Navigating Human Phosphorylation Networks with the SigNET Suite of On-line Knowledge Bases

Presented by Steven Pelech, Ph.D.

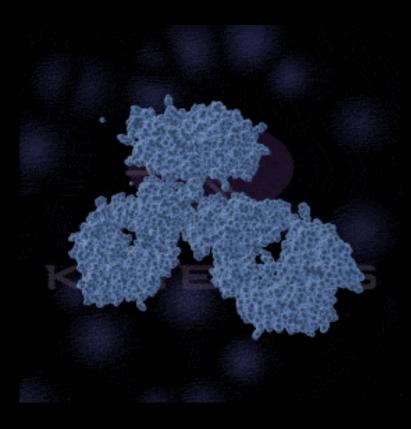
Professor, Department of Medicine, University of British Columbia President & CSO, Kinexus Bioinformatics Corp.







Presented at the MAP Kinase II Meeting at the Life Sciences Baltics 2014 Conference in Vilnius, Lithuania, 2014 September 10



- ◆ Kinetworks[™] and Kinex[™] proprietary analyses uses over 1000 of the world's best antibodies cherry-picked from over 26 vendors and validated in-house
 - Targets low abundance cell signalling proteins
 - Quantifies protein expression and phosphorylation
 - ◆ Kinetworks[™] multi-immunoblotting is more accurate and quantitative than competing methods
 - ◆ Kinex[™]antibody microarray is more comprehensive and sensitive than other methods with unfractionated cell/tissue lysates



www.kinet.ca



- ◆ Open access Kinetworks™ multi-immunoblotting database
- ◆ Features results from >10,000 immunoblots that track protein expression and phosphorylation from data generated with over 330 antibodies
- Over 200,000 protein measurements
- Searchable by protein, treatment or cell/tissue type
- Over 95% unpublished data



www.kinet-am.ca



- ◆ Open access Kinex™ KAM antibody microarray database
- ◆ Features results from >2,500 microarrays that track protein expression and phosphorylations data generated with 650 to 850 antibodies
- Over 3 million protein measurements
- Searchable by protein, treatment or cell/tissue type
- Over 99% unpublished data



PhosphoNET Knowledge Base

www.phosphonet.ca



- Open access human phosphorylation site database
- >177,000 confirmed and 790,000 additional predicted phosphorylation sites in >21,500 human proteins
- Functional information for ~1% of the phosphosites
- Evolutionary analyses in 20 other species
- Kinase specificity prediction



Phosphosite Identification in Proteins

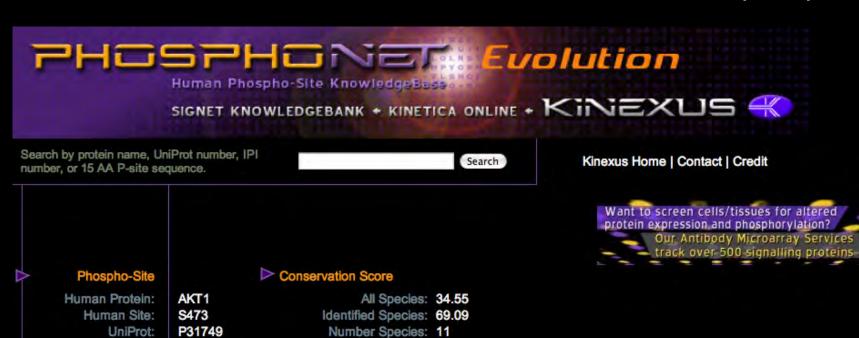
www.phosphonet.ca





Evolutionary Analysis of Phosphosites

www.phosphonet.ca



Charge Score: 0

Phospho-Site Substitution



Evolutionary Analysis of Phosphosites

www.phosphonet.ca

Phospho-Site Sequences																					
Species	Species Scientific Name	HeiDeat ID	NCBI Ref Seq ID	A A 44	Mr(Da)	D Cito	7	6	_	1	2	2	4	0	4	2	3		=	6	,
Human	Homo sapiens	P31749	NP_005154	480	55686	S473	R	P	Н	F	P	Q			Y	S	A	S	G	Т	
Chimpanzee	Pan troglodytes	F31749	XP_512662	481	55720	S474	R	Ŧ	н	F	P	g		S		S	A		9	P	E
Rhesus Macaque	Macaca mulatta		XP_001085623		55679	S473	R		H	F	P	Q			Ÿ	s	A		G	Ť	Ā
Dog	Lupus familis		XP 548000	481	55446	S474		P										S	G	Ť	
Cat	Felis silvestris		74 _010000		00110					۰	н	•		ĭ	•	ď	*	ľ			ľ
Mouse	Mus musculus	P31750		480	55604	S473	R	P	н	F	P	O	F	S	Y	S	A	s	G	Т	A
Rat	Rattus norvegicus	P47196		480	55717													S		Ť	A
Wallaby	Macropus eugenil																	М			
Platypus	Ornith. anatinus		XP_001513899	512	59226																
Chicken	Gallus gallus	Q6U1I9		432	48872	S423	Α	Е	Α	F	L	G	F	s	Y	Α	P	Р	V	D	s
Frog	Xenopus laevis	Q98TY9		481	56023	S474	R	P	н					s		S	A	s	G	N	A
Zebra Danio	Brachydanio rerio	Q7ZTW4		433	48964	S424	T		Α					s				A			
Tiger Blowfish	Takifugu rubipres																				
-	Dros.																				
Fruit Fly	melanogaster	Q8INB9		611	68466	S586	E	P	L	F	P	Q	F	S	Y	Q	G	D	M	A	S
Honey Bee	Apis mellifera																				
And the same of	Caenorhab.	2									_									2	
Nematode Worm	elegans	Q17941		541	62181	S517	Q	S	N	F	Т	Q	F	S	F	Н	N	V	М	G	S
Sea Urchin	Strong. purpuratus																				
Donlar Tree	Populus																				
Poplar Tree Maize	trichocarpa																				
Rice	Zea mays Oryza sativa																				
Rice	Arabidopsis																				
Thale Cress	thaliana																				
Thais Stoss	Sacchar.																				
Baker's Yeast	cerevisiae																				
Red Bread Mold	Neurospora crassa																				



Evolutionary Analysis of Phosphosites

www.phosphonet.ca

Conservation

Percent Protein Identity: Protein Similarity: P-Site Identity: P-Site Similarity:

	1	12		91	•	4	No.	(g)	4	K		•		W. Car	0	
Human	Chimpanzee	Rhesus Macaque	Dog	Cat	Mouse	Rat	Wallaby	Platypus	Chicken	Frog	Zebra Danio	Tiger Blowfish	Fruit Fly	Honey Bee	Nematode Worm	Sea Urchin
100	81.5	99.5	93.9	N.A.	98.1	98.1	N.A.	73	39.7	93.1	39.3	N.A.	49.5	N.A.	52.5	N.A.
100	92.1	99.5	95.2	N.A.	98.7	99.1	N.A.	80.4	56.8	96.2	57.5	N.A.	61.7	N.A.	67.8	N.A.
100	73.3	100	100	N.A.	100	100	N.A.	0	26.6	93.3	26.6	N.A.	46.6	N.A.	26.6	N.A.
100	73.3	100	100	N.A.	100	100	N.A.	0	40	93.3	46.6	N.A.	53.3	N.A.	53.3	N.A.

Percent Protein Identity: Protein Similarity: P-Site Identity: P-Site Similarity:

	12	E	*		1
Poplar Tree	Maize	Rice	Thale Cress	Baker's Yeast	Red Bread Mold
N.A. N.A.	N.A.	N.A. N.A.	N.A. N.A. N.A.	N.A. N.A.	N.A. N.A.



Kiniexus Kinase Substrate Phosphosite Prediction

www.phosphonet.ca



Prediction

Score

228.49

158.34

118.15

117.84

117.65

94.18

86.16

86.10

76.92

76.15

75.50 75.37

Human

P42345

Q13418

Q96SB4

P78362

Q9UPE1

Q13315

P27361

P28482

P78527

P34947

P43250

Q8WTQ7

UniProt. ID

Human Kinase

Short Name

mTOR/FRAP

MSSK1 (STK23)

ERK2 (MAPK1)

ILK SRPK1

SRPK2

ATM

ERK1

DNAPK

GPRK5

GPRK6

GPRK7

Kinase 1:

Kinase 2:

Kinase 3:

Kinase 4:

Kinase 5:

Kinase 6:

Kinase 7:

Kinase 8:

Kinase 9:

Kinase 10:

Kinase 11:

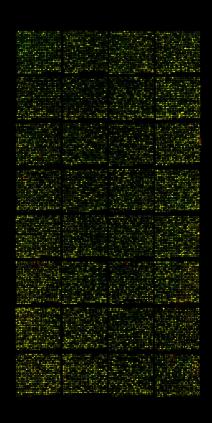
Kinase 12:

- Prediction of kinases is based in silico screening with phospho-site specificity matrices for 500 human protein kinase catalytic domains
- Each matrix is generated with a proprietary algorithm that uses the primary amino acid structure of the kinase for prediction



TranscriptoNET KnowledgeBase

www.transcriptonet.ca



- Gene microarrays permit measurement of mRNA levels
- NCBI Gene Expression Omnibus (GEO) Database features gene chip data from >50,000 studies
- Kinexus developed TranscriptoNET to consolidate and normalize human gene expression data from 6000 normal and tumour cells and tissues to permit comparisons across studies



TranscriptoNET KnowledgeBase

www.transcriptonet.ca



- Open access human mRNA expression knowledgebase
- ◆ >600 human control and cancer tissues and cell lines
- ~21,000 human genes covered
- Contains data from over 125 million measurements
- Identifies highly, commonly and uniquely expressed genes in human tissues and cells
- Identifies differentially expressed genes in about 50 types of human cancers
- Identifies genes that are highly co-expressed
- Shows tissue and cell relatedness



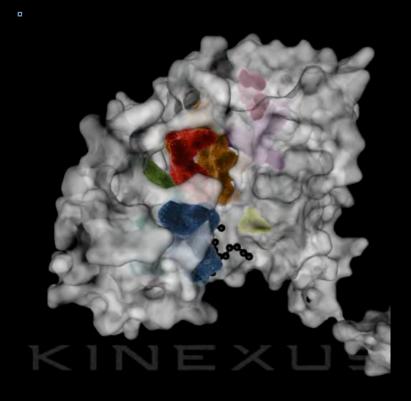
Kiniexus Human Cancer Protein KnowledgeBase

www.onconet.ca



- Open-access human cancer gene knowledgebase
- Beta-version currently available on-line
- Features mRNA expression and mutation information on 3000 proteins previously linked to cancer
- Classifies oncoproteins (OPs), tumour suppressor proteins (TSPs), and tumour-requiring proteins (TRPs)

Approved Kinase Drugs and Those in Development



EGF receptor 3D structure with kinase inhibitor drug Tarceva

- >19 drugs approved
- >150 in clinical trials
- >500 in pre-clinical trials



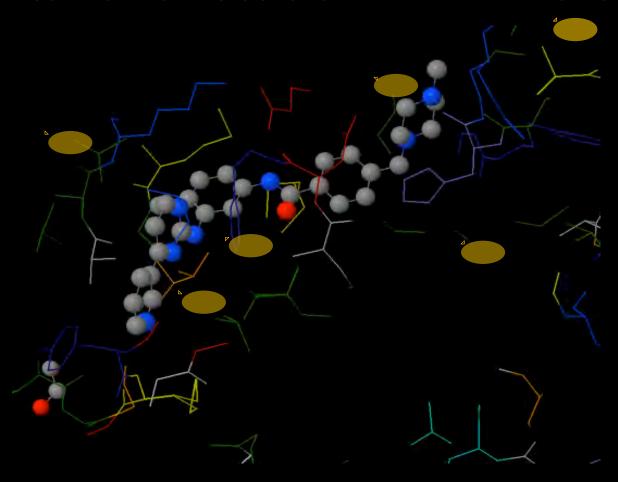
www.drugkinet.ca



- Human protein kinase drug knowledgebase
- Features experimental results for over 105,000 kinase drug pairs (400 kinases, >850 compounds that inhibit kinases)
- Features predictive data for another 200,000 kinasedrug pairs with 500 kinases
- Information and links to other websites provided about each drug



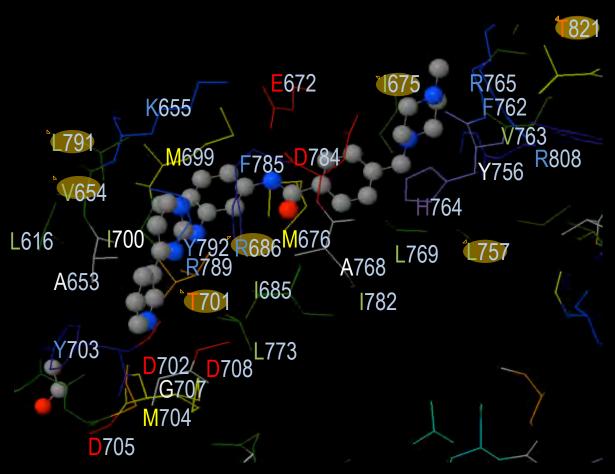
Identified Imatinib Interactions with DDR1 Amino Acid Residues



DrugKiNET identified amino acids are indicated in orange ovals



Identified Imatinib Interactions with DDR1 Amino Acid Residues

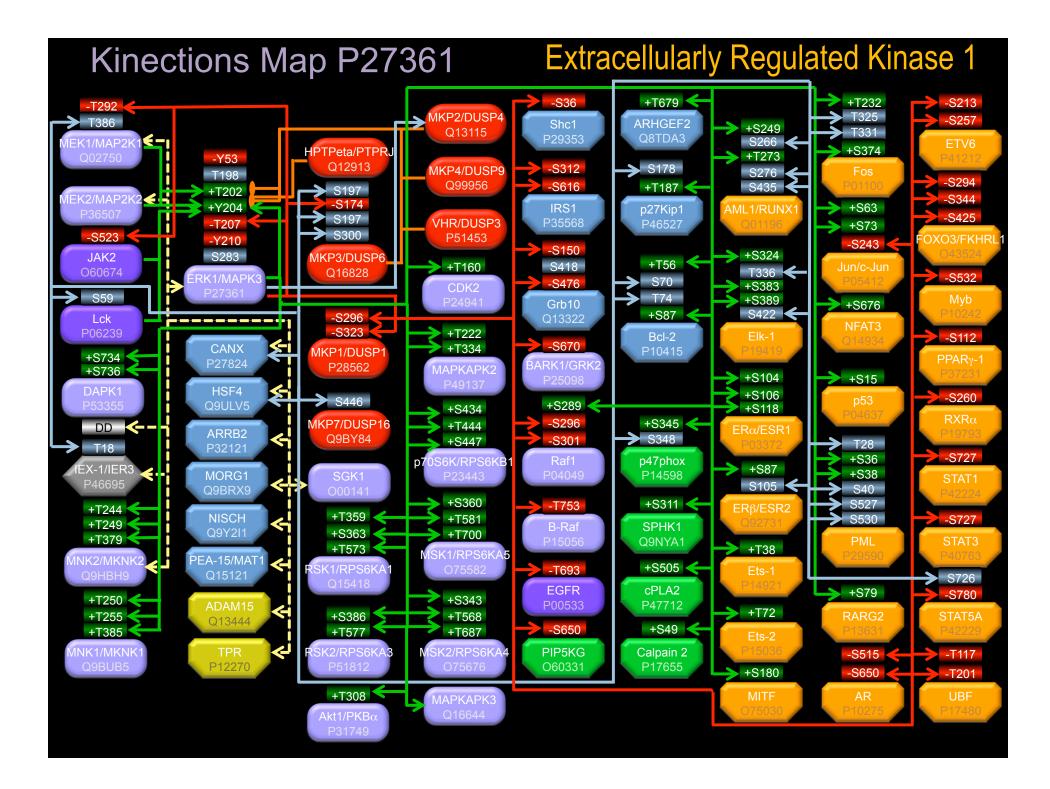


- DrugKiNET identified amino acids are indicated in orange ovals
- Similar analyses may define biomarkers for drug sensitivity



Two mapping initiatives are currently underway at Kinexus

- Kinections Maps
 - Static, hand-annotated mini-maps that are target-centric with immediate upstream and downstream direct and functional interactions tracked
 - To be provided with Kinex™ KAM- 880 Antibody Microarray analyses – An MS-Excel data table is generated with each map based on the data obtained from the comparison of two cell or tissue lysates
 - Will be available as MS-PowerPoint downloads





KinATLAS KnowledgeBase

- Dynamic, customizable tissue/cell-specific maps of protein substrate and drug interactions with kinases based on experimental and predictive data
- Identifies direct protein-protein interactions
- Constructed from PhosphoNET, TranscriptoNET and DrugKiNET data and hyperlinks to these and other websites
- Generates new maps with associated protein as the hub



KINITHES

Human Protein Interaction KnowledgeBase

SIGNET KNOWLEDGEBANK + KINETICA ONLINE + KINETICA

Select type of query desired

Click to view options

Home | Contact | Credits

Want to compare your Kinexus proteomics

Query our KiNET immunoblotting

DataBase online with free access

data with thousands of other studies?

Query Type

Single Target Protein Phosphorylation Interaction

This query identifies the top phosphorylation interactions involving protein kinases and their substrates around a selected protein of interest. The target protein appears in the center of the generated interaction map that is cell, tissue or organ-specific. The stronger the kinase-substrate connection as calculated with our Kinase Substrate Predictor Version 2.0 Algorithm, the closer the associated protein. Apply the following filters to narrow down the most relevant interactions to your individual specifications.

Filters

Step 1 - Target Protein Identification

Provide the gene name, protein name, UniProt ID, RefSeq or IPI ID as a search term.

Type in at least 3 letters of search term

Step 2 - Human Cell/Tissue Specification

Use one of the two pull-down menus to specify the cell, tissue or organ type of interest.

Select from list of organs and tissues

Select from list of established cell lines

Step 4 - Generation of Protein Phosphorylation Map

Click on boxes below to produce a custom map or reset parameters. The map will appear in a new window.

Generate Map

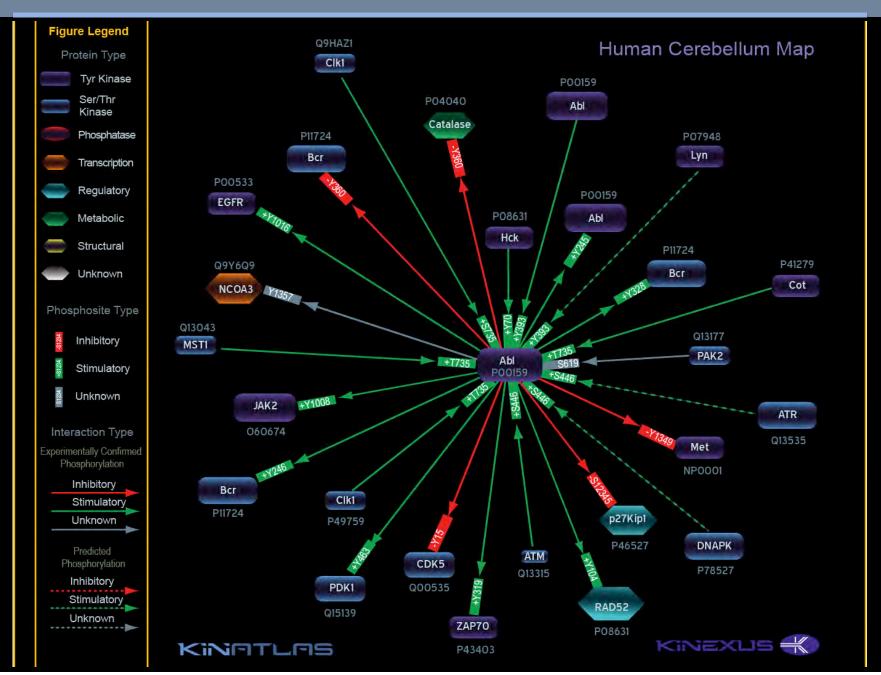
Reset

Step 3 - Selection of Display Parameters

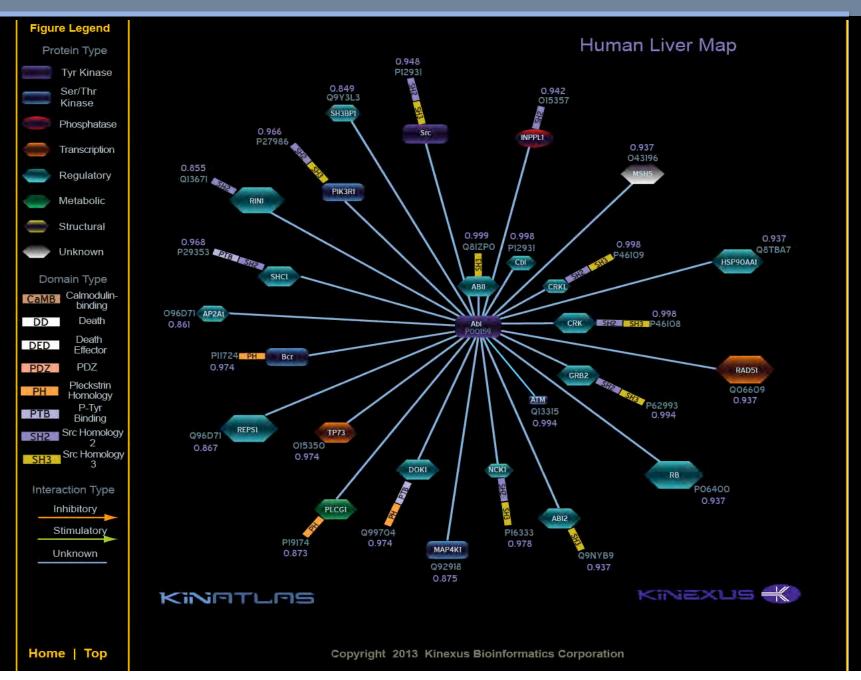
Boxes that are marked are activated to display. Click on boxes to change status.

- M Show experimentally-derived interactions
- Show predicted interactions
- Show upstream inputs
- M Show downstream outputs
- ✓ Show stimulatory phosphosites
- ✓ Show inhibitory phosphosites
- Show non-defined phosphosites
- ✓ Show protein kinases
- ✓ Show protein phosphatases
- Show transcription factors
- M Show regulatory proteins
- ✓ Show metabolic proteins
- ✓ Show structural proteins
- ✓ Show uncharacterized proteins
- ✓ Show black background
- Show icons with uniform size
- ✓ Show UniProt ID

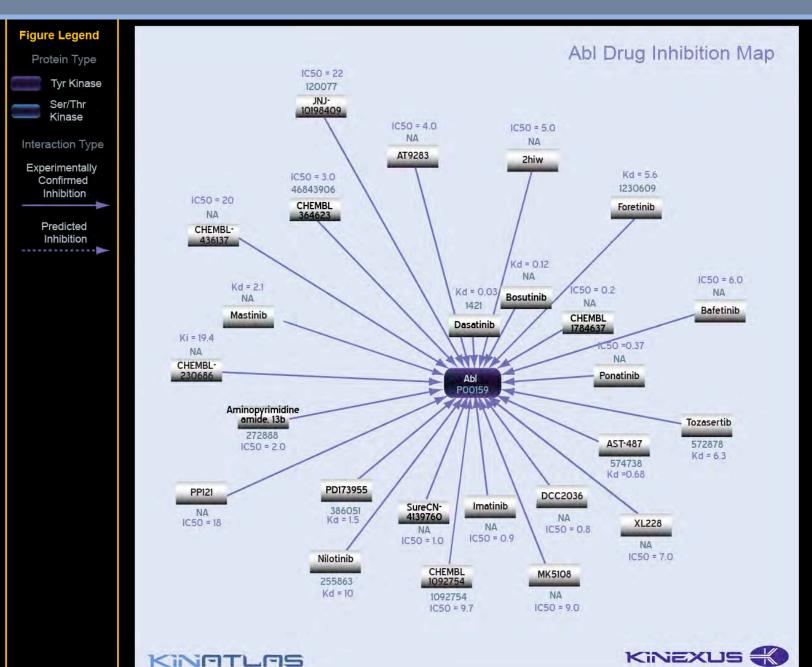












University of British Columbia

Javad Safaei, Dr. Jano Manuch, Shabab Hossein, Alireza Davoodi, Shenshen Lai, Sehyun Cho, Stephen Yiu, Chuen Choi, Pier-Luc Clemont, Christine Eisner, Cameron Rogers, Scott Wilder, Leon, Chew, Erandika Gunaretnam, Anna Isphording, Christopher Laver, Asher Mendelson, Steven Pham, Cecilia Sjoestroem, and Jovian Wat

Simon Fraser University

Dr. Ladislav Stacho

Kinexus Bioinformatics Corporation

Dr. Steven Pelech, Winnie So, Catherine Sutter, Dr. Hong Zhang, Dr. Dirk Winkler, Dr. Jane Shi, Dr. Arthur Yee, Dr. Rod Verdie, Cameron Bowyer, Litsa Blanis, Angie Chu, Mandy Chung, Pringle Comia, Aneesa Din, Nova Do, Bryanna Grace, Eileen Hu, Iris Juan, Joanna Kam, Stephanie Lam, Adam Leigh, Raymond Leung, Sara Marrello, Charrise Pagarigan, Andrew Park, Michael Peabody, Sabrina Rayworth, Ryan Saranchuk, Kevin Sha, Ellen Sung, Sharan Swarup, Amy Tam, Ryan Whitehead, Christine Yu, and Sarah Zaidi

British Columbia Institute of Technology PhosphoNET (www.phosphonet.ca)

Joe Hu, Jonathan Jose, Ysabel Lago, David Liau, John Liau, Christine Livingstone, Melissa Manalac, Travis Nicholson, Kevin Odger, Ryan Pattinson, Nevin Petersen, Hannah Rosellon, Janice Sargent, Brandon Wong, and Alvin Yip

TranscriptoNET (www.transcriptonet.ca)

Isan Chen, Keegan Kelly, Aly Jamani, and Colin Nguyen

DrugKiNET (www.drugkinet.ca)

James Chen, Andy Chow, Sunju Christine Jeong, and Dan Stephenson

OncoNET (www.onconet.ca)

Kyle Li, Theo Mutia, Travis Ryder, and Clarence Sng

KiNET-AM (www.kinet-am.ca)

Simon Ho, Nicholas Tagle, Fausto Faioli, Igor Kozlov, and Justin Ma