

INDEX TO KEY WORDS

A

- A10 smooth muscle cell, distribution, myosin I, *Hasegawa, Tsuwaki, Yamada, Araki, Kimura, Sugawara, Yamamoto, Okamoto*, 421
- absorption maximum, bacterial rhodopsins, *pharaonis* phorbodopsin (ppR), *pharaonis* sensory rhodopsin II (psRII), photocycle, *Shimono, Iwamoto, Sumi, Kamo*, 404
- O-acetyl migration, bovine submandibular gland, Golgi fraction, sialate 7-O-acetyltransferase, sialic acid, *Vandamme-Feldhaus, Schauer*, 111
- acetyl polyamines, diacetyl spermine, ELISA, monoclonal antibody, tumor marker, *Fujiwara, Kaminishi, Kitagawa, Tsuru, Yabuuchi, Kanetake, Nomata*, 244
- Achromopeptidase, β -lytic protease, mass spectrometry, specificity, staphylolysis, *Li, Norioka, Sakiyama*, 332
- acidification, endocytosis, exocytosis, H⁺-ATPase, membrane traffic, *Futai, Oka, Moriyama, Wada*, 259
- acid RNase, base non-specific RNase, *Dictyostelium discoideum*, lysosomal RNase, ribonuclease, *Inokuchi, Saitoh, Kobayashi, Itagaki, Koyama, Uchiyama, Iwama, Ohgi, Irie*, 848
- actin-binding protein, cDNA cloning, heat shock, *Physarum polycephalum*, stress response, *Matsumoto, Ogawa, Kasakura, Shimada, Mitsui, Maruya, Isohata, Yahara, Murakami-Murofushi*, 326
- active site lysine, alanine racemase, pyridoxal 5'-phosphate, reaction mechanism, transamination, *Kurokawa, Watanabe, Yoshimura, Esaki, Soda*, 1163
- active site structure, mushroom, peptidyl-Lys specific metalloendopeptidase, quenched fluorescent substrate, substrate specificity, *Nonaka, Hashimoto, Takio*, 157
- N-acyl chain, glycoside primer, glycosphingolipid, glycosyltransferase, lactoside, lactosyl ceramide, *Nakajima, Miura, Yamagata*, 148
- acyl-CoA dehydrogenase, D-amino acid oxidase, flavoenzyme, hydrogen bond, Raman spectra, *Nishina, Sato, Miura, Matsui, Shiga*, 200
- , androgen, branched chain amino acid, fatty acid synthesis, golden hamster, *Hida, Uchijima, Seyama*, 648
- acyl-CoA synthetase, dietary regulation, intestinal epithelial cell, lipogenesis, proliferation, *Oikawa, Iijima, Suzuki, Sasano, Sato, Kamataki, Nagura, Kang, Fujino, Suzuki, Yamamoto*, 679
- Ad4BP/SF-1, adrenal cortex, *Ftz-F1*, gonad, nuclear receptor, *Nomura, Kawabe, Matsushita, Oka, Hatano, Harada, Nawata, Morohashi*, 217
- adenosine deaminase, dipeptidyl peptidase IV, human serum, kidney, N-terminal amino acid sequence, *Iwaki-Egawa, Watanabe, Kikuya, Fujimoto*, 428
- adenosylcobalamin, coenzyme B₁₂, diol dehydratase, electron paramagnetic resonance, mechanism-based inactivation, *Yamanishi, Yamada, Ishida, Yamauchi, Toraya*, 598
- adenylate kinase, domain exchange, nucleoside monophosphate kinase, substrate specificity, UMP/CMP kinase, *Okajima, Fukamizo, Goto, Fukui, Tanizawa*, 359
- ADP-ribosylation factor, coat protein, Golgi apparatus, N-ethylmaleimide, *Yamaguchi, Nakayama, Hatsuzawa, Tani, Himeno, Tagaya*, 1229
- adrenal cortex, Ad4BP/SF-1, *Ftz-F1*, gonad, nuclear receptor, *Nomura, Kawabe, Matsushita, Oka, Hatano, Harada, Nawata, Morohashi*, 217
- age, fetuin, mRNA, rat, serum concentration, *Kazi, Nakamura, Ohnishi, Arakaki, Kajihara, Nakagawa, Daikuhara*, 179
- aggregate formation, glucose-fructose oxidoreductase, inactivation, renaturation, stabilization, *Zymomonas mobilis*, *Fürlinger, Satory, Haltrich, Kulbe, Nidetzky*, 280
- alanine racemase, active site lysine, pyridoxal 5'-phosphate, reaction mechanism, transamination, *Kurokawa, Watanabe, Yoshimura, Esaki, Soda*, 1163
- Alcaligenes xylooxidans* GIFU, nitrite reductase, type 1 copper, three-dimensional structure, X-ray crystal analysis, *Inoue, Gotowda, Deligeer, Kataoka, Yamaguchi, Suzuki, Watanabe, Gohow, Kai*, 876
- aldo-keto reductase family, dihydrodiol dehydrogenase, 3α -hydroxysteroid dehydrogenase, polymorphism, prostaglandin D₂ 11-ketoreductase, *Matsuura, Shiraiishi, Hara, Sato, Deyashiki, Ninomiya, Sakai*, 940
- ALG-2, apoptosis, calcium, calcium-binding protein, EF-hand, *Maki, Yamaguchi, Kitaura, Satoh, Hitomi*, 1170
- alpha 1,6-linked fucose, Chinese hamster ovary cells, neural cell adhesion molecule, N-glycans, polysialic acid, *Kojima, Tachida, Tsuji*, 726
- alternative splicing, apolipoprotein(a), Kringle domain, plasminogen, reverse transcription-PCR, *Takabatake, Souri, Ichinose*, 540
- Amadori, antithrombin, glycation, glycosaminoglycan, heparin, *Berry, Chan, Andrew*, 434
- amber mutation, co-expression, non-canonical amino acid, suppressor tRNA, tyrosyl-tRNA synthetase, *Ohno, Yokogawa, Fujii, Asahara, Inokuchi, Nishikawa*, 1065
- amino acid, autophagy, density gradient, hepatocyte, proteolysis, *Niioaka, Goto, Ishibashi, Kadowaki*, 1086
- D-amino acid aminotransferase, domain, folding, fragmentary enzyme, pyridoxal 5'-phosphate, *Fuchikami, Yoshimura, Gutierrez, Soda, Esaki*, 905
- D-amino acid oxidase, acyl-CoA dehydrogenase, flavoenzyme, hydrogen bond, Raman spectra, *Nishina, Sato, Miura, Matsui, Shiga*, 200
- amino acid sequence, inorganic pyrophosphatase, molecular cloning, site-directed mutagenesis, *Thermus thermophilus*, *Satoh, Samejima, Watanabe, Nogi, Takahashi, Kaji, Teplyakov, Obmolova, Kuranova, Ishii*, 79
- , Ca²⁺-regulation, Edman degradation, scallop, troponin I, *Tanaka, Ojima, Nishita*, 304
- , bromelain inhibitor, computer modeling, cysteine proteinase inhibitor, isoinhibitor, *Hatano, Tanokura, Takahashi*, 457
- , hyperthermostable enzyme, ionspray mass spectrometry, *Pyrococcus furiosus*, pyrrolidone carboxyl peptidase, *Tsunasawa, Nakura, Tanigawa, Kato*, 778
- aminoacyl-tRNA synthetase, fluorescence titration, lysyl-tRNA synthetase, protein fluorescence, stopped-flow analysis, *Takita, Akita, Inouye, Tomomura*, 45
- ammonia and hydroxylamine oxidation, ammonia starvation, hydroxylamine oxidoreductase, *Nitrosomonas europaea*, *Wilhelm, Abeliovich, Nejidat*, 811
- ammonia starvation, ammonia and hydroxylamine oxidation, ammonia and hydroxylamine oxidoreductase, *Nitrosomonas europaea*, *Wilhelm, Abeliovich, Nejidat*, 811
- androgen, acyl-CoA dehydrogenase, branched chain amino acid, fatty acid synthesis, golden hamster, *Hida, Uchijima, Seyama*, 648
- angiogenesis, antisense oligonucleotide, antisense RNA, bovine aorta endothelial (BAE) cells, connective tissue growth factor (CTGF), *Shimo, Nakanishi, Kimura, Nishida, Ishizeki, Matsumura, Takigawa*, 130
- animal lectin, collectin, conglutinin, gene expression, luciferase, *Kawasaki, Satonaka, Imagawa, Naito, Kawasaki*, 1188
- anionic phospholipids, liquid-crystalline phase, phase separation, phosphatidylcholine, *Ahn, Yun*, 622
- anticancer drug, drug resistance, induction of metallothionein isoform, metallothionein, rat hepatoma cell, *Miyazaki, Naitoh, Nakahashi, Yanagitani, Kuno, Ueno, Okajima, Inoue*, 65
- anti-polyamine antibody, diacetylspermine, ELISA, tumor marker, urine, *Hiramatsu, Miura, Kamei, Iwasaki, Kawakita*, 231
- antisense oligonucleotide, angiogenesis, antisense RNA, bovine aorta endothelial (BAE) cells, connective tissue growth factor (CTGF), *Shimo, Nakanishi, Kimura, Nishida, Ishizeki, Matsumura, Takigawa*, 130
- antisense regulation, blasticidin S resistance, class II transposon, fungal promoter, *Pyricularia oryzae* (*Magnaporthe grisea*), *Kimura, Yamaguchi*, 268

A (cont'd)

- antisense RNA, angiogenesis, antisense oligonucleotide, bovine aorta endothelial (BAE) cells, connective tissue growth factor (CTGF), *Shimo, Nakanishi, Kimura, Nishida, Ishizeki, Matsumura, Takigawa*, 130
- antithrombin, Amadori, glycation, glycosaminoglycan, heparin, *Berry, Chan, Andrew*, 434
- apoE, LDL receptor family, LDL receptor-related protein, lipoprotein, *Kim, Inagaki, Suzuki, Ioka, Yoshioka, Magoori, Kang, Cho, Nakano, Liu, Fujino, Suzuki, Sasano, Yamamoto*, 1072
- apoE receptor, exon shuffling, exon skipping, pseudo exon, repetitive sequence, *Kim, Kim, Magoori, Saeki, Yamamoto*, 451
- apolipoprotein(a), alternative splicing, Kringle domain, plasminogen, reverse transcription-PCR, *Takabatake, Souri, Ichinose*, 540
- apoptosis, caspase-3, geranylgeraniol, HL-60 cells, zinc ions, *Aiuchi, Mihara, Nakaya, Masuda, Nakajo, Nakaya*, 300
- , caspase, ricin, serine protease, toxin, *Komatsu, Oda, Muramatsu*, 1038
- , ALG-2, calcium, calcium-binding protein, EF-hand, *Maki, Yamaguchi, Kitaura, Satoh, Hitomi*, 1170
- ArcB sensor, *Escherichia coli*, HPT domain, phosphotransfer signal transduction, *Matsushika, Mizuno*, 440
- arrays, expression, hybridization, genes, large-scale, *Jordan*, 251
- arsenite, cadmium, heme oxygenase-1, hemin, tyrosine phosphorylation, *Masuya, Hioki, Tokunaga, Taketani*, 628
- ascidian, NADPH, 6-PGDH, tunicate, vanadium, *Uyama, Kinoshita, Takahashi, Satoh, Kanamori, Michibata*, 377
- ascorbate, Fe²⁺ ions, protein phosphatase, *Yu*, 225
- Asn-glycan, Asn-glycan function, α -lactalbumin, lysozyme, protein folding, *Kimura, Uchida, Nishimura, Yamaguchi*, 857
- Asn-glycan function, Asn-glycan, α -lactalbumin, lysozyme, protein folding, *Kimura, Uchida, Nishimura, Yamaguchi*, 857
- aspartic proteinase, fluorescent substrate, kinetic property proteinase A, *Saccharomyces cerevisiae*, substrate specificity, *Kondo, Shibano, Amachi, Cronin, Oda, Dunn*, 141
- association rate constant, dissociation rate constant, lysozyme, site-specific immobilization, surface plasmon resonance, *Ueda, Tsurumaru, Imoto*, 712
- asymmetric phospholipid distribution, electric organ, NBD-labeled phospholipid, phospholipid translocation, synaptic vesicle, *Lee, Anzai, Hirashima, Kirino*, 798
- ATP analog, ATPase, chemical modification, muscle contraction, myosin subfragment-1, *Hiratsuka, Eto, Yazawa, Morita*, 609
- ATP analogue, ATP binding site, fluorescent polarization, myosin, signal transduction, *Maruta, Homma*, 528
- ATP analogues, chemical modification, energy transduction, fluorescent probes, myosin, *Maruta, Homma, Ohki*, 578
- ATPase, ATP analog, chemical modification, muscle contraction, myosin subfragment-1, *Hiratsuka, Eto, Yazawa, Morita*, 609
- F₁F₀-ATPase, ATPase inhibitor (IF₁), ATP synthase, coiled-coil structure, mitochondria, *Ichikawa, Fukuda, Hashimoto, Tagawa*, 886
- H⁺-ATPase, acidification, endocytosis, exocytosis, membrane traffic, *Futai, Oka, Moriyama, Wada*, 259
- , F-ATPase, mitochondria, *Escherichia coli*, H⁺/Cl⁻ symport, *Konno, Matsuya, Okamoto, Sato, Tanaka, Yokoyama, Kataoka, Nagai, Wasserman, Ohkuma*, 547
- ATPase inhibitor (IF₁), ATP synthase, F₁F₀-ATPase, coiled-coil structure, mitochondria, *Ichikawa, Fukuda, Hashimoto, Tagawa*, 886
- ATP binding site, ATP analogue, fluorescent polarization, myosin, signal transduction, *Maruta, Homma*, 528
- ATP synthase, ATPase inhibitor (IF₁), F₁F₀-ATPase, coiled-coil structure, mitochondria, *Ichikawa, Fukuda, Hashimoto, Tagawa*, 886
- autophagy, cathepsin, hepatectomy, lysosome, protein degradation, *Watanabe, Ishidoh, Ueno, Sato, Kominami*, 947
- , amino acid, density gradient, hepatocyte, proteolysis, *Nioka, Goto, Ishibashi, Kadowaki*, 1086

B

- Bacillus subtilis*, RNA polymerase, sigma factor, *Fujita, Sadaie*, 89
- , RNA polymerase, sporulation, transcription factor, *Fujita, Sadaie*, 98
- bacterial rhodopsins, absorption maximum, *pharaonis* phoborhodopsin (ppR), *pharaonis* sensory rhodopsin II (psRII), photocycle, *Shimono, Iwamoto, Sumi, Kamo*, 404
- baculovirus, manganese superoxide dismutase, mitochondrial import, signal peptide, site-directed mutagenesis, *Fujii, Ikeda, Watanabe, Kawasaki, Suzuki, Fujii, Takahashi, Taniguchi*, 340
- , m-calpain, mutant, overexpression, Sf-9 cell, *Masumoto, Yoshizawa, Sorimachi, Nishino, Ishiura, Suzuki*, 957
- band 3 protein, circular dichroism, Fourier transform infrared, liposome, South-East Asian ovalocytosis (SAO) band 3, *Kuma, Inoue, Fu, Ando, Lee, Sugihara, Hama-saki*, 509
- base non-specific RNase, acid RNase, *Dictyostelium discoideum*, lysosomal RNase, ribonuclease, *Inokuchi, Saitoh, Kobayashi, Itagaki, Koyama, Uchiyama, Iwama, Ohgi, Irie*, 848
- binding constant, equilibrium dialysis, GroEL, α -lactalbumin, binding site, *Shimizu, Tanba, Ogata, Ikeguchi, Sugai*, 319
- binding site, equilibrium dialysis, GroEL, α -lactalbumin, binding constant, *Shimizu, Tanba, Ogata, Ikeguchi, Sugai*, 319
- binding specificity, glycosphingolipid, *Haemophilus influenzae*, human oropharyngeal epithelium, *Neisseria meningitidis*, *Hugosson, Ångström, Olsson, Bergström, Fredlund, Olcén, Teneberg*, 1138
- 2,3-bisphosphoglycerate mutase, diabetes, 2,3-DPG, glycation site, phosphoglycerate

- mutase, *Fujita, Suzuki, Tada, Yoshihara, Hamaoka, Uchida, Matuo, Sasaki, Hanafusa, Taniguchi*, 1237
- blastocidin S resistance, antisense regulation, class II transposon, fungal promoter, *Pyricularia oryzae (Magnaporthe grisea)*, *Kimura, Yamaguchi*, 268
- bleomycin-binding protein, bleomycin-resistance, heat shock proteins, nuclear localization, *Streptomyces verticillus, Kumagai, Sugiyama*, 835
- bleomycin-resistance, bleomycin-binding protein, heat shock proteins, nuclear localization, *Streptomyces verticillus, Kumagai, Sugiyama*, 835
- blood cells, central nervous systems, L-selectin ligand, 6-sulfo sialyl Lewis X, sulfotransferase, *Uchimura, Muramatsu, Kaname, Ogawa, Yamakawa, Fan, Mitsuoka, Kannagi, Habuchi, Yokoyama, Yamamura, Ozaki, Nakagawara, Kadomatsu, Muramatsu*, 670
- bovine aorta endothelial (BAE) cells, angiogenesis, antisense oligonucleotide, antisense RNA, connective tissue growth factor (CTGF), *Shimo, Nakanishi, Kimura, Nishida, Ishizeki, Matsumura, Takigawa*, 130
- bovine submandibular gland, Golgi fraction, O-acetyl migration, sialate 7-O-acetyltransferase, sialic acid, *Vandamme-Feldhaus, Schauer*, 111
- brain development and function, gene targeting, mouse model, sphingolipid, sphingolipidosis, *Suzuki, Vanier, Suzuki*, 8
- branched chain amino acid, acyl-CoA dehydrogenase, androgen, fatty acid synthesis, golden hamster, *Hida, Uchijima, Seyama*, 648
- bromelain inhibitor, amino acid sequence, computer modeling, cysteine proteinase inhibitor, isoinhibitor, *Hatano, Tanokura, Takahashi*, 457
- budding, expressed sequence tags, serine protease inhibitor, tunicate, *Kawamura, Hayata, Fujiwara, Yubisui*, 1004

C

- Ca²⁺-regulation, amino acid sequence, Edman degradation, scallop, troponin I, *Tanaka, Ojima, Nishita*, 304
- , force production, myofibril, sarcomere, skeletal muscle, *Yuri, Wakayama, Yamada*, 565
- ⁴⁵Ca²⁺ uptake, microsomal ATPase, thapsigargin, tracheal epithelium, vanadate, *Kim, Sakong, Cho, Lee*, 1094
- cadmium, arsenite, heme oxygenase-1, hemin, tyrosine phosphorylation, *Masuya, Hioki, Tokunaga, Taketani*, 628
- calcium, ALG-2, apoptosis, calcium-binding protein, EF-hand, *Maki, Yamaguchi, Kitaura, Satoh, Hitomi*, 1170
- calcium-binding protein, ALG-2, apoptosis, calcium, EF-hand, *Maki, Yamaguchi, Kitaura, Satoh, Hitomi*, 1170
- calcium ion, fluorescence energy transfer, melittin, structural change, troponin C, *Sano, Takahashi, Iio*, 602
- calf liver, fatty acid metabolism, rat liver, VLDL secretion, *Graulet, Gruffat, Durand, Bauchart*, 1212

C (cont'd)

- calmodulin, MLCK, photocleavage, regulatory mechanism, vanadate, *Maruta, Mitsuhashi, Yamada, Ikebe*, 557
- m-calpain, baculovirus, mutant, overexpression, Sf-9 cell, *Masumoto, Yoshizawa, Sorimachi, Nishino, Ishiura, Suzuki*, 957
- carbamylation, membrane protein, N-terminal sequencing, topology, urea, *Soulić, Denoroy, Le Caer, Hamasaki, Groves, le Maire*, 417
- carboxyl proteinase, Gram-negative bacteria, kinetic property, pepstatin, substrate specificity, *Shibata, Dunn, Oda*, 642
- carboxymethylation of histidine, catalytic histidine residues, catalytic role of phenylalanine, RNase A, *Tanimizu, Ueno, Hayashi*, 410
- carboxypeptidase Y, catalytic histidine, proton-relay system, site-directed mutagenesis, *Jung, Ueno, Hayashi*, 446
- cartilage matrix deficiency, G1 domain, G3 domain, link protein, nanomeria, *Watanabe, Yamada, Kimata*, 687
- caspase, apoptosis, ricin, serine protease, toxin, *Komatsu, Oda, Muramatsu*, 1038
- caspase-3, apoptosis, geranylgeraniol, HL-60 cells, zinc ions, *Aiuchi, Mihara, Nakaya, Masuda, Nakajo, Nakaya*, 300
- catalytic histidine, carboxypeptidase Y, proton-relay system, site-directed mutagenesis, *Jung, Ueno, Hayashi*, 446
- catalytic histidine residues, carboxymethylation of histidine, catalytic role of phenylalanine, RNase A, *Tanimizu, Ueno, Hayashi*, 410
- catalytic mechanism, site-directed mutagenesis, steroid dehydrogenase, X-ray analysis, *Tanabe, Tanaka, Uchikawa, Kabashima, Ito, Nonaka, Mitsui, Tsuru, Yoshimoto*, 634
- , denaturation, enzyme kinetics, Mg^{2+} binding, sphingomyelinase, *Fujii, Inoue, Yamamoto, Ogata, Shinki, Inoue, Tomita, Tamura, Tsukamoto, Ikezawa, Ikeda*, 1178
- catalytic RNA, hairpin ribozyme, iNOS, self-trimming, three-way structure, *Komatsu, Shirai, Ohtsuka*, 986
- catalytic role of phenylalanine, carboxymethylation of histidine, catalytic histidine residues, RNase A, *Tanimizu, Ueno, Hayashi*, 410
- cathepsin, autophagy, hepatectomy, lysosome, protein degradation, *Watanabe, Ishidoh, Ueno, Sato, Kominami*, 947
- cationic liposomes, efficient IFN induction, FITC-poly I:poly C, interferon, poly I:poly C, *Okamoto, Watanabe, Takakura, Hashida*, 697
- caveolin, HeLa cell, human cell hybrids, tumorigenesis, tumor suppressor, *Suzuki, Suzuki, Hanada, Hashimoto, Redpath, Stanbridge, Nishijima, Kitagawa*, 383
- CD4, GD1c, glycoprotein, N-glycolylneuraminic acid, T cell activation, *Nohara, Kunimoto, Fujimaki*, 194
- cdk, microtubule-associated proteins, neurons, phosphorylation, tau, *Wada, Ishiguro, Itoh, Uchida, Hotani, Saito, Kishimoto, Hisanaga*, 738
- CDK inhibitor, differentiation, hepatocyte, proliferation, spheroid, *Hamamoto, Yamada, Kamihira, Iijima*, 972
- cDNA, human, *in vitro* translation, polymorphism, ubiquitin, *Kim, Yamaguchi, Sekine, Saeki, Iwamuro, Kato*, 35
- cDNA and gene cloning, gene expression, *Nicotiana tabacum*, sulfite reductase, sulfur-assimilatory gene, *Yonekura-Sakakibara, Ashikari, Tanaka, Kusumi, Hase*, 615
- cDNA cloning, actin-binding protein, heat shock, *Physarum polycephalum*, stress response, *Matsumoto, Ogawa, Kasakura, Shimada, Mitsui, Maruya, Isohata, Yahara, Murakami-Murofushi*, 326
- , cysteine proteinase, overexpression, phytoecystatin, sunflower, *Doi-Kawano, Kouzuma, Yamasaki, Kimura*, 911
- cDNA expression, deletion mutagenesis, dequalinium, drug interaction, *Saccharomyces cerevisiae*, *Rotenberg, Zhu, Hansen, Li, Sun, Michels, Riedel*, 756
- cell cycle, *Escherichia coli*, gene expression, *prcC*, trypsin-like proteinase, *Jiang, Zhang, Ding, Yao, Chen, Zhu, Muramatsu*, 980
- cell growth, cytoskeleton, differentiation, phosphatidylinositol-3 kinase, vesicle transport, *Fukui, Ihara, Nagata*, 1
- cellobiohydrolase, endoglucanase, exoglucanase, *Humicola grisea*, synergism, *Takashima, Iikura, Nakamura, Hidaka, Masaki, Uozumi*, 717
- central nervous systems, blood cells, L-selectin ligand, 6-sulfo sialyl Lewis X, sulfotransferase, *Uchimura, Muramatsu, Kaname, Ogawa, Yamakawa, Fan, Mitsuoka, Kannagi, Habuchi, Yokoyama, Yamamura, Ozaki, Nahagawara, Kadomatsu, Muramatsu*, 670
- ceramide, Neuro2a cells, sphingosine, sphingosine effects, sphingosine metabolism, *Riboni, Prinetti, Bassi, Viani, Tettamanti*, 900
- characterization, pepsin, shark, specificity, *Nguyen, Nungaray, Martel, Le Goffic, Mollé, Léonil*, 287
- chemical modification, halophilicity, metalloproteinase, salt-activation, thermolysin, tyrosine, *Inouye, Lee, Tonomura*, 72
- , ATP analogues, energy transduction, fluorescent probes, myosin, *Maruta, Homma, Ohki*, 578
- , ATP analog, ATPase, muscle contraction, myosin subfragment-1, *Hiratsuka, Eto, Yazawa, Morita*, 609
- chicken, chromosomal localization, gene regulation, gene structure, ornithine transcarbamylase, *Shimogiri, Kono, Mannen, Mizutani, Tsuji*, 962
- Chinese hamster ovary cells, alpha 1,6-linked glucose, neural cell adhesion molecule, N-glycans, polysialic acid, *Kojima, Tachida, Tsuji*, 726
- chloramphenicol acetyltransferase, β -lactamase, Tet(K), tetracycline, topology, *Hirata, Fujihira, Kimura-Someya, Yamaguchi*, 1206
- chloramphenicol/ H^+ antiport, *Escherichia coli*, multidrug resistance, sequence, *Mine, Morita, Kataoka, Mizushima, Tsuchiya*, 187
- L-2-chloropropionamide, crystal structure, haloacid dehalogenase, reaction intermediate, *Li, Hata, Fujii, Kurihara, Esaki*, 20
- cholesterol, mevalonate pyrophosphate decarboxylase, pravastatin, SHRSP, *Michihara, Sawamura, Nara, Ikeda, Yamori*, 40
- cholesteryl ester transfer protein, fluorescence, high density lipoprotein, low density lipoprotein, pyrene, *Main, Okumura-Noji, Ohnishi, Yokoyama*, 237
- chromatin remodeling, histone acetylation, histone deacetylation, nucleosome, transcription, *Hirose*, 1060
- chromosomal localization, chicken, gene regulation, gene structure, ornithine transcarbamylase, *Shimogiri, Kono, Mannen, Mizutani, Tsuji*, 962
- chymotrypsin inhibitor, *Erythrina variegata*, Kunitz-family protein, primary binding loop, site-directed mutagenesis, *Iwanaga, Yamasaki, Kimura*, 663
- chymotrypsin-type protease, complex formation, endogenous target proteases, gene duplication, *Streptomyces* proteinaceous protease inhibitor, *Taguchi, Yamada, Kojima, Momose*, 804
- circular dichroism, band 3 protein, Fourier transform infrared, liposome, South-East Asian ovalocytosis (SAO) band 3, *Kuma, Inoue, Fu, Ando, Lee, Sugihara, Hamasaki*, 509
- c-Jun N-terminal kinase (JNK), DNA synthesis, extracellular signal-regulated kinase (ERK), lysophosphatidic acid (LPA), *Sasaki, Maehama, Yamamoto, Takasuga, Hoshino, Nishina, Hazeiki, Katada*, 934
- class II transposon, antisense regulation, blasticidin S resistance, fungal promoter, *Pyricularia oryzae* (*Magnaporthe grisea*), *Kimura, Yamaguchi*, 268
- Clostridium tertium*, sialidase gene, sialidase properties, phylogeny of sialidases, putative acylneuraminic pyruvate lyase gene, *Grobe, Sartori, Traving, Schauer, Roggenstein*, 1101
- clycation, diisopropyl fluorophosphate, erythrocyte serine protease, oxidation, protein degradation, *Fujino, Tada, Beppu, Kikugawa*, 1077
- CMP-sialic acid transporter, Golgi apparatus, immunofluorescence microscopy, nucleotide-sugar transporter, peptide antibody, *Ishida, Ito, Yoshioka, Sun-Wada, Kawakita*, 171
- coat protein, ADP-ribosylation factor, Golgi apparatus, N-ethylmaleimide, *Yamaguchi, Nakayama, Hatsuzawa, Tani, Himeno, Tagaya*, 1229
- coenzyme B₁₂, adenosylcobalamin, diol dehydratase, electron paramagnetic resonance, mechanism-based inactivation, *Yamanishi, Yamada, Ishida, Yamauchi, Toraya*, 598
- co-expression, amber mutation, non-canonical amino acid, suppressor tRNA, tyrosyl-tRNA synthetase, *Ohno, Yokogawa, Fujii, Asahara, Inokuchi, Nishikawa*, 1065
- coiled-coil structure, ATPase inhibitor (IF), ATP synthase, F₁F₀-ATPase, mitochondria, *Ichikawa, Fukuda, Hashimoto, Tagawa*, 886
- collagen, hydration, hydroxyproline, model peptide, triple helix, *Nagarajan, Kamitori*,

C (cont'd)

- Okuyama*, 1117
- collagenase buffer perfusion, gene expression, inducible nitric oxide synthase, murine primary hepatocyte, nuclear factor- κ B, *Wang, Gao, Fukumoto, Tadamoto, Sato, Hirai*, 892
- collectin, animal lectin, conglutinin, gene expression, luciferase, *Kawasaki, Satonaka, Imagawa, Naito, Kawasaki*, 1188
- colon carcinoma, MUC1, mucin, transcriptional regulation, tumor antigen, *Shirotani, Irimura*, 585
- complex formation, chymotrypsin-type protease, endogenous target proteases, gene duplication, *Streptomyces* proteinaceous protease inhibitor, *Taguchi, Yamada, Kojima, Momose*, 804
- computer modeling, amino acid sequence, bromelain inhibitor, cysteine proteinase inhibitor, iso-inhibitor, *Hatano, Tanokura, Takahashi*, 457
- concanavalin A, gelatinase A (MMP-2), membrane-type matrix metalloproteinase-1 (MT1-MMP), phorbol ester (TPA), tissue inhibitor of metalloproteinase-2 (TIMP-2), *Shofuda, Moriyama, Nishihashi, Higashi, Mizushima, Yasumitsu, Miki, Sato, Seiki, Miyazaki*, 462
- , gelatinase A (MMP-2), membrane-type matrix metalloproteinase-1 (MT1-MMP), phorbol ester (TPA), tissue inhibitor of metalloproteinase-2 (TIMP-2), *Asakura, Yang, Sottile, Zhang, Jin, Okubo, Sasaki, Matsuda, Hirata, Mosher*, 473
- conglutinin, animal lectin, collectin, gene expression, luciferase, *Kawasaki, Satonaka, Imagawa, Naito, Kawasaki*, 1188
- connective tissue growth factor (CTGF), angiogenesis, antisense oligonucleotide, antisense RNA, bovine aorta endothelial (BAE) cells, *Shimo, Nakanishi, Kimura, Nishida, Ishizeki, Matsumura, Takigawa*, 130
- COPII vesicle formation, *SAR1*, small GTPase, vesicular transport, yeast *Saccharomyces cerevisiae*, *Saito, Kimura, Oka, Nakano*, 816
- Crk-associated substrate, insulin, insulin-like growth factor I, insulin receptor, SHP-2, *Fujita, Maegawa, Kashiwagi, Hirai, Kikkawa*, 1111
- crystal structure, L-2-chloropropionamide, haloacid dehalogenase, reaction intermediate, *Li, Hata, Fujii, Kurihara, Esaki*, 20
- C-terminal peptide, *Fusarium heterosporum*, lipase, stability, *Nagao, Shimada, Sugihara, Tominaga*, 1124
- cyclolinopeptide A, cyclosporin A, cyclopeptides, fluorimetric binding constants, rotamase, PPIase inhibition constants, *Gallo, Rossi, Saviano, Pedone, Colonna, Ragone*, 880
- cyclopeptides, cyclosporin A, cyclolinopeptide A, fluorimetric binding constants, rotamase, PPIase inhibition constants, *Gallo, Rossi, Saviano, Pedone, Colonna, Ragone*, 880
- cyclosporin A, cyclopeptides, cyclolinopeptide A, fluorimetric binding constants, rotamase, PPIase inhibition constants, *Gallo, Rossi, Saviano, Pedone, Colonna, Ragone*, 880
- Gallo, Rossi, Saviano, Pedone, Colonna, Ragone*, 880
- CYP2D, cytochrome P450, degenerate primer, drug metabolism, molecular cloning, *Yamamoto, Ishizuka, Takada, Fujita*, 503
- CYP51, expression, molecular evolution, *Mycobacterium tuberculosis*, P450, *Aoyama, Horiuchi, Gotoh, Noshiro, Yoshida*, 694
- cysteine proteinase, cDNA cloning, overexpression, phyto-cystatin, sunflower, *Doi-Kawano, Kouzuma, Yamasaki, Kimura*, 911
- cysteine proteinase inhibitor, amino acid sequence, bromelain inhibitor, computer modeling, iso-inhibitor, *Hatano, Tanokura, Takahashi*, 457
- cytochrome c, liposome, molecular orientation, photosynthetic reaction center, proteoliposome, *Ueno, Hara, Kamo, Fujii, Miyake*, 485
- cytochrome P450, fatty acid, hydrogen peroxide, α -oxidation, *Sphingomonas paucimobilis*, *Matsunaga, Yamada, Kusunose, Miki, Ichihara*, 105
- , CYP2D, degenerate primer, drug metabolism, molecular cloning, *Yamamoto, Ishizuka, Takada, Fujita*, 503
- cytochrome P450 2B4, electron transfer processes, NH₂-terminus, site-directed mutagenesis, *Lehnerer, Schulze, Pernecky, Lewis, Eulitz, Hlavica*, 396
- cytoskeleton, cell growth, differentiation, phosphatidylinositol-3 kinase, vesicle transport, *Fukui, Ihara, Nagata*, 1

D

- DA-1a, F9, leukemia inhibitory factor, N-glycosylation, recombinant protein, *Sasai, Aikawa, Saburi, Tojo, Tanaka, Ogawa, Shiota*, 999
- degenerate primer, CYP2D, cytochrome P450, drug metabolism, molecular cloning, *Yamamoto, Ishizuka, Takada, Fujita*, 503
- deletion mutagenesis, cDNA expression, dequalinium, drug interaction, *Saccharomyces cerevisiae*, *Rotenberg, Zhu, Hansen, Li, Sun, Michels, Riedel*, 756
- denaturation, catalytic mechanism, enzyme kinetics, Mg²⁺ binding, sphingomyelinase, *Fujii, Inoue, Yamamoto, Ogata, Shinki, Inoue, Tomita, Tamura, Tsukamoto, Ikezawa, Ikeda*, 1178
- denitrification, multi-copper enzyme, nitrous oxide reductase, *Rhodobacter sphaeroides* f. sp. *denitrificans*, *Sato, Okubo, Yamazaki*, 51
- density gradient, amino acid, autophagy, hepatocyte, proteolysis, *Niioka, Goto, Ishibashi, Kadowaki*, 1086
- dequalinium, cDNA expression, deletion mutagenesis, drug interaction, *Saccharomyces cerevisiae*, *Rotenberg, Zhu, Hansen, Li, Sun, Michels, Riedel*, 756
- desensitization, G protein-coupled receptor kinase 2, internalization, muscarinic acetylcholine receptor, sequestration, *Tsuga, Kameyama, Haga*, 863
- dexamethasone, human fibroblast-like synoviocytes, IL-6, 1κ B β , *Miyazawa, Mori, Okudaira*, 1130
- diabetes, 2,3-bisphosphoglycerate mutase, 2,3-DPG, glycation site, phosphoglycerate mutase, *Fujita, Suzuki, Tada, Yoshihara, Hamaoka, Uchida, Matuo, Sasaki, Hanafusa, Taniguchi*, 1237
- diacetylspermine, anti-polyamine antibody, ELISA, tumor marker, urine, *Hiramatsu, Miura, Kamei, Iwasaki, Kawakita*, 231
- , acetyl polyamines, ELISA, monoclonal antibody, tumor marker, *Fujiwara, Kaminishi, Kitagawa, Tsuru, Yabuuchi, Kanetake, Nomata*, 244
- Dictyostelium discoideum*, acid RNase, base non-specific RNase, lysosomal RNase, ribonuclease, *Inokuchi, Saitoh, Kobayashi, Itagaki, Koyama, Uchiyama, Iwama, Ohgi, Irie*, 848
- dietary regulation, acyl-CoA synthetase, intestinal epithelial cell, lipogenesis, proliferation, *Oikawa, Iijima, Suzuki, Sasano, Sato, Kamataki, Nagura, Kang, Fujino, Suzuki, Yamamoto*, 679
- differentiation, cell growth, cytoskeleton, phosphatidylinositol-3 kinase, vesicle transport, *Fukui, Ihara, Nagata*, 1
- , CDK inhibitor, hepatocyte, proliferation, spheroid, *Hamamoto, Yamada, Kamihira, Iijima*, 972
- , G protein γ -subunit, HL-60 cells, immunoblotting, immunoprecipitation, *Ueda, Morishita, Katoh-Semba, Kato, Asano*, 1033
- dihydrodiol dehydrogenase, aldo-keto reductase family, 3 α -hydroxysteroid dehydrogenase, polymorphism, prostaglandin D₂ 11-ketoreductase, *Matsuura, Shiraiishi, Hara, Sato, Deyashiki, Ninomiya, Sakai*, 940
- diisopropyl fluorophosphate, erythrocyte serine protease, oxidation, glycation, protein degradation, *Fujino, Tada, Beppu, Kikugawa*, 1077
- diol dehydratase, adenosylcobalamin, coenzyme B₁₂, electron paramagnetic resonance, mechanism-based inactivation, *Yamanishi, Yamada, Ishida, Yamauchi, Toraya*, 598
- dipeptidyl peptidase IV, adenosine deaminase, human serum, kidney, N-terminal amino acid sequence, *Iwaki-Egawa, Watanabe, Kikuya, Fujimoto*, 428
- dissociation rate constant, association rate constant, lysozyme, site-specific immobilization, surface plasmon resonance, *Ueda, Tsurumaru, Imoto*, 712
- distribution, A10 smooth muscle cell, myosin I, *Hasegawa, Tsuwaki, Yamada, Araki, Kimura, Sugawara, Yamamoto, Okamoto*, 421
- DNA binding protein, DNA-protein interaction, GC-box, HIV, zinc finger, *Suzuki, Yamamoto, Kurabayashi, Nagai, Yazaki, Horikoshi*, 389
- DNA-dependent protein kinase, double-stranded DNA, HMG1, HMG2, Ku protein, *Yumoto, Shirakawa, Yoshida, Suwa, Watanabe, Teraoka*, 519
- DnaJ, DnaK, maltose binding protein, molecular chaperone, zinc finger-like motif, *Ishii, Sonezaki, Iwasaki, Tauchi, Shingu, Okita, I.-Ogawa, Kato, Kondo*, 842
- DnaK, DnaJ, maltose binding protein, molecular chaperone, zinc finger-like motif, *Ishii, Sonezaki, Iwasaki, Tauchi, Shingu, Okita*,

D (cont'd)

- I-Ogawa, Kato, Kondo*, 842
- DNA-protein interaction, DNA binding protein, GC-box, HIV, zinc finger, *Suzuki, Yamamoto, Kurabayashi, Nagai, Yazaki, Horikoshi*, 389
- DNA synthesis, c-Jun N-terminal kinase (JNK), extracellular signal-regulated kinase (ERK), lysophosphatidic acid (LPA), *Sasaki, Maehama, Yamamoto, Takasuga, Hoshino, Nishina, Hazeke, Katada*, 934
- domain, D-amino acid aminotransferase, folding, fragmentary enzyme, pyridoxal 5'-phosphate, *Fuchikami, Yoshimura, Gutierrez, Soda, Esaki*, 905
- domain exchange, adenylate kinase, nucleoside monophosphate kinase, substrate specificity, UMP/CMP kinase, *Okajima, Fukamizo, Goto, Fukui, Tanizawa*, 359
- Dopa, molecular cloning, mouse liver, sulfotransferase, tyrosine, *Saeki, Sakakibara, Araki, Yanagisawa, Suiko, Nakajima, Liu*, 55
- , high performance liquid chromatography, human M-form phenol sulfotransferase, nuclear magnetic resonance spectrometry, substrate specificity, *Suiko, Sakakibara, Awan-Khan, Sakaida, Yoshikawa, Rana-singhe, Liu*, 707
- double-stranded DNA, DNA-dependent protein kinase, HMG1, HMG2, Ku protein, *Yumoto, Shirakawa, Yoshida, Suwa, Watanabe, Teraoka*, 519
- 2,3-DPG, 2,3-bisphosphoglycerate mutase, diabetes, glycation site, phosphoglycerate mutase, *Fujita, Suzuki, Tada, Yoshihara, Hamaoka, Uchida, Matuo, Sasaki, Hanafusa, Taniguchi*, 1237
- drug interaction, cDNA expression, deletion mutagenesis, dequalinium, *Saccharomyces cerevisiae*, *Rotenberg, Zhu, Hansen, Li, Sun, Michels, Riedel*, 756
- drug metabolism, CYP2D, cytochrome P450, degenerate primer, molecular cloning, *Yamamoto, Ishizuka, Takada, Fujita*, 503
- drug resistance, anticancer drug, induction of metallothionein isoform, metallothionein, rat hepatoma cell, *Miyazaki, Naitoh, Nakahashi, Yanagitani, Kuno, Ueno, Okajima, Inoue*, 65
- E
- E box element, gene expression, N-myc, RCC1, transformation, *Tsuneoka, Mekada*, 1013
- Edman degradation, amino acid sequence, Ca²⁺-regulation, scallop, troponin I, *Tanaka, Ojima, Nishita*, 304
- efficient IFN induction, cationic liposomes, FITC-poly I:poly C, interferon, poly I:poly C, *Okamoto, Watanabe, Takakura, Hashida*, 697
- EF-hand, ALG-2, apoptosis, calcium, calcium-binding protein, *Maki, Yamaguchi, Kitaura, Satoh, Hitomi*, 1170
- egg envelope hardening, *Oncorhynchus mykiss*, rainbow trout, transglutaminase, vitelline membrane, *Ha, Iuchi*, 917
- electric organ, asymmetric phospholipid distribution, NBD-labeled phospholipid, phospholipid translocation, synaptic vesicle, *Lee, Anzai, Hirashima, Kirino*, 798
- electron paramagnetic resonance, adenosylcobalamin, coenzyme B₁₂, diol dehydratase, mechanism-based inactivation, *Yamanishi, Yamada, Ishida, Yamauchi, Toraya*, 598
- electron transfer processes, cytochrome P450 2B4, NH₂-terminus, site-directed mutagenesis, *Lehnerer, Schulze, Pernecky, Lewis, Eulitz, Hlavica*, 396
- ELISA, anti-polyamine antibody, diacetylspermine, tumor marker, urine, *Hirama-tsu, Miura, Kamei, Iwasaki, Kawakita*, 231
- , acetyl polyamines, diacetyl spermine, monoclonal antibody, tumor marker, *Fujiwara, Kaminishi, Kitagawa, Tsuru, Yabuuchi, Kanetake, Nomata*, 244
- embryos, nervous system, nuclear protein, proline-rich domain, zinc finger, *Taguchi, Muramatsu, Fan, Kurosawa, Sobue, Muramatsu*, 1220
- endocytosis, acidification, exocytosis, H⁺-ATPase, membrane traffic, *Futai, Oka, Moriyama, Wada*, 259
- endogenous target proteases, chymotrypsin-type protease, complex formation, gene duplication, *Streptomyces* proteinaceous protease inhibitor, *Taguchi, Yamada, Kojima, Momose*, 804
- endoglucanase, cellobiohydrolase, exoglucanase, *Humicola grisea*, synergism, *Takashima, Iikura, Nakamura, Hidaka, Masaki, Uozumi*, 717
- endonuclease M, kinetoplastid protozoa, *Leishmania*, purification, *Mitra, Sadhukhan, Majumder*, 1198
- energy transduction, ATP analogues, chemical modification, fluorescent probes, myosin, *Maruta, Homma, Ohki*, 578
- enzyme kinetics, catalytic mechanism, denaturation, Mg²⁺ binding, sphingomyelinase, *Fujii, Inoue, Yamamoto, Ogata, Shinki, Inoue, Tomita, Tamura, Tsukamoto, Ikezawa, Ikeda*, 1178
- equilibrium dialysis, GroEL, α -lactalbumin, binding constant, binding site, *Shimizu, Tanba, Ogata, Ikeguchi, Sugai*, 319
- ER-targeting sequence, HPC-1/syntaxin 1A, intracellular localization, tail-anchored protein, transmembrane topology, *Masaki, Yamamoto, Akagawa, Tashiro*, 311
- Erythrina variegata*, chymotrypsin inhibitor, Kunitz-family protein, primary binding loop, site-directed mutagenesis, *Iwanaga, Yamasaki, Kimura*, 663
- erythrocyte serine protease, diisopropyl fluorophosphate, oxidation, clycation, protein degradation, *Fujino, Tada, Beppu, Kikugawa*, 1077
- erythropoiesis, hematopoietic microenvironment, monoclonal antibody, *smap-1*, stromal cell, *Sato, Hong, Yanai, Obinata*, 209
- Escherichia coli*, protein translocation, proton motive force, SecA, SecE, *Mori, Sugiyama, Yamanaka, Sato, Tagaya, Mizushima*, 122
- , chloramphenicol/H⁺ antiport, multidrug resistance, sequence, *Mine, Morita, Kataoka, Mizushima, Tsuchiya*, 187
- , ArcB sensor, HPt domain, phosphotransfer signal transduction, *Matsushika, Mizuno*, 440
- , H⁺-ATPase, F-ATPase, mitochondria, H⁺/Cl⁻ symport, *Konno, Matsuya, Okamoto, Sato, Tanaka, Yokoyama, Kataoka, Nagai, Wasserman, Ohkuma*, 547
- , cell cycle, gene expression, *prlC*, trypsin-like proteinase, *Jiang, Zhang, Ding, Yao, Chen, Zhu, Muramatsu*, 980
- N-ethylmaleimide, ADP-ribosylation factor, coat protein, Golgi apparatus, *Yamaguchi, Nakayama, Hatsuzawa, Tani, Himeno, Tagaya*, 1229
- evolution, exon shuffling, multigene family, protease inhibitor, SINE, *Furutani, Kato, Yasue, Alexander, Beattie, Hirose*, 491
- exocytosis, acidification, endocytosis, H⁺-ATPase, membrane traffic, *Futai, Oka, Moriyama, Wada*, 259
- exoglucanase, cellobiohydrolase, endoglucanase, *Humicola grisea*, synergism, *Takashima, Iikura, Nakamura, Hidaka, Masaki, Uozumi*, 717
- exon shuffling, apoE receptor, exon skipping, pseudo exon, repetitive sequence, *Kim, Kim, Magoori, Saeki, Yamamoto*, 451
- , evolution, multigene family, protease inhibitor, SINE, *Furutani, Kato, Yasue, Alexander, Beattie, Hirose*, 491
- exon skipping, apoE receptor, exon shuffling, pseudo exon, repetitive sequence, *Kim, Kim, Magoori, Saeki, Yamamoto*, 451
- expressed sequence tags, budding, serine protease inhibitor, tunicate, *Kawamura, Hayata, Fujiwara, Yubisui*, 1004
- expression, arrays, hybridization, genes, large-scale, *Jordan*, 251
- , CYP51, molecular evolution, *Mycobacterium tuberculosis*, P450, *Aoyama, Horiuchi, Gotoh, Noshiro, Yoshida*, 694
- , mammalian mitochondria, MTF, substrate specificity, translational initiation, *Takeuchi, Ueda, Watanabe*, 1069
- extended and folded conformations, filament assembly, phosphorylation-dependent regulation, single-headed myosin, smooth muscle, *Konishi, Katoh, Morita, Yazawa*, 163
- extracellular signal-regulated kinase (ERK), c-Jun N-terminal kinase (JNK), DNA synthesis, lysophosphatidic acid (LPA), *Sasaki, Maehama, Yamamoto, Takasuga, Hoshino, Nishina, Hazeke, Katada*, 934
- F
- F9, DA-1a, leukemia inhibitory factor, N-glycosylation, recombinant protein, *Sasai, Aikawa, Saburi, Tojo, Tanaka, Ogawa, Shiota*, 999
- F-ATPase, H⁺-ATPase, mitochondria, *Escherichia coli*, H⁺/Cl⁻ symport, *Konno, Matsuya, Okamoto, Sato, Tanaka, Yokoyama, Kataoka, Nagai, Wasserman, Ohkuma*, 547
- fatty acid, cytochrome P450, hydrogen peroxide, α -oxidation, *Sphingomonas paucimobilis*, *Matsunaga, Yamada, Kusunose, Miki, Ichihara*, 105
- fatty acid metabolism, calf liver, rat liver, VLDL secretion, *Graulet, Gruffat, Durand, Bauchart*, 1212
- fatty acid synthesis, acyl-CoA dehydrogenase, androgen, branched chain amino acid, golden hamster, *Hida, Uchijima, Seyama*,

F (cont'd)

- 648
 Fe²⁺ ions, ascorbate, protein phosphatase, Yu, 225
 fetal brain, FOG100, monoclonal antibody, O-glycosylation, sialoglycoprotein, Imamura, Hattori, Shiota, Ogawa, 534
 fetuin, age, mRNA, rat, serum concentration, Kazi, Nakamura, Ohnishi, Arakaki, Kajihara, Nakagawa, Daikuhara, 179
 fibroblast-like synoviocyte, immortalization, MAP kinase, rheumatoid arthritis, Miyazawa, Mori, Okudaira, 1153
 fibrinolysis, α_2 -macroglobulin, pregnancy zone protein, tissue plasminogen activator, trypsin, Sánchez, Chiabrando, Guglielmono, Bonacci, Rabinovich, Vides, 274
 filament assembly, extended and folded conformations, phosphorylation-dependent regulation, single-headed myosin, smooth muscle, Konishi, Katoh, Morita, Yazawa, 163
 FITC-poly I:poly C, cationic liposomes, efficient IFN induction, interferon, poly I:poly C, Okamoto, Watanabe, Takakura, Hashida, 697
 flavoenzyme, acyl-CoA dehydrogenase, D-amino acid oxidase, hydrogen bond, Raman spectra, Nishina, Sato, Miura, Matsui, Shiga, 200
 fluorescence, cholesteryl ester transfer protein, high density lipoprotein, low density lipoprotein, pyrene, Main, Okumura-Noji, Ohnishi, Yokoyama, 237
 fluorescence energy transfer, calcium ion, melittin, structural change, troponin C, Sano, Takahashi, Iio, 602
 fluorescence *in situ* hybridization, gene organization, PTF/SNAPc, VNTR, Maeng, Yoon, 23
 fluorescence titration, aminoacyl-tRNA synthetase, lysyl-tRNA synthetase, protein fluorescence, stopped-flow analysis, Takita, Akita, Inouye, Tonomura, 45
 fluorescent polarization, ATP analogue, ATP binding site, myosin, signal transduction, Maruta, Homma, 528
 fluorescent probes, ATP analogues, chemical modification, energy transduction, myosin, Maruta, Homma, Ohki, 578
 fluorescent substrate, aspartic proteinase, kinetic property proteinase A, *Saccharomyces cerevisiae*, substrate specificity, Kondo, Shibano, Amachi, Cronin, Oda, Dunn, 141
 fluorimetric binding constants, cyclosporin A, cyclopeptides, cyclolinopeptide A, rotamase, PPLase inhibition constants, Gallo, Rossi, Saviano, Pedone, Colonna, Ragone, 880
 para-fluorophenylalanine, receptor recognition, tethered ligand peptide, thrombin, thrombin receptor, Nose, Fujita, Nakajima, Inoue, Costa, Shimohigashi, 354
 FOG100, fetal brain, monoclonal antibody, O-glycosylation, sialoglycoprotein, Imamura, Hattori, Shiota, Ogawa, 534
 folding, D-amino acid aminotransferase, domain, fragmentary enzyme, pyridoxal 5'-phosphate, Fuchikami, Yoshimura, Gutierrez, Soda, Esaki, 905
 force production, Ca²⁺-regulation, myofibril, sarcomere, skeletal muscle, Yuri, Wakayama, Yamada, 565
 Fourier transform infrared, band 3 protein, circular dichroism, liposome, South-East Asian ovalocytosis (SAO) band 3, Kuma, Inoue, Fu, Ando, Lee, Sugihara, Hama-saki, 509
 fragmentary enzyme, D-amino acid aminotransferase, domain, folding, pyridoxal 5'-phosphate, Fuchikami, Yoshimura, Gutierrez, Soda, Esaki, 905
 Ftz-F1, adrenal cortex, Ad4BP/SF-1, gonad, nuclear receptor, Nomura, Kawabe, Matsushita, Oka, Hatano, Harada, Nawata, Morohashi, 217
 fungal promoter, antisense regulation, blastocidin S resistance, class II transposon, *Pyricularia oryzae* (*Magnaporthe grisea*), Kimura, Yamaguchi, 268
Fusarium heterosporum, lipase, stability, C-terminal peptide, Nagao, Shimada, Sugihara, Tominaga, 1124
- G
- G1 domain, cartilage matrix deficiency, G3 domain, link protein, nanomeria, Watanabe, Yamada, Kimata, 687
 G3 domain, cartilage matrix deficiency, G1 domain, link protein, nanomeria, Watanabe, Yamada, Kimata, 687
 GC-box, DNA binding protein, DNA-protein interaction, HIV, zinc finger, Suzuki, Yamamoto, Kurabayashi, Nagai, Yazaki, Horikoshi, 389
 GD1c, CD4, glycoprotein, N-glycolylneuraminic acid, T cell activation, Nohara, Kunimoto, Fujimaki, 194
 gelatinase A (MMP-2), concanavalin A, membrane-type matrix metalloproteinase-1 (MT1-MMP), phorbol ester (TPA), tissue inhibitor of metalloproteinase-2 (TIMP-2), Shofuda, Moriyama, Nishihashi, Higashi, Mizushima, Yasumitsu, Miki, Sato, Seiki, Miyazaki, 462
 —, concanavalin A, membrane-type matrix metalloproteinase-1 (MT1-MMP), phorbol ester (TPA), tissue inhibitor of metalloproteinase-2 (TIMP-2), Asakura, Yang, Sottile, Zhang, Jin, Ohkubo, Sasaki, Matsuda, Hirata, Mosher, 473
 gene duplication, chymotrypsin-type protease, complex formation, endogenous target proteases, *Streptomyces* proteinaceous protease inhibitor, Taguchi, Yamada, Kojima, Momose, 804
 gene expression, cDNA and gene cloning, *Nicotiana tabacum*, sulfite reductase, sulfur-assimilatory gene, Yonekura-Sakakibara, Ashikari, Tanaka, Kusumi, Hase, 615
 —, collagenase buffer perfusion, inducible nitric oxide synthase, murine primary hepatocyte, nuclear factor- κ B, Wang, Gao, Fukumoto, Tadamoto, Sato, Hirai, 892
 —, cell cycle, *Escherichia coli*, *prlC*, trypsin-like proteinase, Jiang, Zhang, Ding, Yao, Chen, Zhu, Muramatsu, 980
 —, E box element, N-myc, RCC1, transformation, Tsuneoka, Mekada, 1013
 —, animal lectin, collectin, conglutinin, luciferase, Kawasaki, Satonaka, Imagawa, Naito, Kawasaki, 1188
 gene organization, fluorescence *in situ* hybridization, PTF/SNAPc, VNTR, Maeng, Yoon, 23
 gene regulation, chicken, chromosomal localization, gene structure, ornithine transcarbamylase, Shimogiri, Kono, Mannen, Mizutani, Tsuji, 962
 genes, arrays, expression, hybridization, large-scale, Jordan, 251
 gene structure, chicken, chromosomal localization, gene regulation, ornithine transcarbamylase, Shimogiri, Kono, Mannen, Mizutani, Tsuji, 962
 gene targeting, brain development and function, mouse model, sphingolipid, sphingolipidosis, Suzuki, Vanier, Suzuki, 8
 gene transcription, melanin, melanocyte, neurofibromatosis, tyrosinase-related protein-2, Suzuki, Takahashi, Yasumoto, Amae, Yoshizawa, Fuse, Shibahara, 992
 genomic structure, Hsp70, MHC, promoter, spermatogenesis, Ito, Ando, Ando, Ando, Saijoh, Inoko, Fujimoto, 347
 geranylgeraniol, apoptosis, caspase-3, HL-60 cells, zinc ions, Aiuchi, Mihara, Nakaya, Masuda, Nakajo, Nakaya, 300
 glucose-fructose oxidoreductase, aggregate formation, inactivation, renaturation, stabilization, *Zymomonas mobilis*, Firlinger, Satory, Haltrich, Kulbe, Nidetzky, 280
 N-glycans, alpha 1,6-linked fucose, Chinese hamster ovary cells, neural cell adhesion molecule, polysialic acid, Kojima, Tachida, Tsuji, 726
 glycation, antithrombin, Amadori, glycosaminoglycan, heparin, Berry, Chan, Andrew, 434
 glycation site, 2,3-bisphosphoglycerate mutase, diabetes, 2,3-DPG, phosphoglycerate mutase, Fujita, Suzuki, Tada, Yoshihara, Hamaoka, Uchida, Matuo, Sasaki, Hanafusa, Taniguchi, 1237
 N-glycolylneuraminic acid, CD4, GD1c, glycoprotein, T cell activation, Nohara, Kunimoto, Fujimaki, 194
 glycoprotein, CD4, GD1c, N-glycolylneuraminic acid, T cell activation, Nohara, Kunimoto, Fujimaki, 194
 glycosaminoglycan, antithrombin, Amadori, glycation, heparin, Berry, Chan, Andrew, 434
 glycoside primer, N-acyl chain, glycosphingolipid, glycosyltransferase, lactoside, lactosyl ceramide, Nakajima, Miura, Yamagata, 148
 glycosphingolipid, N-acyl chain, glycoside primer, glycosyltransferase, lactoside, lactosyl ceramide, Nakajima, Miura, Yamagata, 148
 —, binding specificity, *Haemophilus influenzae*, human oropharyngeal epithelium, *Neisseria meningitidis*, Hugosson, Angström, Olsson, Bergström, Fredlund, Olcén, Teneberg, 1138
 N-glycosylation, DA-1a, F9, leukemia inhibitory factor, recombinant protein, Sasai, Aikawa, Saburi, Tojo, Tanaka, Ogawa, Shiota, 999
 O-glycosylation, fetal brain, FOG100, monoclonal antibody, sialoglycoprotein, Imamura, Hattori, Shiota, Ogawa, 534

G (cont'd)

- glycosyltransferase, *N*-acyl chain, glycoside primer, glycosphingolipid, lactoside, lactosyl ceramide, *Nakajima, Miura, Yamagata*, 148
- golden hamster, acyl-CoA dehydrogenase, androgen, branched chain amino acid, fatty acid synthesis, *Hida, Uchijima, Seyama*, 648
- Golgi apparatus, CMP-sialic acid transporter, immunofluorescence microscopy, nucleotide-sugar transporter, peptide antibody, *Ishida, Ito, Yoshioka, Sun-Wada, Kawakita*, 171
- , ADP-ribosylation factor, coat protein, *N*-ethylmaleimide, *Yamaguchi, Nakayama, Hatsuzawa, Tani, Himeno, Tagaya*, 1229
- Golgi fraction, bovine submandibular gland, *O*-acetyl migration, sialate 7-*O*-acetyltransferase, sialic acid, *Vandamme-Feldhaus, Schauer*, 111
- gonad, adrenal cortex, Ad4BP/SF-1, *Ftz-F1*, nuclear receptor, *Nomura, Kawabe, Matsushita, Oka, Hatano, Harada, Nawata, Morohashi*, 217
- G protein-coupled receptor kinase 2, desensitization, internalization, muscarinic acetylcholine receptor, sequestration, *Tsuga, Kameyama, Haga*, 863
- G protein γ -subunit, differentiation, HL-60 cells, immunoblotting, immunoprecipitation, *Ueda, Morishita, Katoh-Semba, Kato, Asano*, 1033
- Gram-negative bacteria, carboxyl proteinase, kinetic property, pepstatin, substrate specificity, *Shibata, Dunn, Oda*, 642
- GroEL, equilibrium dialysis, α -lactalbumin, binding constant, binding site, *Shimizu, Tanba, Ogata, Ikeguchi, Sugai*, 319
- guanylate kinase, NMDA receptor, palmitoylation, postsynaptic density, receptor clustering, *Nagano, Jourdi, Nawa*, 869
- gustatory papillae, subtraction cDNA library, taste bud, *Asano-Miyoshi, Kusakabe, Abe, Emori*, 927
- H
- H⁺/Cl⁻ symport, H⁺-ATPase, F-ATPase, mitochondria, *Escherichia coli*, *Konno, Matsuya, Okamoto, Sato, Tanaka, Yokoyama, Kataoka, Nagai, Wasserman, Ohkuma*, 547
- Haemophilus influenzae*, binding specificity, glycosphingolipid, human oropharyngeal epithelium, *Neisseria meningitidis*, *Hugosson, Ångström, Olsson, Bergström, Fredlund, Olcén, Teneberg*, 1138
- hairpin ribozyme, catalytic RNA, iNOS, self-trimming, three-way structure, *Komatsu, Shirai, Ohtsuka*, 986
- haloacid dehalogenase, L-2-chloropropionamide, crystal structure, reaction intermediate, *Li, Hata, Fujii, Kurihara, Esaki*, 20
- halophilicity, chemical modification, metalloproteinase, salt-activation, thermolysin, tyrosine, *Inouye, Lee, Tonomura*, 72
- heat shock, actin-binding protein, cDNA cloning, *Physarum polycephalum*, stress response, *Matsumoto, Ogawa, Kasakura, Shimada, Mitsui, Maruya, Isohata, Yahara, Murakami-Murofushi*, 326
- heat shock proteins, bleomycin-binding protein, bleomycin-resistance, nuclear localization, *Streptomyces verticillus*, *Kumagai, Sugiyama*, 835
- HeLa cell, caveolin, human cell hybrids, tumorigenesis, tumor suppressor, *Suzuki, Suzuki, Hanada, Hashimoto, Redpath, Stanbridge, Nishijima, Kitagawa*, 383
- hematopoietic microenvironment, erythropoiesis, monoclonal antibody, *smap-1*, stromal cell, *Sato, Hong, Yanai, Obinata*, 209
- heme oxygenase-1, arsenite, cadmium, heme, hemin, tyrosine phosphorylation, *Masuya, Hioki, Tokunaga, Taketani*, 628
- hemin, arsenite, cadmium, heme oxygenase-1, tyrosine phosphorylation, *Masuya, Hioki, Tokunaga, Taketani*, 628
- heparin, anti-thrombin, Amadori, glycation, glycosaminoglycan, *Berry, Chan, Andrew*, 434
- hepatectomy, autophagy, cathepsin, lysosome, protein degradation, *Watanabe, Ishidoh, Ueno, Sato, Kominami*, 947
- hepatocyte, CDK inhibitor, differentiation, proliferation, spheroid, *Hamamoto, Yamada, Kamihira, Iijima*, 972
- , amino acid, autophagy, density gradient, proteolysis, *Nioka, Goto, Ishibashi, Kadowaki*, 1086
- hepatoma cells, integrin, lung metastasis, tumor invasion, wortmannin, *Saeki, Seya, Hazeke, Ui, Hazeke, Akedo*, 1020
- heteromeric components, isoprenoid biosynthesis, prenyl diphosphate, prenyltransferase, subunit association, *Koike-Takeshita, Koyama, Ogura*, 790
- high density lipoprotein, cholesteryl ester transfer protein, fluorescence, low density lipoprotein, pyrene, *Main, Okumura-Noji, Ohnishi, Yokoyama*, 237
- high performance liquid chromatography, Dopa, human M-form phenol sulfotransferase, nuclear magnetic resonance spectrometry, substrate specificity, *Suiko, Sakakibara, Awan-Khan, Sakaida, Yoshikawa, Ranasinghe, Liu*, 707
- histone acetylation, chromatin remodeling, histone deacetylation, nucleosome, transcription, *Hirose*, 1060
- histone deacetylation, chromatin remodeling, histone acetylation, nucleosome, transcription, *Hirose*, 1060
- HIV, DNA binding protein, DNA-protein interaction, GC-box, zinc finger, *Suzuki, Yamamoto, Kurabayashi, Nagai, Yazaki, Horikoshi*, 389
- HL-60 cells, apoptosis, caspase-3, geranylgeraniol, zinc ions, *Aiuchi, Mihara, Nakaya, Masuda, Nakajo, Nakaya*, 300
- , differentiation, G protein γ -subunit, immunoblotting, immunoprecipitation, *Ueda, Morishita, Katoh-Semba, Kato, Asano*, 1033
- HMG1, DNA-dependent protein kinase, double-stranded DNA, HMG2, Ku protein, *Yumoto, Shirakawa, Yoshida, Suwa, Watanabe, Teraoka*, 519
- HMG2, DNA-dependent protein kinase, double-stranded DNA, HMG1, Ku protein, *Yumoto, Shirakawa, Yoshida, Suwa, Watanabe, Teraoka*, 519
- HPC-1/syntaxin 1A, ER-targeting sequence, intracellular localization, tail-anchored protein, transmembrane topology, *Masaki, Yamamoto, Akagawa, Tashiro*, 311
- HPT domain, ArcB sensor, *Escherichia coli*, phosphotransfer signal transduction, *Matsushita, Mizuno*, 440
- HSP47, human embryonic kidney 293 cells, molecular chaperone, procollagen biosynthesis, procollagen secretion, *Hosokawa, Hohenadl, Satoh, Kühn, Nagata*, 654
- Hsp70, genomic structure, MHC, promoter, spermatogenesis, *Ito, Ando, Ando, Ando, Saijoh, Inoko, Fujimoto*, 347
- human, cDNA, *in vitro* translation, polymorphism, ubiquitin, *Kim, Yamaguchi, Sekine, Saeki, Iwamuro, Kato*, 35
- human cell hybrids, caveolin, HeLa cell, tumorigenesis, tumor suppressor, *Suzuki, Suzuki, Hanada, Hashimoto, Redpath, Stanbridge, Nishijima, Kitagawa*, 383
- human creatine kinase, inactivation, kinetic analysis, phosphotransferase, *Luo, Xie, Bai, Zhou*, 702
- human embryonic kidney 293 cells, HSP47, molecular chaperone, procollagen biosynthesis, procollagen secretion, *Hosokawa, Hohenadl, Satoh, Kühn, Nagata*, 654
- human fibroblast-like synoviocytes, dexamethasone, IL-6, I \times B β , *Miyazawa, Mori, Okudaira*, 1130
- human M-form phenol sulfotransferase, Dopa, high performance liquid chromatography, nuclear magnetic resonance spectrometry, substrate specificity, *Suiko, Sakakibara, Awan-Khan, Sakaida, Yoshikawa, Ranasinghe, Liu*, 707
- human oropharyngeal epithelium, binding specificity, glycosphingolipid, *Haemophilus influenzae*, *Neisseria meningitidis*, *Hugosson, Ångström, Olsson, Bergström, Fredlund, Olcén, Teneberg*, 1138
- human serum, adenosine deaminase, dipeptidyl peptidase IV, kidney, N-terminal amino acid sequence, *Iwaki-Egawa, Watanabe, Kikuya, Fujimoto*, 428
- Humicola grisea*, cellobiohydrolase, endoglucanase, exoglucanase, synergism, *Takashima, Ikura, Nakamura, Hidaka, Masaki, Uozumi*, 717
- hybridization, arrays, expression, genes, large-scale, *Jordan*, 251
- hydration, collagen, hydroxyproline, model peptide, triple helix, *Nagarajan, Kamitori, Okuyama*, 1117
- hydrogen bond, acyl-CoA dehydrogenase, D-amino acid oxidase, flavoenzyme, Raman spectra, *Nishina, Sato, Miura, Matsui, Shiga*, 200
- hydrogen peroxide, cytochrome P450, fatty acid, α -oxidation, *Sphingomonas paucimobilis*, *Matsunaga, Yamada, Kusunose, Miki, Ichihara*, 105
- 2-hydroxychromene-2-carboxylate, *cis-trans* isomerase, naphthalene, naphthalenesulfonate, *Pseudomonas*, *Ohmoto, Kinoshita, Moriyoshi, Sakai, Hamada, Ohe*, 591
- hydroxylamine oxidoreductase, ammonia and hydroxylamine oxidation, ammonia starvation, *Nitrosomonas europaea*, *Wilhelm, Abeliovich, Nejjad*, 811
- hydroxyproline, collagen, hydration, model peptide, triple helix, *Nagarajan, Kamitori*,

H (cont'd)

- Okuyama*, 1117
 3 α -hydroxysteroid dehydrogenase, aldo-keto reductase family, dihydrodiol dehydrogenase, polymorphism, prostaglandin D₂ 11-ketoreductase, *Matsuura, Shiraiishi, Hara, Sato, Deyashiki, Ninomiya, Sakai*, 940
 hyperexpression, 3-ketosteroid- Δ^1 -dehydrogenase, recombinant enzyme, sequence, steroid desaturation, *Morii, Fujii, Miyoshi, Iwami, Itagaki*, 1026
 hyperthermostable enzyme, amino acid sequence, ionspray mass spectrometry, *Pyrococcus furiosus*, pyrrolidone carboxyl peptidase, *Tsunasawa, Nakura, Tanigawa, Kato*, 778

I

- 1 α B β , dexamethasone, human fibroblast-like synoviocytes, IL-6, *Miyazawa, Mori, Okudaira*, 1130
 IL-6, dexamethasone, human fibroblast-like synoviocytes, 1 α B β , *Miyazawa, Mori, Okudaira*, 1130
 immortalization, fibroblast-like synoviocyte, MAP kinase, rheumatoid arthritis, *Miyazawa, Mori, Okudaira*, 1153
 immunoblotting, pepsinogen A, pepsinogen C, protein A, recombinant protein, *Aoki, Satoh, Watabe*, 572
 —, differentiation, G protein γ -subunit, HL-60 cells, immunoprecipitation, *Ueda, Morishita, Katoh-Semba, Kato, Asano*, 1033
 immunofluorescence microscopy, CMP-sialic acid transporter, Golgi apparatus, nucleotide-sugar transporter, peptide antibody, *Ishida, Ito, Yoshioka, Sun-Wada, Kawakita*, 171
 immunoprecipitation, differentiation, G protein γ -subunit, HL-60 cells, immunoblotting, *Ueda, Morishita, Katoh-Semba, Kato, Asano*, 1033
 inactivation, aggregate formation, glucose-fructose oxidoreductase, renaturation, stabilization, *Zymomonas mobilis*, *Fürlinger, Satory, Haltrich, Kulbe, Nidetzky*, 280
 —, human creatine kinase, kinetic analysis, phosphotransferase, *Luo, Xie, Bai, Zhou*, 702
 inducible nitric oxide synthase, collagenase buffer perfusion, gene expression, murine primary hepatocyte, nuclear factor- κ B, *Wang, Gao, Fukumoto, Tademoto, Sato, Hirai*, 892
 induction of metallothionein isoform, anti-cancer drug, drug resistance, metallothionein, rat hepatoma cell, *Miyazaki, Naitoh, Nakahashi, Yanagitani, Kuno, Ueno, Okajima, Inoue*, 65
 inner mitochondrial membrane, mitochondria, precursor, protein import, Tim proteins, *Ishihara, Komiya, Sakaguchi, Ito, Mihara*, 824
 inorganic pyrophosphatase, amino acid sequence, molecular cloning, site-directed mutagenesis, *Thermus thermophilus*, *Satoh, Samejima, Watanabe, Nogi, Takahashi, Kaji, Teplyakov, Obmolova, Kuranova, Ishii*, 79
 iNOS, catalytic RNA, hairpin ribozyme, self-

- trimming, three-way structure, *Komatsu, Shirai, Ohtsuka*, 986
 insulin, Crk-associated substrate, insulin-like growth factor I, insulin receptor, SHP-2, *Fujita, Maegawa, Kashiwagi, Hirai, Kikkawa*, 1111
 insulin-like growth factor I, Crk-associated substrate, insulin, insulin receptor, SHP-2, *Fujita, Maegawa, Kashiwagi, Hirai, Kikkawa*, 1111
 insulin receptor, Crk-associated substrate, insulin, insulin-like growth factor I, SHP-2, *Fujita, Maegawa, Kashiwagi, Hirai, Kikkawa*, 1111
 integrin, hepatoma cells, lung metastasis, tumor invasion, wortmannin, *Saeki, Seya, Hazeki, Ui, Hazeki, Akedo*, 1020
 interferon, cationic liposomes, efficient IFN induction, FITC-poly I:poly C, poly I:poly C, *Okamoto, Watanabe, Takakura, Hashida*, 697
 internalization, desensitization, G protein-coupled receptor kinase 2, muscarinic acetylcholine receptor, sequestration, *Tsuga, Kameyama, Haga*, 863
 intestinal epithelial cell, acyl-CoA synthetase, dietary regulation, lipogenesis, proliferation, *Oikawa, Iijima, Suzuki, Sasano, Sato, Kamataki, Nagura, Kang, Fujino, Suzuki, Yamamoto*, 679
 intracellular localization, ER-targeting sequence, HPC-1/syntaxin 1A, tail-anchored protein, transmembrane topology, *Masaki, Yamamoto, Akagawa, Tashiro*, 311
in vitro translation, cDNA, human, polymorphism, ubiquitin, *Kim, Yamaguchi, Sekine, Saeki, Iwamuro, Kato*, 35
 ionspray mass spectrometry, amino acid sequence, hyperthermostable enzyme, *Pyrococcus furiosus*, pyrrolidone carboxyl peptidase, *Tsunasawa, Nakura, Tanigawa, Kato*, 778
 iso inhibitor, amino acid sequence, bromelain inhibitor, computer modeling, cysteine proteinase inhibitor, *Hatano, Tanokura, Takahashi*, 457
 cis-trans isomerase, 2-hydroxychromene-2-carboxylate, naphthalene, naphthalenesulfonate, *Pseudomonas, Ohmoto, Kinoshita, Moriyo, Sakai, Hamada, Ohe*, 591
 isoprenoid biosynthesis, heteromeric components, prenyl diphosphate, prenyltransferase, subunit association, *Koike-Takeshita, Koyama, Ogura*, 790

K

- 3-ketosteroid- Δ^1 -dehydrogenase, hyperexpression, recombinant enzyme, sequence, steroid desaturation, *Morii, Fujii, Miyoshi, Iwami, Itagaki*, 1026
 kidney, adenosine deaminase, dipeptidyl peptidase IV, human serum, N-terminal amino acid sequence, *Iwaki-Egawa, Watanabe, Kikuya, Fujimoto*, 428
 kinetic analysis, human creatine kinase, inactivation, phosphotransferase, *Luo, Xie, Bai, Zhou*, 702
 kinetic property, carboxyl proteinase, Gram-negative bacteria, pepstatin, substrate specificity, *Shibata, Dunn, Oda*, 642
 kinetic property proteinase A, aspartic proteinase, fluorescent substrate, *Saccharo-*

- myces cerevisiae*, substrate specificity, *Kondo, Shibano, Amachi, Cronin, Oda, Dunn*, 141
 kinetoplastid protozoa, endonuclease M, *Leishmania*, purification, *Mittra, Sadhukhan, Majumder*, 1198
 Kringle domain, alternative splicing, apolipoprotein(a), plasminogen, reverse transcription-PCR, *Takabatake, Souri, Ichinose*, 540
 Kunitz-family protein, chymotrypsin inhibitor, *Erythrina variegata*, primary binding loop, site-directed mutagenesis, *Iwanaga, Yamasaki, Kimura*, 663
 Ku protein, DNA-dependent protein kinase, double-stranded DNA, HMG1, HMG2, *Yumoto, Shirakawa, Yoshida, Suwa, Watanabe, Teraoka*, 519

L

- α -lactalbumin, equilibrium dialysis, GroEL, binding constant, binding site, *Shimizu, Tanba, Ogata, Ikeguchi, Sugai*, 319
 —, Asn-glycan, Asn-glycan function, lysozyme, protein folding, *Kimura, Uchida, Nishimura, Yamaguchi*, 857
 β -lactamase, chloramphenicol acetyltransferase, Tet(K), tetracycline, topology, *Hirata, Fujihira, Kimura-Someya, Yamaguchi*, 1206
 lactoside, N-acyl chain, glycoside primer, glycosphingolipid, glycosyltransferase, lactosyl ceramide, *Nakajima, Miura, Yamagata*, 148
 lactosyl ceramide, N-acyl chain, glycoside primer, glycosphingolipid, glycosyltransferase, lactoside, *Nakajima, Miura, Yamagata*, 148
 large-scale, arrays, expression, hybridization, genes, *Jordan*, 251
 LDL receptor family, LDL receptor related protein, membrane protein, receptor, *Tomita, Kim, Magoori, Fujino, Yamamoto*, 784
 —, apoE, LDL receptor-related protein, lipoprotein, *Kim, Inagaki, Suzuki, Ioka, Yoshioka, Magoori, Kang, Cho, Nakano, Liu, Fujino, Suzuki, Sasano, Yamamoto*, 1072
 LDL receptor related protein, LDL receptor family, membrane protein, receptor, *Tomita, Kim, Magoori, Fujino, Yamamoto*, 784
 LDL receptor-related protein, apoE, LDL receptor family, lipoprotein, *Kim, Inagaki, Suzuki, Ioka, Yoshioka, Magoori, Kang, Cho, Nakano, Liu, Fujino, Suzuki, Sasano, Yamamoto*, 1072
Leishmania, endonuclease M, kinetoplastid protozoa, purification, *Mittra, Sadhukhan, Majumder*, 1198
 leukemia inhibitory factor, DA-1a, F9, N-glycosylation, recombinant protein, *Sasai, Aikawa, Saburi, Tojo, Tanaka, Ogawa, Shiota*, 999
 link protein, cartilage matrix deficiency, G1 domain, G3 domain, nanomeria, *Watanabe, Yamada, Kimata*, 687
 linoleic acid, lipoxygenase-1, oxygenation, phosphatidylcholine, vesicles, *Kato, Nishiyama, Kuninori*, 294
 lipase, *Fusarium heterosporum*, stability, C-terminal peptide, *Nagao, Shimada, Sugihara, Tominaga*, 1124
 lipogenesis, acyl-CoA synthetase, dietary

L (cont'd)

- regulation, intestinal epithelial cell, proliferation, *Oikawa, Iijima, Suzuki, Sasano, Sato, Kamataki, Nagura, Kang, Fujino, Suzuki, Yamamoto*, 679
- lipoprotein, O-linked sugar, splicing variant, VLDL receptor, *Iijima, Miyazawa, Sakai, Magoori, Ito, Suzuki, Nose, Kawarabayasi, Yamamoto*, 747
- , apoE, LDL receptor family, LDL receptor-related protein, *Kim, Inagaki, Suzuki, Ioka, Yoshioka, Magoori, Kang, Cho, Nakano, Liu, Fujino, Suzuki, Sasano, Yamamoto*, 1072
- liposome, cytochrome *c*, molecular orientation, photosynthetic reaction center, proteoliposome, *Ueno, Hara, Kamo, Fujii, Miyake*, 485
- , band 3 protein, circular dichroism, Fourier transform infrared, South-East Asian ovalocytosis (SAO) band 3, *Kuma, Inoue, Fu, Ando, Lee, Sugihara, Hamasaki*, 509
- lipoxygenase-1, linoleic acid, oxygenation, phosphatidylcholine, vesicles, *Kato, Nishiyama, Kuninori*, 294
- liquid-crystalline phase, anionic phospholipids, phase separation, phosphatidylcholine, *Ahn, Yun*, 622
- low density lipoprotein, cholesteryl ester transfer protein, fluorescence, high density lipoprotein, pyrene, *Main, Okumura-Noji, Ohnishi, Yokoyama*, 237
- L-selectin ligand, blood cells, central nervous systems, 6-sulfo sialyl Lewis X, sulfotransferase, *Uchimura, Muramatsu, Kaname, Ogawa, Yamakawa, Fan, Mitsuoka, Kanagi, Habuchi, Yokoyama, Yamamura, Ozaki, Nakagawara, Kadomatsu, Muramatsu*, 670
- luciferase, animal lectin, collectin, conglutinin, gene expression, *Kawasaki, Sato-naka, Imagawa, Naito, Kawasaki*, 1188
- lung metastasis, hepatoma cells, integrin, tumor invasion, wortmannin, *Saeki, Seya, Hazeki, Ui, Hazeki, Akeido*, 1020
- lysophosphatidic acid (LPA), c-Jun N-terminal kinase (JNK), DNA synthesis, extracellular signal-regulated kinase (ERK), *Sasaki, Maehama, Yamamoto, Takasuga, Hoshino, Nishina, Hazeki, Katada*, 934
- lysosomal RNase, acid RNase, base non-specific RNase, *Dictyostelium discoideum*, ribonuclease, *Inokuchi, Saitoh, Kobayashi, Itagaki, Koyama, Uchiyama, Iwama, Ohgi, Irie*, 848
- lysosome, autophagy, cathepsin, hepatectomy, protein degradation, *Watanabe, Ishidoh, Ueno, Sato, Kominami*, 947
- lysozyme, association rate constant, dissociation rate constant, site-specific immobilization, surface plasmon resonance, *Ueda, Tsurumaru, Imoto*, 712
- , Asn-glycan, Asn-glycan function, α -lactalbumin, protein folding, *Kimura, Uchida, Nishimura, Yamaguchi*, 857
- lysyl-tRNA synthetase, aminoacyl-tRNA synthetase, fluorescence titration, protein fluorescence, stopped-flow analysis, *Takita, Akita, Inouye, Tonomura*, 45
- β -lytic protease, Achromopeptidase, mass spectrometry, specificity, staphylolysis, *Li,*

Norioka, Sakiyama, 332

M

- α_2 -macroglobulin, fibrinolysis, pregnancy zone protein, tissue plasminogen activator, trypsin, *Sánchez, Chiabrando, Gugliel-mone, Bonacci, Rabinovich, Vides*, 274
- maltose binding protein, DnaJ, DnaK, molecular chaperone, zinc finger-like motif, *Ishii, Sonezaki, Iwasaki, Tauchi, Shingu, Okita, I.-Ogawa, Kato, Kondo*, 842
- mammalian mitochondria, expression, MTF, substrate specificity, translational initiation, *Takeuchi, Ueda, Watanabe*, 1069
- manganese superoxide dismutase, baculovirus, mitochondrial import, signal peptide, site-directed mutagenesis, *Fujii, Ikeda, Watanabe, Kawasaki, Suzuki, Fujii, Takahashi, Taniguchi*, 340
- MAP kinase, fibroblast-like synoviocyte, immortalization, rheumatoid arthritis, *Miyazawa, Mori, Okudaira*, 1153
- mass spectrometry, Achromopeptidase, β -lytic protease, specificity, staphylolysis, *Li, Norioka, Sakiyama*, 332
- mechanism-based inactivation, adenosylcobalamin, coenzyme B₁₂, diol dehydratase, electron paramagnetic resonance, *Yamanishi, Yamada, Ishida, Yamauchi, Toraya*, 598
- melanin, gene transcription, melanocyte, neurofibromatosis, tyrosinase-related protein-2, *Suzuki, Takahashi, Yasumoto, Amae, Yoshizawa, Fuse, Shibahara*, 992
- melanocyte, gene transcription, melanin, neurofibromatosis, tyrosinase-related protein-2, *Suzuki, Takahashi, Yasumoto, Amae, Yoshizawa, Fuse, Shibahara*, 992
- melittin, calcium ion, fluorescence energy transfer, structural change, troponin C, *Sano, Takahashi, Iio*, 602
- membrane protein, carbamylation, N-terminal sequencing, topology, urea, *Soulié, Denoroy, Le Caer, Hamasaki, Groves, le Maire*, 417
- , LDL receptor family, LDL receptor related protein, receptor, *Tomita, Kim, Magoori, Fujino, Yamamoto*, 784
- , X-ray crystal structure analysis, *Sakai, Tsukihara*, 1051
- membrane traffic, acidification, endocytosis, exocytosis, H⁺-ATPase, *Futai, Oka, Moriyama, Wada*, 259
- membrane-type matrix metalloproteinase-1 (MT1-MMP), concanavalin A, gelatinase A (MMP-2), phorbol ester (TPA), tissue inhibitor of metalloproteinase-2 (TIMP-2), *Shofuda, Moriyama, Nishihashi, Higashi, Mizushima, Yasumitsu, Miki, Sato, Seiki, Miyazaki*, 462
- , concanavalin A, gelatinase A (MMP-2), phorbol ester (TPA), tissue inhibitor of metalloproteinase-2 (TIMP-2), *Asakura, Yang, Sottile, Zhang, Jin, Ohkubo, Sasaki, Matsuda, Hirata, Mosher*, 473
- metalloproteinase, chemical modification, halophilicity, salt-activation, thermolysin, tyrosine, *Inouye, Lee, Tonomura*, 72
- metallothionein, anticancer drug, drug resistance, induction of metallothionein isoform, rat hepatoma cell, *Miyazaki, Naitoh, Nakahashi, Yanagitani, Kuno, Ueno, Oka-*

jima, Inoue, 65

- mevalonate pyrophosphate decarboxylase, cholesterol, pravastatin, SHRSP, *Michihara, Sawamura, Nara, Ikeda, Yamori*, 40
- Mg²⁺ binding, catalytic mechanism, denaturation, enzyme kinetics, sphingomyelinase, *Fujii, Inoue, Yamamoto, Ogata, Shinki, Inoue, Tomita, Tamura, Tsukamoto, Ikezawa, Ikeda*, 1178
- MHC, genomic structure, *Hsp70*, promoter, spermatogenesis, *Ito, Ando, Ando, Ando, Saijoh, Inoko, Fujimoto*, 347
- microsomal ATPase, ⁴⁵Ca²⁺ uptake, thapsigargin, tracheal epithelium, vanadate, *Kim, Sakong, Cho, Lee*, 1094
- microtubule-associated proteins, cdk, neurons, phosphorylation, tau, *Wada, Ishiguro, Itoh, Uchida, Hotani, Saito, Kishimoto, Hisanaga*, 738
- mitochondria, nematode, NMR, stable isotope, tRNA, *Ohtsuki, Kawai, Watanabe*, 28
- , H⁺-ATPase, F-ATPase, *Escherichia coli*, H⁺/Cl⁻ symport, *Konno, Matsuya, Okamoto, Sato, Tanaka, Yokoyama, Kataoka, Nagai, Wasserman, Ohkuma*, 547
- , inner mitochondrial membrane, precursor, protein import, Tim proteins, *Ishihara, Komiya, Sakaguchi, Ito, Mihara*, 824
- , ATPase inhibitor (IF₁), ATP synthase, F₁F₀-ATPase, coiled-coil structure, *Ichikawa, Fukuda, Hashimoto, Tagawa*, 886
- mitochondrial import, baculovirus, manganese superoxide dismutase, signal peptide, site-directed mutagenesis, *Fujii, Ikeda, Watanabe, Kawasaki, Suzuki, Fujii, Takahashi, Taniguchi*, 340
- mitochondrial-import, mitochondrial-protein-degradation, peptidase, processing-protease, substrate-recognition, *Song, Ogi-shima, Ito*, 1045
- mitochondrial-protein-degradation, mitochondrial-import, peptidase, processing-protease, substrate-recognition, *Song, Ogi-shima, Ito*, 1045
- mK13 allozyme, prorenin-converting enzyme, tissue kallikrein, *Hosoi, Tada, Tsumura, Kanamori, Yamanaka*, 368
- MLCK, calmodulin, photocleavage, regulatory mechanism, vanadate, *Maruta, Mitsuhashi, Yamada, Ikebe*, 557
- model peptide, collagen, hydration, hydroxyproline, triple helix, *Nagarajan, Kamitori, Okuyama*, 1117
- modification of an arginine residue, phospholipase A₂, nonpolarity of the active site, snake venom, *Chang, Lin, Chang*, 764
- , phospholipase A₂, nonpolarity of the active site, snake venom, *Iwakura, Take-nawa, Nakamura*, 769
- molecular chaperone, HSP47, human embryonic kidney 293 cells, procollagen biosynthesis, procollagen secretion, *Hosokawa, Hohenadl, Satoh, Kühn, Nagata*, 654
- , DnaJ, DnaK, maltose binding protein, zinc finger-like motif, *Ishii, Sonezaki, Iwasaki, Tauchi, Shingu, Okita, I.-Ogawa, Kato, Kondo*, 842
- molecular cloning, Dopa, mouse liver, sulfotransferase, tyrosine, *Saeki, Sakakibara, Araki, Yanagisawa, Suiko, Nakajima, Liu*, 55

M (cont'd)

- , amino acid sequence, inorganic pyrophosphatase, site-directed mutagenesis, *Thermus thermophilus*, *Sato*, *Samejima*, *Watanabe*, *Nogi*, *Takahashi*, *Kaji*, *Tepljakov*, *Obmolova*, *Kuranova*, *Ishii*, 79
- , CYP2D, cytochrome P450, degenerate primer, drug metabolism, *Yamamoto*, *Ishizuka*, *Takada*, *Fujita*, 503
- molecular evolution, CYP51, expression, *Mycobacterium tuberculosis*, P450, *Aoyama*, *Horiuchi*, *Gotoh*, *Noshiro*, *Yoshida*, 694
- molecular orientation, cytochrome c, liposome, photosynthetic reaction center, proteoliposome, *Ueno*, *Hara*, *Kamo*, *Fujii*, *Miyake*, 485
- monoclonal antibody, erythropoiesis, hematopoietic microenvironment, *smap-1*, stromal cell, *Sato*, *Hong*, *Yanai*, *Obinata*, 209
- , acetyl polyamines, diacetyl spermine, ELISA, tumor marker, *Fujiwara*, *Kaminishi*, *Kitagawa*, *Tsuru*, *Yabuuchi*, *Kanetake*, *Nomata*, 244
- , fetal brain, FOG100, O-glycosylation, sialoglycoprotein, *Imamura*, *Hattori*, *Shiota*, *Ogawa*, 534
- mouse liver, Dopa, molecular cloning, sulfotransferase, tyrosine, *Saeki*, *Sakakibara*, *Araki*, *Yanagisawa*, *Suiko*, *Nakajima*, *Liu*, 55
- mouse model, brain development and function, gene targeting, sphingolipid, sphingolipidosis, *Suzuki*, *Vanier*, *Suzuki*, 8
- mRNA, age, fetuin, rat, serum concentration, *Kazi*, *Nakamura*, *Ohnishi*, *Arakaki*, *Kajihara*, *Nakagawa*, *Daikuhara*, 179
- MTF, expression, mammalian mitochondria, substrate specificity, translational initiation, *Tabeuchi*, *Ueda*, *Watanabe*, 1069
- MUC1, colon carcinoma, mucin, transcriptional regulation, tumor antigen, *Shirotani*, *Irimura*, 585
- mucin, colon carcinoma, MUC1, transcriptional regulation, tumor antigen, *Shirotani*, *Irimura*, 585
- multi-copper enzyme, denitrification, nitrous oxide reductase, *Rhodobacter sphaeroides* f. sp. *denitrificans*, *Sato*, *Okubo*, *Yamazaki*, 51
- multidrug resistance, chloramphenicol/H⁺ antiport, *Escherichia coli*, sequence, *Mine*, *Morita*, *Kataoka*, *Mizushima*, *Tsuchiya*, 187
- multigene family, evolution, exon shuffling, protease inhibitor, SINE, *Furutani*, *Kato*, *Yasue*, *Alexander*, *Beattie*, *Hirose*, 491
- murine primary hepatocyte, collagenase buffer perfusion, gene expression, inducible nitric oxide synthase, nuclear factor- κ B, *Wang*, *Gao*, *Fukumoto*, *Tademoto*, *Sato*, *Hirai*, 892
- muscarinic acetylcholine receptor, desensitization, G protein-coupled receptor kinase 2, internalization, sequestration, *Tsuga*, *Kameyama*, *Haga*, 863
- muscle contraction, ATP analog, ATPase, chemical modification, myosin subfragment-1, *Hiratsuka*, *Eto*, *Yazawa*, *Morita*, 609
- mushroom, active site structure, peptidyl-Lys specific metalloendopeptidase, quenched fluorescent substrate, substrate specificity, *Nonaka*, *Hashimoto*, *Takio*, 157
- mutant, baculovirus, m-calpain, overexpression, Sf-9 cell, *Masumoto*, *Yoshizawa*, *Sorimachi*, *Nishino*, *Ishiura*, *Suzuki*, 957
- Mycobacterium tuberculosis*, CYP51, expression, molecular evolution, P450, *Aoyama*, *Horiuchi*, *Gotoh*, *Noshiro*, *Yoshida*, 694
- myofibril, Ca²⁺-regulation, force production, sarcomere, skeletal muscle, *Yuri*, *Wakayama*, *Yamada*, 565
- myosin, ATP analogue, ATP binding site, fluorescent polarization, signal transduction, *Maruta*, *Homma*, 528
- , ATP analogues, chemical modification, energy transduction, fluorescent probes, *Maruta*, *Homma*, *Ohki*, 578
- myosin I, A10 smooth muscle cell, distribution, *Hasegawa*, *Tsuwaki*, *Yamada*, *Araki*, *Kimura*, *Sugawara*, *Yamamoto*, *Okamoto*, 421
- myosin subfragment-1, ATP analog, ATPase, chemical modification, muscle contraction, *Hiratsuka*, *Eto*, *Yazawa*, *Morita*, 609

N

- NADPH, ascidian, 6-PGDH, tunicate, vanadium, *Uyama*, *Kinoshita*, *Takahashi*, *Sato*, *Kanamori*, *Michibata*, 377
- nanomeria, cartilage matrix deficiency, G1 domain, G3 domain, link protein, *Watanabe*, *Yamada*, *Kimata*, 687
- naphthalene, *cis-trans* isomerase, 2-hydroxychromene-2-carboxylate, naphthalenesulfonate, *Pseudomonas*, *Ohmoto*, *Kinoshita*, *Moriyoshi*, *Sakai*, *Hamada*, *Ohe*, 591
- naphthalenesulfonate, *cis-trans* isomerase, 2-hydroxychromene-2-carboxylate, naphthalene, *Pseudomonas*, *Ohmoto*, *Kinoshita*, *Moriyoshi*, *Sakai*, *Hamada*, *Ohe*, 591
- NBD-labeled phospholipid, asymmetric phospholipid distribution, electric organ, phospholipid translocation, synaptic vesicle, *Lee*, *Anzai*, *Hirashima*, *Kirino*, 798
- Neisseria meningitidis*, binding specificity, glycosphingolipid, *Haemophilus influenzae*, human oropharyngeal epithelium, *Hugosson*, *Ångström*, *Olsson*, *Bergström*, *Fredlund*, *Olčén*, *Teneberg*, 1138
- nematode, mitochondria, NMR, stable isotope, tRNA, *Ohtsuki*, *Kawai*, *Watanabe*, 28
- nervous system, embryos, nuclear protein, proline-rich domain, zinc finger, *Taguchi*, *Muramatsu*, *Fan*, *Kurosawa*, *Sobue*, *Muramatsu*, 1220
- neural cell adhesion molecule, alpha 1,6-linked fucose, Chinese hamster ovary cells, N-glycans, polysialic acid, *Kojima*, *Tachida*, *Tsuji*, 726
- Neuro2a cells, ceramide, sphingosine, sphingosine effects, sphingosine metabolism, *Riboni*, *Prinetti*, *Bassi*, *Viani*, *Tettamanti*, 900
- neurofibromatosis, gene transcription, melanin, melanocyte, tyrosinase-related protein-2, *Suzuki*, *Takahashi*, *Yasumoto*, *Amae*, *Yoshizawa*, *Fuse*, *Shibahara*, 992
- neurons, cdk, microtubule-associated proteins, phosphorylation, tau, *Wada*, *Ishiguro*, *Itoh*, *Uchida*, *Hotani*, *Saito*, *Kishimoto*, *Hisanaga*, 738
- NH₂-terminus, cytochrome P450 2B4, electron transfer processes, site-directed mutagenesis, *Lehnerer*, *Schulze*, *Pernecky*, *Lewis*, *Eulitz*, *Hlavica*, 396
- Nicotiana tabacum*, cDNA and gene cloning, gene expression, sulfite reductase, sulfur-assimilatory gene, *Yonekura-Sakakibara*, *Ashikari*, *Tanaka*, *Kusumi*, *Hase*, 615
- nitrite reductase, *Alcaligenes xylooxidans* GIFU, type 1 copper, three-dimensional structure, X-ray crystal analysis, *Inoue*, *Gotowda*, *Deligeer*, *Kataoka*, *Yamaguchi*, *Suzuki*, *Watanabe*, *Gohow*, *Kai*, 876
- Nitrosomonas europaea*, ammonia and hydroxylamine oxidation, ammonia starvation, hydroxylamine oxidoreductase, *Wilhelm*, *Abeliovich*, *Nejdat*, 811
- nitrous oxide reductase, denitrification, multi-copper enzyme, *Rhodobacter sphaeroides* f. sp. *denitrificans*, *Sato*, *Okubo*, *Yamazaki*, 51
- NMDA receptor, guanylate kinase, palmitoylation, postsynaptic density, receptor clustering, *Nagano*, *Jourdi*, *Nawa*, 869
- NMR, mitochondria, nematode, stable isotope, tRNA, *Ohtsuki*, *Kawai*, *Watanabe*, 28
- N-myc, E box element, gene expression, RCC1, transformation, *Tsuneoka*, *Mekada*, 1013
- non-canonical amino acid, amber mutation, co-expression, suppressor tRNA, tyrosyl-tRNA synthetase, *Ohno*, *Yokogawa*, *Fujii*, *Asahara*, *Inokuchi*, *Nishikawa*, 1065
- nonpolarity of the active site, phospholipase A₁, modification of an arginine residue, snake venom, *Chang*, *Lin*, *Chang*, 764
- , phospholipase A₂, modification of an arginine residue, snake venom, *Iwakura*, *Takenawa*, *Nakamura*, 769
- N-terminal amino acid sequence, adenosine deaminase, dipeptidyl peptidase IV, human serum, kidney, *Iwaki-Egawa*, *Watanabe*, *Kikuya*, *Fujimoto*, 428
- N-terminal sequencing, carbamylation, membrane protein, topology, urea, *Soulié*, *Denoroy*, *Le Caer*, *Hamasaki*, *Groves*, *le Maire*, 417
- nuclear factor- κ B, collagenase buffer perfusion, gene expression, inducible nitric oxide synthase, murine primary hepatocyte, *Wang*, *Gao*, *Fukumoto*, *Tademoto*, *Sato*, *Hirai*, 892
- nuclear localization, bleomycin-binding protein, bleomycin-resistance, heat shock proteins, *Streptomyces verticillus*, *Kumagai*, *Sugiyama*, 835
- nuclear magnetic resonance spectrometry, Dopa, high performance liquid chromatography, human M-form phenol sulfotransferase, substrate specificity, *Suiko*, *Sakakibara*, *Awan-Khan*, *Sakaida*, *Yoshikawa*, *Ranasinghe*, *Liu*, 707
- nuclear protein, embryos, nervous system, proline-rich domain, zinc finger, *Taguchi*, *Muramatsu*, *Fan*, *Kurosawa*, *Sobue*, *Muramatsu*, 1220
- nuclear receptor, adrenal cortex, Ad4BP/SF-1, *Ftz-F1*, gonad, *Nomura*, *Kawabe*, *Matsushita*, *Oka*, *Hatano*, *Harada*, *Nawata*, *Morohashi*, 217

N (cont'd)

- nucleoside monophosphate kinase, adenylate kinase, domain exchange, substrate specificity, UMP/CMP kinase, *Okajima, Fukumizo, Goto, Fukui, Tanizawa*, 359
- nucleosome, chromatin remodeling, histone acetylation, histone deacetylation, transcription, *Hirose*, 1060
- nucleotide-sugar transporter, CMP-sialic acid transporter, Golgi apparatus, immunofluorescence microscopy, peptide antibody, *Ishida, Ito, Yoshioka, Sun-Wada, Kawakita*, 171
- O
- O-linked sugar, lipoprotein, splicing variant, VLDL receptor, *Iijima, Miyazawa, Sakai, Magoori, Ito, Suzuki, Nose, Kawarabayasi, Yamamoto*, 747
- Oncorhynchus mykiss*, egg envelope hardening, rainbow trout, transglutaminase, vitelline membrane, *Ha, Iuchi*, 917
- ornithine transcarbamylase, chicken, chromosomal localization, gene regulation, gene structure, *Shimogiri, Kono, Mannen, Mizutani, Tsuji*, 962
- overexpression, cDNA cloning, cysteine proteinase, phytocystatin, sunflower, *Doi-Kawano, Kouzuma, Yamasaki, Kimura*, 911
- , baculovirus, m-calpain, mutant, Sf-9 cell, *Masumoto, Yoshizawa, Sorimachi, Nishino, Ishiura, Suzuki*, 957
- oxidation, diisopropyl fluorophosphate, erythrocyte serine protease, clycation, protein degradation, *Fujino, Tada, Beppu, Kikugawa*, 1077
- α -oxidation, cytochrome P450, fatty acid, hydrogen peroxide, *Sphingomonas paucimobilis*, *Matsunaga, Yamada, Kusunose, Miki, Ichihara*, 105
- oxygenation, linoleic acid, lipoxygenase-1, phosphatidylcholine, vesicles, *Kato, Nishiyama, Kuninori*, 294
- P
- P450, CYP51, expression, molecular evolution, *Mycobacterium tuberculosis*, *Aoyama, Horiuchi, Gotoh, Noshiro, Yoshida*, 694
- palmitoylation, guanylate kinase, NMDA receptor, postsynaptic density, receptor clustering, *Nagano, Jourdi, Nawa*, 869
- pepsin, characterization, shark, specificity, *Nguyen, Nungaray, Martel, Le Goffic, Mollé, Léonil*, 287
- pepsinogen A, immunoblotting, pepsinogen C, protein A, recombinant protein, *Aoki, Satoh, Watabe*, 572
- pepsinogen C, immunoblotting, pepsinogen A, protein A, recombinant protein, *Aoki, Satoh, Watabe*, 572
- pepstatin, carboxyl proteinase, Gram-negative bacteria, kinetic property, substrate specificity, *Shibata, Dunn, Oda*, 642
- peptidase, mitochondrial-import, mitochondrial-protein-degradation, processing-protease, substrate-recognition, *Song, Ogishima, Ito*, 1045
- peptide antibody, CMP-sialic acid transporter, Golgi apparatus, immunofluorescence microscopy, nucleotide-sugar transporter, *Ishida, Ito, Yoshioka, Sun-Wada, Kawakita*, 171
- peptidyl-Lys specific metalloendopeptidase, active site structure, mushroom, quenched fluorescent substrate, substrate specificity, *Nonaka, Hashimoto, Takio*, 157
- 6-PGDH, ascidian, NADPH, tunicate, vanadium, *Uyama, Kinoshita, Takahashi, Satoh, Kanamori, Michibata*, 377
- pharaonis* phoborhodopsin (ppR), absorption maximum, bacterial rhodopsins, *pharaonis* sensory rhodopsin II (psRII), photocycle, *Shimono, Iwamoto, Sumi, Kamo*, 404
- pharaonis* sensory rhodopsin II (psRII), absorption maximum, bacterial rhodopsins, *pharaonis* phoborhodopsin (ppR), photocycle, *Shimono, Iwamoto, Sumi, Kamo*, 404
- phase separation, anionic phospholipids, liquid-crystalline phase, phosphatidylcholine, *Ahn, Yun*, 622
- phorbol ester (TPA), concanavalin A, gelatinase A (MMP-2), membrane-type matrix metalloproteinase-1 (MT1-MMP), tissue inhibitor of metalloproteinase-2 (TIMP-2), *Shofuda, Moriyama, Nishihashi, Higashi, Mizushima, Yasumitsu, Miki, Sato, Seiki, Miyazaki*, 462
- , concanavalin A, gelatinase A (MMP-2), membrane-type matrix metalloproteinase-1 (MT1-MMP), tissue inhibitor of metalloproteinase-2 (TIMP-2), *Asakura, Yang, Sottile, Zhang, Jin, Ohkubo, Sasaki, Matsuda, Hirata, Mosher*, 473
- phosphatidylcholine, linoleic acid, lipoxygenase-1, oxygenation, vesicles, *Kato, Nishiyama, Kuninori*, 294
- , anionic phospholipids, liquid-crystalline phase, phase separation, *Ahn, Yun*, 622
- phosphatidylinositol-3 kinase, cell growth, cytoskeleton, differentiation, vesicle transport, *Fukui, Ihara, Nagata*, 1
- phosphoglycerate mutase, 2,3-bisphosphoglycerate mutase, diabetes, 2,3-DPG, glycation site, *Fujita, Suzuki, Tada, Yoshihara, Hamaoka, Uchida, Matuo, Sasaki, Hanafusa, Taniguchi*, 1237
- phospholipase A₂, modification of an arginine residue, nonpolarity of the active site, snake venom, *Chang, Lin, Chang*, 764
- , modification of an arginine residue, nonpolarity of the active site, snake venom, *Iwakura, Takenawa, Nakamura*, 769
- phospholipid translocation, asymmetric phospholipid distribution, electric organ, NBD-labeled phospholipid, synaptic vesicle, *Lee, Anzai, Hirashima, Kirino*, 798
- phosphorylation, cdk, microtubule-associated proteins, neurons, tau, *Wada, Ishiguro, Itoh, Uchida, Hotani, Saito, Kishimoto, Hisanaga*, 738
- phosphorylation-dependent regulation, extended and folded conformations, filament assembly, single-headed myosin, smooth muscle, *Konishi, Kato, Morita, Yazawa*, 163
- phosphotransferase, human creatine kinase, inactivation, kinetic analysis, *Luo, Xie, Bai, Zhou*, 702
- phosphotransfer signal transduction, ArcB sensor, *Escherichia coli*, HPT domain, *Matsushika, Mizuno*, 440
- photocleavage, calmodulin, MLCK, regulatory mechanism, vanadate, *Maruta, Mitsuhashi, Yamada, Ikebe*, 557
- photocycle, absorption maximum, bacterial rhodopsins, *pharaonis* phoborhodopsin (ppR), *pharaonis* sensory rhodopsin II (psRII), *Shimono, Iwamoto, Sumi, Kamo*, 404
- photosynthetic reaction center, cytochrome *c*, liposome, molecular orientation, proteoliposome, *Ueno, Hara, Kamo, Fujii, Miyake*, 485
- phylogeny of sialidases, *Clostridium tertium*, sialidase gene, sialidase properties, putative acylneuraminase pyruvate lyase gene, *Grobe, Sartori, Traving, Schauer, Roggen-stein*, 1101
- Physarum polycephalum*, actin-binding protein, cDNA cloning, heat shock, stress response, *Matsumoto, Ogawa, Kasakura, Shimada, Mitsui, Maruya, Isohata, Yahara, Murakami-Murofushi*, 326
- phytocystatin, cDNA cloning, cysteine proteinase, overexpression, sunflower, *Doi-Kawano, Kouzuma, Yamasaki, Kimura*, 911
- plasminogen, alternative splicing, apolipoprotein(a), Kringle domain, reverse transcription-PCR, *Takabatake, Souri, Ichinose*, 540
- poly I:poly C, cationic liposomes, efficient IFN induction, FITC-poly I:poly C, interferon, *Okamoto, Watanabe, Takakura, Hashida*, 697
- polymorphism, cDNA, human, *in vitro* translation, ubiquitin, *Kim, Yamaguchi, Sekine, Saeki, Iwamuro, Kato*, 35
- , aldo-keto reductase family, dihydrodiol dehydrogenase, 3 α -hydroxysteroid dehydrogenase, prostaglandin D, 11-ketoreductase, *Matsuura, Shiraishi, Hara, Sato, Deyashiki, Ninomiya, Sakai*, 940
- polysialic acid, alpha 1,6-linked fucose, Chinese hamster ovary cells, neural cell adhesion molecule, N-glycans, *Kojima, Tachida, Tsuji*, 726
- postsynaptic density, guanylate kinase, NMDA receptor, palmitoylation, receptor clustering, *Nagano, Jourdi, Nawa*, 869
- PPIase inhibition constants, cyclosporin A, cyclopeptides, cyclolinopeptide A, fluorimetric binding constants, rotamase, *Gallo, Rossi, Saviano, Pedone, Colonna, Ragone*, 880
- pravastatin, cholesterol, mevalonate pyrophosphate decarboxylase, SHRSP, *Michihara, Sawamura, Nara, Ikeda, Yamori*, 40
- precursor, inner mitochondrial membrane, mitochondria, Tim protein import, Tim proteins, *Ishihara, Komiya, Sakaguchi, Ito, Mihara*, 824
- pregnancy zone protein, fibrinolysis, α_2 -macroglobulin, tissue plasminogen activator, trypsin, *Sánchez, Chiabrando, Guglielmone, Bonacci, Rabinovich, Vides*, 274
- prenyl diphosphate, heteromeric components, isoprenoid biosynthesis, prenyltransferase, subunit association, *Koike-Takeshita, Koyama, Ogura*, 790
- prenyltransferase, heteromeric components, isoprenoid biosynthesis, prenyl diphosphate, subunit association, *Koike-Takeshita, Koyama, Ogura*, 790

P (cont'd)

- primary binding loop, chymotrypsin inhibitor, *Erythrina variegata*, Kunitz-family protein, site-directed mutagenesis, *Iwanaga, Yamasaki, Kimura*, 663
- prlC*, cell cycle, *Escherichia coli*, gene expression, trypsin-like proteinase, *Jiang, Zhang, Ding, Yao, Chen, Zhu, Muramatsu*, 980
- processing-protease, mitochondrial-import, mitochondrial-protein-degradation, peptidase, substrate-recognition, *Song, Ogi-shima, Ito*, 1045
- procollagen biosynthesis, HSP47, human embryonic kidney 293 cells, molecular chaperone, procollagen secretion, *Hosokawa, Hohenadl, Satoh, Kühn, Nagata*, 654
- procollagen secretion, HSP47, human embryonic kidney 293 cells, molecular chaperone, procollagen biosynthesis, *Hosokawa, Hohenadl, Satoh, Kühn, Nagata*, 654
- proliferation, acyl-CoA synthetase, dietary regulation, intestinal epithelial cell, lipogenesis, *Okawa, Iijima, Suzuki, Sasano, Sato, Kamataki, Nagura, Kang, Fujino, Suzuki, Yamamoto*, 679
- , CDK inhibitor, differentiation, hepatocyte, spheroid, *Hamamoto, Yamada, Kamihira, Iijima*, 972
- proline-rich domain, embryos, nervous system, nuclear protein, zinc finger, *Taguchi, Muramatsu, Fan, Kurosawa, Sobue, Muramatsu*, 1220
- promoter, genomic structure, *Hsp70*, MHC, spermatogenesis, *Ito, Ando, Ando, Saijoh, Inoko, Fujimoto*, 347
- prorenin-converting enzyme, mK13 allozyme, tissue kallikrein, *Hosoi, Tada, Tsumura, Kanamori, Yamanaka*, 368
- prostaglandin D₂ 11-ketoreductase, aldo-keto reductase family, dihydrodiol dehydrogenase, 3 α -hydroxysteroid dehydrogenase, polymorphism, *Matsuura, Shiraishi, Hara, Sato, Deyashiki, Ninomiya, Sakai*, 940
- protease inhibitor, evolution, exon shuffling, multigene family, SINE, *Furutani, Kato, Yasue, Alexander, Beattie, Hirose*, 491
- protein A, immunoblotting, pepsinogen A, pepsinogen C, recombinant protein, *Aoki, Satoh, Watabe*, 572
- protein degradation, autophagy, cathepsin, hepatectomy, lysosome, *Watanabe, Ishidoh, Ueno, Sato, Kominami*, 947
- , diisopropyl fluorophosphate, erythrocyte serine protease, oxidation, clycation, *Fujino, Tada, Beppu, Kikugawa*, 1077
- protein fluorescence, aminoacyl-tRNA synthetase, fluorescence titration, lysyl-tRNA synthetase, stopped-flow analysis, *Takita, Akita, Inouye, Tonomura*, 45
- protein folding, Asn-glycan, Asn-glycan function, α -lactalbumin, lysozyme, *Kimura, Uchida, Nishimura, Yamaguchi*, 857
- protein import, inner mitochondrial membrane, mitochondria, precursor, Tim proteins, *Ishihara, Komiya, Sakaguchi, Ito, Mihara*, 824
- protein phosphatase, ascorbate, Fe²⁺ ions, *Yu*, 225
- protein translocation, *Escherichia coli*, proton motive force, SecA, SecG, *Mori, Sugiyama, Yamanaka, Sato, Tagaya, Mizushima*, 122
- proteoliposome, cytochrome c, liposome, molecular orientation, photosynthetic reaction center, *Ueno, Hara, Kamo, Fujii, Miyake*, 485
- proteolysis, amino acid, autophagy, density gradient, hepatocyte, *Nioka, Goto, Ishibashi, Kadowaki*, 1086
- proton motive force, *Escherichia coli*, protein translocation, SecA, SecG, *Mori, Sugiyama, Yamanaka, Sato, Tagaya, Mizushima*, 122
- proton-relay system, carboxypeptidase Y, catalytic histidine, site-directed mutagenesis, *Jung, Ueno, Hayashi*, 446
- pseudo exon, apoE receptor, exon shuffling, exon skipping, repetitive sequence, *Kim, Kim, Magoori, Saeki, Yamamoto*, 451
- Pseudomonas*, cis-trans isomerase, 2-hydroxychromene-2-carboxylate, naphthalene, naphthalenesulfonate, *Ohmoto, Kinoshita, Moriyoshi, Sakai, Hamada, Ohe*, 591
- PTF/SNAPc, fluorescence *in situ* hybridization, gene organization, VNTR, *Maeng, Yoon*, 23
- purification, endonuclease M, kinetoplastid protozoa, *Leishmania*, *Mitra, Sadhukhan, Majumder*, 1198
- putative acylneuraminase pyruvate lyase gene, *Clostridium tertium*, sialidase gene, sialidase properties, phylogeny of sialidases, *Grobe, Sartori, Traving, Schauer, Roggentin*, 1101
- pyrene, cholesteryl ester transfer protein, fluorescence, high density lipoprotein, low density lipoprotein, *Main, Okumura-Noji, Ohnishi, Yokoyama*, 237
- Pyricularia oryzae* (*Magnaporthe grisea*), antisense regulation, blasticidin S resistance, class II transposon, fungal promoter, *Kimura, Yamaguchi*, 268
- pyridoxal 5'-phosphate, D-amino acid aminotransferase, domain, folding, fragmentary enzyme, *Fuchikami, Yoshimura, Gutierrez, Soda, Esaki*, 905
- , active site lysine, alanine racemase, reaction mechanism, transamination, *Kurokawa, Watanabe, Yoshimura, Esaki, Soda*, 1163
- Pyrococcus furiosus*, amino acid sequence, hyperthermostable enzyme, ionspray mass spectrometry, pyrrolidone carboxyl peptidase, *Tsunasawa, Nakura, Tanigawa, Kato*, 778
- pyrrolidone carboxyl peptidase, amino acid sequence, hyperthermostable enzyme, ionspray mass spectrometry, *Pyrococcus furiosus*, *Tsunasawa, Nakura, Tanigawa, Kato*, 778

Q

quenched fluorescent substrate, active site structure, mushroom, peptidyl-Lys specific metalloendopeptidase, substrate specificity, *Nonaka, Hashimoto, Takio*, 157

R

rainbow trout, egg envelope hardening, *Onchorynchus mykiss*, transglutaminase, vitelline membrane, *Ha, Iuchi*, 917

Raman spectra, acyl-CoA dehydrogenase, D-amino acid oxidase, flavoenzyme, hydrogen bond, *Nishina, Sato, Miura, Matsui, Shiga*, 200

rat, age, fetuin, mRNA, serum concentration, *Kazi, Nakamura, Ohnishi, Arakaki, Kajihara, Nakagawa, Daikuhara*, 179

rat hepatoma cell, anticancer drug, drug resistance, induction of metallothionein isoform, metallothionein, *Miyazaki, Naitoh, Nakahashi, Yanagitani, Kuno, Ueno, Okajima, Inoue*, 65

rat liver, calf liver, fatty acid metabolism, VLDL secretion, *Graulet, Gruffat, Durand, Bauchart*, 1212

RCC1, E box element, gene expression, N-myc, transformation, *Tsuneoka, Mekada*, 1013

reaction intermediate, L-2-chloropropionamide, crystal structure, haloacid dehalogenase, *Li, Hata, Fujii, Kurihara, Esaki*, 20

reaction mechanism, active site lysine, alanine racemase, pyridoxal 5'-phosphate, transamination, *Kurokawa, Watanabe, Yoshimura, Esaki, Soda*, 1163

receptor, LDL receptor family, LDL receptor related protein, membrane protein, *Tomita, Kim, Magoori, Fujino, Yamamoto*, 784

receptor clustering, guanylate kinase, NMDA receptor, palmitoylation, postsynaptic density, *Nagano, Jourdi, Nawa*, 869

receptor recognition, para-fluorophenylalanine, tethered ligand peptide, thrombin, thrombin receptor, *Nose, Fujita, Nakajima, Inoue, Costa, Shimohigashi*, 354

recombinant enzyme, hyperexpression, 3-ketosteroid- Δ^1 -dehydrogenase, sequence, steroid desaturation, *Morii, Fujii, Miyoshi, Iwami, Itagaki*, 1026

recombinant protein, immunoblotting, pepsinogen A, pepsinogen C, protein A, *Aoki, Satoh, Watabe*, 572

—, DA-1a, F9, leukemia inhibitory factor, N-glycosylation, *Sasai, Aikawa, Saburi, Tojo, Tanaka, Ogawa, Shiota*, 999

regulatory mechanism, calmodulin, MLCK, photocleavage, vanadate, *Maruta, Mitsuhashi, Yamada, Ikebe*, 557

renaturation, aggregate formation, glucose-fructose oxidoreductase, inactivation, stabilization, *Zymomonas mobilis*, *Fürlinger, Satory, Haltrich, Kulbe, Nidetzky*, 280

repetitive sequence, apoE receptor, exon shuffling, exon skipping, pseudo exon, *Kim, Kim, Magoori, Saeki, Yamamoto*, 451

reverse transcription-PCR, alternative splicing, apolipoprotein(a), Kringle domain, plasminogen, *Takabatake, Souri, Ichinose*, 540

rheumatoid arthritis, fibroblast-like synovio-cyte, immortalization, MAP kinase, *Miyazawa, Mori, Okudaira*, 1163

Rhodobacter sphaeroides f. sp. *denitrificans*, denitrification, multi-copper enzyme, nitrous oxide reductase, *Sato, Okubo, Yamazaki*, 51

ribonuclease, acid RNase, base non-specific RNase, *Dictyostelium discoideum*, lysosomal RNase, *Inokuchi, Saitoh, Kobayashi, Itagaki, Koyama, Uchiyama, Iwama, Ohgi, Irie*, 848

R (cont'd)

ricin, apoptosis, caspase, serine protease, toxin, *Komatsu, Oda, Muramatsu*, 1038
 RNA polymerase, *Bacillus subtilis*, sigma factor, *Fujita, Sadaie*, 89
 —, *Bacillus subtilis*, sporulation, transcription factor, *Fujita, Sadaie*, 98
 RNase A, carboxymethylation of histidine, catalytic histidine residues, catalytic role of phenylalanine, *Tanimizu, Ueno, Hayashi*, 410
 rotamase, cyclosporin A, cyclopeptides, cyclolinopeptide A, fluorimetric binding constants, PPIase inhibition constants, *Gallo, Rossi, Saviano, Pedone, Colonna, Ragone*, 880

S

Saccharomyces cerevisiae, aspartic proteinase, fluorescent substrate, kinetic property proteinase A, substrate specificity, *Kondo, Shibano, Amachi, Cronin, Oda, Dunn*, 141
 —, cDNA expression, deletion mutagenesis, dequalinium, drug interaction, *Rotenberg, Zhu, Hansen, Li, Sun, Michels, Riedel*, 756
 salt-activation, chemical modification, halophilicity, metalloproteinase, thermolysin, tyrosine, *Inouye, Lee, Tonomura*, 72
 SARI, COPII vesicle formation, small GTPase, vesicular transport, yeast *Saccharomyces cerevisiae*, *Saito, Kimura, Oka, Nakano*, 816
 sarcomere, Ca²⁺-regulation, force production, myofibril, skeletal muscle, *Yuri, Wakayama, Yamada*, 565
 scallop, amino acid sequence, Ca²⁺-regulation, Edman degradation, troponin I, *Tanaka, Ojima, Nishita*, 304
 SecA, *Escherichia coli*, protein translocation, proton motive force, SecG, *Mori, Sugiyama, Yamanaka, Sato, Tagaya, Mizushima*, 122
 SecG, *Escherichia coli*, protein translocation, proton motive force, SecA, *Mori, Sugiyama, Yamanaka, Sato, Tagaya, Mizushima*, 122
 self-trimming, catalytic RNA, hairpin ribozyme, iNOS, three-way structure, *Komatsu, Shirai, Ohtsuka*, 986
 sequence, chloramphenicol/H⁺ antiport, *Escherichia coli*, multidrug resistance, *Mine, Morita, Kataoka, Mizushima, Tsuchiya*, 187
 —, hyperexpression, 3-ketosteroid-Δ¹-dehydrogenase, recombinant enzyme, steroid desaturation, *Morii, Fujii, Miyoshi, Iwami, Itagaki*, 1026
 sequestration, desensitization, G protein-coupled receptor kinase 2, internalization, muscarinic acetylcholine receptor, *Tsuga, Kameyama, Haga*, 863
 serine protease, apoptosis, caspase, ricin, toxin, *Komatsu, Oda, Muramatsu*, 1038
 serine protease inhibitor, budding, expressed sequence tags, tunicate, *Kawamura, Hayata, Fujiwara, Yubisui*, 1004
 serum concentration, age, fetuin, mRNA, rat, *Kazi, Nakamura, Ohnishi, Arakaki, Kajihara, Nakagawa, Daikuhara*, 179
 Sf-9 cell, baculovirus, m-calpain, mutant, overexpression, *Masumoto, Yoshizawa,*

Sorimachi, Nishino, Ishiura, Suzuki, 957
 shark, characterization, pepsin, specificity, *Nguyen, Nungaray, Martel, Le Goffic, Mollé, Léonil*, 287
 SHP-2, Crk-associated substrate, insulin, insulin-like growth factor I, insulin receptor, *Fujita, Maegawa, Kashiwagi, Hirai, Kikkawa*, 1111
 SHRSP, cholesterol, mevalonate pyrophosphate decarboxylase, pravastatin, *Michihara, Sawamura, Nara, Ikeda, Yamori*, 40
 sialate 7-O-acetyltransferase, bovine submandibular gland, Golgi fraction, O-acetyl migration, sialic acid, *Vandamme-Feldhaus, Schauer*, 111
 sialic acid, bovine submandibular gland, Golgi fraction, O-acetyl migration, sialate 7-O-acetyltransferase, *Vandamme-Feldhaus, Schauer*, 111
 sialidase gene, *Clostridium tertium*, sialidase properties, phylogeny of sialidases, putative acylneuraminase pyruvate lyase gene, *Grobe, Sartori, Traving, Schauer, Roggentin*, 1101
 sialidase properties, *Clostridium tertium*, sialidase gene, phylogeny of sialidases, putative acylneuraminase pyruvate lyase gene, *Grobe, Sartori, Traving, Schauer, Roggentin*, 1101
 sialoglycoprotein, fetal brain, FOG100, monoclonal antibody, O-glycosylation, *Imamura, Hattori, Shiota, Ogawa*, 534
 sigma factor, *Bacillus subtilis*, RNA polymerase, *Fujita, Sadaie*, 89
 signal peptide, baculovirus, manganese superoxide dismutase, mitochondrial import, site-directed mutagenesis, *Fujii, Ikeda, Watanabe, Kawasaki, Suzuki, Fujii, Takahashi, Taniguchi*, 340
 signal transduction, ATP analogue, ATP binding site, fluorescent polarization, myosin, *Maruta, Homma*, 528
 SINE, evolution, exon shuffling, multigene family, protease inhibitor, *Furutani, Kato, Yasue, Alexander, Beattie, Hirose*, 491
 single-headed myosin, extended and folded conformations, filament assembly, phosphorylation-dependent regulation, smooth muscle, *Konishi, Katoh, Morita, Yazawa*, 163
 site-directed mutagenesis, amino acid sequence, inorganic pyrophosphatase, molecular cloning, *Thermus thermophilus*, *Sato, Samejima, Watanabe, Nogi, Takahashi, Kaji, Teplyakov, Obmolova, Kuranova, Ishii*, 79
 —, baculovirus, manganese superoxide dismutase, mitochondrial import, signal peptide, *Fujii, Ikeda, Watanabe, Kawasaki, Suzuki, Fujii, Takahashi, Taniguchi*, 340
 —, cytochrome P450 2B4, electron transfer processes, NH₂-terminus, *Lehnerer, Schulze, Pernecky, Lewis, Eulitz, Hlavica*, 396
 —, carboxypeptidase Y, catalytic histidine, proton-relay system, *Jung, Ueno, Hayashi*, 446
 —, catalytic mechanism, steroid dehydrogenase, X-ray analysis, *Tanabe, Tanaka, Uchikawa, Kabashima, Ito, Nonaka, Mitsui, Tsuru, Yoshimoto*, 634
 —, chymotrypsin inhibitor, *Erythrina variegata*, Kunitz-family protein, primary bind-

ing loop, *Iwanaga, Yamasaki, Kimura*, 663
 site-specific immobilization, association rate constant, dissociation rate constant, lysozyme, surface plasmon resonance, *Ueda, Tsurumaru, Imoto*, 712
 skeletal muscle, Ca²⁺-regulation, force production, myofibril, sarcomere, *Yuri, Wakayama, Yamada*, 565
 small GTPase, COPII vesicle formation, SARI, vesicular transport, yeast *Saccharomyces cerevisiae*, *Saito, Kimura, Oka, Nakano*, 816
 smap-1, erythropoiesis, hematopoietic microenvironment, monoclonal antibody, stem cell, *Sato, Hong, Yanai, Obinata*, 209
 smooth muscle, extended and folded conformations, filament assembly, phosphorylation-dependent regulation, single-headed myosin, *Konishi, Katoh, Morita, Yazawa*, 163
 snake venom, phospholipase A₂, modification of an arginine residue, nonpolarity of the active site, *Chang, Lin, Chang*, 764
 —, phospholipase A₂, modification of an arginine residue, nonpolarity of the active site, *Iwakura, Takenawa, Nakamura*, 769
 South-East Asian ovalocytosis (SAO) band 3, band 3 protein, circular dichroism, Fourier transform infrared, liposome, *Kuma, Inoue, Fu, Ando, Lee, Sugihara, Hamasaki*, 509
 specificity, characterization, pepsin, shark, *Nguyen, Nungaray, Martel, Le Goffic, Mollé, Léonil*, 287
 —, Achromopeptidase, β-lytic protease, mass spectrometry, staphylolysis, *Li, Norioka, Sakiyama*, 332
 spermatogenesis, genomic structure, *Hsp70*, MHC, promoter, *Ito, Ando, Ando, Saijoh, Inoko, Fujimoto*, 347
 spheroid, CDK inhibitor, differentiation, hepatocyte, proliferation, *Hamamoto, Yamada, Kamihira, Iijima*, 972
 sphingolipid, brain development and function, gene targeting, mouse model, sphingolipidosis, *Suzuki, Vanier, Suzuki*, 8
 sphingolipidosis, brain development and function, gene targeting, mouse model, sphingolipid, *Suzuki, Vanier, Suzuki*, 8
Sphingomonas paucimobilis, cytochrome P450, fatty acid, hydrogen peroxide, α-oxidation, *Matsunaga, Yamada, Kusunose, Miki, Ichihara*, 105
 sphingomyelinase, catalytic mechanism, denaturation, enzyme kinetics, Mg²⁺ binding, *Fujii, Inoue, Yamamoto, Ogata, Shinki, Inoue, Tomita, Tamura, Tsukamoto, Ikezawa, Ikeda*, 1178
 sphingosine, ceramide, Neuro2a cells, sphingosine effects, sphingosine metabolism, *Riboni, Prinetti, Bassi, Viani, Tettamanti*, 900
 sphingosine effects, ceramide, Neuro2a cells, sphingosine, sphingosine metabolism, *Riboni, Prinetti, Bassi, Viani, Tettamanti*, 900
 sphingosine metabolism, ceramide, Neuro2a cells, sphingosine, sphingosine effects, *Riboni, Prinetti, Bassi, Viani, Tettamanti*, 900
 splicing variant, lipoprotein, O-linked sugar, VLDL receptor, *Iijima, Miyazawa, Sakai,*

S (cont'd)

- Magoori, Ito, Suzuki, Nose, Kawarabayasi, Yamamoto*, 747
- sporulation, *Bacillus subtilis*, RNA polymerase, transcription factor, *Fujita, Sadate*, 98
- stability, *Fusarium heterosporum*, lipase, C-terminal peptide, *Nagao, Shimada, Sugihara, Tominaga*, 1124
- stabilization, aggregate formation, glucose-fructose oxidoreductase, inactivation, renaturation, *Zymomonas mobilis*, *Fürlinger, Satory, Haltrich, Kulbe, Nidetzky*, 280
- stable isotope, mitochondria, nematode, NMR, tRNA, *Ohtsuki, Kawai, Watanabe*, 28
- staphylolysis, Achromopeptidase, β -lytic protease, mass spectrometry, specificity, *Li, Norioka, Sakiyama*, 332
- steroid dehydrogenase, catalytic mechanism, site-directed mutagenesis, X-ray analysis, *Tanabe, Tanaka, Uchikawa, Kabashima, Ito, Nonaka, Mitsui, Tsuru, Yoshimoto*, 634
- steroid desaturation, hyperexpression, 3-ketosteroid- Δ^1 -dehydrogenase, recombinant enzyme, sequence, *Morii, Fujii, Miyoshi, Iwami, Itagaki*, 1026
- stopped-flow analysis, aminoacyl-tRNA synthetase, fluorescence titration, lysyl-tRNA synthetase, protein fluorescence, *Takita, Akita, Inouye, Tonomura*, 45
- Streptomyces* proteinaceous protease inhibitor, chymotrypsin-type protease, complex formation, endogenous target proteases, gene duplication, *Taguchi, Yamada, Kojima, Momose*, 804
- Streptomyces verticillus*, bleomycin-binding protein, bleomycin-resistance, heat shock proteins, nuclear localization, *Kumagai, Sugiyama*, 835
- stress response, actin-binding protein, cDNA cloning, heat shock, *Physarum polycephalum*, *Matsumoto, Ogawa, Kasakura, Shimada, Mitsui, Maruya, Isohata, Yahara, Murakami-Murofushi*, 326
- stromal cell, erythropoiesis, hematopoietic microenvironment, monoclonal antibody, *smap-1*, *Sato, Hong, Yanai, Obinata*, 209
- structural change, calcium ion, fluorescence energy transfer, melittin, troponin C, *Sano, Takahashi, Iio*, 602
- substrate-recognition, mitochondrial-import, mitochondrial-protein-degradation, peptidase, processing-protease, *Song, Ogi-shima, Ito*, 1045
- substrate specificity, aspartic proteinase, fluorescent substrate, kinetic property proteinase A, *Saccharomyces cerevisiae*, *Kondo, Shibano, Amachi, Cronin, Oda, Dunn*, 141
- , active site structure, mushroom, peptidyl-Lys specific metalloendopeptidase, quenched fluorescent substrate, *Nonaka, Hashimoto, Takio*, 157
- , adenylate kinase, domain exchange, nucleoside monophosphate kinase, UMP/CMP kinase, *Okajima, Fukamizo, Goto, Fukui, Tanizawa*, 359
- , carboxyl proteinase, Gram-negative bacteria, kinetic property, pepstatin, *Shibata, Dunn, Oda*, 642
- , Dopa, high performance liquid chromatography, human M-form phenol sulfotransferase, nuclear magnetic resonance spectrometry, *Suiko, Sakakibara, Awan-Khan, Sakaida, Yoshikawa, Ranasinghe, Liu, 707*
- , expression, mammalian mitochondria, MTF, translational initiation, *Takeuchi, Ueda, Watanabe*, 1069
- subtraction cDNA library, gustatory papillae, taste bud, *Asano-Miyoshi, Kusakabe, Abe, Emori*, 927
- subunit association, heteromeric components, isoprenoid biosynthesis, prenyl diphosphate, prenyltransferase, *Koike-Takeshita, Koyama, Ogura*, 790
- sulfite reductase, cDNA and gene cloning, gene expression, *Nicotiana tabacum*, sulfur-assimilatory gene, *Yonekura-Sakakibara, Ashikari, Tanaka, Kusumi, Hase*, 615
- 6-sulfo sialyl Lewis X, blood cells, central nervous systems, L-selectin ligand, sulfotransferase, *Uchimura, Muramatsu, Kaname, Ogawa, Yamakawa, Fan, Mitsuoka, Kannagi, Habuchi, Yokoyama, Yamamura, Ozaki, Nakagawara, Kadomatsu, Muramatsu*, 670
- sulfotransferase, Dopa, molecular cloning, mouse liver, tyrosine, *Saeki, Sakakibara, Araki, Yanagisawa, Suiko, Nakajima, Liu*, 55
- , blood cells, central nervous systems, L-selectin ligand, 6-sulfo sialyl Lewis X, *Uchimura, Muramatsu, Kaname, Ogawa, Yamakawa, Fan, Mitsuoka, Kannagi, Habuchi, Yokoyama, Yamamura, Ozaki, Nakagawara, Kadomatsu, Muramatsu*, 670
- sulfur-assimilatory gene, cDNA and gene cloning, gene expression, *Nicotiana tabacum*, sulfite reductase, *Yonekura-Sakakibara, Ashikari, Tanaka, Kusumi, Hase*, 615
- sunflower, cDNA cloning, cysteine proteinase, overexpression, phytoecystatin, *Doi-Kawano, Kouzuma, Yamasaki, Kimura*, 911
- suppressor tRNA, amber mutation, co-expression, non-canonical amino acid, tyrosyl-tRNA synthetase, *Ohno, Yokogawa, Fujii, Asahara, Inokuchi, Nishikawa*, 1065
- surface plasmon resonance, association rate constant, dissociation rate constant, lysozyme, site-specific immobilization, *Ueda, Tsurumaru, Imoto*, 712
- synaptic vesicle, asymmetric phospholipid distribution, electric organ, NBD-labeled phospholipid, phospholipid translocation, *Lee, Anzai, Hirashima, Kirino*, 798
- synergism, cellobiohydrolase, endoglucanase, exoglucanase, *Humicola grisea, Takashima, Iikura, Nakamura, Hidaka, Masaki, Uozumi*, 717

T

- tail-anchored protein, ER-targeting sequence, HPC-1/syntaxin 1A, intracellular localization, transmembrane topology, *Masaki, Yamamoto, Akagawa, Tashiro*, 311
- taste bud, gustatory papillae, subtraction cDNA library, *Asano-Miyoshi, Kusakabe, Abe, Emori*, 927
- tau, cdk, microtubule-associated proteins, neurons, phosphorylation, *Wada, Ishiguro, Itoh, Uchida, Hotani, Saito, Kishimoto, Hisanaga*, 738
- T cell activation, CD4, GD1c, glycoprotein, N-glycolylneuraminic acid, *Nohara, Kunitomo, Fujimaki*, 194
- tethered ligand peptide, *para*-fluorophenylalanine, receptor recognition, thrombin, thrombin receptor, *Nose, Fujita, Nakajima, Inoue, Costa, Shimohigashi*, 354
- Tet(K), chloramphenicol acetyltransferase, β -lactamase, tetracycline, topology, *Hirata, Fujihira, Kimura-Someya, Yamaguchi*, 1206
- tetracycline, chloramphenicol acetyltransferase, β -lactamase, Tet(K), topology, *Hirata, Fujihira, Kimura-Someya, Yamaguchi*, 1206
- thapsigargin, $^{45}\text{Ca}^{2+}$ uptake, microsomal ATPase, tracheal epithelium, vanadate, *Kim, Sakong, Cho, Lee*, 1094
- thermolysin, chemical modification, halophilicity, metalloproteinase, salt-activation, tyrosine, *Inouye, Lee, Tonomura*, 72
- Thermus thermophilus*, amino acid sequence, inorganic pyrophosphatase, molecular cloning, site-directed mutagenesis, *Sato, Samejima, Watanabe, Nogi, Takahashi, Kaji, Tplyakov, Obmolova, Kuranova, Ishii*, 79
- three-dimensional structure, nitrite reductase, *Alcaligenes xylooxidans* GIFU, type 1 copper, X-ray crystal analysis, *Inoue, Gotowda, Deligeer, Kataoka, Yamaguchi, Suzuki, Watanabe, Gohow, Kai*, 876
- three-way structure, catalytic RNA, hairpin ribozyme, iNOS, self-trimming, *Komatsu, Shirai, Ohtsuka*, 986
- thrombin, *para*-fluorophenylalanine, receptor recognition, tethered ligand peptide, thrombin receptor, *Nose, Fujita, Nakajima, Inoue, Costa, Shimohigashi*, 354
- thrombin receptor, *para*-fluorophenylalanine, receptor recognition, tethered ligand peptide, thrombin, *Nose, Fujita, Nakajima, Inoue, Costa, Shimohigashi*, 354
- Tim proteins, inner mitochondrial membrane, mitochondria, precursor, protein import, *Ishihara, Komiya, Sakaguchi, Ito, Mihara*, 824
- tissue inhibitor of metalloproteinase-2 (TIMP-2), concanavalin A, gelatinase A (MMP-2), membrane-type matrix metalloproteinase-1 (MT1-MMP), phorbol ester (TPA), *Shofuda, Moriyama, Nishihashi, Higashi, Mizushima, Yasumitsu, Miki, Sato, Seiki, Miyazaki*, 462
- , concanavalin A, gelatinase A (MMP-2), membrane-type matrix metalloproteinase-1 (MT1-MMP), phorbol ester (TPA), *Asakura, Yang, Sottile, Zhang, Jin, Okhuko, Sasaki, Matsuda, Hirata, Mosher*, 473
- tissue kallikrein, mK13 allozyme, prorenin-converting enzyme, *Hosoi, Tada, Tsumura, Kanamori, Yamanaka*, 368
- tissue plasminogen activator, fibrinolysis, α_2 -macroglobulin, pregnancy zone protein, trypsin, *Sánchez, Chiabrando, Gugliel-mone, Bonacci, Rabinovich, Vides*, 274

T (cont'd)

- topology, carbamylation, membrane protein, N-terminal sequencing, urea, *Soulié, Denoroy, Le Caer, Hamasaki, Groves, le Maire*, 417
- , chloramphenicol acetyltransferase, β -lactamase, Tet(K), tetracycline, *Hirata, Fujihira, Kimura-Someya, Yamaguchi*, 1206
- toxin, apoptosis, caspase, ricin, serine protease, *Komatsu, Oda, Muramatsu*, 1038
- tracheal epithelium, $^{45}\text{Ca}^{2+}$ uptake, microsomal ATPase, thapsigargin, vanadate, *Kim, Sakong, Cho, Lee*, 1094
- transamination, active site lysine, alanine racemase, pyridoxal 5'-phosphate, reaction mechanism, *Kurokawa, Watanabe, Yoshimura, Esaki, Soda*, 1163
- transcription, chromatin remodeling, histone acetylation, histone deacetylation, nucleosome, *Hirose*, 1060
- transcriptional regulation, colon carcinoma, MUC1, mucin, tumor antigen, *Shirotani, Irimura*, 585
- transcription factor, *Bacillus subtilis*, RNA polymerase, sporulation, *Fujita, Sadaie*, 98
- transformation, E box element, gene expression, N-myc, RCC1, *Tsuneoka, Mekada*, 1013
- transglutaminase, egg envelope hardening, *Oncorhynchus mykiss*, rainbow trout, vitelline membrane, *Ha, Iuchi*, 917
- translational initiation, expression, mammalian mitochondria, MTF, substrate specificity, *Takeuchi, Ueda, Watanabe*, 1069
- transmembrane topology, ER-targeting sequence, HPC-1/syntaxin 1A, intracellular localization, tail-anchored protein, *Masaki, Yamamoto, Akagawa, Tashiro*, 311
- triple helix, collagen, hydration, hydroxyproline, model peptide, *Nagarajan, Kamitori, Okuyama*, 1117
- tRNA, mitochondria, nematode, NMR, stable isotope, *Ohtsuki, Kawai, Watanabe*, 28
- troponin C, calcium ion, fluorescence energy transfer, melittin, structural change, *Sano, Takahashi, Iio*, 602
- troponin I, amino acid sequence, Ca^{2+} -regulation, Edman degradation, scallop, *Tanaka, Ojima, Nishita*, 304
- trypsin, fibrinolysis, α_2 -macroglobulin, pregnancy zone protein, tissue plasminogen activator, *Sánchez, Chiabrando, Guglielmo, Bonacci, Rabinovich, Vides*, 274
- trypsin-like proteinase, cell cycle, *Escherichia coli*, gene expression, *prlC, Jiang, Zhang, Ding, Yao, Chen, Zhu, Muramatsu*, 980
- tumor antigen, colon carcinoma, MUC1, mucin, transcriptional regulation, *Shirotani, Irimura*, 585
- tumorigenesis, caveolin, HeLa cell, human cell hybrids, tumor suppressor, *Suzuki, Suzuki, Hanada, Hashimoto, Redpath, Stanbridge, Nishijima, Kitagawa*, 383
- tumor invasion, hepatoma cells, integrin, lung metastasis, wortmannin, *Saeki, Seya, Hazeke, Ui, Hazeke, Akedo*, 1020
- tumor marker, anti-polyamine antibody, diacetylspermine, ELISA, urine, *Hiramatsu, Miura, Kamei, Iwasaki, Kawakita*, 231
- , acetyl polyamines, diacetyl spermine, ELISA, monoclonal antibody, *Fujiwara, Kaminishi, Kitagawa, Tsuru, Yabuuchi, Kanetake, Nomata*, 244
- tumor suppressor, caveolin, HeLa cell, human cell hybrids, tumorigenesis, *Suzuki, Suzuki, Hanada, Hashimoto, Redpath, Stanbridge, Nishijima, Kitagawa*, 383
- tunicate, ascidian, NADPH, 6-PGDH, vanadium, *Uyama, Kinoshita, Takahashi, Satoh, Kanamori, Michibata*, 377
- , budding, expressed sequence tags, serine protease inhibitor, *Kawamura, Hayata, Fujiwara, Yubisui*, 1004
- type 1 copper, nitrite reductase, *Alcaligenes xylooxidans* GIFU, three-dimensional structure, X-ray crystal analysis, *Inoue, Gotowda, Deligeer, Kataoka, Yamaguchi, Suzuki, Watanabe, Gohow, Kai*, 876
- tyrosinase-related protein-2, gene transcription, melanin, melanocyte, neurofibromatosis, *Suzuki, Takahashi, Yasumoto, Amai, Yoshizawa, Fuse, Shibahara*, 992
- tyrosine, Dopa, molecular cloning, mouse liver, sulfotransferase, *Saeki, Sakakibara, Araki, Yanagisawa, Suiko, Nakajima, Liu*, 55
- , chemical modification, halophilicity, metalloproteinase, salt-activation, thermolysin, *Inouye, Lee, Tonomura*, 72
- tyrosine phosphorylation, arsenite, cadmium, heme oxygenase-1, hemin, *Masuya, Hioki, Tokunaga, Taketani*, 628
- tyrosyl-tRNA synthetase, amber mutation, co-expression, non-canonical amino acid, suppressor tRNA, *Ohno, Yokogawa, Fujii, Asahara, Inokuchi, Nishikawa*, 1065

U

- ubiquitin, cDNA, human, *in vitro* translation, polymorphism, *Kim, Yamaguchi, Sekine, Saeki, Iwamura, Kato*, 35
- UMP/CMP kinase, adenylate kinase, domain exchange, nucleoside monophosphate kinase, substrate specificity, *Okajima, Fukamizo, Goto, Fukui, Tanizawa*, 359
- urea, carbamylation, membrane protein, N-terminal sequencing, topology, *Soulié, Denoroy, Le Caer, Hamasaki, Groves, le Maire*, 417
- urine, anti-polyamine antibody, diacetylspermine, ELISA, tumor marker, *Hiramatsu, Miura, Kamei, Iwasaki, Kawakita*, 231

V

- vanadate, calmodulin, MLCK, photocleavage, regulatory mechanism, *Maruta, Mitsuhashi, Yamada, Ikebe*, 557
- , $^{45}\text{Ca}^{2+}$ uptake, microsomal ATPase, thapsigargin, tracheal epithelium, *Kim, Sakong, Cho, Lee*, 1094
- vanadium, ascidian, NADPH, 6-PGDH, tunicate, *Uyama, Kinoshita, Takahashi, Satoh, Kanamori, Michibata*, 377
- vesicles, linoleic acid, lipoxigenase-1, oxy-

- genation, phosphatidylcholine, *Kato, Nishiyama, Kuninori*, 294
- vesicle transport, cell growth, cytoskeleton, differentiation, phosphatidylinositol-3 kinase, *Fukui, Ihara, Nagata*, 1
- vesicular transport, COPII vesicle formation, SARI, small GTPase, yeast *Saccharomyces cerevisiae*, *Saito, Kimura, Oka, Nakano*, 816
- vitelline membrane, egg envelope hardening, *Oncorhynchus mykiss*, rainbow trout, transglutaminase, *Ha, Iuchi*, 917
- VLDL receptor, lipoprotein, O-linked sugar, splicing variant, *Iijima, Miyazawa, Sakai, Magoori, Ito, Suzuki, Nose, Kawarabayasi, Yamamoto*, 747
- VLDL secretion, calf liver, fatty acid metabolism, rat liver, *Graulet, Gruffat, Durand, Bauchart*, 1212
- VNTR, fluorescence *in situ* hybridization, gene organization, PTF/SNAPc, *Maeng, Yoon*, 23

W

- wortmannin, hepatoma cells, integrin, lung metastasis, tumor invasion, *Saeki, Seya, Hazeke, Ui, Hazeke, Akedo*, 1020

X

- X-ray analysis, catalytic mechanism, site-directed mutagenesis, steroid dehydrogenase, *Tanabe, Tanaka, Uchikawa, Kabashima, Ito, Nonaka, Mitsui, Tsuru, Yoshimoto*, 634
- X-ray crystal analysis, nitrite reductase, *Alcaligenes xylooxidans* GIFU, type 1 copper, three-dimensional structure, *Inoue, Gotowda, Deligeer, Kataoka, Yamaguchi, Suzuki, Watanabe, Gohow, Kai*, 876
- X-ray crystal structure analysis, membrane protein, *Sakai, Tsukihara*, 1051

Y

- yeast *Saccharomyces cerevisiae*, COPII vesicle formation, SARI, small GTPase, vesicular transport, *Saito, Kimura, Oka, Nakano*, 816

Z

- zinc finger, DNA binding protein, DNA-protein interaction, GC-box, HIV, *Suzuki, Yamamoto, Kurabayashi, Nagai, Yazaki, Horikoshi*, 389
- , embryos, nervous system, nuclear protein, proline-rich domain, *Taguchi, Muramatsu, Fan, Kurosawa, Sobue, Muramatsu*, 1220
- zinc finger-like motif, DnaJ, DnaK, maltose binding protein, molecular chaperone, *Ishii, Sonezaki, Iwasaki, Tauchi, Shingu, Okita, I.-Ogawa, Kato, Kondo*, 842
- zinc ions, apoptosis, caspase-3, geranylgeraniol, HL-60 cells, *Aiuchi, Mihara, Nakaya, Masuda, Nakajo, Nakaya*, 300
- Zymomonas mobilis*, aggregate formation, glucose-fructose oxidoreductase, inactivation, renaturation, stabilization, *Fürlinger, Satory, Haltrich, Kulbe, Nidetzky*, 280