



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:04 AM UTC

PDB ID : 5Q2M / pdb_00005q2m
Title : PanDDA analysis group deposition – Crystal Structure of DCLRE1A after initial refinement with no ligand modelled (structure 14)
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Deposited on : 2017-05-25
Resolution : 1.28 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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

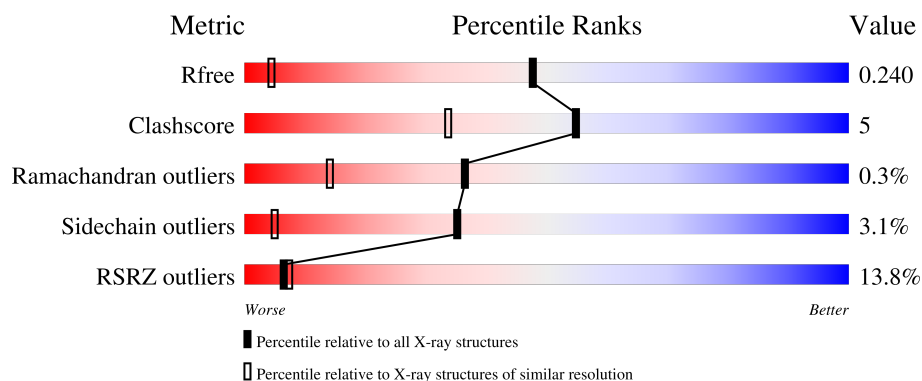
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.28 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}	180053	2836 (1.30-1.26)
Clashscore	190562	2911 (1.30-1.26)
Ramachandran outliers	187476	2841 (1.30-1.26)
Sidechain outliers	187428	2840 (1.30-1.26)
RSRZ outliers	180081	2832 (1.30-1.26)

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 $\leq 5\%$. 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	343	14% 87% 11% ..

2 Entry composition [i](#)

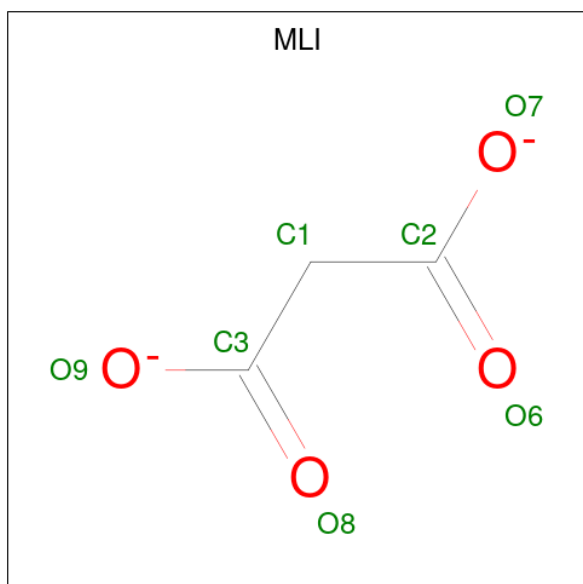
There are 4 unique types of molecules in this entry. The entry contains 3044 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DCLRE1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	341	2726	1765	450	491	20	0	4	0

- Molecule 2 is MALONATE ION (CCD ID: MLI) (formula: $C_3H_2O_4$).



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

- Molecule 3 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

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

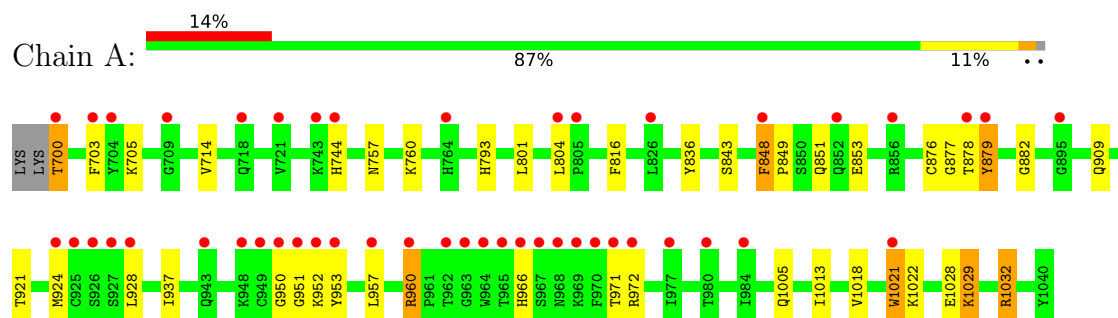
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	310	Total 310	O 310	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: DCLRE1A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.87Å 58.31Å 114.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.18 – 1.28 27.18 – 1.28	Depositor EDS
% Data completeness (in resolution range)	98.1 (27.18-1.28) 98.1 (27.18-1.28)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 1.28Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.210 , 0.234 (Not available) , 0.240	Depositor DCC
R_{free} test set	4360 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	14.8	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 31.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3044	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.60% 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, 0.333 respectively for untwinned datasets, and 0.375, 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: MLI, NI

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	1.50	18/2802 (0.6%)	1.26	11/3809 (0.3%)

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1021	TRP	CB-CG	-10.62	1.17	1.50
1	A	971	THR	CA-C	9.46	1.65	1.52
1	A	1021	TRP	CE3-CZ3	-8.65	1.12	1.38
1	A	879	TYR	N-CA	8.49	1.55	1.46
1	A	971	THR	CA-CB	7.41	1.62	1.53
1	A	700	THR	N-CA	6.81	1.59	1.46
1	A	1021	TRP	CA-C	-6.00	1.45	1.52
1	A	966	HIS	CA-C	5.99	1.60	1.52
1	A	757	ASN	N-CA	5.98	1.53	1.46
1	A	1005	GLN	N-CA	5.48	1.53	1.46
1	A	714	VAL	CA-CB	5.47	1.61	1.54
1	A	882	GLY	N-CA	5.45	1.51	1.45
1	A	843	SER	N-CA	5.41	1.54	1.46
1	A	760	LYS	N-CA	5.29	1.52	1.46
1	A	921	THR	N-CA	5.22	1.52	1.46
1	A	878	THR	N-CA	5.15	1.52	1.45
1	A	793	HIS	N-CA	5.05	1.49	1.46
1	A	1032	ARG	N-CA	5.00	1.52	1.46

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1021	TRP	CB-CA-C	-10.04	95.12	110.88
1	A	966	HIS	N-CA-C	6.76	119.51	111.33
1	A	1021	TRP	CA-C-O	-6.46	114.04	120.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	700	THR	N-CA-C	6.27	128.55	111.00
1	A	1021	TRP	O-C-N	5.98	128.23	122.07
1	A	848	PHE	N-CA-CB	5.50	116.88	111.10
1	A	853	GLU	CA-CB-CG	5.47	125.03	114.10
1	A	1022	LYS	N-CA-C	-5.19	104.88	111.11
1	A	848	PHE	CB-CA-C	5.18	117.05	110.22
1	A	700	THR	N-CA-CB	-5.07	102.88	111.50
1	A	1021	TRP	N-CA-C	5.07	116.49	111.07

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	2726	0	2676	26	0
2	A	7	0	2	0	0
3	A	1	0	0	0	0
4	A	310	0	0	18	0
All	All	3044	0	2678	26	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 5.

All (26) 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:700:THR:HB	4:A:1210:HOH:O	1.32	1.25
1:A:744:HIS:CE1	4:A:1207:HOH:O	2.08	1.07
1:A:876[B]:CYS:SG	4:A:1204:HOH:O	2.17	1.02
1:A:953:TYR:OH	4:A:1203:HOH:O	2.03	0.77
1:A:700:THR:CB	4:A:1210:HOH:O	2.06	0.76
1:A:744:HIS:HE1	4:A:1207:HOH:O	1.55	0.74
1:A:1032:ARG:CZ	4:A:1231:HOH:O	2.40	0.70
1:A:1021:TRP:HA	1:A:1021:TRP:CE3	2.28	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:877:GLY:O	4:A:1204:HOH:O	2.13	0.66
1:A:1028[B]:GLU:OE1	4:A:1205:HOH:O	2.15	0.64
1:A:1029:LYS:NZ	4:A:1208:HOH:O	2.31	0.62
1:A:1032:ARG:NH2	4:A:1206:HOH:O	2.31	0.62
1:A:909:GLN:NE2	4:A:1211:HOH:O	2.37	0.57
1:A:851:GLN:NE2	4:A:1202:HOH:O	1.98	0.56
1:A:1021:TRP:CE3	1:A:1021:TRP:CA	2.86	0.56
1:A:836:TYR:CZ	1:A:1013:ILE:HD12	2.43	0.54
1:A:848:PHE:HB2	1:A:849:PRO:CD	2.39	0.52
1:A:848:PHE:HB2	1:A:849:PRO:HD2	1.91	0.51
1:A:705:LYS:NZ	4:A:1215:HOH:O	2.48	0.47
1:A:950:GLY:O	1:A:952:LYS:N	2.48	0.46
1:A:848:PHE:CB	1:A:849:PRO:CD	2.95	0.45
1:A:744:HIS:NE2	4:A:1207:HOH:O	2.31	0.44
1:A:937:ILE:HG21	1:A:960:ARG:HG2	2.00	0.43
1:A:703:PHE:HD1	4:A:1496:HOH:O	2.01	0.43
1:A:1018:VAL:HG22	4:A:1298:HOH:O	2.19	0.42
1:A:924:MET:HG2	4:A:1397:HOH:O	2.20	0.41

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	343/343 (100%)	329 (96%)	13 (4%)	1 (0%)	36 14

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	951	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	299/305 (98%)	290 (97%)	9 (3%)	36 5

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	801	LEU
1	A	804	LEU
1	A	816	PHE
1	A	879	TYR
1	A	928	LEU
1	A	957	LEU
1	A	960	ARG
1	A	972	ARG
1	A	1029	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	744	HIS
1	A	766	GLN
1	A	851	GLN
1	A	869	ASN
1	A	909	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	MLI	A	1101	3	6,6,6	1.60	2 (33%)	7,7,7	1.36	1 (14%)

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	-	3/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	MLI	O9-C3	-2.66	1.22	1.30
2	A	1101	MLI	O7-C2	-2.24	1.23	1.30

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	MLI	O8-C3-C1	-2.61	114.67	122.11

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	MLI	C3-C1-C2-O6
2	A	1101	MLI	C2-C1-C3-O8
2	A	1101	MLI	C2-C1-C3-O9

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	341/343 (99%)	0.96	47 (13%) 6 7	8, 19, 38, 94	4 (1%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	970	PHE	13.5
1	A	967	SER	8.3
1	A	971	THR	8.1
1	A	968	ASN	7.6
1	A	966	HIS	7.5
1	A	700	THR	7.5
1	A	1021	TRP	6.7
1	A	703	PHE	6.4
1	A	879	TYR	5.9
1	A	963	GLY	5.7
1	A	969	LYS	5.3
1	A	950	GLY	5.2
1	A	744	HIS	5.1
1	A	925	CYS	4.7
1	A	977	ILE	4.3
1	A	926	SER	4.1
1	A	848	PHE	4.0
1	A	951	GLY	4.0
1	A	743	LYS	3.6
1	A	953	TYR	3.5
1	A	972	ARG	3.4
1	A	965	THR	3.3
1	A	721	VAL	3.3
1	A	964	TRP	3.2
1	A	962	THR	3.1
1	A	957	LEU	3.1
1	A	943	GLN	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	805	PRO	3.1
1	A	852	GLN	3.0
1	A	826	LEU	2.8
1	A	952	LYS	2.8
1	A	928	LEU	2.8
1	A	704	TYR	2.7
1	A	984	ILE	2.6
1	A	924	MET	2.5
1	A	980	THR	2.5
1	A	709	GLY	2.4
1	A	927	SER	2.3
1	A	960	ARG	2.2
1	A	804	LEU	2.2
1	A	764[A]	HIS	2.2
1	A	895	GLY	2.2
1	A	948	LYS	2.1
1	A	949	CYS	2.0
1	A	856	ARG	2.0
1	A	718	GLN	2.0
1	A	878	THR	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 oligosaccharides 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, 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	B-factors($\text{\AA}^2$)	Q<0.9
2	MLI	A	1101	7/7	0.95	0.08	13,19,23,24	0
3	NI	A	1102	1/1	1.00	0.04	11,11,11,11	0

6.5 Other polymers [i](#)

There are no such residues in this entry.