



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 07:31 PM UTC

PDB ID : 7ORX / pdb_00007orx
Title : Rhodococcus jostii RHA1 thiamine diphosphate-dependent 4-hydroxybenzoyl formate decarboxylase
Authors : Wilkinson, R.C.; Fulop, V.
Deposited on : 2021-06-06
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

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>.

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

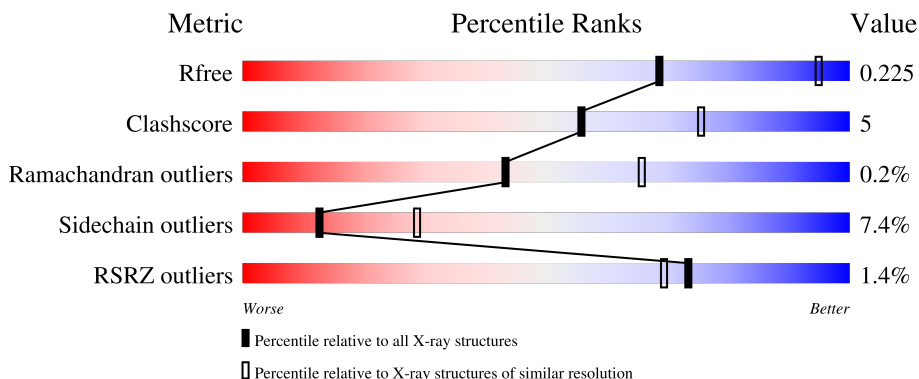
1 Overall quality at a glance

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 ≥ 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	AAA	531	2% 82% 15% ..
1	BBB	531	2% 82% 15% ..
1	CCC	531	2% 84% 14% .
1	DDD	531	84% 14% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15727 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.

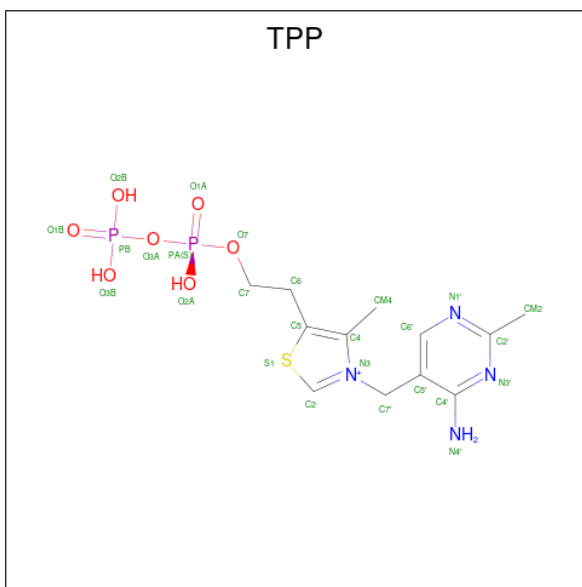
- Molecule 1 is a protein called Probable benzoylformate decarboxylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	AAA	527	Total	C	N	O	P	S	0	0	0
			3881	2456	653	762	1	9			
1	BBB	527	Total	C	N	O	P	S	0	0	0
			3881	2456	653	762	1	9			
1	CCC	531	Total	C	N	O	P	S	0	0	0
			3913	2477	658	767	1	10			
1	DDD	527	Total	C	N	O	P	S	0	0	0
			3881	2456	653	762	1	9			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	-2	PHE	-	expression tag	UNP Q0SCE8
AAA	-1	GLN	-	expression tag	UNP Q0SCE8
AAA	0	GLY	-	expression tag	UNP Q0SCE8
BBB	-2	PHE	-	expression tag	UNP Q0SCE8
BBB	-1	GLN	-	expression tag	UNP Q0SCE8
BBB	0	GLY	-	expression tag	UNP Q0SCE8
CCC	-2	PHE	-	expression tag	UNP Q0SCE8
CCC	-1	GLN	-	expression tag	UNP Q0SCE8
CCC	0	GLY	-	expression tag	UNP Q0SCE8
DDD	-2	PHE	-	expression tag	UNP Q0SCE8
DDD	-1	GLN	-	expression tag	UNP Q0SCE8
DDD	0	GLY	-	expression tag	UNP Q0SCE8

- Molecule 2 is THIAMINE DIPHOSPHATE (CCD ID: TPP) (formula: $C_{12}H_{19}N_4O_7P_2S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	AAA	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0
2	BBB	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0
2	CCC	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0
2	DDD	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	1	Total 1	Na 1	0	0
3	BBB	1	Total 1	Na 1	0	0
3	CCC	1	Total 1	Na 1	0	0
3	DDD	1	Total 1	Na 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	AAA	12	Total O 12 12	0	0

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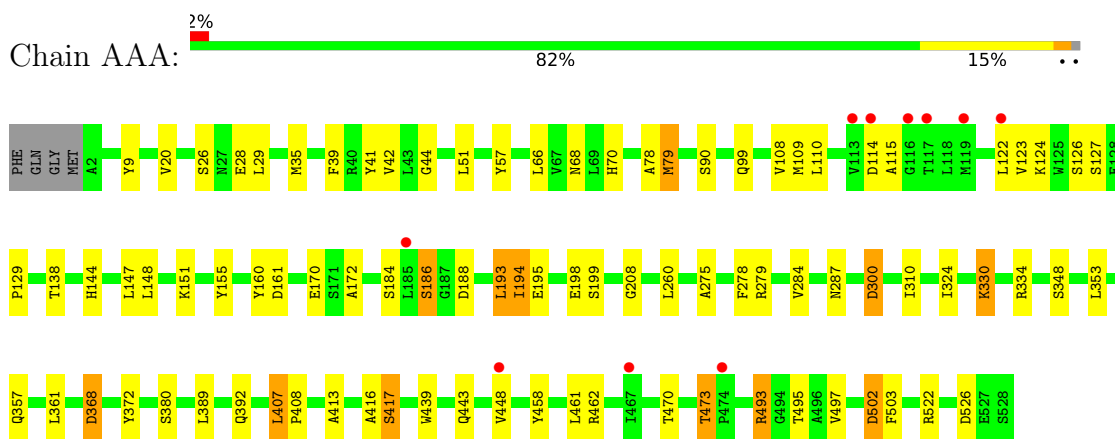
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	BBB	17	Total	O	0	0
			17	17		
4	CCC	15	Total	O	0	0
			15	15		
4	DDD	19	Total	O	0	0
			19	19		

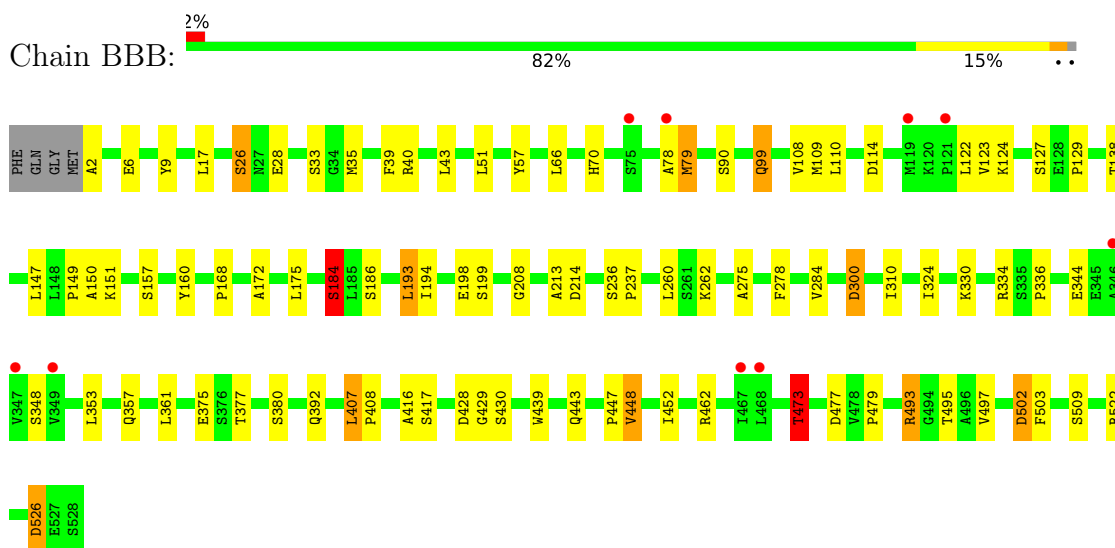
3 Residue-property plots [i](#)

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.

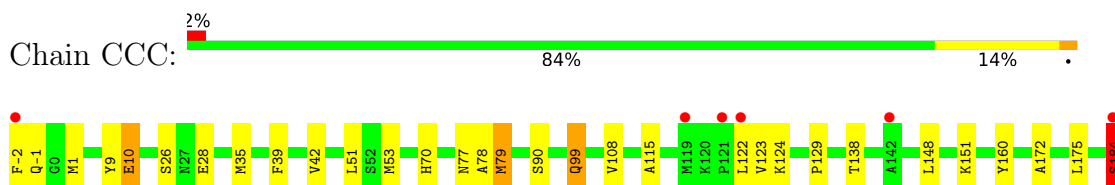
- Molecule 1: Probable benzoylformate decarboxylase

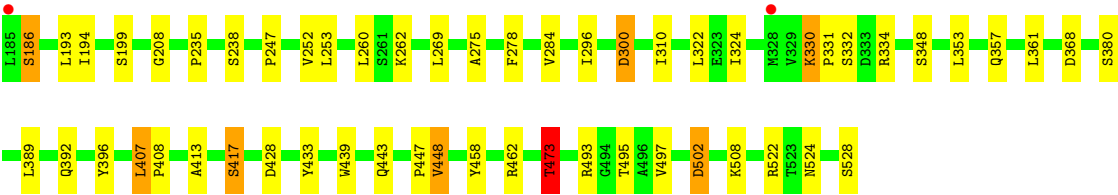


- Molecule 1: Probable benzoylformate decarboxylase

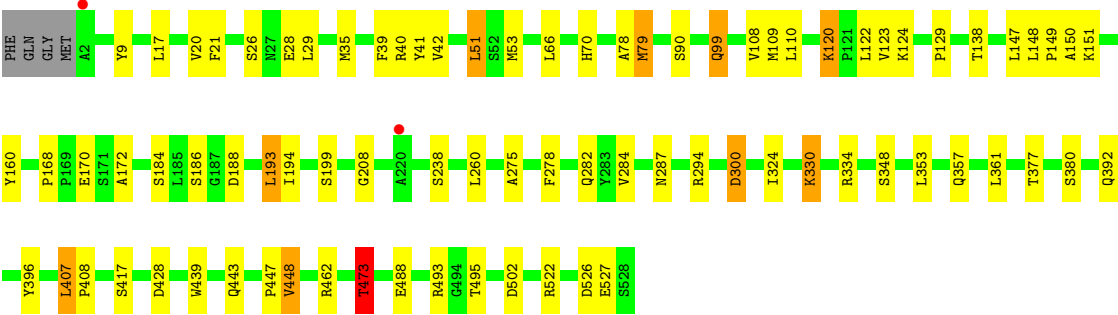
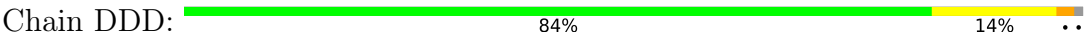


- Molecule 1: Probable benzoylformate decarboxylase





● Molecule 1: Probable benzoylformate decarboxylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	123.50Å 132.24Å 138.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.42 – 2.60 90.42 – 2.60	Depositor EDS
% Data completeness (in resolution range)	100.0 (90.42-2.60) 100.0 (90.42-2.60)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.23 (at 2.62Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.195 , 0.233 (Not available) , 0.225	Depositor DCC
R_{free} test set	2975 reflections (4.22%)	wwPDB-VP
Wilson B-factor (Å ²)	67.8	Xtriage
Anisotropy	0.680	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 61.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.008 for -h,l,k	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15727	wwPDB-VP
Average B, all atoms (Å ²)	88.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: TPP, NA, SEP

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	AAA	1.13	3/3962 (0.1%)	1.51	22/5425 (0.4%)
1	BBB	1.22	6/3962 (0.2%)	1.56	32/5425 (0.6%)
1	CCC	1.18	5/3995 (0.1%)	1.54	21/5468 (0.4%)
1	DDD	1.17	2/3962 (0.1%)	1.52	18/5425 (0.3%)
All	All	1.18	16/15881 (0.1%)	1.53	93/21743 (0.4%)

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	AAA	0	1
1	BBB	0	1
All	All	0	2

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	CCC	235	PRO	C-O	-8.19	1.14	1.23
1	BBB	452	ILE	C-O	-7.01	1.16	1.24
1	CCC	332	SER	C-O	6.22	1.31	1.23
1	BBB	237	PRO	C-O	-6.17	1.17	1.23
1	CCC	524	ASN	C-O	6.00	1.31	1.24

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	CCC	300	ASP	CA-CB-CG	8.23	120.83	112.60
1	BBB	502	ASP	CA-CB-CG	8.16	120.76	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	BBB	300	ASP	CA-CB-CG	8.12	120.72	112.60
1	AAA	300	ASP	CA-CB-CG	7.95	120.55	112.60
1	DDD	300	ASP	CA-CB-CG	7.89	120.49	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AAA	127	SER	Peptide
1	BBB	127	SER	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	AAA	3881	0	3802	42	0
1	BBB	3881	0	3802	34	0
1	CCC	3913	0	3834	36	0
1	DDD	3881	0	3802	36	0
2	AAA	26	0	16	4	0
2	BBB	26	0	16	0	0
2	CCC	26	0	16	1	0
2	DDD	26	0	16	1	0
3	AAA	1	0	0	0	0
3	BBB	1	0	0	0	0
3	CCC	1	0	0	0	0
3	DDD	1	0	0	0	0
4	AAA	12	0	0	1	0
4	BBB	17	0	0	0	0
4	CCC	15	0	0	1	0
4	DDD	19	0	0	1	0
All	All	15727	0	15304	144	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 5.

The worst 5 of 144 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:BBB:79:MET:HE2	1:BBB:122:LEU:HD12	1.60	0.82
1:DDD:79:MET:HE2	1:DDD:122:LEU:HD12	1.61	0.81
1:CCC:79:MET:HE2	1:CCC:122:LEU:HD12	1.64	0.77
1:AAA:79:MET:HE2	1:AAA:122:LEU:HD12	1.70	0.71
2:AAA:601:TPP:HN42	2:AAA:601:TPP:H2	1.54	0.71

There are no symmetry-related clashes.

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	AAA	524/531 (99%)	502 (96%)	21 (4%)	1 (0%)	43	66
1	BBB	524/531 (99%)	501 (96%)	22 (4%)	1 (0%)	43	66
1	CCC	528/531 (99%)	505 (96%)	22 (4%)	1 (0%)	43	66
1	DDD	524/531 (99%)	502 (96%)	21 (4%)	1 (0%)	43	66
All	All	2100/2124 (99%)	2010 (96%)	86 (4%)	4 (0%)	43	66

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	BBB	123	VAL
1	AAA	123	VAL
1	DDD	123	VAL
1	CCC	123	VAL

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	AAA	406/409 (99%)	378 (93%)	28 (7%)	14	32
1	BBB	406/409 (99%)	377 (93%)	29 (7%)	13	31
1	CCC	409/409 (100%)	375 (92%)	34 (8%)	10	23
1	DDD	406/409 (99%)	377 (93%)	29 (7%)	13	31
All	All	1627/1636 (99%)	1507 (93%)	120 (7%)	13	29

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	CCC	-2	PHE
1	DDD	380	SER
1	CCC	262	LYS
1	DDD	361	LEU
1	DDD	526	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	SEP	CCC	26	1	8,9,10	2.44	3 (37%)	7,12,14	3.16	1 (14%)
1	SEP	BBB	26	1	8,9,10	2.48	3 (37%)	7,12,14	3.19	2 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	SEP	DDD	26	1	8,9,10	2.28	3 (37%)	7,12,14	3.22	2 (28%)
1	SEP	AAA	26	1	8,9,10	2.12	3 (37%)	7,12,14	3.08	1 (14%)

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
1	SEP	CCC	26	1	-	3/6/8/10	-
1	SEP	BBB	26	1	-	3/6/8/10	-
1	SEP	DDD	26	1	-	3/6/8/10	-
1	SEP	AAA	26	1	-	3/6/8/10	-

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	BBB	26	SEP	P-OG	5.65	1.78	1.60
1	CCC	26	SEP	P-OG	5.40	1.77	1.60
1	DDD	26	SEP	P-OG	4.55	1.74	1.60
1	AAA	26	SEP	P-OG	4.44	1.74	1.60
1	BBB	26	SEP	CB-CA	3.04	1.60	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	DDD	26	SEP	OG-CB-CA	8.18	116.10	108.14
1	CCC	26	SEP	OG-CB-CA	8.18	116.10	108.14
1	AAA	26	SEP	OG-CB-CA	7.93	115.86	108.14
1	BBB	26	SEP	OG-CB-CA	7.75	115.69	108.14
1	BBB	26	SEP	O3P-P-OG	2.88	114.19	106.67

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	AAA	26	SEP	N-CA-CB-OG
1	AAA	26	SEP	C-CA-CB-OG
1	AAA	26	SEP	CA-CB-OG-P
1	BBB	26	SEP	N-CA-CB-OG

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Mol	Chain	Res	Type	Atoms
1	BBB	26	SEP	C-CA-CB-OG

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	BBB	26	SEP	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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$
2	TPP	BBB	601	3	26,27,27	0.53	0	38,40,40	0.79	0
2	TPP	CCC	601	3	26,27,27	0.56	0	38,40,40	0.92	2 (5%)
2	TPP	DDD	601	3	26,27,27	0.56	0	38,40,40	0.89	3 (7%)
2	TPP	AAA	601	3	26,27,27	0.48	0	38,40,40	0.87	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
2	TPP	BBB	601	3	-	2/17/17/17	0/2/2/2
2	TPP	CCC	601	3	-	4/17/17/17	0/2/2/2
2	TPP	DDD	601	3	-	2/17/17/17	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TPP	AAA	601	3	-	6/17/17/17	0/2/2/2

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	CCC	601	TPP	C2-S1-C5	-3.06	89.19	91.22
2	DDD	601	TPP	C2-S1-C5	-2.67	89.45	91.22
2	CCC	601	TPP	O7-PA-O1A	2.31	118.11	108.94
2	DDD	601	TPP	O2A-PA-O1A	2.29	123.11	112.44
2	DDD	601	TPP	O3A-PA-O1A	-2.05	104.55	110.70

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	AAA	601	TPP	C7-O7-PA-O1A
2	AAA	601	TPP	C7-O7-PA-O2A
2	AAA	601	TPP	C7-O7-PA-O3A
2	AAA	601	TPP	PB-O3A-PA-O7
2	BBB	601	TPP	PA-O3A-PB-O3B

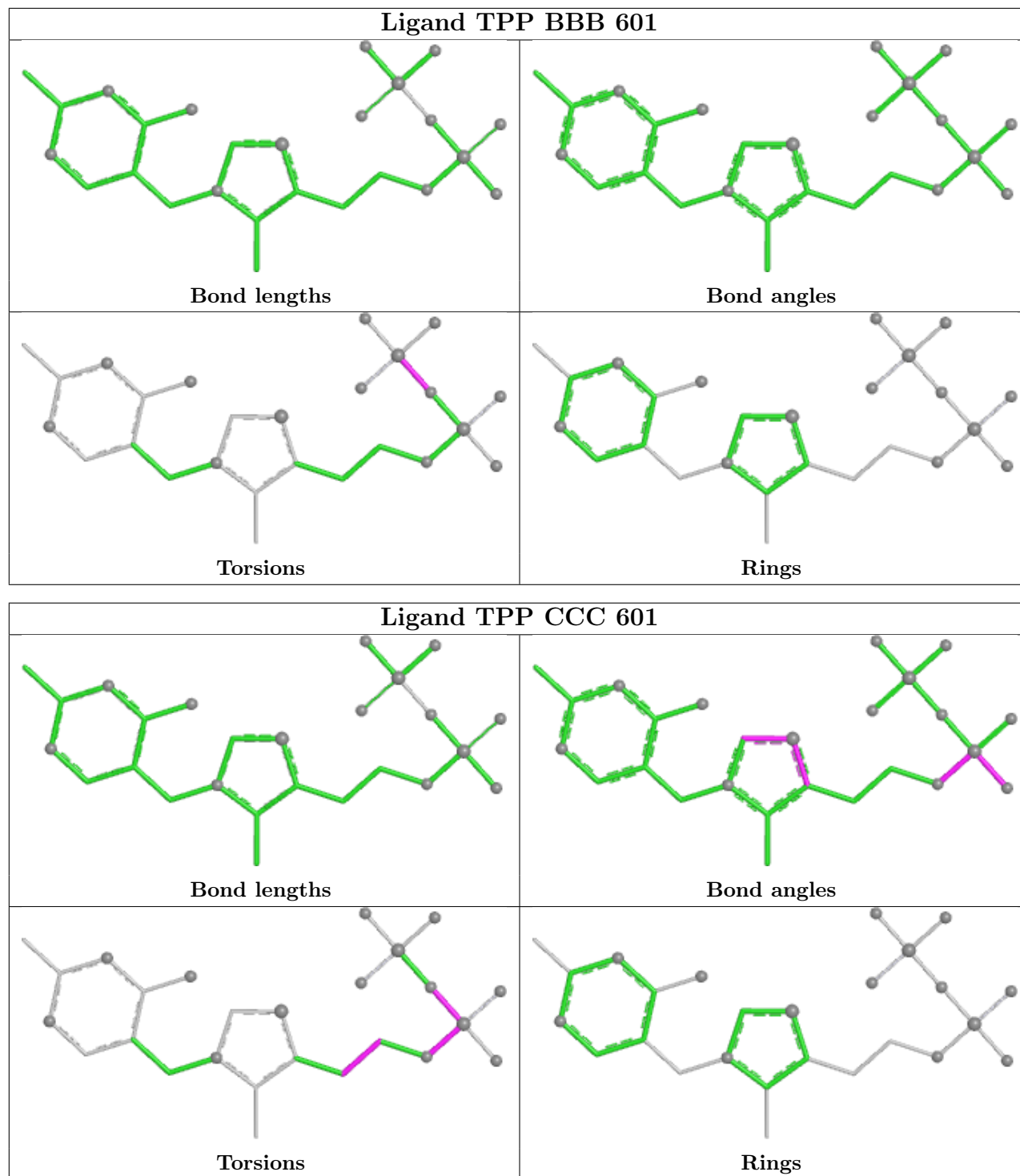
There are no ring outliers.

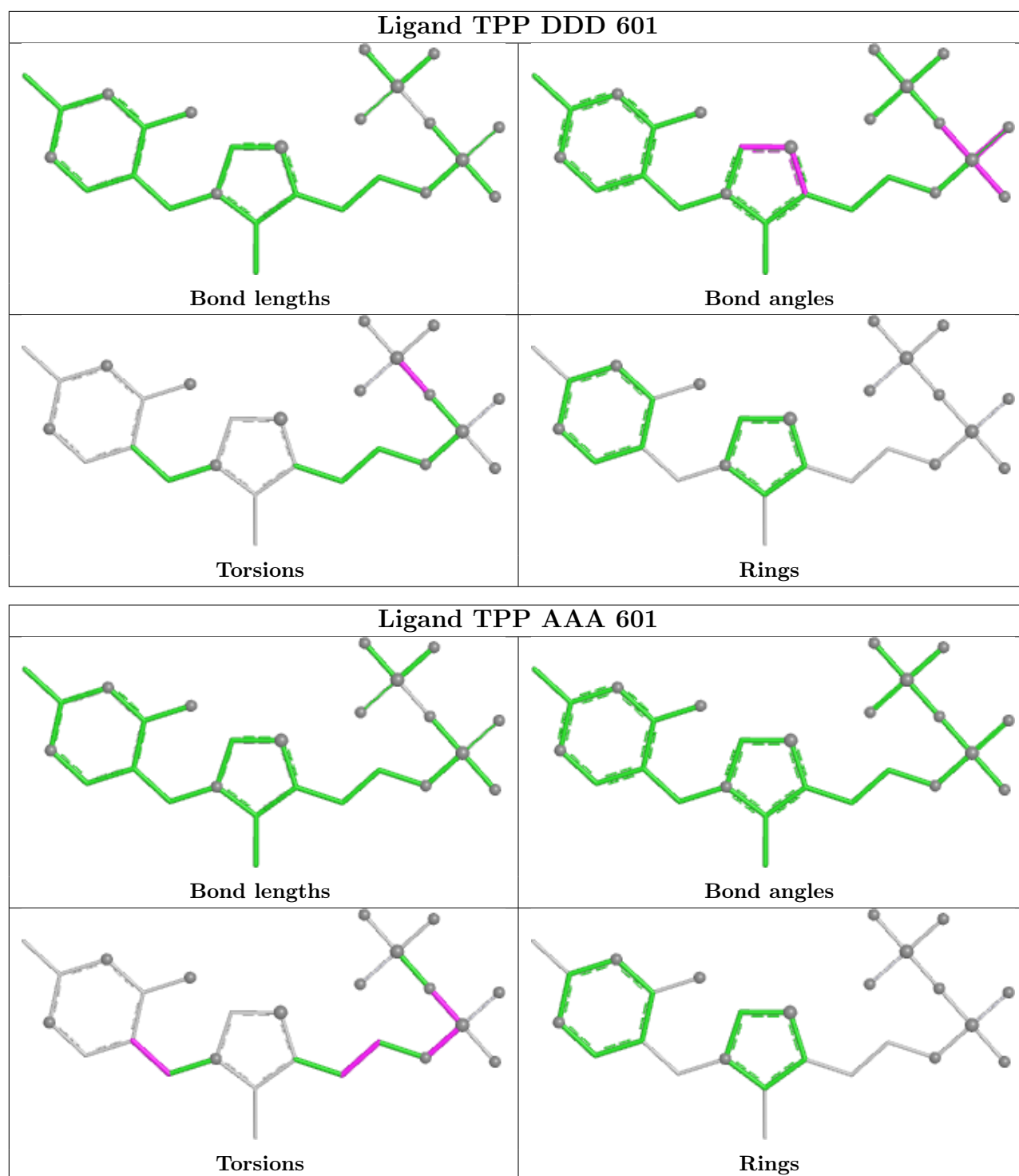
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	CCC	601	TPP	1	0
2	DDD	601	TPP	1	0
2	AAA	601	TPP	4	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 ⓘ

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, 95th 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 ²)	Q<0.9
1	AAA	526/531 (99%)	-0.05	10 (1%) 66 61	70, 93, 133, 159	0
1	BBB	526/531 (99%)	-0.18	9 (1%) 69 64	57, 80, 122, 174	0
1	CCC	530/531 (99%)	-0.19	8 (1%) 72 68	59, 79, 108, 150	0
1	DDD	526/531 (99%)	-0.19	2 (0%) 88 86	63, 87, 131, 160	0
All	All	2108/2124 (99%)	-0.15	29 (1%) 73 69	57, 85, 127, 174	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	121	PRO	4.4
1	BBB	347	VAL	3.9
1	DDD	220	ALA	3.8
1	AAA	119	MET	3.2
1	BBB	78	ALA	3.1

6.2 Non-standard residues in protein, DNA, RNA chains [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, 95th 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 ²)	Q<0.9
1	SEP	CCC	26	10/11	0.89	0.14	88,90,95,100	0
1	SEP	BBB	26	10/11	0.91	0.13	87,95,102,104	0
1	SEP	DDD	26	10/11	0.91	0.10	85,95,106,109	0
1	SEP	AAA	26	10/11	0.95	0.09	116,123,132,135	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

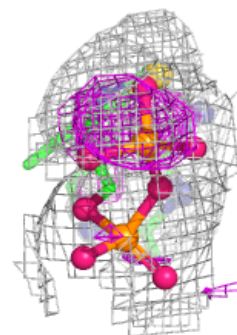
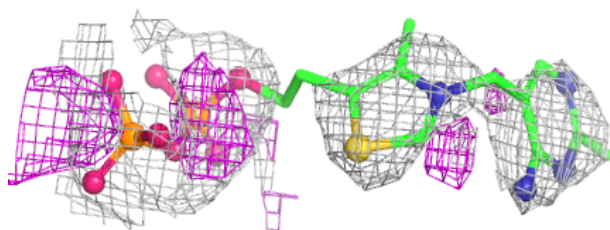
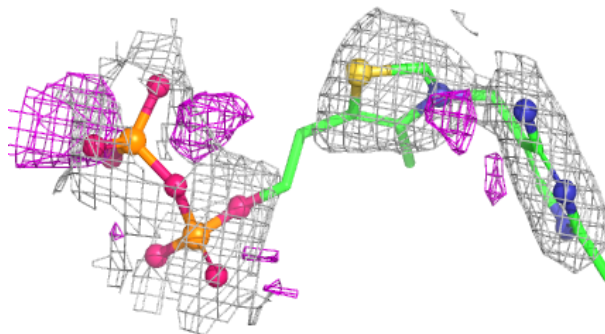
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	TPP	BBB	601	26/26	0.93	0.08	90,112,126,132	0
2	TPP	AAA	601	26/26	0.94	0.08	76,96,106,108	0
2	TPP	CCC	601	26/26	0.95	0.07	64,83,90,109	0
2	TPP	DDD	601	26/26	0.95	0.07	69,80,99,104	0
3	NA	AAA	602	1/1	0.98	0.06	84,84,84,84	0
3	NA	BBB	602	1/1	0.98	0.09	83,83,83,83	0
3	NA	CCC	602	1/1	0.98	0.04	66,66,66,66	0
3	NA	DDD	602	1/1	0.98	0.03	67,67,67,67	0

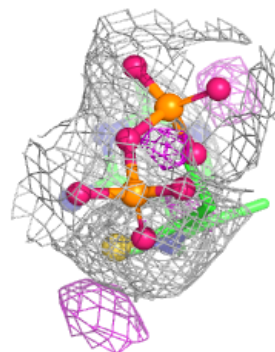
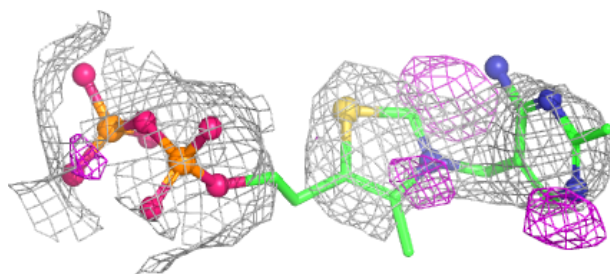
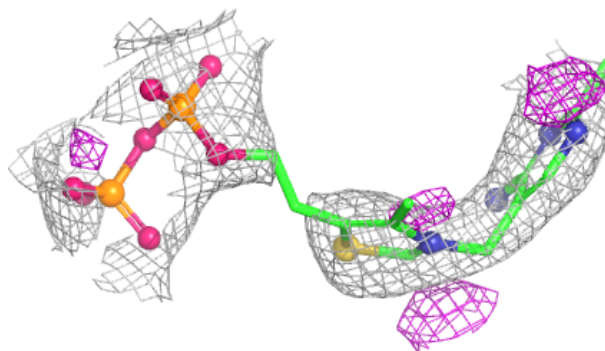
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around TPP BBB 601:

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

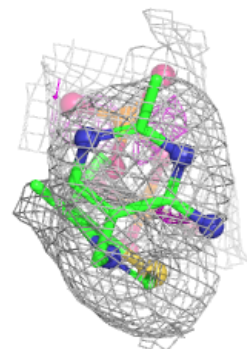
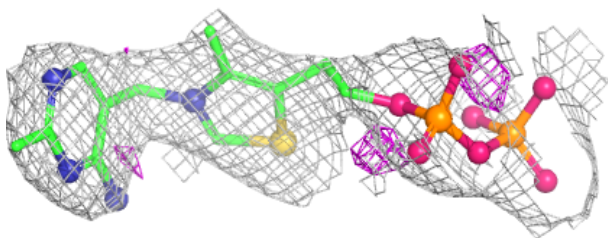
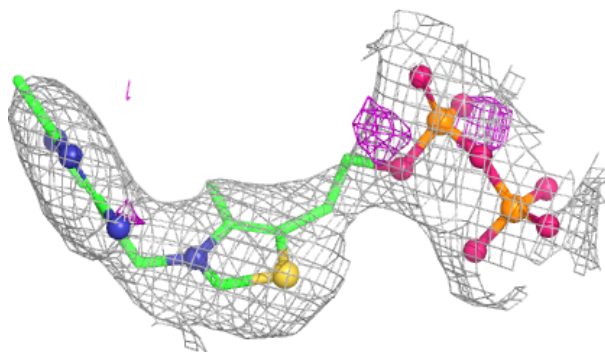
**Electron density around TPP AAA 601:**

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

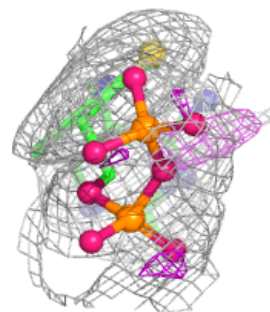
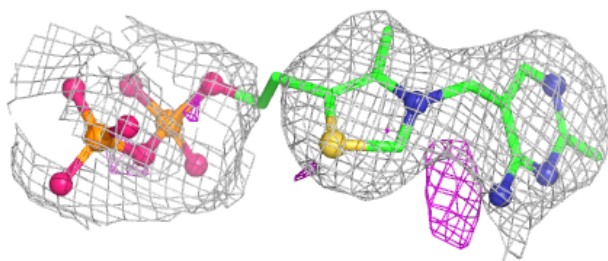
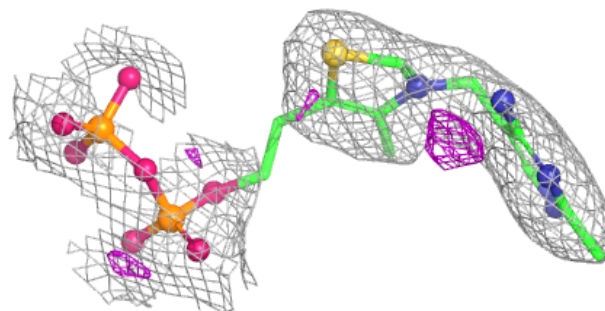


Electron density around TPP CCC 601:

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

**Electron density around TPP DDD 601:**

$2mF_o-DF_c$ (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.