



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:30 AM GMT

PDB ID : 2R0Z  
Title : PFA1 FAB complexed with GripI peptide fragment  
Authors : Gardberg, A.S.; Dealwis, C.  
Deposited on : 2007-08-21  
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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

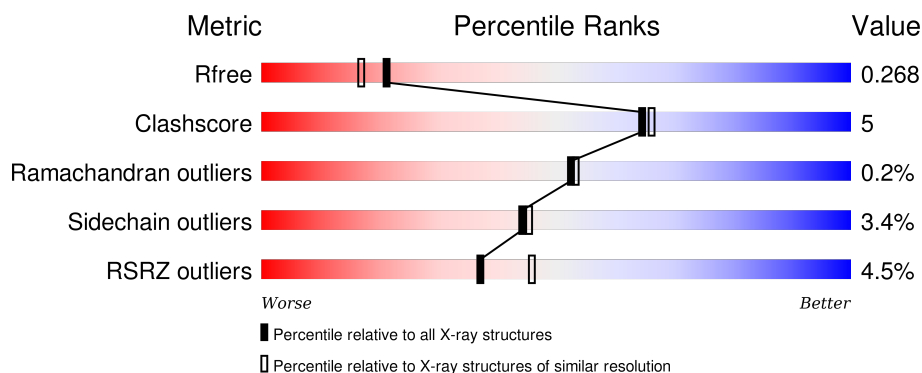
# 1 Overall quality at a glance

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))
$R_{free}$	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	L	219	<div> <div>87%</div> <div>12%</div> <div>•</div> </div>
2	H	223	<div> <div>8%</div> <div>83%</div> <div>13%</div> <div>••</div> </div>
3	Q	6	<div> <div>17%</div> <div>67%</div> <div>33%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	GOL	L	214	-	-	-	X
4	GOL	L	215	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3517 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 IgG2a Fab fragment light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	219	Total	C	N	O	S	0	2	0
			1707	1066	288	346	7			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	27E	SER	THR	CONFLICT	UNP A2NHM3
L	96	LEU	ARG	CONFLICT	UNP A2NHM3
L	100	ALA	GLY	CONFLICT	UNP A2NHM3
L	106	LEU	ILE	CONFLICT	UNP A2NHM3
L	213	YCM	CYS	MODIFIED RESIDUE	UNP A2NHM3

- Molecule 2 is a protein called IgG2a Fab fragment heavy chain, Fd portion.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	216	Total	C	N	O	S	0	0	0
			1630	1040	272	312	6			

- Molecule 3 is a protein called Gripl peptide fragment.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	Q	6	Total	C	N	O	0	0	0
			55	34	12	9			

- Molecule 4 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
4	L	1	Total	C	O	0	0
			6	3	3		
4	L	1	Total	C	O	0	0
			6	3	3		

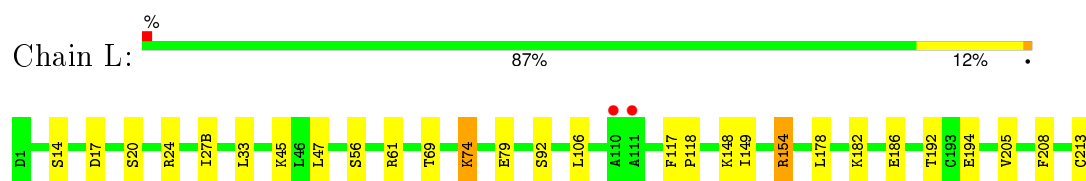
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	H	49	Total	O	0	0
			49	49		
5	L	62	Total	O	0	0
			62	62		
5	Q	2	Total	O	0	0
			2	2		

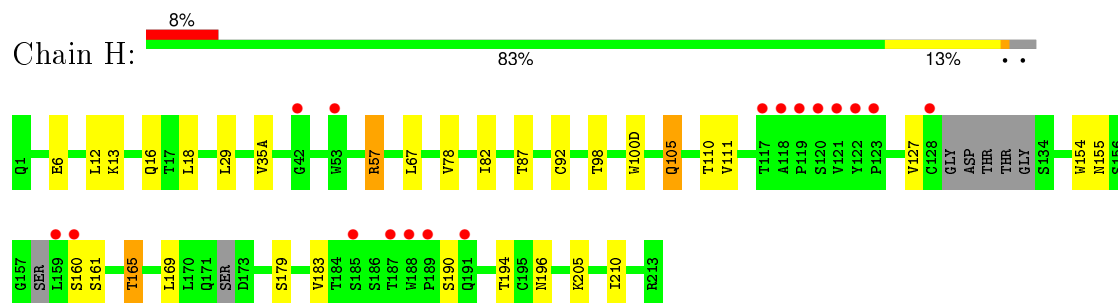
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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.

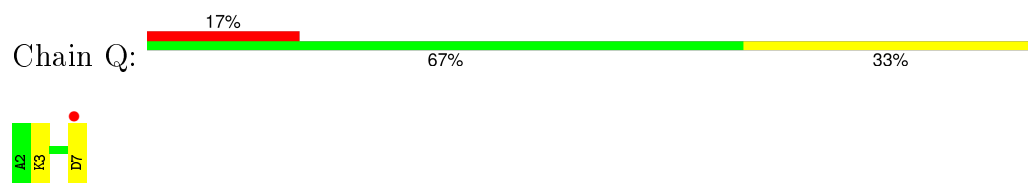
- Molecule 1: IgG2a Fab fragment light chain



- Molecule 2: IgG2a Fab fragment heavy chain, Fd portion



- Molecule 3: GriPI peptide fragment



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	41.47Å 112.24Å 43.17Å 90.00° 93.43° 90.00°	Depositor
Resolution (Å)	33.31 – 2.10 29.69 – 2.10	Depositor EDS
% Data completeness (in resolution range)	86.5 (33.31-2.10) 86.5 (29.69-2.10)	Depositor EDS
$R_{merge}$	0.16	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.92 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2	Depositor
R, $R_{free}$	0.201 , 0.261 0.212 , 0.268	Depositor DCC
$R_{free}$ test set	1000 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	32.9	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 43.9	EDS
Estimated twinning fraction	0.042 for l,-k,h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 19995 reflections (0.005%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	3517	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.22% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, YCM

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	L	0.45	0/1740	0.59	0/2361
2	H	0.44	0/1672	0.58	0/2286
3	Q	0.49	0/56	0.55	0/71
All	All	0.45	0/3468	0.58	0/4718

There are no bond length outliers.

There are no bond angle outliers.

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	L	1707	0	1653	15	0
2	H	1630	0	1587	19	0
3	Q	55	0	50	2	0
4	L	12	0	16	1	0
5	H	49	0	0	1	0
5	L	62	0	0	1	0
5	Q	2	0	0	0	0
All	All	3517	0	3306	34	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 (34) 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)
2:H:154:TRP:HZ3	2:H:210:ILE:HD11	1.59	0.66
1:L:45:LYS:HD3	5:L:242:HOH:O	1.99	0.61
1:L:27(B):ILE:HD11	1:L:33:LEU:HD23	1.84	0.59
2:H:87:THR:HG23	2:H:110:THR:HA	1.85	0.58
2:H:154:TRP:CZ3	2:H:210:ILE:HD11	2.37	0.58
2:H:67:LEU:HD23	2:H:82:ILE:HG12	1.86	0.57
2:H:155:ASN:ND2	5:H:247:HOH:O	2.37	0.56
2:H:13:LYS:O	2:H:16:GLN:HG2	2.05	0.56
2:H:98:THR:HG22	3:Q:7:ASP:OD2	2.08	0.55
1:L:27(B):ILE:CD1	1:L:33:LEU:HD23	2.38	0.54
2:H:154:TRP:HZ3	2:H:210:ILE:CD1	2.19	0.54
2:H:57:ARG:HG2	2:H:57:ARG:HH11	1.74	0.52
2:H:18:LEU:HD23	2:H:82:ILE:HD12	1.92	0.51
2:H:35(A):VAL:HB	2:H:78:VAL:HG21	1.94	0.49
1:L:24:ARG:HA	1:L:69:THR:O	2.14	0.48
1:L:61:ARG:NH1	1:L:79:GLU:OE1	2.46	0.48
1:L:20:SER:HB3	1:L:74:LYS:HG3	1.95	0.48
2:H:6:GLU:HG3	2:H:92:CYS:HB2	1.96	0.47
1:L:182:LYS:HE2	1:L:186:GLU:OE2	2.14	0.47
1:L:149:ILE:HD11	1:L:178:LEU:HD21	1.96	0.47
2:H:165:THR:HB	2:H:179:SER:HB2	1.97	0.45
1:L:148:LYS:HB2	1:L:192:THR:HB	2.00	0.44
4:L:214:GOL:H31	2:H:169:LEU:HD11	2.00	0.44
1:L:154:ARG:HD2	1:L:178:LEU:HD11	1.99	0.44
2:H:161:SER:HB3	2:H:183:VAL:HG12	1.99	0.43
2:H:105:GLN:HE21	2:H:105:GLN:HB3	1.62	0.43
1:L:117:PHE:HA	1:L:118:PRO:HD3	1.85	0.43
1:L:14:SER:O	1:L:17:ASP:HB2	2.18	0.43
1:L:194:GLU:HG3	1:L:205:VAL:HG22	2.01	0.42
2:H:12:LEU:O	2:H:111:VAL:HA	2.20	0.41
1:L:92:SER:O	3:Q:3:LYS:HB2	2.21	0.41
1:L:208:PHE:CD1	1:L:213:YCM:HD2	2.56	0.41
2:H:194:THR:HG22	2:H:196:ASN:OD1	2.20	0.41
2:H:12:LEU:HG	2:H:16:GLN:HG3	2.04	0.40

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	L	219/219 (100%)	216 (99%)	3 (1%)	0	100	100
2	H	208/223 (93%)	200 (96%)	7 (3%)	1 (0%)	34	30
3	Q	4/6 (67%)	4 (100%)	0	0	100	100
All	All	431/448 (96%)	420 (97%)	10 (2%)	1 (0%)	52	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	190	SER

### 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	L	197/195 (101%)	192 (98%)	5 (2%)	55	59
2	H	181/194 (93%)	173 (96%)	8 (4%)	35	33
3	Q	5/5 (100%)	5 (100%)	0	100	100
All	All	383/394 (97%)	370 (97%)	13 (3%)	44	45

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	L	47	LEU
1	L	56	SER

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Mol	Chain	Res	Type
1	L	74	LYS
1	L	106	LEU
1	L	154	ARG
2	H	29	LEU
2	H	57	ARG
2	H	100(D)	TRP
2	H	105	GLN
2	H	127	VAL
2	H	160	SER
2	H	165	THR
2	H	205	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	L	53	ASN
1	L	156	ASN
2	H	16	GLN
2	H	76	ASN
2	H	105	GLN
2	H	155	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue 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	$\# Z  > 2$
1	YCM	L	213	1	7,10,10	1.10	1 (14%)	4,12,12	0.30	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
1	YCM	L	213	1	-	0/6/10/10	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	213	YCM	CD-SG	-2.13	1.77	1.81

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	L	213	YCM	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

2 ligands are 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	$\# Z  > 2$
4	GOL	L	214	-	5,5,5	0.26	0	5,5,5	0.43	0
4	GOL	L	215	-	5,5,5	0.32	0	5,5,5	0.25	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
4	GOL	L	214	-	-	0/4/4/4	0/0/0/0
4	GOL	L	215	-	-	0/4/4/4	0/0/0/0

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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	L	214	GOL	1	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 ⓘ

### 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	L	218/219 (99%)	0.06	2 (0%) 85 88	29, 35, 41, 46	0
2	H	216/223 (96%)	0.43	17 (7%) 15 21	28, 36, 43, 48	0
3	Q	6/6 (100%)	0.61	1 (16%) 2 3	34, 37, 41, 42	0
All	All	440/448 (98%)	0.25	20 (4%) 37 46	28, 36, 42, 48	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	121	VAL	9.8
2	H	122	TYR	8.7
2	H	123	PRO	6.9
2	H	187	THR	5.8
2	H	185	SER	5.7
2	H	120	SER	4.8
2	H	118	ALA	4.1
2	H	188	TRP	4.0
1	L	111	ALA	3.4
2	H	119	PRO	3.3
2	H	191	GLN	3.2
2	H	42	GLY	3.2
3	Q	7	ASP	2.8
2	H	128	CYS	2.6
2	H	160	SER	2.6
2	H	117	THR	2.5
2	H	189	PRO	2.3
2	H	53	TRP	2.2
2	H	159	LEU	2.2
1	L	110	ALA	2.2

## 6.2 Non-standard residues in protein, DNA, RNA chains [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. 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	YCM	L	213	11/11	0.86	0.26	-	44,46,48,48	0

## 6.3 Carbohydrates [i](#)

There are no carbohydrates 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. 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	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	GOL	L	215	6/6	0.89	0.27	5.62	54,55,56,56	0
4	GOL	L	214	6/6	0.75	0.25	3.12	59,61,61,61	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.