BASIC DNA assembly

Biopart Assembly Standard for Idempotent Cloning

Fast, accurate and modular DNA assembly method
for synthetic biology and general molecular biology applications

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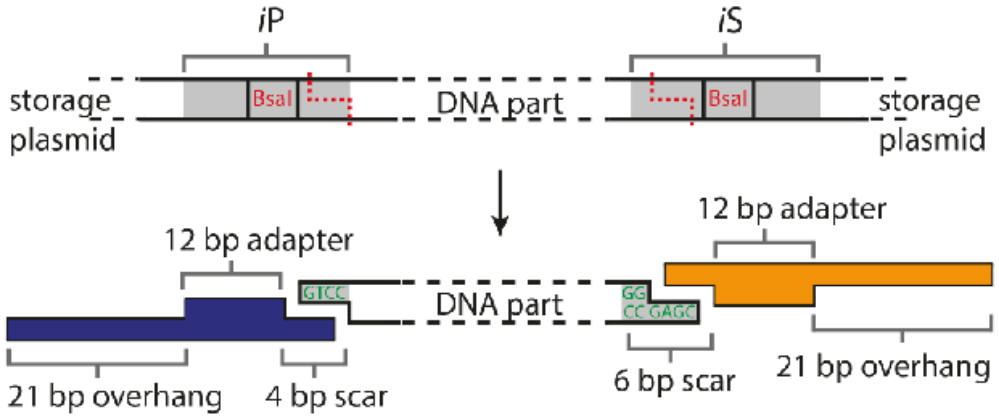
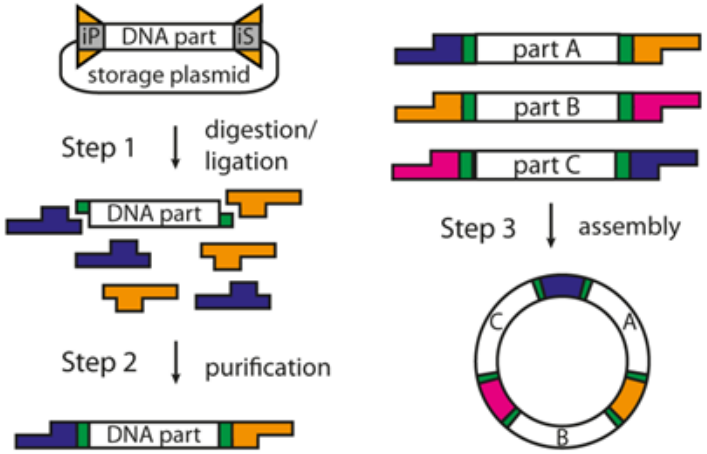
Parts in BASIC format are released and linkers ligated



- Parts are released from vector by BsaI digestion
- Oligonucleotide linkers are simultaneously ligated onto each specific end

Simple 3 step protocol



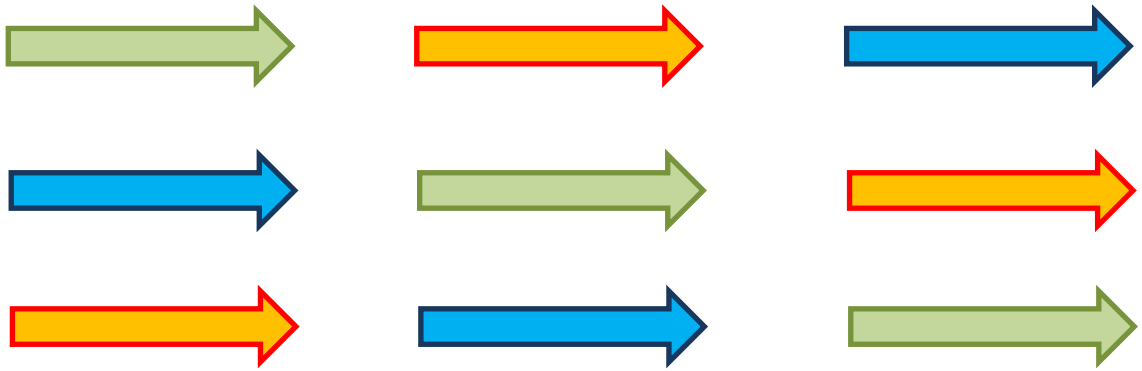
Purified parts are assembled by annealing at 50°C (no ligase!)

Storch et al. ACS SynBio 2015 4 (7), pp 781–787 DOI: 10.1021/sb500356d

Combinatorial pathway assembly

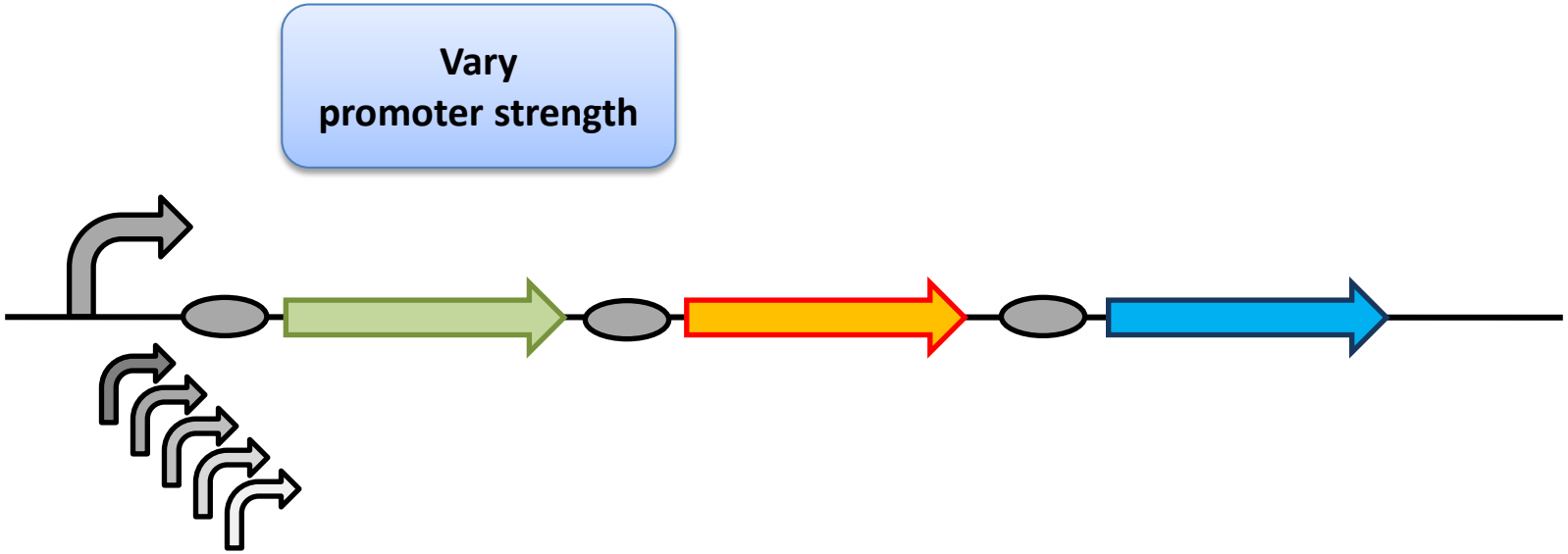
Combining parts in different order

Combine genes in any order



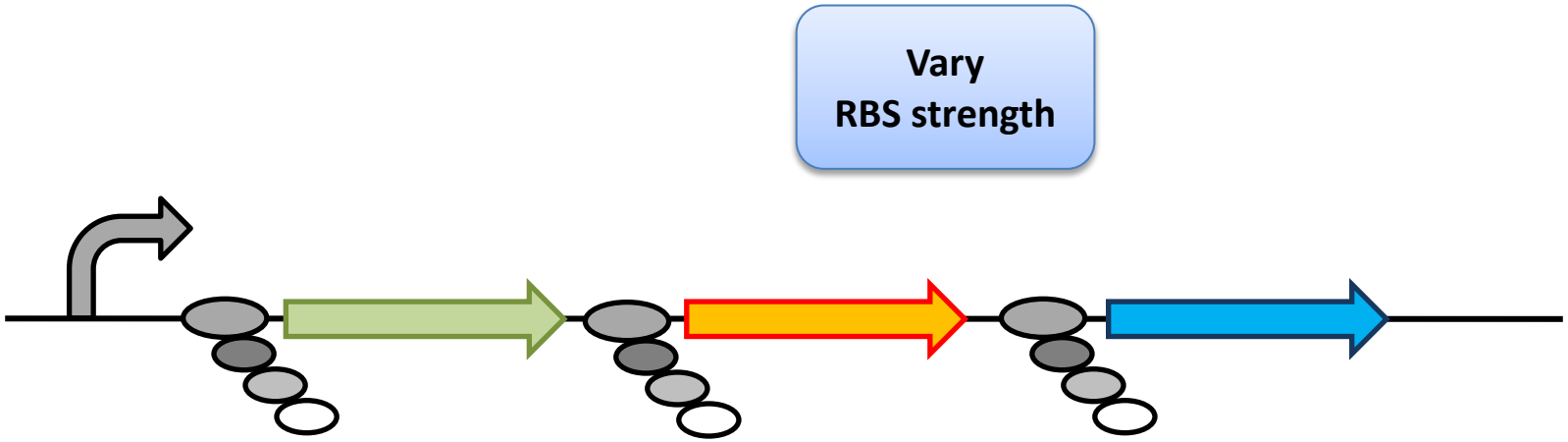
Combinatorial pathway assembly

Driving operon with different promoters



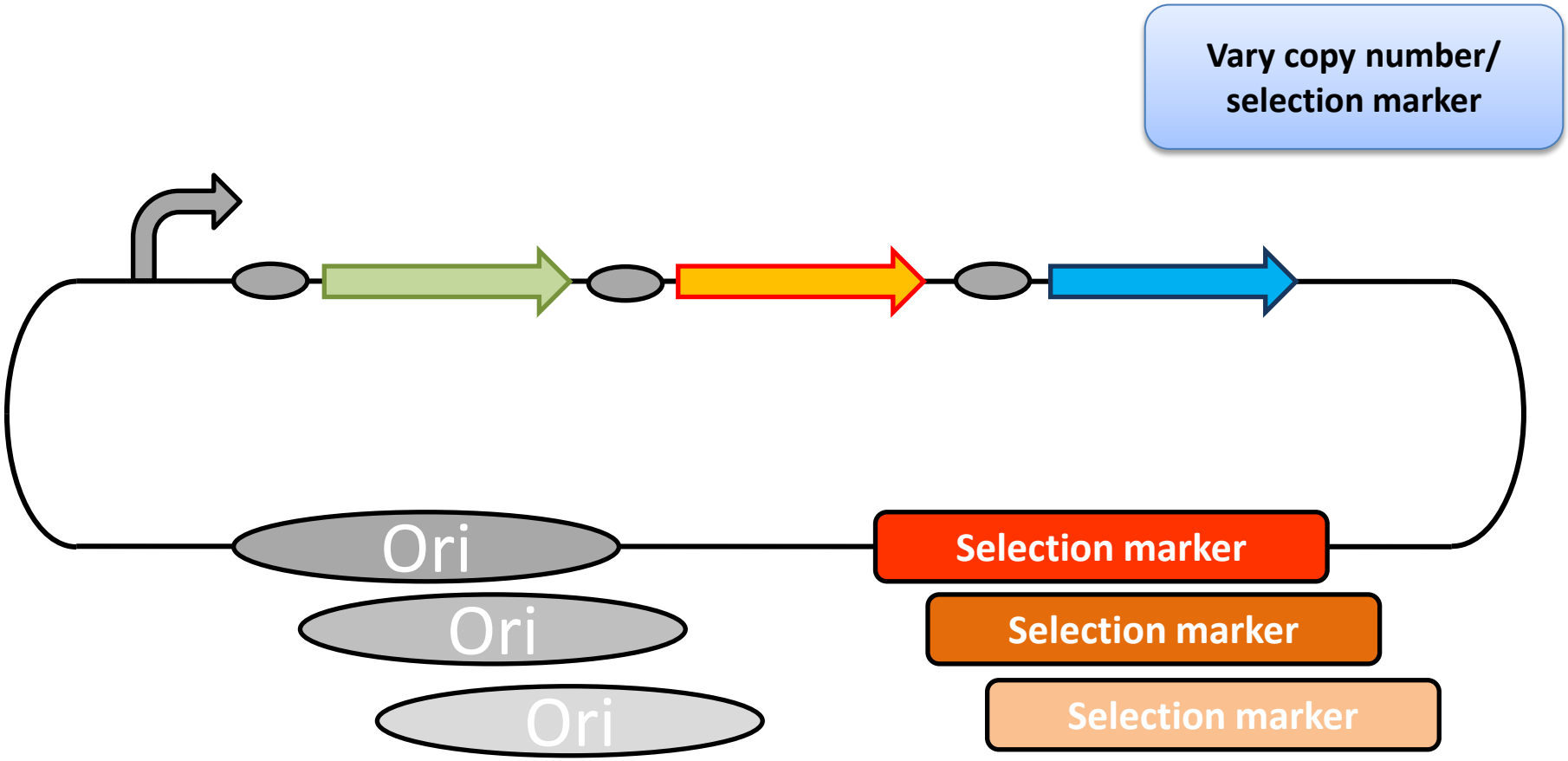
Combinatorial pathway assembly

Balancing gene expression via RBS tuning



Combinatorial pathway assembly

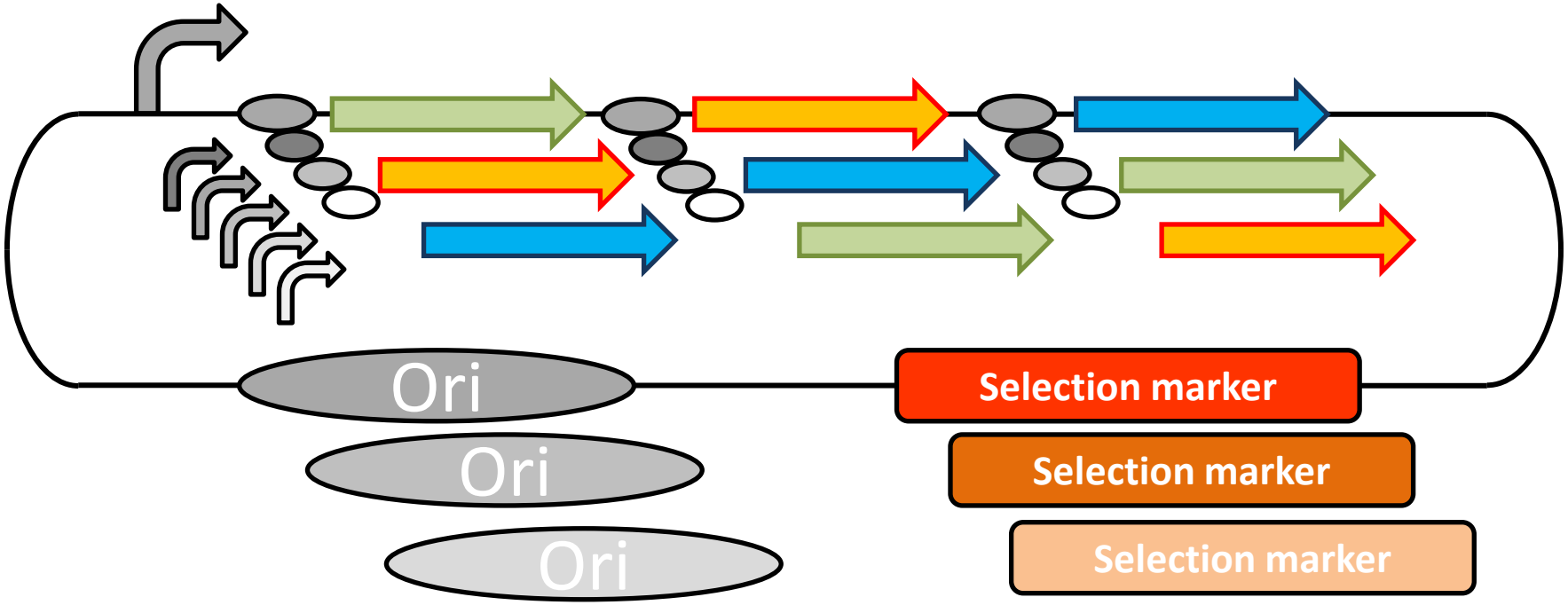
Adjusting copy number and selection marker



Combinatorial pathway assembly

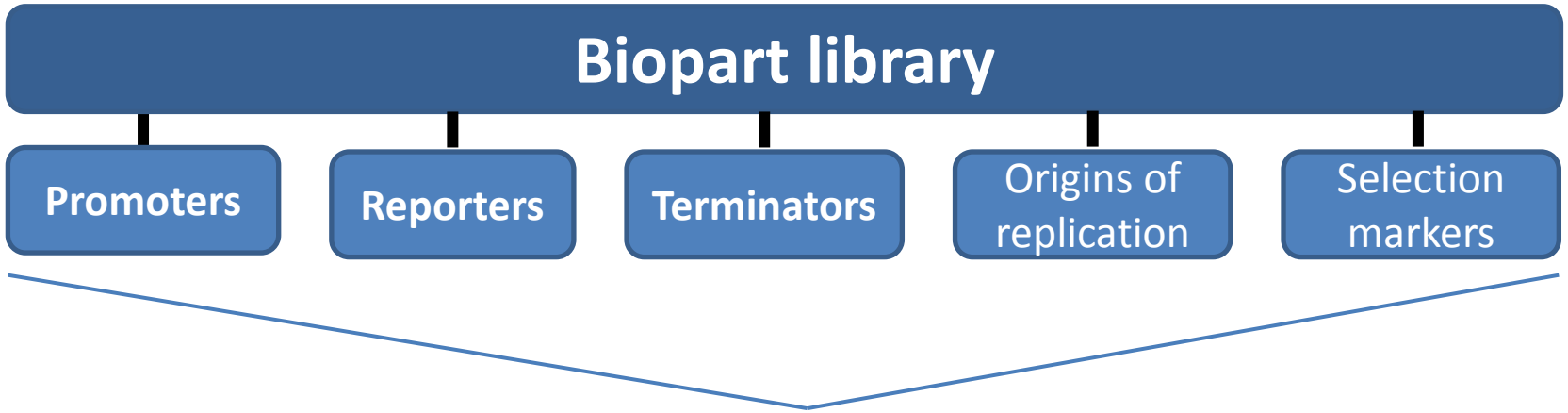
Combinations quickly add up to large libraries

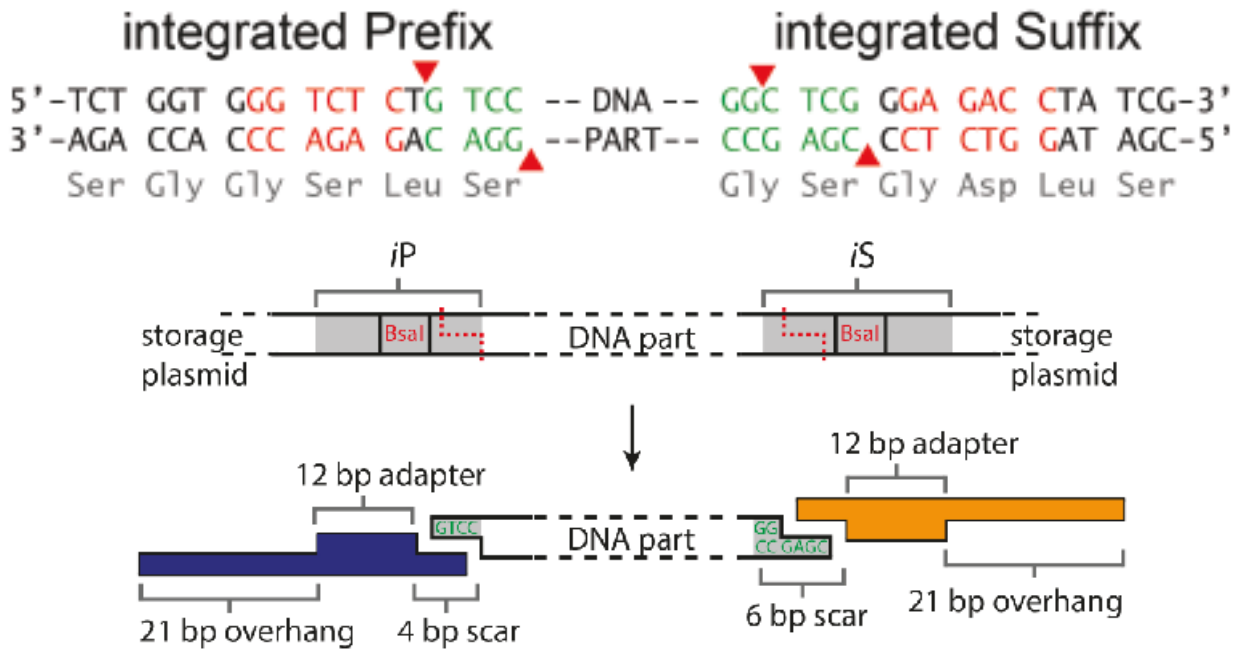
Combine Genes in any order **X** Vary Promoter strength **X** Vary RBS strength **X** Vary copy number/ Selection marker



= 7290 plasmids

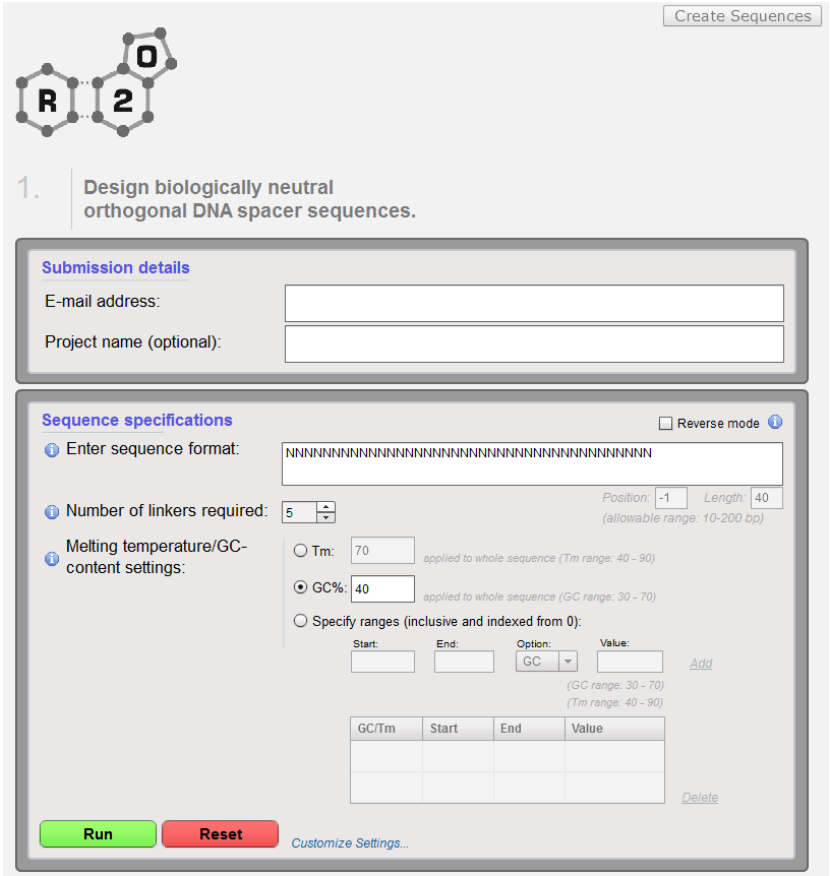
BASIC standard format and parts library



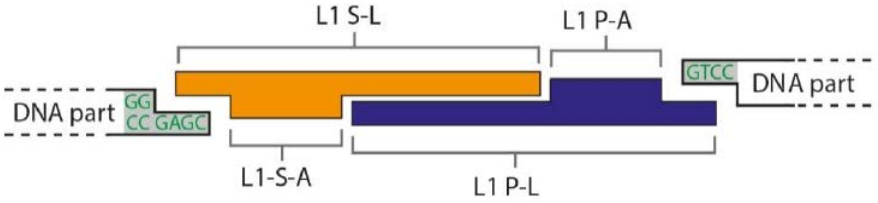


BASIC linkers are optimized using bioinformatics

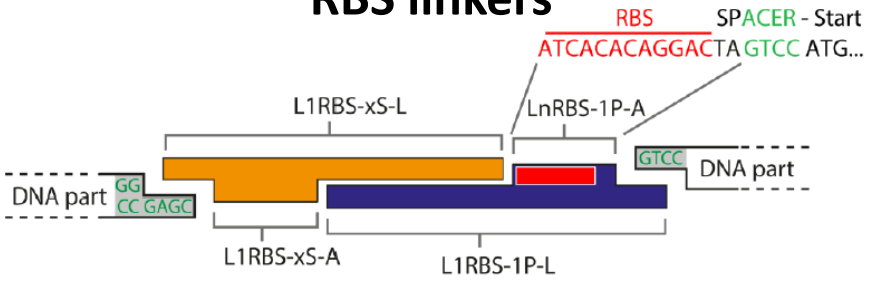
http://www.r2odna.com



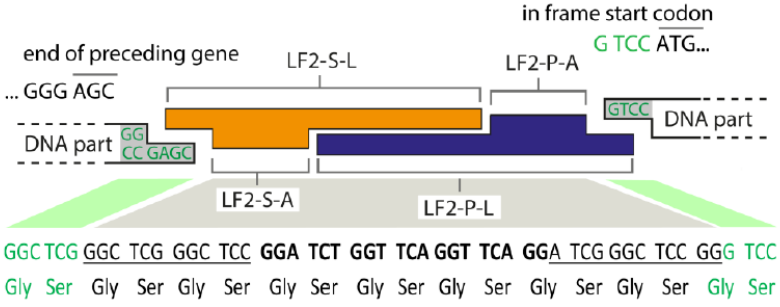
Neutral linkers



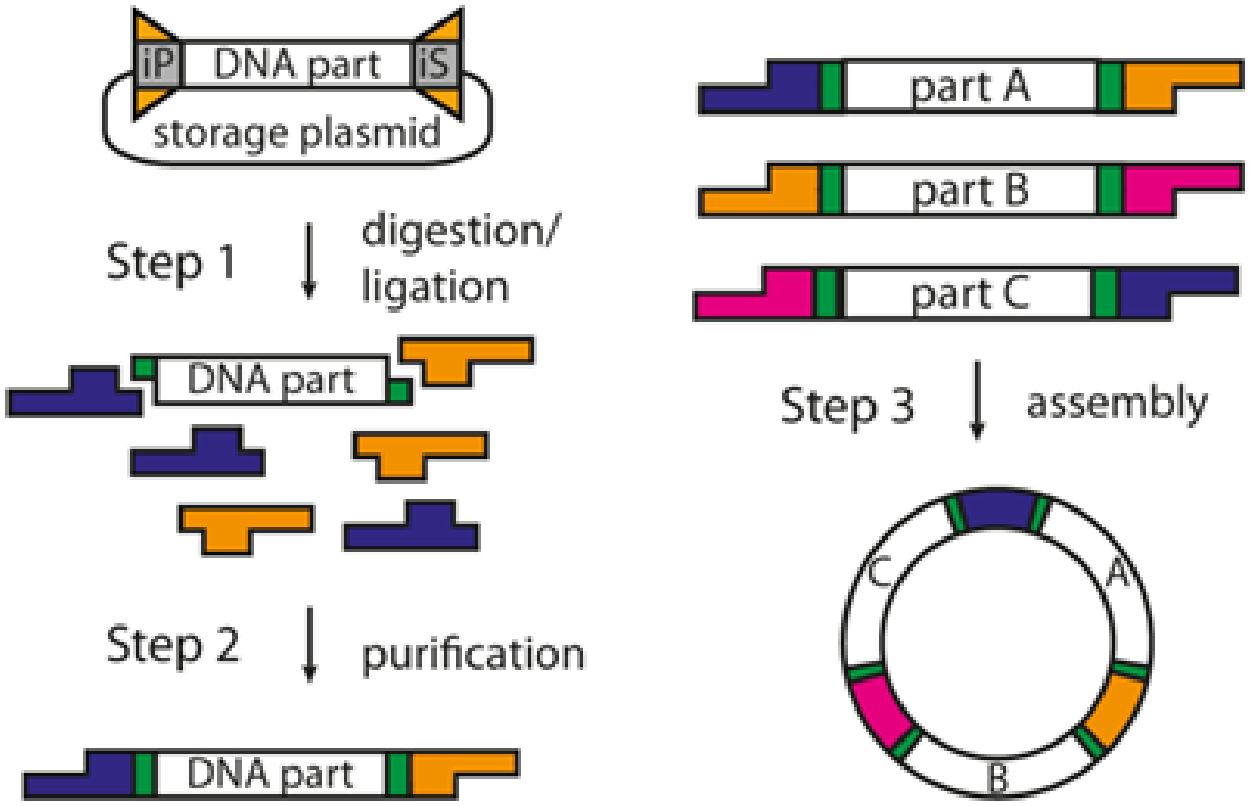
RBS linkers



Fusion protein linkers



BASIC DNA assembly method is simple, robust and can be automated



Per assembly stage:

7 part assembly with 90% accuracy

BASIC DNA assembly summary

- BASIC allows simple and accurate multipart DNA assembly
- Assembled parts can be treated as single part in next stage
- A single BASIC part standard facilitates re-use of parts
- Basic parts and libraries can be shared easily
- BASIC can be completely streamlined
- BASIC can be automated start to end
- BASIC allows simple promoter and RBS tuning
- BASIC covers all prokaryotic construct designs
- BASIC supports defined and random library strategies