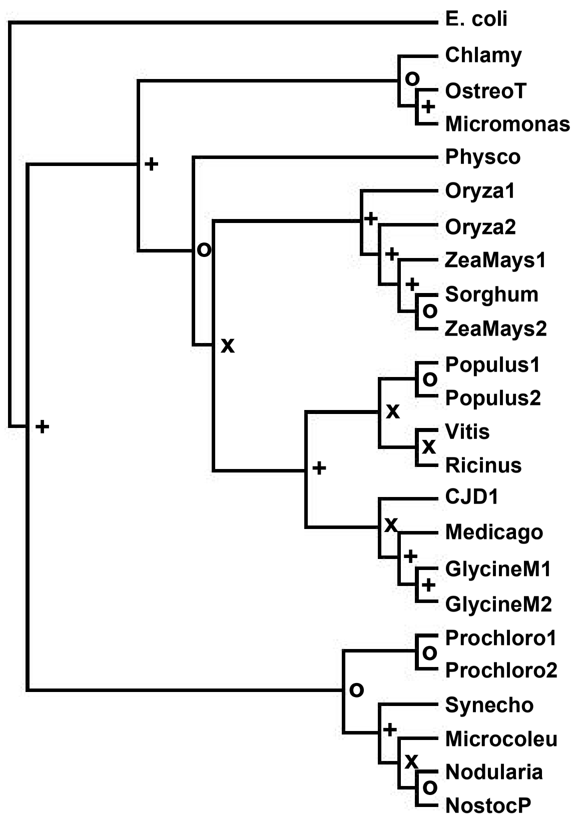

**Figure S1. Rooted tree indicating the relatedness of predicted CJD1 protein homologues in representative organisms.** The *E. coli* DNAJ protein was used as an outgroup. Boot strapping values >900 are marked by a plus sign, those between 500 and 900 are marked with an open circle and those under 500 by a cross. Protein sequences in addition to those already described in Figure 2 (GenBank Protein ID): E.coli, *Escherichia coli*, 16128009; Micromonas, *Micromonas pusilla* (RCC299), 255073349; Physco, *Physcomitrella patens*, 162675779; Oryza2, *Oryza sativa*,113622873; Populus2, *Populus trichocarpa*, 224123536; Sorghum, *Sorghum bicolor*, 242080423; Ricinus, *Ricinus communis*, 255561927; Medicago, *Medicago truncatula*, 217075548; GlycineM1, *Glycine max*, 255638094; Prochloro2, *Prochlorococcus marinus* (MIT9515), 123200338; Microcoleu, *Microcoleus chthonoplastes* (PCC7420), 254411043; Nodularia, *Nodularia spumigena* (CCY9414), 119513416; NostocP, *Nostoc punctiforme* (PCC7312), 186684227. Locus identifiers for ZeaMays2 and GlycineM2 are GRMZM2G050118 and Glyma03g41110, respectively.