

# Resource Summary Report

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## Webproanalyst

RRID:SCR\_008348

Type: Tool

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### Proper Citation

Webproanalyst (RRID:SCR\_008348)

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### Resource Information

**URL:** <http://wwwmgs.bionet.nsc.ru/mgs/programs/panalyst/>

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**Description:** WebProAnalyst provides web-accessible analysis for scanning the quantitative structure-activity relationships in protein families. It searches for a sequence region, whose substitutions are correlated with variations in the activities of a homologous protein set, the so-called activity modulating sites. WebProAnalyst allows users to search for the key physicochemical characteristics of the sites that affect the changes in protein activities. It enables the building of multiple linear regression and neural networks models that relate these characteristics to protein activities. WebProAnalyst implements multiple linear regression analysis, back propagation neural networks and the Structure-Activity Correlation/Determination Coefficient (SACC/SADC). A back propagation neural network is implemented as a two-layered network, one layer as input, the other as output (Rumelhart et al, 1986). WebProAnalyst uses alignment of amino acid sequences and data on protein activity (pK, Km, ED50, among others). The input data are the numerical values for the physicochemical characteristics of a site in the multiple alignment given by a slide window. The output data are the predicted activity values. The current version of WebProAnalyst handles a single activity for a single protein. The SACC/SADC may be defined as an estimate of the strongest multiple correlation between the physicochemical characteristics of a site in a multiple alignment and protein activities. The SACC/SADC coefficient makes possible the calculation of the possible highest correlation achievable for the quantitative relationship between the physicochemical properties of sites and protein activities. The SACC/SADC is a convenient means for an arrangement of positions by their functional significance. WebProAnalyst outputs a list of multiple alignment positions, the respective correlation values, also regression analysis parameters for the relationships between the amino acid physicochemical characteristics at these positions and the protein activity values.

**Synonyms:** Webproanalyst

**Resource Type:** analysis service resource, data analysis service, production service resource, service resource

**Keywords:** family, functional, activity, alignment, amino acid, homologous, modulating site, neural, physicochemical, propagation, protein, quantitative, region, relationship, scan, sequence, structure, substitution, variation, bio.tools

**Resource Name:** Webproanalyst

**Resource ID:** SCR\_008348

**Alternate IDs:** nif-0000-25212, biotools:webproanalyst

**Alternate URLs:** <https://bio.tools/webproanalyst>

**Record Creation Time:** 20220129T080246+0000

**Record Last Update:** 20260808T190414+0000

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## Ratings and Alerts

No rating or validation information has been found for Webproanalyst.

No alerts have been found for Webproanalyst.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.