



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 17, 2020 – 04:37 PM EST

PDB ID : 5RVW
Title : PanDDA analysis group deposition – Crystal Structure of DHTKD1 in complex with Z1587220559
Authors : Bezerra, G.A.; Foster, W.R.; Bailey, H.J.; Shrestha, L.; Krojer, T.; Brandao-Neto, J.; Douangamath, A.; Burgess-Brown, N.; von Delft, F.; Arrowsmith, C.H.; Edwards, A.; Bountra, C.; Yue, W.W.
Deposited on : 2020-10-27
Resolution : 1.61 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.14.6
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.14.6

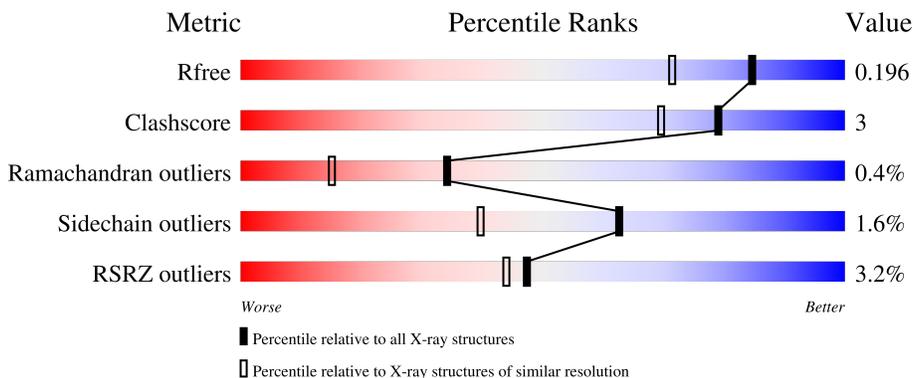
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.61 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4693 (1.64-1.60)
Clashscore	141614	5002 (1.64-1.60)
Ramachandran outliers	138981	4888 (1.64-1.60)
Sidechain outliers	138945	4887 (1.64-1.60)
RSRZ outliers	127900	4609 (1.64-1.60)

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 on 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	A	898	
1	B	898	

2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 15390 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 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	867	6775	4317	1169	1249	40	0	5	0
1	B	867	6740	4296	1163	1243	38	0	2	0

There are 46 discrepancies between the modelled and reference sequences:

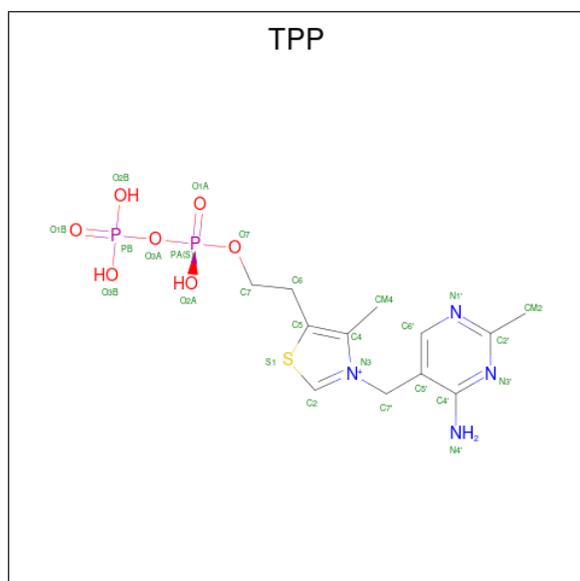
Chain	Residue	Modelled	Actual	Comment	Reference
A	22	MET	-	initiating methionine	UNP Q96HY7
A	23	HIS	-	expression tag	UNP Q96HY7
A	24	HIS	-	expression tag	UNP Q96HY7
A	25	HIS	-	expression tag	UNP Q96HY7
A	26	HIS	-	expression tag	UNP Q96HY7
A	27	HIS	-	expression tag	UNP Q96HY7
A	28	HIS	-	expression tag	UNP Q96HY7
A	29	SER	-	expression tag	UNP Q96HY7
A	30	SER	-	expression tag	UNP Q96HY7
A	31	GLY	-	expression tag	UNP Q96HY7
A	32	VAL	-	expression tag	UNP Q96HY7
A	33	ASP	-	expression tag	UNP Q96HY7
A	34	LEU	-	expression tag	UNP Q96HY7
A	35	GLY	-	expression tag	UNP Q96HY7
A	36	THR	-	expression tag	UNP Q96HY7
A	37	GLU	-	expression tag	UNP Q96HY7
A	38	ASN	-	expression tag	UNP Q96HY7
A	39	LEU	-	expression tag	UNP Q96HY7
A	40	TYR	-	expression tag	UNP Q96HY7
A	41	PHE	-	expression tag	UNP Q96HY7
A	42	GLN	-	expression tag	UNP Q96HY7
A	43	SER	-	expression tag	UNP Q96HY7
A	44	MET	-	expression tag	UNP Q96HY7
B	22	MET	-	initiating methionine	UNP Q96HY7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	23	HIS	-	expression tag	UNP Q96HY7
B	24	HIS	-	expression tag	UNP Q96HY7
B	25	HIS	-	expression tag	UNP Q96HY7
B	26	HIS	-	expression tag	UNP Q96HY7
B	27	HIS	-	expression tag	UNP Q96HY7
B	28	HIS	-	expression tag	UNP Q96HY7
B	29	SER	-	expression tag	UNP Q96HY7
B	30	SER	-	expression tag	UNP Q96HY7
B	31	GLY	-	expression tag	UNP Q96HY7
B	32	VAL	-	expression tag	UNP Q96HY7
B	33	ASP	-	expression tag	UNP Q96HY7
B	34	LEU	-	expression tag	UNP Q96HY7
B	35	GLY	-	expression tag	UNP Q96HY7
B	36	THR	-	expression tag	UNP Q96HY7
B	37	GLU	-	expression tag	UNP Q96HY7
B	38	ASN	-	expression tag	UNP Q96HY7
B	39	LEU	-	expression tag	UNP Q96HY7
B	40	TYR	-	expression tag	UNP Q96HY7
B	41	PHE	-	expression tag	UNP Q96HY7
B	42	GLN	-	expression tag	UNP Q96HY7
B	43	SER	-	expression tag	UNP Q96HY7
B	44	MET	-	expression tag	UNP Q96HY7

- Molecule 2 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: C₁₂H₁₉N₄O₇P₂S).

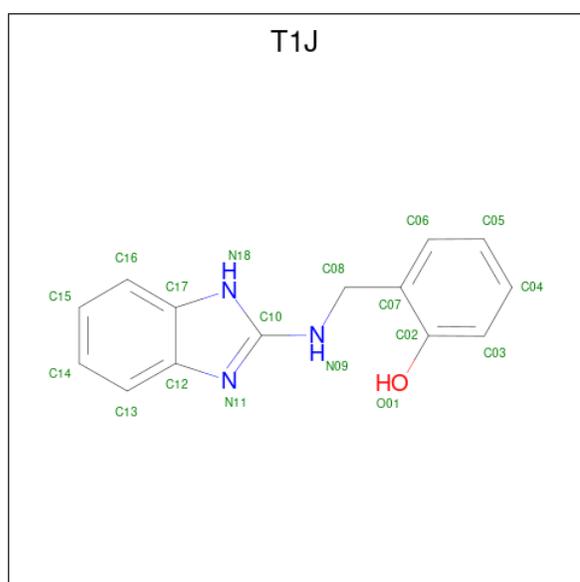


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
2	A	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		
2	B	1	Total	C	N	O	P	S	0	0
			26	12	4	7	2	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is 2-[[[(1H-benzimidazol-2-yl)amino]methyl]phenol (three-letter code: T1J) (formula: C₁₄H₁₃N₃O) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			18	14	3	1		

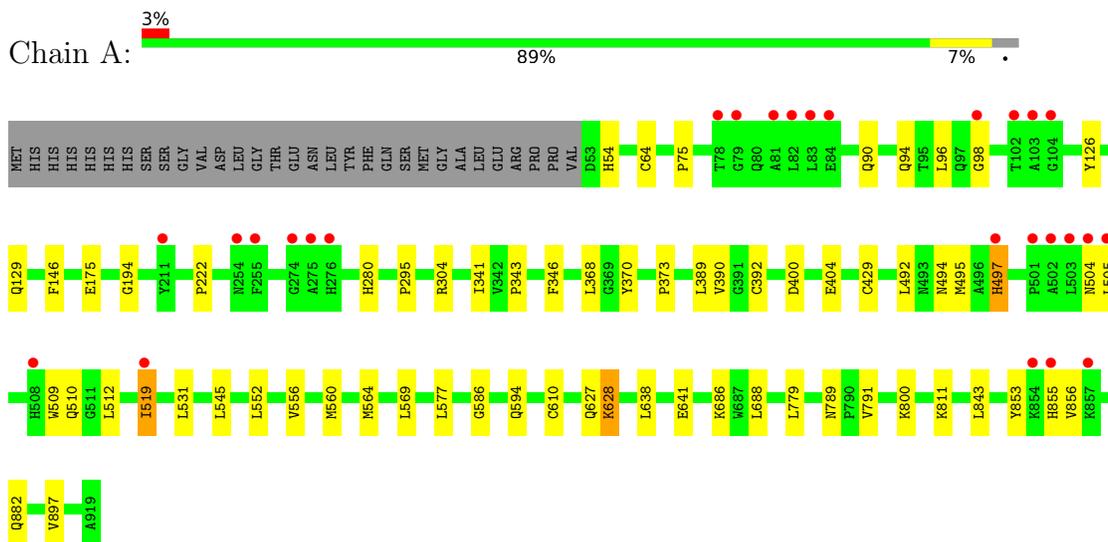
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1008	Total	O	0	0
			1008	1008		
5	B	794	Total	O	0	0
			794	794		

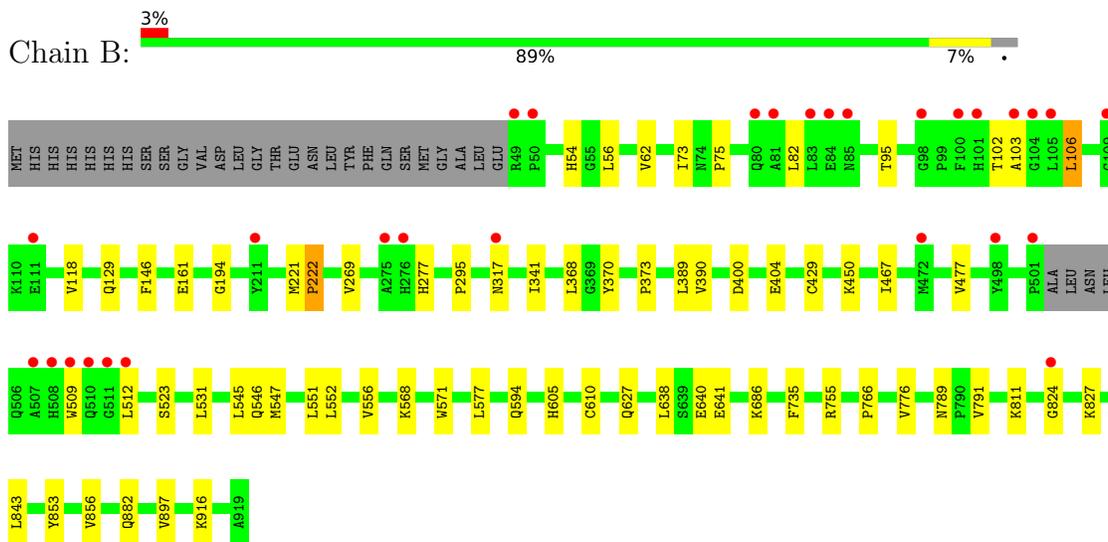
3 Residue-property plots [i](#)

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 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial



- Molecule 1: Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	78.07Å 147.03Å 87.38Å 90.00° 102.70° 90.00°	Depositor
Resolution (Å)	85.24 – 1.61 85.24 – 1.61	Depositor EDS
% Data completeness (in resolution range)	55.6 (85.24-1.61) 55.6 (85.24-1.61)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 1.62Å)	Xtrriage
Refinement program	BUSTER 2.10.3 (20-MAY-2020)	Depositor
R, R_{free}	0.164 , 0.189 0.170 , 0.196	Depositor DCC
R_{free} test set	6725 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	17.1	Xtrriage
Anisotropy	0.126	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	15390	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% 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: MG, T1J, TPP

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	0.42	0/6959	0.58	0/9439
1	B	0.41	0/6914	0.57	0/9385
All	All	0.41	0/13873	0.57	0/18824

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6775	0	6624	42	0
1	B	6740	0	6571	40	0
2	A	26	0	16	4	0
2	B	26	0	16	1	0
3	A	1	0	0	0	0
3	B	2	0	0	0	0
4	B	18	0	0	0	0
5	A	1008	0	0	0	1
5	B	794	0	0	1	1
All	All	15390	0	13227	76	1

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 3.

All (76) 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:824:GLY:O	1:B:827:LYS:HG2	1.84	0.78
1:A:54:HIS:HE1	1:B:95:THR:HG22	1.55	0.72
1:A:90:GLN:O	1:A:94:GLN:HG2	1.94	0.68
1:A:853:TYR:HA	1:A:855:HIS:CE1	2.29	0.67
1:A:494:ASN:HA	1:A:497[A]:HIS:CE1	2.33	0.62
1:A:54:HIS:CE1	1:B:95:THR:HG22	2.34	0.62
1:B:853:TYR:HB3	1:B:856:VAL:HG23	1.84	0.59
1:B:545:LEU:HG	1:B:610:CYS:HB2	1.84	0.58
1:A:280[A]:HIS:CD2	1:A:304:ARG:HH12	2.23	0.56
1:A:494:ASN:ND2	1:A:497[B]:HIS:CD2	2.75	0.55
1:B:102:THR:HG23	1:B:106:LEU:HB3	1.89	0.55
1:A:389:LEU:HD12	1:A:390:VAL:HG13	1.89	0.54
1:B:106:LEU:HD21	1:B:118:VAL:HG13	1.90	0.54
1:A:569:LEU:HD21	1:A:779:LEU:HD13	1.90	0.54
1:A:545:LEU:HG	1:A:610:CYS:HB2	1.89	0.53
1:B:389:LEU:HD12	1:B:390:VAL:HG13	1.89	0.53
1:A:54:HIS:HE1	1:B:95:THR:CG2	2.20	0.53
1:A:494:ASN:ND2	1:A:497[B]:HIS:HD2	2.09	0.51
1:B:547:MET:SD	1:B:556:VAL:HG21	2.51	0.51
1:A:64:CYS:HG	1:A:126:TYR:HH	1.58	0.50
1:A:531:LEU:HD22	1:A:577:LEU:HB3	1.94	0.49
1:A:843:LEU:HD13	1:A:882:GLN:HB3	1.93	0.49
1:A:594:GLN:OE1	2:B:1002:TPP:H6'	2.12	0.49
1:A:494:ASN:HD21	1:A:497[B]:HIS:CD2	2.30	0.49
2:A:1001:TPP:C2	2:A:1001:TPP:HN42	2.27	0.48
1:A:75:PRO:HB3	1:A:400:ASP:HB2	1.96	0.47
1:A:492:LEU:HD12	1:A:495:MET:HE2	1.96	0.47
1:A:494:ASN:HA	1:A:497[A]:HIS:HE1	1.74	0.47
1:B:853:TYR:HB3	1:B:856:VAL:CG2	2.45	0.47
1:B:194:GLY:O	1:B:429:CYS:HB2	2.14	0.47
1:A:853:TYR:HB3	1:A:856:VAL:HG23	1.96	0.47
1:B:75:PRO:HB3	1:B:400:ASP:HB2	1.96	0.47
2:A:1001:TPP:H6'	1:B:594:GLN:OE1	2.14	0.47
1:A:96:LEU:HD23	1:B:54:HIS:NE2	2.30	0.47
1:B:509:TRP:CE3	1:B:512:LEU:HD12	2.50	0.47
1:B:56:LEU:HD11	1:B:106:LEU:HD22	1.96	0.47
1:B:843:LEU:HD13	1:B:882:GLN:HB3	1.98	0.46
2:A:1001:TPP:HN42	2:A:1001:TPP:H2	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:TRP:CE3	1:A:512:LEU:HD12	2.50	0.46
1:B:467:ILE:HD11	1:B:477:VAL:HG21	1.97	0.46
1:B:735:PHE:CE2	1:B:755:ARG:NH2	2.84	0.46
1:A:789[A]:ASN:OD1	1:A:791:VAL:O	2.33	0.46
1:A:194:GLY:O	1:A:429:CYS:HB2	2.16	0.46
1:B:531:LEU:HD22	1:B:577:LEU:HB3	1.96	0.46
1:B:789:ASN:OD1	1:B:791:VAL:O	2.34	0.45
1:A:54:HIS:CE1	1:B:95:THR:CG2	2.99	0.45
1:A:556:VAL:HG12	1:A:560:MET:CE	2.47	0.45
1:B:368:LEU:HD23	1:B:373:PRO:HA	1.98	0.45
1:B:450:LYS:HE2	1:B:450:LYS:HB3	1.75	0.45
1:A:504:ASN:HA	1:A:688:LEU:HD13	1.99	0.44
1:B:295:PRO:HG3	1:B:341:ILE:HD11	2.00	0.43
1:A:552:LEU:HA	1:A:556:VAL:HB	2.00	0.43
1:B:916:LYS:NZ	5:B:1117:HOH:O	2.49	0.43
2:A:1001:TPP:N1'	1:B:640:GLU:OE2	2.52	0.43
1:A:628:LYS:HG2	1:A:628:LYS:H	1.70	0.43
1:A:295:PRO:HG3	1:A:341:ILE:HD11	2.01	0.42
1:B:341:ILE:HD12	1:B:641:GLU:HG2	2.01	0.42
1:B:571:TRP:CE2	1:B:766:PRO:HG3	2.54	0.42
1:A:897:VAL:HG11	1:B:686:LYS:HG3	2.01	0.42
1:A:341:ILE:HD12	1:A:641:GLU:HG2	2.02	0.42
1:A:368:LEU:HD23	1:A:373:PRO:HA	2.01	0.41
1:A:343:PRO:HB3	1:A:389:LEU:CD2	2.50	0.41
1:A:586:GLY:HA2	1:A:628:LYS:HG3	2.02	0.41
1:A:96:LEU:HD23	1:B:54:HIS:CE1	2.56	0.41
1:A:686:LYS:HG3	1:B:897:VAL:HG11	2.01	0.41
1:B:916:LYS:HE3	1:B:916:LYS:HB2	1.89	0.41
1:A:346:PHE:CE1	1:A:392[B]:CYS:SG	3.13	0.41
1:A:129:GLN:HB2	1:A:404:GLU:HG3	2.02	0.41
1:B:221:MET:HG3	1:B:222:PRO:HD2	2.02	0.41
1:B:552:LEU:HA	1:B:556:VAL:HB	2.03	0.41
1:A:519:ILE:HD13	1:A:519:ILE:HA	1.96	0.40
1:B:73:ILE:HD11	1:B:82:LEU:HD13	2.03	0.40
1:A:556:VAL:HG12	1:A:560:MET:HE2	2.02	0.40
1:B:129:GLN:HB2	1:B:404:GLU:HG3	2.03	0.40
1:B:551:LEU:HD21	1:B:605:HIS:CE1	2.56	0.40
1:B:568:LYS:HA	1:B:776:VAL:HB	2.04	0.40

All (1) 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)
5:A:1190:HOH:O	5:B:1666:HOH:O[1_655]	2.14	0.06

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	870/898 (97%)	834 (96%)	32 (4%)	4 (0%)	29 11
1	B	865/898 (96%)	833 (96%)	29 (3%)	3 (0%)	41 21
All	All	1735/1796 (97%)	1667 (96%)	61 (4%)	7 (0%)	34 15

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	98	GLY
1	B	103	ALA
1	A	222	PRO
1	A	510	GLN
1	B	222	PRO
1	B	277	HIS
1	A	505	LEU

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	729/776 (94%)	717 (98%)	12 (2%)	62 40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	723/776 (93%)	711 (98%)	12 (2%)	60	36
All	All	1452/1552 (94%)	1428 (98%)	24 (2%)	62	36

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	146	PHE
1	A	175	GLU
1	A	370	TYR
1	A	497[A]	HIS
1	A	497[B]	HIS
1	A	519	ILE
1	A	564	MET
1	A	627	GLN
1	A	628	LYS
1	A	638	LEU
1	A	800	LYS
1	A	811	LYS
1	B	62	VAL
1	B	106	LEU
1	B	146	PHE
1	B	161	GLU
1	B	269	VAL
1	B	317	ASN
1	B	370	TYR
1	B	523	SER
1	B	546	GLN
1	B	627	GLN
1	B	638	LEU
1	B	811	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	123	ASN
1	A	317	ASN
1	A	418	GLN
1	A	494	ASN
1	A	518	GLN
1	B	280	HIS
1	B	317	ASN

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Mol	Chain	Res	Type
1	B	494	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	T1J	B	1001	-	20,20,20	0.74	0	20,27,27	1.03	2 (10%)
2	TPP	A	1001	3	22,27,27	0.67	0	29,40,40	0.84	1 (3%)
2	TPP	B	1002	3	22,27,27	0.66	0	29,40,40	0.92	1 (3%)

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	T1J	B	1001	-	-	0/3/5/5	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TPP	A	1001	3	-	4/16/17/17	0/2/2/2
2	TPP	B	1002	3	-	3/16/17/17	0/2/2/2

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	TPP	C7'-N3-C2	-2.73	120.42	125.35
2	B	1002	TPP	C7'-N3-C2	-2.64	120.58	125.35
4	B	1001	T1J	C14-C13-C12	-2.34	116.71	120.08
4	B	1001	T1J	C08-N09-C10	-2.28	120.09	123.28

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	TPP	C4-C5-C6-C7
2	A	1001	TPP	PA-O3A-PB-O2B
2	A	1001	TPP	PA-O3A-PB-O3B
2	B	1002	TPP	PA-O3A-PB-O3B
2	B	1002	TPP	PA-O3A-PB-O2B
2	B	1002	TPP	C4-C5-C6-C7
2	A	1001	TPP	PA-O3A-PB-O1B

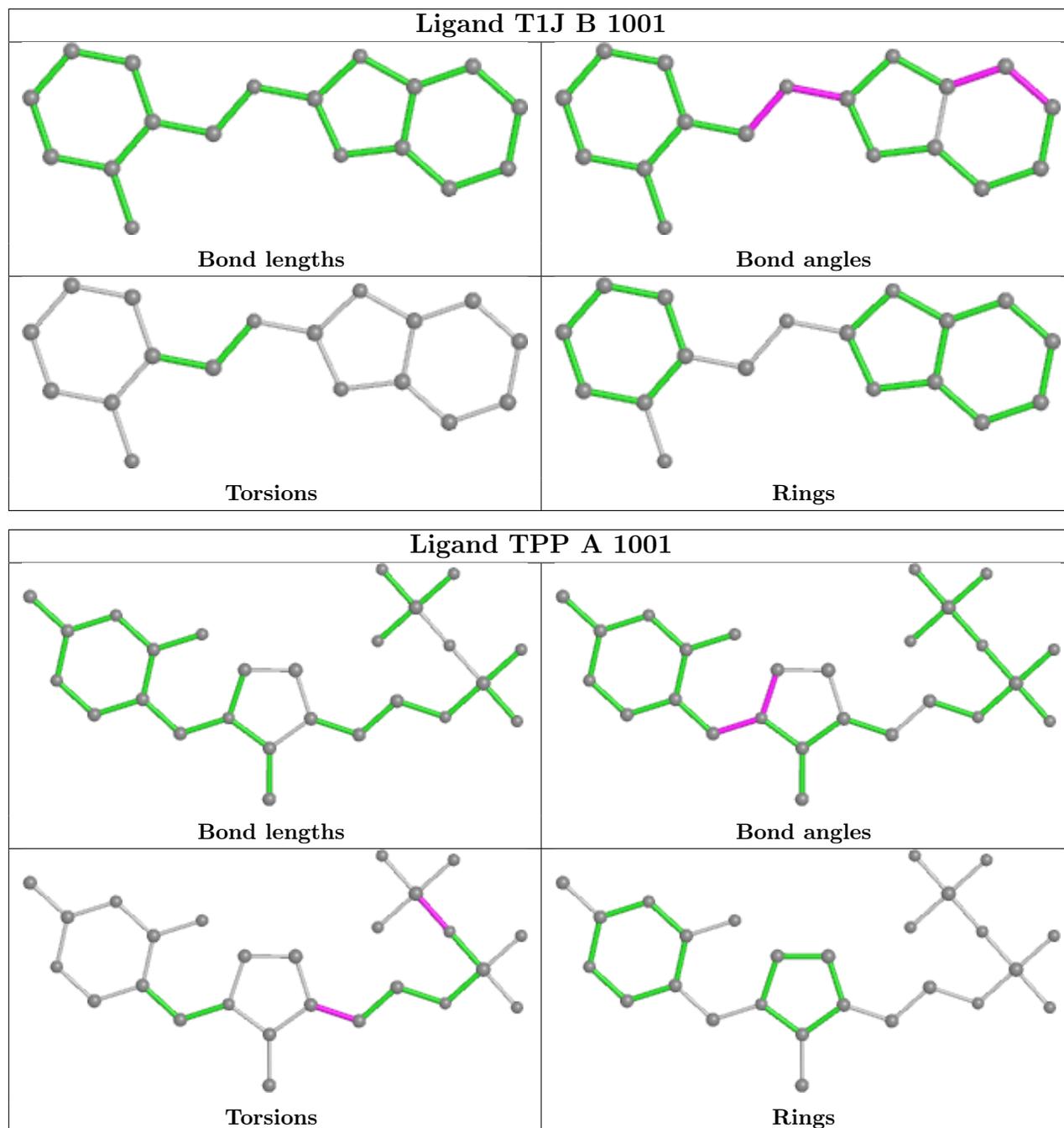
There are no ring outliers.

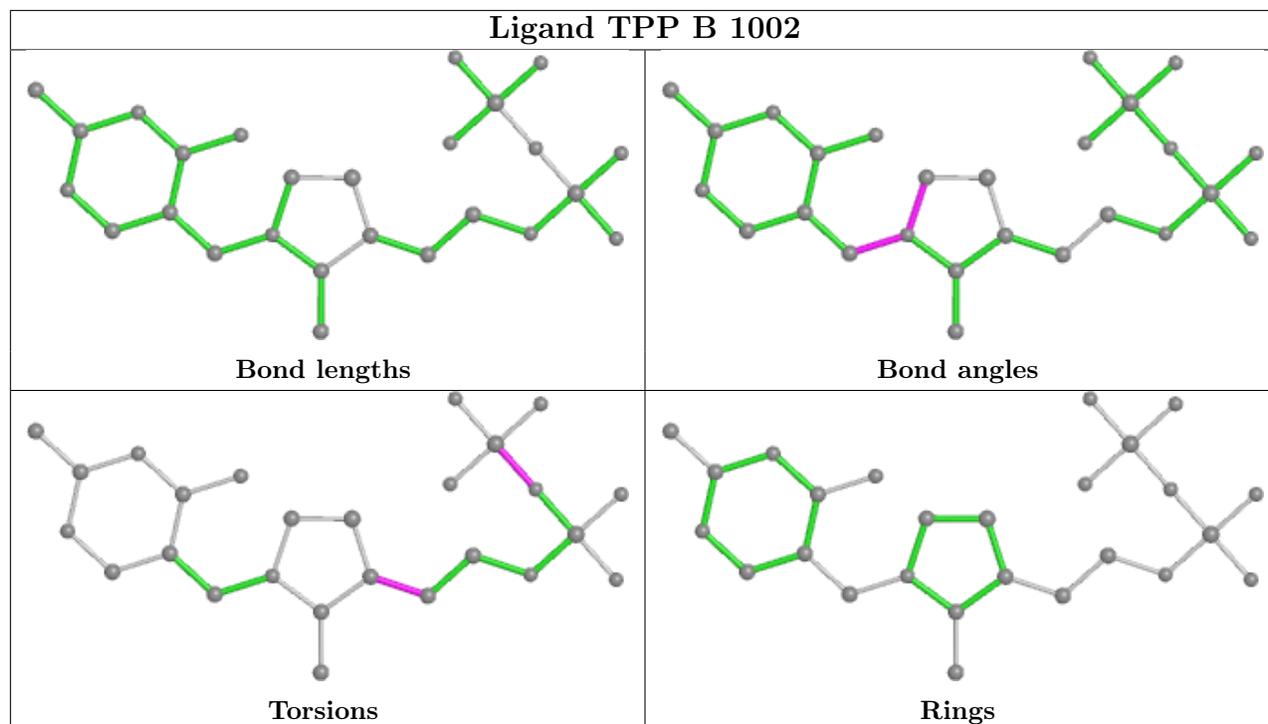
2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	TPP	4	0
2	B	1002	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 [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, 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	A	867/898 (96%)	-0.36	27 (3%) 49 46	9, 19, 44, 60	0
1	B	867/898 (96%)	-0.24	29 (3%) 46 42	9, 23, 53, 77	0
All	All	1734/1796 (96%)	-0.30	56 (3%) 47 44	9, 21, 49, 77	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	505	LEU	8.5
1	B	104	GLY	7.3
1	A	82	LEU	7.0
1	A	276	HIS	6.8
1	B	98	GLY	6.6
1	B	511	GLY	5.5
1	A	504	ASN	5.3
1	B	276	HIS	5.3
1	B	508	HIS	5.3
1	A	83	LEU	5.1
1	B	509	TRP	5.1
1	B	109	GLY	5.0
1	A	104	GLY	4.9
1	A	503	LEU	4.8
1	B	103	ALA	4.7
1	B	510	GLN	4.5
1	A	103	ALA	4.4
1	A	275	ALA	4.2
1	A	81	ALA	4.0
1	A	519	ILE	3.9
1	B	101	HIS	3.8
1	B	317	ASN	3.6
1	B	275	ALA	3.6
1	B	211	TYR	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	78	THR	3.6
1	B	83	LEU	3.5
1	A	98	GLY	3.4
1	B	100	PHE	3.0
1	A	79	GLY	2.9
1	A	855	HIS	2.9
1	A	274	GLY	2.9
1	B	512	LEU	2.7
1	B	50	PRO	2.7
1	B	81	ALA	2.6
1	A	497[A]	HIS	2.6
1	B	85	ASN	2.5
1	B	80	GLN	2.5
1	A	211	TYR	2.5
1	A	102	THR	2.5
1	A	502	ALA	2.4
1	B	84	GLU	2.4
1	B	507	ALA	2.4
1	B	824	GLY	2.3
1	A	255	PHE	2.3
1	A	857	LYS	2.2
1	A	501	PRO	2.2
1	B	111	GLU	2.2
1	A	854	LYS	2.2
1	A	254	ASN	2.2
1	A	84	GLU	2.1
1	B	105	LEU	2.1
1	B	49	ARG	2.0
1	B	472	MET	2.0
1	A	508	HIS	2.0
1	B	498	TYR	2.0
1	B	501	PRO	2.0

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

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

6.3 Carbohydrates [i](#)

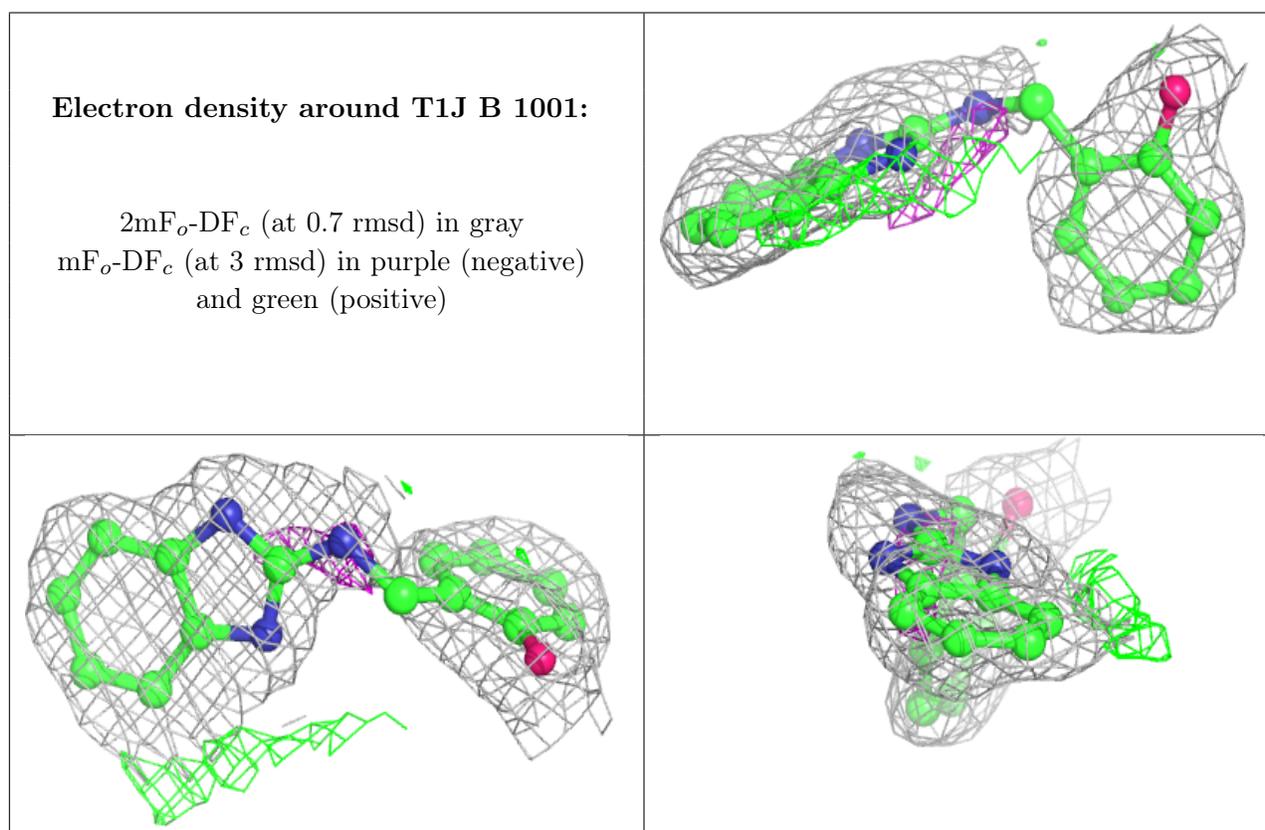
There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

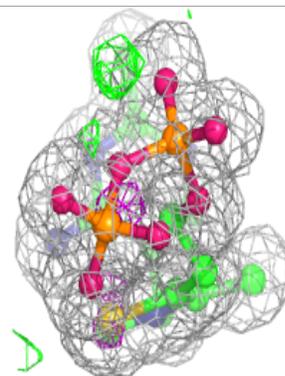
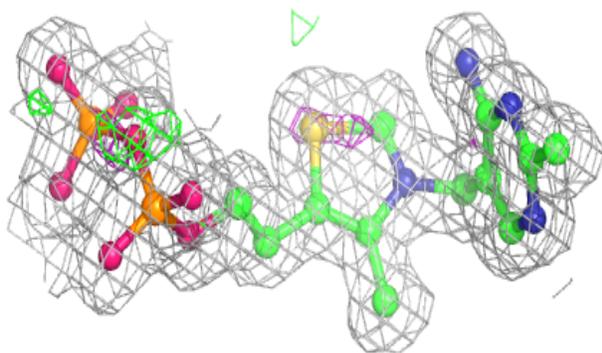
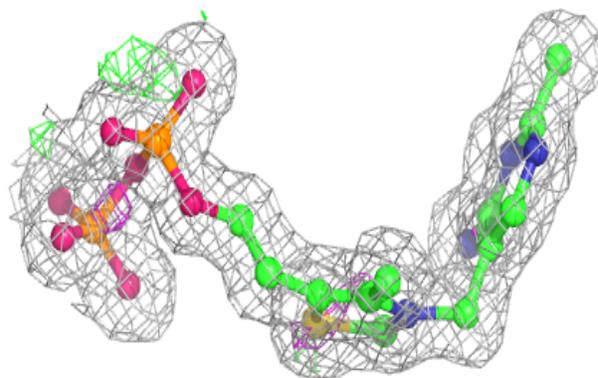
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	T1J	B	1001	18/18	0.81	0.13	38,38,39,39	18
2	TPP	B	1002	26/26	0.98	0.06	10,13,15,16	0
3	MG	B	1003	1/1	0.99	0.06	14,14,14,14	0
2	TPP	A	1001	26/26	0.99	0.06	9,10,11,12	0
3	MG	B	1004	1/1	1.00	0.07	13,13,13,13	0
3	MG	A	1002	1/1	1.00	0.05	12,12,12,12	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.

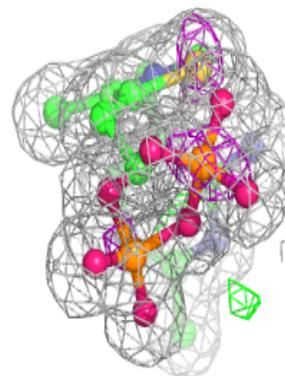
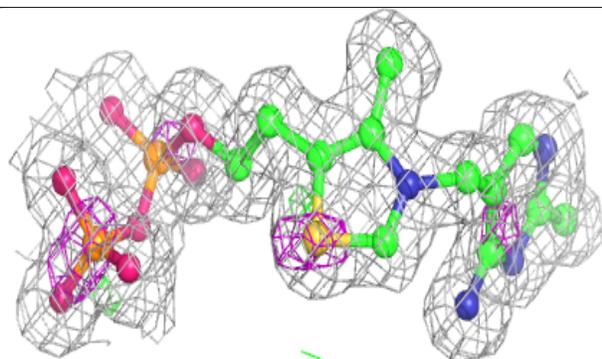
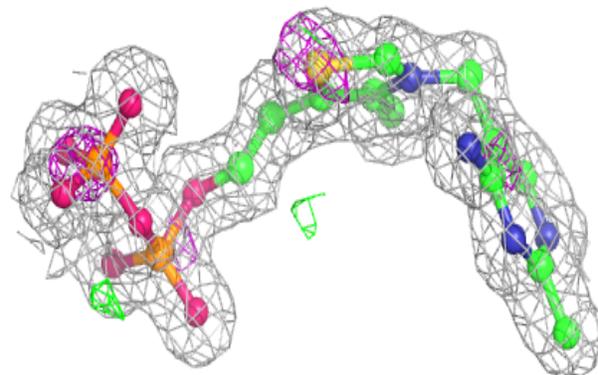


Electron density around TPP B 1002:

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

**Electron density around TPP A 1001:**

$2mF_o-DF_c$ (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.