



## Biopython Project Update 2015

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Website: <http://biopython.org>

Repository: <https://github.com/biopython/biopython>

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The Biopython Project is a long-running distributed collaborative effort, supported by the Open Bioinformatics Foundation, which develops a freely available Python library for biological computation [1].

We present here details of the latest Biopython release - version 1.65. New features include: extended Bio.KEGG and Bio.Graphics modules to support the KEGG REST API, as well as parsing, representing, and drawing KGML pathways; inclusion of the new NCBI genetic code table 24 (Pterobranchia Mitochondrial) and corresponding translation functionality in Bio.Data; improvements to Bio.SeqIO (parse and index\_db methods) and Bio.SearchIO (hit retrieval using alternative IDs); and a rewritten Bio.SeqUtils.MeltingTemp with additional methods to calculate oligonucleotide melting temperatures. Additionally, we continued our efforts to abide by the PEP8 coding style guidelines, namely using lowercase module names in new experimental modules.

We are currently preparing a new release - version 1.66 - that will feature additional improvements to the Bio.KEGG and Bio.Graphics modules (support for transparency in KGML pathways), extended support for the “abi” format in Bio.SeqIO, miscellaneous improvements to the test suite, and further adherence to PEP8. In addition, our participation in Google Summer of Code 2014 had Evan Parker adding lazy-parsing support for Bio.SeqIO. The additions are currently under review and should soon be integrated.

Finally, complementary to these developments, we created a new repository for Docker containers. The included containers support both Python versions 2 & 3 and install all of Biopython’s dependencies. They are, therefore, useful for development, but also for teaching due to the inclusion of IPython Notebooks.

## References

- [1] Cock, P.J.A., Antao, T., Chang, J.T., Chapman, B.A., Cox, C.J., Dalke, A., Friedberg, I., Hamelryck, T., Kauff, F., Wilczynski, B., de Hoon, M.J. (2009) Biopython: freely available Python tools for computational molecular biology and bioinformatics. *Bioinformatics* **25**(11) 1422-3. doi:10.1093/bioinformatics/btp163

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