



# Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 11:35 am BST

PDB ID : 5WJA  
Title : Crystal structure of H107A peptidylglycine alpha-hydroxylating monooxygenase (PHM) in complex with citrate  
Authors : Maheshwari, S.; Rudzka, K.; Gabelli, S.B.; Amzel, L.M.  
Deposited on : 2017-07-21  
Resolution : 2.30 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 : 2.11  
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

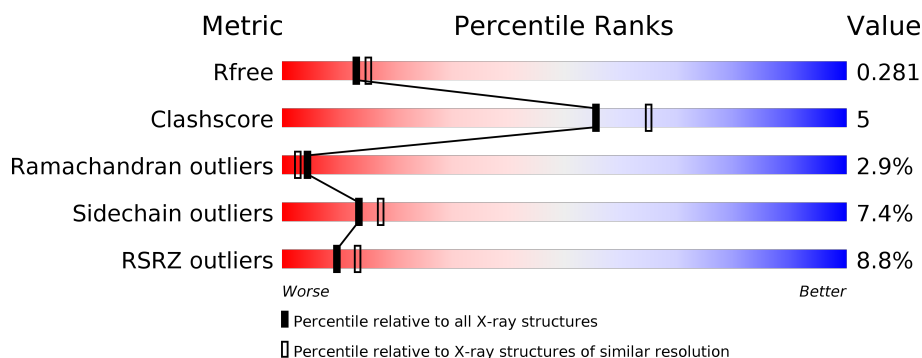
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	312	
1	D	312	

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
5	FLC	D	1002	-	-	X	-

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5004 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 Peptidyl-glycine alpha-amidating monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	305	Total	C	N	O	S	0	0	0
			2378	1516	401	436	25			
1	D	311	Total	C	N	O	S	0	2	0
			2431	1549	408	447	27			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	ALA	HIS	engineered mutation	UNP P14925
D	107	ALA	HIS	engineered mutation	UNP P14925

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Cu	0	0
			2	2		
2	D	1	Total	Cu	0	0
			1	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).

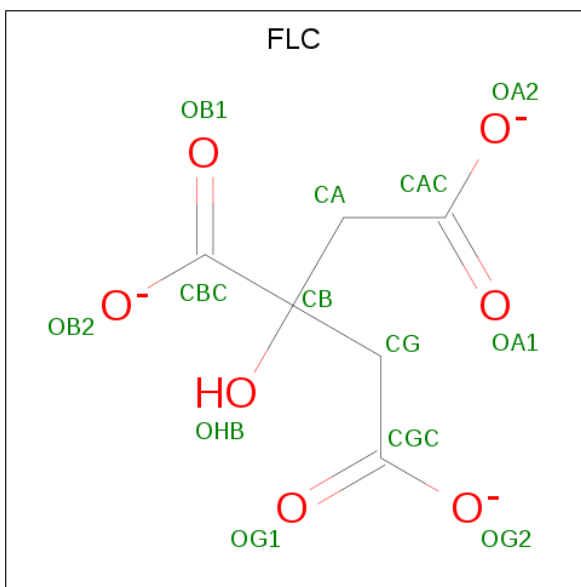


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ni	0	0
			1	1		

- Molecule 5 is CITRATE ANION (three-letter code: FLC) (formula: C<sub>6</sub>H<sub>5</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			13	6	7		

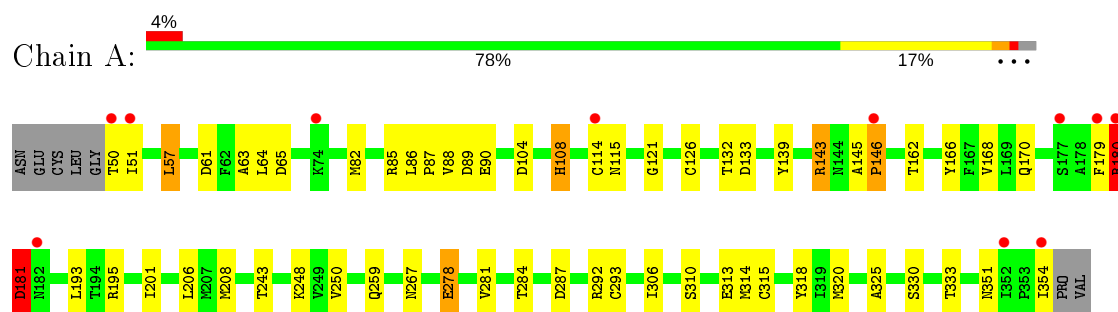
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	81	Total	O	0	0
			81	81		
6	D	61	Total	O	0	0
			61	61		

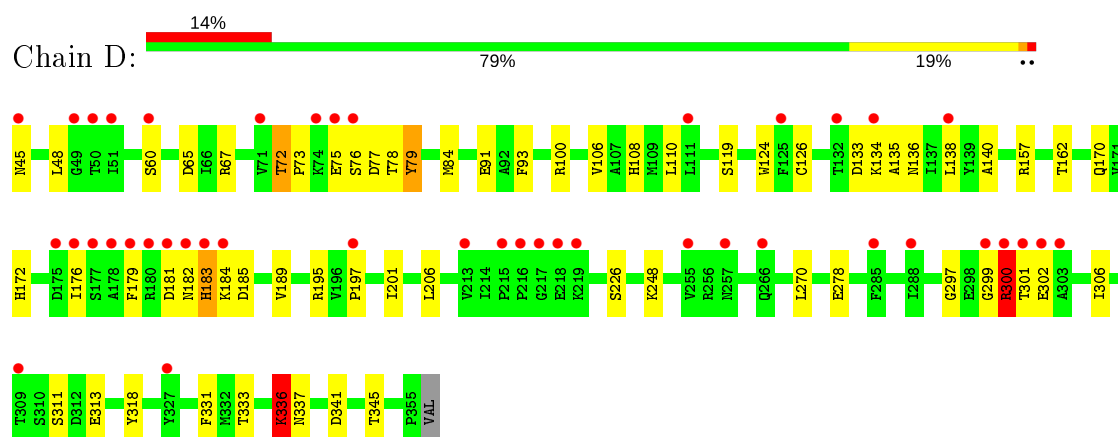
### 3 Residue-property plots [i](#)

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: Peptidyl-glycine alpha-amidating monooxygenase



- Molecule 1: Peptidyl-glycine alpha-amidating monooxygenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.54Å 100.61Å 101.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.77 – 2.30 29.77 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (29.77-2.30) 99.6 (29.77-2.30)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.44 (at 2.31Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.198 , 0.273 0.208 , 0.281	Depositor DCC
$R_{free}$ test set	1390 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	43.4	Xtriage
Anisotropy	0.581	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 50.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.017 for -h,l,k	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5004	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.10% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, FLC, CU, NI

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	0.65	0/2445	0.88	2/3326 (0.1%)
1	D	0.60	0/2505	0.81	1/3407 (0.0%)
All	All	0.63	0/4950	0.85	3/6733 (0.0%)

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	D	0	2
All	All	0	6

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	287	ASP	CB-CG-OD1	6.56	124.20	118.30
1	D	300	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	A	195	ARG	NE-CZ-NH1	5.26	122.93	120.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	121	GLY	Peptide
1	A	132	THR	Peptide
1	A	179	PHE	Peptide

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Mol	Chain	Res	Type	Group
1	A	50	THR	Peptide
1	D	135	ALA	Peptide
1	D	336	LYS	Peptide

## 5.2 Too-close contacts

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	2378	0	2306	28	0
1	D	2431	0	2357	22	0
2	A	2	0	0	0	0
2	D	1	0	0	0	0
3	A	36	0	48	4	0
4	A	1	0	0	0	0
5	D	13	0	5	5	0
6	A	81	0	0	0	0
6	D	61	0	0	0	0
All	All	5004	0	4716	49	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 5.

All (49) 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:108:HIS:NE2	5:D:1002:FLC:CBC	2.40	0.84
1:D:172:HIS:ND1	5:D:1002:FLC:OB2	2.18	0.76
1:D:108:HIS:NE2	5:D:1002:FLC:OB2	2.24	0.70
1:A:259:GLN:HE21	3:A:1003:GOL:H12	1.61	0.66
1:D:110:LEU:HD13	1:D:140:ALA:HB2	1.85	0.59
1:D:297:GLY:O	1:D:299:GLY:N	2.36	0.59
1:A:292:ARG:HH11	1:A:351:ASN:HD21	1.52	0.58
1:A:139:TYR:HA	3:A:1007:GOL:H11	1.89	0.54
1:D:76:SER:HA	1:D:176:ILE:HG12	1.90	0.54
1:A:85:ARG:NH2	1:A:89:ASP:OD1	2.41	0.54
1:A:267:ASN:HB2	1:A:354:ILE:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:170:GLN:HE22	5:D:1002:FLC:HA1	1.72	0.53
1:A:57:LEU:HD21	1:A:63:ALA:HB2	1.93	0.51
1:A:206:LEU:HD13	1:A:318:TYR:CD2	2.45	0.50
1:D:79:TYR:CD2	1:D:126:CYS:HB2	2.46	0.50
1:A:180:ARG:O	1:A:181:ASP:HB3	2.13	0.48
1:D:93:PHE:CE1	1:D:197:PRO:HA	2.48	0.48
1:A:88:VAL:HB	1:A:90:GLU:OE1	2.14	0.47
1:A:108:HIS:C	1:A:108:HIS:CD2	2.89	0.46
5:D:1002:FLC:HA2	5:D:1002:FLC:OG1	2.15	0.46
1:A:64:LEU:HD11	1:A:87:PRO:HD3	1.97	0.46
1:A:85:ARG:NH1	1:D:278:GLU:OE2	2.49	0.46
1:D:226:SER:OG	1:D:337:ASN:OD1	2.35	0.45
1:A:250:VAL:HG22	1:A:293:CYS:SG	2.56	0.45
1:D:91:GLU:OE2	1:D:157:ARG:NH1	2.49	0.45
1:D:157:ARG:HD3	1:D:201:ILE:HD13	1.99	0.45
1:D:136:ASN:HD22	1:D:331:PHE:HB2	1.81	0.45
1:A:143:ARG:NE	1:A:143:ARG:HA	2.32	0.44
1:A:330:SER:HB3	3:A:1006:GOL:H31	2.00	0.44
1:A:201:ILE:HG12	1:A:325:ALA:HA	1.98	0.44
1:D:206:LEU:HD13	1:D:318:TYR:CD2	2.52	0.44
1:D:206:LEU:HD13	1:D:318:TYR:CE2	2.52	0.44
1:D:67:ARG:NH2	1:D:100:ARG:HG2	2.33	0.44
1:D:181:ASP:HB2	1:D:183:HIS:ND1	2.32	0.43
1:A:143:ARG:HE	1:A:143:ARG:HA	1.82	0.43
1:A:57:LEU:HD12	1:A:61:ASP:HB2	2.00	0.43
1:A:114:CYS:HB3	1:A:168:VAL:HG23	2.01	0.43
1:A:306:ILE:HA	1:A:313:GLU:O	2.18	0.43
1:A:208:MET:HA	1:A:315:CYS:O	2.18	0.43
1:A:126:CYS:SG	1:A:170:GLN:HG3	2.59	0.42
1:A:145:ALA:O	1:A:146:PRO:C	2.58	0.42
1:D:119:SER:HB3	1:D:124:TRP:CE3	2.54	0.42
1:A:166:TYR:OH	1:D:278:GLU:OE2	2.33	0.41
1:A:82:MET:C	1:A:82:MET:SD	2.98	0.41
1:D:306:ILE:HA	1:D:313:GLU:O	2.20	0.41
1:D:73:PRO:HG2	1:D:176:ILE:HD12	2.02	0.41
1:A:162:THR:HG22	1:A:162:THR:O	2.21	0.41
1:A:243:THR:HA	1:A:314:MET:O	2.21	0.41
1:A:320:MET:SD	3:A:1007:GOL:H32	2.61	0.41

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	303/312 (97%)	281 (93%)	14 (5%)	8 (3%)	5	4
1	D	311/312 (100%)	277 (89%)	24 (8%)	10 (3%)	4	2
All	All	614/624 (98%)	558 (91%)	38 (6%)	18 (3%)	4	3

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	115	ASN
1	A	133	ASP
1	A	181	ASP
1	A	278	GLU
1	D	134	LYS
1	D	183	HIS
1	D	336	LYS
1	D	72	THR
1	D	300	ARG
1	D	301	THR
1	A	180	ARG
1	D	78	THR
1	D	133	ASP
1	D	185	ASP
1	A	51	ILE
1	A	104	ASP
1	D	179	PHE
1	A	146	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	260/266 (98%)	246 (95%)	14 (5%)	22	30
1	D	267/266 (100%)	241 (90%)	26 (10%)	8	9
All	All	527/532 (99%)	487 (92%)	40 (8%)	13	16

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	LEU
1	A	65	ASP
1	A	86	LEU
1	A	108	HIS
1	A	143	ARG
1	A	180	ARG
1	A	181	ASP
1	A	193	LEU
1	A	248	LYS
1	A	278	GLU
1	A	281	VAL
1	A	284	THR
1	A	310	SER
1	A	333	THR
1	D	45	ASN
1	D	48	LEU
1	D	60	SER
1	D	65	ASP
1	D	72	THR
1	D	75	GLU
1	D	77	ASP
1	D	79	TYR
1	D	84[A]	MET
1	D	84[B]	MET
1	D	106	VAL
1	D	138	LEU
1	D	162	THR
1	D	182	ASN
1	D	184	LYS
1	D	189	VAL
1	D	195	ARG
1	D	248	LYS
1	D	270	LEU

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Mol	Chain	Res	Type
1	D	300	ARG
1	D	302	GLU
1	D	311	SER
1	D	333	THR
1	D	336	LYS
1	D	341	ASP
1	D	345	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	ASN
1	A	136	ASN
1	A	222	ASN
1	A	259	GLN
1	A	316	ASN
1	A	351	ASN
1	D	45	ASN
1	D	136	ASN
1	D	170	GLN
1	D	316	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 4 are monoatomic - leaving 7 for Mogul analysis.

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	A	1005	-	5,5,5	0.28	0	5,5,5	0.38	0
3	GOL	A	1004	-	5,5,5	0.45	0	5,5,5	0.41	0
3	GOL	A	1003	-	5,5,5	0.40	0	5,5,5	1.61	2 (40%)
3	GOL	A	1008	-	5,5,5	0.45	0	5,5,5	0.63	0
3	GOL	A	1007	-	5,5,5	0.85	0	5,5,5	0.91	0
5	FLC	D	1002	-	3,12,12	2.13	1 (33%)	3,17,17	3.43	1 (33%)
3	GOL	A	1006	-	5,5,5	0.46	0	5,5,5	0.79	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
3	GOL	A	1005	-	-	2/4/4/4	-
3	GOL	A	1004	-	-	4/4/4/4	-
3	GOL	A	1003	-	-	2/4/4/4	-
3	GOL	A	1008	-	-	2/4/4/4	-
3	GOL	A	1007	-	-	2/4/4/4	-
5	FLC	D	1002	-	-	3/6/16/16	-
3	GOL	A	1006	-	-	2/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	1002	FLC	OHB-CB	3.45	1.48	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	1002	FLC	CG-CB-CA	5.86	124.99	109.33
3	A	1003	GOL	C3-C2-C1	-2.35	102.57	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1003	GOL	O2-C2-C3	2.31	119.31	109.12

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1005	GOL	O2-C2-C3-O3
3	A	1004	GOL	C1-C2-C3-O3
3	A	1007	GOL	O1-C1-C2-C3
5	D	1002	FLC	CAC-CA-CB-CBC
5	D	1002	FLC	CA-CB-CG-CGC
3	A	1006	GOL	O1-C1-C2-C3
3	A	1006	GOL	O1-C1-C2-O2
3	A	1005	GOL	C1-C2-C3-O3
3	A	1003	GOL	O1-C1-C2-C3
3	A	1008	GOL	O1-C1-C2-C3
3	A	1007	GOL	O1-C1-C2-O2
3	A	1004	GOL	O2-C2-C3-O3
3	A	1003	GOL	O1-C1-C2-O2
3	A	1004	GOL	O1-C1-C2-O2
5	D	1002	FLC	CBC-CB-CG-CGC
3	A	1008	GOL	O1-C1-C2-O2
3	A	1004	GOL	O1-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1003	GOL	1	0
3	A	1007	GOL	2	0
5	D	1002	FLC	5	0
3	A	1006	GOL	1	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	305/312 (97%)	0.14	11 (3%) 42 49	28, 41, 78, 110	4 (1%)
1	D	311/312 (99%)	0.66	43 (13%) 2 4	28, 54, 97, 127	2 (0%)
All	All	616/624 (98%)	0.40	54 (8%) 10 13	28, 47, 87, 127	6 (0%)

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	176	ILE	8.9
1	D	180	ARG	6.0
1	D	179	PHE	5.5
1	D	50	THR	5.2
1	D	217	GLY	5.0
1	A	50	THR	5.0
1	A	180	ARG	4.9
1	D	216	PRO	4.4
1	A	146	PRO	4.3
1	D	303	ALA	4.1
1	A	51	ILE	3.9
1	D	51	ILE	3.9
1	D	301	THR	3.8
1	D	181	ASP	3.7
1	D	302	GLU	3.7
1	A	354	ILE	3.5
1	D	183	HIS	3.3
1	D	182	ASN	3.3
1	D	177	SER	3.2
1	D	300	ARG	3.1
1	D	134	LYS	3.1
1	D	327	TYR	3.0
1	D	45	ASN	3.0
1	A	179	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	266	GLN	2.9
1	D	49	GLY	2.8
1	D	76	SER	2.8
1	D	255	VAL	2.7
1	D	138	LEU	2.7
1	A	74	LYS	2.6
1	D	71	VAL	2.5
1	D	309	THR	2.5
1	D	125	PHE	2.4
1	D	285	PHE	2.4
1	D	257	ASN	2.4
1	D	184	LYS	2.3
1	A	114	CYS	2.3
1	A	182	ASN	2.3
1	D	175	ASP	2.3
1	D	215	PRO	2.3
1	A	352	ILE	2.3
1	D	299	GLY	2.3
1	D	60	SER	2.2
1	D	111	LEU	2.2
1	D	288	ILE	2.2
1	D	132	THR	2.2
1	D	74	LYS	2.2
1	D	213	VAL	2.1
1	D	178	ALA	2.1
1	D	75	GLU	2.1
1	D	218	GLU	2.1
1	A	177	SER	2.1
1	D	197	PRO	2.1
1	D	219	LYS	2.0

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

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

## 6.3 Carbohydrates ⓘ

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	1007	6/6	0.59	0.23	42,51,55,58	0
3	GOL	A	1008	6/6	0.68	0.39	73,78,80,81	0
3	GOL	A	1004	6/6	0.82	0.25	75,78,79,85	0
3	GOL	A	1005	6/6	0.88	0.23	64,68,72,77	0
3	GOL	A	1006	6/6	0.90	0.19	50,55,56,57	0
3	GOL	A	1003	6/6	0.92	0.17	37,39,42,42	0
5	FLC	D	1002	13/13	0.93	0.17	35,56,68,69	0
2	CU	A	1001	1/1	0.98	0.06	73,73,73,73	0
2	CU	D	1001	1/1	0.98	0.10	48,48,48,48	0
2	CU	A	1002	1/1	0.98	0.08	46,46,46,46	0
4	NI	A	1009	1/1	0.99	0.06	47,47,47,47	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.