

Index

A

ACTA2, 333, 338, 340
AEC. *See* Apical epithelial cap
AER. *See* Apical ectodermal ridge
Aging
 dietary interventions, 429–431
 exercise interventions, 431–432
 parabiosis, 432–434
 prospects for study, 435–436
 stem cell
 life span extension and stem cell activity
 maintenance, 428–429
 potency loss, 428
 rejuvenation, 434–435
 tissue function loss, 427
aldh1a2, 93
alx4a, 113
AMPK, 429
and1, 93
ANGPTL4, 280
ANGPTL7, 280
AP1, 49, 51, 96–97, 165–166
Apc, 317
APC, 72–73
Apical ectodermal ridge (AER), 125, 129
Apical epithelial cap (AEC), 125–127, 130
Arid1a, 260, 263
ARX, 195, 199
Ascl1, 180, 182–183, 185, 412
Ask1, 48
ATF3, 356, 361–362
Atoh1, 317–318
Atoh7, 180
Autophagy, *Hydra* regeneration role, 28
Axin, 72
Axin2, 260
Axon regeneration
 axonal decisions
 cell body informing, 359, 361
 growth cone versus retraction bulb
 formation, 359
 axonal transport and translation, 365–366
 cell body decisions
 apoptosis versus survival, 361–362
 growth competence, 362–364

 history of study, 354–357
 inhibitory scar formation, 364–365
 membrane insertion of building blocks, 366
 models
 injury models in mammals
 in vitro, 358
 optic nerve, 358
 peripheral nervous system, 358
 spinal cord, 359
 invertebrates, 357–358
 zebrafish, 358
 overview, 353–354
 prospects for study, 366
5-Azacytidine, cell reprogramming, 411–412

B

Baf60c, 166
Baf180, 166
BAP, 55
BDNF, 363
 β -cell
 artificial cells, 203
 dedifferentiation, 198
 derivation from cultured stem cells, 200–201
 development, 194–195
 encapsulation devices, 202–203
 functional heterogeneity, 191, 195–196
 genetic kill switches, 202
 redifferentiation, 198
 reprogramming from other cells, 413–414
 synthetic gene circuits and lineage control
 networks, 202
trans-differentiation
 α -cells, 199
 exocrine cells, 199
 hepatocytes, 199–200
 overview, 198–199
bglap, 93
Blastema. *See* Digit tip regeneration; Limb
 regeneration; Zebrafish fin regeneration
blitzschnell, 8
BMP
 Hydra regeneration signaling, 32
 imaginal disc regeneration role, 51

Index

- BMP (*Continued*)
 regeneration diversity, 385
 zebrafish fin regeneration role, 95
Bmp2, 319
BMP2, 130, 132
Bmp4, 319
BMP4, 134, 283
BMP6, 278
BMP7, 129–130, 133, 308–309
BMP9, 132, 141
BRG1, 166
Brn2, 412
Broad, 52–53
Bronchoalveolar stem cell, 340–341
- C**
- Calcium signaling
 Drosophila gut regeneration, 77
 imaginal disc regeneration role, 46
Caloric restriction, aging studies, 429–430
Cardiomyocyte. *See* Heart regeneration
Cartilage regeneration, vertebrates, 382–383
CBP, 8, 411
CCL1, 280
CCL2, 280
CCL11, 434
CCL19, 320
CD34, 319–320
CD44, 333
Cdh, 261
Cdh1, 394
Cdk1, 264
Cdk1, 399
Cdk2, 394
C/EBP, 413
C/EBPa, 215
CFTR, 332
CGRP, 332, 341
CHD4, 7
chinmo, 53
Chronic myelogenous leukemia (CML), 220
Cic, 74
Ciliary marginal zone (CMZ), retina regeneration,
 174, 178–179, 181
CML. *See* Chronic myelogenous leukemia
CMZ. *See* Ciliary marginal zone
CNTF, 364
col10a1, 95
COL17A1, 289
COPD, 335
CREB, 33, 322, 385
CRISPR/Cas9, cell reprogramming, 410–411
- Crx, 185
CtBP, 53
ctgfa, 96
CTGFa, 364
Ctnnb1, 263
CTNNB1, 263
CXCL12, 215
CXCR4, 218, 300
cycE, 397
Cyclin A, 394
Cyclin B, 394
Cyclin D, 432
Cyp2e1, 259
CYP2E, 332
cyp26b1, 93–94
- D**
- Ddr-1, 7
Deer antler regeneration, 377
Dermal papilla. *See* Skin
DGC. *See* Dystrophin glycoprotein complex
Diabetes, types, 191–192
Diffuse large B-cell lymphoma (DLBCL), 220
Digit tip regeneration
 amputation in mice, 125–127
 blastema in mice
 cells
 characterization, 300–301
 origin, 298–300
 recruitment, 300
 types, 301–302
 overview, 298
 bone, 302–304
 limb development context, 306–308
 nail, 304–305
 overview, 297–298
 peripheral nerve, 305–306
 prospects for study, 308–309
Distal airway stem cell, 341
dkk1, 90, 92, 95
DKK1, 31
Dl, 72
DLBCL. *See* Diffuse large B-cell lymphoma
DLK, 358, 361
DLK-1, 359
DLL, 317
Dll1, 317
DLL1, 216
Dll4, 317
DLL4, 216, 244
dlx5a, 114
DNA damage response, 401–402

- dnfgr1*, 90
Dnmt3a, 215
Dpp, 64, 74, 76–77
DPP, 49
DRONC, 49
Drosophila. See Imaginal disc regeneration; Insect gut regeneration
DUOX, 75, 77
DYRK1A, 197
Dystrophin glycoprotein complex (DGC), 161–162
- E**
- E2F1*, 397
E2F7, 397
E2F8, 397
E47, 215
ECM. See Extracellular matrix
EcR, 64
EDN1, 286
EGF, 413
EGFR, 7, 74–75, 398
Egr-1, 215
Elf4, 217
Embryonic stem cell
 derivation, 407–408
 nuclear transfer, 408
EMT. See Epithelial-to-mesenchymal transition
Endomitosis, 394
Endothelial cell
 reprogramming from other cells, 414
 skeletal muscle regeneration, 244
EphA5, 194
Epidermal stem cell
 cell competition, differentiation,
 and turnover, 289
 growth balancing with differentiation, 287–288
 overview, 286
 protection, 288
 stress response, 288
 stretching and growth, 288–289
 wound healing, 290
Epithelial-to-mesenchymal transition (EMT), 8
ErbB2, 162
ERG, 219
Erk, planarian regeneration signaling, 14
Evi-1, 217
Exercise, aging interventions, 431–432
Extracellular matrix (ECM)
 cardiomyocyte proliferation capacity, 159
 Hydra regeneration role, 28, 34
 limb regeneration role, 125, 128, 133
 liver regeneration remodeling, 256–257
 planarian regeneration role, 7
- F**
- FAH, 255, 260, 274
Fak, 401
FAPs. See Fibroadipogenic progenitors
Fate-specific transcription factors (FSTFs), planarian
 regeneration, 3, 6
FGF1, 125
FGF2, 125, 129–130, 132, 176
FGF4, 125, 130
Fgf5, 281
FGF7, 290
Fgf8, 102–104, 109
FGF8, 125, 129–132, 134
FGF10, 125, 131, 290
fgf10a, 92
FGF18, 278, 283
FGF20, 131
fgf20a, 90, 92, 96
FGFR
 Fgfr1, 281
 FGFR1, 14
 Fgfr2, 281
 zebrafish fin regeneration role, 90
FGFRL proteins, 10
Fibroadipogenic progenitors (FAPs), skeletal muscle
 regeneration, 244–245
Fin regeneration. See Zebrafish fin regeneration
FK506, 110–111
Flnc, 240
Flt3, 216
follistatin, 13
FOX1, 332
Foxa1, 413
Foxa2, 413
FoxA2, 113, 116
FOXA2, 195
Foxa3, 413
Foxl1, 319
FoxO, 28
Foxo3a, 215
FSTFs. See Fate-specific transcription factors
Zr, 394, 397
- G**
- gadd45*, 96
Gadd45, 48
Gal4/UAS system, imaginal disc regeneration studies,
 45–46
GAP43, 356

Index

- Gastrin, 199
gata4, 155
GATA6, 290
GcgR, 193
G-CSE, 218
GDF11, 434
Germline stem cell (GSC), aging effects, 429–430
GFAP, 305
Gli1, 319–320
GLP-1, 195
GLP-1R, 193, 200
GLUT2, 195, 198
GLUT2, 197
Grem1, 319
Gs, 259, 261
GSC. *See* Germline stem cell
GSK3, 363
GSK-3 β , 31
Gut regeneration. *See* Insect gut regeneration;
Intestinal regeneration
GVHD, 217–218, 221, 321–322
- H**
- Hair follicle stem cell (HFSC)
immune cell interactions, 283–284
melanocyte stem cell coordination, 284
niche, 278–280
overview, 278
stress response, 286
transit-amplifying cell, 278, 280–281, 284
Hamp2, 261–262
hand2, 114, 155
Harmine, 197
HAS-7, 31
HDAC5, 361
Heart regeneration
animal model differences in capacity, 155
cardiomyocyte
induction from other cells, 413
maturation, 155–156
metabolism, 158–159
ploidy, 156–158, 399–400
proliferation
chromatin dynamics, 164–167
signaling pathways, 159–164
sarcomere complexity, 159
telomere length, 159
history of study, 154–155
overview, 153–154
prospects for study, 167
Hematopoietic stem cell (HSC)
aging interventions
diet, 430
exercise, 432
bone marrow transplantation, 212–213
cell therapy, 217–222
dormancy, 213–215
history of study, 211–212
proliferation, 215–217
prospects for study, 222
reprogramming from other cells, 414
Hepatocyte
 β -cell *trans*-differentiation, 199–200
induction from fibroblasts, 413
lineage plasticity, 262–263
liver regeneration. *See* Liver regeneration
Hepatocyte growth factor (HGF), 257, 263
Hes1, 317
HFSC. *See* Hair follicle stem cell
HGF. *See* Hepatocyte growth factor
HIF-1, 215
HIF-1 α , 136
Hippo, 74–76, 160, 258, 397
Hnf1 α , 413
Hnf4 α , 413
House dust mite, lung injury, 337
Hox, 9–10
HOXA5, 219
HoxA9, 102
HOXA9, 219
HoxA10, 116
HOXA10, 219
HoxA11, 116
HoxA13, 102, 105
HOXB4, 217
HoxD11, 116
HSC. *See* Hematopoietic stem cell
HSF1, 411
Hydra regeneration
autophagy role, 28
bisection studies
asymmetric injury
reactive oxygen species signaling, 33–34
somatic tissue transformation into head
organizer, 33
extracellular matrix remodeling, 34
epithelial cells in development, 27–28
extracellular matrix role, 28, 30
history of study, 23–25
organizer centers
dynamic modeling, 30–31
foot organizer components, 31–32
head organizer
components, 31
transplantation studies, 30

- overview, 29–30
 - prospects for study, 34–35
 - stem cells
 - cell death sensitivity of epidermal stem cells and interstitial stem cells, 27
 - G2 pausing, 26–27
 - populations and regulators in central body column, 25–26
- I
- IBD. *See* Inflammatory bowel disease
 - Idh3b, 135
 - IFN- γ , 239, 291, 322
 - IGF1, 239, 290, 363, 413
 - IGF2, 162
 - igf2b*, 90
 - Igfbp2*, 262
 - IL-4, 322
 - IL-6, 215–216, 257, 322
 - IL-10, 239, 322
 - IL-13, 322
 - Il13ra1*, 338
 - IL-22, 321–322
 - IL33*, 320
 - IL-33, 239
 - Ilp8*, 51
 - Ilp8, 55
 - Imaginal disc regeneration
 - damage-responsive enhancers and regenerative capacity, 51–53
 - early events, 46–51
 - genetic tissue-ablation systems, 45–46
 - history of study, 42, 44–45
 - overview, 41–43
 - plasticity and repatterning, 53–55
 - prospects for study, 55
 - transdetermination, 44
 - Induced pluripotent stem cell
 - aging rejuvenation, 434–435
 - derivation from fibroblasts
 - Klf, 409
 - LIN28, 409
 - Myc, 409
 - Nanog, 409
 - overview, 408
 - Pou5f1*, 408–409
 - Sox, 409
 - transgene expression, 409–410
 - disease modeling, 415–416
 - neuronal lineage reprogramming, 412
 - regenerative medicine, 414–415
 - tissue engineering, 419, 436
 - Inflammatory bowel disease (IBD), 314, 322–323
 - Influenza, 337, 341
 - INS1*, 200
 - INS2*, 200
 - Insect gut regeneration
 - Drosophila* studies
 - digestive tract development, 64–65
 - epithelial maintenance and regeneration, cellular dynamics, 67–68, 71
 - interorgan communication, 77–78
 - intestinal stem cell
 - aging, 430
 - intrinsic functions during regeneration, 77
 - pool size regulation, 71
 - midgut cell types and compartmentalization, 65–67
 - signaling mechanisms
 - components, 69–70
 - EGFR, 74–75
 - Hippo/Warts/Yorkie, 75–76
 - JAK/STAT, 73–74
 - JNK, 75
 - Notch, 71–72
 - p38 MAPK, 75
 - Wnt, 72–73
 - Lepidoptera, 78
 - mosquito, 78
 - overview, 63–64
 - polyploidy, 397
 - prospects for study, 79
 - Insulin receptor, 162
 - Intestinal regeneration
 - cell composition, 314
 - dedifferentiation pathways, 316
 - epithelial renewal, 315
 - gut microbiome role, 322–323
 - immune system activation, 321–322
 - innate lymphoid cells, 321–322
 - intestinal stem cell niche
 - mesenchymal cells
 - injury studies, 320–321
 - organoid coculture, 320
 - overview, 318–320
 - signaling
 - Notch, 317
 - organoid studies, 317–318
 - Paneth cells, 318
 - Wnt, 315, 317
 - overview, 313–315
 - prospects for study, 323–324
 - Intestinal stem cell. *See* Insect gut regeneration; Intestinal regeneration
 - Islet. *See* Pancreas
 - Islet1, 180

Index

J

JAG1, 263

JAK/STAT

axon regeneration, 363–364

Drosophila gut regeneration signaling, 73–74

imaginal disc regeneration role, 48–51, 54–55

skin signaling, 282

JIP3, 361

JNK

Drosophila gut regeneration signaling, 71, 75

imaginal disc regeneration role, 48–51, 54–55

K

Keratin. *See also specific KRTs*

epidermal stem cell protection, 288

K5, 300, 304

K6, 278, 283

K14, 300, 304

Keren, 65, 74

KITL, 286

KLF, 362

Klf4, 180, 409

KLF4, 362–363

Klf5, 409

KLF6, 362

KLF7, 362

KLF9, 362

Kmt2d, 260

Krt4, 332, 338

KRT5, 330, 333, 341–342

KRT8, 342

Krt13, 332, 338

KRT13, 332

KRT14, 330, 341

KynA, 51

L

LC3A, 28

LCOR, 219

LDHA, 198

lef1, 90, 92

Lens regeneration, amphibians, 384

Lepidoptera, gut regeneration, 78

LEPR, 432

let7, 180

Lgr4, 260

LGR4, 317

Lgr5, 260, 315, 317–318, 320

LGR5, 317

Lgr6, 304

Lhx2, 182

lhx9, 113

LIF, 199

Limb regeneration

digit tip. *See* Digit tip regeneration

overview in vertebrates, 123–125

promotion

biochemical pathway target interventions,
129–133

bioelectric interventions, 137–141

blastemal transplantation, 125

cell membrane potential manipulation,
135–137

digit tip amputation in mice, 125–127

extracellular matrix grafting, 125, 128–129

fibroblast role, 126, 128

mechanisms, 141–143

porcine small intestinal mucosa scaffold, 128

wound covering, 127

salamander. *See* Salamander limb regeneration

transgenic mice studies, 133–135

Lin28, 135, 180, 183, 185

Lipopolysaccharide (LPS), lung injury

model, 336–337

Liver regeneration

cancer risk association, 263–264

cell heterogeneity in homeostasis, regeneration,
and disease, 258–260

cellular contributions to homeostasis and
regeneration, 260–262

cholangiocyte lineage plasticity, 262–263

genetic regulation, 256–258

hepatocyte

induction from fibroblasts, 413

lineage plasticity, 262–263

liver function and organization, 253–254

principles, 254–256

prospects for study, 264–265

Lmnb2, 157–158

Lmx1b, 104, 113

LPS. *See* Lipopolysaccharide

LTF, 333

Lung regeneration

anatomy, 330

cell types, 330–333

large airway regeneration, 337–340

models of injury repair and regeneration

biological agent injury, 336–337

chemical injury, 333, 335–336

overview, 333–335

pneumonectomy, 337

radiation injury, 337

overview, 329–330, 382

prospects for study, 343

small airway epithelial stem cells, 340–343

- LYZ, 333
LZK, 361
- M**
- MAFA, 198–199
MAFB, 195, 198
MAPK. *See also* JNK; p38 MAPK
 Hydra regeneration signaling, 33–34
 pancreatic cell reprogramming, 414
MC1R, 286
McSC. *See* Melanocyte stem cell
MCT4, 198
mdka, 96
Mef, 217
Meis1, 105, 109, 114
Meis1, 215
Melanocyte stem cell (McSC)
 hair follicle stem cell coordination, 284
 overview, 284
 stress response, 285–286
 ultraviolet radiation response, 284–285
Membrane potential, limb regeneration studies,
 135–137
Mesp1, 243
Mfsd2a, 261
MG. *See* Müller glia
MicroRNA
 neuronal lineage reprogramming, 412
 regeneration roles, 386
Miro, 365
Missing tissue response (MTR), planarian
 regeneration, 2, 8, 13, 15
MKK4, 260
MLLT3, 217
Mmp1, 52
Mmp9, 95, 256
MNX1, 195
Morphallaxis, 34
Mosquito, gut regeneration, 78
MRF4, 238
MS2, 411
Msx1, 113
Msx1, 134, 136, 307
Msx2, 134, 307
mTOR, 356, 363–364, 398, 429–430
MTR. *See* Missing tissue response
MUC5AC, 332
MUC5B, 332–333, 338
Müller glia (MG), retina regeneration, 176–177,
 180–185
Muscle regeneration. *See* Heart regeneration; Skeletal
 muscle regeneration
Myc, 49, 397
MYC, 263
Myo1D, 49
Myocardial infarction. *See* Heart regeneration
myoD, 13–14
MyoD, 238, 411, 413
Myogenin, 238
MyoIA, 66
Myomaker, 239
Myomerger, 239
Myt11, 412
- N**
- NAFLD. *See* Nonalcoholic fatty liver disease
Nanog, 409
NBL1, 32
Ndufb3, 135
Ndufb8, 135
Neoblast. *See* Planarian regeneration
Nephronectin, 282
Nerve regeneration. *See* Axon regeneration;
 Digit tip regeneration
NEUROD1, 195
Neurokinin A, 386
Neuron, lineage reprogramming, 412–413
NF- κ B, 94, 215
Ng2, 320
NGFR, 330
NGN3, 198–199
NICD1, 338
NKX2.2, 195, 200
nkx2.5, 155
NKX6.1, 195–196, 198, 200
Nonalcoholic fatty liver disease (NAFLD), 254, 264
Nonperiodic regeneration
 blastema, 377–378
 dedifferentiation, 378
 overview, 376–377
Notch, 71–72, 163, 198
NOTCH, 263
Notch2, 338
notum, 13
NPY, 195
NR5A2, 197
NRG1, 160, 162
Nrg-1, 8
Nrg-7, 7
Nrl, 185
NuRD, 7–8, 96
- O**
- Oct4, 409
OCT4, 363

Index

- Olfm4*, 320
Optic nerve, injury models, 358
OSM, 306
Osteoblast, fate in zebrafish fin regeneration, 93–95
Otx2, 180, 185
Ovalbumin, lung injury, 337
- P**
- p38 MAPK
 Drosophila gut regeneration signaling, 75
 imaginal disc regeneration role, 48
p53, 179, 286, 401
p65, 411
p300, 411
Pancreas
 cell reprogramming from other cells, 413–414
 islet
 cell–cell contact, 194
 histology, 192–193
 hormones, 193
 intra-islet communication, 193
 vasculature and nerves, 193–194
 regeneration. *See also* β -cell
 endocrine pancreas, 197–198
 exocrine pancreas, 196–197
 prospects for study, 203
Pancreatic polypeptide (PP), 193
Paneth cell, intestinal stem cell niche, 318
Parabiosis, youth restoration to aged
 tissues, 432–434
Parkinson's disease, regenerative medicine, 415
PAX4, 195, 199
Pax6, 180, 182
Pax7, 113, 116
Pax7, 243, 246
PCGs. *See* Position control genes
PCNA, 399
PDGF, 200, 306
Pdgfra, 319–320
PDGFR α , 246
Pdha1, 135
Pdm1, 72
PDX1, 195–196, 198–200
Periodic regeneration
 deer antler regeneration, 377
 endometrium, 374–375
 invertebrates, 375–376
 overview, 374
Pfkp, 135
PGP9.5, 332
Pitx2, 243
Plkd1, 260
Planarian regeneration
 neoblast
 fate specification, 3, 5
 pluripotency, 5–8
 source of new cells, 2–3
 specialized neoblasts, 4
 overview, 1–2
 positional information
 muscle role, 11–12
 neoblast fate studies, 14
 position control genes, 11–15
 reestablishment of pattern, 14
 resetting
 regeneration requirement, 13–14
 wound signaling, 12–13
 scaling, 12
 tissue turnover and regeneration
 control, 8–11
 prospects for study, 14–15
 stem cell response to injury, 8
Plant regeneration
 conservation of strategies, 385
 mammalian comparison, 381
 meristems, 380
 overview, 378, 380
PlexA, 50
PMA1.2, 136
pola2, 109–110
Polyploidy
 cardiomyocyte, 156–158, 399–400
 generation of cells, 394
 genotoxic stress interplay, 401–402
 heterogeneity and diversity, 398–399
 mechanical force as driver, 400–401
 organ size maintenance, 395–398
 overview, 393–394
 prospects for study, 402
 tissue mass restoration, 395–398
POMC, 286
PORCN, 317
Position control genes (PCGs), planarian
 regeneration, 11–15
Positional memory. *See* Planarian regeneration;
 Salamander limb regeneration
Pou5f1, 408–409
PP. *See* Pancreatic polypeptide
PP1R1A, 195
PRC2, 52
Prod1, 95, 105, 109, 114–115
Prostaglandin E2, 216
Ptbp1, 185
PTEN, 356, 361, 363, 365
PTF1A, 197
PU.1, 215

PVF2, 76
PW1, 245–246

R

RA. *See* Retinoic acid
Rab5, 394
Rab11, 394
RAG, 362
rarb, 109
Rax, 182
Reactive oxygen species (ROS)
 Hydra regeneration signaling, 33–34
 imaginal disc regeneration role, 46, 48–50
Regeneration-organizing cell (ROC), 384
Regeneration-response enhancer (RRE), 386–387
Restricted regeneration
 amphibians, 378
 overview, 378–379
Retina regeneration
 anatomy, 173–174
 development, 173–174
 fish and amphibian studies
 functional circuit generation, 181–182
 retinal cell types, 179–180
 history of study, 174–175
 neuron sources
 ciliary marginal zone, 174, 178–179, 181
 Müller glia, 176–177, 180–181
 retinal pigment epithelium, 175–176,
 180–181
 promotion in Müller glia, 182–185
 prospects for study, 186
Retinoic acid (RA), 162, 386
Robo, 50
ROC. *See* Regeneration-organizing cell
ROS. *See* Reactive oxygen species
RRE. *See* Regeneration-response enhancer
Rspo1, 319
R-spondins, 317, 320
RUNX, 219
runx2, 93–94

S

Salamander limb regeneration
 development versus regeneration, 102–104
 model features and strengths, 102
 overview, 101–102, 382
 positional memory
 cell types, 111
 confrontation between memories, 107–109
 embryonic information passing to adults,
 113–114

 experimental manipulation, 109–111
 humans, 116–117
 maintenance in adults, 114
 molecules, 105
 overview, 104
 patterning connection models, 111–113
 patterning gene expression, 114
 patterning information, 105–107
 positional codes
 body-wide compatibility, 115
 conservation, 115
 quantification, 114
 regeneration termination, 114–115
 therapeutic application, 116
 prospects for study, 117
SAPK, 257
Satellite cell. *See* Skeletal muscle regeneration
Sca1, 315
Sca1, 246
SCF, 216
SCGB1A1, 332, 340
SCGB3A1, 332
Schwann cell precursor, 132
Scl, 215
Sd, 76
SDF-1, 215, 300
Sdha, 135
Serpent, 64
Serpine1, 163
Shaggy, 72
Shh, 104, 109, 113, 115–116
Shh, 125, 131, 385
SHH, 280, 291
Skeletal muscle regeneration
 cell types in regeneration
 endothelial cells, 244
 fibroadipogenic progenitors, 244–245
 nonsatellite progenitors, 245–246
 degeneration and inflammation, 236, 238
 diversity of regeneration
 muscle group and associated satellite cells,
 241–244
 stimulus, 241
 exercise and muscle stem cells, 432
 immune myogenic cross talk, 239–240
 muscle repair mechanisms across
 species, 234
 myocyte induction from other cells, 413
 myofiber maturation, 240
 overview, 233–234, 236–237
 prospects for study, 246
 satellite cell activation, differentiation, and fusion,
 238–239

Index

Skin

- cell types and niches, 276, 278
- development, 275–276
- environmental response, 282–283
- epithelial–mesenchymal interactions
 - adipocytes and dermal sheath, 281–282
 - dermal papilla, 280–281
- glossary of terms, 277
- immune cells, 283–284
- organ connectivity, 282
- regeneration overview, 381–382
- stem cells. *See* Epidermal stem cell;
Hair follicle stem cell;
Melanocyte stem cell
- vascular interactions, 283
- wound healing. *See* Wound healing

Slit, 10, 50, 72

SMAD4, 215

SOCS, 73

SOCS3, 364

SOX1, 362

SOX2, 363, 409

Sox9, 260

SOX9, 198

Sox11, 356

SOX11, 362

SP. *See* Substance P

Sp5, 31

Sp7, 95

SPG. *See* Subperineural glia

SPI1, 219

Spinal cord, injury models, 359

Spitz, 65, 74

SPRR1a, 356

STAT3, 356, 362, 414

Streptozotocin (STZ), 197

STRIPAK, 12

STZ. *See* Streptozotocin

Subperineural glia (SPG), 399

Substance P (SP), 386

SUR2, 195

SWI/SNF, 166

SYT4, 195

T

TAC. *See* Transit-amplifying cell

Talin, 401

TAZ, 257, 289, 343

Tbx3, 289

tbx5a, 155

TCE, 31

TCE, 317

Tcf15, 215

Tcf17l2, 317

TEAD, 76, 166

TEP. *See* Transepithelial potential

Tet2, 215

TFF2, 333

Tgfb1, 258

TGFBR2, 215

TGF- β , 179, 215, 239, 281, 342–343

TH. *See* Thyroid hormone

th2, 378

Thymosin β 4, 131–132

Thyroid hormone (TH), cardiomyocyte proliferation
studies, 163–164

Tig1, 105, 109, 114

Tissue engineering, cell reprogramming
applications, 419

TNF- α , 215, 257

Tnni3k, 157, 400

TNSF14, 320

TP63, 330, 333, 340–342

tph1b, 93

TPO, 216

TRACS. *See* Transient regeneration-activating
cell state

TRAK, 365

Transepithelial potential (TEP), limb regeneration
studies, 135–136

Transient regeneration-activating cell state
(TRACS), 384

Transit-amplifying cell (TAC), 278, 280–281, 284

T regulatory cell, hair follicle stem cell
interactions, 283

TREM2, 283

TSC2, 363

TSP, 33

TSPAN-1, 5–6

Ttk69, 72

TUBB4, 332

Twist2, 246

U

UCN3, 195

ULK1, 28

Upd2, 73, 75

Upd3, 51, 73, 75

UPK3a, 340

V

VEGF, 395

Vegfa, 162

VEGFA, 194, 244

Vein, 74

- Vitamin D
 cardiomyocyte proliferation studies, 164
 hematopoietic stem cell renewal, 217
VP64, 411
Vsx2, 182
- W**
- Warts, *Drosophila* gut regeneration signaling,
 75–76
Wg, 49, 51, 64, 72–73
WIPI2, 28
WISP-1, 322
Wls, 320
WLS, 317
Wnt
 digit tip regeneration role, 304–305
 Drosophila gut regeneration signaling, 72–73
 Hydra regeneration role, 31, 33
 imaginal disc regeneration role, 51
 planarian regeneration role, 9–10, 12–14
 skin signaling, 281, 283
 zebrafish fin regeneration role, 90, 92
Wnt2b, 319
WNT2b, 320
Wnt3a, 131–132
WNT3a, 320
Wnt5a, 319
Wnt5a, 131
Wnt7a, 103
Wound healing
 cell formation after large wounds, 291
 epithelial–immune cell interactions, 290–291
 overview, 290
 stem cell behavior, 290
- X**
- XIRP1, 240
- Y**
- Yap, 160, 167
YAP, 263
YAP, 257, 291, 322, 343
YAP1, 289
Yap5SA, 161, 166
Yorkie, 49, 75–76, 397
Ythdf2, 215
- Z**
- Zebrafish fin regeneration
 blastema organization and formation, 91–93
 caudal fin model features, 88–89
 epigenetics, 96
 osteoblast fate, 93–95
 overview, 87–88
 prospects for study, 97
 wound healing, 89–90, 92
Znhit1, 215