Cyrus automates a set of Rosetta protein design software protocols as an easy-to-use, SaaS offering proven to reliably identify stabilizing mutations in a wide variety of proteins:

- Correctly predict stabilizing single protein point mutants faster and more accurately than FEP.
- Category-leading performance in quantitatively calculating energy change upon point mutation.
- Experimentally proven protein stabilization algorithms.

Highest prediction accuracy and confidence
Cyrus delivers software that is refined and tested on large experimental data sets. Cyrus has recently released an improved version of the protein mutational free energy calculator in Rosetta, based on work from the DiMaio lab at UW (1).

Experimentally demonstrated thermo-stabilization
Thermo-stabilization is often achieved by re-designing a protein core. Our custom-built stabilization protocol has been experimentally validated on a number of proteins (2,3).

<table>
<thead>
<tr>
<th></th>
<th>Rosetta***</th>
<th>FEP*</th>
<th>CC/PBSA**</th>
<th>EGAD**</th>
<th>Imutant2**</th>
<th>FoldX**</th>
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</thead>
<tbody>
<tr>
<td>Exp’t correlation</td>
<td>0.69</td>
<td>0.63</td>
<td>0.56</td>
<td>0.59</td>
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<td>1065</td>
<td>933</td>
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</tbody>
</table>

Preliminary computational accuracy and throughput results:

- FEP*: Throughput: 2-4 mutations/day per GPU card
- Rosetta***: Throughput: 5,000-10,000 mutations/day

Predictions for the FoldX experimentally stability data set (Guerois, Nielson & Serrano JMB 320 369 (2002))
**From: Potapov, Cohen & Schreiber PEDS 22 553 (2009)
***From: Kellogg, Leaver-Fay & Baker Proteins 79 830 (2011)