

GEP Project Management System: Basic Usage

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Version

GEP Project Management System (Version alpha)

Introduction

About the Genomics Education Partnership:

The Genomics Education Partnership (GEP) attempts to create a scientist-student partnership by bringing genomics education into the undergraduate curriculum. The GEP has developed a web-based Project Management System in order to enable GEP faculty members to coordinate their annotation and sequence improvement efforts: GEP faculty can use this system to claim and submit GEP projects. Students can use the Project Management System to design and submit reaction orders for sequence improvement projects.

This document provides a general overview of the GEP Project Management System. For a more technical discussion of the system, see the technical manual for system administrators.

Questions about the GEP Project Management System

Please contact Wilson with questions or suggestions at wleung@wustl.edu

Account Management

User Accounts

You must be a member of the GEP in order to access the Project Management System. Members include faculty, TA's, students, and research scientists who are involved in GEP projects. Faculty username and passwords are only issued to members who have participated in the GEP Faculty Workshop. Faculty members can create student accounts using the Project Management System.

Passwords

If you forgot your password, you can email the GEP staff at wleung@wustl.edu to reset your password.

Navigation Options

Login procedure

1. Navigate to the GEP Project Management System through the GEP home page (<http://gep.wustl.edu> → 'Projects' → 'Project Management System')
2. Enter the username and password issued to you by the GEP:
 - a. Username: [<first letter of first name><lastname>] (e.g., selgin)
 - b. Default password: [gep<year joined>] (e.g., gep2007)
3. Click "Login"

Drop-Down Menu

The drop-down menu is visible on all the pages within the Project Management System. You can use the drop-down menu to navigate to different pages within the system. Alternatively, you can click on the items on the main menu bar to navigate to a page with a list of sub-menu items.

The Home Page

Besides the drop down menus, you can also use the homepage to access the different functionalities of the Project Management System. Simply click on the image that corresponds to the page you wish to visit.

The Footer Links

At the bottom of each page are external links to other parts of the GEP web framework.

Logout procedure

Click on the link labeled "Logout" on the Drop-Down Menu to exit the system.

Sections Available to Faculty:

Account:

Section	Purpose
Edit Account	Allow faculty members to update the account information
Change Password	Update the faculty password
Add Student Accounts	Create new user accounts for students
Edit Student Accounts	Edit student information for existing student accounts

Projects:

Section	Purpose
Claim Annotation Projects	Claim and download annotation projects from the GEP.
Submit Annotation Projects	Submit completed annotation projects to the GEP
Review Annotation Claim Status	Allow faculty members to review the list of annotation projects they have claimed and submitted
Claim Finishing Projects	Claim and download finishing projects from the GEP
Submit Finishing Projects	Submit completed finishing projects to the GEP
Review Finishing Claim Status	Allow faculty members to review the list of sequence improvement projects they have claimed and submitted
Claim TSS Projects	Claim and download transcription start sites (TSS) projects from the GEP
Submit TSS Projects	Submit completed TSS projects to the GEP
Review TSS Claim Status	Allow faculty members to review the list of TSS projects they have claimed and submitted

Sections Available to Students:

Account:

Section	Purpose
Edit Account	Allow students to update their account information
Change Password	Update the student account password

Resources:

Section	Purpose
Order Finishing Reactions	Allow students to order finishing reactions
Review Reaction Order Status	Allow students to check the status of their past and current reaction orders and to download traces generated by the McDonnell Genome Institute at Washington University