CITATION REPORT List of articles citing

The genome sequence of Schizosaccharomyces pombe

DOI: 10.1038/nature724 Nature, 2002, 415, 871-80.

Source: https://exaly.com/paper-pdf/34728768/citation-report.pdf

Version: 2024-04-10

This report has been generated based on the citations recorded by exaly.com for the above article. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

#	Paper	IF	Citations
1419	A complex of the Srb8, -9, -10, and -11 transcriptional regulatory proteins from yeast. 2002 , 277, 44202-7	7	131
1418	Structural characterization of the human proteome. 2002 , 12, 1625-41		57
1417	tRNomics: analysis of tRNA genes from 50 genomes of Eukarya, Archaea, and Bacteria reveals anticodon-sparing strategies and domain-specific features. 2002 , 8, 1189-232		290
1416	Ctr6, a vacuolar membrane copper transporter in Schizosaccharomyces pombe. 2002 , 277, 46676-86		69
1415	The unique centromeric chromatin structure of Schizosaccharomyces pombe is maintained during meiosis. 2002 , 277, 19817-22		4
1414	What is finished, and why does it matter. 2002 , 12, 669-71		50
1413	Conservation of a portion of the S. cerevisiae Ure2p prion domain that interacts with the full-length protein. 2002 , 99 Suppl 4, 16384-91		76
1412	Histone H3 lysine 4 methylation is mediated by Set1 and promotes maintenance of active chromatin states in fission yeast. 2002 , 99 Suppl 4, 16438-45		100
1411	GTP-yeast actin. 2002 , 277, 41101-9		12
1410	Identification of mammalian mitochondrial translational initiation factor 3 and examination of its role in initiation complex formation with natural mRNAs. 2002 , 277, 35541-9		93
1409	Fep1, an iron sensor regulating iron transporter gene expression in Schizosaccharomyces pombe. 2002 , 277, 22950-8		100
1408	Replicational organization of three weakly expressed loci in Physarum polycephalum. 2002 , 30, 2261-9		3
1407	Abundant poly(A)-bearing RNAs that lack open reading frames in Schizosaccharomyces pombe. 2002 , 9, 209-15		19
1406	Phosphorylation of eukaryotic initiation factor 2 by heme-regulated inhibitor kinase-related protein kinases in Schizosaccharomyces pombe is important for fesistance to environmental stresses. 2002 , 22, 7134-46		60
1405	Dicer is required for chromosome segregation and gene silencing in fission yeast cells. 2002 , 99, 16648-	53	109
1404	Focus on InterPro. 2002 , 3, 221-223		1
1403	GenomeHistory: a software tool and its application to fully sequenced genomes. 2002 , 30, 3378-86		59

(2002-2002)

1402	A fourth component of the fission yeast gamma-tubulin complex, Alp16, is required for cytoplasmic microtubule integrity and becomes indispensable when gamma-tubulin function is compromised. 2002, 13, 2360-73	56
1401	Distinct roles for glutathione S-transferases in the oxidative stress response in Schizosaccharomyces pombe. 2002 , 277, 35523-31	105
1400	Minimal introns are not "junk". 2002 , 12, 1185-9	65
1399	The Ran GTPase system in fission yeast affects microtubules and cytokinesis in cells that are competent for nucleocytoplasmic protein transport. 2002 , 22, 8491-505	28
1398	Two ras pathways in fission yeast are differentially regulated by two ras guanine nucleotide exchange factors. 2002 , 22, 4598-606	63
1397	Identification and characterization of transcription factor IIIA from Schizosaccharomyces pombe. 2002 , 30, 2772-81	14
1396	Interactions between two fission yeast serine/arginine-rich proteins and their modulation by phosphorylation. 2002 , 368, 527-34	17
1395	The transposable elements of the Drosophila melanogaster euchromatin: a genomics perspective. 2002 , 3, RESEARCH0084	387
1394	Hmo1, an HMG-box protein, belongs to the yeast ribosomal DNA transcription system. 2002 , 21, 5498-507	84
1393	Second Fungal Genome Sequenced. 2002 , 106, 386	2
1392	Regulation of heterochromatic silencing and histone H3 lysine-9 methylation by RNAi. 2002, 297, 1833-7	1653
1391	RNAi hushes heterochromatin. 2002 , 3, REVIEWS1035	12
1390	The model unicellular eukaryote, Schizosaccharomyces pombe. 2002 , 3, COMMENT2003	26
1389	Allosteric cascade of spliceosome activation. 2002 , 36, 333-60	296
1388	Patterning and cell differentiation in Hydra: novel genes and the limits to conservation. 2002 , 80, 1670-1677	30
1387	Old Yellow Enzyme from Candida macedoniensis catalyzes the stereospecific reduction of the C=C bond of ketoisophorone. 2002 , 66, 2651-7	68
1386	Conformational changes during the catalytic cycle of gluconate kinase as revealed by X-ray crystallography. 2002 , 318, 1057-69	33
1385	The constraints protein-protein interactions place on sequence divergence. 2002 , 324, 399-407	92

1384	Functional characterization of 4?-phosphopantetheinyl transferase genes of bacterial and fungal origin by complementation of Saccharomyces cerevisiae lys5. 2002 , 213, 51-57	8
1383	Predicting the distribution, conservation, and functions of SNAREs and related proteins in fungi. 2002 , 36, 1-21	56
1382	Meiotic recombination remote from prominent DNA break sites in S. pombe. 2002 , 9, 253-63	106
1381	Is the number of genes we possess limited by the presence of an adaptive immune system?. 2002 , 23, 351-5	10
1380	The 22nd International Specialized Symposium on Yeasts (ISSY 2002) Meast Fermentations and Other Yeast Bioprocesses (12002, 2, 429-432)	
1379	Genomic approaches to fungal pathogenicity. 2002 , 5, 372-8	33
1378	Genomics of parasitic and symbiotic fungi. 2002 , 5, 513-9	66
1377	Conflict begets complexity: the evolution of centromeres. 2002 , 12, 711-8	161
1376	The evolution of developmental regulatory pathways. 2002 , 12, 695-700	11
1375	The evolution of spliceosomal introns. 2002 , 12, 701-10	124
1375 1374	The evolution of spliceosomal introns. 2002 , 12, 701-10 Fission yeast blooms in Kyoto. 2002 , 18, 342-3	124
1374		124
1374	Fission yeast blooms in Kyoto. 2002 , 18, 342-3	124
1374 1373	Fission yeast blooms in Kyoto. 2002 , 18, 342-3 In this Issue. 2002 , 106, 385-386	
1374 1373 1372	Fission yeast blooms in Kyoto. 2002, 18, 342-3 In this Issue. 2002, 106, 385-386 Genome sequencing: and then there were six. 2002, 12, R294-6	2
1374 1373 1372 1371	Fission yeast blooms in Kyoto. 2002, 18, 342-3 In this Issue. 2002, 106, 385-386 Genome sequencing: and then there were six. 2002, 12, R294-6 Evolution of protein kinase signaling from yeast to man. 2002, 27, 514-20 Eukaryotic genomes contain a [2Fez.sbnd;2S] ferredoxin isoform with a conserved C-terminal	725
1374 1373 1372 1371 1370	Fission yeast blooms in Kyoto. 2002, 18, 342-3 In this Issue. 2002, 106, 385-386 Genome sequencing: and then there were six. 2002, 12, R294-6 Evolution of protein kinase signaling from yeast to man. 2002, 27, 514-20 Eukaryotic genomes contain a [2Fez.sbnd;2S] ferredoxin isoform with a conserved C-terminal sequence motif. 2002, 27, 545-7	2 725 14

1366	Website review: how to get the best from fission yeast genome data. 2002 , 3, 282-8		8
1365	Featured organism: Schizosaccharomyces pombe, the fission yeast. 2002 , 3, 194-204		7
1364	Dictyostelium mobile elements: strategies to amplify in a compact genome. 2002 , 59, 2097-111		17
1363	Intron positions delineate the evolutionary path of a pervasively appended peptide in five human aminoacyl-tRNA synthetases. 2002 , 55, 727-33		20
1362	Prospects for functional genomics in Schizosaccharomyces pombe. 2002 , 42, 73-84		19
1361	Phylogenetic classification of transporters and other membrane proteins from Saccharomyces cerevisiae. 2002 , 2, 154-70		50
1360	Calcineurin phosphatase in signal transduction: lessons from fission yeast. 2002 , 7, 619-27		42
1359	Current awareness on yeast. 2002 , 19, 805-12		
1358	What similarity between human and fission yeast proteins is required for orthology?. 2002 , 19, 1125-6		11
1357	Genome-wide search of Schizosaccharomyces pombe genes causing overexpression-mediated cell cycle defects. 2002 , 19, 1139-51		18
1356	Sequence and analysis of chromosome 2 of Dictyostelium discoideum. <i>Nature</i> , 2002 , 418, 79-85	50.4	158
1355	Genome sequence of the human malaria parasite Plasmodium falciparum. <i>Nature</i> , 2002 , 419, 498-511	50.4	3336
1354	Brouhaha over the other yeast. <i>Nature</i> , 2002 , 415, 845-8	50.4	15
1353	How insects lose their limbs. <i>Nature</i> , 2002 , 415, 848-9	50.4	31
1352	The transcriptional program of meiosis and sporulation in fission yeast. 2002 , 32, 143-7		409
1351	The origin and evolution of model organisms. 2002 , 3, 838-49		593
1350	Functional characterization of 4'-phosphopantetheinyl transferase genes of bacterial and fungal origin by complementation of Saccharomyces cerevisiae lys5. 2002 , 213, 51-7		54
1349	The 22nd International Specialized Symposium on Yeasts (ISSY 2002) 'yeast fermentations and other yeast bioprocesses'. 2002 , 2, 429-32		O

1348	Gene expression profiling: methodological challenges, results, and prospects for addiction research. 2002 , 121, 241-56	41
1347	Nobel Lecture. Cyclin dependent kinases and cell cycle control. 2002 , 22, 487-99	101
1346	Pre-spliceosome formation in S.pombe requires a stable complex of SF1-U2AF(59)-U2AF(23). 2002 , 21, 5516-26	48
1345	Plo1(+) regulates gene transcription at the M-G(1) interval during the fission yeast mitotic cell cycle. 2002 , 21, 5745-55	34
1344	Crawling into a new era-the Dictyostelium genome project. 2003 , 22, 1941-6	27
1343	Pre-mRNA splicing in Schizosaccharomyces pombe: regulatory role of a kinase conserved from fission yeast to mammals. 2003 , 42, 241-51	38
1342	Functional characterization of the Frt1 sugar transporter and of fructose uptake in Kluyveromyces lactis. 2003 , 43, 281-8	27
1341	An inventory of the P-type ATPases in the fission yeast Schizosaccharomyces pombe. 2003 , 43, 273-80	11
1340	Revamp a model-status and prospects of the Dictyostelium genome project. 2003 , 44, 59-72	13
1339	Ibp1p, a novel Cdc25-related phosphatase, suppresses Schizosaccharomyces pombe hsk1 (cdc7). 2003 , 44, 38-48	5
1338	Structure, function and evolution of haspin and haspin-related proteins, a distinctive group of eukaryotic protein kinases. 2003 , 60, 446-62	37
1337	Strand compositional asymmetries of nuclear DNA in eukaryotes. 2003 , 57, 325-34	18
1336	Terminal deoxynucleotidyl transferases from elasmobranchs reveal structural conservation within vertebrates. 2003 , 55, 594-604	14
1335	Candicidin biosynthesis in Streptomyces griseus. 2003 , 60, 633-42	27
1334	MCB-mediated regulation of cell cycle-specific cdc22+ transcription in fission yeast. 2003 , 269, 765-75	12
1333	Comparative genomics of yeast species: new insights into their biology. 2003 , 6, 183-90	13
1332	Fungal biotechnology. 2003 , 6, 191-9	112
1331	Genome comparisons and analysis. 2003 , 13, 344-52	23

(2003-2003)

1330	A new role for the transcriptional corepressor SIN3; regulation of centromeres. 2003 , 13, 68-72	60
1329	S. pombe aurora kinase/survivin is required for chromosome condensation and the spindle checkpoint attachment response. 2003 , 13, 590-7	125
1328	Sir2 regulates histone H3 lysine 9 methylation and heterochromatin assembly in fission yeast. 2003 , 13, 1240-6	162
1327	Neurospora Crassa has Twice the Genes of Schizosaccharomyces Pombe. 2003 , 107, 1011	
1326	The COG database: an updated version includes eukaryotes. 2003 , 4, 41	3212
1325	Molecular phylogeny of the kelch-repeat superfamily reveals an expansion of BTB/kelch proteins in animals. 2003 , 4, 42	126
1324	No simple dependence between protein evolution rate and the number of protein-protein interactions: only the most prolific interactors tend to evolve slowly. 2003 , 3, 1	158
1323	Whole-genome microarrays of fission yeast: characteristics, accuracy, reproducibility, and processing of array data. 2003 , 4, 27	176
1322	Regulated mRNA stability of the Cdk inhibitor Rum1 links nutrient status to cell cycle progression. 2003 , 13, 2015-24	23
1321	Cytokinesis in fission yeast: a story of rings, rafts and walls. 2003 , 19, 403-8	46
1320	Model systems in drug discovery: chemical genetics meets genomics. 2003 , 99, 183-220	37
1319	Growing Yeast for Fun and Profit: Use of Saccharomyces Cerevisiae as a Model System in Drug Discovery. 9-39	O
1318	A relational database for the discovery of genes encoding amino acid biosynthetic enzymes in pathogenic fungi. 2003 , 4, 4-15	9
1317	Microbial ferric iron reductases. 2003 , 27, 427-47	220
1316	K+ fluxes in Schizosaccharomyces pombe. 2003 , 4, 1-6	8
1315	A brute force postgenome approach to identify temperature-sensitive mutations that negatively interact with separase and securin plasmids. 2003 , 8, 341-55	8
1314	Overlapping omt1+ and omt2+ genes are required for spore wall maturation in Schizosaccharomyces pombe. 2003 , 8, 547-58	9
1313	Glycerol dehydrogenase, encoded by gldB is essential for osmotolerance in Aspergillus nidulans. 2003 , 49, 131-41	56

1312	Schizosaccharomyces pombe as a model for metal homeostasis in plant cells: the phytochelatin-dependent pathway is the main cadmium detoxification mechanism. 2003 , 159, 323-330	59
1311	Characterization of vps33+, a gene required for vacuolar biogenesis and protein sorting in Schizosaccharomyces pombe. 2003 , 20, 845-55	36
1310	DNA sequence of the mat2,3 region of Schizosaccharomyces kambucha shares high homology with the corresponding sequence from Sz. pombe. 2003 , 20, 1273-8	8
1309	Structural characterization of chromosome I size variants from a natural yeast strain. 2003, 20, 171-83	22
1308	Isolation and characterization of the plasma membrane biotin transporter from Schizosaccharomyces pombe. 2003 , 20, 221-31	23
1307	Transcriptome characterization of the dimorphic and pathogenic fungus Paracoccidioides brasiliensis by EST analysis. 2003 , 20, 263-71	65
1306	cDNA cloning, biochemical and phylogenetic characterization of beta- and beta'-subunits of Candida albicans protein kinase CK2. 2003 , 20, 471-8	2
1305	A 'marker switch' approach for targeted mutagenesis of genes in Schizosaccharomyces pombe. 2003 , 20, 587-94	29
1304	Verification of a new gene on Saccharomyces cerevisiae chromosome III. 2003 , 20, 731-8	4
1303	Systematic functional analysis of the Caenorhabditis elegans genome using RNAi. <i>Nature</i> , 2003 , 421, 231-7	2758
	421, 231 7	1/3
1302	Genome-wide distribution of DNA replication origins at A+T-rich islands in Schizosaccharomyces pombe. 2003 , 4, 1048-53	133
1302	Genome-wide distribution of DNA replication origins at A+T-rich islands in Schizosaccharomyces	, ,
	Genome-wide distribution of DNA replication origins at A+T-rich islands in Schizosaccharomyces pombe. 2003 , 4, 1048-53 GermOnline, a new cross-species community annotation database on germ-line development and gametogenesis. 2003 , 35, 291-2	133
1301	Genome-wide distribution of DNA replication origins at A+T-rich islands in Schizosaccharomyces pombe. 2003 , 4, 1048-53 GermOnline, a new cross-species community annotation database on germ-line development and gametogenesis. 2003 , 35, 291-2	133
1301 1300 1299	Genome-wide distribution of DNA replication origins at A+T-rich islands in Schizosaccharomyces pombe. 2003, 4, 1048-53 GermOnline, a new cross-species community annotation database on germ-line development and gametogenesis. 2003, 35, 291-2 Chipping away at the chip bias: RNA degradation in microarray analysis. 2003, 35, 292-3	133 18 168
1301 1300 1299	Genome-wide distribution of DNA replication origins at A+T-rich islands in Schizosaccharomyces pombe. 2003, 4, 1048-53 GermOnline, a new cross-species community annotation database on germ-line development and gametogenesis. 2003, 35, 291-2 Chipping away at the chip bias: RNA degradation in microarray analysis. 2003, 35, 292-3 Fungal genomics beyond Saccharomyces cerevisiae?. 2003, 14, 226-31	133 18 168 27
1301 1300 1299 1298	Genome-wide distribution of DNA replication origins at A+T-rich islands in Schizosaccharomyces pombe. 2003, 4, 1048-53 GermOnline, a new cross-species community annotation database on germ-line development and gametogenesis. 2003, 35, 291-2 Chipping away at the chip bias: RNA degradation in microarray analysis. 2003, 35, 292-3 Fungal genomics beyond Saccharomyces cerevisiae?. 2003, 14, 226-31 Astrophysics in 2002. 2003, 115, 514-591	133 18 168 27

(2003-2003)

1294	ABC-transporters: implications on drug resistance from microorganisms to human cancers. 2003 , 22, 188-99	201
1293	Evolution of key cell signaling and adhesion protein families predates animal origins. 2003, 301, 361-3	322
1292	Eukaryotic domain evolution inferred from genome comparisons. 2003 , 13, 623-8	31
1291	Identification of a SNARE protein required for vacuolar protein transport in Schizosaccharomyces pombe. 2003 , 311, 77-82	13
1290	HmCRIP, a cysteine-rich intestinal protein, is expressed by an identified regenerating nerve cell. 2003 , 533, 124-8	13
1289	Cyclophilin sensitivity to sanglifehrin A can be correlated to the same specific tryptophan residue as cyclosporin A. 2003 , 555, 335-40	5
1288	The mitochondrial genome of the thermal dimorphic fungus Penicillium marneffei is more closely related to those of molds than yeasts. 2003 , 555, 469-77	54
1287	Schizosaccharomyces pombe Int6 and Ras homologs regulate cell division and mitotic fidelity via the proteasome. 2003 , 112, 207-17	74
1286	Plasmodium biology: genomic gleanings. 2003 , 115, 771-85	258
1285	Conservation of the heterochronic regulator Lin-28, its developmental expression and microRNA complementary sites. 2003 , 258, 432-42	247
1284	The kic1 kinase of schizosaccharomyces pombe is a CLK/STY orthologue that regulates cell-cell separation. 2003 , 283, 101-15	13
1283	Distinguishing plant and fungal sequences in ESTs from infected plant tissues. 2003 , 54, 339-51	16
1282	Retrotransposons and their recognition of pol II promoters: a comprehensive survey of the transposable elements from the complete genome sequence of Schizosaccharomyces pombe. 2003 , 13, 1984-97	115
1281	Characterization of the genomic organization of the region bordering the centromere of chromosome V of Podospora anserina by direct sequencing. 2003 , 39, 250-63	22
1280	Overview of Schizosaccharomyces pombe. 2003 , Chapter 13, Unit 13.14	5
1279	Reinvestigation of the Saccharomyces cerevisiae genome annotation by comparison to the genome of a related fungus: Ashbya gossypii. 2003 , 4, R45	91
1278	Translational recoding signals between gag and pol in diverse LTR retrotransposons. 2003 , 9, 1422-30	68
1277	Candida albicans secreted aspartyl proteinases in virulence and pathogenesis. 2003 , 67, 400-28, table of contents	760

1276	Phylogenomics: intersection of evolution and genomics. 2003 , 300, 1706-7	244
1275	Cpc2/RACK1 is a ribosome-associated protein that promotes efficient translation in Schizosaccharomyces pombe. 2003 , 278, 49119-28	64
1274	A comparison of three fission yeast mitochondrial genomes. 2003 , 31, 759-68	100
1273	MGAlignIt: A web service for the alignment of mRNA/EST and genomic sequences. 2003 , 31, 3533-6	28
1272	Functional genetics of industrial yeasts; of ancient skills and modern applications. 2003, 1-16	2
1271	The genetic basis of cellular morphogenesis in the filamentous fungus Neurospora crassa. 2003 , 14, 4352-64	161
127 0	Evolution of the Fungi and their Mitochondrial Genomes. 2003 , 3, 133-159	9
1269	SimiTrivisualizing similarity relationships for groups of sequences. 2003 , 19, 390-5	59
1268	Rpn5 is a conserved proteasome subunit and required for proper proteasome localization and assembly. 2003 , 278, 30669-76	32
1267	The phylogenetic diversity of eukaryotic transcription. 2003 , 31, 653-60	36
1266	FELINES: a utility for extracting and examining EST-defined introns and exons. 2003, 31, e141	15
1265	Assessment of genome-wide protein function classification for Drosophila melanogaster. 2003 , 13, 2118-28	35
1264	Retention but not recruitment of Crb2 at double-strand breaks requires Rad1 and Rad3 complexes. 2003 , 23, 6150-8	82
1263	An ordered collection of expressed sequences from Cryphonectria parasitica and evidence of genomic microsynteny with Neurospora crassa and Magnaporthe grisea. 2003 , 149, 2373-2384	35
1262	Dimethyl sulfoxide exposure facilitates phospholipid biosynthesis and cellular membrane proliferation in yeast cells. 2003 , 278, 33185-93	62
1261	Rpb7 subunit of RNA polymerase II interacts with an RNA-binding protein involved in processing of transcripts. 2003 , 31, 4696-701	38
1260	Viewing and annotating sequence data with Artemis. 2003, 4, 124-32	121
1259	Gef1p and Scd1p, the Two GDP-GTP exchange factors for Cdc42p, form a ring structure that shrinks during cytokinesis in Schizosaccharomyces pombe. 2003 , 14, 3617-27	52

1258	A novel jmjC domain protein modulates heterochromatization in fission yeast. 2003 , 23, 4356-70	115
1257	Schizosaccharomyces pombe Rdh54 (TID1) acts with Rhp54 (RAD54) to repair meiotic double-strand breaks. 2003 , 14, 4707-20	43
1256	Schizosaccharomyces pombe essential genes: a pilot study. 2003 , 13, 399-406	61
1255	Molecular characterization of the Schizosaccharomyces pombe nbs1+ gene involved in DNA repair and telomere maintenance. 2003 , 23, 6553-63	48
1254	Nuclear factories for signalling and repairing DNA double strand breaks in living fission yeast. 2003 , 31, 5064-73	61
1253	Global transcriptional responses of fission yeast to environmental stress. 2003 , 14, 214-29	629
1252	Comparative analysis of the base biases at the gene terminal portions in seven eukaryote genomes. 2003 , 31, 5195-201	28
1251	A reticular rhapsody: phylogenic evolution and nomenclature of the RTN/Nogo gene family. 2003 , 17, 1238-47	132
1250	Correlations between gene expression and gene conservation in fission yeast. 2003 , 13, 2686-90	29
1249	Sequence Evolution Function. 2003,	103
.,	Sequence Evolution Function. 2003, Parallel evolution by gene duplication in the genomes of two unicellular fungi. 2003, 13, 794-9	103
.,		
1248	Parallel evolution by gene duplication in the genomes of two unicellular fungi. 2003 , 13, 794-9 Dsl1p, an essential component of the Golgi-endoplasmic reticulum retrieval system in yeast, uses	36
1248	Parallel evolution by gene duplication in the genomes of two unicellular fungi. 2003, 13, 794-9 Dsl1p, an essential component of the Golgi-endoplasmic reticulum retrieval system in yeast, uses the same sequence motif to interact with different subunits of the COPI vesicle coat. 2003, 278, 51722-34	36 76
1248 1247 1246	Parallel evolution by gene duplication in the genomes of two unicellular fungi. 2003, 13, 794-9 Dsl1p, an essential component of the Golgi-endoplasmic reticulum retrieval system in yeast, uses the same sequence motif to interact with different subunits of the COPI vesicle coat. 2003, 278, 51722-34 Preferential attachment in the protein network evolution. 2003, 91, 138701 What's in the genome of a filamentous fungus? Analysis of the Neurospora genome sequence.	36 76 153
1248 1247 1246 1245	Parallel evolution by gene duplication in the genomes of two unicellular fungi. 2003, 13, 794-9 Dsl1p, an essential component of the Golgi-endoplasmic reticulum retrieval system in yeast, uses the same sequence motif to interact with different subunits of the COPI vesicle coat. 2003, 278, 51722-34 Preferential attachment in the protein network evolution. 2003, 91, 138701 What's in the genome of a filamentous fungus? Analysis of the Neurospora genome sequence. 2003, 31, 1944-54	36 76 153 55
1248 1247 1246 1245	Parallel evolution by gene duplication in the genomes of two unicellular fungi. 2003, 13, 794-9 Dsl1p, an essential component of the Golgi-endoplasmic reticulum retrieval system in yeast, uses the same sequence motif to interact with different subunits of the COPI vesicle coat. 2003, 278, 51722-34 Preferential attachment in the protein network evolution. 2003, 91, 138701 What's in the genome of a filamentous fungus? Analysis of the Neurospora genome sequence. 2003, 31, 1944-54 RNA interference, transposons, and the centromere. 2003, 15, 297-301 Schizosaccharomyces pombe cells deficient in triacylglycerols synthesis undergo apoptosis upon	36761535552

1240	Relationship between RNA lariat debranching and Ty1 element retrotransposition. 2003 , 77, 12795-806	23
1239	Spoilage yeasts with emphasis on the genus Zygosaccharomyces. 2003 , 171-191	13
1238	INT6: A Link Between the Proteasome and Tumorigenesis. 2003 , 2, 80-82	11
1237	Sim4: a novel fission yeast kinetochore protein required for centromeric silencing and chromosome segregation. 2003 , 161, 295-307	99
1236	Asymmetric sequence divergence of duplicate genes. 2003 , 13, 2052-8	175
1235	Genome Sequencing, Assembly and Gene Prediction in Fungi. 2003 , 3, 65-81	1
1234	Molecular evolution of eukaryotic genomes: hemiascomycetous yeast spliceosomal introns. 2003 , 31, 1121-35	101
1233	Azollaa model organism for plant genomic studies. 2003 , 1, 15-25	12
1232	Super models. 2003 , 13, 15-24	61
1231	Increasing biological complexity is positively correlated with the relative genome-wide expansion of non-protein-coding DNA sequences. 2003 , 5, P1	30
1230	Vesicle-mediated protein transport pathways to the vacuole in Schizosaccharomyces pombe. 2003 , 28, 399-417	43
1229	A report on single exon genes (SEG) in eukaryotes. 2004 , 9, 3262-7	21
1228	Cell cycle molecules and mechanisms of the budding and fission yeasts. 2005 , 296, 3-29	17
1227	Parasite Genomics Protocols. 2004,	2
1226	The nucleolus is involved in mRNA export from the nucleus in fission yeast. 2004 , 117, 2887-95	37
1225	Meiotic chromosome segregation mutants identified by insertional mutagenesis of fission yeast Schizosaccharomyces pombe; tandem-repeat, single-site integrations. 2004 , 32, 4400-10	10
1224	Differential gene expression in auristatin PHE-treated Cryptococcus neoformans. 2004 , 48, 561-7	8
1223	A comparative analysis of an orthologous proteomic environment in the yeasts Saccharomyces cerevisiae and Schizosaccharomyces pombe. 2004 , 3, 125-32	31

(2004-2004)

	2004 , 24, 4229-40	37
1221	Forespore membrane assembly in yeast: coordinating SPBs and membrane trafficking. 2004 , 117, 389-96	80
1220	Genome-wide prediction of stop codon readthrough during translation in the yeast Saccharomyces cerevisiae. 2004 , 32, 6605-16	57
1219	pdf1, a palmitoyl protein thioesterase 1 Ortholog in Schizosaccharomyces pombe: a yeast model of infantile Batten disease. 2004 , 3, 302-10	11
1218	Global gene expression responses of fission yeast to ionizing radiation. 2004 , 15, 851-60	56
1217	Role of the alpha-glucanase Agn1p in fission-yeast cell separation. 2004 , 15, 3903-14	99
1216	Proteomic study for the cellular responses to Cd2+ in Schizosaccharomyces pombe through amino acid-coded mass tagging and liquid chromatography tandem mass spectrometry. 2004 , 3, 596-607	59
1215	Suppressors of an adenylate cyclase deletion in the fission yeast Schizosaccharomyces pombe. 2004 , 3, 610-9	40
1214	Five genes involved in biosynthesis of the pyruvylated Galbeta1,3-epitope in Schizosaccharomyces pombe N-linked glycans. 2004 , 279, 35644-55	28
1213	Requirements of fission yeast septins for complex formation, localization, and function. 2004 , 15, 5551-64	68
1212	Control of Late Meiosis and Ascospore Formation. 2004 , 311-327	21
1212		21 72
1211	A novel phosphatidylinositol(3,4,5)P3 pathway in fission yeast. 2004 , 166, 205-11 A novel type of silencing factor, Clr2, is necessary for transcriptional silencing at various	72
1211	A novel phosphatidylinositol(3,4,5)P3 pathway in fission yeast. 2004, 166, 205-11 A novel type of silencing factor, Clr2, is necessary for transcriptional silencing at various chromosomal locations in the fission yeast Schizosaccharomyces pombe. 2004, 32, 4421-8	7 ² 8
1211 1210 1209	A novel phosphatidylinositol(3,4,5)P3 pathway in fission yeast. 2004, 166, 205-11 A novel type of silencing factor, Clr2, is necessary for transcriptional silencing at various chromosomal locations in the fission yeast Schizosaccharomyces pombe. 2004, 32, 4421-8 Genome update: Length distributions of sequenced prokaryotic genomes. 2004, 150, 513-516 Eukaryotic regulatory element conservation analysis and identification using comparative	7 ² 8
1211 1210 1209 1208	A novel phosphatidylinositol(3,4,5)P3 pathway in fission yeast. 2004, 166, 205-11 A novel type of silencing factor, Clr2, is necessary for transcriptional silencing at various chromosomal locations in the fission yeast Schizosaccharomyces pombe. 2004, 32, 4421-8 Genome update: Length distributions of sequenced prokaryotic genomes. 2004, 150, 513-516 Eukaryotic regulatory element conservation analysis and identification using comparative genomics. 2004, 14, 451-8 Comparative genomics of transcriptional control in the human malaria parasite Plasmodium	7 ² 8 9 113

1204	Rice Blast: Interaction with Rice and Control. 2004,	1
1203	Neurospora in Temperate Forests of Western North America. 2004 , 96, 66	31
1202	In vivo activation of protein kinase A in Schizosaccharomyces pombe requires threonine phosphorylation at its activation loop and is dependent on PDK1. 2004 , 168, 1843-53	19
1201	The Ashbya Genome Database (AGD)a tool for the yeast community and genome biologists. 2005 , 33, D348-52	15
12 00	Comparative analysis detects dependencies among the 5' splice-site positions. 2004 , 10, 828-40	151
1199	Fkh2p and Sep1p regulate mitotic gene transcription in fission yeast. 2004 , 117, 5623-32	57
1198	CYGD: the Comprehensive Yeast Genome Database. 2005 , 33, D364-8	242
1197	Schizosaccharomyces pombe Pmr1p is essential for cell wall integrity and is required for polarized cell growth and cytokinesis. 2004 , 3, 1124-35	32
1196	Introns and splicing elements of five diverse fungi. 2004 , 3, 1088-100	215
1195	Conserved and nonconserved proteins for meiotic DNA breakage and repair in yeasts. 2004 , 167, 593-605	94
1194	A workshop report on wheat genome sequencing: International Genome Research on Wheat Consortium. 2004 , 168, 1087-96	245
1193	Robustness of metabolic map reconstruction. 2004 , 2, 589-93	1
1192	The Ashbya gossypii genome as a tool for mapping the ancient Saccharomyces cerevisiae genome. 2004 , 304, 304-7	558
1191	Enrichment of transcriptional regulatory sites in non-coding genomic region. 2004 , 20, 569-75	5
1190	Expression and complexity of the PRT1 multigene family of Pneumocystis carinii. 2004, 150, 293-300	23
1189	Conservation and evolution of cis-regulatory systems in ascomycete fungi. 2004 , 2, e398	174
1188	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. 2004 , 2, e162	255
1187	A phylogenomic approach to reconstructing the diversification of serine proteases in fungi. 2004 , 17, 1204-14	58

(2004-2004)

	2004, 271, 2561-72		11
1185	An interactive gene network for securin-separase, condensin, cohesin, Dis1/Mtc1 and histones constructed by mass transformation. 2004 , 9, 1069-82		31
1184	Yeast genome sequencing: the power of comparative genomics. 2004 , 53, 381-9		84
1183	Characterisation and expression of a gene encoding a mutarotase from the fungus Rhizopus nigricans. 2004 , 235, 101-108		2
1182	Genome sequence of the lignocellulose degrading fungus Phanerochaete chrysosporium strain RP78. 2004 , 22, 695-700		710
1181	Periodic gene expression program of the fission yeast cell cycle. 2004 , 36, 809-17		402
1180	How did alternative splicing evolve?. 2004 , 5, 773-82		429
1179	PRMT3 is a ribosomal protein methyltransferase that affects the cellular levels of ribosomal subunits. 2004 , 23, 2641-50		129
1178	A chromodomain protein, Chp1, is required for the establishment of heterochromatin in fission yeast. 2004 , 23, 3825-35		174
1177	Genome sequence of the ultrasmall unicellular red alga Cyanidioschyzon merolae 10D. <i>Nature</i> , 2004 , 428, 653-7	50.4	907
1176	Concern qualities in veneta Natura 2004 420 25 44		1324
1176	Genome evolution in yeasts. <i>Nature</i> , 2004 , 430, 35-44	50.4	J 1
,	Conservation of protein-protein interactions - lessons from ascomycota. 2004 , 20, 72-6	50.4	33
,		50.4	
1175	Conservation of protein-protein interactions - lessons from ascomycota. 2004 , 20, 72-6	50.4	33
1175	Conservation of protein-protein interactions - lessons from ascomycota. 2004 , 20, 72-6 New type of polyubiquitin-like genes with intein-like autoprocessing domains. 2004 , 20, 538-42	50.4	33
1175 1174 1173	Conservation of protein-protein interactions - lessons from ascomycota. 2004 , 20, 72-6 New type of polyubiquitin-like genes with intein-like autoprocessing domains. 2004 , 20, 538-42 Evolutionary dynamics of transposable elements at the centromere. 2004 , 20, 611-6 Production of recombinant human lysosomal acid lipase in Schizosaccharomyces pombe:	50.4	33 20 70
1175 1174 1173 1172	Conservation of protein-protein interactions - lessons from ascomycota. 2004, 20, 72-6 New type of polyubiquitin-like genes with intein-like autoprocessing domains. 2004, 20, 538-42 Evolutionary dynamics of transposable elements at the centromere. 2004, 20, 611-6 Production of recombinant human lysosomal acid lipase in Schizosaccharomyces pombe: development of a fed-batch fermentation and purification process. 2004, 98, 366-73 Characterization of two fructosyl-amino acid oxidase homologs of Schizosaccharomyces pombe.	50.4	33 20 70 23

1168	Kinetochore and heterochromatin domains of the fission yeast centromere. 2004 , 12, 521-34	100
1167	Changes in gene expression at the precursor> stem cell transition in leech. 2004 , 22, 514-21	2
1166	The transcription factor Pap1/Caf3 plays a central role in the determination of caffeine resistance in Schizosaccharomyces pombe. 2004 , 271, 161-70	15
1165	Glutamic protease distribution is limited to filamentous fungi. 2004 , 239, 95-101	37
1164	A distinct type of alcohol dehydrogenase, adh4+, complements ethanol fermentation in an adh1-deficient strain of Schizosaccharomyces pombe. 2004 , 4, 649-54	13
1163	Ferrichrome in Schizosaccharomyces pombean iron transport and iron storage compound. 2004 , 17, 647-54	49
1162	The Metarhizium anisopliae trp1 gene: cloning and regulatory analysis. 2004 , 49, 66-70	3
1161	RNA polymerase II transcription apparatus in Schizosaccharomyces pombe. 2004 , 44, 287-94	16
1160	A fission yeast strain expressing human CDC25A phosphatase: a tool for selectivity studies of pharmacological inhibitors of CDC25. 2004 , 45, 283-8	5
1159	Molecular evolution of FtsZ protein sequences encoded within the genomes of archaea, bacteria, and eukaryota. 2004 , 58, 19-29	144
1159 1158		144
	and eukaryota. 2004 , 58, 19-29	
1158	and eukaryota. 2004 , 58, 19-29 Molecular evolution in large genetic networks: does connectivity equal constraint?. 2004 , 58, 203-11 The origin of eukaryotes is suggested as the symbiosis of pyrococcus into gamma-proteobacteria	121
1158	And eukaryota. 2004, 58, 19-29 Molecular evolution in large genetic networks: does connectivity equal constraint?. 2004, 58, 203-11 The origin of eukaryotes is suggested as the symbiosis of pyrococcus into gamma-proteobacteria by phylogenetic tree based on gene content. 2004, 59, 606-19	121
1158 1157 1156	And eukaryota. 2004, 58, 19-29 Molecular evolution in large genetic networks: does connectivity equal constraint?. 2004, 58, 203-11 The origin of eukaryotes is suggested as the symbiosis of pyrococcus into gamma-proteobacteria by phylogenetic tree based on gene content. 2004, 59, 606-19 Function-dependent clustering of orthologues and paralogues of cyclophilins. 2004, 56, 808-20	121 38 37
1158 1157 1156 1155	A DNA microarray for fission yeast: minimal changes in global gene expression after temperature	121383775
1158 1157 1156 1155 1154	Molecular evolution in large genetic networks: does connectivity equal constraint?. 2004, 58, 203-11 The origin of eukaryotes is suggested as the symbiosis of pyrococcus into gamma-proteobacteria by phylogenetic tree based on gene content. 2004, 59, 606-19 Function-dependent clustering of orthologues and paralogues of cyclophilins. 2004, 56, 808-20 Has the yo-yo stopped? An assessment of human protein-coding gene number. 2004, 4, 1712-26 A DNA microarray for fission yeast: minimal changes in global gene expression after temperature shift. 2004, 21, 25-39 A new approach to species determination for yeast strains: DNA microarray-based comparative genomic hybridization using a yeast DNA microarray with 6000 genes. 2004, 21, 351-65	12138377537

(2004-2004)

1150	Posttranslational activation, site-directed mutation and phylogenetic analyses of the lysine biosynthesis enzymes alpha-aminoadipate reductase Lys1p (AAR) and the phosphopantetheinyl transferase Lys7p (PPTase) from Schizosaccharomyces pombe. 2004 , 21, 1279-88	9
1149	Hop: more than an Hsp70/Hsp90 adaptor protein. 2004 , 26, 1058-68	177
1148	A note on clustering the functionally-related paralogues and orthologues of proteins: a case of the FK506-binding proteins (FKBPs). 2004 , 28, 129-40	30
1147	A set of loxP marker cassettes for Cre-mediated multiple gene disruption in Schizosaccharomyces pombe. 2004 , 68, 545-50	44
1146	The structure of cell wall alpha-glucan from fission yeast. 2005 , 15, 245-57	82
1145	Recent progress, developments, and issues in comparative fungal genomics. 2004 , 26, 19-30	7
1144	Analysis of Phenetic Trees Based on Metabolic Capabilites Across the Three Domains of Life. 2004 , 48, 491-491	
1143	Structure, function, and mechanism of ribonucleotide reductases. 2004 , 1699, 1-34	199
1142	Glutathione, altruistic metabolite in fungi. 2004 , 49, 1-76	205
1141	Cell Cycle Control. 2004 ,	1
1140	The Molecular Biology of Schizosaccharomyces pombe. 2004 ,	21
1140	The Molecular Biology of Schizosaccharomyces pombe. 2004 ,	
,	The Molecular Biology of Schizosaccharomyces pombe. 2004 , Complete genome sequence of the apicomplexan, Cryptosporidium parvum. 2004 , 304, 441-5	21
1139	The Molecular Biology of Schizosaccharomyces pombe. 2004 , Complete genome sequence of the apicomplexan, Cryptosporidium parvum. 2004 , 304, 441-5	21 757
1139	The Molecular Biology of Schizosaccharomyces pombe. 2004, Complete genome sequence of the apicomplexan, Cryptosporidium parvum. 2004, 304, 441-5 GeneDB: a resource for prokaryotic and eukaryotic organisms. 2004, 32, D339-43 Plant Surface Microbiology. 2004,	21 757 190
1139 1138 1137	The Molecular Biology of Schizosaccharomyces pombe. 2004, Complete genome sequence of the apicomplexan, Cryptosporidium parvum. 2004, 304, 441-5 GeneDB: a resource for prokaryotic and eukaryotic organisms. 2004, 32, D339-43 Plant Surface Microbiology. 2004,	21 757 190
1139 1138 1137 1136	The Molecular Biology of Schizosaccharomyces pombe. 2004, Complete genome sequence of the apicomplexan, Cryptosporidium parvum. 2004, 304, 441-5 GeneDB: a resource for prokaryotic and eukaryotic organisms. 2004, 32, D339-43 Plant Surface Microbiology. 2004, Global expression changes resulting from loss of telomeric DNA in fission yeast. 2005, 6, R1 A comprehensive evolutionary classification of proteins encoded in complete eukaryotic genomes.	21 757 190 9

1132	Characterisation and expression of a gene encoding a mutarotase from the fungus Rhizopus nigricans. 2004 , 235, 101-8	1
1131	Evolution of the gene encoding mitochondrial intermediate peptidase and its cosegregation with the A mating-type locus of mushroom fungi. 2004 , 41, 381-90	44
1130	Insight into the genome of Aspergillus fumigatus: analysis of a 922 kb region encompassing the nitrate assimilation gene cluster. 2004 , 41, 443-53	50
1129	A comparative genomic analysis of the calcium signaling machinery in Neurospora crassa, Magnaporthe grisea, and Saccharomyces cerevisiae. 2004 , 41, 827-41	113
1128	A comparison of the nature and abundance of microsatellites in 14 fungal genomes. 2004 , 41, 1025-36	103
1127	Differential expression and role of two dithiol glutaredoxins Grx1 and Grx2 in Schizosaccharomyces pombe. 2004 , 321, 922-9	15
1126	Protocols for experimentation with Schizosaccharomyces pombe. 2004 , 33, 187-8	9
1125	Analysis of phenetic trees based on metabolic capabilites across the three domains of life. 2004 , 340, 491-512	27
1124	The human protein translin specifically binds single-stranded microsatellite repeats, d(GT)n, and G-strand telomeric repeats, d(TTAGGG)n: a study of the binding parameters. 2004 , 344, 939-50	28
1123	The fission yeast TOR proteins and the rapamycin response: an unexpected tale. 2004 , 279, 85-95	26
1122	Proteomics and data standardisation. 2004 , 2, 91-93	2
1121	Functional roles for evolutionarily conserved Spt4p at centromeres and heterochromatin in Saccharomyces cerevisiae. 2004 , 23, 1804-14	47
112 0	Expressed sequence tags: medium-throughput protocols. 2004 , 270, 75-92	8
1119	Cloning and overexpression of the old yellow enzyme gene of Candida macedoniensis, and its application to the production of a chiral compound. 2004 , 114, 1-9	75
1118	Genomic and Proteomic Databases and Applications: A Challenge for Database Technology. 2004 , 1-24	1
1117	Functional Genomic Analysis of the Rice Blast Fungus Magnaporthe grisea. 2004 , 331-352	1
1116	Molecular analysis of muskelin identifies a conserved discoidin-like domain that contributes to protein self-association. 2004 , 381, 547-59	17
1115	Genomics in Neurospora crassa: From One-Gene-One-Enzyme to 10,000 Genes. 2004 , 295-313	

1114	Yeast transport-ATPases and the genome-sequencing project. 2004 , 43, 493-536	4
1113	Neurospora in temperate forests of western North America. 2004 , 96, 66-74	53
1112	Unsupervised Machine Learning to Support Functional Characterization of Genes: Emphasis on Cluster Description and Class Discovery. 2005 , 175-192	
1111	Gene Silencing as a Tool for the Identification of Gene Function in Fungi. 2005 , 93-116	
1110	Phanerochaete chrysosporium Genomics. 2005 , 5, 315-352	6
1109	Completed Genomes: Bacteria and Archaea. 2005 , 464-500	
1108	[Yeast as a model system for drug discovery]. 2005 , 125, 213-8	1
1107	Nep1, a Schizosaccharomyces pombe deneddylating enzyme. 2005 , 389, 307-14	19
1106	Manganese superoxide dismutase in pathogenic fungi: an issue with pathophysiological and phylogenetic involvements. 2005 , 45, 411-22	35
1105	Evolutionary patterns of non-coding RNAs. 2005 , 123, 301-69	59
1104	Efficient conversion of 11-deoxycortisol to cortisol (hydrocortisone) by recombinant fission yeast Schizosaccharomyces pombe. 2005 , 5, 621-5	52
1103	Multiple genetic and biochemical interactions of Brr2, Prp8, Prp31, Prp1 and Prp4 kinase suggest a function in the control of the activation of spliceosomes in Schizosaccharomyces pombe. 2005 , 48, 151-61	28
1102	Yeast evolution and comparative genomics. 2005 , 59, 135-53	106
1101	Comprehensive analysis of heterochromatin- and RNAi-mediated epigenetic control of the fission yeast genome. 2005 , 37, 809-19	395
1100	Synergy between sequence and size in large-scale genomics. 2005 , 6, 699-708	223
1099	Deciphering the model pathogenic fungus Cryptococcus neoformans. 2005 , 3, 753-64	247
1098	Structure of palmitoylated BET3: insights into TRAPP complex assembly and membrane localization. 2005 , 24, 875-84	51
1097	Integration of tools and resources for display and analysis of genomic data for protozoan parasites. 2005 , 35, 481-93	8

1096	A large-scale screen in S. pombe identifies seven novel genes required for critical meiotic events. 2005 , 15, 2056-62	91
1095	Manifestations of multicellularity: Dictyostelium reports in. 2005 , 21, 392-8	32
1094	RNA interference and heterochromatin in the fission yeast Schizosaccharomyces pombe. 2005 , 21, 450-6	120
1093	Large scale hierarchical clustering of protein sequences. 2005 , 6, 15	44
1092	The evolution of the Sin1 gene product, a little known protein implicated in stress responses and type I interferon signaling in vertebrates. 2005 , 5, 13	11
1091	The impact of bacterial genomics on natural product research. 2005 , 44, 6828-46	201
1090	Der Einfluss bakterieller Genomik auf die Naturstoff-Forschung. 2005 , 117, 6988-7007	37
1089	Identification and comparative analysis of the peptidyl-prolyl cis/trans isomerase repertoires of H. sapiens, D. melanogaster, C. elegans, S. cerevisiae and Sz. pombe. 2005 , 6, 277-300	43
1088	Gene organization features in A/T-rich organisms. 2005 , 60, 90-8	22
1087	Heterogeneity of intron presence or absence in rDNA genes of the lichen species Physcia aipolia and P. stellaris. 2005 , 47, 389-99	25
Í		25
Í	and P. stellaris. 2005 , 47, 389-99	
1086	and P. stellaris. 2005 , 47, 389-99 Identification of genes expressed during spore germination of Mycosphaerella pinodes. 2005 , 71, 190-195 Association between SCMV Resistance and Macroarray-based Expression Patterns in Maize Inbreds.	2
1086	and P. stellaris. 2005, 47, 389-99 Identification of genes expressed during spore germination of Mycosphaerella pinodes. 2005, 71, 190-195 Association between SCMV Resistance and Macroarray-based Expression Patterns in Maize Inbreds. 2005, 16, 173-184	2
1086 1085 1084	Identification of genes expressed during spore germination of Mycosphaerella pinodes. 2005, 71, 190-195 Association between SCMV Resistance and Macroarray-based Expression Patterns in Maize Inbreds. 2005, 16, 173-184 Telomere maintenance, function and evolution: the yeast paradigm. 2005, 13, 535-48 A high-throughput structural biology/proteomics beamline at the SRS on a new multipole wiggler.	2 5 47
1086 1085 1084 1083	Identification of genes expressed during spore germination of Mycosphaerella pinodes. 2005, 71, 190-195 Association between SCMV Resistance and Macroarray-based Expression Patterns in Maize Inbreds. 2005, 16, 173-184 Telomere maintenance, function and evolution: the yeast paradigm. 2005, 13, 535-48 A high-throughput structural biology/proteomics beamline at the SRS on a new multipole wiggler. 2005, 12, 455-66	2 5 47 29
1086 1085 1084 1083	Identification of genes expressed during spore germination of Mycosphaerella pinodes. 2005, 71, 190-195 Association between SCMV Resistance and Macroarray-based Expression Patterns in Maize Inbreds. 2005, 16, 173-184 Telomere maintenance, function and evolution: the yeast paradigm. 2005, 13, 535-48 A high-throughput structural biology/proteomics beamline at the SRS on a new multipole wiggler. 2005, 12, 455-66 Pro-oxidant action of phloxine B on fission yeast Schizosaccharomyces pombe. 2005, 22, 91-7	2 5 47 29

(2005-2005)

1078	Additional vectors for PCR-based gene tagging in Saccharomyces cerevisiae and Schizosaccharomyces pombe using nourseothricin resistance. 2005 , 22, 1061-8	80
1077	Mass spectrometry and database search in the analysis of proteins from the fungus Pleurotus ostreatus. 2005 , 5, 67-75	13
1076	The first two-dimensional reference map of the fission yeast, Schizosaccharomyces pombe proteins. 2005 , 5, 1574-9	13
1075	Stress-induced changes in the Schizosaccharomyces pombe proteome using two-dimensional difference gel electrophoresis, mass spectrometry and a novel integrated robotics platform. 2005 , 5, 1669-85	21
1074	Fungal Genetics: A Post-Genomic Perspective. 2005 , 65-88	
1073	Genome organization and three kinds of heritable changes: general description and stochastic factors (a review). 2005 , 10, 335-44	6
1072	Completed Genomes and the Tree of Life. 2005 , 395-435	
1071	Human Disease. 2005 , 646-694	
1070	. 2005,	13
1069	Eukaryotic genomics. 2005 ,	
1068	Eukaryotic Genomes: Fungi. 2005 , 502-537	
1067	Conserved locus-specific silencing functions of Schizosaccharomyces pombe sir2+. 2005 , 169, 1243-60	49
1066	Except in every detail: comparing and contrasting G-protein signaling in Saccharomyces cerevisiae and Schizosaccharomyces pombe. 2005 , 4, 495-503	63
1065	Comparative genomics and disorder prediction identify biologically relevant SH3 protein interactions. 2005 , 1, e26	35
1064	Comparing the Dictyostelium and Entamoeba genomes reveals an ancient split in the Conosa lineage. 2005 , 1, e71	35
1063	A human-curated annotation of the Candida albicans genome. 2005 , 1, 36-57	249
1062	Expression of a RecQ helicase homolog affects progression through crisis in fission yeast lacking telomerase. 2005 , 280, 5249-57	41
1061	Regulation of Cdc2p and Cdc13p is required for cell cycle arrest induced by defective RNA splicing in fission yeast. 2005 , 280, 32640-8	5

1060	Identification of cell cycle-regulated genes in fission yeast. 2005 , 16, 1026-42	141
1059	The monocarboxylate transporter homolog Mch5p catalyzes riboflavin (vitamin B2) uptake in Saccharomyces cerevisiae. 2005 , 280, 39809-17	55
1058	Exonic splicing enhancers in fission yeast: functional conservation demonstrates an early evolutionary origin. 2005 , 19, 242-54	31
1057	The roles of fission yeast ase1 in mitotic cell division, meiotic nuclear oscillation, and cytokinesis checkpoint signaling. 2005 , 16, 1378-95	125
1056	Amiloride uptake and toxicity in fission yeast are caused by the pyridoxine transporter encoded by bsu1+ (car1+). 2005 , 4, 319-26	17
1055	The role of heterochromatin in centromere function. 2005 , 360, 569-79	118
1054	Impairment of the TFIIH-associated CDK-activating kinase selectively affects cell cycle-regulated gene expression in fission yeast. 2005 , 16, 2734-45	50
1053	Identification and functional analysis of 20 Box H/ACA small nucleolar RNAs (snoRNAs) from Schizosaccharomyces pombe. 2005 , 280, 16446-55	26
1052	Sequence and comparative genomic analysis of actin-related proteins. 2005 , 16, 5736-48	89
1051	Cohesins are required for meiotic DNA breakage and recombination in Schizosaccharomyces pombe. 2005 , 102, 10952-7	71
1050	Overexpression Phenotypes of Plk1 and Ndrg2 in Schizosaccharomyces Pombe: Fission Yeast System for Mammalian Gene Study. 2005 , 277-279, 1-6	1
1049	Natural meiotic recombination hot spots in the Schizosaccharomyces pombe genome successfully predicted from the simple sequence motif M26. 2005 , 25, 9054-62	41
1048	Understanding protein dispensability through machine-learning analysis of high-throughput data. 2005 , 21, 575-81	76
1047	Ase1p organizes antiparallel microtubule arrays during interphase and mitosis in fission yeast. 2005 , 16, 1756-68	153
1046	Sequence finishing and gene mapping for Candida albicans chromosome 7 and syntenic analysis against the Saccharomyces cerevisiae genome. 2005 , 170, 1525-37	18
1045	Evolutionary diversification of DNA methyltransferases in eukaryotic genomes. 2005 , 22, 1119-28	104
1044	Moving toward a systems biology approach to the study of fungal pathogenesis in the rice blast fungus Magnaporthe grisea. 2005 , 57, 177-215	15
1043	Effects of the tumor inhibitory triterpenoid avicin G on cell integrity, cytokinesis, and protein ubiquitination in fission yeast. 2005 , 102, 12771-6	21

(2005-2005)

1042	Conformational changes induced in the human protein translin and in the single-stranded oligodeoxynucleotides d(GT)(12) and d(TTAGGG)(5) upon binding of these oligodeoxynucleotides by translin. 2005 , 23, 257-65	6
1041	Genomics of the fungal kingdom: insights into eukaryotic biology. 2005 , 15, 1620-31	222
1040	Evolution of a large ribosomal RNA multigene family in filamentous fungi: birth and death of a concerted evolution paradigm. 2005 , 102, 5084-9	149
1039	The role of the regulatory subunit of fission yeast calcineurin for in vivo activity and its relevance to FK506 sensitivity. 2005 , 280, 12231-8	28
1038	A cysteine-sulfinic acid in peroxiredoxin regulates H2O2-sensing by the antioxidant Pap1 pathway. 2005 , 102, 8875-80	198
1037	A mammalian actin substitution in yeast actin (H372R) causes a suppressible mitochondria/vacuole phenotype. 2005 , 280, 36494-501	22
1036	Systematic deletion analysis of fission yeast protein kinases. 2005 , 4, 799-813	78
1035	DNA replication origins in the Schizosaccharomyces pombe genome. 2005 , 102, 337-42	102
1034	Gene discovery and expression profile analysis through sequencing of expressed sequence tags from different developmental stages of the chytridiomycete Blastocladiella emersonii. 2005 , 4, 455-64	21
1033	A natural meiotic DNA break site in Schizosaccharomyces pombe is a hotspot of gene conversion, highly associated with crossing over. 2005 , 169, 595-605	41
1032	Survey of simple sequence repeats in completed fungal genomes. 2005 , 22, 639-49	195
1031	Schizosaccharomyces pombe mst2+ encodes a MYST family histone acetyltransferase that negatively regulates telomere silencing. 2005 , 25, 8887-903	41
1030	The fission yeast Schizosaccharomyces pombe has two importin-alpha proteins, Imp1p and Cut15p, which have common and unique functions in nucleocytoplasmic transport and cell cycle progression. 2005 , 171, 7-21	22
1029	A pre-tRNA carrying intron features typical of Archaea is spliced in yeast. 2005 , 11, 70-6	10
1028	Analysis of mutant phenotypes and splicing defects demonstrates functional collaboration between the large and small subunits of the essential splicing factor U2AF in vivo. 2005 , 16, 584-96	12
1027	Transfer RNA gene-targeted integration: an adaptation of retrotransposable elements to survive in the compact Dictyostelium discoideum genome. 2005 , 110, 288-98	27
1026	The evolution of transposons in Schizosaccharomyces pombe. 2005 , 110, 566-74	10
1025	Role of septins and the exocyst complex in the function of hydrolytic enzymes responsible for fission yeast cell separation. 2005 , 16, 4867-81	71

1024	Systematic genome-wide annotation of spliceosomal proteins reveals differential gene family expansion. 2006 , 16, 66-77	75
1023	Psc3 cohesin of Schizosaccharomyces pombe: cell cycle analysis and identification of three distinct isoforms. 2005 , 386, 613-21	1
1022	Genome evolution: Lessons from Genolevures. 2005 , 165-196	8
1021	Cloning and characterization of the Schizosaccharomyces pombe homologs of the human protein Translin and the Translin-associated protein TRAX. 2005 , 33, 4128-39	23
1020	Open reading frames provide a rich pool of potential natural antisense transcripts in fungal genomes. 2005 , 33, 5034-44	22
1019	Fungal Intervening Sequences. 2005 , 71-92	3
1018	Characterization of three essential residues in the conserved ATP-binding region of Epstein-Barr virus thymidine kinase. 2005 , 44, 4785-93	5
1017	Putting microarrays in a context: integrated analysis of diverse biological data. 2005 , 6, 34-43	55
1016	The three-dimensional structure of the bifunctional 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase/dihydropteroate synthase of Saccharomyces cerevisiae. 2005 , 348, 655-70	47
1015	Comparative genomics of Dictyostelium discoideum and Entamoeba histolytica. 2005, 8, 606-11	25
1014	How genomics has affected the concept of microbiology. 2005 , 8, 564-71	35
1013	A cell-free mRNA stability assay reveals conservation of the enzymes and mechanisms of mRNA decay between mosquito and mammalian cell lines. 2005 , 35, 1321-34	23
1012	Localization and function of three monothiol glutaredoxins in Schizosaccharomyces pombe. 2005 , 330, 604-10	33
1011	Hemiascomycetous yeasts at the forefront of comparative genomics. 2005 , 15, 614-20	43
1010	Characterisation of two novel fork-head gene homologues of Schizosaccharomyces pombe: their involvement in cell cycle and sexual differentiation. 2005 , 348, 101-9	24
1009	Fission yeast mating-type switching: programmed damage and repair. 2005 , 4, 525-36	32
1008	A dual selection based, targeted gene replacement tool for Magnaporthe grisea and Fusarium oxysporum. 2005 , 42, 483-92	111
1007	A continuous enzyme assay and characterisation of fructosyl amine oxidase enzymes (EC 1.5.3). 2005 , 434, 60-6	3

(2006-2005)

1006	Aquaporins in yeasts and filamentous fungi. 2005 , 97, 487-500	95
1005	Comparative Genomics in Eukaryotes. 2005 , 521-583	7
1004	DNA Bendability and Nucleosome Positioning in Transcriptional Regulation. 2005 , 189-202	1
1003	Toward predictive models of mammalian cells. 2005 , 34, 319-49	69
1002	The rarity of gene shuffling in conserved genes. 2005 , 6, R50	13
1001	The genome of Rhizobium leguminosarum has recognizable core and accessory components. 2006 , 7, R34	421
1000	Fungal Genomics. 2006 ,	5
999	Investigating the Evolution of Fungal Virulence by Functional Genomics. 2006 , 35-49	2
998	Diversity of Nitrogen Metabolism Among Yeast Species: Regulatory and Evolutionary Aspects. 2006 , 123-153	4
997	pEg6, a spire family member, is a maternal gene encoding a vegetally localized mRNA in Xenopus embryos. 2006 , 98, 697-708	13
996	Chromatin insulators. 2006 , 40, 107-38	151
995	Structural features of fungal genomes. 47-77	2
994	Genomics and Biodiversity in Yeasts. 2006 , 45-66	4
993	Schizosaccharomyces pombe comparative genomics; from sequence to systems. 233-285	17
992	Mutation impact on dysferlin inferred from database analysis and computer-based structural predictions. 2006 , 250, 71-8	40
991	Extracellular alpha-galactosidase from Debaryomyces hansenii UFV-1 and its use in the hydrolysis of raffinose oligosaccharides. 2006 , 54, 2385-91	44
990	Transcription regulation of the alpha-glucanase gene agn1 by cell separation transcription factor Ace2p in fission yeast. 2006 , 580, 3099-106	10
989	Transcriptome analysis of Neotyphodium and Epichlolgrass endophytes. 2006 , 43, 465-75	29

988	Meiotic proteins bqt1 and bqt2 tether telomeres to form the bouquet arrangement of chromosomes. 2006 , 125, 59-69	272
987	A role for TFIIIC transcription factor complex in genome organization. 2006 , 125, 859-72	240
986	Comparative genome analyses of nervous system-specific genes. 2006 , 365, 130-6	9
985	Three-dimensional structure of a type III glutamine synthetase by single-particle reconstruction. 2006 , 361, 796-810	17
984	Hybridization monitor: a method for identifying differences between complex genomes. 2006, 64, 305-15	1
983	Repositioning of the reaction intermediate within the catalytic center of the spliceosome. 2006 , 21, 543-53	99
982	The genome of the filamentous fungus Ashbya gossypii: annotation and evolutionary implications. 197-232	2
981	. 2006,	103
980	Identification of Differentially Expressed Genes by cDNA-Amplified Fragment Length Polymorphism in the Biocontrol Agent Pichia anomala (Strain Kh5). 2006 , 96, 80-6	19
979	Comparative genomics and gene finding in fungi. 1-28	2
979 978	Comparative genomics and gene finding in fungi. 1-28 Beer Fermentation. 301-347	2
		2
978	Beer Fermentation. 301-347	
978 977	Beer Fermentation. 301-347 Slicing and spreading of heterochromatic silencing by RNA interference. 2006, 71, 497-503 A parallel proteomic and metabolomic analysis of the hydrogen peroxide- and Sty1p-dependent	12
978 977 976	Beer Fermentation. 301-347 Slicing and spreading of heterochromatic silencing by RNA interference. 2006, 71, 497-503 A parallel proteomic and metabolomic analysis of the hydrogen peroxide- and Sty1p-dependent stress response in Schizosaccharomyces pombe. 2006, 6, 2772-96 Proteome analysis of Schizosaccharomyces pombe by two-dimensional gel electrophoresis and	12 67
978 977 976 975	Beer Fermentation. 301-347 Slicing and spreading of heterochromatic silencing by RNA interference. 2006, 71, 497-503 A parallel proteomic and metabolomic analysis of the hydrogen peroxide- and Sty1p-dependent stress response in Schizosaccharomyces pombe. 2006, 6, 2772-96 Proteome analysis of Schizosaccharomyces pombe by two-dimensional gel electrophoresis and mass spectrometry. 2006, 6, 4115-29 Spsgt1, a new essential gene of Schizosaccharomyces pombe, is involved in carbohydrate	12 67 17
978977976975974	Beer Fermentation. 301-347 Slicing and spreading of heterochromatic silencing by RNA interference. 2006, 71, 497-503 A parallel proteomic and metabolomic analysis of the hydrogen peroxide- and Sty1p-dependent stress response in Schizosaccharomyces pombe. 2006, 6, 2772-96 Proteome analysis of Schizosaccharomyces pombe by two-dimensional gel electrophoresis and mass spectrometry. 2006, 6, 4115-29 Spsgt1, a new essential gene of Schizosaccharomyces pombe, is involved in carbohydrate metabolism. 2006, 23, 35-53	12 67 17

(2006-2006)

	Increased TCA cycle activity and reduced oxygen consumption during cytochrome P450-dependent biotransformation in fission yeast. 2006 , 23, 779-94	25
969	Recombineering reagents for improved inducible expression and selection marker re-use in Schizosaccharomyces pombe. 2006 , 23, 813-23	24
968	Comparative analysis of regulatory transcription factors in Schizosaccharomyces pombe and budding yeasts. 2006 , 23, 929-35	10
967	DNA replication in the fission yeast: robustness in the face of uncertainty. 2006 , 23, 951-62	13
966	Simplified primer design for PCR-based gene targeting and microarray primer database: two web tools for fission yeast. 2006 , 23, 921-8	19
965	The epigenetic magic of histone lysine methylation. 2006 , 273, 3121-35	201
964	Comparative genomic analysis of phytopathogenic fungi using expressed sequence tag (EST) collections. 2006 , 7, 61-70	35
963	ORFeome cloning and global analysis of protein localization in the fission yeast Schizosaccharomyces pombe. 2006 , 24, 841-7	443
962	tRNA genes as chromatin barriers. 2006 , 13, 192-3	18
961	Genome-wide characterization of fission yeast DNA replication origins. 2006 , 25, 5171-9	169
960	Complete, precise, and innocuous loss of multiple introns in the currently intronless, active cathepsin L-like genes, and inference from this event. 2006 , 38, 685-96	11
959	alpha-Synuclein fission yeast model: concentration-dependent aggregation without plasma membrane localization or toxicity. 2006 , 28, 179-91	23
959 958		² 3
	membrane localization or toxicity. 2006 , 28, 179-91	
958	membrane localization or toxicity. 2006 , 28, 179-91 Nickel resistance in fission yeast associated with the magnesium transport system. 2006 , 32, 139-46 Functional analysis through site-directed mutations and phylogeny of the Candida albicans	9
958 957	membrane localization or toxicity. 2006 , 28, 179-91 Nickel resistance in fission yeast associated with the magnesium transport system. 2006 , 32, 139-46 Functional analysis through site-directed mutations and phylogeny of the Candida albicans LYS1-encoded saccharopine dehydrogenase. 2006 , 275, 74-80	9
958 957 956	membrane localization or toxicity. 2006, 28, 179-91 Nickel resistance in fission yeast associated with the magnesium transport system. 2006, 32, 139-46 Functional analysis through site-directed mutations and phylogeny of the Candida albicans LYS1-encoded saccharopine dehydrogenase. 2006, 275, 74-80 Pol5p, a novel binding partner to Cdc10p in fission yeast involved in rRNA production. 2006, 276, 391-401 Studies on inositol-mediated expression of MAL gene encoding maltase and phospholipid	9 1 4

952	Characterization of the arom gene in Rhizoctonia solani, and transcription patterns under stable and induced hypovirulence conditions. 2006 , 49, 166-77	14
951	Comparative genomics of the HOG-signalling system in fungi. 2006 , 49, 137-51	68
950	Comparative analysis of HOG pathway proteins to generate hypotheses for functional analysis. 2006 , 49, 152-65	45
949	Regulation of gene expression and cell division by Polo-like kinases. 2006 , 50, 73-80	9
948	Beyond the data deluge: data integration and bio-ontologies. 2006 , 39, 314-20	101
947	Centromere formation: from epigenetics to self-assembly. 2006 , 16, 70-8	68
946	Yeasts illustrate the molecular mechanisms of eukaryotic genome evolution. 2006, 22, 375-87	177
945	Bystander effects in unicellular organisms. 2006 , 597, 78-86	14
944	Genomics of the filamentous fungi Imoving from the shadow of the bakers yeast. 2006 , 20, 10-14	5
943	Erratum to Taylor and Alexander (2005) Mycologist 19: 102-112. 2006 , 20, 14	1
942	A fungal phylogeny based on 42 complete genomes derived from supertree and combined gene analysis. 2006 , 6, 99	371
941	Comparative EST analysis provides insights into the basal aquatic fungus Blastocladiella emersonii. 2006 , 7, 177	9
940	Identification and comparative analysis of sixteen fungal peptidyl-prolyl cis/trans isomerase repertoires. 2006 , 7, 244	35
939	Highly expressed proteins have an increased frequency of alanine in the second amino acid position. 2006 , 7, 28	25
938	Genomewide identification of pheromone-targeted transcription in fission yeast. 2006 , 7, 303	38
937	Generation, annotation, and analysis of an extensive Aspergillus niger EST collection. 2006 , 6, 7	27
936	Ancient origin, functional conservation and fast evolution of DNA-dependent RNA polymerase III. 2006 , 34, 3615-24	16
935	Spatial organization of transcription by RNA polymerase III. 2006 , 34, 4826-36	69

934	Fungal Genomic Annotation. 2006 , 123-142	16
933	Issues in Comparative Fungal Genomics. 2006 , 99-122	
932	Expression of the Candida albicans morphogenesis regulator gene CZF1 and its regulation by Efg1p and Czf1p. 2006 , 5, 825-35	54
931	Building Biological Complexity with Limited Genes. 2006 , 7, 97-114	3
930	Comparing gene expression networks in a multi-dimensional space to extract similarities and differences between organisms. 2006 , 22, 1359-66	14
929	Modelling in molecular biology: describing transcription regulatory networks at different scales. 2006 , 361, 483-94	21
928	Comparative genomics and genome evolution in yeasts. 2006 , 361, 403-12	51
927	Evidence on the chromosomal location of centromeric DNA in Plasmodium falciparum from etoposide-mediated topoisomerase-II cleavage. 2006 , 103, 6706-11	42
926	A survey of all 11 ABC transporters in fission yeast: two novel ABC transporters are required for red pigment accumulation in a Schizosaccharomyces pombe adenine biosynthetic mutant. 2006 , 152, 2309-2321	34
925	Sequential processing of a mitochondrial tandem protein: insights into protein import in Schizosaccharomyces pombe. 2006 , 5, 997-1006	17
924	Schizosaccharomyces pombe Git1 is a C2-domain protein required for glucose activation of adenylate cyclase. 2006 , 173, 49-61	12
923	The fission yeast transforming acidic coiled coil-related protein Mia1p/Alp7p is required for formation and maintenance of persistent microtubule-organizing centers at the nuclear envelope. 2006 , 17, 2212-22	22
922	Analysis of aldosterone-induced differential receptor-independent protein patterns using 2D-electrophoresis and mass spectrometry. 2006 , 387, 917-29	6
921	The RNA polymerase III-dependent family of genes in hemiascomycetes: comparative RNomics, decoding strategies, transcription and evolutionary implications. 2006 , 34, 1816-35	77
920	A "holistic" kinesin phylogeny reveals new kinesin families and predicts protein functions. 2006 , 17, 1734-43	128
919	Reconstruction of the kinetochore during meiosis in fission yeast Schizosaccharomyces pombe. 2006 , 17, 5173-84	28
918	An alpha-amylase homologue, aah3, encodes a GPI-anchored membrane protein required for cell wall integrity and morphogenesis in Schizosaccharomyces pombe. 2006 , 70, 1454-63	16
917	Introduction. 1-28	2

916	Duplication of genes and genomes in yeasts. 79-99	4
915	Sterol regulatory element binding protein is a principal regulator of anaerobic gene expression in fission yeast. 2006 , 26, 2817-31	137
914	Encyclopedic Reference of Genomics and Proteomics in Molecular Medicine. 2005 , 587-587	
913	Encyclopedic Reference of Genomics and Proteomics in Molecular Medicine. 2005, 576-578	1
912	Codon Signature Extremes In Eukaryote genomes. 2006 , 52, 281-297	1
911	Mechanism of action of a flavin-containing monooxygenase. 2006 , 103, 9832-7	119
910	Evolutionary-conserved telomere-linked helicase genes of fission yeast are repressed by silencing factors, RNAi components and the telomere-binding protein Taz1. 2006 , 34, 78-88	62
909	9 Transcript Analysis: A Microarray Approach. 2007 , 189-703	2
908	Identification, molecular cloning, and characterization of the sixth subunit of human transcription factor TFIIIC. 2007 , 282, 17179-89	29
907	Mutations in the SF1-U2AF59-U2AF23 complex cause exon skipping in Schizosaccharomyces pombe. 2007 , 282, 2221-8	15
906	Proteomic analysis of the U1 snRNP of Schizosaccharomyces pombe reveals three essential organism-specific proteins. 2007 , 35, 1391-401	11
905	Eukaryotic genome size databases. 2007 , 35, D332-8	304
904	A discrete class of intergenic DNA dictates meiotic DNA break hotspots in fission yeast. 2007, 3, e141	72
903	Assessment of phylogenomic and orthology approaches for phylogenetic inference. 2007 , 23, 815-24	63
902	Propping up our knowledge of G protein signaling pathways: diverse functions of putative	6
	noncanonical Gbeta subunits in fungi. 2007 , 2007, pe3	
901	crops on the comparative fungal genomics platform. 2008 , 36, D562-71	72
901		72 4

898 Class 2 Transferases VIII. 2007,

897	Dysferlin homozygous mutation G1418D causes limb-girdle type 2B in a Mexican family. 2007 , 11, 391-6	6
896	Loss of the TOR kinase Tor2 mimics nitrogen starvation and activates the sexual development pathway in fission yeast. 2007 , 27, 3154-64	155
895	The role and aims of the FYSSION project. 2007 , 6, 3-7	2
894	Isolation of the Schizosaccharomyces pombe proteasome subunit Rpn7 and a structure-function study of the proteasome-COP9-initiation factor domain. 2007 , 282, 32414-23	16
893	The hermes transposon of Musca domestica is an efficient tool for the mutagenesis of Schizosaccharomyces pombe. 2007 , 177, 2519-23	26
892	Interaction of Epe1 with the heterochromatin assembly pathway in Schizosaccharomyces pombe. 2007 , 175, 1549-60	32
891	Convergent domestication of pogo-like transposases into centromere-binding proteins in fission yeast and mammals. 2008 , 25, 29-41	94
890	Rescuing yeast mutants with human genes. 2007 , 6, 104-11	31
889	A conditional role of U2AF in splicing of introns with unconventional polypyrimidine tracts. 2007 , 27, 7334-44	22
888	A new paradigm for developmental biology. 2007 , 210, 1526-47	188
887	Protein arginine methylation in Candida albicans: role in nuclear transport. 2007 , 6, 1119-29	26
886	Comparative proteomic and transcriptomic profiling of the fission yeast Schizosaccharomyces pombe. 2007 , 3, 79	91
885	Preface. 2007 , 36, xiii-xvi	
884	Identification of a mitochondrial alcohol dehydrogenase in Schizosaccharomyces pombe: new insights into energy metabolism. 2007 , 401, 459-64	12
883	Dsk1p kinase phosphorylates SR proteins and regulates their cellular localization in fission yeast. 2007 , 405, 21-30	18
882	Comparative genomics and evolution of eukaryotic phospholipid biosynthesis. 2007, 46, 171-99	73
881	Structural organization of dynamic chromatin. 2007 , 41, 3-28	2

880	Arginine catabolism in Aspergillus nidulans is regulated by the rrmA gene coding for the RNA-binding protein. 2007 , 44, 1285-97	10
879	Identification of moulds in the diagnostic laboratoryan algorithm implementing molecular and phenotypic methods. 2007 , 59, 49-60	30
878	Exploration of pairing constraints identifies a 9 base-pair core within box C/D snoRNA-rRNA duplexes. 2007 , 369, 771-83	24
877	A network of multiple regulatory layers shapes gene expression in fission yeast. 2007 , 26, 145-55	161
876	Competition between the ATPase Prp5 and branch region-U2 snRNA pairing modulates the fidelity of spliceosome assembly. 2007 , 28, 838-49	88
875	Comparative genomic analysis of fungal genomes reveals intron-rich ancestors. 2007 , 8, R223	100
874	Global transcriptional responses of fission and budding yeast to changes in copper and iron levels: a comparative study. 2007 , 8, R73	44
873	Місгоаггауs. 2007 ,	1
872	Differential expression of Rho1GTPase and Rho3GTPase during isotropic and polarized growth of Mucor circinelloides. 2007 , 53, 168-76	5
871	Genome survey sequencing of the wine spoilage yeast Dekkera (Brettanomyces) bruxellensis. 2007 , 6, 721-33	92
870	Genome assembly, rearrangement, and repeats. 2007, 107, 3391-406	19
869	Gene expression and distribution of Swi6 in partial aneuploids of the fission yeast Schizosaccharomyces pombe. 2007 , 32, 149-61	27
868	Functional genomics of plant infection by the rice blast fungus Magnaporthe grisea. 227-254	
867	Chromatin dynamics of unfolding and refolding controlled by the nucleosome repeat length and the linker and core histones. 2007 , 85, 295-307	10
866	A 100%-complete sequence reveals unusually simple genomic features in the hot-spring red alga Cyanidioschyzon merolae. 2007 , 5, 28	220
865	Meiosis specific coiled-coil proteins in Shizosaccharomyces pombe. 2007 , 2, 14	8
864	Role of the alpha-glucanase Agn2p in ascus-wall endolysis following sporulation in fission yeast. 2007 , 24, 279-88	17
863	The txl1+ gene from Schizosaccharomyces pombe encodes a new thioredoxin-like 1 protein that participates in the antioxidant defence against tert-butyl hydroperoxide. 2007 , 24, 481-90	15

862	A history of research on yeasts 10: foundations of yeast genetics. 2007 , 24, 799-845	32
861	Modelling dynamic processes in yeast. 2007 , 24, 943-59	21
860	Classification and functional annotation of eukaryotic protein kinases. 2007 , 68, 893-914	121
859	Construction of conditional analog-sensitive kinase alleles in the fission yeast Schizosaccharomyces pombe. 2007 , 2, 2996-3000	42
858	Soil eukaryotic functional diversity, a metatranscriptomic approach. 2007 , 1, 632-42	161
857	Natural history and evolutionary principles of gene duplication in fungi. <i>Nature</i> , 2007 , 449, 54-61 50.4	517
856	Two-step, extensive alterations in the transcriptome from G0 arrest to cell division in Schizosaccharomyces pombe. 2007 , 12, 677-92	51
855	Dyneins across eukaryotes: a comparative genomic analysis. 2007 , 8, 1708-1721	215
854	Schizosaccharomyces pombe possesses two plasma membrane alkali metal cation/H antiporters differing in their substrate specificity. 2007 , 7, 188-95	11
853	Why do some yeast species require niacin for growth? Different modes of NAD synthesis. 2007 , 7, 657-64	22
852	Evolution of the carboxylate Jen transporters in fungi. 2007 , 7, 646-56	19
851	Biochemical characterization and structural prediction of a novel cytosolic leucyl aminopeptidase of the M17 family from Schizosaccharomyces pombe. 2007 , 274, 6228-40	14
850	Fungal CSL transcription factors. 2007 , 8, 233	14
849	Comparison of protein coding gene contents of the fungal phyla Pezizomycotina and Saccharomycotina. 2007 , 8, 325	38
848	Biotechnological synthesis of drug metabolites using human cytochrome P450 2D6 heterologously expressed in fission yeast exemplified for the designer drug metabolite 4'-hydroxymethyl-alpha-pyrrolidinobutyrophenone. 2007 , 74, 511-20	42
847	Schizosaccharomyces pombe minimum genome factory. 2007 , 46, 147-55	55
846	Genomic evolution of the proteasome system among hemiascomycetous yeasts. 2007 , 65, 529-40	15
845	Six new amino acid-auxotrophic markers for targeted gene integration and disruption in fission yeast. 2007 , 52, 97-105	24

844	tRNase Z: the end is not in sight. 2007 , 64, 2404-12	35
843	Sugarcane Phosphoribosyl Pyrophosphate Synthetase: Molecular Characterization of a Phosphate-independent PRS. 2008 , 26, 301-315	7
842	Identification of small molecules inducing apoptosis by cell-based assay using fission yeast deletion mutants. 2008 , 26, 299-307	10
841	Low-copy episomal vector pFY20 and high-saturation coverage genomic libraries for the fission yeast Schizosaccharomyces pombe. 2008 , 25, 643-50	5
840	The gap-filling sequence on the left arm of chromosome 2 in fission yeast Schizosaccharomyces pombe. 2008 , 25, 673-9	8
839	A history of research on yeasts 13. Active transport and the uptake of various metabolites. 2008 , 25, 689-731	20
838	Improved tools for efficient mapping of fission yeast genes: identification of microtubule nucleation modifier mod22-1 as an allele of chromatin- remodelling factor gene swr1. 2008 , 25, 913-25	11
837	Epigenetics regulate centromere formation and kinetochore function. 2008 , 104, 2027-39	32
836	Fungal genome sequencing and bioenergy. 2008 , 22, 1-5	19
835	Soft computing methods to predict gene regulatory networks: An integrative approach on time-series gene expression data. 2008 , 8, 1189-1199	13
834	Recent advances in three-dimensional multicellular spheroid culture for biomedical research. 2008 , 3, 1285-1285	6
833	A vector system for genomic FLAG epitope-tagging in Schizosaccharomyces pombe. 2008 , 3, 1280-5	27
832	Human mobile genetic elements: Structure, distribution and functional role. 2008, 42, 420-430	3
831	The Ypt/Rab family and the evolution of trafficking in fungi. 2008, 9, 27-38	56
830	The endogenous adrenodoxin reductase-like flavoprotein arh1 supports heterologous cytochrome P450-dependent substrate conversions in Schizosaccharomyces pombe. 2008 , 8, 432-41	29
829	Characterization of Sro1, a novel stress responsive protein in Schizosaccharomyces pombe. 2008 , 8, 564-73	3
828	Loss of Zhf and the tightly regulated zinc-uptake system SpZrt1 in Schizosaccharomyces pombe reveals the delicacy of cellular zinc balance. 2008 , 8, 883-96	19
827	Host genome surveillance for retrotransposons by transposon-derived proteins. <i>Nature</i> , 2008 , 451, 431-60.4	143

(2008-2008)

826	Dynamic repertoire of a eukaryotic transcriptome surveyed at single-nucleotide resolution. <i>Nature</i> , 2008 , 453, 1239-43	810
825	Genome sequencing and analysis of the biomass-degrading fungus Trichoderma reesei (syn. Hypocrea jecorina). 2008 , 26, 553-60	920
824	Dynamic transcriptome of Schizosaccharomyces pombe shown by RNA-DNA hybrid mapping. 2008 , 40, 977-86	85
823	Evolution of SET-domain protein families in the unicellular and multicellular Ascomycota fungi. 2008 , 8, 190	30
822	Metabolic innovations towards the human lineage. 2008 , 8, 247	14
821	Fungal cytochrome P450 database. 2008 , 9, 402	96
820	SNUGB: a versatile genome browser supporting comparative and functional fungal genomics. 2008 , 9, 586	17
819	Fisher: a program for the detection of H/ACA snoRNAs using MFE secondary structure prediction and comparative genomics - assessment and update. 2008 , 1, 49	7
818	A yeast PAF acetylhydrolase ortholog suppresses oxidative death. 2008 , 45, 434-42	27
817	Radiation induction of delayed recombination in Schizosaccharomyces pombe. 2008 , 7, 1250-61	6
816	Wine Fermentation. 2008 , 162-192	10
815	The origins of multicellularity and the early history of the genetic toolkit for animal development. 2008 , 42, 235-51	219
814	Molecular Techniques in the Microbial Ecology of Fermented Foods. 2008,	13
813	The genome sequence of the model ascomycete fungus Podospora anserina. 2008, 9, R77	237
812	Cross-kingdom patterns of alternative splicing and splice recognition. 2008 , 9, R50	103
811	Finding exonic islands in a sea of non-coding sequence: splicing related constraints on protein composition and evolution are common in intron-rich genomes. 2008 , 9, R29	34
810	RNA Interference. 2008,	3
809	Chromosome fusions following telomere loss are mediated by single-strand annealing. 2008 , 31, 463-473	57

808	Aldosterone: from biosynthesis to non-genomic action onto the proteome. 2008 , 73, 966-72	7
807	Phosphoproteome analysis of fission yeast. 2008 , 7, 1088-97	161
806	Gene tagging and gene replacement using recombinase-mediated cassette exchange in Schizosaccharomyces pombe. 2008 , 407, 63-74	56
805	Sites of strong Rec12/Spo11 binding in the fission yeast genome are associated with meiotic recombination and with centromeres. 2008 , 117, 431-44	24
804	Cloning of the ATP sulphurylase gene of Schizosaccharomyces pombe by functional complementation. 2008 , 54, 71-4	2
803	Dicistronic tRNA-5S rRNA genes in Yarrowia lipolytica: an alternative TFIIIA-independent way for expression of 5S rRNA genes. 2008 , 36, 5832-44	23
802	Mug27 is a meiosis-specific protein kinase that functions in fission yeast meiosis II and sporulation. 2008 , 121, 1547-58	16
801	Site-specific recombination in Schizosaccharomyces pombe and systematic assembly of a 400kb transgene array in mammalian cells using the integrase of Streptomyces phage phiBT1. 2008 , 36, e9	23
800	A genome-wide screen of genes involved in cadmium tolerance in Schizosaccharomyces pombe. 2008 , 106, 124-39	46
799	Copper distributed by Atx1 is available to copper amine oxidase 1 in Schizosaccharomyces pombe. 2008 , 7, 1781-94	18
798	Schizosaccharomyces pombe Hsp90/Git10 is required for glucose/cAMP signaling. 2008, 178, 1927-36	18
797	Global analysis of gel mobility of proteins and its use in target identification. 2008 , 283, 10745-52	95
796	Recombination and Meiosis. 2008,	
795	Stochastic hybrid modeling of DNA replication across a complete genome. 2008 , 105, 12295-300	62
794	Chromodomains direct integration of retrotransposons to heterochromatin. 2008, 18, 359-69	139
793	Cds1 controls the release of Cdc14-like phosphatase Flp1 from the nucleolus to drive full activation of the checkpoint response to replication stress in fission yeast. 2008 , 19, 2488-99	24
79 ²	Comparative genomics and molecular dynamics of DNA repeats in eukaryotes. 2008, 72, 686-727	356
791	The actomyosin ring recruits early secretory compartments to the division site in fission yeast. 2008 , 19, 1125-38	31

(2009-2008)

790	Schizosaccharomyces pombe Bub3 is dispensable for mitotic arrest following perturbed spindle formation. 2008 , 179, 785-92	18
789	The S. pombe SAGA complex controls the switch from proliferation to sexual differentiation through the opposing roles of its subunits Gcn5 and Spt8. 2008 , 22, 3184-95	66
788	Meiotic Recombination in Schizosaccharomyces pombe: A Paradigm for Genetic and Molecular Analysis. 2008 , 3, 195	21
787	Characterization of a fission yeast P(5)-type ATPase homologue that is essential for Ca(2+)/Mn(2+)homeostasis in the absence of P(2)-type ATPases. 2008 , 83, 373-81	12
786	Centromeric chromatin in fission yeast. 2008 , 13, 3896-905	6
7 ⁸ 5	Yeast Cells as a Discovery Platform for Parkinson's Disease and other Protein Misfolding Diseases. 2008 , 505-536	
784	Fusion and fission of genes define a metric between fungal genomes. 2008 , 4, e1000200	21
783	Meiotic recombination hotspots of fission yeast are directed to loci that express non-coding RNA. 2008 , 3, e2887	29
782	. 2009,	7
781	The secret message of heterochromatin: new insights into the mechanisms and function of centromeric and pericentric repeat sequence transcription. 2009 , 53, 259-68	81
780	The Schizosaccharomyces pombe Hsp104 disaggregase is unable to propagate the [PSI] prion. 2009 , 4, e6939	16
779		
	Common themes in siRNA-mediated epigenetic silencing pathways. 2009 , 53, 245-57	105
778	Common themes in siRNA-mediated epigenetic silencing pathways. 2009, 53, 245-57 {beta}-glucanase Eng2 is required for ascus wall endolysis after sporulation in the fission yeast Schizosaccharomyces pombe. 2009, 8, 1278-86	105
778 777	{beta}-glucanase Eng2 is required for ascus wall endolysis after sporulation in the fission yeast	
	{beta}-glucanase Eng2 is required for ascus wall endolysis after sporulation in the fission yeast Schizosaccharomyces pombe. 2009 , 8, 1278-86 The PRY/SPRY/B30.2 domain of butyrophilin 1A1 (BTN1A1) binds to xanthine oxidoreductase:	22
777	{beta}-glucanase Eng2 is required for ascus wall endolysis after sporulation in the fission yeast Schizosaccharomyces pombe. 2009, 8, 1278-86 The PRY/SPRY/B30.2 domain of butyrophilin 1A1 (BTN1A1) binds to xanthine oxidoreductase: implications for the function of BTN1A1 in the mammary gland and other tissues. 2009, 284, 22444-22456 Mapping epigenetic mutations in fission yeast using whole-genome next-generation sequencing.	22 47
777 776	{beta}-glucanase Eng2 is required for ascus wall endolysis after sporulation in the fission yeast Schizosaccharomyces pombe. 2009, 8, 1278-86 The PRY/SPRY/B30.2 domain of butyrophilin 1A1 (BTN1A1) binds to xanthine oxidoreductase: implications for the function of BTN1A1 in the mammary gland and other tissues. 2009, 284, 22444-22456 Mapping epigenetic mutations in fission yeast using whole-genome next-generation sequencing. 2009, 19, 1077-83	22 47

772	Exploring the conservation of synthetic lethal genetic interaction networks. 2009 , 2, 78-81	18
771	tRNA genes in eukaryotic genome organization and reorganization. 2009 , 8, 3102-6	27
770	Biotechnological synthesis of drug metabolites using human cytochrome P450 isozymes heterologously expressed in fission yeast. 2009 , 1, 821-30	13
769	Functional differentiation of tbf1 orthologues in fission and budding yeasts. 2009 , 8, 207-16	9
768	A simple method for directional transcriptome sequencing using Illumina technology. 2009 , 37, e148	77
767	Comparative genomics of protoploid Saccharomycetaceae. 2009 , 19, 1696-709	171
766	Cyclin-dependent kinase inhibits reinitiation of a normal S-phase program during G2 in fission yeast. 2009 , 29, 4025-32	19
765	Cellular quiescence: are controlling genes conserved?. 2009 , 19, 705-15	68
764	More than just orphans: are taxonomically-restricted genes important in evolution?. 2009 , 25, 404-13	301
763	Evolutionary flexibility of protein complexes. 2009 , 9, 155	7
763 762	Evolutionary flexibility of protein complexes. 2009 , 9, 155 Phylogenetic diversity of stress signalling pathways in fungi. 2009 , 9, 44	7
762	Phylogenetic diversity of stress signalling pathways in fungi. 2009 , 9, 44 Dissecting the fission yeast regulatory network reveals phase-specific control elements of its cell	143
762 761	Phylogenetic diversity of stress signalling pathways in fungi. 2009 , 9, 44 Dissecting the fission yeast regulatory network reveals phase-specific control elements of its cell cycle. 2009 , 3, 93 Screening a genome-wide S. pombe deletion library identifies novel genes and pathways involved	143
762 761 760	Phylogenetic diversity of stress signalling pathways in fungi. 2009, 9, 44 Dissecting the fission yeast regulatory network reveals phase-specific control elements of its cell cycle. 2009, 3, 93 Screening a genome-wide S. pombe deletion library identifies novel genes and pathways involved in genome stability maintenance. 2009, 8, 672-9 A new Schizosaccharomyces pombe chronological lifespan assay reveals that caloric restriction	143 10 47
762 761 760 759	Phylogenetic diversity of stress signalling pathways in fungi. 2009, 9, 44 Dissecting the fission yeast regulatory network reveals phase-specific control elements of its cell cycle. 2009, 3, 93 Screening a genome-wide S. pombe deletion library identifies novel genes and pathways involved in genome stability maintenance. 2009, 8, 672-9 A new Schizosaccharomyces pombe chronological lifespan assay reveals that caloric restriction promotes efficient cell cycle exit and extends longevity. 2009, 44, 493-502	143 10 47
762 761 760 759 758	Phylogenetic diversity of stress signalling pathways in fungi. 2009, 9, 44 Dissecting the fission yeast regulatory network reveals phase-specific control elements of its cell cycle. 2009, 3, 93 Screening a genome-wide S. pombe deletion library identifies novel genes and pathways involved in genome stability maintenance. 2009, 8, 672-9 A new Schizosaccharomyces pombe chronological lifespan assay reveals that caloric restriction promotes efficient cell cycle exit and extends longevity. 2009, 44, 493-502 Chemical Genomics Based on Yeast Genetics. 223-238 Functional studies of an evolutionarily conserved, cytochrome b5 domain protein reveal a specific role in axonemal organisation and the general phenomenon of post-division axonemal growth in	143 10 47 35

(2009-2009)

754	Nitric oxide as a signaling molecule in the fission yeast Schizosaccharomyces pombe. 2009 , 238, 59-66	26
753	Long-term evolution of 5S ribosomal DNA seems to be driven by birth-and-death processes and selection in Ensis razor shells (Mollusca: Bivalvia). 2009 , 47, 635-44	30
752	Yeast Ste23p shares functional similarities with mammalian insulin-degrading enzymes. 2009 , 26, 595-610	12
751	Codon usage bias is correlated with gene expression levels in the fission yeast Schizosaccharomyces pombe. 2009 , 14, 499-509	62
750	Silent chromatin at the middle and ends: lessons from yeasts. 2009 , 28, 2149-61	60
749	Analysis of small RNA in fission yeast; centromeric siRNAs are potentially generated through a structured RNA. 2009 , 28, 3832-44	63
748	Tdp1 protects against oxidative DNA damage in non-dividing fission yeast. 2009 , 28, 632-40	41
747	Dancing genomes: fungal nuclear positioning. 2009 , 7, 875-86	53
746	Eukaryotization of the early biosphere: A biogeochemical aspect. 2009 , 47, 1265-1333	12
745	Hexose and pentose transport in ascomycetous yeasts: an overview. 2009 , 9, 511-25	103
745 744	Hexose and pentose transport in ascomycetous yeasts: an overview. 2009 , 9, 511-25 Cloning and heterologous expression in Escherichia coli of the fission yeast vip1 gene, showing differential expression after aldosterone treatment. 2009 , 12, 1127-1139	0
	Cloning and heterologous expression in Escherichia coli of the fission yeast vip1 gene, showing	
744	Cloning and heterologous expression in Escherichia coli of the fission yeast vip1 gene, showing differential expression after aldosterone treatment. 2009 , 12, 1127-1139 Production of heterologous proteins using the fission-yeast (Schizosaccharomyces pombe)	0
744 743	Cloning and heterologous expression in Escherichia coli of the fission yeast vip1 gene, showing differential expression after aldosterone treatment. 2009 , 12, 1127-1139 Production of heterologous proteins using the fission-yeast (Schizosaccharomyces pombe) expression system. 2009 , 53, 227-35 Metabolic profiling of the fission yeast S. pombe: quantification of compounds under different	o 54
744 743 742	Cloning and heterologous expression in Escherichia coli of the fission yeast vip1 gene, showing differential expression after aldosterone treatment. 2009, 12, 1127-1139 Production of heterologous proteins using the fission-yeast (Schizosaccharomyces pombe) expression system. 2009, 53, 227-35 Metabolic profiling of the fission yeast S. pombe: quantification of compounds under different temperatures and genetic perturbation. 2010, 6, 182-98 Debaryomyces hansenii UFV-1 intracellular alpha-galactosidase characterization and comparative	o 54 64
744 743 742 741	Cloning and heterologous expression in Escherichia coli of the fission yeast vip1 gene, showing differential expression after aldosterone treatment. 2009, 12, 1127-1139 Production of heterologous proteins using the fission-yeast (Schizosaccharomyces pombe) expression system. 2009, 53, 227-35 Metabolic profiling of the fission yeast S. pombe: quantification of compounds under different temperatures and genetic perturbation. 2010, 6, 182-98 Debaryomyces hansenii UFV-1 intracellular alpha-galactosidase characterization and comparative studies with the extracellular enzyme. 2009, 57, 2515-22	o 54 64 18
744 743 742 741 740	Cloning and heterologous expression in Escherichia coli of the fission yeast vip1 gene, showing differential expression after aldosterone treatment. 2009, 12, 1127-1139 Production of heterologous proteins using the fission-yeast (Schizosaccharomyces pombe) expression system. 2009, 53, 227-35 Metabolic profiling of the fission yeast S. pombe: quantification of compounds under different temperatures and genetic perturbation. 2010, 6, 182-98 Debaryomyces hansenii UFV-1 intracellular alpha-galactosidase characterization and comparative studies with the extracellular enzyme. 2009, 57, 2515-22 Annotation of stress-response proteins in the aspergilli. 2009, 46 Suppl 1, S105-20	o 54 64 18

736	Meiosis. Volume 1, molecular and genetic methods. Preface. 2009 , 557, v-vi	6
735	Yeast Biotechnology: Diversity and Applications. 2009,	33
734	Class 2 Transferases. 2009 ,	
733	Completed Genomes. 517-565	
732	Unrepaired oxidative DNA damage induces an ATR/ATM apoptotic-like response in quiescent fission yeast. 2009 , 8, 2326-31	8
731	Transcriptional interference and gene orientation in yeast: noncoding RNA connections. 2010 , 75, 299-311	15
730	Fission Yeast TOR and Rapamycin. 2010 , 27, 251-269	4
729	????????ASPEX??? ?????????? 2010 , 48, 794-798	
728	Saccharomyces cerevisiae and DNA microarray analyses: what did we learn from it for a better understanding and exploitation of yeast biotechnology?. 2010 , 87, 391-400	22
727	Centromere identity: a challenge to be faced. 2010 , 284, 75-94	20
726	Discrete DNA sites regulate global distribution of meiotic recombination. 2010 , 26, 202-8	38
725	Identification and analysis of candidate fungal tRNA 3'-end processing endonucleases tRNase Zs, homologs of the putative prostate cancer susceptibility protein ELAC2. 2010 , 10, 272	10
724	Evolutionary history of the poly(ADP-ribose) polymerase gene family in eukaryotes. 2010 , 10, 308	83
723	Fungal secretome database: integrated platform for annotation of fungal secretomes. 2010 , 11, 105	128
722	Comparative analysis of fungal protein kinases and associated domains. 2010 , 11, 133	36
721	Large-scale transcriptome data reveals transcriptional activity of fission yeast LTR retrotransposons. 2010 , 11, 167	18
720	Genome-wide in silico screen for CCCH-type zinc finger proteins of Trypanosoma brucei, Trypanosoma cruzi and Leishmania major. 2010 , 11, 283	63
719	Autophagy in the fission yeast Schizosaccharomyces pombe. 2010 , 584, 1327-34	33

718 Evolutionary Genomics of Yeasts. **2010**, 95-120

717	Novel episomal vectors and a highly efficient transformation procedure for the fission yeast Schizosaccharomyces japonicus. 2010 , 27, 1049-60	30
716	Dead time loss correction of mass errors occurring in high-throughput proteomics based on electrospray ionization time-of-flight tandem mass spectrometry. 2010 , 24, 1490-5	2
715	The Kinesin motor protein Cut7 regulates biogenesis and function of Ago1-complexes. 2010 , 11, 25-36	8
714	Ribosomal RNA genes in eukaryotic microorganisms: witnesses of phylogeny?. 2010 , 34, 59-86	81
713	Splicing-dependent NMD does not require the EJC in Schizosaccharomyces pombe. 2010 , 29, 1537-51	46
712	Specific splicing defects in S. pombe carrying a degron allele of the Survival of Motor Neuron gene. 2010 , 29, 1817-29	39
711	Analysis of a genome-wide set of gene deletions in the fission yeast Schizosaccharomyces pombe. 2010 , 28, 617-623	510
710	Yeast evolutionary genomics. 2010 , 11, 512-24	262
709	Genomic binding profiling of the fission yeast stress-activated MAPK Sty1 and the bZIP transcriptional activator Atf1 in response to H2O2. 2010 , 5, e11620	46
708	Early Steps in the DNA Base Excision Repair Pathway of a Fission Yeast Schizosaccharomyces pombe. 2010 , 2010,	8
707	The N-terminus of Prp1 (Prp6/U5-102 K) is essential for spliceosome activation in vivo. 2010 , 38, 1610-22	11
706	Glucuronide production by whole-cell biotransformation using genetically engineered fission yeast Schizosaccharomyces pombe. 2010 , 38, 509-15	25
7°5	Centromeric localization of dispersed Pol III genes in fission yeast. 2010 , 21, 254-65	102
704	High-throughput sequencing of retrotransposon integration provides a saturated profile of target activity in Schizosaccharomyces pombe. 2010 , 20, 239-48	55
703	Genome-wide mapping of nuclear mitochondrial DNA sequences links DNA replication origins to chromosomal double-strand break formation in Schizosaccharomyces pombe. 2010 , 20, 1250-61	24
702	Glutaredoxins Grx4 and Grx3 of Saccharomyces cerevisiae play a role in actin dynamics through their Trx domains, which contributes to oxidative stress resistance. 2010 , 76, 7826-35	30
701	Microtubule-dependent spatial organization of mitochondria in fission yeast. 2010 , 97, 203-21	5

Disruption of PDC1 Gene to Enhance Pyruvic Acid Accumulation of Saccharomyces cerevisiae. **2010**,

699	Fission yeast a cellular model well suited for electron microscopy investigations. 2010 , 96, 235-58	4
698	Tay1 protein, a novel telomere binding factor from Yarrowia lipolytica. 2010 , 285, 38078-92	24
697	RNAi and heterochromatin repress centromeric meiotic recombination. 2010 , 107, 8701-5	80
696	cDNA cloning and expression pattern of two enolase genes from the Chinese oak silkworm, Antheraea pernyi. 2010 , 42, 816-26	13
695	Rad3 decorates critical chromosomal domains with gammaH2A to protect genome integrity during S-Phase in fission yeast. 2010 , 6, e1001032	58
694	The Universal Protein Resource (UniProt) in 2010. 2010 , 38, D142-8	1035
693	S. pombe genome deletion project: an update. 2010 , 9, 2399-402	32
692	Mannosylinositol phosphorylceramide is a major sphingolipid component and is required for proper localization of plasma-membrane proteins in Schizosaccharomyces pombe. 2010 , 123, 1578-87	34
691	Rga4, a Rho-GAP from fission yeast: Finding specificity within promiscuity. 2010 , 3, 436-9	8
690	A genome-wide screen for Schizosaccharomyces pombe deletion mutants that affect telomere length. 2010 , 20, 963-5	13
689	Molecular genetics of Schizosaccharomyces pombe. 2010 , 470, 759-95	110
688	Synthetic genetic array (SGA) analysis in Saccharomyces cerevisiae and Schizosaccharomyces pombe. 2010 , 470, 145-79	136
687	The calculation of information and organismal complexity. 2010 , 5, 59	12
686	Mapping of long-range associations throughout the fission yeast genome reveals global genome organization linked to transcriptional regulation. 2010 , 38, 8164-77	188
685	The Role of ACC Deaminase Producing PGPR in Sustainable Agriculture. 2010 , 365-385	22
684	Bioinformatics for LC-MS/MS-based proteomics. 2010 , 658, 61-91	20
683	Global fitness profiling of fission yeast deletion strains by barcode sequencing. 2010 , 11, R60	59

(2011-2011)

682	Microarray-based target identification using drug hypersensitive fission yeast expressing ORFeome. 2011 , 7, 1463-72	16
681	The 5S rDNA gene family in mollusks: characterization of transcriptional regulatory regions, prediction of secondary structures, and long-term evolution, with special attention to Mytilidae mussels. 2011 , 102, 433-47	19
680	The Awesome Power of Yeast Evolutionary Genetics: New Genome Sequences and Strain Resources for the Saccharomyces sensu stricto Genus. 2011 , 1, 11-25	231
679	Microtubule Dynamics. 2011,	3
678	Development of a Process Chain for Nanoparticles Production by Yeasts. 2011 , 197-221	1
677	Comparative functional genomics of the fission yeasts. 2011 , 332, 930-6	364
676	Metal Nanoparticles in Microbiology. 2011 ,	61
675	Comparative genomics of xylose-fermenting fungi for enhanced biofuel production. 2011 , 108, 13212-7	131
674	Genome-wide analysis of fungal manganese transporters, with an emphasis on Phanerochaete chrysosporium. 2011 , 3, 367-82	7
673	Atg8: an autophagy-related ubiquitin-like protein family. 2011 , 12, 226	331
672	References. 2011 , r1-r178	3
671	A piggyBac transposon-based mutagenesis system for the fission yeast Schizosaccharomyces pombe. 2011 , 39, e40	30
670	An outlook on ion signaling and ionome of mycorrhizal symbiosis. 2011 , 23, 79-89	15
669	Genome characterization of the oleaginous fungus Mortierella alpina. 2011 , 6, e28319	102
668	The FUN30 chromatin remodeler, Fft3, protects centromeric and subtelomeric domains from euchromatin formation. 2011 , 7, e1001334	61
667	The reconstruction of condition-specific transcriptional modules provides new insights in the evolution of yeast AP-1 proteins. 2011 , 6, e20924	9
666	The global transcriptional response of fission yeast to hydrogen sulfide. 2011 , 6, e28275	8
665	Ribosomal proteins' association with transcription sites peaks at tRNA genes in Schizosaccharomyces pombe. 2011 , 17, 1713-26	14

664	LAMMER kinase Kic1 is involved in pre-mRNA processing. 2011 , 317, 2308-20	10
663	Schizosaccharomyces pombe encodes a mutated AP endonuclease 1. 2011 , 10, 296-305	7
662	RITS-connecting transcription, RNA interference, and heterochromatin assembly in fission yeast. 2011 , 2, 632-46	32
661	Heterologous expression and characterization of processing Eglucosidase I from Aspergillus brasiliensis ATCC 9642. 2011 , 28, 563-71	14
660	A first partial Aplysia californica proteome. 2011 , 41, 955-68	4
659	Absence of positive selection on centromeric histones in Tetrahymena suggests unsuppressed centromere: drive in lineages lacking male meiosis. 2011 , 72, 510-20	14
658	Proteomics of industrial fungi: trends and insights for biotechnology. 2011 , 89, 225-37	48
657	Binary classification of protein molecules into intrinsically disordered and ordered segments. 2011 , 11, 29	56
656	Why eukaryotic cells use introns to enhance gene expression: splicing reduces transcription-associated mutagenesis by inhibiting topoisomerase I cutting activity. 2011 , 6, 24	41
655	Molecular organization and phylogenetic analysis of 5S rDNA in crustaceans of the genus Pollicipes reveal birth-and-death evolution and strong purifying selection. 2011 , 11, 304	14
654	The genetic interaction network of CCW12, a Saccharomyces cerevisiae gene required for cell wall integrity during budding and formation of mating projections. 2011 , 12, 107	27
653	Minimal regulatory spaces in yeast genomes. 2011 , 12, 320	4
652	Construction of diploid zygotes by interallelic complementation of ade6 in Schizosaccharomyces japonicus. 2011 , 28, 747-54	4
651	Complementation of the pha2 yeast mutant suggests functional differences for arogenate dehydratases from Arabidopsis thaliana. 2011 , 49, 882-90	17
650	Augmented annotation of the Schizosaccharomyces pombe genome reveals additional genes required for growth and viability. 2011 , 187, 1207-17	25
649	Revisiting the yeast PPR proteinsapplication of an Iterative Hidden Markov Model algorithm reveals new members of the rapidly evolving family. 2011 , 28, 2935-48	39
648	Genome evolution in the eremothecium clade of the Saccharomyces complex revealed by comparative genomics. 2011 , 1, 539-48	32
647	Expansion of hexose transporter genes was associated with the evolution of aerobic fermentation in yeasts. 2011 , 28, 131-42	60

646	Genomic mRNA profiling reveals compensatory mechanisms for the requirement of the essential splicing factor U2AF. 2011 , 31, 652-61	19
645	Mediator head subcomplex Med11/22 contains a common helix bundle building block with a specific function in transcription initiation complex stabilization. 2011 , 39, 6291-304	38
644	A meiotic gene regulatory cascade driven by alternative fates for newly synthesized transcripts. 2011 , 22, 66-77	20
643	Diversity in requirement of genetic and epigenetic factors for centromere function in fungi. 2011 , 1384-95	33
642	Spt6 is required for heterochromatic silencing in the fission yeast Schizosaccharomyces pombe. 2011 , 31, 4193-204	29
641	Comparative whole genome sequencing reveals phenotypic tRNA gene duplication in spontaneous Schizosaccharomyces pombe La mutants. 2011 , 39, 4728-42	15
640	Topoisomerase II binds nucleosome-free DNA and acts redundantly with topoisomerase I to enhance recruitment of RNA Pol II in budding yeast. 2011 , 108, 12693-8	58
639	The solute carrier families have a remarkably long evolutionary history with the majority of the human families present before divergence of Bilaterian species. 2011 , 28, 1531-41	115
638	Programmed fluctuations in sense/antisense transcript ratios drive sexual differentiation in S. pombe. 2011 , 7, 559	36
637	Deconvolution of chromatin immunoprecipitation-microarray (ChIP-chip) analysis of MBF occupancies reveals the temporal recruitment of Rep2 at the MBF target genes. 2011 , 10, 130-41	2
636	Protein arginine methylation in parasitic protozoa. 2011 , 10, 1013-22	46
635	Production of ibuprofen acyl glucosides by human UGT2B7. 2011 , 39, 2174-81	26
634	Systematic localization study on novel proteins encoded by meiotically up-regulated ORFs in fission yeast. 2011 , 75, 2364-70	10
633	Tra1 has specific regulatory roles, rather than global functions, within the SAGA co-activator complex. 2011 , 30, 2843-52	48
632	Cadmium-induced proteome remodeling regulated by Spc1/Sty1 and Zip1 in fission yeast. 2012 , 129, 200-12	13
631	Evidence that RNA polymerase II and not TFIIB is responsible for the difference in transcription initiation patterns between Saccharomyces cerevisiae and Schizosaccharomyces pombe. 2012 , 40, 6495-507	11
630	Network evolution: rewiring and signatures of conservation in signaling. 2012 , 8, e1002411	27
629	The CCR4-NOT complex is implicated in the viability of aneuploid yeasts. 2012 , 8, e1002776	12

628	OriDB, the DNA replication origin database updated and extended. 2012 , 40, D682-6	103
627	A stochastic model of kinetochore-microtubule attachment accurately describes fission yeast chromosome segregation. 2012 , 196, 757-74	46
626	tRNAomics: tRNA gene copy number variation and codon use provide bioinformatic evidence of a new anticodon:codon wobble pair in a eukaryote. 2012 , 18, 1358-72	39
625	The Schizosaccharomyces pombe inv1+ regulatory region is unusually large and contains redundant cis-acting elements that function in a SAGA- and Swi/Snf-dependent fashion. 2012 , 11, 1067-74	4
624	Ensuring the faithful execution of cytokinesis in Schizosaccharomyces pombe. 2012 , 5, 265-71	1
623	Simultaneous Segmentation of Cell and Nucleus in Schizosaccharomyces pombe Images with Focus Gradient. 2012 ,	
622	CUE domain-containing protein Vps901 is required for vacuolar protein transport in Schizosaccharomyces pombe. 2012 , 76, 652-9	3
621	Yeast sterol regulatory element-binding protein (SREBP) cleavage requires Cdc48 and Dsc5, a ubiquitin regulatory X domain-containing subunit of the Golgi Dsc E3 ligase. 2012 , 287, 672-681	41
620	PomBase: a comprehensive online resource for fission yeast. 2012 , 40, D695-9	221
619	Growth of transplastomic cells expressing D-amino acid oxidase in chloroplasts is tolerant to D-alanine and inhibited by D-valine. 2012 , 160, 2219-26	24
618	How can satellite DNA divergence cause reproductive isolation? Let us count the chromosomal ways. 2012 , 2012, 430136	40
617	Schizosaccharomyces pombe Hat1 (Kat1) is associated with Mis16 and is required for telomeric silencing. 2012 , 11, 1095-103	16
616	Production of recombinant proteins by yeast cells. 2012 , 30, 1108-18	238
615	Origin and evolution of carnivorism in the Ascomycota (fungi). 2012 , 109, 10960-5	64
614	Centromeric heterochromatin assembly in fission yeastbalancing transcription, RNA interference and chromatin modification. 2012 , 20, 521-34	21
613	Genome-wide identification and characterization of replication origins by deep sequencing. 2012 , 13, R27	73
612	Yeast Genomics Technique for High-Throughput Drug Target Discovery. 2012 , 73, 398-405	1
611	Quantitative analysis of fission yeast transcriptomes and proteomes in proliferating and quiescent cells. 2012 , 151, 671-83	388

610	Analyzing fission yeast multidrug resistance mechanisms to develop a genetically tractable model system for chemical biology. 2012 , 19, 893-901	28
609	SKIP is a component of the spliceosome linking alternative splicing and the circadian clock in Arabidopsis. 2012 , 24, 3278-95	147
608	Interacting factors and cellular localization of SR protein-specific kinase Dsk1. 2012, 318, 2071-84	2
607	Unexpected contribution of cytochrome P450 enzymes CYP11B2 and CYP21, as well as CYP3A4 in xenobiotic androgen elimination - insights from metandienone metabolism. 2012 , 213, 381-91	34
606	DNA replication through hard-to-replicate sites, including both highly transcribed RNA Pol II and Pol III genes, requires the S. pombe Pfh1 helicase. 2012 , 26, 581-93	77
605	Functional repurposing revealed by comparing S. pombe and S. cerevisiae genetic interactions. 2012 , 149, 1339-52	122
604	Fungal Smn and Spf30 homologues are mainly present in filamentous fungi and genomes with many introns: implications for spinal muscular atrophy. 2012 , 491, 135-41	8
603	Generation and analysis of a barcode-tagged insertion mutant library in the fission yeast Schizosaccharomyces pombe. 2012 , 13, 161	13
602	Centromere-associated repeat arrays on Trypanosoma brucei chromosomes are much more extensive than predicted. 2012 , 13, 29	20
601	Identification of novel genes involved in DNA damage response by screening a genome-wide Schizosaccharomyces pombe deletion library. 2012 , 13, 662	17
600	Genome-scale metabolic model of the fission yeast Schizosaccharomyces pombe and the reconciliation of in silico/in vivo mutant growth. 2012 , 6, 49	21
599	A functional selection model explains evolutionary robustness despite plasticity in regulatory networks. 2012 , 8, 619	40
598	RNA Interference and Functional Genomics in Fungi. 2012, 773-792	1
597	Keystone SpeciesIbf Molecular Interaction Networks. 2012, 25, 73-88	
596	Characterization of triglyceride lipase genes of fission yeast Schizosaccharomyces pombe. 2012 , 96, 981-91	22
595	Comparative Genomics Methods for the Prediction of Small RNA-Binding Sites. 2012 , 592-601	
594	1.15 Analysis of 2-D Crystals of Membrane Proteins by Electron Microscopy. 2012 , 277-310	5
593	Cuf2 is a novel meiosis-specific regulatory factor of meiosis maturation. 2012 , 7, e36338	13

592	Genome and transcriptome analysis of the food-yeast Candida utilis. 2012, 7, e37226	25
591	Identification and functional analysis of the erh1(+) gene encoding enhancer of rudimentary homolog from the fission yeast Schizosaccharomyces pombe. 2012 , 7, e49059	12
590	Evolutionary Analysis of Sequence Divergence and Diversity of Duplicate Genes in Aspergillus fumigatus. 2012 , 8, 623-44	6
589	Construction of an insertion marker collection of Sz. japonicus (IMACS) for genetic mapping and a fosmid library covering its genome. 2012 , 29, 241-9	6
588	The non-hierarchical, non-uniformly branching topology of a leuconoid sponge aquiferous system revealed by 3D reconstruction and morphometrics using corrosion casting and X-ray microtomography. 2012 , 93, 160-170	11
587	A dominant role for meiosis-specific 3' RNA processing in controlling expression of a fission yeast cyclin gene. 2012 , 18, 1408-20	3
586	Independent evolution of striated muscles in cnidarians and bilaterians. <i>Nature</i> , 2012 , 487, 231-4 50.4	172
585	Engineered high content of ricinoleic acid in fission yeast Schizosaccharomyces pombe. 2012 , 95, 179-87	42
584	Synthesis and production of unsaturated and polyunsaturated fatty acids in yeast: current state and perspectives. 2012 , 95, 1-12	62
583	RNA and epigenetic silencing: insight from fission yeast. 2012 , 54, 129-41	28
582	EAryl-Eamino acid aminotransferase from Variovorax sp. JH2 is useful for enantioselective Ephenylalanine production. 2012 , 1, 253-258	4
581	Chemical-genomic profiling: systematic analysis of the cellular targets of bioactive molecules. 2012 , 20, 1952-60	33
580	Toward genome-enabled mycology. 2013 , 105, 1339-49	29
579	Noncoding RNAs prevent spreading of a repressive histone mark. 2013 , 20, 994-1000	56
578	Genome architecture is a selectable trait that can be maintained by antagonistic pleiotropy. 2013 , 4, 2235	49
577	Dissection of a redox relay: H2O2-dependent activation of the transcription factor Pap1 through the peroxidatic Tpx1-thioredoxin cycle. 2013 , 5, 1413-24	44
576	Small RNAs, big impact: small RNA pathways in transposon control and their effect on the host stress response. 2013 , 21, 587-600	39
575	Return of the Fungi. 2013 , 9, 328-330	

(2013-2013)

574	Identification and characterisation of non-coding small RNAs in the pathogenic filamentous fungus Trichophyton rubrum. 2013 , 14, 931	6
573	Robust cell segmentation for schizosaccharomyces pombe images with focus gradient. 2013,	3
572	The process of kinetochore assembly in yeasts. 2013 , 338, 107-17	8
571	Bioremediation and Genetically Modified Organisms. 2013 , 433-451	9
570	The secretory pathway: exploring yeast diversity. 2013 , 37, 872-914	126
569	Mechanisms and dynamics of heterochromatin formation during mammalian development: closed paths and open questions. 2013 , 104, 1-45	37
568	Coexpression of CPR from various origins enhances biotransformation activity of human CYPs in S. pombe. 2013 , 170, 1751-66	17
567	A Changing Landscape of Fungal Genomics. 2013 , 1-20	2
566	Integration profiling of gene function with dense maps of transposon integration. 2013, 195, 599-609	45
565	Extensive mass spectrometry-based analysis of the fission yeast proteome: the Schizosaccharomyces pombe PeptideAtlas. 2013 , 12, 1741-51	21
564	Mate and fuse: how yeast cells do it. 2013, 3, 130008	144
563	Influence of long terminal repeat retrotransposons in the genomes of fission yeasts. 2013 , 41, 1629-33	4
562	The repertoires of ubiquitinating and deubiquitinating enzymes in eukaryotic genomes. 2013, 30, 1172-87	54
561	Introns regulate gene expression in Cryptococcus neoformans in a Pab2p dependent pathway. 2013 , 9, e1003686	29
560	Quantitative control of protein S-palmitoylation regulates meiotic entry in fission yeast. 2013 , 11, e1001597	50
559	The genome and development-dependent transcriptomes of Pyronema confluens: a window into fungal evolution. 2013 , 9, e1003820	65
558	Systematic genetic analysis of transcription factors to map the fission yeast transcription-regulatory network. 2013 , 41, 1696-700	5
557	Interactions of photosynthesis with genome size and function. 2013 , 368, 20120264	38

556	Characterization of genome-reduced fission yeast strains. 2013 , 41, 5382-99	14
555	Complete DNA sequence of Kuraishia capsulata illustrates novel genomic features among budding yeasts (Saccharomycotina). 2013 , 5, 2524-39	33
554	Detection and characterization of megasatellites in orthologous and nonorthologous genes of 21 fungal genomes. 2013 , 12, 794-803	7
553	Cross-species protein interactome mapping reveals species-specific wiring of stress response pathways. 2013 , 6, ra38	29
552	FYPO: the fission yeast phenotype ontology. 2013 , 29, 1671-8	35
551	Replisome stall events have shaped the distribution of replication origins in the genomes of yeasts. 2013 , 41, 9705-18	37
550	Systems biology methods and developments for Saccharomyces cerevisiae and other industrial yeasts in relation to the production of fermented food and food ingredients. 2013 , 42-80	
549	Lariat sequencing in a unicellular yeast identifies regulated alternative splicing of exons that are evolutionarily conserved with humans. 2013 , 110, 12762-7	56
548	New vectors for epitope tagging and gene disruption in Schizosaccharomyces pombe. 2013 , 55, 257-63	11
547	Splicing-related features of introns serve to propel evolution. 2013 , 8, e58547	4
547 546	Splicing-related features of introns serve to propel evolution. 2013 , 8, e58547 Paralogous ribosomal protein l32-1 and l32-2 in fission yeast may function distinctively in cellular proliferation and quiescence by changing the ratio of rpl32 paralogs. 2013 , 8, e60689	4 0
	Paralogous ribosomal protein l32-1 and l32-2 in fission yeast may function distinctively in cellular	
546	Paralogous ribosomal protein l32-1 and l32-2 in fission yeast may function distinctively in cellular proliferation and quiescence by changing the ratio of rpl32 paralogs. 2013 , 8, e60689	0
546 545	Paralogous ribosomal protein l32-1 and l32-2 in fission yeast may function distinctively in cellular proliferation and quiescence by changing the ratio of rpl32 paralogs. 2013 , 8, e60689 Mechanisms of intron loss and gain in the fission yeast Schizosaccharomyces. 2013 , 8, e61683 Identification of a lifespan extending mutation in the Schizosaccharomyces pombe cyclin gene	0 21
546545544	Paralogous ribosomal protein l32-1 and l32-2 in fission yeast may function distinctively in cellular proliferation and quiescence by changing the ratio of rpl32 paralogs. 2013, 8, e60689 Mechanisms of intron loss and gain in the fission yeast Schizosaccharomyces. 2013, 8, e61683 Identification of a lifespan extending mutation in the Schizosaccharomyces pombe cyclin gene clg1+ by direct selection of long-lived mutants. 2013, 8, e69084 New insights into the RNA-based mechanism of action of the anticancer drug 5'-fluorouracil in	0 21 15
546545544543	Paralogous ribosomal protein l32-1 and l32-2 in fission yeast may function distinctively in cellular proliferation and quiescence by changing the ratio of rpl32 paralogs. 2013, 8, e60689 Mechanisms of intron loss and gain in the fission yeast Schizosaccharomyces. 2013, 8, e61683 Identification of a lifespan extending mutation in the Schizosaccharomyces pombe cyclin gene clg1+ by direct selection of long-lived mutants. 2013, 8, e69084 New insights into the RNA-based mechanism of action of the anticancer drug 5'-fluorouracil in eukaryotic cells. 2013, 8, e78172	0 21 15 27
546545544543542	Paralogous ribosomal protein l32-1 and l32-2 in fission yeast may function distinctively in cellular proliferation and quiescence by changing the ratio of rpl32 paralogs. 2013, 8, e60689 Mechanisms of intron loss and gain in the fission yeast Schizosaccharomyces. 2013, 8, e61683 Identification of a lifespan extending mutation in the Schizosaccharomyces pombe cyclin gene clg1+ by direct selection of long-lived mutants. 2013, 8, e69084 New insights into the RNA-based mechanism of action of the anticancer drug 5'-fluorouracil in eukaryotic cells. 2013, 8, e78172 PombeX: robust cell segmentation for fission yeast transillumination images. 2013, 8, e81434	0 21 15 27 12

538	Characterization of the nuclear import mechanism of the CCAAT-regulatory subunit Php4. 2014 , 9, e110721	4
537	Genome-wide analyses and functional classification of proline repeat-rich proteins: potential role of eIF5A in eukaryotic evolution. 2014 , 9, e111800	54
536	The Little Fly that Could: Wizardry and Artistry of Drosophila Genomics. 2014 , 5, 385-414	8
535	The early diverging ascomycetous budding yeast Saitoella complicata has three histone deacetylases belonging to the Clr6, Hos2, and Rpd3 lineages. 2014 , 60, 7-12	4
534	Medical Yeasts, 1800 to 2000. 2014 , 227-253	
533	Fungal Genomics. 2014 , 1-52	15
532	Evolutionary and Adaptive Role of Transposable Elements in Fungal Genomes. 2014 , 79-107	11
531	Conservation and divergence of transcriptional coregulations between box C/D snoRNA and ribosomal protein genes in Ascomycota. 2014 , 20, 1376-85	5
530	Proteins involved in the degradation of cytoplasmic mRNA in the major eukaryotic model systems. 2014 , 11, 1122-36	51
529	Unexpected role of the steroid-deficiency protein ecdysoneless in pre-mRNA splicing. 2014 , 10, e1004287	25
528	Gene expansion shapes genome architecture in the human pathogen Lichtheimia corymbifera: an evolutionary genomics analysis in the ancient terrestrial mucorales (Mucoromycotina). 2014 , 10, e1004496	55
527	The proper splicing of RNAi factors is critical for pericentric heterochromatin assembly in fission yeast. 2014 , 10, e1004334	21
526	Endoplasmic reticulum stress response in yeast and humans. 2014 , 34,	67
525	Functional toxicology: tools to advance the future of toxicity testing. 2014 , 5, 110	30
524	On the role of some ARGONAUTE proteins in meiosis and DNA repair in Arabidopsis thaliana. 2014 , 5, 177	38
523	On the current status of Phakopsora pachyrhizi genome sequencing. 2014 , 5, 377	16
522	Characterization and in vivo functional analysis of the Schizosaccharomyces pombe ICLN gene. 2014 , 34, 595-605	6
521	Mutations in the proteolipid subunits of the vacuolar H+-ATPase provide resistance to indolotryptoline natural products. 2014 , 53, 7123-31	7

520	Proteome-wide search for PP2A substrates in fission yeast. 2014 , 14, 1367-80	6
519	Synchronized fission yeast meiosis using an ATP analog-sensitive Pat1 protein kinase. 2014 , 9, 223-31	14
518	Mudi, a web tool for identifying mutations by bioinformatics analysis of whole-genome sequence. 2014 , 19, 517-27	14
517	Centromeric barrier disruption leads to mitotic defects in Schizosaccharomyces pombe. 2014 , 4, 633-42	4
516	Chromosome conformation maps in fission yeast reveal cell cycle dependent sub nuclear structure. 2014 , 42, 12585-99	20
515	Comparative genomics suggests that the human pathogenic fungus Pneumocystis jirovecii acquired obligate biotrophy through gene loss. 2014 , 6, 1938-48	38
514	Does a shift to limited glucose activate checkpoint control in fission yeast?. 2014 , 588, 2373-8	11
513	The ribosomal protein rpl26 promoter is required for its 3' sense terminus ncRNA transcription in Schizosaccharomyces pombe, implicating a new transcriptional mechanism for ncRNAs. 2014 , 444, 86-91	4
512	Physical methods for genetic transformation of fungi and yeast. 2014 , 11, 184-203	37
511	Fungal RNA Biology. 2014 ,	3
510	Fungal RNA Biology. 2014 , Not your ordinary yeast: non-Saccharomyces yeasts in wine production uncovered. 2014 , 14, 215-37	3 475
510	Not your ordinary yeast: non-Saccharomyces yeasts in wine production uncovered. 2014 , 14, 215-37	475
510 509	Not your ordinary yeast: non-Saccharomyces yeasts in wine production uncovered. 2014 , 14, 215-37 Subtelomeres. 2014 ,	475
510 509 508	Not your ordinary yeast: non-Saccharomyces yeasts in wine production uncovered. 2014, 14, 215-37 Subtelomeres. 2014, Automatic phenotyping of multi-channel Schizosaccharomyces pombe images. 2014, A genomic Multiprocess survey of machineries that control and link cell shape, microtubule	475
510 509 508	Not your ordinary yeast: non-Saccharomyces yeasts in wine production uncovered. 2014, 14, 215-37 Subtelomeres. 2014, Automatic phenotyping of multi-channel Schizosaccharomyces pombe images. 2014, A genomic Multiprocess survey of machineries that control and link cell shape, microtubule organization, and cell-cycle progression. 2014, 31, 227-239 The phosphopantetheinyl transferases: catalysis of a post-translational modification crucial for life.	475
510 509 508 507 506	Not your ordinary yeast: non-Saccharomyces yeasts in wine production uncovered. 2014, 14, 215-37 Subtelomeres. 2014, Automatic phenotyping of multi-channel Schizosaccharomyces pombe images. 2014, A genomic Multiprocess survey of machineries that control and link cell shape, microtubule organization, and cell-cycle progression. 2014, 31, 227-239 The phosphopantetheinyl transferases: catalysis of a post-translational modification crucial for life. 2014, 31, 61-108	475 6 26 210

502	Unexpected similarities between the Schizosaccharomyces and human blood metabolomes, and novel human metabolites. 2014 , 10, 2538-51	35
501	Improving industrial yeast strains: exploiting natural and artificial diversity. 2014 , 38, 947-95	260
500	The role of frataxin in fission yeast iron metabolism: implications for Friedreich's ataxia. 2014 , 1840, 3022-33	12
499	Evolutionarily diverse determinants of meiotic DNA break and recombination landscapes across the genome. 2014 , 24, 1650-64	70
498	DNA replication components as regulators of epigenetic inheritancelesson from fission yeast centromere. 2014 , 5, 411-9	12
497	Prevalence of transcription factors in ascomycete and basidiomycete fungi. 2014 , 15, 214	75
496	Secondary Metabolism. 2014 , 376-395	7
495	Fission yeast kinesin-8 controls chromosome congression independently of oscillations. 2015 , 128, 3720-30	22
494	The Long Terminal Repeat Retrotransposons Tf1 and Tf2 of Schizosaccharomyces pombe. 2015 , 3,	11
493	Widespread alternative and aberrant splicing revealed by lariat sequencing. 2015 , 43, 8488-501	36
492	Cnidaria: fast, reference-free clustering of raw and assembled genome and transcriptome NGS data. 2015 , 16, 352	10
491	Polyglutamine toxicity in yeast induces metabolic alterations and mitochondrial defects. 2015 , 16, 662	13
490	RNA-based regulation of transposon expression. 2015 , 6, 687-708	19
489	Genome Evolution in Yeasts. 2015 , 1-16	5
488	Yeast Cell Culture. 2015 , 1-5	
487	The Long Terminal Repeat Retrotransposons Tf1 and Tf2 of Schizosaccharomyces pombe. 2015 , 997-1010	2
486	AnGeLi: A Tool for the Analysis of Gene Lists from Fission Yeast. 2015 , 6, 330	33
485	PRIMED: PRIMEr database for deleting and tagging all fission and budding yeast genes developed using the open-source genome retrieval script (GRS). 2015 , 10, e0116657	5

484	Cwf16p Associating with the Nineteen Complex Ensures Ordered Exon Joining in Constitutive Pre-mRNA Splicing in Fission Yeast. 2015 , 10, e0136336	5
483	Study of Cellular Processes in Higher Eukaryotes Using the Yeast Schizosaccharomyces pombe as a Model. 2015 ,	3
482	Objects and processes: Two notions for understanding biological information. 2015 , 380, 115-22	1
481	The spatial and temporal organization of origin firing during the S-phase of fission yeast. 2015 , 25, 391-401	41
480	Bulk Segregant Analysis Reveals the Genetic Basis of a Natural Trait Variation in Fission Yeast. 2015 , 7, 3496-510	16
479	Global transcriptomic profiling of Schizosaccharomyces pombe in response to nitrosative stress. 2015 , 558, 241-53	11
478	The genomic and phenotypic diversity of Schizosaccharomyces pombe. 2015 , 47, 235-41	111
477	Mechanisms of expression and translocation of major fission yeast glucose transporters regulated by CaMKK/phosphatases, nuclear shuttling, and TOR. 2015 , 26, 373-86	41
476	Transcriptional profiling analysis of individual kinase-deletion strains of fission yeast in response to nitrogen starvation. 2015 , 290, 1067-83	3
475	Parallel profiling of fission yeast deletion mutants for proliferation and for lifespan during long-term quiescence. 2014 , 5, 145-55	23
474	Nonsense codon suppression in fission yeast due to mutations of tRNA(Ser.11) and translation release factor Sup35 (eRF3). 2015 , 61, 165-73	4
473	Condensin targets and reduces unwound DNA structures associated with transcription in mitotic chromosome condensation. 2015 , 6, 7815	64
472	Basic principles of yeast genomics, a personal recollection. 2015 , 15, fov047	9
471	Genetic interaction mapping reveals a role for the SWI/SNF nucleosome remodeler in spliceosome activation in fission yeast. 2015 , 11, e1005074	18
470	Epigenetic Regulation of Chromatin States in Schizosaccharomyces pombe. 2015 , 7, a018770	113
469	Considerations for the use of transcriptomics in identifying the 'genes that matter' for environmental adaptation. 2015 , 218, 1925-35	76
468	Sequence features and transcriptional stalling within centromere DNA promote establishment of CENP-A chromatin. 2015 , 11, e1004986	70
467	Metagenomics and Metatranscriptomics for the Exploration of Natural Products from Soil Fungi. 2015 , 67-79	2

466	How gene expression in fast-proliferating cells keeps pace. 2015 , 37, 514-24	7
465	Phylogenomic analysis of Emiliania huxleyi provides evidence for haptophyte-stramenopile association and a chimeric haptophyte nuclear genome. 2015 , 21, 31-42	6
464	Metabolic engineering of Saccharomyces cerevisiae for accumulating pyruvic acid. 2015 , 65, 2323-2331	15
463	Hybrid sterility of the yeast Schizosaccharomyces pombe: Genetic genus and many species in statu nascendi?. 2015 , 84, 159-169	9
462	Genetic basis of the highly efficient yeast Kluyveromyces marxianus: complete genome sequence and transcriptome analyses. 2015 , 8, 47	102
461	Fungal Transposable Elements. 2015 , 79-96	O
460	PomBase 2015: updates to the fission yeast database. 2015 , 43, D656-61	74
459	Pharmacovigilance. 2015 , 165-174	
458	Genome-wide analysis of core promoter structures in Schizosaccharomyces pombe with DeepCAGE. 2015 , 12, 525-37	38
457	Inner Kinetochore Protein Interactions with Regional Centromeres of Fission Yeast. 2015 , 201, 543-61	20
456	mRNA export through an additional cap-binding complex consisting of NCBP1 and NCBP3. 2015 , 6, 8192	47
455	Evaluation of BLAST-based edge-weighting metrics used for homology inference with the Markov Clustering algorithm. 2015 , 16, 218	9
454	AnABlast: a new in silico strategy for the genome-wide search of novel genes and fossil regions. 2015 , 22, 439-49	9
453	Suppression of Meiotic Recombination by CENP-B Homologs in Schizosaccharomyces pombe. 2015 , 201, 897-904	7
452	Dynamic transition of transcription and chromatin landscape during fission yeast adaptation to glucose starvation. 2015 , 20, 392-407	18
45 ¹	Adaptive regulation of glucose transport, glycolysis and respiration for cell proliferation. 2015 , 6, 423-30	2
450	An Ancient Yeast for Young Geneticists: A Primer on the Schizosaccharomyces pombe Model System. 2015 , 201, 403-23	112
449	Biostimulation of Oil Sands Process-Affected Water with Phosphate Yields Removal of Sulfur-Containing Organics and Detoxification. 2015 , 49, 13012-20	17

448	Typical Features of Genomes in the Mamiellophyceae. 2015 , 107-127	2
447	Widespread exon skipping triggers degradation by nuclear RNA surveillance in fission yeast. 2015 , 25, 884-96	33
446	Comparative genomics suggests primary homothallism of Pneumocystis species. 2015 , 6,	32
445	Nucleotide sequence composition adjacent to intronic splice sites improves splicing efficiency via its effect on pre-mRNA local folding in fungi. 2015 , 21, 1704-18	19
444	Candida albicans commensalism in the gastrointestinal tract. 2015 , 15,	81
443	Intron evolution in Neurospora: the role of mutational bias and selection. 2015 , 25, 100-10	8
442	Genetic Transformation Systems in Fungi, Volume 2. 2015 ,	6
441	Autophagy in Model Organisms: Insights into Cancer. 2016 ,	1
440	Similar Mutation Rates but Highly Diverse Mutation Spectra in Ascomycete and Basidiomycete Yeasts. 2016 , 8, 3815-3821	26
439	Modulation of Epigenetics by Environmental Toxic Molecules. 2016 , 10, 361-389	O
438	A Survey of the Gene Repertoire of Gigaspora rosea Unravels Conserved Features among Glomeromycota for Obligate Biotrophy. 2016 , 7, 233	79
437	Repeat-Associated Fission Yeast-Like Regional Centromeres in the Ascomycetous Budding Yeast Candida tropicalis. 2016 , 12, e1005839	40
436	The fission yeast MTREC and EJC orthologs ensure the maturation of meiotic transcripts during meiosis. 2016 , 22, 1349-59	4
435		
	Global Fitness Profiling Identifies Arsenic and Cadmium Tolerance Mechanisms in Fission Yeast. 2016 , 6, 3317-3333	15
434		23
	2016, 6, 3317-3333 Shugoshin forms a specialized chromatin domain at subtelomeres that regulates transcription and	
434	2016, 6, 3317-3333 Shugoshin forms a specialized chromatin domain at subtelomeres that regulates transcription and replication timing. 2016, 7, 10393 Regulating retrotransposon activity through the use of alternative transcription start sites. 2016,	23

430	Selection on Position of Nonsense Codons in Introns. 2016 , 204, 1239-1248	2
429	Preferential Protection of Genetic Fidelity within Open Chromatin by the Mismatch Repair Machinery. 2016 , 291, 17692-705	17
428	Centromeres of the Yeast Komagataella phaffii (Pichia pastoris) Have a Simple Inverted-Repeat Structure. 2016 , 8, 2482-92	29
427	Transcriptomic responses of a simplified soil microcosm to a plant pathogen and its biocontrol agent reveal a complex reaction to harsh habitat. 2016 , 17, 838	10
426	Intron retention-dependent gene regulation in Cryptococcus neoformans. 2016 , 6, 32252	33
425	Meiotic chromosome mobility in fission yeast is resistant to environmental stress. 2016 , 6, 24222	1
424	Genome-Wide Estimates of Mutation Rates and Spectrum in Schizosaccharomyces pombe Indicate CpG Sites are Highly Mutagenic Despite the Absence of DNA Methylation. 2015 , 6, 149-60	34
423	A Brief History of Schizosaccharomyces pombe Research: A Perspective Over the Past 70 Years. 2016 , 203, 621-9	28
422	Selection for reduced translation costs at the intronic 5' end in fungi. 2016 , 23, 377-94	6
421	Ian Dawes-the third Pope-lucky to be a researcher. 2016 , 16,	
420	Condensin Promotes Position Effects within Tandem DNA Repeats via the RITS Complex. 2016 , 14, 1018-1024	1 16
420 419	Condensin Promotes Position Effects within Tandem DNA Repeats via the RITS Complex. 2016 , 14, 1018-1024 The AP-2 complex is required for proper temporal and spatial dynamics of endocytic patches in fission yeast. 2016 , 100, 409-24	4 16
	The AP-2 complex is required for proper temporal and spatial dynamics of endocytic patches in	
419	The AP-2 complex is required for proper temporal and spatial dynamics of endocytic patches in fission yeast. 2016 , 100, 409-24	9
419	The AP-2 complex is required for proper temporal and spatial dynamics of endocytic patches in fission yeast. 2016 , 100, 409-24 Fungal genome sequencing: basic biology to biotechnology. 2016 , 36, 743-59 A Proteome-wide Fission Yeast Interactome Reveals Network Evolution Principles from Yeasts to	9 34
419 418 417	The AP-2 complex is required for proper temporal and spatial dynamics of endocytic patches in fission yeast. 2016, 100, 409-24 Fungal genome sequencing: basic biology to biotechnology. 2016, 36, 743-59 A Proteome-wide Fission Yeast Interactome Reveals Network Evolution Principles from Yeasts to Human. 2016, 164, 310-323	9 34 67
419 418 417 416	The AP-2 complex is required for proper temporal and spatial dynamics of endocytic patches in fission yeast. 2016, 100, 409-24 Fungal genome sequencing: basic biology to biotechnology. 2016, 36, 743-59 A Proteome-wide Fission Yeast Interactome Reveals Network Evolution Principles from Yeasts to Human. 2016, 164, 310-323 Meiotic DSB patterning: A multifaceted process. 2016, 15, 13-21	9 34 67 36

412	Copper(I) stabilization by cysteine/tryptophan motif in the extracellular domain of Ctr4. 2016, 159, 45-9	10
411	Advances in identification and validation of protein targets of natural products without chemical modification. 2016 , 33, 719-30	64
410	Water Transport in Yeasts. 2016 , 892, 107-124	4
409	Genome-wide functional analysis of SSR for an edible mushroom Pleurotus ostreatus. 2016 , 575, 524-530	19
408	Strong nucleosomes of yeasts. 2016 , 34, 439-47	
407	Model Organisms for Studying the Cell Cycle. 2016 , 1342, 21-57	3
406	Are all repeats created equal? Understanding DNA repeats at an individual level. 2017, 63, 57-63	13
405	Transient structural variations have strong effects on quantitative traits and reproductive isolation in fission yeast. 2017 , 8, 14061	212
404	Genome sequencing and analysis of Kloeckera apiculata strain 34-9, a biocontrol agent against postharvest pathogens in citrus. 2017 , 39, 87-99	5
403	Unsupervised detection of regulatory gene expression information in different genomic regions enables gene expression ranking. 2017 , 18, 77	3
402	Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. 2017 , 355,	101
401	Ablation of RNA interference and retrotransposons accompany acquisition and evolution of transposases to heterochromatin protein CENPB. 2017 , 28, 1132-1146	9
400	Cellular factories for coenzyme Q production. 2017 , 16, 39	33
399	Polycomb Group Systems in Fungi: New Models for Understanding Polycomb Repressive Complex 2. 2017 , 33, 220-231	24
398	The histone variant H2A.Z promotes splicing of weak introns. 2017 , 31, 688-701	17
397	Centromere and Kinetochore: Essential Components for Chromosome Segregation. 2017, 259-288	O
396	Yeast Genetics as a Powerful Tool to Study Human Diseases. 2017 , 191-214	1
395	Incorporating comparative genomics into the design-test-learn cycle of microbial strain engineering. 2017 , 17,	6

(2017-2017)

394	Crystal structure of the Entamoeba histolytica RNA lariat debranching enzyme EhDbr1 reveals a catalytic Zn /Mn heterobinucleation. 2017 , 591, 2003-2010		4
393	Tailing and degradation of Argonaute-bound small RNAs protect the genome from uncontrolled RNAi. 2017 , 8, 15332		22
392	Crystal structure of the GLP-1 receptor bound to a peptide agonist. <i>Nature</i> , 2017 , 546, 254-258	0.4	126
391	A mutated dph3 gene causes sensitivity of Schizosaccharomyces pombe cells to cytotoxic agents. 2017 , 63, 1081-1091		4
390	Phylogenomic evolutionary surveys of subtilase superfamily genes in fungi. 2017 , 7, 45456		20
389	Phosphoribosyl Diphosphate (PRPP): Biosynthesis, Enzymology, Utilization, and Metabolic Significance. 2017 , 81,		67
388	CK2 phospho-independent assembly of the Tel2-associated stress-signaling complexes in Schizosaccharomyces pombe. 2017 , 22, 59-70		8
387	Fungal Genomes and Insights into the Evolution of the Kingdom. 2017 , 5,		47
386	Fungal Genetics. 2017 , 91-118		
385	Metabolic engineering of via CRISPR-Cas9 genome editing for lactic acid production from glucose and cellobiose. 2017 , 5, 60-67		15
384	New Genes and Functional Innovation in Mammals. 2017 , 9, 1886-1900		31
383	The Yeast Genomes in Three Dimensions: Mechanisms and Functions. 2017 , 51, 23-44		15
382	Genome Diversity and Evolution in the Budding Yeasts (Saccharomycotina). 2017, 206, 717-750		71
381	Mating response and construction of heterothallic strains of the fission yeast Schizosaccharomyces octosporus. 2017 , 17,		8
380	Nineteen complex-related factor Prp45 is required for the early stages of cotranscriptional spliceosome assembly. 2017 , 23, 1512-1524		3
379	Screening and purification of natural products from actinomycetes that affect the cell shape of fission yeast. 2017 , 130, 3173-3185		6
378	The molecular mechanisms of Monascus purpureus M9 responses to blue light based on the transcriptome analysis. 2017 , 7, 5537		8
377	Genetic Analysis of. 2017 , 2017, pdb.top079772		12

376	Bacterial endosymbionts influence host sexuality and reveal reproductive genes of early divergent fungi. 2017 , 8, 1843	38
375	Multiple Approaches to Phylogenomic Reconstruction of the Fungal Kingdom. 2017 , 100, 211-266	15
374	How causal analysis can reveal autonomy in models of biological systems. 2017 , 375,	28
373	Determinants of Histone H3K4 Methylation Patterns. 2017 , 68, 773-785.e6	95
372	OrthoFiller: utilising data from multiple species to improve the completeness of genome annotations. 2017 , 18, 390	11
371	Proximity ligation scaffolding and comparison of two strains genomes. 2017 , 10, 151	22
370	A fission yeast cell-based system for multidrug resistant HIV-1 proteases. 2017 , 7, 5	4
369	Spatial organization of the Schizosaccharomyces pombe genome within the nucleus. 2017 , 34, 55-66	9
368	Genetic controls of DNA damage avoidance in response to acetaldehyde in fission yeast. 2017, 16, 45-58	15
367	5 LUTR introns enhance protein expression in the yeast Saccharomyces cerevisiae. 2017 , 101, 241-251	32
366	Big data mining powers fungal research: recent advances in fission yeast systems biology approaches. 2017 , 63, 427-433	5
365	In vitro reconstitution and biochemical analyses of the Schizosaccharomyces pombe nucleosome. 2017 , 482, 896-901	5
364	Advances in Fungal Phylogenomics and Their Impact on Fungal Systematics. 2017, 100, 309-328	10
363	Eroded telomeres are rearranged in quiescent fission yeast cells through duplications of subtelomeric sequences. 2017 , 8, 1684	20
362	Yeast Genome Sequencing: Basic Biology, Human Biology, and Biotechnology. 2017 , 201-226	
361	Non-Saccharomyces (and Bacteria) Yeasts That Produce Ethanol. 2017 , 389-413	
360	Fungal Genomes and Insights into the Evolution of the Kingdom. 2017 , 619-633	9
359	Generation of gua1 deletion using polymerase chain reaction (PCR)-mediated gene disruption method in fission yeast, Schizosaccharomyces pombe. 2017 , 16, 1501-1506	

(2018-2017)

	electrons to oxidized ribonucleotide reductase. 2017 , 13, e1006858	3
357	Unique molecular mechanisms for maintenance and alteration of genetic information in the budding yeast. 2017 , 39, 28	5
356	Identification of 15 candidate structured noncoding RNA motifs in fungi by comparative genomics. 2017 , 18, 785	8
355	Yeast for virus research. 2017 , 4, 311-330	21
354	Centromere Stability: The Replication Connection. 2017 , 8,	6
353	Iron homeostasis regulates facultative heterochromatin assembly in adaptive genome control. 2018 , 25, 372-383	20
352	RNAi drives nonreciprocal translocations at eroding chromosome ends to establish telomere-free linear chromosomes. 2018 , 32, 537-554	7
351	Sequence requirement of the ade6-4095 meiotic recombination hotspot in Schizosaccharomyces pombe. 2018 , 146, 65-74	2
350	Construction of Designer Selectable Marker Deletions with a CRISPR-Cas9 Toolbox in and New Design of Common Entry Vectors. 2018 , 8, 789-796	6
349	Schizosaccharomyces pombe. 2018 ,	1
348	Total RNA Isolation and Quantification of Specific RNAs in Fission Yeast. 2018 , 1721, 63-72	8
348 347	Total RNA Isolation and Quantification of Specific RNAs in Fission Yeast. 2018 , 1721, 63-72 Repeated evolution of self-compatibility for reproductive assurance. 2018 , 9, 1639	8
348 347 346		
347	Repeated evolution of self-compatibility for reproductive assurance. 2018 , 9, 1639	
347 346	Repeated evolution of self-compatibility for reproductive assurance. 2018, 9, 1639 Splicing and Alternative Splicing Impact on Gene Design. 2018, 131-168	10
347 346 345	Repeated evolution of self-compatibility for reproductive assurance. 2018, 9, 1639 Splicing and Alternative Splicing Impact on Gene Design. 2018, 131-168 The natural diversity and ecology of fission yeast. 2018, 35, 253-260	10 15
347 346 345 344	Repeated evolution of self-compatibility for reproductive assurance. 2018, 9, 1639 Splicing and Alternative Splicing Impact on Gene Design. 2018, 131-168 The natural diversity and ecology of fission yeast. 2018, 35, 253-260 Spurious transcription and its impact on cell function. 2018, 9, 182-189	10 15 21

340	The essential genome of the crenarchaeal model Sulfolobus islandicus. 2018, 9, 4908		44
339	Gene Essentiality Analyzed by Transposon Mutagenesis and Machine Learning in a Stable Haploid Isolate of. 2018 , 9,		57
338	Assembly of Schizosaccharomyces cryophilus chromosomes and their comparative genomic analyses revealed principles of genome evolution of the haploid fission yeasts. 2018 , 8, 14629		5
337	Sequana coverage: detection and characterization of genomic variations using running median and mixture models. 2018 , 7,		6
336	Uncovering Natural Longevity Alleles from Intercrossed Pools of Aging Fission Yeast Cells. 2018 , 210, 733-744		7
335	How Do Yeast and Other Fungi Recognize and Respond to Genome Perturbations?. 2018 , 87-130		2
334	Chromatin-mediated regulators of meiotic recombination revealed by proteomics of a recombination hotspot. 2018 , 11, 64		11
333	Novel diagnostic marker genes differentiate Saccharomyces with respect to their potential application. 2018 , 124, 416-424		1
332	Physical basis for long-distance communication along meiotic chromosomes. 2018 , 115, E9333-E9342		19
331	Functional genomics for the oleaginous yeast Yarrowia lipolytica. 2018, 48, 184-196		18
330	PomBase: The Scientific Resource for Fission Yeast. 2018 , 1757, 49-68		15
329	A Heterochromatin Domain Forms Gradually at a New Telomere and Is Dynamic at Stable Telomeres. 2018 , 38,		4
328	The Pif1 signature motif of Pfh1 is necessary for both protein displacement and helicase unwinding activities, but is dispensable for strand-annealing activity. 2018 , 46, 8516-8531		15
327	Creating a functional single-chromosome yeast. <i>Nature</i> , 2018 , 560, 331-335	50.4	106
326	The genome of Rhizophagus clarus HR1 reveals a common genetic basis for auxotrophy among arbuscular mycorrhizal fungi. 2018 , 19, 465		45
325	Using in vivo oxidation status of one- and two-component redox relays to determine HO levels linked to signaling and toxicity. 2018 , 16, 61		11
324	Identification of in the guts of healthy individuals and patients with colorectal cancer: preliminary evidence from a gut microbiome secretome study. 2018 , 10, 29		4
323	Quantitative Phosphoproteomics Reveals the Signaling Dynamics of Cell-Cycle Kinases in the Fission Yeast Schizosaccharomyces pombe. 2018 , 24, 503-514		39

322	Genome Mining of Non-Conventional Yeasts: Search and Analysis of Clusters and Proteins. 2018, 9,	10
321	Genomics and evolution of Pneumocystis species. 2018 , 65, 308-320	9
320	The Transcriptome-wide Landscape and Modalities of EJC Binding in Adult Drosophila. 2019 , 28, 1219-1236.6	<u>:</u> 118
319	An Evaluation of Machine Learning Approaches for the Prediction of Essential Genes in Eukaryotes Using Protein Sequence-Derived Features. 2019 , 17, 785-796	18
318	Heterogeneous transposable elements as silencers, enhancers and targets of meiotic recombination. 2019 , 128, 279-296	13
317	Discovery of Teneurins. 2019 , 13, 230	5
316	Ent3 and GGA adaptors facilitate diverse anterograde and retrograde trafficking events to and from the prevacuolar endosome. 2019 , 9, 10747	3
315	Genome sequencing and comparison of five species to identify candidate genes for the detection of regulated species infecting wheat. 2019 , 10, 11	14
314	The Use of Algae and Fungi for Removal of Pharmaceuticals by Bioremediation and Biosorption Processes: A Review. 2019 , 11, 1555	49
313	Phosphorus Transport in Mycorrhiza: How Far Are We?. 2019 , 24, 794-801	24
312	Identification of putative G-quadruplex DNA structures in S. pombe genome by quantitative PCR stop assay. 2019 , 82, 102678	10
311	Intraspecific Diversity of Fission Yeast Mitochondrial Genomes. 2019 , 11, 2312-2329	10
310	Measuring the impact of gene prediction on gene loss estimates in Eukaryotes by quantifying falsely inferred absences. 2019 , 15, e1007301	22
309	Potential of Thermotolerant Ethanologenic Yeasts Isolated from ASEAN Countries and Their Application in High-Temperature Fermentation. 2019 ,	4
308	Multivariate analysis of genomic variables, effective population size, and mutation rate. 2019 , 12, 60	1
307	The ESCRT Complexes. 2019 ,	1
306	The Impact of Centromeres on Spatial Genome Architecture. 2019 , 35, 565-578	33
305	Simplified Transformation of Using Polyethylene Glycol. 2019 , 10,	8

304	Using genetics to understand biology. 2019 , 123, 4-13	5
303	Ancestral Admixture Is the Main Determinant of Global Biodiversity in Fission Yeast. 2019 , 36, 1975-1989	29
302	TASks for subtelomeres: when nucleosome loss and genome instability are favored. 2019 , 65, 1153-1160	2
301	Positive Selection Evidence in Xylose-Related Genes Suggests Methylglyoxal Reductase as a Target for the Improvement of Yeasts' Fermentation in Industry. 2019 , 11, 1923-1938	5
300	Chitin Prevalence and Function in Bacteria, Fungi and Protists. 2019 , 1142, 19-59	6
299	Fitness Landscape of the Fission Yeast Genome. 2019 , 36, 1612-1623	2
298	Evolution of Genomic Base Composition: From Single Cell Microbes to Multicellular Animals. 2019 , 17, 362-370	15
297	Killer Meiotic Drive and Dynamic Evolution of the wtf Gene Family. 2019 , 36, 1201-1214	24
296	Functional Genomics Approach Towards Dissecting Out Abiotic Stress Tolerance Trait in Plants. 2019 , 1-24	1
295	XPG-related nucleases are hierarchically recruited for double-stranded rDNA break resection. 2019 , 294, 7632-7643	4
294	AYbRAH: a curated ortholog database for yeasts and fungi spanning 600 million years of evolution. 2019 , 2019,	5
293	Biological and chemical diversity go hand in hand: Basidiomycota as source of new pharmaceuticals and agrochemicals. 2019 , 37, 107344	52
292	Established and Upcoming Yeast Expression Systems. 2019 , 1923, 1-74	13
291	Immediate visualization of recombination events and chromosome segregation defects in fission yeast meiosis. 2019 , 128, 385-396	4
2 90	The conservation of polyol transporter proteins and their involvement in lichenized Ascomycota. 2019 , 123, 318-329	7
289	Torsional Turning Motion of Chromosomes as an Accelerating Force to Align Homologous Chromosomes during Meiosis. 2019 , 88, 023801	2
288	Tiny Models to Answer Big Questions: The Worm and the Yeast as Tools in Human Genetics Research. 2019 , 49-68	
287	Crosstalk between autophagy and apoptosis induced by camphor in Schizosaccharomyces pombe. 2019 , 43, 382-390	3

(2020-2019)

286	The Use of Whole Genome and Next-Generation Sequencing in the Diagnosis of Invasive Fungal Disease. 2019 , 13, 284-291	2
285	Comparative Genomics and Transcriptomics To Analyze Fruiting Body Development in Filamentous Ascomycetes. 2019 , 213, 1545-1563	5
284	A DNA Sequence Corpus for Compression Benchmark. 2019 , 208-215	2
283	Ribosomal DNA instability and genome adaptability. 2019 , 27, 73-87	29
282	Andr[Goffeau's imprinting on second generation yeast "genomologists". 2019 , 36, 167-175	1
281	Inevitability or contingency: how many chromosomes do we really need?. 2019 , 62, 140-143	2
280	Towards Quantitative Microbiome Community Profiling Using Internal Standards. 2019, 85,	27
279	MCAT: Motif Combining and Association Tool. 2019 , 26, 1-15	4
278	Cellular models of Batten disease. 2020 , 1866, 165559	10
277	Minimal Cells: Design, Construction, Biotechnological Applications. 2020 ,	O
276	Set1/COMPASS repels heterochromatin invasion at euchromatic sites by disrupting Suv39/Clr4 activity and nucleosome stability. 2020 , 34, 99-117	5
275	Metabolism of phospholipids in the yeast Schizosaccharomyces pombe. 2020 , 37, 73-92	5
274	Stabilization of G-quadruplex DNA structures in Schizosaccharomyces pombe causes single-strand DNA lesions and impedes DNA replication. 2020 , 48, 10998-11015	6
273	A universal and independent synthetic DNA ladder for the quantitative measurement of genomic features. 2020 , 11, 3609	1
272	Microtubule nucleation promoters Mto1 and Mto2 regulate cytokinesis in fission yeast. 2020 , 31, 1846-1856	2
271	Comparing the utility of in vivo transposon mutagenesis approaches in yeast species to infer gene essentiality. 2020 , 66, 1117-1134	7
270	Functional Expression of All Human Sulfotransferases in Fission Yeast, Assay Development, and Structural Models for Isoforms SULT4A1 and SULT6B1. 2020 , 10,	4
269	The occurrence and function of alternative splicing in fungi. 2020 , 34, 178-188	2

268	Genome Sequencing of Provides Insights into Its Phylogenetic Placement and Mycoparasitism Mechanisms on Morel Mushrooms. 2020 , 9,	8
267	Cadmium-Induced Cell Homeostasis Impairment is Suppressed by the Tor1 Deficiency in Fission Yeast. 2020 , 21,	4
266	Pomegranate: 2D segmentation and 3D reconstruction for fission yeast and other radially symmetric cells. 2020 , 10, 16580	1
265	Molecular Tools for Gene Analysis in Fission Yeast. 2020 ,	
264	The conserved elongation factor Spn1 is required for normal transcription, histone modifications, and splicing in Saccharomyces cerevisiae. 2020 , 48, 10241-10258	6
263	The Absence of C-5 DNA Methylation in Allows DNA Enrichment from Complex Samples. 2020 , 8,	4
262	Centromeres under Pressure: Evolutionary Innovation in Conflict with Conserved Function. 2020 , 11,	9
261	Identification of Genomewide Alternative Splicing Events in Sequential, Isogenic Clinical Isolates of Candida albicans Reveals a Novel Mechanism of Drug Resistance and Tolerance to Cellular Stresses. 2020 , 5,	2
260	Nuclear Envelope Proteins Modulating the Heterochromatin Formation and Functions in Fission Yeast. 2020 , 9,	3
259	Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota. 2020 , 6,	24
258	The mechanisms and significance of the positional control of centromeres and telomeres in plants. 2020 , 133, 471-478	3
257	Resurrection from lethal knockouts: Bypass of gene essentiality. 2020 , 528, 405-412	1
256	Bistability and oscillations in cooperative microtubule and kinetochore dynamics in the mitotic spindle. 2020 , 22, 053008	3
255	Genetic investigation of formaldehyde-induced DNA damage response in Schizosaccharomyces pombe. 2020 , 66, 593-605	8
254	Dramatically diverse Schizosaccharomyces pombe wtf meiotic drivers all display high gamete-killing efficiency. 2020 , 16, e1008350	15
253	Nuclear envelope attachment of telomeres limits TERRA and telomeric rearrangements in quiescent fission yeast cells. 2020 , 48, 3029-3041	6
252	Telomeric Transcription and Telomere Rearrangements in Quiescent Cells. 2020 , 432, 4220-4231	2
251	Nascent Polypeptide-Associated Complex Involved in the Development and Pathogenesis of Fusarium graminearum on Wheat. 2020 , 6, 546-552	1

(2021-2020)

250	Metatranscriptomics: an approach for retrieving novel eukaryotic genes from polluted and related environments. 2020 , 10, 71	16
249	The Catalytic-Dependent and -Independent Roles of Lsd1 and Lsd2 Lysine Demethylases in Heterochromatin Formation in. 2020 , 9,	2
248	Telomere Formation Systems in Budding and Fission Yeasts. 2020 ,	
247	Diverse transposable element landscapes in pathogenic and nonpathogenic yeast models: the value of a comparative perspective. 2020 , 11, 16	4
246	Autophagy-Related Protein MAP1LC3C Plays a Crucial Role in Odontogenic Differentiation of Human Dental Pulp Cells. 2021 , 18, 265-277	4
245	Calcium signaling is involved in diverse cellular processes in fungi. 2020 , 12, 10-24	4
244	Experimental evolution of adaptive divergence under varying degrees of gene flow. 2021, 5, 338-349	5
243	Bioinformatics Approaches for Fungal Biotechnology. 2021 , 536-554	
242	Architecture and evolution of subtelomeres in the unicellular green alga Chlamydomonas reinhardtii.	
241	Distribution of methionine sulfoxide reductases in fungi and conservation of the free-methionine-R-sulfoxide reductase in multicellular eukaryotes.	
240	TOR targets an RNA processing network to regulate facultative heterochromatin, developmental gene expression and cell proliferation. 2021 , 23, 243-256	5
239	Analysis of the SNARE Stx8 recycling reveals that the retromer-sorting motif has undergone evolutionary divergence. 2021 , 17, e1009463	О
238	Thyroid hormone action in epidermal development and homeostasis and its implications in the pathophysiology of the skin. 2021 , 44, 1571-1579	12
237	Expression of the cancer-associated DNA polymerase IP286R in fission yeast leads to translesion synthesis polymerase dependent hypermutation and defective DNA replication.	
236	In-depth phylogenomic analysis of arbuscular mycorrhizal fungi based on a comprehensive set of de novo genome assemblies.	
235	Biomechanics of chromosome alignment at the spindle midplane. 2021 , 31, R574-R585	4
234	The cell cycle and differentiation as integrated processes: Cyclins and CDKs reciprocally regulate Sox and Notch to balance stem cell maintenance. 2021 , 43, e2000285	2
233	A single mA modification in U6 snRNA diversifies exon sequence at the 5' splice site. 2021 , 12, 3244	8

232	TORC2 inhibition of Berrestin Aly3 mediates cell surface persistence of S. pombe Ght5 glucose transporter in low glucose. 2021 , 134,	3
231	Distribution of methionine sulfoxide reductases in fungi and conservation of the free-methionine-R-sulfoxide reductase in multicellular eukaryotes. 2021 , 169, 187-215	2
230	Affects the Virulence of the Fungal Plant Pathogen. 2021 , 12,	O
229	Comprehensive predictions of secondary structures for comparative analysis in different species. 2021 , 213, 107735	
228	Fission Yeast Schizosaccharomyces pombe: A Unicellular "Micromammal" Model Organism. 2021 , 1, e151	4
227	Architecture and evolution of subtelomeres in the unicellular green alga Chlamydomonas reinhardtii. 2021 , 49, 7571-7587	2
226	Rapid and inexpensive preparation of genome-wide nucleosome footprints from model and non-model organisms. 2021 , 2, 100486	O
225	Saccharomyces: Is a Necessary Organism or a Biological Warrior?.	
224	Yesprit and Yeaseq: Applications for designing primers and browsing sequences for research using the four Schizosaccharomyces species. 2021 , 38, 583-591	
223	Exomer Is Part of a Hub Where Polarized Secretion and Ionic Stress Connect. 2021 , 12, 708354	O
222	R-loops and regulatory changes in chronologically ageing fission yeast cells drive non-random patterns of genome rearrangements. 2021 , 17, e1009784	
221	Reactivation of transposable elements following hybridization in fission yeast.	
220	Harnessing model organism genomics to underpin the machine learning-based prediction of essential genes in eukaryotes - Biotechnological implications. 2021 , 107822	О
219	Application of omics- and multi-omics-based techniques for natural product target discovery. 2021 , 141, 111833	4
218	In-depth Phylogenomic Analysis of Arbuscular Mycorrhizal Fungi Based on a Comprehensive Set of de novo Genome Assemblies. 2021 , 2,	2
217	Anaerobic Fungal Mevalonate Pathway Genomic Biases Lead to Heterologous Toxicity Underpredicted by Codon Adaptation Indices. 2021 , 9,	2
216	Subtelomeric Chromatin in the Fission Yeast. 2021 , 9,	O
215	Complete sequences of Schizosaccharomyces pombe subtelomeres reveal multiple patterns of genome variation. 2021 , 12, 611	2

214	as Emerging Model Organism in Fundamental Research. 2020 , 11, 607028	8
213	The Genomics of Stress Response in Fission Yeast. 2006 , 97-111	1
212	Yeast functional genomics and metabolic engineering: past, present and future. 2003, 331-360	2
211	Epigenetic Silencing of Pericentromeric Heterochromatin by RNA Interference in Schizosaccharomyces pombe. 2009 , 149-162	1
210	Nucleic Acid and Protein Sample Preparation from Yeasts. 2016 , 285-305	3
209	Duplication and Transformation of the Schizosaccharomyces pombe Collection of Deletion Strains. 2018 , 1721, 197-215	1
208	Genetic and Cytological Methods to Study ESCRT Cell Cycle Function in Fission Yeast. 2019 , 1998, 239-250	1
207	Integrated analysis of microarray results. 2007 , 382, 429-37	1
206	Genetic analysis of meiotic recombination in Schizosaccharomyces pombe. 2009, 557, 65-76	32
205	Systematic cloning of an ORFeome using the Gateway system. 2009 , 577, 11-24	15
204	Purification of tubulin from the fission yeast Schizosaccharomyces pombe. 2011 , 777, 29-55	23
203	Deducing intracellular distributions of metabolic pathways from genomic data. 2014 , 1083, 187-211	11
202	The pre-mRNA splicing reaction. 2014 , 1126, 3-12	3
201	Pre-mRNA Splicing and the Spliceosome: Assembly, Catalysis, and Fidelity. 2014 , 27-57	1
200	Sexual Communication in Archaea, the Precursor to Eukaryotic Meiosis. 2017 , 103-117	1
199	RNAi-mediated chromatin silencing in fission yeast. 2008 , 320, 157-83	47
198	Chromatin proteins are determinants of centromere function. 2003 , 274, 23-52	19
197	Electrophoretic Karyotyping. 2004 , 53-70	1

196	Centromere and Kinetochore Structure and Function. 2004 , 149-169	3
195	Initiation of Meiosis. 2004 , 297-309	33
194	The Genome and Beyond. 2004 , 13-25	4
193	DNA Replication in S. pombe. 2004 , 73-99	5
192	Genetic approaches to aging in budding and fission yeasts: new connections and new opportunities. 2012 , 57, 291-314	8
191	The C- and G-value paradox with polyploidy, repeatomes, introns, phenomes and cell economy. 2020 , 42, 699-714	6
190	Genome-wide distribution of DNA replication origins at A+T-rich islands in Schizosaccharomyces pombe. 2003 , 4, 1048-1053	85
189	Nonrandom homolog segregation at meiosis I in Schizosaccharomyces pombe mutants lacking recombination. 2003 , 163, 857-74	61
188	Repair of damaged and mismatched DNA by the XPC homologues Rhp41 and Rhp42 of fission yeast. 2003 , 164, 457-67	11
187	Fission yeast Mus81.Eme1 Holliday junction resolvase is required for meiotic crossing over but not for gene conversion. 2003 , 165, 2289-93	96
186	'New uses for an Old Enzyme'the Old Yellow Enzyme family of flavoenzymes. 2002 , 148, 1607-1614	216
185	Transient structural variations have strong effects on quantitative traits and reproductive isolation in fission yeast.	1
184	OmicsDB::Pathogens - A database for exploring functional networks of plant pathogens.	1
183	Genome-scale phylogeny and contrasting modes of genome evolution in the fungal phylum Ascomycota.	4
182	The absence of C-5 DNA methylation in Leishmania donovani allows DNA enrichment from complex samples.	1
181	Rapid and Inexpensive Preparation of Genome-Wide Nucleosome Footprints from Model and Non-Model Organisms.	1
180	Trilogies of histone lysine methylation as epigenetic landmarks of the eukaryotic genome. 2004 , 69, 209-18	61
179	Sorangium cellulosum. 329-348	2

178	Carbon metabolism. 2004 , 42-103	11
177	A novel gene family controls species-specific morphological traits in Hydra. 2008 , 6, e278	70
176	Swi1Timeless Prevents Repeat Instability at Fission Yeast Telomeres. 2016 , 12, e1005943	15
175	The intron in centromeric noncoding RNA facilitates RNAi-mediated formation of heterochromatin. 2017 , 13, e1006606	8
174	Two separate pathways regulate protein stability of ATM/ATR-related protein kinases Mec1 and Tel1 in budding yeast. 2017 , 13, e1006873	7
173	Global profiling of DNA replication timing and efficiency reveals that efficient replication/firing occurs late during S-phase in S. pombe. 2007 , 2, e722	20
172	Evidence for a minimal eukaryotic phosphoproteome?. 2007 , 2, e777	38
171	Comparative genome analysis of filamentous fungi reveals gene family expansions associated with fungal pathogenesis. 2008 , 3, e2300	140
170	Genome-wide identification of molecular mimicry candidates in parasites. 2011 , 6, e17546	29
169	N-termini of fungal CSL transcription factors are disordered, enriched in regulatory motifs and inhibit DNA binding in fission yeast. 2011 , 6, e23650	8
168	Comparative analysis of serine/arginine-rich proteins across 27 eukaryotes: insights into sub-family classification and extent of alternative splicing. 2011 , 6, e24542	46
167	The fission yeast GATA factor, Gaf1, modulates sexual development via direct down-regulation of ste11+ expression in response to nitrogen starvation. 2012 , 7, e42409	13
166	Klf1, a C2H2 zinc finger-transcription factor, is required for cell wall maintenance during long-term quiescence in differentiated G0 phase. 2013 , 8, e78545	14
165	DNA sequences at a glance. 2013 , 8, e79922	11
164	Single site suppressors of a fission yeast temperature-sensitive mutant in cdc48 identified by whole genome sequencing. 2015 , 10, e0117779	6
163	Comparative 3D genome structure analysis of the fission and the budding yeast. 2015 , 10, e0119672	16
162	Evolution of the SH3 Domain Specificity Landscape in Yeasts. 2015 , 10, e0129229	6
161	Genetic Interactions between the Members of the SMN-Gemins Complex in Drosophila. 2015 , 10, e0130974	15

160	Pyruvate kinase variant of fission yeast tunes carbon metabolism, cell regulation, growth and stress resistance. 2020 , 16, e9270	11
159	Yeast and its uses 2012 , 58, 326-335	2
158	Involvement of Dcr1 in post-transcriptional regulation of gene expression in Schizosaccharomyces pombe. 2008 , 13, 2203-15	7
157	Biofuel Production: A Promising Alternative Energy for Environmental Cleanup and Fuelling Through Renewable Resources. 2008 , 8, 693-701	10
156	Length-Weight Relationship and Growth Pattern of Sepioteuthis lessoniana Lesson 1830 (Cephalopoda:Teuthida) from the Jaffna Lagoon, Sri Lanka. 2009 , 9, 357-361	9
155	Galactose-Specific Recognition System in the Fission Yeast Schizosaccharomyces pombe. 2012 , 24, 24-42	2
154	Proteomic Differences between Azole-Susceptible and -Resistant <i>Aspergillus fumigatus</i> Strains. 2018 , 08, 77-99	4
153	A Review of Genome Sequencing in the Largest Cereal Genome, <i>Triticum aestivum</i> L 2017 , 08, 194-207	1
152	Yeast as a touchstone in post-genomic research: strategies for integrative analysis in functional genomics. 2004 , 37, 93-106	46
151	Mutation Analysis of Synthetic DNA Barcodes in a Fission Yeast Gene Deletion Library by Sanger Sequencing. 2018 , 16, 22-29	2
150	Statistical analysis of pentose phosphate pathway genes from eubacteria and eukarya reveals translational selection as a major force in shaping codon usage pattern. 2013 , 9, 349-56	1
149	A histone H3K9M mutation traps histone methyltransferase Clr4 to prevent heterochromatin spreading. 2016 , 5,	26
148	A large gene family in fission yeast encodes spore killers that subvert Mendel's law. 2017, 6,	50
147	Distinct 'safe zones' at the nuclear envelope ensure robust replication of heterochromatic chromosome regions. 2018 , 7,	13
146	Large domains of heterochromatin direct the formation of short mitotic chromosome loops. 2020 , 9,	6
145	Characterisation of Schizosaccharomyces pombe ե ctinin. 2016 , 4, e1858	6
144	An automated and combinative method for the predictive ranking of candidate effector proteins of fungal plant pathogens. 2021 , 11, 19731	6
143	Balance of osmotic pressures determines the volume of the cell nucleus.	Ο

(2009-2021)

142	Genome Comparisons of the Fission Yeasts Reveal Ancient Collinear Loci Maintained by Natural Selection. 2021 , 7,	
141	Sulfide-quinone oxidoreductase is required for cysteine synthesis and indispensable to mitochondrial health. 2021 , 47, 102169	3
140	Biochemical Genetics. 2001 , 1473-1527	
139	Fission statement. <i>Nature</i> ,	50.4
138	Literatur. 2002 , 258-266	
137	Proteomics of Magnaporthe Grisea: Liquid Chromatography Mass Spectrometry for the Identification of Extracellular Proteins. 2004 , 39-46	
136	Trilogies of Histone Lysine Methylation as Epigenetic Landmarks of the Eukaryotic Genome. 2004 , 69, 1-10	
135	RNA Polymerases and Accessory Factors. 2004 , 329-342	
134	Genomics of Filamentous Fungi. 2004 , 15-29	
133	Schizosaccharomyces pombe (Fission Yeast).	
132	. 2005,	
131	Data Mining for Expressivity of Recombinant Protein Expression. 2006 , 21, 9-19	
130	Mycorrhizal Development and Cytoskeleton. 2008, 293-329	
129	Dual-specificity kinase. 2009 , 372-391	
128	Cyclin-dependent kinase. 2009 , 156-219	
127	Polo kinase. 2009 , 134-155	
126	Ca2+/Calmodulin-dependent protein kinase. 2009 , 1-53	
125	Mitogen-activated protein kinase. 2009 , 233-277	

124	Mitogen-activated protein kinase kinase. 2009 , 278-302
123	Non-specific serine/threonine protein kinase. 2009 , 1-123
122	tau-Protein kinase. 2009 , 303-325
121	Mitogen-activated protein kinase kinase. 2009 , 392-413
120	2 Wat is metabolisme?. 2010 , 41-76
119	Fungal Genetics: A Post-Genomic Perspective. 95-123
118	Leucyl Aminopeptidase yspII (Yeast). 2013 , 1476-1480
117	Genomics of Subtelomeres: Technical Problems, Solutions and the Future. 2014 , 259-271
116	Insights into Metabolism and the Galactose Recognition System from Microarray Analysis in the Fission Yeast Schizosaccharomyces pombe. 2014 , 109-118
115	Regulation of Pericentric Heterochromatin by ncRNA in Schizosaccharomyces pombe. 2014 , 315-345
114	Minimum Genome Factories in Schizosaccharomyces pombe. 2014 , 17-24
113	Comparative Genomics and Evolutionary Genetics of Yeast Carbon Metabolism. 2014 , 97-120
112	Genomic Perspectives on the Fungal Kingdom. 657-666
111	Studying Fungal Virulence by Using Genomics. 589-P1
110	References. 275-359
109	Comparative Genomics of Candida Species. 27-43
108	Wat is metabolisme?. 2015 , 41-76
107	Centromeres of the yeast Komagataella phaffii (Pichia pastoris) have a simple inverted-repeat structure.

106	Detection and characterization of low and high genome coverage regions using an efficient running median and a double threshold approach.	2
105	New genes and functional innovation in mammals.	1
104	A heterochromatin domain forms gradually at a new telomere and is highly dynamic at stable telomeres.	
103	A non-genetic meiotic repair program inferred from spore survival values in fission yeast wild isolates: a clue for an epigenetic ratchet-like model of ageing?.	
102	AYbRAH: a curated ortholog database for yeasts and fungi spanning 600 million years of evolution.	
101	Uncovering Natural Longevity Alleles from Intercrossed Pools of Aging Fission Yeast Cells.	O
100	Fitness Landscape of the Fission Yeast Genome.	
99	The essential genome of the crenarchaeal model Sulfolobus islandicus.	1
98	Killer meiotic drive and dynamic evolution of the wtf gene family.	O
97	The transcriptome-wide landscape and modalities of EJC binding in adult Drosophila.	O
96	Torsional turning motion of chromosomes as an accelerating force to align homolog ous chromosomes during meiosis.	
95	R-loops and regulatory changes in chronologically ageing fission yeast cells drive non-random patterns of genome rearrangements.	
94	Intraspecific diversity of fission yeast mitochondrial genomes.	
93	Set1/COMPASS repels heterochromatin invasion at euchromatic sites by disrupting Suv39/Clr4 activity and nucleosome stability.	
92	Dramatically diverseS. pombe wtfmeiotic drivers all display high gamete-killing efficiency.	O
91	Comparing the utility of in vivo transposon mutagenesis approaches in yeast species to infer gene essentiality.	O
90	A natural variant of the sole pyruvate kinase of fission yeast lowers glycolytic flux triggering increased respiration and oxidative-stress resistance but decreased growth.	O
89	Microtubule Nucleation Promoters Mto1 and Mto2 Regulate Cytokinesis in Fission Yeast.	

88	Reduction of the Saccharomyces cerevisiae Genome: Challenges and Perspectives. 2020, 117-139	1
87	Saccharomyces cerevisiae as Model Organism to Study Biological Activities of Nanoparticles. 2020 , 101-115	1
86	Measurement of the torque in braided DNAs using a thermodynamic Maxwell relation.	
85	The conserved elongation factor Spn1 is required for normal transcription, histone modifications, and splicing in Saccharomyces cerevisiae.	
84	Intron distribution and emerging role of alternative splicing in fungi. 2021, 368,	1
83	Assays to Study Mitotic Recombination Outcomes. 2020 , 11,	O
82	Complete sequences of Schizosaccharomyces pombe subtelomeres reveal multiple patterns of genome variation.	
81	Pomegranate: 2D segmentation and 3D reconstruction for fission yeast and other radially symmetric cells.	1
80	Molecular Genetic Approach to Identify Inhibitors of Signal Transduction Pathways. 2008, 439-443	О
79	Protein kinase (dual specificity kinase). 2007 , 497-505	
78	Phosphatidylinositol 3-kinase. 2007 , 170-191	
77	Protein kinase (CaMK, MLCK, PhK, SNF, KIN, NIM1, MAPKAP, POLO, CHK, ULK, RSK-2nd domain). 2007 , 489-528	
76	Protein kinase (CDK/MAK). 2007 , 529-551	
75	Protein kinase (CK1). 2007 , 552-560	
74	Protein kinase (CK2). 2007 , 561-566	
73	Protein kinase (dual specificity kinase). 2007 , 567-575	
72	Protein kinase (GSK-3). 2007 , 582-588	
71	Protein kinase (MEK, PAK, MEKK). 2007 , 615-636	

53

Protein kinase (various). 2007, 662-687 70 Comparative Genomics and Evolutionary Genetics of Yeast Carbon Metabolism. 2014, 97-120 69 Transcript-specific determinants of pre-mRNA splicing revealed through in vivo kinetic analyses of 68 the 1st and 2nd chemical steps. PROTEIN I-ISOASPARTYL METHYLTRANSFERASE (PIMT) in plants: regulations and functions. 2020, 67 477, 4453-4471 Experimental evolution of adaptive divergence under varying degrees of gene flow. 66 1 Essential histone chaperones collaborate to regulate transcription and chromatin integrity. 65 64 Molecular Mechanisms and Evolutionary Consequences of Spore Killers in Ascomycetes. 2021, e0001621 3 Segregating Complete Tf2 Elements Are Largely Neutral in Fission Yeast. 2021, 13, 63 Transposon Extermination Reveals Their Adaptive Fitness Contribution. 62 \circ 61 Evolution of the Early Spliceosomal Complex-From Constitutive to Regulated Splicing. 2021, 22, 1 The Metaxin Mitochondrial Import Proteins: Multiple Metaxin-like Proteins in Fungi. 60 O The search for Schizosaccharomyces fission yeasts in environmental meta-transcriptomes.. 2021, 59 In Silico Predictions of Ecological Plasticity Mediated by Protein Family Expansions in 58 O Early-Diverging Fungi.. 2022, 8, Genomic Characterization of the Titan-like Cell Producing, the First Novel Eukaryote Isolated from 57 the International Space Station.. 2022, 8, Prediction of serine phosphorylation sites mapping on Schizosaccharomyces Pombe by fusing three 56 \circ encoding schemes with the random forest classifier.. 2022, 12, 2632 Nematode chromosomes.. 2022, 55 Deletion of can1/cat1 genes and expression of a dominant any1 mutation establish an effective 54 canavanine selection in fission yeast.

Genetics Matters: Voyaging from the Past into the Future of Humanity and Sustainability.. 2022, 23,

52	Phenotypic Characterization and Comparative Genomics of the Melanin-Producing Yeast Reveals a Distinct Stress Tolerance Profile and Reduced Ribosomal Genetic Content 2021 , 7,	0
51	CUT&RUN Identifies Centromeric DNA Regions of Rhodotorula toruloides IFO0880 2021,	O
50	Reactivation of transposable elements following hybridization in fission yeast 2021,	2
49	Differential Gene Expression of under Aerobic and Anaerobic Conditions 2022, 8,	O
48	Isolated THATCH domain of End4 is unable to bind F-actin independently in the fission yeast 2022 , 2022,	
47	RNA Interference (RNAi) as a Tool for High-Resolution Phenotypic Screening of the Pathogenic Yeast Candida glabrata 2022 , 2477, 313-330	
46	Balance of osmotic pressures determines the nuclear-to-cytoplasmic volume ratio of the cell 2022 , 119, e2118301119	О
45	Characterization of canavanine-resistance of cat1 and vhc1 deletions and a dominant any1 mutation in fission yeast. 2022 , 17, e0269276	O
44	Native RNA sequencing in fission yeast reveals frequent alternative splicing isoforms. 2022 , 32, 1215-1227	O
43	Contribution of Model Organisms to Investigating the Far-Reaching Consequences of PRPP Metabolism on Human Health and Well-Being. 2022 , 11, 1909	
42	Perturbed fatty-acid metabolism is linked to localized chromatin hyperacetylation, increased stress-response gene expression and resistance to oxidative stress.	
41	Divergent evolution of early terrestrial fungi reveals the evolution of Mucormycosis pathogenicity factors.	
40	The wtf meiotic driver gene family has unexpectedly persisted for over 100 million years.	
39	A multiplexed, three-dimensional pooling and next-generation sequencing strategy for creating barcoded mutant arrays: construction of a Schizosaccharomyces pombe transposon insertion library.	
38	Transcript-specific determinants of pre-mRNA splicing revealed through in vivo kinetic analyses of the 1st and 2nd chemical steps. 2022 ,	О
37	Yeast Genomics and Its Applications in Biotechnological Processes: What Is Our Present and Near Future?. 2022 , 8, 752	1
36	Fungal resilience and hostpathogen interactions: Future perspectives and opportunities.	
35	Single-chromosome fission yeast models reveal the configuration robustness of a functional genome. 2022 , 40, 111237	O

34	Metabolic engineering of Schizosaccharomyces pombe for itaconic acid production. 2022, 358, 111-117	1
33	Detecting Cell Cycle Stage and Progression in Fission Yeast, Schizosaccharomyces pombe. 2022 , 235-246	O
32	Meiotic crossover interference: Methods of analysis and mechanisms of action. 2022,	0
31	Cell Cycle Synchrony Methods for Fission Yeast, Schizosaccharomyces pombe. 2022 , 169-179	O
30	Witches Droom disease of birch. 2023, 121-136	0
29	Interpreting alignment-free sequence comparison: what makes a score a good score?. 2022, 4,	O
28	SAGA histone acetyltransferase module facilitates chromatin accessibility to SMC5/6.	O
27	Fission yeast Ish1 and Les1 interact with each other in the lumen of the nuclear envelope.	O
26	The wtf meiotic driver gene family has unexpectedly persisted for over 100 million years. 11,	1
25	Altered cohesin dynamics and histone H3K9 modifications contribute to mitotic defects in thecbf11llpid metabolism mutant.	O
24	Epigenetic Regulation of Fungal Genes Involved in Plant Colonization. 2023, 255-281	О
23	A high-quality reference genome for the fission yeastSchizosaccharomyces osmophilus.	O
22	An ESCRT grommet cooperates with a diffusion barrier to maintain nuclear integrity.	O
21	Chromatin localization of nucleophosmin organizes ribosome biogenesis. 2022 , 82, 4443-4457.e9	O
20	Chromosome arm length, and a species-specific determinant, define chromosome arm width. 2022 , 41, 111753	О
19	Myco- and phyco-remediation of polychlorinated biphenyls in the environment: a review.	O
18	Remarkably high rate of meiotic recombination in the fission yeastSchizosaccharomyces pombe.	0
17	Perturbed fatty-acid metabolism is linked to localized chromatin hyperacetylation, increased stress-response gene expression and resistance to oxidative stress. 2023 , 19, e1010582	O

16	Silver nanoparticles elevate mutagenesis of eukaryotic genomes.	O
15	The genome of Lyophyllum shimeji provides insight into the initial evolution of ectomycorrhizal fungal genomes.	O
14	Do mitochondria use efflux pumps to protect their ribosomes from antibiotics?. 2023, 169,	0
13	Yeast Cell Factory for Production of Biomolecules. 2023 , 211-251	O
12	Neutral models ofde novogene emergence suggest that gene evolution has a preferred trajectory.	O
11	Neutral models of de novo gene emergence suggest that gene evolution has a preferred trajectory.	O
10	Comparative Research: Regulatory Mechanisms of Ribosomal Gene Transcription in Saccharomyces cerevisiae and Schizosaccharomyces pombe. 2023 , 13, 288	0
9	A high-quality reference genome for the fission yeast Schizosaccharomyces osmophilus. 2023 , 13,	o
8	Conservation and Expansion of Transcriptional Factor Repertoire in theFusarium oxysporumSpecies Complex.	0
7	Cryo-EM structure and function of S. pombe complex IV with bound respiratory supercomplex factor. 2023 , 6,	O
6	The SAGA histone acetyltransferase module targets SMC5/6 to specific genes. 2023, 16,	O
5	Regulation of Pre-mRNA Splicing: Indispensable Role of Post-Translational Modifications of Splicing Factors. 2023 , 13, 604	O
4	Uracil Repair - A Source of DNA Glycosylase Dependent Genome Instability.	0
3	Conservation and Expansion of Transcriptional Factor Repertoire in the Fusarium oxysporum Species Complex. 2023 , 9, 359	O
2	Interaction hub critical for telomerase recruitment and primer-template handling for catalysis. 2023 , 6, e202201727	0
1	Broad functional profiling of fission yeast proteins using phenomics and machine learning.	O