


Attachment 1B: Survey Screenshots for TCGA researchers

TCGA Survey Page 1

[SURVEY PREVIEW MODE] Clinical Proteomic Tumor Analysis Consortium Survey: TCGA - Google Chrome

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Clinical Proteomic Tumor Analysis Consortium Survey: TCGA

Survey for Clinical Proteomic Tumor Analysis Consortium (CPTAC, Phase II)

Survey of The Cancer Genome Atlas (TCGA) researchers

The National Cancer Institute (NCI) launched the Clinical Proteomic Technologies for Cancer (CPTC) initiative in 2006 (Phase I) to specifically address barriers in proteomics research to ensure any findings are due to the biology and not analytical variability. Building upon the accomplishments of CPTC Phase I, the **Clinical Proteomic Tumor Analysis Consortium (CPTAC) program (Phase II)** was launched in August 2011 to apply the analytical workflows developed in Phase I to better understand cancer biology. CPTAC is a comprehensive and coordinated effort to accelerate the understanding of the molecular basis of cancer through the application of robust, quantitative, proteomic technologies and workflows. CPTAC has developed a range of products, including antibodies and a centralized data repository for the dissemination of proteomic data to the public.

NCI has retained Westat, an independent research organization, to conduct a survey of CPTAC (Phase II) that will provide information on the degree to which CPTAC is meeting its goals and identify opportunities for program improvement. The views of individuals involved with The Cancer Genome Atlas (TCGA) are critical to understanding and improving the efforts of CPTAC. Participation in this survey is voluntary, but your views are important and **we hope you will complete it even if you know little about CPTAC**. All data will be reported to NCI in aggregate form. No reports will contain findings linked to individual respondents or institutions.

If you have questions about this survey, please contact Dr. Eden Segal at edensegal@westat.com or 240-314-7583. If you have questions about your rights and welfare as a research participant, please call the Westat Human Subjects Protections office at 1-888-920-7631. Please leave a message with your full name, the name of this study—CPTAC Survey for NIH—and a phone number beginning with the area code. Someone will return your call as soon as possible. If you have questions about the CPTAC program itself, contact Dr. Tara Hiltke at hiltket@mail.nih.gov or 301-451-8511.

OMB No.: 0925-0642; Expiration Date: 09/30/2014
Public reporting burden for this collection of information is estimated to average 10 minutes per response, including the time for reviewing instructions, searching existing data sources, gathering and maintaining the data needed, and completing and reviewing the collection of information. **An agency may not conduct or sponsor, and a person is not required to respond to, a collection of information unless it displays a currently valid OMB control number.** Send comments regarding this burden estimate or any other aspect of this collection of information, including suggestions for reducing this burden to: NIH, Project Clearance Branch, 6705 Rockledge Drive, MSC 7974, Bethesda, MD 20892-7974, ATTN: PRA (0925-0048). Do not return the completed form to this address. .


If you agree to participate in this short survey click Next, below.

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CPTAC is a comprehensive and coordinated effort to accelerate the understanding of the molecular basis of cancer through the application of robust, quantitative, proteomic technologies and workflows. CPTAC has developed a range of products, including antibodies and a centralized data repository for the dissemination of proteomic data to the public.

The first set of questions asks about your relationship to the Clinical Proteomic Tumor Analysis Consortium (CPTAC) program, if any.

1. What is your level of familiarity with proteomics as a basis for understanding the molecular basis of cancer? (select one response)

Very familiar

Somewhat familiar

Not at all familiar

2. Is or has your work been funded in any way by CPTAC? (select one response)

Yes, only Phase II

Yes, only Phase I

Yes, both Phases I and II

No

3. What is your level of familiarity with CPTAC (Phase II)? (select one response)

Very familiar

Somewhat familiar


Not at all familiar

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[Q3 Not at all familiar skips to survey Page 7]

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The next set of questions asks about your views on proteomics and products of CPTAC.

4. What do you see as the main obstacle(s) to improving the scientific understanding of cancer biology through the analysis of proteins? (select all that apply)


- Difficulty in experimental reproducibility
- Insufficient availability and/or reliability of technologies (e.g., instrument platforms, informatics tools)
- Insufficient agreement/standardization of research protocols
- Insufficient availability of quality reagents
- Insufficient availability of quality biospecimens with well-defined clinical information
- Insufficient understanding of cancer biology
- Lack of well characterized proteomes
- Other (please specify)

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5. Which of the following CPTAC resources available to the public have you used? (select all that apply)

Informatics tools developed by CPTAC

Affinity reagents (monoclonal antibodies)
The NCI makes affinity reagents available to the public for research purposes through the Developmental Studies Hybridoma bank at the University of Iowa at low cost at <http://dshb.biology.uiowa.edu/>.

The NCI antibody portal
The NCI antibodies and affinity reagents characterization data is available to the public through the NCI antibody portal at <http://antibodies.cancer.gov>.

Proteogenomic data available through the CPTAC Data Coordinating Center
The CPTAC data portal is a centralized data repository for the dissemination of proteomic data collected by the Proteome Characterization Centers for the CPTAC program. All data are freely available for secondary analysis, subject to data use guidelines. It is available at <https://cptac-data-portal.georgetown.edu/cptacPublic/>


In-depth characterization of monoclonal antibodies for cancer-related protein targets by NCI.
NCI offers affinity reagent, characterization and distribution through the CPTAC data portal provided approximately annually. More information is available at <http://proteomics.cancer.gov/newsevents/eprotein/june2013/researcher-opportunities/acptargetrequest>

CPTAC assay portal
The Assay Portal serves as a public resource of well-characterized quantitative mass spectrometry-based proteomic assays comprising standard operating procedures, reagents, and assay validation data. It is available at <http://cptac.cancer.gov/>

None

Other (please specify)

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Clinical Proteomic Tumor Analysis Consortium Survey: TCGA

6. What is your overall impression of the Clinical Proteomic Tumor Analysis Consortium (CPTAC Phase II)? (Select one response)

- Positive
- Neutral
- Negative

- Unsure: I am not sufficiently familiar with CPTAC

7. What is your overall impression of the products that have emerged from CPTAC (Phase II)? (Select one response)


- Positive
- Neutral
- Negative

- Too soon to tell
- Unsure: I am not sufficiently familiar with CPTAC products

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To further scientific understanding of cancer biology at the protein level, CPTAC is applying standardized proteomic technologies to comprehensively interrogate tumors previously analyzed by investigators in The Cancer Genome Atlas (TCGA).

8. To what extent has CPTAC prompted new collaborations or strengthened existing genomic-proteomic collaborations? (select one response)

- Positive
- Neutral
- Negative


- Too soon to tell
- Unsure: I am not sufficiently familiar with CPTAC products

9. What additional factors, if any, would facilitate greater use of CPTAC-generated resources by the scientific research community? (select all that apply)

- Availability of more raw data for secondary analysis
- Availability of extensive analysis to accompany available data
- Conference presentations
- Production of more data and/or resources
- Publications in well-regarded peer-reviewed journals
- Outreach to particular scientific community (please specify)

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The last set of questions asks about you and your work.

10. What is your main area of expertise? (select all that apply)

- Bioinformatics
- Cancer biology
- Clinical chemistry
- Experimental design
- Genomics
- Oncology
- Proteomics
- Statistics
- Other (please specify)

11. At what type of institution do you work? (select one)

- Academic
- Clinical
- Government /Military
- Industry
- Other (please specify)

12. If there is anything else you would like to share about the CPTAC program, including what improvements might make program efforts more useful to cancer research, please do so in the box below.

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Display a "Thank You" Page?

- No, do not display a thank you page. After finishing the survey, respondents will proceed directly to the completion option you specify below.
- Yes, display a thank you page after finishing the survey.

Thank you very much for your participation.