



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 12, 2024 – 09:45 PM EDT

PDB ID : 3BRS  
Title : Crystal structure of sugar transporter from Clostridium phytofermentans  
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Deposited on : 2007-12-21  
Resolution : 2.00 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
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
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)	:	2.36.2

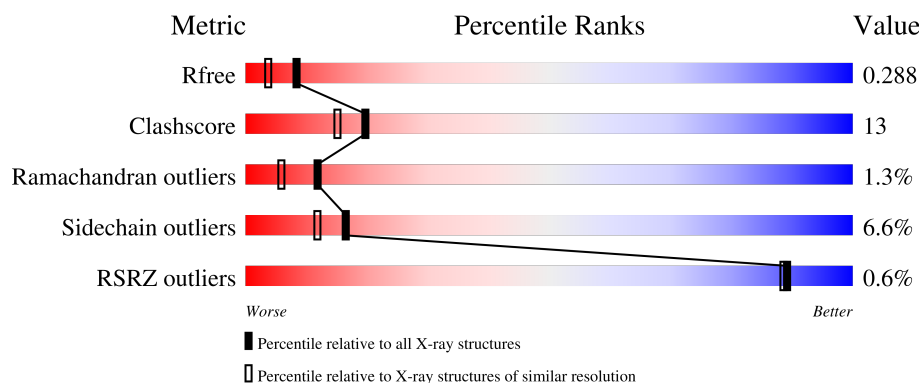
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*



The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	289	 70% 20% • • 6%
1	B	289	 66% 24% • 6%

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4477 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 Periplasmic binding protein/LacI transcriptional regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	271	Total	C	N	O	S	0	1	0
			2108	1344	334	417	13			
1	B	271	Total	C	N	O	S	0	0	0
			2104	1340	333	418	13			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q1FMG2
A	2	SER	-	expression tag	UNP Q1FMG2
A	3	LEU	-	expression tag	UNP Q1FMG2
A	282	GLU	-	expression tag	UNP Q1FMG2
A	283	GLY	-	expression tag	UNP Q1FMG2
A	284	HIS	-	expression tag	UNP Q1FMG2
A	285	HIS	-	expression tag	UNP Q1FMG2
A	286	HIS	-	expression tag	UNP Q1FMG2
A	287	HIS	-	expression tag	UNP Q1FMG2
A	288	HIS	-	expression tag	UNP Q1FMG2
A	289	HIS	-	expression tag	UNP Q1FMG2
B	1	MET	-	expression tag	UNP Q1FMG2
B	2	SER	-	expression tag	UNP Q1FMG2
B	3	LEU	-	expression tag	UNP Q1FMG2
B	282	GLU	-	expression tag	UNP Q1FMG2
B	283	GLY	-	expression tag	UNP Q1FMG2
B	284	HIS	-	expression tag	UNP Q1FMG2
B	285	HIS	-	expression tag	UNP Q1FMG2
B	286	HIS	-	expression tag	UNP Q1FMG2
B	287	HIS	-	expression tag	UNP Q1FMG2
B	288	HIS	-	expression tag	UNP Q1FMG2
B	289	HIS	-	expression tag	UNP Q1FMG2

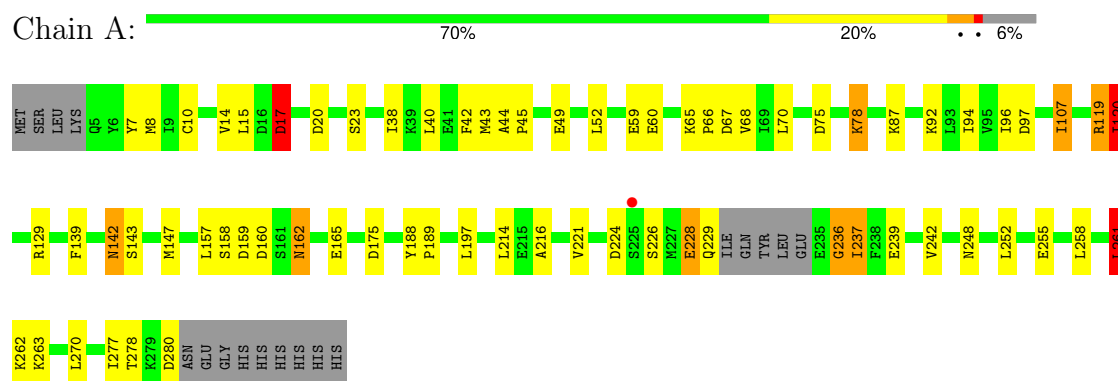
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	131	Total 131	O 131	0	0
2	B	134	Total 134	O 134	0	0

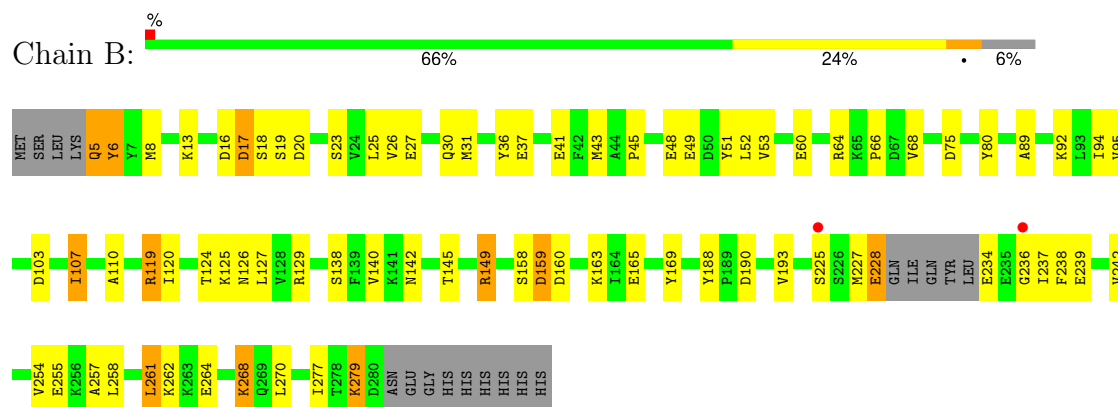
### 3 Residue-property plots

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: Periplasmic binding protein/LacI transcriptional regulator



- Molecule 1: Periplasmic binding protein/LacI transcriptional regulator



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	68.62Å 54.70Å 90.24Å 90.00° 111.78° 90.00°	Depositor
Resolution (Å)	19.68 – 2.00 27.35 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.68-2.00) 97.3 (27.35-2.00)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.69 (at 1.99Å)	Xtriage
Refinement program	REFMAC	Depositor
R, $R_{free}$	0.203 , 0.283 0.210 , 0.288	Depositor DCC
$R_{free}$ test set	2122 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	33.2	Xtriage
Anisotropy	0.174	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 41.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.379 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4477	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.72% 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

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	1.29	5/2136 (0.2%)	1.16	9/2874 (0.3%)
1	B	1.26	7/2129 (0.3%)	1.15	4/2864 (0.1%)
All	All	1.27	12/4265 (0.3%)	1.15	13/5738 (0.2%)

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	3
1	B	0	1
All	All	0	4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	60	GLU	CB-CG	6.81	1.65	1.52
1	B	60	GLU	CG-CD	6.56	1.61	1.51
1	A	7	TYR	CE2-CZ	6.31	1.46	1.38
1	B	89	ALA	CA-CB	6.00	1.65	1.52
1	A	60	GLU	CG-CD	5.90	1.60	1.51
1	B	80	TYR	CG-CD2	5.48	1.46	1.39
1	A	7	TYR	CG-CD1	5.47	1.46	1.39
1	B	110	ALA	CA-CB	5.33	1.63	1.52
1	A	139	PHE	CE2-CZ	5.31	1.47	1.37
1	A	59	GLU	CG-CD	5.27	1.59	1.51
1	B	95	VAL	CB-CG2	5.22	1.63	1.52
1	B	140	VAL	CB-CG1	5.12	1.63	1.52

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	43	MET	CG-SD-CE	7.18	111.69	100.20
1	B	149	ARG	NE-CZ-NH1	6.97	123.78	120.30
1	A	261	LEU	CB-CG-CD2	-6.66	99.69	111.00
1	A	261	LEU	CB-CG-CD1	6.63	122.27	111.00
1	B	261	LEU	CB-CG-CD1	6.02	121.23	111.00
1	B	75	ASP	CB-CG-OD2	5.87	123.58	118.30
1	A	14	VAL	CB-CA-C	-5.83	100.32	111.40
1	A	175	ASP	CB-CG-OD2	-5.80	113.08	118.30
1	B	149	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	261	LEU	CA-CB-CG	5.39	127.71	115.30
1	A	120	ILE	CB-CA-C	5.33	122.26	111.60
1	A	120	ILE	CG1-CB-CG2	5.22	122.89	111.40
1	A	175	ASP	CB-CG-OD1	5.00	122.80	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	17	ASP	Peptide
1	A	236	GLY	Peptide
1	A	237	ILE	Peptide
1	B	159	ASP	Peptide

## 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	2108	0	2159	52	0
1	B	2104	0	2148	57	0
2	A	131	0	0	8	0
2	B	134	0	0	6	0
All	All	4477	0	4307	108	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 13.

All (108) 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:B:8:MET:HG2	1:B:68:VAL:CG2	1.68	1.20
1:B:8:MET:HG2	1:B:68:VAL:HG22	1.19	1.14
1:B:119:ARG:HG2	1:B:119:ARG:HH11	1.23	1.02
1:A:87:LYS:HG3	2:A:376:HOH:O	1.60	1.01
1:B:8:MET:CG	1:B:68:VAL:CG2	2.41	0.99
1:A:94:ILE:HD12	1:A:107:ILE:HG23	1.49	0.94
1:A:8:MET:HG2	1:A:68[B]:VAL:HG12	1.54	0.87
1:A:119:ARG:HH11	1:A:119:ARG:HG2	1.42	0.84
1:A:255:GLU:O	1:A:258:LEU:HB2	1.79	0.81
1:B:107:ILE:HD11	1:B:270:LEU:HG	1.62	0.80
1:B:239:GLU:OE1	2:B:539:HOH:O	2.02	0.78
1:B:8:MET:SD	1:B:68:VAL:HG21	2.23	0.77
1:A:236:GLY:HA3	2:A:419:HOH:O	1.85	0.77
1:A:17:ASP:HA	1:A:23:SER:OG	1.85	0.77
1:A:107:ILE:HD11	1:A:270:LEU:HD12	1.68	0.76
1:B:165:GLU:HG2	1:B:188:TYR:CG	2.23	0.73
1:B:8:MET:HG2	1:B:68:VAL:HG21	1.67	0.73
1:A:38:ILE:O	2:A:303:HOH:O	2.07	0.72
1:B:255:GLU:O	1:B:258:LEU:HB2	1.90	0.72
1:A:120:ILE:HG12	1:A:242:VAL:HG23	1.71	0.72
1:B:8:MET:CG	1:B:68:VAL:HG21	2.18	0.72
1:B:279:LYS:O	1:B:279:LYS:HG3	1.91	0.70
1:B:119:ARG:HG2	1:B:119:ARG:NH1	1.98	0.70
1:A:8:MET:SD	1:A:68[B]:VAL:HG11	2.32	0.69
1:B:66:PRO:O	2:B:538:HOH:O	2.09	0.69
1:A:75:ASP:OD1	1:A:78:LYS:HG3	1.95	0.67
1:A:165:GLU:HG2	1:A:188:TYR:CG	2.30	0.66
1:B:17:ASP:HA	1:B:23:SER:OG	1.95	0.66
1:B:20:ASP:CB	1:B:225:SER:HB2	2.26	0.65
1:B:20:ASP:HB3	1:B:225:SER:HB2	1.77	0.65
1:B:145:THR:O	1:B:149:ARG:HG3	1.97	0.64
1:B:119:ARG:HH11	1:B:119:ARG:CG	2.04	0.64
1:A:8:MET:HG2	1:A:68[B]:VAL:CG1	2.27	0.64
1:B:190:ASP:HB2	2:B:437:HOH:O	1.98	0.63
1:A:162:ASN:HD22	1:A:162:ASN:H	1.45	0.63
1:A:8:MET:CG	1:A:68[B]:VAL:HG12	2.28	0.61
1:A:262:LYS:O	1:A:263:LYS:HB2	1.99	0.61
1:A:15:LEU:HD12	1:A:44:ALA:HB3	1.82	0.60
1:A:162:ASN:HD22	1:A:162:ASN:N	2.00	0.60
1:A:8:MET:CG	1:A:68[B]:VAL:CG1	2.80	0.59
1:A:94:ILE:HD12	1:A:107:ILE:CG2	2.29	0.58
1:A:216:ALA:HB1	2:A:309:HOH:O	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:20:ASP:HB2	1:B:225:SER:CB	2.34	0.57
1:A:45:PRO:O	2:A:333:HOH:O	2.17	0.57
1:B:107:ILE:CD1	1:B:270:LEU:HG	2.33	0.57
1:B:234:GLU:N	1:B:238:PHE:HE1	2.03	0.56
1:A:49:GLU:OE2	2:A:339:HOH:O	2.18	0.56
1:A:75:ASP:CG	1:A:78:LYS:HG3	2.26	0.55
1:A:120:ILE:HD12	1:A:221:VAL:HB	1.86	0.55
1:A:17:ASP:HA	1:A:23:SER:HG	1.72	0.55
1:A:107:ILE:HD11	1:A:270:LEU:CD1	2.35	0.55
1:A:68[B]:VAL:HG23	1:A:92:LYS:HB2	1.90	0.54
1:A:248:ASN:O	1:A:252:LEU:HG	2.07	0.54
1:B:94:ILE:HD12	1:B:107:ILE:HG23	1.90	0.54
1:B:124:THR:HG23	1:B:193:VAL:HG11	1.91	0.53
1:B:25:LEU:C	1:B:25:LEU:HD23	2.29	0.53
1:B:23:SER:O	1:B:27:GLU:HG3	2.08	0.53
1:A:224:ASP:OD2	1:A:229:GLN:HB2	2.09	0.52
1:A:119:ARG:HG2	1:A:119:ARG:NH1	2.17	0.52
1:A:119:ARG:HH11	1:A:119:ARG:CG	2.19	0.52
1:B:94:ILE:CD1	1:B:107:ILE:HG23	2.40	0.52
1:B:254:VAL:O	1:B:257:ALA:HB3	2.10	0.52
1:B:45:PRO:HB3	1:B:53:VAL:HG12	1.91	0.52
1:B:68:VAL:HG12	1:B:92:LYS:HB2	1.91	0.51
1:A:65:LYS:N	1:A:66:PRO:CD	2.74	0.50
1:B:51:TYR:OH	2:B:503:HOH:O	2.19	0.50
1:A:20:ASP:OD2	1:A:228:GLU:HG2	2.11	0.49
1:A:92:LYS:HG3	1:A:261:LEU:HD13	1.93	0.49
1:B:6:TYR:N	2:B:454:HOH:O	2.22	0.49
1:B:190:ASP:CB	2:B:437:HOH:O	2.59	0.48
1:B:268:LYS:HE3	1:B:268:LYS:HB2	1.61	0.48
1:A:8:MET:SD	1:A:68[B]:VAL:CG1	3.02	0.47
1:B:227:MET:O	1:B:228:GLU:HB3	2.14	0.47
1:B:13:LYS:HB3	1:B:48:GLU:HG2	1.96	0.47
1:A:143:SER:O	1:A:147:MET:HG3	2.14	0.47
1:B:160:ASP:O	1:B:163:LYS:HB2	2.16	0.46
1:B:165:GLU:HG2	1:B:188:TYR:CD1	2.50	0.46
1:A:70:LEU:N	1:A:70:LEU:HD12	2.30	0.46
1:A:224:ASP:OD2	1:A:229:GLN:CB	2.64	0.46
1:B:19:SER:O	1:B:23:SER:HB2	2.16	0.46
1:B:20:ASP:HB2	1:B:225:SER:HB2	1.95	0.46
1:B:36:TYR:O	1:B:37:GLU:HB2	2.16	0.46
1:A:158:SER:HB3	1:A:159:ASP:H	1.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:CYS:HB3	1:A:42:PHE:CD1	2.51	0.45
1:B:126:ASN:O	1:B:129:ARG:HB2	2.16	0.45
1:B:138:SER:HB3	1:B:169:TYR:CD1	2.52	0.45
1:B:277:ILE:O	1:B:277:ILE:HG13	2.16	0.44
1:B:262:LYS:O	1:B:264:GLU:HG3	2.18	0.44
1:B:5:GLN:O	1:B:6:TYR:HB2	2.18	0.43
1:A:189:PRO:HB2	2:A:336:HOH:O	2.17	0.43
1:A:52:LEU:HD11	1:B:49:GLU:HG2	2.01	0.42
1:A:67:ASP:HB3	1:A:261:LEU:HD11	2.00	0.42
1:B:52:LEU:HD23	1:B:52:LEU:HA	1.92	0.42
1:B:92:LYS:HA	1:B:92:LYS:HD3	1.87	0.42
1:B:129:ARG:CZ	1:B:129:ARG:CB	2.98	0.42
1:A:197:LEU:HD23	1:A:197:LEU:HA	1.85	0.42
1:A:120:ILE:CD1	1:A:221:VAL:HB	2.50	0.42
1:B:41:GLU:OE1	1:B:64:ARG:NH1	2.51	0.42
1:B:8:MET:CB	1:B:68:VAL:CG2	2.97	0.41
1:B:125:LYS:HG3	1:B:160:ASP:OD2	2.21	0.41
1:B:26:VAL:O	1:B:30:GLN:HG3	2.19	0.41
1:B:120:ILE:HD13	1:B:242:VAL:HG23	2.02	0.41
1:A:157:LEU:O	1:A:158:SER:HB2	2.21	0.41
1:A:142:ASN:HB2	2:A:319:HOH:O	2.20	0.41
1:A:96:ILE:O	1:A:97:ASP:HB3	2.21	0.40
1:A:214:LEU:HD23	1:A:214:LEU:HA	1.81	0.40
1:B:16:ASP:OD2	1:B:16:ASP:C	2.59	0.40
1:A:162:ASN:H	1:A:162:ASN:ND2	2.17	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	268/289 (93%)	252 (94%)	13 (5%)	3 (1%)	<b>14</b> <b>8</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	267/289 (92%)	244 (91%)	19 (7%)	4 (2%)	10	4
All	All	535/578 (93%)	496 (93%)	32 (6%)	7 (1%)	12	6

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	237	ILE
1	B	236	GLY
1	A	160	ASP
1	A	228	GLU
1	B	6	TYR
1	B	17	ASP
1	A	237	ILE

### 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	230/246 (94%)	215 (94%)	15 (6%)	17	12
1	B	229/246 (93%)	214 (93%)	15 (7%)	16	12
All	All	459/492 (93%)	429 (94%)	30 (6%)	16	12

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ASP
1	A	40	LEU
1	A	78	LYS
1	A	107	ILE
1	A	119	ARG
1	A	120	ILE
1	A	129	ARG
1	A	142	ASN
1	A	162	ASN

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Mol	Chain	Res	Type
1	A	226	SER
1	A	239	GLU
1	A	261	LEU
1	A	277	ILE
1	A	278	THR
1	A	280	ASP
1	B	5	GLN
1	B	18	SER
1	B	31	MET
1	B	43	MET
1	B	103	ASP
1	B	107	ILE
1	B	119	ARG
1	B	127	LEU
1	B	142	ASN
1	B	158	SER
1	B	159	ASP
1	B	228	GLU
1	B	261	LEU
1	B	268	LYS
1	B	279	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	162	ASN
1	A	248	ASN
1	B	5	GLN
1	B	126	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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, 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	271/289 (93%)	-0.12	1 (0%) 92 92	21, 34, 56, 70	0
1	B	271/289 (93%)	-0.31	2 (0%) 87 87	22, 34, 55, 78	0
All	All	542/578 (93%)	-0.21	3 (0%) 89 88	21, 34, 56, 78	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	225	SER	3.9
1	B	236	GLY	3.1
1	A	225	SER	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 monosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

### 6.5 Other polymers [i](#)

There are no such residues in this entry.