



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 08:17 am GMT

PDB ID : 5INW  
Title : Structure of reaction loop cleaved lamprey angiotensinogen  
Authors : Wei, H.; Zhou, A.  
Deposited on : 2016-03-08  
Resolution : 2.70 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

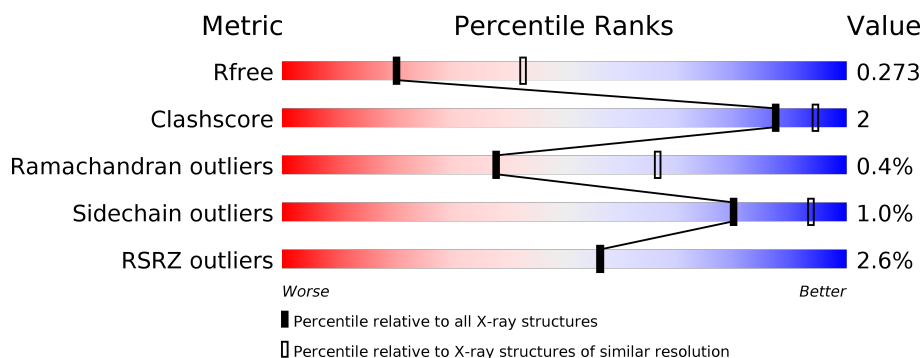
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	100719	2259 (2.70-2.70)
Clashscore	112137	2590 (2.70-2.70)
Ramachandran outliers	110173	2550 (2.70-2.70)
Sidechain outliers	110143	2550 (2.70-2.70)
RSRZ outliers	101464	2275 (2.70-2.70)

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	421	<div> <div>%</div> <div> <div></div> <div>73%</div> <div>6%</div> <div>20%</div> </div> </div>
1	B	421	<div> <div>4%</div> <div> <div></div> <div>72%</div> <div>6%</div> <div>21%</div> </div> </div>
2	C	35	<div> <div></div> <div> <div></div> <div>74%</div> <div>14%</div> <div>11%</div> </div> </div>
2	D	35	<div> <div></div> <div> <div></div> <div>83%</div> <div>9%</div> <div>9%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5704 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 Putative angiotensinogen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	0	0	0
			2616	1673	447	484	12			
1	B	331	Total	C	N	O	S	0	0	0
			2578	1646	440	480	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP C0MNC6
A	416A	ALA	-	insertion	UNP C0MNC6
A	416B	ALA	-	insertion	UNP C0MNC6
A	418	ARG	ILE	engineered mutation	UNP C0MNC6
B	0	GLY	-	expression tag	UNP C0MNC6
B	416A	ALA	-	insertion	UNP C0MNC6
B	416B	ALA	-	insertion	UNP C0MNC6
B	418	ARG	ILE	engineered mutation	UNP C0MNC6

- Molecule 2 is a protein called C-terminal peptide of Putative angiotensinogen.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	31	Total	C	N	O	S	0	0	0
			248	162	42	43	1			
2	D	32	Total	C	N	O	S	0	0	0
			255	167	43	44	1			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		

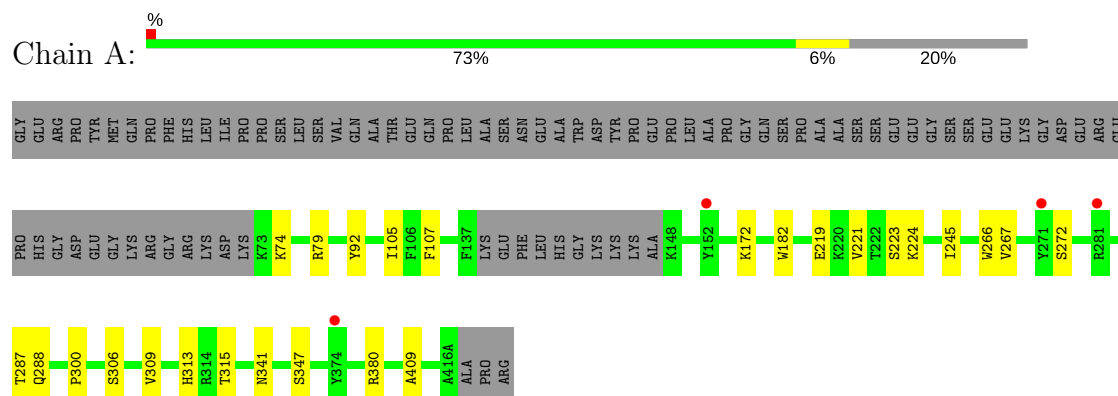
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	O	0	0
			2	2		

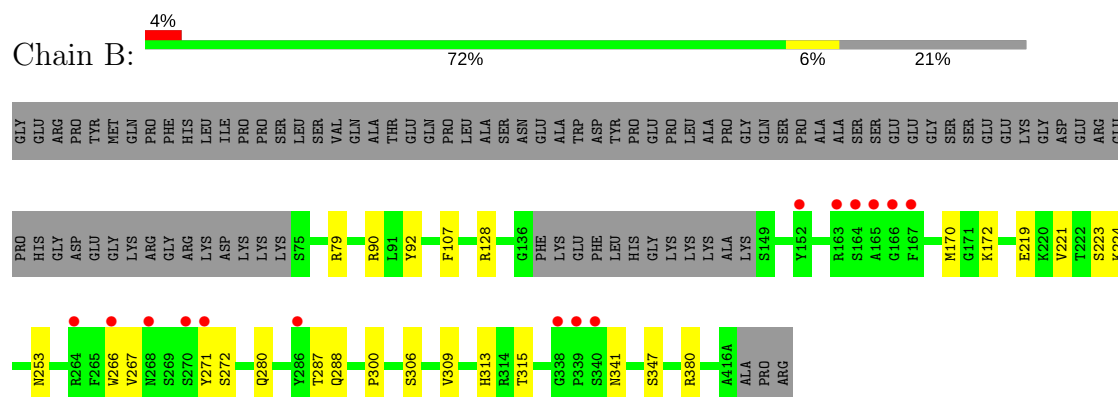
### 3 Residue-property plots

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

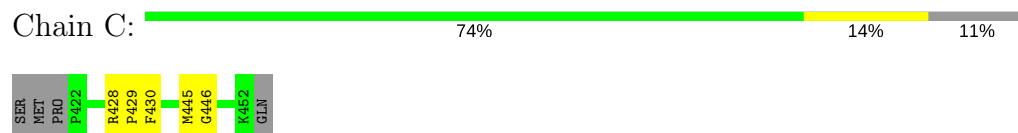
#### • Molecule 1: Putative angiotensinogen



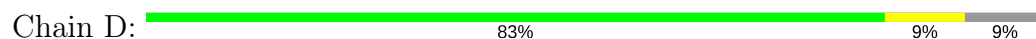
#### • Molecule 1: Putative angiotensinogen



#### • Molecule 2: C-terminal peptide of Putative angiotensinogen



#### • Molecule 2: C-terminal peptide of Putative angiotensinogen





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	42.40Å 119.36Å 141.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	91.26 – 2.70 91.26 – 2.70	Depositor EDS
% Data completeness (in resolution range)	90.6 (91.26-2.70) 90.7 (91.26-2.70)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.56 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.204 , 0.277 0.206 , 0.273	Depositor DCC
$R_{free}$ test set	930 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	62.3	Xtriage
Anisotropy	0.399	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 41.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5704	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	74.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.77	1/2668 (0.0%)	0.87	2/3596 (0.1%)
1	B	0.69	0/2629	0.88	5/3547 (0.1%)
2	C	0.73	0/253	0.96	0/343
2	D	0.72	0/261	0.89	0/355
All	All	0.73	1/5811 (0.0%)	0.88	7/7841 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	182	TRP	CB-CG	5.13	1.59	1.50

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	79	ARG	NE-CZ-NH1	6.38	123.49	120.30
1	B	128	ARG	NE-CZ-NH1	6.11	123.36	120.30
1	B	271	TYR	CA-CB-CG	5.93	124.67	113.40
1	B	90	ARG	NE-CZ-NH2	-5.65	117.47	120.30
1	A	79	ARG	NE-CZ-NH1	5.54	123.07	120.30
1	B	380	ARG	NE-CZ-NH1	5.36	122.98	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	380	ARG	NE-CZ-NH1	5.12	122.86	120.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	267	VAL	Peptide
1	A	341	ASN	Peptide
1	B	267	VAL	Peptide
1	B	341	ASN	Peptide

## 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	2616	0	2658	14	0
1	B	2578	0	2610	14	0
2	C	248	0	261	6	0
2	D	255	0	268	5	0
3	B	5	0	0	0	0
4	A	2	0	0	0	0
All	All	5704	0	5797	28	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 2.

All (28) 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:A:315:THR:HG21	2:C:429:PRO:HD2	1.87	0.57
1:B:172:LYS:HE3	1:B:221:VAL:HG11	1.88	0.56
1:A:172:LYS:HE3	1:A:221:VAL:HG11	1.87	0.56
1:A:300:PRO:HA	1:A:306:SER:HB3	1.88	0.56
1:B:266:TRP:CZ3	1:B:272:SER:HB3	2.42	0.56
1:A:266:TRP:CZ3	1:A:272:SER:HB3	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:VAL:O	1:A:221:VAL:HG12	2.06	0.53
1:B:300:PRO:HA	1:B:306:SER:HB3	1.90	0.53
1:B:221:VAL:HG12	1:B:221:VAL:O	2.09	0.52
1:A:309:VAL:HG13	2:C:430:PHE:CD1	2.46	0.51
1:B:253:ASN:HB2	1:B:280:GLN:HE22	1.77	0.50
1:A:300:PRO:HA	1:A:306:SER:CB	2.44	0.47
1:B:315:THR:HG21	2:D:429:PRO:HD2	1.96	0.47
1:A:219:GLU:HG3	1:A:224:LYS:HA	1.96	0.47
1:B:92:TYR:HB2	2:D:445:MET:HE1	1.97	0.45
1:B:219:GLU:HG3	1:B:224:LYS:HA	1.98	0.45
1:B:92:TYR:HB2	2:D:445:MET:CE	2.47	0.45
1:B:300:PRO:HA	1:B:306:SER:CB	2.47	0.44
1:A:288:GLN:OE1	1:A:313:HIS:NE2	2.50	0.43
1:A:105:ILE:O	2:C:446:GLY:HA3	2.19	0.43
1:A:92:TYR:HB2	2:C:445:MET:HE1	2.00	0.43
1:A:107:PHE:CZ	2:C:445:MET:HE2	2.54	0.42
1:B:107:PHE:CZ	2:D:445:MET:HE2	2.55	0.42
1:B:309:VAL:HG13	2:D:430:PHE:CD1	2.56	0.41
1:A:92:TYR:HB2	2:C:445:MET:CE	2.50	0.41
1:B:253:ASN:HB2	1:B:280:GLN:NE2	2.34	0.41
1:A:245:ILE:CG2	1:A:409:ALA:HB3	2.51	0.40
1:B:288:GLN:OE1	1:B:313:HIS:NE2	2.52	0.40

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	331/421 (79%)	320 (97%)	9 (3%)	2 (1%)	28	56
1	B	327/421 (78%)	317 (97%)	9 (3%)	1 (0%)	44	73
2	C	29/35 (83%)	27 (93%)	2 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	30/35 (86%)	29 (97%)	1 (3%)	0	100	100
All	All	717/912 (79%)	693 (97%)	21 (3%)	3 (0%)	38	66

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	74	LYS
1	A	223	SER
1	B	223	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	A	287/357 (80%)	285 (99%)	2 (1%)	87	96
1	B	283/357 (79%)	280 (99%)	3 (1%)	78	93
2	C	28/32 (88%)	27 (96%)	1 (4%)	40	70
2	D	29/32 (91%)	29 (100%)	0	100	100
All	All	627/778 (81%)	621 (99%)	6 (1%)	80	93

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	287	THR
1	A	347	SER
1	B	170	MET
1	B	287	THR
1	B	347	SER
2	C	428	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	94	GLN
1	B	280	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand 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	$\# Z  > 2$
3	SO4	B	501	-	4,4,4	0.34	0	6,6,6	0.67	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
3	SO4	B	501	-	-	0/0/0/0	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.

No monomer is involved in short contacts.

## 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	335/421 (79%)	-0.18	4 (1%) 79 80	35, 62, 104, 139	0
1	B	331/421 (78%)	0.21	15 (4%) 34 32	45, 81, 119, 180	0
2	C	31/35 (88%)	-0.40	0 100 100	42, 60, 86, 87	0
2	D	32/35 (91%)	-0.14	0 100 100	57, 76, 106, 120	0
All	All	729/912 (79%)	-0.01	19 (2%) 56 56	35, 70, 115, 180	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	340	SER	11.1
1	B	163	ARG	5.4
1	B	338	GLY	4.9
1	B	164	SER	4.3
1	B	152	TYR	4.3
1	B	165	ALA	3.4
1	B	270	SER	3.2
1	B	286	TYR	2.8
1	B	339	PRO	2.6
1	B	167	PHE	2.6
1	A	281	ARG	2.4
1	A	374	TYR	2.3
1	B	264	ARG	2.3
1	A	271	TYR	2.2
1	B	268	ASN	2.1
1	B	266	TRP	2.1
1	B	166	GLY	2.1
1	A	152	TYR	2.1
1	B	271	TYR	2.0

## 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 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	SO4	B	501	5/5	0.99	0.11	-1.53	53,54,57,58	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.