



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:14 PM UTC

PDB ID : 1EG3 / pdb_00001eg3
Title : STRUCTURE OF A DYSTROPHIN WW DOMAIN FRAGMENT IN COM-
PLEX WITH A BETA-DYSTROGLYCAN PEPTIDE
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Deposited on : 2000-02-11
Resolution : 2.00 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

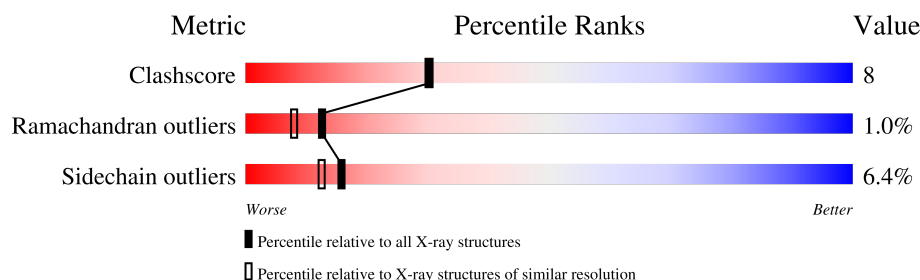
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	261	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2355 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 DYSTROPHIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	260	Total	C	N	O	S	0	0	0
			2089	1321	370	383	15			

- Molecule 2 is water.

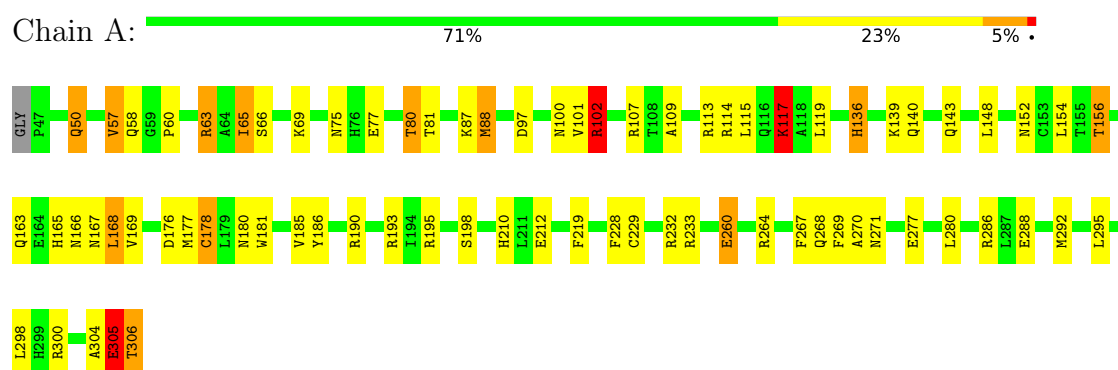
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	266	Total	O	0	0
			266	266		

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.

Note EDS was not executed.

• Molecule 1: DYSTROPHIN



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	49.71Å 67.47Å 85.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00	Depositor
% Data completeness (in resolution range)	99.2 (20.00-2.00)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.194 , 0.257	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2355	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	0.94	0/2135	1.86	53/2897 (1.8%)

There are no bond length outliers.

All (53) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	114	ARG	CG-CD-NE	16.03	147.27	112.00
1	A	114	ARG	CD-NE-CZ	12.43	141.80	124.40
1	A	102	ARG	CD-NE-CZ	9.94	138.32	124.40
1	A	269	PHE	CA-CB-CG	9.27	123.07	113.80
1	A	63	ARG	NE-CZ-NH2	-9.23	110.89	119.20
1	A	168	LEU	N-CA-C	-9.22	100.61	112.23
1	A	169	VAL	N-CA-C	8.90	120.70	107.80
1	A	264	ARG	NE-CZ-NH2	8.54	126.89	119.20
1	A	63	ARG	CD-NE-CZ	-8.35	112.72	124.40
1	A	63	ARG	NE-CZ-NH1	7.59	129.09	121.50
1	A	97	ASP	CA-CB-CG	7.48	120.08	112.60
1	A	195	ARG	NE-CZ-NH1	-7.43	114.06	121.50
1	A	180	ASN	OD1-CG-ND2	-7.31	115.29	122.60
1	A	102	ARG	N-CA-C	7.07	118.78	111.14
1	A	232	ARG	NE-CZ-NH2	7.00	125.50	119.20
1	A	264	ARG	NE-CZ-NH1	-6.96	114.54	121.50
1	A	232	ARG	NE-CZ-NH1	-6.92	114.58	121.50
1	A	75	ASN	OD1-CG-ND2	-6.82	115.78	122.60
1	A	57	VAL	N-CA-CB	-6.80	101.02	112.44
1	A	195	ARG	CD-NE-CZ	6.80	133.92	124.40
1	A	152	ASN	OD1-CG-ND2	-6.77	115.83	122.60
1	A	102	ARG	NE-CZ-NH1	-6.68	114.82	121.50
1	A	228	PHE	CA-CB-CG	-6.58	107.22	113.80
1	A	267	PHE	CA-CB-CG	-6.34	107.46	113.80
1	A	107	ARG	CD-NE-CZ	6.17	133.03	124.40
1	A	260	GLU	CB-CG-CD	6.05	122.89	112.60
1	A	178	CYS	CA-C-O	6.02	126.80	120.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	102	ARG	CA-C-N	-5.99	113.75	122.19
1	A	102	ARG	C-N-CA	-5.99	113.75	122.19
1	A	65	ILE	N-CA-C	5.96	116.70	108.12
1	A	300	ARG	NE-CZ-NH1	-5.86	115.64	121.50
1	A	114	ARG	NE-CZ-NH2	-5.83	113.95	119.20
1	A	65	ILE	CB-CA-C	-5.77	101.91	110.33
1	A	113	ARG	NE-CZ-NH1	5.67	127.17	121.50
1	A	210	HIS	CA-CB-CG	-5.65	108.15	113.80
1	A	114	ARG	NH1-CZ-NH2	5.64	126.63	119.30
1	A	156	THR	CA-C-O	5.63	126.39	120.42
1	A	115	LEU	CA-C-N	5.54	127.65	120.44
1	A	115	LEU	C-N-CA	5.54	127.65	120.44
1	A	57	VAL	CB-CA-C	5.52	118.93	110.55
1	A	117	LYS	CA-CB-CG	-5.50	103.11	114.10
1	A	88	MET	CA-C-O	5.49	126.24	120.42
1	A	136	HIS	CA-CB-CG	-5.43	108.37	113.80
1	A	286	ARG	CD-NE-CZ	-5.39	116.86	124.40
1	A	195	ARG	NH1-CZ-NH2	5.38	126.30	119.30
1	A	288	GLU	CA-C-O	5.36	127.51	120.16
1	A	113	ARG	NE-CZ-NH2	-5.34	114.40	119.20
1	A	100	ASN	CA-CB-CG	-5.26	107.34	112.60
1	A	148	LEU	CA-C-O	-5.15	114.96	120.42
1	A	101	VAL	CA-C-O	-5.15	115.17	121.04
1	A	305	GLU	N-CA-CB	5.05	119.02	110.49
1	A	102	ARG	CA-C-O	-5.03	115.52	120.70
1	A	166	ASN	CA-CB-CG	-5.01	107.58	112.60

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	2089	0	2078	35	0
2	A	266	0	0	15	1
All	All	2355	0	2078	35	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 8.

All (35) 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:50:GLN:OE1	1:A:63:ARG:HD3	1.93	0.68
1:A:63:ARG:HH22	1:A:176:ASP:CG	2.06	0.64
1:A:233:ARG:NE	2:A:561:HOH:O	2.34	0.61
1:A:143:GLN:HG2	2:A:516:HOH:O	1.99	0.61
1:A:117:LYS:NZ	1:A:306:THR:O	2.31	0.61
1:A:140:GLN:NE2	2:A:533:HOH:O	2.34	0.59
1:A:277:GLU:HB2	2:A:456:HOH:O	2.03	0.59
1:A:167:ASN:HA	2:A:568:HOH:O	2.02	0.58
1:A:167:ASN:N	2:A:568:HOH:O	2.35	0.56
1:A:193:ARG:CD	2:A:549:HOH:O	2.54	0.55
1:A:304:ALA:O	1:A:305:GLU:HB2	2.07	0.53
1:A:136:HIS:HE1	1:A:156:THR:OG1	1.92	0.52
1:A:270:ALA:HB2	1:A:280:LEU:HD11	1.93	0.51
1:A:87:LYS:HD3	2:A:527:HOH:O	2.11	0.50
1:A:80:THR:HB	2:A:562:HOH:O	2.10	0.50
1:A:69:LYS:HE2	2:A:569:HOH:O	2.11	0.49
1:A:268:GLN:HG2	2:A:534:HOH:O	2.12	0.49
1:A:109:ALA:HB1	1:A:298:LEU:HA	1.94	0.48
1:A:165:HIS:HB3	1:A:168:LEU:HD12	1.94	0.48
1:A:167:ASN:CA	2:A:568:HOH:O	2.61	0.48
1:A:233:ARG:CZ	2:A:561:HOH:O	2.62	0.46
1:A:280:LEU:C	1:A:280:LEU:HD13	2.41	0.46
1:A:102:ARG:HD2	1:A:102:ARG:H	1.81	0.45
1:A:292:MET:HE3	1:A:292:MET:HB3	1.79	0.44
1:A:154:LEU:HD13	1:A:178:CYS:HB3	1.98	0.43
1:A:63:ARG:NH2	1:A:176:ASP:OD2	2.49	0.43
1:A:65:ILE:HG22	1:A:66:SER:O	2.19	0.43
1:A:80:THR:HG22	2:A:562:HOH:O	2.18	0.42
1:A:88:MET:HA	1:A:88:MET:HE2	2.00	0.42
1:A:60:PRO:HB3	1:A:77:GLU:HG3	2.02	0.41
1:A:88:MET:HE3	1:A:177:MET:HB3	2.01	0.41
1:A:219:PHE:CZ	1:A:229:CYS:HB2	2.56	0.41
1:A:186:TYR:CD2	1:A:198:SER:HB3	2.56	0.40
1:A:163:GLN:NE2	2:A:556:HOH:O	2.54	0.40
1:A:181:TRP:O	1:A:185:VAL:HG23	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)
2:A:307:HOH:O	2:A:429:HOH:O[3_745]	2.15	0.05

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	101/261 (39%)	98 (97%)	2 (2%)	1 (1%)	12 8

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	305	GLU

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	233/233 (100%)	218 (94%)	15 (6%)	16 12

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	GLN
1	A	57	VAL
1	A	58	GLN
1	A	80	THR
1	A	81	THR

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Mol	Chain	Res	Type
1	A	102	ARG
1	A	117	LYS
1	A	119	LEU
1	A	139	LYS
1	A	190	ARG
1	A	212	GLU
1	A	260	GLU
1	A	271	ASN
1	A	295	LEU
1	A	306	THR

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	136	HIS
1	A	140	GLN
1	A	247	GLN
1	A	271	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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.