



## Result

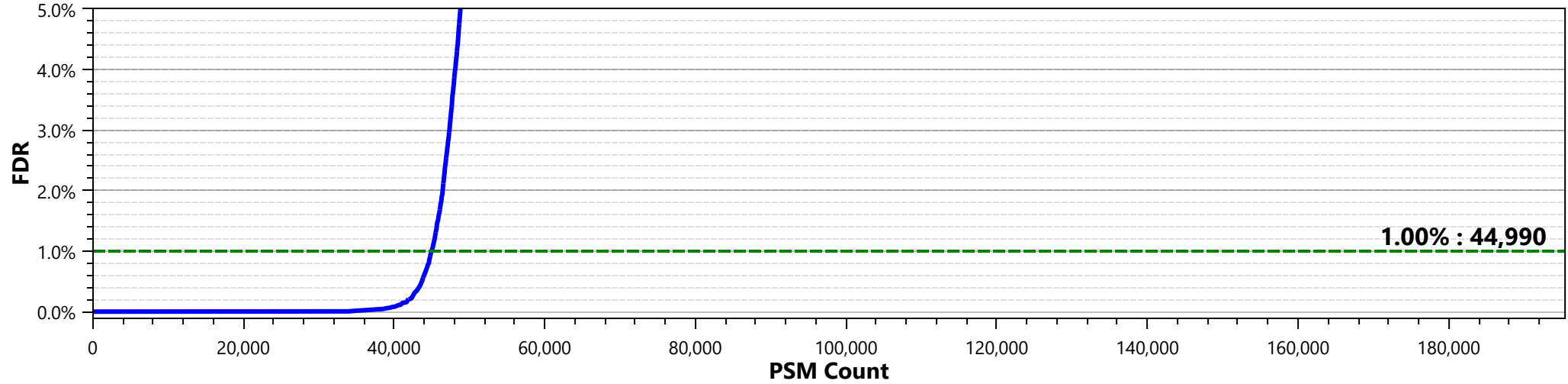
Property	Value	
Peptide Level:		
spectra number	44,734	
scans number	40,692	
peptides number	20,343	
sequences number	17,563	
proteins number	7,058	
protein groups number	6,154	
decoy spectra number	256	
decoy peptides number	203	
decoy proteins number	408	
decoy protein groups number	61	
Cleavage:		
Specific	98.50% (20,038/20,343)	
C-term specific	1.50% (305/20,343)	
N-term specific	0.00% (0/20,343)	
Non specific	0.00% (0/20,343)	
Modifications:		
TMT6plex[AnyN-term]	99.16% (20,172/20,343)	
TMT6plex[K]	54.80% (11,147/20,343)	
Oxidation[M]	14.81% (3,013/20,343)	
Carbamidomethyl[C]	3.77% (767/20,343)	
Missed Cleavage:		
number=0	81.26% (16,531/20,343)	
number=1	18.74% (3,812/20,343)	
Mixed Spectra:		
number=1	90.28% (36,735/40,692)	
number=2	9.52% (3,873/40,692)	
number=3	0.20% (83/40,692)	
number=4	0.00% (1/40,692)	
Charge:		
charge=2	71.32% (14,508/20,343)	
charge=3	25.58% (5,204/20,343)	
charge=4	2.92% (593/20,343)	
charge=5	0.18% (37/20,343)	
charge=6	0.00% (1/20,343)	
MassError:		
Precursor mass error: (mean)	0.60ppm	
Precursor mass error: (std)	±1.54ppm	
ID Rate:		
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr07	38.08% (13,128/34,474)	
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr08	40.74% (13,964/34,275)	
GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr09	39.99% (13,600/34,005)	
Overall	39.60% (40,692/102,754)	



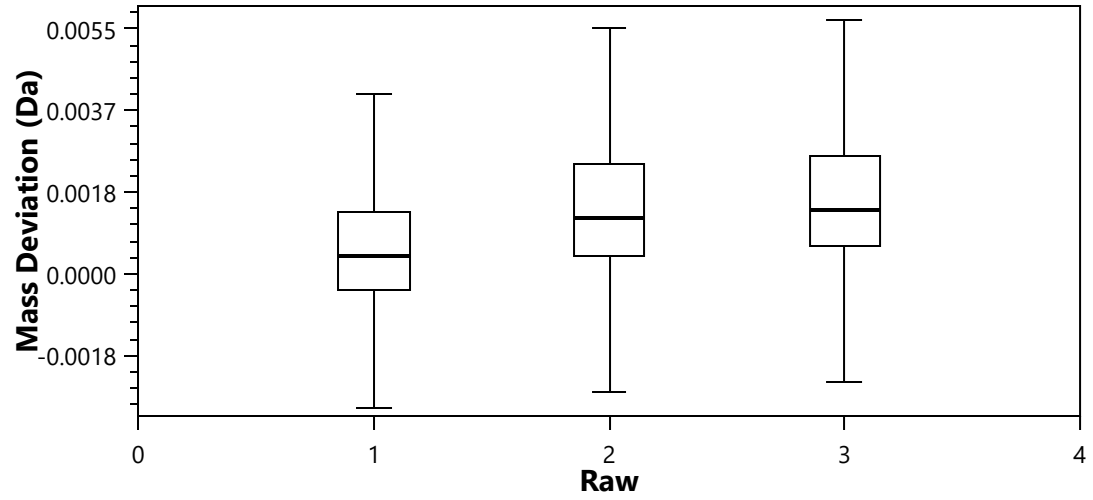
## Parameter

Property	Value	
Param:		
thread number	2	
ms tolerance	10ppm	
msms tolerance	0.02Da	
open search	False	
input format	raw	
fix modification	Carbamidomethyl[C];TMT6plex[AnyN-term];TMT6plex[K];	
variable modification	Oxidation[M];	
enzyme	Trypsin KR _ C	
max missing cleavage number	1	
co elute	True	
ll info label	1 none;	
File:		
aa path 1	C:\Users\LehtioPD\Desktop\Pfind3\pFindTask2\result\1.aa	
modification path	F:\Yanbo\pFind3\bin\modification.ini	
fasta path	F:\Yanbo\Uniprot_sp-Human_refp-EcoliK12_20190626.fasta	
contaminant path	NULL	
task path	C:\Users\LehtioPD\Desktop\Pfind3\pFindTask2\result\pFindTask2	
Raws:		
raw path 1	F:\Yanbo\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr07.raw	
raw path 2	F:\Yanbo\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr08.raw	
raw path 3	F:\Yanbo\GMHJYZ_DeqMSvalidation_300ug_TMT10_IPG3-10_fr09.raw	

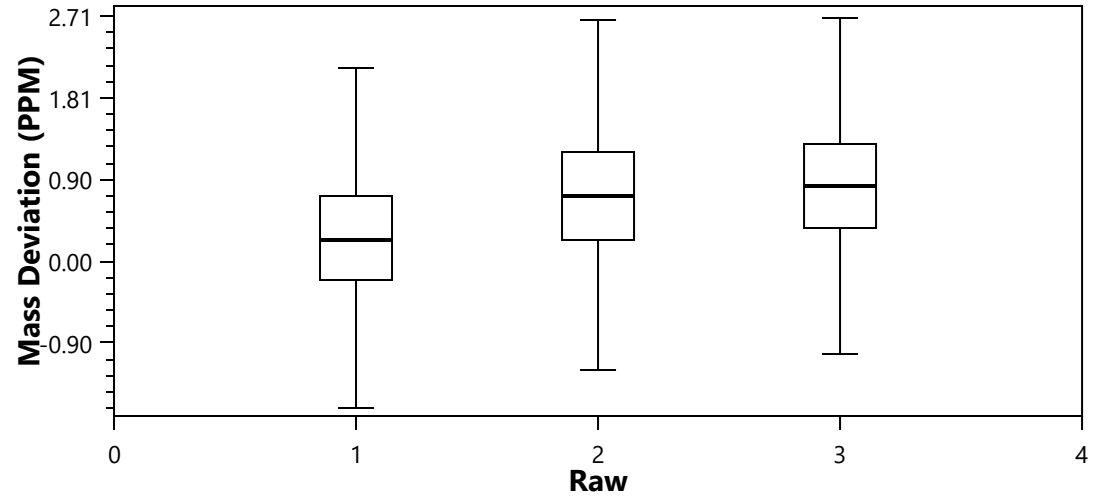
FDR Curve



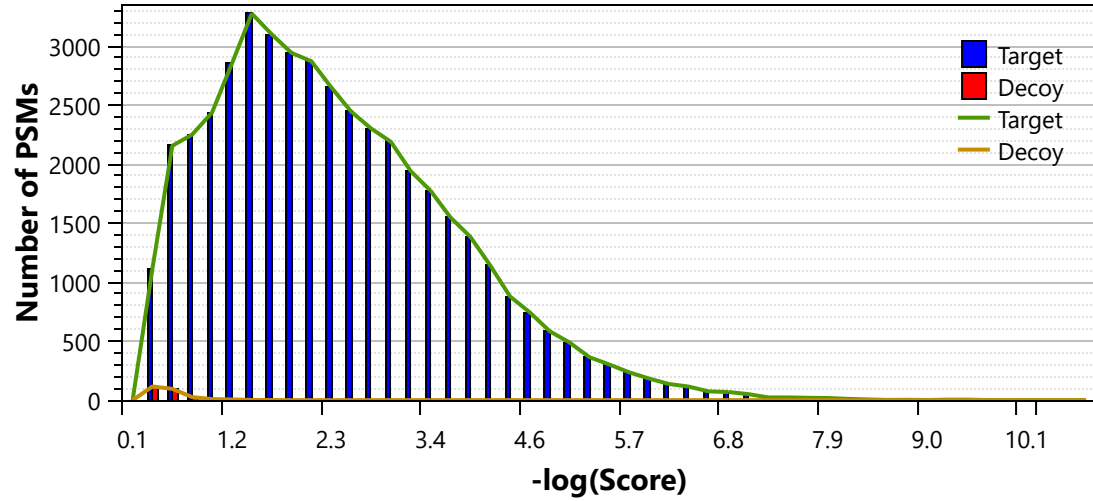
Mass Deviation



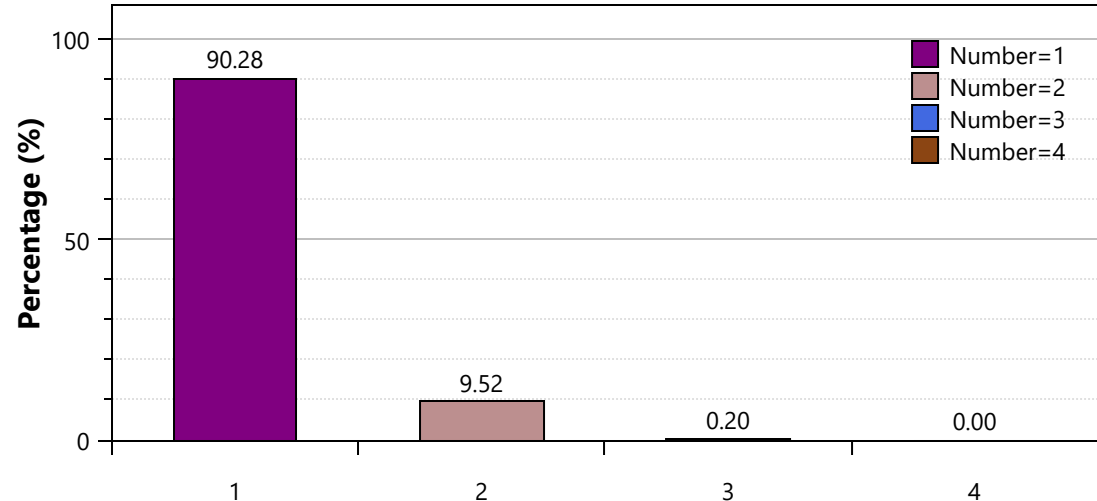
Mass Deviation



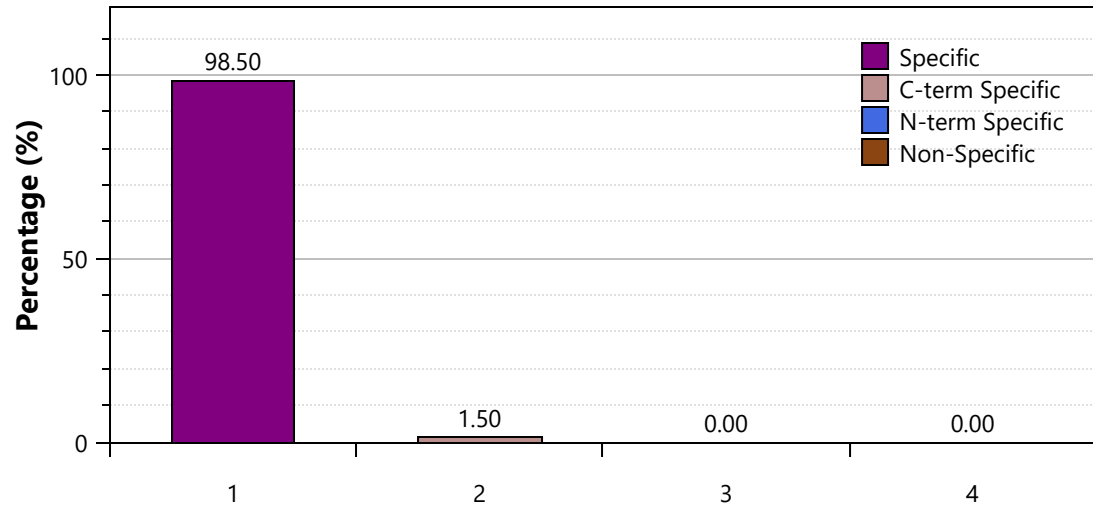
Score Distribution



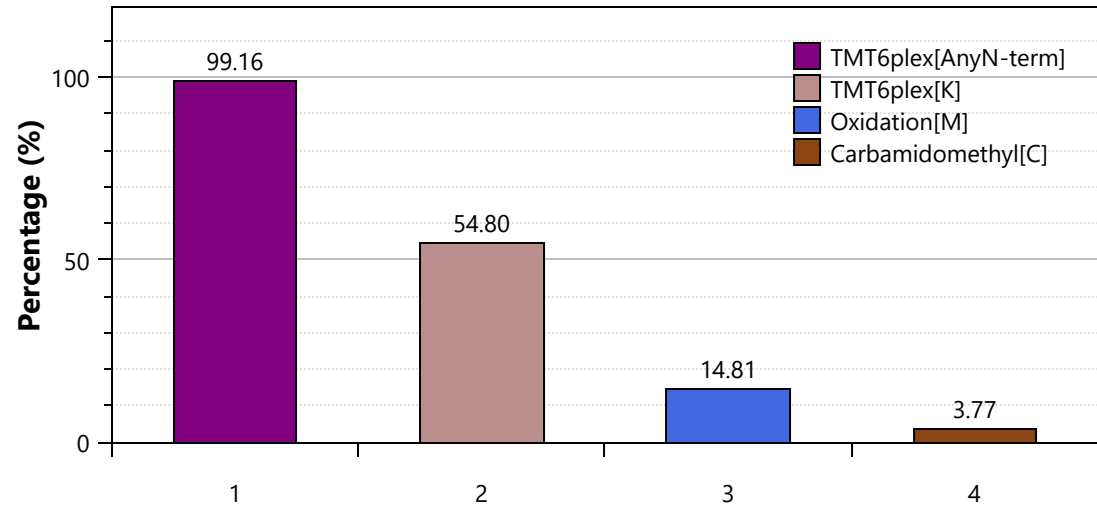
Mixture Spectra Percentage (%)



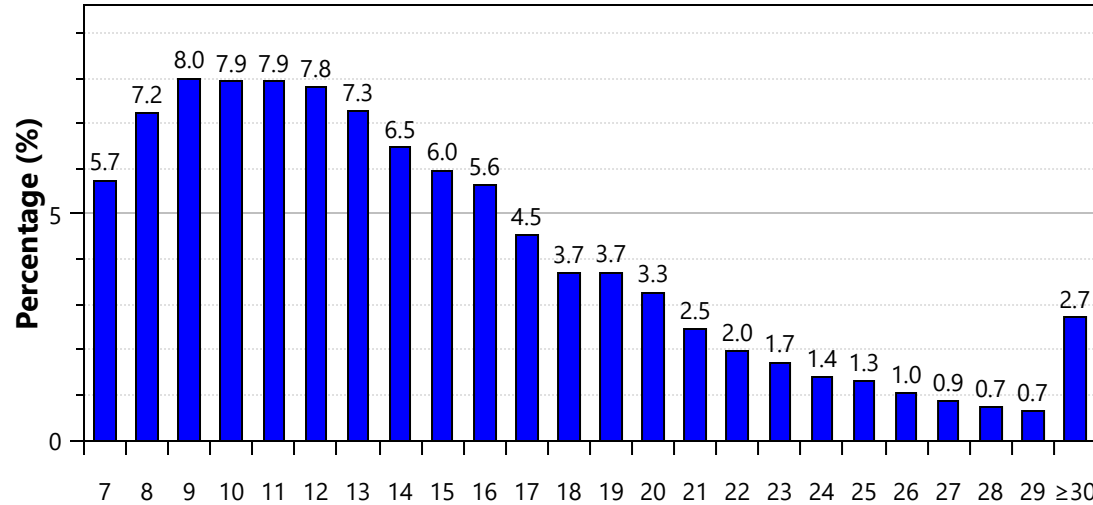
Cleavage Specific Percentage (%)



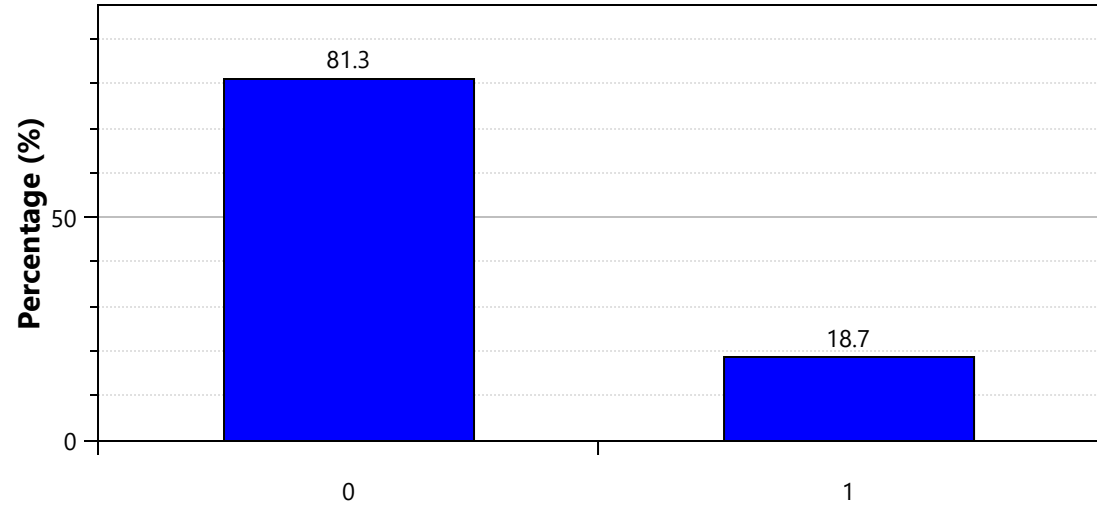
Modification Percentage (%)



Length Percentage (%)



Missed Cleavage Percentage (%)



ID Rate (%)

