Conclusions:

1) The R-T model unifies the description of elastic and inelastic neutron scattering spectra of solvated proteins, covering a wide range in time and momentum exchange. Accounting for resolution effects the „dynamical transition” disappears. This result demonstrates the validity of scattering theory even for complex systems like proteins.

2) Heterogeneity does not play a dominant role in neutron spectra of proteins, two slightly distributed components cover the full parameter range.