

wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID : 8I5W

Title : Crystal structure of the DHR-2 domain of DOCK10 in complex with Rac1 Authors : Kukimoto-Niino, M.; Mishima-Tsumagari, C.; Ihara, K.; Fukui, Y.; Yokoyama,

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Deposited on : 2023-01-26

Resolution : 2.43 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
A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

 $Mol Probity \quad : \quad 4.02b\text{--}467$

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.32.1

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

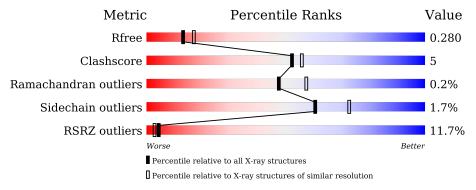
Validation Pipeline (wwPDB-VP) : 2.32.1

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 2.43 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}({\rm \AA})) \end{array}$
R_{free}	130704	1564 (2.46-2.42)
Clashscore	141614	1631 (2.46-2.42)
Ramachandran outliers	138981	1617 (2.46-2.42)
Sidechain outliers	138945	1617 (2.46-2.42)
RSRZ outliers	127900	1547 (2.46-2.42)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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	282	83%	15%	
2	В	184	79%	17%	·



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 3793 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 Dedicator of cytokinesis protein 10.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	۸	276	Total	С	N	О	S	0	0	0
1	A	210	2260	1434	381	436	9	0	U	

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1869	GLY	-	expression tag	UNP Q8BZN6
A	1870	SER	-	expression tag	UNP Q8BZN6
A	1871	SER	-	expression tag	UNP Q8BZN6
A	1872	GLY	_	expression tag	UNP Q8BZN6
A	1873	SER	-	expression tag	UNP Q8BZN6
A	1874	SER	-	expression tag	UNP Q8BZN6

• Molecule 2 is a protein called Ras-related C3 botulinum toxin substrate 1.

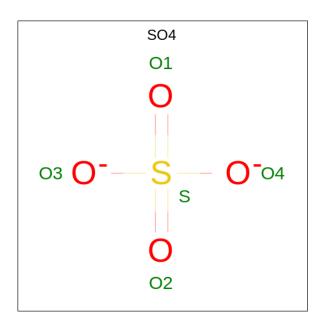
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	В	177	Total	С	N	О	S	0	0	0
_		111	1384	889	228	259	8			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
В	-6	GLY	-	expression tag	UNP P63000
В	-5	SER	-	expression tag	UNP P63000
В	-4	SER	-	expression tag	UNP P63000
В	-3	GLY	-	expression tag	UNP P63000
В	-2	SER	-	expression tag	UNP P63000
В	-1	SER	-	expression tag	UNP P63000
В	0	GLY	-	expression tag	UNP P63000

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).





Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
3	В	1	Total 5	O 4	S 1	0	0

• Molecule 4 is water.

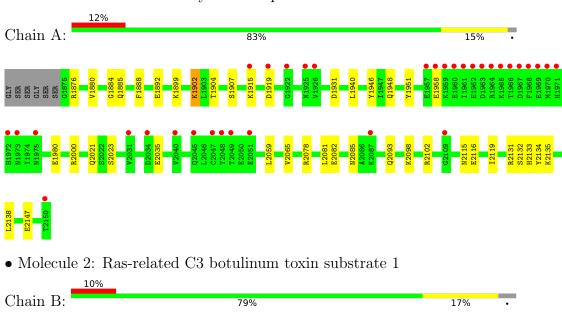
\mathbf{Mol}	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
4	A	96	Total O 96 96	0	0
4	В	48	Total O 48 48	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Dedicator of cytokinesis protein 10





4 Data and refinement statistics (i)

Property	Value	Source	
Space group	C 2 2 21	Depositor	
Cell constants	60.28Å 106.86Å 187.11Å	Donositon	
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor	
Resolution (Å)	46.78 - 2.43	Depositor	
Resolution (A)	46.78 - 2.43	EDS	
% Data completeness	99.7 (46.78-2.43)	Depositor	
(in resolution range)	99.7 (46.78-2.43)	EDS	
R_{merge}	(Not available)	Depositor	
R_{sym}	(Not available)	Depositor	
$< I/\sigma(I) > 1$	1.55 (at 2.42Å)	Xtriage	
Refinement program	PHENIX 1.13	Depositor	
D.D.	0.220 , 0.280	Depositor	
R, R_{free}	0.220 , 0.280	DCC	
R_{free} test set	2012 reflections (8.71%)	wwPDB-VP	
Wilson B-factor (Å ²)	31.8	Xtriage	
Anisotropy	0.833	Xtriage	
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	$0.39\;,55.4$	EDS	
L-test for twinning ²	$< L > = 0.48, < L^2> = 0.31$	Xtriage	
Estimated twinning fraction	0.019 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l	Xtriage	
Latiniated twinning fraction	0.035 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Alliage	
F_o, F_c correlation	0.90	EDS	
Total number of atoms	3793	wwPDB-VP	
Average B, all atoms (Å ²)	38.0	wwPDB-VP	

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.64% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: SO4

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		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.39	0/2301	0.53	0/3094	
2	В	0.36	0/1414	0.54	0/1922	
All	All	0.38	0/3715	0.54	0/5016	

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	2260	0	2247	25	1
2	В	1384	0	1405	16	0
3	В	5	0	0	0	0
4	A	96	0	0	4	3
4	В	48	0	0	2	0
All	All	3793	0	3652	40	4

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 5.

The worst 5 of 40 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:2093:GLN:OE1	4:A:2202:HOH:O	1.90	0.88
1:A:1931:ASP:OD1	4:A:2204:HOH:O	1.92	0.87
1:A:1907:SER:HB2	2:B:162:GLN:HB3	1.80	0.64
1:A:1915:LYS:NZ	4:A:2205:HOH:O	2.22	0.63
2:B:155:LEU:HD13	2:B:168:VAL:HA	1.81	0.62

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{(Å)} \end{aligned}$	Clash overlap (Å)
4:A:2238:HOH:O	4:A:2266:HOH:O[3_554]	1.92	0.28
4:A:2274:HOH:O	4:A:2278:HOH:O[3_554]	1.98	0.22
4:A:2249:HOH:O	4:A:2285:HOH:O[1_655]	2.03	0.17
1:A:2021:GLN:NE2	1:A:2023:SER:OG[3_554]	2.16	0.04

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	Perce	\mathbf{ntiles}	
1	A	274/282 (97%)	265 (97%)	8 (3%)	1 (0%)	34	41	
2	В	175/184~(95%)	170 (97%)	5 (3%)	0	100	100	
All	All	449/466 (96%)	435 (97%)	13 (3%)	1 (0%)	47	57	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1884	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	Rotameric Outliers	
1	A	249/253 (98%)	245 (98%)	4 (2%)	62 74
2	В	153/157 (98%)	150 (98%)	3 (2%)	55 67
All	All	402/410 (98%)	395 (98%)	7 (2%)	60 73

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2132	SER
2	В	63	ASP
2	В	121	ASP
2	В	71	SER
1	A	2059	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2093	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 monosaccharides 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).

	/[a]	Type	Chain	Res	Link	Bond lengths			Bond angles		
1	Mol Typ	туре	Chain	rtes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
	3	SO4	В	401	-	4,4,4	0.21	0	6,6,6	0.35	0

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 (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^{th} 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	$\langle { m RSRZ} \rangle$	# RSRZ > 2		$OWAB(A^2)$	Q<0.9	
1	A	$276/282 \ (97\%)$	1.05	34 (12%)	4	2	18, 33, 95, 136	0
2	В	177/184 (96%)	0.95	19 (10%)	6	4	21, 35, 66, 88	0
All	All	453/466 (97%)	1.01	53 (11%)	4	3	18, 34, 73, 136	0

The worst 5 of 53 RSRZ outliers are listed below:

Mol	Chain	Res Type		RSRZ
1	A	1968	PHE	13.5
1	A	1967	ASP	10.7
1	A	1971	HIS	10.0
1	A	1961	ILE	9.1
1	A	1966	THR	8.8

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 monosaccharides 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. The B-factors column lists the minimum, median, 95^{th} 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.



ľ	Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
	3	SO4	В	401	5/5	0.98	0.13	23,30,35,38	0

6.5 Other polymers (i)

There are no such residues in this entry.

