

# SmetSearch tutorial

## Objective

This project is to develop the formula 'identification' method by ultrahigh resolution MS instrument (we used FT-ICR). The point of this program is to utilize two type of data; 1) fully labeled (in our case, by 34S) biological samples; and 2) non-labeled samples as the control. The program generates formula candidates by means of non-labeled biological datum in combination with the strict mass tolerance (less than 2 mDa). The 34S labeled datum is used to check the 'metabolite peak shift' derived from its labeled element with respect to the formula candidates. The users can quickly perform the metabolite screenings from living organisms of interest.

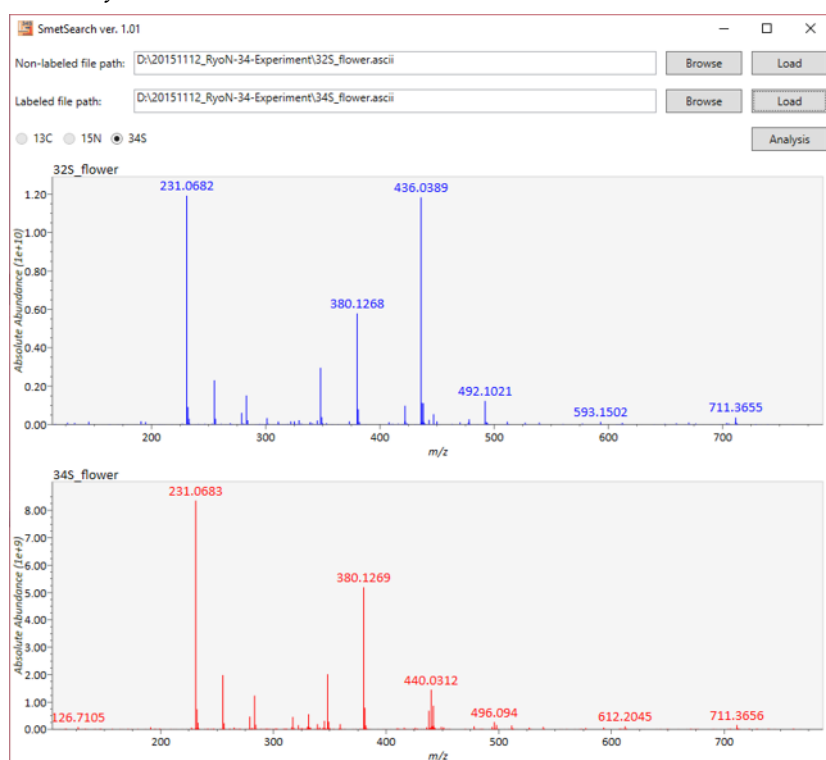
## Limitation:

- 1) The program needs two type 'direct infusion MS' data; 1) a 34S labeled biological datum 2) a non-labeled sample datum.
- 2) The current SmetSearch program accepts the ASCII format file exported from Bruker DataAnalysis software.

Therefore, we produce the source code itself and please let us ([hiroshi.tsugawa@riken.jp](mailto:hiroshi.tsugawa@riken.jp)) know if you are using the different instrument (ex. Orbitrap or QTOF). We can help you as much as possible.

## Main window

Graphical user interface of SmetSearch is simply developed for checking raw infusion MS spectra. The user can import two data, i.e. a labeled datum and a non-labeled datum. The result is generated in the same directory as the above files.



## Quick tutorial of the SmetSearch program

1. Select a file of non-labeled datum from 'Browse'. From 'Load', you can see raw MS spectra.
2. Select a file of labeled datum from 'Browse'. From 'Load', you can see raw MS spectra.
3. Click 'Analysis'.
4. The output will be generated in the same directory as the above files.

## Result

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
	Rank 1	Identification level	Formula	Mass error	Total score	Mass score	Isotopic score	Database score	Database	Non labeled	Non labeled	labeled ma	labeled inter	Rank 2	Identification	Formula	Mass error 1
1																	
2	1	1	1 C10H16SO4	0.0008935	2.468	0.905	0.986	0.576923	ChEBI,UNF	231.0688	1.7E+10	233.0648	3.03E+08				
3	1	1	1 C11H20SO6	1.29E-05	2.515	1	0.977	0.538462	UNPD	279.0908	7.1E+08	281.0867	13665036	2	6	C12H24S3	0.000882
4	1	1	4 C14H32N2SO2	0.0013228	0.811	0.804	0.507	0		291.2099	30013630	293.2069	8715278				
5	1	1	5 C10H20N2SO4	-0.000257	2.516	0.992	0.986	0.538462	ChEBI	295.0794	46893688	0	0	2	6	C18H16S	0.000394
6	1	1	3 C14H30SO5	-0.000441	1.975	0.976	0.961	0.538462	T3DB	309.1746	32416342	311.1691	23518958				
7	1	1	4 C16H36N2SO2	0.0009829	1.034	0.886	0.648	0		319.2415	22037060	321.2386	6960800				
8	1	1	1 C15H21N3SO3	-0.000524	2.628	0.966	0.97	0.692308	ChEBI,Drug	322.1236	1.45E+08	324.1195	5537181				
9	1	1	4 C16H34SO5	-0.000691	1.234	0.942	0.792	0		337.2061	9653801	339.2007	15351761	2	4	C17H30N4	0.000646
10	1	1	6 C12H40N2S4	-0.000533	1.763	0.965	0.798	0		339.2007	45804816	0	0	2	6	C19H32CS	-0.000751
11	1	1	4 C11H26N2SO6	-0.000738	1.243	0.934	0.809	0		345.1167	6128790	349.1065	3.15E+08				
12	1	1	6 C20H42S2	8.69E-05	1.758	0.999	0.759	0		345.2654	34496364	0	0				
13	1	1	1 C16H19N3SO4	-0.000549	2.458	0.963	0.803	0.692308	ChEBI,Drug	348.1029	3.14E+09	350.0987	17559776	2	6	C9H27N5S	-0.000332
14	1	1	4 C13H22N2SO7	0.0010856	1.262	0.863	0.899	0		349.1064	4.05E+08	351.1023	9253539	2	4	C25H18S	-0.000765
15	1	1	4 C10H22N2SO11	0.0005441	1.109	0.964	0.645	0		377.0866	28881096	379.0837	12787804	2	4	C23H14N4	3.10E-05
16	1	1	4 C16H30N2SO2	-0.000175	1.151	0.996	0.655	0		377.1398	9110776	383.1288	24089934	2	4	C24H26S2	0.000476
17	1	1	2 C17H23N3SO5	-0.000625	1.917	0.952	0.965	0		380.1292	4.68E+09	382.1243	5945733	2	6	C18H27N2	0.000244
18	1	1	4 C10H27N3SO10	0.0004386	1.343	0.976	0.867	0		380.134	7660319	382.1301	5604678	2	4	C22H23N5	-0.001412
19	1	1	4 C15H22N4SO6	-0.001071	1.152	0.866	0.786	0		385.1198	33159850	387.1156	5227140				
20	1	1	4 C10H29N5SO6	-0.00028	1.225	0.99	0.735	0		410.121	17666718	416.1063	1.2E+08				
21	1	1	6 C7H17N3SO11	-0.000235	1.857	0.993	0.864	0		413.9955	16465915	0	0	2	6	C15H13N5	0.000417
22	1	1	6 C15H31N4SO4	-6.40E-05	1.963	0.999	0.964	0		416.1064	1.01E+08	0	0	2	6	C15H23N5	0.000404
23	1	1	4 C7H19N5SO17	-1.73E-05	0.946	1	0.446	0		420.0301	51090308	422.0273	6148451	2	4	C8H15N5S	0.00132
24	1	1	3 C13H17N5SO8	-0.001262	1.801	0.82	0.75	0.730769	ChEBI,Drug	434.0458	11983925	438.0381	11261674	2	4	C8H21NS	-9.72E-05
25	1	1	1 C12H23N5SO10	-0.001148	2.589	0.848	0.972	0.769231	ChEBI,Fool	436.0423	73094424	442.0297	13361795	2	2	C13H19N5	0.00019
26	1	1	3 C16H20N2SO9	-0.001174	1.82	0.842	0.709	0.769231	ChEBI,Fool	447.0549	21144086	451.0466	13928907	2	4	C12H20N2	0.001328
27	1	1	4 C8H21N5SO18	-5.26E-05	0.934	1	0.434	0		450.0407	8492443	452.0378	7080681	2	4	C9H17N5S	0.001285
28	1	1	3 C17H22N2SO10	-0.00118	1.795	0.84	0.686	0.769231	ChEBI,Fool	477.0655	14714493	481.057	9882625	2	4	C13H22N2	0.001323
29	1	1	6 C18H29N3S4O4	-0.000296	1.729	0.989	0.74	0		478.0971	17053582	0	0	2	6	C26H25N5	0.000356
30	1	1	6 C17H36SO16	0.0003096	1.956	0.988	0.968	0		527.1648	95931768	0	0	2	6	C30H28N2	-0.000204
31	1	1	6 C19H43N5SO11	-0.000616	1.584	0.954	0.63	0		612.2055	1.85E+08	0	0	2	6	C27H39N2	3.54E-05
32	1	1	4 C30H44SO13	0.000786	1.246	0.926	0.82	0		643.2422	19423026	645.2392	16998336	2	4	C43H36N2	0.000273
33	1	1	6 C34H58N4S3O2	-0.000126	1.472	0.998	0.474	0		649.365	80021320	0	0	2	6	C42H54N2	0.000525
34	1	1	4 C30H57N3SO10	0.0005196	0.885	0.967	0.418	0		650.3687	22892350	652.3658	9336955				

The program generates up to five candidates for a metabolite peak with the identification level as follows.

**Level 1.** Finding 34S isotopic ions (M+2) in non-labeled sample, AND finding the peak shift in labeled sample, AND reported in metabolome databases.

**Level 2.** Finding 34S isotopic ions (M+2) in non-labeled sample, AND finding the peak shift in labeled sample, AND unreported in metabolome databases.

**Level 3.** Cannot find 34S isotopic ions (M+2) in non-labeled sample, AND finding the peak shift in labeled sample, AND reported in metabolome databases.

**Level 4.** Cannot find 34S isotopic ions (M+2) in non-labeled sample, AND finding the peak shift in labeled sample, AND unreported in metabolome databases.

**Level 5.** Finding 34S isotopic ions (M+2) in non-labeled sample, AND cannot find the peak shift in labeled sample, AND reported in metabolome databases.

**Level 6.** Finding 34S isotopic ions (M+2) in non-labeled sample, AND cannot find the peak shift in labeled sample, AND unreported in metabolome databases.