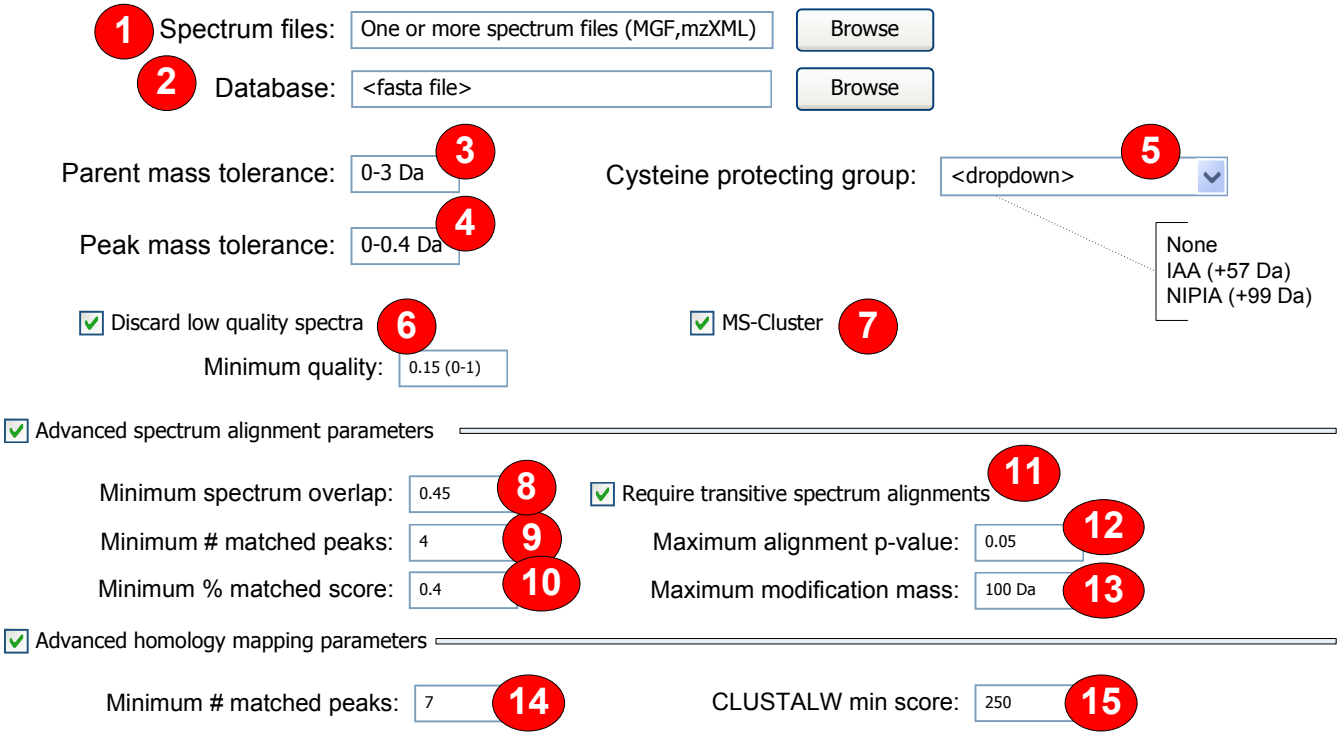

1. Input spectrum files (INPUT_SPECS_MS)
2. Input protein sequence files (FASTA_DATABASE)
3. Parent mass tolerance, in Da (TOLERANCE_PM=0-3Da)
4. Peak mass tolerance, in Da (TOLERANCE_PEAK=0.0.4Da)
5. Cysteine protecting group (AMINO_ACID_MASSES)
6. Minimum spectrum quality (MIN_SPECTRUM_QUALITY=0-1.0)
7. Cluster repeated spectra (CLUSTER_MIN_SIZE=0/1)
8. Minimum percentage of spectrum mass overlap (MIN_OVERLAP_AREA=0-1.0)
9. Minimum number of matched peaks (MIN_MATCHED_PEAKS=0-8)
10. Minimum percentage of matched peaks score (MIN_RATIO-0-1.0)
11. Require transitive spectrum alignments (FILTER_TRIGS=1/0)
12. Maximum alignment p-value (MAX_PVALUE=0-1.0)
13. Maximum modification mass (MAX_MOD_MASS=0-200)
14. Minimum number of matched peaks (MIN_MATCHED_PEAKS_DB=0-12)
15. Minimum score for clustalw protein/protein sequence alignments (CLUSTALW_MINSCORE)