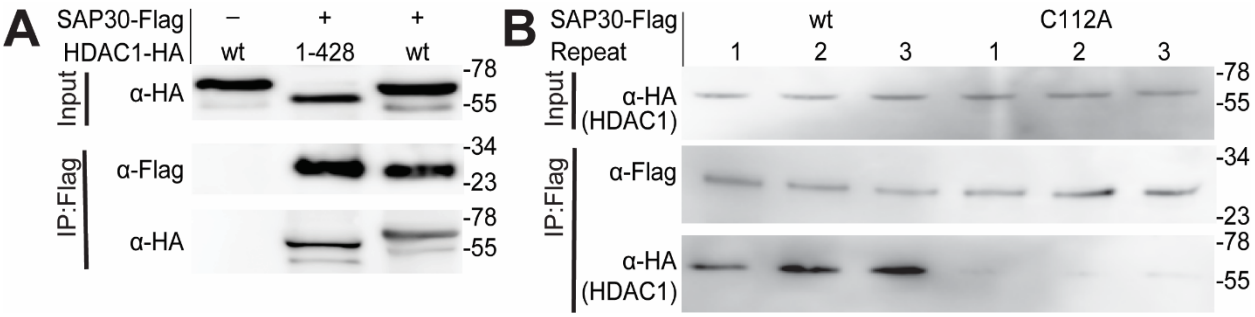
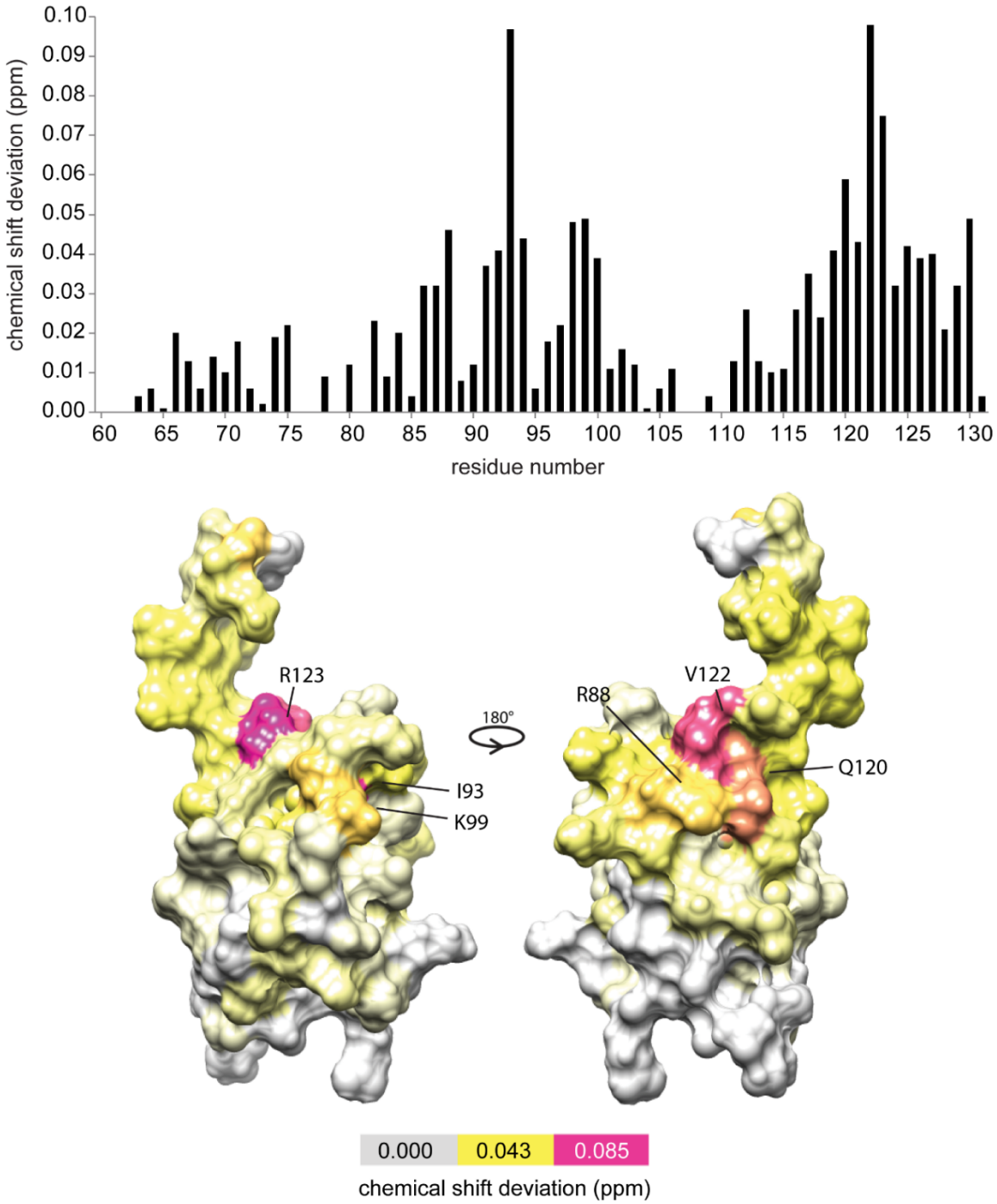
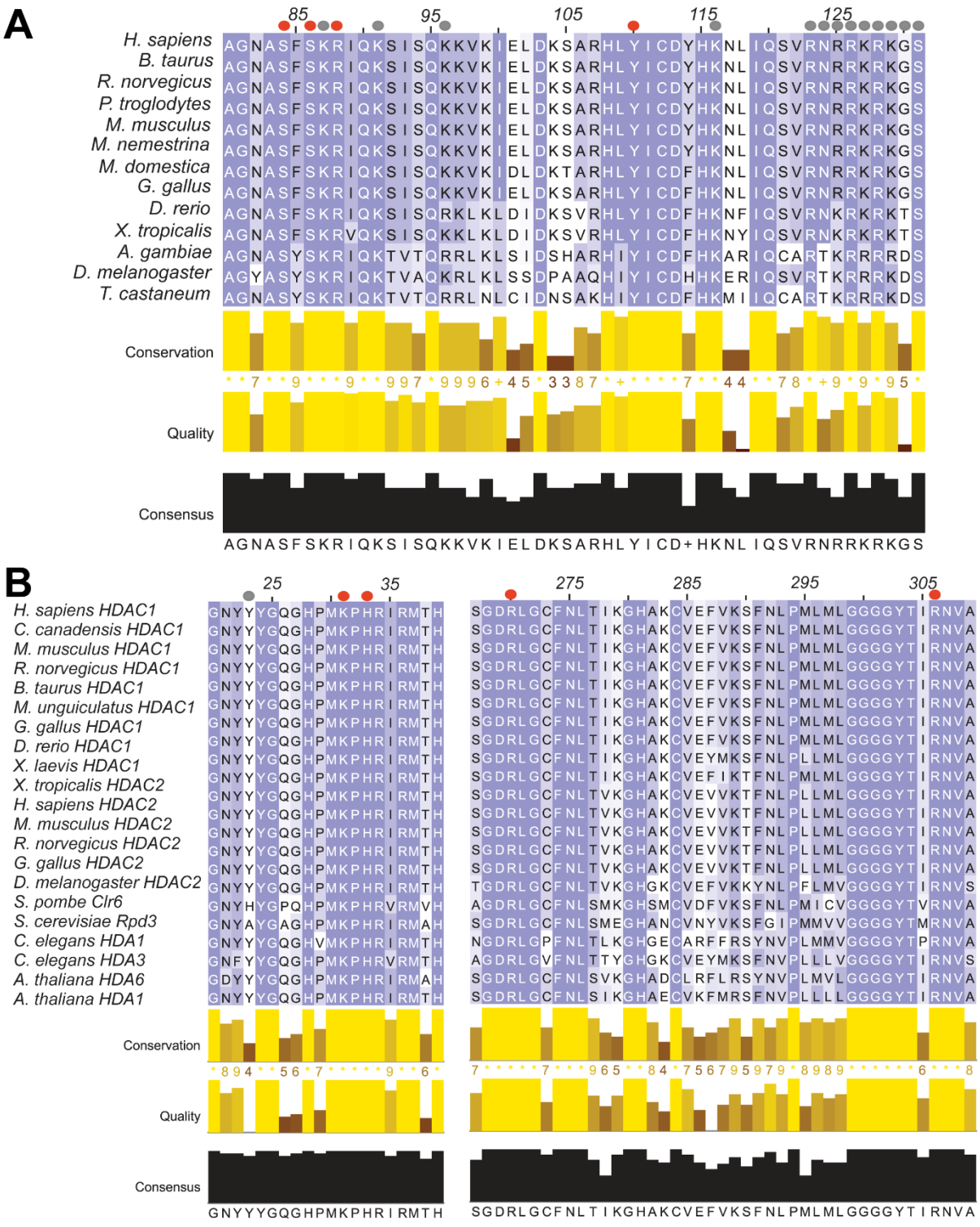


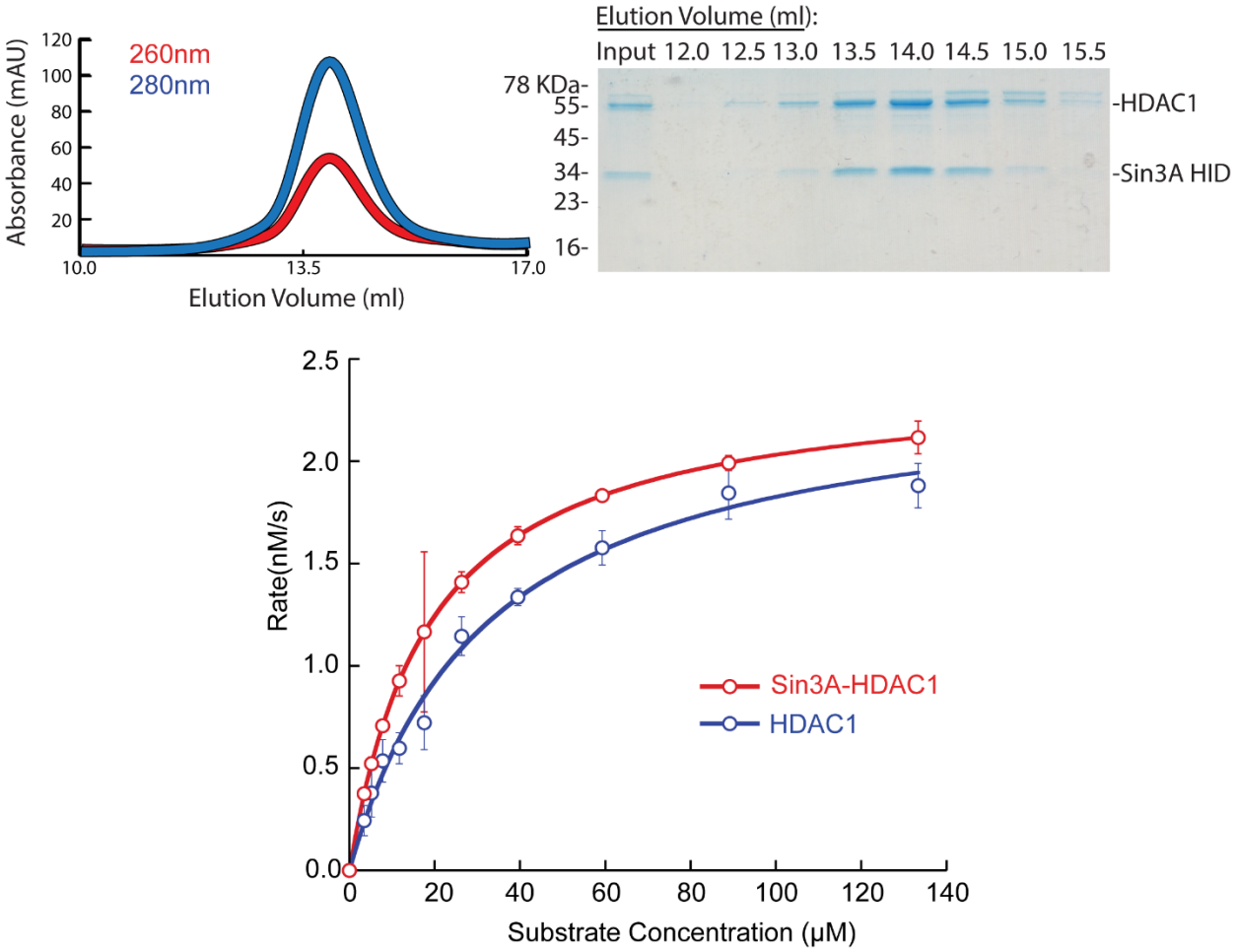
Supplementary Figure S1. (**A**) Co-IP of full-length (lanes designated 'wt') and a 'tail-less' (aa 1-428) construct of HA-tagged HDAC1 by Flag-tagged SAP30. (**B**) Immunoprecipitates of HA-tagged HDAC1 by Flag-tagged SAP30 wild-type (wt) and the C112A mutant used for deacetylase activity assays. Results of three independent experiments used to measure HDAC1 deacetylase activity (cf. Fig. 1C) are shown. In both panels, molecular weights (in KDa) are shown on the right-hand side of each blot.



Supporting Figure S2. Chemical shift deviations in ^{15}N-SAP30 ZnF upon titrating with 8 equivalents of $InsP_6$. The perturbations were calculated using the formula: $\Delta\delta_{H,N} = \sqrt{(((\Delta\delta_H)^2 + 0.04*(\Delta\delta_N)^2)/2)}$ and are graphed as a function of residue number (*top panel*). Two views of the SAP30 ZnF molecular surface with the chemical shift deviations mapped on to the surface of protein (*bottom panel*). The intermediate and high values in the color key correspond to $<\Delta\delta_{H,N}> + 1\sigma$ (yellow) and $<\Delta\delta_{H,N}> + 3\sigma$ (magenta), respectively, where $<\Delta\delta_{H,N}>$ is the average value and σ is the standard deviation. Colors are linearly interpolated to reflect the intermediate values.



Supporting Figure S3. Clustal Ω-guided multiple sequence alignments of (A) SAP30 ZnF and (B) HDAC1/2 orthologs (*bottom panel*). Residues are shaded by sequence conservation profiles as indicated by the substitution scores in the BLOSUM62 scoring matrix. Figures were generated using Jalview. Mutated residues are indicated by circles above the alignment (*gray circles*: mutations with little or no effect on activity; *red circles*: significant effect on activity).



Supporting Figure S4. Formation of a stable complex between Sin3 HID and HDAC1 as established by size exclusion chromatography and SDS-PAGE followed by Coomassie staining (*top panel*) and plots of Michealis-Menten kinetics measuring the deacetylase activity of HDAC1 in the absence or presence of an equimolar amount of Sin3A HID (*bottom panel*).