Index

Page references followed by f denote figures; those followed by t denote tables.

A

ABC model of flower development, 112–115
Actin microfilaments, 58f, 59, 94, 96, 133
Activation energy, 72, 133
Activator, 31, 31f–32f, 33, 85, 106, 133
Active site, 72, 73f, 133
Adapters, 21, 133
Additive genetic interaction, 115, 133
Adenine, 4, 4f–5f
Adenosine, in poly(A) tails, 29
Adenosine diphosphate (ADP), 52–53, 52f, 54f–55f, 133
Adenosine triphosphate (ATP)
  defined, 133
  in glycolysis, 53–54, 54f–55f
  synthesis in Krebs cycle, 54, 56f
  synthesis in photosynthesis, 52, 52f
  use in Calvin cycle, 52, 53f
Afymetrix, 38, 133
Agamous (ag) mutation, 111–114, 111f, 112t, 113f–115f, 133
Agarose, 15
Alleles, 14, 133
Alon, Uri, 86
α-helix, 70, 134
Alternative splicing, 14, 41–42, 41f, 134
Alu retrotransposons, 124, 134
Amino acids
  defined, 134
  genetic code and, 12–13, 12f
  peptide bond between, 70, 143
  protein structure and, 70–71, 71f–72f
  role in translation, 68–69, 68f–69f
Amino-acyl site, 69, 69f, 134
Anaphase-promoting complex (APC), 92–93, 93f, 95f, 134
Annealing, 8–9, 19, 20f, 134
Antibodies, 84
Anticodon, 68–69, 69f, 134
Antisense oligonucleotides, morpholino, 106
APC (anaphase-promoting complex), 92–93, 93f, 95f, 134
Apes, humans compared to, 121
Apetala2 (ap2) mutation, 111–114, 111f, 112t, 113f–115f, 134
Apetala3 (ap3) mutation, 111–114, 112–115f, 112t, 134
Apoptosis (programmed cell death), 79–80, 79f, 134
Arabidopsis thaliana
  described, 134
  flower organization, 110–114, 110f–115f, 112t
  as model organism, 104
  oscillating expression of genes in roots, 101f–102f
  root development in, 107–108, 108f
Asymmetric division, 95, 134
ATP synthase, 52f
Attractor, 99, 99f, 134
Autocrine signaling, 74, 134

B
Balancing selection, 127, 134
Bar codes, 42
Basal transcription, 32, 134
Bases
complementarity of, 5–7, 6f–8f
described, 4, 4f, 134
in DNA sequencing reactions, 17, 18f
gene code, 12, 12f
RNA, 28–29
Basic local alignment search tool (BLAST), 24, 135
Beam lines, 88, 135
Behavior, genes involved in, 127
Bell curve, 110, 135
β-galactosidase, 30–31
β-sheet, 70, 135
Biological oscillators
cell cycle, 89–99
circadian rhythm, 89, 100, 101f
cyclin–CDK interaction, 91–99, 92f–95f, 98f
molecular networks underlying circadian, 100
negative-feedback oscillator, 92–93, 93f
networks controlling, 89–102
positioning lateral roots, 100–102,
101f–102f
testing cyclin–CDK model, 96–98, 98f
Biological replicate, 42, 135
Biologicals, 87, 135
BLAST (basic local alignment search tool), 24, 135
Body plan, 135
Boolean, 98–99, 99f, 135
Brains, of humans and chimpanzees
compared, 124

C
Caenorhabditis elegans
cell division in, 95–96
described, 135
as model organism, 104
noncoding RNAs in, 34
RNA interference in, 96
Calmodulin (calcium-modulated protein), 77, 135
Calvin cycle, 52–53, 53f
cAMP, 77
Cancer, 75, 76–77, 78, 89
Candidate gene, 118, 135
Capecchi, Mario, 105
Capping, 30, 70, 135
Carbon dioxide, fixation of, 53, 53f
Carpels, 110–112, 110f–114f, 112t, 114, 135
Catalytic, 72, 135
CDK (cyclin-dependent kinase), 92–94, 92f–93f,
95f, 96–97, 99, 135, 136
cDNA, See Complementary DNA
Celera, 18
Cell cycle, 89–99
cell cycle, 89–99
circadian rhythm, 89, 100, 101f
cyclin–CDK interaction, 91–99, 92f–95f, 98f
molecular networks underlying circadian, 100
negative-feedback oscillator, 92–93, 93f
networks controlling, 89–102
positioning lateral roots, 100–102,
101f–102f
testing cyclin–CDK model, 96–98, 98f
Biological replicate, 42, 135
Biologicals, 87, 135
BLAST (basic local alignment search tool), 24, 135
Body plan, 135
Boolean, 98–99, 99f, 135
Brains, of humans and chimpanzees
compared, 124

© 2014 by Cold Spring Harbor Laboratory Press. All rights reserved.
Chromatin, 35, 136
Chromatin immunoprecipitation sequencing, 85, 136
Chromatin-remodeling enzymes, 35, 36f, 136
Chromosomes
in cell division, 94–95
described, 13, 136
human and chimpanzee compared, 121–122
quantitative trait loci (QTLs), 117–118, 145
repetitive elements in, 124
Circadian rhythm, 89, 100, 101f
Circuit diagram, of development in sea urchin, 106, 107f
cis-elements, 30, 31, 136
cis-regulatory code, 34, 136
cM (centiMorgan), 116
CNV (copy number variation), 124–125, 136
Codons, 12–13, 12f, 68–69, 136
Cognition, genes involved in, 127
Complementary DNA (cDNA)
defined, 135
generating with reverse transcriptase, 38
library, 41–42
microarrays, 38–39
Complex traits, 109–119
Arabidopsis flower organization example, 110–114, 110f–115f, 112t
defined, 136
environmental factors, role of, 115–116
gene identification, 117–118
gene interactions, 110–115f
heritability of, 110
mapping of genes involved in, 116–117
prevalence of, 109
systems biology and analysis of, 118–119
testing a multigene model, 113–115
Confocal microscopy, 60–61, 61f, 136
Conformation, 72, 136
Continuous distribution, 110
Contractile ring, 94, 136
Copy number variation (CNV), 124–125, 136
Crick, Francis, 3, 5
Cristae, 49, 50f, 136
cRNA, 38–39, 136
Crohn’s disease, 117–118, 136
Cyanobacteria, 51
Cyclin, 91–99, 92f–95f, 98f, 136
Cyclin-dependent kinase (CDK), 92–94,
92f–93f, 95f, 96–97, 99, 135, 136
Cytokines, 74, 74f, 137
Cytokinesis, 90, 94, 96, 137
Cytoplasm, 45, 46f, 137
Cytoplasmic domain, 74, 137
Cytosine, 4, 4f–5f
Cytoskeleton, 58–59, 58f, 137

D
Dairy products, evolution of adult tolerance to, 126
DARC (Duffy antigen/chemokine receptor), 127
Dario rerio, 104, 137
Denticle belts, 104, 137
Deoxyribonucleic acid. See DNA
Development
body plan, 104
circuit diagram, 106, 107f
defined, 103, 137
homeobox genes, 104–106
how scientists study, 103–104
model organisms, 103–104
in plants, 106–108, 108f
in sea urchin, 106, 107f
transcriptional networks in, 103–108
Diabetes, adult-onset, 115–116
Dideoxynucleotides, 17, 137
Differential-equation-based modeling, 129
Differentiation, 59–60, 137
Diploid genome, 116, 137
Disulfide bridge, 71, 137
DNA (deoxyribonucleic acid), 3–25
in chloroplasts, 49, 51
in chromosomes, 13
complementary DNA (cDNA), 38–39,
41–42
defined, 137
fragment separation by gel electrophoresis,
15, 16f
genesis, 13–14
information storage in, 12–13
junk, 24
major groove, 33
in mitochondria, 49, 51
repetitive DNA elements, 25, 124, 145
RNA expression, role of global DNA structure in, 34–36, 35f–36f
role of, 27
single-stranded, 7
structure, 3–5, 4f–6f, 34–36, 35f–36f
template for RNA synthesis, 28–30, 29f
DNA-binding domain, 33, 33f, 137
DNA ligase, 10f, 11, 137
DNA methylation, 35–36
DNA polymerase
defined, 137
in DNA replication process, 7–8, 7f–8f,
10–11, 10f–11f
in PCR, 19, 20f
in Sanger DNA sequencing, 17
DNA primase, 10f, 11, 137

© 2014 by Cold Spring Harbor Laboratory Press. All rights reserved.
DNA replication, 5–11, 7f–11f
   - defined, 137
   - lagging-strand, 10f–11f, 11, 140
   - leading-strand, 11, 11f, 140
   - semiconservative, 9, 9f, 146
   - S phase of cell cycle, 90, 90f, 94, 96–97, 98f, 146
DNA sequencing
   - analysis of sequence data, 23
   - chain-termination sequencing, 17, 18f
   - changing methods, 19, 21
   - finishing, 18
   - 454 sequencing, 21
   - genome, 15, 17–19, 24–25
   - of human genome, 17–18
   - Illumina sequencing, 22
   - massively parallel signature sequencing (MPSS), 41
   - next-generation sequencing, 19, 21–23, 22f, 125
   - production, 18
   - pyrosequencing, 21, 22f
   - read-lengths, 22
   - single-molecule sequencing technologies, 22–23
   - what we have learned from genome sequencing, 24–25
   - whole-genome shotgun, 18–19, 148
Dominant mutation, 104
Double-stranded RNA (dsRNA), 96, 137
   - Drosophila melanogaster, 104, 137
Drug discovery, 88
dsRNA (double-stranded RNA), 96, 137
Duffy antigen/chemokine receptor (DARC), 127, 137

Environment
   - affect on transcription, 33–34
   - role in complex disease traits, 115–116
Enzymes, 7, 72–73, 73f, 138. See also specific enzymes
Epidermal growth factor (EGF) receptor, 75, 76f
Epigenetic, 35–36, 138
Epilepsy, temporal lobe, 127
Epistatic, 115, 138
ES cells (embryonic stem cells), 59–60, 138
ESI (electrospray ionization), 80–81, 81f, 137, 138
Ethanol, generated by fermentation, 54
   - Ethyl methanesulfonate (EMS), 91, 138
Eukaryotic cells
   - defined, 29–30, 138
   - mRNAs in, 29–30, 70
   - Even-skipped mutation, 104, 138
Even-skipped, 104
Evolution, human, 121–127
Exit site, 69, 69f, 138
Exocytosis, 47, 138
Exons, 14, 14f, 41–42, 41f, 138
Extracellular domain, 73, 138

F
Feedforward loop, 86–87, 86f, 138
Fermentation, 54, 138
Flower organization in Arabidopsis, 110–114, 110f–115f, 112t
Folding, 70–71, 71f–72f, 138
454 sequencing, 21
Franklin, Rosalind, 3

G
G1 (first gap phase), 90, 90f, 138
G2 (second gap phase), 90, 90f, 138
Gal 4 transcription factor, 82
GATA1 transcription factor, 127
Gel electrophoresis, 15, 16f, 138
Gene(s), 13–14
   - alleles, 14
   - candidate, 118
   - in complex traits, 109–119
   - copy number variation (CNV), 124–125
   - defined, 139
   - identification of disease-predisposing, 117–118
   - mapping, 116–117
   - minimum number of genes for function of cells, 62–63
   - negative selection on, 122

E
EGF (epidermal growth factor) receptor, 75, 76f
   - Electron transport chain, 52, 52f, 137
   - Electrospray ionization (ESI), 80–81, 81f, 137, 138
   - Elongation, in transcription, 29, 137
   - Embryogenesis, in Caenorhabditis elegans, 95–96
   - Embryonic stem cells (ES cells), 59–60, 138
   - EMS (ethyl methanesulfonate), 91, 138
   - ENCyclopedia Of DNA Elements (ENCODE), 125, 138
   - Endocytosis, 47, 138
   - Endoplasmic reticulum, 49
   - Energy generation in cells, 51–54, 52f–56f
   - Enhancers, 31–32, 32f, 138
   - Entrained, 100, 138
number in human genome, 14
positive selection on, 123–124, 123t
GeneChips, 38, 139
Gene expression, 27–43
cell-specific, 33–34
control of, 30–36, 31f–33f
activation by transcription factors, 32–34, 32f, 33f
role of global DNA structure, 34–36, 35f–36f
role of noncoding RNAs, 34
defined, 139
genome-wide expression analysis, 38–43
level of, 30
selective pressure on, 122–124
General transcription factors, 32, 139
Gene-regulatory network (GRN), 85–87, 86f, 139
Genetic code, 12–13, 12f
Genetic map, 117, 139
Genetic markers, 117, 139
Genetics
complex traits, 109–119
defined, 13, 139
Mendelian traits, 109
monogenic traits, 109
reverse, 95–96
Genetic screen, 91, 95–96, 139
Genome
defined, 139
differences among humans, 124–125
diploid, 116
duplication in S phase of cell cycle, 90
haploid, 13, 116
human and chimpanzee compared, 121–24, 122f, 123t
number of genes in human, 14
Genome sequencing, 15, 17–19, 24–25, 139
Genome-side association study (GWAS), 117, 139
Genome-wide expression analysis, 38–43, 139
Genomics, structural, 88, 147
Gilbert, Walter von, 114
Glycolysis, 53–54, 54f–55f, 139
Goethe, Johann Wolfgang von, 114
Golgi apparatus, 49
G-protein complex, 77, 78f, 139
G-protein-coupled receptor (GPCR), 77, 78f, 139
Grana, 51f
GRN (gene-regulatory network), 85–87, 86f, 139
Growth factors, 74, 139
GTPase, 76, 139
GTP-dependent switches, 77, 78f
Guanine, 4, 4f–5f
GWAS (genome-side association study), 117, 139

H

Haemophilus influenzae, 62
Haploid genome, 13, 116, 139
Haplotypes, 125, 139
HapMap Project, 125, 139
Hartwell, Lee, 91, 92
Heme, 67, 71f
Hemoglobin, 67, 70, 71f
Heritability of complex traits, 110
Hidden Markov models (HMMs), 23, 140
Hierarchical clustering, 43
High-pressure liquid chromatography (HPLC), 58, 140
High-throughput microscopy for imaging cellular responses, 60–61, 61f–62f
His tag, 87, 140
Histone acetyl transferase, 35
Histones, 34–35, 35f, 140
HMMs (hidden Markov models), 23, 140
Homeobox, 104–106, 140
Homologous recombination, 105, 116, 140
Hooke, Robert, 60
Hormones, 74, 140
HPLC (high-pressure liquid chromatography), 58, 140
Human Epigenome Project, 125, 140
Human evolution
in adult tolerance to dairy products, 126
continuing, 126–127
 genetic differences between humans and chimpanzees, 121–124, 122f, 123t
genomic differences among humans, 124–125
networks in, 121–127
in pigmentation pathway, 126
shaped by infectious pathogens, 127
Human Genome Project, 18–19
Hunt, Tim, 92
Hybridization, in northern blotting, 36–37, 37f

I

Illumina sequencing, 22, 140
Indeterminate, 111, 140
Information transfer by proteins, 73–77, 74f–76f, 78f
Inositol triphosphate, 77
Insulin, 73
Interferon, 74, 140
Intermediate filaments, 58f, 59, 140
Introns, 14, 14f, 123, 140
IP3 signaling pathway, 77
J
Jacob, François, 30–31
Janus kinase (JAK), 74, 74f, 140

K
Kinase, 73, 140
k-means clustering, 43
Knock-out mice, for study of homeobox genes, 105–106
Krebs cycle, 54, 56f, 140

L
Lactase persistence, 126
Lactase-phlorizin hydrolase, 126, 140
Lactate, 54
Lactic acidosis, 54
Lactose, 30, 126
Lactose tolerance, 126
Lagging strand, 10f–11f, 11, 140
Lateral roots, 100–102, 101f–102f
LCT gene, 126
Leading strand, 11, 11f, 140
Library, 18, 140
Ligand, 73, 140
LINEs (long interspersed nuclear elements), 124
Linkage, 116–117, 140
Lipid bilayer, 46–47, 47f, 141
Lipids, in membranes, 45–47, 47f, 73
Liposome, 46
Lipid chromatography, 80
Logical operators, 98
Long interspersed nuclear elements (LINEs), 124
Luciferase, 21
Luciferin, 21
Lysosomes, 49

M
Machine learning algorithms, 23, 141
Major groove, 33, 141
Malaria, 67, 127
MALDI (matrix-assisted laser desorption/ionization), 80–81, 81f, 141
Map-based strategy, 18, 141
MAP kinases, 76–77, 141
Mapping, genes underlying complex traits, 116–117
Massively parallel signature sequencing (MPSS), 41
Mass spectrometry, 58, 80–82, 81f, 141
Matrix-assisted laser desorption/ionization (MALDI), 80–81, 81f, 141
McClelland, Barbara, 25
Mediator, 32, 32f, 141
Meiosis, 116, 141
Melanocortin 1 receptor gene (MC1R) (melanocyte-stimulating hormone receptor), 12, 141
Melting, 29, 141
Membranes
chloroplast, 49, 51f, 52, 52f
lipids in, 45–47, 47f, 73
mitochondria, 49, 50f
nuclear, 49
proteins in, 46–47, 48f
vesicles, 47
Mendelian traits, 109, 141
Meselson, Matt, 9
Messenger RNA (mRNA)
defined, 141
in eukaryotic cells, 29–30, 70
miRNA interaction with, 34
modification of, 29–30, 70
poly(A) tails, 29, 38
primary, 30
role of, 28
spliced, 30
splicing, 14
synthesis of, 29, 29f
transcription, 13
in translation, 68–70, 68f–69f
Metabolic network, 54–55, 57f, 58, 141
Metabolism, positive selection associated with genes involved in, 123f
Metabolomics, 55, 141
Methionine, 12–13
Methylation
of DNA, 35–36
of histones, 35
Mice, homeobox genes of, 105–106
Microarray
Affymetrix GeneChips, 38
of cell cycle progression, 40, 40f
defined, 38, 141
drawbacks of, 40–41
how they work, 37–39, 39f
periodic expression of genes in root, 100, 102, 102f
photolithography, 38, 39f
Microfilaments, 58f, 59
MicroRNA (miRNA), 14, 28, 34, 141
Microscopy
automated image analysis, 61, 62f
confocal, 60–61, 61f

© 2014 by Cold Spring Harbor Laboratory Press. All rights reserved.
high-throughput microscopy for imaging cellular responses, 60–61, 61f–62f
Microtubules, 58f, 59, 141
miRNA (microRNA), 14, 28, 34, 141
Mitochondria, 49–51, 50f, 141
Mitogen-activated protein kinases (MAP kinases), 76–77, 141
Mitosis, 142
Mitotic cyclin, 93, 142
Modeling, and quantitative approaches in biology, 129–130
Model organisms, 103–104, 142
Monod, Jacques, 30–31
Monogenic traits, 109, 142
Moore’s law, 19
Morgan, Thomas Hunt, 116
Morphogen gradient, 104, 142
Morpholino antisense oligonucleotides, 106, 142
M (mitosis) phase, 90, 90f, 96–97, 98f, 141
MPSS (massively parallel signature sequencing), 41
mRNA. See Messenger RNA
Multiple reaction monitoring, 82, 142
Multiplexing, 42, 142
Mus musculus, 104, 142
Mutations
dominant, 104
genetic screen, 91
induction with ethyl methanesulfonate (EMS), 91
recessive, 104, 145
temperature-sensitive mutants, 91, 147
Mytilus genitalium, 62
Myosin, 94

N
NAD+, 53, 54f
NADH, 53, 54f
NADP, 52, 52f–53f, 142
NADPH, 52, 52f–53f, 142
Nanopore, 23, 142
National Center for Biotechnology Information (NCBI), 24
Negative-feedback oscillator, 92–93, 93f, 100
Negative selection, 105, 122, 142
Network motifs, 86, 86f, 142
Networks
controlling biological oscillators, 89–102
in human evolution, 121–127
rational network design, 63, 65
signaling, 77–80, 79f
synthetic, 63, 65
Neural functioning, positive selection associated with genes involved in, 123t
Neutral selective pressure, 123, 124, 142
Next-generation sequencing, 19, 21–23, 22f, 125
454 sequencing, 21
Illumina sequencing, 22
pyrosequencing, 21, 22f
single-molecule sequencing technologies, 22–23
Nicotinamide adenine dinucleotide phosphate, 52, 52f–53f, 142
NMR (nuclear magnetic resonance), 88, 142
NOD2 gene, 111
Noncoding regions, natural selection in, 123–124
Normal distribution, 110, 142
Northern blotting, 36–37, 37f, 142
Nuclear magnetic resonance (NMR), 88, 142
Nuclear membrane, 49
Nuclear pores, 49, 143
Nucleolus, 49, 143
Nucleoplasm, 49, 143
Nucleosome, 34–35, 35f–36f, 143
Nucleotide, 4–5, 5f, 143
Nurse, Paul, 92
Nüsslein-Volhard, Christiane, 104
Nüsslein-Volhard screen, 104

O
Odd-skipped mutation, 104, 143
Okazaki fragments, 11, 11f, 143
Oligonucleotide, 5, 143
Oncogene, 77–78, 78f, 143
1000 Genomes Project, 125, 143
Open reading frames (ORFs), 23, 83, 143
Organelles, 46f, 49–51, 50f–51f, 143
Oscillators. See Biological oscillators
Oxygen, released in photosynthesis, 52, 52f

P
p21, 79, 143
p53, 77–80, 79f, 143
Pacific Biosciences, 22–23
Paracrine signaling, 74, 143
Pauling, Linus, 3
PCA (principle components analysis), 43
PCR (polymerase chain reaction), 18, 19, 20f, 21, 42, 143, 144
PDYN (proenkephalin-B gene), 127, 144
Peptide bond, 70, 143
INDEX

Peptidyl site, 69, 69f, 143
Permissive temperature, 91, 143
Petals, 110–113, 110f–111f, 112t, 113f–114f, 143
Phenotypes, 91, 143
Phosphate backbone, of DNA, 4, 5f–6f, 143
Phosphorylation, 73, 143
Photolithography, 38, 39f, 144
Photosynthesis
ATP generation in, 52, 52f
Calvin cycle, 52–53, 53f
by cyanobacteria, 51
defined, 144
in thylakoids, 49, 51f, 52f
Photosystem II, 52, 52f, 144
Pigmentation pathway, human, 126
Pima Indian tribe, 116
Pistillata (pi) mutation, 111–114, 112t, 113f, 144
Plants, development in, 106–108, 108f
Plasmodesmata, 144
Plasmodium vivax, 127
Polyacrylamide, 15
Polymerase chain reaction (PCR), 18, 19, 20f, 21, 42, 143, 144
Polymorphisms, 126
Poly(A) tails, 29, 38, 144
Population structure, 117, 144
Positional information, moving transcription factor and, 108
Positive selectable marker, 105, 144
Positive selection, 123–124, 123t
PPi (pyrophosphate), 7f, 21, 144
Prebranch sites, 100, 101f, 144
Primary metabolites, 54, 144
Primary mRNA, 30, 144
Primary structure, 70, 144
Primase, 10f, 11
Primer
defined, 144
in PCR, 19, 20f, 21, 42
RNA, 10–11, 10f–11f, 38
sequencing, 17
Principle components analysis (PCA), 43
Production sequencing, 18, 144
Proenkephalin-B (prodynorphin) (PDYN) gene, 127, 144
Prokaryotic, 30, 144
Promoter, 31, 31f, 144
Protease, 80, 144
Protein–protein interaction, 82–84, 83f
Proteins, 67–88
catalytic activity, 71–73, 73f
chaperonins, 71, 136
DNA binding identification, 84–85
folding, 70–71, 71f–72f
in gene-regulatory network, 85–87, 86f
identification in complex mixtures, 80–81, 81f
information transfer by, 73–77, 74f–76f, 78f
measurement of differences between sample, 82
in membranes, 46–47, 48f
protein–protein interaction identification, 82–84, 83f
purification, 87
roles of, 67
structure of, 70–71, 71f, 87–88
synthesis of, 68–70, 68f–69f
Pyrophosphate (PPi), 7f, 21, 144
Pyrosequencing, 21, 22f, 145
Pyruvate, 54, 54f–57f

Q
Quantitative approaches in biology, 129–130
Quantitative trait, 110, 117, 145
Quantitative trait loci (QTLs), 117–118, 145
Quaternary structure, 70, 145

R
Radiation, mutations induced by, 91
RAS, 76, 145
RAS pathway, 75–77, 75f–76f, 145
Rational network design, 63, 65, 145
Real-time PCR, 42
Receptors, 47, 73
defined, 145
domains of, 73–74
signal transduction and, 74–77, 74f–76f, 78f
Recessive mutation, 104, 145
Recombinant DNA technology, 87, 145
Recombination
defined, 145
haplotypes broken up by, 125
homologous, 105, 116, 140
in meiosis, 116
Repetitive DNA elements, 25, 124, 145
Replicates, 42, 145
Replication fork, 11, 145
Repressilator, 64f, 65, 145
Repressor, 31, 31f, 85, 106, 145
Restrictive temperature, 91, 145
Retrotransposons, 25, 145
Reverse genetics, 95–96, 145
Reverse transcriptase, 38, 145
Ribonucleic acid. See RNA
Ribosomal RNA (rRNA)
    genes, 14
    in nucleolus, 49
    role of, 28, 68
    tandem repeats in, 49
Ribosomes
    defined, 145
    RNA in, 28, 68
    role in translation, 68–70, 68f–69f
Rickettsia prowazekii, 51
RNA (ribonucleic acid)
    concentration measurement, 36–37
    control of amount in cell, 27–28, 30–32
    cRNA, 38–39
    defined, 10, 145
    double-stranded RNA (dsRNA), 96
    modification of, 29–30, 70
    noncoding, 34
    northern blotting, 36–37, 37f
    primer, 10–11, 10f–11f, 38
    retrotransposons, 25
    role of, 27
    stability of, 27
    structure, 27, 28f, 30
    synthesis of, 28–30, 29f
RNA interference (RNAi), 96, 146
RNA polymerase, 28–33, 29f, 31f–33f, 38–39, 146
RNA secondary structure, 30, 146
RNase H, 10f, 11, 38, 146
RNA-Seq, 40–42, 41f, 60, 146
Roots
    positioning lateral, 100–102, 101f–102f
rRNA. See Ribosomal RNA
RuBisCo, 52–53, 53f, 146

S
Saccharomyces cerevisiae, 91
Sanger, Fred, 16–17
SCARECROW, 108
Schizophrenia, 127
Sea urchin, development in, 106, 107
Secondary structure
    defined, 146
    protein, 70
    RNA, 30
Second messengers, 77, 146
Secretion, 47, 146
Selected ion monitoring, 82, 146
Selection
    balancing, 127
    negative, 122
neutral, 123, 124
    positive, 123–124, 123t
Selective sweep, 122, 146
Semiconservative DNA replication, 9, 9f, 146
Sepals, 110–113, 110f–113f, 112t, 146
Sequence alignment, 23, 24
Sequence depth, 42, 146
Sequence, 18
Sequence reads, 18, 146
Sequencing. See DNA sequencing
454 sequencing, 138
Sequencing primer, 17, 146
SH2 (Src-homology 2) domains, 74f, 75
Short interfering RNA (siRNA), 28, 35, 146
Short interspersed nuclear elements (SINEs), 124
SHORT-ROOT, 108
Short-term memory, computer, 27
Shotgun sequencing, 18–19
Sickle cell disease, 67
Signaling cross talk, 77, 146
Signaling network, 77–80, 79f
Signal transduction pathway
    defined, 74, 146
    G-protein-coupled receptor pathways, 77, 78f
    RAS pathway, 75–77, 75f–76f
    second messengers, 77
    STAT pathway, 74–75, 74f
SINEs (short interspersed nuclear elements), 124
Single-molecule sequencing technologies, 22–23, 146
Single-nucleotide polymorphism (SNP), 117, 125, 126, 147
Single-stranded, 7, 147
siRNA (short interfering RNA), 28, 35, 146
Smithies, Oliver, 105
SNP (single-nucleotide polymorphism), 117, 125, 126, 147
Somatic cells, 95, 147
S (synthesis) phase, 90, 90f, 94, 96–97, 98f, 146
Spliced mRNA, 30, 147
Splicing, 14, 14f, 70
    alternative, 14, 41–42, 41f
    defined, 147
Src-homology 2 (SH2) domains, 74f, 75
Stahl, Frank, 9
Stamens, 110–112, 110f–111f, 112t, 113f–114f, 147
STAT pathway, 74–75, 74f, 147
Stem cells, 59–60, 147
Stop codon, 12f, 13
Strongylocentrotus purpuratus, 106, 147

© 2014 by Cold Spring Harbor Laboratory Press. All rights reserved.
Structural genomics, 88, 147
Sucrose, breakdown of, 72, 73f
Supervised algorithms, 43
Support vector machine (SVM) model, 43
Suprachiasmatic nucleus, 100
Synergistic interactions, 115
Synthetic biology, 63–65, 64f, 147
Synthetic cell, 63, 147
Systems biology, 118–119

Tag, 84, 87, 147
TaqMan, 42
TATA box, 32, 32f, 147
Technical replicate, 42, 147
Temperature-sensitive mutant, 91, 147
Template strand, 29, 29f, 147
Tertiary structure, 70, 147
Testosterone, 73
TFIID, 32, 32f, 147
Thylakoids, 49, 51f, 52f, 147
Thymine, 4, 4f–5f
Time of flight (TOF), 81, 81f, 147
Transcription
basal, 32
defined, 13, 148
process, 29
Transcriptional networks in development, 103–108
Transcription factors
in circuit diagram of sea urchin development, 106, 107f
cis-elements, 30, 31
cyclin–CDK oscillator model and, 97
defined, 30, 148
general, 32
homeobox, 104–106
location of DNA binding, 84–85
as morphogen gradient, 104
p53 activity as, 78–79
phosphorylation of, 77
positional information from moving, 108
role of, 13
structure of, 32–33, 33f
Transfer RNA (tRNA), 28, 68–69, 68f–69f, 148
Transformation, 84, 148
Translation, 30, 68–70, 68f–69f, 148
Transmembrane domain, 73, 148
Transporters, protein, 46–47, 48f
Transposable elements. See Transposons
Transposase, 25, 148
Transposons, 25, 62–63, 148
tRNA (transfer RNA), 28, 68–69, 68f–69f
T7 RNA polymerase, 39
Trypsin, 80
Tubulin, 58f, 59
Tumor suppressor, 78, 148
Tyrosine kinase receptor, 75, 76f, 148

Unsupervised algorithms, 43
Uracil, 29, 148

Vacuoles, 49
Venter, Craig, 18, 63
Vesicles, 47, 148

Warfarin, 118
Watson, Jim, 3, 5
Weinberg, Robert, 76, 77
Whole-genome shotgun sequencing, 18–19, 148
Whorls, of Arabidopsis flower, 110f–115f, 111–114, 112t, 148
Wieschaus, Eric, 104
Wild type, 91, 148

X-ray crystallography, 87–88, 148

Yeast one-hybrid method, 84–85, 148
Yeast two-hybrid method, 82–84, 83f, 148