



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 7, 2020 – 01:56 am BST

PDB ID : 6H2S  
Title : Sulfolobus solfataricus 2 - k e t o - 3 - d e o x y g l u c o n a t e aldolase  
T157V/D181Q/A198L variant, pyruvate complex  
Authors : Crennell, S.J.; Danson, M.J.; Royer, S.  
Deposited on : 2018-07-16  
Resolution : 2.17 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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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 : 2.11  
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) : 2.11

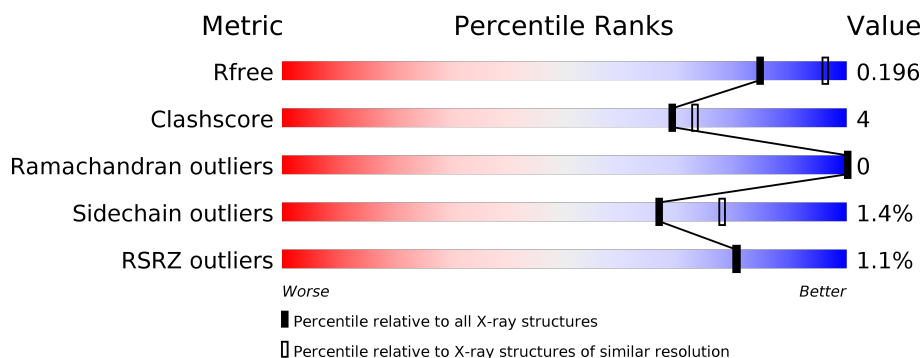
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.17 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	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)
RSRZ outliers	127900	6738 (2.20-2.16)

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	293	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>10%</div> <div>.</div> </div> </div>
1	B	293	<div> <div>%</div> <div> <div></div> <div>91%</div> <div>9%</div> </div> </div>
1	C	293	<div> <div>2%</div> <div> <div></div> <div>92%</div> <div>8%</div> </div> </div>
1	D	293	<div> <div>%</div> <div> <div></div> <div>91%</div> <div>9%</div> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 20168 atoms, of which 9876 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-dehydro-3-deoxy-phosphogluconate/2-dehydro-3-deoxy-6-phosphogalactonate aldolase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	293	Total	C	H	N	O	S	0	15	0
			4886	1554	2480	394	452	6			
1	B	293	Total	C	H	N	O	S	0	13	0
			4824	1534	2452	386	446	6			
1	C	293	Total	C	H	N	O	S	0	3	0
			4751	1512	2413	382	438	6			
1	D	293	Total	C	H	N	O	S	0	12	0
			4796	1528	2435	384	443	6			

There are 12 discrepancies between the modelled and reference sequences:

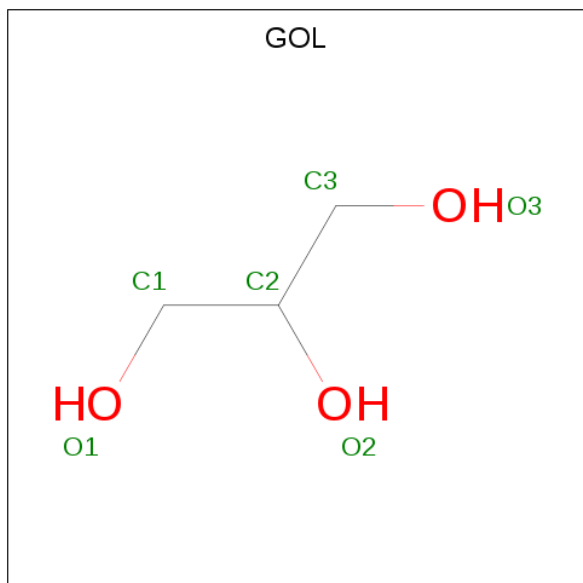
Chain	Residue	Modelled	Actual	Comment	Reference
A	157	VAL	THR	engineered mutation	UNP O54288
A	181	GLN	ASP	engineered mutation	UNP O54288
A	198	LEU	ALA	engineered mutation	UNP O54288
B	157	VAL	THR	engineered mutation	UNP O54288
B	181	GLN	ASP	engineered mutation	UNP O54288
B	198	LEU	ALA	engineered mutation	UNP O54288
C	157	VAL	THR	engineered mutation	UNP O54288
C	181	GLN	ASP	engineered mutation	UNP O54288
C	198	LEU	ALA	engineered mutation	UNP O54288
D	157	VAL	THR	engineered mutation	UNP O54288
D	181	GLN	ASP	engineered mutation	UNP O54288
D	198	LEU	ALA	engineered mutation	UNP O54288

- Molecule 2 is PYRUVIC ACID (three-letter code: PYR) (formula: C<sub>3</sub>H<sub>4</sub>O<sub>3</sub>).



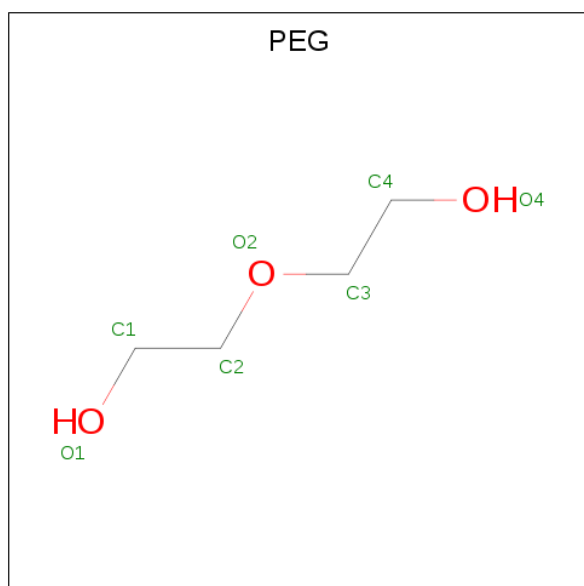
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			9	3	3	3		
2	B	1	Total	C	H	O	0	0
			9	3	3	3		
2	C	1	Total	C	H	O	0	0
			9	3	3	3		
2	D	1	Total	C	H	O	0	0
			9	3	3	3		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



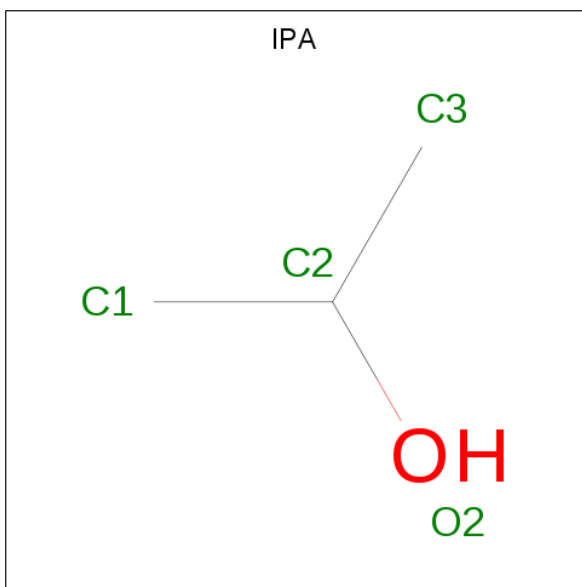
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	C	1	Total	C	H	O	0	0
			14	3	8	3		
3	D	1	Total	C	H	O	0	0
			14	3	8	3		
3	D	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula:  $C_4H_{10}O_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			17	4	10	3		
4	C	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 5 is ISOPROPYL ALCOHOL (three-letter code: IPA) (formula:  $C_3H_8O$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			12	3	8	1		

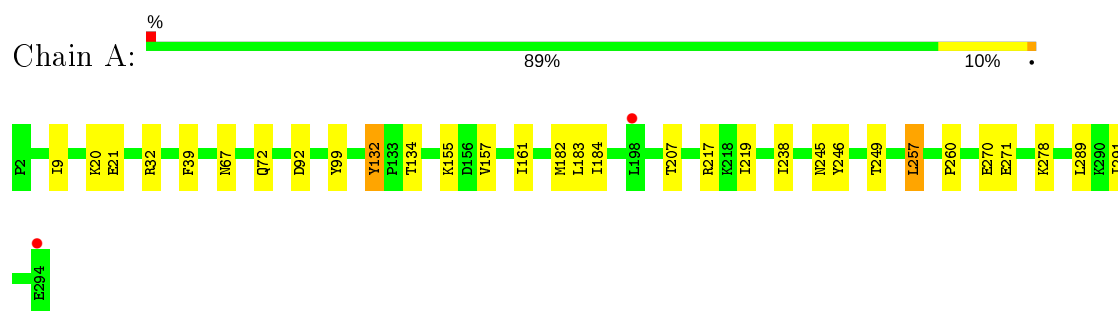
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	200	Total	O	0	0
			200	200		
6	B	164	Total	O	0	0
			164	164		
6	C	158	Total	O	0	0
			158	158		
6	D	209	Total	O	0	0
			209	209		

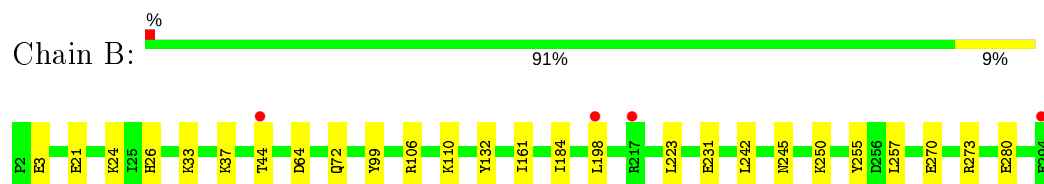
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

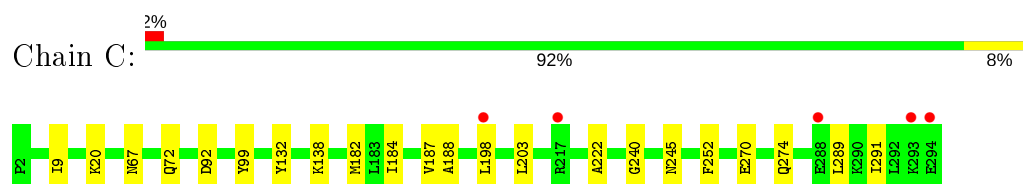
- Molecule 1: 2-dehydro-3-deoxy-phosphogluconate/2-dehydro-3-deoxy-6-phosphogalactonate aldolase



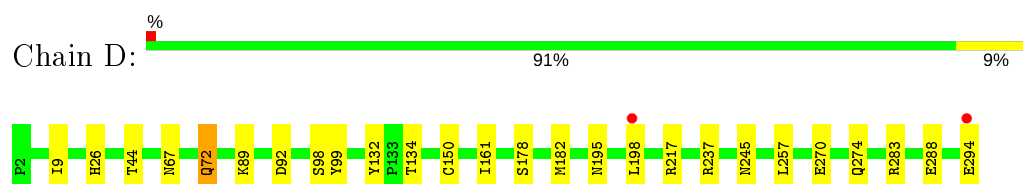
- Molecule 1: 2-dehydro-3-deoxy-phosphogluconate/2-dehydro-3-deoxy-6-phosphogalactonate aldolase



- Molecule 1: 2-dehydro-3-deoxy-phosphogluconate/2-dehydro-3-deoxy-6-phosphogalactonate aldolase



- Molecule 1: 2-dehydro-3-deoxy-phosphogluconate/2-dehydro-3-deoxy-6-phosphogalactonate aldolase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	76.56Å 87.02Å 92.00Å 90.00° 95.74° 90.00°	Depositor
Resolution (Å)	28.79 – 2.17 28.79 – 2.17	Depositor EDS
% Data completeness (in resolution range)	95.2 (28.79-2.17) 95.2 (28.79-2.17)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.71 (at 2.18Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.145 , 0.196 0.145 , 0.196	Depositor DCC
$R_{free}$ test set	3069 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.2	Xtriage
Anisotropy	0.137	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 49.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	20168	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.68% 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: GOL, PYR, PEG, IPA

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	0.52	0/2510	0.66	0/3392
1	B	0.50	0/2481	0.63	0/3355
1	C	0.49	0/2401	0.62	0/3245
1	D	0.53	0/2464	0.65	0/3333
All	All	0.51	0/9856	0.64	0/13325

There are no bond length outliers.

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	2406	2480	2398	24	0
1	B	2372	2452	2369	17	0
1	C	2338	2413	2388	13	0
1	D	2361	2435	2367	18	0
2	A	6	3	3	0	0
2	B	6	3	3	0	0
2	C	6	3	3	0	0
2	D	6	3	3	0	0
3	A	12	16	16	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	12	16	16	1	0
3	C	6	8	8	1	0
3	D	12	16	16	2	0
4	A	7	10	10	1	0
4	C	7	10	10	0	0
5	A	4	8	8	0	0
6	A	200	0	0	8	0
6	B	164	0	0	6	0
6	C	158	0	0	2	0
6	D	209	0	0	8	0
All	All	10292	9876	9618	71	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 4.

The worst 5 of 71 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:67[A]:ASN:OD1	6:C:401:HOH:O	1.85	0.95
1:B:270:GLU:OE1	1:B:273:ARG:NH1	2.13	0.81
1:D:288:GLU:OE2	6:D:401:HOH:O	2.01	0.78
1:D:283:ARG:NH2	1:D:294:GLU:OXT	2.19	0.75
1:D:89:LYS:NZ	6:D:402:HOH:O	2.15	0.72

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	306/293 (104%)	298 (97%)	8 (3%)	0	100	100
1	B	304/293 (104%)	296 (97%)	8 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	294/293 (100%)	287 (98%)	7 (2%)	0	100	100
1	D	303/293 (103%)	295 (97%)	8 (3%)	0	100	100
All	All	1207/1172 (103%)	1176 (97%)	31 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	273/259 (105%)	268 (98%)	5 (2%)	59	70
1	B	271/259 (105%)	267 (98%)	4 (2%)	65	76
1	C	262/259 (101%)	259 (99%)	3 (1%)	73	83
1	D	269/259 (104%)	266 (99%)	3 (1%)	73	83
All	All	1075/1036 (104%)	1060 (99%)	15 (1%)	67	78

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	72	GLN
1	B	99	TYR
1	D	72	GLN
1	B	33	LYS
1	C	132	TYR

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 [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

14 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	$\# Z  > 2$
3	GOL	D	302	-	5,5,5	1.18	0	5,5,5	0.90	0
4	PEG	A	304	-	6,6,6	0.65	0	5,5,5	0.32	0
3	GOL	B	302	-	5,5,5	0.78	0	5,5,5	1.18	1 (20%)
3	GOL	A	303	-	5,5,5	0.43	0	5,5,5	0.73	0
2	PYR	A	301	-	2,5,5	2.03	1 (50%)	2,6,6	1.32	0
5	IPA	A	305	-	3,3,3	0.47	0	3,3,3	0.52	0
3	GOL	A	302	-	5,5,5	0.63	0	5,5,5	1.04	0
3	GOL	C	302	-	5,5,5	1.06	0	5,5,5	1.21	1 (20%)
3	GOL	D	303	-	5,5,5	0.68	0	5,5,5	0.46	0
2	PYR	D	301	-	2,5,5	2.01	1 (50%)	2,6,6	1.70	1 (50%)
4	PEG	C	303	-	6,6,6	0.69	0	5,5,5	0.59	0
2	PYR	C	301	-	2,5,5	2.02	1 (50%)	2,6,6	0.98	0
3	GOL	B	303	-	5,5,5	0.59	0	5,5,5	0.75	0
2	PYR	B	301	-	2,5,5	1.70	1 (50%)	2,6,6	1.57	1 (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
3	GOL	D	302	-	-	0/4/4/4	-
4	PEG	A	304	-	-	3/4/4/4	-
3	GOL	B	302	-	-	2/4/4/4	-
2	PYR	B	301	-	-	0/0/4/4	-
2	PYR	A	301	-	-	0/0/4/4	-
3	GOL	A	302	-	-	0/4/4/4	-
3	GOL	C	302	-	-	2/4/4/4	-
3	GOL	D	303	-	-	2/4/4/4	-
2	PYR	D	301	-	-	0/0/4/4	-
4	PEG	C	303	-	-	3/4/4/4	-
2	PYR	C	301	-	-	0/0/4/4	-
3	GOL	B	303	-	-	2/4/4/4	-
3	GOL	A	303	-	-	0/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	PYR	O3-C2	2.83	1.31	1.22
2	D	301	PYR	O3-C2	2.82	1.31	1.22
2	C	301	PYR	O3-C2	2.75	1.31	1.22
2	B	301	PYR	O3-C2	2.36	1.30	1.22

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	PYR	O3-C2-C3	2.38	125.53	120.17
3	C	302	GOL	C3-C2-C1	-2.22	103.08	111.70
2	B	301	PYR	O3-C2-C3	2.17	125.06	120.17
3	B	302	GOL	C3-C2-C1	-2.14	103.38	111.70

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	302	GOL	C1-C2-C3-O3
3	B	303	GOL	O1-C1-C2-C3
3	B	303	GOL	O1-C1-C2-O2
4	C	303	PEG	O1-C1-C2-O2
4	C	303	PEG	C1-C2-O2-C3

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	304	PEG	1	0
3	B	302	GOL	1	0
3	C	302	GOL	1	0
3	D	303	GOL	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 [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	293/293 (100%)	-0.35	2 (0%) 87 88	14, 23, 44, 92	0
1	B	293/293 (100%)	-0.27	4 (1%) 75 75	14, 24, 50, 79	0
1	C	293/293 (100%)	-0.31	5 (1%) 70 70	14, 26, 54, 81	0
1	D	293/293 (100%)	-0.41	2 (0%) 87 88	14, 22, 42, 69	0
All	All	1172/1172 (100%)	-0.34	13 (1%) 80 80	14, 24, 47, 92	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	294	GLU	5.8
1	B	198[A]	LEU	4.4
1	A	198	LEU	3.5
1	C	217	ARG	3.2
1	C	198	LEU	3.1

### 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 carbohydrates 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
3	GOL	A	303	6/6	0.75	0.31	50,79,95,114	0
3	GOL	D	303	6/6	0.79	0.30	42,63,94,94	0
3	GOL	B	303	6/6	0.82	0.43	40,65,78,93	0
4	PEG	C	303	7/7	0.82	0.34	39,48,70,70	0
4	PEG	A	304	7/7	0.88	0.35	30,48,79,79	0
3	GOL	D	302	6/6	0.92	0.11	23,37,48,48	0
5	IPA	A	305	4/4	0.92	0.11	29,37,48,57	0
2	PYR	C	301	6/6	0.93	0.21	26,39,44,58	0
2	PYR	D	301	6/6	0.93	0.24	17,33,40,45	0
2	PYR	B	301	6/6	0.93	0.23	21,37,44,44	0
3	GOL	A	302	6/6	0.94	0.13	27,38,46,52	0
2	PYR	A	301	6/6	0.95	0.20	19,33,39,39	0
3	GOL	B	302	6/6	0.96	0.11	29,42,56,56	0
3	GOL	C	302	6/6	0.97	0.12	27,43,51,52	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.