



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 09:16 PM UTC

PDB ID : 2QAP / pdb\_00002qap  
Title : Fructose-1,6-bisphosphate aldolase from *Leishmania mexicana*  
Authors : Lafrance-Vanasse, J.; Sygusch, J.  
Deposited on : 2007-06-15  
Resolution : 1.59 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)

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<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  
Mogul : 2022.3.0, CSD as543be (2022)  
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

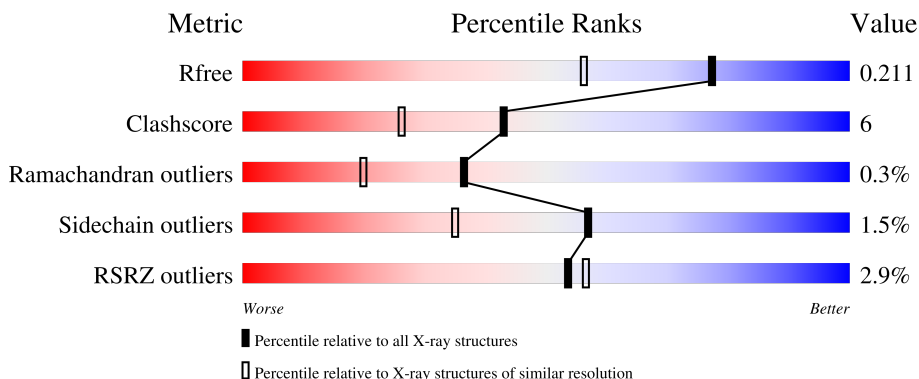
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.59 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))
$R_{free}$	180053	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	391	 80% 11% 8%
1	B	391	 7% 75% 15% 8%
1	C	391	 78% 13% 8%
1	D	391	 78% 12% 8%

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13201 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
			Total	C	N	O	S			
1	A	358	2782	1748	494	521	19	0	3	0
1	B	358	2768	1741	491	517	19	0	0	0
1	C	358	2782	1748	494	521	19	0	3	0
1	D	358	2782	1748	494	521	19	0	3	0

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP Q9U5N6
A	-18	GLY	-	expression tag	UNP Q9U5N6
A	-17	SER	-	expression tag	UNP Q9U5N6
A	-16	SER	-	expression tag	UNP Q9U5N6
A	-15	HIS	-	expression tag	UNP Q9U5N6
A	-14	HIS	-	expression tag	UNP Q9U5N6
A	-13	HIS	-	expression tag	UNP Q9U5N6
A	-12	HIS	-	expression tag	UNP Q9U5N6
A	-11	HIS	-	expression tag	UNP Q9U5N6
A	-10	HIS	-	expression tag	UNP Q9U5N6
A	-9	SER	-	expression tag	UNP Q9U5N6
A	-8	SER	-	expression tag	UNP Q9U5N6
A	-7	GLY	-	expression tag	UNP Q9U5N6
A	-6	LEU	-	expression tag	UNP Q9U5N6
A	-5	VAL	-	expression tag	UNP Q9U5N6
A	-4	PRO	-	expression tag	UNP Q9U5N6
A	-3	ARG	-	expression tag	UNP Q9U5N6
A	-2	GLY	-	expression tag	UNP Q9U5N6
A	-1	SER	-	expression tag	UNP Q9U5N6
A	0	HIS	-	expression tag	UNP Q9U5N6
B	-19	MET	-	expression tag	UNP Q9U5N6

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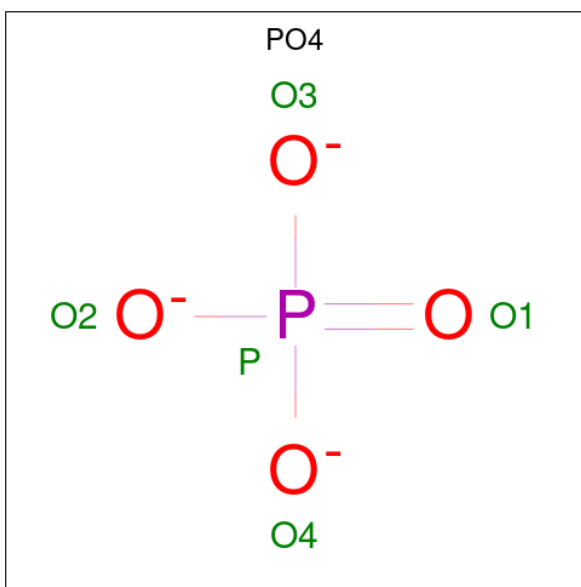
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	expression tag	UNP Q9U5N6
B	-17	SER	-	expression tag	UNP Q9U5N6
B	-16	SER	-	expression tag	UNP Q9U5N6
B	-15	HIS	-	expression tag	UNP Q9U5N6
B	-14	HIS	-	expression tag	UNP Q9U5N6
B	-13	HIS	-	expression tag	UNP Q9U5N6
B	-12	HIS	-	expression tag	UNP Q9U5N6
B	-11	HIS	-	expression tag	UNP Q9U5N6
B	-10	HIS	-	expression tag	UNP Q9U5N6
B	-9	SER	-	expression tag	UNP Q9U5N6
B	-8	SER	-	expression tag	UNP Q9U5N6
B	-7	GLY	-	expression tag	UNP Q9U5N6
B	-6	LEU	-	expression tag	UNP Q9U5N6
B	-5	VAL	-	expression tag	UNP Q9U5N6
B	-4	PRO	-	expression tag	UNP Q9U5N6
B	-3	ARG	-	expression tag	UNP Q9U5N6
B	-2	GLY	-	expression tag	UNP Q9U5N6
B	-1	SER	-	expression tag	UNP Q9U5N6
B	0	HIS	-	expression tag	UNP Q9U5N6
C	-19	MET	-	expression tag	UNP Q9U5N6
C	-18	GLY	-	expression tag	UNP Q9U5N6
C	-17	SER	-	expression tag	UNP Q9U5N6
C	-16	SER	-	expression tag	UNP Q9U5N6
C	-15	HIS	-	expression tag	UNP Q9U5N6
C	-14	HIS	-	expression tag	UNP Q9U5N6
C	-13	HIS	-	expression tag	UNP Q9U5N6
C	-12	HIS	-	expression tag	UNP Q9U5N6
C	-11	HIS	-	expression tag	UNP Q9U5N6
C	-10	HIS	-	expression tag	UNP Q9U5N6
C	-9	SER	-	expression tag	UNP Q9U5N6
C	-8	SER	-	expression tag	UNP Q9U5N6
C	-7	GLY	-	expression tag	UNP Q9U5N6
C	-6	LEU	-	expression tag	UNP Q9U5N6
C	-5	VAL	-	expression tag	UNP Q9U5N6
C	-4	PRO	-	expression tag	UNP Q9U5N6
C	-3	ARG	-	expression tag	UNP Q9U5N6
C	-2	GLY	-	expression tag	UNP Q9U5N6
C	-1	SER	-	expression tag	UNP Q9U5N6
C	0	HIS	-	expression tag	UNP Q9U5N6
D	-19	MET	-	expression tag	UNP Q9U5N6
D	-18	GLY	-	expression tag	UNP Q9U5N6
D	-17	SER	-	expression tag	UNP Q9U5N6

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	expression tag	UNP Q9U5N6
D	-15	HIS	-	expression tag	UNP Q9U5N6
D	-14	HIS	-	expression tag	UNP Q9U5N6
D	-13	HIS	-	expression tag	UNP Q9U5N6
D	-12	HIS	-	expression tag	UNP Q9U5N6
D	-11	HIS	-	expression tag	UNP Q9U5N6
D	-10	HIS	-	expression tag	UNP Q9U5N6
D	-9	SER	-	expression tag	UNP Q9U5N6
D	-8	SER	-	expression tag	UNP Q9U5N6
D	-7	GLY	-	expression tag	UNP Q9U5N6
D	-6	LEU	-	expression tag	UNP Q9U5N6
D	-5	VAL	-	expression tag	UNP Q9U5N6
D	-4	PRO	-	expression tag	UNP Q9U5N6
D	-3	ARG	-	expression tag	UNP Q9U5N6
D	-2	GLY	-	expression tag	UNP Q9U5N6
D	-1	SER	-	expression tag	UNP Q9U5N6
D	0	HIS	-	expression tag	UNP Q9U5N6

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	P		
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0
2	A	1	5	4	1	0	0

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

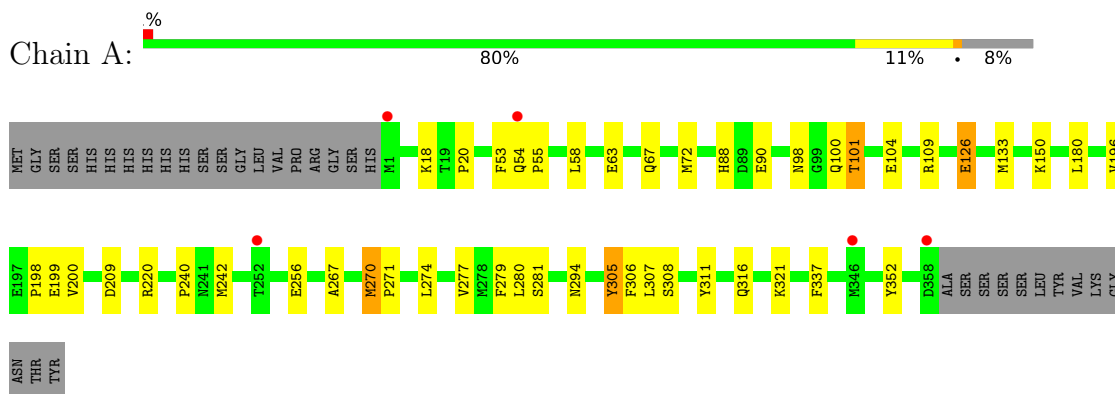
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	533	Total	O	0	0
			533	533		
3	B	437	Total	O	0	0
			437	437		
3	C	561	Total	O	0	0
			561	561		
3	D	501	Total	O	0	0
			501	501		

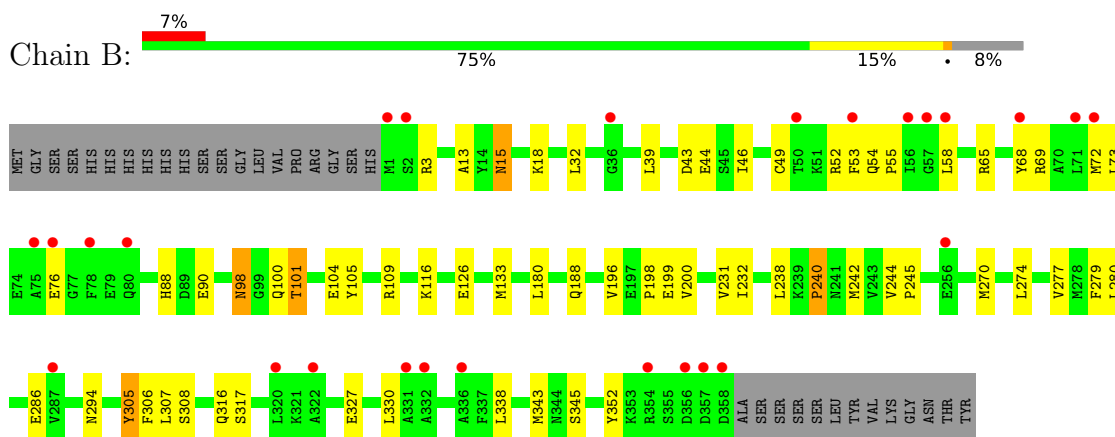
### 3 Residue-property plots [i](#)

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.

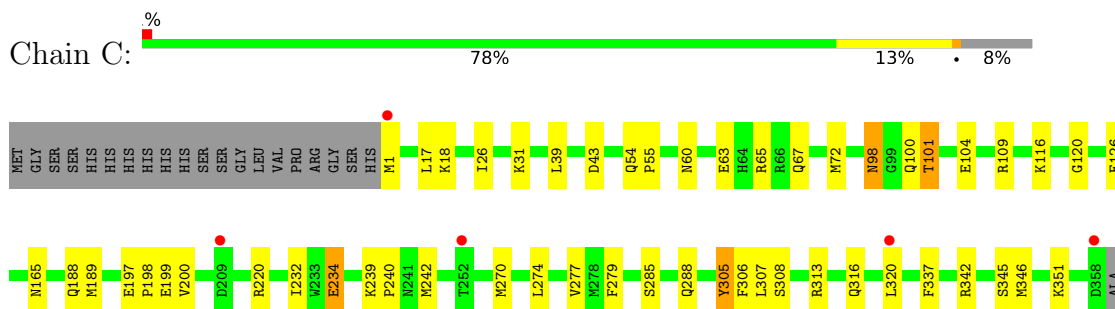
- Molecule 1: Fructose-1,6-bisphosphate aldolase



- Molecule 1: Fructose-1,6-bisphosphate aldolase



- Molecule 1: Fructose-1,6-bisphosphate aldolase



SER  
SER  
SER  
SER  
LEU  
TYR  
VAL  
VAL  
LYS  
GLY  
ASN  
THR  
TYR

• Molecule 1: Fructose-1,6-bisphosphate aldolase

Chain D: %

MET  
GLY  
SER  
SER  
SER  
HIS  
HIS  
HIS  
HIS  
HIS  
HIS  
HIS  
SER  
SER  
SER  
GLY  
LEU  
VAL  
PRO  
ARG  
GLY  
SER  
HIS  
HIS  
M1  
R16  
E22  
I26  
R52  
F53  
Q54  
P55  
Y68  
L71  
M72  
T101  
E104  
K116  
P123  
L124  
L125  
M133  
Y140  
E197  
P198  
E199  
V200  
W219  
R220

I232  
K239  
P240  
R241  
M242  
T252  
E256  
M270  
P271  
A272  
M273  
L274  
V277  
M278  
F279  
L280  
S281  
S285  
Q288  
Y305  
F306  
L307  
Y311  
Q316  
L320  
W323  
F337  
L338  
H339  
M343  
R344  
S345  
M346  
L349  
S356  
D357  
D358  
ALA  
SER  
SER  
SER  
SER  
SER  
TYR

VAL  
LYS  
GLY  
ASN  
THR  
TYR

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	85.78Å 117.31Å 160.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.59 20.00 – 1.59	Depositor EDS
% Data completeness (in resolution range)	75.8 (20.00-1.59) 82.7 (20.00-1.59)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.43 (at 1.59Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.173 , 0.203 0.180 , 0.211	Depositor DCC
$R_{free}$ test set	9351 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	16.7	Xtrriage
Anisotropy	0.665	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 49.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	13201	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.34	0/2837	0.82	8/3832 (0.2%)
1	B	0.32	0/2823	0.81	9/3814 (0.2%)
1	C	0.36	0/2837	0.85	9/3832 (0.2%)
1	D	0.35	0/2837	0.84	9/3832 (0.2%)
All	All	0.34	0/11334	0.83	35/15310 (0.2%)

There are no bond length outliers.

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	242	MET	N-CA-C	-6.98	101.12	110.55
1	C	242	MET	N-CA-C	-6.47	101.81	110.55
1	A	270	MET	N-CA-C	6.23	117.50	109.65
1	D	101	THR	N-CA-C	-6.20	102.35	110.53
1	C	101	THR	N-CA-C	-6.17	102.38	110.53

There are no chirality outliers.

There are no planarity outliers.

### 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	2782	0	2787	30	0
1	B	2768	0	2777	42	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2782	0	2787	35	0
1	D	2782	0	2787	34	0
2	A	15	0	0	0	0
2	B	10	0	0	0	0
2	C	15	0	0	1	0
2	D	15	0	0	0	0
3	A	533	0	0	9	0
3	B	437	0	0	6	0
3	C	561	0	0	8	0
3	D	501	0	0	5	0
All	All	13201	0	11138	139	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 6.

The worst 5 of 139 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:71:LEU:HG	1:D:72:MET:HE3	1.24	1.18
1:C:72:MET:HE1	1:C:316:GLN:HG2	1.53	0.88
1:A:72:MET:HE1	1:A:316:GLN:HG2	1.65	0.79
1:B:188:GLN:HE22	1:B:232:ILE:H	1.31	0.77
1:C:72:MET:CE	1:C:316:GLN:HG2	2.16	0.76

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	359/391 (92%)	351 (98%)	7 (2%)	1 (0%)	36 20
1	B	356/391 (91%)	347 (98%)	8 (2%)	1 (0%)	36 20

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	C	359/391 (92%)	351 (98%)	7 (2%)	1 (0%)	36 20
1	D	359/391 (92%)	352 (98%)	6 (2%)	1 (0%)	36 20
All	All	1433/1564 (92%)	1401 (98%)	28 (2%)	4 (0%)	36 20

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	198	PRO
1	B	198	PRO
1	C	198	PRO
1	D	198	PRO

### 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	294/321 (92%)	290 (99%)	4 (1%)	59 38
1	B	293/321 (91%)	289 (99%)	4 (1%)	59 38
1	C	294/321 (92%)	289 (98%)	5 (2%)	53 30
1	D	294/321 (92%)	289 (98%)	5 (2%)	53 30
All	All	1175/1284 (92%)	1157 (98%)	18 (2%)	57 35

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	116	LYS
1	D	305	TYR
1	D	240	PRO
1	C	39	LEU
1	D	72	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	67	GLN
1	C	188	GLN
1	C	165	ASN
1	C	288	GLN
1	B	67	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](#)

11 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	PO4	C	3008	-	4,4,4	1.77	1 (25%)	6,6,6	0.46	0
2	PO4	D	3009	-	4,4,4	1.76	1 (25%)	6,6,6	0.47	0
2	PO4	C	3006	-	4,4,4	1.77	0	6,6,6	0.45	0
2	PO4	A	3001	-	4,4,4	1.77	2 (50%)	6,6,6	0.46	0
2	PO4	D	3011	-	4,4,4	1.74	1 (25%)	6,6,6	0.46	0
2	PO4	D	3010	-	4,4,4	1.73	1 (25%)	6,6,6	0.46	0
2	PO4	A	3002	-	4,4,4	1.73	0	6,6,6	0.47	0
2	PO4	C	3007	-	4,4,4	1.74	1 (25%)	6,6,6	0.47	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	PO4	B	3004	-	4,4,4	1.75	0	6,6,6	0.46	0
2	PO4	A	3003	-	4,4,4	1.78	2 (50%)	6,6,6	0.46	0
2	PO4	B	3005	-	4,4,4	1.72	2 (50%)	6,6,6	0.47	0

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3008	PO4	P-O4	-2.10	1.48	1.54
2	A	3003	PO4	P-O2	-2.06	1.48	1.54
2	A	3003	PO4	P-O3	-2.05	1.48	1.54
2	B	3005	PO4	P-O2	-2.02	1.48	1.54
2	A	3001	PO4	P-O4	-2.02	1.48	1.54

There are no bond angle outliers.

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
2	C	3006	PO4	1	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 [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	358/391 (91%)	0.04	5 (1%) 73 78	11, 20, 37, 56	3 (0%)
1	B	358/391 (91%)	0.62	26 (7%) 21 21	13, 25, 48, 69	0
1	C	358/391 (91%)	-0.18	5 (1%) 73 78	10, 18, 29, 54	3 (0%)
1	D	358/391 (91%)	-0.14	5 (1%) 73 78	11, 18, 31, 58	3 (0%)
All	All	1432/1564 (91%)	0.09	41 (2%) 53 56	10, 20, 39, 69	9 (0%)

The worst 5 of 41 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	320	LEU	4.2
1	D	1	MET	4.0
1	A	1	MET	3.6
1	C	358	ASP	3.4
1	B	358	ASP	3.4

### 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](#)

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. 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	B-factors( $\text{\AA}^2$ )	Q<0.9
2	PO4	A	3002	5/5	0.57	0.25	25,27,28,28	5
2	PO4	B	3004	5/5	0.78	0.19	39,40,40,40	5
2	PO4	A	3001	5/5	0.80	0.23	33,33,33,34	5
2	PO4	C	3006	5/5	0.81	0.24	37,37,38,38	5
2	PO4	C	3007	5/5	0.85	0.14	20,24,25,25	5
2	PO4	D	3010	5/5	0.85	0.12	22,25,26,26	5
2	PO4	D	3009	5/5	0.87	0.14	34,34,35,36	5
2	PO4	B	3005	5/5	0.87	0.13	29,30,32,33	5
2	PO4	A	3003	5/5	0.89	0.12	28,29,30,31	5
2	PO4	D	3011	5/5	0.91	0.11	32,32,33,34	5
2	PO4	C	3008	5/5	0.93	0.13	31,32,33,35	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.