



An Algorithm For Protein Hinge Prediction Using Elastic Network Models

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Input Protein	Chain	GNM Cutoff Radius	ANM Cutoff Radius
23904.B99990030_MSE.pdb	A	10.0	18.0

click [here](#) for downloadable files !

Slow mode 1

Slow mode 2

Atomistic Representation ANM Motion :

Cartoon Representation ANM Motion :

-----> Slowest mode 1:

Rigid Part No

Residues

1	A:0-733	Score : 0.98
2	A:734-1165	Score : 0.96

Hinge residues: 733A

-----> Slowest mode 2:

Rigid Part No	Residues	
1	A:0-51	Score : 0.76
2	A:52-484	Score : 0.98
3	A:485-895	Score : 0.98
4	A:896-1165	Score : 0.98

Hinge residues: 51A 484A 895A

Short Flexible Fragments:

For comments: appserv AT prc.boun.edu.tr