



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 03:06 pm BST

PDB ID : 3IAX  
Title : The crystal structure of the TolB box of Colicin A in complex with TolB reveals important differences in the recruitment of the common TolB translocation portal used by group A colicins  
Authors : Li, C.  
Deposited on : 2009-07-15  
Resolution : 2.60 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

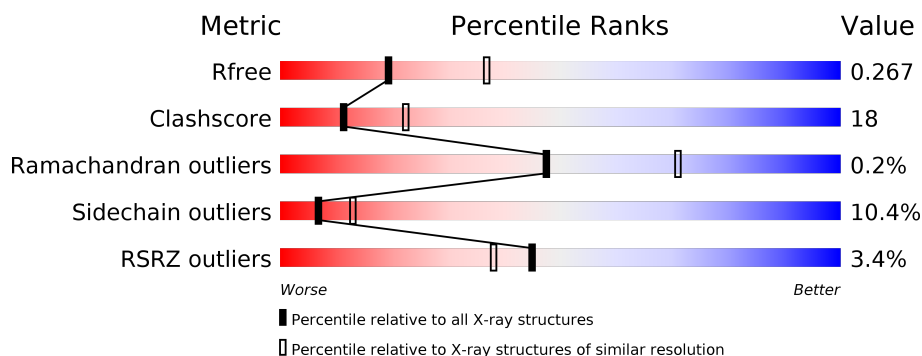
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	438	<div> <div>3%</div> <div> <div></div> <div>62%</div> <div>24%</div> <div>5%</div> <div>9%</div> </div> </div>
2	B	115	<div> <div>5%</div> <div> <div></div> <div>90%</div> </div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3175 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 Protein tolB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	0	2	0
			3020	1895	536	583	6			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	431	LEU	-	EXPRESSION TAG	UNP P0A855
A	432	GLU	-	EXPRESSION TAG	UNP P0A855
A	433	HIS	-	EXPRESSION TAG	UNP P0A855
A	434	HIS	-	EXPRESSION TAG	UNP P0A855
A	435	HIS	-	EXPRESSION TAG	UNP P0A855
A	436	HIS	-	EXPRESSION TAG	UNP P0A855
A	437	HIS	-	EXPRESSION TAG	UNP P0A855
A	438	HIS	-	EXPRESSION TAG	UNP P0A855

- Molecule 2 is a protein called Colicin-A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	12	Total	C	N	O	0	0	0
			85	50	17	18			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	108	LEU	-	EXPRESSION TAG	UNP P04480
B	109	GLU	-	EXPRESSION TAG	UNP P04480
B	110	HIS	-	EXPRESSION TAG	UNP P04480
B	111	HIS	-	EXPRESSION TAG	UNP P04480
B	112	HIS	-	EXPRESSION TAG	UNP P04480
B	113	HIS	-	EXPRESSION TAG	UNP P04480
B	114	HIS	-	EXPRESSION TAG	UNP P04480
B	115	HIS	-	EXPRESSION TAG	UNP P04480

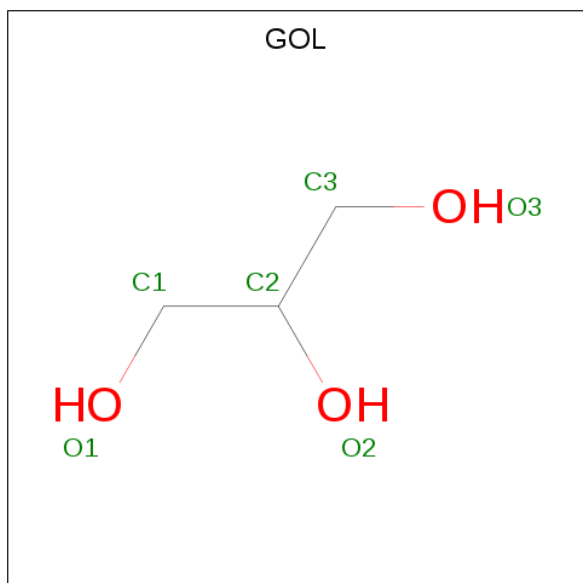
- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 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
5	A	1	Total	C	O	0	0
			6	3	3		

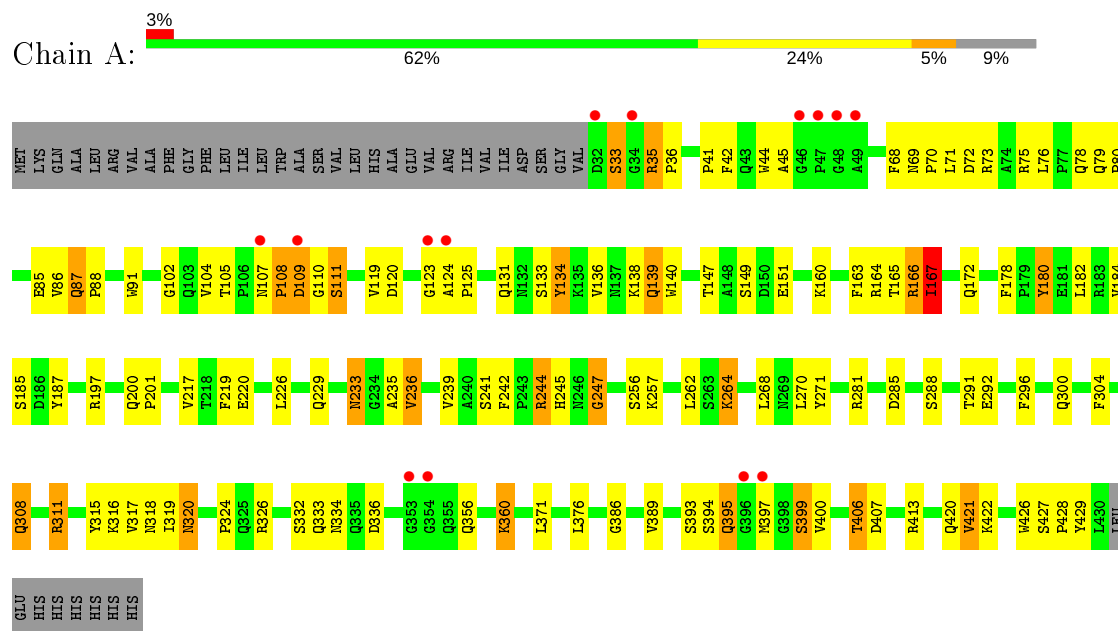
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	58	Total	O	0	0
			58	58		
6	B	4	Total	O	0	0
			4	4		

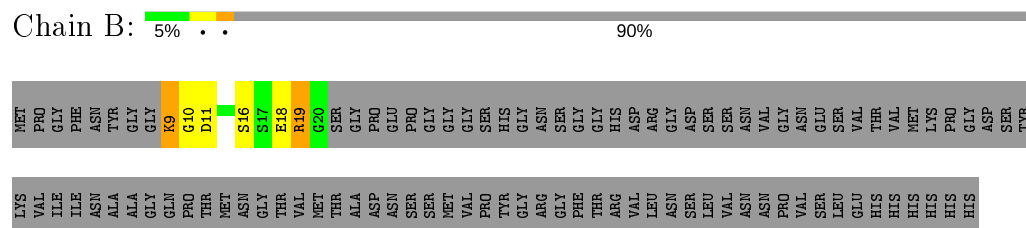
### 3 Residue-property plots

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: Protein tolB



#### • Molecule 2: Colicin-A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	61.95Å 40.17Å 80.87Å 90.00° 97.18° 90.00°	Depositor
Resolution (Å)	30.00 – 2.60 29.98 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.0 (30.00-2.60) 98.0 (29.98-2.60)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.21 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.190 , 0.257 0.200 , 0.267	Depositor DCC
$R_{free}$ test set	583 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.9	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 36.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	3175	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.05% 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

### 5.1 Standard geometry

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

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	1.38	14/3100 (0.5%)	0.93	11/4224 (0.3%)
2	B	1.68	2/86 (2.3%)	0.89	0/113
All	All	1.39	16/3186 (0.5%)	0.93	11/4337 (0.3%)

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	315	TYR	CD2-CE2	-5.78	1.30	1.39
2	B	18	GLU	CD-OE1	-5.73	1.19	1.25
1	A	426	TRP	CE3-CZ3	-5.68	1.28	1.38
1	A	315	TYR	CD1-CE1	-5.62	1.30	1.39
1	A	180	TYR	CD1-CE1	-5.38	1.31	1.39
1	A	317	VAL	CB-CG2	-5.31	1.41	1.52
2	B	18	GLU	CD-OE2	-5.30	1.19	1.25
1	A	315	TYR	CE2-CZ	-5.25	1.31	1.38
1	A	236	VAL	CB-CG2	-5.19	1.42	1.52
1	A	389	VAL	CB-CG2	-5.18	1.42	1.52
1	A	247	GLY	C-O	-5.10	1.15	1.23
1	A	167	ILE	C-O	-5.08	1.13	1.23
1	A	334	ASN	C-O	-5.05	1.13	1.23
1	A	184	VAL	CB-CG2	-5.04	1.42	1.52
1	A	296	PHE	CD2-CE2	-5.02	1.29	1.39
1	A	421	VAL	CB-CG2	-5.01	1.42	1.52

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	407	ASP	CB-CG-OD1	5.95	123.65	118.30
1	A	134	TYR	O-C-N	5.93	132.18	122.70
1	A	134	TYR	CA-C-N	-5.83	104.36	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	242	PHE	N-CA-C	-5.83	95.26	111.00
1	A	33	SER	N-CA-C	-5.74	95.51	111.00
1	A	285	ASP	CB-CG-OD1	5.41	123.17	118.30
1	A	281	ARG	CB-CA-C	-5.33	99.75	110.40
1	A	166[A]	ARG	N-CA-C	5.28	125.24	111.00
1	A	166[B]	ARG	N-CA-C	5.28	125.24	111.00
1	A	241	SER	N-CA-C	-5.26	96.81	111.00
1	A	285	ASP	N-CA-C	-5.25	96.82	111.00

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	3020	0	2932	107	0
2	B	85	0	74	7	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	6	0	8	0	0
6	A	58	0	0	1	0
6	B	4	0	0	0	0
All	All	3175	0	3014	109	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 18.

All (109) 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:41:PRO:HG3	1:A:73:ARG:HE	1.00	1.07
1:A:78:GLN:NE2	1:A:91:TRP:HE1	1.52	1.07
1:A:41:PRO:HG3	1:A:73:ARG:NE	1.85	0.91
1:A:139:GLN:OE1	1:A:139:GLN:HA	1.73	0.84
1:A:104:VAL:O	1:A:104:VAL:HG12	1.79	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:GLN:CA	1:A:139:GLN:OE1	2.29	0.81
1:A:244:ARG:HG3	1:A:264:LYS:HA	1.64	0.80
1:A:395:GLN:CG	1:A:395:GLN:O	2.30	0.80
1:A:78:GLN:HE22	1:A:87:GLN:H	1.30	0.79
1:A:395:GLN:HG2	1:A:395:GLN:O	1.83	0.78
1:A:399:SER:H	1:A:420:GLN:HG3	1.49	0.78
1:A:78:GLN:O	1:A:80:PRO:HD2	1.86	0.76
1:A:44:TRP:HE3	1:A:104:VAL:HG12	1.51	0.75
1:A:229:GLN:HG3	1:A:236:VAL:HG22	1.67	0.75
1:A:400:VAL:HG11	1:A:413:ARG:HD2	1.68	0.74
1:A:386:GLY:O	1:A:406:THR:HG21	1.87	0.74
1:A:318:ASN:HD22	1:A:320:ASN:H	1.36	0.72
1:A:138:LYS:CE	1:A:139:GLN:HE22	2.03	0.72
1:A:233:ASN:HB3	1:A:235:ALA:H	1.54	0.72
1:A:78:GLN:NE2	1:A:87:GLN:H	1.87	0.71
1:A:226:LEU:HD21	1:A:247:GLY:HA2	1.73	0.68
1:A:78:GLN:HE21	1:A:91:TRP:HE1	0.73	0.68
1:A:400:VAL:HG23	6:A:476:HOH:O	1.95	0.67
1:A:229:GLN:HG3	1:A:236:VAL:CG2	2.24	0.66
1:A:376:LEU:HB2	1:A:394:SER:HB2	1.77	0.66
1:A:107:ASN:O	1:A:109:ASP:N	2.30	0.64
1:A:138:LYS:C	1:A:139:GLN:OE1	2.35	0.64
1:A:138:LYS:HE3	1:A:139:GLN:HE22	1.63	0.64
1:A:360:LYS:HE2	1:A:406:THR:O	1.98	0.63
1:A:109:ASP:OD2	1:A:111:SER:HB3	1.99	0.63
1:A:399:SER:H	1:A:420:GLN:CG	2.11	0.63
1:A:80:PRO:HB3	1:A:85:GLU:O	1.97	0.63
1:A:245:HIS:HD2	1:A:268:LEU:HD21	1.62	0.62
1:A:245:HIS:NE2	2:B:11:ASP:HB3	2.14	0.62
1:A:104:VAL:CG1	1:A:104:VAL:O	2.47	0.62
1:A:78:GLN:C	1:A:80:PRO:CD	2.69	0.61
1:A:245:HIS:CD2	1:A:268:LEU:HD21	2.38	0.58
1:A:219:PHE:CD2	2:B:9:LYS:HG3	2.37	0.58
1:A:138:LYS:HE2	1:A:139:GLN:HE22	1.68	0.58
1:A:109:ASP:O	1:A:109:ASP:CG	2.42	0.58
1:A:120:ASP:OD1	1:A:124:ALA:O	2.21	0.58
1:A:226:LEU:O	1:A:239:VAL:HB	2.03	0.58
1:A:44:TRP:HE3	1:A:104:VAL:CG1	2.17	0.58
1:A:165:THR:O	1:A:187:TYR:HB3	2.04	0.57
1:A:72:ASP:HB3	1:A:75:ARG:HG3	1.87	0.57
1:A:123:GLY:C	1:A:125:PRO:HD3	2.26	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:GLN:HE22	1:A:87:GLN:N	2.01	0.56
1:A:138:LYS:HG2	1:A:139:GLN:OE1	2.05	0.56
1:A:300:GLN:O	1:A:319:ILE:HG12	2.06	0.55
1:A:139:GLN:OE1	1:A:139:GLN:N	2.39	0.55
1:A:311:ARG:NH1	1:A:333:GLN:OE1	2.41	0.54
1:A:35:ARG:HD3	1:A:68:PHE:CE2	2.43	0.54
1:A:107:ASN:C	1:A:109:ASP:N	2.61	0.54
1:A:78:GLN:C	1:A:80:PRO:HD3	2.29	0.53
1:A:149:SER:HB3	1:A:163:PHE:CD2	2.43	0.53
1:A:86:VAL:O	1:A:88:PRO:HD3	2.09	0.52
1:A:291:THR:HG23	1:A:292:GLU:HG3	1.91	0.52
1:A:316:LYS:O	1:A:324:PRO:HA	2.08	0.52
1:A:107:ASN:O	1:A:108:PRO:C	2.48	0.52
1:A:320:ASN:N	1:A:320:ASN:OD1	2.42	0.52
1:A:107:ASN:O	1:A:110:GLY:N	2.41	0.51
1:A:45:ALA:HB3	1:A:105:THR:HG22	1.92	0.51
1:A:245:HIS:CE1	2:B:11:ASP:HB3	2.45	0.51
1:A:120:ASP:HB3	1:A:124:ALA:O	2.10	0.51
2:B:10:GLY:HA3	2:B:19:ARG:O	2.10	0.50
1:A:311:ARG:NH1	1:A:333:GLN:HB2	2.27	0.50
1:A:138:LYS:O	1:A:139:GLN:OE1	2.30	0.50
1:A:200:GLN:HB3	1:A:201:PRO:CD	2.42	0.50
1:A:178:PHE:HB3	1:A:197:ARG:HB3	1.93	0.49
1:A:270:LEU:HD11	1:A:304:PHE:CG	2.47	0.48
1:A:44:TRP:CE3	1:A:104:VAL:HG12	2.41	0.48
1:A:78:GLN:C	1:A:80:PRO:HD2	2.33	0.48
1:A:256:SER:C	1:A:257:LYS:HG3	2.33	0.48
1:A:399:SER:HB3	1:A:421:VAL:O	2.14	0.48
1:A:44:TRP:CE3	1:A:104:VAL:CG1	2.97	0.48
1:A:109:ASP:O	1:A:109:ASP:OD2	2.30	0.48
1:A:288:SER:CB	1:A:308:GLN:HB2	2.44	0.47
1:A:147:THR:O	1:A:151:GLU:HG3	2.14	0.47
1:A:180:TYR:N	1:A:180:TYR:CD1	2.82	0.47
1:A:360:LYS:CE	1:A:406:THR:O	2.63	0.47
1:A:166[B]:ARG:HB3	1:A:185:SER:O	2.13	0.47
1:A:166[A]:ARG:HB3	1:A:185:SER:O	2.14	0.46
1:A:123:GLY:O	1:A:125:PRO:HD3	2.16	0.46
1:A:399:SER:HB2	1:A:420:GLN:HG2	1.96	0.46
1:A:42:PHE:CE2	1:A:102:GLY:HA3	2.50	0.46
1:A:136:VAL:HB	1:A:140:TRP:HB2	1.98	0.46
1:A:264:LYS:H	1:A:264:LYS:HG3	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:427:SER:HB2	1:A:428:PRO:HD2	1.99	0.45
1:A:71:LEU:HD23	1:A:76:LEU:HD12	1.99	0.45
1:A:226:LEU:HD21	1:A:247:GLY:CA	2.46	0.44
1:A:245:HIS:NE2	2:B:11:ASP:CB	2.79	0.44
1:A:399:SER:N	1:A:420:GLN:HG3	2.24	0.44
1:A:167:ILE:HG12	1:A:187:TYR:HA	2.00	0.43
1:A:200:GLN:HB3	1:A:201:PRO:HD2	2.00	0.43
1:A:233:ASN:HD22	1:A:233:ASN:HA	1.54	0.42
1:A:262:LEU:HB2	1:A:271:TYR:CE1	2.53	0.42
2:B:16:SER:O	2:B:19:ARG:HG3	2.18	0.42
1:A:160:LYS:HG2	1:A:429:TYR:CE1	2.54	0.42
1:A:107:ASN:C	1:A:109:ASP:H	2.22	0.42
1:A:245:HIS:CD2	2:B:11:ASP:HB2	2.54	0.42
1:A:217:VAL:HG22	1:A:247:GLY:HA2	2.00	0.42
1:A:311:ARG:HH12	1:A:333:GLN:HB2	1.83	0.42
1:A:360:LYS:HE3	1:A:371:LEU:HD21	2.01	0.42
1:A:68:PHE:O	1:A:70:PRO:HD3	2.20	0.41
1:A:147:THR:HG23	1:A:164:ARG:NH1	2.36	0.40
1:A:138:LYS:HE2	1:A:139:GLN:NE2	2.36	0.40
1:A:79:GLN:N	1:A:80:PRO:CD	2.84	0.40
1:A:78:GLN:NE2	1:A:91:TRP:NE1	2.30	0.40
1:A:35:ARG:HA	1:A:36:PRO:HD3	1.96	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	399/438 (91%)	383 (96%)	15 (4%)	1 (0%)	41	64
2	B	10/115 (9%)	10 (100%)	0	0	100	100
All	All	409/553 (74%)	393 (96%)	15 (4%)	1 (0%)	47	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	108	PRO

### 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	320/351 (91%)	288 (90%)	32 (10%)	7	14
2	B	8/90 (9%)	6 (75%)	2 (25%)	0	1
All	All	328/441 (74%)	294 (90%)	34 (10%)	7	13

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	SER
1	A	35	ARG
1	A	69	ASN
1	A	87	GLN
1	A	109	ASP
1	A	111	SER
1	A	119	VAL
1	A	131	GLN
1	A	133	SER
1	A	134	TYR
1	A	139	GLN
1	A	167	ILE
1	A	172	GLN
1	A	182	LEU
1	A	220	GLU
1	A	233	ASN
1	A	244	ARG
1	A	264	LYS
1	A	308	GLN
1	A	311	ARG
1	A	320	ASN
1	A	326	ARG

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Mol	Chain	Res	Type
1	A	332	SER
1	A	336	ASP
1	A	356	GLN
1	A	360	LYS
1	A	393	SER
1	A	395	GLN
1	A	397	MET
1	A	399	SER
1	A	406	THR
1	A	422	LYS
2	B	9	LYS
2	B	19	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	78	GLN
1	A	87	GLN
1	A	229	GLN
1	A	233	ASN
1	A	300	GLN
1	A	308	GLN
1	A	318	ASN
1	A	335	GLN
1	A	355	GLN
1	A	357	HIS

### 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](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	$\# Z  > 2$
5	GOL	A	502	-	5,5,5	0.95	0	5,5,5	1.08	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
5	GOL	A	502	-	-	3/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	502	GOL	C1-C2-C3-O3
5	A	502	GOL	O2-C2-C3-O3
5	A	502	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 ⓘ

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	399/438 (91%)	-0.11	14 (3%) 44 36	7, 15, 29, 39	0
2	B	12/115 (10%)	0.34	0 100 100	21, 25, 32, 38	0
All	All	411/553 (74%)	-0.09	14 (3%) 45 38	7, 15, 29, 39	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	49	ALA	6.6
1	A	47	PRO	5.2
1	A	48	GLY	5.1
1	A	32	ASP	3.7
1	A	46	GLY	3.5
1	A	123	GLY	3.5
1	A	396	GLY	2.9
1	A	397	MET	2.7
1	A	34	GLY	2.5
1	A	353	GLY	2.4
1	A	124	ALA	2.4
1	A	109	ASP	2.3
1	A	107	ASN	2.1
1	A	354	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 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
5	GOL	A	502	6/6	0.79	0.24	57,57,58,61	0
3	NA	A	500	1/1	0.96	0.12	24,24,24,24	0
4	CA	A	501	1/1	0.96	0.30	56,56,56,56	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.