

## L6 – Engineering Transcriptional Responses with a Chemical Probe

February 28, 2019



*D. melanogaster*

**13,600**



*C. elegans*

**19,500**



*Homo sapiens*

**21,000**



*Oryza sativa*

**45,000**



*Zea mays*

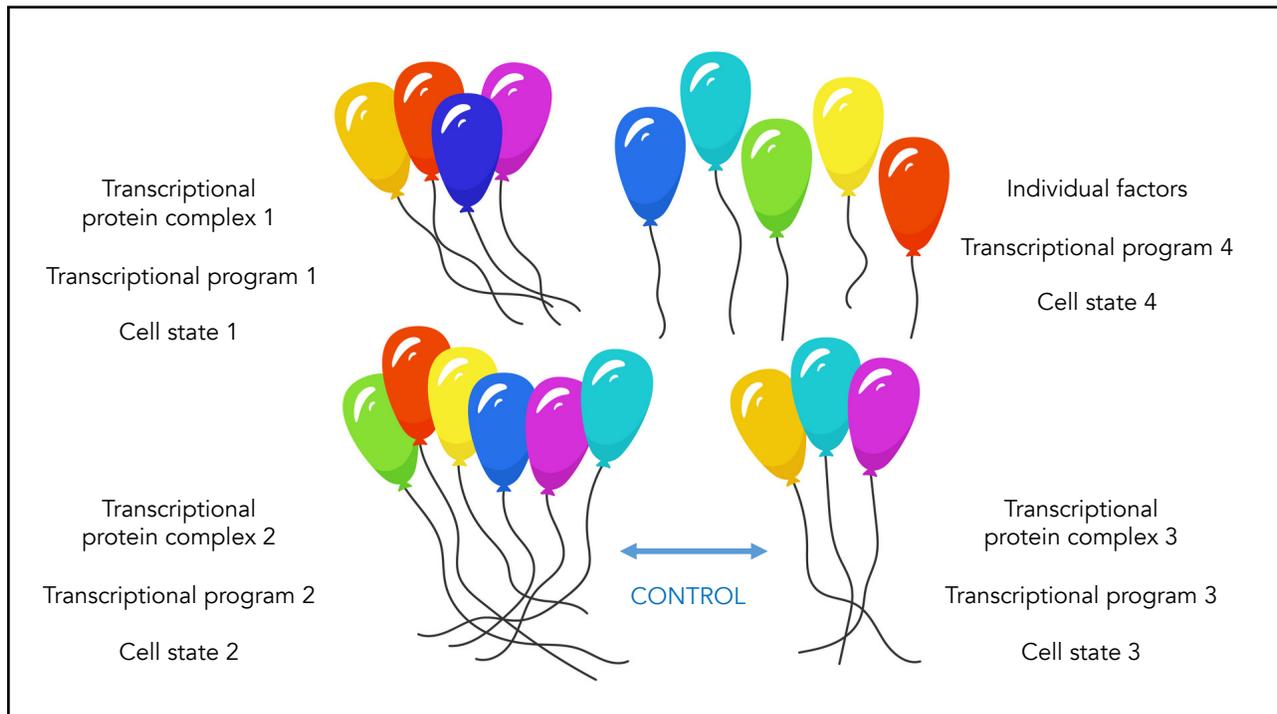
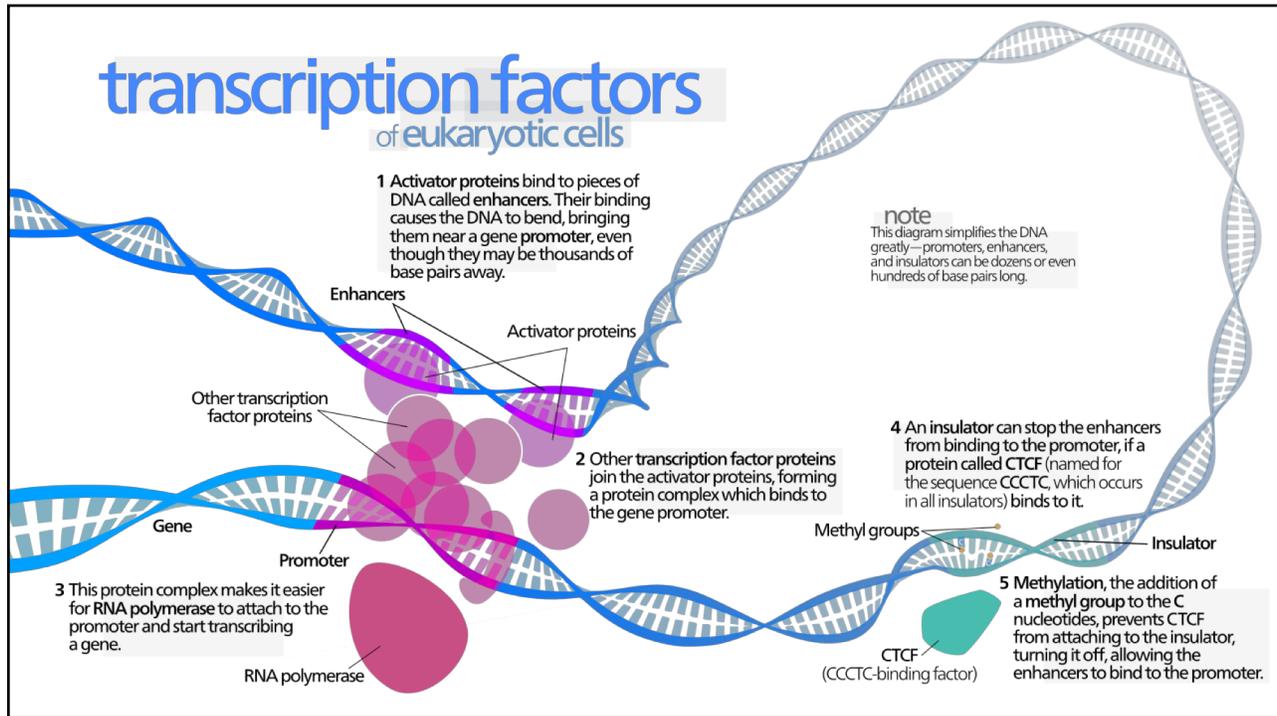
**50,000**

alternative  
splicing

post-translational  
processing

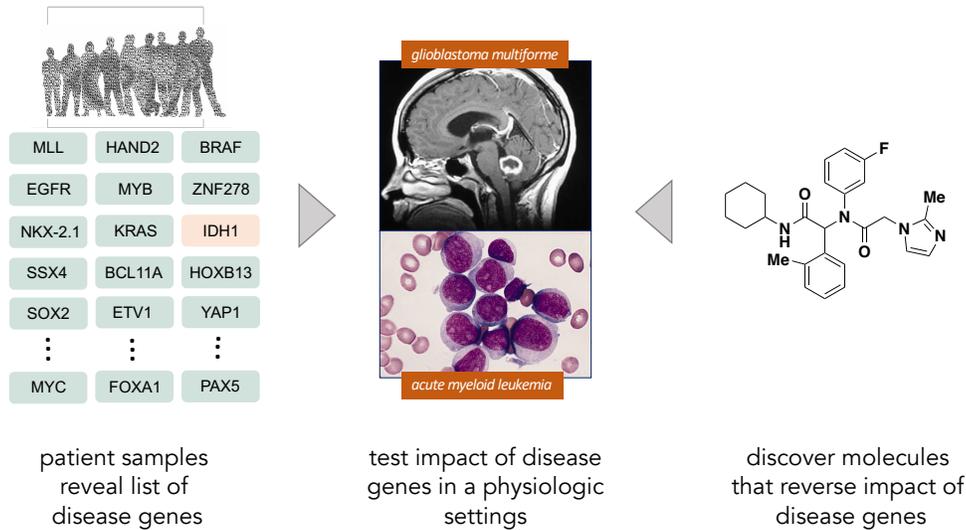


>100,000 proteins of unknown structure or function  
How do these parts give rise to organismal complexity?



## Therapeutically-driven probe discovery

target cause of disease revealed by human genetics



## Transcription factors

implicated in a broad spectrum of disease

<i>AVGR8</i>	central corneal thickness	<i>MEIS1</i>	restless leg syndrome
<i>BCL11A</i>	$\beta$ -hemoglobin disorders	<i>MLXIPL</i>	coronary artery disease
<i>CAMTA1</i>	episodic memory deficit	<i>NFATC2</i>	T1D
<i>ELF1</i>	systemic lupus erythematosus	<i>NOTCH2</i>	T2D
<i>ETS1</i>	systemic lupus erythematosus	<i>PBX4</i>	coronary artery disease
<i>GATA3</i>	periodontitis	<i>PPARG</i>	T2D
<i>GTF2H1</i>	amyloidosis	<i>RELA</i>	rheumatoid arthritis
<i>HHEX-IDE</i>	T2D	<i>RFX4</i>	Parkinson's disease
<i>HIF2A</i>	RCC	<i>SP7</i>	BMD
<i>HNF1B</i>	T2D	<i>STAT3</i>	various AI disorders and cancers
<i>HPB1</i>	osteoarthritis	<i>STAT4</i>	systemic lupus erythematosus
<i>IRF5</i>	various AI disorders	<i>TCF4</i>	schizophrenia, corneal dystrophy
<i>IRF8</i>	MS	<i>TCF7L2</i>	T2D
<i>LBXCOR1</i>	restless leg syndrome	<i>THAP1</i>	early-onset torsion dystonia
<i>MAF</i>	early-onset obesity	<i>ZNF469</i>	central corneal thickness
<i>MECP2</i>	autism	<i>ZNF804A</i>	schizophrenia

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# Transcription factors

misregulation in cancer

## amplified TF cancer genes

<i>JUN</i>	sarcoma
<i>LMO1</i>	T-ALL, neuroblastoma
<i>MITF</i>	melanoma
<i>MYC</i>	various cancers
<i>MYCL1</i>	small cell lung
<i>MYCN</i>	neuroblastoma
<i>NKX2-1</i>	follicular lymphoma
<i>REL</i>	Hodgkin lymphoma
<i>SOX2</i>	NSCLC, esophageal SCC

## germline mutated TF cancer genes

<i>HNF1</i>	HCC, hepatic adenoma
<i>LMO1</i>	neuroblastoma
<i>PHOX2B</i>	neuroblastoma
<i>RB1</i>	various cancers
<i>SMAD4</i>	gastrointestinal polyps
<i>SMARCB1</i>	malignant rhabdoid
<i>SUFU</i>	medulloblastoma
<i>TP53</i>	various cancers
<i>WT1</i>	Wilms tumor

## TF cancer genes with frameshift mutations

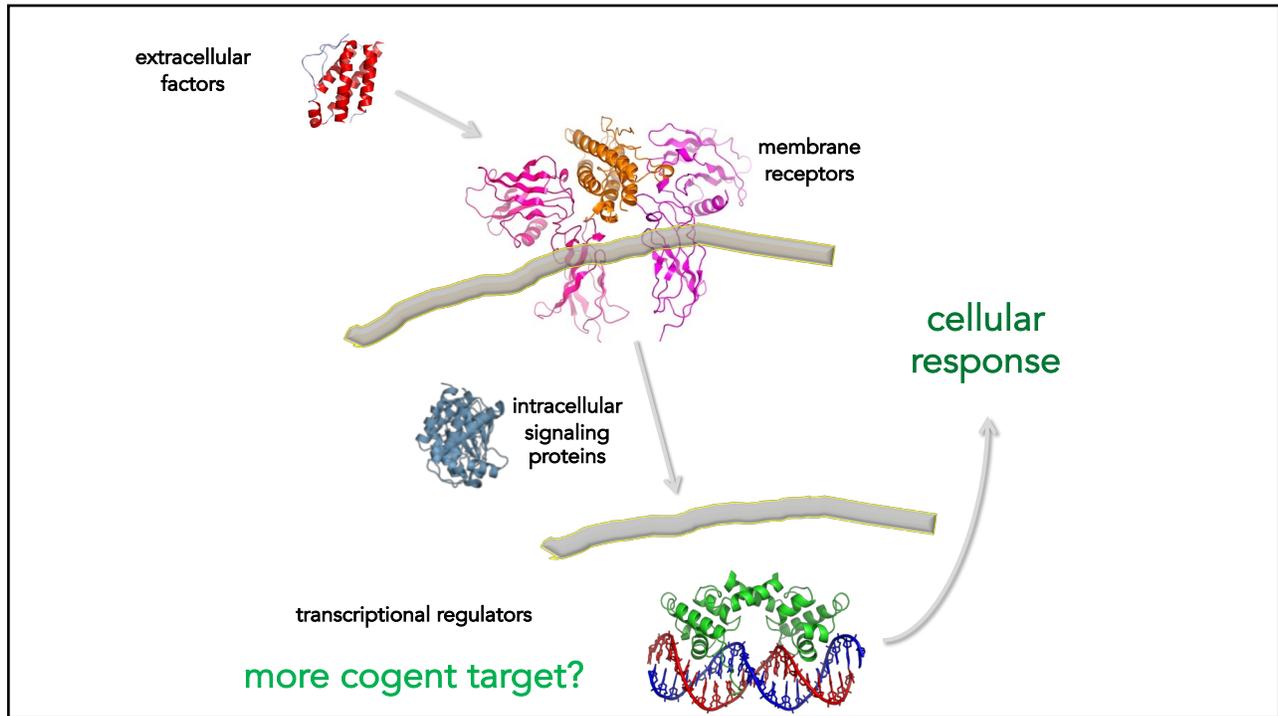
<i>ARID1A</i>	clear cell ovarian carcinoma, RCC
<i>ASXL1</i>	MDS, CMML
<i>ATRX</i>	pancreatic neuroendocrine
<i>CEBPA</i>	AML, MDS
<i>CREBBP</i>	ALL, AML, DLBCL, B-NHL
<i>DAXX</i>	pancreatic neuroendocrine
<i>EP300</i>	various cancers
<i>GATA1</i>	megakaryoblastic leukemia
<i>GATA3</i>	breast
<i>HNF1</i>	HCC, hepatic adenoma
<i>HRPT2</i>	parathyroid adenoma
<i>NOTCH2</i>	marginal zone lymphoma, DLBCL
<i>PBRM1</i>	breast, clear cell renal carcinoma
<i>PHOX2B</i>	neuroblastoma
<i>PRDM1</i>	DLBCL
<i>RB1</i>	various cancers
<i>SMAD4</i>	gastrointestinal polyps
<i>SMARCA4</i>	NSCLC
<i>SMARCB1</i>	malignant rhabdoid
<i>SUFU</i>	medulloblastoma
<i>TP53</i>	various cancers
<i>WT1</i>	Wilms tumor

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## somatically mutated TF cancer genes

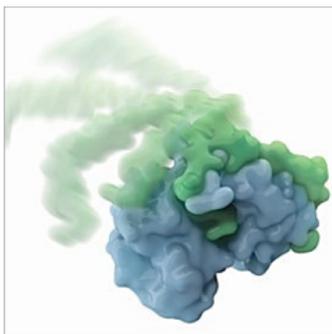
<i>AFF4</i>	ALL	<i>IRF4</i>	MM	<i>POU2AF1</i>	NHL
<i>ARNT</i>	AML	<i>JAZF1</i>	endometrial stromal tumors	<i>POU5F1</i>	sarcoma
<i>ATF1</i>	melanoma, AFH	<i>JUN</i>	sarcoma	<i>PPARG</i>	follicular thyroid
<i>BTG1</i>	BCLL	<i>KLF6</i>	prostate, glioma	<i>PRDM1</i>	DLBCL
<i>CBFB</i>	AML	<i>LAF4</i>	ALL	<i>PRDM16</i>	MDS, AML
<i>CDX2</i>	AML	<i>LMO1</i>	T-ALL, neuroblastoma	<i>RARA</i>	APL
<i>CEBPA</i>	AML, MDS	<i>LMO2</i>	T-ALL	<i>RB1</i>	various cancers
<i>CIC</i>	soft tissue sarcoma	<i>LMO2</i>	lipoma, leukemia	<i>REL</i>	Hodgkin lymphoma
<i>CIITA</i>	PMBL, Hodgkin lymphoma	<i>LPP</i>	T-ALL	<i>RUNX1</i>	AML, pre B-ALL
<i>CREB1</i>	clear cell sarcoma	<i>LYL1</i>	MM	<i>RUNXP2</i>	AML
<i>CREBBP</i>	ALL, AML, DLBCL, B-NHL	<i>MAFB</i>	salivary gland	<i>SMAD4</i>	colorectal, pancreatic
<i>CRT3</i>	salivary gland mucoepidermoid	<i>MAML2</i>	MDS, AML	<i>SMARCA4</i>	NSCLC
<i>DUX4</i>	soft tissue sarcoma	<i>MDS1</i>	MDS	<i>SMARCB1</i>	malignant rhabdoid
<i>EBF1</i>	lipoma	<i>MDS2</i>	salivary gland	<i>SOX2</i>	NSCLC, esophageal SCC
<i>ELF4</i>	AML	<i>MECT1</i>	head-neck squamous cell, renal	<i>SS18</i>	synovial sarcoma
<i>ELK4</i>	prostate	<i>MHC2TA</i>	melanoma	<i>SS18L1</i>	synovial sarcoma
<i>ELK5</i>	papillary thyroid	<i>MITF</i>	AML	<i>SSX1</i>	synovial sarcoma
<i>EP300</i>	various cancers	<i>MKL1</i>	AML	<i>SSX2</i>	synovial sarcoma
<i>ERG</i>	AML, Ewing sarcoma, prostate	<i>MLF1</i>	AML	<i>SSX4</i>	synovial sarcoma
<i>ETV1</i>	Ewing sarcoma, prostate	<i>MLL1</i>	ALL	<i>SUFU</i>	medulloblastoma
<i>ETV4</i>	Ewing sarcoma, prostate	<i>MLL2</i>	ALL, colorectal	<i>SUZ12</i>	endometrial stromal tumors
<i>ETV5</i>	prostate	<i>MLL3</i>	ALL, breast cancers	<i>TAF15</i>	ALL, EMC
<i>ETV6</i>	various cancers	<i>MLL7</i>	AML	<i>TAL1</i>	lymphoblastic leukemia
<i>EV11</i>	AML, CML	<i>MLL7</i>	ALL	<i>TAL2</i>	T-ALL
<i>EWSR1</i>	Ewing sarcoma, ALL	<i>MYB</i>	adenoid cystic sarcoma	<i>TCEA1</i>	salivary adenoma
<i>FEV</i>	Ewing sarcoma	<i>MYC</i>	various cancers	<i>TCF12</i>	EMC
<i>FLI1</i>	Ewing sarcoma	<i>MYCL1</i>	small cell lung	<i>TCF3</i>	pre B-ALL
<i>FOXL2</i>	ovarian	<i>MYCN</i>	neuroblastoma	<i>TFE3</i>	renal, alveolar soft sarcoma
<i>FOXO1A</i>	alveolar rhabdomyosarcomas	<i>NCOA1</i>	alveolar rhabdomyosarcoma	<i>TFEB</i>	renal (child epithelioid)
<i>FOXO3A</i>	AL	<i>NCOA2</i>	AML	<i>TFPI</i>	pre B-ALL
<i>FOXP1</i>	ALL	<i>NCOA4</i>	papillary thyroid	<i>THRAP3</i>	aneurysmal bone cysts
<i>GATA1</i>	megakaryoblastic leukemia	<i>NF1B</i>	lipoma, ACC	<i>TIF1</i>	APL
<i>GATA2</i>	AML	<i>NFKB2</i>	B-NHL	<i>TLX1</i>	T-ALL
<i>GATA3</i>	breast	<i>NKX2-1</i>	NSCLC	<i>TLX3</i>	T-ALL
<i>HLF</i>	ALL	<i>NOTCH1</i>	T-ALL	<i>TP53</i>	various cancers
<i>HIXB9</i>	AML	<i>NOTCH2</i>	DLBCL, marginal zone lymphoma	<i>TRIM27</i>	papillary thyroid
<i>HMGGA1</i>	various cancers	<i>NRF2</i>	EMC	<i>TRIM33</i>	papillary thyroid
<i>HMGGA2</i>	various cancers	<i>OLIG2</i>	NSCLC, HNSCC	<i>TSHR</i>	toxic thyroid adenoma
<i>HOXA11</i>	CML	<i>PAX3</i>	T-ALL	<i>WT1</i>	Wilms tumor
<i>HOXA13</i>	AML	<i>PAX5</i>	alveolar rhabdomyosarcoma	<i>ZNF145</i>	APL
<i>HOXA9</i>	AML	<i>PAX7</i>	NHL	<i>ZNF198</i>	MFD, NHL
<i>HOXC11</i>	AML	<i>PAX8</i>	alveolar rhabdomyosarcoma	<i>ZNF278</i>	Ewing sarcoma
<i>HOXC13</i>	AML	<i>PBX1</i>	NHL	<i>ZNF331</i>	follicular thyroid adenoma
<i>HOXD13</i>	AML	<i>PHOX2B</i>	alveolar rhabdomyosarcoma	<i>ZNF384</i>	ALL
<i>HOXD13</i>	AML	<i>PLAG1</i>	follicular thyroid	<i>ZNF521</i>	ALL
<i>HNF1</i>	HCC	<i>PMX1</i>	pre B-ALL	<i>ZNF9</i>	aneurysmal bone cysts
<i>HRPT2</i>	HCC		neuroblastoma	<i>ZNFN1A1</i>	'ALL, DLBCL
<i>IKZF1</i>	parathyroid adenoma		salivary adenoma		
	ALL		AML1		

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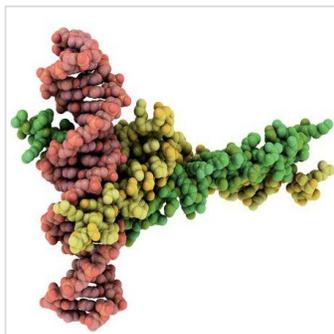


## A complex task?

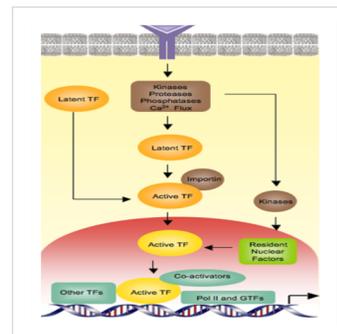
transcription factors are the prototype of an 'undruggable' target



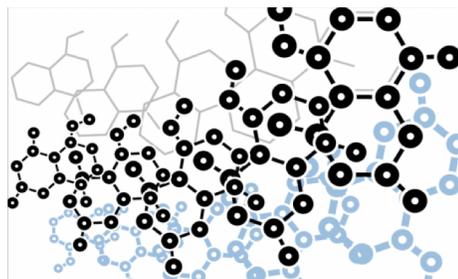
disordered when isolated from binding partners



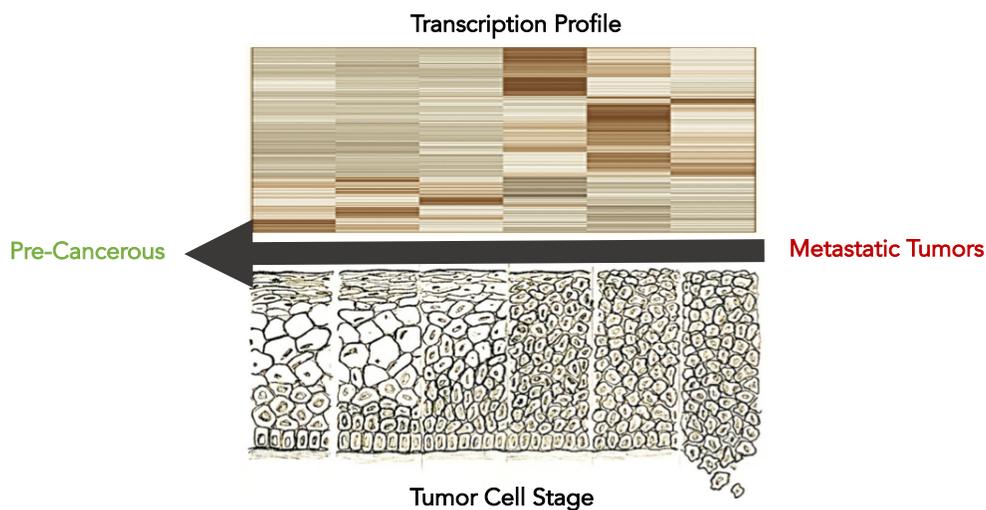
DNA-binding domains lack obvious pockets



transit to reach resident nuclear factors



Can we build general and systematic platforms for developing **chemical probes** for transcriptional regulators?



Can we tune dysregulated gene expression programs and impact cell state?

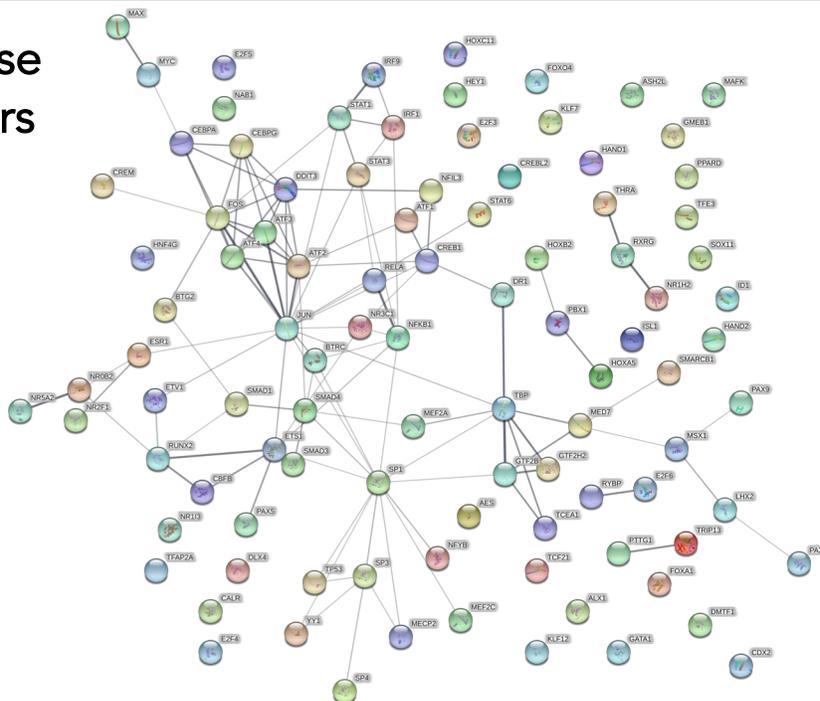
## Profiling 100 diverse transcription factors

commercially available  
purified, His-tagged

145 InterPro domains  
e.g. bZip, Znf\_C2H2, Fbox, Ets, etc.

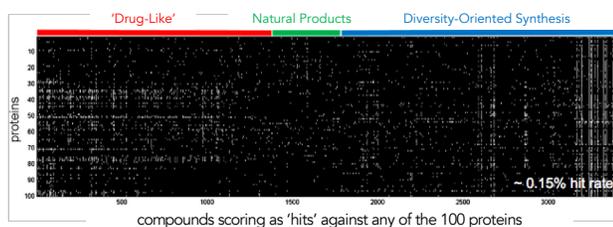
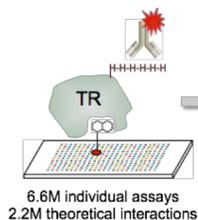
>500 GO terms  
e.g. nuclear, chromatin remodeling,  
basal transcription, etc.

>100 KEGG pathways  
e.g. Wnt signaling, chronic myeloid  
leukemia, circadian entrainment, etc.

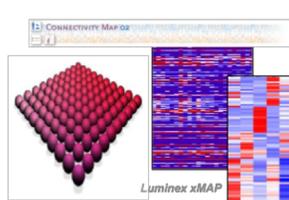
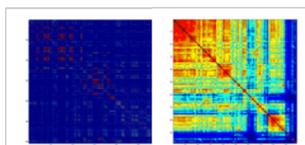


Clemons et al., PNAS 107, 18787-18792, 2010

## '100 Transcription Factor' SMM Screen

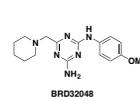
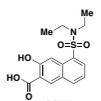
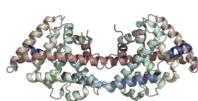


Clemons et al., PNAS 107, 18787-18792, 2010  
Clemons et al., PNAS 108, 6817-6822, 2011



HT-gene expression studies

Chemical stabilizer of Small Heterodimer  
Partner Yang et al., Mol Cancer Ther, 15,  
2294-2301, 2016



Chemical inhibitor of ETV1  
Pop et al., Mol Cancer Ther 13,  
1492-1502, 2014

characterize and optimize probes for individual TFs

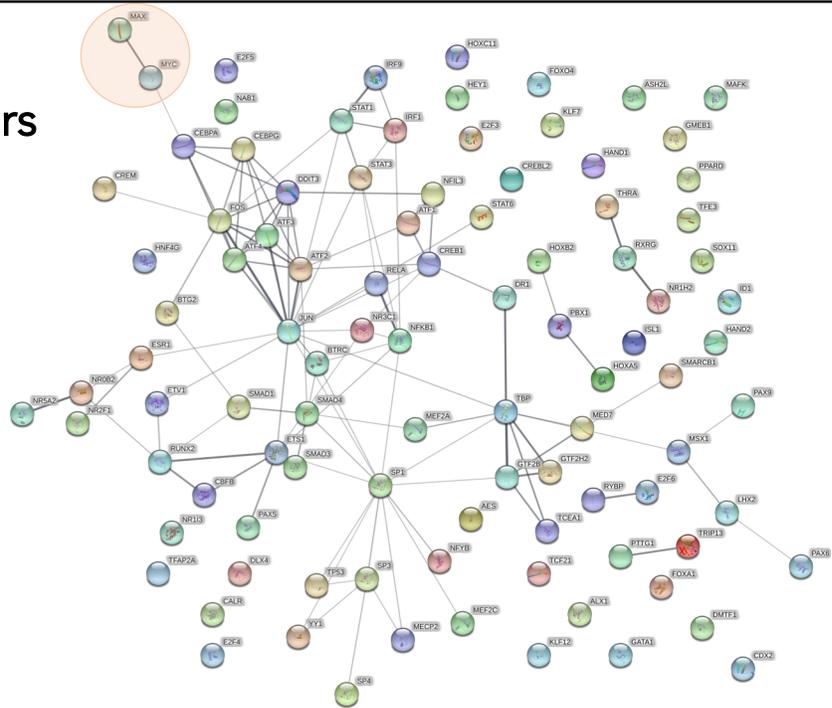
# 100 diverse transcription factors

commercially available  
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145 InterPro domains  
e.g. bZip, Znf\_C2H2, Fbox, Ets, etc.

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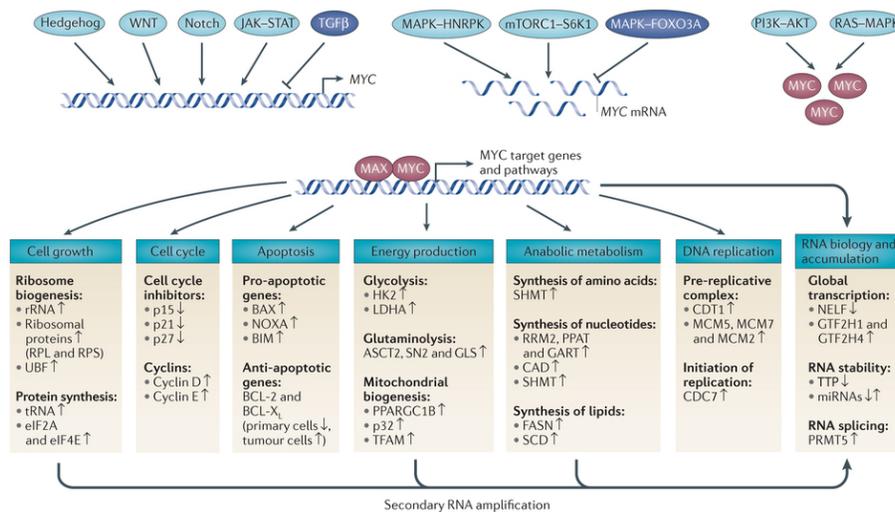
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e.g. Wnt signaling, chronic myeloid  
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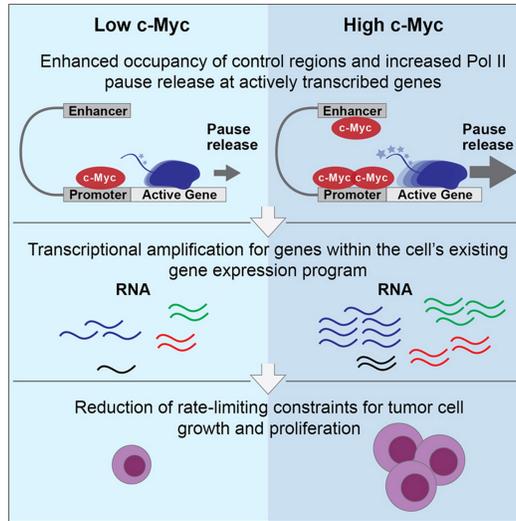
# MYC family of transcription factors

master regulators of broad cellular processes



# c-Myc

accumulates in promoter regions and amplifies transcription when overexpressed in cancer



Lin et al., Cell, 151, 56-67 (2012); Nie et al, Cell 151, 68-79 (2012)

# MYC expression in haploinsufficient mice

amelioration of age-associated phenotypes

**Article**

Hofmann et al., Cell, 160, 477-488 (2015)

**Reduced Expression of MYC Increases Longevity and Enhances Healthspan**

Jeffrey W. Hofmann,<sup>1,2</sup> Xiaoli Zhao,<sup>1,2</sup> Marco De Cecco,<sup>1</sup> Abigail L. Peterson,<sup>1</sup> Luca Pagliarini,<sup>1</sup> Jayameenakshi Manivannan,<sup>1</sup> Gene B. Hubbard,<sup>2</sup> Yuji Ikeno,<sup>2</sup> Yongqing Zhang,<sup>2</sup> Bin Feng,<sup>2</sup> Xiaoli Li,<sup>2</sup> Thomas Serre,<sup>2</sup> Wenbo Qi,<sup>2</sup> Holly Van Remmen,<sup>2</sup> Richard A. Miller,<sup>1</sup> Kevin G. Bath,<sup>3</sup> Rafael de Cabo,<sup>2</sup> Haiyan Xu,<sup>4</sup> Nicola Nereetti,<sup>1</sup> and John M. Sedivy<sup>1,2\*</sup>

<sup>1</sup>Department of Molecular Biology, Cell Biology and Biochemistry, Brown University, Providence, RI 02912, USA  
<sup>2</sup>Department of Cellular and Structural Biology, Barshop Institute for Longevity and Aging Studies, University of Texas Health Science Center at San Antonio, San Antonio, TX 78229, USA  
<sup>3</sup>Translational Gerontology Branch, National Institute on Aging, 251 Bayview Boulevard, Suite 100, Baltimore, MD 21224, USA  
<sup>4</sup>Hallett Center for Diabetes and Endocrinology, Rhode Island Hospital, Warren Alpert Medical School of Brown University, Providence, RI 02903, USA  
<sup>5</sup>Department of Cognitive, Linguistic, and Psychological Sciences, Brown University, Providence, RI 02912, USA  
<sup>6</sup>Department of Pathology and Geriatrics Center, University of Michigan, Ann Arbor, MI 48109, USA  
<sup>7</sup>Co-first author  
<sup>\*</sup>Correspondence: john\_sedivy@brown.edu  
<http://dx.doi.org/10.1016/j.cell.2014.12.016>

**Cell**

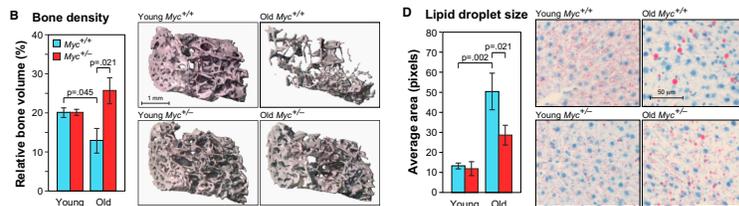
**Myc<sup>-/-</sup> Mice**

↓ Reduced MYC Levels

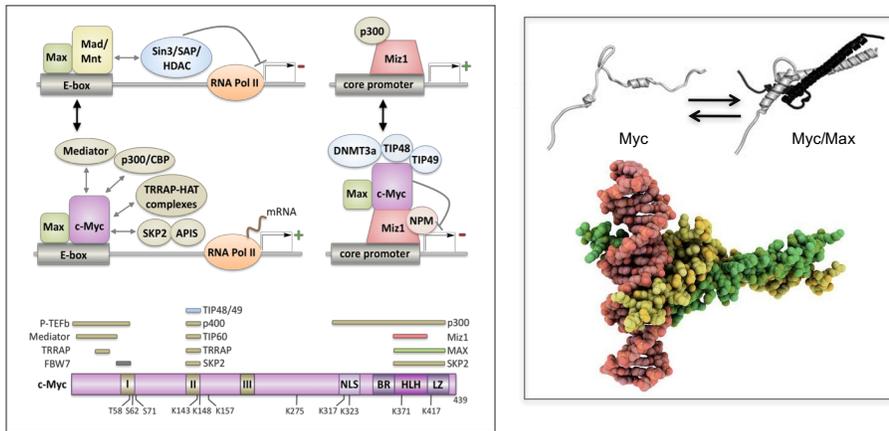
↓ Nutrient & Energy-sensing Pathways    Protein Translation    Somatotropic Signaling

↓

Increased Lifespan and Healthspan  
Resistance to Some Age-associated Pathologies  
Elevated Metabolic Activity  
Normal Development and Fecundity



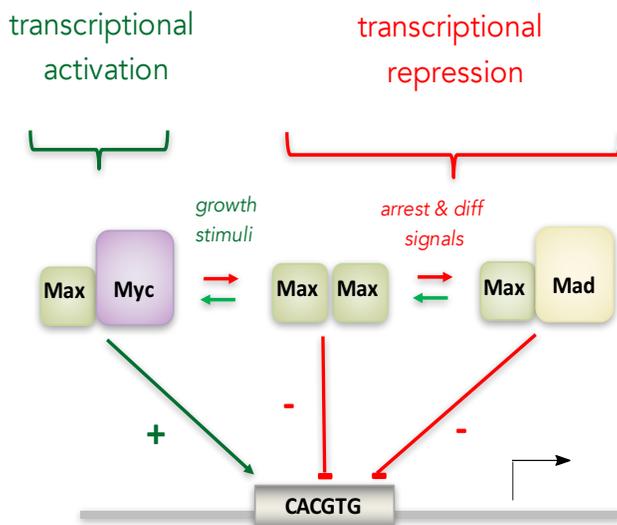
## An obstinate therapeutic target



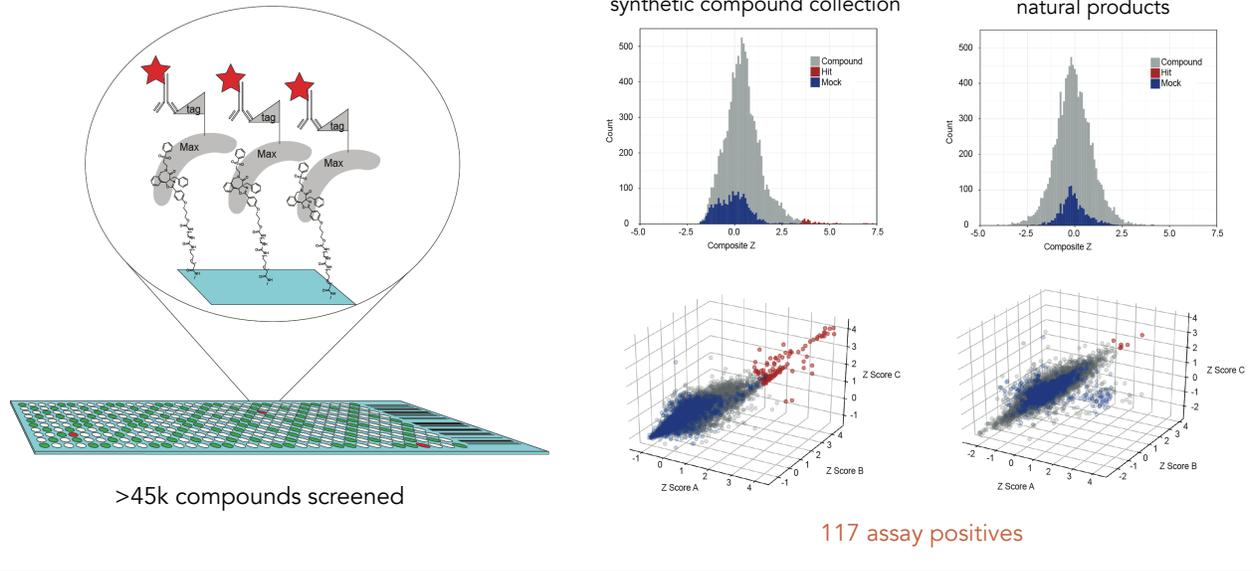
many protein-protein interactions

unstructured domains  
no traditional binding pockets  
large buried interface

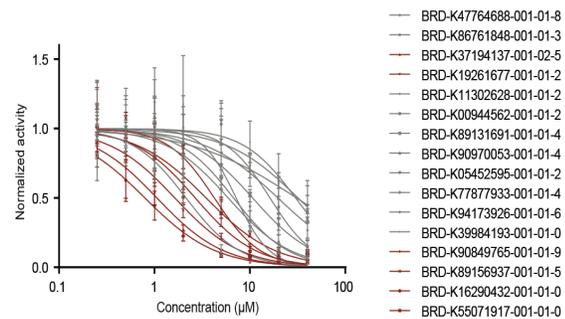
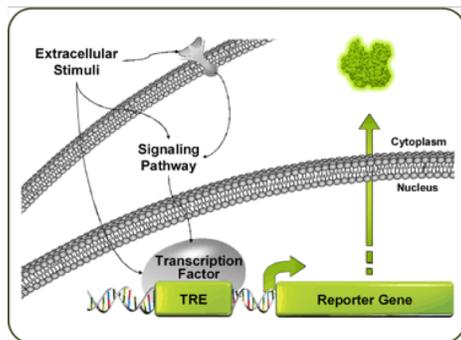
## Max as a target: heterodimer/homodimer dynamics



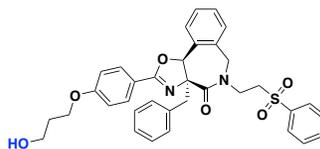
## SMM screens: purified Max transcription factor



## Reporter gene assays: putative Max binders modulate Myc-driven transcription



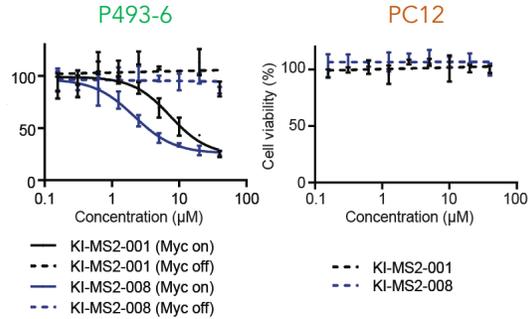
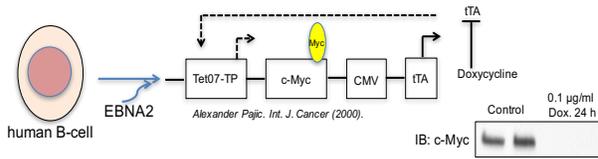
'KI-MS2'



IC<sub>50</sub> = 1.06 µM  
MW = 610.73  
cLogP = 5.15

## Cell viability assays: Are Myc or Max required?

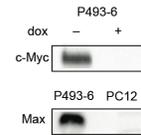
P493-6 Dox-repressible cells for MYC 'on/off' studies



Max-deficient PC12 pheochromocytoma cells



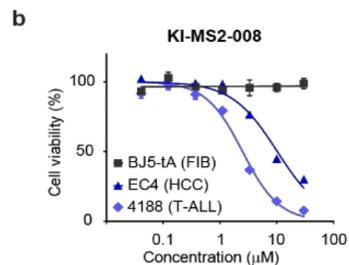
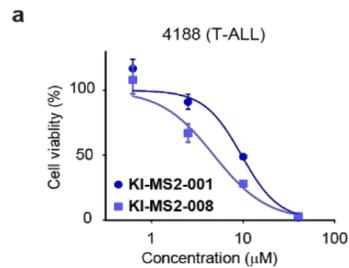
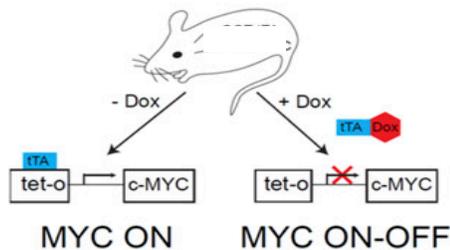
	KI-MS2-001	KI-MS2-008
Myc reporter	1.98 µM	1.28 µM
P493-6 Myc on	7.36 µM	2.15 µM
P493-6 Myc off	>50 µM	>50 µM
PC12	>50 µM	>50 µM



## Conditional cellular models of MYC expression

Myc 'on/off' mouse models:

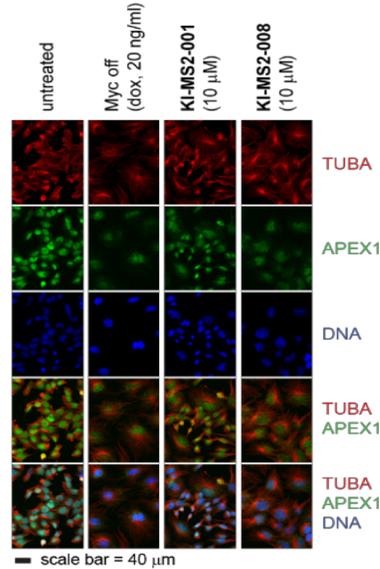
- lymphoma
- HCC
- RCC
- osteosarcoma



Anja Deutzmann, Felsher Lab Stanford

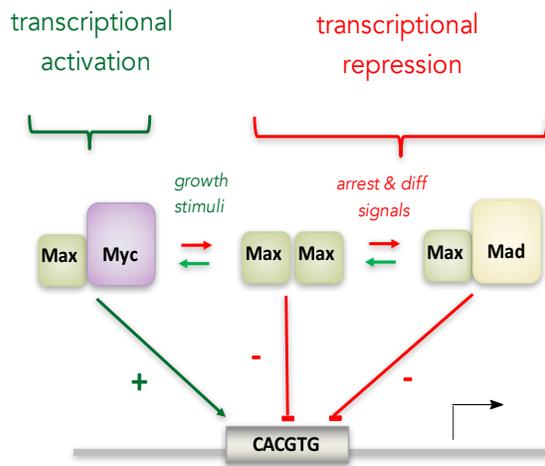
## Imaging of biomarkers: conditional vs. chemical modulation

modulating Myc in an engineered osteosarcoma model

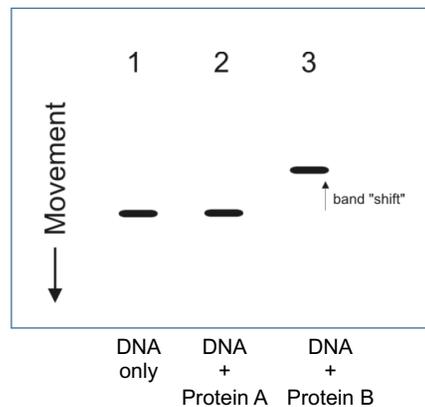


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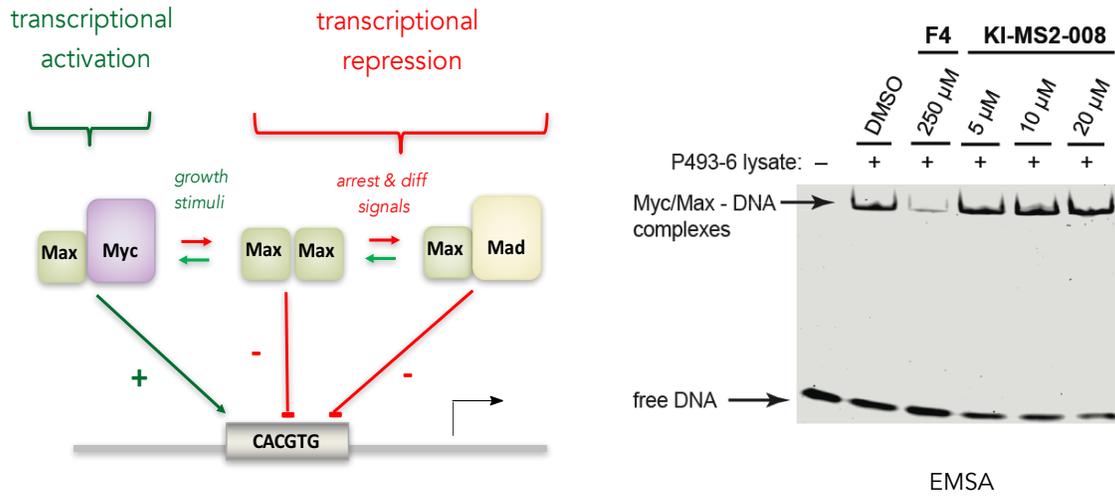
## Does the probe antagonize the Myc/Max heterodimer?



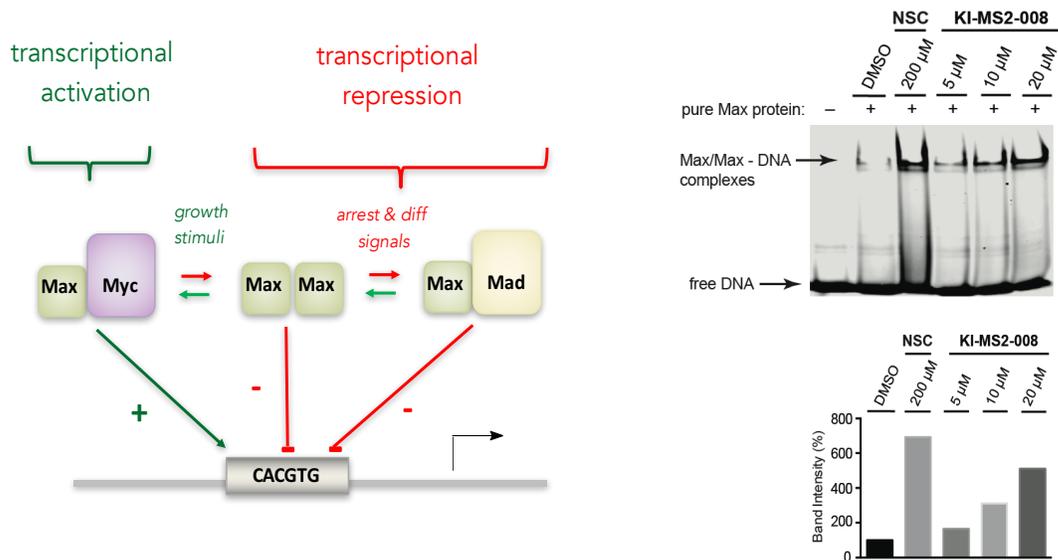
Electrophoretic Mobility Shift Assay (EMSA)  
aka Gel Shift Assay



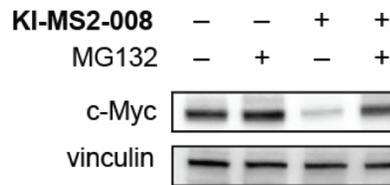
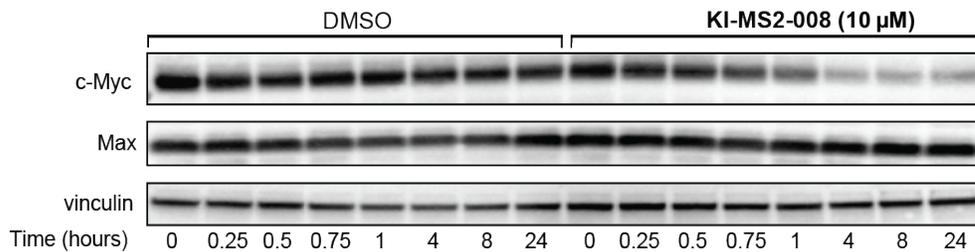
## Does the probe antagonize the Myc/Max heterodimer?



## Does the probe stabilize the Max/Max homodimer?

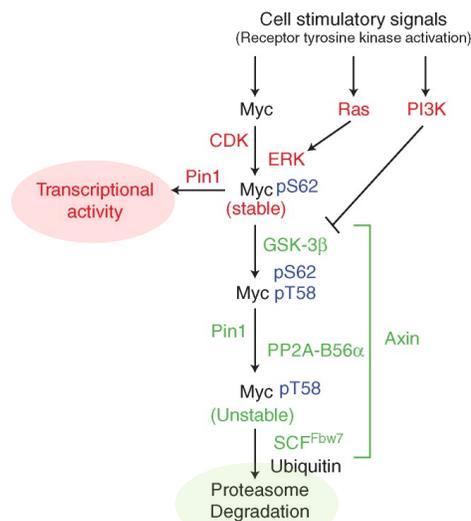


## Western blots: KI-MS2-008 alters Myc protein levels

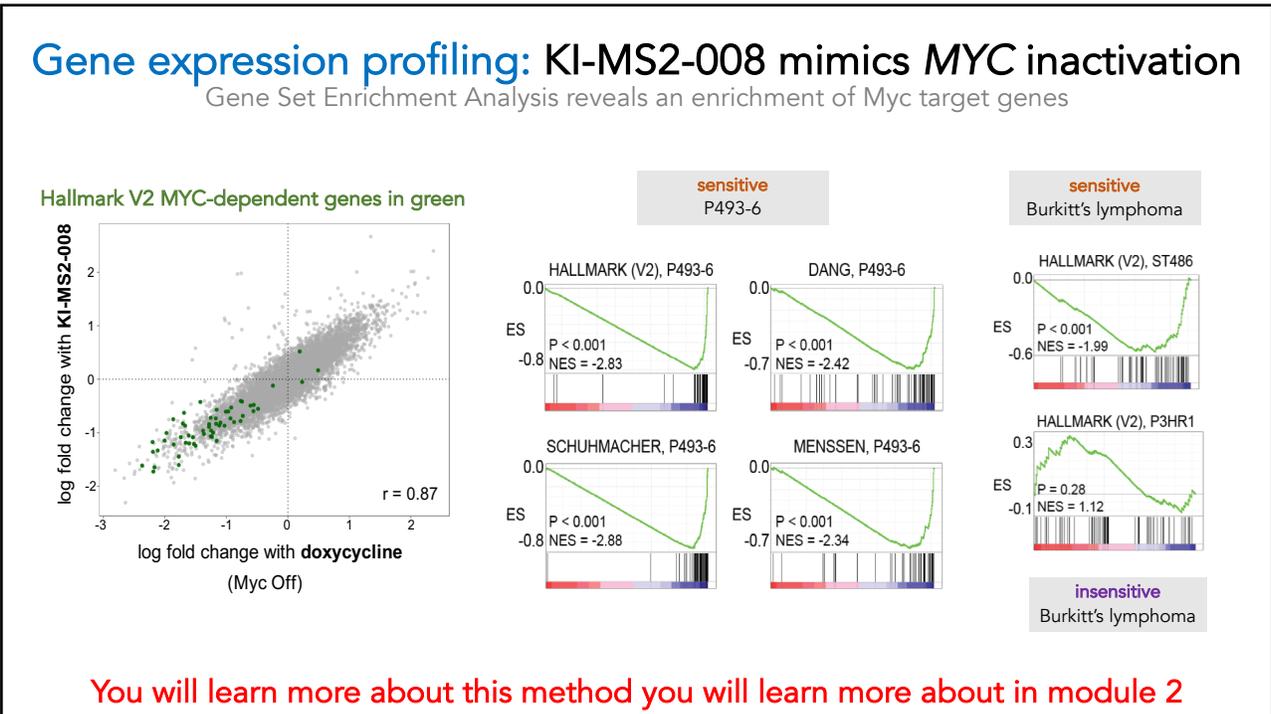
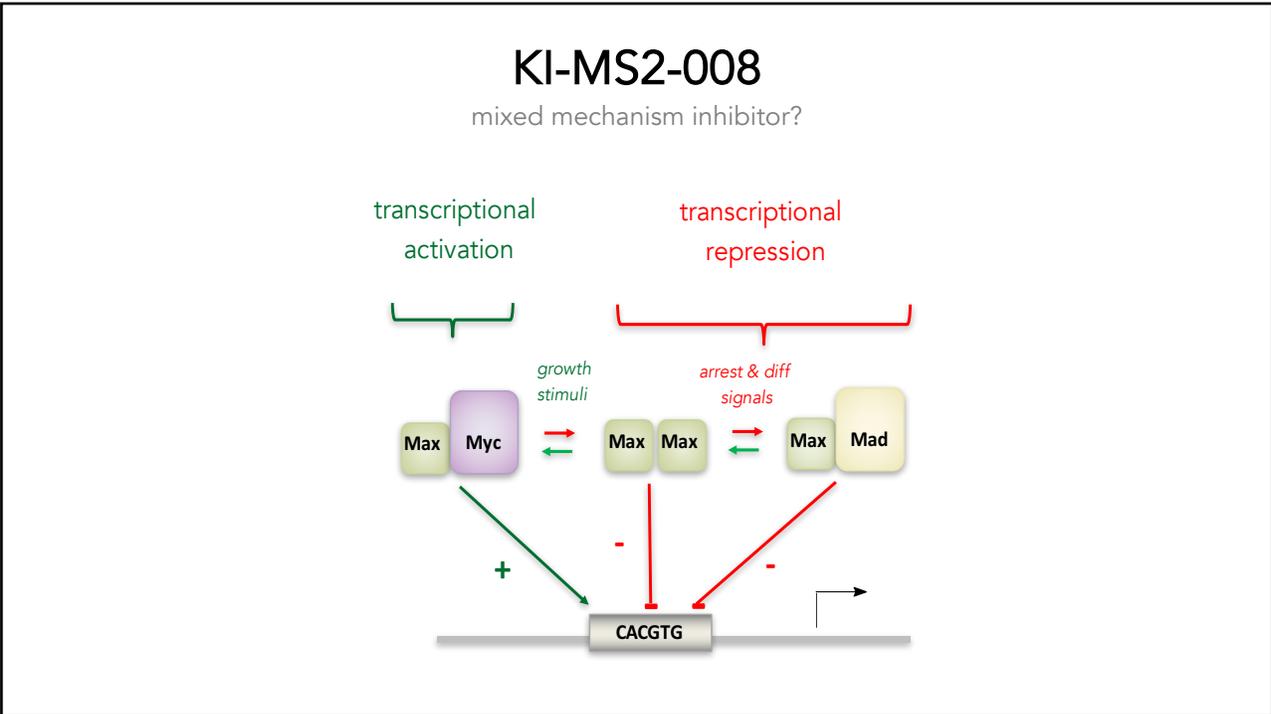


rescue experiment with  
10 μM proteasome inhibitor  
MG132

## Myc protein stability is regulated by the ubiquitin-proteasome system

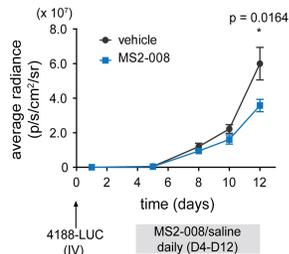
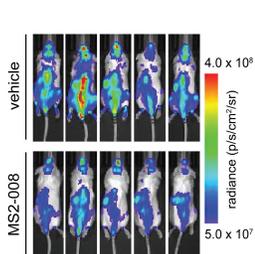


Farrell & Sears, Cold Spring Harb Perspect Med, 4 (2014)



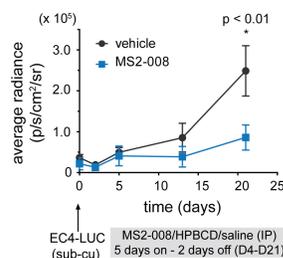
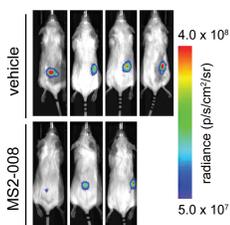
## In vivo studies: KI-MS2-008 modulates tumor volume in Myc-dependent mouse models of cancer

T-cell acute  
lymphoblastic  
leukemia  
blood cancer



0.06 mg/kg  
daily IV administration

hepatocellular  
carcinoma  
solid tumor



0.24 mg/kg  
subcutaneous administration  
5d on/2d off cycles

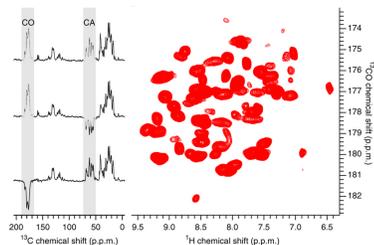
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## Current directions

optimize potency and solubility, PK/PD-guided medicinal chemistry



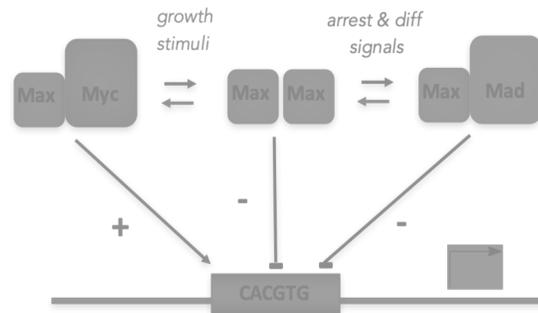
structural biology



additional tumor models  
same tumor models + new readouts



*stabilizing repressive states vs. inhibiting activating states?*



*stabilizing vs. inhibiting PPIs?*

## Our path to evaluate ligands - lectures

2/9/19	Lecture 1	Intro to chemical biology: small molecules, probes, and screens
2/12/19	Lecture 2	Small Molecule Microarrays
2/14/19	Lecture 3	For the love of proteins: FKBP12 and immunophilins
2/19/19	No Lecture	
2/21/19	Lecture 4	Quantitative evaluation of protein-ligand interactions
2/26/19	Lecture 5	A ligand discovery vignette: sonic hedgehog
2/28/19	Lecture 6	Engineering transcriptional responses with a small molecule
3/5/19	<b>Lecture 7</b>	<b>Wrap up discussion: suggestions for how to report your findings</b>