

The following index is composed of keywords selected by presenting authors from a list in the Annual Meeting *Call for Abstracts*. Abstract program numbers follow each keyword.

■ Cytoskeleton and Cellular Biology

adhesion
48

autophagy
260B

border cells
256A

cell adhesion
252C

cell polarity
248B

CLIC (chloride intracellular channel)
245B

copper
261C

cytoskeleton
39 41 42 43 44 45 199A 200B 201C 202A
203B 204C 205A 206B 207C 208A 209B 210C 211A 212B
213C 214A 215B 216C 217A 218B

development
246C

dorsal closure head involution segmentation
255C

dorsal closure JNK P-element
257B

endocytosis
51

epithelium
250A

extracellular matrix
258C

flight musculature
254B

genomics
253A

GTPases Rho
249C

intracellular transport
40 46 47 50 52 219C 220A 221B 222C 223A
224B 225C 226A 227B 228C 229A 230B 231C 232A 233B
234C 235A 236B 237C 238A 239B 240C 241A 242B

invasion
250A

microvilli
49

migration
243C

morphogenesis
259A

muscle
262A

myopathy
247A

polarity
250A 251B

RNAi screen
246C

septate junctions
244A

■ Drosophila Models of Human Diseases

aging
149 939C 940A 941B 942C 943A 944B

alcohol sensitivity
952A

cancer
155 924C 925A 926B 927C 928A 929B 930C 931A 932B

developmental disorders
933C 934A 935B 936C 937A 938B

DNA repair mechanisms
946A

drug discovery
945C

epithelial
958A

epithelial polarity
958A

HIV-1
957C

hyperoxia oxidative injury
959B

hypoxia

951C

infection

949A

laminopathies

955A

muscle degeneration

956B

neural degeneration

150 151 152 153 154 156 907A 908B 909C 910A
 911B 912C 913A 914B 915C 916A 917B 918C 919A 920B
 921C 922A 923B

obesity

948C

pathogenesis

947B

polycystic kidney disease

950B

pyrimidine metabolism

954C

stress

953B

tumor suppressor

958A

■ Evolution and Quantitative Genetics

evolution and development

53 54 55 56 57 789C 790A 791B 792C 793A
 794B 795C 796A 797B 798C 799A

gene expression

825C

genome evolution

58 59 60 764B 765C 766A 767B 768C 769A 770B
 771C 772A 773B 774C 775A 776B 777C 778A 779B 780C

host-symbiont evolution

827B

insecticide resistance

823A

meiotic drive

826A

molecular evolution

824B 828C

mutation and developmental stress

829A

phylogenetics

821B 822C

population variation

61 62 63 781A 782B 783C 784A 785B 786C 787A
 788B

quantitative traits

64 65 800B 801C 802A 803B 804C 805A 806B 807C
 808A

speciation

66 809B 810C 811A 812B 813C 814A 815B 816C 817A
 818B 819C 820A

■ Gametogenesis and Sex Determination

actin cytoskeleton

590B

fertilization

586A 587B 588C

oogenesis (germ line)

537C 538A 539B 540C 541A 542B 543C 544A 545B 546C
 547A 548B 549C 550A 551B 552C 553A 554B 555C

oogenesis (soma)

147 556A 557B 558C 559A 560B 561C 562A 563B 564C
 565A

pre-gametogenic germ cell development

141 142

sex determination (germ line)

144

sex determination (soma)

145 580A 581B

sex-specific traits and molecules

582C 583A 584B 585C

spermatogenesis

143 566B 567C 568A 569B 570C 571A 572B 573C 574A
 575B 576C 577A 578B 579C

Wolbachia

589A

■ Genome and Chromosome Structure

centromere

80 287B

chromatin and remodeling complexes

75 263B 264C 265A 266B 267C 268A 269B 270C 271A
 272B 273C

chromatin folding

300C

DNA methylation

298A

DNA repair

294C 296B

dosage compensation

283A

dystrophin

299B

gene structure

299B

genome

295A

insulators/boundary elements

76 274A 275B 276C

MAR DNA

301A

melanogaster subgroup

301A

mitochondrion

292A

mRNA transport

293B

nuclear transport

293B

polycomb/trithorax complexes

77 277A 278B 279C 280A 281B

position effect variegation

78 282C

PTGS and RNAi

297C

somatic homologue pairing

302B

telomere

79 284B 285C 286A

transgene silencing and RNAi

82

transposons

81 288C 289A 290B 291C

■ Immune System and Cell Death

aging

870C

autophagy

869B

caspases

843C 844A

cellular and humoral immunity

867C

cellular immunity

119 120 830B 831C 832A 833B 834C

death mutants/genes121 122 845B 846C 847A 848B 849C 850A 851B 852C
853A 854B**engulfment**

124

hemolymph coagulation and melanisation

865A

humoral immunity

835A 836B 837C 838A 839B 840C 841A 842B

immunosenescence

868A

inhibitors of apoptosis (iaps)

123 855C

interactions with plasmodium (parasites)

866B

proteasome

872B

RNAi machinery/viral infection

873C

signal transduction

871A

transcriptional regulation

125 856A 857B 858C 859A 860B 861C 862A 863B 864C

■ Meiosis, Mitosis, and Cell Division

checkpoint

86 174C 175A 176B 177C

cytokinesis

189C 190A 191B 192C

developmental modulation

87 182B 183C 184A 185B 186C

DNA replication

194B 195C

histone methylation

196A

kinase/phosphatase/cyclin

88 178A 179B 180C 181A

kinetochores and cohesion

89 90 187A

meiosis84 85 160A 161B 162C 163A 164B 165C 166A 167B
168C 169A 170B 171C 172A 173B**mitosis**

83 157A 158B 159C

mitotic recombination and sex-chromosome loss

197B

protein degradation
198C

replication
193A

spindles and motors
188B

■ Neural Physiology and Behavior

circadian rhythms
12 751A 752B 753C 754A

coordination
761B

courtship and mating
10 14 738C 739A 740B 741C 742A 743B 744C 745A
746B 747C 748A 749B 750C

feeding behavior
758B

functional senescence
759C

glycosylation
761B

hormones
755B 756C

ion channels
11 730A 731B 732C 733A 734B

learning/memory
735C 736A 737B

locomotion
757A

neuropeptides
724A 725B 726C 727A 728B 729C

neurotransmitters
721A 722B 723C

oviposition
762C

oxidative stress
760A

sialyltransferase
761B

sensory
9 13 16 702C 703A 704B 705C 706A 707B 708C
709A 710B 711C 712A 713B 714C 715A 716B

synapse
15 717C 718A 719B 720C

synapse and locomotion
763A

■ Neurogenetics and Neural Development

axon guidance
91 92 93 94 100 101 632B 633C 634A 635B
636C 637A 638B 639C 640A 641B 642C 643A

cell polarity and asymmetric neuroblast division
696C

CNS
96 670A 671B 672C 673A 674B 675C 676A 677B 678C
679A 680B 681C 682A 683B

dendrite
701B

development
697A

disease model
698B 699C

glia
103 104 666C 667A

hormonal control
668B 669C

neurodegeneration
700A

neuronal specification
95 97 98 99 650B 651C 652A 653B 654C 655A
656B 657C 658A 659B 660C 661A 662B 663C

postembryonic
692B 693C 694A 695B

programmed cell death
664A 665B

sensory
684C 685A 686B 687C 688A 689B 690C 691A

synaptogenesis
102 644B 645C 646A 647B 648C 649A

■ Organogenesis

Dip3
628A

ectodermal derivatives (nonneural)
131 132 608B 609C 610A 611B 612C 613A 614B 615C
616A 617B 618C

extracellular matrix/cell adhesion
130 619A 620B 621C

eye development, ey
631A

eye development, eyg
629B 631A

eye development, homothorax

622A

eye development, Jak/STAT signaling

627C

eye development, unpaired, cis-element

624C

eye development, wg

631A

gastrulation

126

GTPase-GEF signaling

626B

mesodermal derivatives (muscle)127 128 129 591C 592A 593B 594C 595A 596B 597C
598A 599B 600C 601A 602B**mesodermal derivatives (muscle and nonmuscle)**

623B

mesodermal derivatives (nonmuscle)

603C 604A 605B 606C 607A

Notch

627C 628A

supernumerary spermathecae

626B

trachea, FGF, ubiquitin ligase

625A

tubulogenesis

630C

■ Pattern Formation**axis specification**25 26 32 476B 477C 478A 479B 480C 481A 482B
483C 484A 485B 486C 487A**cell migration and motility**

28 146 498C

cell polarity

36 37 38 499A 500B 501C 502A 503B 504C

commitment

29 35 505A 506B 507C

compartments and boundaries72 488B 489C 490A 491B 492C 493A 494B 495C 496A
497B**Drosophila/Su(Hw) insulator/Mod(mdg4)/BTB do**

530B

gastrulation

533B

Growth

33

Hh, Fu, Fz, Drok

527B

homeotics

74 473B 474C 475A

imaginal disk derivatives27 30 31 508A 509B 510C 511A 512B 513C 514A
515B 516C 517A 518B 519C 520A 521B 522C 523A**microRNA**

73 534C

mis-specification, transformation, cell death

526A

morphogen distribution

535A

non-Drosophila patterning

67 68 70 524B 525C

organ size

34

precision in patterning

69

regulation of cell-cell contacts

531C

segmentation

71 468C 469A 470B 471C 472A

shape determination

532A

tissue polarity

529A

transdetermination

536B

■ Regulation of Gene Expression**3D image**

358A 374B

activators/coactivators

105 318C 319A 320B 321C 322A 323B 324C 325A

activators/repressors

375C

aging, biomarker, GFP, immune peptide, hsp

376A

automation of embryo injection

349A

chromatin

346A

comparative genome

369C

core promoters and general transcription

303C 304A 305B

DNA methylation

360C

dosage compensation

114 362B 367A

Drosophila/Su(Hw) insulator/enhancer-blocking

359B

ecdysone

343A

enhancer-promoter communication

351C

enhancers110 306C 307A 308B 309C 310A 311B 312C 313A 314B
315C 316A 317B**evolution**

353B

gene regulation network

357C 364A 365B

gene regulatory networks

117 118 350B 356B 368B

gene structure

355A

genetic modifiers

352A

genetic screen

343A

hormonal regulation

347B

mRNA turnover, TTP, ARE

348C

non-coding RNAs

344B

nuclear receptors

366C

physiology

354C

proximal promoter

345C

Redox

373A

repressors/corepressors

106 107 108 109 326B 327C 328A

RNA interference

112

RNA localization

335B 336C 337A 338B 339C 340A 341B 342C

RNA modification and editing

113 330C 331A 332B

RNA stability

361A

splicing and its regulation

115 329B

sumolyation, proteomics

363C

transcription factor conditional mutants

370A

transcription, stress, metal response element

377B

transcriptional feedback

372C

translational control

116 333C 334A

transvection

111 371B

■ Signal Transduction**adaptor proteins**

140

aging

458B

cell-cell communication3 135 387C 388A 389B 390C 391A 392B 393C 394A
395B 396C 397A 398B 399C 400A 401B 402C 403A 404B**cell proliferation**

3 464B

cop9 signalosome

462C

dorsal closure

465C

downstream cascades and targets7 428B 429C 430A 431B 432C 433A 434B 435C 436A
437B 438C 439A 440B 441C 442A 443B 444C 445A 446B
447C 448A 449B 450C 451A 452B 453C**endocytosis**

454A 456C 466A

G protein

405C 406A

GMP synthase

460A

growth

457A

growth control

463A

Hedgehog

467B

interactions between pathways

455B

kinase/phosphatase4 5 6 136 138 378C 379A 380B 381C 382A
383B 384C 385A 386B**lipid metabolism**

461B

Notch

466A

phosphorylation

467B

protease

137 422B 423C 424A 425B

protein degradation

459C

receptor-ligand1 2 134 407B 408C 409A 410B 411C 412A 413B
414C 415A**second messengers**

133 426C 427A

Smoothened

467B

tumorigenesis

8 139 416B 417C 418A 419B 420C 421A

■ Techniques and Genomics

computational analyses

20 21 892A 893B 894C 895A 896B

dual expression control in MARCM

24

gene disruption and targeting

885C 886A 887B

gene mapping

19 888C 889A 890B 891C

heterochromatin

905B

microarrays

17 18 874A 875B 876C 877A 878B 879C

microRNA

22

microscopy

23 884B

molecular interactions

903C

mutational screens

897C 898A 899B 900C 901A 902B

non-coding RNAs

904A

P-element transformation

906C

RNAi

880A 881B 882C 883A

