



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 23, 2024 – 09:09 PM EDT

PDB ID : 2AKA
Title : Structure of the nucleotide-free myosin II motor domain from Dictyostelium discoideum fused to the GTPase domain of dynamin 1 from Rattus norvegicus
Authors : Reubold, T.F.; Eschenburg, S.; Becker, A.; Leonard, M.; Schmid, S.L.; Vallee, R.B.; Kull, F.J.; Manstein, D.J.
Deposited on : 2005-08-03
Resolution : 1.90 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	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

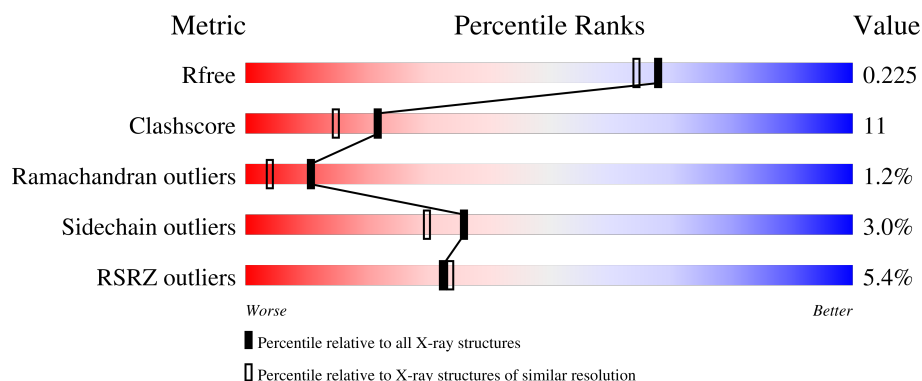
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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}	164625	7293 (1.90-1.90)
Clashscore	180529	8090 (1.90-1.90)
Ramachandran outliers	177936	8022 (1.90-1.90)
Sidechain outliers	177891	8022 (1.90-1.90)
RSRZ outliers	164620	7292 (1.90-1.90)

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	776	<div> <div>6%</div> <div> <div></div> <div>81%</div> <div>15%</div> <div>••</div> </div> </div>
2	L	13	<div> <div>8%</div> <div> <div></div> <div>31%</div> <div>15%</div> <div>54%</div> </div> </div>
3	B	299	<div> <div>4%</div> <div> <div></div> <div>79%</div> <div>19%</div> <div>•</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9377 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 myosin II heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	764	6227	3948	1081	1182	16	0	20	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	insertion	UNP P08799
A	-9	HIS	-	insertion	UNP P08799
A	-8	HIS	-	insertion	UNP P08799
A	-7	HIS	-	insertion	UNP P08799
A	-6	HIS	-	insertion	UNP P08799
A	-5	HIS	-	insertion	UNP P08799
A	-4	HIS	-	insertion	UNP P08799
A	-3	HIS	-	insertion	UNP P08799
A	-2	ASP	-	insertion	UNP P08799
A	-1	GLY	-	insertion	UNP P08799
A	0	THR	-	insertion	UNP P08799
A	1	GLU	-	insertion	UNP P08799

- Molecule 2 is a protein called LINKER.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	L	6	51	32	12	7	0	0	0

- Molecule 3 is a protein called Dynamin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	B	299	2345	1474	420	442	9	0	3	0

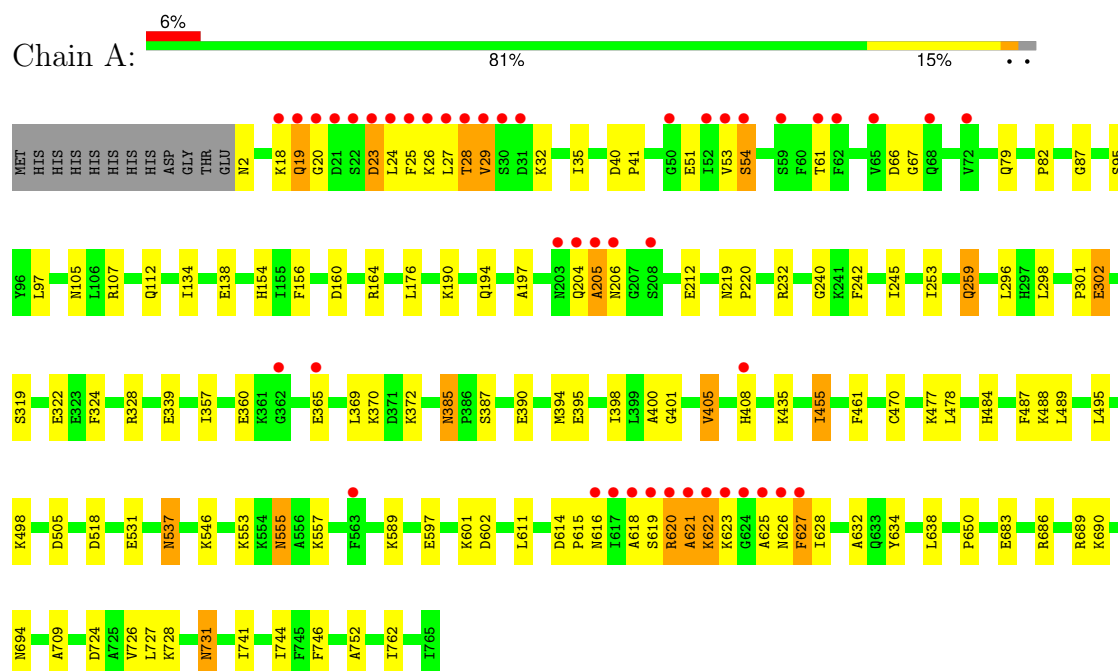
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	584	Total 584	O 584	0	0
4	B	170	Total 170	O 170	0	0

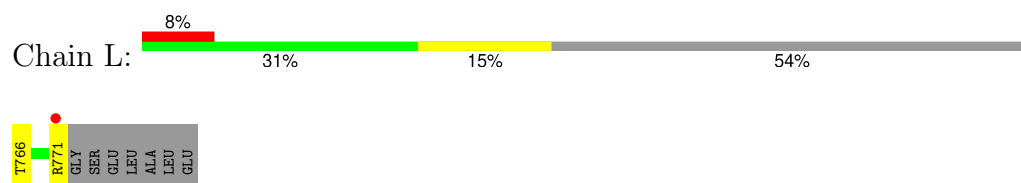
3 Residue-property plots

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.

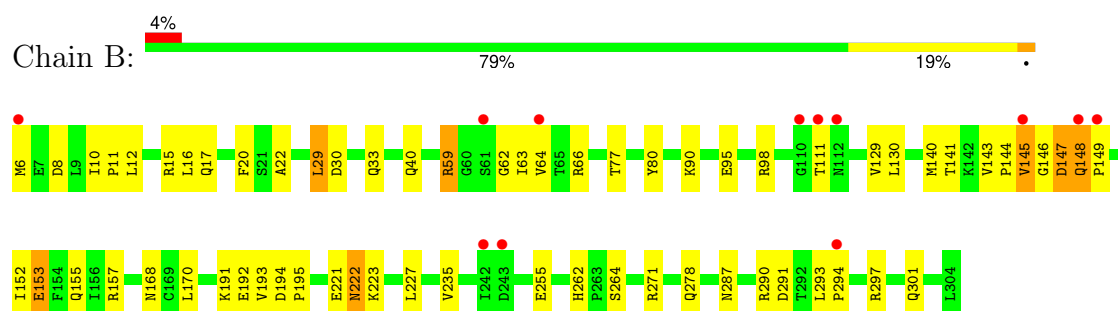
• Molecule 1: myosin II heavy chain



• Molecule 2: LINKER



• Molecule 3: Dynamin-1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.42Å 126.99Å 160.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.93 – 1.90 19.93 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.1 (19.93-1.90) 99.1 (19.93-1.90)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.81 (at 1.90Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.185 , 0.224 0.187 , 0.225	Depositor DCC
R_{free} test set	2317 reflections (2.50%)	wwPDB-VP
Wilson B-factor (Å ²)	24.8	Xtriage
Anisotropy	0.570	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 48.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9377	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.57% 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	0.81	0/6427	0.80	3/8670 (0.0%)
2	L	0.53	0/51	0.61	0/68
3	B	0.69	0/2393	0.81	0/3238
All	All	0.78	0/8871	0.80	3/11976 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	107	ARG	NE-CZ-NH1	-5.60	117.50	120.30
1	A	245	ILE	N-CA-C	-5.17	97.05	111.00
1	A	401	GLY	N-CA-C	-5.10	100.35	113.10

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	6227	0	6170	136	0
2	L	51	0	59	4	0
3	B	2345	0	2402	48	0
4	A	584	0	0	9	0
4	B	170	0	0	3	0
All	All	9377	0	8631	184	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 11.

The worst 5 of 184 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:154:HIS:HD2	1:A:156:PHE:H	1.12	0.97
3:B:40:GLN:NE2	3:B:141:THR:HG21	1.85	0.91
3:B:40:GLN:HB2	3:B:141:THR:HG22	1.57	0.84
1:A:589:LYS:HD3	4:A:1018:HOH:O	1.79	0.82
1:A:154:HIS:CD2	1:A:156:PHE:H	1.98	0.81

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	782/776 (101%)	744 (95%)	28 (4%)	10 (1%)	10	3
2	L	4/13 (31%)	4 (100%)	0	0	100	100
3	B	300/299 (100%)	283 (94%)	14 (5%)	3 (1%)	13	5
All	All	1086/1088 (100%)	1031 (95%)	42 (4%)	13 (1%)	11	4

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	23	ASP
1	A	205	ALA
1	A	620	ARG
1	A	621	ALA
1	A	622	LYS

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	688/679 (101%)	666 (97%)	22 (3%)	34	27
2	L	6/11 (54%)	6 (100%)	0	100	100
3	B	263/261 (101%)	254 (97%)	9 (3%)	32	25
All	All	957/951 (101%)	926 (97%)	31 (3%)	36	27

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	553	LYS
3	B	153	GLU
1	A	602[B]	ASP
3	B	222	ASN
3	B	64	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	532	GLN
3	B	278	GLN
1	A	613	ASN
3	B	287	ASN
3	B	75	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	764/776 (98%)	-0.09	45 (5%)	29 30	10, 25, 64, 102	20 (2%)
2	L	6/13 (46%)	0.88	1 (16%)	5 5	40, 46, 53, 66	0
3	B	299/299 (100%)	0.03	12 (4%)	43 44	18, 30, 63, 76	3 (1%)
All	All	1069/1088 (98%)	-0.05	58 (5%)	32 34	10, 26, 64, 102	23 (2%)

The worst 5 of 58 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	29	VAL	7.3
1	A	25	PHE	6.0
1	A	20	GLY	5.8
1	A	621	ALA	5.6
1	A	625	ALA	5.4

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 monosaccharides 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.