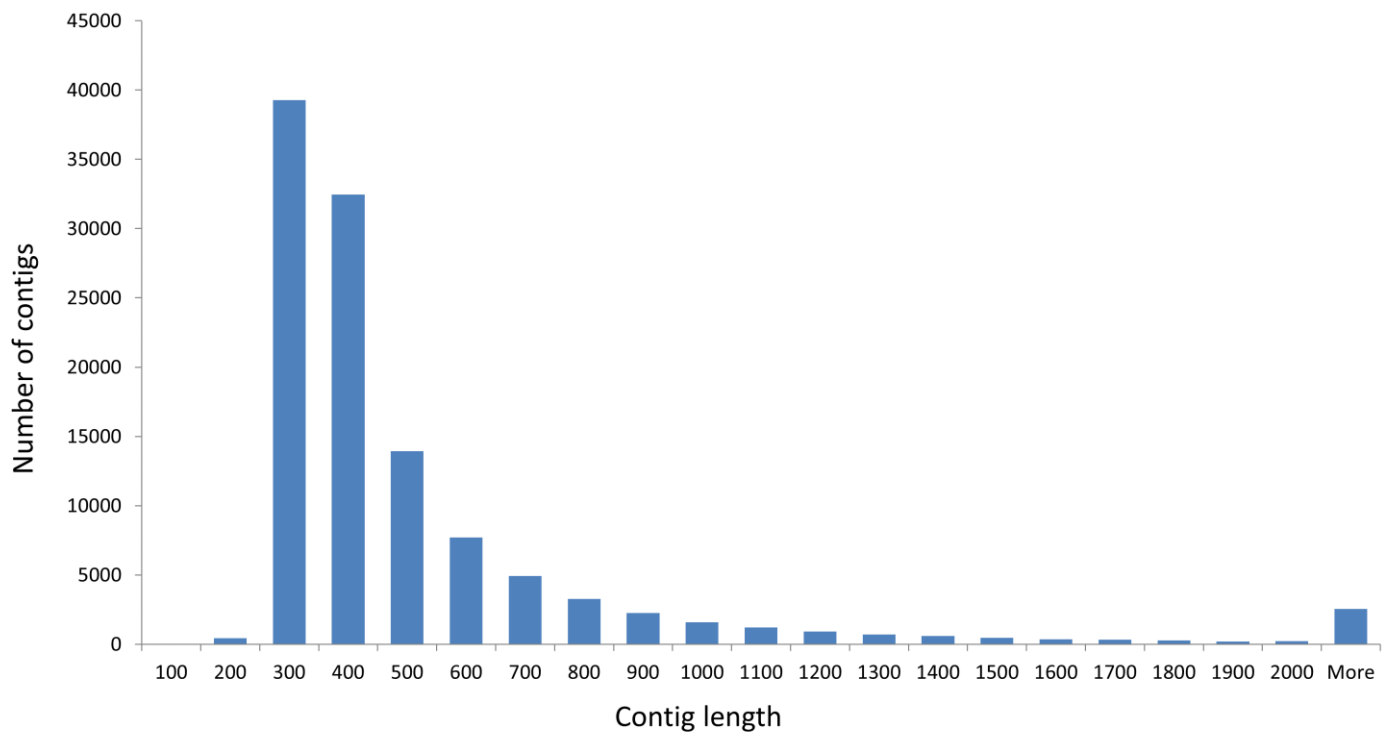
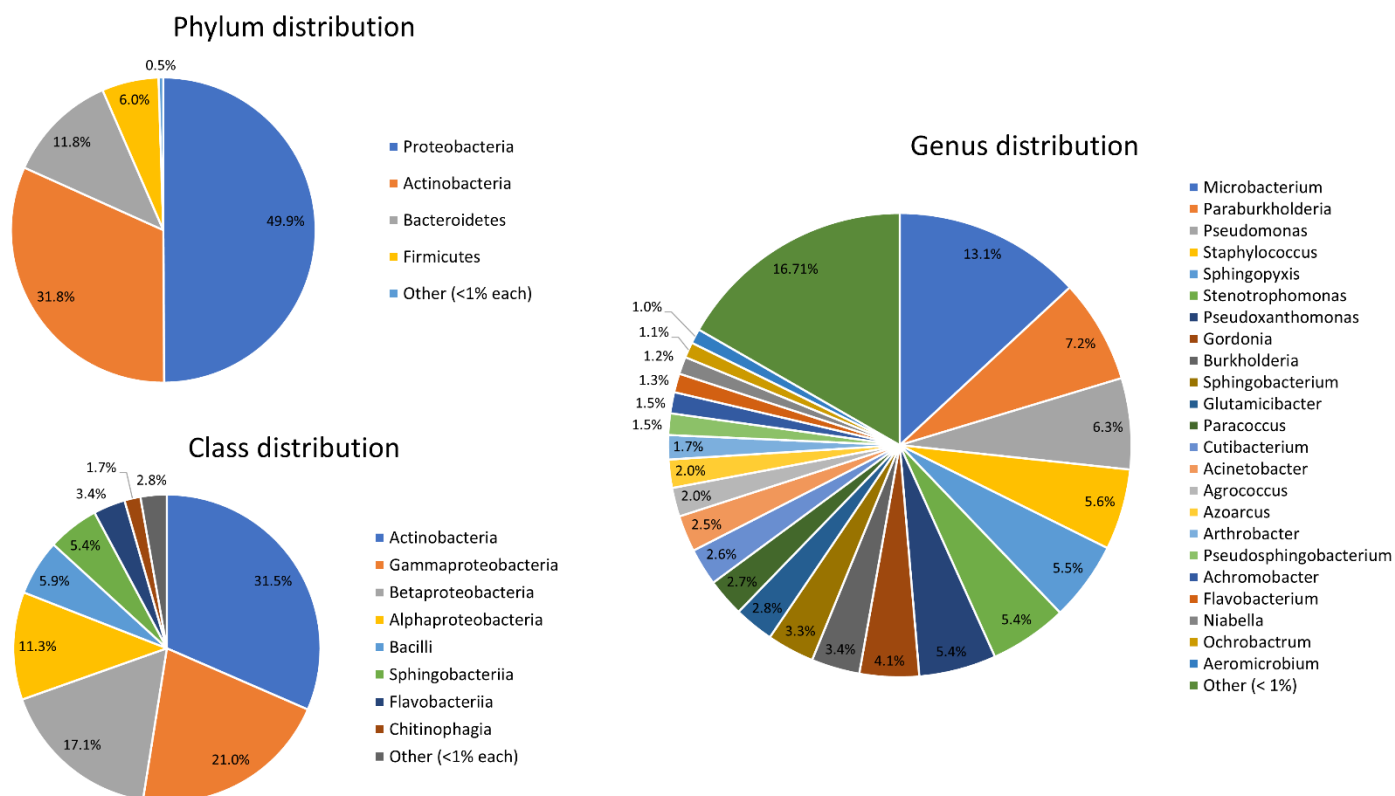


Antimicrobial activity and carbohydrate metabolism in the bacterial metagenome of the soil-living invertebrate *Folsomia candida*

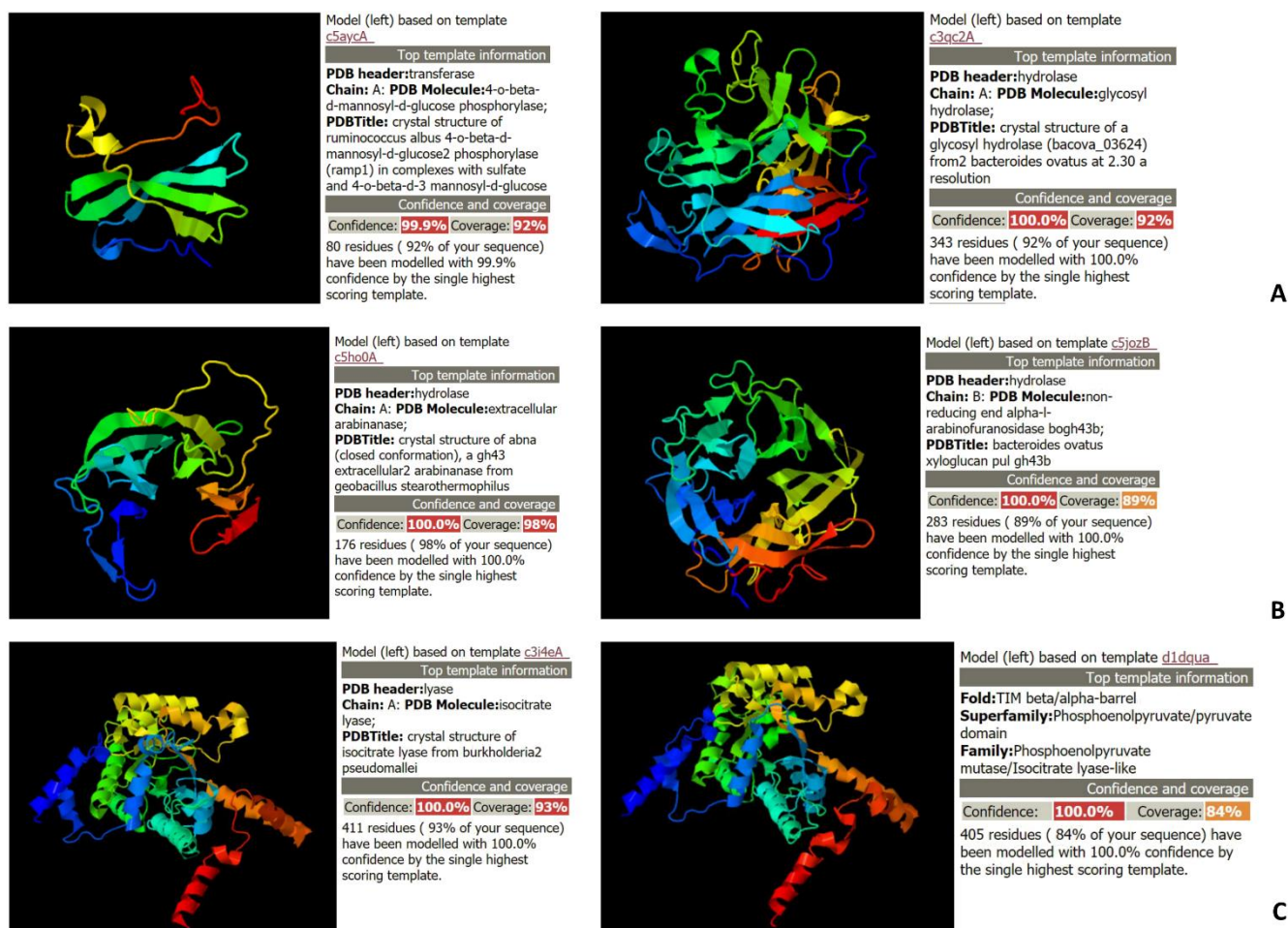
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Supplementary Figure 1. Contig length distribution.



Supplementary Figure 2. Identified taxonomic groups at the phylum, class and genus level.



Supplementary Figure 4. Predicted protein structures of the top three reciprocal blast hits between the metagenome and the genome of *F. candida*, corresponding to a glycosidase (A), an arabinosidase (B), an isocitrate lyase (C). The predicted structures of the microbial genes are on the left, the predicted proteins of the springtail are on the right.

Supplementary Table 1. Summary of antiSMASH results

Cluster type	Number of contigs
Arylpolyene	1
Bacteriocin	4
Cf_fatty_acid	14
Cf_fatty_acid -Cf_saccharide	1
Cf_putative	96
Cf_saccharide	18
Cf_saccharide-Cf_fatty_acid	1
Ectoine	1
Hserlactone	3
Nrps	13
Nrps-Arylpolyene	1
Other	2
Siderophore	2
T1pks	1
T1pks-Nrps	1
T3pks	1
T3pks-Cf_saccharide	1
Terpene	5
TOTAL	166

For each type of secondary metabolite cluster, the number of contigs in *F. candida*'s metagenome in which the cluster was detected is indicated. Cf indicates a putative cluster identified with the ClusterFinder algorithm. Pks = polyketide synthase. Nrps = non-ribosomal peptide synthetase. The complete output of the antiSMASH analysis is given in Supplementary File 3.