

Full wwPDB X-ray Structure Validation Report (i)

Jun 13, 2020 – 09:18 pm BST

PDB ID : 5Q1W

Title: PanDDA analysis group deposition - Crystal Structure of DCLRE1A in com-

plex with FMOPL000546a

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Deposited on : 2017-05-15

Resolution : 1.68 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 following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

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

Xtriage (Phenix) : 1.13 EDS : 2.11

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

Refmac : 5.8.0158

CCP4 : 7.0.044 (Gargrove)

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

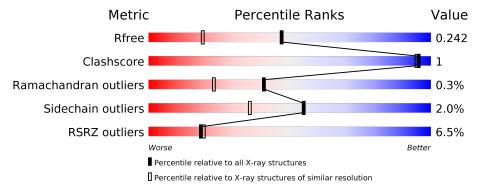
Validation Pipeline (wwPDB-VP) : 2.11

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 1.68 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar resolution} \\ (\#{\rm Entries, resolution range(\AA)}) \end{array}$
R_{free}	130704	6780 (1.70-1.66)
Clashscore	141614	7310 (1.70-1.66)
Ramachandran outliers	138981	7173 (1.70-1.66)
Sidechain outliers	138945	7172 (1.70-1.66)
RSRZ outliers	127900	6661 (1.70-1.66)

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 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
			6%
1	A	343	96%



2 Entry composition (i)

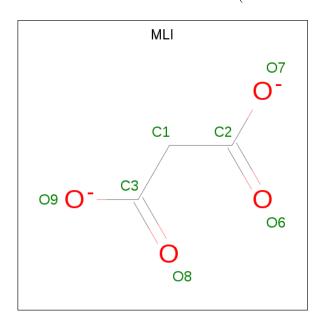
There are 5 unique types of molecules in this entry. The entry contains 3198 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DNA cross-link repair 1A protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Λ	9.41	Total	С	N	О	S	0	10	0
1	A	341	2843	1840	469	513	21	0	19	0

• Molecule 2 is MALONATE ION (three-letter code: MLI) (formula: C₃H₂O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 7	C 3	O 4	0	0

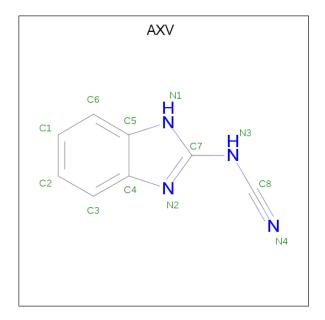
• Molecule 3 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

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

• Molecule 4 is 1 {H}-benzimidazol-2-ylcyanamide (three-letter code: AXV) (formula:



 $C_8H_6N_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N 12 8 4	0	1
4	A	1	Total C N 12 8 4	0	1
4	A	1	Total C N 12 8 4	0	1

• Molecule 5 is water.

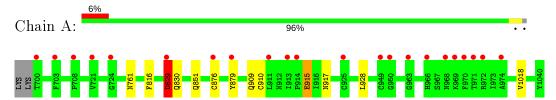
Mo	ol	Chain	Residues	Atoms	ZeroOcc	AltConf
5		A	310	Total O 311 311	0	2



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 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: DNA cross-link repair 1A protein





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	52.10Å 57.13Å 114.98Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.73 - 1.68	Depositor
resolution (A)	23.73 - 1.68	EDS
% Data completeness	99.8 (23.73-1.68)	Depositor
(in resolution range)	99.9 (23.73-1.68)	EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.45 (at 1.68Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
P. P.	0.195 , 0.229	Depositor
R, R_{free}	0.204 , 0.242	DCC
R_{free} test set	1931 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å ²)	22.3	Xtriage
Anisotropy	0.028	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33, 47.5	EDS
L-test for twinning ²	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3198	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.15% 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: NI, MLI, AXV

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	Boı	nd lengths	Bo	nd angles
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	3.98	$2/2924 \ (0.1\%)$	0.80	2/3975 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	${ m Observed}({ m \AA})$	$\mathbf{Ideal}(\mathbf{\AA})$
1	A	915[C]	GLU	CB-CG	150.62	4.38	1.52
1	A	915[D]	GLU	CB-CG	150.62	4.38	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^o)$
1	A	915[C]	GLU	CB-CG-CD	17.07	160.28	114.20
1	A	915[D]	GLU	CB-CG-CD	17.07	160.28	114.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	${f Res}$	Type	Group
1	A	829	ASP	Peptide



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	Α	2843	0	2806	6	0
2	A	7	0	2	0	0
3	A	1	0	0	0	0
4	A	36	0	0	0	0
5	A	311	0	0	5	1
All	All	3198	0	2808	6	1

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 1.

All (6) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${f distance}\;({f \AA})$	overlap(A)
1:A:876[B]:CYS:SG	5:A:1207:HOH:O	1.92	1.27
1:A:909[C]:GLN:NE2	5:A:1201:HOH:O	2.14	0.73
1:A:851:GLN:NE2	5:A:1203:HOH:O	2.36	0.58
1:A:1018:VAL:HG22	5:A:1344:HOH:O	2.12	0.48
1:A:917[D]:ASN:ND2	5:A:1202:HOH:O	2.30	0.47
1:A:761:ASN:HB2	1:A:910[D]:CYS:SG	2.62	0.40

All (1) 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)
5:A:1203:HOH:O	5:A:1298:HOH:O[3_545]	2.08	0.12

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	358/343 (104%)	350 (98%)	7 (2%)	1 (0%)	41 23	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	\mathbf{Type}	
1	A	829	ASP	

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	Analysed Rotameric		Percentiles	
1	A	315/305 (103%)	308 (98%)	7 (2%)	52 32	

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	816	PHE
1	A	829	ASP
1	A	830	GLN
1	A	879	TYR
1	A	915[C]	GLU
1	A	915[D]	GLU
1	A	928	LEU

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

Mol	Chain	${f Res}$	Type
1	A	851	GLN
1	A	869	ASN
1	A	943	GLN
1	A	968	ASN



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 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 for Mogul analysis.

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	Tune	Chain	Dog Limb		es Link Bond lengths			Bond angles		
10101	Type	Chain	m Res	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MLI	A	1101	3	$0,\!6,\!6$	0.00	-	0,7,7	0.00	-
4	AXV	A	1105[D]	-	12,13,13	1.02	1 (8%)	8,17,17	1.27	1 (12%)
4	AXV	A	1104[D]	-	12,13,13	1.02	0	8,17,17	1.26	1 (12%)
4	AXV	A	1103[D]	-	12,13,13	0.99	0	8,17,17	1.33	1 (12%)

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	MLI	A	1101	3	-	0/0/4/4	-
4	AXV	A	1105[D]	-	-	0/0/3/3	0/2/2/2
4	AXV	A	1104[D]	-	-	0/0/3/3	0/2/2/2
4	AXV	A	1103[D]	_	_	0/0/3/3	0/2/2/2



All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	${ m Observed}({ m \AA})$	$Ideal(\AA)$
4	Α	1105[D]	AXV	C7-N3	2.01	1.40	1.36

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}(^{o})$
4	A	1103[D]	AXV	C1-C6-C5	-2.38	116.66	120.08
4	A	1104[D]	AXV	C1-C6-C5	-2.26	116.82	120.08
4	A	1105[D]	AXV	C1-C6-C5	-2.21	116.90	120.08

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	<RSRZ $>$	$\#\mathrm{RSRZ}{>}2$		$OWAB(m \AA^2)$	Q < 0.9
1	A	341/343 (99%)	0.30	22 (6%) 18	19	12, 25, 45, 60	1 (0%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	A	950	GLY	6.7	
1	A	703	PHE	4.9	
1	A	879	TYR	3.8	
1	A	925	CYS	3.6	
1	A	971	THR	3.5	
1	A	966	HIS	3.3	
1	A	724	GLY	3.2	
1	A	968	ASN	3.1	
1	A	970	PHE	3.1	
1	A	829	ASP	3.0	
1	A	721	VAL	3.0	
1	A	949	CYS	2.8	
1	A	700	THR	2.8	
1	A	972	ARG	2.6	
1	A	911[C]	LEU	2.4	
1	A	974	ALA	2.3	
1	A	914[C]	PRO	2.3	
1	A	913[C]	ILE	2.3	
1	A	969	LYS	2.1	
1	A	708	PRO	2.1	
1	A	876[A]	CYS	2.0	
1	A	963	GLY	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. 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.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	${f B-factors}({f \AA}^2)$	Q<0.9
4	AXV	A	1105[D]	12/12	0.66	0.21	49,51,56,60	0
4	AXV	A	1103[D]	12/12	0.74	0.21	23,24,30,32	12
4	AXV	A	1104[D]	12/12	0.75	0.16	33,35,43,48	12
2	MLI	A	1101	7/7	0.96	0.15	20,22,26,26	0
3	NI	A	1102	1/1	1.00	0.02	17,17,17,17	0

6.5 Other polymers (i)

There are no such residues in this entry.

