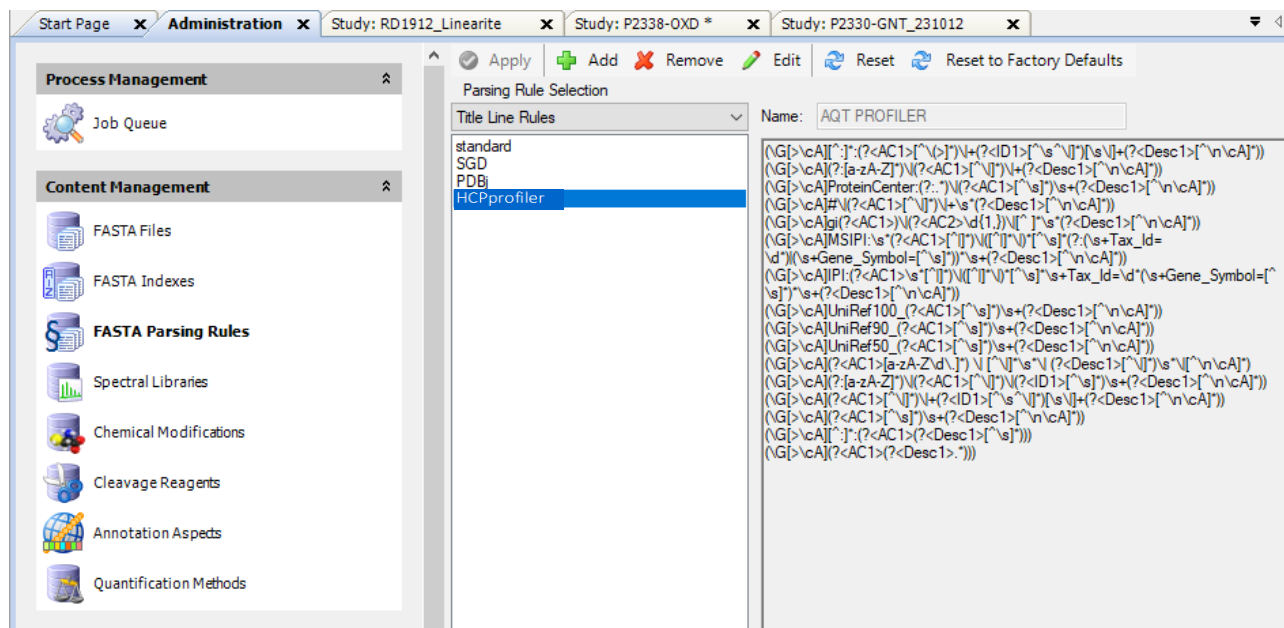


The Proteome Discoverer parsing rules are defined in the **Administration** tab → **FASTA Parsing Rules**



When using proteome Discoverer for HCPprofiler analysis, register the following parsing rules in the proteome discoverer software and make sure to use them in the analysis workflow:

```
(\G[>\cA][^:]*:(?<AC1>[^\(\>]*)|(?<ID1>[^\s^\|]*)[\\s\\|]+(?<Desc1>[^\n\cA]*))
(\G[>\cA](?:[a-zA-Z]*)\\|(?<AC1>[^\|]*)\\|(?<Desc1>[^\n\cA]*))
(\G[>\cA]ProteinCenter:(?:.*)\\|(?<AC1>[^\s]*)\\s+(?<Desc1>[^\n\cA]*))
(\G[>\cA]#\\|(?<AC1>[^\|]*)\\|+\\s*(?<Desc1>[^\n\cA]*))
(\G[>\cA]gi\\|(?<AC1>\\|(?<AC2>\\d{1,}))\\|\\[^\s]*\\s*(?<Desc1>[^\n\cA]*))
(\G[>\cA]MSIPI:\\s*(?<AC1>[^\|]*)\\|\\[^\s]*\\s*(?:\\s+Tax_Id=\\d*)\\|\\s+Gene_Symbol=[^\s]*\\s*(?<Desc1>[^\n\cA]*))
(\G[>\cA]IPI:(?<AC1>\\s*[^\|]*)\\|\\[^\s]*\\s*(?:\\s+Tax_Id=\\d*\\|\\s+Gene_Symbol=[^\s]*\\s*(?<Desc1>[^\n\cA]*))
(\G[>\cA]UniRef100_(?<AC1>[^\s]*)\\s+(?<Desc1>[^\n\cA]*))
(\G[>\cA]UniRef90_(?<AC1>[^\s]*)\\s+(?<Desc1>[^\n\cA]*))
(\G[>\cA]UniRef50_(?<AC1>[^\s]*)\\s+(?<Desc1>[^\n\cA]*))
(\G[>\cA](?<AC1>[a-zA-Z\\d\\.]*\\|\\[^\s]*\\s*\\|(?<Desc1>[^\|]*)\\s*\\|\\[^\n\cA]*)
(\G[>\cA](?:[a-zA-Z]*)\\|(?<AC1>[^\|]*)\\|(?<ID1>[^\s]*)\\s+(?<Desc1>[^\n\cA]*))
(\G[>\cA](?<AC1>[^\|]*)\\|(?<ID1>[^\s^\|]*)[\\s\\|]+(?<Desc1>[^\n\cA]*))
(\G[>\cA](?<AC1>[^\s]*)\\s+(?<Desc1>[^\n\cA]*))
(\G[>\cA][^:]*:(?<AC1>(?<Desc1>[^\s]*)))
(\G[>\cA](?<AC1>(?(?<Desc1>.*)))
```

Warning: a copy of a .pdf file may add a space between lines. Remove extra spaces after copying the parsing rules.