



These figures show counts of protein gene matches to genomes. tBLASTn is used to match query proteomes to target genomes. Figures A show matches at significance level $p \leq 1e-10$, while figures B have match significance of $p \leq 1e-3$. Figure A1 counts full match regions, while A1 counts all match parts (HSPs), as do figures B1 and B2. Target genomes are twelve *Drosophila* species (Dmel .. Dgri), the insect *Anopheles gambia* (Agam), the crustacean *Daphnia pulex* (Dpulx), and *C. elegans* (Cele). Note that Dmel, Agam, and Cele are used as both query proteomes and target genomes. Counts include many duplicate matches, to different as well as same genome locations.