wwPDB X-ray Structure Validation Summary Report (i)

Jul 22, 2024 – 06:23 PM JST

PDB ID	:	8XW8
Title	:	Crystal structure of Streptococcus pneumoniae pyruvate kinase in complex with oxalate and fructose 1,6-bisphosphate and GDP
Authors	:	Nakashima, R.; Taguchi, A.
Deposited on	:	2024-01-16
Resolution	:	2.00 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 (i) 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 (i)) were used in the production of this report:

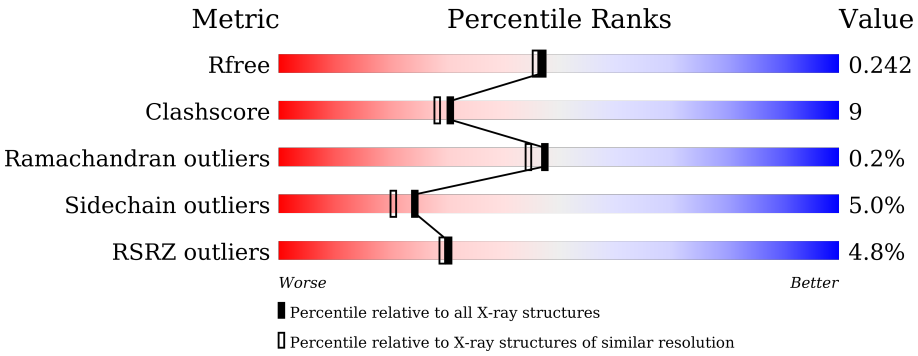
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 <=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	521	3% 83% 12%
1	B	521	% 85% 10%
1	C	521	7% 76% 17%
1	D	521	7% 79% 14%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	GOL	A	608	-	-	X	-

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 17430 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 kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	501	Total	C	N	O	S	0	0	0
			3840	2399	664	760	17			
1	B	501	Total	C	N	O	S	0	0	0
			3840	2399	664	760	17			
1	C	501	Total	C	N	O	S	0	0	0
			3840	2399	664	760	17			
1	D	501	Total	C	N	O	S	0	0	0
			3840	2399	664	760	17			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q8DQ84
A	-18	GLY	-	expression tag	UNP Q8DQ84
A	-17	SER	-	expression tag	UNP Q8DQ84
A	-16	SER	-	expression tag	UNP Q8DQ84
A	-15	HIS	-	expression tag	UNP Q8DQ84
A	-14	HIS	-	expression tag	UNP Q8DQ84
A	-13	HIS	-	expression tag	UNP Q8DQ84
A	-12	HIS	-	expression tag	UNP Q8DQ84
A	-11	HIS	-	expression tag	UNP Q8DQ84
A	-10	HIS	-	expression tag	UNP Q8DQ84
A	-9	SER	-	expression tag	UNP Q8DQ84
A	-8	SER	-	expression tag	UNP Q8DQ84
A	-7	GLY	-	expression tag	UNP Q8DQ84
A	-6	LEU	-	expression tag	UNP Q8DQ84
A	-5	VAL	-	expression tag	UNP Q8DQ84
A	-4	PRO	-	expression tag	UNP Q8DQ84
A	-3	ARG	-	expression tag	UNP Q8DQ84
A	-2	GLY	-	expression tag	UNP Q8DQ84
A	-1	SER	-	expression tag	UNP Q8DQ84
A	0	HIS	-	expression tag	UNP Q8DQ84
B	-19	MET	-	initiating methionine	UNP Q8DQ84

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP Q8DQ84
B	-17	SER	-	expression tag	UNP Q8DQ84
B	-16	SER	-	expression tag	UNP Q8DQ84
B	-15	HIS	-	expression tag	UNP Q8DQ84
B	-14	HIS	-	expression tag	UNP Q8DQ84
B	-13	HIS	-	expression tag	UNP Q8DQ84
B	-12	HIS	-	expression tag	UNP Q8DQ84
B	-11	HIS	-	expression tag	UNP Q8DQ84
B	-10	HIS	-	expression tag	UNP Q8DQ84
B	-9	SER	-	expression tag	UNP Q8DQ84
B	-8	SER	-	expression tag	UNP Q8DQ84
B	-7	GLY	-	expression tag	UNP Q8DQ84
B	-6	LEU	-	expression tag	UNP Q8DQ84
B	-5	VAL	-	expression tag	UNP Q8DQ84
B	-4	PRO	-	expression tag	UNP Q8DQ84
B	-3	ARG	-	expression tag	UNP Q8DQ84
B	-2	GLY	-	expression tag	UNP Q8DQ84
B	-1	SER	-	expression tag	UNP Q8DQ84
B	0	HIS	-	expression tag	UNP Q8DQ84
C	-19	MET	-	initiating methionine	UNP Q8DQ84
C	-18	GLY	-	expression tag	UNP Q8DQ84
C	-17	SER	-	expression tag	UNP Q8DQ84
C	-16	SER	-	expression tag	UNP Q8DQ84
C	-15	HIS	-	expression tag	UNP Q8DQ84
C	-14	HIS	-	expression tag	UNP Q8DQ84
C	-13	HIS	-	expression tag	UNP Q8DQ84
C	-12	HIS	-	expression tag	UNP Q8DQ84
C	-11	HIS	-	expression tag	UNP Q8DQ84
C	-10	HIS	-	expression tag	UNP Q8DQ84
C	-9	SER	-	expression tag	UNP Q8DQ84
C	-8	SER	-	expression tag	UNP Q8DQ84
C	-7	GLY	-	expression tag	UNP Q8DQ84
C	-6	LEU	-	expression tag	UNP Q8DQ84
C	-5	VAL	-	expression tag	UNP Q8DQ84
C	-4	PRO	-	expression tag	UNP Q8DQ84
C	-3	ARG	-	expression tag	UNP Q8DQ84
C	-2	GLY	-	expression tag	UNP Q8DQ84
C	-1	SER	-	expression tag	UNP Q8DQ84
C	0	HIS	-	expression tag	UNP Q8DQ84
D	-19	MET	-	initiating methionine	UNP Q8DQ84
D	-18	GLY	-	expression tag	UNP Q8DQ84
D	-17	SER	-	expression tag	UNP Q8DQ84

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP Q8DQ84
D	-15	HIS	-	expression tag	UNP Q8DQ84
D	-14	HIS	-	expression tag	UNP Q8DQ84
D	-13	HIS	-	expression tag	UNP Q8DQ84
D	-12	HIS	-	expression tag	UNP Q8DQ84
D	-11	HIS	-	expression tag	UNP Q8DQ84
D	-10	HIS	-	expression tag	UNP Q8DQ84
D	-9	SER	-	expression tag	UNP Q8DQ84
D	-8	SER	-	expression tag	UNP Q8DQ84
D	-7	GLY	-	expression tag	UNP Q8DQ84
D	-6	LEU	-	expression tag	UNP Q8DQ84
D	-5	VAL	-	expression tag	UNP Q8DQ84
D	-4	PRO	-	expression tag	UNP Q8DQ84
D	-3	ARG	-	expression tag	UNP Q8DQ84
D	-2	GLY	-	expression tag	UNP Q8DQ84
D	-1	SER	-	expression tag	UNP Q8DQ84
D	0	HIS	-	expression tag	UNP Q8DQ84

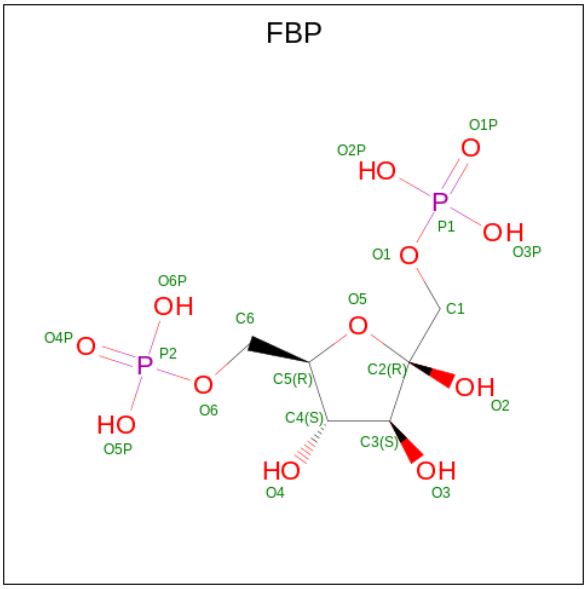
- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Mg 2 2	0	0
2	B	2	Total Mg 2 2	0	0
2	C	2	Total Mg 2 2	0	0
2	D	2	Total Mg 2 2	0	0

- Molecule 3 is POTASSIUM ION (three-letter code: K) (formula: K).

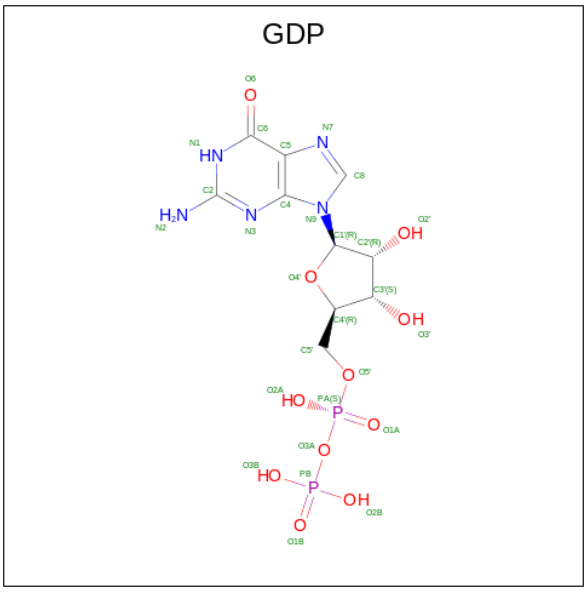
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total K 1 1	0	0
3	B	1	Total K 1 1	0	0
3	C	1	Total K 1 1	0	0
3	D	1	Total K 1 1	0	0

- Molecule 4 is 1,6-di-O-phosphono-beta-D-fructofuranose (three-letter code: FBP) (formula: $C_6H_{14}O_{12}P_2$).



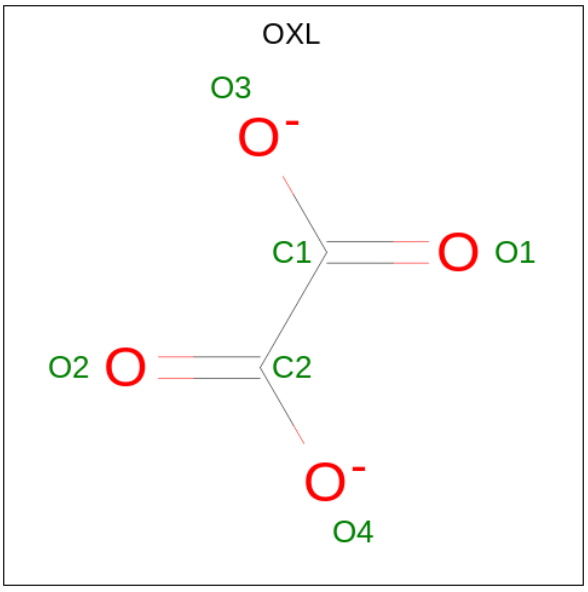
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	P	0	0
			20	6	12	2		
4	B	1	Total	C	O	P	0	0
			20	6	12	2		
4	C	1	Total	C	O	P	0	0
			20	6	12	2		
4	D	1	Total	C	O	P	0	0
			20	6	12	2		

- Molecule 5 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



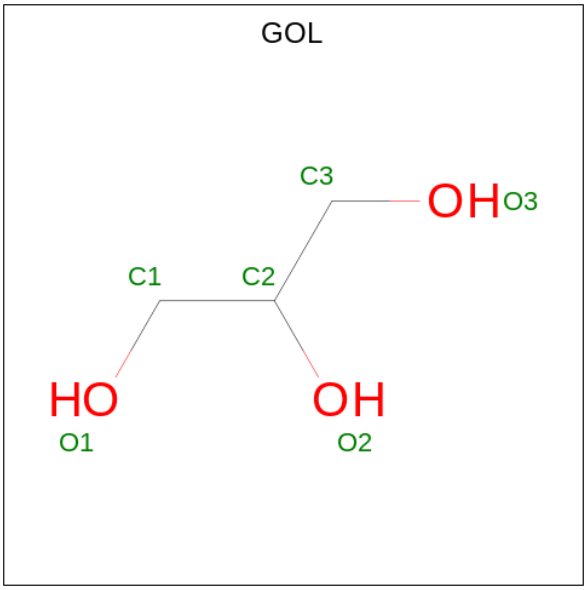
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
5	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
5	C	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
5	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 6 is OXALATE ION (three-letter code: OXL) (formula: C_2O_4).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 6 2 4	0	0
6	B	1	Total C O 6 2 4	0	0
6	C	1	Total C O 6 2 4	0	0
6	D	1	Total C O 6 2 4	0	0

- Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 6 3 3	0	0
7	A	1	Total C O 6 3 3	0	0
7	B	1	Total C O 6 3 3	0	0
7	B	1	Total C O 6 3 3	0	0
7	C	1	Total C O 6 3 3	0	0
7	D	1	Total C O 6 3 3	0	0

- Molecule 8 is water.

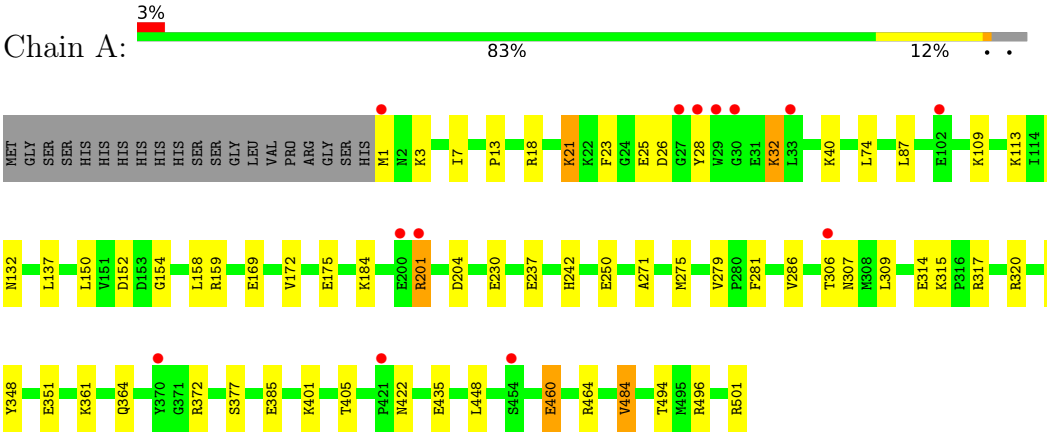
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	524	Total O 524 524	0	0
8	B	540	Total O 540 540	0	0
8	C	379	Total O 379 379	0	0
8	D	363	Total O 363 363	0	0

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.

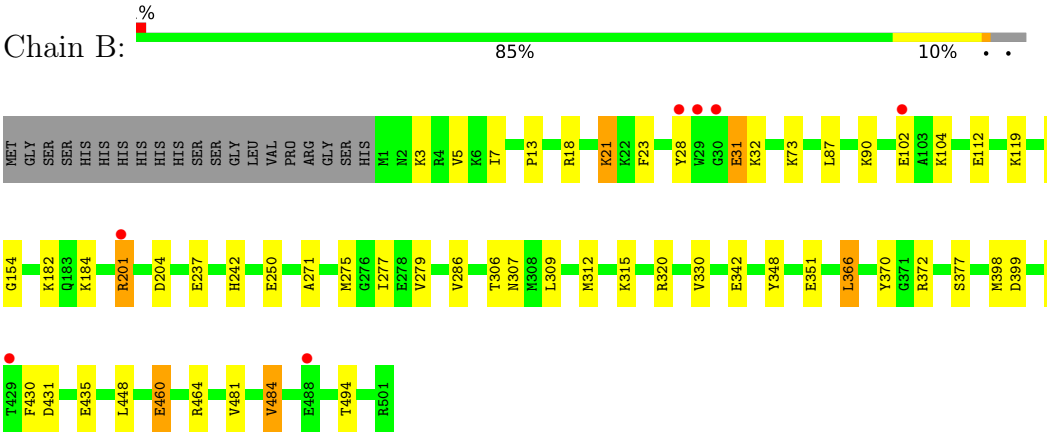
• Molecule 1: Pyruvate kinase

Chain A:



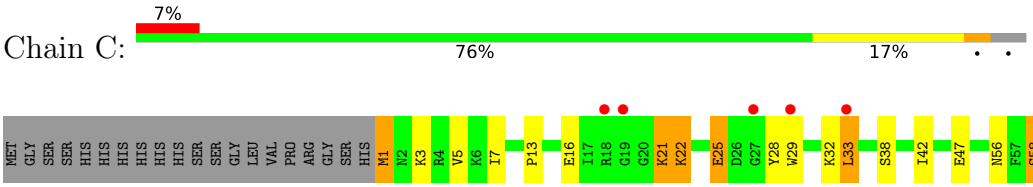
• Molecule 1: Pyruvate kinase

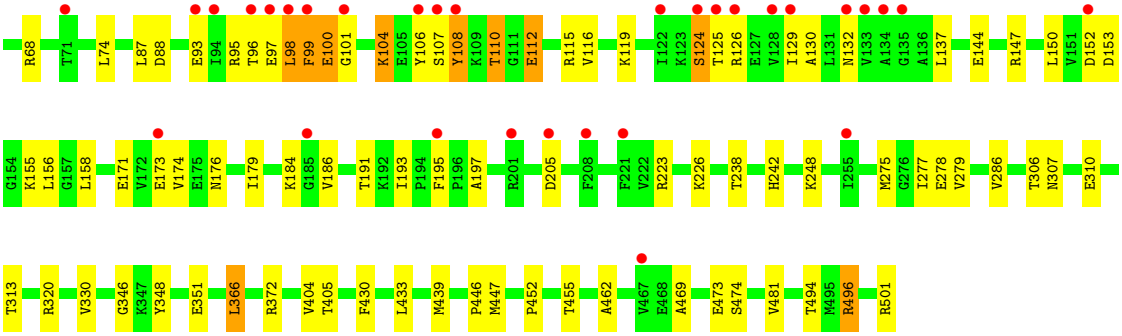
Chain B:



• Molecule 1: Pyruvate kinase

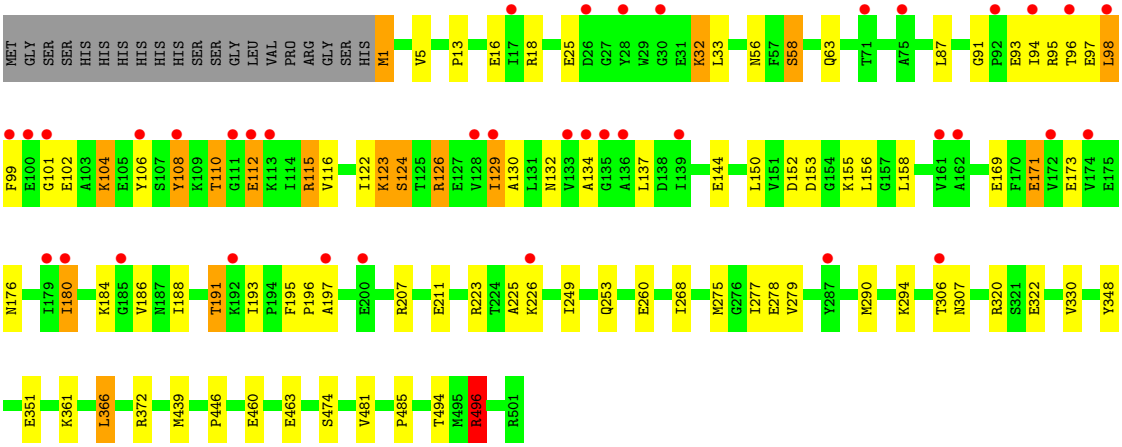
Chain C:





• Molecule 1: Pyruvate kinase

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	123.33Å 256.08Å 88.58Å 90.00° 90.04° 90.00°	Depositor
Resolution (Å)	47.30 – 2.00 47.30 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.9 (47.30-2.00) 97.8 (47.30-2.00)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.76 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.198 , 0.234 0.206 , 0.242	Depositor DCC
R_{free} test set	9061 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	27.3	Xtriage
Anisotropy	0.038	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 34.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.477 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	17430	wwPDB-VP
Average B, all atoms (Å^2)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% of the height of the origin peak. No significant pseudotranslation is detected.*

[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, GOL, FBP, GDP, K, OXL

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	0.96	5/3885 (0.1%)	0.87	1/5238 (0.0%)
1	B	0.97	4/3885 (0.1%)	0.86	0/5238
1	C	0.89	1/3885 (0.0%)	0.95	4/5238 (0.1%)
1	D	0.89	3/3885 (0.1%)	0.95	5/5238 (0.1%)
All	All	0.93	13/15540 (0.1%)	0.91	10/20952 (0.0%)

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	112	GLU	CD-OE1	-6.84	1.18	1.25
1	D	278	GLU	CD-OE1	-6.03	1.19	1.25
1	A	175	GLU	CD-OE2	-5.62	1.19	1.25
1	A	435	GLU	CD-OE2	-5.57	1.19	1.25
1	B	435	GLU	CD-OE1	-5.44	1.19	1.25

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	496	ARG	CG-CD-NE	6.26	124.94	111.80
1	C	110	THR	C-N-CA	5.87	134.62	122.30
1	D	110	THR	C-N-CA	5.73	134.33	122.30
1	D	112	GLU	CB-CA-C	-5.71	98.97	110.40
1	C	112	GLU	CB-CA-C	-5.70	99.00	110.40

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	3840	0	3887	47	0
1	B	3840	0	3887	62	0
1	C	3840	0	3888	110	0
1	D	3840	0	3888	82	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	20	0	10	0	0
4	B	20	0	10	0	0
4	C	20	0	10	0	0
4	D	20	0	10	0	0
5	A	28	0	12	0	0
5	B	28	0	12	0	0
5	C	28	0	12	1	0
5	D	28	0	12	1	0
6	A	6	0	0	1	0
6	B	6	0	0	1	0
6	C	6	0	0	0	0
6	D	6	0	0	0	0
7	A	12	0	16	4	0
7	B	12	0	16	2	0
7	C	6	0	8	0	0
7	D	6	0	8	0	0
8	A	524	0	0	10	0
8	B	540	0	0	10	0
8	C	379	0	0	14	0
8	D	363	0	0	8	0
All	All	17430	0	15686	288	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 9.

The worst 5 of 288 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:D:152:ASP:O	1:D:155:LYS:HG3	1.28	1.27
1:B:204:ASP:HB2	8:B:792:HOH:O	1.36	1.25
1:A:422:ASN:HB2	8:A:1072:HOH:O	1.41	1.18
1:C:97:GLU:HG2	1:C:132:ASN:HB2	1.12	1.11
1:C:106:TYR:HB3	1:C:126:ARG:NH1	1.64	1.11

There are no symmetry-related clashes.

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	499/521 (96%)	494 (99%)	4 (1%)	1 (0%)	47	44
1	B	499/521 (96%)	492 (99%)	6 (1%)	1 (0%)	47	44
1	C	499/521 (96%)	488 (98%)	10 (2%)	1 (0%)	47	44
1	D	499/521 (96%)	488 (98%)	10 (2%)	1 (0%)	47	44
All	All	1996/2084 (96%)	1962 (98%)	30 (2%)	4 (0%)	47	44

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	306	THR
1	B	306	THR
1	C	306	THR
1	D	306	THR

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	411/428 (96%)	392 (95%)	19 (5%)	27	23
1	B	411/428 (96%)	399 (97%)	12 (3%)	42	43
1	C	411/428 (96%)	384 (93%)	27 (7%)	16	12
1	D	411/428 (96%)	387 (94%)	24 (6%)	20	15
All	All	1644/1712 (96%)	1562 (95%)	82 (5%)	24	20

5 of 82 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	501	ARG
1	D	150	LEU
1	D	25	GLU
1	D	115	ARG
1	D	191	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	307	ASN
1	D	253	GLN
1	C	242	HIS
1	D	242	HIS
1	C	132	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 30 ligands modelled in this entry, 12 are monoatomic - leaving 18 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	$\#\|Z\| > 2$
7	GOL	D	607	-	5,5,5	0.17	0	5,5,5	0.42	0
5	GDP	A	605	2	24,30,30	1.07	2 (8%)	30,47,47	1.09	1 (3%)
6	OXL	A	606	2	5,5,5	1.35	1 (20%)	6,6,6	1.15	0
4	FBP	A	604	-	18,20,20	0.72	0	23,32,32	1.09	2 (8%)
4	FBP	B	604	-	18,20,20	0.86	0	23,32,32	1.12	2 (8%)
6	OXL	B	606	2	5,5,5	1.60	1 (20%)	6,6,6	1.01	0
7	GOL	A	607	-	5,5,5	0.22	0	5,5,5	0.27	0
5	GDP	C	605	2	24,30,30	1.22	2 (8%)	30,47,47	1.62	9 (30%)
5	GDP	B	605	2	24,30,30	0.93	0	30,47,47	1.19	1 (3%)
5	GDP	D	605	2	24,30,30	1.13	2 (8%)	30,47,47	1.50	5 (16%)
7	GOL	B	607	-	5,5,5	0.22	0	5,5,5	0.40	0
7	GOL	B	608	-	5,5,5	0.13	0	5,5,5	0.46	0
6	OXL	D	606	2	5,5,5	1.62	2 (40%)	6,6,6	0.97	0
6	OXL	C	606	2	5,5,5	1.46	1 (20%)	6,6,6	1.32	0
4	FBP	C	604	-	18,20,20	0.78	0	23,32,32	0.73	0
7	GOL	C	607	-	5,5,5	0.14	0	5,5,5	0.44	0
4	FBP	D	604	-	18,20,20	0.97	0	23,32,32	0.96	1 (4%)
7	GOL	A	608	-	5,5,5	0.13	0	5,5,5	0.78	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
7	GOL	D	607	-	-	4/4/4/4	-
5	GDP	A	605	2	-	0/12/32/32	0/3/3/3
6	OXL	A	606	2	-	1/4/4/4	-
4	FBP	A	604	-	-	4/13/32/32	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	FBP	B	604	-	-	5/13/32/32	0/1/1/1
6	OXL	B	606	2	-	1/4/4/4	-
7	GOL	A	607	-	-	0/4/4/4	-
5	GDP	C	605	2	-	0/12/32/32	0/3/3/3
5	GDP	B	605	2	-	0/12/32/32	0/3/3/3
5	GDP	D	605	2	-	1/12/32/32	0/3/3/3
7	GOL	B	607	-	-	1/4/4/4	-
7	GOL	B	608	-	-	2/4/4/4	-
6	OXL	D	606	2	-	3/4/4/4	-
6	OXL	C	606	2	-	0/4/4/4	-
4	FBP	C	604	-	-	5/13/32/32	0/1/1/1
7	GOL	C	607	-	-	3/4/4/4	-
4	FBP	D	604	-	-	6/13/32/32	0/1/1/1
7	GOL	A	608	-	-	4/4/4/4	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	605	GDP	O4'-C1'	3.03	1.45	1.41
6	B	606	OXL	O3-C1	-2.79	1.22	1.30
6	C	606	OXL	O4-C2	-2.53	1.23	1.30
6	A	606	OXL	O4-C2	-2.41	1.23	1.30
5	C	605	GDP	C5-C4	2.39	1.49	1.43

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	D	605	GDP	O3A-PB-O1B	-3.22	93.31	111.19
5	C	605	GDP	O5'-PA-O1A	-3.01	97.31	109.07
5	C	605	GDP	O2B-PB-O3A	-2.98	94.62	104.64
4	B	604	FBP	O6P-P2-O5P	2.87	118.60	107.64
5	D	605	GDP	O2B-PB-O3A	2.87	114.25	104.64

There are no chirality outliers.

5 of 40 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	604	FBP	C1-O1-P1-O3P
4	A	604	FBP	O1-C1-C2-C3
4	A	604	FBP	O1-C1-C2-O5

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Mol	Chain	Res	Type	Atoms
4	B	604	FBP	O1-C1-C2-C3
4	B	604	FBP	O1-C1-C2-O5

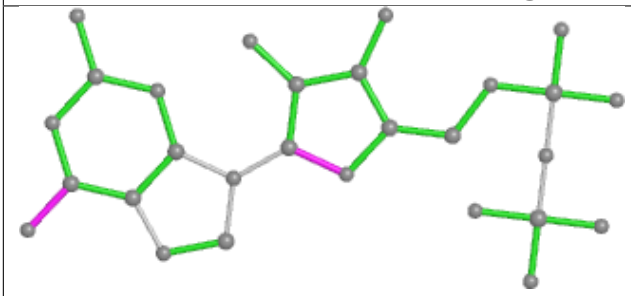
There are no ring outliers.

6 monomers are involved in 10 short contacts:

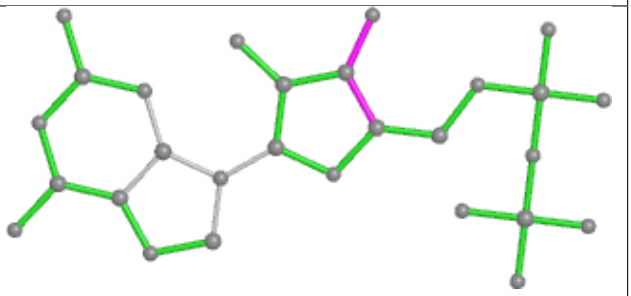
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	606	OXL	1	0
6	B	606	OXL	1	0
5	C	605	GDP	1	0
5	D	605	GDP	1	0
7	B	608	GOL	2	0
7	A	608	GOL	4	0

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 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.

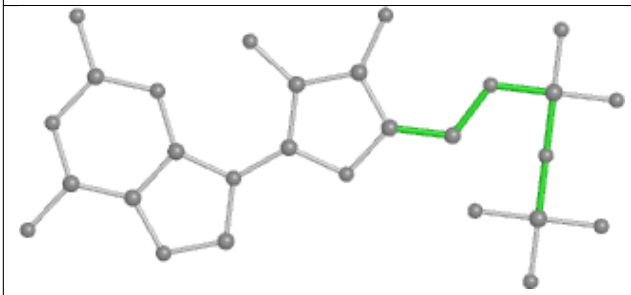
Ligand GDP A 605



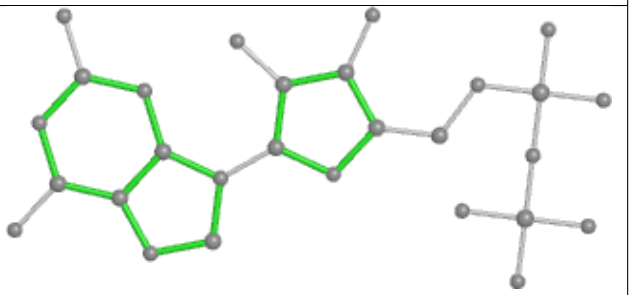
Bond lengths



Bond angles

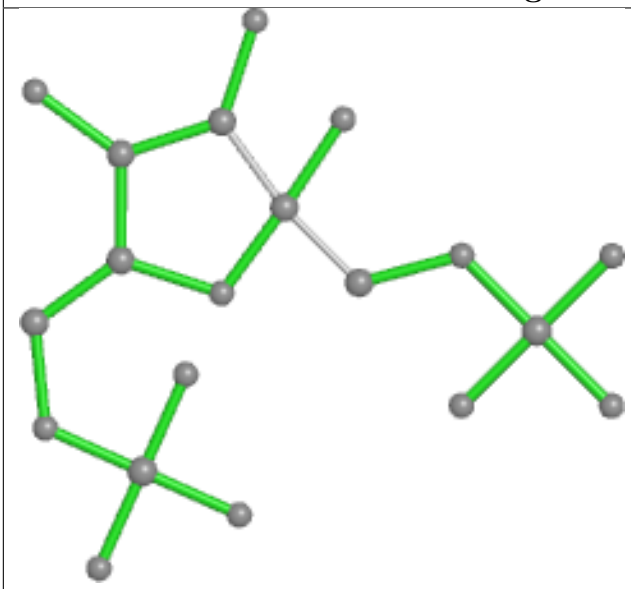


Torsions

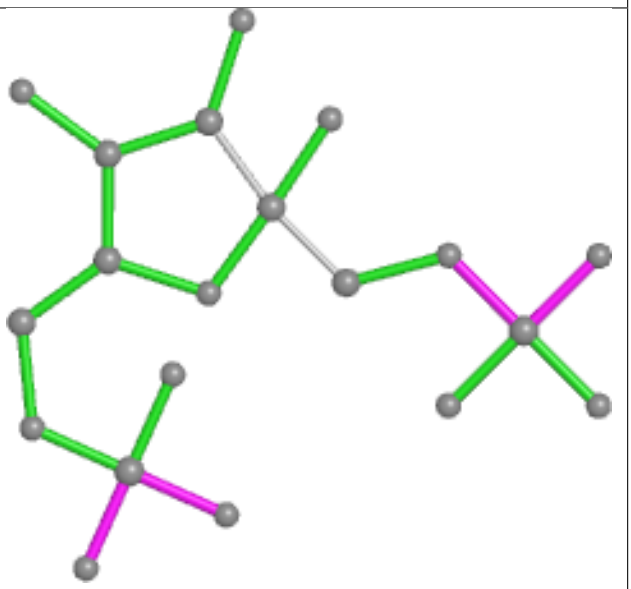


Rings

Ligand FBP A 604



Bond lengths



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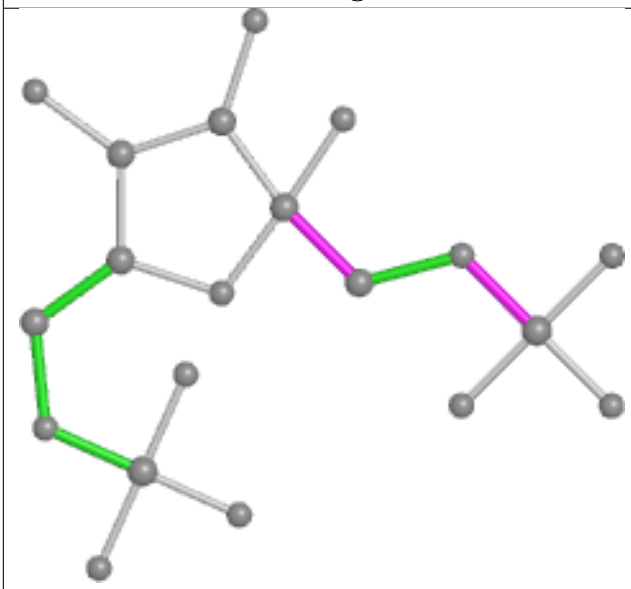

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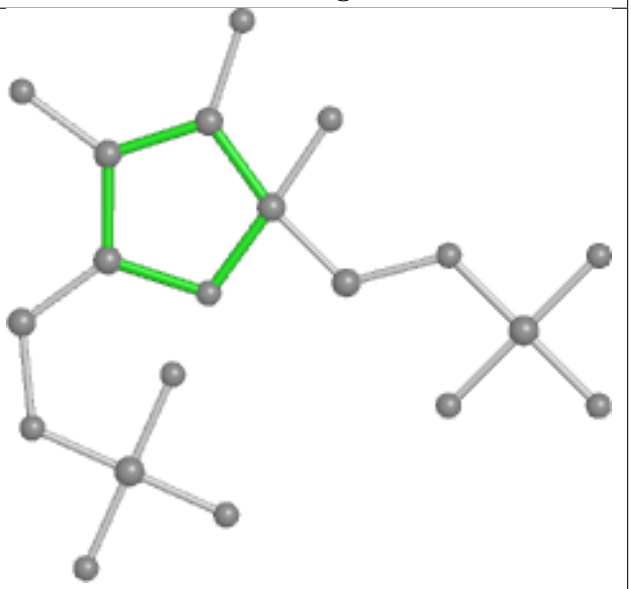
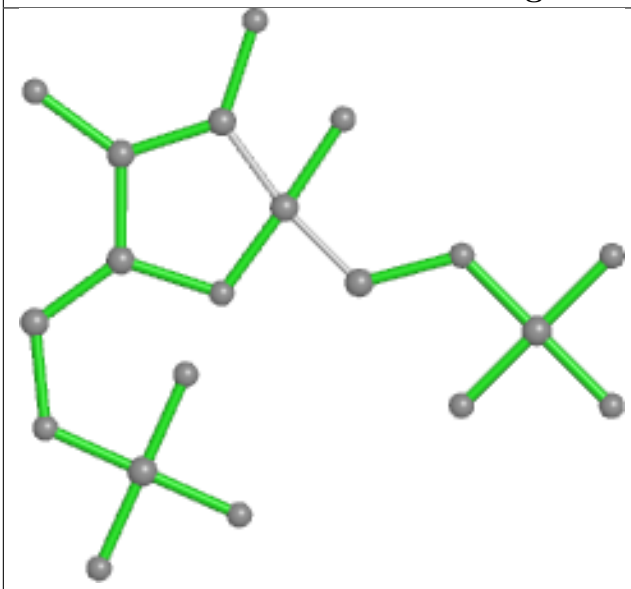
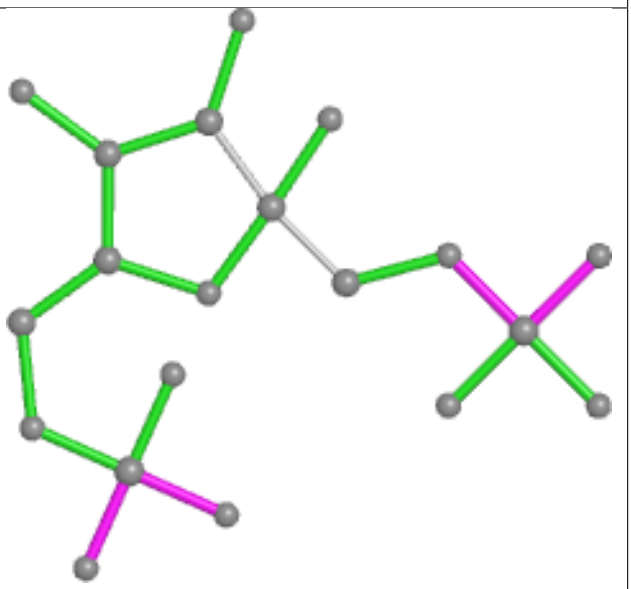


Rings

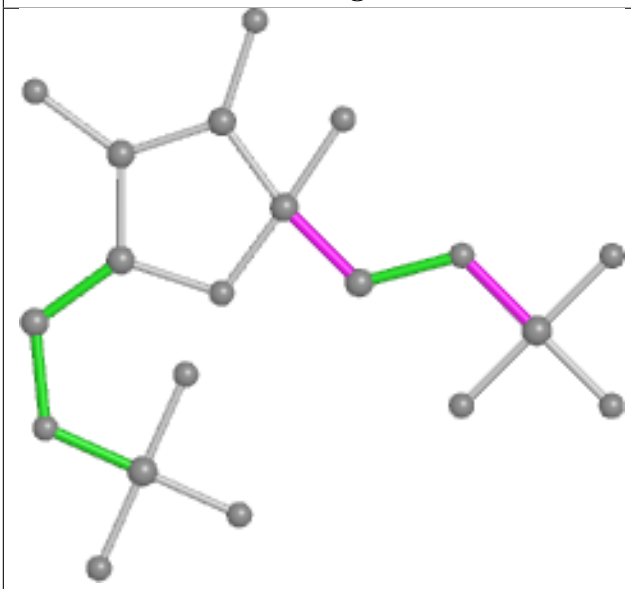
Ligand FBP B 604



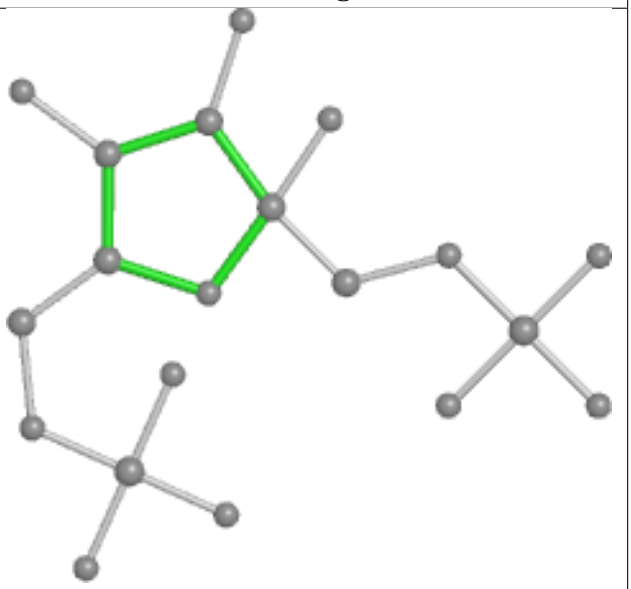
Bond lengths



Bond angles

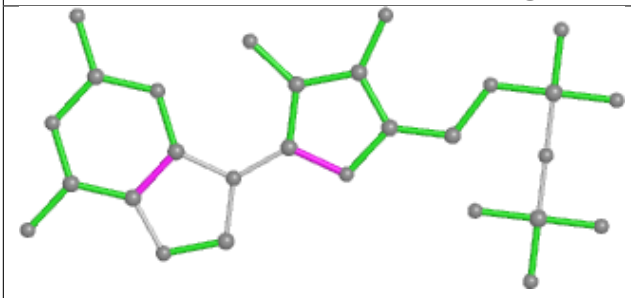


Torsions

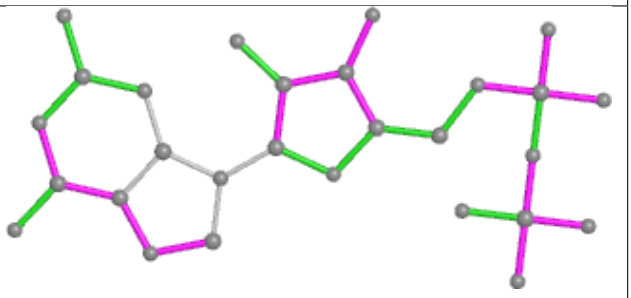


Rings

Ligand GDP C 605



Bond lengths



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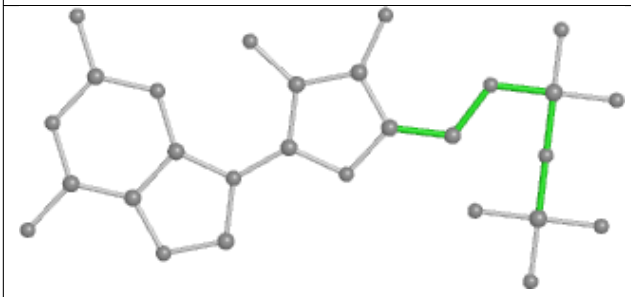
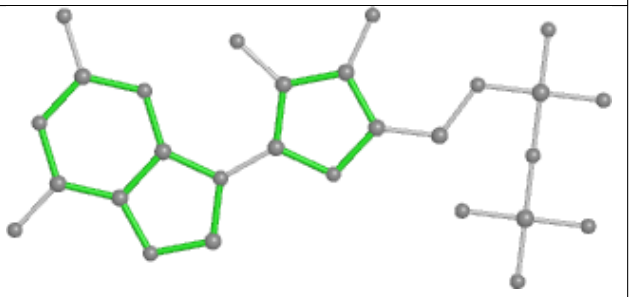
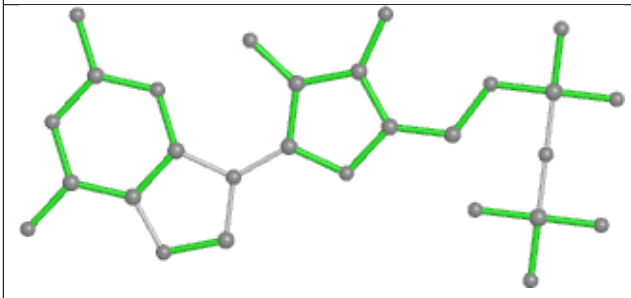


Torsions

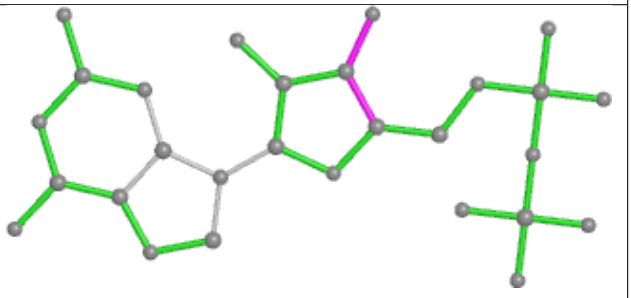


Rings

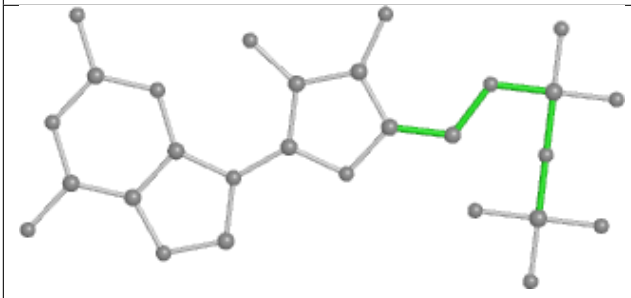
Ligand GDP B 605



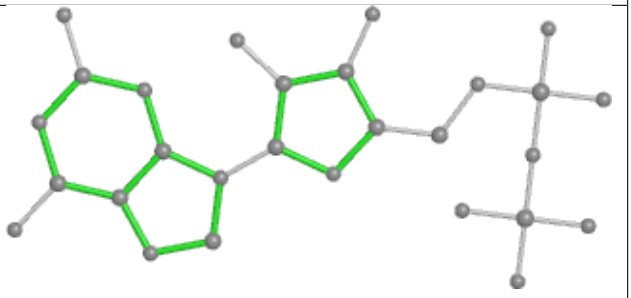
Bond lengths



Bond angles

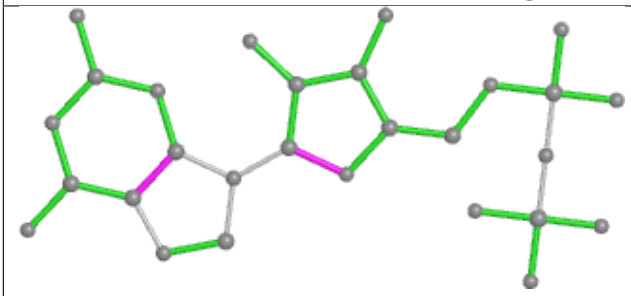


Torsions



Rings

Ligand GDP D 605



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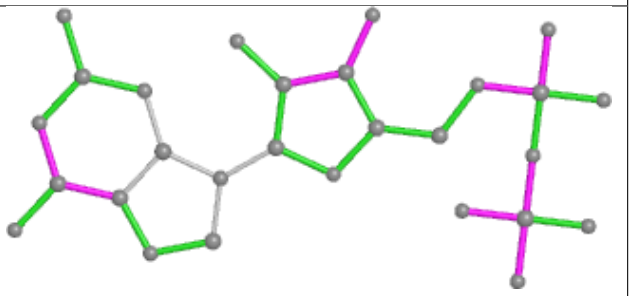

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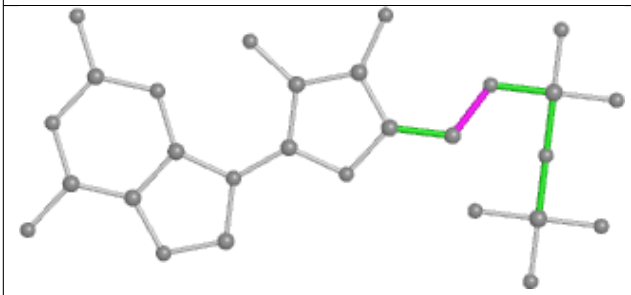

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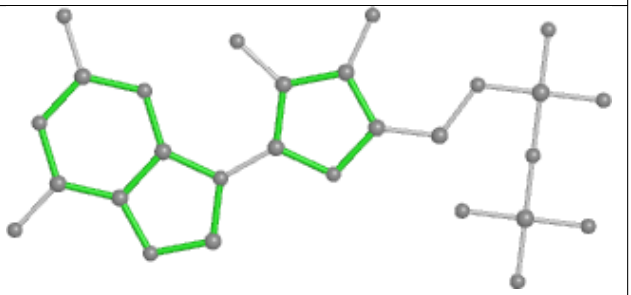
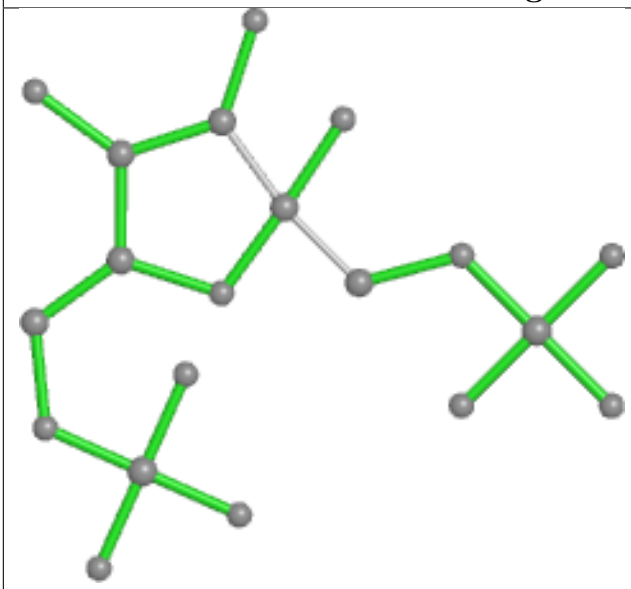
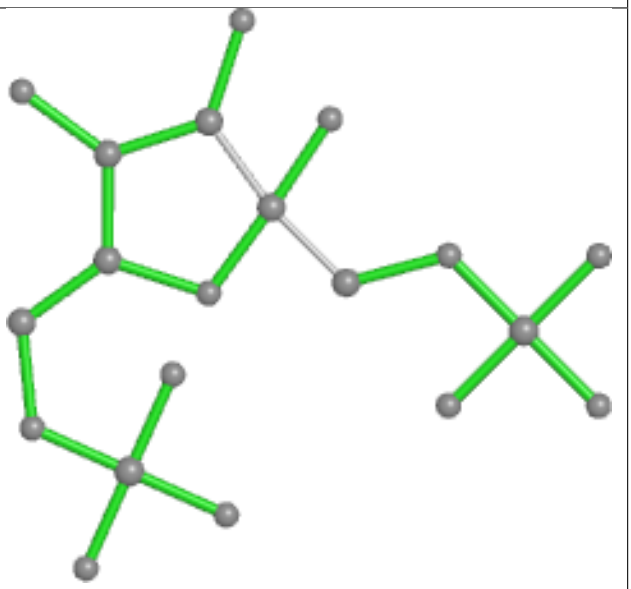


Rings

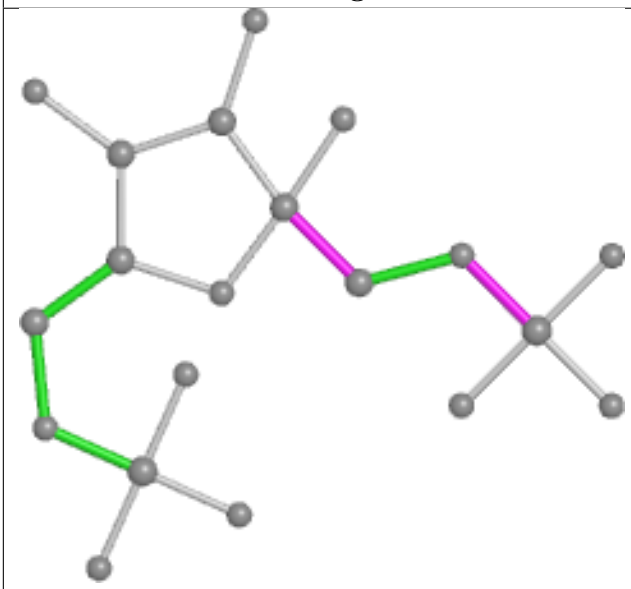
Ligand FBP C 604



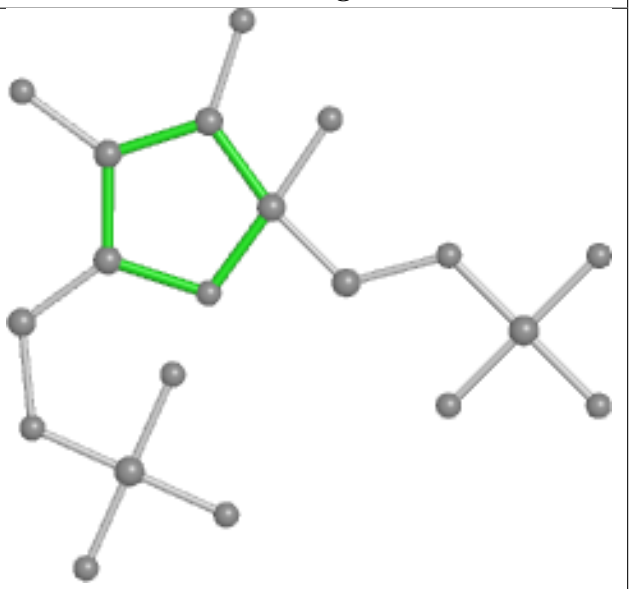
Bond lengths



Bond angles

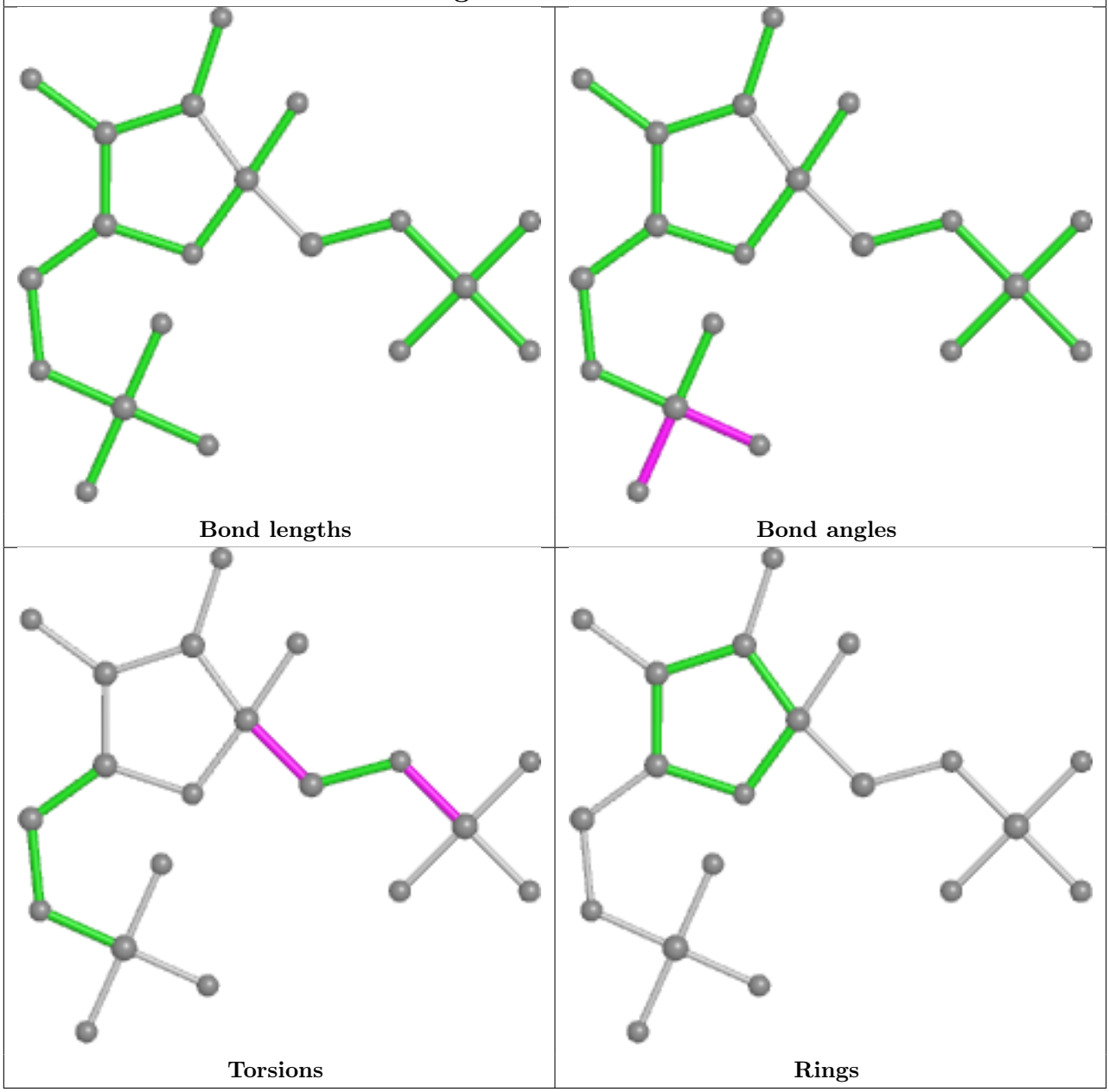


Torsions



Rings

Ligand FBP D 604



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

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, 95^{th} 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	501/521 (96%)	0.17	14 (2%)	53	51	15, 25, 49, 79	0
1	B	501/521 (96%)	0.09	7 (1%)	75	74	15, 24, 49, 79	0
1	C	501/521 (96%)	0.51	37 (7%)	14	13	18, 32, 63, 88	0
1	D	501/521 (96%)	0.53	38 (7%)	13	13	18, 32, 63, 91	0
All	All	2004/2084 (96%)	0.32	96 (4%)	30	29	15, 28, 58, 91	0

The worst 5 of 96 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	134	ALA	7.8
1	C	134	ALA	7.7
1	C	135	GLY	7.2
1	D	135	GLY	6.6
1	C	107	SER	6.5

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

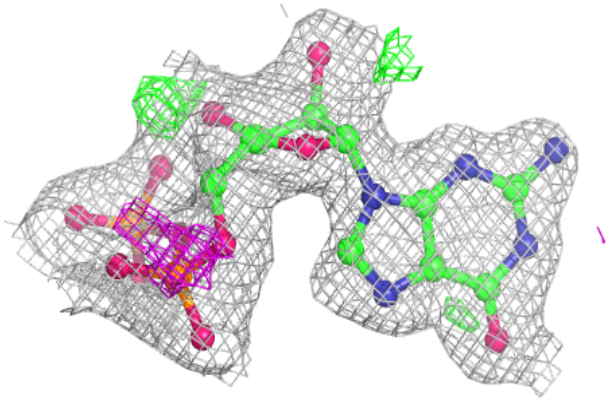
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

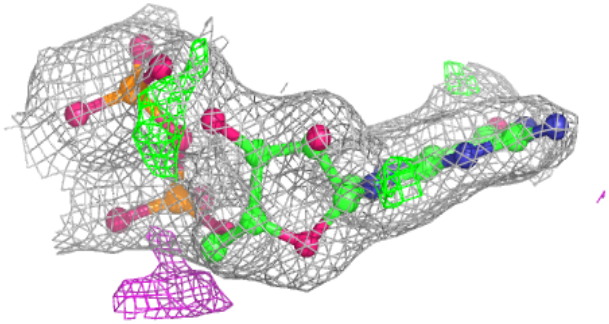
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	MG	D	601	1/1	0.85	0.08	31,31,31,31	0
2	MG	D	602	1/1	0.88	0.10	49,49,49,49	0
7	GOL	B	608	6/6	0.88	0.11	52,53,57,59	0
3	K	D	603	1/1	0.90	0.10	53,53,53,53	0
7	GOL	C	607	6/6	0.90	0.15	29,33,38,44	0
7	GOL	B	607	6/6	0.91	0.15	24,32,42,48	0
6	OXL	D	606	6/6	0.91	0.19	31,35,39,40	0
7	GOL	A	607	6/6	0.91	0.12	26,31,41,50	0
7	GOL	D	607	6/6	0.91	0.15	31,33,38,39	0
6	OXL	C	606	6/6	0.92	0.10	30,34,37,37	0
7	GOL	A	608	6/6	0.93	0.18	29,38,41,47	0
5	GDP	D	605	28/28	0.93	0.13	30,41,54,56	0
2	MG	C	601	1/1	0.93	0.15	46,46,46,46	0
2	MG	B	602	1/1	0.93	0.06	23,23,23,23	0
5	GDP	C	605	28/28	0.93	0.14	30,41,57,58	0
2	MG	A	601	1/1	0.94	0.09	24,24,24,24	0
6	OXL	A	606	6/6	0.94	0.12	23,23,28,30	0
2	MG	C	602	1/1	0.95	0.07	30,30,30,30	0
3	K	C	603	1/1	0.95	0.15	50,50,50,50	0
4	FBP	C	604	20/20	0.96	0.12	22,27,33,33	0
5	GDP	A	605	28/28	0.97	0.10	18,22,29,31	0
6	OXL	B	606	6/6	0.97	0.11	23,24,28,30	0
5	GDP	B	605	28/28	0.97	0.10	18,22,28,32	0
4	FBP	A	604	20/20	0.97	0.11	19,26,30,34	0
4	FBP	D	604	20/20	0.97	0.11	21,26,32,33	0
2	MG	B	601	1/1	0.98	0.06	23,23,23,23	0
4	FBP	B	604	20/20	0.98	0.11	20,26,30,34	0
3	K	B	603	1/1	0.98	0.07	37,37,37,37	0
3	K	A	603	1/1	0.99	0.21	37,37,37,37	0
2	MG	A	602	1/1	0.99	0.06	21,21,21,21	0

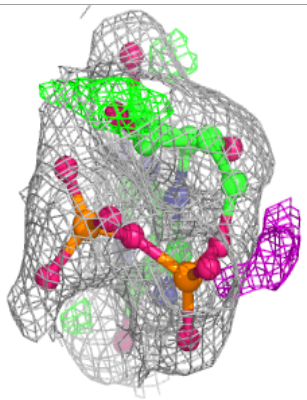
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GDP D 605:

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

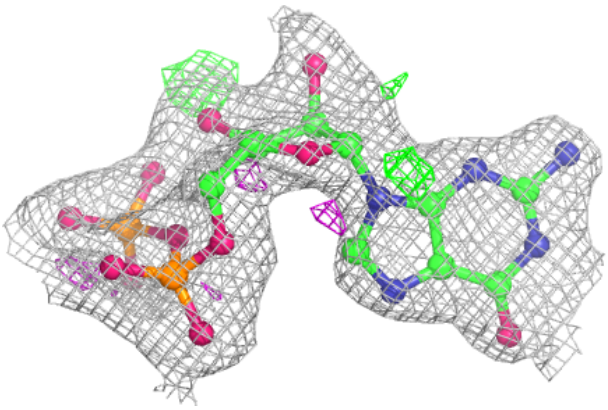


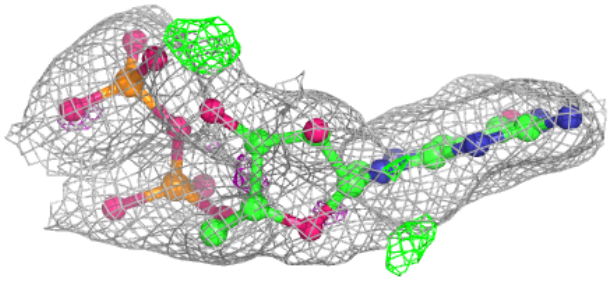


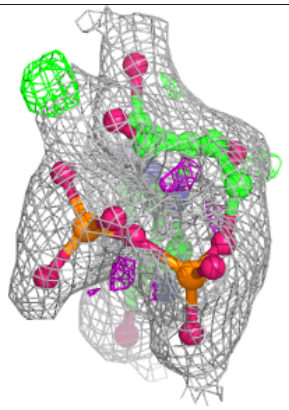


Electron density around GDP C 605:

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

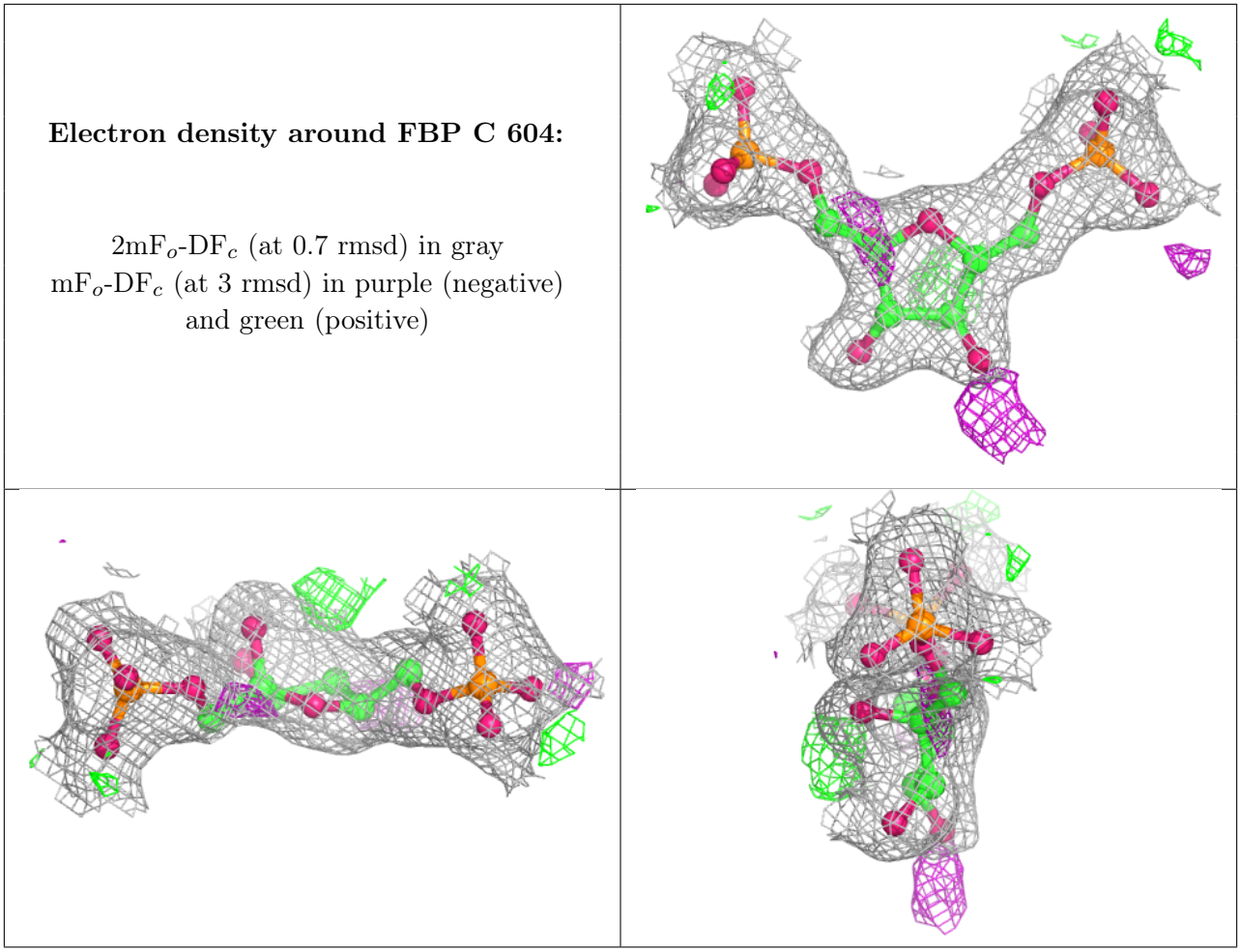






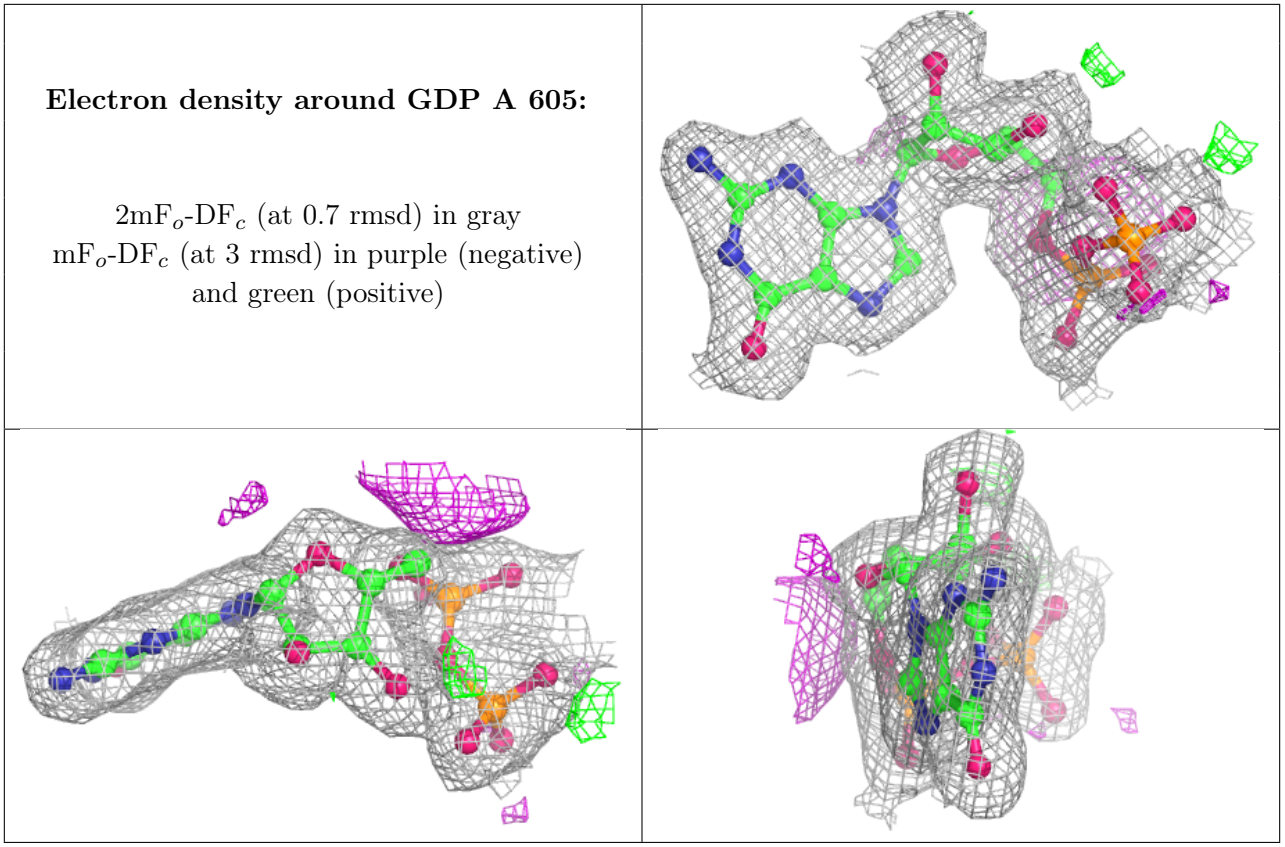
Electron density around FBP C 604:

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



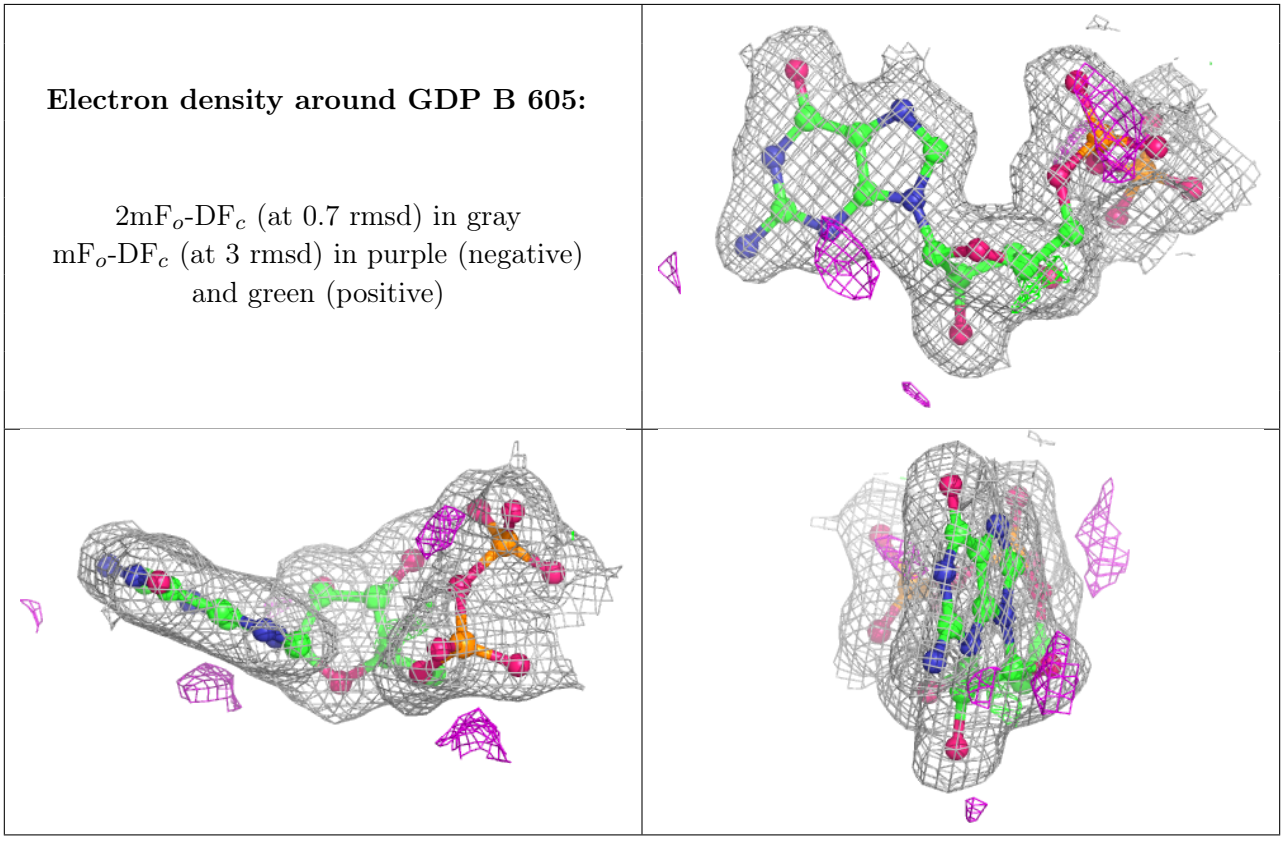
Electron density around GDP A 605:

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



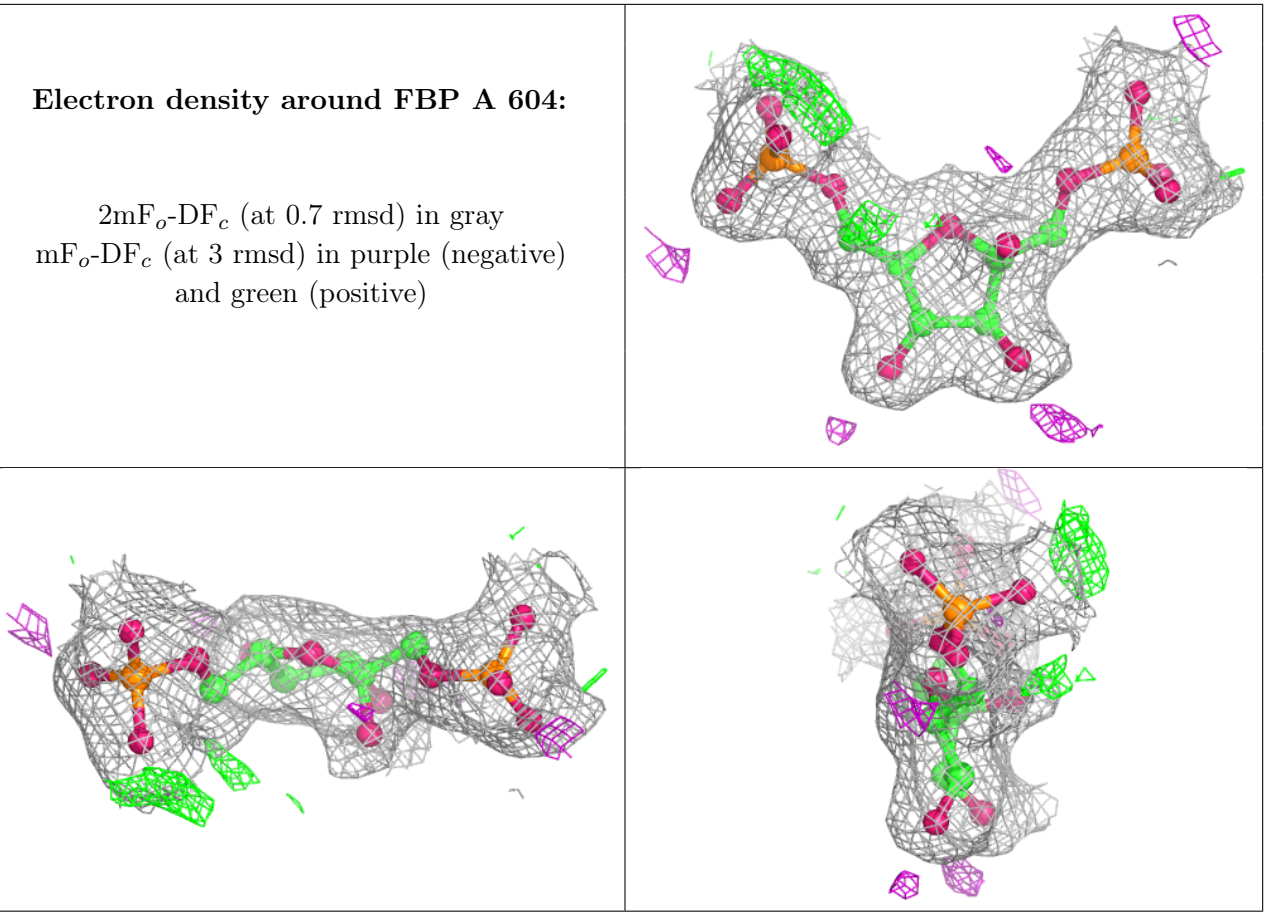
Electron density around GDP B 605:

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



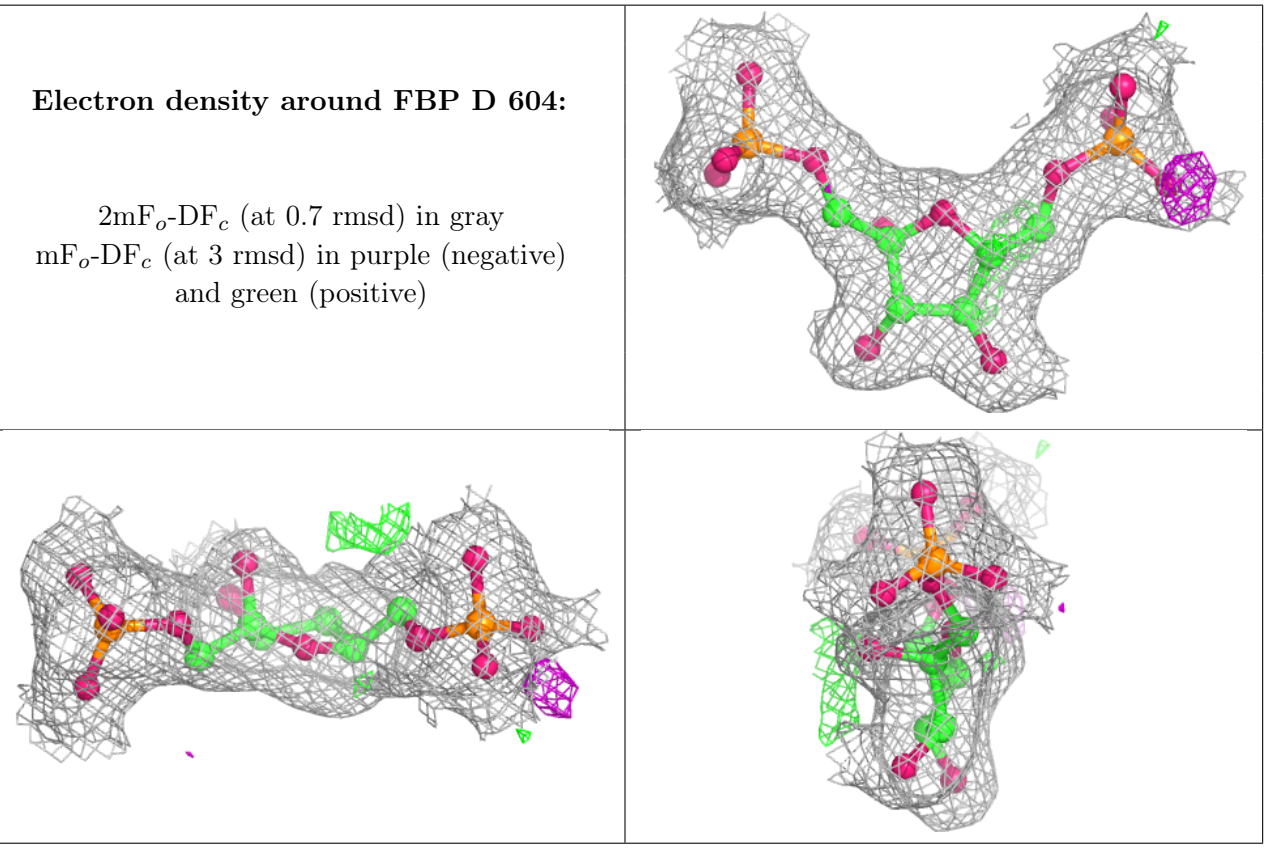
Electron density around FBP A 604:

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



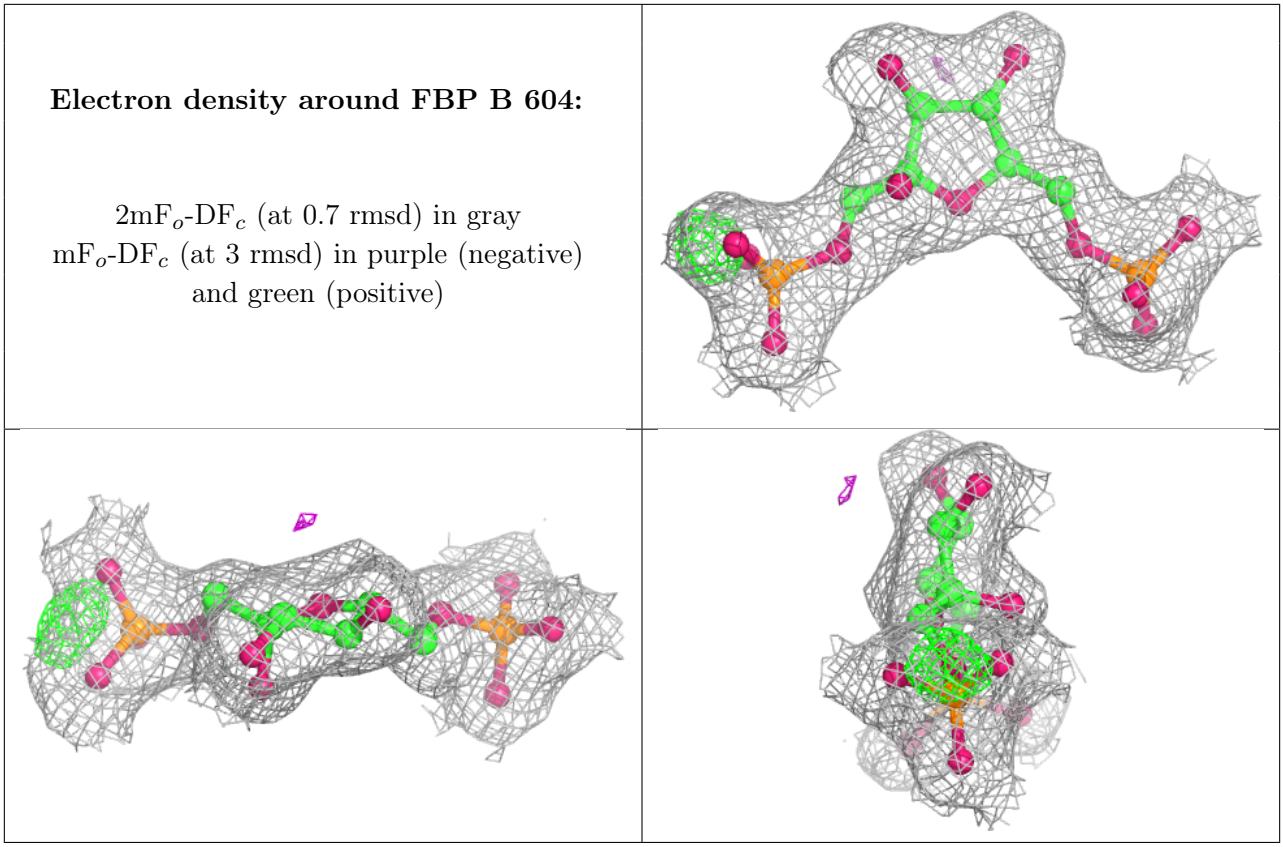
Electron density around FBP D 604:

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



Electron density around FBP B 604:

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



6.5 Other polymers

There are no such residues in this entry.