



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 09:18 PM UTC

PDB ID : 4CI8 / pdb_00004ci8
Title : Crystal structure of the tandem atypical beta-propeller domain of EML1
Authors : Richards, M.W.; Bayliss, R.
Deposited on : 2013-12-06
Resolution : 2.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

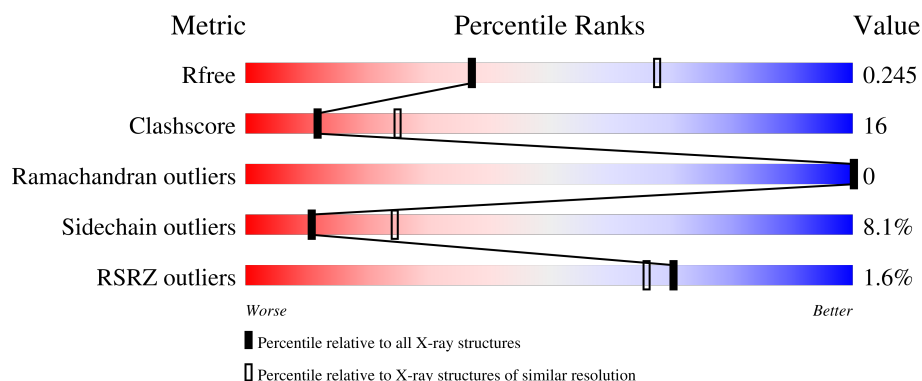
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	655	% 66% 28% ..
1	B	655	2% 66% 29% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	1819	-	-	X	-
2	SO4	A	1824	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10193 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.

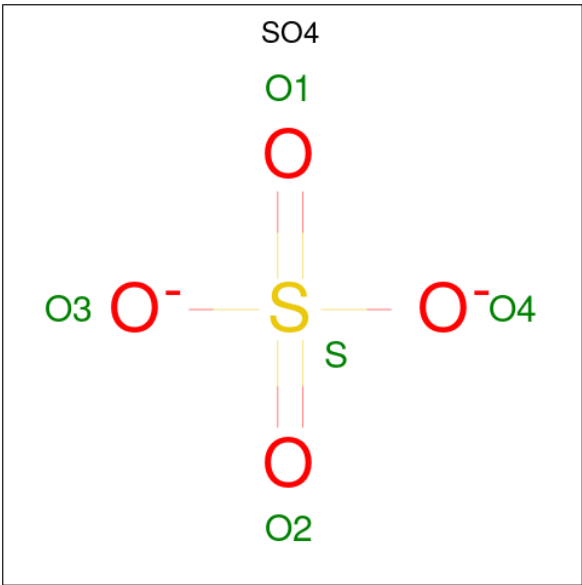
- Molecule 1 is a protein called ECHINODERM MICROTUBULE-ASSOCIATED PROTEIN-LIKE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	640	Total	C	N	O	S	0	0	0
			4936	3131	850	933	22			
1	B	640	Total	C	N	O	S	0	0	0
			4924	3124	843	935	22			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	161	GLY	-	expression tag	UNP O00423
A	162	PRO	-	expression tag	UNP O00423
A	163	HIS	-	expression tag	UNP O00423
A	164	MET	-	expression tag	UNP O00423
A	165	SER	-	expression tag	UNP O00423
A	166	MET	-	expression tag	UNP O00423
B	161	GLY	-	expression tag	UNP O00423
B	162	PRO	-	expression tag	UNP O00423
B	163	HIS	-	expression tag	UNP O00423
B	164	MET	-	expression tag	UNP O00423
B	165	SER	-	expression tag	UNP O00423
B	166	MET	-	expression tag	UNP O00423

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

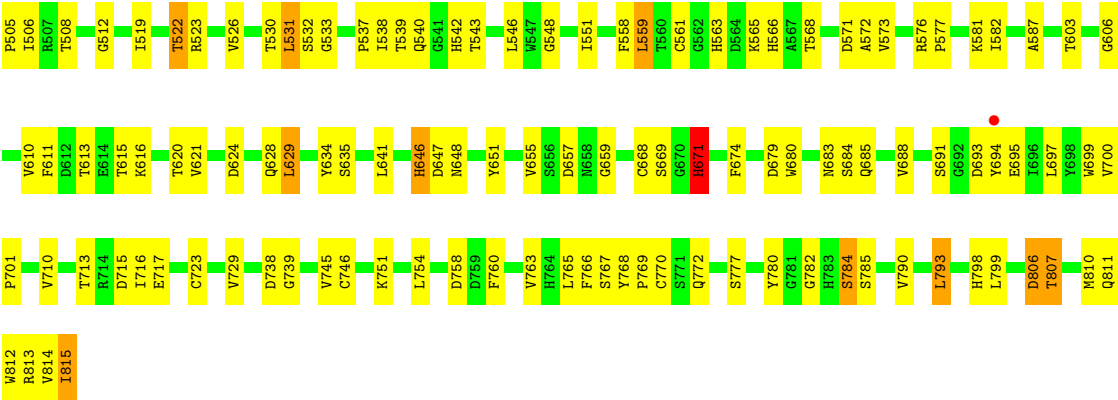
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	116	Total	O	0	0
			116	116		
3	B	92	Total	O	0	0
			92	92		



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	91.98Å 83.98Å 115.52Å 90.00° 96.61° 90.00°	Depositor
Resolution (Å)	47.38 – 2.60 47.38 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.2 (47.38-2.60) 99.3 (47.38-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 2.61Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.200 , 0.251 0.196 , 0.245	Depositor DCC
R_{free} test set	2731 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	42.4	Xtriage
Anisotropy	0.509	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 45.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10193	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 29.03 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.6635e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: SO4

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	0.35	0/5064	0.76	6/6892 (0.1%)
1	B	0.34	0/5052	0.77	7/6879 (0.1%)
All	All	0.35	0/10116	0.77	13/13771 (0.1%)

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	784	SER	N-CA-C	6.99	118.98	111.36
1	A	192	ARG	N-CA-C	-5.96	98.01	108.08
1	A	413	GLU	N-CA-C	-5.91	98.21	110.80
1	B	700	VAL	CA-C-N	5.86	125.56	119.05
1	B	700	VAL	C-N-CA	5.86	125.56	119.05

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	4936	0	4716	159	0
1	B	4924	0	4687	148	0
2	A	65	0	0	5	0
2	B	60	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	116	0	0	3	0
3	B	92	0	0	2	0
All	All	10193	0	9403	306	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 16.

The worst 5 of 306 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:321:ILE:H	1:A:321:ILE:HD12	1.33	0.93
1:A:240:LEU:HD23	1:A:512:GLY:HA2	1.52	0.90
1:A:616:LYS:NZ	2:A:1824:SO4:O4	2.03	0.90
1:B:531:LEU:HD12	1:B:531:LEU:H	1.39	0.86
1:A:517:ILE:HG13	1:A:531:LEU:HD13	1.60	0.83

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	638/655 (97%)	599 (94%)	39 (6%)	0	100	100
1	B	638/655 (97%)	592 (93%)	46 (7%)	0	100	100
All	All	1276/1310 (97%)	1191 (93%)	85 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	532/562 (95%)	496 (93%)	36 (7%)	14	32
1	B	530/562 (94%)	480 (91%)	50 (9%)	8	18
All	All	1062/1124 (94%)	976 (92%)	86 (8%)	11	24

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	407	LYS
1	B	629	LEU
1	B	428	GLU
1	B	559	LEU
1	B	693	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	394	HIS
1	B	575	HIS
1	B	628	GLN
1	B	262	GLN
1	A	786	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

25 ligands are modelled in this entry.

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	SO4	A	1826	-	4,4,4	0.25	0	6,6,6	0.08	0
2	SO4	A	1821	-	4,4,4	0.26	0	6,6,6	0.07	0
2	SO4	A	1820	-	4,4,4	0.25	0	6,6,6	0.08	0
2	SO4	B	1823	-	4,4,4	0.23	0	6,6,6	0.11	0
2	SO4	B	1827	-	4,4,4	0.24	0	6,6,6	0.10	0
2	SO4	A	1822	-	4,4,4	0.25	0	6,6,6	0.09	0
2	SO4	A	1825	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	B	1817	-	4,4,4	0.25	0	6,6,6	0.07	0
2	SO4	A	1817	-	4,4,4	0.25	0	6,6,6	0.09	0
2	SO4	B	1818	-	4,4,4	0.23	0	6,6,6	0.09	0
2	SO4	B	1822	-	4,4,4	0.23	0	6,6,6	0.10	0
2	SO4	A	1818	-	4,4,4	0.22	0	6,6,6	0.07	0
2	SO4	A	1819	-	4,4,4	0.25	0	6,6,6	0.05	0
2	SO4	B	1821	-	4,4,4	0.23	0	6,6,6	0.10	0
2	SO4	B	1825	-	4,4,4	0.23	0	6,6,6	0.15	0
2	SO4	A	1823	-	4,4,4	0.24	0	6,6,6	0.10	0
2	SO4	A	1827	-	4,4,4	0.23	0	6,6,6	0.12	0
2	SO4	B	1826	-	4,4,4	0.25	0	6,6,6	0.10	0
2	SO4	B	1819	-	4,4,4	0.26	0	6,6,6	0.08	0
2	SO4	A	1828	-	4,4,4	0.24	0	6,6,6	0.11	0
2	SO4	A	1816	-	4,4,4	0.25	0	6,6,6	0.16	0
2	SO4	A	1824	-	4,4,4	0.25	0	6,6,6	0.09	0
2	SO4	B	1816	-	4,4,4	0.25	0	6,6,6	0.24	0
2	SO4	B	1824	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	B	1820	-	4,4,4	0.21	0	6,6,6	0.09	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1819	SO4	2	0
2	B	1825	SO4	1	0
2	B	1826	SO4	1	0
2	A	1824	SO4	3	0

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, 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	640/655 (97%)	-0.08	8 (1%) 75 71	27, 44, 71, 95	0
1	B	640/655 (97%)	0.08	12 (1%) 66 61	29, 48, 78, 94	0
All	All	1280/1310 (97%)	0.00	20 (1%) 70 66	27, 46, 74, 95	0

The worst 5 of 20 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	412	PHE	3.5
1	A	299	LYS	3.2
1	B	338	GLY	3.0
1	B	339	GLY	2.8
1	A	338	GLY	2.7

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	SO4	A	1822	5/5	0.68	0.09	84,92,101,120	0
2	SO4	B	1822	5/5	0.72	0.11	86,94,118,119	0
2	SO4	B	1818	5/5	0.73	0.20	85,86,102,115	0
2	SO4	B	1827	5/5	0.75	0.10	83,84,108,118	0
2	SO4	B	1826	5/5	0.79	0.06	93,99,111,126	0
2	SO4	A	1821	5/5	0.80	0.10	87,90,105,114	0
2	SO4	B	1821	5/5	0.81	0.15	75,78,104,107	0
2	SO4	A	1825	5/5	0.81	0.16	66,88,116,121	0
2	SO4	A	1826	5/5	0.82	0.19	70,86,110,110	0
2	SO4	A	1827	5/5	0.84	0.17	72,80,100,106	0
2	SO4	B	1819	5/5	0.84	0.12	68,69,89,107	0
2	SO4	A	1828	5/5	0.85	0.15	82,84,110,113	0
2	SO4	B	1823	5/5	0.85	0.08	80,92,103,110	0
2	SO4	A	1824	5/5	0.86	0.18	66,84,102,105	0
2	SO4	A	1820	5/5	0.87	0.14	74,88,96,103	0
2	SO4	A	1817	5/5	0.87	0.14	58,69,107,112	0
2	SO4	A	1818	5/5	0.87	0.11	76,78,95,101	0
2	SO4	A	1823	5/5	0.87	0.22	68,73,97,98	0
2	SO4	A	1819	5/5	0.90	0.18	64,81,90,98	0
2	SO4	B	1824	5/5	0.90	0.17	73,78,94,96	0
2	SO4	B	1817	5/5	0.92	0.15	54,72,91,102	0
2	SO4	B	1820	5/5	0.93	0.15	44,52,74,88	0
2	SO4	B	1825	5/5	0.93	0.14	53,69,74,83	0
2	SO4	B	1816	5/5	0.98	0.06	31,41,46,47	0
2	SO4	A	1816	5/5	0.98	0.07	35,35,40,42	0

6.5 Other polymers ⓘ

There are no such residues in this entry.