



For each experimental MS/MS spectrum, gather all the peptides in the database that have a m/z value matching the precursor ion's m/z value. For each peptide sequence, compute the HyperScore. With all the HyperScore values, go on with the calculation of the expectation value for the peptide set. The peptidic E-value should be the smallest possible, as it is an indication of the possibility that the match between the experimental MS/MS spectrum and the theoretical mass spectrum occurred by chance.