Issues

#	Project	Tracker	Status	Priority	Subject	Assignee	Updated
69	Pathogen outbreak study - Pseudomonas single isolate WGS	Feature	New	High	Implement/adapt Tychus Nextflow pipeline	Katie Lennard	01/31/2019 05:16 PM
60	Setting up a portable metagenome assembly pipeline for CBIO	Support	New	Normal	Setup Nextflow metagenomics pipeline YAMP on hex		07/24/2018 12:13 PM
58	The effect of tadpole-tail blastema extract on rhabdomyosarcoma	Support	New	Normal	Pathway analysis		07/10/2018 11:17 AM
57	The effect of tadpole-tail blastema extract on rhabdomyosarcoma	Support	New	Normal	Perform proteomics differential abundance testing		07/05/2018 11:18 AM
50	Setting up a portable metagenome assembly pipeline for CBIO	Support	New	Normal	Validate binning using single copy core genes		05/16/2018 02:41 PM
46	Setting up a portable metagenome assembly pipeline for CBIO	Bug	New	Normal	Read binning with CONCOCT		04/30/2018 04:00 PM
45	Setting up a portable metagenome assembly pipeline for CBIO	Support	New	Normal	Quality trimming with Trimmomatic		04/26/2018 05:17 PM
38	Setting up a portable metagenome assembly pipeline for CBIO	Support	New	Normal	How to download SRA files to hex		04/20/2018 03:35 PM
30	Setting up a portable RNA-Seq pipeline for CBIO	Support	In Progress	Normal	Update Nextflow to version 0.27.6	Gerrit Botha	04/09/2018 12:56 PM
25	Setting up a portable RNA-Seq pipeline for CBIO	Support	In Progress	Normal	Configure NGI-RNAseq pipeline to run on hex		05/17/2018 02:54 PM