Subscription Rates for Texas A&M University Researchers FY23

<table>
<thead>
<tr>
<th>Subscription Type</th>
<th>Number of Users with Access to LMS Software and Hardware</th>
<th>Consulting Hours Included</th>
<th>Cost per year</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>PI &amp; 1 researcher</td>
<td>5</td>
<td>$500</td>
</tr>
<tr>
<td>2</td>
<td>PI &amp; 2 researchers</td>
<td>10</td>
<td>$1000</td>
</tr>
<tr>
<td>3</td>
<td>PI &amp; 3 researchers</td>
<td>15</td>
<td>$1500</td>
</tr>
<tr>
<td>4</td>
<td>PI &amp; 4+ researchers</td>
<td>20</td>
<td>$2000</td>
</tr>
</tbody>
</table>

Consulting Fee for non-subscribers and additional hours for subscribers: $65/hour

In addition to the consulting hours, an annual subscription to the LMS gives the PI and designated researcher(s) access to the licensed software and hardware outlined below.

### Licensed Software

**Company** | **Software**
---|---
**Dassault Systèmes** | **BIOVIA Materials Studio** Visualizer, Conformers, Forcite Plus, Gaussian Interface, QSAR+, Reflex, VAMP, MS Pipeline Pilot Collection, Adsorption Locator, Amorphous Cell, Blends, Compass, GULP, Mesocite, Mesodyn, Sorption, Synthia, CASTEP, DFTB+, DMOL3, NMR CASTEP, ONETEP, QMERA
**Dassault Systèmes** | **BIOVIA Discovery Studio** Visualizer, Analysis, Biopolymer, Catalyst (Conformation, Score DB Build, Search, Hypothesis, SBP & Shape), CHARMM, DMOL3, MMFF, Protein Refine, QUANTUMm, CFF FF, De Novo Evolution, De Novo Ligand Builder, Flexible Docking, LibDock, LigandFit, LigandScore, Ludi, MCSS, MODELER, Protein Docking: ZDOCK and RDOCK, Protein Families, Protein Health, Sequence Analysis, X-ray.
**Materials Design** | **MedeA Software** MedeA Environment (includes MedeA GUI, MedeA Analysis, MedeA Builders, MedeA JobServer and TaskServer, MedeA InfoMaticA, MedeA COD GUI, MedeA LAMMPS GUI, and MedeA Forcefield)
**Schrödinger** | **Schrödinger** suite of software: Maestro, CombiGlide, Glide, Liaison, Strike, QikProp, Canvas, LigPrep, BioLuminate GUI, Prime, Qsite, MacroModel, ConfGen, Jaguar, pKa Predictor, Epik, SiteMap, and PIPER.
**CCG** | **MOE**: Molecular Operating Environment. A fully integrated drug discovery software package, including structure-based design, fragment-based design, pharmacophore discovery, medicinal and biologics applications, protein and antibody modeling, molecular mechanics/dynamics, cheminformatics and QSAR.
**Gaussian** | **Gaussian** (09 & 16)
**GaussView** | **GaussView 6 with GMMX add-on**
**Molpro** | **Molpro**
**SCM** | **ADF & ADF-GUI**
**TK Gristmill** | **AIMALL Professional**
**NBO** | **NBO7**
**Chemissian** | **Chemissian**

### Hardware:

**Computer** | Configuration
**LMS** | 10 Dell Precision T3420 workstations NVIDIA Quadro K620 GPU
**MM** | 2060 core cluster. 76 20-core cpu nodes & 27 20-core gpu nodes (K20).