



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 04:25 pm GMT

PDB ID : 1U4D  
Title : Structure of the ACK1 Kinase Domain bound to Debromohymenialdisine  
Authors : Loughheed, J.C.; Chen, R.H.; Mak, P.; Stout, T.J.  
Deposited on : 2004-07-23  
Resolution : 2.10 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

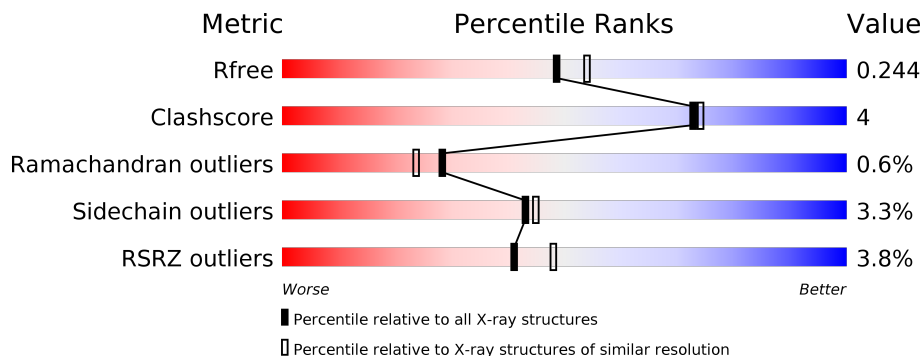
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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	291	<div> <div>4%</div> <div> <div></div> <div>78%</div> <div>10%</div> <div>11%</div> </div> </div>
1	B	291	<div> <div>3%</div> <div> <div></div> <div>79%</div> <div>10%</div> <div>10%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4362 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 Activated CDC42 kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	0	0	0
			2065	1320	364	366	15			
1	B	262	Total	C	N	O	S	0	0	0
			2103	1340	374	374	15			

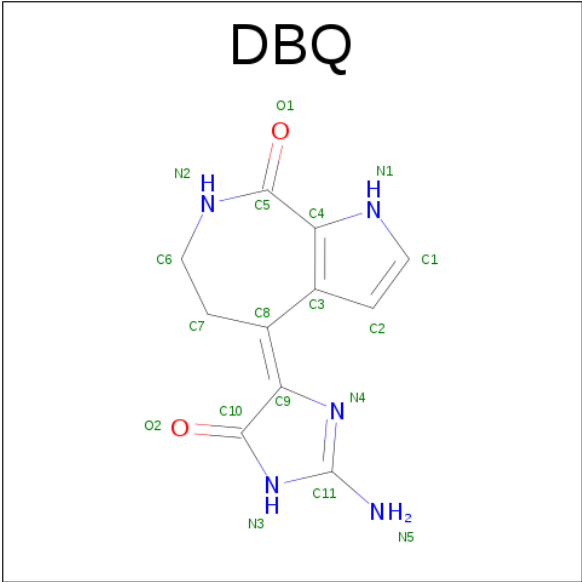
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	107	GLY	-	CLONING ARTIFACT	UNP Q07912
A	108	SER	-	CLONING ARTIFACT	UNP Q07912
A	396	GLU	-	CLONING ARTIFACT	UNP Q07912
A	397	PHE	-	CLONING ARTIFACT	UNP Q07912
B	107	GLY	-	CLONING ARTIFACT	UNP Q07912
B	108	SER	-	CLONING ARTIFACT	UNP Q07912
B	396	GLU	-	CLONING ARTIFACT	UNP Q07912
B	397	PHE	-	CLONING ARTIFACT	UNP Q07912

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cl	0	0
			1	1		

- Molecule 3 is DEBROMOHYMENIALDISINE (three-letter code: DBQ) (formula: C<sub>11</sub>H<sub>11</sub>N<sub>5</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			18	11	5	2		
3	B	1	Total	C	N	O	0	0
			18	11	5	2		

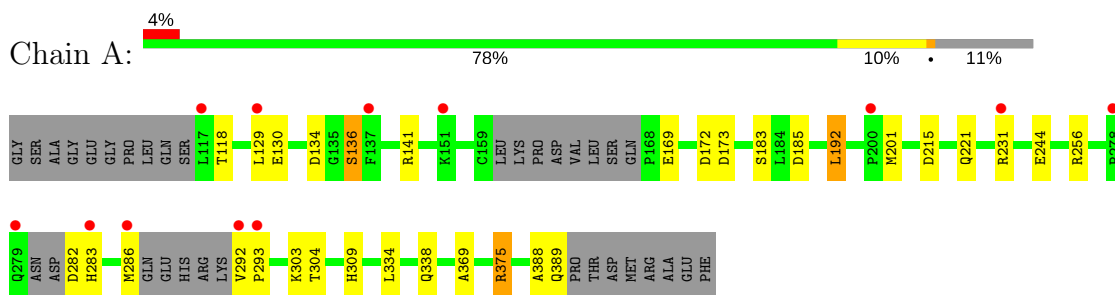
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	53	Total	O	0	0
			53	53		
4	B	104	Total	O	0	0
			104	104		

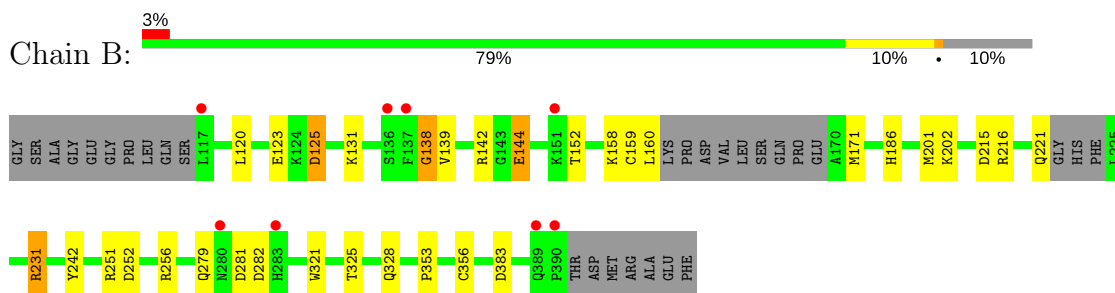
### 3 Residue-property plots [i](#)

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: Activated CDC42 kinase 1



- Molecule 1: Activated CDC42 kinase 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.55Å 42.92Å 85.15Å 90.00° 112.02° 90.00°	Depositor
Resolution (Å)	46.60 – 2.10 46.57 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.60-2.10) 99.7 (46.57-2.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.46 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, $R_{free}$	0.203 , 0.248 0.212 , 0.244	Depositor DCC
$R_{free}$ test set	1621 reflections (5.29%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.2	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 45.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.021 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	4362	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.82% 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: DBQ, CL

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	0/2113	0.94	7/2855 (0.2%)
1	B	0.87	0/2151	1.02	14/2908 (0.5%)
All	All	0.82	0/4264	0.98	21/5763 (0.4%)

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	142	ARG	NE-CZ-NH2	-11.38	114.61	120.30
1	A	375	ARG	NE-CZ-NH1	10.98	125.79	120.30
1	B	231	ARG	NE-CZ-NH2	-8.45	116.07	120.30
1	B	142	ARG	NE-CZ-NH1	8.33	124.47	120.30
1	A	375	ARG	NE-CZ-NH2	-7.81	116.40	120.30
1	B	125	ASP	CB-CG-OD2	6.77	124.39	118.30
1	B	252	ASP	CB-CG-OD1	6.68	124.31	118.30
1	B	231	ARG	NE-CZ-NH1	6.49	123.55	120.30
1	B	256	ARG	NE-CZ-NH2	-6.40	117.10	120.30
1	A	215	ASP	CB-CG-OD2	6.39	124.05	118.30
1	B	256	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	A	185	ASP	CB-CG-OD2	6.06	123.75	118.30
1	B	251	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	B	215	ASP	CB-CG-OD2	5.56	123.30	118.30
1	B	383	ASP	CB-CG-OD2	5.54	123.29	118.30
1	A	282	ASP	CB-CG-OD2	5.46	123.22	118.30
1	B	251	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	B	282	ASP	CB-CG-OD2	5.24	123.01	118.30
1	A	172	ASP	CB-CG-OD2	5.16	122.94	118.30
1	B	281	ASP	CB-CG-OD2	5.11	122.90	118.30
1	A	173	ASP	CB-CG-OD2	5.01	122.81	118.30

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	2065	0	2063	12	0
1	B	2103	0	2106	20	0
2	B	1	0	0	0	0
3	A	18	0	11	0	0
3	B	18	0	11	0	0
4	A	53	0	0	0	0
4	B	104	0	0	3	0
All	All	4362	0	4191	32	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 4.

All (32) 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:123:GLU:OE1	1:B:202:LYS:HE3	1.80	0.82
1:A:129:LEU:O	1:A:141:ARG:NH1	2.22	0.72
1:A:292:VAL:N	1:A:293:PRO:CD	2.54	0.70
1:A:292:VAL:N	1:A:293:PRO:HD2	2.08	0.69
1:B:123:GLU:OE1	1:B:202:LYS:CE	2.44	0.66
1:B:186:HIS:HD2	1:B:242:TYR:HB2	1.64	0.63
1:B:144:GLU:HG3	4:B:543:HOH:O	2.04	0.57
1:B:144:GLU:OE1	1:B:152:THR:OG1	2.20	0.57
1:A:388:ALA:O	1:A:389:GLN:HB2	2.07	0.55
1:B:144:GLU:OE1	1:B:152:THR:CB	2.56	0.54
1:A:244:GLU:HG3	1:A:309:HIS:CD2	2.43	0.54
1:B:186:HIS:CD2	1:B:242:TYR:HB2	2.44	0.53
1:B:159:CYS:O	1:B:160:LEU:HB2	2.07	0.53
1:B:158:LYS:NZ	4:B:584:HOH:O	2.41	0.52
1:A:283:HIS:C	1:A:283:HIS:CD2	2.83	0.51
1:B:353:PRO:HB2	1:B:356:CYS:HB2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:GLU:OE1	1:B:152:THR:HB	2.12	0.48
1:A:334:LEU:HB3	1:A:338:GLN:HG3	1.96	0.48
1:B:171:MET:SD	1:B:201:MET:HE1	2.53	0.48
1:A:303:LYS:HB3	1:A:304:THR:HG23	1.97	0.47
1:B:138:GLY:HA3	1:B:159:CYS:O	2.15	0.46
1:B:171:MET:SD	1:B:201:MET:CE	3.05	0.45
1:B:231:ARG:HD2	4:B:521:HOH:O	2.16	0.44
1:A:141:ARG:HH11	1:A:141:ARG:HG2	1.83	0.44
1:B:120:LEU:N	1:B:120:LEU:HD23	2.33	0.44
1:B:160:LEU:HD12	1:B:160:LEU:HA	1.79	0.43
1:A:369:ALA:O	1:A:375:ARG:HD2	2.19	0.43
1:B:131:LYS:HG2	1:B:139:VAL:HG11	2.01	0.42
1:B:321:TRP:O	1:B:325:THR:HG23	2.19	0.42
1:A:118:THR:HG23	1:A:192:LEU:HD13	2.02	0.42
1:B:159:CYS:O	1:B:160:LEU:CB	2.66	0.42
1:A:256:ARG:HH22	1:A:293:PRO:HB3	1.85	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	250/291 (86%)	241 (96%)	7 (3%)	2 (1%)	22	17
1	B	256/291 (88%)	246 (96%)	9 (4%)	1 (0%)	38	35
All	All	506/582 (87%)	487 (96%)	16 (3%)	3 (1%)	28	24

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	SER
1	B	138	GLY

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Mol	Chain	Res	Type
1	A	221	GLN

### 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	222/250 (89%)	213 (96%)	9 (4%)	35	35
1	B	227/250 (91%)	221 (97%)	6 (3%)	51	55
All	All	449/500 (90%)	434 (97%)	15 (3%)	43	45

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	130	GLU
1	A	134	ASP
1	A	136	SER
1	A	169	GLU
1	A	183	SER
1	A	192	LEU
1	A	201	MET
1	A	231	ARG
1	A	286	MET
1	B	125	ASP
1	B	144	GLU
1	B	216	ARG
1	B	221	GLN
1	B	279	GLN
1	B	328	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	179	ASN
1	A	220	HIS

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Mol	Chain	Res	Type
1	A	283	HIS
1	A	309	HIS
1	A	328	GLN
1	A	341	HIS
1	B	220	HIS

### 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](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\# Z  > 2$
3	DBQ	A	398	-	15,20,20	2.89	3 (20%)	9,29,29	4.82	6 (66%)
3	DBQ	B	401	-	15,20,20	2.95	4 (26%)	9,29,29	2.69	4 (44%)

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	DBQ	A	398	-	-	0/0/30/30	0/2/3/3
3	DBQ	B	401	-	-	0/0/30/30	0/2/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	398	DBQ	C10-N3	-3.06	1.31	1.37
3	B	401	DBQ	C10-N3	-2.08	1.33	1.37
3	B	401	DBQ	C2-C3	2.12	1.51	1.42
3	A	398	DBQ	C2-C3	2.13	1.51	1.42
3	B	401	DBQ	O2-C10	4.05	1.31	1.23
3	B	401	DBQ	C2-C1	9.49	1.51	1.38
3	A	398	DBQ	C2-C1	9.73	1.51	1.38

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	398	DBQ	C1-C2-C3	-3.46	97.66	106.78
3	B	401	DBQ	C1-C2-C3	-3.00	98.88	106.78
3	A	398	DBQ	N5-C11-N3	-2.66	119.40	122.56
3	B	401	DBQ	N5-C11-N4	-2.38	121.65	125.05
3	A	398	DBQ	O2-C10-N3	-2.17	119.81	125.11
3	A	398	DBQ	C2-C3-C4	2.20	109.61	106.58
3	A	398	DBQ	C1-N1-C4	2.72	111.42	104.39
3	B	401	DBQ	C1-N1-C4	3.16	112.56	104.39
3	B	401	DBQ	C9-C10-N3	5.97	109.21	106.10
3	A	398	DBQ	C9-C10-N3	13.11	112.93	106.10

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 [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	258/291 (88%)	0.22	12 (4%)	32 38	22, 39, 65, 74	12 (4%)
1	B	262/291 (90%)	0.17	8 (3%)	49 56	20, 33, 54, 68	12 (4%)
All	All	520/582 (89%)	0.20	20 (3%)	41 48	20, 36, 60, 74	24 (4%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	137	PHE	10.6
1	A	137	PHE	4.4
1	B	117	LEU	4.3
1	A	286	MET	3.5
1	B	390	PRO	3.4
1	A	292	VAL	3.4
1	B	280	ASN	3.3
1	A	283	HIS	3.0
1	A	151	LYS	2.9
1	A	231	ARG	2.7
1	B	151	LYS	2.5
1	A	278	PRO	2.4
1	B	389	GLN	2.4
1	B	283	HIS	2.3
1	B	136	SER	2.2
1	A	129	LEU	2.2
1	A	279	GLN	2.1
1	A	117	LEU	2.1
1	A	200	PRO	2.1
1	A	293	PRO	2.1

## 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(Å <sup>2</sup> )	Q<0.9
3	DBQ	B	401	18/18	0.89	0.15	0.89	30,32,34,34	0
3	DBQ	A	398	18/18	0.94	0.15	0.67	33,37,42,43	0
2	CL	B	502	1/1	0.99	0.12	-0.25	35,35,35,35	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.