



Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 03:43 pm BST

PDB ID : 3WE7
Title : Crystal Structure of Diacetylchitobiose Deacetylase from *Pyrococcus horikoshii*
Authors : Mine, S.; Nakamura, T.; Fukuda, Y.; Inoue, T.; Uegaki, K.; Sato, T.
Deposited on : 2013-07-01
Resolution : 1.55 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 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

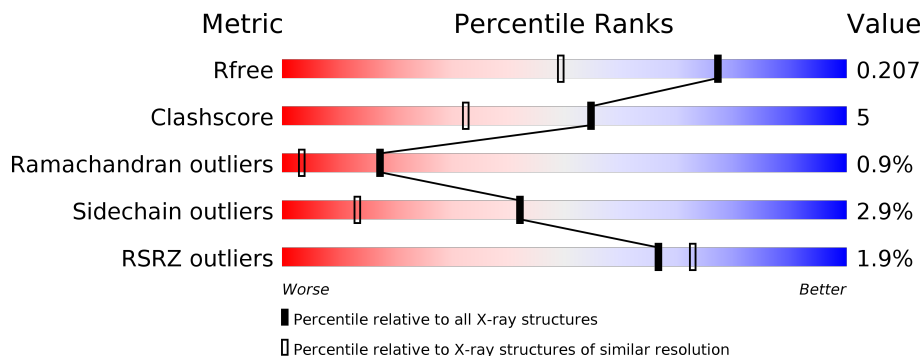
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION




The reported resolution of this entry is 1.55 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	1483 (1.56-1.56)
Clashscore	141614	1529 (1.56-1.56)
Ramachandran outliers	138981	1498 (1.56-1.56)
Sidechain outliers	138945	1495 (1.56-1.56)
RSRZ outliers	127900	1465 (1.56-1.56)

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 ≥ 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	272	 3% 83% 11% . .
1	B	272	 % 84% 11% . .
1	C	272	 % 83% 13% . .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	A	302	-	X	X	-
3	GOL	B	302	-	X	-	-
3	GOL	C	303	-	-	X	-
6	HEZ	B	306	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7295 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.

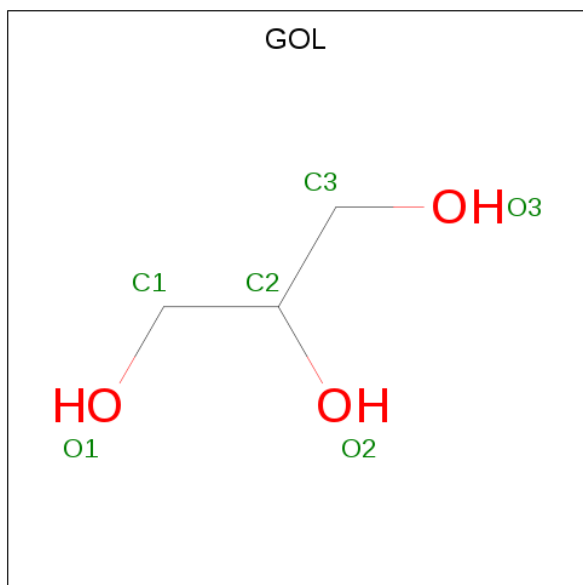
- Molecule 1 is a protein called Putative uncharacterized protein PH0499.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	267	2235	1437	367	420	11	0	6	0
1	B	267	2219	1429	363	416	11	0	4	0
1	C	267	2204	1421	361	411	11	0	2	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

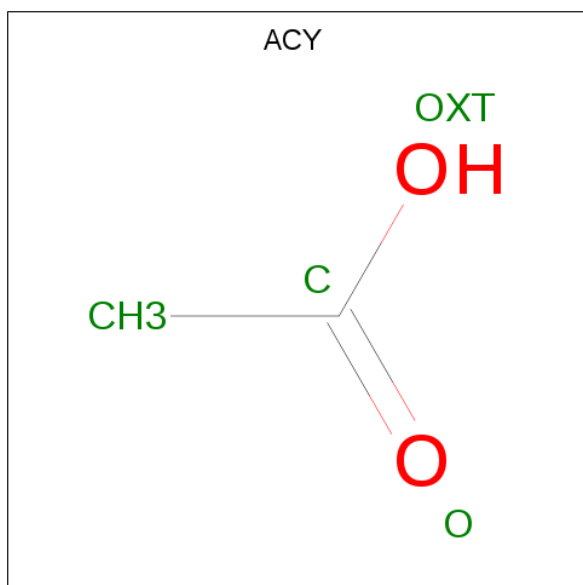
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		
2	A	1	Total	Zn	0	0
			1	1		
2	C	1	Total	Zn	0	0
			1	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	1
			18	9	9		
3	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is ACETIC ACID (three-letter code: ACY) (formula: C₂H₄O₂).

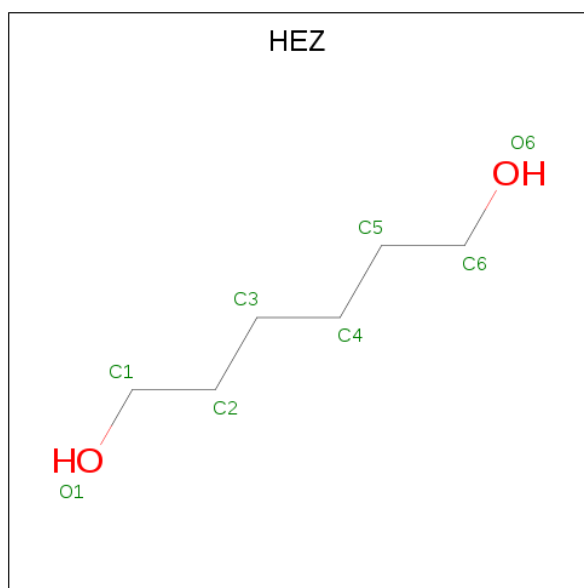


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 4 2 2	0	0
4	B	1	Total C O 4 2 2	0	0
4	C	1	Total C O 4 2 2	0	0

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total Na 1 1	0	0
5	C	1	Total Na 1 1	0	0

- Molecule 6 is HEXANE-1,6-DIOL (three-letter code: HEZ) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C O 8 6 2	0	0
6	B	1	Total C O 8 6 2	0	0
6	C	1	Total C O 8 6 2	0	0
6	C	1	Total C O 8 6 2	0	0

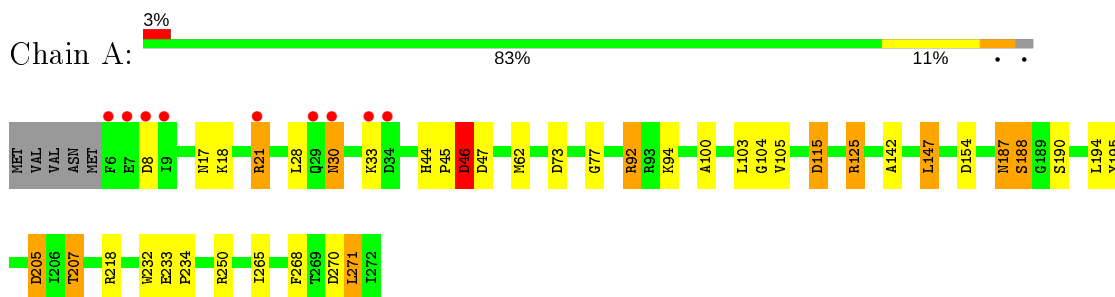
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	205	Total 207	O 207	0	2
7	B	175	Total 178	O 178	0	3
7	C	167	Total 167	O 167	0	0

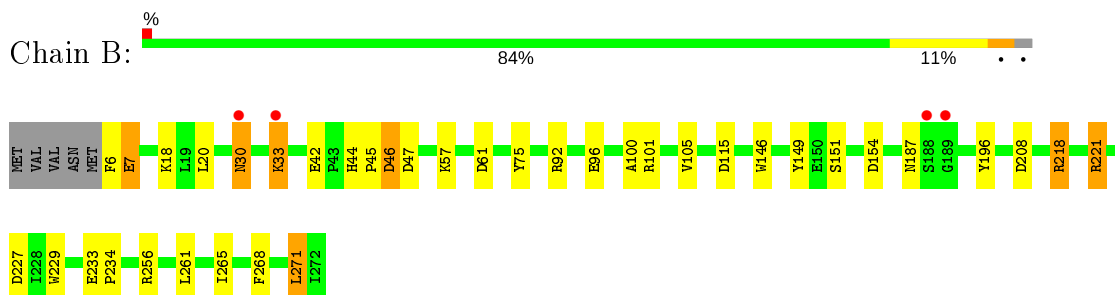
3 Residue-property plots [i](#)

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

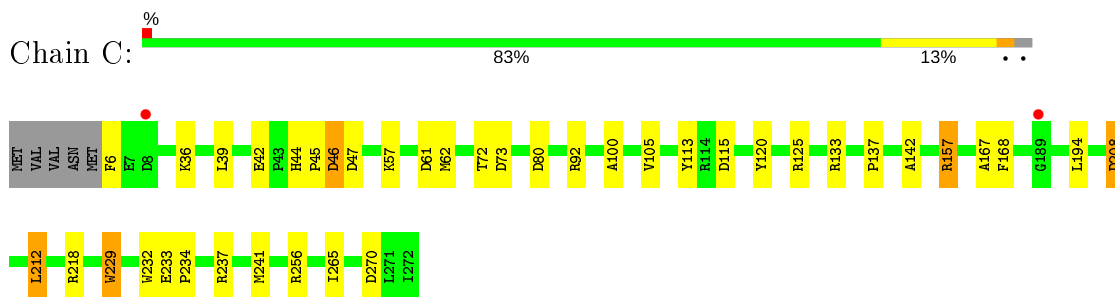
- Molecule 1: Putative uncharacterized protein PH0499



- Molecule 1: Putative uncharacterized protein PH0499



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4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	77.37Å 77.37Å 230.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.62 – 1.55 29.62 – 1.55	Depositor EDS
% Data completeness (in resolution range)	98.4 (29.62-1.55) 98.4 (29.62-1.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 1.54Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.173 , 0.207 0.172 , 0.207	Depositor DCC
R_{free} test set	5792 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	17.5	Xtrriage
Anisotropy	0.130	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 44.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7295	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, ACY, HEZ, 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	1.19	3/2294 (0.1%)	1.22	19/3105 (0.6%)
1	B	1.24	4/2278 (0.2%)	1.24	16/3084 (0.5%)
1	C	1.19	3/2263 (0.1%)	1.24	14/3063 (0.5%)
All	All	1.21	10/6835 (0.1%)	1.23	49/9252 (0.5%)

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	2

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	104	GLY	N-CA	7.86	1.57	1.46
1	B	208	ASP	CB-CG	6.06	1.64	1.51
1	B	146	TRP	NE1-CE2	-5.91	1.29	1.37
1	A	92	ARG	CZ-NH1	5.81	1.40	1.33
1	C	232	TRP	CD2-CE2	5.42	1.47	1.41
1	C	229	TRP	CD2-CE2	5.42	1.47	1.41
1	C	120	TYR	CG-CD2	5.39	1.46	1.39
1	A	232	TRP	CD2-CE2	5.38	1.47	1.41
1	B	149	TYR	CZ-OH	5.11	1.46	1.37
1	B	229	TRP	CD2-CE2	5.05	1.47	1.41

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	61	ASP	CB-CG-OD2	-12.74	106.83	118.30
1	A	103	LEU	C-N-CA	-11.96	97.17	122.30
1	B	101	ARG	NE-CZ-NH1	10.64	125.62	120.30
1	C	125	ARG	NE-CZ-NH1	9.23	124.91	120.30
1	C	125	ARG	NE-CZ-NH2	-8.50	116.05	120.30
1	B	218	ARG	NE-CZ-NH1	-8.38	116.11	120.30
1	A	115	ASP	CB-CG-OD1	8.22	125.69	118.30
1	A	125	ARG	NE-CZ-NH2	-7.72	116.44	120.30
1	C	157	ARG	NE-CZ-NH1	7.11	123.85	120.30
1	A	47	ASP	CB-CG-OD2	-6.88	112.11	118.30
1	C	256	ARG	NE-CZ-NH1	6.74	123.67	120.30
1	B	115	ASP	CB-CG-OD1	6.72	124.35	118.30
1	A	205	ASP	CB-CG-OD1	6.38	124.04	118.30
1	C	212	LEU	CB-CG-CD2	6.17	121.49	111.00
1	A	103	LEU	O-C-N	-6.06	112.90	123.20
1	C	80	ASP	CB-CG-OD2	-6.04	112.87	118.30
1	A	154	ASP	CB-CG-OD2	5.99	123.69	118.30
1	B	61	ASP	CB-CG-OD2	-5.96	112.94	118.30
1	B	101	ARG	CD-NE-CZ	5.95	131.93	123.60
1	A	195	TYR	CB-CG-CD2	-5.89	117.46	121.00
1	C	73	ASP	CB-CG-OD2	-5.81	113.07	118.30
1	C	61	ASP	CB-CG-OD1	5.78	123.50	118.30
1	C	133	ARG	NE-CZ-NH2	-5.75	117.42	120.30
1	B	256	ARG	NE-CZ-NH2	-5.75	117.42	120.30
1	B	256	ARG	NE-CZ-NH1	5.75	123.17	120.30
1	C	270	ASP	CB-CG-OD1	5.72	123.44	118.30
1	B	149	TYR	CB-CG-CD1	-5.67	117.60	121.00
1	A	195	TYR	CD1-CE1-CZ	-5.61	114.75	119.80
1	B	61	ASP	CB-CG-OD1	5.55	123.29	118.30
1	B	20	LEU	CB-CG-CD1	-5.46	101.71	111.00
1	B	154	ASP	CB-CG-OD2	5.41	123.17	118.30
1	C	168	PHE	CB-CG-CD2	-5.40	117.02	120.80
1	B	196	TYR	CD1-CE1-CZ	-5.40	114.94	119.80
1	A	73	ASP	CB-CG-OD2	-5.39	113.45	118.30
1	A	205	ASP	CB-CG-OD2	-5.37	113.47	118.30
1	B	96	GLU	OE1-CD-OE2	-5.32	116.92	123.30
1	A	147	LEU	CB-CG-CD1	5.31	120.03	111.00
1	C	57	LYS	CD-CE-NZ	-5.29	99.54	111.70
1	A	62	MET	CA-CB-CG	5.29	122.28	113.30
1	B	57	LYS	CD-CE-NZ	-5.27	99.57	111.70
1	A	218	ARG	NE-CZ-NH2	5.26	122.93	120.30
1	A	270	ASP	CB-CG-OD1	5.24	123.01	118.30
1	A	188	SER	N-CA-C	5.18	124.98	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	80	ASP	CB-CG-OD1	5.18	122.96	118.30
1	B	261	LEU	CB-CG-CD1	-5.13	102.28	111.00
1	A	46	ASP	CB-CG-OD1	5.08	122.88	118.30
1	A	115	ASP	CB-CG-OD2	-5.06	113.75	118.30
1	B	101	ARG	CA-CB-CG	5.03	124.46	113.40
1	A	73	ASP	CB-CG-OD1	5.01	122.81	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	125	ARG	Sidechain
1	A	190[B]	SER	Peptide

5.2 Too-close contacts [\(i\)](#)

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	2235	0	2168	22	0
1	B	2219	0	2159	21	0
1	C	2204	0	2149	24	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
3	A	6	0	8	7	0
3	B	24	0	31	4	0
3	C	6	0	8	8	0
4	A	4	0	3	0	0
4	B	4	0	3	0	0
4	C	4	0	3	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
6	B	16	0	28	6	0
6	C	16	0	28	4	0
7	A	207	0	0	0	0
7	B	178	0	0	4	0
7	C	167	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7295	0	6588	70	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 (70) 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)
3:B:303[C]:GOL:O3	7:B:459:HOH:O	1.63	1.11
1:C:92:ARG:HH12	3:C:303:GOL:H32	1.03	1.08
1:A:92:ARG:HH12	3:A:302:GOL:H11	0.93	1.07
1:A:92:ARG:NH1	3:A:302:GOL:H11	1.77	0.98
1:B:30:ASN:O	1:B:33:LYS:HG3	1.69	0.91
1:C:92:ARG:NH1	3:C:303:GOL:H32	1.88	0.89
1:A:92:ARG:HH12	3:A:302:GOL:C1	1.85	0.84
1:A:205:ASP:OD1	1:A:207:THR:HG23	1.77	0.84
1:B:151[B]:SER:OG	6:B:306:HEZ:H51	1.79	0.82
1:A:205:ASP:OD1	1:A:207:THR:CG2	2.31	0.79
6:B:306:HEZ:H22	1:C:167:ALA:HB2	1.64	0.78
1:C:92:ARG:HH12	3:C:303:GOL:C3	1.94	0.75
1:A:268:PHE:HB2	1:A:271:LEU:HD22	1.70	0.73
1:C:62:MET:HG3	6:C:306:HEZ:H32	1.74	0.70
1:C:208[A]:ASP:OD1	7:C:527:HOH:O	2.14	0.66
1:A:250:ARG:NH1	1:B:7:GLU:O	2.29	0.66
1:A:17[A]:ASN:O	1:A:21:ARG:HG3	1.97	0.64
1:A:17[B]:ASN:O	1:A:21:ARG:HG3	2.02	0.59
1:B:151[B]:SER:HG	6:B:306:HEZ:H51	1.69	0.58
1:B:30:ASN:HB3	1:B:33:LYS:CG	2.34	0.58
1:C:62:MET:HG3	6:C:306:HEZ:C3	2.34	0.58
1:A:30:ASN:O	1:A:33:LYS:HB2	2.06	0.55
1:A:205:ASP:OD1	1:A:207:THR:HG22	2.07	0.54
1:A:77:GLY:CA	3:A:302:GOL:O1	2.56	0.54
1:B:30:ASN:HD22	1:B:33:LYS:HB3	1.72	0.54
1:C:237:ARG:O	1:C:241:MET:HG3	2.09	0.52
1:B:268:PHE:HB2	1:B:271:LEU:HD22	1.93	0.51
1:C:42:GLU:HB2	1:C:47:ASP:HB2	1.92	0.51
1:B:42:GLU:HB2	1:B:47:ASP:HB2	1.92	0.51
1:A:233:GLU:HB3	1:A:234:PRO:HD3	1.93	0.50
1:A:100:ALA:HB1	1:A:105:VAL:HB	1.94	0.49
6:B:306:HEZ:H41	1:C:167:ALA:HB2	1.94	0.48
1:C:39:LEU:HG	1:C:137:PRO:HG3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:GLU:HB3	1:C:234:PRO:HD3	1.95	0.48
1:B:151[B]:SER:OG	6:B:306:HEZ:C5	2.57	0.48
1:B:92:ARG:HH22	3:B:302:GOL:C3	2.26	0.48
1:B:6:PHE:N	7:B:504:HOH:O	2.47	0.47
1:B:30:ASN:HB3	1:B:33:LYS:HG3	1.96	0.47
1:B:221:ARG:HA	1:B:221:ARG:HD3	1.62	0.46
1:A:44:HIS:CE1	3:A:302:GOL:H32	2.51	0.46
1:B:30:ASN:HB3	1:B:33:LYS:HG2	1.96	0.46
1:C:44:HIS:NE2	3:C:303:GOL:H11	2.30	0.46
1:C:100:ALA:HB1	1:C:105:VAL:HB	1.96	0.46
1:C:142:ALA:O	1:C:194:LEU:HA	2.16	0.45
1:B:45:PRO:O	1:B:46:ASP:CG	2.55	0.45
1:A:45:PRO:O	1:A:46:ASP:CG	2.55	0.45
6:C:305:HEZ:H42	7:C:441:HOH:O	2.17	0.44
1:C:115:ASP:OD2	3:C:303:GOL:C3	2.66	0.44
6:B:306:HEZ:H32	7:C:563:HOH:O	2.17	0.44
1:C:45:PRO:O	1:C:46:ASP:CG	2.56	0.44
6:C:305:HEZ:H61	7:C:476:HOH:O	2.18	0.44
1:A:187[A]:ASN:C	1:A:187[A]:ASN:ND2	2.71	0.43
1:B:227[B]:ASP:OD1	7:B:562:HOH:O	2.18	0.43
1:C:44:HIS:CE1	3:C:303:GOL:H11	2.53	0.43
1:A:115:ASP:OD2	3:A:302:GOL:H12	2.18	0.43
1:B:44:HIS:CE1	3:B:302:GOL:H11	2.53	0.43
1:C:218:ARG:HD2	1:C:229:TRP:CE2	2.53	0.42
1:A:28:LEU:HD23	1:A:28:LEU:HA	1.67	0.42
1:C:44:HIS:CD2	3:C:303:GOL:H11	2.55	0.42
1:B:100:ALA:HB1	1:B:105:VAL:HB	2.02	0.42
3:B:303[A]:GOL:C3	1:C:157:ARG:HH21	2.32	0.42
1:C:72:THR:HA	1:C:113:TYR:O	2.21	0.41
1:C:36:LYS:HD2	1:C:36:LYS:HA	1.82	0.41
1:C:115:ASP:OD2	3:C:303:GOL:H31	2.20	0.41
1:A:142:ALA:O	1:A:194:LEU:HA	2.21	0.41
1:B:6:PHE:HB2	7:B:504:HOH:O	2.20	0.41
1:B:233[B]:GLU:HB3	1:B:234:PRO:HD3	2.02	0.40
1:B:233[A]:GLU:HB3	1:B:234:PRO:HD3	2.03	0.40
1:A:115:ASP:OD2	3:A:302:GOL:C1	2.69	0.40
1:A:271:LEU:HD12	1:A:271:LEU:HA	1.87	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	271/272 (100%)	258 (95%)	10 (4%)	3 (1%)	14	2
1	B	269/272 (99%)	264 (98%)	3 (1%)	2 (1%)	22	5
1	C	267/272 (98%)	263 (98%)	2 (1%)	2 (1%)	22	5
All	All	807/816 (99%)	785 (97%)	15 (2%)	7 (1%)	17	3

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	188	SER
1	A	46	ASP
1	B	46	ASP
1	C	46	ASP
1	A	265	ILE
1	C	265	ILE
1	B	265	ILE

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	245/244 (100%)	235 (96%)	10 (4%)	30	5
1	B	243/244 (100%)	234 (96%)	9 (4%)	34	7
1	C	241/244 (99%)	237 (98%)	4 (2%)	60	32
All	All	729/732 (100%)	706 (97%)	23 (3%)	42	10

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ASP
1	A	18	LYS
1	A	21	ARG
1	A	30	ASN
1	A	94	LYS
1	A	147	LEU
1	A	187[A]	ASN
1	A	187[B]	ASN
1	A	207	THR
1	A	271	LEU
1	B	7	GLU
1	B	18	LYS
1	B	30	ASN
1	B	33	LYS
1	B	75	TYR
1	B	187	ASN
1	B	218	ARG
1	B	221	ARG
1	B	271	LEU
1	C	6	PHE
1	C	208[A]	ASP
1	C	208[B]	ASP
1	C	212	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	30	ASN
1	B	187	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 5 are monoatomic - leaving 13 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
4	ACY	C	302	2	1,3,3	4.04	1 (100%)	0,3,3	0.00	-
6	HEZ	B	307	-	7,7,7	0.33	0	6,6,6	1.12	0
3	GOL	B	303[A]	-	5,5,5	0.43	0	5,5,5	0.86	0
3	GOL	B	303[B]	-	5,5,5	0.72	0	5,5,5	0.36	0
3	GOL	C	303	-	5,5,5	1.92	2 (40%)	5,5,5	2.37	2 (40%)
3	GOL	B	303[C]	-	5,5,5	0.70	0	5,5,5	0.85	0
4	ACY	B	304	2	1,3,3	4.70	1 (100%)	0,3,3	0.00	-
6	HEZ	B	306	-	7,7,7	0.30	0	6,6,6	0.74	0
3	GOL	A	302	-	5,5,5	2.58	2 (40%)	5,5,5	2.49	3 (60%)
4	ACY	A	303	2	1,3,3	3.65	1 (100%)	0,3,3	0.00	-
6	HEZ	C	306	-	7,7,7	0.34	0	6,6,6	0.73	0
3	GOL	B	302	-	5,5,5	2.22	3 (60%)	5,5,5	3.50	5 (100%)
6	HEZ	C	305	-	7,7,7	0.39	0	6,6,6	1.32	1 (16%)

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
6	HEZ	B	307	-	-	3/5/5/5	-
3	GOL	B	303[A]	-	-	4/4/4/4	-
3	GOL	B	303[B]	-	-	1/4/4/4	-
3	GOL	C	303	-	-	1/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	303[C]	-	-	4/4/4/4	-
6	HEZ	B	306	-	-	5/5/5/5	-
3	GOL	A	302	-	-	2/4/4/4	-
6	HEZ	C	305	-	-	3/5/5/5	-
6	HEZ	C	306	-	-	3/5/5/5	-
3	GOL	B	302	-	-	3/4/4/4	-

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	304	ACY	CH3-C	4.70	1.54	1.48
3	A	302	GOL	O3-C3	4.07	1.59	1.42
4	C	302	ACY	CH3-C	4.04	1.53	1.48
4	A	303	ACY	CH3-C	3.65	1.53	1.48
3	A	302	GOL	O2-C2	3.53	1.53	1.43
3	B	302	GOL	O2-C2	3.01	1.52	1.43
3	B	302	GOL	O1-C1	3.00	1.55	1.42
3	C	303	GOL	O1-C1	2.92	1.54	1.42
3	C	303	GOL	O2-C2	2.50	1.50	1.43
3	B	302	GOL	O3-C3	-2.15	1.33	1.42

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	302	GOL	O2-C2-C1	4.90	130.70	109.12
3	C	303	GOL	O1-C1-C2	3.61	127.51	110.20
3	B	302	GOL	O2-C2-C3	-3.54	93.55	109.12
3	A	302	GOL	O3-C3-C2	3.41	126.57	110.20
3	A	302	GOL	O2-C2-C3	3.39	124.04	109.12
3	B	302	GOL	O1-C1-C2	3.29	125.98	110.20
3	C	303	GOL	O2-C2-C1	3.21	123.25	109.12
3	B	302	GOL	C3-C2-C1	-2.93	100.33	111.70
3	B	302	GOL	O3-C3-C2	-2.33	99.04	110.20
3	A	302	GOL	O2-C2-C1	-2.04	100.12	109.12
6	C	305	HEZ	C4-C3-C2	-2.01	104.24	114.42

There are no chirality outliers.

All (29) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	303[A]	GOL	C1-C2-C3-O3
3	B	303[C]	GOL	O1-C1-C2-C3
3	B	303[C]	GOL	C1-C2-C3-O3
3	B	302	GOL	C1-C2-C3-O3
3	B	302	GOL	O2-C2-C3-O3
3	B	303[C]	GOL	O1-C1-C2-O2
6	C	305	HEZ	C2-C3-C4-C5
6	B	306	HEZ	C2-C3-C4-C5
3	B	303[A]	GOL	O1-C1-C2-C3
6	C	306	HEZ	C2-C3-C4-C5
3	B	303[A]	GOL	O2-C2-C3-O3
3	B	303[C]	GOL	O2-C2-C3-O3
3	B	302	GOL	O1-C1-C2-O2
6	B	307	HEZ	C3-C4-C5-C6
6	B	306	HEZ	O1-C1-C2-C3
6	C	305	HEZ	C4-C5-C6-O6
6	C	306	HEZ	O1-C1-C2-C3
6	B	307	HEZ	C4-C5-C6-O6
6	B	307	HEZ	C1-C2-C3-C4
3	A	302	GOL	O1-C1-C2-O2
6	C	306	HEZ	C1-C2-C3-C4
6	B	306	HEZ	C3-C4-C5-C6
3	B	303[A]	GOL	O1-C1-C2-O2
6	B	306	HEZ	C4-C5-C6-O6
3	B	303[B]	GOL	C1-C2-C3-O3
6	B	306	HEZ	C1-C2-C3-C4
6	C	305	HEZ	O1-C1-C2-C3
3	A	302	GOL	O1-C1-C2-C3
3	C	303	GOL	O2-C2-C3-O3

There are no ring outliers.

8 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	303[A]	GOL	1	0
3	C	303	GOL	8	0
3	B	303[C]	GOL	1	0
6	B	306	HEZ	6	0
3	A	302	GOL	7	0
6	C	306	HEZ	2	0
3	B	302	GOL	2	0
6	C	305	HEZ	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 [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	267/272 (98%)	-0.21	9 (3%) 45 52	15, 24, 46, 76	0
1	B	267/272 (98%)	-0.43	4 (1%) 73 78	14, 19, 39, 66	0
1	C	267/272 (98%)	-0.44	2 (0%) 87 90	14, 22, 37, 57	0
All	All	801/816 (98%)	-0.36	15 (1%) 66 73	14, 22, 42, 76	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	33	LYS	5.8
1	A	6	PHE	4.2
1	A	8	ASP	3.9
1	C	189	GLY	3.7
1	C	8	ASP	3.1
1	B	33	LYS	2.9
1	A	21	ARG	2.8
1	B	189	GLY	2.7
1	A	9	ILE	2.6
1	B	188	SER	2.5
1	A	30	ASN	2.4
1	A	29	GLN	2.3
1	A	7	GLU	2.3
1	A	34	ASP	2.3
1	B	30	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. 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(Å ²)	Q<0.9
6	HEZ	C	306	8/8	0.70	0.16	41,48,56,61	0
6	HEZ	B	307	8/8	0.77	0.15	41,44,49,49	0
3	GOL	B	302	6/6	0.82	0.12	22,30,33,34	0
3	GOL	B	303[A]	6/6	0.83	0.18	13,17,18,19	6
3	GOL	B	303[B]	6/6	0.83	0.18	16,21,24,30	6
3	GOL	B	303[C]	6/6	0.83	0.18	15,20,26,29	6
6	HEZ	B	306	8/8	0.84	0.15	49,51,53,53	0
6	HEZ	C	305	8/8	0.87	0.14	31,37,42,43	0
3	GOL	C	303	6/6	0.88	0.18	26,38,41,55	0
3	GOL	A	302	6/6	0.88	0.14	19,27,30,45	0
4	ACY	B	304	4/4	0.91	0.11	22,26,28,28	0
5	NA	C	304	1/1	0.95	0.13	30,30,30,30	0
5	NA	B	305	1/1	0.96	0.10	32,32,32,32	0
4	ACY	C	302	4/4	0.97	0.08	23,27,30,30	0
4	ACY	A	303	4/4	0.98	0.06	21,29,29,30	0
2	ZN	B	301	1/1	1.00	0.02	17,17,17,17	0
2	ZN	C	301	1/1	1.00	0.01	21,21,21,21	0
2	ZN	A	301	1/1	1.00	0.01	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.