

## 8 Supplementary Material

| <b>Abbreviations</b>      | <b>Module</b>             | <b>Name</b>           | <b>Constructor</b>                 | <b>Description</b>                                                                    |
|---------------------------|---------------------------|-----------------------|------------------------------------|---------------------------------------------------------------------------------------|
| <i>ABC</i>                | <i>ABCIndex</i>           | <i>ABC</i>            | <i>ABCIndex()</i>                  | <i>atom – bond connectivity_index</i>                                                 |
| <i>Top_dia</i>            | <i>Topological Index</i>  | <i>Diameter</i>       | <i>Diameter()</i>                  | <i>topological_diameter</i>                                                           |
| <i>Top_Shape</i>          | <i>Topological Index</i>  | <i>TopoShapeIndex</i> | <i>TopologicalShapeIndex()</i>     | <i>topological_shape_index</i>                                                        |
| <i>Walk_C</i>             | <i>WalkCount</i>          | <i>MWC01</i>          | <i>WalkCount(1, False, False)</i>  | <i>walk_count_(leg – 1)</i>                                                           |
| <i>Top_Charge</i>         | <i>Topological Charge</i> | <i>GGI1</i>           | <i>TopologicalCharge('raw', 1)</i> | <i>1 – ordered raw topological_charge</i>                                             |
| <i>Top_PSA</i>            | <i>TopoPSA</i>            | <i>TopoPSA(NO)</i>    | <i>TopoPSA(True)</i>               | <i>topological_polar surface_area (use_only_nitrogen and_oxygen)</i>                  |
| <i>S_log</i>              | <i>SLogP</i>              | <i>SLogP</i>          | <i>SLogP()</i>                     | <i>Wildman – Crippen_LogP</i>                                                         |
| <i>R_B_C</i>              | <i>RotatableBond</i>      | <i>nRot</i>           | <i>RotatableBondsCount()</i>       | <i>rotatable_bonds_count</i>                                                          |
| <i>Wiener</i>             | <i>WienerIndex</i>        | <i>WPath</i>          | <i>WienerIndex(False)</i>          | <i>Wiener_index</i>                                                                   |
| <i>Z1</i>                 | <i>ZagrebIndex</i>        | <i>Zagreb1</i>        | <i>ZagrebIndex(1, 1)</i>           | <i>Zagreb_index (version_1)</i>                                                       |
| <i>Z2</i>                 | <i>ZagrebIndex</i>        | <i>Zagreb2</i>        | <i>ZagrebIndex(2, 1)</i>           | <i>Zagreb_index (version_2)</i>                                                       |
| <i>mZagreb2</i>           | <i>ZagrebIndex</i>        | <i>mZagreb2</i>       | <i>ZagrebIndex(2, -1)</i>          | <i>modified_Zagreb index_(version_2)</i>                                              |
| <i>Acid_Base</i>          | <i>AcidBase</i>           | <i>nAcid</i>          | <i>AcidicGroupCount()</i>          | <i>acidic group count</i>                                                             |
| <i>Arom_atic</i>          | <i>Aromatic</i>           | <i>nAromAtom</i>      | <i>AromaticAtomsCount()</i>        | <i>aromatic atoms count</i>                                                           |
| <i>Arom_atic_1</i>        | <i>Aromatic</i>           | <i>nAromBond</i>      | <i>AromaticBondsCount()</i>        | <i>aromatic bonds count</i>                                                           |
| <i>Atom_Count</i>         | <i>AtomCount</i>          | <i>nAtom</i>          | <i>AtomCount('Atom')</i>           | <i>number of all atoms</i>                                                            |
| <i>Atom_Count_1</i>       | <i>AtomCount</i>          | <i>nHeavyAtom</i>     | <i>AtomCount('HeavyAtom')</i>      | <i>number of heavy atoms</i>                                                          |
| <i>Atom_Count_2</i>       | <i>AtomCount</i>          | <i>nSpiro</i>         | <i>AtomCount('Spiro')</i>          | <i>number of spiro atoms</i>                                                          |
| <i>Atom_Count_3</i>       | <i>AtomCount</i>          | <i>nBridgehead</i>    | <i>AtomCount('Bridgehead')</i>     | <i>number of bridgehead atoms</i>                                                     |
| <i>Atom_Count_4</i>       | <i>AtomCount</i>          | <i>nHetero</i>        | <i>AtomCount('Hetero')</i>         | <i>number of hetero atoms</i>                                                         |
| <i>Atom_Count_5</i>       | <i>AtomCount</i>          | <i>nX</i>             | <i>AtomCount('X')</i>              | <i>number of halogen atoms</i>                                                        |
| <i>Auto_correlation</i>   | <i>Autocorrelation</i>    | <i>ATS0m</i>          | <i>ATS(0, 'm')</i>                 | <i>moreau – broto autocorrelation of lag 0 weighted by mass</i>                       |
| <i>Auto_correlation_1</i> | <i>Autocorrelation</i>    | <i>AATS0m</i>         | <i>AATS(0, 'm')</i>                | <i>averaged moreau – broto autocorrelation of lag 0 weighted by mass</i>              |
| <i>Auto_correlation_2</i> | <i>Autocorrelation</i>    | <i>ATSC0m</i>         | <i>ATSC(0, 'm')</i>                | <i>centered moreau – broto autocorrelation of lag 0 weighted by mass</i>              |
| <i>Auto_correlation_3</i> | <i>Autocorrelation</i>    | <i>AATSC0m</i>        | <i>AATSC(0, 'm')</i>               | <i>averaged and centered moreau – broto autocorrelation of lag 0 weighted by mass</i> |
| <i>Auto_correlation_4</i> | <i>Autocorrelation</i>    | <i>MATS1m</i><br>20   | <i>MATS(1, 'm')</i>                | <i>moran coefficient of lag 1 weighted by mass</i>                                    |

| <b>Abbreviations</b>                | <b>Module</b>                       | <b>Name</b>         | <b>Constructor</b>                               | <b>Description</b>                                           |
|-------------------------------------|-------------------------------------|---------------------|--------------------------------------------------|--------------------------------------------------------------|
| <i>Auto correlation_5</i>           | <i>Autocorrelation</i>              | <i>GATS1m</i>       | <i>GATS(1, 'm')</i>                              | <i>geary coefficient of lag 1 weighted by mass</i>           |
| <i>Balaban_J</i>                    | <i>BalabanJ</i>                     | <i>BalabanJ</i>     | <i>BalabanJ()</i>                                | <i>Balaban's J index</i>                                     |
| <i>Bertz_CT</i>                     | <i>BertzCT</i>                      | <i>BertzCT</i>      | <i>BertzCT()</i>                                 | <i>Bertz CT</i>                                              |
| <i>Bond_Count</i>                   | <i>BondCount</i>                    | <i>nBonds</i>       | <i>BondCount('any', False)</i>                   | <i>number of all bonds in non-kekulized structure</i>        |
| <i>Carbon_Types</i>                 | <i>CarbonTypes</i>                  | <i>C1SP3</i>        | <i>CarbonTypes(1, 3)</i>                         | <i>SP3 carbon bound to 1 other carbon</i>                    |
| <i>Constitutional</i>               | <i>Constitutional</i>               | <i>Sv</i>           | <i>ConstitutionalSum('v')</i>                    | <i>sum of constitutional weighted by vdw volume</i>          |
| <i>Constitutional_1</i>             | <i>Constitutional</i>               | <i>Mv</i>           | <i>ConstitutionalMean('v')</i>                   | <i>mean of constitutional weighted by vdw volume</i>         |
| <i>Eccentric Connectivity Index</i> | <i>Eccentric Connectivity Index</i> | <i>ECIndex</i>      | <i>EccentricConnectivityIndex()</i>              | <i>eccentric connectivity index</i>                          |
| <i>E_State</i>                      | <i>EState</i>                       | <i>NsLi</i>         | <i>AtomTypeEState('count', 'sLi')</i>            | <i>number of sLi</i>                                         |
| <i>Fragment Complexity</i>          | <i>Fragment Complexity</i>          | <i>fragCpx</i>      | <i>FragmentComplexity()</i>                      | <i>fragment complexity</i>                                   |
| <i>Frame_work</i>                   | <i>Framework</i>                    | <i>fMF</i>          | <i>Framework()</i>                               | <i>molecular framework ratio</i>                             |
| <i>Hydrogen Bond</i>                | <i>HydrogenBond</i>                 | <i>nHBAcc</i>       | <i>HBondAcceptor()</i>                           | <i>number of hydrogen bond acceptor</i>                      |
| <i>Hydrogen Bond_1</i>              | <i>HydrogenBond</i>                 | <i>nHBDon</i>       | <i>HBondDonor()</i>                              | <i>number of hydrogen bond donor</i>                         |
| <i>Information Content</i>          | <i>Information Content</i>          | <i>IC0</i>          | <i>InformationContent(0)</i>                     | <i>0 – ordered neighborhood information content</i>          |
| <i>Information Content_1</i>        | <i>Information Content</i>          | <i>IC1</i>          | <i>InformationContent(1)</i>                     | <i>1 ordered neighborhood information content</i>            |
| <i>Information Content_2</i>        | <i>Information Content</i>          | <i>IC2</i>          | <i>InformationContent(2)</i>                     | <i>2 – ordered neighborhood information content</i>          |
| <i>Information Content_4</i>        | <i>Information Content</i>          | <i>IC4</i>          | <i>InformationContent(4)</i>                     | <i>4 – ordered neighborhood information content</i>          |
| <i>Information Content_5</i>        | <i>Information Content</i>          | <i>IC5</i>          | <i>InformationContent(5)</i>                     | <i>5 – ordered neighborhood information content</i>          |
| <i>Information Content_6</i>        | <i>Information Content</i>          | <i>IC6</i>          | <i>InformationContent(6)</i>                     | <i>6 – ordered neighborhood information content</i>          |
| <i>Lipinski</i>                     | <i>Lipinski</i>                     | <i>Lipinski</i>     | <i>Lipinski()</i>                                | <i>Lipinski rule of five</i>                                 |
| <i>Lipinski_1</i>                   | <i>Lipinski</i>                     | <i>GhoseFilter</i>  | <i>GhoseFilter()</i>                             | <i>Ghose filter</i>                                          |
| <i>Log_S</i>                        | <i>LogS</i>                         | <i>FilterItLogS</i> | <i>LogS()</i>                                    | <i>Filter – it LogS</i>                                      |
| <i>McGowan Volume</i>               | <i>McGowan</i>                      | <i>VMcGowan</i>     | <i>McGowanVolume()</i>                           | <i>McGowan volume</i>                                        |
| <i>Moe_Type</i>                     | <i>MoeType</i>                      | <i>LabuteASA</i>    | <i>LabuteASA()</i>                               | <i>Labute's Approximate Surface Area</i>                     |
| <i>Moe_Type_1</i>                   | <i>MoeType</i>                      | <i>PEOE_VSA1</i>    | <i>PEOE_VSA(1)</i>                               | <i>MOE_Charge_VSA_Descriptor1 (-inf &lt; x &lt; -0.30)</i>   |
| <i>Moe_Type_2</i>                   | <i>MoeType</i>                      | <i>PEOE_VSA2</i>    | <i>PEOE_VSA(2)</i>                               | <i>MOE_Charge_VSA_Descriptor2 (-0.30 &lt;= x &lt; -0.25)</i> |
| <i>Moe_Type_3</i>                   | <i>MoeType</i>                      | <i>PEOE_VSA3</i>    | <i>PEOE_VSA(3)</i>                               | <i>MOE_Charge_VSA_Descriptor3 (-0.25 &lt;= x &lt; -0.20)</i> |
| <i>Moe_Type_4</i>                   | <i>MoeType</i>                      | <i>PEOE_VSA4</i>    | <i>PEOE_VSA(4)</i>                               | <i>MOE_Charge_VSA_Descriptor4 (-0.20 &lt;= x &lt; -0.15)</i> |
| <i>Moe_Type_5</i>                   | <i>MoeType</i>                      | <i>PEOE_VSA5</i>    | <i>PEOE_VSA(5)</i>                               | <i>MOE_Charge_VSA_Descriptor5 (-0.15 &lt;= x &lt; -0.10)</i> |
| <i>Path_Count</i>                   | <i>PathCount</i>                    | <i>MPC2</i>         | <i>PathCount(2, False, False, False)</i>         | <i>1 – ordered path count</i>                                |
| <i>Polariz_ability</i>              | <i>Polarizability</i>               | <i>apol</i>         | <i>APol(False)</i>                               | <i>atomic polarizability</i>                                 |
| <i>Polariz_ability_1</i>            | <i>Polarizability</i>               | <i>bpol</i>         | <i>BPol(False)</i>                               | <i>bond polarizability</i>                                   |
| <i>Ring_Count</i>                   | <i>RingCount</i>                    | <i>nRing</i>        | <i>RingCount(None, False, False, None, None)</i> | <i>ring count</i>                                            |
| <i>MW</i>                           | <i>Weight</i>                       | <i>MW</i>           | <i>Weight(True, False)</i>                       | <i>exact molecular weight</i>                                |