Virtual screening for the discovery of microbiome β -glucuronidase inhibitors to alleviate cancer drug toxicity

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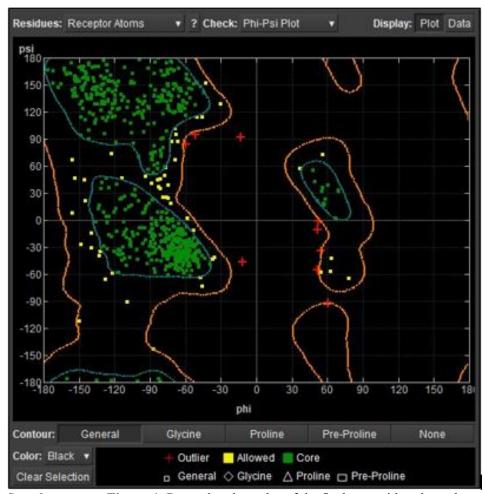
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Supplementary Figure 1. Ramachandran plot of the β -glucuronidase homology model to demonstrate the quality of the predicted 3-dimentioanl structure. The plot is generated using Molecular Operating Environment (MOE) computational software.