



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 24, 2020 – 04:12 PM BST

PDB ID : 6T4V  
Title : Crystal structure of 2-methylisocitrate lyase (PrpB) from *Pseudomonas aeruginosa* in apo form.  
Authors : Wijaya, A.J.; Brear, P.; Dolan, S.K.; Welch, M.  
Deposited on : 2019-10-15  
Resolution : 1.81 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.14.6  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.14.6

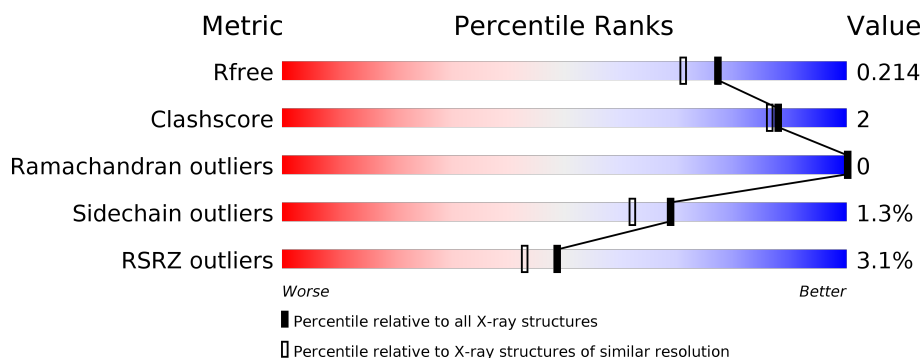
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.81 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))
$R_{free}$	130704	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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 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	298	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 5%, green 87%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>%</span> <span>87%</span> <span>5%</span> <span>7%</span> </div> </div>
1	B	298	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 2%, yellow 7%, green 89%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>2%</span> <span>89%</span> <span>7%</span> </div> </div>
1	C	298	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 2%, orange 2%, yellow 5%, green 88%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>2%</span> <span>88%</span> <span>5%</span> <span>7%</span> </div> </div>
1	D	298	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 6%, orange 6%, yellow 7%, green 85%, grey 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>6%</span> <span>85%</span> <span>7%</span> <span>7%</span> </div> </div>

## 2 Entry composition [i](#)

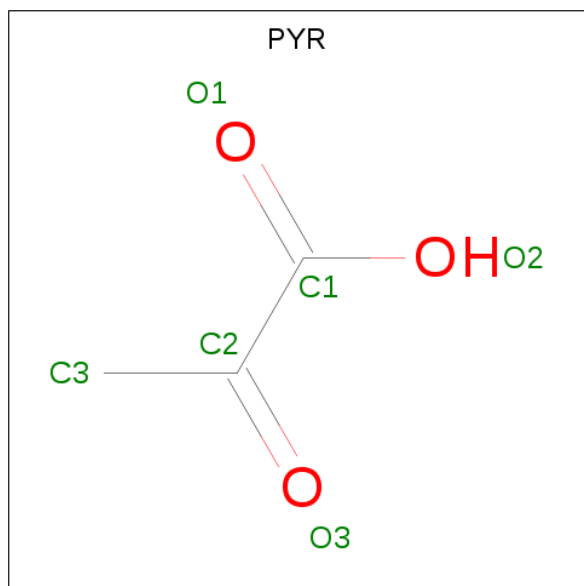
There are 3 unique types of molecules in this entry. The entry contains 8883 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 2-methylisocitrate lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	277	Total	C	N	O	S	0	5	0
			2135	1341	368	413	13			
1	A	276	Total	C	N	O	S	0	2	0
			2104	1323	361	407	13			
1	B	277	Total	C	N	O	S	0	2	0
			2110	1326	361	410	13			
1	D	276	Total	C	N	O	S	0	1	0
			2096	1319	359	405	13			

- Molecule 2 is PYRUVIC ACID (three-letter code: PYR) (formula:  $C_3H_4O_3$ ).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			6	3	3		
2	D	1	Total	C	O	0	0
			6	3	3		

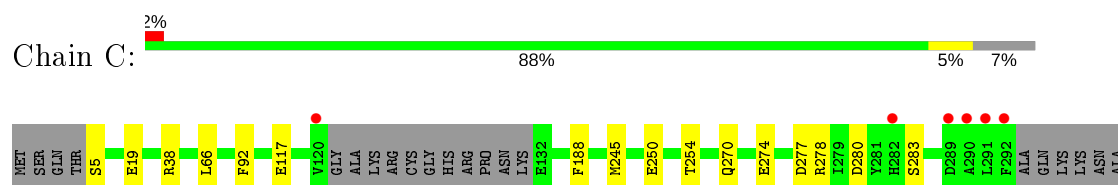
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	148	Total	O	0	2
			150	150		
3	A	90	Total	O	0	0
			90	90		
3	B	114	Total	O	0	0
			114	114		
3	D	60	Total	O	0	0
			60	60		

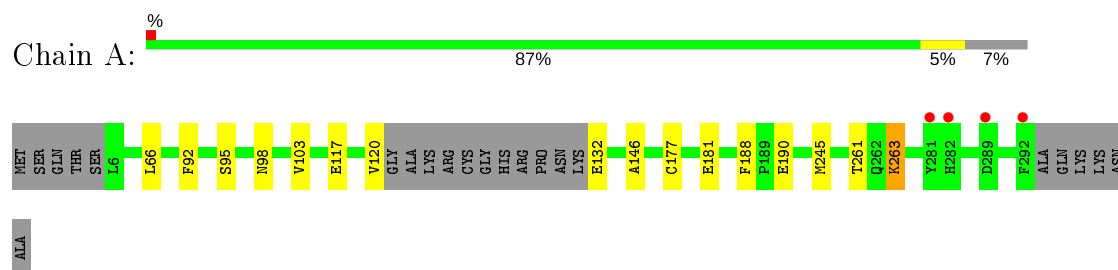
### 3 Residue-property plots [i](#)

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.

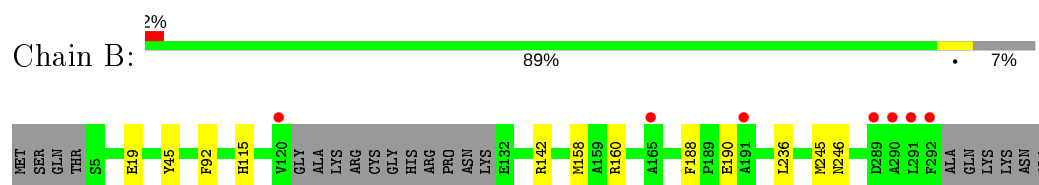
- Molecule 1: 2-methylisocitrate lyase



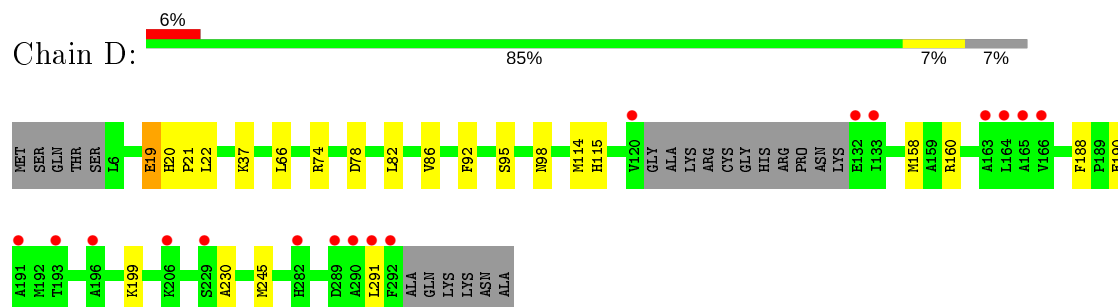
- Molecule 1: 2-methylisocitrate lyase



- Molecule 1: 2-methylisocitrate lyase



- Molecule 1: 2-methylisocitrate lyase



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	152.86 Å   59.19 Å   148.11 Å 90.00°   120.08°   90.00°	Depositor
Resolution (Å)	64.08 – 1.81 64.08 – 1.81	Depositor EDS
% Data completeness (in resolution range)	99.1 (64.08-1.81) 99.1 (64.08-1.81)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.29 (at 1.81 Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, $R_{free}$	0.194 , 0.215 0.194 , 0.214	Depositor DCC
$R_{free}$ test set	5195 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	22.4	Xtriage
Anisotropy	0.694	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 48.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.002 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	8883	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.40% 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: PYR

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	0.82	1/2133 (0.0%)	0.83	0/2889
1	B	0.84	1/2139 (0.0%)	0.86	0/2897
1	C	0.90	3/2164 (0.1%)	0.83	0/2931
1	D	0.80	1/2125 (0.0%)	0.82	0/2878
All	All	0.84	6/8561 (0.1%)	0.83	0/11595

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	19	GLU	CD-OE2	-5.88	1.19	1.25
1	B	19	GLU	CD-OE1	-5.83	1.19	1.25
1	C	117	GLU	CD-OE2	-5.70	1.19	1.25
1	A	117	GLU	CD-OE2	-5.38	1.19	1.25
1	C	19	GLU	CD-OE1	-5.33	1.19	1.25
1	D	19	GLU	CD-OE2	-5.32	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 [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	2104	0	2101	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2110	0	2104	6	0
1	C	2135	0	2132	10	0
1	D	2096	0	2096	12	0
2	A	6	0	3	2	0
2	B	6	0	3	1	0
2	C	6	0	3	2	0
2	D	6	0	3	2	0
3	A	90	0	0	0	0
3	B	114	0	0	0	0
3	C	150	0	0	2	0
3	D	60	0	0	0	0
All	All	8883	0	8445	34	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 2.

All (34) 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:C:66:LEU:HD22	2:C:301:PYR:H33	1.77	0.65
1:C:254[B]:THR:HG21	3:C:478:HOH:O	1.99	0.61
1:C:250:GLU:O	1:C:254[B]:THR:HG22	2.01	0.60
1:A:66:LEU:HD22	2:A:301:PYR:H33	1.85	0.57
1:D:92:PHE:O	2:D:301:PYR:H32	2.07	0.54
1:B:92:PHE:O	2:B:301:PYR:H32	2.07	0.53
1:C:270:GLN:HE22	1:B:246:ASN:HD22	1.59	0.50
1:D:115:HIS:HA	1:D:158:MET:O	2.12	0.49
1:D:66:LEU:HD22	2:D:301:PYR:H33	1.96	0.46
1:D:74[B]:ARG:NH2	1:D:78:ASP:OD2	2.49	0.46
1:C:280:ASP:OD1	1:C:283:SER:HB3	2.16	0.44
1:A:177:CYS:O	1:A:181:GLU:HG2	2.18	0.44
1:A:120:VAL:HG21	1:A:132:GLU:HG2	1.99	0.44
1:D:37:LYS:HA	1:D:82:LEU:HD11	2.00	0.44
1:D:20:HIS:HA	1:D:21:PRO:HA	1.83	0.43
1:D:95:SER:HB3	1:D:98:ASN:OD1	2.19	0.43
1:A:92:PHE:O	2:A:301:PYR:H32	2.18	0.42
1:B:115:HIS:HA	1:B:158:MET:O	2.19	0.42
1:A:103:VAL:HG21	1:A:146:ALA:HA	2.00	0.42
1:A:95:SER:HB3	1:A:98:ASN:OD1	2.19	0.42
1:D:86:VAL:O	1:D:114:MET:HA	2.19	0.42
1:D:19:GLU:HG2	1:D:22:LEU:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:199:LYS:HA	1:D:230:ALA:O	2.20	0.42
1:C:38[B]:ARG:NH2	1:C:277:ASP:OD2	2.52	0.42
1:C:92:PHE:O	2:C:301:PYR:H32	2.20	0.42
1:A:190:GLU:OE1	1:A:190:GLU:HA	2.20	0.41
1:C:270:GLN:NE2	1:B:246:ASN:HD22	2.18	0.41
1:C:274:GLU:O	1:C:278:ARG:HG2	2.20	0.41
1:C:254[B]:THR:HG21	3:C:534:HOH:O	2.21	0.41
1:B:160:ARG:HH21	1:B:190:GLU:CD	2.24	0.40
1:B:45:TYR:CG	1:B:236:LEU:HD11	2.56	0.40
1:D:160:ARG:HH21	1:D:190:GLU:CD	2.25	0.40
1:D:291:LEU:HD23	1:D:291:LEU:HA	1.73	0.40
1:A:261:THR:CG2	1:A:263:LYS:HG2	2.52	0.40

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	274/298 (92%)	268 (98%)	6 (2%)	0	100	100
1	B	275/298 (92%)	270 (98%)	5 (2%)	0	100	100
1	C	278/298 (93%)	272 (98%)	6 (2%)	0	100	100
1	D	273/298 (92%)	267 (98%)	6 (2%)	0	100	100
All	All	1100/1192 (92%)	1077 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	220/235 (94%)	217 (99%)	3 (1%)	67	59
1	B	221/235 (94%)	218 (99%)	3 (1%)	67	59
1	C	224/235 (95%)	221 (99%)	3 (1%)	69	62
1	D	219/235 (93%)	217 (99%)	2 (1%)	78	75
All	All	884/940 (94%)	873 (99%)	11 (1%)	69	65

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	5	SER
1	C	188	PHE
1	C	245	MET
1	A	188	PHE
1	A	245	MET
1	A	263	LYS
1	B	142	ARG
1	B	188	PHE
1	B	245	MET
1	D	188	PHE
1	D	245	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	264	ASN
1	C	270	GLN
1	C	282	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

4 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	PYR	A	301	-	2,5,5	0.39	0	2,6,6	1.61	1 (50%)
2	PYR	D	301	-	2,5,5	0.23	0	2,6,6	1.31	0
2	PYR	B	301	-	2,5,5	0.31	0	2,6,6	1.37	0
2	PYR	C	301	-	2,5,5	0.05	0	2,6,6	0.88	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
2	PYR	A	301	-	-	0/0/4/4	-
2	PYR	D	301	-	-	0/0/4/4	-
2	PYR	B	301	-	-	0/0/4/4	-
2	PYR	C	301	-	-	0/0/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	PYR	C3-C2-C1	-2.19	113.68	120.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	PYR	2	0
2	D	301	PYR	2	0
2	B	301	PYR	1	0
2	C	301	PYR	2	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 ⓘ

### 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	276/298 (92%)	-0.10	4 (1%) 75 72	17, 30, 49, 66	0
1	B	277/298 (92%)	-0.08	7 (2%) 57 52	14, 24, 49, 64	0
1	C	277/298 (92%)	-0.20	6 (2%) 62 57	13, 21, 42, 62	0
1	D	276/298 (92%)	0.29	17 (6%) 20 16	20, 35, 61, 80	0
All	All	1106/1192 (92%)	-0.02	34 (3%) 49 43	13, 28, 52, 80	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	292	PHE	9.9
1	D	292	PHE	9.8
1	B	291	LEU	6.5
1	D	290	ALA	6.5
1	D	291	LEU	5.8
1	D	289	ASP	5.8
1	D	166	VAL	5.0
1	C	292	PHE	4.9
1	D	191	ALA	4.9
1	D	165	ALA	4.0
1	B	191	ALA	4.0
1	B	165	ALA	3.9
1	A	289	ASP	3.5
1	B	120	VAL	3.1
1	D	229	SER	2.9
1	A	292	PHE	2.7
1	D	164	LEU	2.6
1	C	291	LEU	2.5
1	D	120	VAL	2.5
1	D	196	ALA	2.4
1	D	282	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	290	ALA	2.4
1	C	289	ASP	2.4
1	A	281	TYR	2.3
1	D	133	ILE	2.3
1	D	163	ALA	2.3
1	A	282	HIS	2.3
1	B	289	ASP	2.2
1	D	206	LYS	2.2
1	C	290	ALA	2.2
1	C	120	VAL	2.1
1	D	193	THR	2.0
1	C	282	HIS	2.0
1	D	132	GLU	2.0

## 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 monosaccharides 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	PYR	A	301	6/6	0.77	0.25	20,20,20,20	0
2	PYR	D	301	6/6	0.78	0.35	20,20,20,20	0
2	PYR	C	301	6/6	0.85	0.28	20,20,20,20	0
2	PYR	B	301	6/6	0.87	0.28	20,20,20,20	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.