



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 9, 2020 – 01:01 AM BST

PDB ID : 6NN4
Title : The structure of human liver pyruvate kinase, hLPYK-D499N, in complex with Fru-1,6-BP
Authors : McFarlane, J.S.; Ronnebaum, T.A.; Meneely, K.M.; Fenton, A.W.; Lamb, A.L.
Deposited on : 2019-01-14
Resolution : 2.15 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 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 : 2.13.1
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) : 2.13.1

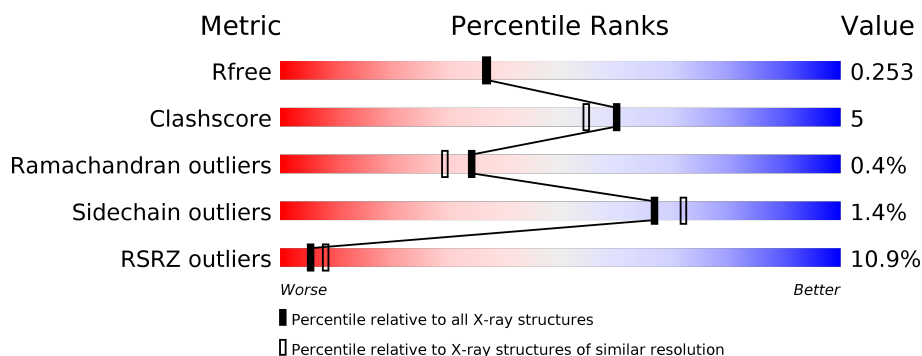
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	1479 (2.16-2.16)
Clashscore	141614	1585 (2.16-2.16)
Ramachandran outliers	138981	1560 (2.16-2.16)
Sidechain outliers	138945	1559 (2.16-2.16)
RSRZ outliers	127900	1456 (2.16-2.16)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	543	<div> <div>9%</div> <div>69%8%23%</div> </div>
1	B	543	<div> <div>8%</div> <div>67%8%24%</div> </div>
1	C	543	<div> <div>8%</div> <div>69%8%23%</div> </div>
1	D	543	<div> <div>8%</div> <div>67%9%24%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 26268 atoms, of which 13032 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.

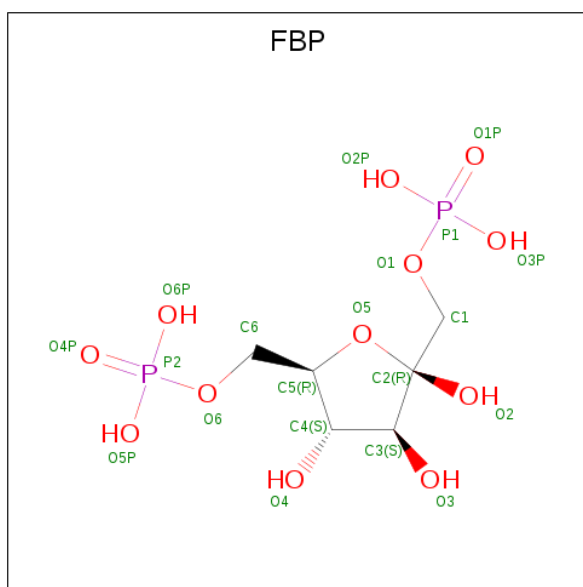
- Molecule 1 is a protein called Pyruvate kinase PKLR.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	418	Total	C	H	N	O	S	0	1	0
			6436	2006	3242	580	590	18			
1	B	414	Total	C	H	N	O	S	0	0	0
			6373	1987	3211	575	582	18			
1	C	419	Total	C	H	N	O	S	0	0	0
			6467	2015	3260	582	592	18			
1	D	414	Total	C	H	N	O	S	0	0	0
			6401	1993	3229	578	583	18			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP P30613
A	2	GLU	-	expression tag	UNP P30613
A	499	ASN	ASP	engineered mutation	UNP P30613
B	1	MET	-	expression tag	UNP P30613
B	2	GLU	-	expression tag	UNP P30613
B	499	ASN	ASP	engineered mutation	UNP P30613
C	1	MET	-	expression tag	UNP P30613
C	2	GLU	-	expression tag	UNP P30613
C	499	ASN	ASP	engineered mutation	UNP P30613
D	1	MET	-	expression tag	UNP P30613
D	2	GLU	-	expression tag	UNP P30613
D	499	ASN	ASP	engineered mutation	UNP P30613

- Molecule 2 is 1,6-di-O-phosphono-beta-D-fructofuranose (three-letter code: FBP) (formula: $C_6H_{14}O_{12}P_2$) (labeled as "Ligand of Interest" by author).



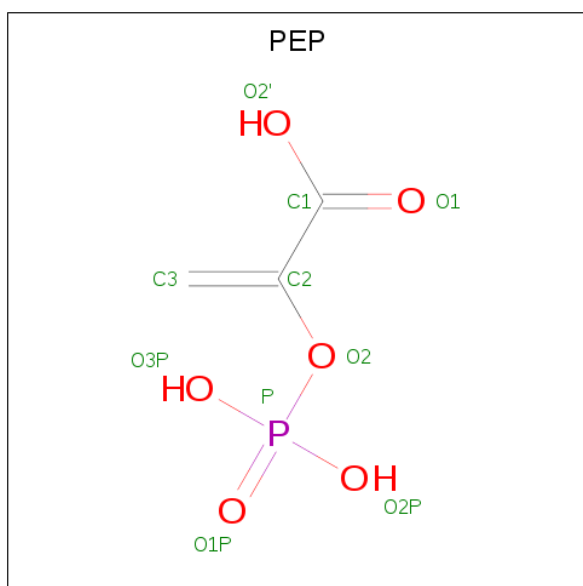
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	O	P	0	0
			30	6	10	12	2		
2	B	1	Total	C	H	O	P	0	0
			30	6	10	12	2		
2	C	1	Total	C	H	O	P	0	0
			30	6	10	12	2		
2	D	1	Total	C	H	O	P	0	0
			30	6	10	12	2		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	A	1	Total	C	H	O	0	0
			10	2	6	2		
3	B	1	Total	C	H	O	0	0
			10	2	6	2		
3	C	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		
3	D	1	Total	C	H	O	0	0
			10	2	6	2		

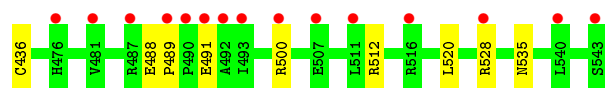
- Molecule 4 is PHOSPHOENOLPYRUVATE (three-letter code: PEP) (formula: $C_3H_5O_6P$).



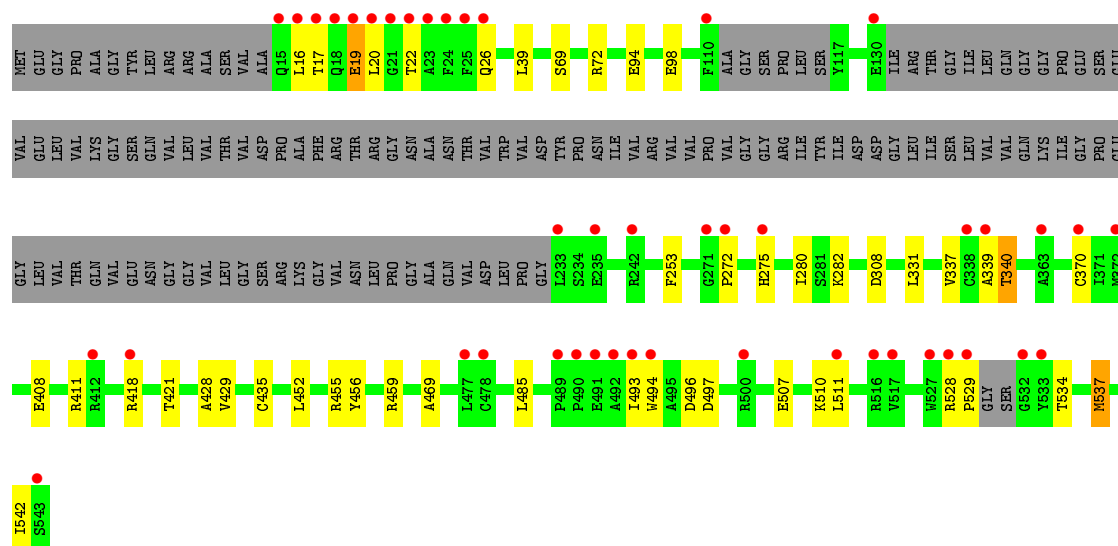
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	H	O	P	0	0
			12	3	2	6	1		
4	B	1	Total	C	H	O	P	0	0
			12	3	2	6	1		
4	C	1	Total	C	H	O	P	0	0
			12	3	2	6	1		
4	D	1	Total	C	H	O	P	0	0
			12	3	2	6	1		

- Molecule 5 is water.

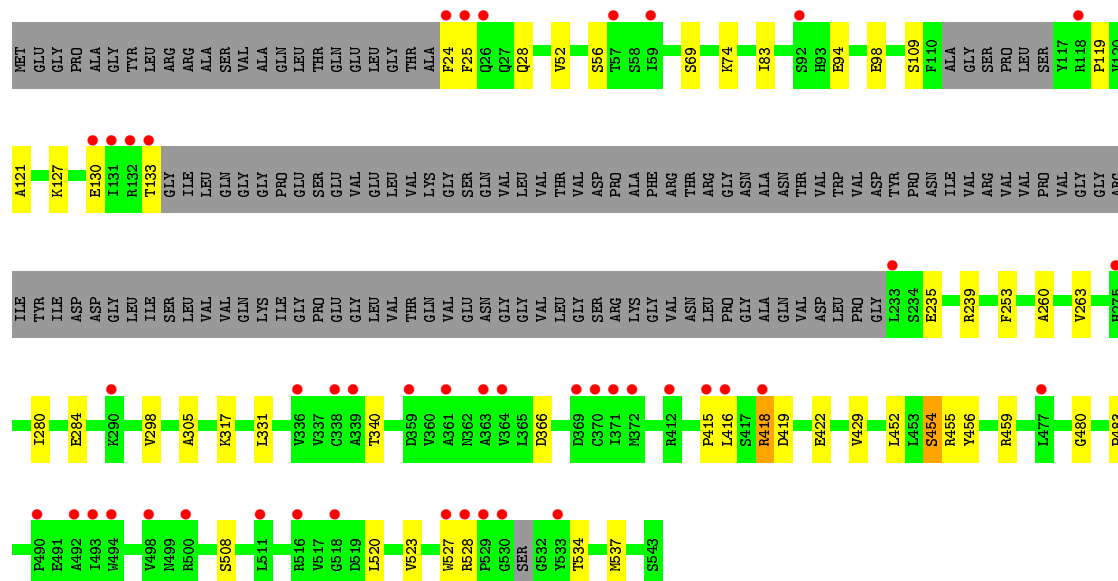
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	111	Total 111	O 111	0	0
5	B	94	Total 94	O 94	0	0
5	C	72	Total 72	O 72	0	0
5	D	76	Total 76	O 76	0	0



• Molecule 1: Pyruvate kinase PKLR



• Molecule 1: Pyruvate kinase PKLR



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	120.57Å 204.66Å 112.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.44 – 2.15 39.44 – 2.15	Depositor EDS
% Data completeness (in resolution range)	98.5 (39.44-2.15) 98.5 (39.44-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.15 (at 2.16Å)	Xtriage
Refinement program	PHENIX (1.13 _2998: ???)	Depositor
R, R_{free}	0.230 , 0.253 0.230 , 0.253	Depositor DCC
R_{free} test set	1982 reflections (1.33%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtriage
Anisotropy	0.910	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 41.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.55$, $\langle L^2 \rangle = 0.39$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	26268	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 51.92 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.2346e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: FBP, PEP, EDO

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	0.57	0/3246	0.67	0/4388
1	B	0.57	0/3214	0.69	0/4344
1	C	0.54	0/3257	0.66	0/4402
1	D	0.56	0/3222	0.70	2/4352 (0.0%)
All	All	0.56	0/12939	0.68	2/17486 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	366	ASP	CB-CG-OD2	-7.13	111.89	118.30
1	D	366	ASP	CB-CG-OD1	6.82	124.44	118.30

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	3194	3242	3239	29	0
1	B	3162	3211	3211	33	0
1	C	3207	3260	3257	32	0
1	D	3172	3229	3225	31	0
2	A	20	10	10	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	20	10	10	0	0
2	C	20	10	10	0	0
2	D	20	10	10	0	0
3	A	8	12	12	1	0
3	B	4	6	6	0	0
3	C	4	6	6	2	0
3	D	12	18	17	1	0
4	A	10	2	2	1	0
4	B	10	2	2	3	0
4	C	10	2	2	3	0
4	D	10	2	2	0	0
5	A	111	0	0	4	0
5	B	94	0	0	2	0
5	C	72	0	0	0	0
5	D	76	0	0	1	0
All	All	13236	13032	13021	118	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 118 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:C:459:ARG:NH2	3:C:602:EDO:O2	1.98	0.95
1:D:260:ALA:O	1:D:263:VAL:HG12	1.76	0.85
1:D:263:VAL:HG11	1:D:298:VAL:CG2	2.16	0.76
1:B:418:ARG:NH2	1:C:20:LEU:HD21	2.04	0.72
1:C:331:LEU:O	1:C:455:ARG:NH2	2.23	0.72

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	413/543 (76%)	400 (97%)	11 (3%)	2 (0%)	29	22
1	B	408/543 (75%)	393 (96%)	13 (3%)	2 (0%)	29	22
1	C	411/543 (76%)	403 (98%)	7 (2%)	1 (0%)	47	46
1	D	406/543 (75%)	395 (97%)	10 (2%)	1 (0%)	47	46
All	All	1638/2172 (75%)	1591 (97%)	41 (2%)	6 (0%)	34	29

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	340	THR
1	A	340	THR
1	A	535	ASN
1	B	340	THR
1	B	535	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	333/433 (77%)	330 (99%)	3 (1%)	78	83
1	B	331/433 (76%)	326 (98%)	5 (2%)	65	69
1	C	336/433 (78%)	332 (99%)	4 (1%)	71	76
1	D	332/433 (77%)	326 (98%)	6 (2%)	59	63
All	All	1332/1732 (77%)	1314 (99%)	18 (1%)	67	72

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	19	GLU
1	C	26	GLN
1	D	418	ARG
1	B	512	ARG
1	B	528	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	403	HIS

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](#)

15 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	FBP	B	601	-	18,20,20	3.85	7 (38%)	23,32,32	0.89	0
2	FBP	D	601	-	18,20,20	3.93	7 (38%)	23,32,32	0.84	0
2	FBP	A	601	-	18,20,20	3.78	5 (27%)	23,32,32	0.80	0
3	EDO	D	603	-	3,3,3	0.89	0	2,2,2	1.19	0
4	PEP	A	604	-	6,9,9	1.25	1 (16%)	8,13,13	1.11	1 (12%)
4	PEP	C	603	-	6,9,9	1.51	1 (16%)	8,13,13	1.45	1 (12%)
3	EDO	B	602	-	3,3,3	0.48	0	2,2,2	0.31	0
3	EDO	D	602	-	3,3,3	0.51	0	2,2,2	0.31	0
3	EDO	A	602	-	3,3,3	0.46	0	2,2,2	0.57	0
3	EDO	C	602	-	3,3,3	0.47	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	PEP	B	603	-	6,9,9	1.40	1 (16%)	8,13,13	1.36	2 (25%)
3	EDO	D	604	-	3,3,3	0.46	0	2,2,2	0.35	0
3	EDO	A	603	-	3,3,3	0.47	0	2,2,2	0.71	0
4	PEP	D	605	-	6,9,9	1.23	1 (16%)	8,13,13	1.00	0
2	FBP	C	601	-	18,20,20	3.80	6 (33%)	23,32,32	0.81	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FBP	B	601	-	-	6/13/32/32	0/1/1/1
2	FBP	D	601	-	-	8/13/32/32	0/1/1/1
2	FBP	A	601	-	-	2/13/32/32	0/1/1/1
3	EDO	D	603	-	-	0/1/1/1	-
4	PEP	A	604	-	-	0/5/9/9	-
4	PEP	C	603	-	-	0/5/9/9	-
3	EDO	B	602	-	-	1/1/1/1	-
3	EDO	D	602	-	-	1/1/1/1	-
3	EDO	A	602	-	-	1/1/1/1	-
3	EDO	C	602	-	-	1/1/1/1	-
4	PEP	B	603	-	-	2/5/9/9	-
3	EDO	D	604	-	-	1/1/1/1	-
3	EDO	A	603	-	-	0/1/1/1	-
4	PEP	D	605	-	-	0/5/9/9	-
2	FBP	C	601	-	-	5/13/32/32	0/1/1/1

The worst 5 of 29 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	FBP	O5-C2	-10.23	1.27	1.43
2	A	601	FBP	O5-C2	-9.84	1.28	1.43
2	B	601	FBP	O5-C2	-9.83	1.28	1.43
2	C	601	FBP	O5-C2	-9.56	1.28	1.43
2	D	601	FBP	O5-C5	8.58	1.62	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	603	PEP	O2-C2-C3	-3.52	118.01	124.79
4	B	603	PEP	O2-C2-C3	-2.48	120.02	124.79
4	A	604	PEP	O2P-P-O2	2.20	111.95	105.25
4	B	603	PEP	O3P-P-O2P	2.01	115.33	107.64

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	FBP	C1-O1-P1-O3P
2	B	601	FBP	O1-C1-C2-O2
2	B	601	FBP	O1-C1-C2-O5
2	D	601	FBP	C1-O1-P1-O1P
2	D	601	FBP	C1-O1-P1-O2P

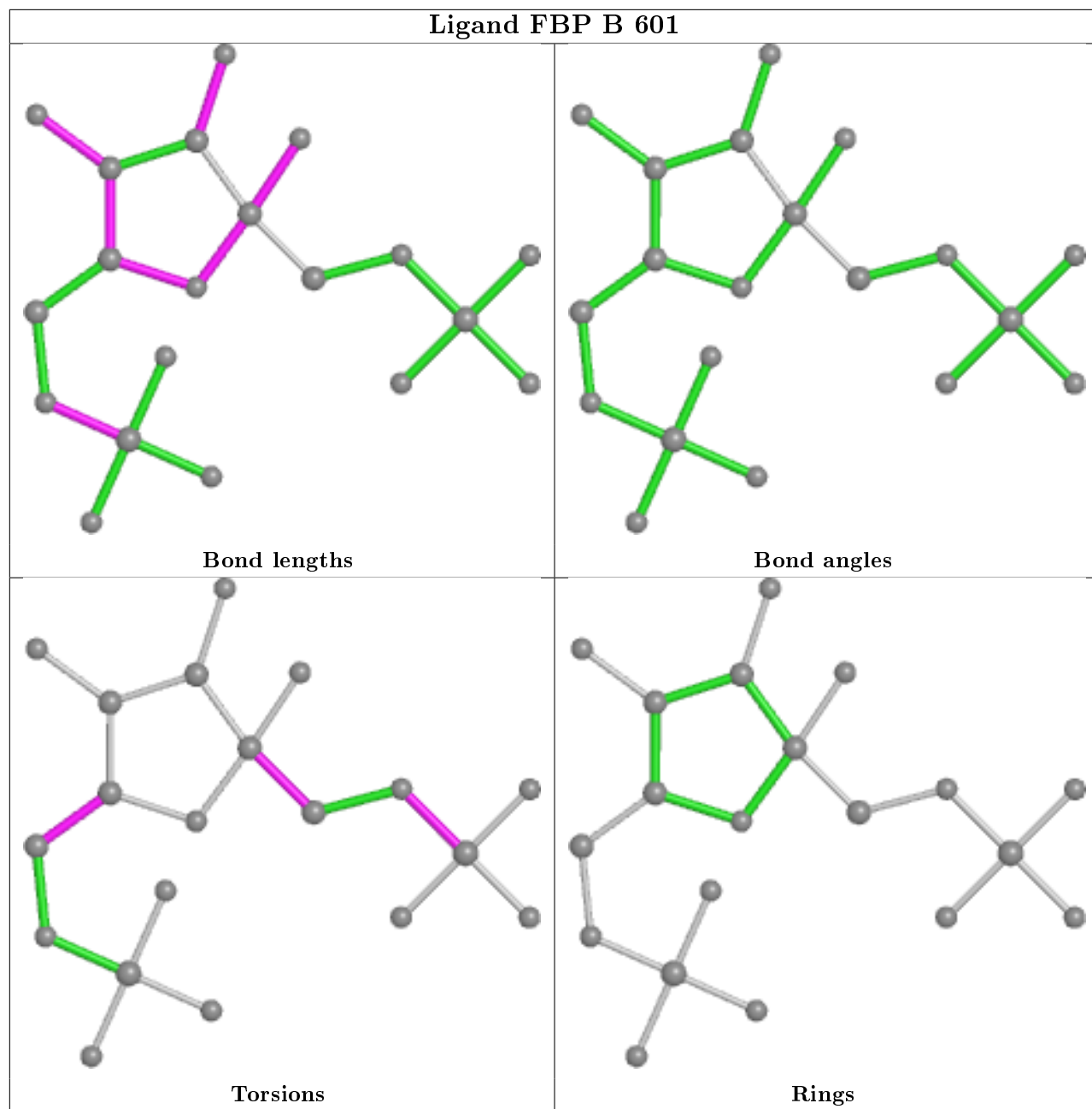
There are no ring outliers.

7 monomers are involved in 12 short contacts:

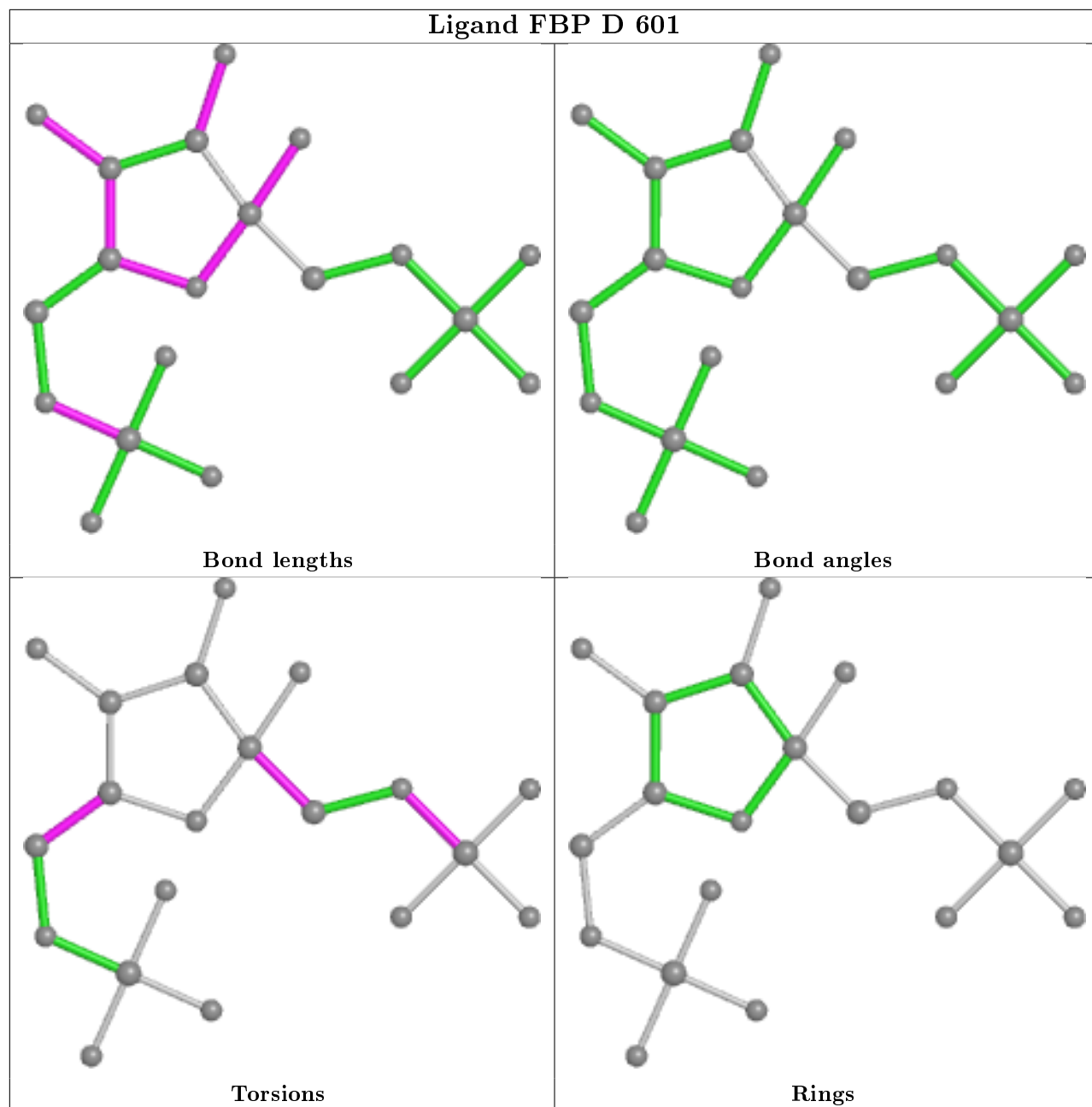
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	FBP	1	0
3	D	603	EDO	1	0
4	A	604	PEP	1	0
4	C	603	PEP	3	0
3	A	602	EDO	1	0
3	C	602	EDO	2	0
4	B	603	PEP	3	0

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.

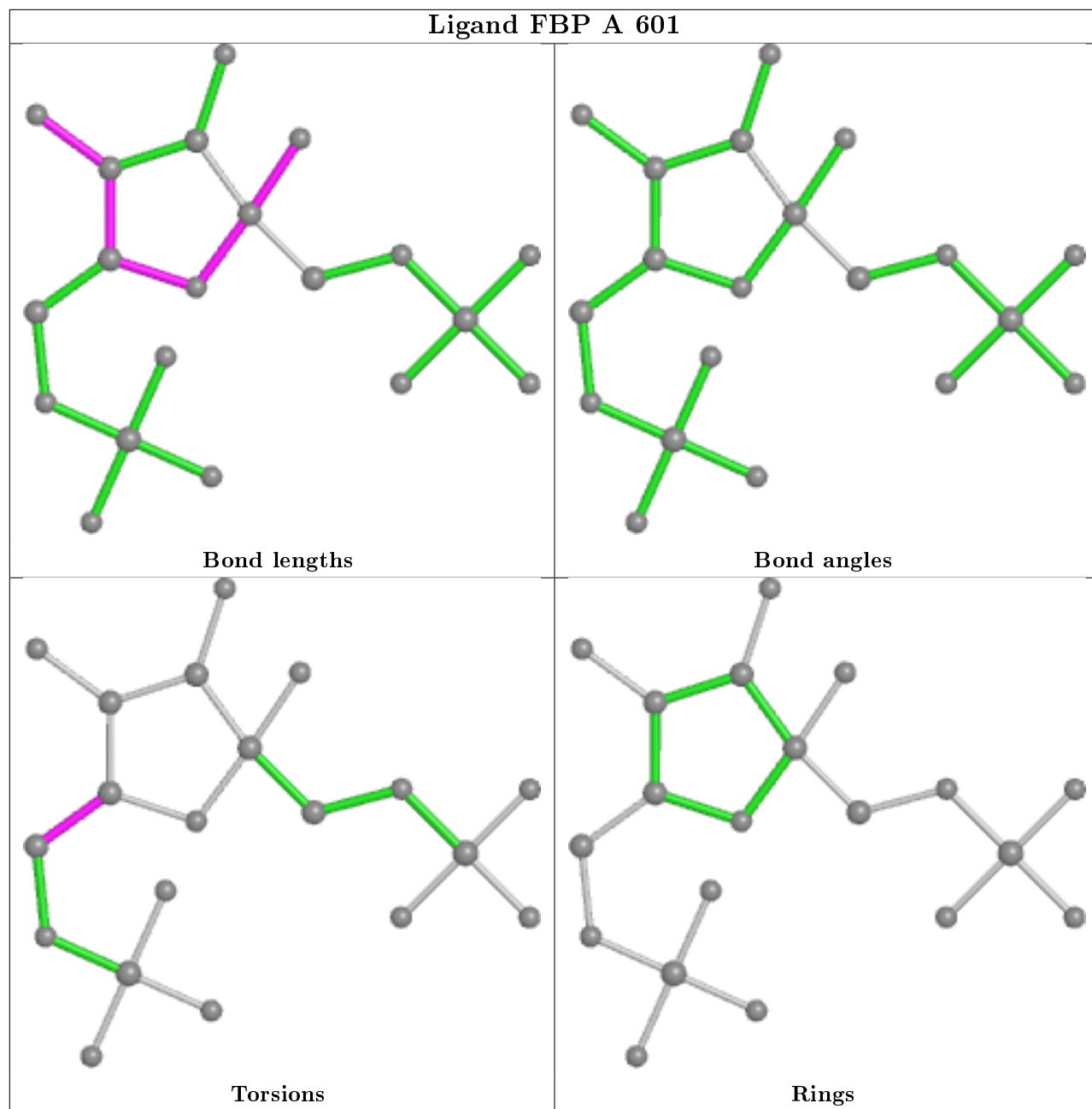
Ligand FBP B 601

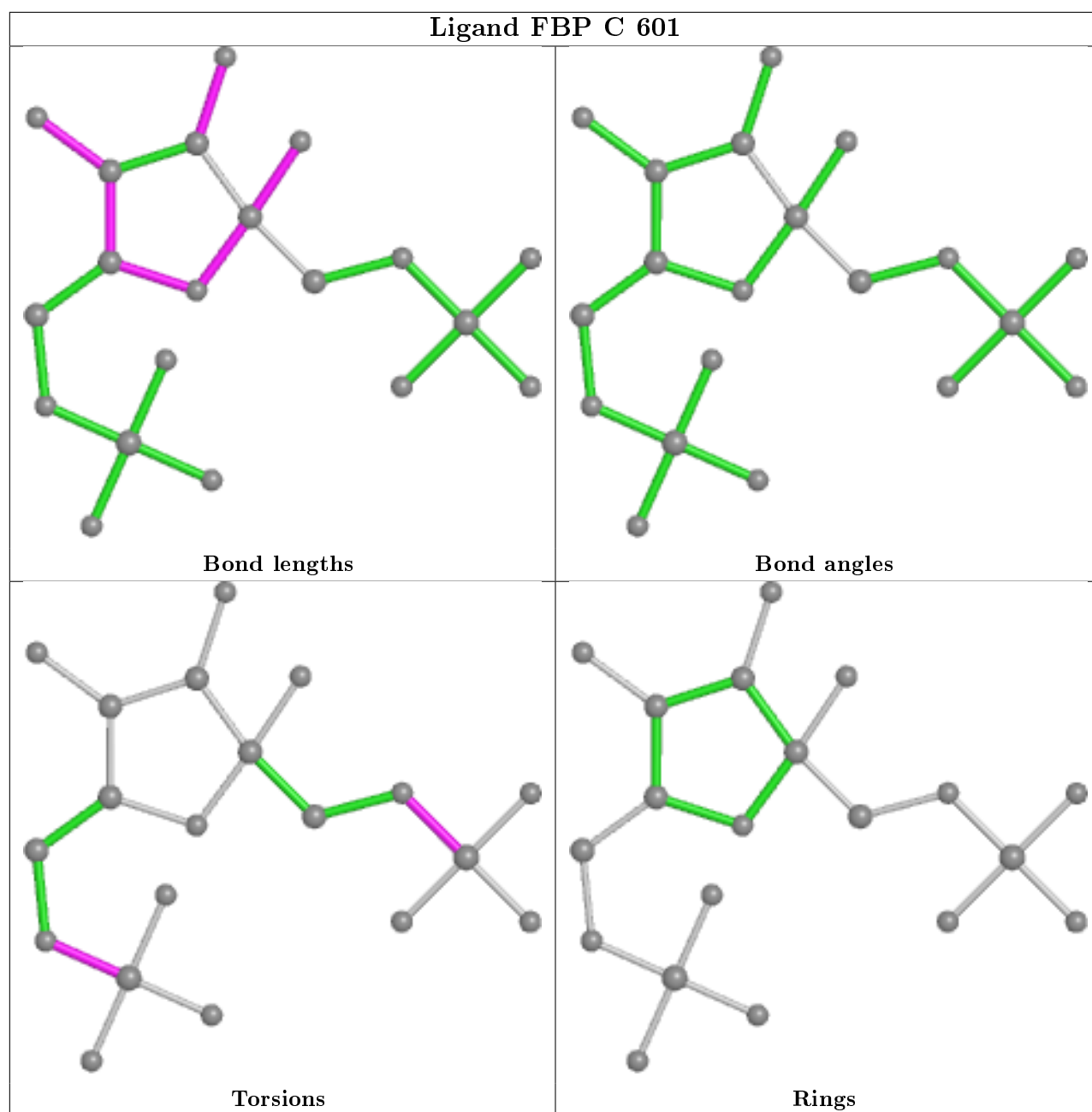


Ligand FBP D 601



Ligand FBP A 601





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	418/543 (76%)	0.67	49 (11%) 4 6	28, 40, 69, 87	0
1	B	414/543 (76%)	0.62	44 (10%) 6 9	28, 41, 73, 109	0
1	C	419/543 (77%)	0.66	45 (10%) 6 8	29, 43, 76, 106	0
1	D	414/543 (76%)	0.59	44 (10%) 6 9	30, 42, 71, 95	0
All	All	1665/2172 (76%)	0.63	182 (10%) 5 8	28, 42, 72, 109	0

The worst 5 of 182 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	528	ARG	7.7
1	C	20	LEU	7.2
1	B	25	PHE	7.2
1	D	133	THR	7.1
1	A	24	PHE	7.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

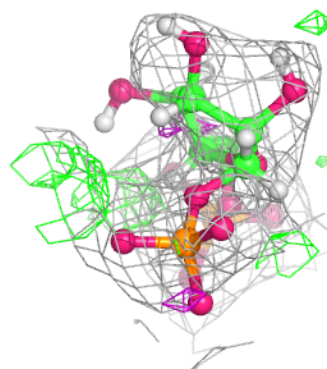
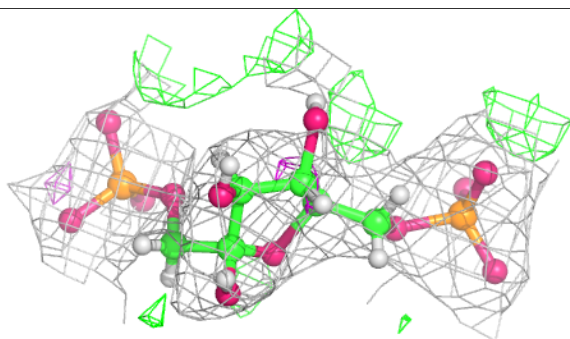
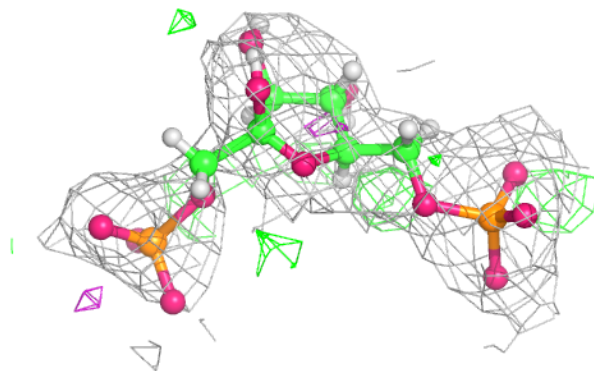
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	PEP	D	605	10/10	0.76	0.22	43,56,67,83	12
3	EDO	B	602	4/4	0.77	0.17	57,69,73,73	0
3	EDO	A	602	4/4	0.78	0.18	60,72,80,83	0
4	PEP	B	603	10/10	0.78	0.18	37,49,58,78	0
4	PEP	A	604	10/10	0.78	0.21	36,50,64,69	12
3	EDO	A	603	4/4	0.79	0.39	56,68,81,92	0
3	EDO	C	602	4/4	0.79	0.39	64,108,153,153	0
3	EDO	D	602	4/4	0.80	0.20	51,65,78,78	0
4	PEP	C	603	10/10	0.82	0.20	40,48,62,76	12
3	EDO	D	604	4/4	0.82	0.34	61,90,141,141	0
2	FBP	C	601	20/20	0.82	0.23	49,80,98,106	0
2	FBP	D	601	20/20	0.88	0.17	44,73,90,93	0
2	FBP	A	601	20/20	0.92	0.18	39,60,71,76	30
3	EDO	D	603	4/4	0.93	0.20	37,44,53,53	0
2	FBP	B	601	20/20	0.93	0.17	42,72,92,110	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.

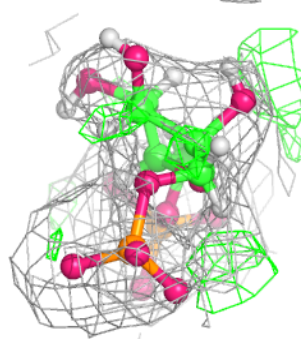
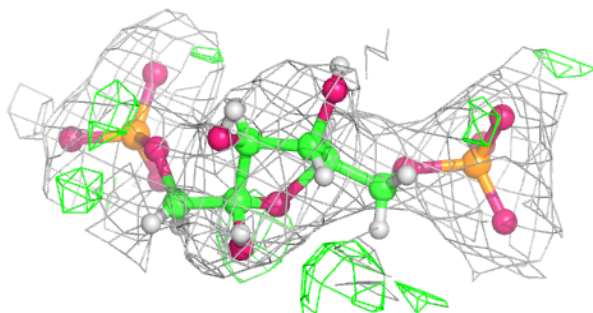
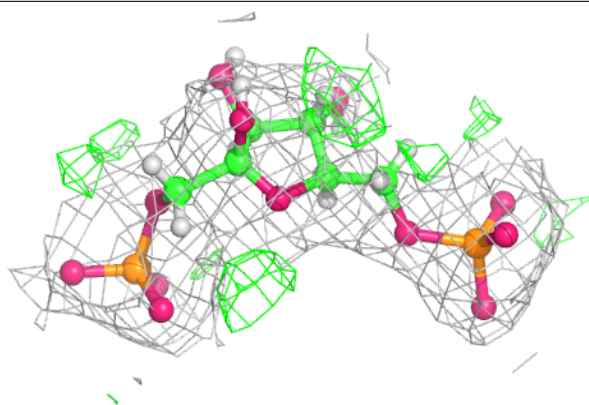
Electron density around FBP C 601:

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



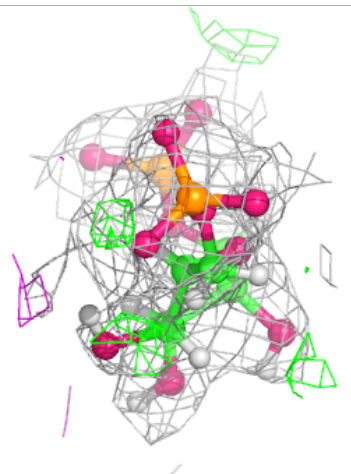
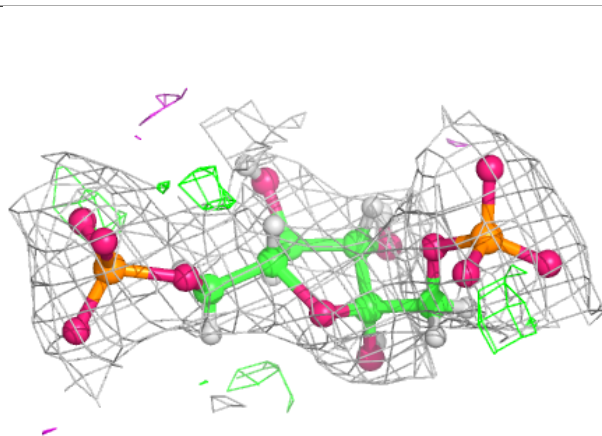
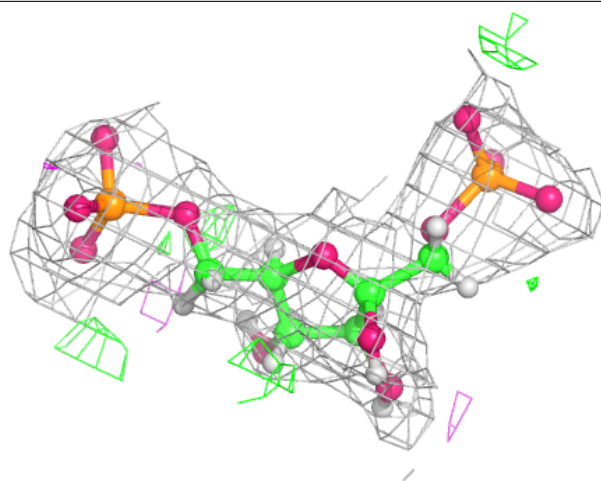
Electron density around FBP D 601:

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



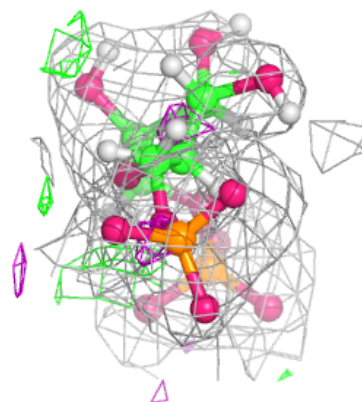
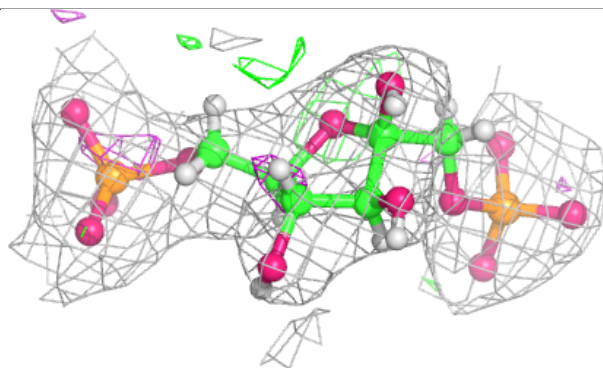
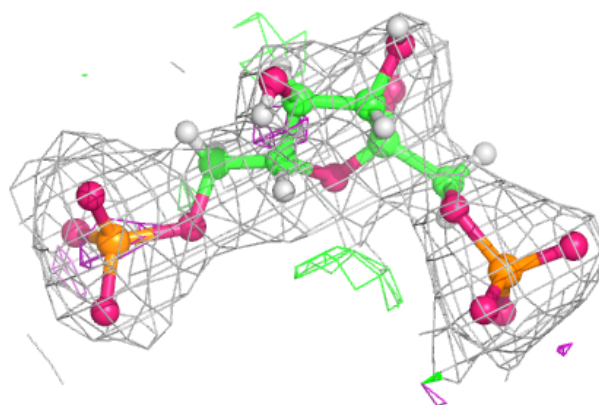
Electron density around FBP A 601:

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



Electron density around FBP 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.