



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 19, 2026 – 12:40 AM UTC

PDB ID : 5Q8S / pdb_00005q8s
Title : PanDDA analysis group deposition – Crystal Structure of DCLRE1A after initial refinement with no ligand modelled (structure 238)
Authors : Newman, J.A.; Aitkenhead, H.; Lee, S.Y.; Kupinska, K.; Burgess-Brown, N.; Tallon, R.; Krojer, T.; von Delft, F.; Arrowsmith, C.H.; Edwards, A.; Bountra, C.; Gileadi, O.
Deposited on : 2017-05-25
Resolution : 1.61 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

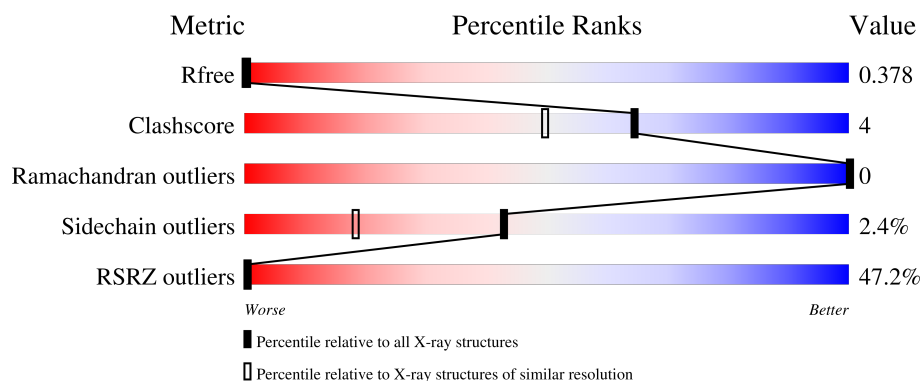
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.61 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	6728 (1.64-1.60)
Clashscore	190562	7023 (1.64-1.60)
Ramachandran outliers	187476	6898 (1.64-1.60)
Sidechain outliers	187428	6896 (1.64-1.60)
RSRZ outliers	180081	6727 (1.64-1.60)

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	47% 89% 10% ..

2 Entry composition [i](#)

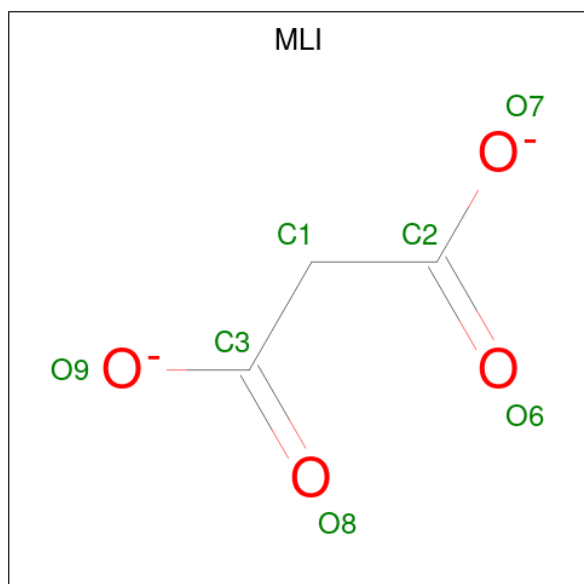
There are 4 unique types of molecules in this entry. The entry contains 3044 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
			Total	Ni		
3	A	1	1	1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	310	Total 310	O 310	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.78Å 57.91Å 114.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	57.30 – 1.61 57.30 – 1.61	Depositor EDS
% Data completeness (in resolution range)	97.9 (57.30-1.61) 97.9 (57.30-1.61)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 1.61Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.302 , 0.362 0.314 , 0.378	Depositor DCC
R_{free} test set	2193 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	20.5	Xtriage
Anisotropy	0.261	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.9	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	0.91	EDS
Total number of atoms	3044	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.43% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.97	0/2802	1.07	3/3809 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	860	ASN	N-CA-C	7.59	119.24	110.97
1	A	830	GLN	N-CA-C	6.08	118.09	108.79
1	A	911	LEU	N-CA-C	5.39	119.48	113.02

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	2726	0	2676	21	0
2	A	7	0	2	0	0
3	A	1	0	0	0	0
4	A	310	0	0	12	0
All	All	3044	0	2678	21	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 4.

All (21) 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:909:GLN:NE2	4:A:1203:HOH:O	2.18	0.76
1:A:815:ASP:OD1	4:A:1201:HOH:O	2.16	0.62
1:A:973:ILE:N	4:A:1206:HOH:O	2.32	0.61
1:A:1018:VAL:HG22	4:A:1298:HOH:O	2.03	0.57
1:A:718:GLN:O	4:A:1202:HOH:O	2.17	0.56
1:A:864:GLU:HB2	4:A:1415:HOH:O	2.08	0.53
1:A:860:ASN:O	1:A:861:THR:C	2.53	0.52
1:A:1032:ARG:NE	4:A:1213:HOH:O	2.42	0.52
1:A:973:ILE:HG22	4:A:1206:HOH:O	2.09	0.51
1:A:804:LEU:HD22	1:A:808:THR:HB	1.94	0.50
1:A:836:TYR:CZ	1:A:1013:ILE:HD12	2.48	0.49
1:A:983:ASN:ND2	4:A:1212:HOH:O	2.39	0.47
1:A:874:VAL:HG11	1:A:890:ILE:HG21	1.97	0.47
1:A:861:THR:HG21	1:A:987:TYR:CZ	2.52	0.44
1:A:871:HIS:CE1	4:A:1281:HOH:O	2.70	0.44
1:A:834:MET:HE2	1:A:1013:ILE:HD11	1.99	0.44
1:A:717:PHE:CE1	1:A:728:TYR:HB3	2.52	0.43
1:A:760:LYS:O	1:A:764[A]:HIS:HA	2.17	0.43
1:A:851:GLN:NE2	4:A:1225:HOH:O	2.52	0.41
1:A:702:PRO:HG2	1:A:705:LYS:HG3	2.02	0.41
1:A:972:ARG:HB3	4:A:1206:HOH:O	2.19	0.41

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	343/343 (100%)	326 (95%)	17 (5%)	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	299/305 (98%)	292 (98%)	7 (2%)	44 20

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	893	VAL
1	A	928	LEU
1	A	1029	LYS

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

Mol	Chain	Res	Type
1	A	851	GLN
1	A	909	GLN
1	A	943	GLN
1	A	966	HIS

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

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	1.37	0	7,7,7	1.26	0

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	-	4/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1101	MLI	C2-C1-C3-O9
2	A	1101	MLI	C2-C1-C3-O8
2	A	1101	MLI	C3-C1-C2-O6
2	A	1101	MLI	C3-C1-C2-O7

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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%)	2.54	161 (47%) 0 0	13, 32, 91, 147	4 (1%)

All (161) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	745	PHE	11.0
1	A	984	ILE	10.9
1	A	973	ILE	10.3
1	A	939	PHE	10.1
1	A	977	ILE	9.8
1	A	970	PHE	9.4
1	A	942	LEU	9.4
1	A	982	GLY	9.1
1	A	780	ILE	8.9
1	A	941	GLY	8.9
1	A	980	THR	8.7
1	A	986	ILE	8.4
1	A	937	ILE	8.4
1	A	765	VAL	8.3
1	A	769	TYR	8.3
1	A	974	ALA	8.1
1	A	978	PRO	7.6
1	A	971	THR	7.6
1	A	711	GLY	7.6
1	A	987	TYR	7.5
1	A	744	HIS	7.2
1	A	976	VAL	7.1
1	A	781	VAL	7.1
1	A	946	LEU	6.9
1	A	747	PHE	6.8
1	A	770	ILE	6.7
1	A	750	TYR	6.7

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Mol	Chain	Res	Type	RSRZ
1	A	966	HIS	6.6
1	A	968	ASN	6.6
1	A	967	SER	6.5
1	A	985	SER	6.4
1	A	938	ASN	6.4
1	A	768	GLN	6.3
1	A	928	LEU	6.3
1	A	746	THR	6.2
1	A	972	ARG	6.2
1	A	741	LEU	6.1
1	A	722	VAL	6.0
1	A	721	VAL	5.9
1	A	988	GLY	5.9
1	A	964	TRP	5.8
1	A	951	GLY	5.8
1	A	983	ASN	5.8
1	A	956	ILE	5.7
1	A	954	ASN	5.7
1	A	784	VAL	5.5
1	A	742	SER	5.4
1	A	861	THR	5.4
1	A	981	LYS	5.3
1	A	979	GLN	5.3
1	A	862	ALA	5.3
1	A	866	VAL	5.2
1	A	940	LYS	5.2
1	A	748	PRO	5.1
1	A	724	GLY	4.8
1	A	743	LYS	4.8
1	A	950	GLY	4.7
1	A	868	LEU	4.7
1	A	943	GLN	4.7
1	A	879	TYR	4.6
1	A	953	TYR	4.6
1	A	965	THR	4.6
1	A	740	GLY	4.6
1	A	766	GLN	4.6
1	A	856	ARG	4.5
1	A	763	LEU	4.5
1	A	717	PHE	4.5
1	A	828	ALA	4.5
1	A	719	TYR	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	867	THR	4.3
1	A	989	ILE	4.3
1	A	857	PHE	4.3
1	A	963	GLY	4.2
1	A	779	CYS	4.2
1	A	957	LEU	4.2
1	A	700	THR	4.2
1	A	935	MET	4.1
1	A	927	SER	4.1
1	A	709	GLY	4.1
1	A	936	GLN	4.1
1	A	764[A]	HIS	4.0
1	A	712	PHE	4.0
1	A	749	VAL	4.0
1	A	782	ASN	4.0
1	A	961	PRO	3.9
1	A	863	PHE	3.9
1	A	969	LYS	3.9
1	A	726	THR	3.8
1	A	944	SER	3.8
1	A	771	HIS	3.8
1	A	723	GLU	3.8
1	A	826	LEU	3.8
1	A	975	ASP	3.7
1	A	894	LEU	3.7
1	A	932	LEU	3.7
1	A	865	ALA	3.7
1	A	767	GLU	3.7
1	A	759	LEU	3.7
1	A	871	HIS	3.7
1	A	925	CYS	3.6
1	A	955	GLN	3.6
1	A	710	THR	3.6
1	A	860	ASN	3.5
1	A	945	HIS	3.5
1	A	870	PRO	3.4
1	A	739	ALA	3.4
1	A	926	SER	3.4
1	A	716	ALA	3.3
1	A	720	GLY	3.3
1	A	893	VAL	3.3
1	A	869	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	774	PRO	3.2
1	A	962	THR	3.2
1	A	773	LEU	3.1
1	A	775	LEU	3.1
1	A	804	LEU	3.1
1	A	829	ASP	3.1
1	A	878	THR	3.1
1	A	948	LYS	3.1
1	A	952	LYS	3.1
1	A	934	MET	3.0
1	A	772	PRO	3.0
1	A	864	GLU	3.0
1	A	735	SER	3.0
1	A	959	PHE	2.9
1	A	847	THR	2.9
1	A	960	ARG	2.9
1	A	827	LEU	2.9
1	A	708	PRO	2.9
1	A	947	LYS	2.9
1	A	873	LEU	2.7
1	A	872	ALA	2.7
1	A	725	CYS	2.7
1	A	852	GLN	2.6
1	A	874	VAL	2.6
1	A	848	PHE	2.6
1	A	728	TYR	2.6
1	A	738	TYR	2.6
1	A	876[A]	CYS	2.6
1	A	949	CYS	2.6
1	A	912	ASN	2.5
1	A	933	PRO	2.5
1	A	831	LYS	2.5
1	A	875	VAL	2.5
1	A	880	SER	2.5
1	A	830	GLN	2.4
1	A	929	VAL	2.4
1	A	727	ALA	2.4
1	A	778	GLU	2.3
1	A	704	TYR	2.3
1	A	783	GLY	2.3
1	A	703	PHE	2.3
1	A	805	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1039	GLY	2.2
1	A	824	ARG	2.2
1	A	736	ASP	2.1
1	A	753	GLU	2.0
1	A	777	THR	2.0
1	A	718	GLN	2.0
1	A	729	PHE	2.0
1	A	958	ALA	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	0.92	0.09	25,32,34,34	0
3	NI	A	1102	1/1	0.99	0.07	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.