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B

Protocol Run: ChimeraModelFromTemplate

Protocol: **chimerax - model from template** [Cite](#) [Help](#)

Run

Run name: **chimerax - model from template** [Edit](#) Comment: [Edit](#)

Run mode: ☒ Continue ☐ Restart [Help](#) Host: **localhost**

Use queue? ☐ Yes ☒ No [Edit](#) [Help](#)

Wait for: [Help](#)

Input [Help](#)

Do you already have a template? ☒ Yes ☐ No [Help](#)

Atomic structure used as template [Search](#) [Trash](#) [Eye](#) [Help](#)

Chain: [Edit](#) [Help](#)

Target sequence [Search](#) [Trash](#) [Eye](#) [Help](#)

Options to improve the alignment: Additional sequences to align [Help](#)

Other sequences to align

Object	Info
Search Trash Eye Help	

Multiple alignment tool: **Clustal Omega** [Help](#)

Additional target sequence to include? ☒ Yes ☐ No [Help](#)

Chain: [Edit](#) [Help](#)

Target sequence [Search](#) [Trash](#) [Eye](#) [Help](#)

Options to improve the alignment: **Provide your own sequence alignment** [Help](#)

Sequence alignment input: [Help](#)

[Close](#) [Save](#) [Execute](#)

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Input

Do you already have a template? ☐ Yes ☒ No [Help](#)

Target sequence [Search](#) [Trash](#) [Eye](#) [Help](#)

Protein sequence database: **PDB** [Help](#)

Similarity matrix: **BLOSUM62** [Help](#)

cutoff value: **0.001** [Help](#)

Maximum number of sequences: **100** [Help](#)