Target Prediction for an Open Access Set of Compounds Active against *Mycobacterium tuberculosis*

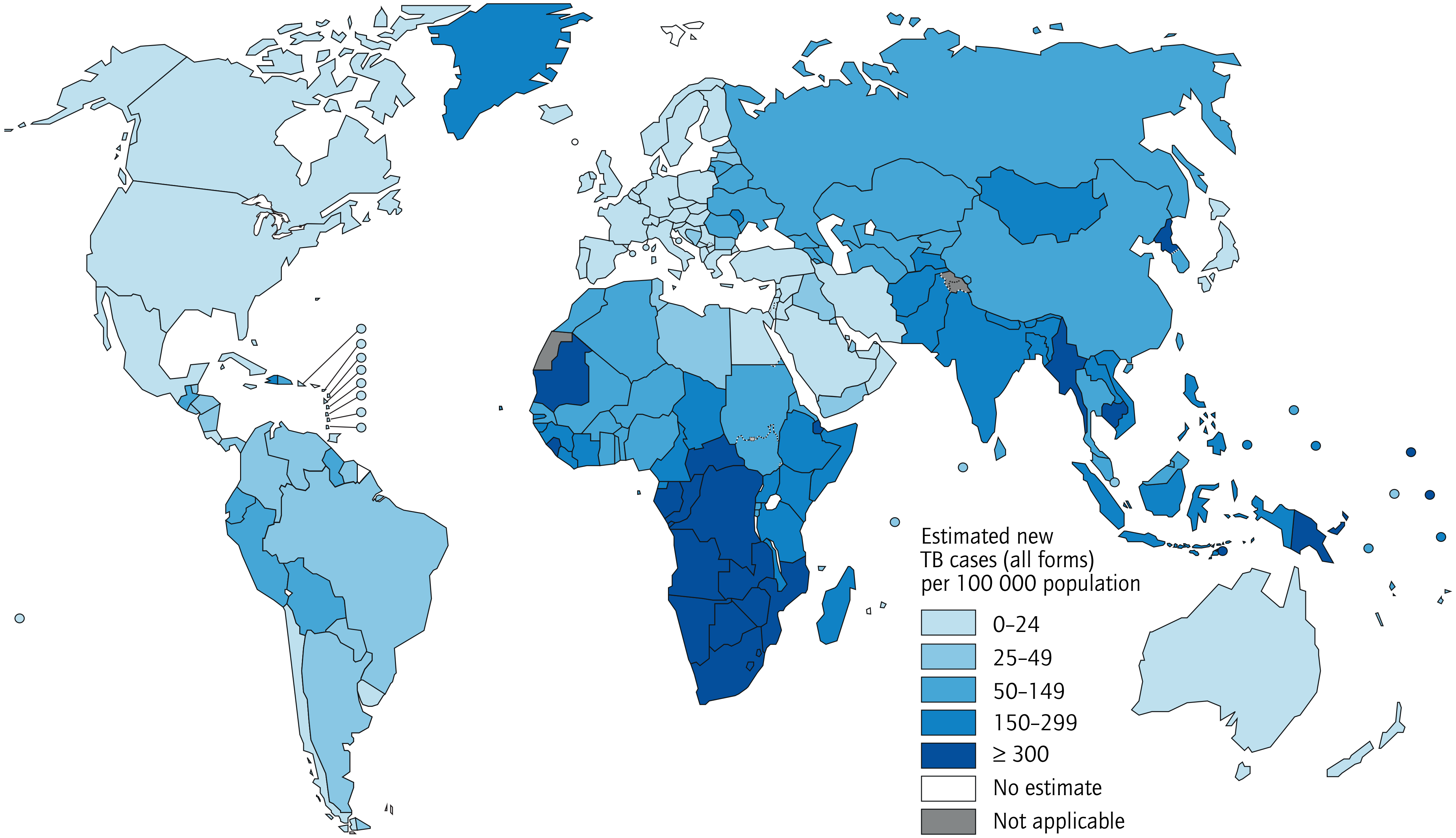
Francisco Martínez-Jiménez

XII Jornadas de Bioinformática, Sevilla

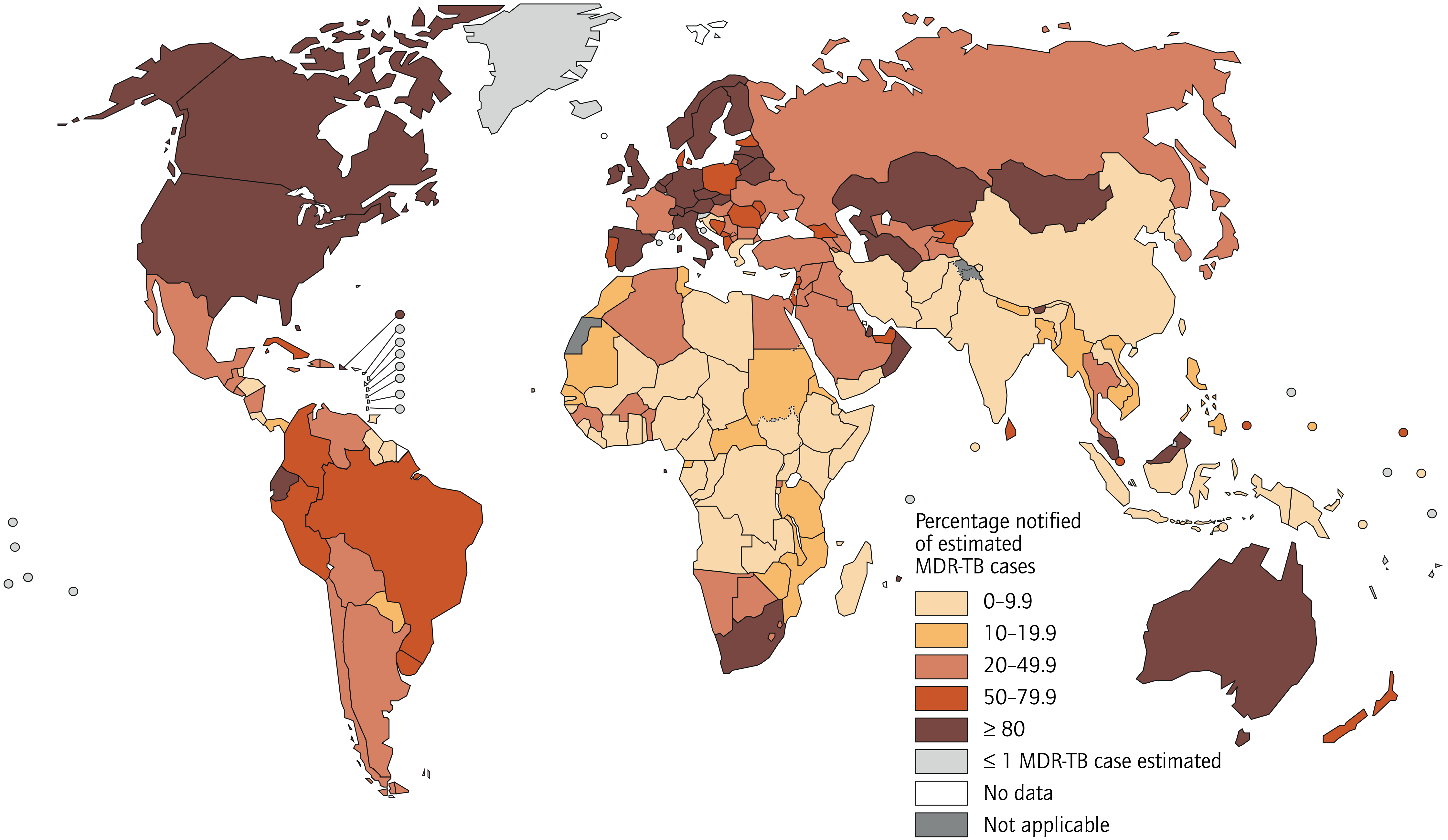
One third of the world's population is infected with Mycobacterium tuberculosis, the causative agent of tuberculosis.

WHOTuber2012. Global Tuberculosis Report 2012.

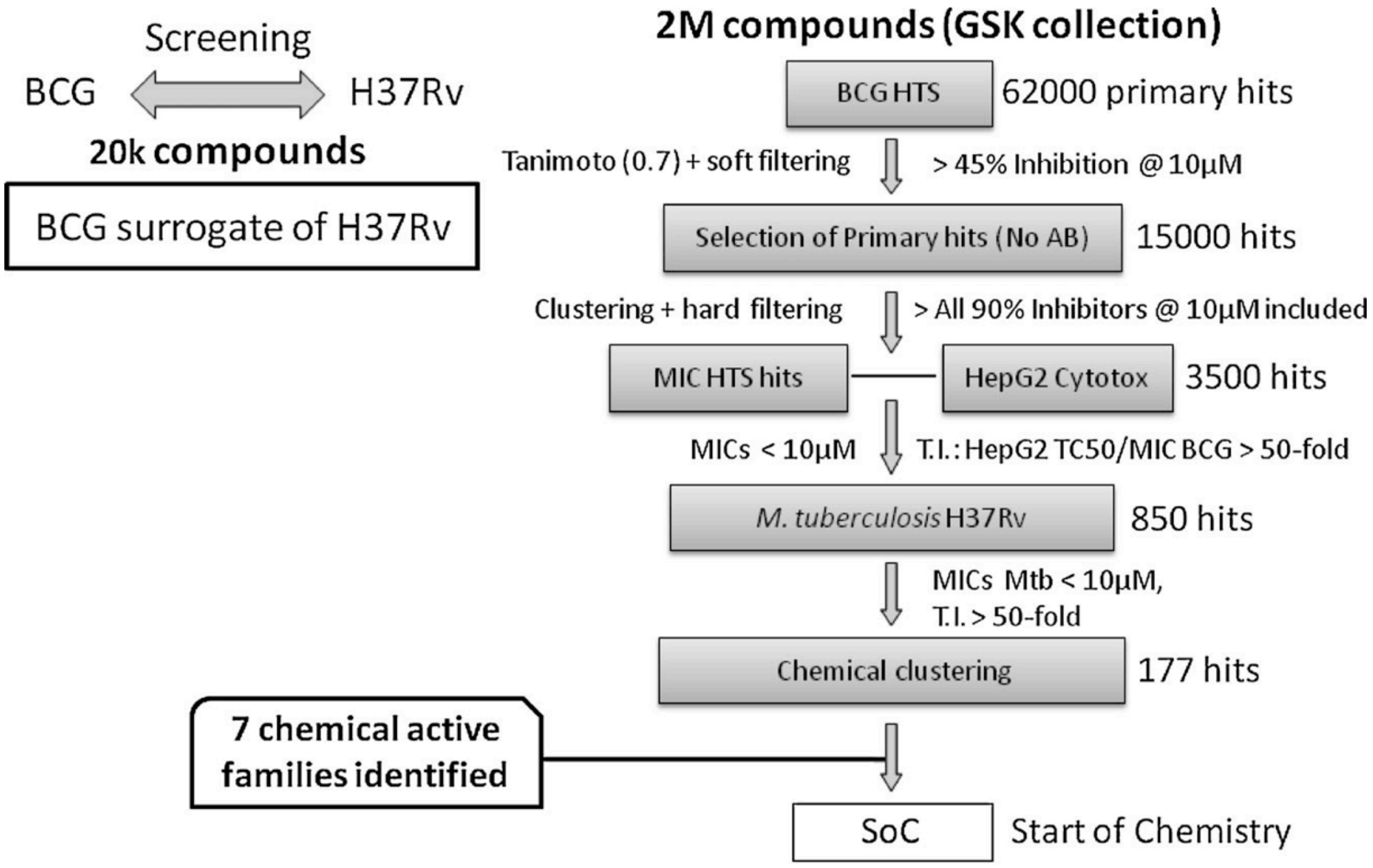
Tuberculosis incidence...



MultiDrugResistant-TB



Phenotypic screening against *Mycobacterium tuberculosis*



Screening

BCG ⟷ H37Rv

20k compounds

BCG surrogate of H37Rv

2M compounds (GSK collection)

BCG HTS — 62000 primary hits

Tanimoto (0.7) + soft filtering ⇩ > 45% Inhibition @ 10μM

Selection of Primary hits (No AB) — 15000 hits

Clustering + hard filtering ⇩ > All 90% Inhibitors @ 10μM included

MIC HTS hits — HepG2 Cytotox — 3500 hits

MICs < 10μM ⇩ T.I.: HepG2 TC50/MIC BCG > 50-fold

M. tuberculosis H37Rv — 850 hits

⇩ MICs Mtb < 10μM,
T.I. > 50-fold

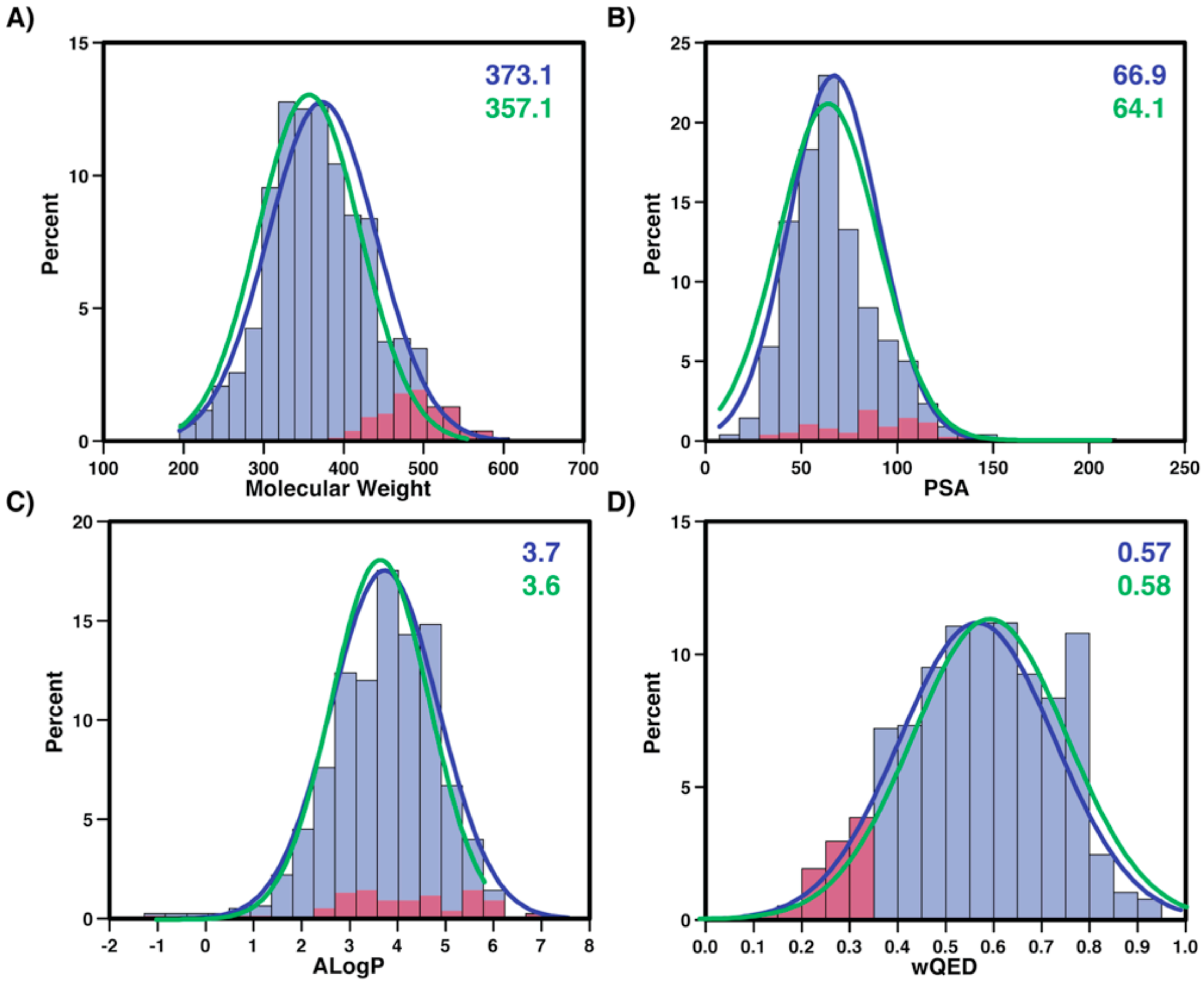
Chemical clustering — 177 hits

7 chemical active families identified

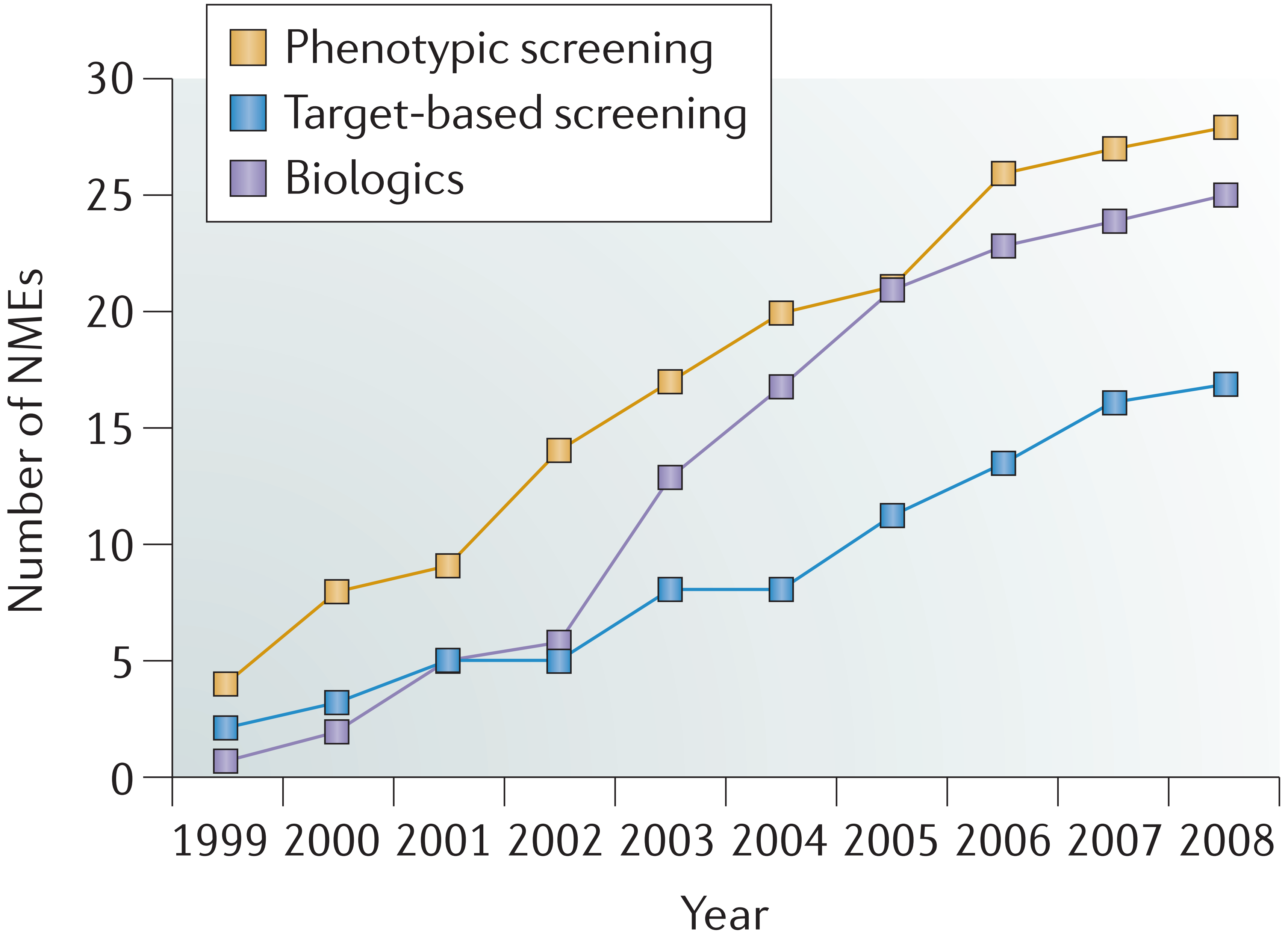
SoC — Start of Chemistry

Ballell, L.et al (2013). Fueling open-source drug discovery: 177 small-molecule leads against tuberculosis. *ChemMedChem*.

776 compounds chemical features

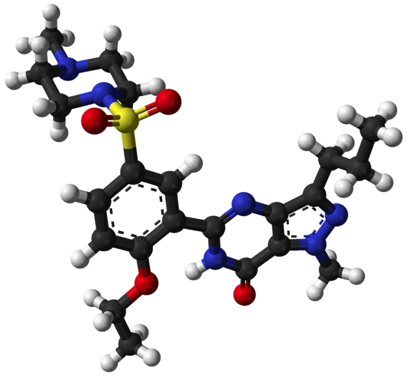


Phenotypic screenings



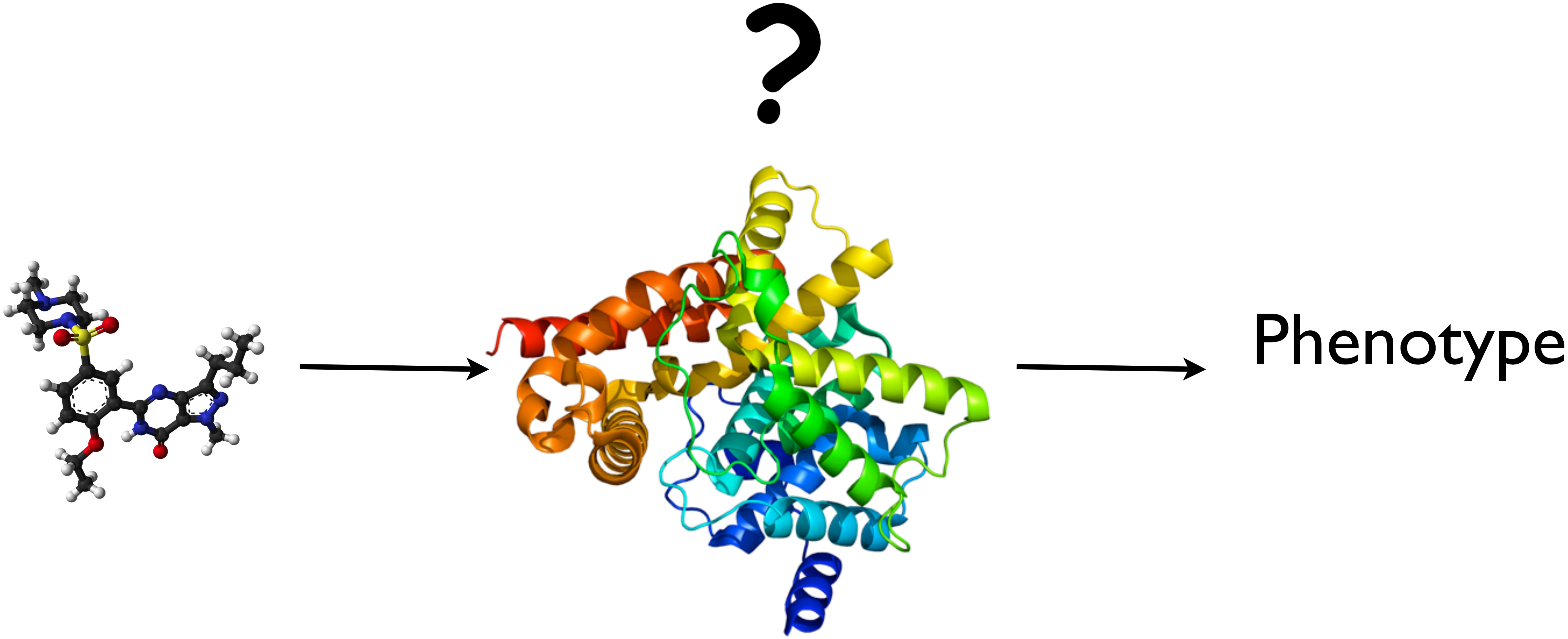
Swinney, D.C. & Anthony, J. How were new medicines discovered? *Nat. Rev. Drug Discov*

Finding out the mode of action...



Phenotype

Finding out the mode of action...

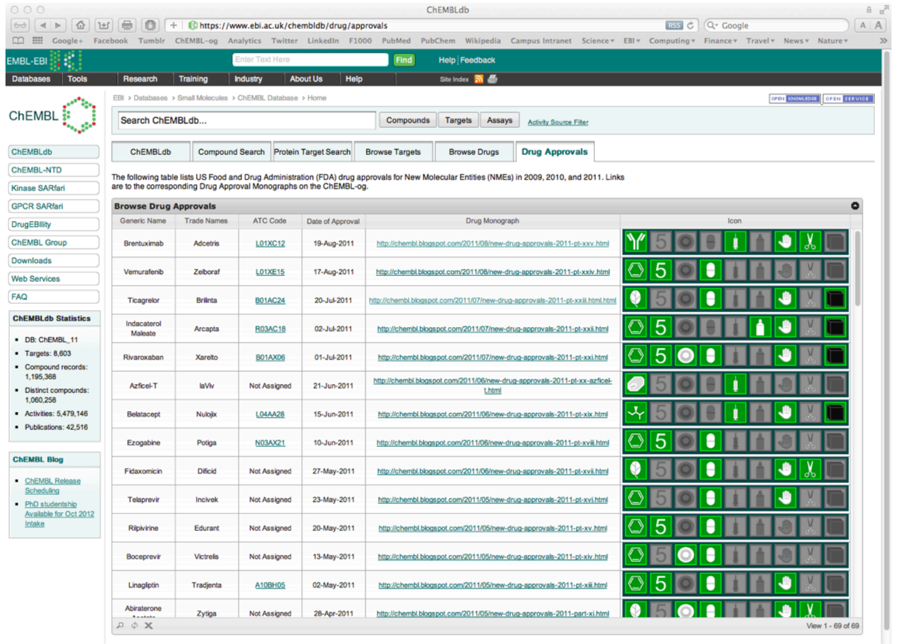


?

Phenotype

Methods

2D-Chemogenomics Approach



ChEMBLdb Statistics

- DB: ChEMBL_11
- Targets: 8,603
- Compound records: 1,195,368
- Distinct compounds: 1,060,258
- Activities: 5,479,146
- Publications: 42,516

ChEMBL Blog

- ChEMBL Release Scheduling
- PhD studentship Available for Oct 2012 Intake

The following table lists US Food and Drug Administration (FDA) drug approvals for New Molecular Entities (NMEs) in 2009, 2010, and 2011. Links are to the corresponding Drug Approval Monographs on the ChEMBL-og.

Browse Drug Approvals

Generic Name	Trade Names	ATC Code	Date of Approval	Drug Monograph	Icon
Brentuximab	Adcetris	L01XC12	19-Aug-2011	http://chembl.blogspot.com/2011/08/new-drug-approvals-2011-pt-xxv.html	
Vemurafenib	Zelboraf	L01XE15	17-Aug-2011	http://chembl.blogspot.com/2011/08/new-drug-approvals-2011-pt-xxiv.html	
Ticagrelor	Brilinta	B01AC24	20-Jul-2011	http://chembl.blogspot.com/2011/07/new-drug-approvals-2011-pt-xxiii.html.html	
Indacaterol Maleate	Arcapta	R03AC18	02-Jul-2011	http://chembl.blogspot.com/2011/07/new-drug-approvals-2011-pt-xxii.html	
Rivaroxaban	Xarelto	B01AX06	01-Jul-2011	http://chembl.blogspot.com/2011/07/new-drug-approvals-2011-pt-xxi.html	
Azficel-T	laViv	Not Assigned	21-Jun-2011	http://chembl.blogspot.com/2011/06/new-drug-approvals-2011-pt-xx-azficel-t.html	
Belatacept	Nulojix	L04AA28	15-Jun-2011	http://chembl.blogspot.com/2011/06/new-drug-approvals-2011-pt-xix.html	
Ezogabine	Potiga	N03AX21	10-Jun-2011	http://chembl.blogspot.com/2011/06/new-drug-approvals-2011-pt-xviii.html	
Fidaxomicin	Dificid	Not Assigned	27-May-2011	http://chembl.blogspot.com/2011/06/new-drug-approvals-2011-pt-xvii.html	
Telaprevir	Incivek	Not Assigned	23-May-2011	http://chembl.blogspot.com/2011/05/new-drug-approvals-2011-pt-xvi.html	
Rilpivirine	Edurant	Not Assigned	20-May-2011	http://chembl.blogspot.com/2011/05/new-drug-approvals-2011-pt-xv.html	
Boceprevir	Victrelis	Not Assigned	13-May-2011	http://chembl.blogspot.com/2011/05/new-drug-approvals-2011-pt-xiv.html	
Linagliptin	Tradjenta	A10BH05	02-May-2011	http://chembl.blogspot.com/2011/05/new-drug-approvals-2011-pt-xiii.html	
Abiraterone	Zytiga	Not Assigned	28-Apr-2011	http://chembl.blogspot.com/2011/05/new-drug-approvals-2011-part-xi.html	

EMBL-EBI

George Papadatos

John P. Overington

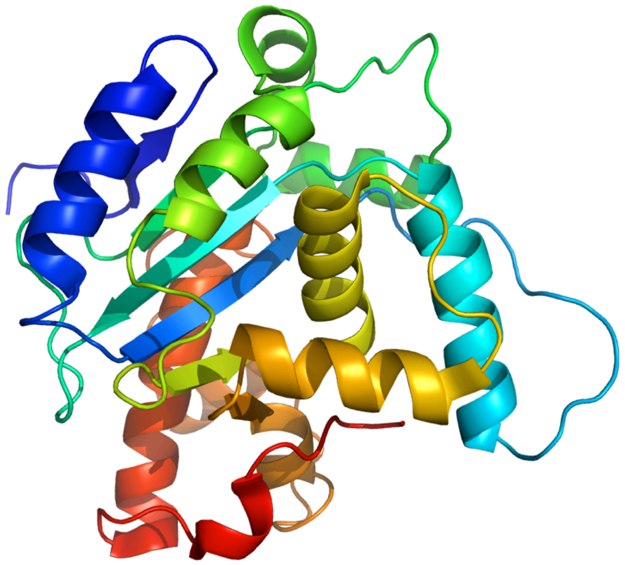
Historical Approach

gsk GlaxoSmithKline

Vinod Kumar

James Brown

3D-Structural Approach



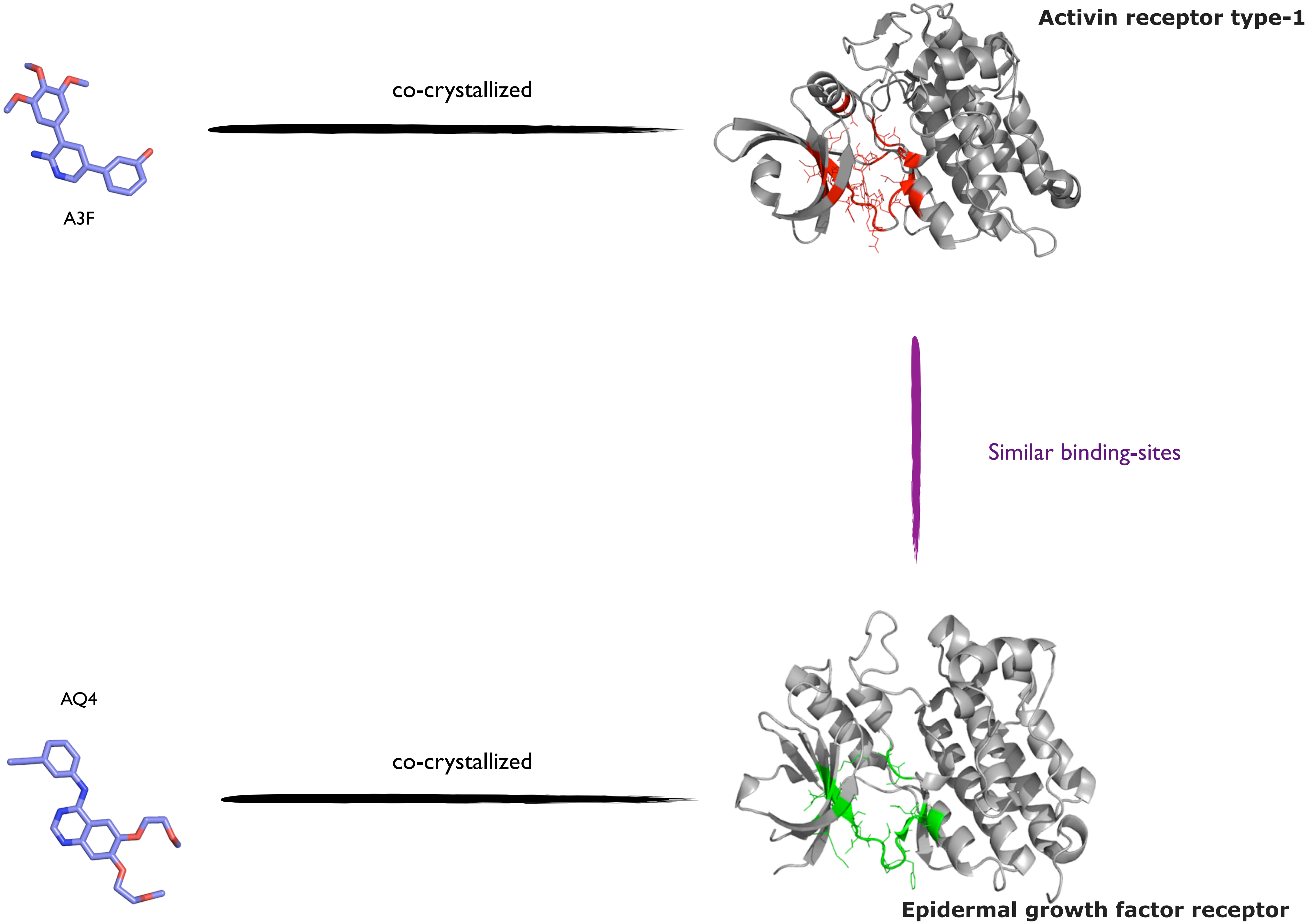
cnag
centre nacional d'anàlisi genòm
centro nacional de análisis gen

CRG
Centre for Genomic Regulation

Francisco Martínez-Jiménez

Marc A. Martí-Renom

Similar binding-sites tend to bind similar ligands



A3F

co-crystallized

Activin receptor type-1

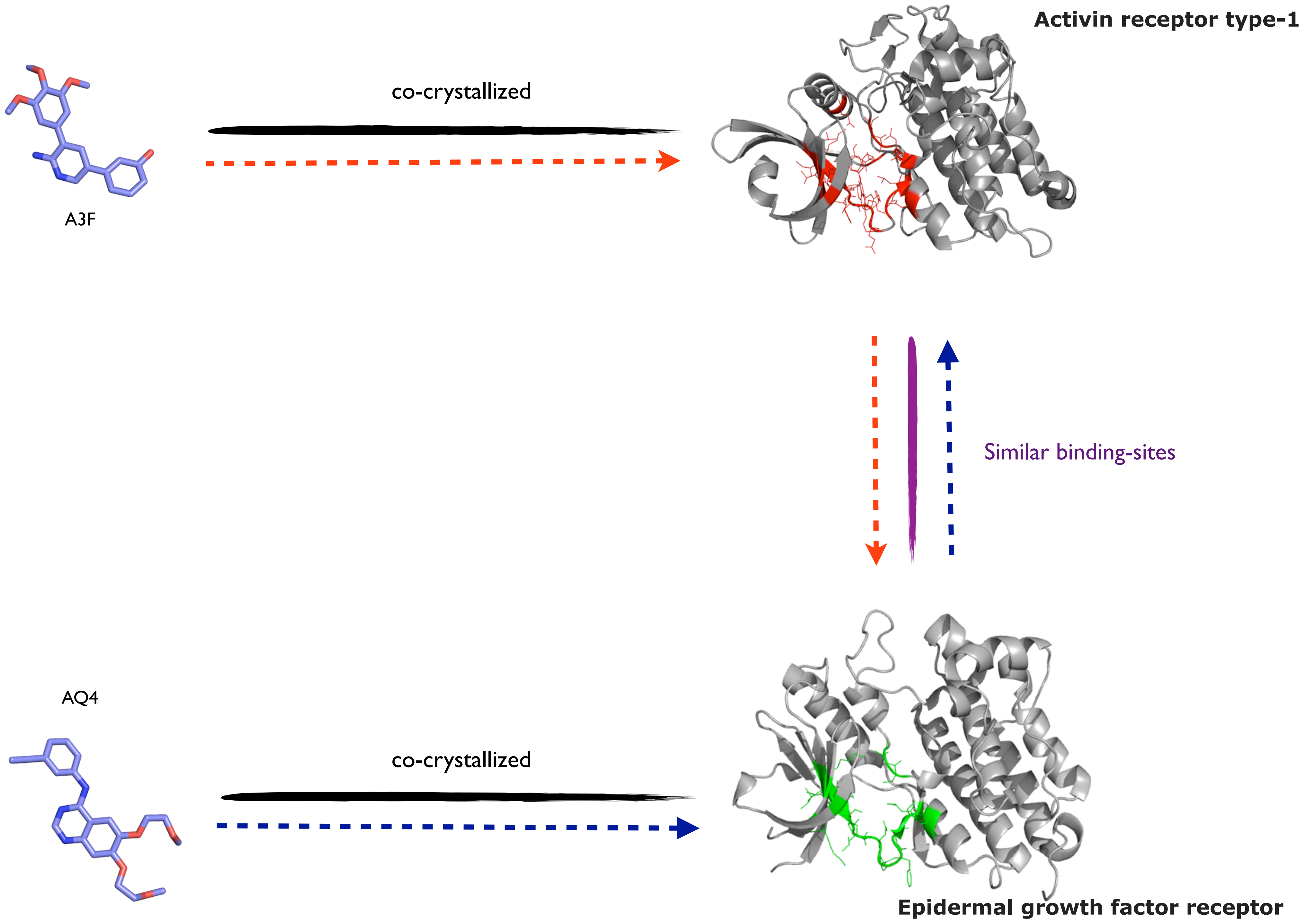
Similar binding-sites

AQ4

co-crystallized

Epidermal growth factor receptor

Similar binding-sites tend to bind similar ligands



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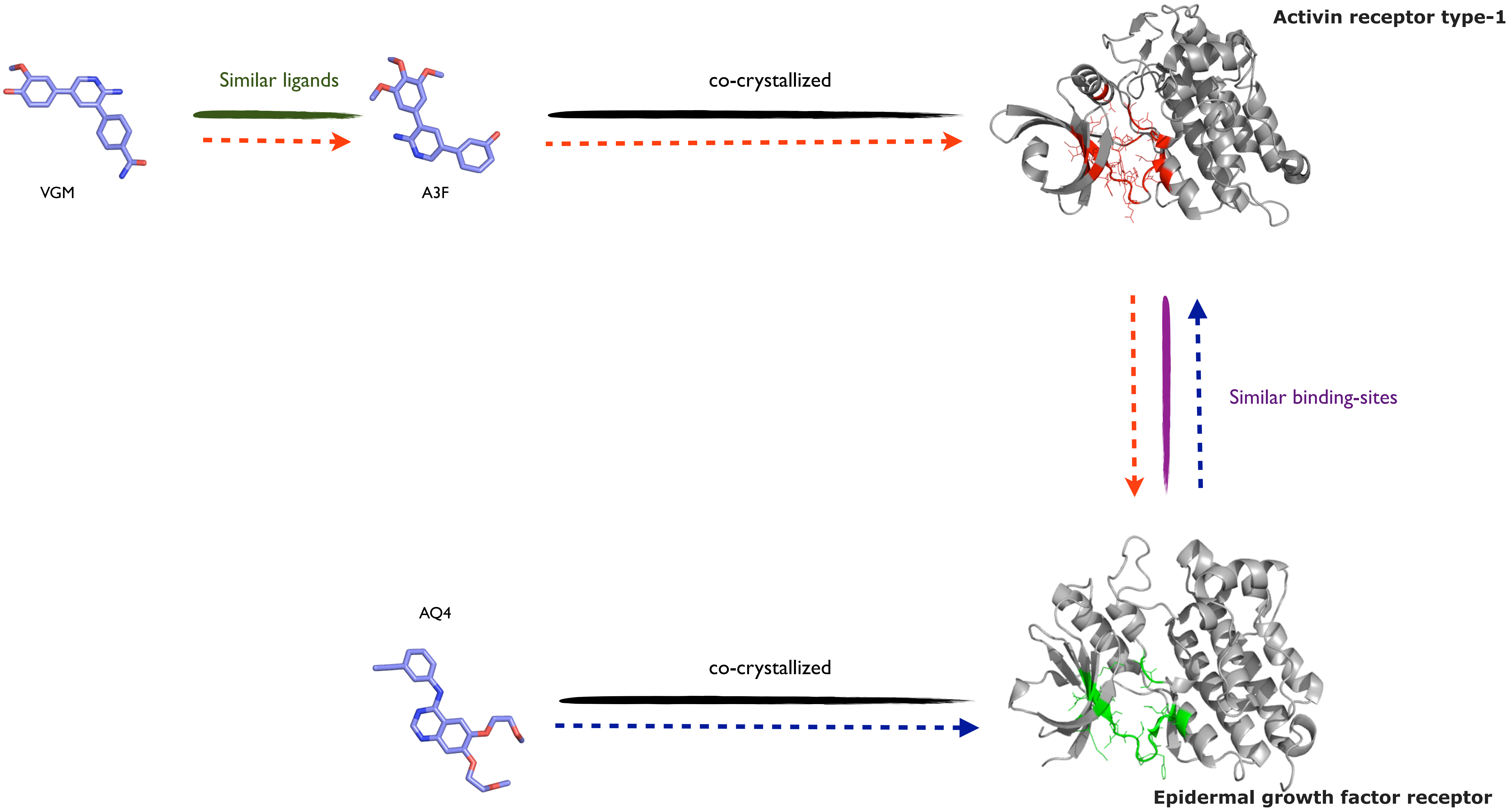


Activin receptor type-1

Similar ligands

co-crystallized

VGM

A3F

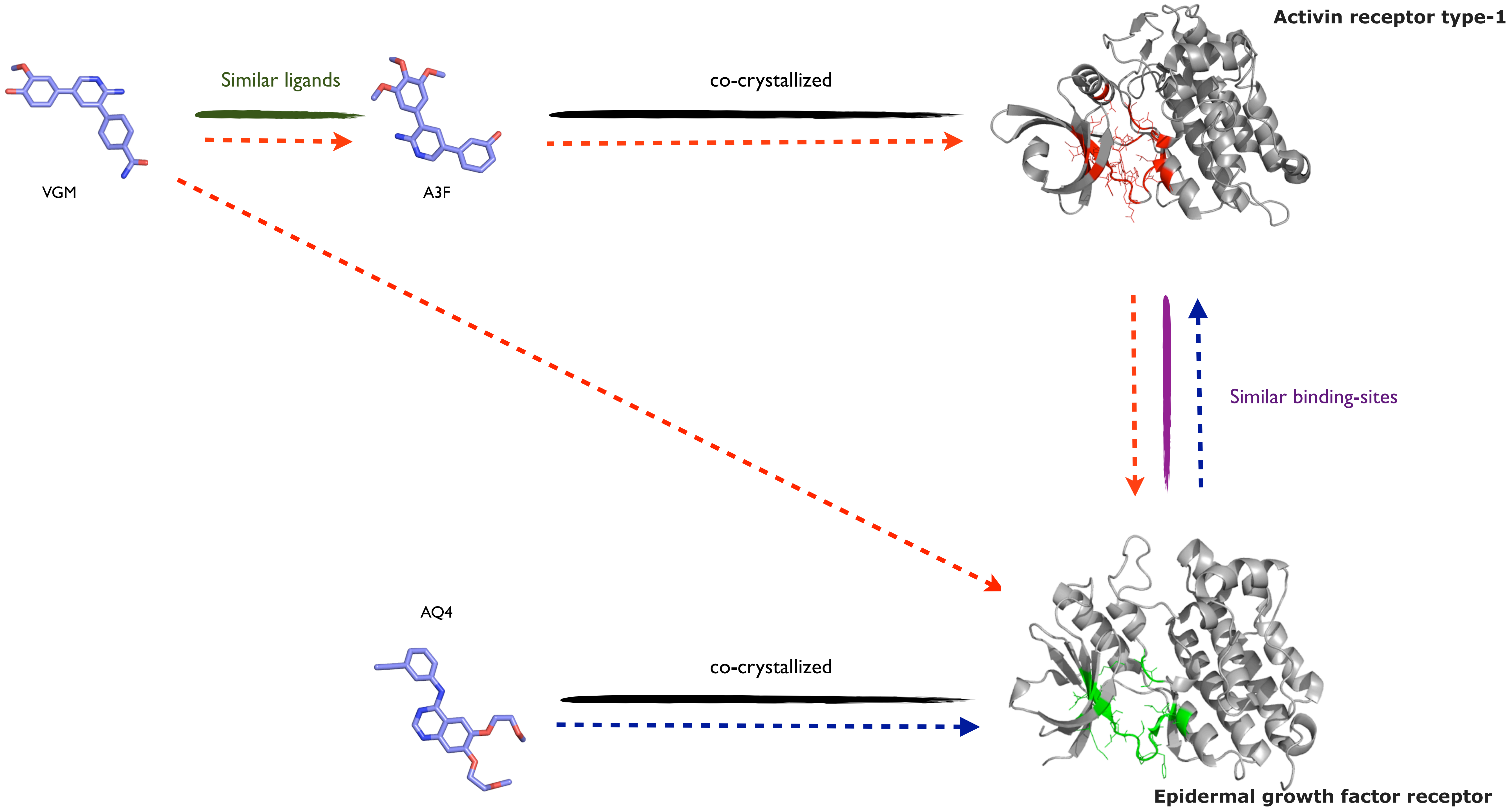
Similar binding-sites

AQ4

co-crystallized

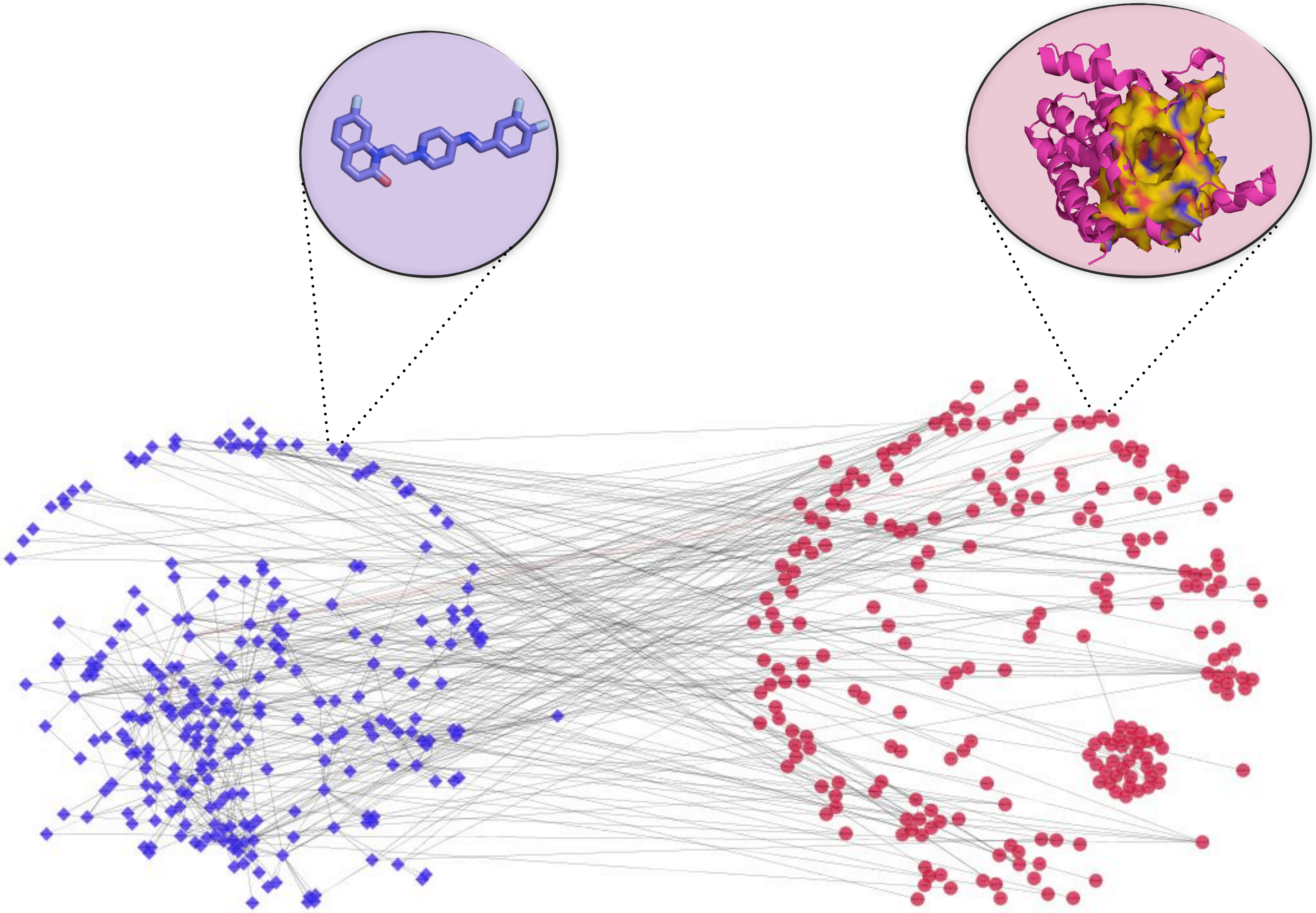
Epidermal growth factor receptor

Similar binding-sites tend to bind similar ligands



Network-based Method

nAnnolyze

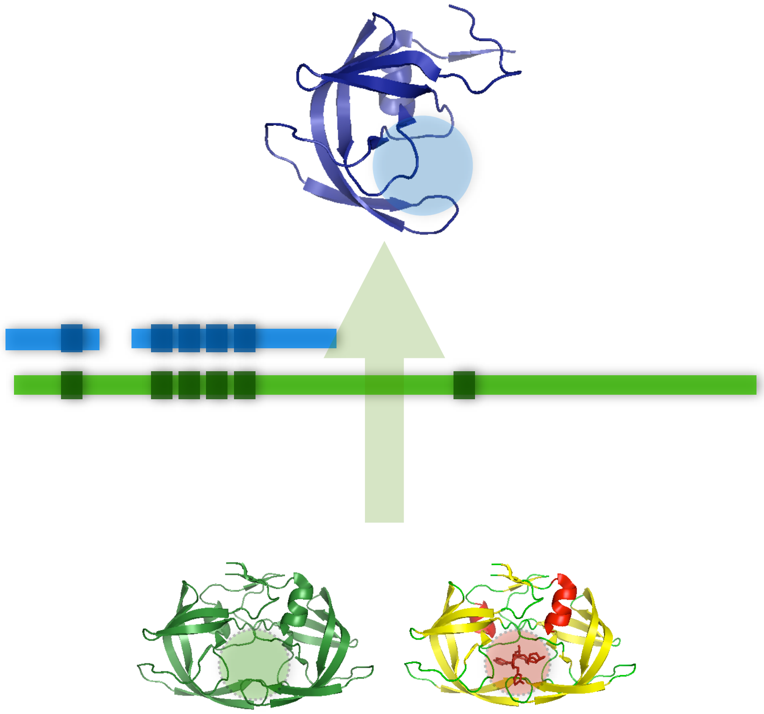


Applying the method, modeling genomes...

1. Modeling

2. Binding-site inheritance

3D model



PDB templates

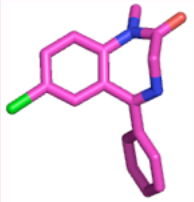
UCSF
University of California
San Francisco

Ursula Pieper

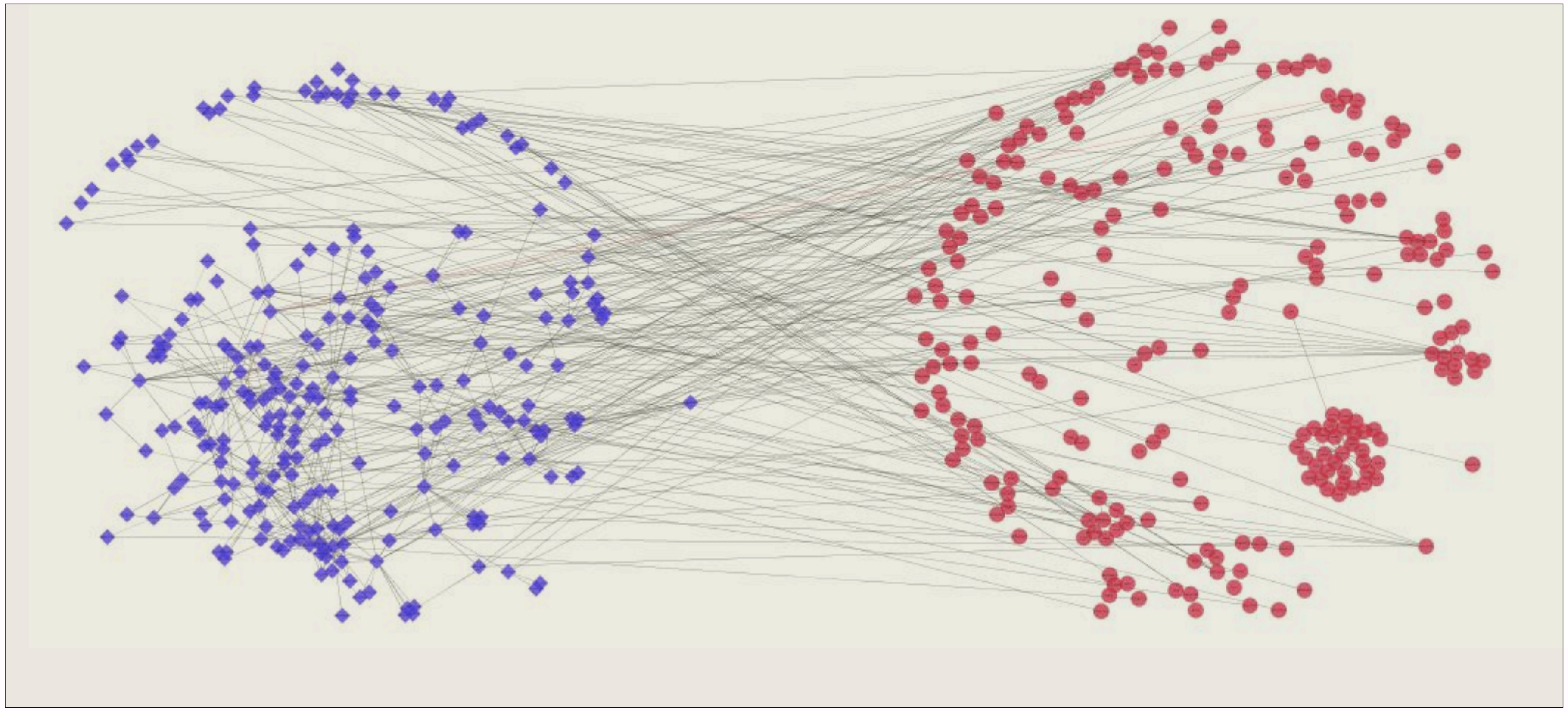
Andrej Sali

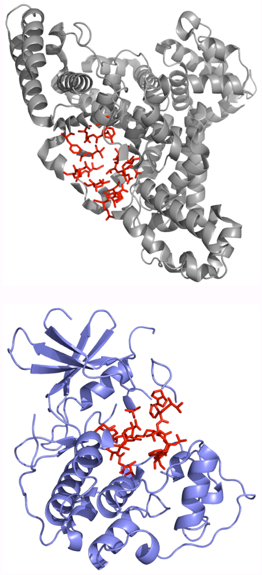
	Bacterial proteomes
3D reliable models	5,008 no overlapping
Different Proteins	5,008 different proteins
Inherited binding-sites	30,000

Looking for targets...



GSK
Drug



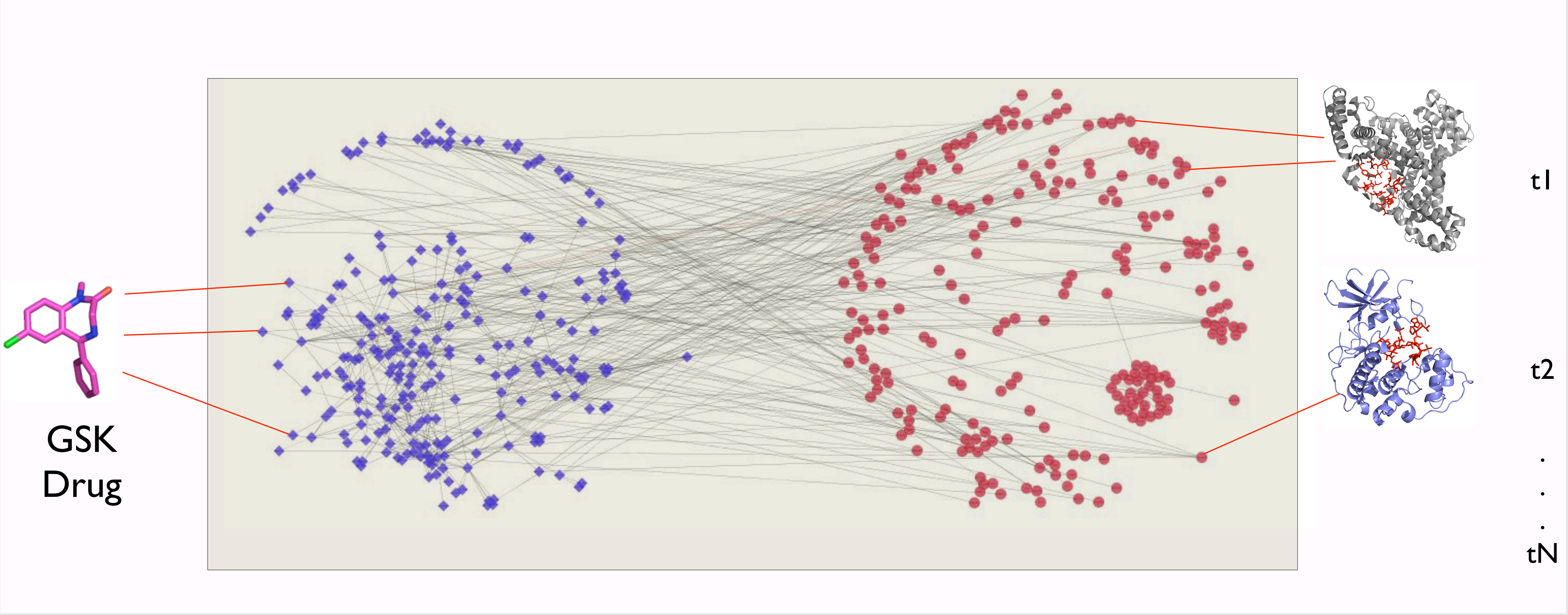


t1

t2

.
.
.
tN

Looking for targets...



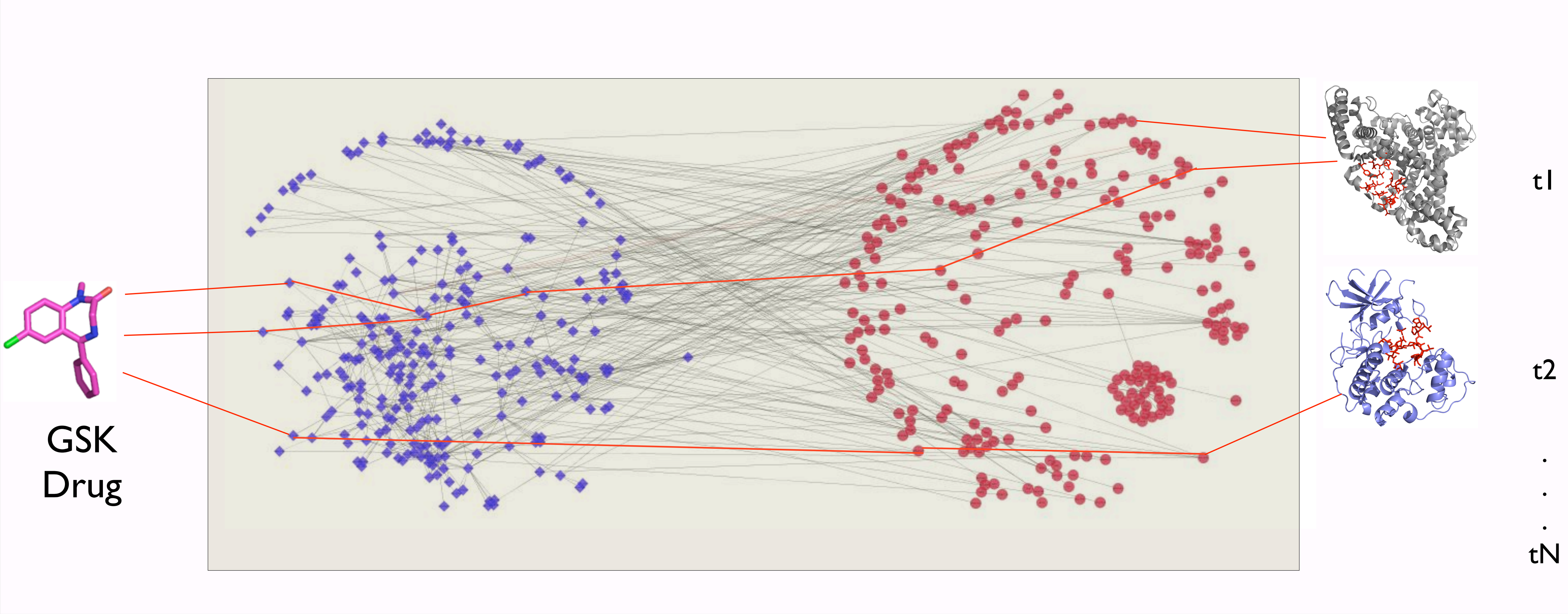
GSK
Drug

t1

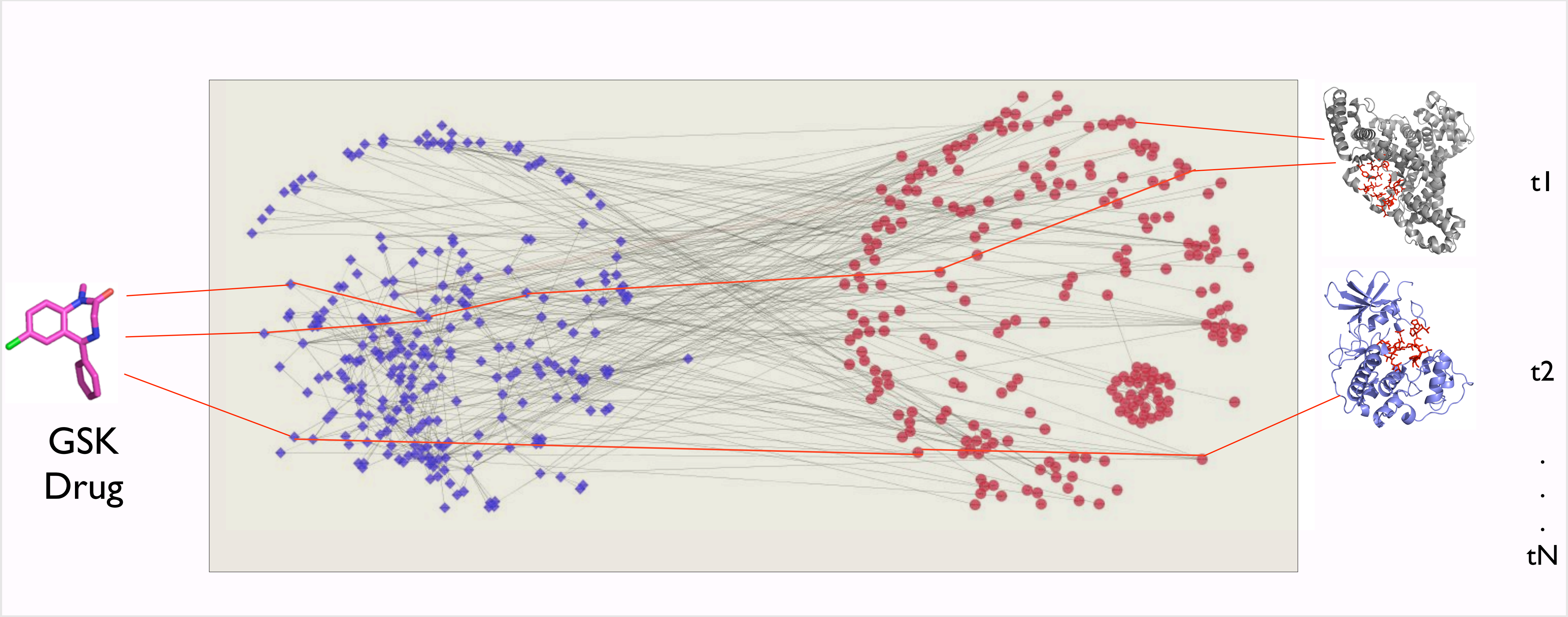
t2

.
.
.
tN

Looking for targets...



Looking for targets...



Ligand	Target	Distance	Global Z-score	Local Z-score
GSK1	pknB Kinase	1.3	-1.6	-2.5
GSK1	mapB	2.5	2.3	1.02
GSK1	sahH	1.9	-1.6	-3.16
GSK1	Mmpl3	2.6	2.42	2.97

Statistical assessment of predicted links between compounds and targets

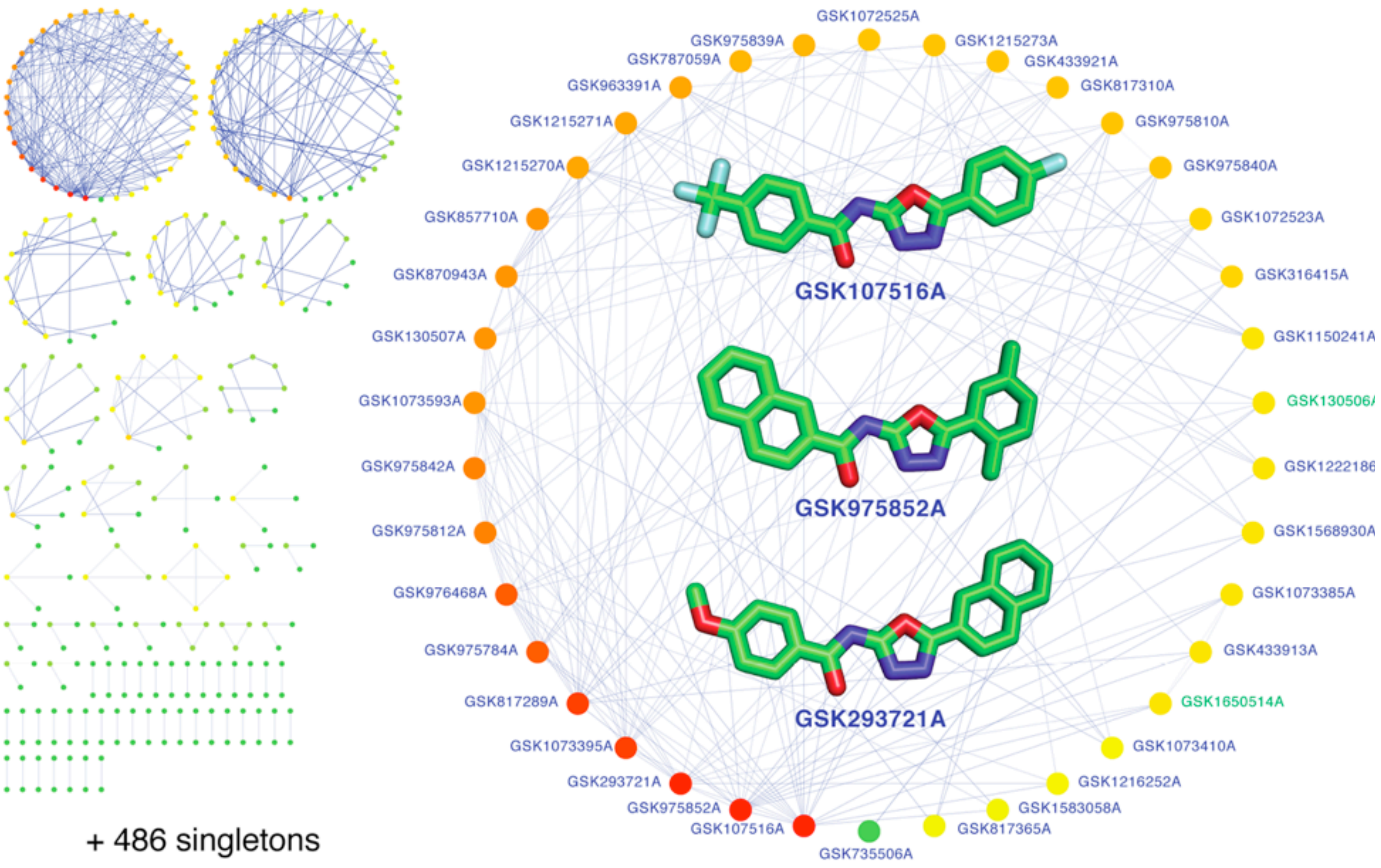
- We merged all the predictions from the 3 methods.

- Significance of links using **groups of similar compounds** and the **targets KEGG pathways**.

- LogOdds. Odds of an observation given its probability.

- p-value using Fisher´s exact test for 2x2 contingency table comparing two groups of annotations.

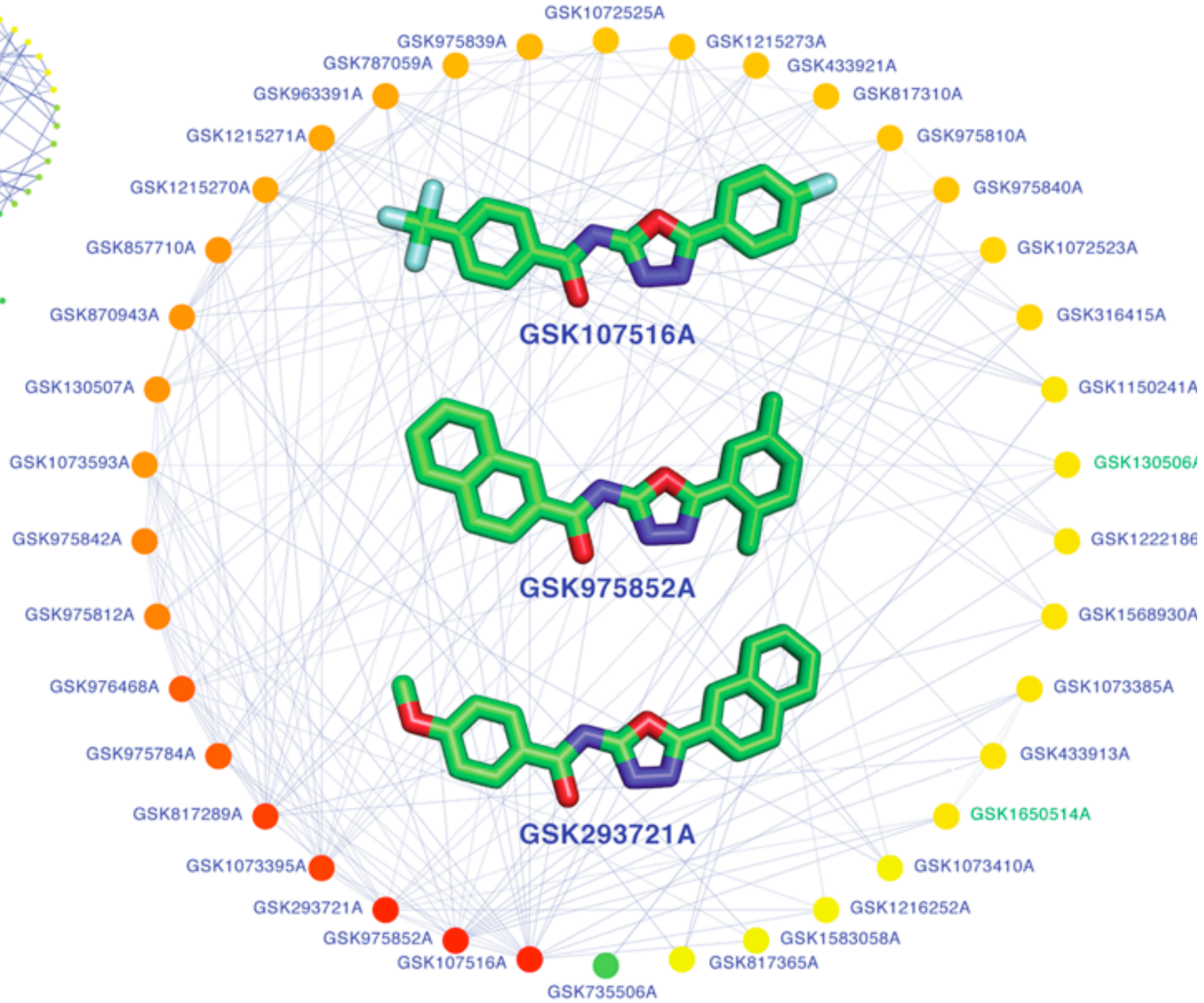
Compound dataset diversity

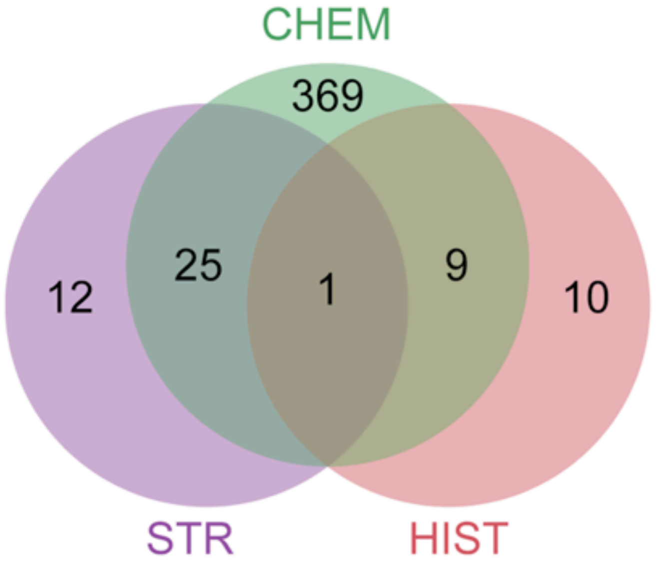


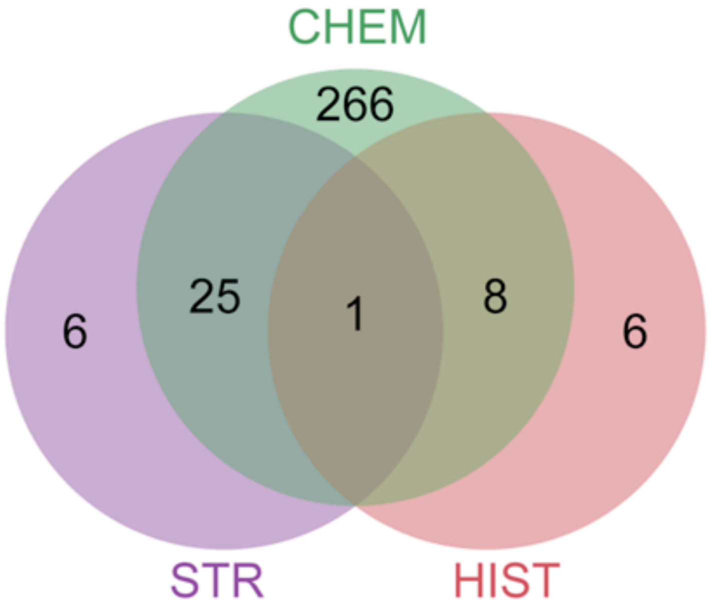
+ 486 singletons

Compound dataset diversity

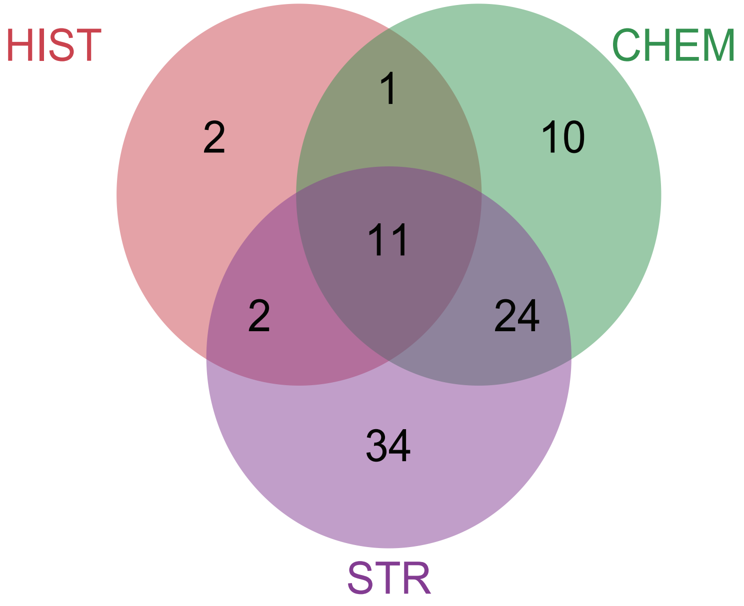
+ 486 singletons

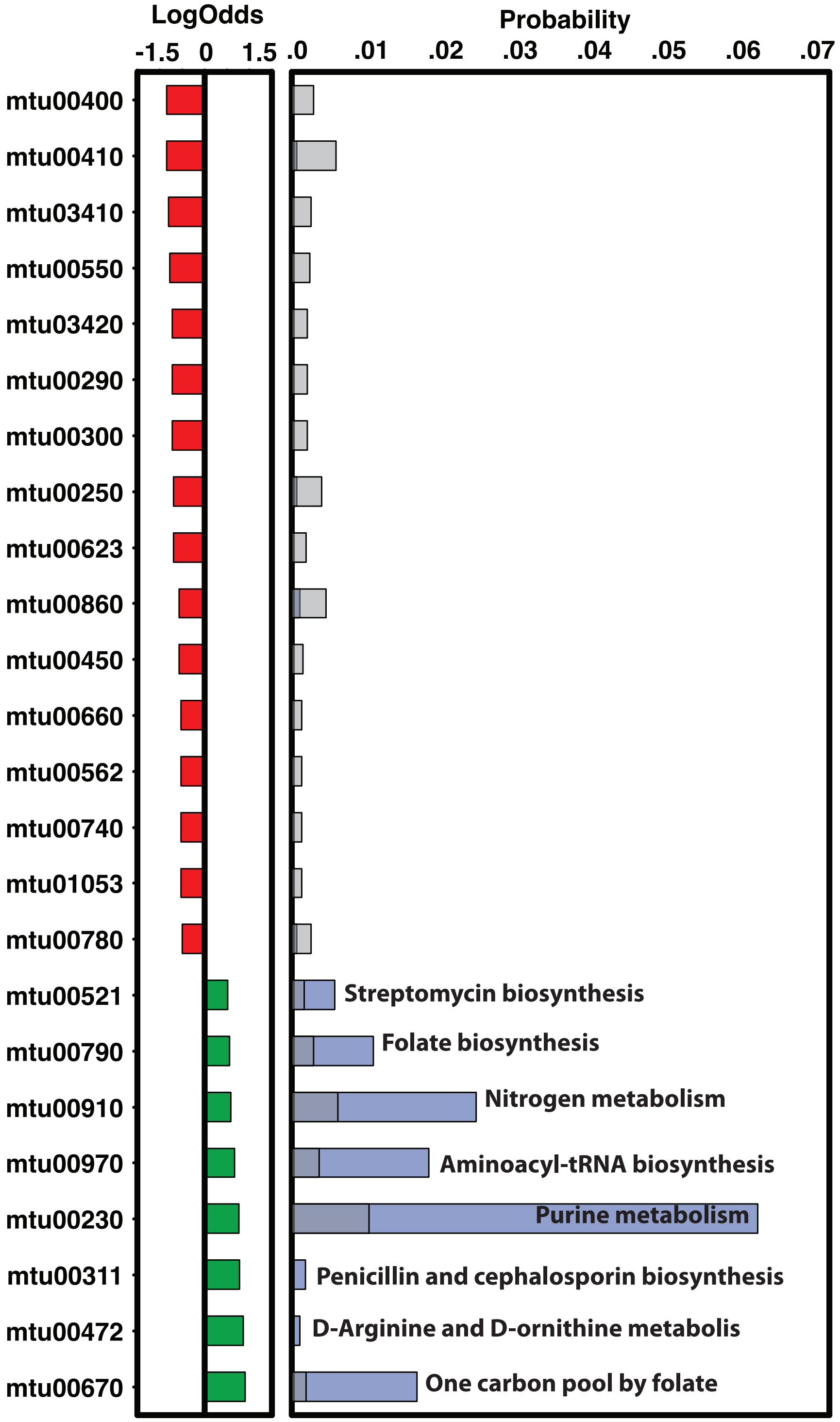






Targeting essential aminoacids metabolism pathways





Significant drug-protein pairs

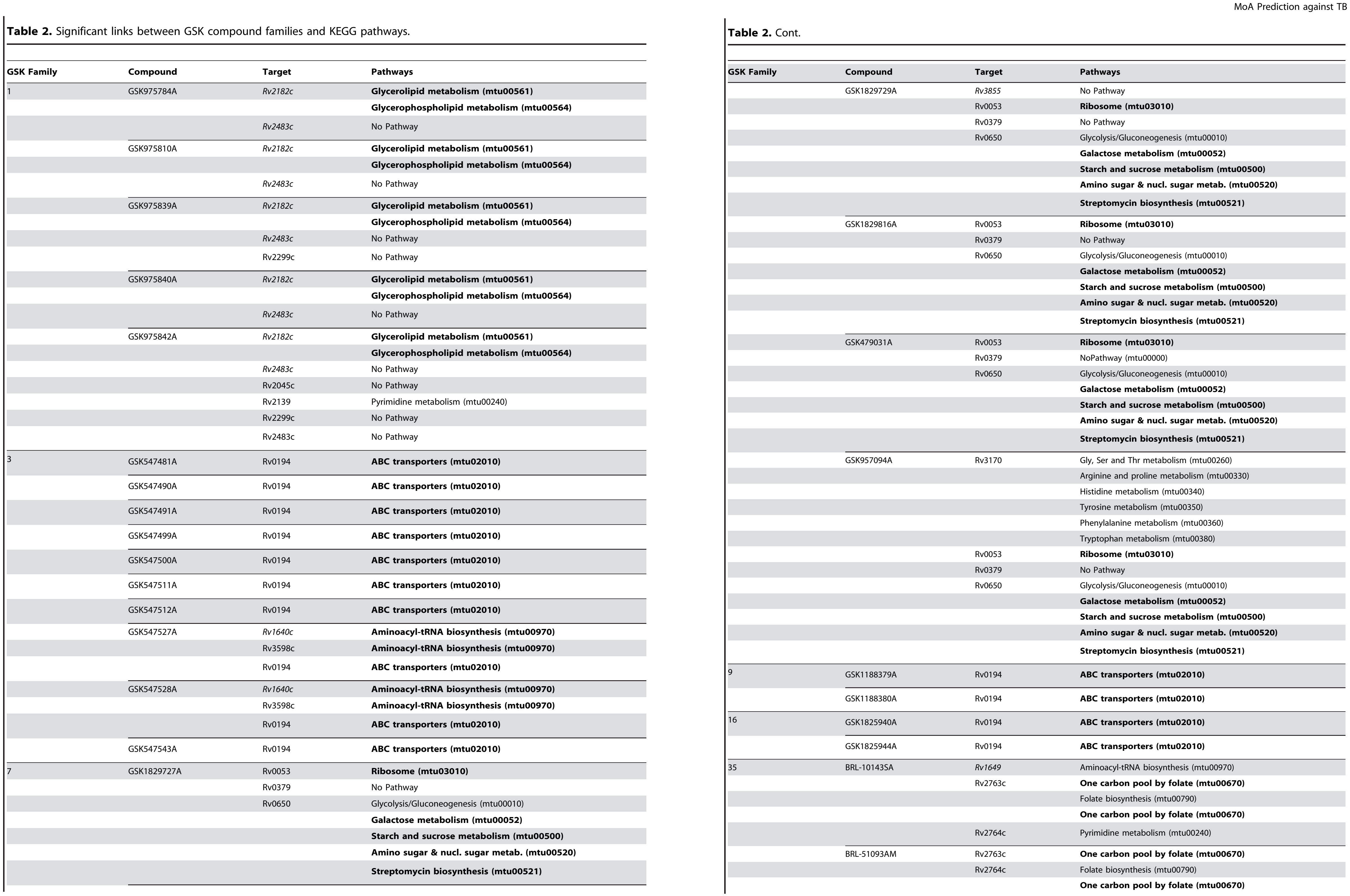


Table 2. Significant links between GSK compound families and KEGG pathways.

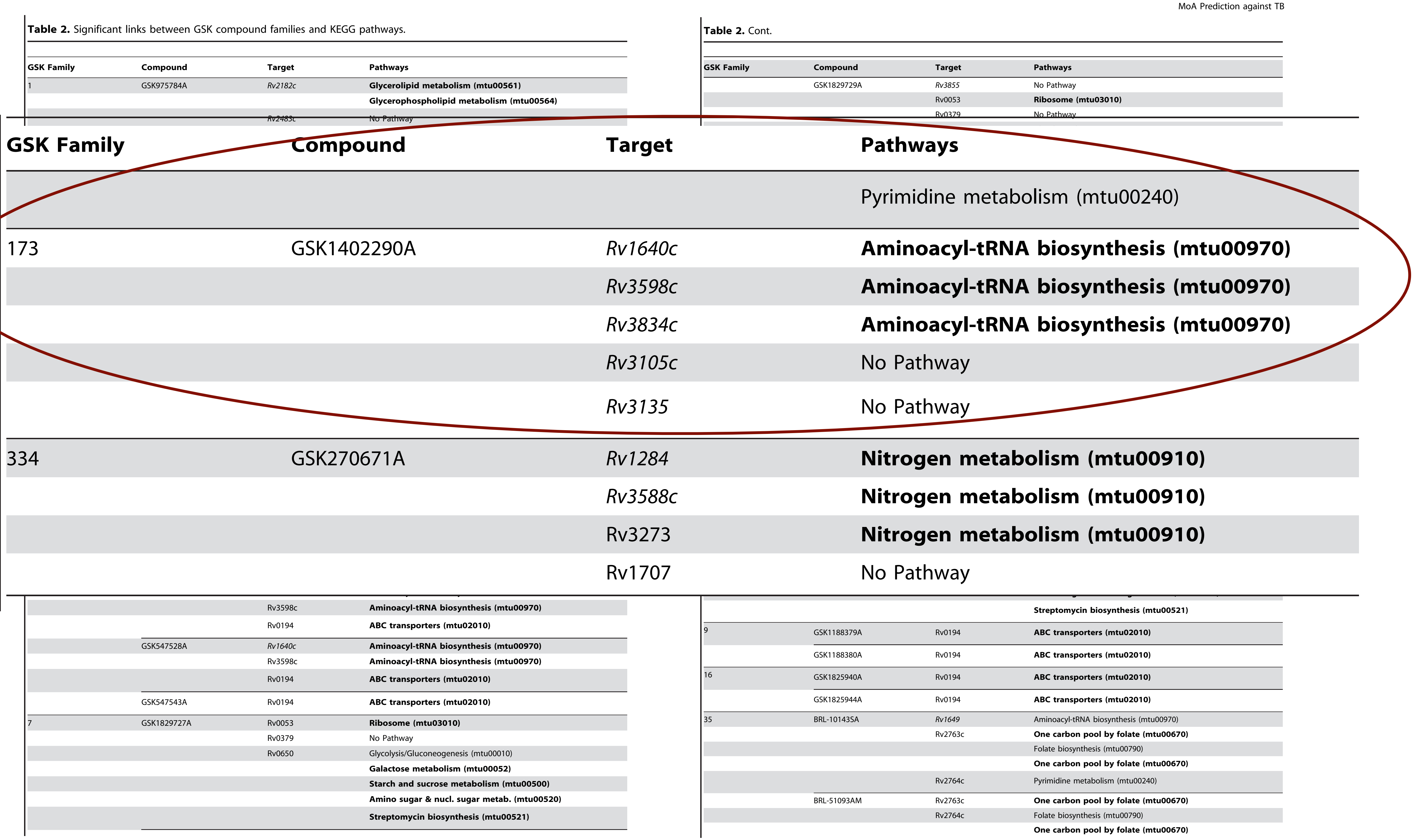
GSK Family	Compound	Target	Pathways
1	GSK975784A	*Rv2182c*	**Glycerolipid metabolism (mtu00561)**
			Glycerophospholipid metabolism (mtu00564)
		Rv2483c	No Pathway
	GSK975810A	*Rv2182c*	**Glycerolipid metabolism (mtu00561)**
			Glycerophospholipid metabolism (mtu00564)
		Rv2483c	No Pathway
	GSK975839A	*Rv2182c*	**Glycerolipid metabolism (mtu00561)**
			Glycerophospholipid metabolism (mtu00564)
		Rv2483c	No Pathway
		Rv2299c	No Pathway
	GSK975840A	*Rv2182c*	**Glycerolipid metabolism (mtu00561)**
			Glycerophospholipid metabolism (mtu00564)
		Rv2483c	No Pathway
	GSK975842A	*Rv2182c*	**Glycerolipid metabolism (mtu00561)**
			Glycerophospholipid metabolism (mtu00564)
		Rv2483c	No Pathway
		Rv2045c	No Pathway
		Rv2139	Pyrimidine metabolism (mtu00240)
		Rv2299c	No Pathway
		Rv2483c	No Pathway
3	GSK547481A	Rv0194	**ABC transporters (mtu02010)**
	GSK547490A	Rv0194	**ABC transporters (mtu02010)**
	GSK547491A	Rv0194	**ABC transporters (mtu02010)**
	GSK547499A	Rv0194	**ABC transporters (mtu02010)**
	GSK547500A	Rv0194	**ABC transporters (mtu02010)**
	GSK547511A	Rv0194	**ABC transporters (mtu02010)**
	GSK547512A	Rv0194	**ABC transporters (mtu02010)**
	GSK547527A	*Rv1640c*	**Aminoacyl-tRNA biosynthesis (mtu00970)**
		Rv3598c	**Aminoacyl-tRNA biosynthesis (mtu00970)**
		Rv0194	**ABC transporters (mtu02010)**
	GSK547528A	*Rv1640c*	**Aminoacyl-tRNA biosynthesis (mtu00970)**
		Rv3598c	**Aminoacyl-tRNA biosynthesis (mtu00970)**
		Rv0194	**ABC transporters (mtu02010)**
	GSK547543A	Rv0194	**ABC transporters (mtu02010)**
7	GSK1829727A	Rv0053	**Ribosome (mtu03010)**
		Rv0379	No Pathway
		Rv0650	Glycolysis/Gluconeogenesis (mtu00010)
			Galactose metabolism (mtu00052)
			Starch and sucrose metabolism (mtu00500)
			Amino sugar & nucl. sugar metab. (mtu00520)
			Streptomycin biosynthesis (mtu00521)

MoA Prediction against TB

Table 2. Cont.

GSK Family	Compound	Target	Pathways
	GSK1829729A	*Rv3855*	No Pathway
		Rv0053	**Ribosome (mtu03010)**
		Rv0379	No Pathway
		Rv0650	Glycolysis/Gluconeogenesis (mtu00010)
			Galactose metabolism (mtu00052)
			Starch and sucrose metabolism (mtu00500)
			Amino sugar & nucl. sugar metab. (mtu00520)
			Streptomycin biosynthesis (mtu00521)
	GSK1829816A	Rv0053	**Ribosome (mtu03010)**
		Rv0379	No Pathway
		Rv0650	Glycolysis/Gluconeogenesis (mtu00010)
			Galactose metabolism (mtu00052)
			Starch and sucrose metabolism (mtu00500)
			Amino sugar & nucl. sugar metab. (mtu00520)
			Streptomycin biosynthesis (mtu00521)
	GSK479031A	Rv0053	**Ribosome (mtu03010)**
		Rv0379	NoPathway (mtu00000)
		Rv0650	Glycolysis/Gluconeogenesis (mtu00010)
			Galactose metabolism (mtu00052)
			Starch and sucrose metabolism (mtu00500)
			Amino sugar & nucl. sugar metab. (mtu00520)
			Streptomycin biosynthesis (mtu00521)
	GSK957094A	Rv3170	Gly, Ser and Thr metabolism (mtu00260)
			Arginine and proline metabolism (mtu00330)
			Histidine metabolism (mtu00340)
			Tyrosine metabolism (mtu00350)
			Phenylalanine metabolism (mtu00360)
			Tryptophan metabolism (mtu00380)
		Rv0053	**Ribosome (mtu03010)**
		Rv0379	No Pathway
		Rv0650	Glycolysis/Gluconeogenesis (mtu00010)
			Galactose metabolism (mtu00052)
			Starch and sucrose metabolism (mtu00500)
			Amino sugar & nucl. sugar metab. (mtu00520)
			Streptomycin biosynthesis (mtu00521)
9	GSK1188379A	Rv0194	**ABC transporters (mtu02010)**
	GSK1188380A	Rv0194	**ABC transporters (mtu02010)**
16	GSK1825940A	Rv0194	**ABC transporters (mtu02010)**
	GSK1825944A	Rv0194	**ABC transporters (mtu02010)**
35	BRL-10143SA	*Rv1649*	Aminoacyl-tRNA biosynthesis (mtu00970)
		Rv2763c	**One carbon pool by folate (mtu00670)**
			Folate biosynthesis (mtu00790)
			One carbon pool by folate (mtu00670)
		Rv2764c	Pyrimidine metabolism (mtu00240)
	BRL-51093AM	Rv2763c	**One carbon pool by folate (mtu00670)**
		Rv2764c	Folate biosynthesis (mtu00790)
			One carbon pool by folate (mtu00670)

Significant drug-protein pairs



MoA Prediction against TB

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			Glycerophospholipid metabolism (mtu00564)
		Rv2483c	No Pathway

Table 2. Cont.

GSK Family	Compound	Target	Pathways
	GSK1829729A	*Rv3855*	No Pathway
		Rv0053	**Ribosome (mtu03010)**
		Rv0379	No Pathway

GSK Family	Compound	Target	Pathways
			Pyrimidine metabolism (mtu00240)
173	GSK1402290A	*Rv1640c*	**Aminoacyl-tRNA biosynthesis (mtu00970)**
		Rv3598c	**Aminoacyl-tRNA biosynthesis (mtu00970)**
		Rv3834c	**Aminoacyl-tRNA biosynthesis (mtu00970)**
		Rv3105c	No Pathway
		Rv3135	No Pathway
334	GSK270671A	*Rv1284*	**Nitrogen metabolism (mtu00910)**
		Rv3588c	**Nitrogen metabolism (mtu00910)**
		Rv3273	**Nitrogen metabolism (mtu00910)**
		Rv1707	No Pathway

		Rv3598c	**Aminoacyl-tRNA biosynthesis (mtu00970)**
		Rv0194	**ABC transporters (mtu02010)**
	GSK547528A	*Rv1640c*	**Aminoacyl-tRNA biosynthesis (mtu00970)**
		Rv3598c	**Aminoacyl-tRNA biosynthesis (mtu00970)**
		Rv0194	**ABC transporters (mtu02010)**
	GSK547543A	Rv0194	**ABC transporters (mtu02010)**
7	GSK1829727A	Rv0053	**Ribosome (mtu03010)**
		Rv0379	No Pathway
		Rv0650	Glycolysis/Gluconeogenesis (mtu00010)
			Galactose metabolism (mtu00052)
			Starch and sucrose metabolism (mtu00500)
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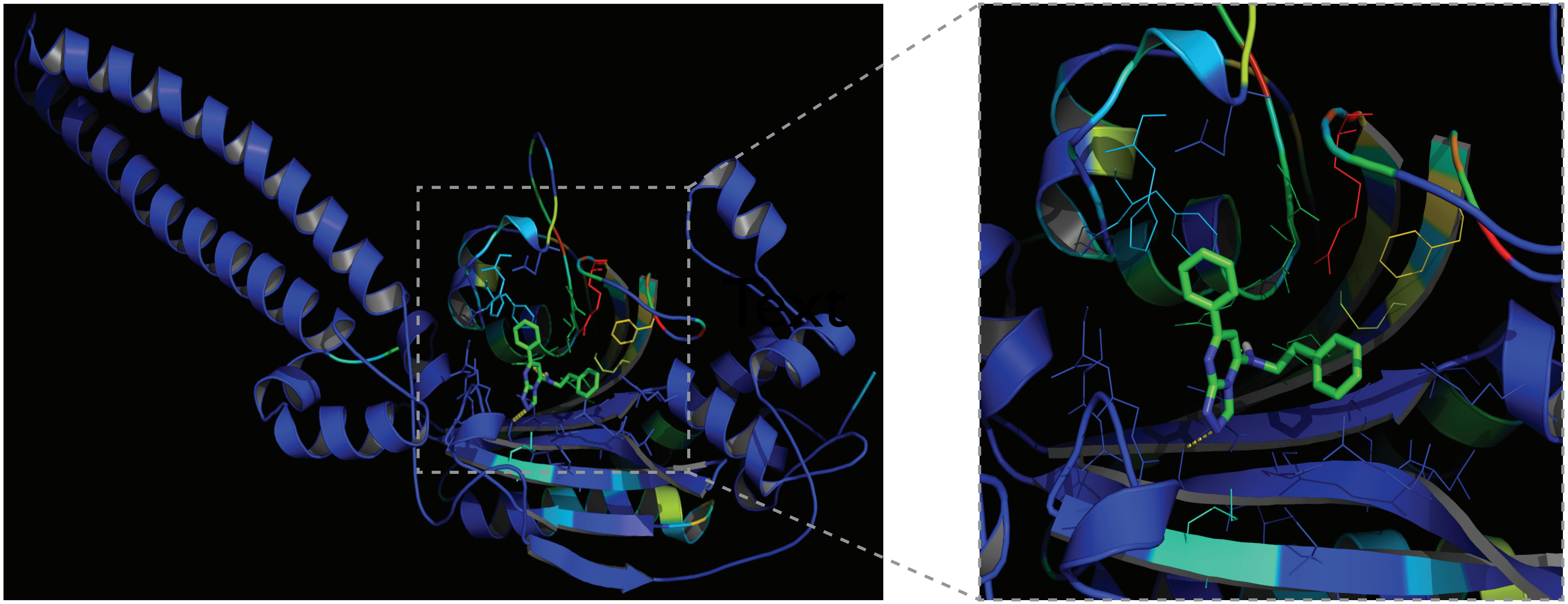
16	GSK1825940A	Rv0194	**ABC transporters (mtu02010)**
	GSK1825944A	Rv0194	**ABC transporters (mtu02010)**
35	BRL-10143SA	*Rv1649*	Aminoacyl-tRNA biosynthesis (mtu00970)
		Rv2763c	**One carbon pool by folate (mtu00670)**
			Folate biosynthesis (mtu00790)
			One carbon pool by folate (mtu00670)
		Rv2764c	Pyrimidine metabolism (mtu00240)
	BRL-51093AM	Rv2763c	**One carbon pool by folate (mtu00670)**
		Rv2764c	Folate biosynthesis (mtu00790)
			One carbon pool by folate (mtu00670)

GSK1402290A attacking *Aminoacyl-tRNA biosynthesis* pathway

lysyl-tRNA synthetase 2

lysS1 Lysine-tRNA ligase

SERYL-tRNA synthetase SerS



nAnnolyze predicted binding-site + Autodock Vina

Experimental validation

a. MapB

b. SahH

c. AofH

d. EphA

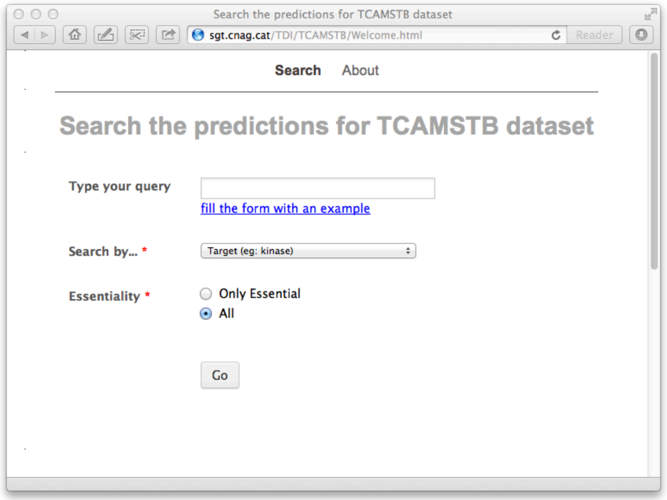
e. SerS?

Stacey Southall

EMBL

Open Access Drug Discovery

http://sgt.cnag.cat/TDI/TCAMSTB/



Search the predictions for TCAMSTB dataset

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fill the form with an example

Search by... * Target (eg: kinase)

Essentiality *
○ Only Essential
● All

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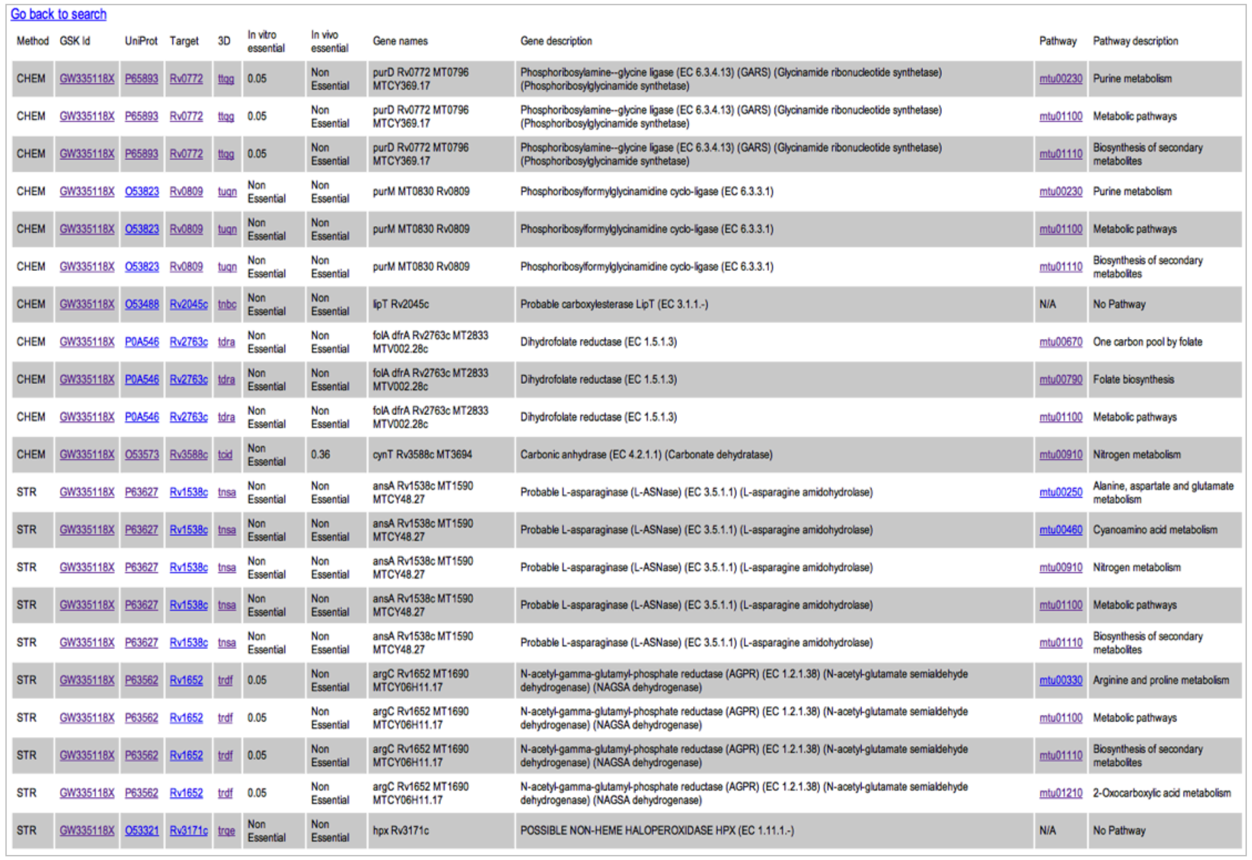
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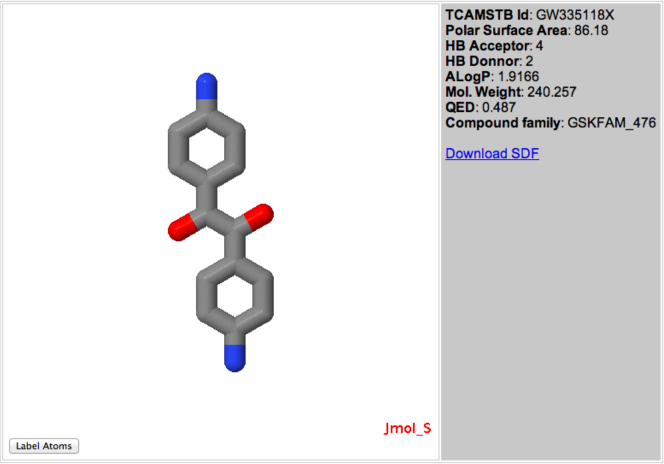
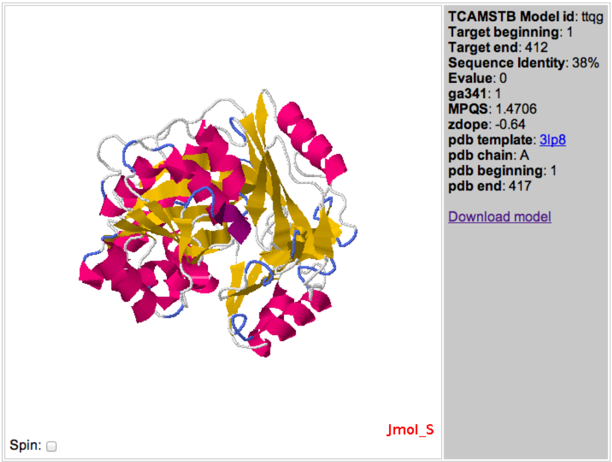
Method	GSK Id	UniProt	Target	3D	In vitro essential	In vivo essential	Gene names	Gene description	Pathway	Pathway description
CHEM	GW335118X	P65893	Rv0772	ttqg	0.05	Non Essential	purD Rv0772 MT0796 MTCY369.17	Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	mtu00230	Purine metabolism
CHEM	GW335118X	P65893	Rv0772	ttqg	0.05	Non Essential	purD Rv0772 MT0796 MTCY369.17	Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	mtu01100	Metabolic pathways
CHEM	GW335118X	P65893	Rv0772	ttqg	0.05	Non Essential	purD Rv0772 MT0796 MTCY369.17	Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (GARS) (Glycinamide ribonucleotide synthetase) (Phosphoribosylglycinamide synthetase)	mtu01110	Biosynthesis of secondary metabolites
CHEM	GW335118X	O53823	Rv0809	tuqn	Non Essential	Non Essential	purM MT0830 Rv0809	Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	mtu00230	Purine metabolism
CHEM	GW335118X	O53823	Rv0809	tuqn	Non Essential	Non Essential	purM MT0830 Rv0809	Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	mtu01100	Metabolic pathways
CHEM	GW335118X	O53823	Rv0809	tuqn	Non Essential	Non Essential	purM MT0830 Rv0809	Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1)	mtu01110	Biosynthesis of secondary metabolites
CHEM	GW335118X	O53488	Rv2045c	tnbc	Non Essential	Non Essential	lipT Rv2045c	Probable carboxylesterase LipT (EC 3.1.1.-)	N/A	No Pathway
CHEM	GW335118X	P0A546	Rv2763c	tdra	Non Essential	Non Essential	folA dfrA Rv2763c MT2833 MTV002.28c	Dihydrofolate reductase (EC 1.5.1.3)	mtu00670	One carbon pool by folate
CHEM	GW335118X	P0A546	Rv2763c	tdra	Non Essential	Non Essential	folA dfrA Rv2763c MT2833 MTV002.28c	Dihydrofolate reductase (EC 1.5.1.3)	mtu00790	Folate biosynthesis
CHEM	GW335118X	P0A546	Rv2763c	tdra	Non Essential	Non Essential	folA dfrA Rv2763c MT2833 MTV002.28c	Dihydrofolate reductase (EC 1.5.1.3)	mtu01100	Metabolic pathways
CHEM	GW335118X	O53573	Rv3588c	tcid	Non Essential	0.36	cynT Rv3588c MT3694	Carbonic anhydrase (EC 4.2.1.1) (Carbonate dehydratase)	mtu00910	Nitrogen metabolism
STR	GW335118X	P63627	Rv1538c	tnsa	Non Essential	Non Essential	ansA Rv1538c MT1590 MTCY48.27	Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase)	mtu00250	Alanine, aspartate and glutamate metabolism
STR	GW335118X	P63627	Rv1538c	tnsa	Non Essential	Non Essential	ansA Rv1538c MT1590 MTCY48.27	Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase)	mtu00460	Cyanoamino acid metabolism
STR	GW335118X	P63627	Rv1538c	tnsa	Non Essential	Non Essential	ansA Rv1538c MT1590 MTCY48.27	Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase)	mtu00910	Nitrogen metabolism
STR	GW335118X	P63627	Rv1538c	tnsa	Non Essential	Non Essential	ansA Rv1538c MT1590 MTCY48.27	Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase)	mtu01100	Metabolic pathways
STR	GW335118X	P63627	Rv1538c	tnsa	Non Essential	Non Essential	ansA Rv1538c MT1590 MTCY48.27	Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase)	mtu01110	Biosynthesis of secondary metabolites
STR	GW335118X	P63562	Rv1652	trdf	0.05	Non Essential	argC Rv1652 MT1690 MTCY06H11.17	N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) (EC 1.2.1.38) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase)	mtu00330	Arginine and proline metabolism
STR	GW335118X	P63562	Rv1652	trdf	0.05	Non Essential	argC Rv1652 MT1690 MTCY06H11.17	N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) (EC 1.2.1.38) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase)	mtu01100	Metabolic pathways
STR	GW335118X	P63562	Rv1652	trdf	0.05	Non Essential	argC Rv1652 MT1690 MTCY06H11.17	N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) (EC 1.2.1.38) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase)	mtu01110	Biosynthesis of secondary metabolites
STR	GW335118X	P63562	Rv1652	trdf	0.05	Non Essential	argC Rv1652 MT1690 MTCY06H11.17	N-acetyl-gamma-glutamyl-phosphate reductase (AGPR) (EC 1.2.1.38) (N-acetyl-glutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase)	mtu01210	2-Oxocarboxylic acid metabolism
STR	GW335118X	O53321	Rv3171c	trqe	Non Essential	Non Essential	hpx Rv3171c	POSSIBLE NON-HEME HALOPEROXIDASE HPX (EC 1.11.1.-)	N/A	No Pathway



TCAMSTB Id: GW335118X
Polar Surface Area: 86.18
HB Acceptor: 4
HB Donnor: 2
ALogP: 1.9166
Mol. Weight: 240.257
QED: 0.487
Compound family: GSKFAM_476

Download SDF



TCAMSTB Model id: ttqg
Target beginning: 1
Target end: 412
Sequence Identity: 38%
Evalue: 0
ga341: 1
MPQS: 1.4706
zdope: -0.64
pdb template: 3lp8
pdb chain: A
pdb beginning: 1
pdb end: 417

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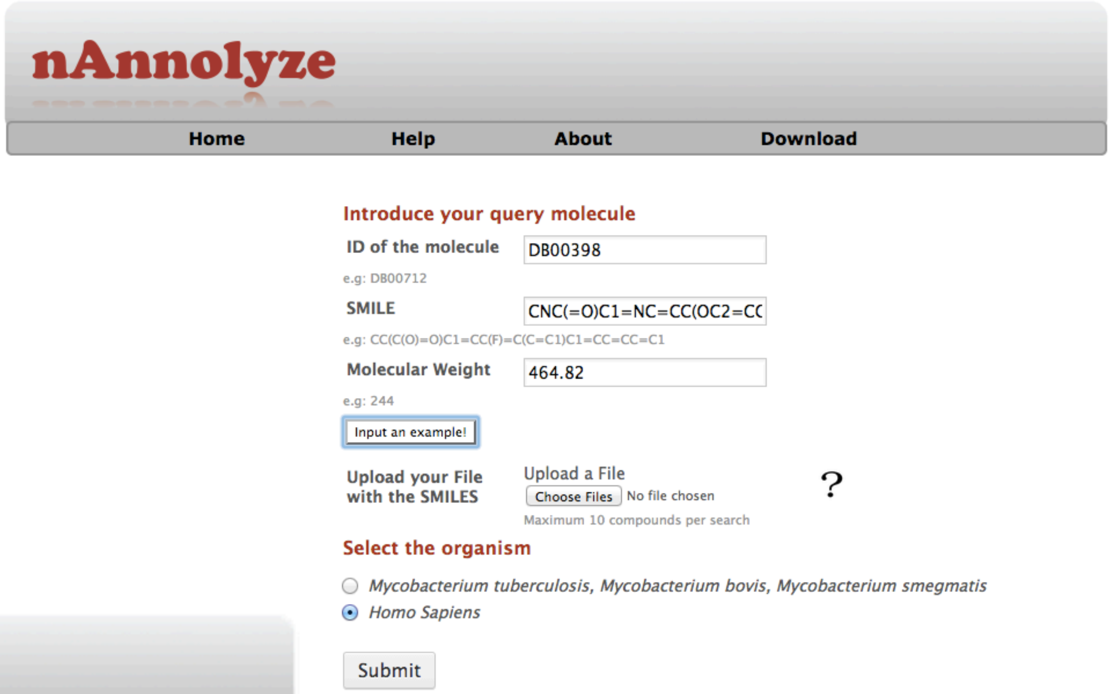


Introduce your query molecule

ID of the molecule: DB00398

e.g: DB00712

SMILE: CNC(=O)C1=NC=CC(OC2=CC

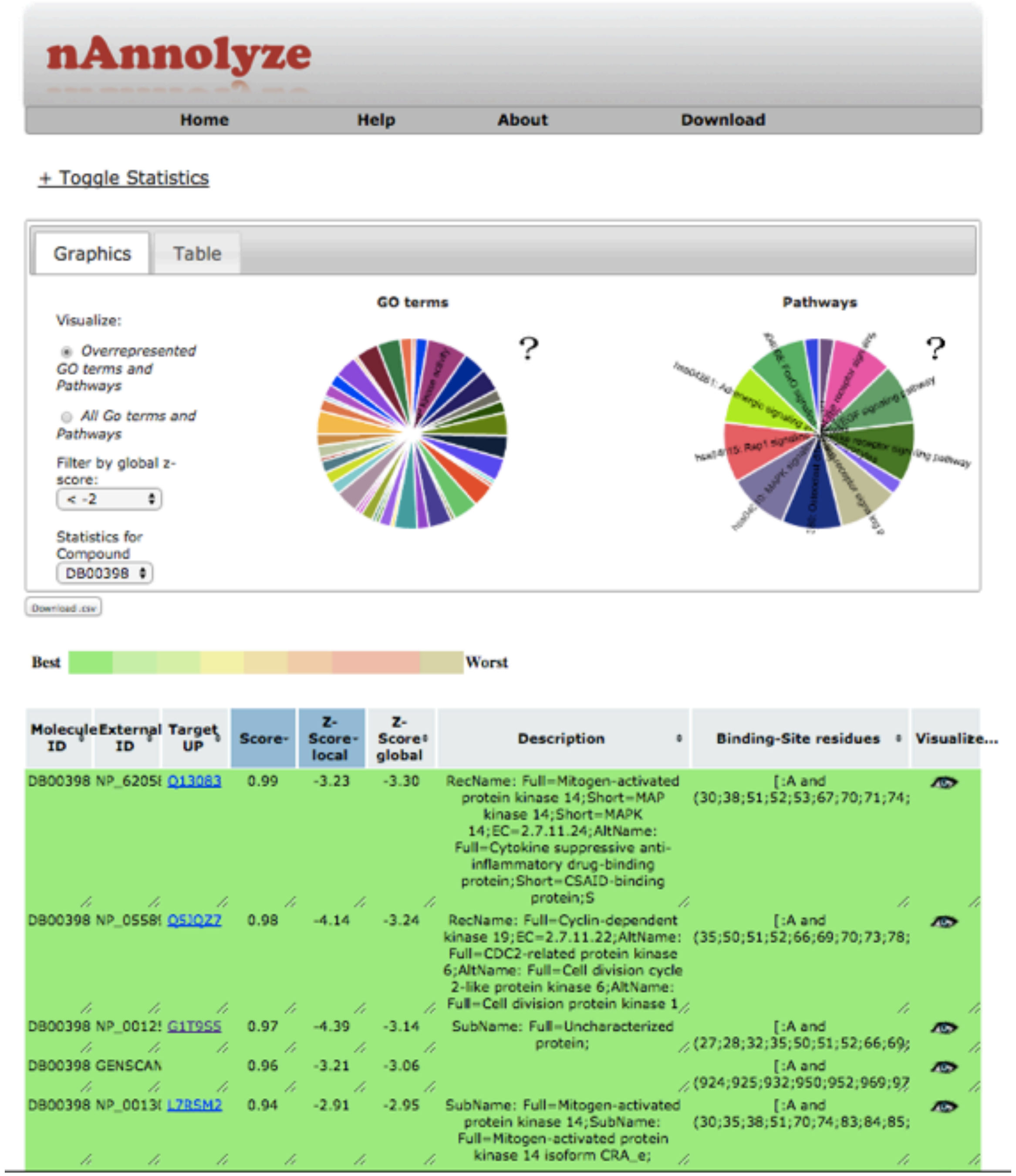
e.g: CC(C(O)=O)C1=CC(F)=C(C=C1)C1=CC=CC=C1

Molecular Weight: 464.82

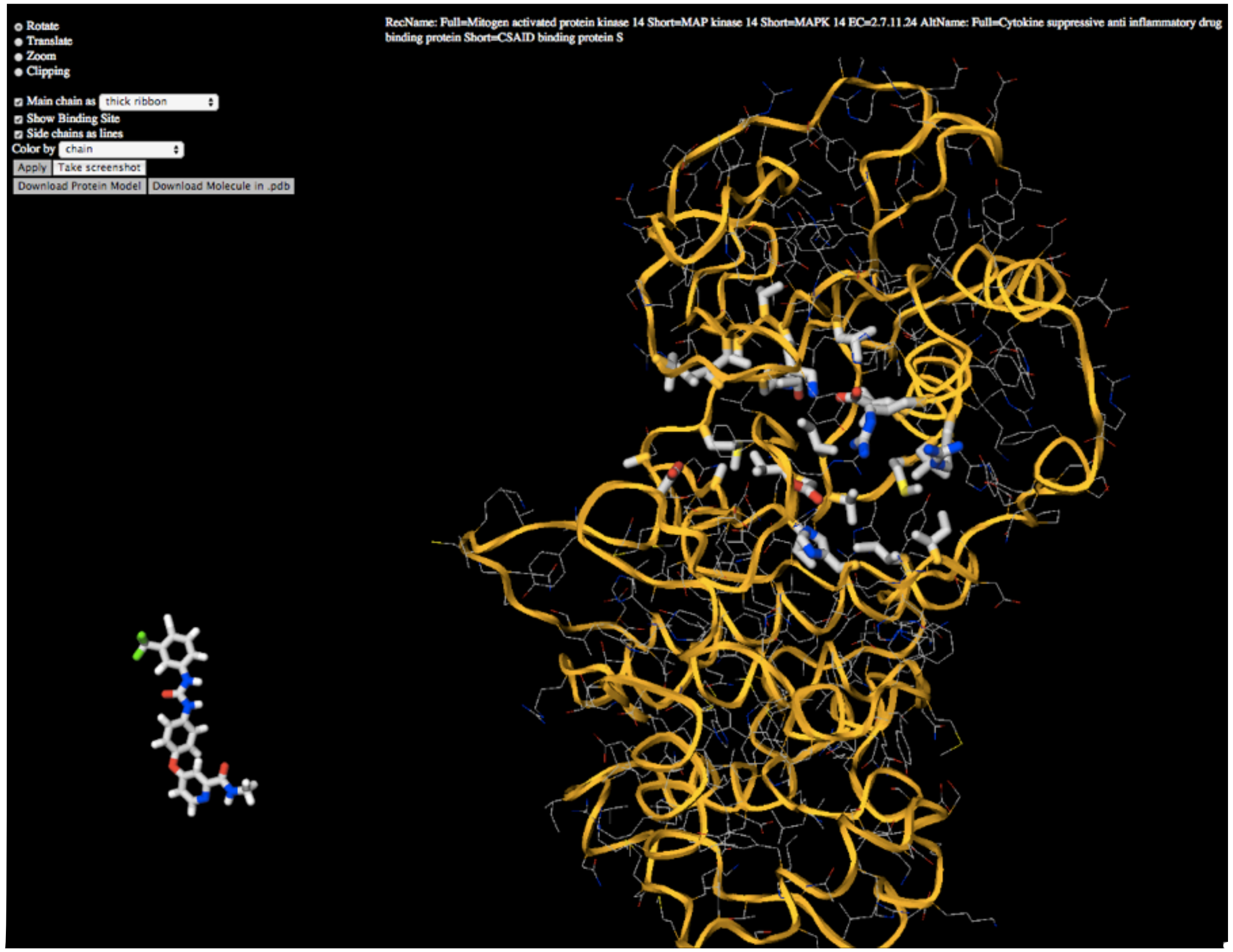
e.g: 244

Select the organism

○ *Mycobacterium tuberculosis, Mycobacterium bovis, Mycobacterium smegmatis*
● *Homo Sapiens*



Molecule ID	External ID	Target UP	Score	Z-Score local	Z-Score global	Description	Binding-Site residues	Visualize...
DB00398	NP_6205	Q13083	0.99	-3.23	-3.30	RecName: Full=Mitogen-activated protein kinase 14;Short=MAP kinase 14;Short=MAPK 14;EC=2.7.11.24;AltName: Full=Cytokine suppressive anti-inflammatory drug-binding protein;Short=CSAID-binding protein;S	[:A and (30;38;51;52;53;67;70;71;74;	
DB00398	NP_0558	Q5JQZ7	0.98	-4.14	-3.24	RecName: Full=Cyclin-dependent kinase 19;EC=2.7.11.22;AltName: Full=CDC2-related protein kinase 6;AltName: Full=Cell division cycle 2-like protein kinase 6;AltName: Full=Cell division protein kinase 1	[:A and (35;50;51;52;66;69;70;73;78;	
DB00398	NP_0012	G1T9S5	0.97	-4.39	-3.14	SubName: Full=Uncharacterized protein;	[:A and (27;28;32;35;50;51;52;66;69;	
DB00398	GENSCAN		0.96	-3.21	-3.06		[:A and (924;925;932;950;952;969;97	
DB00398	NP_0013	L7RSM2	0.94	-2.91	-2.95	SubName: Full=Mitogen-activated protein kinase 14;SubName: Full=Mitogen-activated protein kinase 14 isoform CRA_e;	[:A and (30;35;38;51;70;74;83;84;85;	



RecName: Full=Mitogen activated protein kinase 14 Short=MAP kinase 14 Short=MAPK 14 EC=2.7.11.24 AltName: Full=Cytokine suppressive anti inflammatory drug binding protein Short=CSAID binding protein S

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Acknowledgments

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