



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:34 AM UTC

PDB ID : 6X41 / pdb_00006x41
Title : Crystal structure of inactive enzymatic binary toxin component from *Clostridium difficile*
Authors : Pozharski, E.
Deposited on : 2020-05-21
Resolution : 2.36 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

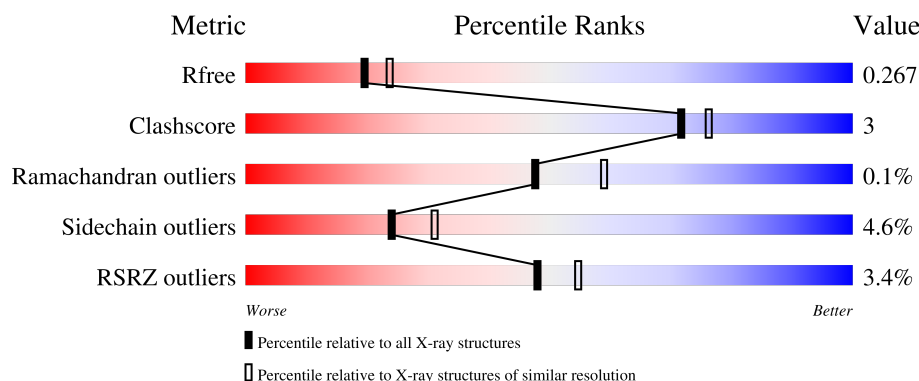
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.36 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	429	
1	B	429	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6998 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 CdtA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	417	Total	C	N	O	S	0	4	0
			3391	2165	566	655	5			
1	B	417	Total	C	N	O	S	0	0	0
			3364	2143	563	653	5			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP F5B5W8
A	1	VAL	-	expression tag	UNP F5B5W8
A	2	ALA	-	expression tag	UNP F5B5W8
A	345	PHE	SER	conflict	UNP F5B5W8
A	385	GLN	GLU	conflict	UNP F5B5W8
A	387	GLN	GLU	conflict	UNP F5B5W8
A	421	LEU	-	expression tag	UNP F5B5W8
A	422	GLU	-	expression tag	UNP F5B5W8
A	423	HIS	-	expression tag	UNP F5B5W8
A	424	HIS	-	expression tag	UNP F5B5W8
A	425	HIS	-	expression tag	UNP F5B5W8
A	426	HIS	-	expression tag	UNP F5B5W8
A	427	HIS	-	expression tag	UNP F5B5W8
A	428	HIS	-	expression tag	UNP F5B5W8
B	0	MET	-	initiating methionine	UNP F5B5W8
B	1	VAL	-	expression tag	UNP F5B5W8
B	2	ALA	-	expression tag	UNP F5B5W8
B	345	PHE	SER	conflict	UNP F5B5W8
B	385	GLN	GLU	conflict	UNP F5B5W8
B	387	GLN	GLU	conflict	UNP F5B5W8
B	421	LEU	-	expression tag	UNP F5B5W8
B	422	GLU	-	expression tag	UNP F5B5W8
B	423	HIS	-	expression tag	UNP F5B5W8
B	424	HIS	-	expression tag	UNP F5B5W8
B	425	HIS	-	expression tag	UNP F5B5W8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	426	HIS	-	expression tag	UNP F5B5W8
B	427	HIS	-	expression tag	UNP F5B5W8
B	428	HIS	-	expression tag	UNP F5B5W8

- 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		
2	B	1	Total	C	O	0	0
			6	3	3		

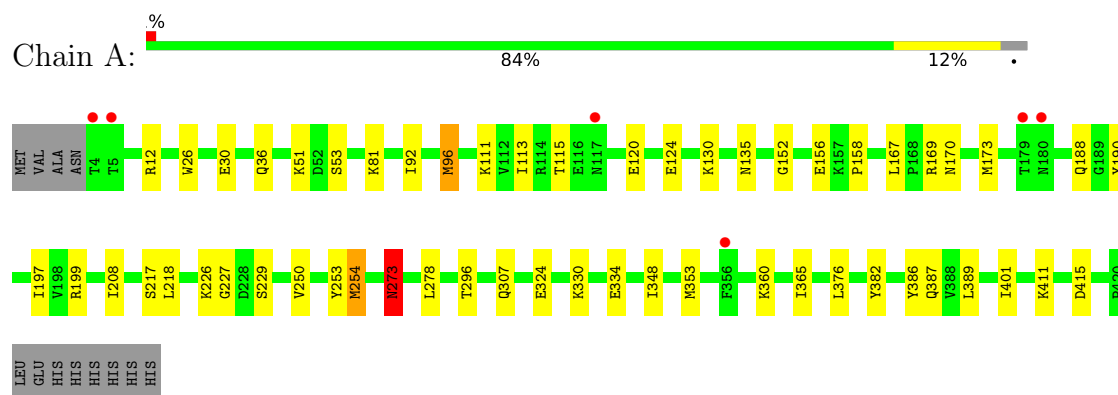
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	138	Total	O	0	0
			138	138		
3	B	93	Total	O	0	0
			93	93		

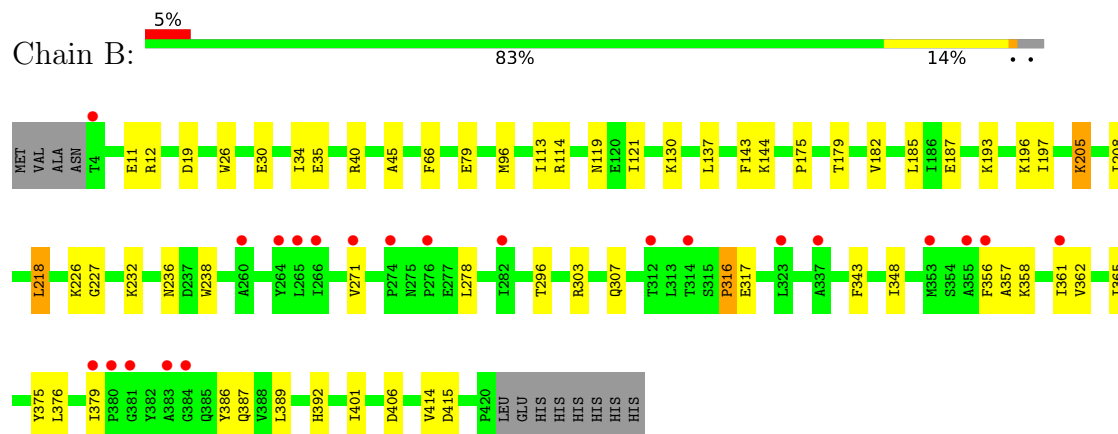
3 Residue-property plots [i](#)

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: CdtA



• Molecule 1: CdtA



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	114.12Å 114.12Å 179.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.66 – 2.36 33.66 – 2.36	Depositor EDS
% Data completeness (in resolution range)	99.3 (33.66-2.36) 99.3 (33.66-2.36)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.42 (at 2.36Å)	Xtriage
Refinement program	BUSTER 2.10.3 (19-MAR-2020)	Depositor
R, R_{free}	0.202 , 0.246 (Not available) , 0.267	Depositor DCC
R_{free} test set	2452 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	49.8	Xtriage
Anisotropy	0.269	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6998	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.17% 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	0.76	0/3471	1.10	8/4687 (0.2%)
1	B	0.73	0/3437	1.09	11/4644 (0.2%)
All	All	0.75	0/6908	1.10	19/9331 (0.2%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	415	ASP	CA-CB-CG	7.03	119.63	112.60
1	A	415	ASP	CA-CB-CG	6.13	118.73	112.60
1	A	273	ASN	CA-CB-CG	5.73	118.33	112.60
1	A	152	GLY	CA-C-N	5.70	127.92	120.28
1	A	152	GLY	C-N-CA	5.70	127.92	120.28
1	A	253	TYR	CA-C-N	5.61	128.36	120.28
1	A	253	TYR	C-N-CA	5.61	128.36	120.28
1	B	387	GLN	N-CA-C	5.56	119.31	109.96
1	B	361	ILE	N-CA-C	5.34	115.55	107.80
1	B	316	PRO	CA-C-N	5.21	127.79	120.28
1	B	316	PRO	C-N-CA	5.21	127.79	120.28
1	A	365	ILE	N-CA-C	5.14	115.49	107.99
1	B	19	ASP	CA-C-N	5.14	127.59	120.29
1	B	19	ASP	C-N-CA	5.14	127.59	120.29
1	B	356	PHE	CA-C-N	5.14	127.48	120.54
1	B	356	PHE	C-N-CA	5.14	127.48	120.54
1	B	357	ALA	N-CA-C	5.12	117.25	111.11
1	A	158	PRO	N-CA-C	5.11	120.32	114.03
1	B	365	ILE	N-CA-C	5.02	115.81	108.58

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	3391	0	3358	22	0
1	B	3364	0	3327	23	0
2	A	6	0	8	2	0
2	B	6	0	8	1	0
3	A	138	0	0	1	0
3	B	93	0	0	0	0
All	All	6998	0	6701	45	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 3.

All (45) 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:227:GLY:HA3	1:A:348:ILE:HD13	1.66	0.76
1:A:330:LYS:HZ3	2:A:501:GOL:H31	1.58	0.69
1:A:330:LYS:NZ	2:A:501:GOL:H31	2.08	0.69
1:A:167:LEU:HD12	1:A:173:MET:HE2	1.75	0.68
1:A:113:ILE:HD13	1:A:208:ILE:HD12	1.76	0.68
1:A:217:SER:HB3	3:A:691:HOH:O	1.94	0.68
1:A:360:LYS:HA	1:A:411:LYS:HG2	1.76	0.67
1:A:382:TYR:OH	1:A:387:GLN:NE2	2.31	0.64
1:B:187:GLU:O	1:B:187:GLU:HG2	1.97	0.63
1:B:227:GLY:HA3	1:B:348:ILE:HD13	1.85	0.58
1:B:316:PRO:HD2	1:B:317:GLU:OE1	2.04	0.58
1:A:348:ILE:HG13	1:A:386:TYR:HB3	1.88	0.54
1:B:343:PHE:CZ	1:B:392:HIS:ND1	2.75	0.54
1:A:12:ARG:HB3	1:A:26:TRP:CD1	2.48	0.49
1:A:334:GLU:HG3	1:A:401:ILE:HD12	1.95	0.49
1:B:34:ILE:CD1	1:B:175:PRO:HD2	2.43	0.49
1:A:26:TRP:CE2	1:A:30:GLU:HG3	2.48	0.48
1:B:66:PHE:HE1	1:B:406:ASP:HA	1.78	0.48
1:B:238:TRP:HZ3	1:B:379:ILE:HD11	1.79	0.48
1:B:113:ILE:HD12	1:B:208:ILE:HD12	1.97	0.47
1:B:119:ASN:HA	1:B:205:LYS:HG3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:ARG:O	1:A:170:ASN:HB2	2.14	0.46
1:B:307:GLN:H	1:B:307:GLN:CD	2.24	0.45
1:A:92:ILE:HD13	1:A:173:MET:HE3	1.98	0.45
1:A:130:LYS:HB2	1:A:197:ILE:HD11	1.98	0.45
1:B:218:LEU:HD12	2:B:501:GOL:H12	1.98	0.45
1:B:137:LEU:HD23	1:B:193:LYS:HB3	1.98	0.45
1:B:114:ARG:HG2	1:B:121:ILE:HG12	1.97	0.45
1:B:143:PHE:HB3	1:B:185:LEU:HD11	2.00	0.44
1:B:232:LYS:O	1:B:236:ASN:HB2	2.18	0.43
1:B:303:ARG:HD3	1:B:362:VAL:HG22	2.01	0.43
1:A:188:GLN:HA	1:A:190:TYR:CE2	2.54	0.43
1:A:26:TRP:CZ2	1:A:30:GLU:HG3	2.54	0.42
1:A:96:MET:HB3	1:A:173:MET:HE1	2.00	0.42
1:A:218:LEU:HD22	1:A:296:THR:HG21	2.02	0.42
1:B:401:ILE:HG12	1:B:414:VAL:HG22	2.02	0.42
1:B:375:TYR:OH	1:B:386:TYR:HA	2.20	0.42
1:A:376:LEU:HD11	1:A:389:LEU:HB2	2.02	0.42
1:A:250:VAL:O	1:A:254:MET:HB2	2.21	0.41
1:B:45:ALA:O	1:B:79:GLU:OE2	2.38	0.41
1:B:12:ARG:HB3	1:B:26:TRP:CD1	2.56	0.40
1:B:26:TRP:CZ2	1:B:30:GLU:HG3	2.56	0.40
1:B:376:LEU:HD11	1:B:389:LEU:HB2	2.04	0.40
1:B:130:LYS:HB2	1:B:197:ILE:HD11	2.02	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	419/429 (98%)	410 (98%)	8 (2%)	1 (0%)	43	52
1	B	415/429 (97%)	401 (97%)	14 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	834/858 (97%)	811 (97%)	22 (3%)	1 (0%)	48 59

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	273	ASN

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	371/386 (96%)	352 (95%)	19 (5%)	21 26
1	B	369/386 (96%)	354 (96%)	15 (4%)	27 36
All	All	740/772 (96%)	706 (95%)	34 (5%)	24 31

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

Mol	Chain	Res	Type
1	A	36	GLN
1	A	51	LYS
1	A	53	SER
1	A	81	LYS
1	A	96	MET
1	A	111	LYS
1	A	115	THR
1	A	120	GLU
1	A	124	GLU
1	A	135	ASN
1	A	156	GLU
1	A	199	ARG
1	A	226	LYS
1	A	229	SER
1	A	254	MET
1	A	278	LEU
1	A	307	GLN

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Mol	Chain	Res	Type
1	A	324	GLU
1	A	353	MET
1	B	11	GLU
1	B	35	GLU
1	B	40	ARG
1	B	96	MET
1	B	144	LYS
1	B	179	THR
1	B	182	VAL
1	B	196	LYS
1	B	205	LYS
1	B	218	LEU
1	B	226	LYS
1	B	271	VAL
1	B	278	LEU
1	B	296	THR
1	B	358	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	119	ASN
1	A	206	HIS
1	A	387	GLN
1	A	391	ASN
1	B	61	GLN
1	B	385	GLN

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

2 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	GOL	B	501	-	5,5,5	0.15	0	5,5,5	0.32	0
2	GOL	A	501	-	5,5,5	0.11	0	5,5,5	0.28	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	B	501	-	-	2/4/4/4	-
2	GOL	A	501	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GOL	C1-C2-C3-O3
2	B	501	GOL	C1-C2-C3-O3
2	B	501	GOL	O2-C2-C3-O3
2	A	501	GOL	O1-C1-C2-C3
2	A	501	GOL	O2-C2-C3-O3
2	A	501	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	501	GOL	1	0
2	A	501	GOL	2	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

6.1 Protein, DNA and RNA chains

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	417/429 (97%)	0.15	6 (1%) 73 78	35, 50, 70, 84	4 (0%)
1	B	417/429 (97%)	0.47	22 (5%) 32 37	40, 57, 83, 99	0
All	All	834/858 (97%)	0.31	28 (3%) 48 55	35, 54, 78, 99	4 (0%)

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	179[A]	THR	5.0
1	B	353	MET	3.4
1	B	383	ALA	3.3
1	A	4	THR	3.3
1	B	380	PRO	3.0
1	B	337	ALA	2.9
1	B	266	ILE	2.8
1	B	271	VAL	2.8
1	B	356	PHE	2.7
1	A	180[A]	ASN	2.7
1	B	384	GLY	2.7
1	B	4	THR	2.6
1	B	265	LEU	2.6
1	B	274	PRO	2.5
1	B	379	ILE	2.4
1	A	117	ASN	2.4
1	B	355	ALA	2.3
1	A	5	THR	2.3
1	B	314	THR	2.3
1	B	260	ALA	2.3
1	B	282	ILE	2.2
1	B	361	ILE	2.2
1	B	264	TYR	2.2
1	A	356	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	381	GLY	2.1
1	B	312	THR	2.0
1	B	323	LEU	2.0
1	B	276	PRO	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($\text{\AA}^2$)	Q<0.9
2	GOL	B	501	6/6	0.81	0.15	63,64,64,64	0
2	GOL	A	501	6/6	0.85	0.13	63,64,64,64	0

6.5 Other polymers [i](#)

There are no such residues in this entry.