



# Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 06:38 pm BST

PDB ID : 4K6J  
Title : Human cohesin inhibitor WapL  
Authors : Tomchick, D.R.; Yu, H.; Ouyang, Z.  
Deposited on : 2013-04-16  
Resolution : 2.62 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	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

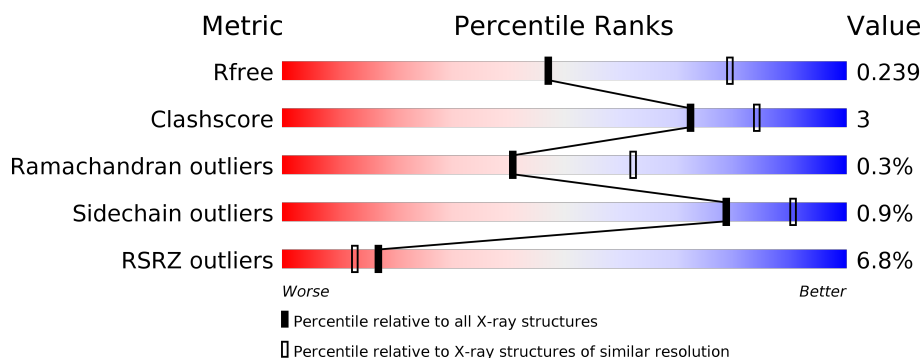
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.62 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))
$R_{free}$	130704	3797 (2.64-2.60)
Clashscore	141614	4168 (2.64-2.60)
Ramachandran outliers	138981	4093 (2.64-2.60)
Sidechain outliers	138945	4093 (2.64-2.60)
RSRZ outliers	127900	3731 (2.64-2.60)

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 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	568	<div> <div>5%</div> <div> <div></div> <div>79%</div> <div>8%</div> <div>13%</div> </div> </div>
1	B	568	<div> <div>7%</div> <div> <div></div> <div>75%</div> <div>7%</div> <div>17%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15557 atoms, of which 7730 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 Wings apart-like protein homolog.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	497	Total	C	H	N	O	S	0	0	0
			7887	2451	3963	689	752	32			
1	B	471	Total	C	H	N	O	S	0	0	0
			7485	2330	3761	654	709	31			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	GLY	-	EXPRESSION TAG	UNP Q7Z5K2
A	-6	PRO	-	EXPRESSION TAG	UNP Q7Z5K2
A	-5	LEU	-	EXPRESSION TAG	UNP Q7Z5K2
A	-4	GLY	-	EXPRESSION TAG	UNP Q7Z5K2
A	-3	SER	-	EXPRESSION TAG	UNP Q7Z5K2
A	-2	GLY	-	EXPRESSION TAG	UNP Q7Z5K2
A	-1	ARG	-	EXPRESSION TAG	UNP Q7Z5K2
A	0	PRO	-	EXPRESSION TAG	UNP Q7Z5K2
B	-7	GLY	-	EXPRESSION TAG	UNP Q7Z5K2
B	-6	PRO	-	EXPRESSION TAG	UNP Q7Z5K2
B	-5	LEU	-	EXPRESSION TAG	UNP Q7Z5K2
B	-4	GLY	-	EXPRESSION TAG	UNP Q7Z5K2
B	-3	SER	-	EXPRESSION TAG	UNP Q7Z5K2
B	-2	GLY	-	EXPRESSION TAG	UNP Q7Z5K2
B	-1	ARG	-	EXPRESSION TAG	UNP Q7Z5K2
B	0	PRO	-	EXPRESSION TAG	UNP Q7Z5K2

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			7	2	3	2		
3	A	1	Total	C	H	O	0	0
			7	2	3	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	58	Total	O	0	0
			58	58		
4	B	48	Total	O	0	0
			48	48		

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

- Chain A:

- Chain B:
- 
- 7% 75% 7% 17%

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.54Å 107.54Å 300.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.68 – 2.62 41.84 – 2.62	Depositor EDS
% Data completeness (in resolution range)	94.8 (29.68-2.62) 94.9 (41.84-2.62)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.42 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.8.1_1168	Depositor
R, $R_{free}$	0.184 , 0.237 0.188 , 0.239	Depositor DCC
$R_{free}$ test set	2587 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	34.7	Xtriage
Anisotropy	0.261	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 58.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	15557	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% 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, ACT

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	0.22	0/3979	0.39	0/5369
1	B	0.22	0/3776	0.40	0/5089
All	All	0.22	0/7755	0.39	0/10458

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	3924	3963	3943	27	0
1	B	3724	3761	3742	27	0
2	A	35	0	0	0	0
2	B	30	0	0	1	0
3	A	8	6	6	0	0
4	A	58	0	0	0	0
4	B	48	0	0	1	0
All	All	7827	7730	7691	52	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 3.



All (52) 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:B:715:ASN:ND2	1:B:765:MET:SD	2.65	0.70
1:A:738:ARG:HG2	1:A:818:LEU:HD13	1.81	0.63
1:B:853:ARG:NH2	4:B:1309:HOH:O	2.31	0.63
1:B:-1:ARG:N	1:B:0:PRO:HD2	2.15	0.61
1:B:992:VAL:O	1:B:999:ARG:NH1	2.34	0.61
1:B:644:ASP:O	1:B:646:VAL:N	2.34	0.60
1:A:946:TRP:CD1	1:B:817:LEU:HD13	2.39	0.58
1:A:1051:GLU:HA	1:A:1054:THR:HG22	1.87	0.57
1:A:638:HIS:NE2	1:A:644:ASP:OD2	2.40	0.55
1:A:738:ARG:HG2	1:A:818:LEU:CD1	2.37	0.55
1:A:-1:ARG:N	1:A:0:PRO:CD	2.72	0.52
1:B:1006:GLU:HA	1:B:1031:HIS:HB3	1.92	0.52
1:A:646:VAL:CG1	1:A:647:GLU:N	2.73	0.51
1:A:1030:VAL:HG22	1:A:1031:HIS:N	2.27	0.50
1:B:1050:ALA:HB3	1:B:1115:HIS:HB2	1.92	0.50
1:B:951:THR:HG22	1:B:957:LEU:HD22	1.93	0.50
1:A:738:ARG:HD3	1:A:818:LEU:HD13	1.95	0.49
1:B:657:ASP:HA	1:B:660:TYR:CE2	2.49	0.48
1:B:968:VAL:N	1:B:969:PRO:CD	2.77	0.47
1:A:968:VAL:N	1:A:969:PRO:CD	2.78	0.47
1:B:765:MET:O	1:B:768:ILE:N	2.48	0.47
1:B:981:ARG:NH2	2:B:1201:SO4:O3	2.48	0.47
1:A:951:THR:HG22	1:A:957:LEU:HD22	1.96	0.46
1:A:891:CYS:HB3	1:A:930:MET:HG3	1.97	0.46
1:B:669:GLN:HG3	1:B:670:PRO:HD2	1.97	0.46
1:B:645:VAL:HG13	1:B:645:VAL:O	2.15	0.46
1:A:669:GLN:HG3	1:A:670:PRO:HD2	1.97	0.45
1:A:913:LEU:HB3	1:A:914:PRO:HD2	1.98	0.45
1:A:967:GLN:O	1:A:970:LYS:HG2	2.17	0.45
1:B:1175:THR:HG23	1:B:1176:GLY:N	2.31	0.44
1:A:642:PHE:O	1:A:643:ASN:HB2	2.17	0.44
1:A:900:ARG:HD2	1:A:923:GLY:HA3	1.99	0.44
1:B:1172:VAL:HG13	1:B:1177:GLN:HG3	2.00	0.43
1:B:657:ASP:HA	1:B:660:TYR:CD2	2.54	0.43
1:B:1041:LEU:O	1:B:1045:ARG:HB2	2.19	0.43
1:A:1151:ASP:CG	1:A:1153:SER:HG	2.22	0.43
1:A:633:TYR:CE2	1:A:637:GLN:HG3	2.54	0.43
1:A:646:VAL:HG12	1:A:647:GLU:N	2.33	0.42
1:A:651:ASN:O	1:A:654:PHE:HB3	2.19	0.42
1:B:824:ILE:CG2	1:B:854:CYS:HB3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:891:CYS:HB3	1:B:930:MET:HG3	2.01	0.42
1:B:714:GLN:HG2	1:B:715:ASN:N	2.35	0.42
1:B:699:MET:O	1:B:703:VAL:HG13	2.20	0.42
1:B:644:ASP:HB3	1:B:646:VAL:HG23	2.02	0.42
1:B:1169:THR:HG22	1:B:1171:ALA:HB2	2.01	0.42
1:B:1172:VAL:HG13	1:B:1177:GLN:CG	2.50	0.42
1:A:646:VAL:HG11	1:A:692:MET:CE	2.50	0.41
1:A:658:ILE:HD11	1:A:694:LEU:HD13	2.01	0.41
1:A:1053:LYS:O	1:A:1057:LEU:HD13	2.20	0.41
1:A:912:PRO:HB2	1:A:919:THR:OG1	2.21	0.41
1:A:1057:LEU:HD21	1:A:1107:LYS:HB3	2.02	0.41
1:A:946:TRP:CD1	1:B:817:LEU:CD1	3.03	0.41

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	489/568 (86%)	471 (96%)	17 (4%)	1 (0%)	47	69
1	B	461/568 (81%)	444 (96%)	15 (3%)	2 (0%)	34	55
All	All	950/1136 (84%)	915 (96%)	32 (3%)	3 (0%)	41	62

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	645	VAL
1	A	651	ASN
1	B	641	HIS

### 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	443/504 (88%)	440 (99%)	3 (1%)	84	93
1	B	418/504 (83%)	413 (99%)	5 (1%)	71	86
All	All	861/1008 (85%)	853 (99%)	8 (1%)	78	90

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	793	HIS
1	A	878	SER
1	A	992	VAL
1	B	660	TYR
1	B	703	VAL
1	B	878	SER
1	B	957	LEU
1	B	1185	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	712	HIS

### 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 ⓘ

15 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	SO4	A	1206	-	4,4,4	0.14	0	6,6,6	0.07	0
2	SO4	B	1204	-	4,4,4	0.11	0	6,6,6	0.21	0
2	SO4	B	1203	-	4,4,4	0.13	0	6,6,6	0.08	0
2	SO4	A	1203	-	4,4,4	0.13	0	6,6,6	0.11	0
2	SO4	B	1201	-	4,4,4	0.16	0	6,6,6	0.11	0
2	SO4	A	1207	-	4,4,4	0.15	0	6,6,6	0.07	0
2	SO4	B	1205	-	4,4,4	0.15	0	6,6,6	0.07	0
2	SO4	B	1202	-	4,4,4	0.14	0	6,6,6	0.16	0
2	SO4	A	1202	-	4,4,4	0.14	0	6,6,6	0.10	0
2	SO4	B	1206	-	4,4,4	0.15	0	6,6,6	0.09	0
3	ACT	A	1208	-	1,3,3	1.63	0	0,3,3	0.00	-
2	SO4	A	1201	-	4,4,4	0.16	0	6,6,6	0.10	0
2	SO4	A	1205	-	4,4,4	0.16	0	6,6,6	0.09	0
3	ACT	A	1209	-	1,3,3	1.52	0	0,3,3	0.00	-
2	SO4	A	1204	-	4,4,4	0.15	0	6,6,6	0.07	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1201	SO4	1	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

### 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	497/568 (87%)	0.04	27 (5%) 25 20	17, 38, 98, 147	0
1	B	471/568 (82%)	0.16	39 (8%) 11 8	19, 43, 104, 148	0
All	All	968/1136 (85%)	0.10	66 (6%) 17 13	17, 40, 101, 148	0

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1060	ASP	7.5
1	A	643	ASN	7.4
1	A	1058	ILE	7.4
1	B	651	ASN	6.3
1	B	652	GLN	6.2
1	B	1109	LEU	6.2
1	B	641	HIS	6.1
1	A	1057	LEU	5.4
1	B	1108	ALA	5.4
1	B	653	GLU	5.4
1	A	837	ARG	5.3
1	A	1059	LYS	5.2
1	B	1052	SER	5.2
1	B	1111	HIS	4.7
1	B	1110	GLN	4.5
1	A	1055	ASP	4.4
1	A	644	ASP	4.3
1	B	1054	THR	4.3
1	B	1053	LYS	4.2
1	B	1112	ALA	4.2
1	B	642	PHE	4.2
1	A	1056	GLU	4.0
1	B	645	VAL	3.8
1	B	654	PHE	3.7

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Mol	Chain	Res	Type	RSRZ
1	B	1049	LEU	3.6
1	B	647	GLU	3.4
1	A	838	ASP	3.3
1	B	838	ASP	3.3
1	B	644	ASP	3.2
1	A	641	HIS	3.2
1	A	1106	ASN	3.2
1	A	1107	LYS	3.1
1	A	836	SER	3.1
1	B	837	ARG	3.1
1	B	1050	ALA	3.0
1	A	907	LEU	2.9
1	A	1054	THR	2.9
1	B	783	HIS	2.8
1	B	655	THR	2.8
1	A	786	LEU	2.8
1	A	760	LEU	2.8
1	B	1113	GLY	2.8
1	B	666	LYS	2.7
1	B	656	ASP	2.7
1	A	1052	SER	2.7
1	A	763	LYS	2.7
1	B	646	VAL	2.6
1	B	1107	LYS	2.6
1	A	1029	GLN	2.5
1	B	668	THR	2.5
1	B	1051	GLU	2.5
1	A	654	PHE	2.4
1	A	1053	LYS	2.4
1	A	1109	LEU	2.4
1	B	643	ASN	2.3
1	B	649	GLY	2.3
1	B	1149	GLU	2.3
1	B	836	SER	2.3
1	A	909	ASP	2.3
1	B	1045	ARG	2.3
1	A	642	PHE	2.2
1	B	786	LEU	2.2
1	B	661	LEU	2.1
1	B	763	LYS	2.1
1	A	1108	ALA	2.1
1	B	660	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. 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
3	ACT	A	1208	4/4	0.83	0.21	34,40,53,63	0
3	ACT	A	1209	4/4	0.85	0.17	25,30,50,55	0
2	SO4	A	1204	5/5	0.90	0.19	66,79,92,94	0
2	SO4	A	1205	5/5	0.94	0.17	63,66,78,86	0
2	SO4	B	1206	5/5	0.95	0.14	45,59,64,71	0
2	SO4	B	1201	5/5	0.96	0.14	34,40,63,69	0
2	SO4	B	1204	5/5	0.97	0.16	34,45,64,75	0
2	SO4	B	1205	5/5	0.97	0.18	47,53,57,73	0
2	SO4	A	1207	5/5	0.97	0.16	49,53,68,69	0
2	SO4	A	1203	5/5	0.98	0.11	46,50,59,66	0
2	SO4	A	1202	5/5	0.98	0.15	39,47,54,66	0
2	SO4	B	1203	5/5	0.98	0.12	42,53,54,56	0
2	SO4	B	1202	5/5	0.99	0.14	27,35,39,49	0
2	SO4	A	1206	5/5	0.99	0.15	50,57,59,59	0
2	SO4	A	1201	5/5	0.99	0.15	34,38,44,44	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.