Protein name	Total Inhibitors	Top 10 inhibitors
CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase	6001	ZINC06507052 ZINC12503116 ZINC03794794 ZINC00020252 ZINC00057358 ZINC20444132 ZINC03830609 ZINC00057147 ZINC03830609 ZINC00057347
CDP-4-dehydro-6-deoxyglucose reductase	5922	ZINC03831425 ZINC08551105 ZINC08551107 ZINC03831427 ZINC03831426 ZINC03831428 ZINC03831426 ZINC03201893 ZINC08551106 ZINC08551106
4-hydroxy-3-methylbut-2-enyl diphosphate	5375	ZINC03831235 ZINC14879972 ZINC01612996 ZINC15668997 ZINC13523524 ZINC14879972 ZINC03874185 ZINC12504524 ZINC00643046 ZINC19702309

Table e. Top 10 hits (inhibitors) obtained after docking for CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase, CDP-4-dehydro-6-deoxyglucose reductase and 4-hydroxy-3-methylbut-2-enyl diphosphate reductase of *Salmonella enterica*

CONCLUSION

In the current study the consolidation of subtractive proteomics methodology, metabolic network reconstruction, structural prediction and docking has been performed to discover possible drug targets in *Salmonella enterica* to enhance the future treatment administration. As of late the act of incorporation of proteomics and bioinformatics information has turned into a promising tool to find novel drug targets. Database of Essential Genes (DEG) that comprises of the genes that are respected to shape useful premise of life was used. 10 key reactions of murB, rfbH, ascD, ddhD, rfbI, dapB, ispH, lytB genes and their inhibitors were conceded that can be utilized for the identification of the ADME/Tox properties, pharmacophore modelling and in experimental analysis so as to find potential drug targets of *Salmonella enterica* in future.

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