Full wwPDB X-ray Structure Validation Report (i)

Jul 14, 2016 – 08:25 PM EDT

PDB ID	:	4ZIM
Title	:	CRYSTAL STRUCTURE OF JANUS KINASE 2 IN COMPLEX WITH A 9 H-CARBAZOLE-1-CARBOXAMIDE INHIBITOR
Authors	:	Sack, J.S.
Deposited on	:	2015-04-28
Resolution	:	2.65 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
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

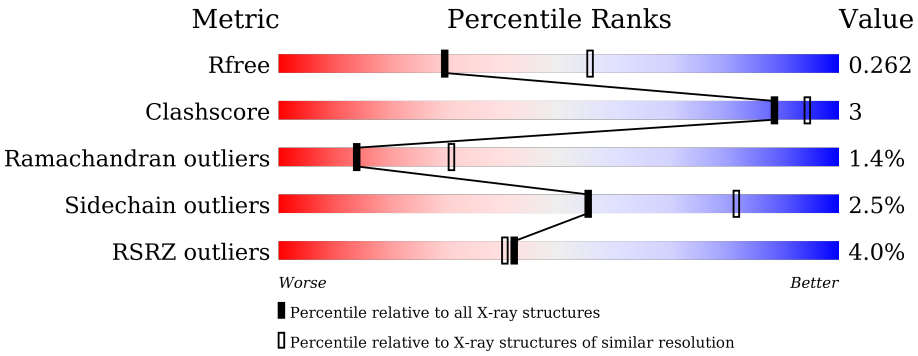
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20027790
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027790

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	3152 (2.70-2.62)
Clashscore	102246	3524 (2.70-2.62)
Ramachandran outliers	100387	3469 (2.70-2.62)
Sidechain outliers	100360	3469 (2.70-2.62)
RSRZ outliers	91569	3161 (2.70-2.62)

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 >=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 <=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	321	4% 80% 10% 11%
1	B	321	3% 82% 9% • 8%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5118 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 Tyrosine-protein kinase JAK2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	287	2379	1509	410	444	2	14	0	1	0
1	B	296	2413	1529	416	452	2	14	0	0	0

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	818	MET	-	initiating methionine	UNP O60674
A	819	GLY	-	expression tag	UNP O60674
A	820	SER	-	expression tag	UNP O60674
A	821	SER	-	expression tag	UNP O60674
A	822	HIS	-	expression tag	UNP O60674
A	823	HIS	-	expression tag	UNP O60674
A	824	HIS	-	expression tag	UNP O60674
A	825	HIS	-	expression tag	UNP O60674
A	826	HIS	-	expression tag	UNP O60674
A	827	HIS	-	expression tag	UNP O60674
A	828	SER	-	expression tag	UNP O60674
A	829	SER	-	expression tag	UNP O60674
A	830	GLY	-	expression tag	UNP O60674
A	831	LEU	-	expression tag	UNP O60674
A	832	VAL	-	expression tag	UNP O60674
A	833	PRO	-	expression tag	UNP O60674
A	834	ARG	-	expression tag	UNP O60674
A	835	GLY	-	expression tag	UNP O60674
A	836	SER	-	expression tag	UNP O60674
A	837	HIS	-	expression tag	UNP O60674
A	838	MET	-	expression tag	UNP O60674
A	1133	HIS	-	expression tag	UNP O60674
A	1134	HIS	-	expression tag	UNP O60674
A	1135	HIS	-	expression tag	UNP O60674
A	1136	HIS	-	expression tag	UNP O60674

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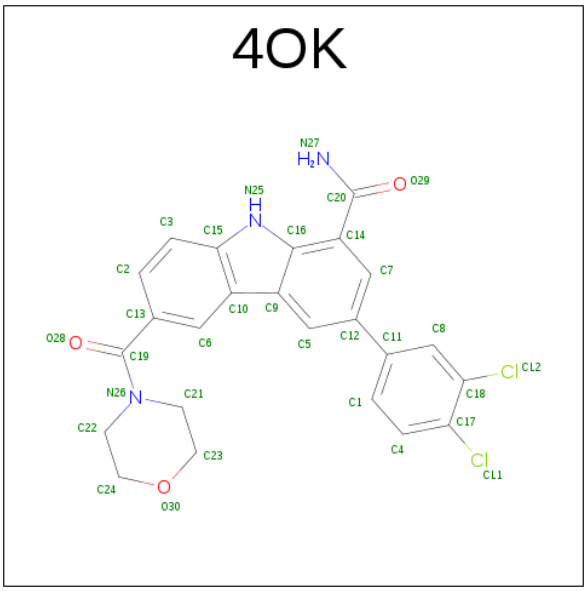
Chain	Residue	Modelled	Actual	Comment	Reference
A	1137	HIS	-	expression tag	UNP O60674
A	1138	HIS	-	expression tag	UNP O60674
B	818	MET	-	initiating methionine	UNP O60674
B	819	GLY	-	expression tag	UNP O60674
B	820	SER	-	expression tag	UNP O60674
B	821	SER	-	expression tag	UNP O60674
B	822	HIS	-	expression tag	UNP O60674
B	823	HIS	-	expression tag	UNP O60674
B	824	HIS	-	expression tag	UNP O60674
B	825	HIS	-	expression tag	UNP O60674
B	826	HIS	-	expression tag	UNP O60674
B	827	HIS	-	expression tag	UNP O60674
B	828	SER	-	expression tag	UNP O60674
B	829	SER	-	expression tag	UNP O60674
B	830	GLY	-	expression tag	UNP O60674
B	831	LEU	-	expression tag	UNP O60674
B	832	VAL	-	expression tag	UNP O60674
B	833	PRO	-	expression tag	UNP O60674
B	834	ARG	-	expression tag	UNP O60674
B	835	GLY	-	expression tag	UNP O60674
B	836	SER	-	expression tag	UNP O60674
B	837	HIS	-	expression tag	UNP O60674
B	838	MET	-	expression tag	UNP O60674
B	1133	HIS	-	expression tag	UNP O60674
B	1134	HIS	-	expression tag	UNP O60674
B	1135	HIS	-	expression tag	UNP O60674
B	1136	HIS	-	expression tag	UNP O60674
B	1137	HIS	-	expression tag	UNP O60674
B	1138	HIS	-	expression tag	UNP O60674

- Molecule 2 is 3-(3,4-dichlorophenyl)-6-(morpholin-4-ylcarbonyl)-9H-carbazole-1-carboxamide (three-letter code: 4OK) (formula: $C_{24}H_{19}Cl_2N_3O_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	Cl	N	O		
2	A	1	32	24	2	3	3	0	0
			Total	C	Cl	N	O		
2	B	1	32	24	2	3	3	0	0

- Molecule 3 is water.

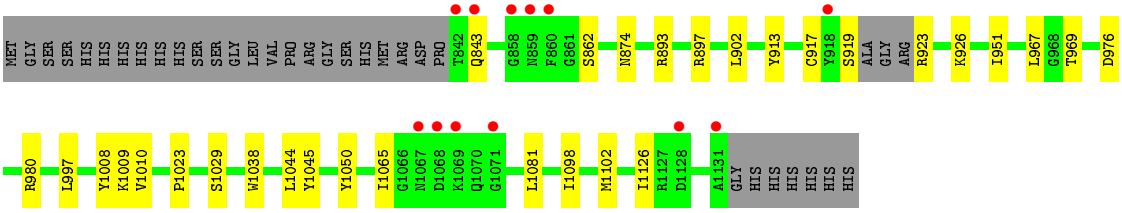
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	134	134	134	0	0
			Total	O		
3	B	128	128	128	0	0

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 errors 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.

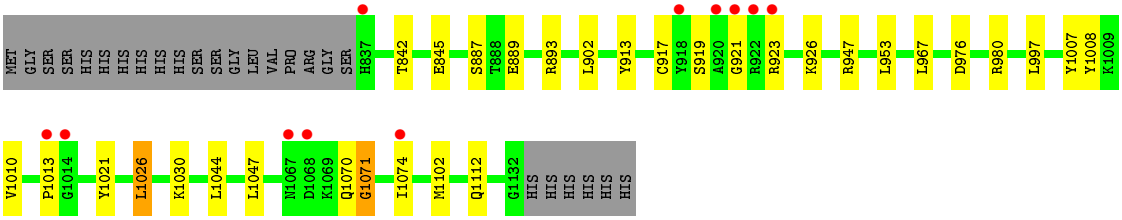
- Molecule 1: Tyrosine-protein kinase JAK2

Chain A:



- Molecule 1: Tyrosine-protein kinase JAK2

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α, β, γ	112.39Å 112.39Å 70.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.46 – 2.65 35.54 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.7 (37.46-2.65) 99.7 (35.54-2.65)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.53 (at 2.65Å)	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
R, R_{free}	0.202 , 0.274 0.200 , 0.262	Depositor DCC
R_{free} test set	656 reflections (2.61%)	DCC
Wilson B-factor (Å^2)	35.4	Xtriage
Anisotropy	0.154	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 50.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.046 for h,-k,-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	5118	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: 4OK, PTR

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	0/2398	0.72	0/3228
1	B	0.50	0/2432	0.72	0/3280
All	All	0.51	0/4830	0.72	0/6508

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 (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	2379	0	2337	14	0
1	B	2413	0	2342	11	0
2	A	32	0	19	0	0
2	B	32	0	19	0	0
3	A	134	0	0	0	0
3	B	128	0	0	0	0
All	All	5118	0	4717	24	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 (24) 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:919:SER:HB2	1:A:923:ARG:HB3	1.80	0.63
1:B:1071:GLY:HA2	1:B:1074:ILE:HD12	1.91	0.53
1:B:917:CYS:HB3	1:B:926:LYS:HB2	1.95	0.49
1:B:976:ASP:HB2	1:B:997:LEU:HD12	1.95	0.49
1:A:1050:TYR:CD1	1:B:1112:GLN:HG3	2.49	0.48
1:A:976:ASP:HB2	1:A:997:LEU:HD12	1.96	0.47
1:A:1009:LYS:HA	1:A:1029:SER:O	2.16	0.46
1:A:917:CYS:HB3	1:A:926:LYS:HB2	1.97	0.45
1:A:1044:LEU:HD23	1:A:1102:MET:HG3	1.98	0.45
1:B:1008:PTR:HD1	1:B:1010:VAL:HG12	1.99	0.44
1:A:1065:ILE:HD11	1:A:1081:LEU:HB2	1.99	0.44
1:B:902:LEU:HG	1:B:913:TYR:HB2	2.00	0.44
1:A:902:LEU:HG	1:A:913:TYR:HB2	2.00	0.43
1:B:1021:TYR:CB	1:B:1026:LEU:HD13	2.49	0.43
1:A:893:ARG:HG2	1:A:897:ARG:HH21	1.84	0.42
1:A:1045:TYR:HB2	1:A:1102:MET:HE3	2.01	0.42
1:B:1007:PTR:CD2	1:B:1030:LYS:HG2	2.49	0.42
1:B:1021:TYR:HB3	1:B:1026:LEU:HD13	2.01	0.42
1:A:951:ILE:H	1:A:951:ILE:HD12	1.84	0.42
1:A:1008:PTR:HE1	1:A:1010:VAL:HB	2.02	0.42
1:B:953:LEU:HD22	1:B:1047:LEU:HB3	2.02	0.42
1:A:1098:ILE:HD11	1:A:1126:ILE:HG21	2.02	0.41
1:A:1023:PRO:HD3	1:A:1038:TRP:CZ3	2.57	0.40
1:B:1044:LEU:HD23	1:B:1102:MET:HG3	2.03	0.40

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	282/321 (88%)	274 (97%)	6 (2%)	2 (1%)	26 51

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	292/321 (91%)	279 (96%)	7 (2%)	6 (2%)	9 20
All	All	574/642 (89%)	553 (96%)	13 (2%)	8 (1%)	14 31

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1013	PRO
1	B	1070	GLN
1	A	843	GLN
1	B	919	SER
1	B	921	GLY
1	B	923	ARG
1	B	1071	GLY
1	A	862	SER

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	259/290 (89%)	255 (98%)	4 (2%)	72 90
1	B	259/290 (89%)	250 (96%)	9 (4%)	43 71
All	All	518/580 (89%)	505 (98%)	13 (2%)	55 82

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	874	ASN
1	A	967	LEU
1	A	969	THR
1	A	980	ARG
1	B	842	THR
1	B	845	GLU
1	B	887	SER
1	B	889	GLU

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Mol	Chain	Res	Type
1	B	893	ARG
1	B	947	ARG
1	B	967	LEU
1	B	980	ARG
1	B	1026	LEU

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	853	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

4 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	PTR	A	1007	1	13,16,17	1.72	2 (15%)	19,22,24	1.64	6 (31%)
1	PTR	A	1008	1	13,16,17	1.66	2 (15%)	19,22,24	1.48	4 (21%)
1	PTR	B	1007	1	13,16,17	1.41	2 (15%)	19,22,24	1.49	2 (10%)
1	PTR	B	1008	1	13,16,17	1.27	1 (7%)	19,22,24	1.25	2 (10%)

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	PTR	A	1007	1	-	0/9/11/13	0/1/1/1
1	PTR	A	1008	1	-	0/9/11/13	0/1/1/1
1	PTR	B	1007	1	-	0/9/11/13	0/1/1/1
1	PTR	B	1008	1	-	0/9/11/13	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1008	PTR	P-O1P	2.38	1.58	1.50
1	B	1007	PTR	CB-CA	2.42	1.58	1.53
1	B	1008	PTR	CE2-CZ	2.69	1.44	1.38
1	B	1007	PTR	CE1-CZ	2.79	1.44	1.38
1	A	1007	PTR	CD2-CG	3.24	1.45	1.38
1	A	1007	PTR	CE1-CZ	3.57	1.46	1.38
1	A	1008	PTR	CE2-CZ	4.01	1.46	1.38

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1007	PTR	O3P-P-O1P	-3.08	100.58	110.63
1	B	1007	PTR	CG-CB-CA	-2.91	107.41	114.12
1	A	1007	PTR	P-OH-CZ	-2.70	116.19	123.85
1	A	1008	PTR	O3P-P-OH	-2.60	97.20	105.47
1	A	1007	PTR	CE1-CD1-CG	-2.40	117.66	121.02
1	A	1008	PTR	O-C-CA	-2.40	119.30	125.72
1	B	1008	PTR	O-C-CA	-2.26	119.67	125.72
1	A	1007	PTR	O-C-CA	-2.10	120.08	125.72
1	A	1007	PTR	O3P-P-O2P	2.02	114.86	107.44
1	A	1008	PTR	CG-CB-CA	2.21	119.22	114.12
1	A	1007	PTR	CD1-CE1-CZ	2.31	122.62	119.74
1	B	1008	PTR	O3P-P-O1P	2.37	118.35	110.63
1	A	1008	PTR	O2P-P-OH	2.78	114.33	105.47
1	B	1007	PTR	O3P-P-OH	3.14	115.48	105.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1008	PTR	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	1007	PTR	1	0
1	B	1008	PTR	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

2 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	4OK	A	1201	-	36,36,36	0.60	0	45,53,53	0.80	2 (4%)
2	4OK	B	1201	-	36,36,36	0.62	0	45,53,53	0.82	1 (2%)

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	4OK	A	1201	-	-	0/16/24/24	0/5/5/5
2	4OK	B	1201	-	-	0/16/24/24	0/5/5/5

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1201	4OK	C6-C10-C15	-3.48	118.97	120.34
2	A	1201	4OK	C6-C10-C15	-3.36	119.01	120.34
2	A	1201	4OK	C2-C3-C15	-2.23	118.39	120.86

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 (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, 95th 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^2)	Q<0.9
1	A	285/321 (88%)	-0.20	12 (4%)	40	38	17, 33, 69, 98	0
1	B	294/321 (91%)	-0.29	11 (3%)	45	44	16, 34, 68, 89	0
All	All	579/642 (90%)	-0.25	23 (3%)	42	40	16, 33, 69, 98	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	921	GLY	6.6
1	B	837	HIS	4.6
1	B	922	ARG	4.3
1	A	842	THR	3.8
1	A	1131	ALA	3.6
1	A	1067	ASN	3.4
1	B	1067	ASN	3.4
1	A	859	ASN	3.2
1	B	918	TYR	3.0
1	B	1068	ASP	3.0
1	B	1014	GLY	2.9
1	A	918	TYR	2.7
1	B	923	ARG	2.7
1	A	1068	ASP	2.7
1	A	843	GLN	2.7
1	A	1071	GLY	2.4
1	A	860	PHE	2.4
1	A	858	GLY	2.4
1	B	1013	PRO	2.3
1	B	1074	ILE	2.2
1	A	1128	ASP	2.1
1	A	1069	LYS	2.1
1	B	920	ALA	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, 95th 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^2)	Q<0.9
1	PTR	A	1008	16/17	0.92	0.15	-	31,43,59,59	0
1	PTR	B	1008	16/17	0.85	0.19	-	44,58,69,69	0
1	PTR	B	1007	16/17	0.92	0.17	-	50,59,71,72	0
1	PTR	A	1007	16/17	0.95	0.12	-	31,42,55,56	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, 95th 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^2)	Q<0.9
2	4OK	A	1201	32/32	0.97	0.12	-0.09	12,26,53,57	0
2	4OK	B	1201	32/32	0.97	0.13	-0.12	18,27,55,58	0

6.5 Other polymers (i)

There are no such residues in this entry.