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## A large family of bacterial activator proteins

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468	A nod at differentiation: the <i>nodD</i> gene product and initiation of <i>Rhizobium</i> nodulation. <b>1989</b> , 5, 199-201		10
467	Molecular cloning and nucleotide sequencing of <i>oxyR</i> , the positive regulatory gene of a regulon for an adaptive response to oxidative stress in <i>Escherichia coli</i> : homologies between OxyR protein and a family of bacterial activator proteins. <b>1989</b> , 218, 371-6		79
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452	Analysis of three nodD genes in <i>Rhizobium leguminosarum</i> biovar phaseoli; nodD1 is preceded by nolE, a gene whose product is secreted from the cytoplasm. <b>1990</b> , 4, 921-32	40
451	Nucleotide sequence and control of transcription of the bacteriophage T4 motA regulatory gene. <b>1990</b> , 4, 1487-96	22
450	Genetics of CO <sub>2</sub> fixation in the chemoautotroph <i>Alcaligenes eutrophus</i> . <b>1990</b> , 87, 445-450	23
449	Genetic analysis of an invasion region by use of a Tn3-lac transposon and identification of a second positive regulator gene, invE, for cell invasion of <i>Shigella sonnei</i> : significant homology of invE with ParB of plasmid P1. <b>1990</b> , 172, 619-29	62
448	Cloning and characterization of tfdS, the repressor-activator gene of tfdB, from the 2,4-dichlorophenoxyacetic acid catabolic plasmid pJP4. <b>1990</b> , 172, 5856-62	51
447	Beta-lactamase expression in <i>Streptomyces cacaoi</i> . <b>1990</b> , 172, 6427-34	9
446	In vitro interactions of CysB protein with the cysJIH promoter of <i>Salmonella typhimurium</i> : inhibitory effects of sulfide. <b>1990</b> , 172, 779-85	49
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444	DNA sequence and translational product of a new nodulation-regulatory locus: syrM has sequence similarity to NodD proteins. <b>1990</b> , 172, 3695-700	44
443	Transcriptional regulation by iron of a <i>Vibrio cholerae</i> virulence gene and homology of the gene to the <i>Escherichia coli</i> fur system. <b>1990</b> , 172, 6863-70	72

- 442 Structure-function studies on Escherichia coli MetR protein, a putative prokaryotic leucine zipper protein. *Proceedings of the National Academy of Sciences of the United States of America*, **1990**, 87, 7076-9<sup>11.5</sup> 61
- 441 Improved detection of helix-turn-helix DNA-binding motifs in protein sequences. **1990**, 18, 5019-26 497
- 440 The roles of indoleglycerol phosphate and the TrpI protein in the expression of trpBA from *Pseudomonas aeruginosa*. **1990**, 18, 979-88 65
- 439 A family of positive regulators related to the *Pseudomonas putida* TOL plasmid XylS and the *Escherichia coli* AraC activators. **1990**, 18, 2149-52 86
- 438 Precise mapping and comparison of two evolutionarily related regions of the *Escherichia coli* K-12 chromosome. Evolution of valU and lysT from an ancestral tRNA operon. **1990**, 214, 825-43 23
- 437 Transcriptional and translational features of a sporulation gene of *Streptomyces griseus*. **1990**, 95, 57-63 31
- 436 Identifying distantly related protein sequences. **1991**, 1, 321-326 11
- 435 Positive regulator for the expression of Mba protein of the virulence plasmid, pKDSC50, of *Salmonella choleraesuis*. **1991**, 10, 459-64 18
- 434 RNA polymerases from *Pseudomonas aeruginosa* and *Pseudomonas syringae* respond to *Escherichia coli* activator proteins. **1991**, 173, 394-7 27
- 433 Activation of the trpBA promoter of *Pseudomonas aeruginosa* by TrpI protein in vitro. **1991**, 173, 3763-9 19
- 432 rbcR [correction of rcbR], a gene coding for a member of the LysR family of transcriptional regulators, is located upstream of the expressed set of ribulose 1,5-bisphosphate carboxylase/oxygenase genes in the photosynthetic bacterium *Chromatium vinosum*. **1991**, 173, 5224-9 83
- 431 Characterization of the *Pseudomonas* sp. strain P51 gene tcbR, a LysR-type transcriptional activator of the tcbCDEF chlorocatechol oxidative operon, and analysis of the regulatory region. **1991**, 173, 3700-8 79
- 430 A family of regulatory genes associated with type II restriction-modification systems. **1991**, 173, 1367-75 137
- 429 Studies of the *Bradyrhizobium japonicum* nodD1 promoter: a repeated structure for the nod box. **1991**, 173, 3356-65 49
- 428 The metR binding site in the *Salmonella typhimurium* metH gene: DNA sequence constraints on activation. **1991**, 173, 3547-53 39
- 427 Functional analysis of the *Pseudomonas putida* regulatory protein CatR: transcriptional studies and determination of the CatR DNA-binding site by hydroxyl-radical footprinting. **1991**, 173, 4717-24 76
- 426 Characterization of a putative periplasmic transport system for octopine accumulation encoded by *Agrobacterium tumefaciens* Ti plasmid pTiA6. **1991**, 173, 6398-405 38
- 425 In vitro determination of the effect of indoleglycerol phosphate on the interaction of purified TrpI protein with its DNA-binding sites. **1991**, 173, 1590-7 38

424	Negative autoregulation of <i>cysB</i> in <i>Salmonella typhimurium</i> : in vitro interactions of CysB protein with the <i>cysB</i> promoter. <b>1991</b> , 173, 2212-8	45
423	Dances with sigmas.. <b>1991</b> , 10, 3559-3566	6
422	Identification of <i>dcmR</i> , the regulatory gene governing expression of dichloromethane dehalogenase in <i>Methylobacterium</i> sp. strain DM4. <b>1991</b> , 173, 6714-21	35
421	The <i>Salmonella typhimurium</i> virulence plasmid encodes a positive regulator of a plasmid-encoded virulence gene. <b>1991</b> , 173, 7176-85	68
420	Growth regulation of a <i>Salmonella</i> plasmid gene essential for virulence. <b>1991</b> , 173, 6783-9	94
419	Involvement of the <i>syrM</i> and <i>nodD3</i> genes of <i>Rhizobium meliloti</i> in <i>nod</i> gene activation and in optimal nodulation of the plant host. <b>1991</b> , 5, 3035-48	47
418	Regulation of methionine synthesis in <i>Escherichia coli</i> . <b>1991</b> , 5, 1593-7	87
417	Purification and mutant analysis of <i>Citrobacter freundii</i> AmpR, the regulator for chromosomal AmpC beta-lactamase. <b>1991</b> , 5, 1715-25	70
416	The role of the NAC protein in the nitrogen regulation of <i>Klebsiella aerogenes</i> . <b>1991</b> , 5, 2575-80	93
415	Identification of <i>cfxR</i> , an activator gene of autotrophic CO <sub>2</sub> fixation in <i>Alcaligenes eutrophus</i> . <b>1991</b> , 5, 2695-705	64
414	<i>Escherichia coli</i> <i>rpoA</i> mutation which impairs transcription of positively regulated systems. <b>1991</b> , 5, 2719-25	73
413	Molecular analysis of the virulence locus of the <i>Salmonella dublin</i> plasmid pSDL2. <b>1991</b> , 5, 307-16	73
412	A new family of bacterial regulatory proteins. <b>1991</b> , 79, 291-296	189
411	Transduction of plant signal molecules by the <i>Rhizobium</i> NodD proteins. <b>1991</b> , 13, 575-81	37
410	The <i>mkaC</i> virulence gene of the <i>Salmonella</i> serovar <i>typhimurium</i> 96 kb plasmid encodes a transcriptional activator. <b>1991</b> , 228, 381-4	36
409	Structural and functional analysis of the <i>rcsA</i> gene from <i>Erwinia stewartii</i> . <b>1991</b> , 229, 155-60	28
408	Identification and organization of carbon dioxide fixation genes in <i>Xanthobacter flavus</i> H4-14. <b>1991</b> , 225, 320-30	65
407	Homology of the ligand-binding regions of <i>Rhizobium</i> symbiotic regulatory protein NodD and vertebrate nuclear receptors. <b>1991</b> , 226, 337-40	32

406	cysB and cysE mutants of Escherichia coli K12 show increased resistance to novobiocin. <b>1991</b> , 228, 307-11	15
405	Genetic and physical analysis of the nodD3 region of Rhizobium meliloti. <b>1991</b> , 19, 921-7	31
404	Positive transcriptional regulation of an iron-regulated virulence gene in Vibrio cholerae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1991</b> , 88, 1125-9	11.5 92
403	Molecular mechanism of negative autoregulation of Escherichia coli crp gene. <b>1991</b> , 19, 4413-9	56
402	iciA, an Escherichia coli gene encoding a specific inhibitor of chromosomal initiation of replication in vitro. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1991</b> , 88, 4066-70	11.5 49
401	Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 to 86.5 minutes. <b>1992</b> , 257, 771-8	250
400	Cloning of genetic loci involved in endoprotease activity in Streptomyces lividans 66: a novel neutral protease gene with an adjacent divergent putative regulatory gene. <b>1992</b> , 38, 912-20	24
399	Nucleotide sequence of the ampC-ampR region from the chromosome of Yersinia enterocolitica. <b>1992</b> , 36, 1049-52	43
398	Conserved motifs in a divergent nod box of Azorhizobium caulinodans ORS571 reveal a common structure in promoters regulated by LysR-type proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1992</b> , 89, 1646-50	11.5 210
397	The alternative sigma factor katF (rpoS) regulates Salmonella virulence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1992</b> , 89, 11978-82	11.5 441
396	Characterization of translation termination mutations in the spv operon of the Salmonella virulence plasmid pSDL2. <b>1992</b> , 174, 6418-23	48
395	The Trp repressor, a ligand-activated regulatory protein. <b>1992</b> , 42, 1-38	27
394	Phenolic Metabolism in Plants. <b>1992</b> ,	8
393	Mutagenesis and regulation of the cysJ promoter of Escherichia coli K-12. <b>1992</b> , 122, 17-25	4
392	Signaling and host range variation in nodulation. <b>1992</b> , 46, 497-531	279
391	Flavonoids: Plant Signals to Soil Microbes. <b>1992</b> , 201-231	41
390	Coordinate regulation of murein peptidase activity and AmpC beta-lactamase synthesis in Escherichia coli. <b>1992</b> , 304, 103-8	14
389	Cloning and sequencing of a gene encoding a novel extracellular neutral proteinase from Streptomyces sp. strain C5 and expression of the gene in Streptomyces lividans 1326. <b>1992</b> , 174, 2797-808	28

388	Regulation of nodulation gene expression by NodD in rhizobia. <b>1992</b> , 174, 5177-82	136
387	Roles of CatR and cis,cis-muconate in activation of the catBC operon, which is involved in benzoate degradation in <i>Pseudomonas putida</i> . <b>1992</b> , 174, 7798-806	95
386	The <i>Escherichia coli</i> K-12 <i>cyn</i> operon is positively regulated by a member of the <i>lysR</i> family. <b>1992</b> , 174, 3645-50	33
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383	XylS domain interactions can be deduced from intraallelic dominance in double mutants of <i>Pseudomonas putida</i> . <b>1992</b> , 235, 406-12	21
382	Induction of a <i>Streptomyces cacaoi</i> beta-lactamase gene cloned in <i>S. lividans</i> . <b>1992</b> , 235, 41-8	8
381	Phylogenetic continuum indicates "galaxies" in the protein universe: preliminary results on the natural group structures of proteins. <b>1992</b> , 34, 358-75	11
380	A systematic search for protein signature sequences. <b>1992</b> , 14, 16-28	25
379	Identification, genetic analysis and DNA sequence of a 7.8-kb virulence region of the <i>Salmonella typhimurium</i> virulence plasmid. <b>1992</b> , 6, 1395-411	74
378	A <i>Salmonella dublin</i> virulence plasmid locus that affects bacterial growth under nutrient-limited conditions. <b>1992</b> , 6, 1631-43	81
377	A metalloprotease gene from <i>Streptomyces coelicolor</i> M162 and its transcriptional activator, a member of the <i>LysR</i> family. <b>1992</b> , 6, 2267-78	19
376	The molecular basis for positive regulation of <i>cys</i> promoters in <i>Salmonella typhimurium</i> and <i>Escherichia coli</i> . <b>1992</b> , 6, 2747-53	136
375	BLAZE: An implementation of the Smith-Waterman sequence comparison algorithm on a massively parallel computer. <b>1993</b> , 17, 203-207	18
374	Molecular mechanism of the regulation of expression of plasmid-encoded mouse bacteremia ( <i>mba</i> ) genes in <i>Salmonella</i> serovar <i>Choleraesuis</i> . <b>1993</b> , 236, 219-26	24
373	Nopaline causes a conformational change in the <i>NocR</i> regulatory protein- <i>nocR</i> promoter complex of <i>Agrobacterium tumefaciens</i> Ti plasmid pTi37. <b>1993</b> , 241, 65-72	18
372	TdcA, a transcriptional activator of the <i>tdcABC</i> operon of <i>Escherichia coli</i> , is a member of the <i>LysR</i> family of proteins. <b>1993</b> , 240, 395-402	27
371	Interactions of wild-type and mutant <i>AmpR</i> of <i>Citrobacter freundii</i> with target DNA. <b>1993</b> , 10, 555-65	36

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369	A <i>Rhizobium tropici</i> DNA region carrying the amino-terminal half of a <i>nodD</i> gene and a <i>nod</i> -box-like sequence confers host-range extension. <b>1993</b> , 9, 1157-68	15
368	AmpG, a signal transducer in chromosomal beta-lactamase induction. <b>1993</b> , 9, 703-15	101
367	Regulation and function of rhizobial nodulation genes. <b>1993</b> , 10, 39-63	74
366	Signal transduction and virulence regulation in human and animal pathogens. <b>1993</b> , 10, 301-26	43
365	Investigation of the <i>Pseudomonas aeruginosa</i> <i>ampR</i> gene and its role at the chromosomal <i>ampC</i> beta-lactamase promoter. <b>1993</b> , 111, 315-20	37
364	Overproduction, solubilization, purification and DNA-binding properties of AmpR from <i>Citrobacter freundii</i> . <b>1993</b> , 213, 405-12	16
363	Molecular biology of the LysR family of transcriptional regulators. <b>1993</b> , 47, 597-626	919
362	Cloning of the <i>lysA</i> gene from <i>Mycobacterium tuberculosis</i> . <b>1993</b> , 124, 105-9	15
361	Molecular mechanism of host specificity in legume-rhizobium symbiosis. <b>1993</b> , 11, 741-79	12
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359	Advances in Molecular Genetics of Plant-Microbe Interactions, Vol. 2. <b>1993</b> ,	2
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348	Altered-function mutations in the <i>Agrobacterium tumefaciens</i> <i>OccR</i> protein and in an <i>OccR</i> -regulated promoter. <b>1993</b> , 175, 7715-9	23
347	Complementation analysis and regulation of CO <sub>2</sub> fixation gene expression in a ribulose 1,5-bisphosphate carboxylase-oxygenase deletion strain of <i>Rhodospirillum rubrum</i> . <b>1993</b> , 175, 5066-77	64
346	Identification of the transcriptional activator <i>pobR</i> and characterization of its role in the expression of <i>pobA</i> , the structural gene for <i>p</i> -hydroxybenzoate hydroxylase in <i>Acinetobacter calcoaceticus</i> . <b>1993</b> , 175, 4499-506	76
345	Regulation of the <i>Salmonella typhimurium</i> <i>metF</i> gene by the <i>MetR</i> protein. <b>1993</b> , 175, 5862-6	43
344	Expression and purification of the <i>cynR</i> regulatory gene product: <i>CynR</i> is a DNA-binding protein. <b>1993</b> , 175, 7990-9	3
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337	DNA sequence and characterization of <i>GcvA</i> , a LysR family regulatory protein for the <i>Escherichia coli</i> glycine cleavage enzyme system. <b>1994</b> , 176, 2862-8	32
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333	Functional analysis of the Escherichia coli K-12 cyn operon transcriptional regulation. <b>1994</b> , 176, 6613-22	22
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330	Identification and characterization of the ilvR gene encoding a LysR-type regulator of Caulobacter crescentus. <b>1994</b> , 176, 1275-81	9
329	The linear Streptomyces plasmid pBL1: analyses of transfer functions. <b>1994</b> , 242, 374-82	11
328	Photosynthetic electron transport and anaerobic metabolism in purple non-sulfur phototrophic bacteria. <b>1994</b> , 66, 151-64	78
327	The molecular basis of the host specificity of the Rhizobium bacteria. <b>1994</b> , 65, 81-98	23
326	Regulation of spvR, the positive regulatory gene of Salmonella plasmid virulence genes. <b>1994</b> , 116, 113-21	15
325	Residue threonine-149 of the Salmonella typhimurium CysB transcription activator: mutations causing constitutive expression of positively regulated genes of the cysteine regulon. <b>1994</b> , 13, 797-805	32
324	Regulation of spvR gene expression of Salmonella virulence plasmid pKDSC50 in Salmonella choleraesuis serovar Choleraesuis. <b>1994</b> , 12, 779-87	29
323	Chapter 23 Mechanisms of chromosomal $\beta$ -lactamase induction in Gram-negative bacteria. <b>1994</b> , 485-503	23
322	Molecular biology of Na <sup>+</sup> /H <sup>+</sup> antiporters: molecular devices that couple the Na <sup>+</sup> and H <sup>+</sup> circulation in cells. <b>1994</b> , 1187, 206-10	15
321	Molecular physiology of Na <sup>+</sup> /H <sup>+</sup> antiporters, key transporters in circulation of Na <sup>+</sup> and H <sup>+</sup> in cells. <b>1994</b> , 1185, 129-51	119
320	Characterization of the CysB protein of Klebsiella aerogenes: direct evidence that N-acetylserine rather than O-acetylserine serves as the inducer of the cysteine regulon. <b>1994</b> , 299 ( Pt 1), 129-36	19
319	Stoichiometry of binding of CysB to the cysJIH, cysK, and cysP promoter regions of Salmonella typhimurium. <b>1994</b> , 176, 3673-82	71
318	Identification and characterization of two nitrogen-regulated genes of the cyanobacterium Synechococcus sp. strain PCC7942 required for maximum efficiency of nitrogen assimilation. <b>1995</b> , 177, 290-6	57
317	A consensus promoter sequence for Caulobacter crescentus genes involved in biosynthetic and housekeeping functions. <b>1995</b> , 177, 4372-6	54

316	Identification of the transcriptional activator controlling the butanediol fermentation pathway in <i>Klebsiella terrigena</i> . <b>1995</b> , 177, 5261-9	51
315	Purification and characterization of an isoaspartyl dipeptidase from <i>Escherichia coli</i> . <b>1995</b> , 270, 4076-87	33
314	Identification and characterization of genes ( <i>xapA</i> , <i>xapB</i> , and <i>xapR</i> ) involved in xanthosine catabolism in <i>Escherichia coli</i> . <b>1995</b> , 177, 5506-16	45
313	Prediction of the Three Dimensional Structure of the DNA-Binding Domain of the LysR Family.. <b>1995</b> , 71, 193-197	4
312	<i>catM</i> encodes a LysR-type transcriptional activator regulating catechol degradation in <i>Acinetobacter calcoaceticus</i> . <b>1995</b> , 177, 5891-8	53
311	In <i>Rhizobium meliloti</i> , the operon associated with the nod box n5 comprises <i>nodL</i> , <i>noeA</i> and <i>noeB</i> , three host-range genes specifically required for the nodulation of particular <i>Medicago</i> species. <b>1995</b> , 17, 687-99	36
310	Regulation of anaerobic citrate metabolism in <i>Klebsiella pneumoniae</i> . <b>1995</b> , 18, 533-46	117
309	Genetic and molecular analysis of a regulatory region of the herbicide 2,4-dichlorophenoxyacetate catabolic plasmid pJP4. <b>1995</b> , 16, 321-31	30
308	Transcriptional regulation of the proton translocating NADH dehydrogenase genes ( <i>nuoA-N</i> ) of <i>Escherichia coli</i> by electron acceptors, electron donors and gene regulators. <b>1995</b> , 16, 521-34	107
307	Hydroxyl radical footprints and half-site arrangements of binding sites for the CysB transcriptional activator of <i>Salmonella typhimurium</i> . <b>1995</b> , 177, 2343-53	40
306	A mutation in the <i>rpoA</i> gene encoding the alpha subunit of RNA polymerase that affects <i>metE-metR</i> transcription in <i>Escherichia coli</i> . <b>1995</b> , 177, 524-9	25
305	Effects of multicopy <i>LeuO</i> on the expression of the acid-inducible lysine decarboxylase gene in <i>Escherichia coli</i> . <b>1995</b> , 177, 810-4	28
304	Characterization of a second <i>MetR</i> -binding site in the <i>metE metR</i> regulatory region of <i>Salmonella typhimurium</i> . <b>1995</b> , 177, 1834-9	14
303	Sites required for <i>GltC</i> -dependent regulation of <i>Bacillus subtilis</i> glutamate synthase expression. <b>1995</b> , 177, 5686-95	43
302	Mutations in <i>GltC</i> that increase <i>Bacillus subtilis</i> <i>gltA</i> expression. <b>1995</b> , 177, 5696-700	19
301	Organization and transcriptional regulation of the <i>Escherichia coli</i> K-12 D-serine tolerance locus. <b>1995</b> , 177, 6456-61	29
300	DNA binding sites of the LysR-type regulator <i>GcvA</i> in the <i>gcv</i> and <i>gcvA</i> control regions of <i>Escherichia coli</i> . <b>1995</b> , 177, 4940-6	33
299	Characterization of an LysR family protein, <i>SmeR</i> from <i>Serratia marcescens</i> S6, its effect on expression of the carbapenem-hydrolyzing beta-lactamase <i>Sme-1</i> , and comparison of this regulator with other beta-lactamase regulators. <b>1995</b> , 39, 629-37	41

298	Biology and clinical significance of virulence plasmids in <i>Salmonella</i> serovars. <b>1995</b> , 21 Suppl 2, S146-51	85
297	The <i>Rhizobium meliloti</i> groELc locus is required for regulation of early nod genes by the transcription activator NodD. <b>1995</b> , 9, 714-29	79
296	Signal exchange in the <i>Bradyrhizobium</i> -soybean symbiosis. <b>1995</b> , 27, 473-483	42
295	Classification of multi-helical DNA-binding domains and application to predict the DBD structures of sigma factor, LysR, OmpR/PhoB, CENP-B, RapI, and Xy1S/Ada/AraC. <b>1995</b> , 372, 215-21	22
294	Sequence analysis of an internal 9.72-kb segment from the 30-kb denitrification gene cluster of <i>Pseudomonas stutzeri</i> . <b>1996</b> , 1277, 6-12	23
293	Scores for sequence searches and alignments. <b>1996</b> , 6, 353-60	48
292	Characterization of PcaQ, a LysR-type transcriptional activator required for catabolism of phenolic compounds, from <i>Agrobacterium tumefaciens</i> . <b>1996</b> , 178, 266-72	44
291	The glutamic acid residue at amino acid 261 of the alpha subunit is a determinant of the intrinsic efficiency of RNA polymerase at the metE core promoter in <i>Escherichia coli</i> . <b>1996</b> , 178, 6810-6	6
290	Positive autoregulation of vipR expression in ViaB region-encoded Vi antigen of <i>Salmonella typhi</i> . <b>1996</b> , 178, 1430-6	17
289	<i>Bradyrhizobium</i> ( <i>Arachis</i> ) sp. strain NC92 contains two nodD genes involved in the repression of nodA and a nola gene required for the efficient nodulation of host plants. <b>1996</b> , 178, 2757-66	37
288	Na <sup>+</sup> -induced transcription of nhaA, which encodes an Na <sup>+</sup> /H <sup>+</sup> antiporter in <i>Escherichia coli</i> , is positively regulated by nhaR and affected by hns. <b>1996</b> , 178, 6508-17	34
287	Transcription start sites for syrM and nodD3 flank an insertion sequence relic in <i>Rhizobium meliloti</i> . <b>1996</b> , 178, 1782-7	26
286	The tfdR gene product can successfully take over the role of the insertion element-inactivated TfdT protein as a transcriptional activator of the tfdCDEF gene cluster, which encodes chlorocatechol degradation in <i>Ralstonia eutropha</i> JMP134(pJP4). <b>1996</b> , 178, 6824-32	74
285	A newly discovered gene, tfuA, involved in the production of the ribosomally synthesized peptide antibiotic trifolixoxin. <b>1996</b> , 178, 4150-6	38
284	Global response of <i>Escherichia coli</i> cells to a treatment with 7-methoxy-2-nitronaphtho[2,1-b]furan (R7000), an extremely potent mutagen. <b>1996</b> , 349, 193-200	5
283	Analysis of a negative regulator, soxR, for the <i>Arthrobacter</i> sarcosine oxidase gene. <b>1996</b> , 81, 64-67	7
282	Analysis of a 23 kb region on the left arm of yeast chromosome IV. <b>1996</b> , 12, 1587-1592	1
281	Evolution of transcriptional regulation system through promiscuous coupling of regulatory proteins with operons; suggestion from protein sequence similarities in <i>Escherichia coli</i> . <b>1996</b> , 178, 183-204	8

280	Isolation and characterization of a <i>Pseudomonas aeruginosa</i> gene, <i>ptxR</i> , which positively regulates exotoxin A production. <b>1996</b> , 21, 97-110	60
279	In vitro characterization of constitutive CysB proteins from <i>Salmonella typhimurium</i> . <b>1996</b> , 21, 247-56	33
278	Use of receiver operating characteristic (ROC) analysis to evaluate sequence matching. <b>1996</b> , 20, 25-33	338
277	Salmonellosis: host immune responses and bacterial virulence determinants. <b>1996</b> , 14, 533-61	330
276	Chapter 22 Bacterial Na <sup>+</sup> /H <sup>+</sup> antiporters [Molecular biology, biochemistry and physiology. <b>1996</b> , 2, 501-531	24
275	Expression of the <i>mau</i> gene cluster of <i>Paracoccus denitrificans</i> is controlled by MauR and a second transcription regulator. <b>1997</b> , 143 ( Pt 3), 793-801	11
274	Analysis of a <i>Rhizobium leguminosarum</i> gene encoding a protein homologous to glutathione S-transferases. <b>1997</b> , 143 ( Pt 3), 813-822	10
273	Identification and characterization of a gene on <i>Rhizobium meliloti</i> pSyma, <i>syrB</i> , that negatively affects <i>syrM</i> expression. <b>1997</b> , 10, 550-9	25
272	Use of model plant hosts to identify <i>Pseudomonas aeruginosa</i> virulence factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>1997</b> , 94, 13245-50	11.5 250
271	Identification and characterization of a new beta-glucoside utilization system in <i>Bacillus subtilis</i> . <b>1997</b> , 179, 496-506	63
270	NodV and NodW, a second flavonoid recognition system regulating nod gene expression in <i>Bradyrhizobium japonicum</i> . <b>1997</b> , 179, 3013-20	66
269	Involvement of CysB and Cbl regulatory proteins in expression of the tauABCD operon and other sulfate starvation-inducible genes in <i>Escherichia coli</i> . <b>1997</b> , 179, 7671-8	66
268	Biosynthesis of Nitrogen-Containing Compounds. <b>1997</b> , 424-469	2
267	Cytosolic intermediates for cell wall biosynthesis and degradation control inducible beta-lactam resistance in gram-negative bacteria. <b>1997</b> , 88, 823-32	265
266	The <i>Agrobacterium tumefaciens</i> virulence gene <i>chvE</i> is part of a putative ABC-type sugar transport operon. <b>1997</b> , 179, 2452-8	56
265	Involvement of NtcB, a LysR family transcription factor, in nitrite activation of the nitrate assimilation operon in the cyanobacterium <i>Synechococcus</i> sp. strain PCC 7942. <b>1997</b> , 179, 4671-5	40
264	Altered transcription activation specificity of a mutant form of <i>Bacillus subtilis</i> GltR, a LysR family member. <b>1997</b> , 179, 1035-43	22
263	Interactions of OxyR with the promoter region of the <i>oxyR</i> and <i>ahpC</i> genes from <i>Mycobacterium leprae</i> and <i>Mycobacterium tuberculosis</i> . <b>1997</b> , 179, 2401-9	58

262	Characterization of the <i>Bacillus subtilis</i> thiC operon involved in thiamine biosynthesis. <b>1997</b> , 179, 3030-5	48
261	The structure of the cofactor-binding fragment of the LysR family member, CysB: a familiar fold with a surprising subunit arrangement. <b>1997</b> , 5, 1017-32	101
260	The Na <sup>+</sup> -specific interaction between the LysR-type regulator, NhaR, and the nhaA gene encoding the Na <sup>+</sup> /H <sup>+</sup> antiporter of <i>Escherichia coli</i> . <b>1997</b> , 16, 5922-9	31
259	A study of the symbiotic importance and location of nod gene inducing compounds in two widely nodulating and two non-nodulating tropical tree species. <b>1997</b> , 188, 77-82	2
258	Embedding strategies for effective use of information from multiple sequence alignments. <b>1997</b> , 6, 698-705	57
257	Cloning, sequence and mutagenesis of the structural gene of <i>Pseudomonas aeruginosa</i> CysB, which can activate algD transcription. <b>1997</b> , 24, 1275-84	38
256	The LysR-like regulator LeuO in <i>Escherichia coli</i> is involved in the translational regulation of rpoS by affecting the expression of the small regulatory DsrA-RNA. <b>1997</b> , 25, 559-69	65
255	Acid-regulated proteins induced by <i>Streptococcus mutans</i> and other oral bacteria during acid shock. <b>1998</b> , 13, 292-300	61
254	The <i>Rhizobium</i> sp. BR816 nodD3 gene is regulated by a transcriptional regulator of the AraC/XylS family. <b>1998</b> , 258, 558-61	8
253	StgR, a new <i>Streptomyces alboniger</i> member of the LysR family of transcriptional regulators. <b>1998</b> , 259, 475-83	2
252	Binding of activator SyrM to the site of nodD3 P1 region of <i>Rhizobium meliloti</i> . <b>1998</b> , 41, 157-62	3
251	A pathway-specific transcriptional activator regulates late steps of clavulanic acid biosynthesis in <i>Streptomyces clavuligerus</i> . <b>1998</b> , 27, 831-43	65
250	The Na <sup>+</sup> and K <sup>+</sup> transport deficiency of an <i>E. coli</i> mutant lacking the NhaA and NhaB proteins is apparent and caused by impaired osmoregulation. <b>1998</b> , 439, 271-4	8
249	Complete sequence of the IncPbeta plasmid R751: implications for evolution and organisation of the IncP backbone. <b>1998</b> , 282, 969-90	187
248	Genetic Organization and Transcriptional Regulation of Rhizobial Nodulation Genes. <b>1998</b> , 361-386	53
247	Activation of gene expression by a ligand-induced conformational change of a protein-DNA complex. <b>1998</b> , 273, 11257-66	38
246	SyrM1 of <i>Rhizobium</i> sp. NGR234 Activates Transcription of Symbiotic Loci and Controls the Level of Sulfated Nod Factors. <b>1998</b> , 11, 343-350	17
245	<i>Salmonella enteritidis</i> : AmpC plasmid-mediated inducible beta-lactamase (DHA-1) with an ampR gene from <i>Morganella morganii</i> . <b>1998</b> , 42, 2352-8	129

244	DNA-binding proteins and evolution of transcription regulation in the archaea. <b>1999</b> , 27, 4658-70	192
243	A new level in the <i>Vibrio cholerae</i> ToxR virulence cascade: AphA is required for transcriptional activation of the tcpPH operon. <b>1999</b> , 31, 763-71	134
242	Dynamics of multigene expression during catabolic adaptation of <i>Ralstonia eutropha</i> JMP134 (pJP4) to the herbicide 2, 4-dichlorophenoxyacetate. <b>1999</b> , 33, 396-406	61
241	Integration of minitransposons for expression of the <i>Escherichia coli</i> elt genes at a preferred site in <i>Salmonella typhimurium</i> identifies a novel putative fimbrial locus. <b>1999</b> , 171, 122-6	4
240	PhoB-dependent transcriptional activation of the <i>iciA</i> gene during starvation for phosphate in <i>Escherichia coli</i> . <b>1999</b> , 262, 448-52	19
239	Cloning and sequence analysis of two catechol-degrading gene clusters from the aniline-assimilating bacterium <i>Frateriella</i> species ANA-18. <b>1999</b> , 226, 189-98	34
238	Molecular analysis of the <i>rlsA</i> gene regulating levan production by the fireblight pathogen <i>Erwinia amylovora</i> . <b>1999</b> , 54, 187-201	17
237	BioS, a biotin-induced, stationary-phase, and possible LysR-type regulator in <i>Sinorhizobium meliloti</i> . <b>1999</b> , 12, 803-12	19
236	Identification of <i>Brucella abortus</i> OxyR and its role in control of catalase expression. <b>2000</b> , 182, 5631-3	20
235	10.1007/s10438-008-2001-3. <b>2000</b> , 1,	
234	The repertoire of DNA-binding transcriptional regulators in <i>Escherichia coli</i> K-12. <b>2000</b> , 28, 1838-47	209
233	In <i>Rhizobium leguminosarum</i> , NodD represses its own transcription by competing with RNA polymerase for binding sites. <b>2000</b> , 28, 2784-93	19
232	ppGpp-dependent <i>leuO</i> expression in bacteria under stress. <b>2000</b> , 276, 64-70	41
231	CcpC, a novel regulator of the LysR family required for glucose repression of the <i>citB</i> gene in <i>Bacillus subtilis</i> . <b>2000</b> , 295, 865-78	92
230	TfdR, the LysR-type transcriptional activator, is responsible for the activation of the <i>tfdCB</i> operon of <i>Pseudomonas putida</i> 2, 4-dichlorophenoxyacetic acid degradative plasmid pEST4011. <b>2000</b> , 245, 161-8	17
229	Survey of genes identified in <i>Sinorhizobium meliloti</i> spp., necessary for the development of an efficient symbiosis. <b>2000</b> , 36, 1-26	16
228	Plant Nitrogen. <b>2001</b> ,	16
227	Na(+)/H(+) antiporters. <b>2001</b> , 1505, 144-57	256



226	<i>Pseudomonas aeruginosa</i> PAO1 kills <i>Caenorhabditis elegans</i> by cyanide poisoning. <b>2001</b> , 183, 6207-14	345
225	Transcription of <i>nhaA</i> , the main Na(+)/H(+) antiporter of <i>Escherichia coli</i> , is regulated by Na(+) and growth phase. <b>2001</b> , 183, 644-53	39
224	Common history at the origin of the position-function correlation in transcriptional regulators in archaea and bacteria. <b>2001</b> , 53, 172-9	56
223	Nucleotide sequence analysis of 5Pflanking region of salicylate hydroxylase gene, and identification and purification of a LysR-type regulator, SalR. <b>2001</b> , 268, 2229-38	4
222	DNA supercoiling-dependent transcriptional coupling between the divergently transcribed promoters of the <i>ilvYC</i> operon of <i>Escherichia coli</i> is proportional to promoter strengths and transcript lengths. <b>2001</b> , 39, 191-8	47
221	Cloning and characterization of the gene cluster for palatinose metabolism from the phytopathogenic bacterium <i>Erwinia rhapontici</i> . <b>2001</b> , 183, 2425-30	52
220	Functional dissection of the LysR-type CysB transcriptional regulator. Regions important for DNA binding, inducer response, oligomerization, and positive control. <b>2001</b> , 276, 2098-107	81
219	Molecular characterization of chromosomal class C beta-lactamase and its regulatory gene in <i>Ochrobactrum anthropi</i> . <b>2001</b> , 45, 2324-30	40
218	Nodule Formation and Function. <b>2001</b> , 101-146	11
217	Involvement of a CbbR homolog in low CO <sub>2</sub> -induced activation of the bicarbonate transporter operon in cyanobacteria. <b>2001</b> , 183, 1891-8	96
216	Inducible AmpC beta-lactamase of a new member Enterobacteriaceae. <b>2002</b> , 46, 3316-9	7
215	Subdivision of the helix-turn-helix GntR family of bacterial regulators in the FadR, HutC, MocR, and YtrA subfamilies. <b>2002</b> , 277, 12507-15	267
214	Constitutive mutations of the OccR regulatory protein affect DNA bending in response to metabolites released from plant tumors. <b>2002</b> , 277, 5866-74	37
213	Mutations in the <i>occQ</i> operator that decrease OccR-induced DNA bending do not cause constitutive promoter activity. <b>2002</b> , 277, 15773-80	46
212	<i>Sinorhizobium fredii</i> HH103 has a truncated <i>nolO</i> gene due to a -1 frameshift mutation that is conserved among other geographically distant <i>S. fredii</i> strains. <b>2002</b> , 15, 150-9	32
211	Promoter analysis of the sodium-responsive V-ATPase ( <i>ntp</i> ) operon in <i>Enterococcus hirae</i> . <b>2002</b> , 178, 172-9	2
210	Activation and silencing of <i>leu-500</i> promoter by transcription-induced DNA supercoiling in the <i>Salmonella</i> chromosome. <b>2000</b> , 37, 583-94	30
209	DNA topology-mediated control of global gene expression in <i>Escherichia coli</i> . <b>2002</b> , 36, 175-203	199



208	The <i>Neisseria meningitidis</i> adhesion regulatory protein CrgA acts through oligomerization and interaction with RNA polymerase. <b>2003</b> , 47, 135-43	11
207	Phenazines and their role in biocontrol by <i>Pseudomonas</i> bacteria. <b>2003</b> , 157, 503-523	272
206	Crystal structure of a full-length LysR-type transcriptional regulator, CbnR: unusual combination of two subunit forms and molecular bases for causing and changing DNA bend. <b>2003</b> , 328, 555-66	148
205	LeuO-mediated transcriptional derepression. <b>2003</b> , 278, 38094-103	20
204	NhaR and RcsB independently regulate the <i>osmCp1</i> promoter of <i>Escherichia coli</i> at overlapping regulatory sites. <b>2003</b> , 185, 4298-304	34
203	Genomic analysis and initial characterization of the chitinolytic system of <i>Microbulbifer degradans</i> strain 2-40. <b>2003</b> , 185, 3352-60	62
202	The structure of full-length LysR-type transcriptional regulators. Modeling of the full-length OxyR transcription factor dimer. <b>2003</b> , 31, 1444-54	48
201	Characterization of the <i>Streptomyces</i> sp. strain C5 <i>snp</i> locus and development of <i>snp</i> -derived expression vectors. <b>2003</b> , 69, 1647-54	10
200	Detection of DNA-binding helix-turn-helix motifs in proteins using the pattern dictionary method. <b>2003</b> , 370, 250-64	4
199	DNA supercoiling and transcription control: a model from the study of suppression of the <i>leu-500</i> mutation in <i>Salmonella typhimurium</i> <i>topA</i> - strains. <b>2003</b> , 73, 43-68	16
198	Transcription-driven DNA supercoiling and gene expression control. <b>2003</b> , 8, d430-9	25
197	Characterization of a gene cluster encoding the maleylacetate reductase from <i>Ralstonia eutropha</i> 335T, an enzyme recruited for growth with 4-fluorobenzoate. <b>2004</b> , 150, 463-472	13
196	The <i>htx</i> and <i>ptx</i> operons of <i>Pseudomonas stutzeri</i> WM88 are new members of the <i>pho</i> regulon. <b>2004</b> , 186, 5876-82	43
195	OmpR and LeuO positively regulate the <i>Salmonella enterica</i> serovar Typhi <i>ompS2</i> porin gene. <b>2004</b> , 186, 2909-20	42
194	Identification of activating region (AR) of <i>Escherichia coli</i> LysR-type transcription factor CysB and CysB contact site on RNA polymerase alpha subunit at the <i>cysP</i> promoter. <b>2004</b> , 53, 791-806	42
193	Analysis in vitro and in vivo of the transcriptional regulator CrgA of <i>Neisseria meningitidis</i> upon contact with target cells. <b>2004</b> , 53, 917-27	16
192	<i>Escherichia coli</i> can tolerate insertions of up to 16 amino acids in the RNA polymerase alpha subunit inter-domain linker. <b>2004</b> , 1678, 47-56	6
191	Crystallization of the effector-binding domains of BenM and CatM, LysR-type transcriptional regulators from <i>Acinetobacter</i> sp. ADP1. <b>2004</b> , 60, 105-8	17

190	Bacterial transcriptional regulators for degradation pathways of aromatic compounds. <b>2004</b> , 68, 474-500, table of contents	304
189	Molecular characterization of the CmbR activator-binding site in the metC-cysK promoter region in <i>Lactococcus lactis</i> . <b>2005</b> , 151, 439-446	18
188	Cloning and characterization of a chromosomal class C beta-lactamase and its regulatory gene in <i>Laribacter hongkongensis</i> . <b>2005</b> , 49, 1957-64	29
187	CrgA is an inducible LysR-type regulator of <i>Neisseria meningitidis</i> , acting both as a repressor and as an activator of gene transcription. <b>2005</b> , 187, 3421-30	47
186	A LysR-type regulator, CidR, is required for induction of the <i>Staphylococcus aureus</i> cidABC operon. <b>2005</b> , 187, 5893-900	61
185	Detailed studies of the binding mechanism of the <i>Sinorhizobium meliloti</i> transcriptional activator ExpG to DNA. <b>2005</b> , 151, 259-268	38
184	Assimilation of nitrogen from nitrite and trinitrotoluene in <i>Pseudomonas putida</i> JLR11. <b>2005</b> , 187, 396-9	47
183	Membrane topology of the <i>Escherichia coli</i> AmpG permease required for recycling of cell wall anhydromuropeptides and AmpC beta-lactamase induction. <b>2005</b> , 49, 1145-9	32
182	The TetR family of transcriptional repressors. <b>2005</b> , 69, 326-56	781
181	Modulating DNA bending affects NodD-mediated transcriptional control in <i>Rhizobium leguminosarum</i> . <b>2005</b> , 33, 2540-8	49
180	Alkaline pH homeostasis in bacteria: new insights. <b>2005</b> , 1717, 67-88	502
179	NahR: effects of replacements at Asn 169 and Arg 248 on promoter binding and inducer recognition. <b>2005</b> , 434, 67-74	29
178	Isolation and characterization of meridamycin biosynthetic gene cluster from <i>Streptomyces</i> sp. NRRL 30748. <b>2006</b> , 377, 109-18	20
177	Biosynthesis and Regulation of the Branched-Chain Amino Acids□ <b>2006</b> , 2,	10
176	Cloning and sequencing of the gene encoding the AmpC beta-lactamase of <i>Morganella morganii</i> . <b>1997</b> , 148, 15-20	16
175	Organization and regulation of cbb CO <sub>2</sub> assimilation genes in autotrophic bacteria. <b>1997</b> , 21, 135-55	106
174	Members of the IclR family of bacterial transcriptional regulators function as activators and/or repressors. <b>2006</b> , 30, 157-86	148
173	Analysis of the ambruticin and jerangolid gene clusters of <i>Sorangium cellulosum</i> reveals unusual mechanisms of polyketide biosynthesis. <b>2006</b> , 13, 1277-86	95

172	Structural characterization of GntR/HutC family signaling domain. <b>2006</b> , 15, 1506-11	28
171	Small molecule inhibitors of a glycoside hydrolase attenuate inducible AmpC-mediated beta-lactam resistance. <b>2007</b> , 282, 21382-91	96
170	SufR coordinates two [4Fe-4S] <sup>2+</sup> , 1+ clusters and functions as a transcriptional repressor of the sufBCDS operon and an autoregulator of sufR in cyanobacteria. <b>2007</b> , 282, 31909-19	62
169	Comparative proteomics of cell division mutants and wild-type of <i>Synechococcus</i> sp. strain PCC 7942. <b>2007</b> , 153, 2505-2517	21
168	Peroxiredoxins in bacterial antioxidant defense. <b>2007</b> , 44, 143-93	79
167	Peroxiredoxin Systems. <b>2007</b> ,	14
166	Oligomerization of BenM, a LysR-type transcriptional regulator: structural basis for the aggregation of proteins in this family. <b>2007</b> , 63, 361-8	30
165	The entire organization of transcription units on the <i>Bacillus subtilis</i> genome. <b>2007</b> , 8, 197	16
164	High crystallizability under air-exclusion conditions of the full-length LysR-type transcriptional regulator Tsar from <i>Comamonas testosteroni</i> T-2 and data-set analysis for a MIRAS structure-solution approach. <b>2008</b> , 64, 764-9	1
163	Crystallization and preliminary X-ray analysis of CrgA, a LysR-type transcriptional regulator from pathogenic <i>Neisseria meningitidis</i> MC58. <b>2008</b> , 64, 797-801	11
162	The att locus of <i>Rhodococcus fascians</i> strain D188 is essential for full virulence on tobacco through the production of an autoregulatory compound. <b>2001</b> , 42, 13-28	49
161	Organization of metabolic pathways and molecular-genetic mechanisms of xenobiotic degradation in microorganisms: A review. <b>2008</b> , 44, 117-135	32
160	A Common System Controls the Induction of Very Different Genes. <b>2008</b> , 226, 149-157	5
159	Expression of the Mau Genes Involved in Methylamine Metabolism in <i>Paracoccus denitrificans</i> is Under Control of a LysR-type Transcriptional Activator. <b>2008</b> , 226, 201-210	
158	Structure and function of the LysR-type transcriptional regulator (LTTR) family proteins. <b>2008</b> , 154, 3609-3623	566
157	Biosynthesis of Cysteine. <b>2008</b> , 3,	43
156	Biochemical evidence for ToxR and ToxJ binding to the tox operons of <i>Burkholderia glumae</i> and mutational analysis of ToxR. <b>2009</b> , 191, 4870-8	15
155	The properties of NodD were affected by mere variation in length within its hinge region. <b>2009</b> , 41, 963-71	2

154	A small functional intramolecular region of NodD was identified by mutation. <b>2009</b> , 41, 822-30	4
153	Characterization of Dutch <i>Staphylococcus aureus</i> from bovine mastitis using a Multiple Locus Variable Number Tandem Repeat Analysis. <b>2009</b> , 136, 277-84	40
152	Sequence analysis of a DNA fragment from <i>Sinorhizobium fredii</i> USDA257 which extends the nitrogen fixation host range of <i>Rhizobium</i> species NGR234 to soybean, <i>Glycine max</i> (L.) Merr cultivar Peking. <b>2009</b> , 48, 110-119	1
151	Functional analysis of a putative regulatory gene, <i>tadR</i> , involved in aniline degradation in <i>Delftia tsuruhatensis</i> AD9. <b>2009</b> , 191, 603-14	10
150	Mutational analysis of the inducer recognition sites of the LysR-type transcriptional regulator TfdT of <i>Burkholderia</i> sp. NK8. <b>2009</b> , 83, 1085-94	5
149	Biodegradation of aromatic compounds: current status and opportunities for biomolecular approaches. <b>2009</b> , 85, 207-28	220
148	Structural and unfolding features of HlyT, a tetrameric LysR type transcription regulator of <i>Vibrio cholerae</i> . <b>2009</b> , 1794, 1134-41	4
147	Quantitative measurement of pH influence on SalR regulated gene expression in <i>Acinetobacter baylyi</i> ADP1. <b>2009</b> , 79, 8-12	2
146	Plant Systems Biology. <b>2009</b> ,	3
145	MhbR, a LysR-type regulator involved in 3-hydroxybenzoate catabolism via gentisate in <i>Klebsiella pneumoniae</i> M5a1. <b>2010</b> , 165, 66-74	9
144	Development of highly-sensitive microbial biosensors by mutation of the <i>nahR</i> regulatory gene. <b>2010</b> , 150, 246-50	24
143	Structural studies on the full-length LysR-type regulator TsaR from <i>Comamonas testosteroni</i> T-2 reveal a novel open conformation of the tetrameric LTTR fold. <b>2010</b> , 75, 1199-214	60
142	<i>ampG</i> gene of <i>Pseudomonas aeruginosa</i> and its role in $\beta$ -lactamase expression. <b>2010</b> , 54, 4772-9	43
141	Molecular characterization of FinR, a novel redox-sensing transcriptional regulator in <i>Pseudomonas putida</i> KT2440. <b>2010</b> , 156, 1487-1496	15
140	Crystal structure of the AmpR effector binding domain provides insight into the molecular regulation of inducible <i>ampC</i> beta-lactamase. <b>2010</b> , 400, 998-1010	40
139	Full-length structures of BenM and two variants reveal different oligomerization schemes for LysR-type transcriptional regulators. <b>2010</b> , 404, 568-86	48
138	Molecular Modeling Studies of AmpR Mediated AmpC $\beta$ -Lactamase Repression. <b>2011</b> ,	0
137	The <i>yfeR</i> gene of <i>Salmonella enterica</i> serovar Typhimurium encodes an osmoregulated LysR-type transcriptional regulator. <b>2011</b> , 315, 63-71	3

136	Molecular characterization of chloranilic acid degradation in <i>Pseudomonas putida</i> TQ07. <b>2011</b> , 49, 974-80	2
135	Integration of metabolic reactions and gene regulation. <b>2011</b> , 47, 70-82	7
134	Integrated regulation of acetoin fermentation by quorum sensing and pH in <i>Serratia plymuthica</i> RVH1. <b>2011</b> , 77, 3422-7	40
133	Most mutant OccR proteins that are defective in positive control hold operator DNA in a locked high-angle bend. <b>2011</b> , 193, 5442-9	3
132	MetR-regulated <i>Vibrio cholerae</i> metabolism is required for virulence. <b>2012</b> , 3,	27
131	Identification and characterization of the LysR-type transcriptional regulator HsdR for steroid-inducible expression of the 3 $\beta$ -hydroxysteroid dehydrogenase/carbonyl reductase gene in <i>Comamonas testosteroni</i> . <b>2012</b> , 78, 941-50	14
130	Oligomerization and negative autoregulation of the LysR-type transcriptional regulator HsdR from <i>Comamonas testosteroni</i> . <b>2012</b> , 132, 203-11	7
129	The control of death and lysis in staphylococcal biofilms: a coordination of physiological signals. <b>2012</b> , 15, 211-5	57
128	Cascades and networks of regulatory genes that control antibiotic biosynthesis. <b>2012</b> , 64, 115-38	30
127	The coming of age of the LeuO regulator. <b>2012</b> , 85, 1026-8	20
126	Transcriptional regulation of <i>sdiA</i> by cAMP-receptor protein, LeuO, and environmental signals in <i>Salmonella enterica</i> serovar Typhimurium. <b>2012</b> , 58, 10-22	5
125	Roles of <i>fkbN</i> in positive regulation and <i>tcs7</i> in negative regulation of FK506 biosynthesis in <i>Streptomyces</i> sp. strain KCTC 11604BP. <b>2012</b> , 78, 2249-55	39
124	Defying stereotypes: the elusive search for a universal model of LysR-type regulation. <b>2012</b> , 83, 453-6	22
123	RcsB-BglJ activates the <i>Escherichia coli</i> <i>leuO</i> gene, encoding an H-NS antagonist and pleiotropic regulator of virulence determinants. <b>2012</b> , 83, 1109-23	38
122	LeuO is a global regulator of gene expression in <i>Salmonella enterica</i> serovar Typhimurium. <b>2012</b> , 85, 1072-89	52
121	Characterization and regulation of the 2,3-butanediol pathway in <i>Serratia marcescens</i> . <b>2012</b> , 93, 2147-59	39
120	The <i>hdhA</i> gene encodes a haloacid dehalogenase that is regulated by the LysR-type regulator, HdhR, in <i>Sinorhizobium meliloti</i> . <b>2013</b> , 54, 148-57	4
119	Molecular evolution of LysR-type transcriptional regulation in <i>Pseudomonas aeruginosa</i> . <b>2013</b> , 66, 1041-9	13

118	The DNA-binding domain of BenM reveals the structural basis for the recognition of a T-N11-A sequence motif by LysR-type transcriptional regulators. <b>2013</b> , 69, 1995-2007	38
117	Purification, crystallization and preliminary X-ray analysis of the effector domain of AlsR, an LysR-type transcriptional regulator from <i>Bacillus subtilis</i> . <b>2013</b> , 69, 581-4	2
116	The <i>Salmonella enterica</i> serovar Typhi LeuO global regulator forms tetramers: residues involved in oligomerization, DNA binding, and transcriptional regulation. <b>2014</b> , 196, 2143-54	18
115	The Subtleties and Contrasts of the LeuO Regulator in <i>Salmonella</i> Typhi: Implications in the Immune Response. <b>2014</b> , 5, 581	8
114	Regulation of <i>Salmonella enterica</i> pathogenicity island 1 (SPI-1) by the LysR-type regulator LeuO. <b>2014</b> , 91, 1057-69	26
113	Microbial degradation of 2,4-dichlorophenoxyacetic acid: Insight into the enzymes and catabolic genes involved, their regulation and biotechnological implications. <b>2016</b> , 42, 194-208	36
112	CRP represses the CRISPR/Cas system in <i>Escherichia coli</i> : evidence that endogenous CRISPR spacers impede phage P1 replication. <b>2014</b> , 92, 1072-91	32
111	YfbA, a <i>Yersinia pestis</i> regulator required for colonization and biofilm formation in the gut of cat fleas. <b>2014</b> , 196, 1165-73	15
110	Comparative genomics reveals new candidate genes involved in selenium metabolism in prokaryotes. <b>2015</b> , 7, 664-76	27
109	Improved PCR assay for the species-specific identification and quantitation of <i>Legionella pneumophila</i> in water. <b>2015</b> , 99, 9227-36	4
108	Transcriptional activation of multiple operons involved in para-nitrophenol degradation by <i>Pseudomonas</i> sp. Strain WBC-3. <b>2015</b> , 81, 220-30	26
107	The solution configurations of inactive and activated DntR have implications for the sliding dimer mechanism of LysR transcription factors. <b>2016</b> , 6, 19988	29
106	Impact of pnpR, a LysR-type regulator-encoding gene, on the cellular processes of <i>Pseudomonas putida</i> DLL-E4. <b>2016</b> , 363,	5
105	FkbN and Tcs7 are pathway-specific regulators of the FK506 biosynthetic gene cluster in <i>Streptomyces tsukubaensis</i> L19. <b>2016</b> , 43, 1693-1703	16
104	Activation of leuO by LrhA in <i>Escherichia coli</i> . <b>2017</b> , 104, 664-676	8
103	The Global Regulators Lrp, LeuO, and HexA Control Secondary Metabolism in Entomopathogenic Bacteria. <b>2017</b> , 8, 209	21
102	<i>Bradyrhizobium elkanii</i> nod regulon: insights through genomic analysis. <b>2017</b> , 40, 703-716	3
101	Coordinating carbon and nitrogen metabolic signaling through the cyanobacterial global repressor NdhR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 403-408 <sup>11.5</sup>	36

100	STRUCTURAL STUDIES OF TRANSCRIPTIONAL REGULATION BY LysR-TYPE TRANSCRIPTIONAL REGULATORS IN BACTERIA. <b>2018</b> , 6, 105-118	3
99	Communication for a Collective Response to Environmental Stress. <b>2018</b> , 169-199	1
98	Functional Mechanism of the Efflux Pumps Transcription Regulators From Based on 3D Structures. <b>2018</b> , 5, 57	24
97	Crystal structure of the effector-binding domain of <i>Synechococcus elongatus</i> CmpR in complex with ribulose 1,5-bisphosphate. <b>2018</b> , 74, 506-511	3
96	Aromatic Compounds and Biofilms: Regulation and Interlinking of Metabolic Pathways in Bacteria. <b>2019</b> , 145-164	1
95	Characterization of the pleiotropic LysR-type transcription regulator LeuO of <i>Escherichia coli</i> . <b>2019</b> , 47, 7363-7379	5
94	Overproduction and purification of the <i>Escherichia coli</i> transcription factors "toxic" to a bacterial cell. <b>2019</b> , 161, 70-77	1
93	Characterization of 17 $\beta$ -hydroxysteroid dehydrogenase and regulators involved in estrogen degradation in <i>Pseudomonas putida</i> SJTE-1. <b>2019</b> , 103, 2413-2425	11
92	The LysR-Type Transcriptional Regulator CrgA Negatively Regulates the Flagellar Master Regulator in <i>Ralstonia solanacearum</i> GMI1000. <b>2020</b> , 203,	0
91	Genomics and transcriptomics analysis reveals the mechanism of isobutanol tolerance of a laboratory evolved <i>Lactococcus lactis</i> strain. <b>2020</b> , 10, 10850	4
90	A central role for the transcriptional regulator VtLR in small RNA-mediated gene regulation in <i>Agrobacterium tumefaciens</i> . <b>2020</b> , 10, 14968	6
89	<i>Rhizobium leguminosarum</i> bv. <i>trifolii</i> NodD2 Enhances Competitive Nodule Colonization in the Clover- <i>Rhizobium</i> Symbiosis. <b>2020</b> , 86,	4
88	Preliminary study on the role of novel LysR family gene kp05372 in <i>Klebsiella pneumoniae</i> of forest musk deer. <b>2020</b> , 21, 137-154	2
87	A novel LysR-type regulator negatively affects biosynthesis of the immunosuppressant brasilicardin. <b>2021</b> , 21, 4-18	
86	Characterization of a LuxR repressor for 3,17 $\beta$ -HSD in <i>Comamonas testosteroni</i> ATCC11996. <b>2021</b> , 336, 109271	1
85	A LysR Family Transcriptional Regulator Modulates <i>Burkholderia cenocepacia</i> Biofilm Formation and Protease Production. <b>2021</b> , 87, e0020221	5
84	The LysR-type transcriptional regulator BsrA (PA2121) controls vital metabolic pathways in <i>Pseudomonas aeruginosa</i> .	
83	First Report of Coexistence of and $\beta$ -Lactamase Genes as Well as Colistin Resistance Gene in a Transferrable Plasmid of a Clinical Isolate of. <b>2021</b> , 12, 676113	5

82	Crystal structure details of <i>Vibrio fischeri</i> DarR and mutant DarR-M202I from LTTR family reveals their activation mechanism. <b>2021</b> , 183, 2354-2363	0
81	The LysR-Type Transcriptional Regulator BsrA (PA2121) Controls Vital Metabolic Pathways in. <b>2021</b> , 6, e0001521	4
80	Comparative genomic and pan-genomic characterisation of <i>Staphylococcus epidermidis</i> from different sources unveils the molecular basis and potential biomarkers of pathogenic strains.	
79	Corrigendum: First Report of Coexistence of $\beta$ -Lactamase Genes as Well as Colistin Resistance Gene in a Transferrable Plasmid of a Clinical Isolate of. <b>2021</b> , 12, 741628	3
78	The molecular mechanism of regulation of the NhaA Na <sup>+</sup> /H <sup>+</sup> antiporter of <i>Escherichia coli</i> , a key transporter in the adaptation to Na <sup>+</sup> and H <sup>+</sup> . <b>1999</b> , 221, 183-96; discussion 196-9	9
77	Detecting the Environment. <b>2000</b> , 367-395	1
76	Activation of Transcription Initiation and Regulation of Tryptophan Biosynthesis in Fluorescent <i>Pseudomonads</i> . <b>2004</b> , 293-322	2
75	The role of nodulation genes in bacterium-plant communication. <b>1991</b> , 13, 115-36	12
74	Cloning and Molecular Analysis of the Gene PRQR Controlling Resistance to Paraquat in <i>Synechocystis</i> sp. PCC 6803. <b>1999</b> , 715-718	1
73	Evolution of Genes for the $\beta$ -Ketoadipate Pathway in <i>Acinetobacter Calcoaceticus</i> . <b>1991</b> , 201-237	27
72	The Nodulation of Legumes by Rhizobia. <b>1992</b> , 315-341	1
71	Homology Recognition During T-DNA Integration into the Plant Genome. <b>1994</b> , 167-189	23
70	Overview on Genetics of Nodule Induction: Factors Controlling Nodule Induction by <i>Rhizobium Meliloti</i> . <b>1991</b> , 111-118	8
69	<i>Rhizobium</i> and Legume Nodulation: A Molecular Dialogue. <b>1993</b> , 19-30	20
68	Na <sup>+</sup> /H <sup>+</sup> antiporters, molecular devices that couple the Na <sup>+</sup> and H <sup>+</sup> circulation in cells. <b>1993</b> , 25, 647-69	61
67	GltC, THE POSITIVE REGULATOR OF GLUTAMATE SYNTHASE GENE EXPRESSION. <b>1990</b> , 141-145	1
66	SIMILAR AMINO ACID SEQUENCES REVISITED. <b>1990</b> , 71-74	1
65	IciA protein, a specific inhibitor of initiation of <i>Escherichia coli</i> chromosomal replication.. <b>1992</b> , 267, 2209-2213	37



64	Multidegenerate DNA recognition by the OxyR transcriptional regulator.. <b>1992</b> , 267, 2038-2045	56
63	In vivo interactions of the NahR transcriptional activator with its target sequences. Inducer-mediated changes resulting in transcription activation. <b>1991</b> , 266, 10830-10838	58
62	Use of saturation mutagenesis to localize probable functional domains in the NahR protein, a LysR-type transcription activator.. <b>1990</b> , 265, 3844-3850	66
61	A family of bacterial regulators homologous to Gal and Lac repressors.. <b>1992</b> , 267, 15869-15874	282
60	NhaR, a protein homologous to a family of bacterial regulatory proteins (LysR), regulates nhaA, the sodium proton antiporter gene in <i>Escherichia coli</i> .. <b>1992</b> , 267, 10433-10438	68
59	nolMNO genes of <i>Bradyrhizobium japonicum</i> are co-transcribed with nodYABCSUIJ, and nolO is involved in the synthesis of the lipo-oligosaccharide nodulation signals.. <b>1993</b> , 268, 27053-27059	32
58	Regulation of syrM and nodD3 in <i>Rhizobium meliloti</i> . <b>1993</b> , 134, 435-44	70
57	The cold-inducible icl gene encoding thermolabile isocitrate lyase of a psychrophilic bacterium, <i>Colwellia maris</i> . <b>2002</b> , 148, 2579-2589	17
56	A common system controls the induction of very different genes. The class-A beta-lactamase of <i>Proteus vulgaris</i> and the enterobacterial class-C beta-lactamase. <b>1994</b> , 226, 149-57	27
55	Expression of the mau genes involved in methylamine metabolism in <i>Paracoccus denitrificans</i> is under control of a LysR-type transcriptional activator. <b>1994</b> , 226, 201-10	25
54	RNA Polymerase and Transcription Factors. 651-667	25
53	The NodD proteins of <i>Rhizobium</i> sp. strain BR816 differ in their interactions with coinducers and in their activities for nodulation of different host plants. <b>1994</b> , 60, 3615-23	15
52	Cloning of nod gene regions from mesquite rhizobia and bradyrhizobia and nucleotide sequence of the nodD gene from mesquite rhizobia. <b>1995</b> , 61, 3422-9	6
51	Identification of the Inducing Agent of the 2,4-Dichlorophenoxyacetic Acid Pathway Encoded by Plasmid pJP4. <b>1997</b> , 63, 317-20	32
50	Molecular characterization of the genes pcaG and pcaH, encoding protocatechuate 3,4-dioxygenase, which are essential for vanillin catabolism in <i>Pseudomonas</i> sp. strain HR199. <b>1999</b> , 65, 951-60	35
49	Lack of expression of the global regulator OxyR in <i>Haemophilus influenzae</i> has a profound effect on growth phenotype. <b>1996</b> , 64, 4618-29	42
48	Molecular analysis of genetic differences between <i>Mycobacterium bovis</i> BCG and virulent <i>M. bovis</i> . <b>1996</b> , 178, 1274-82	791
47	The leuO gene product has a latent ability to relieve bgl silencing in <i>Escherichia coli</i> . <b>1998</b> , 180, 190-3	49

46	Mutation analysis of PobR and PcaU, closely related transcriptional activators in acinetobacter. <b>1998</b> , 180, 5058-69	48
45	A promoter relay mechanism for sequential gene activation. <b>1998</b> , 180, 626-33	41
44	A functional homolog of Escherichia coli NhaR in Vibrio cholerae. <b>1998</b> , 180, 762-5	9
43	The bldD gene of Streptomyces coelicolor A3(2): a regulatory gene involved in morphogenesis and antibiotic production. <b>1998</b> , 180, 1549-55	70
42	The folate branch of the methionine biosynthesis pathway in Streptomyces lividans: disruption of the 5,10-methylenetetrahydrofolate reductase gene leads to methionine auxotrophy. <b>1998</b> , 180, 1586-91	12
41	Regulation of lactose utilization genes in Staphylococcus xylosus. <b>1998</b> , 180, 2273-9	22
40	An additional regulatory gene for actinorhodin production in Streptomyces lividans involves a LysR-type transcriptional regulator. <b>1999</b> , 181, 4353-64	15
39	Bacillus subtilis yckG and yckF encode two key enzymes of the ribulose monophosphate pathway used by methylophs, and yckH is required for their expression. <b>1999</b> , 181, 7154-60	56
38	Characterization of the pyoluteorin biosynthetic gene cluster of Pseudomonas fluorescens Pf-5. <b>1999</b> , 181, 2166-74	211
37	Arac/XylS family of transcriptional regulators. <b>1997</b> , 61, 393-410	369
36	Oxidative stress responses in Escherichia coli and Salmonella typhimurium. <b>1991</b> , 55, 561-85	781
35	Cyclic AMP in prokaryotes. <b>1992</b> , 56, 100-22	419
34	Gene regulation of plasmid- and chromosome-determined inorganic ion transport in bacteria. <b>1992</b> , 56, 195-228	283
33	Molecular mechanisms of genetic adaptation to xenobiotic compounds. <b>1992</b> , 56, 677-94	417
32	Phosphoenolpyruvate:carbohydrate phosphotransferase systems of bacteria. <b>1993</b> , 57, 543-94	1337
31	Functions of the gene products of Escherichia coli. <b>1993</b> , 57, 862-952	300
30	Molecular genetics of Thiobacillus ferrooxidans. <b>1994</b> , 58, 39-55	113
29	The Rhizobium-plant symbiosis. <b>1995</b> , 59, 124-42	365

28	Genetic map of <i>Salmonella typhimurium</i> , edition VIII. <b>1995</b> , 59, 241-303	102
27	Molecular biology of microbial ureases. <b>1995</b> , 59, 451-80	916
26	Specificity of the <i>E. coli</i> LysR-type transcriptional regulators. <b>2010</b> , 5, e15189	20
25	dsdA Does Not Affect Colonization of the Murine Urinary Tract by <i>Escherichia coli</i> CFT073. <b>2015</b> , 10, e0138121	13
24	<i>Sinorhizobium meliloti</i> Megaplasms and Symbiosis in <i>S. meliloti</i> . <b>2009</b> , 91-118	
23	Integration of metabolic reactions and gene regulation. <b>2009</b> , 553, 265-85	
22	<i>Rhizobium meliloti</i> nodulation genes and their regulation. <b>1990</b> , 207-213	
21	THE COMPLEXITY OF THE REGULATION OF EXPRESSION OF NODULATION GENES OF RHIZOBIUM. <b>1990</b> , 249-258	
20	Beta-Lactamase Genes from <i>Streptomyces</i> Species. <b>1991</b> , 195-202	
19	Identification of <i>nif</i> and <i>nod</i> Genes in <i>Frankia</i> . <b>1992</b> , 383-399	
18	Plasmid Genes Involved in Virulence in <i>Salmonella</i> . <b>1993</b> , 181-190	
17	Molecular Analysis of Glutamine Synthetase Genes and Enzymes of <i>Clostridium</i> and <i>Bacteroides</i> . <b>1993</b> , 344-353	
16	Comparison of <i>Yersinia enterocolitica</i> DNA methylation at ambient and host temperatures.	
15	Evolution of structural dynamics in bilobed proteins.	
14	A single amino acid substitution (Glu134-->Ala) in NhaR1 increases the inducibility by Na <sup>+</sup> of the product of <i>nhaA</i> , a Na <sup>+</sup> /H <sup>+</sup> antiporter gene in <i>Escherichia coli</i> . <b>1994</b> , 13, 1981-9	5
13	The <i>Rhizobium meliloti</i> regulatory <i>nodD3</i> and <i>syrM</i> genes control the synthesis of a particular class of nodulation factors N-acylated by (omega-1)-hydroxylated fatty acids. <b>1994</b> , 13, 2139-49	19
12	The <i>Escherichia coli</i> regulatory protein OxyR discriminates between methylated and unmethylated states of the phage Mu <i>mom</i> promoter. <b>1989</b> , 8, 2403-10	33
11	Dances with sigmas. <b>1991</b> , 10, 3559-66	2

10	Mutations in TrpI binding site II that differentially affect activation of the trpBA promoter of <i>Pseudomonas aeruginosa</i> . <b>1991</b> , 10, 4137-44	15
9	Structural dynamics in the evolution of a bilobed protein scaffold. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5 0
8	Comparative Genomic and Pan-Genomic Characterization of From Different Sources Unveils the Molecular Basis and Potential Biomarkers of Pathogenic Strains. <b>2021</b> , 12, 770191	1
7	Human milk oligosaccharides and non-digestible carbohydrates reduce pathogen adhesion to intestinal epithelial cells by decoy effects or by attenuating bacterial virulence.. <b>2022</b> , 151, 110867	1
6	Genetic variation in symbiotic islands of natural variant strains of soybean and differing in competitiveness and in the efficiency of nitrogen fixation.. <b>2022</b> , 8,	
5	Exploring generality of experimental conformational changes with AlphaFold predictions.	
4	Directed evolution of linker helix as an efficient strategy for engineering LysR-type transcriptional regulators as whole-cell biosensors. <b>2023</b> , 222, 115004	0
3	Novel D-glutamate catabolic pathway in marine Proteobacteria and halophilic archaea.	0
2	Phylogeny and cross-regulation of the YjjM and LeuO transcription factors translated as multiple protein forms from one gene in <i>Escherichia coli</i> . <b>2023</b> , 18, 1-14	0
1	Novel rRNA transcriptional activity of NhaR revealed by its growth recovery for the bipA-deleted <i>Escherichia coli</i> at low temperature. 10,	0