To find significantly overrepresented GO terms for the proteins in our dataset, we used DAVID1. For a GO term to be considered significantly overrepresented, we set a Bonferroni adjusted p-value cut off of < 0.05. Visualization of the GO terms as dotplots was carried out in R.



S1 Fig. A dotplot showing significantly overrepresented GO terms (MF - Molecular Function, CC- Cellular Component and BP - Biological Processes) for the transmembrane proteins with 3D structures. The dot sizes indicate the number of proteins within a GO term, the bigger the size of the dot the more the proteins in that ontology.

**References**

1. Huang, D. W. *et al.* DAVID Bioinformatics Resources: expanded annotation database and novel algorithms to better extract biology from large gene lists. *Nucleic Acids Res.* **35**, W169-175 (2007).