



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4V2A / pdb_00004v2a
Title : human Unc5A ectodomain
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Deposited on : 2014-10-08
Resolution : 2.40 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

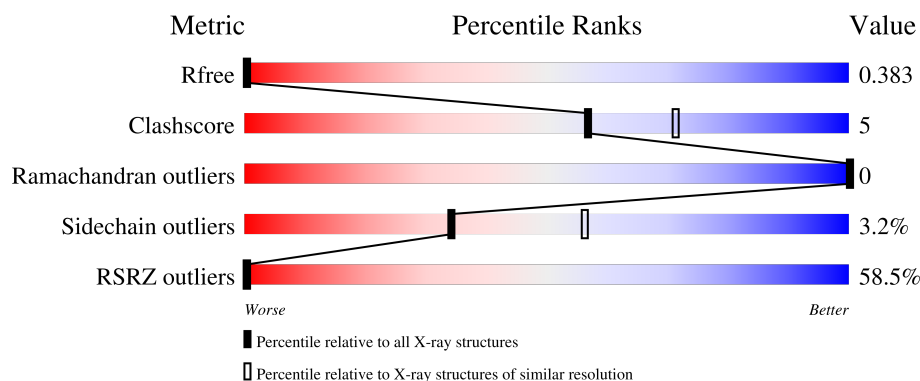
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	303	48% 73% 8% 18%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1995 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.

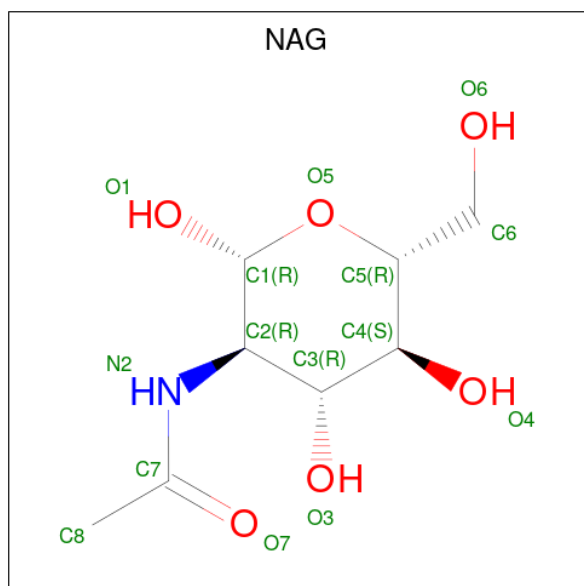
- Molecule 1 is a protein called NETRIN RECEPTOR UNC5A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	248	1962	1230	350	369	13	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	97	ASN	SER	conflict	UNP Q6ZN44

- 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

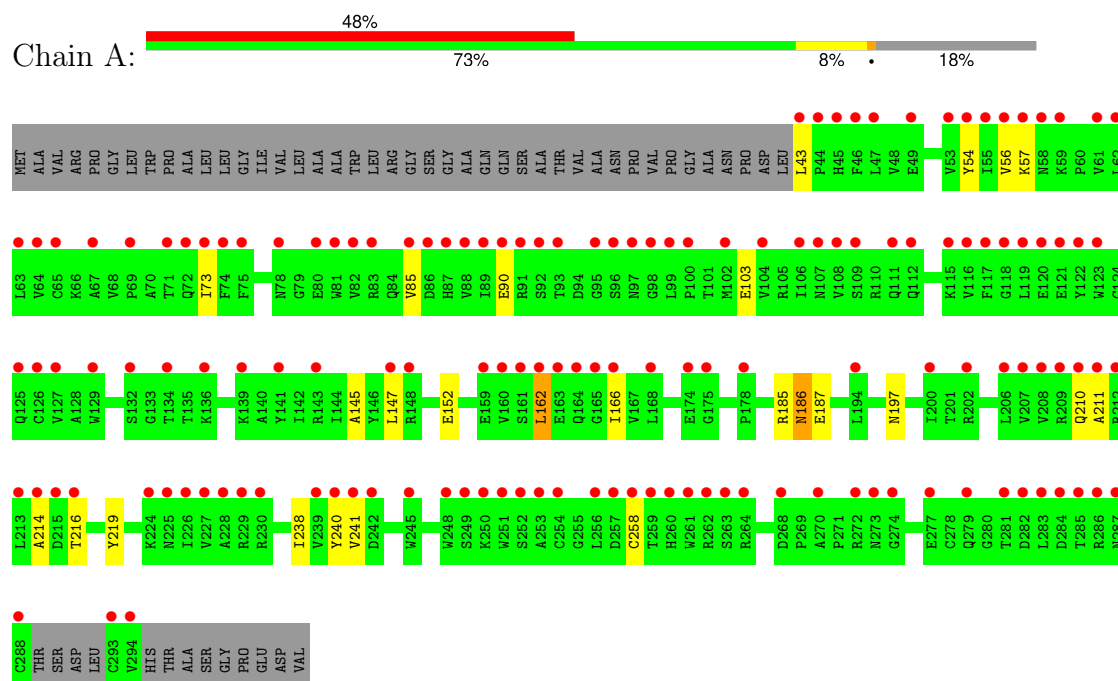
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	19	Total	O	0	0
			19	19		

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: NETRIN RECEPTOR UNC5A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	25.83Å 87.77Å 133.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.88 – 2.40 43.88 – 2.40	Depositor EDS
% Data completeness (in resolution range)	89.9 (43.88-2.40) 89.9 (43.88-2.40)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.39Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.327 , 0.344 0.351 , 0.383	Depositor DCC
R_{free} test set	544 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	57.5	Xtriage
Anisotropy	0.555	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 28.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	1995	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.91% 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: 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	0.68	0/2008	1.07	3/2735 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	187	GLU	N-CA-C	7.44	119.47	111.36
1	A	162	LEU	N-CA-C	5.97	117.79	111.28
1	A	186	ASN	CB-CA-C	-5.00	110.83	116.63

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	1962	0	1903	18	0
2	A	14	0	13	0	0
3	A	19	0	0	0	0
All	All	1995	0	1916	18	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 (18) 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:162:LEU:HD21	1:A:241:VAL:HG22	1.27	1.10
1:A:185:ARG:HH21	1:A:214:ALA:HA	1.32	0.94
1:A:185:ARG:NH2	1:A:214:ALA:HA	1.84	0.92
1:A:162:LEU:CD2	1:A:241:VAL:HG22	2.07	0.82
1:A:162:LEU:HD21	1:A:241:VAL:CG2	2.15	0.71
1:A:162:LEU:HD13	1:A:211:ALA:HB3	1.83	0.60
1:A:162:LEU:HD22	1:A:240:TYR:O	2.11	0.51
1:A:162:LEU:CD2	1:A:240:TYR:O	2.59	0.51
1:A:185:ARG:HH21	1:A:214:ALA:CA	2.15	0.50
1:A:162:LEU:HD23	1:A:241:VAL:HA	1.92	0.49
1:A:54:TYR:HB3	1:A:145:ALA:HB2	1.93	0.49
1:A:162:LEU:HD13	1:A:211:ALA:CB	2.44	0.46
1:A:185:ARG:O	1:A:186:ASN:HB2	2.16	0.45
1:A:185:ARG:HG3	1:A:219:TYR:CE1	2.51	0.45
1:A:56:VAL:O	1:A:57:LYS:HB2	2.16	0.45
1:A:197:ASN:HD21	1:A:210:GLN:H	1.65	0.45
1:A:216:THR:HG22	1:A:238:ILE:HA	2.00	0.44
1:A:90:GLU:HB2	1:A:103:GLU:HB3	2.02	0.42

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	244/303 (80%)	229 (94%)	15 (6%)	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	218/259 (84%)	211 (97%)	7 (3%)	34 56

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	LEU
1	A	73	ILE
1	A	85	VAL
1	A	147	LEU
1	A	152	GLU
1	A	166	ILE
1	A	258	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	HIS
1	A	78	ASN
1	A	153	GLN
1	A	197	ASN
1	A	273	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 oligosaccharides 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	NAG	A	1295	1	14,14,15	0.50	0	17,19,21	1.10	2 (11%)

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	1295	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1295	NAG	C4-C3-C2	-2.35	107.57	111.02
2	A	1295	NAG	C8-C7-N2	2.14	119.66	116.12

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, 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	248/303 (81%)	2.33	145 (58%) 0 0	39, 84, 120, 168	0

All (145) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	294	VAL	8.5
1	A	119	LEU	6.0
1	A	273	ASN	5.9
1	A	73	ILE	5.2
1	A	213	LEU	5.1
1	A	212	ARG	5.0
1	A	174	GLU	4.9
1	A	256	LEU	4.9
1	A	293	CYS	4.9
1	A	89	ILE	4.8
1	A	214	ALA	4.8
1	A	288	CYS	4.7
1	A	43	LEU	4.7
1	A	216	THR	4.5
1	A	283	LEU	4.4
1	A	132	SER	4.3
1	A	272	ARG	4.3
1	A	97	ASN	4.1
1	A	166	ILE	4.1
1	A	211	ALA	4.0
1	A	215	ASP	4.0
1	A	116	VAL	3.9
1	A	208	VAL	3.9
1	A	248	TRP	3.9
1	A	264	ARG	3.8
1	A	162	LEU	3.8
1	A	253	ALA	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	209	ARG	3.7
1	A	159	GLU	3.7
1	A	106	ILE	3.7
1	A	270	ALA	3.6
1	A	117	PHE	3.5
1	A	282	ASP	3.5
1	A	88	VAL	3.5
1	A	112	GLN	3.5
1	A	259	THR	3.5
1	A	49	GLU	3.4
1	A	129	TRP	3.4
1	A	59	LYS	3.4
1	A	72	GLN	3.3
1	A	98	GLY	3.3
1	A	164	GLN	3.3
1	A	287	ASN	3.3
1	A	57	LYS	3.3
1	A	207	VAL	3.3
1	A	75	PHE	3.2
1	A	122	TYR	3.2
1	A	92	SER	3.2
1	A	111	GLN	3.2
1	A	109	SER	3.2
1	A	161	SER	3.1
1	A	224	LYS	3.1
1	A	200	ILE	3.1
1	A	45	HIS	3.1
1	A	251	TRP	3.1
1	A	165	GLY	3.1
1	A	262	ARG	3.1
1	A	83	ARG	3.0
1	A	274	GLY	3.0
1	A	260	HIS	3.0
1	A	85	VAL	3.0
1	A	163	GLU	3.0
1	A	107	ASN	3.0
1	A	125	GLN	3.0
1	A	56	VAL	2.9
1	A	82	VAL	2.9
1	A	99	LEU	2.9
1	A	210	GLN	2.9
1	A	115	LYS	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	47	LEU	2.9
1	A	46	PHE	2.9
1	A	120	GLU	2.9
1	A	143	ARG	2.9
1	A	263	SER	2.8
1	A	225	ASN	2.8
1	A	258	CYS	2.8
1	A	53	VAL	2.8
1	A	93	THR	2.8
1	A	134	THR	2.7
1	A	90	GLU	2.7
1	A	254	CYS	2.7
1	A	74	PHE	2.7
1	A	194	LEU	2.7
1	A	91	ARG	2.7
1	A	227	VAL	2.7
1	A	279	GLN	2.7
1	A	69	PRO	2.7
1	A	147	LEU	2.7
1	A	55	ILE	2.6
1	A	54	TYR	2.6
1	A	281	THR	2.6
1	A	71	THR	2.6
1	A	245	TRP	2.6
1	A	65	CYS	2.6
1	A	81	TRP	2.5
1	A	286	ARG	2.5
1	A	257	ASP	2.5
1	A	118	GLY	2.5
1	A	277	GLU	2.5
1	A	148	ARG	2.5
1	A	285	THR	2.5
1	A	86	ASP	2.4
1	A	226	ILE	2.4
1	A	206	LEU	2.4
1	A	141	TYR	2.4
1	A	178	PRO	2.4
1	A	284	ASP	2.4
1	A	78	ASN	2.4
1	A	249	SER	2.3
1	A	229	ARG	2.3
1	A	242	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	126	CYS	2.3
1	A	80	GLU	2.3
1	A	108	VAL	2.3
1	A	44	PRO	2.3
1	A	175	GLY	2.3
1	A	160	VAL	2.3
1	A	95	GLY	2.3
1	A	250	LYS	2.3
1	A	127	VAL	2.3
1	A	123	TRP	2.2
1	A	104	VAL	2.2
1	A	58	ASN	2.2
1	A	168	LEU	2.2
1	A	239	VAL	2.2
1	A	67	ALA	2.2
1	A	61	VAL	2.2
1	A	241	VAL	2.2
1	A	139	LYS	2.2
1	A	96	SER	2.2
1	A	202	ARG	2.2
1	A	100	PRO	2.2
1	A	63	LEU	2.1
1	A	268	ASP	2.1
1	A	228	ALA	2.1
1	A	62	LEU	2.1
1	A	121	GLU	2.1
1	A	230	ARG	2.1
1	A	240	TYR	2.1
1	A	136	LYS	2.1
1	A	87	HIS	2.1
1	A	102	MET	2.1
1	A	261	TRP	2.1
1	A	252	SER	2.1
1	A	64	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 [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($\text{\AA}^2$)	Q<0.9
2	NAG	A	1295	14/15	0.84	0.13	50,51,52,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.