

Parameter panel

MS/MS dataset: (detailed information)
 cptac_colon_2014_nature

Target event:
 Peptide sequence:
 NPLLDLAAYDQEGR

Input peptide sequence:
 NPLLDLAAYDQEGR

Reference database:
 nature2014_RefSeqDB

Scoring algorithm:
 HyperScore

Unrestricted modification filtering:
 Yes No

Start Stop

Result panels

Identification overview

MS/MS searching parameters:

parameter	value
1 Enzyme	Trypsin
2 No. of missed cleavages	1
3 Fixed modifications	6
4 Variable modifications	107
5 Peptide tol. z	10 ppm
6 MS/MS tol. z	0.6 Da

Identification result

The identification result is presented in the below table:

Show 25 entries

peptide	modification	n	spectrum	sample_name	charge	exp_mass
1 NPLLDLAAYDQEGR	-	137	28448	TCGA-AA-A000	2	1573.7
2 NPLLDLAAYDQEGR	-	137	13425	TCGA-AA-A052	2	1573.7
3 NPLLDLAAYDQEGR	-	137	21872	TCGA-AA-A036	2	1573.7
4 NPLLDLAAYDQEGR	-	137	72807	TCGA-AA-A038	2	1573.7
5 NPLLDLAAYDQEGR	-	137	21054	TCGA-AA-A032	2	1573.7
6 NPLLDLAAYDQEGR	-	137	42207	TCGA-AA-2086	2	1573.7
7 NPLLDLAAYDQEGR	-	137	29133	TCGA-AA-A039	2	1573.7
8 NPLLDLAAYDQEGR	-	137	36361	TCGA-AA-3518	2	1573.7
9 NPLLDLAAYDQEGR	-	137	22566	TCGA-AA-A016	2	1573.7
10 NPLLDLAAYDQEGR	-	137	27416	TCGA-AA-A017	2	1573.7
11 NPLLDLAAYDQEGR	-	137	132465	TCGA-AA-3541	2	1573.7
12 NPLLDLAAYDQEGR	-	137	35701	TCGA-AA-A031	2	1573.7
13 NPLLDLAAYDQEGR	-	137	24936	TCGA-AA-2710	2	1573.7
14 NPLLDLAAYDQEGR	-	137	15595	TCGA-AA-A026	2	1573.7
15 NPLLDLAAYDQEGR	-	137	18888	TCGA-AA-A028	2	1573.7
16 NPLLDLAAYDQEGR	-	137	17287	TCGA-AA-2045	2	1573.7
17 NPLLDLAAYDQEGR	-	137	15985	TCGA-AA-A016	2	1573.7
18 NPLLDLAAYDQEGR	-	137	41274	TCGA-AA-3846	2	1573.7
19 NPLLDLAAYDQEGR	-	137	28394	TCGA-AA-A000	2	1573.7
20 NPLLDLAAYDQEGR	-	137	38034	TCGA-AA-2013	2	1573.7
21 NPLLDLAAYDQEGR	-	137	26466	TCGA-AA-2318	2	1573.7
22 NPLLDLAAYDQEGR	-	137	42966	TCGA-AA-2090	2	1573.7
23 NPLLDLAAYDQEGR	-	137	17784	TCGA-AA-A007	2	1573.7
24 NPLLDLAAYDQEGR	-	137	27661	TCGA-AA-A051	2	1573.7

Showing 1 to 25 of 70 entries

Download the identification result:
 Download

Sample information

ID	TCGA participant ID	Gender	Cancer	Histological.type	Ti
1	TCGA-AA-A000-01A-13	Female	Colon	Colon Adenocarcinoma	3

Spectrum annotation

When a row is selected, the spectrum annotation figure will be shown below:

spectrum_title	peptide	modification	pep_mass	score
1 28448:TCGA-AA-A000-01A-13_W_VU_2012081	NPLLDLAAYDQEGR	-	1573.774	63.565

The best PSM from the reference database searching:

spectrum_title	peptide	modification	pep_mass	score
1 28448:TCGA-AA-A000-01A-13_W_VU_2012081	CFLAFQVRAFTSK	Carbamidomethylation of C@157.0215	1573.808	10.954

The best PSM from the unrestricted modification-based searching:

spectrum_title	peptide	charge	exp_mass	pep_mass	modification	score
1 28448:TCGA-AA-A000-01A-13_W_VU_2012081	LLDLVLSFKR	2	1573.779	1573.756	Carbamidomethylation of C@857.0215;TNBS of N-term@1210.9865	23.239

Supplemental Fig S6: A screenshot of the web interface of PepQuery. The web interface of PepQuery for peptide identification is divided into two parts. One part is for parameter setting and the other part is for result visualization.