

WashU Epigenome Browser - Issues

#	Tracker	Status	Priority	Subject	Assignee	Updated
251	Feature	Closed	Normal	support location following		03/10/2015 04:17 pm
249	Feature	New	Normal	track hub include feature		12/18/2014 05:24 pm
247	Feature	New	Low	Multiple upload of custom tracks		12/17/2014 04:16 pm
246	Feature	New	Low	Change names of custom tracks		12/17/2014 04:14 pm
244	Feature	New	Normal	Pop-up window for confirming zooming in on a region	Xin Zhou	11/09/2014 11:39 pm
242	Feature	New	Normal	Please add the option to remove genome comparison track		11/07/2014 09:37 am
162	Feature	Closed	Normal	Tooltip information		03/13/2014 11:59 pm
161	Feature	New	Normal	Include scaffolds on genome snapshot	Xin Zhou	02/13/2014 03:32 pm
158	Feature	New	Low	wrapping for tooltip read information		02/13/2014 05:59 pm
145	Feature	Closed	Normal	loose format requirement for coordinates format		02/11/2014 10:52 pm
139	Feature	Closed	Low	metadata heatmap compatibility between data hubs		03/12/2014 11:14 am
135	Feature	New	Normal	adjust track order in genome snapshot		01/05/2014 11:11 pm
134	Feature	New	Normal	Track configuration on ipad		01/01/2014 10:09 pm
118	Feature	New	Normal	search auto completion by right clicking from gene tracks		11/29/2013 11:11 pm
117	Feature	New	Normal	add track name to genome snapshot		11/29/2013 11:10 pm
110	Feature	New	Normal	hub check button		11/20/2013 03:13 pm
108	Feature	New	Normal	compute pearson correlation in scatterplot		11/19/2013 08:06 am
99	Feature	New	Normal	function that move track(s) to top or bottom		11/07/2013 05:36 pm
98	Feature	Closed	Normal	multiple selection of tracks		11/18/2013 09:53 pm
97	Feature	New	Normal	user defined track color		11/07/2013 05:33 pm
67	Feature	Closed	Normal	change background color		11/18/2013 10:00 pm
60	Feature	Closed	Normal	"file type" category for custom facet table		11/18/2013 10:17 pm
58	Feature	Closed	Normal	make public hubs for ENCODE tracks	Daofeng Li	05/25/2014 12:13 am
55	Feature	New	Normal	[System] killing subtleKnife process which had been stuck longer than 10min		09/26/2013 09:14 am
52	Feature	New	Normal	Improve gene set view		09/21/2013 07:14 pm
51	Feature	New	Normal	Improve gene search function		09/21/2013 07:14 pm
50	Feature	New	Normal	Improve session?		09/21/2013 07:13 pm
49	Feature	New	Normal	general suggestions from UCSF		09/21/2013 07:13 pm
48	Feature	New	Normal	automatically refresh cache		09/18/2013 10:59 pm
36	Feature	Closed	Normal	add Brassica Rapa genome	Daofeng Li	09/13/2013 09:06 am
35	Feature	Closed	High	add common bean genome	Daofeng Li	09/13/2013 09:06 am
34	Feature	Closed	High	add soybean genome	Daofeng Li	09/13/2013 09:06 am

33	Feature	New	Low	batch GEO id output		08/20/2013 10:57 pm
30	Feature	New	Low	bam track (full) view range limit	Xin Zhou	08/05/2013 04:50 pm
28	Feature	New	Low	add time information for session and status	Xin Zhou	08/03/2013 11:43 pm
25	Feature	New	Normal	Quick capture of the central canvas	Daofeng Li	08/02/2013 07:49 am
21	Feature	New	Low	operation history	Xin Zhou	07/26/2013 02:47 pm
19	Feature	Closed	Low	new url parameter for public hub	Xin Zhou	07/29/2013 12:14 pm
17	Feature	New	Low	public datahub unload button?	Xin Zhou	07/25/2013 09:42 pm
14	Feature	Closed	Normal	Custom categorical track	Xin Zhou	09/13/2013 09:07 am
13	Feature	New	Normal	Line plot	Xin Zhou	09/22/2013 02:50 pm
11	Feature	New	Low	ability to cancel a super-enhancer job	Xin Zhou	07/22/2013 05:40 pm
10	Feature	New	Low	gene set list in hub support url	Xin Zhou	07/22/2013 05:35 pm
7	Feature	Closed	Normal	store gene set info in datahub descriptor file	Xin Zhou	07/26/2013 10:47 am
1	Feature	Rejected	Low	switch genome button		07/23/2013 01:44 pm