

3. Protein Engineering

Outline

- Limitations of proteins in biotech processes
- Definition and aim of protein engineering
- Targeted properties of proteins
- Approaches in protein engineering
 - **Directed evolution**
 - **Rational design**

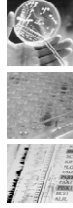
Proteins in biotechnology

- main problem - identify or design optimal protein for specific process
 - **historically** - adapt process
 - **future** - adapt protein



Proteins in biotechnology

- **classical screening**
 - screening culture collections
 - polluted and extreme environment
- **environmental gene libraries**
 - metagenomic DNA
- **data-base mining**
 - genome sequencing projects
 - massive sequencing (Sargasso sea project)
 - numerous uncharacterised enzymes
- **protein engineering**

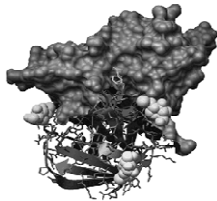


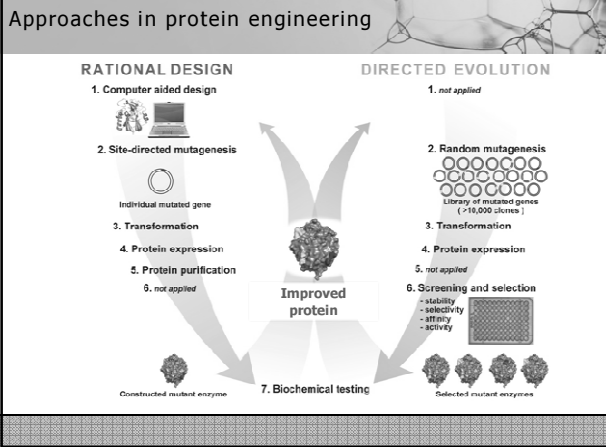
Protein engineering

- the process of **constructing novel protein molecules** by design first principles or altering existing structure
- use of genetic manipulations to alter the coding sequence of a gene and thus **modify the properties of the protein**
- **aims and applications**
 - **technological** - optimisation of the protein to be suitable in particular technology purpose
 - **scientific** - desire to understand what elements of proteins contribute to folding, stability and function

Targeted properties of proteins

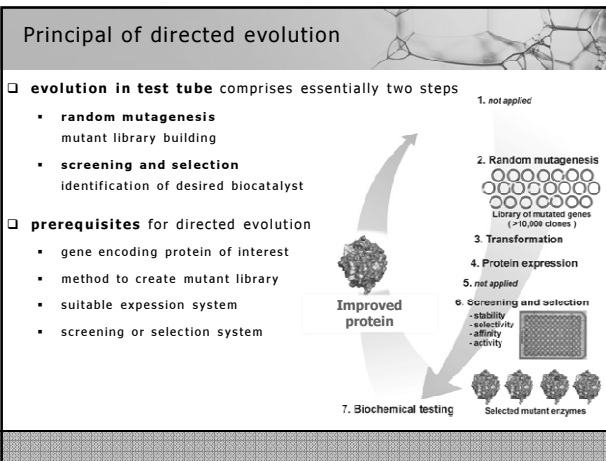
- **structural** properties of proteins
 - stability (temperature, solvents)
 - tolerance to pH, salt
 - resistance to oxidative stress
- **functional** properties of proteins
 - reaction type
 - substrate specificity and selectivity
 - kinetic properties (e.g., K_m , k_{cat} , K_i)
 - cofactor selectivity
 - protein-protein or protein-DNA interactions




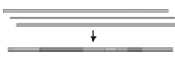


Directed evolution





- directed evolution techniques emerged during mid-1990s
- inspired by natural evolution**
- this form of "evolution" does not match what Darwin had envisioned
 - requires **outside intelligence**, not blind chance
 - does not create brand new species (macroevolution) only improvements (**molecular evolution**)
 - does not take millions of years, but **happens rapidly**







Methods to create mutant libraries

- technology to generate large diversity
 - NON-RECOMBINING** (one parent gene -> variants with point mutations)
 
 - RECOMBINING** (several parental homologous genes -> chimeras)
 

Non-recombining mutagenesis

- UV irradiation** or **chemical mutagens** (traditional)
 
- mutator strains** - lacks DNA repair mechanism mutations during replication (e.g., Epicurian coli XL1-Red)
 
- error-prone polymerase chain reaction (ep-PCR)**
 - gene amplified in imperfect copying process (e.g., unbalanced deoxyribonucleotides concentrations, high Mg²⁺ concentration, Mn²⁺, low annealing temperatures)
 
 - 1 to 20 mutation per 1000 base pairs
- saturation mutagenesis**
 - randomization of single or multiple codons
- other methods**
 - gene site saturation mutagenesis
 - cassette mutagenesis (region mutagenesis)
 

Recombining mutagenesis

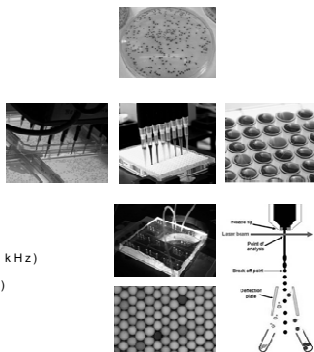
- also referred to as „sexual mutagenesis“
- DNA shuffling**
 - fragmentation step
 
 - random reassembly of segments
 
- StEP** - staggered extension process
 - simpler than shuffling
 - random reannealing combined with limited primer extension
 
- other methods**
 - shuffling of genes with lower homology down to 70% (e.g., RACHITT, ITCHY, SCRATCHY)
 

Screening and selection

- most **critical step** of direct evolution
- isolation of positive mutants hiding in library
 - **HIGH THROUGHPUT SCREENING**
individual assays of variants one by one
 - **DIRECT SELECTION**
display techniques (link between genotype and phenotype)

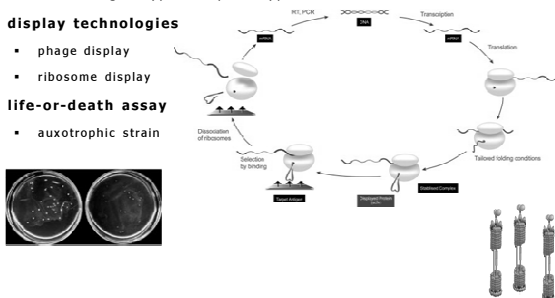
High throughput screening

- common methods not applicable
- **agar plate (pre)screening**
- **microtiter plates screening**
 - 96-, 384- or 1536-well format
 - **robot assistance**
(colony picker, liquid handler)
 - 10^4 libraries
 - volume 10 – 100 μ L
- **microfluidic systems**
 - water in oil emulsions (up to 10 kHz)
 - **FACS sorting** (10^8 events/hour)
 - 10^9 libraries
 - volume 1 – 10 pL



Direct selection from mutant library

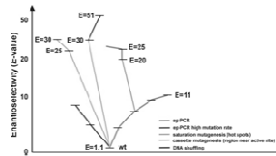
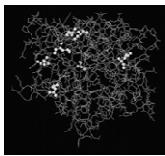
- not generally applicable (mutant libraries $>10^6$ variants)
- link between genotype and phenotype
- **display technologies**
 - phage display
 - ribosome display
- **life-or-death assay**
 - auxotrophic strain



Example of Directed evolution

□ directed evolution of enantioselectivity

- lipase from *P. aeruginosa* (E-value improved from 1.1 into 51)
- **spectrophotometric screening** of (*R*)- and (*S*)-nitrophenyl esters
- the best mutant contains six amino acid substitutions
- **40 000 variants screened**



Approaches in protein engineering

RATIONAL DESIGN

1. Computer aided design
2. Site-directed mutagenesis
3. Transformation
4. Protein expression
5. Protein purification
6. not applied
7. Biochemical testing

DIRECTED EVOLUTION

1. not applied
2. Random mutagenesis
3. Transformation
4. Protein expression
5. not applied
6. Screening and selection
7. Biochemical testing

Improved protein

Constructed mutant enzyme

Selected mutant enzymes

Rational design

- emerged around 1980s as the original protein engineering approach
- combining theory (**knowledge based**) and experiment
- protein engineering cycle:
„**structure-theory-design-mutation-purification-analysis**“
- **difficulty in prediction** of mutation effects on protein property

Construction

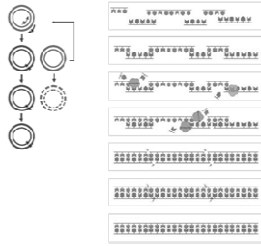
□ site-directed mutagenesis

- introducing point mutations
- QuickChange Kit (one day method)

□ multi site-directed mutagenesis

□ gene synthesis

- commercial service
- codone optimisation



Example of rational design

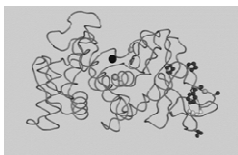
□ rational design of protein stability

- stability to high temperature, extreme pH, oxygen stress, proteases etc.
- stabilizing mutations increase strength of weak interactions
 - salt bridges and H-bonds (*Eijsink et al., Biochem. J. 285: 625-628, 1992*)
 - S-S bonds (*Matsumura et al., Nature 342: 291-293, 1989*)
 - addition of prolines (*Watanabe et al., Eur. J. Biochem. 226: 277-283, 1994*)
 - less glycines (*Margarit et al., Protein Eng. 5: 543-550, 1992*)
 - oligomerisation (*Dalhus et al., J. Mol. Biol. 318: 707-721, 2002*)

Example of rational design

□ rational design of protein stability

- engineering protein to resist boiling (*Burg et al., PNAS 95: 2056-2060, 1998*)
 - reduced rotational freedom - Thr56Ala, Gly58Ala, Ser65Pro and Ala96Pro
 - introduction of disulfide bridge - Gly8Cys + Asn60Cys
 - improved internal hydrogen bond - Ala4Thr
 - filling cavity - Tyr63Phe



Half-lives (min.)	80°C	100°C
wild type	17.5	>0.5
8-fold mutant	stable	170

