



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:35 PM UTC

PDB ID : 2YM0 / pdb_00002ym0
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

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>.

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)
Xtriage (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

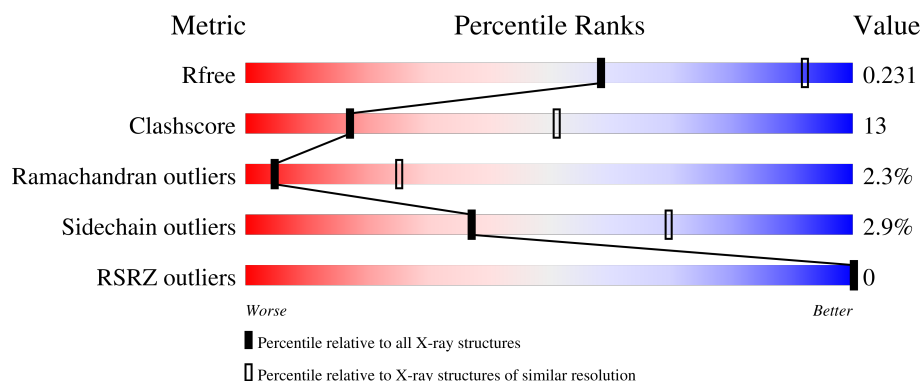
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (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 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 $\leq 5\%$. 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	
1	B	233	

2 Entry composition

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
1	A	199	Total	C	N	O	S	0	0	1
			1529	964	249	309	7			
1	B	200	Total	C	N	O	S	0	0	1
			1536	968	250	311	7			

There are 42 discrepancies between the modelled and reference sequences:

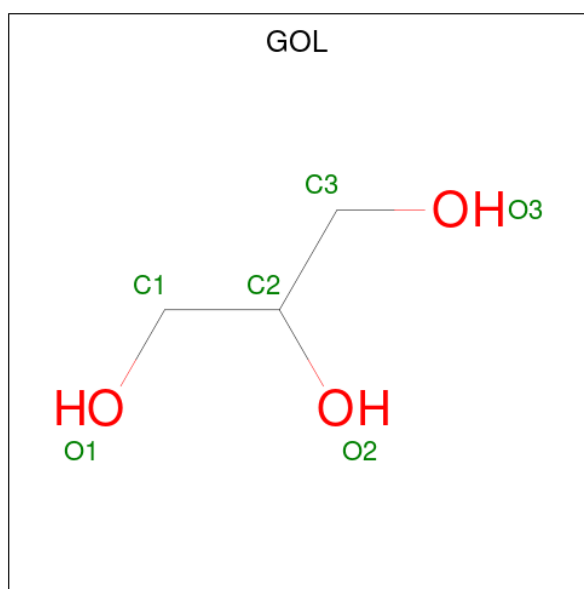
Chain	Residue	Modelled	Actual	Comment	Reference
A	111	MET	-	expression tag	UNP Q56026
A	112	GLY	-	expression tag	UNP Q56026
A	113	SER	-	expression tag	UNP Q56026
A	114	SER	-	expression tag	UNP Q56026
A	115	HIS	-	expression tag	UNP Q56026
A	116	HIS	-	expression tag	UNP Q56026
A	117	HIS	-	expression tag	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 (CCD ID: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	11	Total	O	0	0
			11	11		
3	B	10	Total	O	0	0
			10	10		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 3.01Å)	Xtriage
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 ²)	68.1	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 39.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3092	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage'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.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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	0.50	1/1555 (0.1%)	0.92	8/2110 (0.4%)
1	B	0.46	1/1562 (0.1%)	0.88	9/2120 (0.4%)
All	All	0.48	2/3117 (0.1%)	0.90	17/4230 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	329	THR	C-N	-5.40	1.25	1.33
1	A	328	SER	C-N	-5.28	1.25	1.33

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	213	VAL	N-CA-C	6.25	117.30	108.36
1	A	206	ASN	N-CA-C	-6.19	105.73	113.28
1	B	206	ASN	N-CA-C	-6.06	105.72	113.23
1	B	133	GLU	N-CA-C	6.02	118.33	111.11
1	A	292	SER	N-CA-C	-5.90	104.77	111.14
1	A	310	GLN	N-CA-C	-5.75	104.91	111.07
1	A	220	GLY	N-CA-C	5.64	121.24	110.86
1	A	289	ALA	N-CA-C	-5.39	105.05	111.03
1	B	310	GLN	N-CA-C	-5.35	105.53	111.36
1	A	296	ALA	N-CA-C	-5.31	105.40	111.14
1	A	133	GLU	N-CA-C	5.23	118.44	111.75
1	B	223	VAL	N-CA-C	5.14	115.88	108.93
1	B	174	MET	N-CA-C	5.12	117.53	111.33
1	B	289	ALA	N-CA-C	-5.05	105.47	110.97
1	A	185	ASN	N-CA-C	-5.03	107.19	113.38
1	B	324	LYS	N-CA-C	-5.03	105.49	110.97
1	B	304	THR	N-CA-C	-5.01	105.71	111.07

There are no chirality outliers.

There are no planarity outliers.

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	1529	0	1504	33	0
1	B	1536	0	1511	44	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	77	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 13.

All (77) 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:185:ASN:C	1:B:284:ASN:HD21	1.83	0.86
1:B:284:ASN:HD22	1:B:284:ASN:N	1.75	0.84
1:B:183:ASP:HB2	1:B:185:ASN:HD21	1.43	0.83
1:B:284:ASN:HD22	1:B:284:ASN:H	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:185:ASN:C	1:B:284:ASN:ND2	2.53	0.66
1:B:329:THR:HG22	1:B:329:THR:O	1.99	0.63
1:B:283:ASP:OD2	1:B:285:ALA:HB3	1.99	0.63
1:A:185:ASN:C	1:A:284:ASN:HD21	2.12	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:A:284:ASN:ND2	1:A:284:ASN:H	2.02	0.56
1:B:282:MET:HE3	1:B:287:TYR:HD2	1.71	0.55
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:LYS:HD3	1:A:255:THR:HG21	1.91	0.53
1:B:186:THR:N	1:B:284:ASN:HD21	2.06	0.53
1:B:275:GLY:O	1:B:277:ASP:N	2.42	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: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:258:LEU:O	1:B:259:THR:C	2.56	0.46
1:B:303:THR:HA	1:B:306:GLN:HB2	1.97	0.46
1:A:209:ASN:C	1:A:211:ASN:H	2.24	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
1:B:209:ASN:C	1:B:211:ASN:H	2.23	0.45
1:A:171:LEU:HA	1:A:174:MET:CG	2.46	0.45
1:A:135:TRP:CD1	1:A:135:TRP:C	2.95	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:147:ASP:HA	1:B:319:TYR:HE2	1.81	0.44
1:B:157:VAL:HG21	1:B:312:TYR:CB	2.47	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:B:167:PHE:HB2	1:B:201:LEU:HD21	2.00	0.44
1:A:314:ASN:N	1:A:314:ASN:ND2	2.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:328:SER:C	1:B:330:ILE:N	2.76	0.43
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:A:232:ARG:HG2	1:A:232:ARG:NH1	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:A:235:LEU:HD12	1:A:235:LEU:HA	1.96	0.41
1:B:329:THR:O	1:B:329:THR:CG2	2.68	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:B:151:GLY:O	1:B:154:GLU:HG2	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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%)	8	35
1	B	198/233 (85%)	178 (90%)	14 (7%)	6 (3%)	3	19
All	All	395/466 (85%)	358 (91%)	28 (7%)	9 (2%)	5	25

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 ⓘ

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%)	165 (96%)	6 (4%)	32	65
1	B	172/201 (86%)	168 (98%)	4 (2%)	44	74
All	All	343/402 (85%)	333 (97%)	10 (3%)	37	70

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	157	VAL
1	A	160	TYR
1	A	182	LYS
1	A	183	ASP
1	A	276	LYS
1	A	306	GLN
1	B	160	TYR
1	B	197	ASP
1	B	284	ASN
1	B	304	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	284	ASN
1	A	291	GLN
1	A	314	ASN
1	B	185	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 oligosaccharides 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	0.31	0	5,5,5	0.24	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, 95th 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	199/233 (85%)	-0.46	0 100 100	41, 59, 89, 129	0
1	B	200/233 (85%)	-0.30	0 100 100	39, 61, 114, 154	0
All	All	399/466 (85%)	-0.38	0 100 100	39, 60, 105, 154	0

There are no RSRZ outliers to report.

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 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, 95th 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
2	GOL	A	1329	6/6	0.77	0.20	72,77,80,80	6

6.5 Other polymers [i](#)

There are no such residues in this entry.