

INDEX

A

ASKA collection.....55, 60

C

Campylobacter jejuni1–13, 167–179, 222, 224
Candida albicans.....125–134
CEG_Match206, 208–209, 212, 213, 215
Chronic lung infection100, 101
Complex haploinsufficiency126–128, 130
Constraint-based approaches.....183–201

D

Database of essential genes (DEG)36, 37,
139, 153, 155, 207–209, 211, 212, 219–230
Deletion mutation15–22, 114, 118
Dispensable genes.....1
Domains80, 90,
139–142, 149, 220, 222, 223, 225–230, 235–243

E

Enrichment analysis225, 226
Escherichia coli2, 5, 26–29,
37–40, 45–63, 79, 97, 101, 105, 107–109, 113, 117,
130, 131, 138, 139, 154, 155, 161, 169, 170, 172, 186,
188, 189, 197, 207, 208, 210, 211, 213–215,
220–222, 224–226, 230, 236, 242
Essential gene prediction (EGP).....169, 206–208,
211, 212, 215, 216, 239
Essential genes.....1–13, 15, 16,
19–22, 25–41, 45–63, 79–94, 97–122, 137–150,
153–163, 167–179, 205–216, 219–230, 235–243
Essentiality36, 47, 53,
55–57, 60, 79, 82, 89–94, 97, 138, 142–144,
147–149, 154, 156, 160, 162, 163, 178, 184,
188–189, 194, 195, 206–212, 214, 216, 235, 236,
238, 241–243
Expectation–Maximization (EM) algorithm236,
239, 240, 242

F

FLP Recognition Target (FRT)46, 48, 49, 60, 117
FLP recombinase.....47, 60

Flux balance analysis (FBA)167, 168,
170, 171, 173, 176, 184–190, 193–196, 200, 201
Fusion PCR.....17, 18

G

Gene deletion15, 17–19,
22, 46, 49, 52, 54–58, 62, 79, 80, 184, 206, 220, 236
Gene essentiality.....1, 16,
37, 45, 53–57, 63, 93, 98, 139, 142, 143, 148, 149,
155, 173, 206, 210, 219–230, 235, 236, 241, 242
Gene knockout45, 47, 49, 52–53, 56, 58,
60, 104, 113–119, 184, 186, 188, 194, 195, 198, 200
Gene ontology (GO).....220, 225–230, 237
Genome-scale metabolic networks183, 184,
188, 189, 196, 197, 201
Genome-wide.....15–22, 80,
125–134, 206, 208, 209, 212, 214, 219, 220, 223, 235
Genomic annotations153–163
Genomic features.....140–142
Geptop37, 206, 209–211, 214–216
Glyoxylate cycle.....185, 189, 191
GO terms220, 221, 225–227, 229, 230

H

Himar168
Himar1 mutagenesis.....31, 68
Homologous recombination12, 17, 46, 59, 114, 126, 130
Hyphal development125–127

I

Illumina next generation sequencing.....79
In-frame deletion.....46, 47, 49, 60
Insertional mutagenesis107
Integrative model.....138, 214, 215

K

Keio collection.....47, 58, 60, 63

L

Lambda Red recombinase48, 49
Leptospira67–73
Leptospirosis67–76

M

Machine learning..... 137–150, 206, 214
 Mariner 26, 29, 37, 68
 Metabolic network 169, 175,
 176, 178, 183–189, 196, 197, 201
 Metabolic network analysis 186
 Microarray..... 1–13, 48, 80, 222
Mycobacterium tuberculosis 79–94, 97, 213, 222, 224

N

Network analysis 170, 173, 177, 186

P

Porphyromonas gingivalis..... 25–41, 222
 Prediction 16, 92, 98, 138, 147,
 148, 169, 173, 174, 178, 183–201, 206–210, 213,
 215, 216, 221, 236, 238–243
Pseudomonas aeruginosa 46, 98–101,
 104, 106, 108–110, 112–116, 118–119, 121, 138,
 213, 215, 222, 224, 236, 242

R

Rat model..... 100, 101

S

Shuttle mutagenesis..... 127, 130
 Signature-tagged mutagenesis (STM)..... 97–122
 Statistical framework..... 153–163
Streptococcus sanguinis..... 15–22, 222
 Synthetic biology..... 15,
 219, 235
 Synthetic genetic analysis (SGA) 126

T

TCA cycle 184, 185, 187,
 189–192, 194, 195, 199
 Transposon 1–13, 25–42, 46, 48,
 67–73, 75, 76, 80–93, 99, 103–107, 109, 110, 113,
 125–134, 138, 153–163, 169, 174, 206, 222, 223,
 235, 237
 Transposon based mutant library..... 37
 Transposon mutagenesis 5–6, 11,
 26–30, 34, 37, 46, 48, 67, 68, 80, 104, 109, 125–134,
 138, 153–163, 206, 222, 235, 237
 Transposon mutagenesis analysis..... 169
 Transposon sequencing (TnSeq) 25–41,
 80, 81, 87, 222–224