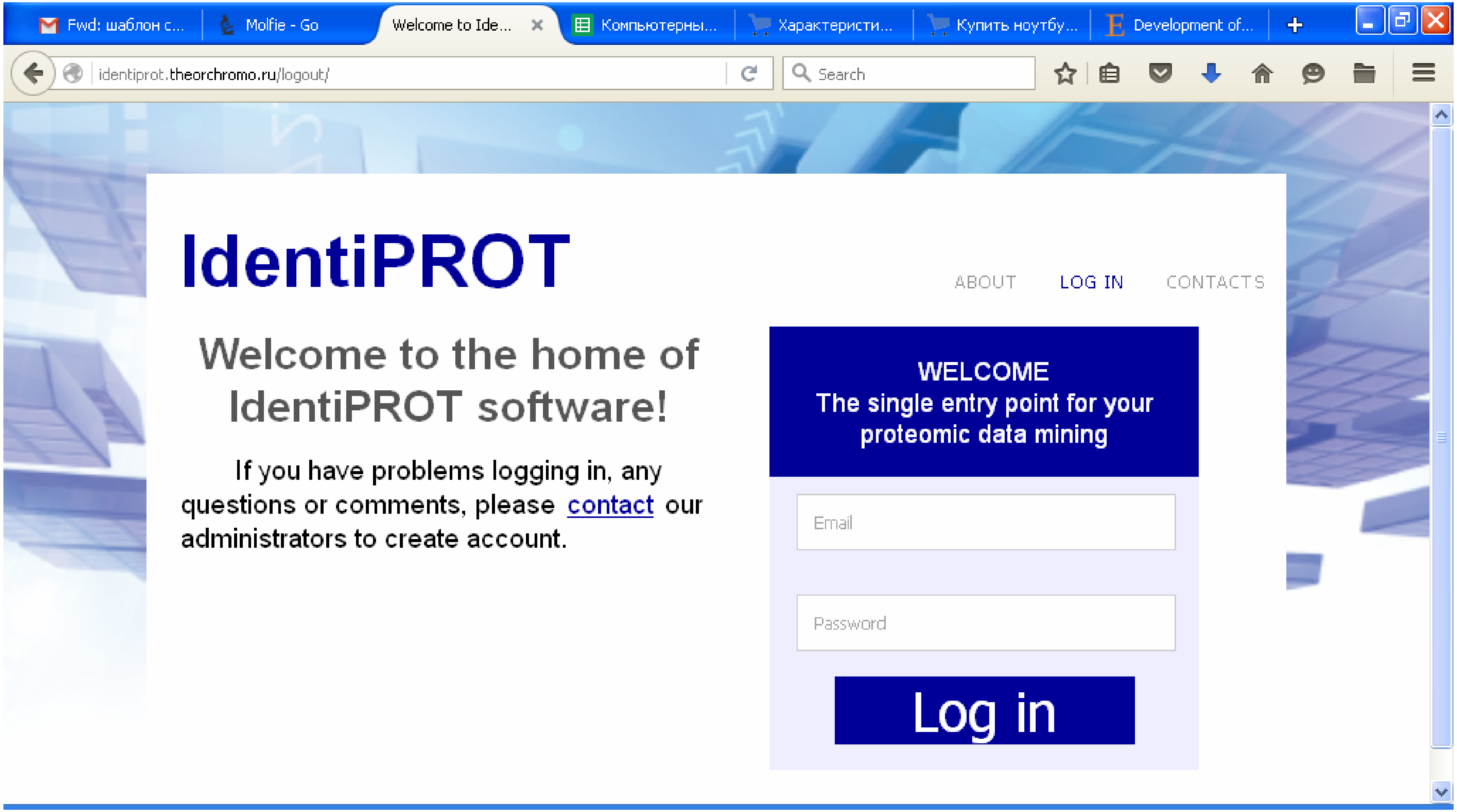
IdentiPROT

комплексное решение для потока протеомных данных по принципу «все включено»



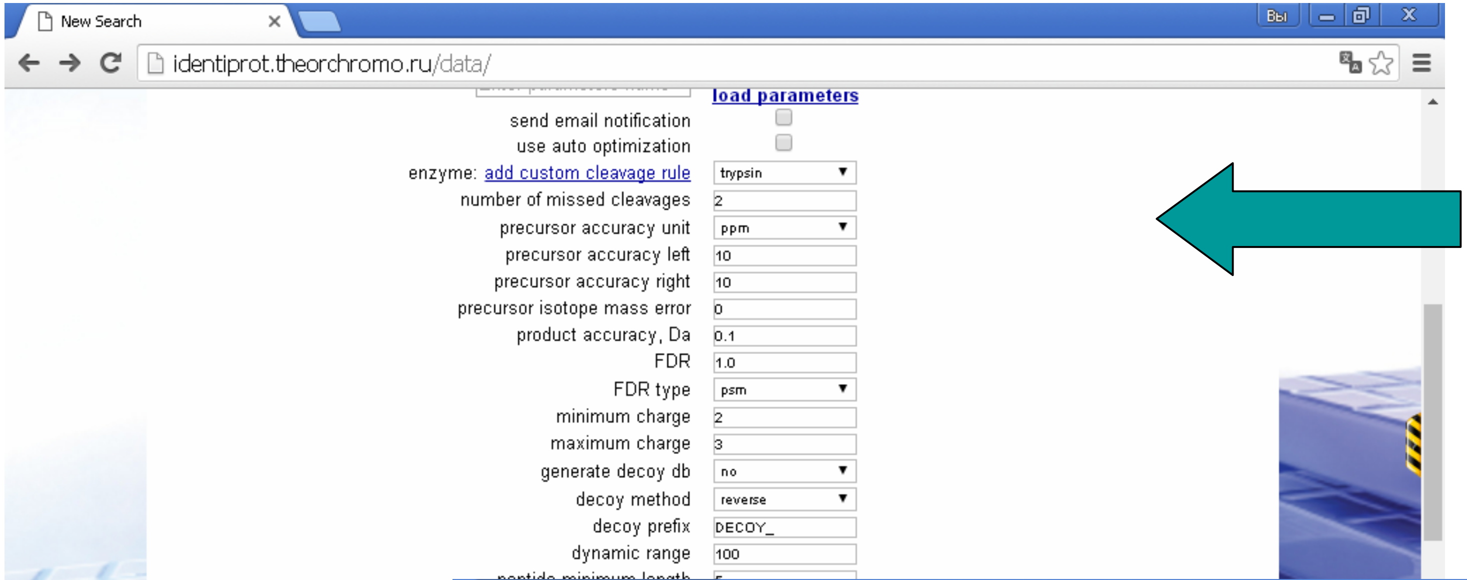
IdentiPROT

Welcome to the home of IdentiPROT software!

If you have problems logging in, any questions or comments, please contact our administrators to create account.

WELCOME
The single entry point for your proteomic data mining

Вход через Интернет из клиентского места, включая мобильные устройства



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

Ввод параметров поиска

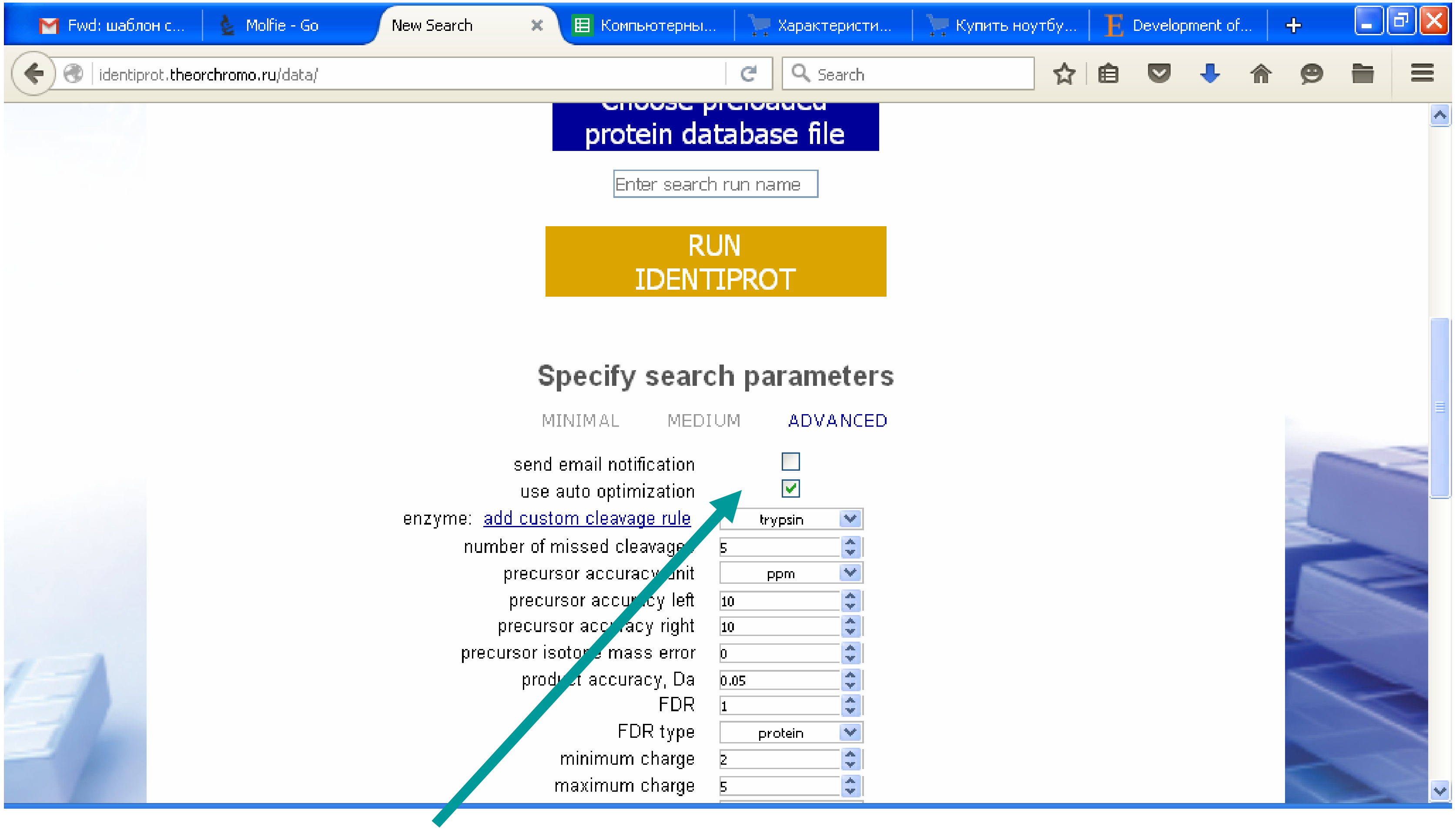
use scoring function: hyperscore
score threshold: 0
show unmached spectra in results: no
report number of sequence candidates: 1
select fixed modifications: camC
select potential modifications:
peptide mass shift: 0

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

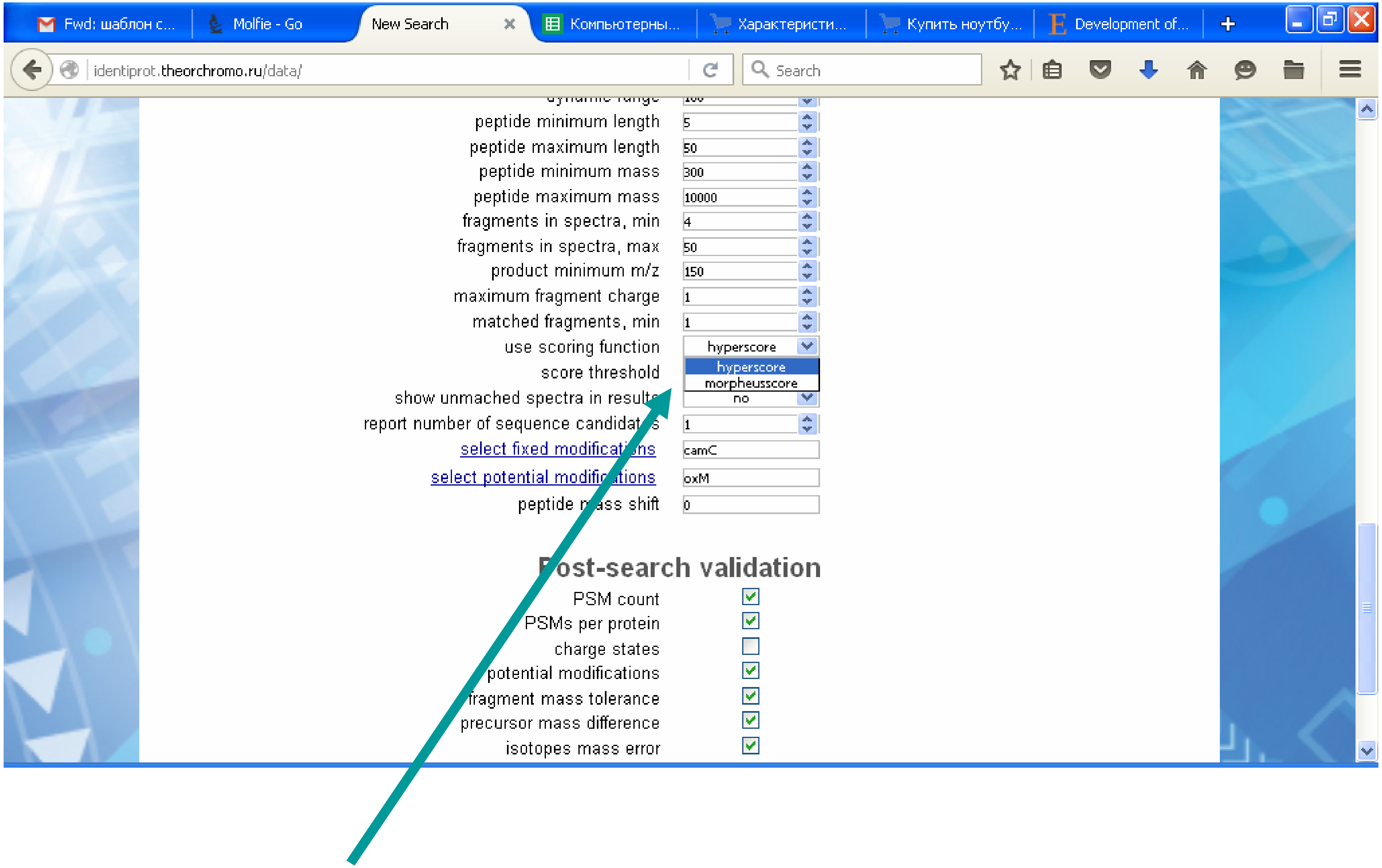
Послепоисковое валидирование идентификаций (до 9 ортогональных критериев)



Specify search parameters

- send email notification ☐
- use auto optimization ☑
- enzyme: add custom cleavage rule — trypsin
- number of missed cleavages — 5
- precursor accuracy unit — ppm
- precursor accuracy left — 10
- precursor accuracy right — 10
- precursor isotope mass error — 0
- product accuracy, Da — 0.05
- FDR — 1
- FDR type — protein
- minimum charge — 2
- maximum charge — 5

Автоматическая оптимизация входных параметров поиска под конкретные данные

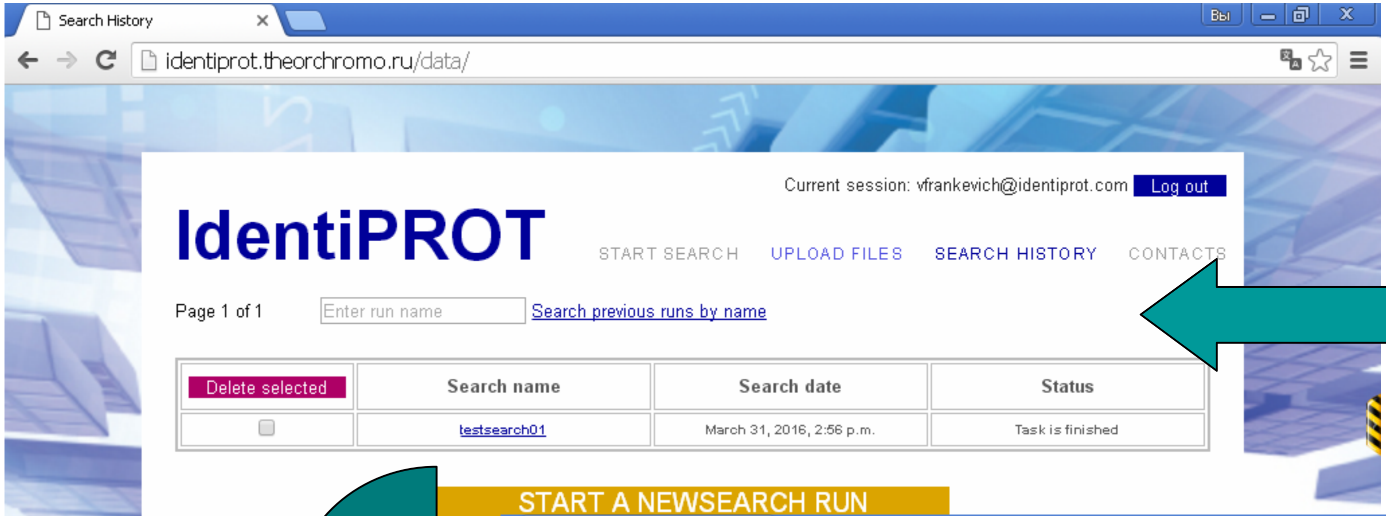


peptide minimum length	5
peptide maximum length	50
peptide minimum mass	300
peptide maximum mass	10000
fragments in spectra, min	4
fragments in spectra, max	50
product minimum m/z	150
maximum fragment charge	1
matched fragments, min	1
use scoring function	hyperscore hyperscore morpheusscore
score threshold	
show unmached spectra in results	no
report number of sequence candidates	1
select fixed modifications	camC
select potential modifications	oxM
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	☑

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



Current session: vfrankevich@identiprot.com

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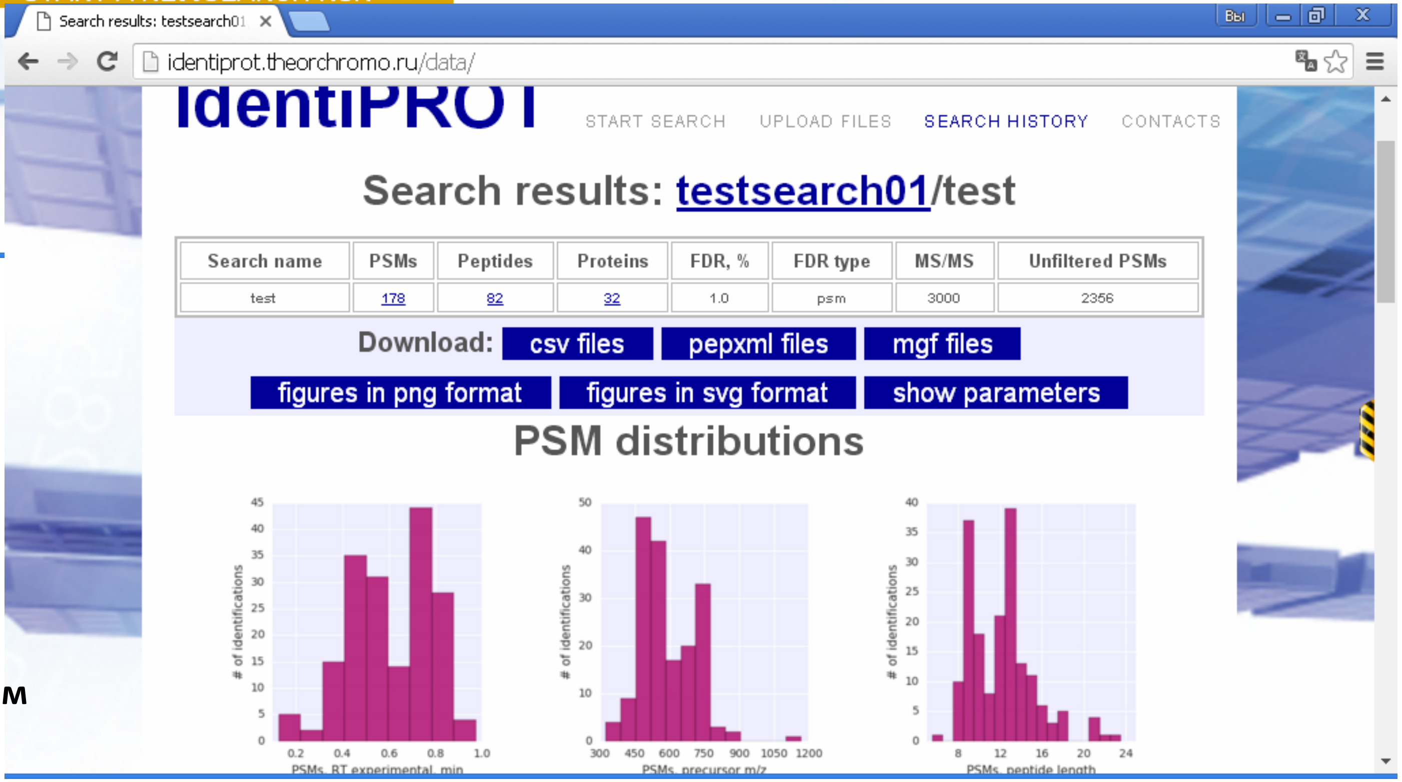
Enter run name

Search previous runs by name

Delete selected	Search name	Search date	Status
☐	testsearch01	March 31, 2016, 2:56 p.m.	Task is finished

Вывод результатов поиска



Search results: testsearch01/test

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

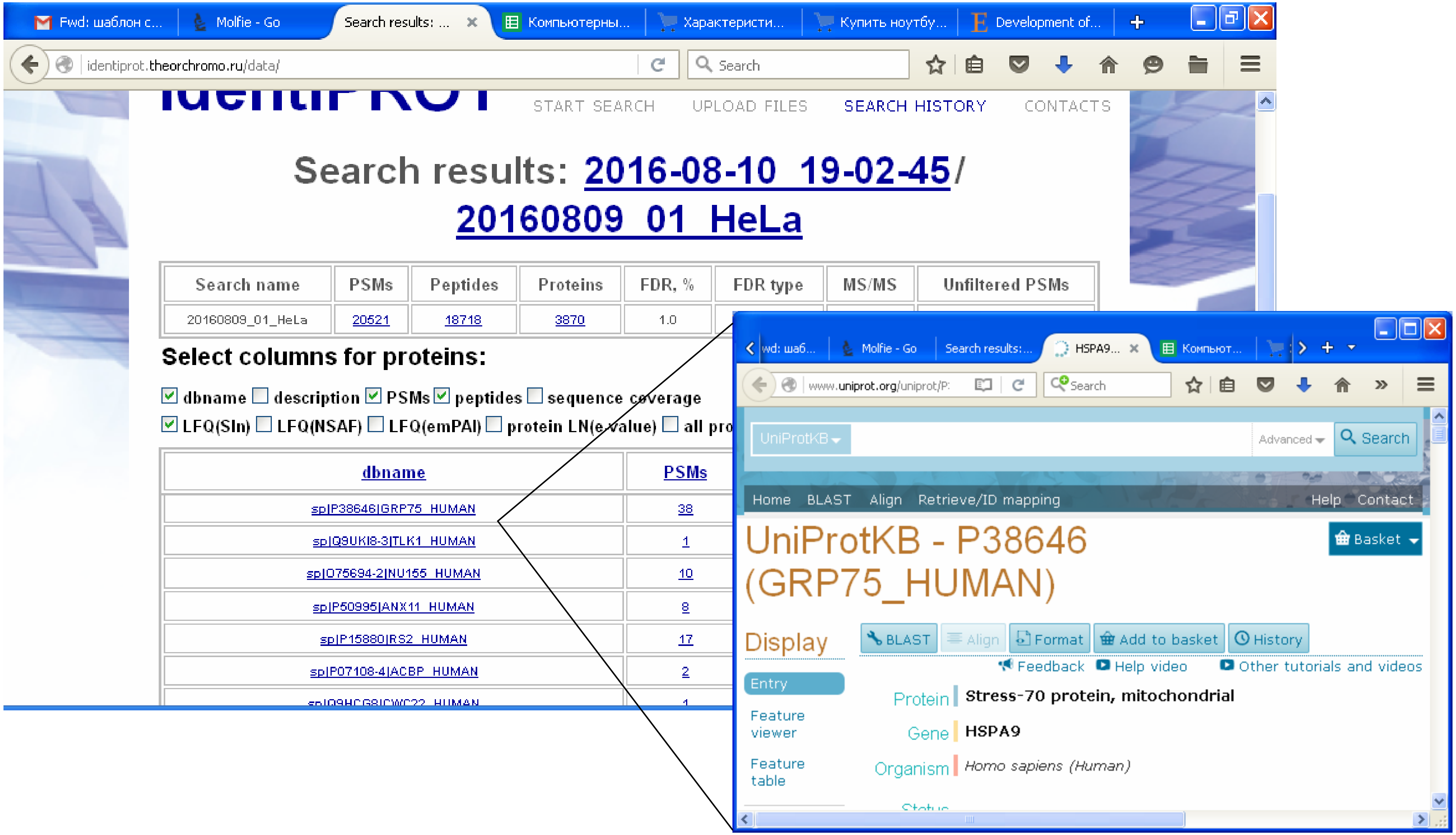
PSM distributions

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

Label-free quantitation

MP-score descriptors

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(SIn) ☐ LFQ(NSAF) ☐ LFQ(emPAI) ☐ protein LN(e-value) ☐ all pro

dbname	PSMs
sp|P38646|GRP75_HUMAN	38
sp|Q9UKI8-3|TLK1_HUMAN	1
sp|O75694-2|NU155_HUMAN	10
sp|P50995|ANX11_HUMAN	8
sp|P15880|RS2_HUMAN	17
sp|P07108-4|ACBP_HUMAN	2
sp|Q9HCG8|CWC22_HUMAN	1

UniProtKB - P38646 (GRP75_HUMAN)

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

Интерактивный режим просмотра белковых идентификаций