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Supplementary material

SUPPLEMENTARY MATERIAL TO

A bioinformatics study concerning the structural and functional properties of human caveolin proteins

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HYDROPHOBICITY, ALPHA-HELIX AND BETA-TURN PROFILES FOR CAVEOLIN 1 OBTAINED USING DIFFERENT WINDOW SIZES

The independence of the hydrophobicity, alpha-helix and beta-turn profiles on the window size used to compute them is illustrated in Figs. S-1 and S-2 for caveolin 1. The hydrophobicity profile of caveolin 1 for three different window sizes, *i.e.*, 9, 13 and 21 residues, is illustrated in Fig. S-1. It could be seen that the profiles do not differ significantly.

This is also true for the alpha-helix and beta-turn profiles, presented in Fig. S-2a and b, respectively.

HOMOLOGY MODELLING USING THE GENO3D TOOL

The use of the Geno3D tool is illustrated in Fig. S-3. For any of the human caveolin sequences, the obtained result was the same "No satisfying template found for sequence 1".

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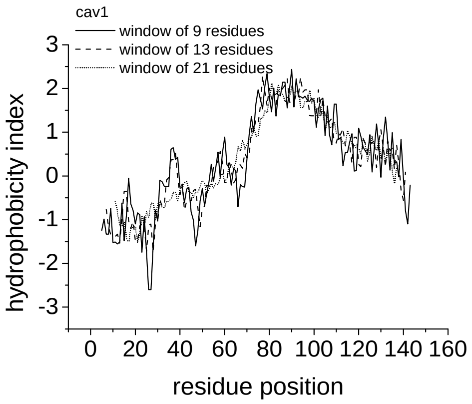
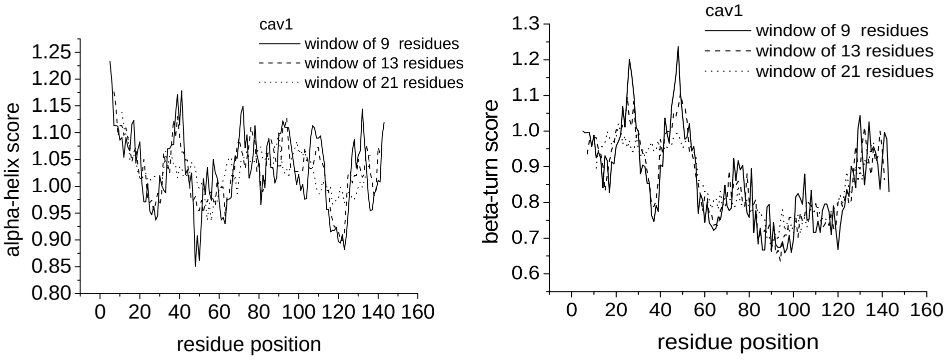
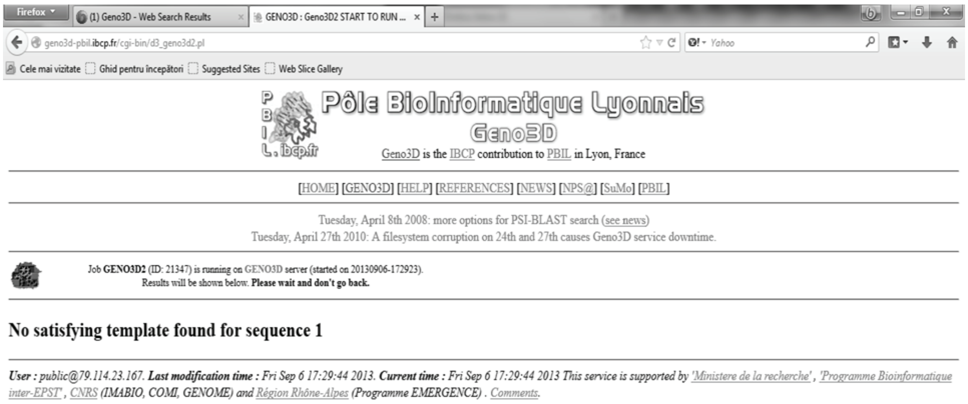


Fig. S-1. The hydrophobicity profile of caveolin 1 for three different window sizes: 9 residues – solid line, 13 residues – dashed line, 21 residues – dotted line.



(a) (b)

Fig. S-2. a) Alpha-helix and b) beta-turn profile of caveolin 1 for three different window sizes: 9 residues – solid line, 13 residues – dashed line, 21 residues – dotted line.



Geno3D is the IBCP contribution to PBIL in Lyon, France

Tuesday, April 8th 2008: more options for PSI-BLAST search (see news)
Tuesday, April 27th 2010: A filesystem corruption on 24th and 27th causes Geno3D service downtime.

Job **GENO3D2** (ID: 21347) is running on GENO3D server (started on 20130906-172923).
Results will be shown below. **Please wait and don't go back.**

No satisfying template found for sequence 1

User : *public@79.114.23.167.* ***Last modification time :*** *Fri Sep 6 17:29:44 2013.* ***Current time :*** *Fri Sep 6 17:29:44 2013 This service is supported by 'Ministere de la recherche', 'Programme Bioinformatique inter-EPST', CNRS (IMABIO, COMI, GENOME) and Région Rhône-Alpes (Programme EMERGENCE) . Comments.*

Fig. S-3. Illustration of using Geno3D tool for human caveolin 1.

MEMBRANE TENDENCY PROFILES FOR HUMAN CAVEOLINS

Membrane tendency profiles for the three caveolins are presented in Fig. S-4 in comparison to the hydrophobicity profile of caveolin 1. The similarity between the membrane tendency profiles and their correspondence to the hydrophobicity profile of cav1 could be evidenced.

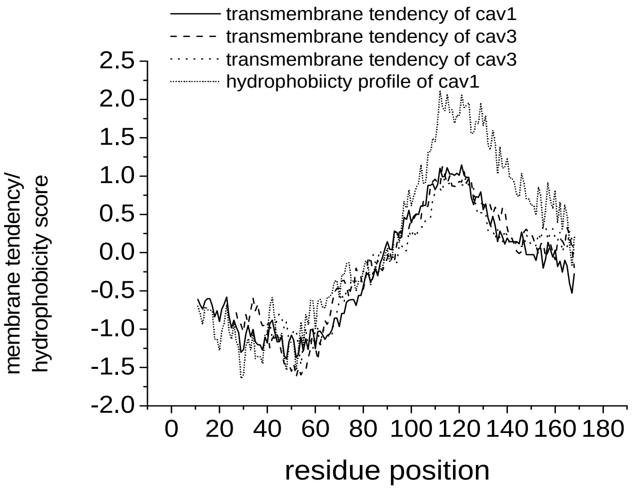


Fig. S-4. Membrane tendency profiles of cav1 (solid line), cav2 (dashed line), cav3 (dotted line) and the hydrophobicity profile of cav1 (short dotted line) obtained using ProtScale tool. For cav2 and cav3 proteins the residue position was translated such as the caveolin signature sequence to correspond for all caveolins. Prediction of disordered regions of cav1 using GlobPlot.

PREDICTION OF DISORDERED REGIONS OF CAV1 USING GLOBPLOT SOFTWARE

Prediction of disordered regions of cav1 using GlobPlot software is presented in Fig. S-5.

Disordered by Russell/Linding definition

>none_Disorder 23-42
spqcavhman cavelinshm sa**PIENSGNC**
AVPESVMSGG KYvdseghly tvpireqgni
ykpnnkamad elsekqvyda htkeidlvnr
dpkhlnddvv kidfedviae pegthsfdgi
wkasfttftv tkywfyrlls alfgipmali
wgiyfailsf lhiwavvpci ksflieiqci
srvysiyvht vcdplfeavg kifsnvrinl
qkei

Fig. S-5. Prediction of the disordered region of human caveolin 1 using the GlobPlot tool.

The predicted disordered region is 23–42.