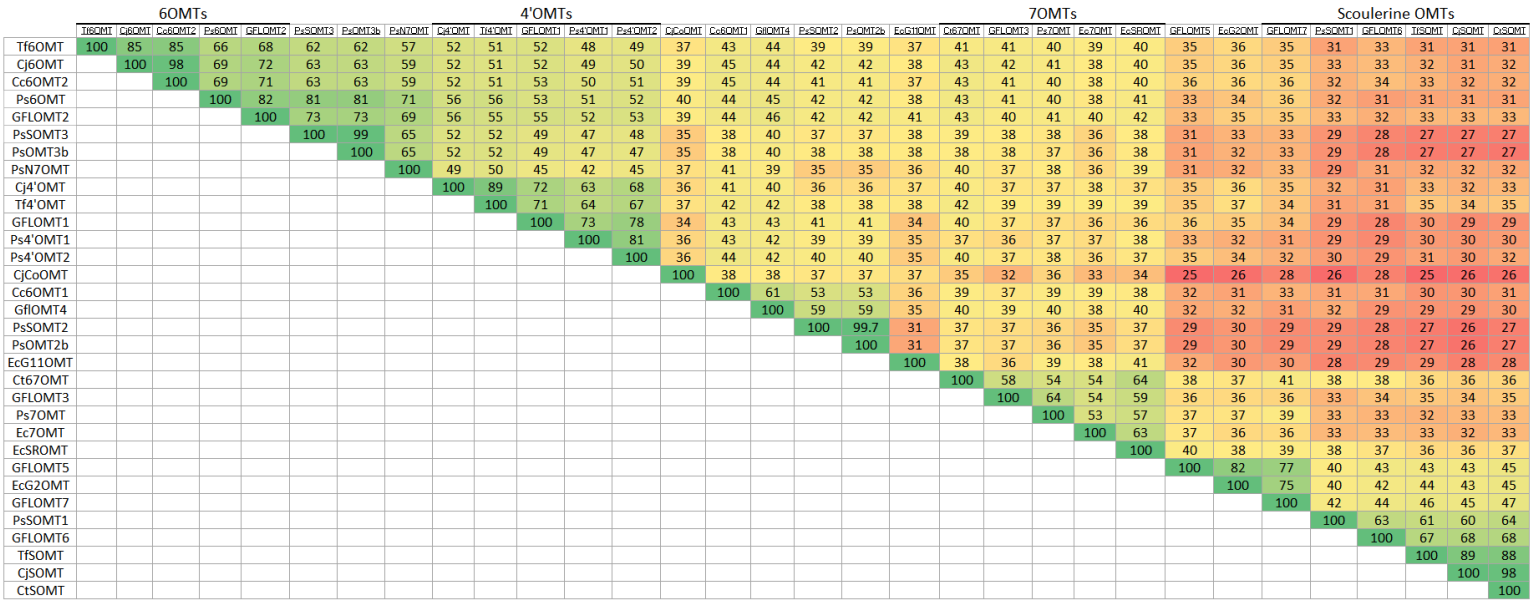

Supplementary Figure 1. Percent identity matrix for amino acid sequences of BIA *O*-methyltransferases characterized at the molecular level. Protein sequences were obtained by translation of nucleotide sequences deposited in Genbank (accession numbers provided in Supplementary Table 1) and aligned using Clustal Omega under default parameters (Chojnacki et al., 2017). Percentage identities are shaded with from green (maximum, 100%) to minimum (red, 25%).

Chojnacki, S., Cowley, A., Lee, J., Foix, A., and Lopez, R. (2017). Programmatic access to bioinformatics tools from EMBL-EBI update: 2017. *Nucleic Acids Res.* 45, W550–W553. doi:10.1093/nar/gkx273.