

# ***In Silico* Identification of Potential PD-L1 and VISTA Inhibitors in Ovarian Cancer: A Computational Approach Combining Virtual Screening and Molecular Dynamics Simulations**



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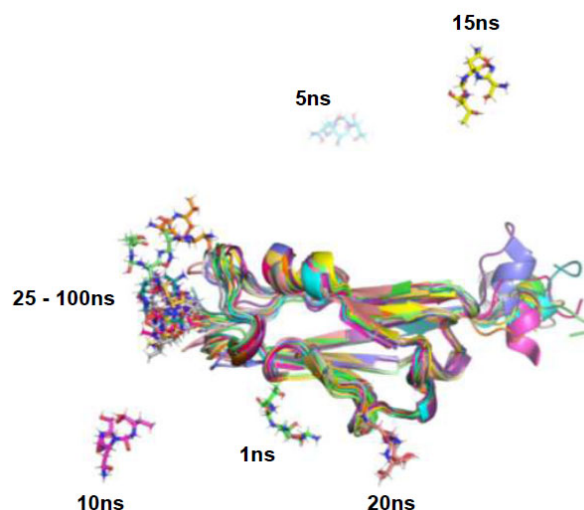
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Published: September 15, 2025

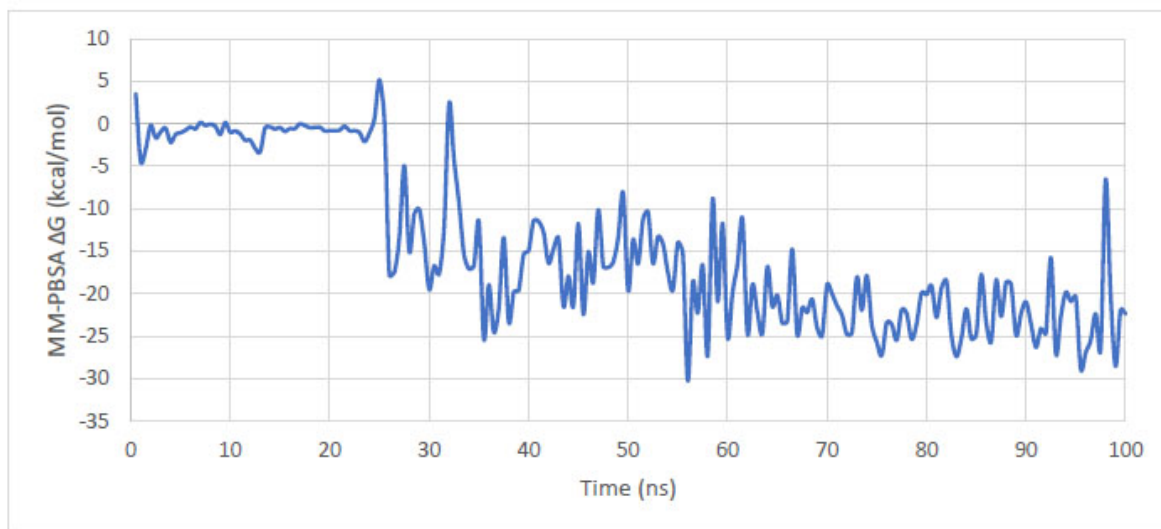
Cite as: Ahmadi N, Hakmi M, Gaouzi Z, Elhafidi N, IBRAHIMI A. *In Silico* Identification of Potential PD-L1 and VISTA Inhibitors in Ovarian Cancer: A Computational Approach Combining Virtual Screening and Molecular Dynamics Simulations. Open Bioinform J, 2025; 18: e18750362429534. <http://dx.doi.org/10.2174/0118750362429534250911103350>



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**Fig. (4).** Snapshots of the PD-L1/CA-170 complex from molecular dynamics simulation showing conformational evolution over time.



**Fig. (4).** Fluctuations of MM-PBSA Binding Free Energy as a Function of Time.

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