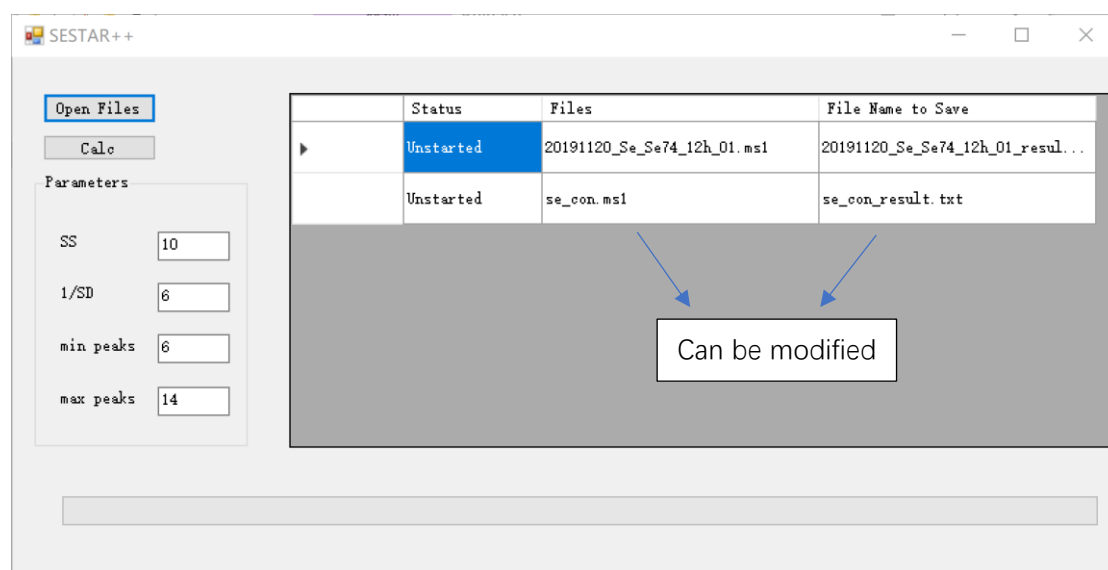How to get results:

1. Open SESTAR_GUI.exe
2. Click "Open Files" button, and select *.ms1 file(s) to be processed.
3. Rows can be deleted if wrong files are selected. File name to open/save can be modified in the sheet (Make sure the file name is available).
4. Set appropriate parameters. Recommended parameters are shown below. Of course, you can set your own parameters within the limits.

	Limit	Loose	Strict
SS	>0 (decimal)	15	10
1/SD	>=0 (decimal)	4	6
Min peaks	>0 (integer)	5	6
Max peaks	<=14 (integer)	14	14

5. Click "Calc" and be patient. ;-)

How to interpret results:
1. Open the result file (Excel is recommended). Every row represents a potential candidate and sorted by the scan number. Candidates with lower "SS.Se" and higher "SD.Se" are more likely containing selenium. More specifically, "SS.Se" discribes the similarity between observed envelope and theoretical envelope with selenium, while "SD.Se" represents the uniqueness of the similarity to only the selenium-containing envelope but not the proteogenic counterpart.

#	retention.t	charge	mass	mz.max	mz	intensity	calc.se.dist	SS.Se	SD.Se	scan.No
2	11.24251	3	1314.585	439.2022	438.5335; ʹ	35258.1; 1ε	0.1546033;	4.590526	10.55418	2079
3	12.16925	3	1318.637	440.5528	439.8796; ʹ	10833.6; 4ε	0.1543758;	7.620584	6.830223	2247
4	12.28828	3	1176.567	393.1962	392.1923; ʹ	5322.5; 12	0.0709472	9.335705	7.006888	2268
5	12.29907	2	1193.579	597.7969	596.2889; ʹ	27757.6; 4ε	0.0706470ʹ	7.674311	8.515975	2270
6	12.34555	2	1193.579	597.7969	596.2895; ʹ	26725.7; 4ε	0.0706470ʹ	7.228959	8.463049	2278
7	12.35095	2	1193.577	597.7959	596.2897; ʹ	23733; 415	0.0706470ʹ	7.46265	8.49293	2279
8	12.39205	2	1028.452	515.2335	513.23; 51ʹ	12927.7; 8ε	0.0551555ʹ	9.616364	8.140587	2286
9	12.83844	2	1309.533	655.774	654.275; 6ε	12056.2; 3ʹ	0.0692453ʹ	5.140306	11.72349	2366
10	12.93456	3	1549.612	517.5445	516.5476; ε	7134.9; 134	0.0658811ʹ	9.956669	6.742762	2383
11	12.93456	3	1352.593	451.8717	450.8684; ʹ	7795.4; 10ε	0.0685342ε	8.257457	6.838684	2383
12	12.98619	2	1309.534	655.7745	654.2745; ε	14701.9; 3ʹ	0.0692453ʹ	8.957527	7.277471	2392
13	12.99698	2	1309.532	655.7734	654.2723; ε	7525.2; 38ʹ	0.0692453ʹ	9.275255	6.951735	2394
14	13.0433	2	1309.534	655.7744	654.275; 6ε	9131.9; 35ε	0.0692453ʹ	7.206026	9.068492	2402
15	13.0487	2	1309.534	655.7743	654.2738; ε	14040.4; 2ʹ	0.0692453ʹ	6.532532	10.09055	2403
16	13.0541	2	1309.534	655.7744	654.7759; ε	30803.8; 1ʹ	0.1546033;	6.29019	8.860815	2404
17	13.10034	2	970.4252	486.2199	484.7144; ʹ	7389.9; 174	0.0733561ʹ	7.265663	8.783823	2412
18	13.11113	2	1309.534	655.7743	654.7766; ʹ	40996.8; 2ʹ	0.1546033;	7.859925	6.342012	2414
19	13.2139	1	459.2053	460.2126	456.1952; ʹ	20960.6; 6ε	0.0753723ʹ	8.769439	9.026943	2432
20	13.38722	2	1155.494	578.7544	577.2546; ε	8922.9; 15ʹ	0.0713081ε	5.024858	11.95937	2463
21	13.46586	3	1306.606	436.5425	435.5381; ʹ	4402.5; 25ε	0.0692453ʹ	7.627582	8.560473	2477
22	13.47125	2	845.4412	423.7279	422.2202; ʹ	5329.2; 13ε	0.0747626ε	8.176275	8.601869	2478
23	13.57338	2	1121.475	561.7449	560.2337; ε	6811; 2709	0.0717399ʹ	6.180169	10.69635	2496
24	13.60135	3	1306.606	436.5427	435.8746; ʹ	37523.5; 2ε	0.1546033;	5.800836	8.378604	2501

2. Sort all rows by "mass" so that candidates with the same mass will get closer. More candidates with the same mass mean this peptide is continuously observed in a serious of full mass scans, so it's less likely a false positive result. If candidates with different charges but the same mass are observed in the same full mass scan, they are very likely true positive results. You can return to raw data to check if selenium-containing isotopic pattern can be observed.
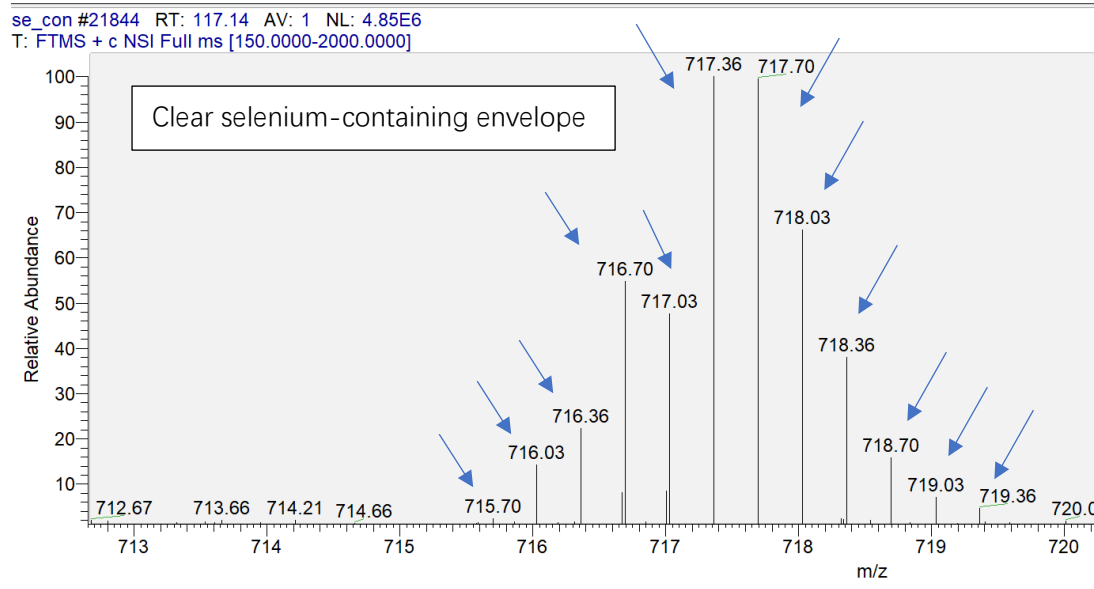
3. Check the MS2 scans of candidates selected from Step 2. If selenium-encoded isotopic patterns are also observed, record them as candidates with very high possibility to be selenium-containing peptides.
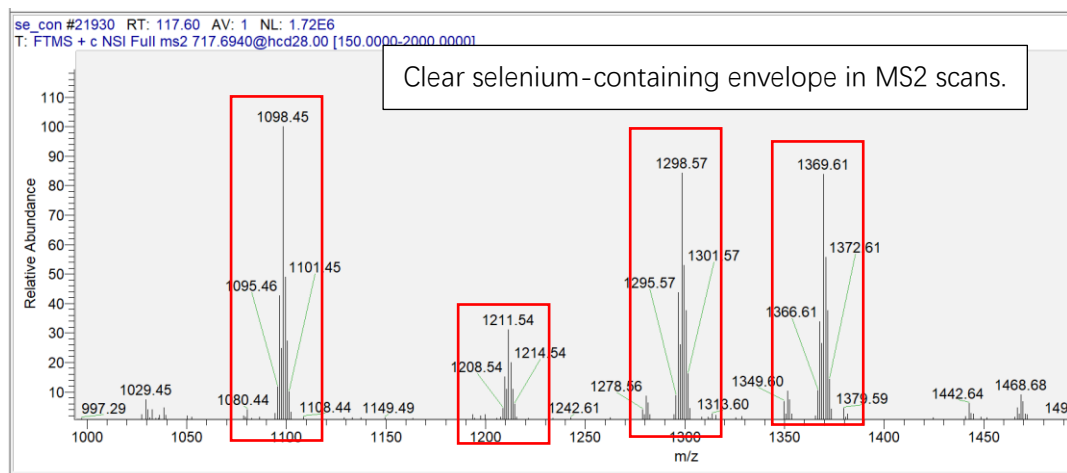
4. Database searching or *de novo* sequencing or other further processing. (The above example is GPX1 according to the database searching results)