



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:05 PM UTC

PDB ID : 6MSV / pdb\_00006msv  
Title : Structure of the 6th type III domain from human fibronectin  
Authors : Loa, S.; Mou, T.C.; Sprang, S.R.; Briknarova, K.  
Deposited on : 2018-10-18  
Resolution : 2.40 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)

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<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

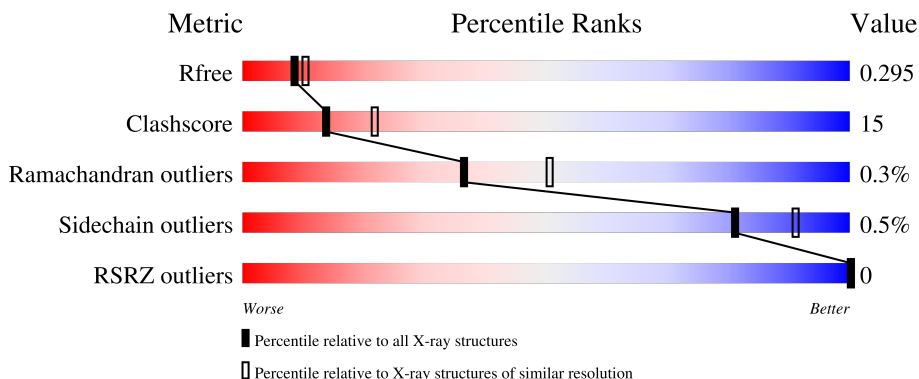
# 1 Overall quality at a glance i

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  $\geq 3$ , 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	92	 70% 24% 7%
1	B	92	 71% 18% 10%
1	C	92	 60% 33% 8%
1	D	92	 74% 23% 3%
1	E	92	 53% 38% 9%

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Mol	Chain	Length	Quality of chain
1	F	92	 79% 11% • 9%
1	G	92	 61% 28% • 10%
1	H	92	 78% 18% •
1	I	92	 57% 32% 12%
1	J	92	 52% 37% • 10%
1	K	92	 55% 36% 9%
1	L	92	 59% 30% • 10%

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7827 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 Fibronectin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	86	645	407	109	129	0	0	0
1	B	83	629	399	106	124	0	0	0
1	C	85	641	405	108	128	0	0	0
1	D	90	673	425	114	134	0	0	0
1	E	84	635	402	107	126	0	0	0
1	F	84	635	402	107	126	0	0	0
1	G	83	629	399	106	124	0	0	0
1	H	89	669	423	113	133	0	0	0
1	I	81	618	393	103	122	0	0	0
1	J	83	629	399	106	124	0	0	0
1	K	84	635	402	107	126	0	0	0
1	L	83	629	399	106	124	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

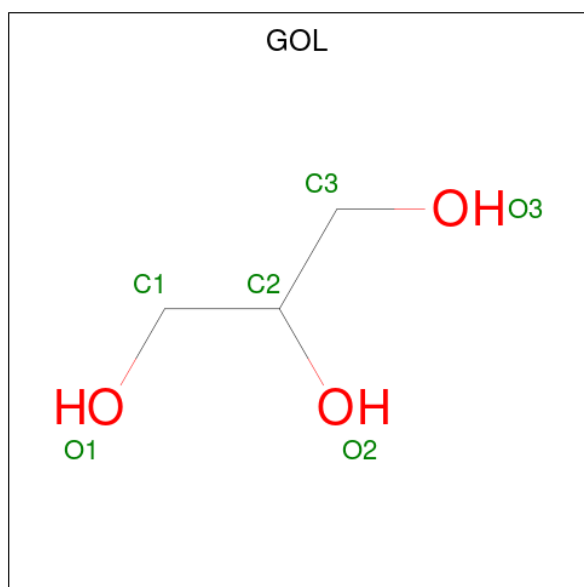
Chain	Residue	Modelled	Actual	Comment	Reference
A	1082	GLY	-	expression tag	UNP P02751
A	1083	SER	-	expression tag	UNP P02751
A	1084	GLY	-	expression tag	UNP P02751
B	1082	GLY	-	expression tag	UNP P02751
B	1083	SER	-	expression tag	UNP P02751

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1084	GLY	-	expression tag	UNP P02751
C	1082	GLY	-	expression tag	UNP P02751
C	1083	SER	-	expression tag	UNP P02751
C	1084	GLY	-	expression tag	UNP P02751
D	1082	GLY	-	expression tag	UNP P02751
D	1083	SER	-	expression tag	UNP P02751
D	1084	GLY	-	expression tag	UNP P02751
E	1082	GLY	-	expression tag	UNP P02751
E	1083	SER	-	expression tag	UNP P02751
E	1084	GLY	-	expression tag	UNP P02751
F	1082	GLY	-	expression tag	UNP P02751
F	1083	SER	-	expression tag	UNP P02751
F	1084	GLY	-	expression tag	UNP P02751
G	1082	GLY	-	expression tag	UNP P02751
G	1083	SER	-	expression tag	UNP P02751
G	1084	GLY	-	expression tag	UNP P02751
H	1082	GLY	-	expression tag	UNP P02751
H	1083	SER	-	expression tag	UNP P02751
H	1084	GLY	-	expression tag	UNP P02751
I	1082	GLY	-	expression tag	UNP P02751
I	1083	SER	-	expression tag	UNP P02751
I	1084	GLY	-	expression tag	UNP P02751
J	1082	GLY	-	expression tag	UNP P02751
J	1083	SER	-	expression tag	UNP P02751
J	1084	GLY	-	expression tag	UNP P02751
K	1082	GLY	-	expression tag	UNP P02751
K	1083	SER	-	expression tag	UNP P02751
K	1084	GLY	-	expression tag	UNP P02751
L	1082	GLY	-	expression tag	UNP P02751
L	1083	SER	-	expression tag	UNP P02751
L	1084	GLY	-	expression tag	UNP P02751

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total C O 6 3 3	0	0
2	F	1	Total C O 6 3 3	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	13	Total O 13 13	0	0
3	B	18	Total O 18 18	0	0
3	C	16	Total O 16 16	0	0
3	D	8	Total O 8 8	0	0
3	E	12	Total O 12 12	0	0
3	F	17	Total O 17 17	0	0
3	G	12	Total O 12 12	0	0
3	H	14	Total O 14 14	0	0
3	I	14	Total O 14 14	0	0
3	J	11	Total O 11 11	0	0

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
3	K	11	Total	O	0	0
			11	11		
3	L	2	Total	O	0	0
			2	2		

### 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: Fibronectin

Chain A: 



- Molecule 1: Fibronectin

Chain B: 



- Molecule 1: Fibronectin

Chain C: 



- Molecule 1: Fibronectin

Chain D: 




- Molecule 1: Fibronectin

Chain E: 



- Molecule 1: Fibronectin

Chain F:  79% 11% 9%




- Molecule 1: Fibronectin

Chain G:  61% 28% 10%



- Molecule 1: Fibronectin

Chain H:  78% 18% 4%



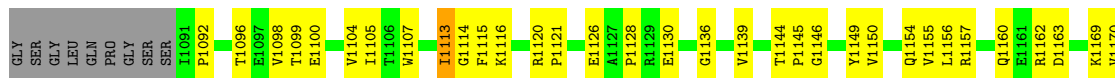
- Molecule 1: Fibronectin

Chain I:  57% 32% 12%



- Molecule 1: Fibronectin

Chain J:  52% 37% 10%



- Molecule 1: Fibronectin

Chain K:  55% 36% 9%



- Molecule 1: Fibronectin

Chain L:  59% 30% 10%

GLY	I1091	T1096	E1100	W1107	A1110	P1111	R1112	I1113	G1114	F1115	V1119	R1120	E1126	A1127	P1128	G1136	V1139	P1145	G1146	V1150	Y1151	Q1154	V1155	L1156	R1157	Q1160	D1163	K1169	V1170	V1171	T1172	P1173			
SER	P1092																																		
LEU																																			
GLN																																			
PRO																																			
GLY																																			
SER																																			

## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.52Å 79.46Å 80.89Å 112.33° 95.88° 94.48°	Depositor
Resolution (Å)	26.64 – 2.40 26.64 – 2.40	Depositor EDS
% Data completeness (in resolution range)	91.8 (26.64-2.40) 85.8 (26.64-2.40)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 2.29Å)	Xtrriage
Refinement program	PHENIX (1.14_3260: ???)	Depositor
R, $R_{free}$	0.235 , 0.295 0.236 , 0.295	Depositor DCC
$R_{free}$ test set	1992 reflections (4.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.4	Xtrriage
Anisotropy	0.431	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 46.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.076 for -h,-l,-k	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7827	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% 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: 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	0.12	0/659	0.31	0/905
1	B	0.12	0/643	0.33	0/884
1	C	0.11	0/655	0.32	0/900
1	D	0.12	0/688	0.36	0/945
1	E	0.14	0/649	0.49	0/892
1	F	0.55	3/649 (0.5%)	0.55	0/892
1	G	0.34	0/643	0.43	1/884 (0.1%)
1	H	0.14	0/684	0.36	0/940
1	I	0.13	0/631	0.37	0/867
1	J	0.13	0/643	0.37	0/884
1	K	0.14	0/649	0.38	0/892
1	L	0.21	0/643	0.50	0/884
All	All	0.22	3/7836 (0.0%)	0.40	1/10769 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	1120	ARG	C-O	-5.08	1.18	1.24
1	F	1120	ARG	C-N	5.03	1.39	1.33
1	F	1119	VAL	C-O	-5.01	1.19	1.24

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	1161	GLU	N-CA-C	-6.42	100.14	109.59

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	645	0	648	23	0
1	B	629	0	635	17	0
1	C	641	0	645	23	0
1	D	673	0	677	13	0
1	E	635	0	640	34	0
1	F	635	0	640	5	0
1	G	629	0	635	19	0
1	H	669	0	674	13	0
1	I	618	0	625	25	0
1	J	629	0	635	32	0
1	K	635	0	640	20	0
1	L	629	0	635	29	0
2	B	6	0	8	2	0
2	F	6	0	8	0	0
3	A	13	0	0	0	0
3	B	18	0	0	0	0
3	C	16	0	0	1	0
3	D	8	0	0	0	0
3	E	12	0	0	0	0
3	F	17	0	0	0	0
3	G	12	0	0	0	0
3	H	14	0	0	1	0
3	I	14	0	0	0	0
3	J	11	0	0	0	0
3	K	11	0	0	0	0
3	L	2	0	0	1	0
All	All	7827	0	7745	224	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 15.

The worst 5 of 224 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:G:1157:ARG:HB3	1:G:1162:ARG:HD2	1.49	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:1120:ARG:HB3	1:L:1128:PRO:HB3	1.50	0.91
1:I:1157:ARG:HD2	1:I:1162:ARG:HE	1.36	0.88
1:G:1116:LYS:CE	1:G:1130:GLU:OE1	2.21	0.88
1:A:1168:ASN:HD22	1:J:1170:VAL:HA	1.39	0.88

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	84/92 (91%)	83 (99%)	1 (1%)	0	100	100
1	B	81/92 (88%)	81 (100%)	0	0	100	100
1	C	83/92 (90%)	79 (95%)	4 (5%)	0	100	100
1	D	88/92 (96%)	83 (94%)	5 (6%)	0	100	100
1	E	82/92 (89%)	78 (95%)	4 (5%)	0	100	100
1	F	82/92 (89%)	79 (96%)	3 (4%)	0	100	100
1	G	81/92 (88%)	79 (98%)	2 (2%)	0	100	100
1	H	87/92 (95%)	83 (95%)	4 (5%)	0	100	100
1	I	77/92 (84%)	75 (97%)	2 (3%)	0	100	100
1	J	81/92 (88%)	77 (95%)	3 (4%)	1 (1%)	10	16
1	K	82/92 (89%)	78 (95%)	3 (4%)	1 (1%)	10	16
1	L	81/92 (88%)	79 (98%)	1 (1%)	1 (1%)	10	16
All	All	989/1104 (90%)	954 (96%)	32 (3%)	3 (0%)	36	50

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	K	1125	GLY
1	J	1113	ILE
1	L	1128	PRO

### 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	74/78 (95%)	74 (100%)	0	100	100
1	B	72/78 (92%)	71 (99%)	1 (1%)	59	79
1	C	74/78 (95%)	74 (100%)	0	100	100
1	D	77/78 (99%)	76 (99%)	1 (1%)	61	80
1	E	73/78 (94%)	73 (100%)	0	100	100
1	F	73/78 (94%)	72 (99%)	1 (1%)	59	79
1	G	72/78 (92%)	71 (99%)	1 (1%)	59	79
1	H	77/78 (99%)	77 (100%)	0	100	100
1	I	72/78 (92%)	72 (100%)	0	100	100
1	J	72/78 (92%)	72 (100%)	0	100	100
1	K	73/78 (94%)	73 (100%)	0	100	100
1	L	72/78 (92%)	72 (100%)	0	100	100
All	All	881/936 (94%)	877 (100%)	4 (0%)	81	91

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1156	LEU
1	D	1129	ARG
1	F	1120	ARG
1	G	1122	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	1123	GLN
1	G	1095	ASN
1	L	1160	GLN
1	H	1095	ASN
1	D	1160	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](#)

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
2	GOL	F	1201	-	5,5,5	0.92	0	5,5,5	1.08	0
2	GOL	B	1201	-	5,5,5	1.01	0	5,5,5	0.98	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
2	GOL	F	1201	-	-	2/4/4/4	-
2	GOL	B	1201	-	-	2/4/4/4	-

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
2	F	1201	GOL	C1-C2-C3-O3
2	B	1201	GOL	O1-C1-C2-C3
2	F	1201	GOL	O2-C2-C3-O3
2	B	1201	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1201	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	86/92 (93%)	-1.26	0 100 100	31, 49, 87, 92	0
1	B	83/92 (90%)	-1.23	0 100 100	33, 50, 73, 82	0
1	C	85/92 (92%)	-1.26	0 100 100	35, 52, 80, 92	0
1	D	90/92 (97%)	-1.17	0 100 100	37, 59, 87, 106	0
1	E	84/92 (91%)	-1.16	0 100 100	38, 53, 91, 102	0
1	F	84/92 (91%)	-1.31	0 100 100	34, 49, 81, 93	0
1	G	83/92 (90%)	-1.29	0 100 100	33, 46, 77, 91	0
1	H	89/92 (96%)	-1.28	0 100 100	32, 51, 83, 102	0
1	I	81/92 (88%)	-1.29	0 100 100	39, 51, 88, 102	0
1	J	83/92 (90%)	-1.13	0 100 100	34, 58, 108, 122	0
1	K	84/92 (91%)	-1.26	0 100 100	34, 51, 81, 97	0
1	L	83/92 (90%)	-1.12	0 100 100	38, 61, 102, 108	0
All	All	1015/1104 (91%)	-1.23	0 100 100	31, 53, 90, 122	0

There are no RSRZ outliers to report.

### 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( $\text{\AA}^2$ )	Q<0.9
2	GOL	F	1201	6/6	0.97	0.07	55,57,64,64	0
2	GOL	B	1201	6/6	0.98	0.04	50,59,63,66	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.