



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 07:54 pm GMT

PDB ID : 2CG1  
Title : AGAO IN COMPLEX WITH WC11B (RU-WIRE INHIBITOR, 11-CARBON LINKER, DATA SET B)  
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Deposited on : 2006-02-27  
Resolution : 1.67 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

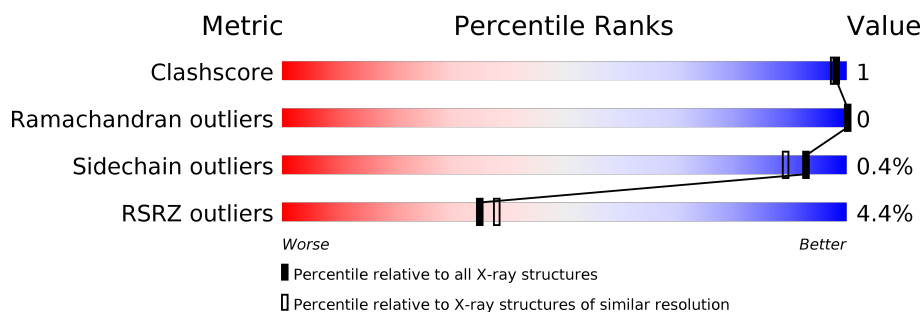
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.67 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))
Clashscore	112137	5803 (1.70-1.66)
Ramachandran outliers	110173	5704 (1.70-1.66)
Sidechain outliers	110143	5703 (1.70-1.66)
RSRZ outliers	101464	5298 (1.70-1.66)

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	646	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	11R	A	1631	X	-	-	X
6	GOL	A	1634	-	-	-	X
6	GOL	A	1635	-	-	-	X
6	GOL	A	1636	-	-	-	X

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 10015 atoms, of which 4573 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 PHENYLETHYLAMINE OXIDASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	620	Total	C	H	N	O	S	0	8	0
			9390	3091	4498	856	934	11			

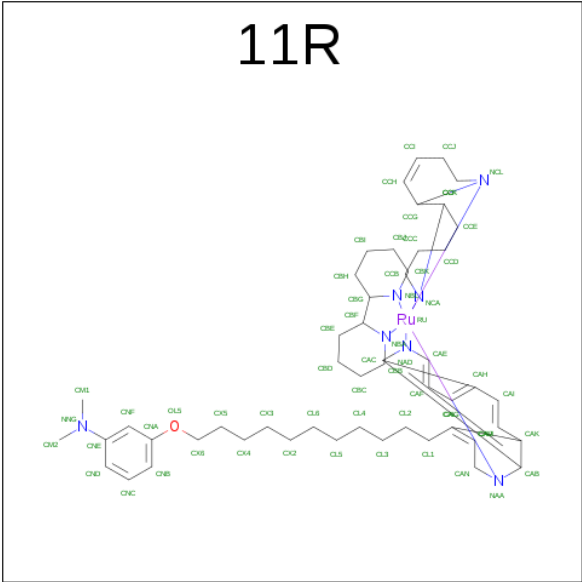
- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cu	0	0
			1	1		

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

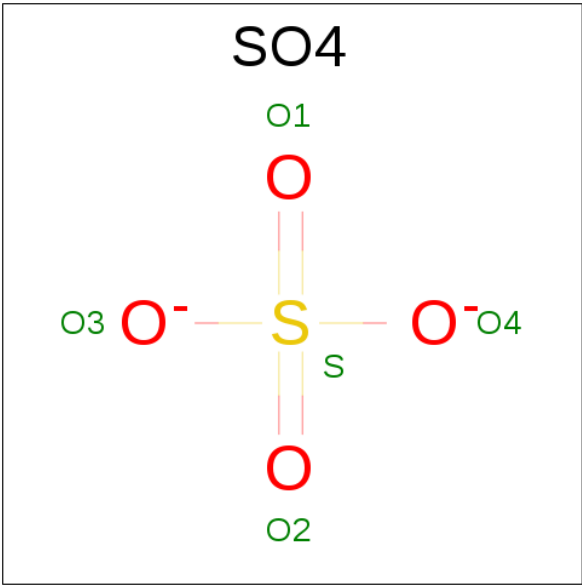
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		

- Molecule 4 is RUTHENIUM WIRE, 11 CARBON LINKER (three-letter code: 11R) (formula: C<sub>51</sub>H<sub>75</sub>N<sub>7</sub>ORu).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
4	A	1	115	51	55	7	1	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			11	3	5	3		
6	A	1	Total	C	H	O	0	0
			11	3	5	3		
6	A	1	Total	C	H	O	0	0
			11	3	5	3		
6	A	1	Total	C	H	O	0	0
			11	3	5	3		

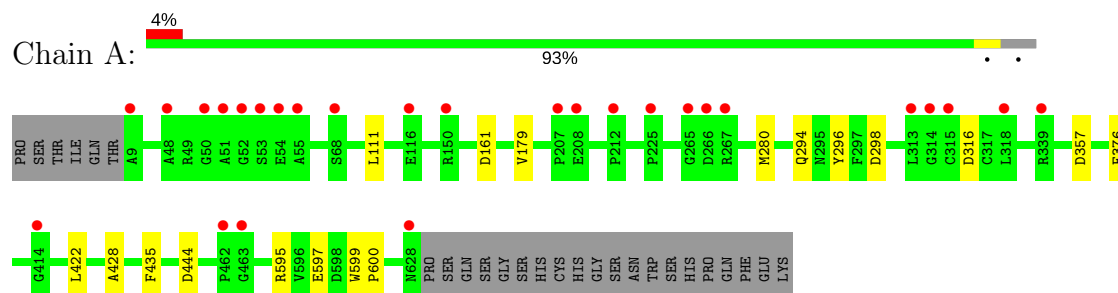
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	459	Total	O	0	0
			459	459		

### 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: PHENYLETHYLAMINE OXIDASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	157.92Å 63.04Å 92.07Å 90.00° 112.19° 90.00°	Depositor
Resolution (Å)	14.99 – 1.67 14.98 – 1.67	Depositor EDS
% Data completeness (in resolution range)	97.3 (14.99-1.67) 97.3 (14.98-1.67)	Depositor EDS
$R_{merge}$	0.03	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.21 (at 1.67Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.160 , 0.179 (Not available) , (Not available)	Depositor DCC
$R_{free}$ test set	NotAvailable	DCC
Wilson B-factor (Å <sup>2</sup> )	20.4	Xtriage
Anisotropy	0.653	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.47 , 57.8	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	0.96	EDS
Total number of atoms	10015	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% 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 [i](#)

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

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NA, SO4, TPQ, 11R, CU

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	0.43	0/5030	0.76	4/6848 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	316	ASP	CB-CG-OD2	5.74	123.46	118.30
1	A	357	ASP	CB-CG-OD2	5.39	123.15	118.30
1	A	298	ASP	CB-CG-OD2	5.28	123.06	118.30
1	A	161	ASP	CB-CG-OD2	5.11	122.90	118.30

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	4892	4498	4706	8	0
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	60	55	64	0	0
5	A	5	0	0	0	0
6	A	24	20	32	0	0
7	A	459	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5442	4573	4802	8	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 (8) 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:294[A]:GLN:HG3	1:A:296:TYR:CZ	2.32	0.64
1:A:599:TRP:CD2	1:A:600:PRO:HA	2.35	0.62
1:A:422:LEU:HD11	1:A:428:ALA:HB2	1.88	0.54
1:A:294[A]:GLN:HG3	1:A:296:TYR:CE2	2.47	0.50
1:A:280[B]:MET:HG3	1:A:435:PHE:CD2	2.50	0.47
1:A:111:LEU:HD12	1:A:179:VAL:HG11	1.96	0.47
1:A:280[B]:MET:HG3	1:A:435:PHE:CE2	2.52	0.45
1:A:595:ARG:HG3	1:A:597:GLU:HB2	2.00	0.42

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	624/646 (97%)	604 (97%)	20 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 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	520/537 (97%)	518 (100%)	2 (0%)	93	89

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	376	PHE
1	A	444	ASP

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	TPQ	A	382	1	14,14,15	1.35	2 (14%)	17,19,21	1.93	3 (17%)

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	TPQ	A	382	1	-	0/4/22/24	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	382	TPQ	O4-C4	-2.76	1.26	1.33
1	A	382	TPQ	C3-C4	2.92	1.40	1.35

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	382	TPQ	CB-CA-C	-5.97	99.91	111.41
1	A	382	TPQ	CB-C1-C6	-2.02	118.51	122.41
1	A	382	TPQ	C6-C1-C2	2.49	120.54	118.54

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](#)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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	$\# Z  > 2$
4	11R	A	1631	-	60,70,70	4.04	24 (40%)	56,108,108	2.70	26 (46%)
5	SO4	A	1632	-	4,4,4	0.14	0	6,6,6	0.24	0
6	GOL	A	1633	-	5,5,5	0.19	0	5,5,5	0.23	0
6	GOL	A	1634	-	5,5,5	0.28	0	5,5,5	0.25	0
6	GOL	A	1635	-	5,5,5	0.28	0	5,5,5	0.43	0
6	GOL	A	1636	-	5,5,5	0.35	0	5,5,5	0.28	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
4	11R	A	1631	-	5/5/19/19	0/19/157/157	0/10/11/11
5	SO4	A	1632	-	-	0/0/0/0	0/0/0/0
6	GOL	A	1633	-	-	0/4/4/4	0/0/0/0
6	GOL	A	1634	-	-	0/4/4/4	0/0/0/0
6	GOL	A	1635	-	-	0/4/4/4	0/0/0/0
6	GOL	A	1636	-	-	0/4/4/4	0/0/0/0

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1631	11R	CCB-NCA	-14.03	1.28	1.48
4	A	1631	11R	CBB-NBA	-13.99	1.28	1.48
4	A	1631	11R	CBK-NBL	-9.70	1.34	1.48
4	A	1631	11R	CCK-NCL	-9.67	1.34	1.48
4	A	1631	11R	CBD-CBE	-7.65	1.33	1.53
4	A	1631	11R	CCD-CCE	-7.61	1.33	1.53
4	A	1631	11R	CBH-CBG	-6.10	1.39	1.53
4	A	1631	11R	CBI-CBH	-5.04	1.39	1.53
4	A	1631	11R	CCB-CCC	-4.61	1.34	1.51
4	A	1631	11R	CBB-CBC	-4.58	1.34	1.51
4	A	1631	11R	CCK-CCJ	-3.96	1.40	1.51
4	A	1631	11R	CAK-CAL	-3.89	1.49	1.54
4	A	1631	11R	CBK-CBJ	-3.07	1.40	1.51
4	A	1631	11R	CBI-CBJ	-2.84	1.40	1.51
4	A	1631	11R	CCG-CCF	-2.81	1.50	1.54
4	A	1631	11R	CCJ-CCI	-2.53	1.40	1.48
4	A	1631	11R	CCE-CCF	-2.16	1.48	1.53
4	A	1631	11R	CBE-CBF	-2.15	1.48	1.53
4	A	1631	11R	CAN-CAM	-2.02	1.41	1.48
4	A	1631	11R	CCH-CCI	2.74	1.39	1.32
4	A	1631	11R	CAM-CAL	3.62	1.41	1.33
4	A	1631	11R	CAC-CAH	3.66	1.46	1.42
4	A	1631	11R	CAC-CAB	4.25	1.45	1.39
4	A	1631	11R	CAI-CAJ	5.25	1.41	1.33

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1631	11R	CAG-CAH-CAC	-3.84	115.69	118.75
4	A	1631	11R	CAC-CAH-CAI	-3.32	118.05	124.08
4	A	1631	11R	CAF-CAE-NAD	-2.12	119.95	122.70
4	A	1631	11R	CCJ-CCI-CCH	-2.02	120.04	123.62
4	A	1631	11R	CAE-NAD-CAC	2.02	118.94	117.40
4	A	1631	11R	CAE-CAF-CAG	2.02	122.49	119.44
4	A	1631	11R	CCJ-CCK-NCL	2.24	119.67	111.94
4	A	1631	11R	CAG-CAH-CAI	2.38	126.27	121.31
4	A	1631	11R	CAK-CAL-CAM	2.82	118.20	112.14
4	A	1631	11R	CBC-CBD-CBE	2.82	117.25	111.42
4	A	1631	11R	CCC-CCD-CCE	2.85	117.31	111.42
4	A	1631	11R	CBF-CBG-NBL	3.01	113.57	109.07
4	A	1631	11R	CCD-CCE-CCF	3.16	117.00	111.22
4	A	1631	11R	CBD-CBE-CBF	3.18	117.02	111.22
4	A	1631	11R	CBI-CBH-CBG	3.99	118.51	111.22
4	A	1631	11R	CBJ-CBK-NBL	4.00	119.52	113.00
4	A	1631	11R	CBJ-CBI-CBH	4.20	120.11	111.42
4	A	1631	11R	CCG-CCF-NCA	4.25	115.42	109.07
4	A	1631	11R	CBG-CBF-NBA	4.55	115.86	109.07
4	A	1631	11R	CAJ-CAK-CAB	4.72	118.42	108.64
4	A	1631	11R	CAL-CAK-CAB	4.91	114.57	108.46
4	A	1631	11R	CCB-CCC-CCD	5.40	119.81	111.43
4	A	1631	11R	CBB-CBC-CBD	5.49	119.94	111.43
4	A	1631	11R	CCC-CCB-NCA	5.60	122.13	113.00
4	A	1631	11R	CBC-CBB-NBA	5.63	122.17	113.00
4	A	1631	11R	CBK-CBJ-CBI	5.68	120.24	111.43

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	1631	11R	CAK
4	A	1631	11R	CBG
4	A	1631	11R	CCF
4	A	1631	11R	CBF
4	A	1631	11R	CCG

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	619/646 (95%)	-0.25	27 (4%) 35 38	13, 20, 33, 60	1 (0%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	52	GLY	9.5
1	A	53	SER	8.9
1	A	628	ASN	7.2
1	A	54	GLU	6.3
1	A	51	ALA	5.2
1	A	314	GLY	4.6
1	A	55	ALA	4.4
1	A	266	ASP	4.2
1	A	9	ALA	4.1
1	A	315	CYS	3.9
1	A	50	GLY	3.8
1	A	313	LEU	3.6
1	A	414	GLY	3.0
1	A	208	GLU	2.8
1	A	265	GLY	2.8
1	A	462	PRO	2.6
1	A	207	PRO	2.5
1	A	68	SER	2.4
1	A	463	GLY	2.4
1	A	225	PRO	2.3
1	A	267	ARG	2.2
1	A	318	LEU	2.2
1	A	116	GLU	2.1
1	A	339	ARG	2.1
1	A	212	PRO	2.1
1	A	48	ALA	2.0
1	A	150	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. 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
1	TPQ	A	382	14/15	0.95	0.10	-	16,23,38,51	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(Å <sup>2</sup> )	Q<0.9
4	11R	A	1631	60/60	0.73	0.43	6.87	38,59,62,62	89
6	GOL	A	1635	6/6	0.80	0.12	4.43	52,53,56,61	0
6	GOL	A	1636	6/6	0.90	0.28	3.83	39,50,53,55	0
6	GOL	A	1634	6/6	0.82	0.16	3.67	36,42,47,49	0
5	SO4	A	1632	5/5	0.94	0.13	1.98	49,50,54,64	0
6	GOL	A	1633	6/6	0.94	0.09	0.66	28,29,30,30	0
3	NA	A	1630	1/1	0.99	0.08	-0.23	26,26,26,26	0
2	CU	A	1629	1/1	0.99	0.03	-2.41	26,26,26,26	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.