

	<i>E. coli</i>			<i>S. cerevisiae</i>		
	Metabolic	Other	All	Metabolic	Other	All
COG	98.7%	76.8%	81.3%	92.1%	31.3%	46.7%
KEGG	99.7%	97.6%	98.0%	96.8%	88.0%	89.0%
BLAST	98.7%	98.9%	99.2%	98.7%	94.3%	94.9%

Gene coverage of different orthology datasets. The table shows fraction of metabolic, non-metabolic (other) and all genes of *E. coli* and *S. cerevisiae* genomes covered by COGs, KEGG-based orthology dataset (best bi-directional hits) and BLAST-based dataset.