Subject Index

a
14-3-3 1002
Aβ 966
Aβ immunization 977
Aβ production 965
ab initio gene-finding software 664
acetylation 1014ff
acetylcholinesterase 458
Achilles’ heel strategy 684
actin 1003ff, 1004
“activation function” domain 994
adaptation 401
Adeno-associated viruses (AAVs) 1125
age of onset 958
Agrobacterium tumefaciens 343
AIDS 571
Akt 1002
Alan Templeton 369
albright hereditary osteodystrophy 202
albumin 364
alignment 371
alkylation of bases
mispairing by 183
Allan Wilson 363, 375ff
allosteric transitions 31
alternate transcripts see alternative splicing
703ff
alternative splicing 702
Alu repeat 677, 684
Alu-PCR 620ff
Alzheimer’s disease 960, 997ff
amyloid 959, 1009ff
amyotrophic lateral sclerosis 997ff
ancestral core 518
ancestral polymorphism 559
anchor markers 40
androgenetic 192, 193
development 489
aneuploid 213
aneuploidy 4
Angelman syndrome 198, 201
anion exchange chromatography (AEX) 1132
annotation 452, 600
Anopheles 445
antibiotic resistance 342
antibodies 977
anticipation 989ff
anticodon 24, 76, 84, 85
codon interaction 85
definition 76
tRNA loop 84
antifreeze proteins (AFPs) 854
anti-oncogene 184
APH-1 968ff
apolipoprotein E 963ff
allele frequency 963
alleles 963, 970
functions 970
gene 963
genetic risk factor 963
molecular mechanisms 970
protein 963
apoptosis 1145
ATM 1145
Bcl2 1145
DNA damage 1145
APP 965ff
alternative splicing 965
FAD mutation 961
gene 960, 965
homologs 965
mRNAs 965
mutations 960
normal function 965
proteolytic processing 965ff
Aristaless related homebox (ARX) protein 1033
armadillo repeats 1035
arrestin domain 1007
assembly 590
assembly software package 661
PhrapView 661
Phred-Phrap-Consed 661
associative expression networks 254
AT-rich or GC-rich repeats 661
ataxin-1 1000
ataxin-2 1003
ataxin-2 binding protein-1 (A2BP1) 1003
ataxin-3 1004
ataxin-7 1006ff
atrophin-1 999
attenuation 4, 31
autologous 864, 873
autophagy 1008
autosomal 11
inheritance 4
autosomes 174
average linkage 369
BAC (bacterial artificial chromosomes) 496, 504, 596, 641, 678, 682, 687
cloning large DNA fragments 641
plasmids 641
BAC-end sequences 597
BACE1 965ff
Bacillus subtilis 341
bacteria
mutagenesis in 183, 184
bacterial artificial chromosomes see BAC
bacterial cloning systems 639
bacteriophages and plasmids 639
cloned DNA 639
polylinkers 639
bacterial conjugation 391
bacterial genomes 681
bacteriophage-mediated transduction 391
balanced lethal stocks 420
Barr body 213
λ-based vectors 609ff
cosmids 611ff
diphasmids 611
hyphages 611
phasmids 611
base analog
base replacement by 183
base calling 586
base excision repair (BER) 174
batched segregant analysis 494
Battista Grassi 444
Bcl2 rearrangement
effect of 178
Beckwith–Wiedemann syndrome 194, 196, 202
binary model 864, 885
biodiversity 404
BLAST 600
blepharophimosis-ptosis-epicanthus inversus syndrome (BPES) 1033
blood meal 455
blue–white selection 606ff
β-galactosidase (lacZ) gene 606
bottom-to-top strategy 567
brain-derived neurotrophic factor (BDNF) 997
branching order 553
c
C83 965ff
C99 965ff
C-value paradox 326, 327
CACNA1A 1005ff
Caenorhabditis elegans 869
calcium channel 1005ff
calpain 1016
β-catenins 1035
cancer 190, 203, 706ff
candidate gene studies 964
CAP3 590
capillary 587
capillary-based sequencers 640
capture step 1132
carboxylesterases 457
cardiac troponin T (cTNT) 1025
cardiomyopathies 1128
gene therapy of 1128
“carriers” 13
caspase 995ff
cathepsins D and E 1016
caveats 897
CBC-SGC 654
CBC-SGS 654
map-directed operation 654
shotgun libraries 654
CBC-SGS approach 640, 641
crop plant genome – the rice genome 640
large-insert clones 641
shotgun cloned 641
small-insert clones 641
Celera effort 235
Center for Biologics Evaluation and Research (CBER) 1130
centimorgan (cM) 4, 39
centromeres 11, 211ff, 511, 513
CFTR mutations 174, 176
chaperone binding site 106
Charles Laveran 444
Charles Sibley 368
chemical mutagenesis 478ff
breeding scheme 480ff
chemicals 393
chemosensation 537, 538
chimeric mouse 864, 883
chimpanzee 569–570, 572
chimpanzee genome project
finishing phase 574
sequencing errors 575
sequencing strategy 573
shotgun phase 574
chloroquine 444
chorea 996
chromatin 200, 210ff, 211ff
chromatogram 584
chromosomal banding
C-bands 238
G-bands 238, 243
H1 R-bands 243
R-bands 238
T-bands 238, 243
chromosomal locus 682
chromosomal segregation 1144
aneuploidy 1144
centrosomal anomalies 1144
chromosome aberrations 35
deletion or deficiency 35
duplication 35
inversion 35
translocation 35
chromosomes 9, 173, 211ff
banding 561
forms 447
inversions 447
microdissection 621
substitution 864, 867
subtelomeric region 562ff
cladistics 373, 374ff
class switch recombination (CSR) 184
cleidocranial dysplasia (CCD) 1032
clinical gene therapy 1129
treatment of diseases 1129
trials 1125
clone coverage 646
clone libraries proper 646
Unbiased 646
clone Fingerprinting 662
clone fingerprints 662
clone gap 650
standard Southern techniques 650
clone linking 688
cloned ordering 687, 688
clone recovery rate 654
measured by colony-PCR 654
clone-by-clone (CBC) 635
clone-by-clone SGS or CBC-SGS 637
cloneless genomic libraries 688
cloneless library 678, 683, 689
cloning 606ff, 607, 841
closing sequence gaps 661
genomic DNAs as PCR templates 661
isolated YAC 661
physical gaps caused by cloning failures 661
CMAH 563
codon 5, 24, 76, 82, 85, 97, 111
anticodon interaction 85
start 82, 97
termination 82, 97
usage 111
coenzyme Q10 1023
coevolution, virus–host 571
cofactors 968ff
colinearity 20
Committee for Proprietary Medicinal Products (CPMP) 1130
comparative genome analyses 671
gene families 671
gene networks 671
genome annotation 671
guiding molecular biologists 671
Mammalian Gene Collection (MGC) 671
comparative genome hybridization (CGH) 678, 689
comparative genomics 671
genome sequencing 671
human-centric to species-focused 671
competition model 350
complementation test 5, 9
complexity hypothesis 350
compositional constraints 402
concatemer 695, 699, 700ff
conditional gene targeting 888, 891
conditional model 864
conditional transgenesis 887, 888
cone-rod dystrophy 1006ff
cone-rod homeobox protein (CRX) 1007
congenital central hypoventilation syndrome (CCHS) 1034
Congo red birefringence 1009
conjugation 342, 397
bacterial conjugation 342
plasmid 342
T-DNA 342
Ti plasmid 342
conserved synteny 496
construction of genomic library
partial filling-in 615
contigs 41, 504, 590, 657
contigs and scaffolds 658
paired sequence reads 658
"scaffold" neighboring contigs 658
 coordinately transcribed genes 255
CoT analysis 449
CpG Islands 519, 621ff, 1017ff
density of CpG islands 250
DNA methylation 248
GC suppression 248
gene silencing 249
tissue-specific expression patterns 250
CRE expression 890, 891
CRE-LoxP 864, 890
CRE-MER 864
CREB 1010
CREB-binding protein (CBP) 995ff
CREM 1010
cross-reactivity 555
crossing-over 5, 38
intrachromosomal 563
CUG-BP1 and ETR-3-like factors (CELF) 1026
cystic fibrosis 174
cytochrome P450s 457
cytoplasmic "dumping" 1004
cytosine deaminase
induced activation of 178, 184

d
2D electrophoresis 556
data integration 651
basic genomic information 651
 functional annotation, of sequenced genomes 651
gene-centric or marker-centric 651
Genetic information 651
markers 651
sequence polymorphisms 651
DDT 444
D. E. Kohne 367
dead on arrival (DOA) elements 328
Helena 328
nonallelic 328
deletion bias (DB) 326, 327, 329
based on small indels 328, 329
drosophila 328
dentatorubral pallidoluysian atrophy 990ff
derived features 374
detoxification 539
developmental genetics 361
diabetes 202
mellitus 202
transient neonatal 202
diploids 9
directed cloning 655
M13 phage 655
plasmid cloning system 655
plasmid-based random cloning system 655
random shotgun protocol 655
disease, human 560
environmental influences 571
 genetic predispositions 571
diseased alleles 871
disomy 191, 194
uniparental 191, 194
distamycin 781
diuretic hormones 459
DM2 1025
DNA 212, 215—217, 219, 221, 223, 583
carcinogens leave no definite mutational
signatures on 184
electroporation into embryos 839, 840
electroporation into sperm 839, 840
gains of 515, 518
losses of 515, 518
methylation 217, 222, 223
methyltransferases 217
microinjection into embryos 838, 839
microinjection into unfertilized eggs 838, 839
mutagenesis of 171, 185
repair of 171, 185
repetitive 212, 215, 216
satellite 216, 219, 221
structure of 173, 176
DNA acquisition 396
DNA chip 700, 706ff
DNA cloning 635
DNA gain 330
DNA heteroduplex 557
DNA hybridization 366, 367ff
DNA lesion 19 mutation 176
DNA loss
due to small indels and genome size 329
DNA marker 607ff
DNA methylation 190, 191, 199, 200
DNA methyltransferases 200
DNA microarray 635
DNA polymerase-based sequencing 638
DNA polymerization errors 181
DNA rearrangements 177, 393, 398
DNA repair 172
systems 393
Subject Index

DNA replication 1144
checkpoint activation 1144
DNA sequence 371, 556ff
deletion 564ff
diversity 560
evolutionary rate 564
insertion 564ff
nonfunctional 558
repetitive 563
substitution 563ff
human-specific 568
multiple/parallel 566
transposable elements 563
variation 560
DNA sequence assembly 657, 658
close the gaps 658
Lander–Waterman gaps 658
Phred-Phrap-Consed package 658
repeat gaps 658
RePS (an assembler, repeat-masked Phrap with scaffolding) 658
DNA sequence comparison 556ff
DNA–DNA hybridization 557
mitochondrial DNA 558
nuclear DNA 558ff
DNA sequence homologies 390
DNA sequencing 635, 638
basic technology 638
concept and technology of 638
DNA methylation sites 635
primer-dependent tactics 638
sequence polymorphisms 635
 shotgun principles 638
DNA transformation 391
DNA triplex 1021
dNA-damaging agents 172, 176
Dobzhansky 366, 378ff
dominance 5, 32
codominant 33
partial dominance 33
recessive 32
dominant-negative 993
Drosophila melanogaster 213, 869
duality of genomic information 403
duplex 173
duplication, segmental 563
dynamic expression linkages 259
dystrophica myotonica protein kinase (DMPK) 1024ff
effective population size (Ne) 326, 327
electron transport chain (ETC) 998
electrophoresis 584
electroporation 832, 838
elongation factors see mRNA translation, protein factors 87
embryonic stem (ES) cells 865, 870, 882, 894
embryos 885
ES cell–derived 885, 887
EMEA (European Agency for the Evaluation of Medicinal Products) 1130
Emile Zuckermandl 363
deri-sequencing 660
endogenous retroviruses derivatives of 536
endosymbiosis 400
enhancer 31, 218
enhancer mutations 34
Ensembl system 234
environmental conditions 388
enzymatic repair systems 393
epidemiology 958ff
epigenesis 376
epigentic 190–192
modifications 191
inheritance 211, 221
episodic ataxia type 2 (EA2) 1006
epistasis 5, 28
epitope 555
equine infectious anemia virus (EIAV) 1124
Erika Hagelberg 370
ES cells see embryonic stem cells
random mutagenesis in 894, 897
EST see expressed sequence tag 694
EST (expressed sequence tag) 694ff, 695, 703, 704ff
euochromatin 210ff, 420, 423, 427, 430, 433, 595
eukaryotes
noncoding DNA evolution 327, 333
noncoding DNA, size of 327, 328
eukaryotic genomes 330, 644
influence of recombination 330
evo-devo 361, 376
evolution 1061
biological 565
DNA sequence 565ff
male-driven 1061
molecular 565
of phenotypes 565
species-specific 563
evolution and development 376
evolution genes 391, 399
evolutionary change 379ff
Subject Index

- evolutionary fitness 399, 400
- evolutionary function of viruses 402
- excitotoxicity 997ff
- exon 5, 21
- expanding trinucleotide repeats 36
- expressed sequence tag (EST) 40, 600, 678, 682, 694ff
- expression controls 261
- expressivity 28

f

- F1 transgenic fish 832
- F2 transgenic fish 850
- F8A 1061
- F8B 1061
- factor V 1062
- factor VII 1063
- factor VIII 1060, 1061
- gene 1061
- factor FVIII 1062
- mRNA 1062
- protein domains 1062
- factor IX 1060, 1063, 1065, 1076
- gene 1063
- inhibitor 1076
- mRNA 1063
- protein domains 1063
- tridimensional structure 1065
- factor X 1062, 1063
- familial hemiplegic migraine (FMH) 1006
- FASTA 600
- feline immunodeficiency virus (FIV) 1124
- FGenesH 600
- fibrinogen domains 454
- fingerprint 596
- fingerprint contig (FPC) 508
- fingerprinting 496
- finished sequence 504
- FISH see fluorescence in situ hybridization 689
- fish model
  - large-size 834, 835
  - medium-size 834
  - small-size 834
- fish species
  - selection of 833, 835
- FISH technique 662
- fish transgenesis 846
- flip-flop system 394
- fluorescence in situ hybridization (FISH) 678
- fluorescence-activated cell sorter (FACS) 619
- FMR2 1020
- FMR3 1020
- Food and Drug Administration (FDA) 1130
- Forkhead L2 (Foxl2) 1033
- forms of genomic damage 1138, 1139
  - chromosomal instability 1139
  - intrachromosomal instability 1139
  - microsatellite instability 1139
- forward genetics 478ff
- founder effect 1004ff
- FOXP2 567
- FPC 597, 598, 662
  - assembling of, sequence-ready clones 662
- fragile site 1017
- fragile X mental retardation-1 (FMR1) gene 1017ff
- fragile X syndrome (FRAXA) 1017ff
- fragile X tremor-ataxia syndrome (FXTAS) 993ff, 1028ff
- fragile XE mental retardation (FRAXE) 988ff, 1018ff
- frameshift mutation 5, 34
- frameshifts 177
- frataxin 1020ff
- Friedreich’s ataxia 993ff
- Friedreich’s ataxia (FRDA) 1020ff
- FTDP-17 969ff
- full genome scans 964
- functional annotation see genome annotation 707ff
- functional coordination 255
- functional genomics 704
- fusion, telomeric 561
- FVIII 1063, 1071, 1072
  - binding sites for FIX 1071
  - inactivation by protein C 1063
  - inhibitors 1072
  - interaction with vWF 1071
  - normandy-type von willebrand disease 1071
  - tridimensional structure 1063
- FVIII and FV 1062
  - combined deficiency 1062
- FVIIIa 1070
  - heterotrimer stability 1070
- g
- α2u globulin pheromones 538, 539
- G + C content 519
- G-protein of vesicular stomatitis virus (VSV-G) 1124
- G-quartet 1018
  - gain-of-function mutation 5, 34, 990ff
- gametogenesis 375
- gap closure 690
  - pseudogaps 690
  - true gaps 690
GC content 239, 557, 663  
problems in cloning, and sequencing  
procedures 664  
GC3 values 241  
Gel filtration (GF) 1132  
gene 8, 172, 376  
evolution of 322, 532  
fusion 394  
homeotic 376  
loss 529, 530  
map 236  
model 245  
number 232  
prediction 233, 600  
regulatory 376  
set  
construction of 522, 523  
size 665  
spaces 666  
empty space 241  
genome core 241  
structural 376  
structure 241  
exon length 242  
intron sizes 242  
number of exons 242  
targeting 771, 865, 870, 879, 884  
basics of 879, 885  
biotechnological procedures of 884, 885  
developments in 870, 871  
technology of 879, 885  
vector design of 879, 882  
therapy 1128  
infectious diseases of 1128, 1129  
transfer 1120  
methodology of 841, 842  
methods of 838, 842, 1120, 1122, 1123, 1125  
naked nucleic acid 1122, 1123  
Nonviral Vectors 1122, 1123  
viral Vectors 1123  
viral vectors 1125  
trap 865, 895  
mutagenesis of 895, 896  
tree 559  
vector 397  
gene density 238  
gene duplications 526, 529  
gene expression see gene expression profiling  
gene expression profile see gene expression  
profiling 705ff  
gene expression profiling 377, 568, 695, 700ff, 704ff  
gene-finding algorithms 664  
gene-finding program 665  
gene-regulatory regions  
conservation of 529  
generators of genetic variations 401  
Genesis 403  
genetic code 77, 82  
deviations from 82  
reading frame 82  
standard 82  
genetic distance 554ff  
genetic diversity 340, 559ff  
genetic drift 560  
genetic engineering 404  
genetic instability 990ff  
genetic locus 682  
genetic map 5, 493ff  
genetic maps 38, 670ff, 682  
assembled, genome sequence map 670  
genetic and functional studies 671  
sequence polymorphism discovery 671  
genetic polymorphism 390  
genetic screens 478  
genetic selection 606ff  
Spi 606  
supF 606  
genetic sequence 173  
genetic variation 388  
genetically identical 867  
genetically modified organisms 339, 349, 404  
lateral gene transfer 339  
transgenic crops 349  
genetics 960ff  
familial Alzheimer’s disease 960  
sporadic Alzheimer’s disease 963  
genome 172, 504  
genome annotation 662–664, 666, 695, 703, 704ff  
and analysis 662  
compositional and structural dynamics 663  
genome and gene structural dynamics, importance of 664  
heterogeneous distributions of DNA composition 663  
sequence variations 666  
SGS 666  
genome duplication 475  
genome evolution 667, 669  
genome duplications and deletions 669  
insect genomes 667  
Vertebrate genomes 667  
genome human chromosome 677  
physical mapping of 677, 691  
Genome organization 390
Subject Index

Genome sequencing 671
Genome, large 671
WG-SGS strategy for, animal genomes 671
genome sequencing 497
BAC clones 497
ESTs 497
whole-genome shotgun 497
genome size 511
genome working draft 644
genome-sequencing project 662, 669
EST sequencing 669
ESTs and cDNAs 669
Full-length cDNA 669
NIAS 669
RIKEN 669
sequencing cDNA clones 669
genomic clone libraries 687, 688
genomic DNA Libraries 652
genomic features
 covariance of 522
genomic imprinting 190, 191
genomic instability as a clinical prognostic tool
array-based approaches 1147
clinically practicable assay methodology 1147
 genomic sampling methodologies 1148
genomic instability begin 1141, 1142
coloctal adenomas 1142
ey in tumor progression 1141
measuring genomic damage 1141
the Loeb model 1141
genomic library 607ff
amplified libraries 611
 classical dephosphorylation 612
construction 612
 classical 612
dephosphorylation 612
 genomic libraries 612
 jumping 615ff
 linking 615ff
 percentage of recombinants 612
 representativity 611ff
 special 607
 genomic mapping 682
 concepts of 682, 683
genomic restriction maps 683, 687, 689
 genomics 15, 573 583
 genotype 174
genotype–phenotype correlation 567
Genscan 600
George H. F. Nuttall 362
George Todaro 367
GGG trinucleotide 251
gibbon 553ff
Glimmer 600
 glutathione reductase 459
 glutathione-S-transferases 457
glycosylation 1062
good manufacturing practice (GMP) 1130
Goodman 365ff
granulocyte-macrophage colony-stimulating factor (GM-CSF) 1128
great apes 553ff
green fluorescent protein 492ff
gynogenetic development 489
h
Haemophilus influenzae 341
hand-foot-genital syndrome (HFGS) 1033
haploinsufficiency 1024ff
haplotypes 451
HDAC3 (histone deacetylase 3) 1002
HDL2 1036ff
α-helical 1031
heat shock proteins (HSP) 375, 994ff
heat shock response 379
hemizygous 13
hemochorial placentation 365
hemoglobin 363, 367ff
hemophilia 1059, 1060, 1077–1080
 genetic counseling 1078
 genetics 1059
 gonadal mosaicism 1078
 incidence 1060
 missense mutation 1077
 mutation at CpG sites 1077
 treatment 1079
 gene therapy 1079
 treatment, gene therapy 1080
 clinical trial 1080
hemophilia A 1059–1060, 1065–1069, 1077
gross gene deletions 1066
inhibitors 1077
inversions 1066
large insertions 1066
 mutation 1067–1069
 affecting mRNA translation 1068
 affecting RNA processing 1067
 amino acid addition 1069
 amino acid deletions 1069
deletion or insertion hotspots 1069
 missense 1069
 nonsense 1068
 small sequence changes 1067
mutation rate 1060
mutations 1065
hemophilia B 1059–1060, 1072, 1073, 1075, 1077
inhibitors 1077
mutation 1073, 1075
founder mutations 1073
large insertions 1073
missense 1075
small sequence changes 1073
mutation affecting 1073
mRNA processing 1074
RNA Processing 1074
transcription 1074
translation 1074
mutation rate 1060
mutations 1072
gross deletions 1072
hepatitis 571
heritability 5, 14
heterochromatin 210ff, 420, 422, 430, 433, 595
satellite 786
heterologous 865, 874
HGT 340, 348, 351
barriers 340, 348, 351
measurements of 340
hidden Markov models (neural network) 665
sequence composition 665
signal to weight 665
high repetitive sequence content 672
histone acetylation 200, 998
histone deacetylase inhibitors (HDAC Is) 998
histone methylation 200
histones 997ff
holoprosencephaly (HPE) 1032ff
homeodomain 1033ff
homeostasis 375, 380ff
hominooids 553ff
homologous recombination 771, 879
homology searching 600
homozygous 867
horizontal gene transfer 339, 391, 397, 398
host preference 457
HOX 1032
HSP 379ff
Human Genome Project (HGP) 637, 639ff
BAC (bacterium artificial chromosome)-based
STS (sequence-tagged site) 637
cosmids 640
gene-space physical mapping effort 640
large-insert clones 640
minimal tiling path (MTP) 637
physical mapping 637
YAC (yeast artificial chromosome)-based
human immunodeficiency virus type 1 (HIV-1) 637, 640
human transcriptome map type 1 (HIV-1) 1124
human–chimpanzee comparison 561
biomedical differences 570ff
cytogenetic differences 561
DNA sequence differences 575
ethical considerations 572
human rights 573ff
infectious diseases 571
qualitative difference 572
huntingtin 996
Huntington's disease 990ff, 1036ff
hybrid cell lines 620
radiation hybrids 620
hybridization 340, 345, 348
hybrid-bridge 345
hybrid-bridges 348
β-hydroxylation 1064
hypoxia response element 995
i
IBD (identical-by-descent) fragments 624
CIS (cloning of identical sequences) 624
GMS (genomic mismatch scanning) 624
CIS (cloning of identical sequences) 624
idebenone 1023
IGF/INS pathway 194, 196
immune-response genes 460
immunological distance 364
imprint 191
imprinted genes 196
imprinting-control region 190, 198, 199–201
imprinting-control regions 198
imprints 192
improvement of a biological function 398
in situ hybridization 420, 425, 450
inbred strain 865, 882
inclusions 998ff
indels 327, 329
polymorphic 329
dependent assortment 6, 37
induced mutations 182, 183
induction 30
inducible enzymes 30
inducible genes 30
infidelities of DNA replication 392
initiation factors see mRNA translation, protein factors 91
institute immune system 460
inositol phosphate-3 receptor (IP3-R) 998
insecticide resistance 457
insertional mutagenesis 480ff, 865, 894
plasmid DNA 480ff
pseudotyped retroviral vectors 480ff
rate of mutagenesis 482
retroviral vector 480ff
transposon 480ff
insulin receptor (IR) 1025
inteins 25
inter-Alu PCR 678, 690
intergenic noncomplementation 29
interphase 211ff
interspersed simple sequence repeats (SSRs) 536
intertwined complementary strands 173
intragenic complementation 29
introgression 340, 352
introgrowth 340
intronic splice signals
conservation of 526
introns 6, 21, 330
inversion 561ff
iron–sulfur cluster-containing proteins 1021
Iron–sulfur clusters (ISCs) 1021
IS elements 395
isochores 240
isogenic DNA 865
isolation 389
reproductive 562

j
Jon Ahlquist 368
Jonathan Marks 371, 380ff
josephin domain 1005
jumping library 678
construction of Not I jumping 616ff
“general” jumping 616
(hopping) 616
jumping clones 616
Not I jumping 616
Jun N-terminal kinase (JNK) 999
junctophilin-3 (JPH3) 1036ff
knockdown 484ff
knockin 865
knockout 486ff
mutant 569
Kpn repeat 678, 684

l
laboratory strains 475ff
lamina 216
nuclear 216
Lander–Waterman curves 648
clone coverage 648
large genome-sequencing projects 637
large-insert clone-based physical mapping 637
large-insert clones 634, 640, 662
BAC 640, 662
BACs or YACs 634
YAC 640
large-scale sequencing (LSS) 635, 640
LSS and physical mapping 640
Large-scale Sequencing Era 638
law of large numbers 361, 369, 380, 381ff
leptospirosis 506
lethal mutations 396
Lewis Wolpert 376
library 588
ligand-binding domain (LBD) 891
ligand-binding proteins 525
LINE (long interspersed) repeat 684
lineage sorting 559
linkage 38
linking libraries 616, 678, 686
Linus Pauling 363
local DNA sequence change 392, 398
locus 679, 690
long interspersed repeat elements (LINEs) 679
long term depression (LTD) 1018
long terminal repeat (LTR) 1119
loss-of-function mutation 6, 34, 993ff
low-complexity repeats (LCR) 657
LSS 655

m
M13 589
Machado–Joseph disease 1003ff
maintenance of genomic integrity 1143
DNA damage repair 1143
homologous recombination repair 1143
mismatch repair 1143
nonhomologous end joining 1143
major histocompatibility complex (MHC) 571
### Subject Index

- **malaria** 444
- **malignant** see cancer 706ff
- **mammals**
  - carcinogenesis in 183, 184
- **markers** 494, 607
  - anonymous markers 608
  - polymorphic 608
  - microsatellites 608ff
  - minisatellites 608
  - single-nucleotide polymorphism (SNP) 608
- **Mary-Claire King** 375ff
- **Maryellen Ruvolo** 373
- **massive parallel signature sequencing** 701
- **massively parallel hybridization** see DNA chip 703ff
- **master gene** 568
- **Master Working Cell Bank (MWCB)** 1132
- **maximum likelihood** 373
- **mechanisms of genetic variation** 389
- **meiosis** 6
- **melting temperature** 557
- **membrane** 212, 216
  - nuclear 212, 216
- **mendel** 14
- **mesothelioma** 184
- **messenger ribonucleoprotein complexes (mRNPs)** 1018
- **messenger RNA (mRNA)** 76–78, 1120
- **meta genomes** 672
  - portions of ruminant stomach 672
- **metabolic pathway** 705
- **metabolic resistance** 457
- **metabotropic glutamate receptors** 459, 1018
- **metaphase** 211ff
- **methylation** 379, 1017ff
- **microaggregates** 1010
- **microarray** 694, 700, 704–707ff
- **hybridization** 493
- **microbial genome sequencing** 639
- **microcomplement fixation** 363
- **microdeletion** 519
- **microinjection** 492
- **microRNAs** 1018
- **microsatellites** 41, 493, 988
- **mitochondrial genome** 702
- **mitosis** 6, 213
- **mixed genomes** 672
- **MMR** 348
- **mutators** 348
- **mobile genetic elements** 391, 395
- **mobility pattern** 556
- **model organism** 569ff
- **modified vaccinia ancanra (MVA)** 1120
- **molecular and cellular mechanisms** 965
- **molecular anthropology** 361
- **molecular assumption** 363, 369, 370, 373–375ff
- **molecular change** 361, 364, 365, 367, 373–375ff
- **molecular clock** 361, 363–365ff, 368, 375ff
- **molecular cloning techniques** 638
- **molecular evolution** 388, 403
- **molecular systematics** 361, 362, 367, 370ff
- **moloney murine leukemia virus (MoMLV)** 840
- **monogenic congenital diseases** 1125
- **gene therapy of** 1125
- **morphogenetic fields** 377
- **morpholino** 484ff, 838
  - structure of morpholino 484ff
- **Morris Goodman** 364
- **morula aggregation** 882
- **mosaic embryos** 882
- **mosquitoes** 443
- **mouse** 866, 868, 891
  - colocalization of SINEs in 535, 536
  - genetics of 866, 867
  - genome 519
  - history of 866, 871
  - knockins of 891, 894
  - lineage	h
different activity of SINEs in 534, 535
  - molecular genetics of 868, 871
  - shift in substitution spectra 519, 520
- **MPSS** see massive parallel signature sequencing 701, 707ff
- **mRNA** see messenger RNA 76
- **mRNA structure** 78–80, 105, 107–111
  - 5′ cap 81
eukaryote 81
  - ferritin 107, 108
  - frameshift 78
  - histone 79
  - internal RNA entry site 110, 111
  - polarity 78
  - polyadenylation 81
  - polycistronic 108, 109
  - prokaryote 81
  - pseudoknot 108
  - Shine–Dalgarno sequence 81, 111
  - stability 105
  - translational control 108
mRNA translation control 76, 104, 105, 107, 108, 111, 113
amino acid abundance 111
antisense polynucleotide 111
codon usage 111
elongation factor activity 108
frameshift 108
initiation factor activity 108
internal RNA entry sites 110, 111
mRNA/protein interactions 107
mRNA stability 105
mRNA structure 108
ribosome activity, modulation 111
ribosome inactivation 112
mRNA translation mechanism 76, 80, 90, 95, 97, 99, 100, 103, 104, 113
initiation of translation 90, 95
peptide bond formation 80, 100, 103
peptide chain elongation 95
peptide chain elongation/translocation cycle 97
termination 97, 99
translocation 103, 104ff
mRNA translation, protein factors 90–93, 95, 97, 99
elongation factors, eukaryotic 97, 99
elongation factors, prokaryotic 95, 97
initiation factors, eukaryotic 91, 93
initiation factors, prokaryotic 90–902
termination factors 95, 99
mt DNA 370
hypervariable zone 370
multiplex analysis 679, 687
murine leukemia virus (MLV) 1123
muscleblind 1026ff
muscleblind-like proteins (MBNL) 1026
mutagenesis 172, 391, 393, 478ff
to produce immunity repertoire 184, 185
mutagenic conditions 393
mutagens 172, 176, 393, 478ff
mutation 6, 32, 172, 378–380, 390, 478ff, 1061
at regulatory sequences 178
chromosomal rearrangement 378
gene duplication 378
load 1061
macromutation 378, 379, 380ff
micromutation 378
point 378
types of 176, 179
mutation hotspots 178
mutation rate, germ line-specific 566
mutation reversions 178
Myoclonic epilepsy type 1 993ff
myoclonic epilepsy type 1 993ff
myoglobin 365
myotonic dystrophy 989ff
myotonic dystrophy type 1 (DM1) 1024ff
myotonic dystrophy type 2 (DM2) 1026ff
n
natural habitats 475
natural killer lymphocytes (NK) 1127
natural selection 365, 388
natural strategies of genetic variation 398
N-ethyl-N-nitrosourea 478ff
mechanism of mutagenesis 479
rate of mutagenesis 479
nearest-neighbor joining 373
Neisseria gonorrhoeae 341
nephron 706
netropsin 781
neurofibrillary tangles 969
neurotransmitter 1005ff
neutral substitution rate 527
new world monkeys 554
nicastrin 968
non-Mendelian inheritance 989
noncoding DNA 327, 331
noncoding lesions 183
noncoding RNA genes 532
nondisjunction 6, 35
monosomy 35
trisomy 35
nonsynonymous mutation 180, 505
nuclear bodies (NBs) 1008ff
nuclear DNA 371
nuclear inclusions 994ff
nuclear transplantation 841
nucleic acids 8
nucleic base loss of 182
nucleoid 9
nucleus 9, 211ff
nucleotide excision repair (NER) 174
nucleotide substitution 392, 557
nucleus 9, 211ff
nutrient transfer 190, 203, 204
nucleopharyngeal muscular dystrophy 993ff, 1030ff
odorant binding proteins 457
odorant receptors 454
Okazaki fragments 17
old world monkeys 554
oligomers 1010
operon fusion 394
operons 31
1:1 orthologs 453
ORF 505
ORs 457
orthologous chromosomal segments 513
large-scale rearrangements 513
orthologous genes
properties of 523, 524
orthology
determination of 522, 523
OTC (ornithine transcarbamylase) 1124
Otto 235
outgroup 575
ovary ecdysteroids 459
overall similarity 363
oxidized base
incorporation of 182

p
P1 transgenic fish 832, 843
P1 artificial chromosomes (PACs) 682, 687
P1-derived artificial chromosomes (PAC) 679
p53 998
p300/CBP-associated factor (PCAF) 1014
parasites 343, 344
parasitic plants 344
Parkinson’s disease 849, 997ff, 1003
parthenogenesis 192, 193, 203, 488
partial transgenesis 898, 900
Partington syndrome (PRTS) 1033
pathogenicity islands 344
pathogens 343
pathology 958ff
PAUP 373
PCR see polymerase chain reaction
PCR-based protocols 643
preparation of sequencing templates 643
PEN-2 968ff
penetrance 28
peptide bond, formation 80, 100, 103
peptide nucleic acids 794
pericentric inversion 562
“perturbed expression” profiling 254
peroxidases 454
PEST (Pink Eye STandard) strain 447
phenotype 174, 388
analysis 897, 898
emergence of new 567
phosphoglycerate kinase (PGK) 875
PHOX-2B 1034
Phrapt 590
Phred 587
Phred-Phrapt-Consed 643
phylogenetic analysis using parsimony 373
phylogeny 475ff
vertebrate lineages 477
phylogeny, human and great ape 553ff
physical colocation and dislocation 257
physical gaps 634, 648, 650
physical mapping 40, 496, 597, 634, 662, 670, 683
approaches for 683
radiation hybrid mapping 662
restriction-digest fingerprints 662
STSs 662
physical mapping methods 670
cloning fingerprinting 670
hybridization-based 670
large-insert clones 670
large-insert, clone-based STS mapping 670
sequence-tagged connectors 670
plant genomes 644, 672
diploid species 672
polyplid crop 672
plaques 959
plasmid 589
plasmid DNA 1119
preparation methods 642, 643
absorbent-based 642
alkaline lysis protocols 642
centrifugation steps 643
isothermal amplification protocols 642
β-pleated sheets 1009
pleiotropy 28
ploidy 35
aneuploidy 35
 euploidy 35
pluripotent 865
point mutations 176, 374
polonies 679, 690
polyadenine-binding protein 2 (PABP2) 1030ff
polyadenylated transcripts see polyadenylation 703ff
polyadenylation 702
polyalanine 993ff
polyamide 781
imidazole 782
pyrrole 781
polyglutamine 988ff
binding protein 1 (PQBP-1) 1002
polylinker 606
polymerase chain reaction (PCR) 533, 635, 640, 679, 683, 694, 699ff, 832, 842

Subject Index | 1171
polymorphic microsatellites 608ff
minisatellites 608
single-nucleotide polymorphism (SNP) 608
polymorphism 694, 703ff
link-up 679, 686
polypeptide chain, polarity 80
polypeptide synthesis see mRNA translation 77
polyploidy 6
polypurine (polypyrimidine) 537, 787
polytene chromosomes 420, 421, 423–427, 430, 434, 435, 447
polyubiquitin 1005
POMC (pro-opiomelanocortin promoter) 887
population genetic theory 327, 328
population size, effective 561
position effect variegation (PEV) 213ff
positional cloning 41
positional information 377
postsegregational killing genes 351
suicide genes 351
posttranscriptional gene silencing 31, 899, 900
posttranslational modification 1002
Presenilin 967ff
PPF2R2B 1035ff
Prader–Willi syndrome 198, 201
premature ovarian failure (POF) 1017
premutation 988ff
presenilin 967ff
CTF 968
endocleavage 962
endoproteolysis 961, 968
FAD mutations 962
genome 961, 967
homologs 967
mutations 961
NTF 968
structure 967
preventive vaccination 1128
infectious diseases of 1128, 1129
primate phylogeny 555
primate–rodent ancestor 518
primer walking 592, 660
primitive features 374
prion diseases 997
process control 655–656
data tracking mistakes 655
equipment-related errors 655
failures in DNA preparation 655
managerial challenges for 655
scales, automation, and robust protocols 656
throughput and efficiency 656
progressive myoclonus epilepsy type 1 (EPM1) 1023ff
promoter 219, 221, 222
promoter/enhancer elements
functional analysis of 846, 847
promyelocytic leukemia (PML) protein 1008
proofreading 16
prosimians 554
proteasome 1016ff
protein C 1063
protein comparison
amino acid sequence comparison 556
electrophoretic comparison 555
immunological comparison 555
protein domains 454
protein family expansions 454
protein phosphatase 2A enzyme (PP2A) 1035ff
protein synthesis see mRNA translation 78
protein-coding sequences
indels in 524, 525
repeats in 524, 525
proteolysis 539, 995ff
proteome 453
prothrombin 1062
protozoan genomes 681
PS1 960
PS2 960
pseudogenes 252, 329, 529, 530
psoralen 790
public consortium 234
pulsed field gel (PFG) electrophoresis 679, 681
Purkinje cells 1000ff
q
quality assessment 653
quality of SGS clone library 653
quantitative traits 14
r
R. J. Britten 367
radiation hybrid mapping 495ff
radiation hybrid maps 679, 683
radiation hybrids 620
radiation mutagenesis 483
γ-radiation 483
ionising radiation 483
mechanism of mutagenesis 483
rate of mutagenesis 483
random Enu mutation 897
random insertion type 882
Subject Index

random mutagenesis 896
  retroviruses elements of 896
  transposable elements of 896
random SGS 655
Raoul Benveniste 367
rapid electrophoresis 653
RARE (RecA-assisted restriction endonuclease) cleavage 680, 684
rat 506, 507
  colocalization of SINEs in 535, 536
  different activity of SINEs in 534, 535
genomes 530, 532
  Shift in Substitution Spectra 519, 520
rat genome 503, 506, 507, 545
  assembly strategy 507, 510
  evolutionary hotspots of 520, 522
  features of 511, 522
  human disease gene orthologs 539, 544
  substitution rates 518, 519
  transcription-associated substitution 525, 526
rat lineage 519
  LINE-1 activity in 532, 534
rat-specific biology 537, 539
reactive oxygen species (ROS) 1022
rearrangement 213
  chromosomal 213, 562
  subchromosomal 562ff
recombinant inbred strain 865, 867
recombination 6, 36
  rate 566
reduced penetrance 1027
regions of increased gene expression (RIDGE) domains 255
regulation of development 376
regulator genes 30
  corepressors 31
  inducers 31
regulatory peptides 459
repeated DNA 368
RepeatMasker 649
Repetitive Sequences 656–657
  Classification of 656
  eukaryotic genomes 656
  simple and complex 657
replacement type vectors 879
  replication 211, 217, 218, 222
  replication forks 773
replication-competent adenovirus (RCA) 1120
replication-competent lentivirus (RCL) 1124
replication-competent retrovirus (RCR) 1123
replisome 19
reporter-function transgenes 837
repression 30
  repressible genes 30
research, biomedical 569
reshuffling of DNA segments 398
restriction endonucleases 397
restriction enzyme 606
  cleavage 687
restriction fragment length polymorphisms (RFLPs) 40, 395
retinal degeneration 1006ff
retinoblastoma protein (Rb) 221
retroposons 680
retroviruses 348
reverse genetics 483
reversed phase (RP) 1132
RGG box 1018
ribosomal protein 697, 698ff
ribosomal RNA 695, 702ff
ribosome 86
ribosome function 76, 78, 84, 86, 95, 97, 100–0104, 106, 110–112
  aminoacyl tRNA binding 97, 102
  chaperone binding 106
  decoding mRNA 76, 104
  elongation factor-G binding 104
  elongation factor-Tu binding 103
  fidelity 76, 78, 84, 86
  GTP hydrolysis 103, 104
  internal RNA entry site 110, 111
  peptide bond formation 100, 103
  peptide chain elongation 95, 100
  peptidyl-tRNA binding 97, 102
  proof reading 101
  ribosome inactivating proteins 112
  translocation 103, 104ff
  tRNA binding 97, 102
ribosome structure 76, 102–104, 106
  aminoacyl-tRNA binding site 102
  conformational change 103ff
  elongation factor-G binding site 104
  elongation factor-Tu binding site 104
  peptidyl-tRNA binding site 102
  tunnel 106
rice genomic data 651
Richard Goldschmidt 378
risk factors 958
RNA 223
  interference 223
RNA analog sugar 789
  2′-O-(2-aminoethyl) (AE) 789
  2′-O-Methyl (2′-OMe) 789
  Bridged Nucleic Acid 789
  Locked Nucleic Acid, LNA 789
RNA editing 22
RNA interference (RNAi) 31, 488, 865, 899, 900
RNA polymerase 219
RNA polymerase II transcription factor D (TFIID) complex 1009
RNA splicing 1003
RNA-induced silencing complex (RISC) 1019
RNP motif 1003
rodents medium-length duplications in 537
Ronald Ross 444
rRNA 216
RST microarrays
   Not I clone microarrays 627
RST microarrays 626ff
   CpG-Island 626
   CGI (CpG-island-containing) microarrays 626
RUNX2 1032
s
SAGA 1007
Sarich 364, 365ff
scaffold 305, 634, 657
SCID-X1 (severe combined immunodeficiency disease) 1124
\(\alpha\)-secretase 961, 965
\(\beta\)-secretase 961, 965ff
   active site motifs 966
   structure 966
\(\gamma\)-secretase 961, 965ff
second-order selection 399, 400
secondary crossover site 394
secretase inhibitors 976
segmental duplications 513, 515
segments, chromosomal 561
segregation 7, 36
selection 1061
   truncating 1061
self-organization 402
semiconservative replication 15
sequence consensus 592
sequence assembly 650, 656, 657, 658
   assembly process 658
   base caller 657
   computational filters 656
   contaminated reads 656
   electrophoresis-based instrument 657
   Lander-Waterman model 656
   low-quality reads 656
   Multiple estimators 650
   operating teams 656
   Phred-Phrap-Consed 657
   Repeats 658
   repetitive sequences 656
   Software Packages for 657
to define “repeats” 658
Validation of 650
sequence assembly software 657
   identifying different reads, and detect overlaps 657
sequence contigs 635, 654
sequence finishing 658, 660, 662
   better contiguity of a target sequence 658
   Clone Fingerprinting 662
   End-sequencing 660
   high-copy repeats 660
   low-copy repeats 660
   PCR-sequencing 660
   Physical Mapping 662
   Primer-walking 660
   Quality-related contig-breakers 660
   sequence contigs 660
   single-read coverage 660
sequence gap 635, 648, 650
sequence heterogeneity 664
sequence homology comparison 664
sequence quality control 648
   poor DNA preparation 649
   poor signal-to-noise ratio 649
   system contamination and malfunction 649
   wet-bench operation 649
sequence slippage 524
sequence-tagged connectors 597
sequence-tagged restriction site (STAR) 680, 688
sequence-tagged site (STS) 40, 606ff 680, 682
sequencing DNA 584
genome 583
shotgun 583, 588
sequencing data acquisition 654
   engine of SGS 654
sequencing reads 636, 637
   a parallel subcloning strategy 637
   stepwise primer-directed “walking” strategy 636
serine proteases 454, 1064
sex-limited 995
sex-linked inheritance 7, 11
SGS 641, 645, 655
clone library construction 645
clone sequencing 645
cloning 641
computing techniques 641
data analysis 645
Subject Index

libraries 652
Methodology 641
related technologies 643
sequence annotation 645
sequence assembly 645
sequencing 641
wet-bench operators 645
SH3 domains 1007
Sherman paradox 989
short interspersed repeating element (SINE) 680, 684
shotgun sequencing see SGS 635
signal transduction pathways 376, 380ff, 705
silencers 31
silent base substitutions 179, 181
simian immunodeficiency virus (SIV) 1124
single nucleotide polymorphism (SNPs) 450, 494
RFLP markers 608
single-copy DNA 367, 368
site-specific DNA inversion 394
site-specific recombination 394
SIX5 1024ff
slab-gel-based sequencers 640
slipped-strand mispairing 182
small fragment homologous replacement, SFHR 793
small indels 328
small ubiquitinlike modifier (SUMO) 999
SMRT (silencing mediator of retinoid and thyroid hormone receptors) 1002
solar radiations 176
somatic gene therapy 1117, 1118, 1125, 1129, 1133
clinical use of 1125, 1129
homologous recombination 1118
manufacture of 1129, 1132
regulatory aspects of 1129, 1132
SOS mutagenic repair 172
source DNA 653
gene heterogeneity of DNA samples 653
using pulse-field gel electrophoresis 653
southern blot hybridization 842
Sp1 998
spaghetti effect 1132
spatio-temporal expression pattern 865
species tree 559
speech impairment 567
spinal and bulbar muscular atrophy 988ff
spinalocerebellar ataxia 990ff
type 1 (SCA1) 1000ff
type 2 (SCA2) 1002ff
type 3 (SCA3) 1003ff
type 6 (SCA6) 1005ff
type 7 (SCA7) 1006ff
type 8 (SCA8) 1027ff
type 10 (SCA10) 1034ff
type 12 (SCA12) 1035ff
type 17 (SCA17) 1009ff
splicing control elements (SCEs) 251
spontaneous mutations 181, 390
generation mechanisms 181, 182
sporogenic developmental cycle 445
STAGA 1007
standard genetic sequence 174
strategies of genetic variation 389
strategies to map and sequence genomes 624ff
hierarchical 624
slalom 624
whole-genome 624
Streptococcus pneumoniae 341
STS see sequence tagged site
subtraction
Not I-CODE 623
subtraction procedures 622ff
Not I linking libraries 622
Not I subtraction see Not I-CODE Fig. 8 622
representational difference analysis 622
sulfation 1062
supF mutation reporter 790
suppressor mutation 7, 34
susceptibility genes 964
symbionts 343
symbiosis islands 344
symbiotic associations 400
synapsis 38
synonymous 505
synteny 453
tangles 959
TATA-binding protein (TBP) 1009
tau 959
biological role 969
hyperphosphorylation 969
isoforms 969
tautomer forms of 392
TBP-associated factors (TAFs) 1010
telomerases 11, 211ff, 511, 513, 1145
bridge-breakage-fusion 1145
dicentric chromosome 1145
telomerase 1145
test gene set 665
tetraploid 865, 885
theodicy 403
theory of molecular evolution 389, 400, 401
therapeutic approaches 977
TILLING 486ff
top-to-bottom strategy 567
training data sets 664
trans heterozygote 9
trans-lesion DNA-synthesis 176
transcription 20, 214, 219, 224
dysregulation 997ff
interference 995ff
transcriptome 694, 700, 703–705, 706ff, 707ff
transduction 343
bacteriophage 343
generalized 343
specialized 343
transfer RNA see tRNA
transformation 341, 397
competence 341
transformants 341
transgene 832, 835, 865, 869, 871, 894
design of 871, 876
expression of 843
gain-of-function 835, 837
inheritance of 843
loss-of-function 838
origin of 871, 873
reporter-function 837
structure of 871, 873
types of 835, 838
transgene donor 872
transgene expression 843
transgene integration
pattern of 842, 843
transgene recipient 872
transgenesis 492, 869, 871, 873, 876, 885
basics of 871, 879
biotechnological procedures in 876, 879
developments in 869, 870
pronuclear injection 876
rates of integration 492
refinements of 885, 894
regulatory elements of 873, 876
stable expression 492
technology of 871, 879
transient expression 492
transgenic fish 831–833, 856
application of 843, 854
as environmental biomonitors 852, 854
characterization of 842, 843
examples of 854
growth hormone 850
human disease modeling 848, 850
identification of 842
in basic research 844, 850
signaling pathways 847, 848
vertebrate developmental biology 845, 846
with different body color 851, 852
with resistance to pathogen infection 850, 851
transgenic mice 863, 971ff
apolipoprotein E transgenic mice 974
APP transgenic mice 971
in biomedical research 863, 900
presenilin 1/2 transgenic mice 972ff
tau transgenic mice 973ff
transgenic crosses 974ff
transgenic mosquitoes 461
transition 7, 33
translation 23
translocation 194
transmembrane regions 525
transposable element (TE) 7, 39, 215–217, 223, 224, 253, 328, 330
evolution of 532, 537
insertion of 178
transposition 213, 394, 395
transposons 39
transversion 7, 33, 177
treatments 975ff
tree
genealogical 560
phylogenetic 560
tricarboxylic acid pathways (TCA) 257
trinucleotide repeat expansion 988ff
triple helical DNA 787
triple helix–forming oligonucleotides 787
tRNA (transfer RNA) 76, 83, 84, 86, 101, 111
abundance 111
aminacylation 84, 86
anticodon loop 83ff
elongation factor Tu•GTP complex 86, 101
nomenclature 83
structure 83ff
trojan gene effect 855
tumor 1127
gene therapy of 1127
tumor necrosis factor (TNF) 1129
tumor therapy 1119
tumor therapy replication-competent adenoviruses 1119
tumor vaccination 1120
u
UAR 368, 369, 375ff
ubiquitin interaction motifs (UIMs) 1005
ultraviolet radiation 375
uniform average rate of genomic change 368
universality of the genetic code 397

V
vaccine 977
variable number tandem repeats 41
variation generator 396f
vascular endothelial growth factor (VEGF) 995

vector
BAC 343, 607, 609, 625
PAC 609, 625
parental vector 607
recombinant vector 607
YAC 609

vertical gene transfer 340
vesicular stomatitis virus (VSV) 840
Vincent Sarich 363
viral shuttles 898, 900
viral vectors 1123–1125
AAV (adeno-associated viral) vectors 1125
adenoviral vectors 1124
lentiviral vectors 1124
poxvirus vectors 1125
retroviral vectors 1123, 1124
virus-mediated transduction 397
vomeronasal receptors 537

W
West syndrome (WS) 1033
WG-SGS 639–640, 643, 654
contigs 654
Drosophila genome 639
genome survey sequence 643
Insect genomes 639
microbial genome, H. influenzae 639
mouse genome 640
ordered within scaffolds 654
rat genome 640
targeted genome sequences 643
working draft 643
WGS (whole-genome shotgun) 448, 505, 507, 635, 637
whole-genome shotgun sequencing 574f
Wilson 364, 381f
World Health Organization-directed worldwide Malaria Eradication Campaign 444
worldview 403

X chromosome 11
X-linked mental retardation (XLMR) 1033ff

Y chromosome 11
YACs (yeast artificial chromosomes) 680f, 687
yeast 213, 217, 222, 223, 704

Z
zebrafish development 472f
external development 473f
generation time 473
numbers of offspring 474
speed of development 472
transparency 473f
ZIC2 1032f
zinc finger 9 protein (ZNF9) 1025
zona pellucida 882