



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 09:22 pm GMT

PDB ID : 2Y25  
Title : Crystal structure of the myomesin domains My11-My13  
Authors : Pinotsis, N.; Chatziefthimiou, S.D.; Wilmanns, M.  
Deposited on : 2010-12-13  
Resolution : 3.50 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

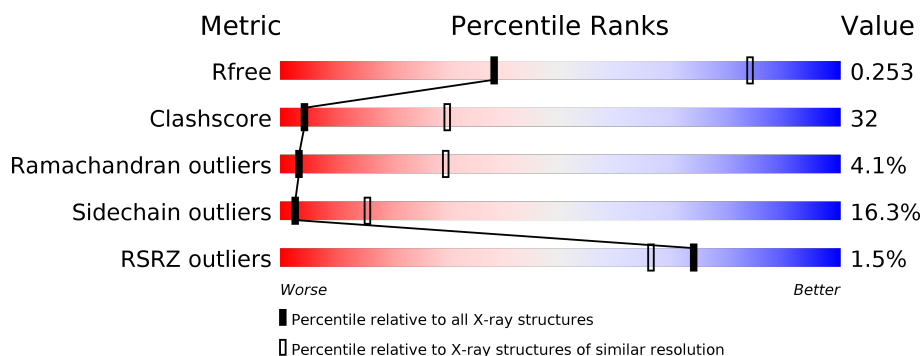
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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))
$R_{free}$	100719	1195 (3.60-3.40)
Clashscore	112137	1322 (3.60-3.40)
Ramachandran outliers	110173	1283 (3.60-3.40)
Sidechain outliers	110143	1284 (3.60-3.40)
RSRZ outliers	101464	1226 (3.60-3.40)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	317	<div> <div>3%</div> <div> <div></div> <div>47%</div> <div>45%</div> <div>6%</div> </div> </div>
1	B	317	<div> <div></div> <div> <div>42%</div> <div>45%</div> <div>11%</div> </div> </div>
1	C	317	<div> <div>3%</div> <div> <div></div> <div>48%</div> <div>44%</div> <div>6%</div> </div> </div>
1	D	317	<div> <div></div> <div> <div>42%</div> <div>44%</div> <div>11%</div> </div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9534 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 MYOMESIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2351	1492	391	459	9			
1	B	314	Total	C	N	O	S	0	0	0
			2416	1531	403	473	9			
1	C	310	Total	C	N	O	S	0	0	0
			2351	1492	391	459	9			
1	D	314	Total	C	N	O	S	0	0	0
			2416	1531	403	473	9			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1351	GLY	-	EXPRESSION TAG	UNP P52179
A	1352	ILE	-	EXPRESSION TAG	UNP P52179
A	1353	ASP	-	EXPRESSION TAG	UNP P52179
A	1354	PRO	-	EXPRESSION TAG	UNP P52179
A	1355	PHE	-	EXPRESSION TAG	UNP P52179
A	1356	THR	-	EXPRESSION TAG	UNP P52179
B	1351	GLY	-	EXPRESSION TAG	UNP P52179
B	1352	ILE	-	EXPRESSION TAG	UNP P52179
B	1353	ASP	-	EXPRESSION TAG	UNP P52179
B	1354	PRO	-	EXPRESSION TAG	UNP P52179
B	1355	PHE	-	EXPRESSION TAG	UNP P52179
B	1356	THR	-	EXPRESSION TAG	UNP P52179
C	1351	GLY	-	EXPRESSION TAG	UNP P52179
C	1352	ILE	-	EXPRESSION TAG	UNP P52179
C	1353	ASP	-	EXPRESSION TAG	UNP P52179
C	1354	PRO	-	EXPRESSION TAG	UNP P52179
C	1355	PHE	-	EXPRESSION TAG	UNP P52179
C	1356	THR	-	EXPRESSION TAG	UNP P52179
D	1351	GLY	-	EXPRESSION TAG	UNP P52179
D	1352	ILE	-	EXPRESSION TAG	UNP P52179
D	1353	ASP	-	EXPRESSION TAG	UNP P52179

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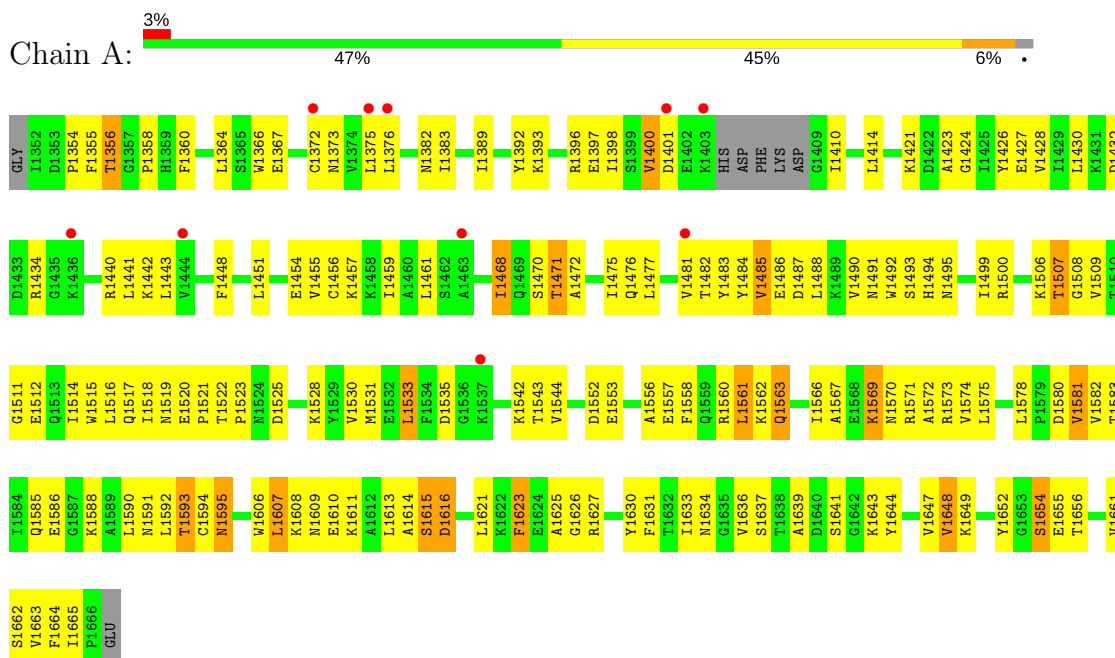
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Chain	Residue	Modelled	Actual	Comment	Reference
D	1354	PRO	-	EXPRESSION TAG	UNP P52179
D	1355	PHE	-	EXPRESSION TAG	UNP P52179
D	1356	THR	-	EXPRESSION TAG	UNP P52179

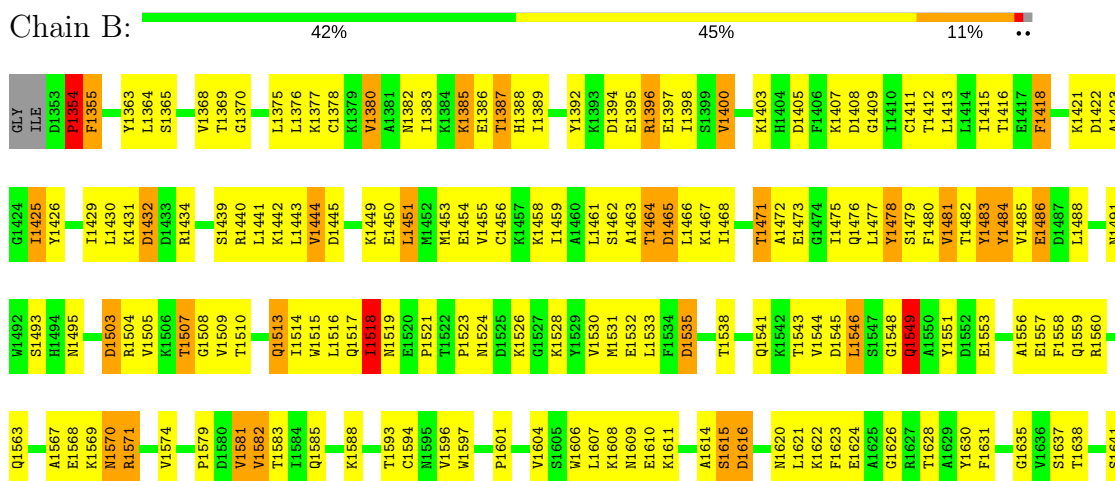
### 3 Residue-property plots [i](#)

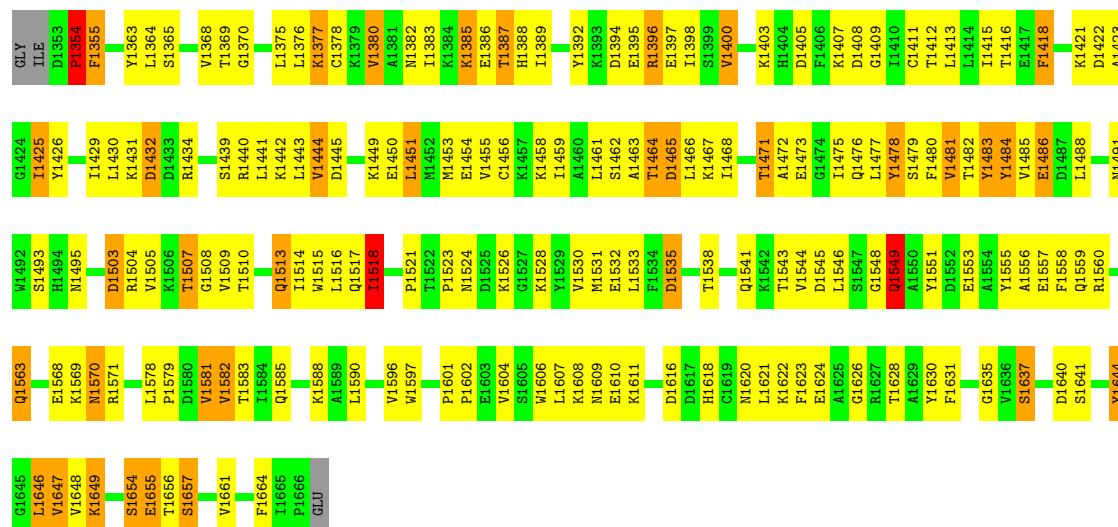
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: MYOMESIN



#### • Molecule 1: MYOMESIN





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 42	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	155.20Å 155.20Å 106.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.95 – 3.50 19.95 – 3.50	Depositor EDS
% Data completeness (in resolution range)	93.8 (19.95-3.50) 93.8 (19.95-3.50)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.80 (at 3.52Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.217 , 0.266 0.201 , 0.253	Depositor DCC
$R_{free}$ test set	1232 reflections (4.12%)	DCC
Wilson B-factor (Å <sup>2</sup> )	92.9	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.24 , 44.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.408 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	9534	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	128.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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

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	0.62	0/2397	0.71	2/3261 (0.1%)
1	B	0.72	0/2464	0.84	3/3346 (0.1%)
1	C	0.62	1/2397 (0.0%)	0.71	3/3261 (0.1%)
1	D	0.72	1/2464 (0.0%)	0.85	3/3346 (0.1%)
All	All	0.67	2/9722 (0.0%)	0.78	11/13214 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	2
1	D	0	2
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	1563	GLN	CG-CD	5.40	1.63	1.51
1	C	1573	ARG	CG-CD	5.05	1.64	1.51

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1581	VAL	CB-CA-C	-6.54	98.98	111.40
1	B	1355	PHE	N-CA-C	6.40	128.28	111.00
1	D	1355	PHE	N-CA-C	6.26	127.91	111.00
1	D	1581	VAL	CB-CA-C	-6.04	99.92	111.40
1	C	1573	ARG	NE-CZ-NH1	5.97	123.29	120.30

There are no chirality outliers.



All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	1354	PRO	Peptide
1	B	1483	TYR	Peptide
1	D	1354	PRO	Peptide
1	D	1483	TYR	Peptide

## 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	2351	0	2223	128	0
1	B	2416	0	2323	174	0
1	C	2351	0	2223	123	0
1	D	2416	0	2323	175	0
All	All	9534	0	9092	596	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 32.

The worst 5 of 596 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:1485:VAL:HG21	1:A:1509:VAL:HG11	1.35	1.06
1:C:1485:VAL:HG21	1:C:1509:VAL:HG11	1.34	1.05
1:B:1615:SER:O	1:B:1616:ASP:OD1	1.76	1.02
1:D:1585:GLN:HB3	1:D:1588:LYS:HD2	1.39	1.02
1:B:1585:GLN:HB3	1:B:1588:LYS:HD2	1.41	1.00

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	306/317 (96%)	250 (82%)	47 (15%)	9 (3%)	5	38
1	B	312/317 (98%)	244 (78%)	51 (16%)	17 (5%)	2	22
1	C	306/317 (96%)	248 (81%)	49 (16%)	9 (3%)	5	38
1	D	312/317 (98%)	242 (78%)	54 (17%)	16 (5%)	2	23
All	All	1236/1268 (98%)	984 (80%)	201 (16%)	51 (4%)	3	29

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1482	THR
1	B	1354	PRO
1	B	1400	VAL
1	B	1418	PHE
1	B	1484	TYR

### 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	242/274 (88%)	211 (87%)	31 (13%)	5	25
1	B	255/274 (93%)	203 (80%)	52 (20%)	1	7
1	C	242/274 (88%)	213 (88%)	29 (12%)	6	28
1	D	255/274 (93%)	205 (80%)	50 (20%)	1	8
All	All	994/1096 (91%)	832 (84%)	162 (16%)	3	15

5 of 162 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1615	SER
1	C	1488	LEU

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Mol	Chain	Res	Type
1	D	1581	VAL
1	B	1637	SER
1	B	1657	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1609	ASN
1	C	1513	GLN
1	D	1524	ASN
1	C	1491	ASN
1	A	1609	ASN

### 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 carbohydrates 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	310/317 (97%)	-0.20	10 (3%) 48 40	43, 158, 290, 454	0
1	B	314/317 (99%)	-0.44	0 100 100	49, 95, 169, 308	0
1	C	310/317 (97%)	-0.18	9 (2%) 52 43	48, 161, 288, 455	0
1	D	314/317 (99%)	-0.43	0 100 100	51, 95, 172, 325	0
All	All	1248/1268 (98%)	-0.31	19 (1%) 74 66	43, 111, 259, 455	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1436	LYS	4.1
1	C	1403	LYS	3.1
1	C	1481	VAL	3.1
1	A	1401	ASP	3.1
1	A	1444	VAL	2.9

### 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 carbohydrates 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.