



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 4F1O
Title : Crystal Structure of the L1180T mutant Roco4 Kinase Domain from *D. discoideum* bound to AppCp
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Deposited on : 2012-05-07
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 : 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

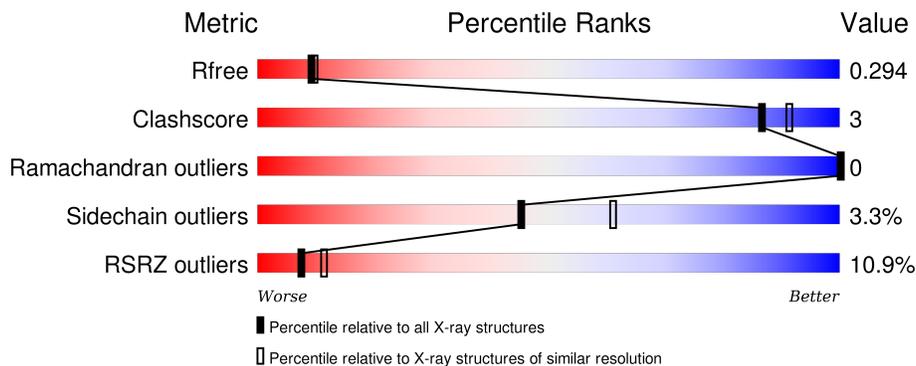
1 Overall quality at a glance i

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	287	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2409 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 Serine/threonine-protein kinase roco4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	276	2213	1418	371	410	14	0	1	0

There are 13 discrepancies between the modelled and reference sequences:

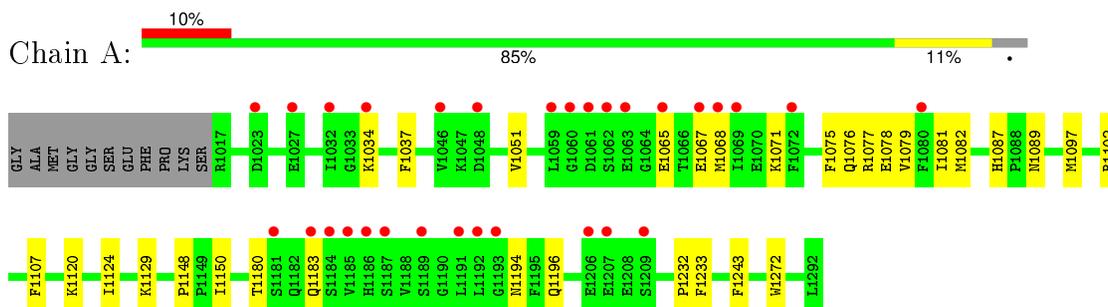
Chain	Residue	Modelled	Actual	Comment	Reference
A	1006	GLY	-	EXPRESSION TAG	UNP Q6XHB2
A	1007	ALA	-	EXPRESSION TAG	UNP Q6XHB2
A	1008	MET	-	EXPRESSION TAG	UNP Q6XHB2
A	1009	GLY	-	EXPRESSION TAG	UNP Q6XHB2
A	1010	GLY	-	EXPRESSION TAG	UNP Q6XHB2
A	1011	SER	-	EXPRESSION TAG	UNP Q6XHB2
A	1012	GLU	-	EXPRESSION TAG	UNP Q6XHB2
A	1013	PHE	-	EXPRESSION TAG	UNP Q6XHB2
A	1014	PRO	-	EXPRESSION TAG	UNP Q6XHB2
A	1015	LYS	-	EXPRESSION TAG	UNP Q6XHB2
A	1016	SER	-	EXPRESSION TAG	UNP Q6XHB2
A	1017	ARG	-	EXPRESSION TAG	UNP Q6XHB2
A	1018	LEU	-	EXPRESSION TAG	UNP Q6XHB2

- Molecule 2 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).

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: Serine/threonine-protein kinase roco4



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	42.32Å 42.32Å 332.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.98 – 2.30 41.98 – 2.30	Depositor EDS
% Data completeness (in resolution range)	100.0 (41.98-2.30) 100.0 (41.98-2.30)	Depositor EDS
R_{merge}	0.22	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.04 (at 2.29Å)	Xtrriage
Refinement program	REFMAC 5.6.0093	Depositor
R, R_{free}	0.250 , 0.296 0.249 , 0.294	Depositor DCC
R_{free} test set	731 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	28.4	Xtrriage
Anisotropy	0.216	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.9	EDS
Estimated twinning fraction	No twinning to report.	Xtrriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtrriage
Outliers	0 of 14603 reflections	Xtrriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	2409	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.37% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ACP

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	0.41	0/2269	0.50	0/3066

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	2213	0	2204	12	0
2	A	31	0	14	0	0
3	A	165	0	0	0	0
All	All	2409	0	2218	12	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 (12) 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:1078:GLU:O	1:A:1082:MET:HG2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1097:MET:HB2	1:A:1102:ARG:HB2	1.87	0.56
1:A:1087:HIS:CD2	1:A:1089:ASN:H	2.26	0.54
1:A:1065:GLU:HG3	1:A:1067:GLU:H	1.72	0.54
1:A:1148:PRO:HG2	1:A:1183:GLN:HG2	1.89	0.53
1:A:1081:ILE:HG23	1:A:1150:ILE:HD12	1.92	0.51
1:A:1077:ARG:HH21	1:A:1180:THR:HA	1.77	0.49
1:A:1051:VAL:HG13	1:A:1107:PHE:HB3	1.96	0.47
1:A:1037:PHE:HA	1:A:1071:LYS:HD2	1.99	0.43
1:A:1232:PRO:O	1:A:1233:PHE:HB2	2.19	0.42
1:A:1124:ILE:O	1:A:1129:LYS:HE3	2.20	0.41
1:A:1075:PHE:O	1:A:1079:VAL:HG23	2.21	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	275/287 (96%)	263 (96%)	12 (4%)	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	245/253 (97%)	237 (97%)	8 (3%)	45 61

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1034	LYS
1	A	1068	MET
1	A	1076	GLN
1	A	1120	LYS
1	A	1194	ASN
1	A	1196	GLN
1	A	1243	PHE
1	A	1272	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1087	HIS
1	A	1115	HIS
1	A	1194	ASN
1	A	1196	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](#)

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](#)

1 ligand 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
2	ACP	A	1301	-	25,33,33	1.67	5 (20%)	31,52,52	2.16	5 (16%)

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	ACP	A	1301	-	-	0/15/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1301	ACP	PB-O2B	-3.25	1.48	1.56
2	A	1301	ACP	PG-O3G	3.12	1.62	1.54
2	A	1301	ACP	PG-O2G	3.17	1.62	1.54
2	A	1301	ACP	PB-O3A	3.42	1.62	1.58
2	A	1301	ACP	O4'-C1'	3.80	1.46	1.41

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1301	ACP	N3-C2-N1	-9.41	121.69	128.89
2	A	1301	ACP	C2'-C1'-N9	-4.18	107.90	114.29
2	A	1301	ACP	PA-O3A-PB	-3.67	122.43	132.73
2	A	1301	ACP	C4-C5-N7	-2.08	107.56	109.48
2	A	1301	ACP	O2B-PB-O1B	2.99	119.53	110.12

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	276/287 (96%)	0.55	30 (10%) 7 11	14, 25, 71, 89	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1207	GLU	7.5
1	A	1185	VAL	5.6
1	A	1061	ASP	5.4
1	A	1192	LEU	5.1
1	A	1184	SER	4.8
1	A	1068	MET	4.6
1	A	1181	SER	4.5
1	A	1187	SER	4.5
1	A	1072	PHE	4.4
1	A	1186	HIS	4.2
1	A	1183	GLN	4.1
1	A	1060	GLY	4.1
1	A	1206	GLU	4.0
1	A	1046	VAL	3.7
1	A	1062	SER	3.7
1	A	1059	LEU	3.6
1	A	1193	GLY	3.5
1	A	1065	GLU	3.5
1	A	1032	ILE	2.9
1	A	1189	SER	2.9
1	A	1034	LYS	2.8
1	A	1063	GLU	2.7
1	A	1209	SER	2.6
1	A	1027	GLU	2.4
1	A	1069	ILE	2.3
1	A	1048	ASP	2.2
1	A	1067	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1191	LEU	2.1
1	A	1023	ASP	2.1
1	A	1080	PHE	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, 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	ACP	A	1301	31/31	0.73	0.28	1.61	49,67,92,92	0

6.5 Other polymers [i](#)

There are no such residues in this entry.