# AntibodyCross-ReactivityTestingUsingtheHuProt™ Human Proteome Microarray

Analysis of several commercially available antibodies against nearly 75% of the human proteome.

A CDI Laboratories in partnership with Arrayjet Ltd. White Paper

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**CONCLUSION:** The use of protein microarrays to evaluate antibodies is likely to set new quality standards to evaluate antibody cross-reactivity and will also address the need for new methods to identify antibodies that can be used in robust scientific investigations, grant proposals and for commercialization.



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### Introduction

A number of recent articles and commentaries published in high impact journals detail the problems with antibody cross- reactivity, its impact on data relevancy and the amount of time and money wasted on the use of poor antibodies. In addition, there is growing demand from the NIH regarding the need for antibody standardization that would ensure that reagents used in publications are actually detecting the proteinsofinterest.

Antibodies are among the most commonly employed biological research reagents - tools used primarily to identify and/or isolate molecules of interest. It is becoming clear that they are also the cause of many problems regarding data interpretation and may hinder researcher's abilities to reach unambiguous conclusions. (Baker M. (2015) Reproducibility crisis: Blame it on the Antibodies. <u>Nature 521:</u> 274-276.)

Scientists - along with non-scientists - contend that the complex system for ensuring the reproducibility of biomedical research is failing at certain levels and is in need of restructuring. (Bradbury Aand PlückthunA(2015) Reproducibility:Standardize antibodies used in research. <u>Nature **518**: 27-29.</u>)

Glenn Begley, chief scientific officer at TetraLogic Pharmaceuticals in Malvern, Pennsylvania, and coauthor of the controversial article "Drug development: Raise standards for preclinical cancer research" (Begley and Ellis, <u>Nature 483:531–533</u>, 2012) suggested that "poorly characterized antibodies probably con- tribute more to the problem than any other laboratory tool". While antibodies are the undisputed workhorses of biological experimentation, they are also littering the field with false find- ings. A few crusaders are pushing for change.

This recent and growing concern over commercial antibody quality indicates that the day is coming when all commercially-

available antibodies will need to undergo standardized testing to meet quality criteria. Only then will the data generated using these antibodies be accepted for journal publication or for inclusion in NIH grants.

As an example, some companies have begun using knockout cell linesto address antibody specificity issues. This is a good move forward but is stillnotacomplete solution. Aknockout cellline does give asnapshot of how a particular antibody behaves in a particular cell line under the given assay conditions. The knock- out does not, however, guarantee that antibody will behave similarly in a different cell line under different conditions, or in a different tissue type. This is because radically different expression levels of proteins can occur across cell lines, tissue types and treatments. In contrast, using high content protein microarrays produces a comprehensive picture of antibody cross-reactivity against a large part of the entire human proteome. Since the proteins spotted on the arrays are robustly expressed, array analysis can give a clear profile of cross-reactivity across proteins that are selectively expressed in a wide rangeofcelllines.

In addition, with tools such as the CDI Labs HuProt<sup>™</sup> array, it is possible to measure antibody cross-reactivity to proteins in their native, folded conformation, (e.g., in an immunoprecipitation or immunofluorescence assay), or to denatured proteins, (as found on western blots, or in IHC) in which antibodies do not recognize native proteins and thus the tissues need to be processed by antigen retrieval methods. The HuProt<sup>™</sup> arrays are ideal for both types of screening, as the proteins are initially spotted in native conformation, but the arrays can also be de- natured with 9M urea and 5mM DTT. See Hu, *et al.* "Proteins on HuProt<sup>™</sup> Array Are Well Folded": A poster presentation included in the Appendix, page 25.

Continued on page 3.



#### Continued from page 2.

In a move aimed at improving the quality and usefulness of commercial antibodies, the NIH started the Protein Capture Reagents Program to produce validated and highly specific antibodies /protein detection reagents. CDI Laboratories is part of this program and uses a patented technique to produce mono- clonal antibodies with unprecedented specificity. All of the antibodies produced by CDI Labs are tested for monospecificity on the HuProt™ protein microarray, which is the world's highest- content proteinmicroarray.

#### **Methods and Materials**

#### HuProt<sup>™</sup> human proteome microarray

The HuProt<sup>™</sup> human proteome microarray provides the largest number of unique hu- man proteins known to be included on a single slide, allowing thousands of interactions to be profiledinhigh-throughput.

The HuProt<sup>™</sup> version 2.0 microarray contains thousands of purified human and ~100 mouse proteins. This content encompasses the encoded products of more than 15,000 unique human genes (~75% of the human proteome) and over 100 unique mouse gene symbols. Recombinant proteins are expressed in the yeast *S. cerevisiae*, individually purified using N-terminal GST or RGS-His6-tags, and printed on glass slides in duplicate. The quality of each microarray batch is determined by GST immunoblot- ting (98% of all proteins show GST signals significantly higher than negative controls).

For most applications, CDI prints the microarray on glass slides that are coated with 3D polymers that contain functional groups. This allows the protein samples to be immobilized on the glass by covalent bonding.

In addition to these proteins, the following are printed as controls: H1 -Histone H1, H2 (A+B) - Histone H2A and H2B mixture, H3 - Histone H3, H4 - Histone H4 (the histones are non-specific binding proteins, used as positive controls in a variety of assays), Alexa Fluor 488/594-labeled IgG, Alexa Fluor 555/647-labeled IgG (positive control and landmarks for fluorescent detection in 555/647 channels), glutathione S-transferase (GST) at 10 ng/5l, GST at 50 ng/5l, GST at 100 ng/5l, GST at 200 ng/5l, mouse anti- biotin IgG, rabbit anti-biotin IgG, biotinylated BSA, BSA (nega- tive control), buffer (printing buffer only, negative control), mouse IgM. In order to demonstrate the usefulness of human proteome microarray analysis of research reagents, a number of commercial MAbs were screened on CDI's HuProt<sup>™</sup> protein microarrays to look at possible cross reactivities.

In the pages that follow, CDI presents cross-reactivity data on a number of commercial antibodies, both as a function of working concentration and protein conformation (native vs denatured).

#### Monoclonal antibody specificity determination assay

HuProt<sup>™</sup> protein microarrays were blocked for 5 min with 3.0 ml of blocking solution (5% BSA/TBS-T). The blocking solution was removed, 3.0 ml of fresh blocking solution was added, and incubation was continuedatroomtemperaturefor1.5–2hrs with gentle shaking.

Primary antibodies were diluted in blocking solution (5% BSA/ TBS-T) to the concentrations detailed in the figures below. Arrays were incubated with gentle shaking on an orbital shaker at room temperature for 1 hr.

After incubation, microarrays were briefly rinsed with 4.0 ml of TBS-T. After the rinse, microarrays were incubated at room temperature in 4.0 ml of TBS-T with gentle shaking for 10 min and buffer was removed by aspiration. This wash was repeated 3 times.

Secondary antibodies were then diluted to manufacturer's recommendations. 3.0 ml of diluted secondary antibody was add- ed and incubation continued at room temperature for 1 hr with gentle shaking. Arrays were washed 3 times with 4.0 ml TBS-T and gentle shaking for 10 min at room temperature. After washing, arrays were brieflyrinsedthreetimes withddH<sub>2</sub>O.

The arrays were put into 50 ml conical tubes that contained Kimwipes at the bottom. The 50 ml conical tubes with arrays were spun at 800 rpm for 3 minutes. Arrays were then immediately analyzedbyscanning with a Genepix scanner.

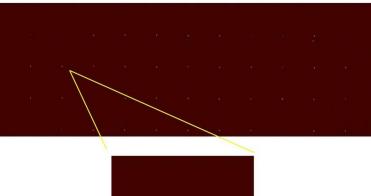
#### Native vs denatured arrays

To determine whether the antibodies bound to native and/or denatured forms of their target proteins, HuProt<sup>™</sup> arrays were blocked as previously described. 3 ml of denaturation buffer (9 M urea with 5 mM DTT) was added and the arrays were incubated at room temperature WITHOUT shaking for 20 min. Arrays were then washed 3 times for 5 min with gentles haking in TBS-T.

Arrays were probed with primary and secondary antibodies and then scanned as described above.



#### Microarray data output and statistical analysis



**Microarray Analysis:** Antibody specificity was evaluated using the CDI HuProt<sup>™</sup> Human Proteome Microarray (~75% of the human proteome) and subsequently analyzed with GenePix Pro Image Acquisition and Analysis Software, the benchmark tool for the acquisition and analysis of microarray images. The top 3 "hits" are identified by cross-reference to the array map which stores the exact location of each protein. If the expected target is ranked #1 and the S-Score (the difference between Rank #1 and #2) is >3, then the antibody is considered monospecific.



**Statistical Analysis:** Thousands of GenePix data points (from the microarray) are analyzed in terms of signalstrengthandrankedaccordingly.

**SUMMARY**: The A-score indicates the number of standard deviations above background seen for the mean signal bound by the target antigen. The S-score represents the difference between the A-score of the target antigen and the next best hit on the array.

S-scores greater than 3 standard deviations over the next listed target are deemed statistically significant and indicate highly specific antibodies.

**IN DEPTH:** The following is excerpted from Jeong JS *et al.* (2012). Rapid identification of monospecific monoclonal antibodies using a hu- man proteome microarray. *Mol Cell Proteomics* **11**(6):O111.016253.



"To quantify the affinity of individual mAbs to specific proteins on the array, we first calculated the mean and standard deviation of the signal intensity across all spots on the chip. We obtain normalized signal intensity for any pair of spots, which we define as A, which is the mean z score for each duplicate pair of spotted proteins, where  $An = (In - m)/\sigma$ . Here, I is the ratio of median foreground and median background fluorescence for any given spot pair n, m is the median value for I for all spots on the array, and  $\sigma$  is the standard deviation for I. mAbsfound in one unique row pool and one column pool that showed z scores greater than 2.8 for both duplicates pots of any given protein were then flagged for individual analysis.

mAbs identified as potentially specific using this pooling strategy were then tested individually against the entire array, and A was measured for each spotted protein. We next quantitatively evaluated the specificity of any individual mAb identified as potentially specific by means of this analysis. Todo this, we calculated a value for specificity that we define as S, where  $S = A_1 - A_2$ . Here,  $A_1$  represents the spotpairon the array that shows the highest value of A, and  $A_2$  represents the spotpairon the array that shows the highest value of A.

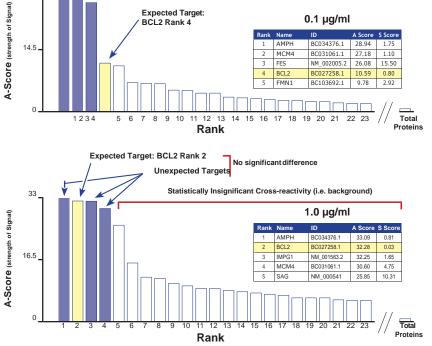
The A-Score (Affinity Score) is the normalized signal intensity of spots on the HuProt<sup>™</sup> Array. The S-Score (Specificity Score) is the difference between the A-score of a target ranking and the A-score of the target ranking that immediately follows. S-scores greater than 3 standard deviations over the next listed target are deemed statistically significant and indicate highly specific antibodies.



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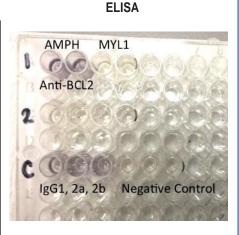






IgG Neg. Control:

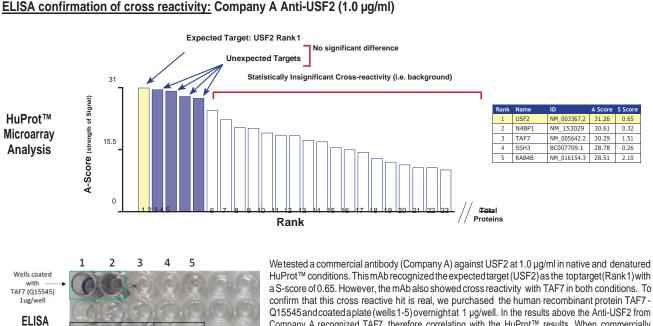
IgG Controls



The BCL2 antibody from Company C exhibited cross-reactivity on the HuProt™ microarray and recognized AMPH as the top target at two different concentrations (0.1 and 1.0 µg/mL). Confirmation of cross-reactivity was done via an ELISA using a commercially available recombinant AMPH (NM\_001635, Origene - TP306620) as the coating material. The plate was coated overnight at a concentration of 1 µg/well. Results from the ELISA clearly show that the Anti-BCL2 from Company C recognized AMPH. When commercially avail- able recombinant MYL1 (NM\_079422, Origene

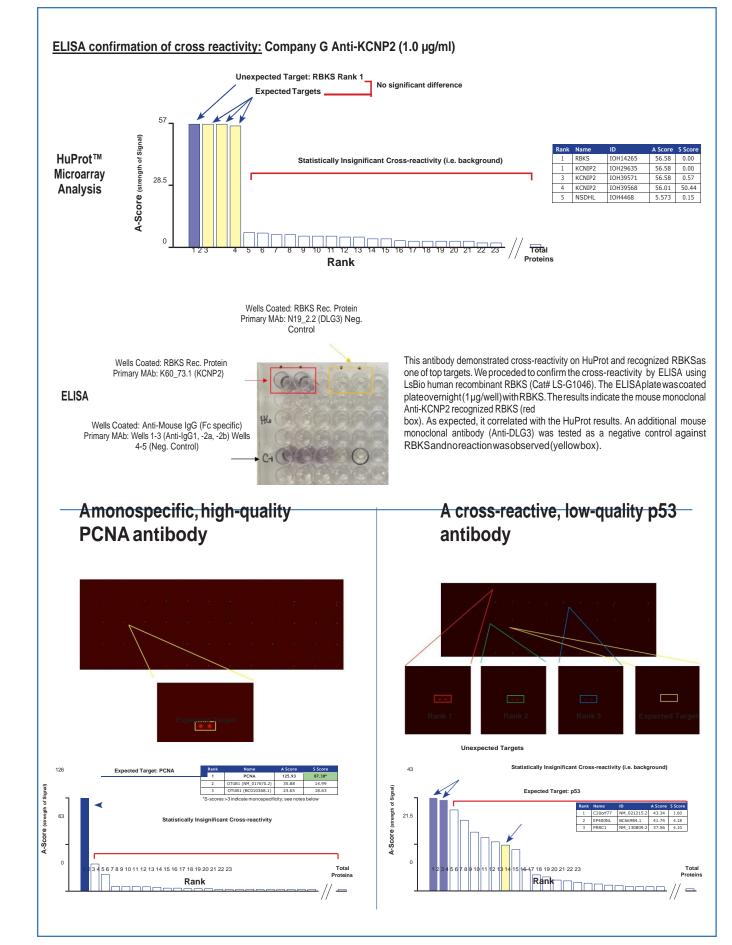
- TP302750) was used to coat wells, the same antibody gave no reaction. These results correlate

with the HuProt<sup>™</sup> findings.



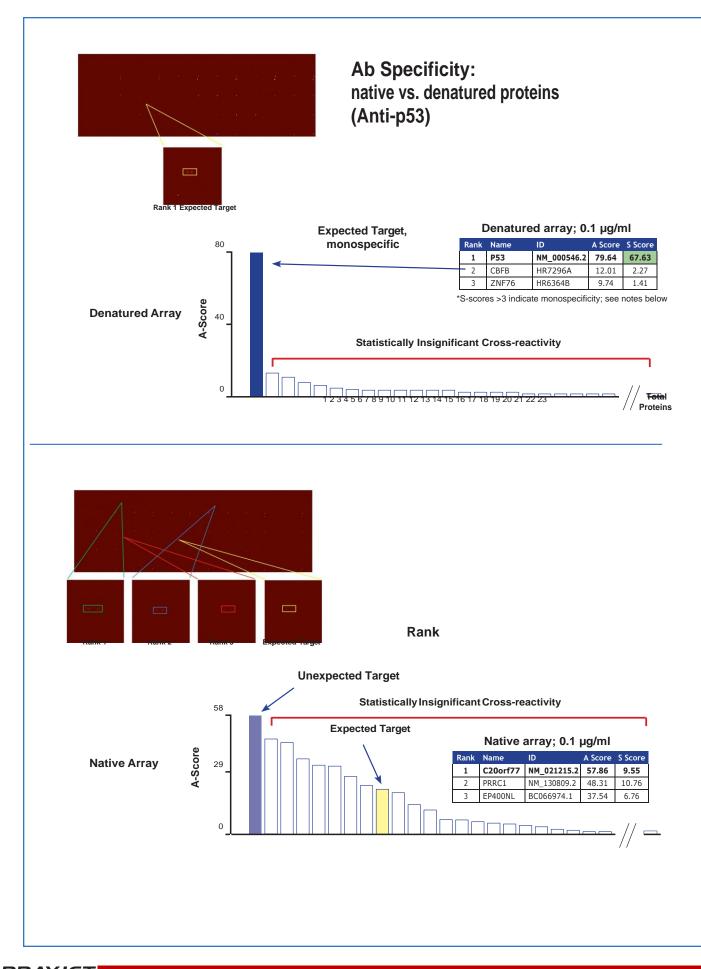
Company A recognized TAF7, therefore correlating with the HuProt™ results. When commercially available recombinant protein TFDP1-Q14186 was used to coat wells, the same antibody gave no reaction.

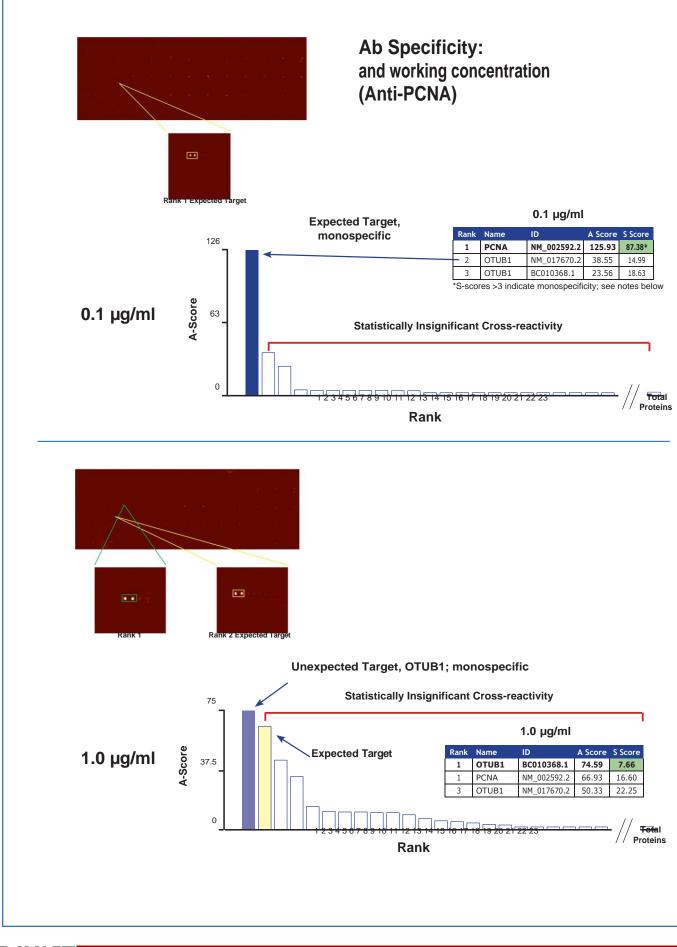


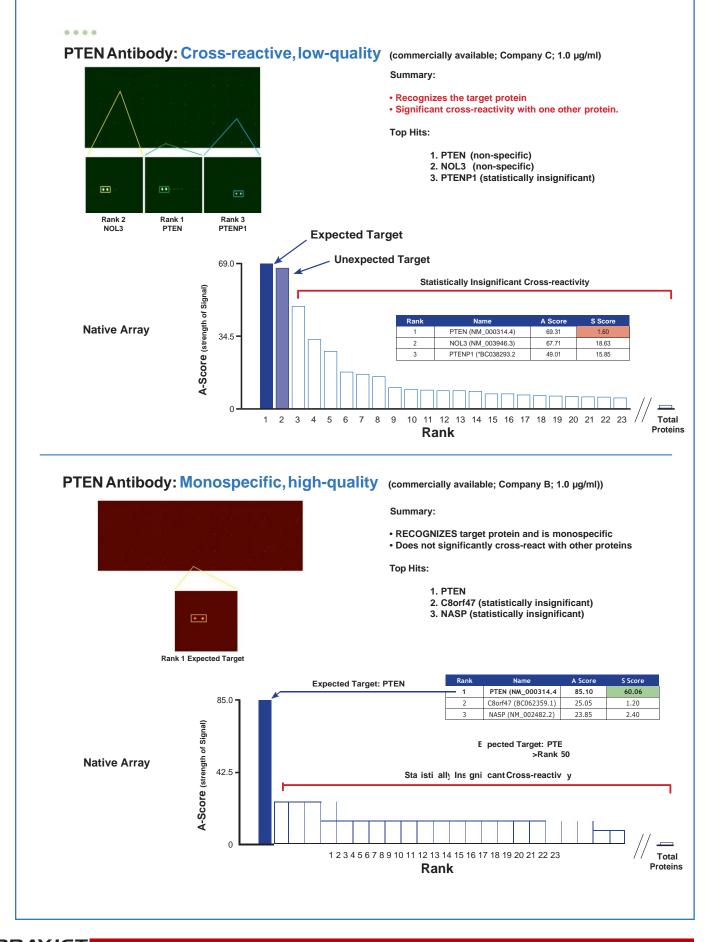


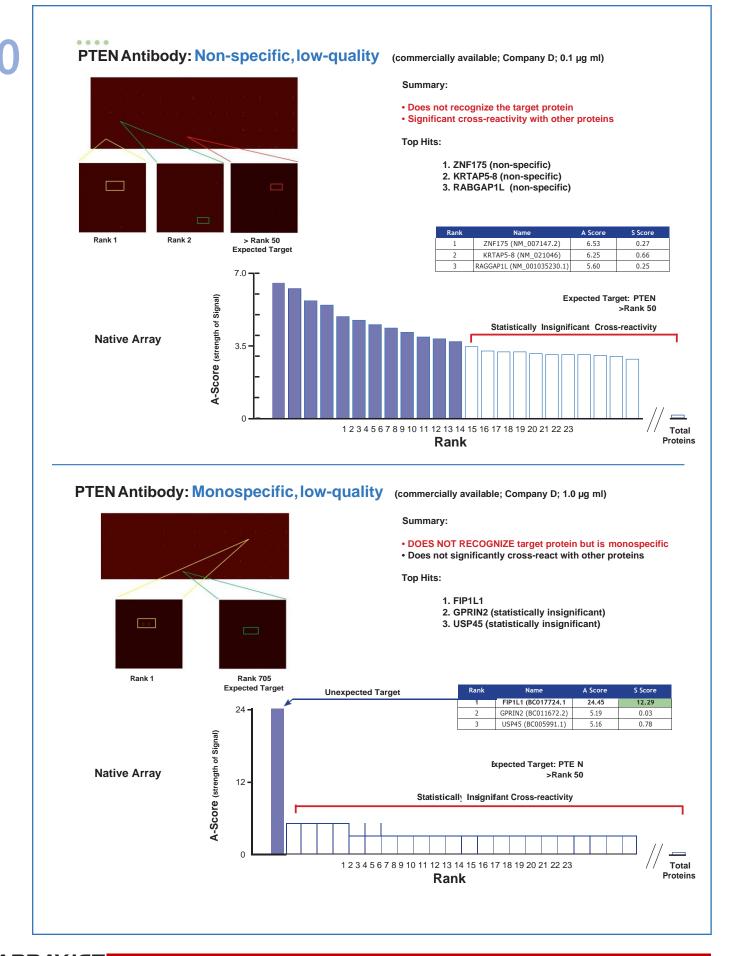
ANTIBODY CROSS-REACTIVIty TESTING USING THE HUPROT<sup>TM</sup> MICROARRAY

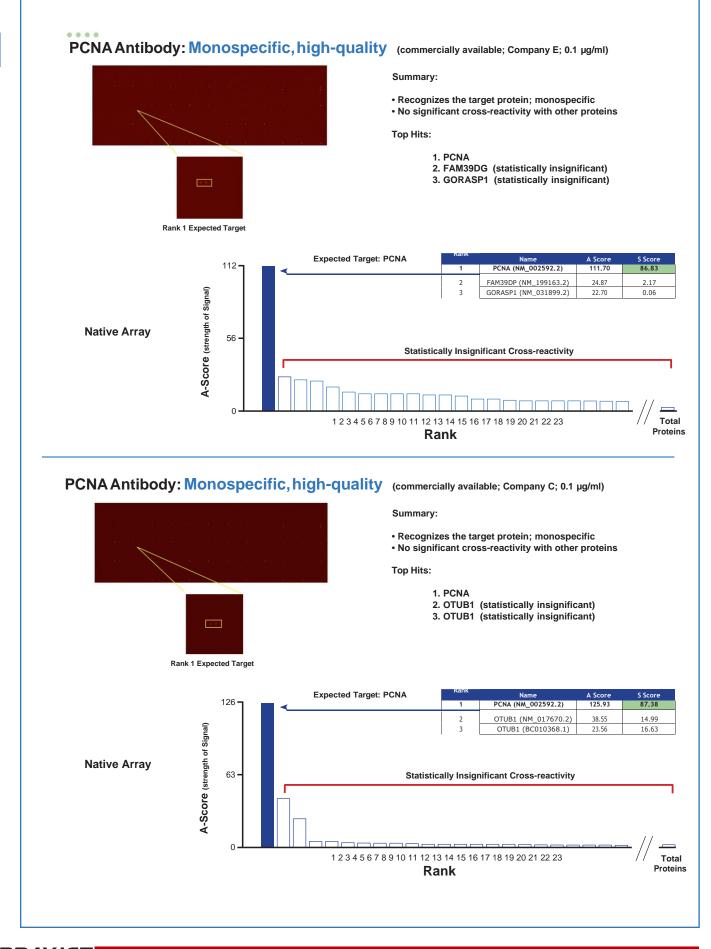
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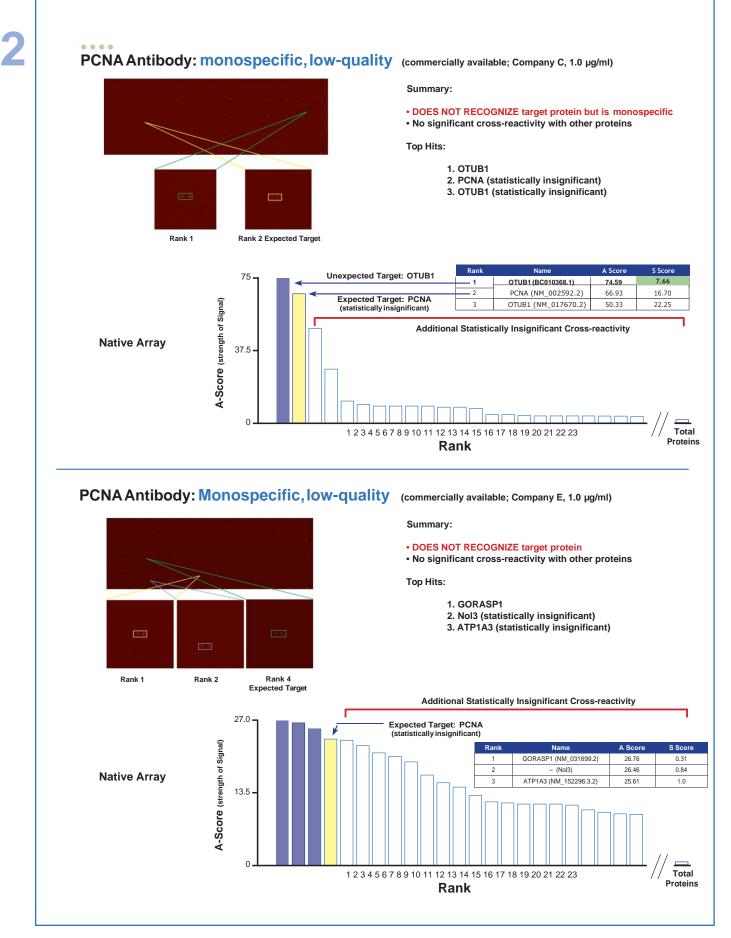


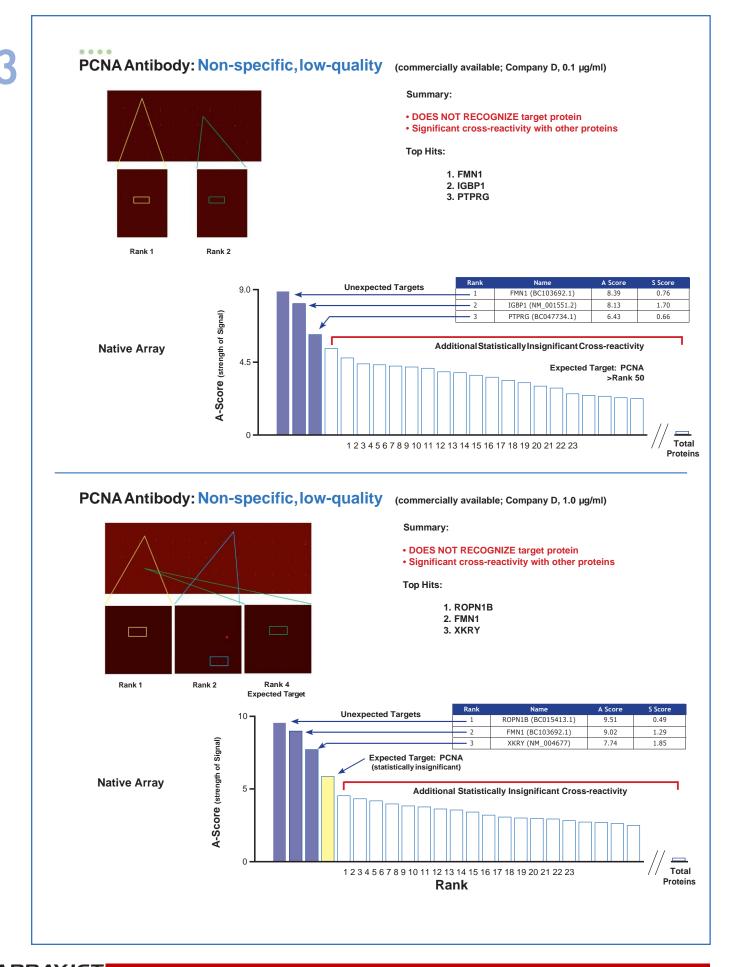


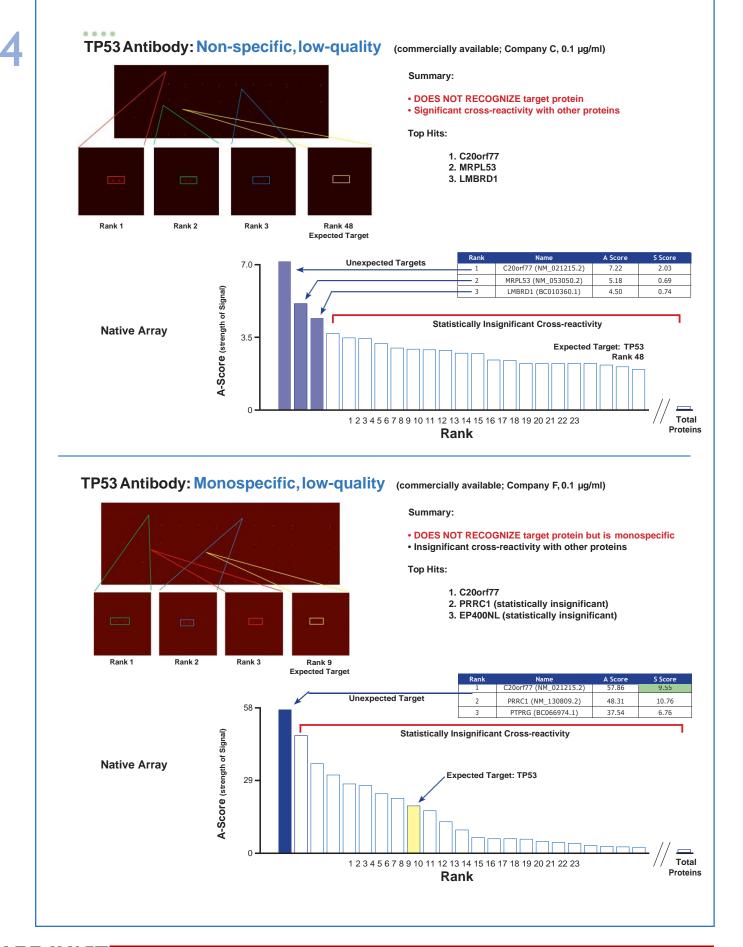


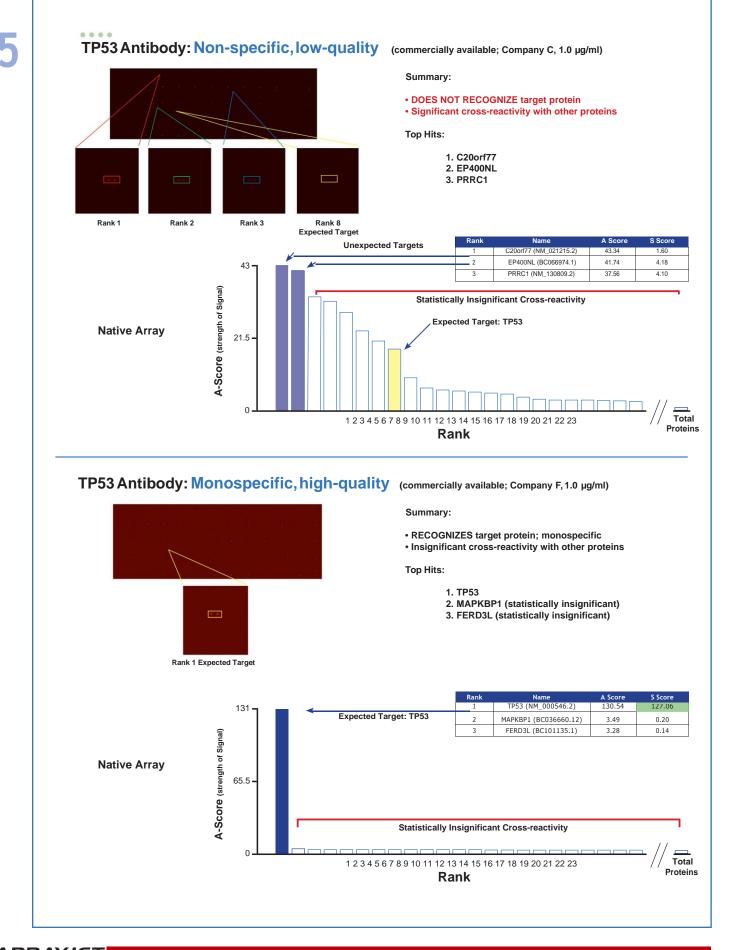




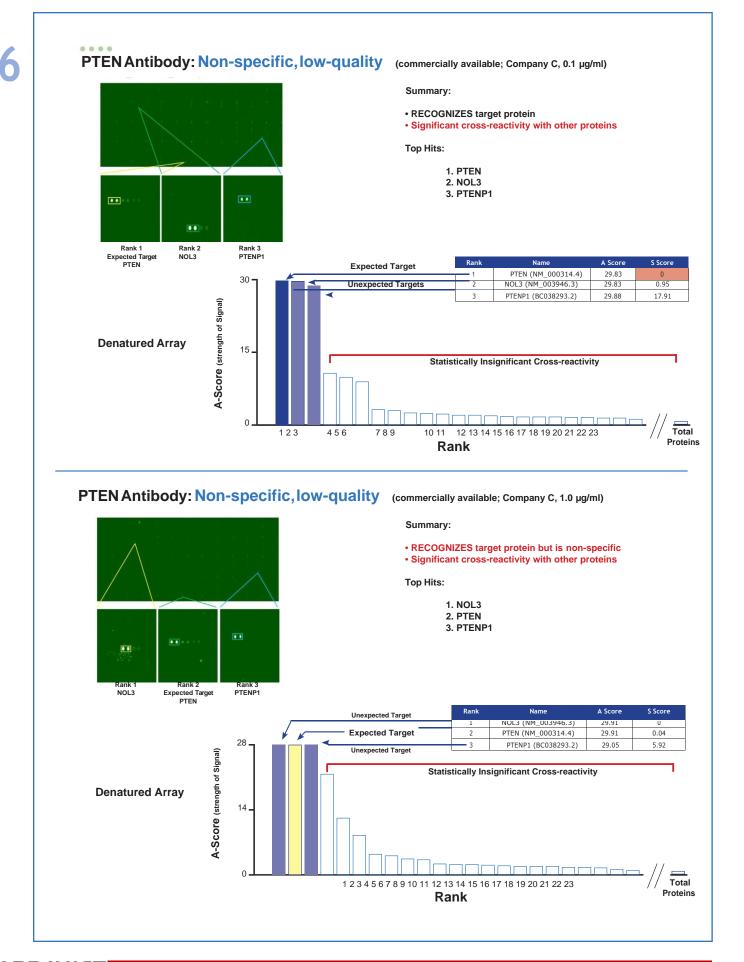


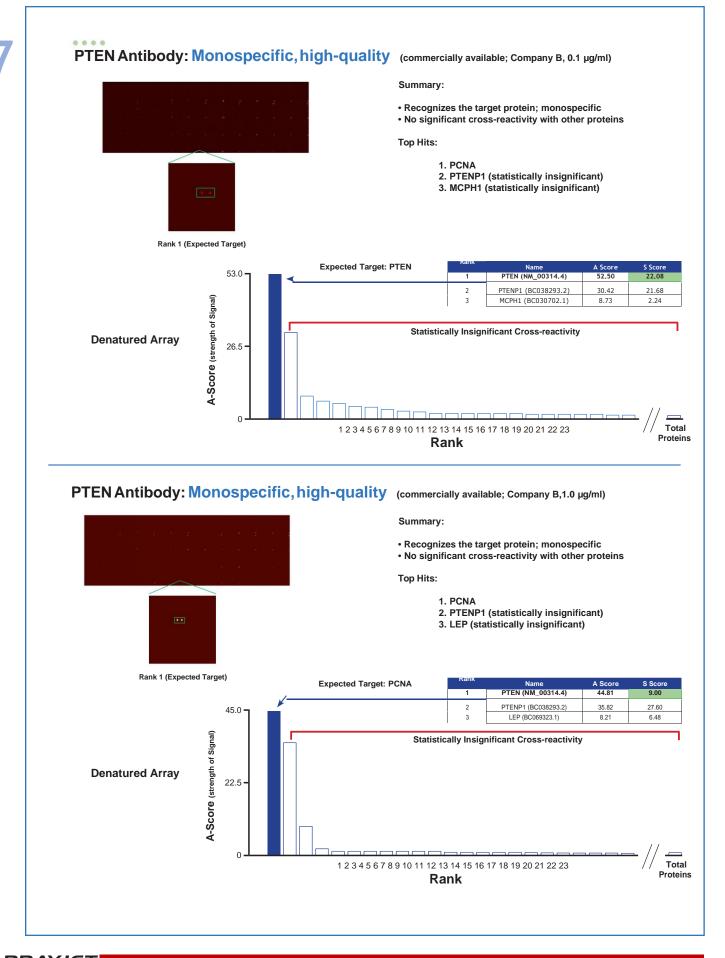




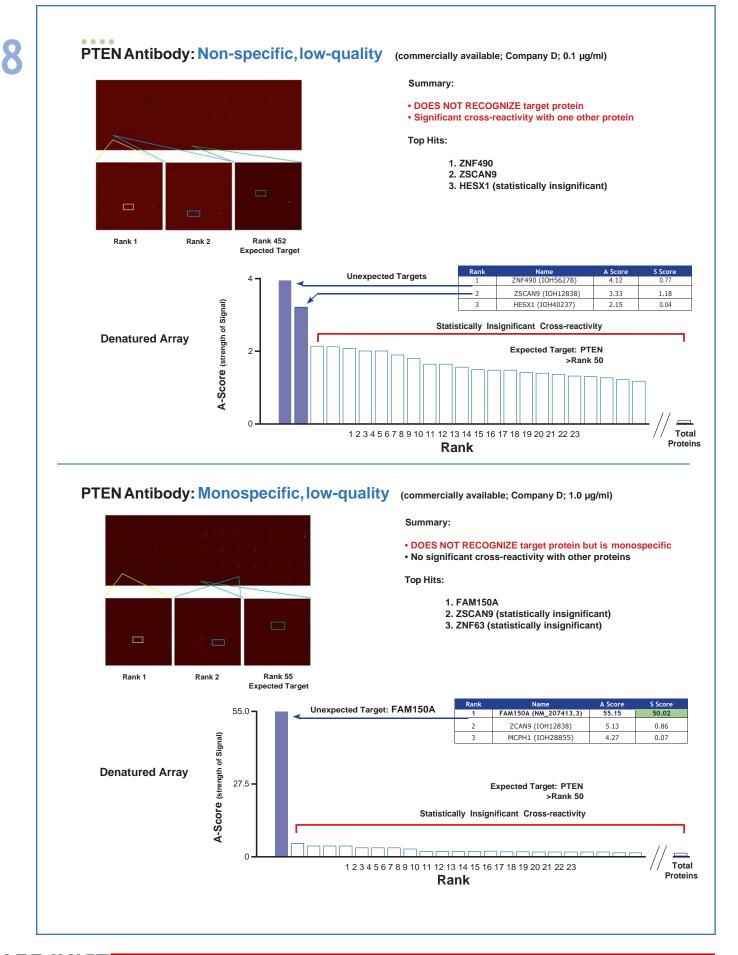


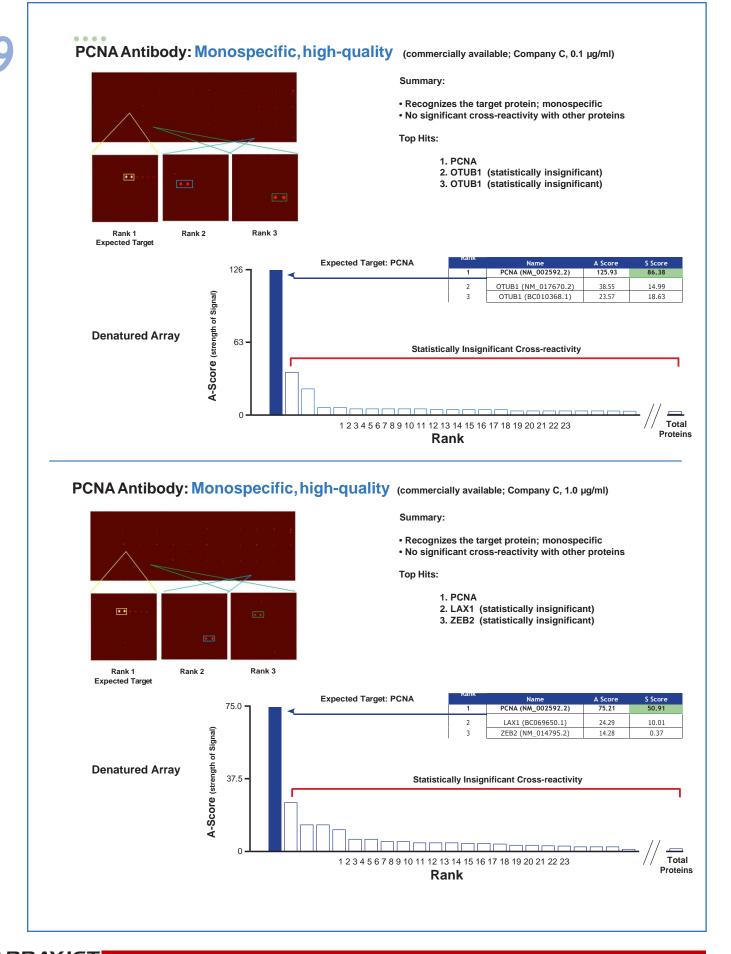
ANTIBODY CROSS-REACTIVITY TESTING USING THE HUPROT<sup>TM</sup> MICROARRAY

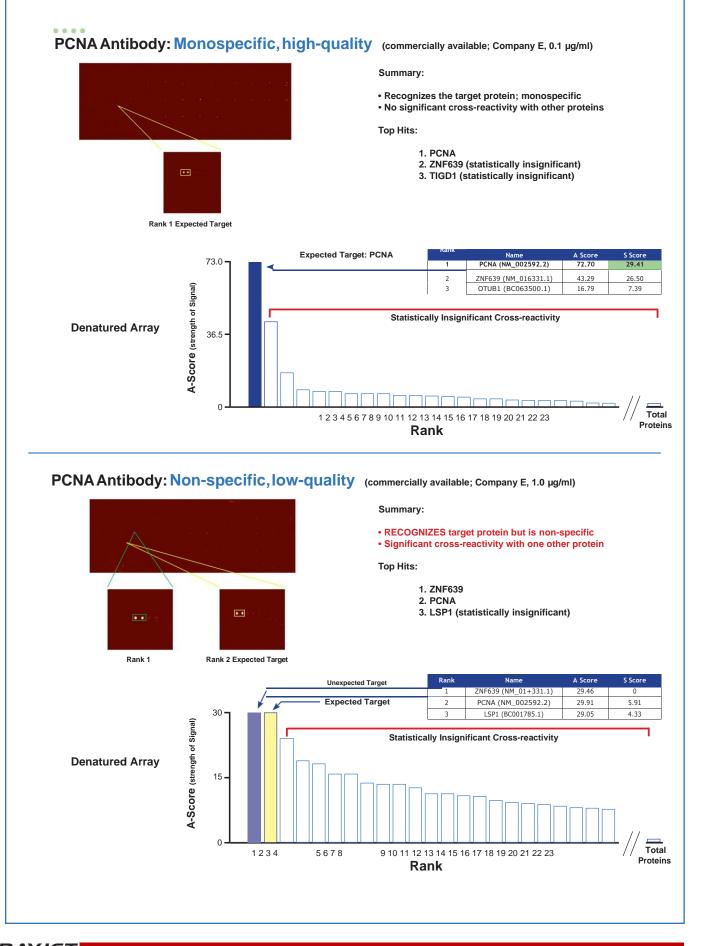


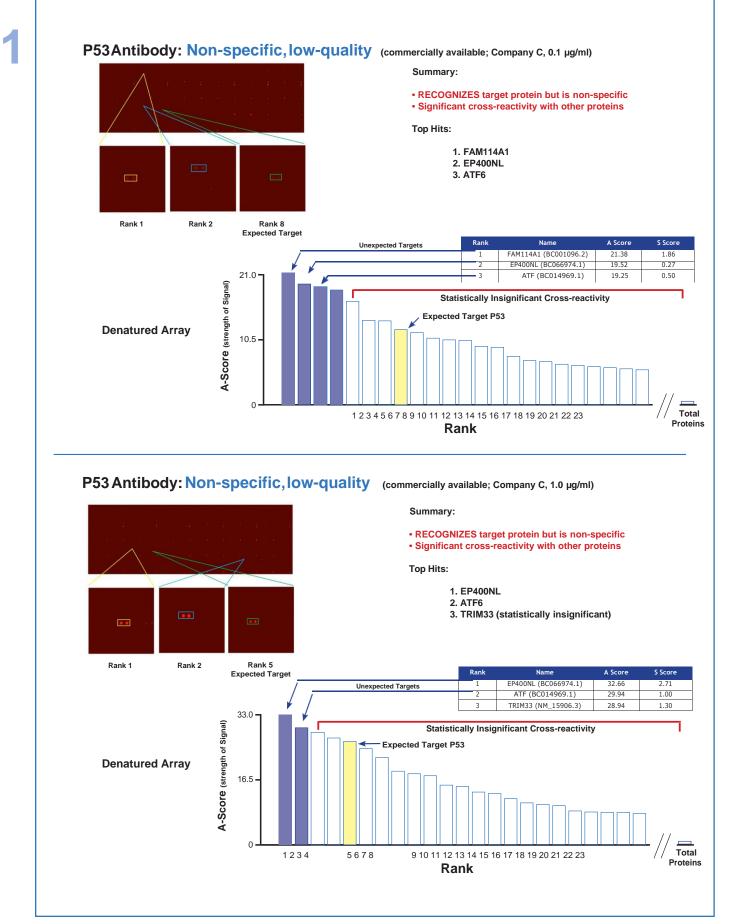


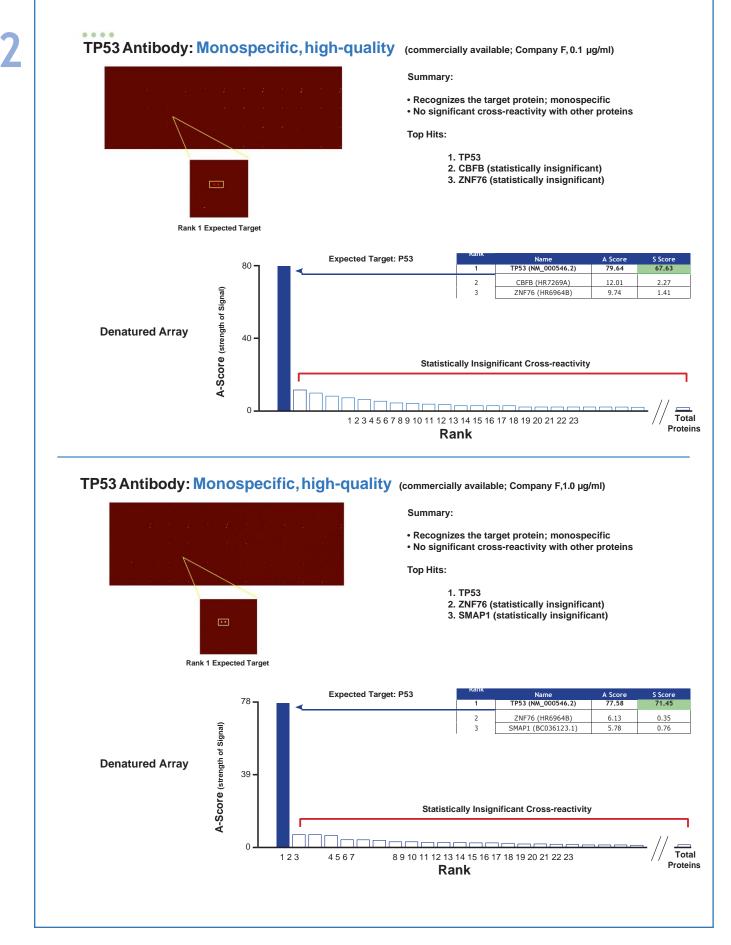
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ANTIBODY CROSS-REACTIVITY TESTING USING THE HUPROT<sup>TM</sup> MICROARRAY

## **Data Summary and Conclusion**

Company	Intended Target (IT)	Dilution µg/ml	Top Target	AScore	S Score*	Specific for IT	Array+	Page	Notes
ELISA Co	nfirmation								
Company C	BCL2	0.1	AMPH	28.94	1.75				
Company A	USF2	1.0	USF2	31.26	0.65	NO	N	p.5	ELISAconfirmationofHuProt <sup>™</sup> analysis;each antibodyisnon-specificfortheintended targe (IT)
Company G	KCNP2	1.0	RBKS	56.58	0.00			p.6	
Native Mid	croarrav								
Company C	PTEN			69.31	1.60	NO YES		p. 9	head-to-head comparison; Company B P TEN A bis also monospecificon denatured array (see below)
Company B		1.0	PTEN	85.10	60.06		Ν		
Company D	PTEN	0.1	ZNF175	6.53	0.27	NO	N	р. 10	monospecific for unintended target at higher concentration
		1.0	FIP1L1	24.45	12.29				
Company E	PCNA	0.1	PCNA	111.70	86.83	YES NO	N	p. 11-12	loss of monospecificity at higher concentra-tion; same results on denatured array (see below)
		1.0	GORASP1	26.76	0.31				
Company C	PCNA	0.1	PCNA	125.93	87.38	YES NO	Ν	p. 11-12	monospecific for unintended target a higher concentration
		1.0	OTUB1	74.59	7.66				
Company D	PCNA	0.1	FMN1	8.39	0.76	NO	Ν	p. 13	no specificity at either concentration
		1.0	ROPN1B	9.51	0.49				
Company C	TP53	0.1	C20orf77	7.22	2.03	ΝΟ	Ν	p. 14-15	no specificity at either concentration
		1.0		43.34	1.60				
Company F	TP53	0.1	C20orf77	57.86	9.55	NO	N	N p. 14-15	monospecific for unintended target at lower concentration; monospecific for
		1.0	TP53	130.54	127.06	YES		•	intended target at higher concentration
Denatured	d Microarray								
Company C	PTEN	0.1	PTEN	29.83	0.00		D	p. 16	no specificity on either array
		1.0	NOL3	29.91	0.00	NO			
Company B	PTEN	0.1		52.50	22.08		D	p. 17	high quality antibody as demonstrated on both native and denatured arrays
		1.0	PTEN	44.81	9.00	YE			
Company D									
		0.1	ZNF490	4 12	0 77	S			
Company D	PTEN	0.1	ZNF490 FAM150A	4.12	0.77 <b>50.02</b>	NO	D	p. 18	monospecific for unintended target at lower concentration
Company D	PTEN	1.0	ZNF490 FAM150A	55.15	50.02		D	p. 18	lower concentration
Company D Company C	PTEN	1.0 0.1		55.15 125.93	50.02 86.38	NO	D	p. 18 p. 19	lower concentration high quality antibody as demonstrated on denatured array; use with caution on nativ
		1.0 0.1 1.0	FAM150A PCNA	55.15 125.93 75.21	50.02 86.38 50.91	NO YE S			lower concentration high quality antibody as demonstrated on
		1.0 0.1 1.0 0.1	FAM150A PCNA PCNA	55.15 125.93 75.21 72.70	50.02 86.38 50.91 29.41	NO YE S YES			Iower concentration high quality antibody as demonstrated on denatured array; use with <b>caution</b> on nativ proteins (seeabove) lossofmonospecificityathigherconcentra- tion.
Company C	PCNA	1.0 0.1 1.0	FAM150A PCNA	55.15 125.93 75.21	50.02 86.38 50.91	NO YE S	D	p. 19	lower concentration high quality antibody as demonstrated on denatured array; use with caution on nativ proteins (seeabove)
Company C	PCNA	1.0 0.1 1.0 0.1 1.0 0.1	FAM150A PCNA PCNA ZNF639 FAM114A1	55.15   125.93   75.21   72.70   29.46   21.38	<b>50.02</b> <b>86.38</b> <b>50.91</b> <b>29.41</b> 0.00 1.86	NO YE S YES NO	D	p. 19	Iower concentration high quality antibody as demonstrated on denatured array; use with <b>caution</b> on nativ proteins (seeabove) lossofmonospecificityathigherconcentra- tion;
Company C Company E	PCNA	1.0 0.1 1.0 0.1 1.0	FAM150A PCNA PCNA ZNF639	55.15 125.93 75.21 72.70 29.46	50.02 86.38 50.91 29.41 0.00	NO YE S YES	D	p. 19 p. 20	Iower concentration   high quality antibody as demonstrated on denatured array; use with caution on nativ proteins (seeabove)   Iossofmonospecificityathigherconcentration; same results on native array (see above)
Company C Company E	PCNA	1.0 0.1 1.0 0.1 1.0 0.1	FAM150A PCNA PCNA ZNF639 FAM114A1	55.15   125.93   75.21   72.70   29.46   21.38	<b>50.02</b> <b>86.38</b> <b>50.91</b> <b>29.41</b> 0.00 1.86	NO YE S YES NO	D	p. 19 p. 20	high quality antibody as demonstrated on denatured array; use with <b>caution</b> on nativ proteins (seeabove) lossofmonospecificityathigherconcentra- tion; sameresultsonnativearray(seeabove)



#### Data Summary and Conclusion ... continued from page 23.

Our analysis of monoclonal antibodies shows that while some high quality, monospecific antibodies are commercially available, there are also many poorly-performing antibodies on the market that are not specific to their intended targets. At present, there is a groundswell from within the research community that advocates higher quality standards for commercial antibodies. Funding agencies such as the NIH have also started to adopthigherstandardsforcommercialantibodies that are to be selected for use in grant-funded research.

The new technical developments we described now make it possible to test monoclonal antibodies for cross-reactivity at an unprecedented level. We recommend that all commercial monoclonal antibodies made against human proteins be evaluated for binding specificity using human protein microarrays, such as the CDI HuProt<sup>™</sup> Array.

As HuProt<sup>™</sup> microarray analysis provides a global snapshot of monoclonal antibody cross-reactivity, this could serve as an authentication standard that is independent of the cell lines or tissues used.

For example, the recent NIH notice NOT-OD-15-103 (Enhancing Reproducibility through Rigor and Transparency, in effect for grants submitted after January, 252016), states:

#### Authentication of Key Biological and/or Chemical Resources

"The quality of the resources used to conduct research is critical to the ability to reproduce the results. NIH expects that key biological and/or chemical resources will be regularly authenticated to ensure their identity and validity for use in the proposed studies. Key biological and/or chemical resources may or may not be generated with NIH funds and: 1) may differ from laboratory to laboratory or over time; 2) may have qualities and/or qualifications that could influence the research data; and 3) are integral to the proposed research. These include, but are not limited to, cell lines, specialty chemicals, antibodies and otherbiologics.

There are not clear consensus guidelines on authenticating different types of resources, and NIH encourages the research community to inform the development of such guidelines. In the absence of clear guidelines, researchers should transparently report on what they have done to authenticate key resources, so that consensus can emerge."

HuProt<sup>™</sup> arrays have also been very useful in determining the best working concentrations for a given antibody, as antibodies sometimes show non-specific binding when used at sub-optimal concentrations. Some antibodies, when used at high concentrations, may bind in a non-specific fashion; such antibodies may need to be diluted in order to show specific binding to the target. In contrast, other antibodies may need to be used at a high concentration in order to show any binding at all; in such cases, monospecificity will be of paramount importance.

HuProt<sup>™</sup> arrays are also very useful for analyzing the cross-reactivity of antibodies to both native and denatured forms of the target proteins. Antibodies that bind to folded proteins often function best for IP, ICC and IHC, as well as for ChIP and ChIP-seq applications. In contrast, antibodies that recognize linear epitopes (denatured protein) are usually best for western blot ap- plications. Experimental results obtained from many of the commercial monoclonal antibodies tested are simply not consistent with the manufacturers' recommendations. By evaluating antibodies on both denatured and native microarrays, it is possible to determine in advance the applications to which they are best suited prior to distribution.