



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 16, 2023 – 12:40 PM EST

PDB ID : 4P3Z  
Title : Chlamydia pneumoniae CopN (D29 construct)  
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Deposited on : 2014-03-10  
Resolution : 1.77 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.

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

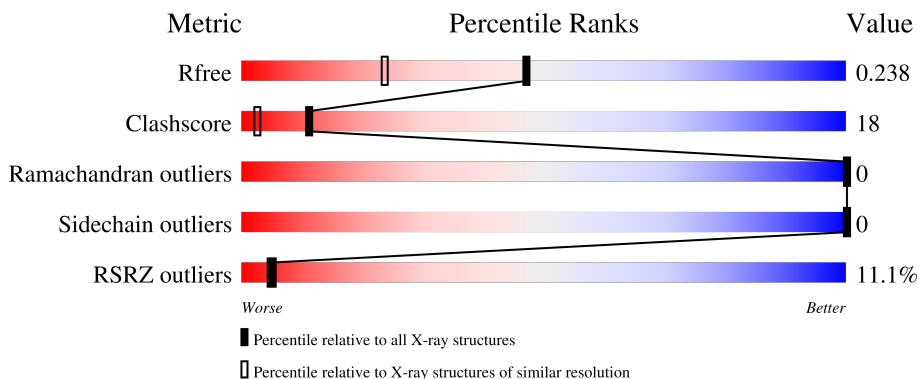
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.77 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	9185 (1.80-1.76)
Clashscore	141614	10184 (1.80-1.76)
Ramachandran outliers	138981	10051 (1.80-1.76)
Sidechain outliers	138945	10050 (1.80-1.76)
RSRZ outliers	127900	9032 (1.80-1.76)

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	425	

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
2	SO4	A	402	-	-	X	-

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<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
3	GOL	A	407	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 4768 atoms, of which 2287 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 CopN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	292	4564	1433	2271	390	463	7	0	4	0

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-25	MET	-	initiating methionine	UNP Q9Z8L4
A	-24	LYS	-	expression tag	UNP Q9Z8L4
A	-23	HIS	-	expression tag	UNP Q9Z8L4
A	-22	HIS	-	expression tag	UNP Q9Z8L4
A	-21	HIS	-	expression tag	UNP Q9Z8L4
A	-20	HIS	-	expression tag	UNP Q9Z8L4
A	-19	HIS	-	expression tag	UNP Q9Z8L4
A	-18	HIS	-	expression tag	UNP Q9Z8L4
A	-17	PRO	-	expression tag	UNP Q9Z8L4
A	-16	MET	-	expression tag	UNP Q9Z8L4
A	-15	SER	-	expression tag	UNP Q9Z8L4
A	-14	ASP	-	expression tag	UNP Q9Z8L4
A	-13	TYR	-	expression tag	UNP Q9Z8L4
A	-12	ASP	-	expression tag	UNP Q9Z8L4
A	-11	ILE	-	expression tag	UNP Q9Z8L4
A	-10	PRO	-	expression tag	UNP Q9Z8L4
A	-9	THR	-	expression tag	UNP Q9Z8L4
A	-8	THR	-	expression tag	UNP Q9Z8L4
A	-7	GLU	-	expression tag	UNP Q9Z8L4
A	-6	ASN	-	expression tag	UNP Q9Z8L4
A	-5	LEU	-	expression tag	UNP Q9Z8L4
A	-4	TYR	-	expression tag	UNP Q9Z8L4
A	-3	PHE	-	expression tag	UNP Q9Z8L4
A	-2	GLN	-	expression tag	UNP Q9Z8L4
A	-1	GLY	-	expression tag	UNP Q9Z8L4
A	0	ALA	-	expression tag	UNP Q9Z8L4

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 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	
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	A	1	Total	C	H	O	0	0
			14	3	8	3		

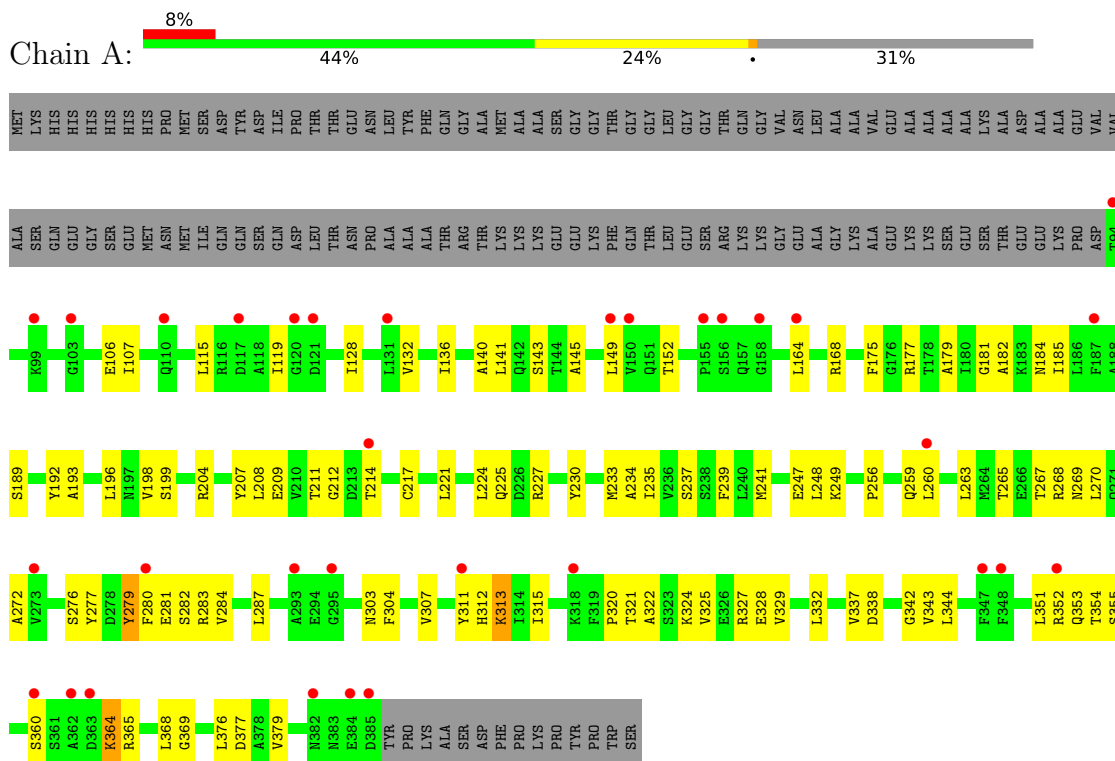
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	151	Total	O	0	0
			151	151		

### 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: CopN



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	62.70Å 62.70Å 85.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	16.29 – 1.77 16.29 – 1.77	Depositor Estimate
% Data completeness (in resolution range)	99.6 (16.29-1.77) 99.6 (16.29-1.77)	Depositor Estimate
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.48 (at 1.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496), BUSTER-TNT, SHELXL	Depositor
R, $R_{free}$	0.180 , 0.235 0.186 , 0.238	Depositor Difference
$R_{free}$ test set	1668 reflections (4.99%)	wwPDB
Wilson B-factor (Å <sup>2</sup> )	28.8	Xtriage
Anisotropy	0.067	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.49 , 34.0	Estimate
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.021 for k,h,-l	Xtriage
$F_o, F_c$ correlation	0.96	Estimate
Total number of atoms	4768	wwPDB
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.00% 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, SO4, MLZ

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	0.58	1/2287 (0.0%)	0.52	0/3095

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	279	TYR	CE1-CZ	-5.56	1.31	1.38

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	2293	2271	2280	83	1
2	A	25	0	0	4	0
3	A	12	16	16	2	0
4	A	151	0	0	1	0
All	All	2481	2287	2296	83	1

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 18.

All (83) 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:221:LEU:O	1:A:225[A]:GLN:HG3	1.83	0.78
1:A:272:ALA:HB1	1:A:355:SER:HB3	1.71	0.72
1:A:268:ARG:NH1	2:A:402:SO4:O4	2.23	0.70
1:A:224:LEU:HD12	1:A:270:LEU:HD21	1.75	0.67
1:A:248:LEU:HD21	1:A:260:LEU:HB2	1.79	0.65
1:A:337:VAL:HG23	1:A:379:VAL:HG12	1.78	0.65
1:A:282:SER:OG	1:A:283:ARG:NH1	2.31	0.64
1:A:311:TYR:OH	1:A:351:LEU:HA	1.98	0.63
1:A:311:TYR:OH	1:A:354:THR:OG1	1.92	0.62
1:A:196:LEU:HD21	1:A:235:ILE:HB	1.82	0.61
1:A:211:THR:HA	1:A:263:LEU:HD13	1.83	0.60
1:A:106:GLU:OE1	1:A:204:ARG:NH1	2.34	0.60
1:A:284:VAL:HG21	1:A:304:PHE:HA	1.81	0.60
1:A:182:ALA:HB2	1:A:208:LEU:HD11	1.81	0.60
1:A:307:VAL:HA	1:A:332:LEU:HD21	1.85	0.58
1:A:107:ILE:HG23	1:A:141:LEU:HD22	1.87	0.57
1:A:128:ILE:HG21	1:A:164:LEU:HD23	1.87	0.57
1:A:321:THR:O	1:A:325:VAL:HG23	2.06	0.56
1:A:221:LEU:HG	1:A:225[A]:GLN:NE2	2.21	0.55
1:A:352:ARG:NH2	2:A:404:SO4:O1	2.40	0.54
1:A:185:ILE:HD13	1:A:207:TYR:CG	2.43	0.54
1:A:140:ALA:HB2	1:A:182:ALA:CB	2.37	0.54
1:A:119:ILE:CD1	1:A:149:LEU:HD13	2.38	0.53
1:A:128:ILE:HD13	1:A:164:LEU:HA	1.92	0.52
1:A:214:THR:HG22	4:A:639:HOH:O	2.10	0.51
1:A:230:TYR:HA	1:A:233:MET:HE3	1.93	0.50
1:A:192:TYR:CG	1:A:239:PHE:HB2	2.47	0.50
1:A:177:ARG:O	1:A:181:GLY:N	2.42	0.50
1:A:193:ALA:HB1	1:A:198:VAL:O	2.12	0.50
1:A:140:ALA:HB2	1:A:182:ALA:HB3	1.93	0.49
1:A:217:CYS:HB2	1:A:269:ASN:HB2	1.94	0.49
1:A:281:GLU:HA	1:A:304:PHE:CG	2.47	0.49
1:A:281:GLU:HA	1:A:304:PHE:CB	2.43	0.48
1:A:351:LEU:HD21	1:A:365:ARG:O	2.13	0.48
1:A:143:SER:HB2	1:A:179:ALA:HB1	1.94	0.48
1:A:276:SER:OG	1:A:312:HIS:NE2	2.36	0.48
1:A:354:THR:O	1:A:365:ARG:NH1	2.41	0.48
1:A:344:LEU:HB3	1:A:376:LEU:HG	1.96	0.48
1:A:175:PHE:CB	1:A:179:ALA:HB2	2.44	0.47
1:A:115:LEU:HD21	1:A:132:VAL:HG22	1.96	0.47
1:A:211:THR:HA	1:A:263:LEU:CD1	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:313:MLZ:HCM2	1:A:328:GLU:OE2	2.14	0.47
1:A:115:LEU:HD21	1:A:132:VAL:HA	1.97	0.47
1:A:185:ILE:HG21	1:A:207:TYR:CZ	2.50	0.47
1:A:207:TYR:CZ	1:A:211:THR:HG21	2.49	0.47
1:A:276:SER:CB	1:A:312:HIS:NE2	2.78	0.47
1:A:322:ALA:H	3:A:406:GOL:H32	1.80	0.47
1:A:287:LEU:HD11	1:A:342:GLY:HA3	1.98	0.46
1:A:149:LEU:HB3	1:A:164:LEU:HD22	1.99	0.45
1:A:177:ARG:NH2	1:A:247:GLU:OE1	2.32	0.45
1:A:351:LEU:O	1:A:365:ARG:NH1	2.50	0.45
1:A:189:SER:HA	1:A:239:PHE:CE1	2.51	0.45
1:A:208:LEU:O	1:A:212:GLY:N	2.50	0.45
1:A:265:THR:HG23	2:A:402:SO4:O2	2.18	0.44
1:A:329:VAL:HG21	1:A:344:LEU:CD2	2.48	0.43
1:A:315:ILE:HG22	1:A:368:LEU:HD13	1.99	0.43
1:A:241:MET:SD	1:A:267:THR:HB	2.58	0.43
1:A:217:CYS:SG	1:A:270:LEU:HA	2.58	0.43
1:A:136:ILE:CD1	1:A:145:ALA:HB2	2.48	0.43
1:A:344:LEU:HD12	1:A:379:VAL:HG21	2.01	0.43
1:A:136:ILE:CG2	1:A:141:LEU:HB2	2.49	0.43
1:A:199:SER:N	2:A:405:SO4:O1	2.48	0.42
1:A:234:ALA:O	1:A:237[A]:SER:OG	2.31	0.42
1:A:185:ILE:HD11	1:A:204:ARG:HA	2.01	0.42
1:A:230:TYR:CE1	1:A:277:TYR:CD2	3.07	0.42
1:A:276:SER:O	1:A:279:TYR:HB3	2.19	0.42
1:A:332:LEU:HD23	1:A:343:VAL:HG11	2.02	0.42
1:A:337:VAL:HG13	1:A:338:ASP:N	2.34	0.42
1:A:209:GLU:CD	1:A:227:ARG:HH22	2.23	0.42
1:A:351:LEU:CD2	1:A:369:GLY:CA	2.97	0.42
1:A:107:ILE:CG2	1:A:141:LEU:HD22	2.49	0.42
1:A:303:ASN:O	1:A:307:VAL:HG23	2.20	0.42
1:A:184:ASN:HB3	1:A:247:GLU:HG2	2.02	0.41
1:A:280:PHE:O	1:A:284:VAL:HG23	2.20	0.41
1:A:360:SER:OG	1:A:364:MLZ:HG2	2.20	0.41
1:A:149:LEU:HA	1:A:152:THR:HG22	2.02	0.41
1:A:320:PRO:HG3	1:A:368:LEU:HD21	2.02	0.41
1:A:327:ARG:NE	1:A:327:ARG:HA	2.36	0.41
1:A:312:HIS:HA	1:A:315:ILE:HG12	2.02	0.41
1:A:351:LEU:CD2	1:A:369:GLY:N	2.84	0.41
1:A:279:TYR:CE1	1:A:353:GLN:HG3	2.57	0.40
1:A:256:PRO:HB2	1:A:259:GLN:HB3	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:ALA:H	3:A:406:GOL:C3	2.33	0.40

All (1) 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)
1:A:168:ARG:HH12	1:A:377:ASP:OD1[2_345]	1.58	0.02

## 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	290/425 (68%)	287 (99%)	3 (1%)	0	<a href="#">100</a> <a href="#">100</a>

There are no Ramachandran outliers to report.

### 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	251/350 (72%)	251 (100%)	0	<a href="#">100</a> <a href="#">100</a>

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

4 non-standard protein/DNA/RNA residues are 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
1	MLZ	A	249	1	8,9,10	0.72	0	4,9,11	2.16	1 (25%)
1	MLZ	A	364	1	8,9,10	0.66	0	4,9,11	1.47	1 (25%)
1	MLZ	A	324	1	8,9,10	0.67	0	4,9,11	1.77	1 (25%)
1	MLZ	A	313	1	8,9,10	0.66	0	4,9,11	1.86	1 (25%)

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
1	MLZ	A	249	1	-	0/7/8/10	-
1	MLZ	A	364	1	-	6/7/8/10	-
1	MLZ	A	324	1	-	4/7/8/10	-
1	MLZ	A	313	1	-	1/7/8/10	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	249	MLZ	CM-NZ-CE	4.02	123.56	111.95
1	A	313	MLZ	CM-NZ-CE	3.51	122.10	111.95
1	A	324	MLZ	CM-NZ-CE	3.35	121.62	111.95
1	A	364	MLZ	CM-NZ-CE	2.79	120.00	111.95

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	324	MLZ	N-CA-CB-CG
1	A	324	MLZ	C-CA-CB-CG
1	A	364	MLZ	C-CA-CB-CG
1	A	313	MLZ	CD-CE-NZ-CM
1	A	364	MLZ	CA-CB-CG-CD
1	A	364	MLZ	CG-CD-CE-NZ
1	A	324	MLZ	CE-CD-CG-CB
1	A	324	MLZ	CD-CE-NZ-CM
1	A	364	MLZ	CE-CD-CG-CB
1	A	364	MLZ	CD-CE-NZ-CM
1	A	364	MLZ	N-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	364	MLZ	1	0
1	A	313	MLZ	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

7 ligands are 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	SO4	A	405	-	4,4,4	0.13	0	6,6,6	0.05	0
2	SO4	A	402	-	4,4,4	0.14	0	6,6,6	0.05	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	A	404	-	4,4,4	0.14	0	6,6,6	0.05	0
3	GOL	A	406	-	5,5,5	0.16	0	5,5,5	0.70	0
2	SO4	A	403	-	4,4,4	0.15	0	6,6,6	0.09	0
2	SO4	A	401	-	4,4,4	0.15	0	6,6,6	0.06	0
3	GOL	A	407	-	5,5,5	0.24	0	5,5,5	0.20	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
3	GOL	A	407	-	-	2/4/4/4	-
3	GOL	A	406	-	-	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
3	A	406	GOL	C1-C2-C3-O3
3	A	406	GOL	O2-C2-C3-O3
3	A	407	GOL	O1-C1-C2-C3
3	A	407	GOL	O1-C1-C2-O2

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	405	SO4	1	0
2	A	402	SO4	2	0
2	A	404	SO4	1	0
3	A	406	GOL	2	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	288/425 (67%)	0.86	32 (11%) <b>5</b> <b>5</b>	22, 30, 54, 77	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	103	GLY	7.1
1	A	385	ASP	5.9
1	A	94	THR	5.6
1	A	384	GLU	5.0
1	A	156	SER	4.8
1	A	155	PRO	4.1
1	A	311	TYR	3.8
1	A	362	ALA	3.2
1	A	110	GLN	3.2
1	A	363	ASP	3.1
1	A	131	LEU	3.1
1	A	149	LEU	3.0
1	A	117	ASP	2.7
1	A	121	ASP	2.7
1	A	187[A]	PHE	2.6
1	A	295	GLY	2.6
1	A	318	LYS	2.6
1	A	360	SER	2.5
1	A	347	PHE	2.5
1	A	150	VAL	2.5
1	A	164	LEU	2.5
1	A	352	ARG	2.3
1	A	293	ALA	2.3
1	A	382	ASN	2.2
1	A	260	LEU	2.2
1	A	99	LYS	2.2
1	A	120	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	348	PHE	2.2
1	A	214	THR	2.2
1	A	273	VAL	2.0
1	A	280	PHE	2.0
1	A	158	GLY	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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
1	MLZ	A	249	10/11	0.84	0.21	24,37,50,50	0
1	MLZ	A	313	10/11	0.90	0.18	26,51,65,65	0
1	MLZ	A	324	10/11	0.92	0.11	24,37,45,45	0
1	MLZ	A	364	10/11	0.92	0.15	35,55,66,66	0

## 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
3	GOL	A	407	6/6	0.53	0.41	76,92,93,94	0
3	GOL	A	406	6/6	0.57	0.39	46,60,74,75	0
2	SO4	A	404	5/5	0.78	0.30	63,64,65,66	5
2	SO4	A	405	5/5	0.89	0.33	66,68,68,69	0
2	SO4	A	403	5/5	0.90	0.18	60,62,63,63	5
2	SO4	A	402	5/5	0.97	0.20	50,53,57,58	5
2	SO4	A	401	5/5	0.97	0.21	61,62,63,63	5

## 6.5 Other polymers [i](#)

There are no such residues in this entry.