

**Ordered conformational change in the protein backbone: prediction of  
conformationally variable positions from sequence and  
low-resolution structural data.**

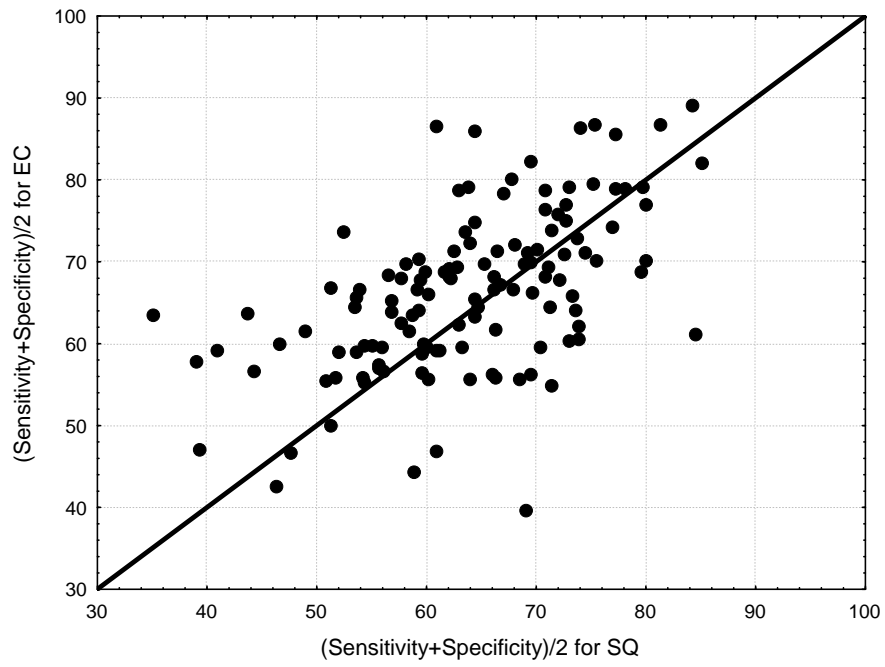
**Igor B. Kuznetsov**

**Supplementary Figures**

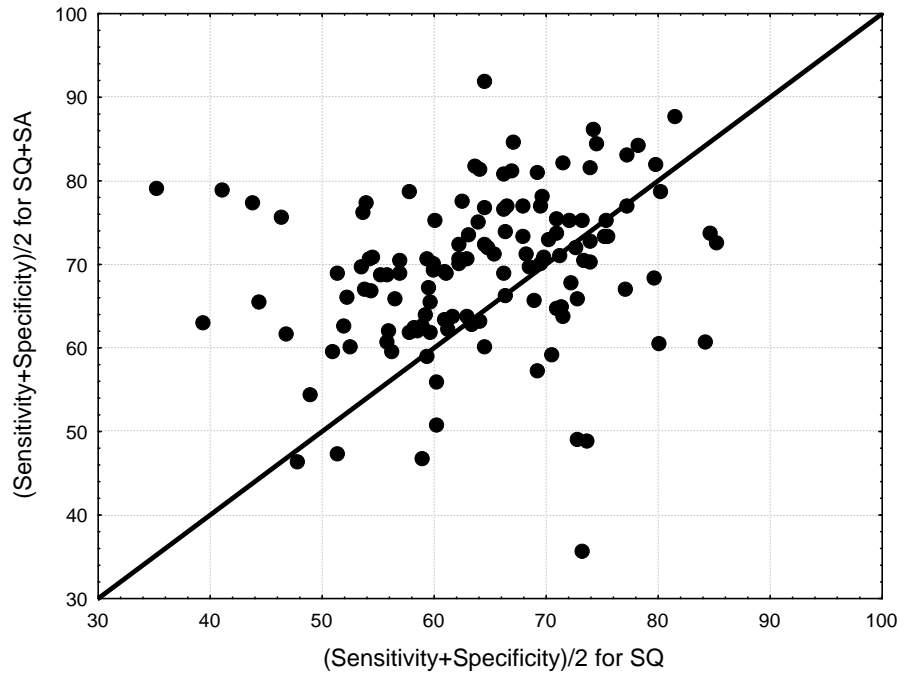
**Supplementary Figure 1.** Scatter plot of the net prediction rate,  $(\text{sensitivity} + \text{specificity})/2$ , of the SQ feature that uses single sequence information vs. the NP of the EC feature that uses evolutionary information. Each point corresponds to one protein. Points above the diagonal correspond to proteins on which EC performs better.

**Supplementary Figure 2.** Scatter plot of the net prediction rate,  $(\text{sensitivity} + \text{specificity})/2$ , of the SQ feature that uses single sequence information vs. the NP of the SQ+SA feature that uses single sequence information and normalized solvent accessibility. Each point corresponds to one protein. Points above the diagonal correspond to proteins on which SQ+SA performs better.

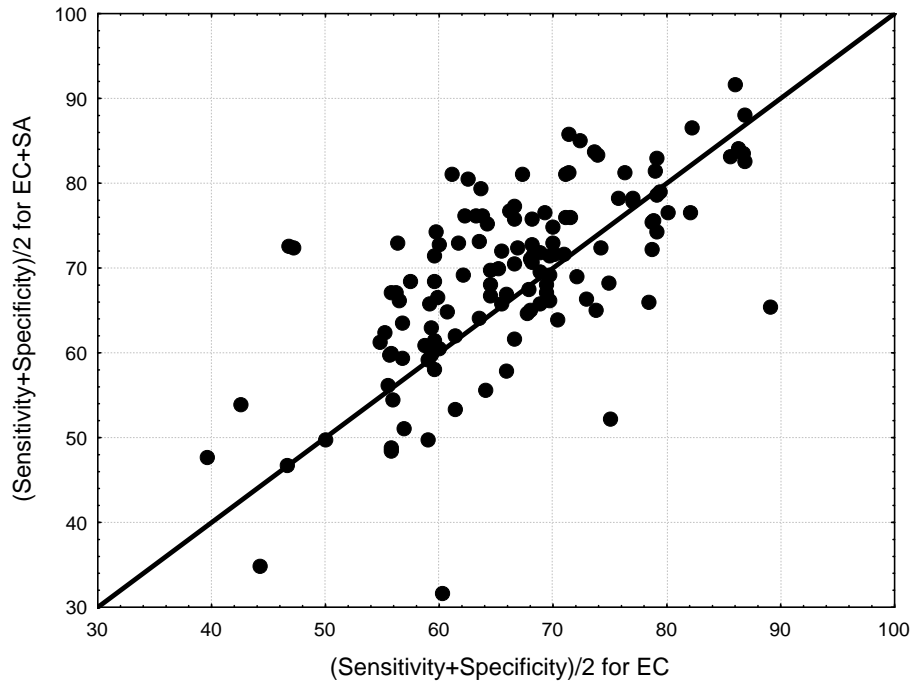
**Supplementary Figure 3.** Scatter plot of the net prediction rate,  $(\text{sensitivity} + \text{specificity})/2$ , of the EC feature that uses evolutionary information vs. the NP of the EC+SA feature that uses evolutionary information and normalized solvent accessibility. Each point corresponds to one protein. Points above the diagonal correspond to proteins on which EC+SA performs better.



**Supplementary Figure 1**



**Supplementary Figure 2**



**Supplementary Figure 3**