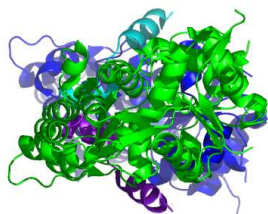


2v51

Evolutionary trace report by **report_maker**

January 16, 2010



4.3.1	Alistat	10
4.3.2	CE	10
4.3.3	DSSP	10
4.3.4	HSSP	10
4.3.5	LaTex	10
4.3.6	Muscle	10
4.3.7	Pymol	10
4.4	Note about ET Viewer	10
4.5	Citing this work	10
4.6	About report_maker	10
4.7	Attachments	10

CONTENTS

1 Introduction

2 Chain 2v51B

- 2.1 Q6IP22 overview
- 2.2 Multiple sequence alignment for 2v51B
- 2.3 Residue ranking in 2v51B
- 2.4 Top ranking residues in 2v51B and their position on the structure
 - 2.4.1 Clustering of residues at 25% coverage.
 - 2.4.2 Overlap with known functional surfaces at 25% coverage.
 - 2.4.3 Possible novel functional surfaces at 25% coverage.

3 Notes on using trace results

- 3.1 Coverage
- 3.2 Known substitutions
- 3.3 Surface
- 3.4 Number of contacts
- 3.5 Annotation
- 3.6 Mutation suggestions

4 Appendix

- 4.1 File formats
- 4.2 Color schemes used
- 4.3 Credits

1 INTRODUCTION

From the original Protein Data Bank entry (PDB id 2v51):

Title: Structure of mal-rpel1 complexed to actin

Compound: Mol id: 1; molecule: actin, alpha skeletal muscle; chain: b, d; synonym: alpha-actin-1; mol id: 2; molecule: mkl/myocardin-like protein 1; chain: e, f; fragment: rpel1 motif, residues 16-41; synonym: myocardin-related transcription factor a, megakaryoblastic leukemia 1 protein homolog, basic sap coiled-coil transcription activator

1 Organism, scientific name: Mus Musculus;

1 2v51 contains a single unique chain 2v51B (351 residues long) and its homologue 2v51D. Not enough homologous sequences could be found to permit analysis for chain 2v51E.

2 CHAIN 2V51B

2.1 Q6IP22 overview

2 From SwissProt, id Q6IP22, 95% identical to 2v51B:

Description: MGC79012 protein.

6 Organism, scientific name: Xenopus laevis (African clawed frog).

8 Taxonomy: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Xenopus.

8 Similarity: Belongs to the actin family.

2.2 Multiple sequence alignment for 2v51B

9 For the chain 2v51B, the alignment 2v51B.msf (attached) with 604 sequences was used. The alignment was downloaded from the HSSP database, and fragments shorter than 75% of the query as well as duplicate sequences were removed. It can be found in the attachment to this report, under the name of 2v51B.msf. Its statistics, from the *alistat* program are the following:

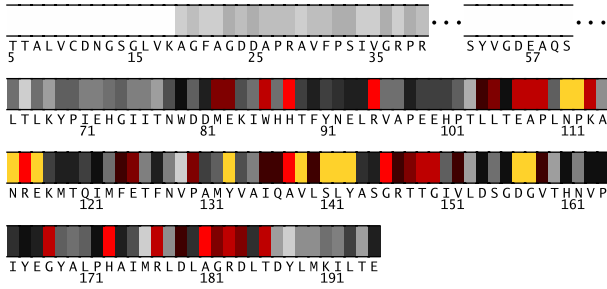


Fig. 1. Residues 5-195 in 2v51B colored by their relative importance. (See Appendix, Fig.15, for the coloring scheme.)

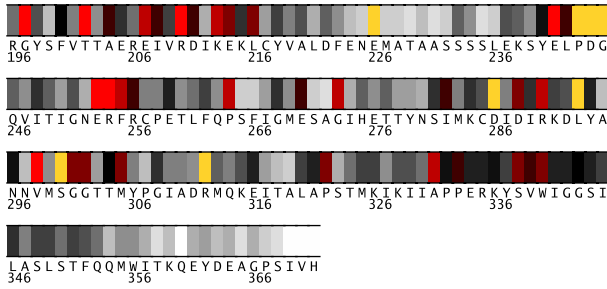


Fig. 2. Residues 196-371 in 2v51B colored by their relative importance. (See Appendix, Fig.15, for the coloring scheme.)

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Format:                MSF
Number of sequences:  604
Total number of residues: 198185
Smallest:             272
Largest:              351
Average length:       328.1
Alignment length:     351
Average identity:     84%
Most related pair:    99%
Most unrelated pair:  59%
Most distant seq:     76%
  
```

Furthermore, <1% of residues show as conserved in this alignment.

The alignment consists of 61% eukaryotic (3% vertebrata, 4% arthropoda, 10% fungi, 16% plantae) sequences. (Descriptions of some sequences were not readily available.) The file containing the sequence descriptions can be found in the attachment, under the name 2v51B.descr.

2.3 Residue ranking in 2v51B

The 2v51B sequence is shown in Figs. 1–2, with each residue colored according to its estimated importance. The full listing of residues in 2v51B can be found in the file called 2v51B.ranks.sorted in the attachment.

2.4 Top ranking residues in 2v51B and their position on the structure

In the following we consider residues ranking among top 25% of residues in the protein . Figure 3 shows residues in 2v51B colored

by their importance: bright red and yellow indicate more conserved/important residues (see Appendix for the coloring scheme). A Pymol script for producing this figure can be found in the attachment.

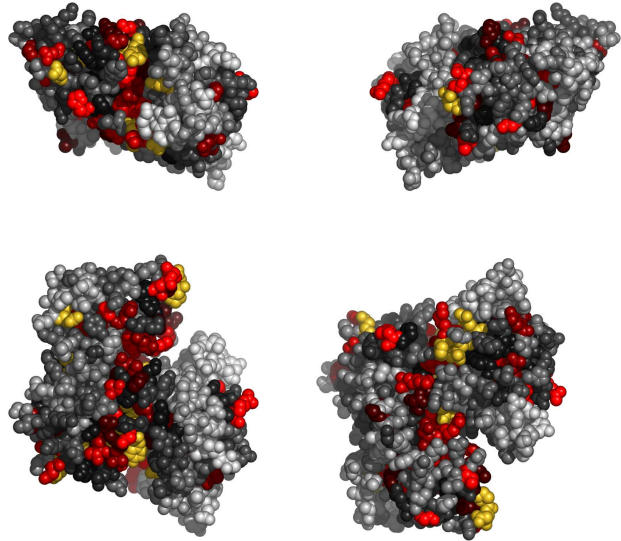


Fig. 3. Residues in 2v51B, colored by their relative importance. Clockwise: front, back, top and bottom views.

2.4.1 Clustering of residues at 25% coverage. Fig. 4 shows the top 25% of all residues, this time colored according to clusters they belong to. The clusters in Fig.4 are composed of the residues listed in Table 1.

Table 1.		
cluster color	size	member residues
red	44	104, 105, 107, 108, 109, 111, 112, 113, 115, 116, 117, 133, 136, 137, 138, 139, 140, 141, 142, 143, 146, 147, 148, 149, 150, 152, 168, 282, 286, 288, 290, 293, 298, 300, 301, 302, 304, 305, 331, 333, 338, 339, 340, 343
blue	30	157, 158, 159, 177, 179, 181, 182, 183, 184, 186, 200, 202, 204, 207, 208, 210, 211, 213, 214, 216, 226, 241, 242, 243, 244, 245, 253, 254, 255, 256
yellow	4	82, 83, 86, 88
green	2	264, 273
purple	2	124, 125

Table 1. Clusters of top ranking residues in 2v51B.