wwPDB X-ray Structure Validation Summary Report (i)

Jun 27, 2024 – 04:08 PM EDT

PDB ID	:	8TX5
Title	:	Crystal structure of an engineered variant of galactose oxidase, GOaseRd4BB, from Fusarium graminearum
Authors	:	Selvaraj, B.; Orth, P.
Deposited on	:	2023-08-22
Resolution	:	1.93 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (1)) were used in the production of this report:

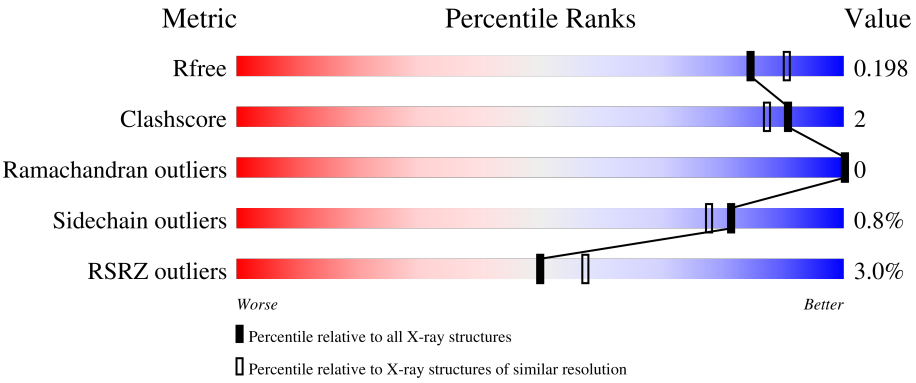
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 1.93 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	4310 (1.96-1.92)
Clashscore	141614	1023 (1.94-1.94)
Ramachandran outliers	138981	1007 (1.94-1.94)
Sidechain outliers	138945	1007 (1.94-1.94)
RSRZ outliers	127900	4250 (1.96-1.92)

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 >=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 <=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	647	2% 94%
1	B	647	3% 94%
1	C	647	4% 95%
1	D	647	3% 94%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 20976 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 Galactose oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	639	Total	C	N	O	S	0	0	0
			4824	3008	840	958	18			
1	B	639	Total	C	N	O	S	0	0	0
			4824	3008	840	958	18			
1	C	639	Total	C	N	O	S	0	0	0
			4824	3008	840	958	18			
1	D	639	Total	C	N	O	S	0	0	0
			4824	3008	840	958	18			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P0CS93
A	10	PRO	SER	conflict	UNP P0CS93
A	70	VAL	MET	conflict	UNP P0CS93
A	195	GLU	GLY	conflict	UNP P0CS93
A	219	SER	VAL	conflict	UNP P0CS93
A	290	PHE	TRP	conflict	UNP P0CS93
A	294	ARG	VAL	conflict	UNP P0CS93
A	295	VAL	PHE	conflict	UNP P0CS93
A	406	GLU	GLN	conflict	UNP P0CS93
A	464	THR	PHE	conflict	UNP P0CS93
A	494	ALA	VAL	conflict	UNP P0CS93
A	535	ASP	ASN	conflict	UNP P0CS93
A	640	GLY	-	expression tag	UNP P0CS93
A	641	HIS	-	expression tag	UNP P0CS93
A	642	HIS	-	expression tag	UNP P0CS93
A	643	HIS	-	expression tag	UNP P0CS93
A	644	HIS	-	expression tag	UNP P0CS93
A	645	HIS	-	expression tag	UNP P0CS93
A	646	HIS	-	expression tag	UNP P0CS93
B	0	MET	-	initiating methionine	UNP P0CS93
B	10	PRO	SER	conflict	UNP P0CS93

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	70	VAL	MET	conflict	UNP P0CS93
B	195	GLU	GLY	conflict	UNP P0CS93
B	219	SER	VAL	conflict	UNP P0CS93
B	290	PHE	TRP	conflict	UNP P0CS93
B	294	ARG	VAL	conflict	UNP P0CS93
B	295	VAL	PHE	conflict	UNP P0CS93
B	406	GLU	GLN	conflict	UNP P0CS93
B	464	THR	PHE	conflict	UNP P0CS93
B	494	ALA	VAL	conflict	UNP P0CS93
B	535	ASP	ASN	conflict	UNP P0CS93
B	640	GLY	-	expression tag	UNP P0CS93
B	641	HIS	-	expression tag	UNP P0CS93
B	642	HIS	-	expression tag	UNP P0CS93
B	643	HIS	-	expression tag	UNP P0CS93
B	644	HIS	-	expression tag	UNP P0CS93
B	645	HIS	-	expression tag	UNP P0CS93
B	646	HIS	-	expression tag	UNP P0CS93
C	0	MET	-	initiating methionine	UNP P0CS93
C	10	PRO	SER	conflict	UNP P0CS93
C	70	VAL	MET	conflict	UNP P0CS93
C	195	GLU	GLY	conflict	UNP P0CS93
C	219	SER	VAL	conflict	UNP P0CS93
C	290	PHE	TRP	conflict	UNP P0CS93
C	294	ARG	VAL	conflict	UNP P0CS93
C	295	VAL	PHE	conflict	UNP P0CS93
C	406	GLU	GLN	conflict	UNP P0CS93
C	464	THR	PHE	conflict	UNP P0CS93
C	494	ALA	VAL	conflict	UNP P0CS93
C	535	ASP	ASN	conflict	UNP P0CS93
C	640	GLY	-	expression tag	UNP P0CS93
C	641	HIS	-	expression tag	UNP P0CS93
C	642	HIS	-	expression tag	UNP P0CS93
C	643	HIS	-	expression tag	UNP P0CS93
C	644	HIS	-	expression tag	UNP P0CS93
C	645	HIS	-	expression tag	UNP P0CS93
C	646	HIS	-	expression tag	UNP P0CS93
D	0	MET	-	initiating methionine	UNP P0CS93
D	10	PRO	SER	conflict	UNP P0CS93
D	70	VAL	MET	conflict	UNP P0CS93
D	195	GLU	GLY	conflict	UNP P0CS93
D	219	SER	VAL	conflict	UNP P0CS93
D	290	PHE	TRP	conflict	UNP P0CS93

Continued on next page...

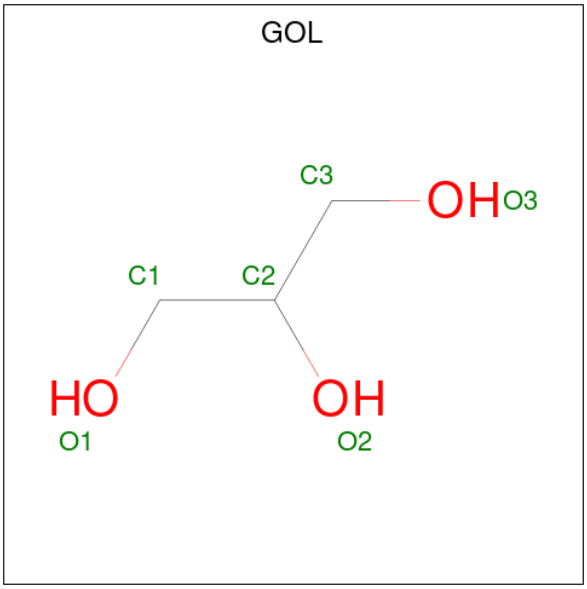
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	294	ARG	VAL	conflict	UNP P0CS93
D	295	VAL	PHE	conflict	UNP P0CS93
D	406	GLU	GLN	conflict	UNP P0CS93
D	464	THR	PHE	conflict	UNP P0CS93
D	494	ALA	VAL	conflict	UNP P0CS93
D	535	ASP	ASN	conflict	UNP P0CS93
D	640	GLY	-	expression tag	UNP P0CS93
D	641	HIS	-	expression tag	UNP P0CS93
D	642	HIS	-	expression tag	UNP P0CS93
D	643	HIS	-	expression tag	UNP P0CS93
D	644	HIS	-	expression tag	UNP P0CS93
D	645	HIS	-	expression tag	UNP P0CS93
D	646	HIS	-	expression tag	UNP P0CS93

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

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

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



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

- Molecule 4 is water.

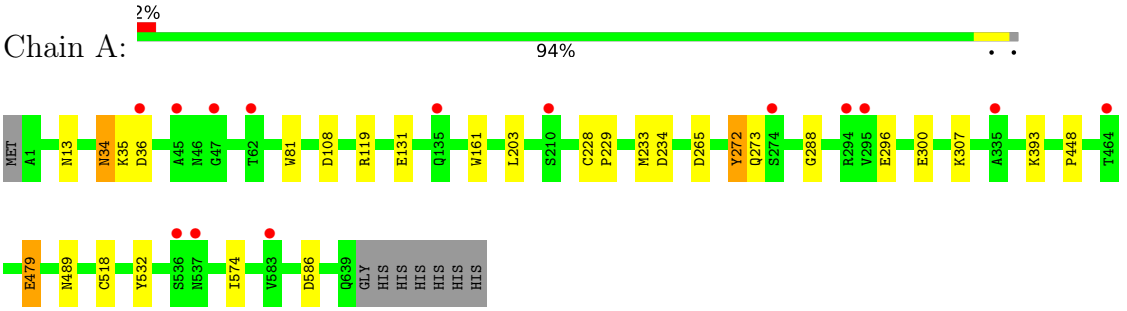
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	426	Total O 426 426	0	0
4	B	404	Total O 404 404	0	0
4	C	425	Total O 425 425	0	0
4	D	397	Total O 397 397	0	0

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.

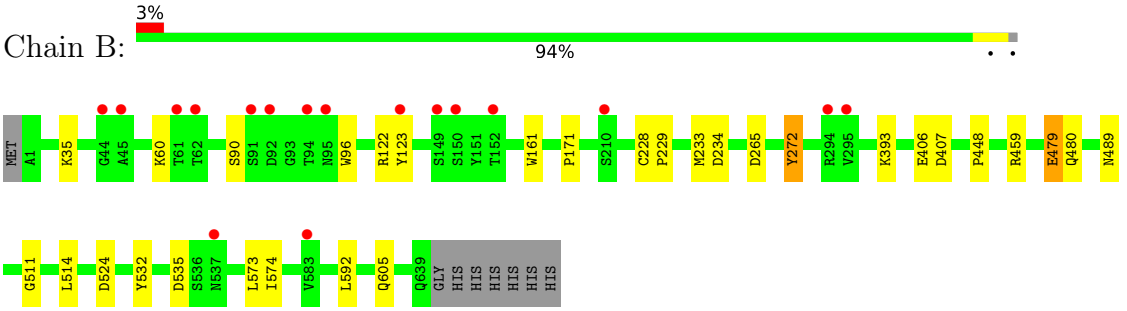
• Molecule 1: Galactose oxidase

Chain A:



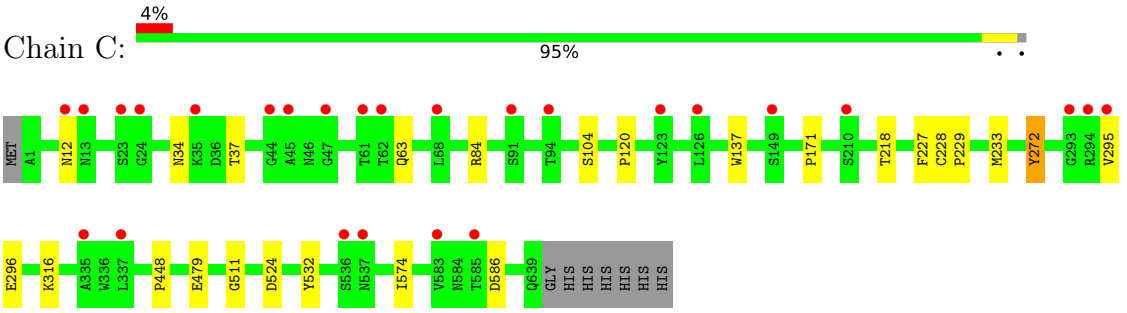
• Molecule 1: Galactose oxidase

Chain B:



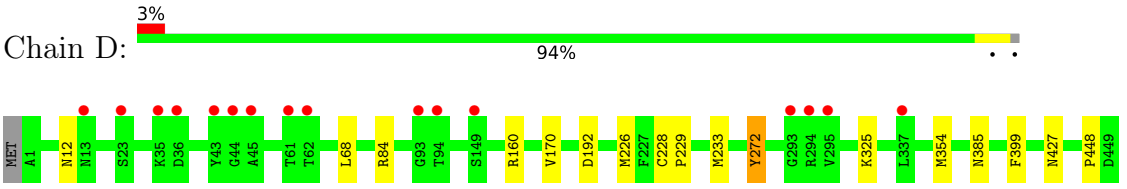
• Molecule 1: Galactose oxidase

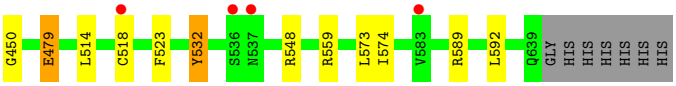
Chain C:



• Molecule 1: Galactose oxidase

Chain D:




G450
E479
L514
C518
F523
Y532
S536
N537
R548
R559
L573
I574
V583
R589
L592
Q639
GLY
HIS
HIS
HIS
HIS
HIS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	89.01Å 205.75Å 89.29Å 90.00° 92.93° 90.00°	Depositor
Resolution (Å)	28.02 – 1.93 28.02 – 1.93	Depositor EDS
% Data completeness (in resolution range)	92.7 (28.02-1.93) 92.7 (28.02-1.93)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.17 (at 1.92Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.163 , 0.198 0.163 , 0.198	Depositor DCC
R_{free} test set	11305 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	24.5	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 42.3	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.011 for l,k,-h 0.025 for h,-k,-l 0.085 for l,-k,h	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	20976	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: CU, GOL

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	0.83	4/4951 (0.1%)	0.85	8/6756 (0.1%)
1	B	0.84	3/4951 (0.1%)	0.85	8/6756 (0.1%)
1	C	0.81	3/4951 (0.1%)	0.84	3/6756 (0.0%)
1	D	0.84	7/4951 (0.1%)	0.83	4/6756 (0.1%)
All	All	0.83	17/19804 (0.1%)	0.84	23/27024 (0.1%)

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	B	0	1

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	518	CYS	CB-SG	7.65	1.95	1.82
1	D	479	GLU	CG-CD	7.41	1.63	1.51
1	D	272	TYR	CD1-CE1	-7.34	1.28	1.39
1	D	272	TYR	CG-CD1	-6.81	1.30	1.39
1	C	272	TYR	CE2-CZ	-6.58	1.29	1.38

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	272	TYR	CD1-CE1-CZ	8.93	127.83	119.80
1	C	272	TYR	CD1-CE1-CZ	8.56	127.51	119.80
1	B	524	ASP	CB-CG-OD1	8.11	125.59	118.30
1	D	272	TYR	CD1-CE1-CZ	8.07	127.06	119.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	272	TYR	CD1-CE1-CZ	7.87	126.89	119.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	459	ARG	Sidechain

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	4824	0	4598	16	0
1	B	4824	0	4598	15	0
1	C	4824	0	4598	15	0
1	D	4824	0	4598	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
3	C	6	0	8	0	0
3	D	6	0	8	0	0
4	A	426	0	0	4	0
4	B	404	0	0	4	1
4	C	425	0	0	3	0
4	D	397	0	0	5	1
All	All	20976	0	18424	64	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 2.

The worst 5 of 64 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:A:228:CYS:SG	1:A:272:TYR:HE1	1.22	1.61
1:B:228:CYS:SG	1:B:272:TYR:HE1	1.28	1.57
1:C:228:CYS:SG	1:C:272:TYR:HE1	1.27	1.54
1:D:228:CYS:SG	1:D:272:TYR:HE1	1.33	1.50
1:C:479:GLU:OE1	4:C:1101:HOH:O	1.57	1.17

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)
4:B:1231:HOH:O	4:D:1106:HOH:O[2_546]	1.84	0.36

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	637/647 (98%)	617 (97%)	20 (3%)	0	100	100
1	B	637/647 (98%)	616 (97%)	21 (3%)	0	100	100
1	C	637/647 (98%)	614 (96%)	23 (4%)	0	100	100
1	D	637/647 (98%)	609 (96%)	28 (4%)	0	100	100
All	All	2548/2588 (98%)	2456 (96%)	92 (4%)	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	526/533 (99%)	522 (99%)	4 (1%)	81	78
1	B	526/533 (99%)	520 (99%)	6 (1%)	73	67
1	C	526/533 (99%)	522 (99%)	4 (1%)	81	78
1	D	526/533 (99%)	523 (99%)	3 (1%)	86	85
All	All	2104/2132 (99%)	2087 (99%)	17 (1%)	81	78

5 of 17 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	12	ASN
1	D	559	ARG
1	B	480	GLN
1	B	532	TYR
1	B	605	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	427	ASN
1	C	427	ASN
1	C	74	GLN
1	B	552	GLN
1	C	135	GLN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	1002	-	5,5,5	0.82	0	5,5,5	1.00	0
3	GOL	D	1002	-	5,5,5	0.34	0	5,5,5	1.23	1 (20%)
3	GOL	B	1002	-	5,5,5	0.53	0	5,5,5	0.94	0
3	GOL	C	1002	-	5,5,5	0.60	0	5,5,5	1.15	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	1002	-	-	4/4/4/4	-
3	GOL	D	1002	-	-	0/4/4/4	-
3	GOL	B	1002	-	-	0/4/4/4	-
3	GOL	C	1002	-	-	0/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	1002	GOL	C3-C2-C1	-2.10	103.54	111.70

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1002	GOL	O1-C1-C2-O2
3	A	1002	GOL	O1-C1-C2-C3
3	A	1002	GOL	C1-C2-C3-O3
3	A	1002	GOL	O2-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

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^{th} 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^2)	Q<0.9
1	A	639/647 (98%)	-0.04	14 (2%)	62	69	15, 24, 42, 67	0
1	B	639/647 (98%)	-0.00	17 (2%)	54	61	15, 24, 45, 68	0
1	C	639/647 (98%)	0.00	26 (4%)	37	44	16, 24, 49, 71	0
1	D	639/647 (98%)	0.02	20 (3%)	49	56	16, 26, 45, 66	0
All	All	2556/2588 (98%)	-0.00	77 (3%)	50	57	15, 25, 46, 71	0

The worst 5 of 77 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	45	ALA	4.9
1	C	23	SER	4.1
1	D	45	ALA	4.0
1	C	44	GLY	3.9
1	A	45	ALA	3.7

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 monosaccharides in this entry.

6.4 Ligands

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^{th} 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^2)	Q<0.9
3	GOL	C	1002	6/6	0.83	0.24	52,54,58,63	0
3	GOL	A	1002	6/6	0.91	0.14	42,44,46,55	0
3	GOL	B	1002	6/6	0.92	0.17	44,46,49,52	0
3	GOL	D	1002	6/6	0.96	0.16	41,43,46,49	0
2	CU	C	1001	1/1	0.99	0.06	38,38,38,38	0
2	CU	D	1001	1/1	0.99	0.09	43,43,43,43	0
2	CU	A	1001	1/1	0.99	0.08	37,37,37,37	0
2	CU	B	1001	1/1	1.00	0.08	39,39,39,39	0

6.5 Other polymers (i)

There are no such residues in this entry.