

iPEP User's Guide

iPEP has been designed to aid in designing sample preparation techniques around the detection of specific sites or motifs in proteins and proteomes. The first application, single protein sequence analysis enables extensive analysis of the potential sites of post-translational modifications in a user-selected proteins. The second application, proteome motif scanning, measures the occurrence of a specific sequence in the proteome and determines the efficacy of digestion and instrument selection on detecting the proteins that contain the motif.

iPEP Front Page <http://ipep.moffitt.org>

Menu

- Main
 - Home
 - About
 - Help
- Search
 - GO Term search
- Analysis
 - Single protein analysis
 - Motif Scanning
 - Protein level tracking

Links

- NCBI
- SwissProt
- GO
- Harvester
- Proteogest
- ExPASy
- PhosphoSite

Search

Google Scholar BETA

Search

Home About Help

iPEP v2.0 Today is 9/17/2008

Introduction

iPEP performs insilico proteome digestion by multiple enzymes/chemicals and mass calculation to help proteomics experiments planning. iPEP also supports motif searching, classification and gene ontology annotation for a given subset of proteins detected by various instruments.

iPEP Tutorial

PDF Description and Example Results

1. Examine Protein Sequence for Post-translational Modification Analysis (p. 3)
2. Monitor Detection of Proteins Containing Specific Motifs or Amino Acid Residues in Entire Proteomes to Design Peptide-based Proteomic Experiments (p. 12)

iPEP Protein Sequence Analysis:

Analysis of Potential Phosphotyrosine Sites in the Human Epidermal Growth Factor Receptor

Menu

- Main
 - Home
 - About
 - Help
- Search
 - GO Term search
 - Analysis
 - Single protein analysis
 - Motif Scanning
 - Protein level tracking
- Links
 - NCBI
 - SwissProt
 - GO
 - Harvester
 - Proteogest
 - ExPASy
 - PhosphoSite
- Search
 - Google Scholar

Home About Help

IPEP v2.0 Today is 9/17/2008

Search single protein

Protein ID*

SwissProt Accession

Enter 1 Letter Code for Amino Acid or Sequence

Following Results Pages are Generated for the Human Epidermal Growth Factor Receptor, SwissProt Entry: EGFR_HUMAN, with Peptide MW 600-4500 and Monitoring Tyrosine (Y) Residues.

iPEP Protein Sequence Analysis Results:

EGFR Accession, Description, and Sequence

Search result for protein: [EGFR_HUMAN](#)

**Click to Access Peptide Lists in Sequence Order
for All Methods (p. 5)**

Protein information ([View all peptides per digest](#))

Accession	P00533	Links to SwissProt Entry
Entry Name	EGFR_HUMAN	
Description	Epidermal growth factor receptor precursor (EC 2.7.10.1) (Receptor tyrosine-protein kinase ErbB-1) - Homo sapiens (Human)	
Sequence (1210 aa)	MRPSGTAGAALLALLAALCPASRALEEEKKVCQGTSNKLTQLGTFEDHFLSLQRMFMNCEVVLGNLEITYVQRNYDLSFLK TIQEVAGYVLIALNTVERIPLNLQIIRGNMYYSYALAVLSNYDANKTGLKELPMRNLQEILHGAVRFSNNPALCNVE SIQWRDIVSSDFLSNMSMDFQNLHGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQQCSGRGRGKSPSDCCHNQCAAGC TGPRESCLVCRKFRDEATCKDTCPLMLYNPTTYQMDVNPEGKYSFGATCVKCCPRNYVVDHGSCVRACGADSYEMEE DGVKCKKCEGPKRVCNGIGIGEFKDSLINATNIKHFKNCTSIGDLHLIPVAFRGDSFTHTPPLDPQELDILKTVKE ITGFLLIQAWPENRTDLHAFENLEIIRGRKQHGQFSLAVVSLNITSLGLRSLKEISDGDVLIISGNKNLCYANTINWKKL FGTSGQKTKIISNRGENSCKATGQVCHALCSPEGCWGPEPRDCVSCRNVSRGRECVDKCNLLEGEPRFVENSECIQCHP ECLPQAMNITCTGRGPDNCIQAHYIDGPHCVKTCPAGVMGMNNTLVWKYADAGHVCHLCHPNCTYGCTGPGLEGCPNG PKIPSIATGMVGALLLLLVVALGIGLFMRRRHIVRKRTLRLQLQERELVEPLTPSGEAPNQALLRILKETEFKKIKVLGS GAFGTVYKGLWIPEGEKVKIPVAIKELEATSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLITQLMPFGCLLD YVREHKDNIGSQYLLNWCQVIAKGMNYLEDRLVHRDLAARNVLVKTTPQHVKITDFGLAKLLGAEKEKYHAEGGKVPKWK MALESILHRIYTHQSDVWSYGVTVWELMTFGSKPYDGIPASEISSILEKGERLPQPPICTIDVYMIMVKCWMIDADSRPK FRELIIEFSKMARDPQRYLVIOGDERMHLPSPTDSNFYRALMDEEDMDVDVDAEYLIIPQQGFFSSPSTSRTPLLSSLSA TSNNSTVACIDRNLQSCPIKEDSFLQRYSSDPTGALTEDSIDDTFLPVPEYINQSVKRPAGSVQNPVYHNQPLNPAPS RDPHYQDPHSTAVGNPEYLNTVQPTCVNSTFDSPAHWAQKGS HQISLDNPDYQQDFFPKAKPNGIFKGSTAENAEYLRV APQSSEFIGA	
Molecular Weight	600~4500 (Da)	

This panel shows the sequence of the selected SwissProt entry. Additional data, including sequence, residue, and peptide coverages, are also displayed as part of the same web page (pages 6, 8, and 10-12).

iPEP Protein Sequence Analysis Results:

Peptide Lists (from p. 4)

Protein Accession: EGFR_HUMAN			
Start	Stop	Peptide Sequence	Molecular Weight
Digestion: Acid			
0	45	MRPSGTAGAALLALLAALCPASRALEEKVKCQGTSNKLTQLGTFED	4730.45562
46	74	HFLSLQRMFNNCEVVLGNLEITYVQRNYD	3514.71249
75	125	LSFLKTIQEVAGYVLIALNTVERIPLNLQIIRGNMYYSYALAVLSNYD	5834.06433
126	165	ANKTGLKELPMRNLQEILHGAVRFSNNPALCNVESIQWRD	4561.34333
166	170	IVSSD	519.25397
171	178	FLSNMSMD	943.37788
179	190	FQNHLGSCQKCD	1378.57574
191	229	PSCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSD	4097.80558
230	246	CCHNQCAAGCTGPRES	1750.62793
247	255	CLVCRKFRD	1138.57388
256	261	EATCKD	665.26897
262	277	TCPPMLLYNPTTYQMD	1886.82522
278	302	VNPEGKYSFGATCVKKCPRNYVVTD	2774.35191
303	313	HGSCVRACGAD	1074.43342
314	320	SYEMEED	901.30106
321	346	GVRKCKKCEGPCRKVCNGIGIGEFKD	2823.41274
347	367	SLSINATNIKHFKNCTSIGD	2249.11095
368	378	LHILPVAFRGD	1236.69779
379	387	SFTHTPPLD	1013.48173
388	392	PQELD	600.27543
393	415	ILKTVKEITGFLLIQAWPENRTD	2684.49002
416	457	LHAFENLEIIRGRTKQHGQFSLAVVSLNITSLGLRSLKEISD	4689.57171
458	459	GD	190.05890

Continues for All Digestion Methods

iPEP Protein Sequence Analysis Results:

Table of Proteolytic Peptide, Sequence, and Residue Coverage

Summary of peptide, sequence and residue coverage.(Click the link to view the residue coverage)

Digestion	Peptide Coverage	Sequence Coverage	Residue Coverage (Y)	Compare
Trypsin	74/122	1054/1210	33/36	<input type="checkbox"/>
Arg C	35/61	673/1210	20/36	<input type="checkbox"/>
Lys C	44/67	770/1210	20/36	<input type="checkbox"/>
Lys N	44/67	770/1210	20/36	<input type="checkbox"/>
Acid	43/62	748/1210	25/36	<input type="checkbox"/>
Asp N	43/62	749/1210	25/36	<input type="checkbox"/>
V8 phosphate	79/139	1016/1210	32/36	<input type="checkbox"/>
V8 bicarbonate	48/78	833/1210	27/36	<input type="checkbox"/>
Pepsin (PH 1.3)	74/148	928/1210	32/36	<input type="checkbox"/>
Pepsin (PH 2.0)	61/394	493/1210	7/36	<input type="checkbox"/>
Proteinase K	63/407	461/1210	9/36	<input type="checkbox"/>
Thermolysin	65/383	502/1210	20/36	<input type="checkbox"/>
Chymo (F/Y/M/M/L)	60/82	1043/1210	27/36	<input type="checkbox"/>
Chymo (F/Y/M)	88/238	856/1210	17/36	<input type="checkbox"/>
CNBr	15/26	349/1210	18/36	<input type="checkbox"/>
IBA	4/14	100/1210	2/36	<input type="checkbox"/>
NTCB	28/61	395/1210	11/36	<input type="checkbox"/>
v8_LysC	85/184	955/1210	31/36	<input type="checkbox"/>
AspN_nGlu	79/139	1015/1210	32/36	<input type="checkbox"/>
AspN_LysC	81/125	1057/1210	28/36	<input type="checkbox"/>
Trypsin_Chymo	91/204	922/1210	18/36	<input type="checkbox"/>
IBA_CNBr	22/39	487/1210	21/36	<input type="checkbox"/>

**User Can
Compare Digests
using Sequence
Alignment
(see p. 7)**

Cyanogen bromide

Iodosobenzoic Acid

2-Nitro-5-thiocyanatobenzoic Acid

iPEP Protein Sequence Analysis Results:

Sequence Alignment of Trypsin and *S. aureus* V8 Protease Digests (from p. 6)

Protein Entry	EGFR_HUMAN
Residue(s)	Y
Molecular Weight	600~4500 (Da)

Coverage comparison (The blue indicates detectable peptide and the red is detectable residue)

```

EGFR_HUMAN MRPSGTAGAALLALLAALCPASRALEEKVKVCGQTSNKLTQLGTFEDHFLSLQRMFMNCEV
Trypsin    MRPSGTAGAALLALLAALCPASR-----VCQGTSNKLTQLGTFEDHFLSLQRMFMNCEV
V8         MRPSGTAGAALLALLAALCPASRALE-KKVCQGTSNKLTQLGTFE-HFLSLQRMFMNCEV
phosphate

EGFR_HUMAN VLGNEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLNLQIRGNMYYENSVALA
Trypsin    VLGNEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLNLQIRGNMYYENSVALA
V8         VLGNEITYVQRNYDLSFLKTIQEVAGYVLIALNTVERIPLNLQIRGNMYYENSVALA
phosphate

EGFR_HUMAN VLSNYDANKTGLKELPMRNLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMMSDF
Trypsin    VLSNYDANK----ELPMRNLQEILHGAVRFSNNPALCNVESIQWRDIVSSDFLSNMMSDF
V8         VLSNYDANKTGLKELPMRNLQEILHGAVRFSNNPALCNVESIQWRD-----FLSNMMSDF
phosphate

EGFR_HUMAN QNHLGSCQKCDPSCPNGSCWGAGEENCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGC
Trypsin    QNHLGSCQKCDPSCPNGSCWGAGEENCQK---IICAQQCSGR----SPSDCCHNQCAAGC
V8         QNHLGSCQKCDPSCPNGSCWGAGE-NCQKLTKIICAQQCSGRCRGKSPSDCCHNQCAAGC
phosphate

EGFR_HUMAN TGPRESDCLVCRKFRDEATCKDTCPPMLLYNPPTYQMDVNPEGKYSFGATCVKKCPRNYV
Trypsin    TGPRESDCLVCR---DEATCKDTCPPMLLYNPPTYQMDVNPEGKYSFGATCVK----NYV
V8         TGPRES--CLVCRKFRD-----TCPPLMLLYNPPTYQMD----GKYSFGATCVKKCPRNYV
phosphate

EGFR_HUMAN VTDHGSCVRACGADSYEMEEDGVRKCKKCEGPCRKVCNGIGIGEFKDSLSINATNIKHFK
Trypsin    VTDHGSCVRACGADSYEMEEDGVR-----CEGPCRVCNGIGIGEFKDSLSINATNIK---
V8         VTDHGSCVRACGAD-----GVRKCKKCEGPCRKVCNGIGIGE---SLSINATNIKHFK
phosphate
    
```

Residue
Tracking

Detectable
Sequence

iPEP Protein Sequence Analysis Results:

Tyrosine Residue Detection in each Proteolytic Method

Summary of coverage of each residue in all enzymes. (Click the link to view all peptides containing the residue at position selected)

(Y) Position	Trypsin	Arg C	Lys C	Lys N	Acid	Asp N	V8 phosphate	V8 bicarbonate	Pepsin (PH 1.3)	Pepsin (PH 2.0)	Proteinase K
68	✓	✓			✓	✓	✓	✓	✓		
73	✓	✓			✓	✓	✓	✓	✓		
87	✓	✓					✓	✓	✓		
111	✓	✓					✓	✓	✓	✓	✓
112	✓	✓					✓	✓	✓		
116	✓	✓					✓	✓	✓		
124	✓	✓					✓	✓	✓		
269	✓		✓	✓	✓	✓	✓	✓	✓		
274	✓		✓	✓	✓	✓	✓	✓	✓		
284	✓		✓	✓	✓	✓	✓	✓	✓		✓
298	✓	✓	✓	✓	✓	✓	✓	✓		✓	✓
315	✓	✓	✓	✓	✓	✓		✓			
470	✓		✓	✓			✓	✓	✓		
584	✓				✓	✓	✓	✓	✓		
609	✓		✓	✓	✓	✓	✓	✓	✓		
625	✓		✓	✓			✓	✓	✓	✓	✓
726	✓		✓	✓			✓	✓			
763	✓	✓			✓	✓	✓		✓		
800	✓	✓			✓	✓	✓	✓	✓		
812	✓	✓	✓	✓	✓	✓	✓	✓			
826	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
868	✓		✓	✓					✓		✓
890			✓	✓			✓	✓	✓		
899			✓	✓	✓	✓	✓	✓	✓		
914			✓	✓	✓	✓	✓	✓	✓		
943	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
977	✓	✓			✓	✓	✓	✓	✓		✓
997	✓	✓			✓	✓	✓	✓			
1015	✓	✓			✓	✓	✓	✓	✓		
1068	✓	✓	✓	✓	✓	✓	✓	✓	✓		
1091	✓	✓	✓	✓	✓	✓	✓	✓	✓		
1109	✓	✓			✓	✓	✓	✓	✓		
1124	✓				✓	✓	✓	✓	✓	✓	✓
1137	✓				✓	✓	✓	✓			
1171	✓		✓	✓	✓	✓	✓	✓	✓	✓	✓
1196	✓				✓	✓	✓	✓	✓		

(Y) Position	Thermolysin	Chymo (F/Y/NW/M/L)	Chymo (F/Y/NM)	CNBr	IBA	NTCB	v8_LysC	AspN_nGlu	AspN_LysC	Trypsin_Chymo	IBA_CNBr
68		✓					✓	✓	✓	✓	
73	✓		✓				✓	✓	✓		
87		✓	✓				✓	✓		✓	
111	✓	✓	✓		✓		✓	✓			✓
112	✓			✓			✓	✓			✓
116	✓			✓			✓	✓			✓
124	✓	✓		✓			✓	✓		✓	✓
269	✓	✓			✓	✓	✓	✓	✓	✓	✓
274	✓			✓	✓	✓	✓	✓	✓		✓
284	✓	✓	✓	✓	✓	✓	✓	✓	✓		✓
298	✓	✓	✓	✓	✓	✓	✓	✓	✓		✓
315		✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
470		✓			✓	✓	✓	✓	✓		
584		✓		✓	✓	✓	✓	✓	✓	✓	✓
609					✓		✓	✓	✓	✓	✓
625	✓	✓	✓				✓	✓	✓	✓	✓
726			✓				✓	✓	✓	✓	
763		✓					✓	✓	✓	✓	✓
800		✓		✓	✓	✓	✓	✓	✓	✓	✓
812			✓	✓	✓	✓	✓	✓	✓	✓	✓
826		✓					✓	✓	✓		
868	✓	✓	✓					✓	✓		
890	✓	✓		✓	✓		✓	✓	✓		✓
899	✓			✓	✓		✓	✓	✓		✓
914	✓			✓			✓	✓	✓	✓	✓
943		✓	✓			✓	✓	✓	✓	✓	✓
977	✓	✓	✓	✓			✓	✓	✓	✓	✓
997				✓			✓	✓	✓	✓	✓
1015		✓	✓				✓	✓	✓	✓	
1068	✓						✓	✓	✓	✓	
1091		✓	✓				✓	✓	✓	✓	
1109	✓	✓	✓				✓	✓	✓	✓	
1124	✓	✓	✓				✓	✓	✓	✓	
1137	✓	✓	✓				✓	✓	✓	✓	
1171	✓	✓	✓				✓	✓	✓	✓	
1196		✓	✓				✓	✓	✓	✓	

Links to Display of Detectable Peptides Containing Tyr 1068 (p. 9)

iPEP Protein Sequence Analysis Results:

Peptides Containing Tyrosine 1068 (from p. 8)

List of detectable peptides containing residue Y

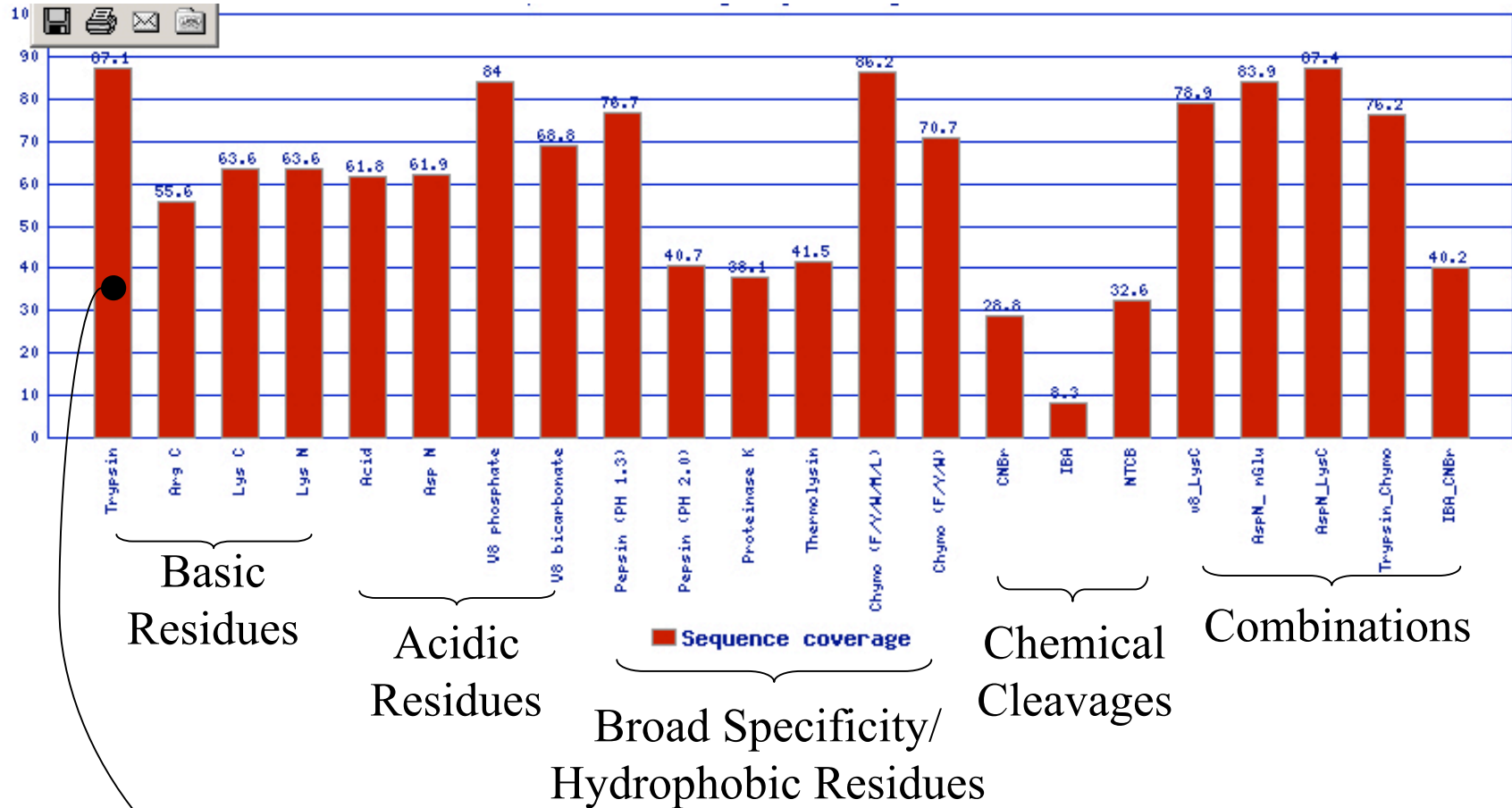
EGFR_HUMAN Tyr 1068

Digestion	Start	Stop	Peptide	Molecular Weight
Trypsin	1068	1098	YSSDPTGALTEDSIDDTFLPVPEYINQSVPK	3397.60881
Arg C	1068	1099	YSSDPTGALTEDSIDDTFLPVPEYINQSVPKR	3553.70992
Lys C	1061	1098	EDSFLQRYSSDPTGALTEDSIDDTFLPVPEYINQSVPK	4273.02253
Lys N	1060	1097	KEDSFLQRYSSDPTGALTEDSIDDTFLPVPEYINQSV	4273.02253
Acid	1063	1071	SFLQRYSSD	1101.50902
Asp N	1062	1070	DSFLQRYSS	1101.50902
V8 phosphate	1063	1071	SFLQRYSSD	1101.50902
V8 bicarbonate	1062	1078	DSFLQRYSSDPTGALTE	1885.86930
Pepsin (PH 1.3)	1066	1076	QRYSSDPTGAL	1193.56759
Thermolysin	1065	1074	LQRYSSDPTG	1122.53048
v8_LysC	1063	1078	SFLQRYSSDPTGALTE	1770.84236
AspN_nGlu	1062	1070	DSFLQRYSS	1101.50902
AspN_LysC	1062	1070	DSFLQRYSS	1101.50902

Enables Quantification using Specific Peptide Sequences

iPEP Protein Sequence Analysis Results:

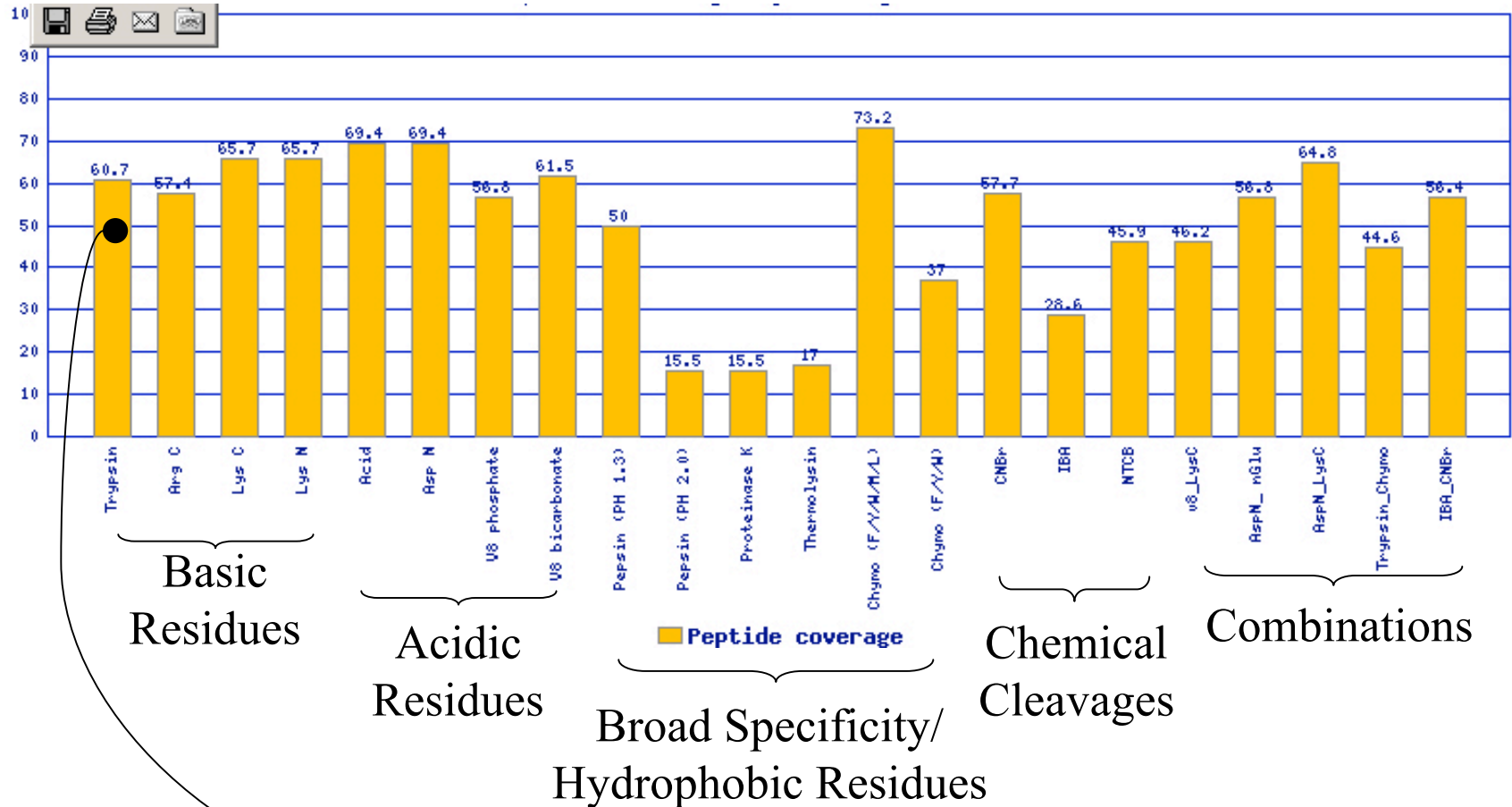
Graph of EGFR Sequence Coverage



87.1% of the Sequence Can Be Detected in Tryptic Peptides from MW 600 to 4,500 Da

iPEP Protein Sequence Analysis Results:

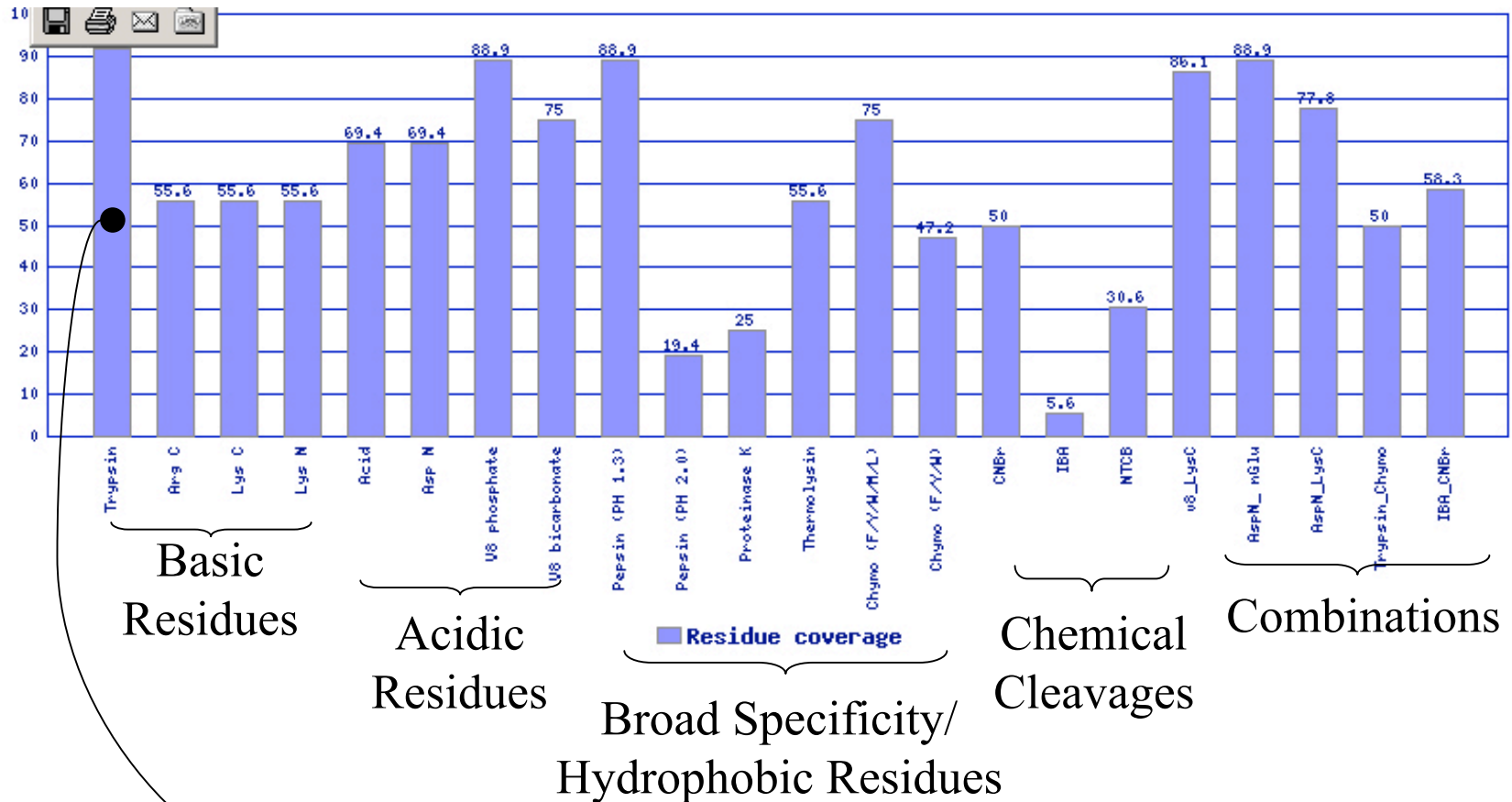
Graph of EGFR Peptide Coverage



60.7% of the Tryptic Peptides Have MW Between 600 and 4,500 Da

iPEP Protein Sequence Analysis Results:

Graph of EGFR Residue Coverage



91.7% of the Tyrosine Residues Can Be Detected in Tryptic Peptides from MW 600 to 4,500 Da

Proteome Motif Scanning

Search Parameter Page

Search

Menu

- Home
- About
- Help
- Search
 - Single protein analysis
 - Protein level tracking
 - GO Term search

Links

- NCBI
- SwissProt
- GO
- Harvester

Proteome motif scanning

Data Source* **Select Database**

Motif* (Prosites: P-X-[ST]-P.)

Select 2 Proteolytic Methods

Digestion *(Choose 2)

<input type="checkbox"/> Trypsin	<input type="checkbox"/> Arg C	<input type="checkbox"/> Lys C	<input type="checkbox"/> Lys N
<input type="checkbox"/> Acid hydrolysis	<input type="checkbox"/> Asp N	<input type="checkbox"/> V8 Phosphate	<input type="checkbox"/> V8 Bicarbonate
<input type="checkbox"/> Pepsin (PH 1.3)	<input type="checkbox"/> Pepsin (PH 2.0)	<input type="checkbox"/> Proteinase K	<input type="checkbox"/> Thermolysin
<input type="checkbox"/> Chymotrypsin high specificity	<input type="checkbox"/> Chymotrypsin low specificity	<input type="checkbox"/> CNBr	<input type="checkbox"/> IBA
<input type="checkbox"/> NTCB	<input type="checkbox"/> V8/Lys C	<input type="checkbox"/> Asp N/N-terminal Glu	<input type="checkbox"/> Asp N/Lys C
<input type="checkbox"/> Trypsin/Chymotrypsin	<input type="checkbox"/> IBA/CNBr		

Molecular weight

MW Filtering

☒ ESI Ion Trap (600-3500 Da)
☐ MALDI TOF/TOF (750-5500 Da)
☐ Other, please specify. Min Max (Da)

1. Enter Motif in single amino acid codes. Use X as a wild card. [OJ] means either O or J. {OJ} means neither O nor J. N-terminus is < and C-terminus is >.

iPEP Proteome Motif Scan Results

MAPK Sites in Human SwissProt Entries

Search criteria

Data source	SwissProt human protein data
Motif ?	P.[ST]P
Digest ?	Trypsin, Lys-C
Instrument	ESI (600~3500)

Complexity of proteome

Total proteins	Motif-containing proteins	Fraction of proteome (%) ?	Total number of motifs
15939	4746	29.776 % (4746/15939)	9235

In the first part of the proteome scanning results, the number of motifs in the proteome and the number of proteins containing the motif are shown. The user can then estimate the difficulty in detecting all of these motif-containing proteins in an LC-MS/MS experiment. This application is illustrated with mitogen-activated protein kinase (MAPK) consensus phosphorylation sequences (Proline-any amino acid-Serine or Threonine-Proline). Results continue on p. 15-16.

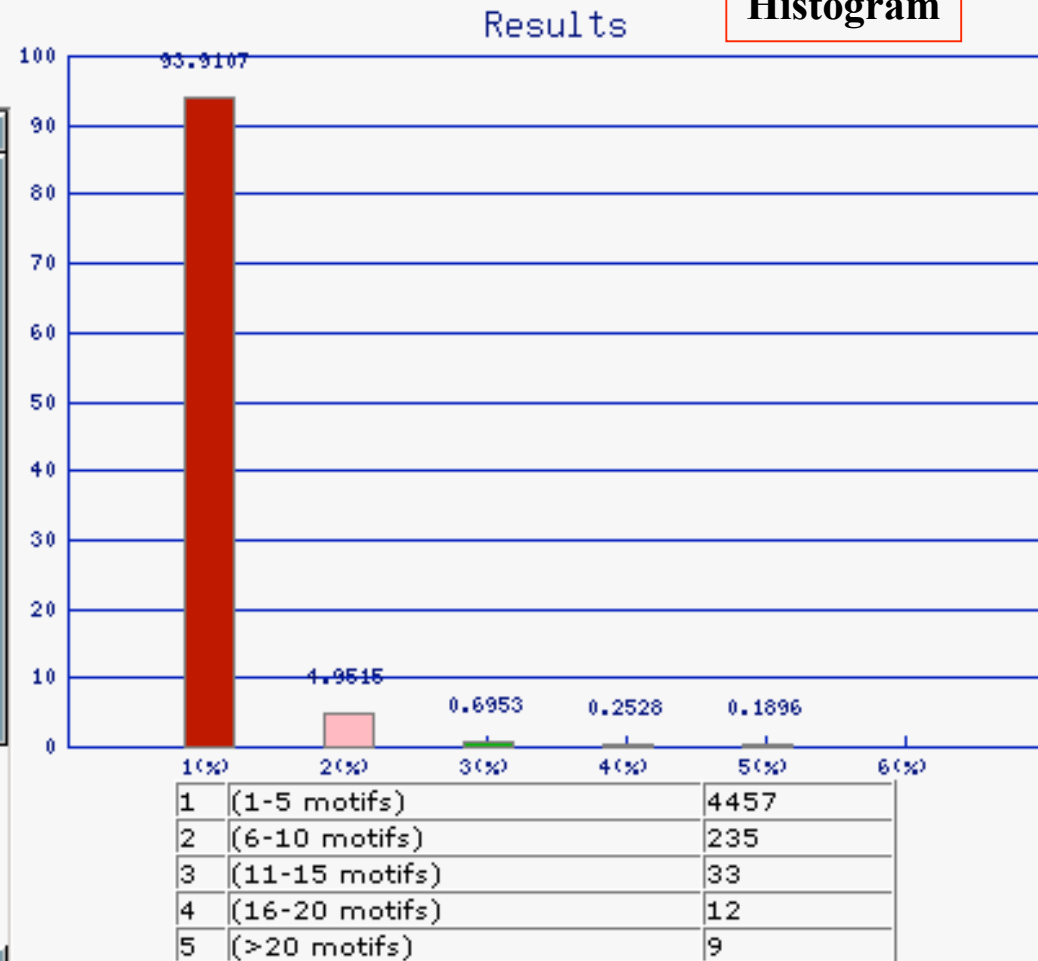
iPEP Proteome Motif Scan Results:

Distribution of Motifs per Protein

Col 1: #primary motifs for each protein
Col 2: #proteins

1	2854
2	997
3	403
4	203
5	99
6	56
7	38
8	24
9	18
10	12
11	5
12	7
13	4
14	5
15	2
16	2
17	4
19	4
20	2
21	1
23	1

Raw Data



Histogram

Most proteins containing MAPK consensus phosphorylation sequences have a small number of motifs within their sequence.





iPEP Proteome Motif Scan Results:

Peptide Statistics and Detection

Trypsin

Total proteolytic peptides	Detectable peptides	Motif-containing peptides	Fraction of peptidome (%)
953610	488492	7510	0.7875





Determines if peptide fractionation techniques are necessary prior to LC-MS/MS.

Detection Results							
Motif	Filter	Peptides from motif-containing proteins	Motif-containing peptides	Motifs	Motif-containing proteins	FASTA Sequence	Compare
P.[ST] P	None	415027	7510	8409	4746		
P.[ST] P	MW	213353	5088	5388	4740		

Lys-C

Total proteolytic peptides	Detectable peptides	Motif-containing peptides	Fraction of peptidome (%)
519240	283171	7574	1.4587

Compare Detection of Peptides, Motifs, and Motif-Containing Proteins to Select Ideal Digestion(s). Trypsin will produce more detectable peptides than Lys-C.

Detection Results							
Motif	Filter	Peptides from motif-containing proteins	Motif-containing peptides	Motifs	Motif-containing proteins	FASTA Sequence	Compare
P.[ST] P	None	219573	7574	8913	4746		
P.[ST] P	MW	118917	2791	2955	4709		

Download Protein in FASTA

View All GO Terms





Compare Two Subsets of Proteins

iPEP Proteome Motif Scan Results:

Peptide Statistics and Detection

Trypsin





Total proteolytic peptides	Detectable peptides	Motif-containing peptides	Fraction of peptidome (%)
953610	488492	7510	0.7875

Detection Results							
Motif	Filter	Peptides from motif-containing proteins	Motif-containing peptides	Motifs	Motif-containing proteins	FASTA Sequence	Compare
P.[ST] P	None	415027	7510	8409	4746		
P.[ST] P	MW	213353	5088	5388	4740		

Download Specific Database Of Motif-Containing Proteins

Lys-C

Total proteolytic peptides	Detectable peptides	Motif-containing peptides	Fraction of peptidome (%)
519240	283171	7574	1.4587

Detection Results							
Motif	Filter	Peptides from motif-containing proteins	Motif-containing peptides	Motifs	Motif-containing proteins	FASTA Sequence	Compare
P.[ST] P	None	219573	7574	8913	4746		
P.[ST] P	MW	118917	2791	2955	4709		

Compare Protein Populations (see p. 18)

Examine Enrichment of Biological Processes/Functions

[View All GO Terms](#)






[Compare Two Subsets of Proteins](#)

Comparison of Proteins Detected:

Extraction of Differences

Data source	SwissProt human protein data
Primary motif ?	P.[ST]P
Digest ?	Trypsin, Lys-C
Modified residue ?	
Instrument	ESI (800~4000)

Result

Set	Difference	Analysis Result	Select	
	Union	4746 proteins in both digestion Trypsin or Lys-C	<input type="radio"/>	<input type="radio"/>
	Intersection	4709 proteins in digestion Trypsin and digestion Lys-C	<input type="radio"/>	<input type="radio"/>
	Set difference	32 proteins in digestion Trypsin	<input type="radio"/>	<input type="radio"/>
	Set difference	5 proteins in digestion Lys-C	<input type="radio"/>	<input type="radio"/>
	Symmetric difference	37 proteins in digestion Trypsin or digestion Lys-C but not in both	<input type="radio"/>	<input type="radio"/>

Trypsin and Lys-C both produce peptides that enable detection of proteins that can not be observed in the other digest. Each set can be viewed in HTML or exported as a FASTA database (see p. 19).

Download Protein in FASTA View Proteins View All GO Terms

Comparison of Proteins Detected:

Extraction of Differences

Data source	SwissProt human protein data
Primary motif ?	P.[ST]P
Digest ?	Trypsin, Lys-C
Modified residue ?	
Instrument	ESI (800~4000)

Result

Set	Difference	Analysis Result	Select	
	Union	4746 proteins in both digestion Trypsin or Lys-C	<input type="radio"/>	<input type="radio"/>
	Intersection	4709 proteins in digestion Trypsin and digestion Lys-C	<input type="radio"/>	<input type="radio"/>
	Set difference	32 proteins in digestion Trypsin	<input type="radio"/>	<input checked="" type="radio"/>
	Set difference	5 proteins in digestion Lys-C	<input type="radio"/>	<input type="radio"/>
	Symmetric difference	37 proteins in digestion Trypsin or digestion Lys-C but not in both	<input type="radio"/>	<input type="radio"/>

[Download Protein in FASTA](#)
[View Proteins](#)
[View All GO Terms](#)

```

ATL5_HUMAN[1].fasta - ...
File Edit Format Help
>ARTN_HUMAN (Q5T4W7)
>BMF_HUMAN (Q96LC9)
>HAX1_HUMAN (O00165)
>CORT_HUMAN (O00230)
>GPM3_HUMAN (Q9Y4H4)
>CXCL_HUMAN (O15255)
>O10V1_HUMAN (Q8NGI7)
>GP152_HUMAN (Q8TDT2)
>GASR_HUMAN (P32239)
>GP137_HUMAN (Q14444)
>FRAT2_HUMAN (O75474)
>SMR3A_HUMAN (Q99954)
>UPK3B_HUMAN (Q9BT76)
>TMG2_HUMAN (O14669)
>CF001_HUMAN (Q86T20)
>TIP39_HUMAN (Q96A98)
>DBND2_HUMAN (Q9BQY9)
>CU119_HUMAN (Q96HZ7)
>DLL3_HUMAN (Q9NYJ7)
>5HT6R_HUMAN (P50406)
>PRTN3_HUMAN (P24158)
>NPBW1_HUMAN (P48145)
>UCN2_HUMAN (Q96RP3)
>IG2AS_HUMAN (Q6U949)
>WBP1_HUMAN (Q96G27)
>BIM_HUMAN (O43521)
>CC056_HUMAN (Q8N813)
>SPG11_HUMAN (Q08648)
>CI122_HUMAN (Q5SY85)
  
```

1






2

Comparison of Proteins Detected:

Extraction of Gene Ontology Data

Data source	SwissProt human protein data
Primary motif ?	P.[ST]P
Digest ?	Trypsin, Lys-C
Modified residue ?	
Instrument	ESI (800~4000)

Result

Set	Difference	Analysis Result	Select	
	Union	4746 proteins in both digestion Trypsin or Lys-C	<input type="radio"/>	<input type="radio"/>
	Intersection	4709 proteins in digestion Trypsin and digestion Lys-C	<input type="radio"/>	<input type="radio"/>
	Set difference	32 proteins in digestion Trypsin	<input type="radio"/>	<input type="radio"/>
	Set difference	5 proteins in digestion Lys-C	<input type="radio"/>	<input type="radio"/>
	Symmetric difference	37 proteins in digestion Trypsin or digestion Lys-C but not in both	<input type="radio"/>	<input type="radio"/>

1

The GO terms can be viewed for each set.

Download Protein in FASTA View Proteins View All GO Terms

2