



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 28, 2025 – 12:37 PM EDT

PDB ID : 3EXF / pdb_00003exf
Title : Crystal structure of the pyruvate dehydrogenase (E1p) component of human pyruvate dehydrogenase complex
Authors : Kato, M.; Wynn, R.M.; Chuang, J.L.; Tso, S.-C.; Machius, M.; Li, J.; Chuang, D.T.
Deposited on : 2008-10-16
Resolution : 3.00 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 Phenix2.0rc1
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

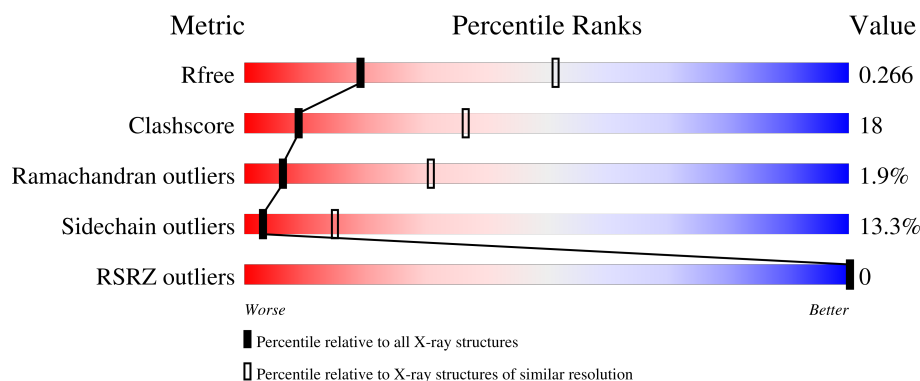
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2511 (3.00-3.00)
Clashscore	180529	2866 (3.00-3.00)
Ramachandran outliers	177936	2778 (3.00-3.00)
Sidechain outliers	177891	2781 (3.00-3.00)
RSRZ outliers	164620	2523 (3.00-3.00)

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	A	382	
1	C	382	
1	E	382	
1	G	382	

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Mol	Chain	Length	Quality of chain
2	B	329	<div><div></div><div>57%</div><div>35%</div><div>9%</div></div>
2	D	329	<div><div></div><div>57%</div><div>35%</div><div>7%</div><div></div></div>
2	F	329	<div><div></div><div>60%</div><div>33%</div><div>7%</div></div>
2	H	329	<div><div></div><div>60%</div><div>33%</div><div>7%</div></div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 21507 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 Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	362	Total	C	N	O	S	0	0	0
			2821	1772	496	529	24			
1	C	363	Total	C	N	O	S	0	0	0
			2834	1780	499	530	25			
1	E	363	Total	C	N	O	S	0	0	0
			2834	1780	499	530	25			
1	G	362	Total	C	N	O	S	0	0	0
			2821	1772	496	529	24			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-20	MET	-	expression tag	UNP P08559
A	-19	GLY	-	expression tag	UNP P08559
A	-18	SER	-	expression tag	UNP P08559
A	-17	SER	-	expression tag	UNP P08559
A	-16	HIS	-	expression tag	UNP P08559
A	-15	HIS	-	expression tag	UNP P08559
A	-14	HIS	-	expression tag	UNP P08559
A	-13	HIS	-	expression tag	UNP P08559
A	-12	HIS	-	expression tag	UNP P08559
A	-11	HIS	-	expression tag	UNP P08559
A	-10	SER	-	expression tag	UNP P08559
A	-9	SER	-	expression tag	UNP P08559
A	-8	GLY	-	expression tag	UNP P08559
A	-7	LEU	-	expression tag	UNP P08559
A	-6	VAL	-	expression tag	UNP P08559
A	-5	PRO	-	expression tag	UNP P08559
A	-4	ARG	-	expression tag	UNP P08559
A	-3	GLY	-	expression tag	UNP P08559
A	-2	SER	-	expression tag	UNP P08559
A	-1	HIS	-	expression tag	UNP P08559

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP P08559
A	203	ALA	SER	engineered mutation	UNP P08559
A	271	ALA	SER	engineered mutation	UNP P08559
C	-20	MET	-	expression tag	UNP P08559
C	-19	GLY	-	expression tag	UNP P08559
C	-18	SER	-	expression tag	UNP P08559
C	-17	SER	-	expression tag	UNP P08559
C	-16	HIS	-	expression tag	UNP P08559
C	-15	HIS	-	expression tag	UNP P08559
C	-14	HIS	-	expression tag	UNP P08559
C	-13	HIS	-	expression tag	UNP P08559
C	-12	HIS	-	expression tag	UNP P08559
C	-11	HIS	-	expression tag	UNP P08559
C	-10	SER	-	expression tag	UNP P08559
C	-9	SER	-	expression tag	UNP P08559
C	-8	GLY	-	expression tag	UNP P08559
C	-7	LEU	-	expression tag	UNP P08559
C	-6	VAL	-	expression tag	UNP P08559
C	-5	PRO	-	expression tag	UNP P08559
C	-4	ARG	-	expression tag	UNP P08559
C	-3	GLY	-	expression tag	UNP P08559
C	-2	SER	-	expression tag	UNP P08559
C	-1	HIS	-	expression tag	UNP P08559
C	0	MET	-	expression tag	UNP P08559
C	203	ALA	SER	engineered mutation	UNP P08559
C	271	ALA	SER	engineered mutation	UNP P08559
E	-20	MET	-	expression tag	UNP P08559
E	-19	GLY	-	expression tag	UNP P08559
E	-18	SER	-	expression tag	UNP P08559
E	-17	SER	-	expression tag	UNP P08559
E	-16	HIS	-	expression tag	UNP P08559
E	-15	HIS	-	expression tag	UNP P08559
E	-14	HIS	-	expression tag	UNP P08559
E	-13	HIS	-	expression tag	UNP P08559
E	-12	HIS	-	expression tag	UNP P08559
E	-11	HIS	-	expression tag	UNP P08559
E	-10	SER	-	expression tag	UNP P08559
E	-9	SER	-	expression tag	UNP P08559
E	-8	GLY	-	expression tag	UNP P08559
E	-7	LEU	-	expression tag	UNP P08559
E	-6	VAL	-	expression tag	UNP P08559
E	-5	PRO	-	expression tag	UNP P08559

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-4	ARG	-	expression tag	UNP P08559
E	-3	GLY	-	expression tag	UNP P08559
E	-2	SER	-	expression tag	UNP P08559
E	-1	HIS	-	expression tag	UNP P08559
E	0	MET	-	expression tag	UNP P08559
E	203	ALA	SER	engineered mutation	UNP P08559
E	271	ALA	SER	engineered mutation	UNP P08559
G	-20	MET	-	expression tag	UNP P08559
G	-19	GLY	-	expression tag	UNP P08559
G	-18	SER	-	expression tag	UNP P08559
G	-17	SER	-	expression tag	UNP P08559
G	-16	HIS	-	expression tag	UNP P08559
G	-15	HIS	-	expression tag	UNP P08559
G	-14	HIS	-	expression tag	UNP P08559
G	-13	HIS	-	expression tag	UNP P08559
G	-12	HIS	-	expression tag	UNP P08559
G	-11	HIS	-	expression tag	UNP P08559
G	-10	SER	-	expression tag	UNP P08559
G	-9	SER	-	expression tag	UNP P08559
G	-8	GLY	-	expression tag	UNP P08559
G	-7	LEU	-	expression tag	UNP P08559
G	-6	VAL	-	expression tag	UNP P08559
G	-5	PRO	-	expression tag	UNP P08559
G	-4	ARG	-	expression tag	UNP P08559
G	-3	GLY	-	expression tag	UNP P08559
G	-2	SER	-	expression tag	UNP P08559
G	-1	HIS	-	expression tag	UNP P08559
G	0	MET	-	expression tag	UNP P08559
G	203	ALA	SER	engineered mutation	UNP P08559
G	271	ALA	SER	engineered mutation	UNP P08559

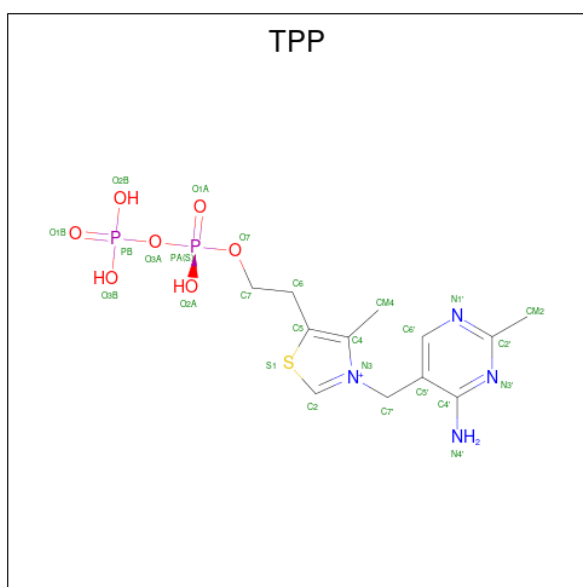
- Molecule 2 is a protein called Pyruvate dehydrogenase E1 component subunit beta, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			
2	D	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			
2	F	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			
2	H	329	Total	C	N	O	S	0	0	0
			2519	1604	427	469	19			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		
3	E	1	Total	Mg	0	0
			1	1		
3	G	1	Total	Mg	0	0
			1	1		

- Molecule 4 is THIAMINE DIPHOSPHATE (CCD ID: TPP) (formula: C₁₂H₁₉N₄O₇P₂S).



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

- Molecule 5 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	K	0	0
			1	1		

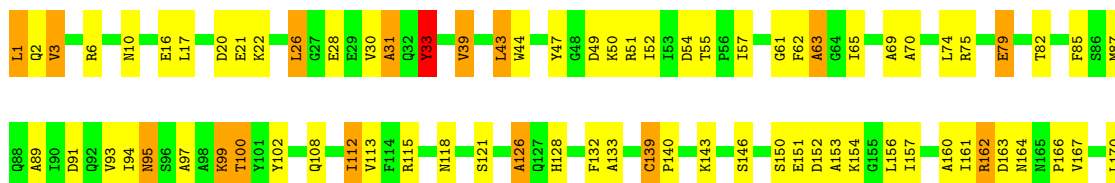
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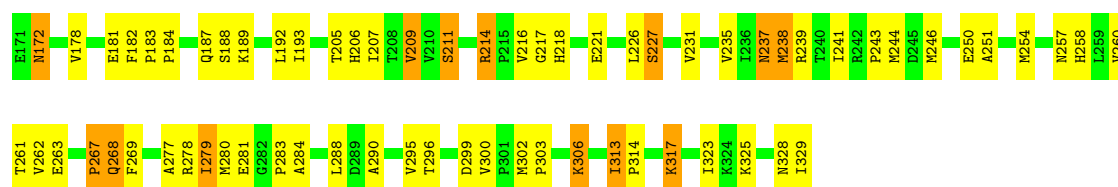
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	D	1	Total K 1 1	0	0
5	F	1	Total K 1 1	0	0
5	H	1	Total K 1 1	0	0

- Molecule 6 is water.

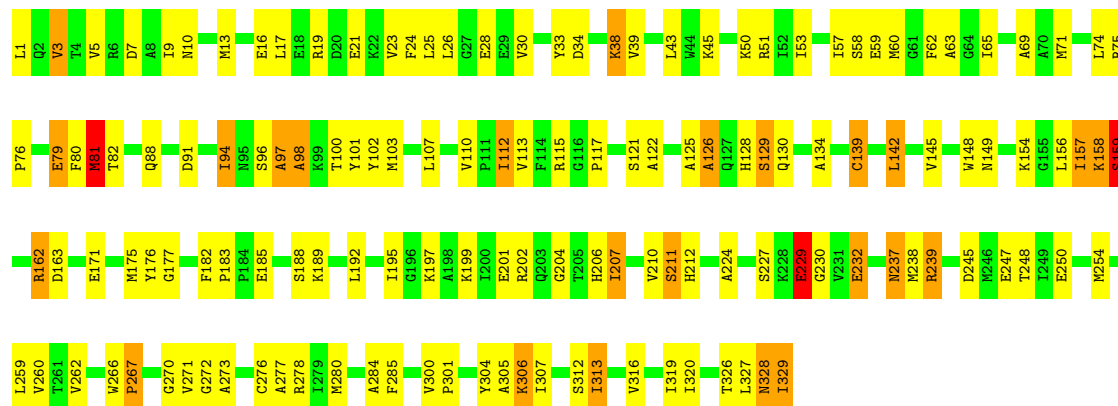
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total O 1 1	0	0
6	C	3	Total O 3 3	0	0
6	D	1	Total O 1 1	0	0
6	E	1	Total O 1 1	0	0
6	F	2	Total O 2 2	0	0
6	H	1	Total O 1 1	0	0





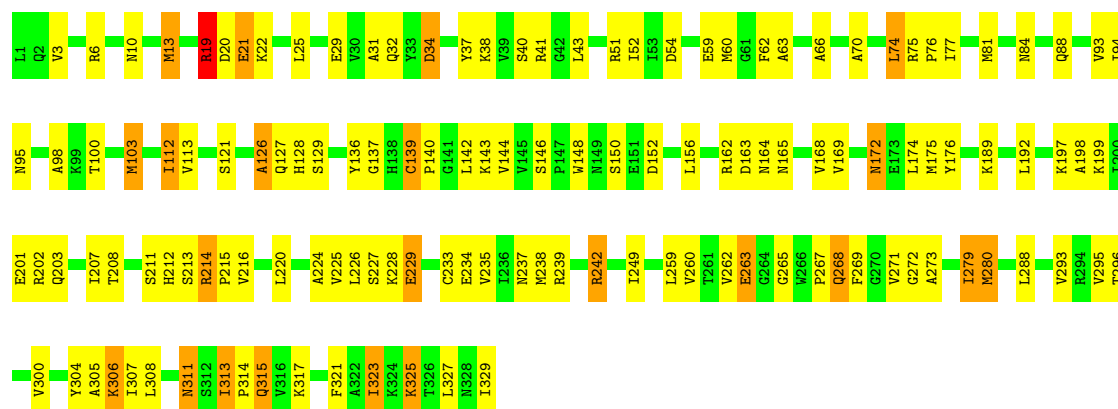
- Molecule 2: Pyruvate dehydrogenase E1 component subunit beta, mitochondrial

Chain D: 57% 35% 7% •



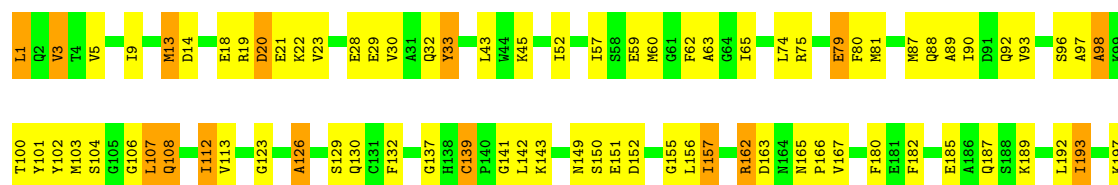
- Molecule 2: Pyruvate dehydrogenase E1 component subunit beta, mitochondrial

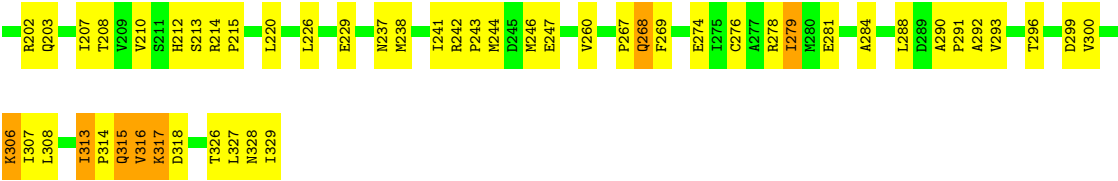
Chain F: 60% 33% 7%



- Molecule 2: Pyruvate dehydrogenase E1 component subunit beta, mitochondrial

Chain H: 60% 33% 7%





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	103.39Å 129.67Å 144.95Å 90.00° 109.15° 90.00°	Depositor
Resolution (Å)	50.00 – 3.00 50.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (50.00-3.00) 99.4 (50.00-3.00)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.58 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.4.0069	Depositor
R, R_{free}	0.185 , 0.263 0.190 , 0.266	Depositor DCC
R_{free} test set	3624 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	35.5	Xtriage
Anisotropy	0.059	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 5.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.117 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	21507	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.44% 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, K, 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	1.14	4/2877 (0.1%)	1.30	15/3875 (0.4%)
1	C	1.17	3/2891 (0.1%)	1.34	20/3893 (0.5%)
1	E	1.13	2/2891 (0.1%)	1.29	19/3893 (0.5%)
1	G	1.15	1/2877 (0.0%)	1.29	16/3875 (0.4%)
2	B	1.20	3/2574 (0.1%)	1.37	23/3488 (0.7%)
2	D	1.17	3/2574 (0.1%)	1.33	19/3488 (0.5%)
2	F	1.21	6/2574 (0.2%)	1.32	15/3488 (0.4%)
2	H	1.19	1/2574 (0.0%)	1.37	15/3488 (0.4%)
All	All	1.17	23/21832 (0.1%)	1.32	142/29488 (0.5%)

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	313	ILE	CA-CB	-8.12	1.46	1.55
2	F	77	ILE	CA-CB	-6.55	1.46	1.54
1	A	149	ALA	CA-CB	-5.64	1.44	1.53
2	B	153	ALA	CA-CB	-5.60	1.44	1.53
2	F	6	ARG	CA-C	5.58	1.60	1.52

The worst 5 of 142 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	249	GLY	CA-C-N	10.65	130.57	120.03
1	A	249	GLY	C-N-CA	10.65	130.57	120.03
1	A	67	GLY	N-CA-C	-9.04	103.90	113.58
1	G	344	PRO	CA-C-N	-8.61	111.02	120.14
1	G	344	PRO	C-N-CA	-8.61	111.02	120.14

There are no chirality outliers.

There are no planarity outliers.

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	2821	0	2777	111	0
1	C	2834	0	2791	119	0
1	E	2834	0	2791	112	0
1	G	2821	0	2777	83	0
2	B	2519	0	2517	97	0
2	D	2519	0	2517	95	0
2	F	2519	0	2517	105	0
2	H	2519	0	2517	110	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
3	E	1	0	0	0	0
3	G	1	0	0	0	0
4	A	26	0	16	2	0
4	C	26	0	16	1	0
4	E	26	0	16	2	0
4	G	26	0	16	2	0
5	B	1	0	0	0	0
5	D	1	0	0	0	0
5	F	1	0	0	0	0
5	H	1	0	0	0	0
6	B	1	0	0	0	0
6	C	3	0	0	1	0
6	D	1	0	0	1	0
6	E	1	0	0	0	0
6	F	2	0	0	0	0
6	H	1	0	0	1	0
All	All	21507	0	21268	780	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 18.

The worst 5 of 780 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)
2:F:280:MET:HE3	2:H:292:ALA:HB3	1.21	1.13

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:214:ARG:HG2	2:F:214:ARG:HH11	0.99	1.10
1:C:144:LEU:HD13	2:D:71:MET:CE	1.81	1.10
1:C:144:LEU:HD13	2:D:71:MET:HE1	1.20	1.09
1:C:314:ARG:HH21	1:C:314:ARG:HG3	0.93	1.09

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	A	360/382 (94%)	321 (89%)	32 (9%)	7 (2%)	6	31
1	C	361/382 (94%)	322 (89%)	31 (9%)	8 (2%)	5	27
1	E	361/382 (94%)	333 (92%)	19 (5%)	9 (2%)	4	24
1	G	360/382 (94%)	318 (88%)	35 (10%)	7 (2%)	6	31
2	B	327/329 (99%)	297 (91%)	26 (8%)	4 (1%)	11	41
2	D	327/329 (99%)	277 (85%)	41 (12%)	9 (3%)	4	21
2	F	327/329 (99%)	287 (88%)	37 (11%)	3 (1%)	14	49
2	H	327/329 (99%)	295 (90%)	28 (9%)	4 (1%)	11	41
All	All	2750/2844 (97%)	2450 (89%)	249 (9%)	51 (2%)	6	31

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	18	GLU
1	C	88	ALA
1	C	204	VAL
2	D	207	ILE
2	D	328	ASN

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	292/310 (94%)	258 (88%)	34 (12%)	4	20
1	C	294/310 (95%)	246 (84%)	48 (16%)	2	9
1	E	294/310 (95%)	258 (88%)	36 (12%)	4	18
1	G	292/310 (94%)	244 (84%)	48 (16%)	2	9
2	B	268/268 (100%)	229 (85%)	39 (15%)	2	12
2	D	268/268 (100%)	234 (87%)	34 (13%)	3	17
2	F	268/268 (100%)	240 (90%)	28 (10%)	5	23
2	H	268/268 (100%)	236 (88%)	32 (12%)	4	19
All	All	2244/2312 (97%)	1945 (87%)	299 (13%)	3	15

5 of 299 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	85	LEU
2	H	185	GLU
1	G	157	LYS
1	G	314	ARG
1	C	218	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	40	GLN
2	H	108	GLN
1	G	55	GLN
1	G	263	HIS
2	H	328	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 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
4	TPP	A	1003	3	23,27,27	1.48	5 (21%)	30,40,40	2.08	10 (33%)
4	TPP	E	1009	3	23,27,27	1.50	5 (21%)	30,40,40	2.08	11 (36%)
4	TPP	G	1012	3	23,27,27	1.70	4 (17%)	30,40,40	2.02	13 (43%)
4	TPP	C	1006	3	23,27,27	1.29	2 (8%)	30,40,40	2.11	11 (36%)

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	TPP	A	1003	3	-	1/16/17/17	0/2/2/2
4	TPP	E	1009	3	-	6/16/17/17	0/2/2/2
4	TPP	G	1012	3	-	0/16/17/17	0/2/2/2
4	TPP	C	1006	3	-	4/16/17/17	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	1012	TPP	C6-C5	5.67	1.54	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1003	TPP	C4-N3	-3.86	1.36	1.39
4	C	1006	TPP	C2'-N1'	3.06	1.39	1.34
4	E	1009	TPP	C6-C5	3.02	1.52	1.51
4	E	1009	TPP	C2'-N3'	3.00	1.39	1.34

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	E	1009	TPP	CM4-C4-N3	5.11	129.05	122.53
4	A	1003	TPP	C5'-C7'-N3	-4.99	104.96	113.28
4	A	1003	TPP	C6'-C5'-C4'	4.70	121.33	115.55
4	C	1006	TPP	C5'-C7'-N3	-4.24	106.22	113.28
4	C	1006	TPP	C6'-N1'-C2'	4.19	122.95	116.07

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	E	1009	TPP	C5-C6-C7-O7
4	E	1009	TPP	C7-O7-PA-O1A
4	E	1009	TPP	C7-O7-PA-O3A
4	C	1006	TPP	C4-C5-C6-C7
4	E	1009	TPP	C4-C5-C6-C7

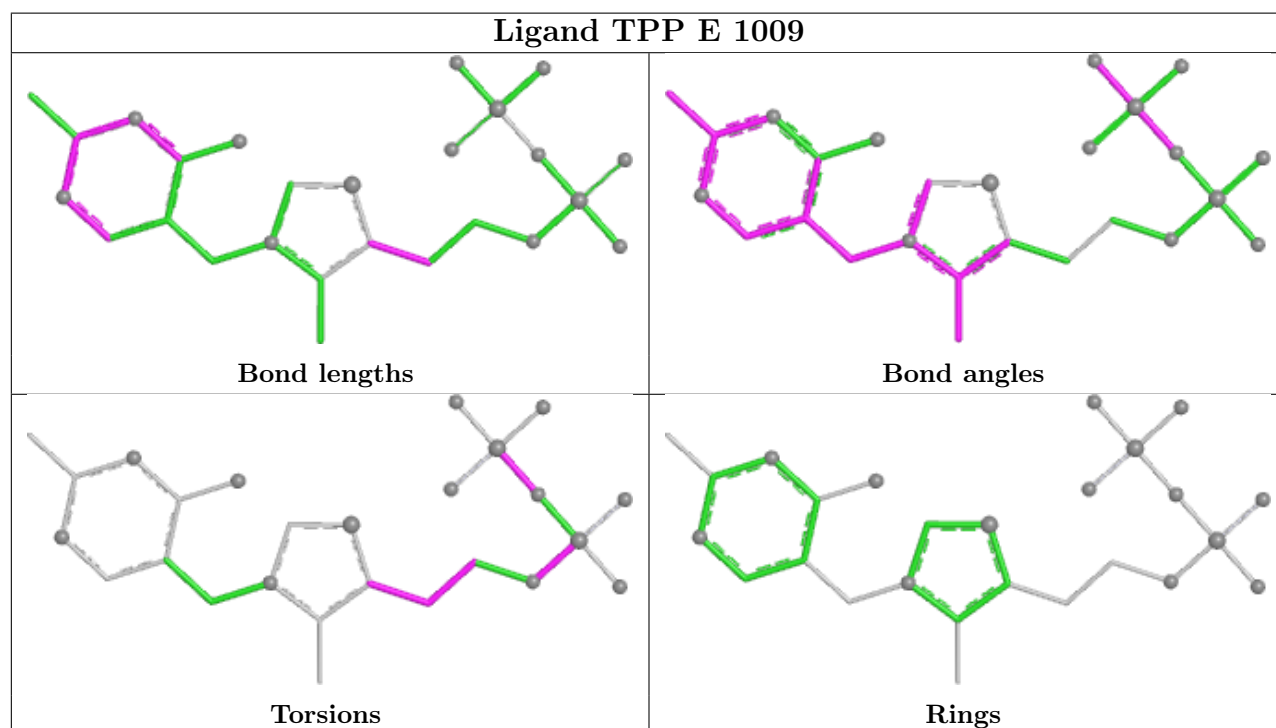
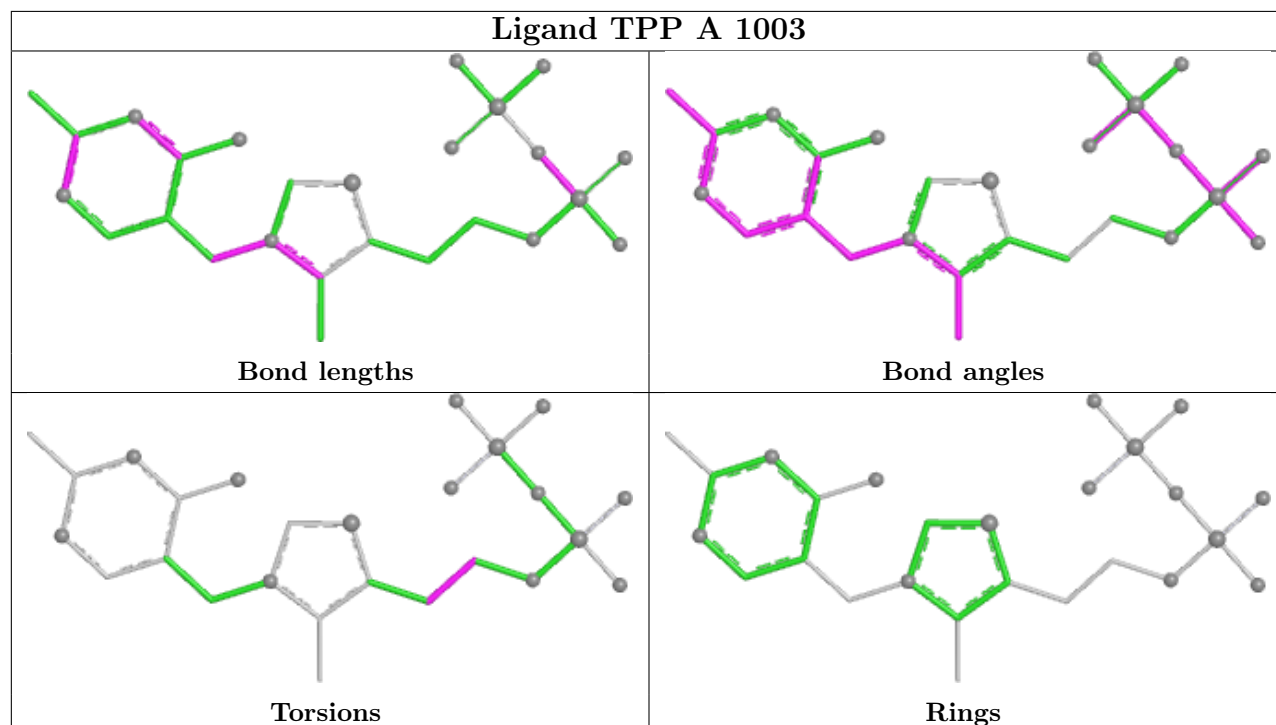
There are no ring outliers.

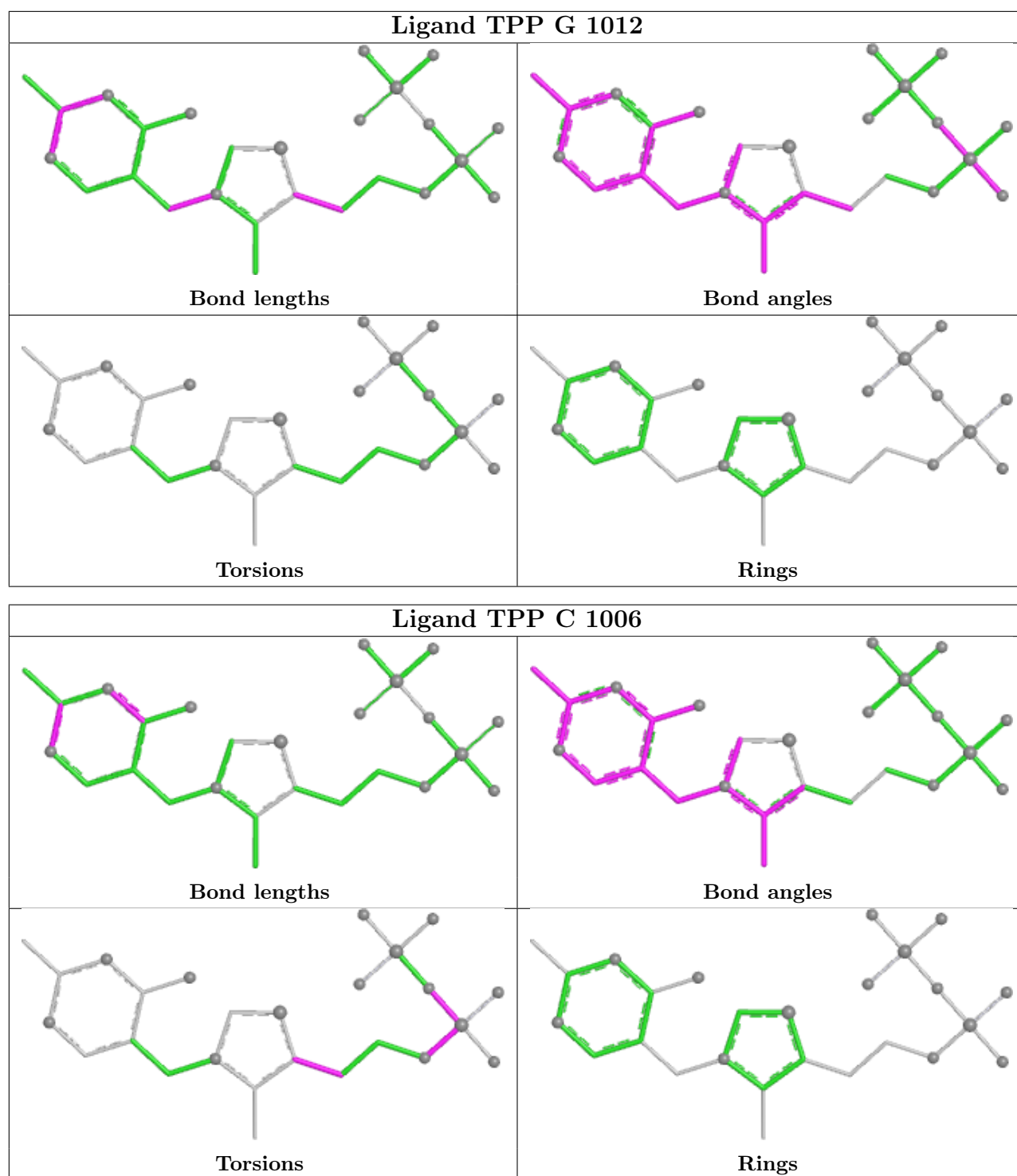
4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1003	TPP	2	0
4	E	1009	TPP	2	0
4	G	1012	TPP	2	0
4	C	1006	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 ⓘ

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	362/382 (94%)	-1.96	0 100 100	8, 21, 37, 52	0
1	C	363/382 (95%)	-1.97	0 100 100	10, 20, 40, 54	0
1	E	363/382 (95%)	-1.95	0 100 100	10, 21, 41, 54	0
1	G	362/382 (94%)	-1.96	0 100 100	9, 20, 39, 53	0
2	B	329/329 (100%)	-1.99	0 100 100	8, 19, 29, 38	0
2	D	329/329 (100%)	-2.00	0 100 100	12, 20, 30, 41	0
2	F	329/329 (100%)	-1.98	0 100 100	10, 20, 29, 40	0
2	H	329/329 (100%)	-1.99	0 100 100	7, 19, 28, 42	0
All	All	2766/2844 (97%)	-1.97	0 100 100	7, 20, 33, 54	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](#)

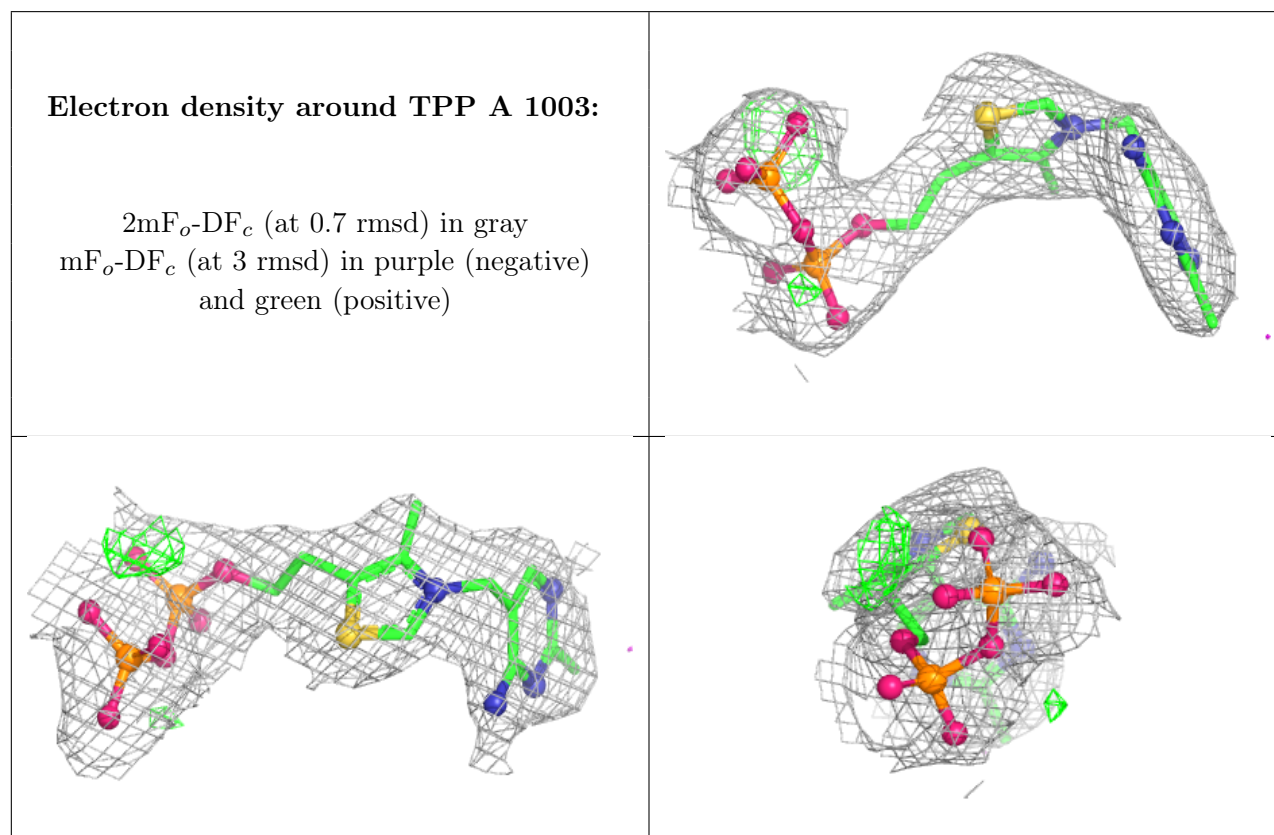
There are no monosaccharides in this entry.

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, 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.

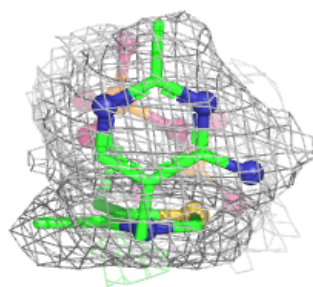
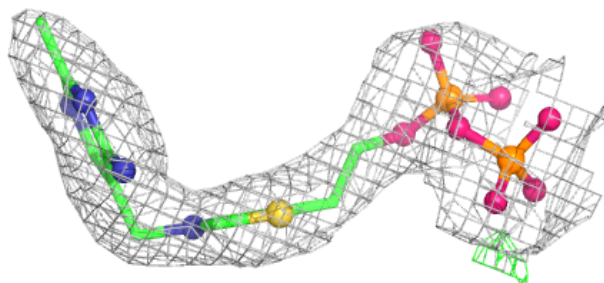
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	K	F	1011	1/1	0.98	0.05	66,66,66,66	0
5	K	D	1002	1/1	0.99	0.03	50,50,50,50	0
5	K	H	1008	1/1	0.99	0.04	36,36,36,36	0
3	MG	G	1010	1/1	1.00	0.02	11,11,11,11	0
4	TPP	A	1003	26/26	1.00	0.02	16,21,29,33	0
4	TPP	C	1006	26/26	1.00	0.02	15,22,34,40	0
4	TPP	E	1009	26/26	1.00	0.02	18,27,37,40	0
4	TPP	G	1012	26/26	1.00	0.02	17,23,35,41	0
5	K	B	1005	1/1	1.00	0.02	37,37,37,37	0
3	MG	A	1001	1/1	1.00	0.03	6,6,6,6	0
3	MG	C	1004	1/1	1.00	0.01	22,22,22,22	0
3	MG	E	1007	1/1	1.00	0.02	30,30,30,30	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.

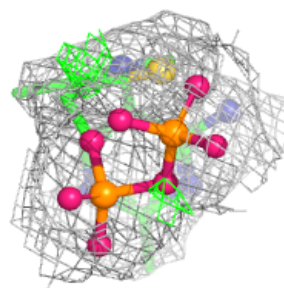
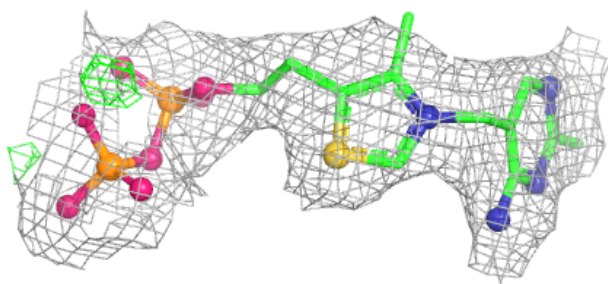
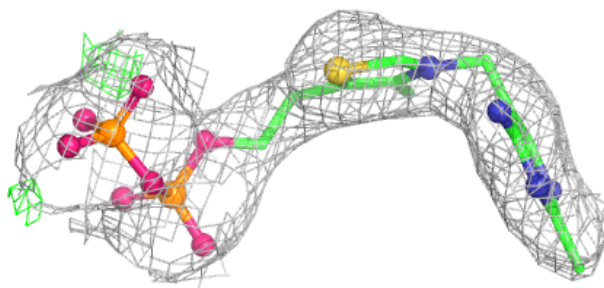


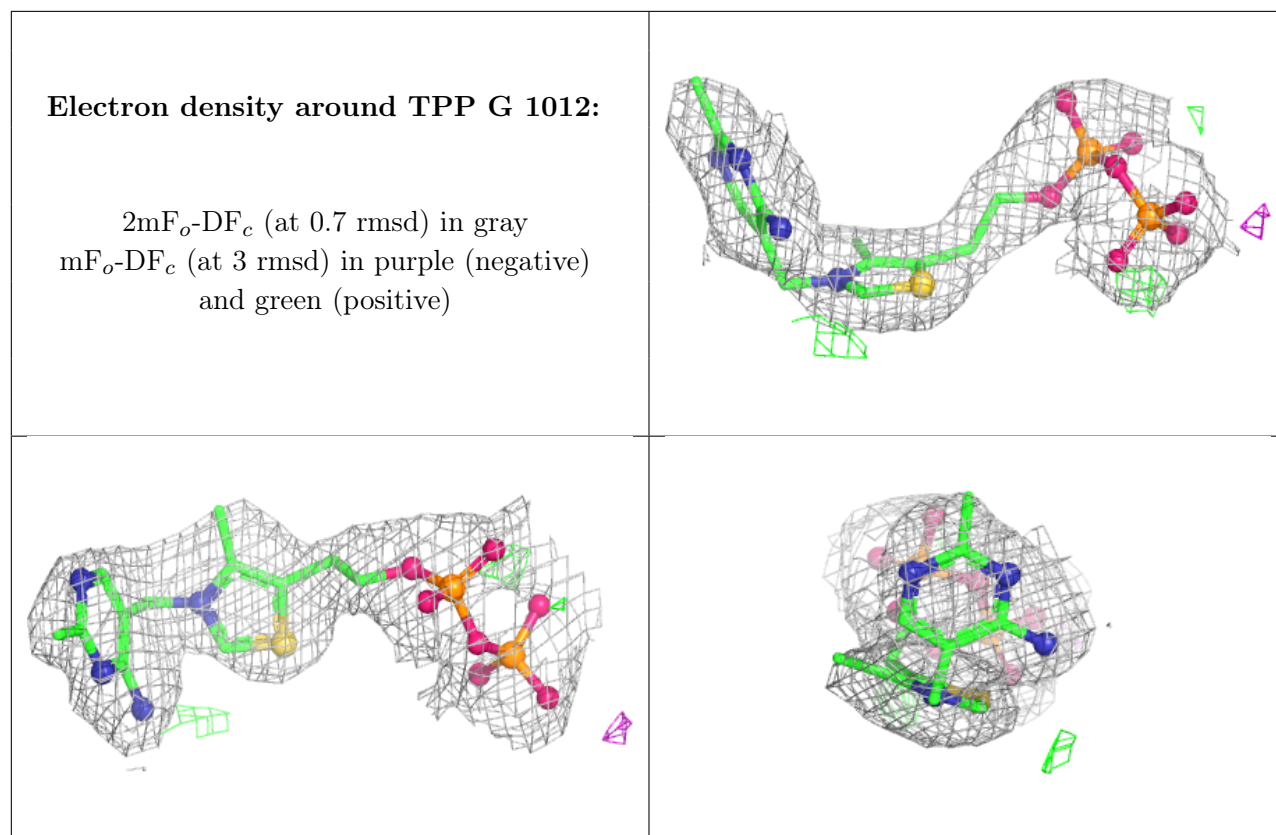
Electron density around TPP C 1006:

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

**Electron density around TPP E 1009:**

$2mF_o-DF_c$ (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.