



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 24, 2016 – 07:53 AM EDT

PDB ID : 5IKJ
Title : Structure of Clr2 bound to the Clr1 C-terminus
Authors : Pfister, Y.; Schalch, T.
Deposited on : 2016-03-03
Resolution : 2.30 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027257
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-20027257

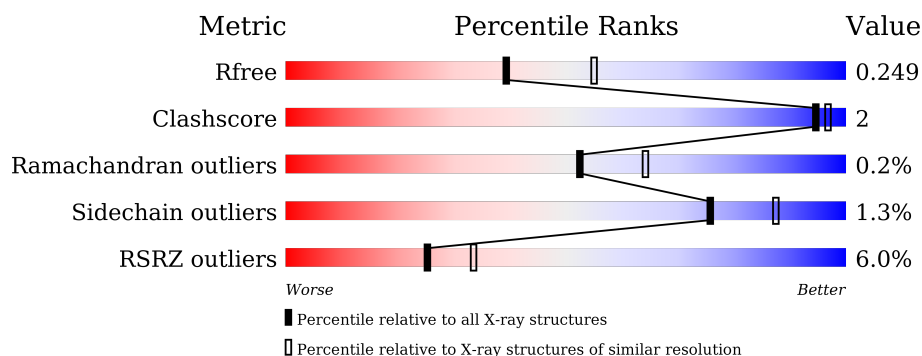
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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 $\leq 5\%$. 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	548	
2	B	88	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8322 atoms, of which 4060 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 Cryptic loci regulator 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	448	Total	C	H	N	O	S	0	0	0
			7190	2352	3513	617	686	22			

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	expression tag	UNP O13881
A	-9	ALA	-	expression tag	UNP O13881
A	-8	SER	-	expression tag	UNP O13881
A	-7	MET	-	expression tag	UNP O13881
A	-6	THR	-	expression tag	UNP O13881
A	-5	GLY	-	expression tag	UNP O13881
A	-4	GLY	-	expression tag	UNP O13881
A	-3	GLN	-	expression tag	UNP O13881
A	-2	GLN	-	expression tag	UNP O13881
A	-1	MET	-	expression tag	UNP O13881
A	0	GLY	-	expression tag	UNP O13881

- Molecule 2 is a protein called Cryptic loci regulator protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	66	Total	C	H	N	O	0	0	0
			1059	328	547	93	91			

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total 1	Cl 1	0	0
4	A	1	Total 1	Cl 1	0	0

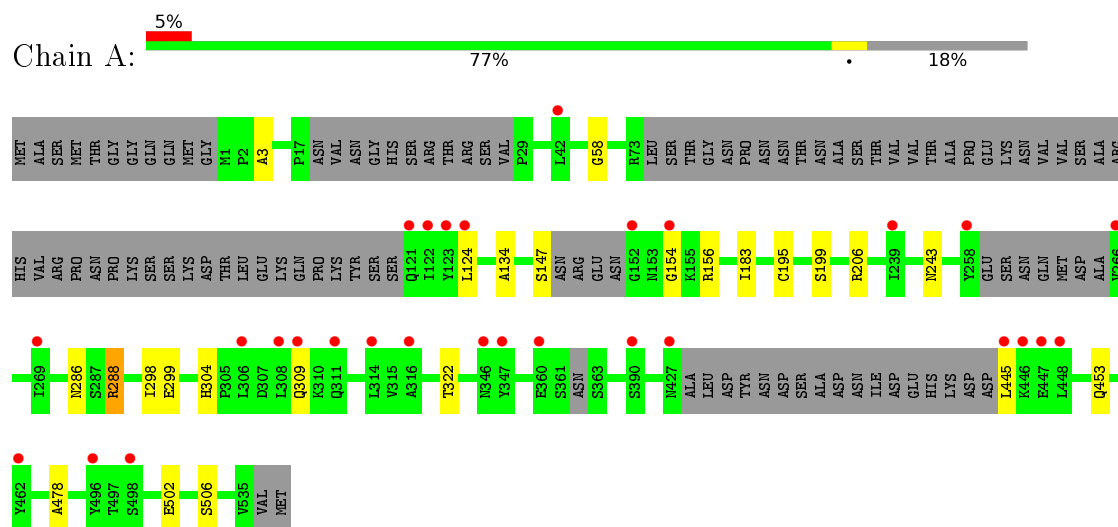
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	64	Total 64	O 64	0	0
5	B	6	Total 6	O 6	0	0

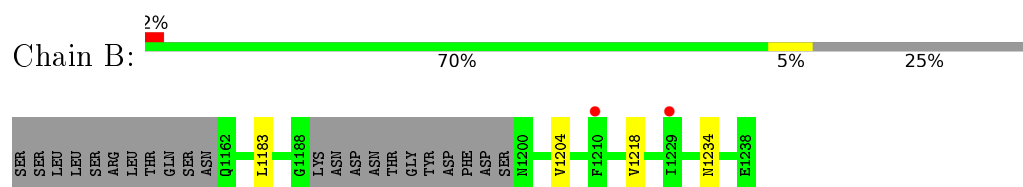
3 Residue-property plots [i](#)

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: Cryptic loci regulator 2



• Molecule 2: Cryptic loci regulator protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	103.50Å 103.50Å 135.09Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.33 – 2.30 48.33 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.33-2.30) 99.9 (48.33-2.30)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.10_2152: ???)	Depositor
R, R_{free}	0.214 , 0.243 0.225 , 0.249	Depositor DCC
R_{free} test set	3590 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	58.0	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8322	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 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	0.28	0/3776	0.45	0/5124
2	B	0.25	0/519	0.44	0/694
All	All	0.27	0/4295	0.45	0/5818

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	3677	3513	3525	13	0
2	B	512	547	545	4	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	64	0	0	2	0
5	B	6	0	0	1	0
All	All	4262	4060	4070	14	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 2.

All (14) 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:506:SER:OG	2:B:1183:LEU:O	1.96	0.83
1:A:298:ILE:O	5:A:701:HOH:O	2.10	0.70
1:A:309:GLN:OE1	1:A:309:GLN:N	2.36	0.58
1:A:299:GLU:OE1	1:A:304:HIS:NE2	2.41	0.53
1:A:147:SER:OG	1:A:154:GLY:N	2.45	0.50
1:A:147:SER:OG	1:A:154:GLY:CA	2.62	0.48
1:A:199:SER:OG	1:A:206:ARG:NH1	2.45	0.48
1:A:445:LEU:O	1:A:453:GLN:NE2	2.48	0.46
2:B:1218:VAL:O	5:B:1401:HOH:O	2.21	0.46
1:A:288:ARG:HD2	5:A:738:HOH:O	2.16	0.46
1:A:183:ILE:HA	2:B:1234:ASN:HB2	1.98	0.46
1:A:478:ALA:HB2	2:B:1204:VAL:HG12	2.01	0.43
1:A:322:THR:HA	1:A:502:GLU:O	2.19	0.43
1:A:3:ALA:HB1	1:A:134:ALA:HB2	2.02	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	434/548 (79%)	424 (98%)	9 (2%)	1 (0%)	52	64
2	B	62/88 (70%)	62 (100%)	0	0	100	100
All	All	496/636 (78%)	486 (98%)	9 (2%)	1 (0%)	52	64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	58	GLY

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	412/500 (82%)	406 (98%)	6 (2%)	72	85
2	B	56/77 (73%)	56 (100%)	0	100	100
All	All	468/577 (81%)	462 (99%)	6 (1%)	76	87

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	124	LEU
1	A	156	ARG
1	A	195	CYS
1	A	243	ASN
1	A	286	ASN
1	A	288	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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, 3 are monoatomic - leaving 0 for Mogul analysis.

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.

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, 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	448/548 (81%)	0.53	29 (6%)	22 30	43, 62, 98, 121	0
2	B	66/88 (75%)	0.49	2 (3%)	54 63	46, 65, 93, 107	0
All	All	514/636 (80%)	0.53	31 (6%)	25 33	43, 62, 97, 121	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	266	VAL	5.2
1	A	121	GLN	4.8
1	A	123	TYR	4.6
1	A	462	TYR	4.5
1	A	269	ILE	4.1
1	A	346	ASN	3.8
1	A	347	TYR	3.6
1	A	308	LEU	3.6
1	A	445	LEU	3.5
1	A	448	LEU	3.5
1	A	309	GLN	3.3
1	A	446	LYS	3.2
1	A	360	GLU	3.2
1	A	306	LEU	3.1
1	A	311	GLN	3.0
1	A	122	ILE	2.7
1	A	42	LEU	2.6
1	A	498	SER	2.6
1	A	390	SER	2.5
1	A	152	GLY	2.5
2	B	1210	PHE	2.4
1	A	314	LEU	2.4
1	A	447	GLU	2.3
1	A	154	GLY	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	1229	ILE	2.2
1	A	496	TYR	2.2
1	A	427	ASN	2.1
1	A	258	TYR	2.1
1	A	124	LEU	2.1
1	A	239	ILE	2.0
1	A	316	ALA	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. 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(\AA^2)	Q<0.9
4	CL	B	1301	1/1	0.86	0.20	1.84	72,72,72,72	0
3	ZN	A	601	1/1	0.98	0.17	1.27	47,47,47,47	0
4	CL	A	602	1/1	0.96	0.13	-	57,57,57,57	0

6.5 Other polymers [i](#)

There are no such residues in this entry.