



# wwPDB X-ray Structure Validation Summary Report (i)

Feb 28, 2014 – 03:23 PM GMT

PDB ID : 2B2X  
Title : VLA1 RdeltaH I-domain complexed with a quadruple mutant of the AQC2 Fab  
Authors : Clark, L.A.; Boriack-Sjodin, P.A.; Eldredge, J.; Fitch, C.; Friedman, B.; Hanf, K.J.; Jarpe, M.; Liparoto, S.F.; Li, Y.; Lugovskoy, A.  
Deposited on : 2005-09-19  
Resolution : 2.20 Å(reported)

This is a wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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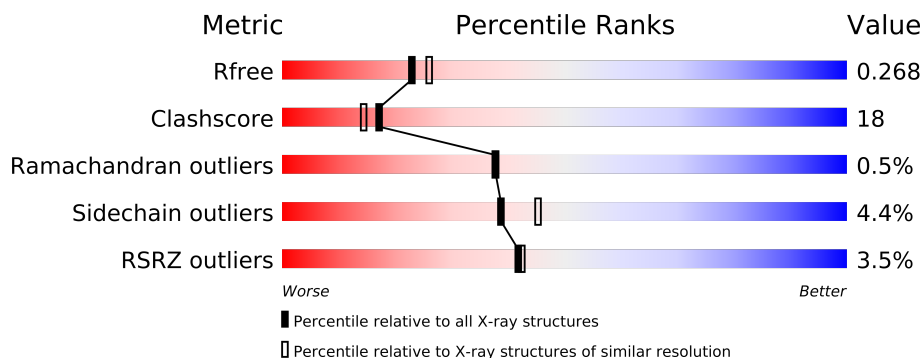
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 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 2.20 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	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)

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  $\geq 3$ , 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	223	
1	B	223	
2	H	226	
2	I	226	
3	L	213	
3	M	213	

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9537 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 Integrin alpha-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	0	0
			1490	940	258	288	4			
1	B	176	Total	C	N	O	S	0	0	0
			1397	884	240	270	3			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	125	GLY	-	CLONING ARTIFACT	UNP P18614
A	126	SER	-	CLONING ARTIFACT	UNP P18614
A	217	VAL	GLY	ENGINEERED	UNP P18614
A	218	GLN	ARG	ENGINEERED	UNP P18614
A	219	ARG	GLN	ENGINEERED	UNP P18614
A	222	ARG	LEU	ENGINEERED	UNP P18614
A	341	LEU	-	CLONING ARTIFACT	UNP P18614
A	342	GLU	-	CLONING ARTIFACT	UNP P18614
A	343	ARG	-	CLONING ARTIFACT	UNP P18614
A	344	PRO	-	CLONING ARTIFACT	UNP P18614
A	345	HIS	-	CLONING ARTIFACT	UNP P18614
A	346	ARG	-	CLONING ARTIFACT	UNP P18614
A	347	ASP	-	CLONING ARTIFACT	UNP P18614
B	125	GLY	-	CLONING ARTIFACT	UNP P18614
B	126	SER	-	CLONING ARTIFACT	UNP P18614
B	217	VAL	GLY	ENGINEERED	UNP P18614
B	218	GLN	ARG	ENGINEERED	UNP P18614
B	219	ARG	GLN	ENGINEERED	UNP P18614
B	222	ARG	LEU	ENGINEERED	UNP P18614
B	341	LEU	-	CLONING ARTIFACT	UNP P18614
B	342	GLU	-	CLONING ARTIFACT	UNP P18614
B	343	ARG	-	CLONING ARTIFACT	UNP P18614
B	344	PRO	-	CLONING ARTIFACT	UNP P18614
B	345	HIS	-	CLONING ARTIFACT	UNP P18614
B	346	ARG	-	CLONING ARTIFACT	UNP P18614

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Chain	Residue	Modelled	Actual	Comment	Reference
B	347	ASP	-	CLONING ARTIFACT	UNP P18614

- Molecule 2 is a protein called Antibody AQC2 Fab.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	210	Total	C	N	O	S	0	0	0
			1575	1000	260	308	7			
2	I	210	Total	C	N	O	S	0	0	0
			1575	1000	260	308	7			

- Molecule 3 is a protein called Antibody AQC2 Fab.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	210	Total	C	N	O	S	0	0	0
			1636	1026	274	330	6			
3	M	210	Total	C	N	O	S	0	0	0
			1636	1026	274	330	6			

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Mg	0	0
			1	1		
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is water.

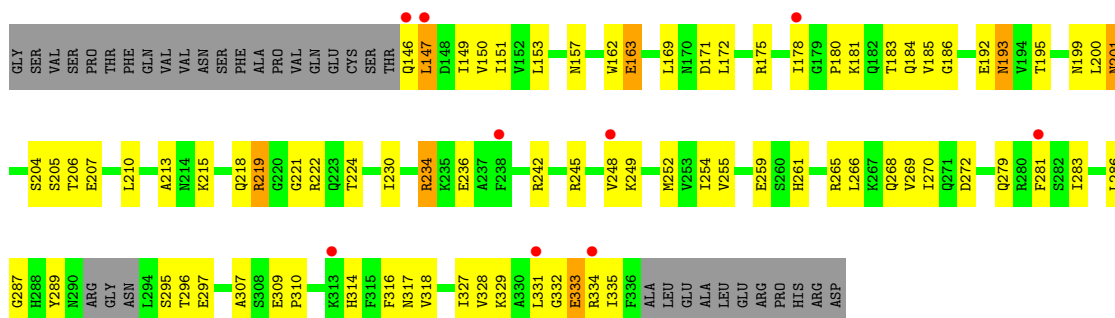
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	13	Total	O	0	0
			13	13		
5	B	5	Total	O	0	0
			5	5		
5	H	73	Total	O	0	0
			73	73		
5	I	77	Total	O	0	0
			77	77		
5	L	30	Total	O	0	0
			30	30		
5	M	28	Total	O	0	0
			28	28		

### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

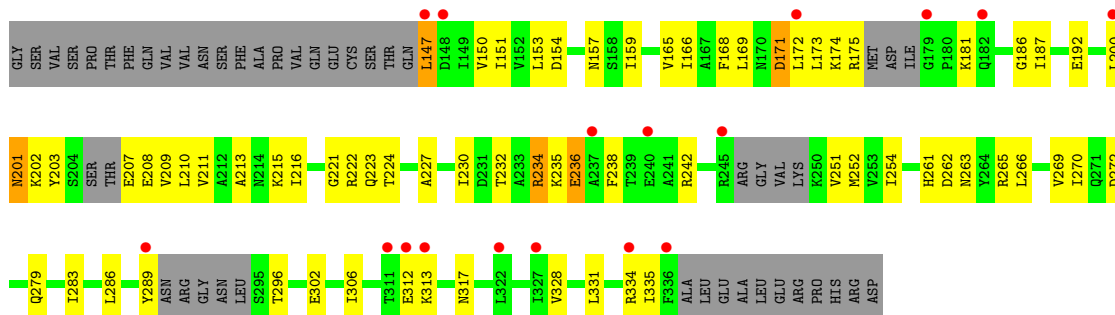
#### • Molecule 1: Integrin alpha-1

Chain A:



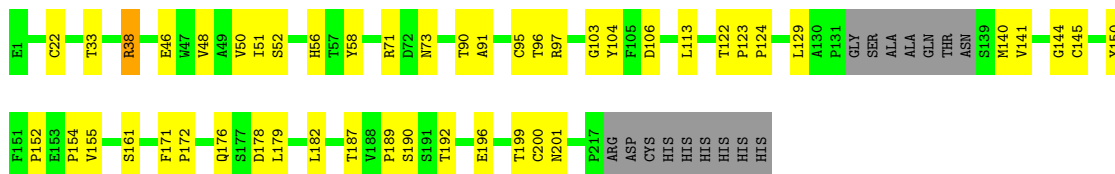
#### • Molecule 1: Integrin alpha-1

Chain B:



#### • Molecule 2: Antibody AQC2 Fab

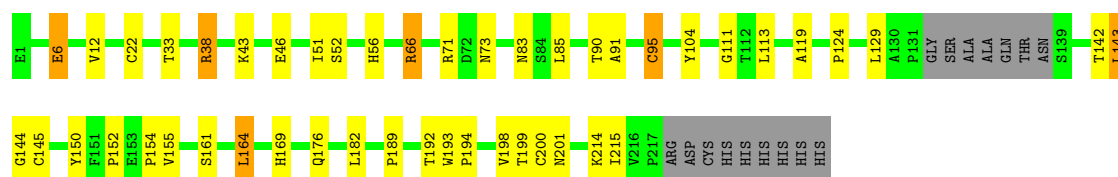
Chain H:



#### • Molecule 2: Antibody AQC2 Fab

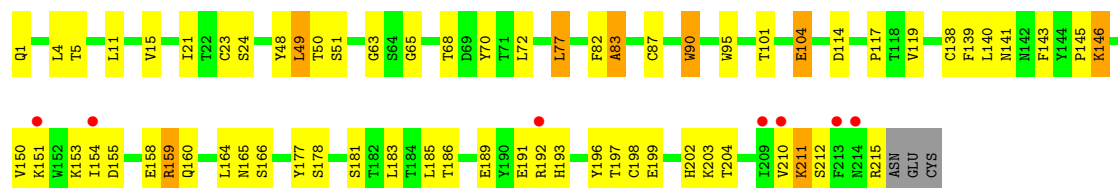
Chain I:





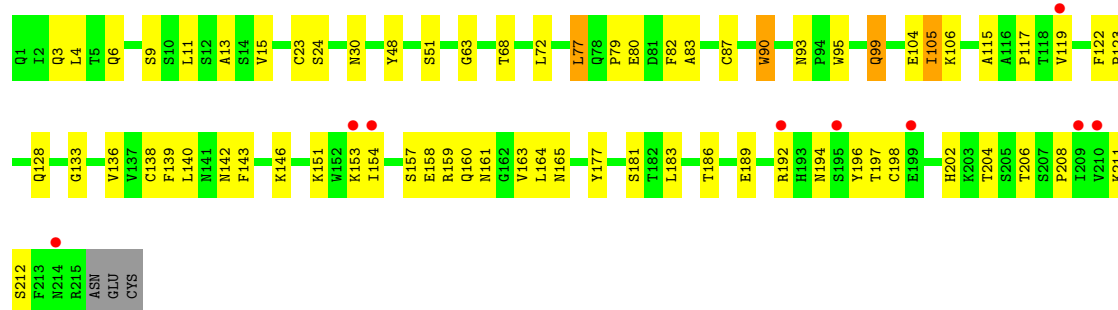
### • Molecule 3: Antibody AQC2 Fab

Chain L:



### • Molecule 3: Antibody AQC2 Fab

Chain M:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	106.12Å 43.68Å 153.88Å 90.00° 104.10° 90.00°	Depositor
Resolution (Å)	35.00 – 2.20 49.75 – 2.20	Depositor EDS
% Data completeness (in resolution range)	94.3 (35.00-2.20) 94.3 (49.75-2.20)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.04 (at 2.20Å)	Xtriage
Refinement program	CNX	Depositor
R, $R_{free}$	0.238 , 0.272 0.236 , 0.268	Depositor DCC
$R_{free}$ test set	3380 reflections (5.35%)	DCC
Wilson B-factor (Å <sup>2</sup> )	38.6	Xtriage
Anisotropy	0.335	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 35.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 66552 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	9537	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.80 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 4.7301e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup>Intensities 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: MG

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	0.28	0/1510	0.56	0/2036
1	B	0.27	0/1414	0.55	0/1903
2	H	0.39	0/1616	0.71	0/2208
2	I	0.37	0/1616	0.70	0/2208
3	L	0.35	0/1680	0.63	0/2288
3	M	0.33	0/1680	0.61	0/2288
All	All	0.34	0/9516	0.63	0/12931

There are no bond length outliers.

There are no bond angle outliers.

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	1490	0	1497	67	0
1	B	1397	0	1395	75	0
2	H	1575	0	1537	39	0
2	I	1575	0	1537	38	0
3	L	1636	0	1561	53	0
3	M	1636	0	1561	56	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	13	0	0	0	0
5	B	5	0	0	0	0
5	H	73	0	0	0	0
5	I	77	0	0	1	0
5	L	30	0	0	1	0
5	M	28	0	0	0	0
All	All	9537	0	9088	315	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 18.

The worst 5 of 315 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:L:191:GLU:HA	3:L:215:ARG:HH12	1.25	0.98
1:B:234:ARG:HH11	1:B:234:ARG:HB3	1.27	0.97
2:H:161:SER:H	2:H:201:ASN:HD21	1.00	0.95
2:I:161:SER:H	2:I:201:ASN:HD21	1.08	0.94
3:M:6:GLN:H	3:M:99:GLN:NE2	1.64	0.94

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	184/223 (82%)	164 (89%)	18 (10%)	2 (1%)	21	16
1	B	166/223 (74%)	147 (89%)	17 (10%)	2 (1%)	19	14
2	H	206/226 (91%)	201 (98%)	5 (2%)	0	100	100
2	I	206/226 (91%)	202 (98%)	4 (2%)	0	100	100
3	L	208/213 (98%)	198 (95%)	9 (4%)	1 (0%)	38	38
3	M	208/213 (98%)	195 (94%)	12 (6%)	1 (0%)	38	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1178/1324 (89%)	1107 (94%)	65 (6%)	6 (0%)	38 38

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	287	GLY
1	B	236	GLU
1	A	333	GLU
3	L	83	ALA
1	B	173	LEU

### 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	164/194 (84%)	157 (96%)	7 (4%)	40 47
1	B	153/194 (79%)	148 (97%)	5 (3%)	50 60
2	H	177/190 (93%)	170 (96%)	7 (4%)	42 51
2	I	177/190 (93%)	166 (94%)	11 (6%)	26 27
3	L	187/190 (98%)	179 (96%)	8 (4%)	40 47
3	M	187/190 (98%)	179 (96%)	8 (4%)	40 47
All	All	1045/1148 (91%)	999 (96%)	46 (4%)	39 45

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	159	ARG
1	B	234	ARG
3	M	90	TRP
3	L	211	LYS
1	B	171	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 41 such sidechains are listed below:

Mol	Chain	Res	Type
3	L	3	GLN
3	L	165	ASN
3	M	99	GLN
3	L	93	ASN
3	L	141	ASN

### 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 ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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, 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	188/223 (84%)	0.46	9 (4%) 29 29	28, 59, 77, 83	0
1	B	176/223 (78%)	0.78	17 (9%) 8 7	33, 66, 91, 96	0
2	H	210/226 (92%)	0.10	0 100 100	22, 31, 49, 58	0
2	I	210/226 (92%)	0.06	0 100 100	24, 34, 50, 61	0
3	L	210/213 (98%)	0.19	7 (3%) 44 45	22, 42, 74, 86	0
3	M	210/213 (98%)	0.20	9 (4%) 34 34	24, 41, 68, 86	0
All	All	1204/1324 (90%)	0.28	42 (3%) 42 42	22, 42, 78, 96	0

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	200	LEU	5.0
1	B	147	LEU	4.5
1	B	179	GLY	4.3
1	B	237	ALA	4.2
1	A	146	GLN	4.1

### 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, 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	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	MG	B	401	1/1	0.15	1.33	54,54,54,54	0
4	MG	A	400	1/1	0.12	-0.30	47,47,47,47	0

## 6.5 Other polymers

There are no such residues in this entry.