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 ⓘ

Feb 13, 2017 – 08:59 pm GMT

PDB ID	:	1FRP
Title	:	CRYSTAL STRUCTURE OF FRUCTOSE-1,6-BISPHOSPHATASE COMPLEXED WITH FRUCTOSE-2,6-BISPHOSPHATE, AMP AND ZN2+ AT 2.0 ANGSTROMS RESOLUTION. ASPECTS OF SYNERGISM BETWEEN INHIBITORS
Authors	:	Xue, Y.; Huang, S.; Liang, J.-Y.; Zhang, Y.; Lipscomb, W.N.
Deposited on	:	1994-08-26
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
http://wwpdb.org/validation/2016/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:

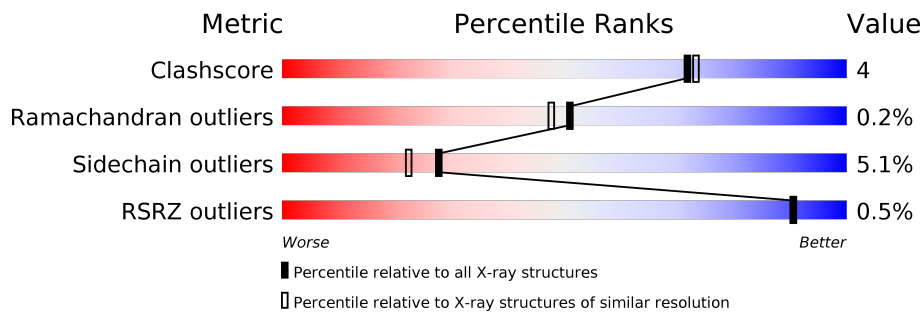|		
MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

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 2.00 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	Percentile Ranks	Value
Clashscore		4
Ramachandran outliers		0.2%
Sidechain outliers		5.1%
RSRZ outliers		0.5%

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))
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (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 on the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	335	79% 14% · ·
1	B	335	% 79% 14% · ·

WORLDWIDE PDB PROTEIN DATA BANK

2 Entry composition ⓘ

There are 5 unique types of molecules in this entry. The entry contains 6789 atoms, of which 1566 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-BISPHOSPHATASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	321	Total	C	H	N	O	S	0	0	1
			2990	1560	542	414	459	15			
1	B	321	Total	C	H	N	O	S	0	0	1
			2990	1560	542	414	459	15			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	GLN	GLU	CONFLICT	UNP P00636
A	62	ALA	SER	CONFLICT	UNP P00636
A	96	THR	SER	CONFLICT	UNP P00636
A	199	ASN	ASP	CONFLICT	UNP P00636
B	20	GLN	GLU	CONFLICT	UNP P00636
B	62	ALA	SER	CONFLICT	UNP P00636
B	96	THR	SER	CONFLICT	UNP P00636
B	199	ASN	ASP	CONFLICT	UNP P00636

- Molecule 2 is SUGAR (FRUCTOSE-2,6-DIPHOSPHATE) (three-letter code: FDP) (formula: $C_6H_{14}O_{12}P_2$).
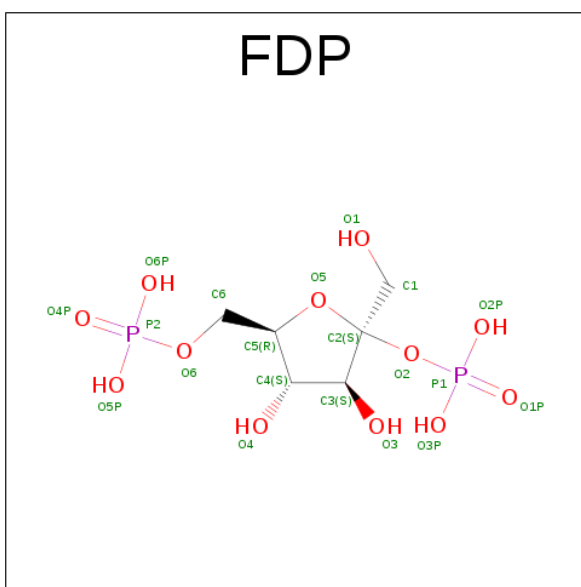
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	O	P	0	0
			22	6	2	12	2		
2	B	1	Total	C	H	O	P	0	0
			22	6	2	12	2		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 4 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: $C_{10}H_{14}N_5O_7P$).
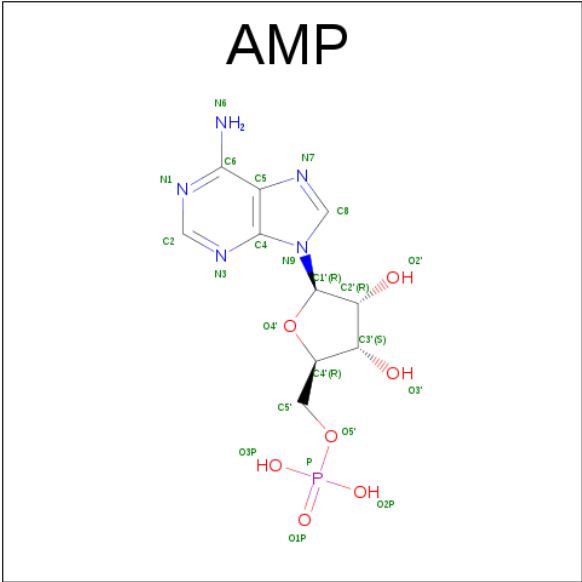
| Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

• Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	128	Total	H	O	0	0
			384	256	128		
5	B	111	Total	H	O	0	0
			333	222	111		

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 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.
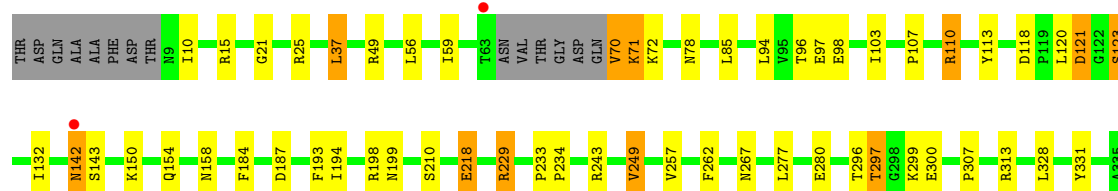
• Molecule 1: FRUCTOSE 1,6-BISPHOSPHATASE

Chain A:
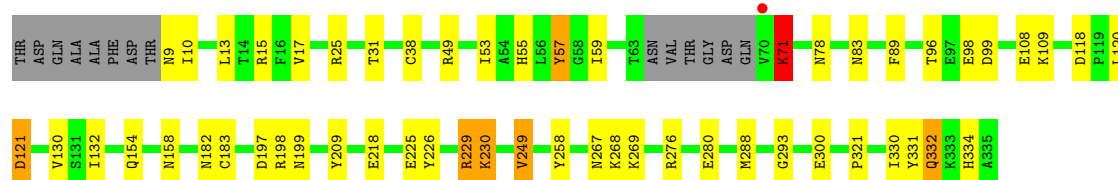
• Molecule 1: FRUCTOSE 1,6-BISPHOSPHATASE

Chain B:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	60.95Å 166.30Å 80.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.00 72.09 – 1.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.00) 76.4 (72.09-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.91 (at 1.90Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.189 , (Not available) 0.168 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å^2)	24.4	Xtriage
Anisotropy	0.393	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 73.3	EDS
L-test for twinning[2]	$< |L| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	6789	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.95% 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: FDP, ZN, AMP

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	0.78	1/2489 (0.0%)	1.39	16/3365 (0.5%)
1	B	0.79	1/2489 (0.0%)	1.39	21/3365 (0.6%)
All	All	0.78	2/4978 (0.0%)	1.39	37/6730 (0.5%)

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	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	280	GLU	CD-OE2	-5.47	1.19	1.25
1	A	280	GLU	CD-OE2	-5.33	1.19	1.25

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	249	VAL	CG1-CB-CG2	-9.81	95.20	110.90
1	A	49	ARG	NE-CZ-NH2	-7.88	116.36	120.30
1	A	118	ASP	CB-CG-OD1	7.70	125.23	118.30
1	B	118	ASP	CB-CG-OD1	7.66	125.19	118.30
1	A	249	VAL	CG1-CB-CG2	-7.46	98.97	110.90

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	57	TYR	Sidechain
1	A	71	LYS	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	2448	542	2513	23	0
1	B	2448	542	2513	19	0
2	A	20	2	10	0	0
2	B	20	2	10	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	23	0	12	0	0
4	B	23	0	12	1	0
5	A	128	256	0	0	0
5	B	111	222	0	1	0
All	All	5223	1566	5070	40	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 4.

The worst 5 of 40 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:A:96:THR:HG22	1:A:98:GLU:H	1.51	0.74
1:B:96:THR:HG22	1:B:98:GLU:H	1.57	0.69
1:A:78:ASN:OD1	1:A:96:THR:HG21	1.94	0.67
1:B:78:ASN:OD1	1:B:96:THR:HG21	1.98	0.63
1:A:182:ASN:HD22	1:A:198:ARG:HA	1.64	0.61

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	317/335 (95%)	307 (97%)	10 (3%)	0	100	100
1	B	317/335 (95%)	308 (97%)	8 (2%)	1 (0%)	44	40
All	All	634/670 (95%)	615 (97%)	18 (3%)	1 (0%)	51	48

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	71	LYS

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	265/277 (96%)	255 (96%)	10 (4%)	38	35
1	B	265/277 (96%)	248 (94%)	17 (6%)	20	15
All	All	530/554 (96%)	503 (95%)	27 (5%)	28	22

5 of 27 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	56	LEU
1	B	72	LYS
1	B	229	ARG
1	B	70	VAL
1	A	99	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	182	ASN
1	A	282	ASN
1	B	35	ASN
1	A	154	GLN
1	B	9	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#$|Z| > 2$	Counts	RMSZ	#$|Z| > 2$
2	FDP	A	336	3	20,20,20	0.93	1 (5%)	30,32,32	1.76	9 (30%)
4	AMP	A	338	-	22,25,25	1.06	3 (13%)	24,38,38	1.93	4 (16%)
2	FDP	B	336	3	20,20,20	0.95	1 (5%)	30,32,32	1.64	8 (26%)
4	AMP	B	338	-	22,25,25	1.10	3 (13%)	24,38,38	2.17	4 (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
2	FDP	A	336	3	-	0/12/34/34	0/1/1/1
4	AMP	A	338	-	-	0/6/26/26	0/3/3/3
2	FDP	B	336	3	-	0/12/34/34	0/1/1/1
4	AMP	B	338	-	-	0/6/26/26	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	338	AMP	O4'-C1'	2.11	1.44	1.41
4	B	338	AMP	C2-N1	2.13	1.37	1.33
2	B	336	FDP	O1-C1	2.17	1.49	1.42
4	A	338	AMP	C2-N1	2.17	1.38	1.33
4	B	338	AMP	C2-N3	2.20	1.35	1.32

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	338	AMP	N3-C2-N1	-8.89	121.11	128.86
4	A	338	AMP	N3-C2-N1	-7.34	122.47	128.86
2	A	336	FDP	O5-C2-C3	-3.37	98.25	105.57
2	B	336	FDP	O5-C2-C3	-3.25	98.51	105.57
4	B	338	AMP	C5-C6-N1	-2.31	112.71	119.70

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	338	AMP	1	0

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	321/335 (95%)	-0.30	1 (0%)	93	93	11, 26, 59, 89	0
1	B	321/335 (95%)	-0.27	2 (0%)	89	88	11, 26, 63, 89	0
All	All	642/670 (95%)	-0.29	3 (0%)	90	90	11, 26, 62, 89	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	63	THR	11.2
1	B	142	ASN	3.3
1	A	70	VAL	2.4

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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
2	FDP	B	336	20/20	0.98	0.12	0.56	0,23,29,35	0
2	FDP	A	336	20/20	0.97	0.11	0.17	0,21,28,36	0
4	AMP	B	338	23/23	0.97	0.10	-0.43	24,25,30,31	0
4	AMP	A	338	23/23	0.97	0.10	-0.54	17,25,28,28	0
3	ZN	B	337	1/1	0.94	0.08	-1.88	50,50,50,50	0
3	ZN	A	337	1/1	0.94	0.06	-3.19	49,49,49,49	0

6.5 Other polymers ⓘ

There are no such residues in this entry.