

Kepler - Bug #2252

Need to add actors for aligning multiple DNA or protein sequences

11/06/2005 06:33 PM - Timothy McPhillips

<b>Status:</b>	Resolved	<b>Start date:</b>	11/06/2005
<b>Priority:</b>	Normal	<b>Due date:</b>	
<b>Assignee:</b>	Timothy McPhillips	<b>% Done:</b>	0%
<b>Category:</b>	actors	<b>Estimated time:</b>	0.00 hour
<b>Target version:</b>	Post-rel-1.0.0	<b>Spent time:</b>	0.00 hour
<b>Bugzilla-Id:</b>	2252		
<b>Description</b> We need to wrap the ClustalW and Gblocks programs in collection-oriented actors. The aligned sequences output by these actors could then be fed into the actors wrapping the Phylip package and used for inferring phylogenetic trees.			

History

#1 - 10/23/2008 04:46 PM - Timothy McPhillips

Actors for running ClustalW and Gblocks are included in the ppod-actors module.

#2 - 03/27/2013 02:19 PM - Redmine Admin

Original Bugzilla ID was 2252