6'-N1'-C2'	4.28	123.10	116.07

There are no chirality outliers.

5 of 25 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	602	TPP	C5'-C7'-N3-C2
3	A	602	TPP	C5-C6-C7-O7
3	A	602	TPP	C7-O7-PA-O1A
3	B	612	TPP	C7-O7-PA-O2A
3	B	612	TPP	C7-O7-PA-O3A

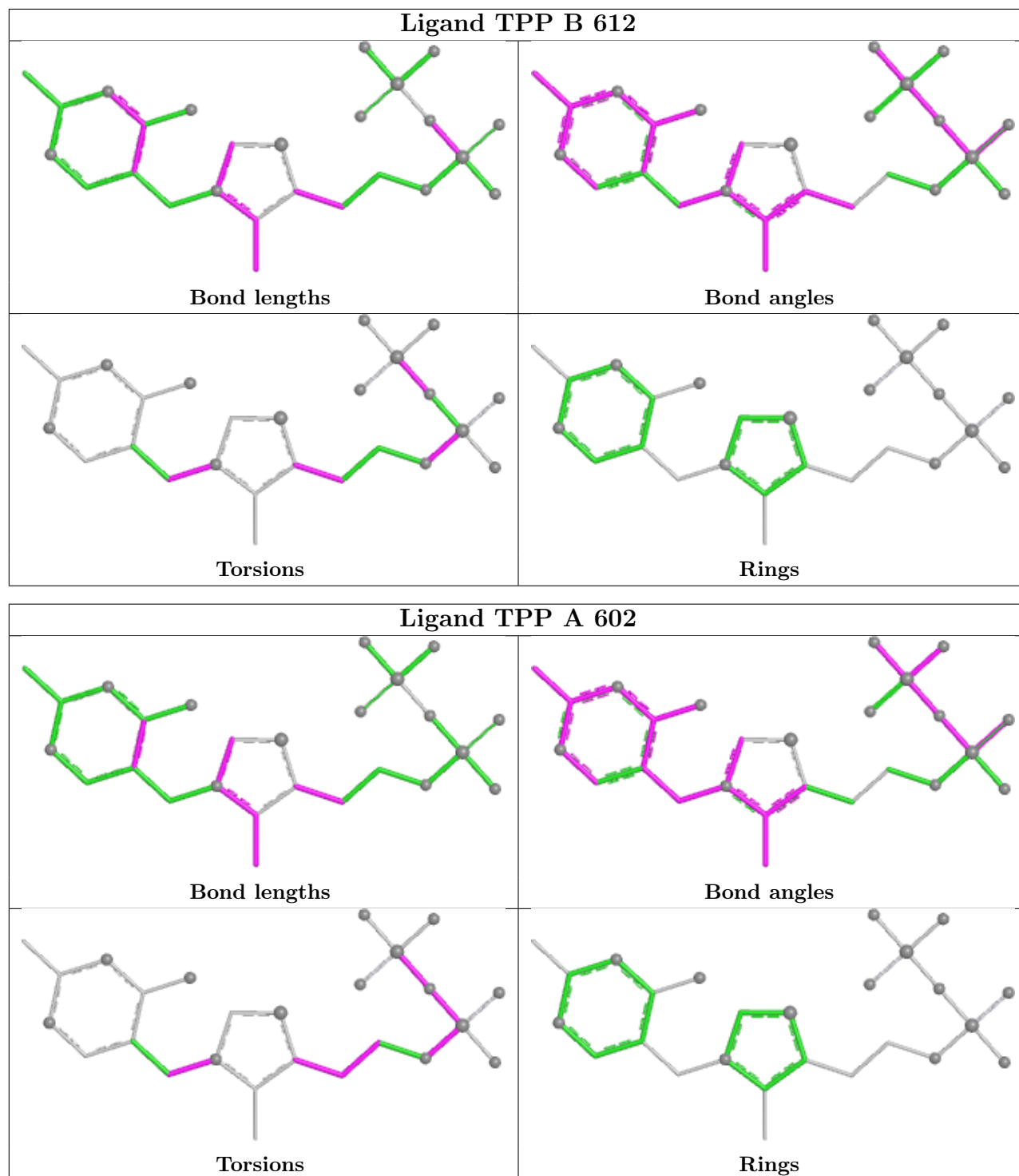
There are no ring outliers.

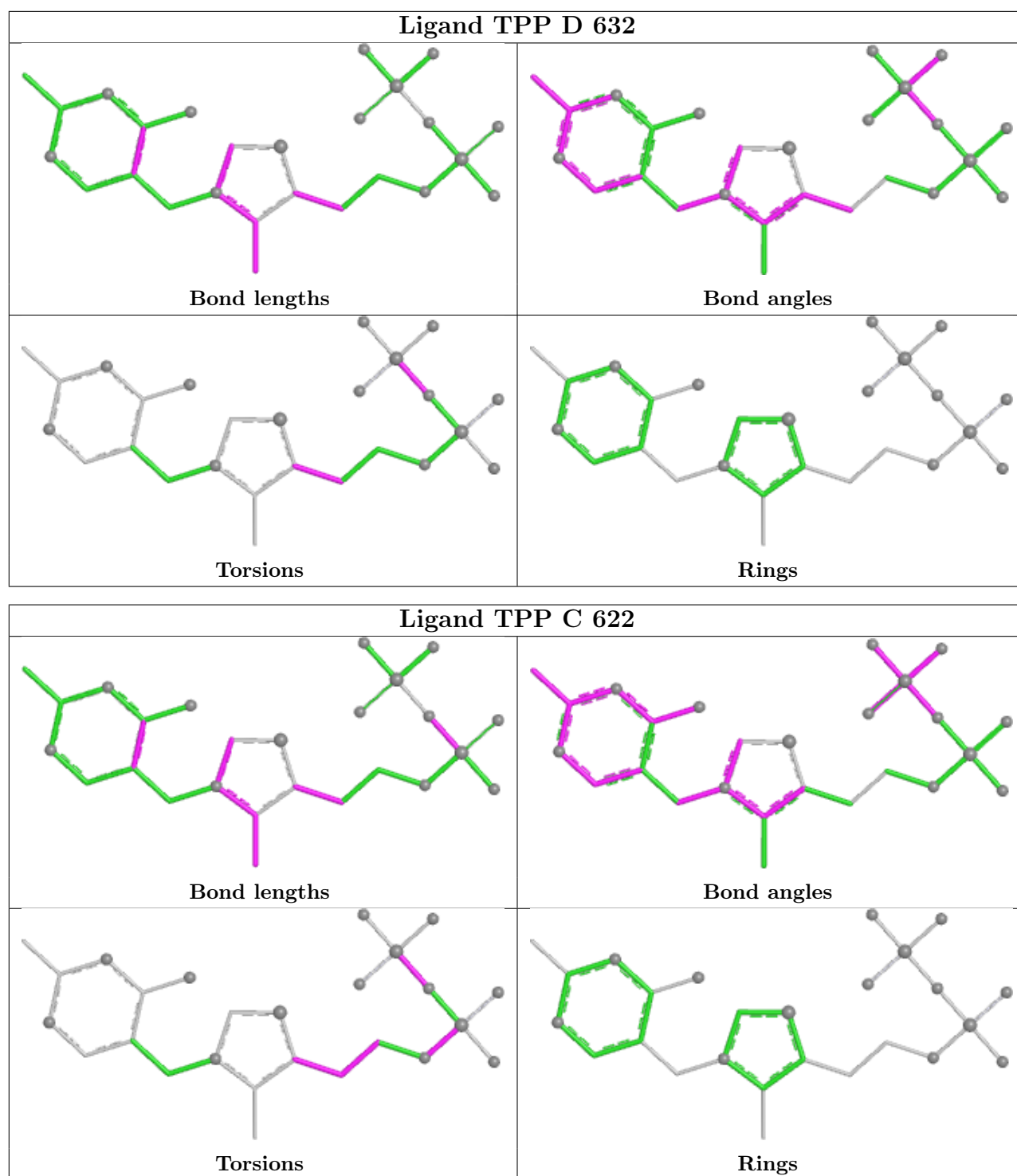
4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	612	TPP	1	0
3	A	602	TPP	4	0
3	D	632	TPP	1	0
3	C	622	TPP	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 ⓘ

There are no such residues in this entry.



## 5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	370:LEU	C	371:HIS	N	1.20

## 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	542/563 (96%)	-1.43	0 100 100	18, 49, 92, 123	0
1	B	542/563 (96%)	-1.37	0 100 100	21, 50, 83, 103	0
1	C	542/563 (96%)	-1.77	0 100 100	13, 31, 59, 77	0
1	D	542/563 (96%)	-1.80	0 100 100	14, 28, 44, 63	0
All	All	2168/2252 (96%)	-1.60	0 100 100	13, 37, 81, 123	0

There are no RSRZ outliers to report.

### 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.

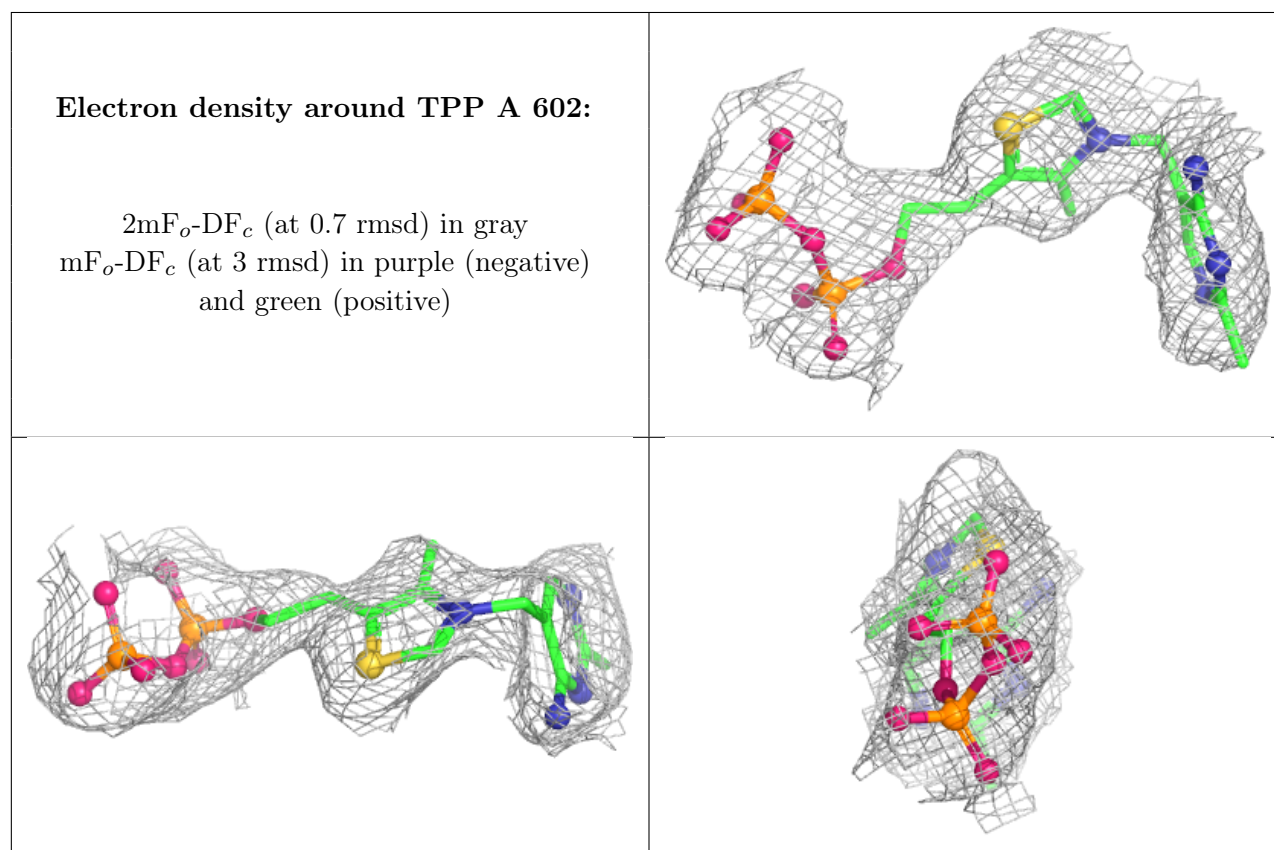
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	MG	A	601	1/1	0.99	0.02	55,55,55,55	0
2	MG	C	621	1/1	0.99	0.02	33,33,33,33	0
3	TPP	A	602	26/26	0.99	0.03	47,54,61,61	0
3	TPP	B	612	26/26	0.99	0.03	30,42,50,51	0

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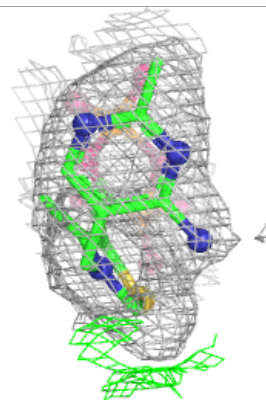
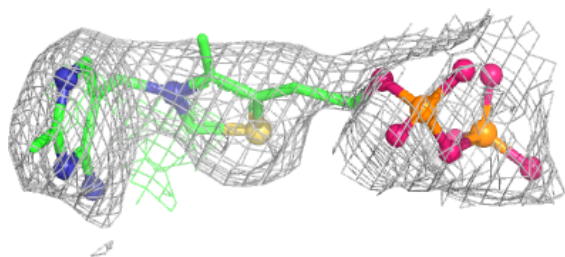
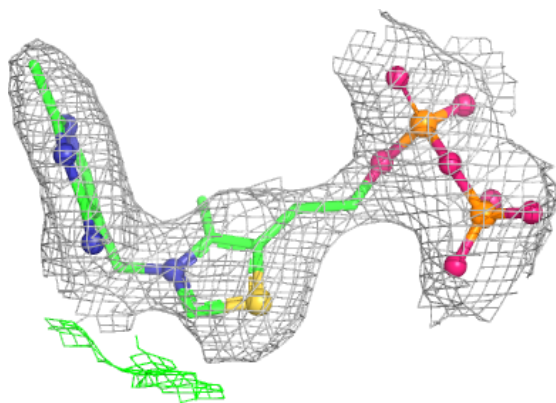
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MG	B	611	1/1	1.00	0.02	44,44,44,44	0
2	MG	D	631	1/1	1.00	0.01	20,20,20,20	0
3	TPP	C	622	26/26	1.00	0.02	25,35,41,42	0
3	TPP	D	632	26/26	1.00	0.02	18,21,26,27	0

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.

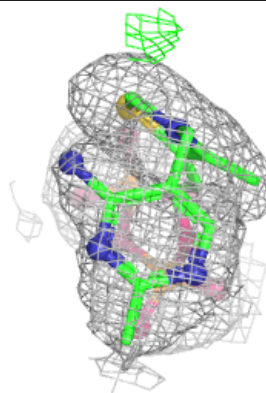
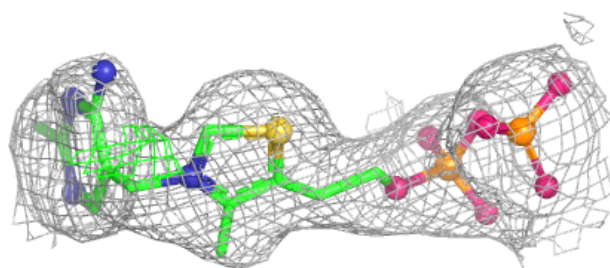
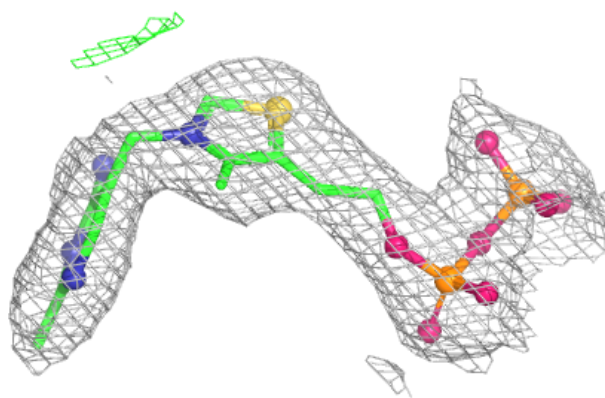


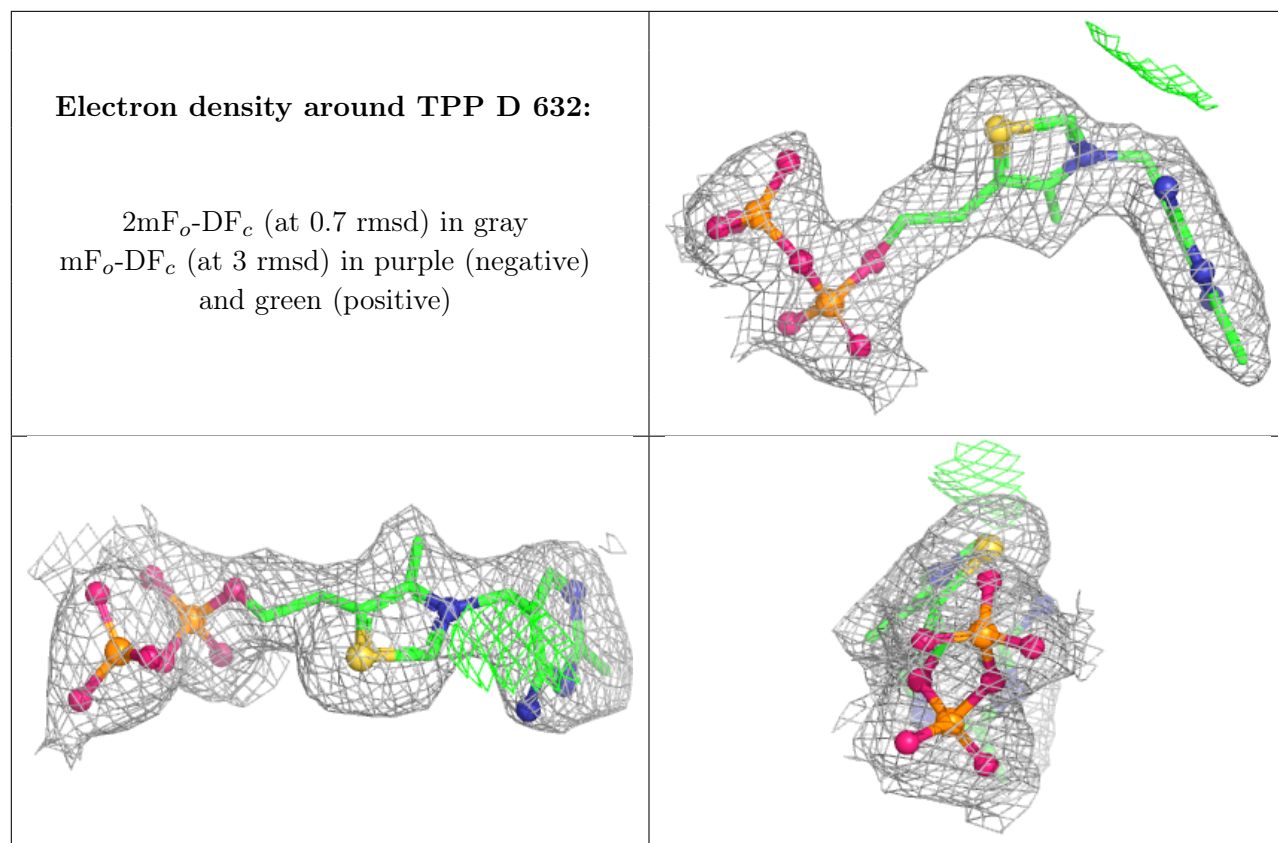
**Electron density around TPP B 612:**

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

**Electron density around TPP C 622:**

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





## 6.5 Other polymers ⓘ

There are no such residues in this entry.