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Author	<b>Johan Geijer</b>	
Title (English)	<b>Databases for the <i>Trypanosoma cruzi</i> genome project</b>	
Title (Swedish)		
Abstract	Three different types of <i>Trypanosoma cruzi</i> sequences (EST, GSS and BACend) have been assembled using Phrap. The resulting contigs have been annotated using open reading frame prediction, gene prediction and homology search. All the results have been stored in newly constructed databases and user-friendly webinterfaces have been developed to access the data. The databases were implemented to facilitate the analysis process of biological data in the <i>Trypanosoma cruzi</i> genome project.	
Keywords	<i>Trypanosoma cruzi</i> , EST, GSS, BACend, PHRAP, assembly, annotation, databases	
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