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An integrated computational approach of molecular dynamics simulations, receptor binding studies and pharmacophore mapping analysis in search of potent inhibitors against tuberculosis

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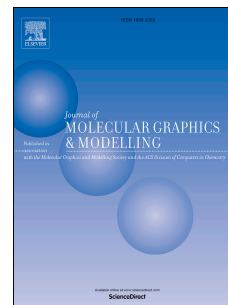
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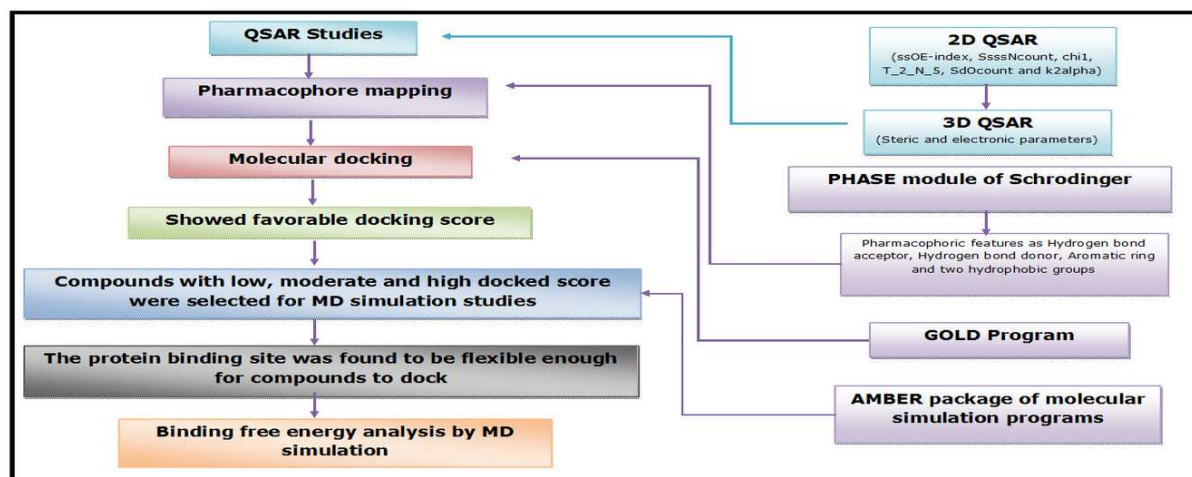
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