

Illuminating the Druggable Genome Program

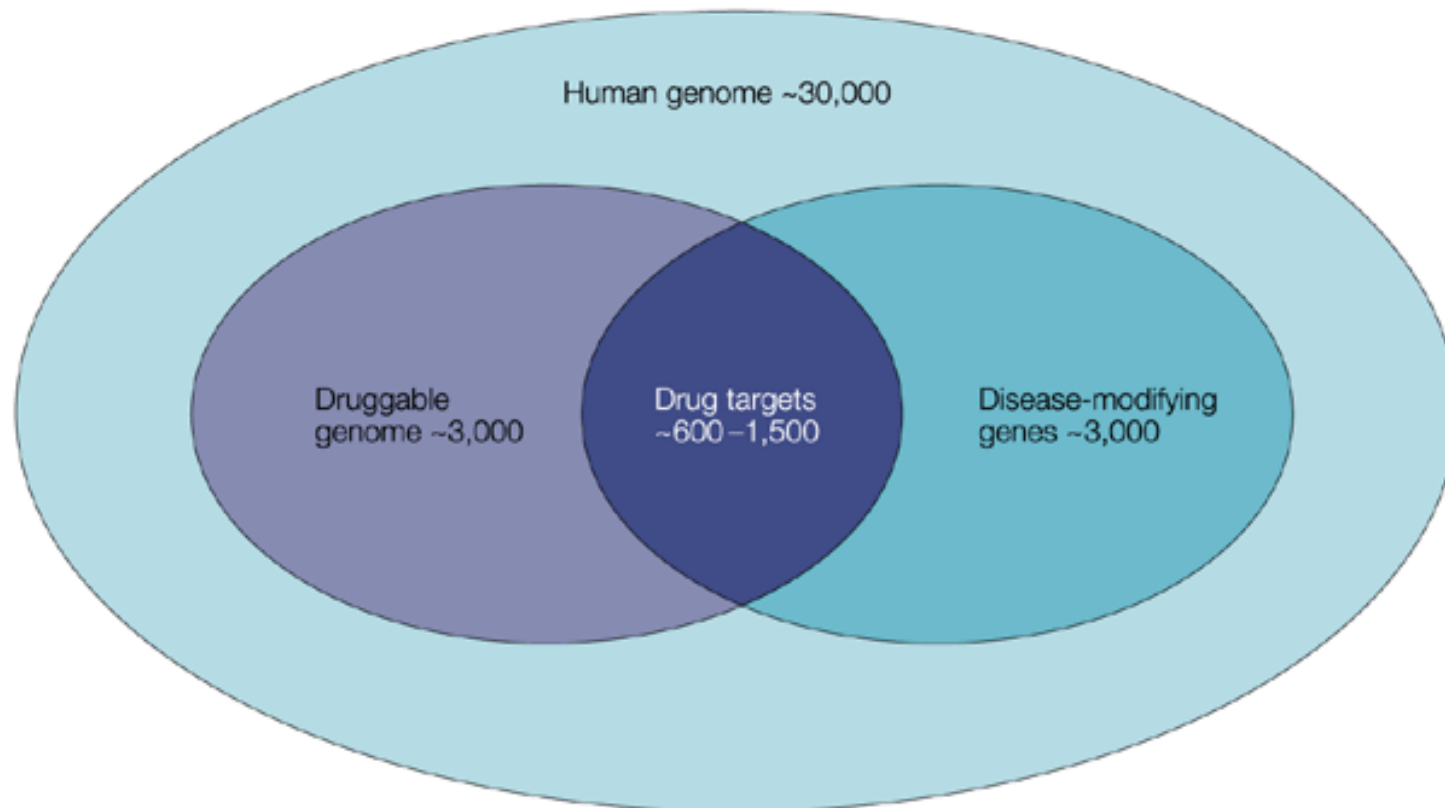
Council of Councils Meeting
January 25-26, 2024

Karlie Sharma, PhD
Program Director, Office of Drug Development Partnership Programs
National Center for Advancing Translational Sciences



National Institutes of Health
Office of Strategic Coordination – The Common Fund

Illuminating the Druggable Genome (IDG) Program: What is the Druggable Genome?



Druggable Genome - the subset of the human genome that expresses proteins potentially able to bind drug-like compounds.

Illuminating the Druggable Genome (IDG) Program: What is the Druggable Genome?

- While the number of proteins in the druggable genome is upwards of 4,500, the existing clinical pharmacopeia is represented by only a few hundred targets, leaving a huge swath of biology that remains unexploited.
- Goal of the IDG Program – catalyze research to improve our understanding of the properties and functions of proteins that are currently not well studied within commonly drug-targeted protein families.

Definition of an Understudied Protein

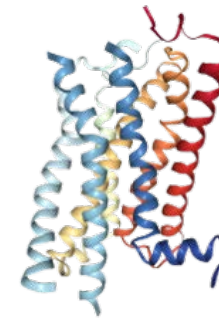
▶ Understudied Proteins Identified by:

- ▶ Few or no publications
- ▶ Lack of R01 Funding

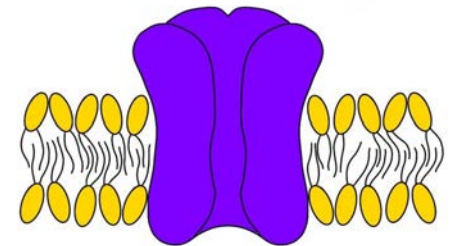
▶ Three protein families:

- ▶ Ion Channels
- ▶ G Protein Coupled Receptors
- ▶ Kinases

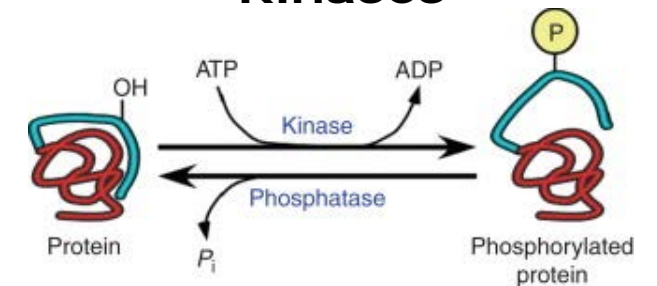
GPCRs



Ion Channels



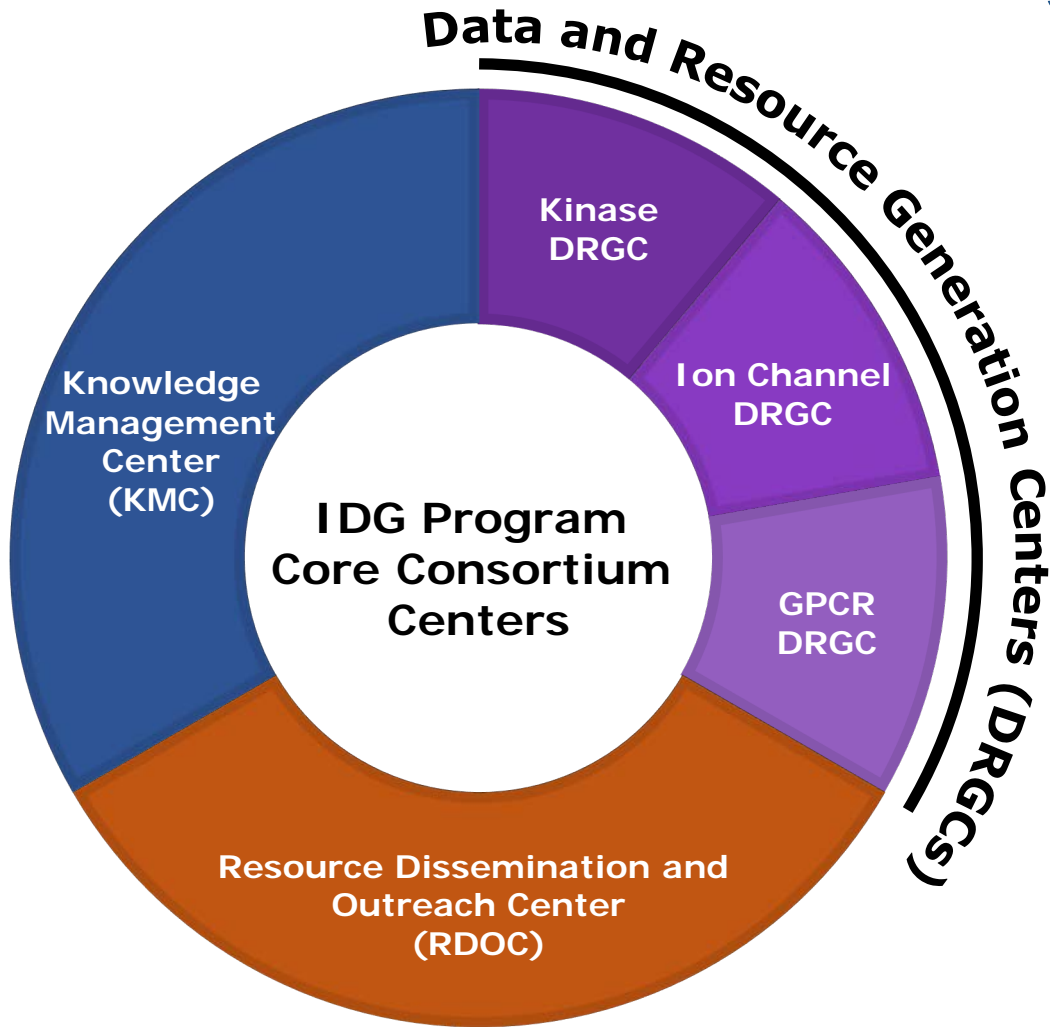
Kinases



IDG Program Timeline and Budget

2014	2015	2016	2017	2018	2019	2020	2021	2022	2023
Pilot Phase (\$25.5M)				Implementation Phase (\$71M)					
Goals: <ul style="list-style-type: none"> • Adapt scalable technology platforms for IDG protein families. • Develop a knowledge/information management platform. 				Goals: <ul style="list-style-type: none"> • Identify phenotypes of understudied proteins. • Provide reagents and tools. • Create an enriched, minable knowledge base (Pharos). 					
Outputs: <ul style="list-style-type: none"> • Core understudied protein datasets. • Understudied protein interrogation platforms. • Predictive algorithms. • Pharos, a protein exploration search engine. 				Outputs: <ul style="list-style-type: none"> • Pharos interface and underlying database. • Reagents available through several repositories. • Improved understanding of nearly 100 understudied proteins and their role in human disease • Updated and improved Expanded high-throughput platforms for interrogating the understudied genome. 					

IDG Program: Implementation Phase Consortium Structure

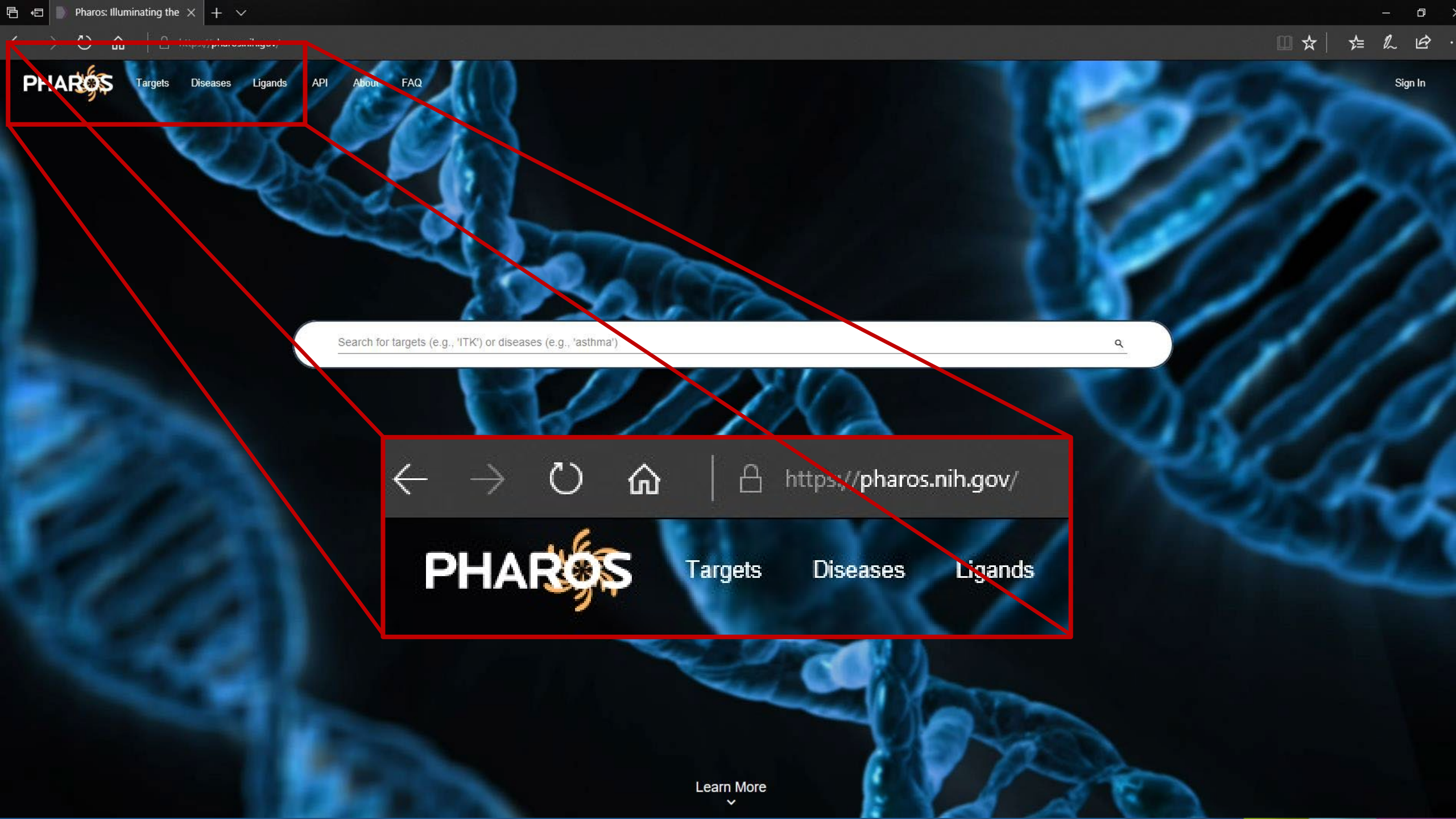


Cutting Edge Informatics Tools (CEIT) Awards - NOFO issued in 2018 and 2021 to deploy tools to enhance the community's ability to process, analyze, and visualize data around the understudied proteins.

R03 Pilot Projects – NOFO issued each year from 2018-2022 to support the generation of preliminary data and tools around eligible understudied protein(s) to:

- elucidate function in the context of human disease
- support R01 applications and/or drug discovery projects

Commercializing Understudied Proteins from the Illuminating the Druggable Genome Project (SBIR and STTR) – NOFO to initiate early research leading to the commercialization of assays or products.



Search for targets (e.g., 'ITK') or diseases (e.g., 'asthma')

Navigation bar with icons: back, forward, refresh, home, lock, and address bar showing `https://pharos.nih.gov/`

PHAROS Targets Diseases Ligands

Pharos: Target Development Levels

Tdark

These are targets about which virtually nothing is known. They do not have known drug or small molecule activities and satisfy two or more of the following criteria: very low publication number (usually <5), gene function annotations <3 and <50 antibodies available.

Tbio

These targets do not have known drug or small molecule activities but do have some publications and data. They satisfy all conditions for Tdark and satisfy one or more of the following criteria: known molecular-level activity and/or a known molecular relationship between a genetic variation and phenotypic expression.

Tchem

These targets have at least one bioactive, drug-like compound with an activity cutoff of <30 nM and satisfy all preceding conditions (Tdark and Tbio).

Tclin

These targets have at least one approved drug and satisfy all preceding conditions (Tdark, Tbio and Tchem).



Jump to section:

Protein Summary

IDG Development Level Summary

Active Ligands

Disease Associations by Source

PDB Viewer

Target Expression Data

Protein to Protein Interactions

Publication Statistics

Related Publications

Sequence Details

Related Targets

Protein Summary

Uniprot Accession IDs

[P01375](#) [O43647](#) [Q9P1Q2](#) [Q9UIV3](#)

Gene Name

[TNF](#)

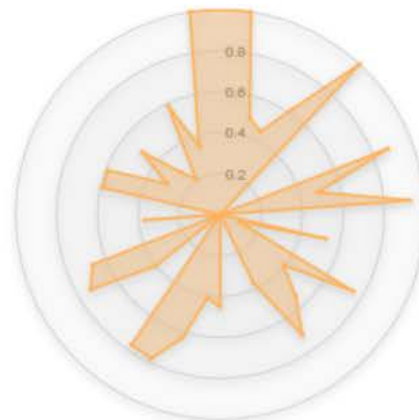
Ensembl ID

ENST00000376122 ENSP00000365290 ENSG00000204490
 ENST00000383496 ENSP00000372988 ENSG00000206439
 ENST00000412275 ENSP00000392858 ENSG00000228321
 ENST00000420425 ENSP00000410668 ENSG00000228849
 ENST00000443707 ENSP00000389492 ENSG00000230108
 ENST00000448781 ENSP00000389490 ENSG00000223952
 ENST00000449264 ENSP00000398698 ENSG00000232810

Symbol

TNFA TNFSF2 DIF TNFA TNFSF2 TNLG1F TNF-alpha

Illumination Graph



Knowledge Table

Most Knowledge About	Knowledge Value (0 to 1 scale)
biological process	1
biological term	1
chemical	1
virus perturbation	1
drug	0.93

IDG Development Level Summary

Tdark

These are targets about which virtually nothing is known. They do not have known drug or small molecule activities

- AND -

satisfy two or more of the following criteria:

✓ Pubmed score: 49978.25 (req: > 5)

✓ Gene RIFs: 4125 (req: > 3)

Tbio

These targets do not have known drug or small molecule activities

- AND -

satisfy the preceding conditions

- AND -

satisfy one or more of the following criteria:

✓ Gene Ontology Molecular Functions: 156

✓ OMIM Phenotypes: 4

Tchem

Target has at least one ChEMBL compound with an activity cutoff of < 30 nM

- AND -

satisfies the preceding conditions

✓ Active Ligands: 352

Tclin

Target has at least one approved drug

- AND -

satisfies the preceding conditions

✓ Active Drugs: 5

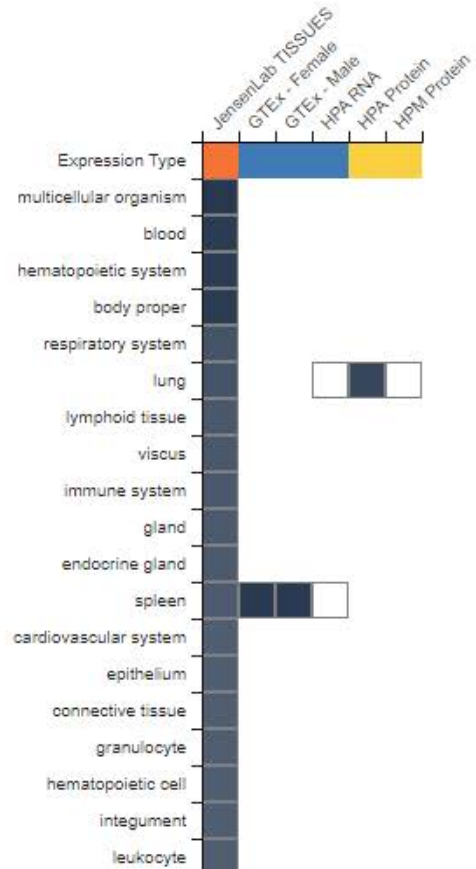
TNF

Tissue Search On

Search Uberon Hierarchy

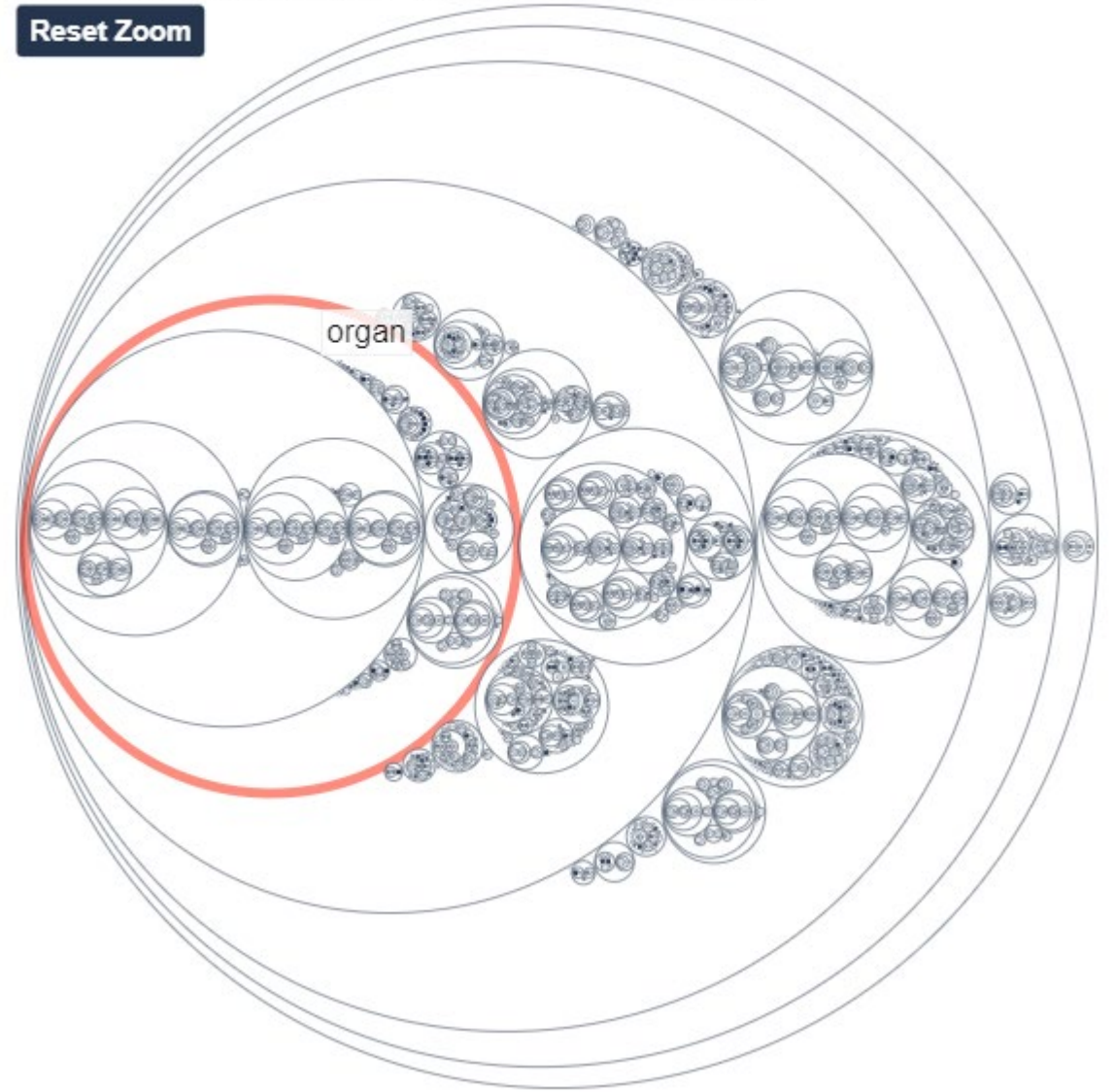
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Sort Column: **JensenLab TISSUES**








root: anatomical entity (UBERON:0001062)

Reset Zoom



Pharos: Other Notable Features

Approved Drugs

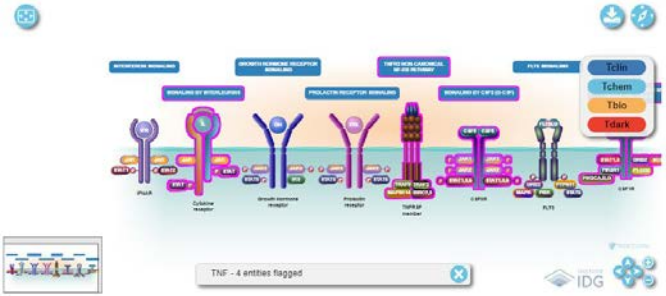
<p>adalimumab</p>  <p>TNF Tclin</p> <p>ANTIBODY BINDING :</p>	<p>golimumab</p>  <p>TNF Tclin</p> <p>ANTIBODY BINDING :</p>	<p>certolizumab pegol</p>  <p>TNF Tclin</p> <p>ANTIBODY BINDING pKd : 10.05</p>	<p>infliximab</p>  <p>TNF Tclin</p> <p>ANTIBODY BINDING :</p>	<p>etanercept</p>  <p>TNF Tclin</p> <p>INHIBITOR :</p>
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Pathways

Pathways (154)

Reactome (15) KEGG (59) PathwayCommons (25) WikiPathways (55)

Cytokine Signaling in Immune system (R-HSA-1280215)



TNF - 4 antibodies flagged

Click on a row in the table to change the structure displayed.






Active Ligands

<p>doramapimod</p>  <p>TNF Tclin</p> <p>pKd : 7.7</p>	<p>CHEMBL187092</p>  <p>TNF Tclin</p> <p>pIC50 : 9.05</p>	<p>marimastat</p>  <p>TNF Tclin</p> <p>pKi : 8.96</p>	<p>rolipram</p>  <p>TNF Tclin</p> <p>pKi : 6.03</p>	<p>CHEMBL72511</p>  <p>TNF Tclin</p> <p>pKi : 8.96</p>
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Structures



Protein-Protein Interactions

<p>TNFRSF1A Tchem</p>  <p>Novelty: 0.00037647 p_int: 0.999996794 p_ni: 0.000002275 p_wrong: 9.3e-7 Score: 0.999 Data Source: BioPlex,Reactome,STRINGDB</p>	<p>DAG1 Tbio</p>  <p>Family: Enzyme Novelty: 0.00149278 p_int: 0.997018043 p_ni: 0.002981832 p_wrong: 1.25e-7 Score: 0.205 Data Source: BioPlex,STRINGDB</p>	<p>HSPA13 Tbio</p>  <p>Novelty: 0.03895652 p_int: 0.988975416 p_ni: 0.011024584 Score: 0.603 Data Source: BioPlex,STRINGDB</p>	<p>GUF1 Tbio</p>  <p>Novelty: 0.00422028 p_int: 0.979527956 p_ni: 0.019640972 p_wrong: 0.000631072 Score: 0.2 Data Source: BioPlex,STRINGDB</p>	<p>SFXN5 Tdark</p>  <p>Novelty: 0.30379915 p_int: 0.974090509 p_ni: 0.024865901 p_wrong: 0.00104359 Data Source: BioPlex</p>
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IDG Program Generated Resources

Jump to section:



Descriptive Data

[Protein Summary](#)[Protein Classes](#)[IDG Development Level Summary](#)[Protein Sequence and Structure](#)[Expression Data](#)[Related Tools](#)

Behavioral Data

[Protein to Protein Interactions](#)[Pathways](#)

Phenotypic Data

[Gene Ontology Terms](#)[Disease Associations by Source](#)[GWAS Traits](#)[Related Targets](#)

Resources

[Orthologs](#)

Publications

[Publication Statistics](#)[Related Publications](#)

Protein Summary

[help](#)

Description

Regulatory subunit of the poly(A)-nuclease (PAN) deadenylation complex, one of two cytoplasmic mRNA deadenylases involved in general and miRNA-mediated mRNA turnover. PAN specifically shortens poly(A) tails of RNA and the activity is stimulated by poly(A)-binding protein (PABP). PAN deadenylation is followed by rapid degradation of the shortened mRNA tails by the CCR4-NOT complex. Deadenylated mRNAs are then degraded by two alternative mechanisms, namely exosome-mediated 3'-5' exonucleolytic degradation, or deadenylation-dependent mRNA decapping and subsequent 5'-3' exonucleolytic degradation by XRN1. PAN3 acts as a positive regulator for PAN activity, recruiting the catalytic subunit PAN2 to mRNA via its interaction with RNA and PABP, and to miRNA targets via its interaction with GW182 family proteins.

Uniprot Accession IDs

[Q58A45](#) [A0N0X1](#) [A1A4Y8](#)[A1A4Y9](#) [B1ALF1](#) [B7Z3W7](#)[Q0D2P2](#) [Q5HYG6](#) [Q5T515](#)[Q5T516](#) [Q5TBA0](#) [Q76E13](#)[Q8NBA6](#)

Illumination Graph



Knowledge Table

Most Knowledge About	Knowledge Value (0 to 1 scale)
molecular function	0.99
transcription factor binding site profile	0.77
cell type or tissue	0.72
histone modification site profile	0.72
microRNA	0.65

Gene Name

[PAN3](#)

Ensembl ID

ENST00000380958 ENSP00000370345
ENSG00000152520

Protein Classes

[help](#)

DTO Classes

Protein / Kinase / Protein Kinase / Other Group / Pan3 Family / Pab-dependent Poly(a)-specific Ribonuclease Subunit Pan3

PAN3 (Tdark)

200

400

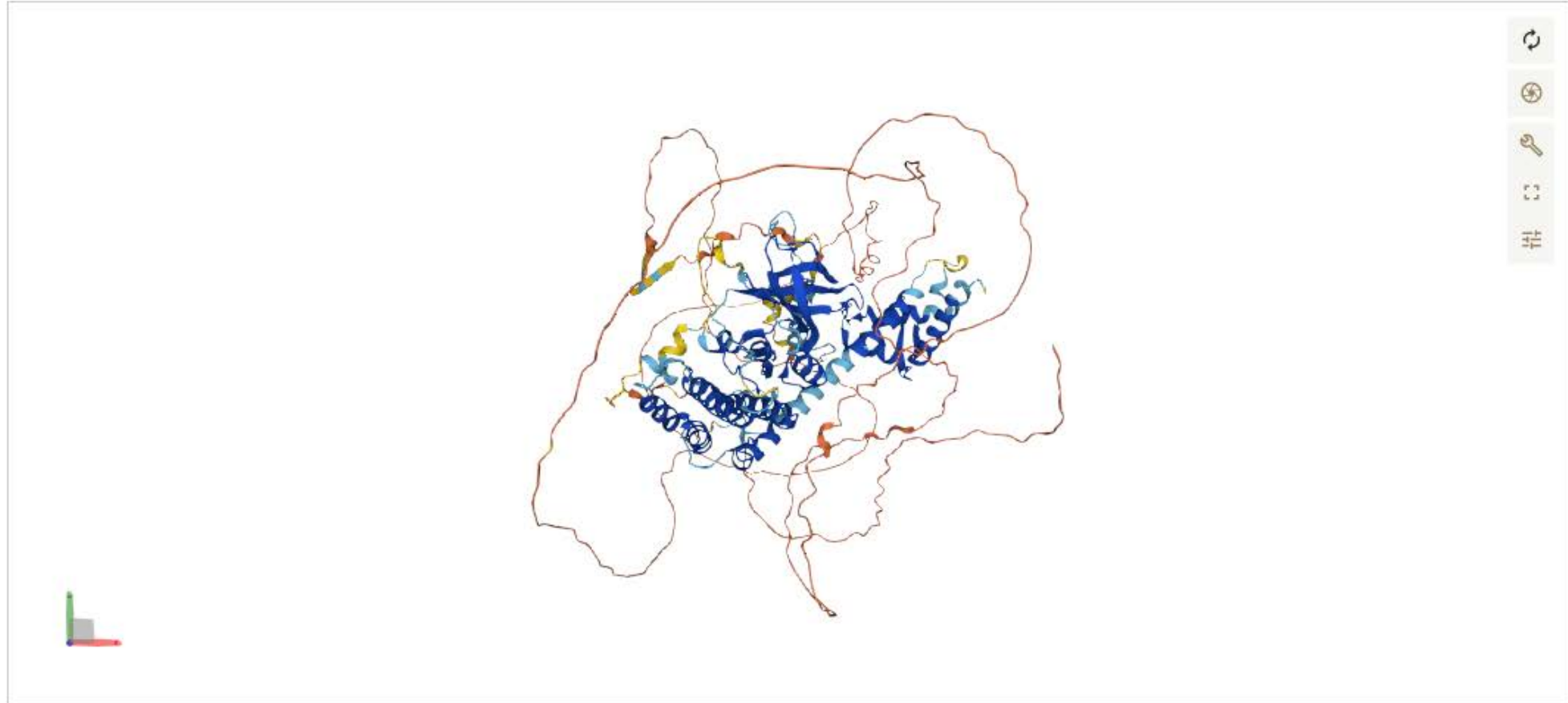
600

800

Model Confidence:

- Very high (pLDDT > 90)
- Confident (90 > pLDDT > 70)
- Low (70 > pLDDT > 50)
- Very low (pLDDT < 50)

AlphaFold produces a per-residue confidence score (pLDDT) between 0 and 100. Some regions with low pLDDT may be unstructured in isolation.



SOURCE

-- Select --

IDENTIFIER

METHOD

-- Select --

RESOLUTION

CHAIN

POSITIONS

LINKS

AlphaFold

AF-Q58A45-F1

Predicted

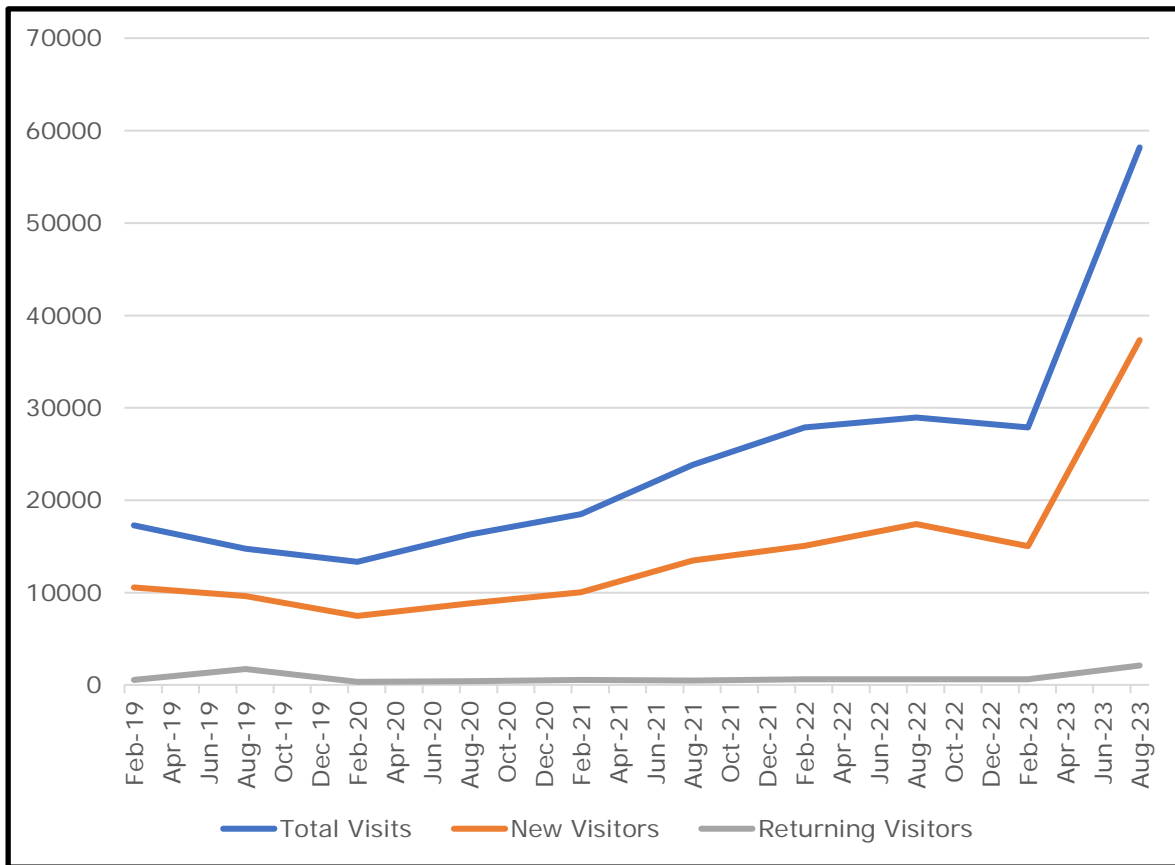
1-887

AlphaFold

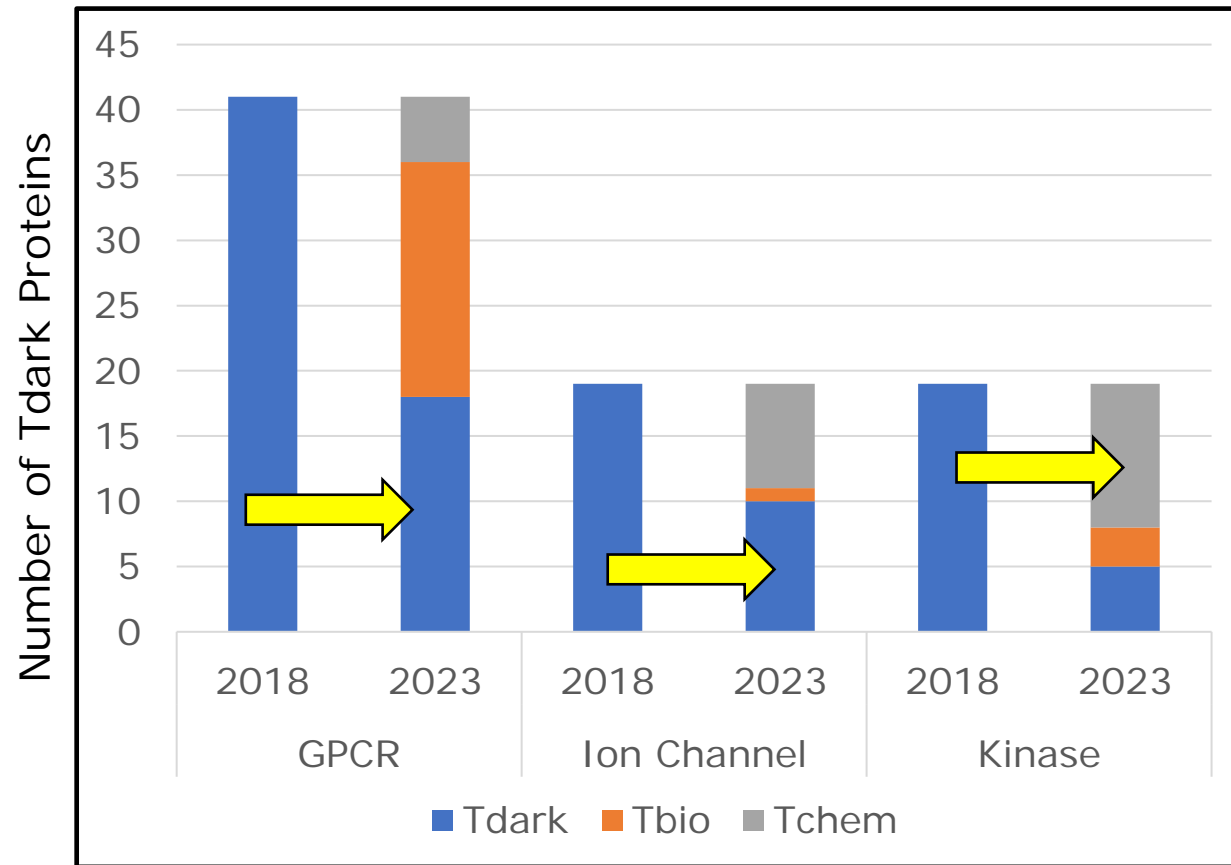


Pharos: Impacts on Evolution of Target Development Levels

Pharos Usage – New and Returning Users



IDG Program Protein Families – Target Development Levels 2018 vs. 2023



Utilization of Pharos for New Opportunities

FONDAZIONE



We've been investing in scientific research since 1990

We've funded more than 2700 projects and 1600 researchers to give people affected by a rare genetic condition a new hope.

01 / 02

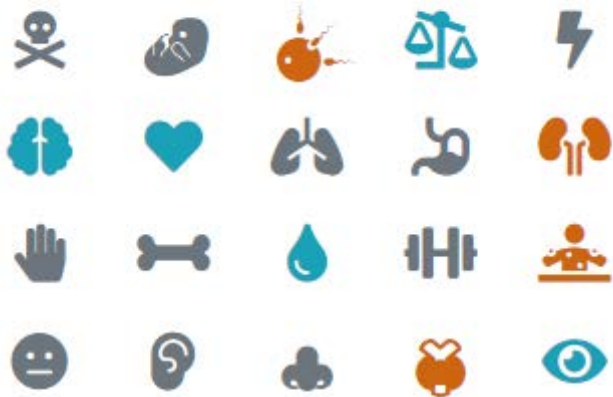
[LEARN MORE](#)



IDG Partners with KOMP2

- IDG partnership with the Knockout Mouse Phenotyping Program (KOMP2) initiated September 2022
- Working together to develop twenty-seven understudied ion channel knockout mouse models

IMPC Phenotype Summary



■ Significant
 ■ Not Significant
 ■ Not tested

[View all our phenotype data below](#) ▼

Phenotype ↕	System ↕	Allele ↕	Zyg ↕	Sex ↕	Life Stage ↕
small kidney		Plip ^{tm1(KOMP)Vlcg}	HOM	♀♂	Early adult
abnormal kidney morphology		Plip ^{tm1(KOMP)Vlcg}	HOM	♀♂	Early adult
enlarged testis		Plip ^{tm1(KOMP)Vlcg}	HOM	♂	Early adult
abnormal testis morphology		Plip ^{tm1(KOMP)Vlcg}	HOM	♂	Early adult
abnormal skin morphology		Plip ^{tm1(KOMP)Vlcg}	HOM	♂	Early adult

R03 Pilot Projects – A Blueprint for Success

R03 Pilot Program: Pilot Projects Investigating Understudied G Protein-Coupled Receptors, Ion Channels, and Protein Kinases

- Over 120 specific dark proteins studied via 98 awards, with over 60 publications to date
- 29 Early Stage and/or New Investigators funded

R03 Pilot Projects – A Blueprint for Success

- Select awardee achievements:
 - R01 projects focused on:
 - Expanding our understanding of the role for the branched-chain a-ketoacid dehydrogenase kinase (BCKDK) in cognition and vocal communication.
 - Interrogation of the NEK family of kinases in cancer (NEK1-11, NEK4-7, 10, 11 considered understudied)
 - R21 awards to:
 - Identify endogenous peptide ligands for orphan GPCRs in order to explore their roles in CNS disorders.
 - Analyze GWAS loci associated with hearing loss – understudied kinases
 - An award to further explore the role of the understudied GPR83 protein in opioid addiction.
 - An award made by the American Heart Association to study a dark kinase in cardiac hypertrophy.

R03 Pilot Projects – A Blueprint for Success



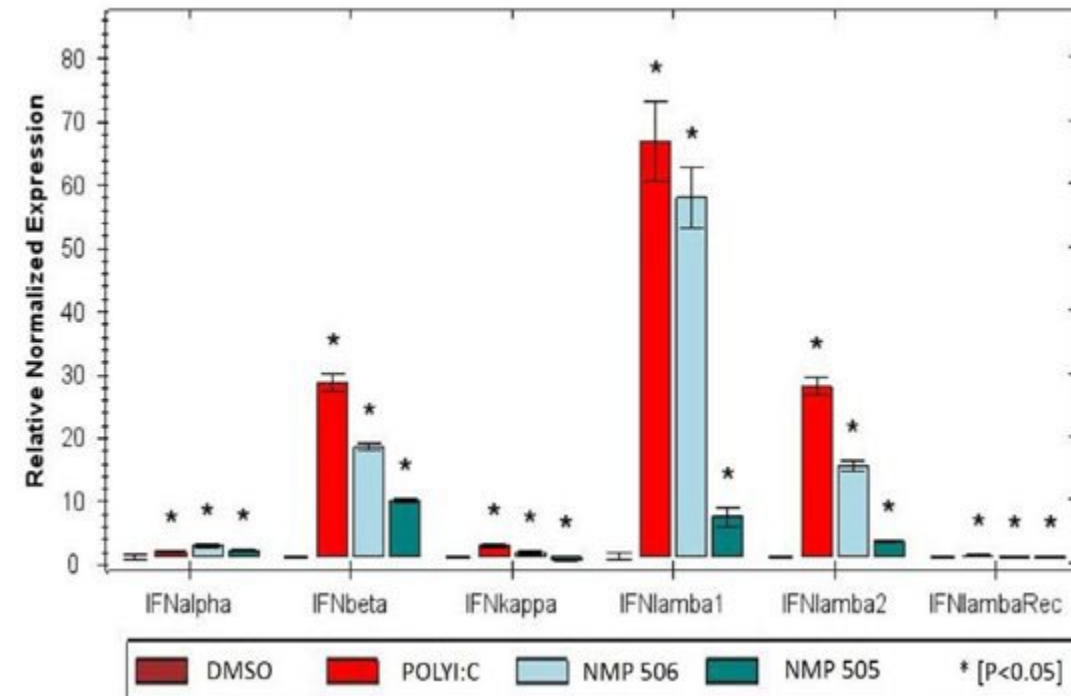
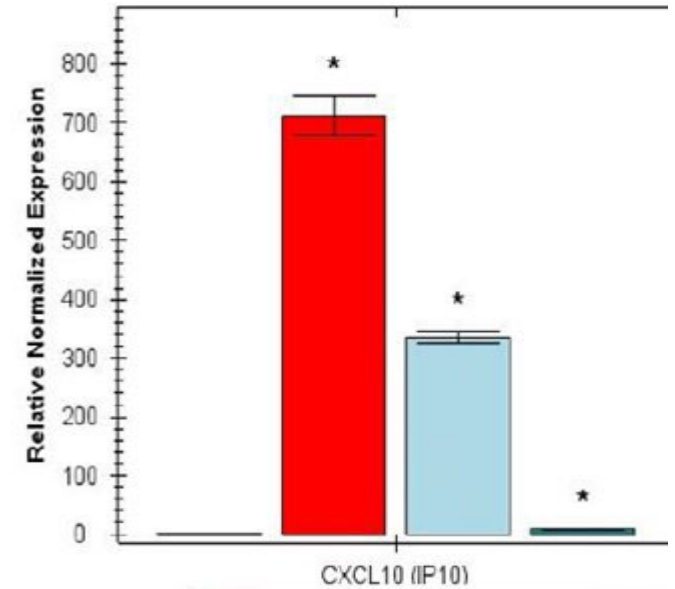
The Atypical Kinase RIOK3 Limits RVFV Propagation and Is Regulated by Alternative Splicing

by Katherine E. Havranek ^{1,†} , Luke Adam White ^{1,†} , Thomas C. Bisom ² ,
 Jean-Marc Lanchy ¹ and J. Stephen Lodmell ^{1,3,*}

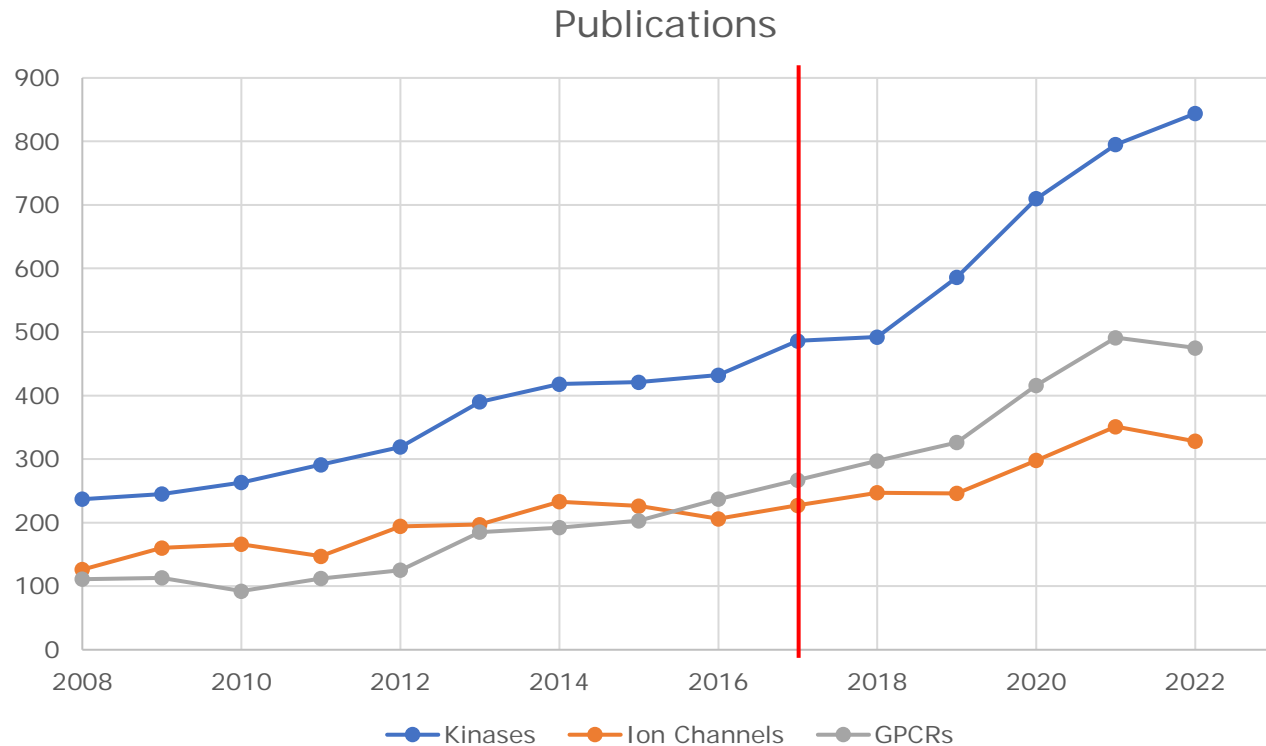
Viruses 2021, 13(3), 367; <https://doi.org/10.3390/v13030367>

Received: 16 January 2021 / Revised: 16 February 2021 / Accepted: 22 February 2021 /
Published: 26 February 2021

- Identification of role for RIOK3 in anti-viral immunity and the inflammatory reaction
- Paired with Dermaxon, LLC on SBIR award to develop RIOK3 as novel therapeutic target for cutaneous lupus
- Now have small molecules and PROTACs that bind to RIOK3 with nanomolar affinity (NMP505 and NMP506).
 - Blockade of RIOK3 also prevents inflammation from spreading to bystander cells

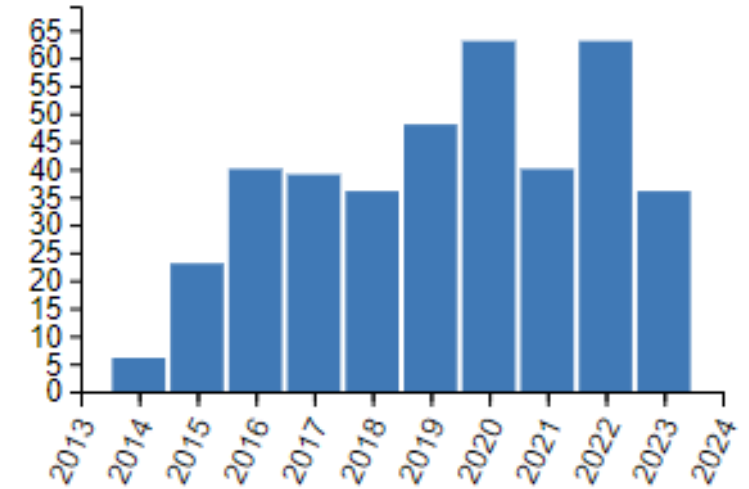


IDG Program – Impacts on the Field

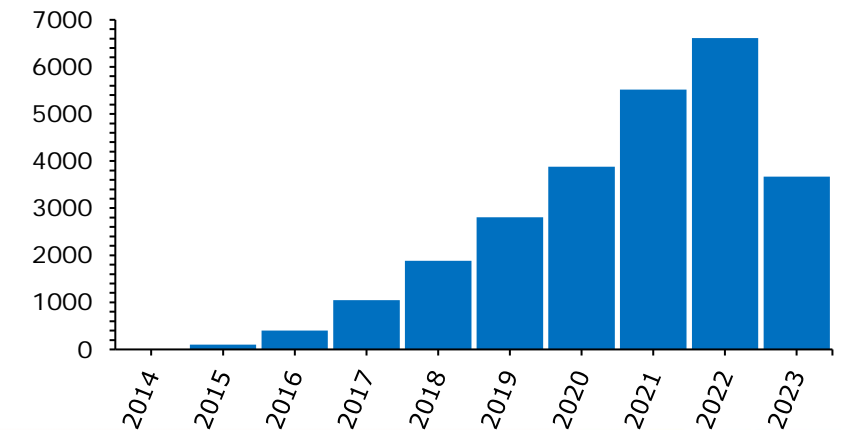


***The above analysis does not include publications from awardees of the IDG Program

Publications



Citations



IDG Program Outputs: Impacts on the Future



- Pharos sustainability
- R03 Pilot award successes still coming in – much impact of this initiative not yet felt
- Common Fund and NIH Institutes/Centers incorporating pilot program format into other initiatives
- Sustainability of many resources through utilization of public repositories
- Increased interest around understudied protein families – demonstration of value of these targets to human disease

Druggable Genome Special Series



Keynote (green)

Illuminating the druggable genome: Pathways to progress

Karlie R. Sharma¹  , Christine M. Colvis¹, Griffin P. Rodgers², Douglas M. Sheeley³

Additional five articles in series:

- Overview of the Knowledge Management Center for Illuminating the Druggable Genome
- Informatic Challenges and Advances in Illuminating the Druggable Proteome
- Illuminating the Understudied GPCR-ome
- Illuminating Function of the Understudied Druggable Kinome
- Best Practices for Managing and Disseminating Resources, Outreach, and Evaluating Impact from IDG Consortium

<https://www.sciencedirect.com/journal/drug-discovery-today/vol/29/issue/3>

IDG Program Leadership

IDG Co-Chairs

Griffin Rodgers, NIDDK
Christine Colvis, NCATS

IDG Common Fund Lead

Becky Miller (OD)

IDG Program Coordinator

Karlie Sharma (NCATS)

IDG Program Analyst

Amber Peters (NCATS)

IDG Working Group

Sam Ananthan (NIDA)	Colin Fletcher (NHGRI)	Mehdi Mesri (NCI)	Ajay Pillai (NHGRI)
Steve Benowitz (NCATS)	Zorina Galis (NHLBI)	Enrique Michelotti (NIMH)	Steve Pittenger (NCATS)
Mark Caprara (CSR)	Brionna Hair (OD)	Laurie Nadler (NIMH)	Lu Wang (NIDDK)
Marc Charette (NHLBI)	Jerry Li (NCI)	Antonio Noronha (NIAAA)	Ashley Xia (NIDDK)
Hemin Chin (NIAAA)	Chris Lindsey (NICHD)	Michael O'Neil (NIAID)	Zuoyu Xu (NIAID)
Ben Churn (NINDS)	Tristan McClure-Begley (NIDA)	Aaron Pawlyk (NICHD)	Yong Yao (NIMH)
David Dzamashvili (OD)		Suzana Petanceska (NIA)	Jean Yuan (OPA)



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