



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 01:07 PM UTC

PDB ID : 4FIR / pdb\_00004fir  
Title : Crystal structure of pyridoxal biosynthesis lyase PdxS from Pyrococcus  
Authors : Matsuura, A.; Yoon, J.Y.; Yoon, H.J.; Lee, H.H.; Suh, S.W.  
Deposited on : 2012-06-11  
Resolution : 3.10 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

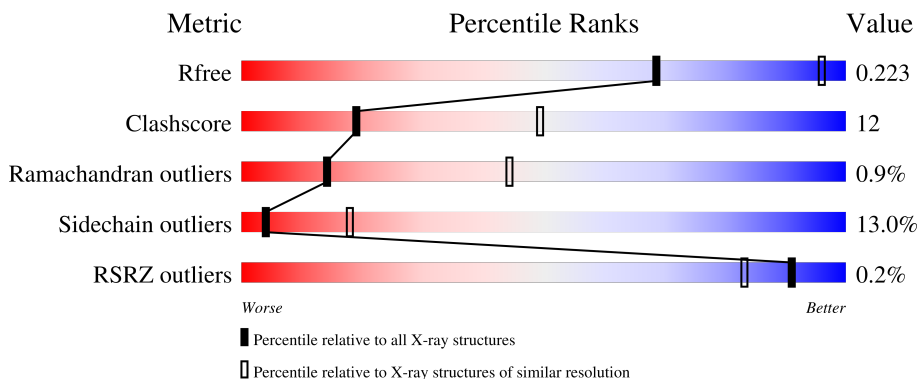
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	335	70% 24% 5% ..
1	B	335	68% 25% 6% ..
1	C	335	70% 22% 7% .
1	D	335	71% 23% 5% ..
1	E	335	70% 23% 6% ..

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Mol	Chain	Length	Quality of chain
1	F	335	 70% 25%

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
2	R5P	F	401	-	-	X	-

## 2 Entry composition [i](#)

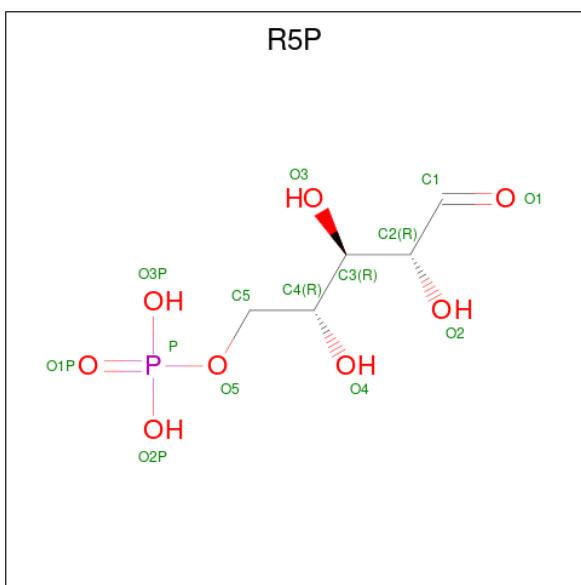
There are 3 unique types of molecules in this entry. The entry contains 15269 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Pyridoxal biosynthesis lyase pdxS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	333	Total 2520	C 1600	N 442	O 460	S 18	0	0	0
1	B	333	Total 2519	C 1599	N 442	O 460	S 18	0	0	0
1	C	333	Total 2520	C 1600	N 442	O 460	S 18	0	0	0
1	D	333	Total 2520	C 1600	N 442	O 460	S 18	0	0	0
1	E	333	Total 2520	C 1600	N 442	O 460	S 18	0	0	0
1	F	333	Total 2520	C 1600	N 442	O 460	S 18	0	0	0

- Molecule 2 is RIBOSE-5-PHOSPHATE (CCD ID: R5P) (formula: C<sub>5</sub>H<sub>11</sub>O<sub>8</sub>P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 13	C 5	O 7	P 1	0	0
2	B	1	Total 13	C 5	O 7	P 1	0	0
2	C	1	Total 13	C 5	O 7	P 1	0	0
2	D	1	Total 13	C 5	O 7	P 1	0	0
2	E	1	Total 13	C 5	O 7	P 1	0	0
2	F	1	Total 13	C 5	O 7	P 1	0	0

- Molecule 3 is water.

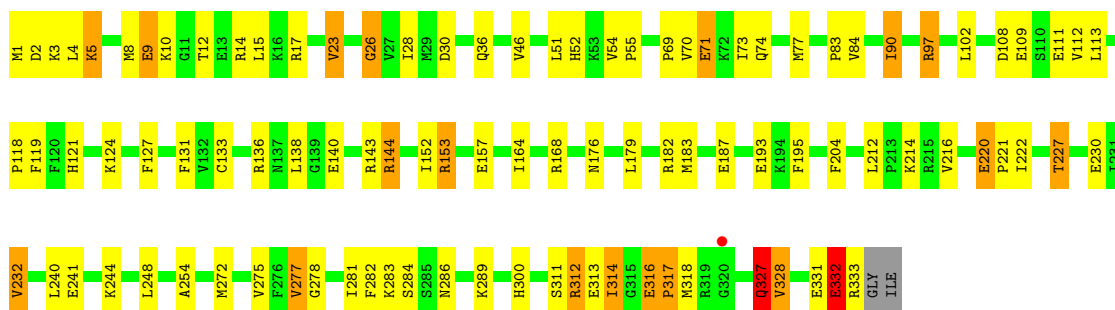
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	14	Total 14	O 14	0	0
3	B	7	Total 7	O 7	0	0
3	C	8	Total 8	O 8	0	0
3	D	13	Total 13	O 13	0	0
3	E	14	Total 14	O 14	0	0
3	F	16	Total 16	O 16	0	0

### 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.

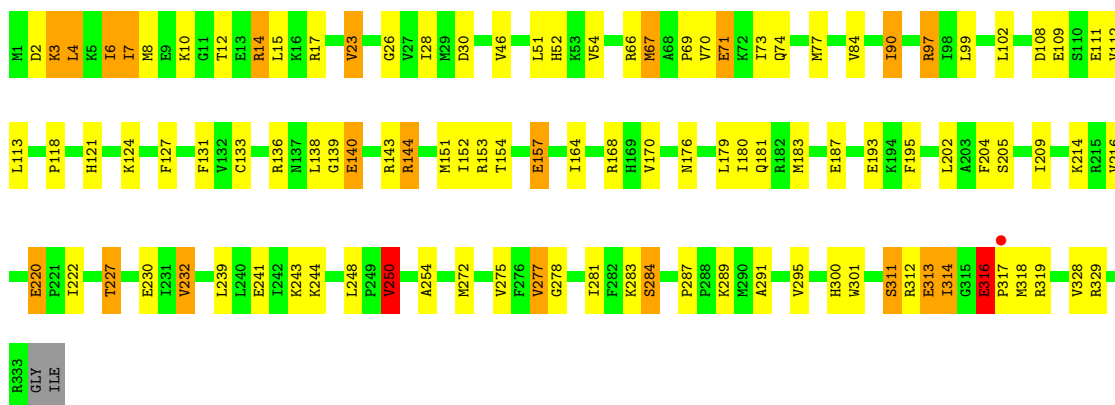
- Molecule 1: Pyridoxal biosynthesis lyase pdxS

Chain A: 



- Molecule 1: Pyridoxal biosynthesis lyase pdxS

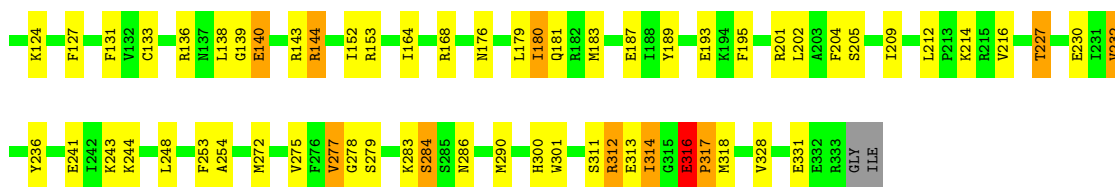
Chain B: 



- Molecule 1: Pyridoxal biosynthesis lyase pdxS

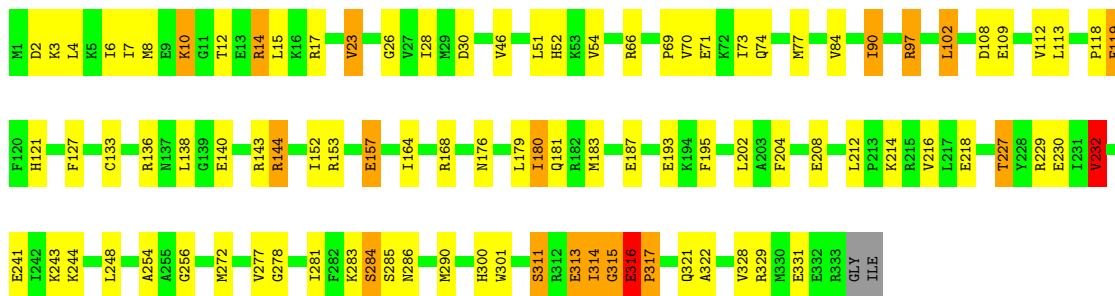
Chain C: 





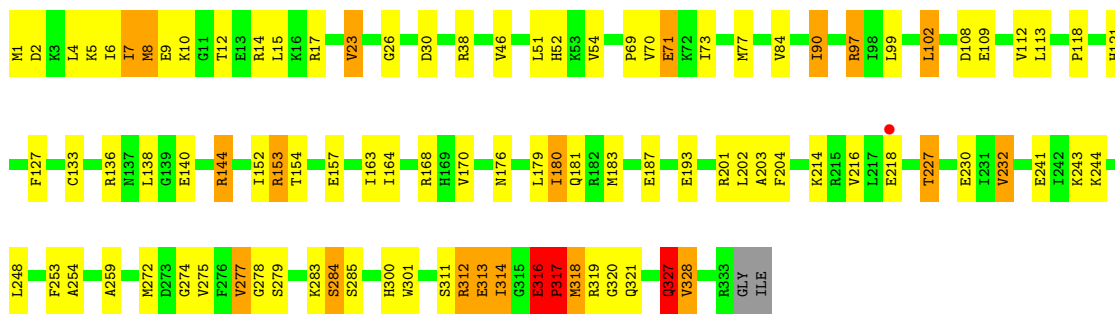
- Molecule 1: Pyridoxal biosynthesis lyase pdxS

Chain D: 71% 23% 5% ..



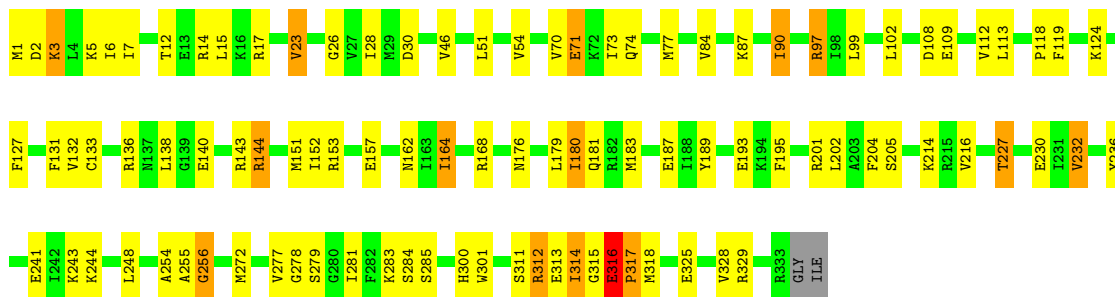
- Molecule 1: Pyridoxal biosynthesis lyase pdxS

Chain E: 70% 23% 6% ..



- Molecule 1: Pyridoxal biosynthesis lyase pdxS

Chain F: 70% 25% ..



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.16Å 179.06Å 109.36Å 90.00° 102.53° 90.00°	Depositor
Resolution (Å)	29.84 – 3.10 29.84 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.2 (29.84-3.10) 98.0 (29.84-3.10)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.77 (at 3.11Å)	Xtrriage
Refinement program	PHENIX 1.7.3_928	Depositor
R, $R_{free}$	0.185 , 0.227 0.184 , 0.223	Depositor DCC
$R_{free}$ test set	1983 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	57.7	Xtrriage
Anisotropy	0.521	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 49.7	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	15269	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	54.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.55% 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: R5P

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	3/2559 (0.1%)	1.13	14/3450 (0.4%)
1	B	0.77	0/2558	1.18	15/3448 (0.4%)
1	C	0.73	0/2559	1.13	10/3450 (0.3%)
1	D	0.79	1/2559 (0.0%)	1.14	13/3450 (0.4%)
1	E	0.86	2/2559 (0.1%)	1.17	16/3450 (0.5%)
1	F	0.77	0/2559	1.16	16/3450 (0.5%)
All	All	0.78	6/15353 (0.0%)	1.15	84/20698 (0.4%)

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	4
1	B	0	2
1	D	0	4
1	E	0	3
All	All	0	13

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	317	PRO	CA-CB	-10.25	1.39	1.53
1	A	318	MET	CA-CB	5.79	1.63	1.53
1	D	316	GLU	CA-C	-5.67	1.46	1.52
1	A	318	MET	CA-C	5.52	1.60	1.52
1	E	316	GLU	CA-C	-5.36	1.46	1.52

The worst 5 of 84 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	317	PRO	N-CA-CB	11.79	113.15	103.36
1	F	316	GLU	CA-C-N	10.75	133.27	119.84
1	F	316	GLU	C-N-CA	10.75	133.27	119.84
1	D	316	GLU	O-C-N	10.66	129.43	121.65
1	C	316	GLU	N-CA-C	9.87	123.56	109.84

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	300	HIS	Mainchain
1	A	327	GLN	Mainchain
1	A	331	GLU	Mainchain
1	A	332	GLU	Mainchain
1	B	66	ARG	Peptide

## 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	2520	0	2551	57	0
1	B	2519	0	2550	69	0
1	C	2520	0	2552	67	0
1	D	2520	0	2551	67	0
1	E	2520	0	2552	53	1
1	F	2520	0	2553	63	0
2	A	13	0	8	1	0
2	B	13	0	8	0	0
2	C	13	0	8	1	0
2	D	13	0	8	1	0
2	E	13	0	8	1	0
2	F	13	0	8	7	0
3	A	14	0	0	0	0
3	B	7	0	0	0	0
3	C	8	0	0	2	0
3	D	13	0	0	0	0
3	E	14	0	0	0	0
3	F	16	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	15269	0	15357	359	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 12.

The worst 5 of 359 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:286:ASN:N	1:D:316:GLU:OE1	1.91	1.02
1:C:1:MET:SD	1:C:2:ASP:N	2.43	0.92
1:D:138:LEU:HB3	1:D:176:ASN:HD22	1.34	0.91
1:B:138:LEU:HB3	1:B:176:ASN:HD22	1.37	0.89
1:D:14:ARG:HG2	1:D:14:ARG:HH11	1.40	0.87

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:E:38:ARG:NH1	1:E:218:GLU:OE1[1_655]	2.17	0.03

## 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	331/335 (99%)	318 (96%)	9 (3%)	4 (1%)	10 37
1	B	331/335 (99%)	321 (97%)	8 (2%)	2 (1%)	21 52
1	C	331/335 (99%)	320 (97%)	10 (3%)	1 (0%)	36 67
1	D	331/335 (99%)	314 (95%)	14 (4%)	3 (1%)	14 44
1	E	331/335 (99%)	314 (95%)	13 (4%)	4 (1%)	10 37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	F	331/335 (99%)	319 (96%)	9 (3%)	3 (1%)	14	44
All	All	1986/2010 (99%)	1906 (96%)	63 (3%)	17 (1%)	14	44

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	67	MET
1	D	317	PRO
1	D	322	ALA
1	E	317	PRO
1	F	316	GLU

### 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	251/267 (94%)	220 (88%)	31 (12%)	4	19
1	B	251/267 (94%)	213 (85%)	38 (15%)	3	13
1	C	251/267 (94%)	218 (87%)	33 (13%)	4	17
1	D	251/267 (94%)	219 (87%)	32 (13%)	4	18
1	E	251/267 (94%)	217 (86%)	34 (14%)	4	16
1	F	251/267 (94%)	223 (89%)	28 (11%)	6	24
All	All	1506/1602 (94%)	1310 (87%)	196 (13%)	4	18

5 of 196 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	97	ARG
1	E	51	LEU
1	D	144	ARG
1	D	284	SER
1	E	113	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	74	GLN
1	F	176	ASN
1	D	121	HIS
1	F	252	ASN
1	E	176	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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

6 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	R5P	D	401	1	12,12,13	0.63	0	16,17,18	1.98	4 (25%)
2	R5P	F	401	-	12,12,13	0.98	0	16,17,18	2.82	5 (31%)
2	R5P	C	401	1	12,12,13	0.77	0	16,17,18	1.21	1 (6%)
2	R5P	E	401	1	12,12,13	0.68	0	16,17,18	1.66	4 (25%)
2	R5P	B	401	1	12,12,13	0.54	0	16,17,18	2.03	6 (37%)
2	R5P	A	401	1	12,12,13	0.68	0	16,17,18	2.21	8 (50%)

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	R5P	D	401	1	-	7/14/14/16	-
2	R5P	F	401	-	-	11/14/14/16	-
2	R5P	C	401	1	-	9/14/14/16	-
2	R5P	E	401	1	-	6/14/14/16	-
2	R5P	B	401	1	-	6/14/14/16	-
2	R5P	A	401	1	-	9/14/14/16	-

There are no bond length outliers.

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	401	R5P	O2-C2-C3	-7.95	96.60	109.77
2	F	401	R5P	C5-C4-C3	-4.77	103.23	112.22
2	A	401	R5P	C5-C4-C3	-4.51	103.70	112.22
2	D	401	R5P	O2-C2-C3	-4.43	102.44	109.77
2	D	401	R5P	C1-C2-C3	3.77	116.74	112.11

There are no chirality outliers.

5 of 48 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	R5P	C5-O5-P-O2P
2	A	401	R5P	C5-O5-P-O3P
2	B	401	R5P	C1-C2-C3-O3
2	B	401	R5P	C1-C2-C3-C4
2	B	401	R5P	O2-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	401	R5P	1	0
2	F	401	R5P	7	0
2	C	401	R5P	1	0
2	E	401	R5P	1	0
2	A	401	R5P	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	333/335 (99%)	-0.59	1 (0%) 90 80	30, 49, 83, 121	0
1	B	333/335 (99%)	-0.46	1 (0%) 90 80	31, 51, 94, 148	0
1	C	333/335 (99%)	-0.46	0 100 100	31, 52, 85, 118	0
1	D	333/335 (99%)	-0.51	0 100 100	30, 49, 87, 147	0
1	E	333/335 (99%)	-0.52	1 (0%) 90 80	28, 46, 79, 116	0
1	F	333/335 (99%)	-0.58	0 100 100	30, 48, 86, 144	0
All	All	1998/2010 (99%)	-0.52	3 (0%) 91 83	28, 49, 85, 148	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	320	GLY	3.6
1	E	218	GLU	2.4
1	B	317	PRO	2.1

### 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 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(Å <sup>2</sup> )	Q<0.9
2	R5P	E	401	13/14	0.94	0.09	35,53,62,83	0
2	R5P	F	401	13/14	0.94	0.09	28,48,61,63	0
2	R5P	A	401	13/14	0.95	0.08	41,50,66,71	0
2	R5P	D	401	13/14	0.95	0.09	32,51,77,77	0
2	R5P	C	401	13/14	0.96	0.07	49,66,75,75	0
2	R5P	B	401	13/14	0.96	0.08	44,57,65,68	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.