

# Comet

2020.06

김현우

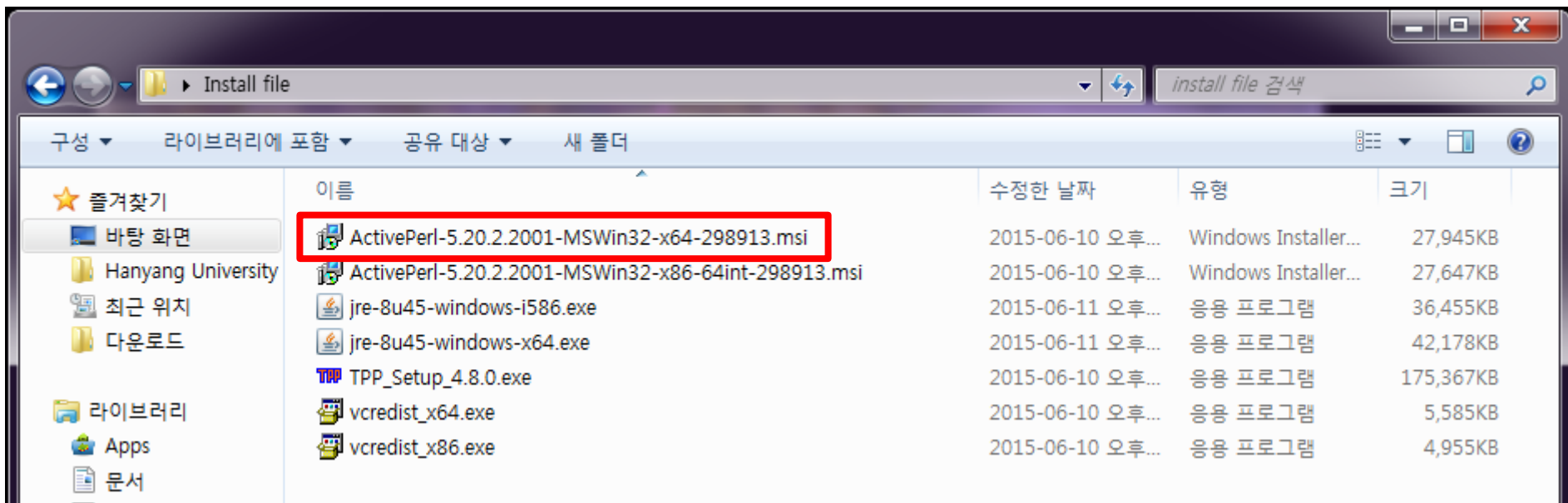
# TPP (Trans-Proteomic Pipeline) 설치

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- **TPP 설치**
  - Perl 설치
  - TPP 설치
  - .dll 파일 설치 (Comet을 실행하기 위한 VC++ 2010관련 dll)

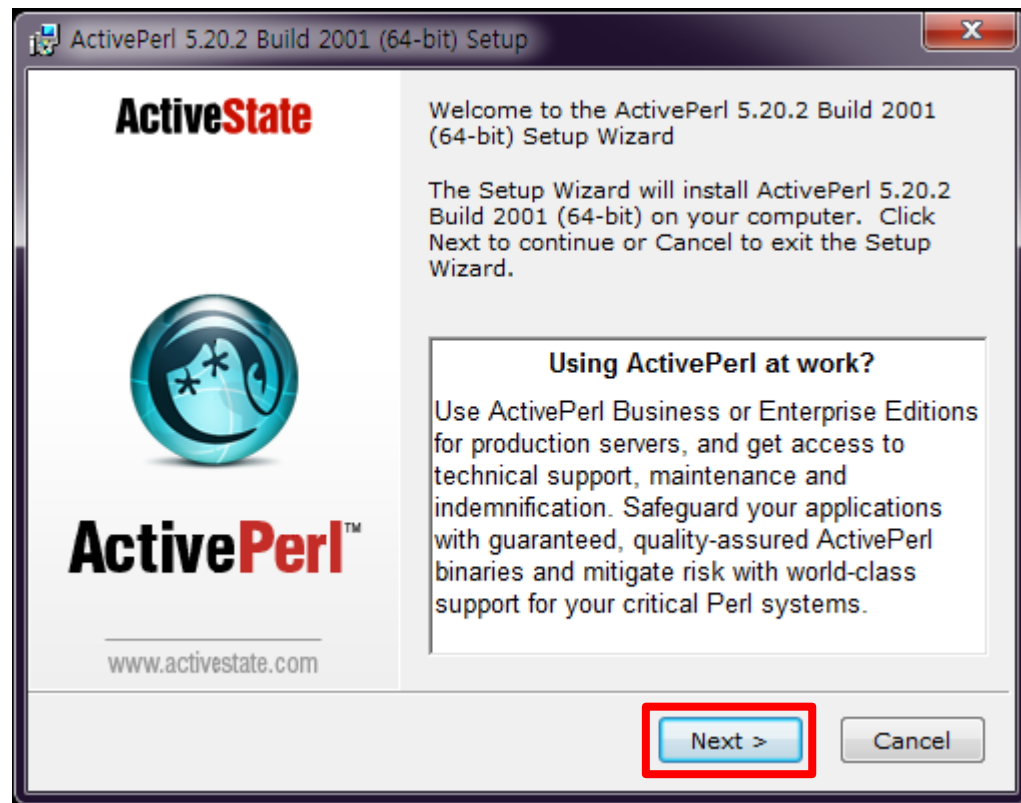
# TPP (Trans-Proteomic Pipeline) 설치

- Perl 설치
  - 설치파일 실행



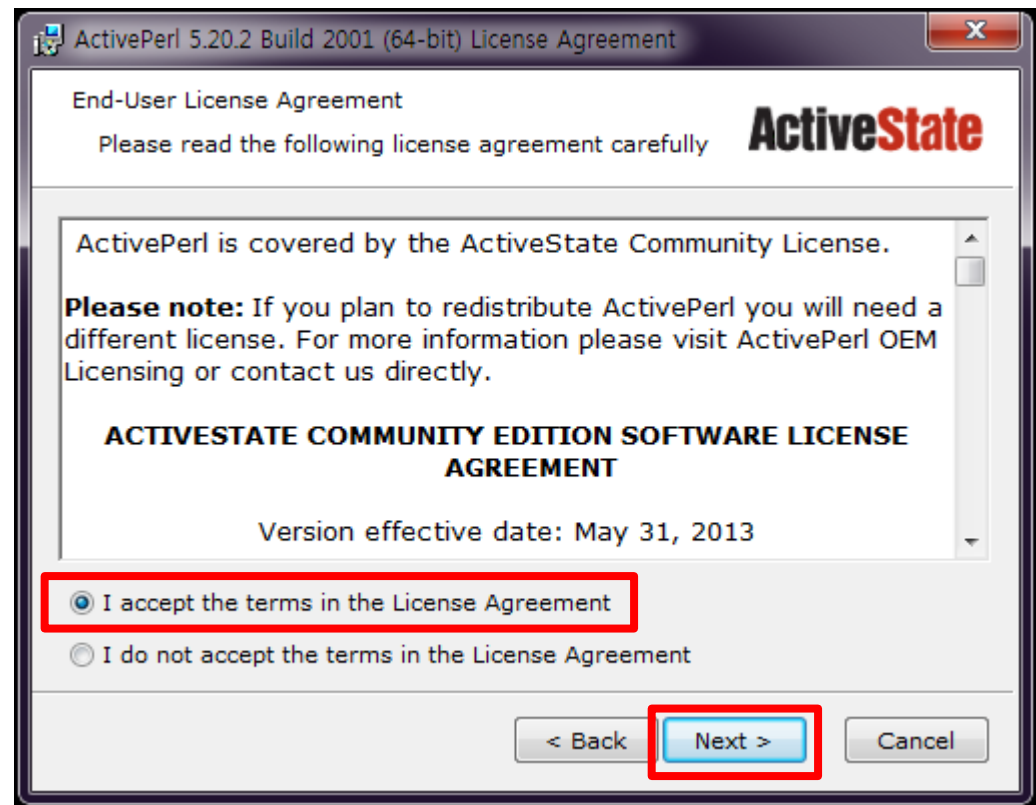
# TPP (Trans-Proteomic Pipeline) 설치

- Perl 설치
  - Next 클릭



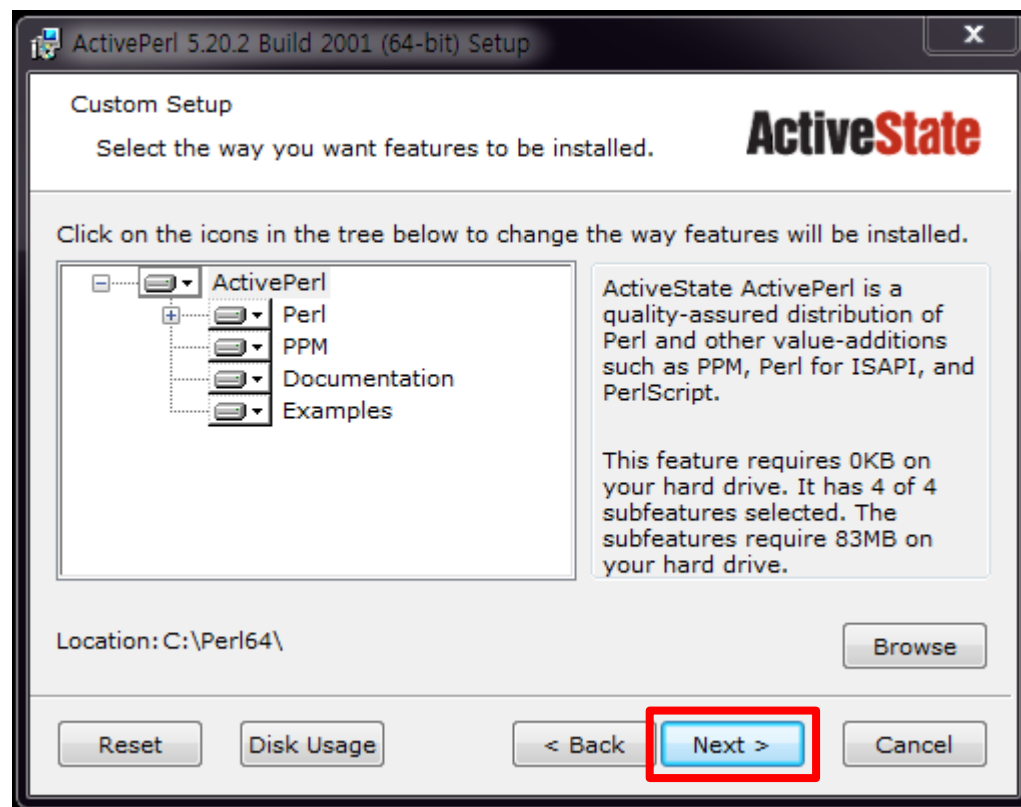
# TPP (Trans-Proteomic Pipeline) 설치

- Perl 설치
  - License Agreement 체크
  - Next 클릭



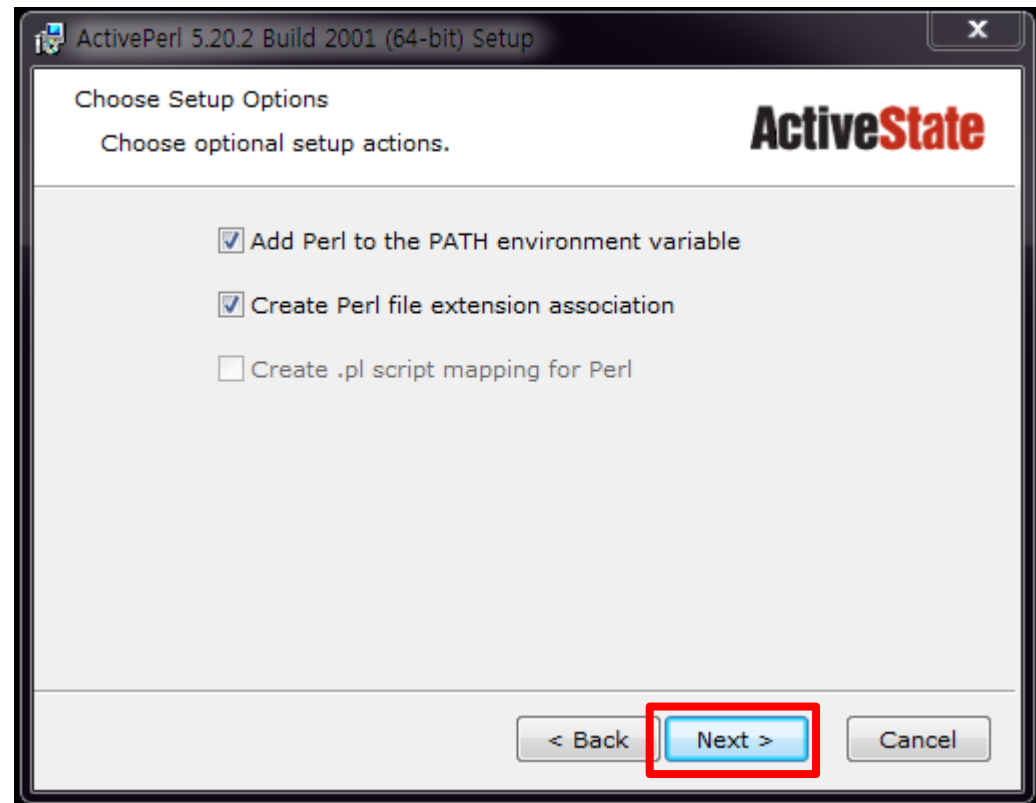
# TPP (Trans-Proteomic Pipeline) 설치

- Perl 설치
  - Next 클릭



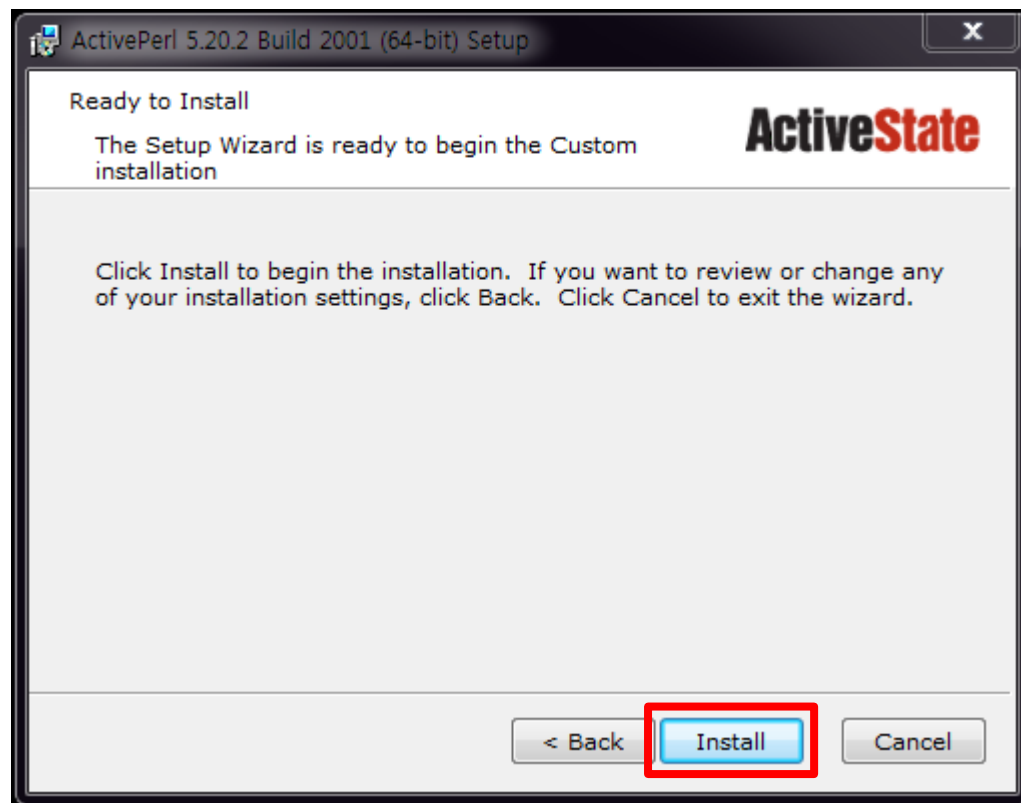
# TPP (Trans-Proteomic Pipeline) 설치

- Perl 설치
  - Next 클릭



# TPP (Trans-Proteomic Pipeline) 설치

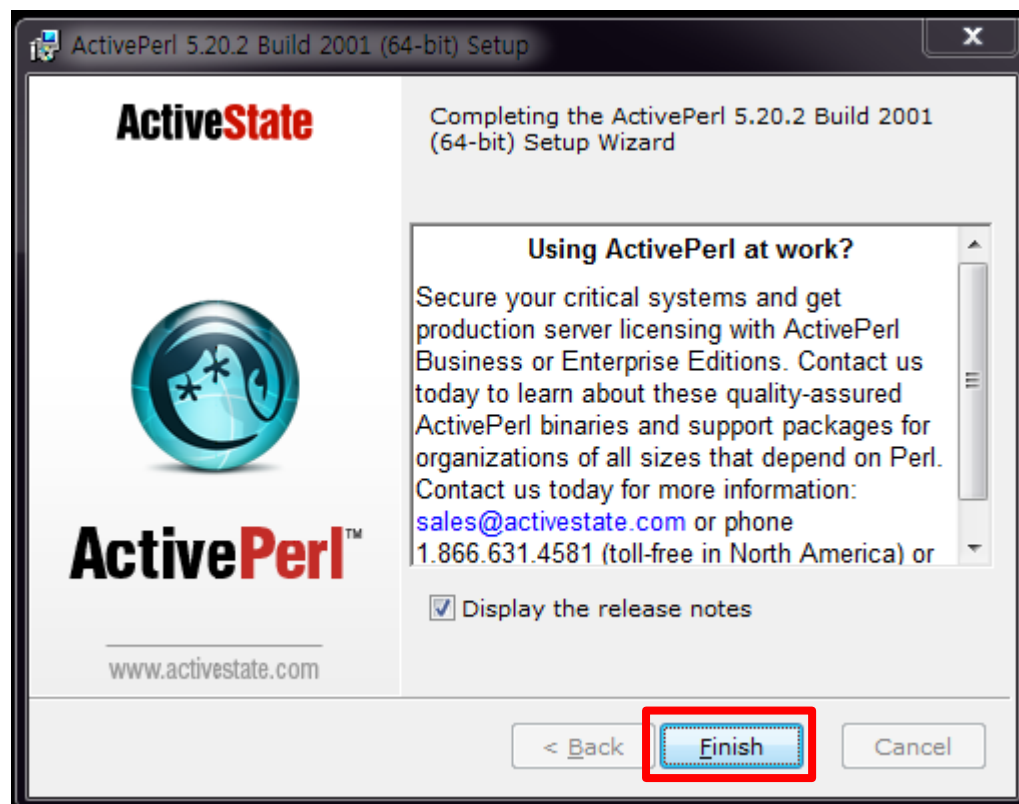
- Perl 설치
  - Install 클릭





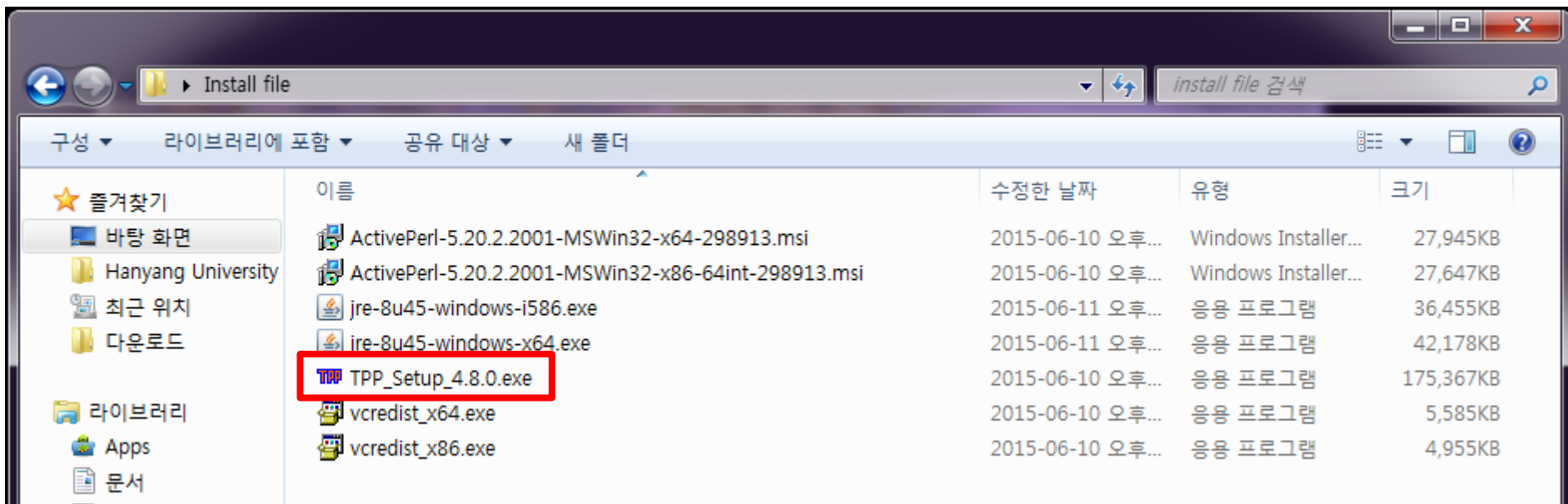
# TPP (Trans-Proteomic Pipeline) 설치

- Perl 설치
  - Finish 클릭



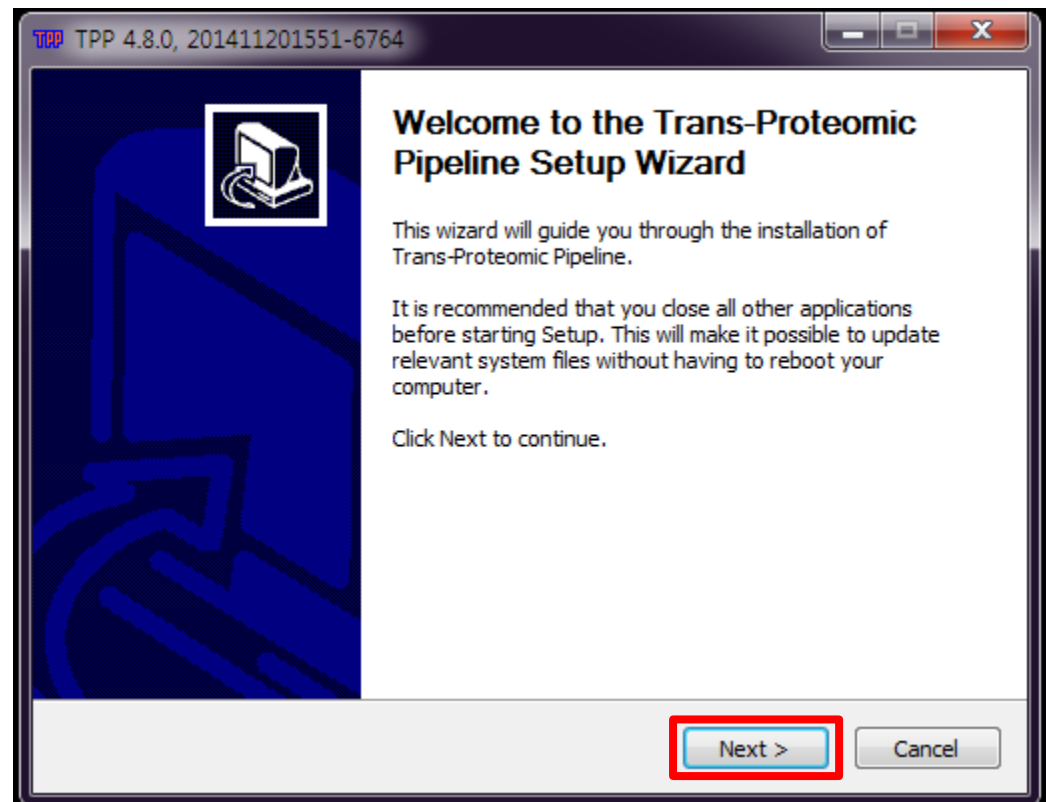
# TPP (Trans-Proteomic Pipeline) 설치

- TPP 설치
  - 설치파일 실행



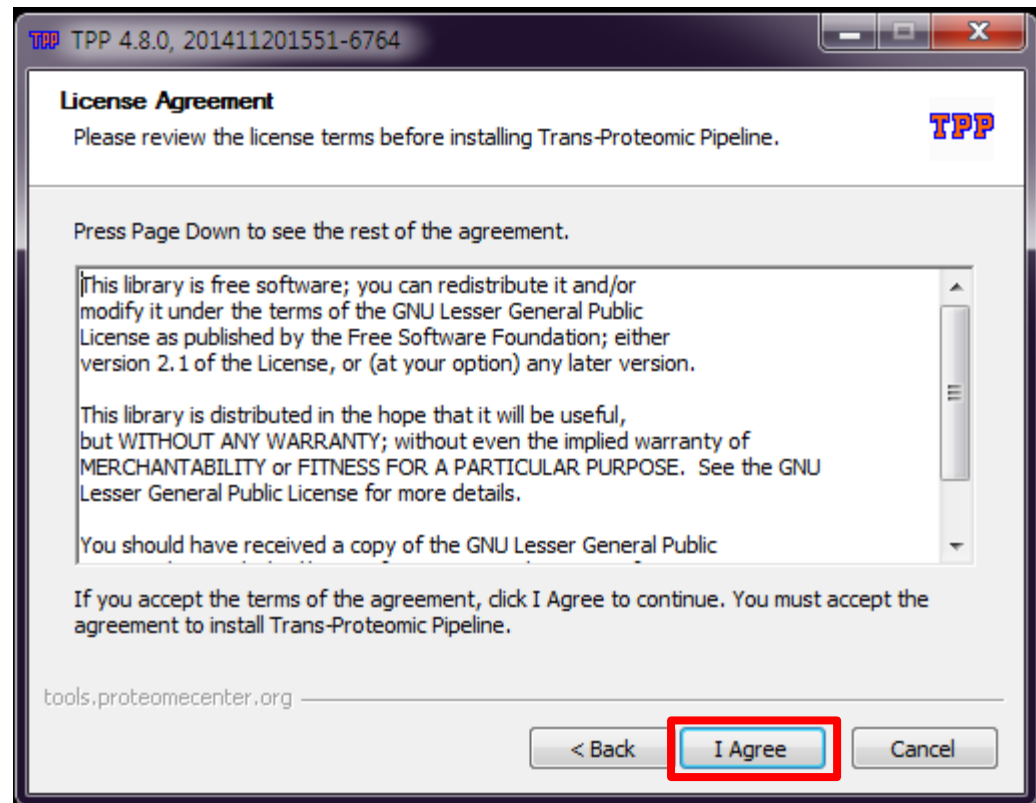
# TPP (Trans-Proteomic Pipeline) 설치

- **TPP 설치**
  - Next 클릭



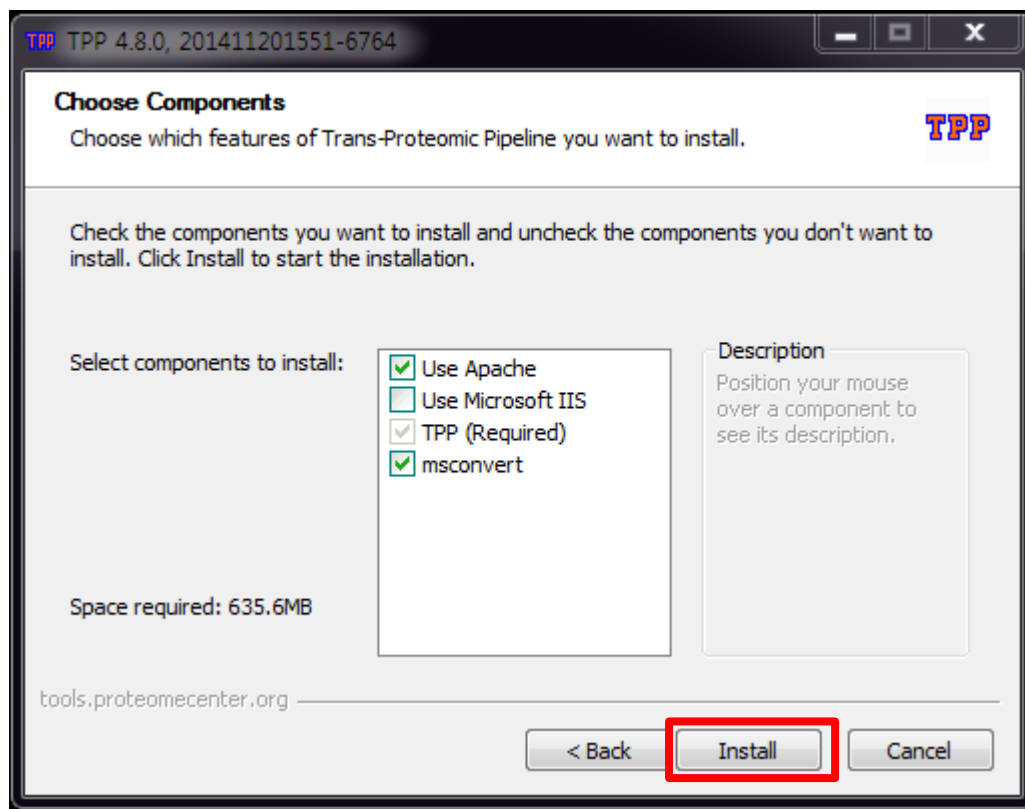
# TPP (Trans-Proteomic Pipeline) 설치

- TPP 설치
  - I Agree 클릭



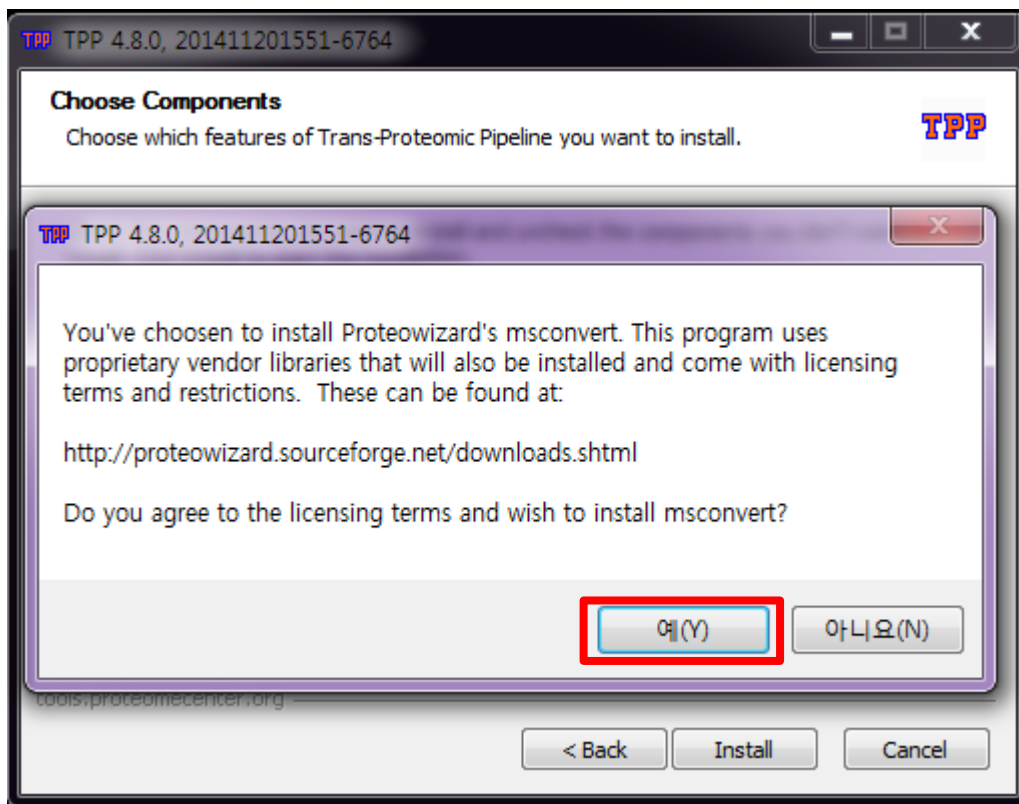
# TPP (Trans-Proteomic Pipeline) 설치

- **TPP 설치**
  - Install 클릭



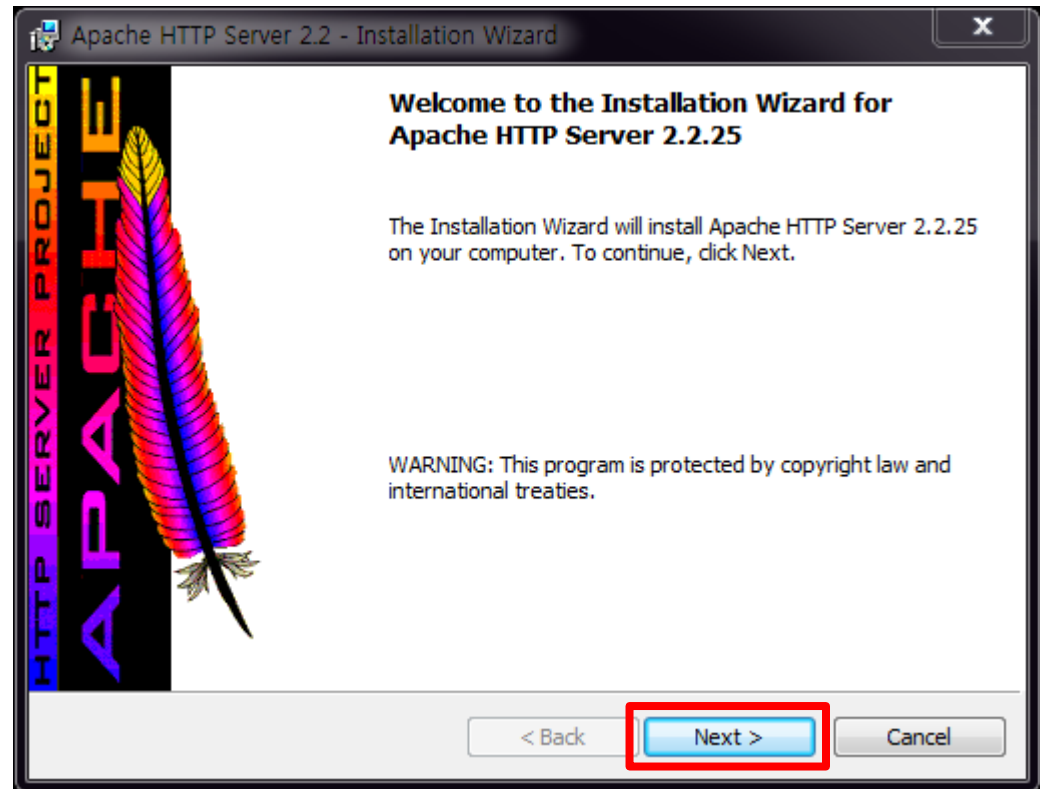
# TPP (Trans-Proteomic Pipeline) 설치

- TPP 설치
  - 예(Y) 클릭



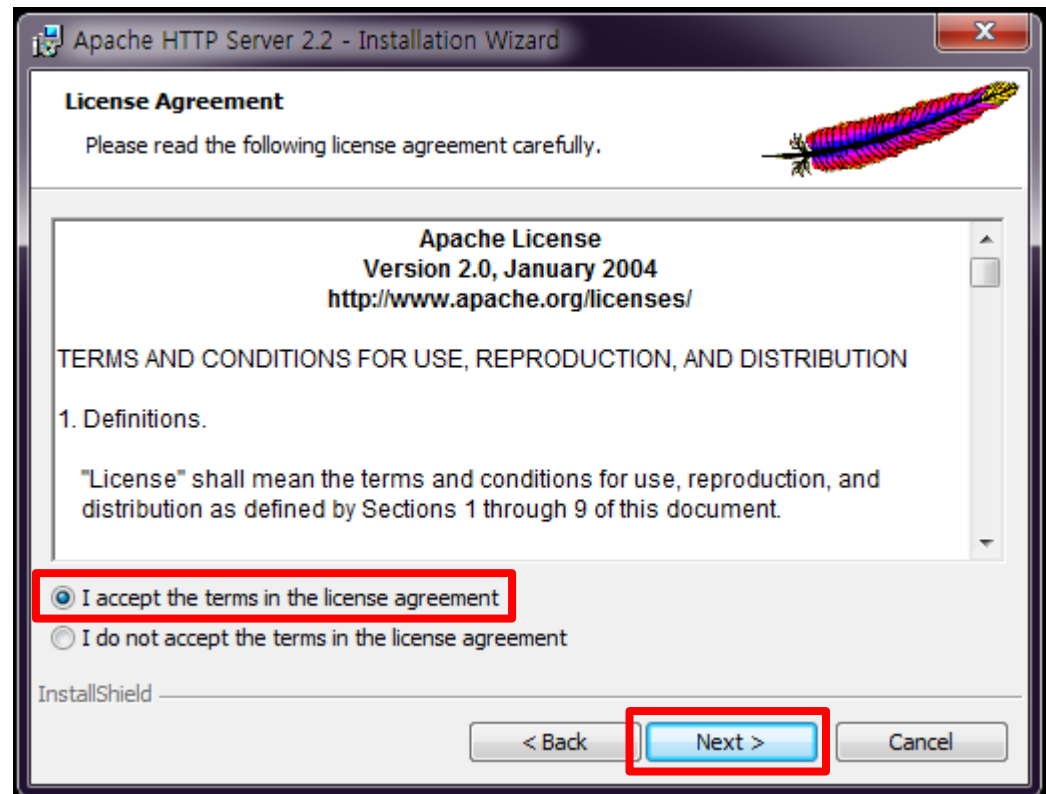
# TPP (Trans-Proteomic Pipeline) 설치

- **TPP 설치**
  - Apache 설치
    - Next 클릭



# TPP (Trans-Proteomic Pipeline) 설치

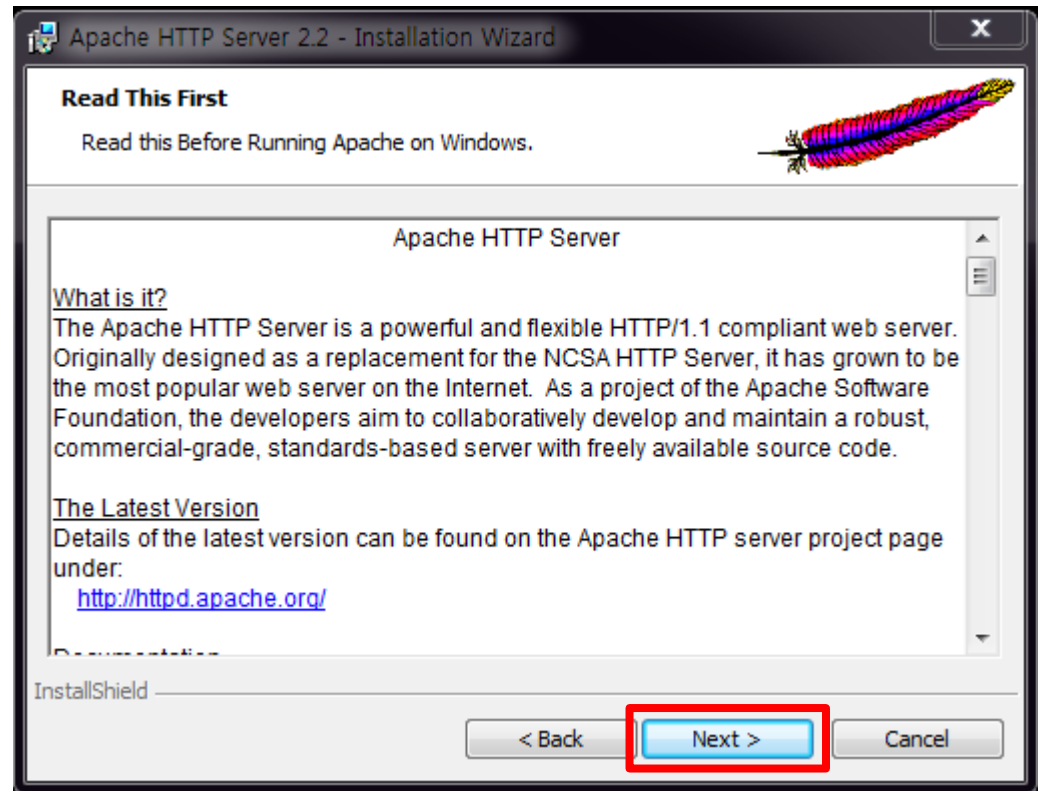
- **TPP 설치**
  - Apache 설치
    - License agreement 체크
    - Next 클릭





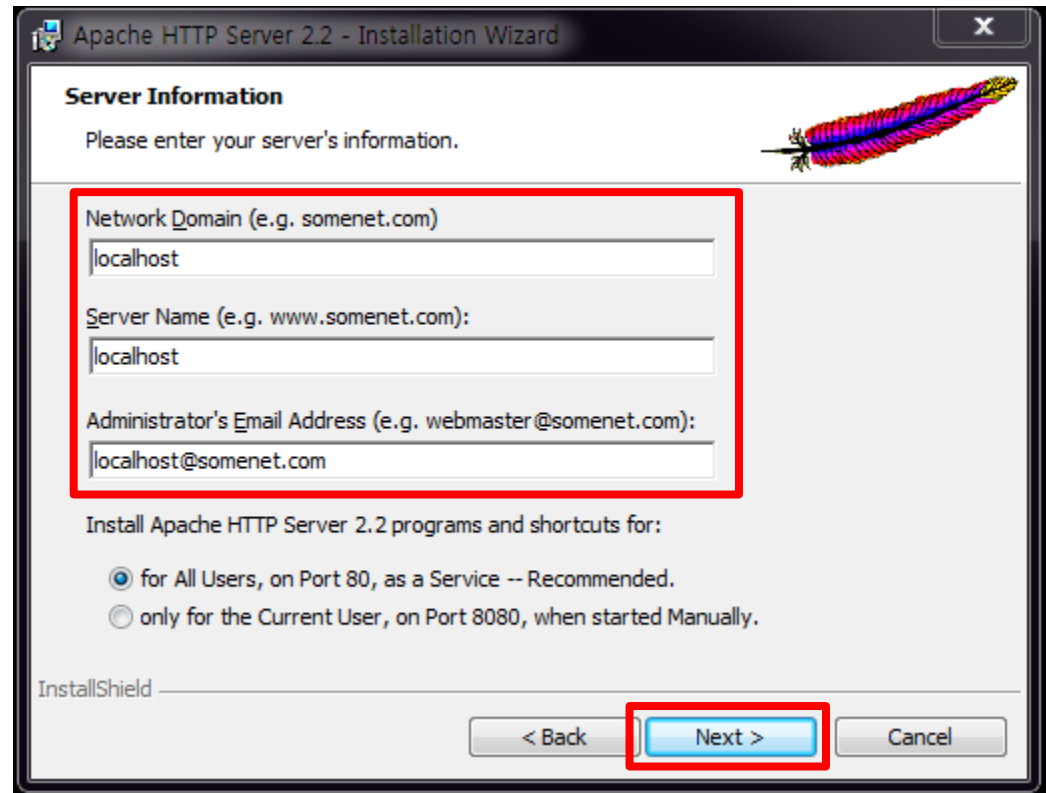
# TPP (Trans-Proteomic Pipeline) 설치

- **TPP 설치**
  - Apache 설치
    - Next 클릭



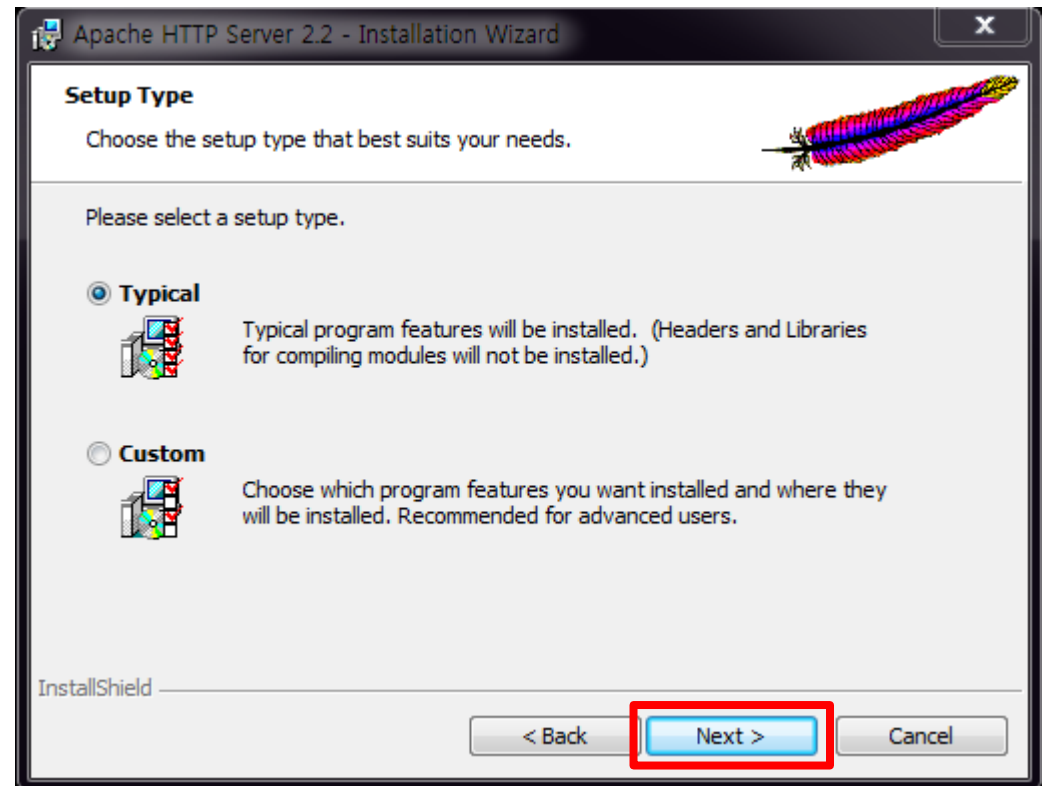
# TPP (Trans-Proteomic Pipeline) 설치

- **TPP 설치**
  - Apache 설치
    - Network Domain, Server name, Email Address 입력
    - Next 클릭



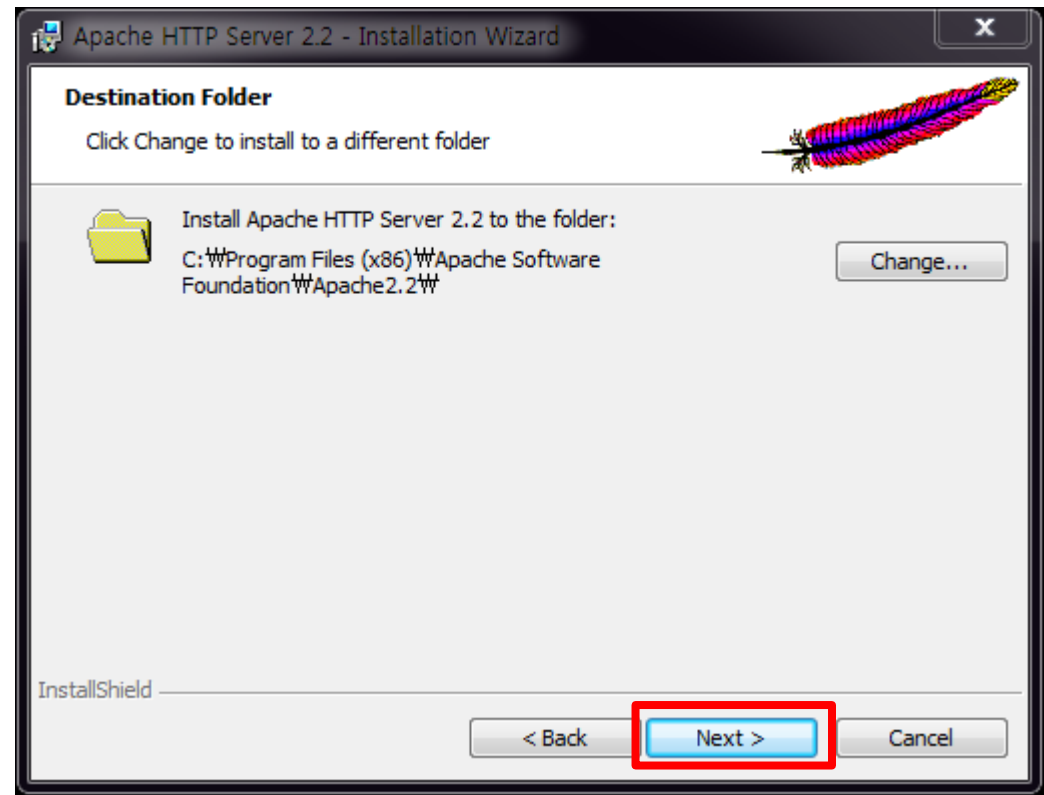
# TPP (Trans-Proteomic Pipeline) 설치

- **TPP 설치**
  - Apache 설치
    - Next 클릭



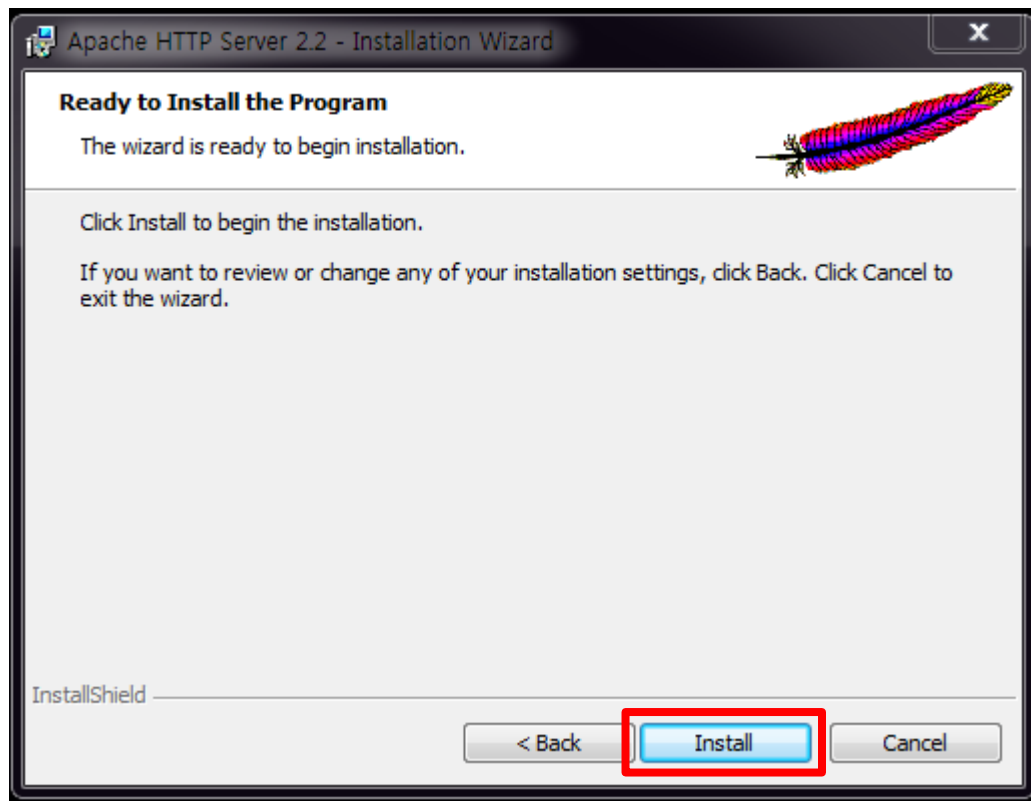
# TPP (Trans-Proteomic Pipeline) 설치

- **TPP 설치**
  - Apache 설치
    - Next 클릭



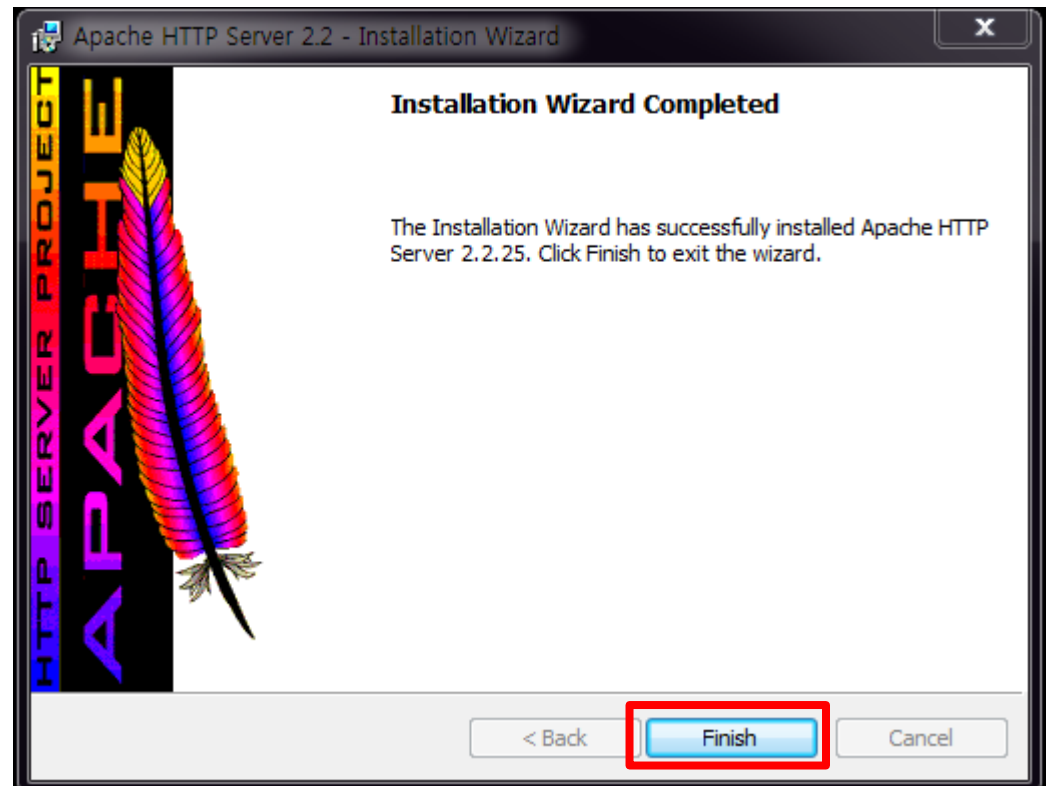
# TPP (Trans-Proteomic Pipeline) 설치

- **TPP 설치**
  - Apache 설치
    - Install 클릭



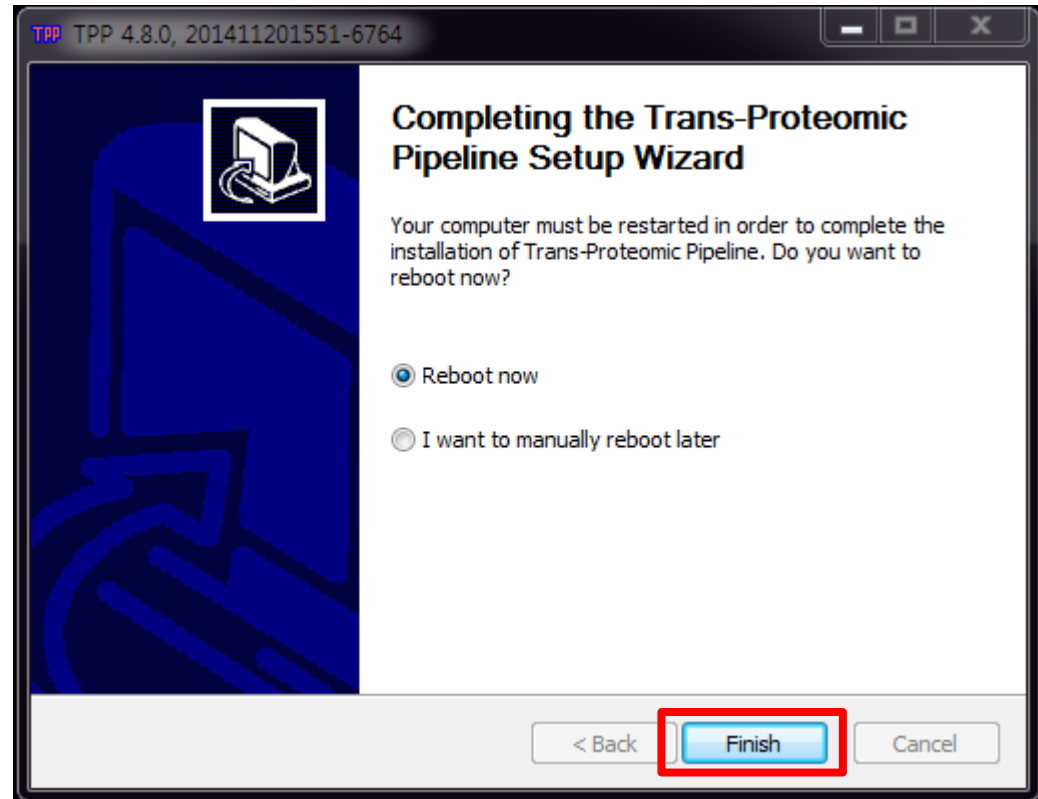
# TPP (Trans-Proteomic Pipeline) 설치

- **TPP 설치**
  - Apache 설치
    - Finish 클릭



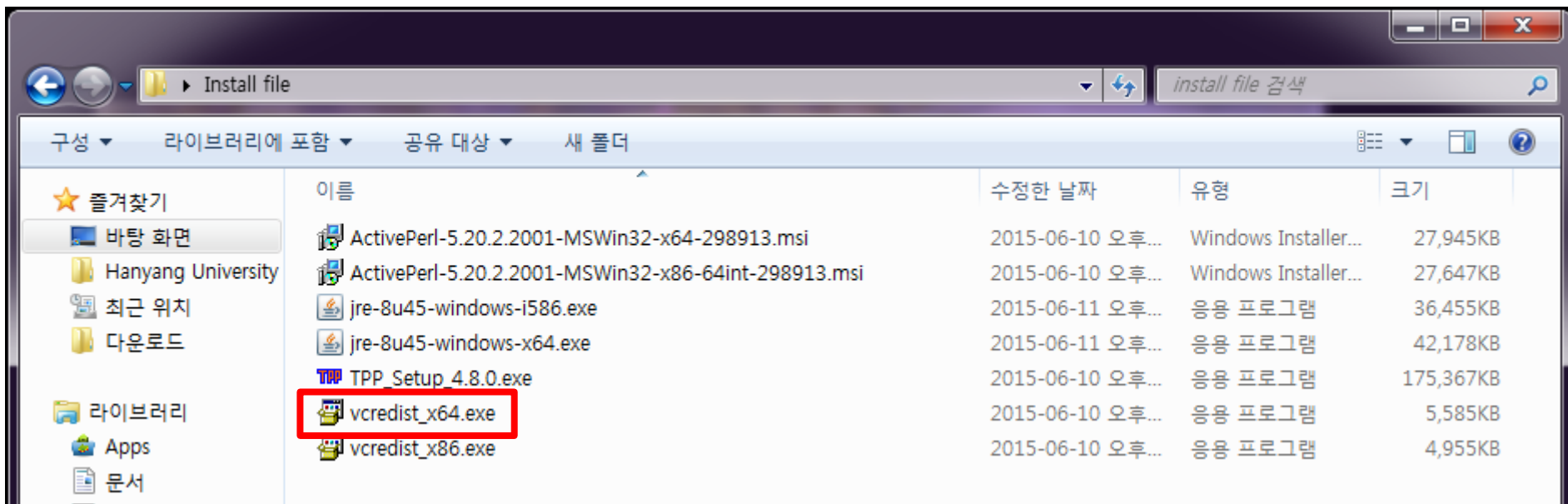
# TPP (Trans-Proteomic Pipeline) 설치

- **TPP 설치**
  - Finish 클릭



# TPP (Trans-Proteomic Pipeline) 설치

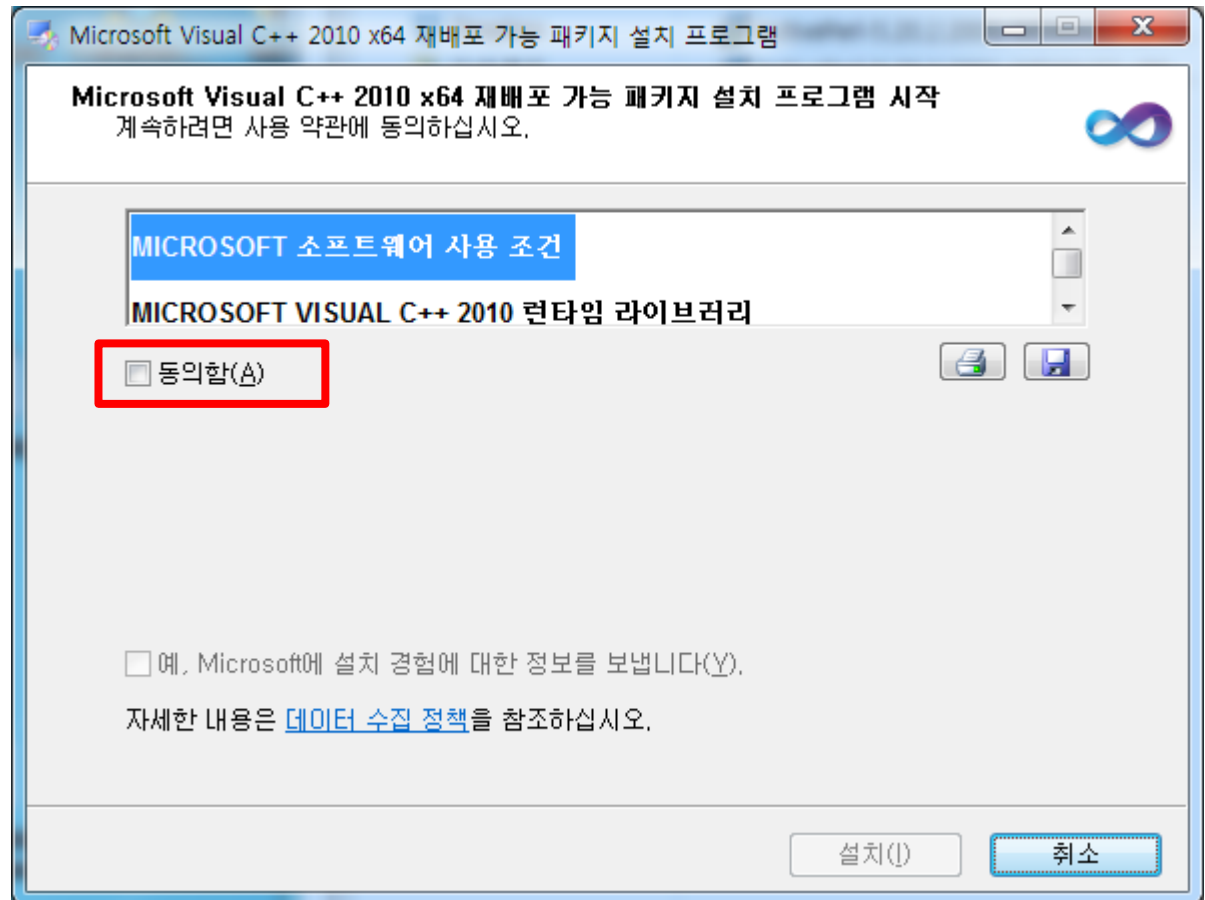
- Dll 파일 설치
  - 설치파일 실행





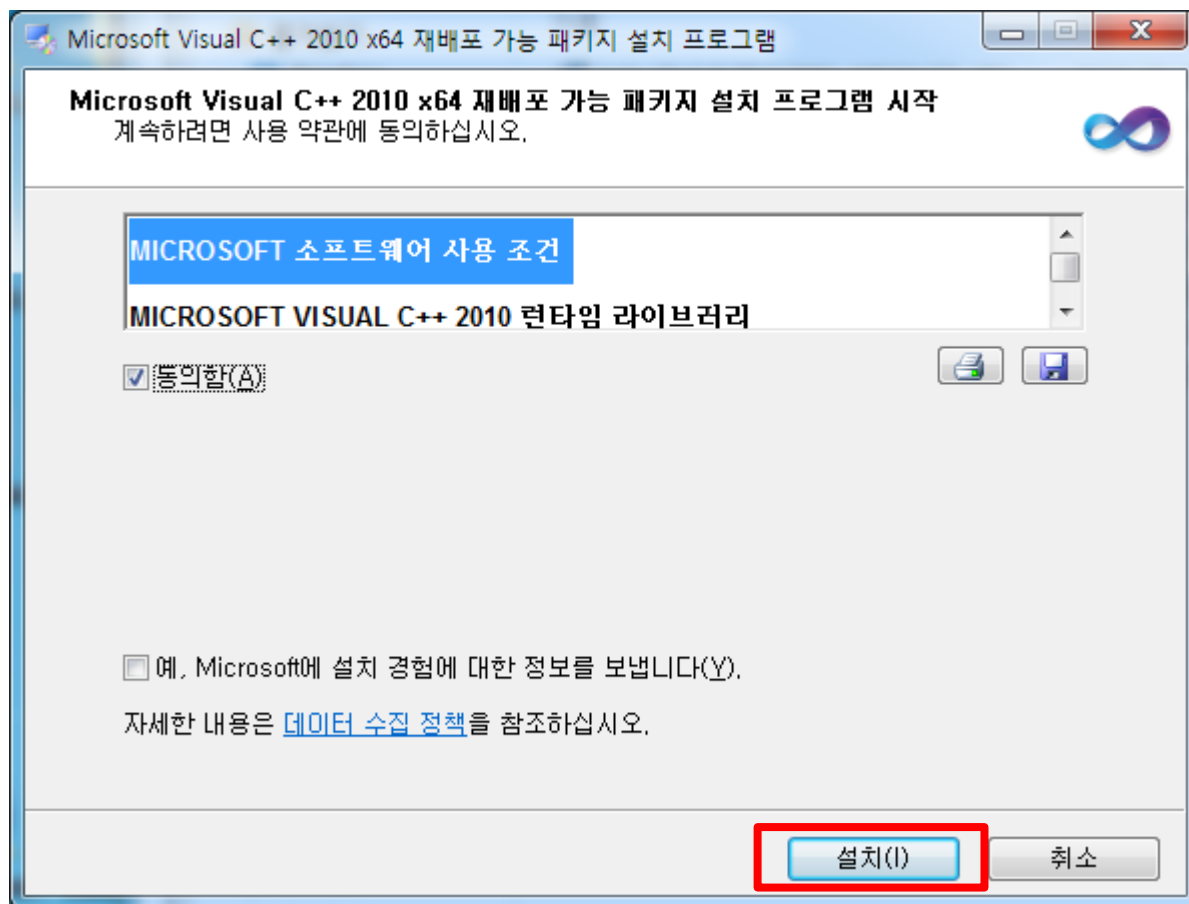
# TPP (Trans-Proteomic Pipeline) 설치

- Dll 파일 설치
  - 동의함



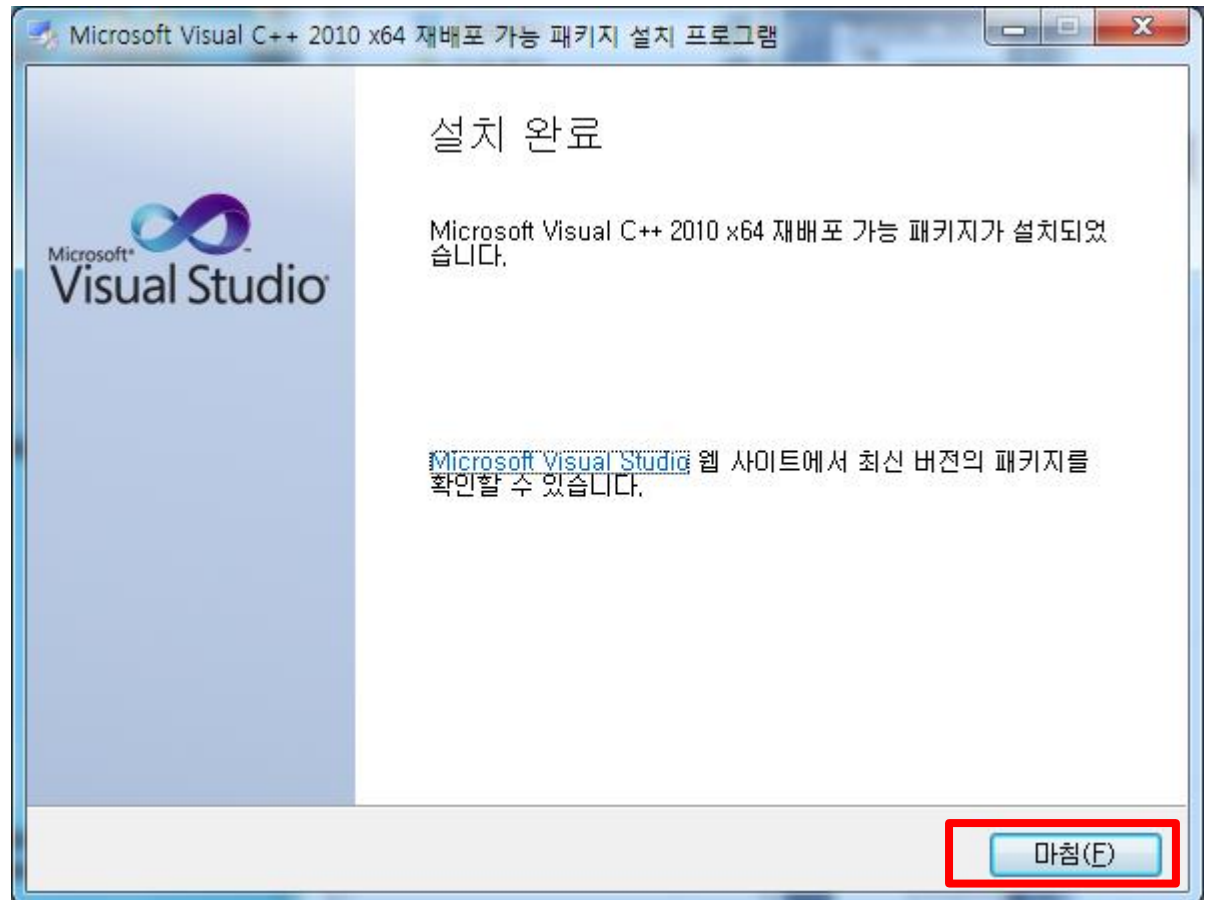
# TPP (Trans-Proteomic Pipeline) 설치

- Dll 파일 설치
  - 설치



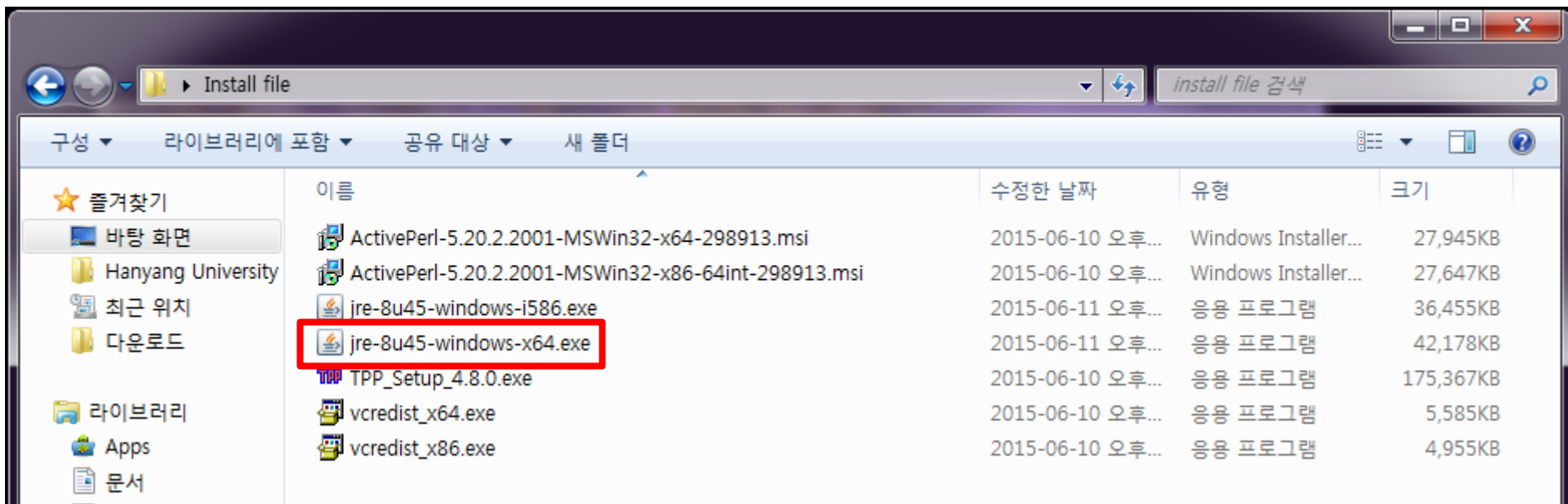
# TPP (Trans-Proteomic Pipeline) 설치

- Dll 파일 설치
  - 마침



# TPP (Trans-Proteomic Pipeline) 설치

- JRE 설치
  - 설치파일 실행



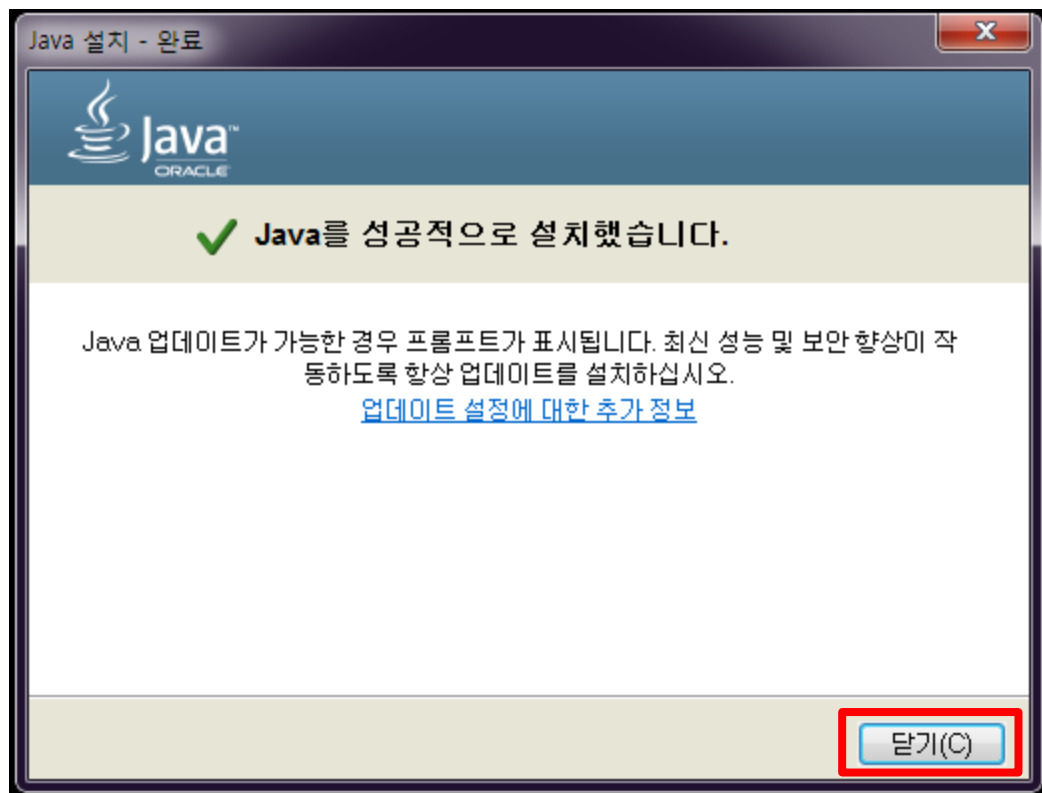
# TPP (Trans-Proteomic Pipeline) 설치

- JRE 설치
  - 설치(I) 클릭



# TPP (Trans-Proteomic Pipeline) 설치

- JRE 설치
  - 닫기(C) 클릭



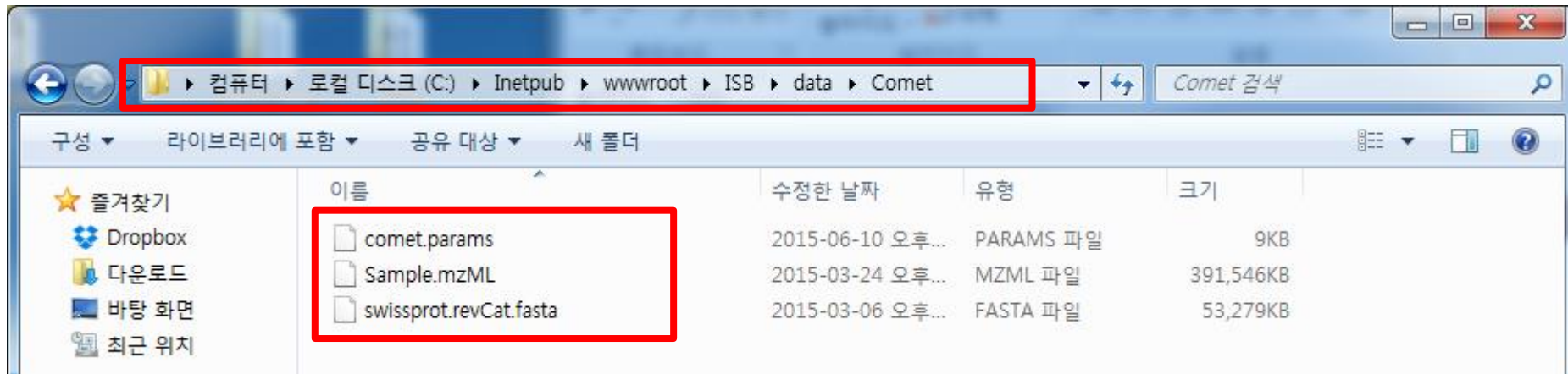
# Comet 실행을 위한 준비

---

- **필요한 파일**
  - Spectrum **파일** (.mzxml or .mzml)
    - Sample.mzML
  - Database **파일** (.fasta)
    - swissprot.revCat.fasta
  - Parameter **파일** (.params)
    - comet.params

# Comet 실행을 위한 준비

- 해당 파일을 TPP에서 사용할 수 있도록 복사
  - C:\Inetpub\wwwroot\ISB\data 폴더에 Comet 폴더를 복사
  - Comet 폴더 안에 있는 3개 파일 확인

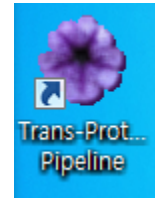
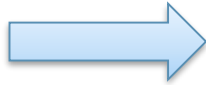




# TPP 실행 및 로그인

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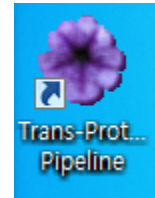
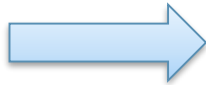
- **TPP 실행**
  - 바탕화면에 아이콘 실행



# TPP 실행 및 로그인

- **TPP 실행**

- 바탕화면에 아이콘 실행



- **TPP 웹페이지에서 로그인**

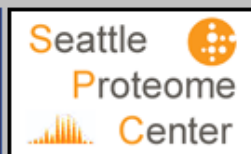
- User Name: guest
  - Password: guest

## ISB/SPC Trans Proteomic Pipeline - login

User Name:

Password:

Login

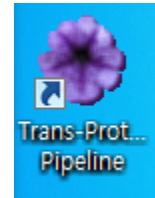
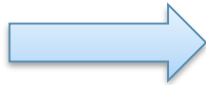


TPP v4.8.0 PHILAE, Build 201411201551-6764 (mingw-i686)

# TPP 실행 및 로그인

- **TPP 실행**

- 바탕화면에 아이콘 실행



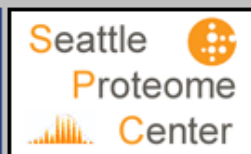
- **TPP 웹페이지에서 로그인**

- User Name: guest
  - Password: guest
  - Login 클릭

## ISB/SPC Trans Proteomic Pipeline - login

User Name:

Password:



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# Comet 실행

- Analysis pipeline 확인
  - Comet으로 선택

ISB/SPC Trans Proteomic Pipeline - home

Home | Files | Account | Pre-Process | mzXML Utils | Analysis Pipeline (Comet) | Decoy | Utilities | SpectraST Tools | Jobs

You are logged in as guest [Log Out](#)

Home	FILES	ACCOUNT	PRE-PROCESS	mzXML UTILS	ANALYSIS PIPELINE	DECOY	UTILITIES	SPECTRAST TOOLS	JOBS
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Messages [\[ Show / Hide \]](#)

- Welcome, guest.

Welcome

Welcome to the Trans-Proteomic Pipeline (TPP) web interface. These tools and interfaces were developed and are being maintained at the [Institute for Systems Biology](#) (ISB) under a grant from [NIGMS](#). Please visit [this page](#) for more information.

Please select analysis pipeline you want to use:

Analysis Pipeline

Follow these steps to convert, search, and analyze your data:

1. RAW to mzML Conversion  
Convert original .RAW files to the standard mzML input format used by the tools
2. Peptide Database Search and Identification

Comet  
Mascot  
Sequest  
SpectraST  
Tandem

Analysis Pipeline

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INSTITUTE FOR Systems Biology Revolutionizing science. Enhancing life.

Seattle Proteome Center

# Comet 실행

- Analysis pipeline 확인
  - Analysis Pipeline(Comet)

The screenshot shows the 'ISB/SPC Trans Proteomic Pipeline - home' interface. The top navigation bar includes links for Home, Files, Account, Pre-Process, **Analysis Pipeline (Comet)**, Decoy, Utilities, SpectraST Tools, and Jobs. A red box highlights the 'Analysis Pipeline (Comet)' link, and a red arrow points from it to a detailed menu overlay.

The menu overlay lists the following options:

- mzML/mzXML
- Database Search
- Analyze Peptides
- Combine Analyses
- Analyze PTMs
- Analyze Proteins

has been changed to: Comet

The footer of the page contains the following information:

- INSTITUTE FOR Systems Biology Revolutionizing science. Enhancing life.
- Seattle Proteome Center
- TPP v4.8.0 PHILAE, Build 201411201551-6764 (mingw-i686)

# Comet 실행

- Analysis pipeline 확인
  - Analysis Pipeline(Comet)
  - Database Search 클릭

The screenshot shows the 'ISB/SPC Trans Proteomic Pipeline - home' page. A red box highlights the 'Analysis Pipeline (Comet)' link in the top navigation bar. A red arrow points from this box to a larger red-bordered box that contains a list of options: 'mzML/mzXML', 'Database Search', 'Analyze Peptides', 'Combine Analyses', 'Analyze PTMs', and 'Analyze Proteins'. The 'Database Search' option is highlighted with a red box. Below this list, the text 'has been changed to: Comet' is visible. The bottom of the page features logos for the 'Institute for Systems Biology' and the 'Seattle Proteome Center', along with version information: 'TPP v4.8.0 PHILAE, Build 201411201551-6764 (mingw-i686)'.

ISB/SPC Trans Proteomic Pipeline - home

Home | Files | Account | Pre-Process | mzXML Utils | Analysis Pipeline (Comet) | Decoy | Utilities | SpectraST Tools | Jobs

Home | FILES | ACCOUNT | PRE-PROCESS | mzXML UTILS | ANALYSIS PIPELINE | DECOY | UTILITIES | SPECTRAST TOOLS | JOBS

messages [ Show / Hide ]

- Welcome, guest.

mzML/mzXML  
**Database Search**  
Analyze Peptides  
Combine Analyses  
Analyze PTMs  
Analyze Proteins

has been changed to: Comet

Institute for Systems Biology (ISB) under a grant from NIGMS. Please visit [here](#) to find out how to join this list.

PeptideProphet and/or use ASAPRatio or XPRESS to calculate the relative abundances

Users should modify.

list. Click [here](#) to find out how to join this list.

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Seattle Proteome Center

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# Comet 실행

- Spectrum data 선택
  - Add Files 클릭

ISB/SPC Trans Proteomic Pipeline - runcomet

[Home](#) | [Files](#) | [Account](#) | [Pre-Process](#) | [mzXML Utils](#) | [Analysis Pipeline \(Comet\)](#) | [Decoy](#) | [Utilities](#) | [SpectraST Tools](#) | [Jobs](#)  You are logged in as guest [Log Out](#)

[Home](#) | [mzML/mzXML](#) | [Database Search](#) | [Analyze Peptides](#) | [Combine Analyses](#) | [Analyze PTMs](#) | [Analyze Proteins](#)

Need more [information on Comet or its parameters?](#)

**1. Specify mz[X]ML Input Files** [ Show / Hide ]

No files selected yet.

[Add Files](#)

**2. Specify Comet Parameters File** [ Show / Hide ]


No files selected yet.

[Add Files](#)

**1. Specify mz[X]ML Input Files** [ Show / Hide ]

No files selected yet.

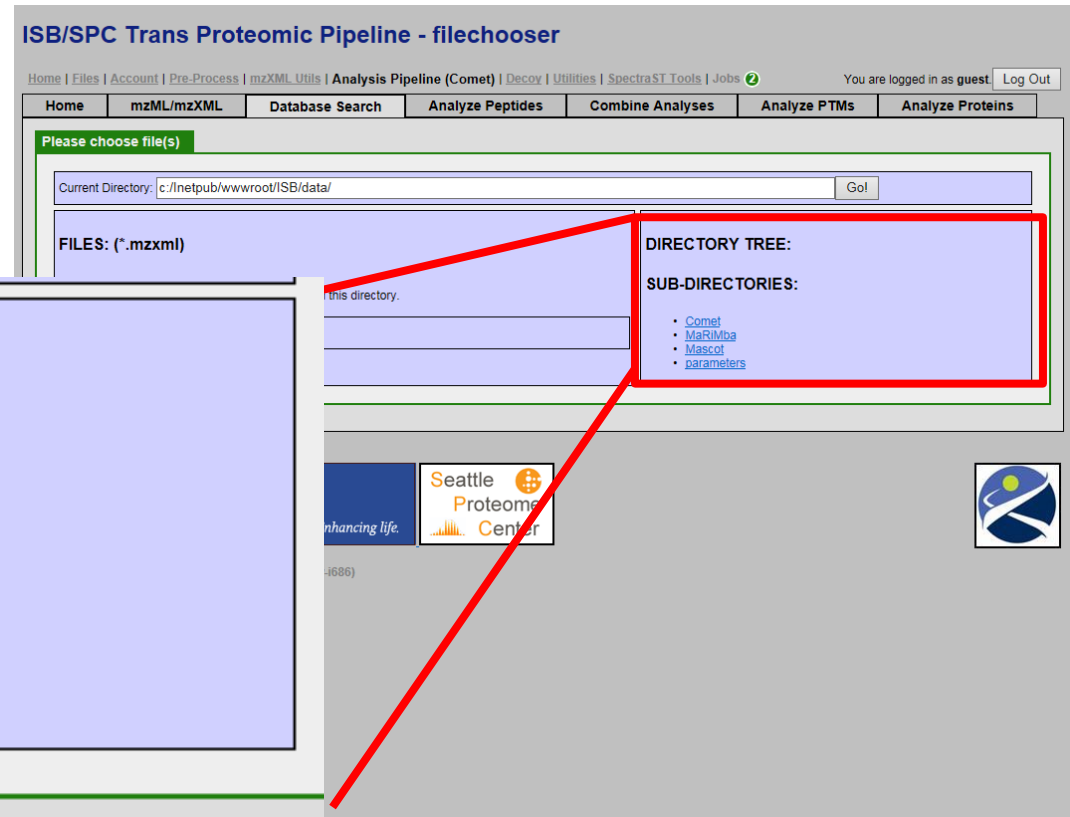
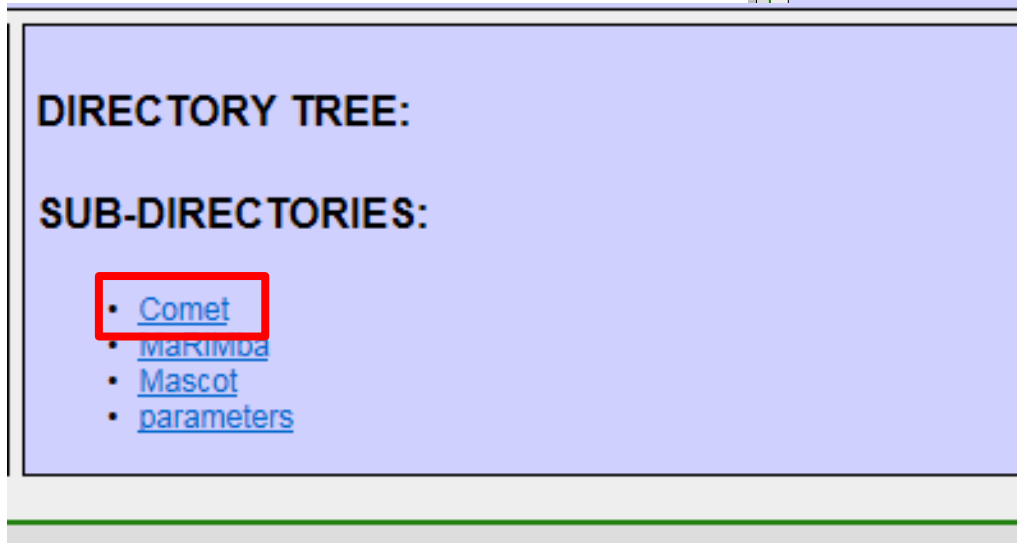
[Add Files](#)



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# Comet 실행

- Spectrum data 선택
  - Comet 클릭





# Comet 실행

- Spectrum data 선택
  - Sample.mzML 체크
  - Select 클릭

ISB/SPC Trans Proteomic Pipeline - filechooser

Home | Files | Account | Pre-Process | mzXML Utils | Analysis Pipeline (Comet) | Decoy | Utilities | SpectraST Tools | Jobs 2 You are logged in as guest Log Out

Home mzML/mzXML Database Search Analyze Peptides Combine Analyses Analyze PTMs Analyze Proteins

Please choose file(s)

Current Directory: c:/inetpub/wwwroot/ISB/data/Comet/ Go!

FILES: (\*.mzxml)

File Name	View?	Size	Date Modified
<input type="checkbox"/> Sample.mzML	[ <a href="#">Pep3D</a> ]	382.4 MB	Tue Mar 24 13:23:52 2015
files found			

Select Cancel

DIRECTORY TREE:

- Go up to: [data](#)
- Current: |--Comet

SUB-DIRECTORIES:

- No subdirectories found in this folder.

1 files found

Select Cancel

# Comet 실행

- Spectrum data 선택
  - 파일 선택 확인

ISB/SPC Trans Proteomic Pipeline - runcomet

Home | Files | Account | Pre-Process | mzXML Utils | Analysis Pipeline (Comet) | Decoy | Utilities | SpectraST Tools | Jobs You are logged in as guest [Log Out](#)

Home | **mzML/mzXML** | Database Search | Analyze Peptides | Combine Analyses | Analyze PTMs | Analyze Proteins

**Messages** [ Show / Hide ]

- Your files have been added:
- Sample.mzML

Need more [information on Comet or its parameters?](#)

**1. Specify mz[X]ML Input Files** [ Show / Hide ]

c:/inetpub/wwwroot/ISB/data/Comet/Sample.mzML ☐

Or choose from list: c:/inetpub/wwwroot/ISB/data/Comet/ [ mzxml ]

**2. Specify Comet Parameters File** [ Show / Hide ]

No files selected yet.

**1. Specify mz[X]ML Input Files** [ Show / Hide ]

c:/inetpub/wwwroot/ISB/data/Comet/Sample.mzML

Or choose from list: c:/inetpub/wwwroot/ISB/data/Comet/ [ mzxml ]

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# Comet 실행

- Parameter 선택
  - comet.params 선택

ISB/SPC Trans Proteomic Pipeline - runcomet

Home | Files | Account | Pre-Process | mzXML Utils | Analysis Pipeline (Comet) | Decoy | Utilities | SpectraST Tools | Jobs You are logged in as guest Log Out

Home | mzML/mzXML | Database Search | Analyze Peptides | Combine Analyses | Analyze PTMs | Analyze Proteins

Messages [ Show / Hide ]

- Your files have been added:
- Sample.mzML

Need more [information on Comet or its parameters?](#)

1. Specify mz[X]ML Input Files [ Show / Hide ]

c:/inetpub/wwwroot/ISB/data/Comet/Sample.mzML Remove

Add Files Or choose from list: c:/inetpub/wwwroot/ISB/data/Comet/ [ mzxml ]

2. Specify Comet Parameters File [ Show / Hide ]

No files selected yet.

Add Files Or choose from list: c:/inetpub/wwwroot/ISB/data/Comet/ [ \*params\* ]

3. Specify a sequence database [ Show / Hide ]

2. Specify Comet Parameters File [ Show / Hide ]

No files selected yet.

Add Files Or choose from list: c:/inetpub/wwwroot/ISB/data/Comet/ [ \*params\* ]

comet.params

# Comet 실행

- Parameter 선택
  - 파일 선택 확인

ISB/SPC Trans Proteomic Pipeline - runcomet

Home | Files | Account | Pre-Process | mzXML Utils | Analysis Pipeline (Comet) | Decoy | Utilities | SpectraST Tools | Jobs You are logged in as guest Log Out

Home | mzML/mzXML | Database Search | Analyze Peptides | Combine Analyses | Analyze PTMs | Analyze Proteins

Messages [ Show / Hide ]

- Your files have been added:
- comet.params

Need more [information on Comet or its parameters?](#)

1. Specify mz[X]ML Input Files [ Show / Hide ]

c:/inetpub/wwwroot/ISB/data/Comet/Sample.mzML

Or choose from list: c:/inetpub/wwwroot/ISB/data/Comet/ [ mzxml ] ▾

2. Specify Comet Parameters File [ Show / Hide ]

c:/inetpub/wwwroot/ISB/data/Comet/comet.params

Or choose from list: c:/inetpub/wwwroot/ISB/data/Comet/ [ \*params\* ] ▾

3. Specify a sequence database [ Show / Hide ]

2. Specify Comet Parameters File [ Show / Hide ]

c:/inetpub/wwwroot/ISB/data/Comet/comet.params

Or choose from list: c:/inetpub/wwwroot/ISB/data/Comet/ [ \*params\* ] ▾

# Comet Parameter

```
1 # comet_version 2014.02 rev. 2
2 # Comet MS/MS search engine parameters file.
3 # Everything following the '#' symbol is treated as a comment.
4
5 database_name = swissprot.revCat.fasta
6 decoy_search = 0 # 0=no (default), 1=concatenated search, 2=separate search
7 num_threads = 0 # 0=poll CPU to set num threads; else specify num threads directly (max 64)
8
9 #
10 # masses
11 #
12 peptide_mass_tolerance = 10
13 peptide_mass_units = 2 # 0=amu, 1=mmu, 2=ppm
14 mass_type_parent = 1 # 0=average masses, 1=monoisotopic masses
15 mass_type_fragment = 1 # 0=average masses, 1=monoisotopic masses
16 isotope_error = 0 # 0=off, 1=on -1/0/1/2/3 (standard C13 error), 2= -8/-4/0/4/8 (for +4/+8 labeling)
17
18 #
19 # search enzyme
20 #
21 search_enzyme_number = 1 # choose from list at end of this params file
22 num_enzyme termini = 2 # valid values are 1 (semi-digested), 2 (fully digested, default), 8 N-term, 9 C-term
23 allowed_missed_cleavage = 0 # maximum value is 5; for enzyme search
24
25 #
26 # Up to 9 variable modifications are supported
27 # format: <mass> <residues> <0=variable/1=binary> <max_mods_per_peptide> <term_distance> <n/c-term>
28 # e.g. 79.966331 STY 0 3 -1 0
29 #
30 variable_mod01 = 0.0 X 0 3 -1 0
31 variable_mod02 = 0.0 X 0 3 -1 0
32 variable_mod03 = 0.0 X 0 3 -1 0
33 variable_mod04 = 0.0 X 0 3 -1 0
34 variable_mod05 = 0.0 X 0 3 -1 0
35 variable_mod06 = 0.0 X 0 3 -1 0
36 variable_mod07 = 0.0 X 0 3 -1 0
37 variable_mod08 = 0.0 X 0 3 -1 0
```

# Comet 실행

- Database 선택
  - Add Files 클릭

ISB/SPC Trans Proteomic Pipeline - runcomet

Home | Files | Account | Pre-Process | mzXML Utils | Analysis Pipeline (Comet) | Decoy | Utilities | SpectraST Tools | Jobs You are logged in as guest [Log Out](#)

Home | mzML/mzXML | Database Search | Analyze Peptides | Combine Analyses | Analyze PTMs | Analyze Proteins

Messages [\[ Show / Hide \]](#)

Your files have been added:

**3. Specify a sequence database** [\[ Show / Hide \]](#)

No files selected yet.

[Add Files](#)

**3. Specify a sequence database** [\[ Show / Hide \]](#)

No files selected yet.

[Add Files](#)

**4. Search!** [\[ Show / Hide \]](#)

No files selected yet.

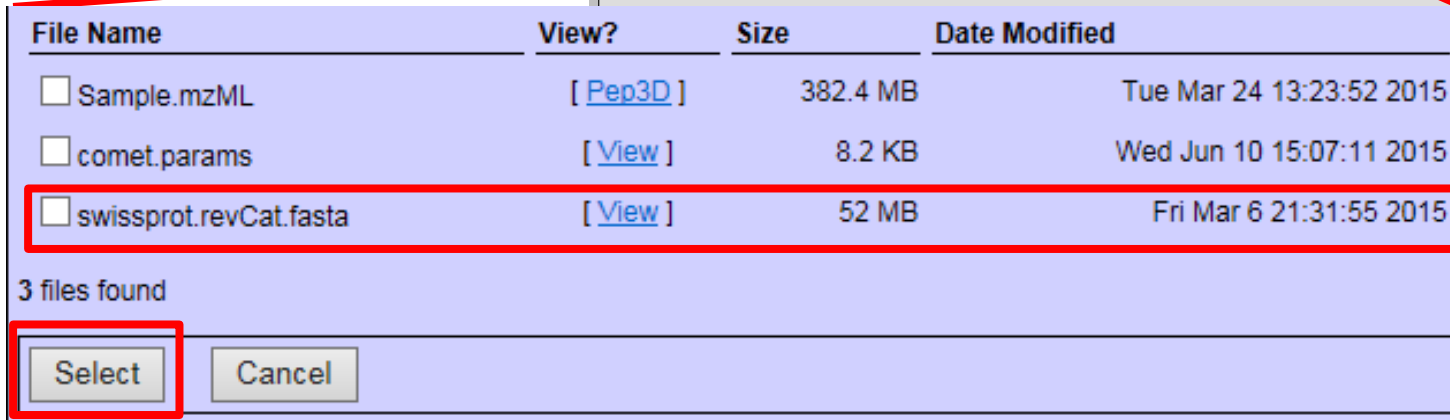
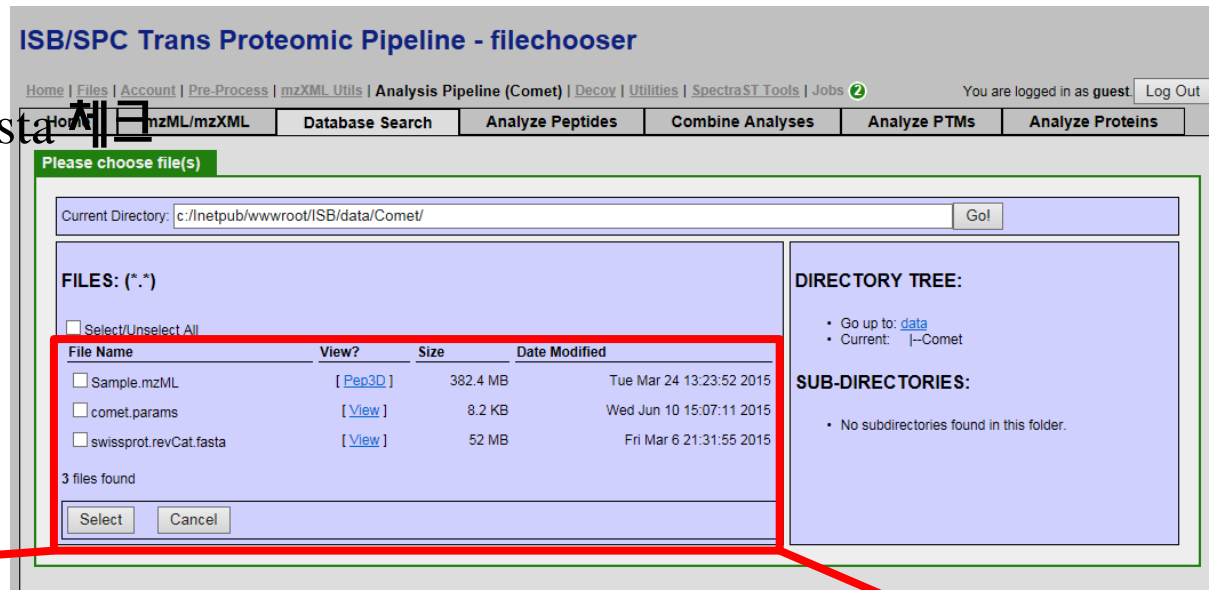
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Proteome  
Center

TPP v4.8.0 PHILAE, Build 201411201551-6764 (mingw-i686)

# Comet 실행

- Database 선택
  - swissprot.revCat.fasta 체크
  - Select 클릭



# Comet 실행

- Comet 실행
  - Run Comet Search 클릭

The screenshot displays the 'ISB/SPC Trans Proteomic Pipeline - runcomet' web interface. A blue header bar at the top contains navigation links: Home, Files, Account, Pre-Process, mzXML Utils, Analysis Pipeline (Comet), Decoy, Utilities, SpectraST Tools, and Jobs. A user status bar indicates 'You are logged in as guest' with a 'Log Out' button. Below the header is a tabbed interface with tabs for Home, mzML/mzXML, Database Search, Analyze Peptides, Combine Analyses, Analyze PTMs, and Analyze Proteins. The 'Database Search' tab is active, showing a 'Messages' section with a notification: 'Your files have been added: swissprot.revCat.fasta'. The main content area lists three files: 'sample.mzML', 'met.params', and 'swissprot.revCat.fasta', each with a 'Remove' button and a '[ Show / Hide ]' link. A red box highlights the 'Run Comet Search' button at the bottom of the interface. A red arrow points from the '4. Search!' section of the slide to this button. The footer contains logos for the Institute for Systems Biology and the Seattle Proteome Center, along with version information: 'TPP v4.8.0 PHILAE, Build 201411201551-6764 (mingw-i686)'.

**4. Search!**

Run Comet Search

ISB/SPC Trans Proteomic Pipeline - runcomet

Home | Files | Account | Pre-Process | mzXML Utils | Analysis Pipeline (Comet) | Decoy | Utilities | SpectraST Tools | Jobs

You are logged in as guest Log Out

Home | mzML/mzXML | Database Search | Analyze Peptides | Combine Analyses | Analyze PTMs | Analyze Proteins

Messages [ Show / Hide ]

- Your files have been added:
- swissprot.revCat.fasta

sample.mzML [ Show / Hide ] Remove

c:/inetpub/wwwroot/ISB/data/Comet/ [ mzxml ]

met.params [ Show / Hide ] Remove

c:/inetpub/wwwroot/ISB/data/Comet/ [ "params" ]

swissprot.revCat.fasta [ Show / Hide ] Remove

Add Files

4. Search!

Run Comet Search

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# Comet 실행

- Comet 실행 중
  - running → finished
  - Refresh 클릭

ISB/SPC Trans Proteomic Pipeline - jobs

Home | Files | Account | Pre-Process | mzXML Utils | Analysis Pipeline (Comet) | Decor | Utilities | SpectraST Tools | Jobs

You are logged in as guest [Log Out](#)

**Home** **Jobs**

**Commands Status** [ Show / Hide ]

Status as of: Wed Jun 10 17:40:24 2015

**All Jobs** [ Show / Hide ]

Session ID	Job	Location	Start date / time	Actions	Status	Output
QPZW0ZA9A	runcomet	localhost	2015-06-10 17:40:23	<a href="#">Kill job</a>	running	<a href="#">Refresh</a>

Output for job id QPZW0ZA9A\_20150610-174023

Command 1 [Wed Jun 10 17:40:23 2015] [ Show / Hide ]

Session ID	Job	Location	Start date / time	Actions	Status	Output
QPZW0ZA9A	runcomet	localhost	2015-06-10 17:40:23	<a href="#">Kill job</a>	running	<a href="#">Refresh</a>

Session ID	Job	Location	Start date / time	Actions	Status	Output
QPZW0ZA9A	runcomet	localhost	2015-06-10 17:40:23	<a href="#">Kill job</a>	* finished	<a href="#">Refresh</a>

# Comet 실행

- Comet 실행 완료
  - Comet version
  - Spectrum 개수
  - 시작시간 및 종료시간

ISB/SPC Trans Proteomic Pipeline - jobs

Home | Files | Account | Pre-Process | mzXML Utils | Analysis Pipeline (Comet) | Decoy | Utilities | SpectraST Tools | Jobs You are logged in as guest Log Out

Home Jobs

Commands Status [ Show / Hide ]

Status as of: Wed Jun 10 17:45:43 2015  
Output from all commands has been viewed; auto-refresh is now OFF.

All Jobs [ Show / Hide ]

Session ID	Job	Location	Start date / time	Actions	Status	Output
QPZW0ZA9A	runcomet	localhost	2015-06-10 17:40:23	<a href="#">Delete Log</a>	viewed	<a href="#">Refresh</a>

Output for job id QPZW0ZA9A\_20150610-174023

Output Files

- c:/inetpub/wwwroot/ISB/data/Comet/Sample.pep.xml [PeoXML](#)

Command 1 [Wed Jun 10 17:40:23 2015] [ Show / Hide ]

```
EXECUTING: cd c:/inetpub/wwwroot/ISB/data/Comet& c:/inetpub/tpp-bin/comet -Pc:/inetpub/wwwroot/ISB/data/Comet/comet.params  
-Nc:/inetpub/wwwroot/ISB/data/Comet/Sample -Dc:/inetpub/wwwroot/ISB/data/Comet/swissprot.revCat.fasta Sample.mzML  
  
Comet version "2014.02 rev. 2"  
Search start: 06/10/2015, 05:40:23 PM  
- Input file: Sample.mzML  
- Load and process input spectra  
- Number of mass-charge spectra loaded: 33223  
- Search progress: 0% 0% 0% 1% 1% 1% 2% 2% 2% 2% 3% 3% 3% 4% 4% 4% 4% 5% 5% 5% 6% 6% 6% 6% 6% 6% 7% 7% 7% 8% 8%  
- Perform post-search analysis  
- Write output  
Search end: 06/10/2015, 05:43:34 PM  
  
Command Successful  
RETURN CODE:0
```

All commands finished at Wed Jun 10 17:43:34 2015

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# Comet 실행

**Command 1 [Wed Jun 10 17:40:23 2015]**

[ Show / Hide ]

```
EXECUTING: cd c:/inetpub/wwwroot/ISB/data/Comet& c:/inetpub  
-Nc:/inetpub/wwwroot/ISB/data/Comet/Sample -Dc:/inetpub/www
```

Comet version "2014.02 rev. 2"

Search start: 06/10/2015, 05:40:23 PM

- ```
- Input file: Sample.mzML
- Load and process input spectra
- Number of mass-charge spectra loaded: 33223
- Search progress: 0% 0% 0% 0% 1% 1% 1% 2% 2%
- Perform post-search analysis
- Write output
```

Search end: 06/10/2015, 05:43:34 PM



Command Successful

RETURN CODE:0

**All commands finished at Wed Jun 10 17:43:34 2015**



- Comet 결과 확인
  - 결과 파일 sample.pep.xml
  - PepXML 클릭

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# Comet 실행

- Comet 결과 확인

SummaryDisplay OptionsPick ColumnsFiltering OptionsOther Actions[ Hide options ]

Sorting: spectrumdescascpepXML file: c:/inetpub/wwwroot/ISB/data/Comet/Sample.pep.xml

Trypsin digest, COMET search engine, quantitation: [none]  
displaying 33223 of 33223 total spectra, page 1 of 665  
25764 unique peptides, 25764 unique stripped peptides, 17751 unique proteins, 10856 single hits  
PepXML Viewer, 2006 SPC188

Update Page

Page 1 of 665

1FIRST1234561151101251501NEXTLAST

| SPECTRUM                                          | SSCAN | XCORR         | DELTAQN       | EXPECT        | IONS2                      | PEPTIDE                           | PROTEIN                                    | CALC_MASS     |
|---------------------------------------------------|-------|---------------|---------------|---------------|----------------------------|-----------------------------------|--------------------------------------------|---------------|
| <a href="#">Sample.00002.00002.3<sup>St</sup></a> | 2     | 0.508         | 0.085         | 1.41E+001     | <a href="#">4/36</a>       | R.LNPINTLLK.M <sup>BA</sup>       | <a href="#">spIQ9UGV2-2INDRG3_HUMAN</a>    | 1125.675760   |
| <a href="#">Sample.00003.00003.3<sup>St</sup></a> | 3     | 1.488         | 0.189         | 3.24E-002     | <a href="#">8/32</a>       | K.FSEPLQVER.C <sup>BA</sup>       | <a href="#">spIQ5K651 SAMD9_HUMAN</a>      | 1103.561124   |
| <a href="#">Sample.00004.00004.3<sup>St</sup></a> | 4     | 0.375         | 0.064         | 1.96E+001     | <a href="#">4/32</a>       | K.LPNILC160.0sHYK.I <sup>BA</sup> | <a href="#">spIQ8N957 ANKF1_HUMAN</a>      | 1092.611385   |
| <a href="#">Sample.00005.00005.3<sup>St</sup></a> | 5     | [unavailable] | [unavailable] | [unavailable] | <a href="#">[spectrum]</a> | .. <sup>BA</sup>                  |                                            | [unavailable] |
| <a href="#">Sample.00006.00006.2<sup>St</sup></a> | 6     | [unavailable] | [unavailable] | [unavailable] | <a href="#">[spectrum]</a> | .. <sup>BA</sup>                  |                                            | [unavailable] |
| <a href="#">Sample.00007.00007.2<sup>St</sup></a> | 7     | 0.889         | 0.093         | 1.00E+000     | <a href="#">5/14</a>       | R.GGQLHEPR.Y <sup>BA</sup>        | <a href="#">XXX_spIQ8TBE0 BAHD1_HUMAN</a>  | 892.451514    |
| <a href="#">Sample.00008.00008.3<sup>St</sup></a> | 8     | 0.889         | 0.303         | 1.00E+000     | <a href="#">5/44</a>       | R.YSSQYTVASELR.H <sup>BA</sup>    | <a href="#">spIQ5T6L9 CF070_HUMAN</a>      | 1274.683030   |
| <a href="#">Sample.00009.00009.3<sup>St</sup></a> | 9     | 0.372         | 0.023         | 2.82E+001     | <a href="#">3/28</a>       | R.EADLLHK.K <sup>BA</sup>         | <a href="#">XXX_spIQ8N323 INXPE1_HUMAN</a> | 937.523282    |
| <a href="#">Sample.00010.00010.2<sup>St</sup></a> | 10    | 0.485         | 0.011         | 1.00E+000     | <a href="#">4/16</a>       | R.YMPGASHGR.E <sup>BA</sup>       | <a href="#">XXX_spIQ9NRC6 SPTN5_HUMAN</a>  | 910.444320    |
| <a href="#">Sample.00011.00011.4<sup>St</sup></a> | 11    | 0.963         | 0.024         | 1.00E+000     | <a href="#">9/66</a>       | R.HVPPWALGPPGR.L <sup>BA</sup>    | <a href="#">XXX_spIA8MTA8 F166B_HUMAN</a>  | 1282.693475   |
| <a href="#">Sample.00013.00013.3<sup>St</sup></a> | 13    | 0.549         | 0.089         | 2.01E+000     | <a href="#">5/36</a>       | R.LSGEPEPTT.- <sup>BA</sup>       | <a href="#">spIP09293 JUL16_VZVD</a>       | 1030.481870   |

# Comet 결과 확인

---

- Text 결과 파일

# Comet 결과 확인

- Spectrum sequence match 확인

