

# Four interesting examples ...

... of how technology developments support new business models.

*Richard Padley, Managing Director, Semantico.*



Monday, 23 April 12

Example #1 is about Researchers. Specifically its about focus on researcher needs. It starts with a piece of researcher focussed technology that creates some interesting opportunities.



Researcher

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Example #1 is about Researchers. Specifically its about focus on researcher needs. It starts with a piece of researcher focussed technology that creates some interesting opportunities.

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**Sample Collection**

10.1038/nature040001  
**Charleworth (2006) The Rate of Adaptive Evolution in Emeric Bacteria** *Molecular Biology and Evolution*

10.1038/nature040002  
**Eisen (2007) Environmental Shotgun Sequencing: Its Potential and Challenges for Studying the Hidden World of Microbes** *Proc Natl Acad Sci U S A*

10.1038/nature040003  
**Duhell, Ganagathy, Hoboth, Malund, Uyenoyama, Schierup (2008) Ancestral Population Genomics: The Coalescent Hidden Markov Model Approach** *Genetics*

10.1038/nature040004  
**Tan, Jones, Zhu, Ye, Hong, Zhou, Zhang, Zhang (2008) Fallacy by Fruit Bats Prolongs Cuspation Time** *Nature*

10.1038/nature040005  
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**DUNCAN J WATTS**

**145** Collective dynamics of 'small-world' networks.

*Nature (2002) Nature Publishing Group, 1998*

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Networks of coupled dynamical systems have been used to model biological oscillators, Josephson-junction arrays, metabolic cycles, social networks, spatial games, genetic control networks and many other self-organizing systems. Ordinarily, the connection topology is assumed to be either completely regular or completely random. But many biological, technological and social networks have intermediate features that can be described using complex network theory. We study three classes of networks: regular lattices, small-world networks and complex networks with a power-law distribution of nearest-neighbour degrees. The small-world networks are characterized by a high degree of clustering, and the complex networks show a high degree of heterogeneity. Models of dynamical systems with small-world coupling display enhanced signal-propagation speed, computational power, and robustness to perturbations. Intermediate features may occur naturally in small-world networks that are regular lattices.

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**Annotating genes and genomes with DNA sequences extracted from biomedical articles**

Ramsey M, Gerner M, Bergman C. *Bioinformatics*. 2011;27(13):980-986  
<http://doi.org/10.1093/bioinformatics/btt644>

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*Nature News*  
 New model suggests that Fukushima's fallout was far worse than the Japanese government has claimed.  
 Global data on Fukushima challenge Japanese estimates.  
 Fallout forensics hike radiation toll - Global data on Fukushima challenge Japanese estimates.  
 Fukushima radiation far worse than reported by Japanese gov. How does it affect dolphins in Japan - or Hawaii or Calif?

**1043** **Quantum theorem shakes foundations**  
*Nature*  
 Forget neutrinos: THIS is the most significant result in quantum mechanics for 50 years.  
 Quantum theorem shakes foundations: Wavefunction is a real physical object after all.  
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 Not sure what to make of this: new paper claims QM wave function is physically real. ?

**561** **Cesium-137 deposition and contamination of Japanese soils due to the Fukushima nuclear accident**  
*Proceedings of the National Academy of Sciences*  
 PNAS: Some Fukushima fallout no longer safe due to high radiation levels in soil - Japan.  
 Original PNAS articles on C137 deposition/contamination from Fukushima accidents.  
 Study about state of Cesium-137 contamination Fukushima.  
 We show that 137Cs strongly contaminated the soils in large areas of eastern and northeastern Japan (Fukushima #1).

**517** **Rebirth of a Dead Belousov-Zhabotinsky Oscillator**  
*The Journal of Physical Chemistry A*  
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**Review of Neighbourhood physical activity environments and adiposity in children and mothers: a three-year longitudinal study** (Tinetti et al., 2012)

**Nevel approach that merits further explanation and development**

by Kate Thomson · 1 week ago · Recommended by 1 · Difficulty level: **Intermediate** · Reviewer expertise: **Intermediate**

This paper was discussed by Public Health Action Journal 1 July in November 2011. A full summary of the discussion and knowledge can be accessed here: <http://publichealthactionjournal.com/2011/07/11/20110711-7-neighbourhood-environments/>. The study generally aligns with my research on neighbourhood environments, focusing on aspects such as 'walkability'. Data on the 'walkability' neighbourhoods measured is generally to park space, houses, rather than official boundaries. Both these aspects are crucial to the literature on health and place and offer interesting analytic potential. The choice of adiposity measure - BMI and a score - could have been discussed more fully. BMI is not more commonly accepted as the best measure, and a score and their interpretation merit further explanation for non-specialists to make sense of the data presented. The paper reports on part of a wider study, and the further (conclusion) findings would be best read in conjunction with published papers from other elements of the study to place the lack of control from the further findings in the wider urban health context. Overall, though an interesting experiment in comparing physical neighbourhood characteristics with obesity in different age groups.

**References** ★★★★★ **Originality** ★★★★★ **Argumentation** ★★★★★ **Readability** ★★★★★

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**Dataset**  
 All tweets contain a link to a scholarly article. Data collected by altmetric.com.

- 467 tweets
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**Activity**

**Most active users**

**Martin Fenner** @mferner  
 Clinical fellow in oncology and science blogger. 91 Classifications

**Ross Mounce** @rmounce  
 Data Research of Palaeo-Phylo-Morpho-favour. Likes Openness. 61 Classifications

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Will feed into Altmetrics phenomenon. Triangulation rather than single measure of impact. Tech: Big data, firehose, hadoop, NoSQL datastores, API level integration. SAAS business model. Returning to h-index is ...

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**Publications**

Title	h5-index	h5-median
1. Nature	295	427
2. New England Journal of Medicine	274	450
3. Science	265	388
4. RePEc	259	356
5. arXiv	256	367
6. The Lancet	205	313
7. Social Science Research Network	205	290
8. Cell	195	279
9. Proceedings of the National Academy of Sciences	189	237
10. Nature Genetics	174	268
11. Journal of Clinical Oncology	173	229
12. JAMA: The Journal of the American Medical Association	171	246
13. Physical Review Letters	162	213
14. Circulation	159	251
15. Chemical reviews	144	248
16. Blood	141	192
17. The Astrophysical Journal	140	181
18. Journal of the American College of Cardiology	139	192

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Who's seen this? Google scholar metrics, launched 1 April. This is no joke. H-index. Another elephant in the room is the biggest business model shift ...



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Researcher focussed business model. Publishing sold is a service, not a physical good, or a licence to access IP. Paraphrase Ahmed Hindawi: increased competition, differentiation around the service. OA raises the bar. Service is for authors; differentiation in adding value for authors.

Royal Marsden Manual: Chapter 3: Infection prevention and control

http://www.rmmonline.co.uk/rmm8/procedure/03/ss9

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## Chapter 3: Infection prevention and control

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- Overview
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  - Definitions
  - Related theory
  - Evidence-based approaches
  - Legal and professional issues
  - Preprocedural considerations
  - Procedure guideline 3.1 Handwashing**
  - Essential equipment
  - Preprocedure

### Procedure guidelines: Handwashing

Audit information

- Date posted: 17 November 2011
- Author: fdsa
- Review date: **09 December 2011**
- Status: This procedure guideline is expired. Please review it.

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Example #2 User Generated Content. RMM in print until 7e; but often supplemented with local notes and modifications. Tech: Flexible XML content database for R/W content. Allows seamless presentation of published & UGC. Like a Wiki BUT private to each subscribing institution. Audit trail. Innovation is delivering Content in Context for clinical practitioners, rather than bus model.



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www.nal.usda.gov/awic/pubs/oldbib/srb94-01.htm  
Swine have been utilized as a biomedical research model in a wide variety of disciplines: the Swine as Models in Biomedical Research M.M. Swindle, D.C.

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[Swine as models in biomedical research. - CAB Direct](#)  
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## Document details

**Title** Swine as models in biomedical research.

**Authors** Pennington, L. R.; Weiskopf, R. B.; Hannon, J. F.

**Editor** Swindle, M. M.

**Book** Swine as models in biomedical research. 1992 pp. xv + 312 pp.

**ISBN** 0-8138-1472-3

**Record Number** 19942200241

## Abstract

The Seventh Charles River International Symposium was held at Danvers, Massachusetts in September 1989. 18 symposium contributions deal with the use of Yucutan and Hanford minipigs and ordinary pigs in cardiovascular research and in a variety of other topics, such as renal transplantation (L. R. Pennington, pp. 35-43), use of swine in the study of anaesthetics, by R. B. Weiskopf and others (96-117), congenital cardiovascular disease in pigs, by M. M. Swindle and others (176-184), and haemorrhagic shock, by J. P. Hannon (197-245). A previous book on swine in biomedical research appeared in 1986 (edited by M. E. Tumbleson, published by Plenum Press, New York).

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Jul 2011

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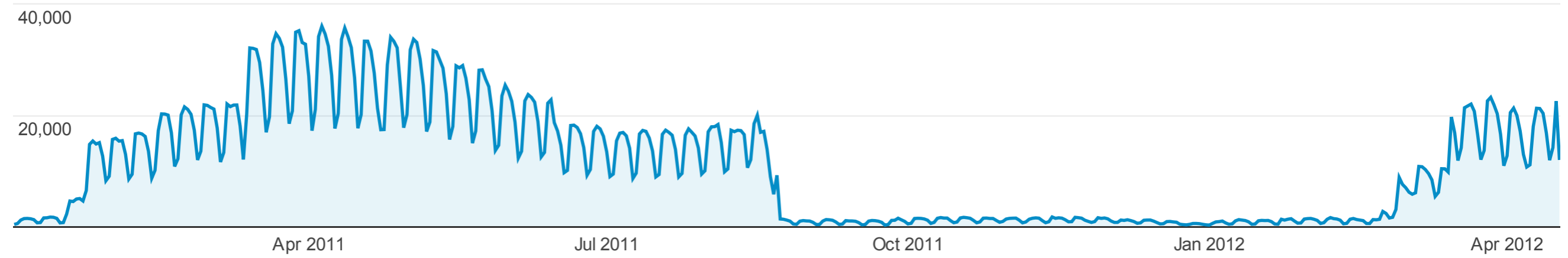
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# The *Mycobacterium tuberculosis* Drugome and Its Polypharmacological Implications

Sarah L. Kinnings<sup>1,2</sup>, Li Xie<sup>3</sup>, Kingston H. Fung<sup>4</sup>, Richard M. Jackson<sup>1</sup>, Lei Xie<sup>3\*</sup>, Philip E. Bourne<sup>2,3\*</sup>

**1** Institute of Molecular and Cellular Biology and Airbury Centre for Structural Molecular Biology, University of Leeds, Leeds, United Kingdom, **2** San Diego Supercomputer Center, University of California, San Diego, La Jolla, California, United States of America, **3** Sloggs School of Pharmacy and Pharmaceutical Sciences, University of California, San Diego, La Jolla, California, United States of America, **4** Bioinformatics Program, University of California, San Diego, La Jolla, California, United States of America

## Abstract

We report a computational approach that integrates structural bioinformatics, molecular modelling and systems biology to construct a drug-target network on a structural proteome-wide scale. The approach has been applied to the genome of *Mycobacterium tuberculosis* (*M.tb*), the causative agent of one of today's most widely spread infectious diseases. The resulting drug-target interaction network for all structurally characterized approved drugs bound to putative *M.tb* receptors, we refer to as the 'TB-drugome'. The TB-drugome reveals that approximately one-third of the drugs examined have the potential to be repositioned to treat tuberculosis and that many currently unexploited *M.tb* receptors may be chemically druggable and could serve as novel anti-tubercular targets. Furthermore, a detailed analysis of the TB-drugome has shed new light on the controversial issues surrounding drug-target networks [1–3]. Indeed, our results support the idea that drug-target networks are inherently modular, and further that any observed randomness is mainly caused by biased target coverage. The TB-drugome (<http://funsite.sdc.edu/drugome/TB>) has the potential to be a valuable resource in the development of safe and efficient anti-tubercular drugs. More generally the methodology may be applied to other pathogens of interest with results improving as more of their structural proteomes are determined through the continued efforts of structural biology/genomics.

**Citation:** Kinnings SL, Xie L, Fung KH, Jackson RM, Xie L, et al. (2010) The Mycobacterium tuberculosis Drugome and Its Polypharmacological Implications. *PLoS Comput Biol* 6(11): e1000976. doi:10.1371/journal.pcbi.1000976

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**Competing Interests:** The authors have declared that no competing interests exist.

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## Introduction

The construction and analysis of molecular interaction networks provides a powerful means to understand the complexity of biological systems and to reveal hidden relationships between drugs, genes, proteins, and diseases. In particular, the study of drug-target networks may facilitate an improved understanding of the principles of polypharmacology and hence improved rational drug design [2]. In recent years, several computational methodologies have been developed to predict drug-target networks based on ligand chemistry [4–6], phenotypic changes resulting from drug perturbation [7–9], or a combination of chemical features of drugs and sequence features of protein targets [10–12]. Extensive experimental and computational evaluation has proven that these methods are valuable for drug repurposing and side effect prediction. However, these methods are biased towards known drug-target pairs, which are mainly derived from well-established human target classes such as G-protein coupled receptors (GPCRs), which only cover a small portion of the human proteome. The lack of a broad spectrum of drug-target pairs is more severe in pathogens than it is in human. For example, amongst the 3,999 proteins encoded by the *Mycobacterium tuberculosis* (*M.tb*) genome, only nine (*cmaA1*, *cyp51*, *embA*, *embB*, *embC*, *folK*, *lahA*, *katG* and *rpoC*) have been pharmaceutically investigated [13]. Thus, drug-target networks that are constructed from only existing drug targets are retrospective, and less capable

of discovering new druggable targets and predicting off-target profiles of new compounds on a proteome-wide scale. In addition, the incompleteness of drug-target data poses questions as to whether or not the topology of drug-target networks is inherently modular or random [1].

It is important to construct and analyze a proteome-wide drug-target network that includes not only the primary targets, but also all of the potential off-targets of the drugs in the network. Such a network, if available, would provide unparalleled opportunities for mapping a comprehensive drug-target space and understanding the molecular basis of drug efficacy, side-effects and drug resistance, thereby providing the foundation for the rational design of polypharmacological (multi-target) drugs. For anti-infectious drug discovery, where pharmaceutically investigated targets only represent a small portion of the whole pathogen's proteome, it is more challenging to establish a proteome-wide drug-target network. The linkage of drugs to less exploited proteins such as virulence factors, transport proteins and transcription factors will greatly expand the repository of anti-infectious drug targets and provide new solutions for combating multi-drug and extensively drug resistant pathogens, and for repurposing existing drugs for new uses.

Structural bioinformatics provides an alternative and complementary way to extend drug-target networks to less characterized proteins on a proteome-wide scale. The structural coverage of a given pathogen proteome is usually much larger than the

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Mycobacterium tuberculosis

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Reactivity	Bacteria
Clonality	Monoclonal
Volume	0.2mg

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# The *Mycobacterium tuberculosis* Drugome and Its Polypharmacological Implications

Sarah L. Kinnings<sup>1,2</sup>, Li Xie<sup>3</sup>, Kingston H. Fung<sup>4</sup>, Richard M. Jackson<sup>1</sup>, Lei Xie<sup>3\*</sup>, Philip E. Bourne<sup>2,3\*</sup>

**1** Institute of Molecular and Cellular Biology and Airbury Centre for Structural Molecular Biology, University of Leeds, Leeds, United Kingdom, **2** San Diego Supercomputer Center, University of California, San Diego, La Jolla, California, United States of America, **3** Sloggs School of Pharmacy and Pharmaceutical Sciences, University of California, San Diego, La Jolla, California, United States of America, **4** Bioinformatics Program, University of California, San Diego, La Jolla, California, United States of America

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**Funding:** This research is funded by National Institutes of Health grant GM078996 (<http://www.nih.gov>). The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**Competing Interests:** The authors have declared that no competing interests exist.

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## Introduction

The construction and analysis of molecular interaction networks provides a powerful means to understand the complexity of biological systems and to reveal hidden relationships between drugs, genes, proteins, and diseases. In particular, the study of drug-target networks may facilitate an improved understanding of the principles of polypharmacology and hence improved rational drug design [2]. In recent years, several computational methodologies have been developed to predict drug-target networks based on ligand chemistry [4–6], phenotypic changes resulting from drug perturbation [7–9], or a combination of chemical features of drugs and sequence features of protein targets [10–12]. Extensive experimental and computational evaluation has proven that these methods are valuable for drug repurposing and side effect prediction. However, these methods are biased towards known drug-target pairs, which are mainly derived from well-established human target classes such as G-protein coupled receptors (GPCRs), which only cover a small portion of the human proteome. The lack of drug-target pairs is even more severe in pathogens than it is in human. For example, amongst the 3,999 proteins encoded by the *Mycobacterium tuberculosis* (*M.tb*) genome, only nine (*cmaA1*, *cyp51*, *embA*, *embB*, *embC*, *embX*, *inhA*, *katG* and *rpoC*) have been pharmacologically investigated [13]. Thus, drug-target networks constructed from only existing drug targets are retrospective, and less capable

of discovering new druggable targets and predicting off-target profiles of new compounds on a proteome-wide scale. In addition, the incompleteness of drug-target data poses questions as to whether or not the topology of drug-target networks is inherently modular or random [1].

It is important to construct and analyze a proteome-wide drug-target network that includes not only the primary targets, but also all of the potential off-targets of the drugs in the network. Such a network, if available, would provide unparalleled opportunities for mapping a comprehensive drug-target space and understanding the molecular basis of drug efficacy, side-effects and drug resistance, thereby providing the foundation for the rational design of polypharmacological (multi-target) drugs. For anti-infectious drug discovery, where pharmacologically investigated targets only represent a small portion of the whole pathogen's proteome, it is more challenging to establish a proteome-wide drug-target network. The linkage of drugs to less exploited proteins such as virulence factors, transport proteins and transcription factors will greatly expand the repository of anti-infectious drug targets and provide new solutions for combating multi-drug and extensively drug resistant pathogens, and for repurposing existing drugs for new uses.

Structural bioinformatics provides an alternative and complementary way to extend drug-target networks to less characterized proteins on a proteome-wide scale. The structural coverage of a given pathogen proteome is usually much larger than the

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Supplier	Novus Biologicals
Host organism	Mouse
Reactivity	Bacteria
Clonality	Monoclonal
Volume	0.2mg

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# The *Mycobacterium tuberculosis* Drugome and Its Polypharmacological Implications

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## Abstract

We report a computational approach that integrates structural bioinformatics, molecular modelling and systems biology to construct a drug-target network on a structural proteome-wide scale. The approach has been applied to the genome of *Mycobacterium tuberculosis* (*M.tb*), the causative agent of one of today's most widely spread infectious diseases. The resulting drug-target interaction network for all structurally characterized approved drugs bound to putative *M.tb* receptors, we refer to as the 'TB-drugome'. The TB-drugome reveals that approximately one-third of the drugs examined have the potential to be repositioned to treat tuberculosis and that many currently unexploited *M.tb* receptors may be chemically druggable and could serve as novel anti-tubercular targets. Furthermore, a detailed analysis of the TB-drugome has shed new light on the controversial issues surrounding drug-target networks [1–3]. Indeed, our results support the idea that drug-target networks are inherently modular, and further that any observed randomness is mainly caused by biased target coverage. The TB-drugome (<http://funsite.sdc.edu/drugome/TB>) has the potential to be a valuable resource in the development of safe and efficient anti-tubercular drugs. More generally the methodology may be applied to other pathogens of interest with results improving as more of their structural proteomes are determined through the continued efforts of structural biology/genomics.

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