



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:00 AM UTC

PDB ID : 3KZH / pdb_00003kzh
Title : Crystal structure of a putative sugar kinase from *Clostridium perfringens*
Authors : Syed Ibrahim, B.; Kumaran, D.; Burley, S.K.; Swaminathan, S.; New York
SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2009-12-08
Resolution : 2.45 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

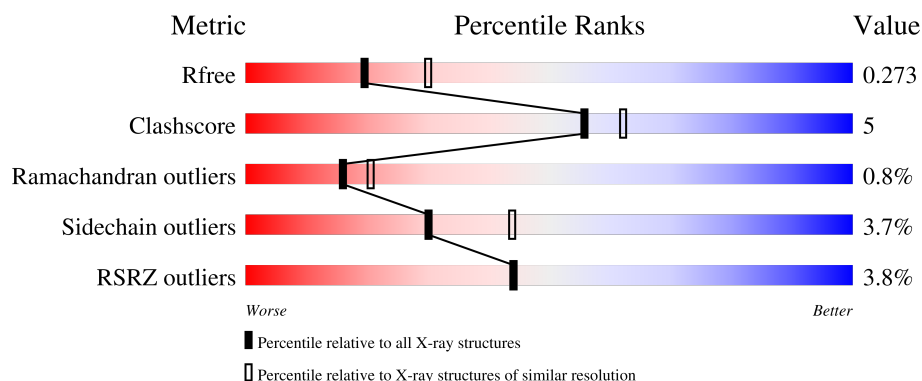
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	328	
1	B	328	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5072 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.

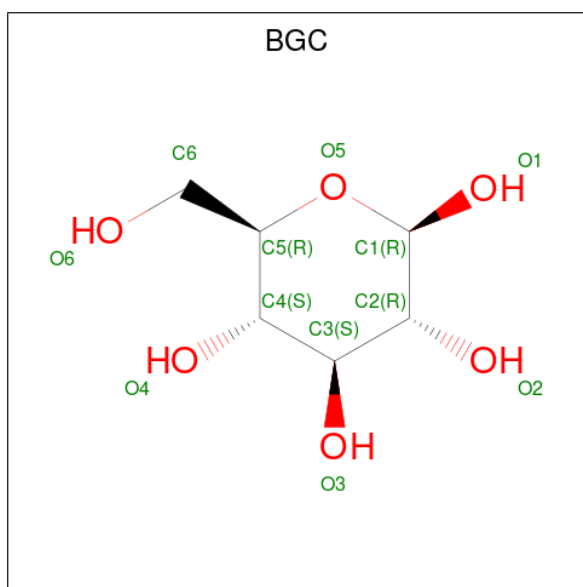
- Molecule 1 is a protein called Probable sugar kinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	316	Total	C	N	O	S	Se	0	0	0
			2451	1560	394	482	2	13			
1	B	314	Total	C	N	O	S	Se	0	0	0
			2379	1515	382	467	2	13			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q8XKB8
A	2	SER	-	expression tag	UNP Q8XKB8
A	321	GLU	-	expression tag	UNP Q8XKB8
A	322	GLY	-	expression tag	UNP Q8XKB8
A	323	HIS	-	expression tag	UNP Q8XKB8
A	324	HIS	-	expression tag	UNP Q8XKB8
A	325	HIS	-	expression tag	UNP Q8XKB8
A	326	HIS	-	expression tag	UNP Q8XKB8
A	327	HIS	-	expression tag	UNP Q8XKB8
A	328	HIS	-	expression tag	UNP Q8XKB8
B	1	MET	-	expression tag	UNP Q8XKB8
B	2	SER	-	expression tag	UNP Q8XKB8
B	321	GLU	-	expression tag	UNP Q8XKB8
B	322	GLY	-	expression tag	UNP Q8XKB8
B	323	HIS	-	expression tag	UNP Q8XKB8
B	324	HIS	-	expression tag	UNP Q8XKB8
B	325	HIS	-	expression tag	UNP Q8XKB8
B	326	HIS	-	expression tag	UNP Q8XKB8
B	327	HIS	-	expression tag	UNP Q8XKB8
B	328	HIS	-	expression tag	UNP Q8XKB8

- Molecule 2 is beta-D-glucopyranose (CCD ID: BGC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			11	6	5		
2	B	1	Total	C	O	0	0
			11	6	5		

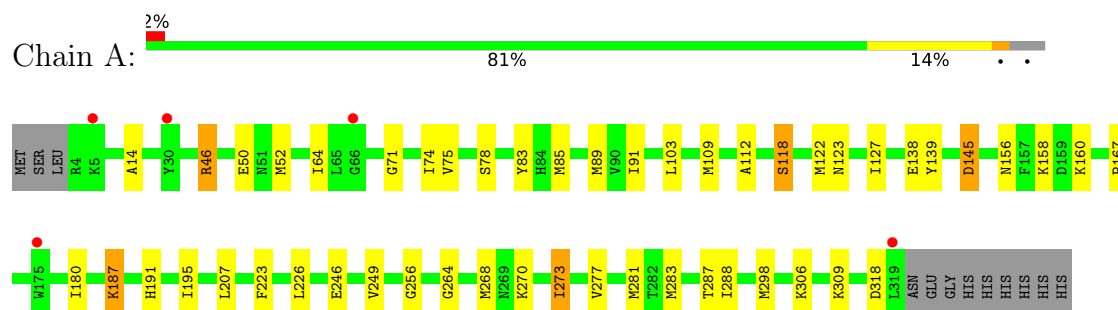
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	143	Total	O	0	0
			143	143		
3	B	77	Total	O	0	0
			77	77		

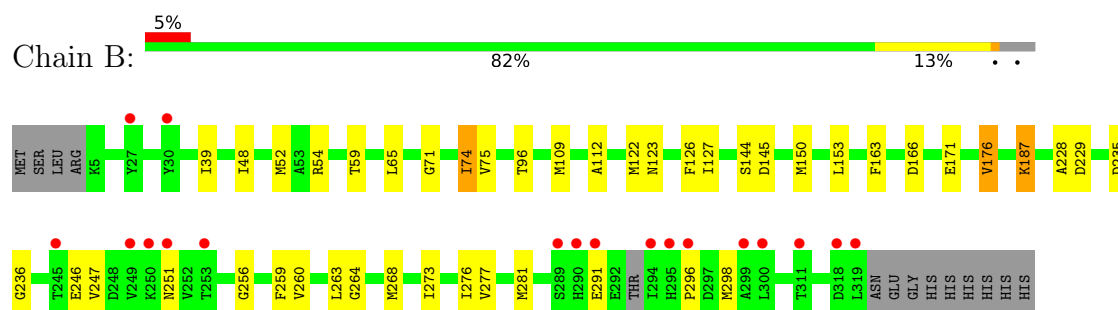
3 Residue-property plots [i](#)

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: Probable sugar kinase



- Molecule 1: Probable sugar kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.40Å 108.10Å 110.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.71 – 2.45 38.71 – 2.45	Depositor EDS
% Data completeness (in resolution range)	92.6 (38.71-2.45) 97.0 (38.71-2.45)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.50 (at 2.45Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.231 , 0.273 0.235 , 0.273	Depositor DCC
R_{free} test set	1123 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	37.7	Xtriage
Anisotropy	0.302	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 37.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.015 for -h,l,k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5072	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.93% 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: BGC

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	0.75	0/2488	1.13	10/3341 (0.3%)
1	B	0.72	0/2412	1.15	12/3240 (0.4%)
All	All	0.74	0/4900	1.14	22/6581 (0.3%)

There are no bond length outliers.

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	247	VAL	N-CA-C	7.10	118.95	109.37
1	B	236	GLY	N-CA-C	-7.01	105.54	114.37
1	A	273	ILE	N-CA-C	6.86	118.44	110.62
1	A	180	ILE	N-CA-C	6.66	119.37	111.05
1	A	14	ALA	N-CA-C	6.50	119.67	110.50
1	A	118	SER	N-CA-C	6.28	120.04	112.38
1	B	263	LEU	N-CA-C	-6.20	104.61	111.36
1	B	59	THR	N-CA-C	6.12	119.21	109.24
1	A	145	ASP	N-CA-C	5.85	117.45	111.14
1	B	144	SER	N-CA-C	5.63	119.23	112.93
1	A	112	ALA	N-CA-C	5.50	116.88	108.52
1	A	158	LYS	N-CA-C	5.47	118.76	111.75
1	B	112	ALA	N-CA-C	5.47	117.42	108.55
1	A	167	PRO	N-CA-C	5.39	120.94	113.98
1	B	163	PHE	N-CA-C	5.32	117.94	109.96
1	B	166	ASP	CA-C-N	5.28	125.00	119.82
1	B	166	ASP	C-N-CA	5.28	125.00	119.82
1	B	145	ASP	N-CA-C	5.22	116.66	111.07
1	B	276	ILE	N-CA-C	-5.10	105.73	110.53
1	A	156	ASN	N-CA-C	5.09	118.64	112.23
1	B	96	THR	N-CA-C	-5.04	103.30	109.65
1	A	246	GLU	N-CA-C	5.04	118.69	112.24

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	2451	0	2387	26	0
1	B	2379	0	2271	19	0
2	A	11	0	5	1	0
2	B	11	0	5	0	0
3	A	143	0	0	3	0
3	B	77	0	0	0	0
All	All	5072	0	4668	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 5.

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:122:MSE:HE2	1:A:127:ILE:HG13	1.59	0.84
1:A:138:GLU:HB2	1:A:268:MSE:HE1	1.63	0.78
1:A:139:TYR:HD2	1:A:268:MSE:HE2	1.56	0.71
1:A:139:TYR:CD2	1:A:268:MSE:HE2	2.38	0.58
1:A:122:MSE:HE3	1:A:123:ASN:O	2.03	0.57
1:B:122:MSE:HE1	1:B:126:PHE:HB3	1.87	0.57
1:B:127:ILE:HD12	1:B:153:LEU:HD21	1.87	0.57
1:B:277:VAL:HG12	1:B:281:MSE:HE2	1.87	0.56
1:B:273:ILE:O	1:B:277:VAL:HG23	2.06	0.56
1:A:64:ILE:HG23	1:A:89:MSE:HE2	1.88	0.56
1:B:187:LYS:HD3	1:B:259:PHE:HD2	1.71	0.55
1:B:150:MSE:SE	1:B:176:VAL:HG21	2.59	0.53
1:B:256:GLY:O	1:B:260:VAL:HG23	2.09	0.53
1:B:71:GLY:O	1:B:75:VAL:HG23	2.08	0.52
1:A:89:MSE:HE3	1:A:91:ILE:HD11	1.93	0.50
1:A:277:VAL:HG12	1:A:281:MSE:CE	2.42	0.50
1:A:277:VAL:O	1:A:281:MSE:HB2	2.12	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:TYR:HD2	1:A:268:MSE:CE	2.26	0.48
1:B:187:LYS:HB3	1:B:187:LYS:HE3	1.64	0.48
1:B:122:MSE:HE3	1:B:123:ASN:H	1.79	0.48
1:A:122:MSE:CE	1:A:127:ILE:HG13	2.39	0.47
1:A:74:ILE:HG22	1:A:85:MSE:SE	2.64	0.47
1:B:122:MSE:HE2	1:B:127:ILE:HG12	1.97	0.46
1:B:54:ARG:HD3	1:B:298:MSE:HB3	1.98	0.46
3:A:345:HOH:O	1:B:39:ILE:HD13	2.17	0.45
1:A:64:ILE:HD11	1:A:122:MSE:HB2	1.98	0.45
1:A:287:THR:HG22	3:A:379:HOH:O	2.16	0.44
1:B:264:GLY:O	1:B:268:MSE:HG2	2.17	0.44
1:A:78:SER:HB2	1:A:83:TYR:O	2.18	0.43
1:A:191:HIS:O	1:A:195:ILE:HG12	2.17	0.43
1:B:48:ILE:O	1:B:52:MSE:HG3	2.19	0.43
1:A:306:LYS:NZ	3:A:434:HOH:O	2.48	0.43
1:A:207:LEU:HD21	1:A:226:LEU:HD21	2.01	0.43
1:A:256:GLY:HA3	2:A:329:BGC:H5	2.00	0.42
1:A:64:ILE:HG21	1:A:118:SER:O	2.20	0.41
1:B:65:LEU:HD21	1:B:74:ILE:HG21	2.03	0.41
1:B:122:MSE:HE3	1:B:123:ASN:O	2.20	0.41
1:A:283:MSE:HE2	1:A:283:MSE:HB3	2.00	0.41
1:B:277:VAL:O	1:B:281:MSE:HB2	2.21	0.41
1:A:273:ILE:O	1:A:277:VAL:HG23	2.21	0.41
1:A:71:GLY:O	1:A:75:VAL:HG23	2.21	0.41
1:A:46:ARG:NH2	1:A:50:GLU:OE1	2.54	0.40
1:A:52:MSE:HE2	1:A:264:GLY:HA3	2.03	0.40
1:A:187:LYS:HG2	1:A:223:PHE:HB2	2.03	0.40
1:B:150:MSE:SE	1:B:176:VAL:CG2	3.19	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	314/328 (96%)	304 (97%)	10 (3%)	0	100	100
1	B	310/328 (94%)	286 (92%)	19 (6%)	5 (2%)	7	7
All	All	624/656 (95%)	590 (95%)	29 (5%)	5 (1%)	16	20

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	296	PRO
1	B	246	GLU
1	B	291	GLU
1	B	228	ALA
1	B	251	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	268/269 (100%)	256 (96%)	12 (4%)	24	37
1	B	250/269 (93%)	243 (97%)	7 (3%)	38	54
All	All	518/538 (96%)	499 (96%)	19 (4%)	30	44

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	ARG
1	A	103	LEU
1	A	109	MSE
1	A	145	ASP
1	A	160	LYS
1	A	187	LYS
1	A	249	VAL
1	A	270	LYS
1	A	288	ILE
1	A	298	MSE
1	A	309	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	318	ASP
1	B	74	ILE
1	B	109	MSE
1	B	171	GLU
1	B	176	VAL
1	B	187	LYS
1	B	229	ASP
1	B	235	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	HIS
1	A	146	ASN
1	A	156	ASN
1	A	162	ASN
1	A	251	ASN
1	B	31	ASN
1	B	51	ASN
1	B	162	ASN
1	B	269	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](#)

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	BGC	A	329	1	11,11,12	3.65	7 (63%)	16,16,17	1.50	2 (12%)
2	BGC	B	329	1	11,11,12	3.68	7 (63%)	16,16,17	1.29	2 (12%)

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	BGC	A	329	1	-	-	0/1/1/1
2	BGC	B	329	1	-	-	0/1/1/1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	329	BGC	O2-C2	-6.33	1.27	1.43
2	B	329	BGC	O2-C2	-5.83	1.28	1.43
2	A	329	BGC	O3-C3	-5.73	1.28	1.43
2	B	329	BGC	O3-C3	-5.71	1.28	1.43
2	B	329	BGC	O4-C4	-5.21	1.30	1.43
2	A	329	BGC	O1-C1	-4.77	1.24	1.39
2	B	329	BGC	O1-C1	-4.72	1.24	1.39
2	A	329	BGC	O4-C4	-4.37	1.32	1.43
2	A	329	BGC	O5-C1	3.07	1.50	1.42
2	B	329	BGC	C4-C5	3.02	1.59	1.52
2	B	329	BGC	O5-C1	2.99	1.50	1.42
2	B	329	BGC	C4-C3	2.97	1.60	1.52
2	A	329	BGC	C4-C5	2.89	1.59	1.52
2	A	329	BGC	C4-C3	2.60	1.59	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	329	BGC	C4-C3-C2	-4.05	103.71	110.83

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	329	BGC	C4-C3-C2	-4.02	103.78	110.83
2	A	329	BGC	O3-C3-C2	-2.84	103.68	110.38
2	B	329	BGC	O3-C3-C2	-2.15	105.31	110.38

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	329	BGC	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	303/328 (92%)	-0.09	5 (1%) 69 71	11, 34, 53, 66	0
1	B	301/328 (91%)	0.61	18 (5%) 27 24	25, 51, 75, 78	0
All	All	604/656 (92%)	0.26	23 (3%) 44 44	11, 42, 71, 78	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	300	LEU	3.5
1	B	245	THR	3.5
1	A	175	TRP	3.5
1	B	296	PRO	3.3
1	B	251	ASN	3.2
1	B	319	LEU	3.1
1	B	311	THR	2.9
1	B	289	SER	2.8
1	A	319	LEU	2.7
1	B	250	LYS	2.7
1	B	318	ASP	2.6
1	A	66	GLY	2.5
1	B	290	HIS	2.5
1	A	5	LYS	2.4
1	B	295	HIS	2.3
1	B	253	THR	2.3
1	B	291	GLU	2.3
1	B	27	TYR	2.3
1	B	249	VAL	2.2
1	B	299	ALA	2.1
1	B	294	ILE	2.1
1	A	30	TYR	2.0
1	B	30	TYR	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	BGC	B	329	11/12	0.60	0.16	63,70,71,72	0
2	BGC	A	329	11/12	0.72	0.14	51,58,59,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.