



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:49 PM UTC

PDB ID : 1BCD / pdb\_00001bcd  
Title : X-RAY CRYSTALLOGRAPHIC STRUCTURE OF A COMPLEX BETWEEN HUMAN CARBONIC ANHYDRASE II AND A NEW TOPICAL INHIBITOR, TRIFLUOROMETHANE SULPHONAMIDE  
Authors : Hakansson, K.; Liljas, A.  
Deposited on : 1993-08-31  
Resolution : 1.90 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](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.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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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)  
Xtrriage (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

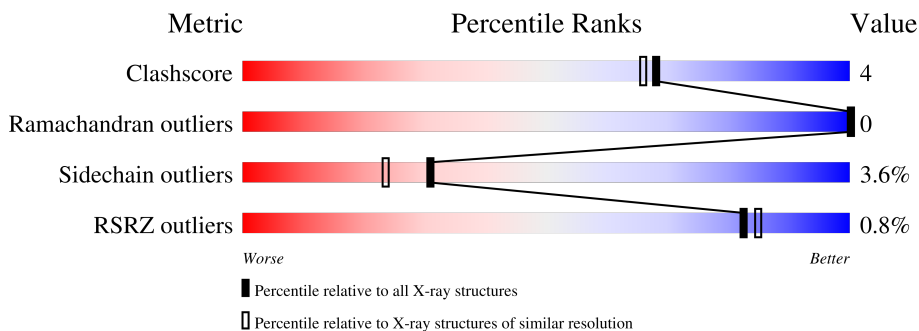
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	259	

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2303 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.

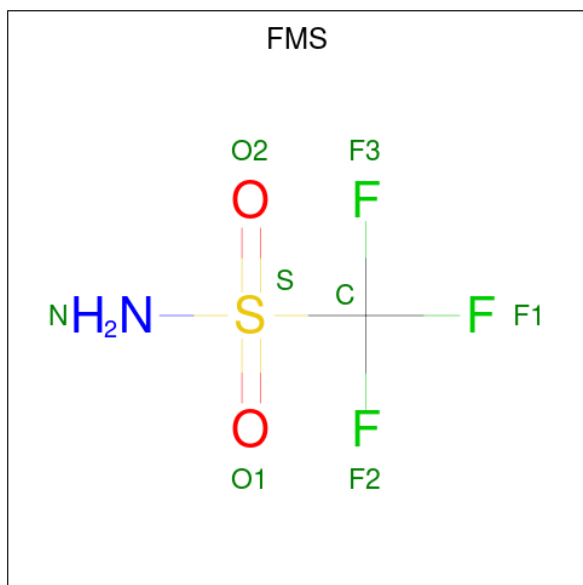
- Molecule 1 is a protein called CARBONIC ANHYDRASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	258	2079	1333	360	384	2	0	4	0

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is TRIFLUOROMETHANE SULFONAMIDE (CCD ID: FMS) (formula: CH<sub>2</sub>F<sub>3</sub>NO<sub>2</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	F	N	O			S
3	A	1	8	1	3	1	2	1	0	0

- Molecule 4 is water.

<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
4	A	215	Total 215	O 215	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: CARBONIC ANHYDRASE II



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	42.70Å 41.70Å 73.00Å 90.00° 104.60° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.90 70.64 – 1.94	Depositor EDS
% Data completeness (in resolution range)	(Not available) ((Not available)-1.90) 68.9 (70.64-1.94)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.09 (at 1.93Å)	Xtrriage
Refinement program	PROFFT	Depositor
R, $R_{free}$	0.154 , (Not available) 0.151 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	12.0	Xtrriage
Anisotropy	0.270	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 72.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.046 for h,-k,-h-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	2303	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.56% 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 [i](#)

### 5.1 Standard geometry [i](#)

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

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	1.46	6/2161 (0.3%)	2.09	83/2931 (2.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	151	GLY	C-N	-5.79	1.25	1.33
1	A	205	GLU	CA-C	-5.75	1.47	1.53
1	A	119	HIS	C-O	5.73	1.30	1.24
1	A	55	THR	CA-CB	5.33	1.62	1.53
1	A	253	ASN	C-O	5.17	1.30	1.24
1	A	120	LEU	N-CA	5.02	1.52	1.46

All (83) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	237	PRO	CB-CA-C	10.47	124.97	111.46
1	A	182	ARG	NE-CZ-NH1	9.02	130.52	121.50
1	A	101	ASP	CA-CB-CG	8.16	120.76	112.60
1	A	41	ASP	CB-CA-C	8.02	120.76	110.34
1	A	230	ASN	CA-CB-CG	8.00	120.60	112.60
1	A	226	PHE	CA-CB-CG	8.00	121.80	113.80
1	A	254	ARG	NE-CZ-NH2	-7.77	112.20	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	58	ARG	N-CA-CB	-7.72	99.59	111.56
1	A	94	HIS	CA-CB-CG	-7.52	106.28	113.80
1	A	96	HIS	CA-CB-CG	-7.42	106.39	113.80
1	A	221	GLU	CG-CD-OE1	7.32	135.23	118.40
1	A	92	GLN	OE1-CD-NE2	-7.31	115.29	122.60
1	A	68	VAL	CA-C-O	-7.16	112.78	120.59
1	A	11	ASN	OD1-CG-ND2	-7.16	115.44	122.60
1	A	98	GLY	O-C-N	7.12	129.79	123.59
1	A	87	THR	O-C-N	7.10	131.29	123.27
1	A	85	ASP	CA-CB-CG	7.06	119.66	112.60
1	A	254	ARG	NH1-CZ-NH2	7.02	128.43	119.30
1	A	206	CYS	N-CA-CB	-6.97	99.70	111.27
1	A	192	TRP	N-CA-CB	6.81	121.65	110.69
1	A	180	ASP	CB-CA-C	6.52	116.63	110.17
1	A	67	ASN	CA-C-O	-6.44	113.88	120.71
1	A	107	HIS	N-CA-CB	6.36	119.33	110.17
1	A	44	LEU	O-C-N	6.34	130.49	123.01
1	A	182	ARG	NH1-CZ-NH2	-6.32	111.08	119.30
1	A	248	ALA	O-C-N	-6.30	115.12	122.87
1	A	144	LEU	N-CA-CB	-6.19	100.33	110.42
1	A	68	VAL	N-CA-C	-6.16	99.00	107.99
1	A	26	GLU	CB-CG-CD	6.10	122.97	112.60
1	A	236	GLU	CA-CB-CG	6.08	126.26	114.10
1	A	248	ALA	CB-CA-C	6.06	119.78	109.72
1	A	20	PHE	O-C-N	6.05	126.82	121.37
1	A	203	LEU	N-CA-CB	-5.96	103.07	112.08
1	A	130	ASP	CA-CB-CG	5.95	118.55	112.60
1	A	27	ARG	CB-CG-CD	5.91	124.89	111.30
1	A	253	ASN	N-CA-CB	-5.88	100.56	110.49
1	A	217	SER	CB-CA-C	-5.87	99.62	109.48
1	A	103	GLN	OE1-CD-NE2	-5.86	116.74	122.60
1	A	191	TYR	CA-C-N	5.86	131.42	122.93
1	A	191	TYR	C-N-CA	5.86	131.42	122.93
1	A	133	LYS	CB-CG-CD	5.84	124.73	111.30
1	A	219	SER	CA-C-O	5.73	128.48	121.72
1	A	236	GLU	CB-CG-CD	5.61	122.14	112.60
1	A	237	PRO	CA-C-N	5.55	129.24	121.24
1	A	237	PRO	C-N-CA	5.55	129.24	121.24
1	A	227	ARG	CD-NE-CZ	5.54	132.16	124.40
1	A	95	PHE	CA-CB-CG	5.53	119.33	113.80
1	A	122	HIS	CA-CB-CG	5.51	119.31	113.80
1	A	74	GLN	OE1-CD-NE2	5.51	128.11	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	97	TRP	CA-C-N	-5.49	116.63	122.67
1	A	97	TRP	C-N-CA	-5.49	116.63	122.67
1	A	91	ILE	CA-CB-CG2	5.49	119.83	110.50
1	A	238	GLU	CB-CG-CD	5.45	121.86	112.60
1	A	198	LEU	N-CA-C	-5.42	102.86	110.50
1	A	67	ASN	CA-CB-CG	5.42	118.02	112.60
1	A	14[A]	GLU	CA-C-O	5.39	126.06	119.05
1	A	14[B]	GLU	CA-C-O	5.39	126.06	119.05
1	A	197	SER	N-CA-C	5.37	116.44	108.86
1	A	201	PRO	N-CA-C	-5.36	104.17	110.70
1	A	215	PRO	CA-C-N	-5.34	114.76	122.45
1	A	215	PRO	C-N-CA	-5.34	114.76	122.45
1	A	244	ASN	OD1-CG-ND2	-5.34	117.26	122.60
1	A	175	ASP	N-CA-C	-5.32	102.52	110.23
1	A	158	GLN	N-CA-C	5.30	117.06	111.28
1	A	89	ARG	NE-CZ-NH2	-5.29	114.44	119.20
1	A	119	HIS	ND1-CE1-NE2	-5.28	103.12	108.40
1	A	37	THR	CA-CB-CG2	5.27	119.45	110.50
1	A	238	GLU	CG-CD-OE2	5.24	130.44	118.40
1	A	151	GLY	N-CA-C	-5.20	100.86	113.18
1	A	27	ARG	CA-CB-CG	5.17	124.44	114.10
1	A	175	ASP	CB-CG-OD1	5.17	130.28	118.40
1	A	145	GLY	O-C-N	-5.16	119.05	123.80
1	A	232	ASN	CA-C-O	5.16	127.85	121.87
1	A	213	LYS	CB-CG-CD	5.14	123.13	111.30
1	A	236	GLU	CG-CD-OE1	5.14	130.22	118.40
1	A	200	THR	O-C-N	5.14	125.72	121.35
1	A	146	ILE	CB-CG1-CD1	5.10	124.52	113.80
1	A	207	VAL	N-CA-C	5.07	115.87	108.53
1	A	239	GLU	CA-CB-CG	5.05	124.20	114.10
1	A	151	GLY	CA-C-N	5.04	128.37	120.75
1	A	151	GLY	C-N-CA	5.04	128.37	120.75
1	A	96	HIS	CA-C-O	-5.04	114.73	120.32
1	A	248	ALA	CA-C-O	5.01	126.70	121.19

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	89	ARG	Sidechain

## 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	2079	0	2021	15	0
2	A	1	0	0	0	0
3	A	8	0	2	0	0
4	A	215	0	0	0	0
All	All	2303	0	2023	15	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 4.

All (15) 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:236:GLU:HB3	1:A:237:PRO:HD2	1.82	0.61
1:A:59:ILE:HG12	1:A:167:ILE:HD13	1.90	0.53
1:A:134:ALA:O	1:A:140:GLY:HA3	2.12	0.49
1:A:30:PRO:HG3	1:A:106:GLU:HB3	1.96	0.46
1:A:45:LYS:O	1:A:82:GLY:HA2	2.16	0.46
1:A:255:GLN:HG2	1:A:257:LYS:HE2	1.97	0.46
1:A:47:LEU:HD21	1:A:210:ILE:HD13	1.97	0.45
1:A:201:PRO:HA	1:A:203:LEU:HG	1.98	0.44
1:A:128:TYR:CZ	1:A:137:GLN:HG3	2.53	0.43
1:A:106:GLU:OE1	1:A:119:HIS:HE1	2.02	0.42
1:A:128:TYR:CE1	1:A:137:GLN:HG3	2.55	0.42
1:A:17:HIS:CG	1:A:24:LYS:HE2	2.55	0.41
1:A:4[B]:HIS:CG	1:A:5:TRP:H	2.38	0.41
1:A:194:TYR:HA	1:A:195:PRO:HD3	1.86	0.41
1:A:243:ASP:HA	1:A:245:TRP:CD1	2.56	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	260/259 (100%)	249 (96%)	11 (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	227/224 (101%)	219 (96%)	8 (4%)	32	24

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	THR
1	A	39	LYS
1	A	60	LEU
1	A	201	PRO
1	A	202	PRO
1	A	213	LYS
1	A	253	ASN
1	A	255	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	255	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$
3	FMS	A	500	2	5,7,7	1.19	0	9,12,12	2.31	3 (33%)

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	FMS	A	500	2	-	0/9/9/9	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	500	FMS	F2-C-S	-4.41	105.08	110.56
3	A	500	FMS	O1-S-C	3.51	110.02	104.09
3	A	500	FMS	O2-S-O1	-3.09	114.26	120.39

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 [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	258/259 (99%)	-0.50	2 (0%) 82 85	2, 11, 24, 31	5 (1%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	3	HIS	4.3
1	A	253	ASN	2.9

### 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 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, 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(Å <sup>2</sup> )	Q<0.9
3	FMS	A	500	8/8	0.98	0.05	5,6,7,9	0
2	ZN	A	262	1/1	1.00	0.01	6,6,6,6	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.