



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 07:23 PM GMT

PDB ID : 1FDJ  
Title : FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE FROM RABBIT LIVER  
Authors : Blom, N.S.; White, A.; Sygusch, J.  
Deposited on : 2000-07-20  
Resolution : 2.10 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

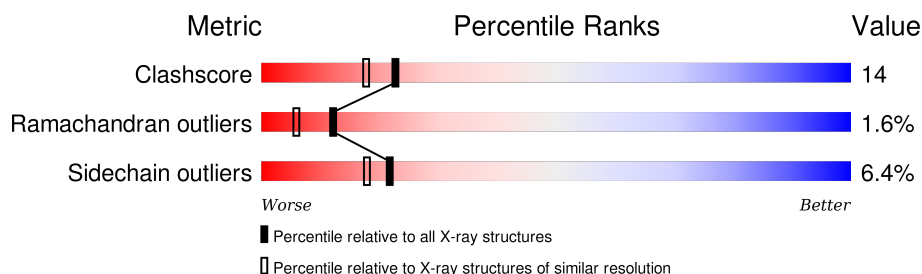
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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))
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	363	
1	B	363	
1	C	363	
1	D	363	

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
3	2FP	A	5001	X	-	-	-
4	2FP	B	6001	X	-	-	-
5	G3P	B	6003	X	-	-	-
6	13P	C	7001	-	-	X	-
6	13P	D	8002[A]	-	-	X	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 15089 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 FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	363	Total	C	N	O	S	0	6	0
			2820	1766	506	535	13			
1	B	363	Total	C	N	O	S	0	18	0
			2918	1834	517	554	13			
1	C	363	Total	C	N	O	S	0	17	0
			2914	1827	524	550	13			
1	D	363	Total	C	N	O	S	0	9	0
			2850	1787	506	544	13			

There are 4 discrepancies between the modelled and reference sequences:

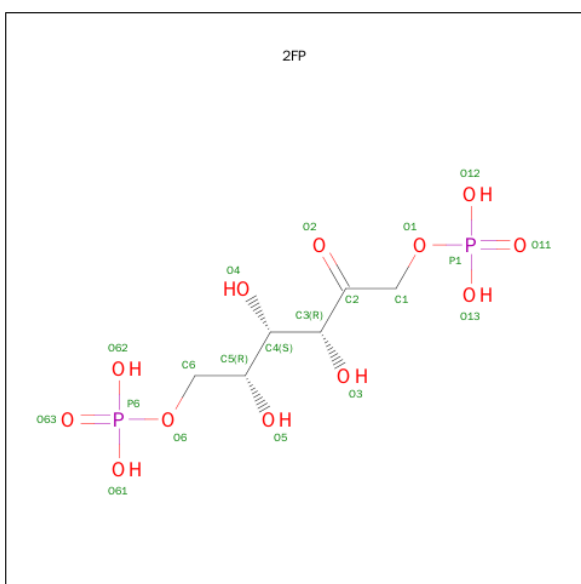
Chain	Residue	Modelled	Actual	Comment	Reference
A	1051	SER	THR	CONFLICT	UNP P79226
B	2051	SER	THR	CONFLICT	UNP P79226
C	3051	SER	THR	CONFLICT	UNP P79226
D	4051	SER	THR	CONFLICT	UNP P79226

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 3 is 1,6-FRUCTOSE DIPHOSPHATE (LINEAR FORM) (three-letter code: 2FP) (formula:  $C_6H_{14}O_{12}P_2$ ).

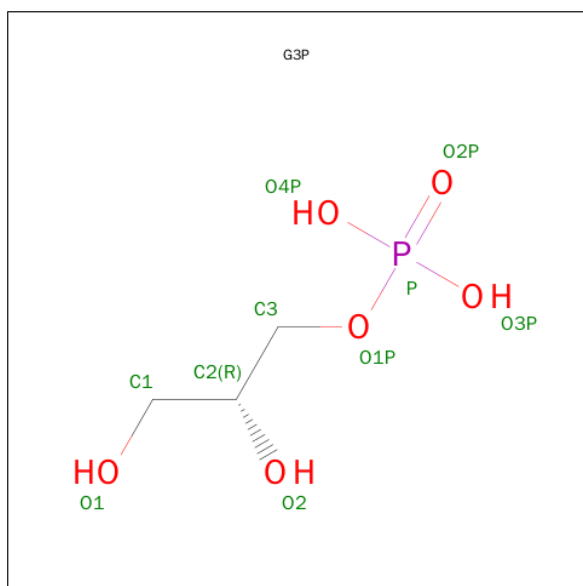


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			20	6	12	2		

- Molecule 4 is a polymer of unknown type called 1,6-FRUCTOSE DIPHOSPHATE (LINEAR FORM).

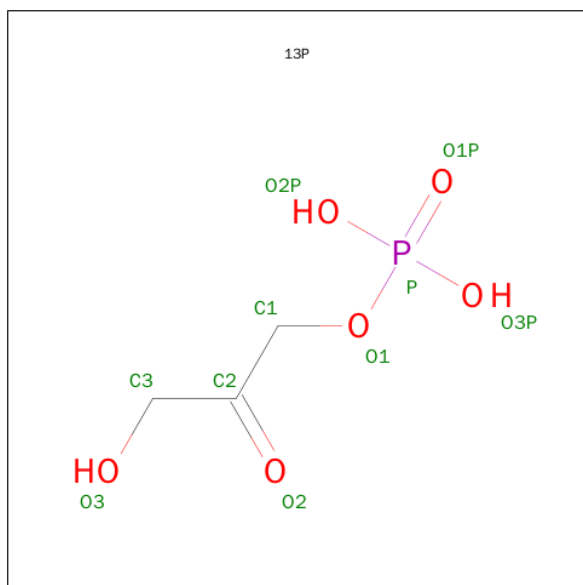
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	2	Total	C	O	P	0	0
			30	9	18	3		

- Molecule 5 is SN-GLYCEROL-3-PHOSPHATE (three-letter code: G3P) (formula:  $C_3H_9O_6P$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	O	P	0	0
			10	3	6	1		

- Molecule 6 is 1,3-DIHYDROXYACETONEPHOSPHATE (three-letter code: 13P) (formula:  $C_3H_7O_6P$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	O	P	0	0
			10	3	6	1		
6	D	1	Total	C	O	P	0	1
			10	3	6	1		
6	D	1	Total	C	O	P	0	1
			10	3	6	1		

- Molecule 7 is water.

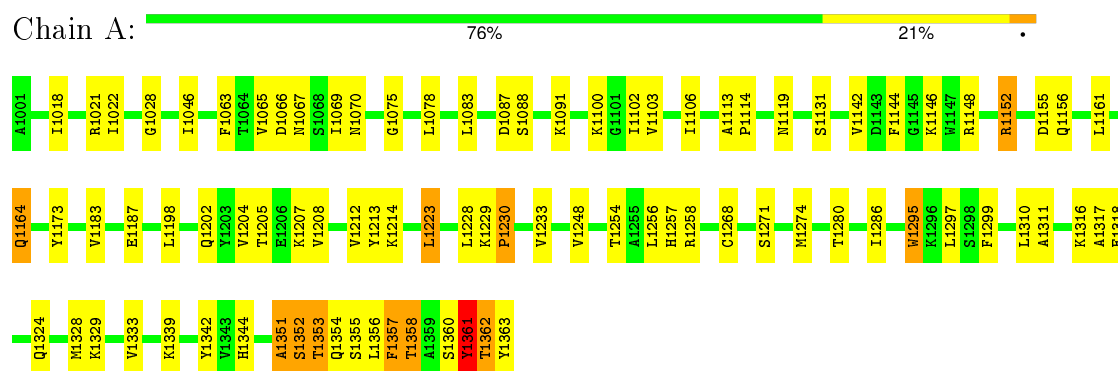
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	775	Total	O	0	0
			775	775		
7	B	858	Total	O	0	0
			858	858		
7	C	917	Total	O	0	0
			917	917		
7	D	927	Total	O	0	0
			927	927		

### 3 Residue-property plots

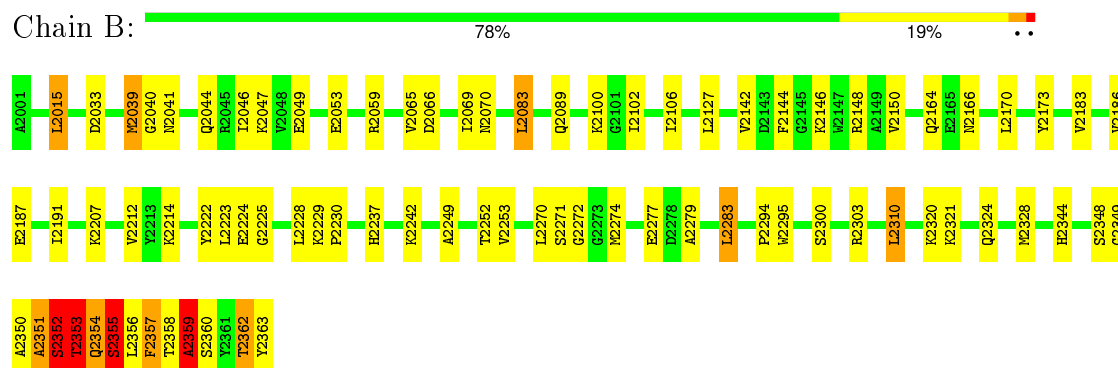
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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.

Note EDS was not executed.

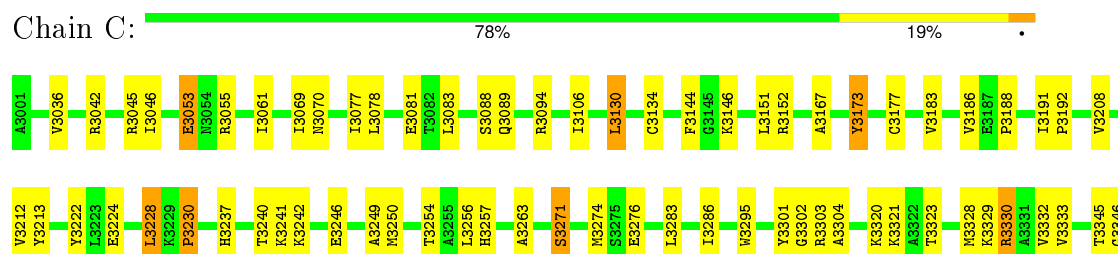
#### • Molecule 1: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE



#### • Molecule 1: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE



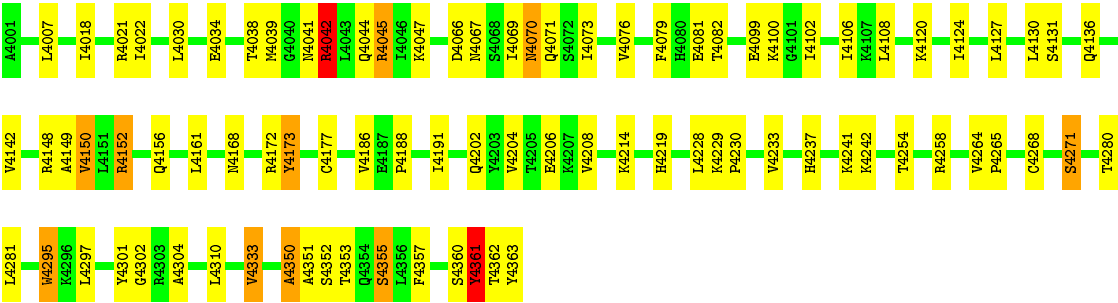
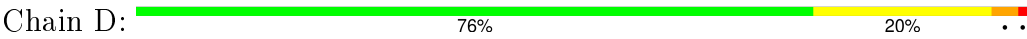
#### • Molecule 1: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE







● Molecule 1: FRUCTOSE 1,6-BISPHOSPHATE ALDOLASE



## 4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	377.25Å 130.54Å 80.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 2.10	Depositor
% Data completeness (in resolution range)	8.0 (12.00-2.10)	Depositor
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.171 , 0.214	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	15089	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: G3P, 2FP, SO4, 13P

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	0.35	0/2869	0.64	0/3880
1	B	0.44	1/2973 (0.0%)	0.73	7/4023 (0.2%)
1	C	0.33	0/2966	0.62	0/4010
1	D	0.41	0/2900	0.69	2/3922 (0.1%)
All	All	0.38	1/11708 (0.0%)	0.67	9/15835 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
4	B	2	0
All	All	2	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	2352	SER	N-CA	-6.02	1.34	1.46

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2353	THR	N-CA-C	7.00	129.89	111.00
1	B	2352	SER	CA-C-N	-6.77	102.30	117.20
1	B	2354	GLN	N-CA-C	-6.73	92.84	111.00
1	B	2353	THR	CA-C-N	-6.60	102.68	117.20
1	D	4042[A]	ARG	NE-CZ-NH2	6.33	123.46	120.30

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	6001	2FP	C3,C4

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1213	TYR	Sidechain
1	B	2353	THR	Mainchain

## 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	2820	0	2831	60	0
1	B	2918	0	2912	89	0
1	C	2914	0	2928	68	0
1	D	2850	0	2853	92	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
3	A	20	0	10	2	0
4	B	30	0	9	6	0
5	B	10	0	4	3	0
6	C	10	0	5	6	0
6	D	20	0	10	7	0
7	A	775	0	0	12	0
7	B	858	0	0	33	0
7	C	917	0	0	24	0
7	D	927	0	0	32	0
All	All	15089	0	11562	315	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 14.

The worst 5 of 315 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:4363[B]:TYR:CD2	7:D:8916:HOH:O	1.72	1.28
1:D:4042[A]:ARG:HG3	1:D:4042[A]:ARG:HH11	0.97	1.10
1:D:4363[B]:TYR:OH	7:D:8918:HOH:O	1.74	1.04
1:D:4042[A]:ARG:HG3	1:D:4042[A]:ARG:NH1	1.74	0.98
1:D:4363[B]:TYR:CE1	7:D:8917:HOH:O	2.16	0.98

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	367/363 (101%)	337 (92%)	22 (6%)	8 (2%)	8	3
1	B	379/363 (104%)	352 (93%)	20 (5%)	7 (2%)	11	5
1	C	378/363 (104%)	356 (94%)	17 (4%)	5 (1%)	15	9
1	D	369/363 (102%)	343 (93%)	22 (6%)	4 (1%)	17	11
All	All	1493/1452 (103%)	1388 (93%)	81 (5%)	24 (2%)	12	6

5 of 24 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1344	HIS
1	A	1353	THR
1	A	1361	TYR
1	B	2357	PHE
1	B	2359	ALA

### 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	297/293 (101%)	280 (94%)	17 (6%)	25	22
1	B	307/293 (105%)	293 (95%)	14 (5%)	33	31
1	C	307/293 (105%)	287 (94%)	20 (6%)	21	17
1	D	301/293 (103%)	273 (91%)	28 (9%)	11	7
All	All	1212/1172 (103%)	1133 (94%)	79 (6%)	22	17

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	3228[A]	LEU
1	C	3283	LEU
1	D	4281	LEU
1	C	3228[B]	LEU
1	C	3246	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 23 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	2110	GLN
1	B	2220	HIS
1	D	4219	HIS
1	B	2164	GLN
1	B	2237	HIS

### 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 ⓘ

2 carbohydrates 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	$\# Z  > 2$
4	2FP	B	6001	1,5,4	19,19,19	1.02	1 (5%)	18,28,28	2.32	8 (44%)
4	13P	B	6002	4	9,9,9	1.04	1 (11%)	9,12,12	1.29	1 (11%)

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	2FP	B	6001	1,5,4	2/2/6/6	0/24/24/24	0/0/0/0
4	13P	B	6002	4	-	0/7/8/8	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	6001	2FP	P6-O63	2.02	1.57	1.51
4	B	6002	13P	P-O1P	2.26	1.58	1.51

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	6001	2FP	O12-P1-O11	-4.66	95.59	110.58
4	B	6001	2FP	O3-C3-C2	-3.44	104.63	111.01
4	B	6001	2FP	O13-P1-O11	-2.90	101.26	110.58
4	B	6002	13P	O2P-P-O1P	-2.68	101.94	110.58
4	B	6001	2FP	O4-C4-C5	-2.04	103.61	108.75

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	B	6001	2FP	C3
4	B	6001	2FP	C4

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	6001	2FP	5	0
4	B	6002	13P	1	0

## 5.6 Ligand geometry ⓘ

9 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	SO4	A	5000	-	4,4,4	0.98	0	6,6,6	0.21	0
3	2FP	A	5001	-	19,19,19	1.14	2 (10%)	18,28,28	1.73	6 (33%)
2	SO4	B	6000	-	4,4,4	1.22	0	6,6,6	0.23	0
5	G3P	B	6003	4	9,9,9	2.01	2 (22%)	10,12,12	1.16	1 (10%)
2	SO4	C	7000	-	4,4,4	1.17	0	6,6,6	0.45	0
6	13P	C	7001	-	9,9,9	1.09	1 (11%)	9,12,12	1.59	2 (22%)
2	SO4	D	8000	-	4,4,4	1.35	0	6,6,6	0.16	0
6	13P	D	8001[B]	-	9,9,9	1.06	1 (11%)	9,12,12	1.44	2 (22%)
6	13P	D	8002[A]	-	9,9,9	1.00	1 (11%)	9,12,12	1.44	2 (22%)

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	SO4	A	5000	-	-	0/0/0/0	0/0/0/0
3	2FP	A	5001	-	2/2/6/6	0/24/24/24	0/0/0/0
2	SO4	B	6000	-	-	0/0/0/0	0/0/0/0
5	G3P	B	6003	4	1/1/2/2	0/8/8/8	0/0/0/0
2	SO4	C	7000	-	-	0/0/0/0	0/0/0/0
6	13P	C	7001	-	-	1/7/8/8	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	D	8000	-	-	0/0/0/0	0/0/0/0
6	13P	D	8001[B]	-	-	1/7/8/8	0/0/0/0
6	13P	D	8002[A]	-	-	2/7/8/8	0/0/0/0

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	6003	G3P	O1-C1	-4.83	1.21	1.42
6	D	8002[A]	13P	P-O1P	2.15	1.58	1.51
6	C	7001	13P	P-O1P	2.23	1.58	1.51
3	A	5001	2FP	C4-C3	2.25	1.59	1.53
3	A	5001	2FP	O2-C2	2.42	1.25	1.21

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	5001	2FP	O3-C3-C2	-2.71	105.99	111.01
6	D	8001[B]	13P	O2P-P-O1P	-2.67	101.99	110.58
3	A	5001	2FP	O12-P1-O11	-2.49	102.58	110.58
6	C	7001	13P	O2P-P-O1P	-2.11	103.79	110.58
6	D	8002[A]	13P	O1-P-O1P	2.07	112.41	107.14

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	B	6003	G3P	C2
3	A	5001	2FP	C3
3	A	5001	2FP	C4

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	7001	13P	O2-C2-C3-O3
6	D	8002[A]	13P	P-O1-C1-C2
6	D	8001[B]	13P	O2-C2-C3-O3
6	D	8002[A]	13P	O2-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	5001	2FP	2	0
5	B	6003	G3P	3	0
6	C	7001	13P	6	0
6	D	8001[B]	13P	2	0
6	D	8002[A]	13P	5	0

## 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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.