



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 14, 2021 – 06:07 PM JST

PDB ID : 7EAL  
Title : The structure of the A20-Binding Inhibitor of NF- $\kappa$ B 1 in complex with di-ubiquitin  
Authors : Lo, Y.C.; Lin, S.C.  
Deposited on : 2021-03-07  
Resolution : 2.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.22
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)	:	2.22

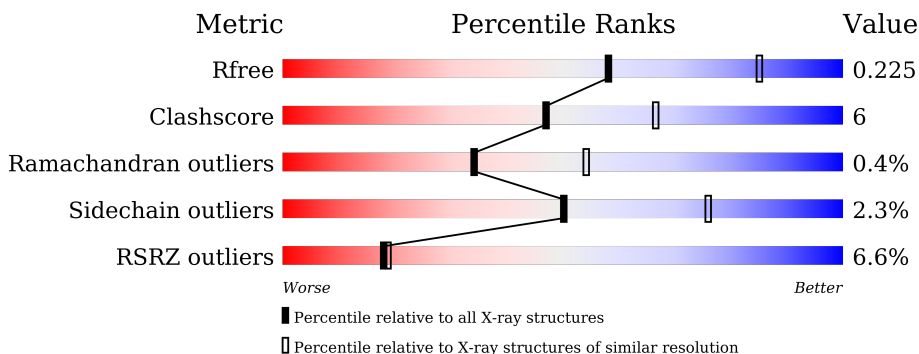
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	152	<div> <div>3%</div> <div>80%</div> <div>19%</div> <div>.</div> </div>
1	D	152	<div> <div>4%</div> <div>88%</div> <div>11%</div> <div>.</div> </div>
2	B	109	<div> <div>6%</div> <div>39%</div> <div>17%</div> <div>.</div> <div>43%</div> </div>
2	C	109	<div> <div>6%</div> <div>41%</div> <div>13%</div> <div>..</div> <div>44%</div> </div>
2	E	109	<div> <div>2%</div> <div>54%</div> <div>6%</div> <div>.</div> <div>40%</div> </div>
2	F	109	<div> <div>10%</div> <div>48%</div> <div>12%</div> <div>.</div> <div>39%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4579 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 ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	152	Total	C	N	O	S	0	0	0
			1202	756	210	234	2			
1	D	152	Total	C	N	O	S	0	0	0
			1202	756	210	234	2			

- Molecule 2 is a protein called TNFAIP3-interacting protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	62	Total	C	N	O	S	0	0	0
			529	326	95	107	1			
2	C	61	Total	C	N	O	S	0	0	0
			520	320	93	106	1			
2	E	65	Total	C	N	O	S	0	0	0
			556	344	101	110	1			
2	F	66	Total	C	N	O	S	0	0	0
			553	342	101	109	1			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	506	THR	ALA	conflict	UNP Q15025
C	506	THR	ALA	conflict	UNP Q15025
E	506	THR	ALA	conflict	UNP Q15025
F	506	THR	ALA	conflict	UNP Q15025

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



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

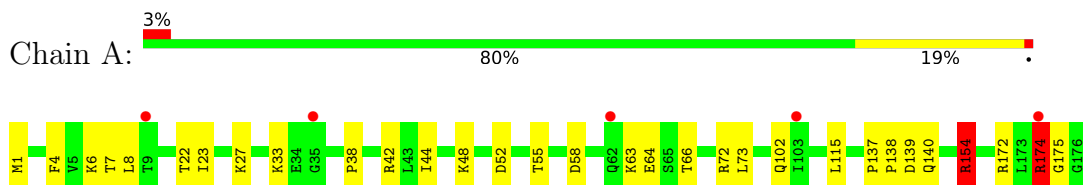
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	O	0	0
			3	3		
4	D	7	Total	O	0	0
			7	7		
4	E	1	Total	O	0	0
			1	1		

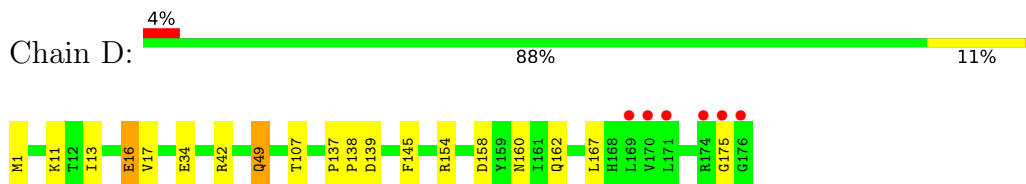
### 3 Residue-property plots [i](#)

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.

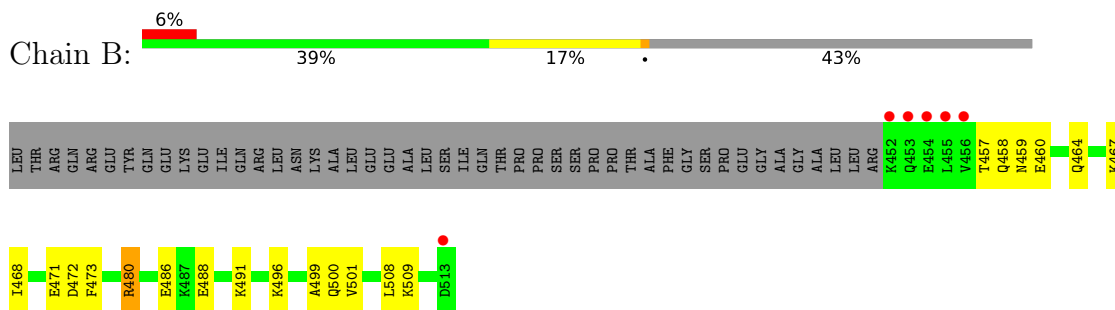
- Molecule 1: ubiquitin



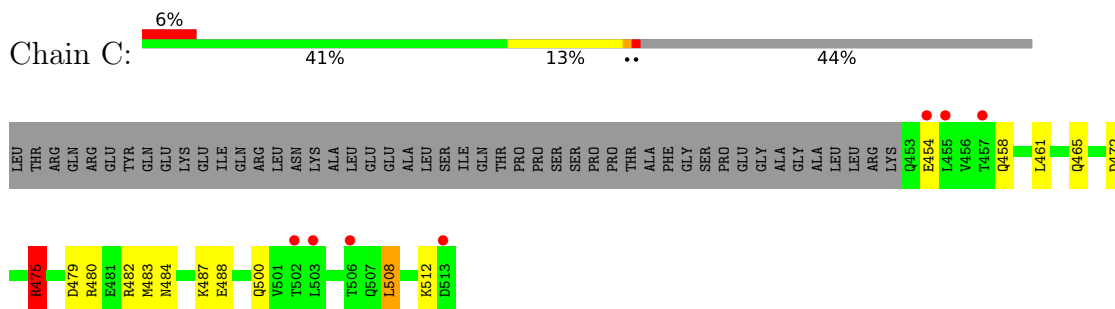
- Molecule 1: ubiquitin



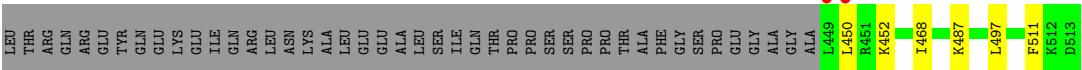
- Molecule 2: TNFAIP3-interacting protein 1



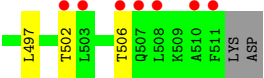
- Molecule 2: TNFAIP3-interacting protein 1



- Molecule 2: TNFAIP3-interacting protein 1



● Molecule 2: TNFAIP3-interacting protein 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.75Å 59.99Å 84.06Å 90.00° 109.71° 90.00°	Depositor
Resolution (Å)	23.56 – 2.50 23.56 – 2.48	Depositor EDS
% Data completeness (in resolution range)	98.0 (23.56-2.50) 93.1 (23.56-2.48)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.77 (at 2.47Å)	Xtriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, $R_{free}$	0.184 , 0.224 0.183 , 0.225	Depositor DCC
$R_{free}$ test set	1301 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	38.7	Xtriage
Anisotropy	0.193	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 65.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.015 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4579	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.45% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

### 5.1 Standard geometry

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

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	0.43	0/1215	0.67	3/1635 (0.2%)
1	D	0.53	2/1215 (0.2%)	0.59	0/1635
2	B	0.43	0/531	0.54	0/704
2	C	0.55	1/522 (0.2%)	0.84	2/693 (0.3%)
2	E	0.51	1/558 (0.2%)	0.53	0/740
2	F	0.52	0/555	0.84	2/737 (0.3%)
All	All	0.49	4/4596 (0.1%)	0.66	7/6144 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	16	GLU	CD-OE2	-9.52	1.15	1.25
2	C	475	ARG	CZ-NH1	-7.23	1.23	1.33
1	D	16	GLU	CD-OE1	6.18	1.32	1.25
2	E	511	PHE	CE1-CZ	5.04	1.47	1.37

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	475	ARG	NE-CZ-NH2	-15.95	112.33	120.30
2	C	475	ARG	NE-CZ-NH1	15.31	127.95	120.30
1	A	154	ARG	CG-CD-NE	-9.10	92.70	111.80
2	F	475	ARG	NH1-CZ-NH2	7.56	127.72	119.40
1	A	48	LYS	CD-CE-NZ	-6.93	95.76	111.70

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-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 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	1202	0	1256	21	1
1	D	1202	0	1256	12	5
2	B	529	0	537	16	0
2	C	520	0	524	9	5
2	E	556	0	572	4	1
2	F	553	0	568	10	0
3	D	6	0	8	2	0
4	A	3	0	0	0	0
4	D	7	0	0	0	0
4	E	1	0	0	0	0
All	All	4579	0	4721	58	6

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 6.

The worst 5 of 58 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:4:PHE:HB2	1:A:66:THR:HG22	1.49	0.91
1:D:42:ARG:HG2	2:E:468:ILE:HD11	1.59	0.83
2:C:479:ASP:OD2	2:C:482:ARG:NH2	2.13	0.81
2:E:487:LYS:NZ	2:F:486:GLU:OE2	2.14	0.80
2:C:508:LEU:HD21	2:C:512:LYS:HD3	1.71	0.71

The worst 5 of 6 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:475:ARG:NH2	1:D:16:GLU:CD[2_956]	1.53	0.67
2:C:475:ARG:NH2	1:D:16:GLU:CG[2_956]	1.62	0.58
2:C:475:ARG:NH2	1:D:16:GLU:OE2[2_956]	1.85	0.35
2:C:475:ARG:CZ	1:D:16:GLU:OE2[2_956]	1.92	0.28
2:C:475:ARG:NH1	1:D:16:GLU:OE2[2_956]	2.10	0.10

## 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	150/152 (99%)	148 (99%)	0	2 (1%)	12	21
1	D	150/152 (99%)	148 (99%)	2 (1%)	0	100	100
2	B	60/109 (55%)	58 (97%)	2 (3%)	0	100	100
2	C	59/109 (54%)	58 (98%)	1 (2%)	0	100	100
2	E	63/109 (58%)	63 (100%)	0	0	100	100
2	F	64/109 (59%)	63 (98%)	1 (2%)	0	100	100
All	All	546/740 (74%)	538 (98%)	6 (1%)	2 (0%)	34	54

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	174	ARG
1	A	175	GLY

### 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	136/136 (100%)	133 (98%)	3 (2%)	52	77
1	D	136/136 (100%)	135 (99%)	1 (1%)	84	94
2	B	60/99 (61%)	59 (98%)	1 (2%)	60	82
2	C	59/99 (60%)	55 (93%)	4 (7%)	16	30
2	E	63/99 (64%)	62 (98%)	1 (2%)	62	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	F	61/99 (62%)	59 (97%)	2 (3%)	38	64
All	All	515/668 (77%)	503 (98%)	12 (2%)	50	76

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	508	LEU
1	D	49	GLN
2	F	475	ARG
2	E	450	LEU
2	B	480	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	149	GLN
2	F	505	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules 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 monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

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	$\# Z  > 2$
3	GOL	D	201	-	5,5,5	0.62	0	5,5,5	1.41	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
3	GOL	D	201	-	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	201	GOL	O1-C1-C2-O2
3	D	201	GOL	O1-C1-C2-C3
3	D	201	GOL	C1-C2-C3-O3
3	D	201	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	201	GOL	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	152/152 (100%)	0.23	5 (3%)	46	50	30, 53, 82, 97	0
1	D	152/152 (100%)	0.15	6 (3%)	39	42	29, 42, 69, 114	0
2	B	62/109 (56%)	0.53	6 (9%)	7	7	32, 63, 95, 113	0
2	C	61/109 (55%)	0.73	7 (11%)	4	4	30, 63, 91, 107	0
2	E	65/109 (59%)	0.39	2 (3%)	49	52	30, 57, 97, 121	0
2	F	66/109 (60%)	0.84	11 (16%)	1	1	32, 61, 96, 114	0
All	All	558/740 (75%)	0.39	37 (6%)	18	19	29, 52, 91, 121	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	176	GLY	10.2
2	E	449	LEU	10.0
2	F	446	ALA	6.2
2	B	452	LYS	5.9
2	F	449	LEU	5.5

### 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, 95<sup>th</sup> 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
3	GOL	D	201	6/6	0.94	0.23	42,51,55,57	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.