## Index

A	В
Actomyosin, cleavage furrow ingression, 150-153	BAF, 188
AICAR. See Aminoimidazole carboxamide ribonucleotide	Bfa1, 88
ALIX, 157	BLM, 60-62
Aminoimidazole carboxamide ribonucleotide	Boveri, Theodor, 4, 67
(AICAR), 179	BRCA1, 90, 169
Ana2, 74–76, 89	Bub1, 138, 140, 176–177, 191
Anaphase	Bub3, 140, 168
chromosome dynamics, 53–54	BUBR1, 23, 168-169, 178
overview, 3	
sister chromatid separation and dynamics, 60	C
Anaphase-promoting complex (APC)	C
activation, 18, 22	CAK. See Cdk-activating kinase
discovery, 7–8	CALK, 84
ubiquitin ligase activity, 21-22	CAP350, 78
Aneuploidy	CBB, 89
effects	CBF3, 131
cell fitness, 171	CCDK. See Cyclin-dependent kinase
genome stability, 172-174	CDC10, 8
health, 165–166	Cdc14, 24, 87
transcription and protein composition, 171-172	CDC20, 22–23, 168
molecular mechanisms	Cdc25, mitosis entry role, 16–18
cohesion defects, 170-171	Cdc31, 71
merotelic attachments, 169-170	cdc mutants, history of yeast cell cycle studies, 6–7
spindle assembly checkpoint defects, 168-169	Cdk-activating kinase (CAK), mitosis entry role, 16
overview, 166	Cdk2, 72–73
prospects for study, 179–180	CDKRAP2, 81
therapeutic targeting, 178–179	Cell cycle <i>cdc</i> mutants, history of yeast cell cycle studies, 6–7
tolerating mutations, 174–175	overview of phases, 1–2
tumorigenesis	CEN3, 8
driver, 175–177	CENP-A
inhibition, 177–178	assembly
Anillin, 152	constitutive centromere proteins in assembly, 117–118
APC	HJURP chaperone, 115–116, 133
anaphase-promoting complex. See	Mis18 complex, 117
Anaphase-promoting complex	overview, 114–116
tumor suppression, 177–178	centromere longevity and CENP-A maintenance during
Arf6, 154	DNA replication, 119–121
Arp2/3, 193	centromere protein recognition of CENP-A chromatin,
ASE1, metaphase spindle function, 41	111–112
Asl, 79, 89	depletion studies, 111
ASPM, 90	functional overview, 9–10, 105
Aurora A	histone H3 comparison, 108
cilium cycle role, 84	nucleosome
mitosis entry role, 19–20	deposition at centromeres, 131–133
Aurora B	distribution during DNA replication, 120
anaphase function, 60	structure, 105–108
cytokinesis role, 150	prospects for study, 121
kinetochore regulation, 138–139	CENP-B box, 111

## Index

CENP-C, 111–112, 117–118, 121, 134	merotelic attachments, 169–170
CENP-E, 137, 140	overview, 166
CENP-H, 113, 118-119	Chromosomal passenger complex (CPC), 191-192, 194
CENP-N, 108, 111-112, 119, 121	Cilia, assembly and disassembly cycle, 82-94
CENP-S, 109, 119, 133	CIN. See Chromosomal instability
CENP-T, 109, 113, 119, 121, 133-135	CIT-K. See Citron kinase
CENP-U, 113	Citron kinase (CIT-K), 152-153, 156
CENP-W, 109, 119, 133	CLASP, 38, 138, 150, 169
CENP-X, 109, 119, 133	C-Nap1, 78-79
Centriole	CNN, 80-81
assembly	Cnp1, 9
cartwheel structure, 73–75	Cohesin
elongation, 77–78	functional overview, 12
Plk4 role, 73, 75–77	meiosis and stepwise removal, 190–191
species comparison, 74	prophase condensation and cohesin release from
asymmetry and cell fate decisions, 88–89	chromosome arms, 58–59
duplication cycle, 72–73	sister chromatid adhesion in S phase, 55–57
structure, 72	subunit organization, 54–55
Centromere. See also CENP-A	
CENPs	Common fragile site (CFS), 61
architecture, 109–110	Condensin
CENP-B box, 111	condensin I function, 59–60, 62
interactions, 111–112	condensin II function, 57–58
composition, 112–113	cytokinesis and chromosome segregation
epigenetic nature, 105–107, 131	coordination, 62
functional overview, 103–104	prophase condensation and cohesin release from
histone modifications, 108–109	chromosome arms, 58–59
history of study, 8–9, 103	subunit organization, 54–55
longevity and CENP-A maintenance during DNA	CP110, 77–78, 83
replication, 119–121	CPAP, 75, 77–78, 90
prospects for study, 121	CPC. See Chromosomal passenger complex
	CREST syndrome, 105
Centrosome asymmetry and cell fate decisions, 88–89	CUEDC2, 169
control center activity, 84–86	Cut2, 8
disengagement of mother–daughter linkage, 81–82	Cut12, 84–86
disjunction at G2/M, 78–79	Cyclin A, mitosis entry role, 18
duplication cycle, 68	Cyclin B. mitosis entry role, 16–19
÷ .	Cyclin-dependent kinase (CDK)
history of study, 67, 69	history of study, $6-7$ , $11$
pericentriolar material assembly, 79–81	kinetochore regulation, 138
spindle pole body similarity, 69 structure, 68	meiosis, 186
	mitosis entry role, 16–19
Cep55, 157	Cyclosome. See Anaphase-promoting complex
CEP67, 120	Cytokinesis
CEP63, 90 Cep83, 83	chromosome segregation coordination, 62
	cleavage furrow ingression, 150-153
Cep89, 83	defects and disease, 157-158
Cep97, 78, 83	division plane positioning, 147–150
CEP120, 77	membrane formation and composition, 153-155
Cep135, 75	midbody dynamics, 155-157
Cep152, 75, 79, 90	overview, 147–148
Cep164, 83	prospects for study, 158
Cep192, 76, 79, 81	
CEP290, 77	
CFS. See Common fragile site	D
Chk1, 86, 90	
CHMP4 proteins, 157	Dam1, 136
Chromosomal instability (CIN). See also Aneuploidy	DSCR1, 178
cohesion defects, 170–171	Dynein, metaphase spindle function, 39–40
measurement, 166–168	DYRK1A, 178

E	Kinesin-14, metaphase spindle function, 41
EB1, metaphase spindle function, 37–38	Kinetochore
Eg5, 79	assembly, 133-135
ENSA, mitosis exit role, 24	centromere association, 103-104, 131-133
ESCO1, 55	components, 133
ESCO2, 55	composition, 112–113
ESCRT complexes, cytokinesis role, 156–158	DNA segregation, 129–131
1 ,	force generation, 136–138
	regulation
F	microtubule binding, 138-140
Fa1, 83	spindle assembly checkpoint signaling,
Fa2, 83	140-141
FANCD2, 61–62	spindle microtubules
FANCI, 62	binding, 135–136
FBF1, 83	dynamics, 137-138
Fbxw5, 77	Klo10A, 77
Fin1, 85	KLP-19, 193
FIP3, 154	KNL, 140
FIP4, 154	KNL1, 113
Flemming, Walther, 2–4, 103	KNL2, 117
FOP, 78	,
, / -	
	L
G	LIS1, 40
$\gamma$ -Tubulin ring complex ( $\gamma$ -TuRC), spindle pole body, 69–70	Lte1, 88
γ-TuRC. See γ-Tubulin ring complex	
GOLPH3, 154	
GOLI 113, 134	M
	Ma31, 140
Н	Mad1, 140, 176
HDAC6, 83	Mad2, 140-141, 168-169, 176-177
HDAC8, 55	Maize, history of chromosome studies, 4-5
HEC1, 176	Maturation-promoting factor (MPF), history
HEF1, 79, 83–84	of study, 6–7
Histone H3, CENP-A comparison, 108	MCAK, 170–171, 191
HJURP, 108, 115–118, 133	MCAK. See Mitotic centromere-associated kinesin
HP-1, 9	MCC. See Mitotic checkpoint complex
HRAS, 177	McClintock, Barbara, 4–5
hSav1, 79	MCPH1, 57-58, 90
HSET, 179	MCRS1, 38
HURP, 191	Meiosis
110Ki, 191	acentrosomal spindle formation, 191–192
	asymmetric division of oocytes, 192–193
K	cell cycle control, 185–186
K-RAS, 177	chromosomal segregation, 188–191
Karl, 71	cohesin stepwise removal, 190–191
KIF4, 59	
KIF4A, cytokinesis role, 149–150	pairing and recombination, 186–188
•	postrecombination events, 188
KIF14, 156	sister chromatids, monopolar attachment in meiosis I
KIF20A, cytokinesis role, 149	188, 190
KIF23, cytokinesis role, 149–150, 152, 156–157	spindle assembly checkpoint, 194
KIF2B, 170–171	spindle–chromosome interactions,
Kin4, 87–88	193–194
Kinesin-4, metaphase spindle function, 38–41	MEN, 87–88
Kinesin-8, metaphase spindle function, 36	MET, 177
Kinesin-13	Metaphase
kinetochore regulation, 138	chromosome dynamics, 53-54
metaphase spindle function, 35–38	overview, 3

Index

Metaphase spindle	r
assembly modeling in Xenopus extracts, 41-42	P53, 175, 177, 180
forces and functions	Patronin, metaphase spindle function, 38
ASE1, 41	PCM. See Pericentriolar material
dynein, 39–40	PCM1, 84
kinesin-4, 38-41	Pds1, 8
kinesin-14, 41	Pds5, 56
overview, 39	Pericentriolar material (PCM), assembly, 79–81
PRC1, 41	PICH, 60–61
microtubules	Plk1
amplification, 34	anaphase role, 60
depolymerases, 35-37	centrosome function, 81–82
dynamics, 35	cilium cycle role, 84
minus end stabilizers, 38-39	cytokinesis role, 157
nucleation, 32-34	kinetochore regulation, 138
plus end	mitosis entry role, 18–19
dynamics, 35	pericentriolar material assembly, 81
tracking proteins, 37–38)	Plk4
severing, 34–35	centriole assembly role, 73, 75–77
organizers, 32	pericentriolar material assembly role, 79
prospects for study, 44	PLK4, 170
size control and scaling, 42–44	Plo1, 18, 84–86
MgcRacGAP, 118, 154	POC5, 77
Microcephaly, defects in division symmetry, 89–90	PP1
Microtubule. See Metaphase spindle	inhibition studies, 20–21
Microtubule-organizing center. See Centrosome	kinetochore regulation, 139
Mis12, 9, 113, 121, 134	mitosis exit role, 24
Mis16, 118	PP2A
Mis18, 117	centriole assembly role, 76
Mitotic centromere-associated kinesin (MCAK), 35,	inhibition studies, 20–21
170–171, 191	
Mitotic checkpoint complex (MCC), components and	kinetochore regulation, 139
function, 22–23	mitosis exit role, 24
Mitotic spindle, eukaryote distribution, 5–6	PRC1, 41, 149–150, 152, 156
MPF. See Maturation-promoting factor	Prdm9, 186
Mps1, 19–20, 138	Prometaphase, overview, 3
Mps3, 71	Prophase condensation and cohesin release from chromosome
Mst2, 79	
MUS81, 82	arms, 58–59
Myosin II, 193	overview, 3
	Psh1, 118
	Pyp2, 85
N	
Ndc80, 113, 134-136, 140	R
NEBD. See Nuclear envelope breakdown	
Nek2, 76, 78–79	Rab11, 154
NHK-1, 188–189	Rab35, 154
Nuclear envelope breakdown (NEBD), 19, 59	Rad51, 187
Nucleosome. See CENP-A	Ran, 32–34, 191
NudE, 40	Rec8, 190–191
Nuf, 154	RhoA, cytokinesis role, 150
	Rootlein, 78
NuMA, 191 NuSAP, 191	
1140/11, 1/1	S
0	SA, 56–57
Ofd1, 77	SAC, 24–25 Salamander chromosome history of mitosis studies 1. 4
Oocyte. See Meiosis	Salamander chromosome, history of mitosis studies, 1–4 SAPK. See Stress-activated protein kinase
0.00, 10.000 111010010	or it is, occounted protein killase

Sas-4, 79, 89	Stress-activated protein kinase (SAPK), 73
SAS-5, 73–76	SUN-KASH domain, 187
SAS-6, 73–76, 89	Syndapin, 155
SCLT1, 83	
Sea urchin embryo, history of mitosis studies, 4–5	
Securin, degradation in mitosis, 7–8	Т
Sfi1, 71	TACC3, 81
Sgo1, 190-191	Telomere, isolation from Tetrahymena, 9
Shugosin, 24	Telophase
Sister chromatids	chromosome dynamics, 53-54
cohesin and adhesion in S phase, 55-57	overview, 3
separation and dynamics in anaphase, 60	Topoisomerase I, 11
separation mechanism, 21-24	Topoisomerase II, 10, 60, 62
Ska1, 136	TPX2, 33, 43, 191
SLC19A1, 178	TTBK2, 83
SOC. See Spindle orientation checkpoint	
SPB. See Spindle pole body	
Spd-2, 76, 79–81	U
SPICE1, 77	UBCH10, 169
Spindle. See Metaphase spindle; Mitotic spindle	Ubiquitinylation, sister chromatid separation role, 21
Spindle assembly checkpoint, 140–141, 168–169, 194	UBP6, 175
Spindle orientation checkpoint (SOC), 87	UFB. See Ultrafine DNA bridge
Spindle pole body (SPB)	Ultrafine DNA bridge (UFB), 60-62
asymmetry	
cellular asymmetry and spindle alignment in	***
budding yeast, 86-87	W
extrinsic control and end of budding yeast cell cycle,	Wap1, 56
87-88	Wee1, mitosis entry role, 17
spindle pole body asymmetry and spindle alignment	
in budding yeast, 87	
centrosome similarity, 69	X
control center activity, 84-86	XIST, 171
duplication cycle, 70–72	XMAP215, metaphase spindle function, 37, 39
mitosis entry, 18	
structure, 69–70	<b>~</b>
STAG2, 170	Z
STIL, 74–75, 77, 90	ZYG-1, 75–76

This is a free sample of content from Mitosis.

Click here for more information on how to buy the book.