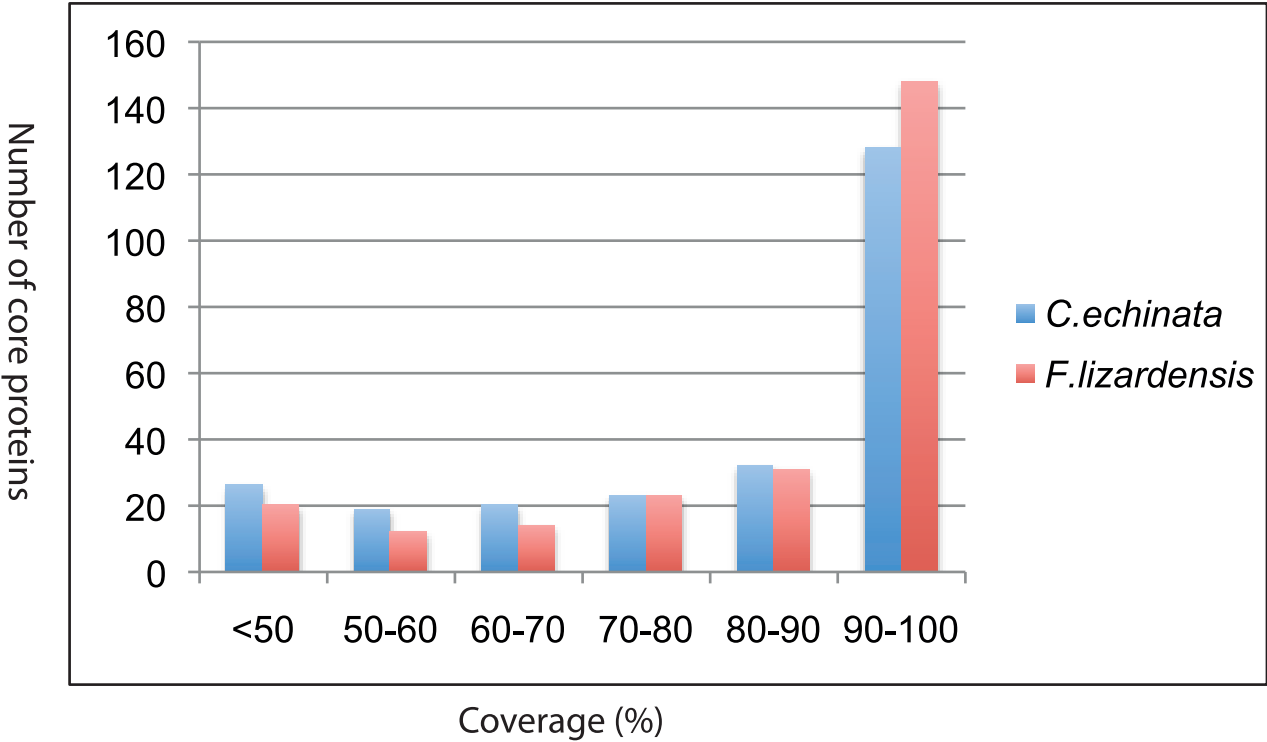




Coverage of 248 core eukaryotic proteins in the *C.echinata* and *F.lizardensis* transcriptomes. The human set of the core protein dataset was used for the analysis.