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



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...





Thursday, September 25, 14



Methods

2D-Chemogenomics Approach

Historical Approach

3D-Structural Approach

					(ChEMBLdb									8
60 a > 6	u 🖶 🔘 🗆	+ 🛛 🚯 https://w	ww.ebi.ac.uk,	/chembldb/drug/ap	provals					RSS	Q. Goo	jle) [A]
C III Google+ Fa	cebook Tumblr	ChEMBL-og An	alytics Twi	tter LinkedIn F10	000 PubMed Pu	bChem Wikipe	dia Ca	ampus Intranet Scie	nce + EBI	Computing	• Finance •	Travel +	News v	Nature	
EMBL-EBI			Enter Text Her	0	Find	Help Feedbac									
Databases Tools	Research	Training I	ndustry	About Us Help		Site Index 🔂 (5								
1	EBI > Databases :	Small Molecules >	ChEMBL Datab	ase > Home									28N 10004.83	AT OPEN	SERVICE
ChEMBL	Search ChEM	MBLdb			Compounds	Targets	Assays	Activity Source Filter							
ChEMBLdb	ChEMBLdb	Compound	Search Pro	tein Target Search	Browse Targets	Browse Dru	lgs	Drug Approvals							
ChEMBL-NTD								L							
Kinase SARfari	are to the corresp	onding Drug Appre	oval Monogra	stration (FDA) drug a phs on the ChEMBL-o	ipprovals for New M 9g.	olecular Entities (NMES) I	n 2009, 2010, and 201	1. Links						
GPCR SARfari	Browse Drug	Approvals													0
DrugEBIlity	Generic Name	Trade Names	ATC Code	Date of Approval		Drug M	lonograph				lco				
ChEMBL Group	Brentuximab	Adcetris	L01XC12	19-Aug-2011	http://chembi.blo	gspot.com/2011/08/	Inew-drug	-approvals-2011-pt-xxv.l	html 🏻	5		A	(ا	(🔲	
Downloads															1
Web Services	Vemurafenib	Zelboraf	L01XE15	17-Aug-2011	http://chembl.blog	25pot.com/2011/06/	new-drug	-approvals-2011-pt-xxiv.	html	259					
FAQ	Ticagrelor	Brilinta	B01AC24	20-Jul-2011	http://chembil.blogs;	pot.com/2011/07/ne	w-drug-a	pprovals-2011-pt-xxiii.htm	ni.htmi	50		A	•		
ChEMBLdb Statistics	Indacaterol Maleate	Arcapta	R03AC18	02-Jul-2011	htp://chembl.blo	gspot.com/2011/07	Inew-drus	p-approvals-2011-pt-xxii.h	ttml 🤇	5			•		
Targets: 8,603 Compound records:	Rivaroxaban	Xarelto	B01AX06	01-Jul-2011	http://chembl.blo	gspot.com/2011/07	Ynew-drug	p-approvals-2011-pt-xxi.h	-	50					
1,195,368 Distinct compounds:	Azficei-T	laViv	Not Assigne	ad 21-Jun-2011	http://chembl.blog	spot.com/2011/06/n L	www.drug-	approvals-2011-pl-xx-az	ficele 🖌	50					
1,080,258 Activities: 5,479,146 Dublications: 42,516	Belatacept	Nulojix	L04AA28	15-Jun-2011	http://chembl.blo	gspot.com/2011/06	Vnew-drus	p-approvals-2011-pt-xix h	-	50		Î	•		
	Ezogabine	Potiga	N03AX21	10-Jun-2011	http://chembi.blog	gspot.com/2011/06	Inew-drug	p-approvals-2011-pt-xviii.	htmi 【	5		Î			
ChEMBL Blog ChEMBL Release	Fidaxomicin	Dificid	Not Assigne	ed 27-May-2011	http://chembl.blo	gspot.com/2011/06	(new-drug	p-approvals-2011-pt-xvil/	tani 🤇	50			(ا		
Scheduling PhD studentship	Telaprevir	Incivek	Not Assigne	id 23-May-2011	http://chembl.bio	gspot.com/2011/05	inew-dru	p-approvals-2011-pt-xvi.h	-	50			•		
Intake	Ripivirine	Edurant	Not Assigne	ad 20-May-2011	http://chembl.blo	gspot.com/2011/05	/new-dru	g-approvals-2011-pl-xv.h	5ml 🤇	5					
	Boceprevir	Victrelis	Not Assigne	nd 13-May-2011	http://chembl.bio	gspot.com/2011/05	inew-drug	g-approvals-2011-pt-xiv.h		50					
	Linagliptin	Tradjenta	A108H05	02-May-2011	http://chembl.blo	gspot.com/2011/05	Vnew-dru	o-approvals-2011-pt-xill h		5			•		
	Abiraterone	Zytiga	Not Assigne	ad 28-Apr-2011	http://chembl.blo	gspot.com/2011/05	inew-drug	a-approvals-2011-part-xi.	html	50				/ew 1 - 69 c	68 10







George Papadatos

John P. Overington



Vinod Kumar

James Brown

centre nacional d'anàlisi genòm centro nacional de análisis geno



Francisco Martínez-Jiménez

Marc A. Martí-Renom









Network-based Method nAnnolyze



Applying the method, modeling genomes...











Ligand	Target	Distance	Global Z-score	Local Z-score
GSKI	pknB Kinase	1.3	-1.6	-2.5
GSKI	mapB	2.5	2.3	1.02
GSKI	sahH	1.9	-1.6	-3.16
GSKI	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



Compound dataset diversity

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)				
	GRIDZYZIA	Rv0379	No Pathway				
		Rv0650	Glycolysis/Gluconeogenesis (mtu00010)				
			Galactose metabolism (mtu00052)				
			Starch and sucrose metabolism (mtu00500)				
			Amino sugar & nucl. sugar metab. (mtu00520)				

Table 2. Cont.

SK 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)
	GSK1188379A	Rv0194	ABC transporters (mtu02010)
	GSK1188380A	Rv0194	ABC transporters (mtu02010)
	GSK1825940A	Rv0194	ABC transporters (mtu02010)
	GSK1825944A	Rv0194	ABC transporters (mtu02010)
	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 need by falate (mtu00670)

MoA Prediction against TB

Significant drug-protein pairs

GSK Family	Compound	Target	Pathways		GSK Family	Compound	Target	Pathways
1	GSK975784A	Rv2182c	Glycerolipid metabolism (mtu00561)			GSK1829729A	Rv3855 Rv0053	No Pathway Ribosome (mtu03010)
		8v2463c	Giyceropnospholipid metabolism (mtu00564)				Rv0379	No Pathway
SK Family		ing lost		Toward		Det		
ISK Family		Com	ipouna	Target		Pau	nways	
						Pyrir	midine metab	olism (mtu00240)
73		GSK1	402290A	Rv1640c		Ami	inoacyl-tRN	A biosynthesis (mtu00970)
				Rv3598c		Ami	inoacyl-tRN	A biosynthesis (mtu00970)
				Rv3834c		Ami	inoacyl-tRN	A biosynthesis (mtu00970)
				Rv3105c		No F	Pathway	
				Rv3135		No F	Pathway	
34		GSK2	270671A	Rv1284		Nitr	ogen metak	oolism (mtu00910)
5.		00112					- <u>-</u>	
				Rv3588c		Nitr	ogen metak	oolism (mtu00910)
				Rv3273		Nitr	ogen metak	oolism (mtu00910)
				Rv1707		No f	Pathway	
		Rv3598c	Aminoacyl-tRNA biosynthesis (mtu00970)					Streptomycin biosynthesis (mtu00521)
		Rv0194	ABC transporters (mtu02010)		9	GSK1188379A	Rv0194	ABC transporters (mtu02010)
	GSK547528A	Rv1640c	Aminoacyl-tRNA biosynthesis (mtu00970)			GSK1188380A	Rv0194	ABC transporters (mtu02010)
1		KV3598C	AMINOACYI-TKINA DIOSYNTHESIS (MTUUU970)		16	GSK1825940A	Rv0194	ABC transporters (mtu02010)
	GSK547542A	D-0104	ABC transporters (mtu02010)			GSK1825944A	Rv0194	ABC transporters (mtu02010)
	UJUJ4/J45A	NVU194			35	BRI -1014354	Rv1649	AminoacyLtRNA biosynthesis (mtu00970)
-	66//1000707		Kibosome (mtu03010)				Rv2763c	One carbon pool by folate (mtu00570)
7	GSK1829727A	RV0053	No Pathway					One carbon poor by forate (introdot/o)
7	GSK1829727A	Rv0053 Rv0379 Rv0650	No Pathway Glycolysis/Gluconeogenesis (mtu00010)					Folate biosynthesis (mtu00790)
7	GSK1829727A	Rv0053 Rv0379 Rv0650	No Pathway Glycolysis/Gluconeogenesis (mtu00010) Galactose metabolism (mtu00052)					Folate biosynthesis (mtu00070) One carbon pool by folate (mtu00670)
7	G5K1829727A	Rv0053 Rv0379 Rv0650	No Pathway Glycolysis/Gluconeogenesis (mtu00010) Galactose metabolism (mtu00052) Starch and sucrose metabolism (mtu00500)				Rv2764c	Folate biosynthesis (mtu00070) One carbon pool by folate (mtu00070) Pyrimidine metabolism (mtu00240)
7	GSK1829727A	Rv0053 Rv0379 Rv0650	No Pathway Glycolysis/Gluconeogenesis (mtu00010) Galactose metabolism (mtu00052) Starch and sucrose metabolism (mtu00500) Amino sugar & nucl. sugar metab. (mtu00520)			BRL-51093AM	Rv2764c Rv2763c	Folate Carbon pool by folate (mtu00070) One carbon pool by folate (mtu00670) Pyrimidine metabolism (mtu00240) 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/

Method GSK id UnProt Target 30 In vbro method Gene description Gene description Pathony de Pathony de <t< th=""><th>description etabolism : pathways esis of secondary es etabolism : pathways :sis of secondary es</th></t<>	description etabolism : pathways esis of secondary es etabolism : pathways :sis of secondary es
CHEM 04V335118X De5883 Rv0772 fiss 0.05 Non MICV208.17 PProsphor/booylightimegyboine ligase (EC 6.3.4.13) (CARS) (Olycinamide rbonucleotide synthetase) mb.0020 Purice metal MICV208.17 CHEM 04V335118X De5893 Rv0772 liss 0.05 Non Essential pu/C RV072 MI0796 MICV208.17 Phosphor/booylightimegyboine ligase (EC 6.3.4.13) (CARS) (Olycinamide rbonucleotide synthetase) mb.0110 Metabolic p CHEM 04V335118X De5893 Rv072 liss 0.05 Non Essential pu/C RV072 MI0796 Phosphor/booylightimegyboine ligase (EC 6.3.4.13) (CARS) (Olycinamide rbonucleotide synthetase) mb.0110 Metabolic p CHEM 04V335118X 05822 Rv689 liss Non Essential pu/M MT0830 Rv0809 Phosphor/booylightiam-diplocaligase (EC 6.3.3.1) mb.0110 Metabolic p CHEM 04V335118X 058282 Rv689 liss Non Essential pu/M MT0830 Rv0809 Phosphor/booylightiam-diplocaligase (EC 6.3.3.1) mb.01102 Metabolic p CHEM 04V335118X 05848 Rv689 liss Phosphor/booylightimdiplocaligase (EC 6.3.3.1) mb.01100 <td>etabolism : pathways sis of secondary etabolism : pathways sis of secondary es ay</td>	etabolism : pathways sis of secondary etabolism : pathways sis of secondary es ay
CHE GW335118X P6589 FW372 Ito 0.05 Non Essential PUP RV772 WT0796 WT0CV309.17 Phosphorboorylepic-apice ligase (EC 6.3.4.13) (GARS) (Glycinamide roboruciotide synthetase) mtu0110 Besorthal Besorthal CHEM GW335118X P6589 Rv072 tite 0.05 Non Essential purD Rv0772 WT0796 Phosphorboorylepic-apice ligase (EC 6.3.4.13) (GARS) (Glycinamide roboruciotide synthetase) mtu0110 Besorthal CHEM GW335118X 05382 Rv089 Iso Non Essential purD Rv0772 WT0796 Phosphorboorylepic-apice ligase (EC 6.3.13) (GARS) (Glycinamide roboruciotide synthetase) mtu0110 Besorthal CHEM GW335118X 05382 Rv089 Iso Phosphorboorylepic-syloire ligase (EC 6.3.3.1) mtu0110 Metabole propriotice synthetase) CHEM GW335118X 05382 Rv089 Iso Phosphorboorylepic-syloire ligase (EC 6.3.3.1) mtu0110 Metabole propriotice synthetase) CHEM GW335118X 05382 Rv089 Iso Phosphorboorylepic-syloire asse (EC 6.3.1) mtu0110 Metabole propriotice synthetase) CHEM GW335118X 05382 <td< td=""><td>c pathways esis of secondary es etabolism : pathways es es ray</td></td<>	c pathways esis of secondary es etabolism : pathways es es ray
CHEM GW335118X P6589 Fx0772 Itra O.O Non Essential puD Rx0772 MT0796 Phosphorbooyleminegloine lgase (EC 6.3.4.13) (GARS) (Gloinamide rhonucleoide synthetase) mul0110 Brogenbrace metabolies CHEM GW335118X O53821 kx0892 ku0 Non Essential purl M10303 Rx0809 Phosphorbooyleminegloine lgase (EC 6.3.3.1) mul0110 Mul0220 Purl meter CHEM GW335118X O53821 kx0892 ku0 Non Essential purl M10303 Rx0809 Phosphorbooylemmydychamidne cydo-lgase (EC 6.3.3.1) mul0110 Mul01100 Mul0	esis of secondary tes etabolism : pathways sis of secondary es ay
CHEM GM335118X G5822 Kv0592 Iun Non Essential pur/M MT0830 Rv0809 Phosphorbosyformyglychamidine cyclo-igase (EC 6.3.3.1) mtu02022 Purie metric metric/018 CHEM GM335118X G5823 Rv0592 Iun Non Essential pur/M MT0830 Rv0809 Phosphorbosyformyglychamidine cyclo-igase (EC 6.3.3.1) mtu02022 Purie metric/018 CHEM GW335118X G5823 Rv0592 Iun Non Essential pur/M MT0830 Rv0809 Phosphorbosyformyglychamidine cyclo-igase (EC 6.3.3.1) mtu02022 Purie metric/018 CHEM GW335118X G5843 Rv0592 Iun Non Essential pur/M MT0830 Rv0809 Phosphorbosyformyglychamidine cyclo-igase (EC 6.3.1) mtu02020 Purie metric/018 CHEM GW335118X G5845 Rv0592 Iun Non Essential pur/M MT0830 Rv0809 Phosphorbosyformyglychamidine cyclo-igase (EC 6.3.1) mtu02020 Purie metric/018 GHEM GW335118X G5845 Rv0592 Iun Non Essential pur/M MT0830 Rv0809 Phosphorbosyformyglychamidine cyclo-igase (EC 6.3.1.1) mtu02020 Purie metric/018 Purie metric/018 GHEM GW335118X D6345 Rv0255	etabolism : pathways sis of secondary es ray
CHEM GW335118X Q53821 Rv0892 Ium Non Essential Pur/M MT0830 Rv0809 Phosphorbosyformytglychamidne cyclo-ligase (EC 6.3.1) mtullition mtullition Metabole predictions CHEM GW335118X Q53823 Rv0892 Ium Non Essential pur/M MT0830 Rv0809 Phosphorbosyformytglychamidne cyclo-ligase (EC 6.3.1) mtullition Biosphorbosyformytglychamidne cyclo-ligase (EC 6.3.1) mtullition Biosphorbosyformytglychamidne cyclo-ligase (EC 6.3.1) Nullition Nullition Rv0801 Mtullition Rv0801 Mtullition Rv0801 Nullition Rv0801 Rv0801 <td>pathways esis of secondary es ray</td>	pathways esis of secondary es ray
CHEM GM335118X GS382 BxX892 Ixin Non Essential PM MT 0830 Rv0809 Phosphorbosyformyglychamdine cyclo-ligase (EC 6.3.1) mbml 01110 Biosphorbasilies CHEM GW335118X GS488 Rx2085 Ixin Non Essential Ip Rv2045c Phosphorbosyformyglychamdine cyclo-ligase (EC 6.3.1.1) NA NA No Pathway CHEM GW335118X PA645 Rx2055 Ixin Non Essential Ip Rv2045c Phosphorbosyformyglychamdine cyclo-ligase (EC 6.3.1.1) NA No Pathway CHEM GW335118X PA645 Rx2055 Ixin Non Essential Ip Rv2045c Dhydrofolate reductase (EC 1.5.1.3) mbu0202 Oc carbon CHEM GW335118X PA645 Rx2755 Ixin Non Essential Ip Rv2755c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mbu0202 Pice boxy CHEM GW335118X PA6456 Rx2755c Ixin Non Essential In Arc/155c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mbu0202 Mebboxy CHEM GW335118X PA5557 Ixin Non Essential In Arc/155c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mbu02010 Mebboxy	esis of secondary les ray
CHEM GW335118X Q63488 Rx2055 tito Non Essential IP Rv2045c Probable carboxylestarase L/DT (EC 3.1.1-) NA NA NA Pathway CHEM GW335118X P0A546 Rx2753c tito Non Essential fold drik Rv2753c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mtw00270 One arbon CHEM GW335118X P0A546 Rx2753c tito Non Essential fold drik Rv2753c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mtw00270 One arbon CHEM GW335118X P0A546 Rx2753c tito Non Essential fold drik Rv2753c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mtw00270 One arbon CHEM GW335118X P0A546 Rx2753c tito Non Essential fold drik Rv2753c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mtw00270 mtw00270 Mtw002 28c CHEM GW335118X P0A546 Rx2753c tito Non Essential fold drik Rv2753c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mtw00270 mtw00270 Mtw002 28c CHEM GW335118X P0535	vay
CHEM GW335118X P0A64 Bx2753 tim Non Essential Non Essential Non Essential Non Essential Non Essential Mon Essential Dhydrofolate reductase (EC 1.5.1.3) mb/00220 mb/00270 Chearbon mb/00270 Chearbon CHEM GW335118X P0A646 Rx2753 tim Non Essential StA drfs Rx2763c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mb/00270 Felde borg CHEM GW335118X P0A646 Rx2753c trans Non Essential StA drfs Rx2763c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mb/00270 Felde borg CHEM GW335118X P0A646 Rx2753c trans Non Essential StA drfs Rx2763c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mb/00270 Melabolic put MTV00228c CHEM GW335118X P05367 Rx558c mt3684 Carbonic anhydrase (EC 4.2.1.1) (Carbonate dehydratase) mb/00270 Non enabolic put MTV00228c STR GW335118X P05367 Rx1538c MT3694 Carbonic anhydrase (EC 4.2.1.1) (Carbonate dehydratase) mb/00400 Alanine, ass MTC/44 2/7 STR GW335118X P053627<	
CHEM GW335118X P0A546 Rx2753c total Non Essential fold drA Rx2753c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mtx002790 Folate box CHEM GW335118X P0A546 Rx2753c total Non Essential fold drA Rx2753c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mtx002790 Folate box CHEM GW335118X P0A546 Rx2753c total Non Essential Sol drfA Rx2753c MT2833 Dhydrofolate reductase (EC 1.5.1.3) mtx002790 Mt3002100 Metabolic put CHEM GW335118X P03572 Rx958bs total Non Essential opt Rx536s MT3694 Carbonic anhydrase (EC 4.2.1.1) (Carbonate dehydratase) mtx002790 Mt002790 Anine, ass metabolism STR GW335118X P63827 Rx1538s tosa Non Essential anxA Rx1538c MT1590 Probable L-asparaginese (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolese) mtx02420 Quenominic	on pool by folate
CHEM GW335118X P0A546 Bx/2753c tdra Non Essential IolA drfA RV2763c MT2803 Dihydrofolate reductase (EC 1.5.1.3) mb/0100 Metabolic processor CHEM GW335118X P0A546 Bx/2753c tdra Non Essential OldA drfA RV2763c MT2803 Dihydrofolate reductase (EC 1.5.1.3) mb/0100 Metabolic processor CHEM GW335118X P03572 RV1558c tdra Non Essential opnT Rv1598c MT3694 Carbonic anhydrase (EC 4.2.1.1) (Carbonate dehydratase) mb/0100 Metabolic processor STR GW335118X P03827 RV1538c tma Non Essential msA RV1538c MT1590 Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase) Mato/250 Alanine, asp metabolism STR GW335118X P63827 RV1538c tma Non Essential RNn Proable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase) mb/02400 Quanamid	osynthesis
CHEM QW335118X Q5577 Rv3588 tid Non Essential 0.36 oyn Rv3588c M1369 Carbonic anhydrase (EC 4.2.1.1) (Carbonate dehydratase) mtu00910 Nitrogen mtu00910 STR GW335118X P63827 Rv1538c tva Non Essential ansA Rv1538c M1369 MTCY48.27 Probable L-asparaginese (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase) mtu00450 Almine, asg mtu00450 STR GW335118X P63827 Rv1538c tva Non Essential Non MTCY48.27 Probable L-asparaginese (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase) mtu00450 Almine, asg mtu00450 mtu00460 Qynoamine	; pathways
STR GW335118X P63827 Rv1538e Image Non Essential Non Essential ansA Rv1538c MT1590 MTCV48.27 Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase) mbd02250 mdb00250 Alanine, asg metabolism STR GW335118X P63827 Rv1538c Image Non Essential Non Amin An Rv1530c MT1590 Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase) mbd02250 Alanine, asg metabolism STR GW335118X P63827 Rv1538c Image Non Essential Non MTCV48.27 Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase) mbd0250 Alanine, asg metabolism	metabolism
STR GW035118X P63627 Rv1536 tma Rom Non ansA Rv1538c M11590 Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase) mtu00460 Cyanoamino	aspartate and glutamate sm
	nino acid metabolism
STR <u>GW335118X P63627 Rv1538c Insa</u> Non Non Essential Ssential Essential MTCV48.27 Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase) <u>mtu00910</u> Ntrogen me	metabolism
STR QW335118X P63627 Rv1538e Image Non Essential Non Essential ansA Rv1538e //11590 MTCV48 27 Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase) mtu01100 Metabolic prime	; pathways
STR <u>GW335118X P63827 Rv1538c Insa</u> Non Non ansA Rv1538c MT1590 Probable L-asparaginase (L-ASNase) (EC 3.5.1.1) (L-asparagine amidohydrolase) mtu01110 Biosynthesis metabolites	isis of secondary les
STR QW335118X P63562 Rv1652 trd 0.05 Non Essential argC Rv1652 MT1690 MTCV06H11.17 N-acety-gamma-gutamy-phosphate reductase (AGPR) (EC 1.2.1.38) (N-acety-gutamate semialdehyde dehydrogenase) (NAGSA dehydrogenase) Macety-gamma-gutamy-phosphate reductase (AGPR) (EC 1.2.1.38) (N-acety-gutamate semialdehyde dehydrogenase) Argaine and dehydrogenase)	and proline metabolism
STR <u>GW335118X P63562</u> <u>Rv1652</u> trdf 0.05 Non argC Rv1652 MT1690 Stemial MTCV06H11.17 Metabolic participanase) (NAGSA dehydrogenase) (NAGSA dehydrogenase)	a pathways
STR 0W335118X P63562 Rv1652 trd 0.05 Non Essential arCV0652/MT1690 N-acety-gamma-gutamy-phosphate reductase (AGPR) (EC 1.2.1.38) (N-acety-gutamate semialdehyde mtu01110 Bosynthesis metabolites	isis of secondary les
STR <u>GW335118X P63562</u> Rv1652 Irdf 0.05 Non argC Rv1652 IIT1690 MTCV06H11.17 Nacetyl-gamma-gutamyl-phosphate reductase (AGPR) (EC 1.2.1.38) (N-acetyl-gutamate semialdehyde mtu01210 2-Oxocarbo	boxylic acid metabolism
STR QW335118X Q53321 Rv3171c Image Non Essential Non Essential Non Possible NON-HEME HALOPEROXIDASE HPX (EC 1.11.1) N/A No Pathway	vay

nAn	noly	ze			
	Home	Help	About	Download	
		Introduce your qu ID of the molecule	DB00398		

Select the organism

O Mycobacterium tuberculosis, Mycobacterium bovis, Mycobacterium smegmatis

Homo Sapiens

Submit

+ Toggle Statistics

Download

http://nannolyze.cnag.cat

Acknowledgments

Davide Baù Gireesh K. Bogu François le Dily Marc A. Marti-Renom David Dufour François Serra Michael Goodstadt Yasmina Cuartero

COLLABORATORS

Jim Brown (GSK) LLuís Ballell (GSK) John Overington (EBI-EMBL) Andrej Sali (UCSF) Anna Tramontano (Sapienza University)

http://marciuslab.org
http://integrativemodeling.org
http://cnag.cat · http://crg.cat

MINISTERIO DE ECONOMÍA Y COMPETITIVIDAD

