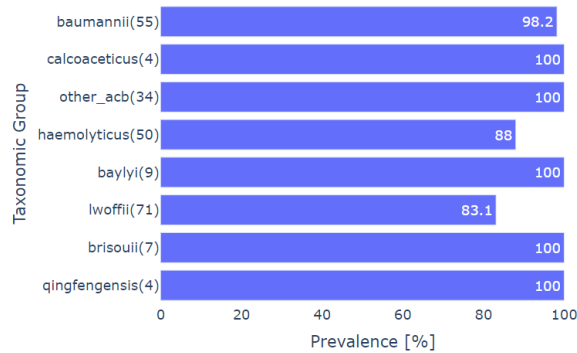
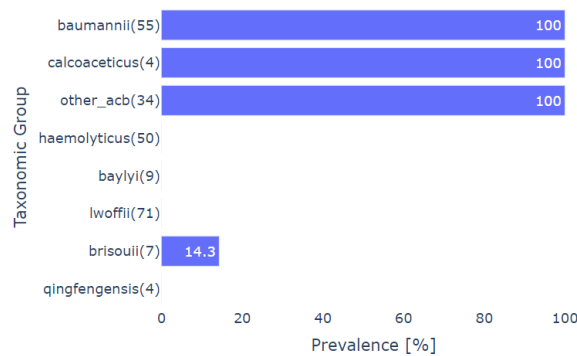


A Ortho-Family: HOG135.fa



Predicted SCL class [GN]:	PER
This class % across HOG:	98.65
KEGG KO(s):	K00117
KEGG Description(s):	gcd; quinoprotein glucose dehydrogenase [EC:1.1.5.2]
COG ID:	COG4993
COG Letter:	G
COG Description:	Glucose dehydrogenase
VIR Factor Hit ID:	N/A
VIR evalue:	N/A
VIR Description	N/A

B Ortho-Family: HOG3408.fa



Predicted SCL class [GN]:	IMB
This class % across HOG:	16.18
KEGG KO(s):	N/A
KEGG Description(s):	N/A
COG ID:	COG2133
COG Letter:	G
COG Description:	Glucose/arabinose dehydrogenase, beta-propeller fold
VIR Factor Hit ID:	N/A
VIR evalue:	N/A
VIR Description	N/A

Supplementary Figure F3: Abundance of the two glucose dehydrogenase encoding genes in *A. baumannii* ATCC 19606. The abundance pattern and annotations of the almost ubiquitously present membrane-bound *gdhA* (WP_001075590.1). B) The abundance pattern and annotations of the soluble *gdhB* (WP_001032867.1). This gene is, with a sole exception, confined to the ACB clade. The plots were derived from Aci-Dash (<https://aci-dash.ingress.rancher.computational.bio>)