



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:54 AM GMT

PDB ID : 2V7N  
Title : Unusual twinning in crystals of the CitS binding antibody Fab fragment f3p4  
Authors : Frey, D.; Huber, T.; Plueckthun, A.; Gruetter, M.G.  
Deposited on : 2007-07-31  
Resolution : 1.92 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

---

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

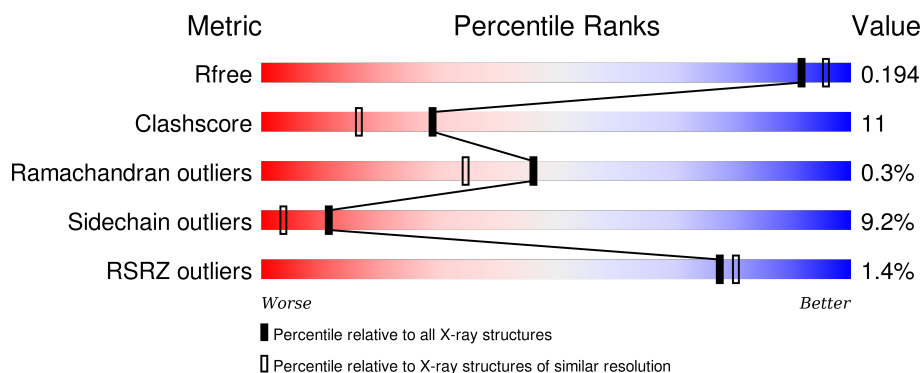
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.92 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	5832 (1.94-1.90)
Clashscore	102246	6540 (1.94-1.90)
Ramachandran outliers	100387	6464 (1.94-1.90)
Sidechain outliers	100360	6465 (1.94-1.90)
RSRZ outliers	91569	5846 (1.94-1.90)

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 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	A	215	 71% 23% . .
1	C	215	 71% 24% . .
1	E	215	 69% 25% 5% .
1	G	215	 74% 23% . .
2	B	229	 70% 21% . 7%

*Continued on next page...*

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	D	229	<div><div></div><div>4%</div><div>68%</div><div>21%</div><div>7%</div></div>
2	F	229	<div><div></div><div>2%</div><div>63%</div><div>25%</div><div>7%</div></div>
2	H	229	<div><div></div><div>2%</div><div>66%</div><div>22%</div><div>8%</div></div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13417 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 IMMUNOGLOBULIN LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	213	Total	C	N	O	S	0	0	0
			1631	1019	275	333	4			
1	C	212	Total	C	N	O	S	0	0	0
			1627	1017	274	332	4			
1	E	213	Total	C	N	O	S	0	0	0
			1631	1019	275	333	4			
1	G	212	Total	C	N	O	S	0	0	0
			1627	1017	274	332	4			

- Molecule 2 is a protein called IMMUNOGLOBULIN HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	214	Total	C	N	O	S	0	0	0
			1598	1011	272	309	6			
2	D	213	Total	C	N	O	S	0	0	0
			1595	1010	272	307	6			
2	F	212	Total	C	N	O	S	0	0	0
			1586	1005	270	305	6			
2	H	211	Total	C	N	O	S	0	0	0
			1582	1003	269	304	6			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	85	Total	O	0	0
			85	85		
3	B	58	Total	O	0	0
			58	58		
3	C	80	Total	O	0	0
			80	80		
3	D	61	Total	O	0	0
			61	61		

*Continued on next page...*

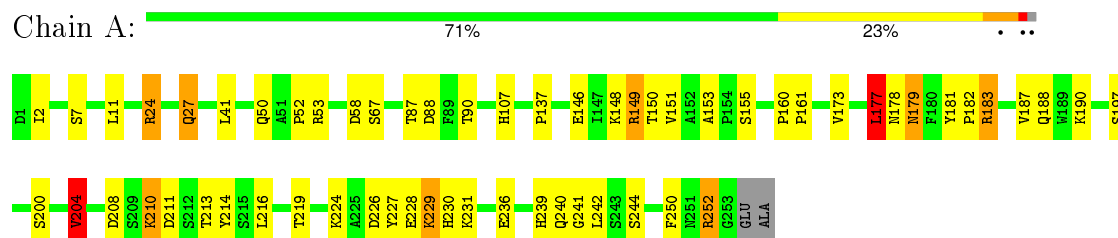
*Continued from previous page...*

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	64	Total 64	O 64	0	0
3	F	51	Total 51	O 51	0	0
3	G	80	Total 80	O 80	0	0
3	H	61	Total 61	O 61	0	0

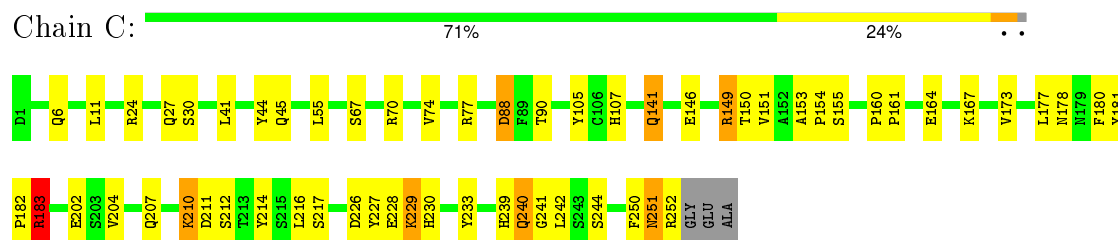
### 3 Residue-property plots

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

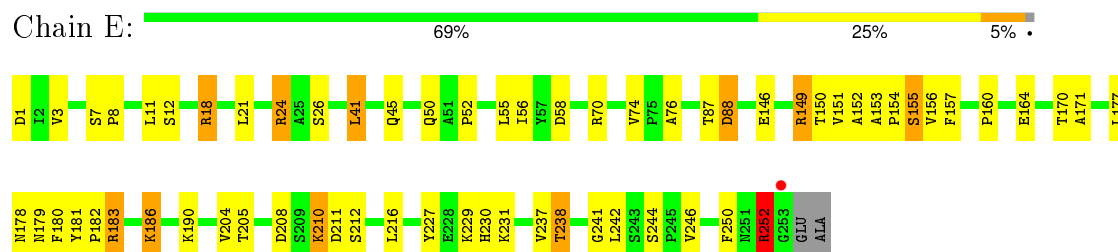
#### • Molecule 1: IMMUNOGLOBULIN LIGHT CHAIN



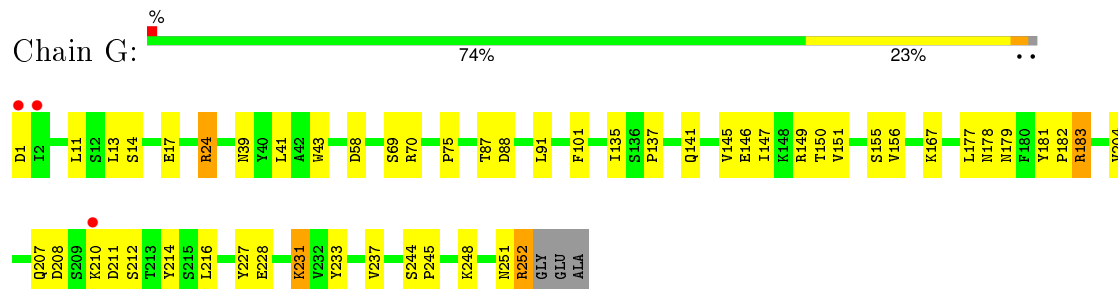
#### • Molecule 1: IMMUNOGLOBULIN LIGHT CHAIN



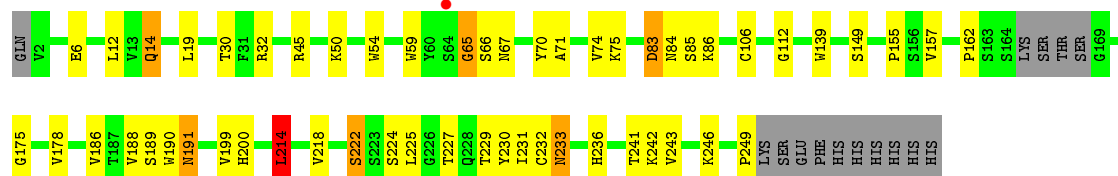
#### • Molecule 1: IMMUNOGLOBULIN LIGHT CHAIN



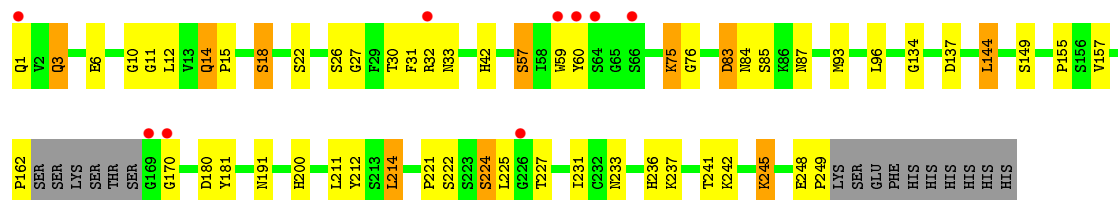
#### • Molecule 1: IMMUNOGLOBULIN LIGHT CHAIN



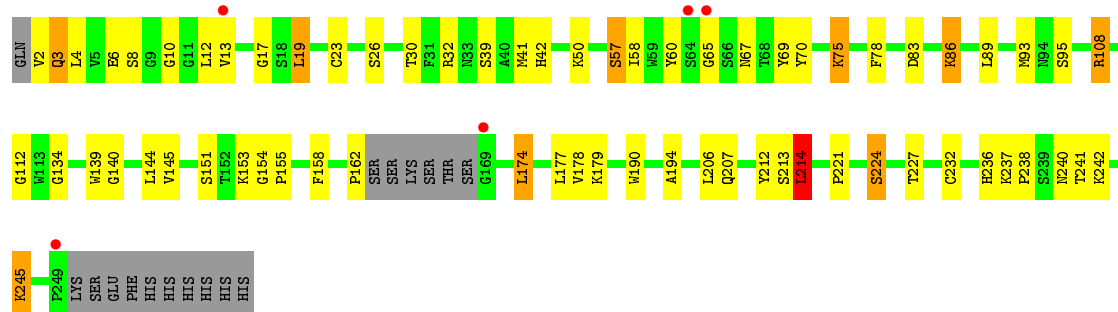
## • Molecule 2: IMMUNOGLOBULIN HEAVY CHAIN

Chain B: 

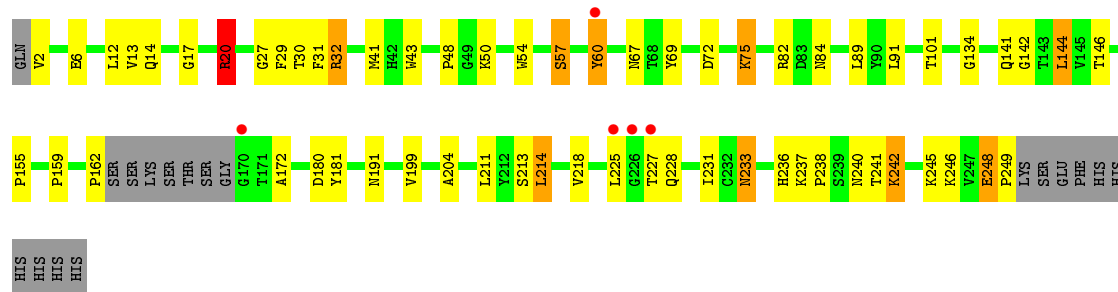
## • Molecule 2: IMMUNOGLOBULIN HEAVY CHAIN

Chain D: 

## • Molecule 2: IMMUNOGLOBULIN HEAVY CHAIN

Chain F: 

## • Molecule 2: IMMUNOGLOBULIN HEAVY CHAIN

Chain H: 

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	102.79Å 185.92Å 102.99Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 1.92 29.99 – 1.90	Depositor EDS
% Data completeness (in resolution range)	95.1 (15.00-1.92) 96.7 (29.99-1.90)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.29 (at 1.91Å)	Xtriage
Refinement program	SHELXL-97	Depositor
R, $R_{free}$	0.155 , 0.202 0.151 , 0.194	Depositor DCC
$R_{free}$ test set	4227 reflections (2.97%)	DCC
Wilson B-factor (Å <sup>2</sup> )	18.7	Xtriage
Anisotropy	0.227	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.389 for l,-k,h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.37$ , $\langle L^2 \rangle = 0.19$	Xtriage
Outliers	0 of 151548 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	13417	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.25% 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 ⓘ

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	0.39	0/1667	1.00	6/2267 (0.3%)
1	C	0.38	0/1663	1.03	5/2262 (0.2%)
1	E	0.39	0/1667	1.04	5/2267 (0.2%)
1	G	0.39	0/1663	1.02	4/2262 (0.2%)
2	B	0.37	0/1639	1.02	6/2234 (0.3%)
2	D	0.37	0/1636	0.98	5/2230 (0.2%)
2	F	0.37	0/1627	1.04	6/2218 (0.3%)
2	H	0.36	0/1623	0.97	3/2213 (0.1%)
All	All	0.38	0/13185	1.01	40/17953 (0.2%)

There are no bond length outliers.

The worst 5 of 40 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	183	ARG	CD-NE-CZ	14.47	143.87	123.60
1	E	252	ARG	NE-CZ-NH1	-10.07	115.27	120.30
2	F	214	LEU	CA-CB-CG	9.60	137.38	115.30
1	A	252	ARG	NE-CZ-NH1	-8.86	115.87	120.30
2	B	83	ASP	CB-CG-OD2	8.74	126.17	118.30

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	1631	0	1580	35	0
1	C	1627	0	1577	39	0
1	E	1631	0	1580	51	0
1	G	1627	0	1577	27	0
2	B	1598	0	1549	38	0
2	D	1595	0	1550	28	0
2	F	1586	0	1539	40	0
2	H	1582	0	1536	42	0
3	A	85	0	0	1	0
3	B	58	0	0	2	0
3	C	80	0	0	1	0
3	D	61	0	0	1	0
3	E	64	0	0	3	0
3	F	51	0	0	1	0
3	G	80	0	0	0	0
3	H	61	0	0	1	0
All	All	13417	0	12488	288	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 11.

The worst 5 of 288 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:B:229:THR:HG23	2:B:246:LYS:HE3	1.55	0.88
1:C:6:GLN:H	1:C:141:GLN:HE22	1.20	0.87
1:G:204:VAL:HG22	1:G:216:LEU:HD12	1.59	0.84
2:F:236:HIS:HB3	2:F:241:THR:HB	1.61	0.83
1:C:164:GLU:HA	1:C:167:LYS:HD3	1.60	0.81

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	211/215 (98%)	206 (98%)	5 (2%)	0	100	100
1	C	210/215 (98%)	203 (97%)	7 (3%)	0	100	100
1	E	211/215 (98%)	205 (97%)	6 (3%)	0	100	100
1	G	210/215 (98%)	206 (98%)	4 (2%)	0	100	100
2	B	210/229 (92%)	201 (96%)	8 (4%)	1 (0%)	34	20
2	D	209/229 (91%)	200 (96%)	7 (3%)	2 (1%)	19	7
2	F	208/229 (91%)	200 (96%)	7 (3%)	1 (0%)	34	20
2	H	207/229 (90%)	200 (97%)	6 (3%)	1 (0%)	34	20
All	All	1676/1776 (94%)	1621 (97%)	50 (3%)	5 (0%)	46	34

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	F	134	GLY
2	D	10	GLY
2	H	134	GLY
2	D	134	GLY
2	B	65	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	186/187 (100%)	166 (89%)	20 (11%)	8	2
1	C	186/187 (100%)	169 (91%)	17 (9%)	12	4
1	E	186/187 (100%)	171 (92%)	15 (8%)	15	5
1	G	186/187 (100%)	172 (92%)	14 (8%)	17	6
2	B	175/190 (92%)	164 (94%)	11 (6%)	22	10
2	D	174/190 (92%)	155 (89%)	19 (11%)	8	2
2	F	173/190 (91%)	153 (88%)	20 (12%)	7	2
2	H	173/190 (91%)	157 (91%)	16 (9%)	11	4

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1439/1508 (95%)	1307 (91%)	132 (9%)	11 4

5 of 132 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	222	SER
1	E	149	ARG
2	H	75	LYS
2	D	227	THR
1	E	7	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	230	HIS
2	D	84	ASN
2	H	84	ASN
1	C	251	ASN
2	D	14	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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	A	213/215 (99%)	-0.12	0 100 100	13, 21, 34, 51	0
1	C	212/215 (98%)	-0.19	0 100 100	13, 21, 33, 51	0
1	E	213/215 (99%)	-0.12	1 (0%) 91 92	14, 22, 34, 51	0
1	G	212/215 (98%)	-0.17	3 (1%) 78 80	13, 21, 33, 51	0
2	B	214/229 (93%)	0.06	1 (0%) 91 92	14, 24, 45, 60	0
2	D	213/229 (93%)	0.18	9 (4%) 40 44	15, 24, 46, 59	0
2	F	212/229 (92%)	0.12	5 (2%) 62 66	16, 24, 44, 60	0
2	H	211/229 (92%)	0.01	5 (2%) 62 66	15, 24, 43, 60	0
All	All	1700/1776 (95%)	-0.03	24 (1%) 78 80	13, 23, 40, 60	0

The worst 5 of 24 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	169	GLY	7.5
2	F	169	GLY	3.5
2	H	225	LEU	3.3
2	H	227	THR	3.2
2	F	65	GLY	3.1

### 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

There are no ligands in this entry.

## 6.5 Other polymers

There are no such residues in this entry.