S2 Fig. Full-length alignment of PexRD54 and PexRD54-like proteins from Fig 1. A 482 amino acid alignment (MUSCLE (25)) of the full-length PexRD54 and PexRD54-like proteins from Fig 1. The proteins are listed in the same order (top-bottom) as Fig 1, with the numeric ID (1-20) corresponding to the key and to Table S1. The predicted WY domain boundaries were mapped based on the PiPexRD54 sequence (WY-1 – WY-5) (18) and identification of key residues based on the WY domain MEME (WY-6) (16). The RxLR-dEER motif is noted, as is the location of the PexRD54 C-terminal AIM site.