

Things that will cause Welkin to return your annotation for revisions prior to acceptance:

Incomplete notes

Duplicate notes---post merging, please delete duplicate notes from the notes field such that there is only one set of notes per gene

A file that returns anything other than “All ORFs are valid” when I press the validate button---unless you have already noted that you are having a specific problem and ask for attention to that area in your cover letter

A file that has not been renumbered such that all genes are now numbered sequentially

A file that doesn't have your phagename as the locus tag header (you do this during validation and renumbering)

A file whose documentation has not been recreated to match the information in your feature table

A file that has entries in the Function field

A file that has not been cleared of old BLAST hits and reBLASTed such that embedded BLAST hits do not match your current gene predictions

If during QC, it becomes clear that all the evidence has not been routinely weighed for each gene prediction.

Multiple wildly speculative functions without sufficient documentation –if you find something cool that you truly believe is a putative function never before seen in mycobacteriophages (not just the top HHPred hit so you feel like you should write it down), put it in the cover letter.