



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 06:28 AM GMT

PDB ID : 3F9M
Title : Human pancreatic glucokinase in complex with glucose and activator showing a mobile flap
Authors : Petit, P.; Gluais, L.; Lagarde, A.; Vuillard, L.; Boutin, J.A.; Ferry, G.
Deposited on : 2008-11-14
Resolution : 1.50 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

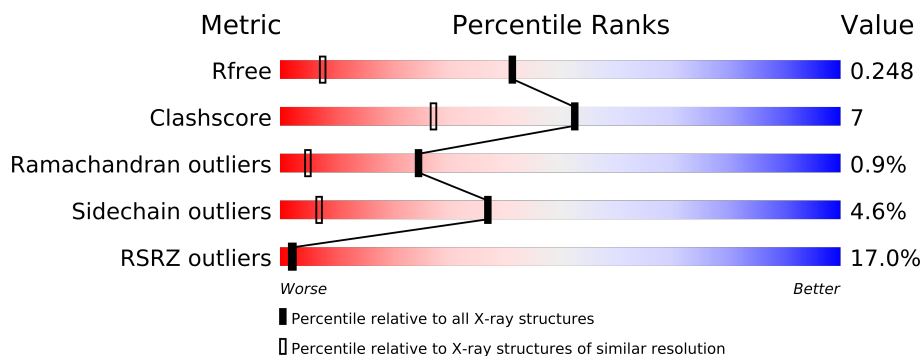
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance


The reported resolution of this entry is 1.50 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}	66092	1513 (1.50-1.50)
Clashscore	79885	1768 (1.50-1.50)
Ramachandran outliers	78287	1720 (1.50-1.50)
Sidechain outliers	78261	1718 (1.50-1.50)
RSRZ outliers	66119	1514 (1.50-1.50)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	470	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4065 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

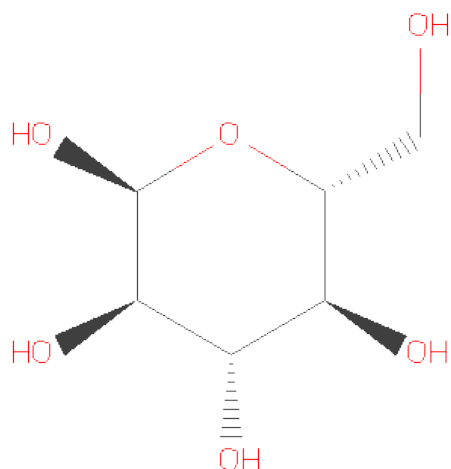
- Molecule 1 is a protein called Glucokinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	451	3590	2239	620	698	33	26	8	0

There are 16 discrepancies between the modelled and reference sequences:

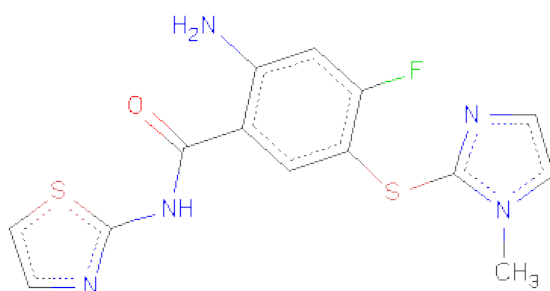
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	MET	-	EXPRESSION TAG	UNP P35557
A	-3	GLY	-	EXPRESSION TAG	UNP P35557
A	-2	HIS	-	EXPRESSION TAG	UNP P35557
A	-1	HIS	-	EXPRESSION TAG	UNP P35557
A	0	HIS	-	EXPRESSION TAG	UNP P35557
A	1	HIS	-	EXPRESSION TAG	UNP P35557
A	2	HIS	-	EXPRESSION TAG	UNP P35557
A	3	HIS	-	EXPRESSION TAG	UNP P35557
A	4	GLU	-	EXPRESSION TAG	UNP P35557
A	5	ASN	-	EXPRESSION TAG	UNP P35557
A	6	LEU	-	EXPRESSION TAG	UNP P35557
A	7	TYR	-	EXPRESSION TAG	UNP P35557
A	8	PHE	-	EXPRESSION TAG	UNP P35557
A	9	GLN	-	EXPRESSION TAG	UNP P35557
A	10	GLY	-	EXPRESSION TAG	UNP P35557
A	11	MET	-	EXPRESSION TAG	UNP P35557

- Molecule 2 is SUGAR (ALPHA-D-GLUCOSE) (three-letter code: GLC) (formula: C₆H₁₂O₆).



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

- Molecule 3 is 2-AMINO-4-FLUORO-5-[(1-METHYL-1H-IMIDAZOL-2-YL)SULFANYL]-N-(1,3-THIAZOL-2-YL)BENZAMIDE (three-letter code: MRK) (formula: $C_{14}H_{12}FN_5OS_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	F	N	O	0	0
			23	14	1	5	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	440	Total 440	O 440	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.70Å 81.20Å 85.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.74 – 1.50 19.74 – 1.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.74-1.50) 99.2 (19.74-1.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.190 , 0.222 0.227 , 0.248	Depositor DCC
R_{free} test set	3663 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	18.7	Xtriage
Anisotropy	0.201	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 35.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 73275 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4065	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.80% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, MRK

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	0.62	2/3665 (0.1%)	0.81	6/4921 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	191	ARG	CZ-NH2	-5.54	1.25	1.33
1	A	394	ARG	C-N	-5.22	1.22	1.34

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	191	ARG	NE-CZ-NH2	-17.90	111.35	120.30
1	A	191	ARG	NE-CZ-NH1	17.85	129.23	120.30
1	A	394	ARG	NE-CZ-NH1	-9.93	115.34	120.30
1	A	191	ARG	O-C-N	-6.70	111.98	122.70
1	A	394	ARG	NE-CZ-NH2	6.46	123.53	120.30
1	A	191	ARG	CD-NE-CZ	5.09	130.72	123.60

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3590	0	3546	50	0
2	A	12	0	12	0	0
3	A	23	0	12	3	0
4	A	440	0	0	7	0
All	All	4065	0	3570	51	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

All (51) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:4:GLU:HA	1:A:9[A]:GLN:HE21	1.13	1.13
1:A:65:THR:H	1:A:66:PRO:HA	0.93	1.09
1:A:4:GLU:HG2	1:A:5:ASN:N	1.64	1.08
1:A:4:GLU:HG2	1:A:5:ASN:H	0.91	1.06
1:A:139:MET:HE1	4:A:898:HOH:O	1.63	0.98
1:A:65:THR:H	1:A:66:PRO:CA	1.77	0.97
1:A:65:THR:N	1:A:66:PRO:HA	1.74	0.93
1:A:4:GLU:HA	1:A:9[A]:GLN:NE2	1.84	0.92
1:A:106:GLN:HE22	1:A:136:LYS:HD2	1.35	0.90
1:A:4:GLU:O	1:A:9[B]:GLN:HG2	1.75	0.86
1:A:439:ILE:HD11	4:A:777:HOH:O	1.90	0.72
1:A:4:GLU:O	1:A:5:ASN:C	2.29	0.71
1:A:146:LEU:HB2	1:A:197:MET:HE3	1.74	0.68
1:A:106:GLN:NE2	1:A:136:LYS:HD2	2.13	0.60
1:A:140:LYS:HB2	1:A:195:PHE:HB3	1.83	0.60
1:A:65:THR:N	1:A:66:PRO:CA	2.47	0.57
1:A:106:GLN:HE22	1:A:136:LYS:CD	2.13	0.56
1:A:140:LYS:HB2	1:A:195:PHE:CB	2.35	0.56
3:A:501:MRK:O8	3:A:501:MRK:S1	2.63	0.56
1:A:146:LEU:HD12	1:A:197:MET:HE2	1.88	0.55
1:A:341:ASP:O	1:A:368:ARG:NH2	2.42	0.53
1:A:87:MET:HG2	1:A:89:VAL:HG12	1.89	0.53
1:A:4:GLU:CG	1:A:5:ASN:N	2.49	0.52
1:A:102:LYS:HD3	1:A:105:HIS:CD2	2.45	0.51
1:A:28:GLU:HG3	4:A:618:HOH:O	2.11	0.51
1:A:215:TYR:CE2	1:A:451:LEU:HD13	2.46	0.50
1:A:4:GLU:O	1:A:5:ASN:O	2.29	0.50
1:A:137:HIS:O	1:A:139:MET:HG2	2.12	0.50
1:A:420:LYS:HG2	1:A:424:HIS:CE1	2.47	0.49
1:A:92:GLY:HA3	1:A:99:TRP:CZ2	2.48	0.49
1:A:219:GLN:HG3	4:A:819:HOH:O	2.12	0.49
1:A:50:HIS:NE2	1:A:155[A]:ARG:NH1	2.61	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:46[A]:ARG:NH2	1:A:48[A]:GLU:HG3	2.29	0.47
1:A:138:GLN:C	1:A:139:MET:HG2	2.36	0.46
1:A:144:LEU:HB2	1:A:197:MET:HE1	1.99	0.45
1:A:137:HIS:HE1	4:A:858:HOH:O	2.00	0.44
1:A:146:LEU:HB2	1:A:197:MET:CE	2.42	0.44
1:A:420:LYS:CG	1:A:424:HIS:CE1	3.00	0.44
1:A:4:GLU:O	1:A:9[A]:GLN:HG3	2.17	0.44
1:A:432:PRO:O	1:A:433:SER:HB2	2.18	0.44
1:A:134:LEU:HB3	1:A:140:LYS:HB3	2.01	0.43
1:A:22:GLU:HG2	1:A:271:LEU:HD22	2.00	0.43
1:A:220:CYS:O	3:A:501:MRK:H221	2.19	0.42
1:A:5:ASN:OD1	1:A:5:ASN:C	2.58	0.42
1:A:7:TYR:O	1:A:11:MET:HG2	2.19	0.42
1:A:139:MET:CE	4:A:898:HOH:O	2.43	0.42
1:A:42[B]:ASP:OD1	1:A:392:ARG:NH1	2.53	0.42
1:A:53:ALA:HB1	4:A:852:HOH:O	2.19	0.41
1:A:211:ILE:HD12	3:A:501:MRK:C13	2.50	0.41
1:A:143:LYS:HE2	1:A:196:GLU:HB3	2.02	0.41
1:A:41:MET:HB3	1:A:41:MET:HE2	1.81	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	454/470 (97%)	442 (97%)	8 (2%)	4 (1%)	25 5

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	66	PRO
1	A	5	ASN
1	A	80	GLY
1	A	65	THR

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	396/403 (98%)	378 (96%)	18 (4%)	38 7

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	THR
1	A	67	GLU
1	A	69	SER
1	A	93	GLU
1	A	102	LYS
1	A	104	LYS
1	A	113	ASP
1	A	139	MET
1	A	140	LYS
1	A	141	HIS
1	A	166	ASN
1	A	216	GLU
1	A	218	HIS
1	A	248	GLU
1	A	257	TRP
1	A	315	LEU
1	A	398	SER
1	A	442	GLU

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

Mol	Chain	Res	Type
1	A	106	GLN
1	A	137	HIS
1	A	317	HIS
1	A	337	GLN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

2 ligands are 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	GLC	A	500	-	12,12,12	0.57	0	17,17,17	0.74	0
3	MRK	A	501	-	25,25,25	1.33	2 (8%)	33,35,35	1.85	8 (24%)

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	GLC	A	500	-	-	0/2/22/22	0/1/1/1
3	MRK	A	501	-	-	0/10/12/12	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	MRK	C12-S16	-4.65	1.71	1.78
3	A	501	MRK	C18-N17	-2.72	1.33	1.35

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	MRK	C18-S16-C12	5.01	110.54	102.28
3	A	501	MRK	C21-N17-C18	-4.59	104.34	108.61
3	A	501	MRK	C22-N17-C18	2.88	128.34	125.63
3	A	501	MRK	C2-S1-C5	-2.78	88.14	89.96
3	A	501	MRK	C20-C21-N17	2.77	108.80	106.33
3	A	501	MRK	C15-C13-C12	-2.54	120.34	122.70
3	A	501	MRK	C9-C10-C7	2.52	121.97	120.26
3	A	501	MRK	S16-C18-N19	-2.22	123.27	126.67

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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, 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	450/470 (95%)	1.00	77 (17%) 2 2	6, 15, 28, 40	5 (1%)

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	457	CYS	7.0
1	A	99	TRP	6.3
1	A	215	TYR	5.7
1	A	141	HIS	5.7
1	A	195	PHE	5.5
1	A	194	ASP	5.2
1	A	65	THR	5.2
1	A	82	THR	5.2
1	A	196	GLU	4.1
1	A	358	ARG	4.0
1	A	216	GLU	4.0
1	A	93	GLU	3.9
1	A	346	LYS	3.8
1	A	193	GLY	3.8
1	A	400	ASP	3.7
1	A	66	PRO	3.7
1	A	8	PHE	3.7
1	A	349	TYR	3.6
1	A	139	MET	3.6
1	A	395	GLU	3.6
1	A	77	LEU	3.5
1	A	458	LYS	3.5
1	A	344	ASP	3.4
1	A	399	GLU	3.3
1	A	138	GLN	3.3
1	A	68	GLY	3.3
1	A	343	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	143	LYS	3.2
1	A	71	VAL	3.2
1	A	134	LEU	3.2
1	A	113	ASP	3.0
1	A	6	LEU	3.0
1	A	7	TYR	3.0
1	A	342	THR	3.0
1	A	70	GLU	3.0
1	A	67	GLU	2.9
1	A	98	GLN	2.9
1	A	140	LYS	2.9
1	A	146	LEU	2.8
1	A	147	GLY	2.8
1	A	101	VAL	2.8
1	A	197	MET	2.7
1	A	401	VAL	2.7
1	A	433	SER	2.7
1	A	79	LEU	2.7
1	A	135	ASP	2.7
1	A	432	PRO	2.7
1	A	4	GLU	2.7
1	A	442	GLU	2.7
1	A	69	SER	2.7
1	A	142	LYS	2.7
1	A	361	THR	2.7
1	A	123	PHE	2.7
1	A	148	PHE	2.5
1	A	103	THR	2.5
1	A	150	PHE	2.5
1	A	317	HIS	2.5
1	A	386	LEU	2.5
1	A	378	ALA	2.4
1	A	403	ARG	2.4
1	A	5	ASN	2.4
1	A	126	ILE	2.4
1	A	112	GLU	2.4
1	A	136	LYS	2.4
1	A	247	ASP	2.3
1	A	350	ASN	2.3
1	A	33	VAL	2.3
1	A	84	PHE	2.3
1	A	86	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	382	CYS	2.2
1	A	443	GLU	2.2
1	A	92	GLY	2.2
1	A	218	HIS	2.1
1	A	313	ASN	2.1
1	A	75	LEU	2.1
1	A	41	MET	2.0
1	A	406	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	GLC	A	500	12/12	0.13	0.63	10,11,13,14	0
3	MRK	A	501	23/23	0.12	-0.25	18,23,28,29	0

6.5 Other polymers ⓘ

There are no such residues in this entry.