



# Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 12:36 am BST

PDB ID : 2YM0  
Title : Truncated SipD from Salmonella typhimurium  
Authors : Lunelli, M.; Kolbe, M.  
Deposited on : 2011-06-06  
Resolution : 3.00 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

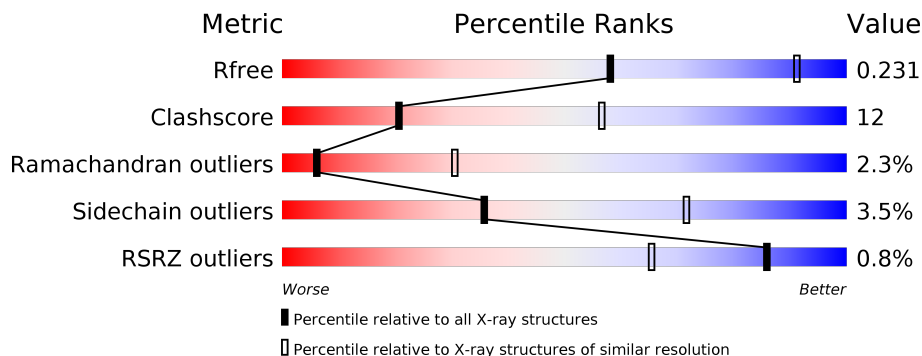
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	233	 62% 22% 15%
1	B	233	 61% 21% 14%

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 3092 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 CELL INVASION PROTEIN SIPD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	199	1529	964	249	309	7	0	0	1
1	B	200	1536	968	250	311	7	0	0	1

There are 42 discrepancies between the modelled and reference sequences:

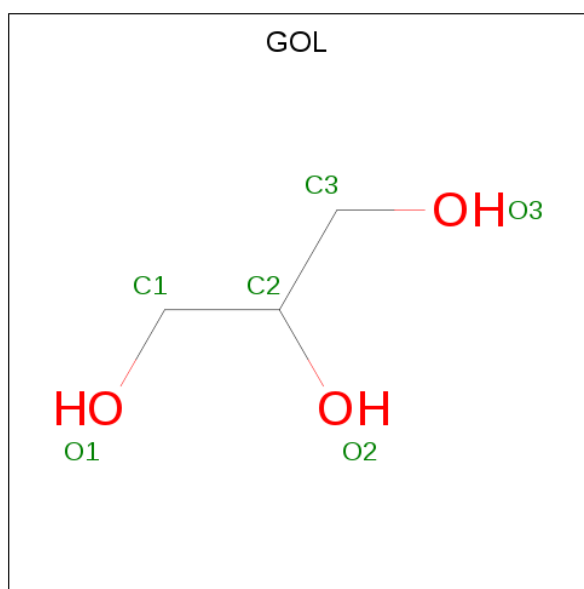
Chain	Residue	Modelled	Actual	Comment	Reference
A	111	MET	-	expression tag	UNP Q56026
A	112	GLY	-	expression tag	UNP Q56026
A	113	SER	-	expression tag	UNP Q56026
A	114	SER	-	expression tag	UNP Q56026
A	115	HIS	-	expression tag	UNP Q56026
A	116	HIS	-	expression tag	UNP Q56026
A	117	HIS	-	expression tag	UNP Q56026
A	118	HIS	-	expression tag	UNP Q56026
A	119	HIS	-	expression tag	UNP Q56026
A	120	HIS	-	expression tag	UNP Q56026
A	121	SER	-	expression tag	UNP Q56026
A	122	SER	-	expression tag	UNP Q56026
A	123	GLY	-	expression tag	UNP Q56026
A	124	LEU	-	expression tag	UNP Q56026
A	125	VAL	-	expression tag	UNP Q56026
A	126	PRO	-	expression tag	UNP Q56026
A	127	ARG	-	expression tag	UNP Q56026
A	128	GLY	-	expression tag	UNP Q56026
A	129	SER	-	expression tag	UNP Q56026
A	130	HIS	-	expression tag	UNP Q56026
A	131	MET	-	expression tag	UNP Q56026
B	111	MET	-	expression tag	UNP Q56026
B	112	GLY	-	expression tag	UNP Q56026
B	113	SER	-	expression tag	UNP Q56026
B	114	SER	-	expression tag	UNP Q56026

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Chain	Residue	Modelled	Actual	Comment	Reference
B	115	HIS	-	expression tag	UNP Q56026
B	116	HIS	-	expression tag	UNP Q56026
B	117	HIS	-	expression tag	UNP Q56026
B	118	HIS	-	expression tag	UNP Q56026
B	119	HIS	-	expression tag	UNP Q56026
B	120	HIS	-	expression tag	UNP Q56026
B	121	SER	-	expression tag	UNP Q56026
B	122	SER	-	expression tag	UNP Q56026
B	123	GLY	-	expression tag	UNP Q56026
B	124	LEU	-	expression tag	UNP Q56026
B	125	VAL	-	expression tag	UNP Q56026
B	126	PRO	-	expression tag	UNP Q56026
B	127	ARG	-	expression tag	UNP Q56026
B	128	GLY	-	expression tag	UNP Q56026
B	129	SER	-	expression tag	UNP Q56026
B	130	HIS	-	expression tag	UNP Q56026
B	131	MET	-	expression tag	UNP Q56026

- 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
			Total	C	O		
2	A	1	6	3	3	0	0

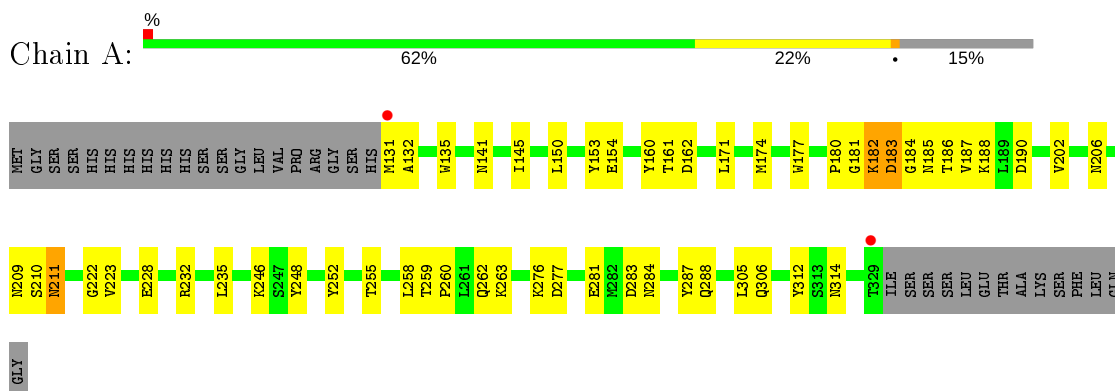
- Molecule 3 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	A	11	Total 11	O 11	0	0
3	B	10	Total 10	O 10	0	0

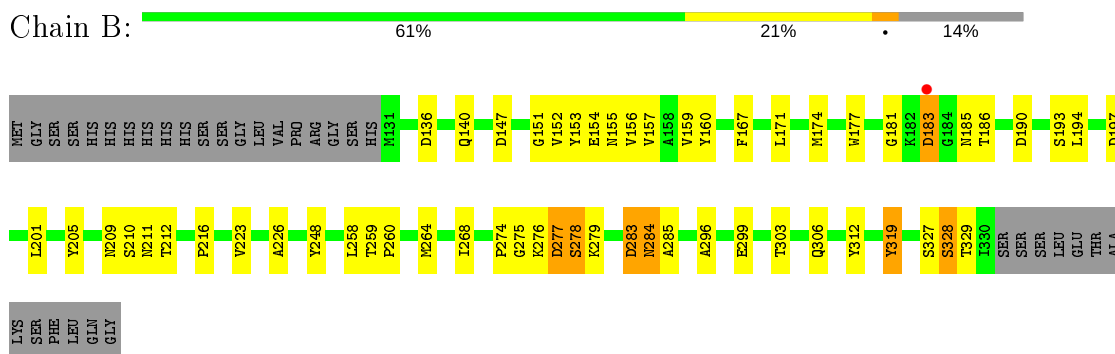
### 3 Residue-property plots [i](#)

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: CELL INVASION PROTEIN SIPD



- Molecule 1: CELL INVASION PROTEIN SIPD



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.80Å 94.37Å 117.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.21 – 3.00 37.21 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.3 (37.21-3.00) 99.4 (37.21-3.00)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.86 (at 3.01Å)	Xtrriage
Refinement program	CNS 1.2.1	Depositor
R, $R_{free}$	0.198 , 0.224 0.200 , 0.231	Depositor DCC
$R_{free}$ test set	647 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	68.1	Xtrriage
Anisotropy	0.139	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 39.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	3092	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.92% 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

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	0.39	0/1555	0.57	0/2110
1	B	0.38	0/1562	0.56	0/2120
All	All	0.39	0/3117	0.57	0/4230

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	1529	0	1504	33	0
1	B	1536	0	1511	42	0
2	A	6	0	8	1	0
3	A	11	0	0	0	0
3	B	10	0	0	0	0
All	All	3092	0	3023	75	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 12.

All (75) 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:B:183:ASP:HB2	1:B:185:ASN:ND2	1.89	0.87
1:B:284:ASN:N	1:B:284:ASN:HD22	1.75	0.84
1:B:183:ASP:HB2	1:B:185:ASN:HD21	1.43	0.83
1:B:185:ASN:C	1:B:284:ASN:HD21	1.83	0.81
1:B:284:ASN:H	1:B:284:ASN:HD22	1.32	0.77
1:B:284:ASN:N	1:B:284:ASN:ND2	2.40	0.69
1:A:186:THR:HG22	1:A:283:ASP:HA	1.74	0.68
1:B:329:THR:O	1:B:329:THR:HG22	1.99	0.63
1:B:283:ASP:OD2	1:B:285:ALA:HB3	1.99	0.63
1:B:185:ASN:C	1:B:284:ASN:ND2	2.53	0.61
1:A:284:ASN:ND2	1:A:284:ASN:H	2.02	0.57
1:A:171:LEU:HA	1:A:174:MET:HG2	1.87	0.56
1:B:152:VAL:O	1:B:156:VAL:HG23	2.05	0.56
1:B:327:SER:O	1:B:328:SER:HB3	2.07	0.53
1:B:157:VAL:HG21	1:B:312:TYR:HB2	1.90	0.53
1:A:153:TYR:HB3	1:A:312:TYR:HD1	1.74	0.53
1:A:246:LYS:HD3	1:A:255:THR:HG21	1.91	0.53
1:B:275:GLY:O	1:B:277:ASP:N	2.42	0.53
1:B:186:THR:N	1:B:284:ASN:HD21	2.06	0.53
1:B:185:ASN:O	1:B:284:ASN:ND2	2.43	0.52
1:A:180:PRO:HA	1:A:187:VAL:HG12	1.91	0.52
1:B:155:ASN:O	1:B:159:VAL:HG23	2.08	0.52
1:A:185:ASN:C	1:A:284:ASN:HD21	2.12	0.52
1:A:202:VAL:O	1:A:206:ASN:HB2	2.10	0.51
1:B:216:PRO:HG3	1:B:226:ALA:HB2	1.92	0.51
1:B:153:TYR:HB3	1:B:312:TYR:HD1	1.76	0.50
1:A:228:GLU:HB2	1:A:252:TYR:CE2	2.46	0.50
1:A:258:LEU:O	1:A:262:GLN:HG3	2.12	0.49
1:B:296:ALA:O	1:B:299:GLU:HB2	2.12	0.49
1:A:186:THR:HG22	1:A:283:ASP:CA	2.43	0.49
1:B:209:ASN:OD1	1:B:211:ASN:HB2	2.13	0.49
1:B:205:TYR:HA	1:B:212:THR:CG2	2.42	0.49
1:A:263:LYS:HG2	2:A:1329:GOL:H12	1.96	0.48
1:B:299:GLU:O	1:B:303:THR:HG23	2.14	0.47
1:A:171:LEU:O	1:A:174:MET:HB2	2.15	0.47
1:B:171:LEU:HA	1:B:174:MET:HG2	1.95	0.47
1:A:177:TRP:HB3	1:A:190:ASP:HB3	1.97	0.47
1:B:147:ASP:HA	1:B:319:TYR:CE2	2.50	0.46
1:B:303:THR:HA	1:B:306:GLN:HB2	1.97	0.46
1:A:259:THR:N	1:A:260:PRO:CD	2.79	0.46
1:A:314:ASN:N	1:A:314:ASN:HD22	2.14	0.46
1:A:150:LEU:O	1:A:154:GLU:HG3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:LEU:HA	1:A:174:MET:CG	2.46	0.45
1:A:154:GLU:HG2	1:A:312:TYR:HE1	1.82	0.45
1:B:274:PRO:HB2	1:B:279:LYS:O	2.17	0.45
1:A:188:LYS:HA	1:A:281:GLU:HA	1.99	0.45
1:A:287:TYR:HD2	1:A:288:GLN:HG3	1.81	0.45
1:B:136:ASP:O	1:B:140:GLN:HG3	2.17	0.45
1:B:157:VAL:HG21	1:B:312:TYR:CB	2.47	0.44
1:B:147:ASP:HA	1:B:319:TYR:HE2	1.81	0.44
1:A:223:VAL:HB	1:A:248:TYR:CE2	2.53	0.44
1:B:277:ASP:O	1:B:278:SER:HB2	2.18	0.44
1:A:314:ASN:ND2	1:A:314:ASN:N	2.65	0.44
1:B:167:PHE:HB2	1:B:201:LEU:HD21	2.00	0.44
1:A:131:MET:HG3	1:A:132:ALA:N	2.34	0.43
1:A:188:LYS:HE2	1:A:277:ASP:OD2	2.19	0.43
1:A:183:ASP:O	1:A:185:ASN:N	2.52	0.43
1:B:190:ASP:OD2	1:B:193:SER:HB2	2.19	0.42
1:B:259:THR:HB	1:B:260:PRO:HD3	2.01	0.42
1:A:181:GLY:O	1:A:182:LYS:HG3	2.20	0.42
1:B:181:GLY:HA3	1:B:186:THR:O	2.19	0.42
1:B:264:MET:O	1:B:268:ILE:HG13	2.19	0.42
1:B:258:LEU:O	1:B:259:THR:C	2.56	0.41
1:A:209:ASN:C	1:A:211:ASN:H	2.24	0.41
1:A:232:ARG:NH1	1:A:232:ARG:HG2	2.34	0.41
1:B:277:ASP:HB3	1:B:278:SER:H	1.70	0.41
1:A:141:ASN:O	1:A:145:ILE:HG13	2.20	0.41
1:A:161:THR:HG22	1:A:305:LEU:HD11	2.03	0.41
1:B:209:ASN:C	1:B:211:ASN:H	2.23	0.41
1:B:329:THR:CG2	1:B:329:THR:O	2.68	0.41
1:A:235:LEU:HA	1:A:235:LEU:HD12	1.96	0.41
1:B:223:VAL:HB	1:B:248:TYR:CE2	2.56	0.40
1:B:177:TRP:HZ3	1:B:194:LEU:HD12	1.87	0.40
1:A:135:TRP:CD1	1:A:135:TRP:C	2.95	0.40
1:B:151:GLY:O	1:B:154:GLU:HG2	2.21	0.40

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	197/233 (84%)	180 (91%)	14 (7%)	3 (2%)	10	42
1	B	198/233 (85%)	178 (90%)	14 (7%)	6 (3%)	4	24
All	All	395/466 (85%)	358 (91%)	28 (7%)	9 (2%)	6	30

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	278	SER
1	B	328	SER
1	B	210	SER
1	B	276	LYS
1	B	277	ASP
1	A	210	SER
1	A	222	GLY
1	B	283	ASP
1	A	184	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	171/201 (85%)	164 (96%)	7 (4%)	30	67
1	B	172/201 (86%)	167 (97%)	5 (3%)	42	76
All	All	343/402 (85%)	331 (96%)	12 (4%)	36	71

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	160	TYR
1	A	162	ASP
1	A	182	LYS
1	A	183	ASP
1	A	211	ASN
1	A	276	LYS
1	A	306	GLN
1	B	160	TYR
1	B	183	ASP
1	B	197	ASP
1	B	284	ASN
1	B	319	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	284	ASN
1	B	284	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](#)

1 ligand is 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	A	1329	-	5,5,5	0.30	0	5,5,5	0.21	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	1329	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1329	GOL	1	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	199/233 (85%)	-0.60	2 (1%) 82 59	41, 59, 89, 129	0
1	B	200/233 (85%)	-0.53	1 (0%) 91 75	39, 61, 114, 154	0
All	All	399/466 (85%)	-0.57	3 (0%) 86 65	39, 60, 105, 154	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	329	THR	3.3
1	B	183	ASP	2.9
1	A	131	MET	2.1

### 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(Å <sup>2</sup> )	Q<0.9
2	GOL	A	1329	6/6	0.87	0.49	72,77,80,80	6

## 6.5 Other polymers

There are no such residues in this entry.