



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:02 AM UTC

PDB ID : 2WD6 / pdb_00002wd6
Title : Crystal structure of the Variable Domain of the Streptococcus gordonii Surface Protein SspB
Authors : Forsgren, N.; Persson, K.
Deposited on : 2009-03-20
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

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

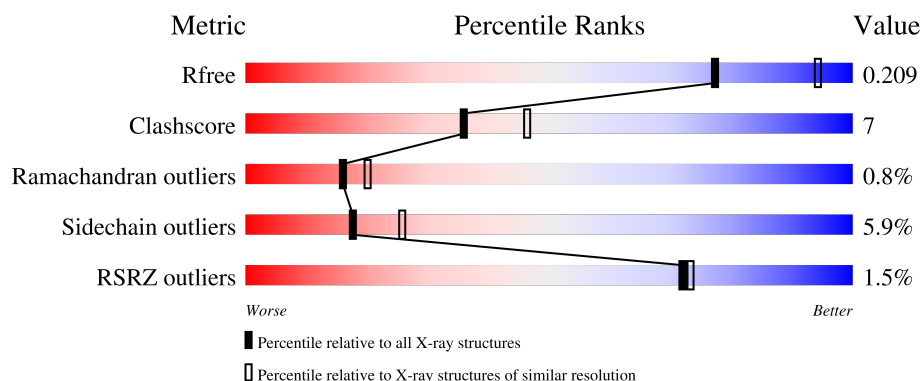
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 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	349	0% 75% 10% • 13%
1	B	349	2% 69% 12% • 16%

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
3	GOL	A	1767	-	X	-	-
3	GOL	B	1765	-	X	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4946 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 AGGLUTININ RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	302	Total	C	N	O	S	0	0	0
			2356	1480	398	474	4			
1	B	293	Total	C	N	O	S	0	0	0
			2282	1429	387	462	4			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total K 1 1	0	0

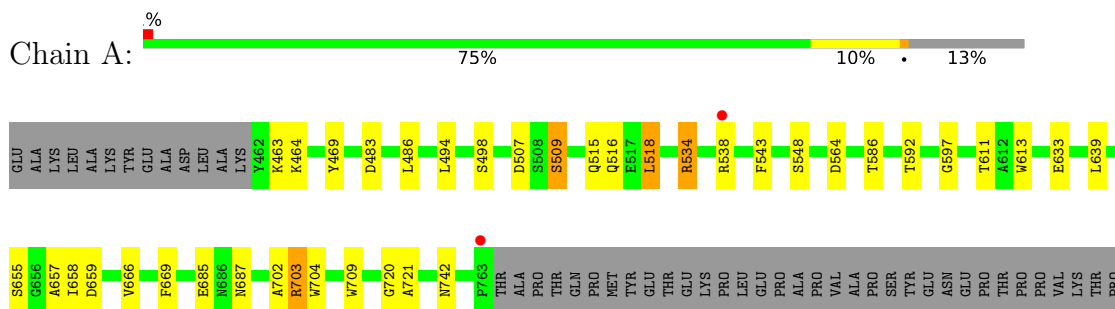
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	173	Total O 173 173	0	0
5	B	108	Total O 108 108	0	0

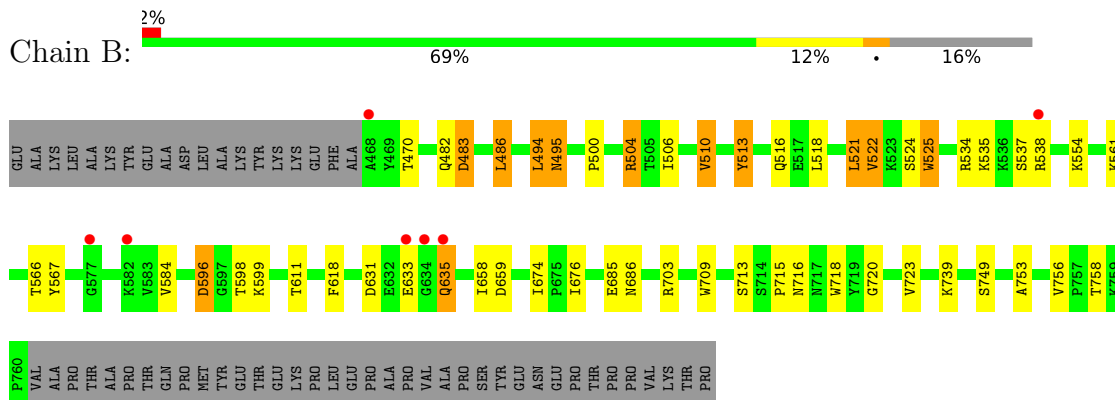
3 Residue-property plots

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: AGGLUTININ RECEPTOR



• Molecule 1: AGGLUTININ RECEPTOR



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	110.17Å 110.17Å 121.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	95.35 – 2.30 95.35 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (95.35-2.30) 99.9 (95.35-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.35 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.176 , 0.209 0.176 , 0.209	Depositor DCC
R_{free} test set	1853 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	28.7	Xtriage
Anisotropy	0.371	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 40.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.048 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4946	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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: K, CA, 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	1.00	2/2409 (0.1%)	0.98	1/3264 (0.0%)
1	B	0.97	2/2332 (0.1%)	0.95	2/3160 (0.1%)
All	All	0.99	4/4741 (0.1%)	0.97	3/6424 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	596	ASP	N-CA	6.66	1.54	1.46
1	A	702	ALA	C-O	-5.39	1.17	1.23
1	A	721	ALA	CA-CB	5.18	1.64	1.54
1	B	596	ASP	CA-C	5.06	1.60	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	525	TRP	N-CA-C	-5.77	105.57	113.30
1	A	703	ARG	N-CA-C	5.71	117.96	111.11
1	B	596	ASP	O-C-N	5.50	129.49	122.39

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	2356	0	2267	28	0
1	B	2282	0	2191	39	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	12	0	16	1	0
3	B	12	0	15	6	0
4	B	1	0	0	0	0
5	A	173	0	0	0	0
5	B	108	0	0	5	0
All	All	4946	0	4489	67	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 7.

All (67) 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:715:PRO:HD2	3:B:1765:GOL:H11	1.39	1.04
1:B:513:TYR:HE1	1:B:521:LEU:HD12	1.47	0.79
1:B:513:TYR:CE1	1:B:521:LEU:HD12	2.19	0.78
1:A:534:ARG:HG3	1:A:538:ARG:NH2	1.99	0.76
1:A:538:ARG:HE	1:A:657:ALA:CB	1.99	0.75
1:A:534:ARG:HG3	1:A:534:ARG:HH11	1.53	0.74
1:A:534:ARG:O	1:A:538:ARG:HG3	1.88	0.74
1:B:715:PRO:HD2	3:B:1765:GOL:C1	2.17	0.73
1:B:596:ASP:OD1	1:B:598:THR:HG22	1.90	0.71
1:B:703:ARG:HD2	5:B:2076:HOH:O	1.90	0.70
1:A:669:PHE:O	1:A:687:ASN:ND2	2.24	0.69
1:A:538:ARG:HE	1:A:657:ALA:HB1	1.56	0.69
1:B:521:LEU:HD23	1:B:521:LEU:O	1.94	0.67
1:B:521:LEU:HD23	1:B:521:LEU:C	2.24	0.63
1:A:507:ASP:OD2	1:A:509:SER:HB2	1.99	0.62
1:A:534:ARG:HG3	1:A:538:ARG:CZ	2.29	0.62
1:B:521:LEU:CD2	1:B:525:TRP:CZ2	2.83	0.61
1:B:598:THR:HG23	1:B:599:LYS:HG3	1.82	0.60
1:A:742:ASN:HD22	3:B:1765:GOL:H32	1.66	0.60
1:B:685:GLU:O	1:B:686:ASN:HB2	2.02	0.59
1:A:704:TRP:HE1	3:A:1766:GOL:H31	1.67	0.58
1:B:535:LYS:HG2	1:B:658:ILE:HG12	1.86	0.58
1:B:703:ARG:CD	5:B:2076:HOH:O	2.49	0.58
1:A:534:ARG:HH11	1:A:534:ARG:CG	2.16	0.57
1:B:486:LEU:HD13	1:B:753:ALA:CB	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:613:TRP:CZ3	3:B:1765:GOL:H31	2.41	0.55
1:A:494:LEU:HD13	1:A:639:LEU:HD13	1.88	0.55
1:B:521:LEU:HD21	1:B:525:TRP:CZ2	2.41	0.55
1:B:631:ASP:HB2	5:B:2046:HOH:O	2.07	0.54
1:A:592:THR:HG23	1:A:597:GLY:HA2	1.91	0.53
1:B:521:LEU:C	1:B:521:LEU:CD2	2.80	0.53
1:B:521:LEU:CD2	1:B:525:TRP:CE2	2.92	0.53
1:B:521:LEU:HD22	1:B:525:TRP:CZ2	2.44	0.52
1:B:495:ASN:HD22	1:B:495:ASN:C	2.17	0.52
1:A:534:ARG:O	1:A:538:ARG:CG	2.56	0.51
1:B:482:GLN:O	1:B:483:ASP:C	2.54	0.51
1:B:566:THR:HG23	1:B:584:VAL:HG22	1.93	0.51
1:B:518:LEU:O	1:B:522:VAL:HG13	2.11	0.51
1:A:483:ASP:OD2	1:A:703:ARG:NH2	2.22	0.50
1:B:618:PHE:CG	1:B:658:ILE:HD13	2.47	0.50
1:B:494:LEU:HD13	1:B:749:SER:HB3	1.94	0.49
1:A:463:LYS:HA	1:A:463:LYS:HE2	1.95	0.49
1:B:535:LYS:HE2	1:B:658:ILE:HG23	1.95	0.48
1:A:534:ARG:CG	1:A:534:ARG:NH1	2.77	0.47
1:A:534:ARG:HH11	1:A:538:ARG:HH22	1.63	0.47
1:A:613:TRP:HZ3	3:B:1765:GOL:H31	1.79	0.46
1:A:703:ARG:HG2	1:A:704:TRP:CE3	2.51	0.45
1:B:676:ILE:HG21	1:B:718:TRP:HB2	1.99	0.45
1:B:500:PRO:HD2	5:B:2011:HOH:O	2.17	0.45
1:A:709:TRP:CZ3	1:A:720:GLY:HA3	2.52	0.43
1:A:515:GLN:NE2	1:A:548:SER:HA	2.34	0.43
1:B:635:GLN:HE21	1:B:635:GLN:HB2	1.61	0.43
1:B:504:ARG:HG3	1:B:567:TYR:CE2	2.54	0.43
1:A:534:ARG:HG3	1:A:538:ARG:HH22	1.78	0.42
1:B:506:ILE:HG22	1:B:510:VAL:HG13	2.00	0.42
1:B:486:LEU:HD11	1:B:723:VAL:HG21	1.99	0.42
1:A:515:GLN:HE21	1:A:548:SER:HA	1.84	0.42
1:B:716:ASN:OD1	3:B:1764:GOL:H31	2.19	0.42
1:A:564:ASP:OD1	1:A:586:THR:HG23	2.20	0.41
1:B:659:ASP:HB3	1:B:739:LYS:HD2	2.03	0.41
1:A:518:LEU:HD13	1:A:543:PHE:HE1	1.86	0.41
1:B:534:ARG:O	1:B:538:ARG:HB2	2.21	0.41
1:B:486:LEU:HD22	1:B:756:VAL:HG22	2.04	0.40
1:B:513:TYR:CE1	1:B:521:LEU:CD1	2.98	0.40
1:B:635:GLN:HG2	5:B:2048:HOH:O	2.22	0.40
1:B:709:TRP:CZ3	1:B:720:GLY:HA3	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:486:LEU:HA	1:A:486:LEU:HD12	1.89	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	300/349 (86%)	290 (97%)	8 (3%)	2 (1%)	18	23
1	B	291/349 (83%)	274 (94%)	14 (5%)	3 (1%)	12	15
All	All	591/698 (85%)	564 (95%)	22 (4%)	5 (1%)	16	20

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	483	ASP
1	B	611	THR
1	A	611	THR
1	A	659	ASP
1	B	513	TYR

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	258/298 (87%)	246 (95%)	12 (5%)	23	35
1	B	251/298 (84%)	233 (93%)	18 (7%)	13	18
All	All	509/596 (85%)	479 (94%)	30 (6%)	18	26

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	464	LYS
1	A	469	TYR
1	A	498	SER
1	A	509	SER
1	A	516	GLN
1	A	518	LEU
1	A	534	ARG
1	A	633	GLU
1	A	655	SER
1	A	658	ILE
1	A	666	VAL
1	A	685	GLU
1	B	470	THR
1	B	486	LEU
1	B	494	LEU
1	B	495	ASN
1	B	504	ARG
1	B	510	VAL
1	B	516	GLN
1	B	521	LEU
1	B	522	VAL
1	B	524	SER
1	B	537	SER
1	B	554	LYS
1	B	561	LYS
1	B	633	GLU
1	B	635	GLN
1	B	674	ILE
1	B	713	SER
1	B	758	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	482	GLN
1	A	501	ASN
1	A	511	HIS
1	A	515	GLN
1	A	572	ASN
1	A	576	ASN
1	A	615	ASN
1	A	716	ASN
1	A	742	ASN
1	B	495	ASN
1	B	512	GLN
1	B	547	ASN
1	B	615	ASN
1	B	624	ASN
1	B	635	GLN
1	B	668	ASN
1	B	752	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](#)

Of 7 ligands modelled in this entry, 3 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	1766	-	5,5,5	0.48	0	5,5,5	0.49	0
3	GOL	B	1765	-	5,5,5	1.52	1 (20%)	5,5,5	4.44	3 (60%)
3	GOL	B	1764	-	5,5,5	0.31	0	5,5,5	0.70	0
3	GOL	A	1767	-	5,5,5	1.10	1 (20%)	5,5,5	1.30	1 (20%)

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	1766	-	-	4/4/4/4	-
3	GOL	B	1765	-	-	3/4/4/4	-
3	GOL	B	1764	-	-	3/4/4/4	-
3	GOL	A	1767	-	-	4/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1765	GOL	C3-C2	-2.72	1.41	1.51
3	A	1767	GOL	O2-C2	-2.24	1.36	1.43

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1765	GOL	O2-C2-C3	-8.71	73.11	109.18
3	B	1765	GOL	O3-C3-C2	-4.29	91.06	110.38
3	A	1767	GOL	O2-C2-C3	-2.71	97.98	109.18
3	B	1765	GOL	O2-C2-C1	2.04	117.64	109.18

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1766	GOL	O1-C1-C2-O2
3	A	1766	GOL	O1-C1-C2-C3
3	A	1766	GOL	C1-C2-C3-O3
3	A	1767	GOL	C1-C2-C3-O3
3	A	1767	GOL	O2-C2-C3-O3
3	A	1767	GOL	O1-C1-C2-C3

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Mol	Chain	Res	Type	Atoms
3	B	1764	GOL	O1-C1-C2-C3
3	B	1764	GOL	C1-C2-C3-O3
3	B	1765	GOL	O1-C1-C2-C3
3	B	1765	GOL	C1-C2-C3-O3
3	A	1766	GOL	O2-C2-C3-O3
3	A	1767	GOL	O1-C1-C2-O2
3	B	1765	GOL	O2-C2-C3-O3
3	B	1764	GOL	O2-C2-C3-O3

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1766	GOL	1	0
3	B	1765	GOL	5	0
3	B	1764	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	302/349 (86%)	-0.06	2 (0%) 84 85	17, 23, 31, 47	0
1	B	293/349 (83%)	0.44	7 (2%) 59 62	17, 24, 33, 38	0
All	All	595/698 (85%)	0.19	9 (1%) 72 73	17, 24, 32, 47	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	468	ALA	4.2
1	B	634	GLY	3.2
1	A	763	PRO	3.0
1	B	582	LYS	2.9
1	A	538	ARG	2.7
1	B	633	GLU	2.5
1	B	635	GLN	2.3
1	B	538	ARG	2.1
1	B	577	GLY	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 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($\text{\AA}^2$)	Q<0.9
3	GOL	A	1766	6/6	0.81	0.19	59,61,62,64	0
3	GOL	A	1767	6/6	0.88	0.17	33,35,40,46	0
3	GOL	B	1764	6/6	0.89	0.15	42,45,46,47	0
3	GOL	B	1765	6/6	0.92	0.21	15,27,28,33	0
4	K	B	1762	1/1	0.95	0.18	37,37,37,37	0
2	CA	B	1763	1/1	0.99	0.14	22,22,22,22	0
2	CA	A	1765	1/1	0.99	0.10	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.