

LECTURE 1 – INTRODUCTION

1. Choosing a disease

- Economic vs scientific issues
- Have to recoup costs if development is to be *sustainable*
- Therefore the ideal disease for drug discovery has:
 - o Lots of patients
 - o Someone is able to pay for treatment
 - Rich governments
 - Rich patients
- Multiple effective drugs to treat HIV/AIDS
 - o Initially affected economically privileged patients
- Few effective drugs to treat malaria
 - o Most patients in less economically well-off countries

2. Hits and leads

- A compound that is identified in an assay with the desired activity
- E.g. binds to a receptor with micromolar affinity or better = **HIT**
- Success of hit in further
- Biological characterization
- E.g. agonist versus antagonist
- Chemical characterisation
- E.g. ease of synthesis = **LEAD** (compound you can start investigating further)
- What compounds do you synthesise and test?
- How do you find hits?
 - o How do you optimise the hits and come up with a lead?
- Assume the compound is “out there”
 - o How do you find it?
- Molecular diversity

3. Finding a hit

- Searching a “library” – collection of compounds (**SCREENING**)
 - o Natural products
 - o Artificially prepared library - combinatorial chemistry
- Chemically modifying a natural ligand (**DESIGN**)
- Designing a compound to fit a receptor (DESIGN)

4. Optimising a lead (lead optimisation)

- Take a “hit” and examine pharmacological properties
- Often *in vitro* – looking at: pharmacodynamics, signalling, pharmacokinetics
 - o e.g. Receptor binding
 - o e.g. Cellular function
 - o e.g. Enzymatic stability
- Sometimes *in vivo* – looking at in vivo pharmacology and pharmacokinetics
 - o e.g. Animal model of disease
 - o e.g. Pharmacokinetics (ADME)
- When a hit fails some step, select a new compound
 - o Chemically related analogue
- And go through pharmacological studies again

- Hope to identify compounds that are
 - “Better” than initial hit
 - So much “better” that they become a lead
- **Things one may wish to optimise** (reflected in the assays)
 - Potency
 - Selectivity
 - Metabolic stability
 - Pharmacokinetic behaviour
 - Toxicity/safety
- How to optimise a lead:
 - Screening a “focussed” library
 - Natural products
 - Combinatorial chemistry
 - Chemically modifying a lead – medicinal chemistry
 - Redesigning to fit receptor

LECTURE 17-18 – STRUCTURE BASED DRUG DESIGN

- **What is a lead?**
 - A new chemical entity that could potentially be developed into a new drug by optimising its beneficial effects and minimising its side effects
- Target validation establishes the relevance of a target in a certain disease pathway
- Drug discovery overview
 - What compounds do you synthesise and test?
 - How do you identify hits?
 - How do you select a lead?
 - How do you optimise the lead?
 - What aspect do you optimise?
 - A pharmacodynamic entity:
 - Affinity, potency, efficacy, selectivity
 - A pharmacokinetic entity:
 - A good lead compound shows good pharmacokinetics early on in the process of discovery
 - Oral bioavailability
 - Stability
 - Blood-brain barrier penetration
 - **ASSAY is important**
 - If you assay for oral bioavailability you are selecting for a compound that has good oral bioavailability
 - Need to have appropriate assays to ensure good drug discovery → critical to the success of drug discovery
 - How do you catch a drug [**lead**]?
 - **Screening**
 - ‘catch’ a broad range of molecules
 - May not catch the drug that you want
 - Currently high throughput screening is the main approach for the identification of lead compounds
 - **Design**

- Trying to 'catch' a particular drug
 - Set out to design a particular drug
 - You will end up with a drug either way, but will you end up with the molecule you want?
- **Finding/discovering a lead compound (hit)**
 - Start with:
 - **A library**
 - A collection of **natural** products or **synthetic** compounds
 - Using combinatorial chemistry to create synthetic libraries of compounds
 - **Structural information**
 - Known **ligand** – e.g. substrate, NT, etc.
 - **Receptor** 3D structure