(§) Newly added seqs are pre- and post-filtered for their inclusion in a longer (or equally-long) seq from the very same organism in the ALI or in the NON file. As in the original forty, seqs lengthened by newly added seqs can be removed.

(∞) BLAST alignment is as in the original forty:
- The 5 first transcripts are used as templates as long as coverage is increased.
- Each (translated) BLASTX HSP is added separately to the ALI.

(∞) exonerate alignment is as follows:
- The transcript with the best coverage among the 5 first hits is selected as the template.
- The single exonerate (protein2genome:bestfit) translated transcript is added to the ALI.

(†) Newly added seqs can be optionally tagged as potential contaminations if they do not satisfy user-specified org-specific taxonomic filters.