

Table 1. Numbers of distinct gene families versus numbers of predicted genes and their duplicated copies in *H. influenzae*, *S. cerevisiae*, *C. elegans*, and *D. melanogaster*. Row one shows the total number of genes in each species. Row two shows the total number of all genes in each genome that appear to have arisen by gene duplication. Row three is the total number of distinct gene families for each genome. Each proteome was compared to itself using the same parameters as described in (63).

	<i>H. influenzae</i>	<i>S. cerevisiae</i>	<i>C. elegans</i>	<i>D. melanogaster</i>
Total no. of predicted genes	1709	6241	18424	13601
No. of genes duplicated	284	1858	8971	5536
Total no. of distinct families	1425	4383	9453	8065