Full wwPDB X-ray Structure Validation Report (i)

Mar 1, 2026 – 08:04 PM UTC

PDB ID	:	1RP1 / pdb_00001rp1
Title	:	DOG PANCREATIC LIPASE RELATED PROTEIN 1
Authors	:	Roussel, A.; Cambillau, C.
Deposited on	:	1998-04-02
Resolution	:	2.10 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 (1)) were used in the production of this report:

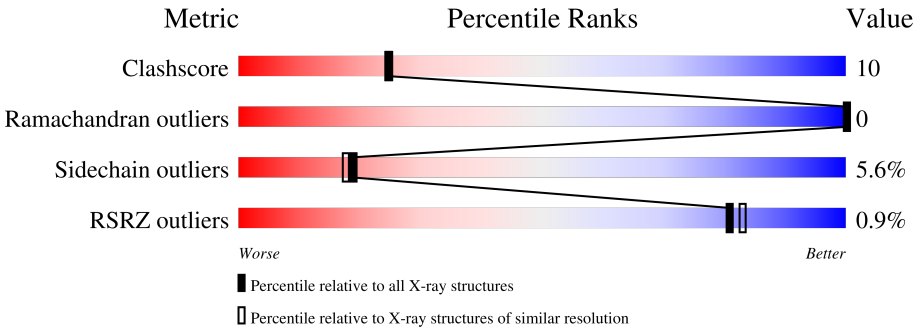
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 2.10 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	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	450	% 75% 20%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 3798 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.

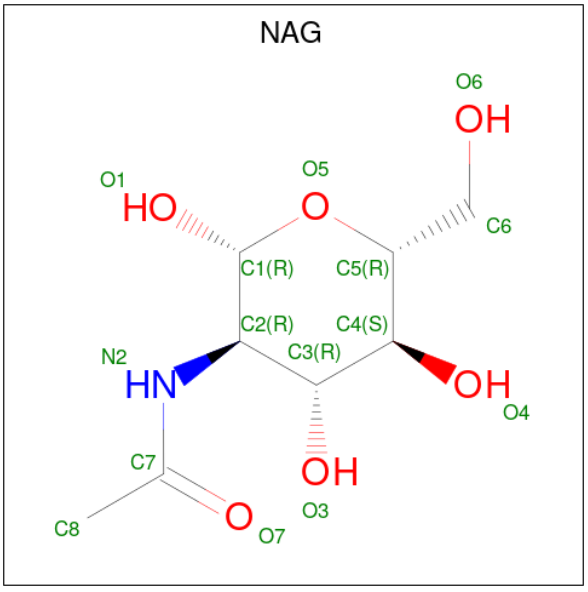
- Molecule 1 is a protein called PANCREATIC LIPASE RELATED PROTEIN 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	441	3425	2169	585	651	20	10	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	GLY	GLU	conflict	UNP P06857

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	14	8	1	5	0	0

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Ca 1 1	0	0

- Molecule 4 is water.

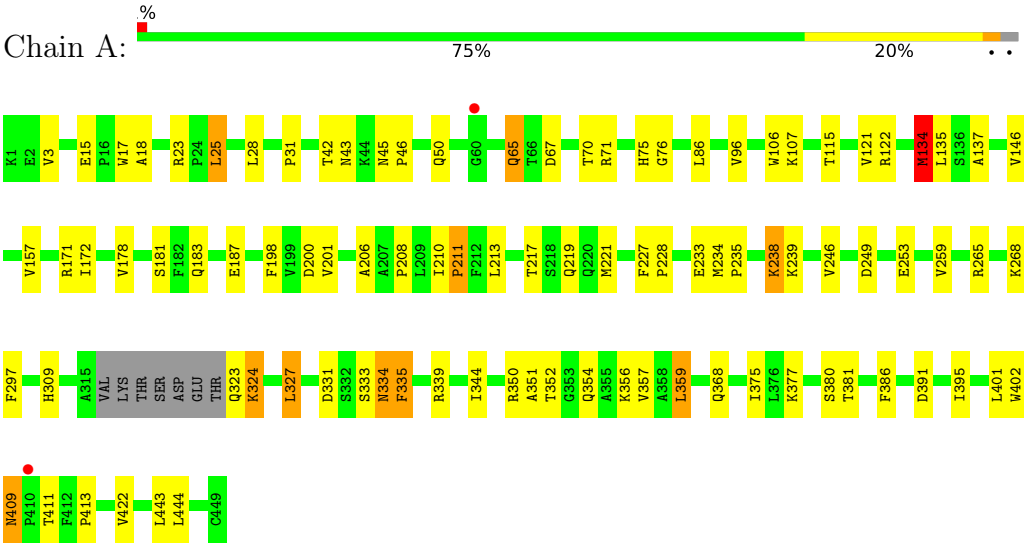
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	358	Total O 358 358	0	0

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: PANCREATIC LIPASE RELATED PROTEIN 1

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	54.03Å 150.75Å 132.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	9.00 – 2.10 9.00 – 2.11	Depositor EDS
% Data completeness (in resolution range)	97.3 (9.00-2.10) 95.6 (9.00-2.11)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.50 (at 2.12Å)	Xtriage
Refinement program	X-PLOR 3.843	Depositor
R, R_{free}	0.195 , 0.256 0.208 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	31.7	Xtriage
Anisotropy	0.296	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.42 , 50.8	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	0.94	EDS
Total number of atoms	3798	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.69% 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

5.1 Standard geometry

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

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	0.70	1/3511 (0.0%)	1.06	15/4757 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	134	MET	SD-CE	-6.84	1.62	1.79

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	309	HIS	N-CA-C	6.79	119.54	111.33
1	A	157	VAL	N-CA-C	-6.46	104.22	110.42
1	A	206	ALA	N-CA-C	6.34	120.69	113.15
1	A	334	ASN	N-CA-C	-6.29	97.39	110.80
1	A	25	LEU	N-CA-C	6.26	119.35	109.96
1	A	201	VAL	N-CA-C	5.86	116.56	108.12
1	A	333	SER	N-CA-C	5.83	118.51	110.35
1	A	391	ASP	N-CA-C	-5.69	99.91	108.96
1	A	268	LYS	N-CA-C	-5.65	105.04	111.14
1	A	238	LYS	N-CA-C	-5.36	103.31	110.55
1	A	107	LYS	N-CA-C	5.26	117.70	111.33
1	A	335	PHE	N-CA-C	-5.08	106.34	112.54
1	A	50	GLN	N-CA-C	-5.05	100.66	108.90
1	A	137	ALA	N-CA-C	5.01	116.43	110.97
1	A	96	VAL	CB-CA-C	-5.00	105.75	110.70

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	3425	0	3301	66	0
2	A	14	0	13	0	0
3	A	1	0	0	0	0
4	A	358	0	0	7	0
All	All	3798	0	3314	66	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 10.

All (66) 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:171:ARG:HD3	1:A:198:PHE:HD2	1.46	0.80
1:A:71:ARG:HH11	1:A:147:GLN:NE2	1.83	0.76
1:A:171:ARG:HD3	1:A:198:PHE:CD2	2.20	0.76
1:A:227:PHE:CE1	1:A:324:LYS:HG2	2.21	0.75
1:A:3:VAL:HG13	1:A:28:LEU:HD13	1.73	0.70
1:A:409:ASN:HD22	1:A:411:THR:H	1.40	0.68
1:A:187:GLU:HG3	4:A:963:HOH:O	1.97	0.64
1:A:359:LEU:HD21	1:A:386:PHE:HZ	1.62	0.64
1:A:75:HIS:HE1	1:A:106:TRP:H	1.46	0.63
1:A:350:ARG:NH2	1:A:375:ILE:HD13	2.12	0.63
1:A:265:ARG:NH1	1:A:335:PHE:HE1	1.97	0.63
1:A:147:GLN:HG3	1:A:171:ARG:HG2	1.80	0.62
1:A:368:GLN:NE2	1:A:401:LEU:HD22	2.14	0.62
1:A:265:ARG:NH1	1:A:335:PHE:CE1	2.68	0.61
1:A:42:THR:OG1	1:A:45:ASN:ND2	2.34	0.60
1:A:153:LEU:HD13	1:A:178:VAL:HG21	1.82	0.60
1:A:217:THR:HG21	1:A:221:MET:SD	2.44	0.58
1:A:171:ARG:HG3	1:A:172:ILE:N	2.17	0.57
1:A:75:HIS:CE1	1:A:106:TRP:H	2.23	0.57
1:A:265:ARG:NH1	4:A:859:HOH:O	2.38	0.56
1:A:409:ASN:ND2	1:A:411:THR:H	2.04	0.56
1:A:339:ARG:NH2	4:A:779:HOH:O	2.31	0.55
1:A:297:PHE:CE2	1:A:339:ARG:HG2	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:TRP:CZ3	1:A:404:ASN:HB3	2.42	0.54
1:A:356:LYS:HE3	1:A:403:ASN:ND2	2.23	0.54
1:A:368:GLN:HE21	1:A:443:LEU:HD21	1.72	0.54
1:A:17:TRP:CZ3	1:A:122:ARG:HD3	2.42	0.54
1:A:359:LEU:HD21	1:A:386:PHE:CZ	2.42	0.53
1:A:75:HIS:HD2	1:A:76:GLY:O	1.91	0.53
1:A:65:GLN:HG2	1:A:67:ASP:OD1	2.08	0.53
1:A:344:ILE:O	1:A:381:THR:HA	2.08	0.53
1:A:235:PRO:HB2	1:A:331:ASP:HB3	1.92	0.52
1:A:86:LEU:H	1:A:86:LEU:HD12	1.75	0.52
1:A:249:ASP:O	1:A:253:GLU:HG2	2.09	0.52
1:A:76:GLY:HA3	1:A:152:SER:HB3	1.91	0.52
1:A:134:MET:HE2	1:A:134:MET:C	2.35	0.52
1:A:352:THR:HG22	1:A:375:ILE:HG12	1.92	0.51
1:A:17:TRP:CE3	1:A:122:ARG:HD3	2.45	0.51
1:A:43:ASN:O	1:A:46:PRO:HD3	2.11	0.51
1:A:395:ILE:HD13	1:A:422:VAL:HG11	1.92	0.51
1:A:210:ILE:HD11	4:A:959:HOH:O	2.12	0.50
1:A:183:GLN:HG3	1:A:219:GLN:OE1	2.12	0.49
1:A:233:GLU:HG2	1:A:239:LYS:NZ	2.28	0.49
1:A:259:VAL:HG13	4:A:1050:HOH:O	2.12	0.48
1:A:289:ARG:HD3	1:A:289:ARG:HA	1.42	0.47
1:A:409:ASN:ND2	1:A:411:THR:OG1	2.47	0.47
1:A:71:ARG:HH11	1:A:147:GLN:HE21	1.59	0.47
1:A:210:ILE:HA	1:A:211:PRO:HA	1.72	0.47
1:A:228:PRO:HA	1:A:327:LEU:HD13	1.97	0.46
1:A:23:ARG:HD2	1:A:181:SER:O	2.15	0.46
1:A:75:HIS:HB3	1:A:86:LEU:HD21	1.97	0.46
1:A:134:MET:HE2	1:A:135:LEU:HA	1.98	0.45
1:A:18:ALA:HA	1:A:23:ARG:O	2.17	0.45
1:A:198:PHE:CZ	1:A:200:ASP:HB3	2.52	0.44
1:A:228:PRO:O	1:A:234:MET:HE1	2.17	0.44
1:A:134:MET:HE2	1:A:135:LEU:N	2.32	0.44
1:A:171:ARG:HD2	1:A:200:ASP:OD1	2.17	0.44
1:A:238:LYS:HB2	4:A:1050:HOH:O	2.18	0.43
1:A:409:ASN:HB3	1:A:413:PRO:HD2	2.01	0.43
1:A:71:ARG:NH1	1:A:147:GLN:NE2	2.62	0.42
1:A:377:LYS:HG2	4:A:1046:HOH:O	2.19	0.42
1:A:151:HIS:O	1:A:152:SER:HB3	2.19	0.42
1:A:354:GLN:O	1:A:402:TRP:HA	2.20	0.41
1:A:377:LYS:HG3	1:A:380:SER:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:THR:HB	1:A:146:VAL:HG22	2.03	0.40
1:A:350:ARG:HG2	1:A:351:ALA:N	2.36	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	435/450 (97%)	426 (98%)	9 (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	373/382 (98%)	352 (94%)	21 (6%)	19 18

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	GLU
1	A	25	LEU
1	A	31	PRO
1	A	65	GLN

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Mol	Chain	Res	Type
1	A	115	THR
1	A	121	VAL
1	A	134	MET
1	A	153	LEU
1	A	208	PRO
1	A	211	PRO
1	A	213	LEU
1	A	246	VAL
1	A	276	ASN
1	A	323	GLN
1	A	324	LYS
1	A	327	LEU
1	A	334	ASN
1	A	357	VAL
1	A	359	LEU
1	A	409	ASN
1	A	444	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	47	ASN
1	A	75	HIS
1	A	130	GLN
1	A	147	GLN
1	A	183	GLN
1	A	328	ASN
1	A	368	GLN
1	A	406	ASN
1	A	409	ASN
1	A	423	GLN

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 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\#\|Z\| > 2$
2	NAG	A	500	1	14,14,15	0.59	0	17,19,21	0.70	1 (5%)

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	NAG	A	500	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	500	NAG	C2-N2-C7	-2.26	119.87	122.90

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 (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

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^{th} 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	441/450 (98%)	-0.29	4 (0%)	81	83	19, 29, 43, 52	3 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	410	PRO	3.4
1	A	60	GLY	2.9
1	A	404	ASN	2.0
1	A	406	ASN	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 oligosaccharides 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. The B-factors column lists the minimum, median, 95^{th} 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	NAG	A	500	14/15	0.80	0.10	43,45,48,49	0
3	CA	A	501	1/1	0.98	0.05	21,21,21,21	0

6.5 Other polymers (i)

There are no such residues in this entry.