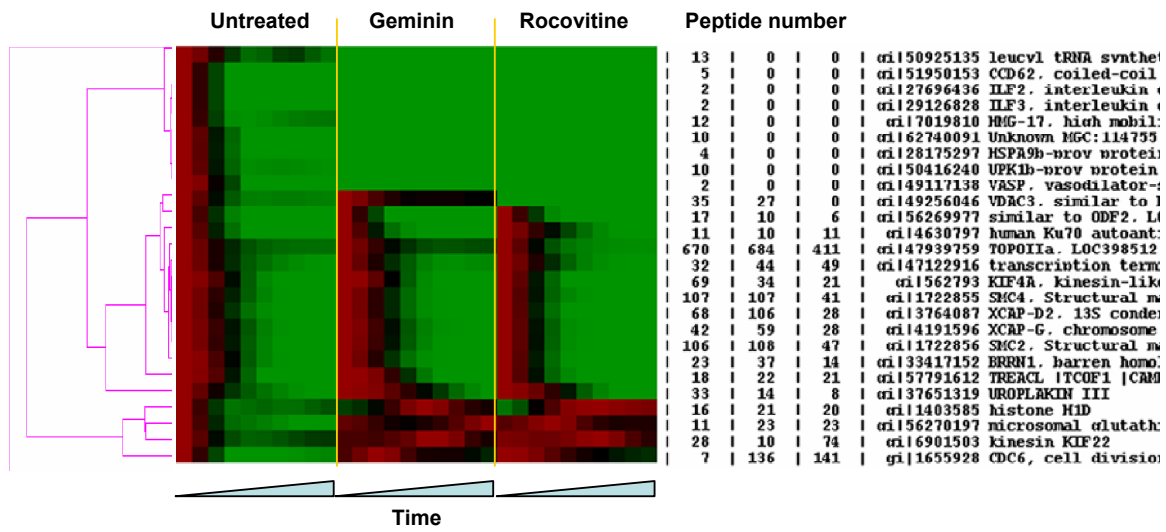
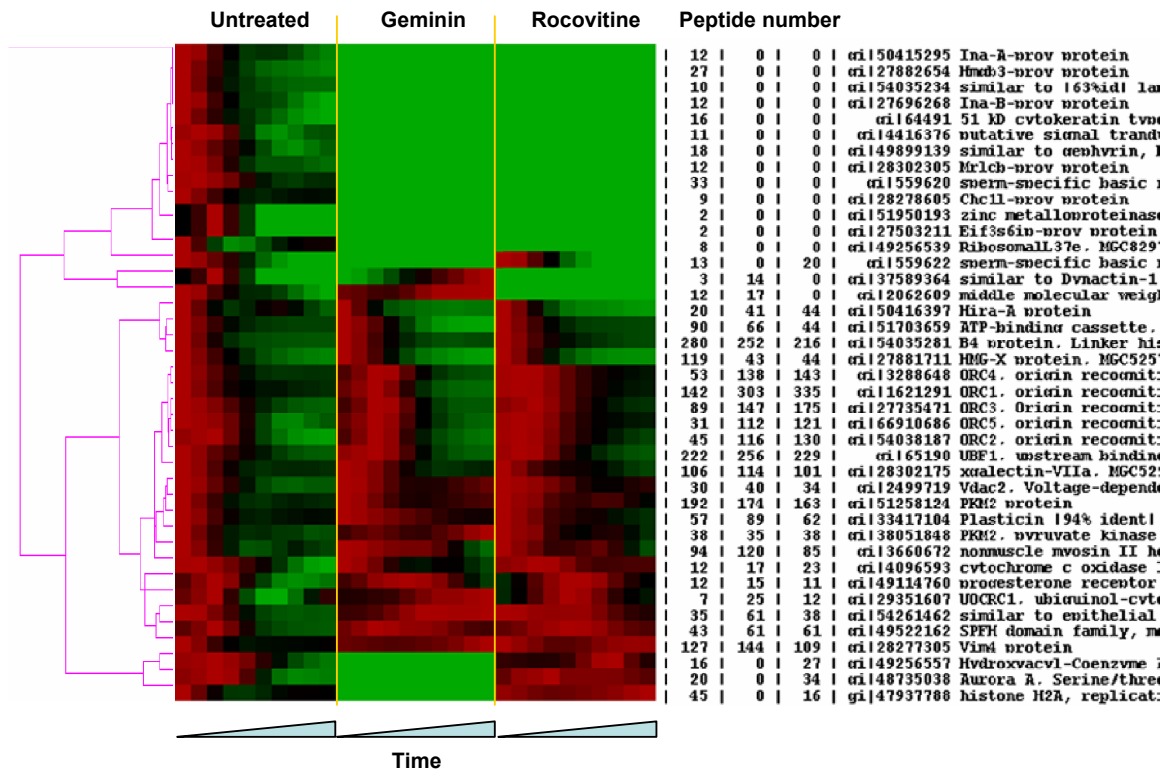


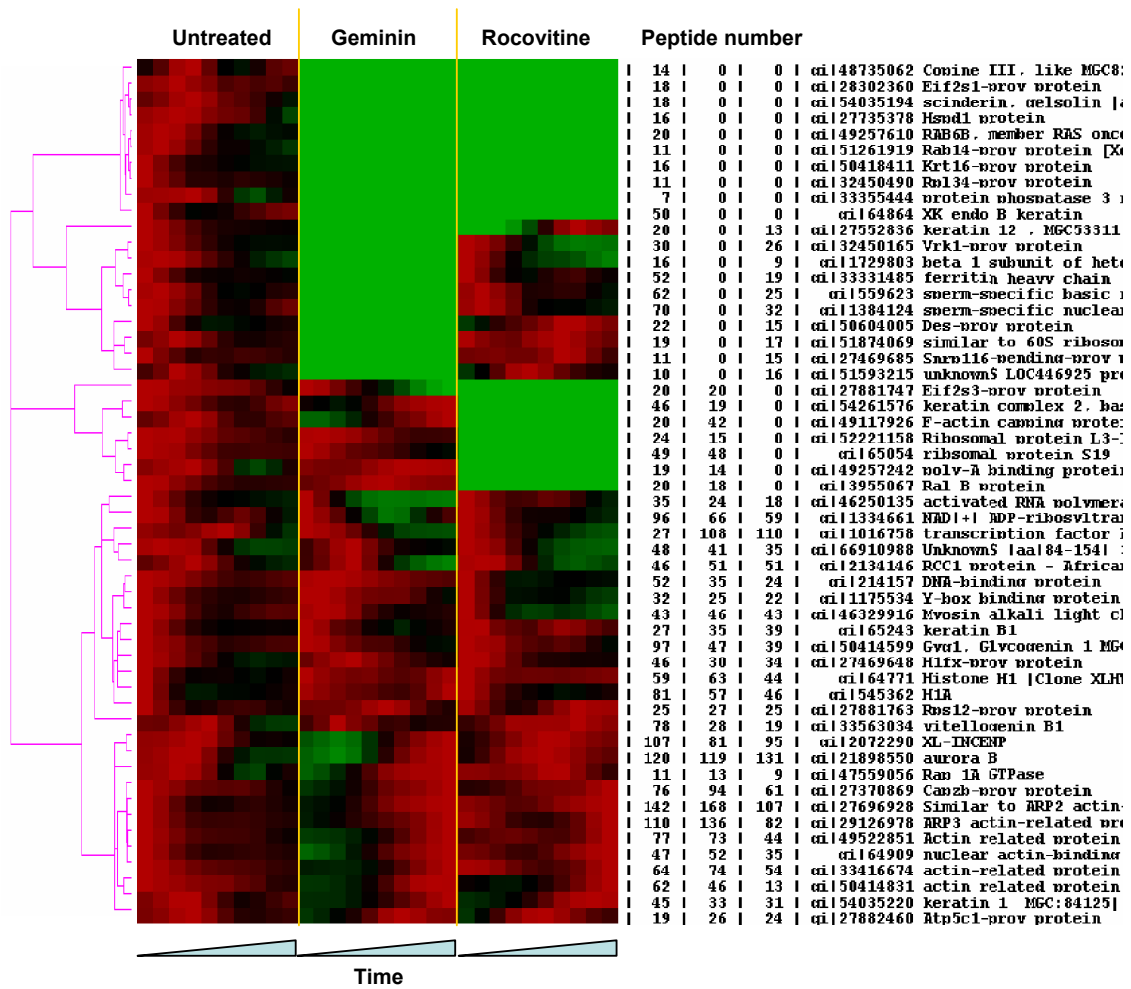
A. FCM cluster E1



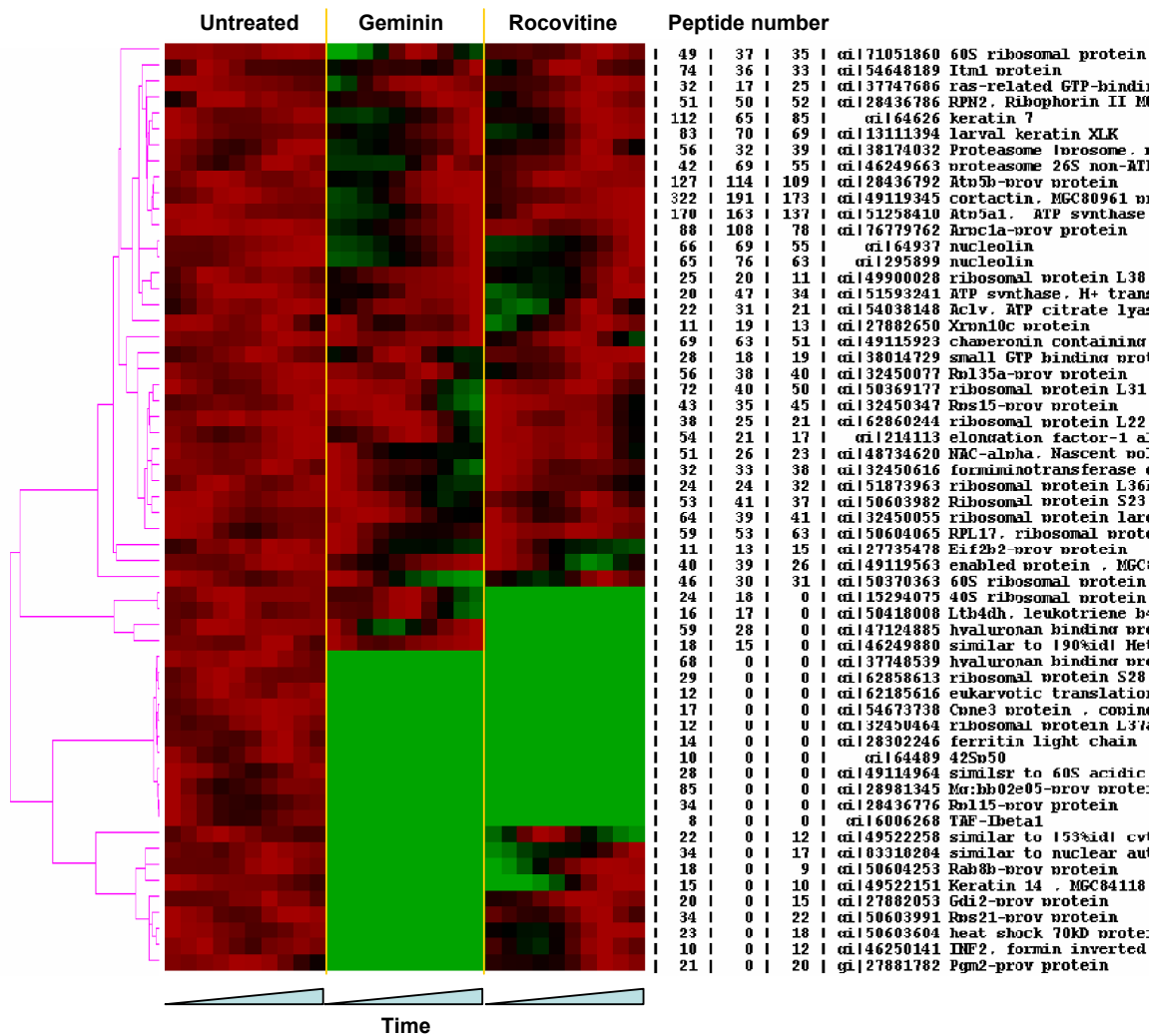
B. FCM cluster E2



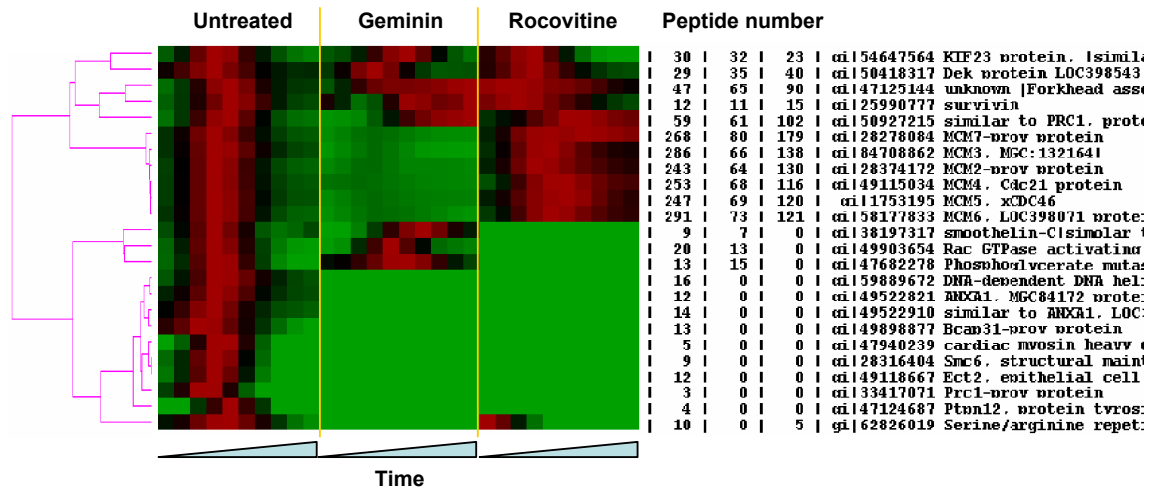
C. FCM cluster E3



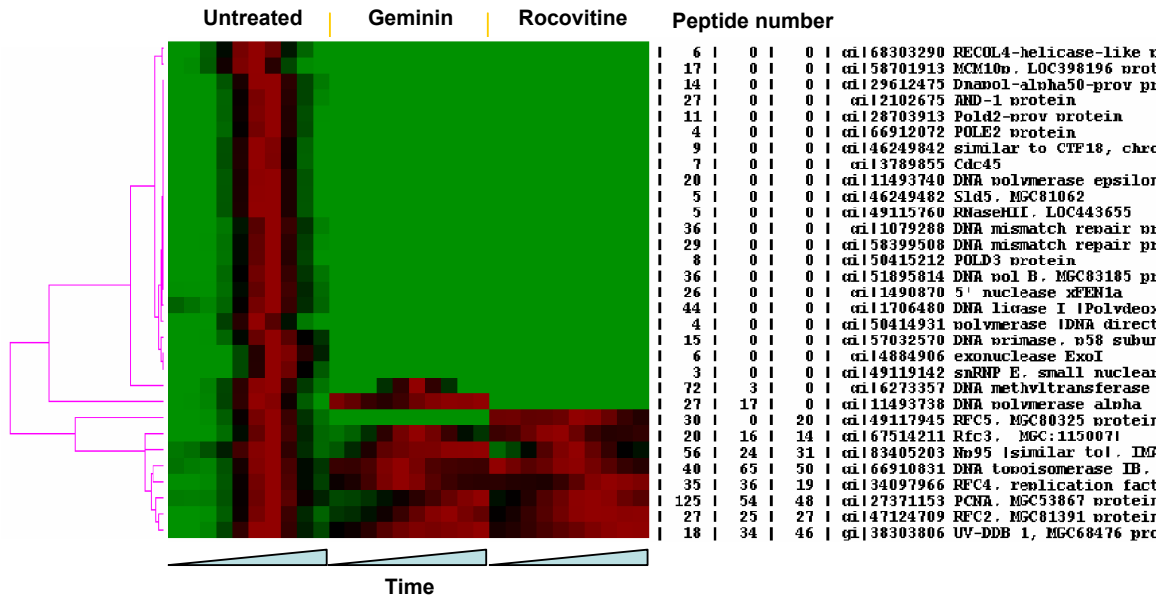
E. FCM cluster E4



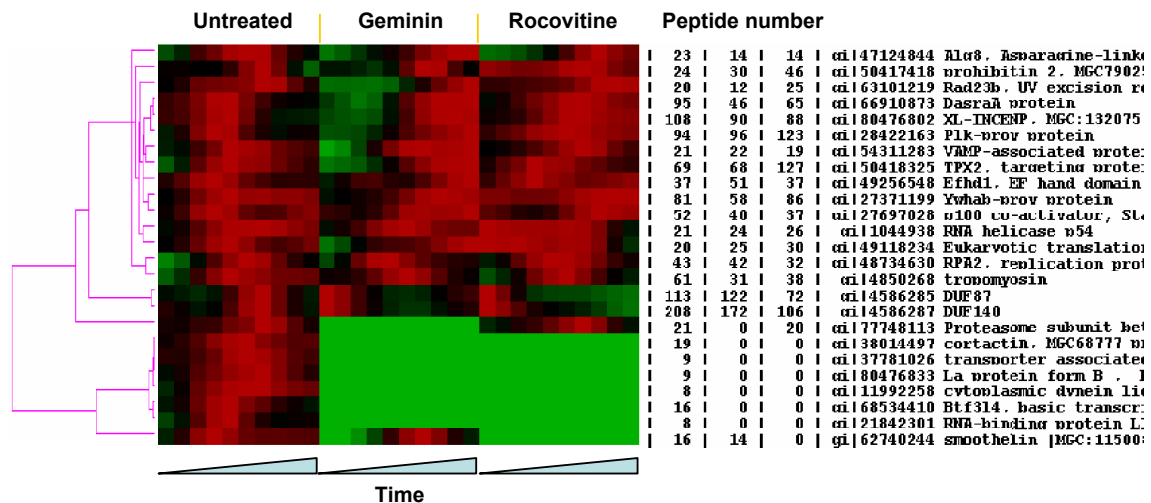
F. FCM cluster I1



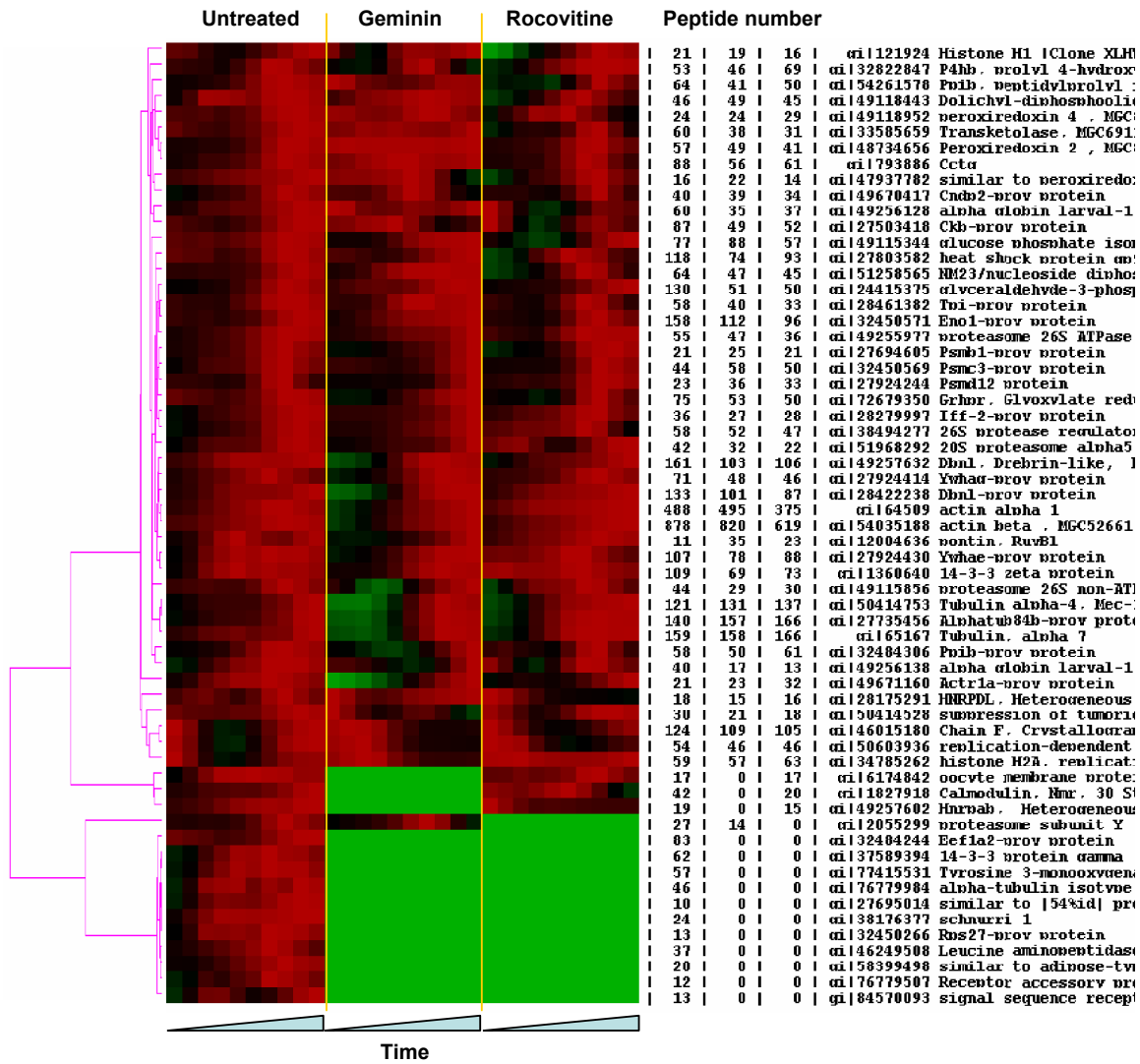
G. FCM cluster I2



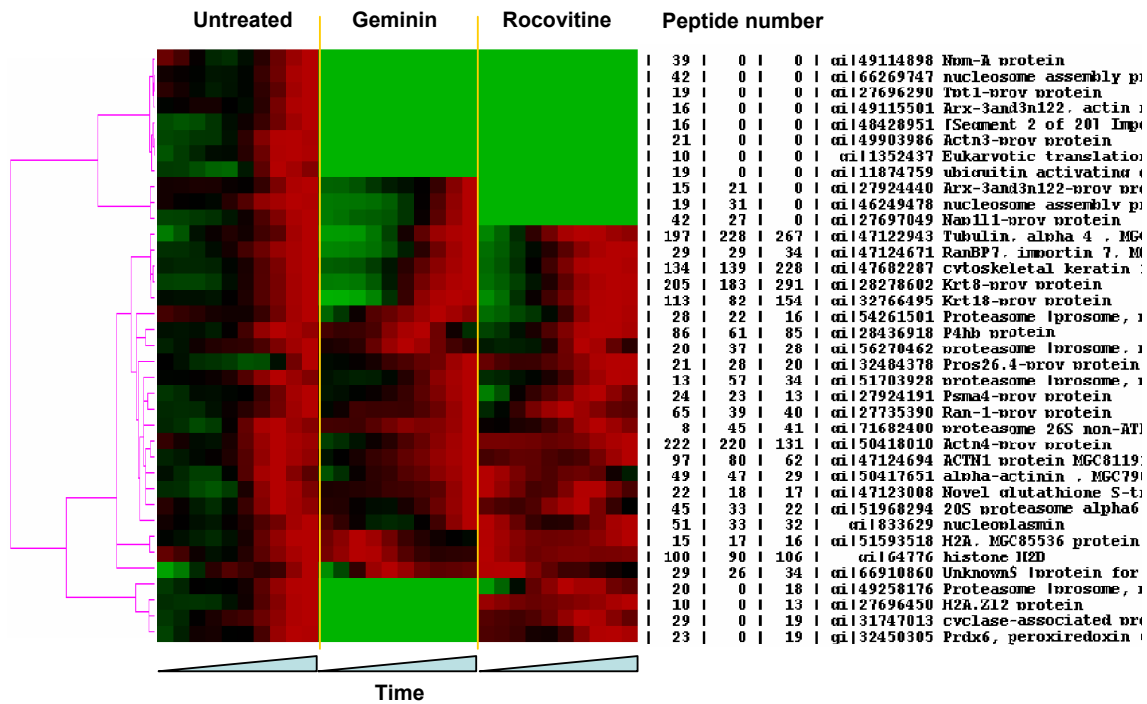
H. FCM cluster I3



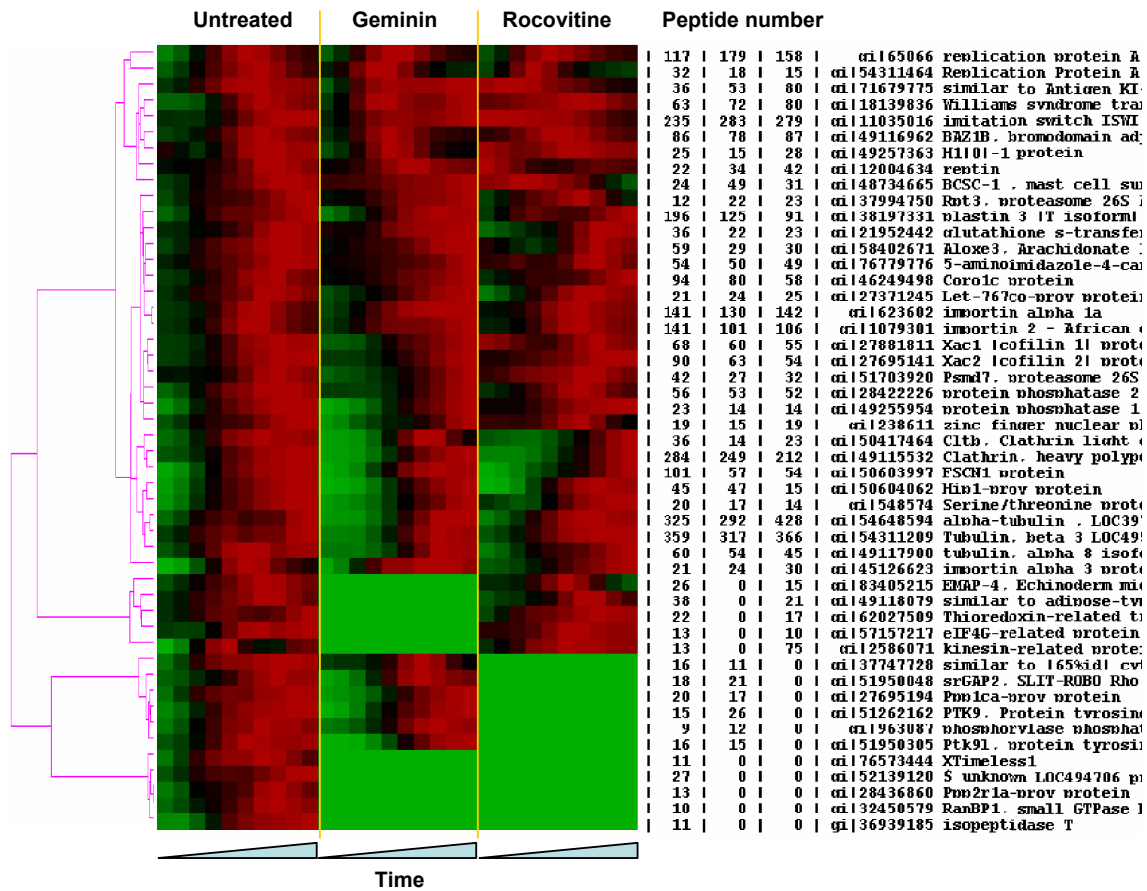
I. FCM cluster L1



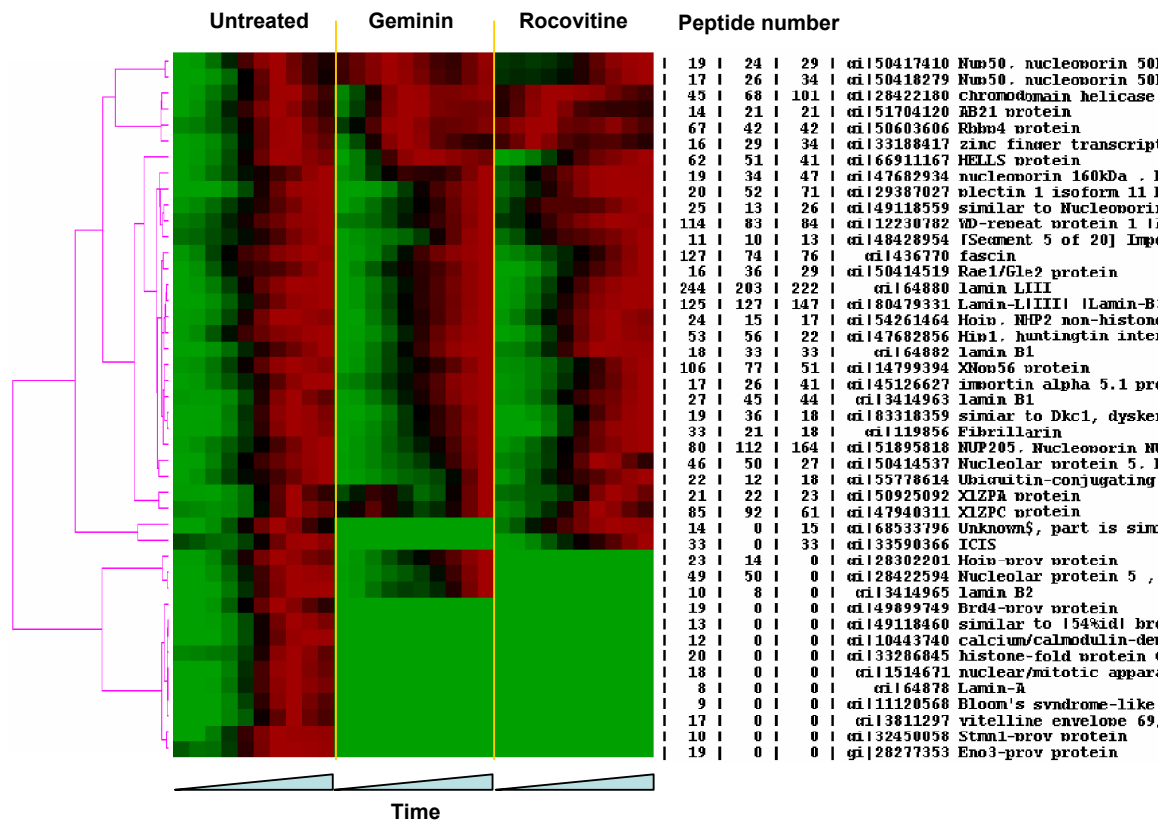
J. FCM cluster L2



K. FCM cluster L3



L. FCM cluster L4



M. FCM cluster L5

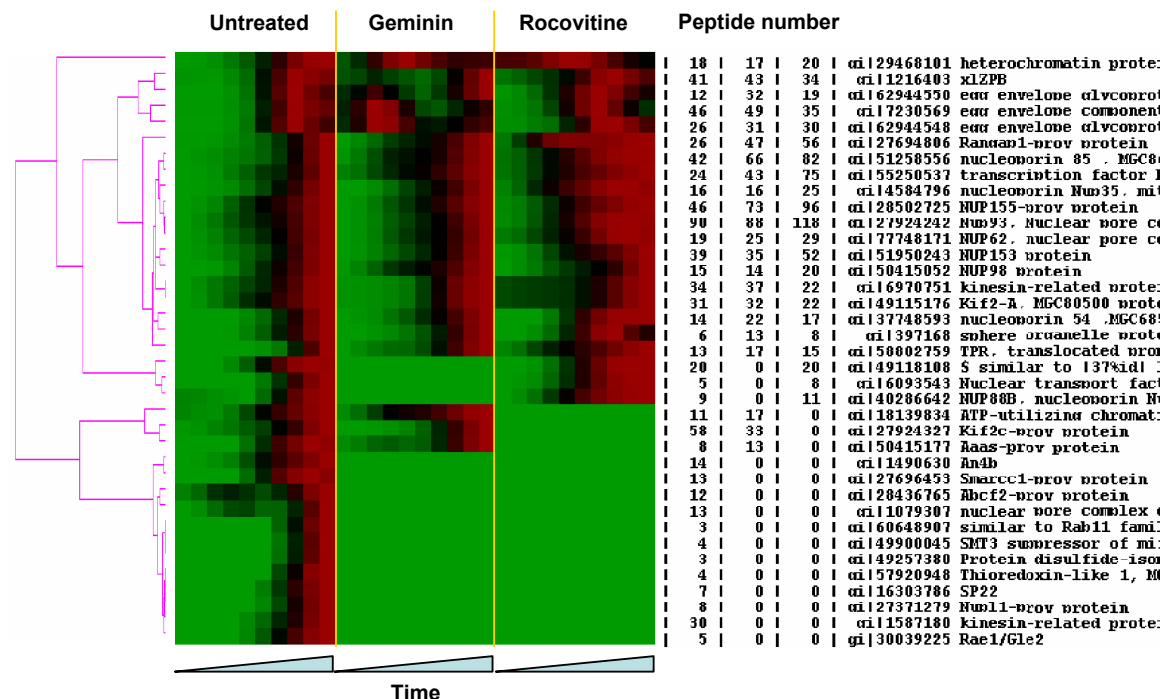


Figure S4. Heatmap of FCM clusters and hierarchical clustering results. For hierarchical clustering the combined dataset was generated by integrating profiles from inhibitor-free, geminin and roscovitine experiments for each protein. Hierarchical clustering was performed inside each of 12 FCM groups. Colour coding: 0.0 - green, 0.5 - black and 1.0 - red. Number of peptides identified for proteins in each treatment is also indicated.