



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:58 AM GMT

PDB ID : 3KDM  
Title : Crystal Structure of Human Anti-steroid Fab 5F2 in Complex with Testosterone  
Authors : Niemi, M.H.; Rouvinen, J.  
Deposited on : 2009-10-23  
Resolution : 1.50 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.

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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

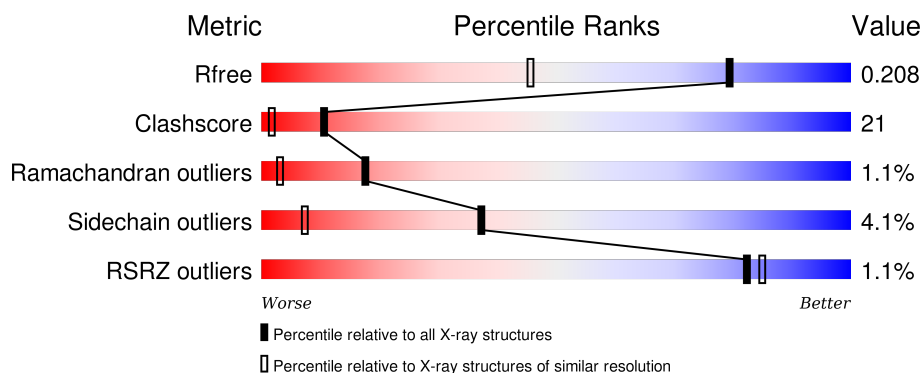
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.50 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	2072 (1.50-1.50)
Clashscore	102246	2274 (1.50-1.50)
Ramachandran outliers	100387	2218 (1.50-1.50)
Sidechain outliers	100360	2216 (1.50-1.50)
RSRZ outliers	91569	2075 (1.50-1.50)

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	218	<div> <div></div> <div>77%21%..</div> </div>
1	L	218	<div> <div></div> <div>72%25%..</div> </div>
2	B	225	<div> <div>2%</div> <div>64%31%5%.</div> </div>
2	H	225	<div> <div>2%</div> <div>61%34%..</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7532 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.

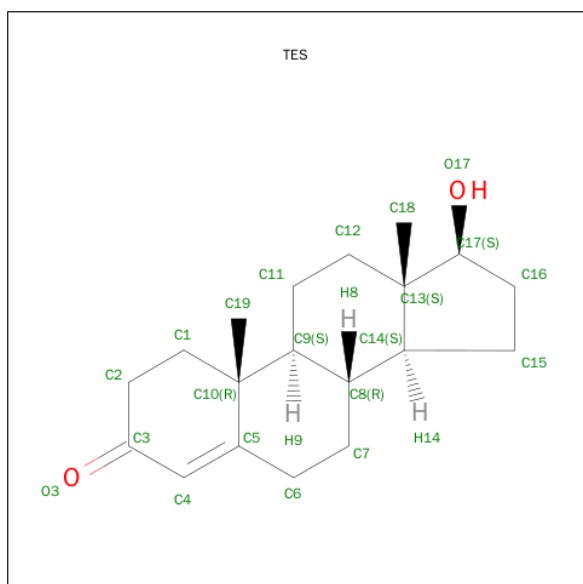
- Molecule 1 is a protein called Immunoglobulin light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	L	216	Total	C	N	O	S	0	2	0
			1631	1013	275	337	6			
1	A	216	Total	C	N	O	S	0	0	0
			1627	1009	275	337	6			

- Molecule 2 is a protein called Immunoglobulin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	223	Total	C	N	O	S	0	0	0
			1655	1044	275	329	7			
2	B	223	Total	C	N	O	S	0	1	0
			1658	1047	275	329	7			

- Molecule 3 is TESTOSTERONE (three-letter code: TES) (formula:  $C_{19}H_{28}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	C	O	0	0
			21	19	2		
3	B	1	Total	C	O	0	0
			21	19	2		

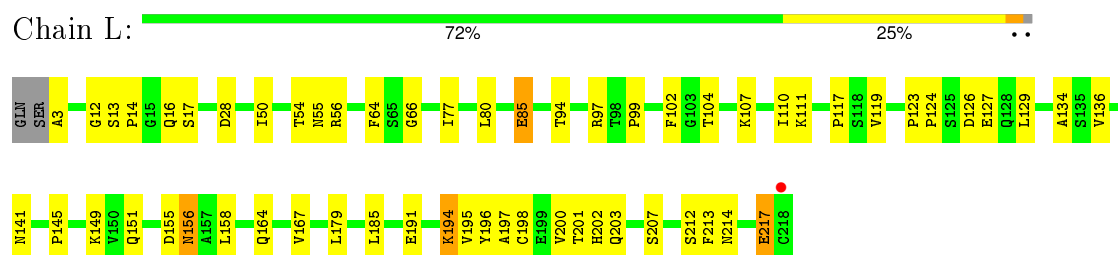
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	238	Total	O	0	0
			238	238		
4	H	223	Total	O	0	0
			223	223		
4	A	239	Total	O	0	0
			239	239		
4	B	219	Total	O	0	0
			219	219		

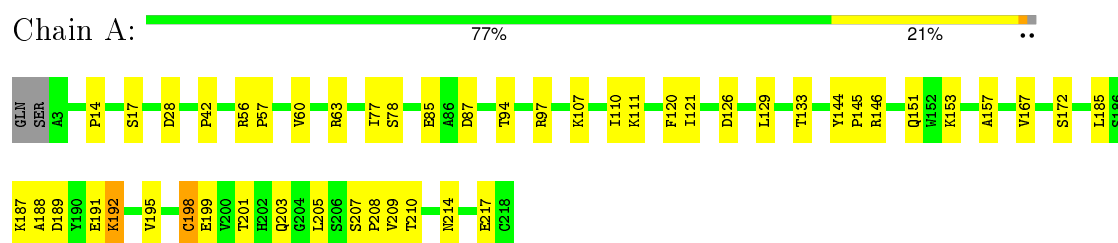
### 3 Residue-property plots

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.

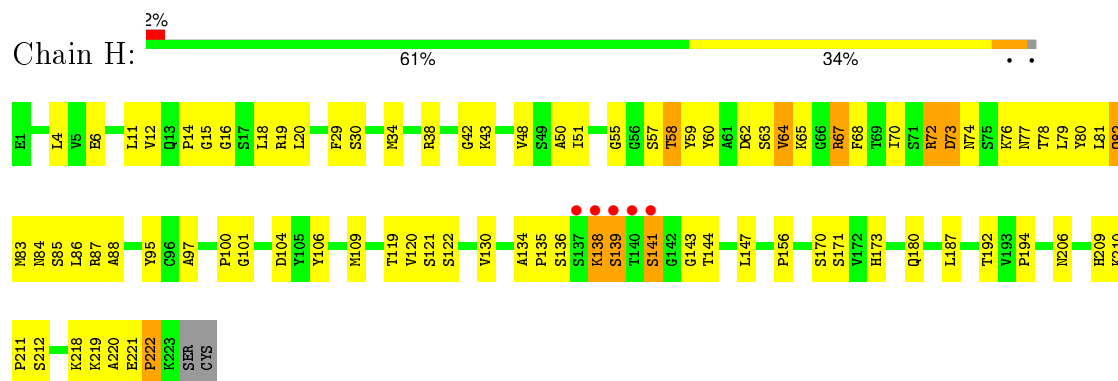
- Molecule 1: Immunoglobulin light chain



- Molecule 1: Immunoglobulin light chain

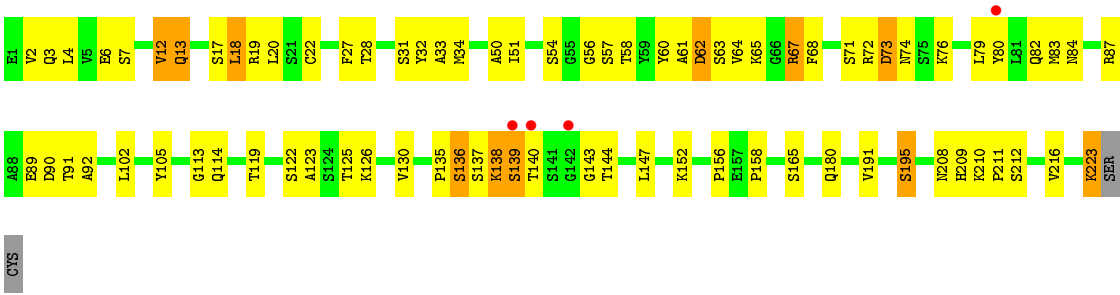


- Molecule 2: Immunoglobulin heavy chain



- Molecule 2: Immunoglobulin heavy chain





CYS

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	66.75Å 67.08Å 67.06Å 81.32° 69.30° 69.27°	Depositor
Resolution (Å)	48.25 – 1.50 48.25 – 1.50	Depositor EDS
% Data completeness (in resolution range)	93.3 (48.25-1.50) 92.4 (48.25-1.50)	Depositor EDS
$R_{merge}$	0.03	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.23 (at 1.50Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.180 , 0.208 0.179 , 0.208	Depositor DCC
$R_{free}$ test set	7595 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	15.3	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 43.0	EDS
Estimated twinning fraction	0.501 for -h,-l,-k 0.469 for -h,-l,-k	Xtriage
Reported twinning fraction	0.501 for -h,-l,-k	Depositor
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 151891 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	7532	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.52% 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 [i](#)

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

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

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	0.63	1/1662 (0.1%)	0.74	0/2257
1	L	0.62	1/1677 (0.1%)	0.71	0/2278
2	B	0.64	0/1696	0.81	1/2313 (0.0%)
2	H	0.67	0/1689	0.80	3/2303 (0.1%)
All	All	0.64	2/6724 (0.0%)	0.77	4/9151 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	198	CYS	CB-SG	-10.05	1.65	1.82
1	L	198	CYS	CB-SG	-5.34	1.73	1.81

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	73	ASP	CB-CG-OD1	6.03	123.72	118.30
2	H	82	GLN	N-CA-C	-5.83	95.26	111.00
2	H	58	THR	N-CA-C	-5.83	95.27	111.00
2	B	56	GLY	N-CA-C	5.76	127.49	113.10

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	1627	0	1564	40	0
1	L	1631	0	1568	63	0
2	B	1658	0	1613	81	0
2	H	1655	0	1608	102	0
3	B	21	0	28	0	0
3	H	21	0	28	3	0
4	A	239	0	0	7	0
4	B	219	0	0	7	1
4	H	223	0	0	7	0
4	L	238	0	0	12	1
All	All	7532	0	6409	277	1

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 21.

The worst 5 of 277 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:L:145:PRO:HG3	1:L:203:GLN:HE22	1.19	1.05
1:L:119:VAL:HG21	1:L:200[A]:VAL:HG21	1.37	1.03
2:B:68:PHE:HA	2:B:82:GLN:O	1.61	1.00
2:H:82:GLN:NE2	2:H:84:ASN:OD1	1.95	1.00
2:B:87:ARG:HD3	2:B:89:GLU:OE1	1.61	0.99

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:L:273:HOH:O	4:B:271:HOH:O[1_465]	2.09	0.11

## 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	214/218 (98%)	204 (95%)	9 (4%)	1 (0%)	34	10
1	L	216/218 (99%)	207 (96%)	9 (4%)	0	100	100
2	B	222/225 (99%)	206 (93%)	12 (5%)	4 (2%)	11	1
2	H	221/225 (98%)	207 (94%)	9 (4%)	5 (2%)	8	1
All	All	873/886 (98%)	824 (94%)	39 (4%)	10 (1%)	17	3

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	139	SER
1	A	217	GLU
2	H	15	GLY
2	H	63	SER
2	H	222	PRO

### 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	185/187 (99%)	182 (98%)	3 (2%)	70	41
1	L	187/187 (100%)	178 (95%)	9 (5%)	31	5
2	B	184/185 (100%)	172 (94%)	12 (6%)	21	2
2	H	183/185 (99%)	177 (97%)	6 (3%)	45	12
All	All	739/744 (99%)	709 (96%)	30 (4%)	37	7

5 of 30 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	138	LYS
1	A	94	THR
2	B	139	SER
1	A	28	ASP
1	A	192	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	209	HIS
2	B	209	HIS
2	B	13	GLN
1	L	203	GLN
1	A	214	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	PCA	B	1	2	7,8,9	1.68	1 (14%)	9,10,12	2.78	4 (44%)
2	PCA	H	1	2	7,8,9	1.59	1 (14%)	9,10,12	1.96	4 (44%)

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	PCA	B	1	2	-	0/0/11/13	0/1/1/1
2	PCA	H	1	2	-	0/0/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	1	PCA	CD-N	4.01	1.47	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1	PCA	CD-N	4.30	1.48	1.33

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	PCA	CB-CA-C	-6.28	104.17	112.76
2	B	1	PCA	CA-N-CD	-3.71	101.38	113.81
2	H	1	PCA	CA-N-CD	-3.19	103.12	113.81
2	B	1	PCA	O-C-CA	-2.55	118.72	125.44
2	H	1	PCA	O-C-CA	-2.35	119.22	125.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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	$\# Z  > 2$
3	TES	B	226	-	24,24,24	0.70	0	39,39,39	1.45	6 (15%)
3	TES	H	226	-	24,24,24	0.71	0	39,39,39	1.34	5 (12%)

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	TES	B	226	-	-	0/0/58/58	0/4/4/4
3	TES	H	226	-	-	0/0/58/58	0/4/4/4

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	226	TES	C6-C5-C4	-3.79	116.08	120.89
3	H	226	TES	C16-C17-C13	-3.33	101.99	104.58
3	H	226	TES	C6-C5-C4	-3.07	116.99	120.89
3	B	226	TES	C16-C17-C13	-2.84	102.37	104.58
3	H	226	TES	C11-C12-C13	-2.74	107.94	112.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	226	TES	3	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	216/218 (99%)	-0.28	0 100 100	12, 18, 27, 50	0
1	L	216/218 (99%)	-0.30	1 (0%) 91 93	12, 18, 26, 45	0
2	B	222/225 (98%)	-0.07	4 (1%) 71 75	13, 20, 28, 42	0
2	H	222/225 (98%)	-0.11	5 (2%) 64 67	13, 19, 29, 38	0
All	All	876/886 (98%)	-0.19	10 (1%) 82 85	12, 19, 27, 50	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	H	139	SER	5.5
2	B	142	GLY	3.5
2	H	141	SER	3.0
2	B	140	THR	2.7
2	B	139	SER	2.6

### 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
2	PCA	H	1	8/9	0.91	0.10	-	29,32,34,36	0
2	PCA	B	1	8/9	0.84	0.14	-	32,37,40,40	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( $\text{\AA}^2$ )	Q<0.9
3	TES	B	226	21/21	0.96	0.07	-0.60	15,16,19,20	0
3	TES	H	226	21/21	0.95	0.07	-0.90	15,17,19,20	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.