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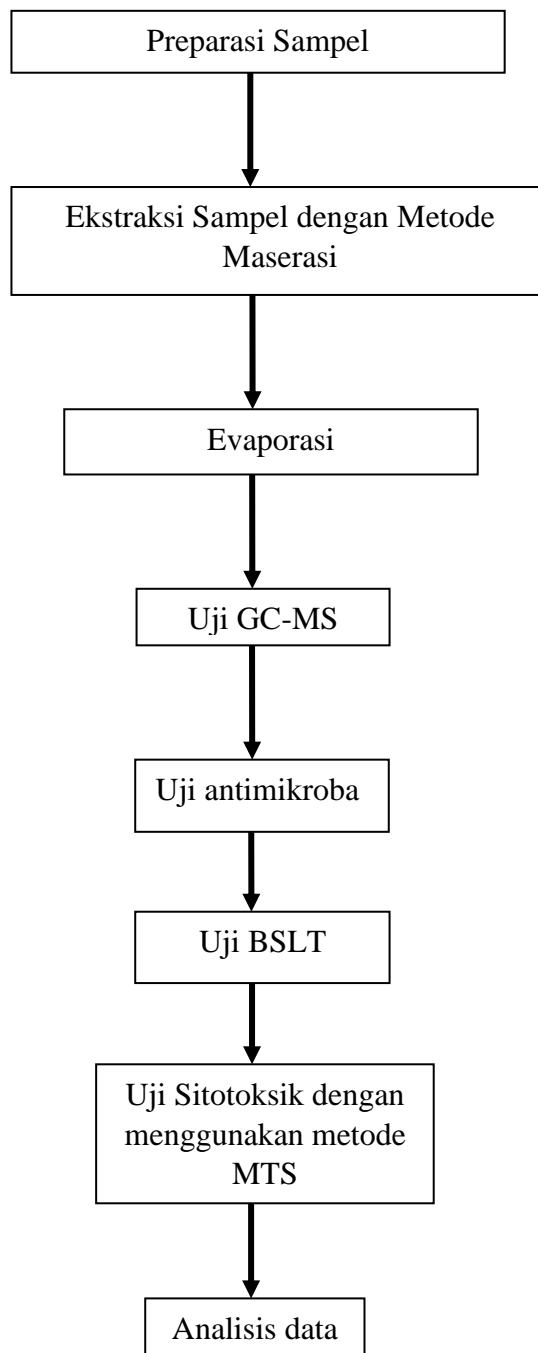
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LAMPIRAN

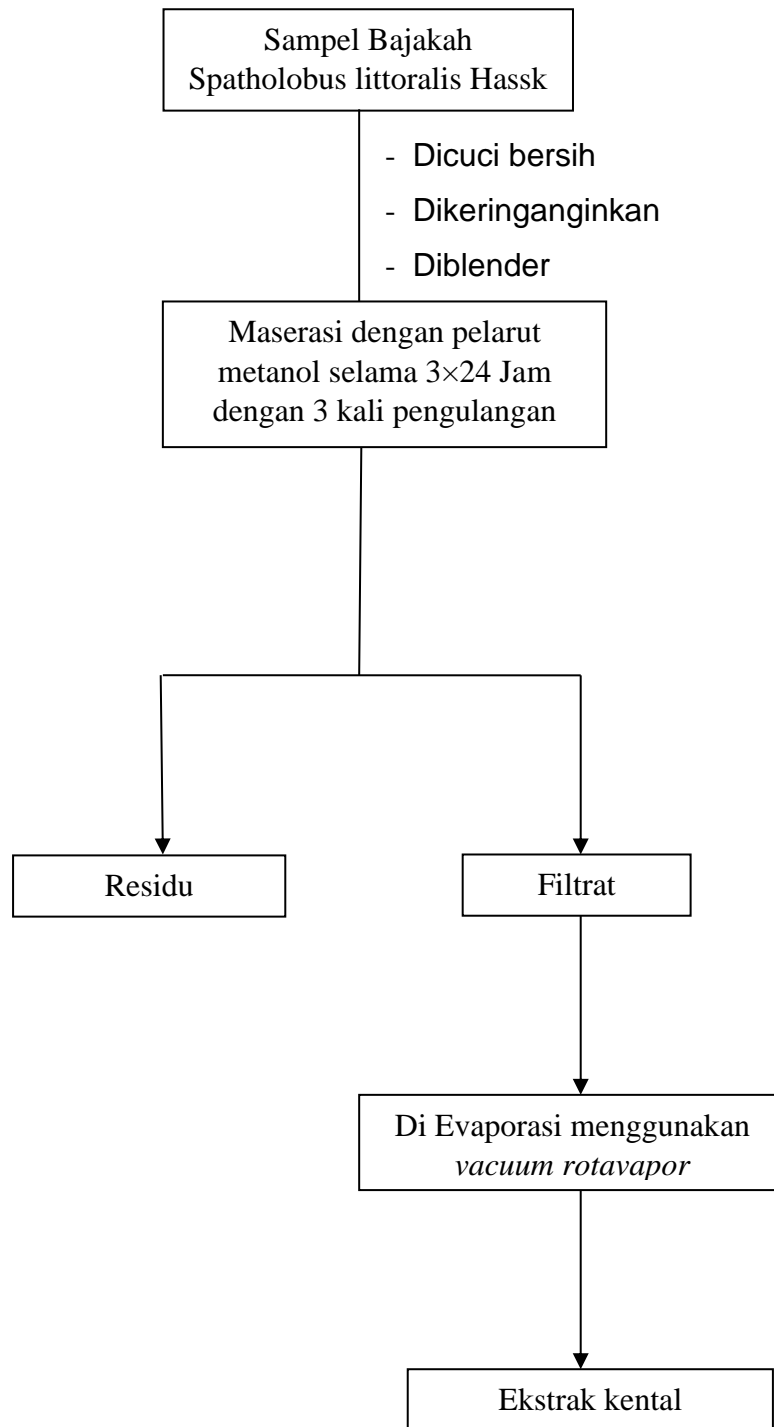
Lampiran 1. Skema Alur Penelitian

Tahapan prosedur penelitian yang akan dilakukan disajikan pada skema dibawah ini:



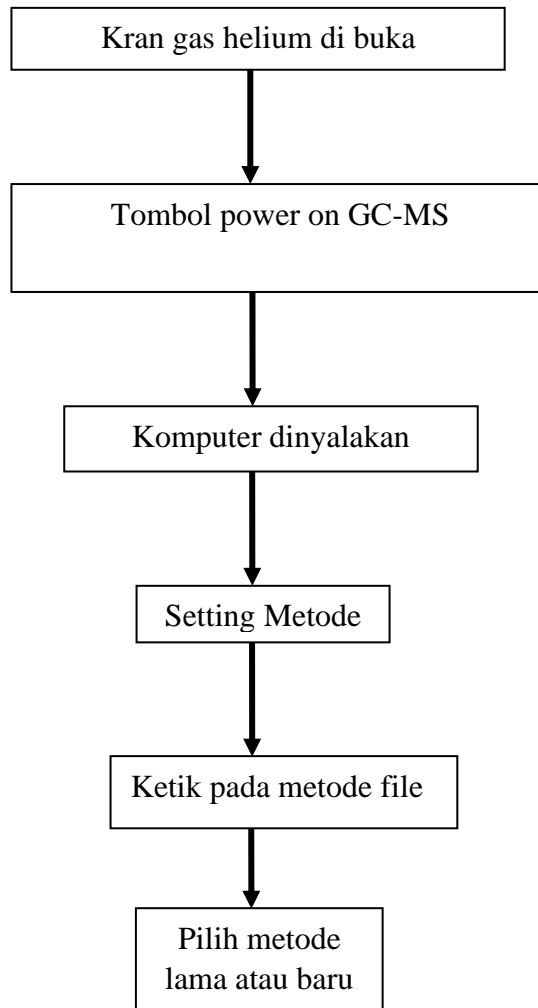
Lampiran 2. Skema Ekstraksi dengan Metode Maserasi

Adapun skema ekstraksi menggunakan metode maserasi adalah sebagai berikut:



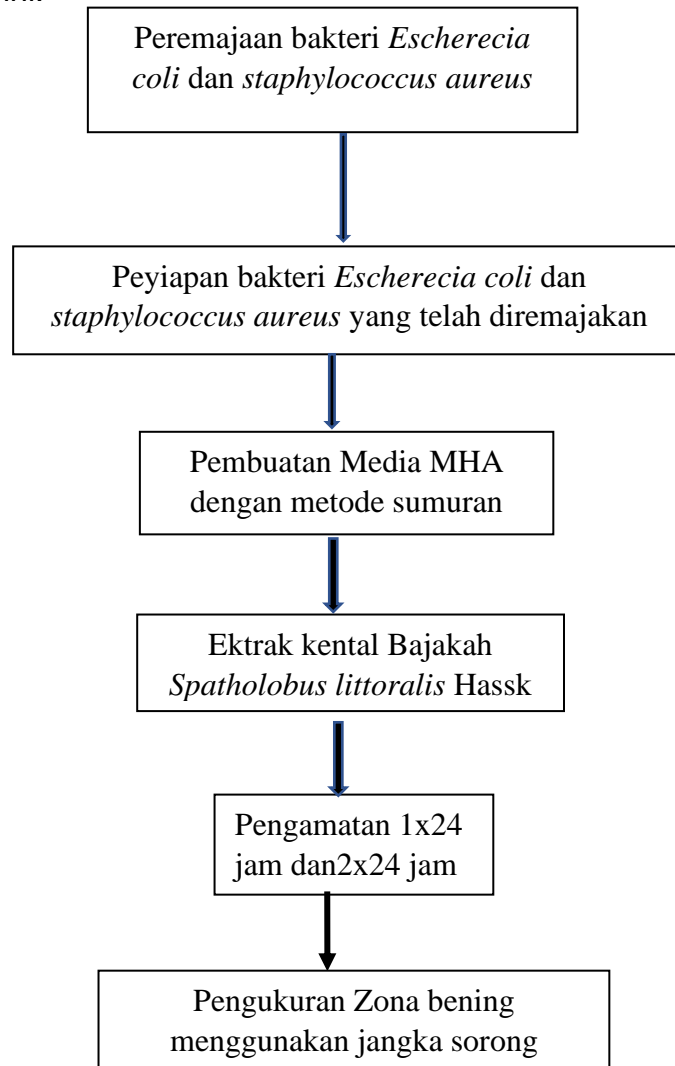
Lampiran 3. Skema uji GC-MS

Tahapan prosedur penelitian yang akan dilakukan disajikan pada skema dibawah ini:



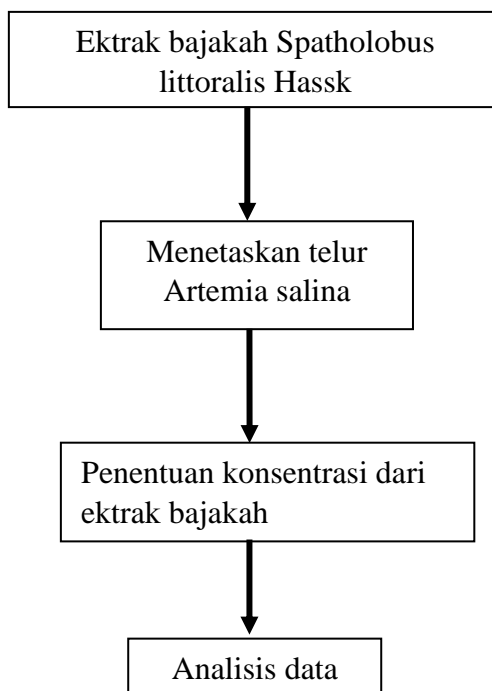
Lampiran 4. Skema uji antimikroba

Tahapan prosedur penelitian yang akan dilakukan disajikan pada skema dibawah ini:



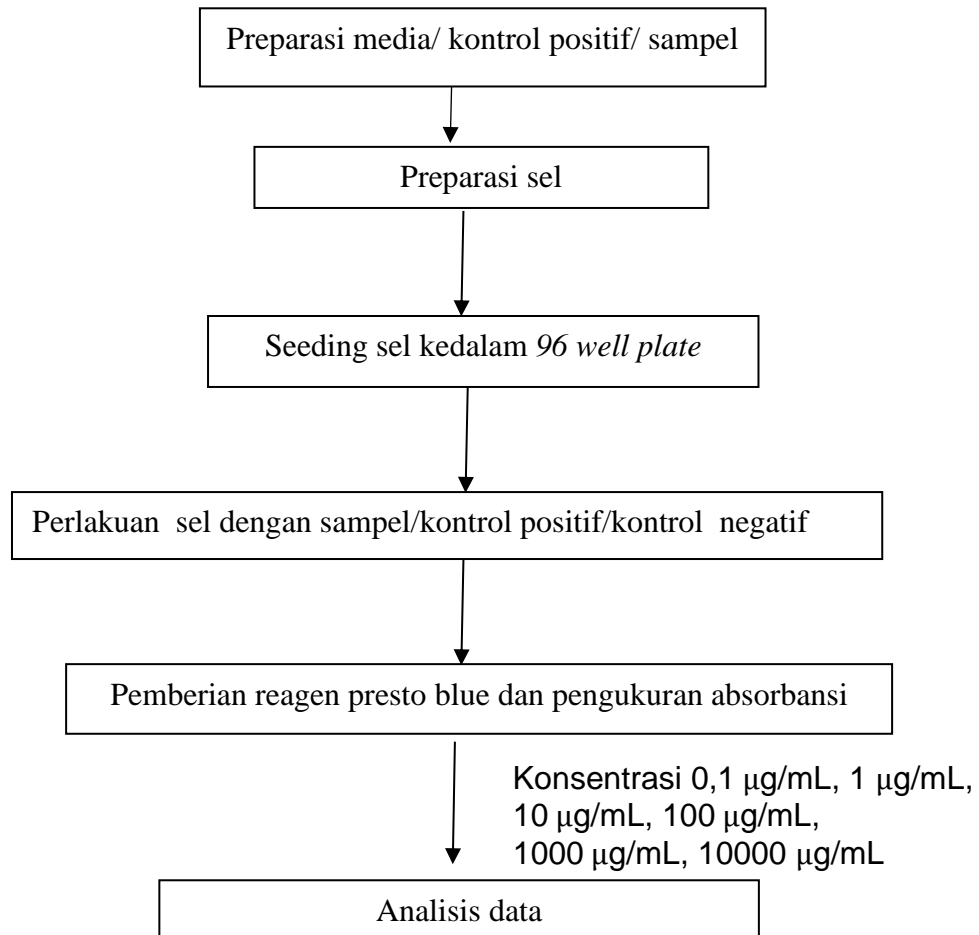
Lampiran 5. Skema Alur Penelitian

Tahapan prosedur penelitian yang akan dilakukan disajikan pada skema dibawah ini:



Lampiran 6. Skema Uji Sitotoksik dengan Metode MTS

skema uji sitotoksik menggunakan metode MTS adalah sebagai berikut:



Lampiran 7. Dokumentasi penelitian



The screenshot shows the Vina Wizard software interface. The 'Molecules' list on the left includes:

- dpp_fix
- dpp_fix_3-pepindinol
- dpp_fix_chloromphenicol
- dpp_fix_cyanoacetyl_urea

The 'Results' table shows the following data:

| Ligand | Binding Affinity (kcal/mol) | Mode | RMSD lower bound | RMSD upper bound |
|--------------------------|-----------------------------|------|------------------|------------------|
| dpp_fix_chloromphenicol | -4.9 | 8 | 2.743 | 3.479 |
| dpp_fix_cyanoacetyl_urea | -5.0 | 0 | 0.0 | 0.0 |
| dpp_fix_cyanoacetyl_urea | -4.9 | 1 | 3.542 | 4.954 |
| dpp_fix_cyanoacetyl_urea | -4.9 | 2 | 4.033 | 6.07 |
| dpp_fix_cyanoacetyl_urea | -4.7 | 3 | 1.629 | 2.583 |
| dpp_fix_cyanoacetyl_urea | -4.4 | 4 | 23.333 | 24.936 |
| dpp_fix_cyanoacetyl_urea | -4.4 | 5 | 2.676 | 3.606 |
| dpp_fix_cyanoacetyl_urea | -4.3 | 6 | 2.911 | 6.662 |
| dpp_fix_cyanoacetyl_urea | -4.3 | 7 | 33.189 | 34.245 |
| dpp_fix_cyanoacetyl_urea | -4.2 | 8 | 23.503 | 24.25 |

The screenshot shows the Vina Wizard software interface. The 'Molecules' list on the left includes:

- dpp_fix
- dpp_fix_3-pepindinol
- dpp_fix_chloromphenicol
- dpp_fix_cyanoacetyl_urea

The 'Results' table shows the following data:

| Ligand | Binding Affinity (kcal/mol) | Mode | RMSD lower bound | RMSD upper bound |
|-------------------------|-----------------------------|------|------------------|------------------|
| dpp_fix_3-pepindinol | -4.4 | 0 | 0.0 | 0.0 |
| dpp_fix_3-pepindinol | -4.3 | 1 | 3.741 | 4.422 |
| dpp_fix_3-pepindinol | -4.1 | 2 | 2.3 | 2.9 |
| dpp_fix_3-pepindinol | -4.0 | 3 | 2.482 | 2.916 |
| dpp_fix_3-pepindinol | -4.0 | 4 | 2.377 | 3.176 |
| dpp_fix_3-pepindinol | -4.0 | 5 | 3.657 | 4.353 |
| dpp_fix_3-pepindinol | -4.0 | 6 | 2.398 | 2.849 |
| dpp_fix_3-pepindinol | -3.9 | 7 | 17.638 | 18.101 |
| dpp_fix_3-pepindinol | -3.8 | 8 | 23.204 | 23.834 |
| dpp_fix_chloromphenicol | -5.9 | 0 | 0.0 | 0.0 |

Molecules

- dpp_fix
- dpp_fix_3-pepidinol
- dpp_fix_chloromphenicol
- dpp_fix_cyanoacetyl_urea

Controls

Vina Wizard | AutoDock Wizard | Open Babel | Python Shell | Logger

Start Here | Select Molecules | Run Vina | Analyze Results

View: No filter | Results: All 27 items

| Ligand | Binding Affinity (kcal/mol) | Mode | RMSD lower bound | RMSD |
|-------------------------|-----------------------------|------|------------------|--------|
| dpp_fix_3-pepidinol | -5.8 | 0 | 23.207 | 23.207 |
| dpp_fix_chloromphenicol | -5.9 | 0 | 0.0 | 0.0 |
| dpp_fix_chloromphenicol | -5.7 | 1 | 2.84 | 6.109 |
| dpp_fix_chloromphenicol | -5.6 | 2 | 3.65 | 6.849 |
| dpp_fix_chloromphenicol | -5.5 | 3 | 1.903 | 2.349 |
| dpp_fix_chloromphenicol | -5.2 | 4 | 27.877 | 29.925 |
| dpp_fix_chloromphenicol | -5.1 | 5 | 2.724 | 3.452 |
| dpp_fix_chloromphenicol | -5.0 | 6 | 15.198 | 16.188 |
| dpp_fix_chloromphenicol | -5.0 | 7 | 3.225 | 4.436 |
| dpp_fix_chloromphenicol | -4.9 | 8 | 2.743 | 3.479 |

Molecules

- dpp_fix
- dpp_fix_3-pepidinol
- dpp_fix_chloromphenicol
- dpp_fix_cyanoacetyl_urea

Controls

Vina Wizard | AutoDock Wizard | Open Babel | Python Shell | Logger

Start Here | Select Molecules | Run Vina | Analyze Results

View: No filter | Results: All 27 items

| Ligand | Binding Affinity (kcal/mol) | Mode | RMSD lower bound | RMSD |
|--------------------------|-----------------------------|------|------------------|--------|
| dpp_fix_chloromphenicol | -4.9 | 8 | 2.743 | 3.479 |
| dpp_fix_cyanoacetyl_urea | -5.0 | 0 | 0.0 | 0.0 |
| dpp_fix_cyanoacetyl_urea | -4.9 | 1 | 3.542 | 4.954 |
| dpp_fix_cyanoacetyl_urea | -4.9 | 2 | 4.033 | 6.07 |
| dpp_fix_cyanoacetyl_urea | -4.7 | 3 | 1.629 | 2.583 |
| dpp_fix_cyanoacetyl_urea | -4.4 | 4 | 23.333 | 24.936 |
| dpp_fix_cyanoacetyl_urea | -4.4 | 5 | 2.676 | 3.606 |
| dpp_fix_cyanoacetyl_urea | -4.3 | 6 | 2.911 | 6.662 |
| dpp_fix_cyanoacetyl_urea | -4.3 | 7 | 33.189 | 34.245 |
| dpp_fix_cyanoacetyl_urea | -4.2 | 8 | 23.503 | 24.25 |

Python - Virtual Screening tool

You are screen sharing | Stop Share

Navigator: Molecules, AutoDock, TVTK, Mayavi

View: 3D Scene, 2D Plots, Documents, Tables

Vina Wizard: AutoDock Wizard, Open Babel, Python Shell, Logger

Start Here | Select Molecules | Run Vina | Analyze Results

View: No filter | Results: All 27 items

| Ligand | Binding Affinity (kcal/mol) | Mode | RMSD lower bound | RMSD upper bound |
|-------------------------|-----------------------------|------|------------------|------------------|
| erb_fixfx_3-pepidinol | -4.5 | 0 | 0.0 | 0.0 |
| erb_fixfx_3-pepidinol | -4.3 | 1 | 3.729 | 4.414 |
| erb_fixfx_3-pepidinol | -4.2 | 2 | 2.349 | 2.932 |
| erb_fixfx_3-pepidinol | -4.1 | 3 | 2.476 | 2.902 |
| erb_fixfx_3-pepidinol | -4.0 | 4 | 2.04 | 2.445 |
| erb_fixfx_3-pepidinol | -4.0 | 5 | 2.577 | 2.899 |
| erb_fixfx_3-pepidinol | -3.9 | 6 | 2.749 | 3.255 |
| erb_fixfx_3-pepidinol | -3.8 | 7 | 23.192 | 23.824 |
| erb_fixfx_3-pepidinol | -3.3 | 8 | 23.65 | 24.475 |
| erb_fixfx_cisplatin_pdb | -6.0 | 0 | 0.0 | 0.0 |
| erb_fixfx_cisplatin_pdb | -5.6 | 1 | 2.218 | 5.16 |
| erb_fixfx_cisplatin_pdb | -5.3 | 2 | 2.119 | 3.888 |
| erb_fixfx_cisplatin_pdb | -5.3 | 3 | 2.278 | 4.238 |
| erb_fixfx_cisplatin_pdb | -5.2 | 4 | 2.638 | 4.64 |
| erb_fixfx_cisplatin_pdb | -5.1 | 5 | 1.908 | 3.537 |
| erb_fixfx_cisplatin_pdb | -5.1 | 6 | 2.173 | 5.365 |
| erb_fixfx_cisplatin_pdb | -4.9 | 7 | 24.077 | 27.058 |
| erb_fixfx_cisplatin_pdb | -4.9 | 8 | 2.191 | 5.198 |

Type here to search

24°C | 6:39 | 25/08/2021

Navigator: Molecules, AutoDock, TVTK, Mayavi

View: 3D Scene, 2D Plots, Documents, Tables, Run AutoGrid, Run AutoGrid, Run AutoGrid

Vina Wizard: AutoDock Wizard, Open Babel, Python Shell, Logger

Start Here | Select Molecules | Run Vina | Analyze Results

View: No filter | Results: All 27 items

| Ligand | Binding Affinity (kcal/mol) | Mode | RMSD lower bound | RMSD upper bound |
|------------------------|-----------------------------|------|------------------|------------------|
| erb_pppp_3-pepidinol | -1.9 | 0 | 0.0 | 0.0 |
| erb_pppp_3-pepidinol | -1.8 | 1 | 8.685 | 9.238 |
| erb_pppp_3-pepidinol | -1.6 | 2 | 8.414 | 9.249 |
| erb_pppp_3-pepidinol | -1.5 | 3 | 8.631 | 8.798 |
| erb_pppp_3-pepidinol | -1.5 | 4 | 9.042 | 9.574 |
| erb_pppp_3-pepidinol | -1.5 | 5 | 2.471 | 2.575 |
| erb_pppp_3-pepidinol | -1.4 | 6 | 9.065 | 9.684 |
| erb_pppp_3-pepidinol | -1.4 | 7 | 9.484 | 10.218 |
| erb_pppp_3-pepidinol | -1.0 | 8 | 7.243 | 8.126 |
| erb_pppp_cisplatin_pdb | -2.1 | 0 | 0.0 | 0.0 |
| erb_pppp_cisplatin_pdb | -1.8 | 1 | 7.852 | 10.769 |
| erb_pppp_cisplatin_pdb | -1.8 | 2 | 3.451 | 6.149 |
| erb_pppp_cisplatin_pdb | -1.8 | 3 | 9.335 | 11.282 |
| erb_pppp_cisplatin_pdb | -1.7 | 4 | 1.763 | 2.641 |
| erb_pppp_cisplatin_pdb | -1.6 | 5 | 2.469 | 3.871 |
| erb_pppp_cisplatin_pdb | -1.4 | 6 | 2.65 | 4.182 |
| erb_pppp_cisplatin_pdb | -1.3 | 7 | 5.452 | 8.276 |

PyMol - Virtual Screening Tool

You are screen sharing Stop Share

File Edit View Help

3D Scene 3D Plots Documents Tables

Vina Wizard AutoDock Wizard Open Babel Python Shell Logger

Start Here Select Molecules Run Vina Analyze Results

View: No filter Results: All 27 items

| Ligand | Binding Affinity (kcal/mol) | Mode | RMSD lower bound | RMSD upper bound |
|--------------------------------|-----------------------------|------|------------------|------------------|
| erb_palingfx_3_pepidinol | -4.4 | 0 | 0.0 | 0.0 |
| erb_palingfx_3_pepidinol | -4.3 | 1 | 2.534 | 3.425 |
| erb_palingfx_3_pepidinol | -4.2 | 2 | 2.696 | 3.799 |
| erb_palingfx_3_pepidinol | -4.1 | 3 | 8.557 | 9.145 |
| erb_palingfx_3_pepidinol | -4.1 | 4 | 7.895 | 8.414 |
| erb_palingfx_3_pepidinol | -4.0 | 5 | 2.102 | 2.652 |
| erb_palingfx_3_pepidinol | -4.0 | 6 | 8.21 | 8.696 |
| erb_palingfx_3_pepidinol | -4.0 | 7 | 8.154 | 8.591 |
| erb_palingfx_3_pepidinol | -3.9 | 8 | 14.287 | 14.983 |
| erb_palingfx_cisplatin_pdb | -5.6 | 0 | 0.0 | 0.0 |
| erb_palingfx_cisplatin_pdb | -5.6 | 1 | 1.383 | 4.248 |
| erb_palingfx_cisplatin_pdb | -5.5 | 2 | 19.382 | 22.079 |
| erb_palingfx_cisplatin_pdb | -5.4 | 3 | 21.524 | 23.941 |
| erb_palingfx_cisplatin_pdb | -5.2 | 4 | 27.106 | 29.962 |
| erb_palingfx_cisplatin_pdb | -5.2 | 5 | 2.373 | 5.548 |
| erb_palingfx_cisplatin_pdb | -5.2 | 6 | 22.278 | 24.77 |
| erb_palingfx_cisplatin_pdb | -5.2 | 7 | 24.845 | 27.246 |
| erb_palingfx_cisplatin_pdb | -5.1 | 8 | 22.016 | 24.429 |
| erb_palingfx_cyanosacetil_urea | -6.3 | 0 | 0.0 | 0.0 |

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PyMol - Virtual Screening Tool

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Vina Wizard AutoDock Wizard Open Babel Python Shell Logger

Start Here Select Molecules Run Vina Analyze Results

View: No filter Results: All 27 items

| Ligand | Binding Affinity (kcal/mol) | Mode | RMSD lower bound | RMSD upper bound |
|--------------------------------|-----------------------------|------|------------------|------------------|
| erb_palingfx_cisplatin_pdb | -5.6 | 0 | 0.0 | 0.0 |
| erb_palingfx_cisplatin_pdb | -5.6 | 1 | 1.383 | 4.248 |
| erb_palingfx_cisplatin_pdb | -5.5 | 2 | 19.382 | 22.079 |
| erb_palingfx_cisplatin_pdb | -5.4 | 3 | 21.524 | 23.941 |
| erb_palingfx_cisplatin_pdb | -5.2 | 4 | 27.106 | 29.962 |
| erb_palingfx_cisplatin_pdb | -5.2 | 5 | 2.373 | 5.548 |
| erb_palingfx_cisplatin_pdb | -5.2 | 6 | 22.278 | 24.77 |
| erb_palingfx_cisplatin_pdb | -5.2 | 7 | 24.845 | 27.246 |
| erb_palingfx_cisplatin_pdb | -5.1 | 8 | 22.016 | 24.429 |
| erb_palingfx_cyanosacetil_urea | -6.3 | 0 | 0.0 | 0.0 |
| erb_palingfx_cyanosacetil_urea | -6.2 | 1 | 0.0 | 0.0 |
| erb_palingfx_cyanosacetil_urea | -6.1 | 2 | 0.0 | 0.0 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 3 | 0.0 | 0.0 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 4 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 5 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 6 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 7 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 8 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 9 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 10 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 11 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 12 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 13 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 14 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 15 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 16 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 17 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 18 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 19 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 20 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 21 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 22 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 23 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 24 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 25 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 26 | 11.536 | 16.075 |
| erb_palingfx_cyanosacetil_urea | -6.0 | 27 | 11.536 | 16.075 |

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