



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 17, 2019 – 11:32 PM EDT

PDB ID : 6HMK  
Title : POLYADPRIBOSYL GLYCOHYDROLASE IN COMPLEX WITH  
PDD00016690  
Authors : Tucker, J.A.; Barkauskaite, E.  
Deposited on : 2018-09-12  
Resolution : 2.06 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : rb-20031633  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20031633

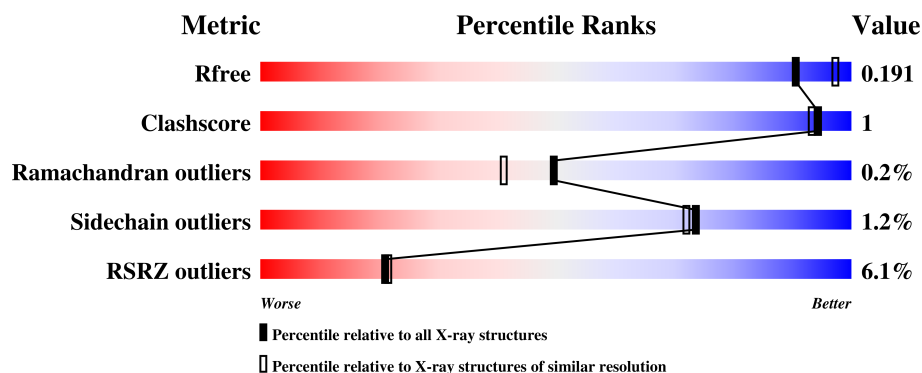
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.06 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))
$R_{free}$	111664	2250 (2.08-2.04)
Clashscore	122126	2358 (2.08-2.04)
Ramachandran outliers	120053	2339 (2.08-2.04)
Sidechain outliers	120020	2339 (2.08-2.04)
RSRZ outliers	108989	2211 (2.08-2.04)

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	531	<div> <div>6%</div> <div>91%</div> <div>5%</div> </div>

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4628 atoms, of which 20 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.

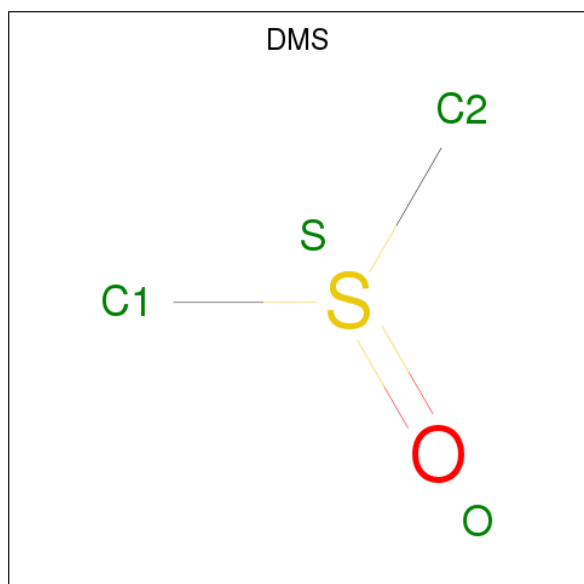
- Molecule 1 is a protein called Poly(ADP-ribose) glycohydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	506	4098	2615	710	746	27	0	8	0

There are 9 discrepancies between the modelled and reference sequences:

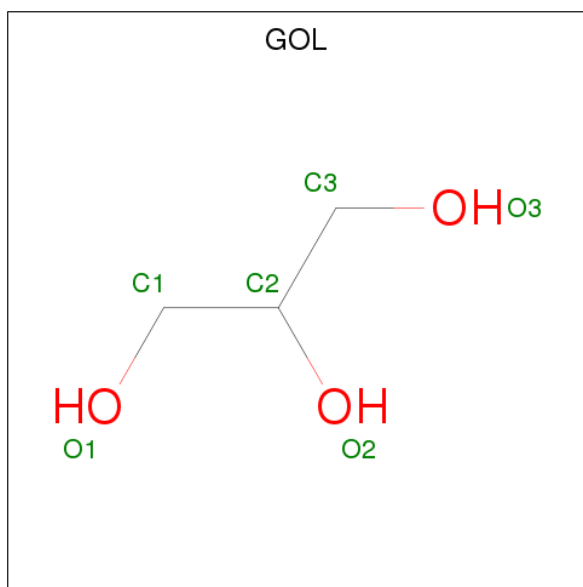
Chain	Residue	Modelled	Actual	Comment	Reference
A	446	GLY	-	expression tag	UNP Q86W56
A	447	SER	-	expression tag	UNP Q86W56
A	616	ALA	LYS	engineered mutation	UNP Q86W56
A	617	ALA	GLN	engineered mutation	UNP Q86W56
A	618	ALA	LYS	engineered mutation	UNP Q86W56
A	681	6WK	CYS	conflict	UNP Q86W56
A	688	ALA	GLU	engineered mutation	UNP Q86W56
A	689	ALA	LYS	engineered mutation	UNP Q86W56
A	690	ALA	LYS	engineered mutation	UNP Q86W56

- Molecule 2 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C<sub>2</sub>H<sub>6</sub>OS).



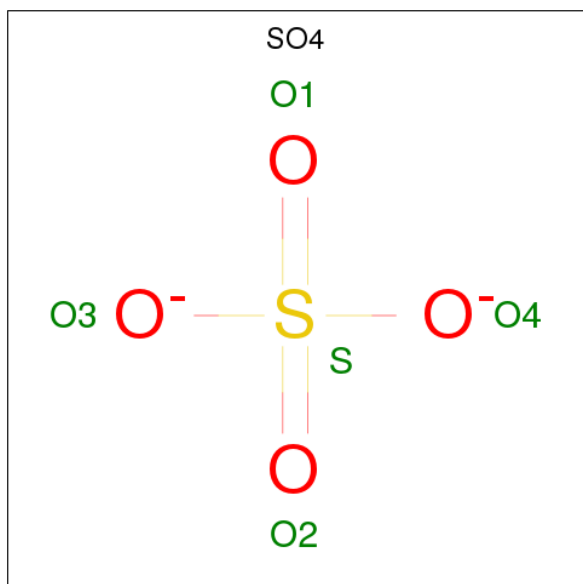
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			4	2	1	1		
2	A	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



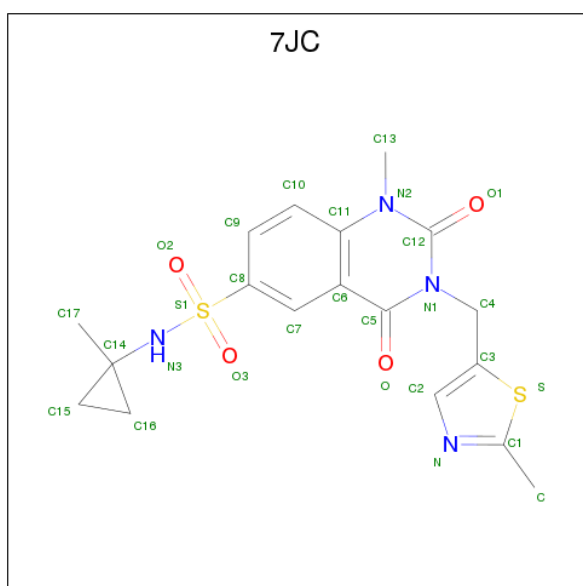
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



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

- Molecule 5 is 1-methyl- {N}-(1-methylcyclopropyl)-3-[(2-methyl-1,3-thiazol-5-yl)methyl]-2,4-bis(oxidanylidene)quinazoline-6-sulfonamide (three-letter code: 7JC) (formula: C<sub>18</sub>H<sub>20</sub>N<sub>4</sub>O<sub>4</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C H N O S 48 18 20 4 4 2	0	0

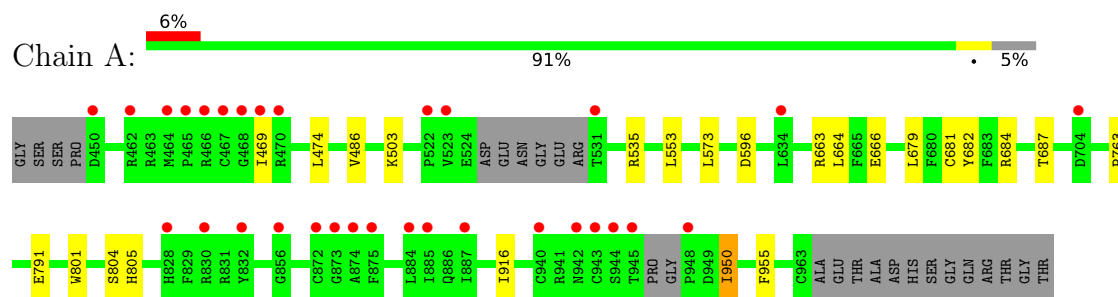
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	448	Total O 448 448	0	1

### 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 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: Poly(ADP-ribose) glycohydrolase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.09Å 90.11Å 95.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.77 – 2.06 28.76 – 2.06	Depositor EDS
% Data completeness (in resolution range)	99.7 (28.77-2.06) 99.7 (28.76-2.06)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.08 (at 2.06Å)	Xtriage
Refinement program	BUSTER	Depositor
R, $R_{free}$	0.154 , 0.189 0.153 , 0.191	Depositor DCC
$R_{free}$ test set	1823 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	23.9	Xtriage
Anisotropy	0.701	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 66.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4628	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.68% 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: GOL, DMS, 7JC, 6WK, 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	0.51	0/4183	0.61	0/5675

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	A	4098	0	3935	11	0
2	A	8	0	12	0	0
3	A	6	0	8	0	0
4	A	20	0	0	0	0
5	A	28	20	0	0	0
6	A	448	0	0	0	0
All	All	4608	20	3955	11	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 1.

All (11) 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:681:6WK:SD	1:A:804:SER:HB2	2.20	0.82
1:A:681:6WK:SD	1:A:801:TRP:HZ2	2.19	0.64
1:A:791:GLU:HG3	1:A:805:HIS:HB2	1.91	0.52
1:A:553:LEU:HD23	1:A:573:LEU:HD21	1.92	0.51
1:A:663:ARG:O	1:A:666:GLU:HG2	2.11	0.49
1:A:664:LEU:HD21	1:A:679:LEU:HD12	1.94	0.49
1:A:474:LEU:O	1:A:486:VAL:HG11	2.16	0.45
1:A:950:ILE:HD11	1:A:955:PHE:HA	1.99	0.45
1:A:596:ASP:HB3	1:A:687:THR:HB	1.99	0.43
1:A:681:6WK:SD	1:A:801:TRP:CZ2	3.08	0.43
1:A:682:TYR:HB2	1:A:763:PRO:HG2	2.01	0.43

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	507/531 (96%)	493 (97%)	13 (3%)	1 (0%)	49 41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	469	ILE

### 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	425/461 (92%)	420 (99%)	5 (1%)	74 72

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	503	LYS
1	A	535	ARG
1	A	684	ARG
1	A	916	ILE
1	A	950	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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	6WK	A	681	1	12,13,14	0.86	1 (8%)	8,15,17	1.08	1 (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
1	6WK	A	681	1	-	0/12/15/17	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	681	6WK	CA-C	2.70	1.53	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	681	6WK	C4-SD-SG	2.01	107.70	103.82

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
1	A	681	6WK	3	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

8 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	DMS	A	1001	-	3,3,3	0.33	0	3,3,3	0.57	0
2	DMS	A	1002	-	3,3,3	0.35	0	3,3,3	0.33	0
3	GOL	A	1003	-	5,5,5	0.20	0	5,5,5	0.37	0
4	SO4	A	1004	-	4,4,4	0.37	0	6,6,6	0.47	0
4	SO4	A	1005	-	4,4,4	0.19	0	6,6,6	0.07	0
4	SO4	A	1006	-	4,4,4	0.28	0	6,6,6	0.43	0
4	SO4	A	1007	-	4,4,4	0.21	0	6,6,6	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	7JC	A	1008	-	26,31,31	1.15	3 (11%)	33,49,49	1.02	2 (6%)

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	DMS	A	1001	-	-	0/0/0/0	0/0/0/0
2	DMS	A	1002	-	-	0/0/0/0	0/0/0/0
3	GOL	A	1003	-	-	0/4/4/4	0/0/0/0
4	SO4	A	1004	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1005	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1006	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1007	-	-	0/0/0/0	0/0/0/0
5	7JC	A	1008	-	-	0/12/20/20	0/3/4/4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1008	7JC	C2-N	2.13	1.39	1.36
5	A	1008	7JC	C7-C8	2.29	1.40	1.36
5	A	1008	7JC	C5-C6	3.43	1.47	1.41

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1008	7JC	C2-C3-S	-3.13	108.89	112.00
5	A	1008	7JC	C6-C5-N1	-2.11	114.71	116.15

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 [i](#)

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	505/531 (95%)	0.05	31 (6%) 21 21	13, 27, 61, 118	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	873	GLY	7.6
1	A	944	SER	7.3
1	A	874	ALA	7.0
1	A	465	PRO	6.9
1	A	856	GLY	6.0
1	A	943	CYS	5.5
1	A	945	THR	5.4
1	A	468	GLY	4.7
1	A	467	CYS	4.2
1	A	531	THR	4.2
1	A	464	MET	4.1
1	A	875	PHE	4.0
1	A	469	ILE	3.7
1	A	828	HIS	3.7
1	A	885	ILE	3.6
1	A	872[A]	CYS	3.4
1	A	942	ASN	3.4
1	A	940	CYS	3.1
1	A	523	VAL	2.9
1	A	948	PRO	2.9
1	A	884	LEU	2.8
1	A	887	ILE	2.6
1	A	704	ASP	2.5
1	A	466	ARG	2.4
1	A	450	ASP	2.4
1	A	462	ARG	2.2
1	A	522	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	830	ARG	2.1
1	A	832	TYR	2.0
1	A	634	LEU	2.0
1	A	470	ARG	2.0

## 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. 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(Å <sup>2</sup> )	Q<0.9
1	6WK	A	681	14/15	0.88	0.19	17,56,69,72	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. 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(Å <sup>2</sup> )	Q<0.9
4	SO4	A	1007	5/5	0.81	0.25	115,116,116,116	0
4	SO4	A	1005	5/5	0.86	0.28	96,96,96,97	0
4	SO4	A	1004	5/5	0.88	0.72	164,164,165,165	0
3	GOL	A	1003	6/6	0.91	0.26	38,43,45,51	0
2	DMS	A	1002	4/4	0.94	0.29	53,56,57,58	0
4	SO4	A	1006	5/5	0.94	0.16	39,45,48,50	0
2	DMS	A	1001	4/4	0.96	0.14	56,56,57,58	0
5	7JC	A	1008	28/28	0.98	0.09	19,24,33,34	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.