17 July 1998

Science

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Pages 297–476 $7

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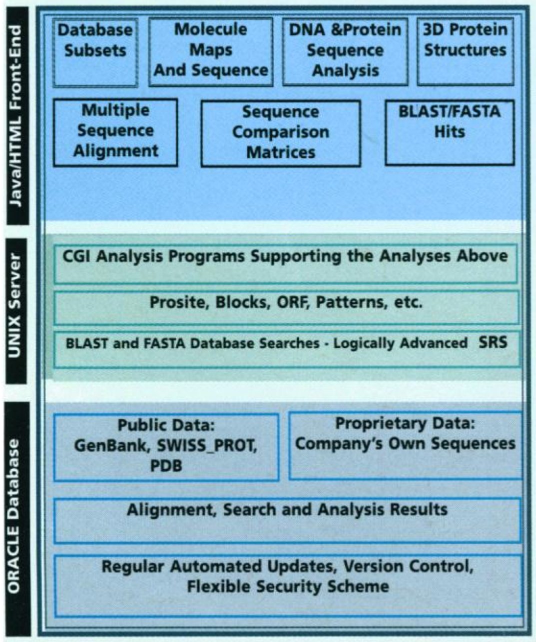

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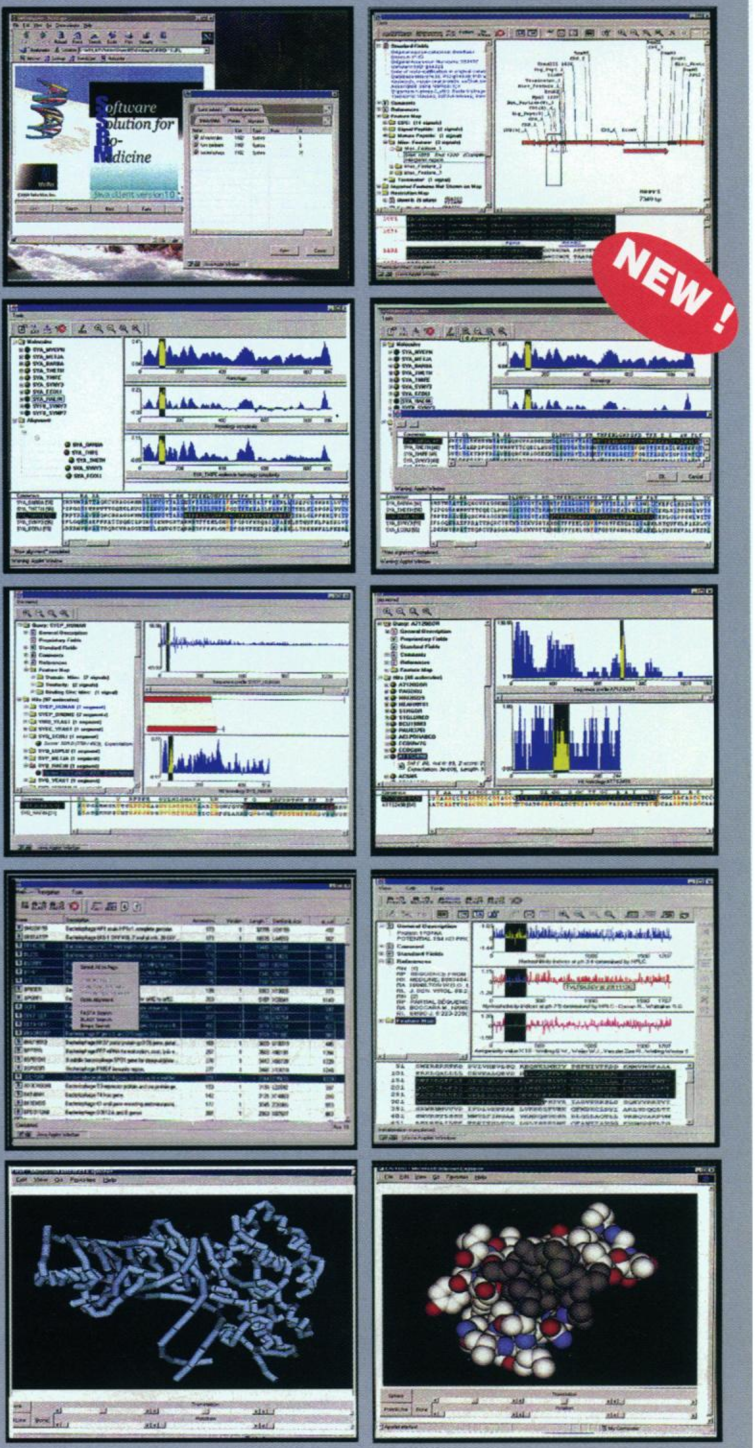

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Science

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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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An intimate look at an extinct sloth

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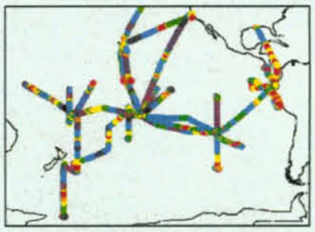

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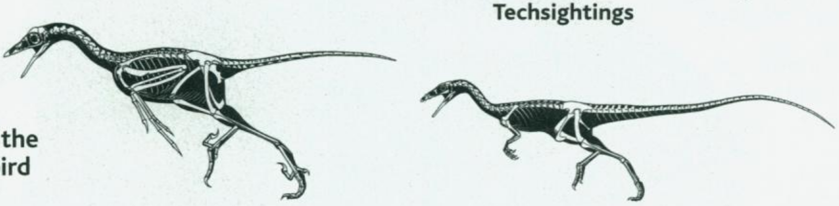

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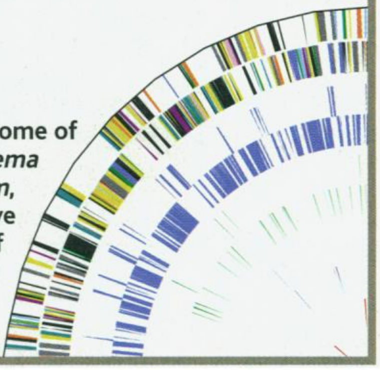

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The genome of *Treponema pallidum*, causative agent of syphilis

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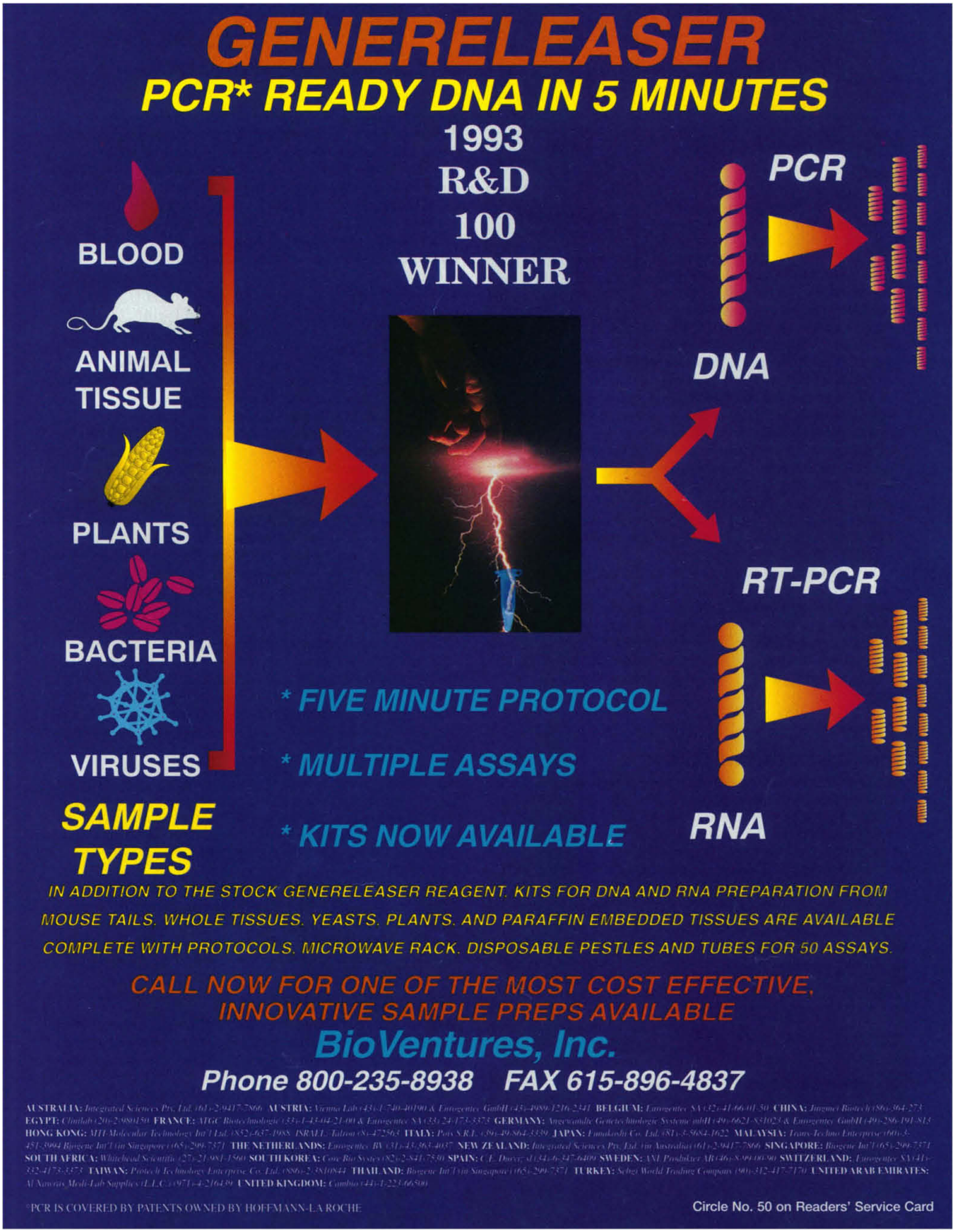

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THIS WEEK IN *SCIENCE*

edited by PHIL SZUROMI

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

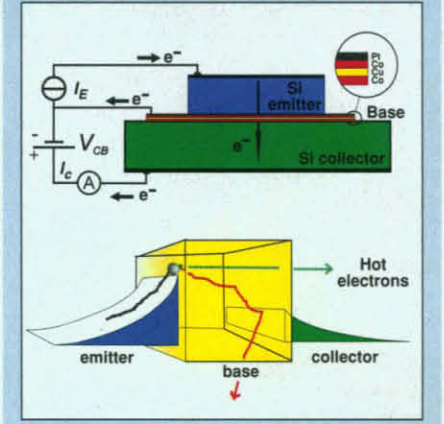
Methyl bromide is the main atmospheric component containing bromine and plays a role in ozone destruction in the stratosphere. Many of the sources and sinks of methyl bromide are incompletely understood, which results in large uncertainties in estimating the relative importance of natural and anthropogenic 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_4O tetrahedra formed by shortening of hydrogen bonds, which suggests 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 nonmagnetic 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. Rubin *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

CONTINUED ON PAGE 307

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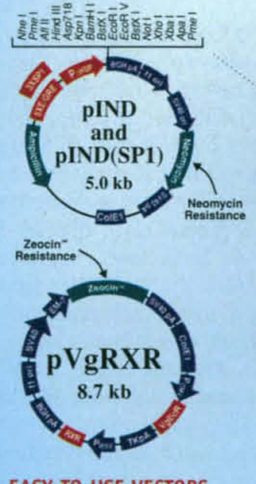

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INDUCE WITH PONASTERONE A OR MURISTERONE A

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

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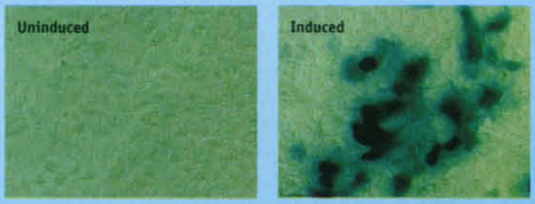

Uninduced and induced transiently transfected 293 cells stained with X-gal.

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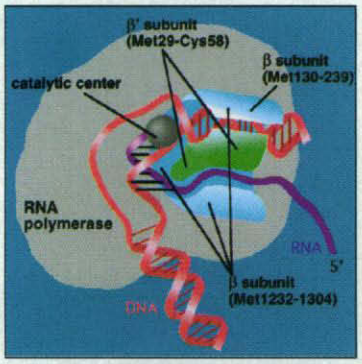
CONTINUED FROM PAGE 305

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 chord 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-γ1 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.

BEETLE 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

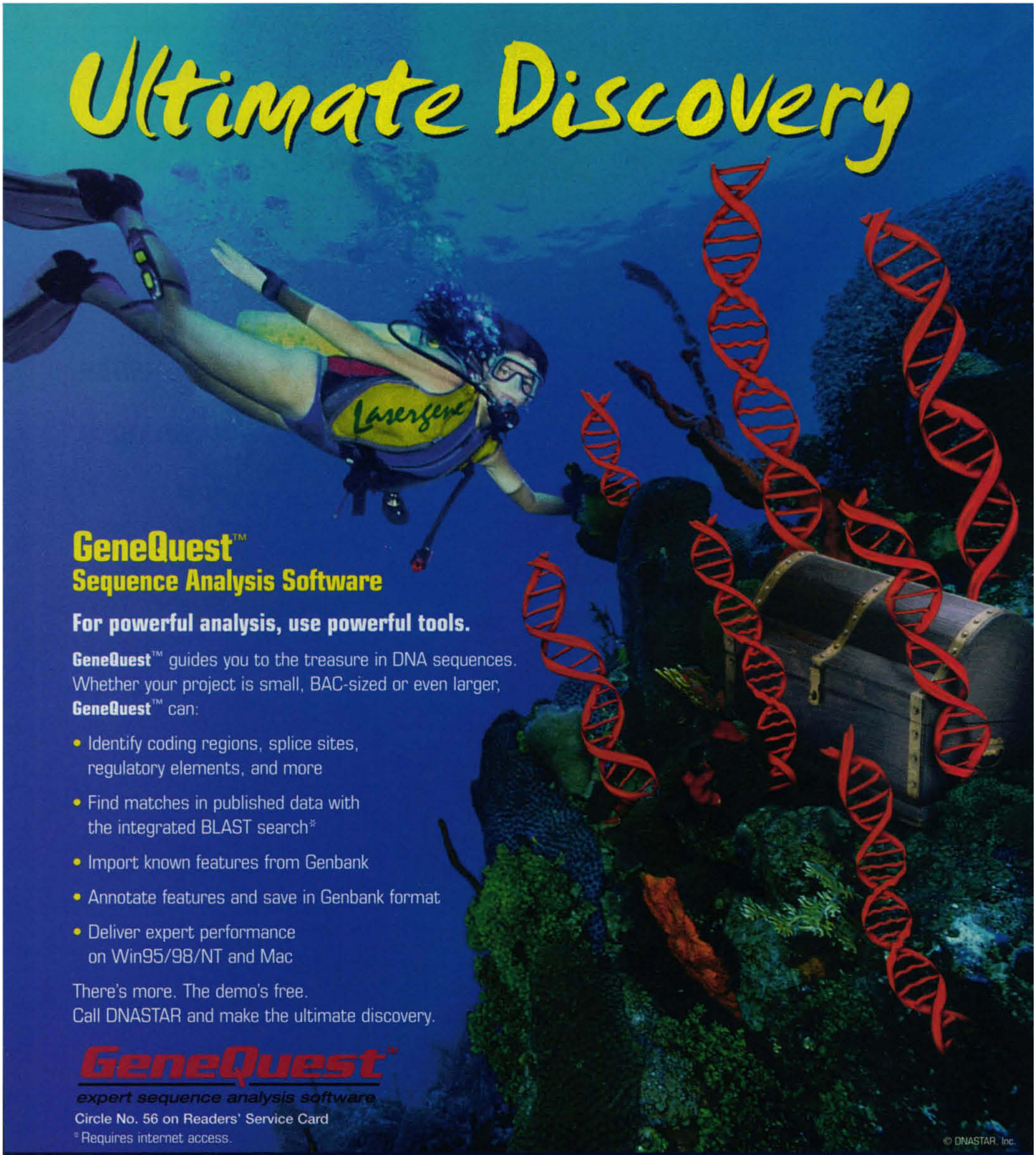
Feasibility of a Colliding Beam Fusion Reactor

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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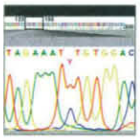

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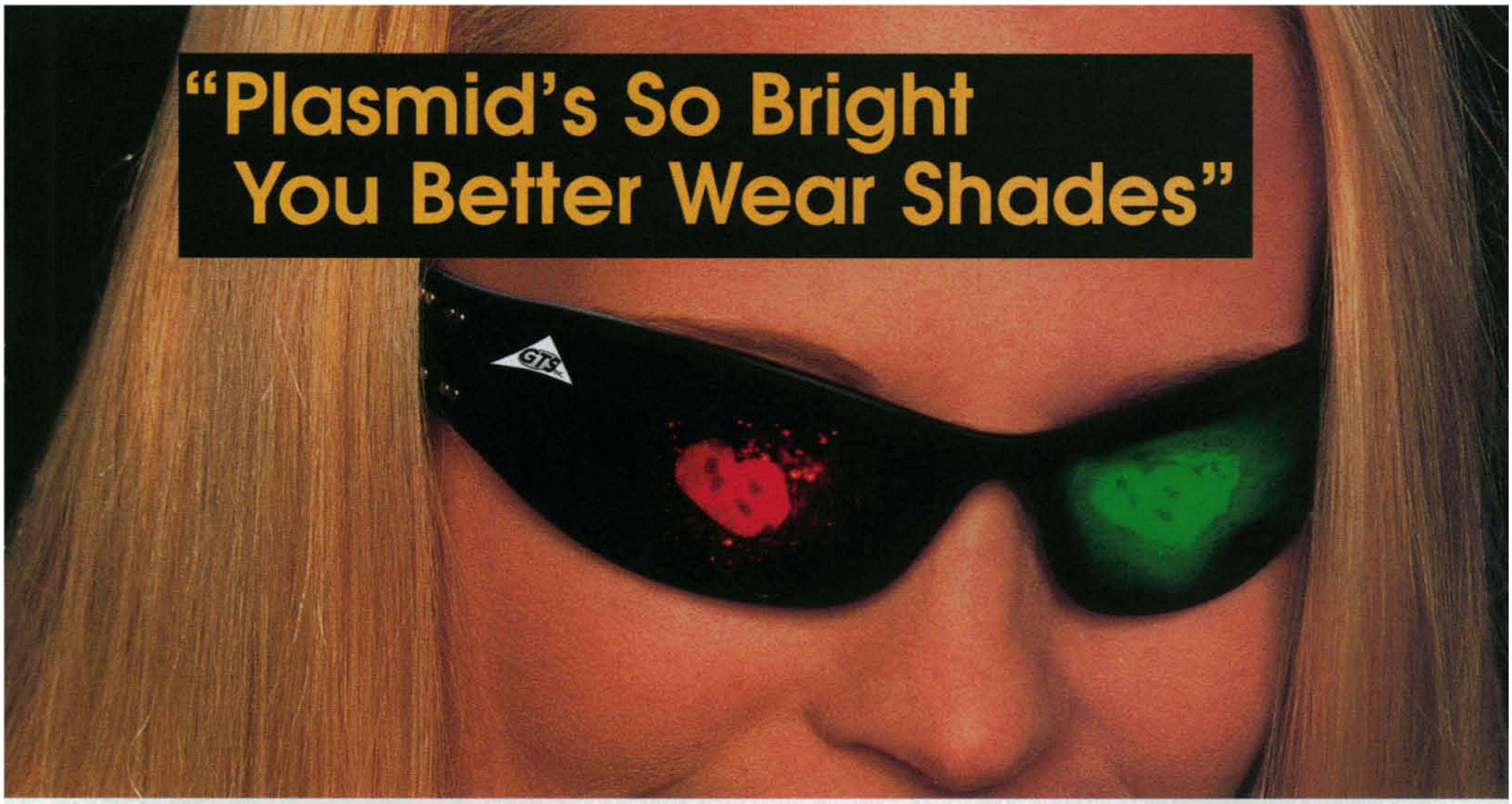
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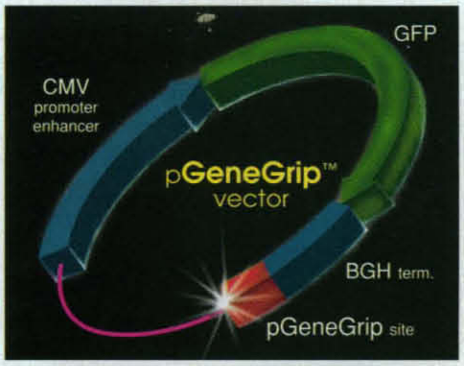
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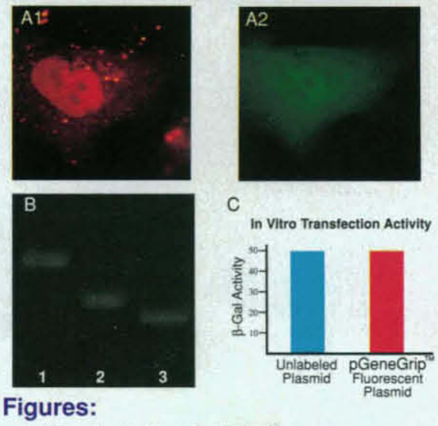
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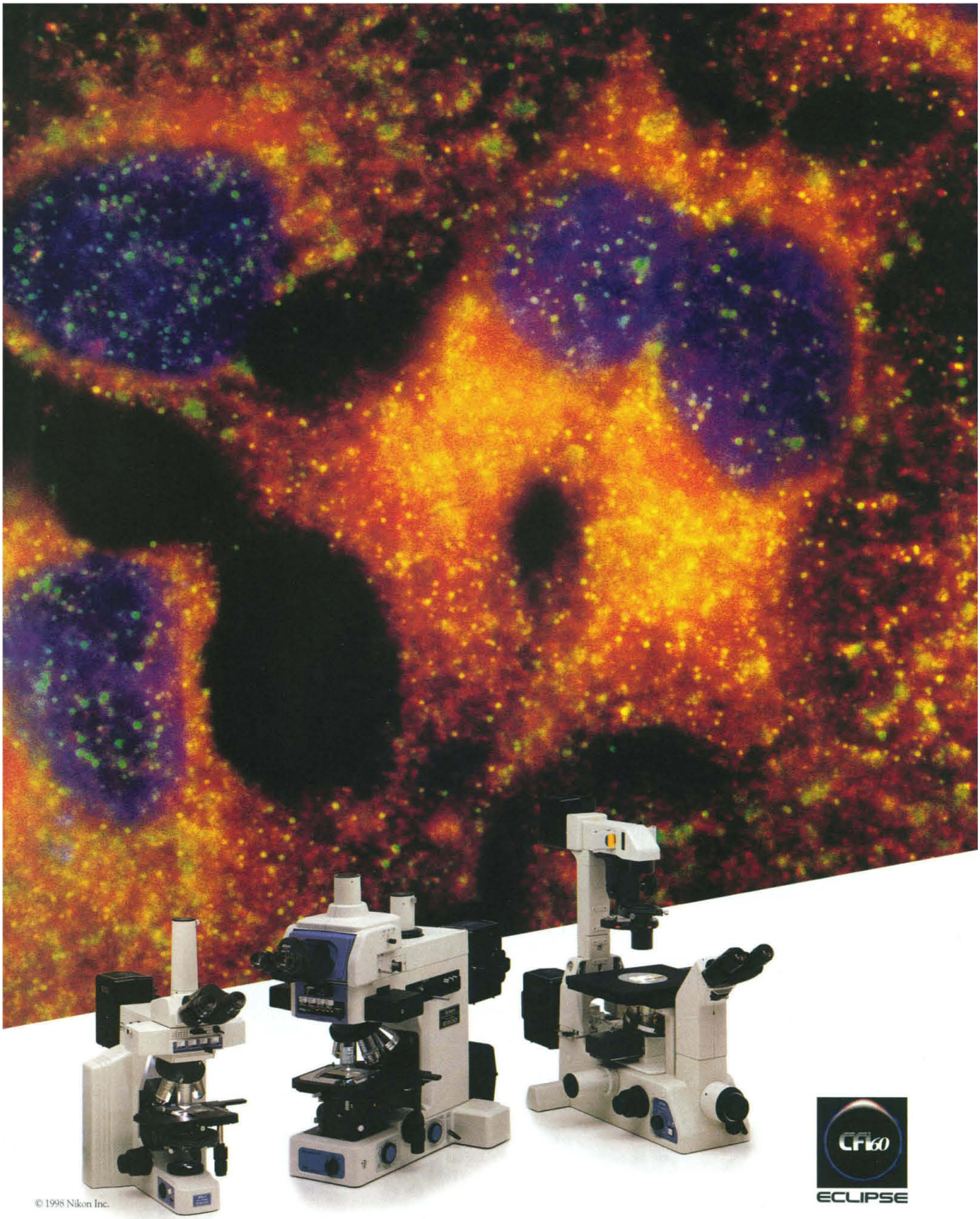
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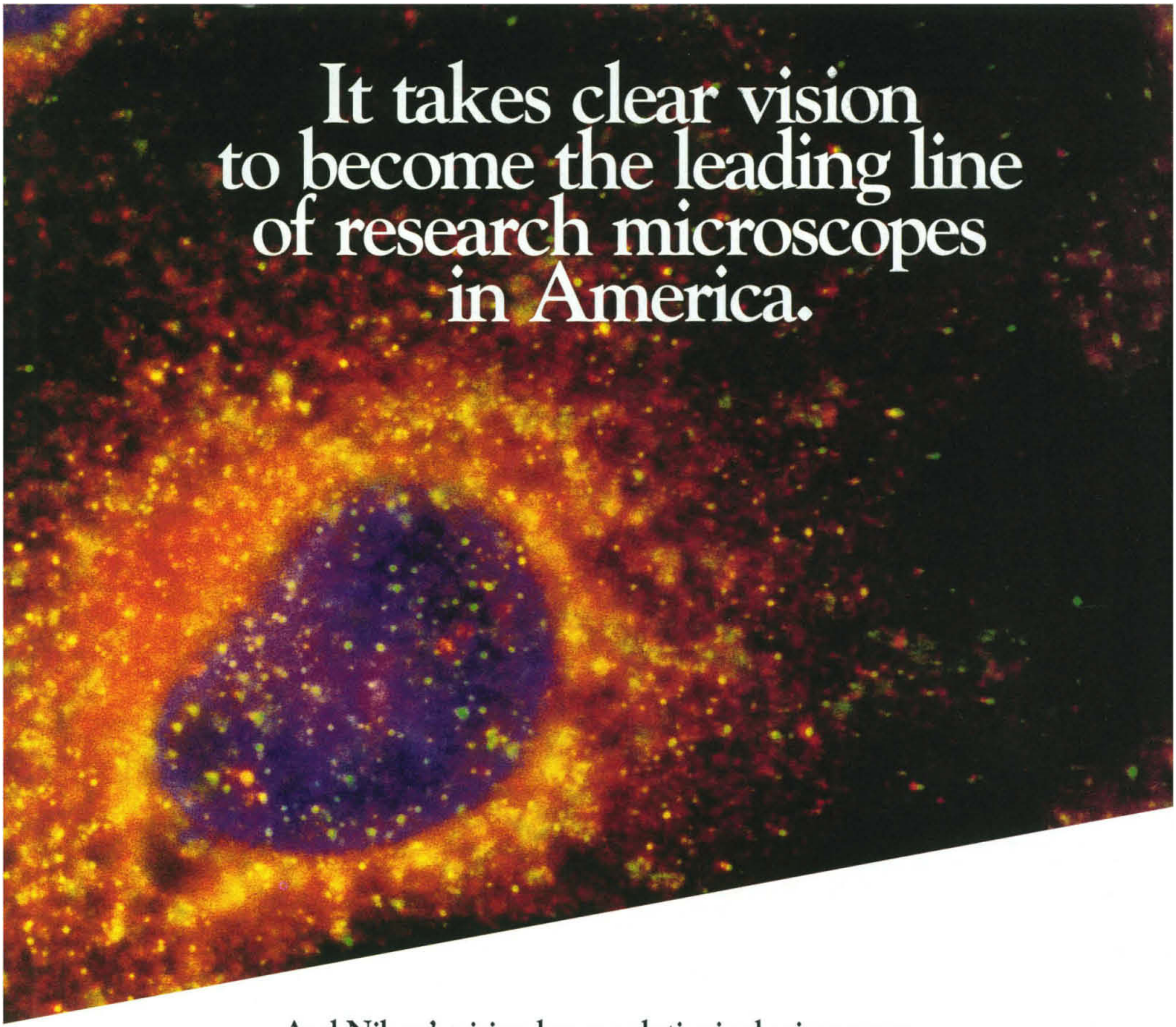
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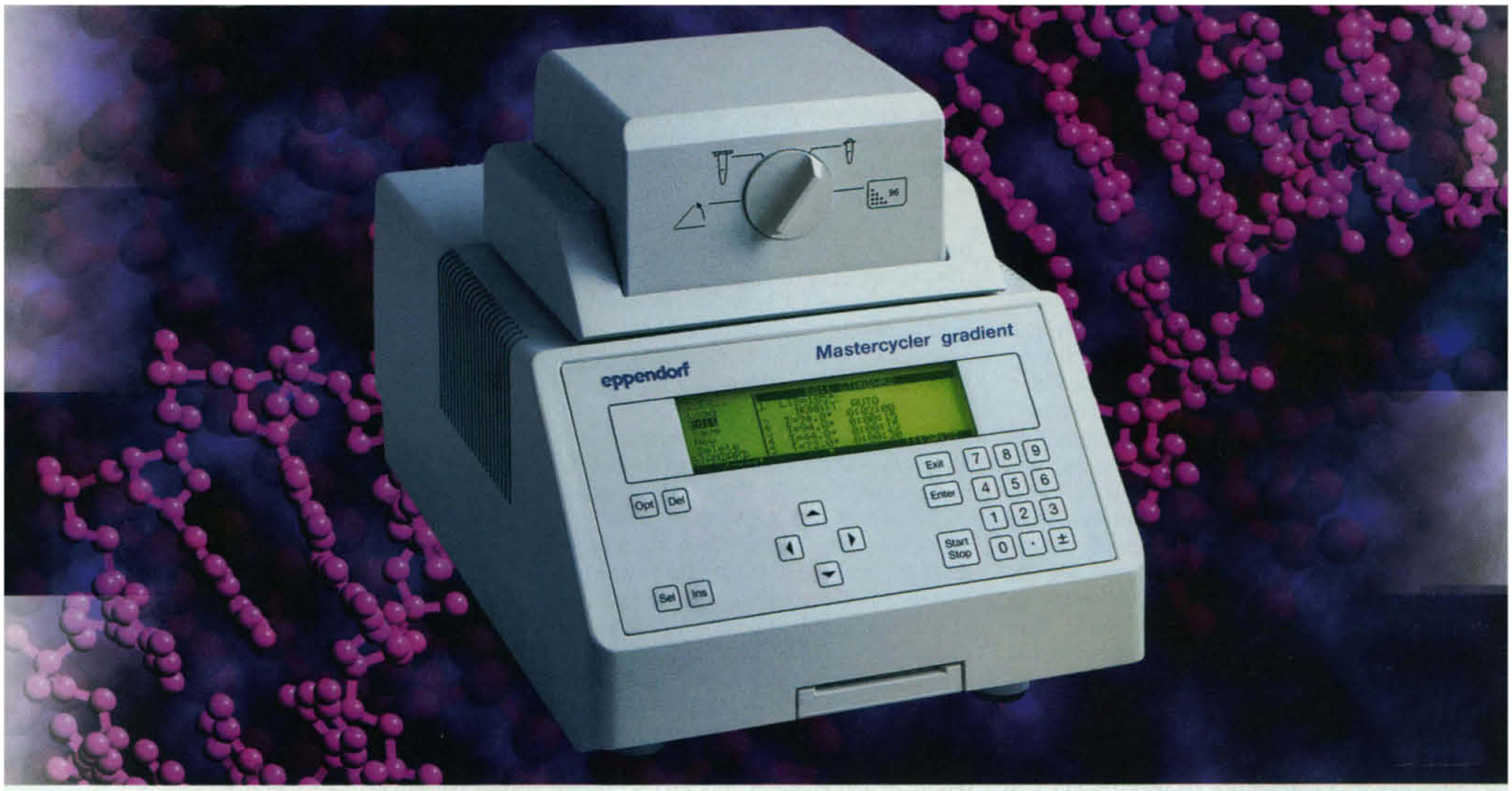

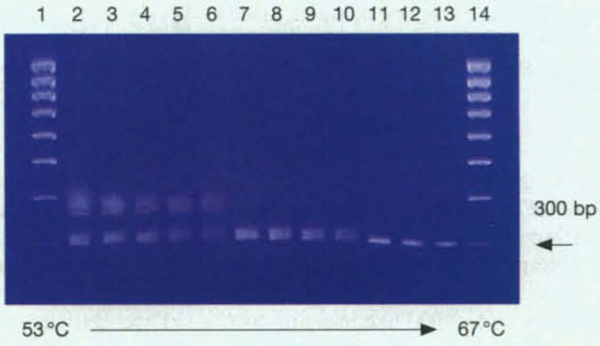

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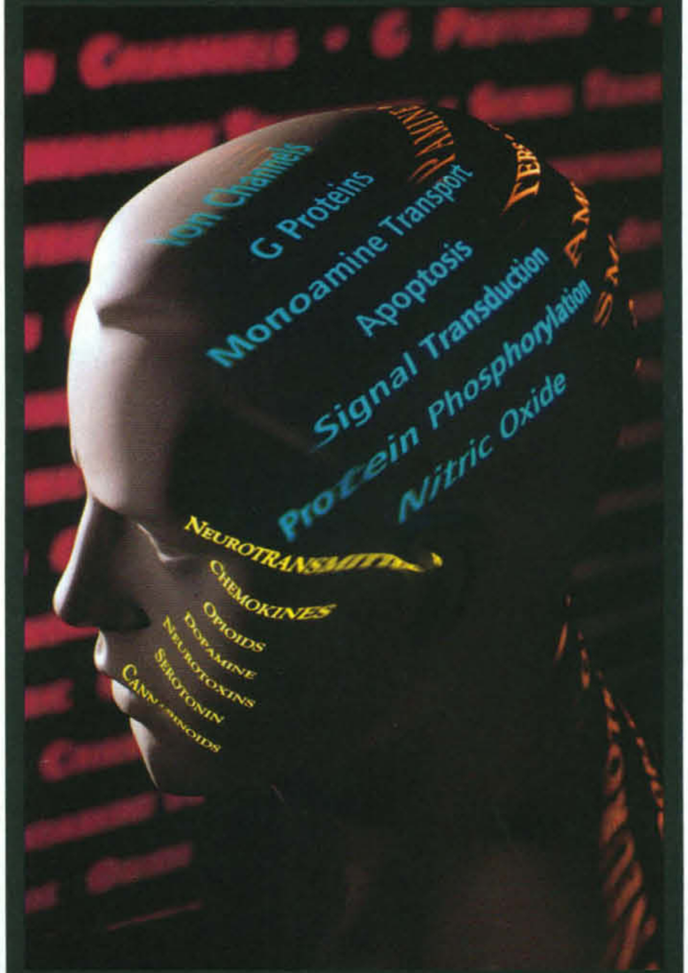

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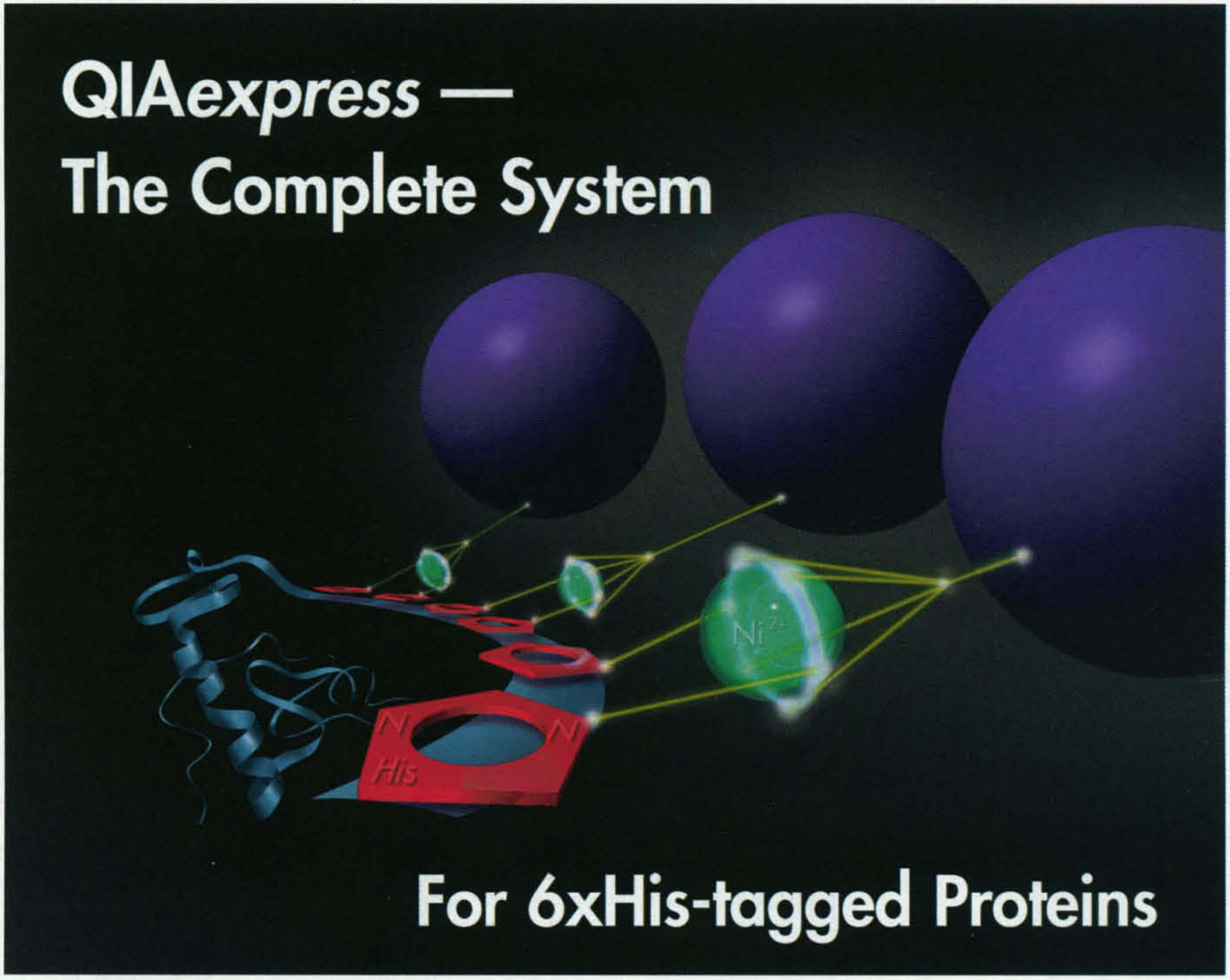
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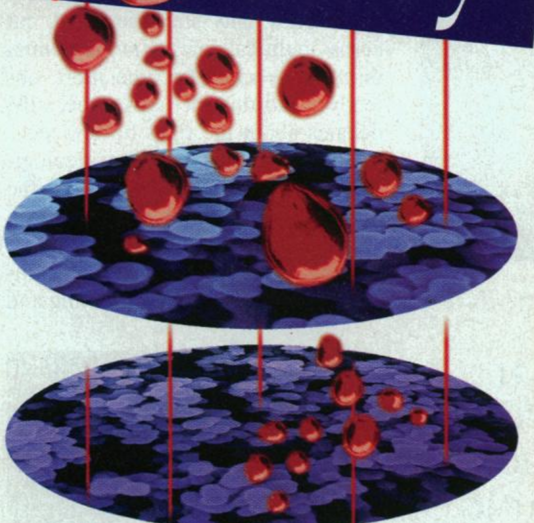

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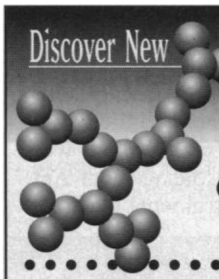

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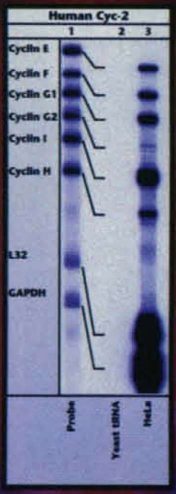

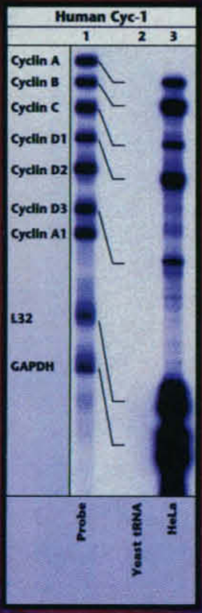

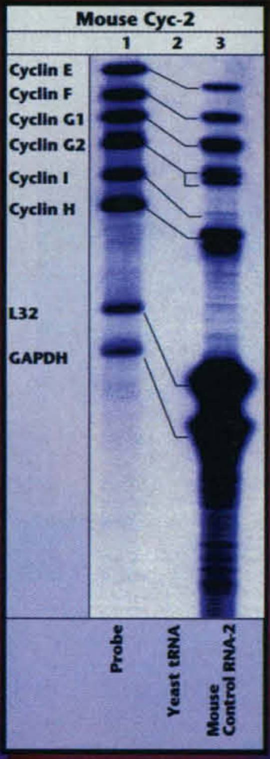

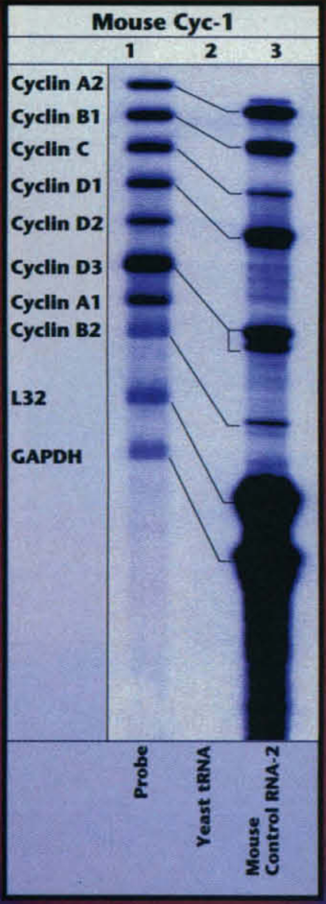

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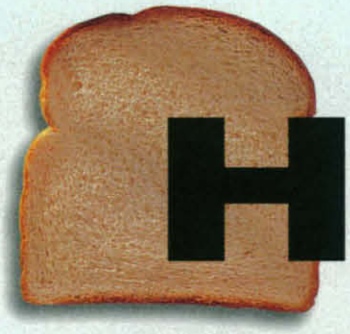

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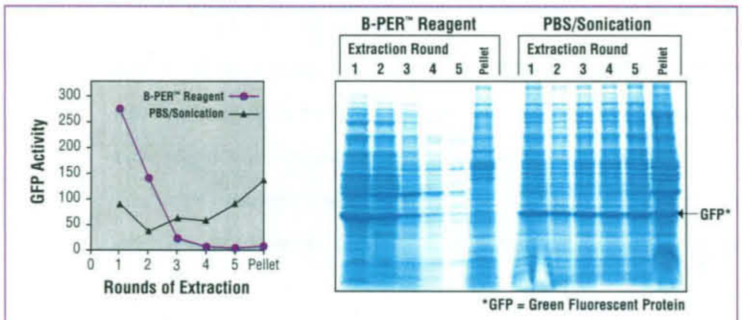

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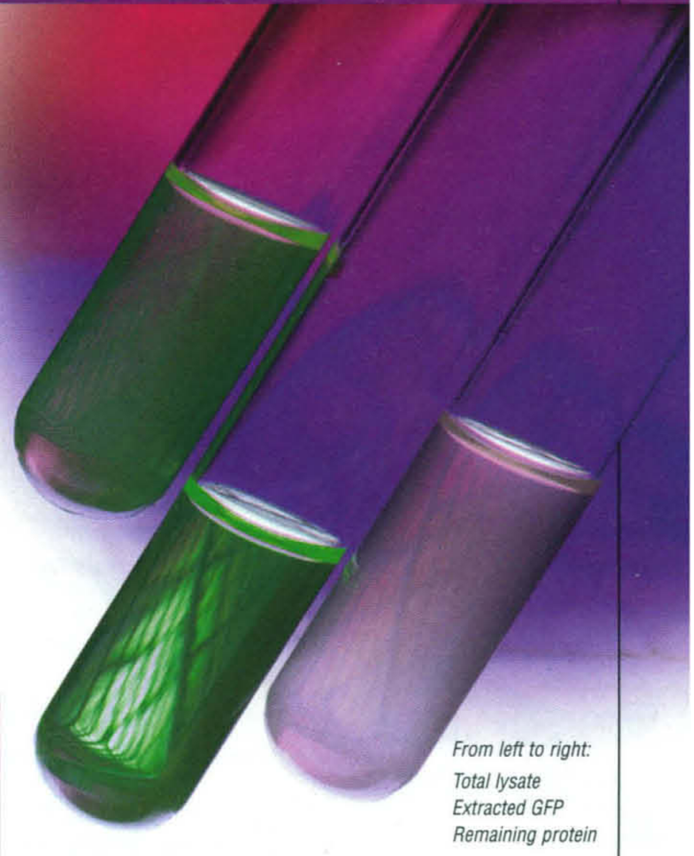

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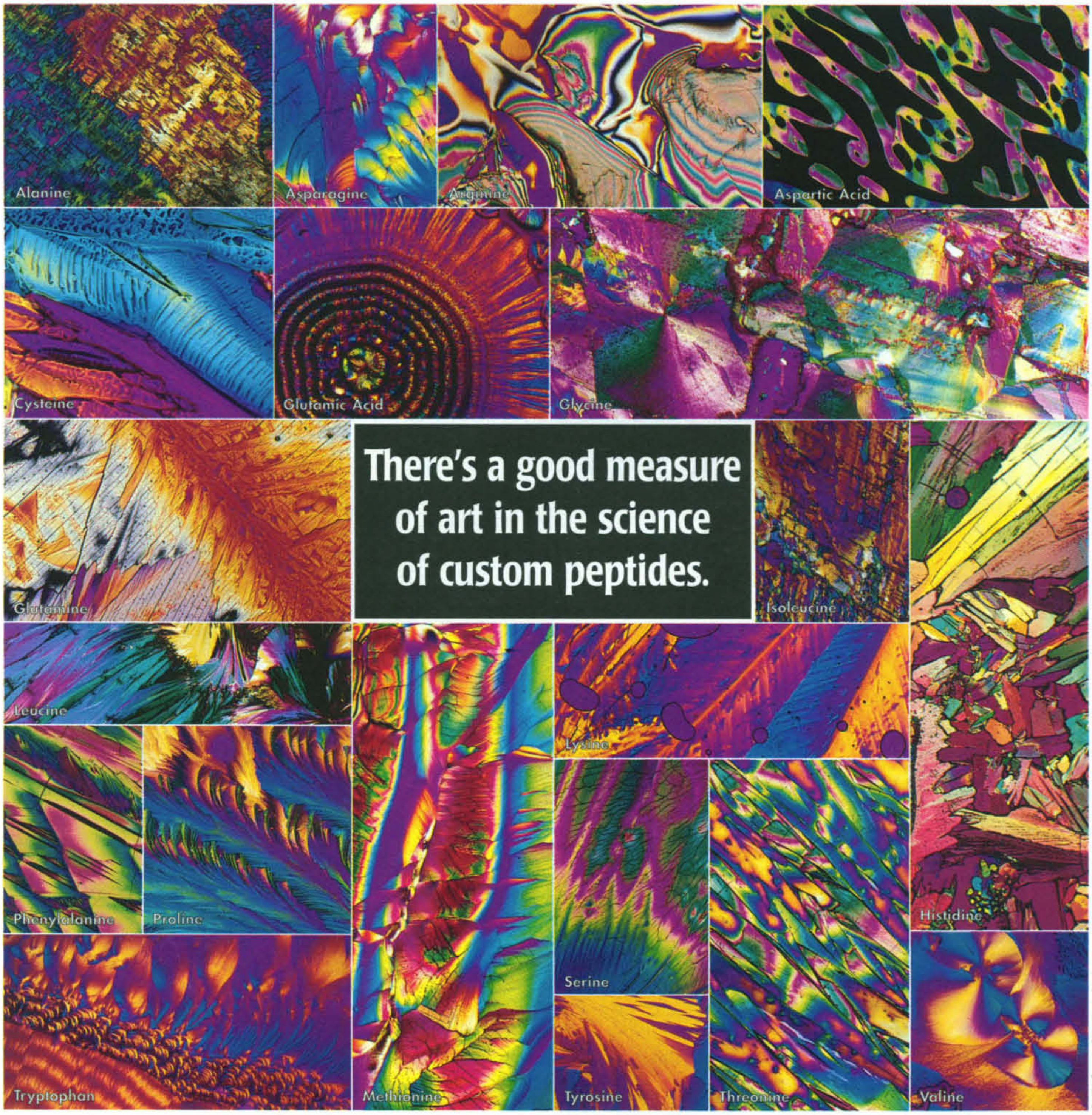
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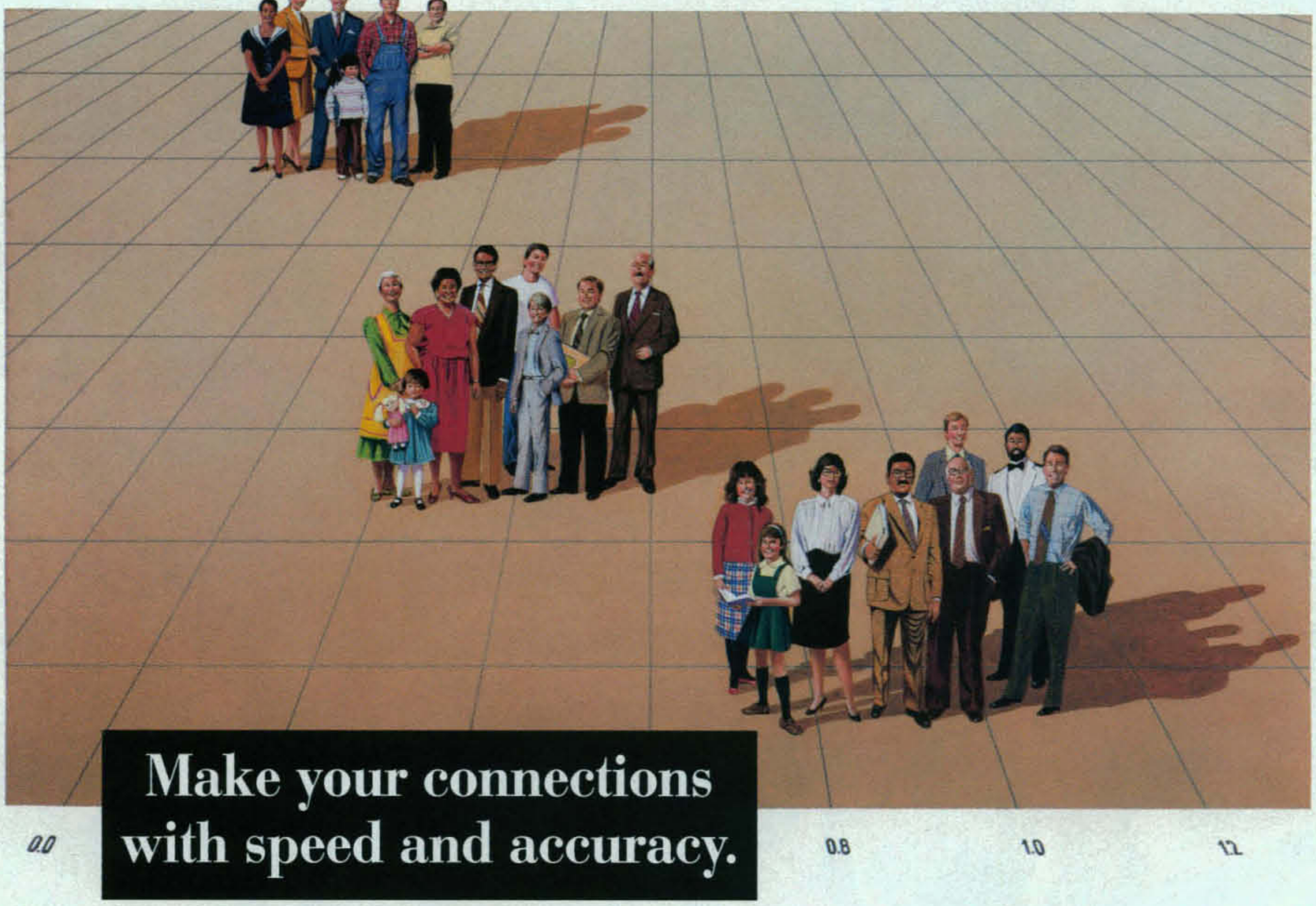
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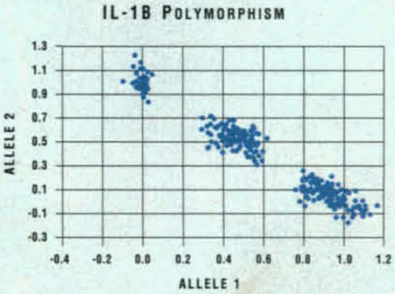
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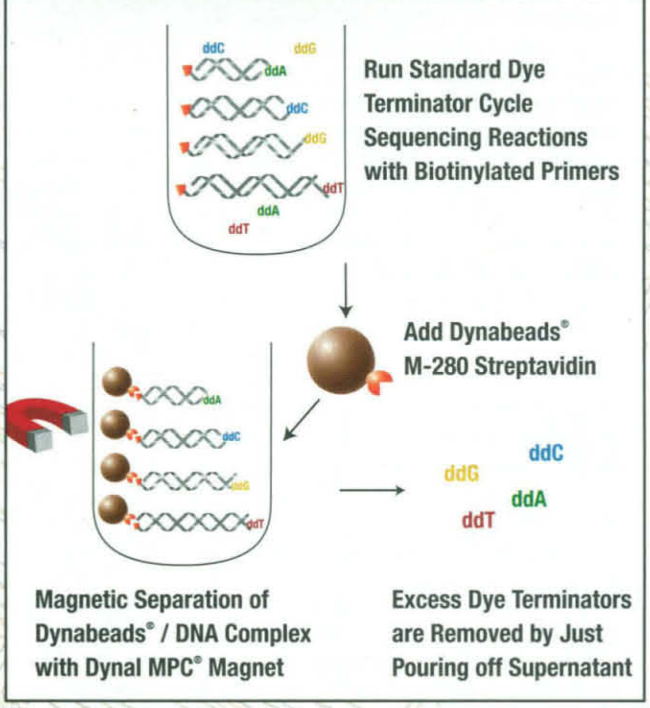
Avoid labor-intensive ethanol precipitation and costly spin column purification procedures.

Methodology



	Ethanol Precipitation	*Spin Column Purification*	*DYNAPURE*
Centrifugation	*15 - 30 min.*	*2 x 2 min.*	....
Ice Cooling	*10 min.*	....	....
Vacuum Drying	*30 min.*	*30 min.*	....
Binding, Washing and Elution	....	....	*<10 min.*
Total Time	*>60 min.*	*>30 min.*	*<10 min.*

A time comparison for cleaning up sequencing products after cycle sequencing with dye terminators.

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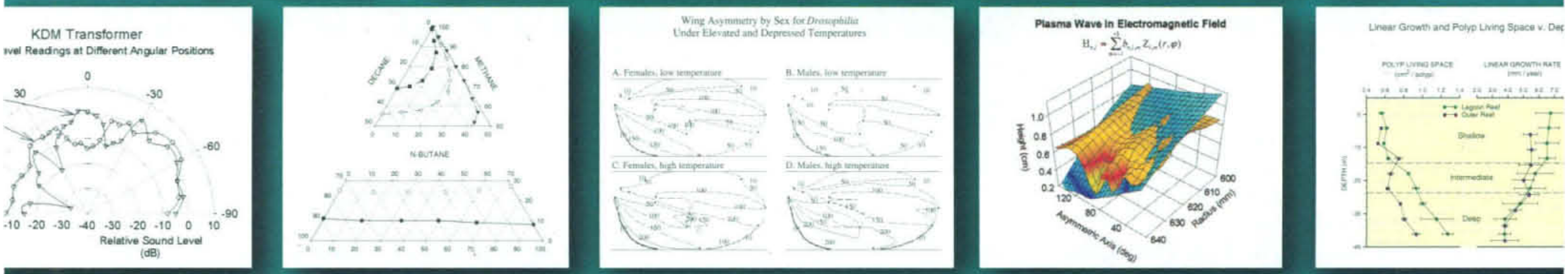

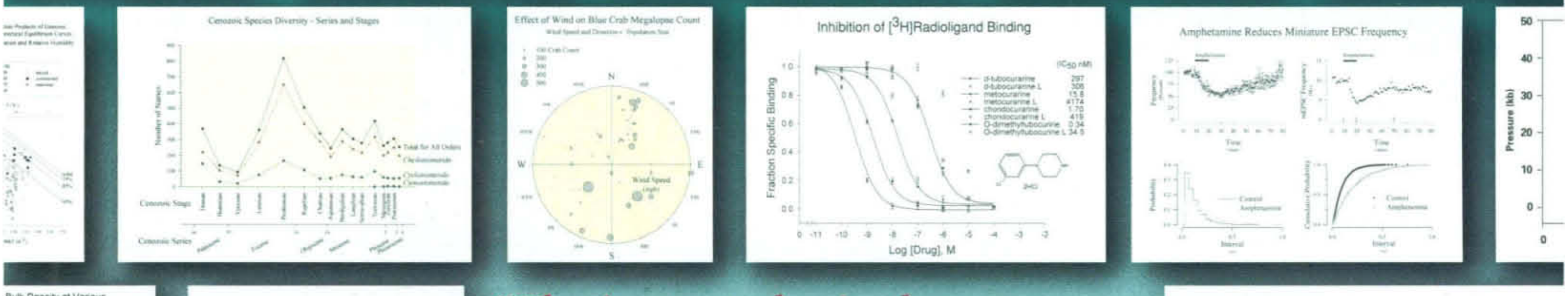

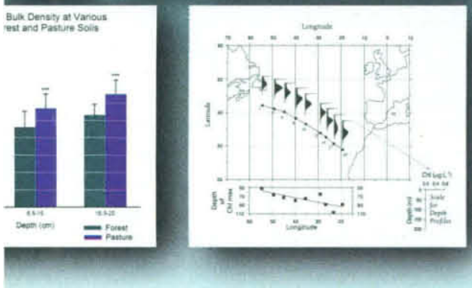

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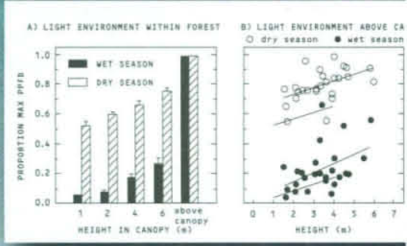

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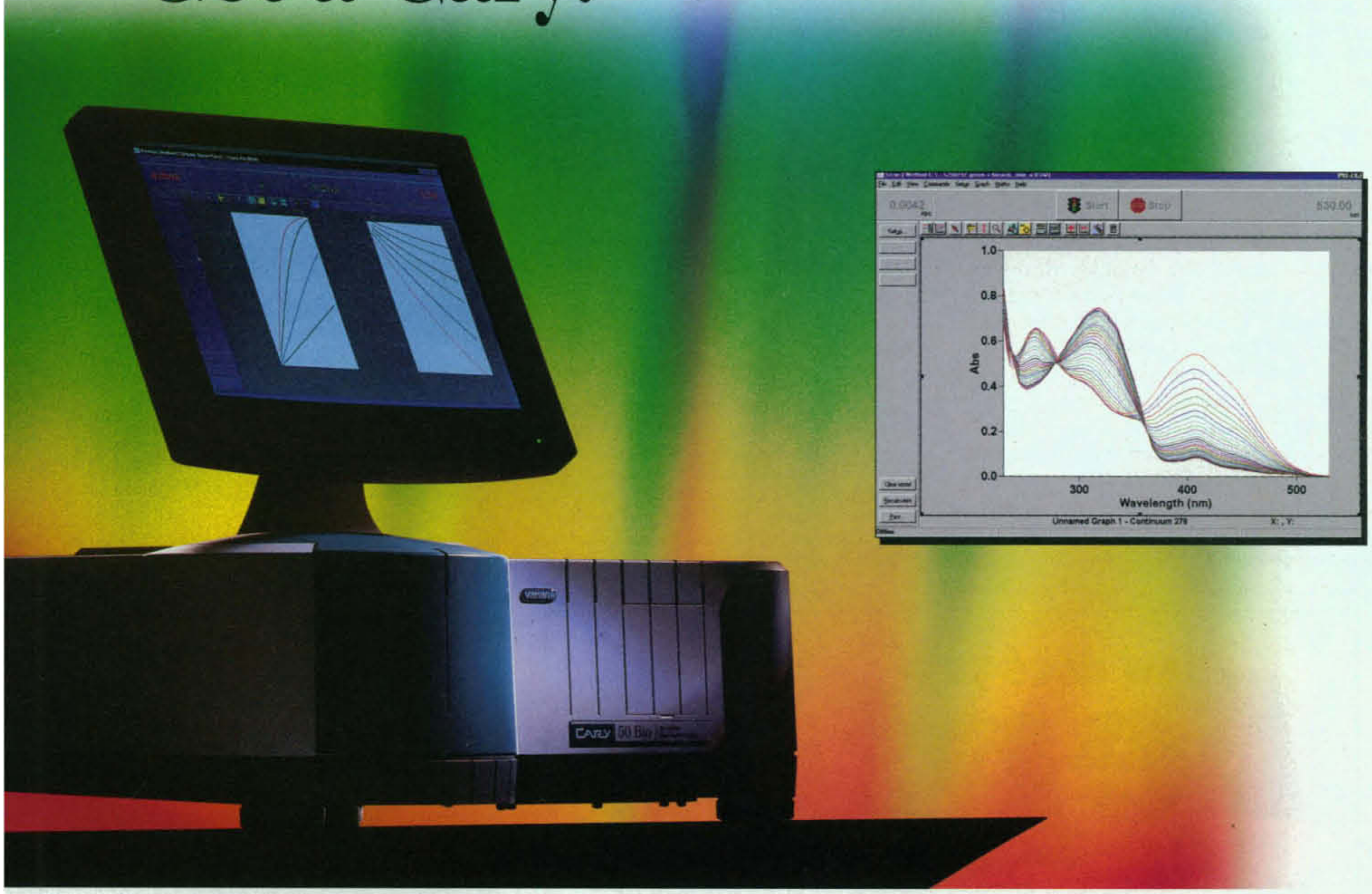

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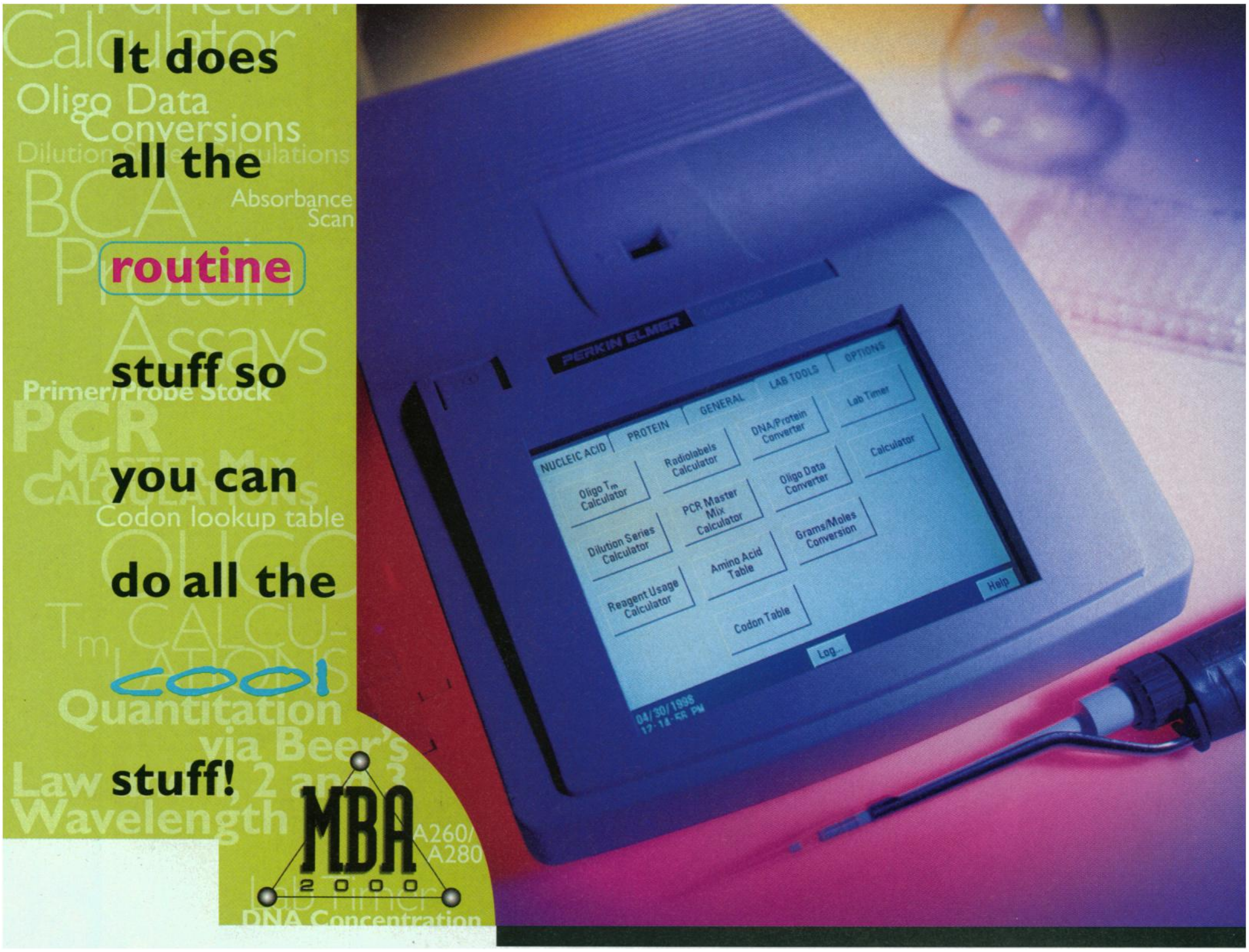
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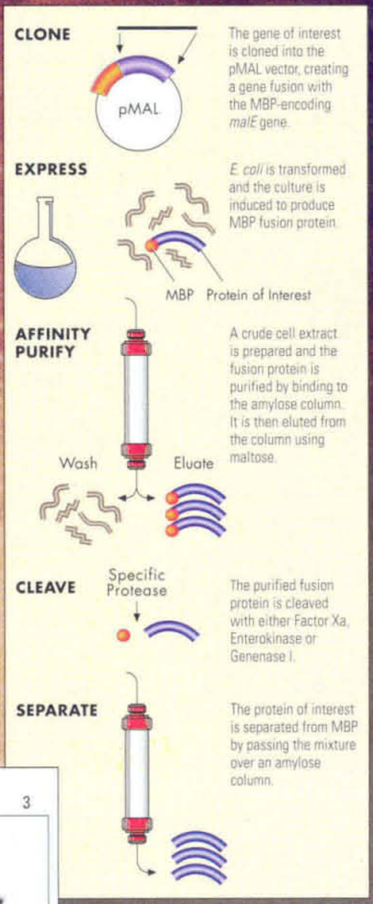


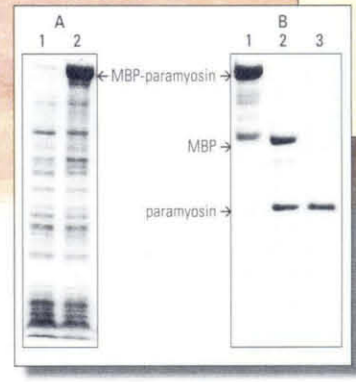
CLONE The gene of interest is cloned into the pMAL vector, creating a gene fusion with the MBP-encoding *malE* gene.

EXPRESS *E. coli* is transformed and the culture is induced to produce MBP fusion protein.

AFFINITY PURIFY A crude cell extract is prepared and the fusion protein is purified by binding to the amylose column. It is then eluted from the column using maltose.

CLEAVE The purified fusion protein is cleaved with either Factor Xa, Enterokinase or Genenase I.

SEPARATE The protein of interest is separated from MBP by passing the mixture over an amylose column.



◀ SDS-polyacrylamide gel electrophoresis of fractions from the purification of MBP-paramyosin-ΔSal. A: Lane 1: uninduced cells. Lane 2: induced cells. B: Lane 1: purified protein eluted from amylose column with maltose. Lane 2: purified protein after Factor Xa cleavage. Lane 3: paramyosin fragment eluted from second amylose column.

THE MOST FLEXIBLE SYSTEM AVAILABLE

A proven alternative to conventional methods for the expression and purification of recombinant proteins. The gene of interest is fused to the *malE* gene, which encodes maltose-binding protein (MBP), and expressed at levels constituting up to 40% of the total cell protein.

- The kit supplies reagents to clone, express and purify your target protein and yields up to 100 mg of fusion protein per liter.
- MBP fusion proteins are extremely soluble, virtually eliminating problems with insoluble protein (inclusion bodies).
- Fusion protein can be expressed in the cytoplasm or targeted for export to the periplasm to facilitate formation of disulfide bonds.
- The pMAL System is designed for Factor Xa cleavage of fusion protein. Alternative pMAL vectors allow for cleavage with Enterokinase or Genenase I.

ORDERING INFORMATION:

pMAL Protein Fusion and Purification System	**#800**

The System includes: pMAL vectors, amylose resin, Factor Xa and test substrate, anti-MBP antiserum, a marker for SDS-polyacrylamide gels, *E. coli* host and a comprehensive instruction manual. System components are also available separately.

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TP#	Identification (species match)	% similarity
TP0925	flavodoxin {C b}	61
TP0939	pyruvate oxidoRDase {S PCC}	73
TP0991	rubredoxin {C p}	76
TP0919	thioredoxin (trx) {B s}	75
TP0100	thioredoxin, put {B j}	60
Entner-Doudoroff		
TP056	4-OH-2-oxoglutarate aldolase/2-dehydro-3-deoxyP-gluconate aldolase (eda) {H i}	65
Fermentation		
TP0476	acetate Kase (ack) {M th}	66
TP0094	P AcTase (pta) {M th}	63
Glycolysis/gluconeogenesis		
TP0817	enolase (eno) {T p}	99
TP0662	fru-bisP aldolase (cbbA) {A e}	65
TP0475	glu-6-P isomerase (gpi) {B b}	67
TP0844	glyceraldehyde 3-P DHase (gap) {T b}	82
TP0505	hexoKase (hxk) {S po}	47
TP0122	phosphoenolpyruvate carboxyKase (pckA) {C l}	72
TP0538	phosphoglycerate Kase (pgk) {B b}	71
TP0168	phosphoglycerate mutase (pgm) {T p}	100
TP0108	pyroP-fru 6-P 1-PPTase (pfk) {B b}	73
TP0542	pyroP-fru 6-P 1-PPTase, beta sub {B b}	72
TP0746	pyruvate, P diKase {E vi}	56
TP0537	trioseP isomerase (tpi) {B b}	67
Pentose phosphate pathway		
TP0478	glu-6-P 1-DHase (zwf) {H i}	68
TP0477	glu-6-P 1-DHase, put {R c}	61
TP0331	phosphogluconate DHase (gnd) {H i}	72
TP0616	ribose 5-P isomerase (rpiA) {S PCC}	67
TP0945	ribulose-P 3-epimerase (cfxE) {R c}	64
TP0560	transketolase A (tktA) {B s}	66
TP0824	transketolase B (tktB) {H i}	60
Polysaccharides		
TP0413	phosphoglucomutase {B b}	57
TP0642	phosphomannomutase (manB) {B s}	62
Sugars		
TP0147	alpha-amylase 1, put {D t}	52
TP0295	carbohydrate Kase (xylB) {B b}	50
TP0418	galactoKase {H s}	49
TP0407	phosphoglycolate PPase (gph-1) {E c}	55
TP0554	phosphoglycolate PPase (gph-2) {H i}	51
Other		
TP0736	hydrogenase, gamma chain (hydG) {M j}	52
Fatty acid and phospholipid metabolism		
Biosynthesis		
TP0808	acyl carrier prt (acpP) {B b}	71
TP0256	CDP-diacylglycerol-glycerol-3-P 3-phosphatidylTase (pgsA) {B s}	60
TP0828	holo-acyl-carrier prt Sase (acpS) {B b}	59
TP0602	phosphatidate cytidylylTase (cdsA) {B b}	56
TP0671	sn-1,2-diacylglycerol cholinePPTase, put {S c}	44
Degradation		
TP0902	carboxylesterase (est) {B st}	49
TP0257	glycerophosphoryldiester phosphodiesterase (glpQ) {T p}	100
TP0952	lipase, put {S al}	45
TP0145	long-chain-fatty-acid-CoA ligase {B b}	60
TP0812	long-chain-fatty-acid-CoA ligase, auth FS {A f}	48
Other		
TP0361	lysophosphatidic acid acylTase, put {H s}	57
Purines, pyrmidines, nucleosides, and nucleotides		
2'-Deoxyribonucleotide metabolism		
TP0264	deoxyribose-P aldolase (deoC) {B s}	62
TP0885	deoxyuridine 5'-triP nucleotidohydrolase (dut) {H p}	65
TP0053	ribonucleoside-diP RDase, sub beta (nrdB) {H p}	62
TP1008	ribonucleoside-diP RDase, sub alpha (nrdA) {H p}	63
TP0814	thioredoxin RDase (trxB) {B s}	65
Nucleotide and nucleoside interconversions		
TP0595	adenylate Kase (adk) {B s}	66
TP0342	cytidylate Kase (cmk) {B b}	63
TP0354	thymidylate Kase (tmk) {M j}	57
TP0099	uridylate Kase (smbA) {B b}	66
TP1010	nucleoside-diP Kase (ndk) {A f}	72
TP0104	5'-nucleotidase (ushA) {H i}	70
Purine ribonucelotide biosynthesis		
TP0294	phosphoribosyl pyroP Sase (prs) {B b}	66
TP0695	phosphoribosylglycinamide formylTase, put {B s}	46
Pyrimidine ribonucelotide biosynthesis		
TP0305	CTP Sase (pyrG) {S PCC}	72
Salvage of nucleosides and nucleotides		
TP0045	adenosine deaminase, put {S c}	55
TP1039	adenine phosphoribosylTase (apt) {H i}	63
TP0274	deoxycytidylate deaminase, put {A f}	61
TP0170	pfs prt (pfs) {T p}	99
TP0734	purine nucleoside phosphorylase (deoD) {B st}	79
TP0448	uracil phosphoribosylTase, put {B s}	58
TP0667	uridine Kase (udk) {B b}	55
TP1027	uridine phosphorylase (udp) {E c}	58
Regulatory functions		
TP0485	adenylate cyclase {A sp}	67
TP0220	anti-sigma F factor antagonist (spoIIAA-1) {B l}	62
TP0540	anti-sigma F factor antagonist (spoIIAA-2) {B s}	58
TP0233	anti-sigma F factor antagonist, put {B l}	54
TP0657	carbon storage regulator (csrA) {B s}	74
TP0262	catabolite gene activator (crp) {E c}	43
TP0261	catabolite gene activator, put {S PCC}	53
TP0167	cation-activated repressor prt (troR) {T p}	100
TP0995	cyclic nucleotide BP {S PCC}	57
TP0089	cyclic nucleotide BP {P te}	51
TP0980	histidine phosphoKase/phophatase (ntrB) {M l}	55
TP0591	HPr Kase (ptsK) {B s}	67
TP0953	pheromone shutdown prt (traB) {B b}	60
TP0589	phosphocarrier prt HPr (ptsH) {B s} _	65
TP0575	Penolpyruvate-prt PPTase (ptsI), auth FS {B st}	57
TP0085	PTS sys, N2 regulatory IIA component (ptsN-1) {P p}	55
TP0755	PTS sys, N2 regulatory IIA component (ptsN-2) {E c}	50
TP0633	pilin repressor (pilB) {M g}	73
TP0038	regulatory prt (pfoS/R) {T p}	100
TP0519	response regulatory prt (atoC) {B b}	75
TP0520	sensory transduction histidine Kase, auth FS {B b}	61
TP0981	sensory transduction histidine Kase, put {S PCC}	52
TP0219	sigma factor SigG regulation prt, put {B s}	51
TP0218	sigma factor SigB regulation prt, put {S a}	50
DNA metabolism		
Degradation of DNA		
TP0898	ATP-dependent nuclease, sub A, put {B s}	48
TP0125	exodeoxyribonuclease (exoA) {M tm}	69
DNA replication, recombination, and repair		
TP0343	A/G-specific adenine glycosylase, put {H p}	63
TP0526	ATP-dependent helicase (hrpA) {B b}	70
TP0103	ATP-dependent DNA helicase, put {E c}	56
TP0001	chrom replication initiator prt (dnaA) {B b}	60
TP0810	DNA adenine MTase (dam) {T p}	100
TP0251	DNA-BP II {B s}	60
TP0005	DNA gyrase, sub A (gyrA) {B s}	68
TP1006	DNA gyrase, sub B (gyrB) {T p}	100
TP1028	DNA helicase II (uvrD) {T t}	58
TP0634	DNA ligase (lig) {T a}	51
TP0303	DNA mismatch repair prt (mutL) {B b}	53
TP0328	DNA mismatch repair prt (mutS) {B b}	63
TP0229	DNA polymerase, bacteriophage-type {A f}	64
TP0105	DNA polymerase I (polA) {T p}	99
TP0002	DNA polymerase III, sub beta (dnaN) {P p}	54
TP0669	DNA polymerase III, sub alpha (dnaE) {B s}	58
TP0643	DNA polymerase III, sub epsilon (dnaQ) {E c}	56
TP1005	DNA polymerase III, subs gamma/tau (dnaH) {B b}	67
TP0521	DNA polymerase III, subs gamma/tau, put {B s}	56
TP0492	DNA primase (dnaG) {C a}	53
TP0687	DNA recombinase (recG) {T p}	100
TP1022	DNA repair prt (sms) {B s}	61
TP0442	DNA repair prt (recN) {B s}	56
TP0380	DNA repair helicase, put {S c}	54
TP0394	DNA topoisomerase I (topA) {B s}	66
TP0514	excinuclease ABC, sub A (uvrA) {B s}	76
TP0116	excinuclease ABC, sub B (uvrB) {M tm}	74
TP0472	excinuclease ABC, sub C (uvrC) {M tm}	60
TP0627	exonuclease (sbcC) {E c}	47
TP0626	exonuclease, put {B s}	49
TP0775	endonuclease III (nth) {E c}	70
TP0044	glu inhibited division prt A (gidA) {B b}	71
TP0946	glu-inhibited division prt B (gidB) {E c}	50
TP0517	Holliday junction nuclease (ruvC) {E c}	63
TP0162	Holliday junction DNA helicase (ruvB) {H i}	76
TP0543	Holliday junction DNA helicase (ruvA) {H i}	56
TP0391	integrase/recombinase (codV) {B s}	68
TP0395	integrase/recombinase (xprB) {E c}	56
TP0141	methylated-DNA-prt-cysteine S-MTase (dat) {B s}	57
TP0230	primosomal prt N (priA) {B b}	57
TP0692	recA prt (recA) {B b}	83
TP0003	recF prt (recF) {S PCC}	52
TP1023	recX prt (recX) {P f}	47
TP1004	recombination prt (recR) {H i}	64
TP0102	rep helicase, ss DNA-dependent ATPase (rep) {B b}	66
TP0058	replicative DNA helicase (dnaB) {B s}	64
TP0062	single-strand DNA BP (ssb) {B b}	68
TP0704	ss-DNA-specific exonuclease (recJ) {B b}	49
TP0344	transcription-repair coupling factor (trcF) {B b}	63
Transcription		
Degradation of DNA		
TP0805	exoribonuclease II (rnb) {S PCC}	48
TP0886	polyribonucleotide nucleotidylTase (pnp) {B b}	74
TP0353	ribonuclease H (rnhA) {E c}	65
TP0809	ribonuclease III (rnc) {B b}	62
DNA-dependent RNA polymerase		
TP0701	DNA-directed RNA polymerase, put {E c}	52
TP0709	RNA polymerase sigma-28 factor {S co}	72
TP1012	RNA polymerase sigma-43 factor (sigA) {T m}	64
TP0092	RNA polymerase sigma-24 factor (rpoE) {M l}	48
TP0493	RNA polymerase sigma-70 factor (rpoD) {B b}	68
TP0111	RNA polymerase sigma-54 factor (rpoN) {A e}	52
TP0242	DNA-directed RNA polymerase, beta' sub {B b}	80
TP0241	DNA-directed RNA polymerase, beta sub (rpoB) {B b}	77
TP0212	DNA-directed RNA polymerase, alpha sub (rpoA) {B b}	63
RNA processing		
TP0596	polynucleotide adenylylTase (pcnB) {E c}	61
TP0270	polynucleotide adenylylTase (pcnA) {B b}	59
Transcription factors		
TP0082	formate hydrogenlyase transcriptional activator (fhlA) {E c}	62
TP0892	N utilization substance prt A (nusA) {B b}	64
TP1015	N utilization substance prt B (nusB) {B s}	58
TP0236	transcription antitermination prt (nusG) {B b}	67
TP0018	transcription elongation factor {B b}	58
TP0019	transcription elongation factor (greA) {B b}	61
TP0511	transcription factor (carD) {B s}	52
TP0254	transcription termination factor Rho (rho) {B b}	83
Other		
TP0924	tex prt (tex) {B p}	61
Translation		
Amino acyl tRNA synthetases		
TP1017	alanyl-tRNA Sase (alaS) {B b}	73
TP0831	arginyl-tRNA Sase (argS) {B b}}	68
TP0609	asparaginyl-tRNA Sase (asnS) {S PCC}	71
TP0985	aspartyl-tRNA Sase (aspS) {B b}	71
TP0091	cysteinyl-tRNA Sase (cysS) {B b}	63
TP0672	glycyl-tRNA Sase (glyS) {B b}	74
TP0673	glutamyl-tRNA Sase (gltX) {B b}	70
TP0641	histidyl-tRNA Sase (hisS) {B b}	61
TP0452	isoleucyl-tRNA Sase (ileS) {B b}	70
TP0586	leucyl-tRNA Sase (leuS) {B b}	71
TP0644	lysyl-tRNA Sase (lysS-1) {B b}	71
TP1040	lysyl-tRNA Sase (lysS-2) {E c}	56
TP0798	methionyl-tRNA Sase (metG) {B b}	69
TP0015	phenylalanyl-tRNA Sase beta sub (pheT) {B b}	63
TP0973	phenylalanyl-tRNA Sase alpha sub (pheS) {B b}	69
TP0160	prolyl-tRNA Sase (proS) {E c}	63
TP0647	seryl-tRNA Sase (serS) {B b}	75
TP0837	threonyl-tRNA Sase (thrS) {H i}	67
TP0632	tryptophanyl-tRNA Sase (trsA) {B b}	76

TP#	Identification (species match)	% similarity
TP0834	tyrosyl-tRNA Sase (tyrS) {B b}	68
TP1035	valyl-tRNA Sase (valS) {B b}}	67
	Degradation of proteins, peptides and glycopeptides	
TP0112	aminopeptidase C (pepC) {S s}	64
TP0569	aminopeptidase P {H s}	56
TP0549	ATPase (clpC) {B s}	65
TP0016	ATP-dependent protease LA (lon-1) {H i}	54
TP0524	ATP-dependent protease LA (lon-2) {B b}	69
TP0801	ATP-dependent Clp protease sub A (clpA) {E c}	70
TP0071	ATP-dependent Clp protease sub B (clpB) {C g}	76
TP1041	ATP-dependent Clp protease proteolytic component (clpP-2) {B b}	78
TP0507	ATP-dependent Clp protease proteolytic component (clpP-1) {H i}	83
TP0508	ATP-dependent Clp protease sub X (clpX) {E c}	76
TP0277	carboxyl-terminal protease (ctp) {B ba}	63
TP0113	Lambda CII stability-governing prt (hflK) {T p}	99
TP0114	Lambda CII stability-governing prt (hflC) {B b}	65
TP0680	o-sialoglycoprt endopeptidase (gcp) {B b}	62
TP1026	oligoendopeptidase F, put {L l}	45
TP0773	periplasmic serine protease DO (htrA-1) {H i}	63
TP0841	periplasmic serine protease DO (htrA-2) {B b}	63
TP0546	periplasmic serine protease, put {M l}	53
TP0488	protease {T p}	99
TP0997	protease IV (sppA) {E c}	53
TP0600	zinc protease, put {H i}	54
	Protein modification	
TP0842	methionine aminopeptidase (map) {B s}	63
TP0947	peptidyl-prolyl cis-trans isomerase, cyclophilin-binding (cyp) {M t}	71
TP0349	peptidyl-prolyl cis-trans isomerase, FKBP-type (slyD) {H i}	57
TP0862	peptidyl-prolyl cis-trans isomerase, FKBP-type, 22 kD (fklB) {E c}	62
TP0757	polypeptide deformylase (def) {S PCC}	66
TP0633	prt-methionine-S-oxide RDase (msrA) {M tm}	66
	Ribosomal proteins: synthesis and modification	
TP0238	ribosomal prt L1 (rplA) {B b}	76
TP0192	ribosomal prt L2 (rplB) {B b}	75
TP0189	ribosomal prt L3 (rplC) {B b}	66
TP0190	ribosomal prt L4 (rplD) {B b}	76
TP0201	ribosomal prt L5 (rplE) {B b}	83
TP0204	ribosomal prt L6 (rplF) {B b}	69
TP0240	ribosomal prt L7/L12 (rplL) {H i}	72
TP0060	ribosomal prt L9 (rplI) {B s}	61
TP0239	ribosomal prt L10 (rplJ) {S an}	61
TP0237	ribosomal prt L11 (rplK) {T m}	80
TP1025	ribosomal prt L13 (rplM) {B b}	75
TP0199	ribosomal prt L14 (rplN) {B b}	85
TP0207	ribosomal prt L15 (rplO) {B b}	70
TP0196	ribosomal prt L16 (rplP) {S PCC}	79
TP0213	ribosomal prt L17 (rplQ) {B b}	78
TP0205	ribosomal prt L18 (rplR) {B st}	70
TP0909	ribosomal prt L19 (rplS) {B b}	81
TP0848	ribosomal prt L20 (rplT) {B b}	70
TP0745	ribosomal prt L21 (rplU) {B s}	67
TP0194	ribosomal prt L22 (rplV) {B b}	74
TP0191	ribosomal prt L23 (rplW) {T m}	61
TP0200	ribosomal prt L24 (rplX) {B s}	73
TP0743	ribosomal prt L27 (rpl27) {S PCC}	78
TP0362	ribosomal prt L28 (rpmB) {T p}	100
TP0197	ribosomal prt L29 (rpmC) {B st}	63
TP0255	ribosomal prt L31 (rpmE) {H i}	80
TP0807	ribosomal prt L32 (rpmF) {B b}	72
TP0234	ribosomal prt L33 (rpmG) {T a}	76
TP0951	ribosomal prt L34 (rpmH) {B b}	86
TP0849	ribosomal prt L35 (rpmI) {B b}	75
TP0209	ribosomal prt L36 (rpmJ-1) {C v}	86
TP0590	ribosomal prt L36 (rpmJ-2) {A l}	61
TP0279	ribosomal prt S1 (rpsA) {E c}	57
TP0606	ribosomal prt S2 (rpsB) {B b}	84
TP0195	ribosomal prt S3 (rpsC) {B s}	71
TP0306	ribosomal prt S4 {B b}	69
TP0206	ribosomal prt S5 (rpsE) {B b}	77
TP0063	ribosomal prt S6 (rpsF) {B b}	53
TP0244	ribosomal prt S7 {B b}	76
TP0203	ribosomal prt S8 (rpsH) {B b}	73
TP1024	ribosomal prt S9 (rpsI) {B st}	72
TP0188	ribosomal prt S10 (rpsJ) {B b}	88
TP0211	ribosomal prt S11 (rpsK) {B b}	87
TP0243	ribosomal prt S12 (rpsL) {L b}	91
TP0210	ribosomal prt S13 (rpsM) {B b}	82
TP0202	ribosomal prt S14 (rpsN) {B b}	79
TP0887	ribosomal prt S15 (rpsO) {B b}	71
TP0905	ribosomal prt S16 (rpsP) {B s}	74
TP0198	ribosomal prt S17 (rpsQ) {B st}	74
TP0061	ribosomal prt S18 (rpsR) {B st}	73
TP0193	ribosomal prt S19 (rpsS) {B b}	84
TP0758	ribosomal prt S21 (rpsU) {M x}	75
TP0109	rRNA methylase, put {B s}	58
	Translation factors	
TP0770	ATP-dependent RNA helicase {A f}	68
TP0510	GTP-binding memb prt (lepA) {B b}	79
TP0051	peptide chain release factor 1 (prfA) {B b}	74
TP0576	peptide chain release factor 2 (prfB) {B b}	71
TP0604	ribosome recycling factor {B s}	74
TP0450	translation elongation factor G (fusA-1) {T m}	67
TP0767	translation elongation factor G (fusA-2) {B b}	84
TP0187	translation elongation factor TU (tuf) {E c}	84
TP0525	translation elongation factor P (efp) {B b}	65
TP0605	translation elongation factor TS (tsf) {S pl}	57
TP0097	translation initiation factor 1 (infA) {B b}	91
TP0850	translation initiation factor 3 (infC) {B b}	73
TP0891	translation initiation factor 2 (infB) {B b}	71
	tRNA modification	
TP1019	glu-tRNA amidoTase, sub C (gatC) {B b}	65
TP1021	glu-tRNA amidoTase, sub B (gatB) {B b}	66
TP1020	glu-tRNA amidoTase, sub A (gatA) {A f}	68
TP0756	methionyl-tRNA formylTase (fmt) {H i}	59
TP1011	peptidyl-tRNA hydrolase (pth) {H i}	63
TP0830	pseudouridylate Sase (hisT) {B b}	57
TP0889	tRNA pseudouridine 55 Sase (truB) {B b}	60
TP0908	tRNA (guanine-N1)-MTase (trmD) {B b}	75
TP0637	tRNA delta(2)-isopentenylPP Tase (miaA) {B s}	54
	Other	
TP0890	ribosome-binding factor A (rbfA) {B s}	62

Transport and binding proteins

TP#	Identification (species match)	% similarity
	Unknown substrate	
TP0964	ABC transporter, ATP-BP {B s}	72
TP0581	ABC transporter, ATP-BP {B b}	72
TP0838	ABC transporter, ATP-BP {B b}	75
TP0035	ABC transporter, ATP-BP {S PCC}	61
TP0611	ABC transporter, ATP-BP {S PCC}	69
TP0881	ABC transporter, ATP-BP (natA) {B s}	62
TP0786	ABC transporter, ATP-BP, put {E c}	76
TP0034	ABC transporter, periplasmic BP {P a}	55
TP0036	ABC transporter, permease prt {S g}	55
TP0023	Na+- and Cl— dependent transporter {M j}	53
	Amino acids, peptides, and amines	
TP0120	AA ABC transporter, ATP-BP (abc) {H p}	70
TP0265	AA ABC transporter, permease prt (braC) {B s}	54
TP0119	AA ABC transporter, permease prt (yaeE) {H p}	73
TP0309	AA ABC transporter, periplasmic BP {B s}	47
TP0308	AA ABC transporter, periplasmic BP (hisJ) {S ch}	48
TP0106	carnitine transporter, put {E c}	51
TP0414	D-alanine glycine permease (dagA) {H i}	64
TP0934	glutamate transporter, put {B b}	45
TP0555	glutamate/ aspartate transporter, put {M m}	51
TP0585	OP ABC transporter, periplasmic BP (oppA) {B s}	50
TP0998	Na+/proton-dependent alanine transporter {H i}	69
TP0653	SP ABC transporter, permease prt (potB) {A f}	58
TP0654	SP ABC transporter, permease prt (potC) {H i}	68
TP0652	SP ABC transporter, ATP-BP (potA) {A f}	66
TP0655	SP ABC transporter, periplasmic BP (potD) {E c}	52
	Carhohydrates, organic alcohols, acids	
TP0958	dicarboxylate transporter (dctM) {R c}	57
TP0685	MG ABC transporter, ATP BP (mglA) {T p}	100
TP0686	MG ABC transporter, permease prt (mglC) {T p}	100
TP0684	MG ABC transporter, periplasmic galactose-BP (mglB-2) {T p}	100
TP0545	MG ABC transporter, periplasmic galactose-BP (mglB-1) { C f}	57
TP0804	sugar ABC transporter, ATP-BP (ugpC) {E c}	70
TP0075	sugar ABC transporter, permease prt (y4oQ) {R sp}	60
TP0076	sugar ABC transporter, permease prt (y4oR) {R sp}	60
TP0074	sugar ABC transporter, periplasmic BP (y4oP) {R sp.}	44
TP0737	sugar ABC transporter, periplasmic BP (msmE) {B s}	43
TP0321	RG ABC transporter, ATP-BP (rbsA-2) {B b}	67
TP0300	RG ABC transporter, ATP-BP (rbsA-1) {A f}	54
TP0322	RG ABC transporter, permease prt (rbsC-1) {B b}	52
TP0323	RG ABC transporter, permease prt (rbsC-2) {B b}	55
	Cations	
TP0163	ABC transporter, periplasmic BP (troA) {T p}	100
TP0164	ABC transporter, ATP-BP (troB) {T p}	100
TP0165	ABC transporter, permease prt (troC) {T p}	100
TP0166	ABC transporter, permease prt (troD) {T p}	99
TP1038	bacterioferrin (TpF1) {T p}	100
TP1036	cation-transporting ATPase, P-type {A f}	60
TP0227	cobalt ABC transporter, ATP-BP {M j}	59
TP0513	K+ transport prt (trkA) {E c}	46
TP0140	K+ transport prt (ntpJ) {B s}	64
TP0917	Mg2+ transport prt (mgtE) {B b}	69
TP0774	Mg2+ transport prt (mgtC) {S PCC}	68
TP0056	oxaloacetate DCase, sub alpha (oadA) {K p}	67
TP0057	oxaloacetate DCase, sub beta (oadB) {S ch}	79
	Other	
TP0790	antibiotic transport prt, put {M l}	47
TP0146	chromate resistance prt A, auth FS {M j}	54
TP0142	thiamine ABC transporter, ATP-BP, put {H i}	62
TP0143	thiamine ABC transporter, permease prt, put {N g}	48
TP0144	thiamine ABC transporter, thiamine-binding periplasmic prt, put {E c}	50

Other categories

TP#	Identification (species match)	% similarity
	Adaptations and atypical conditions	
TP0372	general stress prt (ctc) {B s}	49
TP0272	SpoOJ regulator (soj) {B s}	72
TP0419	survival prt, put {S me}	55
TP0516	virulence factor (mviN) {H i}	57
	Other	
TP0835	ankyrin, put {H s}	46
TP0614	N2 fixation prt (nifS-1) {B s}	60
TP0615	N2 fixation prt (nifU) {M l}	53
TP0152	N2 fixation prt (rnfC) {R c}	44
TP0863	N2 fixation prt (nifS-2) {R s}	58
TP0551	PPase {T d}	56
	Unknown	
TP0712	ATP-BP (ylxH-1) {T p}	100
TP0853	ATP-BP (ylxH-2) {B b}	67
TP0779	dedA prt (dedA) {H i}	50
TP0096	dnaK suppressor, put {B b}	56
TP0446	gcpE prt (gcpE) {B s}	59
TP0225	leucine-rich repeat prt TpLRR {T p}	100
TP0778	mazG prt (mazG) {E c}	55
TP0880	memb spanning prt, put {B b}	58
TP0393	smf prt (smf) {B b}	54
TP0689	GTP-BP {T p}	100
TP0356	RNA-BP, put {A th}	64
TP0184	small prt (smpB) {S PCC}	70
TP0948	spoIIIJ-associated prt (jag) {B b}	63
TP0009	tpr prt A (tprA), auth FS {T p}	61
TP0011	tpr prt B (tprB) {T p}	56
TP0117	tpr prt C (tprC) {T p}	66
TP0131	tpr prt D (tprD) {T p}	66
TP0313	tpr prt E (tprE) {T p}	78
TP0316	tpr prt F (tprF), auth FS {T p}	66
TP0317	tpr prt G (tprG) {T p}	89
TP0610	tpr prt H (tprH) {T p}	63
TP0620	tpr prt I (tprI) {T p}	67
TP0621	tpr prt J (tprJ) {T p}	100
TP0897	tpr prt K (tprK) {T p}	55
TP1031	tpr prt L (tprL), FS {T p}	61
TP0729	treponemal aqueous prt (tap1) {T p}	100
TP1007	thymidylate Sase-complementing prt (thy1) {B b}	68
TP0845	P23 prt, put {P le}	58
TP0989	P26 {B b}	50
TP0020	76K prt {T p}	99
TP0006	Tp75 prt {T p}	100
TP0571	Tp70 prt {T p}	98
TP0957	Tp33 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 acetobutylicum*; 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
Amino acid biosynthesis		
Aspartate family		
TP0556	asparagine Sase (asnA) {H i}	84
TP0223	aspartate aminoTase (tpaaT) {T p}	99
Glutamate family		
TP0735	glutamate Sase (gltA) {P sp}	68
TP0351	glutamate 5-Kase (proB) {T p}	100
TP0350	glutamate-5-semialdehyde DHase (proA) {T p}	99
TP0797	1-pyrroline-5-carboxylate RDase (proC) {T p}	94
Serine family		
TP0329	serine OHMTase (glyA) {B s}	68
Biosyn of cofactors/prosthetic groups/carriers		
Biotin		
TP0357	biotin-Ac-CoA-carboxylase ligase (birA) {M t}	45
TP0228	biotin Sase, put {B sp}	62
Folic acid		
TP0340	folylpolyglutamate Sase (folC) {B s}	56
TP0694	5,10-methenyltetrahydrofolate Sase, put {H s}	42
TP0732	methylenetetrahydrofolate DHase (folD) {B s}	65
Heme and porphyrin		
TP0186	O2-ind. coproporphyrinogen III ODase, put {B s}	53
TP0052	protoporphyrinogen ODase (hemK) {H i}	53
Menaquinone and ubiquinone		
TP0683	octaprenyl-diP Sase {T p}	100
Pyridine nucleotides		
TP0780	NH(3)-dependent NAD(+) Sase (nadE) {R c}	46
Riboflavin		
TP0888	riboflavin Kase/FMN adenylylTase (ribF) {E c}	48
Thiamine		
TP0115	phosphomethypyrimidine Kase (thiD) {B s}	69
TP0445	4-methyl-5(b-OHethyl)-thiazole monoP biosyn enzyme (thiJ) {B b}	57
Cell envelope		
Lipoproteins		
TP0821	lipoprt (tpn32) {T p}	100
TP0171	lipoprt, 15 kD (tpp15) {T p}	98
TP0435	lipoprt, 17 kD (tpp17) {T p}	100
TP0319	memb lipoprt (tmpC) {T p}	99
TP0993	rare lipoprt A, put {B b}	73
Biosynthesis of murein sacculus and peptidoglycan		
TP0247	N-Acmur-L-alanine amidase (amiA) {E c}	55
TP0670	D-alanine-D-alanine ligase (ddlA) {S ch}	61
TP0681	alanine racemase (alr) {T p}	100
TP0574	CPDase, 47 kD {T p}	99
TP0221	D,D-CPDase, put {B b}	62
TP0806	femA prt, put {B b}	60
TP0861	glucosamine-fru-6-P aminoTase (glmS) {H i}	74
TP0406	glutamate racemase (murI) {E c}	54
TP0623	memb-bound lytic murein TGLase D (dniR) {E c}	52
TP0500	penicillin-BP (pbp-1) {B b}	62
TP0705	penicillin-BP (pbp-2) {B b}	65
TP0760	penicillin-BP (pbp-3) {B b}	52
TP0345	P-N-Acmur-pentapeptide-Tase (mraY) {H p}	53
TP0497	rod shape-determining prt (mreB) {B b}	85
TP0498	rod shape-determining prt (mreC) {B b}	60
TP0499	rod shape-determining prt (mreD) {E c}	51
TP0501	rod shape-determining prt (rodA) {B b}	63
TP0800	serine-type D-Ala-D-Ala CPDase (dacC) {B b}	53
TP0043	soluble lytic TGLase, put {E c}	55
TP0090	UDP-N-Acmuramate DHase (murB) {B b}	58
TP0341	UDP-N-Acmuramate-alanine ligase (murC) {B b}	60
TP0903	UDP-N-Acmuralanine-D-glutamate ligase (murD) {B b}	62
TP0029	UDP-N-Acglucosamine 1-carboxyvinylTase (murA) {B b}	71
TP0933	UDP-N-Acmuralanyl-D-glutamate-2,6-diamino -pimelate ligase (murE) {B b}	59
TP0386	UDP-N-Acmuralanyl-D-glutamyl-2,6-diamino -pimelate-D-alanyl-D-alanine ligase (murF) {S PCC}	55
TP0523	UDP-N-glucosamine-N-Acmuramyl-(pentapeptide)pyrophosphoryl-undecaprenol N-Acglucosamine Tase (murG) {B b}	61
Biosynthesis of surface polysccharides and lipopolysacchararides		
TP0566	alginate O-Acation prt (algI) {P a}	56
TP0486	antigen, p83/100 {B b}	47
TP0077	capsular polysacch biosyn prt (cap5D) {S a}	63
TP0107	licC prt (licC) {H i}	53
TP0283	lipopolysacch core biosyn prt (kdtB) {E c}	58
TP0078	spore coat polysacch biosyn prt (spsC) {B s}	61
TP0288	spore coat polysacch biosyn prt (spsF) {B s}	50
TP0562	spore coat polysacch biosyn prt (spsE) {B s}	50
TP0440	spore coat polysacch biosyn prt, put {S PCC}	48
TP0275	UDP-N-Ac-D-mannosamine Tase, put {P a}	46
Surface structures		
TP0943	flgr prt (fliS) {B s}	61
TP0722	flgr prt (fliL) {T p}	100
TP0726	flgr prt (flbD) {T p}	100
TP0378	flgr prt, put {T p}	52
TP0403	flgr prt, put {T d}	49
TP0727	flgr hook prt (flgE) {T p}	100
TP0401	flgr assembly prt (fliH) {T d}	70
TP0714	flgr biosyn prt (flhA) {T p}	100
TP0715	flgr biosynthetic prt (flhB) {T p}	99
TP0716	flgr biosynthetic prt (fliR) {T p}	100
TP0717	flgr biosynthetic prt (fliQ) {T p}	100
TP0718	flgr biosynthetic prt (fliP) {T p}	100
TP0720	flgr motor switch prt (fliY) {T p}	100
TP0721	flgr motor switch prt (fliM) {T p}	100
TP0748	cytoplasmic filament prt A (cfpA) {T p}	100
TP0402	flgm-specific ATP Sase (fliI) {T d}	75
TP0724	flgr motor rotation prt (motB) {T p}	100
TP0725	flgr motor rotation prt (motA) {T p}	100
TP0872	flgr filament cap prt (fliD) {B b}	55
TP0026	flgr motor switch prt (fliG-1) {T d}	52
TP0396	flgr basal-body rod prt (flgB) {T d}	80
TP0397	flgr basal-body rod prt (flgC) {T d}	82
TP0400	flgr motor switch prt (fliG-2) {T d}	94
TP0399	flgr basal-body M ring prt (fliF) {T d}	79
TP0960	flgr basal-body rod prt (flgG-1) {B b}	80
TP0961	flgr basal-body rod prt (flgG-2) {B b}	71
TP0659	flgr hook-associated prt 3 (flgL) {B b}	57
TP0660	flgr hook-associated prt 1 (flgK) {B b}	67
TP0792	flgr filament 33 kD core prt (flaB2) {T p}	100
TP0870	flgr filament 31 kD core prt (flaB3) {T p}	100
TP0249	flgr filament outer layer prt (flaA-1) {T p}	100
TP0664	flgr filament outer layer prt (flaA-2) {T p}	98
TP0713	flgr-associated GTP-BP (flhF) {T p}	100
TP0868	flgr filament 34.5 kD core prt (flaB1) {T p}	100
TP0398	flgr hook-basal body complex prt (fliE) {T d}	76
TP0728	flgr hook assembly scaffolding prt (flgD) {T p}	100
Other		
TP1016	basic memb prt (tpn39b) {T p}	100
TP0327	cationic outer memb prt (ompH) {Y e}	46
TP0298	exported prt (tpn38b) {T p}	100
TP0971	memb antigen, pathogen-specific (tpd) {T p}	100
TP0965	memb fusion prt, put {H i}	44
TP0949	memb prt {B b}	63
TP0768	memb prt (tmpA) {T p}	100
TP0326	outer memb prt {H p}	49
TP0769	outer memb prt (tmpB) {T p}	100
TP0292	outer memb prt (tpn50) {T p}	100
TP0663	outer memb prt, put {T p}	99
TP0658	transmemb prt, put {B s}	57
Cellular processes		
Cell division		
TP0578	cell division prt (ftsY) {B s}	61
TP0765	cell division prt (ftsH) {H p}	73
TP0387	cell division prt (ftsW) {B b}	63
TP0388	cell division prt (ftsQ) {B b}	48
TP0389	cell division prt (ftsA) {B b}	64
TP0390	cell division prt (ftsZ) {B b}	75
TP0682	cell division prt (ftsJ) {B b}	58
TP0999	cell division prt, put {B b}	78
TP0330	cell division prt, put {M g}	48
TP0271	chromosome partitioning prt (parB) {C c}	61
TP0367	chromosome segregation prt, put {B s}	61
Toxin production and resistance		
TP0935	N-Acphosphinothricin-tripetide-deAcase, put {S v}	56
TP0337	dimethyladenosine Tase (ksgA) {B s}	53
TP0649	hemolysin (tlyC) {B b}	73
TP1037	hemolysin III (hlyIII) {B c}	66
TP0027	hemolysin, put {B b}	53
TP0028	hemolysin, put {S PCC}	50
TP0936	hemolysin, put {S PCC}	50
TP0688	immunity prt (mccF) {T p}	100
TP0405	mcbG prt, put {E c}	48
TP0696	nicotinamidase, put {M k}	49
TP0547	penicillin tolerance prt (lytB) {H p}	54
Chaperones		
TP1013	chaperonin (groES) {B st}	78
TP0215	grpE prt (grpE) {B b}	59
TP0030	heat shock prt (groEL) {T p}	99
TP0217	heat shock prt (dnaJ), auth FS {E c}	64
TP0216	heat shock prt 70 (dnaK) {B b}	82
TP0984	heat shock prt 90 (htpG) {B b}	72
TP0843	heat shock prt, put {M g}	59
TP0098	heat shock prt, put {L p}	60
Detoxification		
TP0509	alkyl hydroperoxide RDase (ahpC) {B s}	72
TP0550	thiophene and furan oxidation prt (thdF) {B b}	58
Protein and peptide secretion		
TP0417	apolipoprt N-acylTase (cutE) {E c}	49
TP0252	apolipoprt N-acylTase, put {H i}	48
TP0235	preprt translocase sub (secE) {T m}	66
TP0208	preprt translocase sub (secY) {B b}	71
TP0379	preprt translocase sub (secA) {B b}	72
TP0852	prolipoprt diacylglyceryl Tase (lgt) {H i}	62
TP0410	prt-export memb prt (secD) {B b}	64
TP0411	prt-export memb prt (secF) {B s}	67
TP0185	signal peptidase I (sip) {B s}	56
TP0978	signal peptidase II (lsp) {B b}	64
TP0926	signal peptidase I, put {L p}	62
TP0416	signal recognition particle prt (ffh) {B b}	69
TP0506	trigger factor (tig) {B b}	52
Transformation		
TP0336	comE prt, put {S PCC}	52
Other		
TP0363	chemotaxis histidine Kase (cheA) {T p}	99
TP0365	chemotaxis prt (cheX) {T p}	100
TP0630	chemotaxis prt MTase (cheR) {B b}	64
TP0366	chemotaxis response regulator (cheY) {T p}	100
TP0541	GTP-BP (era) {B b}	65
TP0742	GTP-BP (obg) {B b}	66
TP0040	MC prt (mcp1) {T p}	100
TP0488	MC prt (mcp2-1) {T p}	100
TP0639	MC prt (mcp2-2) {T p}	56
TP0640	MC prt (mcp2-3) {T p}	56
TP0364	purine-binding chemotaxis prt (cheW-1) {T p}	100
TP0439	purine-binding chemotaxis prt (cheW-2) {B b}	63
TP0631	prt-glutamate methylesterase (cheB) {S ch}	61
Central intermediary metabolism		
TP0080	quinoline 2-oxidoRDase {P p}	47
TP0794	SAM Sase (metK) {E c}	75
Energy metabolism		
Aerobic		
TP0921	NADH ODase {S m}	79
TP1009	glycerol-3-P DHase (gpsA) {B s}	59
TP0037	D-specific D-2-OHacid DHase {S a}	63
Anaerobic		
TP0982	glpG prt, put {E c}	51
ATP-proton motive force interconversion		
TP0426	V-type ATPase, sub A (atpA-1) {B b}	79
TP0529	V-type ATPase, sub A (atpA-2) {S ac}	69
TP0427	V-type ATPase, sub B (atpB-1) {B b}	86
TP0528	V-type ATPase, sub B (atpB-2) {M j}	74
TP0428	V-type ATPase, sub D (atpD-1) {B b}	67
TP0527	V-type ATPase, sub D (atpD-2) {M m}	54
TP0530	V-type ATPase, sub E, put {D sp}	54
TP0424	V-type ATPase, sub E, put {T t}	55
TP0531	V-type ATPase, sub F, put {M mi}	49
TP0429	V-type ATPase, sub I (atpI-1) {M j}	51
TP0533	V-type ATPase, sub I (atpI-2) {M j}	52
TP0430	V-type ATPase, sub K (atpK-1) {B b}	74
TP0532	V-type ATPase, sub K (atpK-2), auth FS {T p}	99
Electron transport		
TP0101	cytochrome c biogenesis prt (ccdA) {H p}	67
TP0823	desulfoferrodoxin (rbo) {D v}	58