

A black and white scanning electron micrograph (SEM) showing several plant structures. In the foreground, a large, bulbous, spherical structure sits atop a long, slender, textured stalk. Other similar but smaller structures are visible in the background and foreground, some on stalks and others more isolated. The background is dark, and the structures are illuminated from the side, creating strong highlights and shadows that emphasize their three-dimensional forms.

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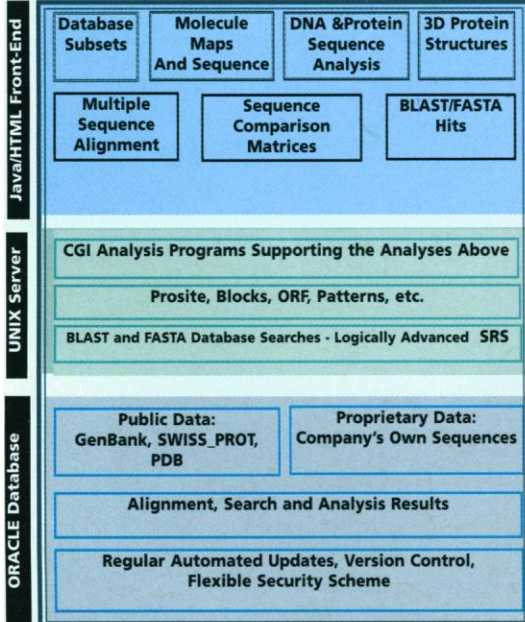
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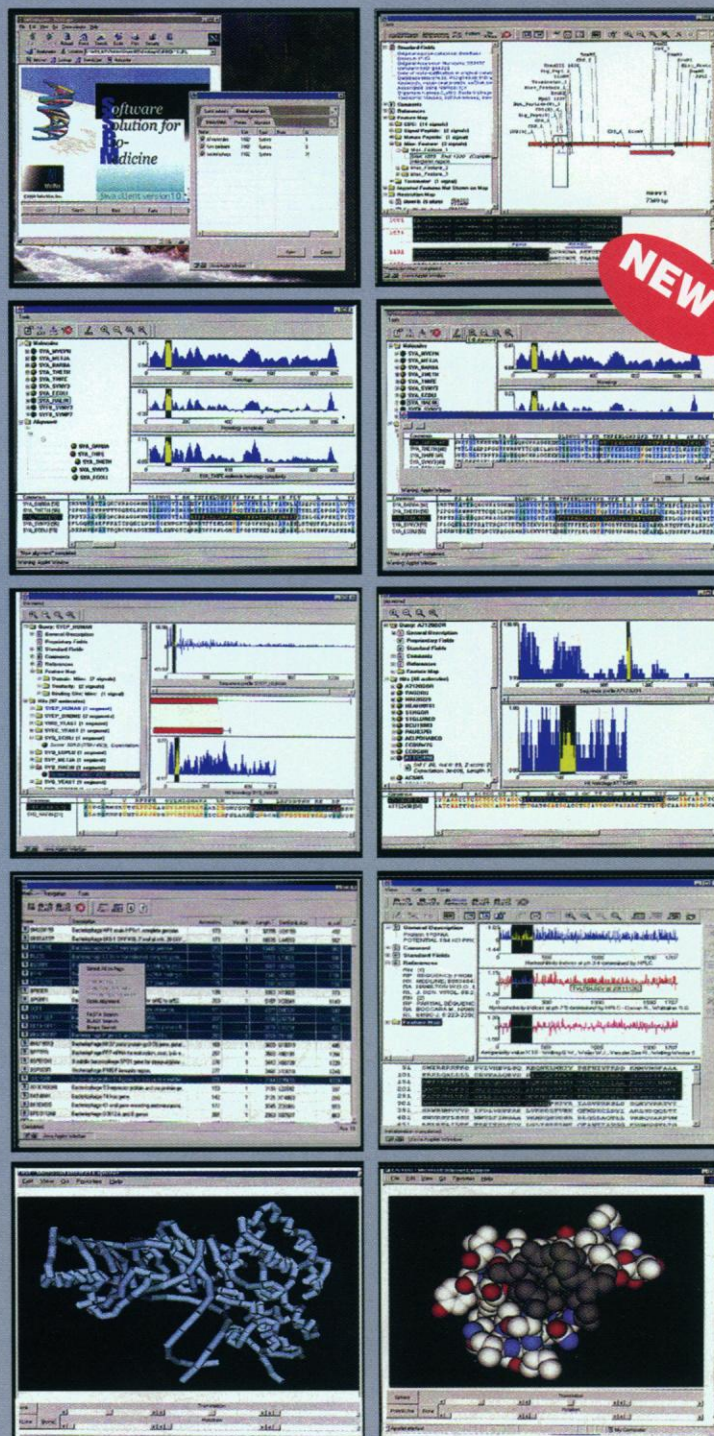
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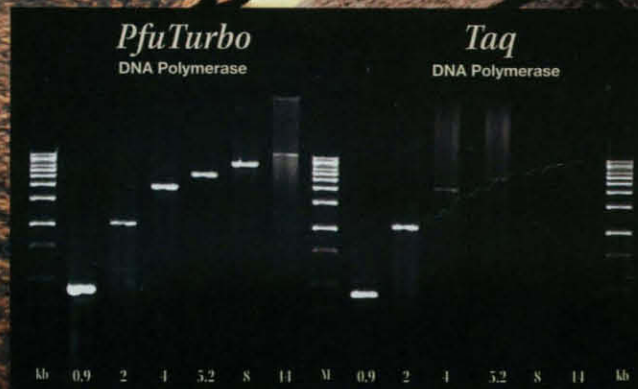


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COVER A scanning electron micrograph of glandular hairs (about 275 micrometers long) on the surface of the pupa of the ladybird beetle *Epilachna borealis*. The droplets that have been secreted at the tips of these hairs contain a variety of macrocyclic alkaloids, all made of a random assembly of three closely related molecular building blocks. These chemicals protect the pupa from predation. [Image: Maria Eisner]



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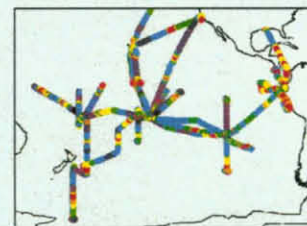
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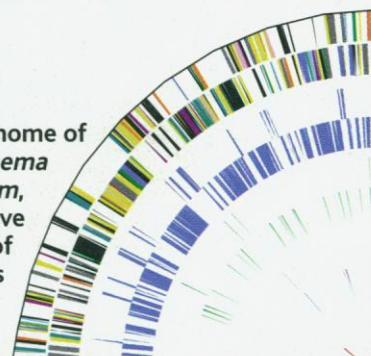
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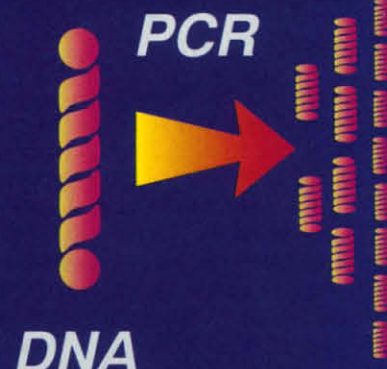
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SYPHILIS GENOME

The agent that causes syphilis, *Treponema pallidum*, cannot be cultured continuously in vitro, which has hampered studies of its pathogenesis and virulence. The complete genome sequence of *T. pallidum* has now been determined by Fraser *et al.* (p. 375; see the Policy Forum on syphilis elimination by St. Louis and Wasserheit, p. 353, and the news story by Pennisi, p. 324). Analysis of the metabolic pathways used by this spirochete should aid in efforts to culture the organism, and evaluation of the outer membrane proteins indicates possible vaccine candidates. Comparison with other bacteria, such as the Lyme disease agent *Borrelia burgdorferi* and another metabolically limited bacterium *Mycoplasma genitalium*, provide clues to the basis for microbial diversity.

PINNING DOWN METHYL BROMIDE

Methyl bromide is the main atmospheric component containing bromine and plays a role in ozone destruction in the stratosphere. Many of the sources and sinks of methyl bromide are incompletely understood, which results in large uncertainties in estimating the relative importance of natural and anthropogenic sources and the residence lifetime of this compound (which is an important factor in determining how much will reach the stratosphere). Colman *et al.* (p. 392) now provide an independent estimate of the residence lifetime, independent from source and sink estimates, which is based on determining its spatial variability relative to other atmospheric compounds with known lifetimes. The result is consistent with previous estimates from source and sink strength.

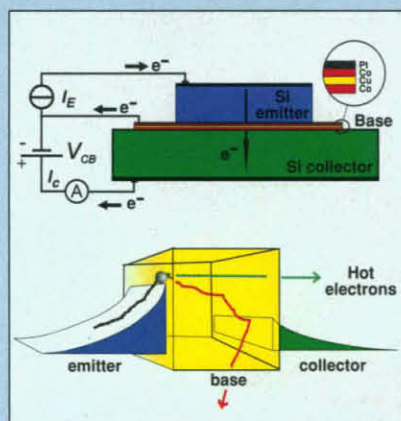
FROM WATER TO ICE

Small amounts of water in silicate magmas, either dissolved as hydroxyl ions (OH^-) or present as molecular water, can change the bulk properties of the melt and alter the ascent rate of the magma, which affects not only eruptive processes observed on the surface but also the amount of chemical fractionation in magma reservoirs below. Richet and Polian (p. 396) determined the partial molar volume and bulk modulus of water dissolved in iron-free, andesitic glasses through density and Brillouin-scattering measurements. The volume and bulk modulus of the dissolved water was independent of the water concentration and similar to ice VII. Ice VII is a network of H_2O tetrahedra formed by shortening of hydrogen bonds, which sug-

gests that the main mechanism of compression of water in the glasses may also be hydrogen bond shortening through a clustering of OH^- ions.

HOT ELECTRONS FOR SPIN-VALVE TRANSISTORS

Layered structures of magnetic and non-magnetic metals can produce a "spin-valve" effect useful in magnetic sensing—application of a magnetic field aligns the magnetizations of the magnetic layers and lowers the resistance for electrons aligned parallel to the field. For transistors based on the spin-valve effect, interfacial defects between metal



and semiconductor layers have tended to limit the operation of these devices to cryogenic temperatures. Monsma *et al.* (p. 407; see the Perspective by De Boeck, p. 357) show that room-temperature devices can be prepared by vacuum bonding; a platinum layer bonds the silicon emitter to a metal-multilayer-silicon collector. The collector accepts only "hot" ballistic electrons transported through the layers rather than parallel to them, which makes the device highly sensitive to magnetic fields.

L.A.'S SEISMIC HISTORY

The greatest seismic risk in Los Angeles may not be from the more distant San Andreas fault but from smaller nearby thrust faults, such as the ones that ruptured during the 1994 Northridge (magnitude $M 6.7$) and 1971 San Fernando ($M 6.7$) earthquakes. The size and frequency of potential earthquakes on these faults has been uncertain because the record of prehistoric ruptures is poorly resolved, and there are some suggestions that earthquakes greater than $M 7$ are unlikely. Ru-

bin *et al.* (p. 398) obtained a paleoseismic record for the Sierra Madre fault, which extends along the base of the San Gabriel Mountains and ruptured in the 1971 earthquake. Offsets of markers in a trench through the fault and radiocarbon dates imply that the fault ruptured twice in large magnitude events (7.2 to 7.6) during the past 15,000 years.

DIGGING INTO OLD DIETS

Understanding the life-styles of extinct animals is a daunting task that has been made easier by findings of Poinar *et al.* (p. 402; see the news story by Stokstad, p. 319). They have determined that it is possible to amplify DNA sequences from a coprolite (ancient dung) of a ground sloth that lived in the Pleistocene era. This analysis could be performed only after the DNA was first freed from sugar-derived condensation products through an agent that cleaves chemical crosslinks. Analysis of the amplified DNA, which ranged in size from 153 to 273 base pairs, indicated that the sloth had ingested representatives of six families and two orders of plants.

SELF-ASSEMBLING PROTEIN GELS

Materials that can reversibly transform from liquids to gels with changes in temperature or pH have numerous uses, such as controlled release of drugs, yet the materials that show this behavior as hydrogels are complex and their behavior at the molecular level is often poorly understood. Petka *et al.* (p. 389) have used protein engineering to create reversible hydrogels that undergo transitions in gelation near neutral pH and ambient temperatures; leucine zipper domains were incorporated that can aggregate through coiled-coil interactions to control the formation of three-dimensional networks.

REGULATING NOTCH

The specification of tissue boundaries in vertebrates and invertebrates has been shown to involve the Notch family of receptors. In *Drosophila*, Notch is broadly distributed in the wing; however, wing development requires tight regulation of Notch, limiting target gene activation to the dorsoventral boundary. One mechanism to limit Notch activity involves the protein Fringe, where Fringe modulates the sensitivity of Notch for its two ligands. Neumann and Cohen (p. 409) report another Notch regulatory mechanism. For this mechanism, the POU domain protein Nubbin competes with Notch-dependent

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The Ecdysone-Inducible Mammalian Expression System.

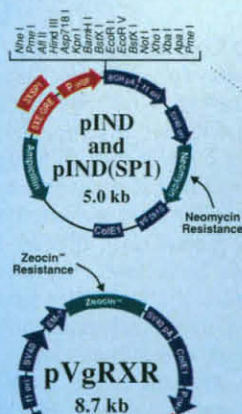
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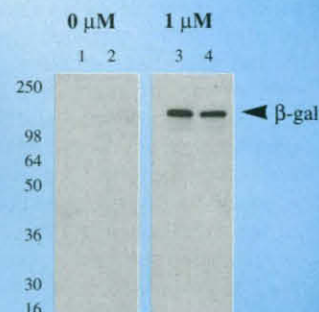
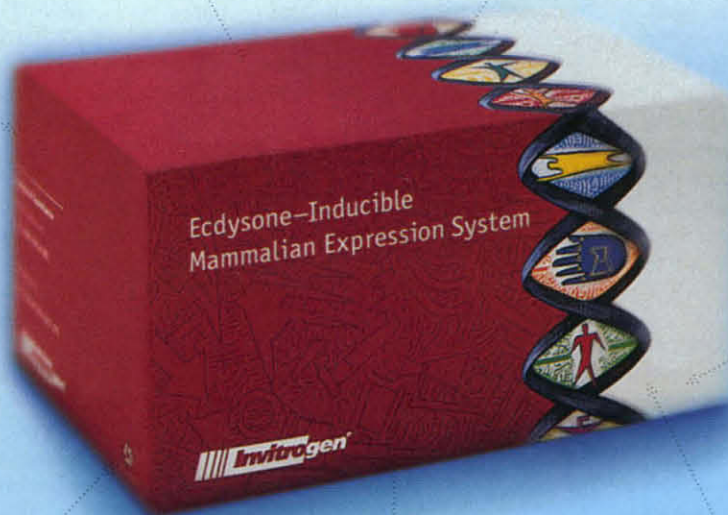
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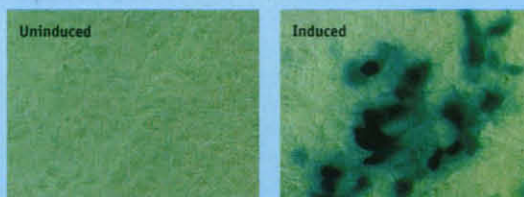
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CHO cells stably transfected with *pIND(SP1)/Hygro/lacZ*. Lanes 1 and 2: Uninduced. Lane 3: Induced with Muristerone A. Lane 4: Induced with Ponasterone A.



Uninduced and induced transiently transfected 293 cells stained with X-gal.

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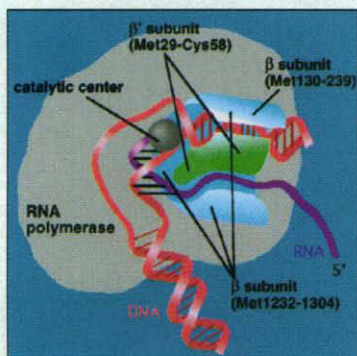
THIS WEEK IN SCIENCE

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activating signals to repress Notch target genes, further limiting Notch activation to cells near the wing margin.

GETTING THE GUIDE INTO THE WORK

The decoding of genetic information begins with RNA polymerase, the enzyme that uses double-stranded, helical DNA as a template to transcribe a single strand of



RNA. The helix must be unwound and the hydrogen bonds between the deoxynucleotide pairs must be broken in order to sequentially order substrate ribonucleotides before polymerizing them into RNA. Nudler *et al.* (p. 424) have mapped the relative locations of portions of the enzyme complex and the DNA-RNA hybrid at various stages of transcription. The catalytic site where polymerization occurs is near the portion of the enzyme that guides the nascent strand of RNA. This juxtaposition may explain how double-stranded regions of RNA promote termination of transcription.

DOUBLY FAST

It has been widely accepted that a single neuron could only release one neurotransmitter, and even the discovery of peptides and slowly acting neuromodulators has

not changed this general rule for fast neurotransmitters. Jonas *et al.* (p. 419; see the Perspective by Nicoll and Malenka, p. 360) show that inhibitory interneurons in the spinal cord corelease two fast neurotransmitters, glycine and γ -aminobutyric acid (GABA). They also provide evidence that a substantial amount of miniature postsynaptic currents are composed of a GABA and a glycine component.

ADAPTER PROTEIN ACTIVITIES

Some white blood cells express an "adapter protein," SLP-76, which has been thought to bring together various types of signal transduction molecules in T cells after the T cell receptor binds an antigen. Yablonski *et al.* (p. 413) determined that SLP-76 is critical for transmission of activation signals through phospholipase C- γ 1 and the Ras-signaling pathway. In an examination of SLP-76-deficient mice by Clements *et al.* (p. 416), SLP-76 was found to be required for the maturation of T cells, but not for B cells or other lineages. Together, these studies provide a framework for understanding the mechanism of action and the in vivo function of SLP-76.

BETLE CHEMISTRY

The pupa of the squash beetle (*Epilachna borealis*) is the unusual source of a combinatorial library described by Schröder *et al.* (p. 428; see the cover and the news story by Campos, p. 321). The family, comprising a hundred polyamino macrocyclic structures, is derived from just three parent components. Termed polyazamacrolides, these compounds are involved in the defense of the insect against predation, although their precise mode of action and the possible evolutionary benefits conferred by the combinatorial phenomenon remain to be determined.

TECHNICAL COMMENT SUMMARIES

Feasibility of a Colliding Beam Fusion Reactor

The full text of these comments can be seen at www.sciencemag.org/cgi/content/full/281/5375/307a

N. Rostoker *et al.* proposed (21 Nov., p. 1419) a "colliding beam fusion reactor" with "an alternate confinement system, the field-reversed configuration [that would confine] beams of protons and boron-11." The design might "solve the major problems of Tokamak reactors."

W. M. Nevins discusses "nonthermal ion distributions" and concludes that "the fusion gain ... would be much lower than the value of 2.7 stated by Rostoker *et al.*" A. Carlson comments that "a large power input would ... be required" and that maintaining equilibrium would be "a serious problem."

Rostoker *et al.* respond to Nevins by providing detailed calculations "of heating of electrons by boron scattering." They address Carlson's concerns by presenting a "formula for the power density required to overcome the friction between proton and boron beams" that includes the force of the magnetic field.

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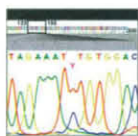
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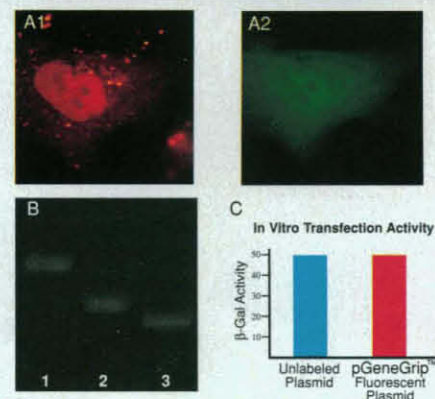
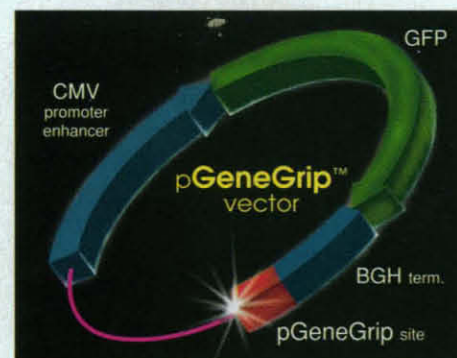
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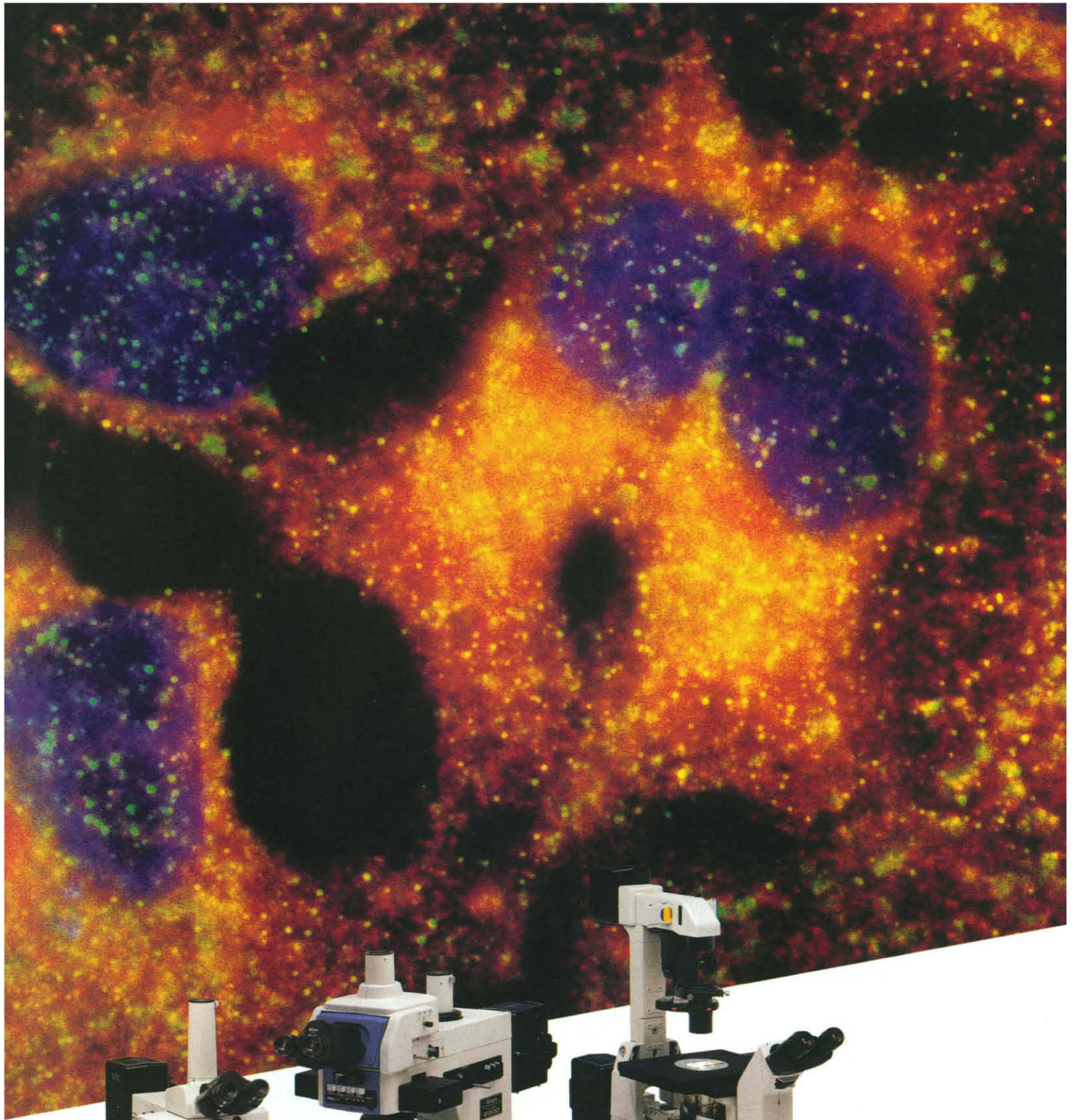
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2. GFP expression
- B.** Electrophoresis of pGeneGrip™ Rhodamine labeled fluorescent vector
Lanes: 1. β -gal, 2. GFP, 3. Blank
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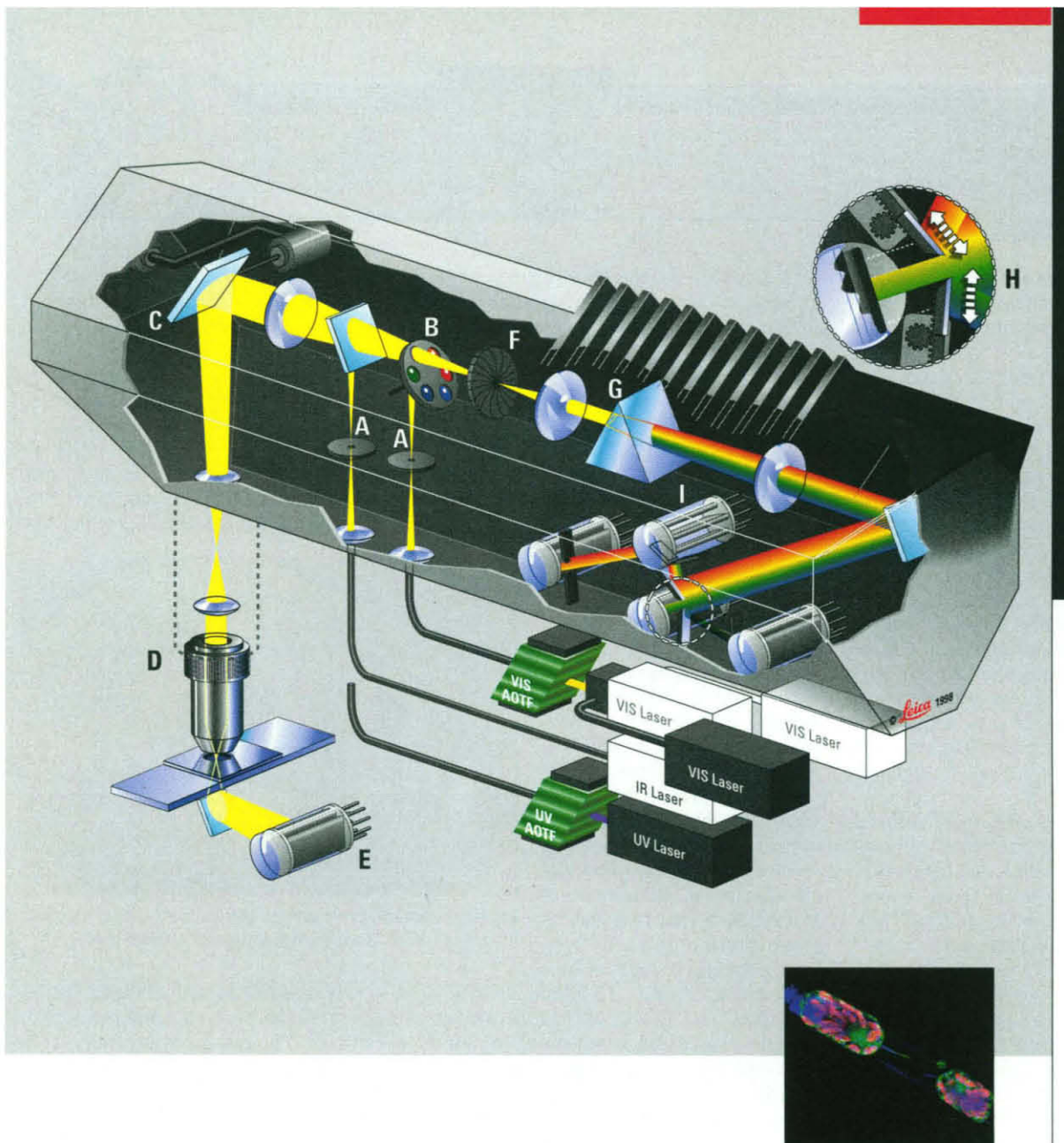
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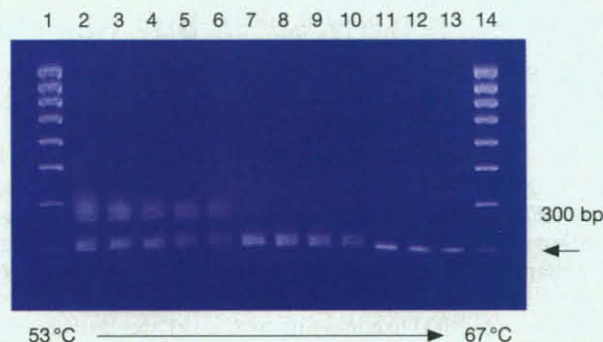
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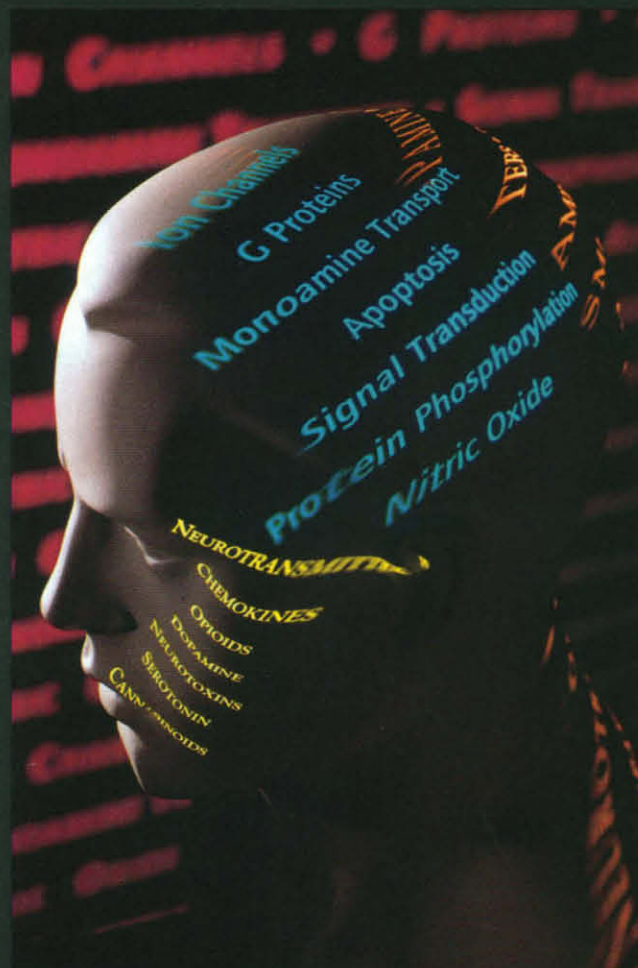
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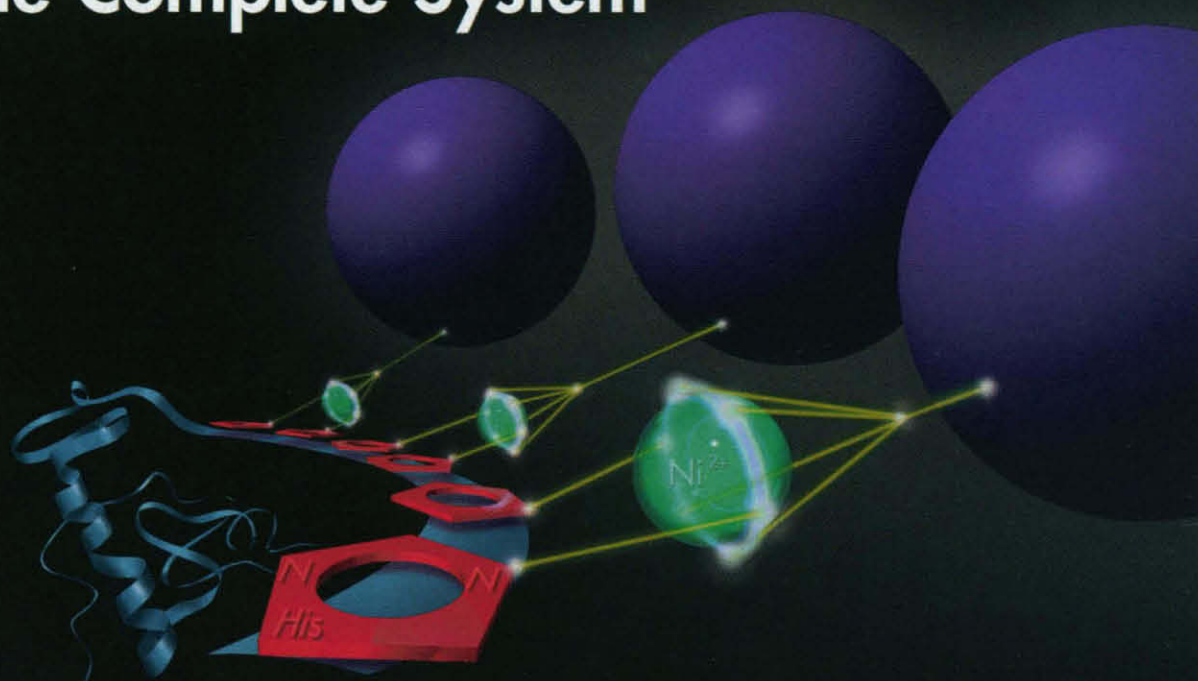
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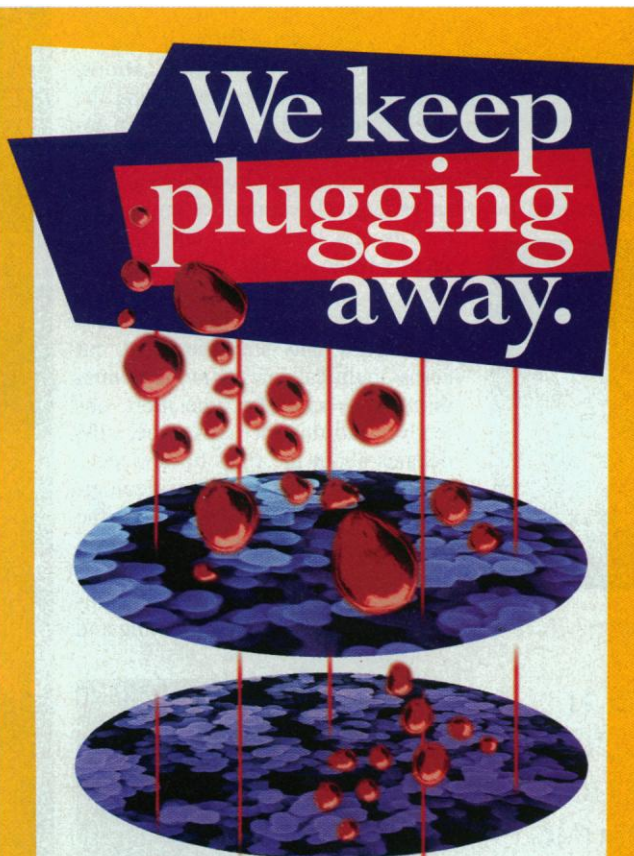
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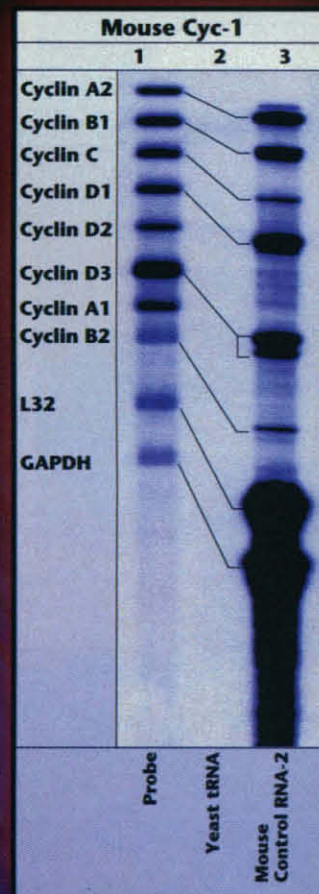
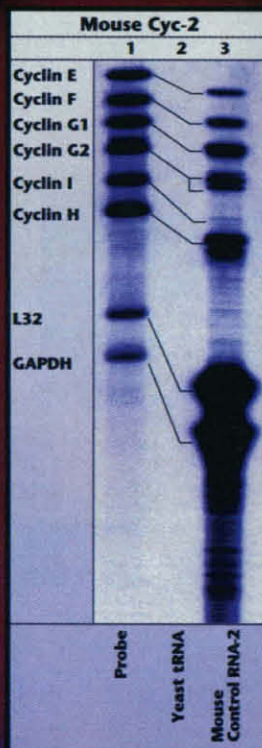
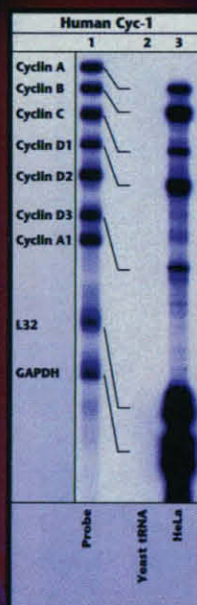
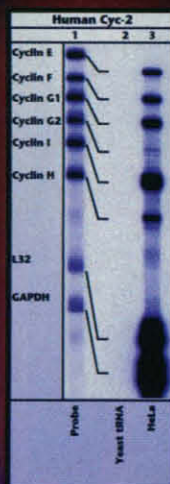
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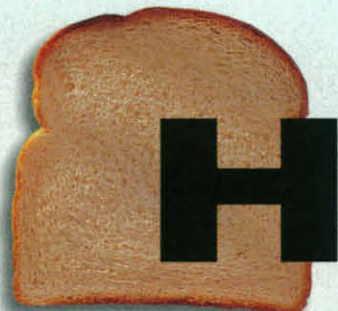
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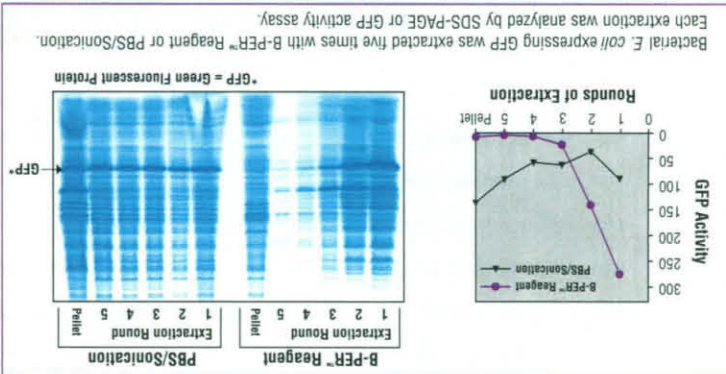
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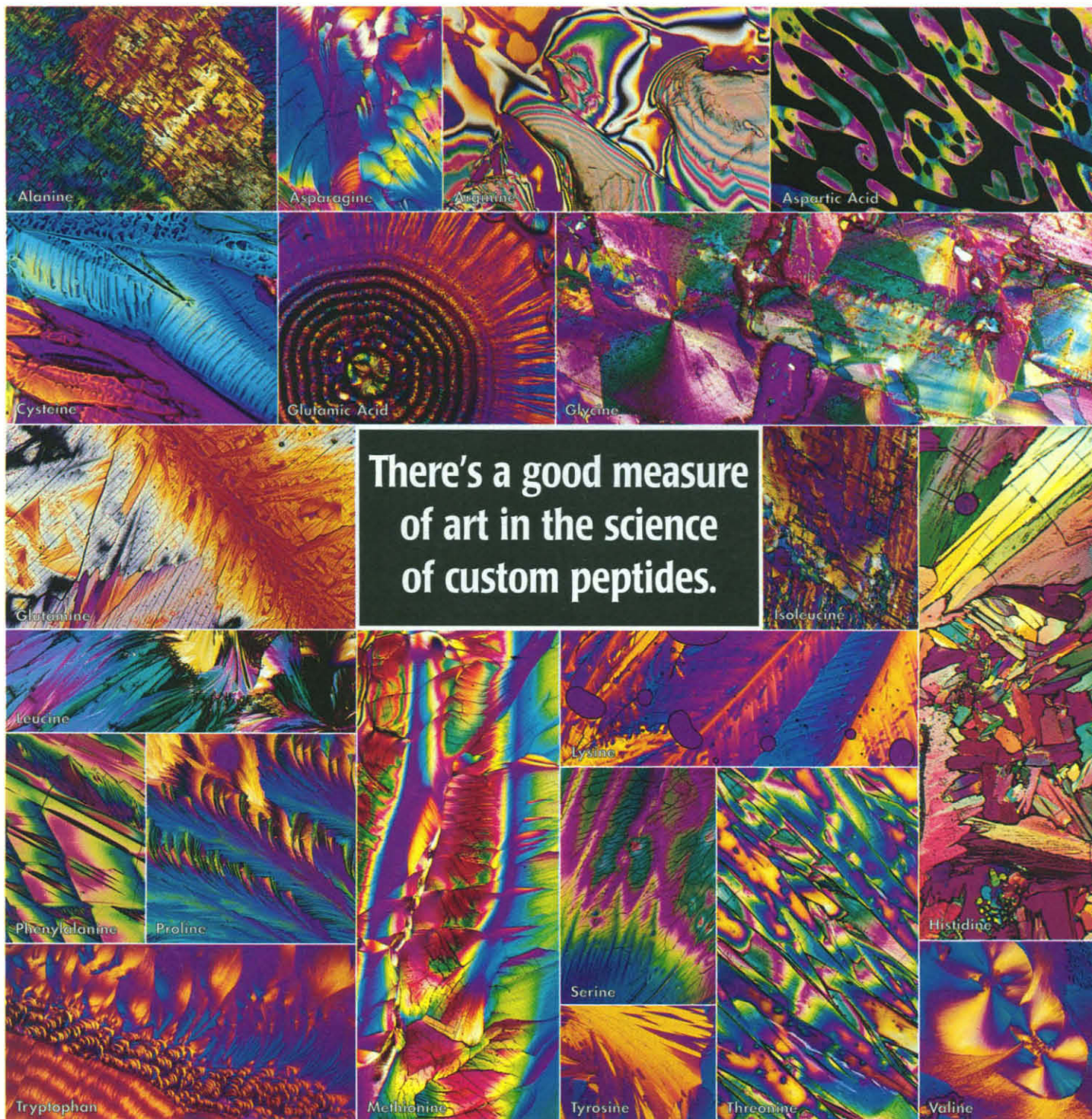
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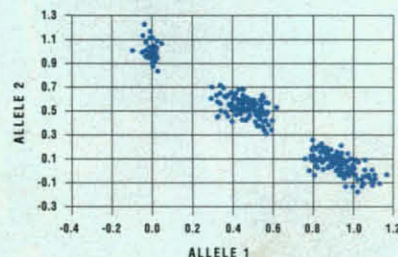
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Genotyping of the single nucleotide IL-1B polymorphism: Genotyping of the two alleles of the human Interleukin-1 beta (IL-1B) promoter polymorphism at position -511 was performed using the fluorogenic 5' nuclease assay. The graph shows genotyping results for 454 individuals. (Results courtesy of Franco di Giovine and Adeel Chaudhry, University of Sheffield, UK.)

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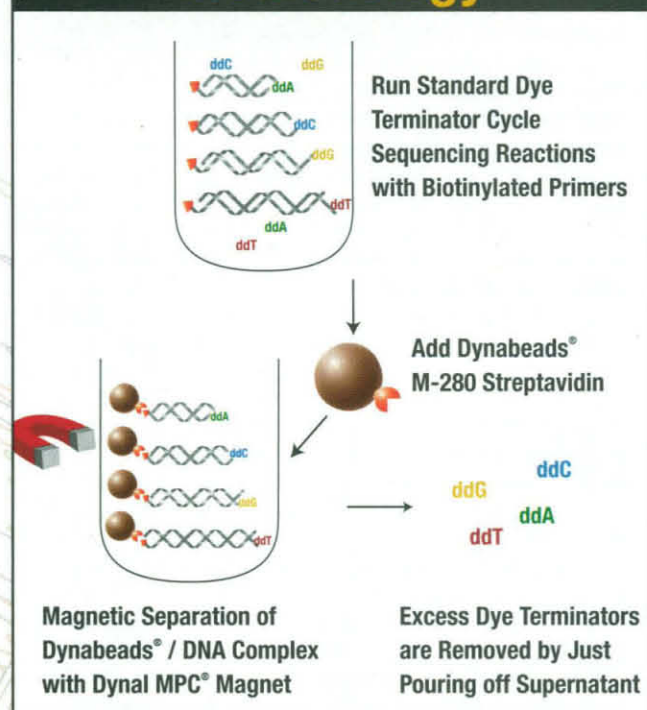
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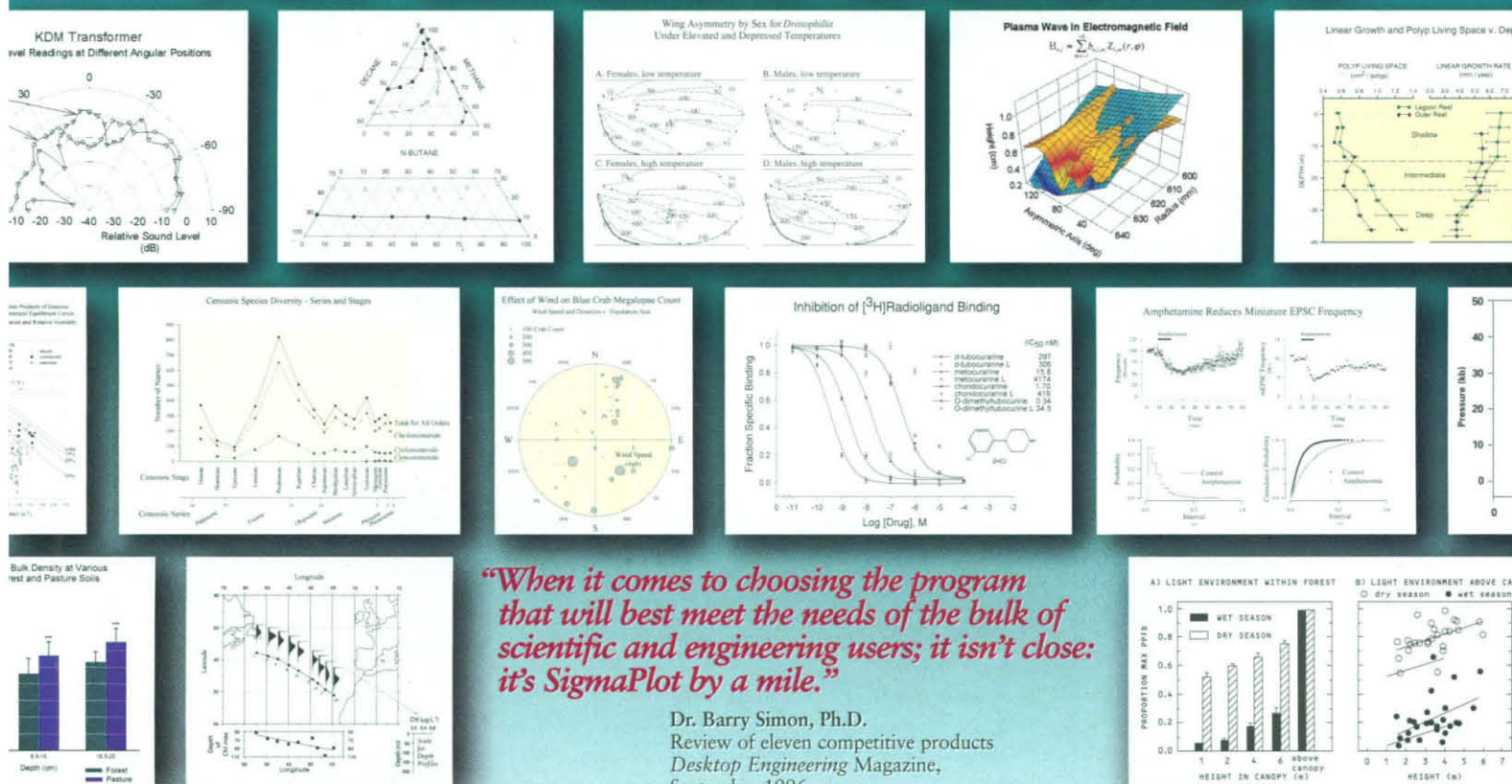


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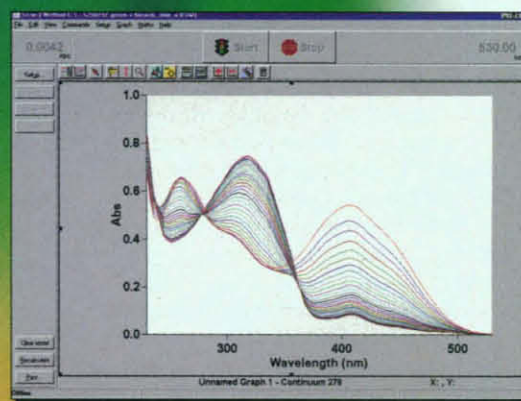
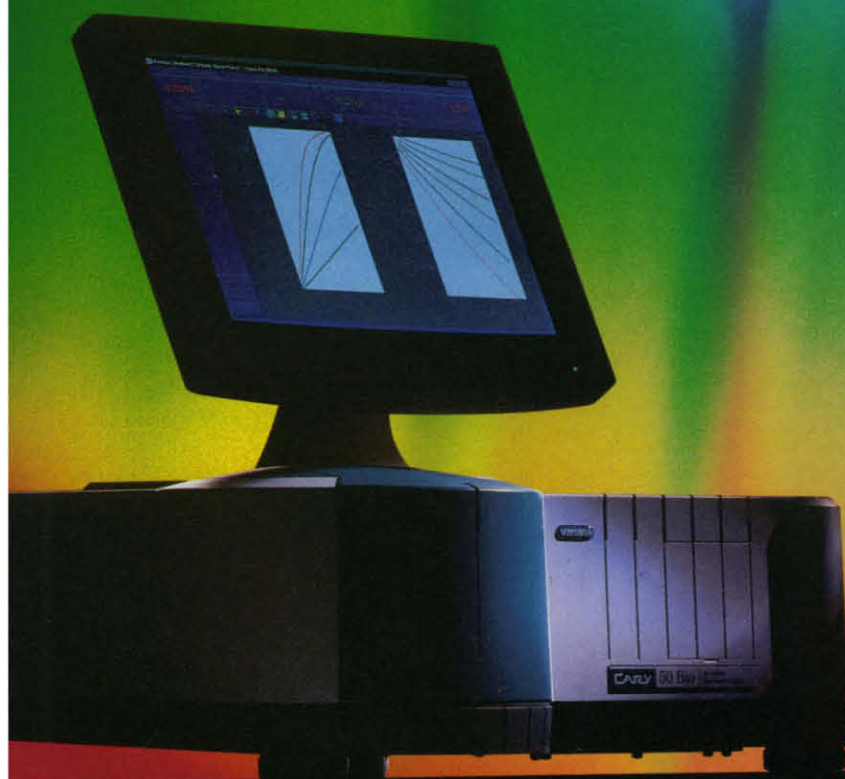
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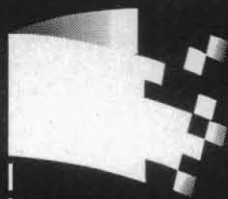
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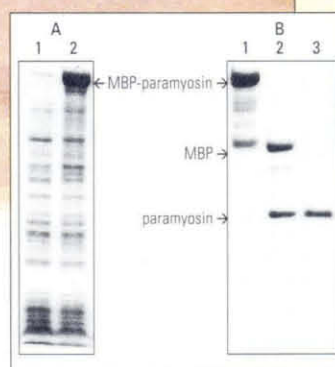
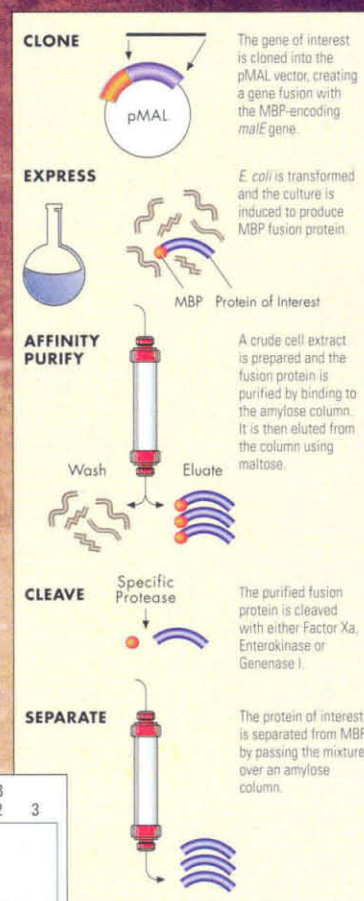
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TP0939	pyruvate oxidase [S PCC]	73	TP1010	nucleoside-diP Kase (ndk) [A f]	72	TP0472	excinuclease ABC, sub C (uvrC) [M tm]	60
TP0991	rubredoxin [C p]	76	TP0104	5'-nucleotidase (ushA) [H i]	70	TP0627	exonuclease (sbcC) [E c]	47
TP0919	thioredoxin (trx) [B s]	75	Purine ribonucleotide biosynthesis			TP0626	exonuclease, put [B s]	49
TP0100	thioredoxin, put [B j]	60	TP0294	phosphoribosyl pyroP Sase (prs) [B b]	66	TP0775	endonuclease III (nth) [E c]	70
Entner-Doudoroff			TP0695	phosphoribosylglycinamide formylase, put [B s]	46	TP0044	glu inhibited division prt A (gidA) [B b]	71
TP056	4-OH-2-oxoglutarate aldolase/2-dehydro-3-deoxyP-glucuronate aldolase (eda) [H i]	65	Pyrimidine ribonucleotide biosynthesis			TP0946	glu-inhibited division prt B (gidB) [E c]	50
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TP0476	acetate Kase (ack) [M th]	66	Salvage of nucleosides and nucleotides			TP0162	Holliday junction DNA helicase (ruvB) [H i]	76
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Glycolysis/gluconeogenesis			TP1039	adenine phosphoribosylase (apt) [H i]	63	TP0391	integrase/recombinase (codV) [B s]	68
TP0817	enolase (eno) [T p]	99	TP0274	deoxycytidylate deaminase, put [A f]	61	TP0395	integrase/recombinase (xprB) [E c]	56
TP0662	fru-bisP aldolase (cbba) [A e]	65	TP0170	pfs prt (pfs) [T p]	99	TP0141	methylated-DNA-prt-cysteine S-MTase (dat) [B s]	57
TP0475	glu-6-P isomerase (gpi) [B b]	67	TP0734	purine nucleoside phosphorylase (deoD) [B st]	79	TP0230	primosomal prt N (priA) [B b]	57
TP0844	glyceraldehyde 3-P DHase (gap) [T b]	82	TP0448	uracil phosphoribosylase, put [B s]	58	TP0692	recA prt (recA) [B b]	83
TP0505	hexoKase (hvk) [S po]	47	TP0667	uridine Kase (udk) [B b]	55	TP0003	recF prt (recF) [S PCC]	52
TP0122	phosphoenolpyruvate carboxyKase (pckA) [C l]	72	TP1027	uridine phosphorylase (udp) [E c]	58	TP1023	recX prt (recX) [P f]	47
TP0538	phosphoglycerate Kase (pgk) [B b]	71	Regulatory functions			TP1004	recombination prt (recR) [H i]	64
TP0168	phosphoglycerate mutase (pgm) [T p]	100	TP0485	adenylate cyclase [A sp]	67	TP0102	rep helicase, ss DNA-dependent ATPase (rep) [B b]	66
TP0108	pyroP-fru 6-P 1-PPase (pfk) [B b]	73	TP0220	anti-sigma F factor antagonist (spolIAA-1) [B l]	62	TP0058	replicative DNA helicase (dnaB) [B s]	64
TP0542	pyroP-fru 6-P 1-PPase, beta sub [B b]	72	TP0540	anti-sigma F factor antagonist (spolIAA-2) [B s]	58	TP0062	single-strand DNA BP (ssb) [B b]	68
TP0746	pyruvate, P diKase [E vi]	56	TP0233	anti-sigma F factor antagonist, put [B l]	54	TP0704	ss-DNA-specific exonuclease (recJ) [B b]	49
TP0537	trioseP isomerase (tpi) [B b]	67	TP0657	carbon storage regulator (csrA) [B s]	74	TP0344	transcription-repair coupling factor (trcF) [B b]	63
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TP0478	glu-6-P 1-DHase (zwf) [H i]	68	TP0261	catabolite gene activator, put [S PCC]	53	Degradation of DNA		
TP0477	glu-6-P 1-DHase, put [R c]	61	TP0167	cation-activated repressor prt (troR) [T p]	100	TP0805	exoribonuclease II (rnb) [S PCC]	48
TP0331	phosphogluconate DHase (gnd) [H i]	72	TP0995	cyclic nucleotide BP [S PCC]	57	TP0886	polynucleotide nucleotidylase (pnp) [B b]	74
TP0616	ribose 5-P isomerase (rpiA) [S PCC]	67	TP0089	cyclic nucleotide BP [P te]	51	TP0353	ribonuclease H (rnhA) [E c]	65
TP0945	ribulose-5-P-epimerase (cfeE) [R c]	64	TP0980	histidine phosphoKase/phosphatase (ntrB) [M l]	55	TP0809	ribonuclease III (rnc) [B b]	62
TP0560	transketolase A (tktA) [B s]	66	TP0591	HPr Kase (ptsK) [B s]	67	DNA-dependent RNA polymerase		
TP0824	transketolase B (tktB) [H i]	60	TP0953	pheromone shutdown prt (traB) [B b]	60	TP0701	DNA-directed RNA polymerase, put [E c]	52
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TP0642	phosphomannomutase (manB) [B s]	62	TP0085	PTS sys, N2 regulatory IIA component (ptsN-1) [P p]	55	TP0092	RNA polymerase sigma-24 factor (rhoE) [M l]	48
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TP0554	phosphoglycolate PPase (gph-2) [H i]	51	TP0981	sensory transduction histidine Kase, put [S PCC]	52	RNA processing		
Other			TP0219	sigma factor SigG regulation prt, put [B s]	51	TP0596	polynucleotide adenylase (pcnB) [E c]	61
TP0736	hydrogenase, gamma chain (hydG) [M j]	52	TP0218	sigma factor SigG regulation prt, put [S a]	50	TP0270	polynucleotide adenylase (pcnA) [B b]	59
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Biosynthesis			Degradation of DNA			TP0082	formate hydrogenlyase transcriptional activator (fhA) [E c]	62
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TP0812	long-chain-fatty-acid-CoA ligase, auth FS [A f]	48	TP1006	DNA gyrase, sub B (gyrB) [T p]	100	Amino acyl tRNA synthetases		
Other			TP1028	DNA helicase II (uvrD) [T t]	58	TP1017	alanyl-tRNA Sase (alaS) [B b]	73
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TP0885	deoxyuridine 5'-triphosphate nucleotidohydrolase (dut) [H p]	65	TP0105	DNA polymerase I (polA) [T p]	99	TP0672	glycyl-tRNA Sase (glyS) [B b]	74
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			TP1022	DNA repair prt (sms) [B s]	61	TP0015	phenylalanyl-tRNA Sase beta sub (pheT) [B b]	63
			TP0442	DNA repair prt (recN) [B s]	56	TP0973	phenylalanyl-tRNA Sase alpha sub (pheS) [B b]	69
			TP0380	DNA repair helicase, put [S c]	54	TP0160	prolyl-tRNA Sase (proS) [E c]	63
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Degradation of proteins, peptides and glycopeptides			TP0905	ribosomal prt S16 (rpsP) {B s}	74	TP0321	RG ABC transporter, ATP-BP (rbsA-2) {B b}	67
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TP0114	Lambda CII stability-governing prt (hflC) {B b}	65	TP0767	translation elongation factor G (fusA-2) {B b}	84	TP0227	cobalt ABC transporter, ATP-BP {M j}	59
TP0680	o-sialoglycoprt endopeptidase (gcp) {B b}	62	TP0187	translation elongation factor TU (tuf) {E c}	84	TP0513	K+ transport prt (trkA) {E c}	46
TP1026	oligoendopeptidase F, put {L l}	45	TP0525	translation elongation factor P (efp) {B b}	65	TP0140	K+ transport prt (ntpJ) {B s}	64
TP0773	periplasmic serine protease DO (htrA-1) {H i}	63	TP0605	translation elongation factor TS (tsf) {S pl}	57	TP0917	Mg2+ transport prt (mgfE) {B b}	69
TP0841	periplasmic serine protease DO (htrA-2) {B b}	63	TP0097	translation initiation factor 1 (infA) {B b}	91	TP0774	Mg2+ transport prt (mgfC) {S PCC}	68
TP0546	periplasmic serine protease, put {M l}	53	TP0850	translation initiation factor 3 (infC) {B b}	73	TP0056	oxaloacetate DCase, sub alpha (oadA) {K p}	67
TP0488	protease {T p}	99	TP0891	translation initiation factor 2 (infB) {B b}	71	TP0057	oxaloacetate DCase, sub beta (oadB) {S ch}	79
TP0997	protease IV (sppA) {E c}	53	tRNA modification			Other		
TP0600	zinc protease, put {H i}	54	TP1019	glu-tRNA amidoTase, sub C (gatC) {B b}	65	TP0790	antibiotic transport prt, put {M l}	47
Protein modification			TP1021	glu-tRNA amidoTase, sub B {gatB} {B b}	66	TP0146	chromate resistance prt A, auth FS {M j}	54
TP0842	methionine aminopeptidase (map) {B s}	63	TP1020	glu-tRNA amidoTase, sub A (gata) {A f}	68	TP0142	thiamine ABC transporter, ATP-BP, put {H i}	62
TP0947	peptidyl-prolyl cis-trans isomerase, cyclophilin-binding (cyp) {M t}	71	TP0756	methionyl-tRNA formylTase (fmt) {H i}	59	TP0143	thiamine ABC transporter, permease prt,	
TP0349	peptidyl-prolyl cis-trans isomerase, FKBP-type (slyD) {H i}	57	TP1011	peptidyl-tRNA hydrolase (pth) {H i}	63	put {N g}	48	
TP0862	peptidyl-prolyl cis-trans isomerase, FKBP-type, 22 kD (fklB) {E c}	62	TP0830	pseudouridylate Sase (hisT) {B b}	57	TP0144	thiamine ABC transporter, thiamine-binding	
TP0757	polypeptide deformylase (def) {S PCC}	66	TP0889	tRNA pseudouridine 55 Sase (truB) {B b}	60	periplasmic prt, put {E c}	50	
TP0633	prt-methionine-S-oxide RDase (msrA) {M tm}	66	TP0908	tRNA (guanine-N1)-MTase (trmD) {B b}	75	Other categories		
Ribosomal proteins: synthesis and modification			TP0637	tRNA delta(2)-isopentenylPP Tase (miaA) {B s}	54	Adaptations and atypical conditions		
TP0238	ribosomal prt L1 (rplA) {B b}	76	Other			TP0372	general stress prt (ctc) {B s}	49
TP0192	ribosomal prt L2 (rplB) {B b}	75	TP0890	ribosome-binding factor A (rbfA) {B s}	62	TP0272	SpoOJ regulator (soj) {B s}	72
TP0189	ribosomal prt L3 (rplC) {B b}	66	Transport and binding proteins			TP0419	survival prt, put {S me}	55
TP0190	ribosomal prt L4 (rplD) {B b}	76	Unknown substrate			TP0516	virulence factor (mviN) {H i}	57
TP0201	ribosomal prt L5 (rplE) {B b}	83	TP0964	ABC transporter, ATP-BP {B s}	72	Other		
TP0204	ribosomal prt L6 (rplF) {B b}	69	TP0581	ABC transporter, ATP-BP {B b}	72	TP0835	ankyrin, put {H s}	46
TP0240	ribosomal prt L7/L12 (rplL) {H i}	72	TP0838	ABC transporter, ATP-BP {B b}	75	TP0614	N2 fixation prt (nifS-1) {B s}	60
TP0060	ribosomal prt L9 (rplI) {B s}	61	TP0035	ABC transporter, ATP-BP {S PCC}	61	TP0615	N2 fixation prt (nifU) {M l}	53
TP0239	ribosomal prt L10 (rplJ) {S an}	61	TP0611	ABC transporter, ATP-BP {S PCC}	69	TP0152	N2 fixation prt (rnfC) {R c}	44
TP0237	ribosomal prt L11 (rplK) {T m}	80	TP0881	ABC transporter, ATP-BP (natA) {B s}	62	TP0863	N2 fixation prt (nifS-2) {R s}	58
TP1025	ribosomal prt L13 (rplM) {B b}	75	TP0786	ABC transporter, ATP-BP, put {E c}	76	TP0551	PPase {T d}	56
TP0199	ribosomal prt L14 (rplN) {B b}	85	TP0034	ABC transporter, periplasmic BP {P a}	55	Unknown		
TP0207	ribosomal prt L15 (rplO) {B b}	70	TP0036	ABC transporter, permease prt {S g}	55	TP0712	ATP-BP (ybhH-1) {T p}	100
TP0196	ribosomal prt L16 (rplP) {S PCC}	79	TP0023	Na+- and Cl- dependent transporter {M j}	53	TP0853	ATP-BP (ybhH-2) {B b}	67
TP0213	ribosomal prt L17 (rplQ) {B b}	78	Amino acids, peptides, and amines			TP0779	dedA prt (dedA) {H i}	50
TP0205	ribosomal prt L18 (rplR) {B st}	70	TP0120	AA ABC transporter, ATP-BP (abc) {H p}	70	TP0096	dnaK suppressor, put {B b}	56
TP0909	ribosomal prt L19 (rplS) {B b}	81	TP0265	AA ABC transporter, permease prt (braC) {B s}	54	TP0446	gcpE prt (gcpE) {B s}	59
TP0848	ribosomal prt L20 (rplT) {B b}	70	TP0119	AA ABC transporter, permease prt (yaeE) {H p}	73	TP0225	leucine-rich repeat prt TplRR {T p}	100
TP0745	ribosomal prt L21 (rplU) {B s}	67	TP0309	AA ABC transporter, periplasmic BP {B s}	47	TP0778	mazG prt (mazG) {E c}	55
TP0194	ribosomal prt L22 (rplV) {B b}	74	TP0308	AA ABC transporter, periplasmic BP (hisJ) {S ch}	48	TP0880	memb spanning prt, put {B b}	58
TP0191	ribosomal prt L23 (rplW) {T m}	61	TP0106	carnitine transporter, put {E c}	51	TP0393	smf prt (smf) {B b}	54
TP0200	ribosomal prt L24 (rplX) {B s}	73	TP0414	D-alanine glycine permease (dagA) {H i}	64	TP0689	GTP-BP {T p}	100
TP0743	ribosomal prt L27 (rpl27) {S PCC}	78	TP0934	glutamate transporter, put {B b}	45	TP0356	RNA-BP, put {A th}	64
TP0362	ribosomal prt L28 (rpmB) {T p}	100	TP0555	glutamate/ aspartate transporter, put {M m}	51	TP0184	small prt (smpB) {S PCC}	70
TP0197	ribosomal prt L29 (rpmC) {B st}	63	TP0585	OP ABC transporter, periplasmic BP (oppA) {B s}	50	TP0948	spoIIJ-associated prt (jag) {B b}	63
TP0255	ribosomal prt L31 (rpmE) {H i}	80	TP0998	Na+/proton-dependent alanine transporter {H i}	69	TP0009	tpr prt A (tprA), auth FS {T p}	61
TP0807	ribosomal prt L32 (rpmF) {B b}	72	TP0653	SP ABC transporter, permease prt (potB) {A f}	58	TP0011	tpr prt B (tprB) {T p}	56
TP0234	ribosomal prt L33 (rpmG) {T a}	76	TP0654	SP ABC transporter, permease prt (potC) {H i}	68	TP0117	tpr prt C (tprC) {T p}	66
TP0951	ribosomal prt L34 (rpmH) {B b}	86	TP0652	SP ABC transporter, ATP-BP (potA) {A f}	66	TP0131	tpr prt D (tprD) {T p}	66
TP0849	ribosomal prt L35 (rpmI) {B b}	75	TP0655	SP ABC transporter, periplasmic BP (potD) {E c}	52	TP0313	tpr prt E (tprE) {T p}	78
TP0209	ribosomal prt L36 (rpmJ-1) {C v}	86	Carbohydrates, organic alcohols, acids			TP0316	tpr prt F (tprF), auth FS {T p}	66
TP0590	ribosomal prt L36 (rpmJ-2) {A l}	61	TP0958	dicarboxylate transporter (dctM) {R c}	57	TP0317	tpr prt G (tprG) {T p}	89
TP0279	ribosomal prt S1 (rpsA) {E c}	57	TP0685	MG ABC transporter, ATP BP (mgIA) {T p}	100	TP0610	tpr prt H (tprH) {T p}	63
TP0606	ribosomal prt S2 (rpsB) {B b}	84	TP0686	MG ABC transporter, permease prt (mgIC) {T p}	100	TP0620	tpr prt I (tprI) {T p}	67
TP0195	ribosomal prt S3 (rpsC) {B s}	71	TP0684	MG ABC transporter, periplasmic galactose-BP (mgIB-2) {T p}	100	TP0621	tpr prt J (tprJ) {T p}	100
TP0306	ribosomal prt S4 {B b}	69	TP0545	MG ABC transporter, periplasmic galactose-BP (mgIB-1) {C f}	57	TP0897	tpr prt K (tprK) {T p}	55
TP0206	ribosomal prt S5 (rpsE) {B b}	77	TP0804	sugar ABC transporter, ATP-BP (ugpC) {E c}	70	TP1031	tpr prt L (tprL), FS {T p}	61
TP0063	ribosomal prt S6 (rpsF) {B b}	53	TP0075	sugar ABC transporter, permease prt		TP0729	treponemal aqueous prt (tap1) {T p}	100
TP0244	ribosomal prt S7 {B b}	76	(y4oQ) {R sp}	60	TP1007	thymidylate Sase-complementing prt (thy1) {B b}	68	
TP0203	ribosomal prt S8 (rpsH) {B b}	73	TP0076	sugar ABC transporter, permease prt		TP0845	p23 prt, put {P le}	58
TP1024	ribosomal prt S9 (rpsI) {B st}	72	(y4oR) {R sp}	60	TP0989	P26 {B b}	50	
TP0188	ribosomal prt S10 (rpsJ) {B b}	88	TP0074	sugar ABC transporter, periplasmic BP		TP0020	76K prt {T p}	99
TP0211	ribosomal prt S11 (rpsK) {B b}	87	(y4oP) {R sp}	44	TP0006	7p75 prt {T p}	100	
TP0243	ribosomal prt S12 (rpsL) {L b}	91				TP0571	7p70 prt {T p}	98
TP0210	ribosomal prt S13 (rpsM) {B b}	82				TP0957	7p33 prt {T p}	93

Science

The Genome of *Treponema pallidum*

Table 1. Identification of *T. pallidum* genes. Gene identification numbers that correspond to those in Fig. 1 are listed here with the prefix TP. Each gene identified is listed in its functional role category [adopted from (11)]. The percentage of similarity to the best match is also shown. Three ORFs, TP0279, TP0488, and TP0633, are represented in this table more than once because each contains complete, nonoverlapping matches to more than one sequence. An expanded version of this table with additional information is available on the World Wide Web at www.tigr.org/tdb/mdb/tpdb/tpdb.html. Abbreviations are as follows. Gene names: AA, amino acid; Ac, acetyl; auth, authentic; BP, binding protein; biosyn, biosynthesis; CPDase, carboxypeptidase; Dcase, decarboxylase; DHase, dehydrogenase; flgr, flagellar/flagellum; fru, fructose; glu, glucose; Kase, kinase; MC, methyl-accepting chemotaxis; MG, methylgalactoside; MTase, methyltransferase; memb, membrane; mur, muramoyl; O₂, oxygen; ODase, oxidase; OH, hydroxy; OP, oligopeptide; N₂, nitrogen; P, phosphate or phospho-; PPTase, phosphotransferase; PPase, phosphatase; prt, protein; put, putative; RDase, reductase; RG, ribose/galactose; SAM, S-adenosylmethionine; Sase, synthetase/synthase; SP, spermidine/putrescine; ss, single-stranded; sub, subunit; sys, system; Tase, transferase; TGLase, transglycosylase. Genus/species: Aa, *Actinobacillus actinomycetemcomitans*; Ae, *Alcaligenes eutrophus*; Af, *Archaeoglobus fulgidus*; Al, *Astasia longa*; Asp, *Anabaena species*; Ath, *Arabidopsis thaliana*; Bb, *Borrelia burgdorferi*; Bba, *Bartonella bacilliformis*; Bc, *Bacillus cereus*; Bj, *Bradyrhizobium japonicum*; Bl, *Bacillus licheniformis*; Bp, *Bordetella pertussis*; Bs, *Bacillus subtilis*; Bsp, *Bacillus sphaericus*; Bst, *Bacillus stearothermophilus*; Ca, *Clostridium aceto-*

butylicum; Cb, *Clostridium beijerinckii*; Cc, *Caulobacter crescentus*; Cf, *Citrobacter freundii*; Cg, *Corynebacterium glutamicum*; Cl, *Chlorobium linicola*; Cp, *Clostridium perfringens*; Cv, *Chlorella vulgaris*; Dsp, *Desulfurococcus species*; Dt, *Dictyoglomus thermophilum*; Dv, *Desulfovibrio vulgaris*; Ec, *Escherichia coli*; Evi, *Eleocharis vivipara*; Hi, *Haemophilus influenzae*; Hp, *Helicobacter pylori*; Hs, *Homo sapiens*; Kp, *Klebsiella pneumoniae*; Lb, *Leptospira biflexa*; Ll, *Lactococcus lactis*; Lp, *Legionella pneumophila*; Mg, *Mycoplasma genitalium*; Mj, *Methanococcus jannaschii*; Mk, *Mycobacterium kansasii*; Ml, *Mycobacterium leprae*; Mm, *Methanosarcina mazei*; Mmu, *Mus musculus*; Mt, *Mycobacterium tuberculosis*; Mth, *Methanosarcina thermophila*; Mtm, *Methanobacterium thermoautotrophicum*; Mx, *Myxococcus xanthus*; Ng, *Neisseria gonorrhoeae*; Pa, *Pseudomonas aeruginosa*; Pf, *Pseudomonas fluorescens*; Ple, *Pseudomonas lemoignei*; Pp, *Pseudomonas putida*; Psp, *Pyrococcus species*; Pte, *Paramecium tetraurelia*; Rm, *Rhizobium meliloti*; Rc, *Rhodobacter capsulatus*; Rs, *Rhodobacter sphaeroides*; Rsp, *Rhizobium species*; Sa, *Staphylococcus aureus*; Sac, *Sulfolobus acidocaldarius*; Sal, *Streptomyces albus*; San, *Streptomyces antibioticus*; Sc, *Saccharomyces cerevisiae*; Sch, *Salmonella choleraesuis*; Sco, *Streptomyces coelicolor*; Sg, *Streptococcus gordonii*; Sm, *Streptococcus mutans*; Sme, *Sinorhizobium meliloti*; Sp, *Streptococcus pneumoniae*; Spl, *Spirulina platensis*; St, *Salmonella typhimurium*; Spo, *Schizosaccharomyces pombe*; Ss, *Streptococcus salivarius*; SPCC, *Synechocystis* PCC6803; Sv, *Streptomyces viridochromogenes*; Ta, *Thermus aquaticus*; Tb, *Trypanosoma borreli*; Td, *Treponema denticola*; Tt, *Thermus thermophilus*; Tm, *Thermotoga maritima*; Tp, *Treponema pallidum*; Ye, *Yersinia enterocolitica*.

Table 1. Predicted functions of *T. pallidum* genes

TP#	Identification (species match)	% similarity	TP#	Identification (species match)	% similarity	TP#	Identification (species match)	% similarity
Amino acid biosynthesis			Biosynthesis of surface polysaccharides and lipopolysacchararides			TP0028 hemolysin, put [S PCC]		
Aspartate family			TP0566 alginate O-Acation prt (algI) [P a]			TP0936 hemolysin, put [S PCC]		
TP0556 asparagine Sase (asnA) [H i]			TP0486 antigen, p83/100 [B b]			TP0688 immunity prt (mccF) [T p]		
TP0223 aspartate aminoTase (tpaaT) [T p]			TP0077 capsular polysacch biosyn prt (cap5D) [S a]			TP0405 mcbG prt, put [E c]		
Glutamate family			TP0107 licC prt (licC) [H i]			TP0696 nicotinamidase, put [M k]		
TP0735 glutamate Sase (gltA) [P sp]			TP0283 lipopolysacch core biosyn prt (kdtB) [E c]			TP0547 penicillin tolerance prt (lytB) [H p]		
TP0351 glutamate 5-Kase (proB) [T p]			TP0078 spore coat polysacch biosyn prt (spsC) [B s]			Chaperones		
TP0350 glutamate-5-semialdehyde DHase (proA) [T p]			TP0288 spore coat polysacch biosyn prt (spsF) [B s]			TP1013 chaperonin (groES) [B st]		
TP0797 1-pyrroline-5-carboxylate RDase (proC) [T p]			TP0562 spore coat polysacch biosyn prt (spsE) [B s]			TP0215 grpE prt (grpE) [B b]		
Serine family			TP0440 spore coat polysacch biosyn prt, put [S PCC]			TP0030 heat shock prt (groEL) [T p]		
TP0329 serine OHMTase (glyA) [B s]			TP0275 UDP-N-Ac-D-mannosamine Tase, put [P a]			TP0217 heat shock prt (dnaJ), auth FS [E c]		
Biosyn of cofactors/prosthetic groups/carriers			Surface structures			TP0216 heat shock prt 70 (dnaK) [B b]		
Biotin			TP0943 flgr prt (fliS) [B s]			TP0984 heat shock prt 90 (htpG) [B b]		
TP0357 biotin-Ac-CoA-carboxylase ligase (birA) [M t]			TP0722 flgr prt (fliL) [T p]			TP0843 heat shock prt, put [M g]		
TP0228 biotin Sase, put [B sp]			TP0726 flgr prt (fliD) [T p]			TP0098 heat shock prt, put [L p]		
Folic acid			TP0378 flgr prt, put [T p]			Detoxification		
TP0340 folylpolyglutamate Sase (folC) [B s]			TP0403 flgr prt, put [T d]			TP0509 alkyl hydroperoxide RDase (ahpC) [B s]		
TP0694 5,10-methenyltetrahydrofolate Sase, put [H s]			TP0727 flgr hook prt (flgE) [T p]			TP0550 thiophene and furan oxidation prt (thdF) [B b]		
TP0732 methylenetetrahydrofolate DHase (folD) [B s]			TP0401 flgr assembly prt (fliH) [T d]			Protein and peptide secretion		
Heme and porphyrin			TP0714 flgr biosyn prt (flhA) [T p]			TP0417 apolipoprt N-acylTase (cutE) [E c]		
TP0186 O2-ind. coproporphyrinogen III ODase, put [B s]			TP0715 flgr biosynthetic prt (flhB) [T p]			TP0252 apolipoprt N-acylTase, put [H i]		
TP0052 protoporphyrinogen ODase (hemK) [H i]			TP0716 flgr biosynthetic prt (fliR) [T p]			TP0235 preprt translocase sub (secE) [T m]		
Menaquinone and ubiquinone			TP0720 flgr motor switch prt (fliY) [T p]			TP0208 preprt translocase sub (secY) [B b]		
TP0683 octaprenyl-diP Sase [T p]			TP0721 flgr motor switch prt (fliM) [T p]			TP0379 preprt translocase sub (secA) [B b]		
Pyridine nucleotides			TP0748 cytoplasmic filament prt A (cfaA) [T p]			TP0852 prolipoprt diacylglyceryl Tase (lgt) [H i]		
TP0780 NH(3)-dependent NAD(+) Sase (nadE) [R c]			TP0402 flgm-specific ATP Sase (fliI) [T d]			TP0410 prt-export memb prt (secD) [B b]		
Riboflavin			TP0724 flgr motor rotation prt (motB) [T p]			TP0411 prt-export memb prt (secF) [B s]		
TP0888 riboflavin Kase/FMN adenylTase (ribF) [E c]			TP0725 flgr motor rotation prt (motA) [T p]			TP0185 signal peptidase I (sip) [B s]		
Thiamine			TP0872 flgr filament cap prt (fliD) [B b]			TP0978 signal peptidase II (lsp) [B b]		
TP0115 phosphomethylpyrimidine Kase (thiD) [B s]			TP0026 flgr motor switch prt (fliG-1) [T d]			TP0926 signal peptidase I, put [L p]		
TP0445 4-methyl-5(b-OHethyl)-thiazole monoP biosyn enzyme (thiJ) [B b]			TP0396 flgr basal-body rod prt (flgB) [T d]			TP0416 signal recognition particle prt (ffh) [B b]		
Cell envelope			TP0397 flgr basal-body rod prt (flgC) [T d]			TP0506 trigger factor (tig) [B b]		
Lipoproteins			TP0400 flgr motor switch prt (fliG-2) [T d]			Transformation		
TP0821 lipoprt (tpn32) [T p]			TP0399 flgr basal-body M ring prt (fliF) [T d]			TP0336 comE prt, put [S PCC]		
TP0171 lipoprt, 15 kD (tpp15) [T p]			TP0960 flgr basal-body rod prt (flgG-1) [B b]			Other		
TP0435 lipoprt, 17 kD (tpp17) [T p]			TP0961 flgr basal-body rod prt (flgG-2) [B b]			TP0363 chemotaxis histidine Kase (cheA) [T p]		
TP0319 memb lipoprt (tmpC) [T p]			TP0659 flgr hook-associated prt 3 (flgL) [B b]			TP0365 chemotaxis prt (cheX) [T p]		
TP0993 rare lipoprt A, put [B b]			TP0660 flgr hook-associated prt 1 (flgK) [B b]			TP0630 chemotaxis prt MTase (cheR) [B b]		
Biosynthesis of murein sacculus and peptidoglycan			TP0792 flgr filament 33 kD core prt (flaB2) [T p]			TP0366 chemotaxis response regulator (cheY) [T p]		
TP0247 N-Acmur-L-alanine amidase (amiA) [E c]			TP0870 flgr filament 31 kD core prt (flaB3) [T p]			TP0541 GTP-BP (era) [B b]		
TP0670 D-alanine-D-alanine ligase (ddlA) [S ch]			TP0249 flgr filament outer layer prt (flaA-1) [T p]			TP0742 GTP-BP (obg) [B b]		
TP0681 alanine racemase (alr) [T p]			TP0664 flgr filament outer layer prt (flaA-2) [T p]			TP0040 MC prt (mcp1) [T p]		
TP0574 CPDase, 47 kD [T p]			TP0713 flgr-associated GTP-BP (flhF) [T p]			TP0488 MC prt (mcp2-1) [T p]		
TP0221 D,D-CPDase, put [B b]			TP0868 flgr filament 34.5 kD core prt (flaB1) [T p]			TP0639 MC prt (mcp2-2) [T p]		
TP0806 femA prt, put [B b]			TP0398 flgr hook-basal body complex prt (fliE) [T d]			TP0640 MC prt (mcp2-3) [T p]		
TP0861 glucosamine-fru-6-P aminoTase (glmS) [H i]			TP0728 flgr hook assembly scaffolding prt (flgD) [T p]			TP0364 purine-binding chemotaxis prt (cheW-1) [T p]		
TP0406 glutamate racemase (murI) [E c]			Other			TP0439 purine-binding chemotaxis prt (cheW-2) [B b]		
TP0623 memb-bound lytic murein TGLase D (dniR) [E c]			TP1016 basic memb prt (tpn39b) [T p]			TP0631 prt-glutamate methylesterase (cheB) [S ch]		
TP0500 penicillin-BP (pbp-1) [B b]			TP0327 cationic outer memb prt (ompH) [Y e]			Central intermediary metabolism		
TP0705 penicillin-BP (pbp-2) [B b]			TP0298 exported prt (tpn38b) [T p]			TP0080 quinoline 2-oxidoRDase [P p]		
TP0760 penicillin-BP (pbp-3) [B b]			TP0971 memb antigen, pathogen-specific (tpd) [T p]			TP0794 SAM Sase (metK) [E c]		
TP0345 P-N-Acmur-pentapeptide-Tase (mraY) [H p]			TP0965 memb fusion prt, put [H i]			Energy metabolism		
TP0497 rod shape-determining prt (mreB) [B b]			TP0949 memb prt [B b]			Aerobic		
TP0498 rod shape-determining prt (mreC) [B b]			TP0768 memb prt (tmpA) [T p]			TP0921 NADH ODase [S m]		
TP0499 rod shape-determining prt (mreD) [E c]			TP0326 outer memb prt [H p]			TP1009 glycerol-3-P DHase (gpsA) [B s]		
TP0501 rod shape-determining prt (rodA) [B b]			TP0769 outer memb prt (tmpB) [T p]			TP0037 D-specific D-2-OHacid DHase [S a]		
TP0800 serine-type D-Ala-D-Ala CPDase (dacC) [B b]			TP0292 outer memb prt (tpn50) [T p]			Anaerobic		
TP0043 soluble lytic TGLase, put [E c]			TP0663 outer memb prt, put [T p]			TP0982 glpG prt, put [E c]		
TP0090 UDP-N-Acmuramate DHase (murB) [B b]			TP0658 transmemb prt, put [B s]			ATP-proton motive force interconversion		
TP0341 UDP-N-Acmuramate-alanine ligase (murC) [B b]			Cellular processes			TP0426 V-type ATPase, sub A (atpA-1) [B b]		
TP0903 UDP-N-Acmuralanine-D-glutamate ligase (murD) [B b]			Cell division			TP0529 V-type ATPase, sub A (atpA-2) [S ac]		
TP0029 UDP-N-Acglucosamine 1-carboxyvinylTase (murA) [B b]			TP0578 cell division prt (ftsY) [B s]			TP0427 V-type ATPase, sub B (atpB-1) [B b]		
TP0933 UDP-N-Acmuralanyl-D-glutamate-2,6-diamino -pimelate ligase (murE) [B b]			TP0765 cell division prt (ftsH) [H p]			TP0528 V-type ATPase, sub B (atpB-2) [M j]		
TP0386 UDP-N-Acmuralanyl-D-glutamyl-2,6-diamino -pimelate-D-alanyl-D-alanine ligase (murF) [S PCC]			TP0387 cell division prt (ftsW) [B b]			TP0428 V-type ATPase, sub D (atpD-1) [B b]		
TP0523 UDP-N-glucosamine-N-Acmuramyl-(penta-peptide)pyrophosphoryl-undecaprenol N-Acglucosamine Tase (murG) [B b]			TP0388 cell division prt (ftsQ) [B b]			TP0527 V-type ATPase, sub D (atpD-2) [M m]		
			TP0389 cell division prt (ftsA) [B b]			TP0530 V-type ATPase, sub E, put [D sp]		
			TP0390 cell division prt (ftsZ) [B b]			TP0424 V-type ATPase, sub E, put [T t]		
			TP0682 cell division prt (ftsJ) [B b]			TP0531 V-type ATPase, sub F, put [M mi]		
			TP0999 cell division prt, put [B b]			TP0429 V-type ATPase, sub I (atpI-1) [M j]		
			TP0330 cell division prt, put [M g]			TP0533 V-type ATPase, sub I (atpI-2) [M j]		
			TP0271 chromosome partitioning prt (parB) [C c]			TP0430 V-type ATPase, sub K (atpK-1) [B b]		
			TP0367 chromosome segregation prt, put [B s]			TP0532 V-type ATPase, sub K (atpK-2), auth FS [T p]		
			Toxin production and resistance			Electron transport		
			TP0935 N-Acphosphinothricin-tripetide-deAcase, put [S v]			TP0101 cytochrome c biogenesis prt (ccdA) [H p]		
			TP0337 dimethyladenosine Tase (ksgA) [B s]			TP0823 desulfoferrodoxin (rbo) [D v]		
			TP0649 hemolysin (tlyC) [B b]					
			TP1037 hemolysin III (hlyIII) [B c]					
			TP0027 hemolysin, put [B b]					