Full wwPDB X-ray Structure Validation Report (i)

Nov 6, 2023 – 03:54 am GMT

PDB ID	:	2JAI
Title	:	DDAH1 complexed with citrulline
Authors	:	Murray-Rust, J.; O'Hara, B.P.; Rossiter, S.; Leiper, J.M.; Vallance, P.; McDonald, N.Q.
Deposited on	:	2006-11-29
Resolution	:	2.30 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 (i) 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 (i)) were used in the production of this report:

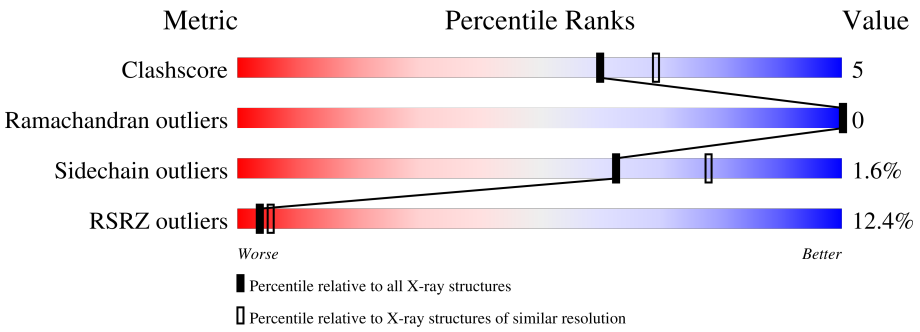
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

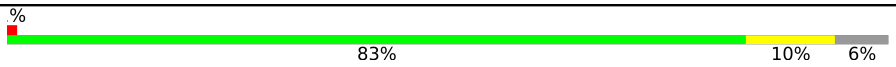
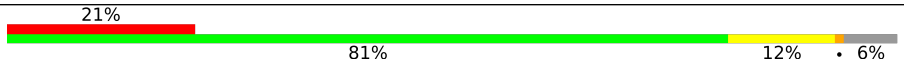
The reported resolution of this entry is 2.30 Å.

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))
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 <=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	
1	B	289	

2 Entry composition (i)

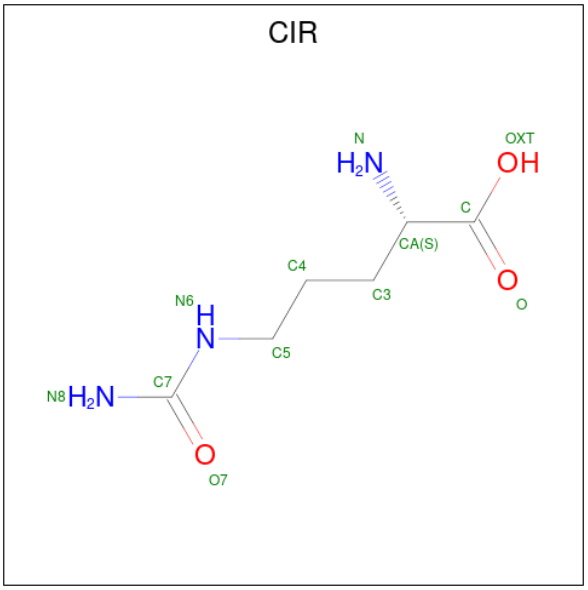
There are 3 unique types of molecules in this entry. The entry contains 4056 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 NG, NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	271	2042	1288	347	391	7	9	0	3	0
1	B	271	1877	1192	326	345	6	8	0	0	0

- Molecule 2 is CITRULLINE (three-letter code: CIR) (formula: $C_6H_{13}N_3O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	12	6	3	3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	114	114	114	0	0

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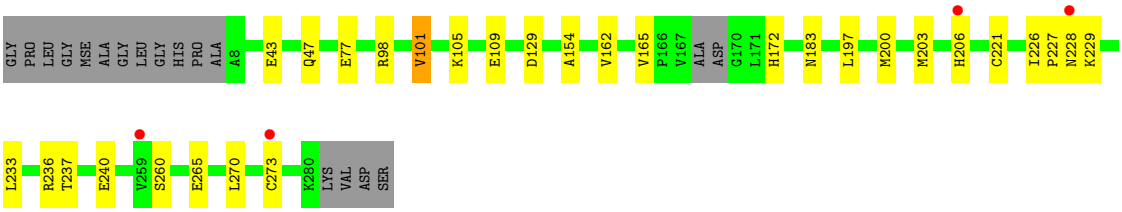
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	B	11	11	11	0	0

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.

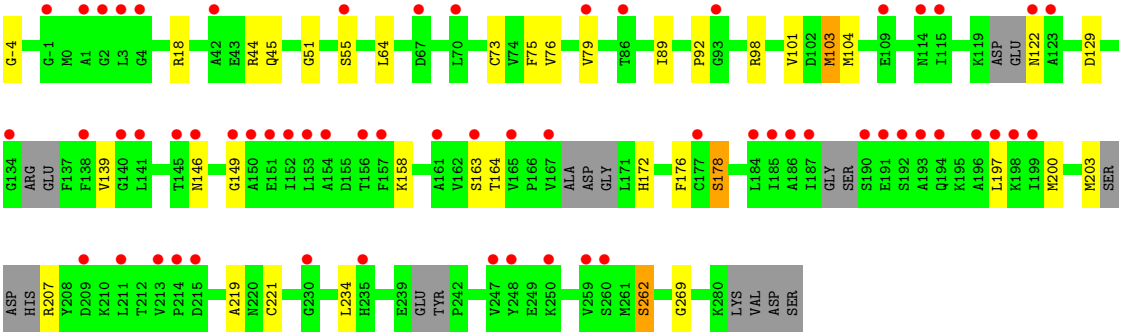
• Molecule 1: NG, NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1

Chain A:



• Molecule 1: NG, NG-DIMETHYLARGININE DIMETHYLAMINOHYDROLASE 1

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	44.83Å 46.80Å 147.79Å 90.00° 94.64° 90.00°	Depositor
Resolution (Å)	50.00 – 2.30 44.68 – 2.30	Depositor EDS
% Data completeness (in resolution range)	92.8 (50.00-2.30) 92.8 (44.68-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.80 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.198 , 0.258 0.201 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	28.8	Xtriage
Anisotropy	0.442	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 51.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	4056	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.51% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: CIR

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	0.80	0/2071	0.80	1/2794 (0.0%)
1	B	0.89	11/1895 (0.6%)	0.72	1/2570 (0.0%)
All	All	0.84	11/3966 (0.3%)	0.76	2/5364 (0.0%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	146	ASN	CG-OD1	9.77	1.45	1.24
1	B	146	ASN	CG-ND2	9.76	1.57	1.32
1	B	122	ASN	CG-ND2	8.94	1.55	1.32
1	B	122	ASN	CG-OD1	8.66	1.43	1.24
1	B	122	ASN	C-N	6.97	1.50	1.34
1	B	207	ARG	N-CA	6.21	1.58	1.46
1	B	158	LYS	C-O	6.03	1.34	1.23
1	B	176	PHE	CG-CD1	5.53	1.47	1.38
1	B	122	ASN	N-CA	5.23	1.56	1.46
1	B	207	ARG	CA-CB	5.04	1.65	1.53
1	B	149	GLY	C-O	5.03	1.31	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	146	ASN	CB-CG-OD1	-5.10	111.40	121.60
1	A	165	VAL	CB-CA-C	-5.04	101.82	111.40

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	2042	0	2007	20	0
1	B	1877	0	1750	16	0
2	A	12	0	7	2	0
3	A	114	0	0	1	0
3	B	11	0	0	0	0
All	All	4056	0	3764	35	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 (35) 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:183:ASN:ND2	1:A:206[A]:HIS:NE2	2.33	0.75
1:A:270:LEU:O	1:A:273[B]:CYS:SG	2.47	0.73
1:B:178:SER:HB2	1:B:219:ALA:O	1.88	0.71
1:B:163:SER:HB3	1:B:203:MSE:SE	2.41	0.70
1:A:236:ARG:NH2	1:A:265:GLU:OE1	2.29	0.63
1:A:203:MSE:SE	1:B:-4:GLY:HA2	2.50	0.60
1:A:154:ALA:HA	1:A:162:VAL:HG21	1.84	0.58
1:A:98:ARG:O	1:A:101:VAL:HB	2.06	0.56
1:A:206[B]:HIS:HE1	3:A:2083:HOH:O	1.89	0.55
1:A:273[B]:CYS:HB3	2:A:1281:CIR:C7	2.38	0.53
1:A:43:GLU:OE2	1:A:47:GLN:NE2	2.33	0.51
1:A:197:LEU:HA	1:A:200:MSE:HE3	1.92	0.51
1:A:221:CYS:SG	1:A:233:LEU:HD11	2.51	0.50
1:A:270:LEU:N	1:A:273[B]:CYS:SG	2.85	0.50
1:A:183:ASN:HD21	1:A:206[A]:HIS:CD2	2.28	0.50
1:B:75:PHE:CE2	1:B:269:GLY:HA3	2.48	0.49
1:B:64:LEU:HD13	1:B:103:MSE:HG2	1.95	0.48
1:A:227:PRO:O	1:A:228:ASN:HB2	2.13	0.48
1:B:221:CYS:HB2	1:B:234:LEU:O	2.14	0.48
1:B:76:VAL:HB	1:B:104:MSE:CE	2.44	0.47
1:A:129:ASP:OD1	1:A:172:HIS:HA	2.16	0.46
1:B:197:LEU:HA	1:B:200:MSE:HE3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:139:VAL:O	1:B:164:THR:HA	2.17	0.44
1:B:89:ILE:CG2	1:B:101:VAL:HG13	2.48	0.43
1:B:129:ASP:OD1	1:B:172:HIS:HA	2.18	0.43
1:B:92:PRO:HD2	1:B:98:ARG:HG2	2.01	0.43
1:A:237:THR:OG1	1:A:240:GLU:HG3	2.19	0.43
1:B:45:GLN:HE22	1:B:262:SER:HB2	1.83	0.43
1:A:273[B]:CYS:HB3	2:A:1281:CIR:O7	2.19	0.42
1:A:226:ILE:HB	1:A:229:LYS:HB2	2.02	0.41
1:A:105:LYS:O	1:A:109:GLU:HG3	2.20	0.41
1:B:18:ARG:HD3	1:B:73:CYS:HB2	2.03	0.41
1:B:51:GLY:O	1:B:55:SER:HB3	2.20	0.41
1:B:79:VAL:HG23	1:B:104:MSE:HG2	2.03	0.40
1:A:77:GLU:HB3	1:A:273[B]:CYS:HA	2.03	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	270/289 (93%)	260 (96%)	10 (4%)	0	100	100
1	B	257/289 (89%)	248 (96%)	9 (4%)	0	100	100
All	All	527/578 (91%)	508 (96%)	19 (4%)	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	216/232 (93%)	214 (99%)	2 (1%)	78	89
1	B	173/232 (75%)	169 (98%)	4 (2%)	50	67
All	All	389/464 (84%)	383 (98%)	6 (2%)	62	79

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	VAL
1	A	260	SER
1	B	44	ARG
1	B	103	MSE
1	B	178	SER
1	B	262	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	GLN
1	A	183	ASN
1	B	235	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	CIR	A	1281	1	10,11,11	0.84	0	12,13,13	0.78	0

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	CIR	A	1281	1	-	1/11/11/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1281	CIR	OXT-C-CA-N

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1281	CIR	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	263/289 (91%)	0.63	4 (1%)	73	79	31, 35, 42, 52	0
1	B	262/289 (90%)	1.34	61 (23%)	0	1	28, 36, 44, 55	0
All	All	525/578 (90%)	0.99	65 (12%)	4	5	28, 36, 42, 55	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	163	SER	5.4
1	B	115	ILE	4.9
1	B	190	SER	4.8
1	B	161	ALA	4.7
1	B	140	GLY	4.5
1	B	3	LEU	4.3
1	B	154	ALA	4.3
1	B	165	VAL	4.3
1	B	197	LEU	3.8
1	B	213	VAL	3.8
1	B	123	ALA	3.8
1	B	186	ALA	3.8
1	B	193	ALA	3.7
1	B	156	THR	3.7
1	B	1	ALA	3.7
1	B	149	GLY	3.3
1	B	150	ALA	3.3
1	B	67	ASP	3.3
1	B	167	VAL	3.2
1	B	70	LEU	3.1
1	B	138	PHE	3.1
1	B	141	LEU	3.0
1	B	114	ASN	3.0
1	B	215	ASP	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	146	ASN	3.0
1	B	184	LEU	2.9
1	B	191	GLU	2.9
1	B	153	LEU	2.9
1	B	55	SER	2.9
1	B	187	ILE	2.8
1	B	199	ILE	2.8
1	B	259	VAL	2.8
1	B	134	GLY	2.7
1	B	194	GLN	2.7
1	B	248	TYR	2.7
1	B	235	HIS	2.6
1	B	4	GLY	2.6
1	B	247	VAL	2.6
1	B	145	THR	2.5
1	B	230	GLY	2.5
1	B	198	LYS	2.5
1	B	192	SER	2.4
1	B	2	GLY	2.4
1	B	79	VAL	2.4
1	A	206[A]	HIS	2.4
1	B	185	ILE	2.4
1	B	196	ALA	2.3
1	B	211	LEU	2.3
1	B	177	CYS	2.3
1	B	93	GLY	2.2
1	B	122	ASN	2.2
1	B	151	GLU	2.2
1	B	152	ILE	2.2
1	B	214	PRO	2.2
1	B	-1	GLY	2.2
1	B	86	THR	2.2
1	B	250	LYS	2.2
1	B	109	GLU	2.1
1	A	273[A]	CYS	2.1
1	B	157	PHE	2.1
1	A	228	ASN	2.0
1	B	42	ALA	2.0
1	B	260	SER	2.0
1	A	259	VAL	2.0
1	B	209	ASP	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 monosaccharides 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
2	CIR	A	1281	12/12	0.93	0.21	11,13,17,17	12

6.5 Other polymers (i)

There are no such residues in this entry.