# Identification of antiviral compounds against Monkeypox virus profilin-like protein A42R from *Plantago lanceolata*

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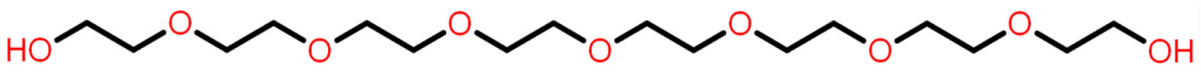
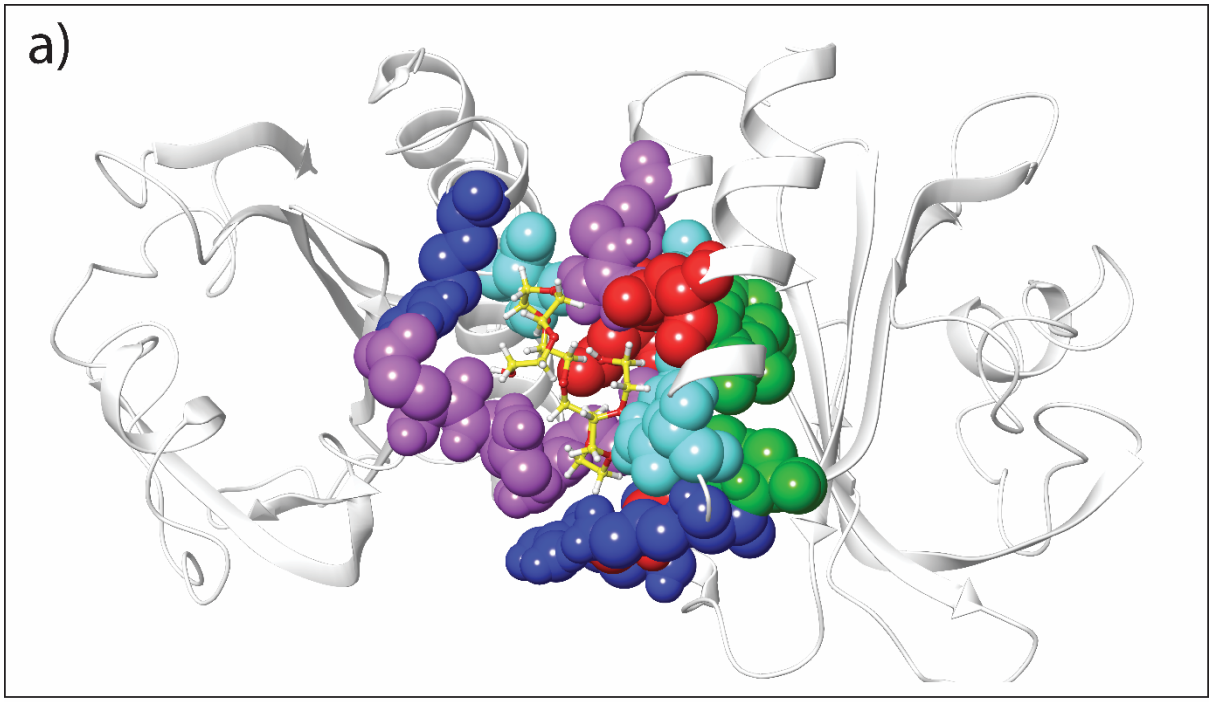



**Figure S1-** control 3,6,9,12,15,18,21-HEPTAOXATRICOSANE-1,23-DIOL



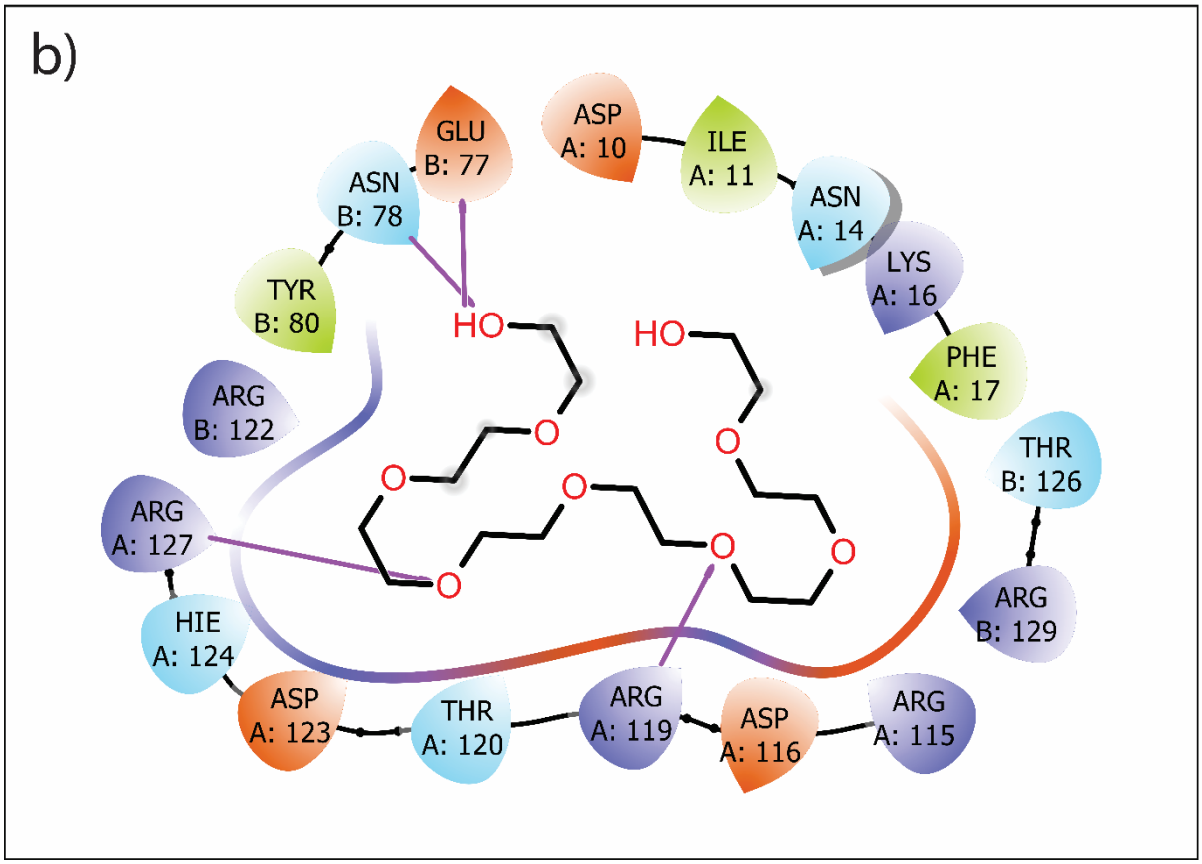




**Figure S2-** 2d and 3d pose of control

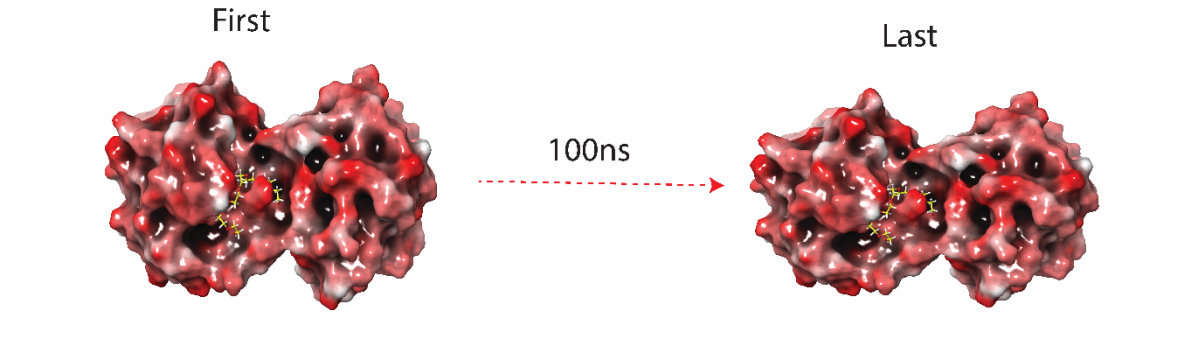



**Figure S3** – first and last pose of control

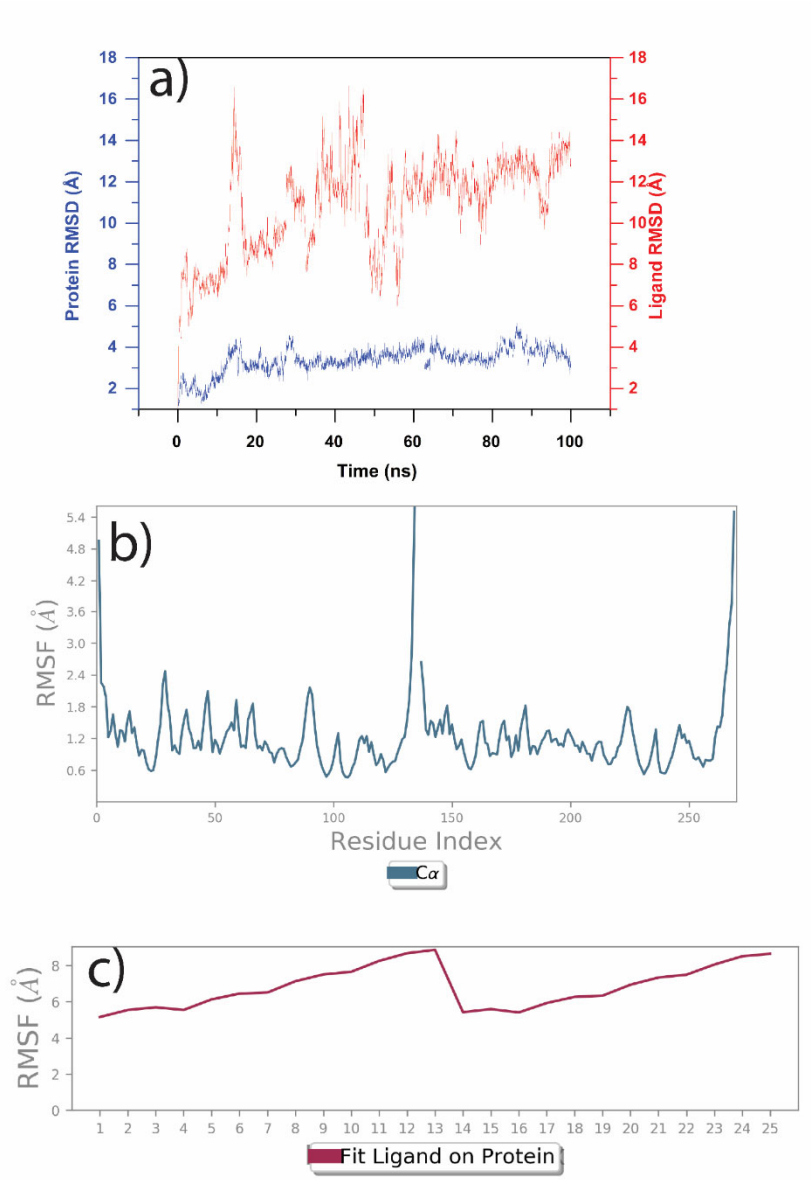



**Figure S4-** a) RMSD of control b) RMSF plot of protein- control c) RMSF Plot of ligand-control

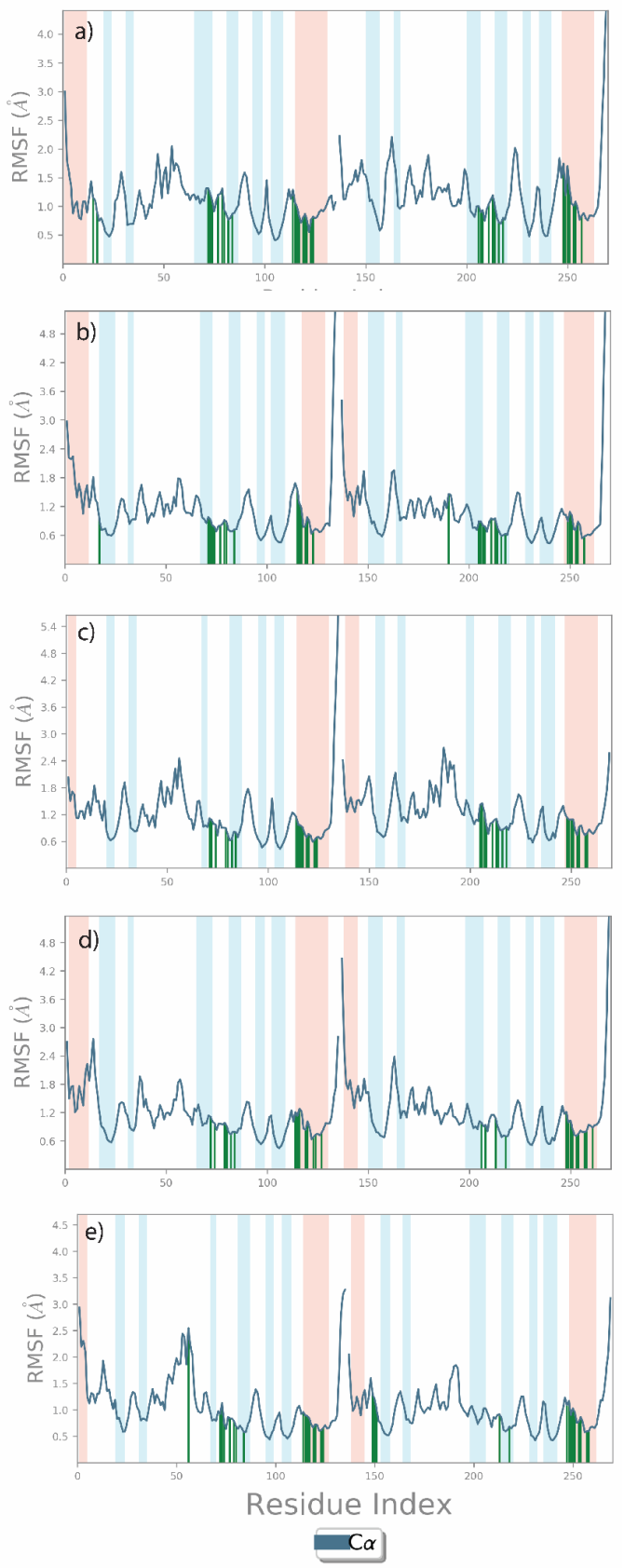



**Figure S5.** RMSF plots for protein docked with natural compounds, i.e., a) Luteolin 7,3'-diglucuronide b) Luteolin 7-glucuronide-3'-glucoside c) Plantagoside d) Narcissoside e) (alphaE,8S,9R)-N-(3,4-Dihydroxyphenethyl)-8-[(3,4-dihydroxyphenethyl)carbamoyl]-9-(1,3-

benzodioxole-5-yl)-3a alpha,7a alpha-ethano-1,3-benzodioxole-5-acrylamide as function of 100 ns simulation interval.

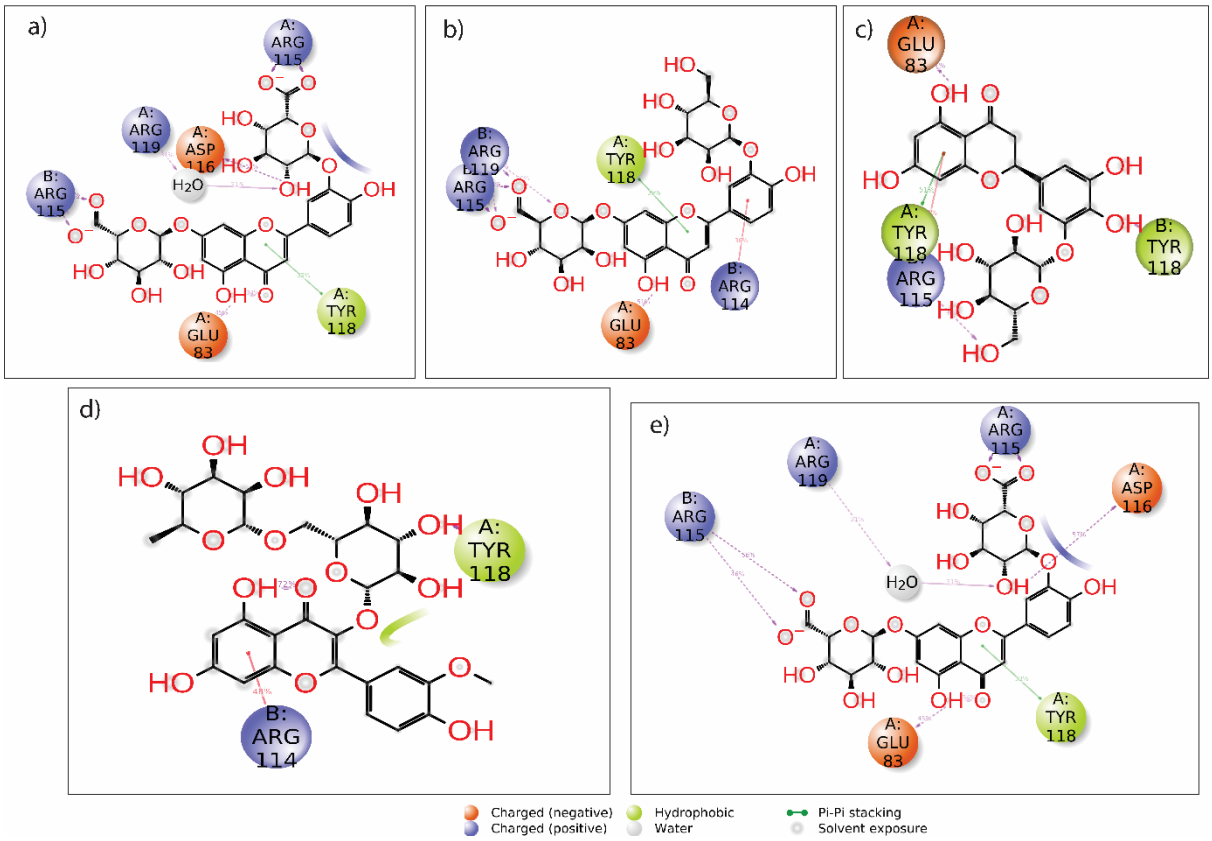



**Figure S6.** Ligand protein contact of PE8 and selected natural compounds, i.e., (a) Luteolin 7,3'-diglucuronide b) Luteolin 7-glucuronide-3'-glucoside c) Plantagoside d) Narcissoside e) (alphaE,8S,9R)-N-(3,4-Dihydroxyphenethyl)-8-[(3,4-dihydroxyphenethyl)carbamoyl]-9-(1,3-benzodioxole-5-yl)-3aalpha,7aalpha-ethano-1,3-benzodioxole-5-acrylamide fit on protein were extracted from 100 ns MD simulation trajectories of respective docked complexes.

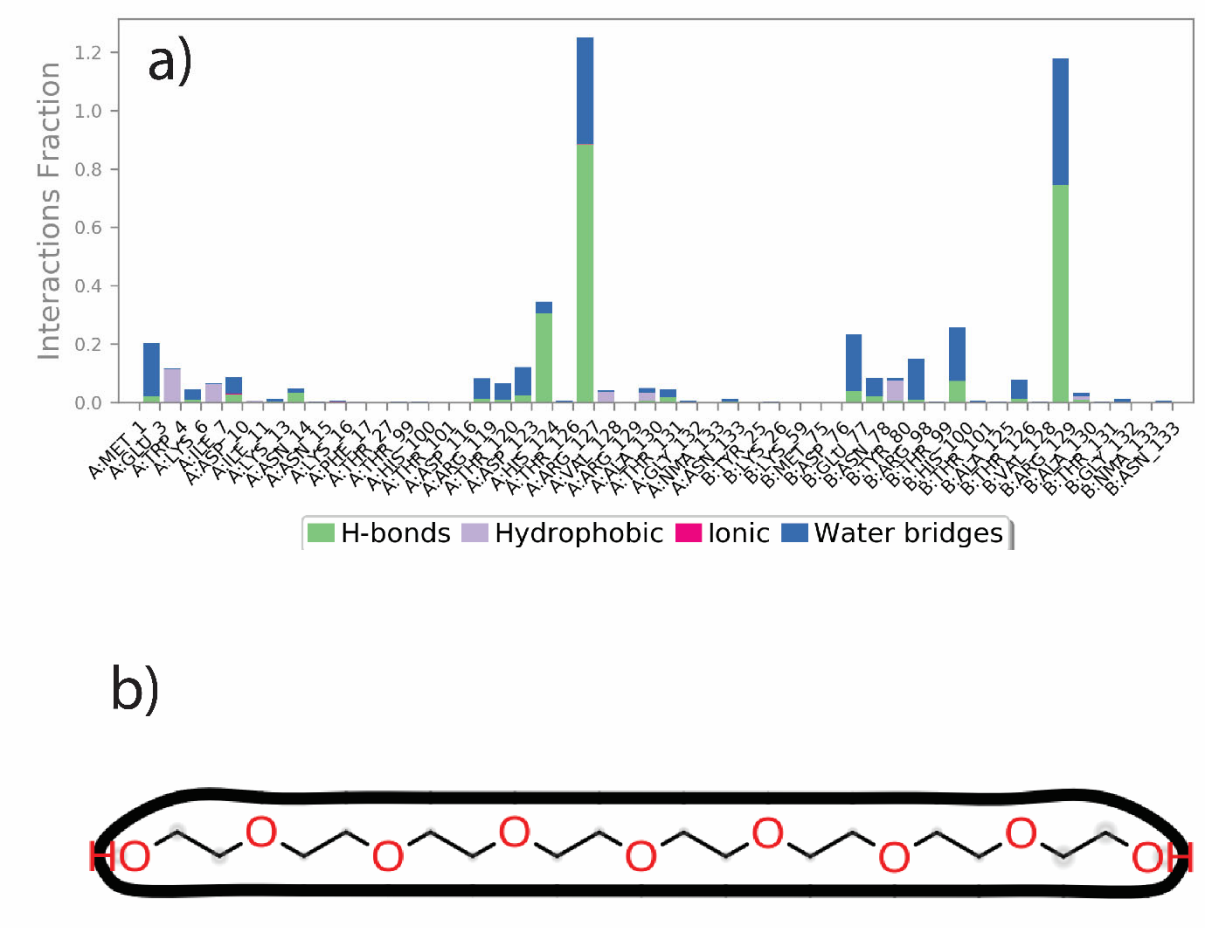



**Figure S7** a) protein-ligand interaction of control b) protein-ligand contact of control

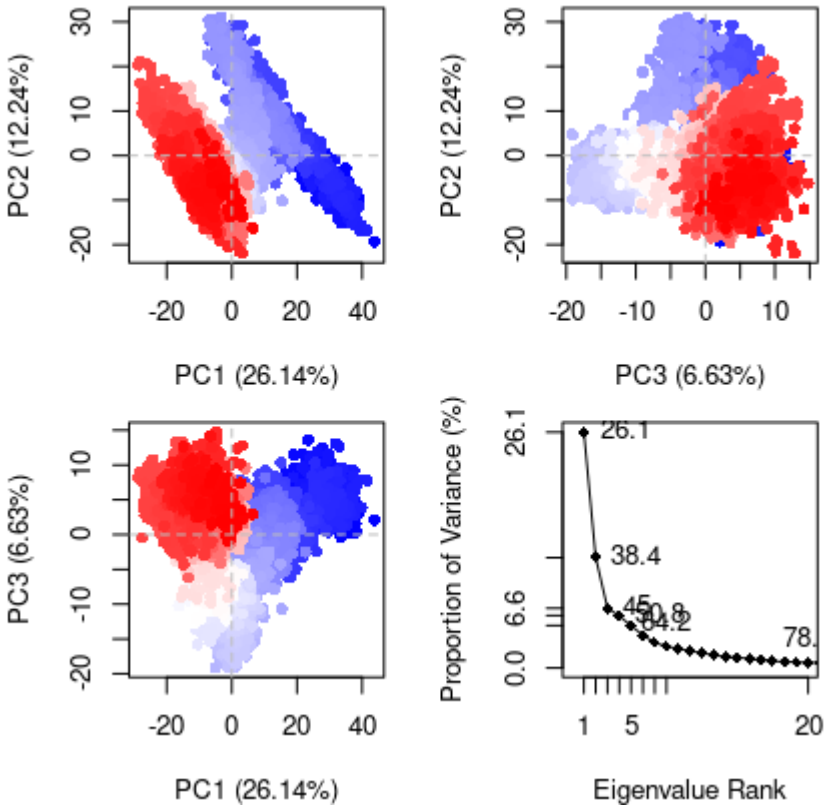



**Figure S8.** PCA of control

**Table S1.** ADME analysis of all the selected compounds.

| **Molecule** | **44258091** | **44258090** | **174157** | **5481663** | **101131595** |
|---|---|---|---|---|---|
| Formula | C27H26O18 | C27H28O17 | C21H22O12 | C28H32O16 | C36H34N2O10 |
| MW | 638.48 | 624.5 | 466.39 | 624.54 | 654.66 |
| #Heavy atoms | 45 | 44 | 33 | 44 | 48 |
| #Aromatic heavy atoms | 16 | 16 | 12 | 16 | 18 |
| Fraction Csp3 | 0.37 | 0.41 | 0.38 | 0.46 | 0.28 |
| #Rotatable bonds | 7 | 7 | 4 | 7 | 12 |
| #H-bond acceptors | 18 | 17 | 12 | 16 | 10 |
| #H-bond donors | 10 | 10 | 8 | 9 | 6 |
| MR | 141.48 | 140.87 | 107.74 | 145.85 | 171.93 |
| TPSA | 303.57 | 286.5 | 206.6 | 258.43 | 176.04 |
| iLOGP | 1.32 | 1.16 | 1.65 | 2.62 | 3.58 |
| XLOGP3 | 0.15 | -0.1 | -0.06 | -0.01 | 2.9 |
| WLOGP | -2.59 | -2.68 | -0.93 | -1.38 | 3.2 |
| MLOGP | -4.13 | -4.15 | -2.4 | -3.69 | 1.26 |
| Silicos-IT Log P | -3.12 | -2.68 | -1.06 | -1.55 | 3.8 |
| Consensus Log P | -1.67 | -1.69 | -0.56 | -0.8 | 2.95 |
| ESOL Log S | -3.69 | -3.46 | -2.7 | -3.51 | -5.21 |
| ESOL Solubility (mg/ml) | 0.129 | 2.19E-01 | 9.33E-01 | 1.92E-01 | 4.02E-03 |
| ESOL Solubility (mol/l) | 0.000202 | 3.50E-04 | 2.00E-03 | 3.07E-04 | 6.15E-06 |
| ESOL Class | Soluble | Soluble | Soluble | Soluble | Moderately soluble |
| Ali Log S | -6.08 | -5.46 | -3.83 | -4.97 | -6.26 |
| Ali Solubility (mg/ml) | 0.000529 | 2.15E-03 | 6.94E-02 | 6.73E-03 | 3.62E-04 |
| Ali Solubility (mol/l) | 0.00000828 | 3.44E-06 | 1.49E-04 | 1.08E-05 | 5.53E-07 |
| Ali Class | Poorly soluble | Moderately soluble | Soluble | Moderately soluble | Poorly soluble |
| Silicos-IT LogSw | 0.65 | 0.17 | -0.52 | -0.97 | -6.99 |
| Silicos-IT Solubility (mg/ml) | 2820 | 9.22E+02 | 1.40E+02 | 6.66E+01 | 6.75E-05 |
| Silicos-IT Solubility (mol/l) | 4.42 | 1.48E+00 | 2.99E-01 | 1.07E-01 | 1.03E-07 |
| Silicos-IT class | Soluble | Soluble | Soluble | Soluble | Poorly soluble |
| GI absorption | Low | Low | Low | Low | Low |
| BBB permeant | No | No | No | No | No |
| Pgp substrate | Yes | Yes | No | Yes | No |
| CYP1A2 inhibitor | No | No | No | No | No |
| CYP2C19 inhibitor | No | No | No | No | No |
| CYP2C9 inhibitor | No | No | No | No | No |
| CYP2D6 inhibitor | No | No | No | No | No |
| CYP3A4 inhibitor | No | No | No | No | No |

| | | | | | |
|---|---|---|---|---|---|
| log Kp (cm/s) | -10.09 | -10.18 | -9.19 | -10.12 | -8.23 |
| Lipinski #violations | 3 | 3 | 2 | 3 | 3 |
| Ghose #violations | 4 | 4 | 1 | 4 | 3 |
| Veber #violations | 1 | 1 | 1 | 1 | 2 |
| Egan #violations | 1 | 1 | 1 | 1 | 1 |
| Muegge #violations | 4 | 4 | 3 | 4 | 3 |
| Bioavailability Score | 0.11 | 0.11 | 0.17 | 0.17 | 0.17 |
| PAINS #alerts | 0 | 0 | 1 | 0 | 1 |
| Brenk #alerts | 0 | 0 | 1 | 0 | 2 |
| Leadlikeness #violations | 1 | 1 | 1 | 1 | 2 |
| Synthetic Accessibility | 6.29 | 6.33 | 5.14 | 6.64 | 6.91 |