



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 23, 2018 – 09:11 PM EST

PDB ID : 1DFK  
Title : NUCLEOTIDE-FREE SCALLOP MYOSIN S1-NEAR RIGOR STATE  
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Deposited on : 1999-11-19  
Resolution : 4.20 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) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030736

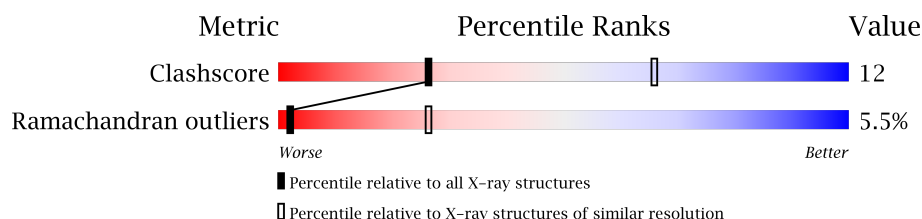
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 4.20 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	112137	1025 (4.72-3.66)
Ramachandran outliers	110173	1024 (4.76-3.62)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	830	 74% 12% •• 12%
2	Y	139	 81% 17% •
3	Z	152	 81% 18% •

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5032 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 HEAD.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	728	Total	C	N	O	0	0	0
			3597	2140	728	729			

- Molecule 2 is a protein called MYOSIN HEAD.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	Y	139	Total	C	N	O	0	0	0
			688	409	139	140			

- Molecule 3 is a protein called MYOSIN HEAD.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	Z	152	Total	C	N	O	0	0	0
			746	441	152	153			

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	Z	1	Total	Ca	0	0
			1	1		



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.50 Å   52.10 Å   164.60 Å 90.00°   100.30°   90.00°	Depositor
Resolution (Å)	20.00 – 4.20	Depositor
% Data completeness (in resolution range)	95.0 (20.00-4.20)	Depositor
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	CNS	Depositor
R, $R_{free}$	0.415 , 0.410	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5032	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA

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	0.97	9/3587 (0.3%)	1.33	26/4978 (0.5%)
2	Y	0.42	0/687	0.80	2/954 (0.2%)
3	Z	0.58	1/745 (0.1%)	0.76	0/1031
All	All	0.86	10/5019 (0.2%)	1.20	28/6963 (0.4%)

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	A	0	8

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	268	GLU	C-N	-31.26	0.62	1.34
1	A	705	LYS	C-N	23.07	1.74	1.33
1	A	706	GLY	C-N	19.97	1.79	1.34
1	A	683	ASP	C-N	-18.55	0.91	1.34
3	Z	7	GLU	C-N	11.26	1.59	1.34

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	515	ASP	O-C-N	-39.30	59.82	122.70
1	A	268	GLU	O-C-N	-35.48	65.94	122.70
1	A	268	GLU	C-N-CA	-24.70	59.95	121.70
1	A	268	GLU	CA-C-N	-24.51	63.29	117.20
1	A	515	ASP	CA-C-N	16.06	152.53	117.20

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	268	GLU	Mainchain
1	A	445	THR	Mainchain
1	A	515	ASP	Mainchain,Peptide
1	A	600	ASP	Mainchain
1	A	601	PRO	Mainchain

## 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	3597	0	1592	58	0
2	Y	688	0	307	17	0
3	Z	746	0	340	11	0
4	Z	1	0	0	0	0
All	All	5032	0	2239	85	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 12.

The worst 5 of 85 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:705:LYS:C	1:A:706:GLY:N	1.74	1.40
1:A:706:GLY:C	1:A:707:PHE:N	1.80	1.35
1:A:584:ALA:HB1	1:A:693:CYS:HA	1.37	1.07
1:A:770:LEU:O	1:A:774:ARG:CB	2.10	0.99
1:A:507:TRP:O	1:A:508:GLU:C	2.07	0.89

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	708/830 (85%)	576 (81%)	95 (13%)	37 (5%)	2	27
2	Y	137/139 (99%)	96 (70%)	34 (25%)	7 (5%)	2	27
3	Z	150/152 (99%)	106 (71%)	33 (22%)	11 (7%)	1	19
All	All	995/1121 (89%)	778 (78%)	162 (16%)	55 (6%)	2	26

5 of 55 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	268	GLU
1	A	269	LYS
1	A	542	ALA
1	A	601	PRO
1	A	623	LYS

### 5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

### 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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	6

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	706:GLY	C	707:PHE	N	1.80
1	A	705:LYS	C	706:GLY	N	1.74
1	A	489:ASN	C	490:HIS	N	1.20
1	A	445:THR	C	446:LEU	N	1.10
1	A	683:ASP	C	684:ALA	N	0.91

## 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.