

Projects

- Kinase_32
 - [Generate Protein List](#)
 - [Validate Protein List](#)
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- Diabetes
 - [Generate Protein List](#)
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Edit

Project: **Kinase_32**
 Date: 2010.04.02 12:42:29.000000000
 Author: **Mi-YounBrosniak**

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Step 3: Generate Transition List

Load Transitions

Get Transitions From:

Upload Transitions From:

Maximum Transition Calculator

Proteins x Peptides x Transitions = Maximum SRM Transitions

Target

Choose: [Add Labeled Pairs](#)

Modification:

- Mystery_NTERM
- ICPL_light_K
- ICPL-N_heavy_NTERM
- ICPL_heavy_K
- ICAT_heavy_C
- OLDICAT_light_C
- OLDICAT_heavy_C
- ICPL-N_light_NTERM
- ICAT_light_C
- AQUA_heavy_K_K**
- AQUA_heavy_R_R**
- Cys_CAM_C
- MetOx_M


Decoy Generation

Algorithm: [Simple No Overlap Algorithm](#)

- [About SRM](#)
- [Help](#)

ATAQS PeptideAtlas

[PeptideAtlas Home](#)



PeptideAtlas Home

Get PABST List

Protein Accession:

Upload File Of Proteins:

Peptide Sequence:

Peptide Length:

Empirical Proteolytic Score:

Number of Proteins Mapped:

Number of Genome Locations Mapped:

Num of highest bits Frag tags to Keep:

Number of peptides per protein constraint:

Adjust penalties:

Parameter	Value	Description
4H:	1	Avoid 4 consecutive hydrophobic residues: C,F,I,L,V,W,Y
5H:	1	Avoid 5 straight hydrophobic residues: F,I,L,V,W,M
BA:	1	Penalize high basic (protonatable) sites: H, K, R, n-term
C:	0.95	Avoid C
D:	1	Slightly penalize D or S in general?
DG:	1	Avoid dipeptide DG
DP:	1	Avoid dipeptide DP
Hper:	1	Hydrophobic residues (F,I,L,V,W,M) not to exceed 75%
M:	0.95	Avoid M
NG:	1	Avoid dipeptide NG
NxST:	1	Penalize peptides without NxST motif
P:	0.95	Avoid P
QG:	1	Avoid dipeptide QG
R:	1	Avoid R
S:	1	Slightly penalize D or S in general?