



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 02:23 AM UTC

PDB ID : 1DCU / pdb\_00001dcu  
Title : REDOX SIGNALING IN THE CHLOROPLAST: STRUCTURE OF OXIDIZED PEA FRUCTOSE-1,6-BISPHOSPHATE PHOSPHATASE  
Authors : Chiadmi, M.; Navaza, A.; Miginiac-Maslow, M.; Jacquot, J.P.; Cherfils, J.  
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

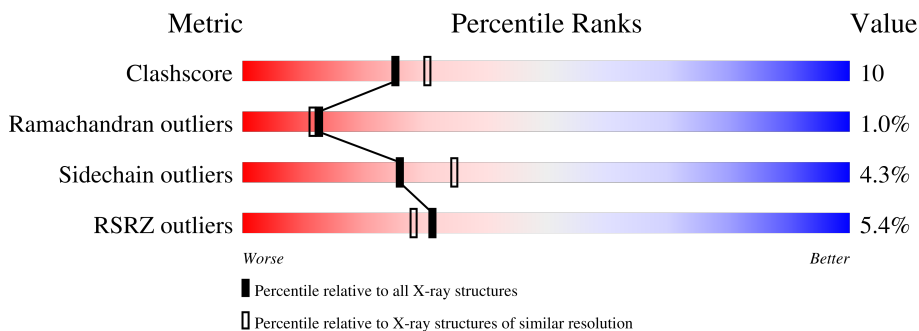
# 1 Overall quality at a glance

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	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	357	
1	B	357	
1	C	357	
1	D	357	

## 2 Entry composition [i](#)

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

There are 8 discrepancies between the modelled and reference sequences:

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

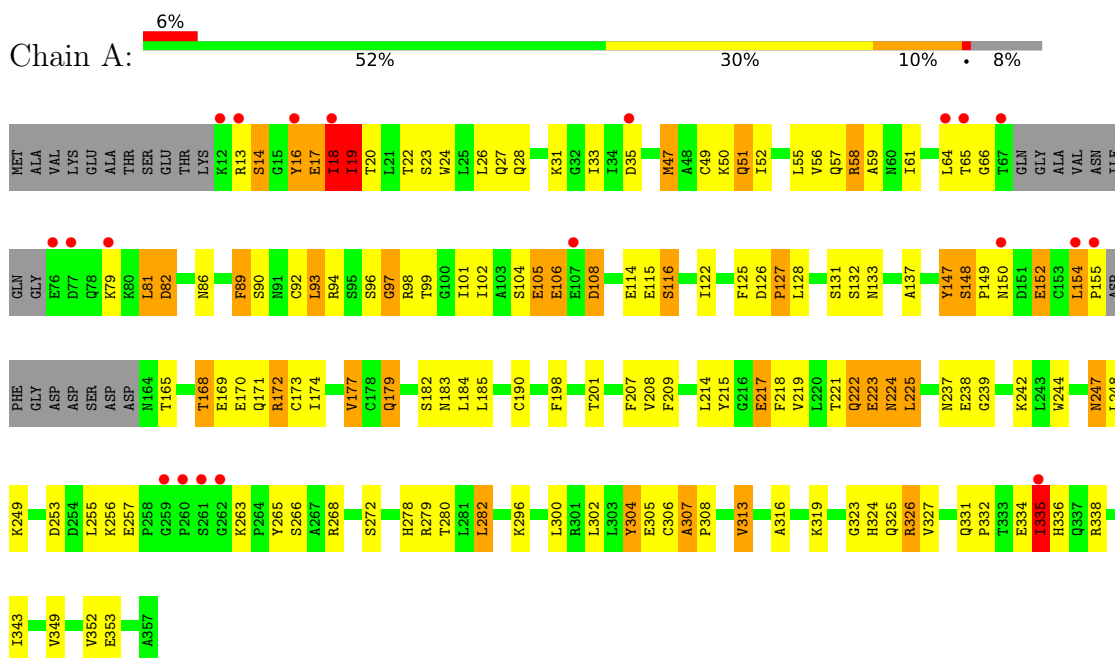
- Molecule 2 is water.

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

### 3 Residue-property plots

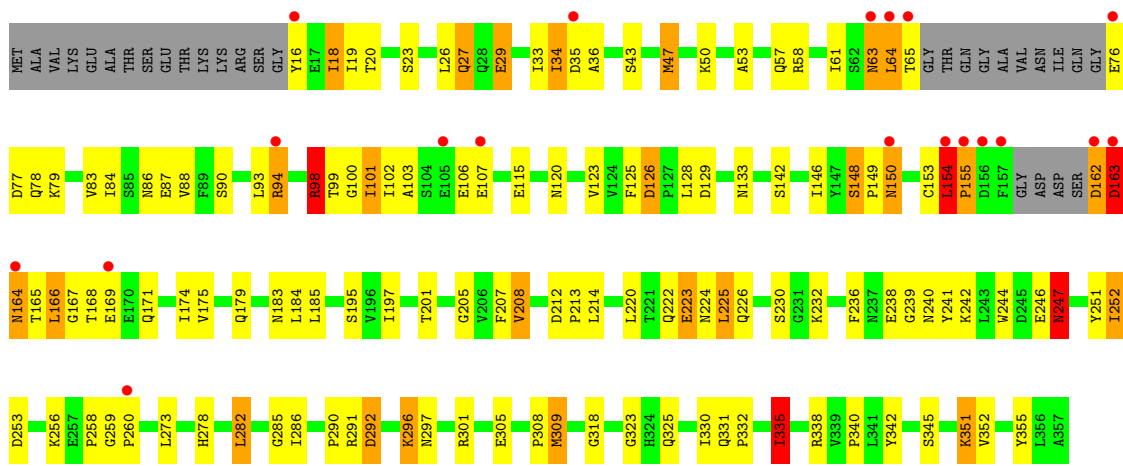
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: FRUCTOSE-1,6-BISPHOSPHATASE

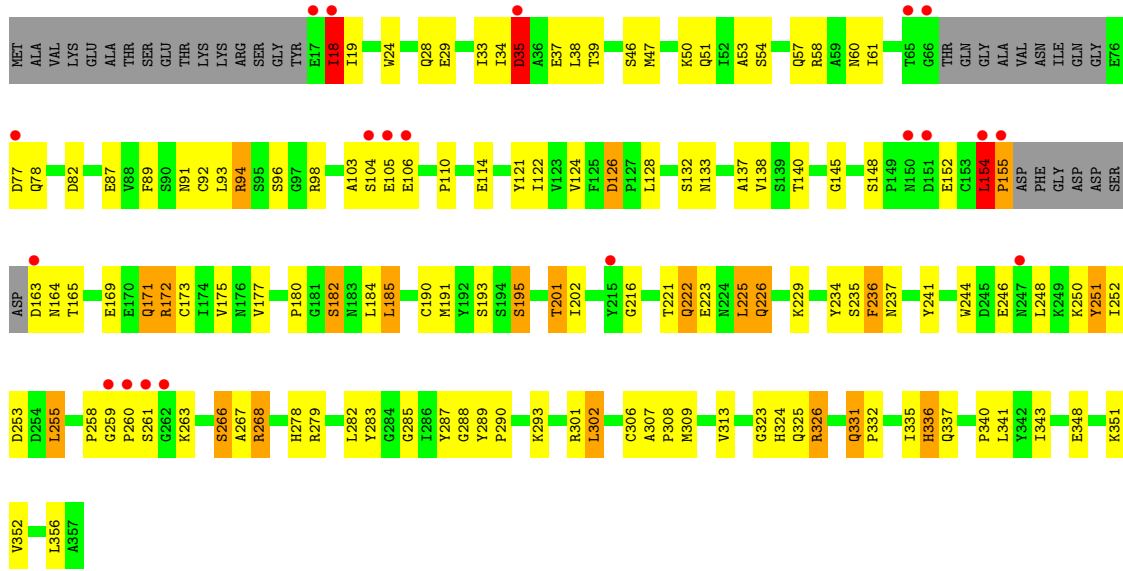




● Molecule 1: FRUCTOSE-1,6-BISPHOSPHATASE



● 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, $\alpha$ , $\beta$ , $\gamma$	71.60Å 126.32Å 78.02Å 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) 99.5 (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 2.19Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.189 , 0.247 0.184 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.7	Xtrriage
Anisotropy	0.164	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 75.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10102	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtrriage'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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality i

### 5.1 Standard geometry i

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	1.13	2/2553 (0.1%)	2.30	131/3463 (3.8%)
1	B	1.33	6/2493 (0.2%)	2.42	126/3383 (3.7%)
1	C	1.20	2/2541 (0.1%)	2.39	132/3444 (3.8%)
1	D	1.19	4/2499 (0.2%)	2.27	128/3393 (3.8%)
All	All	1.21	14/10086 (0.1%)	2.35	517/13683 (3.8%)

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

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	202	ILE	C-O	11.04	1.37	1.24
1	B	202	ILE	CA-C	-8.43	1.42	1.52
1	B	278	HIS	CE1-NE2	-6.48	1.26	1.32
1	B	219	VAL	N-CA	-5.99	1.39	1.46
1	A	57	GLN	N-CA	-5.78	1.39	1.46

The worst 5 of 517 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	202	ILE	CA-C-O	-32.56	80.08	120.78
1	C	162	ASP	CA-C-N	27.90	174.83	121.54
1	C	162	ASP	C-N-CA	27.90	174.83	121.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	108	ASP	CA-CB-CG	16.77	129.37	112.60
1	B	120	ASN	CA-CB-CG	-13.63	98.97	112.60

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 [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	2507	0	2420	61	0
1	B	2449	0	2375	34	3
1	C	2497	0	2428	60	0
1	D	2454	0	2376	51	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	9599	189	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 10.

The worst 5 of 189 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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:LEU:H	1:A:155:PRO:CD	1.71	1.04
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 [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	324/357 (91%)	305 (94%)	12 (4%)	7 (2%)	<b>5</b> <b>3</b>
1	B	317/357 (89%)	306 (96%)	10 (3%)	1 (0%)	36 42
1	C	322/357 (90%)	306 (95%)	13 (4%)	3 (1%)	<b>14</b> <b>14</b>
1	D	319/357 (89%)	304 (95%)	13 (4%)	2 (1%)	<b>21</b> <b>23</b>
All	All	1282/1428 (90%)	1221 (95%)	48 (4%)	13 (1%)	<b>12</b> <b>11</b>

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%)	261 (96%)	11 (4%)	28	38
1	B	264/307 (86%)	254 (96%)	10 (4%)	29	40
1	C	270/307 (88%)	258 (96%)	12 (4%)	25	34
1	D	264/307 (86%)	251 (95%)	13 (5%)	22	29
All	All	1070/1228 (87%)	1024 (96%)	46 (4%)	26	35

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	154	LEU
1	D	154	LEU
1	C	230	SER
1	C	335	ILE
1	D	177	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	336	HIS
1	D	176	ASN
1	C	164	ASN
1	D	331	GLN
1	D	78	GLN

### 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 oligosaccharides 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%)	0.30	20 (6%) 27 24	21, 40, 74, 93	0
1	B	323/357 (90%)	0.07	11 (3%) 48 45	21, 34, 70, 96	0
1	C	328/357 (91%)	0.19	19 (5%) 29 25	23, 39, 71, 90	0
1	D	325/357 (91%)	0.26	20 (6%) 26 23	23, 38, 68, 97	0
All	All	1306/1428 (91%)	0.20	70 (5%) 31 28	21, 38, 72, 97	0

The worst 5 of 70 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	65	THR	7.7
1	C	64	LEU	6.0
1	D	105	GLU	5.1
1	D	261	SER	4.9
1	A	260	PRO	4.7

### 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 oligosaccharides 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.