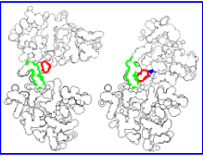


Database of Macromolecular Movements - Netscape

YALE GERSTEIN LAB



## Database of Macromolecular Movements

### with Associated Tools for Geometric Analysis

This describes the motions that occur in proteins and other macromolecules, particularly using movies. Associated with it are a variety of free software tools and servers for structural analysis.

View entry:  OR Search motions database:

**Movies**  
[Gallery of movies \(new ranker interface\)](#) of protein motions. If you want to make your own movie, we have a [Morph Server](#) that will interpolate between any two protein conformations, generating a movie. Also, a server with a [simplified interface](#). The [highlights page](#) shows some of the best movies in the database, all generated by the morph server. (Alternate, [MPPEGs-only](#) page.)

**Papers**  
 • A general *Scientific American* article on water and protein motions [[full-text](#)]  
 • The database citation: M. Gerstein & WG Krebs (1998). *Nuc. Acid. Res.* **26**:4280-4290 [[medline](#)].  
 • [More papers...](#)

**Software**  
 This includes [freeware](#) for calculating volumes, surfaces, axes, angles, and distances. Also, there is information about [VRML](#).


**Browse**  
 The main database is arranged around a multi-level classification scheme (e.g. motions of loops, domains, or subunits). It can either be viewed as individual motions by selecting from the menu above, or as a [full outline](#). The overall classification scheme is briefly described on the [help page](#). Also available are: a focus page on [motions in membrane proteins, schematic](#), or a raw [SQL data dump](#).

**Edit**  
 You can add a comment, including a link or reference, to any motion report by clicking on "Add a comment" at the top of each motion page. Other comments, suggestions, and submissions are highly encouraged and should be emailed to [motions@bioinfo.mibb.yale.edu](mailto:motions@bioinfo.mibb.yale.edu). If you want to link directly to entries in the database, [more information](#) is available.

http://mekor.csb.yale.edu/MolMovDB/exp/tcxray.html

Movie Gallery - Netscape


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## Movie Gallery of Macromolecular Motions

Below is a listing of movies associated with the [Database](#) of Macromolecular Movements. Most of these were automatically generated by our [morph server](#). There is also a page illustrating [outstanding morphs](#) generated by the server.

Search morphs:


 [Order movies by other attributes in a custom table.](#)

morph ID	Motion ID	Motion name (in DB, as submitted)	PDB ID		Submitter Info	# of residues	maximum CA deviation	# of frames
			#1	#2				
86390-22634	trpsyn	TRP repressor	1ttq	1ubs	2001-02-14 16:38:30	268	1.64816	10
86414-22674	trpsyn	TRP repressor	1ttp	1ubs	2001-02-14 16:38:36	268	1.98394	10
86440-22702	trpsyn	TRP repressor	1ttq	1ttq	2001-02-14 16:37:07	268	0.76212	10
15439-7452	tropc	troponin	1ncx	1ncy	2001-02-15 00:38:05	162	0.0891075	10
d1ncx__d1ahr__	tropc		1ncx	1ahr	1999-11-06 17:37:57	146	23.438	10
d1ncx__d1ap4__	tropc		1ncx	1ap4	1999-11-06 22:01:40	89	13.3166	10
d1ncx__d1cfd__	tropc		1ncx	1cfd	1999-11-06 17:50:53	148	11.707	10
d1ncx__d1osa__	tropc		1ncx	1osa	1999-11-06 18:21:18	148	9.78271	10
d1ncx__d1tcob__	tropc		1ncx	1tco	1999-11-07 02:05:27	375	41.803	10
d1ncx__d2sas__	tropc		1ncx	2sas	2000-07-20 14:20:12	185	9.869	10
d1ncx__d2scpa__	tropc		1ncx	2scp	2000-07-19 03:03:19	174	8.71277	10

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cm [cm] - Netscape

cm [cm]




Representation  Ribbon  CA trace  Ball-and-Stick

Video Format  MultiG  QuickT

VRML 2.0 3D Animations:

- [CA trace \[low-end hardware\]](#)
- [solid tubes \[high-end hardware\]](#)

 A VRML 2.0 Browser such as CosmoPlayer is required to view the above 3-D Animations.

Download CosmoPlayer now!

[Download tar'ed PDB file](#)

## Entry from Macromolecular Movements Database:

### Motion in Calmodulin [cm]

Classification

**Known Domain Motion, Hinge Mechanism**  
[\[D-h-2\]](#)

Structures

- Closed is 1CDL ; mammalian, recomb., X-ray (Links to [PDB](#), [SCOP](#), [Core-Structures](#), and [VRML-tubes](#)).
- Closed is 2BBM ; fly, NMR, closed with peptide (Links to [PDB](#), [SCOP](#), [Core-Structures](#), and

Document: Done