

Full wwPDB X-ray Structure Validation Report (i)

Dec 2, 2023 – 09:43 pm GMT

PDB ID : 2JI0

Title : CRYSTAL STRUCTURE OF RHOGDI K138Y, K141Y MUTANT

Authors: Cooper, D.R.; Boczek, T.; Derewenda, Z.S.

Deposited on : 2007-02-23

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
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:

MolProbity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.36

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)

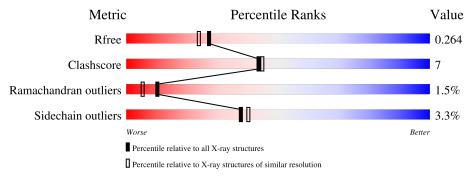
 $\begin{tabular}{lll} Validation Pipeline (wwPDB-VP) & : & 2.36 \end{tabular}$

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 2.10 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	Similar resolution
14160116	(# Entries)	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (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 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%

Mol	Chain	Length	Quality of chain		
1	A	138	77%	20%	



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1191 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.

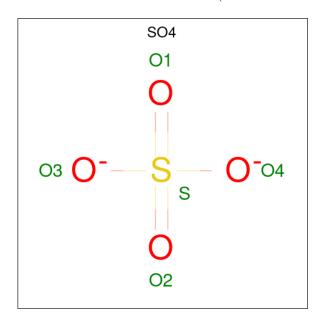
• Molecule 1 is a protein called RHO GDP-DISSOCIATION INHIBITOR 1.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	138	Total	С	N	О	S	0	1	0
1	Λ	130	1122	721	183	213	5	0	1	U

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	138	TYR	LYS	engineered mutation	UNP P52565
A	141	TYR	LYS	engineered mutation	UNP P52565

• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
2	A	1	Total 5	O 4	S 1	0	0

• Molecule 3 is water.



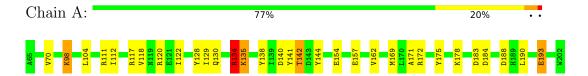
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	64	Total O 64 64	0	0



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. 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. 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: RHO GDP-DISSOCIATION INHIBITOR 1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	32.01Å 55.12Å 38.94Å	Donositor
a, b, c, α , β , γ	90.00° 107.50° 90.00°	Depositor
Resolution (Å)	37.14 - 2.10	Depositor
Resolution (A)	22.13 - 2.10	EDS
% Data completeness	67.5 (37.14-2.10)	Depositor
(in resolution range)	67.6 (22.13-2.10)	EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.20 (at 2.09Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D.	0.184 , 0.259	Depositor
R, R_{free}	0.184 , 0.264	DCC
R_{free} test set	241 reflections (4.66%)	wwPDB-VP
Wilson B-factor (Å ²)	32.7	Xtriage
Anisotropy	0.150	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.30, 36.0	EDS
L-test for twinning ²	$ < L > = 0.50, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	1191	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 13.85% 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	Во	ond angles
MOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.54	0/1152	1.56	15/1558~(1.0%)

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathbf{Ideal}(^o)$
1	A	134	ARG	NE-CZ-NH1	8.62	124.61	120.30
1	A	117	ARG	NE-CZ-NH2	-8.41	116.09	120.30
1	A	120	ARG	NE-CZ-NH2	-7.94	116.33	120.30
1	A	140	ASP	CB-CG-OD1	-7.27	111.75	118.30
1	A	111	ARG	NE-CZ-NH2	-7.12	116.74	120.30
1	A	183	ASP	CB-CG-OD1	6.65	124.29	118.30
1	A	104	LEU	CA-CB-CG	6.44	130.10	115.30
1	A	188	ASP	CB-CG-OD2	6.29	123.96	118.30
1	A	98	LYS	CD-CE-NZ	6.10	125.74	111.70
1	A	112	ILE	CG1-CB-CG2	-5.70	98.87	111.40
1	A	193	GLU	OE1-CD-OE2	-5.42	116.79	123.30
1	A	184	ASP	CB-CG-OD2	-5.34	113.49	118.30
1	A	188	ASP	CB-CG-OD1	-5.33	113.50	118.30
1	A	122	ILE	CG1-CB-CG2	-5.30	99.75	111.40
1	A	135	LYS	CD-CE-NZ	-5.05	100.08	111.70

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.

Mo	l Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1122	0	1109	15	0
2	A	5	0	0	0	0
3	A	64	0	0	4	0
Al	All	1191	0	1109	15	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 7.

All (15) 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:157:GLU:HG2	3:A:2027:HOH:O	1.48	1.11
1:A:154:GLU:HB2	3:A:2042:HOH:O	1.72	0.88
1:A:134:ARG:HG2	1:A:175:TYR:CE2	2.25	0.72
1:A:178:LYS:HG2	1:A:193:GLU:HG3	1.79	0.64
1:A:134:ARG:NH2	1:A:172:ARG:O	2.36	0.59
1:A:157:GLU:HG3	3:A:2044:HOH:O	2.02	0.59
1:A:157:GLU:CG	3:A:2044:HOH:O	2.52	0.56
1:A:171:ALA:O	1:A:175:TYR:OH	2.27	0.49
1:A:128:TYR:CE2	1:A:130:GLN:HG3	2.49	0.48
1:A:138:TYR:OH	1:A:141:TYR:HB2	2.16	0.45
1:A:98:LYS:HG2	1:A:193:GLU:HB3	2.00	0.44
1:A:128:TYR:HD2	1:A:144:TYR:HD2	1.66	0.44
1:A:142:THR:HG21	1:A:144:TYR:OH	2.18	0.43
1:A:70:VAL:HG22	1:A:118:VAL:HG22	2.00	0.43
1:A:129:ILE:HG23	1:A:141:TYR:CE1	2.56	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	137/138 (99%)	132 (96%)	3 (2%)	2 (2%)	10 5

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type		
1	A	169	MET		
1	A	190	LEU		

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	124/123 (101%)	120 (97%)	4 (3%)	39 41	

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type		
1	A	134	ARG		
1	A	135	LYS		
1	A	142	THR		
1	A	162	VAL		

Sometimes 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 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).

Mol Type	Chain Re	Res	Res Link	Bond lengths		Bond angles				
	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	1203	-	4,4,4	0.33	0	6,6,6	0.82	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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

