Netscape: Protein Motions DataBase 1.5

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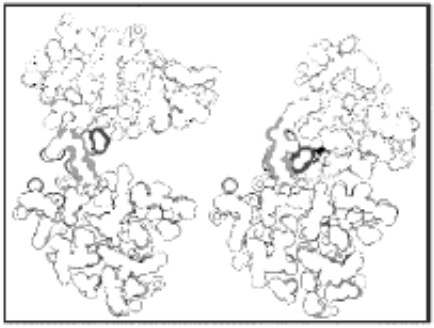
Location: http://hyper.stanford.edu/~mbg/ProtMotDB/



Protein Motions Database

This database lists protein motions. It is arranged around a multi-level classification scheme and includes domain motions, loop motions, and subunit motions. The database in outline form follows. You can view it with condensed subheadings (the normal way), with fully expanded subheadings, with just main headings or as straight-ASCII records (raw database and references). You can also search the database for a simple text string (e.g. 'calmodulin', no regular expressions or special characters such as '+' and '%').

Enter Search Text: Adenylate Search

The citation and other relevant references for the database are available. If you want to add an entry or point out a mistake, please e-mail mbg@hyper.stanford.edu. If your browser supports forms, you are encouraged to use a standard form for submissions. If you want to link directly to entries in the database, more information is available. This is version 1.5 of the database.

(A) Domain Motions

(1) Proteins for which open and closed conformations are known

(i) Motion is predominantly shear

- Citrate Synthase
- Aspartate Amino Transferase (AAT)
- Trp Repressor (TrpR)
- Hexokinase
- Glyceraldehyde-3-phosphate Dehydrogenase (GAPDH)
- Alcohol Dehydrogenase (ADH)
- Endothiapepsin