Supporting Information

Assessing Potential Inhibitors for SARS-CoV-2 Main Protease from Available Drugs using Free Energy Perturbation Simulations

Son Tung Ngo,[a,b*] Hung Minh Nguyen,[c,d] Le Thi Thuy Huong,[e,f] Pham Minh Quan,[e,f] Vi Khanh Truong,[g] Nguyen Thanh Tung,[h] Van V. Vu[i*]

[a]*Laboratory of Theoretical and Computational Biophysics, Ton Duc Thang University, Ho Chi Minh City 700000, Vietnam.*

[b]*Faculty of Applied Sciences, Ton Duc Thang University, Ho Chi Minh City 700000, Vietnam*

[c]*Center for Molecular Biology, Institute of Research and Development, Duy Tan University, Da Nang, 550000, Vietnam*

[d]*Faculty of Pharmacy, Duy Tan University, Da Nang, 550000, Vietnam*

[e]*Institute of Natural Products Chemistry, Vietnam Academy of Science and Technology, Hanoi 100000, Vietnam*

[f]*Graduate University of Science and Technology, Vietnam Academy of Science and Technology, Hanoi 100000, Vietnam*

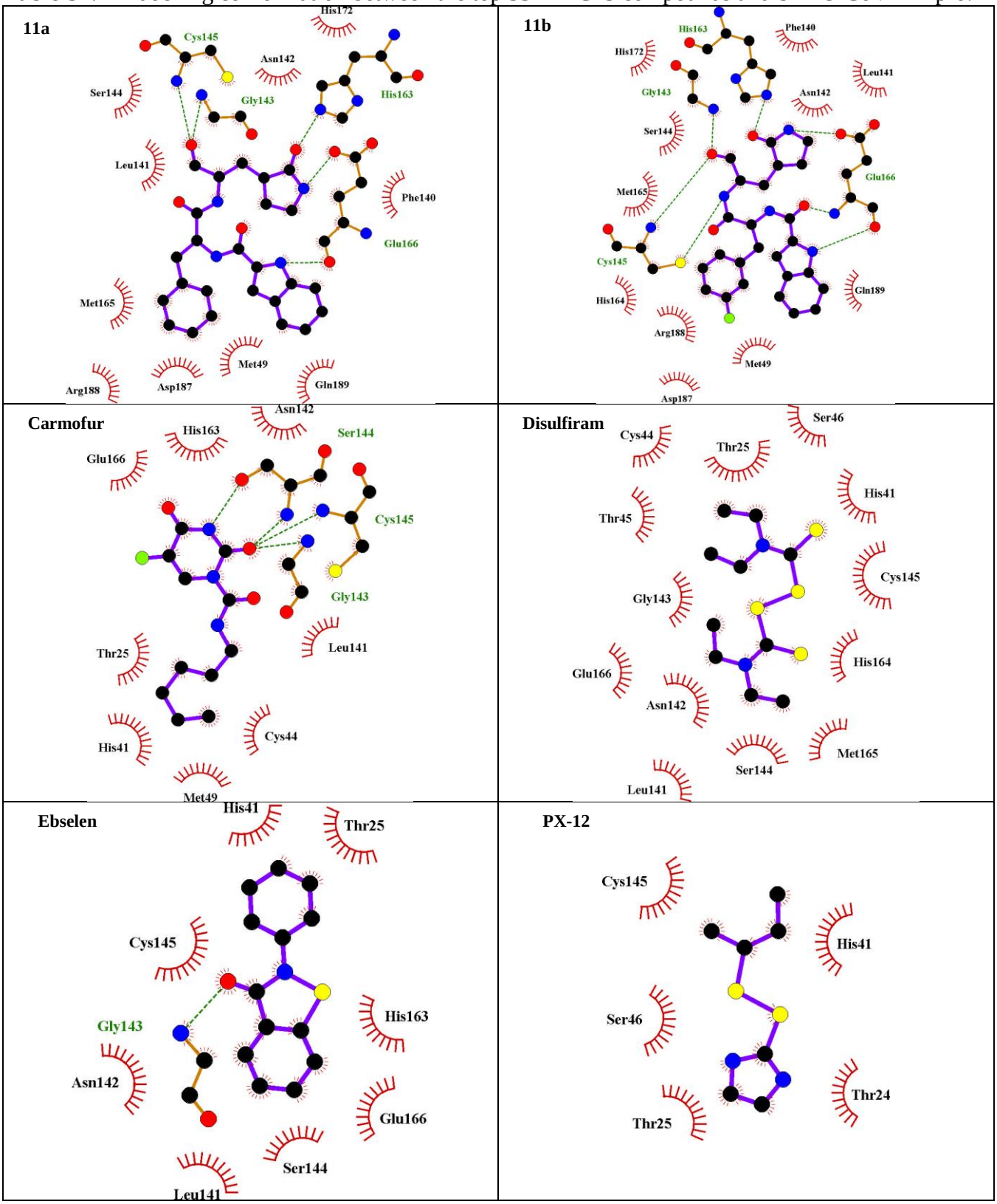
[g]*School of Science, RMIT University, GPO Box 2476, Melbourne 3001, Australia*

[h]*Institute of Materials Science, Vietnam Academy of Science and Technology, Hanoi 100000, Vietnam*

iNTT Hi-Tech Institute, Nguyen Tat Thanh University, Ho Chi Minh City 700000, Vietnam

*Email: ngosontung@tdtu.edu.vn; vanvu@ntt.edu.vn

Table S1. 2D docking conformation between the top 33 ZINC15 compounds and SARS-CoV-2 Mpro.



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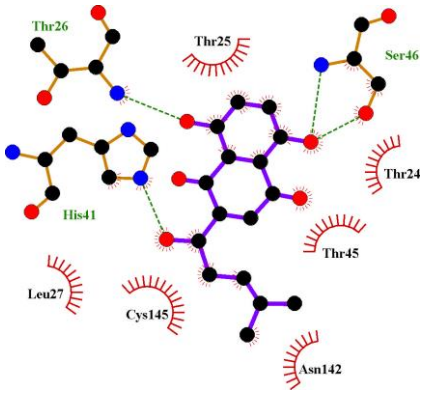

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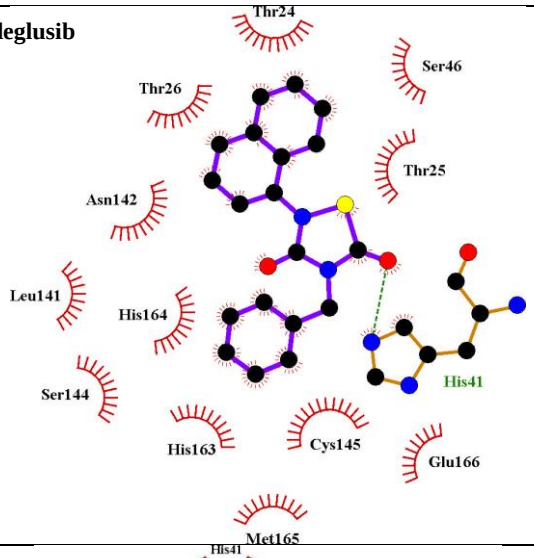

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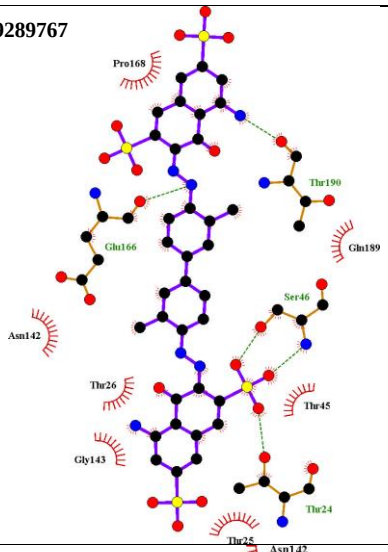

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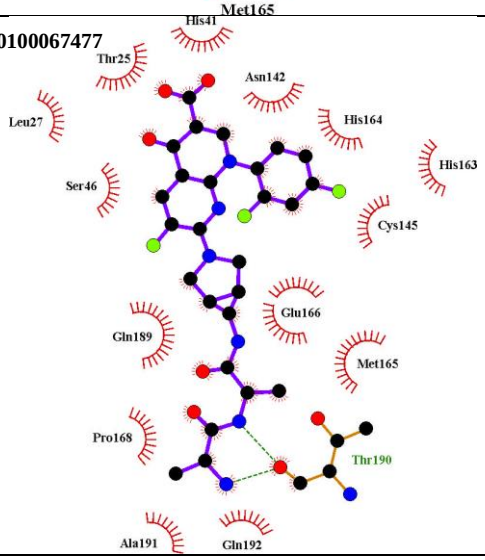

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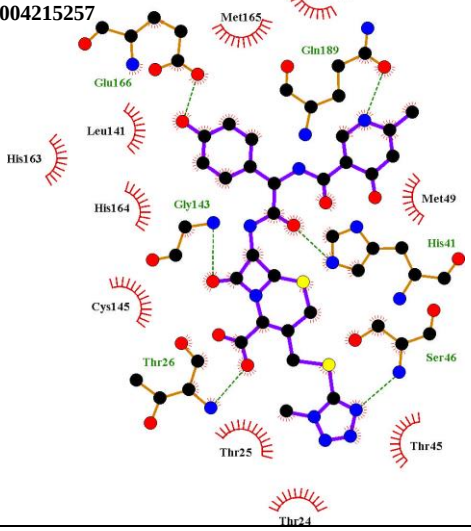

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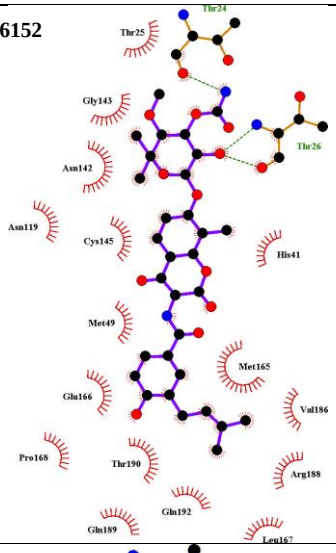

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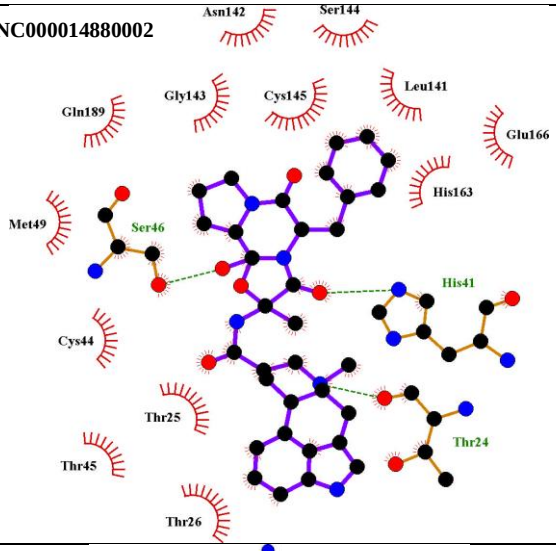

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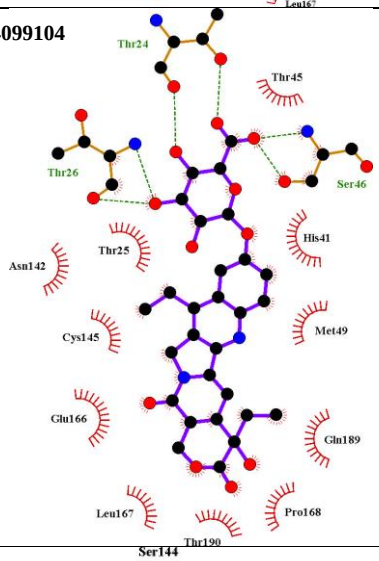

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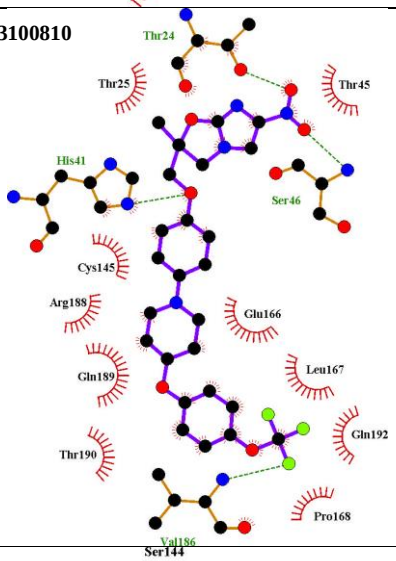

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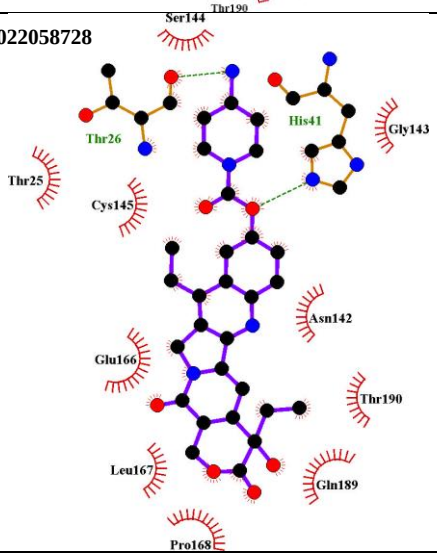

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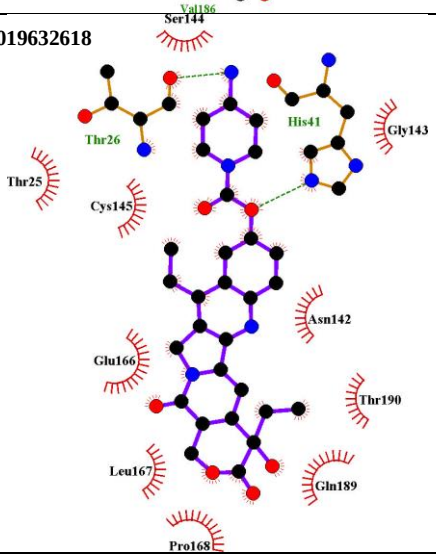

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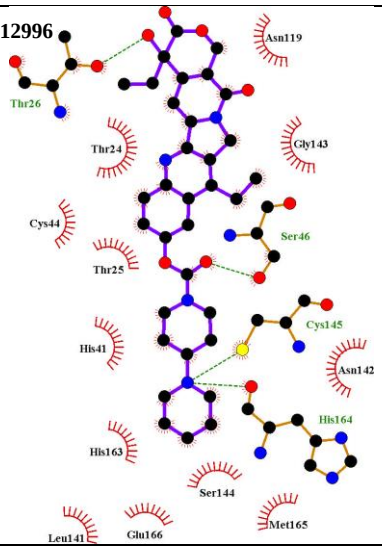

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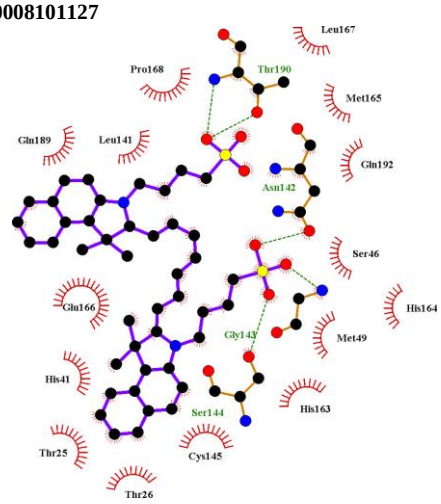

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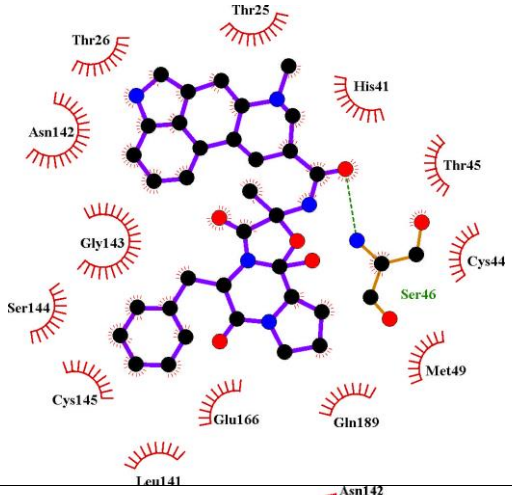

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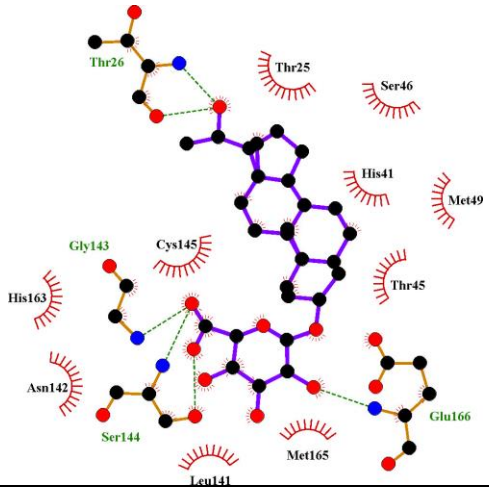

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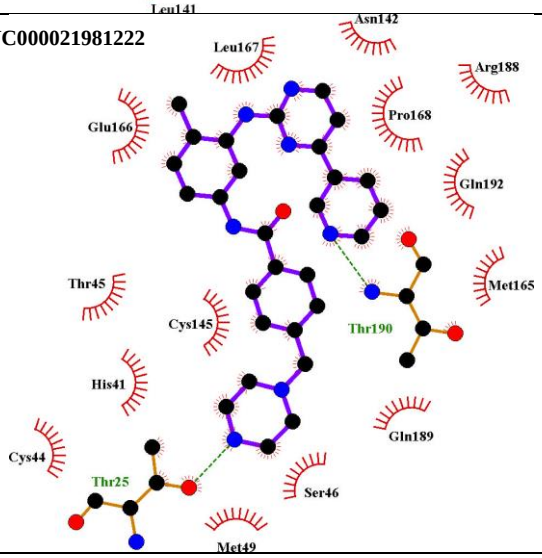

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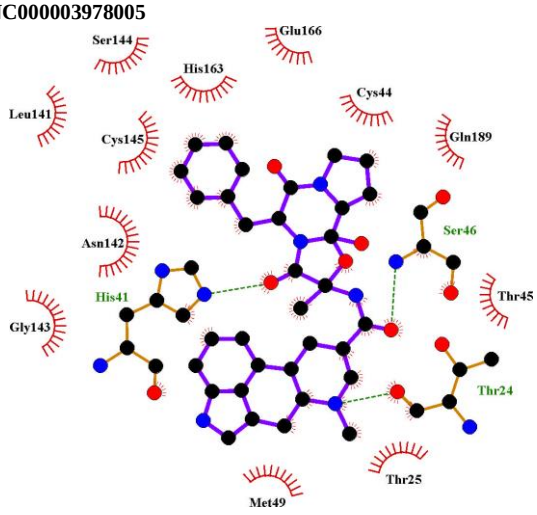

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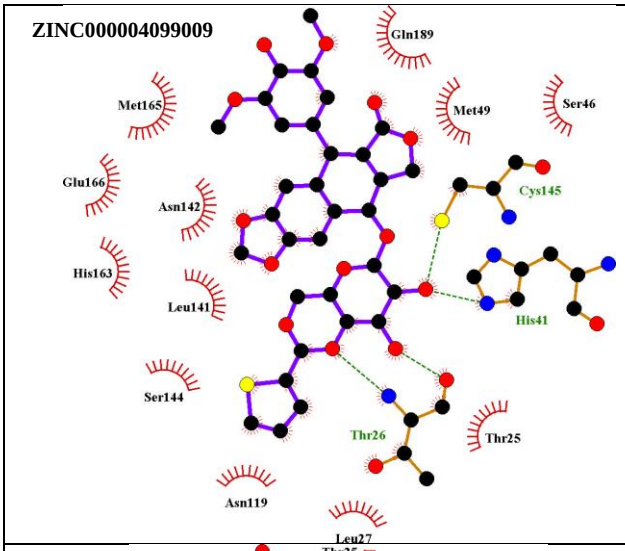

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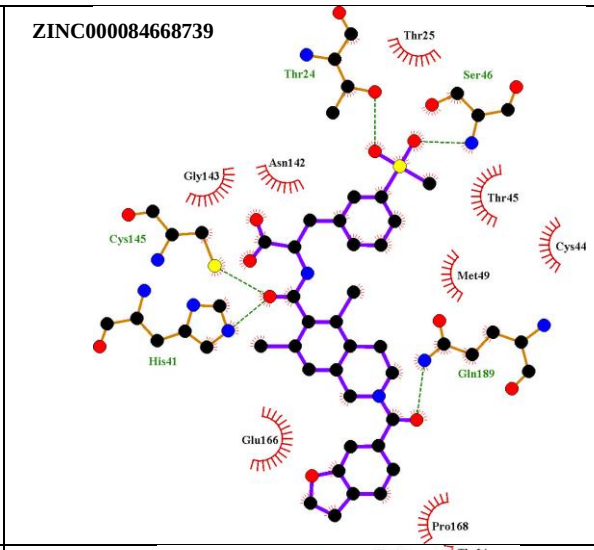

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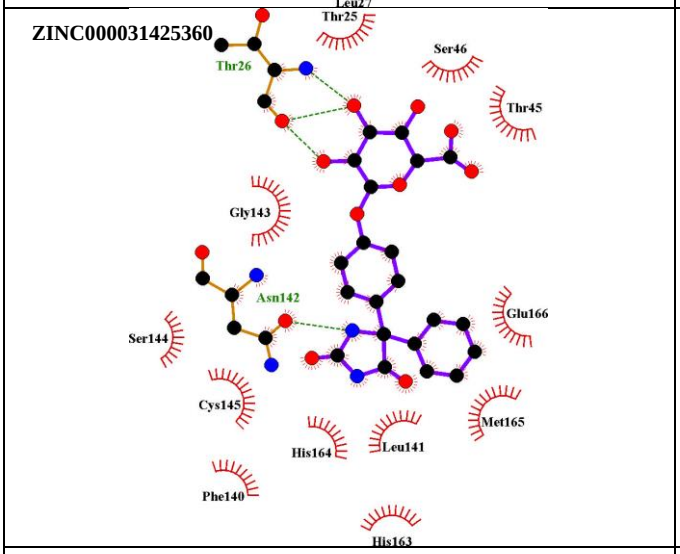

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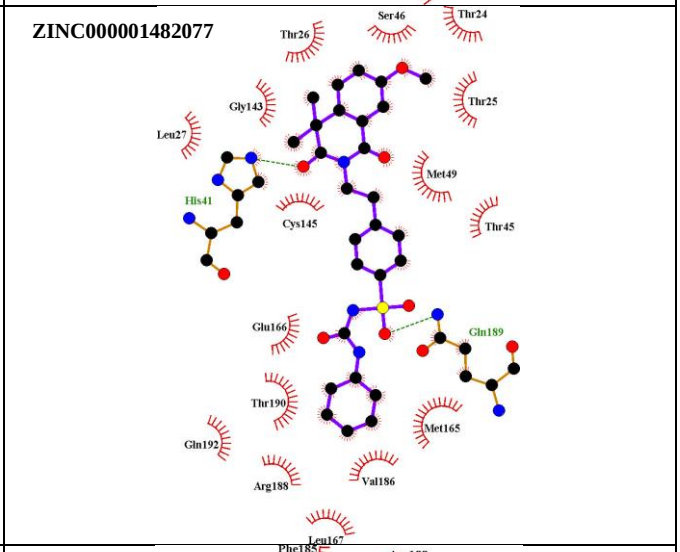

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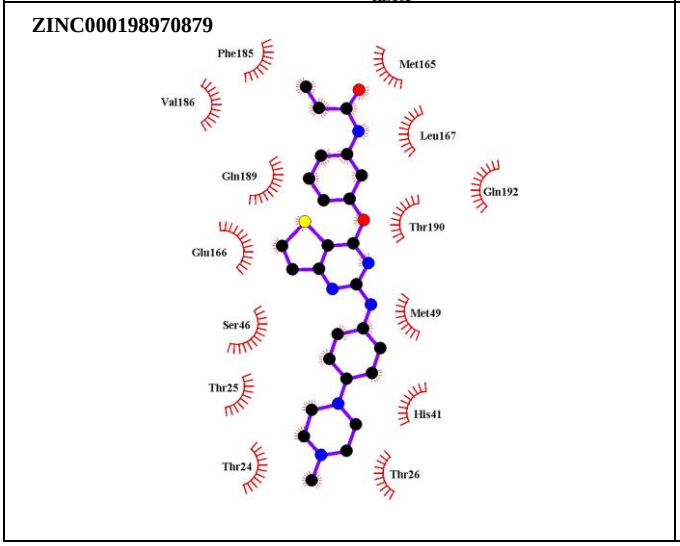

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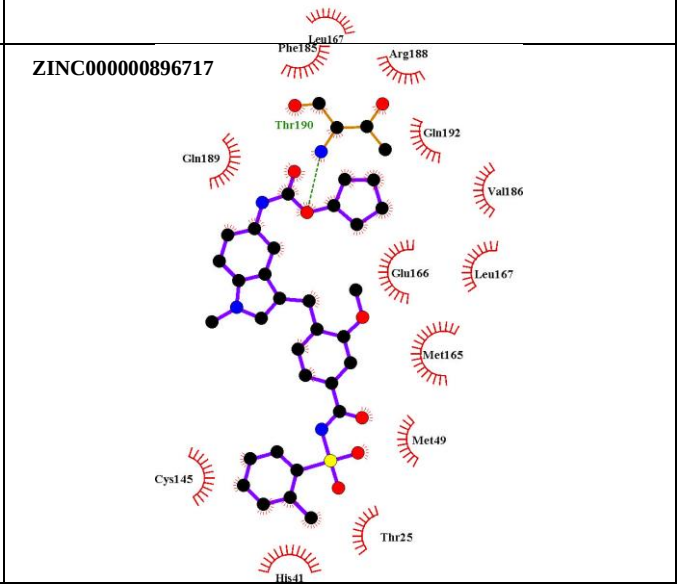

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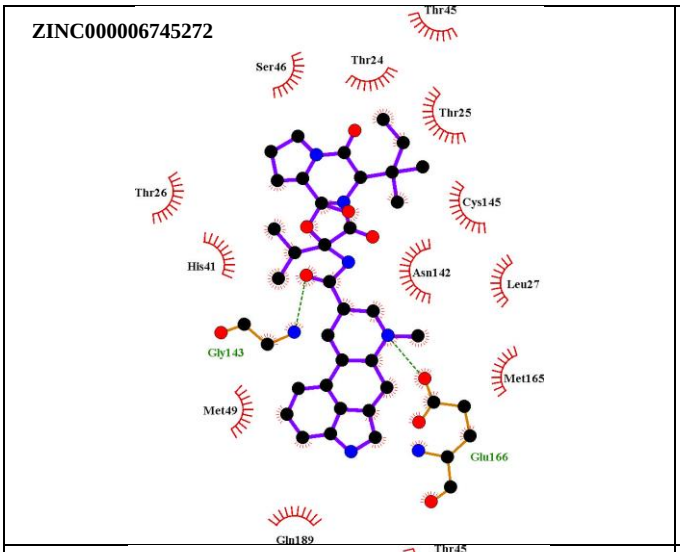

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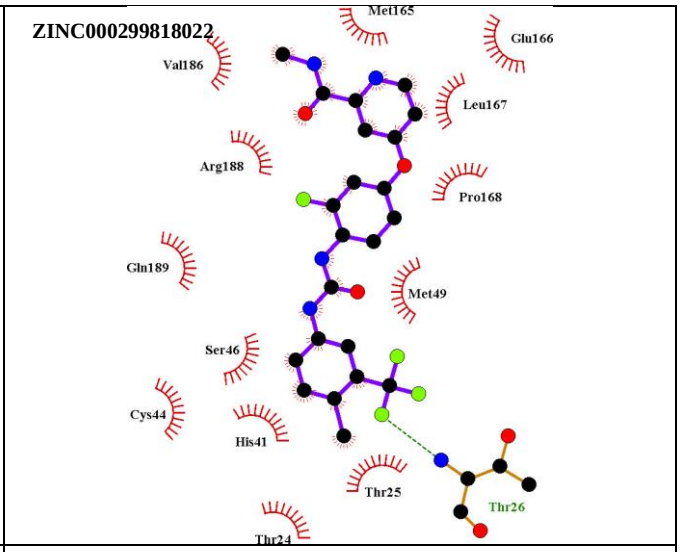

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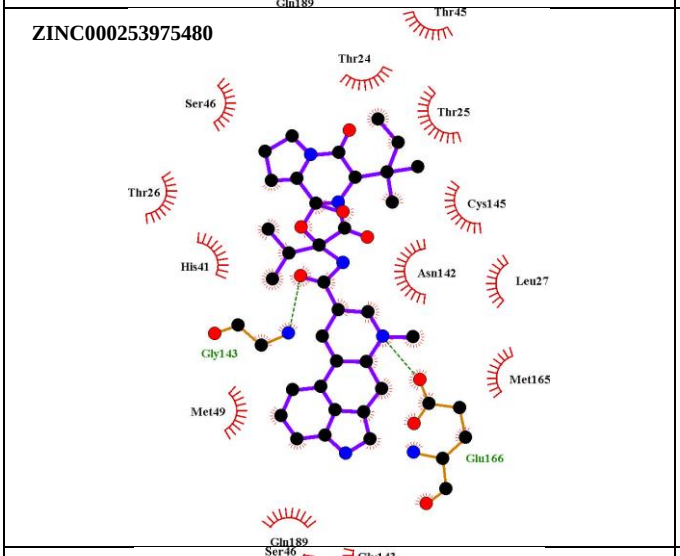

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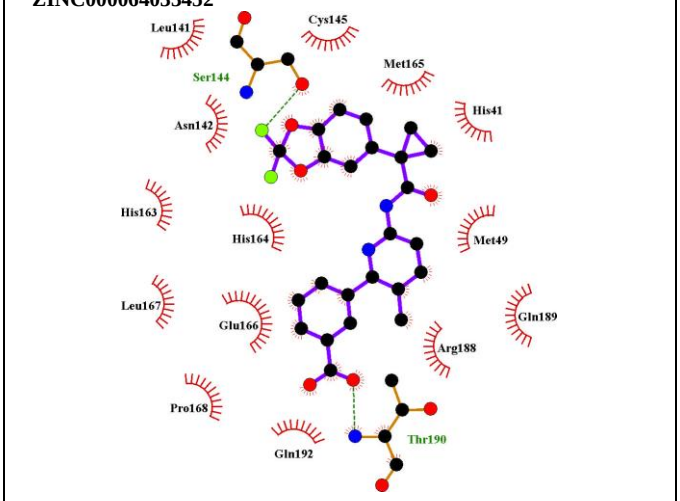

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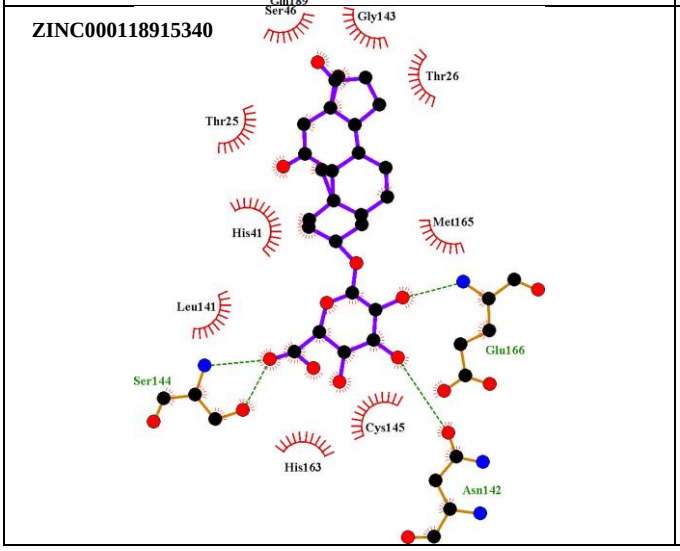

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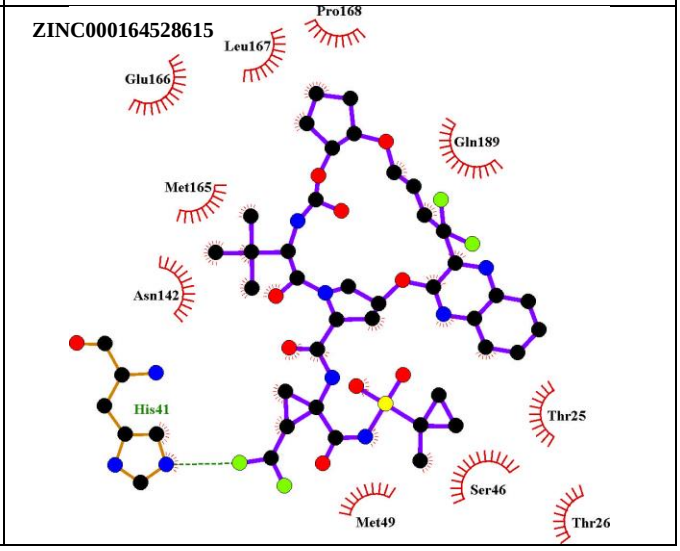

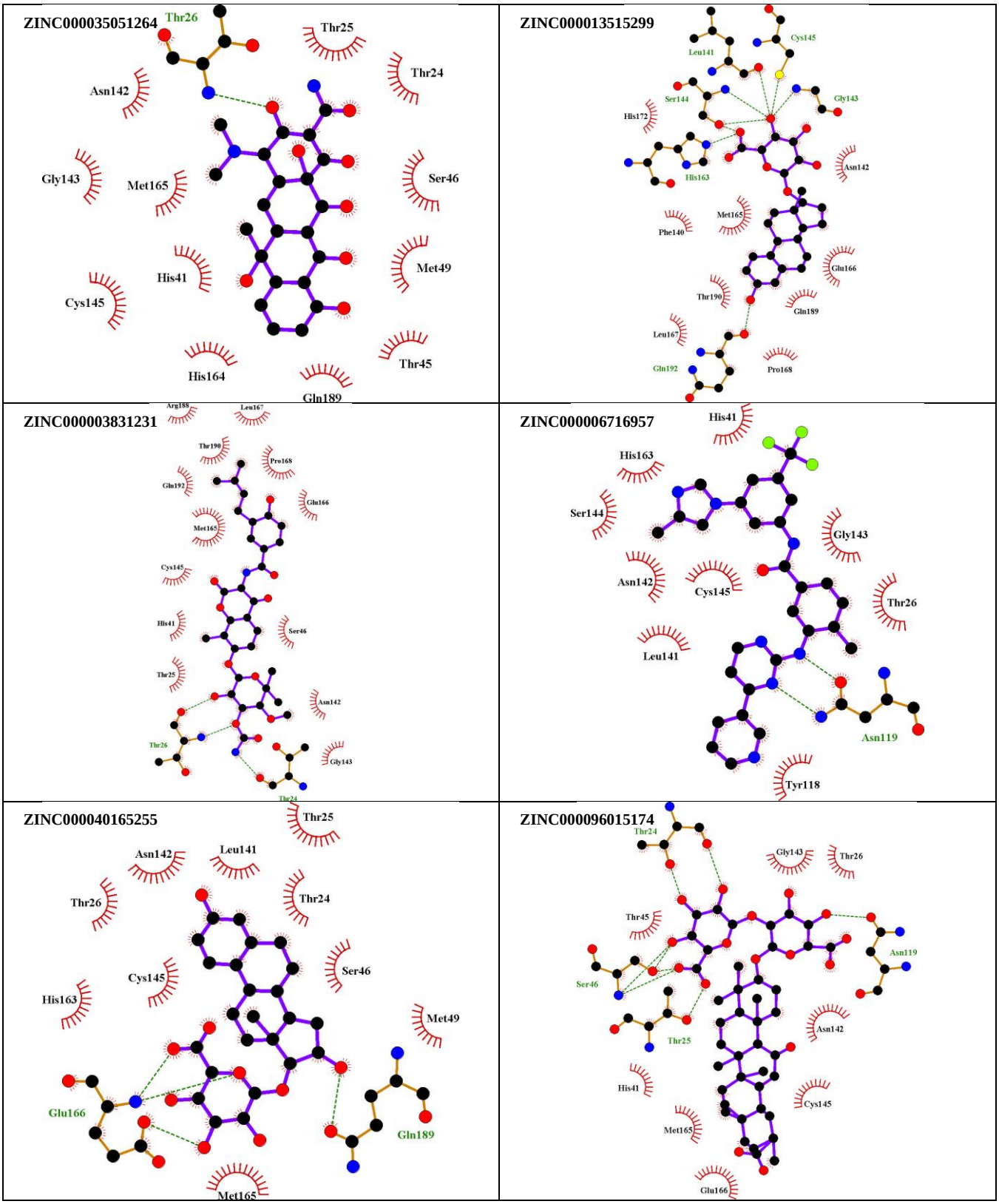
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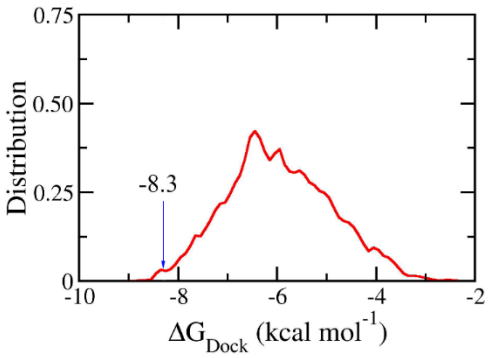
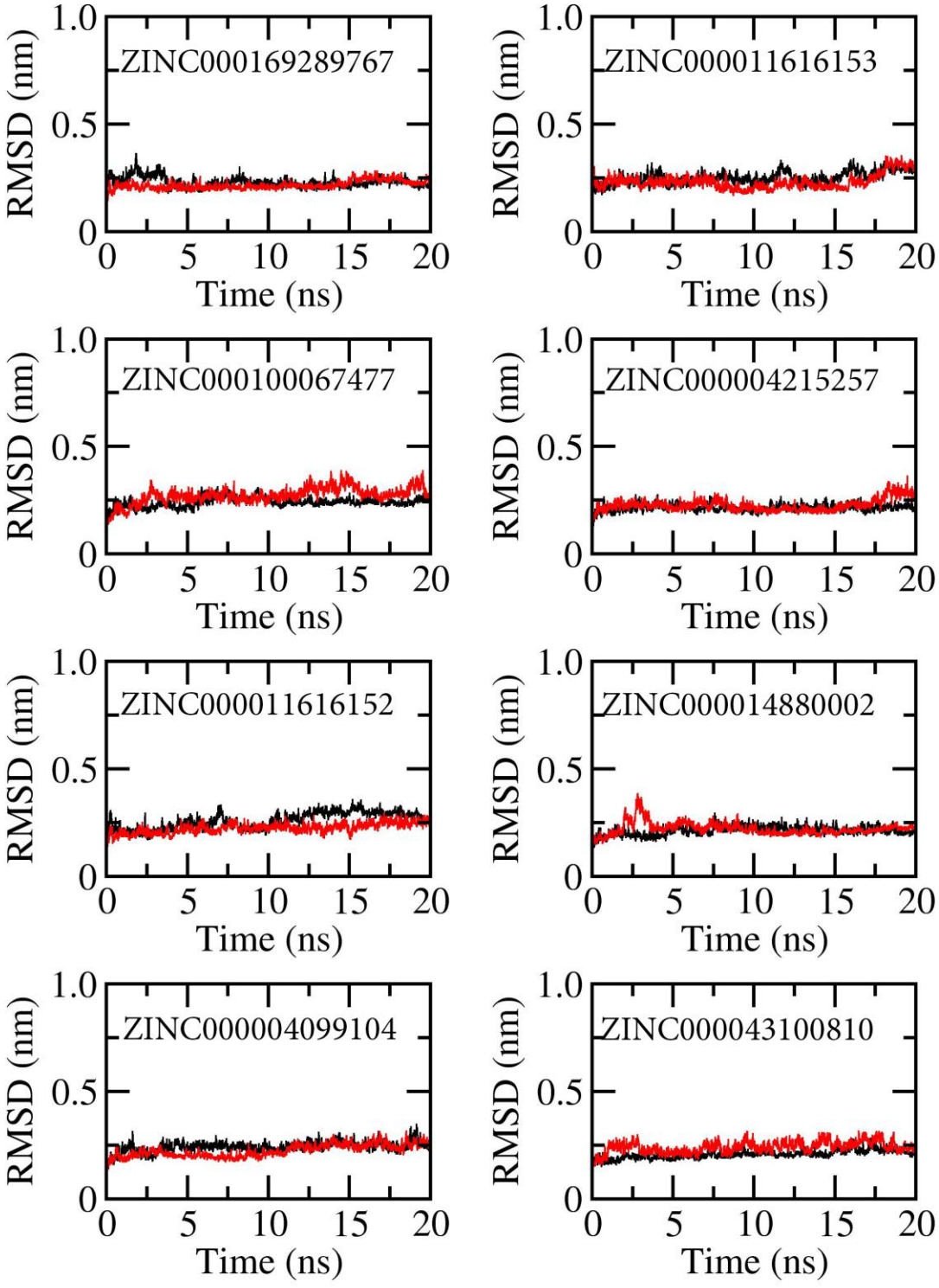


Figure S1. Distribution of docking energy between 6363 ZINC15 compounds and SARS-CoV-2 Mpro.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RMSD (nm)
Time (ns)
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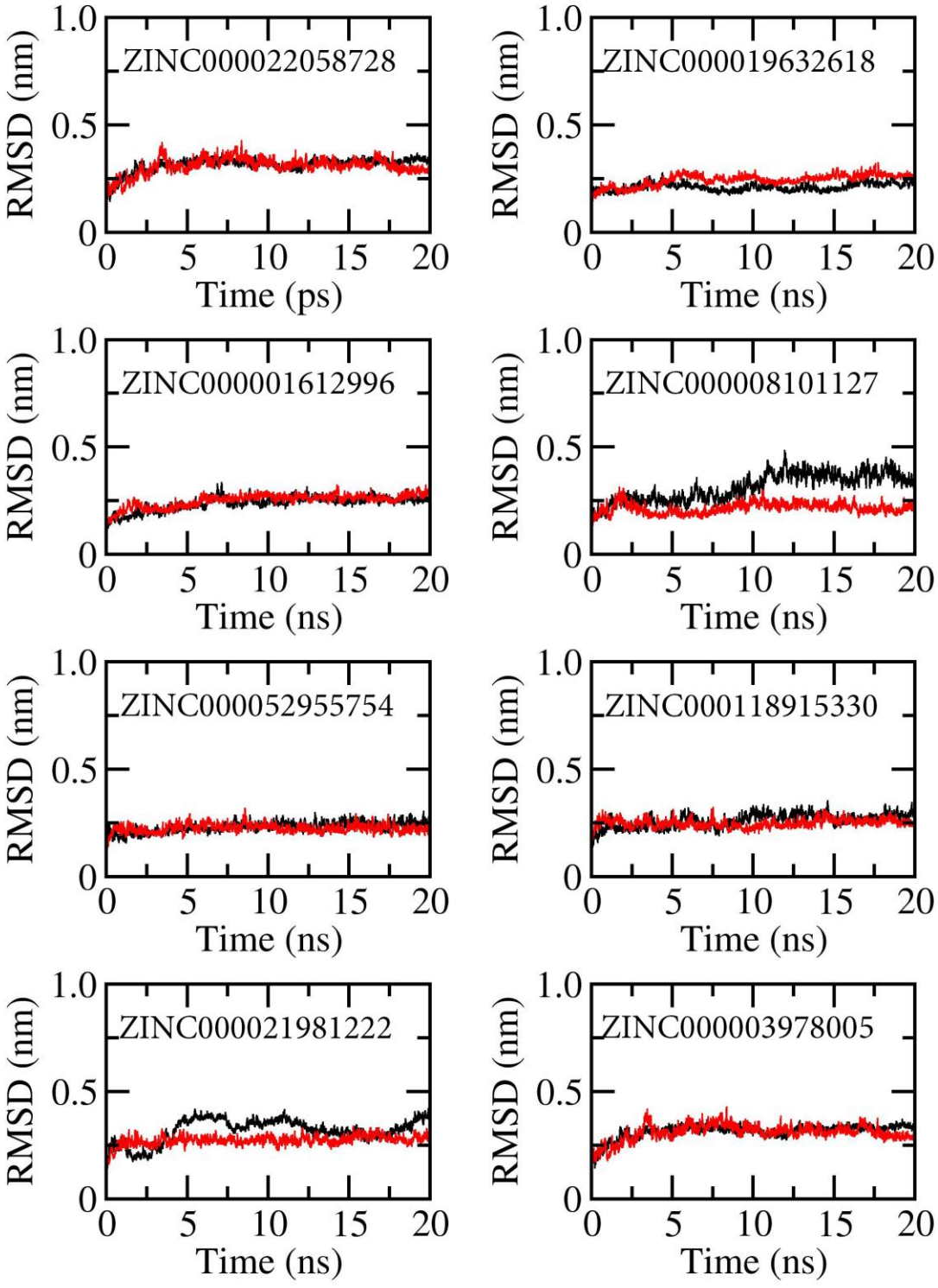
0
5
10
15
20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Time (ps)
Time (ns)
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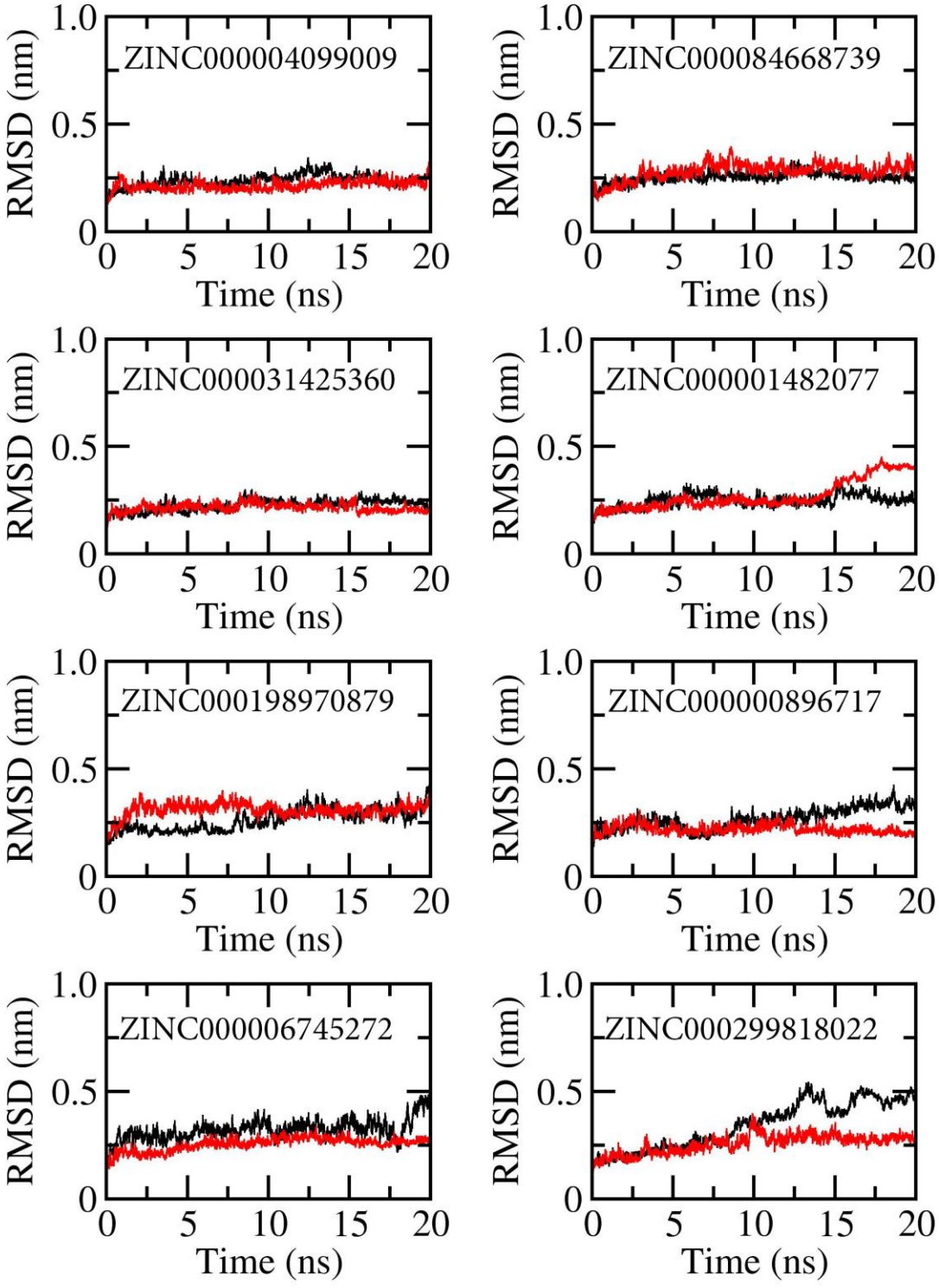
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Time (ns)
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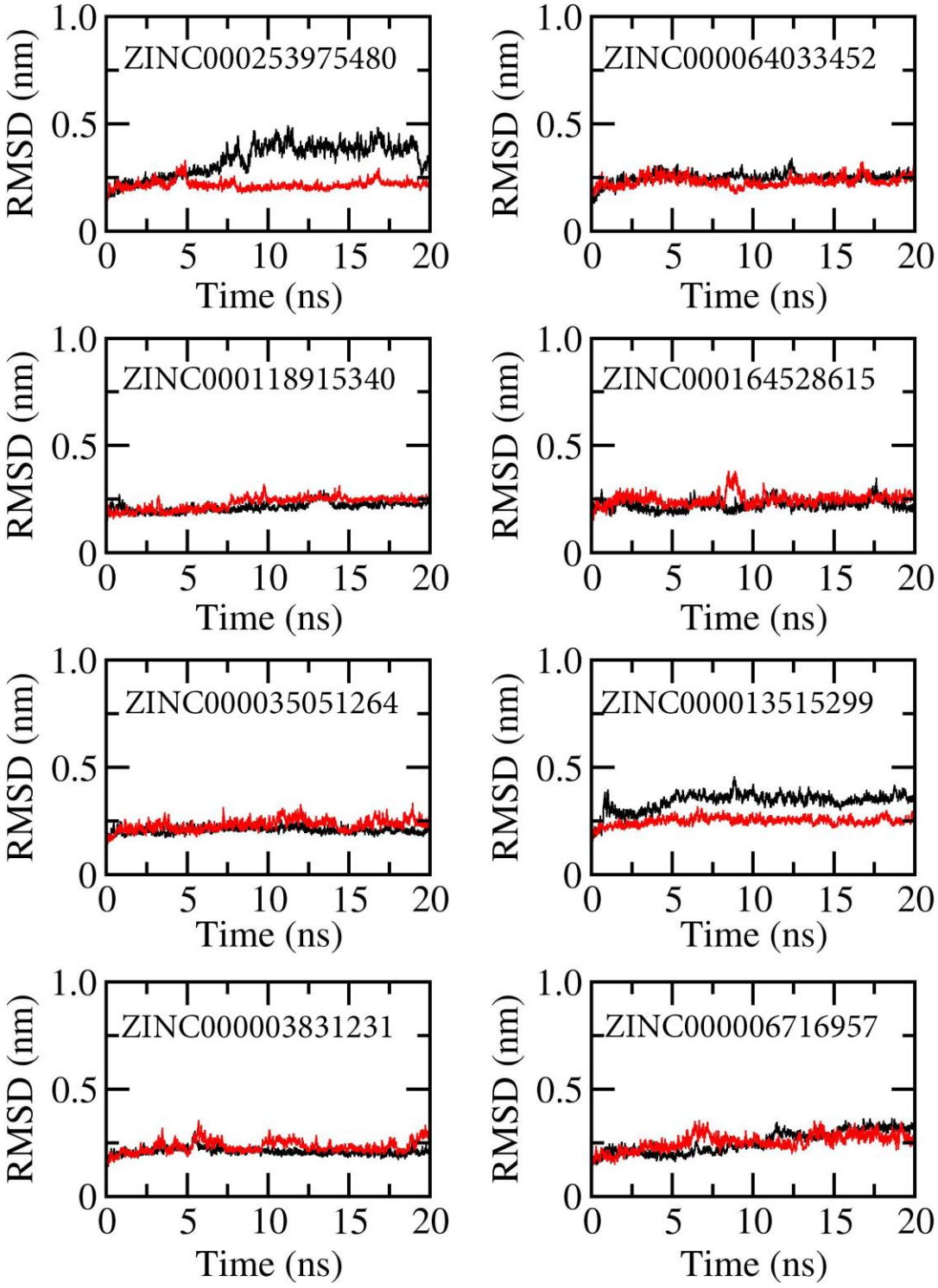
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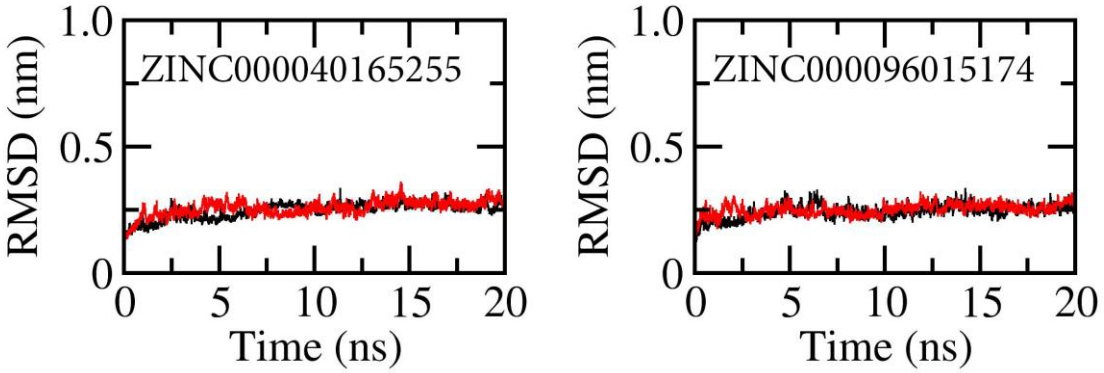


Figure S2. All-atom RMSD of SARS-CoV-2 Mpro+inhibitors complexes during two independent 20ns-long MD simulations.

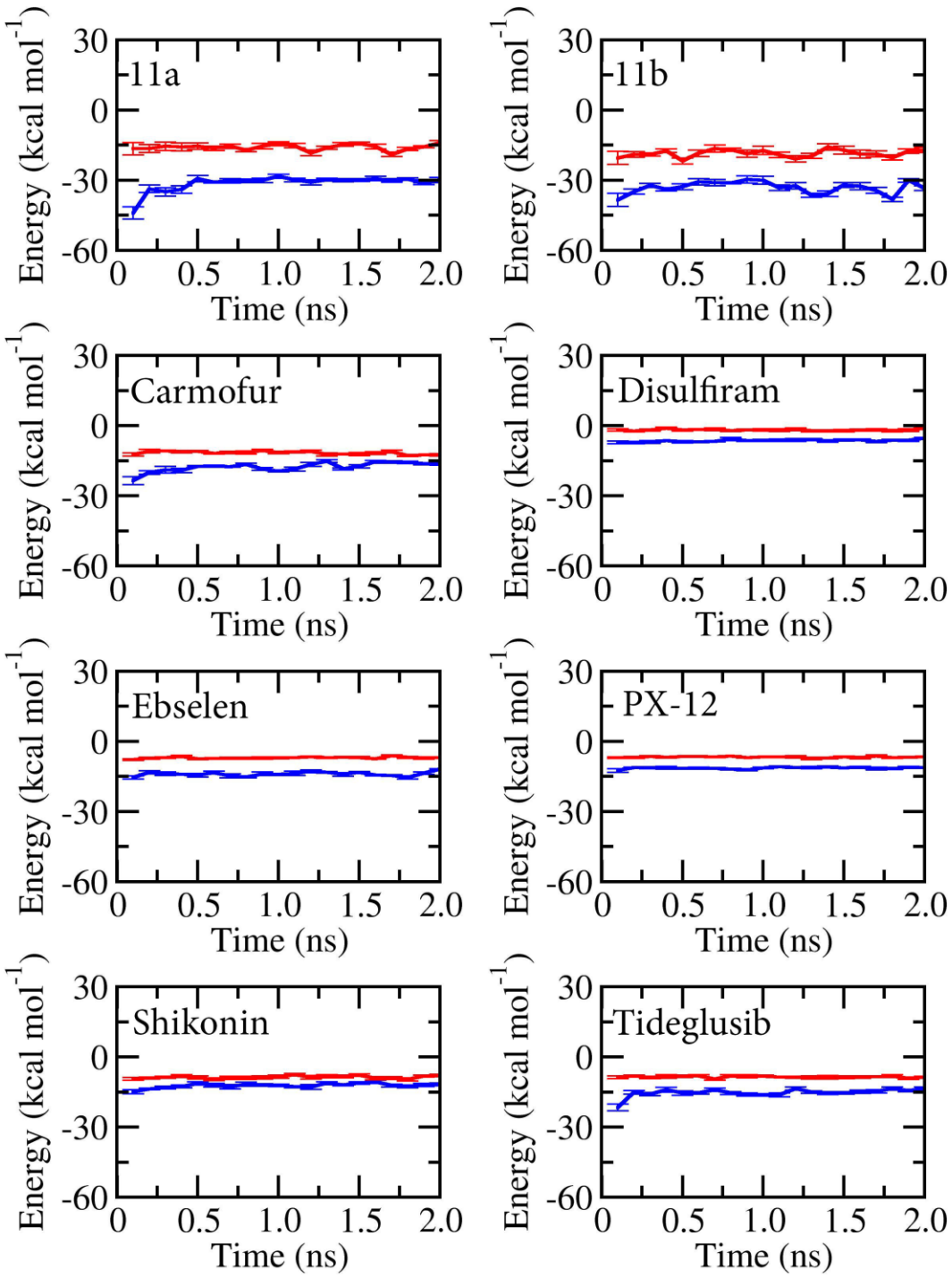
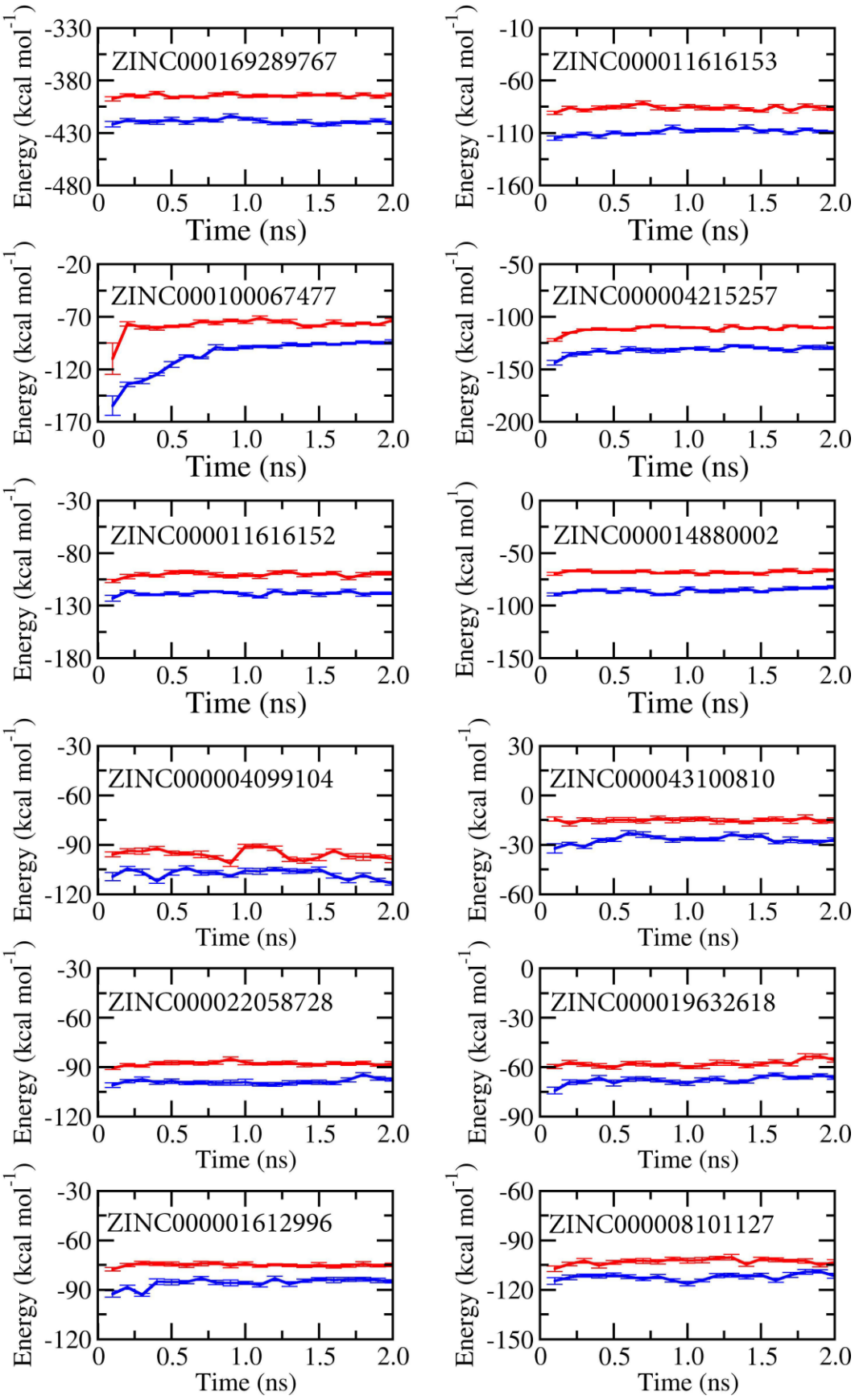


Figure S3. Desolvation free energy of experimentally characterized inhibitors of SARS-CoV-2 Mpro from solvated complex system (blue) and solvated ligand system (red). The difference between two metrics is the binding free energy between the ligand to SARS-CoV-2 Mpro, which obtained via FEP simulations.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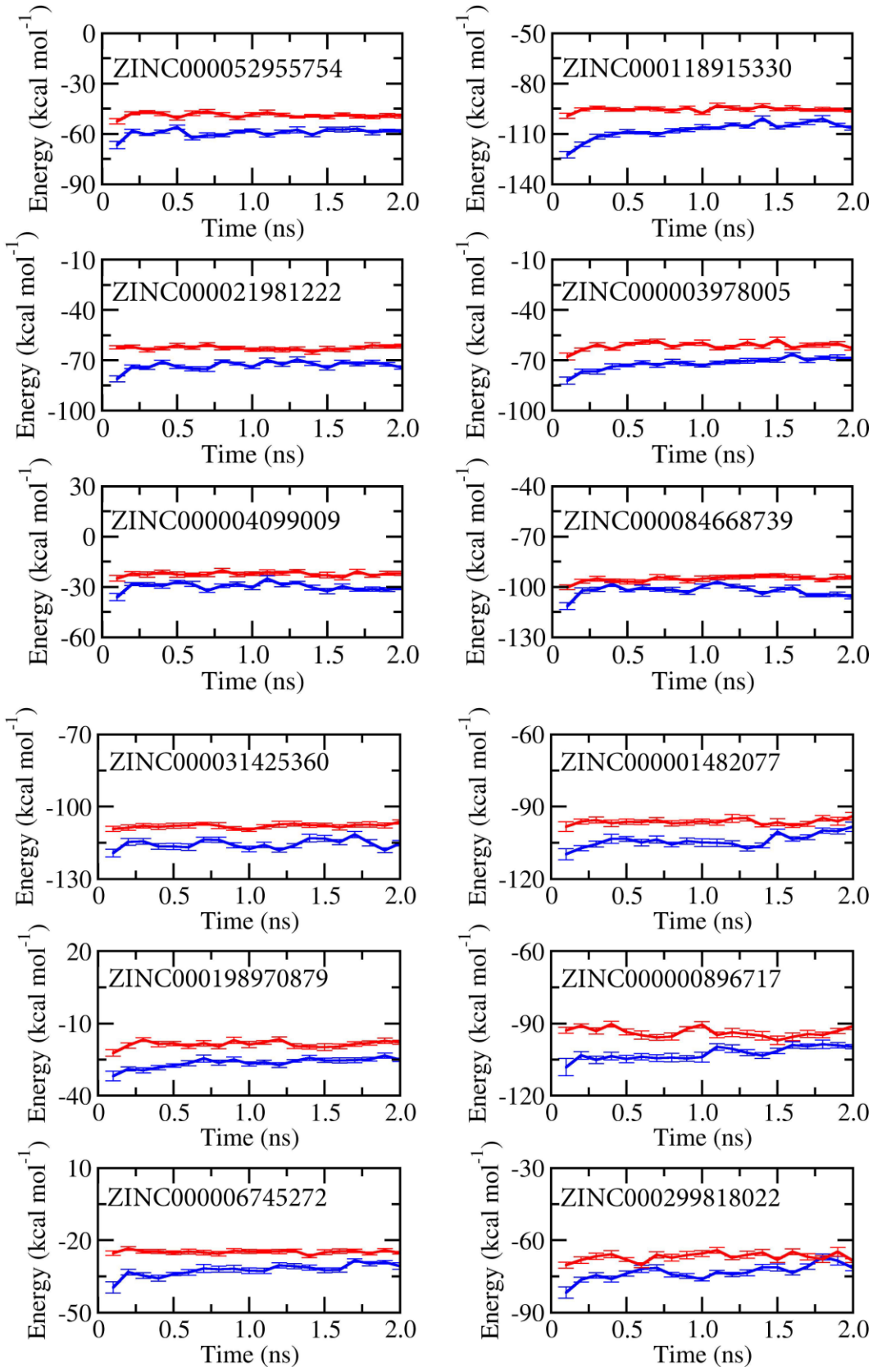
Energy (kcal mol-1)
Time (ns)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Energy (kcal mol-1)
Time (ns)

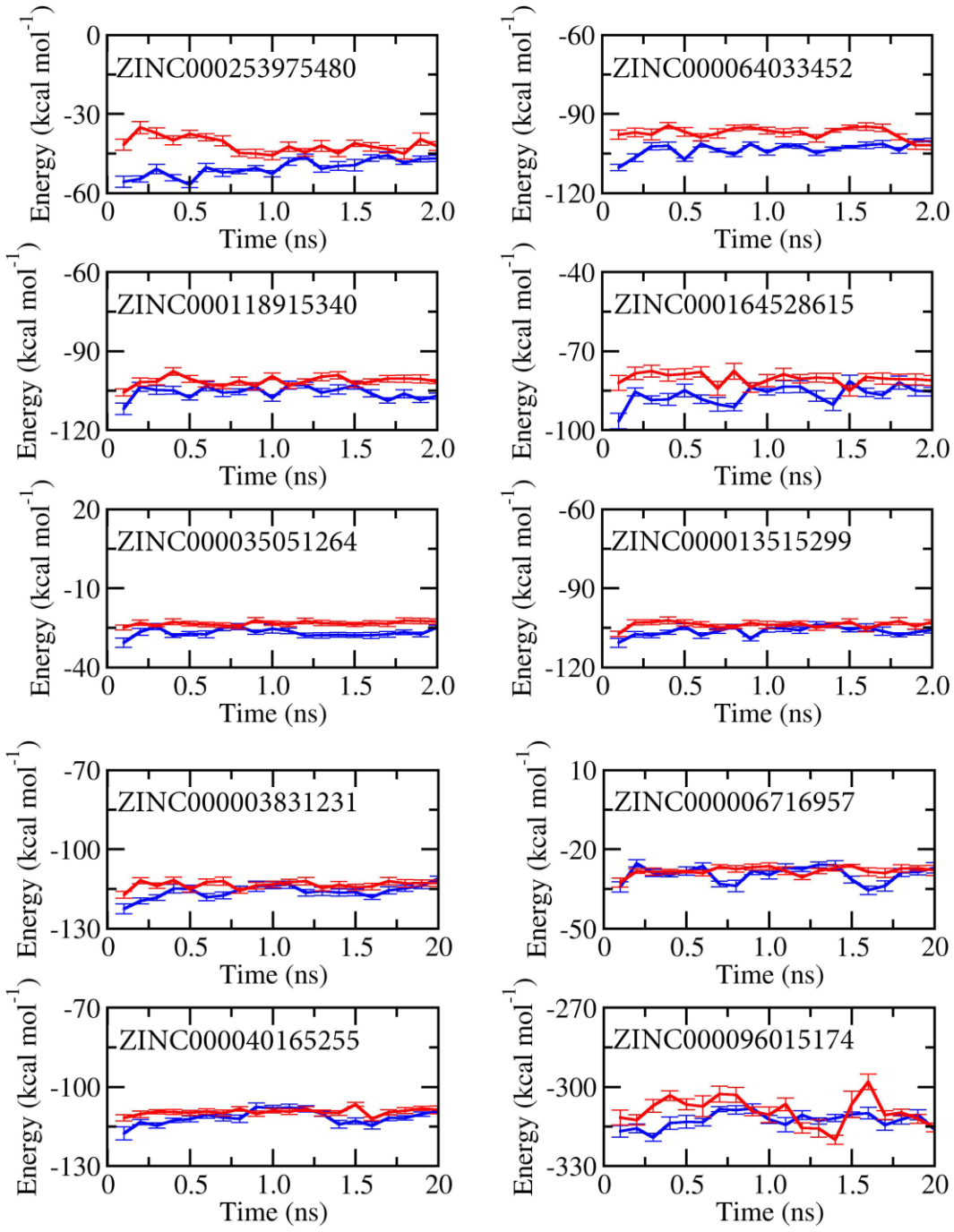

Figure S4. Desolvation free energy of the top 33 ZINC15 compounds of SARS-CoV-2 Mpro from solvated complex system (blue) and solvated ligand system (red). The difference between two metrics is the binding free energy between the ligand to SARS-CoV-2 Mpro, which obtained via FEP simulation.