



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:57 PM GMT

PDB ID : 1DCU  
Title : REDOX SIGNALING IN THE CHLOROPLAST: STRUCTURE OF OXIDIZED PEA FRUCTOSE-1,6-BISPHOSPHATE PHOSPHATASE  
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Deposited on : 1999-11-05  
Resolution : 2.20 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) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

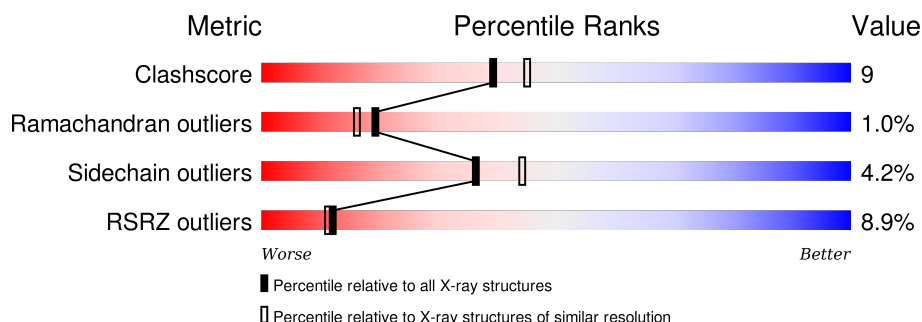
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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.

Mol	Chain	Length	Quality of chain
1	A	357	<div> <div>10%</div> <div>62% 24% 7% 8%</div> </div>
1	B	357	<div> <div>5%</div> <div>66% 21% • 10%</div> </div>
1	C	357	<div> <div>7%</div> <div>64% 24% • • 8%</div> </div>
1	D	357	<div> <div>10%</div> <div>68% 18% • • 9%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10102 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-BISPHOSPHATASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	330	Total	C	N	O	S	0	0	0
			2507	1590	408	499	10			
1	B	323	Total	C	N	O	S	0	0	0
			2449	1558	401	480	10			
1	C	328	Total	C	N	O	S	0	0	0
			2497	1586	411	490	10			
1	D	325	Total	C	N	O	S	0	0	0
			2454	1561	402	481	10			

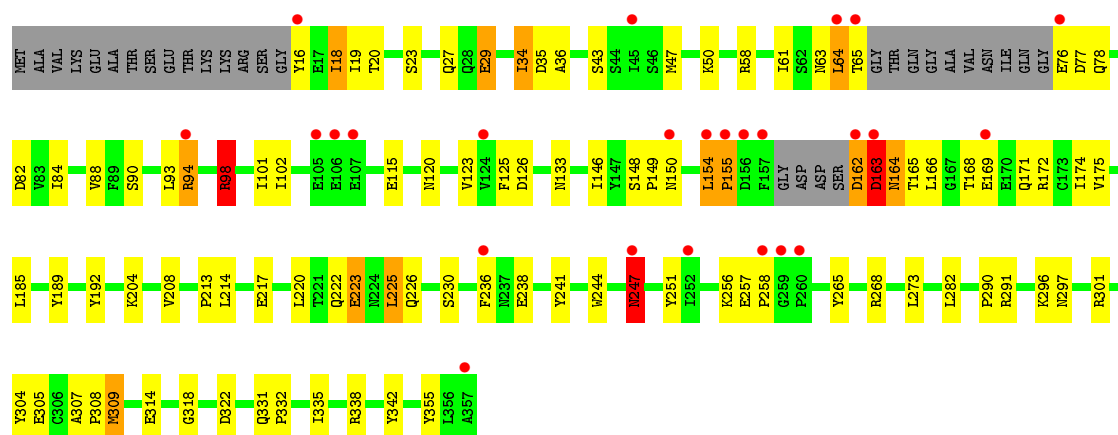
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	ALA	ILE	ENGINEERED	UNP P46275
B	103	ALA	ILE	ENGINEERED	UNP P46275
C	103	ALA	ILE	ENGINEERED	UNP P46275
D	103	ALA	ILE	ENGINEERED	UNP P46275
A	232	LYS	GLU	ENGINEERED	UNP P46275
B	232	LYS	GLU	ENGINEERED	UNP P46275
C	232	LYS	GLU	ENGINEERED	UNP P46275
D	232	LYS	GLU	ENGINEERED	UNP P46275

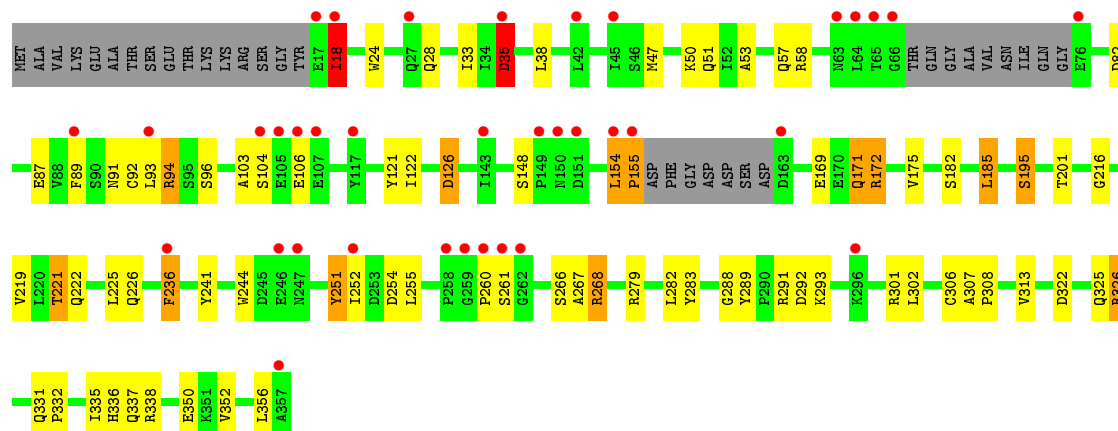
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	40	Total	O	0	0
			40	40		
2	B	56	Total	O	0	0
			56	56		
2	C	47	Total	O	0	0
			47	47		
2	D	52	Total	O	0	0
			52	52		





• Molecule 1: FRUCTOSE-1,6-BISPHOSPHATASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.60 Å 126.32 Å 78.02 Å 90.00° 97.73° 90.00°	Depositor
Resolution (Å)	23.80 – 2.20 23.80 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (23.80-2.20) 99.6 (23.80-2.20)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.54 (at 2.19 Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.189 , 0.247 0.185 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	32.7	Xtriage
Anisotropy	0.164	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 69.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 69336 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	10102	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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	0.87	0/2553	1.92	63/3463 (1.8%)
1	B	1.01	3/2493 (0.1%)	1.97	63/3383 (1.9%)
1	C	0.92	0/2541	1.85	52/3444 (1.5%)
1	D	0.92	1/2499 (0.0%)	1.80	40/3393 (1.2%)
All	All	0.93	4/10086 (0.0%)	1.89	218/13683 (1.6%)

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	5
1	B	0	3
1	C	0	1
1	D	0	2
All	All	0	11

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	202	ILE	C-O	7.30	1.37	1.23
1	D	195	SER	CA-CB	7.23	1.63	1.52
1	B	241	TYR	CE2-CZ	-5.06	1.31	1.38
1	B	230	SER	CB-OG	-5.03	1.35	1.42

The worst 5 of 218 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	202	ILE	CA-C-N	21.39	158.98	116.20
1	C	162	ASP	C-N-CA	21.25	174.83	121.70
1	A	147	TYR	CB-CG-CD1	19.57	132.74	121.00
1	B	202	ILE	CA-C-O	-19.06	80.08	120.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	326	ARG	NE-CZ-NH1	17.35	128.98	120.30

There are no chirality outliers.

5 of 11 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	148	SER	Mainchain
1	A	170	GLU	Mainchain
1	A	217	GLU	Mainchain
1	A	224	ASN	Mainchain
1	A	26	LEU	Mainchain

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2507	0	2420	57	0
1	B	2449	0	2374	31	3
1	C	2497	0	2428	54	0
1	D	2454	0	2376	48	0
2	A	40	0	0	0	3
2	B	56	0	0	2	0
2	C	47	0	0	2	0
2	D	52	0	0	2	0
All	All	10102	0	9598	174	3

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 174 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:B:309:MET:HG2	2:B:409:HOH:O	1.51	1.10
1:A:105:GLU:HG2	1:A:106:GLU:HG3	1.31	1.06
1:A:154:LEU:H	1:A:155:PRO:CD	1.71	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:115:GLU:HB2	1:C:154:LEU:HD13	1.55	0.89
1:C:154:LEU:HD12	1:C:154:LEU:H	1.37	0.88

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:ILE:O	2:A:382:HOH:O[2_656]	1.50	0.70
1:B:202:ILE:C	2:A:382:HOH:O[2_656]	2.07	0.13
1:B:203:GLY:N	2:A:382:HOH:O[2_656]	2.13	0.07

## 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	324/357 (91%)	305 (94%)	12 (4%)	7 (2%)	8	4
1	B	317/357 (89%)	306 (96%)	10 (3%)	1 (0%)	46	50
1	C	322/357 (90%)	306 (95%)	13 (4%)	3 (1%)	21	19
1	D	319/357 (89%)	304 (95%)	13 (4%)	2 (1%)	30	29
All	All	1282/1428 (90%)	1221 (95%)	48 (4%)	13 (1%)	19	16

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	65	THR
1	A	154	LEU
1	A	335	ILE
1	C	155	PRO
1	C	163	ASP

### 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	272/307 (89%)	260 (96%)	12 (4%)	35	42
1	B	264/307 (86%)	255 (97%)	9 (3%)	44	54
1	C	270/307 (88%)	259 (96%)	11 (4%)	37	45
1	D	264/307 (86%)	251 (95%)	13 (5%)	31	36
All	All	1070/1228 (87%)	1025 (96%)	45 (4%)	36	44

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	321	SER
1	C	126	ASP
1	D	266	SER
1	C	64	LEU
1	C	150	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	63	ASN
1	C	171	GLN
1	D	240	ASN
1	C	78	GLN
1	C	164	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	330/357 (92%)	0.58	36 (10%) 7 7	21, 40, 74, 93	0
1	B	323/357 (90%)	0.28	19 (5%) 26 25	21, 34, 70, 96	0
1	C	328/357 (91%)	0.38	25 (7%) 17 16	23, 39, 71, 90	0
1	D	325/357 (91%)	0.48	36 (11%) 7 7	23, 38, 68, 97	0
All	All	1306/1428 (91%)	0.43	116 (8%) 12 11	21, 38, 72, 97	0

The worst 5 of 116 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	157	PHE	9.8
1	D	260	PRO	9.3
1	A	260	PRO	9.1
1	D	259	GLY	9.1
1	D	105	GLU	9.1

### 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 carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.