

Deciphering the long distance-glycosylation preferences of GalNAc-Ts

SY07-03

M. de las Rivas^I, E. Lira-Navarrete^{II}, J. Earnest^{III}, H. Coelho^{IV}, I. Compañón^V, H. Clausen^{II}, G. Jiménez-Osés^V, F. Corzana^V, F. Marcelo^{IV}, T.A. Gerken^{III}, R. Hurtado-Guerrero^I

^IInstituto de Biocomputación y Física de Sistemas Complejos, Zaragoza, Spain, ^{II}Copenhagen Center for Glycomics, Copenhagen, Denmark, ^{III}Case Western Reserve University, Cleveland, United States of America, ^{IV}Universidade de Nova de Lisboa, Caparica, Portugal, ^VUniversidad de La Rioja, Logroño, Spain

GalNAc-Ts are a large family of glycosyltransferases that uniquely feature both a catalytic and lectin domain and that are responsible of the mucin-like glycosylation found in higher eukaryotes. To date, the underlying molecular basis of how GalNAc-Ts present distinct long distance-glycosylation preferences remained elusive. Here, through the first crystal structures of complexes of GalNAc-T2 with glycopeptides, we show how the activity profile of GalNAc-T2 is dictated by conformational heterogeneity and relies on a flexible linker located between the catalytic and the lectin domains. Our results also shed light on how GalNAc-Ts generate dense decoration of proteins with O-glycans, and suggest that the flexible linker dictates the lectin domain rotation, which in turn is responsible for the long distance-glycosylation preferences.