



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:32 PM UTC

PDB ID : 5X83 / pdb_00005x83
Title : Structure of DCC FN456 domains
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Deposited on : 2017-02-28
Resolution : 3.00 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
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

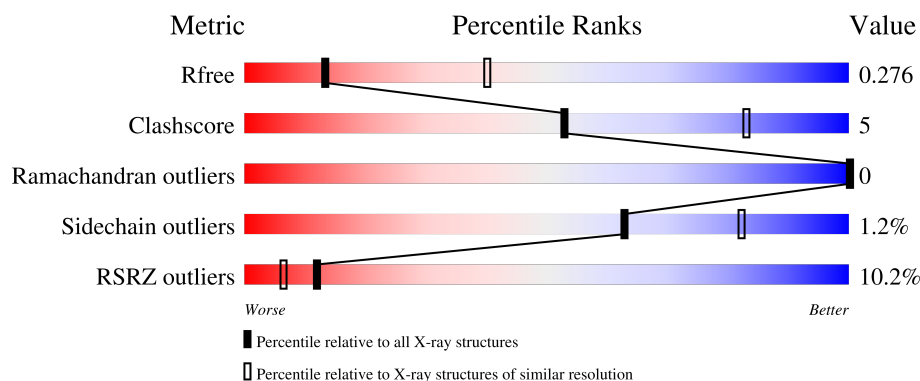
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	116	 11% 69% 12% 19%
1	C	116	 11% 66% 16% 18%
2	B	207	 10% 84% 13% ..
2	D	207	 7% 82% 12% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4627 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 Netrin receptor DCC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	94	Total	C	N	O	S	0	0	0
			734	463	128	141	2			
1	C	95	Total	C	N	O	S	0	0	0
			740	466	129	143	2			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	816	GLY	-	linker	UNP P43146
A	817	SER	-	linker	UNP P43146
A	818	GLY	-	linker	UNP P43146
A	819	GLY	-	linker	UNP P43146
A	820	SER	-	linker	UNP P43146
A	821	GLY	-	linker	UNP P43146
A	822	GLY	-	linker	UNP P43146
A	823	SER	-	linker	UNP P43146
A	824	GLY	-	linker	UNP P43146
A	825	GLY	-	linker	UNP P43146
A	826	SER	-	linker	UNP P43146
A	827	GLY	-	linker	UNP P43146
A	828	GLY	-	linker	UNP P43146
A	829	SER	-	linker	UNP P43146
A	830	GLY	-	linker	UNP P43146
A	831	GLY	-	linker	UNP P43146
A	832	SER	-	linker	UNP P43146
A	833	GLY	-	linker	UNP P43146
A	834	GLY	-	linker	UNP P43146
A	835	SER	-	linker	UNP P43146
A	836	GLY	-	linker	UNP P43146
C	816	GLY	-	linker	UNP P43146
C	817	SER	-	linker	UNP P43146
C	818	GLY	-	linker	UNP P43146
C	819	GLY	-	linker	UNP P43146

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Chain	Residue	Modelled	Actual	Comment	Reference
C	820	SER	-	linker	UNP P43146
C	821	GLY	-	linker	UNP P43146
C	822	GLY	-	linker	UNP P43146
C	823	SER	-	linker	UNP P43146
C	824	GLY	-	linker	UNP P43146
C	825	GLY	-	linker	UNP P43146
C	826	SER	-	linker	UNP P43146
C	827	GLY	-	linker	UNP P43146
C	828	GLY	-	linker	UNP P43146
C	829	SER	-	linker	UNP P43146
C	830	GLY	-	linker	UNP P43146
C	831	GLY	-	linker	UNP P43146
C	832	SER	-	linker	UNP P43146
C	833	GLY	-	linker	UNP P43146
C	834	GLY	-	linker	UNP P43146
C	835	SER	-	linker	UNP P43146
C	836	GLY	-	linker	UNP P43146

- Molecule 2 is a protein called Netrin receptor DCC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	202	Total	C	N	O	S	0	0	0
			1600	1022	271	300	7			
2	D	195	Total	C	N	O	S	0	0	0
			1553	994	263	289	7			

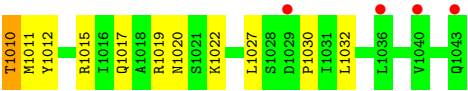
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	837	GLY	-	linker	UNP P43146
B	1038	LEU	-	expression tag	UNP P43146
B	1039	GLU	-	expression tag	UNP P43146
B	1040	VAL	-	expression tag	UNP P43146
B	1041	LEU	-	expression tag	UNP P43146
B	1042	PHE	-	expression tag	UNP P43146
B	1043	GLN	-	expression tag	UNP P43146
D	837	GLY	-	linker	UNP P43146
D	1038	LEU	-	expression tag	UNP P43146
D	1039	GLU	-	expression tag	UNP P43146
D	1040	VAL	-	expression tag	UNP P43146
D	1041	LEU	-	expression tag	UNP P43146
D	1042	PHE	-	expression tag	UNP P43146

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1043	GLN	-	expression tag	UNP P43146



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.46Å 126.97Å 57.16Å 90.00° 99.68° 90.00°	Depositor
Resolution (Å)	42.14 – 3.00 42.14 – 3.00	Depositor EDS
% Data completeness (in resolution range)	96.4 (42.14-3.00) 96.8 (42.14-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.221 , 0.278 0.224 , 0.276	Depositor DCC
R_{free} test set	722 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.773	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 31.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	4627	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.22% 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](#)

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	0.30	0/753	0.72	0/1028
1	C	0.29	0/759	0.72	0/1036
2	B	0.29	0/1638	0.71	0/2231
2	D	0.28	0/1590	0.68	0/2166
All	All	0.29	0/4740	0.70	0/6461

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	734	0	718	8	1
1	C	740	0	723	12	0
2	B	1600	0	1607	15	1
2	D	1553	0	1561	15	0
All	All	4627	0	4609	46	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 5.

All (46) 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)
2:D:1011:MET:HE3	2:D:1032:LEU:HB3	1.77	0.66
1:C:778:GLN:O	1:C:779:ARG:NH1	2.30	0.65
2:D:878:ARG:HE	2:D:913:SER:HB2	1.61	0.64
2:D:1015:ARG:HE	2:D:1030:PRO:HG3	1.63	0.64
1:C:728:GLN:HB3	1:C:806:VAL:HG13	1.79	0.63
2:B:1011:MET:HE3	2:B:1032:LEU:HB3	1.80	0.63
2:B:980:LEU:HD21	2:B:1010:THR:HB	1.81	0.62
1:A:726:PRO:HA	1:A:753:ILE:HD12	1.83	0.60
2:B:874:LEU:HD11	2:B:893:ASP:HB3	1.85	0.59
1:A:728:GLN:HB3	1:A:806:VAL:HG13	1.87	0.57
2:D:962:GLN:HG3	2:D:963:PRO:HD2	1.86	0.56
2:B:1015:ARG:HE	2:B:1030:PRO:HG3	1.70	0.56
2:B:955:ARG:NH1	1:C:811:SER:OG	2.37	0.55
2:B:1009:ASP:HB2	2:B:1037:LYS:HD3	1.88	0.55
1:C:797:LYS:HG2	1:C:807:PRO:HB3	1.90	0.54
2:B:915:MET:HE3	2:B:925:TRP:CE2	2.44	0.53
2:B:962:GLN:HG3	2:B:963:PRO:HD2	1.92	0.52
1:A:811:SER:OG	2:D:955:ARG:NH1	2.42	0.51
2:B:939:THR:OG1	2:B:966:GLU:OE1	2.23	0.51
2:D:980:LEU:HD11	2:D:1010:THR:HB	1.93	0.50
2:B:955:ARG:HH12	1:C:811:SER:HG	1.60	0.49
2:B:1017:GLN:HB3	2:B:1027:LEU:HD23	1.95	0.48
2:D:980:LEU:HD13	2:D:1012:TYR:CZ	2.48	0.48
1:A:787:GLU:OE1	1:A:792:TYR:OH	2.31	0.48
2:B:981:ASP:HB3	2:B:984:ILE:HG12	1.96	0.48
1:C:787:GLU:OE1	1:C:792:TYR:OH	2.31	0.47
2:D:951:GLU:HA	2:D:952:GLY:HA2	1.67	0.47
2:D:915:MET:HE3	2:D:925:TRP:CE2	2.49	0.47
2:D:1019:ARG:HG2	2:D:1020:ASN:H	1.81	0.45
2:D:981:ASP:HB3	2:D:984:ILE:HG12	1.99	0.45
2:D:1017:GLN:HB3	2:D:1027:LEU:HD23	1.98	0.45
1:C:756:ARG:HE	1:C:801:ASN:ND2	2.16	0.44
1:A:752:ASN:OD1	1:A:753:ILE:N	2.51	0.43
1:C:759:ILE:HG13	1:C:799:PHE:CD1	2.53	0.43
2:D:1022:LYS:HD3	2:D:1022:LYS:HA	1.73	0.43
1:C:776:SER:O	1:C:779:ARG:NH2	2.45	0.42
1:C:744:SER:HB3	1:C:780:TYR:CE2	2.54	0.42
1:C:806:VAL:HA	1:C:807:PRO:HD3	1.79	0.42
2:B:949:THR:HA	2:B:957:VAL:HG12	2.01	0.42
1:A:730:SER:OG	1:A:746:THR:OG1	2.31	0.42
1:A:775:ASP:OD1	1:A:776:SER:N	2.53	0.41
2:B:951:GLU:HA	2:B:952:GLY:HA2	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:808:LEU:HD23	1:C:808:LEU:HA	1.93	0.41
1:A:797:LYS:HG2	1:A:807:PRO:HB3	2.02	0.40
2:B:849:LEU:HD22	2:D:1019:ARG:HD3	2.03	0.40
2:D:905:LYS:O	2:D:933:THR:HG21	2.21	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	Interatomic distance (Å)	Clash overlap (Å)
1:A:787:GLU:OE2	2:B:995:SER:OG[2_657]	2.17	0.03

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	92/116 (79%)	88 (96%)	4 (4%)	0	100	100
1	C	93/116 (80%)	89 (96%)	4 (4%)	0	100	100
2	B	198/207 (96%)	189 (96%)	9 (4%)	0	100	100
2	D	191/207 (92%)	181 (95%)	10 (5%)	0	100	100
All	All	574/646 (89%)	547 (95%)	27 (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	83/92 (90%)	83 (100%)	0	100	100
1	C	84/92 (91%)	83 (99%)	1 (1%)	63	82
2	B	178/183 (97%)	175 (98%)	3 (2%)	53	78
2	D	172/183 (94%)	170 (99%)	2 (1%)	63	82
All	All	517/550 (94%)	511 (99%)	6 (1%)	63	82

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	863	VAL
2	B	980	LEU
2	B	1010	THR
1	C	789	SER
2	D	982	LYS
2	D	1010	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1001	HIS
1	C	801	ASN
2	D	919	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

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	94/116 (81%)	1.10	13 (13%) 6 4	34, 57, 93, 132	0
1	C	95/116 (81%)	1.05	13 (13%) 6 4	37, 62, 101, 128	0
2	B	202/207 (97%)	0.94	20 (9%) 13 7	27, 47, 84, 122	0
2	D	195/207 (94%)	0.93	14 (7%) 21 11	28, 48, 83, 116	0
All	All	586/646 (90%)	0.98	60 (10%) 12 6	27, 52, 93, 132	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	749	LEU	4.1
2	B	865	LYS	4.1
2	B	952	GLY	3.8
1	C	727	ASP	3.6
2	B	872	VAL	3.6
2	D	1009	ASP	3.5
1	C	738	THR	3.3
2	B	935	GLU	3.1
1	C	753	ILE	3.1
1	A	739	ASN	3.1
2	D	1029	ASP	3.1
1	C	775	ASP	3.0
1	C	743	MET	3.0
1	A	775	ASP	3.0
2	B	1040	VAL	2.9
1	A	724	GLN	2.9
1	C	752	ASN	2.9
2	D	1040	VAL	2.8
1	C	777	LYS	2.7
2	D	952	GLY	2.7
1	C	749	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	909	MET	2.6
2	D	997	ASP	2.6
2	B	953	LYS	2.5
1	C	780	TYR	2.5
1	C	787	GLU	2.5
2	B	839	LEU	2.5
2	B	927	MET	2.5
2	D	887	ALA	2.5
1	A	738	THR	2.5
1	A	816	GLY	2.4
2	D	883	PHE	2.4
2	B	878	ARG	2.4
1	C	724	GLN	2.4
2	B	883	PHE	2.3
1	A	784	GLU	2.3
2	B	951	GLU	2.3
2	B	902	THR	2.3
2	B	997	ASP	2.3
1	A	777	LYS	2.3
2	B	857	SER	2.3
2	B	954	PRO	2.2
1	A	780	TYR	2.2
2	B	850	THR	2.2
2	D	993	THR	2.2
2	D	978	TYR	2.2
1	A	752	ASN	2.2
2	B	1029	ASP	2.2
1	A	788	SER	2.1
1	C	751	PRO	2.1
1	A	728	GLN	2.1
2	D	1036	LEU	2.1
1	C	741	ILE	2.1
2	B	914	VAL	2.1
1	A	750	ASN	2.1
2	B	871	GLU	2.1
2	D	1043	GLN	2.0
2	D	966	GLU	2.0
2	D	857	SER	2.0
2	D	972	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.