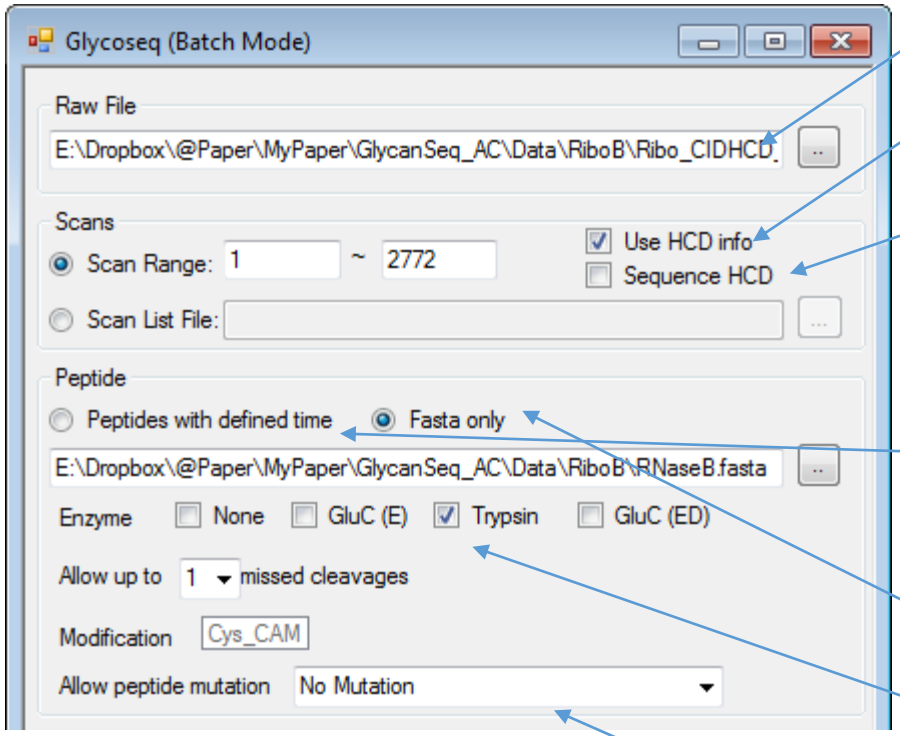
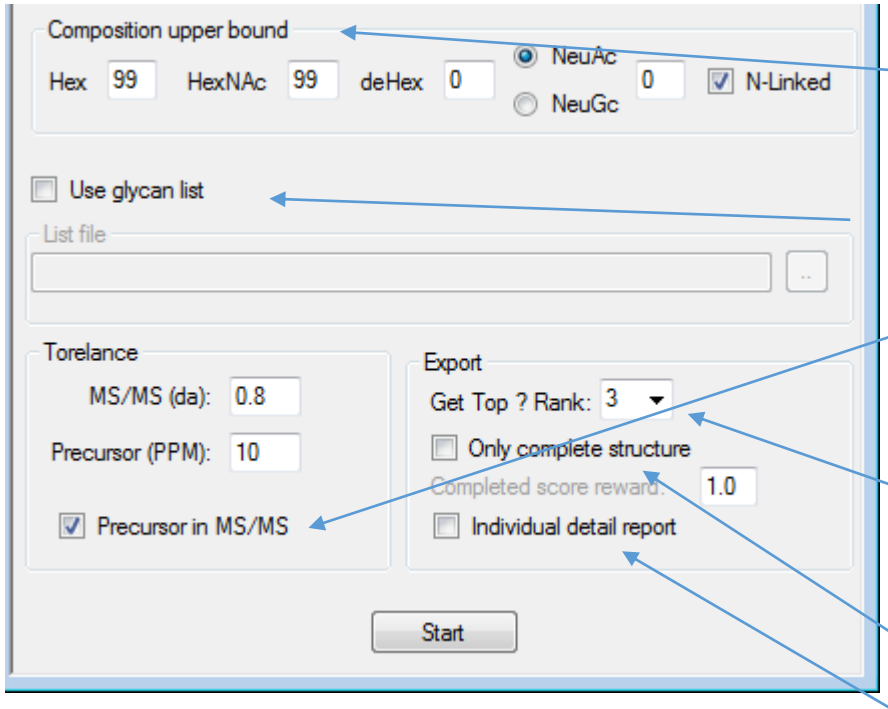
Suggestion setting are shown in the picture



- Raw File: Theomo Raw or mzXML
- Use HCD Info: if your raw file contain HCD scan, this can help guide CID sequencing
- Sequence HCD: sometimes HCD contains glycosidic bond fragments, and can be used for sequencing.
- Peptide with defined time: CSV format contain peptide search time information (Page 3)
- Fasta Only: input protein/peptide sequence in fasta format
  - Enzyme, missed cleavage: for protein sequence
  - For peptide fasta choose None and 0
  - Peptide mutation: generate and add mutated peptides



- Composition upper bound: limit the number of glycan in the structure. eg. high mannose sample can be set as the picture shown
- Use glycan list: check if you have csv format glycan list
- Precursor in MS/MS: if CID contains precursor, it can help for sequencing
- Get top: export top n results
- Only complete structure: export completed structure
- Generate detail report: generate report for each scan (caution : lots of files, and long time)

Peptide with defined time

- CSV format
- Header name
  - Protein_Name
  - Peptide_Sequence
  - Start_Search_Time_(Mins)
  - End_Search_Time_(Mins)

```
Protein_Name,Peptide_Sequence,Start_Search_Time_(Mins),End_Search_Time_(Mins)
CC112 HUMAN,AISSK,99.79108,101.01841
```

Protein/peptide fasta

```
>sp|P03455|HEMA_I76AI Hemagglutinin OS=Influenza A virus (stra
MKAILLVLLCTFAATNADTLCIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDRHNGKLCK
LGGIAPLHLGKCNIAGRLLGNPECELLLTVSSWSYIVETSKSDNGTCYPGDFINYEELRE
QLSSVSSFERFEIFPKTSSWPNHETNRGVTAACPYAGANSFYRNLIWLVKKENSYPKLSK
SYVNNKGKEVLVLWGIHHPPTSTDQQSLYQNADAYVFVGSSKYNRKFKPEIAARPKVRGQ
AGRMSYYWTLIEPGDTITFEATGNLVVPRYAFAMNRGSGSGIIIWDAPVHDCNTKCQTPK
GAINTSLPFQNIHPVTIGECPKYVKSTKLRMATGLRNVPSIQSRGLFGAIAGFIEGGWTG
MIDGWYGYHHQNEQGSGYAADQRSTQNAIDGITNKVNSVIEKMNTQFTAVGKEFNHLEKR
IENLNKKVDDGFLDIWTYNAELLVLLENERTLDFHDSNVKNLYEKVRSQLRNNAKEIGNG
CFEFYHKCDDTCMESVKNGTYDYPKYSEESKLNREEIDGVKLESTRIYQILAIYSTVASS
LVLLVSLGAISFWMCSNGSLOCRICI
```

```
>IIIB-C1
VVLVNVTE
>IIIB-V1/V2_1
CTNLKNDTNTNSSSGR
>IIIB-V1/V2_2
NCSFNISTSIR
>IIIB-V1/V2/C2
LDIIPIDNDTTSYTLTSCNTSVITQACPK
>IIIB-C2_1
TFNGTGPCTNVSTVQCTHGIR
>IIIB-C2_2
PVVSTQLLLNGSLAEEEVVIR
>IIIB-C2_3
SANFTDNAK
>IIIB-C2_4
TIIVQLNQSVE
>IIIB-C2_5
INCTRPNNNTRK
>IIIB-C3_1
QAHCNISR
>IIIB-C3_2
WNNTLK
>IIIB-C3_3_1
LREQFGNNK
>IIIB-C3_3_2
LREQFGNNKT
>IIIB-V4_1
FFYCNSTQLFNSTWFNSTWSTK
>IIIB-V4_2
GSNNTEGSDTITLPCR
>IIIB-C4
CSSNITGLLLTR
>IIIB-V5
DGGNSNNESEIFR
```