



# **Protein dynamics in response to genotoxic drugs regulated by proteasome system**

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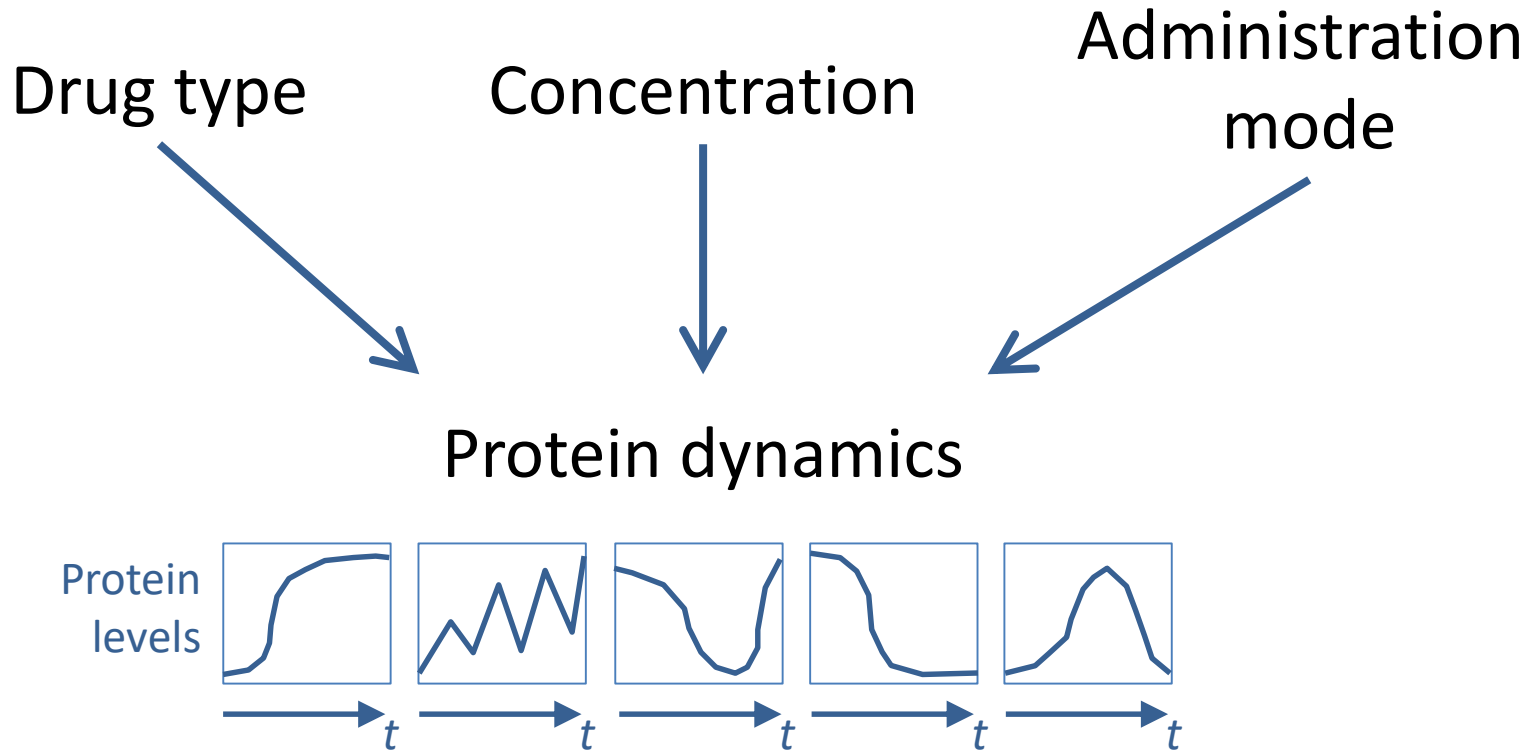
# **COI Disclosure Information**

**Kohei Kume**

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**I have no financial relationships to disclose.**

# Protein dynamics is differentially altered by various drug treatments



Little is known about systematic methods for multidimensional protein dynamics.

## Systematic Protein Level Regulation via Degradation Machinery Induced by Genotoxic Drugs

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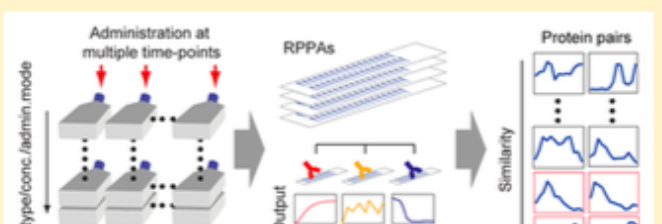
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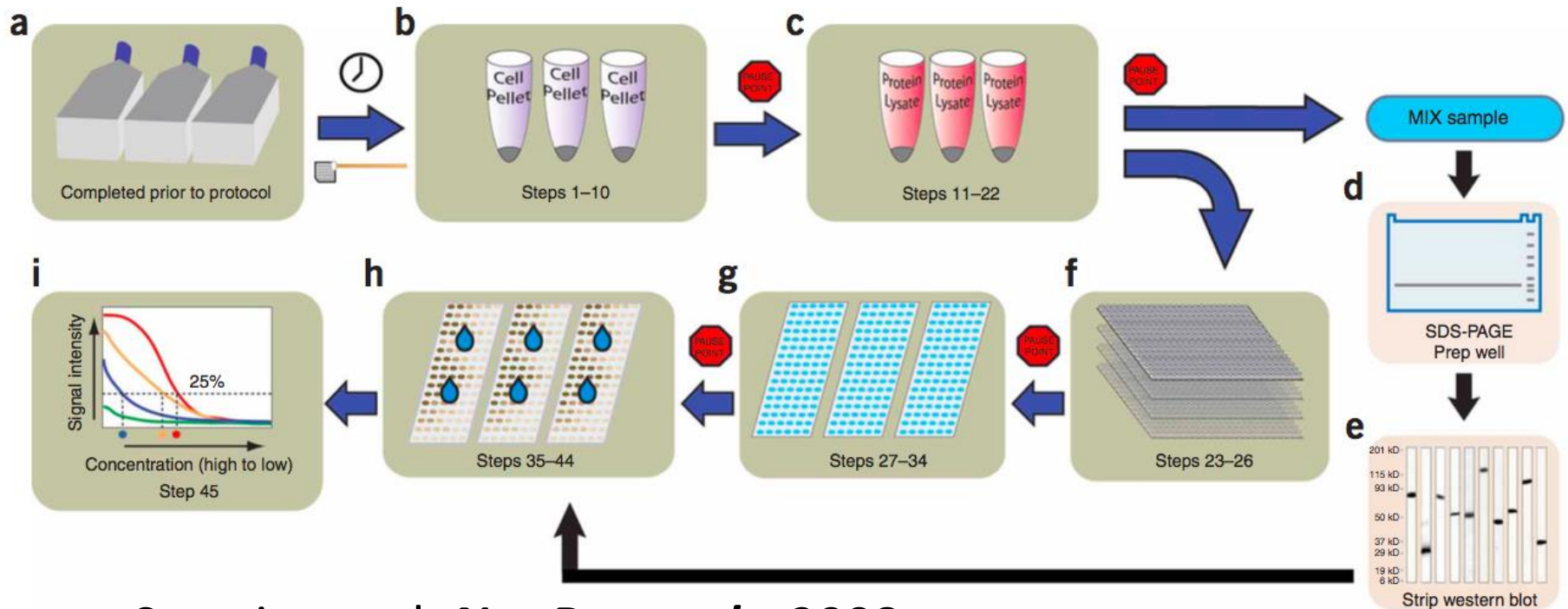
<sup>○</sup>National Institutes of Health (NIH) Library, Division of Library Services, Office of Research Services, National Institutes of Health, Bethesda, Maryland 20892, United States

### **S** Supporting Information

**ABSTRACT:** In this study we monitored protein dynamics in response to cisplatin, 5-fluorouracil, and irinotecan with different concentrations and administration modes using “reverse-phase” protein arrays (RPPAs) in order to gain comprehensive insight into the protein dynamics induced by genotoxic drugs. Among 666 protein time-courses, 38% exhibited an increasing trend, 32% exhibited a steady decrease, and 30% fluctuated within 24 h after



# Reverse-phase protein arrays (RPPAs)



Spurrier et al. *Nat Protocols*, 2008

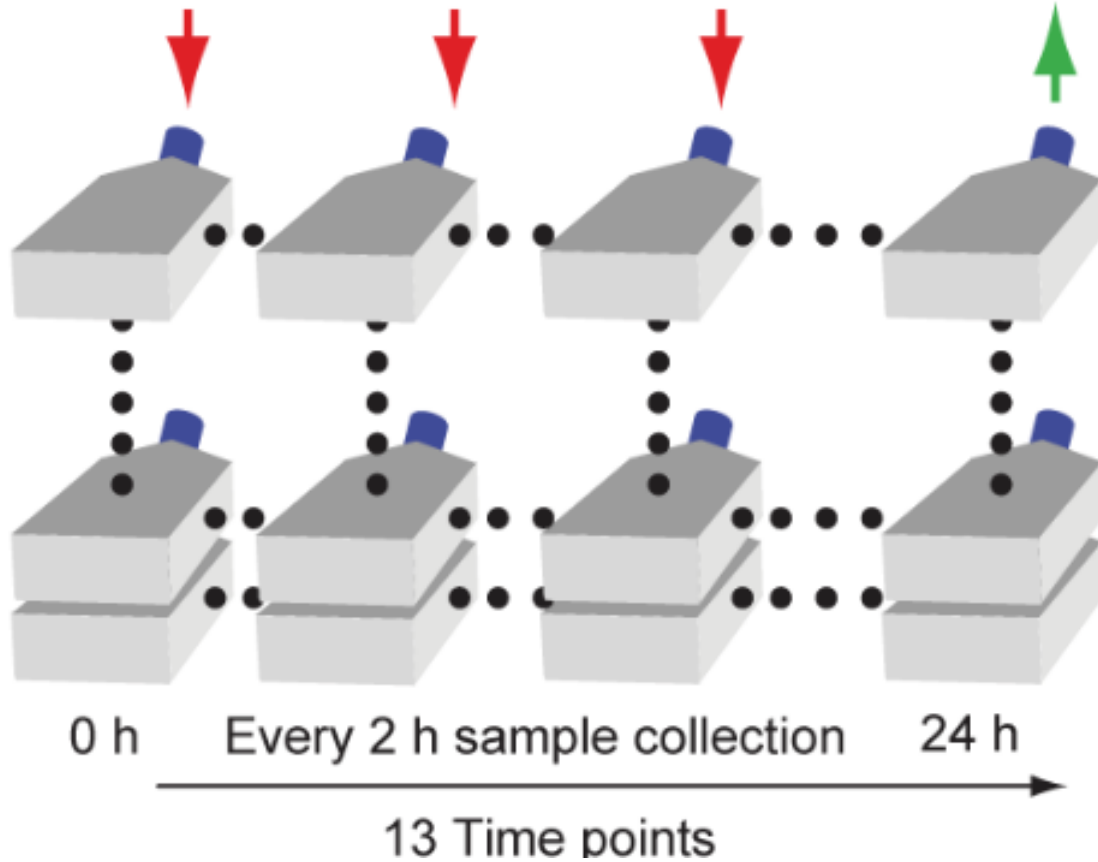
Nishizuka SS, inventor; Japanese patent 2010-081879

A micro-scale dot blot that can monitor protein levels across >10,000 data points.

# Monitoring protein dynamics in response to genotoxic drugs using RPPA

Drug administration  
at multiple time-points

Sample collection  
for lysate preparation



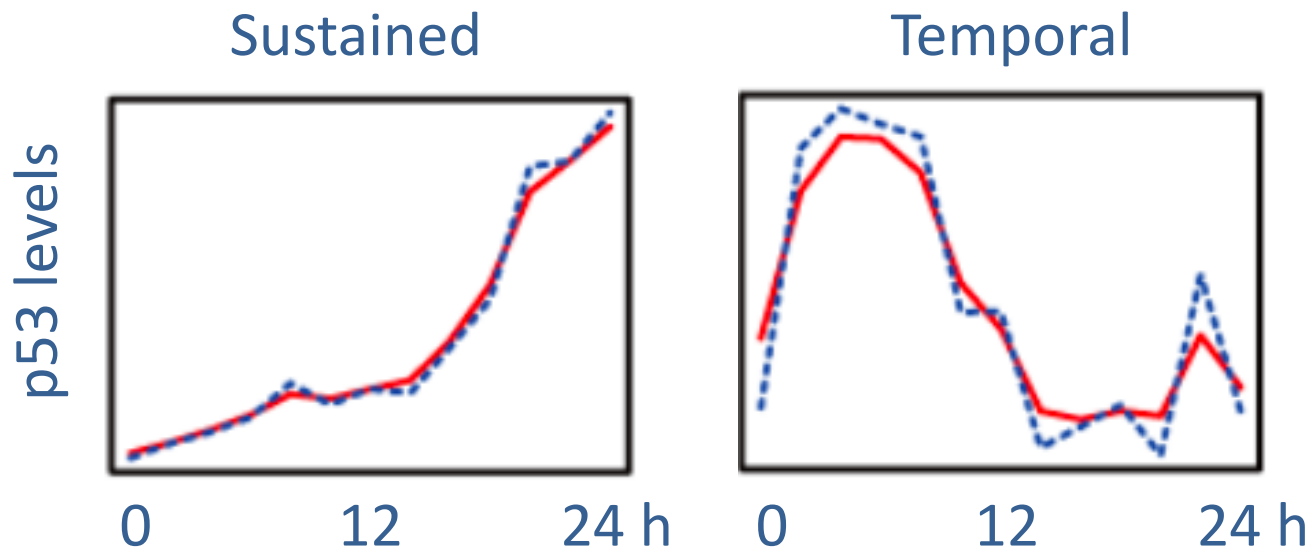
18 Conditions

(  
3 Drug types  
3 Drug concentrations  
2 Administration modes

3 Biological replicates

54 Sample sets

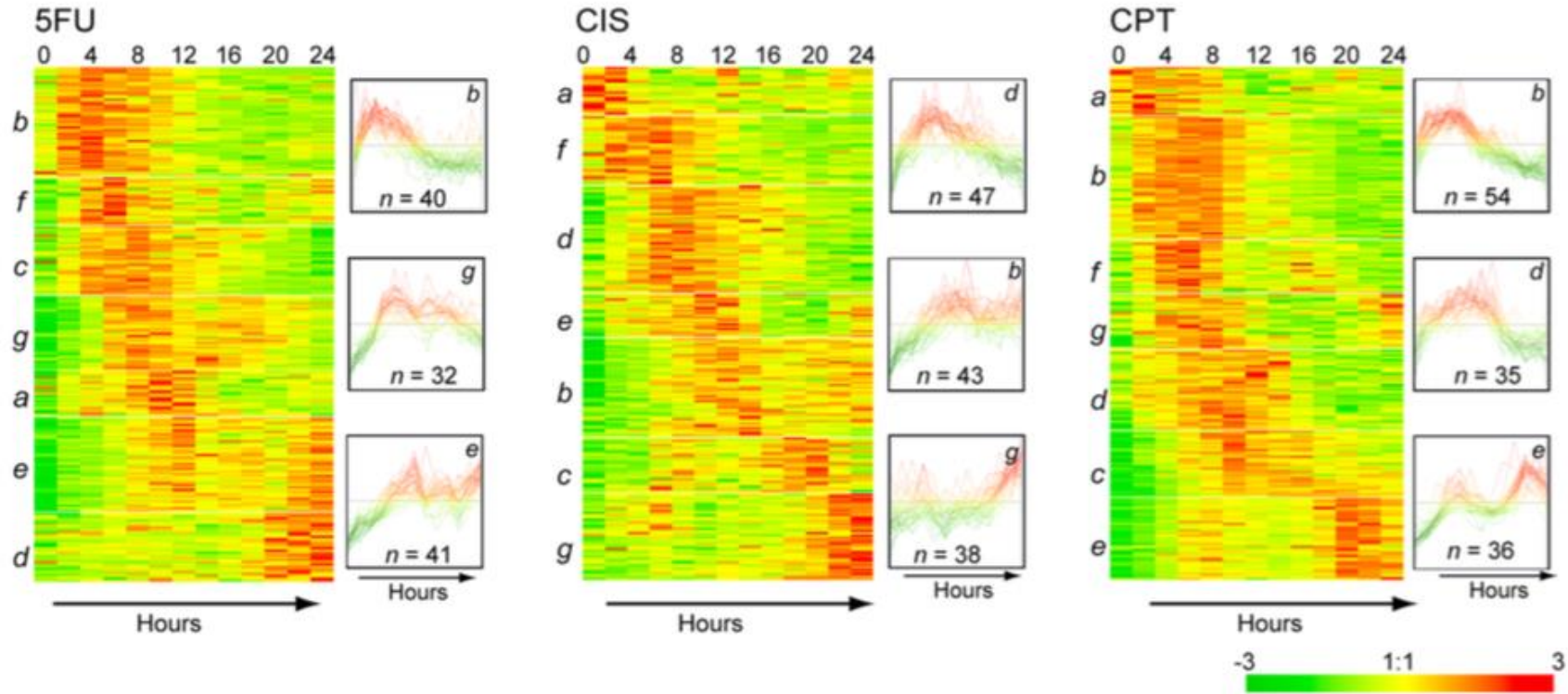
**The genotoxic stress response was immediately reset following drug removal.**



RPPA system is suitable for evaluating the protein dynamics of drug response.

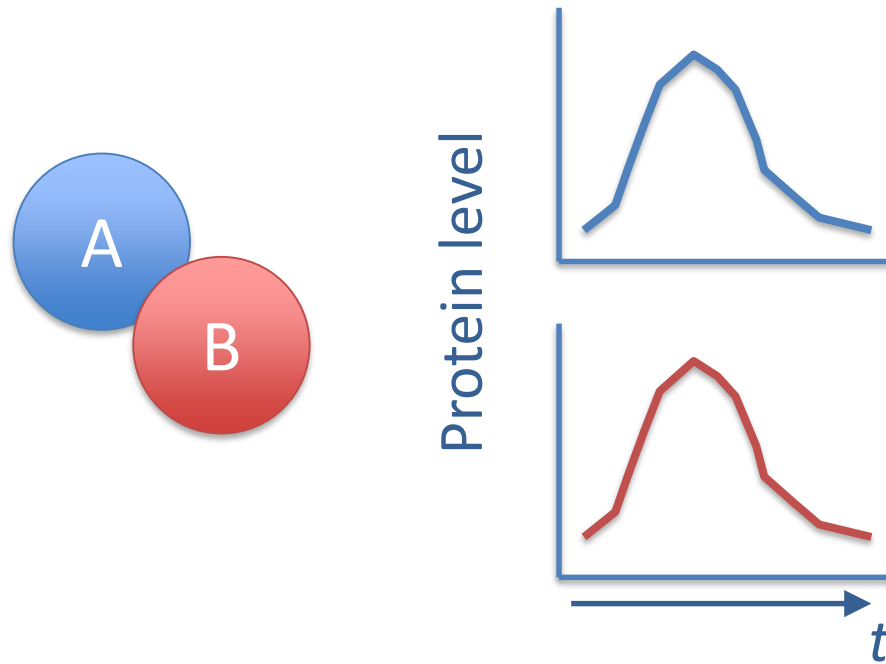
# 666 protein dynamics for 37 proteins over 24 h

222 dynamics of  
37 proteins



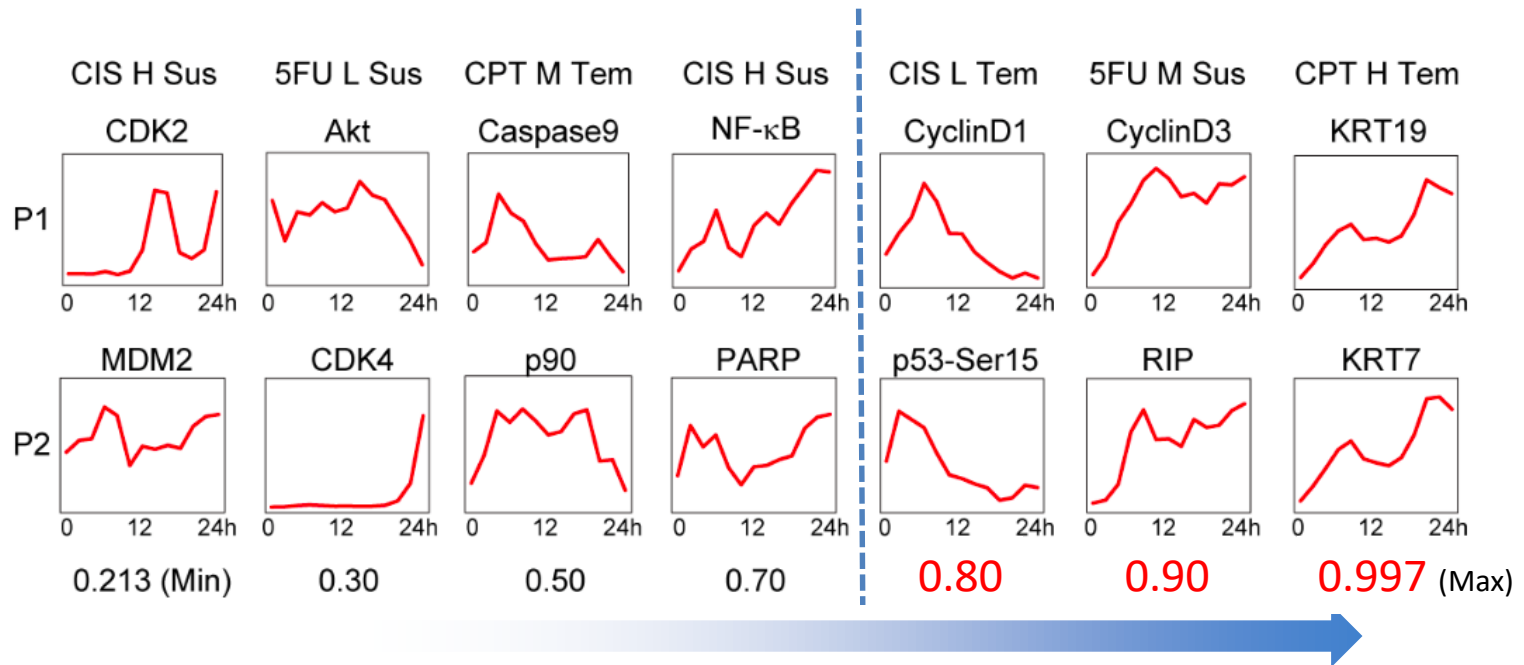


# Similarity measurement of protein dynamics using $dCor$

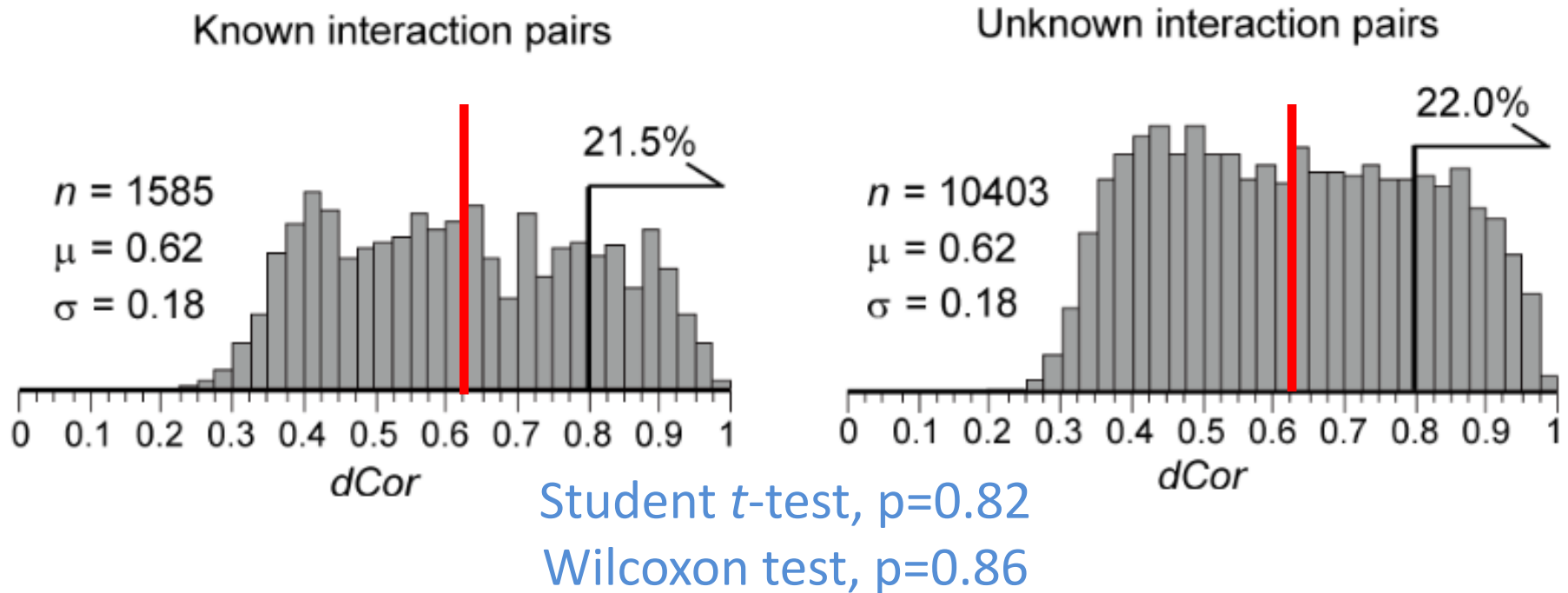


$$dCor(X, Y) = \frac{dCov(X, Y)}{\sqrt{dCov(X, Y) dCov(X, Y)}}$$

# Similarity measurement of protein dynamics using distance correlation, $dCor$

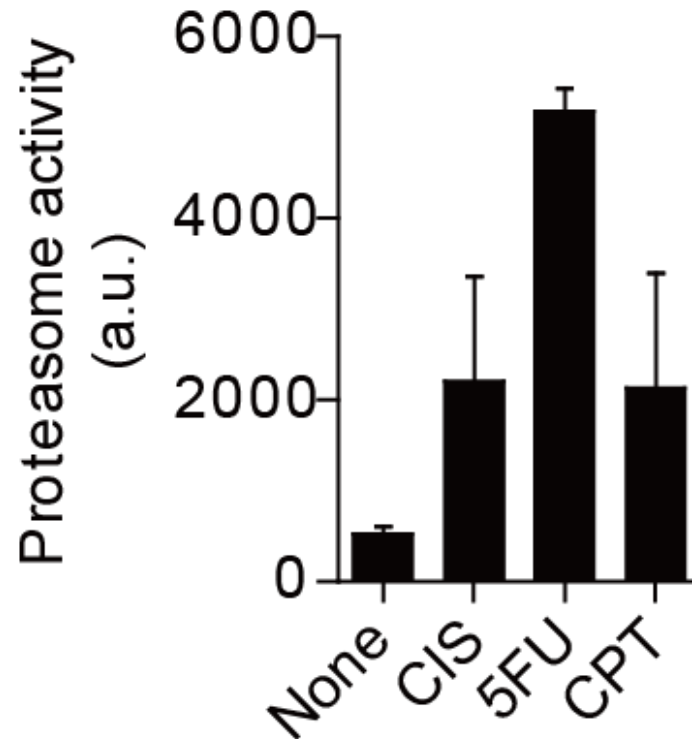


# No significant difference between protein pairs of known and unknown interactions



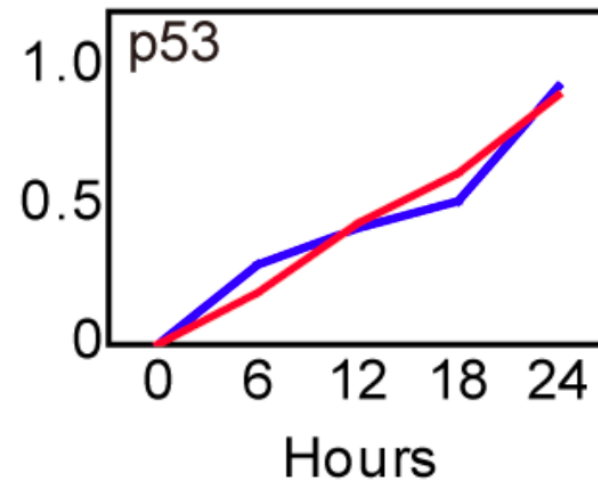
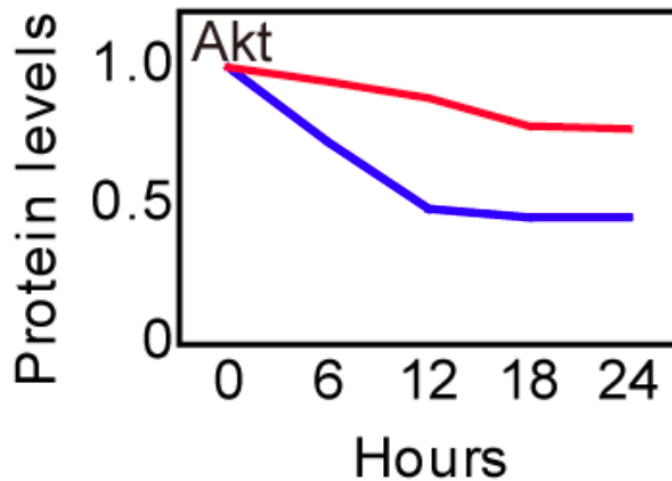
Functionally distinct proteins may be regulated by common degradation machinery.

# Proteasome activity was increased in response to genotoxic drugs

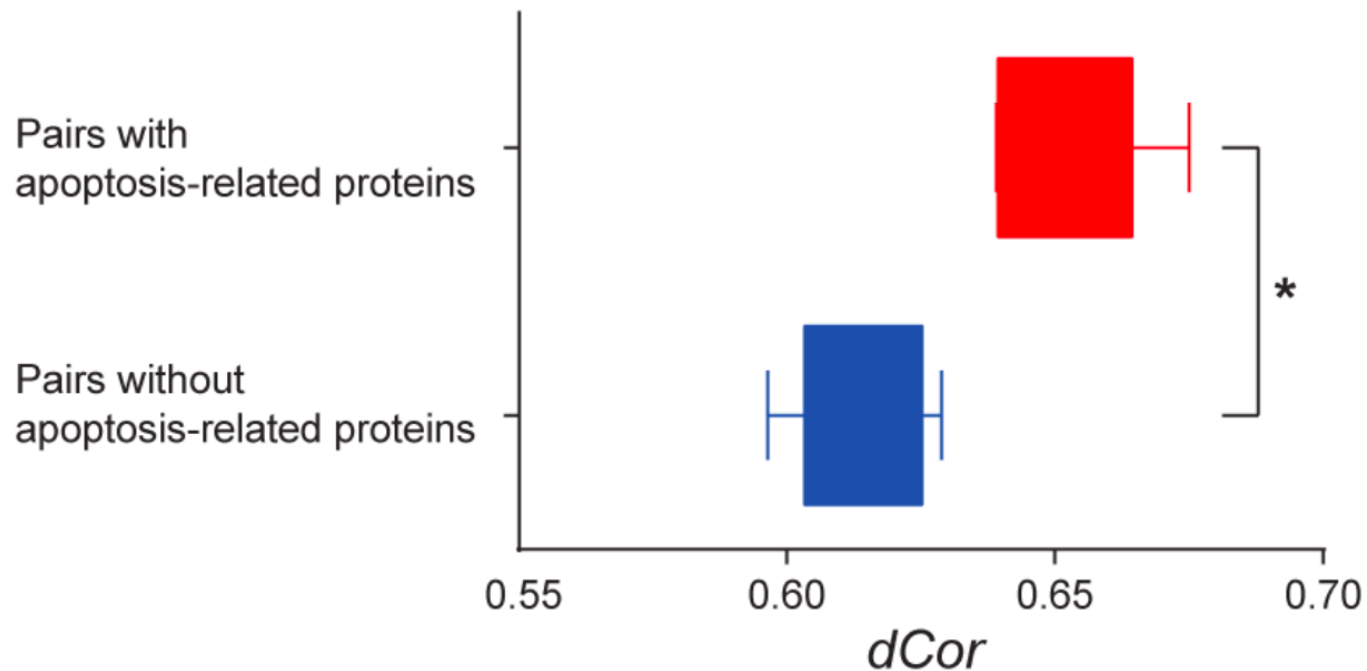


# Protein dynamics altered by a proteasome inhibitor

— 5FU — 5FU/MG132



# *dCor* in protein pairs with or without apoptosis-related proteins



The average *dCor* of pairs that had at least one apoptosis-related protein was significantly higher than those without the apoptosis-related proteins.

# Summary

- Protein levels could be changed immediately after drug administration.
- Functionally distinct proteins may be regulated by common degradation machinery.
- Apoptosis-related degradation machinery may play a key role in systematic protein level regulation.

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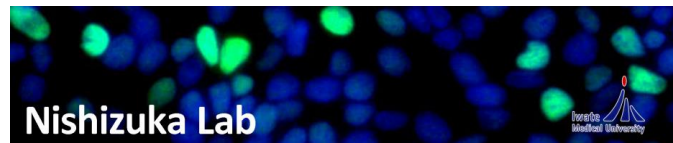
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