



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 13, 2024 – 04:08 PM EST

PDB ID : 3JVA  
Title : Crystal structure of Dipeptide Epimerase from *Enterococcus faecalis* V583  
Authors : Fedorov, A.A.; Fedorov, E.V.; Sakai, A.; Imker, H.; Gerlt, J.A.; Almo, S.C.  
Deposited on : 2009-09-16  
Resolution : 1.70 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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
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) : 2.36

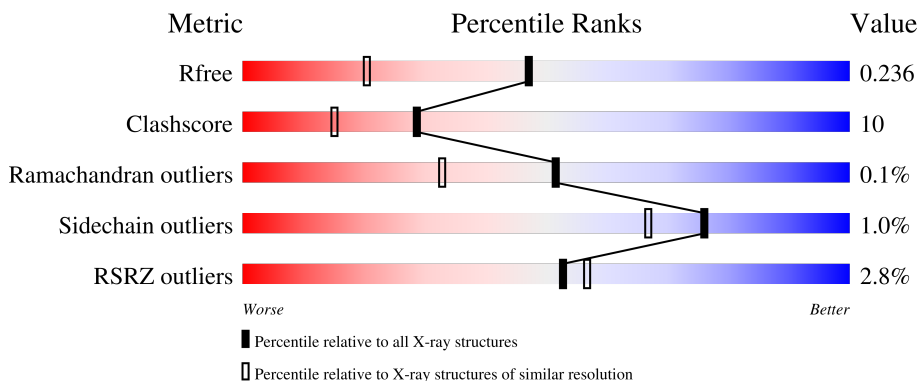
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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	354	
1	B	354	
1	C	354	
1	D	354	
1	E	354	

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Mol	Chain	Length	Quality of chain
1	F	354	 <p>% 86% 14%</p>
1	G	354	 <p>6% 73% 25% .</p>
1	H	354	 <p>% 80% 18% .</p>

## 2 Entry composition

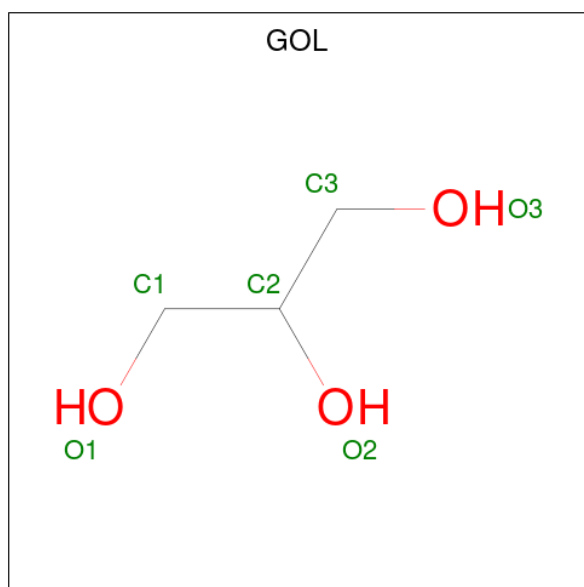
There are 5 unique types of molecules in this entry. The entry contains 21865 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Dipeptide Epimerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	353	2638	1674	434	516	14	0	0	0
1	B	354	2649	1680	437	518	14	0	0	0
1	C	344	2576	1632	427	503	14	0	0	0
1	D	346	2591	1640	429	508	14	0	0	0
1	E	353	2638	1674	434	516	14	0	0	0
1	F	354	2649	1680	437	518	14	0	0	0
1	G	345	2582	1635	428	505	14	0	0	0
1	H	346	2591	1640	429	508	14	0	0	0

- Molecule 2 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
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	B	1	Total C O 6 3 3	0	0
2	F	1	Total C O 6 3 3	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0
3	E	1	Total Mg 1 1	0	0
3	F	1	Total Mg 1 1	0	0
3	G	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	1	Total Mg 1 1	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	E	1	Total O S 5 4 1	0	0
4	G	1	Total O S 5 4 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	97	Total O 97 97	0	0
5	B	153	Total O 153 153	0	0
5	C	78	Total O 78 78	0	0

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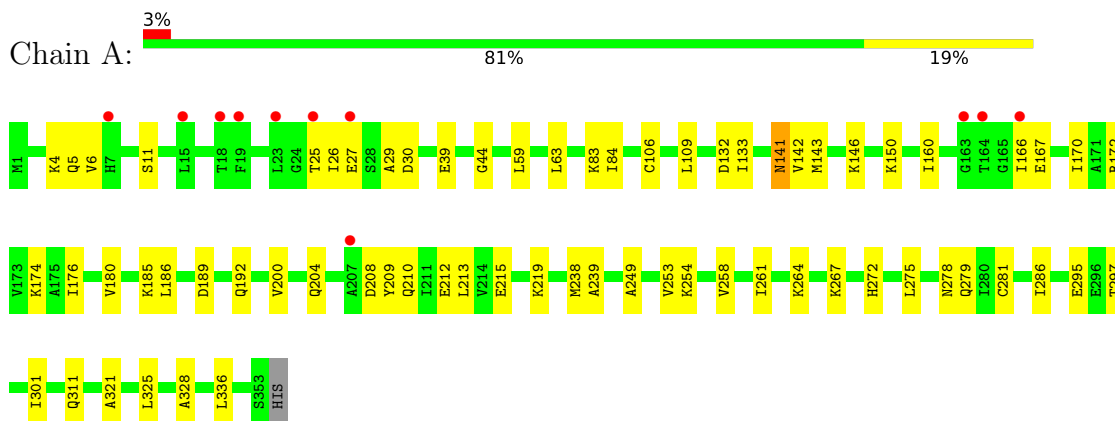
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	131	Total 131	O 131	0	0
5	E	90	Total 90	O 90	0	0
5	F	138	Total 138	O 138	0	0
5	G	76	Total 76	O 76	0	0
5	H	125	Total 125	O 125	0	0

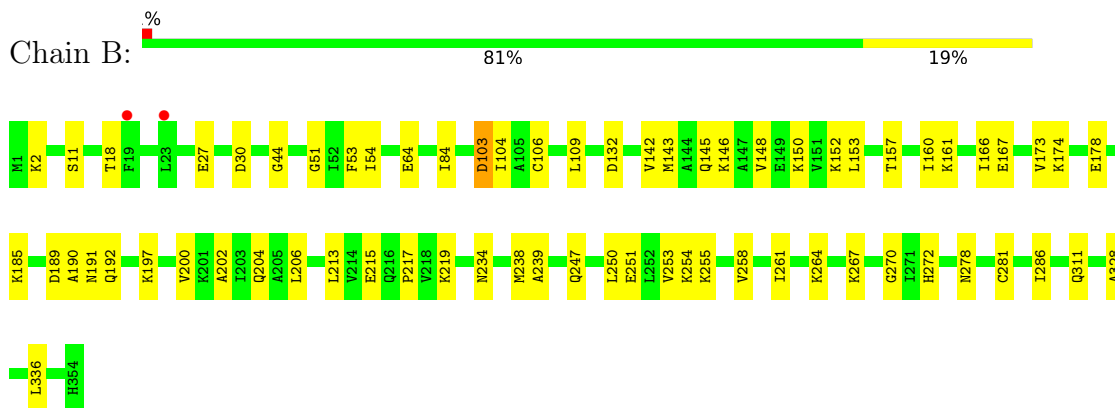
### 3 Residue-property plots [i](#)

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.

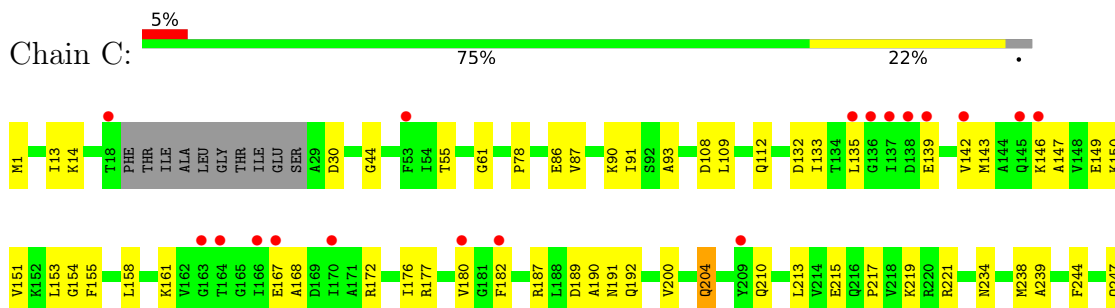
- Molecule 1: Dipeptide Epimerase



- Molecule 1: Dipeptide Epimerase



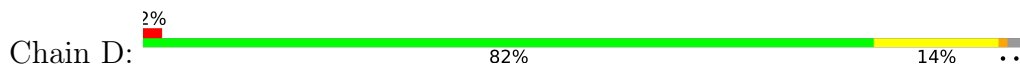
- Molecule 1: Dipeptide Epimerase



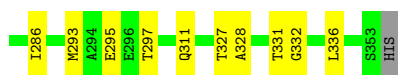
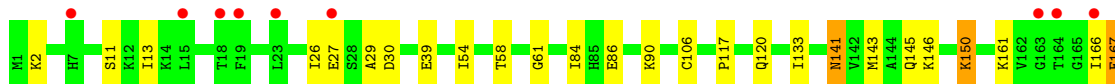
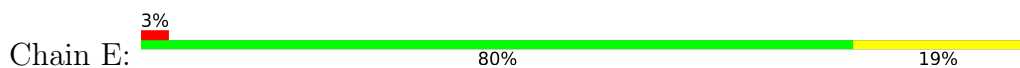




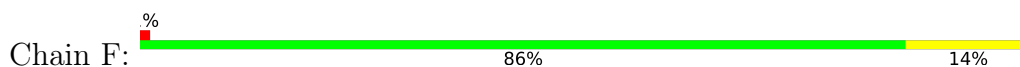
- Molecule 1: Dipeptide Epimerase



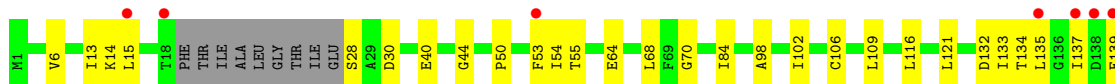
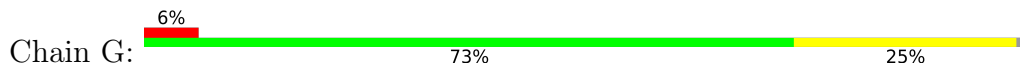
- Molecule 1: Dipeptide Epimerase

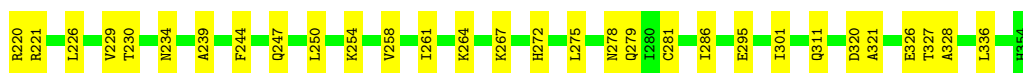


- Molecule 1: Dipeptide Epimerase

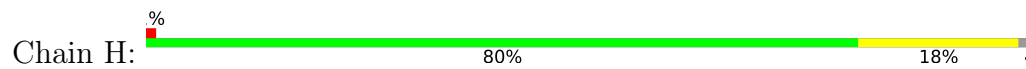


- Molecule 1: Dipeptide Epimerase





● Molecule 1: Dipeptide Epimerase



## 4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	162.27Å 162.27Å 319.56Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	24.93 – 1.70 38.69 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.1 (24.93-1.70) 99.2 (38.69-1.70)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.30 (at 1.70Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.223 , 0.244 0.215 , 0.236	Depositor DCC
$R_{free}$ test set	17272 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	25.2	Xtrriage
Anisotropy	0.184	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 28.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	0.486 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	21865	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 3.06% 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: SO4, MG, 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	0.29	0/2667	0.58	0/3605
1	B	0.30	0/2679	0.60	0/3620
1	C	0.28	0/2604	0.55	0/3516
1	D	0.29	0/2619	0.58	0/3536
1	E	0.29	0/2667	0.58	0/3605
1	F	0.30	0/2679	0.59	0/3620
1	G	0.27	0/2610	0.55	0/3524
1	H	0.29	0/2619	0.58	0/3536
All	All	0.29	0/21144	0.58	0/28562

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	2638	0	2726	56	0
1	B	2649	0	2733	54	0
1	C	2576	0	2657	63	0
1	D	2591	0	2668	48	0
1	E	2638	0	2726	54	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	2649	0	2733	36	0
1	G	2582	0	2662	73	0
1	H	2591	0	2668	48	0
2	A	6	0	8	3	0
2	B	18	0	24	2	0
2	F	6	0	8	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	A	5	0	0	0	0
4	C	10	0	0	1	0
4	E	5	0	0	0	0
4	G	5	0	0	0	0
5	A	97	0	0	2	0
5	B	153	0	0	3	0
5	C	78	0	0	3	0
5	D	131	0	0	4	0
5	E	90	0	0	5	0
5	F	138	0	0	2	0
5	G	76	0	0	3	0
5	H	125	0	0	1	0
All	All	21865	0	21613	413	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 10.

The worst 5 of 413 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:E:328:ALA:HB2	1:E:336:LEU:HD11	1.39	1.04
1:F:328:ALA:HB2	1:F:336:LEU:HD11	1.40	1.04
1:B:328:ALA:HB2	1:B:336:LEU:HD21	1.42	1.02
1:D:328:ALA:HB2	1:D:336:LEU:HD11	1.42	1.01
1:A:328:ALA:HB2	1:A:336:LEU:HD21	1.45	0.98

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	351/354 (99%)	333 (95%)	18 (5%)	0	100	100
1	B	352/354 (99%)	339 (96%)	12 (3%)	1 (0%)	41	24
1	C	340/354 (96%)	327 (96%)	12 (4%)	1 (0%)	41	24
1	D	342/354 (97%)	327 (96%)	14 (4%)	1 (0%)	41	24
1	E	351/354 (99%)	335 (95%)	16 (5%)	0	100	100
1	F	352/354 (99%)	340 (97%)	11 (3%)	1 (0%)	41	24
1	G	341/354 (96%)	328 (96%)	13 (4%)	0	100	100
1	H	342/354 (97%)	326 (95%)	16 (5%)	0	100	100
All	All	2771/2832 (98%)	2655 (96%)	112 (4%)	4 (0%)	51	33

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	210	GLN
1	F	51	GLY
1	B	51	GLY
1	D	51	GLY

### 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	277/278 (100%)	275 (99%)	2 (1%)	84	77

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	278/278 (100%)	275 (99%)	3 (1%)	73	63
1	C	270/278 (97%)	268 (99%)	2 (1%)	84	77
1	D	272/278 (98%)	267 (98%)	5 (2%)	59	43
1	E	277/278 (100%)	272 (98%)	5 (2%)	59	43
1	F	278/278 (100%)	276 (99%)	2 (1%)	84	77
1	G	271/278 (98%)	268 (99%)	3 (1%)	73	63
1	H	272/278 (98%)	271 (100%)	1 (0%)	91	87
All	All	2195/2224 (99%)	2172 (99%)	23 (1%)	76	67

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	145	GLN
1	F	71	GLN
1	E	167	GLU
1	F	251	GLU
1	C	204	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 56 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	141	ASN
1	H	311	GLN
1	F	5	GLN
1	H	272	HIS
1	G	311	GLN

### 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 [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 8 are monoatomic - leaving 10 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	$\# Z  > 2$
4	SO4	C	357	-	4,4,4	0.25	0	6,6,6	0.07	0
4	SO4	A	357	3	4,4,4	0.30	0	6,6,6	0.06	0
4	SO4	G	356	-	4,4,4	0.26	0	6,6,6	0.05	0
2	GOL	A	355	-	5,5,5	0.23	0	5,5,5	0.35	0
4	SO4	E	356	3	4,4,4	0.31	0	6,6,6	0.07	0
2	GOL	B	356	-	5,5,5	0.31	0	5,5,5	0.26	0
2	GOL	B	357	-	5,5,5	0.30	0	5,5,5	0.26	0
4	SO4	C	356	-	4,4,4	0.26	0	6,6,6	0.08	0
2	GOL	F	355	-	5,5,5	0.36	0	5,5,5	0.31	0
2	GOL	B	355	-	5,5,5	0.29	0	5,5,5	0.26	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	GOL	A	355	-	-	4/4/4/4	-
2	GOL	B	356	-	-	0/4/4/4	-
2	GOL	B	357	-	-	4/4/4/4	-
2	GOL	F	355	-	-	4/4/4/4	-
2	GOL	B	355	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.



There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	355	GOL	C1-C2-C3-O3
2	A	355	GOL	O2-C2-C3-O3
2	B	357	GOL	O1-C1-C2-C3
2	F	355	GOL	C1-C2-C3-O3
2	F	355	GOL	O2-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	355	GOL	3	0
4	C	356	SO4	1	0
2	B	355	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	353/354 (99%)	-0.11	11 (3%) 49 53	18, 27, 44, 53	0
1	B	354/354 (100%)	-0.27	2 (0%) 89 91	17, 24, 37, 47	0
1	C	344/354 (97%)	0.11	19 (5%) 25 27	19, 31, 62, 70	0
1	D	346/354 (97%)	-0.20	6 (1%) 70 74	19, 26, 45, 55	0
1	E	353/354 (99%)	-0.09	11 (3%) 49 53	18, 28, 45, 53	0
1	F	354/354 (100%)	-0.27	3 (0%) 86 88	17, 25, 37, 47	0
1	G	345/354 (97%)	0.13	21 (6%) 21 23	19, 31, 63, 71	0
1	H	346/354 (97%)	-0.21	4 (1%) 79 82	19, 26, 44, 54	0
All	All	2795/2832 (98%)	-0.11	77 (2%) 53 57	17, 27, 48, 71	0

The worst 5 of 77 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	137	ILE	4.5
1	A	19	PHE	4.3
1	E	19	PHE	4.3
1	G	135	LEU	4.1
1	B	19	PHE	4.1

### 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 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(Å <sup>2</sup> )	Q<0.9
2	GOL	B	357	6/6	0.57	0.16	53,54,54,55	0
2	GOL	F	355	6/6	0.70	0.18	53,54,55,56	0
2	GOL	B	355	6/6	0.81	0.17	57,58,59,59	0
4	SO4	G	356	5/5	0.81	0.19	69,69,70,70	0
4	SO4	C	357	5/5	0.87	0.26	70,70,70,70	0
2	GOL	A	355	6/6	0.90	0.15	32,33,36,37	0
4	SO4	C	356	5/5	0.93	0.10	52,53,54,54	0
2	GOL	B	356	6/6	0.95	0.14	32,33,36,37	0
4	SO4	A	357	5/5	0.96	0.09	35,37,39,40	0
4	SO4	E	356	5/5	0.96	0.08	35,37,39,40	0
3	MG	C	355	1/1	0.96	0.03	30,30,30,30	0
3	MG	G	355	1/1	0.97	0.03	30,30,30,30	0
3	MG	A	356	1/1	0.97	0.07	29,29,29,29	0
3	MG	E	355	1/1	0.97	0.06	28,28,28,28	0
3	MG	F	356	1/1	0.99	0.03	19,19,19,19	0
3	MG	D	355	1/1	0.99	0.04	24,24,24,24	0
3	MG	H	355	1/1	0.99	0.04	23,23,23,23	0
3	MG	B	358	1/1	0.99	0.03	20,20,20,20	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.