



## Computational studies on the structural variations of MAO-A and MAO-B inhibitors - An *in silico* docking approach

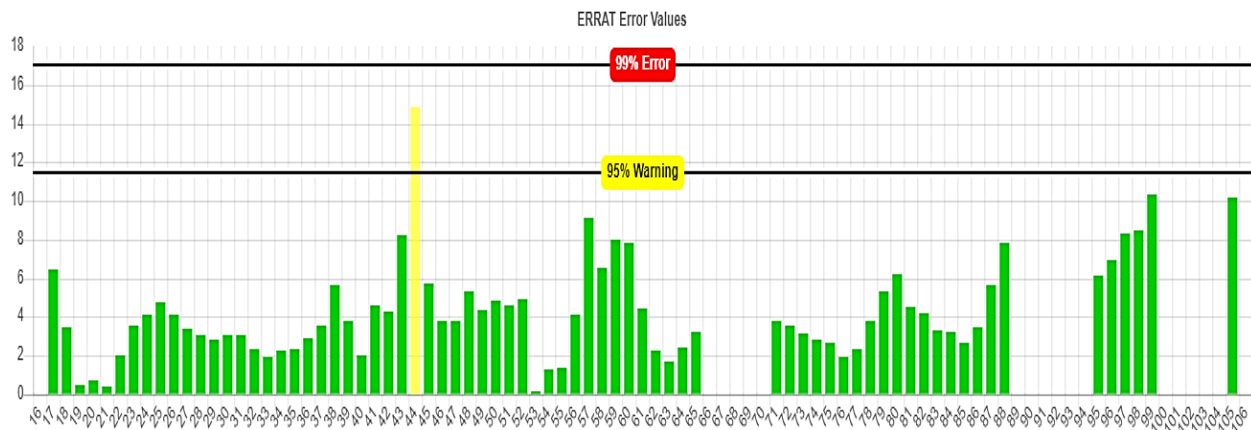
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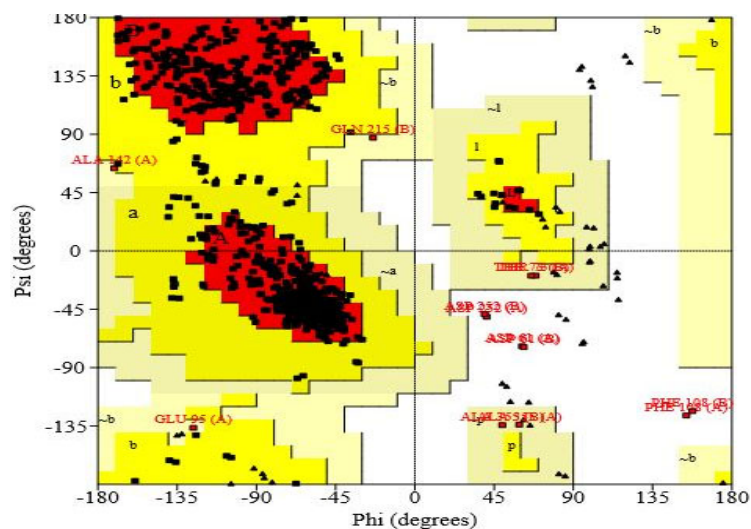
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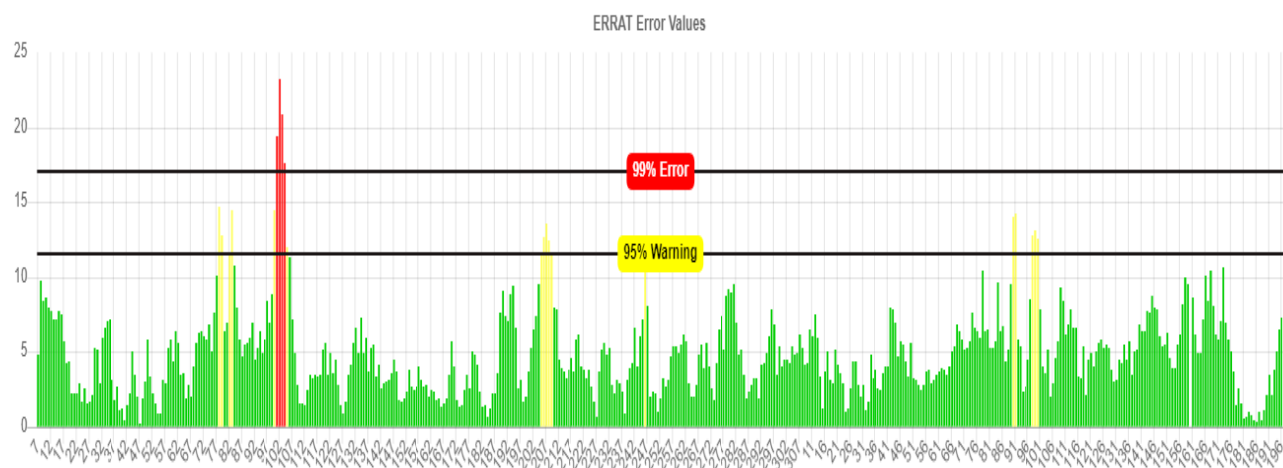
### Supplementary Data



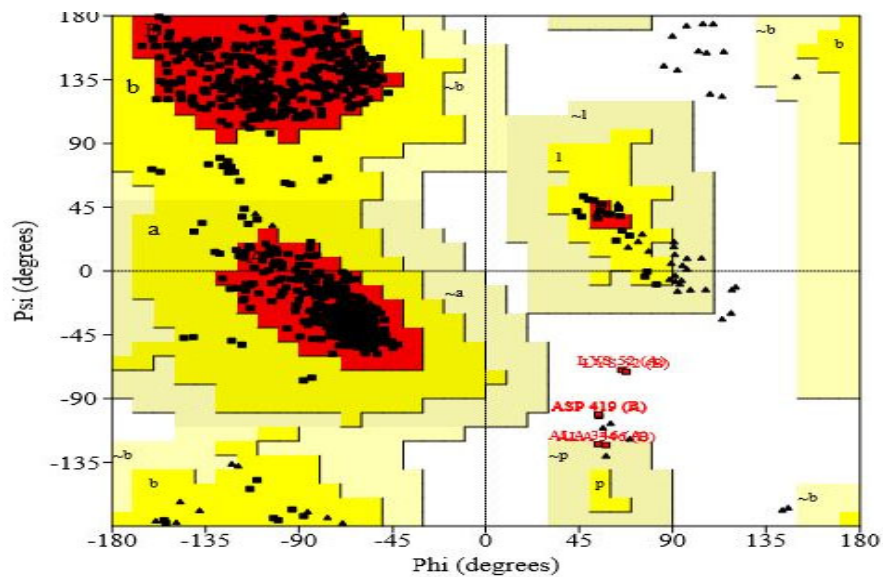
Suppl. Fig. 1 —Errat quality plot of 2BXR, where X-axis provides the amino acid residues and Y-axis it's quality or error percentage



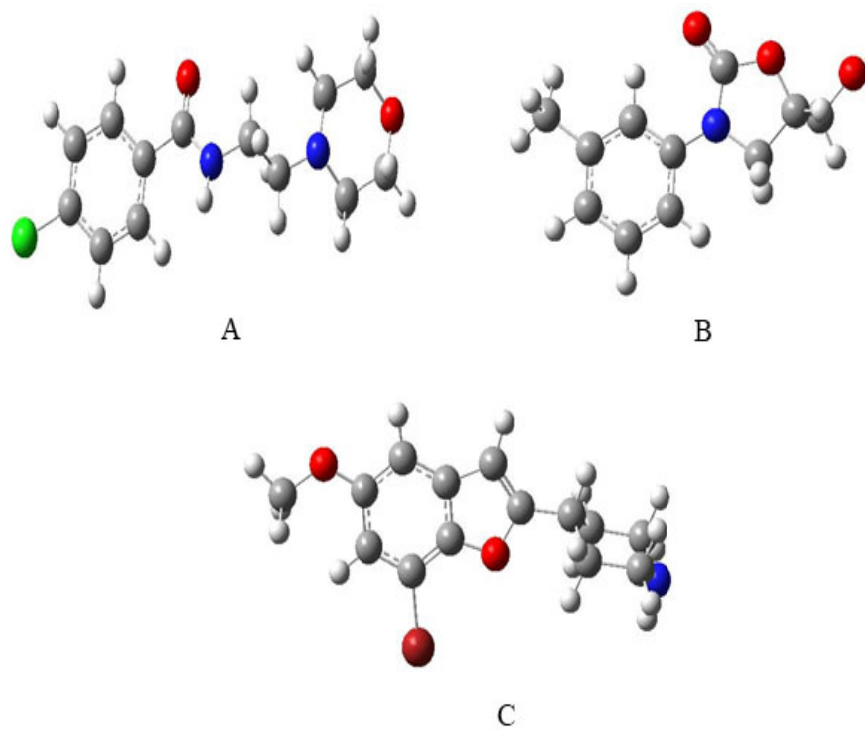
Suppl. Fig. 2 — Ramachandran plot of 2bxx provided by Procheck calculation, with 88.2% [A, B, L] of residues in favored area



Suppl. Fig. 3 — Errat quality plot of 2vz2, where X-axis provides the amino acid residues and Y-axis it's quality or error percentage.



Suppl. Fig. 4 — Ramachandran plot of 2vz2 provided by Procheck calculation, with 88.2% [A, B, L] of residues in the favored area.



Suppl. Fig. 5— Optimized images of (A) Moclobemide; (B) Toloxatone; and (C) Brofaromine