S1 Fig. Distribution of Q, N, and P residues in MUT-16 orthologs.
The frequency of Q, N, and P residues were analyzed in C. elegans MUT-16 (WP:CE40347), C. briggsae MUT-16 (BP:CBP44329), C. remanei MUT-16 (RP:RP48608), and C. japonica MUT-16 (JA:JA63728) proteins. Residues were counted in amino acid 100-mers, starting at position one, shifting 10 residues at a time, and displayed as stacked columns. Indicated residue positions are the mid-point of the 100-mer.