W O R L D W I D E
wwPDB
P R O T E I N   D A T A   B A N K

wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 23, 2023 – 08:12 PM EDT

PDB ID	:	5TMA
Title	:	Zymomonas mobilis pyruvate decarboxylase mutant PDC-2.3
Authors	:	Alahuhta, P.M.; Lunin, V.V.
Deposited on	:	2016-10-12
Resolution	:	1.67 Å(reported)

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)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
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)	:	2.35.1

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 1.67 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	Percentile Ranks	Value
Rfree		0.209
Clashscore		6
Ramachandran outliers		0.3%
Sidechain outliers		1.0%
RSRZ outliers		2.2%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
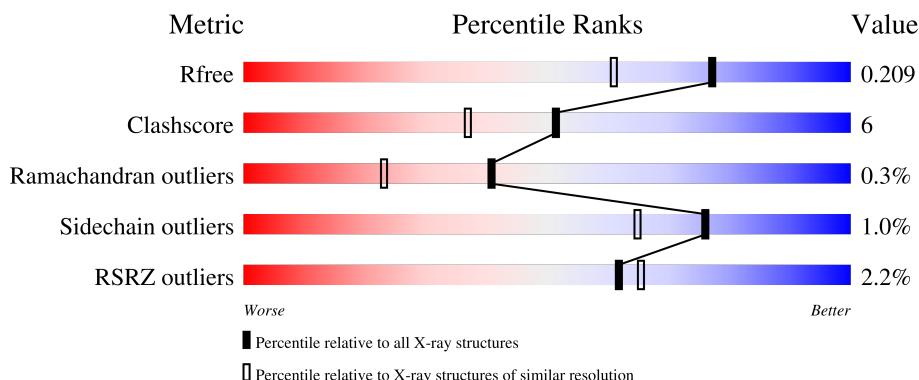
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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 <=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	576	3% / 91% / 8% ·
1	B	576	% / 91% / 6% ··
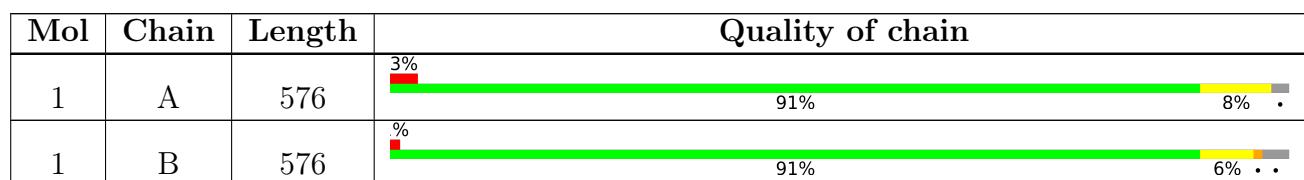
The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SO4	A	606	-	-	X	-
4	SO4	A	607[B]	-	-	X	-
4	SO4	B	606[B]	-	-	X	-
5	EDO	A	615	-	-	X	-
5	EDO	A	617	-	-	X	-
5	EDO	B	621	-	-	X	-

2 Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 10255 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 decarboxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	567	Total 4560	C 2886	N 769	O 879	S 26	0	29	0
1	B	561	Total 4442	C 2816	N 751	O 849	S 26	0	21	0

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	2	ASP	SER	engineered mutation	UNP P06672
A	38	ASP	LEU	engineered mutation	UNP P06672
A	109	ALA	GLY	engineered mutation	UNP P06672
A	207	GLU	ALA	engineered mutation	UNP P06672
A	224	ALA	GLY	engineered mutation	UNP P06672
A	333	GLU	GLN	engineered mutation	UNP P06672
A	357	ASP	ALA	engineered mutation	UNP P06672
A	374	ILE	VAL	engineered mutation	UNP P06672
A	376	ASP	ALA	engineered mutation	UNP P06672
A	491	ALA	GLY	engineered mutation	UNP P06672
A	515	ALA	GLY	engineered mutation	UNP P06672
A	516	ALA	GLY	engineered mutation	UNP P06672
A	519	GLU	ALA	engineered mutation	UNP P06672
A	527	ASP	ALA	engineered mutation	UNP P06672
A	540	ALA	GLY	engineered mutation	UNP P06672
A	553	GLU	LYS	engineered mutation	UNP P06672
A	569	LEU	-	expression tag	UNP P06672
A	570	GLU	-	expression tag	UNP P06672
A	571	HIS	-	expression tag	UNP P06672
A	572	HIS	-	expression tag	UNP P06672
A	573	HIS	-	expression tag	UNP P06672
A	574	HIS	-	expression tag	UNP P06672
A	575	HIS	-	expression tag	UNP P06672
A	576	HIS	-	expression tag	UNP P06672
B	2	ASP	SER	engineered mutation	UNP P06672

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Chain	Residue	Modelled	Actual	Comment	Reference
B	38	ASP	LEU	engineered mutation	UNP P06672
B	109	ALA	GLY	engineered mutation	UNP P06672
B	207	GLU	ALA	engineered mutation	UNP P06672
B	224	ALA	GLY	engineered mutation	UNP P06672
B	333	GLU	GLN	engineered mutation	UNP P06672
B	357	ASP	ALA	engineered mutation	UNP P06672
B	374	ILE	VAL	engineered mutation	UNP P06672
B	376	ASP	ALA	engineered mutation	UNP P06672
B	491	ALA	GLY	engineered mutation	UNP P06672
B	515	ALA	GLY	engineered mutation	UNP P06672
B	516	ALA	GLY	engineered mutation	UNP P06672
B	519	GLU	ALA	engineered mutation	UNP P06672
B	527	ASP	ALA	engineered mutation	UNP P06672
B	540	ALA	GLY	engineered mutation	UNP P06672
B	553	GLU	LYS	engineered mutation	UNP P06672
B	569	LEU	-	expression tag	UNP P06672
B	570	GLU	-	expression tag	UNP P06672
B	571	HIS	-	expression tag	UNP P06672
B	572	HIS	-	expression tag	UNP P06672
B	573	HIS	-	expression tag	UNP P06672
B	574	HIS	-	expression tag	UNP P06672
B	575	HIS	-	expression tag	UNP P06672
B	576	HIS	-	expression tag	UNP P06672

- Molecule 2 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: $C_{12}H_{19}N_4O_7P_2S$).
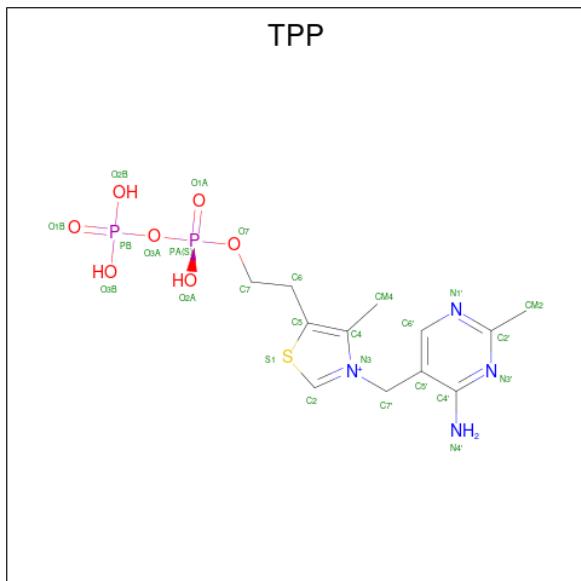
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0
2	B	1	Total 26	C 12	N 4	O 7	P 2	S 1	0	0

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

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

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 5	O 4	S 1	0	0
4	A	1	Total 5	O 4	S 1	0	0
4	A	1	Total 5	O 4	S 1	0	0
4	A	1	Total 5	O 4	S 1	0	0
4	A	1	Total 10	O 8	S 2	0	1
4	A	1	Total 5	O 4	S 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total 5	O 4	S 1	0	0
4	B	1	Total 5	O 4	S 1	0	0
4	B	1	Total 5	O 4	S 1	0	0
4	B	1	Total 10	O 8	S 2	0	1
4	B	1	Total 10	O 8	S 2	0	1
4	B	1	Total 5	O 4	S 1	0	0
4	B	1	Total 5	O 4	S 1	0	0
4	B	1	Total 5	O 4	S 1	0	0
4	B	1	Total 5	O 4	S 1	0	0
4	B	1	Total 5	O 4	S 1	0	0

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total 4	C 2	O 2	0	0
5	A	1	Total 4	C 2	O 2	0	0
5	A	1	Total 4	C 2	O 2	0	0
5	A	1	Total 4	C 2	O 2	0	0
5	A	1	Total 4	C 2	O 2	0	0
5	A	1	Total 4	C 2	O 2	0	0
5	A	1	Total 8	C 4	O 4	0	1
5	A	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0
5	B	1	Total 4	C 2	O 2	0	0

- Molecule 6 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	507	Total 520	O 520	0	13
6	B	497	Total 508	O 508	0	11

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: Pyruvate decarboxylase

Chain A:

• Molecule 1: Pyruvate decarboxylase

Chain B:
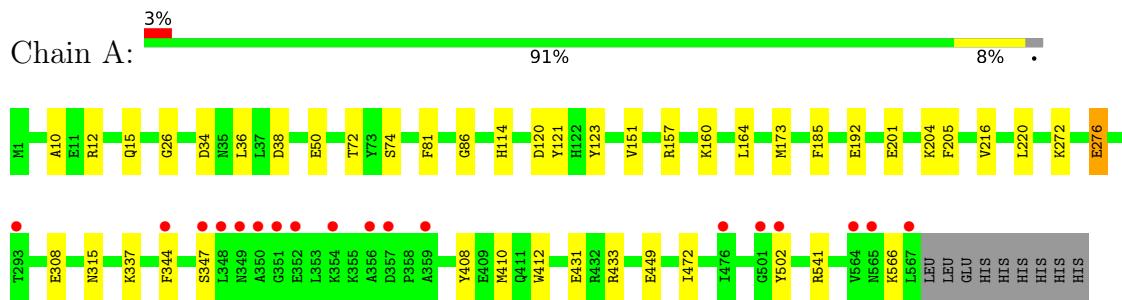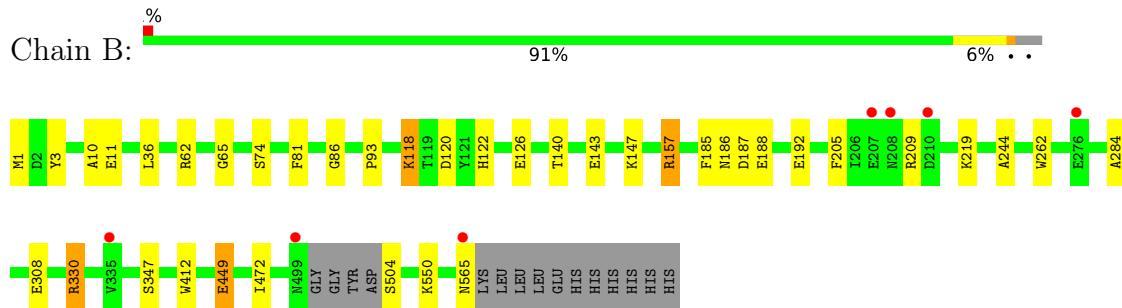
4 Data and refinement statistics   ⓘ

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	124.44Å 124.44Å 173.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	101.18 – 1.67 52.53 – 1.67	Depositor EDS
% Data completeness (in resolution range)	99.5 (101.18-1.67) 99.5 (52.53-1.67)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	1.17 (at 1.67Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.170 , 0.203 0.181 , 0.209	Depositor DCC
R_{free} test set	7707 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å^2)	19.1	Xtriage
Anisotropy	0.004	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 50.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50, < L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	10255	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< \|L\| >$, $< L^2 >$ 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: MG, TPP, EDO, SO4

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	1.06	6/4655 (0.1%)	0.98	10/6322 (0.2%)
1	B	1.03	4/4534 (0.1%)	1.00	14/6157 (0.2%)
All	All	1.04	10/9189 (0.1%)	0.99	24/12479 (0.2%)

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	74	SER	CB-OG	-6.88	1.33	1.42
1	B	308	GLU	CG-CD	6.87	1.62	1.51
1	B	120	ASP	CB-CG	6.42	1.65	1.51
1	A	50	GLU	CD-OE1	6.37	1.32	1.25
1	B	118	LYS	C-O	6.07	1.34	1.23

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	157[A]	ARG	NE-CZ-NH1	9.63	125.11	120.30
1	B	157[B]	ARG	NE-CZ-NH1	9.63	125.11	120.30
1	B	62	ARG	NE-CZ-NH2	-8.90	115.85	120.30
1	B	308	GLU	OE1-CD-OE2	-7.78	113.96	123.30
1	B	157[A]	ARG	NE-CZ-NH2	-7.10	116.75	120.30

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	4560	0	4460	47	0
1	B	4442	0	4371	33	0
2	A	26	0	16	2	0
2	B	26	0	16	4	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	35	0	0	5	0
4	B	60	0	0	6	0
5	A	40	0	57	19	0
5	B	36	0	54	9	0
6	A	520	0	0	28	0
6	B	508	0	0	20	0
All	All	10255	0	8974	102	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 6.

The worst 5 of 102 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)
5:A:616[B]:EDO:H12	6:A:741:HOH:O	1.21	1.30
1:A:114[A]:HIS:HD2	6:A:735:HOH:O	1.19	1.25
4:B:611:SO4:O1	6:B:708:HOH:O	1.57	1.20
4:B:606[B]:SO4:O4	6:B:709:HOH:O	1.58	1.18
4:A:606:SO4:O1	6:A:710:HOH:O	1.56	1.17

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	594/576 (103%)	583 (98%)	9 (2%)	2 (0%)	41	23
1	B	577/576 (100%)	565 (98%)	10 (2%)	2 (0%)	41	23
All	All	1171/1152 (102%)	1148 (98%)	19 (2%)	4 (0%)	41	23

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	186	ASN
1	A	74[A]	SER
1	A	74[B]	SER
1	B	347	SER

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	470/450 (104%)	460 (98%)	10 (2%)	53	33
1	B	458/450 (102%)	455 (99%)	3 (1%)	84	76
All	All	928/900 (103%)	915 (99%)	13 (1%)	76	51

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	337	LYS
1	A	347	SER
1	B	565	ASN
1	B	449	GLU
1	B	504	SER

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 ⓘ

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

5.5   Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6   Ligand geometry ⓘ

Of 42 ligands modelled in this entry, 2 are monoatomic - leaving 40 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	$\#|Z| > 2$
5	EDO	A	612	-	3,3,3	0.53	0	2,2,2	1.15	0
2	TPP	A	601	3	22,27,27	1.47	3 (13%)	29,40,40	1.75	7 (24%)
5	EDO	A	615	-	3,3,3	0.50	0	2,2,2	0.83	0
5	EDO	B	621	-	3,3,3	0.38	0	2,2,2	0.53	0
4	SO4	B	610	-	4,4,4	0.61	0	6,6,6	0.46	0
5	EDO	B	617	-	3,3,3	0.40	0	2,2,2	0.33	0
4	SO4	B	608	-	4,4,4	0.70	0	6,6,6	1.28	1 (16%)
5	EDO	A	610	-	3,3,3	0.49	0	2,2,2	0.58	0
5	EDO	B	620	-	3,3,3	0.73	0	2,2,2	0.26	0
4	SO4	A	607[A]	-	4,4,4	0.38	0	6,6,6	1.09	1 (16%)
5	EDO	B	619	-	3,3,3	0.61	0	2,2,2	0.49	0
4	SO4	A	604	-	4,4,4	0.19	0	6,6,6	0.68	0
2	TPP	B	601	3	22,27,27	1.87	5 (22%)	29,40,40	1.76	6 (20%)
4	SO4	A	605	-	4,4,4	0.55	0	6,6,6	1.01	0
5	EDO	B	615	-	3,3,3	0.56	0	2,2,2	0.59	0
4	SO4	A	607[B]	-	4,4,4	0.35	0	6,6,6	0.49	0
5	EDO	A	616[A]	-	3,3,3	0.29	0	2,2,2	0.81	0
4	SO4	A	603	-	4,4,4	0.51	0	6,6,6	0.65	0
4	SO4	B	611	-	4,4,4	0.39	0	6,6,6	0.41	0
4	SO4	B	606[A]	-	4,4,4	0.40	0	6,6,6	0.42	0
5	EDO	A	616[B]	-	3,3,3	0.37	0	2,2,2	0.44	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
4	SO4	B	606[B]	-	4,4,4	0.32	0	6,6,6	0.50	0
5	EDO	A	609	-	3,3,3	0.35	0	2,2,2	0.18	0
4	SO4	B	607[A]	-	4,4,4	0.46	0	6,6,6	1.22	0
4	SO4	B	603	-	4,4,4	0.25	0	6,6,6	1.29	1 (16%)
4	SO4	B	612	-	4,4,4	0.34	0	6,6,6	0.37	0
5	EDO	B	614	-	3,3,3	0.51	0	2,2,2	0.91	0
5	EDO	A	614	-	3,3,3	0.38	0	2,2,2	1.07	0
5	EDO	B	616	-	3,3,3	0.37	0	2,2,2	0.81	0
5	EDO	A	617	-	3,3,3	0.63	0	2,2,2	0.64	0
5	EDO	B	613	-	3,3,3	0.50	0	2,2,2	0.27	0
5	EDO	B	618	-	3,3,3	0.33	0	2,2,2	0.75	0
5	EDO	A	613	-	3,3,3	0.49	0	2,2,2	0.67	0
5	EDO	A	611	-	3,3,3	0.50	0	2,2,2	0.25	0
4	SO4	B	607[B]	-	4,4,4	0.41	0	6,6,6	0.61	0
4	SO4	B	604	-	4,4,4	0.34	0	6,6,6	0.74	0
4	SO4	B	605	-	4,4,4	0.13	0	6,6,6	0.66	0
4	SO4	A	608	-	4,4,4	0.44	0	6,6,6	0.24	0
4	SO4	A	606	-	4,4,4	0.36	0	6,6,6	0.67	0
4	SO4	B	609	-	4,4,4	0.41	0	6,6,6	1.26	1 (16%)

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
5	EDO	A	612	-	-	1/1/1/1	-
2	TPP	A	601	3	-	0/16/17/17	0/2/2/2
5	EDO	A	615	-	-	1/1/1/1	-
5	EDO	B	621	-	-	1/1/1/1	-
5	EDO	B	617	-	-	1/1/1/1	-
5	EDO	A	610	-	-	0/1/1/1	-
5	EDO	B	620	-	-	0/1/1/1	-
5	EDO	B	619	-	-	0/1/1/1	-
2	TPP	B	601	3	-	2/16/17/17	0/2/2/2
5	EDO	B	615	-	-	0/1/1/1	-
5	EDO	A	616[A]	-	-	1/1/1/1	-
5	EDO	A	616[B]	-	-	1/1/1/1	-
5	EDO	A	609	-	-	0/1/1/1	-
5	EDO	B	616	-	-	0/1/1/1	-
5	EDO	B	614	-	-	0/1/1/1	-
5	EDO	A	614	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	B	618	-	-	1/1/1/1	-
5	EDO	A	617	-	-	0/1/1/1	-
5	EDO	B	613	-	-	1/1/1/1	-
5	EDO	A	613	-	-	1/1/1/1	-
5	EDO	A	611	-	-	1/1/1/1	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	TPP	C5'-C4'	5.33	1.52	1.42
2	A	601	TPP	C5'-C4'	3.81	1.49	1.42
2	B	601	TPP	C2'-N1'	3.66	1.40	1.34
2	A	601	TPP	C2'-N1'	3.06	1.39	1.34
2	B	601	TPP	C4-N3	-3.05	1.37	1.39

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	TPP	C6-C5-C4	5.42	131.78	127.43
2	A	601	TPP	C6-C5-C4	4.98	131.43	127.43
2	B	601	TPP	C5'-C4'-N4'	-3.19	117.66	122.19
2	A	601	TPP	PA-O3A-PB	-3.03	122.42	132.83
2	B	601	TPP	N4'-C4'-N3'	2.76	120.93	117.03

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	TPP	C4-C5-C6-C7
2	B	601	TPP	C5-C6-C7-O7
5	A	612	EDO	O1-C1-C2-O2
5	A	616[A]	EDO	O1-C1-C2-O2
5	A	613	EDO	O1-C1-C2-O2

There are no ring outliers.

18 monomers are involved in 45 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	TPP	2	0
5	A	615	EDO	6	0
5	B	621	EDO	4	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	617	EDO	1	0
5	B	620	EDO	1	0
5	B	619	EDO	1	0
2	B	601	TPP	4	0
5	B	615	EDO	1	0
4	A	607[B]	SO4	3	0
4	B	611	SO4	1	0
4	B	606[A]	SO4	1	0
5	A	616[B]	EDO	3	0
4	B	606[B]	SO4	4	0
5	A	609	EDO	3	0
5	B	616	EDO	1	0
5	A	617	EDO	4	0
5	A	613	EDO	3	0
4	A	606	SO4	2	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 then 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.

Ligand TPP A 601

Bond lengths

Bond angles

Torsions

Rings

Ligand TPP B 601

Bond lengths

Bond angles

Torsions

Rings
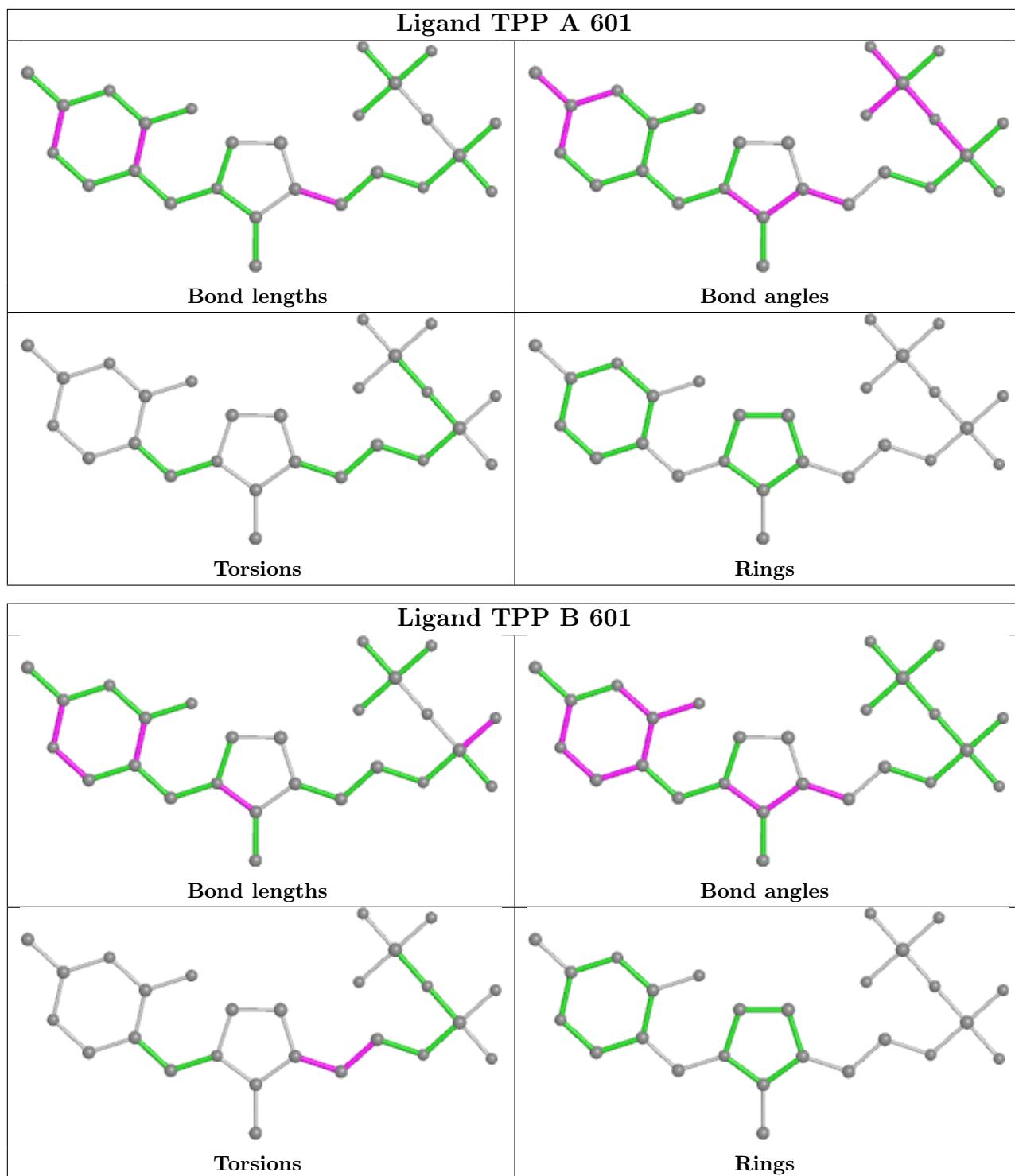
5.7 Other polymers ⓘ

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 ⓘ

6.1   Protein, DNA and RNA chains ⓘ

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	567/576 (98%)	-0.24	18 (3%)	47 50	11, 21, 44, 69	1 (0%)
1	B	561/576 (97%)	-0.33	7 (1%)	79 82	13, 22, 41, 79	2 (0%)
All	All	1128/1152 (97%)	-0.29	25 (2%)	62 65	11, 21, 42, 79	3 (0%)

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	502	TYR	7.4
1	A	356	ALA	4.5
1	A	349	ASN	4.2
1	A	501	GLY	4.0
1	A	348	LEU	4.0

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

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

6.3   Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4   Ligands ⓘ

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
5	EDO	B	620	4/4	0.63	0.24	34,36,39,45	4
5	EDO	B	618	4/4	0.73	0.16	35,37,41,44	4
5	EDO	B	619	4/4	0.77	0.25	32,33,38,40	4
5	EDO	A	609	4/4	0.80	0.20	22,23,23,23	4
5	EDO	A	613	4/4	0.86	0.26	25,32,32,33	4
5	EDO	A	616[A]	4/4	0.86	0.45	32,32,32,34	4
5	EDO	A	616[B]	4/4	0.86	0.45	31,32,32,34	4
5	EDO	A	615	4/4	0.88	0.16	26,27,27,28	4
4	SO4	B	610	5/5	0.89	0.29	36,45,45,50	5
5	EDO	B	616	4/4	0.90	0.17	27,31,33,38	4
4	SO4	B	612	5/5	0.90	0.24	32,37,39,40	5
5	EDO	A	612	4/4	0.90	0.27	31,34,38,39	4
5	EDO	A	617	4/4	0.90	0.14	23,30,33,37	4
5	EDO	B	614	4/4	0.91	0.10	32,33,34,39	0
4	SO4	A	608	5/5	0.93	0.25	35,36,39,46	5
4	SO4	B	604	5/5	0.93	0.12	27,32,37,40	5
5	EDO	B	617	4/4	0.94	0.12	22,26,26,31	4
4	SO4	B	609	5/5	0.94	0.15	29,31,36,39	5
5	EDO	A	610	4/4	0.94	0.09	39,41,43,47	0
5	EDO	A	614	4/4	0.94	0.14	28,42,46,47	0
4	SO4	B	611	5/5	0.95	0.15	26,26,30,32	5
4	SO4	B	608	5/5	0.95	0.09	22,25,29,29	5
4	SO4	B	606[A]	5/5	0.95	0.15	36,43,45,48	5
4	SO4	B	606[B]	5/5	0.95	0.15	28,31,34,34	5
5	EDO	B	615	4/4	0.95	0.09	28,36,36,36	0
5	EDO	B	621	4/4	0.95	0.28	18,19,20,20	4
4	SO4	A	603	5/5	0.96	0.09	22,27,34,39	5
2	TPP	A	601	26/26	0.96	0.08	17,25,33,36	0
2	TPP	B	601	26/26	0.96	0.09	17,23,29,34	26
4	SO4	B	605	5/5	0.96	0.11	46,50,50,56	5
4	SO4	A	607[A]	5/5	0.97	0.10	26,29,31,36	5
4	SO4	A	607[B]	5/5	0.97	0.10	25,26,27,27	5
4	SO4	A	604	5/5	0.97	0.08	41,43,49,50	5
4	SO4	B	607[A]	5/5	0.97	0.17	20,21,26,27	5
4	SO4	B	607[B]	5/5	0.97	0.17	21,30,32,33	5
4	SO4	A	605	5/5	0.97	0.12	25,25,29,34	5
5	EDO	A	611	4/4	0.97	0.10	25,27,27,27	4
5	EDO	B	613	4/4	0.97	0.08	29,31,34,40	0
4	SO4	A	606	5/5	0.98	0.12	32,36,42,45	5
3	MG	B	602	1/1	0.99	0.04	24,24,24,24	0
4	SO4	B	603	5/5	0.99	0.09	36,39,42,44	0
3	MG	A	602	1/1	1.00	0.06	20,20,20,20	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 A 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 B 601:

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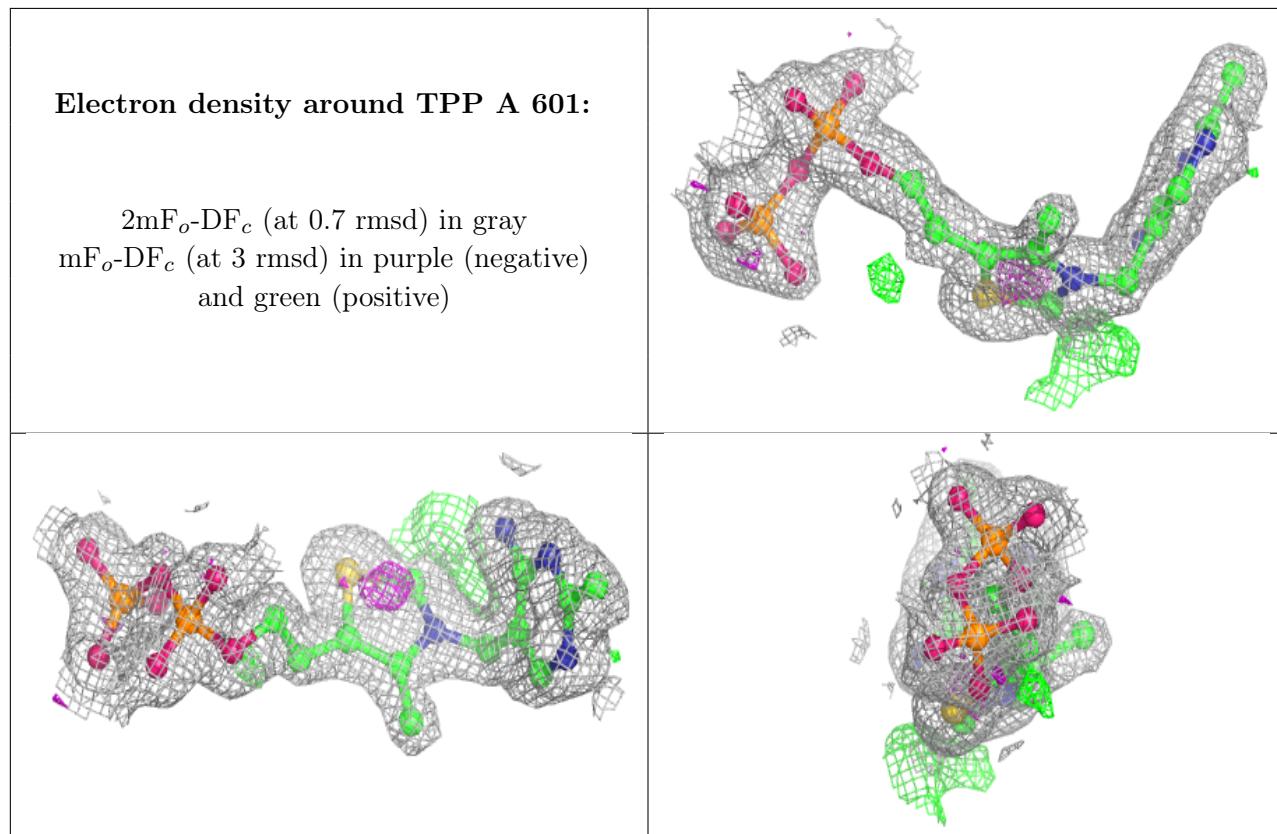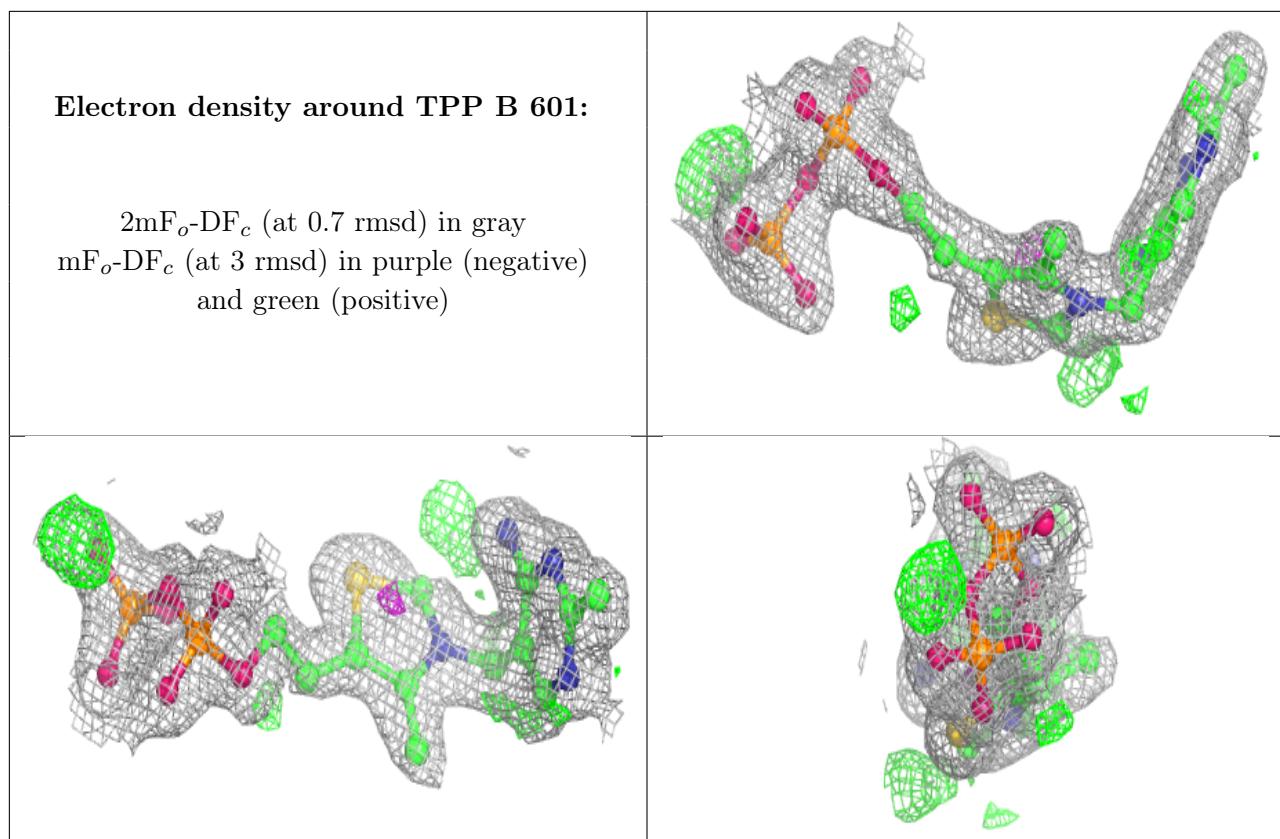
6.5 Other polymers (i)

There are no such residues in this entry.