Proteolytic E-cadherin activation followed by solution NMR and X-ray crystallography

Daniel Häussinger, Thomas Ahrens, Thomas Aberle, Jürgen Engel, Jörg Stetefeld*, and Stephan Grzesiek*

Division of Structural Biology and Division of Biophysical Chemistry, Biozentrum, University of Basel, 4056 Basel, Switzerland

SUPPLEMENTARY MATERIAL

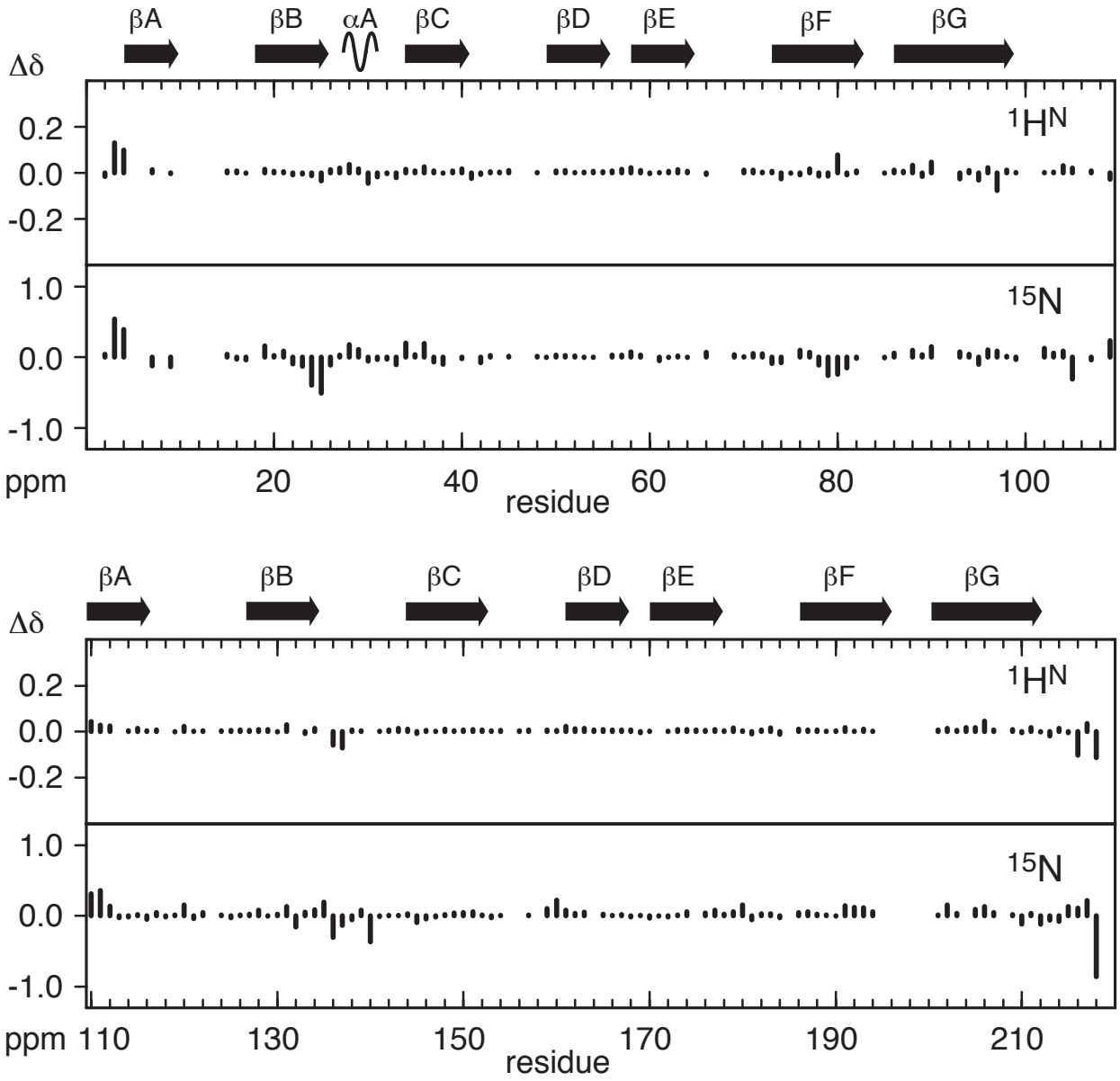

Fig. S1A-D. Differences in chemical shift of backbone amide groups between ECAD12 fragments with different N-terminal extensions. The total concentration of the fragments is indicated in parentheses. Differences are calculated as the second mentioned form subtracted from the first. (A): Differences between M-ECAD12 (0.6 mM) and HisXa-ECAD12 (1.1 mM), both under calcium-free conditions. Please note the five-fold expansion of the vertical axes as compared to B-D.

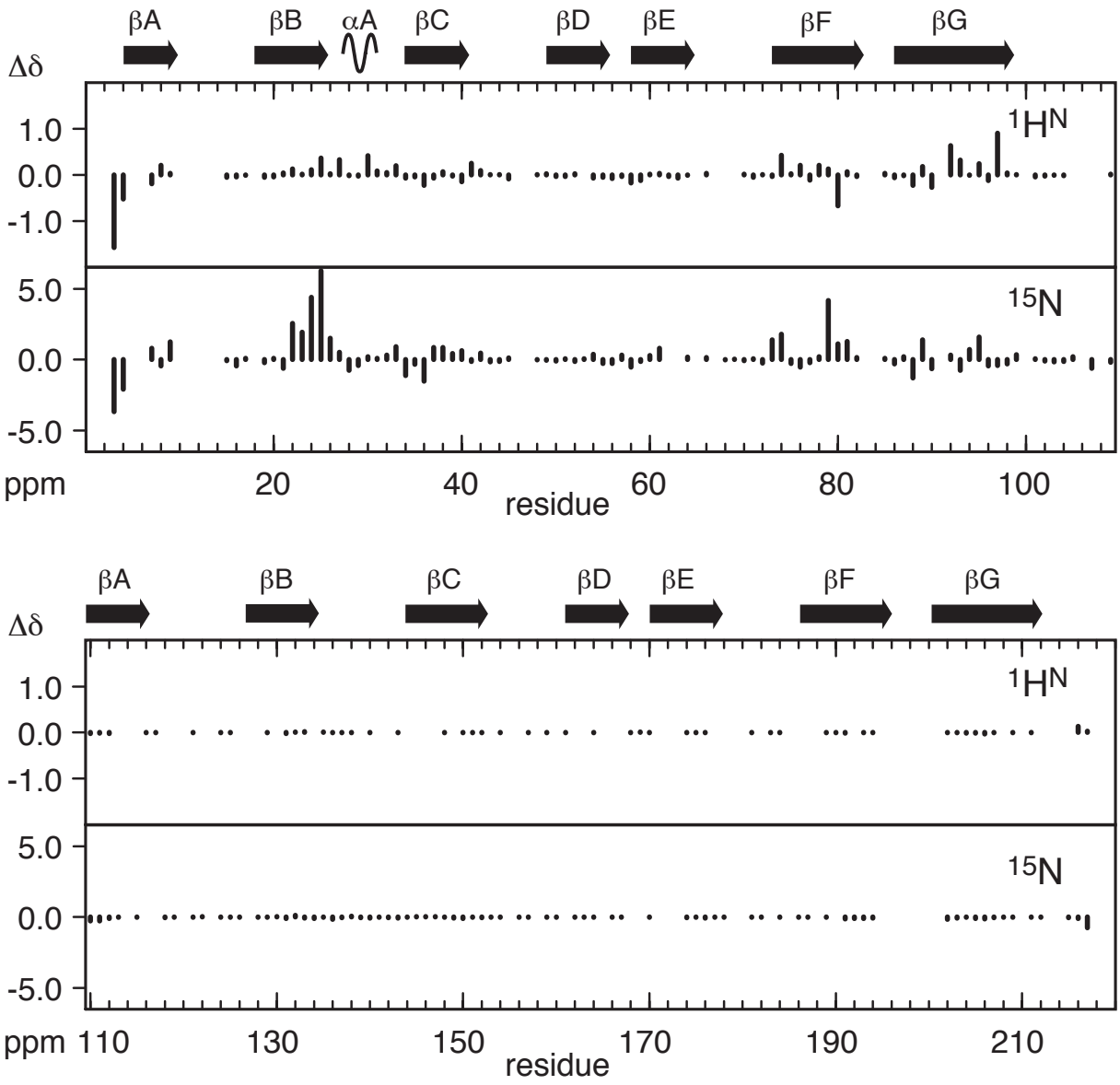

Figure S1B: Shift differences between monomeric HisXa-ECAD12 (1.1 mM) and monomeric ECAD12 (1.0 mM), both under calcium-free conditions.

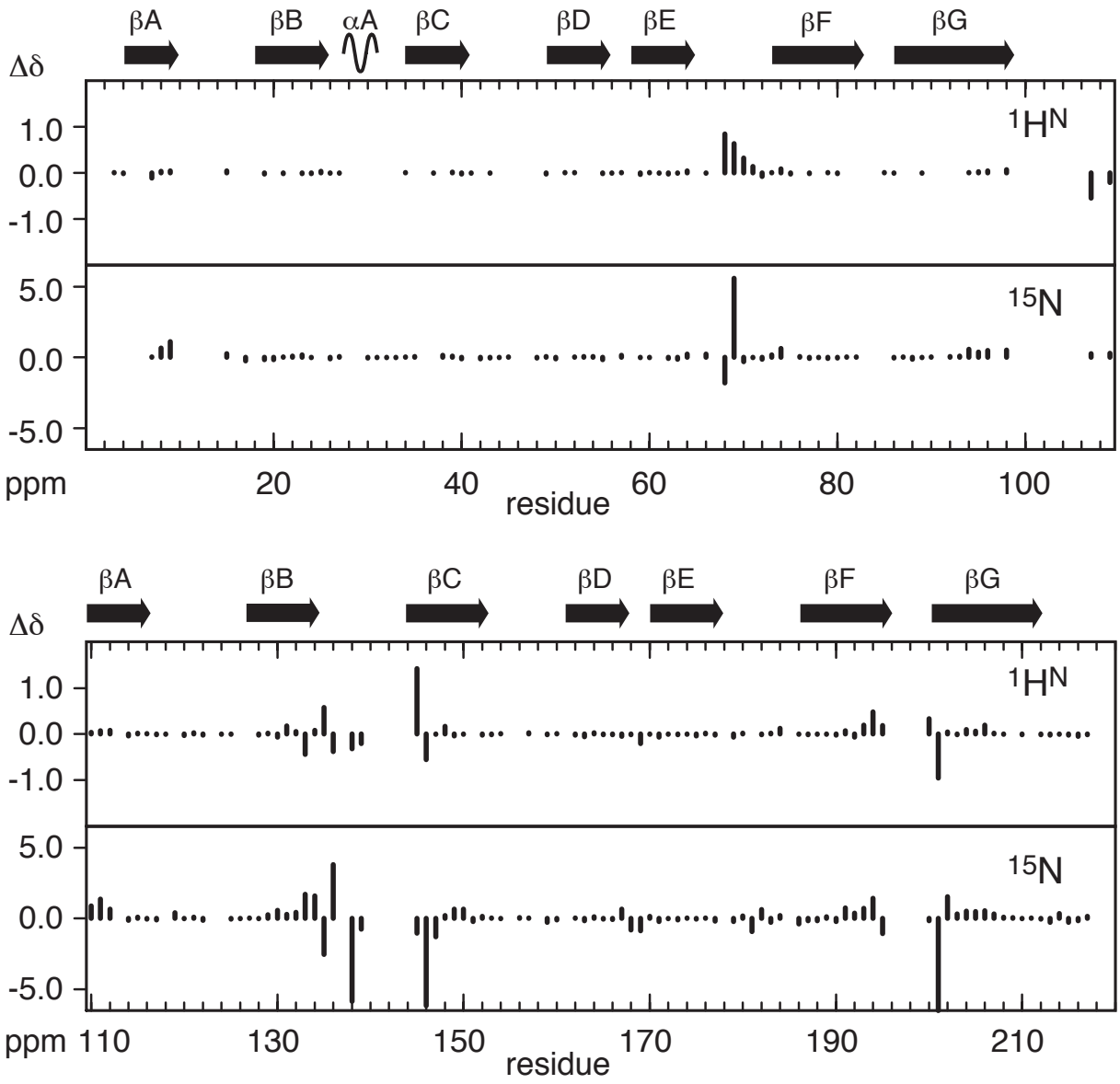

Figure S1C: Shift differences between monomeric, calcium-free ECAD12 (1.0 mM) and monomeric, calcium-bound ECAD12 (0.4 mM).

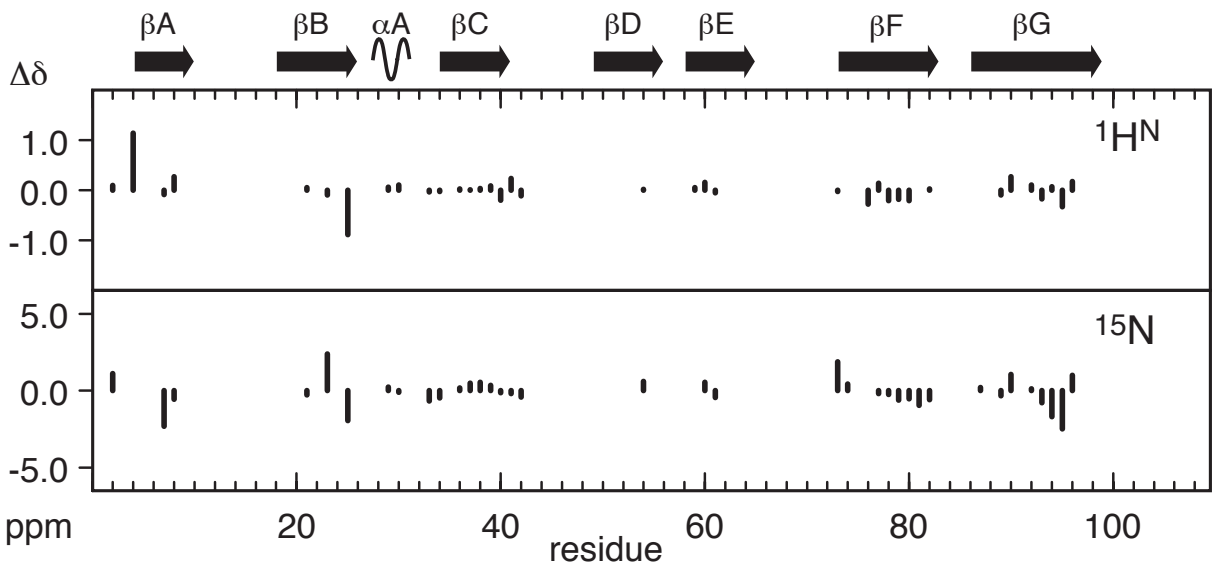

Figure S1D: Chemical shift differences between calcium-bound, associated ECAD12 (0.4 mM) and calcium-bound, monomeric ECAD12 (0.4 mM). No chemical shift differences between monomeric and associated form could be detected beyond residue number 100, i.e. for residues outside of the CAD1 domain.