



IdentiPROT

**комплексное решение для потока протеемных данных
по принципу «все включено»**

The image shows a browser window with several tabs open. The active tab is titled "Welcome to Ide...". The address bar shows the URL "identiprot.theorchromo.ru/logout/". The website content features a large blue header with the text "IdentiPROT" and navigation links for "ABOUT", "LOG IN", and "CONTACTS". A main heading reads "Welcome to the home of IdentiPROT software!". Below this, a message states: "If you have problems logging in, any questions or comments, please [contact](#) our administrators to create account." On the right side, there is a dark blue box with the text "WELCOME The single entry point for your proteomic data mining". Below this box are two input fields labeled "Email" and "Password", followed by a prominent blue "Log in" button.

Вход через Интернет из клиентского места, включая мобильные устройства

New Search

identiprot.theorchromo.ru/data/

load parameters

send email notification

use auto optimization

enzyme: [add custom cleavage rule](#) trypsin

number of missed cleavages 2

precursor accuracy unit ppm

precursor accuracy left 10

precursor accuracy right 10

precursor isotope mass error 0

product accuracy, Da 0.1

FDR 1.0

FDR type psm

minimum charge 2

maximum charge 3

generate decoy db no

decoy method reverse

decoy prefix DECOY_

dynamic range 100

peptide minimum length 5



Ввод параметров поиска

New Search

identiprot.theorchromo.ru/data/

matched fragments, min 1

use scoring function hypescore

score threshold 0

show unmatched spectra in results no

report number of sequence candidates 1

[select fixed modifications](#) camC

[select potential modifications](#)

peptide mass shift 0

Post-search validation

PSM count

PSMs per protein

charge states

potential modifications

fragment mass tolerance

precursor mass difference

isotopes mass error

missed cleavages

RT difference

Enter search run name

RUNIDENTIPROT

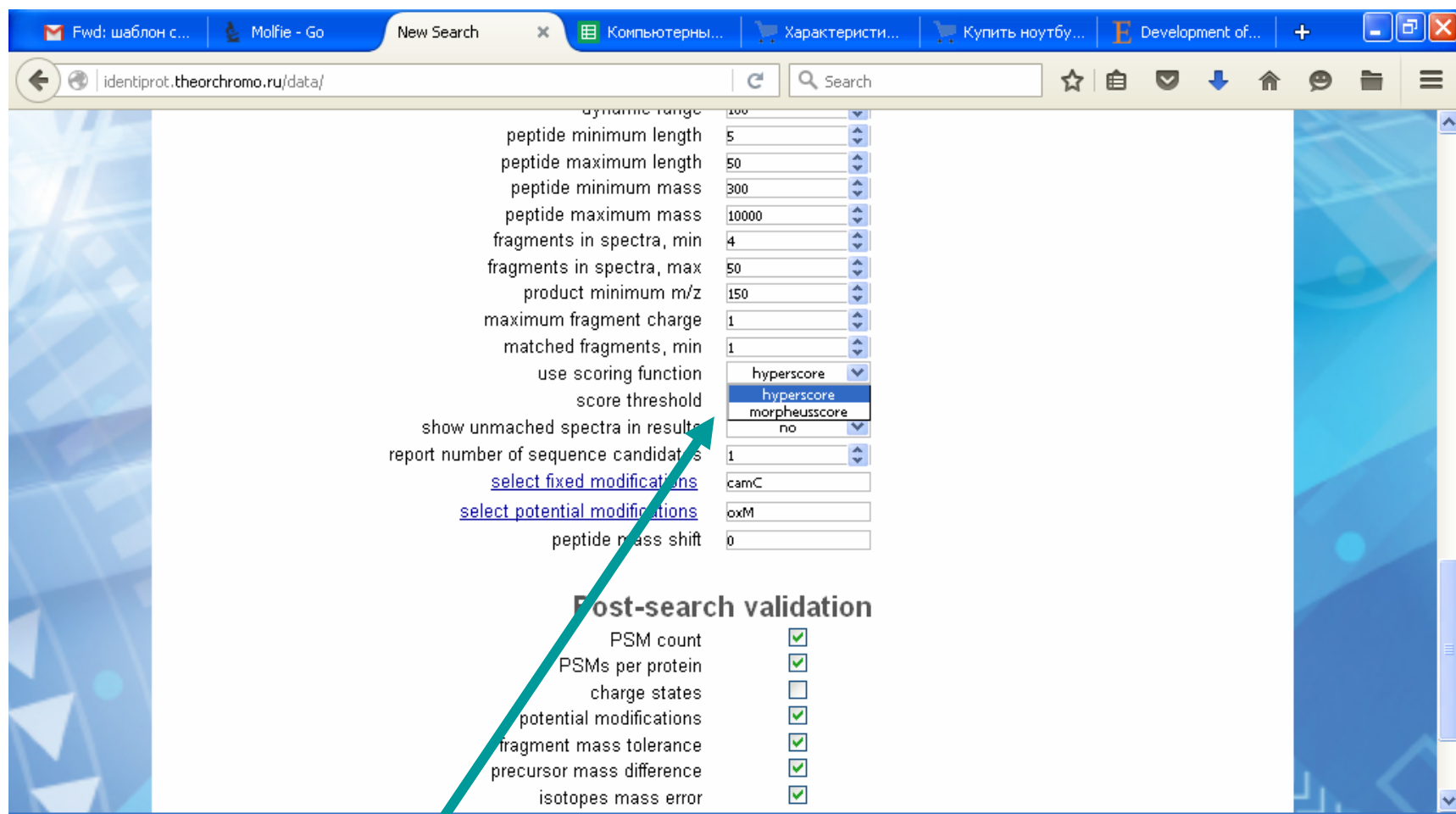
Clear chosen files



Послепоисковое
валидирование
идентификаций
(до 9 ортогональных
критериев)

The screenshot shows the IDENTIPROT web interface. At the top, there is a navigation bar with several tabs: "Fwd: шаблон с...", "Molfie - Go", "New Search", "Компьютерны...", "Характеристи...", "Купить ноутбу...", and "Development of...". Below the navigation bar is a search bar with the URL "identiprot.theorchromo.ru/data/" and a search icon. The main content area is titled "choose preloaded protein database file" and includes a text input field "Enter search run name" and a large orange button labeled "RUN IDENTIPROT". Below this is a section titled "Specify search parameters" with three tabs: "MINIMAL", "MEDIUM", and "ADVANCED". The "ADVANCED" tab is selected. The parameters listed are: "send email notification" (checkbox), "use auto optimization" (checkbox with a checkmark), "enzyme: [add custom cleavage rule](#)" (dropdown menu showing "trypsin"), "number of missed cleavages" (input field with "5"), "precursor accuracy unit" (dropdown menu showing "ppm"), "precursor accuracy left" (input field with "10"), "precursor accuracy right" (input field with "10"), "precursor isotopic mass error" (input field with "0"), "product accuracy, Da" (input field with "0.05"), "FDR" (input field with "1"), "FDR type" (dropdown menu showing "protein"), "minimum charge" (input field with "2"), and "maximum charge" (input field with "5"). A green arrow points from the bottom text to the "use auto optimization" checkbox.

Автоматическая оптимизация входных параметров поиска под конкретные данные



Выбор сторонней скоринг-функции в режиме выбора параметров поиска «Advanced»

The image shows two screenshots of the IdentiPROT web application. The top screenshot displays the main interface with a search history table. A teal arrow points from the 'testsearch01' entry to the second screenshot. The second screenshot shows the search results page for 'testsearch01/test', including a summary table, download options, and three histograms for PSM distributions.

Вывод результатов поиска

START A NEWSEARCH RUN

Интерактивный просмотр идентификаций и их распределений по экспериментальным параметрам и физико=химическим свойствам пептидов

Search name	PSMs	Peptides	Proteins	FDR, %	FDR type	MS/MS	Unfiltered PSMs
test	178	82	32	1.0	psm	3000	2356

Download: [csv files](#) [pepxml files](#) [mgf files](#)
[figures in png format](#) [figures in svg format](#) [show parameters](#)

PSM distributions

- PSMs RT experimental_min
- PSMs precursor m/z
- PSMs peptide length



Расчет трех количественных индексов относительного содержания идентифицированных белков

Search results: 2016-08-10 19-02-45/
20160809 01 HeLa

Search name	PSMs	Peptides	Proteins	FDR, %	FDR type	MS/MS	Unfiltered PSMs
20160809_01_HeLa	20521	18718	3870	1.0			

Select columns for proteins:

dbname description PSMs peptides sequence coverage
 LFQ(S/n) LFQ(NSAF) LFQ(emPAI) protein LN(e value) all proteins

dbname	PSMs
sp P38646 GRP75_HUMAN	38
sp Q9UKI8-3 ITLK1_HUMAN	1
sp O75694-2 INU155_HUMAN	10
sp P50995 JANX11_HUMAN	8
sp P15880 IRS2_HUMAN	17
sp P07108-4 ACBP_HUMAN	2
sp Q9HC68 CWC22_HUMAN	1

UniProtKB - P38646 (GRP75_HUMAN)

Display [BLAST](#) [Align](#) [Format](#) [Add to basket](#) [History](#)

Entry **Protein** | Stress-70 protein, mitochondrial
Gene | HSPA9
Organism | *Homo sapiens (Human)*

Интерактивный режим просмотра белковых identifications