



Open Source Drug Discovery for Infectious Diseases

A case Application on Tuberculosis (Phase I)

INSTITUTE OF GENOMICS AND INTEGRATIVE BIOLOGY

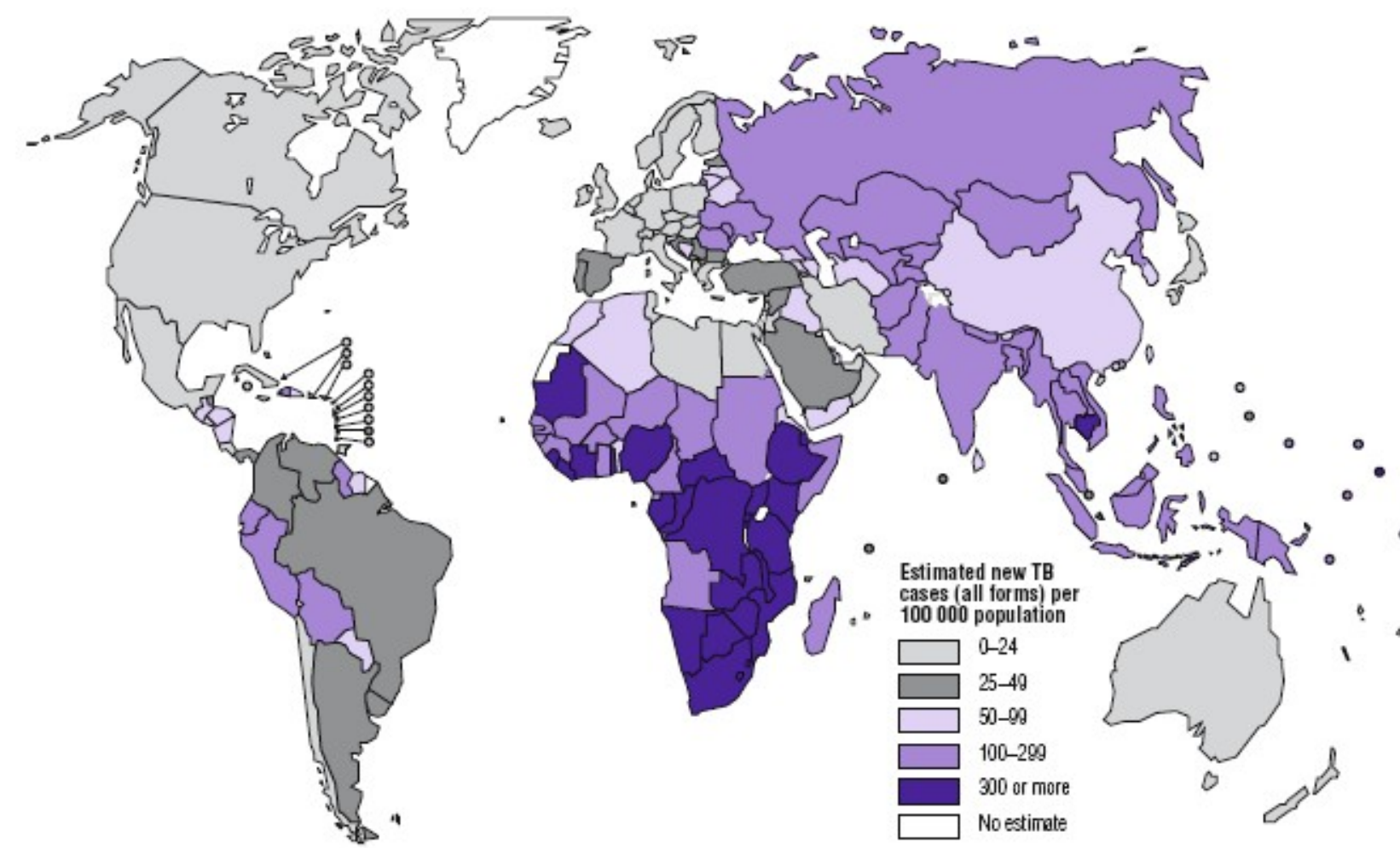


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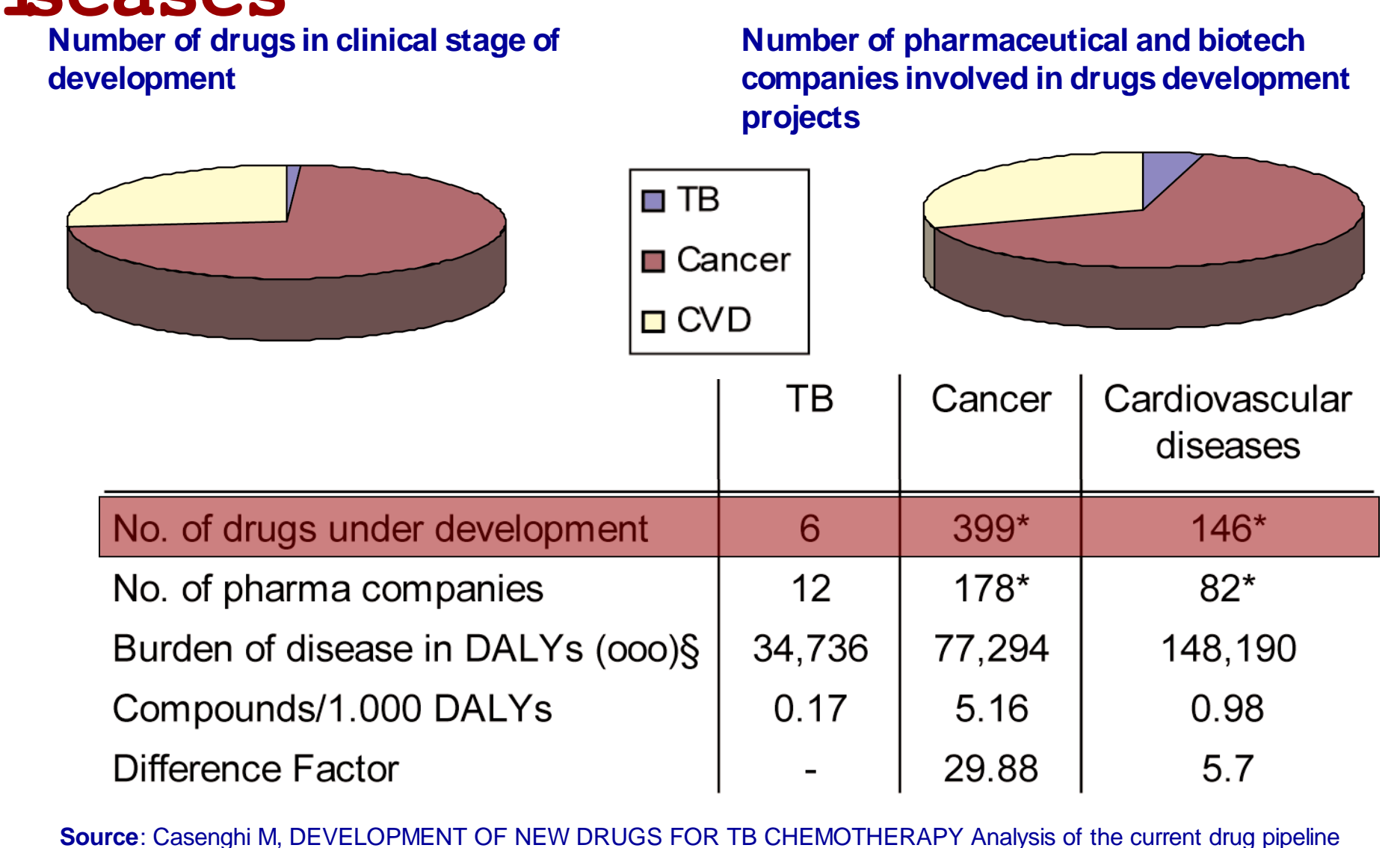
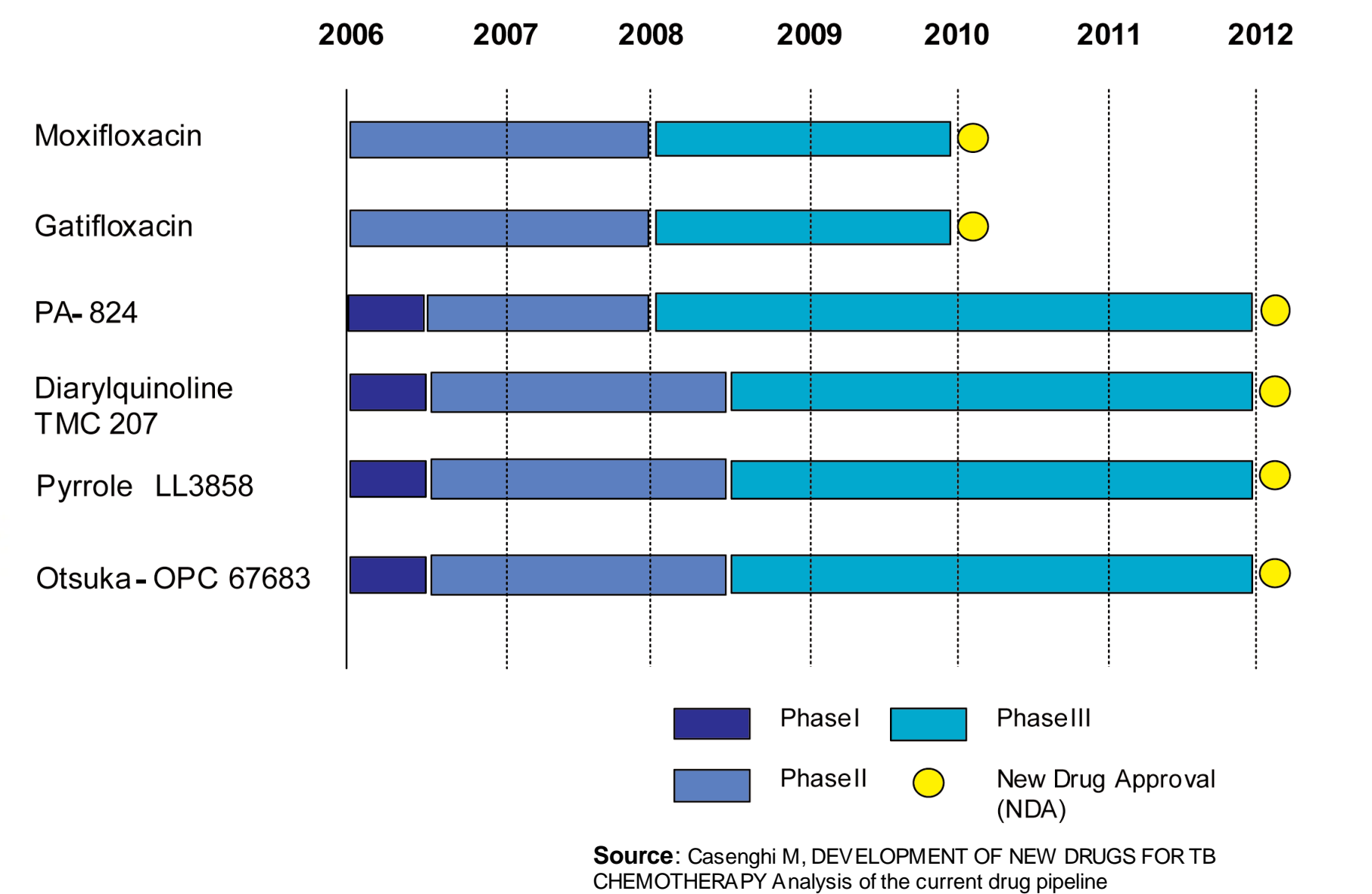
Tuberculosis Facts and Figures

- Someone in the world is newly infected with TB bacilli every three seconds.
- Overall, one-third of the world's population is currently infected with the TB bacillus.
- 5-10% of people who are infected with TB become sick or infectious at some time during their life.
- Left untreated, each person with active TB disease will infect on average between 10 and 15 people every year.
- 450 000 new MDR-TB cases are estimated to occur every year.

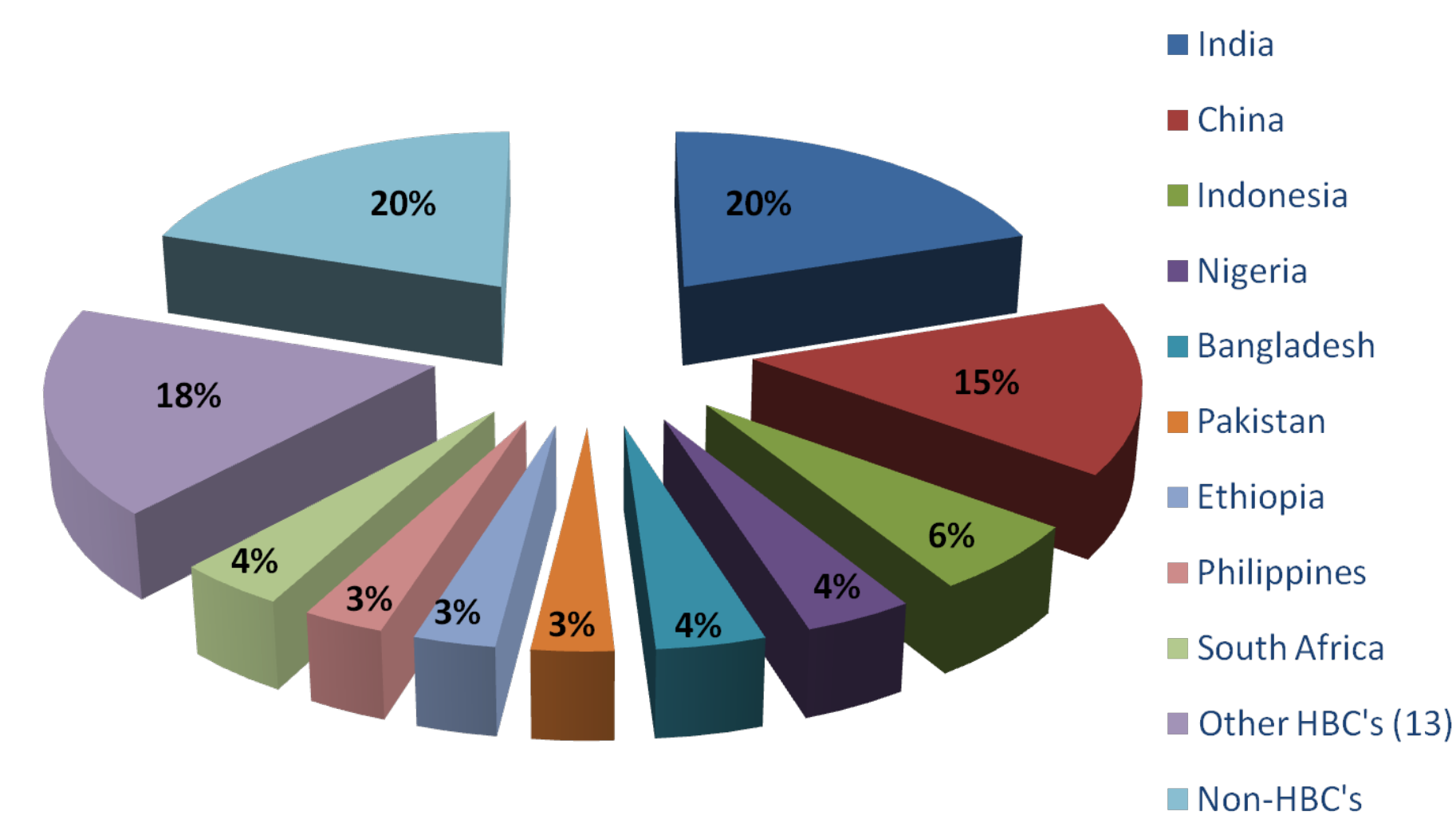
Estimated TB Incidence Rate in 2006



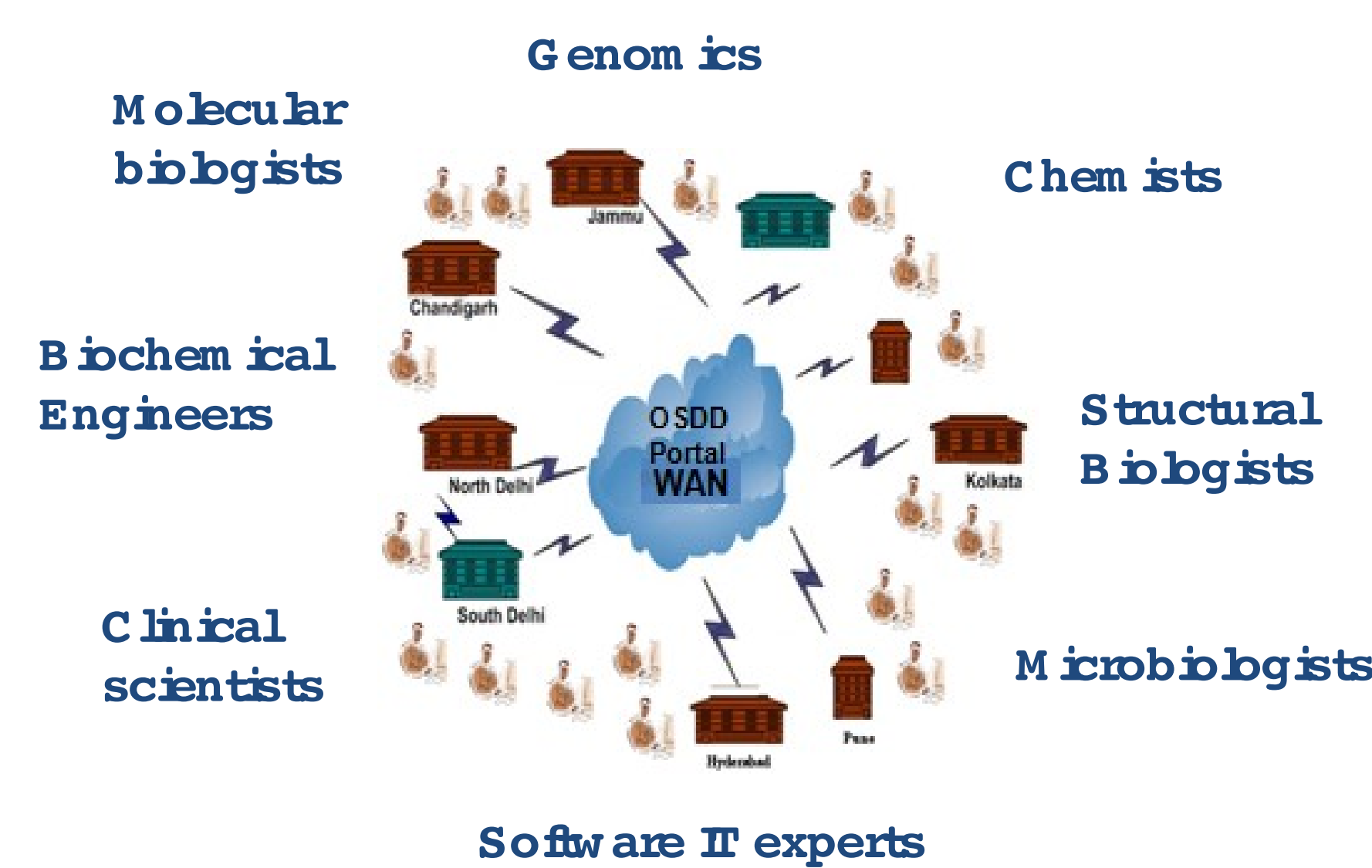
Candidate TB Drugs in Pipeline Drug Pipelines for TB and for other Diseases



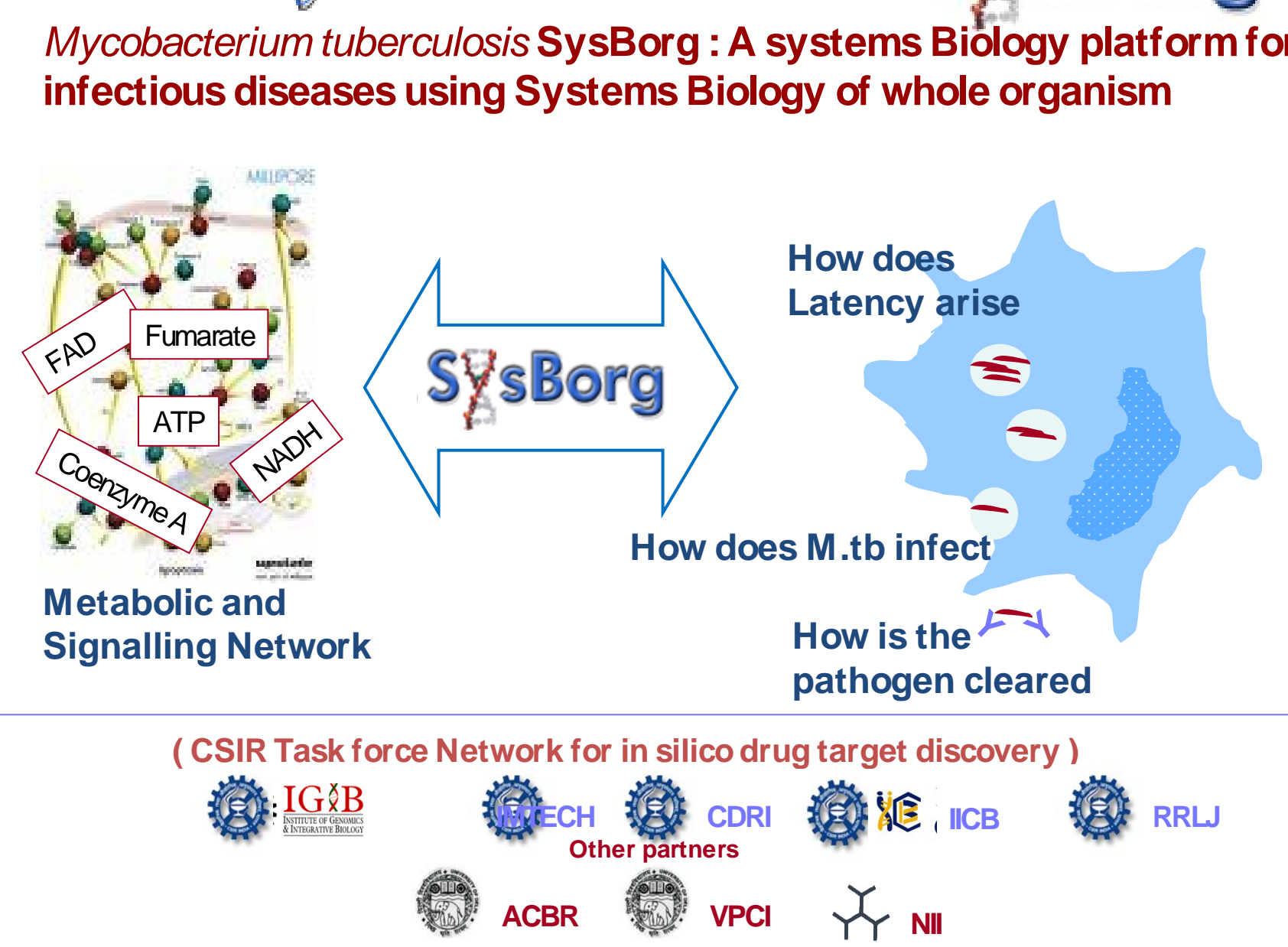
India is the Highest TB Burden Country Globally



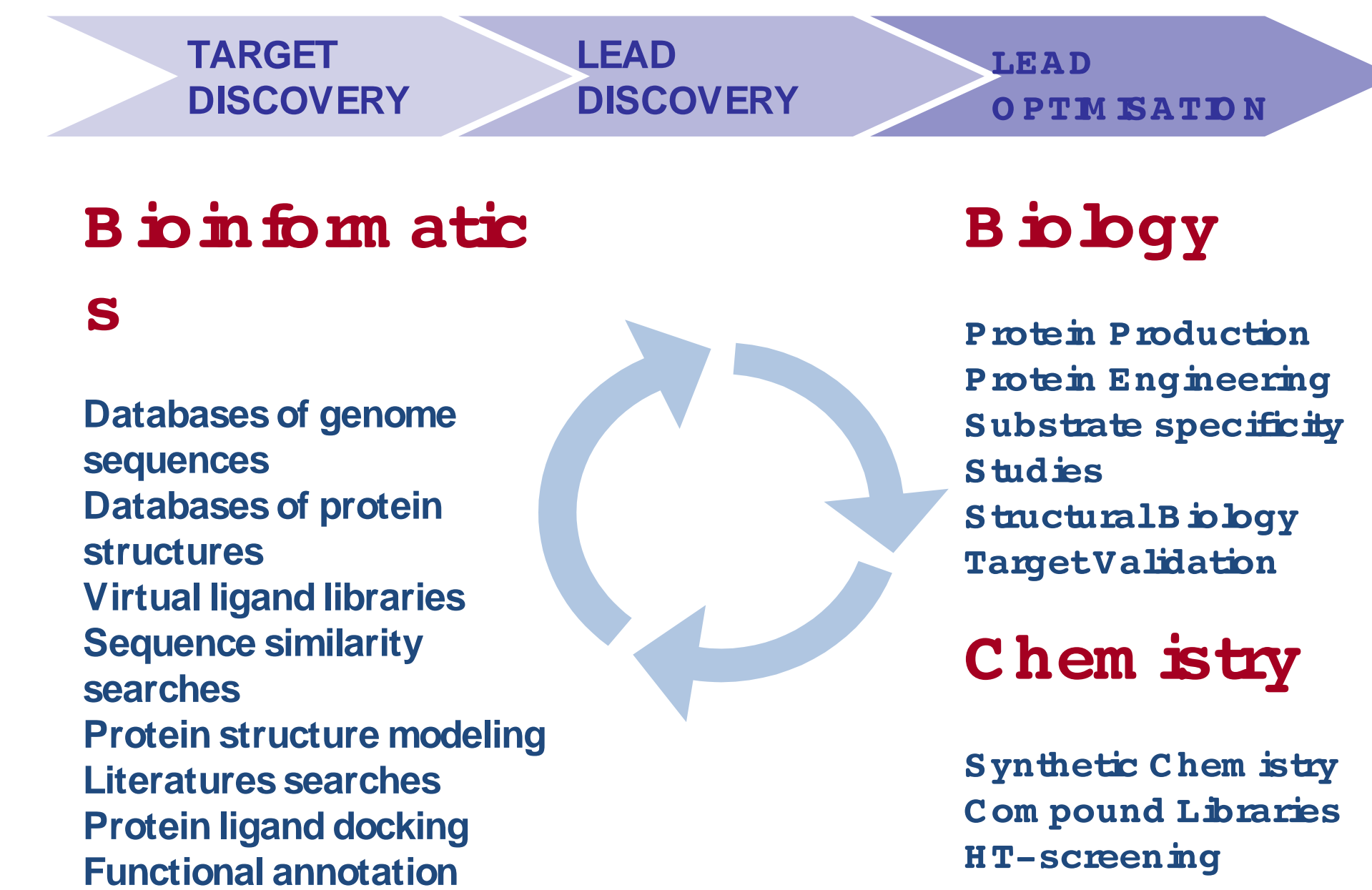
Collaborate, Share, Discover



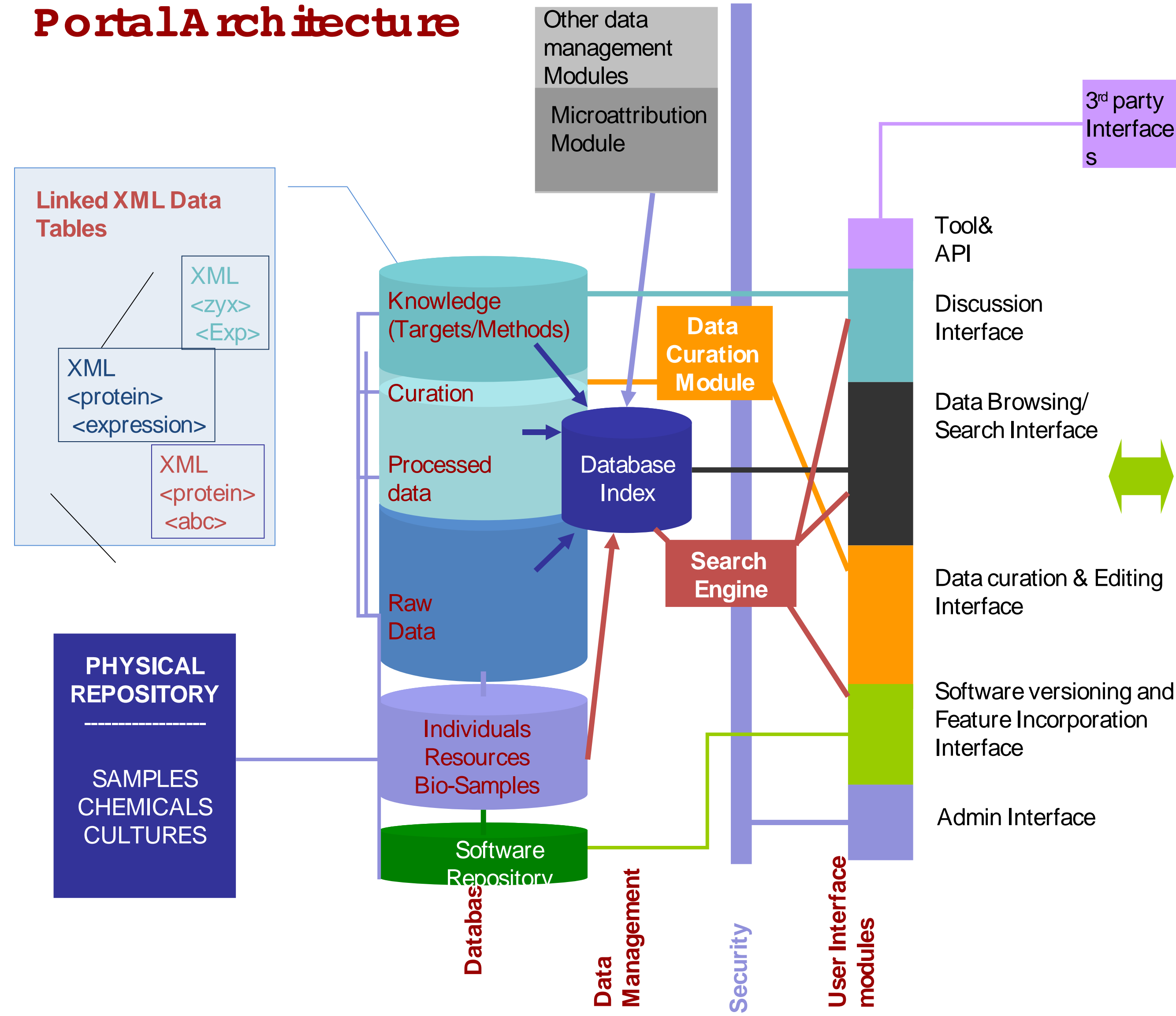
Mycobacterium tuberculosis SysBorg



Work Plan for OSDD



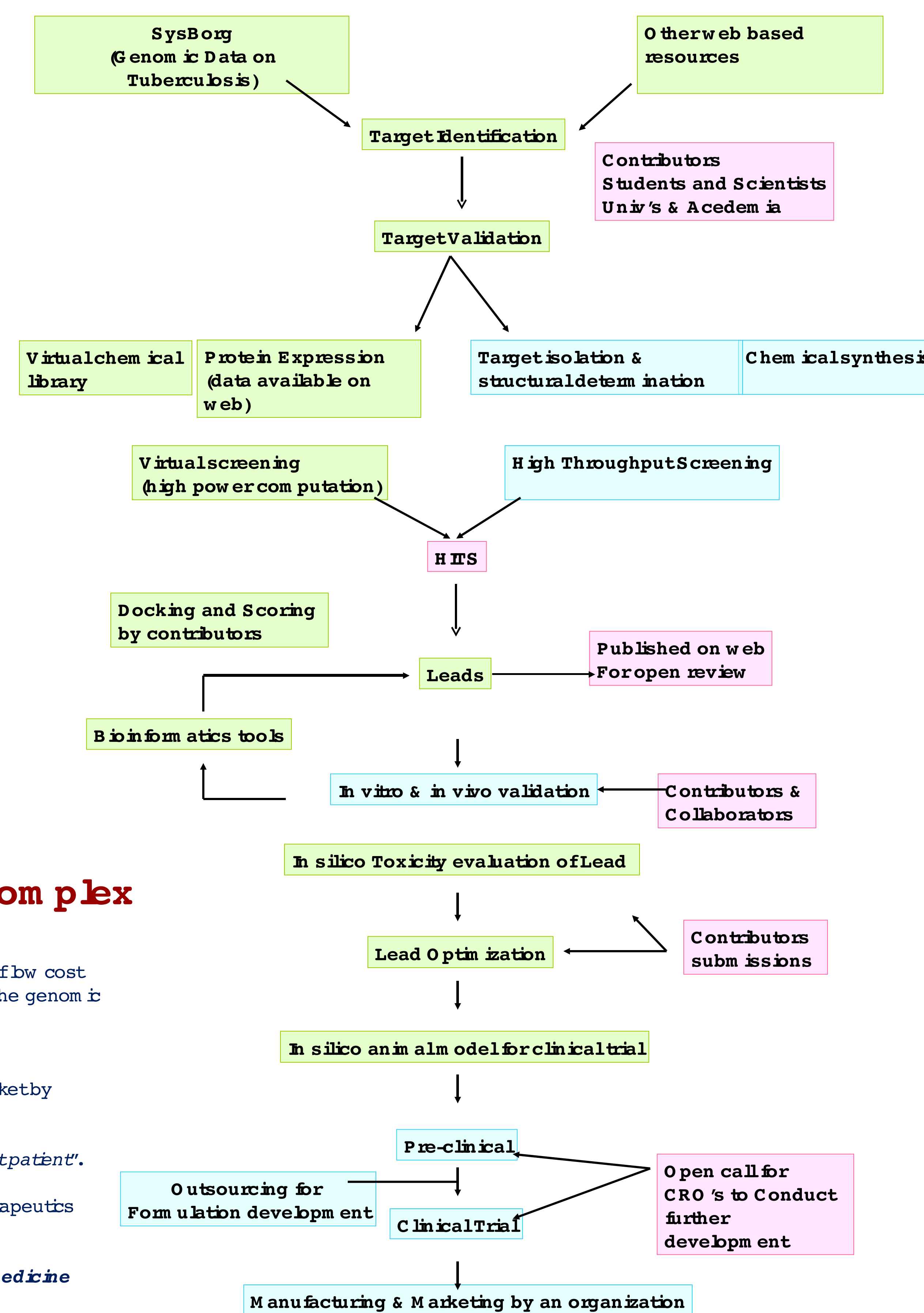
Portal Architecture



Work Packages

- Phase-I
 - WP-1 Identification of Targets (in Silico)
 - WP-2 Expression of Targets
 - WP-3 Validation of targets and Screen Development
 - WP-4 Identification of Chemical library
 - WP-5 Microarray gene expression
 - WP-6 Lead optimization on the non-toxic hits
 - WP-7 Synthesis of analogues
 - WP-8 Identify non specific binding proteins using Phase-2
 - WP-9 Preclinical toxicity
 - WP-10 Clinical Trial

How would it work



The Promise of The Human Genome Open Source Drug Discovery Portal Pharmacogenomics and Predictive Therapy for Complex Diseases

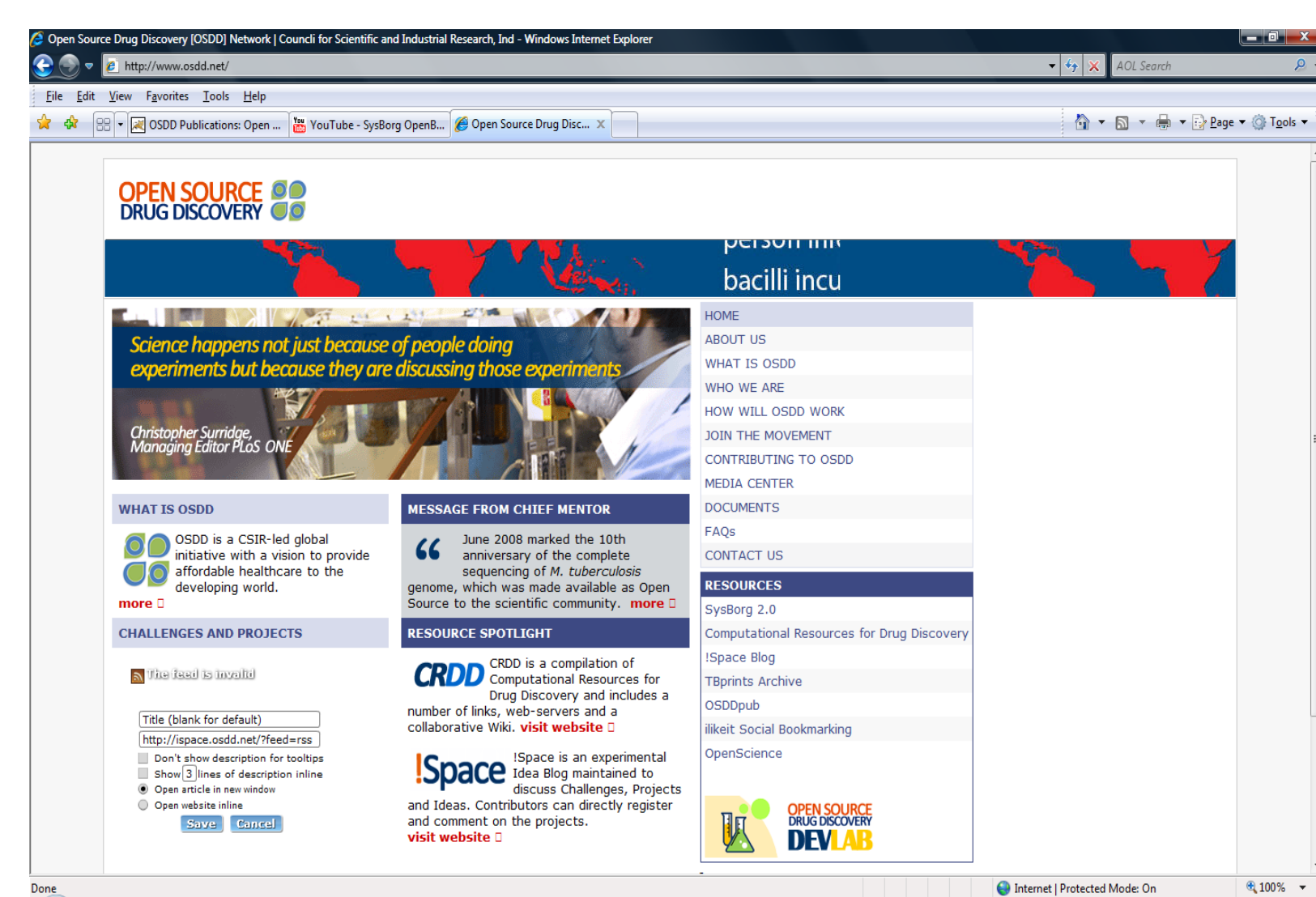
The sequencing of the Human Genome created stir in the scientific community with the promise to make a remarkable difference to healthcare.

Mycobacterium tuberculosis genome was sequenced 10 years ago

With both the genome sequences available to the scientific community

Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome sequence

...discovered! The Human Genome...
S.T. Cowi, R. Brooth, J. Parkhill, T. Garnier, C. Chardon, D. Harris, S.V. Gordon, K. Eigmeier, S. Guo, C. Barry III, R. Takai, K. Bakula, D. Basham, D. Brown, T. Chillingworth, E. Connor, R. Davies, K. Deacon, T. Desjardins, S. Gordon, B. Haubert, S. Haywood, S. Hegerl, A. Hoare, J. Holt, K. Hogg, J. Maitland, R. Squares, S. Squares, J.E. Sutton, K. Taylor, S. Whittaker & S.G. Bellgard



URL: <http://osdd.org> & <http://osdd.net>

Predictive Therapy for Complex Diseases

OSDD Phase-II
Provide the molecular targets for safe usage of low cost drugs in personalized medicine system to decipher the genome based variability in drug response. (eg: Epilepsy, Mental disorders etc)

To keep low cost drugs/orphan drugs in the market by promoting safe and effective usage.

To provide 'right dosage of right drug to the right patient'.

Avoiding adverse events to commonly used therapeutics using pharmacogenomics.

Ref: Brahmachari S. Annual Personalized Medicine Report 2007.