



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:41 PM GMT

PDB ID : 3RPL  
Title : D-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7-bisphosphatase of Synechocystis sp. PCC 6803 in complex with FRUCTOSE-1,6-BISPHOSPHATE  
Authors : Hu, X.; Hui, D.; Lingling, F.; Jian, W.  
Deposited on : 2011-04-26  
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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

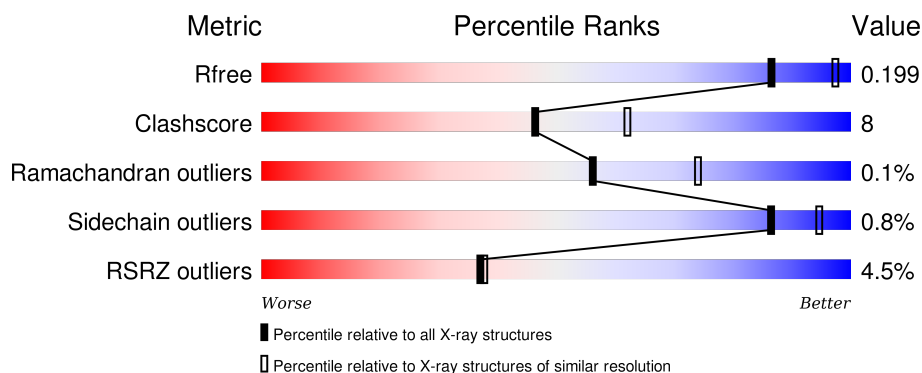
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.40 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))
$R_{free}$	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	379	<div> <div>3%</div> <div>78% 13% 8%</div> </div>
1	C	379	<div> <div>3%</div> <div>79% 12% 8%</div> </div>
1	D	379	<div> <div>5%</div> <div>75% 16% 9%</div> </div>
2	B	379	<div> <div>4%</div> <div>80% 11% 8%</div> </div>

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	MG	A	348	-	-	-	X
3	MG	B	348	-	-	-	X
3	MG	D	348	-	-	-	X
6	SO4	A	353	-	-	-	X
6	SO4	B	351	-	-	-	X
6	SO4	C	351	-	-	X	-
6	SO4	C	353	-	-	-	X
8	GOL	C	358	-	-	-	X

## 2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 11262 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 D-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7-bisphosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	347	Total	C	N	O	S	0	0	0
			2556	1584	452	498	22			
1	C	347	Total	C	N	O	S	0	1	0
			2552	1583	453	494	22			
1	D	346	Total	C	N	O	S	0	4	0
			2577	1600	452	503	22			

There are 105 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-33	MET	-	EXPRESSION TAG	UNP P73922
A	-32	GLY	-	EXPRESSION TAG	UNP P73922
A	-31	SER	-	EXPRESSION TAG	UNP P73922
A	-30	SER	-	EXPRESSION TAG	UNP P73922
A	-29	HIS	-	EXPRESSION TAG	UNP P73922
A	-28	HIS	-	EXPRESSION TAG	UNP P73922
A	-27	HIS	-	EXPRESSION TAG	UNP P73922
A	-26	HIS	-	EXPRESSION TAG	UNP P73922
A	-25	HIS	-	EXPRESSION TAG	UNP P73922
A	-24	HIS	-	EXPRESSION TAG	UNP P73922
A	-23	SER	-	EXPRESSION TAG	UNP P73922
A	-22	SER	-	EXPRESSION TAG	UNP P73922
A	-21	GLY	-	EXPRESSION TAG	UNP P73922
A	-20	LEU	-	EXPRESSION TAG	UNP P73922
A	-19	VAL	-	EXPRESSION TAG	UNP P73922
A	-18	PRO	-	EXPRESSION TAG	UNP P73922
A	-17	ARG	-	EXPRESSION TAG	UNP P73922
A	-16	GLY	-	EXPRESSION TAG	UNP P73922
A	-15	SER	-	EXPRESSION TAG	UNP P73922
A	-14	HIS	-	EXPRESSION TAG	UNP P73922
A	-13	MET	-	EXPRESSION TAG	UNP P73922
A	-12	ALA	-	EXPRESSION TAG	UNP P73922
A	-11	SER	-	EXPRESSION TAG	UNP P73922

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	EXPRESSION TAG	UNP P73922
A	-9	THR	-	EXPRESSION TAG	UNP P73922
A	-8	GLY	-	EXPRESSION TAG	UNP P73922
A	-7	GLY	-	EXPRESSION TAG	UNP P73922
A	-6	GLN	-	EXPRESSION TAG	UNP P73922
A	-5	GLN	-	EXPRESSION TAG	UNP P73922
A	-4	MET	-	EXPRESSION TAG	UNP P73922
A	-3	GLY	-	EXPRESSION TAG	UNP P73922
A	-2	ARG	-	EXPRESSION TAG	UNP P73922
A	-1	GLY	-	EXPRESSION TAG	UNP P73922
A	0	SER	-	EXPRESSION TAG	UNP P73922
A	1	VAL	-	EXPRESSION TAG	UNP P73922
C	-33	MET	-	EXPRESSION TAG	UNP P73922
C	-32	GLY	-	EXPRESSION TAG	UNP P73922
C	-31	SER	-	EXPRESSION TAG	UNP P73922
C	-30	SER	-	EXPRESSION TAG	UNP P73922
C	-29	HIS	-	EXPRESSION TAG	UNP P73922
C	-28	HIS	-	EXPRESSION TAG	UNP P73922
C	-27	HIS	-	EXPRESSION TAG	UNP P73922
C	-26	HIS	-	EXPRESSION TAG	UNP P73922
C	-25	HIS	-	EXPRESSION TAG	UNP P73922
C	-24	HIS	-	EXPRESSION TAG	UNP P73922
C	-23	SER	-	EXPRESSION TAG	UNP P73922
C	-22	SER	-	EXPRESSION TAG	UNP P73922
C	-21	GLY	-	EXPRESSION TAG	UNP P73922
C	-20	LEU	-	EXPRESSION TAG	UNP P73922
C	-19	VAL	-	EXPRESSION TAG	UNP P73922
C	-18	PRO	-	EXPRESSION TAG	UNP P73922
C	-17	ARG	-	EXPRESSION TAG	UNP P73922
C	-16	GLY	-	EXPRESSION TAG	UNP P73922
C	-15	SER	-	EXPRESSION TAG	UNP P73922
C	-14	HIS	-	EXPRESSION TAG	UNP P73922
C	-13	MET	-	EXPRESSION TAG	UNP P73922
C	-12	ALA	-	EXPRESSION TAG	UNP P73922
C	-11	SER	-	EXPRESSION TAG	UNP P73922
C	-10	MET	-	EXPRESSION TAG	UNP P73922
C	-9	THR	-	EXPRESSION TAG	UNP P73922
C	-8	GLY	-	EXPRESSION TAG	UNP P73922
C	-7	GLY	-	EXPRESSION TAG	UNP P73922
C	-6	GLN	-	EXPRESSION TAG	UNP P73922
C	-5	GLN	-	EXPRESSION TAG	UNP P73922
C	-4	MET	-	EXPRESSION TAG	UNP P73922

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	EXPRESSION TAG	UNP P73922
C	-2	ARG	-	EXPRESSION TAG	UNP P73922
C	-1	GLY	-	EXPRESSION TAG	UNP P73922
C	0	SER	-	EXPRESSION TAG	UNP P73922
C	1	VAL	-	EXPRESSION TAG	UNP P73922
D	-33	MET	-	EXPRESSION TAG	UNP P73922
D	-32	GLY	-	EXPRESSION TAG	UNP P73922
D	-31	SER	-	EXPRESSION TAG	UNP P73922
D	-30	SER	-	EXPRESSION TAG	UNP P73922
D	-29	HIS	-	EXPRESSION TAG	UNP P73922
D	-28	HIS	-	EXPRESSION TAG	UNP P73922
D	-27	HIS	-	EXPRESSION TAG	UNP P73922
D	-26	HIS	-	EXPRESSION TAG	UNP P73922
D	-25	HIS	-	EXPRESSION TAG	UNP P73922
D	-24	HIS	-	EXPRESSION TAG	UNP P73922
D	-23	SER	-	EXPRESSION TAG	UNP P73922
D	-22	SER	-	EXPRESSION TAG	UNP P73922
D	-21	GLY	-	EXPRESSION TAG	UNP P73922
D	-20	LEU	-	EXPRESSION TAG	UNP P73922
D	-19	VAL	-	EXPRESSION TAG	UNP P73922
D	-18	PRO	-	EXPRESSION TAG	UNP P73922
D	-17	ARG	-	EXPRESSION TAG	UNP P73922
D	-16	GLY	-	EXPRESSION TAG	UNP P73922
D	-15	SER	-	EXPRESSION TAG	UNP P73922
D	-14	HIS	-	EXPRESSION TAG	UNP P73922
D	-13	MET	-	EXPRESSION TAG	UNP P73922
D	-12	ALA	-	EXPRESSION TAG	UNP P73922
D	-11	SER	-	EXPRESSION TAG	UNP P73922
D	-10	MET	-	EXPRESSION TAG	UNP P73922
D	-9	THR	-	EXPRESSION TAG	UNP P73922
D	-8	GLY	-	EXPRESSION TAG	UNP P73922
D	-7	GLY	-	EXPRESSION TAG	UNP P73922
D	-6	GLN	-	EXPRESSION TAG	UNP P73922
D	-5	GLN	-	EXPRESSION TAG	UNP P73922
D	-4	MET	-	EXPRESSION TAG	UNP P73922
D	-3	GLY	-	EXPRESSION TAG	UNP P73922
D	-2	ARG	-	EXPRESSION TAG	UNP P73922
D	-1	GLY	-	EXPRESSION TAG	UNP P73922
D	0	SER	-	EXPRESSION TAG	UNP P73922
D	1	VAL	-	EXPRESSION TAG	UNP P73922

- Molecule 2 is a protein called D-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7-bisphosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	349	Total	C	N	O	S	0	1	0
			2556	1584	451	499	22			

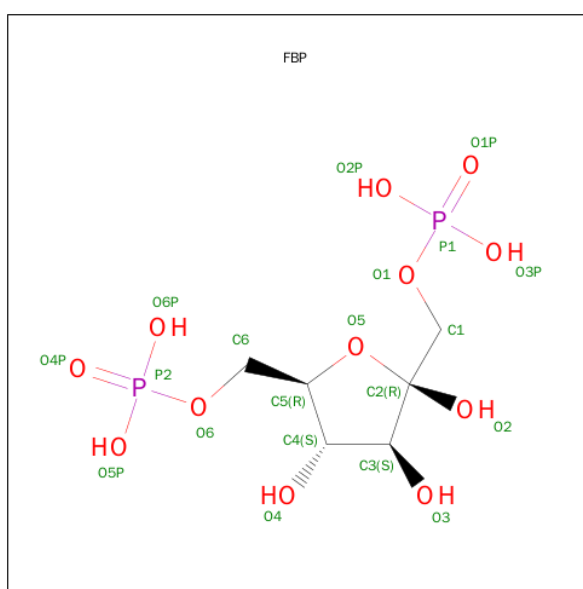
There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-33	MET	-	EXPRESSION TAG	UNP P73922
B	-32	GLY	-	EXPRESSION TAG	UNP P73922
B	-31	SER	-	EXPRESSION TAG	UNP P73922
B	-30	SER	-	EXPRESSION TAG	UNP P73922
B	-29	HIS	-	EXPRESSION TAG	UNP P73922
B	-28	HIS	-	EXPRESSION TAG	UNP P73922
B	-27	HIS	-	EXPRESSION TAG	UNP P73922
B	-26	HIS	-	EXPRESSION TAG	UNP P73922
B	-25	HIS	-	EXPRESSION TAG	UNP P73922
B	-24	HIS	-	EXPRESSION TAG	UNP P73922
B	-23	SER	-	EXPRESSION TAG	UNP P73922
B	-22	SER	-	EXPRESSION TAG	UNP P73922
B	-21	GLY	-	EXPRESSION TAG	UNP P73922
B	-20	LEU	-	EXPRESSION TAG	UNP P73922
B	-19	VAL	-	EXPRESSION TAG	UNP P73922
B	-18	PRO	-	EXPRESSION TAG	UNP P73922
B	-17	ARG	-	EXPRESSION TAG	UNP P73922
B	-16	GLY	-	EXPRESSION TAG	UNP P73922
B	-15	SER	-	EXPRESSION TAG	UNP P73922
B	-14	HIS	-	EXPRESSION TAG	UNP P73922
B	-13	MET	-	EXPRESSION TAG	UNP P73922
B	-12	ALA	-	EXPRESSION TAG	UNP P73922
B	-11	SER	-	EXPRESSION TAG	UNP P73922
B	-10	MET	-	EXPRESSION TAG	UNP P73922
B	-9	THR	-	EXPRESSION TAG	UNP P73922
B	-8	GLY	-	EXPRESSION TAG	UNP P73922
B	-7	GLY	-	EXPRESSION TAG	UNP P73922
B	-6	GLN	-	EXPRESSION TAG	UNP P73922
B	-5	GLN	-	EXPRESSION TAG	UNP P73922
B	-4	MET	-	EXPRESSION TAG	UNP P73922
B	-3	GLY	-	EXPRESSION TAG	UNP P73922
B	-2	ARG	-	EXPRESSION TAG	UNP P73922
B	-1	GLY	-	EXPRESSION TAG	UNP P73922
B	0	SER	-	EXPRESSION TAG	UNP P73922
B	1	VAL	-	EXPRESSION TAG	UNP P73922

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	3	Total Mg 3 3	0	0
3	A	3	Total Mg 3 3	0	0
3	D	3	Total Mg 3 3	0	0
3	C	3	Total Mg 3 3	0	0

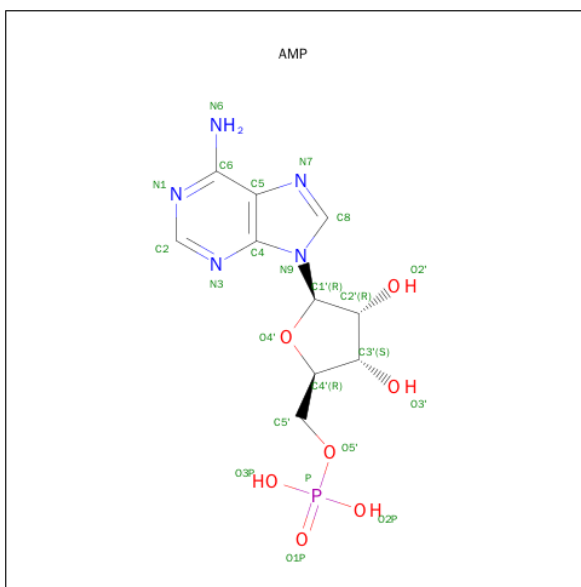
- Molecule 4 is SUGAR (BETA-FRUCTOSE-1,6-DIPHOSPHATE) (three-letter code: FBP) (formula:  $C_6H_{14}O_{12}P_2$ ).



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

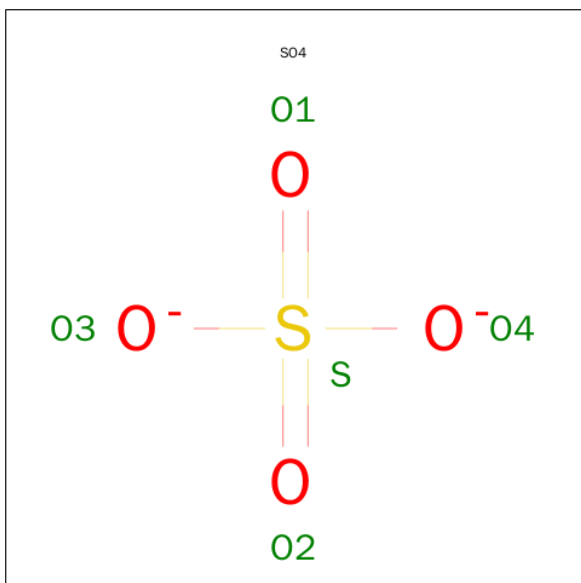
- Molecule 5 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula:  $C_{10}H_{14}N_5O_7P$ ).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
5	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
5	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
5	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 6 is SULFATE ION (three-letter code: SO<sub>4</sub>) (formula: O<sub>4</sub>S).

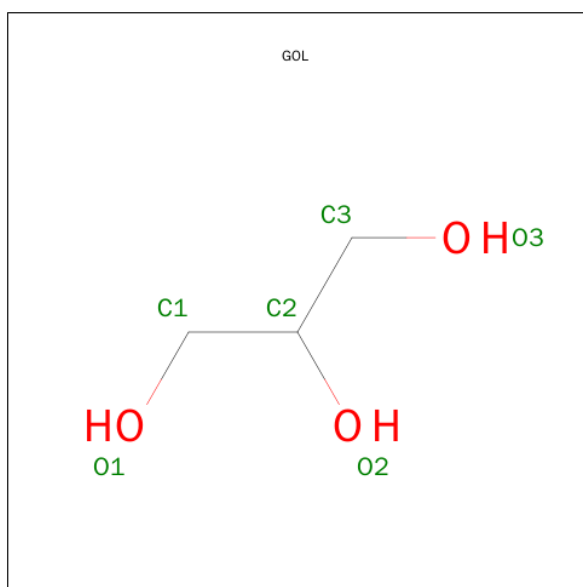


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0
6	A	1	Total O S 5 4 1	0	0
6	B	1	Total O S 5 4 1	0	0
6	B	1	Total O S 5 4 1	0	0
6	B	1	Total O S 5 4 1	0	0
6	C	1	Total O S 5 4 1	0	0
6	C	1	Total O S 5 4 1	0	0
6	C	1	Total O S 5 4 1	0	0
6	D	1	Total O S 5 4 1	0	0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

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total Cl 1 1	0	0
7	D	1	Total Cl 1 1	0	0
7	C	4	Total Cl 4 4	0	0

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			6	3	3		

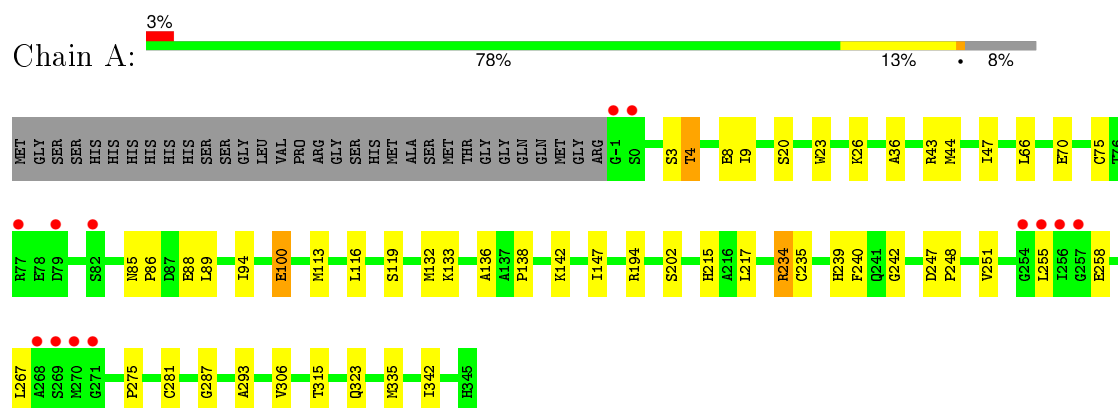
- Molecule 9 is water.

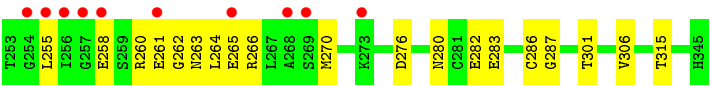
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	194	Total	O	0	0
			194	194		
9	B	214	Total	O	0	0
			214	214		
9	C	177	Total	O	0	0
			177	177		
9	D	185	Total	O	0	0
			185	185		

### 3 Residue-property plots [i](#)

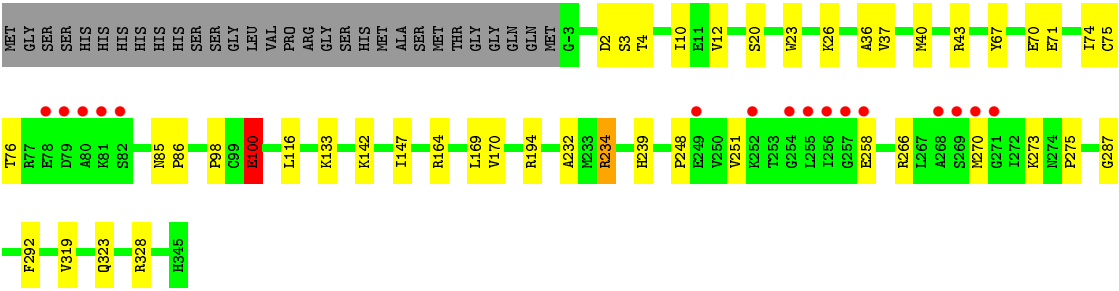
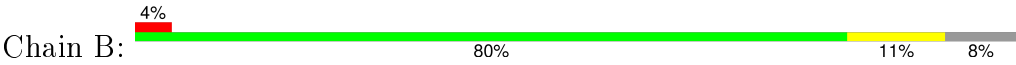
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

- Molecule 1: D-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7-bisphosphatase





● Molecule 2: D-fructose 1,6-bisphosphatase class 2/sedoheptulose 1,7-bisphosphatase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	145.22Å 145.22Å 169.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	25.72 – 2.40 25.72 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.2 (25.72-2.40) 99.2 (25.72-2.40)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.81 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, $R_{free}$	0.166 , 0.207 0.152 , 0.199	Depositor DCC
$R_{free}$ test set	3937 reflections (5.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	24.7	Xtriage
Anisotropy	0.473	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 43.4	EDS
Estimated twinning fraction	0.031 for h,-h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 78132 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11262	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% 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

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CSO, FBP, CL, MG, SO4, 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	0.42	0/2590	0.56	0/3500
1	C	0.46	1/2587 (0.0%)	0.57	0/3496
1	D	0.43	1/2621 (0.0%)	0.53	0/3542
2	B	0.42	1/2577 (0.0%)	0.54	0/3480
All	All	0.43	3/10375 (0.0%)	0.55	0/14018

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	281	CYS	CB-SG	-7.25	1.70	1.82
1	D	100	GLU	CD-OE1	-5.91	1.19	1.25
2	B	100	GLU	CD-OE1	-5.61	1.19	1.25

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 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	2556	0	2526	40	0
1	C	2552	0	2511	38	1
1	D	2577	0	2544	48	0
2	B	2556	0	2513	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
4	A	20	0	10	0	0
4	B	20	0	10	0	0
4	C	20	0	10	0	0
4	D	20	0	10	2	0
5	A	23	0	12	1	0
5	B	23	0	12	0	0
5	C	23	0	12	0	0
5	D	23	0	12	2	0
6	A	15	0	0	0	0
6	B	15	0	0	0	0
6	C	15	0	0	2	0
6	D	10	0	0	0	0
7	A	1	0	0	0	0
7	C	4	0	0	0	0
7	D	1	0	0	0	0
8	C	6	0	8	1	0
9	A	194	0	0	2	0
9	B	214	0	0	3	0
9	C	177	0	0	5	0
9	D	185	0	0	4	1
All	All	11262	0	10190	158	1

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 8.

All (158) 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:132:MET:HE3	1:A:242:GLY:HA3	1.38	1.04
1:D:263:ASN:HA	1:D:266:ARG:HD2	1.47	0.93
1:C:263:ASN:HA	1:C:266:ARG:HD3	1.51	0.91
1:A:132:MET:CE	1:A:242:GLY:HA3	2.00	0.90
1:A:3:SER:HA	1:A:323:GLN:OE1	1.78	0.83
1:C:181:GLU:HG2	9:C:432:HOH:O	1.81	0.78
2:B:71:GLU:HB3	2:B:76:THR:HG21	1.66	0.77
2:B:170:VAL:HG11	2:B:194:ARG:NH1	2.03	0.73
1:C:44:MET:HE2	1:C:94:ILE:HD13	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:150:SER:OG	1:D:153[A]:GLU:HG3	1.90	0.71
9:A:405:HOH:O	2:B:26:LYS:HE3	1.91	0.70
1:C:266:ARG:O	1:C:270:MET:HG3	1.92	0.69
1:D:132:MET:CE	1:D:242:GLY:HA3	2.22	0.69
1:C:44:MET:CE	1:C:94:ILE:HG21	2.25	0.67
2:B:71:GLU:HB3	2:B:76:THR:CG2	2.26	0.66
1:A:248:PRO:HG3	1:A:258:GLU:HG2	1.79	0.65
1:D:286:CYS:SG	9:D:521:HOH:O	2.55	0.65
1:C:4:THR:HG22	9:C:707:HOH:O	1.98	0.64
1:A:234:ARG:HD2	9:A:518:HOH:O	2.00	0.62
1:A:132:MET:HE1	1:A:240:PHE:HE2	1.63	0.62
1:D:260:ARG:NH1	1:D:264:LEU:HD11	2.17	0.60
1:C:44:MET:HE2	1:C:94:ILE:HG21	1.83	0.60
1:D:170:VAL:HG11	1:D:194:ARG:NH1	2.17	0.59
1:D:194:ARG:NH1	1:D:213:ASN:O	2.31	0.59
1:A:255:LEU:HD23	1:A:258:GLU:HA	1.83	0.59
1:C:3:SER:HA	1:C:323:GLN:OE1	2.02	0.59
1:D:194:ARG:NH2	9:D:754:HOH:O	2.34	0.59
1:A:44:MET:HE2	1:A:94:ILE:HG21	1.84	0.59
2:B:170:VAL:HG11	2:B:194:ARG:HH11	1.68	0.57
1:D:261:GLU:HA	1:D:264:LEU:HD12	1.87	0.57
1:D:132:MET:HE2	1:D:242:GLY:HA3	1.86	0.56
1:D:138:PRO:HD3	1:D:215:HIS:O	2.05	0.56
1:D:234:ARG:NE	9:D:395:HOH:O	2.37	0.56
2:B:116:LEU:HD12	2:B:116:LEU:C	2.26	0.56
1:A:194:ARG:HD3	9:B:693:HOH:O	2.05	0.55
1:D:100:GLU:O	1:D:100:GLU:HG3	2.06	0.54
1:D:132:MET:HE3	1:D:242:GLY:HA3	1.90	0.54
2:B:234:ARG:NH2	2:B:287:GLY:O	2.37	0.54
2:B:133:LYS:HE2	2:B:147:ILE:HG12	1.90	0.53
1:D:37:VAL:HG22	1:D:98:PRO:HG2	1.90	0.53
1:D:255:LEU:O	1:D:258:GLU:HB2	2.08	0.53
1:C:44:MET:HE1	1:C:94:ILE:HG21	1.90	0.52
1:D:142:LYS:HA	1:D:239:HIS:HB2	1.89	0.52
2:B:71:GLU:CB	2:B:76:THR:HG21	2.38	0.52
1:A:43:ARG:NH1	1:A:43:ARG:O	2.41	0.52
1:A:75:CYS:HB3	1:A:89:LEU:HD23	1.90	0.52
8:C:358:GOL:H12	9:C:385:HOH:O	2.10	0.51
1:A:100:GLU:HG3	1:A:100:GLU:O	2.11	0.51
1:D:44:MET:HE1	1:D:94:ILE:HG21	1.92	0.51
1:A:267:LEU:HD13	1:A:275:PRO:HB3	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:20:SER:HB2	1:C:36:ALA:HB2	1.93	0.51
1:D:132:MET:HE1	1:D:240:PHE:CE2	2.46	0.50
1:D:261:GLU:O	1:D:265:GLU:HG3	2.11	0.50
5:A:349:AMP:O1P	2:B:164:ARG:NH2	2.41	0.50
2:B:234:ARG:HD3	9:B:745:HOH:O	2.11	0.50
1:D:44:MET:CE	1:D:94:ILE:HG21	2.42	0.50
1:C:164:ARG:HD2	1:C:169:LEU:HD23	1.94	0.50
1:D:53:ILE:HD13	1:D:66:LEU:HA	1.94	0.50
2:B:194:ARG:NH2	9:B:489:HOH:O	2.45	0.49
1:A:234:ARG:HG3	1:A:235:CYS:N	2.27	0.49
1:A:44:MET:CE	1:A:94:ILE:HG21	2.42	0.49
1:C:312:GLY:HA2	1:C:336:LYS:HG2	1.94	0.49
2:B:164:ARG:HD2	2:B:169:LEU:HD23	1.95	0.49
1:A:113:MET:HE3	1:A:202:SER:HB2	1.95	0.49
1:A:234:ARG:NH2	1:A:287:GLY:O	2.38	0.48
2:B:85:ASN:HB2	2:B:86:PRO:HD2	1.95	0.48
1:C:113:MET:HE3	1:C:202:SER:HB2	1.95	0.48
1:C:77:ARG:NH2	9:C:483:HOH:O	2.46	0.48
1:A:132:MET:HE1	1:A:240:PHE:CE2	2.47	0.48
1:D:42:GLU:HA	9:D:429:HOH:O	2.13	0.48
1:C:248:PRO:HA	1:C:251:VAL:O	2.12	0.48
2:B:133:LYS:HG2	2:B:147:ILE:HD11	1.94	0.48
1:D:119:SER:OG	1:D:287:GLY:HA3	2.14	0.48
1:C:34:GLN:NE2	1:C:38:GLU:OE1	2.34	0.48
1:C:138:PRO:HD3	1:C:215:HIS:O	2.14	0.48
1:D:255:LEU:CB	1:D:258:GLU:HB2	2.44	0.47
1:C:142:LYS:HA	1:C:239:HIS:HB2	1.96	0.47
1:D:23:TRP:HA	1:D:26:LYS:HG3	1.95	0.47
2:B:23:TRP:HA	2:B:26:LYS:HD2	1.96	0.47
1:C:9:ILE:HD12	1:C:293:ALA:HB2	1.97	0.47
2:B:328:ARG:NH2	1:C:14:GLU:OE2	2.46	0.47
2:B:100:GLU:HG3	2:B:100:GLU:O	2.15	0.47
1:A:335:MET:CE	1:A:342:ILE:HD13	2.45	0.46
2:B:266:ARG:O	2:B:270:MET:HG3	2.16	0.46
1:C:10:ILE:HG12	1:C:319:VAL:HG21	1.96	0.46
1:D:116:LEU:HD12	1:D:116:LEU:C	2.36	0.46
1:D:248:PRO:HB3	1:D:252:LYS:HG2	1.98	0.46
1:D:132:MET:CE	1:D:240:PHE:HE2	2.29	0.46
1:A:248:PRO:HA	1:A:251:VAL:O	2.16	0.45
2:B:142:LYS:HA	2:B:239:HIS:HB2	1.96	0.45
1:D:85:ASN:HB2	1:D:86:PRO:CD	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:132:MET:HE1	1:D:240:PHE:HE2	1.80	0.45
1:A:133:LYS:HG2	1:A:147:ILE:HD11	1.99	0.45
1:C:263:ASN:CA	1:C:266:ARG:HD3	2.35	0.45
1:C:94:ILE:HG12	1:C:118:ILE:HG12	1.99	0.45
1:A:142:LYS:HA	1:A:239:HIS:HB2	1.99	0.44
2:B:74:ILE:C	2:B:76:THR:H	2.20	0.44
1:A:240:PHE:HB3	1:A:281:CYS:HB3	1.98	0.44
1:C:11:GLU:OE2	1:C:43:ARG:NH2	2.49	0.44
2:B:248:PRO:HB3	2:B:258:GLU:OE1	2.18	0.44
1:D:225:GLU:N	1:D:225:GLU:OE2	2.47	0.44
1:D:306:VAL:HG22	1:D:315:THR:HG22	1.99	0.44
1:A:4:THR:HG22	1:A:8:GLU:OE1	2.17	0.44
2:B:248:PRO:HA	2:B:251:VAL:O	2.18	0.43
2:B:67:TYR:CE1	2:B:70:GLU:HB2	2.52	0.43
1:C:164:ARG:HH22	5:D:349:AMP:P	2.40	0.43
1:D:4:THR:HG22	1:D:8:GLU:OE1	2.19	0.43
1:C:234:ARG:HB2	1:C:281:CYS:SG	2.58	0.43
1:D:44:MET:HE2	1:D:94:ILE:HD13	2.01	0.43
1:A:85:ASN:OD1	1:A:88:GLU:HG3	2.18	0.43
1:C:116:LEU:HD12	1:C:116:LEU:C	2.39	0.43
1:C:251:VAL:HG23	6:C:351:SO4:O2	2.18	0.43
1:C:264:LEU:HD12	1:C:264:LEU:HA	1.86	0.43
1:D:198:ASP:OD1	4:D:350:FBP:O2	2.25	0.43
1:C:257:GLY:H	1:C:258:GLU:CB	2.32	0.43
1:A:116:LEU:HD12	1:A:116:LEU:C	2.39	0.43
1:C:25:GLY:HA3	1:D:193:VAL:O	2.19	0.43
1:D:214:ILE:HD12	1:D:301:THR:HG21	2.00	0.43
1:C:178:ARG:HD3	6:C:351:SO4:O2	2.19	0.42
1:A:9:ILE:HD12	1:A:293:ALA:HB2	2.01	0.42
1:A:132:MET:HE2	1:A:242:GLY:HA3	1.92	0.42
1:A:306:VAL:HG22	1:A:315:THR:HG22	2.02	0.42
2:B:3:SER:HA	2:B:323:GLN:OE1	2.19	0.42
1:C:164:ARG:NH2	5:D:349:AMP:O2P	2.49	0.42
2:B:2:ASP:OD2	2:B:4:THR:HB	2.20	0.42
1:D:20:SER:HB2	1:D:36:ALA:HB2	2.02	0.42
1:A:66:LEU:N	1:A:70:GLU:OE2	2.51	0.42
1:D:11:GLU:HB2	1:D:43:ARG:HH21	1.85	0.42
1:A:85:ASN:HB2	1:A:86:PRO:HD2	2.01	0.42
2:B:37:VAL:HG22	2:B:98:PRO:HG2	2.02	0.42
1:A:20:SER:HB2	1:A:36:ALA:HB2	2.02	0.42
1:C:280:ASN:HB3	9:C:741:HOH:O	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:246:TYR:OH	1:D:276:ASP:OD2	2.33	0.42
2:B:12:VAL:CG1	2:B:40:MET:HG3	2.50	0.41
1:A:44:MET:HE2	1:A:94:ILE:HD13	2.02	0.41
1:D:53:ILE:HD11	1:D:66:LEU:HD22	2.02	0.41
2:B:10:ILE:HG12	2:B:319:VAL:HG21	2.02	0.41
1:C:263:ASN:HA	1:C:266:ARG:CD	2.37	0.41
1:C:280:ASN:OD1	1:C:283:GLU:HG3	2.21	0.41
1:D:280:ASN:HB3	1:D:283:GLU:HG3	2.01	0.41
2:B:43:ARG:HD2	2:B:43:ARG:HA	1.84	0.41
1:A:119:SER:OG	1:A:287:GLY:HA3	2.21	0.41
1:A:43:ARG:HD2	1:A:43:ARG:HA	1.87	0.41
1:D:131:TYR:OH	4:D:350:FBP:O6P	2.31	0.41
2:B:20:SER:HB2	2:B:36:ALA:HB2	2.03	0.41
1:D:262:GLY:O	1:D:266:ARG:HG3	2.21	0.41
1:D:282:GLU:H	1:D:282:GLU:CD	2.24	0.41
1:A:138:PRO:HD3	1:A:215:HIS:O	2.21	0.41
2:B:232:ALA:HB2	2:B:292:PHE:CD1	2.56	0.41
1:C:156:LYS:O	1:C:159:SER:HB3	2.20	0.40
1:D:266:ARG:O	1:D:270:MET:HG3	2.21	0.40
1:A:43:ARG:HH12	1:A:47:ILE:HG13	1.86	0.40
1:D:63:ALA:HA	1:D:64:PRO:HD2	1.87	0.40
1:A:23:TRP:CE3	1:A:26:LYS:HG2	2.56	0.40
1:A:136:ALA:HB3	1:A:217:LEU:HB3	2.02	0.40
2:B:273:LYS:O	2:B:275:PRO:HD3	2.21	0.40
1:C:130:PHE:HE1	1:C:263:ASN:HB3	1.85	0.40
1:A:247:ASP:HA	1:A:248:PRO:HD3	1.85	0.40

All (1) 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:C:61:ASP:OD2	9:D:429:HOH:O[2_544]	2.18	0.02

## 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	345/379 (91%)	336 (97%)	9 (3%)	0	100	100
1	C	346/379 (91%)	334 (96%)	12 (4%)	0	100	100
1	D	348/379 (92%)	340 (98%)	8 (2%)	0	100	100
2	B	346/379 (91%)	334 (96%)	11 (3%)	1 (0%)	46	63
All	All	1385/1516 (91%)	1344 (97%)	40 (3%)	1 (0%)	56	74

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	75	CYS

### 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	267/302 (88%)	264 (99%)	3 (1%)	80	92
1	C	264/302 (87%)	263 (100%)	1 (0%)	93	98
1	D	270/302 (89%)	268 (99%)	2 (1%)	88	95
2	B	262/300 (87%)	260 (99%)	2 (1%)	86	94
All	All	1063/1206 (88%)	1055 (99%)	8 (1%)	86	94

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	THR
1	A	100	GLU
1	A	234	ARG
2	B	100	GLU
2	B	234	ARG
1	C	234	ARG
1	D	100	GLU

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Mol	Chain	Res	Type
1	D	198	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	CSO	B	281	2	3,6,7	0.60	0	1,6,8	2.47	1 (100%)
2	CSO	B	286	2	3,6,7	0.55	0	1,6,8	2.08	1 (100%)

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	CSO	B	281	2	-	0/1/5/7	0/0/0/0
2	CSO	B	286	2	-	0/1/5/7	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	281	CSO	O-C-CA	-2.47	119.06	125.49
2	B	286	CSO	O-C-CA	-2.08	120.06	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 38 ligands modelled in this entry, 18 are monoatomic - leaving 20 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	$\# Z  > 2$
5	AMP	A	349	-	20,25,25	0.86	1 (5%)	22,38,38	1.94	5 (22%)
4	FBP	A	350	3	18,20,20	1.02	1 (5%)	21,32,32	0.75	0
6	SO4	A	351	-	4,4,4	0.17	0	6,6,6	0.39	0
6	SO4	A	352	-	4,4,4	0.17	0	6,6,6	0.10	0
6	SO4	A	353	-	4,4,4	0.10	0	6,6,6	0.07	0
5	AMP	B	349	-	20,25,25	0.86	1 (5%)	22,38,38	2.02	5 (22%)
4	FBP	B	350	3	18,20,20	1.09	1 (5%)	21,32,32	0.72	0
6	SO4	B	351	-	4,4,4	0.19	0	6,6,6	0.17	0
6	SO4	B	352	-	4,4,4	0.11	0	6,6,6	0.32	0
6	SO4	B	353	-	4,4,4	0.11	0	6,6,6	0.18	0
5	AMP	C	349	-	20,25,25	0.92	1 (5%)	22,38,38	1.86	5 (22%)
4	FBP	C	350	3	18,20,20	1.04	1 (5%)	21,32,32	0.67	0
6	SO4	C	351	-	4,4,4	0.18	0	6,6,6	0.45	0
6	SO4	C	352	-	4,4,4	0.23	0	6,6,6	0.17	0
6	SO4	C	353	-	4,4,4	0.11	0	6,6,6	0.18	0
8	GOL	C	358	-	5,5,5	0.32	0	5,5,5	0.64	0
5	AMP	D	349	-	20,25,25	0.88	1 (5%)	22,38,38	1.97	4 (18%)
4	FBP	D	350	3	18,20,20	0.90	1 (5%)	21,32,32	0.78	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	SO4	D	351	-	4,4,4	0.23	0	6,6,6	0.13	0
6	SO4	D	352	-	4,4,4	0.16	0	6,6,6	0.12	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
5	AMP	A	349	-	-	0/6/26/26	0/3/3/3
4	FBP	A	350	3	-	0/13/32/32	0/1/1/1
6	SO4	A	351	-	-	0/0/0/0	0/0/0/0
6	SO4	A	352	-	-	0/0/0/0	0/0/0/0
6	SO4	A	353	-	-	0/0/0/0	0/0/0/0
5	AMP	B	349	-	-	0/6/26/26	0/3/3/3
4	FBP	B	350	3	-	0/13/32/32	0/1/1/1
6	SO4	B	351	-	-	0/0/0/0	0/0/0/0
6	SO4	B	352	-	-	0/0/0/0	0/0/0/0
6	SO4	B	353	-	-	0/0/0/0	0/0/0/0
5	AMP	C	349	-	-	0/6/26/26	0/3/3/3
4	FBP	C	350	3	-	0/13/32/32	0/1/1/1
6	SO4	C	351	-	-	0/0/0/0	0/0/0/0
6	SO4	C	352	-	-	0/0/0/0	0/0/0/0
6	SO4	C	353	-	-	0/0/0/0	0/0/0/0
8	GOL	C	358	-	-	0/4/4/4	0/0/0/0
5	AMP	D	349	-	-	0/6/26/26	0/3/3/3
4	FBP	D	350	3	-	0/13/32/32	0/1/1/1
6	SO4	D	351	-	-	0/0/0/0	0/0/0/0
6	SO4	D	352	-	-	0/0/0/0	0/0/0/0

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	350	FBP	O2-C2	2.45	1.45	1.41
5	B	349	AMP	C5-C4	2.61	1.46	1.40
5	D	349	AMP	C5-C4	2.73	1.46	1.40
5	A	349	AMP	C5-C4	2.76	1.46	1.40
5	C	349	AMP	C5-C4	2.84	1.46	1.40
4	A	350	FBP	O2-C2	2.91	1.45	1.41
4	B	350	FBP	O2-C2	3.25	1.46	1.41
4	C	350	FBP	O2-C2	3.29	1.46	1.41



All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	349	AMP	N3-C2-N1	-7.15	123.42	128.89
5	A	349	AMP	N3-C2-N1	-7.04	123.50	128.89
5	B	349	AMP	N3-C2-N1	-6.97	123.56	128.89
5	C	349	AMP	N3-C2-N1	-6.57	123.86	128.89
5	B	349	AMP	C4-C5-N7	-3.77	106.01	109.48
5	D	349	AMP	C4-C5-N7	-3.06	106.67	109.48
5	A	349	AMP	C4-C5-N7	-2.86	106.84	109.48
5	C	349	AMP	C4-C5-N7	-2.86	106.85	109.48
5	A	349	AMP	C2'-C1'-N9	-2.47	110.52	114.29
5	B	349	AMP	C2'-C1'-N9	-2.40	110.62	114.29
5	D	349	AMP	C2'-C1'-N9	-2.23	110.88	114.29
5	C	349	AMP	O3P-P-O5'	-2.23	100.13	106.56
5	A	349	AMP	C1'-N9-C4	-2.21	123.61	126.94
5	B	349	AMP	C1'-N9-C4	-2.20	123.63	126.94
5	C	349	AMP	C2'-C1'-N9	-2.05	111.16	114.29
5	B	349	AMP	O2P-P-O1P	2.34	118.11	110.58
5	D	349	AMP	O2P-P-O1P	2.34	118.13	110.58
5	C	349	AMP	O2P-P-O1P	2.36	118.17	110.58
5	A	349	AMP	O2P-P-O1P	2.45	118.46	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	349	AMP	1	0
6	C	351	SO4	2	0
8	C	358	GOL	1	0
5	D	349	AMP	2	0
4	D	350	FBP	2	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 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	347/379 (91%)	-0.41	13 (3%) 45 46	14, 22, 57, 84	0
1	C	347/379 (91%)	-0.39	13 (3%) 45 46	14, 22, 62, 98	0
1	D	346/379 (91%)	-0.34	20 (5%) 26 27	13, 24, 63, 92	0
2	B	347/379 (91%)	-0.41	16 (4%) 36 37	14, 21, 57, 87	0
All	All	1387/1516 (91%)	-0.39	62 (4%) 37 38	13, 22, 59, 98	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	257	GLY	9.0
1	D	256	ILE	7.9
1	C	254	GLY	6.5
2	B	256	ILE	6.5
1	C	256	ILE	6.1
2	B	79	ASP	5.7
1	D	257	GLY	5.4
1	D	254	GLY	5.1
1	A	255	LEU	5.1
1	C	255	LEU	4.9
1	A	82	SER	4.7
1	A	257	GLY	4.4
2	B	254	GLY	4.2
1	D	255	LEU	4.2
1	A	256	ILE	4.1
2	B	82	SER	4.0
2	B	255	LEU	3.9
1	A	-1	GLY	3.7
2	B	257	GLY	3.7
1	C	253	THR	3.7
1	D	79	ASP	3.6

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Mol	Chain	Res	Type	RSRZ
1	A	269	SER	3.6
1	C	0	SER	3.5
1	C	268	ALA	3.5
1	D	269	SER	3.5
1	D	83	PHE	3.4
1	C	266	ARG	3.3
2	B	78	GLU	3.3
1	D	62	ASP	3.2
2	B	269	SER	3.2
1	A	268	ALA	3.1
1	A	254	GLY	3.1
2	B	270	MET	3.0
1	C	269	SER	3.0
1	D	82	SER	3.0
2	B	268	ALA	3.0
1	A	79	ASP	2.9
1	C	258	GLU	2.8
1	D	60	ARG	2.8
1	D	258	GLU	2.8
2	B	80	ALA	2.7
1	C	-1	GLY	2.7
1	D	273	LYS	2.7
2	B	252	LYS	2.6
1	D	268	ALA	2.6
1	C	62	ASP	2.6
1	D	61	ASP	2.6
1	D	252	LYS	2.6
1	D	250	VAL	2.5
1	D	0	SER	2.4
1	D	261	GLU	2.4
1	A	77	ARG	2.4
2	B	258	GLU	2.3
1	C	259	SER	2.3
2	B	271	GLY	2.3
1	D	86	PRO	2.3
2	B	249	GLU	2.2
2	B	81	LYS	2.2
1	D	265	GLU	2.2
1	A	0	SER	2.1
1	A	270	MET	2.1
1	A	271	GLY	2.0

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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	CSO	B	281	7/8	0.97	0.13	-	21,25,29,42	0
2	CSO	B	286	7/8	0.98	0.10	-	20,20,25,32	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	MG	A	348	1/1	0.98	0.16	8.28	37,37,37,37	0
3	MG	B	348	1/1	0.97	0.17	5.58	35,35,35,35	0
6	SO4	C	353	5/5	0.88	0.34	3.64	47,53,75,85	0
6	SO4	A	353	5/5	0.88	0.40	2.76	52,58,85,91	0
8	GOL	C	358	6/6	0.88	0.18	2.74	29,32,36,39	0
3	MG	D	348	1/1	0.95	0.13	2.20	39,39,39,39	0
6	SO4	B	351	5/5	0.99	0.26	2.05	32,38,41,52	0
6	SO4	C	351	5/5	0.97	0.29	1.94	38,39,49,54	0
6	SO4	A	351	5/5	0.97	0.26	1.35	35,44,44,49	0
6	SO4	D	351	5/5	0.97	0.22	0.33	34,43,49,55	0
3	MG	C	348	1/1	0.95	0.11	-0.08	39,39,39,39	0
4	FBP	D	350	20/20	0.98	0.09	-0.43	19,25,30,31	0
5	AMP	C	349	23/23	0.99	0.09	-0.54	13,17,20,23	0
4	FBP	A	350	20/20	0.98	0.08	-0.55	20,24,32,32	0
4	FBP	B	350	20/20	0.98	0.08	-0.65	20,24,35,36	0
5	AMP	B	349	23/23	0.99	0.09	-0.70	12,15,18,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	AMP	D	349	23/23	0.99	0.08	-0.80	12,15,17,18	0
7	CL	C	354	1/1	0.99	0.08	-1.05	36,36,36,36	0
4	FBP	C	350	20/20	0.98	0.08	-1.26	19,25,33,34	0
5	AMP	A	349	23/23	0.99	0.08	-1.73	13,16,18,19	0
3	MG	B	346	1/1	0.92	0.20	-	43,43,43,43	0
3	MG	A	347	1/1	0.95	0.08	-	29,29,29,29	0
6	SO4	B	353	5/5	0.97	0.26	-	50,57,63,69	0
3	MG	C	347	1/1	0.91	0.14	-	34,34,34,34	0
6	SO4	C	352	5/5	0.95	0.25	-	55,60,69,73	0
3	MG	A	346	1/1	0.96	0.30	-	46,46,46,46	0
7	CL	C	357	1/1	0.88	0.10	-	58,58,58,58	0
7	CL	D	353	1/1	0.98	0.12	-	46,46,46,46	0
7	CL	C	356	1/1	0.81	0.36	-	65,65,65,65	0
3	MG	D	346	1/1	0.96	0.32	-	39,39,39,39	0
6	SO4	A	352	5/5	0.97	0.28	-	53,56,70,71	0
6	SO4	D	352	5/5	0.95	0.27	-	47,55,62,63	0
3	MG	B	347	1/1	0.98	0.06	-	31,31,31,31	0
7	CL	A	354	1/1	0.98	0.10	-	50,50,50,50	0
7	CL	C	355	1/1	0.98	0.10	-	44,44,44,44	0
6	SO4	B	352	5/5	0.94	0.23	-	48,52,67,70	0
3	MG	C	346	1/1	0.93	0.45	-	48,48,48,48	0
3	MG	D	347	1/1	0.98	0.10	-	35,35,35,35	0

## 6.5 Other polymers

There are no such residues in this entry.