



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 25, 2026 – 01:55 AM UTC

PDB ID : 4I8A / pdb\_00004i8a  
Title : Alanine-glyoxylate aminotransferase variant S187F  
Authors : Fodor, K.; Oppici, E.; Williams, C.; Cellini, B.; Wilmanns, M.  
Deposited on : 2012-12-03  
Resolution : 2.90 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.

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)  
Xtrriage (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

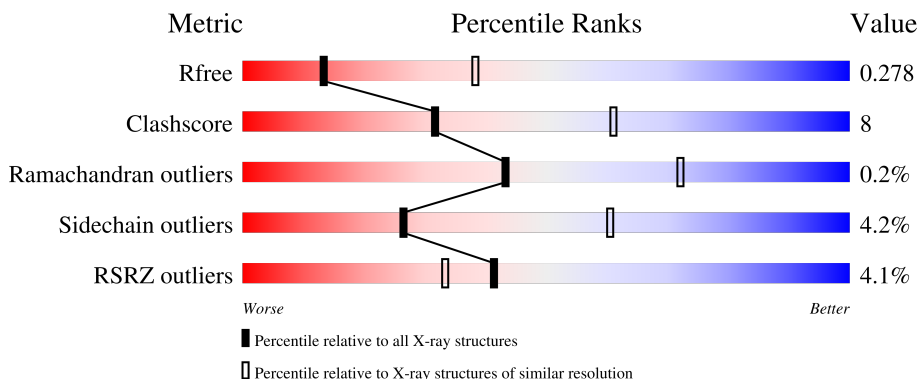
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	394	 4% 81% 16% ..
1	B	394	 4% 78% 18% ..
1	C	394	 3% 79% 17% ..
1	D	394	 6% 78% 19% ..

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	GOL	D	403	-	-	X	-

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11929 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 Serine-pyruvate aminotransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	387	2958	1902	500	539	1	16	0	1	0
1	B	386	2981	1911	512	541	1	16	0	0	0
1	C	385	2960	1899	507	537	1	16	0	0	0
1	D	386	2952	1896	499	540	1	16	0	1	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P21549
A	0	ALA	-	expression tag	UNP P21549
A	187	PHE	SER	engineered mutation	UNP P21549
B	-1	GLY	-	expression tag	UNP P21549
B	0	ALA	-	expression tag	UNP P21549
B	187	PHE	SER	engineered mutation	UNP P21549
C	-1	GLY	-	expression tag	UNP P21549
C	0	ALA	-	expression tag	UNP P21549
C	187	PHE	SER	engineered mutation	UNP P21549
D	-1	GLY	-	expression tag	UNP P21549
D	0	ALA	-	expression tag	UNP P21549
D	187	PHE	SER	engineered mutation	UNP P21549

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).

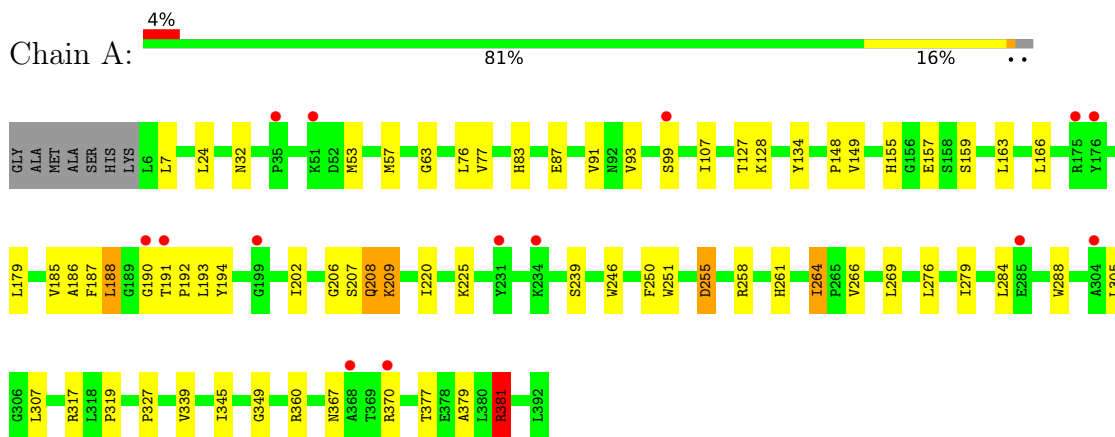


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 6 3 3	0	0
2	A	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	C	1	Total C O 6 3 3	0	0
2	C	1	Total C O 6 3 3	0	0
2	C	1	Total C O 6 3 3	0	0
2	C	1	Total C O 6 3 3	0	0
2	D	1	Total C O 6 3 3	0	0
2	D	1	Total C O 6 3 3	0	0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

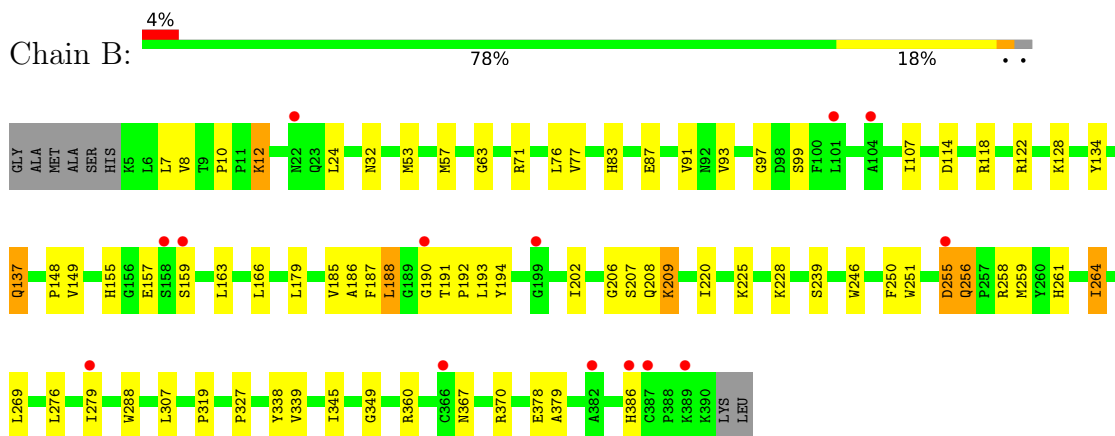
### 3 Residue-property plots [i](#)

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.

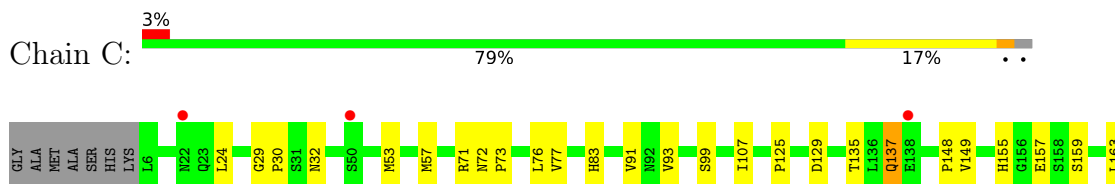
- Molecule 1: Serine-pyruvate aminotransferase

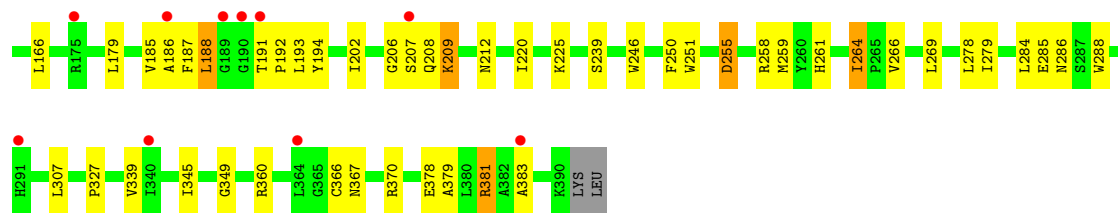


- Molecule 1: Serine-pyruvate aminotransferase

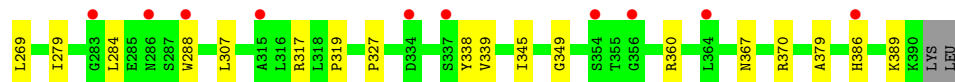
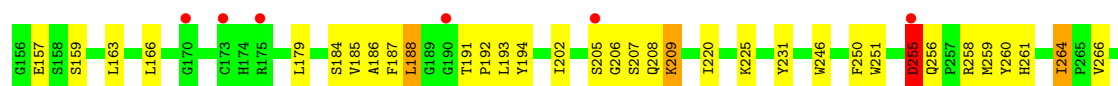
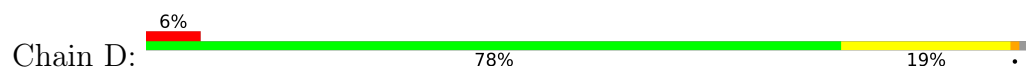


- Molecule 1: Serine-pyruvate aminotransferase





● Molecule 1: Serine-pyruvate aminotransferase



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	78.89Å 101.56Å 116.75Å 90.00° 90.64° 90.00°	Depositor
Resolution (Å)	18.07 – 2.90 18.07 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.8 (18.07-2.90) 98.8 (18.07-2.90)	Depositor EDS
$R_{merge}$	0.20	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.18 (at 2.92Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, $R_{free}$	0.251 , 0.278 0.255 , 0.278	Depositor DCC
$R_{free}$ test set	2055 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.7	Xtrriage
Anisotropy	0.532	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 42.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.44$ , $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	0.048 for h,-k,-l	Xtrriage
$F_o, F_c$ correlation	0.82	EDS
Total number of atoms	11929	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.46% 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, LLP

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	0/3003	0.96	3/4083 (0.1%)
1	B	0.80	0/3026	0.97	1/4109 (0.0%)
1	C	0.81	1/3005 (0.0%)	0.95	0/4084
1	D	0.81	1/2997 (0.0%)	0.95	3/4079 (0.1%)
All	All	0.81	2/12031 (0.0%)	0.96	7/16355 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	6	LEU	N-CA	5.83	1.53	1.46
1	C	383	ALA	CA-C	5.10	1.59	1.52

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	381	ARG	CB-CA-C	6.91	121.81	110.90
1	D	6	LEU	N-CA-C	6.44	120.14	109.46
1	A	7	LEU	N-CA-C	-5.72	105.13	111.71
1	D	255	ASP	N-CA-C	5.59	117.38	111.28
1	D	389	LYS	N-CA-C	5.52	118.19	108.75

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	2958	0	2930	44	0
1	B	2981	0	2991	51	0
1	C	2960	0	2954	48	0
1	D	2952	0	2918	56	0
2	A	12	0	16	0	0
2	B	12	0	16	0	0
2	C	24	0	32	4	0
2	D	30	0	40	11	0
All	All	11929	0	11897	192	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 8.

The worst 5 of 192 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:136[B]:LEU:HD13	1:D:136[B]:LEU:H	1.17	1.03
1:D:136[B]:LEU:HD13	1:D:136[B]:LEU:N	1.89	0.84
1:C:378:GLU:OE2	1:C:381:ARG:NH1	2.14	0.80
1:A:127:THR:OG1	1:C:129:ASP:OD1	2.03	0.76
1:D:136[B]:LEU:H	1:D:136[B]:LEU:CD1	1.86	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	385/394 (98%)	375 (97%)	9 (2%)	1 (0%)	36 65
1	B	383/394 (97%)	373 (97%)	10 (3%)	0	100 100
1	C	382/394 (97%)	373 (98%)	8 (2%)	1 (0%)	36 65

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	D	384/394 (98%)	372 (97%)	11 (3%)	1 (0%)	36 65
All	All	1534/1576 (97%)	1493 (97%)	38 (2%)	3 (0%)	43 72

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	266	VAL
1	A	266	VAL
1	D	266	VAL

### 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	303/325 (93%)	293 (97%)	10 (3%)	33 67
1	B	313/325 (96%)	298 (95%)	15 (5%)	23 55
1	C	308/325 (95%)	296 (96%)	12 (4%)	28 63
1	D	306/325 (94%)	292 (95%)	14 (5%)	24 57
All	All	1230/1300 (95%)	1179 (96%)	51 (4%)	26 61

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	149	VAL
1	C	370	ARG
1	D	264	ILE
1	C	179	LEU
1	C	225	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	124	HIS

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Mol	Chain	Res	Type
1	D	303	GLN
1	D	146	HIS
1	D	212	ASN
1	B	146	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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
1	LLP	D	209	1	23,24,25	1.82	7 (30%)	25,32,34	2.00	4 (16%)
1	LLP	C	209	1	23,24,25	1.94	5 (21%)	25,32,34	1.92	4 (16%)
1	LLP	B	209	1	23,24,25	1.85	5 (21%)	25,32,34	1.85	7 (28%)
1	LLP	A	209	1	23,24,25	1.76	5 (21%)	25,32,34	2.05	5 (20%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	LLP	D	209	1	-	5/16/17/19	0/1/1/1
1	LLP	C	209	1	-	8/16/17/19	0/1/1/1
1	LLP	B	209	1	-	5/16/17/19	0/1/1/1
1	LLP	A	209	1	-	8/16/17/19	0/1/1/1

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	209	LLP	O3-C3	-5.43	1.24	1.36
1	B	209	LLP	O3-C3	-5.36	1.24	1.36
1	A	209	LLP	O3-C3	-5.07	1.25	1.36
1	D	209	LLP	O3-C3	-4.68	1.26	1.36
1	C	209	LLP	C6-N1	3.78	1.42	1.34

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	209	LLP	OP4-C5'-C5	7.05	122.56	109.36
1	A	209	LLP	C4-C4'-NZ	-5.89	96.87	124.04
1	A	209	LLP	OP4-C5'-C5	5.80	120.22	109.36
1	B	209	LLP	OP4-C5'-C5	5.66	119.97	109.36
1	C	209	LLP	C4-C4'-NZ	-5.30	99.58	124.04

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	209	LLP	C5'-OP4-P-OP2
1	B	209	LLP	C5'-OP4-P-OP1
1	B	209	LLP	C5'-OP4-P-OP2
1	B	209	LLP	C5'-OP4-P-OP3
1	C	209	LLP	C5'-OP4-P-OP1

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	D	209	LLP	3	0
1	C	209	LLP	2	0
1	B	209	LLP	2	0
1	A	209	LLP	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

13 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	GOL	D	402	-	5,5,5	0.49	0	5,5,5	0.61	0
2	GOL	D	405	-	5,5,5	0.50	0	5,5,5	0.27	0
2	GOL	B	401	-	5,5,5	0.41	0	5,5,5	0.28	0
2	GOL	A	401	-	5,5,5	0.39	0	5,5,5	0.40	0
2	GOL	C	404	-	5,5,5	0.44	0	5,5,5	0.74	0
2	GOL	D	401	-	5,5,5	0.42	0	5,5,5	0.45	0
2	GOL	D	404	-	5,5,5	0.47	0	5,5,5	0.40	0
2	GOL	C	401	-	5,5,5	0.37	0	5,5,5	0.23	0
2	GOL	C	402	-	5,5,5	0.44	0	5,5,5	0.69	0
2	GOL	C	403	-	5,5,5	0.47	0	5,5,5	0.52	0
2	GOL	D	403	-	5,5,5	0.58	0	5,5,5	0.77	0
2	GOL	B	402	-	5,5,5	0.47	0	5,5,5	0.48	0
2	GOL	A	402	-	5,5,5	0.52	0	5,5,5	0.80	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	D	402	-	-	2/4/4/4	-
2	GOL	D	405	-	-	1/4/4/4	-
2	GOL	B	401	-	-	2/4/4/4	-
2	GOL	A	401	-	-	0/4/4/4	-
2	GOL	C	404	-	-	4/4/4/4	-
2	GOL	D	401	-	-	2/4/4/4	-
2	GOL	D	404	-	-	2/4/4/4	-
2	GOL	C	401	-	-	2/4/4/4	-
2	GOL	C	402	-	-	4/4/4/4	-
2	GOL	C	403	-	-	4/4/4/4	-
2	GOL	D	403	-	-	3/4/4/4	-
2	GOL	B	402	-	-	4/4/4/4	-
2	GOL	A	402	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 31 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	402	GOL	O1-C1-C2-C3
2	C	401	GOL	C1-C2-C3-O3
2	C	402	GOL	C1-C2-C3-O3
2	C	403	GOL	O1-C1-C2-C3
2	C	403	GOL	C1-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	404	GOL	2	0
2	D	401	GOL	1	0
2	C	401	GOL	1	0
2	C	402	GOL	1	0
2	D	403	GOL	10	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	386/394 (97%)	0.60	14 (3%) 46 38	13, 29, 43, 65	2 (0%)
1	B	385/394 (97%)	0.65	14 (3%) 46 38	13, 30, 45, 57	2 (0%)
1	C	384/394 (97%)	0.49	13 (3%) 48 39	18, 28, 41, 57	1 (0%)
1	D	385/394 (97%)	0.76	22 (5%) 29 23	13, 31, 46, 70	3 (0%)
All	All	1540/1576 (97%)	0.63	63 (4%) 41 33	13, 30, 45, 70	8 (0%)

The worst 5 of 63 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	386	HIS	7.8
1	D	386	HIS	7.6
1	D	136[A]	LEU	3.8
1	A	51[A]	LYS	3.5
1	D	288	TRP	3.4

### 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	LLP	B	209	24/25	0.90	0.11	25,33,34,36	0
1	LLP	A	209	24/25	0.92	0.12	26,30,33,34	0
1	LLP	C	209	24/25	0.92	0.11	25,28,29,30	0
1	LLP	D	209	24/25	0.93	0.12	26,31,34,36	0

### 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	GOL	B	401	6/6	0.53	0.21	47,50,50,50	0
2	GOL	D	403	6/6	0.53	0.32	49,52,53,65	0
2	GOL	D	402	6/6	0.63	0.18	44,47,49,51	0
2	GOL	D	404	6/6	0.71	0.15	45,47,48,48	0
2	GOL	D	401	6/6	0.77	0.11	30,33,33,35	0
2	GOL	B	402	6/6	0.77	0.14	34,38,40,40	0
2	GOL	C	403	6/6	0.80	0.15	32,34,34,34	0
2	GOL	C	404	6/6	0.82	0.15	38,45,47,51	0
2	GOL	A	402	6/6	0.83	0.14	42,48,51,51	0
2	GOL	C	402	6/6	0.84	0.12	33,34,39,42	0
2	GOL	C	401	6/6	0.85	0.11	26,27,28,30	0
2	GOL	D	405	6/6	0.87	0.09	34,37,37,38	0
2	GOL	A	401	6/6	0.88	0.11	50,52,53,57	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.