



# wwPDB X-ray Structure Validation Summary Report

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PDB ID : 3IW4  
Title : Crystal structure of PKC alpha in complex with NVP-AEB071  
Authors : Stark, W.; Rummel, G.; Strauss, A.; Cowan-Jacob, S.W.  
Deposited on : 2009-09-02  
Resolution : 2.80 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

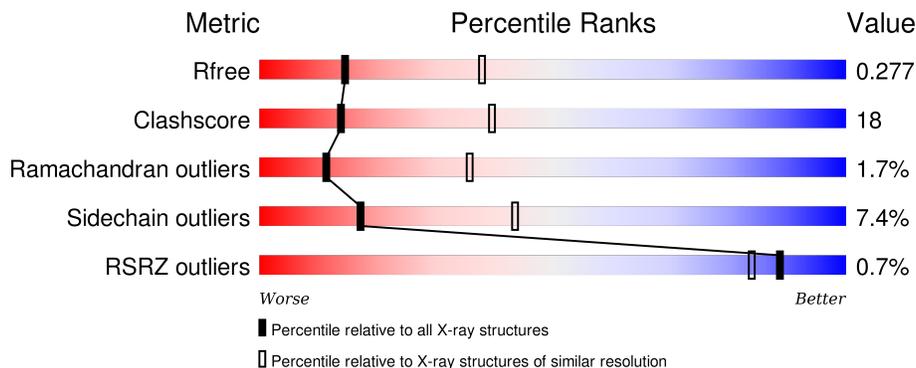
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	360	
1	B	360	
1	C	360	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 8196 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 Protein kinase C alpha type.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	332	Total 2686	C 1730	N 441	O 495	P 2	S 18	0	0	0
1	B	327	Total 2658	C 1714	N 436	O 488	P 2	S 18	0	0	0
1	C	334	Total 2707	C 1742	N 445	O 500	P 2	S 18	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

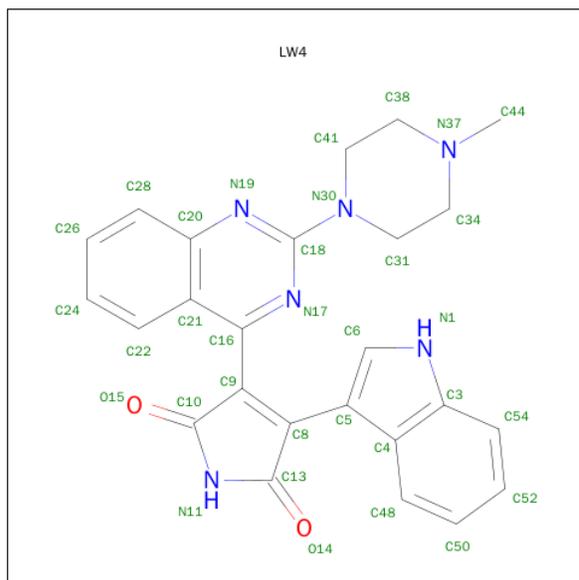
Chain	Residue	Modelled	Actual	Comment	Reference
A	319	MET	-	CLONING ARTIFACT	UNP P17252
A	497	GLU	THR	ENGINEERED	UNP P17252
A	673	HIS	-	EXPRESSION TAG	UNP P17252
A	674	HIS	-	EXPRESSION TAG	UNP P17252
A	675	HIS	-	EXPRESSION TAG	UNP P17252
A	676	HIS	-	EXPRESSION TAG	UNP P17252
A	677	HIS	-	EXPRESSION TAG	UNP P17252
A	678	HIS	-	EXPRESSION TAG	UNP P17252
B	319	MET	-	CLONING ARTIFACT	UNP P17252
B	497	GLU	THR	ENGINEERED	UNP P17252
B	673	HIS	-	EXPRESSION TAG	UNP P17252
B	674	HIS	-	EXPRESSION TAG	UNP P17252
B	675	HIS	-	EXPRESSION TAG	UNP P17252
B	676	HIS	-	EXPRESSION TAG	UNP P17252
B	677	HIS	-	EXPRESSION TAG	UNP P17252
B	678	HIS	-	EXPRESSION TAG	UNP P17252
C	319	MET	-	CLONING ARTIFACT	UNP P17252
C	497	GLU	THR	ENGINEERED	UNP P17252
C	673	HIS	-	EXPRESSION TAG	UNP P17252
C	674	HIS	-	EXPRESSION TAG	UNP P17252
C	675	HIS	-	EXPRESSION TAG	UNP P17252
C	676	HIS	-	EXPRESSION TAG	UNP P17252
C	677	HIS	-	EXPRESSION TAG	UNP P17252

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Chain	Residue	Modelled	Actual	Comment	Reference
C	678	HIS	-	EXPRESSION TAG	UNP P17252

- Molecule 2 is 3-(1H-INDOL-3-YL)-4-[2-(4-METHYLPIPERAZIN-1-YL)QUINAZOLIN-4-YL]-1H-PYRROLE-2,5-DIONE (three-letter code: LW4) (formula: C<sub>25</sub>H<sub>22</sub>N<sub>6</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	
			Total	C	N			O
2	A	1	Total	C	N	O	0	0
			33	25	6	2		
2	B	1	Total	C	N	O	0	0
			33	25	6	2		
2	C	1	Total	C	N	O	0	0
			33	25	6	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	19	Total	O	0	0
			19	19		
3	B	7	Total	O	0	0
			7	7		
3	C	20	Total	O	0	0
			20	20		



MET	I439	V526	F626
PRO	Q430	L527	D627
SER	F435	L528	L637
GLU	K436	T638	T638
ASP	E437	E530	P639
ARG	P438	E531	L643
LYS	Q439	L532	V644
GLN	A440	D539	I645
PRO	V441	G540	I645
SER	F442	E541	F656
ASN	Y443	D544	V664
ASN	A444	E545	V664
I330	I447	S549	I667
L331	S448	L561	S670
D332	L451	S562	ALA
L345	L454	A565	VAL
L345	I459	Y566	HIS
S349	I460	K570	HIS
F350	L464	H573	HIS
L355	D467	T574	HIS
A356	M470	K575	HIS
D357	E474	E586	HIS
R358	I477	G587	HIS
K359	K478	E588	HIS
L364	I479	R589	HIS
L364	C383	D590	HIS
K371	A480	Y591	HIS
K372	D481	R592	HIS
I376	C485	D601	HIS
E382	K486	H602	HIS
C383	R389	E603	HIS
T384	Y390	K604	HIS
H385	H488	L605	HIS
K388	M489	E606	HIS
R389	M490	I607	HIS
Y390	D491	R608	HIS
T401	G492	P612	HIS
H404	V493	F613	HIS
S405	T494	F614	HIS
C406	T495	K615	HIS
D411	R496	P616	HIS
E418	T501	R617	HIS
M421	P507	V618	HIS
G422	A511	CYS	HIS
G423	Y512	GLY	HIS
D424	Y513	LYS	HIS
L425	Q513	GLY	HIS
H426	Y427	ALA	HIS
Y427	G525	GLU	HIS
H428		ASN	HIS

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	43.87Å 100.67Å 251.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	64.42 – 2.80 53.30 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.5 (64.42-2.80) 99.5 (53.30-2.80)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.05 (at 2.81Å)	Xtrriage
Refinement program	REFMAC 5.5.0063	Depositor
R, $R_{free}$	0.192 , 0.277 0.193 , 0.277	Depositor DCC
$R_{free}$ test set	1417 reflections (5.27%)	DCC
Wilson B-factor (Å <sup>2</sup> )	49.1	Xtrriage
Anisotropy	0.077	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 45.5	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtrriage
Outliers	1 of 28329 reflections (0.004%)	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8196	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.06% 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: TPO, LW4, SEP

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	0.57	1/2730 (0.0%)	0.69	0/3681
1	B	0.53	0/2702	0.65	0/3640
1	C	0.61	2/2751 (0.1%)	0.71	0/3709
All	All	0.57	3/8183 (0.0%)	0.68	0/11030

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	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	406	CYS	CB-SG	-8.07	1.68	1.82
1	C	406	CYS	CB-SG	-7.46	1.69	1.82
1	C	383	CYS	CB-SG	-5.09	1.73	1.81

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	420	VAL	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	2686	0	2635	88	0
1	B	2658	0	2611	120	0
1	C	2707	0	2661	86	0
2	A	33	0	22	5	0
2	B	33	0	22	3	0
2	C	33	0	22	6	0
3	A	19	0	0	1	0
3	B	7	0	0	0	0
3	C	20	0	0	2	0
All	All	8196	0	7973	296	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 18.

The worst 5 of 296 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:C:436:LYS:HE2	1:C:438:PRO:HB2	1.28	1.09
1:C:437:GLU:O	1:C:441:VAL:HG23	1.62	0.97
1:A:460:ILE:HG22	1:A:462:ARG:HG3	1.48	0.94
1:A:350:PHE:O	1:A:368:LYS:HE3	1.72	0.90
1:C:501:THR:HG22	3:C:17:HOH:O	1.77	0.84

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	326/360 (91%)	286 (88%)	37 (11%)	3 (1%)	21	55
1	B	319/360 (89%)	281 (88%)	27 (8%)	11 (3%)	5	16
1	C	328/360 (91%)	295 (90%)	30 (9%)	3 (1%)	21	55
All	All	973/1080 (90%)	862 (89%)	94 (10%)	17 (2%)	11	36

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	594	HIS
1	B	362	GLU
1	B	559	LYS
1	B	606	GLU
1	B	613	PRO

### 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	289/316 (92%)	268 (93%)	21 (7%)	17	44
1	B	287/316 (91%)	262 (91%)	25 (9%)	13	35
1	C	293/316 (93%)	275 (94%)	18 (6%)	23	55
All	All	869/948 (92%)	805 (93%)	64 (7%)	17	43

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	401	THR
1	B	474	GLU
1	C	590	ASP
1	B	410	VAL
1	B	421	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 20 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	340	ASN
1	B	421	ASN
1	C	428	HIS
1	A	647	ASN
1	A	665	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

6 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$
1	TPO	A	638	1	8,10,11	0.77	0	7,14,16	1.43	1 (14%)
1	SEP	A	657	1	8,9,10	1.72	2 (25%)	8,12,14	0.87	0
1	TPO	B	638	1	8,10,11	0.79	0	7,14,16	1.93	3 (42%)
1	SEP	B	657	1	8,9,10	1.58	1 (12%)	8,12,14	0.94	0
1	TPO	C	638	1	8,10,11	0.67	0	7,14,16	1.74	3 (42%)
1	SEP	C	657	1	8,9,10	1.61	2 (25%)	8,12,14	1.28	2 (25%)

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	TPO	A	638	1	-	0/8/11/13	0/0/0/0
1	SEP	A	657	1	-	0/6/8/10	0/0/0/0
1	TPO	B	638	1	-	0/8/11/13	0/0/0/0
1	SEP	B	657	1	-	0/6/8/10	0/0/0/0
1	TPO	C	638	1	-	0/8/11/13	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	C	657	1	-	0/6/8/10	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	657	SEP	P-O2P	2.04	1.62	1.54
1	C	657	SEP	P-O2P	2.09	1.62	1.54
1	B	657	SEP	P-O1P	3.32	1.62	1.51
1	C	657	SEP	P-O1P	3.41	1.62	1.51
1	A	657	SEP	P-O1P	3.63	1.63	1.51

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	638	TPO	CG2-CB-CA	-3.31	106.44	113.17
1	C	638	TPO	CG2-CB-CA	-3.00	107.07	113.17
1	B	638	TPO	O-C-CA	-2.52	118.79	125.44
1	C	638	TPO	O-C-CA	-2.06	119.99	125.44
1	C	657	SEP	O-C-CA	-2.03	120.19	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	638	TPO	2	0
1	B	638	TPO	2	0
1	B	657	SEP	1	0
1	C	638	TPO	2	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

3 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	LW4	A	901	-	35,38,38	2.22	4 (11%)	46,56,56	2.20	20 (43%)
2	LW4	B	901	-	35,38,38	2.17	6 (17%)	46,56,56	2.38	17 (36%)
2	LW4	C	901	-	35,38,38	2.11	5 (14%)	46,56,56	2.50	18 (39%)

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	LW4	A	901	-	-	0/7/38/38	0/6/6/6
2	LW4	B	901	-	-	0/7/38/38	0/6/6/6
2	LW4	C	901	-	-	0/7/38/38	0/6/6/6

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	901	LW4	C5-C8	-3.07	1.44	1.50
2	C	901	LW4	C16-C21	-3.06	1.39	1.43
2	B	901	LW4	C16-C21	-2.75	1.40	1.43
2	C	901	LW4	C6-N1	-2.50	1.31	1.36
2	B	901	LW4	C6-N1	-2.36	1.31	1.36

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	901	LW4	C31-C34-N37	-7.56	102.80	110.79
2	B	901	LW4	C41-C38-N37	-5.00	105.51	110.79
2	B	901	LW4	N19-C18-N17	-4.43	118.90	126.36
2	B	901	LW4	C21-C16-N17	-4.25	118.86	122.14
2	A	901	LW4	N19-C18-N17	-3.99	119.64	126.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	LW4	5	0
2	B	901	LW4	3	0
2	C	901	LW4	6	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	330/360 (91%)	-0.28	1 (0%) 94 92	18, 37, 61, 72	0
1	B	325/360 (90%)	-0.12	6 (1%) 71 61	21, 43, 70, 82	0
1	C	332/360 (92%)	-0.37	0 100 100	16, 33, 53, 72	0
All	All	987/1080 (91%)	-0.26	7 (0%) 89 84	16, 38, 65, 82	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	604	LYS	3.4
1	B	559	LYS	3.1
1	B	602	TRP	3.0
1	B	599	ARG	2.6
1	B	584	GLY	2.5

### 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	TPO	B	638	11/12	0.90	0.16	-	50,53,71,72	0
1	TPO	C	638	11/12	0.88	0.14	-	50,52,74,75	0
1	SEP	B	657	10/11	0.96	0.12	-	30,32,49,50	0
1	TPO	A	638	11/12	0.92	0.14	-	63,65,69,70	0
1	SEP	C	657	10/11	0.96	0.15	-	27,28,40,41	0
1	SEP	A	657	10/11	0.97	0.13	-	33,34,44,46	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
2	LW4	C	901	33/33	0.97	0.15	-0.30	20,28,35,38	0
2	LW4	B	901	33/33	0.97	0.14	-0.82	23,30,33,39	0
2	LW4	A	901	33/33	0.96	0.13	-1.05	26,32,36,38	0

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

There are no such residues in this entry.