



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:58 PM GMT

PDB ID : 3VNI  
Title : Crystal structures of D-Psicose 3-epimerase from *Clostridium cellulolyticum* H10 and its complex with ketohexose sugars  
Authors : Chan, H.C.; Zhu, Y.; Hu, Y.; Ko, T.P.; Huang, C.H.; Ren, F.; Chen, C.C.; Guo, R.T.; Sun, Y.  
Deposited on : 2012-01-16  
Resolution : 1.98 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

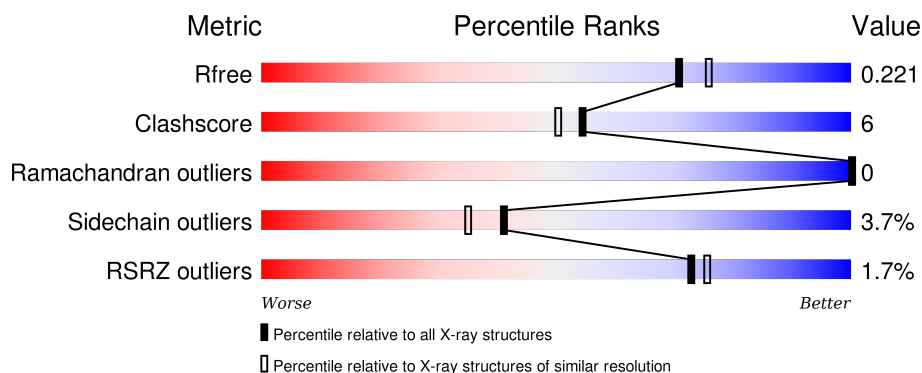
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.98 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))
$R_{free}$	91344	8664 (2.00-1.96)
Clashscore	102246	9905 (2.00-1.96)
Ramachandran outliers	100387	9792 (2.00-1.96)
Sidechain outliers	100360	9791 (2.00-1.96)
RSRZ outliers	91569	8679 (2.00-1.96)

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. 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	294	<div> <div>2%</div> <div>82% 15% ..</div> </div>
1	B	294	<div> <div>2%</div> <div>83% 12% ..</div> </div>
1	C	294	<div> <div>%</div> <div>86% 11% ..</div> </div>
1	D	294	<div> <div>2%</div> <div>83% 14% ..</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10344 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 Xylose isomerase domain protein TIM barrel.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	289	Total	C	N	O	S	0	0	0
			2293	1459	388	435	11			
1	B	289	Total	C	N	O	S	0	0	0
			2292	1459	388	435	10			
1	C	288	Total	C	N	O	S	0	0	0
			2287	1456	387	434	10			
1	D	288	Total	C	N	O	S	0	0	0
			2287	1456	387	434	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	EXPRESSION TAG	UNP B8I944
B	0	ALA	-	EXPRESSION TAG	UNP B8I944
C	0	ALA	-	EXPRESSION TAG	UNP B8I944
D	0	ALA	-	EXPRESSION TAG	UNP B8I944

- Molecule 2 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mn	0	0
			1	1		
2	A	1	Total	Mn	0	0
			1	1		
2	D	1	Total	Mn	0	0
			1	1		
2	C	1	Total	Mn	0	0
			1	1		

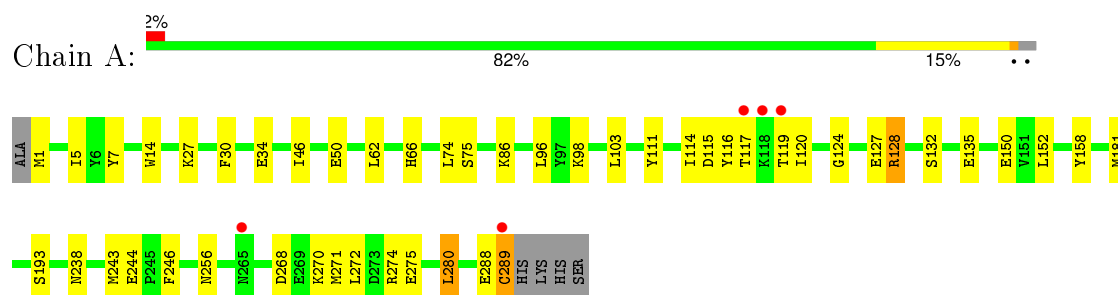
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	339	Total 339	O 339	0	0
3	B	282	Total 282	O 282	0	0
3	C	295	Total 295	O 295	0	0
3	D	265	Total 265	O 265	0	0

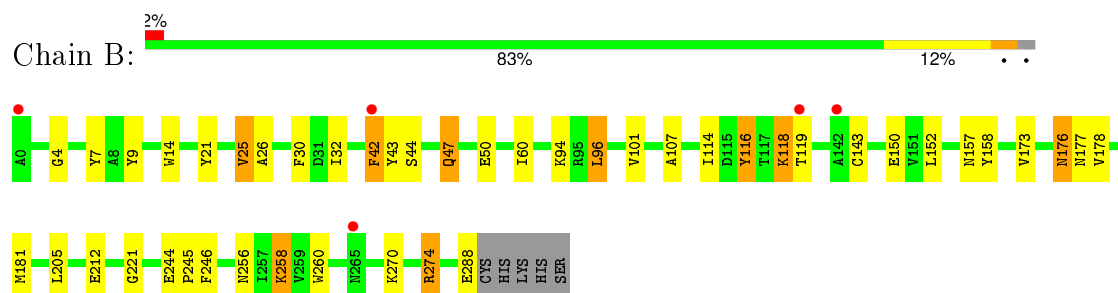
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

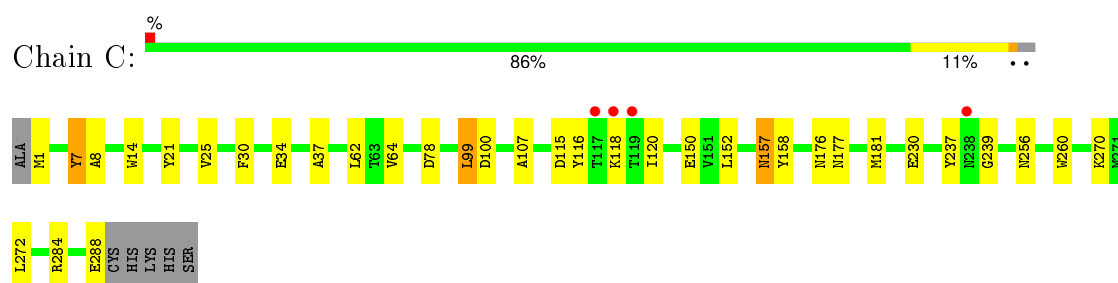
- Molecule 1: Xylose isomerase domain protein TIM barrel



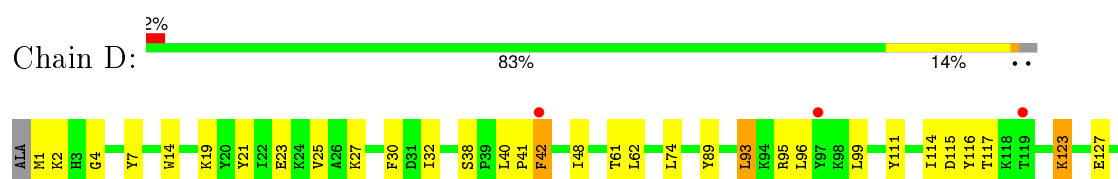
- Molecule 1: Xylose isomerase domain protein TIM barrel

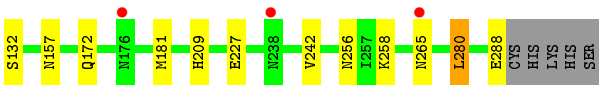


- Molecule 1: Xylose isomerase domain protein TIM barrel



- Molecule 1: Xylose isomerase domain protein TIM barrel





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	79.76 Å 115.44 Å 91.63 Å 90.00° 105.45° 90.00°	Depositor
Resolution (Å)	25.00 – 1.98 24.74 – 1.98	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-1.98) 93.5 (24.74-1.98)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.00 (at 1.98 Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.175 , 0.220 0.176 , 0.221	Depositor DCC
$R_{free}$ test set	5270 reflections (5.05%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.6	Xtriage
Anisotropy	0.175	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 56.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 104493 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10344	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MN

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	0.88	1/2346 (0.0%)	0.84	2/3177 (0.1%)
1	B	0.76	0/2345	0.78	1/3176 (0.0%)
1	C	0.75	1/2340 (0.0%)	0.79	1/3169 (0.0%)
1	D	0.73	0/2340	0.79	0/3169
All	All	0.78	2/9371 (0.0%)	0.80	4/12691 (0.0%)

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	1
1	B	0	1
1	C	0	2
1	D	0	1
All	All	0	5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	34	GLU	CD-OE1	6.80	1.33	1.25
1	C	34	GLU	CD-OE1	6.12	1.32	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	268	ASP	CB-CG-OD1	6.16	123.84	118.30
1	B	176	ASN	N-CA-C	5.37	125.50	111.00
1	A	128	ARG	NE-CZ-NH1	-5.34	117.63	120.30

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	176	ASN	N-CA-C	5.02	124.55	111.00

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	7	TYR	Sidechain
1	B	7	TYR	Sidechain
1	C	21	TYR	Sidechain
1	C	7	TYR	Sidechain
1	D	7	TYR	Sidechain

## 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	2293	0	2228	30	0
1	B	2292	0	2228	40	0
1	C	2287	0	2223	24	0
1	D	2287	0	2223	25	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	339	0	0	6	1
3	B	282	0	0	1	0
3	C	295	0	0	0	0
3	D	265	0	0	3	1
All	All	10344	0	8902	116	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 6.

All (116) 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:C:118:LYS:HE2	1:C:118:LYS:HA	1.57	0.86
1:A:75:SER:O	1:A:128:ARG:NH1	2.13	0.81
1:D:123:LYS:HE3	1:D:123:LYS:HA	1.62	0.81
1:D:14:TRP:HE1	1:D:256:ASN:HD22	1.29	0.81
1:D:23:GLU:O	1:D:27:LYS:HG2	1.81	0.80
1:A:98:LYS:HD3	3:A:7402:HOH:O	1.84	0.77
1:D:32:ILE:HD13	1:D:61:THR:HB	1.66	0.77
1:C:157:ASN:HD22	1:C:158:TYR:H	1.33	0.77
1:A:14:TRP:HE1	1:A:256:ASN:HD22	1.35	0.74
1:D:4:GLY:HA3	1:D:32:ILE:HB	1.71	0.72
1:C:25:VAL:HG13	1:C:30:PHE:HB2	1.71	0.72
1:B:274:ARG:CG	1:B:274:ARG:HH11	2.03	0.71
1:B:14:TRP:HE1	1:B:256:ASN:HD22	1.39	0.69
1:B:270:LYS:NZ	1:B:274:ARG:HE	1.92	0.67
1:A:271:MET:HE2	1:A:275:GLU:HG2	1.76	0.67
1:B:274:ARG:CB	1:B:274:ARG:HH11	2.08	0.67
1:A:1:MET:HE2	1:A:288:GLU:HG2	1.78	0.66
1:D:123:LYS:O	1:D:127:GLU:HG2	1.94	0.66
1:C:14:TRP:HE1	1:C:256:ASN:HD22	1.44	0.66
1:A:14:TRP:HE1	1:A:256:ASN:ND2	1.95	0.65
1:B:274:ARG:HG2	1:B:274:ARG:NH1	2.11	0.64
1:C:157:ASN:ND2	1:C:158:TYR:H	1.96	0.64
1:A:115:ASP:OD2	1:A:117:THR:HB	1.98	0.64
1:A:289:CYS:HB3	3:A:7321:HOH:O	1.98	0.63
1:D:14:TRP:HE1	1:D:256:ASN:ND2	1.94	0.63
1:B:14:TRP:HE1	1:B:256:ASN:ND2	1.97	0.62
1:A:66:HIS:HD2	3:A:7421:HOH:O	1.81	0.61
1:C:284:ARG:O	1:C:288:GLU:HG3	2.01	0.60
1:C:14:TRP:HE1	1:C:256:ASN:ND2	1.98	0.60
1:B:274:ARG:HG2	1:B:274:ARG:HH11	1.66	0.59
1:B:270:LYS:HZ3	1:B:274:ARG:HE	1.50	0.59
1:C:157:ASN:HD22	1:C:158:TYR:N	2.02	0.57
1:C:150:GLU:HB2	1:C:181:MET:HE2	1.85	0.57
1:A:271:MET:HE2	1:A:275:GLU:CG	2.35	0.57
1:C:150:GLU:HB2	1:C:181:MET:CE	2.35	0.57
1:D:115:ASP:OD2	1:D:117:THR:HB	2.05	0.56
1:B:25:VAL:HG13	1:B:30:PHE:HB2	1.86	0.56
1:A:150:GLU:HB2	1:A:181:MET:CE	2.36	0.55
1:D:1:MET:HG3	1:D:288:GLU:OE2	2.05	0.55
1:A:1:MET:N	3:A:7183:HOH:O	2.40	0.55
1:A:46:ILE:O	1:A:50:GLU:HG3	2.06	0.55
1:D:181:MET:CE	1:D:209:HIS:CE1	2.89	0.55

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:244:GLU:HG2	1:A:246:PHE:CE2	2.43	0.54
1:B:107:ALA:HB2	1:B:152:LEU:HD11	1.89	0.53
3:A:7431:HOH:O	1:D:258:LYS:HE2	2.07	0.53
1:D:42:PHE:CD1	1:D:42:PHE:N	2.72	0.53
1:B:47:GLN:HA	1:B:50:GLU:HG2	1.91	0.53
1:D:48:ILE:HD11	1:D:95:ARG:HH11	1.74	0.52
1:C:115:ASP:OD2	1:C:118:LYS:HG2	2.10	0.52
1:D:227:GLU:OE1	3:D:644:HOH:O	2.19	0.51
1:D:181:MET:HE3	1:D:209:HIS:CE1	2.45	0.51
1:D:172:GLN:HG3	3:D:549:HOH:O	2.12	0.50
1:B:9:TYR:CD1	1:B:245:PRO:HG2	2.48	0.48
1:B:94:LYS:HD2	1:B:143:CYS:SG	2.53	0.48
1:D:209:HIS:HA	1:D:242:VAL:O	2.14	0.48
1:B:150:GLU:HB2	1:B:181:MET:HE1	1.96	0.47
1:A:5:ILE:HG13	1:A:243:MET:HG3	1.96	0.47
1:C:37:ALA:HB2	1:C:64:VAL:CG1	2.44	0.47
1:C:107:ALA:HB2	1:C:152:LEU:HD11	1.97	0.47
1:B:44:SER:H	1:B:47:GLN:CG	2.27	0.47
1:A:150:GLU:HB2	1:A:181:MET:HE2	1.97	0.47
1:D:38:SER:O	1:D:41:PRO:HD2	2.15	0.47
1:C:237:TYR:CZ	1:C:239:GLY:HA3	2.50	0.47
1:D:89:TYR:O	1:D:93:LEU:HB2	2.15	0.47
1:D:74:LEU:HD22	1:D:132:SER:HB3	1.96	0.46
1:B:177:ASN:HD22	1:B:177:ASN:N	2.14	0.46
1:D:40:LEU:HB2	1:D:41:PRO:HD3	1.97	0.46
1:C:157:ASN:ND2	1:C:158:TYR:N	2.62	0.46
1:B:21:TYR:O	1:B:25:VAL:HB	2.16	0.46
1:B:260:TRP:CD1	1:C:158:TYR:HA	2.51	0.45
1:A:124:GLY:O	1:A:127:GLU:HG2	2.16	0.45
1:B:270:LYS:NZ	1:B:274:ARG:NE	2.64	0.45
1:B:288:GLU:O	3:B:479:HOH:O	2.21	0.45
1:B:42:PHE:CD1	1:B:42:PHE:N	2.84	0.45
1:A:271:MET:CE	1:A:275:GLU:HG2	2.45	0.45
1:B:150:GLU:HB2	1:B:181:MET:CE	2.46	0.45
1:A:271:MET:CE	1:A:274:ARG:NH1	2.80	0.45
1:B:116:TYR:CE1	1:C:260:TRP:CZ2	3.05	0.45
1:C:118:LYS:HE2	1:C:118:LYS:CA	2.34	0.45
1:B:96:LEU:HG	1:B:101:VAL:HG22	1.98	0.45
1:C:120:ILE:HD12	1:C:158:TYR:CE2	2.53	0.44
1:B:157:ASN:ND2	1:B:158:TYR:H	2.15	0.44
1:B:4:GLY:HA3	1:B:32:ILE:HB	1.99	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:GLU:OE1	1:A:152:LEU:HD21	2.18	0.44
1:A:150:GLU:HB2	1:A:181:MET:HE3	1.99	0.44
1:A:30:PHE:CE1	1:A:280:LEU:HG	2.53	0.44
1:B:274:ARG:HB2	1:B:274:ARG:HH11	1.83	0.44
1:D:21:TYR:O	1:D:25:VAL:HG22	2.18	0.44
1:A:238:ASN:C	3:A:7420:HOH:O	2.55	0.43
1:B:43:TYR:HA	1:B:47:GLN:OE1	2.18	0.43
1:A:86:LYS:NZ	1:A:135:GLU:OE2	2.38	0.43
1:B:212:GLU:CD	1:B:221:GLY:HA3	2.38	0.43
1:A:74:LEU:HD22	1:A:132:SER:HB3	2.00	0.43
1:B:44:SER:H	1:B:47:GLN:CD	2.22	0.43
1:C:177:ASN:N	1:C:177:ASN:HD22	2.17	0.43
1:B:244:GLU:HG2	1:B:246:PHE:CE2	2.54	0.43
1:B:176:ASN:HB3	1:B:177:ASN:HD22	1.83	0.42
1:B:26:ALA:HA	1:B:60:ILE:HD11	2.01	0.42
1:D:111:TYR:CE2	1:D:114:ILE:HA	2.54	0.42
1:B:118:LYS:HZ2	1:B:119:THR:H	1.65	0.42
1:B:270:LYS:HZ2	1:B:274:ARG:NE	2.18	0.42
1:B:114:ILE:HG13	1:B:114:ILE:O	2.19	0.42
1:B:173:VAL:HG11	1:B:178:VAL:HG21	2.02	0.42
1:A:271:MET:HE1	1:A:274:ARG:NH1	2.35	0.42
1:B:96:LEU:HG	1:B:101:VAL:CG2	2.50	0.41
1:C:99:LEU:O	1:C:100:ASP:HB3	2.20	0.41
1:D:30:PHE:CE1	1:D:280:LEU:HG	2.55	0.41
1:B:258:LYS:HG3	1:B:260:TRP:CZ2	2.56	0.41
1:C:7:TYR:CG	1:C:8:ALA:N	2.89	0.41
1:D:157:ASN:HB3	3:D:639:HOH:O	2.21	0.41
1:A:111:TYR:CE1	1:A:114:ILE:HG12	2.56	0.41
1:A:120:ILE:HD12	1:A:158:TYR:CE2	2.55	0.41
1:A:193:SER:HB2	1:C:230:GLU:OE2	2.20	0.41
1:C:78:ASP:C	1:C:78:ASP:OD1	2.60	0.41
1:B:42:PHE:HD1	1:B:42:PHE:H	1.67	0.40
1:A:103:LEU:C	1:A:103:LEU:HD23	2.42	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)
3:A:7236:HOH:O	3:D:645:HOH:O[2_545]	2.19	0.01

## 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	287/294 (98%)	281 (98%)	6 (2%)	0	100	100
1	B	287/294 (98%)	278 (97%)	9 (3%)	0	100	100
1	C	286/294 (97%)	280 (98%)	6 (2%)	0	100	100
1	D	286/294 (97%)	279 (98%)	7 (2%)	0	100	100
All	All	1146/1176 (97%)	1118 (98%)	28 (2%)	0	100	100

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	241/245 (98%)	232 (96%)	9 (4%)	41	35
1	B	240/245 (98%)	231 (96%)	9 (4%)	40	33
1	C	240/245 (98%)	233 (97%)	7 (3%)	50	46
1	D	240/245 (98%)	229 (95%)	11 (5%)	33	25
All	All	961/980 (98%)	925 (96%)	36 (4%)	41	35

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LYS
1	A	62	LEU

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	96	LEU
1	A	116	TYR
1	A	119	THR
1	A	270	LYS
1	A	272	LEU
1	A	280	LEU
1	A	289	CYS
1	B	25	VAL
1	B	42	PHE
1	B	47	GLN
1	B	96	LEU
1	B	116	TYR
1	B	118	LYS
1	B	205	LEU
1	B	258	LYS
1	B	274	ARG
1	C	1	MET
1	C	62	LEU
1	C	99	LEU
1	C	116	TYR
1	C	157	ASN
1	C	270	LYS
1	C	272	LEU
1	D	2	LYS
1	D	19	LYS
1	D	42	PHE
1	D	62	LEU
1	D	93	LEU
1	D	96	LEU
1	D	99	LEU
1	D	116	TYR
1	D	123	LYS
1	D	265	ASN
1	D	280	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	66	HIS
1	A	256	ASN
1	A	277	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	12	GLN
1	B	176	ASN
1	B	177	ASN
1	B	256	ASN
1	C	49	ASN
1	C	66	HIS
1	C	84	ASN
1	C	157	ASN
1	C	177	ASN
1	C	256	ASN
1	D	12	GLN
1	D	177	ASN
1	D	256	ASN
1	D	265	ASN
1	D	277	GLN

### 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 ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

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

### 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, 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	289/294 (98%)	-0.37	5 (1%) 73 75	16, 23, 38, 58	0
1	B	289/294 (98%)	-0.17	5 (1%) 73 75	17, 27, 44, 58	0
1	C	288/294 (97%)	-0.21	4 (1%) 78 80	17, 28, 42, 62	0
1	D	288/294 (97%)	-0.08	6 (2%) 67 69	17, 30, 47, 61	0
All	All	1154/1176 (98%)	-0.21	20 (1%) 73 75	16, 27, 44, 62	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	42	PHE	7.5
1	B	0	ALA	4.9
1	C	119	THR	4.1
1	D	119	THR	3.8
1	A	289	CYS	3.4
1	B	42	PHE	3.3
1	D	265	ASN	3.3
1	C	238	ASN	2.9
1	A	119	THR	2.9
1	D	238	ASN	2.9
1	A	117	THR	2.8
1	B	265	ASN	2.7
1	C	117	THR	2.5
1	B	119	THR	2.4
1	B	142	ALA	2.4
1	C	118	LYS	2.2
1	A	265	ASN	2.1
1	A	118	LYS	2.1
1	D	97	TYR	2.1
1	D	176	ASN	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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	MN	A	7001	1/1	0.98	0.05	-1.55	41,41,41,41	0
2	MN	B	301	1/1	0.99	0.03	-2.05	37,37,37,37	0
2	MN	D	301	1/1	0.99	0.03	-2.84	39,39,39,39	0
2	MN	C	301	1/1	0.96	0.04	-3.44	44,44,44,44	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.