

Resource Summary Report

Generated by [nidm-terms](#) on Aug 9, 2026

BCM ET

RRID:SCR_008495

Type: Tool

Proper Citation

BCM ET (RRID:SCR_008495)

Resource Information

URL: <http://mammoth.bcm.tmc.edu/server.html>

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Description: It ranks amino acid residues in a protein sequence by their relative evolutionary importance, and when a structure is available for that protein, it also can display a structural map of where top-ranked residues fall. This can be useful for rational function re-design and protein engineering because biologist can then efficiently target mutations to the most relevant parts of a protein. For example, one may selectively block, separate, rewire, or mimic functions. ET-based functional annotations may also be useful to suggest protein function (see the ET Annotation Server). ET rank essentially captures the extent of evolutionary pressure at a given sequence position. It is obtained by correlating the sequence variations in an alignment of a protein family with its evolutionary divergences. Top-ranked residues are associated with variations that correlate with large divergences near the root of the evolutionary tree, and presumably linked to significant functional changes. Poorly-ranked residues in contrast are associated with variations near the leaves of the tree, presumably linked to modest functional differences, if any at all. We provide two means of generating and visualizing the ET ranks of importance: the ET Viewer and the ET report_maker. 0. The ET Viewer runs real-value ET or integer ET and displays results. Its ET Wizard takes a PDB identifier, or file, for input, and it outputs ranks of evolutionary importance for every sequence position in the protein. All trace parameters may be adjusted; custom alignments and phylogenetic trees may be used. The ET Viewer then displays a color map of the structure showing which residues are ranked among the top nth percentile, where n is adjustable, and whether they cluster (a z-score indicates whether these top-ranked residues cluster in a statistically significant manner). A multiple sequence alignment viewer and phylogenetic tree viewer display the underlying data. 0. (06/19/2009)A special note for Mac users: 0. The latest Java update for Mac, Java for Mac OS X 10.5 Update 4, moves the Java Web Start application to a new location, causing problems launching ET viewer and other Java Web Start programs. In order to fix this, you need to show your computer where the new location is for Java Web Start. In Finder, select the ET_Viewer_2_pub.jnlp file (which is probably in your downloads folder). Under the File menu, select Get Info. In the resulting window, there's a section called Open With:

Click the drop-down menu and select Other.... A new window will open. Navigate to your hard drive, select System, then Library, then CoreServices, and then select Java Web Start.app. Then click the Change All... button in the Open With: section to make this change permanent. Sponsor. A.D.W., S.E. and R.M.W. were also supported by training fellowships from the National Library of Medicine to the Keck Center for Interdisciplinary Bioscience Training of the Gulf Coast Consortia.

Abbreviations: BCM, ET

Synonyms: Evolutionary Trace, Baylor College of Medicine, Evolutionary Trace Server

Resource Type: database, data or information resource

Resource Name: BCM ET

Resource ID: SCR_008495

Alternate IDs: nif-0000-30501

Record Creation Time: 20220129T080247+0000

Record Last Update: 20260808T190422+0000

Ratings and Alerts

No rating or validation information has been found for BCM ET.

No alerts have been found for BCM ET.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.