



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 4, 2026 – 09:49 PM UTC

PDB ID : 9OZL / pdb_00009ozl
Title : Crystal structure of the polysaccharide lyase RbmB from *Vibrio cholerae*
Authors : Weerasekera, R.; Moreau, A.; Huang, X.; Potapova, A.; Schwechheimer, C.; Huynh, Y.; Cannizzo, O.; Gordon, R.; Hinbest, A.J.; Yang, Y.; Jiang, X.; Yan, J.; Yildiz, F.; Olson, R.
Deposited on : 2025-06-05
Resolution : 2.10 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

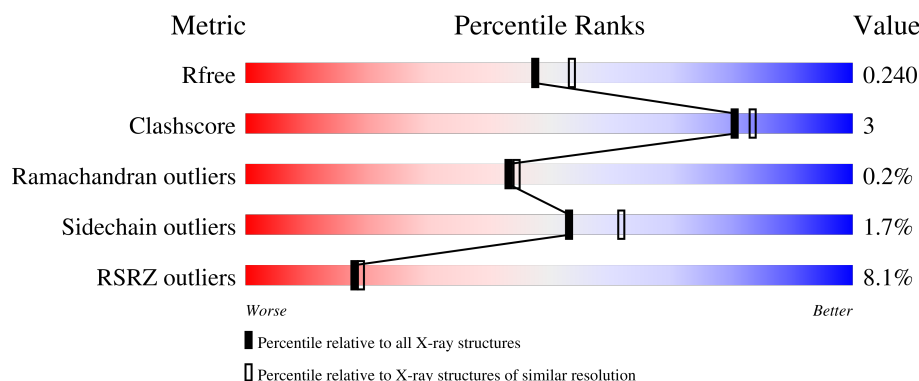
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	380	<div> <div>10%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>6%</div> </div> </div>
1	B	380	<div> <div>5%</div> <div> <div></div> <div>86%</div> <div>6%</div> <div>8%</div> </div> </div>
1	C	380	<div> <div>7%</div> <div> <div></div> <div>87%</div> <div>8%</div> <div>6%</div> </div> </div>
1	D	380	<div> <div>9%</div> <div> <div></div> <div>87%</div> <div>8%</div> <div>5%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 21935 atoms, of which 10294 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 Polysaccharide lyase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	348	Total	C	H	N	O	S	0	8	0
			5266	1697	2548	466	547	8			
1	C	359	Total	C	H	N	O	S	0	6	0
			5401	1741	2614	481	559	6			
1	D	360	Total	C	H	N	O	S	0	5	0
			5340	1725	2571	481	557	6			
1	A	359	Total	C	H	N	O	S	0	5	0
			5261	1706	2529	472	548	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	29	GLY	-	expression tag	UNP Q9KTH3
B	30	SER	-	expression tag	UNP Q9KTH3
B	31	THR	-	expression tag	UNP Q9KTH3
C	29	GLY	-	expression tag	UNP Q9KTH3
C	30	SER	-	expression tag	UNP Q9KTH3
C	31	THR	-	expression tag	UNP Q9KTH3
D	29	GLY	-	expression tag	UNP Q9KTH3
D	30	SER	-	expression tag	UNP Q9KTH3
D	31	THR	-	expression tag	UNP Q9KTH3
A	29	GLY	-	expression tag	UNP Q9KTH3
A	30	SER	-	expression tag	UNP Q9KTH3
A	31	THR	-	expression tag	UNP Q9KTH3

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	H	O	0	0
			14	3	8	3		
2	C	1	Total	C	H	O	0	0
			14	3	8	3		
2	D	1	Total	C	H	O	0	0
			14	3	8	3		
2	A	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	177	Total	O	0	0
			177	177		

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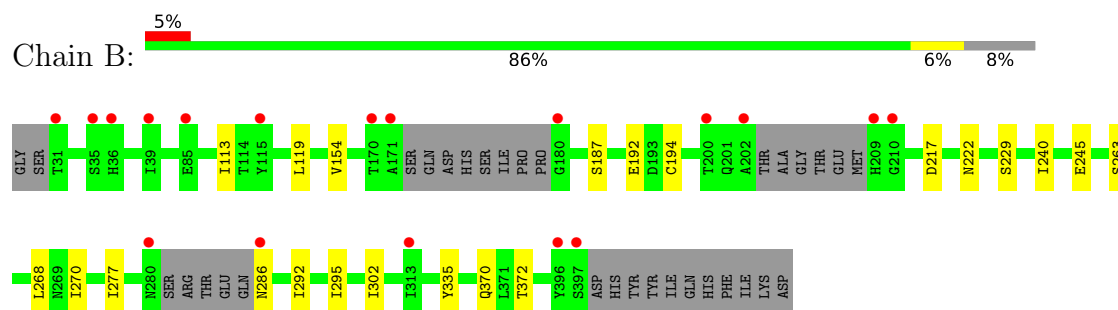
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	190	Total 190	O 190	0	0
4	D	136	Total 136	O 136	0	0
4	A	104	Total 104	O 104	0	0

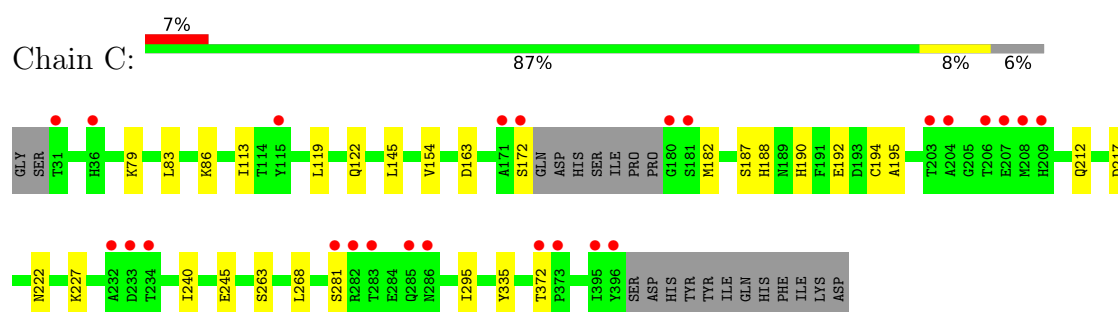
3 Residue-property plots

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.

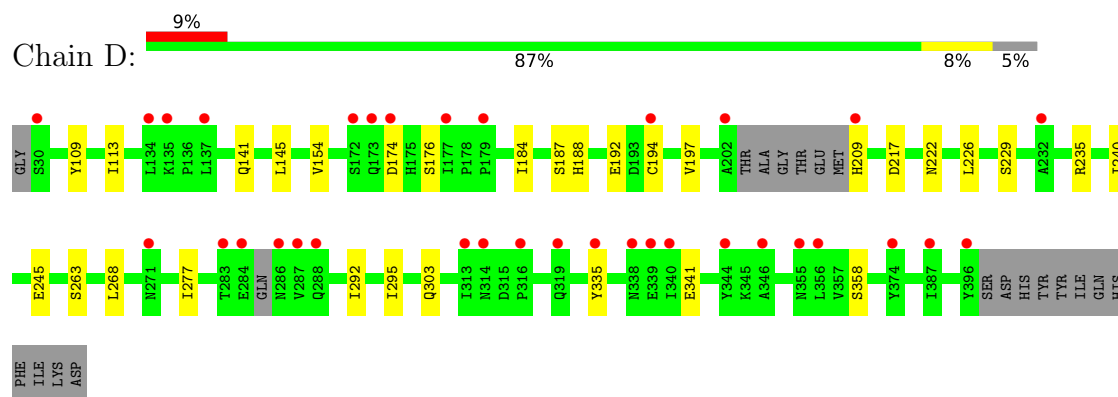
• Molecule 1: Polysaccharide lyase



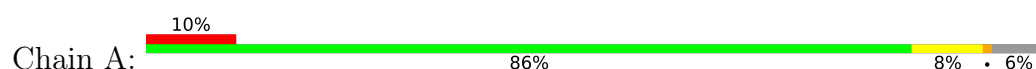
• Molecule 1: Polysaccharide lyase

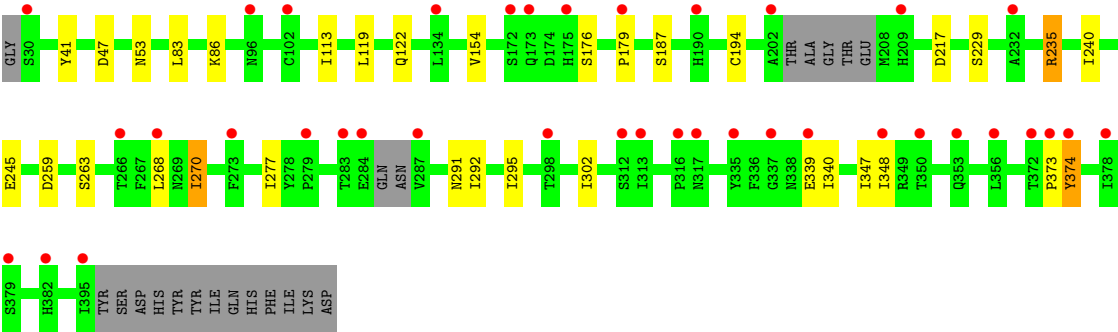


• Molecule 1: Polysaccharide lyase



• Molecule 1: Polysaccharide lyase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	118.44Å 48.42Å 134.90Å 90.00° 109.70° 90.00°	Depositor
Resolution (Å)	72.50 – 2.10 72.50 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.5 (72.50-2.10) 99.5 (72.50-2.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, R_{free}	0.197 , 0.242 0.197 , 0.240	Depositor DCC
R_{free} test set	2000 reflections (2.35%)	wwPDB-VP
Wilson B-factor (Å ²)	30.5	Xtriage
Anisotropy	0.617	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 63.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	21935	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.70% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, CA

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	0.09	0/2791	0.30	0/3791
1	B	0.10	0/2781	0.31	0/3771
1	C	0.09	0/2851	0.31	0/3867
1	D	0.11	0/2831	0.31	0/3841
All	All	0.10	0/11254	0.31	0/15270

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	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	235	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	2732	2529	2535	18	0
1	B	2718	2548	2558	10	0
1	C	2787	2614	2625	15	0
1	D	2769	2571	2576	13	0
2	A	6	8	8	0	0
2	B	6	8	8	0	0
2	C	6	8	8	0	0
2	D	6	8	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
4	A	104	0	0	2	2
4	B	177	0	0	0	1
4	C	190	0	0	3	1
4	D	136	0	0	0	2
All	All	11641	10294	10326	56	3

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 3.

All (56) 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:259[A]:ASP:OD1	1:A:291:ASN:ND2	2.24	0.70
1:C:190[A]:HIS:NE2	4:C:602:HOH:O	2.29	0.65
1:D:187:SER:OG	1:D:188:HIS:ND1	2.34	0.59
1:A:47:ASP:OD2	4:A:601:HOH:O	2.17	0.59
1:A:277:ILE:CD1	1:A:292:ILE:HG21	2.33	0.57
1:C:335:TYR:HA	1:C:372:THR:HG21	1.93	0.50
1:C:187:SER:OG	1:C:188:HIS:ND1	2.43	0.48
1:D:277:ILE:CD1	1:D:292:ILE:HG21	2.44	0.48
1:A:270:ILE:HB	1:A:302[A]:ILE:HG23	1.95	0.48
1:D:335:TYR:O	1:D:335:TYR:CG	2.67	0.48
1:D:263:SER:HA	1:D:295:ILE:O	2.14	0.48
1:B:245:GLU:HA	1:B:268:LEU:O	2.14	0.48
1:C:263:SER:HA	1:C:295:ILE:O	2.15	0.47
1:A:263:SER:HA	1:A:295:ILE:O	2.15	0.46
1:B:335:TYR:HA	1:B:372:THR:HG21	1.98	0.46
1:A:235:ARG:HH21	1:A:259[A]:ASP:CG	2.24	0.46
1:A:154:VAL:HA	1:A:187:SER:O	2.16	0.45
1:D:245:GLU:HA	1:D:268:LEU:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:GLU:HA	1:B:222:ASN:O	2.17	0.45
1:C:217:ASP:HA	1:C:240:ILE:O	2.16	0.45
1:A:41:TYR:OH	4:A:603:HOH:O	2.21	0.45
1:D:154:VAL:HA	1:D:187:SER:O	2.17	0.44
1:B:270:ILE:HB	1:B:302:ILE:HG23	1.99	0.44
1:D:303:GLN:HA	1:D:335:TYR:O	2.16	0.44
1:C:192:GLU:HA	1:C:222:ASN:O	2.17	0.44
1:B:263:SER:HA	1:B:295:ILE:O	2.18	0.44
1:B:277[A]:ILE:CD1	1:B:292:ILE:HG21	2.48	0.44
1:B:270:ILE:HD12	1:B:302:ILE:HD12	2.00	0.43
1:B:113:ILE:HG21	1:B:119:LEU:HD22	2.00	0.43
1:B:217:ASP:HA	1:B:240:ILE:O	2.18	0.43
1:C:154:VAL:HA	1:C:187:SER:O	2.18	0.43
1:A:270:ILE:HB	1:A:302[B]:ILE:HG23	2.00	0.43
1:C:245:GLU:HA	1:C:268:LEU:O	2.19	0.43
1:A:122:GLN:HA	1:A:154:VAL:O	2.18	0.43
1:A:339:GLU:C	1:A:340:ILE:HD13	2.44	0.43
1:A:217:ASP:HA	1:A:240:ILE:O	2.18	0.42
1:D:217:ASP:HA	1:D:240:ILE:O	2.18	0.42
1:C:227:LYS:NZ	4:C:605:HOH:O	2.34	0.42
1:C:113:ILE:HB	1:C:145:LEU:HD23	2.01	0.42
1:D:109:TYR:CD1	1:D:141:GLN:HB2	2.55	0.41
1:D:187:SER:HA	1:D:217:ASP:O	2.19	0.41
1:A:83:LEU:HD11	1:A:86:LYS:HD2	2.02	0.41
1:A:245:GLU:HA	1:A:268:LEU:O	2.20	0.41
1:C:83:LEU:HD11	1:C:86:LYS:HD2	2.02	0.41
1:B:154:VAL:HA	1:B:187:SER:O	2.20	0.41
1:C:163:ASP:O	1:C:195:ALA:HB3	2.20	0.41
1:A:347:ILE:HG22	1:A:348:ILE:HG13	2.03	0.41
1:D:113:ILE:HB	1:D:145:LEU:HD23	2.03	0.41
1:A:373:PRO:O	1:A:374:TYR:CB	2.68	0.41
1:C:122:GLN:HA	1:C:154:VAL:O	2.21	0.41
1:D:192:GLU:HA	1:D:222:ASN:O	2.20	0.41
1:C:79:LYS:NZ	4:C:622:HOH:O	2.53	0.40
1:A:113:ILE:HG21	1:A:119:LEU:HD22	2.03	0.40
1:D:197:VAL:O	1:D:226:LEU:HD12	2.21	0.40
1:A:176:SER:OG	1:A:179:PRO:HA	2.21	0.40
1:C:113:ILE:HG21	1:C:119:LEU:HD22	2.04	0.40

All (3) 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:D:654:HOH:O	4:A:695:HOH:O[1_655]	2.03	0.17
4:B:764:HOH:O	4:A:662:HOH:O[2_545]	2.11	0.09
4:C:686:HOH:O	4:D:725:HOH:O[2_655]	2.16	0.04

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	358/380 (94%)	338 (94%)	19 (5%)	1 (0%)	36	36
1	B	348/380 (92%)	334 (96%)	14 (4%)	0	100	100
1	C	361/380 (95%)	343 (95%)	18 (5%)	0	100	100
1	D	359/380 (94%)	331 (92%)	26 (7%)	2 (1%)	21	18
All	All	1426/1520 (94%)	1346 (94%)	77 (5%)	3 (0%)	43	44

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	174	ASP
1	D	358	SER
1	A	374	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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	287/333 (86%)	283 (99%)	4 (1%)	59	67

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	295/333 (89%)	290 (98%)	5 (2%)	53	62
1	C	299/333 (90%)	294 (98%)	5 (2%)	53	62
1	D	295/333 (89%)	288 (98%)	7 (2%)	43	49
All	All	1176/1332 (88%)	1155 (98%)	21 (2%)	53	60

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	194[A]	CYS
1	B	194[B]	CYS
1	B	229	SER
1	B	286	ASN
1	B	370	GLN
1	C	172	SER
1	C	182	MET
1	C	194	CYS
1	C	212	GLN
1	C	281	SER
1	D	176	SER
1	D	184	ILE
1	D	194	CYS
1	D	209	HIS
1	D	229	SER
1	D	235	ARG
1	D	341	GLU
1	A	53	ASN
1	A	194	CYS
1	A	229	SER
1	A	270	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	87	ASN
1	B	88	ASN
1	B	118	ASN
1	B	309	GLN
1	B	351	ASN
1	B	353	GLN
1	C	130	ASN

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Mol	Chain	Res	Type
1	C	309	GLN
1	C	351	ASN
1	C	353	GLN
1	C	370	GLN
1	D	130	ASN
1	D	246	ASN
1	D	269	ASN
1	D	323	ASN
1	A	53	ASN
1	A	130	ASN
1	A	212	GLN
1	A	246	ASN
1	A	323	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 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	$\# Z > 2$
2	GOL	A	501	-	5,5,5	0.33	0	5,5,5	0.36	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	GOL	B	501	-	5,5,5	0.33	0	5,5,5	0.40	0
2	GOL	C	501	-	5,5,5	0.35	0	5,5,5	0.41	0
2	GOL	D	501	-	5,5,5	0.35	0	5,5,5	0.41	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	501	-	-	2/4/4/4	-
2	GOL	B	501	-	-	0/4/4/4	-
2	GOL	C	501	-	-	0/4/4/4	-
2	GOL	D	501	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GOL	O1-C1-C2-C3
2	D	501	GOL	O1-C1-C2-C3
2	A	501	GOL	O1-C1-C2-O2
2	D	501	GOL	O1-C1-C2-O2

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 [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	359/380 (94%)	0.77	38 (10%)	11 12	23, 56, 96, 154	5 (1%)
1	B	348/380 (91%)	0.18	18 (5%)	33 35	18, 40, 68, 131	8 (2%)
1	C	359/380 (94%)	0.31	25 (6%)	22 24	16, 42, 81, 179	6 (1%)
1	D	360/380 (94%)	0.67	34 (9%)	14 14	24, 52, 98, 139	5 (1%)
All	All	1426/1520 (93%)	0.49	115 (8%)	18 19	16, 47, 89, 179	24 (1%)

All (115) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	287	VAL	5.6
1	C	206	THR	5.3
1	B	171	ALA	5.3
1	D	202	ALA	5.2
1	A	395	ILE	5.0
1	C	207	GLU	5.0
1	D	335	TYR	4.7
1	A	202	ALA	4.7
1	D	340	ILE	4.7
1	B	36	HIS	4.6
1	C	180	GLY	4.6
1	C	282	ARG	4.4
1	A	374	TYR	4.3
1	C	285	GLN	4.1
1	C	232	ALA	4.0
1	C	283	THR	3.9
1	A	284	GLU	3.9
1	A	356	LEU	3.7
1	D	374	TYR	3.7
1	C	208	MET	3.7
1	D	134	LEU	3.5

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Mol	Chain	Res	Type	RSRZ
1	D	284	GLU	3.4
1	D	172	SER	3.4
1	B	209	HIS	3.4
1	D	283	THR	3.4
1	D	316	PRO	3.3
1	A	287	VAL	3.3
1	A	190	HIS	3.3
1	A	173	GLN	3.2
1	A	382	HIS	3.2
1	A	350	THR	3.1
1	D	177	ILE	3.1
1	C	171	ALA	3.1
1	C	396	TYR	3.0
1	C	373	PRO	3.0
1	A	353	GLN	3.0
1	B	31	THR	3.0
1	D	209	HIS	3.0
1	A	316	PRO	3.0
1	A	373	PRO	3.0
1	A	279	PRO	2.9
1	B	397	SER	2.9
1	B	286	ASN	2.8
1	D	396	TYR	2.8
1	B	202	ALA	2.8
1	A	339	GLU	2.8
1	A	30	SER	2.8
1	B	115	TYR	2.8
1	B	180	GLY	2.7
1	C	36	HIS	2.7
1	C	209	HIS	2.7
1	C	372	THR	2.7
1	A	134	LEU	2.7
1	D	319	GLN	2.6
1	D	179	PRO	2.6
1	A	313	ILE	2.6
1	A	317	ASN	2.6
1	A	268	LEU	2.6
1	C	286	ASN	2.6
1	B	170	THR	2.6
1	C	203	THR	2.6
1	C	234	THR	2.6
1	C	172	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	281	SER	2.6
1	B	280	ASN	2.6
1	D	314	ASN	2.6
1	A	266	THR	2.6
1	D	137	LEU	2.6
1	A	102	CYS	2.5
1	A	179	PRO	2.5
1	A	379	SER	2.5
1	A	378	ILE	2.5
1	D	173	GLN	2.4
1	C	204	ALA	2.4
1	A	232	ALA	2.4
1	D	356	LEU	2.4
1	A	273	PHE	2.4
1	B	313	ILE	2.4
1	D	313	ILE	2.4
1	A	175	HIS	2.4
1	B	210	GLY	2.4
1	C	233	ASP	2.4
1	A	209	HIS	2.4
1	D	232	ALA	2.4
1	B	85	GLU	2.4
1	D	355	ASN	2.3
1	A	96	ASN	2.3
1	D	339	GLU	2.3
1	C	115	TYR	2.3
1	A	312	SER	2.3
1	C	31	THR	2.3
1	D	346	ALA	2.3
1	D	338	ASN	2.3
1	B	396	TYR	2.2
1	D	344	TYR	2.2
1	A	335	TYR	2.2
1	A	372	THR	2.2
1	C	395	ILE	2.2
1	D	174	ASP	2.2
1	D	288	GLN	2.1
1	C	181	SER	2.1
1	D	135	LYS	2.1
1	A	172	SER	2.1
1	A	298	THR	2.1
1	A	283	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	337	GLY	2.1
1	B	39	ILE	2.1
1	A	348	ILE	2.1
1	B	35	SER	2.1
1	D	30	SER	2.1
1	D	271	ASN	2.0
1	D	286	ASN	2.0
1	D	387	ILE	2.0
1	D	194	CYS	2.0
1	B	200	THR	2.0

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	D	501	6/6	0.80	0.13	18,28,39,43	14
2	GOL	A	501	6/6	0.80	0.15	37,46,66,66	11
2	GOL	B	501	6/6	0.83	0.17	36,46,61,74	10
2	GOL	C	501	6/6	0.93	0.10	32,40,59,70	13
3	CA	C	502	1/1	0.94	0.08	61,61,61,61	0
3	CA	D	502	1/1	0.94	0.08	29,29,29,29	1
3	CA	B	502	1/1	0.96	0.04	35,35,35,35	0
3	CA	A	502	1/1	0.96	0.10	36,36,36,36	1

6.5 Other polymers [i](#)

There are no such residues in this entry.