



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 10:43 AM UTC

PDB ID : 3ITC / pdb_00003itc
Title : Crystal structure of Sco3058 with bound citrate and glycerol
Authors : Nguyen, T.T.; Cummings, J.A.; Tsai, C.-L.; Barondeau, D.P.; Raushel, F.M.
Deposited on : 2009-08-28
Resolution : 1.70 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

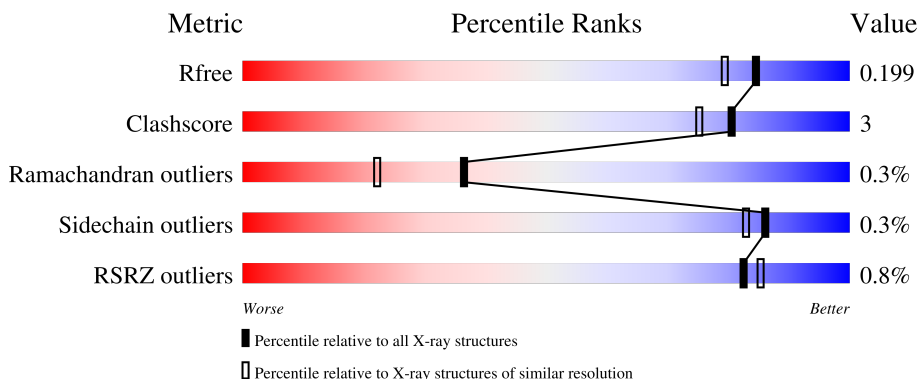
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	400	

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
4	GOL	A	504	-	X	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3580 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.

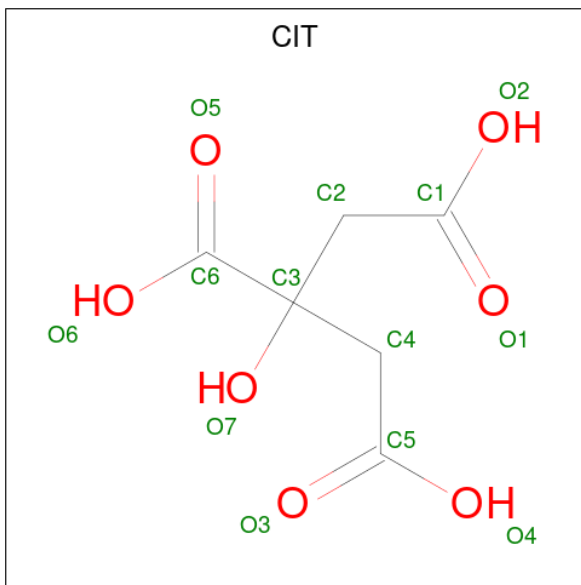
- Molecule 1 is a protein called renal dipeptidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	392	3054	1877	568	594	15	0	15	0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Zn	0	0
			2	2		

- Molecule 3 is CITRIC ACID (CCD ID: CIT) (formula: C₆H₈O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 6 3 3	0	0

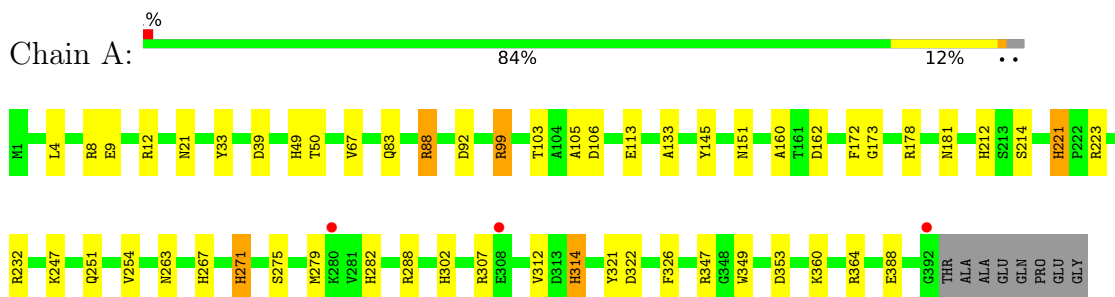
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	505	Total O 505 505	0	0

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: renal dipeptidase



4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	97.29Å 97.29Å 104.41Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.70 20.00 – 1.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-1.70) 92.8 (20.00-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.30 (at 1.70Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.167 , 0.203 0.167 , 0.199	Depositor DCC
R_{free} test set	3134 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	22.2	Xtrriage
Anisotropy	0.268	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 63.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.021 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3580	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.63% 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 i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, GOL, CIT

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	0.63	0/3168	1.64	70/4303 (1.6%)

There are no bond length outliers.

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	212	HIS	ND1-CE1-NE2	-11.15	97.25	108.40
1	A	214	SER	CA-C-N	10.84	136.90	122.81
1	A	214	SER	C-N-CA	10.84	136.90	122.81
1	A	221	HIS	CB-CG-CD2	10.54	144.90	131.20
1	A	214	SER	O-C-N	-10.37	111.43	122.84
1	A	221	HIS	CG-CD2-NE2	10.26	117.46	107.20
1	A	388	GLU	CA-C-N	10.07	133.53	120.44
1	A	388	GLU	C-N-CA	10.07	133.53	120.44
1	A	212	HIS	CA-CB-CG	9.86	123.66	113.80
1	A	321	TYR	CA-C-N	9.31	139.33	121.54
1	A	321	TYR	C-N-CA	9.31	139.33	121.54
1	A	105	ALA	CA-C-N	9.26	133.43	120.29
1	A	105	ALA	C-N-CA	9.26	133.43	120.29
1	A	4	LEU	CA-C-O	9.24	130.34	120.55
1	A	321	TYR	O-C-N	-9.24	111.96	122.86
1	A	172	PHE	CA-C-N	9.11	130.28	119.99
1	A	172	PHE	C-N-CA	9.11	130.28	119.99
1	A	212	HIS	ND1-CG-CD2	-8.83	97.27	106.10
1	A	212	HIS	CB-CG-CD2	8.83	142.68	131.20
1	A	151	ASN	CA-CB-CG	8.69	121.29	112.60
1	A	221	HIS	ND1-CG-CD2	-8.65	97.45	106.10
1	A	162	ASP	CA-CB-CG	8.61	121.21	112.60
1	A	67	VAL	CA-C-N	8.43	133.87	121.31
1	A	67	VAL	C-N-CA	8.43	133.87	121.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	99	ARG	CD-NE-CZ	8.38	136.13	124.40
1	A	4	LEU	O-C-N	-8.32	113.30	122.12
1	A	212	HIS	CG-ND1-CE1	8.32	123.44	109.30
1	A	302	HIS	CB-CG-CD2	8.21	141.87	131.20
1	A	67	VAL	CA-C-O	8.06	130.85	120.78
1	A	21	ASN	OD1-CG-ND2	7.64	130.24	122.60
1	A	105	ALA	O-C-N	-7.55	113.39	122.22
1	A	4	LEU	CA-C-N	7.34	130.43	120.44
1	A	4	LEU	C-N-CA	7.34	130.43	120.44
1	A	49	HIS	CB-CG-ND1	7.33	133.70	122.70
1	A	151	ASN	OD1-CG-ND2	-7.28	115.32	122.60
1	A	271	HIS	CA-CB-CG	6.91	120.71	113.80
1	A	83	GLN	OE1-CD-NE2	-6.86	115.74	122.60
1	A	145	TYR	CA-CB-CG	6.86	126.25	113.90
1	A	49	HIS	ND1-CG-CD2	-6.78	99.32	106.10
1	A	314	HIS	CA-CB-CG	-6.49	107.31	113.80
1	A	347	ARG	NE-CZ-NH2	6.48	125.04	119.20
1	A	288	ARG	CD-NE-CZ	6.47	133.46	124.40
1	A	353	ASP	CA-CB-CG	6.35	118.95	112.60
1	A	67	VAL	O-C-N	-6.30	114.69	122.57
1	A	326	PHE	CA-CB-CG	-6.26	107.54	113.80
1	A	133	ALA	CA-C-N	6.23	129.14	120.29
1	A	133	ALA	C-N-CA	6.23	129.14	120.29
1	A	221	HIS	CE1-NE2-CD2	-6.20	102.80	109.00
1	A	106	ASP	N-CA-C	-6.14	104.66	111.36
1	A	302	HIS	CA-CB-CG	-6.02	107.78	113.80
1	A	49	HIS	ND1-CE1-NE2	-5.91	102.49	108.40
1	A	321	TYR	CA-C-O	5.87	127.95	121.56
1	A	302	HIS	ND1-CE1-NE2	-5.82	102.58	108.40
1	A	232	ARG	NE-CZ-NH2	5.81	124.43	119.20
1	A	50	THR	CA-CB-OG1	-5.74	100.98	109.60
1	A	39	ASP	CA-CB-CG	5.73	118.33	112.60
1	A	33	TYR	OH-CZ-CE2	5.71	137.04	119.90
1	A	103	THR	OG1-CB-CG2	-5.63	98.04	109.30
1	A	106	ASP	CA-CB-CG	5.61	118.21	112.60
1	A	223	ARG	N-CA-C	-5.49	106.08	112.89
1	A	302	HIS	ND1-CG-CD2	-5.49	100.61	106.10
1	A	347	ARG	NE-CZ-NH1	-5.44	116.06	121.50
1	A	160	ALA	CA-C-N	5.41	131.14	122.86
1	A	160	ALA	C-N-CA	5.41	131.14	122.86
1	A	223	ARG	NE-CZ-NH2	5.38	124.04	119.20
1	A	49	HIS	CG-ND1-CE1	5.25	118.23	109.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	364	ARG	NE-CZ-NH2	5.24	123.91	119.20
1	A	173	GLY	N-CA-C	-5.20	106.35	112.64
1	A	181	ASN	O-C-N	5.07	127.29	122.07
1	A	282	HIS	CA-CB-CG	-5.05	108.75	113.80

There are no chirality outliers.

There are no planarity outliers.

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	3054	0	2948	15	0
2	A	2	0	0	0	0
3	A	13	0	5	0	0
4	A	6	0	7	1	0
5	A	505	0	0	7	0
All	All	3580	0	2960	16	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 (16) 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:247:LYS:O	1:A:254[B]:VAL:HG13	1.95	0.67
4:A:504:GOL:H31	5:A:887:HOH:O	2.00	0.61
1:A:251:GLN:O	1:A:254[B]:VAL:HG23	2.05	0.57
1:A:307[B]:ARG:HD3	1:A:349:TRP:CH2	2.43	0.54
1:A:221:HIS:HE1	5:A:780:HOH:O	1.91	0.52
1:A:263:ASN:O	1:A:267:HIS:HD2	1.93	0.52
1:A:271:HIS:HD2	5:A:560:HOH:O	1.91	0.51
1:A:178:ARG:HD3	5:A:544:HOH:O	2.17	0.45
1:A:360:LYS:NZ	5:A:907:HOH:O	2.50	0.45
1:A:99:ARG:HH11	1:A:113:GLU:CD	2.27	0.43
1:A:275:SER:O	1:A:279:MET:HG2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:VAL:HG22	5:A:901:HOH:O	2.18	0.42
1:A:88[A]:ARG:NH2	1:A:92:ASP:OD1	2.51	0.42
1:A:8[B]:ARG:HD3	1:A:12:ARG:NH1	2.36	0.40
1:A:9:GLU:HG3	5:A:945:HOH:O	2.21	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	404/400 (101%)	390 (96%)	13 (3%)	1 (0%)	43 28

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	322	ASP

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	324/314 (103%)	322 (99%)	2 (1%)	78 72

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88[A]	ARG
1	A	88[B]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	GLN
1	A	130	ASN
1	A	267	HIS
1	A	271	HIS

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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	GOL	A	504	2	5,5,5	2.19	2 (40%)	5,5,5	2.30	2 (40%)
3	CIT	A	503	2	12,12,12	0.74	0	17,17,17	1.47	3 (17%)

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
4	GOL	A	504	2	-	2/4/4/4	-
3	CIT	A	503	2	-	0/16/16/16	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	504	GOL	C3-C2	-3.37	1.38	1.51
4	A	504	GOL	O3-C3	-3.34	1.28	1.42

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	504	GOL	C3-C2-C1	3.93	126.22	111.80
3	A	503	CIT	C3-C4-C5	-2.99	105.74	113.92
4	A	504	GOL	O3-C3-C2	2.84	123.14	110.38
3	A	503	CIT	O7-C3-C6	2.39	112.34	108.96
3	A	503	CIT	C4-C3-C6	-2.31	104.93	110.03

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	504	GOL	O1-C1-C2-C3
4	A	504	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	504	GOL	1	0

5.7 Other polymers [i](#)

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 [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	392/400 (98%)	-0.33	3 (0%) 82 85	12, 21, 36, 64	15 (3%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	392	GLY	2.5
1	A	280	LYS	2.4
1	A	308[A]	GLU	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 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(Å ²)	Q<0.9
4	GOL	A	504	6/6	0.74	0.21	30,33,41,66	0
3	CIT	A	503	13/13	0.94	0.08	18,23,32,35	0
2	ZN	A	501	1/1	1.00	0.01	19,19,19,19	0
2	ZN	A	502	1/1	1.00	0.01	18,18,18,18	0

6.5 Other polymers [i](#)

There are no such residues in this entry.