

# pNovo 3 User Guide

pFind Group

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# Before software installation

## ❖ **Windows 7 or above**

- **64 bit version**
- **.Net Framework 4.5 environment or above**

# pNovo 3 Introduction

- ❖ **The kernel in pNovo 3 is written with C++**
- ❖ **The interface in pNovo 3 is written with C# / WPF**
- ❖ **pNovo 3 cannot run on Linux and Mac systems**

# How to register

- ❖ Please visit the website to fill in the registered table:  
<http://pfind.ict.ac.cn/software/pNovo/index.html>
- ❖ Please email the table to [pnovo@ict.ac.cn](mailto:pnovo@ict.ac.cn) to get the registered code

* First name	
* Last name	
* University/Company	
* Department	
* Lab leader/Supervisor:	
* Work email address	
* Country	
City / ZIP	
Phone	
* How do you hear about pNovo?	
* What can pNovo do for you?	

Notice:

1. The item with the "\*" **must be** filled.
2. **For Chinese, please fill in the table with Chinese.** Thanks.
3. Please email this table to [pnovo@ict.ac.cn](mailto:pnovo@ict.ac.cn) to get the registered code.
4. **Please let us know if you use pNovo in your publication.**

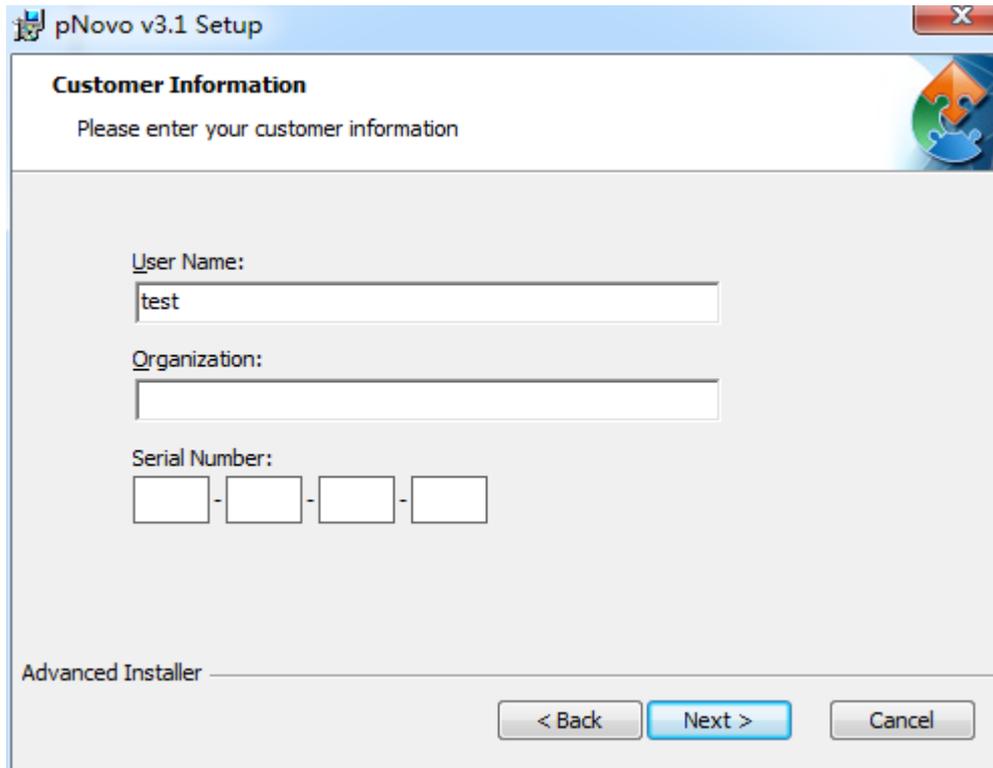
# How to install

❖ Double click the “EXE” setup file:



# How to install

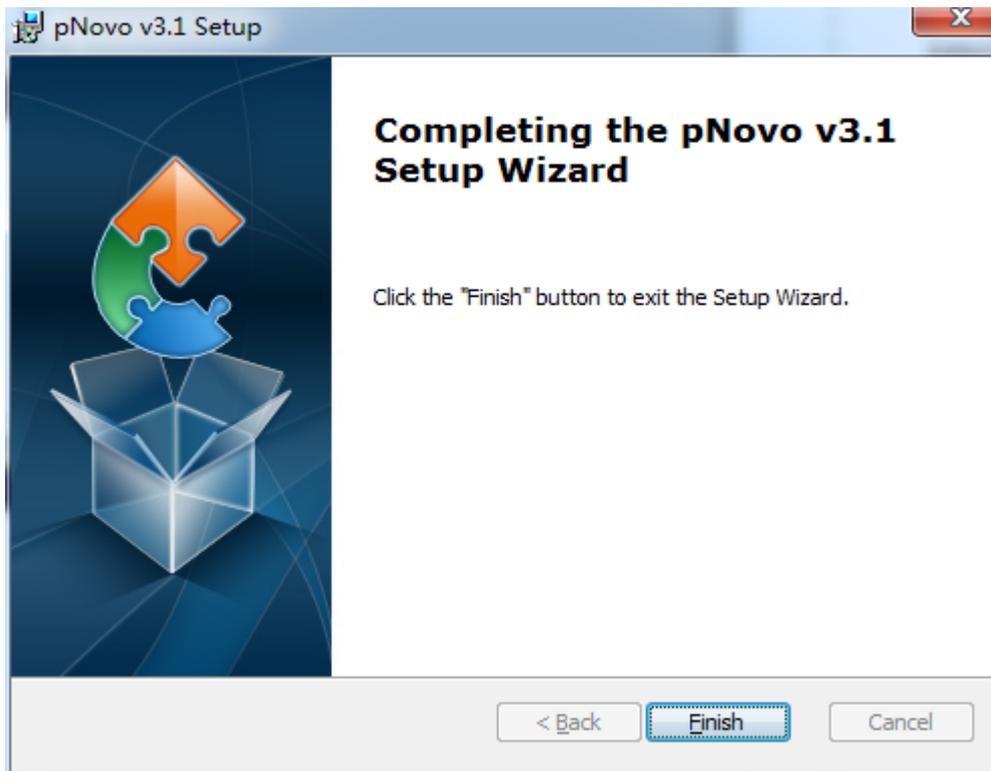
- ❖ You should input the registered code in the installation process:



The screenshot shows a Windows-style dialog box titled "pNovo v3.1 Setup". The main heading is "Customer Information" with a sub-instruction "Please enter your customer information". There are three input fields: "User Name:" containing "test", "Organization:" which is empty, and "Serial Number:" which consists of four empty boxes separated by hyphens. At the bottom, there are three buttons: "< Back", "Next >" (highlighted in blue), and "Cancel". The text "Advanced Installer" is visible in the bottom left corner of the dialog.

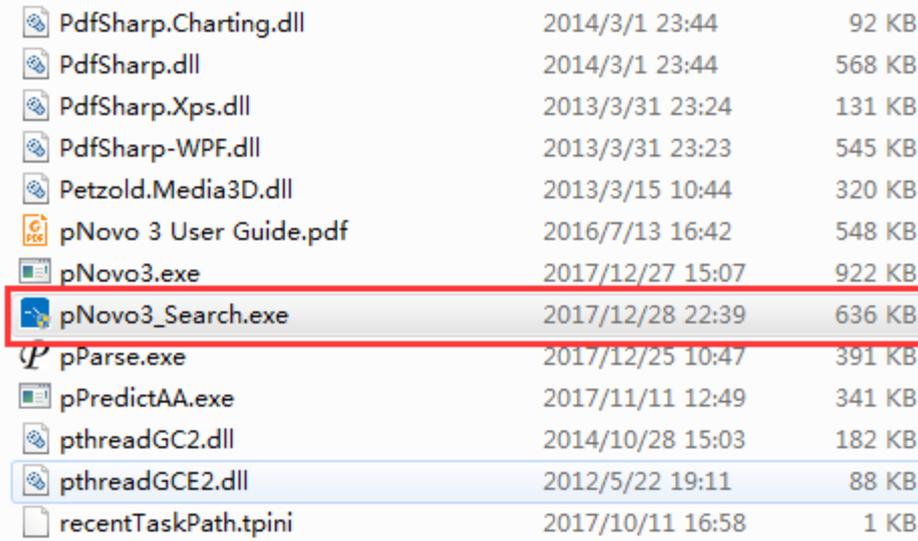
# How to install

- ❖ You can always input “Next” step in each process, pNovo will be successfully installed:



# How to run pNovo 3

- ❖ pNovo 3 is successfully installed in your computer, the default installation directory is “C:\Program Files\ict\pNovo v3.1\”
- ❖ You can double click “pNovo3\_Search.exe” file in the installation directory to start pNovo 3:



 PdfSharp.Charting.dll	2014/3/1 23:44	92 KB
 PdfSharp.dll	2014/3/1 23:44	568 KB
 PdfSharp.Xps.dll	2013/3/31 23:24	131 KB
 PdfSharp-WPF.dll	2013/3/31 23:23	545 KB
 Petzold.Media3D.dll	2013/3/15 10:44	320 KB
 pNovo 3 User Guide.pdf	2016/7/13 16:42	548 KB
 pNovo3.exe	2017/12/27 15:07	922 KB
 pNovo3_Search.exe	2017/12/28 22:39	636 KB
 pParse.exe	2017/12/25 10:47	391 KB
 pPredictAA.exe	2017/11/11 12:49	341 KB
 pthreadGC2.dll	2014/10/28 15:03	182 KB
 pthreadGCE2.dll	2012/5/22 19:11	88 KB
 recentTaskPath.tpini	2017/10/11 16:58	1 KB

❖ **Search Parameters**

❖ **Displaying Results**

# Search Parameters

The screenshot shows the pNovo software interface with the following sections highlighted by red boxes and numbered labels:

- 1. General parameters:** A box at the top containing dropdown menus for MS Data Format (MGF), MS Instrument (HCD), Enzyme (Trypsin KR C), and Thread Number (1).
- 2. Data input:** A box containing a table with columns 'Files' and 'Size', and buttons for 'Add', 'Delete', and 'Clear'.
- 3. Precursor/Fragment tolerance:** A box containing input fields for Precursor Tolerance (± 20 ppm) and Fragment Tolerance (± 20 ppm).
- 4. Modifications:** A box containing 'Add Modification' options, including 'Fixed' and 'Variable' lists, a list of modification types (e.g., Acetyl, Amidated, Biotin), and an 'Edit...' button.
- 5. Output path:** A box containing 'Open Search' (false), 'Keep' (Top-10), 'Results', and a 'File Output:' text field with a 'Select' button.
- 6. Start/Stop search:** A box containing 'Search' and 'Stop' buttons.
- 7. Report progress:** A box containing an 'Output' section with a 'Save Report' button.

# Search Parameters

- ❖ MS Data Format
- ❖ MS Instrument
- ❖ Enzyme
- ❖ Thread Number
- ❖ Data File List
- ❖ Precursor Tolerance/Fragment Tolerance
- ❖ Fixed Modification/Variable Modification
- ❖ Open Search
- ❖ Keep Top-1/Top-10 Results
- ❖ File Output

# Fundamental Parameter

- ❖ MS Data Format: MGF/DTA/MS2
- ❖ MS Instrument: HCD/ETD/CID
- ❖ Enzyme: Trypsin/AspN/ArgC/GluC...
- ❖ Thread Number: 1/2/.../8

MS Data Format:	MGF	MS Instrument:	HCD
Enzyme:	Trypsin KR C	Thread Number:	1

- ❖ pNovo can support all enzymes in “enzyme.ini” file, you can modify this file to support your individual enzyme.

# Data File List

- ❖ You can add all data files by clicking “Add” button.
- ❖ You can delete some data files by clicking “Delete” button.
- ❖ Also, you can delete all data files by clicking “Clear” button.



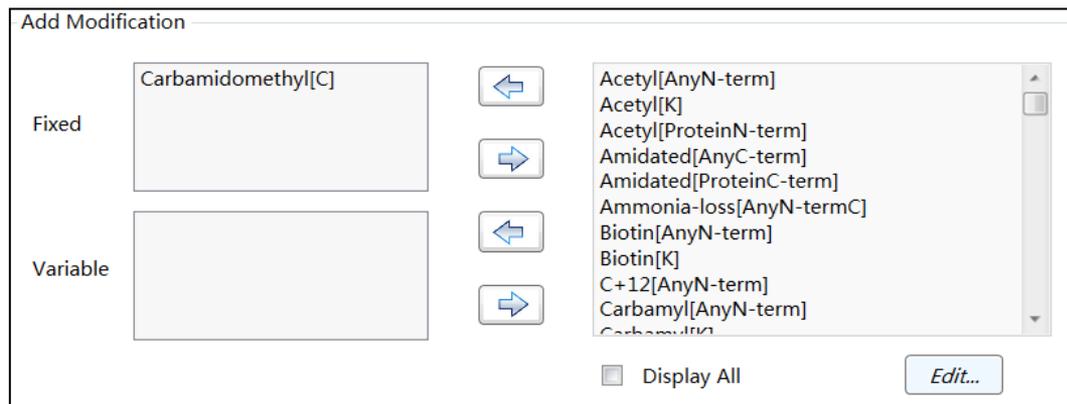
# Precursor/Fragment Tolerance

- ❖ You can set the precursor tolerance and fragment tolerance in “Da” or “ppm” format.

Precursor Tolerance	±	<input type="text" value="20"/>	ppm ▾	Fragment Tolerance	±	<input type="text" value="20"/>	ppm ▾
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# Fixed/Variable Modification

- ❖ You can add some modifications as fixed modification or variable modification by clicking “” button.
- ❖ You can delete some fixed modification or variable modification by clicking “” button.
- ❖ Also, you can see all modifications in Unimod by clicking “Display All” checkbox while pNovo defaultly displays common modifications.
- ❖ Finally, you can modify all modifications in Unimod in “modification.ini” file.



# Open Search

- ❖ pNovo has a very important function of searching “unexpected” modification.
- ❖ You can only add “Carbamidomethyl[C]” as fixed modification and few modifications as variable modifications, and set the “Open Search” as “true”, then pNovo will automatically find credible “unexpected” modifications in Unimod.

# Keep Top-1/Top-10 Results

- ❖ pNovo can support the very fast searching by keeping only Top-1 result when you set “Keep Top-1 Result”.
- ❖ pNovo defaultly set “Keep Top-10 Results” because the results will be much more credible although the speed is slow.

# File Output

- ❖ You can select a path as the output path and you should insure that the selected path is existing.
- ❖ pNovo will create two folders (“param” and “result” folder) in the selected path. The param folder has only one file named “pNovo.param” which contains all searching parameters while the result folder has two files, one file is “pNovo.res” which contains all searching result and the other file is “time.txt” which displays the searching time.
- ❖ Finally, you can click “Search” button to start searching!!!

File Output:	<input type="text"/>	Select
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❖ **Search Parameters**

❖ **Displaying Results**

# Displaying Results

❖ **Result File Format**

❖ **Peptide List**

❖ **Peptide-Spectrum-Matching Graph**

# Displaying Results

- ❖ pNovo will create a folder named “result”, which restores all result files.
- ❖ This folder contains three main result files:
  - “results.res” records the top-one PSM per spectrum
  - “pNovo.res” records the top-ten PSMs per spectrum
  - “time.txt” records the searching time in this searching task

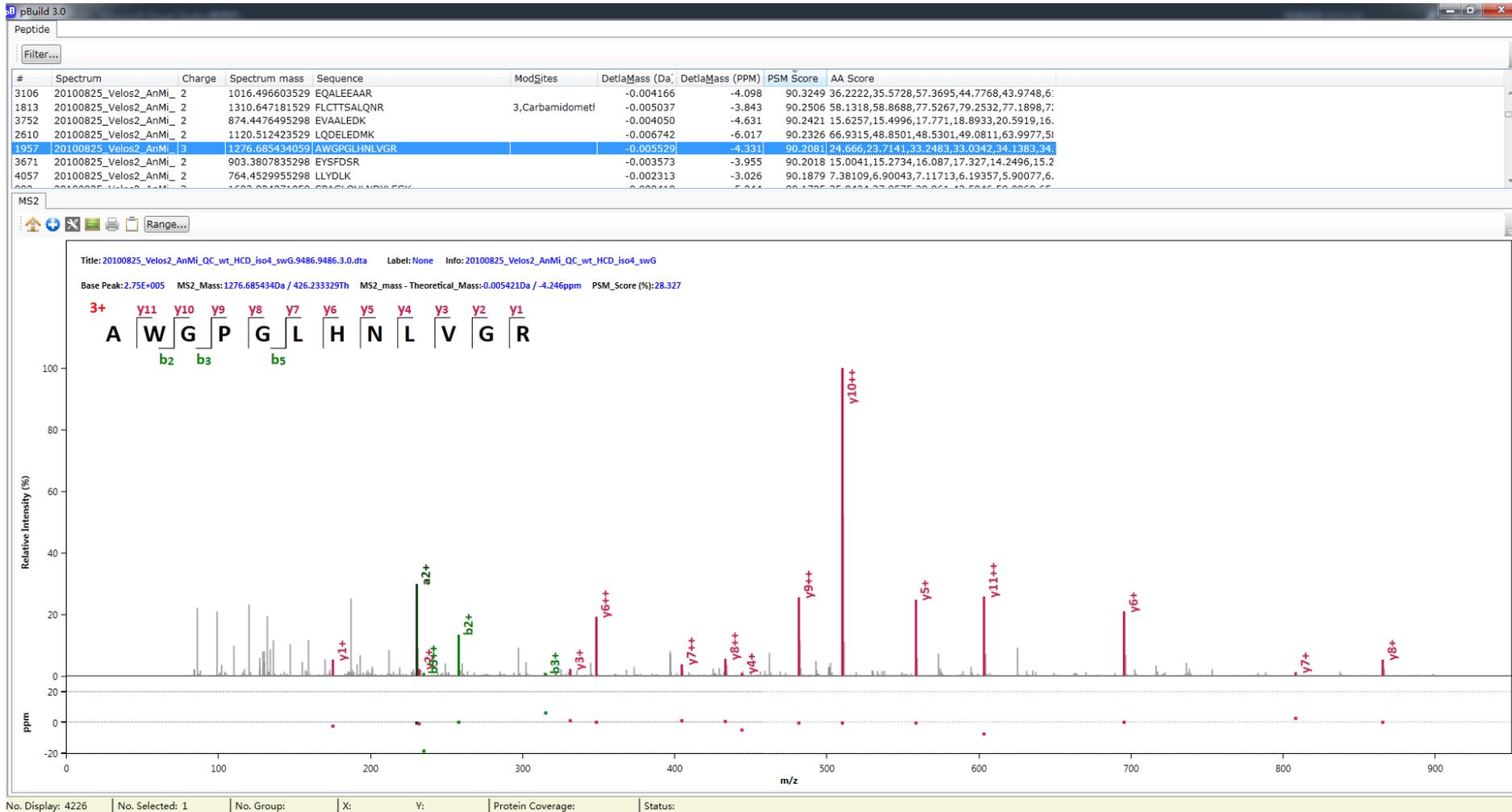
# Displaying Results

- ❖ The format of “results.res” file
- ❖ Each row contains one PSM for each spectrum and it has 9 columns, the following will introduce these columns:
  - **Spectrum title**
  - **Sequence**
  - **Modifications**
  - Average score of all amino acids in this sequence
  - **Final score of this sequence**
  - All scores of amino acids (using “,” to split)
  - The best sequence in background candidates
  - Modifications of this best sequence
  - Precursor mass deviation of the original sequence

# Displaying Results

- ❖ The format of “pNovo.res” file, the line starts with “S” records the spectrum title:
- ❖ The line starts with “P” records top-ten PSMs of this spectrum (from the first column to last column):
  - “P1” to “P10” means the first 1 to 10 candidate result
  - **Sequence**
  - **Final score of this result**
  - Modification abundance (if result doesn't contain modification, it is 1.0)
  - Precursor mass deviation
  - Path rank in the spectrum graph
  - Score of main ions
  - Score of internal ions
  - Continuity score of b ions
  - Continuity score of y ions
  - Enzyme score
  - Std. fragment mass deviations
  - Max. fragment mass deviations
  - Charge feature
  - Raw score of peptide-spectrum matching
  - Spearman correlation between the real and theoretical ion intensities
  - Gap feature
  - Gap feature for N-terminal sequence

# Displaying Results



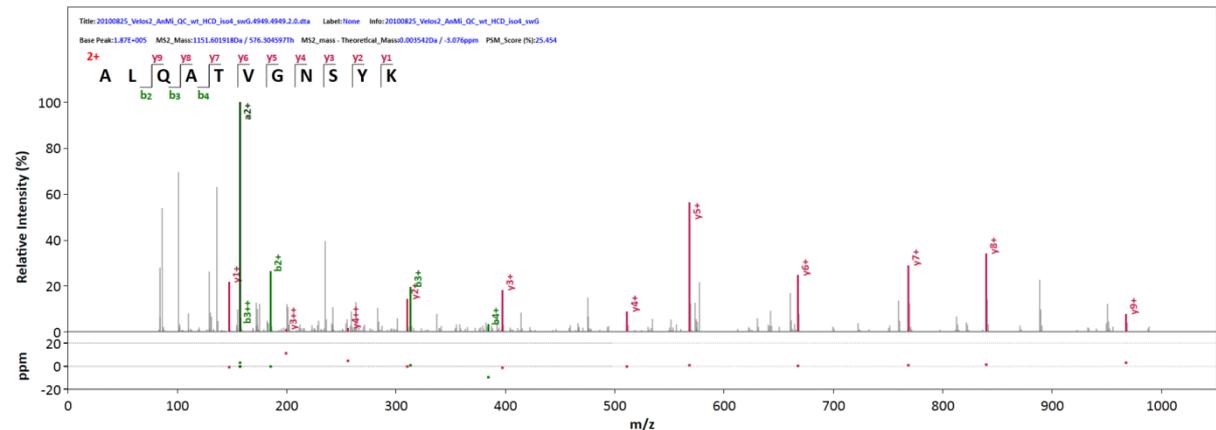
# Peptide List

❖ pNovo will display all searching results which contain the title and charge of spectrum, the sequence and modifications of peptide.

#	Spectrum	Charge	Spectrum mass	Sequence	ModSites	DeltaMass (Da)	DeltaMass (PPM)	PSM Score	AA Score
3106	20100825_Velos2_AnMi_2	2	1016.496603529	EQALEEAAR		-0.004166	-4.098	90.3249 36.2222,35.5728,57.3695,44.7768,43.9748,61.9872,58.2665,53.68,58.5509	
1813	20100825_Velos2_AnMi_2	2	1310.647181529	FLCTTSALQNR	3,Carbamidometi	-0.005037	-3.843	90.2506 58.1318,58.8688,77.5267,79.2532,77.1898,72.9922,68.6975,73.4063,65.1435,53.3508,64.5376	
3752	20100825_Velos2_AnMi_2	2	874.4476495298	EVAALDEK		-0.004050	-4.631	90.2421 15.6257,15.4996,17.771,18.8933,20.5919,16.9963,16.1662,17.4287	
2610	20100825_Velos2_AnMi_2	2	1120.512423529	LQDELEDMK		-0.006742	-6.017	90.2326 66.9315,48.8501,48.5301,49.0811,63.9977,58.7425,58.0835,65.027,65.7872	
1957	20100825_Velos2_AnMi_3	3	1276.685434059	AWGPGLHNLVGR		-0.005529	-4.331	90.2081 24.666,23.7141,33.2483,33.0342,34.1383,34.0924,28.3314,23.466,23.1274,16.7401,17.3826,20.221	
3671	20100825_Velos2_AnMi_2	2	903.3807835298	EYSFDSR		-0.003573	-3.955	90.2018 15.0041,15.2734,16.087,17.327,14.2496,15.2974,15.0217	
4057	20100825_Velos2_AnMi_2	2	764.4529955298	LLYDLK		-0.002313	-3.026	90.1879 7.38109,6.90043,7.11713,6.19357,5.90077,6.10736	
992	20100825_Velos2_AnMi_3	3	1603.824271059	SPAGQLVINDYLEGK		-0.008410	-5.244	90.1725 35.8434,37.9575,39.961,43.5846,59.0969,65.3083,68.2589,68.7975,60.4357,59.0147,55.2496,44.8304	
3547	20100825_Velos2_AnMi_2	2	933.5056075298	MVLNLESK		-0.001800	-1.929	90.1372 25.554,24.5401,30.0771,24.5792,25.1699,17.8601,17.6659,24.8212	
1355	20100825_Velos2_AnMi_3	3	1441.651141059	PNMVTPGHACTEK	10,Carbamidome	-0.005162	-3.581	90.101 86.4819,76.0616,94.0065,95.0569,95.1556,92.1839,91.9984,87.0515,79.5969,67.6415,65.132,73.1309	
2901	20100825_Velos2_AnMi_2	2	1055.542857529	TPGGAESALR		-0.005207	-4.933	90.1006 67.4762,68.8808,83.1992,80.1005,46.4961,45.0688,68.3379,59.4903,56.6764,60.9396,63.3482	
2321	20100825_Velos2_AnMi_3	3	1191.593539059	HMYHSLYLK		-0.004453	-3.737	89.9754 73.2959,70.5134,64.4153,92.3771,96.2282,95.2941,88.8753,91.5386,91.9403	
2897	20100825_Velos2_AnMi_2	2	1057.620351529	LLLLGAGESGK		-0.004888	-4.621	89.9011 69.2428,69.1773,87.2617,81.5448,59.8472,55.9012,58.9159,70.6328,65.3996,66.1602,71.5286	
3927	20100825_Velos2_AnMi_2	2	818.4399555298	VPMTSGVK		-0.004183	-5.111	89.9 37.2744,35.4711,33.915,27.5262,21.2455,19.9556,20.8822,26.7701	
552	20100825_Velos2_AnMi_3	3	1880.976307059	LPQFGLSTPGSDLHVNK		-0.010248	-5.448	89.8246 40.5997,38.9631,42.3.59.0855,33.0017,32.0896,42.4111,60.0389,61.8855,62.3444,56.5164,50.5773,51.	
4145	20100825_Velos2_AnMi_2	2	705.3912015298	LGFSGPK		-0.001829	-2.593	89.7968 29.1624,26.8303,25.4813,30.9401,21.7269,22.5209,27.4492	
2431	20100825_Velos2_AnMi_3	3	1167.663421059	VRHPVSTMLK		-0.003294	-2.821	89.7835 61.5504,65.2982,76.1123,92.7921,91.5943,95.2533,92.486,90.3942,85.2538,85.1227	
1746	20100825_Velos2_AnMi_3	3	1328.687410059	AENPGAAVTRNK		-0.004333	-3.261	89.7615 10.8554,10.5064,10.3276,10.168,9.63623,9.15852,10.6045,12.735,12.7474,10.2398,9.62697,9.38333,5	
3206	20100825_Velos2_AnMi_2	2	993.5682115298	PFTLLSLK		-0.006815	-6.859	89.754 18.3093,17.8236,18.0097,19.3485,18.5556,21.0713,17.7632,17.0673,19.2455	
1691	20100825_Velos2_AnMi_3	3	1345.741591059	TFLALPKDQANK		-0.005893	-4.379	89.7037 56.3161,58.3302,71.2653,71.1724,78.7773,75.9969,68.1076,57.5868,50.47.9475,51.8158,59.3173	
1257	20100825_Velos2_AnMi_2	2	1480.697305529	LLELSGSSSEDESK		-0.004048	-2.734	89.6978 33.9376,31.2725,30.4049,36.0227,34.5867,39.2929,38.8935,39.6679,33.8411,32.7827,32.0168,25.417	
3512	20100825_Velos2_AnMi_2	2	941.5012695298	PTHVNFAR		-0.006234	-6.622	89.6958 15.4567,15.0841,13.4981,14.6773,14.0355,12.1411,11.1929,13.0804	
1359	20100825_Velos2_AnMi_3	3	1440.665335059	PNMVTPGHACTQK	10,Carbamidome	-0.006982	-4.847	89.6765 65.8393,56.3734,65.9723,81.8404,81.458,40.6467,42.5657,64.6207,47.1105,48.3662,47.9475,50.5922	
2444	20100825_Velos2_AnMi_2	2	1166.599515529	AASLTSEVFNK		-0.005739	-4.920	89.6336 62.1528,62.6405,62.3087,73.7978,88.2065,82.0782,82.2277,81.6553,85.418,66.1265,79.7612	
1411	20100825_Velos2_AnMi_2	2	1422.660317529	NQSFCTVNLDK	5,Carbamidometi	-0.007974	-5.605	89.6019 44.8672,46.0375,70.1314,79.5725,82.0747,74.6659,72.8987,77.0922,72.0504,66.6574,65.805,75.387	
2914	20100825_Velos2_AnMi_3	3	1052.548654059	YRNFDLPK		-0.003755	-3.567	89.5013 19.3465,19.9846,21.5535,19.9825,20.9617,19.731,19.7834,18.9739	
2949	20100825_Velos2_AnMi_2	2	1046.543949529	VLDLTLNR		-0.003770	-3.602	89.4615 65.645,67.7372,75.9581,50.5008,71.9966,66.3088,65.2581,68.1723	

# Peptide-Spectrum-Matching Graph

- ❖ pNovo will display the peptide-spectrum-matching graph.
- ❖ You can hold down the mouse button to zoom in the graph while you can also scroll the mouse button to zoom in or zoom out.
- ❖ You can also input “Ctrl+C” to copy the graph to clipboard and “Ctrl+V” to paste the graph to word or PPT.
- ❖ Finally, there are other useful functions in pNovo. You can try it by yourself and we will wish you to have a good time.





❖ **Thank you for using pNovo 3 software!**

❖ **If you have any questions, please contact**  
**[pnovo@ict.ac.cn](mailto:pnovo@ict.ac.cn)**.