Figure S6. Alignments for regions surrounding the residues that coordinate IP_6 in hADAR2 are shown, with hADAR2 numbering indicated in blue. IP_6 coordinating residues for backbone interactions (red capitals) and side chain interactions (bold, red capitals) are indicated. The alignment was prepared with the entire catalytic domain as input, using GCG software (Wisconsin Package Version 10.3, Accelrys Inc., San Diego, CA). Pileup, using default parameters, was used to align the following sequences (accession number; amino acids aligned, start-end): ADAR1, human (NM_001111; 833-1226), mouse (AF052506; 756-1152), rat (U18942; 779-1175), Xenopus laevis (U88065; 879-1270), pufferfish (AAF69764; 790-1194), zebrafish (NM_131596; 952-1382); ADAR2, human (NM_001112; 317-701), rat (NP_037026; 317-711), mouse (AF403106; 317-701), chicken (AF403119; 318-701), pufferfish (AF533143; 309-694), zebrafish (AF403113; 305-689), *D. melanogaster* (AF208535; 252-632), *C. elegans* (AF051275; 113-495); the entire open-reading frame for ADAT1, human (AF125188), mouse (NM_013925), chicken (NM_001012779), *Xenopus tropicalis* (CR762003), *D. melanogaster* (AF192530). This multiple sequence alignment was used as input to the program HmmerBuild to create a profile hidden Markov model (HMM) of the consensus (global alignment setting). The HMM file was then used with the program HmmerAlign to add the following to the alignment *S. cerevisiae* ADAT1, (AJ007297; 11-401), *C. elegans adr-1c* (AY150815; 617-964) and human ADAR3 (AF034837; 355-739). The alignment was optimized by selective manual manipulation using the program Seaview (*S18*). Manual manipulation was guided by alignments of the subgroups alone. Sequences diverge considerably in the region surrounding K483; the alignment shown was chosen because the conserved lysine of various subfamilies is aligned with K483 of hADAR2.