Oregon Health & Science University

Proteomics Shared Resource

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MRB524

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MRB524

Quote:

Identifier: DAVI-113
As of:
October 23, 2018
Expires on:
September 30, 2015

Summary

Service Requested:	Proteomics Project Request
Requester:	John Klimek
E-mail:	klimekj@ohsu.edu
Phone:	
Lab:	David, Larry (OHSU) Lab
Billing address:	,,,,,
PIs:	Larry David - 503-494-8625 - davidl@ohsu.edu
Financial Contacts:	Larry David - 503-494-8625 - davidl@ohsu.edu

Request Summary:

Forms

Sample Submission Form		
★	I acknowledge that I've read the Sample Preparation Considerations page listed in the OHSU website and my samples are mass spectrometry compatible. (Please Initial):	jk
	Affiliations:	○ Knight Cancer Center ○ Casey Eye Institute ○ None of the above
	Project Information:	
	Requested Analysis (Check all that apply):	☐ Protein Identification (partial sequencing) ☐ Post Translational Modification Identification and Localization ☐ Relative quantitative analysis via label-free methods ☐ Relative quantitative analysis via TMT method ☐ MRM Targeted Analysis on Known Proteins: prior consultation required ☐ Whole Protein Mass Determination ☐ Silac Based Quantitation ☑ Other
	If other, please explain:	Project to produce example billings for website. Not a real project.
	Please provide attachment(s):	

Milestones

Name	Description	Duration	Target Date	Notes	Status

Projected Cost: $1.00

Known Charges: $1,830.00

Name	Billing Status	Quantity	Unit Price	Extended Price
Labor	Not ready to bill	17.0	$80.00	$1,360.00
Orbitrap Fusion	Not ready to bill	4.0	$80.00	$320.00
Supplies (Varies)	Not ready to bill	150.0	$1.00	$150.00

Notes:

An example billing for a quantitative experiment with 2 samples (experimental and control), each with 3 replicates, with some minor sample processing and basic data analysis. About 1/3 of the Staff time is assumed to be for sample prep work (protein assay, TMT labeling, etc.) and the rest if for informatics time. A sample of this nature would be expected to yield quantitative data on anywhere from several hundred to a couple thousand proteins. This kind of experiment is not usually recommended for Co-IP samples as it tends to be more expensive. Also the ideal candidate in a Co-IP sample is usually in one sample but not the other; so accurate ratio data is generally not possible to generate.