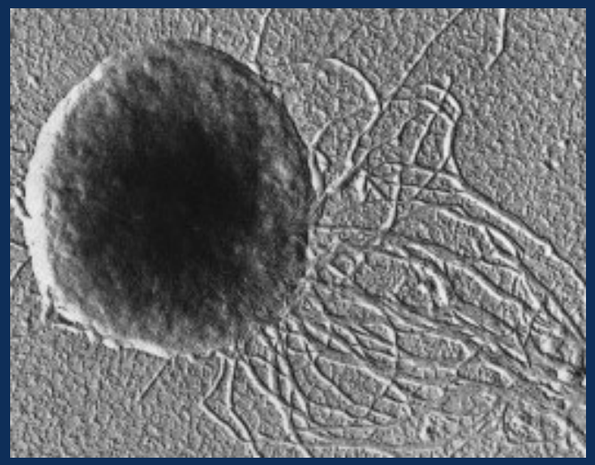
Adaptation to ”deep-sea” environment of IF6 protein.



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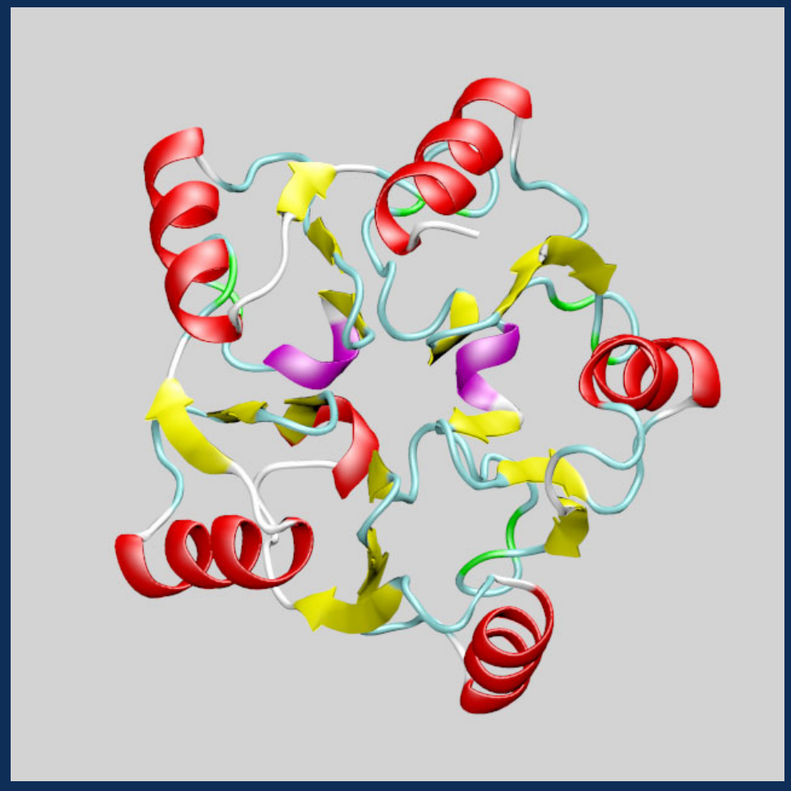
Initiation Factor 6 (IF6)

The assembly of 80S ribosomes requires joining of the 40S and 60S subunits, which is triggered by the formation of an initiation complex on the 40S subunit.

IF6 binds specifically to the free 60S ribosomal subunit and prevents its association with the 40S ribosomal subunit ribosomes.



The biological role of IF6 is:

-rate-limiting for DNA translation

-sensitive to external stimuli

IF6 works almost the same way in:

-Saccharomyces cerevisiae :Mesophile Eukaryote; It's the simplest eukaryote, i.e. yeast it lives at **~300K** and **1atm**.

-Methanococcus Jannaschii : Archaeon (Barophile); it lives at **353K** and **~200atm** near hydrothermal Chimneys. Its metabolism produces ***methane*** **(!)**

How come?

..we look for structural and dynamical adaptation…

Structural changes

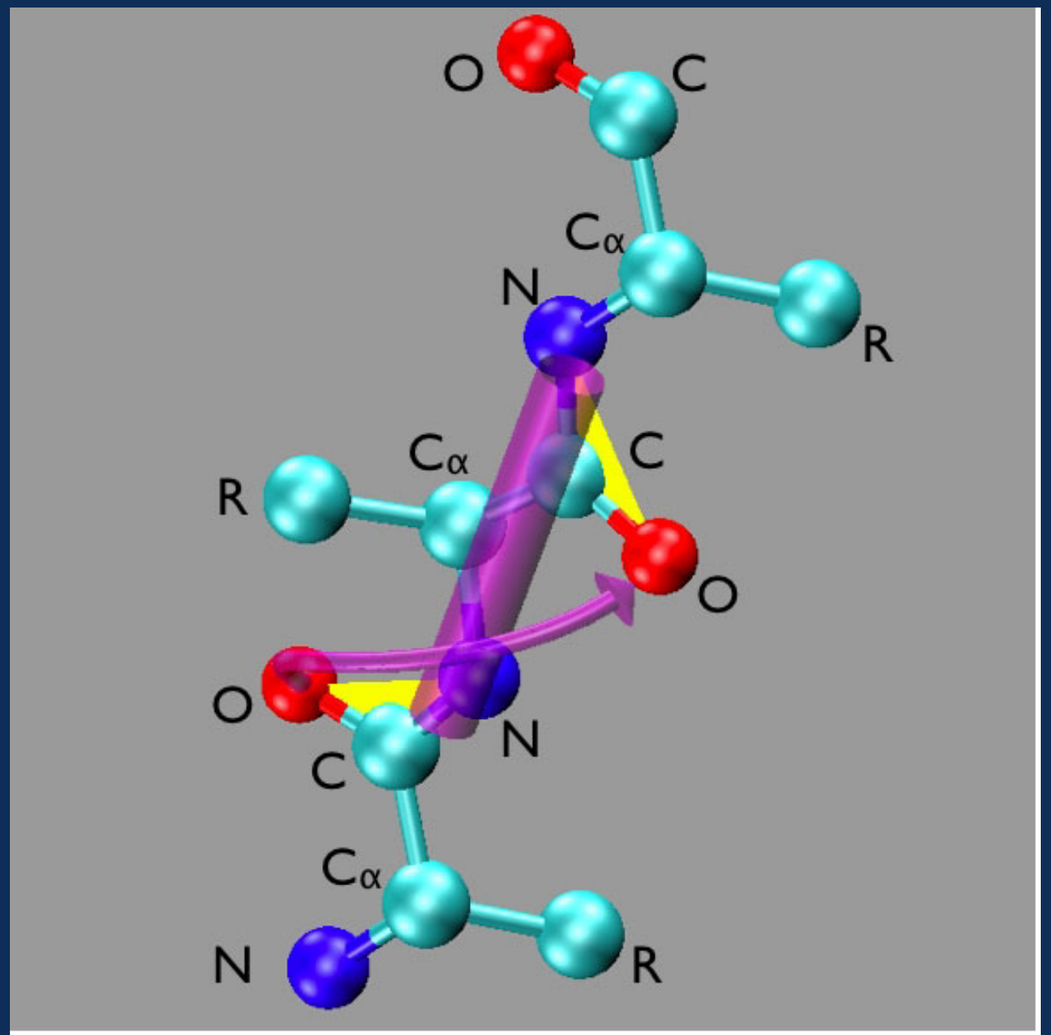
IF6 : 228 amino acids , ~3400 atoms:

-changes in structure could be difficult to quantify

- The characterization of structural changes can be done using ScrewFit method *

The model describes backbone structure using *quaternion-based* superposition fits of peptide planes in conjunction with *Charles' theorem* ("every rigid-body displacement can be described by a screw motion").

- Parameters of "local helix" from the screw motion can easily determine motifs in secondary structure and their deviations from ideal motifs (kinks, curvatures, etc..)



-good agreement with DSSP method and other common methods for secondary structure determination.

* Kneller, G. and Calligari, P. *Acta Cryst. D* , 2006 (in press)

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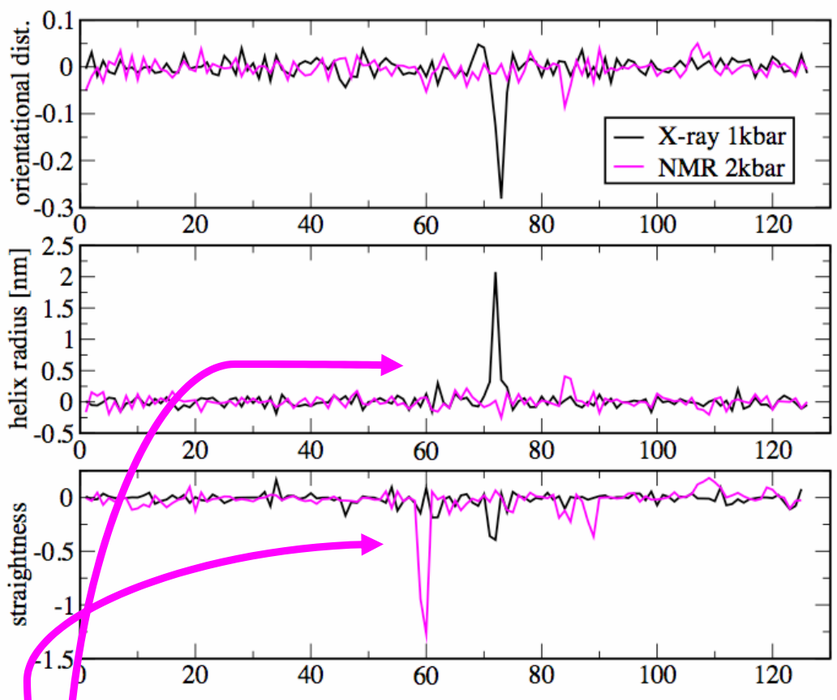
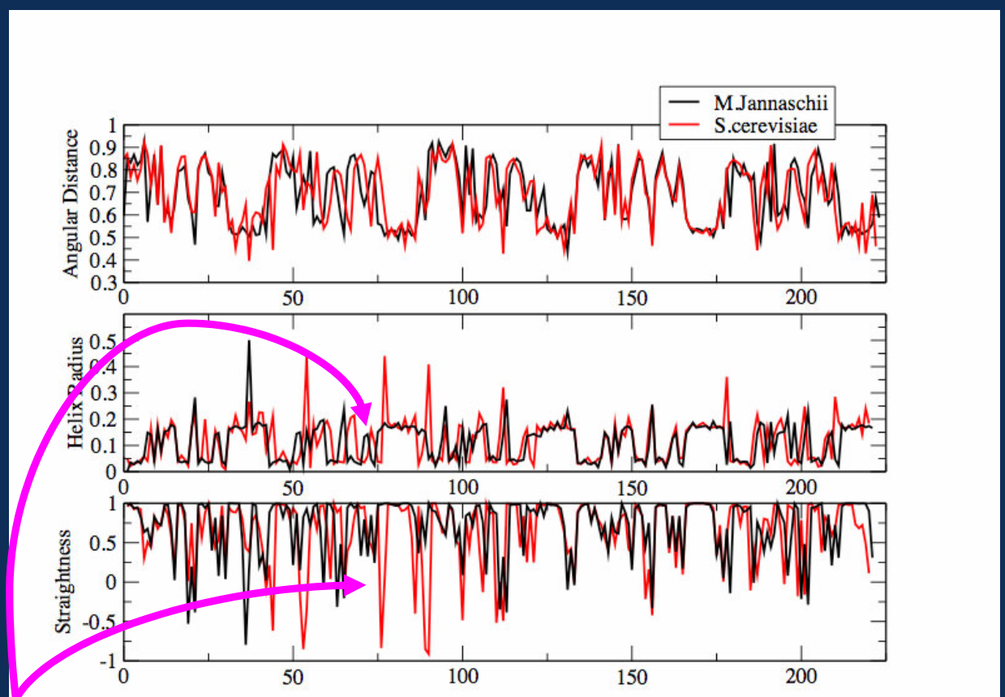
ScrewFit pinpoints small differences between structures.

pressure effects



Example: Lysozyme
Changes between parameters at high pressure and at 1atm.

differences between homologous



Parameters from IF6/M.Jannaschii and IF6/S.cerevisiae.
X-ray data at 300K and 1atm

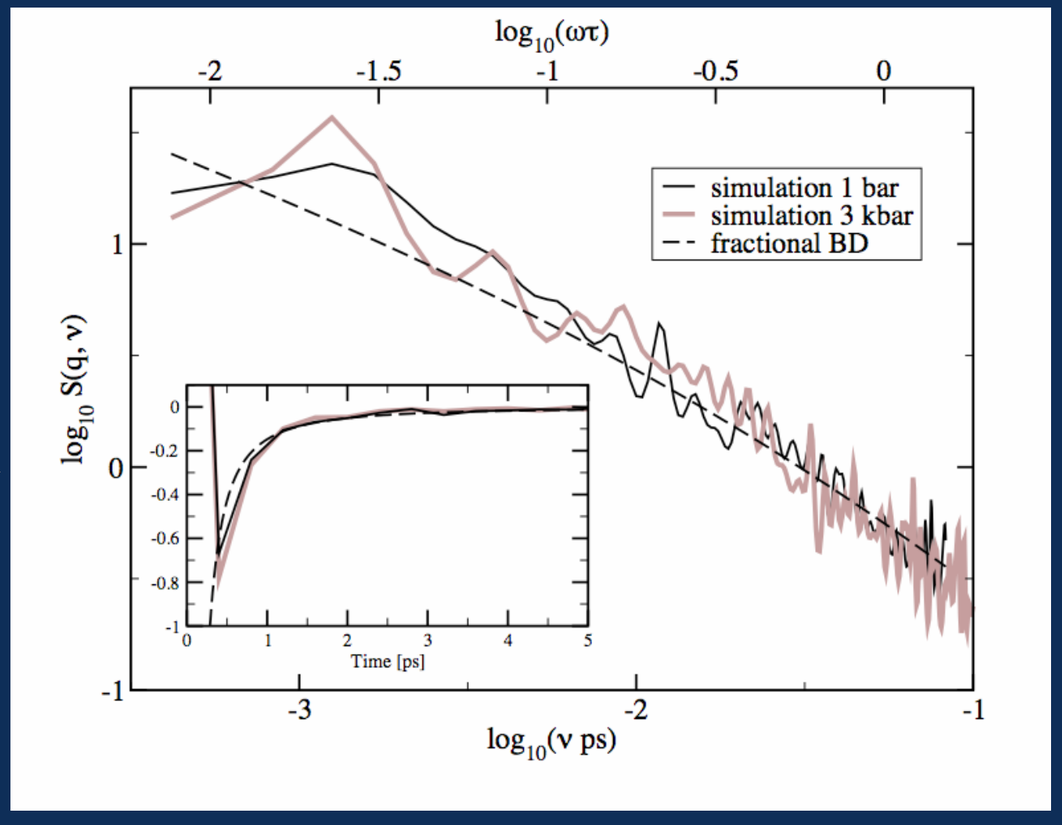
… and now... effects on dynamics

Molecular Dynamics Simulations:

- MD simulations in NPT-ensemble at natural and “extreme” conditions.

- Comparison with analytical model of fractional Brownian Dynamics*.

- Mean structures from MD simulations will be used as “under-pressure structures” and studied with ScrewFit.



Experiments:

- Quasielastic neutron scattering experiments at different temperatures and pressures.

  Expression and purification of IF6 protein (from M.Jannaschii and S.cerevisiae) (***at D-Lab***).

* Kneller, G. and Hinsen, K., J. Chem. Phys., 121, (2004)

Acknowledgements

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Everybody!!