Table 3: Byonic Search Parameters

Recorded protein search configuration:		
Num	**Rule**	**Value**
0	Protein database	A_thaliana_RefProt_3702_08032018
1	Spectrum-level FDR	Auto cut
2	Cleavage residues	RK
3	Digest cutter	C-terminal cutter
4	Peptide termini	Fully specific
5	Maximum number of missed cleavages	2
6	Fragmentation type	CID low energy
7	Precursor tolerance	10.0 ppm
8	Fragment tolerance	20.0 ppm
9	Charges applied to charge- unassigned spectra:	
10	Precursor mass max	10000.0
11	N-glycan search	None
12	O-glycan search	None
13	Skip bad spectrum	true
14	Off by x isotopes	Too high or low (narrow)
15	Contaminants added	true
16	Decoys added	true
17	%Additional parameters:	
18	Disulfide Enable	false
19	Trisulfide Enable	false
20	DSS Crosslink Enable	false
21	Custom Crosslink Enable	false
22	Wildcard Enable	false
23	Combyne cut off score	Auto
24	Protein FDR cutoff	1% (or 20 reverse count)
25	Focused DB created	false
26	Export mzIdentML	true
27	Score version	2
28	precursor_assignment_flags	Compute from MS1
29	po_NumberMonosReturn	2
30	%Modification searches:	
31	common_modifications_max	2
32	rare_modifications_max	1