

1/345

12AP1/E5 -- Viventia Biotech	AI-201 -- AutoImmune
1964 -- Aventis	AI-301 -- AutoImmune
20K growth hormone -- AMUR	AIDS vaccine -- ANRS, CIBG, Hoesel
28P6/E6 -- Viventia Biotech	Biomed, Hollis-Eden, Rome, United
3-Hydroxyphthaloyl-beta-lactoglobulin --	Biomedical, American Home Products,
4-IBB ligand gene therapy --	Maxygen
64-Cu MAb conjugate TETA-1A3 --	airway receptor ligand -- IC Innovations
Mallinckrodt Institute of Radiology	AJvW 2 -- Ajinomoto
64-Cu MAb conjugate TETA-cT84.66	AK 30 NGF -- Alkermes
64-Cu Trastuzumab TETA conjugate --	Albuferon -- Human Genome Sciences
Genentech	albumin -- Biogen, DSM Anti-Infectives,
A 200 -- Amgen	Genzyme Transgenics, PPL Therapeutics,
A10255 -- Eli Lilly	TranXenoGen, Welfide Corp.
A1PDX -- Hedral Therapeutics	aldesleukin -- Chiron
A6 -- Angstrom	alefacept -- Biogen
aaAT-III -- Genzyme	Alemtuzumab --
Abciximab -- Centocor	Allergy therapy -- ALK-Abello/Maxygen,
ABI.001 -- Atlantic BioPharmaceuticals	ALK-Abello/RP Scherer
ABT-828 -- Abbott	allergy vaccines -- Allergy Therapeutics
Accutin	Alnidofibatide -- Aventis Pasteur
Actinohivin	Alnorine -- SRC VB VECTOR
activin -- Biotech Australia, Human	ALP 242 -- Gruenenthal
Therapeutics	Alpha antitrypsin -- Arriva/Hyland
activin -- Curis	Immuno/ProMetic/Protease Sciences
AD 439 -- Tanox	Alpha-1 antitrypsin -- Cutter, Bayer, PPL
AD 519 -- Tanox	Therapeutics, Profile, ZymoGenetics,
Adalimumab -- Cambridge Antibody Tech.	Arriva
Adenocarcinoma vaccine -- Biomira -- NIS	Alpha-1 protease inhibitor -- Genzyme
Adenosine A2B receptor antagonists --	Transgenics, Welfide Corp.
Adenosine Therapeutics	Alpha-galactose fusion protein --
ADP-001 -- Axis Genetics	Immunomedics
AF 13948 -- Affymax	Alpha-galactosidase A -- Research
Afelimomab -- Knoll	Corporation Technologies
AFP-SCAN -- Immunomedics	Alpha-glucosidase -- Genzyme, Novazyme
AG 2195 -- Corixa	Alpha-lactalbumin
agalsidase alfa -- Transkaryotic Therapies	Alpha-L-iduronidase -- Transkaryotic
agalsidase beta -- Genzyme	Therapies, BioMarin
AGENT-- Antisoma	alteplase -- Genentech
AI 300 -- AutoImmune	alvircept sudotox -- NIH
AI-101 -- Teva	ALX1-11 --sNPS Pharmaceuticals
AI-102 -- Teva	Alzheimer's disease gene therapy --

FIG. 1A

2/345

AM-133 -- AMRAD	Anti-B4 MAb-DC1 conjugate -- ImmunoGen
Amb a 1 immunostim conj. -- Dynavax	Anti-B7 antibody PRIMATIZED -- IDEC
AMD 3100 -- AnorMED -- NIS	Anti-B7-1 MAb 16-10A1
AMD 3465 -- AnorMED -- NIS	Anti-B7-1 MAb 1G10
AMD 3465 -- AnorMED -- NIS	Anti-B7-2 MAb GL-1
AMD Fab -- Genentech	Anti-B7-2-gelonin immunotoxin --
Amediplase -- Menarini, Novartis	Antibacterials/antifungals --
AM-F9	Diversa/IntraBiotics
Amoebiasis vaccine	Anti-beta-amyloid monoclonal antibodies --
Amphiregulin -- Octagene	Cambridge Antibody Tech., Wyeth-Ayerst
anakinra -- Amgen	Anti-BLyS antibodies -- Cambridge
analgesic -- Nobex	Antibody Tech. /Human Genome Sciences
ancestim -- Amgen	Antibody-drug conjugates -- Seattle
AnergiX.RA -- Corixa, Organon	Genetics/Eos
Angiocidin -- InKine	Anti-C5 MAb BB5-1 -- Alexion
angiogenesis inhibitors -- ILEX	Anti-C5 MAb N19-8 -- Alexion
AngioMab -- Antisoma	Anti-C8 MAb
Angiopoietins -- Regeneron/Procter & Gamble	anticancer cytokines -- BioPulse
angiostatin -- EntreMed	anticancer matrix -- Telios Integra
Angiostatin/endostatin gene therapy --	Anticancer monoclonal antibodies -- ARIUS,
Genetix Pharmaceuticals	Immunex
angiotensin-II, topical -- Maret	anticancer peptides -- Maxygen, Micrologix
Anthrax -- EluSys Therapeutics/US Army	Anticancer prodrug Tech. -- Alexion
Medical Research Institute	Antibody Technologies
Anthrax vaccine	anticancer Troy-Bodies -- Affite -- Affitech
Anti platelet-derived growth factor D human	anticancer vaccine -- NIH
monoclonal antibodies -- CuraGen	anticancers -- Epimmune
Anti-17-1A MAb 3622W94 --	Anti-CCR5/CXCR4 sheep MAb -- KS
GlaxoSmithKline	Biomedix Holdings
Anti-2C4 MAb -- Genentech	Anti-CD11a MAb KBA --
anti-4-1BB monoclonal antibodies -- Bristol-	Anti-CD11a MAb M17
Myers Squibb	Anti-CD11a MAb TA-3 --
Anti-Adhesion Platform Tech. -- Cytovax	Anti-CD11a MAb WT.1 --
Anti-adipocyte MAb -- Cambridge Antibody	Anti-CD11b MAb -- Pharmacia
Tech./ObeSys	Anti-CD11b MAb LM2
antiallergics -- Maxygen	Anti-CD154 MAb -- Biogen
antiallergy vaccine -- Acambis	Anti-CD16-anti-CD30 MAb -- Biotest
Anti-alpha-4-integrin MAb	Anti-CD18 MAb -- Pharmacia
Anti-angiogenesis monoclonal antibodies --	Anti-CD19 MAb B43 --
KS Biomedix/Schering AG	Anti-CD19 MAb -liposomal sodium butyrate
	conjugate --

FIG. 1B

3/345

Anti-CD19 MAb-saporin conjugate –	Anti-CD4 MAb KT6
Anti-CD19-dsFv-PE38-immunotoxin –	Anti-CD4 MAb OX38
Anti-CD2 MAb 12-15 –	Anti-CD4 MAb PAP conjugate -- Bristol-Myers Squibb
Anti-CD2 MAb B-E2 – Diaclone	Anti-CD4 MAb RIB 5-2
Anti-CD2 MAb OX34 –	Anti-CD4 MAb W3/25
Anti-CD2 MAb OX54 –	Anti-CD4 MAb YTA 3.1.2
Anti-CD2 MAb OX55 –	Anti-CD4 MAb YTS 177-9
Anti-CD2 MAb RM2-1	Anti-CD40 ligand MAb 5c8 -- Biogen
Anti-CD2 MAb RM2-2	Anti-CD40 MAb
Anti-CD2 MAb RM2-4	Anti-CD40 MAb 5D12 – Tanox
Anti-CD20 MAb BCA B20	Anti-CD44 MAb A3D8
Anti-CD20-anti-Fc alpha RI bispecific MAb – Medarex, Tenovus	Anti-CD44 MAb GKWA3
Anti-CD22 MAb-saporin-6 complex –	Anti-CD44 MAb IM7
Anti-CD3 immunotoxin –	Anti-CD44 MAb KM81
Anti-CD3 MAb 145-2C11 – Pharming	Anti-CD44 variant monoclonal antibodies -- Corixa/Hebrew University
Anti-CD3 MAb CD4IgG conjugate -- Genentech	Anti-CD45 MAb BC8-I-131
Anti-CD3 MAb humanised – Protein Design, RW Johnson	Anti-CD45RB MAb
Anti-CD3 MAb WT32	Anti-CD48 MAb HuLy-m3
Anti-CD3 MAb-ricin-chain-A conjugate –	Anti-CD48 MAb WM-63
Anti-CD3 MAb-xanthine-oxidase conjugate –	Anti-CD5 MAb -- Becton Dickinson
Anti-CD30 MAb BerH2 -- Medac	Anti-CD5 MAb OX19
Anti-CD30 MAb-saporin conjugate	Anti-CD6 MAb
Anti-CD30-scFv-ETA'-immunotoxin	Anti-CD7 MAb-PAP conjugate
Anti-CD38 MAb AT13/5	Anti-CD7 MAb-ricin-chain-A conjugate
Anti-CD38 MAb-saporin conjugate	Anti-CD8 MAb – Amerimmune, Cytodyn, Becton Dickinson
Anti-CD3-anti-CD19 bispecific MAb	Anti-CD8 MAb 2-43
Anti-CD3-anti-EGFR MAb	Anti-CD8 MAb OX8
Anti-CD3-anti-interleukin-2-receptor MAb	Anti-CD80 MAb P16C10 -- IDEC
Anti-CD3-anti-MOV18 MAb -- Centocor	Anti-CD80 MAb P7C10 -- ID Vaccine
Anti-CD3-anti-SCLC bispecific MAb	Anti-CD8-Idarubicin conjugate
Anti-CD4 idiotype vaccine	Anti-CEA MAb CE-25
Anti-CD4 MAb – Centocor, IDEC Pharmaceuticals, Xenova Group	Anti-CEA MAb MN 14 – Immunomedics
Anti-CD4 MAb 16H5	Anti-CEA MAb MN14-PE40 conjugate – Immunomedics
Anti-CD4 MAb 4162W94 -- GlaxoSmithKline	Anti-CEA MAb T84.66-interleukin-2 conjugate
Anti-CD4 MAb B-F5 – Diaclone	Anti-CEA sheep MAb – KS Biomedix Holdings
Anti-CD4 MAb GK1-5	

FIG. 1C

4/345

Anti-cell surface monoclonal antibodies --	Anti-HIV antibody -- Epicyte
Cambridge Antibody Tech. /Pharmacia	anti-HIV catalytic antibody -- Hesed Biomed
Anti-c-erbB2-anti-CD3 bifunctional MAb --	anti-HIV fusion protein -- Idun
Otsuka	anti-HIV proteins -- Cangene
Anti-CMV MAb -- Scotgen	Anti-HM1-24 MAb -- Chugai
Anti-CTLA-4 MAb	Anti-hR3 MAb
Anti-EGFR catalytic antibody -- Hesed	Anti-Human-Carcinoma-Antigen MAb --
Biomed	Epicyte
anti-EGFR immunotoxin -- IVAX	Anti-ICAM-1 MAb -- Boehringer Ingelheim
Anti-EGFR MAb -- Abgenix	Anti-ICAM-1 MAb 1A-29 -- Pharmacia
Anti-EGFR MAb 528	Anti-ICAM-1 MAb HA58
Anti-EGFR MAb KSB 107 -- KS Biomedix	Anti-ICAM-1 MAb YN1/1.7.4
Anti-EGFR MAb-DM1 conjugate --	Anti-ICAM-3 MAb ICM3 -- ICOS
ImmunoGen	Anti-idiotypic breast cancer vaccine 11D10
Anti-EGFR MAb-LA1 --	Anti-idiotypic breast cancer vaccine
Anti-EGFR sheep MAb -- KS Biomedix	ACA14C5 --
Anti-FAP MAb F19-I-131	Anti-idiotypic cancer vaccine -- ImClone
Anti-Fas IgM MAb CH11	Systems/Merck KGaA ImClone, Viventia
Anti-Fas MAb Jo2	Biotech
Anti-Fas MAb RK-8	Anti-idiotypic cancer vaccine 1A7 -- Titan
Anti-Flt-1 monoclonal antibodies -- ImClone	Anti-idiotypic cancer vaccine 3H1 -- Titan
Anti-fungal peptides -- State University of	Anti-idiotypic cancer vaccine TriAb -- Titan
New York	Anti-idiotypic Chlamydia trachomatis
antifungal tripeptides -- BTG	vaccine
Anti-ganglioside GD2 antibody-interleukin-2	Anti-idiotypic colorectal cancer vaccine --
fusion protein -- Lexigen	Novartis
Anti-GM2 MAb -- Kyowa	Anti-idiotypic colorectal cancer vaccine --
Anti-GM-CSF receptor monoclonal	Onyvax
antibodies -- AMRAD	Anti-idiotypic melanoma vaccine -- IDEC
Anti-gp130 MAb -- Tosoh	Pharmaceuticals
Anti-HCA monoclonal antibodies --	Anti-idiotypic ovarian cancer vaccine ACA
AltaRex/Epigen	125
Anti-hCG antibodies -- Abgenix/AVI	Anti-idiotypic ovarian cancer vaccine AR54 -
BioPharma	- AltaRex
Anti-heparanase human monoclonal	Anti-idiotypic ovarian cancer vaccine CA-
antibodies -- Oxford	125 -- AltaRex, Biomira
Glycosciences/Medarex	Anti-IgE catalytic antibody -- Hesed Biomed
Anti-hepatitis C virus human monoclonal	Anti-IgE MAb E26 -- Genentech
antibodies -- XTL Biopharmaceuticals	Anti-IGF-1 MAb
Anti-HER-2 antibody gene therapy	anti-inflammatory -- GeneMax
Anti-herpes antibody -- Epicyte	anti-inflammatory peptide -- BTG

FIG. 1D

5/345

anti-integrin peptides -- Burnha	Anti-mu MAb -- Novartis
Anti-interferon-alpha-receptor MAb 64G12 -- Pharma Pacific Management	Anti-MUC-1 MAb
Anti-interferon-gamma MAb -- Protein Design Labs	Anti-Nogo-A MAb IN1
Anti-interferon-gamma polyclonal antibody - - Dompe	Anti-nuclear autoantibodies -- Procyon
- Advanced Biotherapy	Anti-ovarian cancer monoclonal antibodies -
Anti-interleukin-10 MAb --	Anti-p185 monoclonal antibodies
Anti-interleukin-12 MAb --	Anti-p43 MAb
Anti-interleukin-1-beta polyclonal antibody -- R&D Systems	Antiparasitic vaccines
Anti-interleukin-2 receptor MAb 2A3	Anti-PDGF/bFGF sheep MAb -- KS Biomedix
Anti-interleukin-2 receptor MAb 33B3-1 -- Immunotech	Anti-properdin monoclonal antibodies -- Abgenix/Gllatech
Anti-interleukin-2 receptor MAb ART-18	Anti-PSMA MAb J591 -- BZL Biologics
Anti-interleukin-2 receptor MAb LO-Tact-1	Anti-Rev MAb gene therapy --
Anti-interleukin-2 receptor MAb Mikbeta1	Anti-RSV antibodies -- Epicyte, Intracell
Anti-interleukin-2 receptor MAb NDS61	Anti-RSV monoclonal antibodies -- Medarex/MedImmune, Applied Molecular Evolution/MedImmune
Anti-interleukin-4 MAb 11B11	Anti-RSV MAb, inhalation -- Alkermes/MedImmune
Anti-interleukin-5 MAb -- Wallace Laboratories	Anti-RT gene therapy
Anti-interleukin-6 MAb -- Centocor, Diaclone, Pharmadigm	Antisense K-ras RNA gene therapy
Anti-interleukin-8 MAb -- Xenotech	Anti-SF-25 MAb
Anti-JL1 MAb	Anti-sperm antibody -- Epicyte
Anti-Klebsiella sheep MAb -- KS Biomedix Holdings	Anti-Tac(Fv)-PE38 conjugate
Anti-Laminin receptor MAb-liposomal doxorubicin conjugate	Anti-TAPA/CD81 MAb AMP1
Anti-LCG MAb -- Cytoclonal	Anti-tat gene therapy
Anti-lipopolysaccharide MAb -- VitaResc	Anti-TCR-alphabeta MAb H57-597
Anti-L-selectin monoclonal antibodies -- Protein Design Labs, Abgenix, Stanford University	Anti-TCR-alphabeta MAb R73
Anti-MBL monoclonal antibodies -- Alexion/Brigham and Women's Hospital	Anti-tenascin MAb BC-4-I-131
Anti-MHC monoclonal antibodies	Anti-TGF-beta human monoclonal antibodies -- Cambridge Antibody Tech., Genzyme
Anti-MIF antibody humanised -- IDEC, Cytokine PharmaSciences	Anti-TGF-beta MAb 2G7 -- Genentech
Anti-MRSA/VRSA sheep MAb -- KS Biomedix Holdings	Anti-thrombin III -- Genzyme Transgenics, Aventis, Bayer, Behringwerke, CSL, Myriad
	Anti-Thy1 MAb
	Anti-Thy1.1 MAb

FIG. 1E

6/345

Anti-tissue factor/factor VIIA sheep MAb -- KS Biomedix	ARGENT gene delivery systems -- ARIAD
Anti-TNF monoclonal antibodies -- Centocor, Chiron, Peptech, Pharacia, Serono	Arresten
Anti-TNF sheep MAb -- KS Biomedix Holdings	ART-123 -- Asahi Kasei
Anti-TNFalpha MAb -- Genzyme	arylsulfatase B -- BioMarin
Anti-TNFalpha MAb B-C7 -- Diaclone	Arylsulfatase B, Recombinant human -- BioMarin
Anti-tooth decay MAb -- Planet BioTech.	AS 1051 -- Ajinomoto
antitumour RNases -- NIH	ASI-BCL -- Intracell
Anti-VCAM MAb 2A2 -- Alexion	ATL-101 -- Alizyme
Anti-VCAM MAb 3F4 -- Alexion	atrial natriuretic peptide -- Pharis
Anti-VCAM-1 MAb	Aurintricarboxylic acid-high molecular weight
Anti-VEC MAb -- ImClone	autoimmune disorders -- GPC Biotech/MorphoSys
Anti-VEGF MAb -- Genentech	Autoimmune disorders and transplant rejection -- Bristol-Myers Squibb/Genzyme
Anti-VEGF MAb 2C3	Tra
Anti-VEGF sheep MAb -- KS Biomedix Holdings	Autoimmune disorders/cancer -- Abgenix/Chiron, /CuraGen
Anti-VLA-4 MAb HP1/2 -- Biogen	Autotaxin
Anti-VLA-4 MAb PS/2	Avicidin -- NeoRx
Anti-VLA-4 MAb R1-2	axogenesis factor-1 -- Boston Life Sciences
Anti-VLA-4 MAb TA-2	Axokine -- Regeneron
Anti-VRE sheep MAb -- KS Biomedix Holdings	B cell lymphoma vaccine -- Biomira
ANUP -- TranXenoGen	B7-1 gene therapy --
ANUP-1 -- Pharis	BABS proteins -- Chiron
AOP-RANTES -- Senetek	BAM-002 -- Novelos Therapeutics
Apan-CH -- Praecis Pharmaceuticals	Bay-16-9996 -- Bayer
APC-8024 -- Demegen	Bay-39-9437 -- Bayer
ApoA-1 -- Milano, Pharmacia	Bay-50-4798 -- Bayer
Apogen -- Alexion	BB-10153 -- British Biotech
apolipoprotein A1 -- Avanir	BBT-001 -- Bolder BioTech.
Apolipoprotein E -- Bio-Tech. General	BBT-002 -- Bolder BioTech.
Applaggin -- Biogen	BBT-003 -- Bolder BioTech.
aprotinin -- ProdiGene	BBT-004 -- Bolder BioTech.
APT-070C -- AdProTech	BBT-005 -- Bolder BioTech.
AR 177 -- Aronex Pharmaceuticals	BBT-006 -- Bolder BioTech.
AR 209 -- Aronex Pharmaceuticals, Antigenics	BBT-007 -- Bolder BioTech.
AR545C	BCH-2763 -- Shire
	BCSF -- Millenium Biologix
	BDNF -- Regeneron -- Amgen

FIG. 1F

7/345

Becaplermin -- Johnson & Johnson, Chiron	BST-3002 -- BioStratum
Bectumomab -- Immunomedics	BTI 322 --
Beta-adrenergic receptor gene therapy -- University of Arkansas	butyrylcholinesterase -- Shire
BI 51013 -- Behringwerke AG	C 6822 -- COR Therapeutics
BIBH 1 -- Boehringer Ingelheim	C1 esterase inhibitor -- Pharming
BIM-23190 -- Beaufour-Ipsen	C3d adjuvant -- AdProTech
birch pollen immunotherapy -- Pharmacia	CAB-2.1 -- Millennium
bispecific fusion proteins -- NIH	calcitonin -- Inhale Therapeutics Systems, Aventis, Genetronics, TranXenoGen, Unigene, Rhone Poulenc Rohrer
Bispecific MAb 2B1 -- Chiron	calcitonin -- oral -- Nobex, Emisphere, Pharmaceutical Discovery
Bitistatin	Calcitonin gene-related peptide -- Asahi Kasei -- Unigene
BIWA 4 -- Boehringer Ingelheim	calcitonin, human -- Suntory
blood substitute -- Northfield, Baxter Intl.	calcitonin, nasal -- Novartis, Unigene
BLP-25 -- Biomira	calcitonin, Panoderm -- Elan
BLS-0597 -- Boston Life Sciences	calcitonin, Peptitrol -- Shire
BlyS -- Human Genome Sciences	calcitonin, salmon -- Therapicon
BlyS radiolabelled -- Human Genome Sciences	calin -- Biopharm
BM 06021 -- Boehringer Mannheim	Calphobindin I
BM-202 -- BioMarin	calphobindin I -- Kowa
BM-301 -- BioMarin	calreticulin -- NYU
BM-301 -- BioMarin	Campath-1G
BM-302 -- BioMarin	Campath-1M
BMP 2 -- Genetics Institute/Medtronic-Sofamor Danek, Genetics Institute/Collagenesis, Genetics Institute/Yamanouch	cancer therapy -- Cangene
BMP 2 gene therapy	cancer vaccine -- Aixlie, Aventis Pasteur, Center of Molecular Immunology, YM BioSciences, Cytos, Genzyme, Transgenics, Globelimmune, Igeneon, ImClone, Virogenetics, InterCell, Iomai, Jenner Biotherapies, Memorial Sloan-Kettering Cancer Center, Sydney Kimmel Cancer Center, Novavax, Protein Sciences, Argonex, SIGA
BMP 52 -- Aventis Pasteur, Biopharm	Cancer vaccine ALVAC-CEA B7.1 -- Aventis Pasteur/Therion Biologics
BMP-2 -- Genetics Institute	Cancer vaccine CEA-TRICOM -- Aventis Pasteur/Therion Biologics
BMS 182248 -- Bristol-Myers Squibb	Cancer vaccine gene therapy -- Cantab Pharmaceuticals
BMS 202448 -- Bristol-Myers Squibb	
bone growth factors -- IsoTis	
BPC-15 -- Pfizer	
brain natriuretic peptide --	
Breast cancer -- Oxford GlycoSciences/Medarex	
Breast cancer vaccine -- Therion Biologics, Oregon	
BSSL -- PPL Therapeutics	
BST-2001 -- BioStratum	

FIG. 1G

8/345

Cancer vaccine HER-2/neu -- Corixa	CETP vaccine -- Avant
Cancer vaccine THERATOPE -- Biomira	Cetorelix
cancer vaccine, PolyMASC -- Valentis	Cetuximab
Candida vaccine -- Corixa, Inhibitex	CGH 400 -- Novartis
Canstatin -- ILEX	CGP 42934 -- Novartis
CAP-18 -- Panorama	CGP 51901 -- Tanox
Cardiovascular gene therapy -- Collateral Therapeutics	CGRP -- Unigene
carperitide -- Suntory	CGS 27913 -- Novartis
Casocidin-1 -- Pharis	CGS 32359 -- Novartis
CAT 152 -- Cambridge Antibody Tech.	Chagas disease vaccine -- Corixa
CAT 192 -- Cambridge Antibody Tech.	chemokines -- Immune Response
CAT 213 -- Cambridge Antibody Tech.	CHH 380 -- Novartis
Catalase -- Enzon	chitinase -- Genzyme, ICOS
Cat-PAD -- Circassia	Chlamydia pneumoniae vaccine -- Antex Biologics
CB 0006 -- Celltech	Chlamydia trachomatis vaccine -- Antex Biologics
CCK(27-32) -- Akzo Nobel	Chlamydia vaccine -- GlaxoSmithKline
CCR2-64I -- NIH	Cholera vaccine CVD 103-HgR -- Swiss Serum and Vaccine Institute Berne
CD, Procept -- Paligent	Cholera vaccine CVD 112 -- Swiss Serum and Vaccine Institute Berne
CD154 gene therapy	Cholera vaccine inactivated oral -- SBL Vaccin
CD39 -- Immunex	Chrysalin -- Chrysalis BioTech.
CD39-L2 -- Hyseq	CI-782 -- Hitachi Kase
CD39-L4 -- Hyseq	Ciliary neurotrophic factor -- Fidia, Roche
CD4 fusion toxin -- Senetek	CIM project -- Active Biotech
CD4 IgG -- Genentech	CL 329753 -- Wyeth-Ayerst
CD4 receptor antagonists -- Pharmacopeia/Progenics	CL22, Cobra -- ML Laboratories
CD4 soluble -- Progenics	Clenoliximab -- IDEC
CD4, soluble -- Genzyme Transgenics	Clostridium difficile antibodies -- Epicyte
CD40 ligand -- Immunex	clotting factors -- Octogene
CD4-ricin chain A -- Genentech	CMB 401 -- Celltech
CD59 gene therapy -- Alexion	CNTF -- Sigma-Tau
CD8 TIL cell therapy -- Aventis Pasteur	Cocaine abuse vaccine -- Cantab, ImmuLogic, Scripps
CD8, soluble -- Avidex	coccidiomycosis vaccine -- Arizo
CD95 ligand -- Roche	collagen -- Type I -- Pharming
CDP 571 -- Celltech	Collagen formation inhibitors -- FibroGen
CDP 850 -- Celltech	
CDP 870 -- Celltech	
CDS-1 -- Ernest Orlando	
Cedelizumab -- Ortho-McNeil	
Cetermin -- Insmed	

FIG. 1H

9/345

Collagen/hydroxyapatite/bone growth factor	CY 1747 -- Epimmune
-- Aventis Pasteur, Biopharm, Orquest	CY 1748 -- Epimmune
collagenase -- BioSpecifics	Cyanovirin-N
Colorectal cancer vaccine -- Wistar Institute	Cystic fibrosis therapy -- CBR/IVAX
Component B, Recombinant -- Serono	CYT 351
Connective tissue growth factor inhibitors --	cytokine Traps -- Regeneron
FibroGen/Taisho	cytokines -- Enzon, Cytoclonal
Contortrostatin	Cytomegalovirus glycoprotein vaccine --
contraceptive vaccine -- Zonagen	Chiron, Aquila Biopharmaceuticals,
Contraceptive vaccine hCG	Aventis Pasteur, Virogenetics
Contraceptive vaccine male reversible --	Cytomegalovirus vaccine live -- Aventis
IMMUCON	Pasteur
Contraceptive vaccine zona pellucida --	Cytosine deaminase gene therapy --
Zonagen	GlaxoSmithKline
Copper-64 labelled MAb TETA-1A3 -- NCI	DA-3003 -- Dong-A
Coralyne	DAB389interleukin-6 -- Senetek
Corsevin M	DAB389interleukin-7
C-peptide analogues -- Schwarz	DAMP [^] -- Incyte Genomics
CPI-1500 -- Consensus	Daniplestim -- Pharmacia
CRF -- Neurobiological Tech.	darbepoetin alfa -- Amgen
cRGDFV pentapeptide --	DBI-3019 -- Diabetogen
CRL 1095 -- CytRx	DCC -- Genzyme
CRL 1336 -- CytRx	DDF -- Hyseq
CRL 1605 -- CytRx	decorin -- Integra, Telios
CS-560 -- Sankyo	defensins -- Large Scale Biology
CSF -- ZymoGenetics	DEGR-VIIa
CSF-G -- Hangzhou, Dong-A, Hanmi	Deimmunised antibody 3B6/22 AGEN
CSF-GM -- Cangene, Hunan, LG Chem	Deimmunised anti-cancer antibodies --
CSF-M -- Zarix	Biovation/Viragen
CT 1579 -- Merck Frosst	Dendroamide A
CT 1786 -- Merck Frosst	Dengue vaccine -- Bavarian Nordic, Merck
CT-112 [^] -- BTG	denileukin diftitox -- Ligand
CTB-134L -- Xenova	DES-1101 -- Desmos
CTC-111 -- Kaketsuken	desirudin -- Novartis
CTGF -- FibroGen	desmopressin -- Unigene
CTLA4-Ig -- Bristol-Myers Squibb	Desmoteplase -- Merck, Schering AG
CTLA4-Ig gene therapy --	Destabilase
CTP-37 -- AVI BioPharma	Diabetes gene therapy -- DeveloGen, Pfizer
C-type natriuretic peptide -- Suntory	Diabetes therapy -- Crucell
CVS 995 -- Corvas Intl.	Diabetes type 1 vaccine -- Diamyd
CX 397 -- Nikko Kyodo	Therapeutics

FIG. 11

10/345

DiaCIM -- YM BioSciences	EGF-P64k vaccine -- Center of Molecular Immunology
dialytic oligopeptides -- Research Corp	EL 246 -- LigoCyte
Diamyd -- Diamyd Therapeutics	elastase inhibitor -- Synergen
DiaPep227 -- Pepgen	elcatonin -- Therapicon
DiavaX -- Corixa	EMD 72000 -- Merck KGaA
Diphtheria tetanus pertussis-hepatitis B vaccine -- GlaxoSmithKline	Emdogain -- BIORA
DIR therapy -- Solis Therapeutics --	emfilermin -- AMRAD
DNase -- Genentech	Emoctakin -- Novartis
Dornase alfa -- Genentech	enamel matrix protein -- BIORA
Dornase alfa, inhalation -- Genentech	Endo III -- NYU
Doxorubicin-anti-CEA MAb conjugate -- Immunomedics	endostatin -- EntreMed, Pharis
DP-107 -- Trimeris	Enhancins -- Micrologix
drotrecogin alfa -- Eli Lilly	Enlimomab -- Isis Pharm.
DTctGMCSF	Enoxaparin sodium -- Pharmuka
DTP-polio vaccine -- Aventis Pasteur	enzyme linked antibody nutrient depletion therapy -- KS Biomedix Holdings
DU 257-KM231 antibody conjugate -- Kyowa	Eosinophil-derived neutralizing agent --
dural graft matrix -- Integra	EP-51216 -- Asta Medica
Dutiplase -- Baxter Intl.	EP-51389 -- Asta Medica
DWP-401 -- Daewoong	EPH family ligands -- Regeneron
DWP-404 -- Daewoong	Epidermal growth factor -- Hitachi Kasei, Johnson & Johnson
DWP-408 -- Daewoong	Epidermal growth factor fusion toxin -- Senetek
E coli O157 vaccine -- NIH	Epidermal growth factor-genistein --
E21-R -- BresaGen	EPI-HNE-4 -- Dyax
Eastern equine encephalitis virus vaccine --	EPI-KAL2 -- Dyax
Echicetin --	Epoetin-alfa -- Amgen, Dragon Pharmaceuticals, Nanjing Huaxin
Echinhibin 1 --	Epratuzumab -- Immunomedics
Echistatin -- Merck	Epstein-Barr virus vaccine --
Echitamine --	Aviron/SmithKline Beecham, Bioresearch
EC-SOD -- PPL Therapeutics	Eptacog alfa -- Novo Nordisk
EDF -- Ajinomoto	Eptifibatide -- COR Therapeutics
EDN derivative -- NIH	erb-38 --
EDNA -- NIH	Erlizumab -- Genentech
Edobacomab -- XOMA	
Edrecolomab -- Centocor	
EF 5077	
Efalizumab -- Genentech	
EGF fusion toxin -- Seragen, Ligand	

FIG. 1J

11/345

erythropoietin -- Alkermes, ProLease, Dong-Fas TR -- Human Genome Sciences	
A, Elanex, Genetics Institute, LG Chem,	Felvizumab -- Scotgen
Protein Sciences, Serono, Snow Brand,	FFR-VIIa -- Novo Nordisk
SRC VB VECTOR, Transkaryotic	FG-001 -- F-Gene
Therapies	FG-002 -- F-Gene
Erythropoietin Beta -- Hoffman La Roche	FG-004 -- F-Gene
Erythropoietin/Epoetin alfa -- Chugai	FG-005 -- F-Gene
Escherichia coli vaccine -- North American	FGF + fibrin -- Repair
Vaccine, SBL Vaccin, Swiss Serum and	Fibrimage -- Bio-Tech. General
Vaccine Institute Berne	fibrin-binding peptides -- ISIS Innovation
etanercept -- Immunex	fibrinogen -- PPL Therapeutics, Pharming
examorelin -- Mediolanum	fibroblast growth factor -- Chiron, NYU,
exonuclease VII	Ramot, ZymoGenetics
F 105 -- Centocor	fibrolase conjugate -- Schering AG
F-992 -- Fornix	Filgrastim -- Amgen
Factor IX -- Alpha Therapeutics, Welfide	filgrastim -- PDA modified -- Xencor
Corp., CSL, Genetics Institute/AHP,	FLT-3 ligand -- Immunex
Pharmacia, PPL Therapeutics	FN18 CRM9 --
Factor IX gene therapy -- Cell Genesys	folliculin -- Biotech Australia, Human
Factor VII -- Novo Nordisk, Bayer, Baxter	Therapeutics
Intl.	folliculin alfa -- Alkermes, ProLease,
Factor VIIa -- PPL Therapeutics,	PowderJect, Serono, Akzo Nobel
ZymoGenetics	Folliculin Beta -- Bayer, Organon
Factor VIII -- Bayer Genentech, Beaufour-	FP 59
Ipsen, CLB, Inex, Octagen, Pharmacia,	FSH -- Ferring
Pharming	FSH + LH -- Ferring
Factor VIII -- PEGylated -- Bayer	F-spondin -- CeNeS
Factor VIII fragments -- Pharmacia	fusion protein delivery system -- UAB
Factor VIII gene therapy -- Targeted	Research Foundation
Genetics	fusion toxins -- Boston Life Sciences
Factor VIII sucrose formulation -- Bayer,	G 5598 -- Genentech
Genentech	GA-II -- Transkaryotic Therapies
Factor VIII-2 -- Bayer	Gamma-interferon analogues -- SRC VB
Factor VIII-3 -- Bayer	VECTOR
Factor Xa inhibitors -- Merck, Novo Nordisk,	Ganirelix -- Roche
Mochida	gastric lipase -- Meristem
Factor XIII -- ZymoGenetics	Gavilimomab --
Factors VIII and IX gene therapy -- Genetics	G-CSF -- Amgen, SRC VB VECTOR
Institute/Targeted Genetics	GDF-1 -- CeNeS
Famoxin -- Genset	GDF-5 -- Biopharm
Fas (delta) TM protein -- LXR BioTech.	GDNF -- Amgen

FIG. 1K

12/345

gelsolin -- Biogen	H5N1 influenza A virus vaccine -- Protein Sciences
Gemtuzumab ozogamicin -- Celltech	haemoglobin -- Biopure
Gene-activated epoetin-alfa -- Aventis Pharma -- Transkaryotic Therapies	haemoglobin 3011, Recombinant -- Baxter Healthcare
Glanzmann thrombasthenia gene therapy --	haemoglobin crosfumaril -- Baxter Intl.
Glatiramer acetate -- Yeda	haemoglobin stabilized -- Ajinomoto
glial growth factor 2 -- CeNeS	haemoglobin, recombinant -- Apex
GLP-1 -- Amylin, Suntory, TheraTech, Watson	HAF -- Immune Response
GLP-1 peptide analogues -- Zealand Pharmaceuticals	Hantavirus vaccine
glucagon -- Eli Lilly, ZymoGenetics	HB 19
Glucagon-like peptide-1 7-36 amide -- Suntory	HBNF -- Regeneron
Glucocerebrosidase -- Genzyme	HCC-1 -- Pharis
glutamate decarboxylase -- Genzyme Transgenics	hCG -- Milkhaus
Glycoprotein S3 -- Kureha	hCG vaccine -- Zonagen
GM-CSF -- Immunex	HE-317 -- Hollis-Eden Pharmaceuticals
GM-CSF tumour vaccine -- PowderJect	Heat shock protein cancer and influenza vaccines -- StressGen
GnRH immunotherapeutic -- Protherics	Helicobacter pylori vaccine -- Acambis, AstraZeneca/CSL, Chiron, Provalis
gp75 antigen -- ImClone	Helistat-G -- GalaGen
gp96 -- Antigenics	Hemolink -- Hemosol
GPI 0100 -- Galenica	hepapoietin -- Snow Brand
GR 4991W93 -- GlaxoSmithKline	heparanase -- InSight
Granulocyte colony-stimulating factor -- Dong-A	heparinase I -- Ibex
Granulocyte colony-stimulating factor conjugate	heparinase III -- Ibex
grass allergy therapy -- Dynavax	Hepatitis A vaccine -- American Biogenetic Sciences
GRF1-44 -- ICN	Hepatitis A vaccine inactivated
Growth Factor -- Chiron, Atrigel, Atrix, Innogenetics, ZymoGenetics, Novo	Hepatitis A vaccine Nothav -- Chiron
growth factor peptides -- Biotherapeutics	Hepatitis A-hepatitis B vaccine -- GlaxoSmithKline
growth hormone -- LG Chem	hepatitis B therapy -- Tripep
growth hormone, Recombinant human -- Serono	Hepatitis B vaccine -- Amgen, Chiron SpA, Meiji Milk, NIS, Prodeva, PowderJect, Rhein Biotech
GT 4086 -- Gliatech	Hepatitis B vaccine recombinant -- Evans Vaccines, Epitex Combiotech, Genentech, MedImmune, Merck Sharp & Dohme, Rhein Biotech, Shantha Biotechnics, Vector, Yeda
GW 353430 -- GlaxoSmithKline	
GW-278884 -- GlaxoSmithKline	
H 11 -- Viventia Biotech	

FIG. 1L

13/345

Hepatitis B vaccine recombinant TGP 943 -- Takeda	HIV peptides -- American Home Products
Hepatitis C vaccine -- Bavarian Nordic, Chiron, Innogenetics Acambis,	HIV vaccine -- Applied bioTech., Axis
Hepatitis D vaccine -- Chiron Vaccines	Genetics, Biogen, Bristol-Myers Squibb,
Hepatitis E vaccine recombinant -- Genelabs/GlaxoSmithKline, Novavax	Genentech, Korea Green Cross, NIS,
hepatocyte growth factor -- Panorama, Sosei	Oncogen, Protein Sciences Corporation,
hepatocyte growth factor kringle fragments - - EntreMed	Terumo, Tonen Corporation, Wyeth-
Her-2/Neu peptides -- Corixa	Ayerst, Wyeth-Lederle Vaccines-Malvern,
Herpes simplex glycoprotein DNA vaccine -- Merck, Wyeth-Lederle Vaccines-Malvern, Genentech, GlaxoSmithKline, Chiron, Takeda	Advanced BioScience Laboratories,
Herpes simplex vaccine -- Cantab Pharmaceuticals, CEL-SCI, Henderson Morley	Bavarian Nordic, Bavarian Nordic/Statens
Herpes simplex vaccine live -- ImClone Systems/Wyeth-Lederle, Aventis Pasteur	Serum Institute, GeneCure, Immune
HGF derivatives -- Dompe	Response, Progenics, Therion Biologics,
hIAPP vaccine -- Crucell	United Biomedical, Chiron
Hib-hepatitis B vaccine -- Aventis Pasteur	HIV vaccine vCP1433 -- Aventis Pasteur
HIC 1	HIV vaccine vCP1452 -- Aventis Pasteur
HIP-- Altachem	HIV vaccine vCP205 -- Aventis Pasteur
Hirudins -- Biopharma, Cangene, Dongkook, Japan Energy Corporation, Pharmacia Corporation, SIR International, Sanofi-Synthelabo, Sotragene, Rhein Biotech	HL-9 -- American BioScience
HIV edible vaccine -- ProdiGene	HM-9239 -- Cytran
HIV gp120 vaccine -- Chiron, Ajinomoto, GlaxoSmithKline, ID Vaccine, Progenics, VaxGen	HML-103 -- Hemosol
HIV gp120 vaccine gene therapy --	HML-104 -- Hemosol
HIV gp160 DNA vaccine -- PowderJect, Aventis Pasteur, Oncogen, Hyland Immuno, Protein Sciences	HML-105 -- Hemosol
HIV gp41 vaccine -- Panacos	HML-109 -- Hemosol
HIV HGP-30W vaccine -- CEL-SCI	HML-110 -- Hemosol
HIV immune globulin -- Abbott, Chiron	HML-121 -- Hemosol
	hNLP -- Pharis
	Hookworm vaccine
	host-vector vaccines -- Henogen
	HPM 1 -- Chugai
	HPV vaccine -- MediGene
	HSA -- Meristem
	HSF -- StressGen
	HSP carriers --Weizmann, Yeda, Peptor
	HSPPC-70 -- Antigenics
	HSPPC-96 -- pathogen-derived -- Antigenics
	HSV 863 -- Novartis
	HTLV-I DNA vaccine
	HTLV-I vaccine
	HTLV-II vaccine -- Access
	HU 901 -- Tanox
	Hu23F2G -- ICOS
	HuHMFG1

FIG. 1M

14/345

HumaLYM -- Intracell	HuMax-IL15 -- Genmab
Human krebs statika -- Yamanouchi	HYB 190 -- Hybridon
human monoclonal antibodies --	HYB 676 -- Hybridon
Abgenix/Biogen, Abgenix/ Corixa,	I-125 MAb A33 -- Celltech
Abgenix/Immunex, Abgenix/Lexicon,	Ibritumomab tiuxetan -- IDEC
Abgenix/ Pfizer, Athersys/Medarex,	IBT-9401 -- Ibex
Biogen/MorphoSys, CAT/Searle,	IBT-9402 -- Ibex
Centocor/Medarex, Corixa/Kirin Brewery,	IC 14 -- ICOS
Corixa/Medarex, Eos BioTech./Medarex,	Idarubicin anti-Ly-2.1 --
Eos/Xenerex, Exelixis/Protein Design	IDEC 114 -- IDEC
Labs, ImmunoGen/ Raven,	IDEC 131 -- IDEC
Medarex/B.Twelve,	IDEC 152 -- IDEC
MorphoSys/ImmunoGen, XTL	IDM 1 -- IDM
Biopharmaceuticals/Dyax,	IDPS -- Hollis-Eden Pharmaceuticals
Human monoclonal antibodies --	Iduronate-2-sulfatase -- Transkaryotic
Medarex/Northwest Biotherapeutics,	Therapies
Medarex/Seattle Genetics	IGF/IBP-2-13 -- Pharis
human netrin-1 -- Exelixis	IGN-101 -- Igeneon
human papillomavirus antibodies -- Epicyte	IK HIR02 -- Iketon
Human papillomavirus vaccine -- Biotech	IL-11 -- Genetics Institute/AHP
Australia, IDEC, StressGen	IL-13-PE38 -- NeoPharm
Human papillomavirus vaccine MEDI 501 --	IL-17 receptor -- Immunex
MedImmune/GlaxoSmithKline	IL-18BP -- Yeda
Human papillomavirus vaccine MEDI	IL-1Hy1 -- Hyseq
503/MEDI 504 --	IL-1 β -- Celltech
MedImmune/GlaxoSmithKline	IL-1 β adjuvant -- Celltech
Human papillomavirus vaccine TA-CIN --	IL-2 -- Chiron
Cantab Pharmaceuticals	IL-2 + IL-12 -- Hoffman La-Roche
Human papillomavirus vaccine TA-HPV --	IL-6/sIL-6R fusion -- Hadasit
Cantab Pharmaceuticals	IL-6R derivative -- Tosoh
Human papillomavirus vaccine TH-GW --	IL-7-Dap 389 fusion toxin -- Ligand
Cantab/GlaxoSmithKline	IM-862 -- Cytran
human polyclonal antibodies -- Biosite/Eos	IMC-1C11 -- ImClone
BioTech./ Medarex	imiglucerase -- Genzyme
human type II anti factor VIII monoclonal	Immune globulin intravenous (human) --
antibodies -- ThromboGenics	Hoffman La Roche
humanised anti glycoprotein Ib murine	immune privilege factor -- Proneuron
monoclonal antibodies -- ThromboGenics	Immunocal -- Immunotec
HumaRAD -- Intracell	Immunogene therapy -- Briana Bio-Tech
HuMax EGFR -- Genmab	Immunoliposomal 5-fluorodeoxyuridine-
HuMax-CD4 -- Medarex	dipalmitate --

FIG. 1N

15/345

immunosuppressant vaccine -- Aixlie	integrin antagonists -- Merck
immunotoxin -- Antisoma, NIH	interferon (Alpha2) -- SRC VB VECTOR,
ImmuRAIT-Re-188 -- Immunomedics	Viragen, Dong-A, Hoffman La-Roche,
imreg-1 -- Imreg	Genentech
infertility -- Johnson & Johnson, E-TRANS	interferon -- BioMedicines, Human Genome
Influenza virus vaccine -- Aventis Pasteur,	Sciences
Protein Sciences	interferon (Alfa-n3)—Interferon Sciences
inhibin -- Biotech Australia, Human	Intl.
Therapeutics	interferon (Alpha), Biphasix -- Helix
Inhibitory G protein gene therapy	interferon (Alpha)—Amgen, BioNative,
INKP-2001 -- InKine	Novartis, Genzyme Transgenics,
Inolimomab -- Diaclone	Hayashibara, Inhale Therapeutics
insulin -- AutoImmune, Altea, Biobras,	Systems, Medusa, Flamel, Dong-A,
BioSante, Bio-Tech. General, Chong Kun	GeneTrol, Nastech, Shantha,
Dang, Emisphere, Flamel, Provalis, Rhein	Wassermann, LG Chem, Sumitomo,
Biotech, TranXenoGen	Aventis, Behring EGIS, Pepgen, Servier,
insulin (bovine) -- Novartis	Rhein Biotech,
insulin analogue -- Eli Lilly	interferon (Alpha2A)
Insulin Aspart -- Novo Nordisk	interferon (Alpha2B) -- Enzon, Schering-
insulin detemir -- Novo Nordisk	Plough, Biogen, IDEA
insulin glargine -- Aventis	interferon (Alpha-N1) -- GlaxoSmithKline
insulin inhaled -- Inhale Therapeutics	interferon (beta) -- Rentschler, GeneTrol,
Systems, Alkermes	Meristem, Rhein Biotech, Toray, Yeda,
insulin oral -- Inovax	Daiichi, Mochida
insulin, AeroDose -- AeroGen	interferon (Beta1A) -- Serono, Biogen
insulin, AERx -- Aradigm	interferon (beta1A), inhale -- Biogen
insulin, BEODAS -- Elan	interferon (β 1b)—Chiron
insulin, Biphasix -- Helix	interferon (tau)—Pepgen
insulin, buccal -- Generex	Interferon alfacon-1 -- Amgen
Insulin, I2R -- Flemington	Interferon alpha-2a vaccine
insulin, intranasal -- Bentley	Interferon Beta 1b -- Schering/Chiron,
insulin, oral -- Nobex, Unigene	InterMune
insulin, Orasome -- Endorex	Interferon Gamma -- Boehringer Ingelheim,
insulin, ProMaxx -- Epic	Sheffield, Rentschler, Hayashibara
insulin, Quadrant -- Elan	interferon receptor, Type I -- Serono
insulin, recombinant -- Aventis	interferon(Gamma1B) -- Genentech
insulin, Spiros -- Elan	Interferon-alpha-2b + ribavirin -- Biogen,
insulin, Transfersome -- IDEA	ICN
insulin, Zymo, recombinant -- Novo Nordisk	Interferon-alpha-2b gene therapy --
insulinotropin -- Scios	Schering-Plough
Insulysin gene therapy --	Interferon-con1 gene therapy --

FIG. 10

16/345

interleukin-1 antagonists -- Dompe	IPF -- Metabolex
Interleukin-1 receptor antagonist -- Abbott	IR-501 -- Immune Response
Bioresearch, Pharmacia	ISIS 9125 -- Isis Pharmaceuticals
Interleukin-1 receptor type I -- Immunex	ISURF No. 1554 -- Millennium
interleukin-1 receptor Type II -- Immunex	ISURF No. 1866 -- Iowa State Univer.
Interleukin-10 -- DNAX, Schering-Plough	ITF-1697 -- Italfarmaco
Interleukin-10 gene therapy --	IxC 162 -- Ixion
interleukin-12 -- Genetics Institute, Hoffman	J 695 -- Cambridge Antibody Tech.,
La-Roche	Genetics Inst., Knoll
interleukin-13 -- Sanofi	Jagged + FGF -- Repair
interleukin-13 antagonists -- AMRAD	JKC-362 -- Phoenix Pharmaceuticals
Interleukin-13-PE38QQR	JTP-2942 -- Japan Tobacce
interleukin-15 -- Immunex	Juman monoclonal antibodies --
interleukin-16 -- Research Corp	Medarex/Raven
interleukin-18 -- GlaxoSmithKline	K02 -- Axys Pharmaceuticals
Interleukin-1-alpha -- Immunex/Roche	Keliximab -- IDEC
interleukin-2 -- SRC VB VECTOR,	Keyhole limpet haemocyanin
Ajinomoto, Biomira	KGF -- Amgen
Interleukin-3 -- Cangene	KM 871 -- Kyowa
Interleukin-4 -- Immunology Ventures,	KPI 135 -- Scios
Sanofi Winthrop, Schering-Plough,	KPI-022 -- Scios
Immunex/ Sanofi Winthrop, Bayer, Ono	Kringle 5
interleukin-4 + TNF-Alpha -- NIH	KSB 304
interleukin-4 agonist -- Bayer	KSB-201 -- KS Biomedix
interleukin-4 fusion toxin -- Ligand	L 696418 -- Merck
Interleukin-4 receptor -- Immunex, Immun	L 703801 -- Merck
Interleukin-6 -- Ajinomoto, Cangene, Yeda,	L1 -- Acorda
Genetics Institute, Novartis	L-761191 -- Merck
interleukin-6 fusion protein --	lactoferrin -- Meristem, Pharming, Agennix
interleukin-6 fusion toxin -- Ligand, Serono	lactoferrin cardio -- Pharming
interleukin-7 -- IC Innovations	LAG-3 -- Serono
interleukin-7 receptor -- Immunex	LAIT -- GEMMA
interleukin-8 antagonists -- Kyowa	LAK cell cytotoxin -- Arizona
Hakko/Millennium/Pfizer	lamellarins -- PharmaMar/University of
interleukin-9 antagonists -- Genaera	Malaga
interleukins -- Cel-Sci	laminin A peptides -- NIH
Iodine I 131 tositumomab -- Corixa	lanotriplase -- Genetics Institute
ior EPOCIM -- Center of Molecular	laronidase -- BioMarin
Immunology	Lassa fever vaccine
Ior-P3 -- Center of Molecular Immunology	LCAT -- NIH
IP-10 -- NIH	LDP 01 -- Millennium

FIG. 1P

17/345

LDP 02 -- Millennium
 Lecithinized superoxide dismutase --
 Seikagaku
 LeIF adjuvant -- Corixa
 leishmaniasis vaccine -- Corixa
 lenercept -- Hoffman La-Roche
 Lenograstim -- Aventis, Chugai
 lepirudin -- Aventis
 leptin -- Amgen, IC Innovations
 Leptin gene therapy -- Chiron Corporation
 leptin, 2nd-generation -- Amgen
 leridistim -- Pharmacia
 leuprolide, ProMaxx -- Epic
 leuprorelin, oral -- Unigene
 LeuTech -- Papatin
 LEX 032 -- SuperGen
 LiDEPT -- Novartis
 lipase -- Altus Biologics
 lipid A vaccine -- EntreMed
 lipid-linked anchor Tech. -- ICRT, ID
 Biomedical
 liposome-CD4 Tech. -- Sheffield
 Listeria monocytogenes vaccine
 LMB 1
 LMB 7
 LMB 9 -- Battelle Memorial Institute, NIH
 LM-CD45 -- Cantab Pharmaceuticals
 lovastatin -- Merck
 LSA-3
 LT- β receptor -- Biogen
 lung cancer vaccine -- Corixa
 lusupultide -- Scios
 L-Vax -- AVAX
 LY 355455 -- Eli Lilly
 LY 366405 -- Eli Lilly
 LY-355101 -- Eli Lilly
 Lyme disease DNA vaccine -- Vical/Aventis
 Pasteur
 Lyme disease vaccine -- Aquila
 Biopharmaceuticals, Aventis, Pasteur,
 Symbicom, GlaxoSmithKline, Hyland
 Immuno, MedImmune
 Lymphocytic choriomeningitis virus vaccine
 lymphoma vaccine -- Biomira, Genitope
 LYP18
 lys plasminogen, recombinant
 Lysosomal storage disease gene therapy --
 Avigen
 lysostaphin -- Nutrition 21
 M 23 -- Gruenenthal
 M1 monoclonal antibodies -- Acorda
 Therapeutics
 MA 16N7C2 -- Corvas Intl.
 malaria vaccine -- GlaxoSmithKline,
 AdProTech, Antigenics, Apovia, Aventis
 Pasteur, Axis Genetics, Behringwerke,
 CDCP, Chiron Vaccines, Genzyme
 Transgenics, Hawaii, MedImmune, NIH,
 NYU, Oxxon, Roche/Saramane, Biotech
 Australia, Rx Tech
 Malaria vaccine CDC/NIIMALVAC-1
 malaria vaccine, multicomponent
 mammaglobin -- Corixa
 mammastatin -- Biotherapeutics
 mannan-binding lectin -- NatlImmu
 mannan-MUC1 -- Psiron
 MAP 30
 Marinovir -- Phytera
 MARstem -- Maret
 MB-015 -- Mochida
 MBP -- ImmuLogic
 MCI-028 -- Mitsubishi-Tokyo
 MCIF -- Human Genome Sciences
 MDC -- Advanced BioScience -- Akzo
 Nobel, ICOS
 MDX 11 -- Medarex
 MDX 210 -- Medarex
 MDX 22 -- Medarex
 MDX 22

FIG. 1Q

18/345

MDX 240 -- Medarex	Methionine lyase gene therapy --
MDX 33	AntiCancer
MDX 44 -- Medarex	Met-RANTES -- Genexa Biomedical,
MDX 447 -- Medarex	Serono
MDX H210 -- Medarex	Metreleptin
MDX RA -- Houston BioTech., Medarex	MGDF -- Kirin
ME-104 -- Pharmexa	MGV -- Progenics
Measles vaccine	micrin -- Endocrine
Mecasermin -- Cephalon/Chiron, Chiron	microplasmin -- ThromboGenics
MEDI 488 -- MedImmune	MIF -- Genetics Institute
MEDI 500	migration inhibitory factor -- NIH
MEDI 507 -- BioTransplant	Mim CD4.1 -- Xycte Therapies
melanin concentrating hormone --	mirostipen -- Human Genome Sciences
Neurocrine Biosciences	MK 852 -- Merck
melanocortins -- OMRF	Mobenakin -- NIS
Melanoma monoclonal antibodies -- Viragen	molgramostim -- Genetics Institute, Novartis
melanoma vaccine -- GlaxoSmithKline,	monoclonal antibodies -- Abgenix/Celltech,
Akzo Nobel, Avant, Aventis Pasteur,	Immusol/ Medarex, Viragen/ Roslin
Bavarian Nordic, Biovector, CancerVax,	Institute, Cambridge Antibody Tech./Elan
Genzyme Molecular Oncology, Humbolt,	MAB 108 --
ImClone Systems, Memorial, NYU, Oxxon	MAB 10D5 --
Melanoma vaccine Magevac -- Therion	MAB 14.18-interleukin-2 immunocytokine --
memory enhancers -- Scios	Lexigen
meningococcal B vaccine -- Chiron	MAB 14G2a --
meningococcal vaccine -- CAMR	MAB 15A10 --
Meningococcal vaccine group B conjugate -	MAB 170 -- Biomira
- North American Vaccine	MAB 177Lu CC49 --
Meningococcal vaccine group B	MAB 17F9
recombinant -- BioChem Vaccines,	MAB 1D7
Microscience	MAB 1F7 -- Immune Network
Meningococcal vaccine group Y conjugate -	MAB 1H10-doxorubicin conjugate
- North American Vaccine	MAB 26-2F
Meningococcal vaccine groups A B and C	MAB 2A11
conjugate -- North American Vaccine	MAB 2E1 -- RW Johnson
Mepolizumab -- GlaxoSmithKline	MAB 2F5
Metastatin -- EntreMed, Takeda	MAB 31.1 -- International BioImmune
Met-CkB7 -- Human Genome Sciences	Systems
met-enkephalin -- TNI	MAB 32 -- Cambridge Antibody Tech.,
METH-1 -- Human Genome Sciences	Peptech
methioninase -- AntiCancer	MAB 323A3 -- Centocor
	MAB 3C5

FIG. 1R

19/345

MAB 3F12	MAB C242-PE conjugate
MAB 3F8	MAB c30-6
MAB 42/6	MAB CA208-cytorhodin-S conjugate --
MAB 425 -- Merck KGaA	Hoechst Japan
MAB 447-52D -- Merck Sharp & Dohme	MAB CC49 -- Enzon
MAB 45-2D9- -- haematoporphyrin	MAB ch14.18 --
conjugate	MAB CH14.18-GM-CSF fusion protein --
MAB 4B4	Lexigen
MAB 4E3-CPA conjugate -- BCM Oncologia	MAB chCE7
MAB 4E3-daunorubicin conjugate	MAB CI-137 -- AMRAD
MAB 50-6	MAB cisplatin conjugate
MAB 50-61A -- Institut Pasteur	MAB CLB-CD19
MAB 5A8 -- Biogen	MAB CLB-CD19v
MAB 791T/36-methotrexate conjugate	MAB CLL-1 -- Peregrine
MAB 7c11.e8	MAB CLL-1-GM-CSF conjugate
MAB 7E11 C5-selenocystamine conjugate	MAB CLL-1-IL-2 conjugate -- Peregrine
MAB 93KA9 -- Novartis	MAB CLN IgG -- doxorubicin conjugates
MAB A5B7-cisplatin conjugate --	MAB conjugates -- Tanox
Biodynamics Research, Pharmacia	MAB D612
MAB A5B7-I-131	MAB Dal B02
MAB A7	MAB DC101 -- ImClone
MAB A717 -- Exocell	MAB EA 1 --
MAB A7-zinostatin conjugate	MAB EC708 -- Biovation
MAB ABX-RB2 -- Abgenix	MAB EP-5C7 -- Protein Design Labs
MAB ACA 11	MAB ERIC-1 -- ICRT
MAB AFP-I-131 -- Immunomedics	MAB F105 gene therapy
MAB AP1	MAB FC 2.15
MAB AZ1	MAB G250 -- Centocor
MAB B3-LysPE40 conjugate	MAB GA6
MAB B4 -- United Biomedical	MAB GA733
MAB B43 Genistein-conjugate	MAB Gliomab-H -- Viventia Biotech
MAB B43.13-Tc-99m -- Biomira	MAB HB2-saporin conjugate
MAB B43-PAP conjugate	MAB HD 37 --
MAB B4G7-gelonin conjugate	MAB HD37-ricin chain-A conjugate
MAB BCM 43-daunorubicin conjugate --	MAB HNK20 -- Acambis
BCM Oncologia	MAB huN901-DM1 conjugate --
MAB BIS-1	ImmunoGen
MAB BMS 181170 -- Bristol-Myers Squibb	MAB I-131 CC49 -- Corixa
MAB BR55-2	MAB ICO25
MAB BW494	MAB ICR12-CPG2 conjugate
MAB C 242-DM1 conjugate -- ImmunoGen	MAB ICR-62

FIG. 1S

20/345

MAb IRac-ricin A conjugate	MAb R-24
MAb K1	MAb R-24 α Human GD3 -- Celltech
MAb KS1-4-methotrexate conjugate	MAb RFB4-ricin chain A conjugate
MAb L6 -- Bristol-Myers Squibb, Oncogen	MAb RFT5-ricin chain A conjugate
MAb LiCO 16-88	MAb SC 1
MAb LL2-I-131 -- Immunomedics	MAb SM-3 -- ICRT
MAb LL2-Y-90	MAb SMART 1D10 -- Protein Design Labs
MAb LS2D617 -- Hybritech	MAb SMART ABL 364 -- Novartis
MAb LYM-1-gelonin conjugate	MAb SN6f
MAb LYM-1-I-131	MAb SN6f-deglycosylated ricin A chain
MAb LYM-1-Y-90	conjugate --
MAb LYM-2 -- Peregrine	MAb SN6j
MAb M195	MAb SN7-ricin chain A conjugate
MAb M195-bismuth 213 conjugate --	MAb T101-Y-90 conjugate -- Hybritech
Protein Design Labs	MAb T-88 -- Chiron
MAb M195-gelonin conjugate	MAb TB94 -- Cancer ImmunoBiology
MAb M195-I-131	MAb TEC 11
MAb M195-Y-90	MAb TES-23 -- Chugai
MAb MA 33H1 -- Sanofi	MAb TM31 -- Avant
MAb MAD11	MAb TNT-1 -- Cambridge Antibody Tech.,
MAb MGB2	Peregrine
MAb MINT5	MAb TNT-3
MAb MK2-23	MAb TNT-3 -- IL2 fusion protein --
MAb MOC31 ETA(252-613) conjugate	MAb TP3-At-211
MAb MOC-31-In-111	MAb TP3-PAP conjugate --
MAb MOC-31-PE conjugate	MAb UJ13A -- ICRT
MAb MR6 --	MAb UN3
MAb MRK-16 -- Aventis Pasteur	MAb ZME-018-gelonin conjugate
MAb MS11G6	MAb-BC2 -- GlaxoSmithKline
MAb MX-DTPA BrE-3	MAb-DM1 conjugate -- ImmunoGen
MAb MY9	MAb-ricin-chain-A conjugate -- XOMA
MAb Nd2 -- Tosoh	MAb-temoporfin conjugates
MAb NG-1 -- Hygeia	Monopharm C -- Viventia Biotech
MAb NM01 -- Nissin Food	monteplase -- Eisai
MAb OC 125	montirelin hydrate -- Gruenenthal
MAb OC 125-CMA conjugate	moroctocog alfa -- Genetics Institute
MAb OKI-1 -- Ortho-McNeil	Moroctocog-alfa -- Pharmacia
MAb OX52 -- Bioproducts for Science	MP 4
MAb PMA5	MP-121 -- Biopharm
MAb PR1	MP-52 -- Biopharm
MAb prost 30	MRA -- Chugai

FIG. 1T

21/345

MS 28168 -- Mitsui Chemicals, Nihon Schering	Neuroprotective vaccine -- University of Auckland
MSH fusion toxin -- Ligand	neurotrophic chimaeras -- Regeneron
MSI-99 -- Genaera	neurotrophic factor -- NsGene, CereMedix
MT 201 -- Micromet	NeuroVax -- Immune Response
Muc-1 vaccine -- Corixa	neurturin -- Genentech
mucosal tolerance -- Aberdeen	neutral endopeptidase -- Genentech
mullerian inhibiting subst	NGF enhancers -- NeuroSearch
muplestim -- Genetics Institute, Novartis, DSM Anti-Infectives	NHL vaccine -- Large Scale Biology
murine MAb -- KS Biomedix	NIP45 -- Boston Life Sciences
Mutant somatropin -- JCR Pharmaceutical	NKI-B20
MV 833 -- Toagosei	NM 01 -- Nissin Food
Mycoplasma pulmonis vaccine	NMI-139 -- NitroMed
Mycoprex -- XOMA	NMMP -- Genetics Institute
myeloperoxidase -- Henogen	NN-2211 -- Novo Nordisk
myostatin -- Genetics Institute	Noggin -- Regeneron
Nacolumab tafenatox -- Pharmacia	Nonacog alfa
nagrestipen -- British Biotech	Norelin -- Biostar
NAP-5 -- Corvas Intl.	Norwalk virus vaccine
NAPc2 -- Corvas Intl.	NRLU 10 -- NeoRx
nartograstim -- Kyowa	NRLU 10 PE -- NeoRx
Natalizumab -- Protein Design Labs	NT-3 -- Regeneron
Nateplase -- NIH, Nihon Schering	NT-4/5 -- Genentech
nateplase -- Schering AG	NU 3056
NBI-3001 -- Neurocrine Biosci.	NU 3076
NBI-5788 -- Neurocrine Biosci.	NX 1838 -- Gilead Sciences
NBI-6024 -- Neurocrine Biosci.	NY ESO-1/CAG-3 antigen -- NIH
Nef inhibitors -- BRI	NYVAC-7 -- Aventis Pasteur
Neisseria gonorrhoea vaccine -- Antex Biologics	NZ-1002 -- Novazyme
Neomycin B-arginine conjugate	obesity therapy -- Nobex
Nerelimomab -- Chiron	OC 10426 -- Ontogen
Nerve growth factor -- Amgen -- Chiron, Genentech	OC 144093 -- Ontogen
Nerve growth factor gene therapy	OCIF -- Sankyo
nesiritide citrate -- Scios	Oct-43 -- Otsuka
neuregulin-2 -- CeNeS	OK PSA - liposomal
neurocan -- NYU	OKT3-gamma-1-ala-ala
neuronal delivery system -- CAMR	OM 991
	OM 992
	Omalizumab -- Genentech
	oncoimmunin-L -- NIH
	Oncolysin B -- ImmunoGen

FIG. 1U

22/345

Oncolysin CD6 -- ImmunoGen	PAM 4 -- Merck
Oncolysin M -- ImmunoGen	pamiteplase -- Yamanouchi
Oncolysin S -- ImmunoGen	pancreatin, Minitabs -- Eurand
Oncophage -- Antigenics	Pangen -- Fournier
Oncostatin M -- Bristol-Myers Squibb	Pantarin -- Selective Genetics
OncoVax-CL -- Jenner Biotherapies	Parainfluenza virus vaccine -- Pharmacia,
OncoVax-P -- Jenner Biotherapies	Pierre Fabre
oncept -- Yeda	paraoxanase -- Esperion
onychomycosis vaccine -- Boehringer	parathyroid hormone -- Abiogen, Korea
Ingelheim	Green Cross
opebecan -- XOMA	Parathyroid hormone (1-34) --
opioids -- Arizona	Chugai/Suntory
Oprelvekin -- Genetics Institute	Parkinson's disease gene therapy -- Cell
Org-33408 b-- Akzo Nobel	Genesys/ Ceregene
Orolip DP -- EpiCept	Parvovirus vaccine -- MedImmune
oryzacystatin	PCP-Scan -- Immunomedics
OSA peptides -- GenSci Regeneration	PDGF cocktail -- Theratechnologies
osteoblast-cadherin GF -- Pharis	peanut allergy therapy -- Dynavax
Osteocalcin-thymidine kinase gene therapy	PEG anti-ICAM MAb -- Boehringer
osteogenic protein -- Curis	Ingelheim
osteopontin -- OraPharma	PEG asparaginase -- Enzon
osteoporosis peptides -- Integra, Telios	PEG glucocerebrosidase
osteoprotegerin -- Amgen, SnowBrand	PEG hirudin -- Knoll
otitis media vaccines -- Antex Biologics	PEG interferon-alpha-2a -- Roche
ovarian cancer -- University of Alabama	PEG interferon-alpha-2b + ribavirin --
OX40-IgG fusion protein -- Cantab, Xenova	Biogen, Enzon, ICN Pharmaceuticals,
P 246 -- Diatide	Schering-Plough
P 30 -- Alfacell	PEG MAb A5B7 --
p1025 -- Active Biotech	Pegacaristim -- Amgen -- Kirin Brewery --
P-113 ^A -- Demegen	ZymoGenetics
P-16 peptide -- Transition Therapeutics	Pegaldesleukin -- Research Corp
p43 -- Ramot	pegaspargase -- Enzon
P-50 peptide -- Transition Therapeutics	pegfilgrastim -- Amgen
p53 + RAS vaccine -- NIH, NCI	PEG-interferon Alpha -- Viragen
PACAP(1-27) analogue	PEG-interferon Alpha 2A -- Hoffman La-
paediatric vaccines -- Chiron	Roche
Pafase -- ICOS	PEG-interferon Alpha 2B -- Schering-
PAGE-4 plasmid DNA -- IDEC	Plough
PAI-2 -- Biotech Australia, Human	PEG-r-hirudin -- Abbott
Therapeutics	PEG-uricase -- Mountain View
Palivizumab -- MedImmune	Pegvisomant -- Genentech

FIG. 1V

23/345

PEGylated proteins, PolyMASC -- Valentis Pharmaprojects No. 5947 -- StressGen
 PEGylated recombinant native human leptin Pharmaprojects No. 5961 --
 -- Roche Theratechnologies
 Pentumomab Pharmaprojects No. 5962 -- NIH
 Penetratin -- Cyclacel Pharmaprojects No. 5966 -- NIH
 Pepscan -- Antisoma Pharmaprojects No. 5994 -- Pharming
 peptide G -- Peptech, ICRT Pharmaprojects No. 5995 -- Pharming
 peptide vaccine -- NIH, NCI Pharmaprojects No. 6023 -- IMMUCON
 Pexelizumab Pharmaprojects No. 6063 -- Cytoclonal
 pexiganan acetate -- Genaera Pharmaprojects No. 6073 -- SIDDCO
 Pharmaprojects No. 3179 -- NYU Pharmaprojects No. 6115 -- Genzyme
 Pharmaprojects No. 3390 -- Ernest Orlando Pharmaprojects No. 6227 -- NIH
 Pharmaprojects No. 3417 -- Sumitomo Pharmaprojects No. 6230 -- NIH
 Pharmaprojects No. 3777 -- Acambis Pharmaprojects No. 6236 -- NIH
 Pharmaprojects No. 4209 -- XOMA Pharmaprojects No. 6243 -- NIH
 Pharmaprojects No. 4349 -- Baxter Intl. Pharmaprojects No. 6244 -- NIH
 Pharmaprojects No. 4651 Pharmaprojects No. 6281 -- Senetek
 Pharmaprojects No. 4915 -- Avanir Pharmaprojects No. 6365 -- NIH
 Pharmaprojects No. 5156 -- Rhizogenics Pharmaprojects No. 6368 -- NIH
 Pharmaprojects No. 5200 -- Pfizer Pharmaprojects No. 6373 -- NIH
 Pharmaprojects No. 5215 -- Origene Pharmaprojects No. 6408 -- Pan Pacific
 Pharmaprojects No. 5216 -- Origene Pharmaprojects No. 6410 -- Athersys
 Pharmaprojects No. 5218 -- Origene Pharmaprojects No. 6421 -- Oxford
 Pharmaprojects No. 5267 -- ML GlycoSciences
 Laboratories Pharmaprojects No. 6522 -- Maxygen
 Pharmaprojects No. 5373 -- MorphoSys Pharmaprojects No. 6523 -- Pharis
 Pharmaprojects No. 5493 -- Metabolex Pharmaprojects No. 6538 -- Maxygen
 Pharmaprojects No. 5707 -- Genentech Pharmaprojects No. 6554 -- APALEXO
 Pharmaprojects No. 5728 -- Autogen Pharmaprojects No. 6560 -- Ardana
 Pharmaprojects No. 5733 -- BioMarin Pharmaprojects No. 6562 -- Bayer
 Pharmaprojects No. 5757 -- NIH Pharmaprojects No. 6569 -- Eos
 Pharmaprojects No. 5765 -- Gryphon Phenoxazine
 Pharmaprojects No. 5830 -- AntiCancer Phenylase -- Ibex
 Pharmaprojects No. 5839 -- Dyax Pigment epithelium derived factor --
 Pharmaprojects No. 5849 -- Johnson & plasminogen activator inhibitor-1,
 Johnson recombinant -- DuPont Pharmaceuticals
 Pharmaprojects No. 5860 -- Mitsubishi-
 Tokyo
 Pharmaprojects No. 5869 -- Oxford
 GlycoSciences
 Pharmaprojects No. 5883 -- Asahi Brewery

FIG. 1W

24/345

Plasminogen activators -- Abbott Laboratories, American Home Products, Boehringer Mannheim, Chiron Corporation, DuPont Pharmaceuticals, Eli Lilly, Shionogi, Genentech, Genetics Institute, GlaxoSmithKline, Hemispherx Biopharma, Merck & Co, Novartis, Pharmacia Corporation, Wakamoto, Yeda	prostate-specific antigen -- Entremed
plasminogen-related peptides -- Bio-Tech. General/MGH	protein A -- RepliGen
platelet factor 4 -- RepliGen	protein adhesives -- Enzon
Platelet-derived growth factor -- Amgen -- ZymoGenetics	protein C -- Baxter Intl., PPL Therapeutics, ZymoGenetics
plusonemin-- Hayashibara	protein C activator -- Gilead Sciences
PMD-2850 -- Protherics	protein kinase R antags -- NIH
Pneumococcal vaccine -- Antex Biologics, Aventis Pasteur	protirelin -- Takeda
Pneumococcal vaccine intranasal -- BioChem Vaccines/Biovector	protocadherin 2 -- Caprion
PR1A3	Pro-urokinase -- Abbott, Bristol-Myers Squibb, Dainippon, Tosoh -- Welfide
PR-39	P-selectin glycoprotein ligand-1 -- Genetics Institute
pralmorelin -- Kaken	pseudomonal infections -- InterMune
Pretarget-Lymphoma -- NeoRx	Pseudomonas vaccine -- Cytovax
Priliximab -- Centocor	PSGL-Ig -- American Home Products
PRO 140 -- Progenics	PSP-94 -- Procyon
PRO 2000 -- Procept	PTH 1-34 -- Nobex
PRO 367 -- Progenics	Quilimmune-M -- Antigenics
PRO 542 -- Progenics	R 101933
pro-Apo A-I -- Esperion	R 125224 -- Sankyo
prolactin -- Genzyme	RA therapy -- Cardion
Prosaptide TX14(A) -- Bio-Tech. General	Rabies vaccine recombinant -- Aventis Pasteur, BioChem Vaccines, Kaketsuken Pharmaceuticals
prostate cancer antibodies -- Immunex, UroCor	RadioTheraCIM -- YM BioSciences
prostate cancer antibody therapy -- Genentech/UroGenesys, Genotherapeutics	Ramot project No. 1315 -- Ramot
prostate cancer immunotherapeutics -- The PSMA Development Company	Ramot project No. K-734A -- Ramot
prostate cancer vaccine -- Aventis Pasteur, Zonagen, Corixa, Dendreon, Jenner Biotherapies, Therion Biologics	Ramot project No. K-734B -- Ramot
	RANK -- Immunex
	ranpirnase -- Alfacell
	ranpirnase-anti-CD22 MAb -- Alfacell
	RANTES inhibitor -- Milan
	RAPID drug delivery systems -- ARIAD
	rasburicase -- Sanofi
	rBPI-21, topical -- XOMA
	RC 529 -- Corixa
	rCFTR -- Genzyme Transgenics
	RD 62198
	rDnase -- Genentech
	RDP-58 -- SangStat

FIG. 1X

25/345

RecepTox-Fce -- Keryx	Ribozyme gene therapy -- Genset
RecepTox-GnRH -- Keryx, MTR Technologies	Rickettsial vaccine recombinant
RecepTox-MBP -- Keryx, MTR Technologies	RIGScan CR -- Neoprobe
recFSH -- Akzo Nobel, Organon	RIP-3 -- Rigel
REGA 3G12	RK-0202 -- RxKinetix
Regavirumab -- Teijin	RLT peptide -- Esperion
relaxin -- Connetics Corp	rM/NEI -- IVAX
Renal cancer vaccine -- Macropharm	rmCRP -- Immtech
repifermin -- Human Genome Sciences	RN-1001 -- Renovo
Respiratory syncytial virus PFP-2 vaccine -- Wyeth-Lederle	RN-3 -- Renovo
Respiratory syncytial virus vaccine -- GlaxoSmithKline, Pharmacia, Pierre Fabre	RNAse conjugate -- Immunomedics
Respiratory syncytial virus vaccine inactivated	RO 631908 -- Roche
Respiratory syncytial virus-parainfluenza virus vaccine -- Aventis Pasteur, Pharmacia	Rotavirus vaccine -- Merck
Retepase -- Boehringer Mannheim, Hoffman La-Roche	RP 431 -- DuPont Pharmaceuticals
Retropep -- Retroscreen	RP-128 -- Resolution
RFB4 (dsFv) PE38	RPE65 gene therapy --
RFI 641 -- American Home Products	RPR 110173 -- Aventis Pasteur
RFTS -- UAB Research Foundation	RPR 115135 -- Aventis Pasteur
RG 12986 -- Aventis Pasteur	RPR 116258A -- Aventis Pasteur
RG 83852 -- Aventis Pasteur	rPSGL-Ig -- American Home Products
RG-1059 -- RepliGen	r-SPC surfactant -- Byk Gulden
rGCR -- NIH	rV-HER-2/neu -- Therion Biologics
rGLP-1 -- Restoragen	SA 1042 -- Sankyo
rGRF -- Restoragen	sacrosidase -- Orphan Medical
rh Insulin -- Eli Lilly	Sant 7
RHAMM targeting peptides -- Cangene	Sargramostim -- Immunex
rHb1.1 -- Baxter Intl.	saruplase -- Gruenenthal
rhCC10 -- Claragen	Satumomab -- Cytogen
rhCG -- Sero	SB 1 -- COR Therapeutics
Rheumatoid arthritis gene therapy	SB 207448 -- GlaxoSmithKline
Rheumatoid arthritis vaccine -- Veterans Affairs Medical Center	SB 208651 -- GlaxoSmithKline
rhLH -- Sero	SB 240683 -- GlaxoSmithKline
	SB 249415 -- GlaxoSmithKline
	SB 249417 -- GlaxoSmithKline
	SB 6 -- COR Therapeutics
	SB RA 31012 --
	SC 56929 -- Pharmacia
	SCA binding proteins -- Curis, Enzon
	scFv(14E1)-ETA Berlex Laboratories, Schering AG
	ScFv(FRP5)-ETA --

FIG. 1Y

26/345

ScFv6C6-PE40 –
 SCH 55700 – Celltech
 Schistosomiasis vaccine – Glaxo
 Wellcome/Medeira, Brazil
 SCPF – Advanced Tissue Sciences
 scuPA-suPAR complex – Hadasit
 SD-9427 – Pharmacia
 SDF-1 – Ono
 SDZ 215918 – Novartis
 SDZ 280125 – Novartis
 SDZ 89104 – Novartis
 SDZ ABL 364 – Novartis
 SDZ MMA 383 – Novartis
 serine protease inhbs – Pharis
 sermorelin acetate – Serono
 SERP-1 – Viron
 sertenef – Dainippon
 serum albumin, Recombinant human –
 Aventis Behring
 serum-derived factor – Hadasit
 Sevirumab – Novartis
 SGN 14 – Seattle Genetics
 SGN 15 – Seattle Genetics
 SGN 17/19 – Seattle Genetics
 SGN 30 – Seattle Genetics
 SGN-10 – Seattle Genetics
 SGN-11 – Seattle Genetics
 SH 306 – DuPont Pharmaceuticals
 Shanvac-B – Shantha
 Shigella flexneri vaccine – Avant, Acambis,
 Novavax
 Shigella sonnei vaccine –
 sICAM-1 – Boehringer Ingelheim
 Silteplase – Genzyme
 SIV vaccine – Endocon, Institut Pasteur
 SK 896 – Sanwa Kagaku Kenkyusho
 SK-827 – Sanwa Kagaku Kenkyusho
 Skeletex – CellFactors
 SKF 106160 – GlaxoSmithKline
 S-nitroso-AR545C –
 SNTP – Active Biotech
 somatomedin-1 – GroPep, Mitsubishi-
 Tokyo, NIH
 somatomedin-1 carrier protein – Insmed
 somatostatin – Ferring
 Somatotropin/
 Human Growth Hormone – Bio-Tech.
 General, Eli Lilly
 somatropin – Bio-Tech. General, Alkermes,
 ProLease, Aventis Behring, Biovector,
 Cangene, Dong-A, Eli Lilly, Emisphere,
 Enact, Genentech, Genzyme Transgenics,
 Grandis/InfiMed, CSL, InfiMed, MacroMed,
 Novartis, Novo Nordisk, Pharmacia
 Sero, TranXenoGen
 somatropin derivative – Schering AG
 somatropin, AIR – Eli Lilly
 Somatropin, inhaled – Eli Lilly/Alkermes
 somatropin, Kabi – Pharmacia
 somatropin, Orasome – Novo Nordisk
 Sonermin – Dainippon Pharmaceutical
 SP(V5.2)C – Supertek
 SPf66
 sphingomyelinase – Genzyme
 SR 29001 – Sanofi
 SR 41476 – Sanofi
 SR-29001 – Sanofi
 SS1(dsFV)-PE38 – NeoPharm
 β 2 microglobulin – Avidex
 β 2-microglobulin fusion proteins – NIH
 β -amyloid peptides – CeNeS
 β -defensin – Pharis
 Staphylococcus aureus infections –
 Inhibitex/ZLB
 Staphylococcus aureus vaccine conjugate –
 Nabi
 Staphylococcus therapy – Tripep
 Staphylokinase – Biovation, Prothera,
 Thrombogenetics
 Streptococcal A vaccine – M6
 Pharmaceuticals, North American Vaccine
 Streptococcal B vaccine – Microscience

FIG. 1Z

27/345

Streptococcal B vaccine recombinant --	TFPI -- EntreMed
Biochem Vaccines	tgD-IL-2 -- Takeda
Streptococcus pyogenes vaccine	TGF-Alpha -- ZymoGenetics
STRL-33 -- NIH	TGF- β -- Kolon
Subalin -- SRC VB VECTOR	TGF- β 2 -- Insmmed
SUIS -- United Biomedical	TGF- β 3 -- OSI
SUIS-LHRH -- United Biomedical	Thalassaemia gene therapy -- Crucell
SUN-E3001 -- Suntory	TheraCIM-h-R3 -- Center of Molecular
super high affinity monoclonal antibodies --	Immunology, YM BioSciences
YM BioSciences	Theradigm-HBV -- Epimmune
Superoxide dismutase -- Chiron, Enzon,	Theradigm-HPV -- Epimmune
Ube Industries, Bio-Tech, Yeda	Theradigm-malaria -- Epimmune
superoxide dismutase-2 -- OXIS	Theradigm-melanoma -- Epimmune
suppressin -- UAB Research Foundation	TheraFab -- Antisoma
SY-161-P5 -- ThromboGenics	ThGRF 1-29 -- Theratechnologies
SY-162 -- ThromboGenics	ThGRF 1-44 -- Theratechnologies
Systemic lupus erythematosus vaccine --	thrombomodulin -- Iowa, Novocastra
MedClone/VivoRx	Thrombopoietin -- Dragon Pharmaceuticals,
T cell receptor peptide vaccine	Genentech
T4N5 liposomes -- AGI Dermatics	thrombopoietin, Pliva -- Recepton
TACI, soluble -- ZymoGenetics	Thrombospondin 2 --
targeted apoptosis -- Antisoma	thrombostatin -- Thromgen
tasonermin -- Boehringer Ingelheim	thymalfasin -- SciClone
TASP	thymocartin -- Gedeon Richter
TASP-V	thymosin Alpha1 -- NIH
Tat peptide analogues -- NIH	thyroid stimulating hormone -- Genzyme
TBP I -- Yeda	tICAM-1 -- Bayer
TBP II	Tick anticoagulant peptide -- Merck
TBV25H -- NIH	TIF -- Xoma
Tc 99m for cea1 -- Center of Molecular	Tifacogin -- Chiron, NIS, Pharmacia
Immunology	Tissue factor -- Genentech
Tc 99m P 748 -- Diatide	Tissue factor pathway inhibitor
Tc 99m votumumab -- Intracell	TJN-135 -- Tsumura
Tc-99m rh-Annexin V -- Theseus Imaging	TM 27 -- Avant
teceleukin -- Biogen	TM 29 -- Avant
tenecteplase -- Genentech	TMC-151 -- Tanabe Seiyaku
Teriparatide -- Armour Pharmaceuticals,	TNF tumour necrosis factor -- Asahi Kasei
Asahi Kasei, Eli Lilly	TNF Alpha -- Cytimmune
terlipressin -- Ferring	TNF antibody -- Johnson & Johnson
testisin -- AMRAD	TNF binding protein -- Amgen
Tetrafabricin -- Roche	TNF degradation product -- Oncotech

FIG. 1AA . . .

28/345

TNF receptor -- Immunex	TXU-PAP
TNF receptor 1, soluble -- Amgen	TY-10721 -- TOA Eiyo
TNF Tumour necrosis factor-alpha -- Asahi Kasei, Genetech, Mochida	Type I diabetes vaccine -- Research Corp
TNF-Alpha inhibitor -- Tripep	Typhoid vaccine CVD 908
TNFR:Fc gene therapy -- Targeted Genetics	U 143677 -- Pharmacia
TNF-SAM2	U 81749 -- Pharmacia
Tolerimab -- Innogenetics	UA 1248 -- Arizona
Toxoplasma gondii vaccine -- GlaxoSmithKline	UGIF -- Sheffield
TP 9201 -- Telios	UIC 2
TP10 -- Avant	UK 101
TP20 -- Avant	UK-279276 -- Corvas Intl.
tPA -- Centocor	urodilatin -- Pharis
trafermin -- Scios	urofolitrophin -- Serono
TRAIL/Apo2L -- Immunex	uteroferrin -- Pepgen
transferrin-binding proteins -- CAMR	V 20 -- GLYCODESIGN
Transforming growth factor-beta-1 -- Genentech	V2 vasopressin receptor gene therapy
transport protein -- Genesis	vaccines -- Active Biotech
TRH -- Ferring	Varicella zoster glycoprotein vaccine -- Research Corporation Technologies
Triabin -- Schering AG	Varicella zoster virus vaccine live -- Cantab Pharmaceuticals
Triconal	Vascular endothelial growth factor -- Genentech, University of California
Triflavin	Vascular endothelial growth factors -- R&D Systems
troponin I -- Boston Life Sciences	vascular targeting agents -- Peregrine
TRP-2 ^A -- NIH	vasopermeation enhancement agents -- Peregrine
trypsin inhibitor -- Mochida	vasostatin -- NIH
TSP-1 gene therapy --	VCL -- Bio-Tech. General
TT-232	VEGF -- Genentech, Scios
TTS-CD2 -- Active Biotech	VEGF inhibitor -- Chugai
Tuberculosis vaccine -- Aventis Pasteur, Genesis	VEGF-2 -- Human Genome Sciences
Tumor Targeted Superantigens -- Active Biotech -- Pharmacia	VEGF-Trap -- Regeneron
tumour vaccines -- PhotoCure	viscumin, recombinant -- Madaus
tumour-activated prodrug antibody conjugates -- Millennium/ImmunoGen	Vitaxin
tumstatin -- ILEX	Vitrax -- ISTA Pharmaceuticals
Tuvirumab -- Novartis	West Nile virus vaccine -- Bavarian Nordic
TV-4710 -- Teva	WP 652
TWEAK receptor -- Immunex	WT1 vaccine -- Corixa
	WX-293 -- Wilex BioTech.

FIG. 1BB

29/345

WX-360 – Wilex BioTech.	YM 207 – Yamanouchi
WX-UK1 – Wilex BioTech.	YM 337 – Protein Design Labs
XMP-500 – XOMA	Yttrium-90 labelled biotin
XomaZyme-791 – XOMA	Yttrium-90-labeled anti-CEA MAb T84.66 –
XTL 001 – XTL Biopharmaceuticals	ZD 0490 – AstraZeneca
XTL 002 – XTL Biopharmaceuticals	ziconotide – Elan
yeast delivery system – GlobelImmune	ZK 157138 – Berlex Laboratories
Yersinia pestis vaccine	Zolimomab aritox
YIGSR-Stealth – Johnson & Johnson	Zorcell – Immune Response
Yisum Project No. D-0460 – Yisum	ZRXL peptides – Novartis

FIG. 1CC

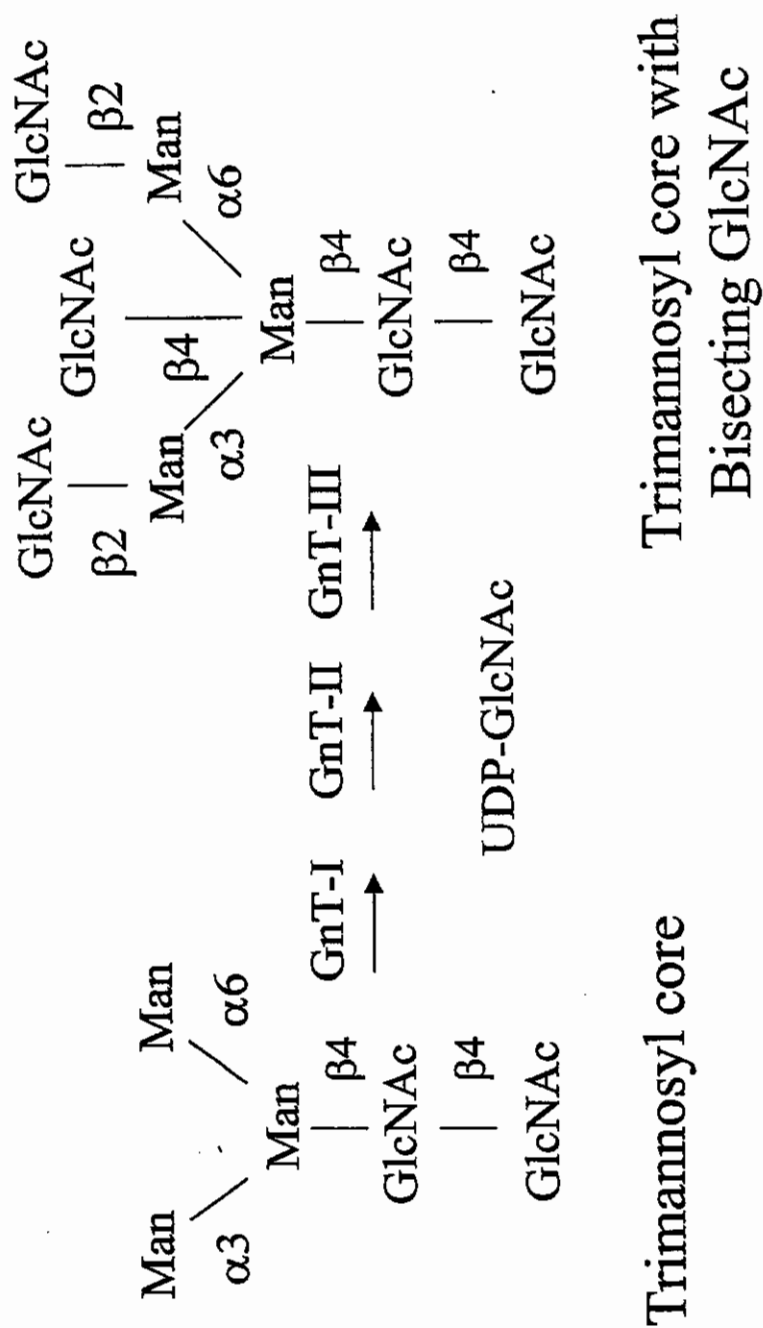


FIG. 2

31/345

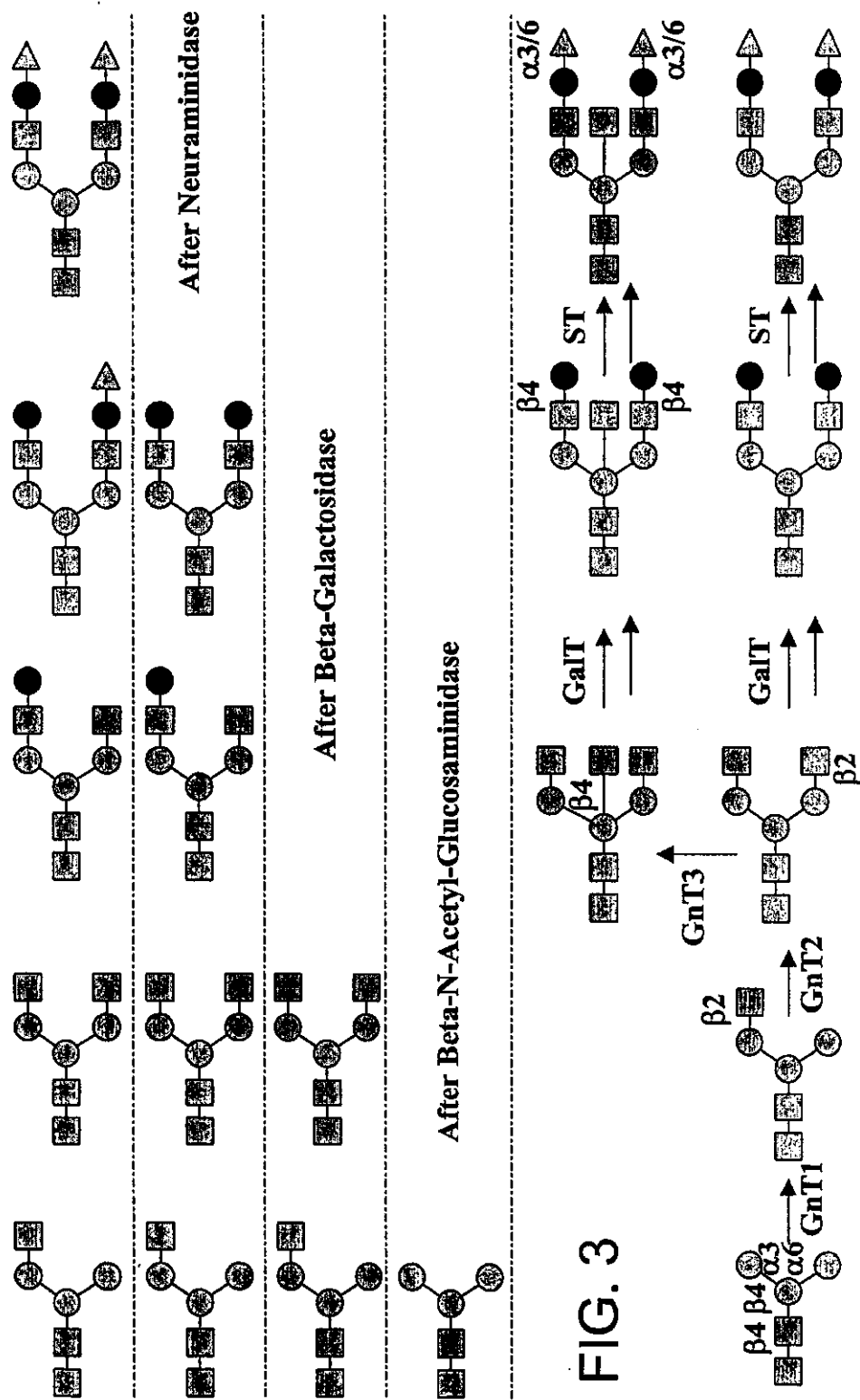


FIG. 3

32/345

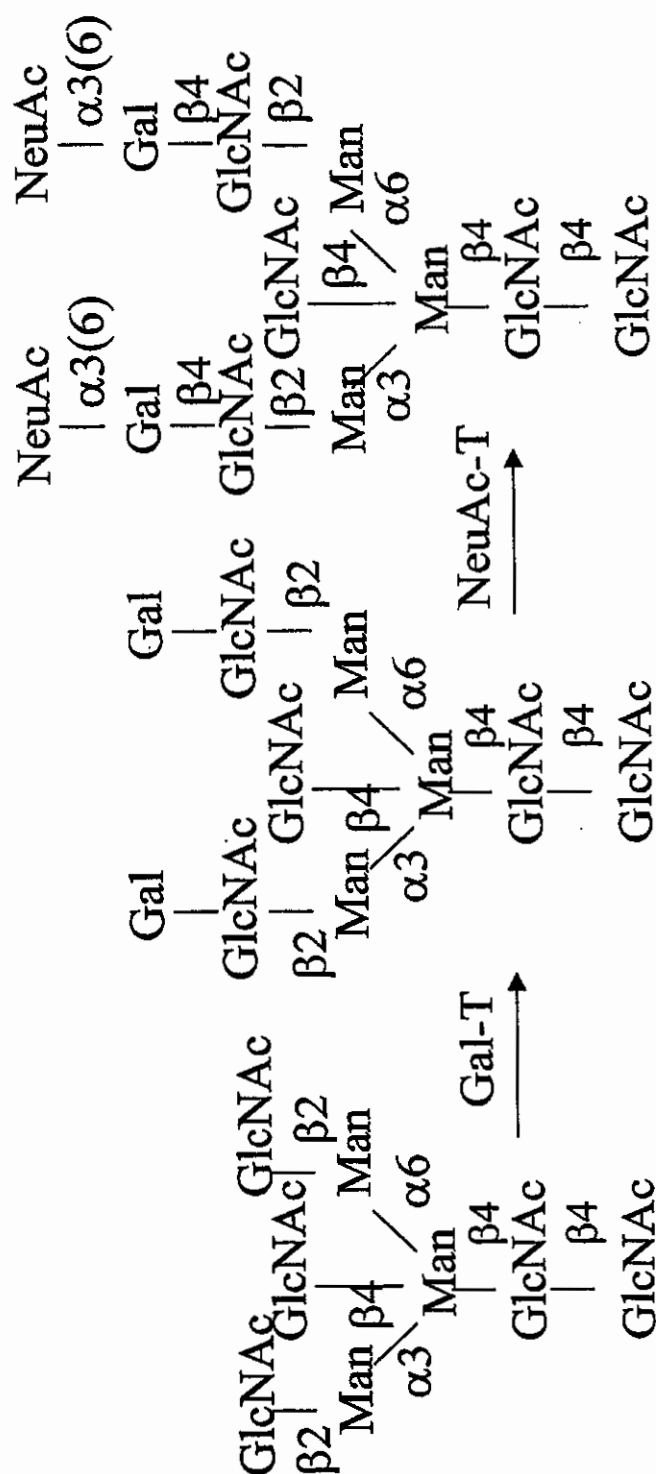


FIG. 4

33/345

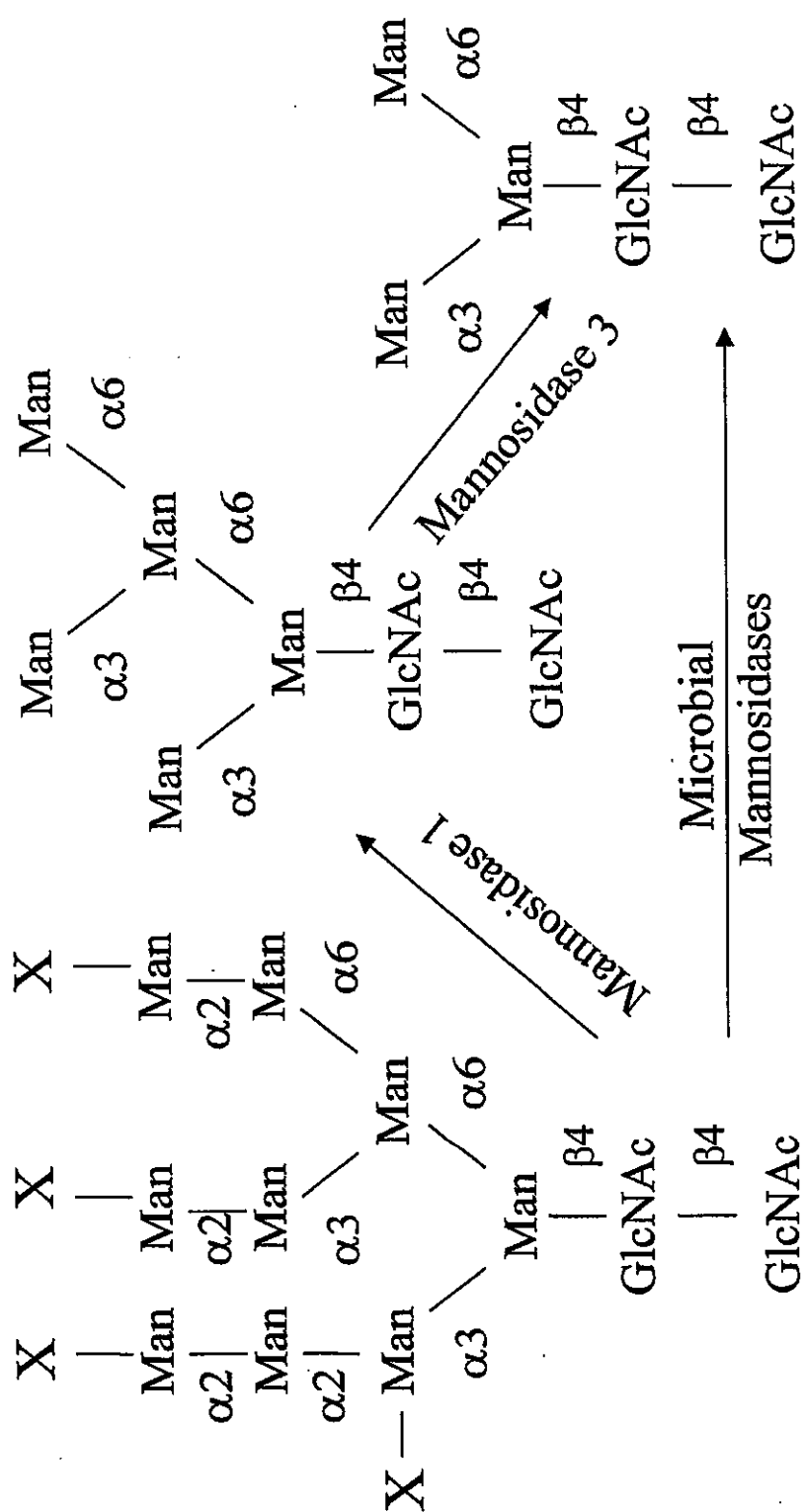


FIG. 5

34/345

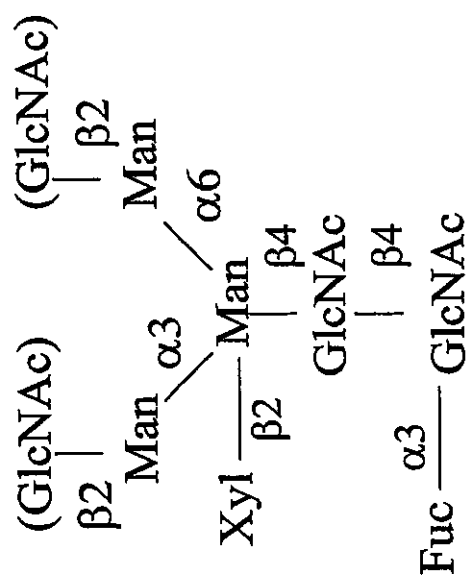


FIG. 6

35/345

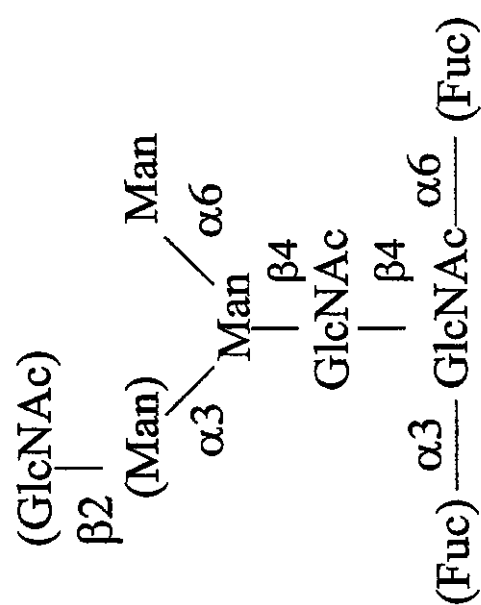


FIG. 7

36/345

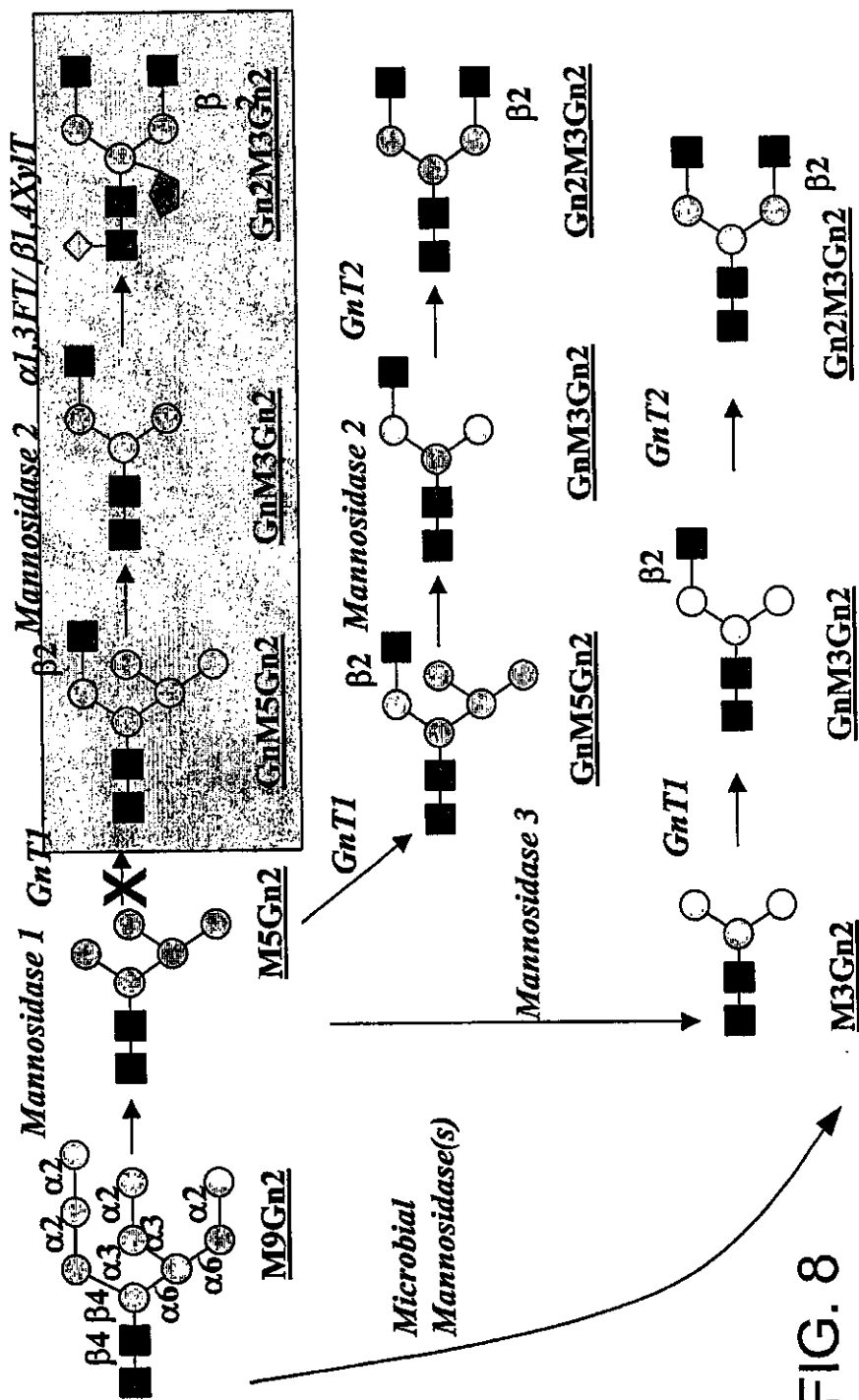


FIG. 8

37/345

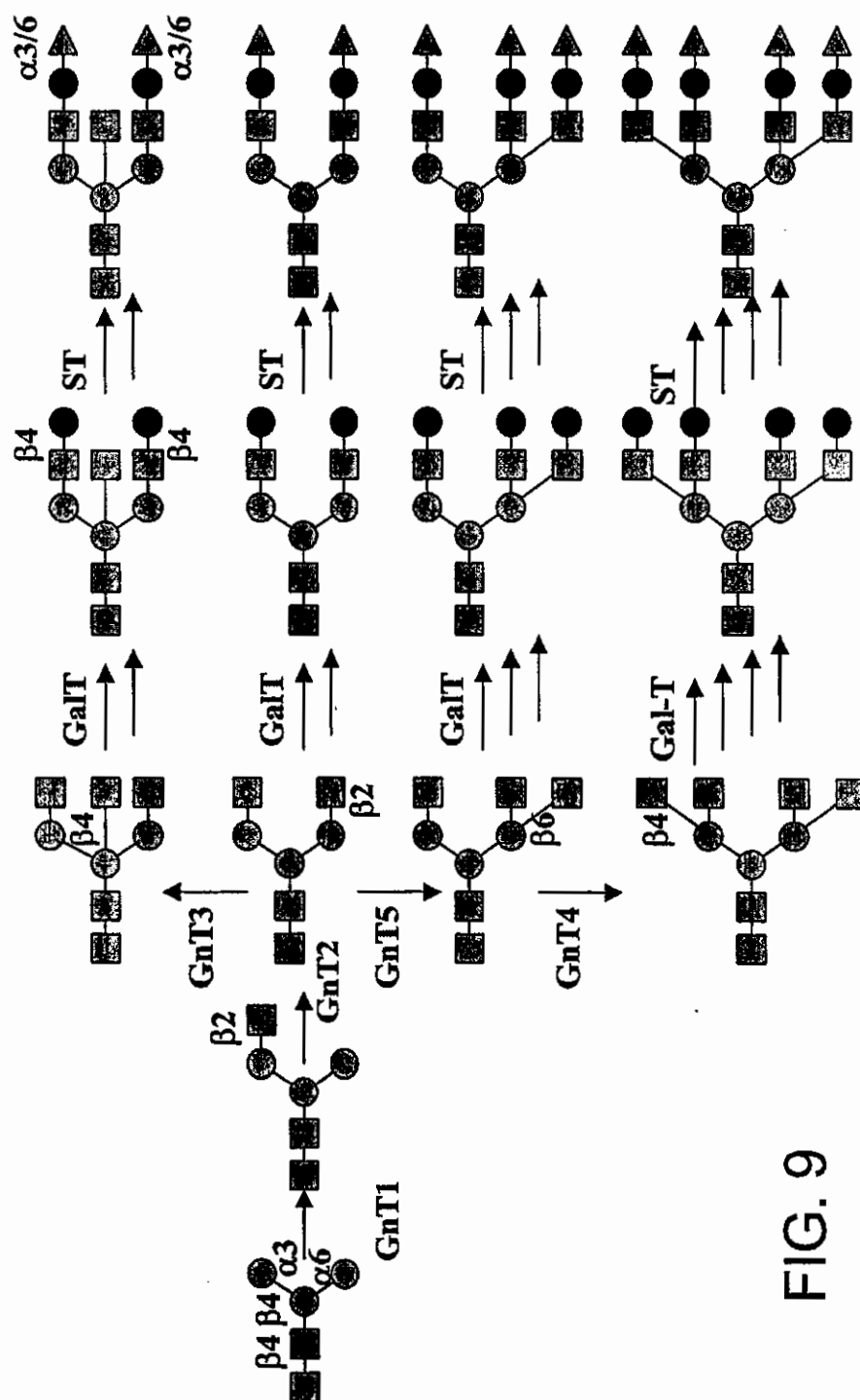


FIG. 9

38/345

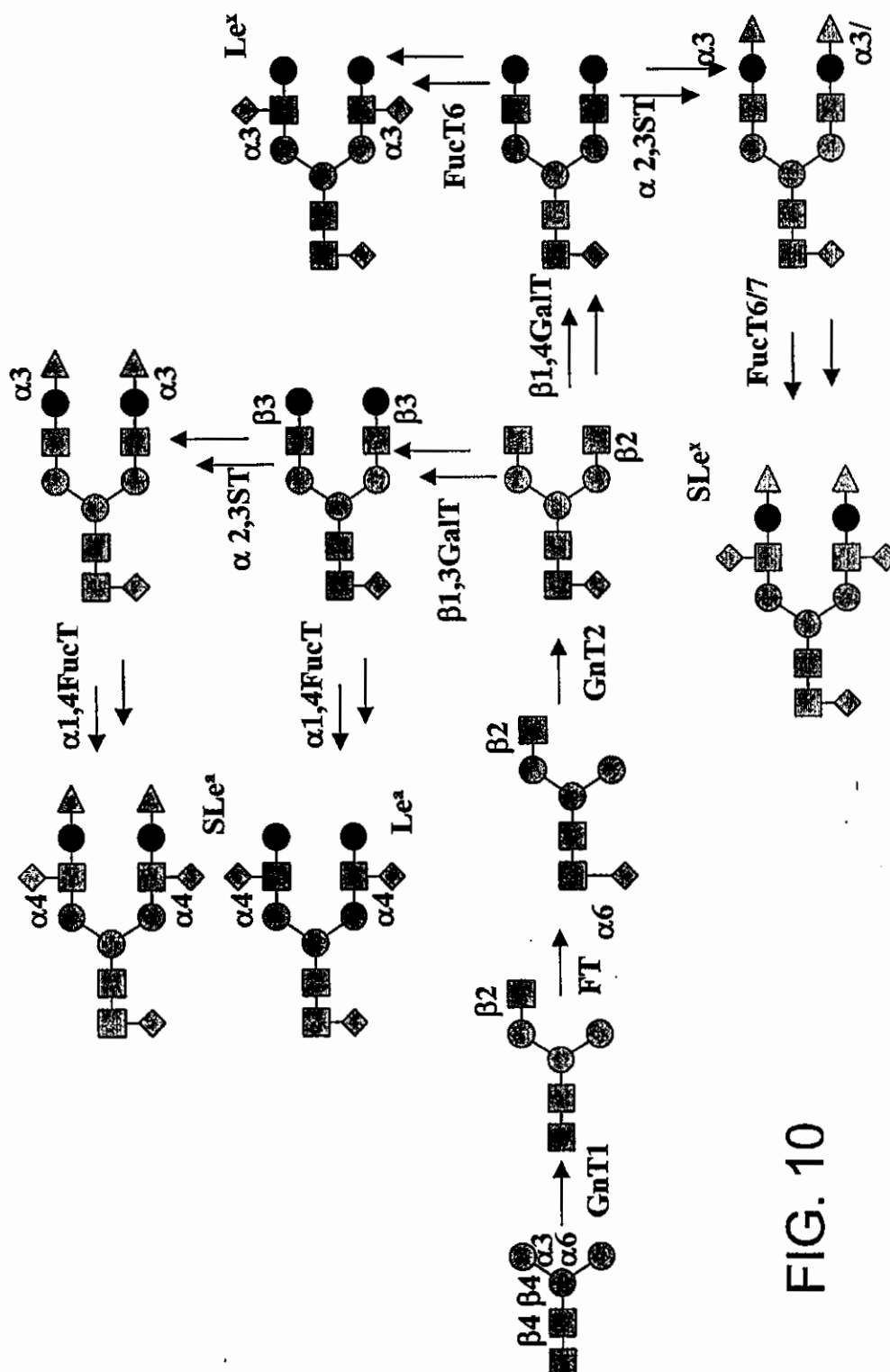


FIG. 10

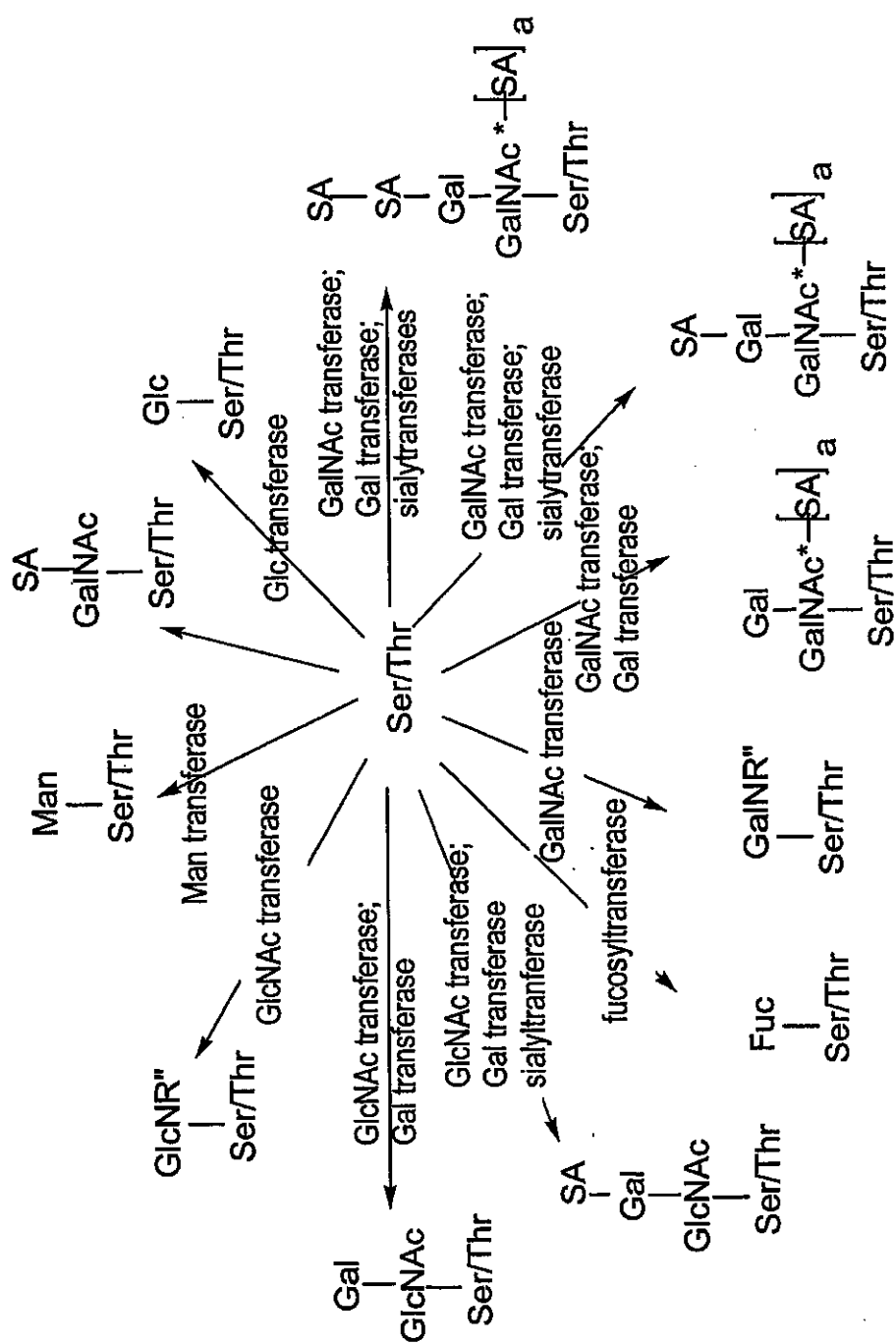


FIG. 11

40/345

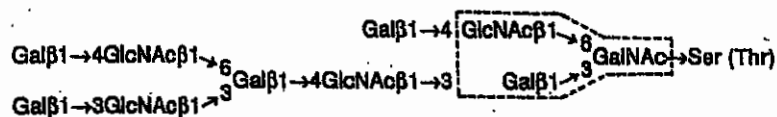
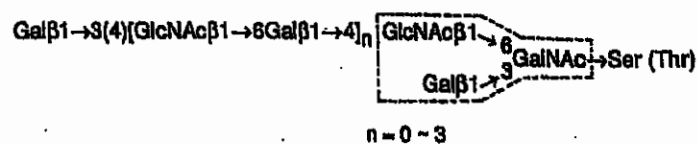
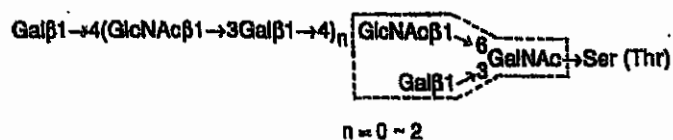
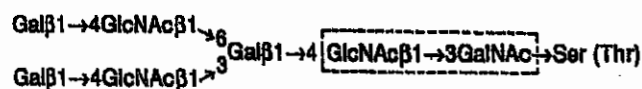
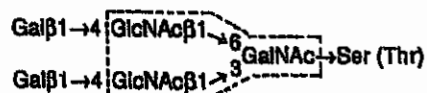
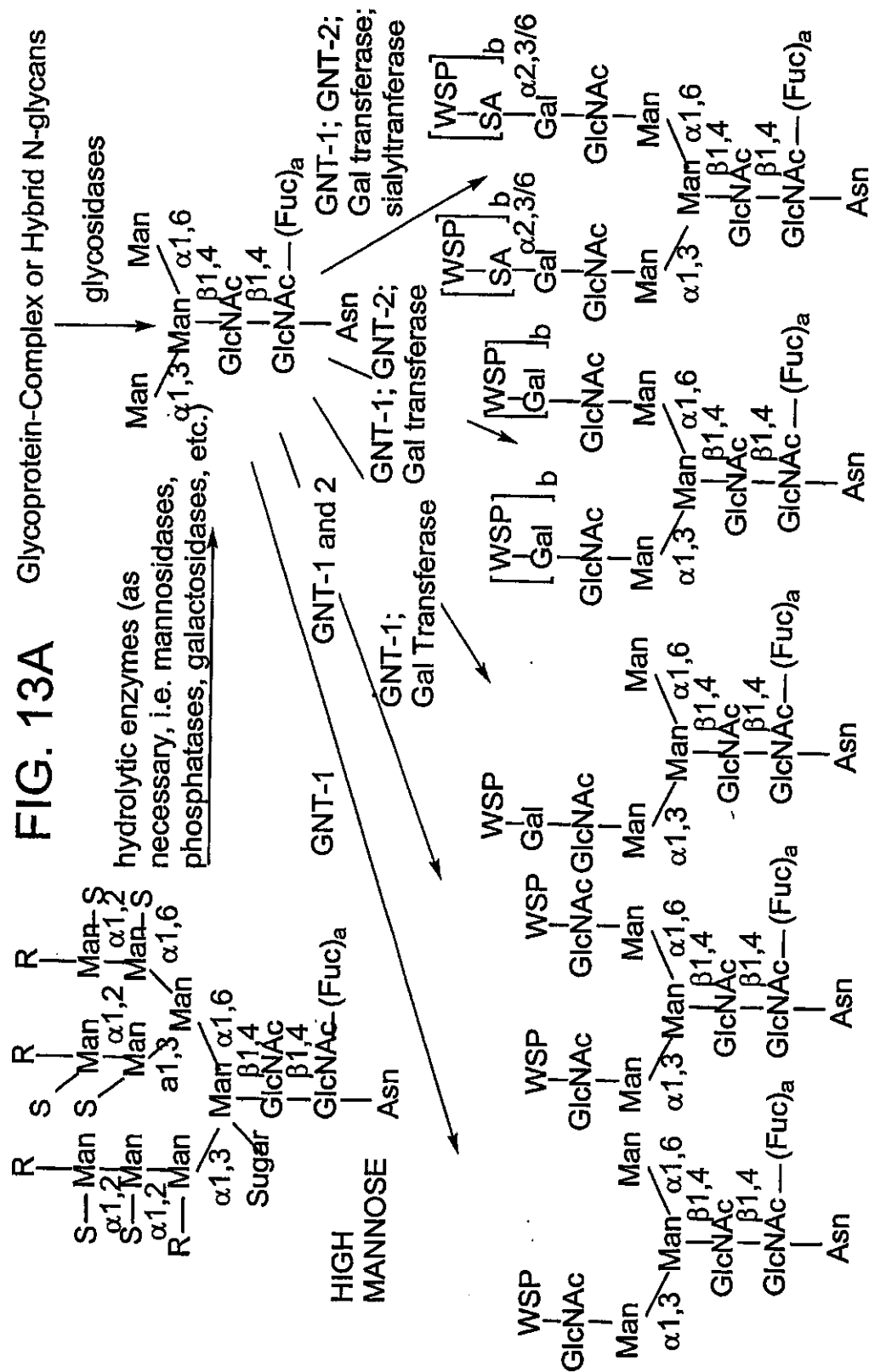
Core 1**Core 2****Core 3****Core 4**

FIG. 12

FIG. 13A



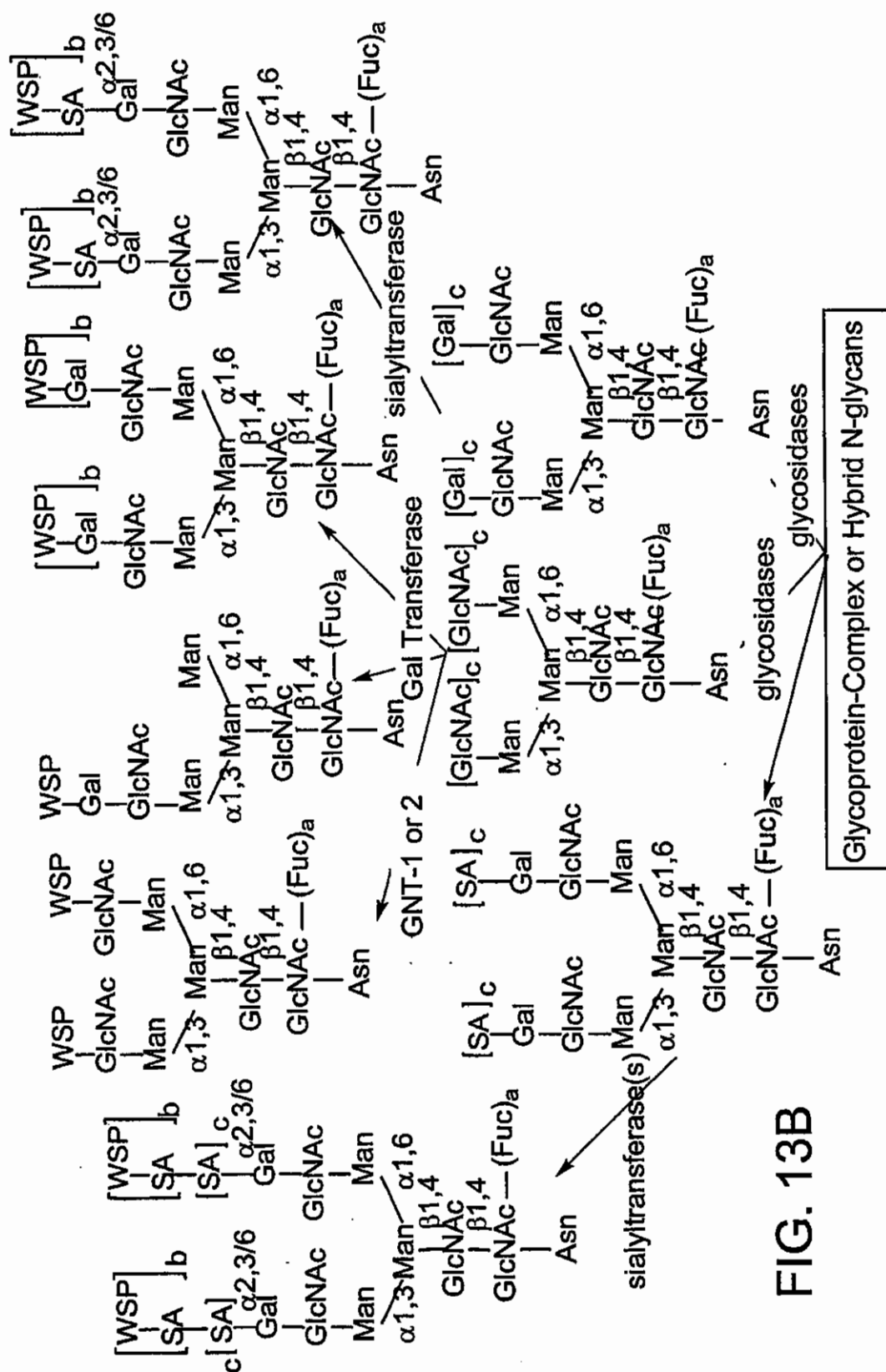


FIG. 13B

43/345

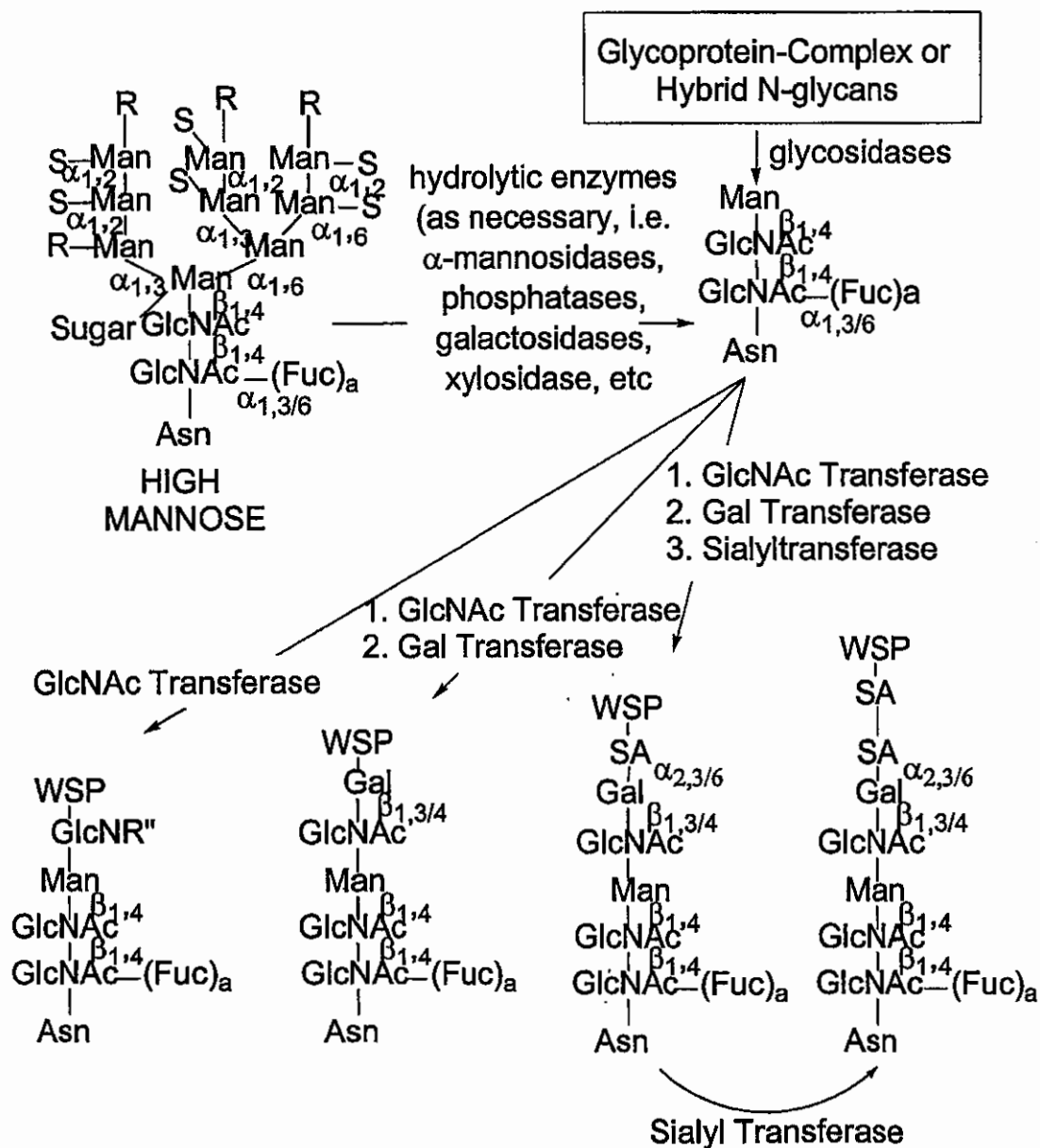


FIG. 14

44/345

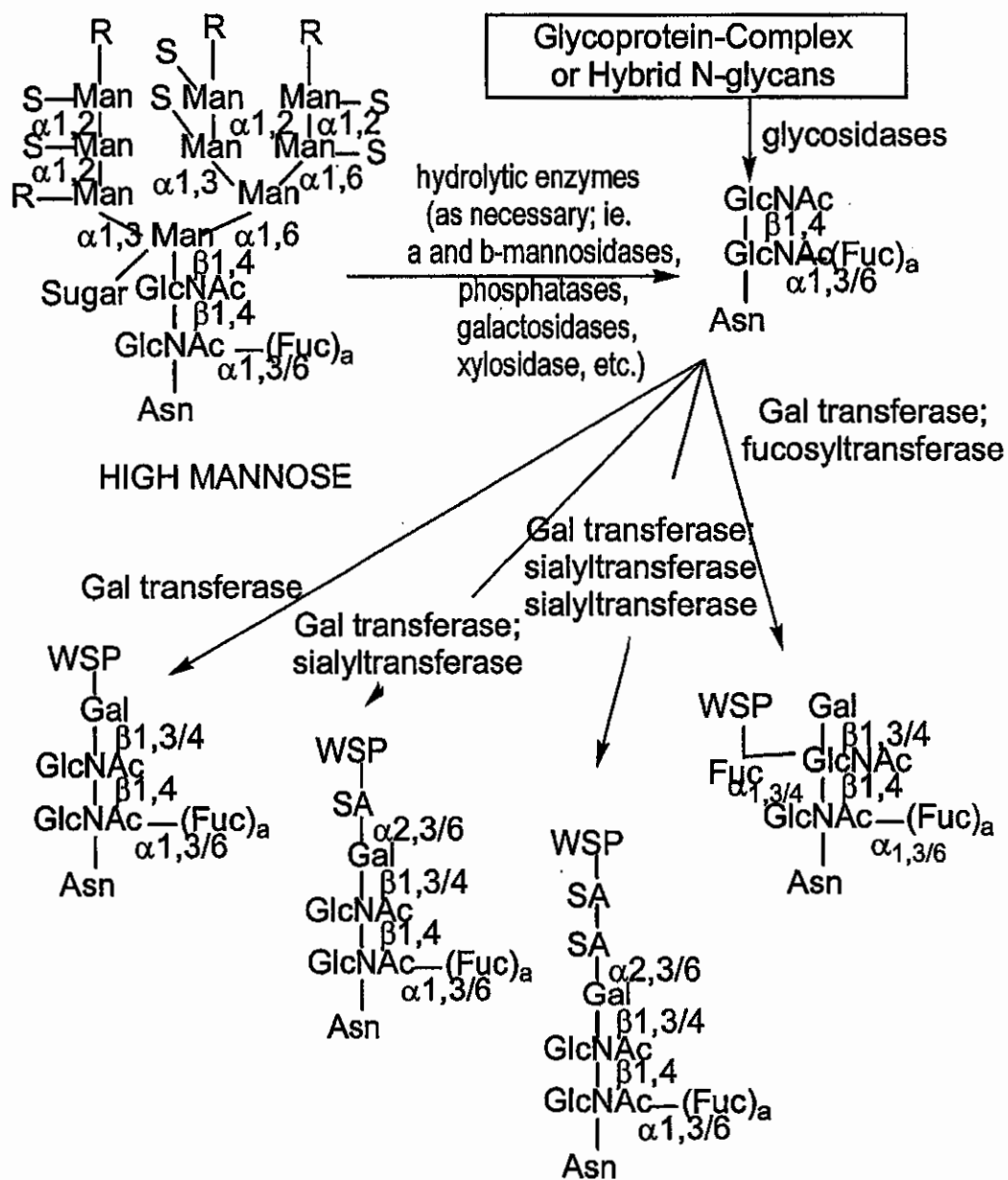


FIG. 15

45/345

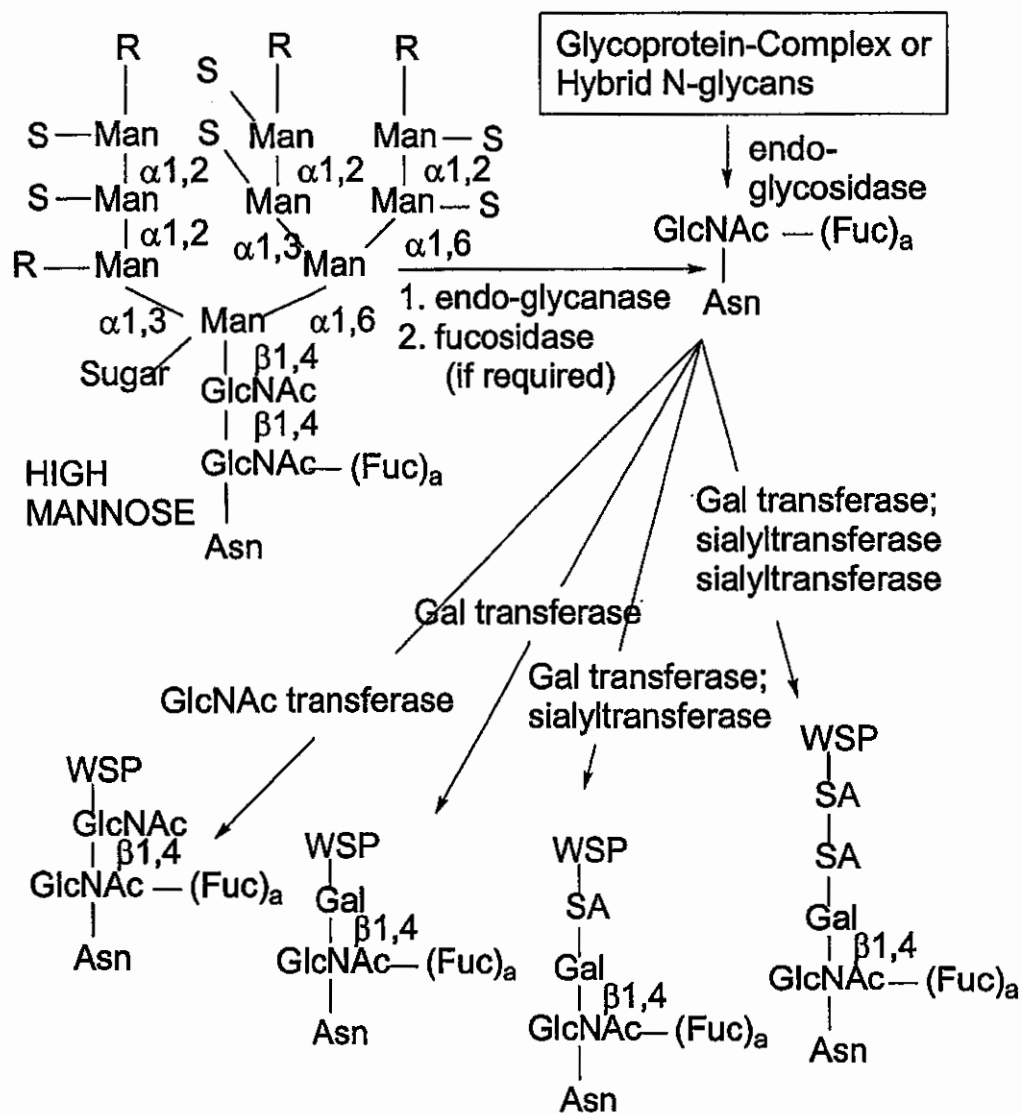
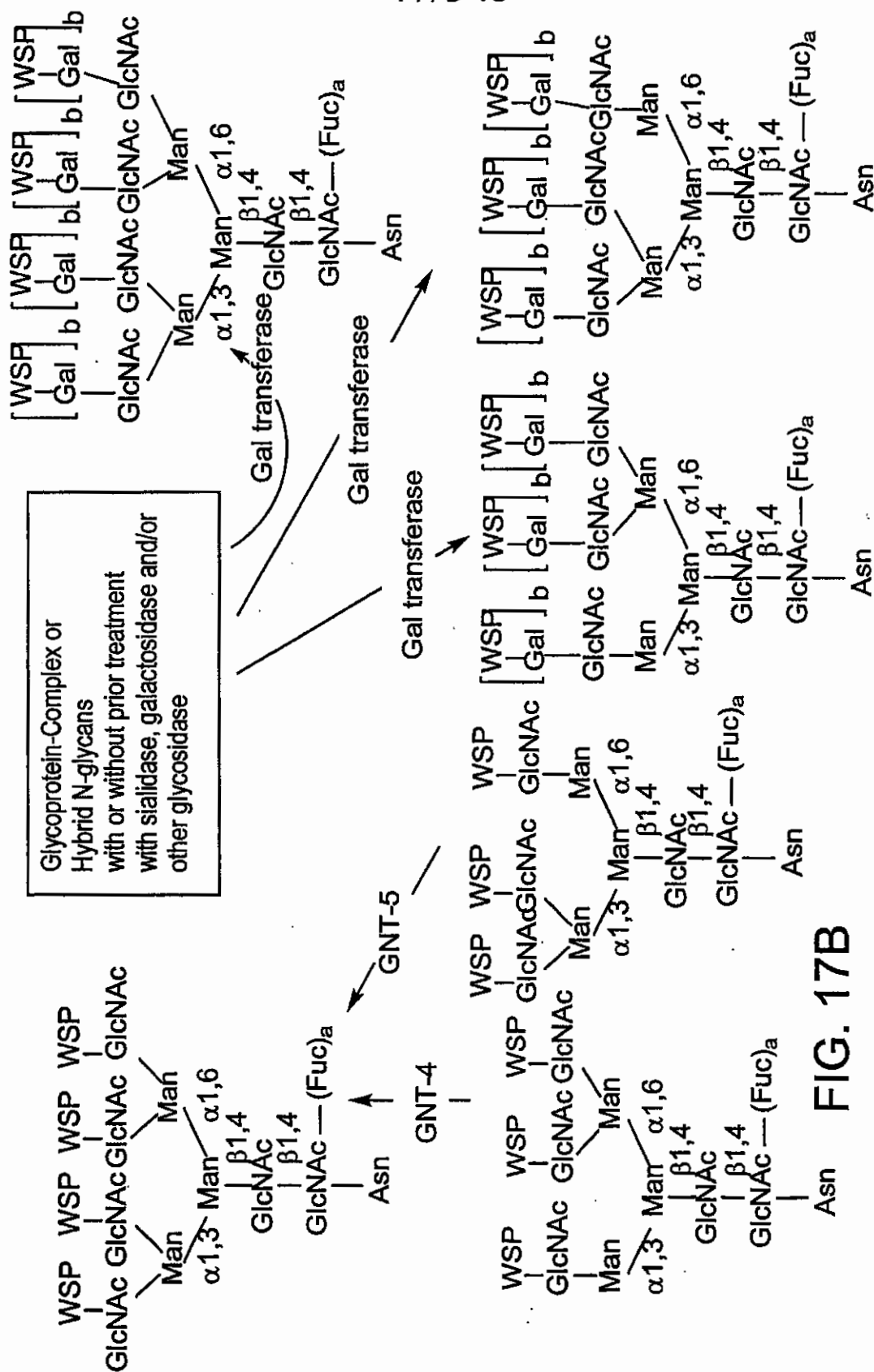
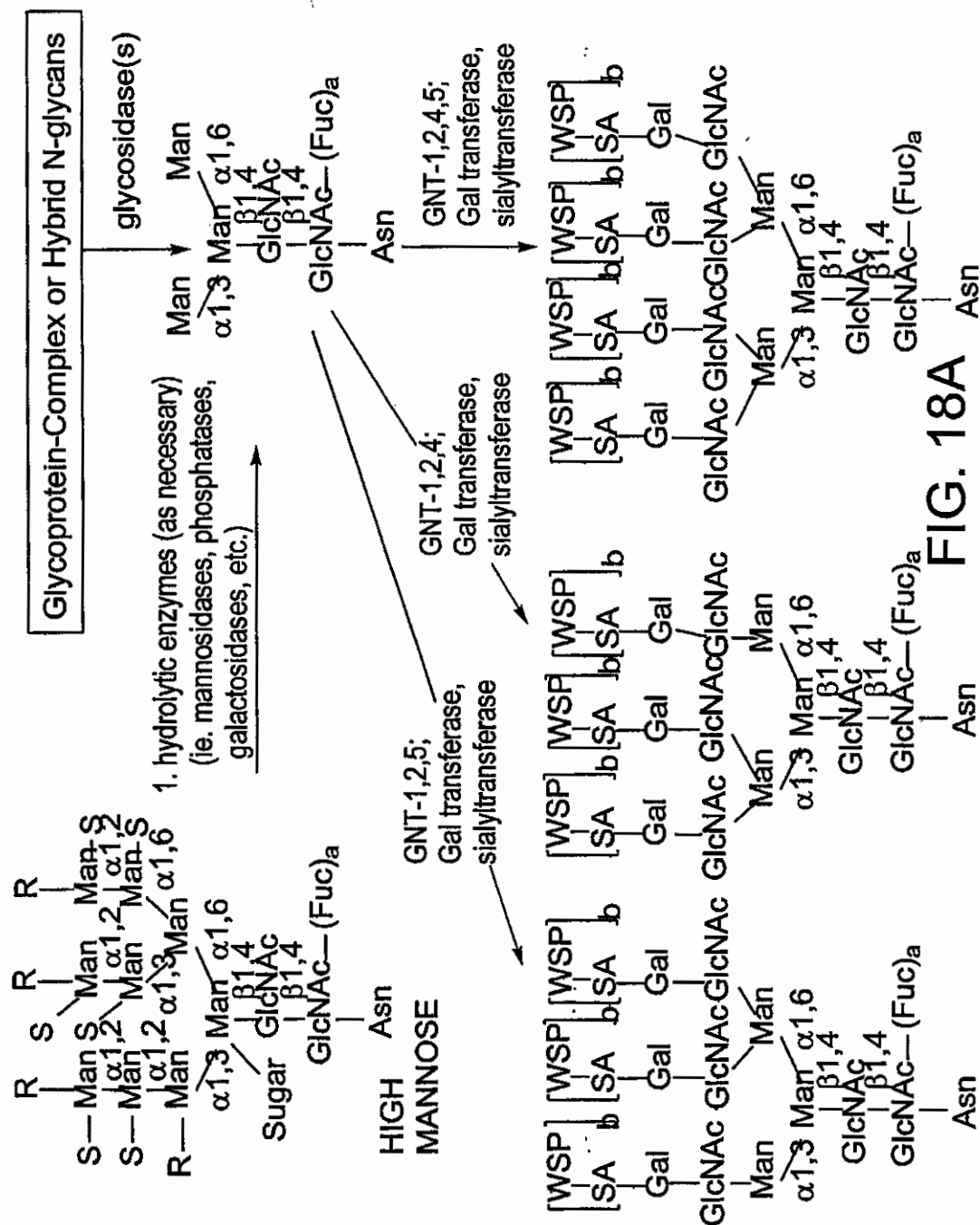


FIG. 16



47/345





49/345

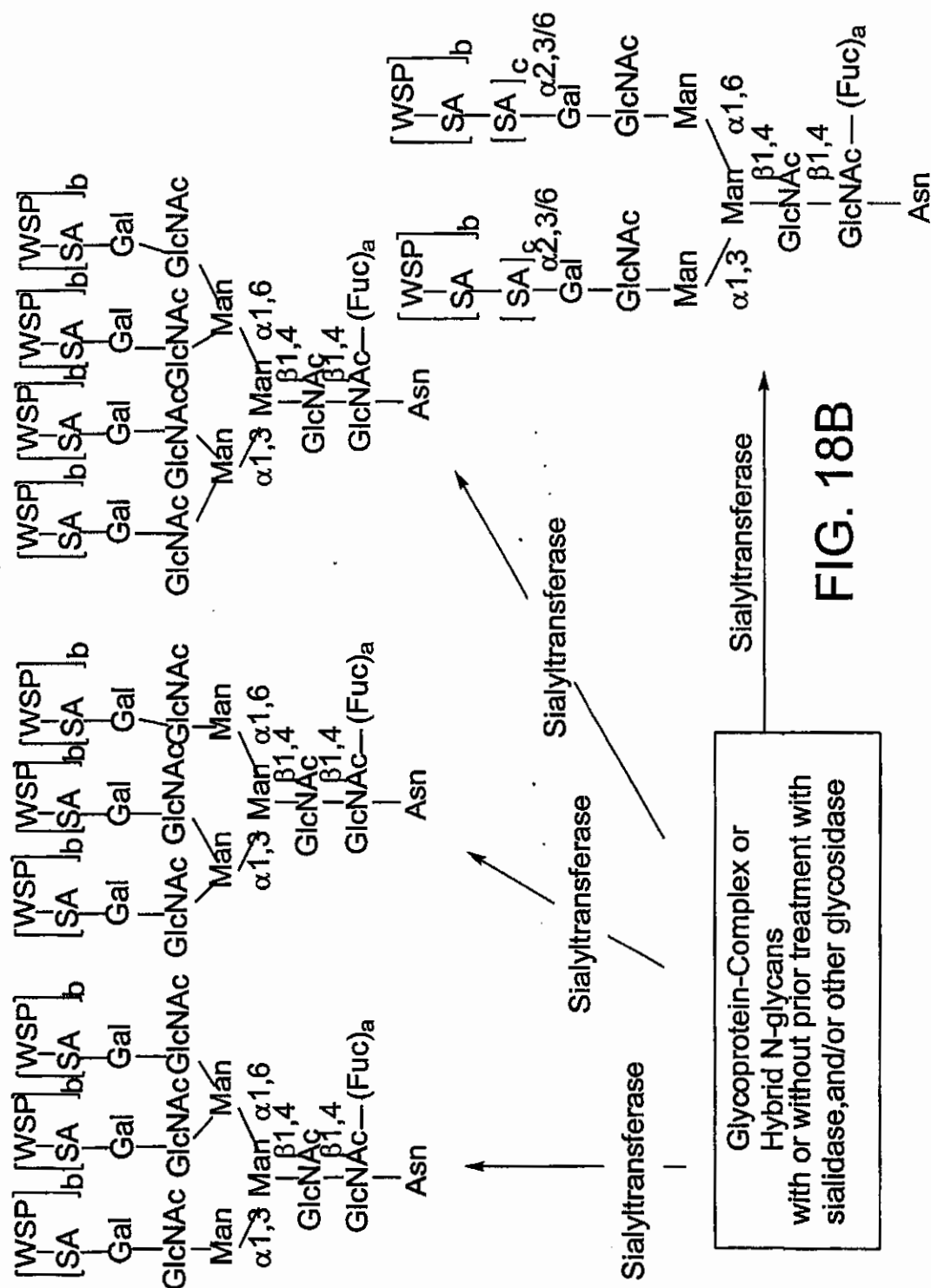


FIG. 18B

50/345

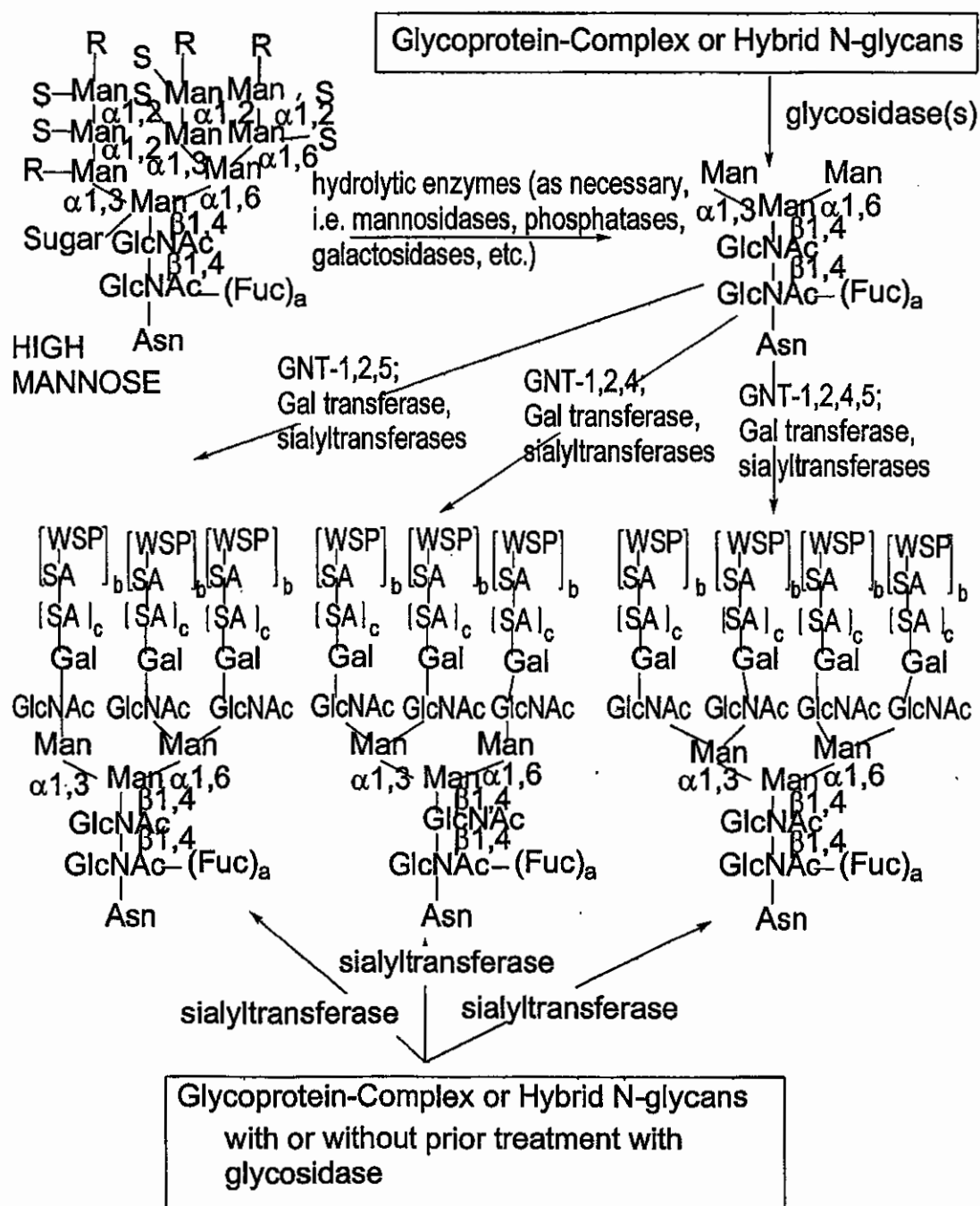
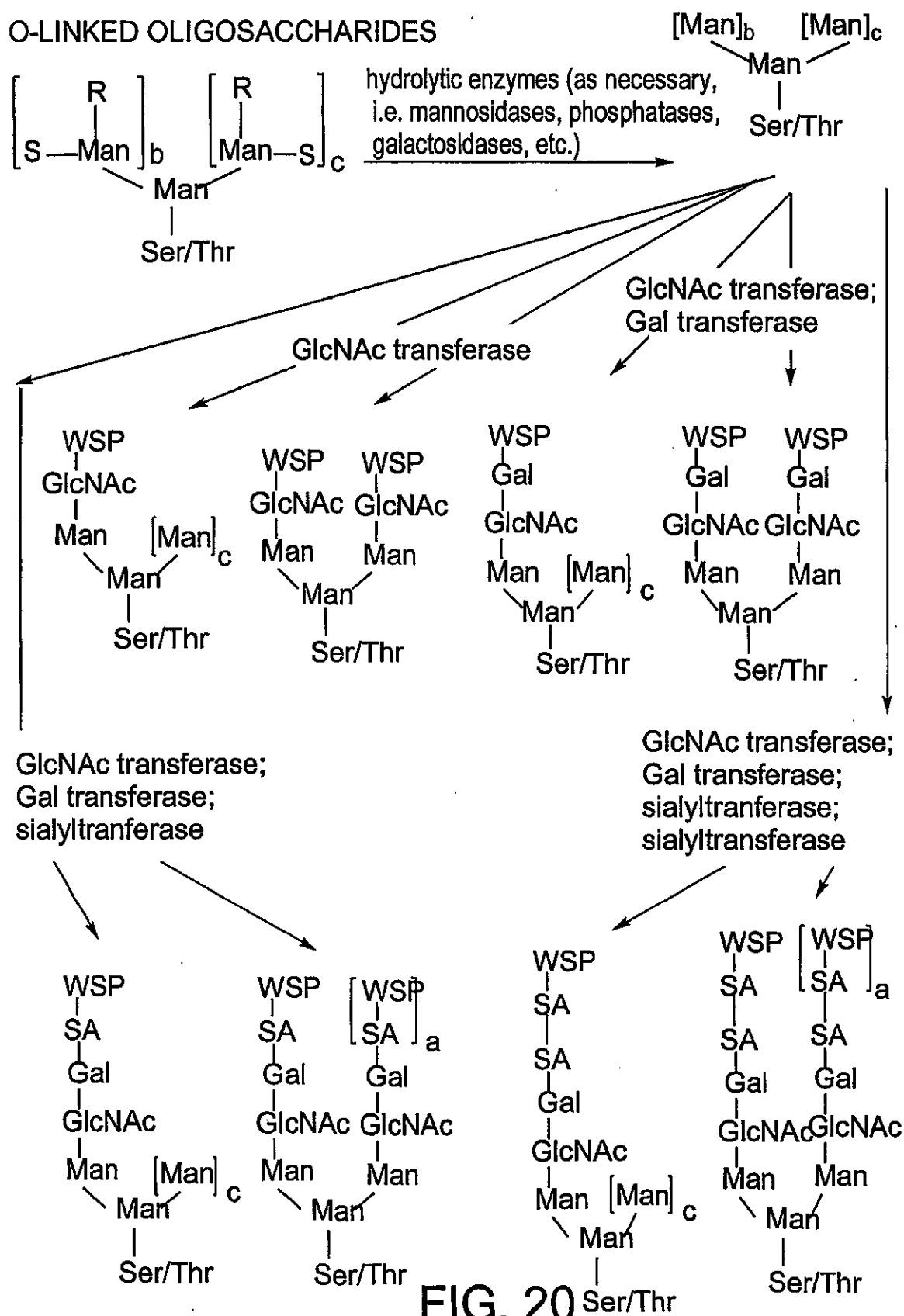


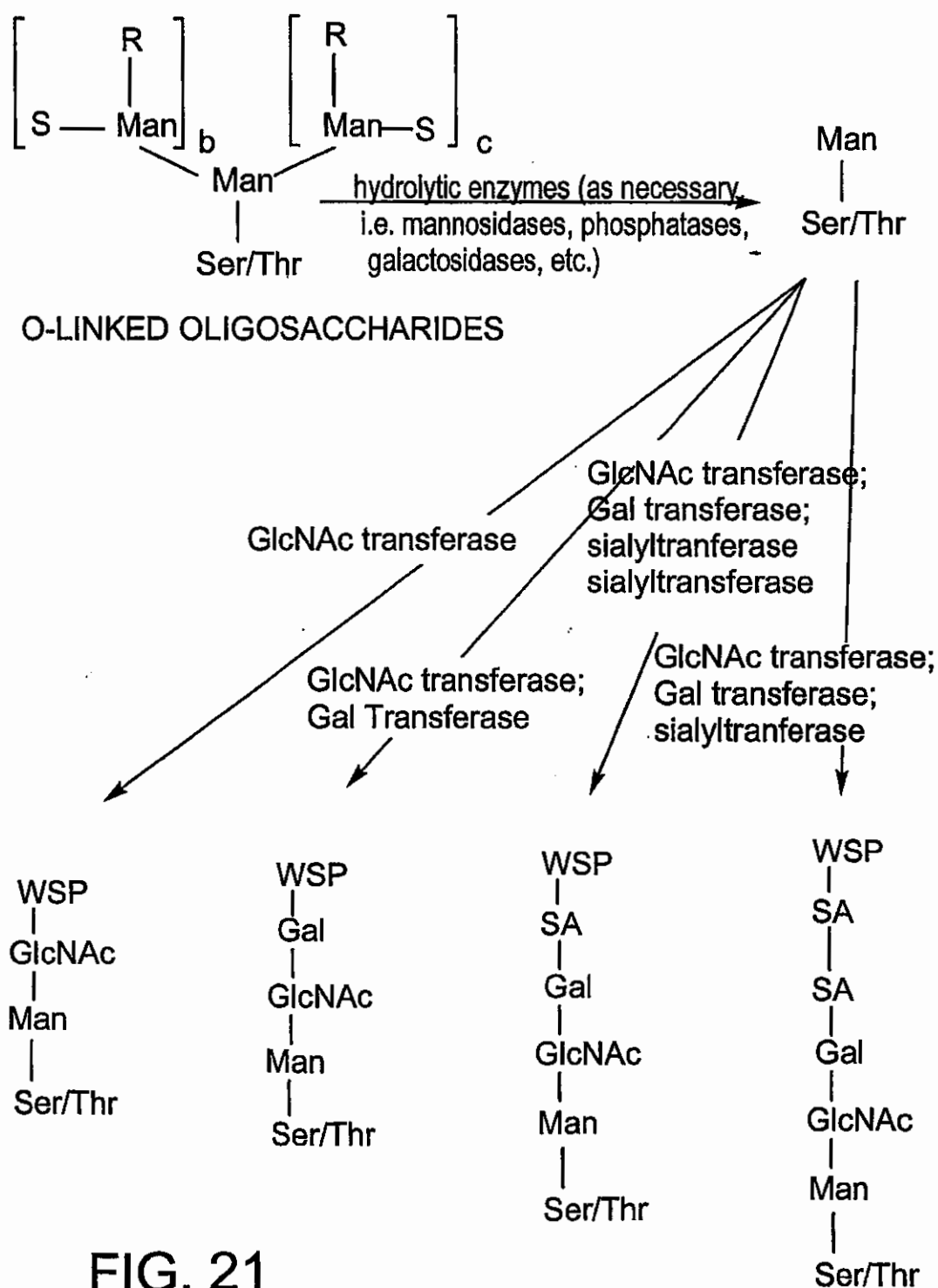
FIG. 19

51/345

O-LINKED OLIGOSACCHARIDES



52/345



53/345

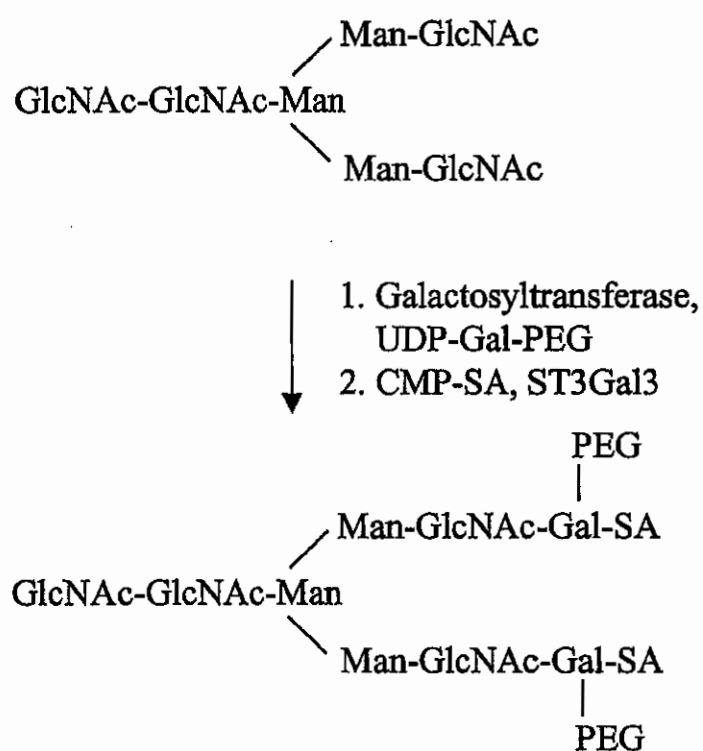


FIG. 22A

54/345

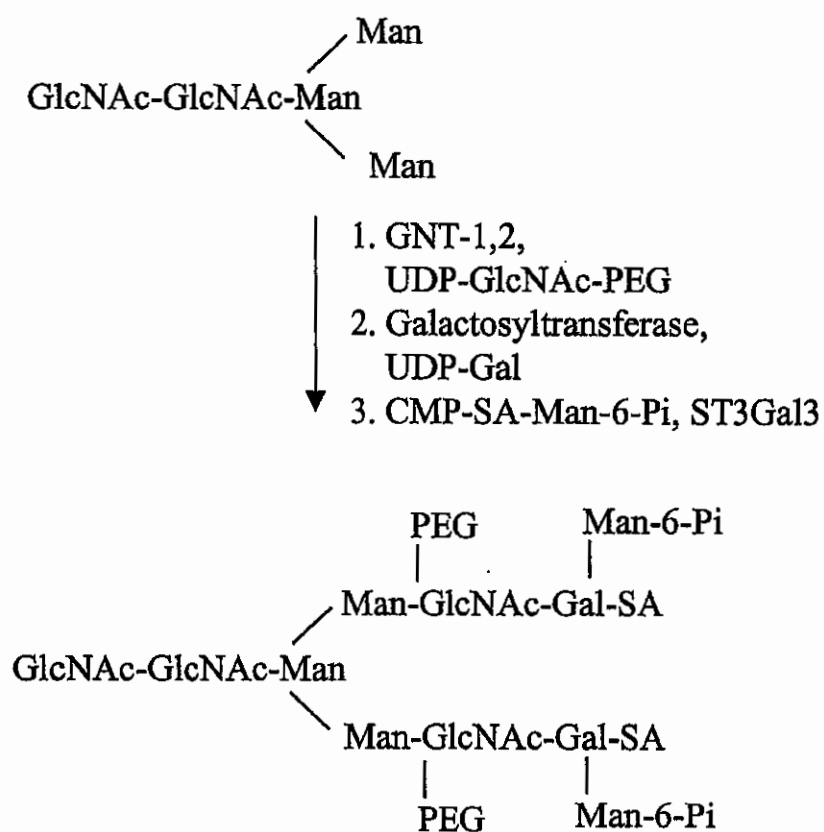


FIG. 22B

55/345

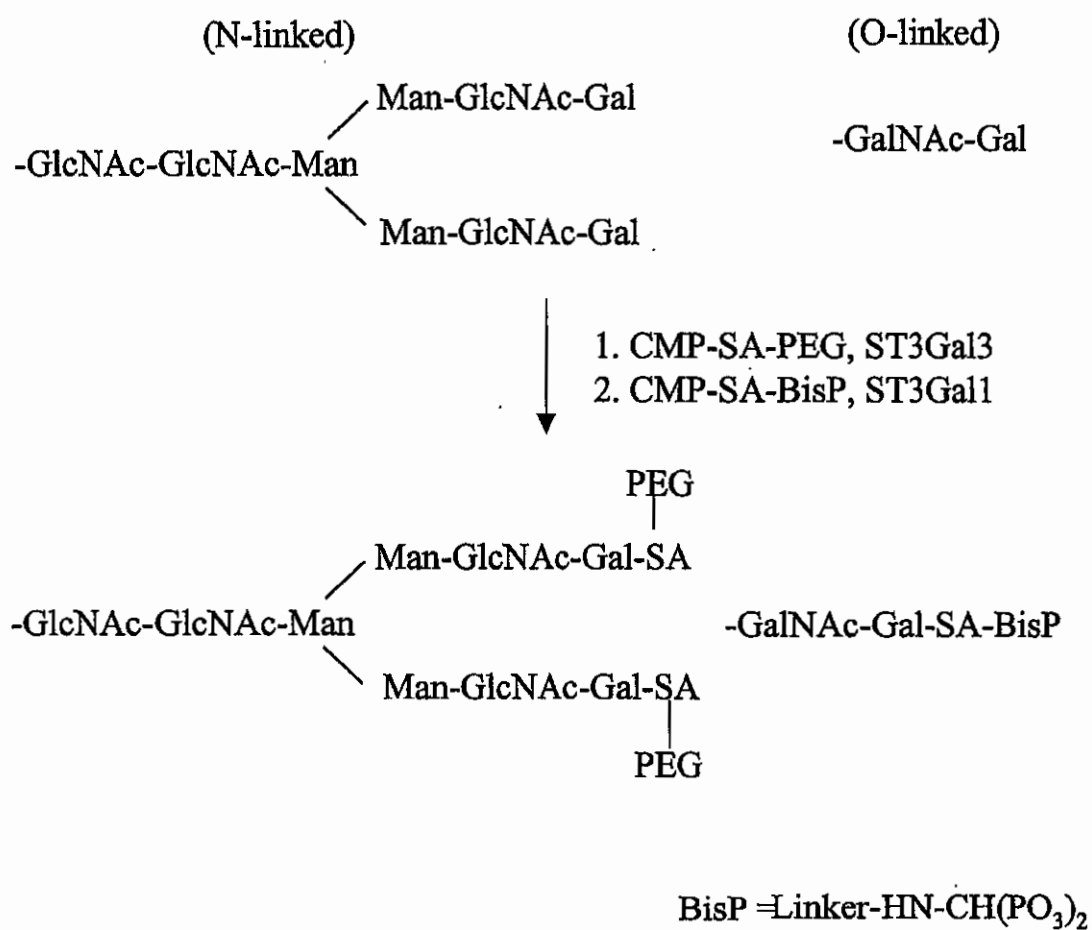


FIG. 22C

56/345

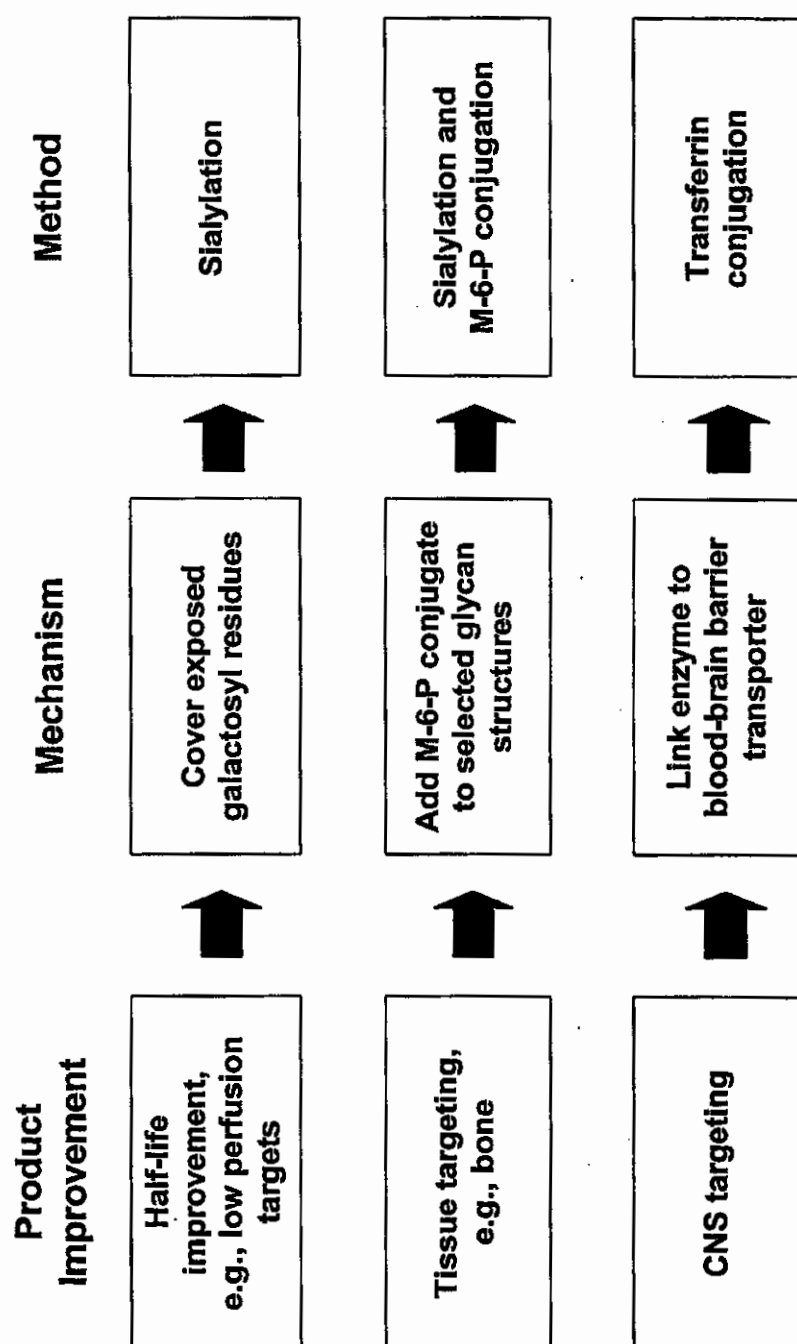


FIG. 23

57/345

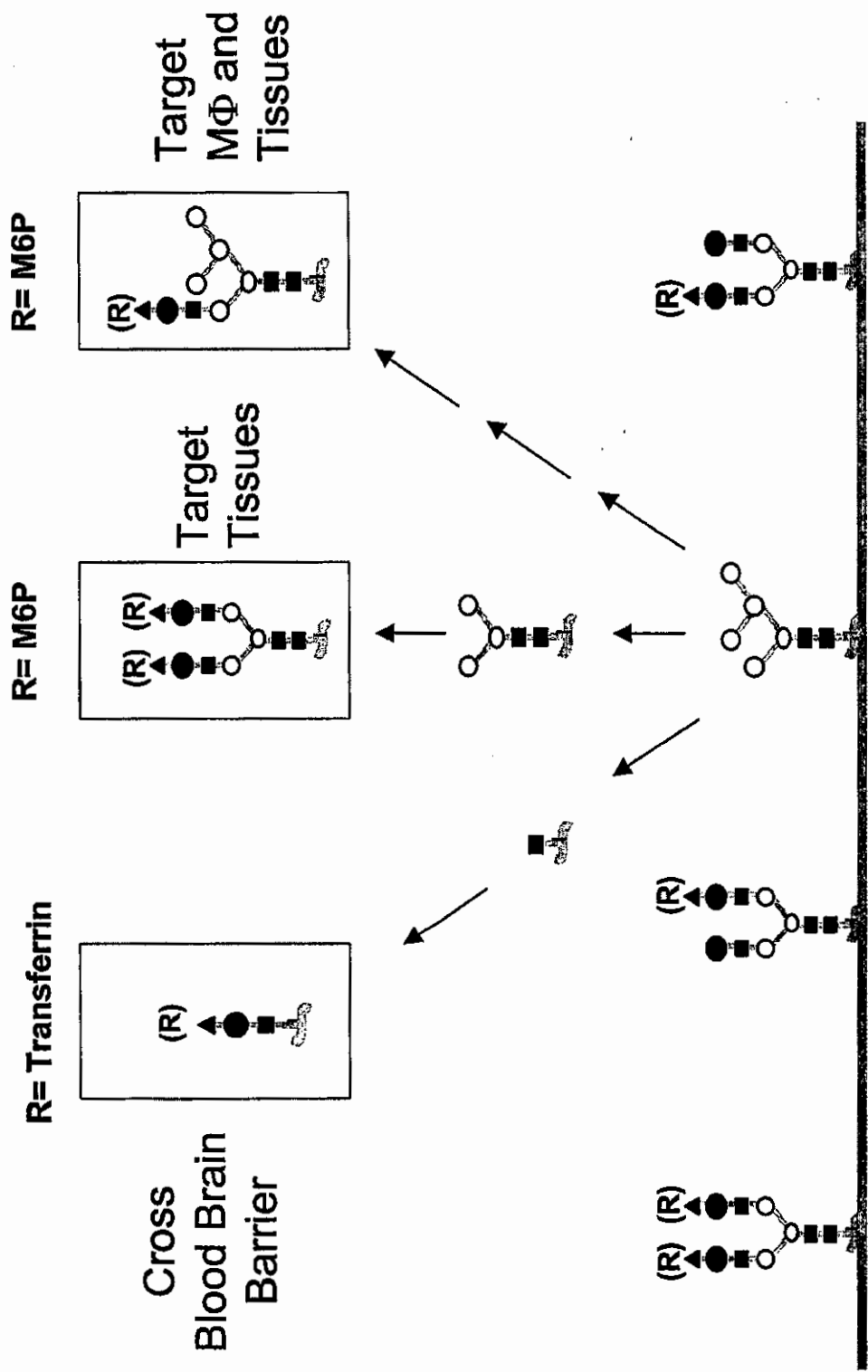


FIG. 24

58/345

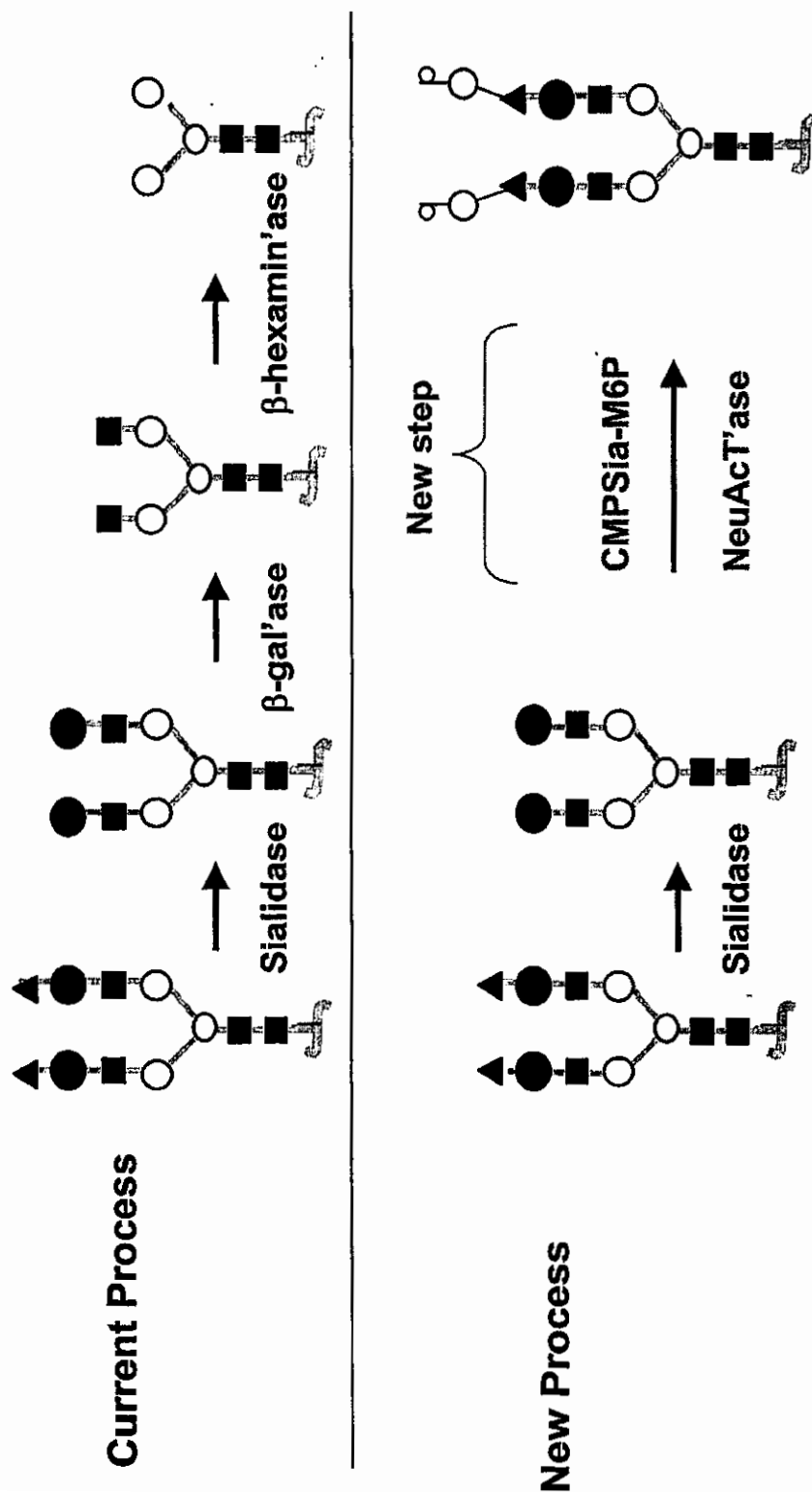


FIG. 25

59/345

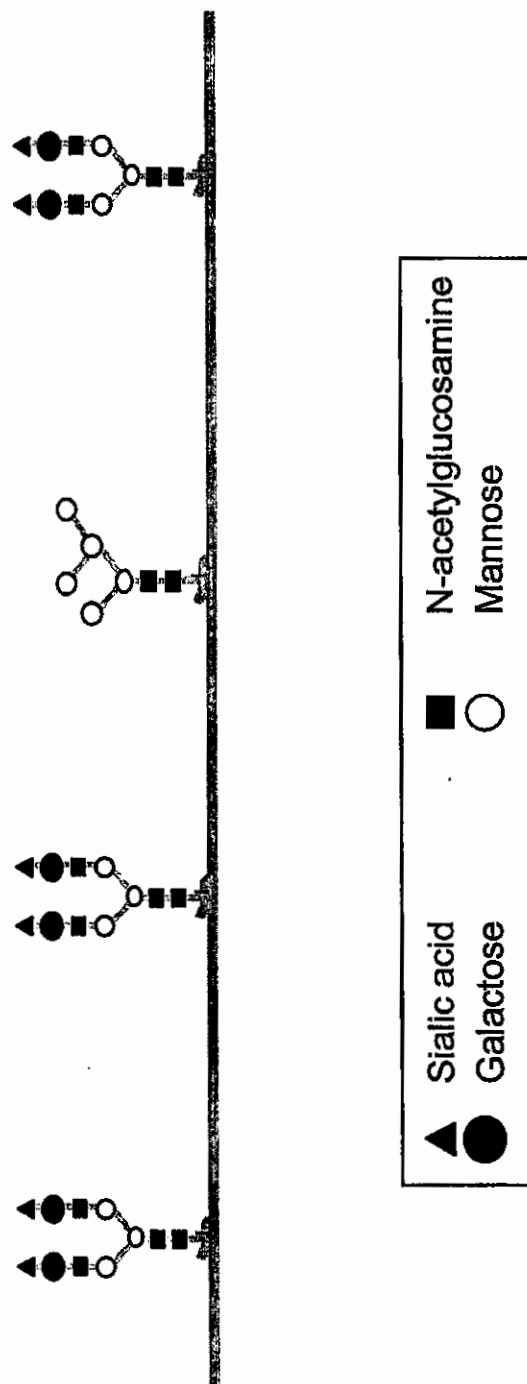
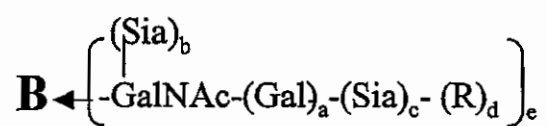
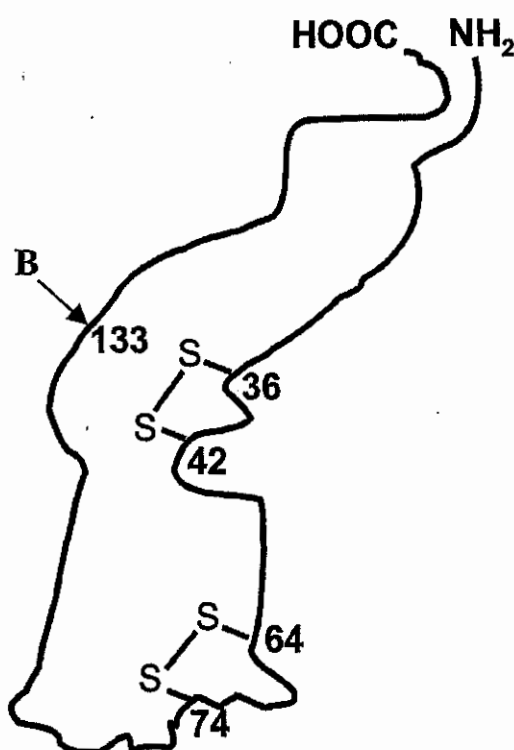


FIG. 26

60/345



a-c, e (independently selected) = 0 or 1;
d = 0;

R = modifying group, mannose, oligo-
mannose

FIG. 27A

61/345

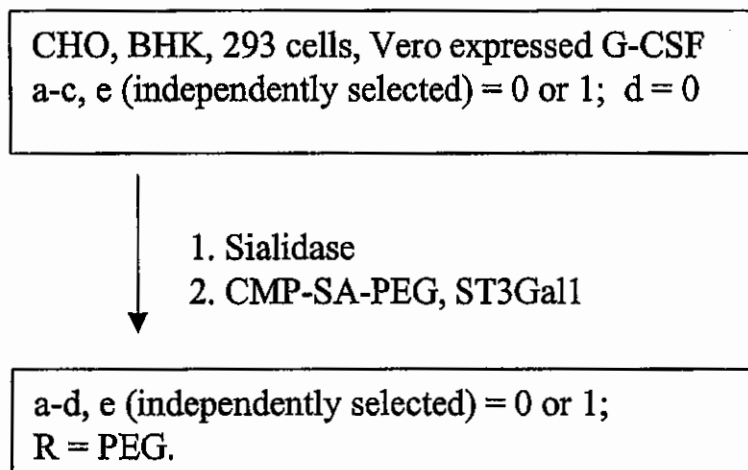


FIG. 27B

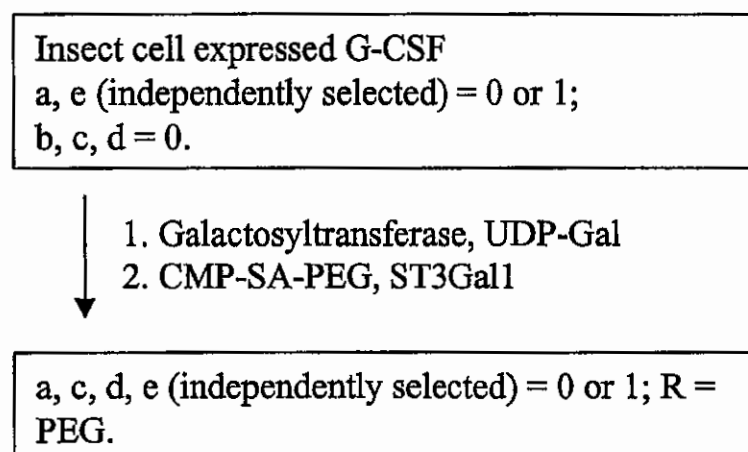


FIG. 27C

62/345

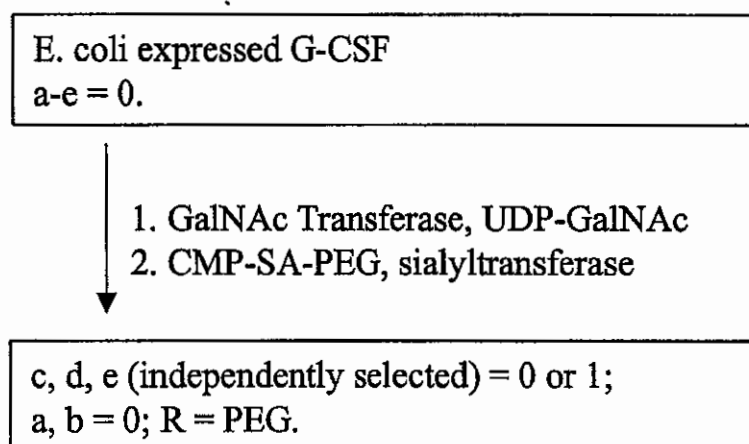


FIG. 27D

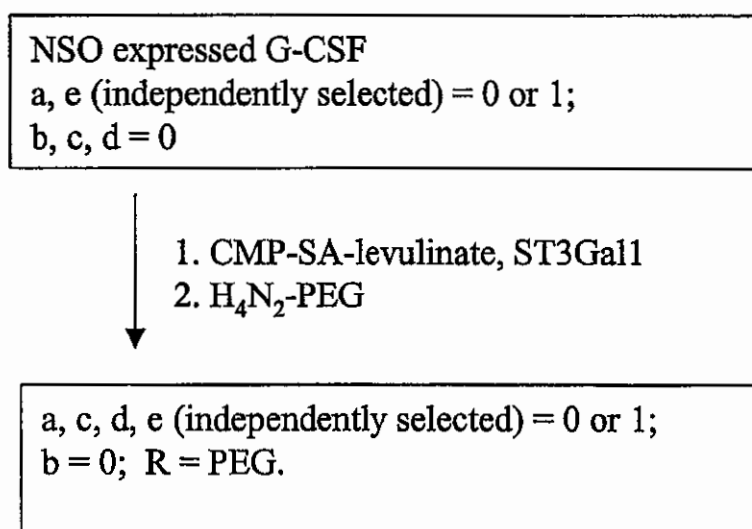


FIG. 27E

63/345

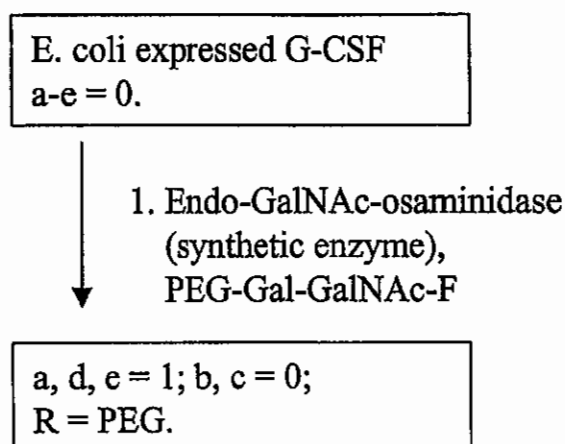


FIG. 27F

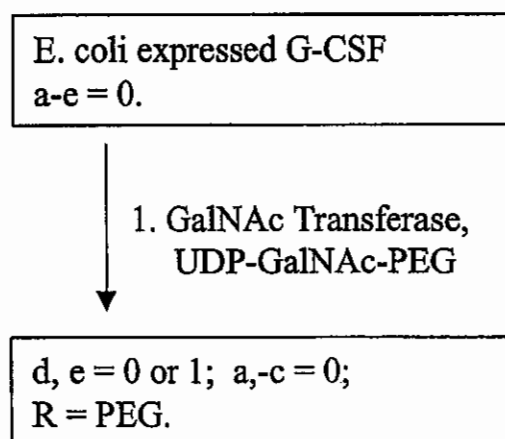
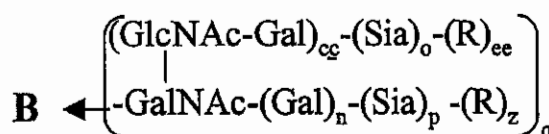
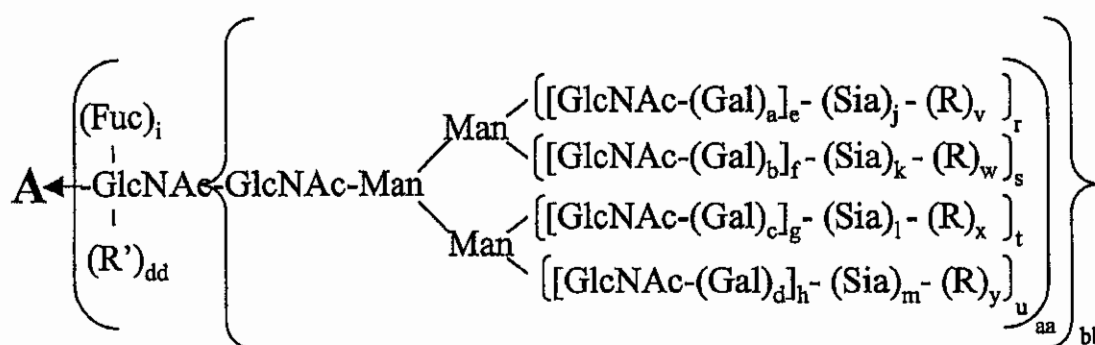
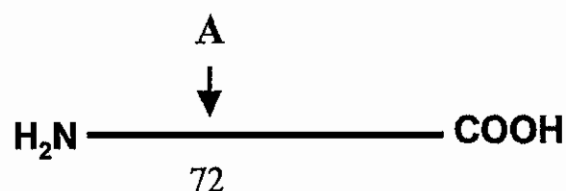


FIG. 27G

64/345



a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 28A

65/345

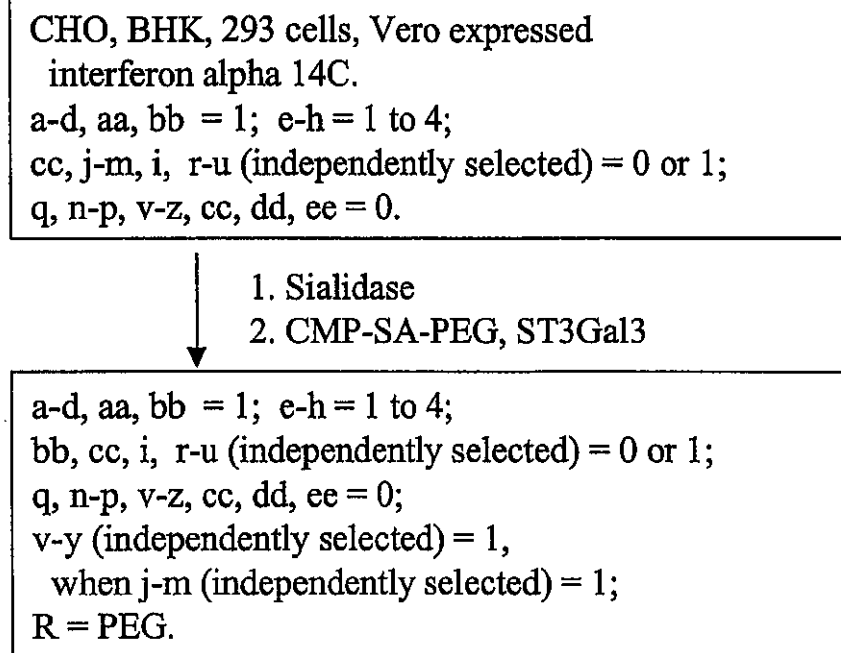


FIG. 28B

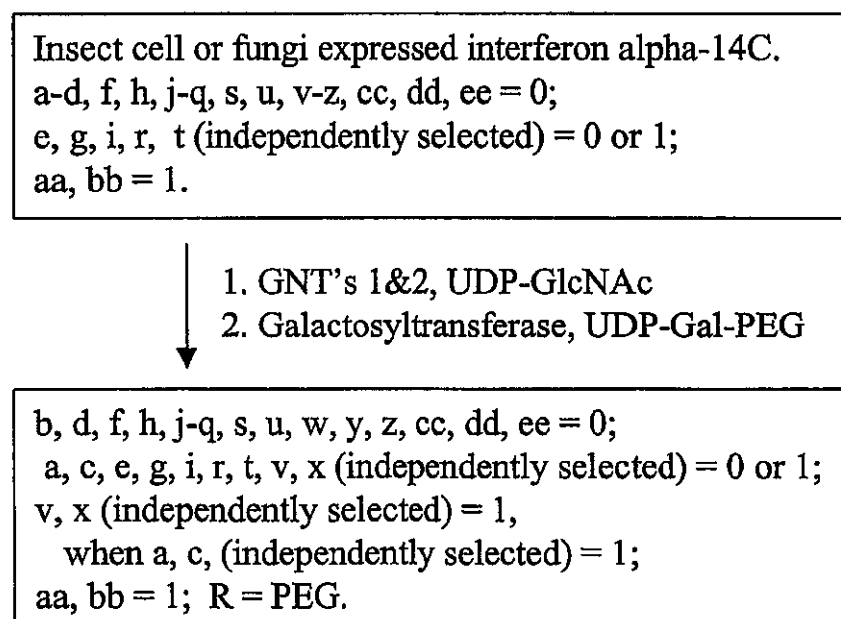


FIG. 28C

66/345

Yeast expressed interferon alpha-14C.

a-q, cc, dd, ee, v-z = 0;

r-y (independently selected) = 0 to 1;

aa, bb = 1;

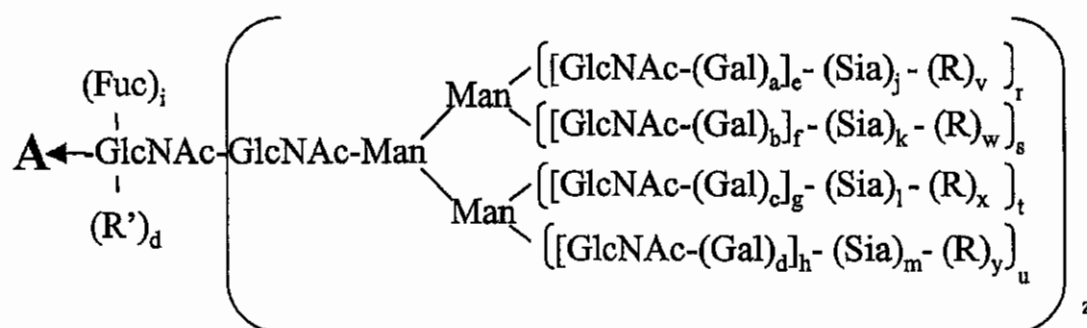
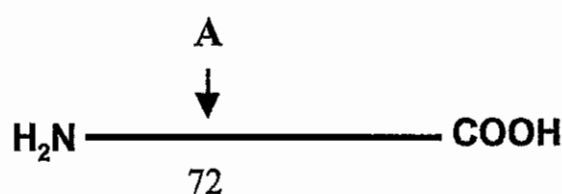
R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - ↓
 - 3.. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 28D

67/345



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 28E

68/345

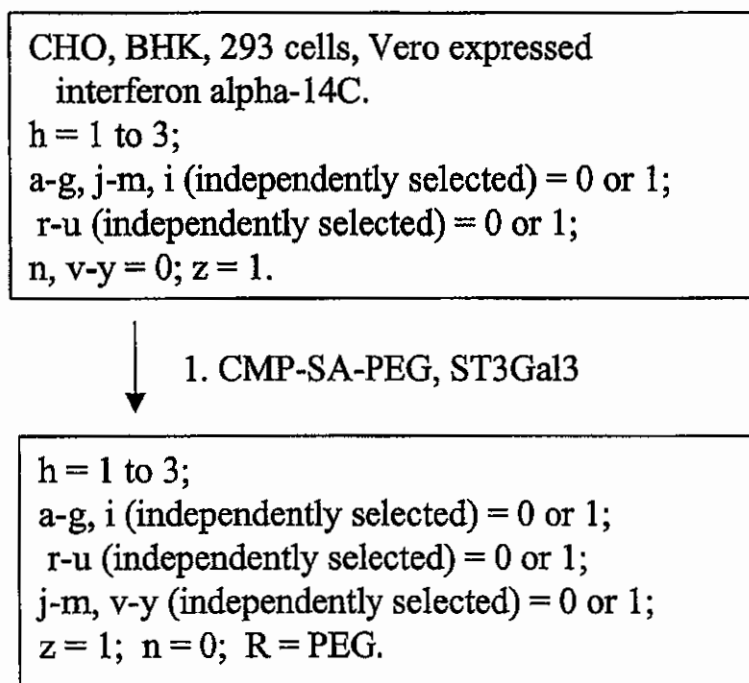


FIG. 28F

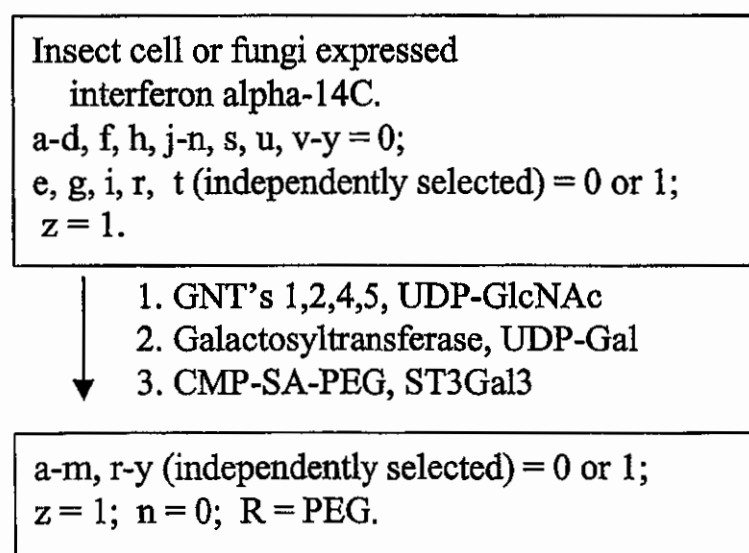


FIG. 28G

69/345

Yeast expressed interferon alpha-14C.
 a-n = 0; r-y (independently selected) = 0 to 1;
 z = 1; R (branched or linear) = Man,
 oligomannose.

1. mannosidases
2. GNT's 1,2,4,5, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal
4. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
 z = 1; n = 0; R = PEG.

FIG. 28H

NSO expressed interferon alpha 14C.
 a-i, r-u (independently selected) = 0 or 1;
 j-m, n, v-y = 0; z = 1.

1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
2. H₄N₂-PEG

a-i, j-m, r-y (independently selected) = 0 or 1;
 n = 0; z = 1; R = PEG.

FIG. 28I

70/345

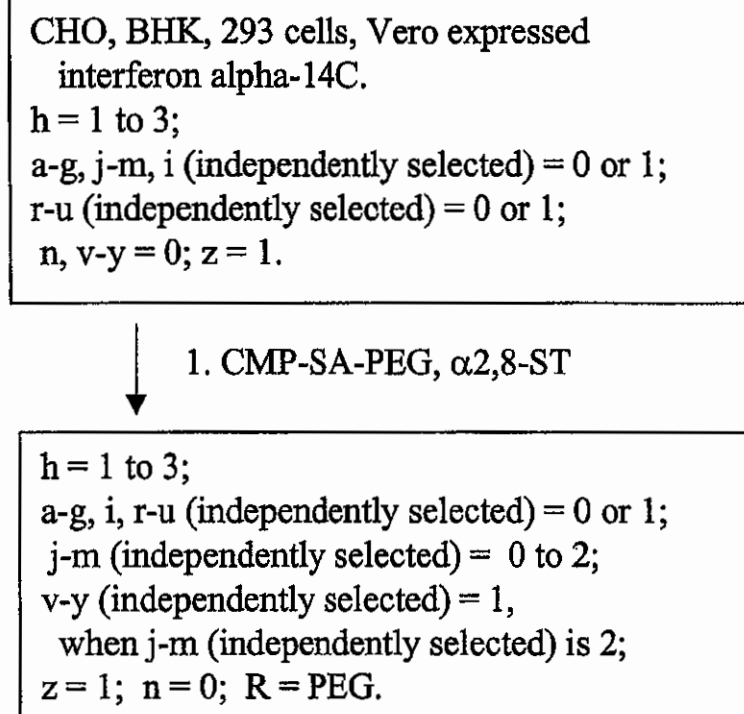


FIG. 28J

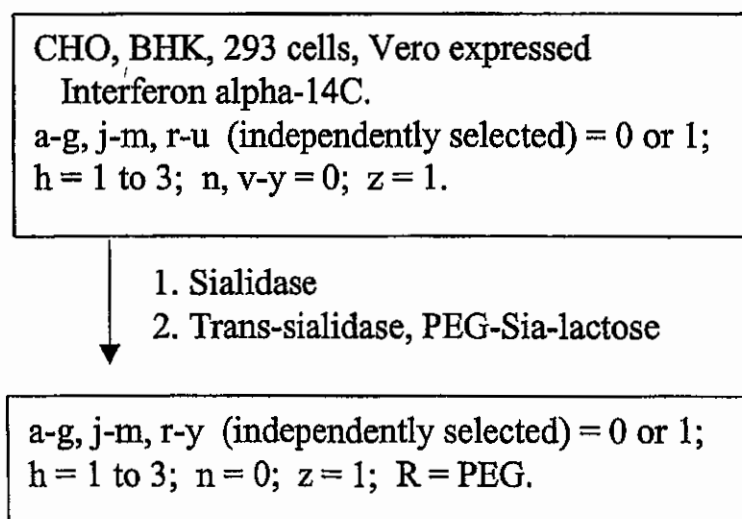


FIG. 28K

71/345

CHO, BHK, 293 cells, Vero expressed
interferon alpha-14C.
h = 1 to 3;
a-g, j-m, i (independently selected) = 0 or 1;
r-u (independently selected) = 0 or 1;
n, v-y = 0; z = 1.



1. CMP-SA, α 2,8-ST

h = 1 to 3;
a-g, i, r-u (independently selected) = 0 or 1;
j-m (independently selected) = 0 to 40;
z = 1; v-y, n = 0.

FIG. 28L

Insect cell or fungi expressed interferon alpha-14C.
a-d, f, h, j-n, s, u, v-y = 0;
e, g, i, r, t (independently selected) = 0 or 1;
z = 1.



1. GNT's 1 & 2, UDP-GlcNAc
2. Galactosyltransferase,
UDP-Gal-linker-SA-CMP
3. ST3Gal3, transferrin

a, c, e, g, i, r, t, v, x (independently selected) = 0 or 1;
z = 1; b, d, f, h, j-n, s, u, w, y = 0;
R = transferrin.

FIG. 28M

72/345

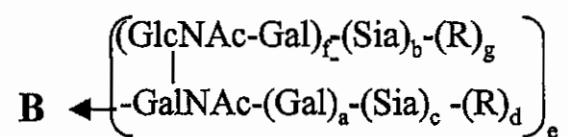
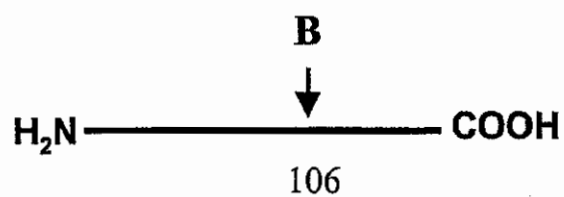
Insect cell or fungi expressed interferon alpha-14C.
a-d, f, h, j-n, s, u, v-y = 0;
e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
 2. Galactosyltransferase,
UDP-Gal-linker-SA-CMP
 3. ST3Gal3, transferrin

i (independently selected) = 0 or 1;
a-h, j-m, r-z = 0;
n = 1; R' = -Gal-linker-transferrin.

FIG. 28N

73/345



a-c, e, f (independently selected) = 0 or 1;
 d, g = 0; R = polymer, glycoconjugate.

FIG. 280

74/345

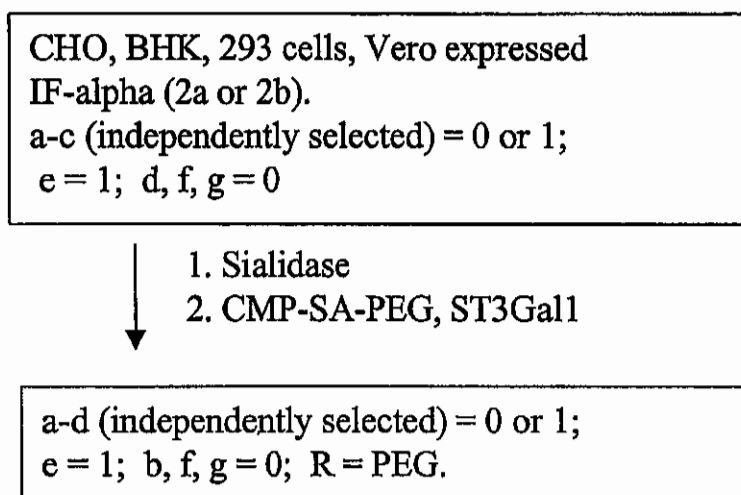


FIG. 28P

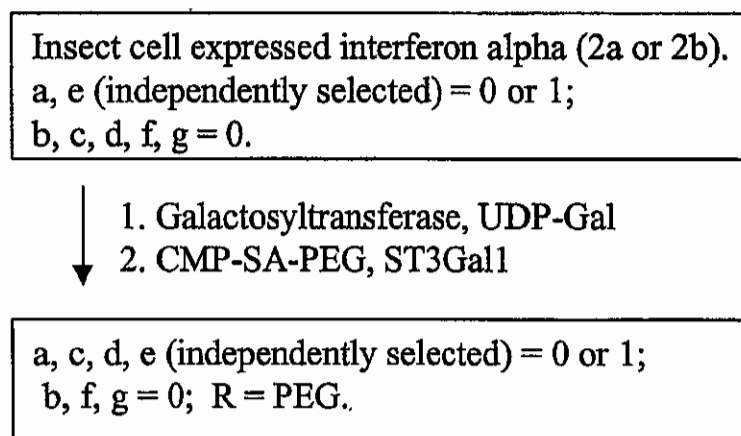


FIG. 28Q

75/345

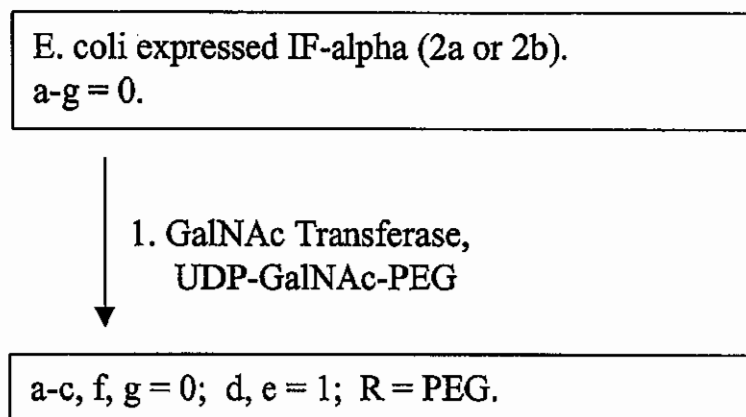


FIG. 28R

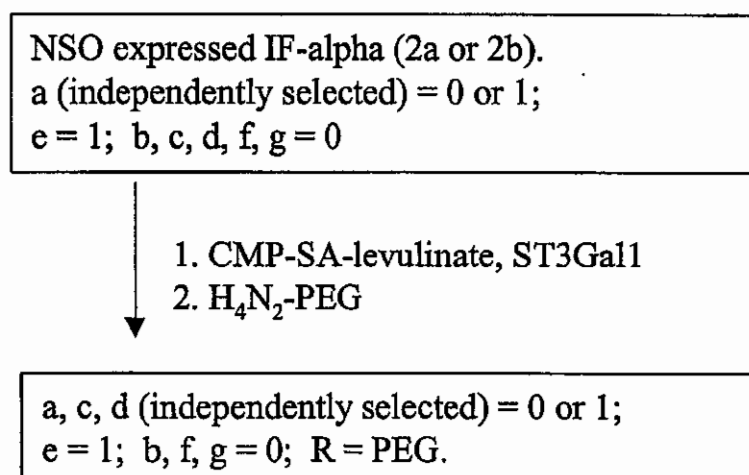


FIG. 28S

76/345

E. coli expressed IF-alpha (2a or 2b).
a-g = 0.



1. Endo-N-acetylgalatosamidase
(synthetic enzyme),
PEG-Gal-GalNAc-F

a, d, e = 1; b, c, f, g = 0; R = PEG.

FIG. 28T

E. coli expressed IF-alpha (2a or 2b).
a-g = 0.



1. GalNAc Transferase, UDP-GalNAc
2. sialyltransferase, CMP-SA-PEG

b, d = 0 or 1; e = 1; a, c, f, g = 0; R = PEG.

FIG. 28U

77/345

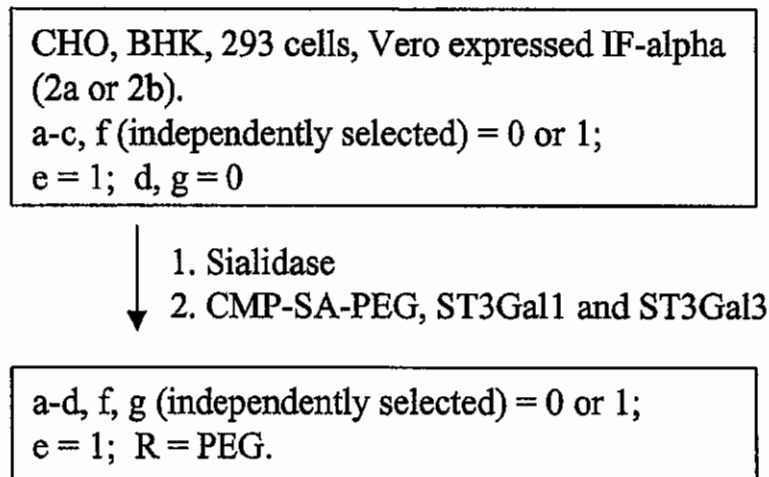


FIG. 28V

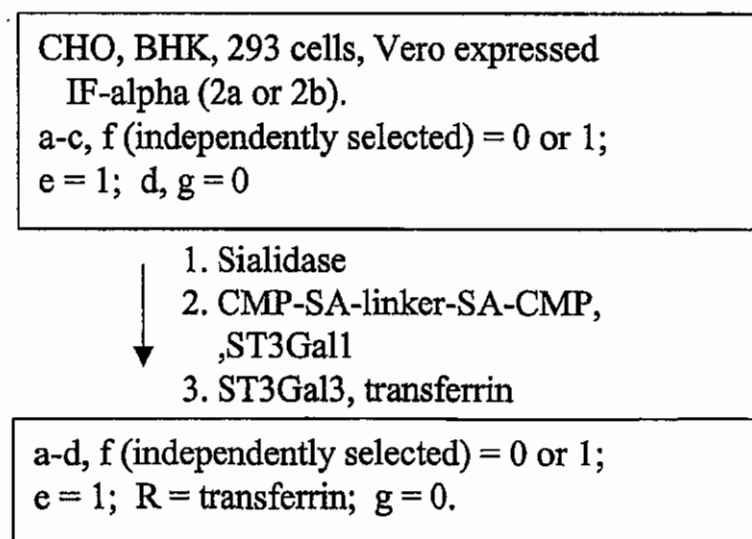


FIG. 28W

79/345

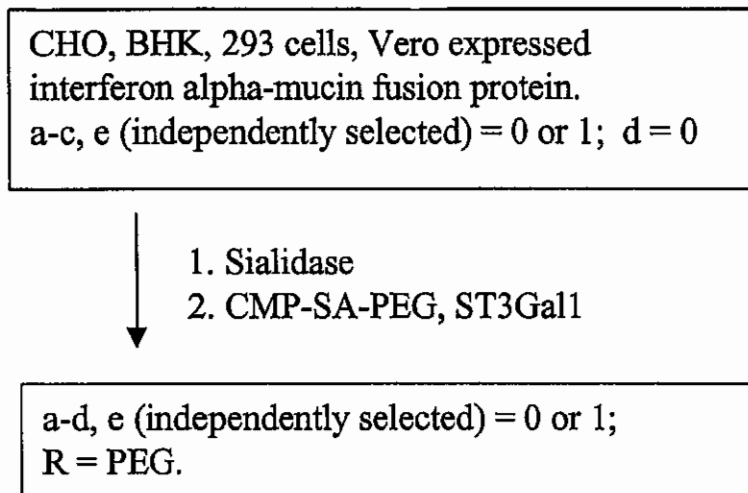


FIG. 28Y

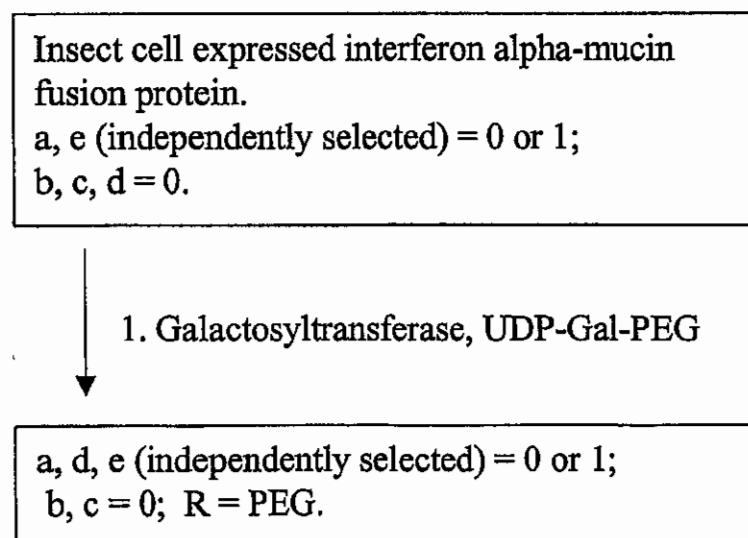


FIG. 28Z

80/345

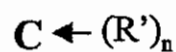
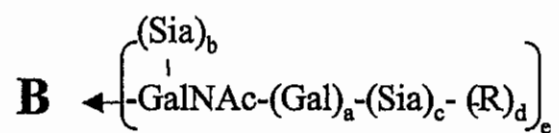
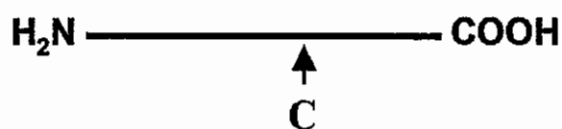
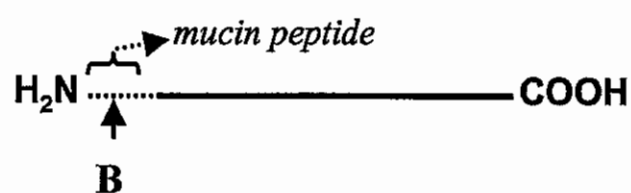
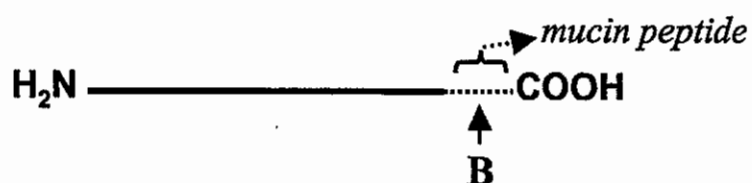
E. coli expressed interferon alpha-mucin
fusion protein.
a-e = 0.

- ↓
1. GalNAc Transferase, UDP-GalNAc
 2. CMP-SA-PEG, sialyltransferase

c, d, e (independently selected) = 0 or 1;
a, b = 0; R = PEG.

FIG. 28AA

81/345



a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 28BB

82/345

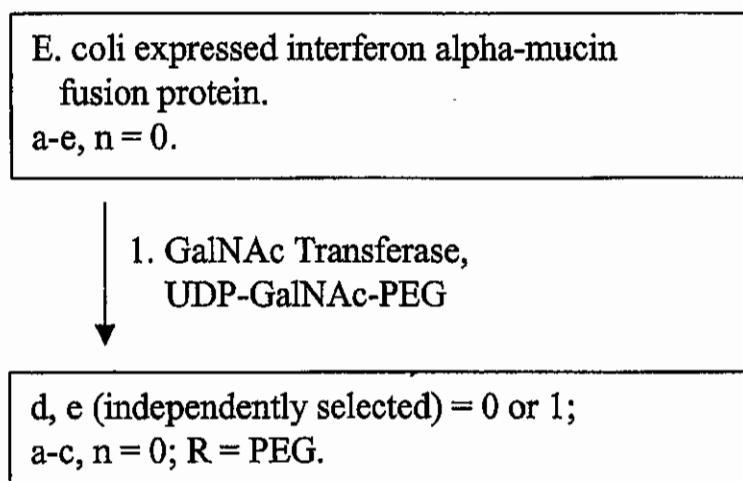


FIG. 28CC

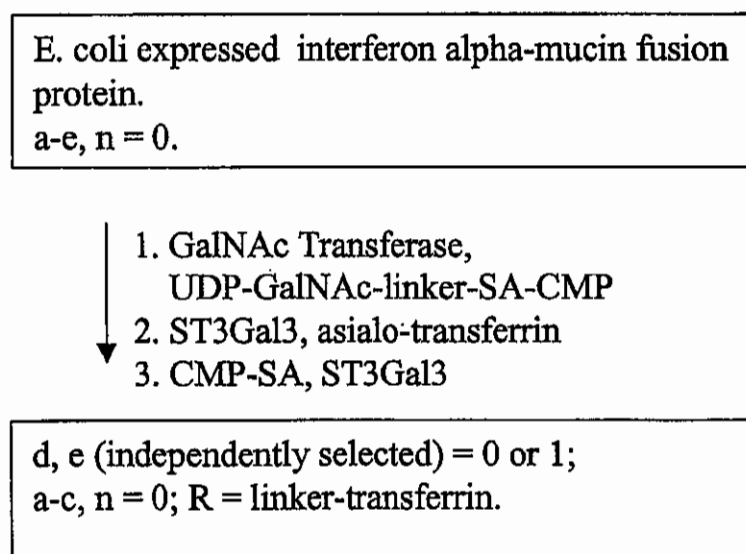


FIG. 28DD

83/345

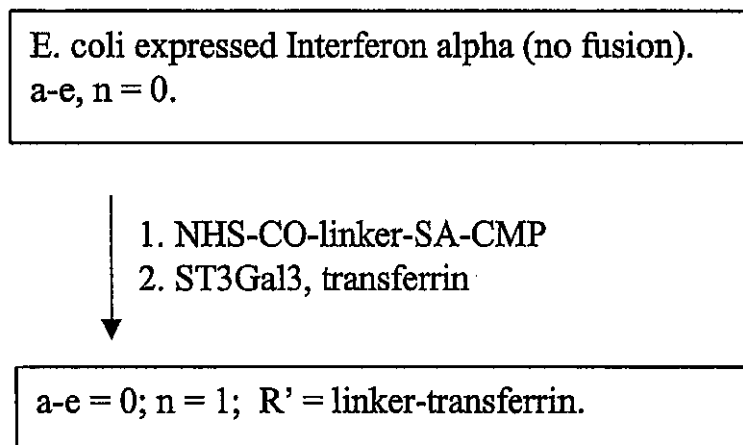
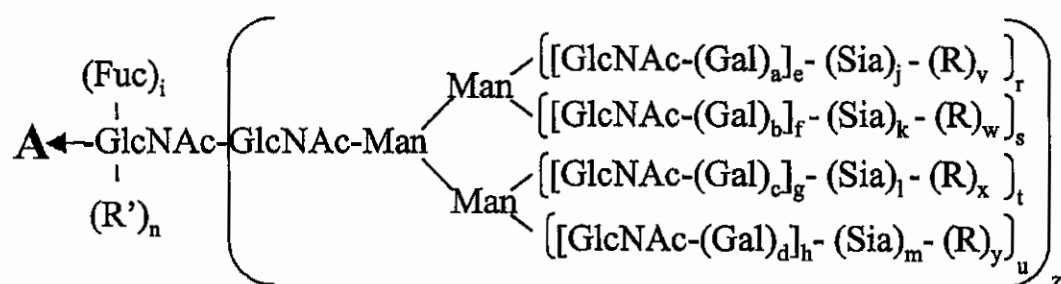
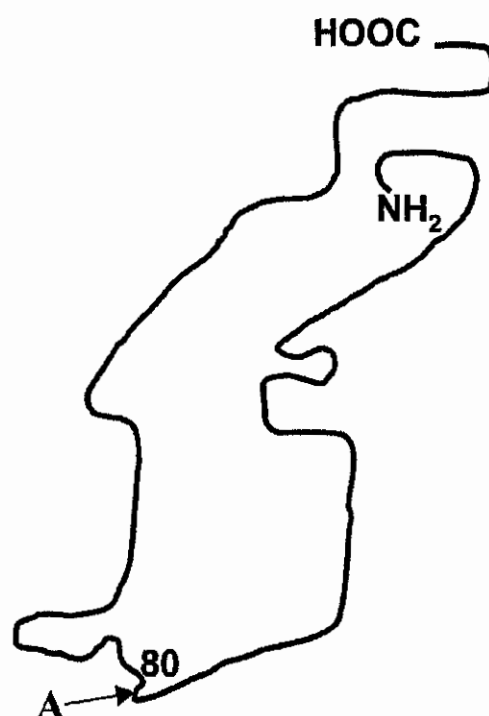


FIG. 28EE

84/345



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer

FIG. 29A

85/345

CHO, BHK, 293 cells, Vero expressed IF-beta
 $h = 1$ to 3 ;
 $a-g, j-m, i$ (independently selected) = 0 or 1 ;
 $r-u$ (independently selected) = 0 or 1 ;
 $n, v-y = 0$; $z = 1$.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

$h = 1$ to 3 ;
 $a-g, i$ (independently selected) = 0 or 1 ;
 $r-u$ (independently selected) = 0 or 1 ;
 $j-m, v-y$ (independently selected) = 0 or 1 ;
 $z = 1$; $n = 0$; $R = \text{PEG}$.

FIG. 29B

Insect cell expressed IF-beta
 $a-d, f, h, j-n, s, u, v-y = 0$;
 e, g, i, r, t (independently selected) = 0 or 1 ;
 $z = 1$.



1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
2. CMP-SA-PEG, ST3Gal3,
buffer, salt

$b, d, f, h, k, m, n, s, u, w, y = 0$;
 a, c, e, g, i, r, t (independently selected) = 0 or 1 ;
 j, l, v, x (independently selected) = 0 or 1 ;
 $z = 1$; $R = \text{PEG}$.

FIG. 29C

86/345

Yeast expressed IF-beta

a-n = 0; z = 1;

r-y (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 29D

CHO, BHK, 293 cells, Vero expressed IF-beta

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.

- ↓
1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;

a-g, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

j-m, v-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 29E

87/345

Insect cell expressed IF-beta

a-d, f, h, j-n, s, u, v-y = 0; e, g, i, r, t
(independently selected) = 0 or 1; z = 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
z = 1; n = 0; R = PEG.

FIG. 29F

Yeast expressed IF-beta

a-n = 0; z = 1;
r-y (independently selected) = 0 to 1;
R (branched or linear) = Man, oligomannose.

- ↓
1. mannosidases
 2. GNT's 1,2,4,5, UDP-GlcNAc
 3. Galactosyltransferase, UDP-Gal
 4. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;
z = 1; n = 0; R = PEG.

FIG. 29G

88/345

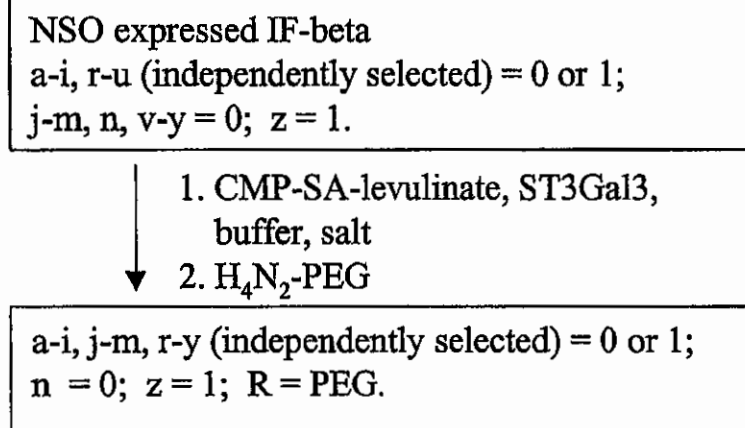


FIG. 29H

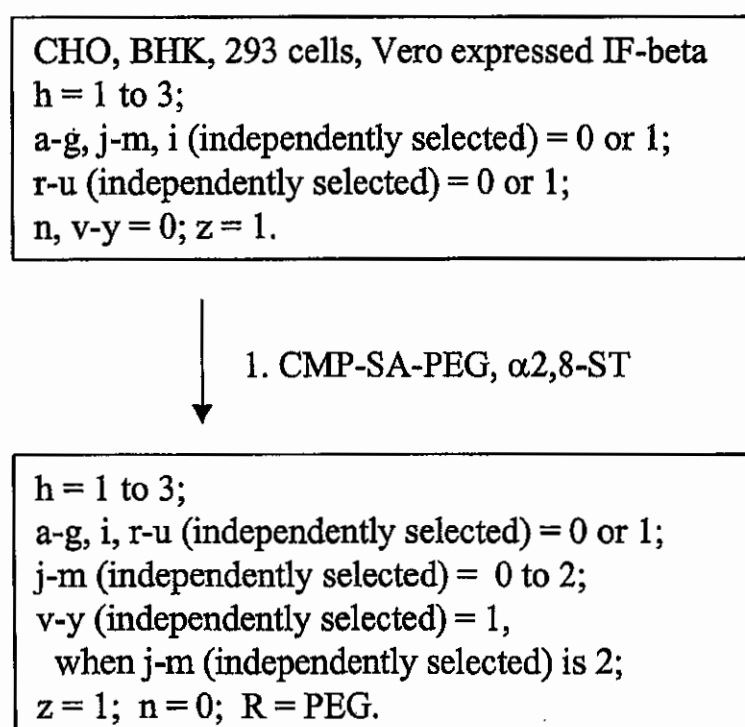


FIG. 29I

89/345

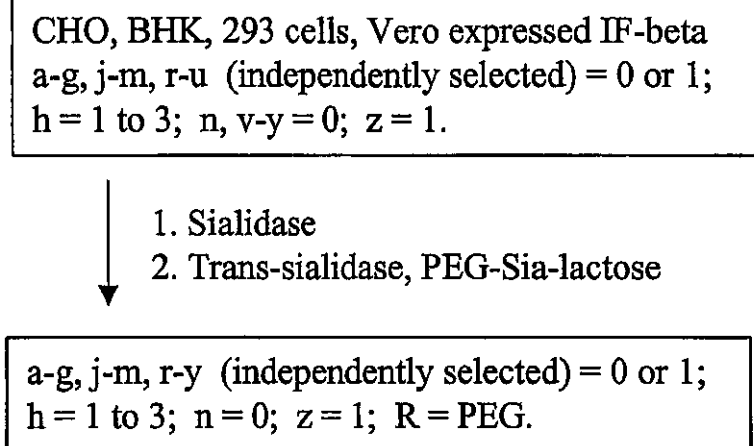


FIG. 29J

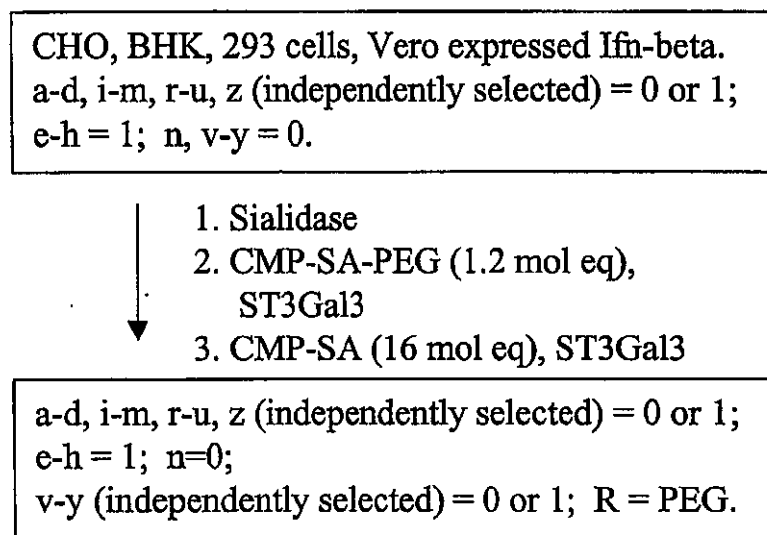


FIG. 29K

90/345

NSO expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; R = PEG

n = 0; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

FIG. 29L

CHO, BHK, 293 cells, Vero expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n = 0;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 29M

91/345

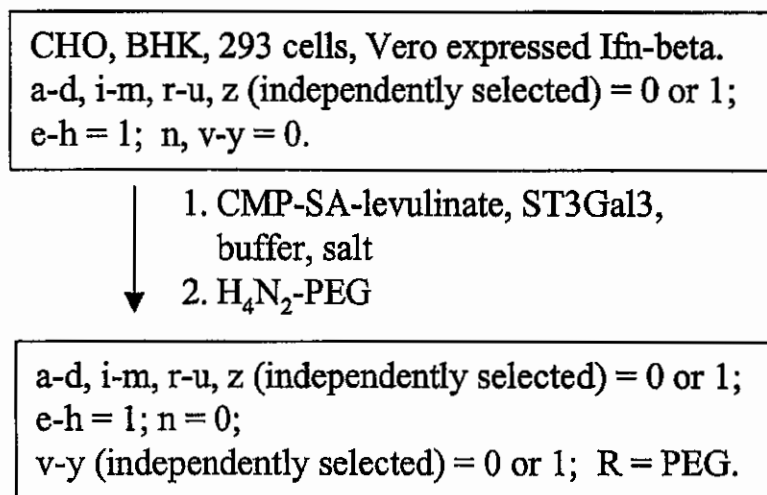


FIG. 29N

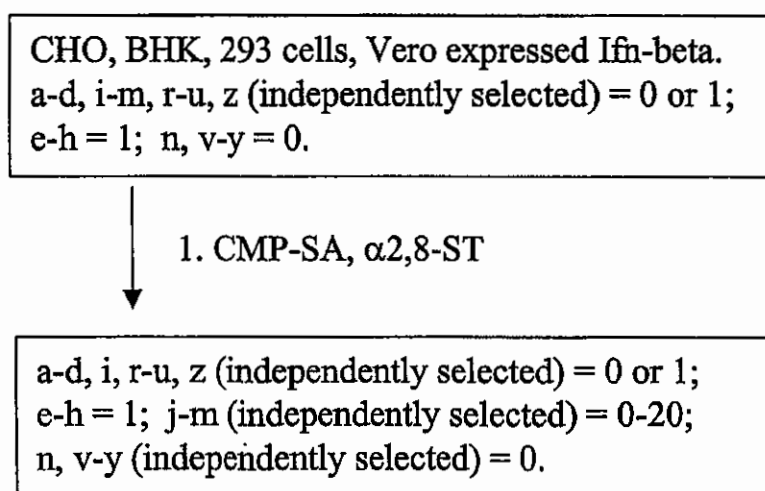
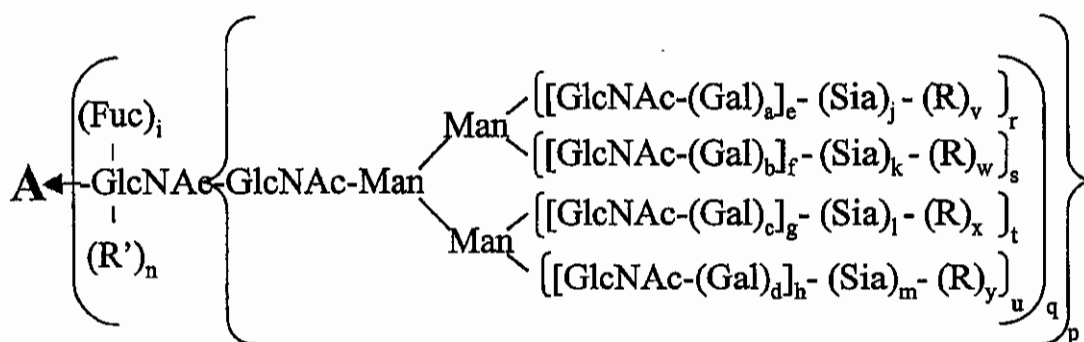
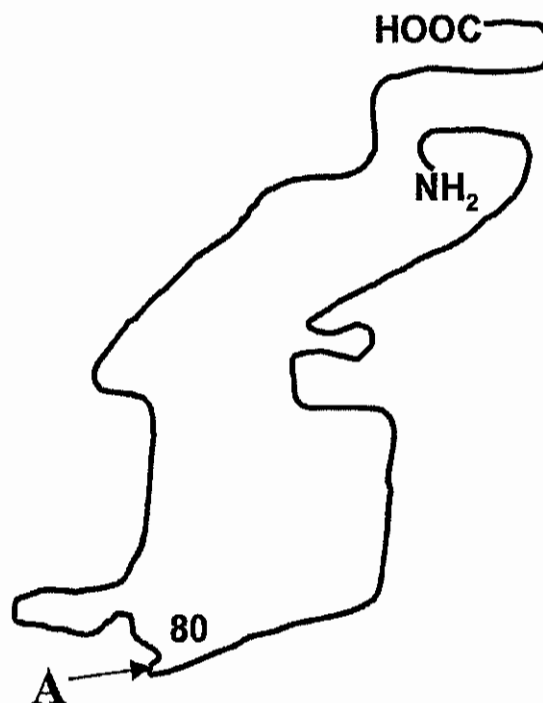


FIG. 29O

92/345



a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group;

R' = H, glycosyl group, modifying group,
glycoconjugate.

FIG. 29P

93/345

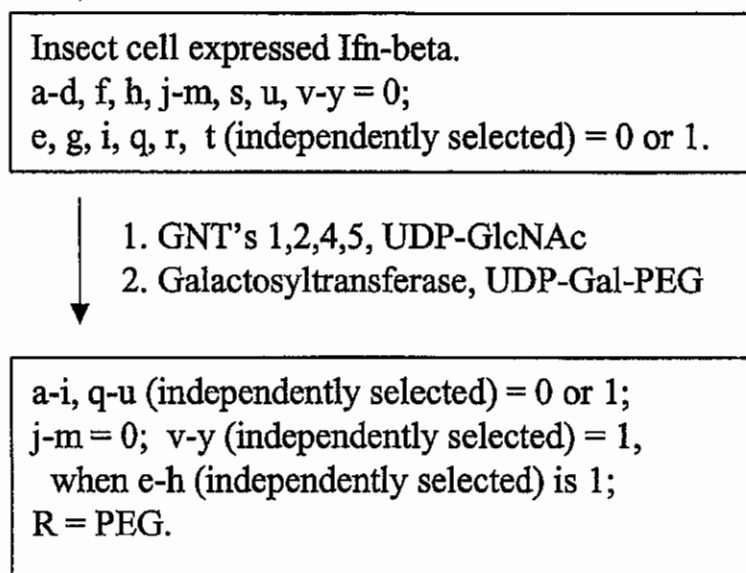


FIG. 29Q

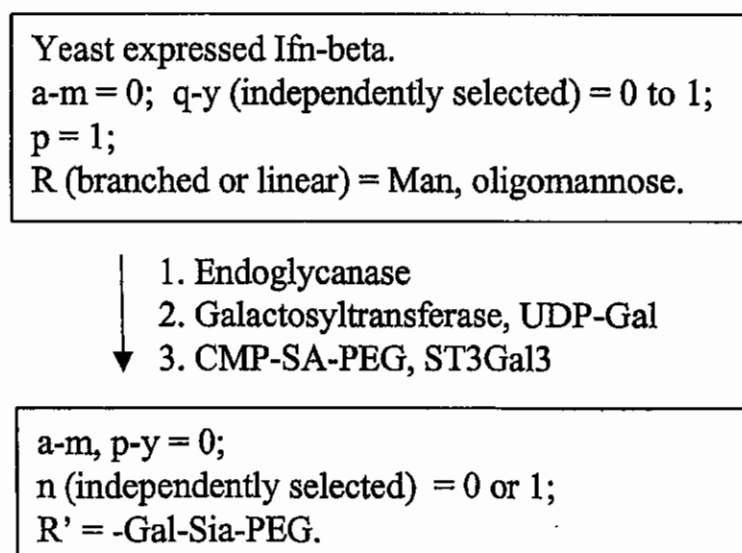


FIG. 29R

94/345

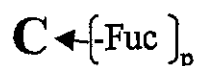
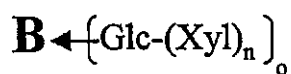
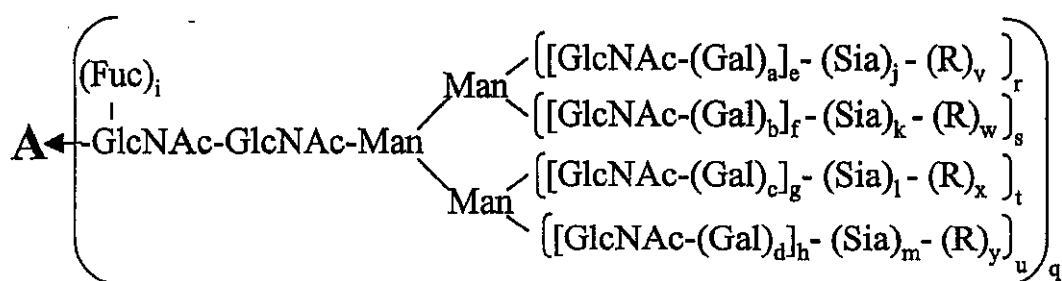
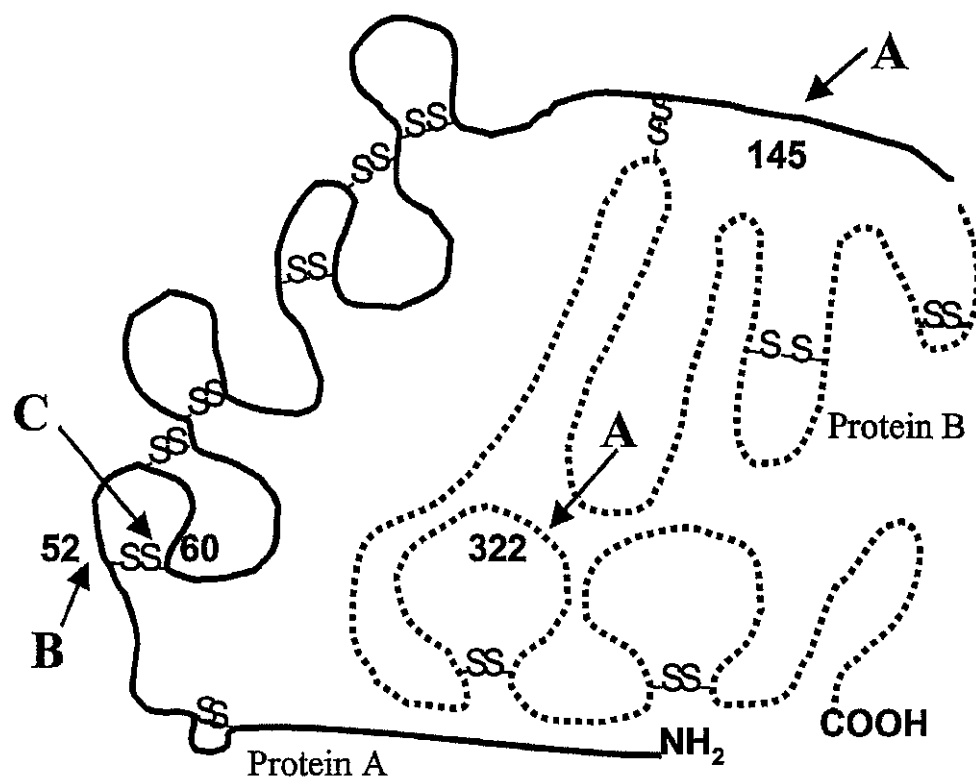
CHO, BHK, 293 cells, Vero expressed Ifn-beta.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 29S

95/345



a-d, i, q-u (independently selected) = 0 or 1.

o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-y = 0;

R = modifying group, mannose, oligo-mannose, Sia-Lewis X, Sia-Lewis A..

FIG. 30A

96/345

BHK expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.



1. Sialidase
2. CMP-SA-PEG (16 mole eq),
ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;
v, x, (independently selected) = 1,
when j, l (respectively, independently selected) is 1;
R = PEG.

FIG. 30B

CHO, BHK, 293 cells, Vero expressed Factor VII or VIIa

a-d, e, i, g, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, v-y = 0; n = 0-4.



1. Sialidase
2. CMP-SA-PEG (1.2 mole eq),
ST3Gal3
3. CMP-SA (8 mol eq), ST3Gal3

a-d, e, g, i, q, j, l, o, p (independently selected) = 0 or 1;
r, t = 1; f, h, k, m, s, u, w, y = 0; n = 0-4;
v or x, (independently selected) = 1,
when j or l, (respectively, independently selected) is 1;
R = PEG.

FIG. 30C

97/345

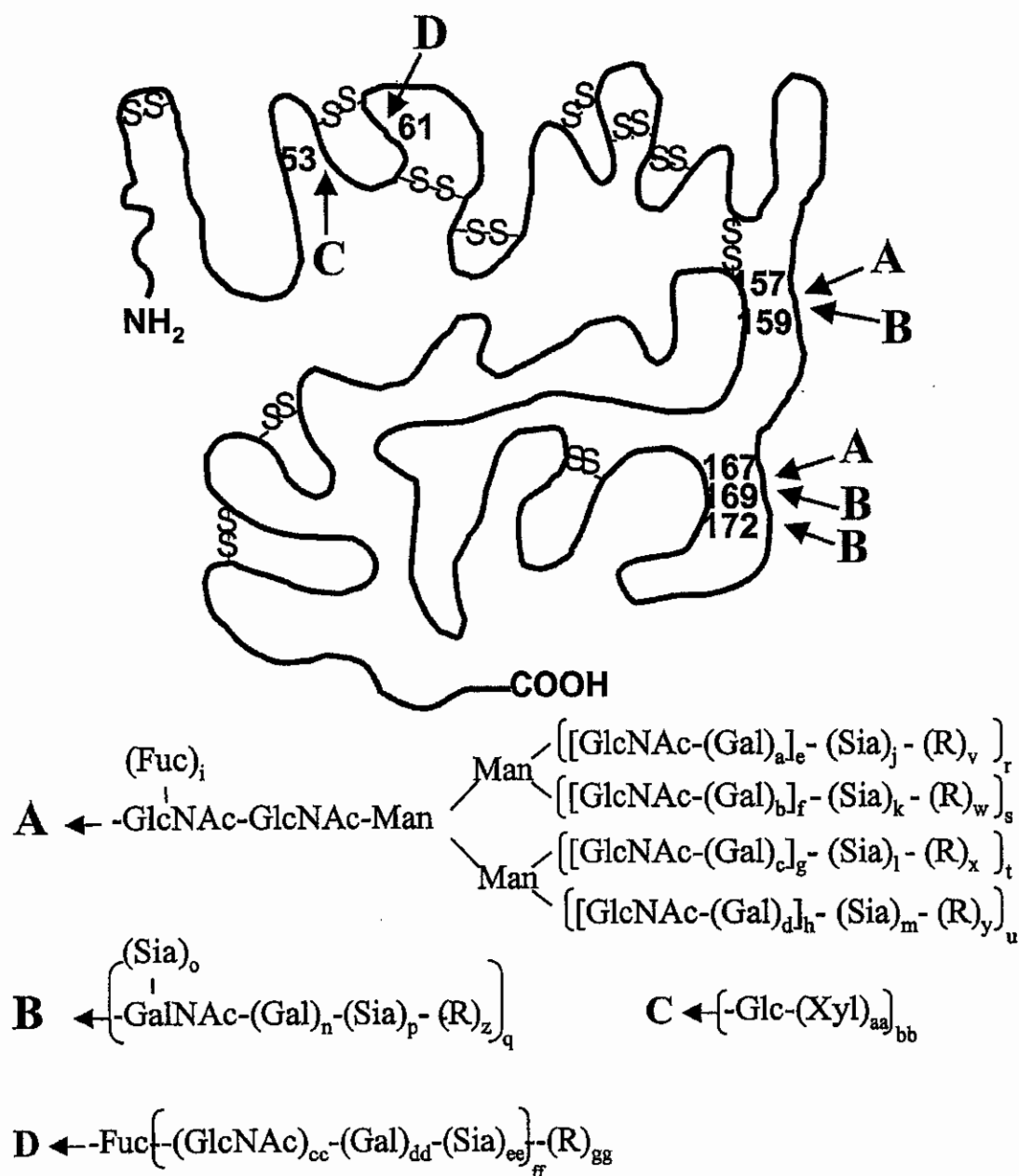
NSO expressed Factor VII or VIIa
a--u (independently selected) = 0 or 1;
v-y = 0; n = 0-4;
Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ▼ 3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;
n = 0-4; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
Sia = Sia; R = PEG.

FIG. 30D

98/345



a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

e-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 31A

99/345

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0;
 j-m, ee, v-y, gg (independently selected) = 0 or 1;
 R = PEG.

FIG. 31B

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3
3. ST3Gal1, CMP-SA

a-d, n, p, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1;
 j-m, ee, v-y, gg (independently selected) = 0 or 1;
 o, z = 0; R = PEG.

FIG. 31C

100/345

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i,
 o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

1. sialidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA, ST3Gal3
- ↓ 4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =
 0 or 1; R = PEG;
 o, v-y, gg = 0;
 j-m, p, ee (independently selected) = 0 or 1, but when
 p = 1, z = 1.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓ CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1; R = PEG;
 o, p, z = 0; j-m, ee, v-y, gg (independently selected) =
 0 or 1.

FIG. 31E

101/345

CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently
 selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee, v-y, gg (independently selected) = 0 or 1.

FIG. 31F

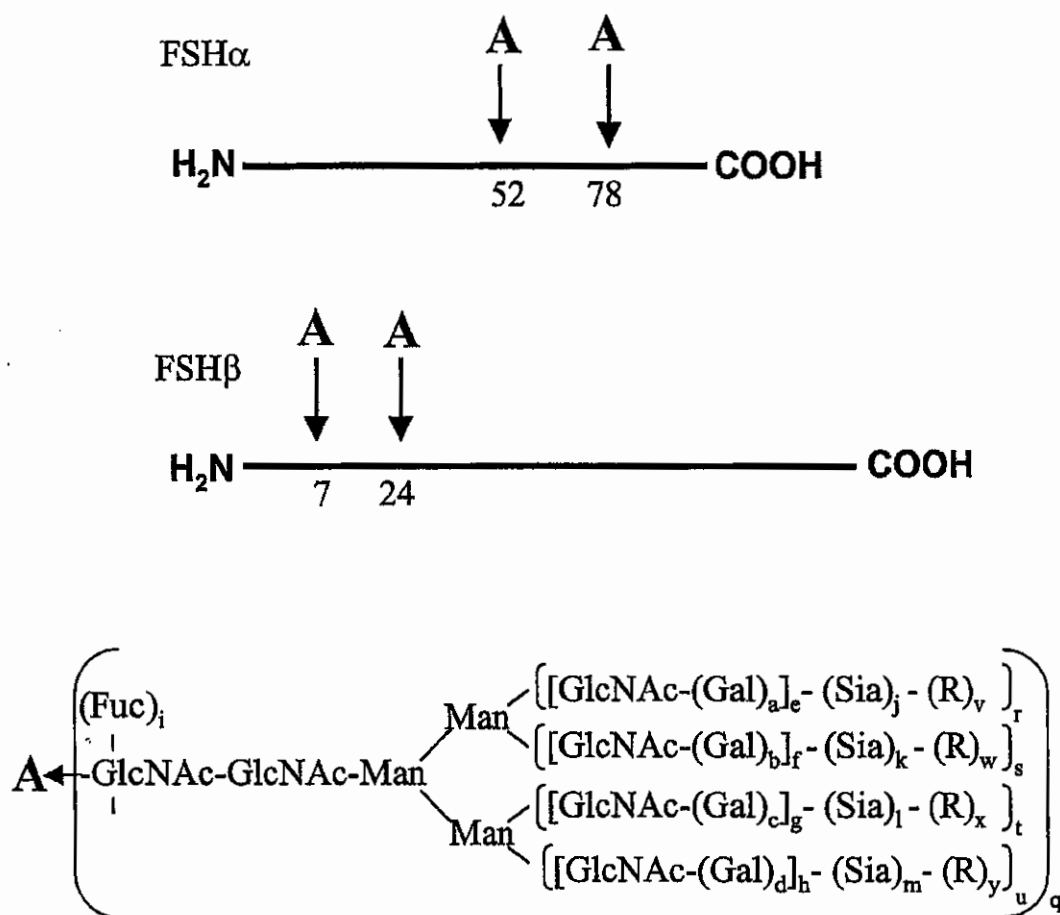
CHO, BHK, 293 cells, Vero expressed Factor IX
 a-d, n, q, bb, cc, dd, ff = 1;
 e-h, aa = 1 to 4;
 ee, j-m, i, o, p, r-u (independently selected) = 0 or 1;
 v-z, gg = 0.

- ↓
1. CMP-SA-PEG, α 2,8-ST

a-d, q = 1; e-h = 1 to 4;
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)
 = 0 or 1;
 o, p, z = 0; R = PEG;
 j-m, ee (independently selected) = 0 to 2;
 v-y, gg (independently selected) = 1, when j-m
 (independently selected) is 2;

FIG. 31G

102/345



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 32A

103/345

CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 32B

CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 32C

104/345

NSO expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA-PEG, ST3Gal1

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 32D

CHO, BHK, 293 cells, Vero expressed FSH.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 32E

105/345

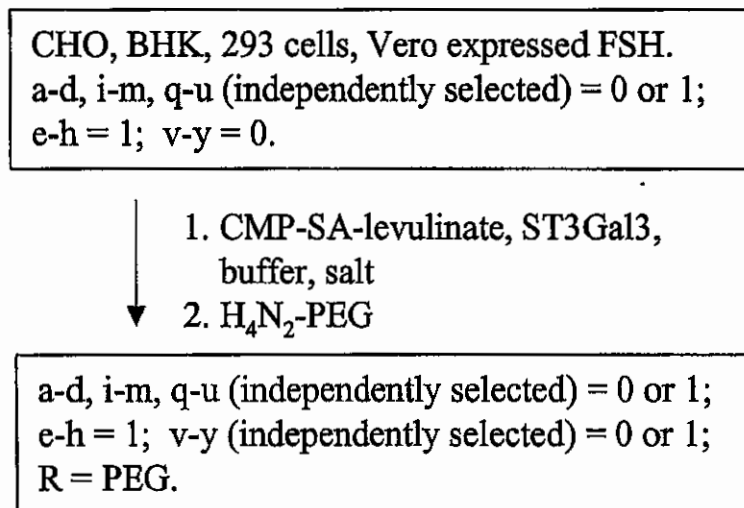


FIG. 32F

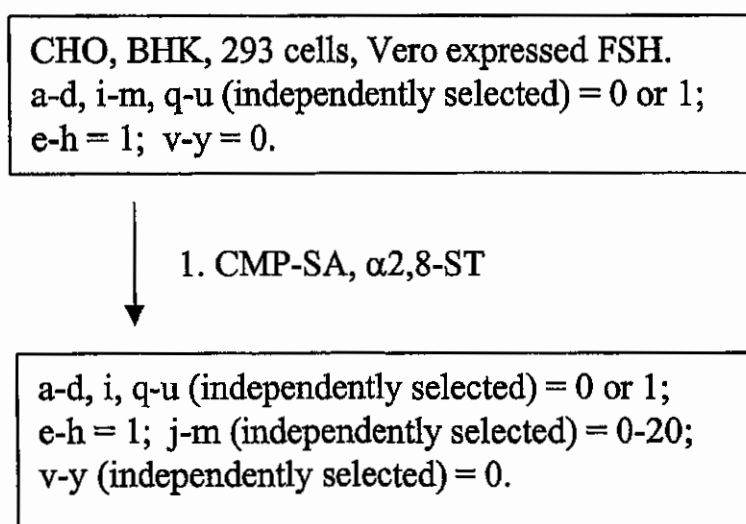


FIG. 32G

106/345

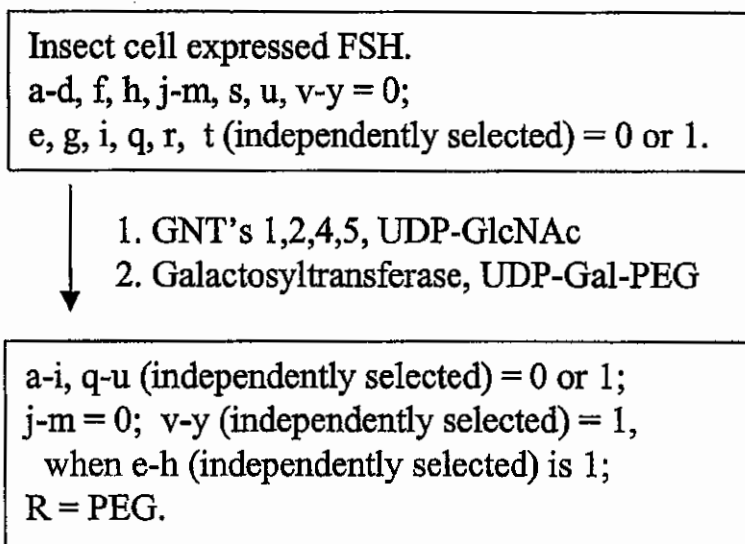


FIG. 32H

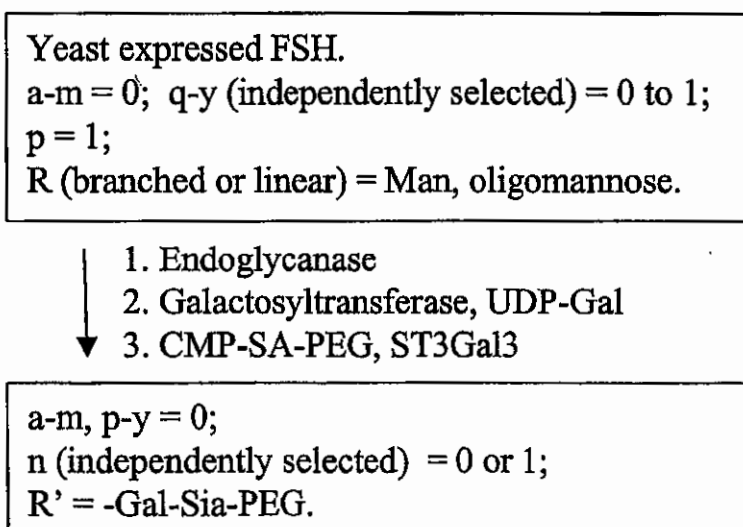


FIG. 32I

107/345

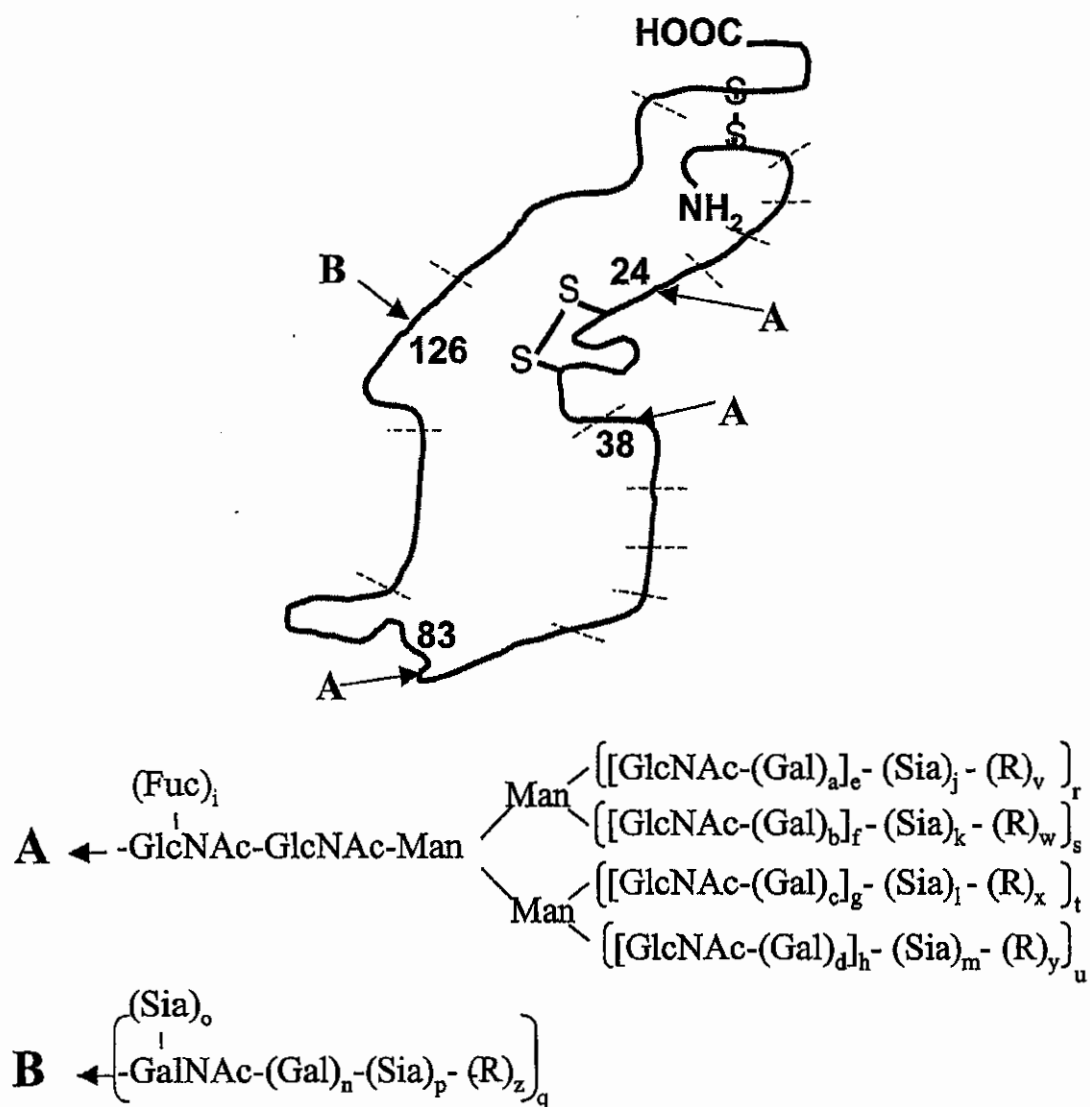
CHO, BHK, 293 cells, Vero expressed FSH.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated chorionic gonadotrophin (CG) produced in CHO.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-CG.

FIG. 32J

108/345



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 33A

109/345

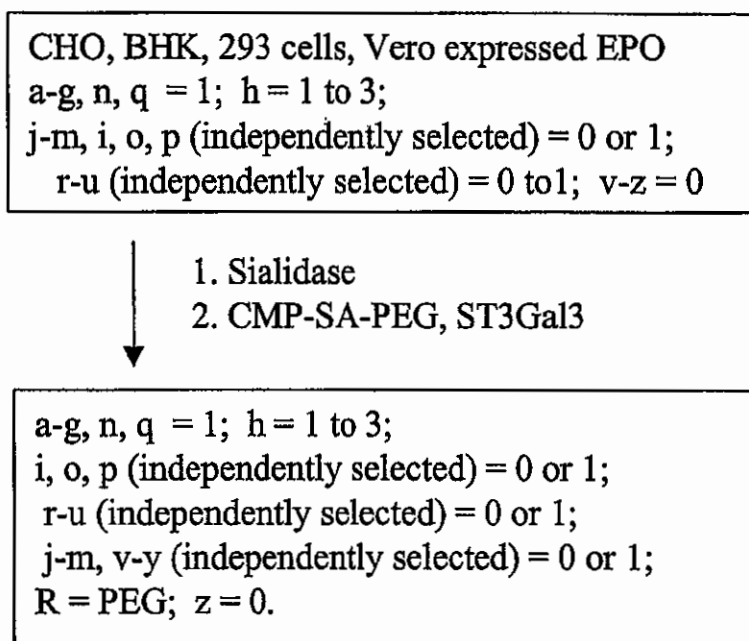


FIG. 33B

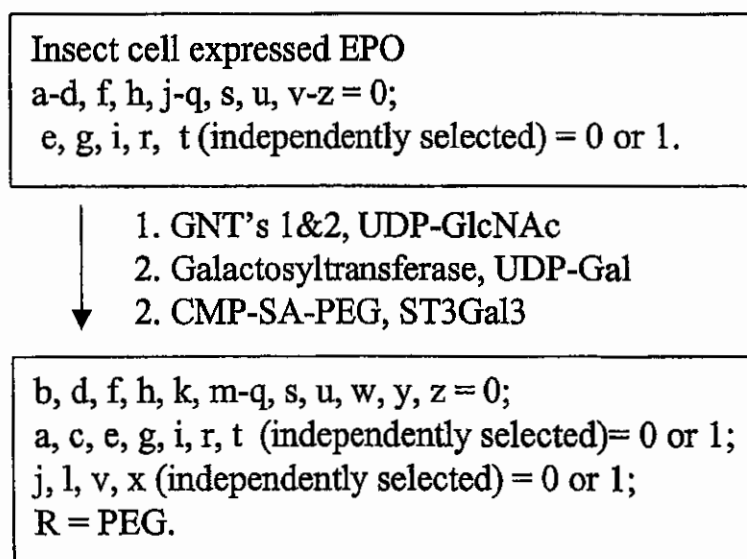


FIG. 33C

110/345

CHO, BHK, 293 cells, Vero expressed EPO
 a-q, r-u (independently selected) = 0 or 1;
 v-z = 0.

- ↓
1. sialidase
 2. Galactosyltransferase, UDP-Gal
 3. CMP-SA, ST3Gal3
 - ↓ 4. CMP-SA-PEG, ST3Gal1

a-h, n, q = 1;
 i-m, o, r-u (independently selected) = 0 or 1;
 v-y = 0; p, z = 0 or 1; R = PEG.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed EPO
 a-g, n, q = 1; h = 1 to 3;
 j-m, i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 or 1;
 v-z = 0

- ↓
1. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;
 i, o, p (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1;
 j-m, v-y (independently selected) = 0 or 1;
 R = PEG; z = 0.

FIG. 33E

111/345

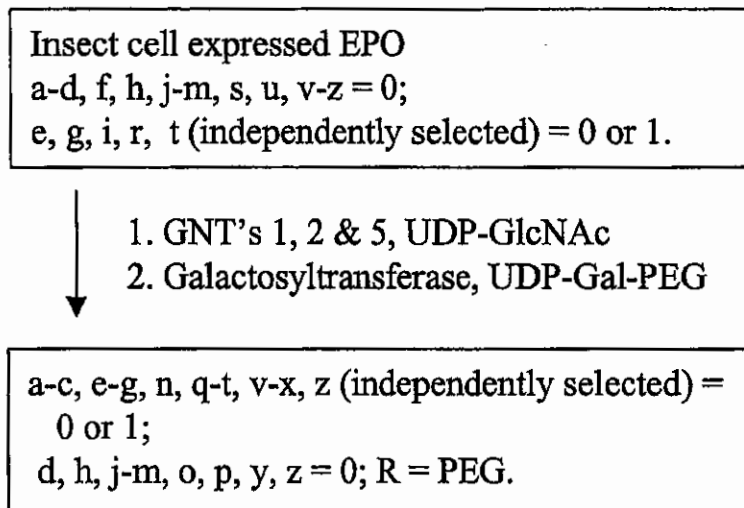


FIG. 33F

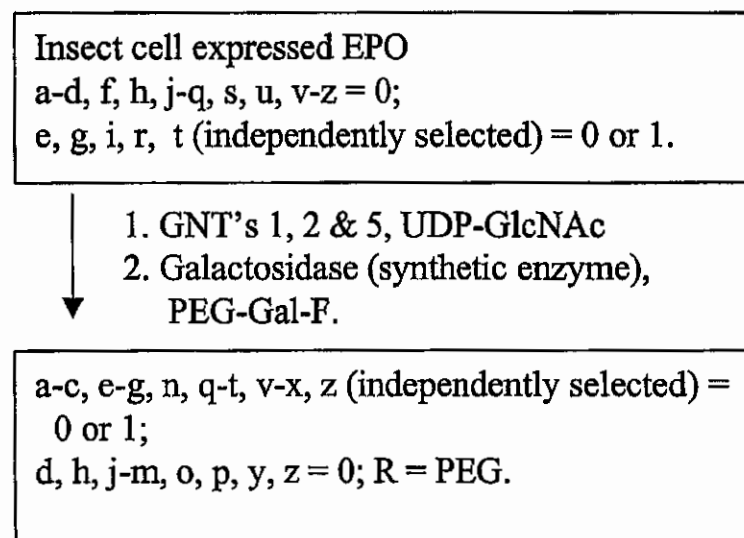


FIG. 33G

112/345

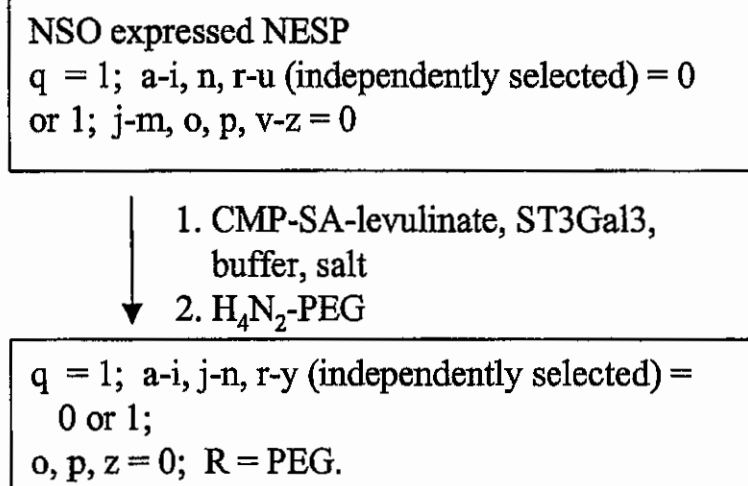


FIG. 33H

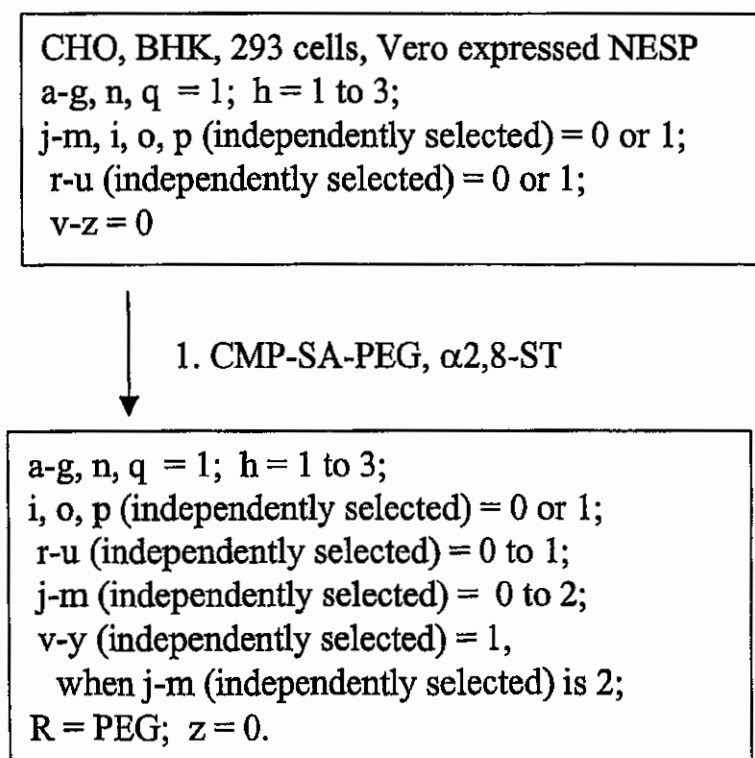


FIG. 33I

113/345

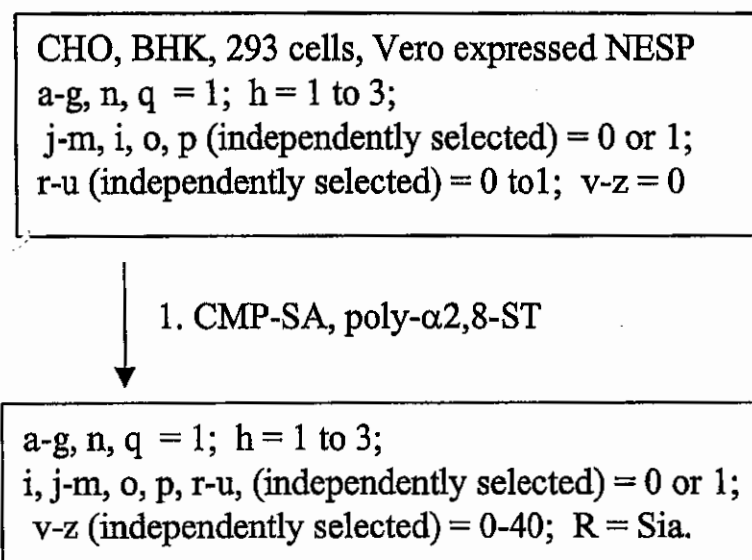
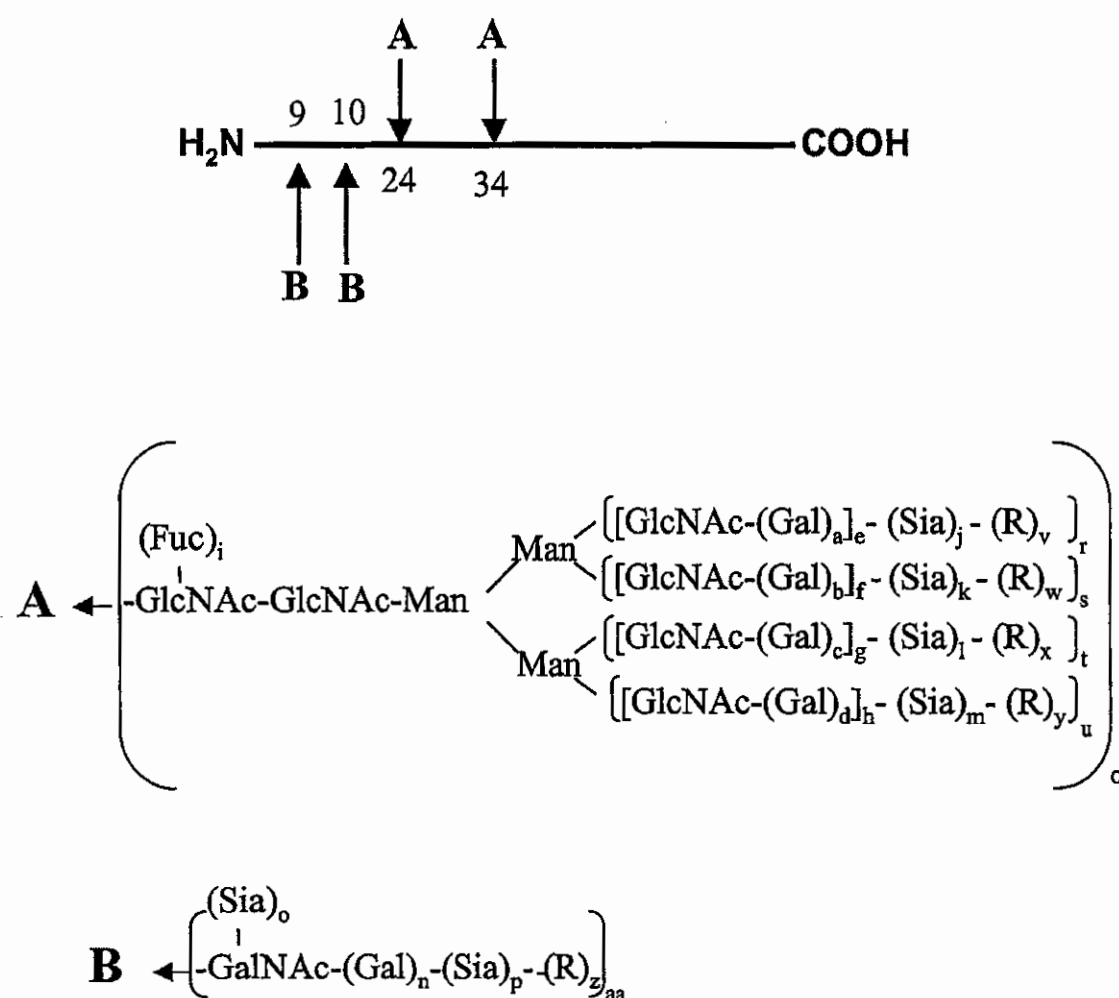


FIG. 33J

114/345



a-d, i, n-u, aa (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 34A

115/345

CHO, BHK, 293 cells, Vero expressed GM-CSF.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
 o, p, z = 0; n, e-h = 1;
 v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 34B

CHO, BHK, 293 cells, Vero expressed GM-CSF.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3 &
ST3Gal1

a-d, i-m, p-u, aa (independently selected) = 0 or 1;
 o, z = 0; n, e-h = 1;
 v-y (independently selected) = 0 or 1; R = PEG.

FIG. 34C

116/345

NSO expressed GM-CSF.

a-d, i-m, o-u, aa (independently selected) = 0 or 1;

n, e-h = 1; v-z = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-PEG, ST3Gal1

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;

n, e-h = 1; o, v-y = 0; z = 1, when p = 1; R = PEG.

FIG. 34D

CHO, BHK, 293 cells, Vero expressed GM-CSF.

a-d, i-m, o-u, aa (independently selected) = 0 or 1;

n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-y, aa (independently selected) = 0 or 1;

o, p, z = 0; n, e-h = 1; R = PEG.

FIG. 34E

117/345

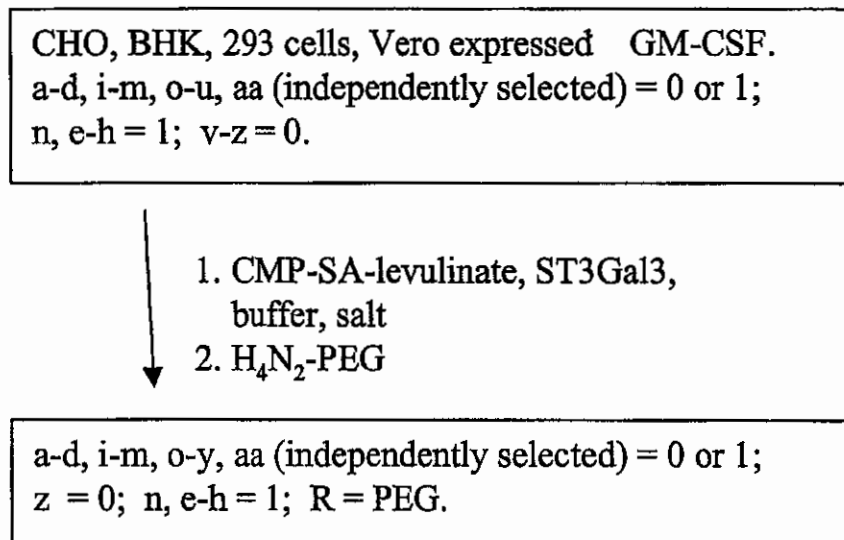


FIG. 34F

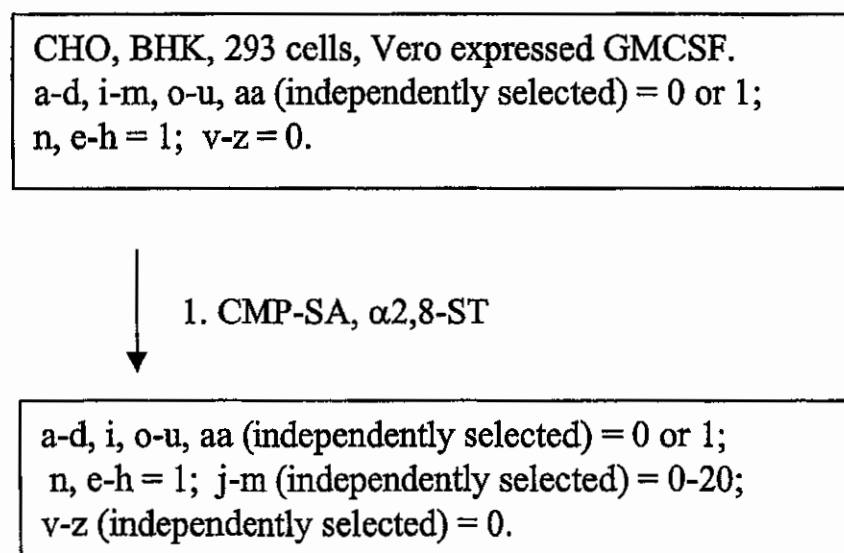
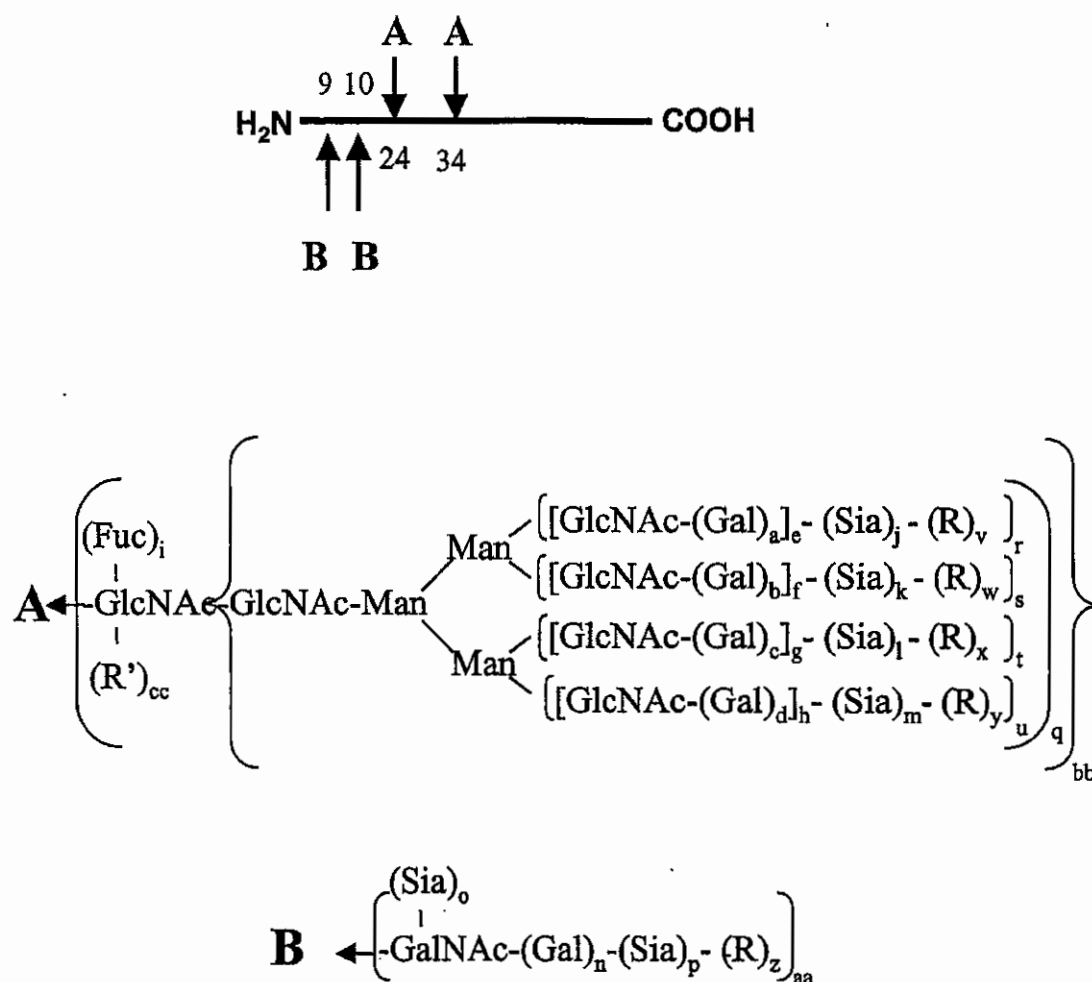


FIG. 34G

118/345



a-d, i, n-u, aa, bb, cc (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group. glycoconjugate.

FIG. 34H

119/345

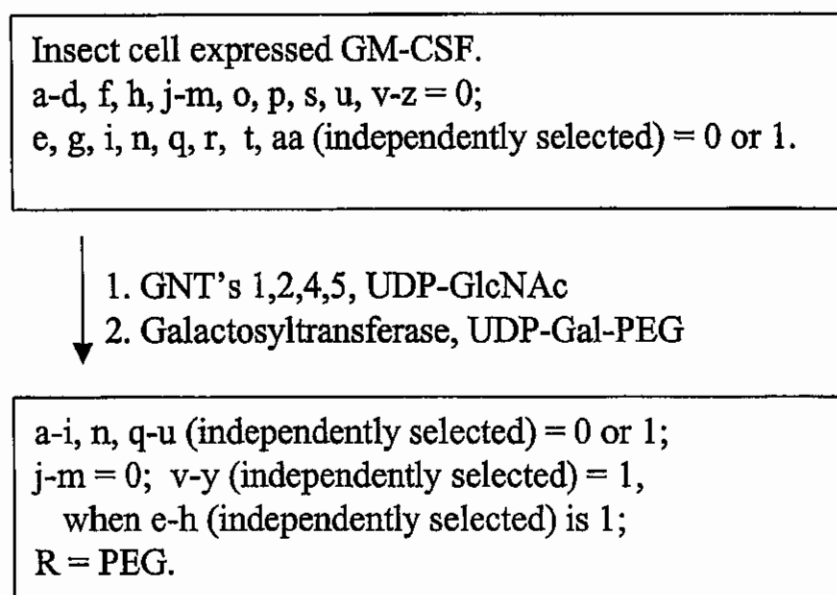


FIG. 34I

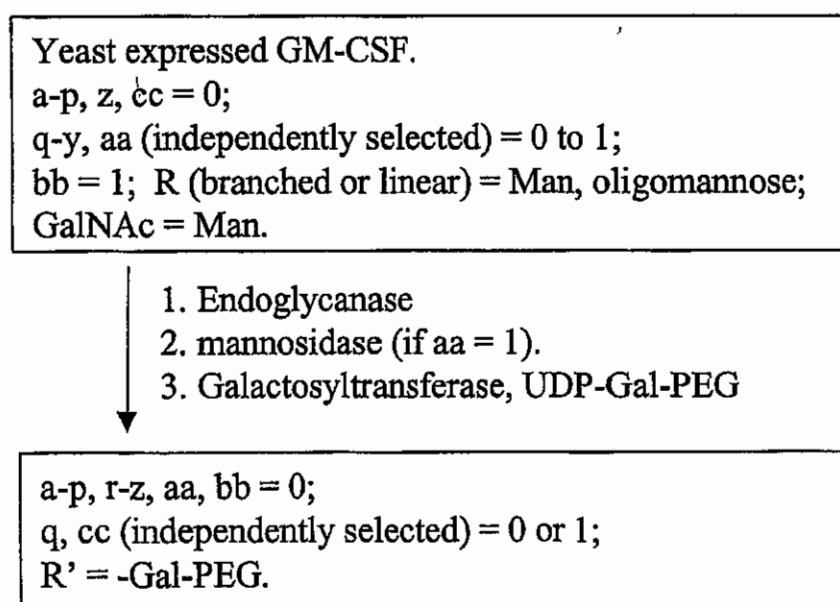


FIG. 34J

120/345

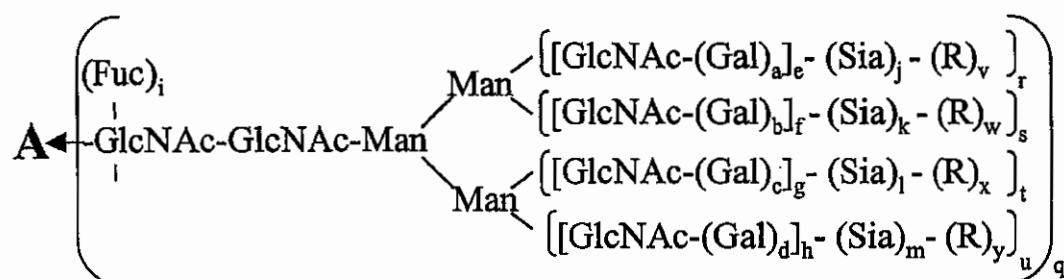
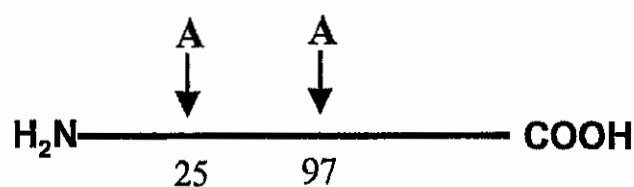
CHO, BHK, 293 cells, Vero expressed GM-CSF.
a--m, o-u, aa, bb (independently selected) = 0 or 1;
n, v-z, cc = 0.

- ↓
1. sialidase
 2. CMP-SA, ST3Gal3
 2. CMP-SA-linker-SA-CMP, ST3Gal1
 3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 34K

121/345



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 35A

122/345

CHO, BHK, 293 cells, Vero expressed IF-gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 35B

CHO, BHK, 293 cells, Vero expressed IF-gamma.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 35C

123/345

NSO expressed Interferon gamma.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 - ↓ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 35D

CHO, BHK, 293 cells, Vero expressed
Interferon gamma.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ↓ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 35E

124/345

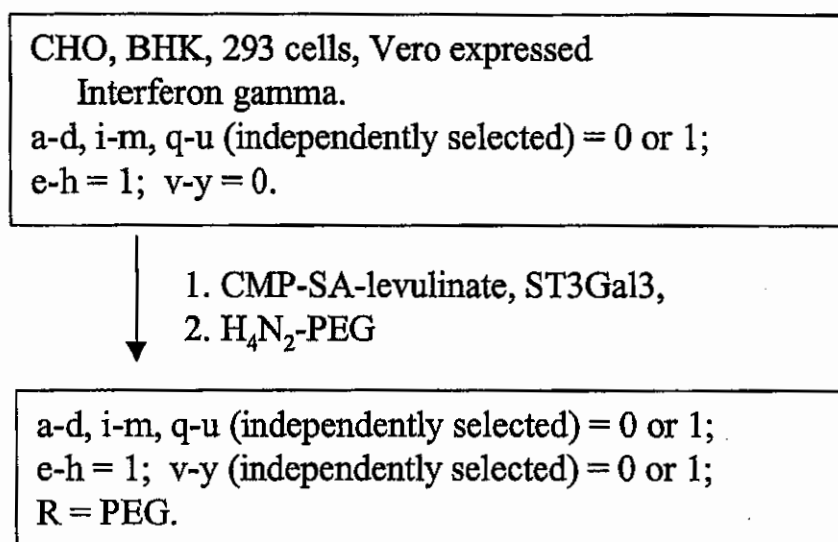


FIG. 35F

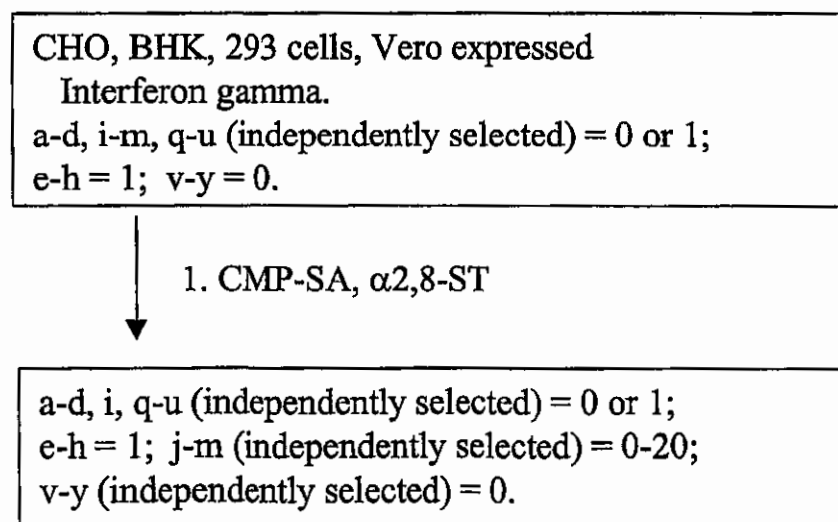
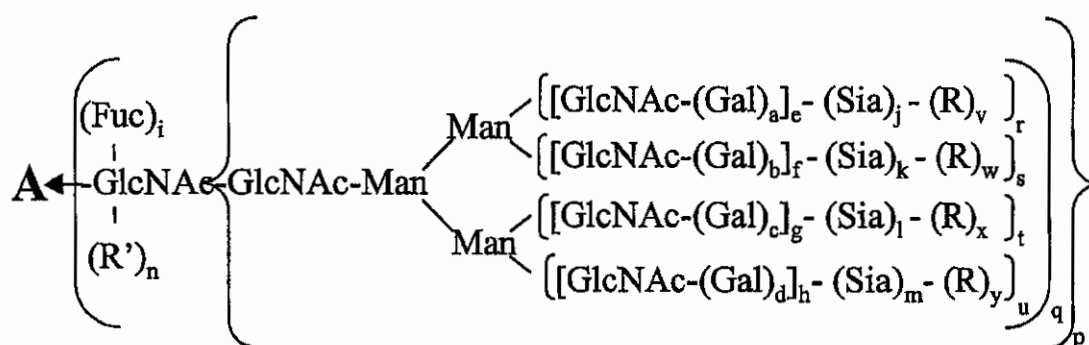
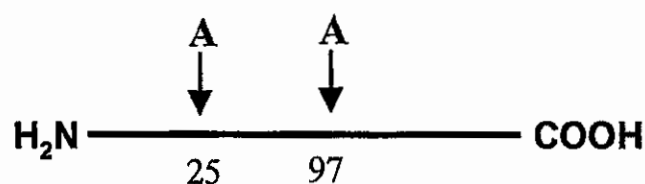


FIG. 35G

125/345



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 35H

126/345

Insect or fungi cell expressed IF-gamma.
 a-d, f, h, j-m, s, u, v-y = 0;
 e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;
 j-m = 0; v-y (independently selected) = 1,
 when e-h (independently selected) is 1;
 R = PEG.

FIG. 35I

Yeast expressed IF-gamma.
 a-m = 0; q-y (independently selected) = 0 to 1; p = 1;
 R (branched or linear) = Man, oligomannose.



1. Endoglycanase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;
 R' = -Gal-Sia-PEG.

FIG. 35J

127/345

CHO, BHK, 293 cells, Vero expressed IF-gamma.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP, ST3Gal3
 2. Galactosyltransferase, transferrin treated
with endoglycanase.

a-m, q-u (independently selected) = 0 or 1;
 p = 1; n = 0;
 v-y (independently selected) = 0 or 1;
 R = linker-transferrin.

FIG. 35K

CHO, BHK, 293 cells, Vero expressed
 Interferon gamma.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h, p = 1; n, v-y = 0.

- ↓
1. CMP-SA-PEG,
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h, p = 1;
 n, v-y (independently selected) = 0 or 1;
 R = PEG.

FIG. 35L

128/345

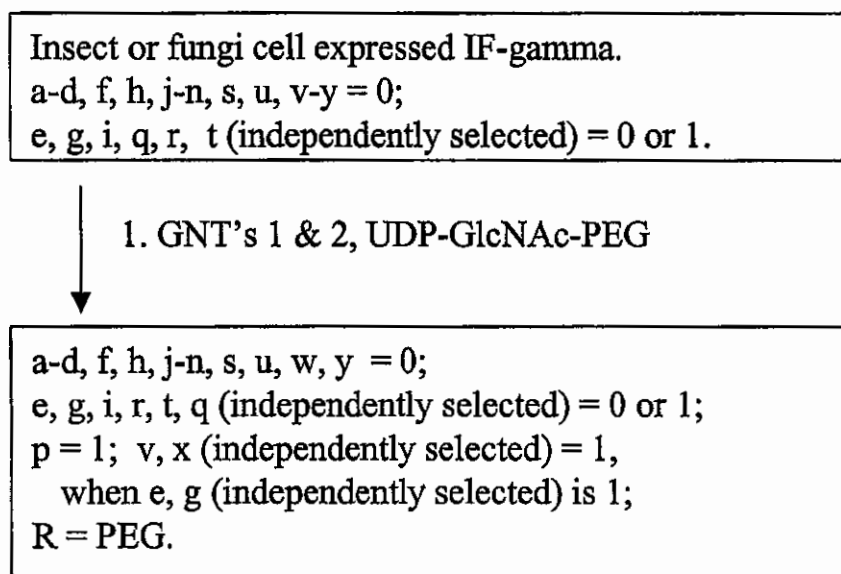


FIG. 35M

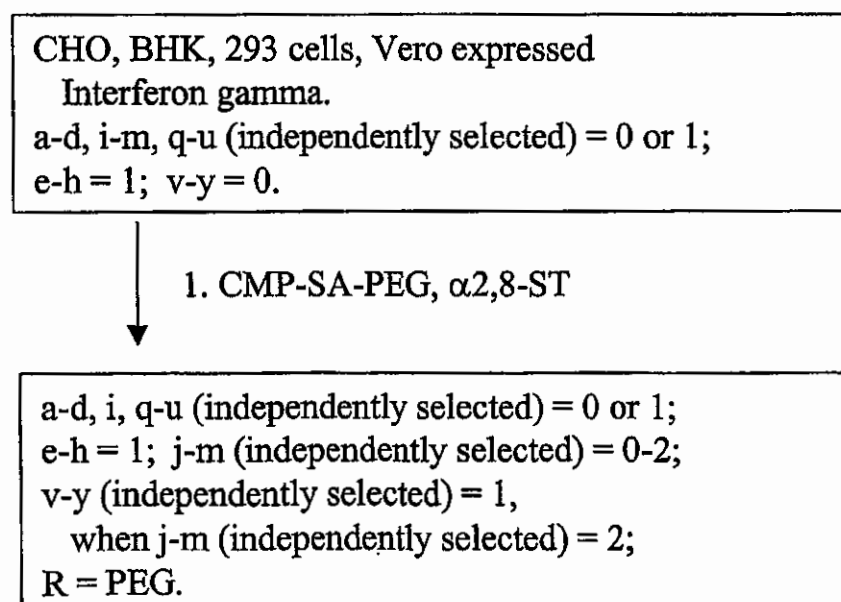


FIG. 35N

130/345

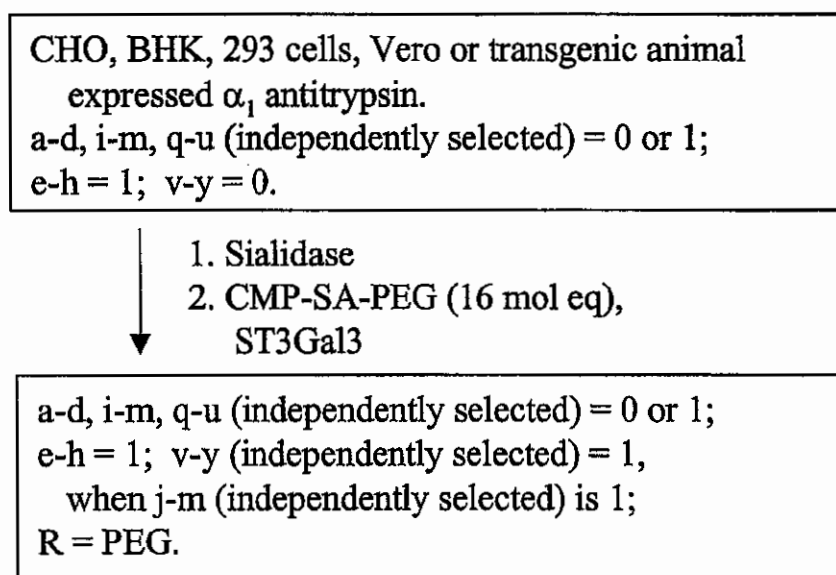


FIG. 36B

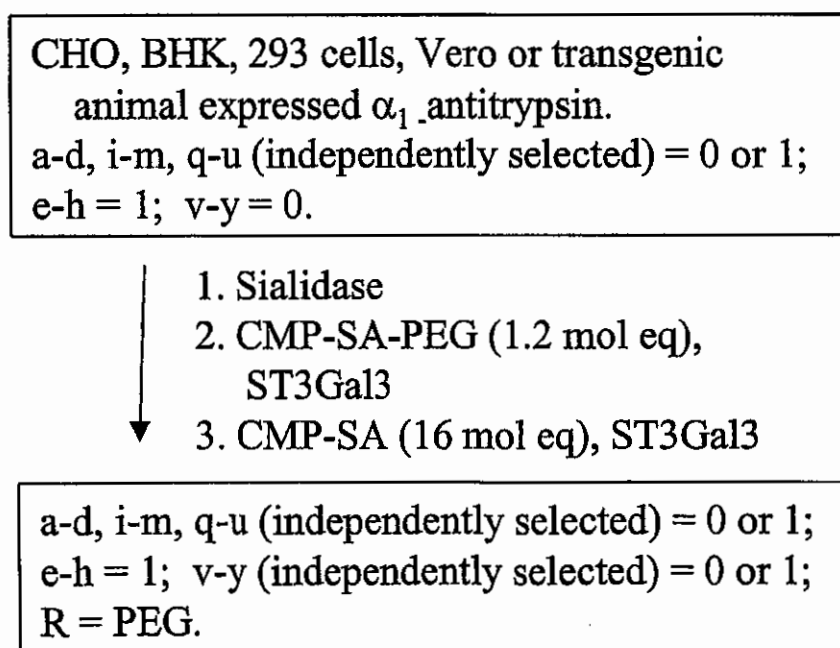


FIG. 36C

131/345

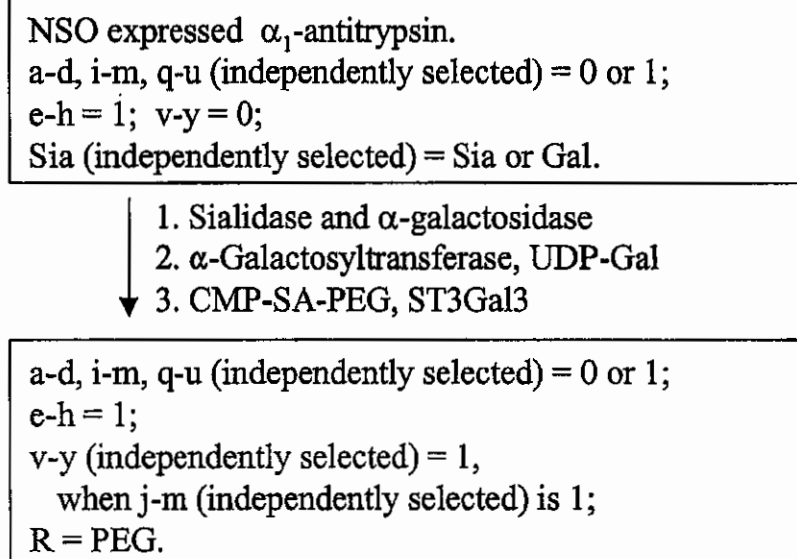


FIG. 36D

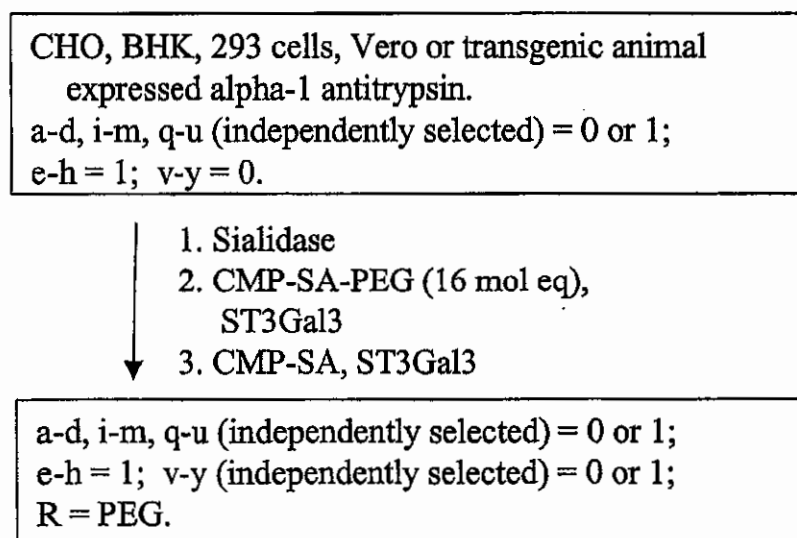


FIG. 36E

132/345

CHO, BHK, 293 cells, Vero or transgenic animal
expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H_4N_2 -PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 36F

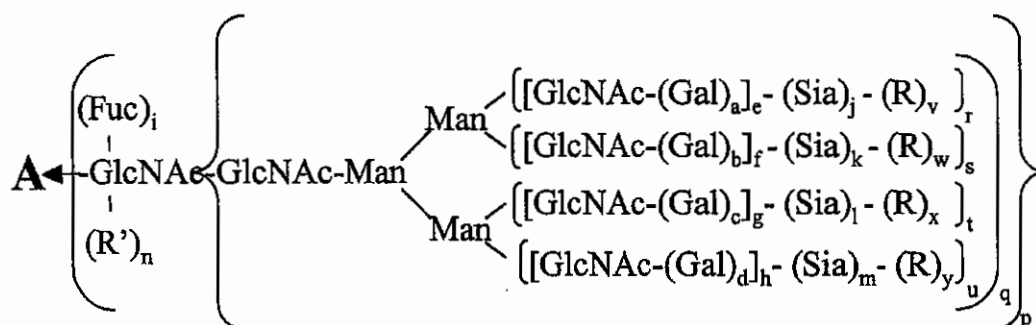
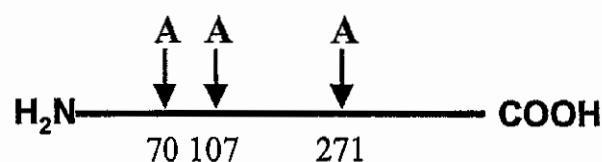
CHO, BHK, 293 cells, Vero expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, $\alpha 2,8$ -ST

a-d, i, q-u (independently selected) = 0 or 1; e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 36G

133/345



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 36H

134/345

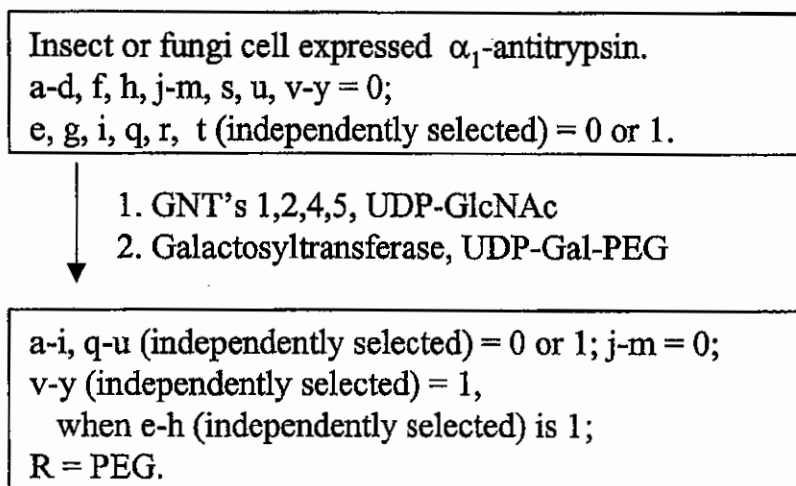


FIG. 36I

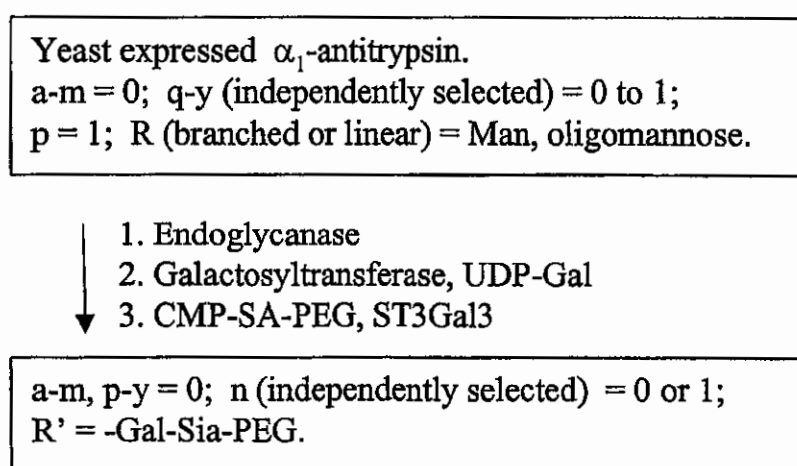


FIG. 36J

135/345

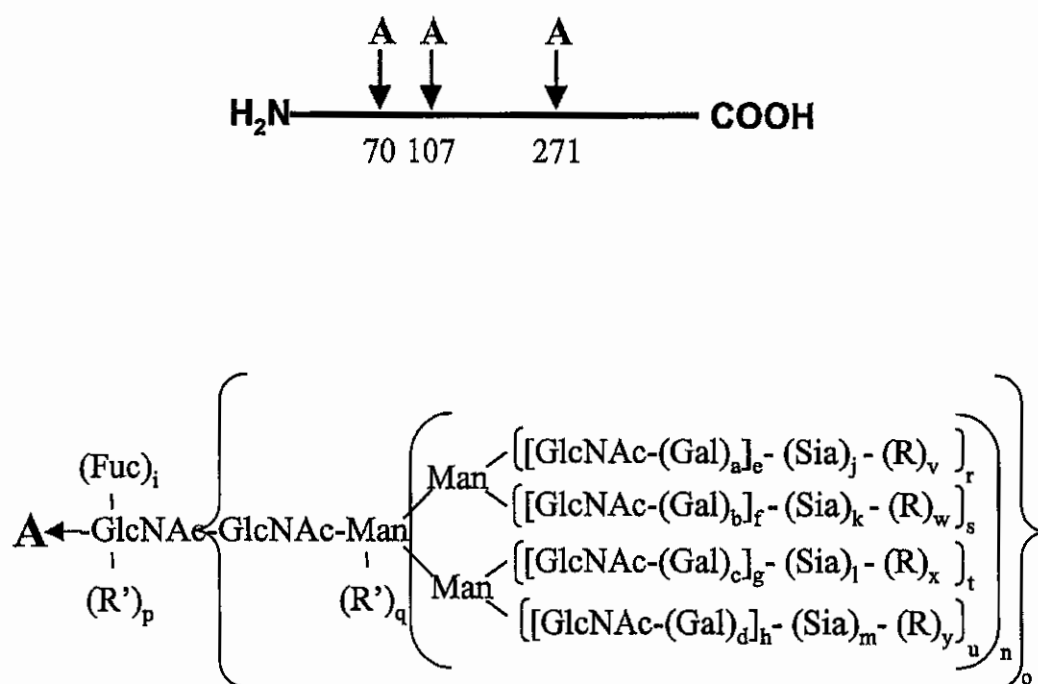
CHO, BHK, 293 cells, Vero expressed α_1 -antitrypsin.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, transferrin treated
with endoglycanase

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 36K

136/345



137/345

Yeast expressed alpha-1 antitrypsin.
 a-h, i-m, p, q = 0;
 R (independently selected) = mannose, oligomannose,
 polymannose;
 r-u, v-y (independently selected) = 0 or 1; n, o = 1.

- ↓ 1. endoglycanase
 ↓ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.
 R'' = Gal-PEG.

FIG. 36M

Plant expressed alpha-1 antitrypsin.
 a-d, f, h, j- m, s, u, v-y = 0;
 e, g, i, q, r, t (independently selected) = 0 or 1;
 n = 1; R' = xylose

- ↓ 1. hexosaminidase,
 ↓ 2. alpha mannosidase and xylosidase
 ↓ 3. GlcNAc transferase, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, v-y = 0;
 e, g, i, r, t (independently selected) = 0;
 q = 1; R' = GlcNAc-PEG.

FIG. 36N

138/345

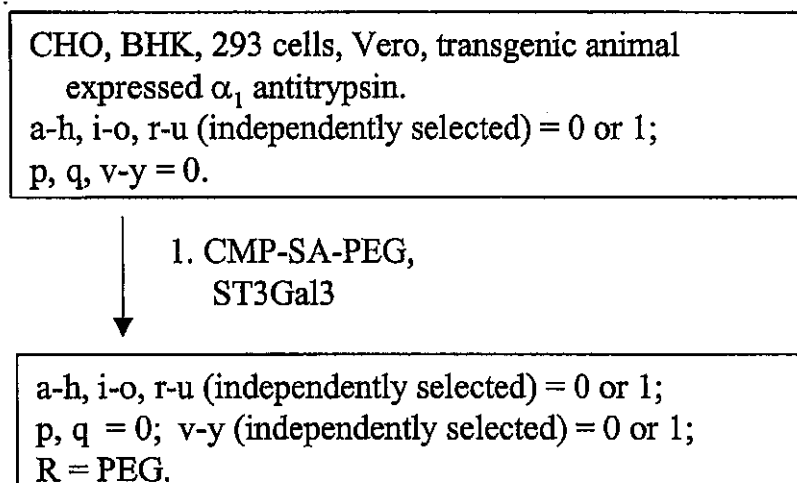
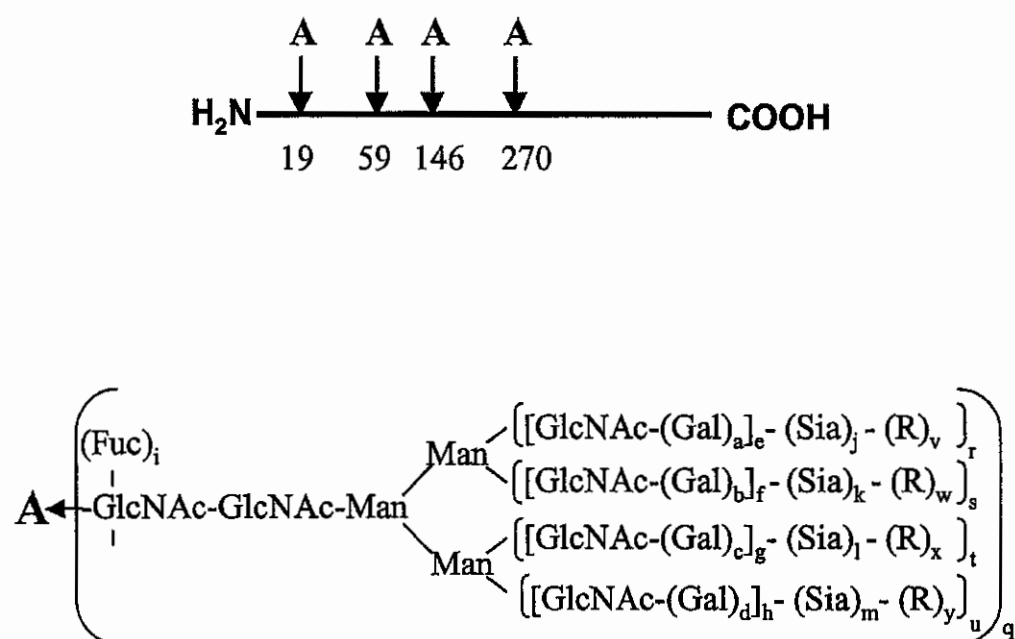


FIG. 36O

139/345



a-d, i, q-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer.

FIG. 37A

140/345

CHO, BHK, 293 cells, Vero expressed Cerezyme
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 37B

CHO, BHK, 293 cells, Vero expressed Cerezyme.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-M-6-P (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 0 or 1;
 R = mannose-6-phosphate

FIG. 37C

141/345

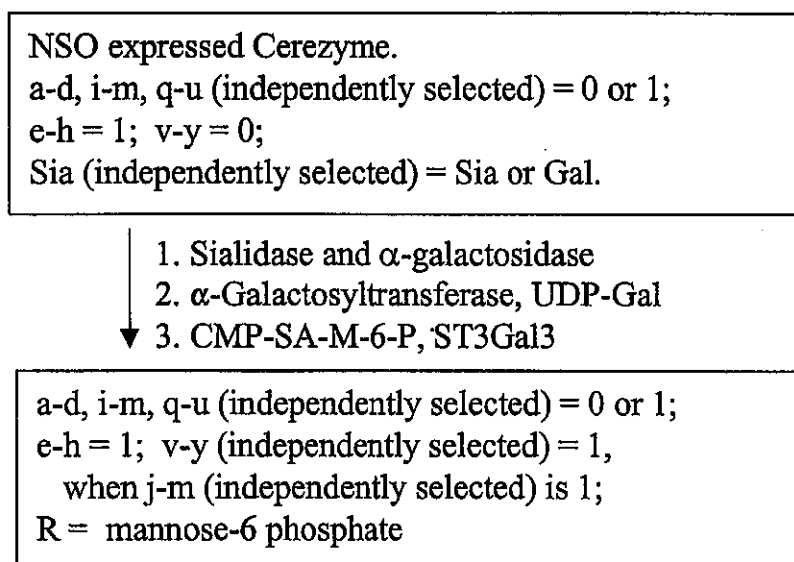


FIG. 37D

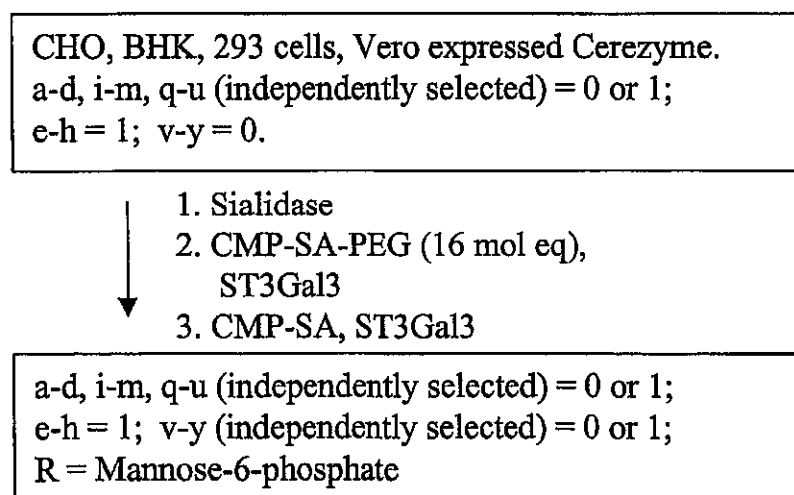


FIG. 37E

142/345

CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3, buffer, salt.
 2. H₄N₂-spacer-M-6-P or clustered M-6-P

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = M-6-P or clustered M-6-P

FIG. 37F

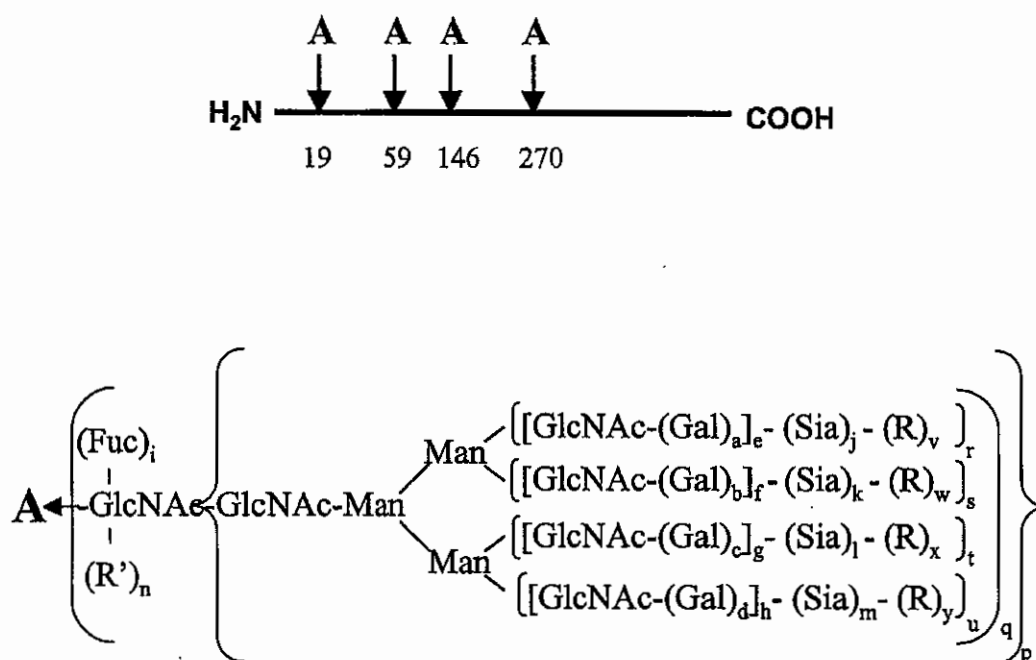
CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 37G

143/345



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 37H

144/345

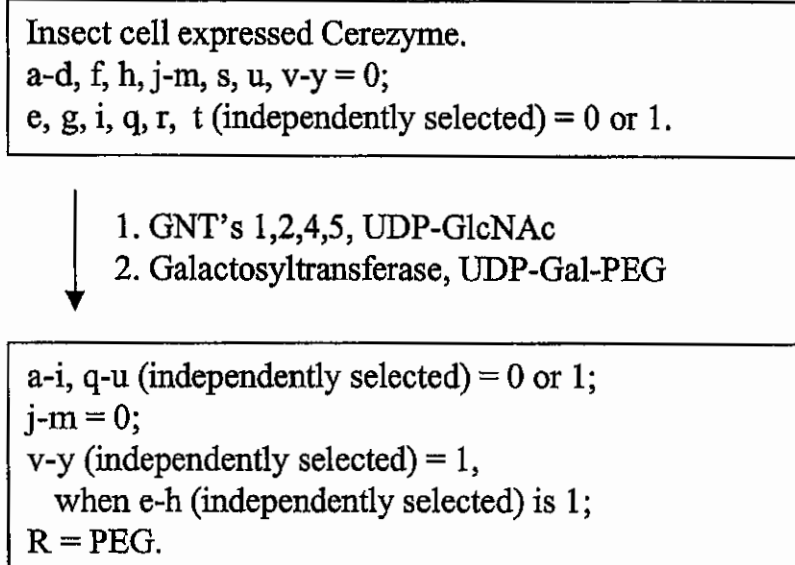


FIG. 37I

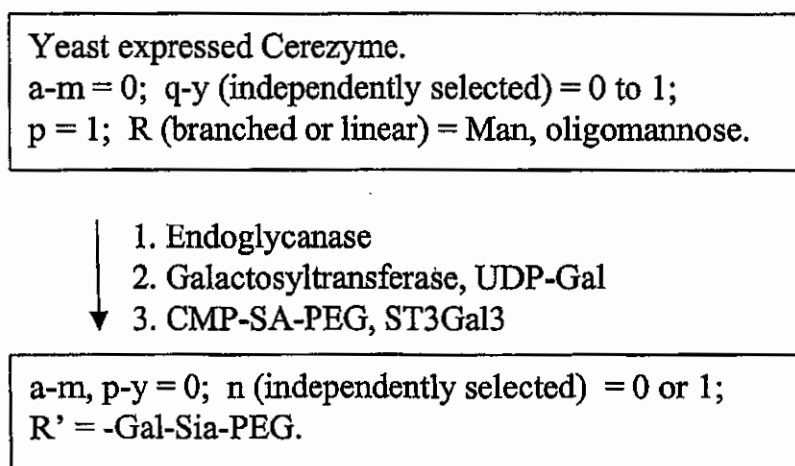


FIG. 37J

145/345

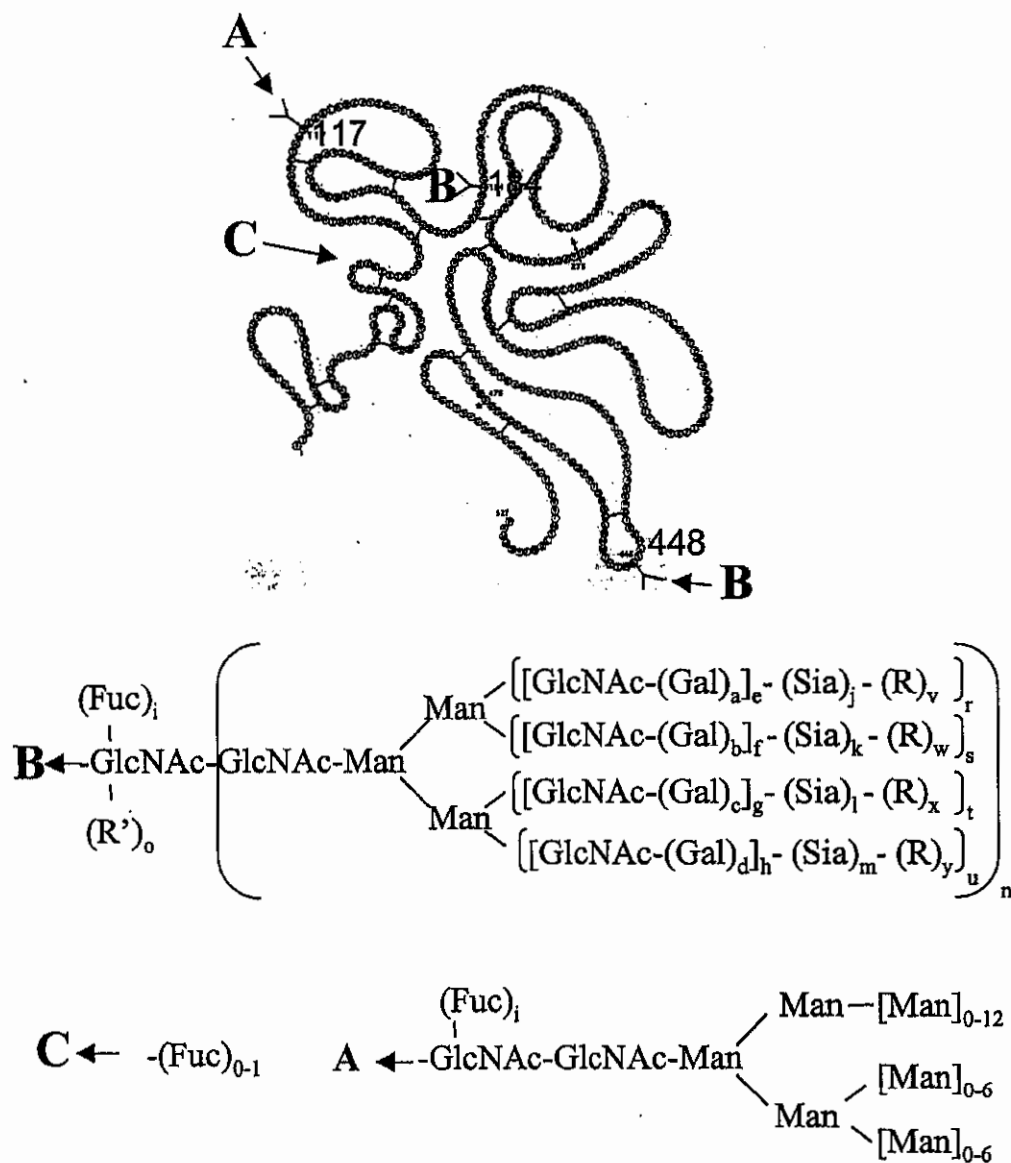
CHO, BHK, 293 cells, Vero expressed Cerezyme.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,
ST3Gal3
 2. ST3Gal3, desialylated transferrin.
 3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0; v-y (independently selected) = 0 or 1;
R = linker-transferrin.

FIG. 37K

146/345



a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 38A

147/345

CHO, BHK, 293 cells, Vero expressed tPA
 a-g, n = 1; h = 1 to 3;
 j-m, i, (independently selected) = 0 or 1;
 r-u (independently selected) = 0 to 1; o, v-y = 0.

1. Mannosidase(s), sialidase
2. GNT1,2 (4 and/or 5) UDP-GlcNAc
3. Gal transferase, UDP-Gal
4. CMP-SA-PEG, ST3Gal3

A = B; a-g, n = 1; h = 1 to 3;
 i, r-u (independently selected) = 0 or 1;
 o = 0; j-m, v-y (independently selected) = 0 or 1;
 R = PEG

FIG. 38B

Insect or fungi cell expressed tPA
 A = B; a-d, f, h, j-o, s, u, v-y = 0;
 e, g, i, n, r, t (independently selected) = 0 or 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

A = B; b, d, f, h, k, m, o, s, u, w, y = 0;
 a, c, e, g, i, r, t (independently selected) = 0 or 1;
 n = 1; j, l, v, x (independently selected) = 0 or 1;
 R = PEG.

FIG. 38C

148/345

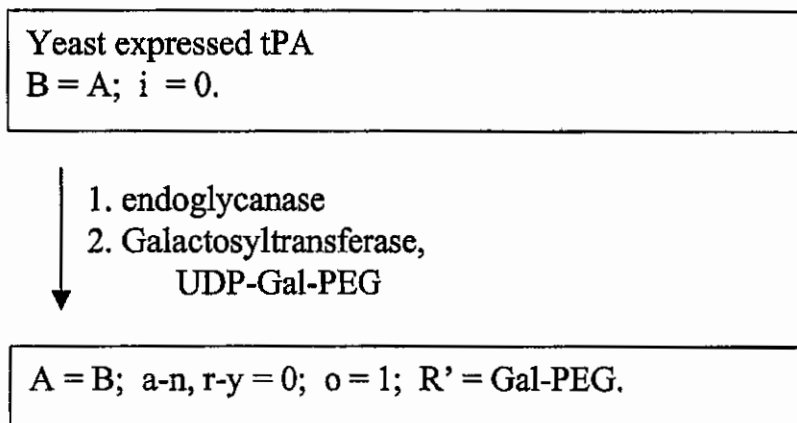


FIG. 38D

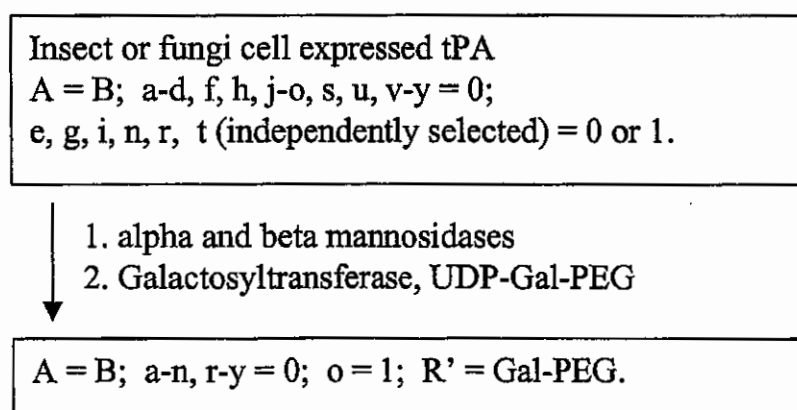


FIG. 38E

149/345

Insect or fungi cell expressed tPA
 $A = B$; a-d, f, h, j-o, s, u, v-y = 0;
 e, g, i, n, r, t (independently selected) = 0 or 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal-PEG

$A = B$; b, d, f, h, j-o, s, u, w, y = 0;
 a, c, e, g, i, r, t, v, x (independently selected) = 0 or 1;
 n = 1; R = PEG.

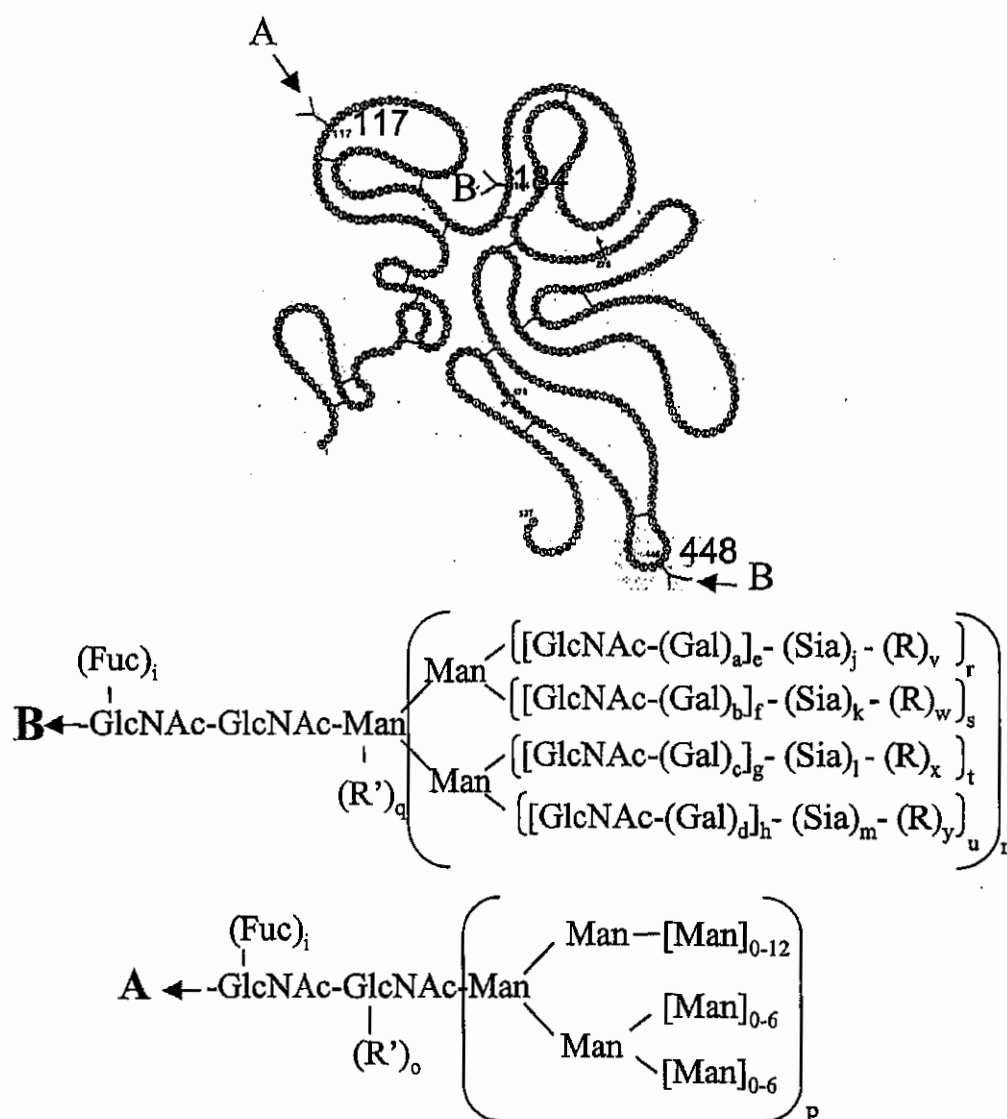
FIG. 38F

Insect or fungi cell expressed tPA
 $A = B$; a-d, f, h, j-o, s, u, v-y = 0;
 e, g, i, n, r, t (independently selected) = 0 or 1.

- ↓
1. GNT's 1 & 2, UDP-GlcNAc
 2. Galactosidase (synthetic enzyme),
PEG-Gal-F.

$A = B$; b, d, f, h, j-o, s, u, w, y = 0;
 a, c, e, g, i, r, t, v, x (independently selected) = 0 or 1;
 n = 1; R = PEG.

FIG. 38G



a-d, i, n-u (independently selected) = 0 or 1.
e-h (independently selected) = 0 to 4.
j-m (independently selected) = 0 to 20.
R = polymer; R' = sugar, glycoconjugate.

FIG. 38H

151/345

NSO expressed tPA

A = B; a-m, r-u (independently selected) = 0 or 1;
n = 1; o, p, q, v-y = 0

- ↓
1. sialidase, alpha-galactosidase
 2. CMP-SA-levulinate, ST3Gal3,
 3. H₄N₂-PEG

A = B; a-m, r-y (independently selected) = 0 or 1;
n = 1; o, p, q = 0;
v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 38I

CHO, BHK, 293 cells, Vero expressed tPA

a-g, n, p = 1; h = 1 to 3;
j-m, i, (independently selected) = 0 or 1;
r-u (independently selected) = 0 to 1; q, o, v-y = 0.

- ↓
1. alpha and beta Mannosidases
 2. CMP-SA, ST3Gal3
 3. Galactosyltransferase, UDP-Gal-PEG

a-g, n = 1; h = 1 to 3;
i, r-u (independently selected) = 0 or 1; o = 1;
q, p, v-y = 0; j-m (independently selected) = 0 or 1;
R' = Gal-PEG

FIG. 38J

152/345

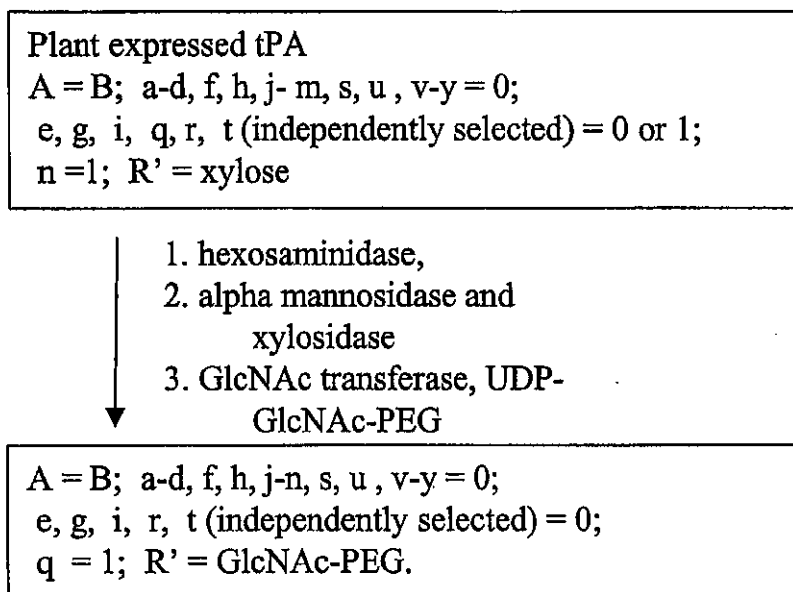
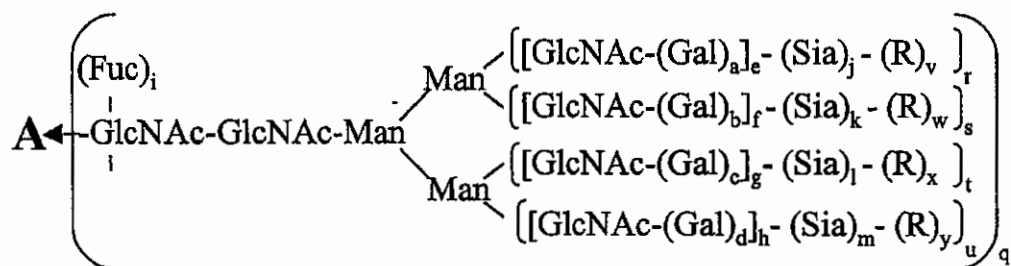
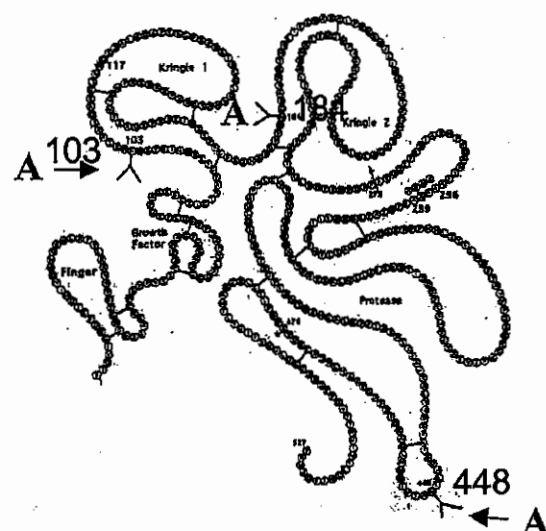


FIG. 38K

153/345



a-d, i, q-u (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 100.
 v-y = 0; R = polymer.

FIG. 38L

154/345

CHO, BHK, 293 cells, Vero expressed TNK tPA
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 38M

CHO, BHK, 293 cells, Vero expressed TNK tPA
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 0 or 1;
 R = PEG.

FIG. 38N

155/345

NSO expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0;
Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. Galactosyltransferase, UDP-Gal
 - ↓ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 380

157/345

CHO, BHK, 293 cells, Vero expressed TNK tPA
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 0 or 1;
 R = PEG.

FIG. 38Q

CHO, BHK, 293 cells, Vero expressed TNK tPA
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 0 or 1;
 R = PEG.

FIG. 38R

158/345

CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

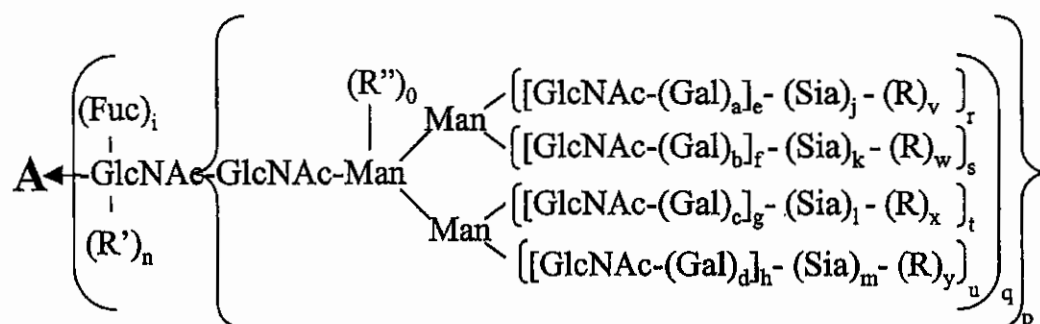
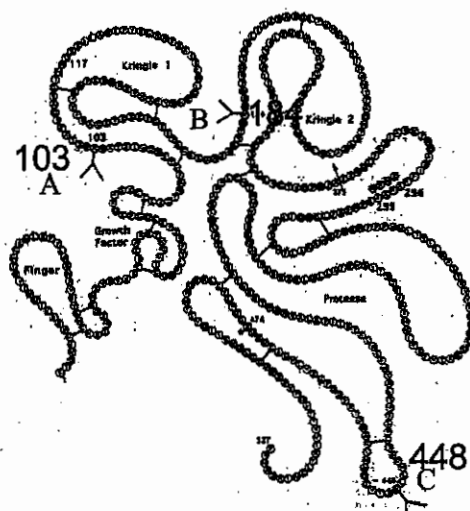


1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1; j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 38S

159/345



a-d, i, n-y (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

R'' = glycosyl residue.

FIG. 38T

160/345

Insect cell expressed TNK tPA
 a-d, f, h, j-m, s, u, v-y = 0;
 e, g, i, q, r, t (independently selected) = 0 or 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
 2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;
 j-m = 0; v-y (independently selected) = 1,
 when e-h (independently selected) is 1;
 R = PEG.

FIG. 38U

Yeast expressed TNK tPA
 a-m = 0; q-y (independently selected) = 0 to 1; p = 1;
 R (branched or linear) = Man, oligomannose.

- ↓
1. Endoglycanase
 2. Galactosyltransferase, UDP-Gal-PEG

a-m, p-y = 0; n (independently selected) = 0 or 1;
 R' = -Gal-PEG.

FIG. 38V

161/345

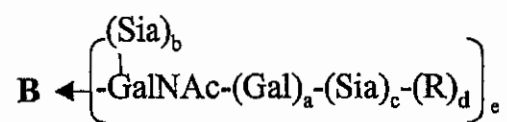
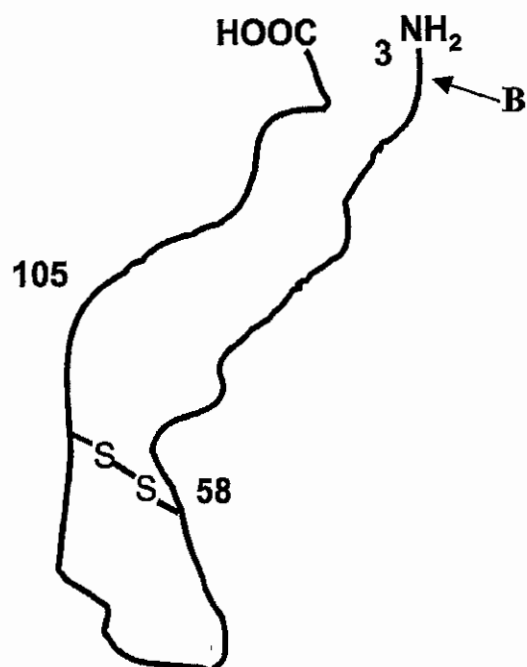
CHO, BHK, 293 cells, Vero expressed TNK tPA
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,
ST3Gal3
 2. Galactosyltransferase, anti-TNF
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;
n = 0; v-y (independently selected) = 0 or 1;
R = linker-anti-TNF IG chimera protein.

FIG. 38W

162/345



a-c, e (independently selected) = 0 or 1;
d = 0;

R = modifying group, mannose, oligo-
mannose.

FIG. 39A

163/345

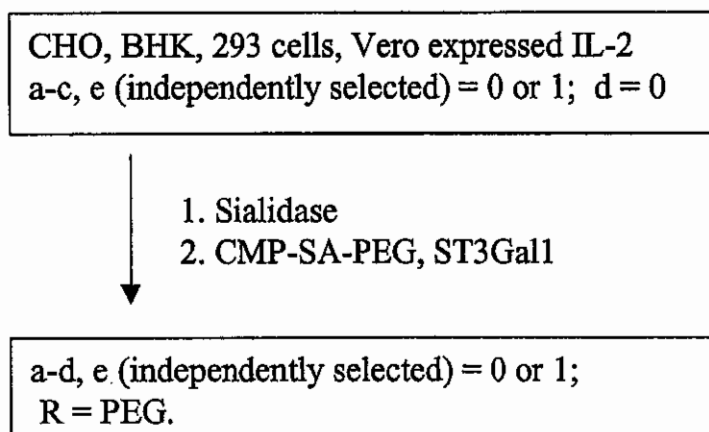


FIG. 39B

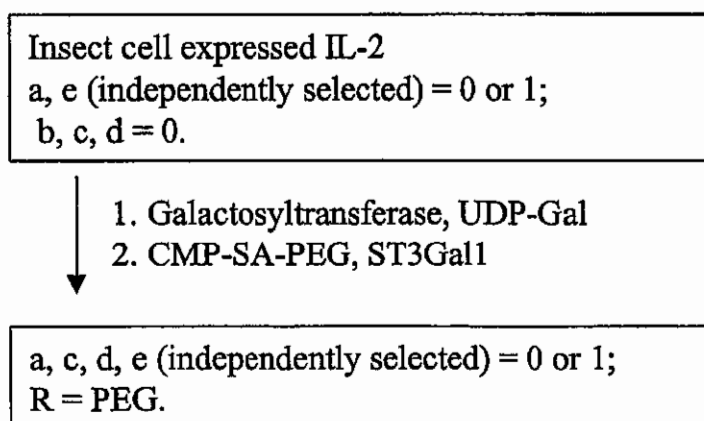


FIG. 39C

164/345

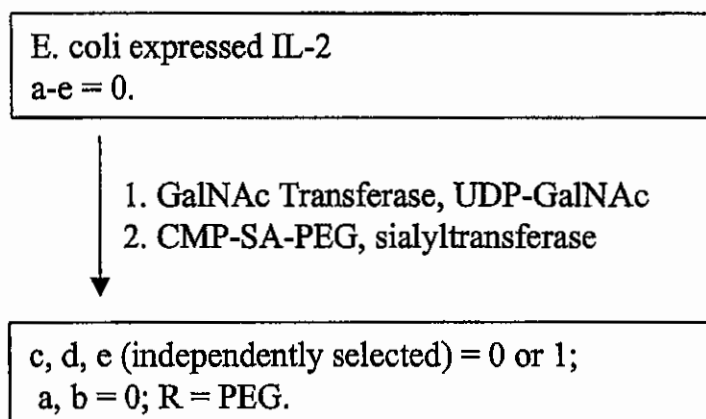


FIG. 39D

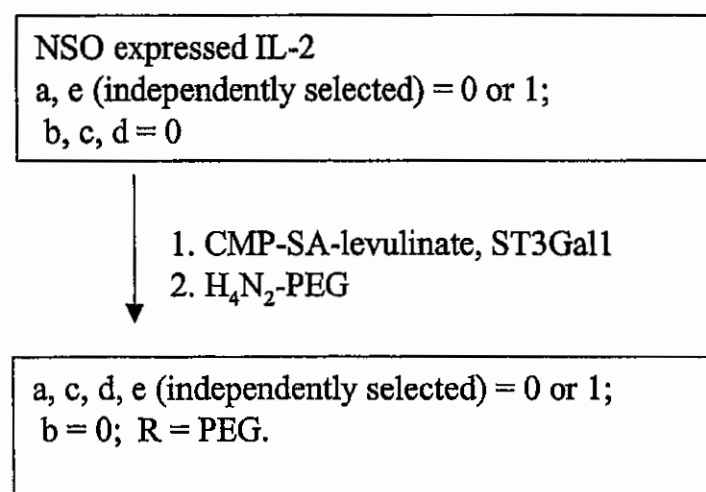


FIG. 39E

165/345

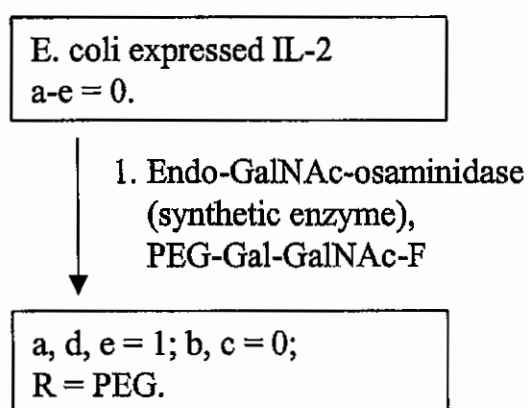


FIG. 39F

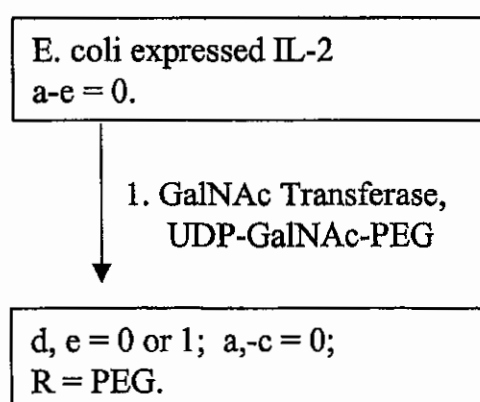
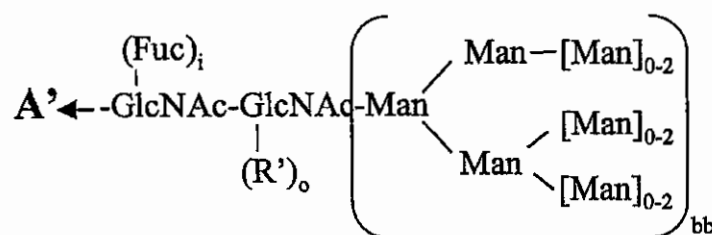
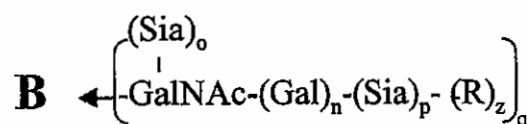
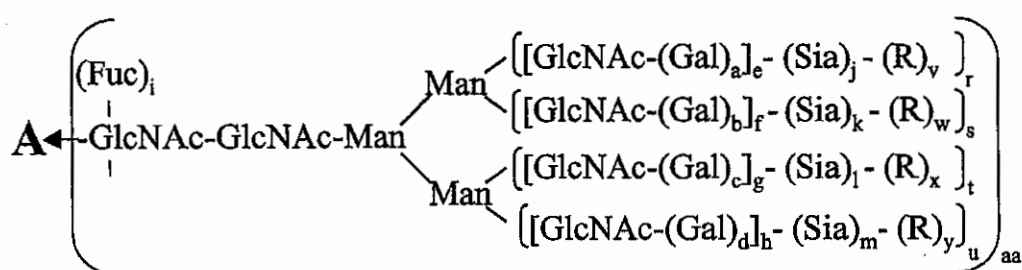


FIG. 39G

166/345

2 peptides
 A and A' - N-linked sites
 B - O-linked sites



Alternate structure
 for some N-linked
 structures of A.

a-d, i, n-u (independently selected) = 0 or 1.
 aa, bb (independently selected) = 0 or 1.
 e-h (independently selected) = 0 to 6.
 j-m (independently selected) = 0 to 20.
 v-z = 0; R = polymer, glycoconjugate.

FIG. 40A

167/345

CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG, ST3Gal3
 3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40C

168/345

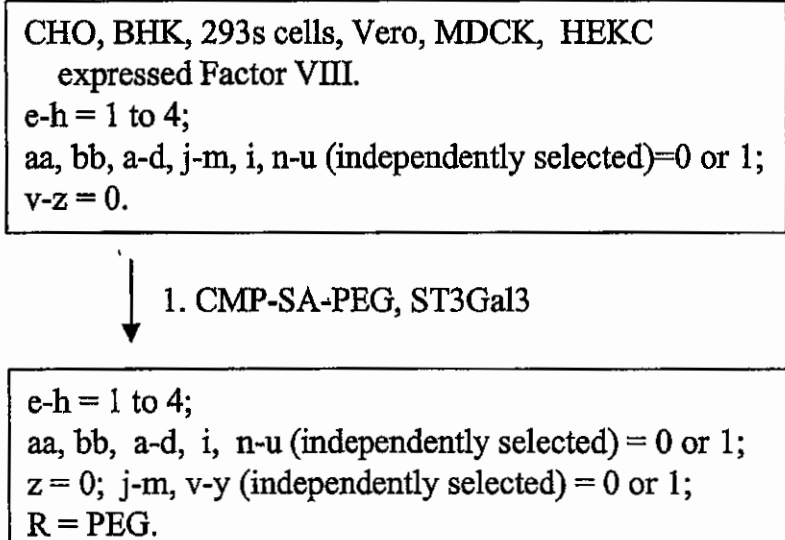


FIG. 40D

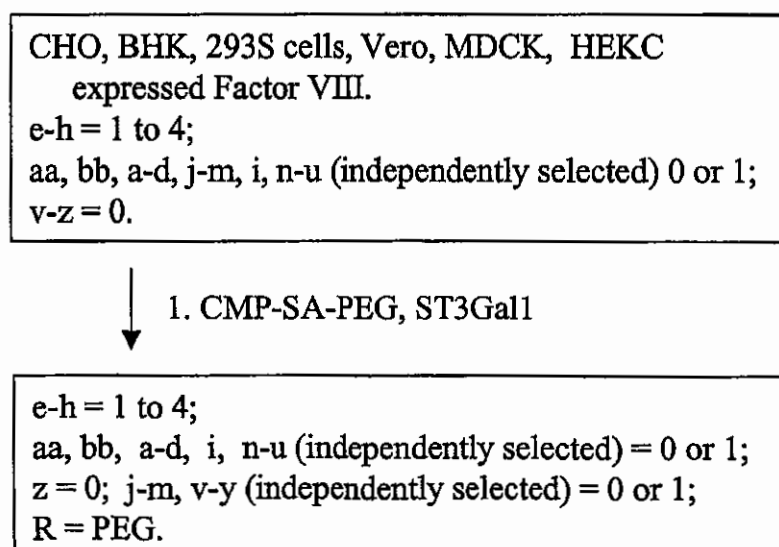


FIG. 40E

169/345

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;

v-z = 0.

↓ 1. CMP-SA-PEG, α 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

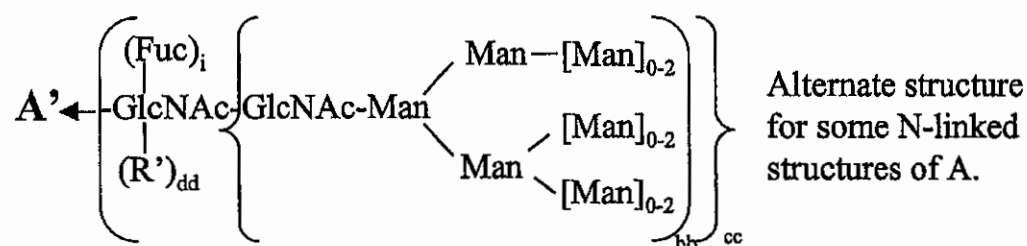
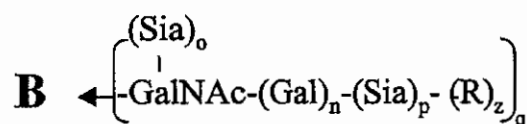
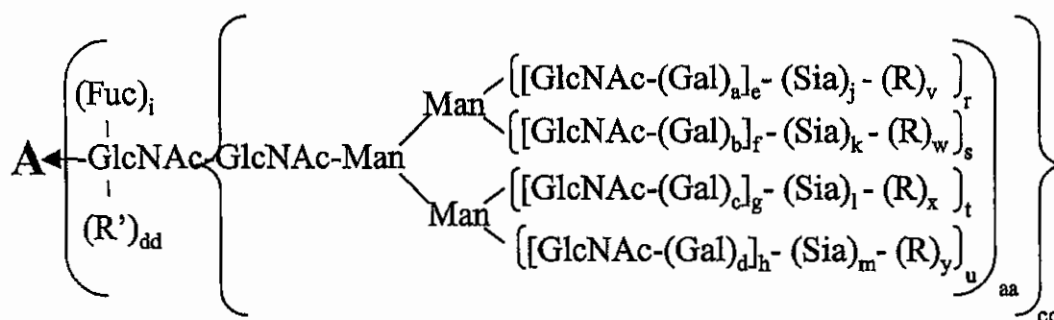
when j-m (independently selected) is 2;

R = PEG.

FIG. 40F

170/345

2 peptides
A or A' - N-linked sites
B - O-linked sites



a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 40G

171/345

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

↓ 1. CMP-SA-levulinate, ST3Gal3,
2. H₄N₂-PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;

dd, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 40H

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

↓ 1. endo-H
2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 40I

172/345

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓ 1. ST3Gal3, CMP-SA
2. endo-H
3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 40J

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓ 1. mannosidases
2. GNT 1 & 2, UDP-GlcNAc
3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0; R = PEG.

FIG. 40K

173/345

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

1. mannosidases

↓ 2. GNT-1, 2, 4 & 5; UDP-GlcNAc

↓ 3. galactosyltransferase, UDP-Gal

4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;

dd, v-z = 0.

FIG. 40L

CHO, BHK, 293S cells, Vero, MDCK, HEKC
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

↓ 1. mannosidases

↓ 2. GNT-1, UDP-GlcNAc-PEG

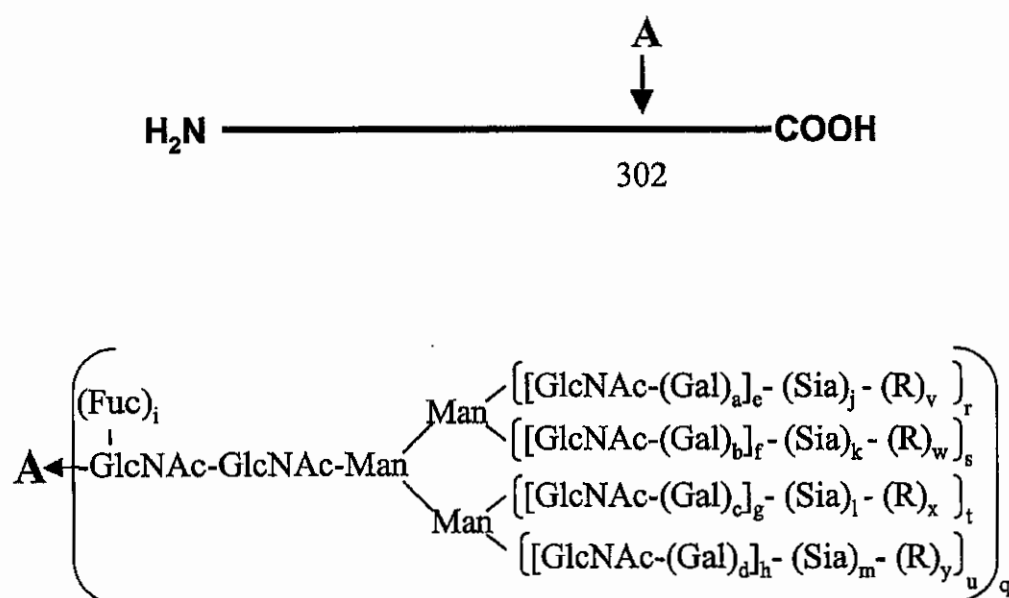
e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0.

FIG. 40M

174/345



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 41A

175/345

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 1,
when j-m (independently selected) is 1;
R = PEG.

FIG. 41B

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq),
ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 41C

176/345

NSO expressed Urokinase.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0;
 Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 - ↓ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 41D

CHO, BHK, 293 cells, Vero expressed Urokinase.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3
 - ↓ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 0 or 1;
 R = PEG.

FIG. 41E

177/345

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 41F

CHO, BHK, 293 cells, Vero expressed Urokinase.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 41G

178/345

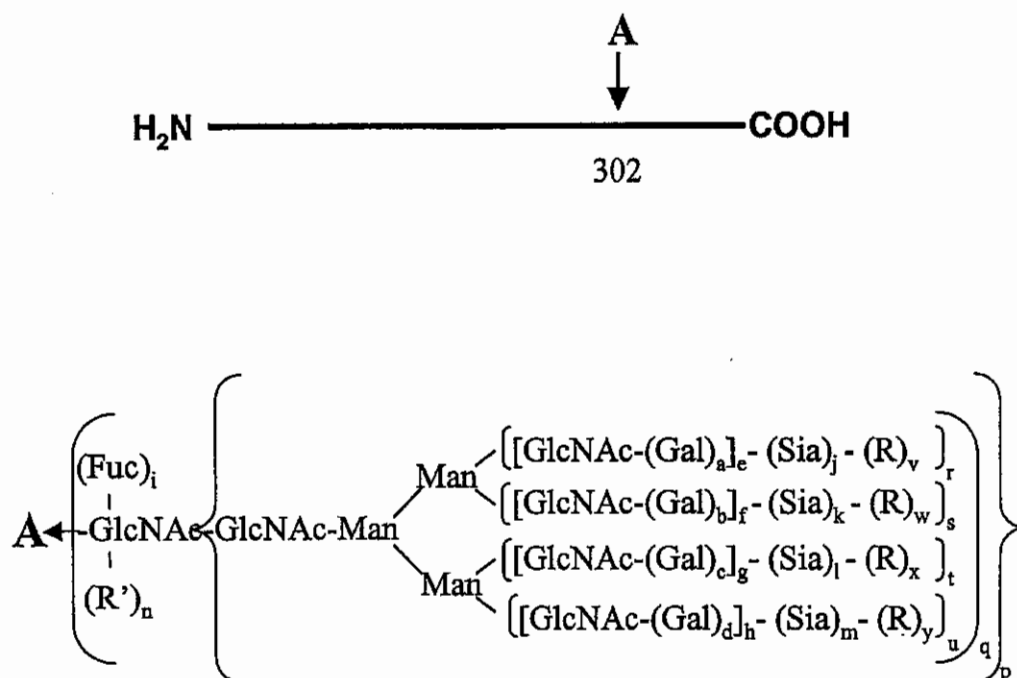


FIG. 41H

179/345

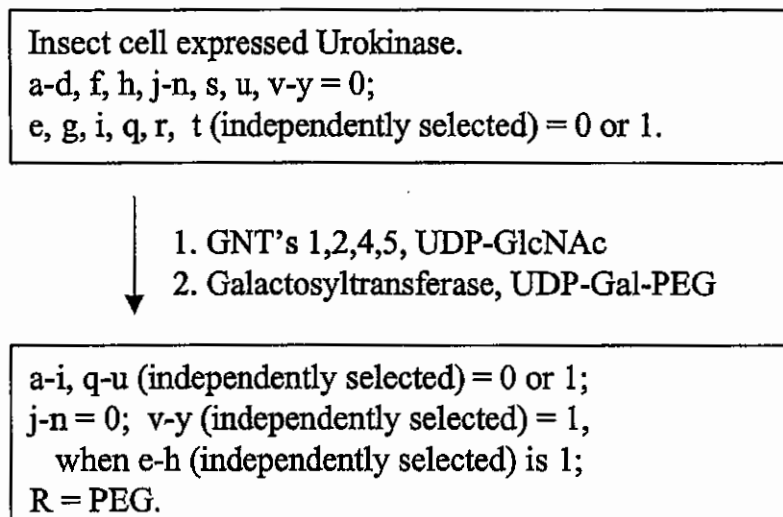


FIG. 41I

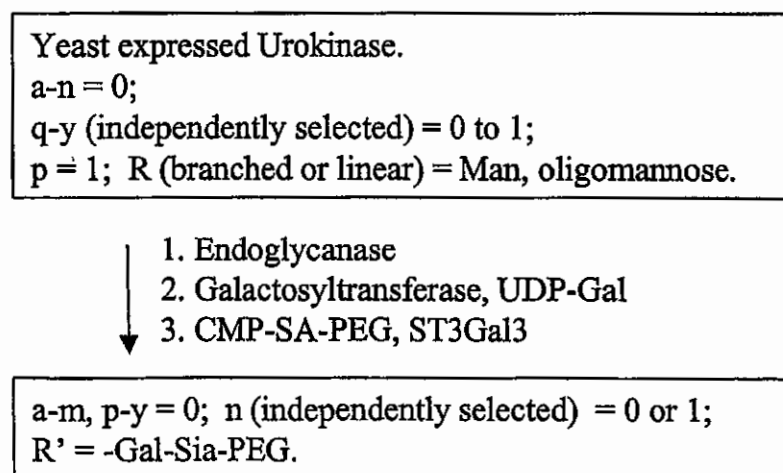


FIG. 41J

180/345

CHO, BHK, 293 cells, Vero expressed Urokinase.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated Urokinase produced in CHO.
 - ↓ 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
 p = 1; n = 0;
 v-y (independently selected) = 0 or 1;
 R = linker-Urokinase.

FIG. 41K

Isolated Urokinase.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0; n = 0;
 Sia (independently selected) = Sia or SO₄;
 Gal (independently selected) = Gal or GalNAc;
 GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase
 2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;
 n = 0; e-h = 1; Sia = Sia;
 Gal (independently selected) = Gal or GalNAc;
 GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.
 v-y (independently selected) = 0 or 1;
 R = PEG.

FIG. 41L

181/345

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO₄;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase, hexosaminidase
 2. UDP-Gal-PEG, galactosyltransferase

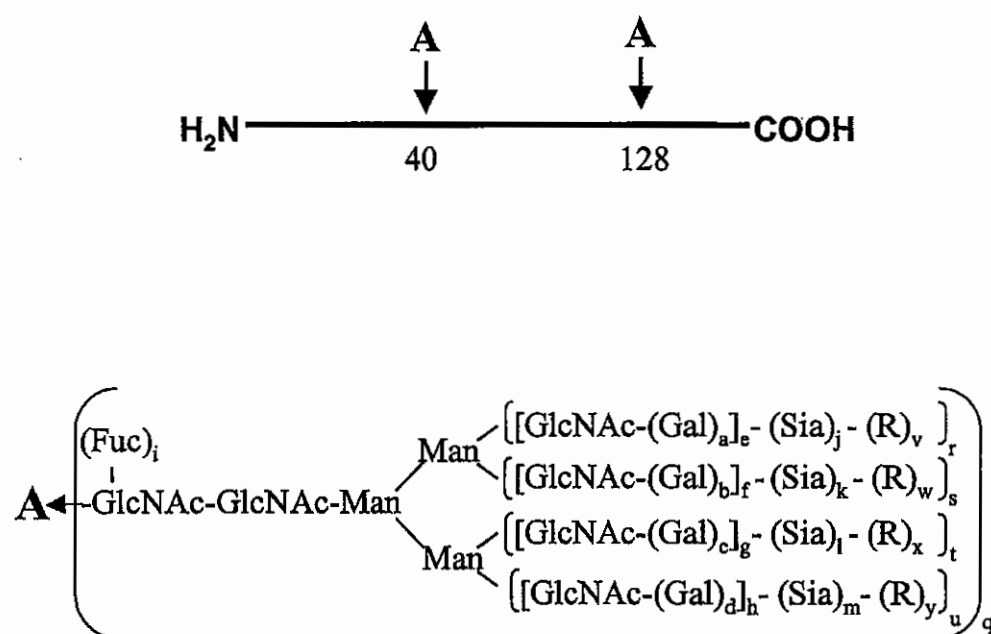
a-d, i, q-u (independently selected) = 0 or 1;

e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 41M



a-d, i, q-u (independently selected) = 0 or 1.
e-h (independently selected) = 0 to 6.
j-m (independently selected) = 0 to 100.
v-y = 0; R = polymer, glycoconjugate.

FIG. 42A

183/345

CHO, BHK, 293 cells, Vero expressed DNase I.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (16 mol eq),
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1;
 v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 42B

CHO, BHK, 293 cells, Vero expressed DNase I.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.

- ↓
1. Sialidase
 2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
 3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 0 or 1;
 R = PEG.

FIG. 42C

184/345

NSO expressed DNase I.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0;
 Sia (independently selected) = Sia or Gal.

- ↓
 1. Sialidase and α -galactosidase
 2. α -Galactosyltransferase, UDP-Gal
 ▼ 3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = PEG.

FIG. 42D

CHO, BHK, 293 cells, Vero expressed DNase I.
 a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y = 0.

- ↓
 1. Sialidase
 2. CMP-SA-PEG (16 mol eq), ST3Gal3
 ▼ 3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;
 e-h = 1; v-y (independently selected) = 0 or 1;
 R = PEG.

FIG. 42E

185/345

CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,
buffer, salt
 2. H₄N₂-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y (independently selected) = 0 or 1;
R = PEG.

FIG. 42F

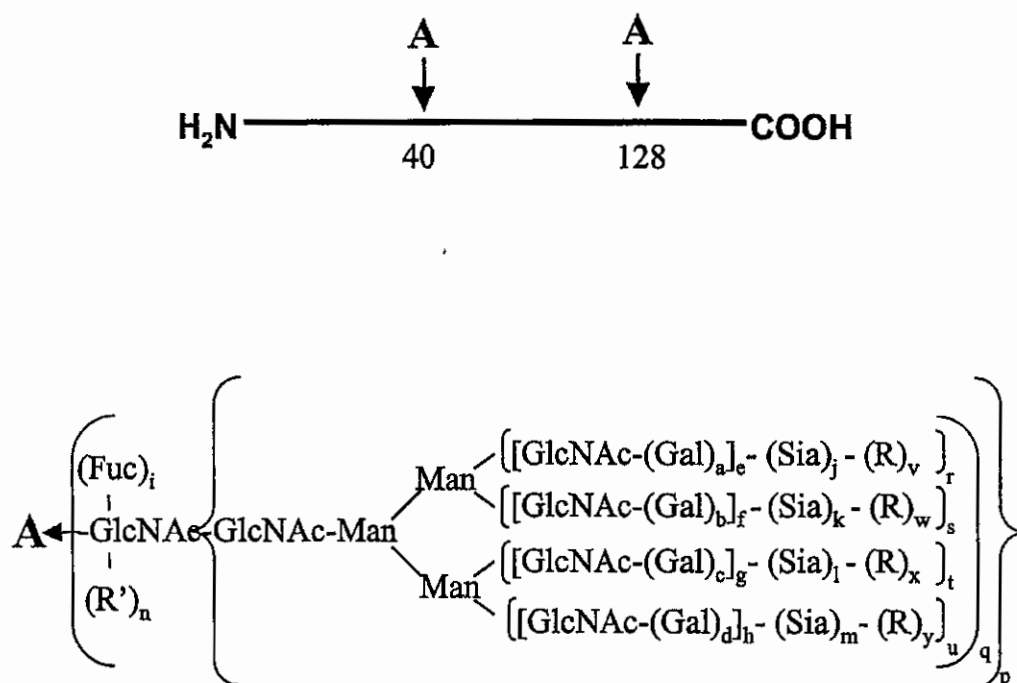
CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; v-y = 0.

- ↓
1. CMP-SA, α 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;
e-h = 1;
j-m (independently selected) = 0-20;
v-y (independently selected) = 0.

FIG. 42G

186/345



a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 42H

187/345

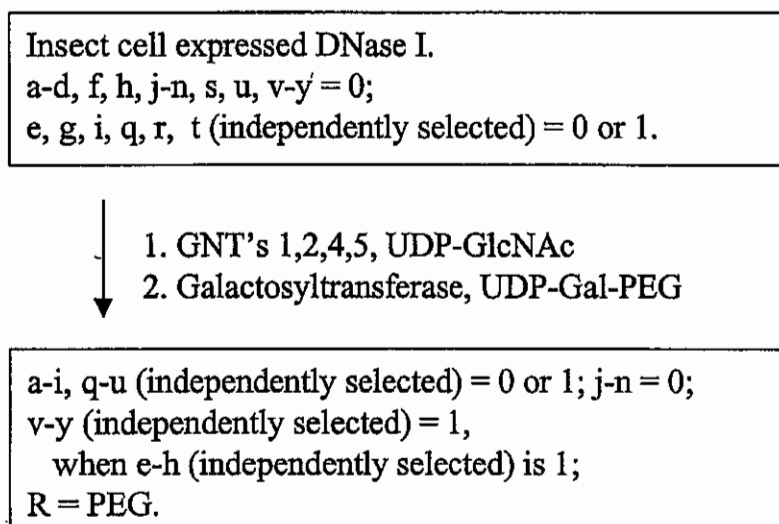


FIG. 42I

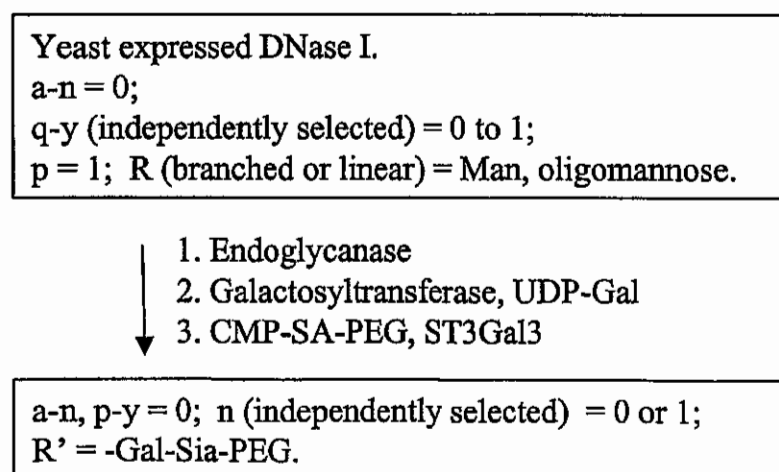


FIG. 42J

188/345

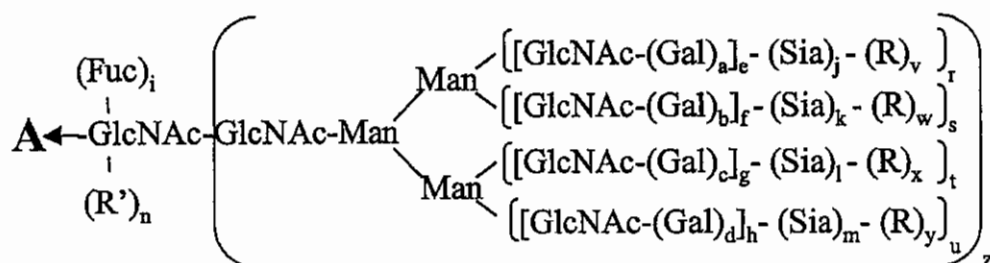
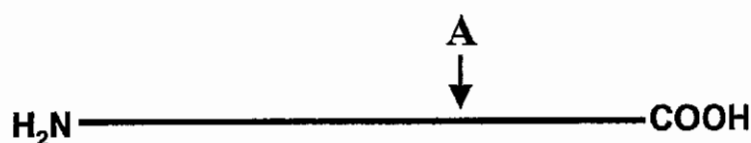
CHO, BHK, 293 cells, Vero expressed DNase I.
a-d, i-m, q-u (independently selected) = 0 or 1;
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
 2. ST3Gal1, desialylated alpha-1-Proteinase inhibitor.
 3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;
p = 1; n = 0;
v-y (independently selected) = 0 or 1;
R = linker- alpha-1-Proteinase inhibitor.

FIG. 42K

189/345



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,

glycoconjugate.

FIG. 43A

190/345

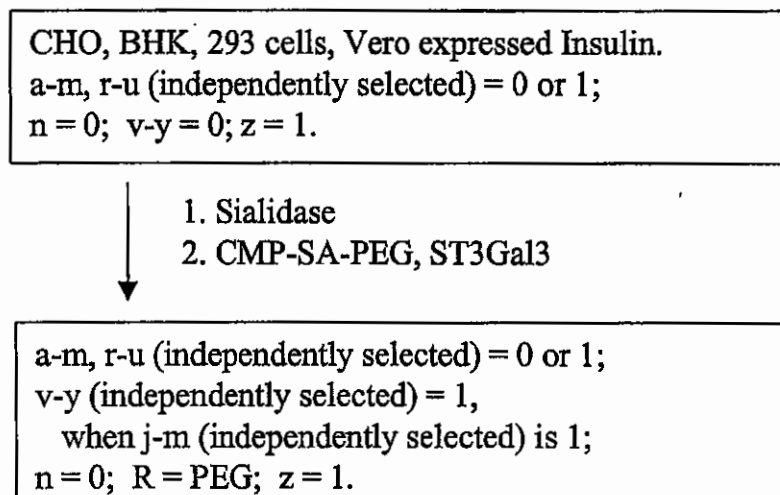


FIG. 43B

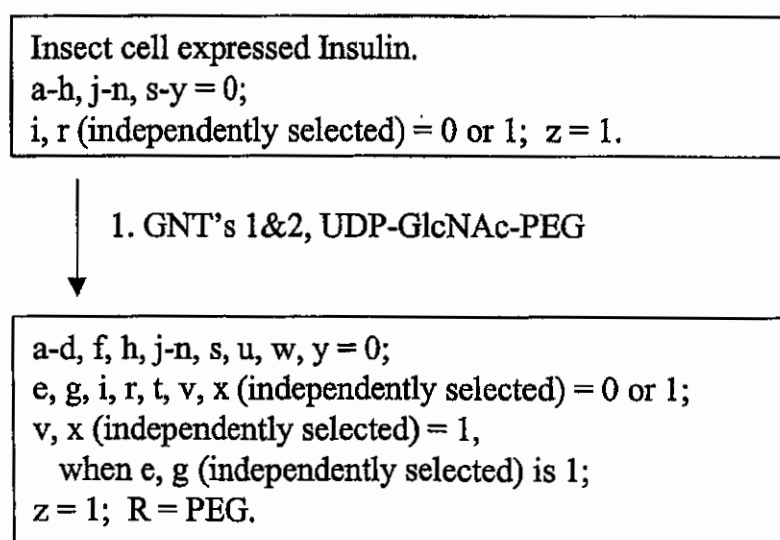


FIG. 43C

191/345

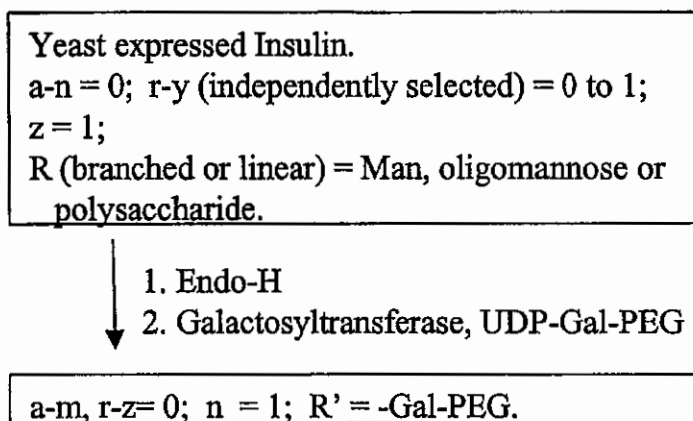
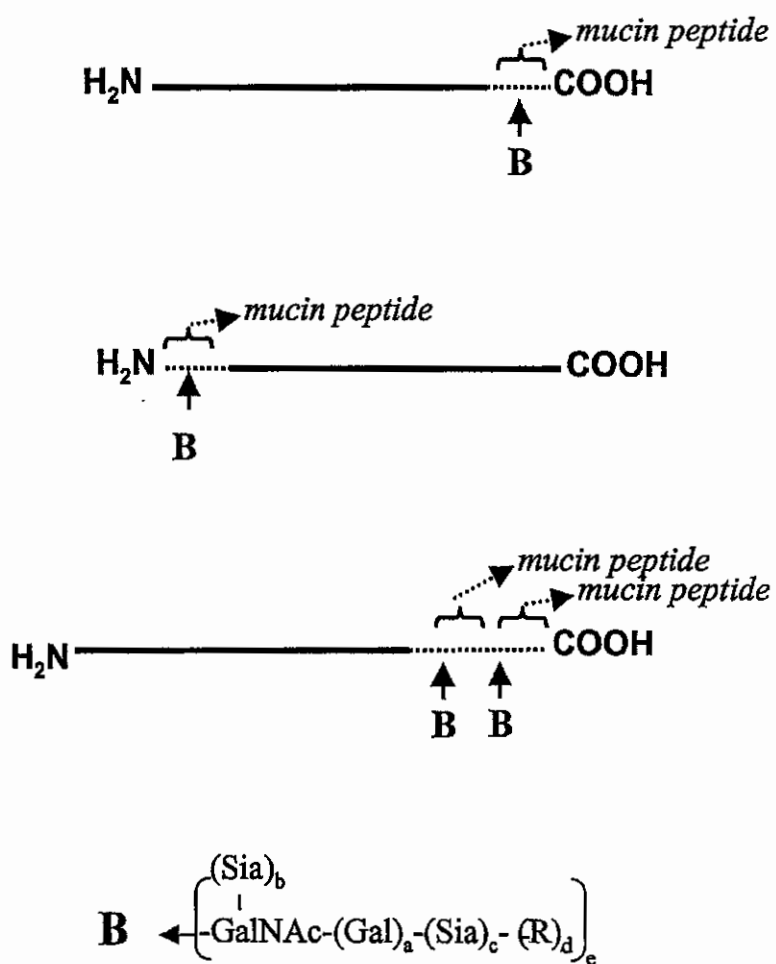


FIG. 43D

192/345



a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 43E

193/345

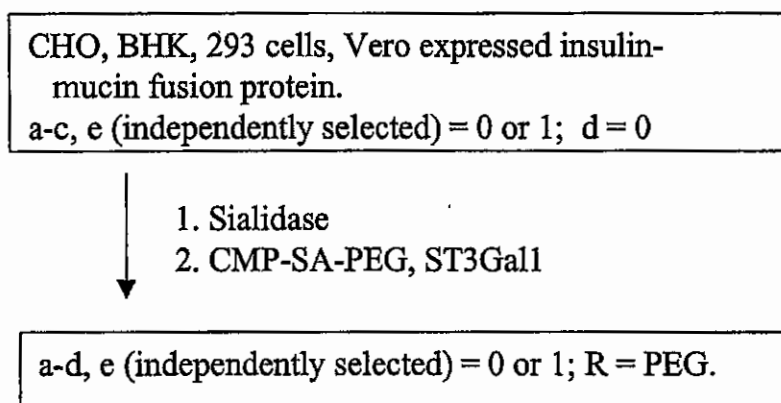


FIG. 43F

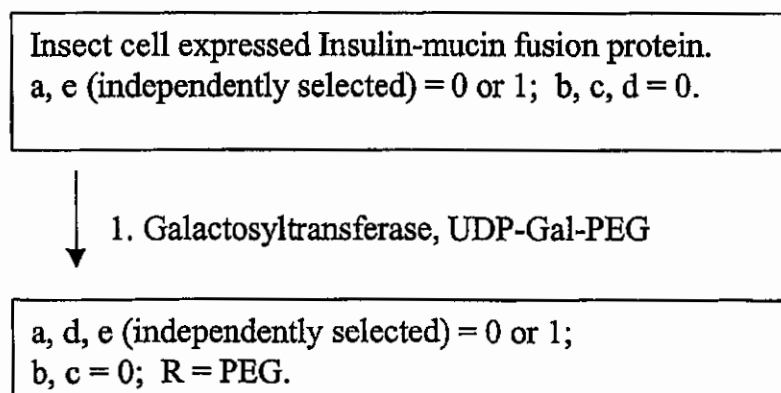


FIG. 43G

194/345

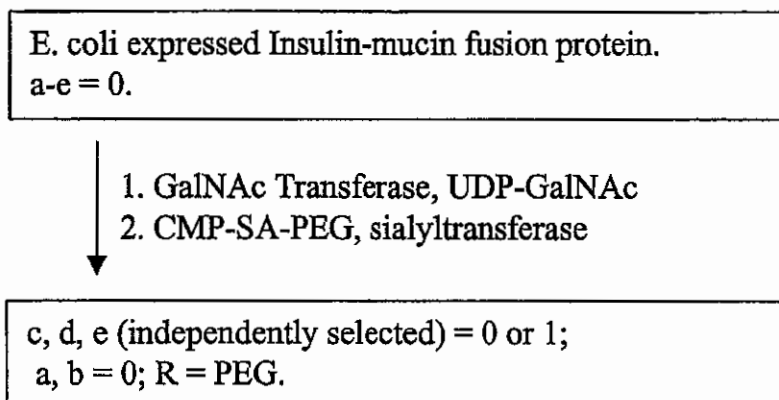
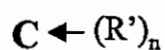
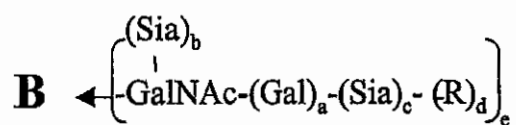
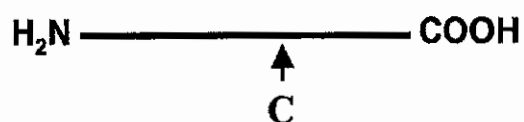
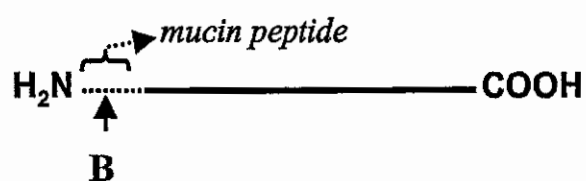
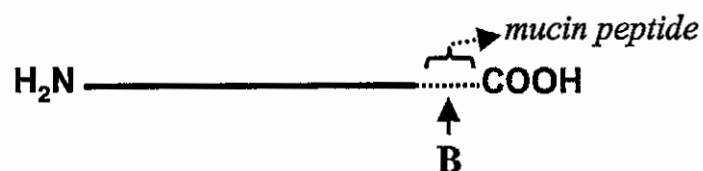


FIG. 43H

195/345



a-c, e (independently selected) = 0 or 1;
 d = 0; R = modifying group, mannose,
 oligo-mannose.

FIG. 43I

196/345

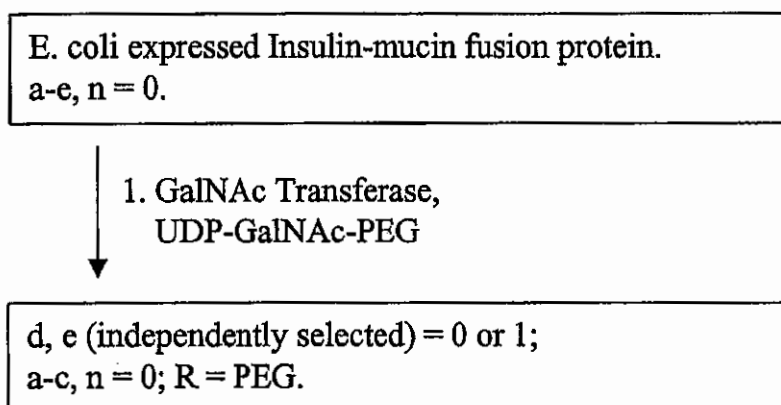


FIG. 43J

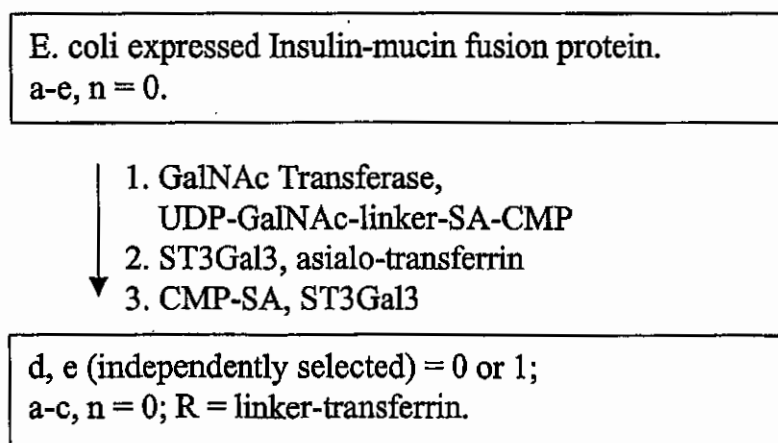


FIG. 43K

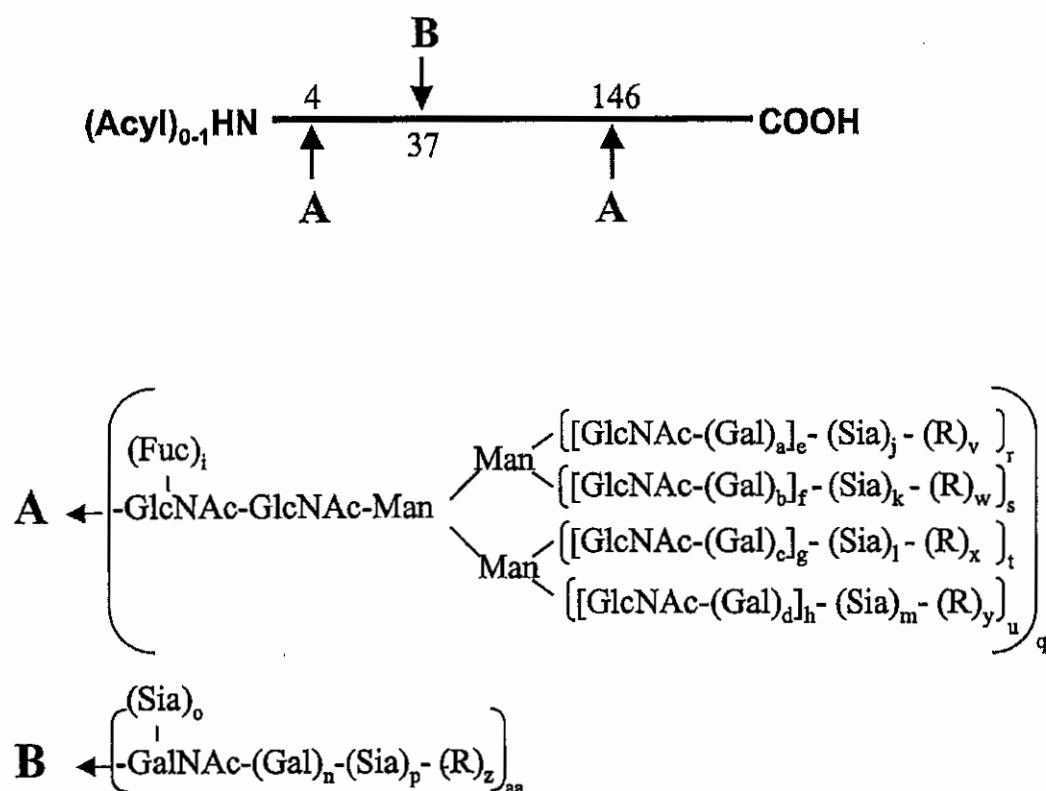
197/345

E. coli expressed Insulin (N)—no mucin peptide.
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
 2. ST3Gal3, asialo-transferrin
 3. CMP-SA, ST3Gal3

a-e = 0; n = 1;
R' = linker-transferrin.

FIG. 43L



a-d, i, n-u, aa (independently selected) = 0 or 1.
e-h (independently selected) = 0 to 6.
j-m (independently selected) = 0 to 100.
v-y = 0; R = polymer, glycoconjugate.

FIG. 44A

199/345

CHO, BHK, 293 cells, Vero expressed M-antigen.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
 2. CMP-SA-linker-lipid-A,
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;
 o, p, z = 0; n, e-h = 1;
 v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 R = linker-lipid-A.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed M-antigen.
 a-d, i-m, o-u, aa (independently selected) = 0 or 1;
 n, e-h = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-linker-tetanus toxin, ST3Gal1
 3. CMP-SA, ST3Gal3

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;
 o, v-y = 0; n, e-h = 1; R = tetanus toxin.

FIG. 44C

200/345

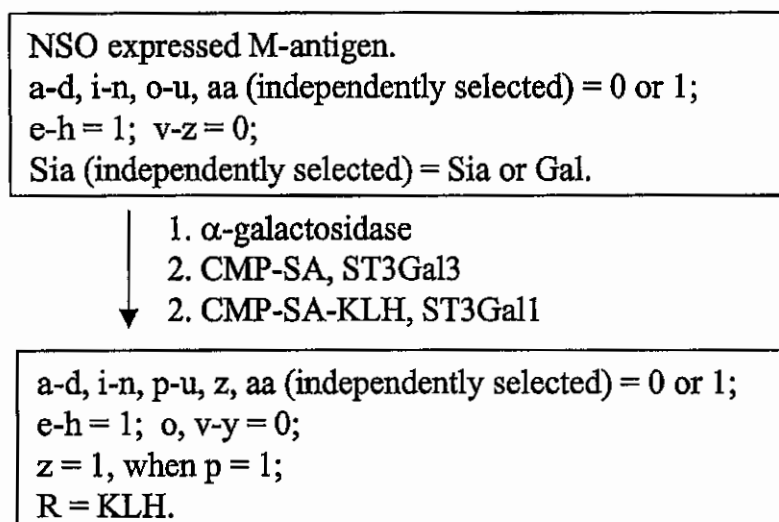


FIG. 44D

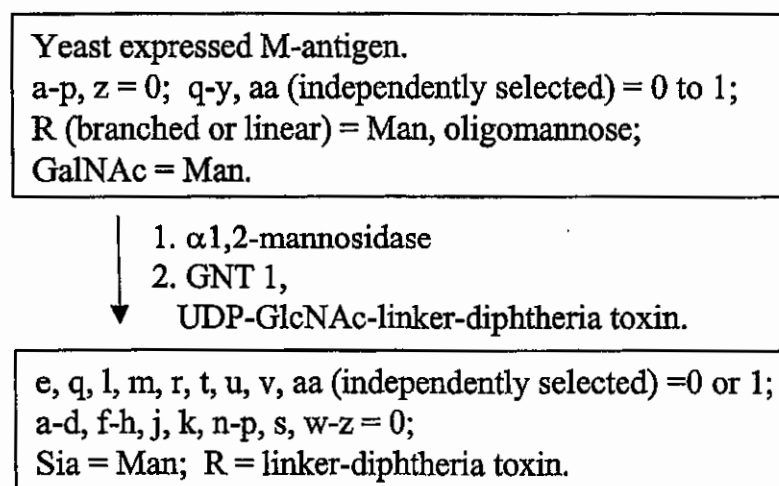


FIG. 44E

201/345

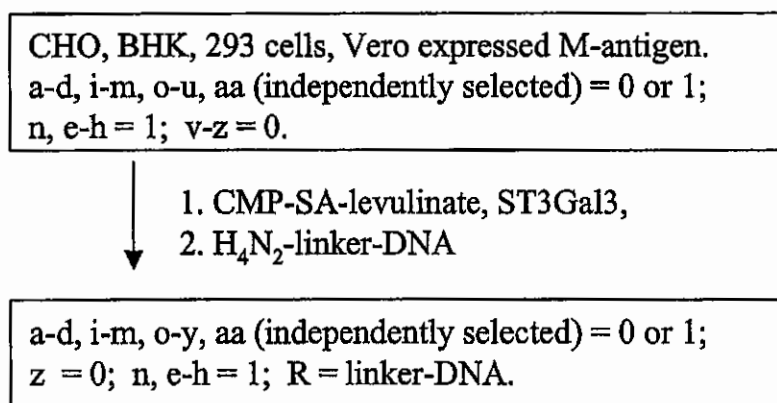


FIG. 44F

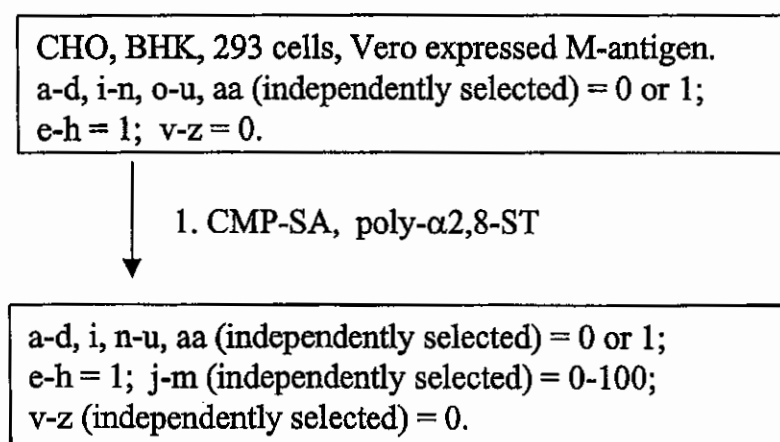
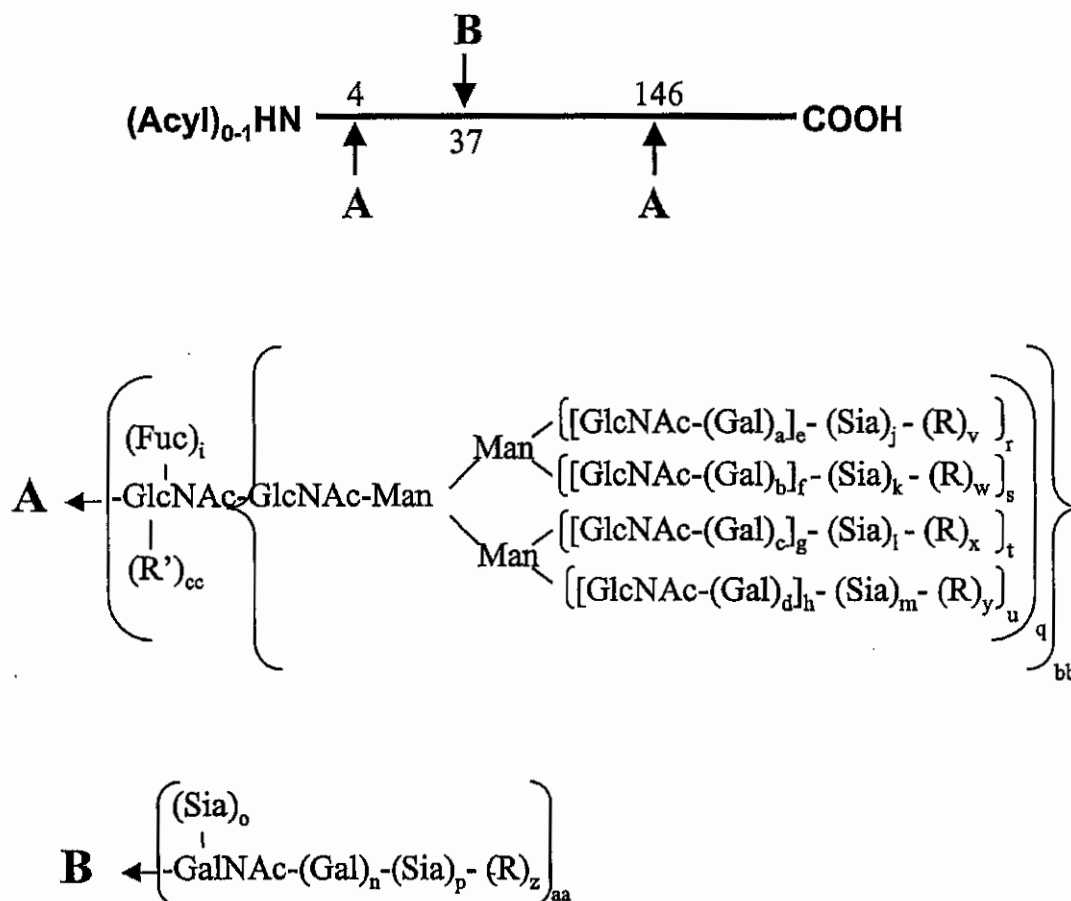


FIG. 44G

202/345



a-d, i, n, q-u, aa, bb, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-p (independently selected) = 0 to 100.

Cc, v-y = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 44H

203/345

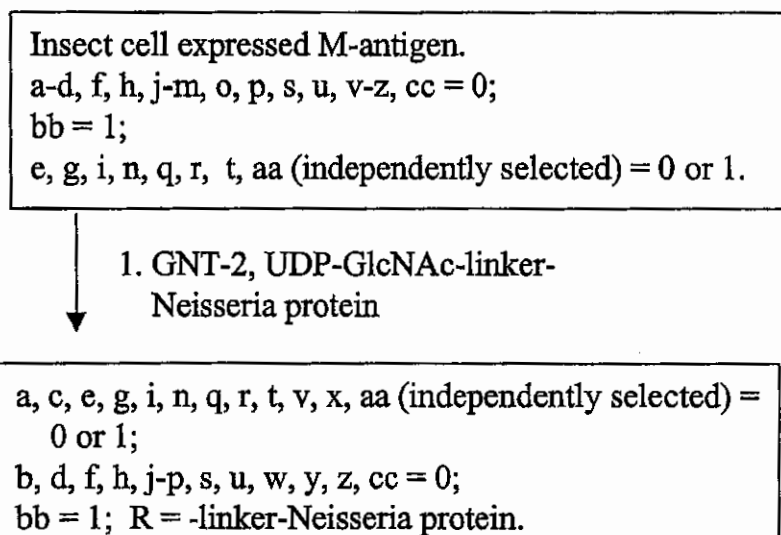


FIG. 44I

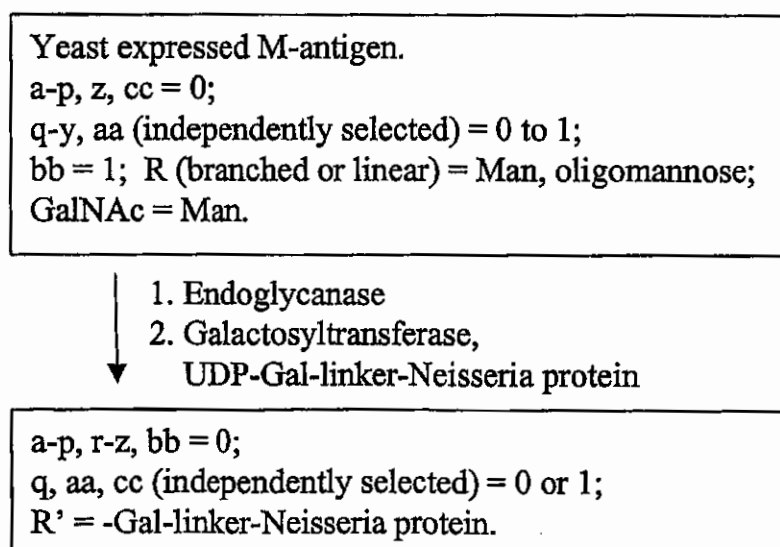


FIG. 44J

204/345

Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

1. mannosidases

2. GNT 1 & 2, UDP-GlcNAc

3. UDP-Gal, Galactosyltransferase,

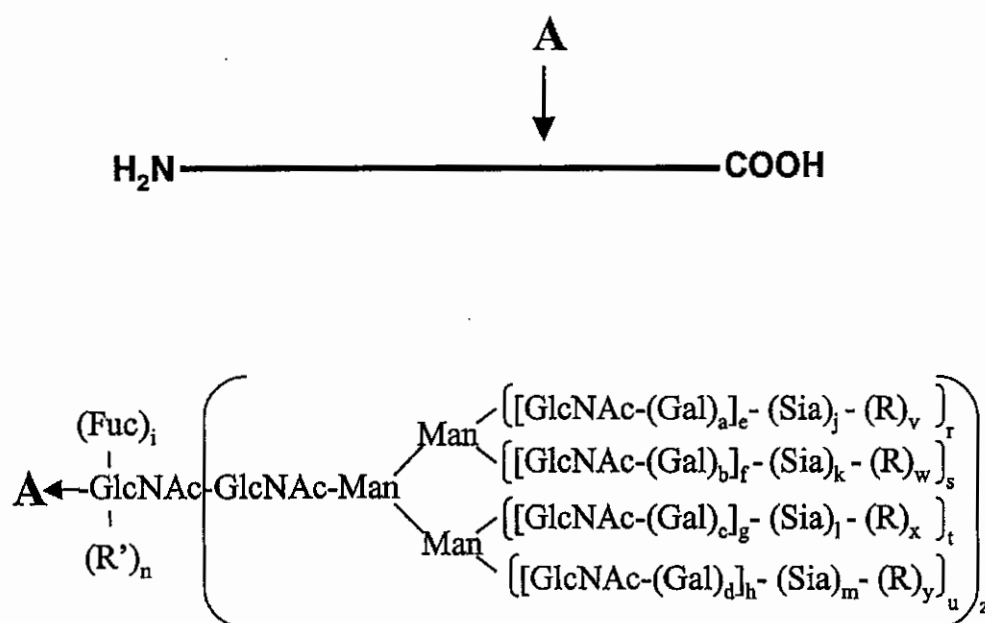
4. CMP-SA, sialyltransferase

a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;

b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 44K

205/345



a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,
glycoconjugate.

FIG. 45A

206/345

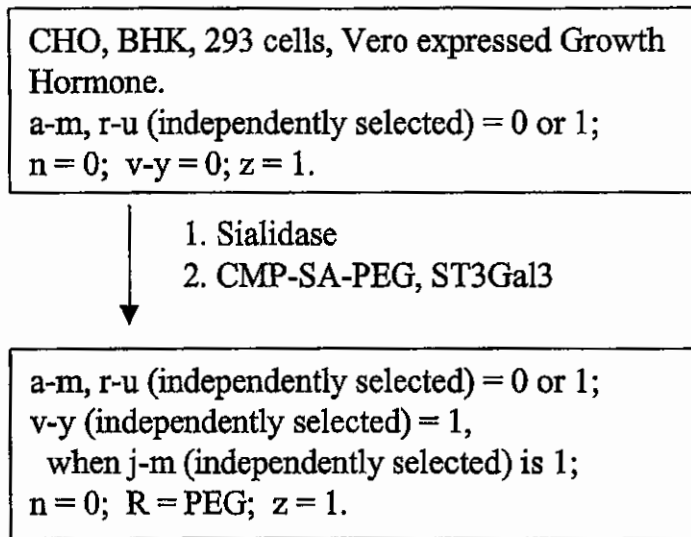


FIG. 45B

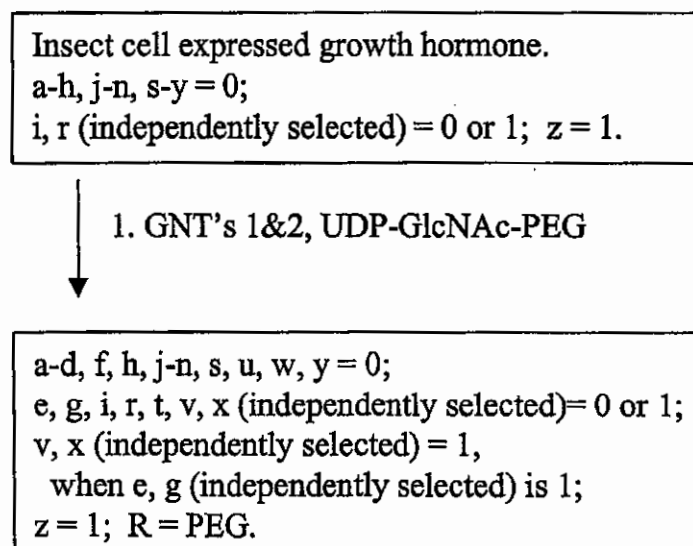


FIG. 45C

207/345

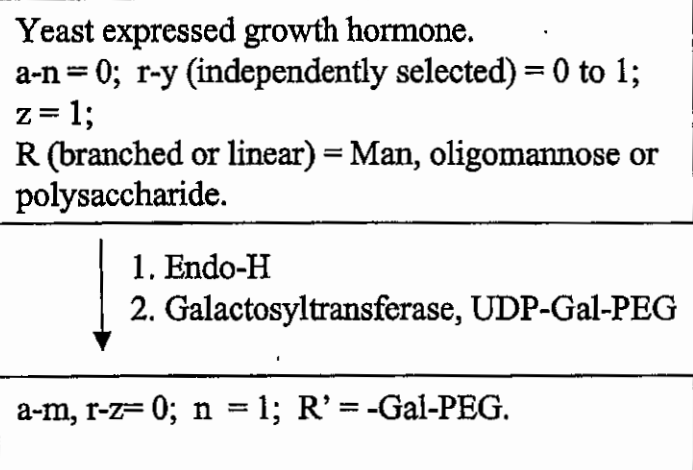
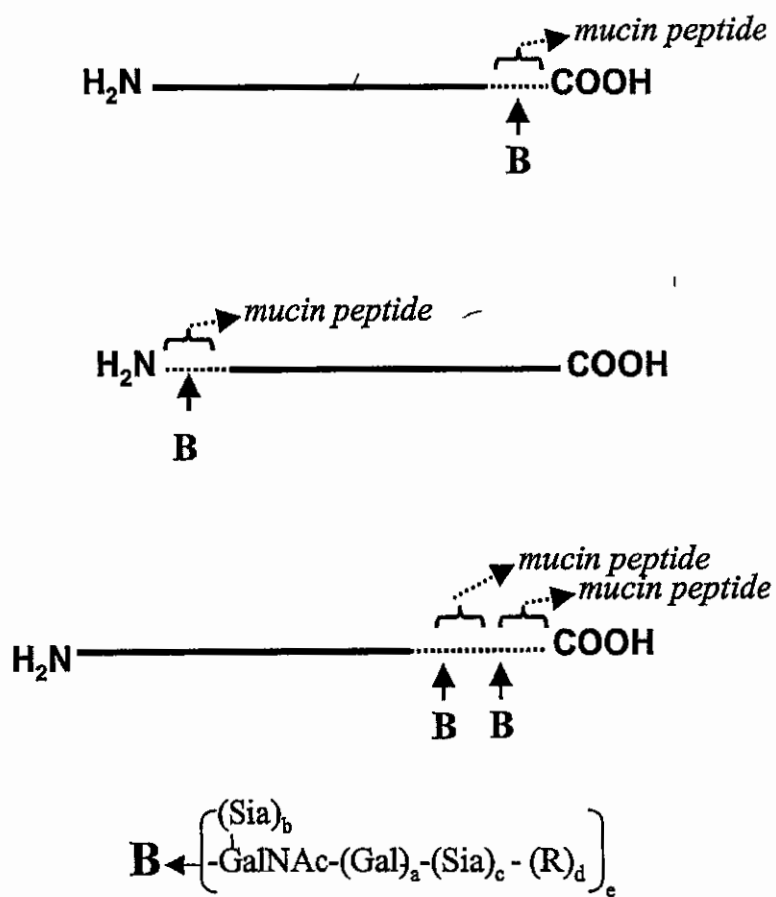


FIG. 45D

208/345



a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 45E

209/345

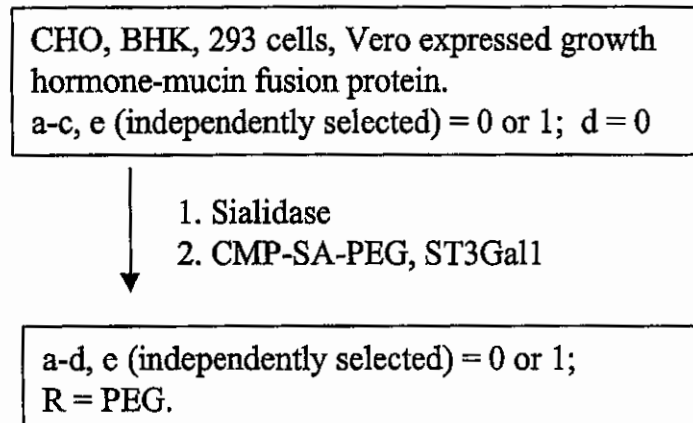


FIG. 45F

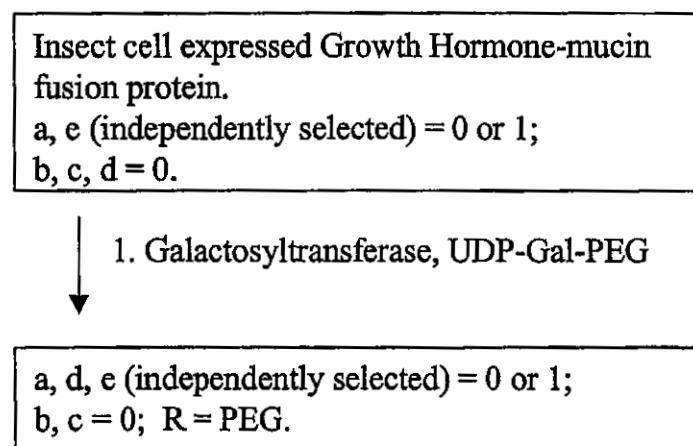


FIG. 45G

210/345

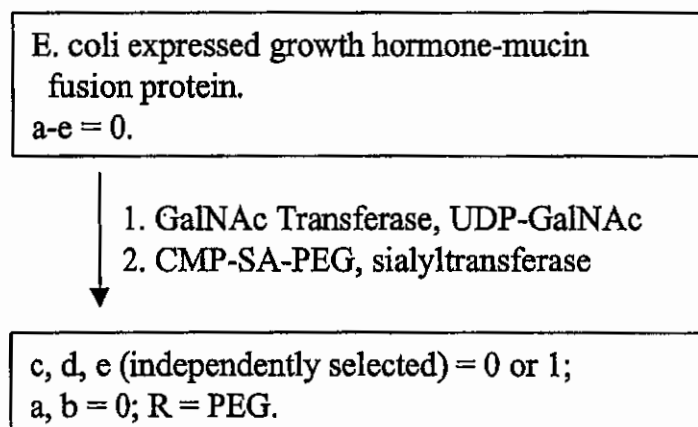


FIG. 45H

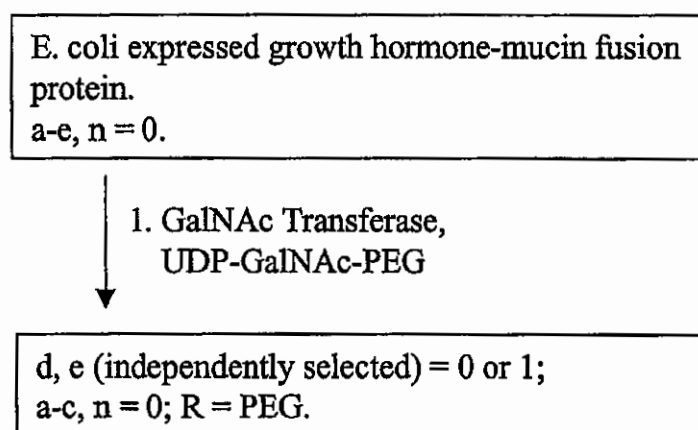


FIG. 45I

211/345

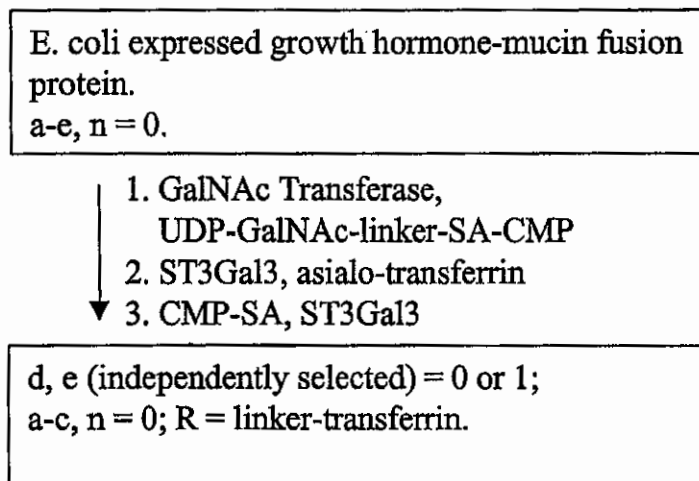


FIG. 45J

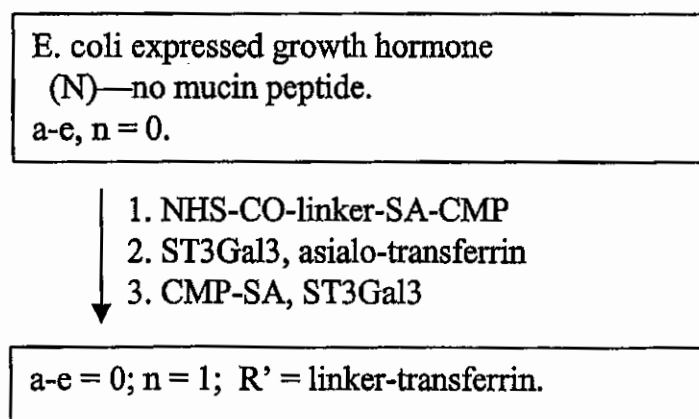
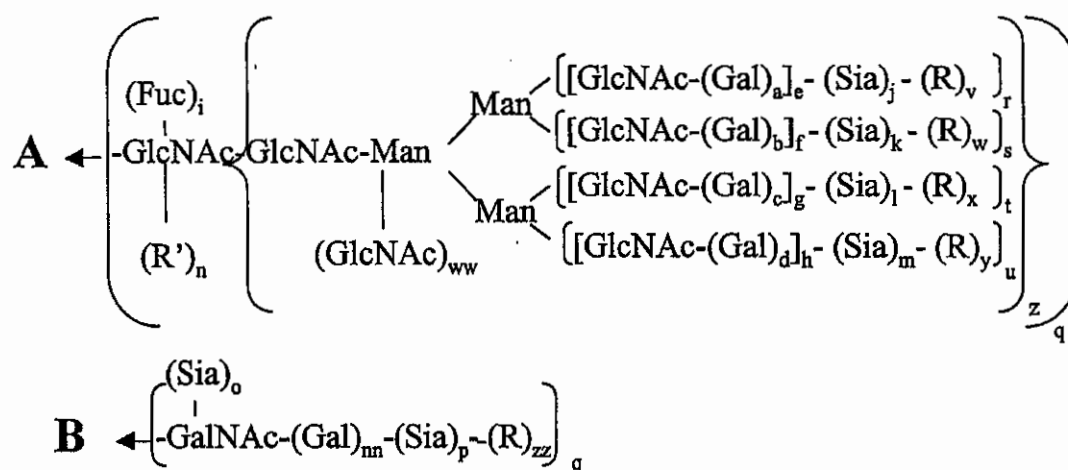
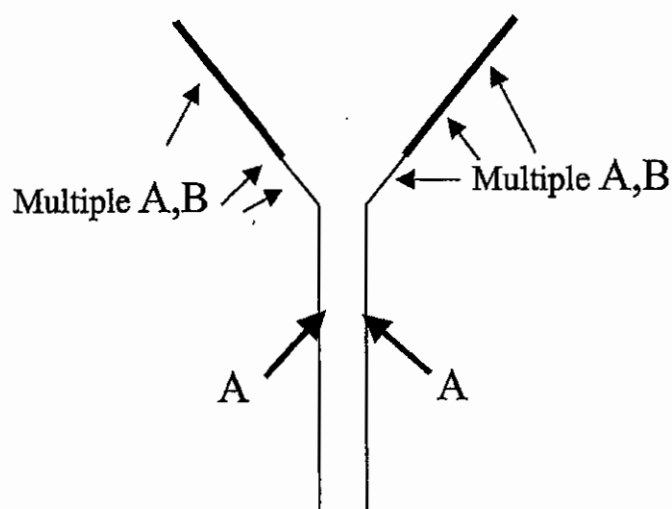


FIG. 45K

212/345



a-d, i-m, q-u, w, z, nn, ww, zz (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

n, v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 46A

213/345

CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. CMP-SA, ST3Gal1
 2. galactosyltransferase, UPD-Gal
 3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

FIG. 46B

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

- ↓
1. sialidase
 2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 46C

214/345

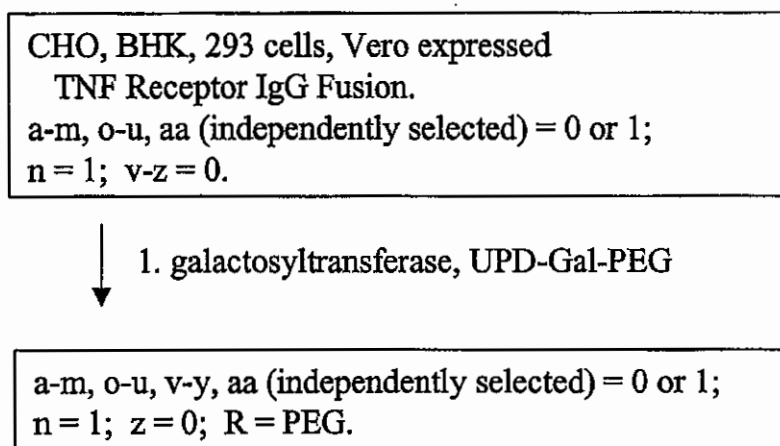


FIG. 46D

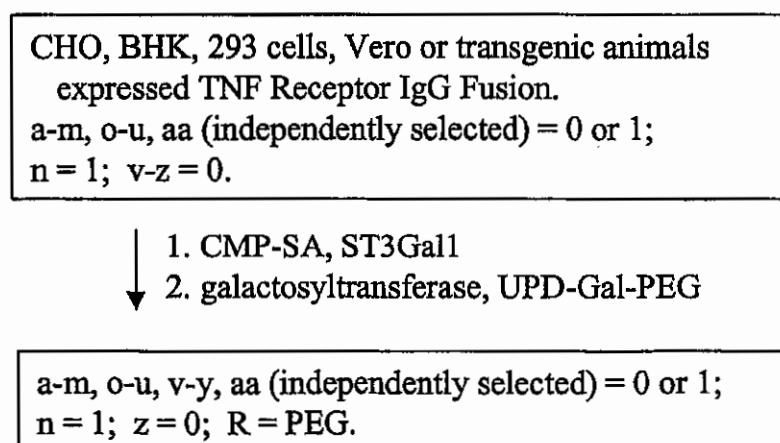


FIG. 46E

215/345

CHO, BHK, 293 cells, Vero or transgenic animals
expressed TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

↓
1. CMP-SA-levulinate, ST3Gal1
2. H₄N₂-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;
n = 1; z = 0; R = PEG.

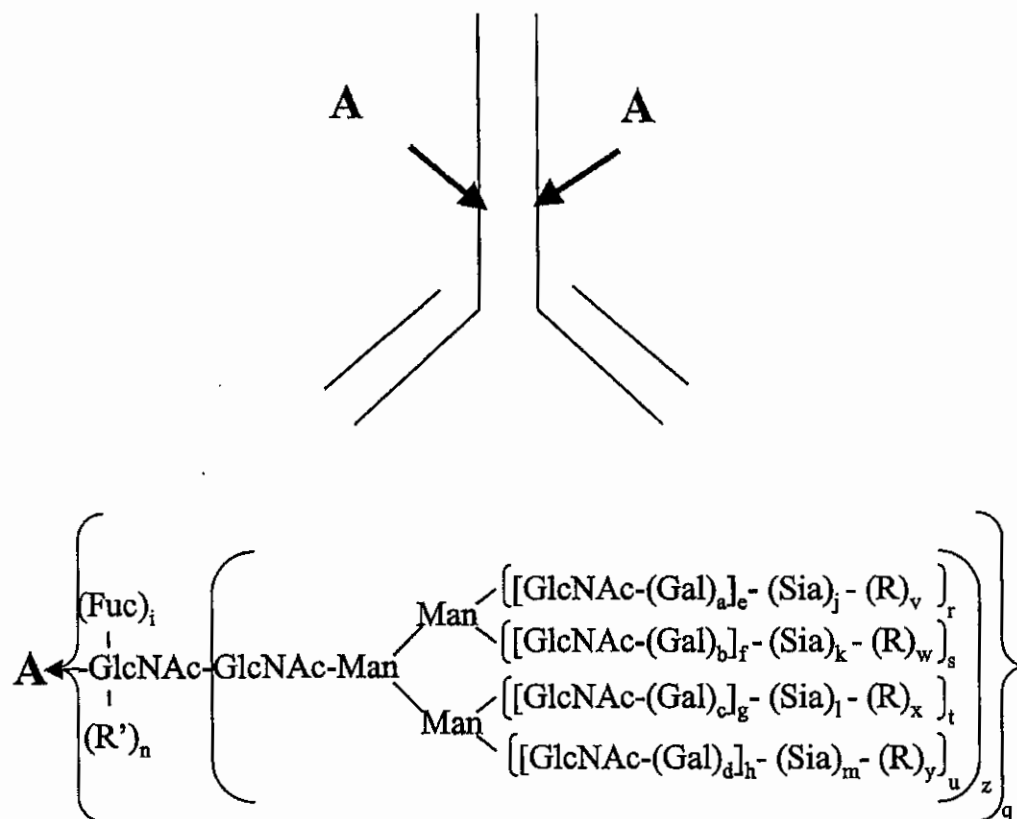
FIG. 46F

CHO, BHK, 293 cells, Vero expressed
TNF Receptor IgG Fusion.
a-m, o-u, aa (independently selected) = 0 or 1;
n = 1; v-z = 0.

↓
1. CMP-SA-PEG, α 2,8-ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;
n = 1; j-m, p (independently selected) = 0 to 2;
v-z (independently selected) = 1,
when j-m, p (independently selected) is 2;
R = PEG.

FIG. 46G



R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 47A

217/345

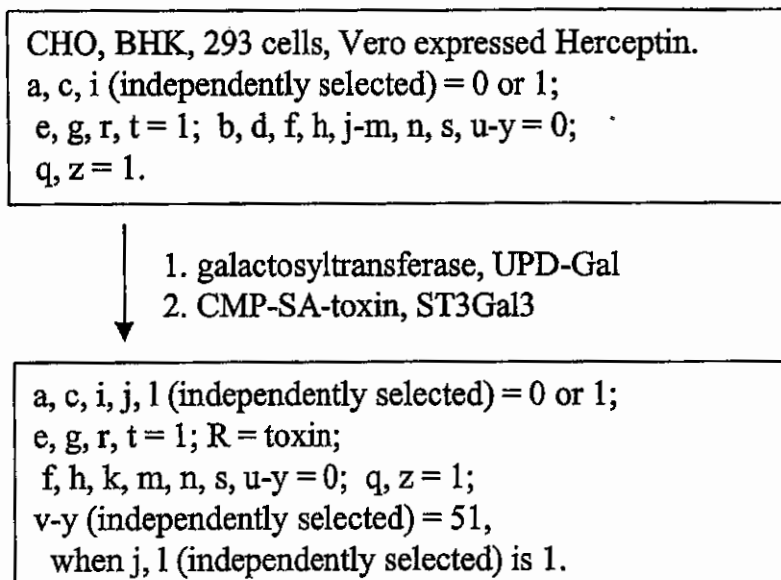


FIG. 47B

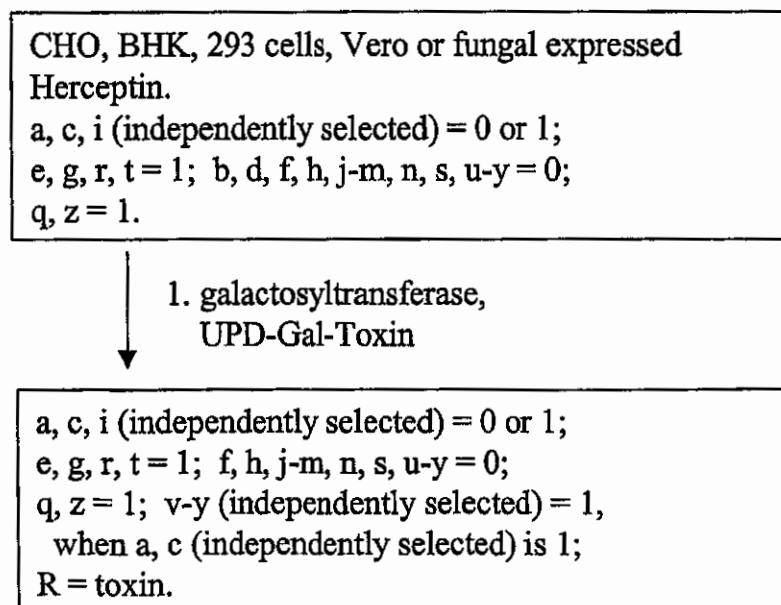


FIG. 47C

218/345

Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

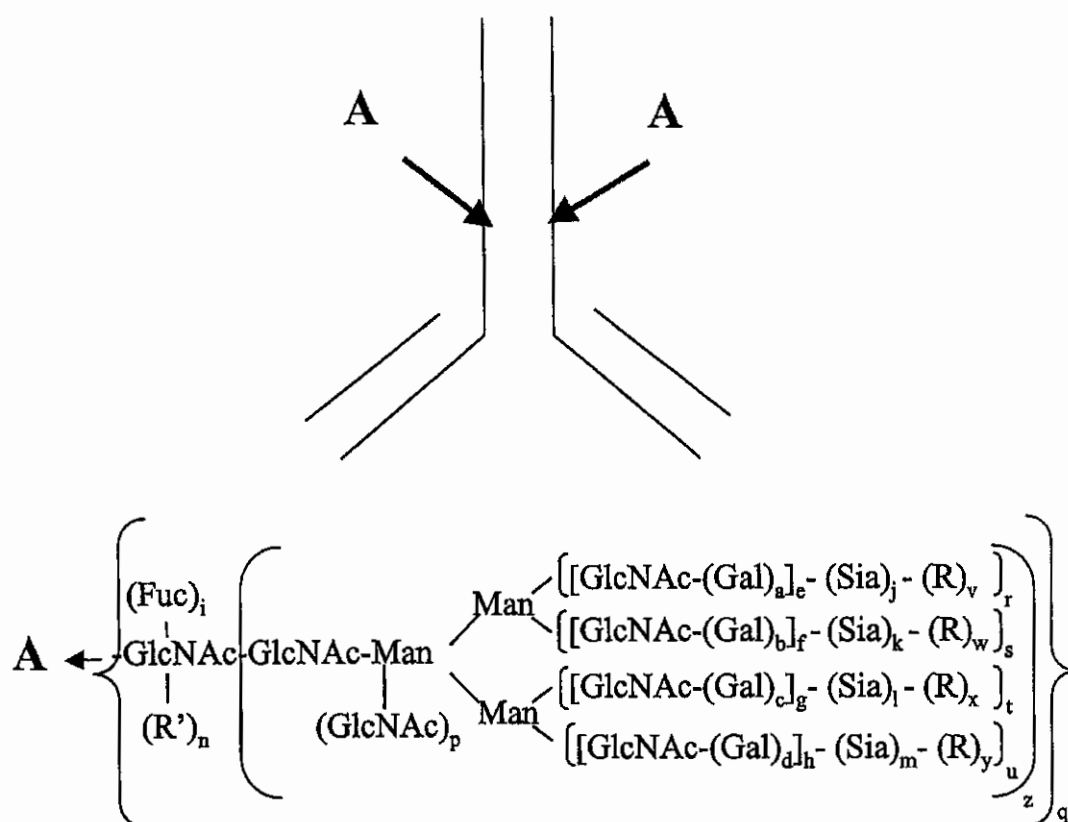
1. Endo-H
2. Galactosyltransferase, UDP-Gal
↓
3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 47D

219/345



a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 48A

220/345

CHO, BHK, 293 cells, Vero expressed Synagis.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1;
 b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.



1. galactosyltransferase, UPD-Gal
 2. CMP-SA-PEG, ST3Gal3

a, c, i, j, w, (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when j, l (independently selected) is 1;
 R = PEG.

FIG. 48B

CHO, BHK, 293 cells, Vero or fungal expressed
 Synagis.
 a, c, i (independently selected) = 0 or 1;
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;
 q, z = 1.



1. galactosyltransferase,
 UPD-Gal-PEG

a, c, i, w (independently selected) = 0 or 1;
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;
 q, z = 1; v-y (independently selected) = 1,
 when a, c (independently selected) is 1;
 R = PEG.

FIG. 48C

221/345

Fungi expressed Synagis.

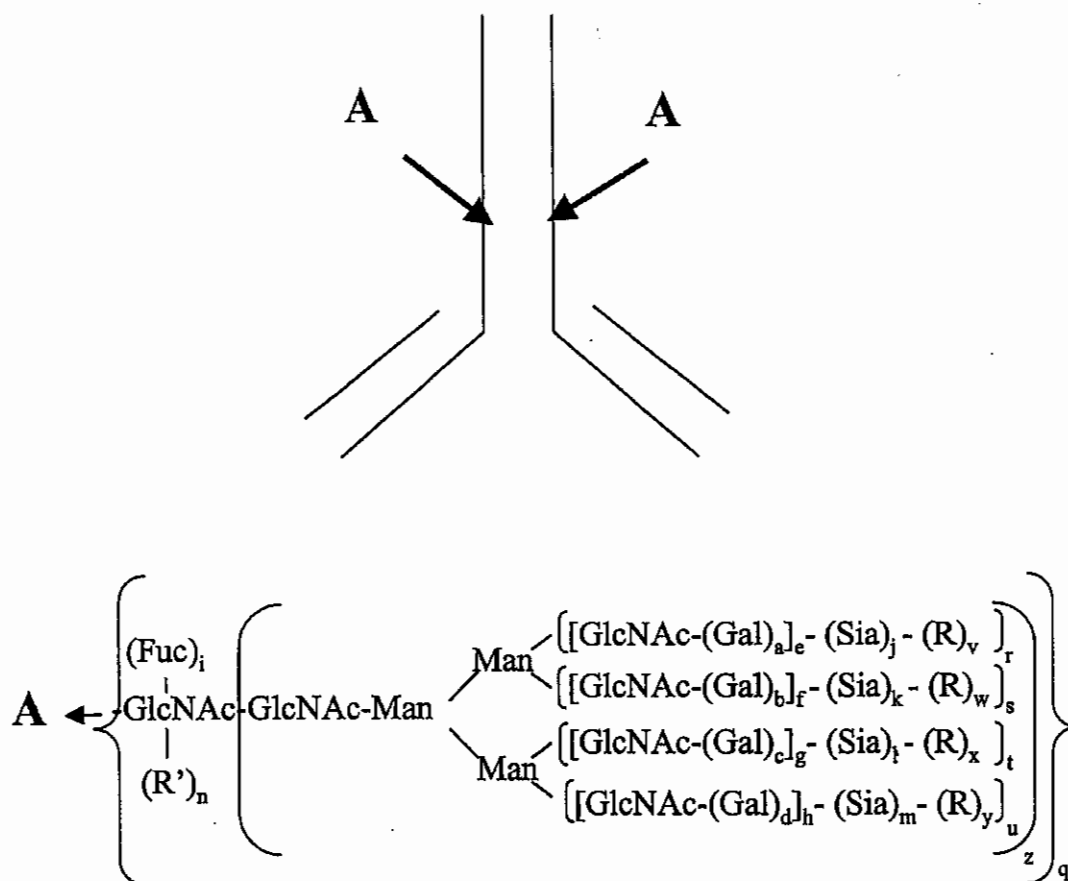
e, g, i, r, t (independently selected) = 0 or 1;
a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
2. Galactosyltransferase, UDP-Gal
3.. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 48D

222/345



a-d, i, q-u, w (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 49A

223/345

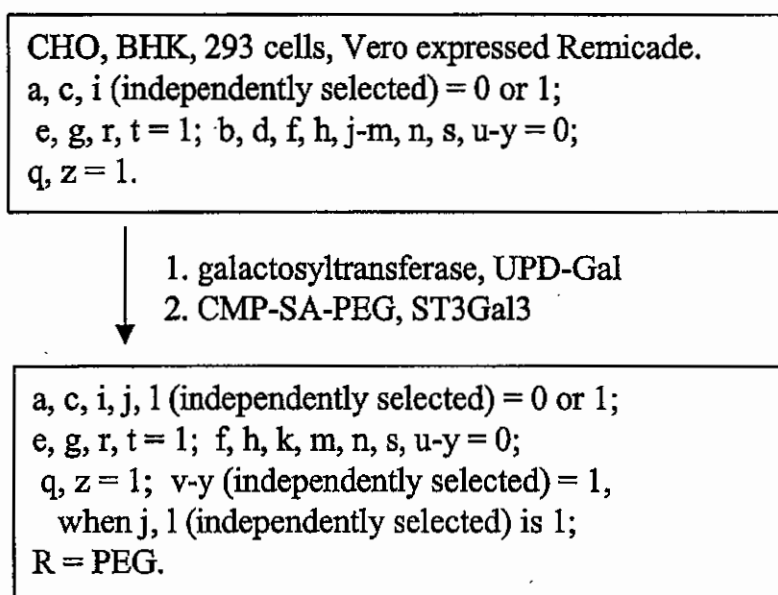


FIG. 49B

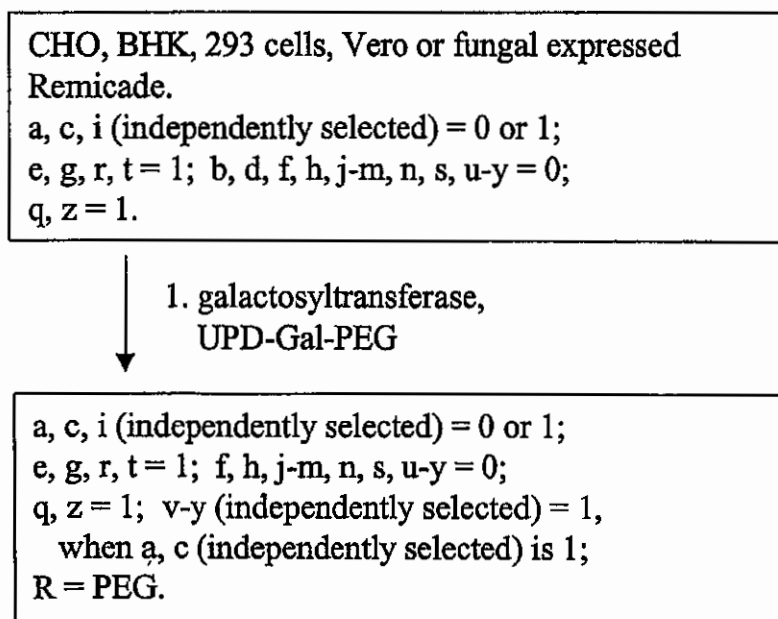


FIG. 49C

224/345

Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

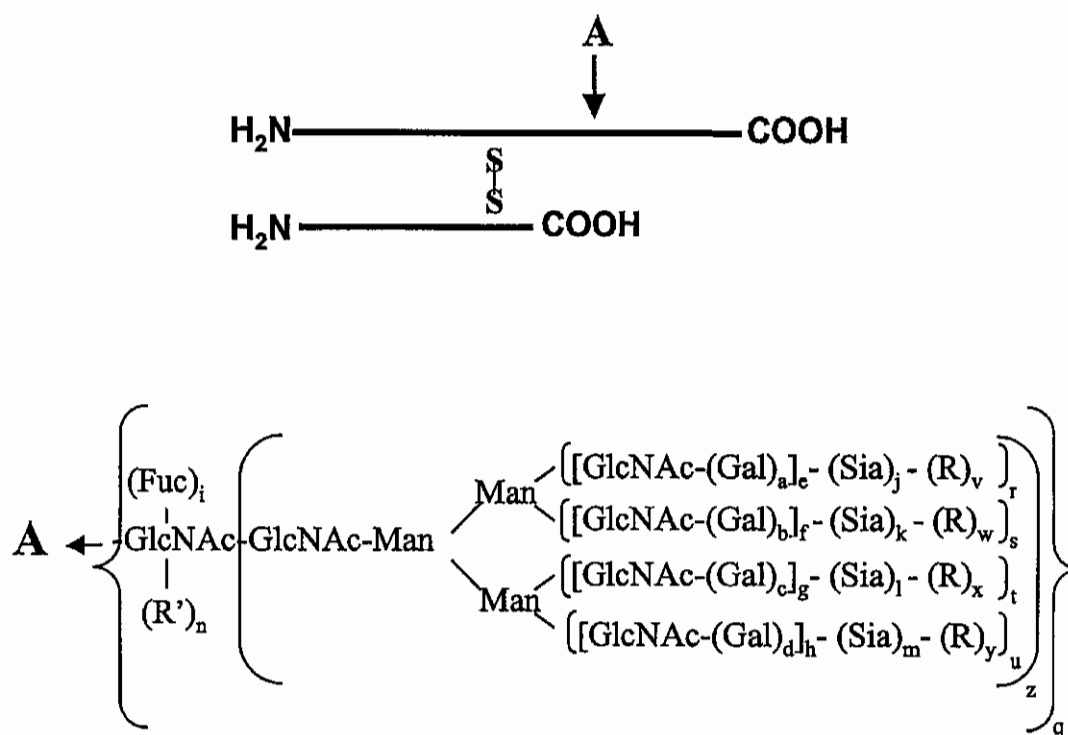
- ↓
1. Endo-H
 2. Galactosyltransferase, UDP-Gal
 - 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z= 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D

225/345



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 50A

226/345

CHO, BHK, 293 cells, Vero expressed Reopro.
 a-m, r-u (independently selected) = 0 or 1;
 n = 0; v-y = 0; z = 1.



1. Sialidase
2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;
 v-y (independently selected) = 1,
 when j-m (independently selected) is 1;
 n = 0; R = PEG; z = 1.

FIG. 50B

Insect cell expressed Reopro.
 a-h, j-n, s-y = 0; i, r (independently selected) = 0 or 1;
 z = 1.



1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;
 e, g, i, r, t, v, x (independently selected) = 0 or 1;
 v, x (independently selected) = 1,
 when e, g (independently selected) is 1;
 z = 1; R = PEG.

FIG. 50C

227/345

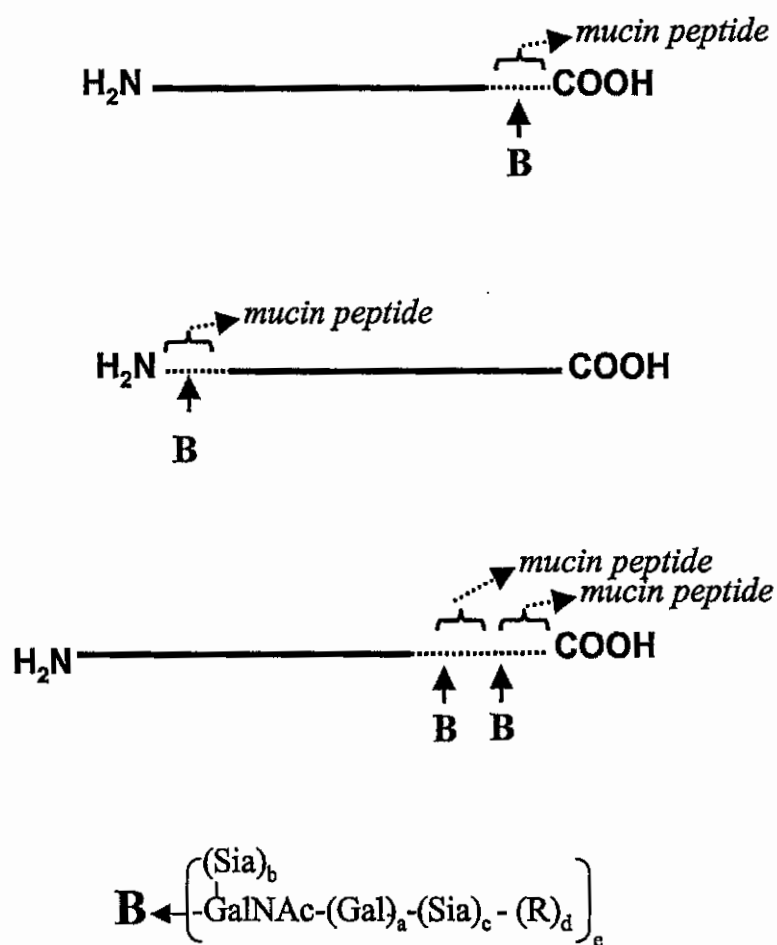
Yeast expressed Reopro.
a-n = 0; r-y (independently selected) = 0 to 1;
z = 1;
R (branched or linear) = Man, oligomannose or
polysaccharide.

1. Endo-H
2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z= 0; n = 1; R' = -Gal-PEG.

FIG. 50D

228/345



a-c, e (independently selected) = 0 or 1;
 d = 0; R = polymer

FIG. 50E

229/345

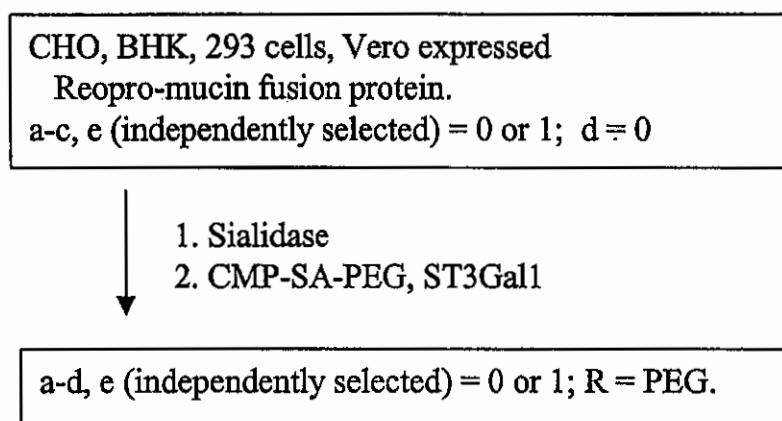


FIG. 50F

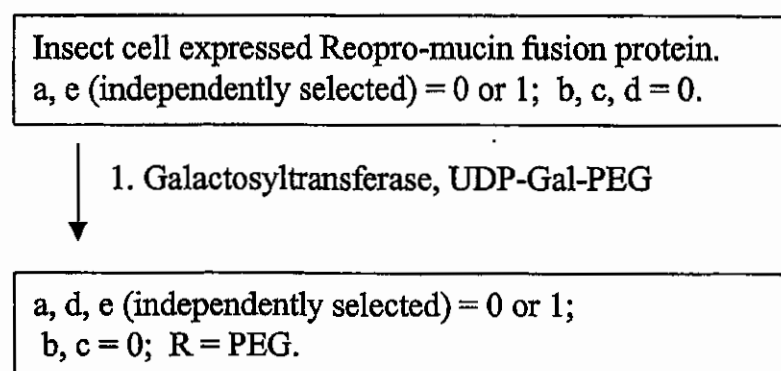


FIG. 50G

230/345

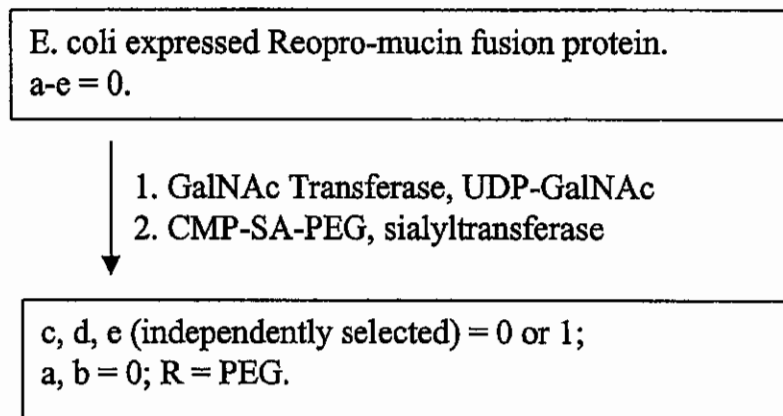
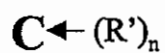
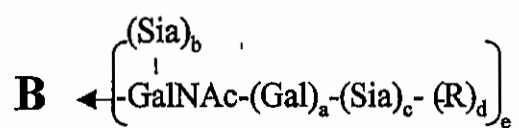
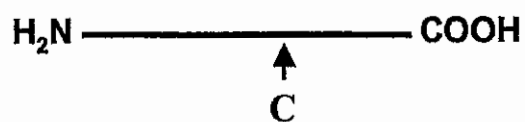
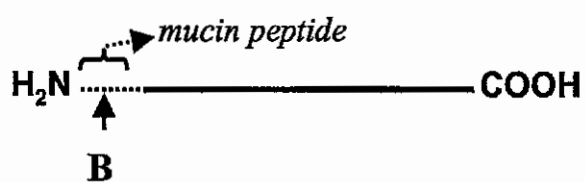
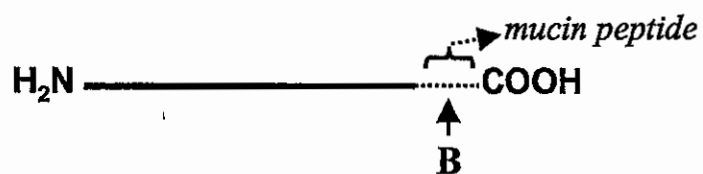


FIG. 50H

231/345



a-c, e (independently selected) = 0 or 1;
d = 0; R = polymer, linker.

FIG. 50I

232/345

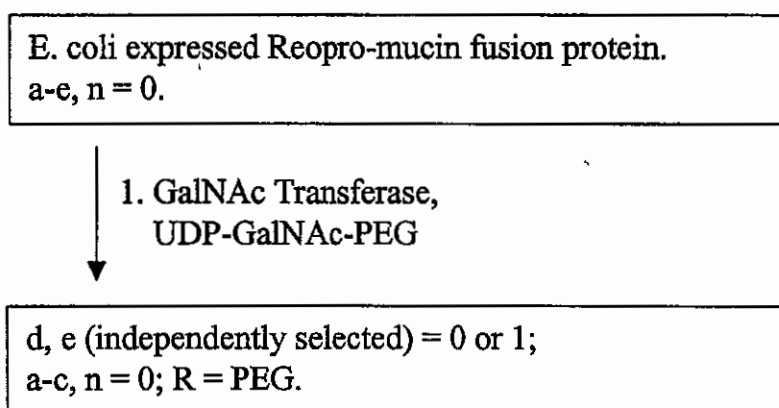


FIG. 50J

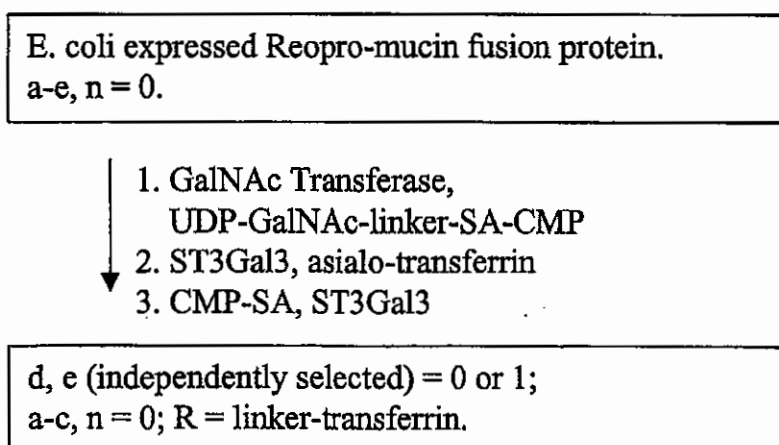


FIG. 50K

233/345

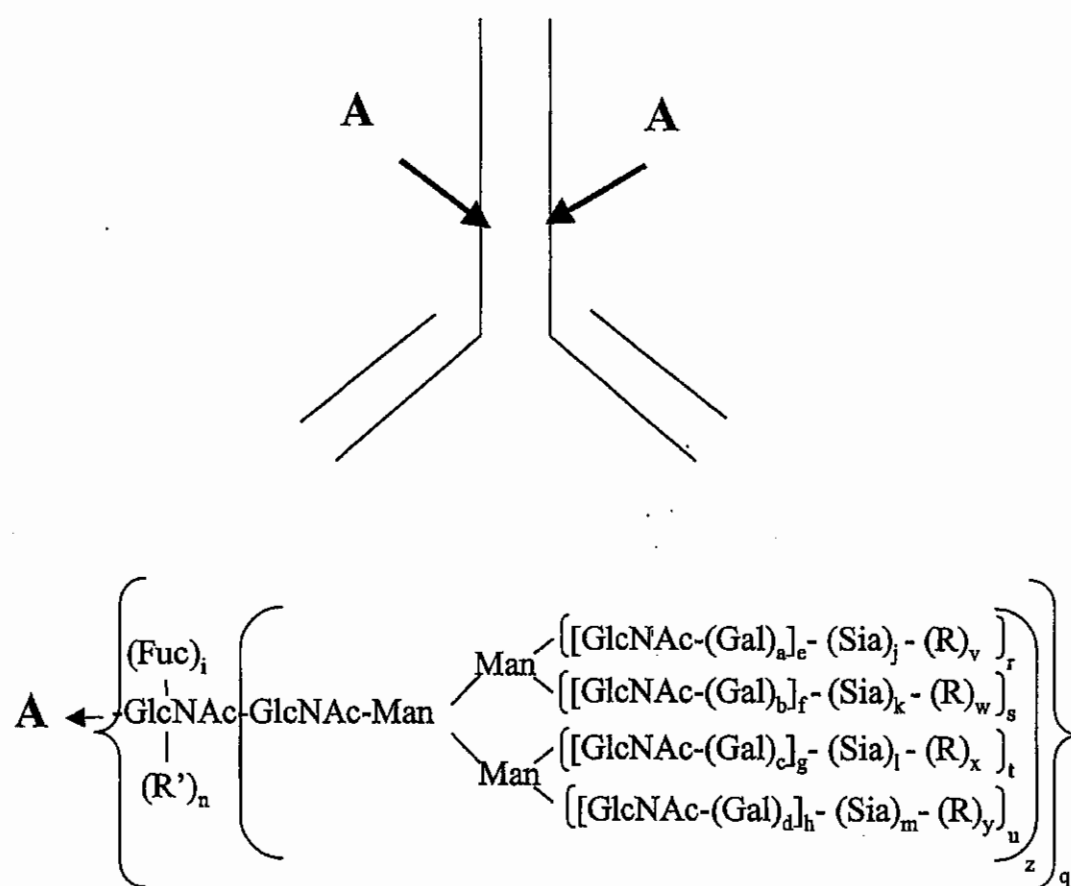
E. coli expressed Reopro(N)—no mucin peptide.
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
 2. ST3Gal3, asialo-transferrin
 3. CMP-SA, ST3Gal3

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 50L

234/345



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

z

FIG. 51A

235/345

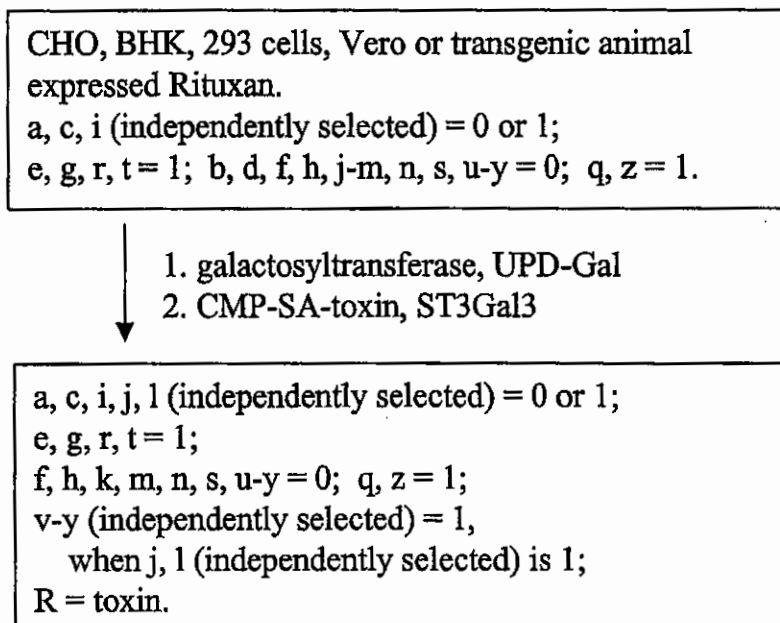


FIG. 51B

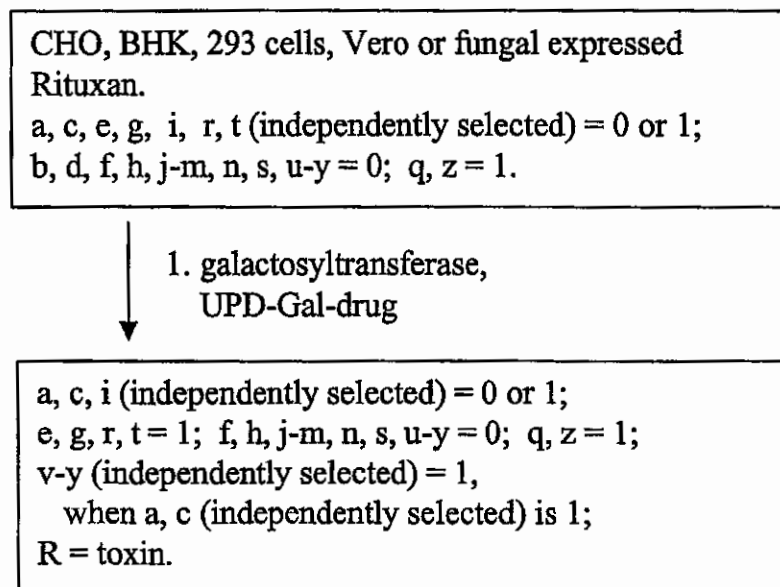


FIG. 51C

236/345

Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

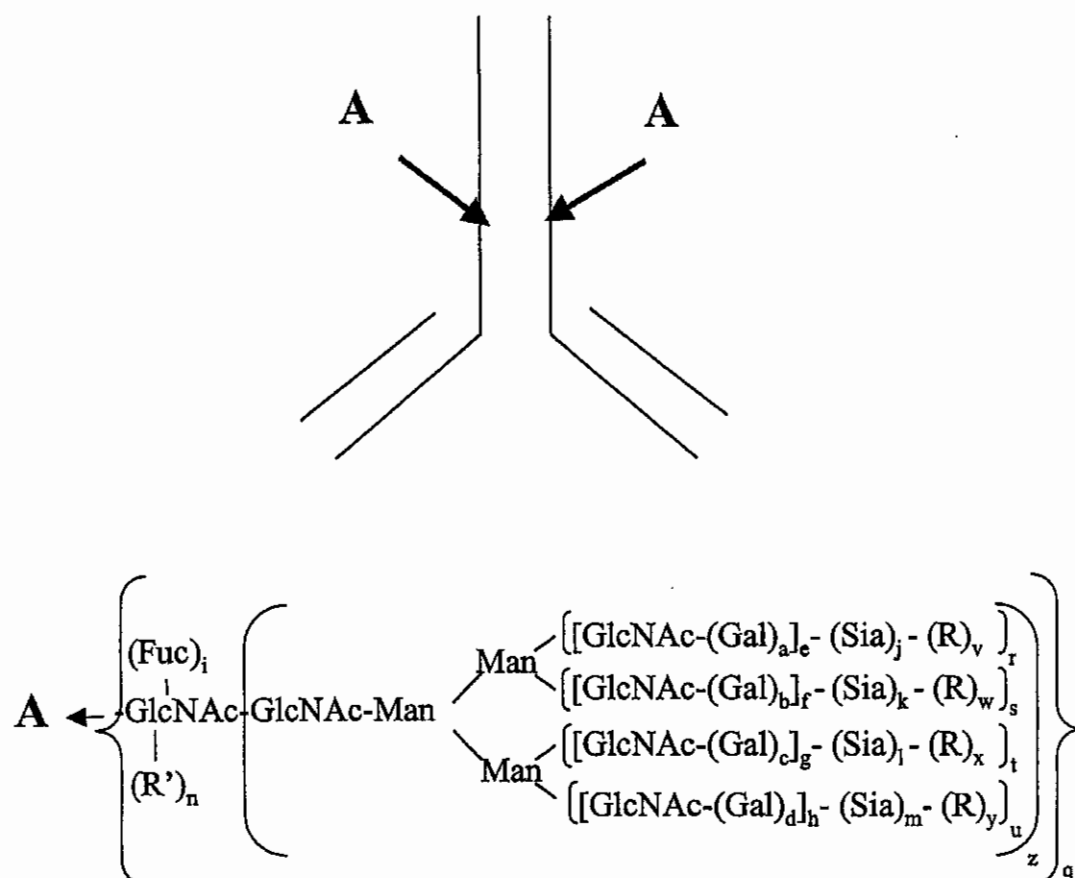
1. Endo-H
2. Galactosyltransferase, UDP-Gal
- ↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D

237/345



a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug,
glycoconjugate, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 51E

238/345

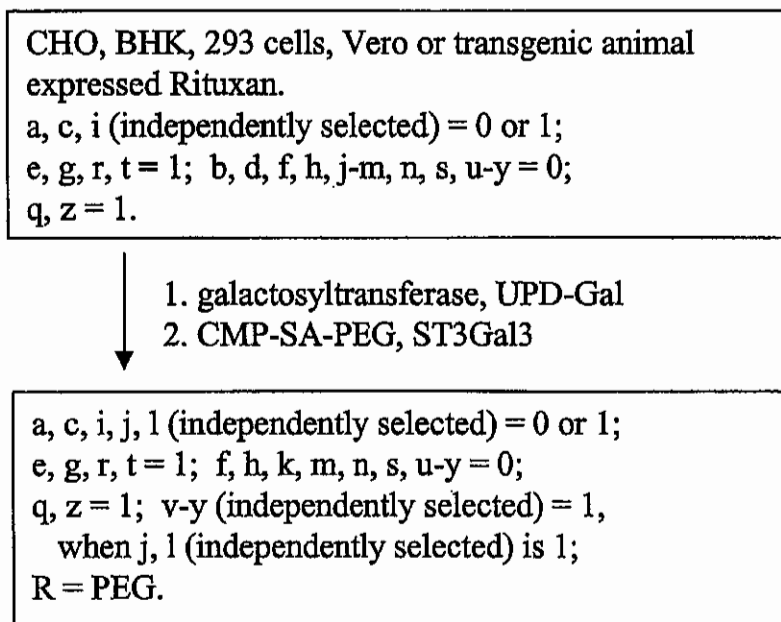


FIG. 51F

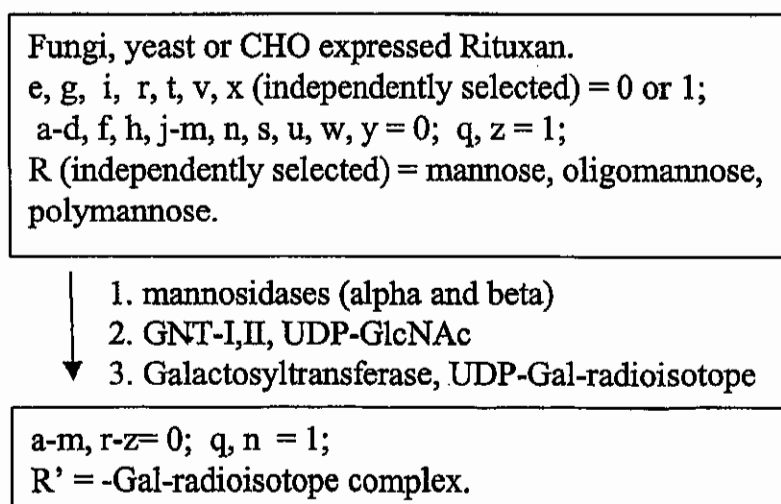


FIG. 51G

239/345

FIG. 52A

ACCCCCCTGGGCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGT
GCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTG
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACCTCCATA
GCGGCCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGATCT
CCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCG
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAAGTGGGAATGGCC
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCT
TTCCAGCGCCGGGCAGGAGGGGTCTGGTTGCCTCCCATCTGCAGAG
CTTCCTGGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTG
A

FIG. 52B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His
Leu Ala Gln Pro

240/345

FIG. 53A

GCGCCTCTTATGTACCCACAAAAATCTATTTTCAAAAAAGTTGCTCTA
AGAATATAGTTATCAAGTTAAGTAAAATGTCAATAGCCTTTTAATTTA
ATTTTAAATTGTTTTATCATTCTTTGCAATAATAAACATTAACCTTTAT
ACTTTTAAATTTAATGTATAGAATAGAGATATACATAGGATATGTAAA
TAGATACACAGTGTATATGTGATTAAAAATATAATGGGAGATTCAATC
AGAAAAAAGTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAGGAAAC
AATAATGAAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTA
AAGAGTGTATAAAGAAAGCAAAAAGAGAAGTAGAAAGTAACACAGG
GGCATTGGAATAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC
CCATTTCAACCAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCCTGGGTAGCAGG
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAATCTCTCTTTTCTCC
TGCTTGAAGGACAGACATGACTTTGGATTTCCCAGGAGGAGTTTGG
CAACCAGTTCCAAAAGGCTGAAACCATCCCTGTCCTCCATGAGATGA
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT
GGGATGAGACCCTCCTAGACAAATTCTACACTGAACTCTACCAGCAG
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGA
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT
TCCAAAGAATCACTCTCTATCTGAAAGAGAAGAAATACAGCCCTTGT
GCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCTTTTTCTTTGTCA
ACAACTTGCAAGAAAGTTTAAGAAGTAAGGAATGAAAACCTGGTTCA
ACATGGAAATGATTTTCATTGATTCGTATGCCAGCTCACCTTTTTATG
ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT
TAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACATTGTATTCAG
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATGCTGACTGATCCATT
ATCTATTTAAATATTTTTTAAAAATATTATTTATTTAACTATTTATAAAC
AACTTATTTTTGTTTCATATTATGTCATGTGCACCTTTGCACAGTGGTTA
ATGTAATAAAATGTGTTCTTTGTATTTGGTAAATTTATTTTGTGTTGTT
CATTGAACCTTTGCTATGGAACCTTTGTACTTGTTTATTCTTTAAATG
AAATTCCAAGCCTAATTGTGCAACCTGATTACAGAATAACTGGTACA
CTTCATTTGTCCATCAATATTATATTCAAGATATAAGTAAAAATAAAC
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACC
TAACAAATACAATTCTGCTCTCTTGTGTATTTGATTTTTGTATGAAAA
AACTAAAAATGGTAATCACTTAATTATCAGTTATGGTAAATGGT
ATGAAGAGAAGAAGGAACG

241/345

FIG. 53B

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser
Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr
Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala
Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr
Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu
Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe
Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val
Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu
Arg Ser Lys Glu

242/345

FIG. 54A

ATGACCAACAAGTGTCTCCTCCAAATTGCTCTCCTGTTGTGCTTCTCC
ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCTTACAAAGA
AGCAGCAATTTTCAGTGTGAGAAGCTCCTGTGGCAATTGAATGGGAG
GCTTGAATATTGCCTCAAGGACAGGATGAACTTTGACATCCCTGAGG
AGATTAAGCAGCTGCAGCAGTTCCAGAAGGAGGACGCCGCATTGACC
ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA
TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA
TGTCTATCATCAGATAAACCATCTGAAGACAGTCCTGGAAGAAAAAC
TGGAGAAAGAAGATTTTACCAGGGGAAAACCTCATGAGCAGTCTGCAC
CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA
GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAAATCCTAAGGA
ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT
CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTTCAAGCATTCCTC
AACCAGCAGATGCTGTTTAAGTGACTGATGGCTAATGTACTGCAAAT
GAAAGGACACTAGAAGATTTTGAAATTTTATTAAATTATGAGTTATT
TTTATTTAT TTAAATTTTATTTTGGAAAATAAATTATTTTGGTGC

FIG. 54B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala
Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly ArgLeu Glu Tyr Cys Leu Lys Asp
Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu
Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp
Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile
Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val
Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

243/345

FIG. 55A

ATGGTCTCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCCACGGCGT
CCTGCACCGGCGCCGGCGCGCCAACGCGTTCTGAGGAGCTGCGGC
CGGGCTCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA
GGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA
GAATGGGGGCTCCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCT
GCCTCCCTGCCTTCGAGGGCCGGAACGTGTGAGACGCACAAGGATGAC
CAGCTGATCTGTGTGAACGAGAACGGCGGCTGTGAGCAGTACTGCAG
TGACCACACGGGCACCAAGCGCTCCTGTGCGTGCCACGAGGGGTACT
CTCTGCTGGCAGACGGGGTGTCTGACACCCACAGTTGAATATCCA
TGTGGAATAATACCTATTCTAGAAAAAAGAAATGCCAGCAAACCCCA
AGGCCGAATTGTGGGGGGCAAGGTGTGCCCCAAAGGGGAGTGTCCA
TGGCAGGTCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG
TCATCATCCCCAGCACGTACGTCCCGGGCACCAACACGACATC
GCGCTGCTCCGCCTGCACCAGCCCGTGGTCCCTCACTGACCATGTGGTG
CCCCTCTGCCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC
GTGCGCTTCTCATTGGTCAGCGGCTGGGGCCAGCTGCTGGACCGTGG
CGCCACGGCCCTGGAGCTCATGGTGCTCAACGTGCCCCGGCTGATGA
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT
ATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA
CTCCTGCAAGGGGGACAGTGGAGGGCCACATGCCACCCACTACCGGG
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGCCAGGGCTGCGCA
ACCGTGGGCCACTTTGGGGTGTACACCAGGGTCTCCAGTACATCGA
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCAGGAGTCCTCC
TGCGAGCCCCATTCCC

244/345

FIG. 55B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys
Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val Leu His Arg Arg Arg
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro

245/345

FIG. 56A

ATGCAGCGCGTGAACATGATCATGGCAGAATCACCAAGCCTCATCAC
CATCTGCCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTTTCTT
GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA
TTCAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAAT
GTATGGAAGAAAAGTGTAGTTTTGAAGAACCACGAGAAGTTTTTGAA
AACACTGAAAAGACAACCTGAATTTTGAAGCAGTATGTTGATGGAGA
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG
ACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGA
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT
GAGGGATATCGACTTGCAGAAAACCAGAAGTCCTGTGAACCAGCAGT
GCCATTTCCATGTGGAAGAGTTTCTGTTTCACAACTTCTAAGCTCAC
CCGTGCTGAGGCTGTTTTTCCTGATGTGGACTATGTAAATCCTACTGA
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA
ATGACTTCACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA
TTCCCTTGGCAGGTTGTTTTGAATGGTAAAGTTGATGCATTCTGTGGA
GGCTCTATCGTTAATGAAAAATGGATTGTAAGTCTGCTGCCCACTGTGTT
GAAACTGGTGTGTTAAAATTACAGTTGTTCGCAGGTGAACATAATATTGA
GGAGACAGAACATACAGAGCAAAAGCGAAATGTGATTTCGAGCAATT
ATTCCTCACCACAACCTACAATGCAGCTATTAATAAGTACAACCATGA
CATTGCCCTTCTGGAAGTGGACGAACCCTTAGTGCTAAACAGCTACG
TTACACCTATTTGCATTGCTGACAAGGAATACACGAACATCTTCCTCA
AATTTGGATCTGGCTATGTAAGTGGCTGGGCAAGAGTCTTCCACAAA
GGGAGATCAGCTTTAGTTCTTCAGTACCTTAGAGTTCCACTTGTTGAC
CGAGCCACATGTCTTCGATCTACAAAGTTCACCATCTATAACAACAT
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTCATGTCAAGGAG
ATAGTGGGGGACCCCATGTTACTGAAGTGGAAGGGACCAGTTTCTTA
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAATA
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAGGAAA
AAACAAAGCTCACTTAATGAAAGATGGATTTCCAAGGTTAATTCATT
GGAATTGAAAATTAACAG

246/345

FIG. 56B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr

247/345

FIG. 57A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCG
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCA
GAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCC
AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCACTCC
ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAG
AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG
GGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTG
TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT
GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT
GTGAGATAAACTCTCCTTTTCCTTACCATAACCACTTTGACACGCTTC
AAGGATATACTGCAGCTTTACTGCCTTCCTCCTTATCCTACAGTACAA
TCAGCAGTCTAGTTCTTTTCATTTGGAATGAATACAGCATTAAGCTTG
TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 57B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His
Lys Ser

248/345

FIG. 57C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTTGGTGTGCTG
GCTACTGCTACACCAGGGATCTGGTGTATAAGGACCCAGCCAGGCCC
AAAATCCAGAAAACATGTACCTTCAAGGAACTGGTATATGAAACAGT
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG
ATTGTACTGTGCGAGGCCTGGGGCCCAGCTACTGCTCCTTTGGTGAAA
TGAAAGAATAA

FIG. 57D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

249/345

FIG. 58A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT
GCACCGCCGAGCTTCCCGGGATGAGGGCCCCCGGTGTGGTCACCCGG
CGCGCCCCAGGTGCTGAGGGACCCCGGCCAGGCGCGGAGATGGGG
GTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCTGCTGTCG
CTCCCTCTGGGCCTCCAGTCCTGGGCGCCCCACCACGCCTCATCTGT
GACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT
ATCACTGTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGAT
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGCCTGGCCCTG
CTGTTCGGAAGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCC
CAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG
CCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGCGAGCCCAGAAGG
AAGCCATCTCCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACA
ATCACTGCTGACACTTTCCGCAAACCTCTTCCGAGTCTACTCCAATTTC
CTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC
TCACCAACATTGCTTGTGCCACACCCTCCCCCGCCACTCCTGAACCCC
GTCGAGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC
AACTCTGAGATCTAAGGATGTCACAGGGCCAACCTTGAGGGCCCAGAG
CAGGAAGCATTGAGAGAGCAGCTTTAAACTCAGGGACAGAGCCATG
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC
AGGACACGCTTTGGAGGCGATTTACCTGTTTTCGCACCTACCATCAGG
GACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAG
GTCTCACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGCTGGCCTCTGG
CTCTCATGGGGTCCAAGTTTTGTGTATTCTTCAACCTCATTGACAAGA
ACTGAAACCACCAAAAAAAAAAAAAA

250/345

FIG. 58B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu Leu Ser
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

251/345

FIG. 59A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT
CTCTGCACCCGCCCCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGC
ATGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGA
GACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAT
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGT
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTG
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA
ACCTGAAGGACTTTCTGCTTGTTCATCCCCTTTGACTGCTGGGAGCCAG
TCCAGGAGTGA

FIG. 59B

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

252/345

FIG. 60A

ATGAAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTTG
GGTTCTCTTGGCTGTTACTGCCAGGACCCATATGTAAAAGAAGCAGA
AAACCTTAAGAAATATTTTAATGCAGGTCATTCAGATGTAGCGGATA
ATGGAACCTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT
GACAGAAAAATAATGCAGAGCCAAATTGTCTCCTTTTACTTCAAACCT
TTTTAAAAACTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG
AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT
GAATGTCCAACGCAAAGCAATACATGAACTCATCCAAGTGATGGCTG
AACTGTGCGCCAGCAGCTAAAACAGGGAAGCGAAAAAGGAGTCAGAT
GCTGTTTCGAGGTCGAAGAGCATCCCAGTAA

FIG. 60B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile
Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln

253/345

FIG. 61A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC
CCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGA
ATTTCAACCTCACGGAGATTCCGGAGGCTCAGATCCATGAAGGCTTC
CAGGAACCTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT
GACCACCGGCAATGGCCTGTTCTCAGCGAGGGCCTGAAGCTAGTGG
ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTC
ACTGTCAACTTCGGGGACACCGAAGAGGCCAAGAAACAGATCAACG
ATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTGTTGGTCAAG
GAGCTTGACAGAGACACAGTTTTTGTCTCTGGTGAATTACATCTTCTTT
AAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAG
AGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATG
AAGCGTTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCTGTCCAG
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACC
CACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGC
CAGCTTACATTTACCCAACTGTCCATTACTGGAACCTATGATCTGAA
GAGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGG
CTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTCTCCAAG
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGC
TGCTGGGGCCATGTTTTTAGAGGCCATACCCATGTCTATCCCCCCCCGA
GGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATAC
CAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAAT
AACTGCCTCTCGCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCC
CTGGATGACATTAAAGAAGGGTTGAGCTGG

254/345

FIG. 61B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val
Phe Ala LeuVal Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys
Phe Leu Glu Asn Glu AspArg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val
Val Asn Pro Thr Gln Lys

255/345

FIG. 62A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTTT
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCT
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTCAAGTCCTTCCA
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTCGTGGGCATCAGGT
GCCCCGCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGT
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCCGACCTTTCCT
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGCGACG
GATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGCACAG
GCCTGCTACTGACCCTGCAGCCAGAACAGAAAGTTCCAGAAAGTGAAG
GGATTTGGAGGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC
CTGTCACCCCCTGCCCAAATTTGCTACTTAAATCGTACTTCTCTGAA
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCCA
GTTGCACAACCTTCAGCCTCCAGAGGAAGATACCAAGCTCAAGATAC
CCCTGATTCACCGAGCCCTGCAGTTGGCCCAGCGTCCCGTTTCACTCC
TTGCCAGCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG
GTGAATGGGAAGGGGTCCTCAAGGGACAGCCCGGAGACATCTACC
ACCAGACCTGGGCCAGATACTTTGTGAAGTTCCTGGATGCCTATGCTG
AGCACAAGTTACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCT
GCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGGGCTTCACCCCT
GAACATCAGCGAGACTTCATTGCCCGTGACCTAGGTCTACCCCTCGCC
AACAGTACTCACCACAATGTCCGCCTACTCATGCTGGATGACCAACGC
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCT
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA
ACACCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTTCTGGG
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC
CACAGCATCATCACGAACCTCCTGTACCATGTGGTCGGCTGGACCGAC
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA
CTTTGTGACAGTCCCATCATTGTAGACATCACCAAGGACACGTTTTTA
CAAACAGCCCATGTTCTACCACCTTGGCCACTTCAGCAAGTTCATTCC
TGAGGGCTCCAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC
TGGACGCAGTGGCACTGATGCATCCCGATGGCTCTGCTGTTGTGGTCG
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG
CTGTGGGCTTCCTGGAGACAATCTCACCTGGCTACTCCATTCACACCT
ACCTGTGGCATCGCCAGTGATGGAGCAGATACTCAAGGAGGCACTGG
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAGCTCACACGCTGTCTG
TGAATAAGAGGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

256/345

FIG. 62A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCCCTCTAGGTGGT
GCCCAGGGCTGGAGGCCCCTAGAAAAAGATCAGTAAGCCCCAGTGTC
CCCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT
TGGAAACT

FIG. 62B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser
Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser
Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys
Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr
Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly
Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu
Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser
Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser
Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser
Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu
Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys
Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile
Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu
His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu
Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp
Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg
Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val
Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu
Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro
Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser
Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn
Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu
Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr
Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu
Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn
Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu
Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

257/345

FIG. 63A

ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG
AGCAGTCTTTCGTTTCGCCCAGCCAGGAAATCCATGCCCCGATTTCAGAA
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAACGCA
GATGATATAACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA
GCAACCGGGTGGAAATATTGCTGGTGCAACAGTGGCAGGGGCACAGTGC
CACTCAGTGCCTGTCAAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG
GGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTTCGTGTGCCAGTG
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATAACCAGGGCCA
CGTGCTACGAGGACCAGGGCATCAGCTACAGGGGACAGTGGAGCAC
AGCGGAGAGTGGCGCCGAGTGCACCAACTGGAACAGCAGCGCGTTG
GCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG
GCCTGGGGAAACCACAACTACTGCAGAAACCCAGATCGAGACTCAA
GCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCT
GCAGCACCCCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGG
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC
CTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACAC
AGCACAGAACCCCAAGTGCCCAAGGCACTGGGCCTGGGCAAACATAATT
ACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTC
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG
GAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCT
TTGCCAAGCACAGGAGGTGCGCCGGGAGAGCGGTTCTGTGCGGGGGC
ATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCACTGCTTCCAG
GAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATA
CCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA
TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACAT
TGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCAGGAGA
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTG
CCGGACTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC
CTTGTCTCCTTTCTATTTCGGAGCGGCTGAAGGAGGCTCATGTCAGACT
GTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAG
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCC
CAGGCAAACCTTGACGACGCCTGCCAGGGCGATTTCGGGAGGCCCCCT
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAG
GTTACCAACTACCTAGACTGGATTCGTGACAACATGCGACCGTGACC
AGGAACACCCGACTCCTCAAAAGCAAATGAGATCC

258/345

FIG. 63B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys
Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg
Asp Asn Met

259/345

FIG. 64A

ATCACTCTCTTTAATCACTACTCACATTAACCTCAACTCCTGCCACAA
TGTACAGGATGCAACTCCTGTCTTGCAATTGCACTAATTCTTGCACTTG
TCACAAACAGTGCACCTACTTCAAGTTCGACAAAGAAAACAAAGAAA
ACACAGCTACAACCTGGAGCATTACTGCTGGATTACAGATGATTTTG
AATGGAATTAATAATTACAAGAATCCCAAACCTCACCAGGATGCTCAC
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC
AGTGTCTAGAAGAAGAAGTCAAACCTCTGGAGGAAGTGCTGAATTTA
GCTCAAAGCAAAAACCTTTCCTTAAGACCCAGGGACTTAATCAGCAA
TATCAACGTAATAGTTCTGGAAGTAAAGGGATCTGAAACAACATTCA
TGTGTGAATATGCAGATGAGACAGCAACCATTGTAGAATTTCTGAAC
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAACTTGATAA
TTAAGTGCTTCCCACTTAAACATATCAGGCCTTCTATTTATTTATTTA
AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG
TAACTATTATTCTTAATCTTAAACTATAAATATGGATCTTTTATGAT
TCTTTTTGTAAAGCCCTAGGGGCTCTAAATGGTTTACCTTATTTATCC
CAAAAATATTTATTATTATGTTGAATGTAAATATAGTATCTATGTAG
ATTGGTTAGTAAACTATTTAATAAATTTGATAAATATAAAAAAAAAA
AAACAAAAAAAAAAAA

FIG. 64B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys
Gln Ser Ile Ile Ser Thr Leu Thr

260/345

FIG. 65A-1

ATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTTCGATTCT
GCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAAGTGTCA
TGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG
ATTTCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGT
GTACAAAAAGACTCTGTTTGTAGAATTACCGGATCACCTTTTCAACAT
CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCC
AGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCT
TCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCT
TCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAG
AAGATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGCAG
GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG
CCTCATTGGAGCCCTACTAGTATGTAGAGAAGGGAGTCTGGCCAAGG
AAAAGACACAGACCTTGCACAAATTTATACTACTTTTTGTCTGTATTG
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATGCA
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCTAAAATGCACACAG
TCAATGGTTATGTAAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAA
GTGCACTCAATATTCCTCGAAGGTCACACATTTCTTGAGGAACCAT
CGCCAGGCGTCCTTGGAATCTCGCCAATAACTTTCTTACTGCTCAA
ACACTCTTGATGGACCTTGGACAGTTTCTACTGTTTTGTATATCTCTT
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT
CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG
ACTATGATGATGATCTTACTGATTCTGAAATGGATGTGGTCAGGTTTG
ATGATGACAACTCTCCTTCCCTTTATCCAAATTCGCTCAGTTGCCAAGA
AGCATCCTAAAACCTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC
TGGGACTATGCTCCCTTAGTCCTCGCCCCGATGACAGAAGTTATAAA
AGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAA
AAAAGTCCGATTTATGGCATAACAGATGAAACCTTTAAGACTCGTG
AAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG
AAGTTGGAGACACACTGTTGATTATATTTAAGAATCAAGCAAGCAGA
CCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTAT
TCAAGGAGATTACCAAAGGTGTAAAACATTTGAAGGATTTTCCAAT
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGACTGTAGAAG
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC
TCCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGATA
ATGTCAGACAAGAGGAATGTCATCCTGTTTTCTGTATTTGATGAGAAC
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTTCTCCCAATCCA
GCTGGAGTGCAGCTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT
GCACAGCATCAATGGCTATGTTTTTGATAGTTTGCAGTTGTCAGTTTG
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTGGAGCACAGA
CTGACTTCCTTTCTGTCTTCTTCTCTGGATATACCTTCAAACACAAAAT

261/345

FIG. 65A-2

GGTCTATGAAGACACACTCACCCCTATTCCCATTCTCAGGAGAAACTGT
CTTCATGTCGATGGAAAACCCAGGTCTATGGATTCTGGGGTGCCACA
ACTCAGACTTTCGGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT
AGTTGTGACAAGAACAACACTGGTGATTATTACGAGGACAGTTATGAAGA
TATTTTCAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCAAGAA
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCCAAAAGCAATTT
AATGCCACCACAATTCCAGAAAATGACATAGAGAAGACTGACCCTTG
GTTTGCACACAGAACACCTATGCCTAAAATACAAAATGTCTCCTCTA
GTGATTTGTTGATGCTCTTGCGACAGAGTCCTACTCCACATGGGCTAT
CCTTATCTGATCTCCAAGAAGCCAAATATGAGACTTTTTCTGATGATC
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA
CACTTCAGGCCACAGCTCCATCACAGTGGGGACATGGTATTTACCCC
TGAGTCAGGCCTCCAATTAAGATTAAATGAGAAACTGGGGACAACCTG
CAGCAACAGAGTTGAAGAACTTGATTTCAAAGTTTCTAGTACATCA
AATAATCTGATTTCAACAATTCCATCAGACAATTTGGCAGCAGGTACT
GATAATACAAGTTCCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT
AGTCAATTAGATAACCACTCTATTTGGCAAAAAGTCATCTCCCCTTACT
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAATAATGATTCAAA
GTTGTTAGAATCAGGTTTAATGAATAGCCAAGAAAGTTCATGGGGAA
AAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGGAAAAGA
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAGTT
AGCATCTCTTTGTTAAAGACAAAACAAAACCTTCCAATAATTCAGCAACT
AATAGAAAGACTCACATTGATGGCCCATCATTATTAATTGAGAATAG
TCCATCAGTCTGGCAAAATATATTAGAAAGTGACACTGAGTTTAAAA
AAGTGACACCTTTGATTCATGACAGAATGCTTATGGACAAAAATGCT
ACAGCTTTGAGGCTAAATCATATGTCAAATAAACTACTTCATCAAA
AAACATGGAAATGGTCCAACAGAAAAAAGAGGGCCCCATTCCACCA
GATGCACAAAATCCAGATATGTCGTTCTTTAAGATGCTATTCTTGCCA
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCCTTAGGACCAG
AAAAATCTGTGGAAGGTCAGAATTTCTTGTCTGAGAAAAACAAAGTG
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA
TGGTTTTTCCAAGCAGCAGAAACCTATTTCTTACTAACTTGGATAATT
TACATGAAAATAATACACACAATCAAGAAAAAAAATTCAGGAAGA
AATAGAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTTGCCTC
AGATACATACAGTGACTGGCACTAAGAATTTTCATGAAGAACCTTTTC
TTACTGAGCACTAGGCCAAAATGTAGAAGGTTTCATATGACGGGGCATA
TGCTCCAGTACTTCAAGATTTTAGGTCATTAAATGATTCAACAAATAG
AACAAAGAAACACACAGCTCATTTCTCAAAAAAAGGGGAGGAAGAA
AACTTGGAAGGCTTGGGAAATCAAACCAGCAAATTGTAGAGAAATAT
GCATGCACCACAAGGAATATCTCCTAATACAAGCCAGCAGAATTTTG
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCCTA

262/345
FIG. 65A-3

GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCTCACAC
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAATAGA
TCTCCATTACCCATTGCAAAGGTATCATCATTTCCATCTATTAGACCTA
TATATCTGACCAGGGTCCTATTCCAAGACAACTCTTCTCATCTTCCAG
CAGCATCTTATAGAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT
TTCTTACAAGGAGCCAAAAAAATAACCTTTCTTTAGCCATTCTAACC
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG
TGCCACAAATTCAGTCACATACAAGAAAGTTGAGAACACTGTTCTCCC
GAAACCAGACTTGCCCAAAACATCTGGCAAAGTTGAATTGCTTCCAA
AAGTTCACATTTATCAGAAGGACCTATTCCCTACGGAACTAGCAATG
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA
CAGAGGGAGCGATTAAGTGGAATGAAGCAAACAGACCTGGAAAAAGT
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAAGACTCCCTCCAA
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC
AAAAGAAGAGTGGAATCCCAAGAGAAGTCACCAGAAAAAACAGCT
TTAAGAAAAAGGATACCATTTTGTCCCTGAACGCTTGTGAAAGCAAT
CATGCAATAGCAGCAATAAATGAGGGACAAAATAAGCCCGAAATAG
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA
AACCACACAGTCTTGAAACGCCATCAACGGGAAATAACTCGTACTAC
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAATC
AGAGCCCCCGCAGCTTTCAAAGAAAACACGACACTATTTTATTGCTG
CAGTGGAGAGGCTCTGGGATTATGGGATGAGTAGCTCCCCACATGTT
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAAGAAAGT
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT
GGAGAACTAAATGAACATTTGGGACTCCTGGGGCCATATATAAGAGC
AGAAGTTGAAGATAATATCATGGTAACTTTCAGAAATCAGGCCTCTC
GTCCCTATTCTTCTATTCTAGCCTTATTTCTTATGAGGAAGATCAGAG
GCAAGGAGCAGAACCTAGAAAAAACTTTGTCAAGCCTAATGAAACCA
AACTTACTTTTGGAAGTGCAACATCATATGGCACCCACTAAAGAT
GAGTTTGACTGCAAAGCCTGGGCTTATTTCTCTGATGTTGACCTGGAA
AAAGATGTGCACTCAGGCCTGATTGGACCCCTTCTGGTCTGCCACACT
AACACACTGAACCCTGCTCATGGGAGACAAGTGACAGTACAGGAATT
TGCTCTGTTTTTCACCATCTTTGATGAGACCAAAAGCTGGTACTTCACT
GAAAATATGGAAAGAACTGCAGGGCTCCCTGCAATATCCAGATGGA
AGATCCCCTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA
TTCGATGGTATCTGCTCAGCATGGGCAGCAATGAAAACATCCATTCT
ATTCATTTCAAGTGGACATGTGTTCACTGTACGAAAAAAAGAGGAGTA
TAAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGAGACAGTGGA

263/345

FIG. 65A-4

AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGGAATGCCTTATTGG
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA
TAAGTGTCAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT
TCAGATTACAGCTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG
CCAGACTTCATTATTCCGGATCAATCAATGCCTGGAGCACCAAGGAG
CCCTTTTCTTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTCAC
GGCATCAAGACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACAT
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA
CTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATG
TGGATTCATCTGGGATAAAACACAATATTTTAAACCCTCCAATTATTG
CTCGATACATCCGTTTGCACCCAACCTCATTATAGCATTTCGAGCACTC
TTCGCATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCAT
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA
TCCTACTTTACCAATATGTTTGCCACCTGGTCTCCTTCAAAGCTCGA
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA
CAGGAGTAACTACTCAGGGAGTAAATCTCTGCTTACCAGCATGTAT
GTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC
TCTCTTTTTTTCAGAATGGCAAAGTAAAGGTTTTTTCAGGGAAATCAAGA
CTCCTTCACACCTGTGGTGAACCTCTCTAGACCCACCGTTACTGACTCG
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAG
GATGGAGGTTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC
CACTGCAGCACCTGCCACTGCCGTACCTCTCCCTCCTCAGCTCCAGG
GCAGTGTCCCTCCCTGGCTTGCCTTCTACCTTTGTGCTAAATCCTAGC
AGACACTGCCTTGAAGCCTCCTGAATTAACATCATCAGTCCTGCATT
TCTTTGGTGGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACTCTTA
CCTATTTTCTGCAGCTGCTCCCAGATTACTCCTTCCTTCCAATATAACT
AGGCAAAAAGAAGTGAGGAGAAACCTGCATGAAAGCATTCTTCCCTG
AAAAGTTAGGCCTCTCAGAGTCACCACTTCCTCTGTTGTAGAAAACT
ATGTGATGAAACTTTGAAAAAGATATTTATGATGTTAACATTTTCAGGT
TAAGCCTCATACGTTTAAAATAAAACTCTCAGTTGTTTATTATCCTGA
TCAAGCATGGAACAAAGCATGTTTCAGGATCAGATCAATACAATCTT
GGAGTCAAAAGGCAAATCATTTGGACAATCTGCAAAATGGAGAGAA
TACAATAACTACTACAGTAAAGTCTGTTTCTGCTTCCTTACACATAGA
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCCAA
AACTAGCATTCTTAAACTGAGAATTATAGATGGGGTTCAAGAATCCC
TAAGTCCCCTGAAATTATATAAGGCATTCTGTATAAATGCAAATGTGC
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT
GACCAATAAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG
AAATAAAATAACAATGTCTTCTTGAAATTTGTGATGGCCAAGAAAGA
AAATGATGA

264/345
FIG. 65B-1

Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser
Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe
Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro
Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr
Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly
Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro
Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys
Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser
Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg
Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu
Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln
Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu
Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn
Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val
Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr
Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro
Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser
Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile
Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser
Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn
Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg
Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln
Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys
His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val
Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe
Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr
Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn
Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln
Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp

265/345

FIG. 65B-2

Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu
Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu
Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val
Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr
Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu
Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu
Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly
Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn
Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly
Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly
Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu
Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp
Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser
Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp
Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser
Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala
Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg
Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro
Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu
Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly
Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp
Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile
Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr
Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln
Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg
Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys
Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val
Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe
Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu
Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn
Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu
Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile
Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile
Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro
Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu
Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr
Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr
Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser
Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro
Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu

266/345

FIG. 65B-3

Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys
 Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu
 Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu
 Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile
 Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly
 Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg
 Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg
 Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu
 Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg
 Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp
 Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val
 Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro
 Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg
 Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro
 Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu
 Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val
 Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr
 Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu
 Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
 Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu
 Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr
 Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro
 Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly
 Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys
 Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr
 Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu
 His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr
 Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln
 Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala
 Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile
 Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser
 Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly
 Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile
 Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr
 His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn
 Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr
 Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu
 His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu
 Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln
 Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser
 Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe
 Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu
 Leu Thr Arg Tyr Leu Arg Ile His

WO 03/031464

PCT/US02/32263

267/345

FIG.65B-4

Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg Met Glu Val Leu Gly Cys Glu
Ala Gln Asp Leu Tyr

268/345

FIG. 66A

TCCACCTGTCCCCGCAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC
GAGCCGCGCTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG
GCGCGCCTGCTTCTCTGCGTCCTGGTCGTGAGCGACTCCAAAGGCAGC
AATGAACTTCATCAAGTTCCATCGAACTGTGACTGTCTAAATGGAGGA
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC
CCAAAGAAATTCGGAGGGCAGCACTGTGAAATAGATAAGTCAAAAAC
CTGCTATGAGGGGAATGGTCACTTTTACCGAGGAAAGGCCAGCACTG
ACACCATGGGCGCGCCCTGCCTGCCCTGGAACCTCTGCCACTGTCCTTC
AGCAAACGTACCATGCCCACAGATCTGATGCTCTTCAGCTGGGCCTGG
GGAAACATAATTACTGCAGGAACCCAGACAACCGGAGGCGACCCCTGG
TGCTATGTGCAGGTGGGCCTAAAGCCGCTTGTCCAAGAGTGCATGGT
GCATGACTGCGCAGATGGAAAAAAGCCCTCCTCTCCTCCAGAAGAAT
TAAAATTTCAGTGTGGCCAAAAGACTCTGAGGCCCCGCTTTAAGATTA
TTGGGGGAGAATTCACCACCATCGAGAACCAGCCCTGGTTTGCGGCC
ATCTACAGGAGGCACCGGGGGGGCTCTGTACCTACGTGTGTGGAGG
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTCTGCTCAA
GGCTTAACCTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGAAAAC
CTCATCCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA
AGCTGATTTCCACCGGGAGTGTCAGCAGCCCCACTACTACGGCTCTG
AAGTCACCACCAAAAATGCTGTGTGCTGCTGACCCACAGTGGAACA
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA
GGGTCCCCAGGGAGGAAACGGGCACCAACCCGCTTTCTTGCTGGTTGTC
ATTTTTCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA
AGAT

269/345

FIG. 66B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

270/345

FIG.67A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA
TAGACTACTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAATTGTCATCA
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGGCGCTGCTG
GCACTGGCGGCCCTACTGCAGGGGGGCCGTGTCCCTGAAGATCGCAGC
CTTCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCT
CGTCAGCTACATTGTGCAGATCCTGAGCCGCTATGACATCGCCCTGGT
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTCGTGTA
CAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT
GTCAGGTTCTTCTCCCGGTTACAGAGGTCAGGGAGTTTGCCATTGTT
CCCCTGCATGCGGCCCCGGGGGACGCAGTAGCCGAGATCGACGCTCT
CTATGACGTCTACCTGGATGTCCAAGAGAAATGGGGCTTGGAGGACG
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT
CCCAGTGGTCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGC
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGCGCCGTTGTTC
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG
CTGAAGTGAGCAGCCCCTCCCCACACCAGTTGAACTGCAG

271/345

FIG. 67B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu Leu Gln
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val
Glu Val Met Leu Lys

272/345

FIG. 68A

GCTGCATCAGAAGAGGCCATCAAGCACATCACTGTCCTTCTGCCATGG
CCCTGTGGATGCGCCTCCTGCCCCTGCTGGCGCTGCTGGCCCTCTGGG
GACCTGACCCAGCCGCAGCCTTTGTGAACCAACACCTGTGCGGCTCAC
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA
GGTGGAGCTGGGCGGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG
CAGCCCGCAGGCAGCCCCCACC CGCCCTCCTGCACCGAGAGAGA
TGGAATAAAGCCCTTGAACCAGC

FIG. 68B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly
Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

273/345

FIG. 69A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT
TTCTGTTCCCAATCCTCTGGGATTCTTTCCCGATCACCAGTTGGACCCT
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC
GGGCCAGGGTTCACCCCAACACACGGCGGTCTTTTGGGGTGGAGCCC
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCCTG
TTTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAATCCACAACA
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGCCTATATTTTCCT
GCTGGTGGCTCCAGTTCCGGAACAGTAAACCCTGTTCCGACTACTGTC
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCTGCACCGAAC
ATGGAGAGCACAAACATCAGGATTCCTAGGACCCCTGCTCGTGTTACA
GGCGGGGTTTTTCTTGTTGACAAGAATCCTCACAATACCACAGAGTCT
AGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGGAGCACCCACGTG
TCCTGGCCAAAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTC
TTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTTT
ATCATATTCCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTC
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCCTGCT
CAAGGAACCTCTATGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC
GGAAACTGCACTTGTATTCCCATCCCATCATCCTGGGCTTTCGCAAGA
TTCTATATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA
GTGCCATTTGTTTCAAGTGGTTCGCAGGGCTTTCCCCCACTGTTTGGCTTT
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT
TGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATAC
ATTTGA

274/345

FIG. 69B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu
Trp Val Tyr Ile

275/345

FIG. 70A

CGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA
CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGC
CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGC
CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT
TTGACACCTACCAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG
AAGTATTCATTCCCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG
TCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAA
CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA
GCCCCGTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG
CGCCTCTGACAGCAACGTCTATGACCTCCTAAAGGACCTAGAGGAAG
GCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGGACT
GGGCAGATCTTCAAGCAGACCTACAGCAAGTTCGACACAAACTCACA
CAACGATGACGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAG
GAAGGACATGGCAAGGTCGAGACATTCCTGCGCATCGTGCAGTGCCG
CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG
TGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGT
GCCACCAAGCCTTGTCCTAATAAAATTAAGTTGCATC

FIG. 70B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp
Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln
Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro
Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr
Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala
Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu
Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr
Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile
Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

276/345

FIG. 71A

ATGGCGCCCGTCGCCGTCTGGGCGCGCTGGCCGTCGGACTGGAGCT
CTGGGCTGCGGCGCACGCCTTGCCCGCCAGGTGGCATTACACCCTA
CGCCCCGGAGCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG
GACAGCACATACACCCAGCTCTGGAAGTGGGTTCCCGAGTGCTTGAG
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAAACTCAAGCCTGCAC
TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCG
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAG
TGCCGCCCCGGGCTTCGGCGTGGCCAGACCAGGAACTGAAACATCAGA
CGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCAACACGACTTC
ATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACGTGGTGGCCAT
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA
CCCGGAGTATGGCCCCAGGGGCAGTACACTTACCCAGCCAGTGTCC
ACACGATCCCAACACACGCAGCCAACCTCCAGAACCCAGCACTGCTCC
AAGCACCTCCTTCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTCATCATGAC
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC
CTCACTTGCTGCGGATAAGGCCCGGGGTACACAGGGCCCCGAGCAG
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA
GAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCCACTCGGAACCAGC
CACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGC
CAGCACCGGGAGCTCAGATTCTTCCCTGGTGGCCATGGGACCCAGG
TCAATGTCACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT
CACAGTGCTCCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC
AGCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCCTTCTCCAAGGA
GGAATGTGCCTTTTCGGTCACAGCTGGAGACGCCAGAGACCCTGCTGG
GGAGCACCGAAGAGAAGCCCCTGCCCTTGGAGTGCCTGATGCTGGG
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTCTGTAGCCAAGG
TGGGCTGAGCCCTGGCAGGATGACCCTGCGAAGGGGCCCTGGTCCTT
CCAGGC

277/345

FIG. 71B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly
Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro
Asp Ala Gly Met Lys Pro Ser

278/345

FIG. 72A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

FIG. 72B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
Gly Thr Leu Val Thr Val Ser Ser

279/345

FIG. 73A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ser

FIG. 73B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

280/345

FIG. 74A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA
GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGC
ATCCACTGGTATCAGCAAAGAACAAATGGTTCTCCAAGGCTTCTCATA
AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGGC
AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT
GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC
ACGTTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA
GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT
CCTGTGTTGCCTCTGGATTCAATTTTACGTAACCACTGGATGAACTGGG
TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA
TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG
AGGTTACACCATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA
ATGACCGACTTAAGAACTGAAGACACTGGCGTTTATTACTGTTCCAGG
AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC
ACAGTCTCC

FIG. 74B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val
Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln
Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn
Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro
Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly
Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu
Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr
LeuGln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg
Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

281/345

FIG. 75A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGTTC
CA GGTTCCACTGGTGACGTCAGGCGAGGGCCCCGGAGCCTGCGGGGCAG
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC
TGCTGGTCCGCCACTGCGTGGCCTGCGGGCTCCTGCGCACGCCGCGGC
CGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAG
CCGCAGGAGTCGGTGGGCGCGGGGGCCGGCGAGGCGGCGGTGACAC
AAACTCACACATGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGA
CCGTCAGTCTTCCTCTTCCCCCAAAACCCAAGGACACCCTCATGATC
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGA
AGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA
CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGG
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT
GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACG
CCTCCCGTGTTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT
CCCTGTCTCCCGGGAAATGA

282/345

FIG. 75B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

283/345

FIG. 76

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

284/345

FIG. 77

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser
Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe
Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr
Leu Val Thr Val Ser Ala

285/345

FIG. 78

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

286/345

FIG. 79

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
Thr Leu Val Thr Val Ser Ser

287/345

FIG. 80

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys
Ser Phe Asn Arg Gly Glu Cys

288/345

FIG. 81

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly

289/345

FIG. 82A

ATGGATTTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA
GTCATAATGTCCAGAGGGCAAATTGTTCTCTCCCAGTCTCCAGCAATC
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCAGGGCCAG
CTCAAGTGTAAGTTACATCCACTGGTTCAGCAGAAGCCAGGATCCTC
CCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCC
TGTTTCGCTTCAGTGGCAGTGGGTCTGGGACTTCTTACTCTCTCACAAT
CAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT
GGACTAGTAACCCACCCACGTTTCGGAGGGGGGACCAAGCTGGAAATC
AAA

FIG. 82B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

290/345

FIG. 83A

ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG
TCCTGTCCCAGGTACAACCTGCAGCAGCCTGGGGCTGAGCTGGTGAAG
CCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACATTT
ACCAGTTACAATATGCACTGGGTAAAACAGACACCTGGTCGGGGCCT
GGAATGGATTGGAGCTATTTATCCCGGAAATGGTGATACTTCCTACAA
TCAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCA
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 83B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly
Thr Thr Val Thr Val Ser Ala

291/345

FIG. 84A

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG
ACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAG
AGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGAACACAGACCC
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTA
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT
CCTCCAAGAGCACCTCTGGGGGACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGC
CCTGACCAGCGGCGTGCACACCTTCCCGGTGTCTACAGTCCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA
TGCCACCGTGCCAGCACCTGAACCTCTGGGGGGACCGTCAGTCTTC
CTCTTCCCCCCTAAACCAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCTGCAACCAGGACTGGCTGAATGGCAAGGACTACAA
GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGATGAGCTGACCAGGAACCAGGTGAGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGA
GCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTG
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTTCGTG
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT
TCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCTTCTTGA
CCCTGGAAGGTGCCACTCCCACTGTCCTTTCCTAATAAAATGAGGAAA
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGGG
TGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA
TGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGACAGC
GCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCATA
ATGAGAAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGAT
TGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

292/345

FIG. 84B

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG
ACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAG
AGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGAACACAGACCC
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTA
CGCGTGTGCTAGCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCT
CCTCCAAGAGCACCTCTGGGGGGCACAGCGGCCCTGGGCTGCCTGGTC
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGC
CCTGACCAGCGGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGG
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA
TGCCCAACCGTGCCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTC
CTCTTCCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCCT
GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC
GTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGACTACAA
GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA
TCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG
CCCCCATCCCGGGATGAGCTGACCAGGAACCAGGTCAGCCTGACCTG
CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGA
GCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTG
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG
TAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTTCGTG
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT
TCTAGTTGCCAGCCATCTGTTGTTTGCCCTCCCCCGTGCCTTCCTTGA
CCCTGGAAGGTGCCACTCCCCTGTCCTTTCTTAATAAAATGAGGAAA
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGGG
TGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGCA
TGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGGCTCGACAGC
GCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCATA
ATGAGAAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGAT
TGAGCAAATGCGTTGCCAAAAGGATGCTTTAGAGACAGTGTTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

293/345

FIG. 84C

GCTGCGATTTTCGCGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTG
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTGAACTGCAT
CGTCGCCGTGTCCCAAATATGGGGATTGGCAAGAACGGAGACCTAC
CCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC
ACAACCTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAG
GAAAACCTGGTTCTCCATTCTGAGAACAAATCGACCTTTAAAGGACA
GAATTAATATAGTTCTCAGTAGAGAACTCAAAGAACCACCACGAGGA
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT
CTTTGTGACAAGGATCATGCAGGAATTTGAAAGTGACACGTTTTTCCC
AGAAATTGATTTGGGGAAATATAAACTTCTCCCAGAATACCCAGGCG
TCCTCTCTGAGGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAA
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTTCAGTTCTCTGC
TCCCCTCCTAAAGTCATGCATTTTTATAAGACCATGGGACTTTTGCTG
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGT
TTGCCCCCTCCCCCGTGCCTTTCCTTGACCCTGGAAGGTGCCACTCCCAC
TGTCCTTTCCTAATAAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG
AGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCT
ATGGAACCAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTT
ATTTGCATAATGAGAAAAAAAGGAAAATTAATTTTAACACCAATTCA
GTAGTTGATTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACA
GTGTTCTCTGCACAGATAAGGACAAACATTATTCAGAGGGAGTACCC
AGAGCTGAGACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGA
AATATGCTTGTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGG
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGG
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTC
TGACATAGTTGTGTTGGGAGCTTGATCGATCCTCTATGGTTGAACAA
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC
GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGT
GTTCCGGCTGTGACGCGAGGGGCGCCCGGTTCTTTTGTCAAGACCGA
CCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTAT
CGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTG
TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG
CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATC
ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC
CCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAATCG
GATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATC
AGGGGCTCGCGCCAGCCGAAGTGTTCGCCAGGCTCAAGGCGCGCATG
CCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG

294/345

FIG. 84D

AATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGC
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG
TGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGT
GCTTTACGGTATCGCCGCTTCCCGATTTCGCAGCGCATCGCCTTCTATC
GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGAC
CGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCCACCG
CCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCG
GCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCC
ACCCCAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATA
GCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTT
GTGGTTTGTCCAACTCATCAATCTATCTTATCATGTCTGGATCGCGG
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC
TGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGG
AGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCAC
ATTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTC
GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT
TGCGTATTGGGCGCTCTTCCGCTTCTCGCTCACTGACTCGCTGCGCTC
GGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA
TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA
GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGC
TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATC
GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC
CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC
CTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG
GCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC
GTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAC
CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGA
CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGA
AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA
CAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATT
ACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC
GGGGTCTGACGCTCAGTGAACGAAAACCTCACGTAAAGGGATTTTGG
TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAA
AATGAAGTTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTG
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC
TATTTGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTAC
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGC
GAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA
GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTC
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTTCG

295/345

FIG. 84E

CAGTTAATAGTTTGGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGG
TGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAAC
GATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTT
AGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTG
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGC
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT
TCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCCGGCGTCAA
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATC
ATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTG
TTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTGATCTTCA
GCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGG
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAA
TACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTA
TTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA
AATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT

296/345

FIG. 85A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAATAAAA
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAACCTGGGCG
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA
CACACATTCACAGAATTAATCCCCTAGTTATTAATAGTAATCAATT
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGCTTACATAA
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCC
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA
CTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCT
TATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATACC
GGTTTGACTCACGCGGATTTCCAAGTCTCCACCCCATTGACGTCAATG
GGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
ACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGG
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG
GAGACGCCATCACAGATCTCTCACTATGGATTTTCAGGTGCAGATTAT
CAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAT
TGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAA
GGTCACAATGACTTGCAGGGGCCAGCTCAAGTGTAAGTTACATCCACT
GGTTCCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTATGCCA
CATCCAACCTGGCTTCTGGAGTCCCTGTTTCGCTTCAGTGGCAGTGGGT
CTGGGACTTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATG
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTCCG
GAGGGGGGACCAAGCTGGAAATCAAACGTACGGTGGCTGCACCATCT
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAACCTGCC
TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA
CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG
TGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA
CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC
TGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT
CAACAGGGGAGAGTGTTGAATTCAGATCCGTTAACGGTTACCAACTA
CCTAGACTGGATTCGTGACAACATGCGGCCGTGATATCTACGTATGAT
CAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCTC
CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTCC

297/345

FIG. 85B

TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCT
ATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGG
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA
GCTGGGGGCTCGACAGCTATGCCAAGTACGCCCCCTATTGACGTCAATG
ACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGG
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT
GGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTG
ACTCACGGGGATTTCCTCAAGTCTCCACCCCATTTGACGTCAATGGGAGTT
TGTTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACT
CCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTC
TATATAAGCAGAGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGA
ACACAGACCCGTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT
CGCTGTTGCTACGCGTGTCTGTCCAGGTACAACCTGCAGCAGCCTGG
GGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGG
CTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAACAGA
CACCTGGTCGGGGCCTGGAATGGATTGGAGCTATTTATCCCGGAAAT
GGTGATACTTCCTACAATCAGAAGTTCAAAGGCAAGGCCACATTGAC
TGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGA
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCACGGTCACC
GTCTCTGCAGCTAGCACCAAGGGGCCCATCGGTCTTCCCCCTGGCACCC
TCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGT
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG
CCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC
AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACAC
ATGCCCACCGTGCCAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTT
CCTCTTCCCCCAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC
TGAGGTACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG
ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG
CGTCCTCACCGTCTTGCACCAGGACTGGCTGAATGGCAAGGAGTACA
AGTGCAAGGTCTCCAACAAAGCCCTCCAGCCCCCATCGAGAAAACC
ATCTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT
GCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT
GCCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAGTGGGAG
AGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGTCT
GGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAA
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG
AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG
GTAAATGAGGATCCGTTAACGGTTACCAACTACCTAGACTGGATTCTGT

298/345

FIG. 85C

GACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCC
TTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTG
ACCCTGGAAGGTGCCACTCCCAGTGTCTTTCTAATAAAATGAGGAA
ATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGTGGG
GTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAGGC
ATGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGACAG
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCAT
AATGAGAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGA
TTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGGGCTGCGATTTTCG
CGCCAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC
CCCGCTGCCATCATGGTTCGACCATTGAACTGCATCGTCGCCGTGTCC
CAAAATATGGGGATTGGCAAGAACGGAGACCTACCCTGGCCTCCGCT
CAGGAACGAGTTCAAGTACTTCCAAAGAATGACCACAACCTCTTCAG
TGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGAAAACCTGGTTC
TCCATTCCTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTT
CTCAGTAGAGAACTCAAAGAACCACCACGAGGAGCTCATTTTCTTGC
CAAAAGTTTGGATGATGCCTTAAGACTTATTGAACAACCGGAATTGG
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTTCTGTTTACC
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG
ATCATGCAGGAATTTGAAAGTGACACGTTTTTCCCAGAAATTGATTTG
GGGAAATATAAACTTCTCCCAGAATAACCCAGGCGTCCTCTCTGA
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA
AGAAAGACTAACAGGAAGATGCTTTCAGTTCTCTGCTCCCCCTCCTAA
AGCTATGCATTTTTATAAGACCATGGGACTTTTGCTGGCTTTAGATCA
GCCTCGACTGTGCCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCC
CCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAGTGTCTTTCTTA
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTAT
TCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAA
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGC
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTTATTTGCATAATG
AGAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGATTGA
GCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCTGCA
CAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAGACT
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTTGTC
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCCAAT
CTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCATATA
AGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAGTTG

299/345

FIG. 85D

TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA,
CGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTG
GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTC
AGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGGTGC
CCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCA
CGACGGGCGTTCCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGG
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTG
TCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCA
ATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCAC
CAAGCGAAACATCGCATCGAGCGAGCACGTA CT CGGATGGAAGCCGG
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGC
CAGCCGAAC TGTTCGCCAGGCTCAAGGCGCGCATGCCCGACGGCGAG
GATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTG
GAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTG
GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA
AGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTAT
CGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGA
GTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGAC
GCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCCTTCTATGA
AAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCT
CCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCAACTTGT
TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTT
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAA
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGCCGCGATCCCGTC
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT
TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTG
TAAAGCCTGGGGTGCTAATGAGTGAGCTAACTCACATTAATTGCGTT
GCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCA
TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGC
GCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTGCTTCGGCT
GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA
CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCA
GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC
ATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT
CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCC
CCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC
CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA
ATGCTCACGCTGTAGGTATCTCAGTTCGGGTGTAGGTGCTTCGCTCCAA
GCTGGGCTGTGTGCACGAACCCCCCGTT CAGCCCGACCGCTGCGCCTT
ATCCGGTA ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

300/345

FIG. 85E

GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG
TAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC
ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC
TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGC
TGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAA
AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC
TCAGTGGAACGAAAACCTCACGTAAAGGGATTTTGGTTCATGAGATTATC
AAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAAATGAAGTTTAA
ATCAATCTAAAGTATATATGAGTAACTTGGTCTGACAGTTACCAATG
CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC
ATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG
CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC
ACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCG
AGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTA
ATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGT
TTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTA
CATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTC
CGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTA
TGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCT
TTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA
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GCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCT
TCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCCG
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CCAGCGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCAAAA
AAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCT
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301/345

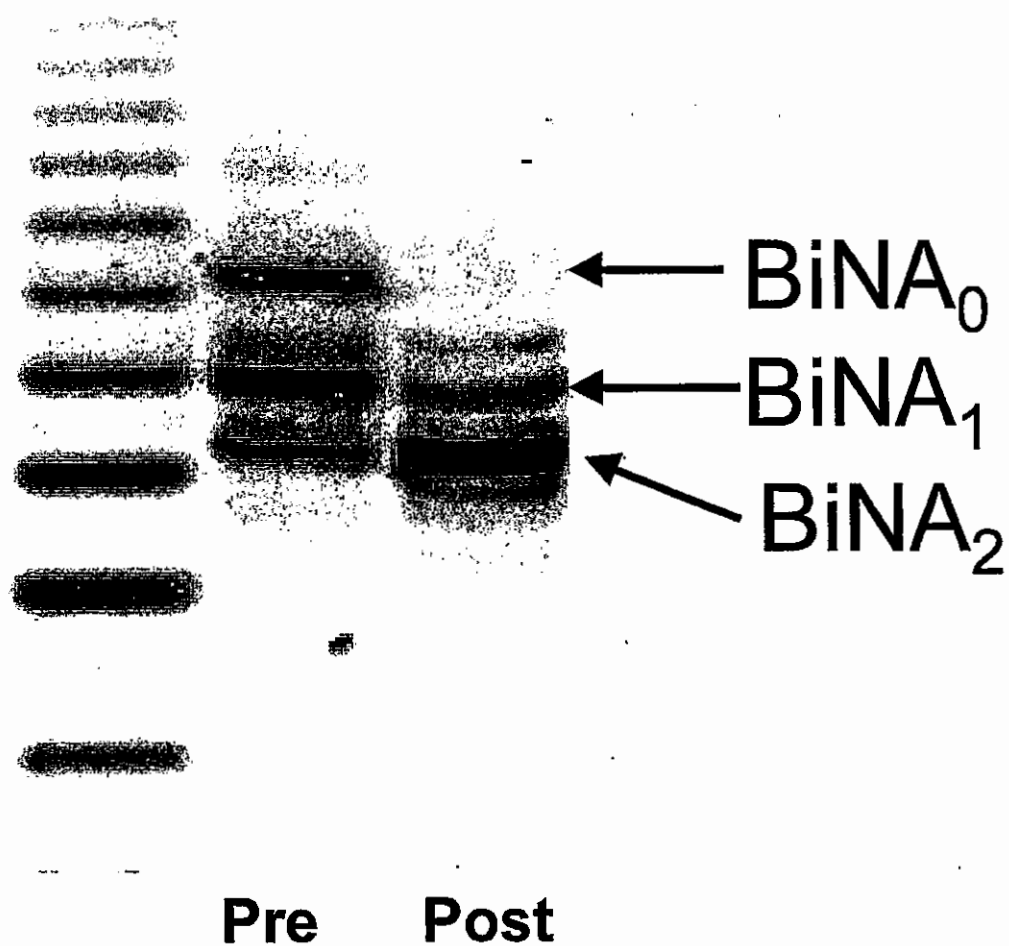


FIG. 86

302/345

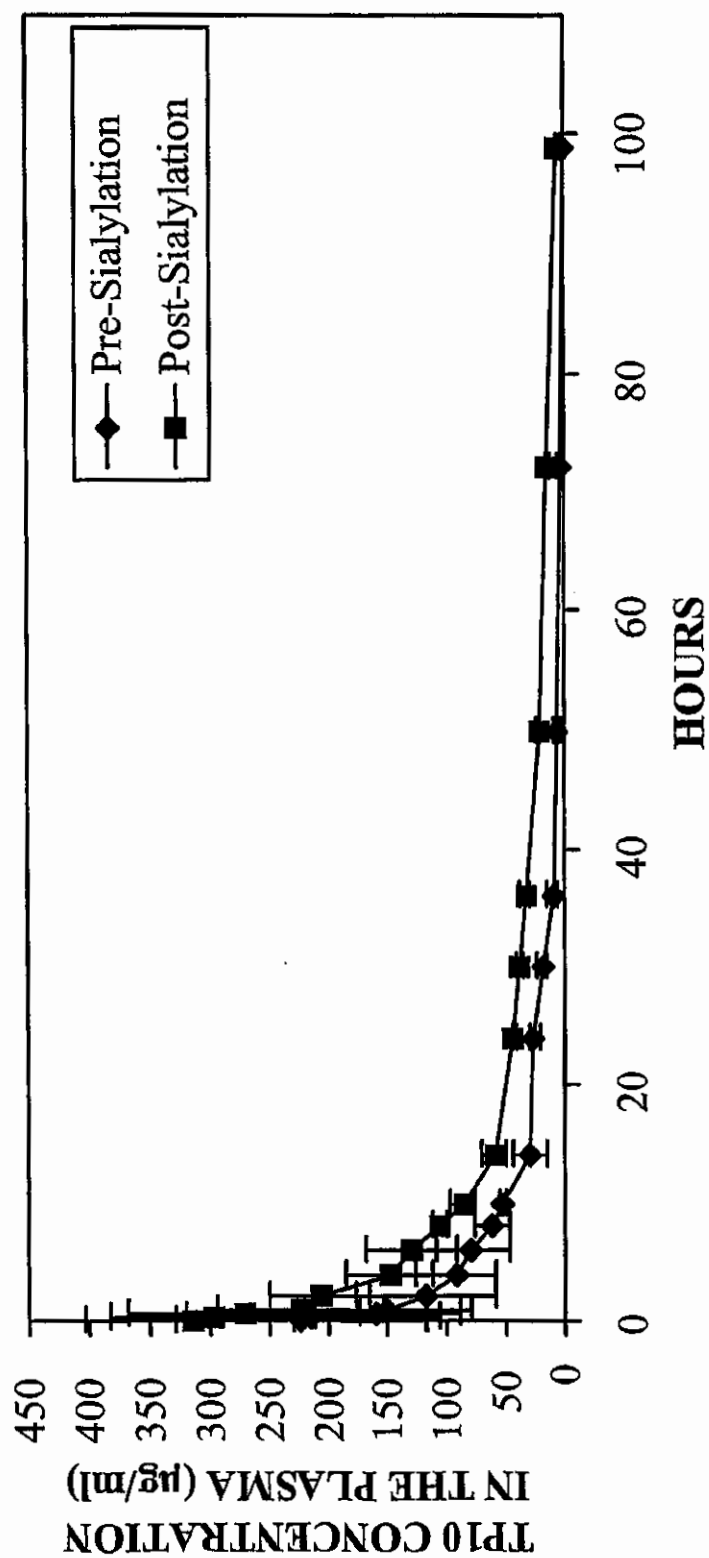


FIG. 87

303/345

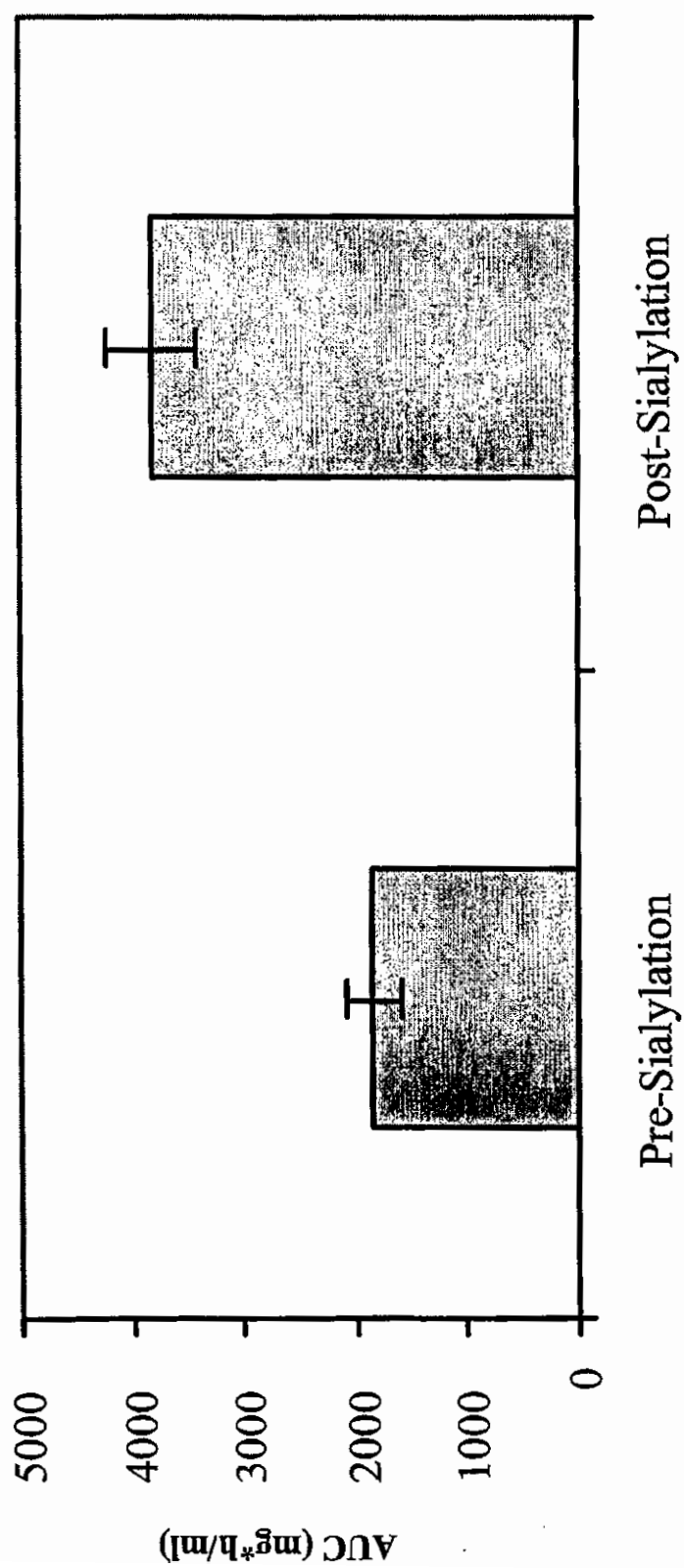


FIG. 88

304/345

← BiNA₂F₂

FIG. 89

TP20

+F

+SA

Pre



305/345

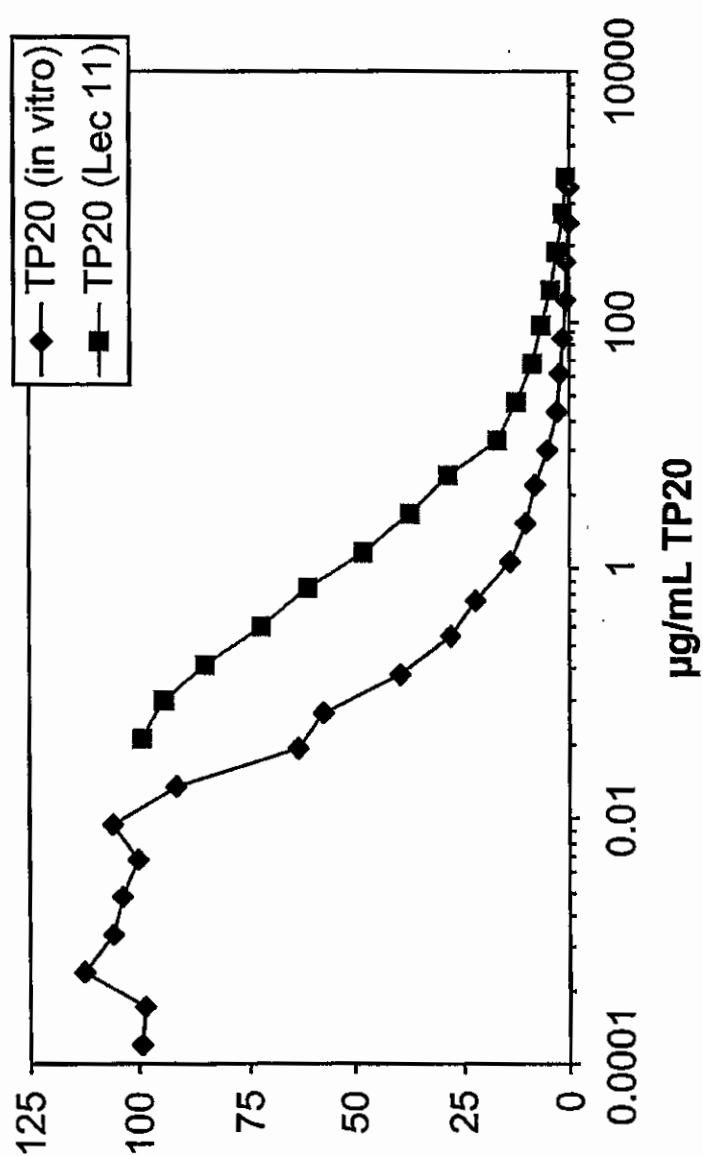


FIG. 90

306/345

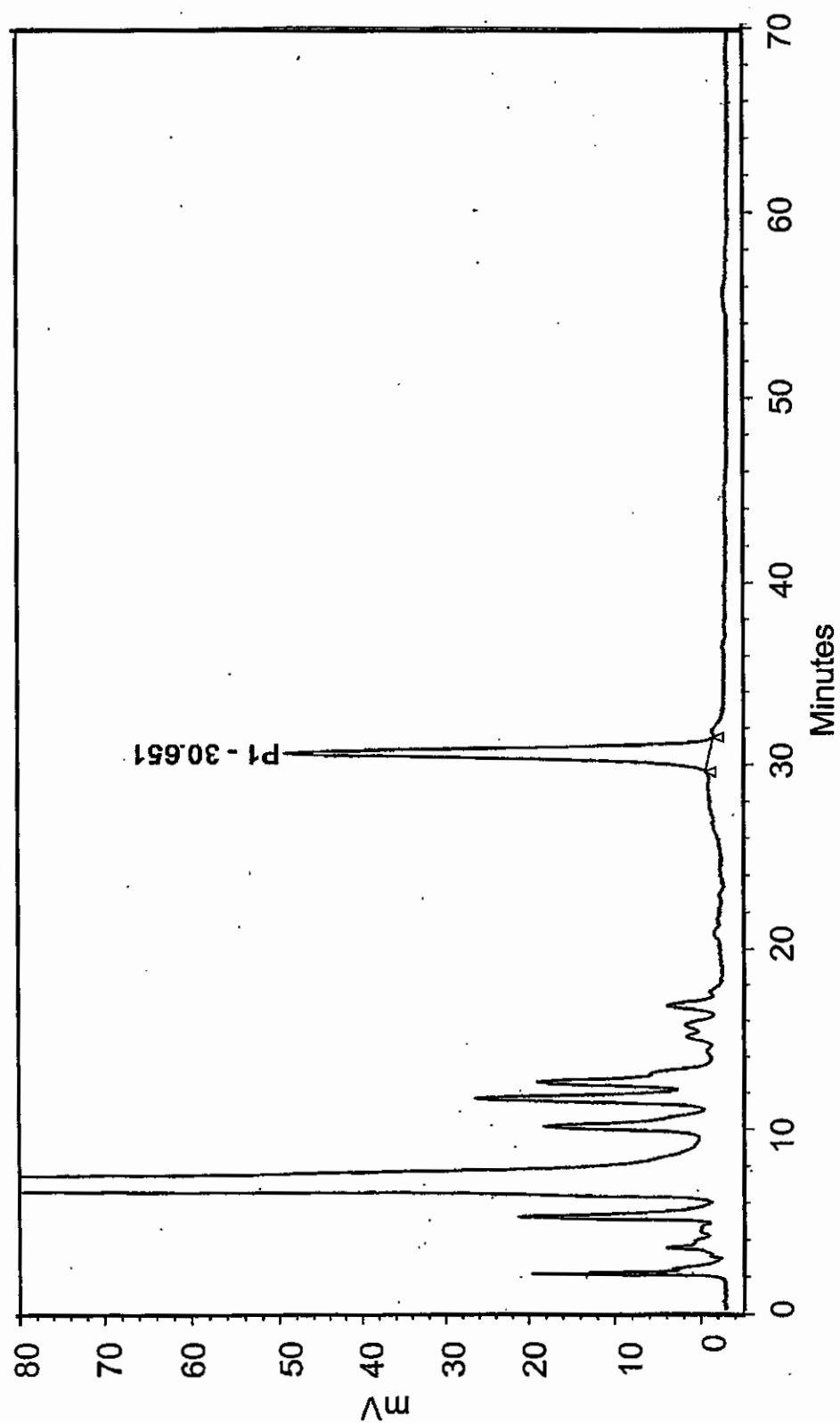


FIG. 91

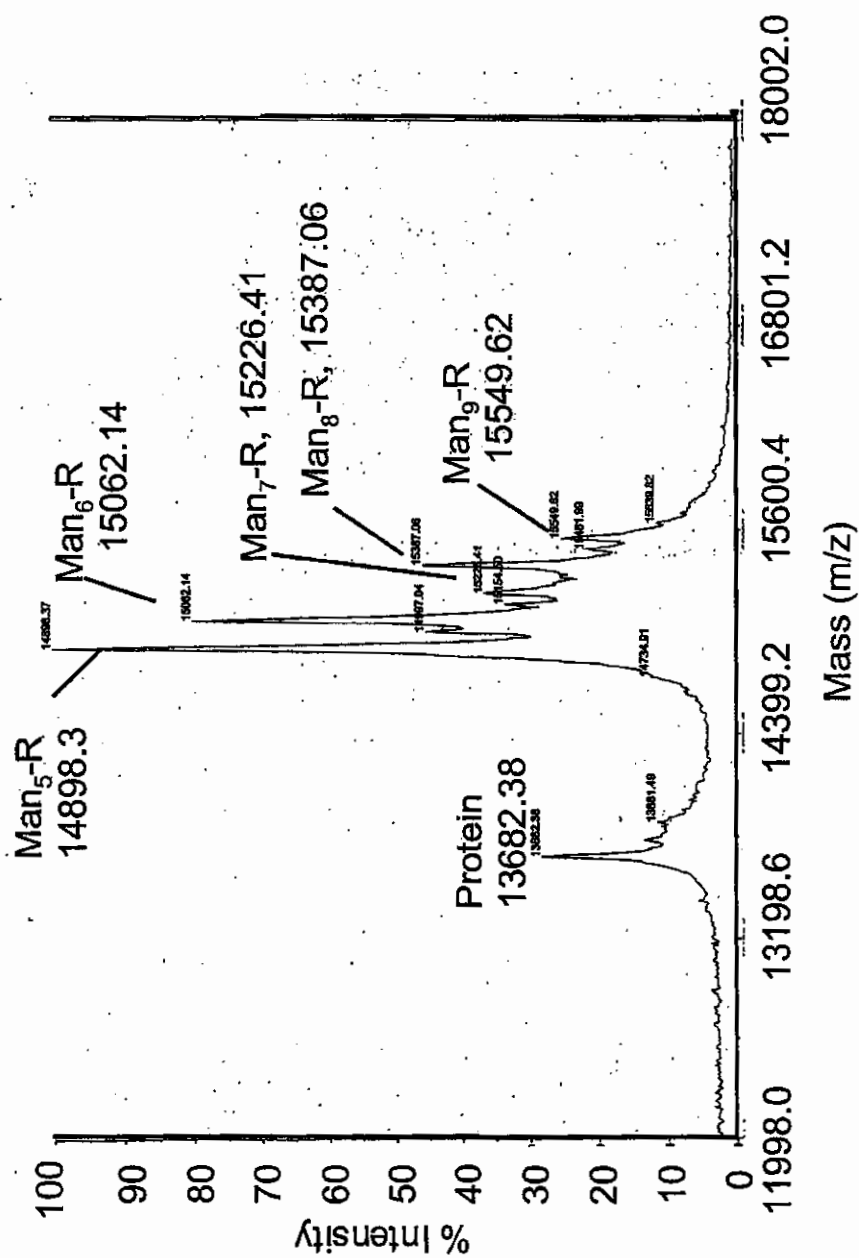


FIG. 92A

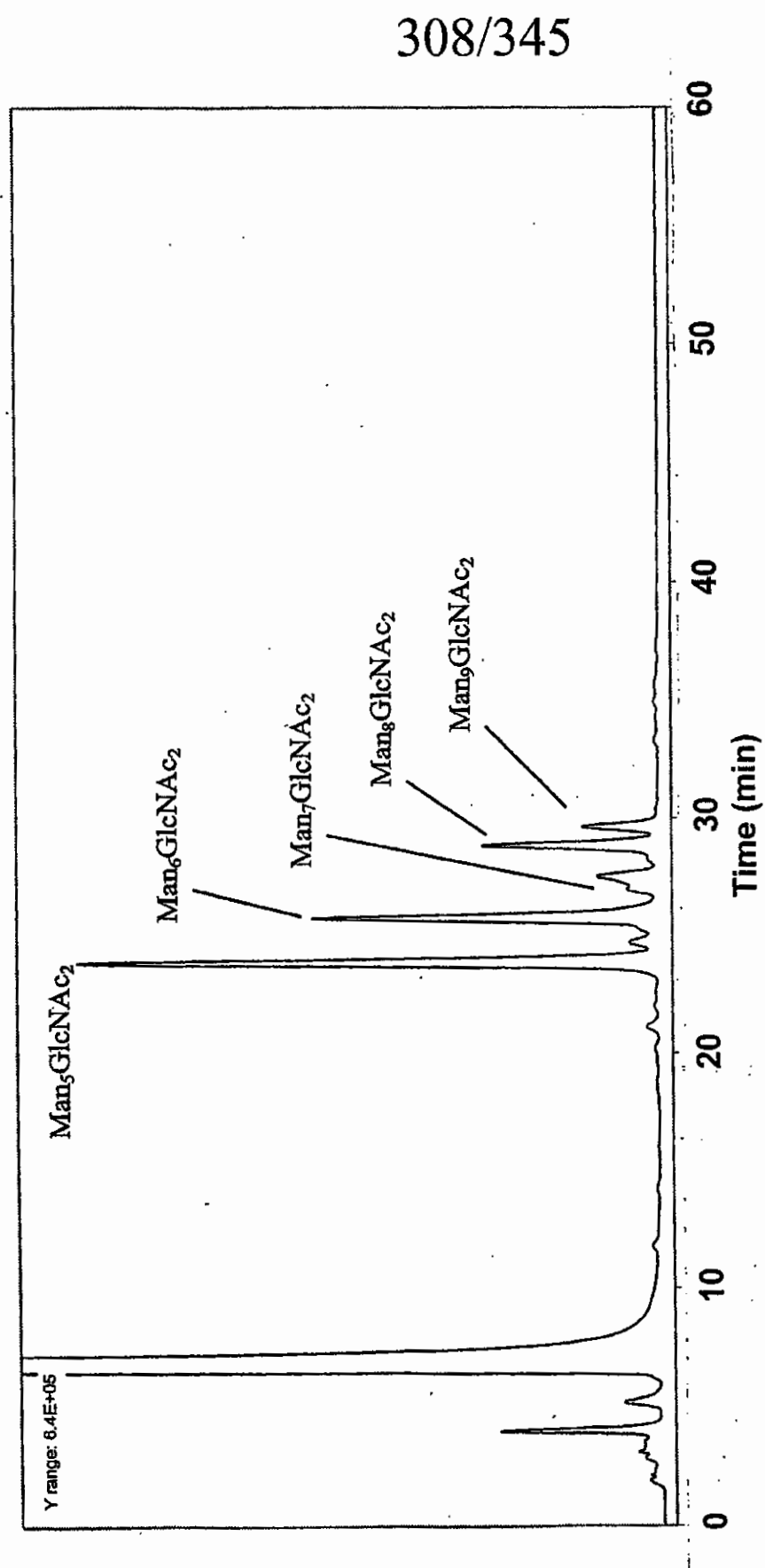


FIG. 92B

309/345

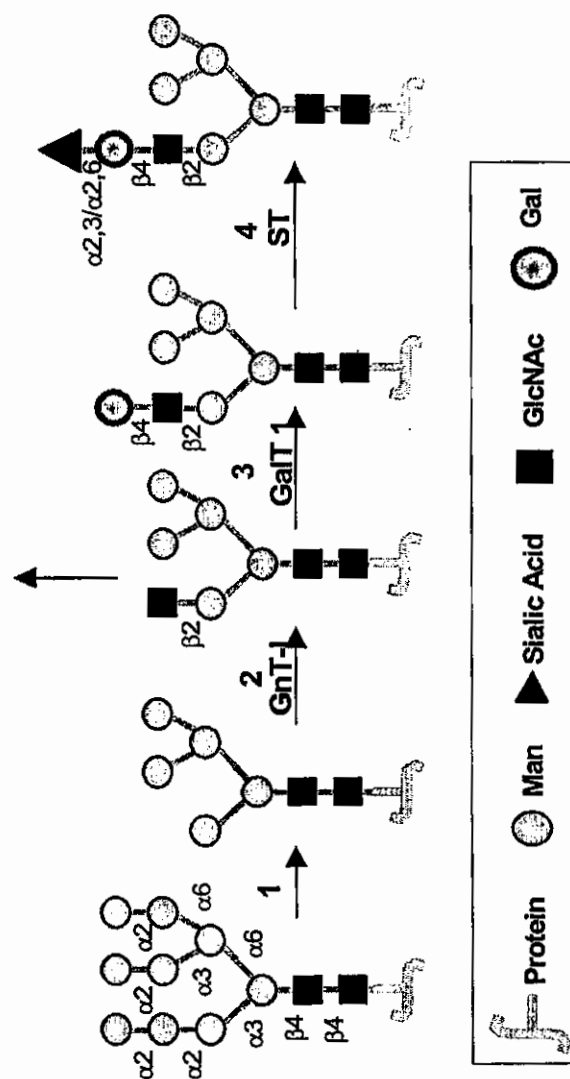
Bisected Hybrid
N-Glycans

FIG. 93

310/345

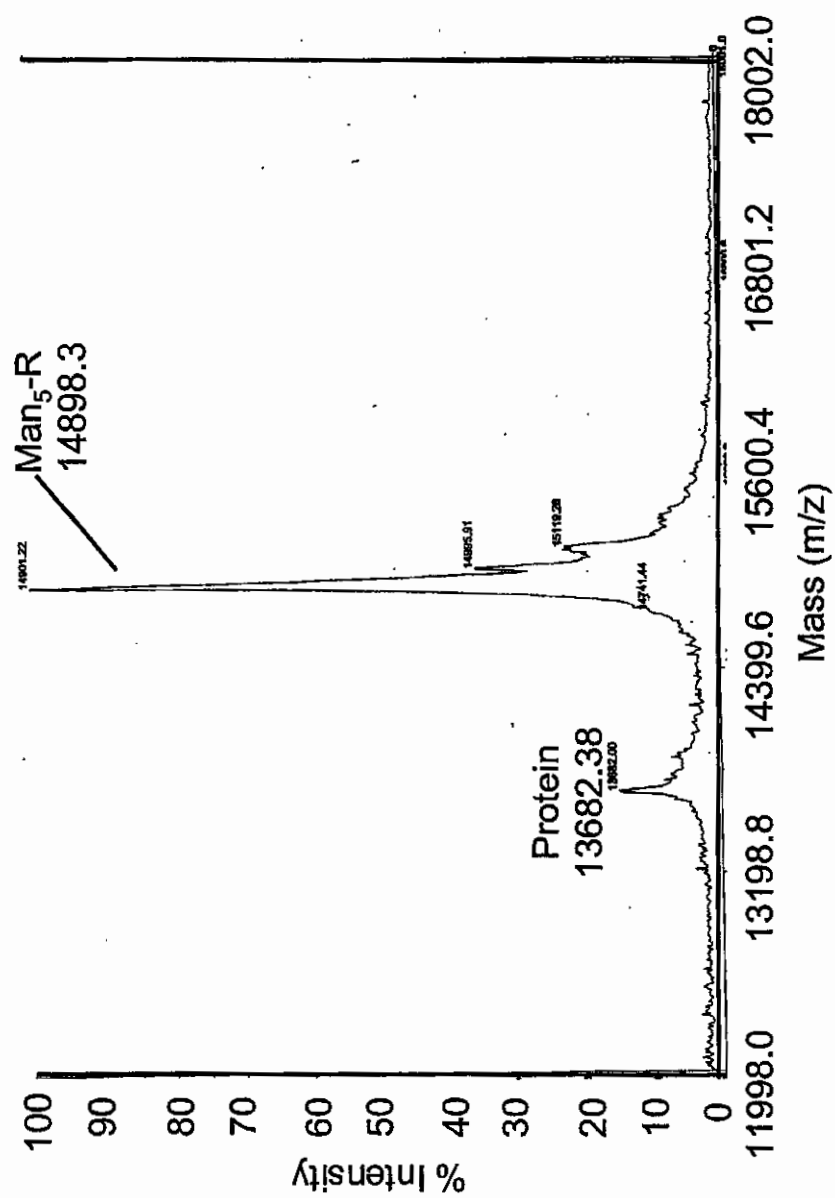


FIG. 94A

311/345

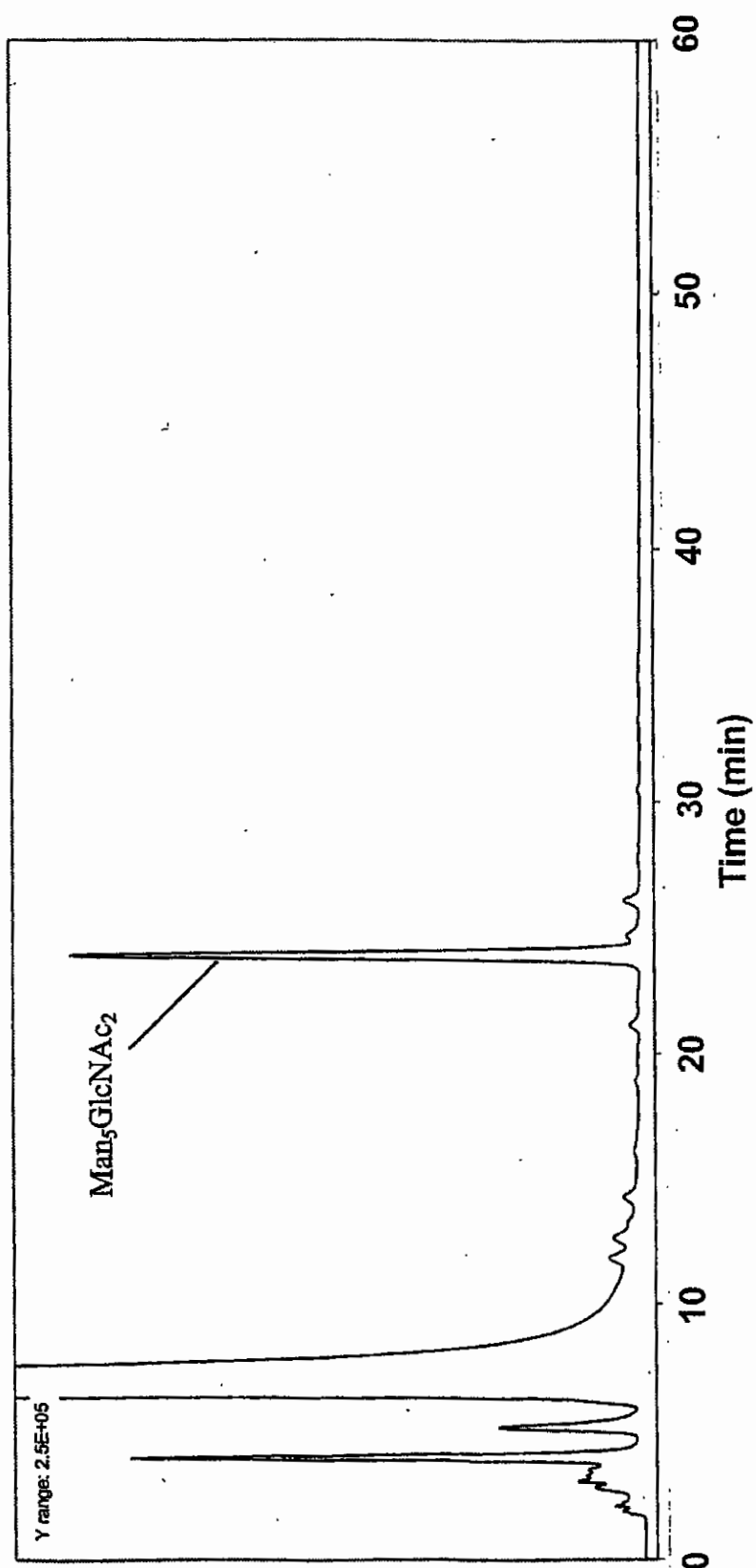


FIG. 94B

312/345

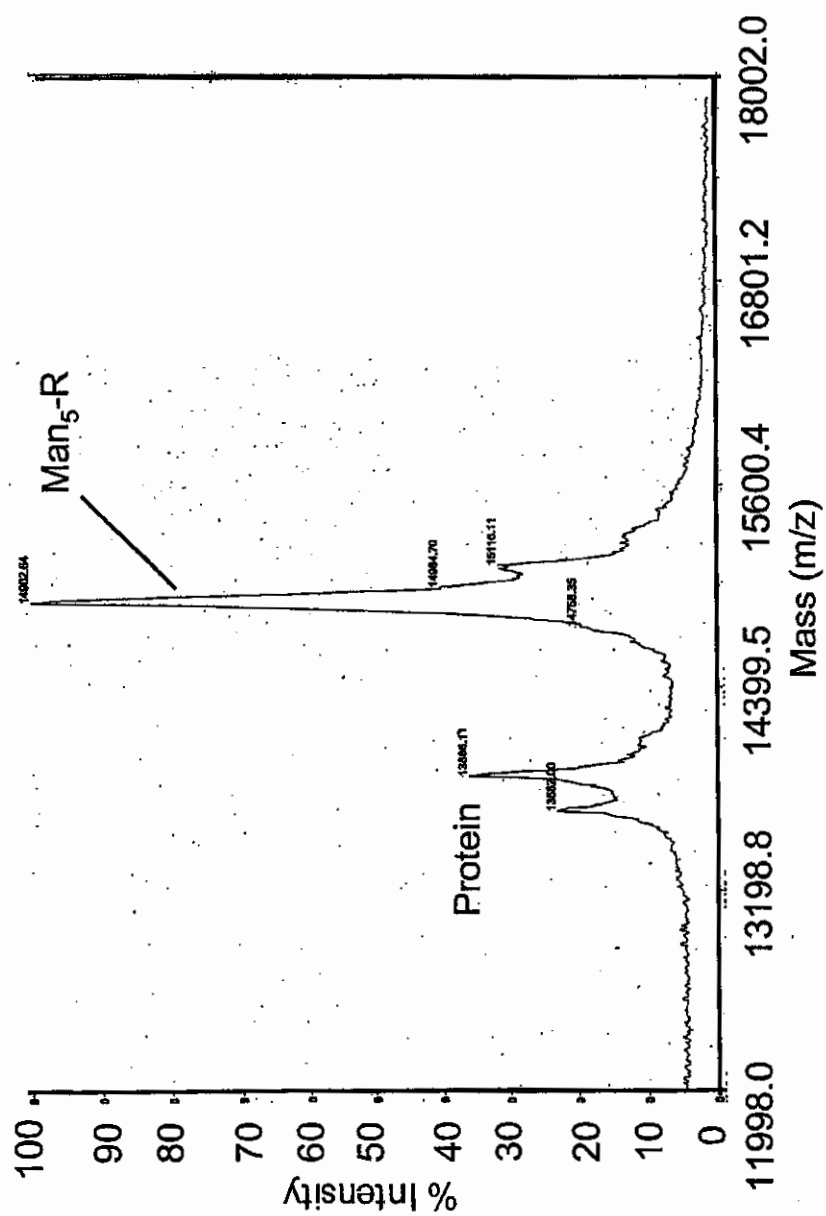


FIG. 95

313/345

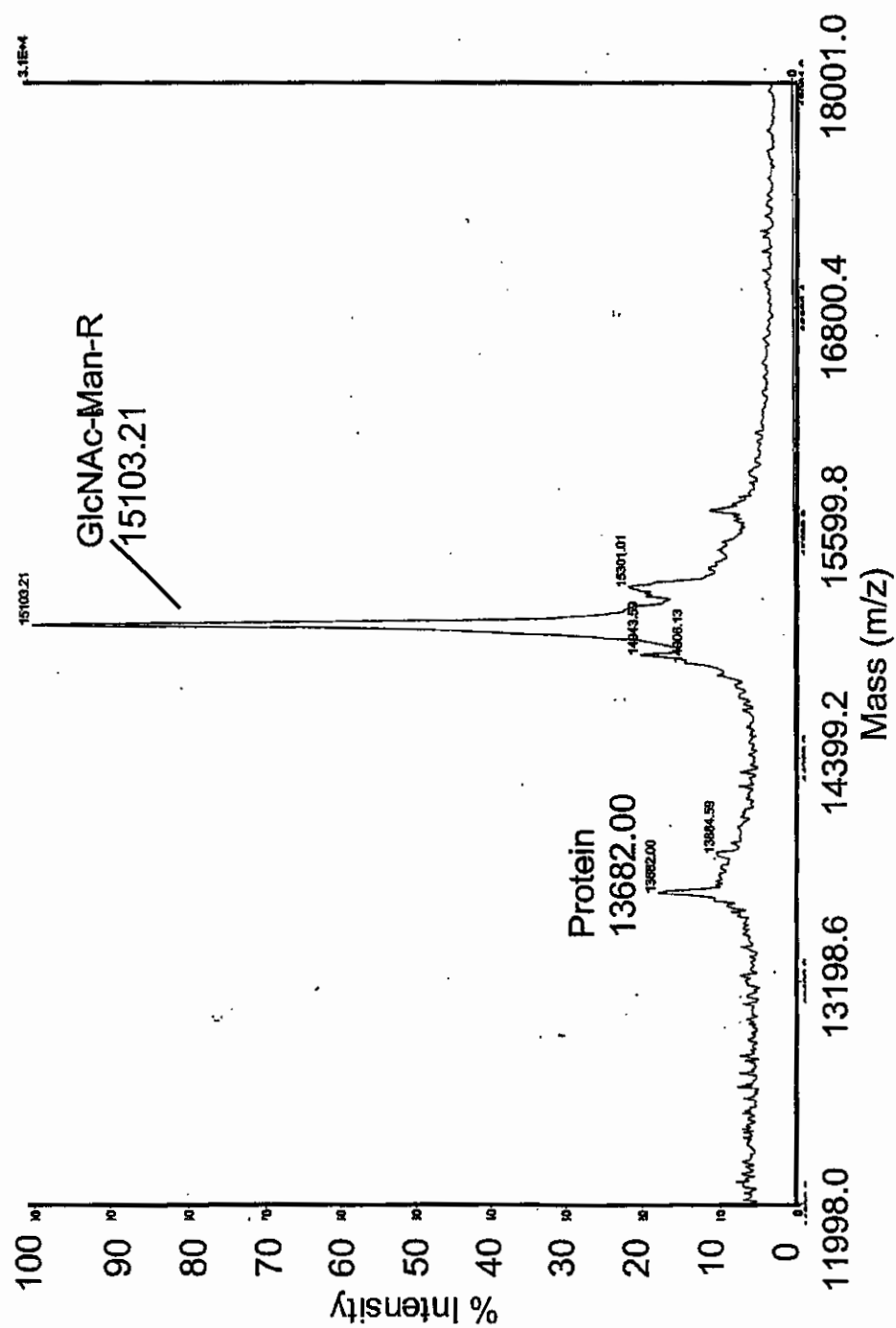


FIG. 96

314/345

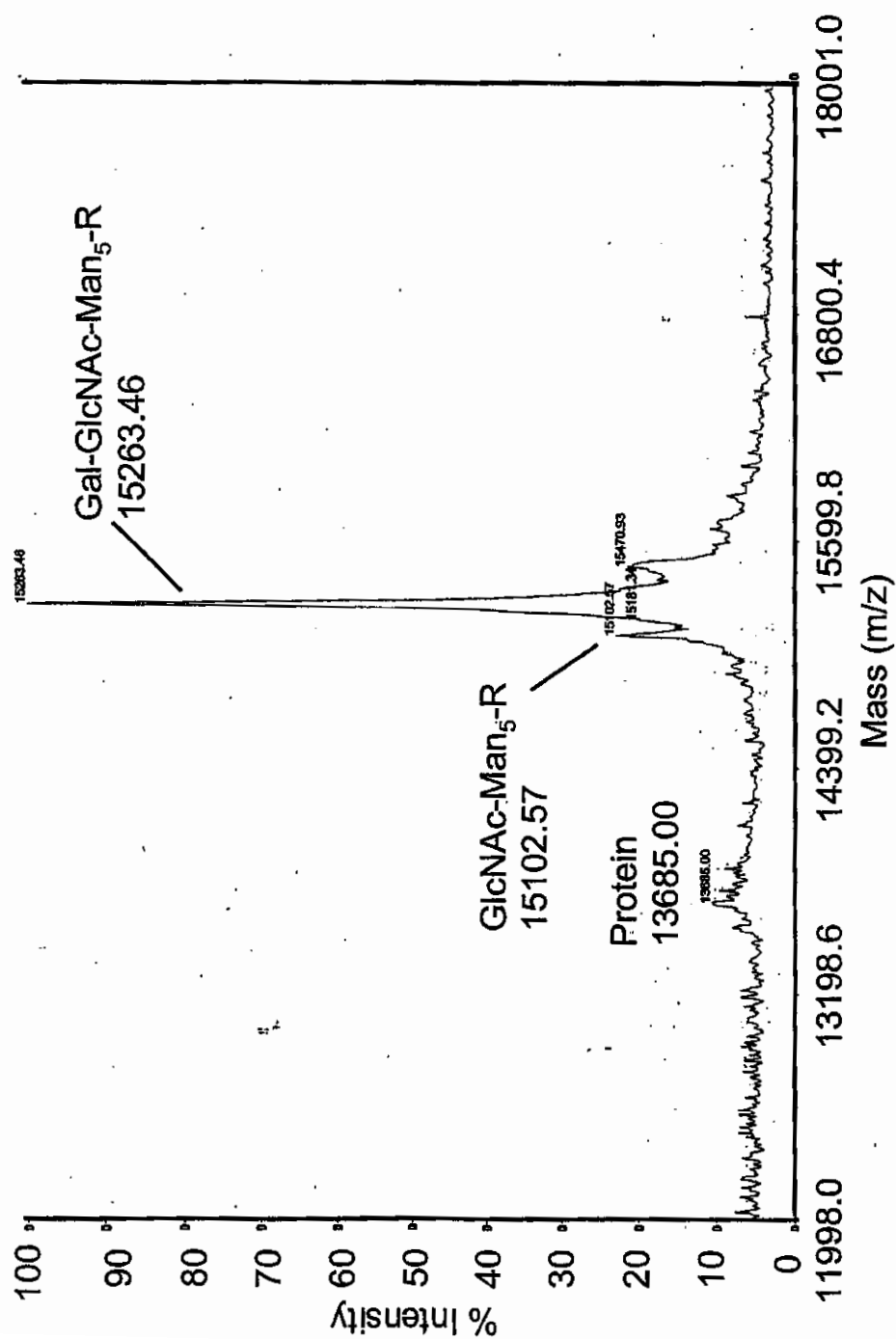


FIG. 97

315/345

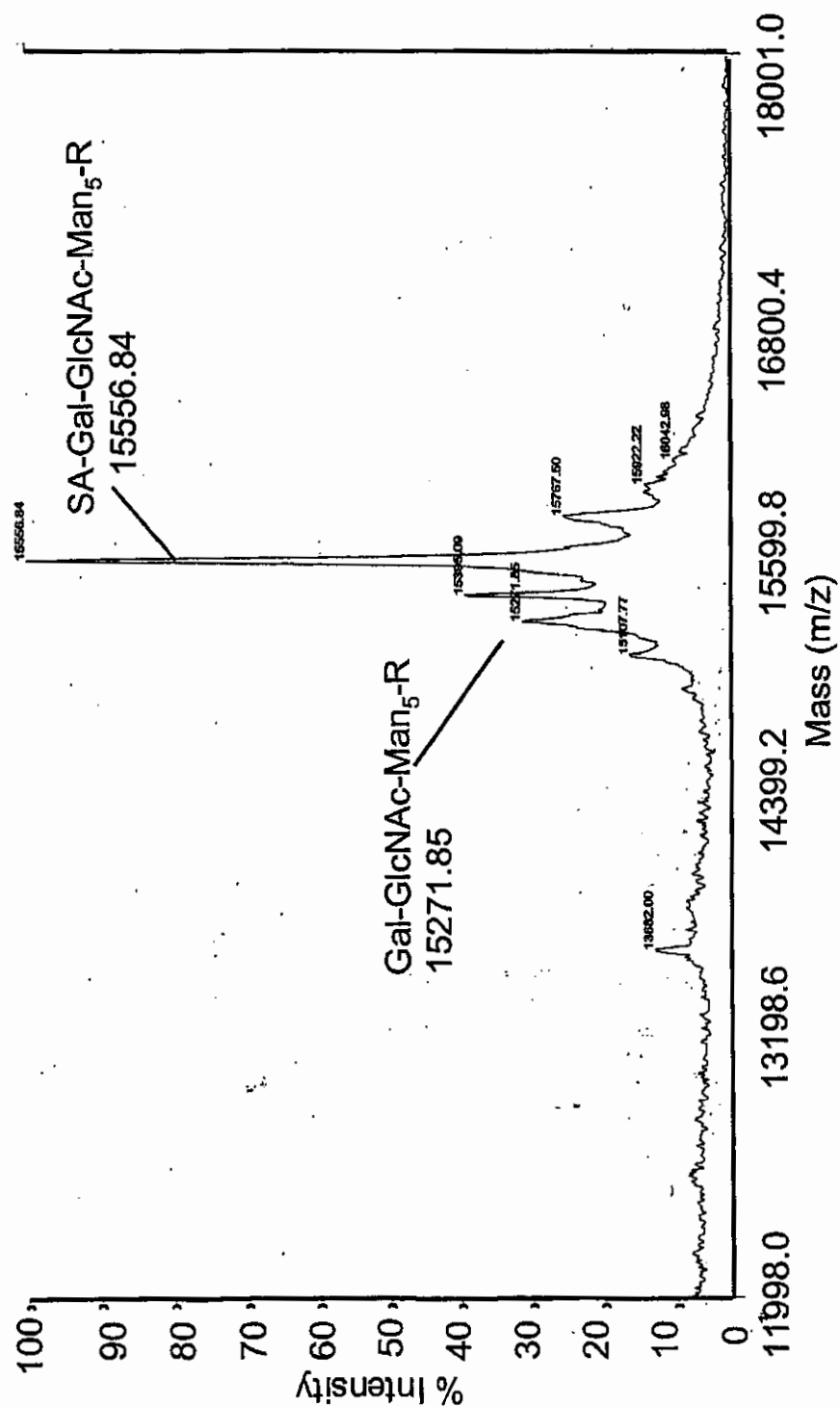


FIG. 98

316/345

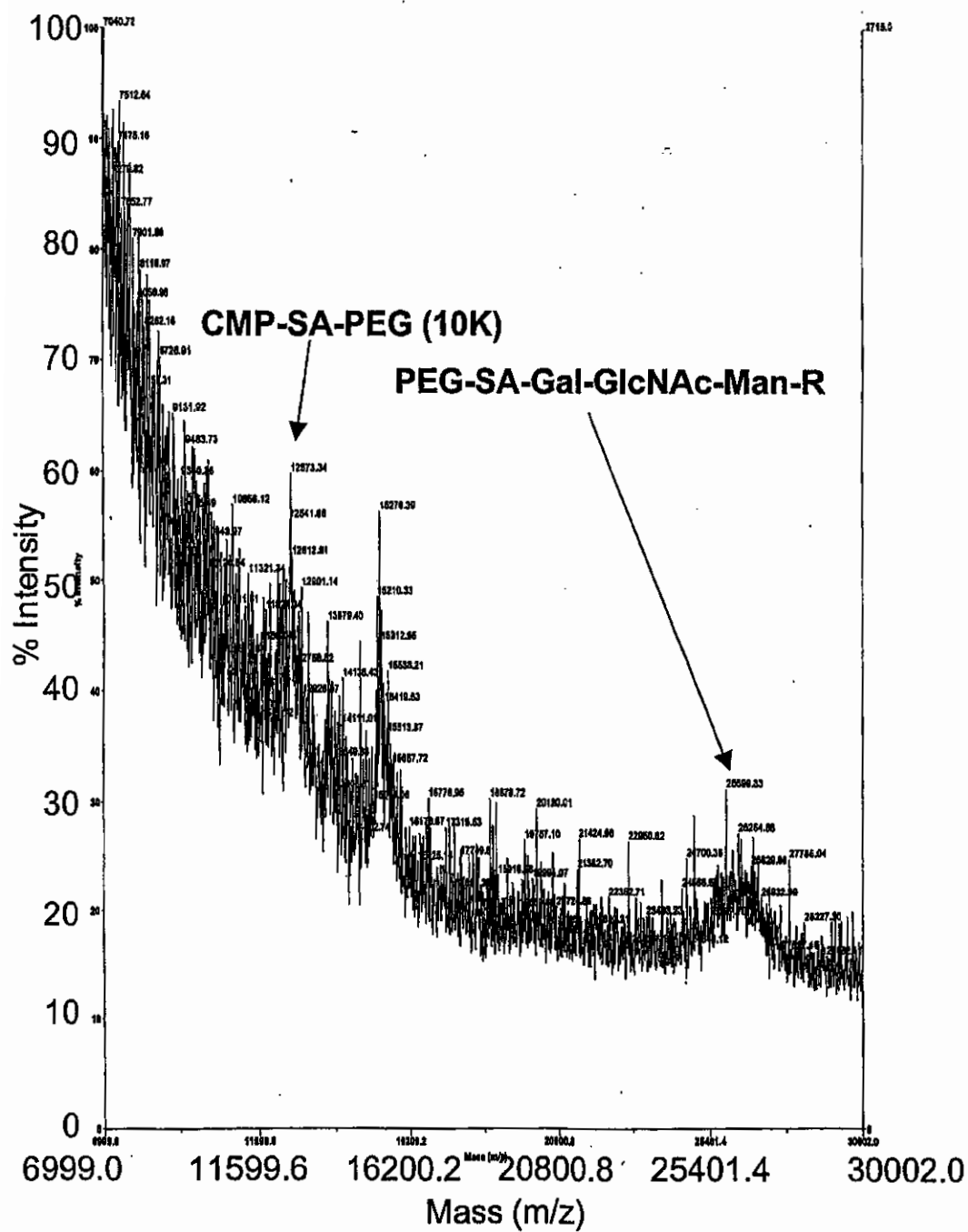


FIG. 99A

318/345

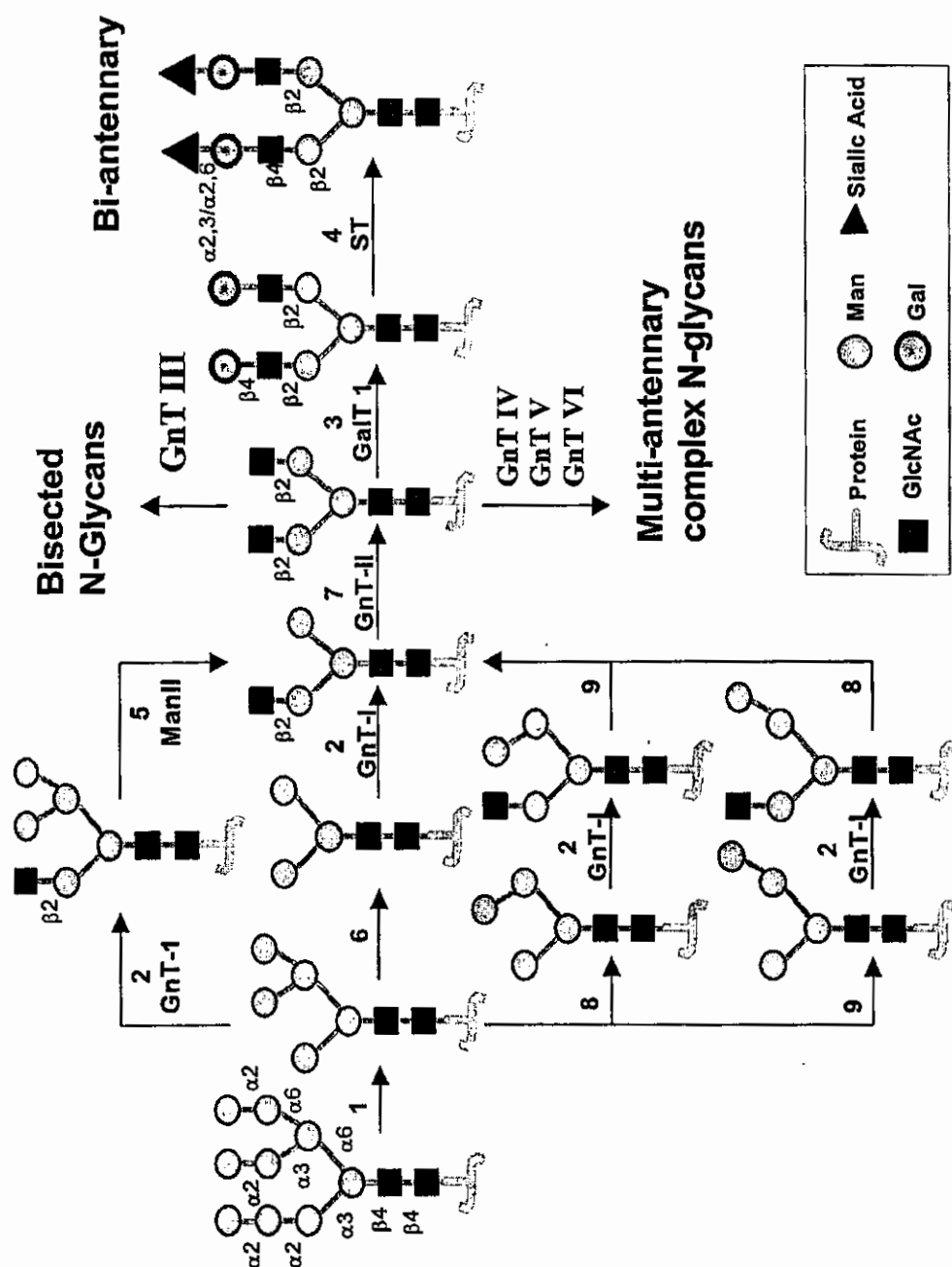


FIG. 100

319/345

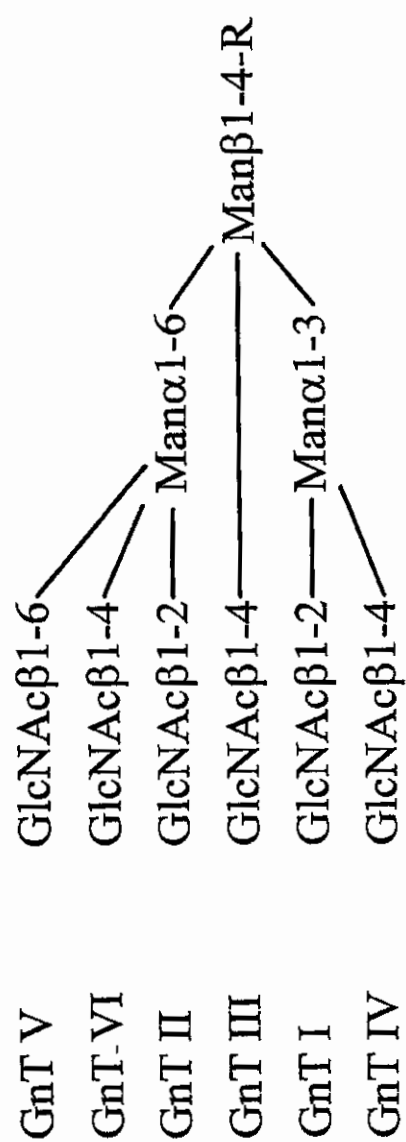


FIG. 101

320/345

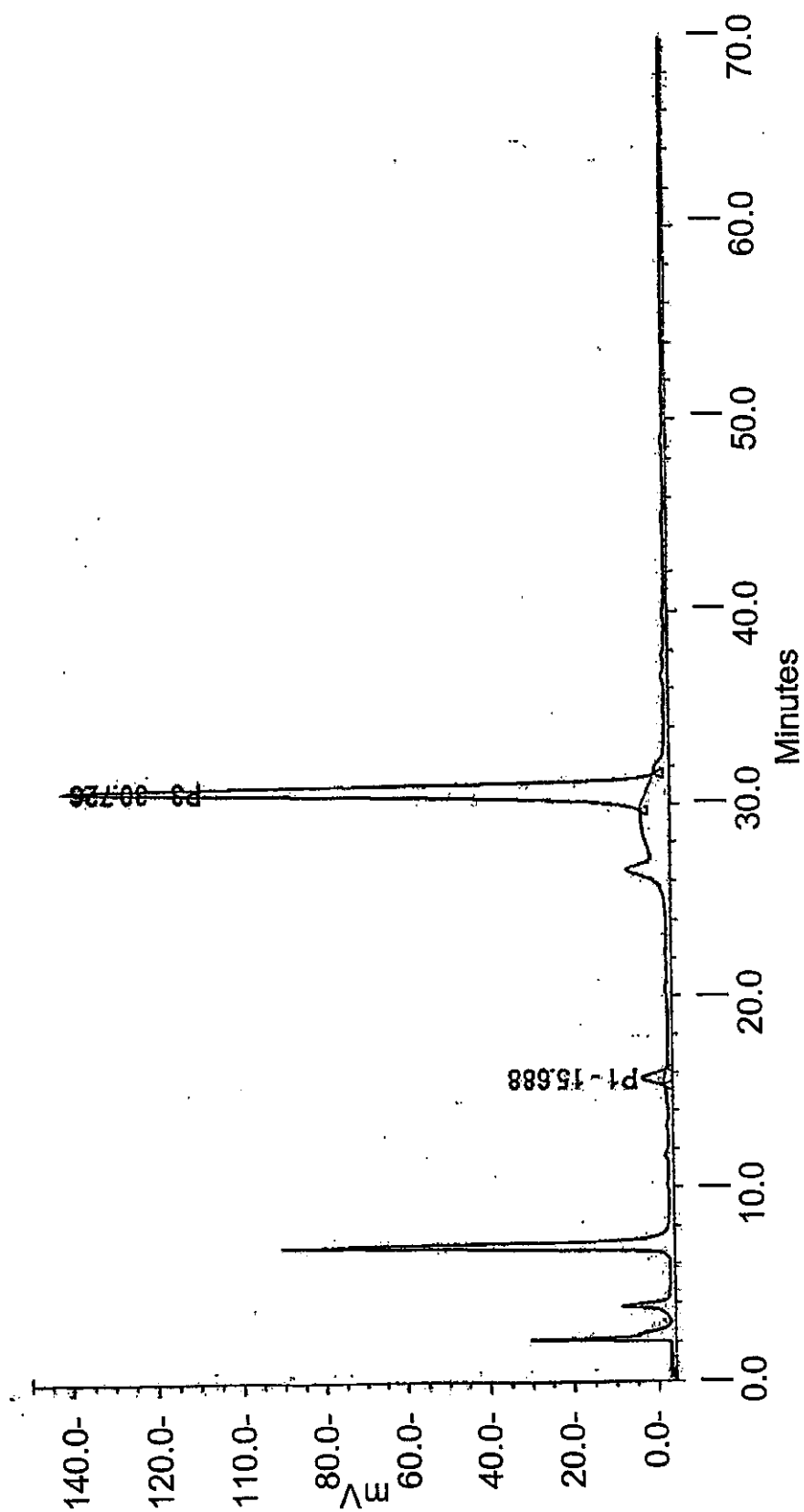


FIG. 102A

321/345

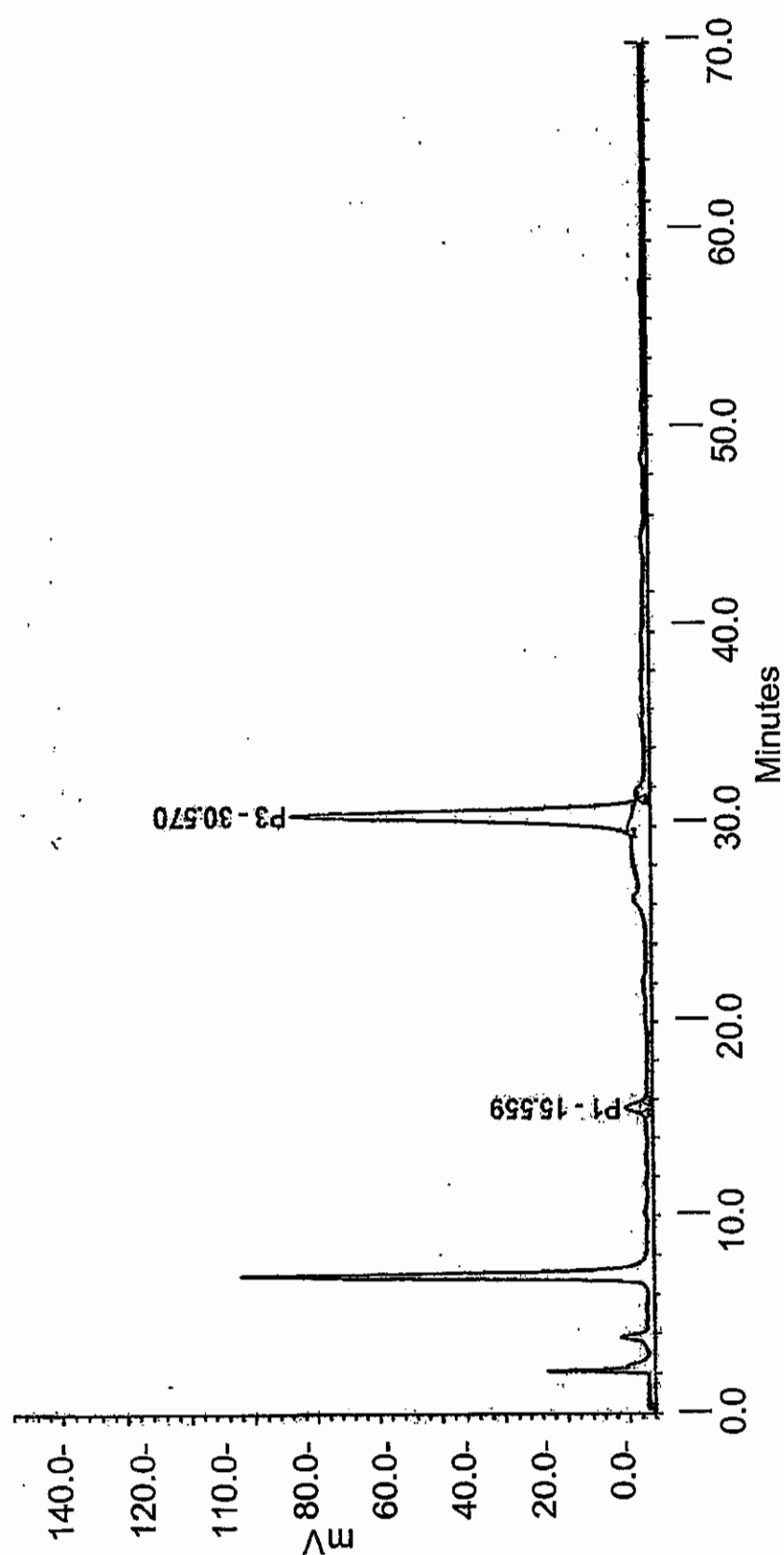


FIG. 102B

322/345

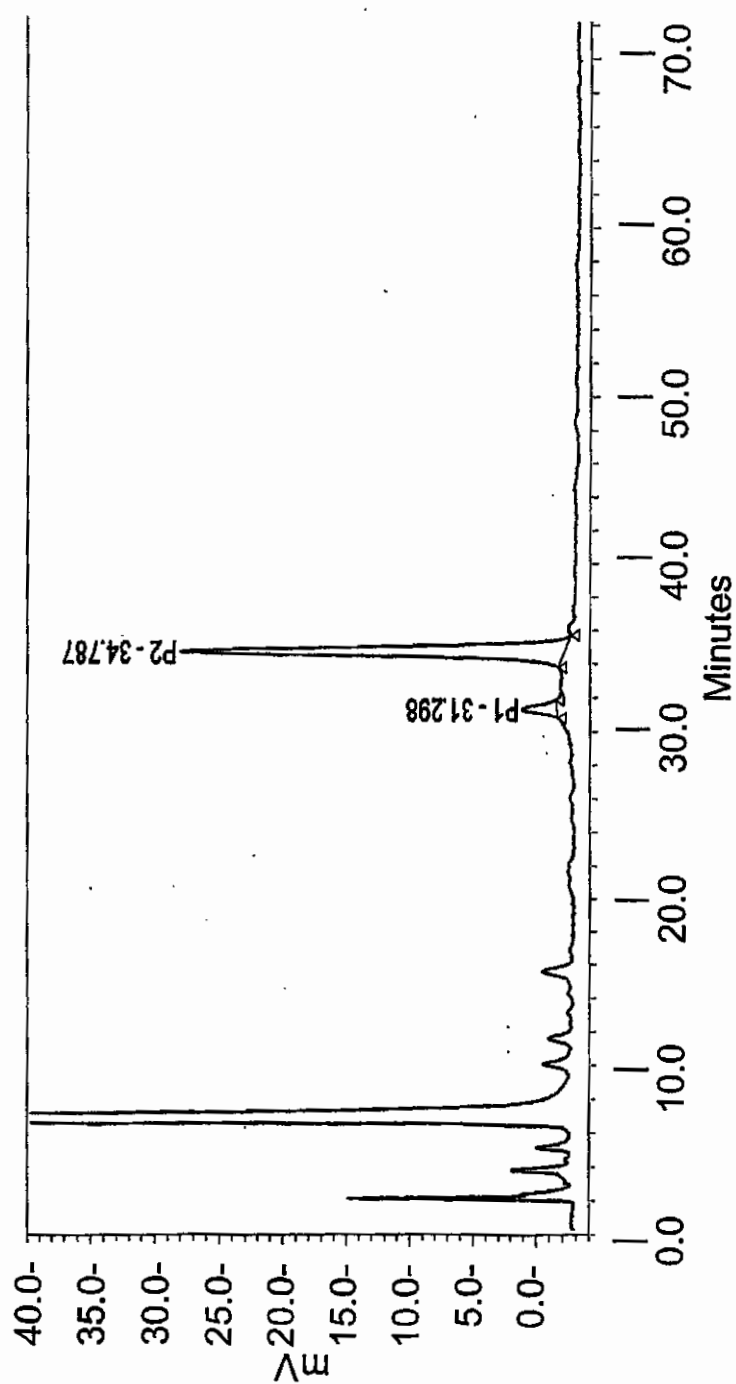


FIG. 103

323/345

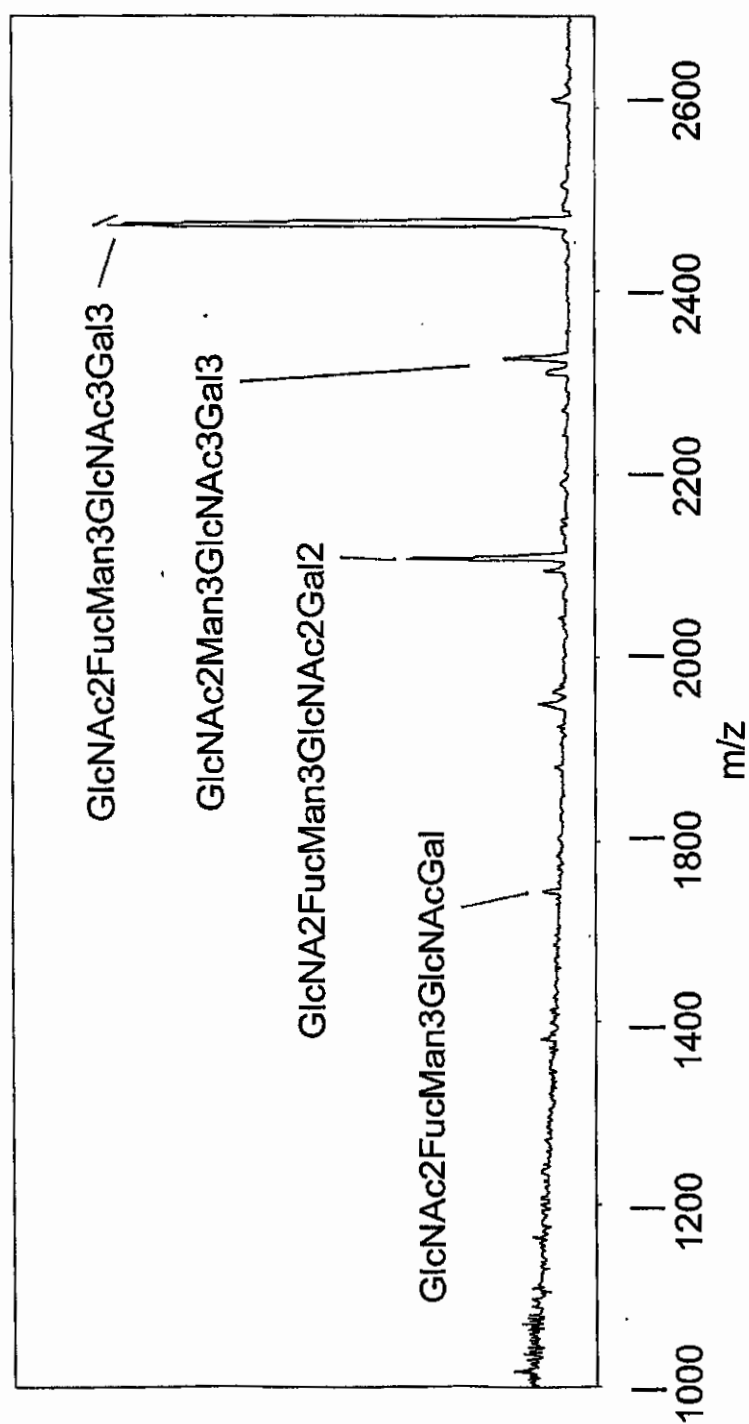


FIG. 104

324/345



FIG. 105

325/345

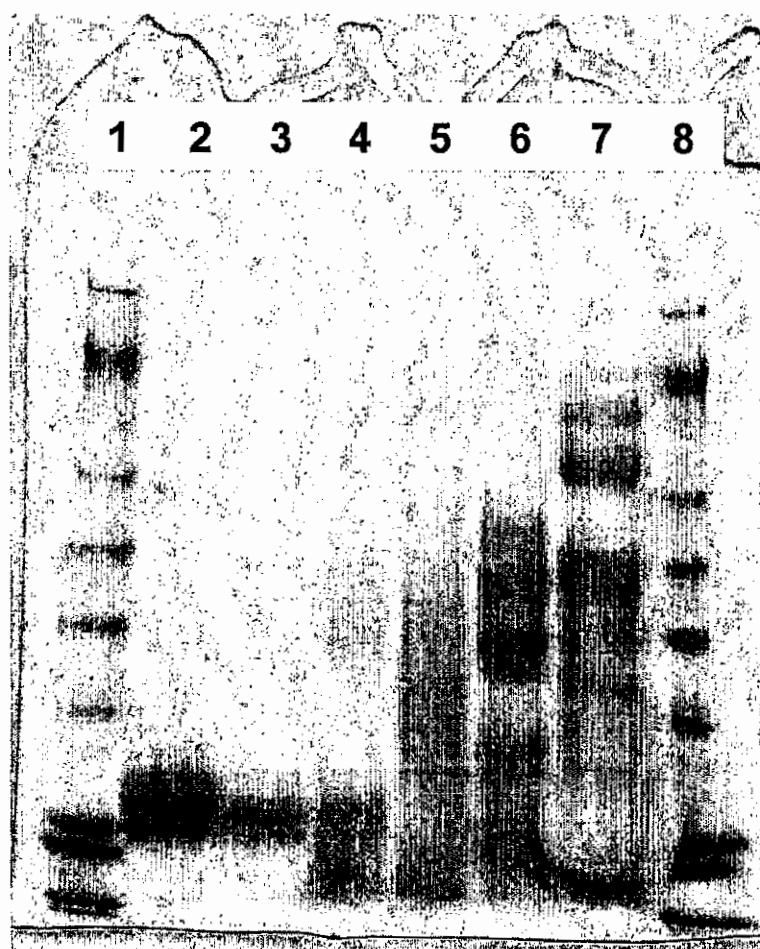


FIG. 106

326/345

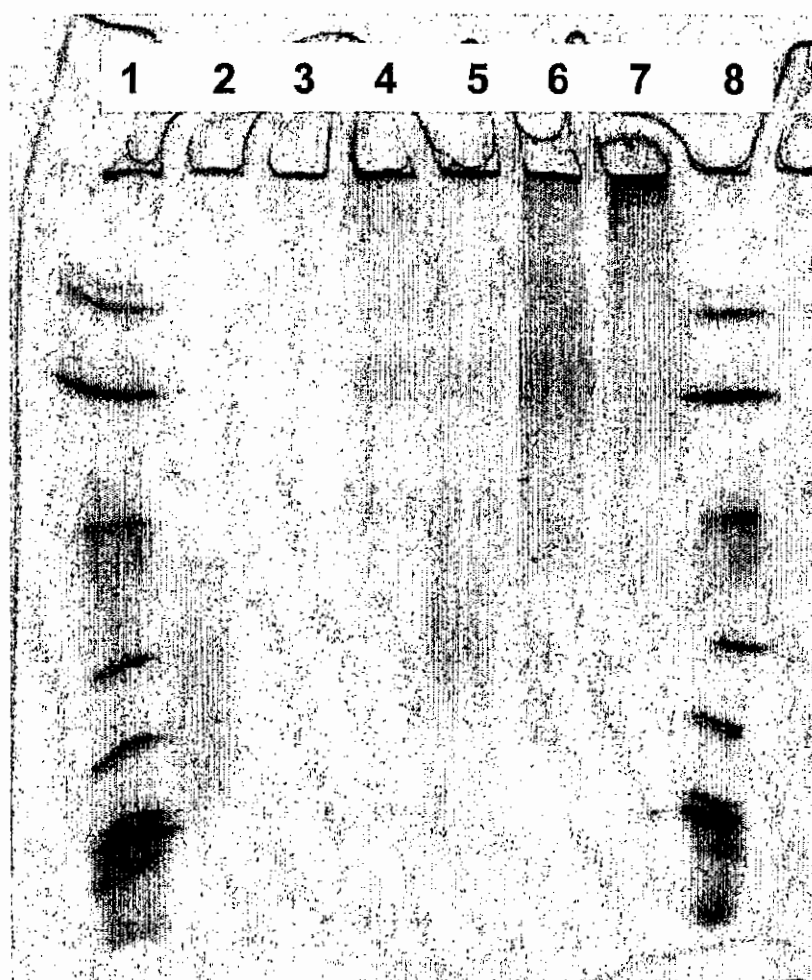


FIG. 107

327/345

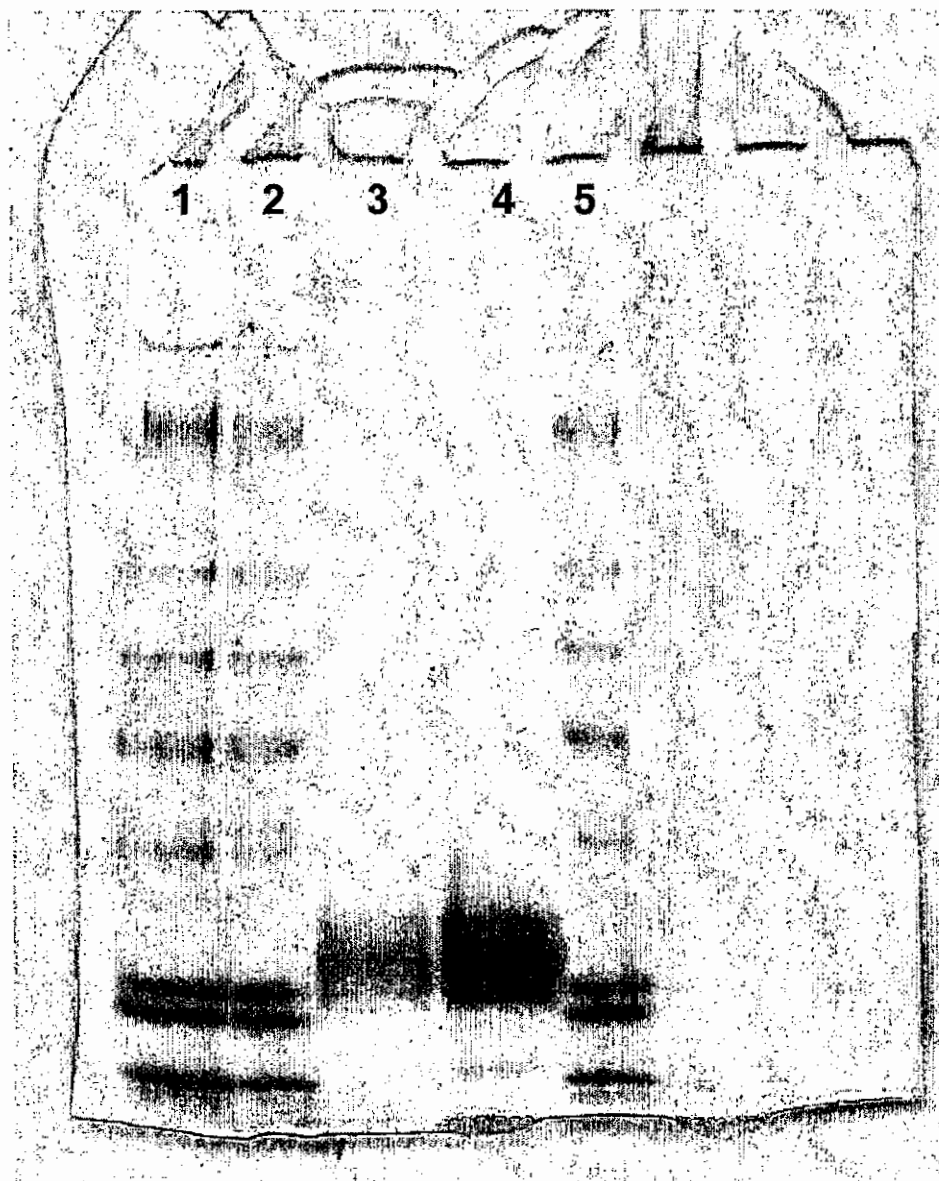


FIG. 108

328/345



FIG. 109

329/345

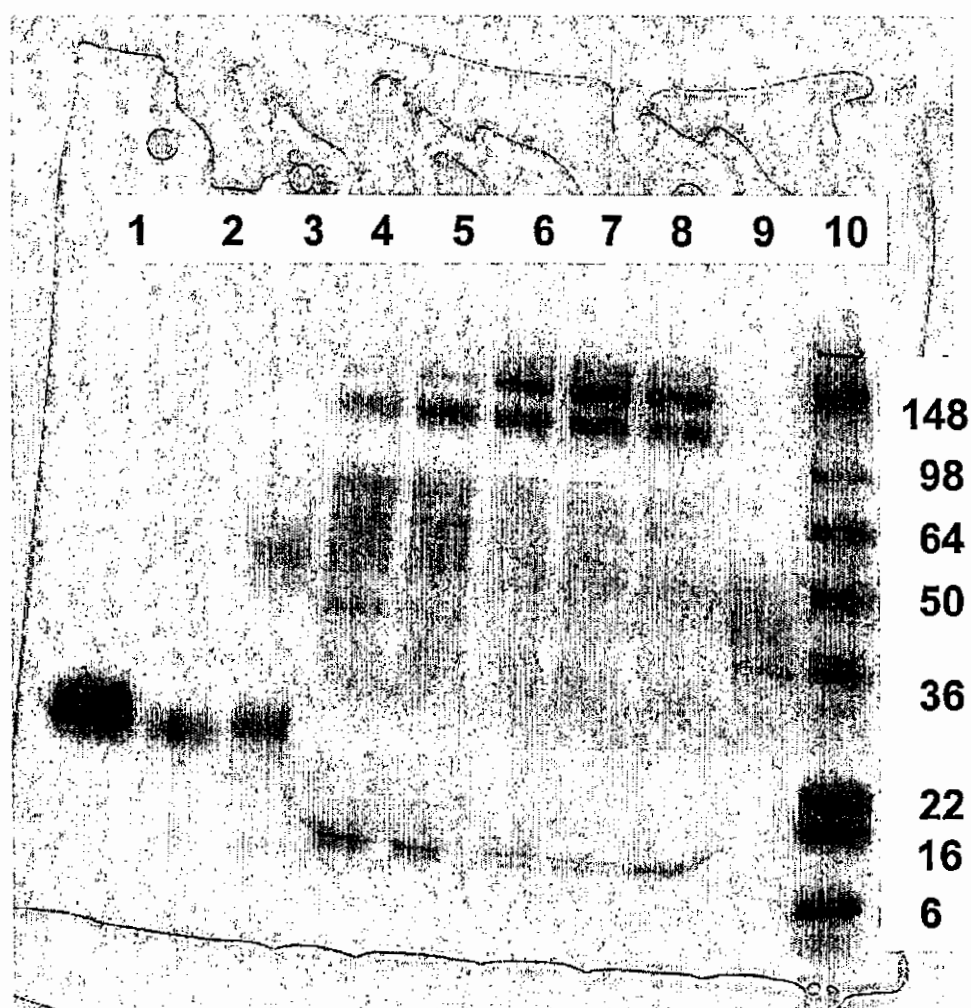


FIG. 110

330/345

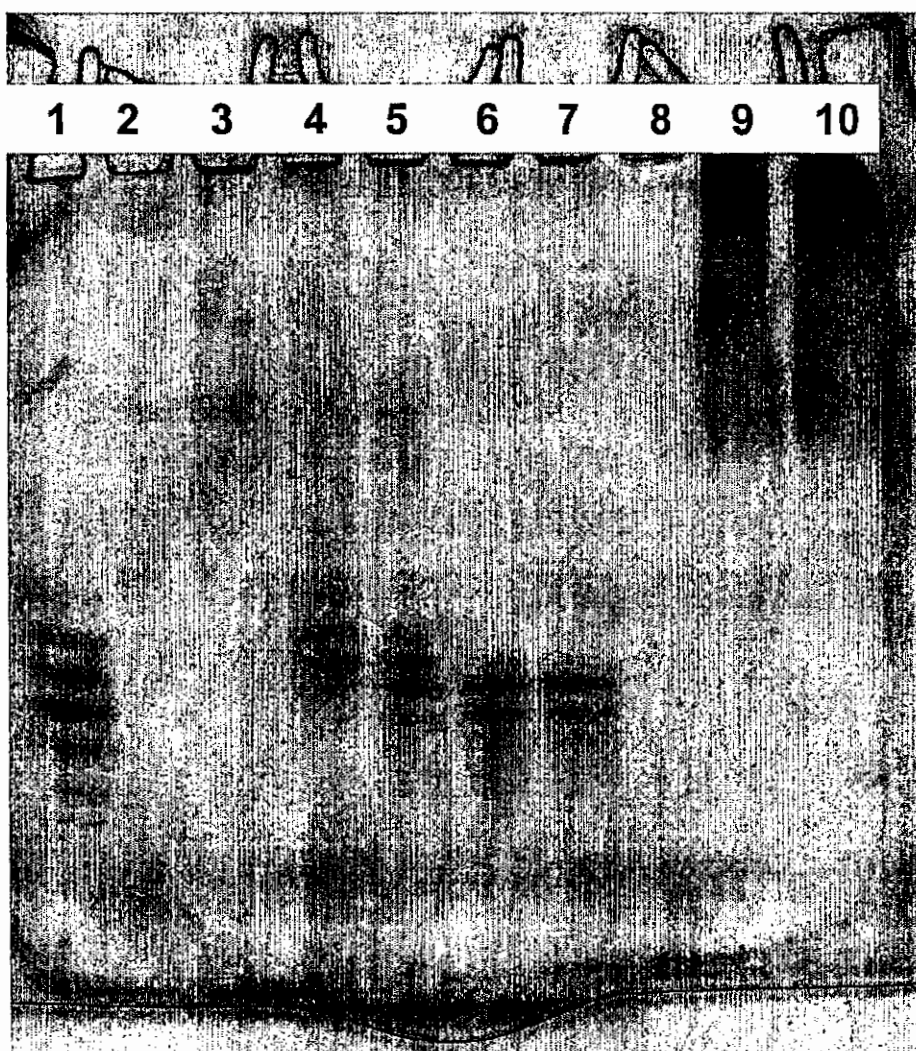


FIG. 111

331/345

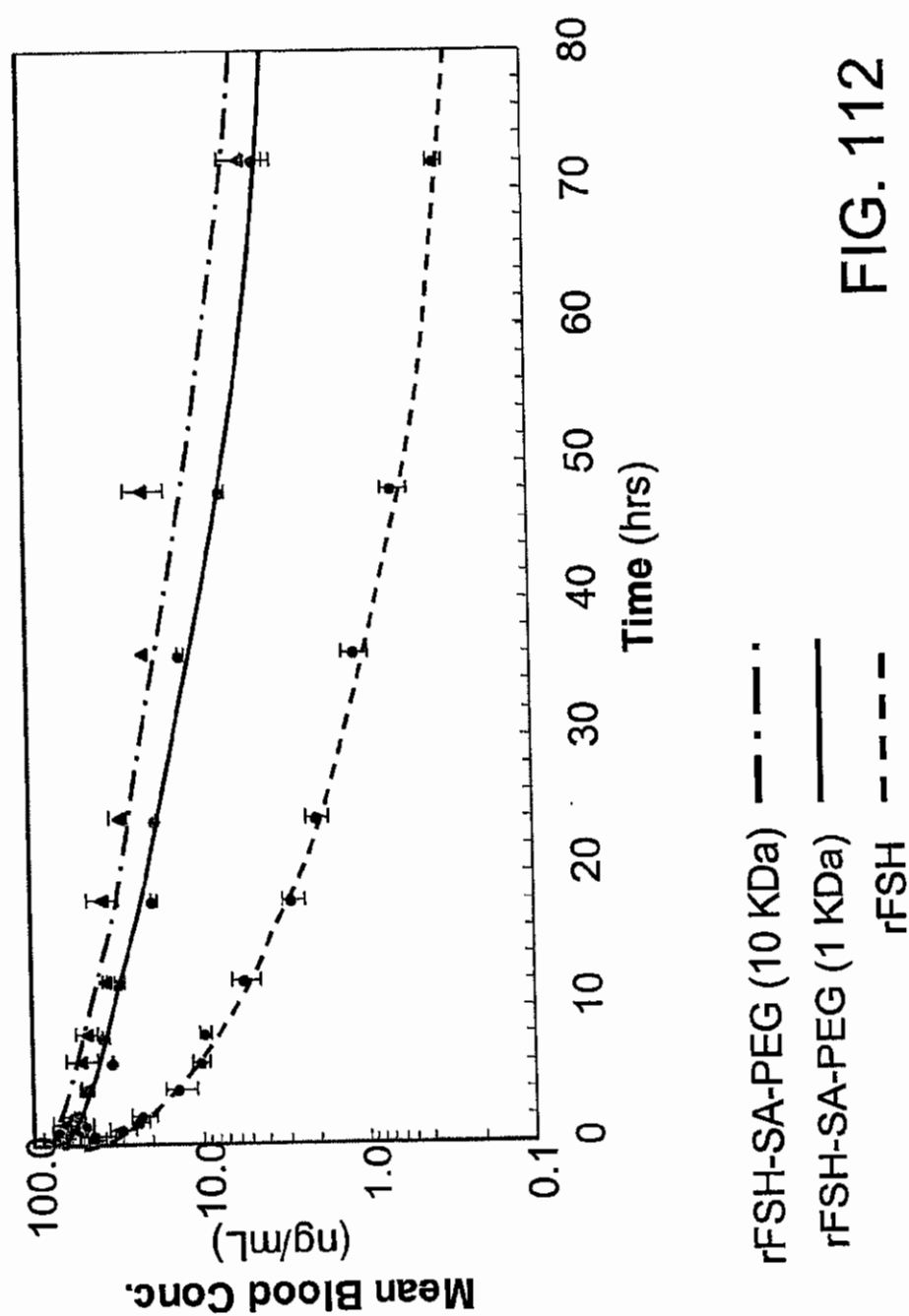


FIG. 112

332/345

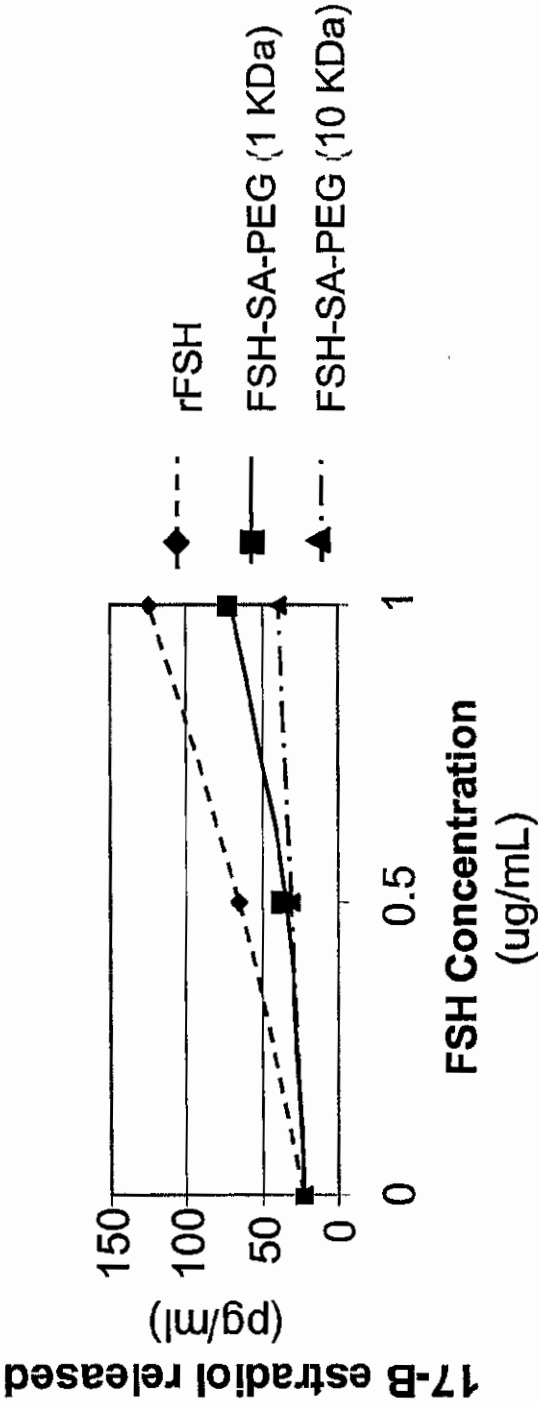


FIG. 113

333/345

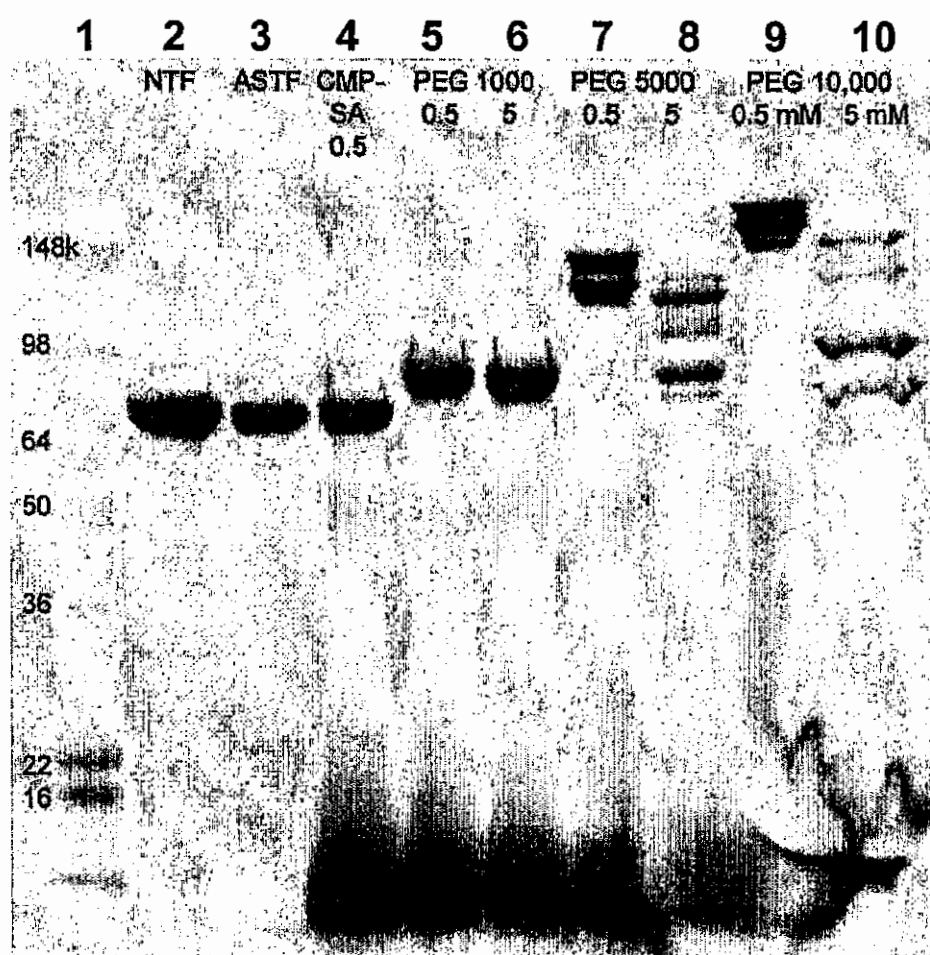


FIG. 114

334/345

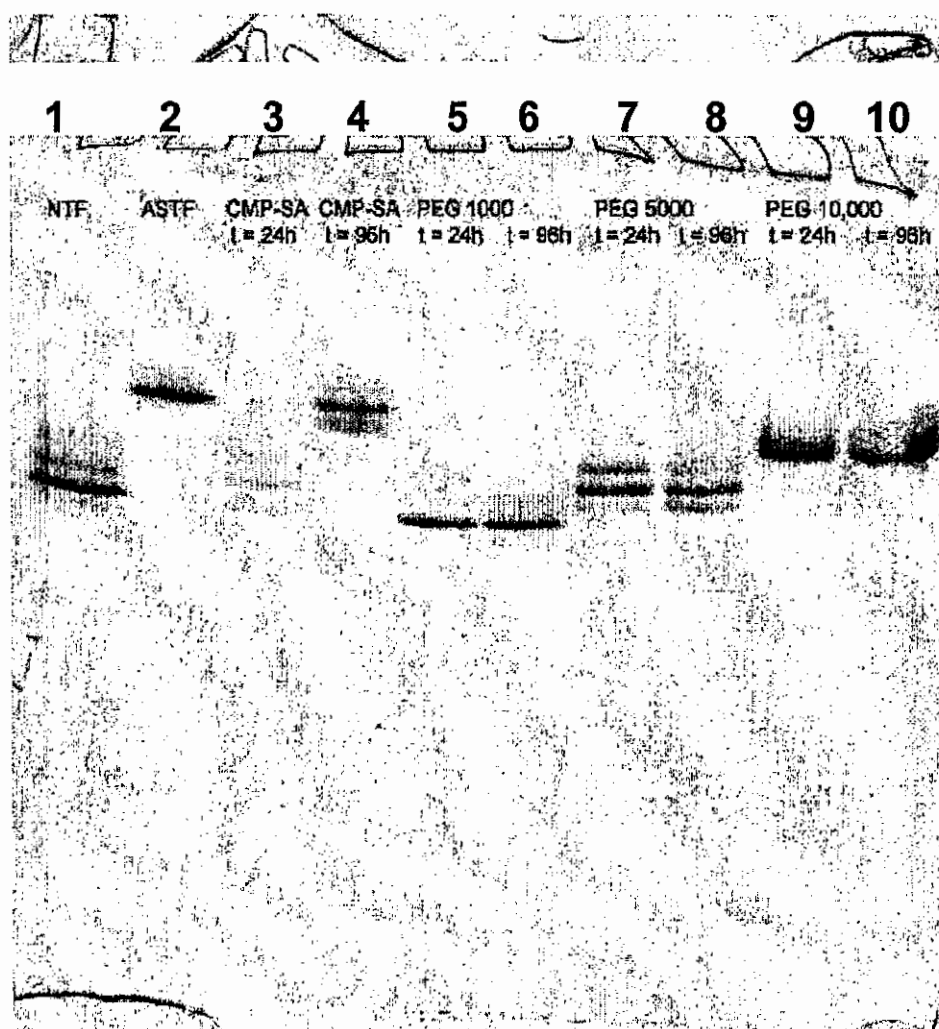


FIG. 115

335/345

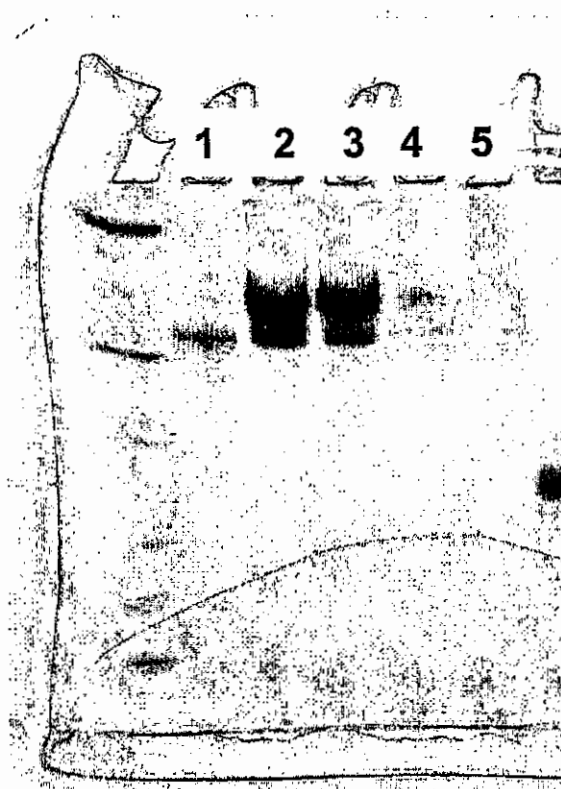


FIG. 116

336/345

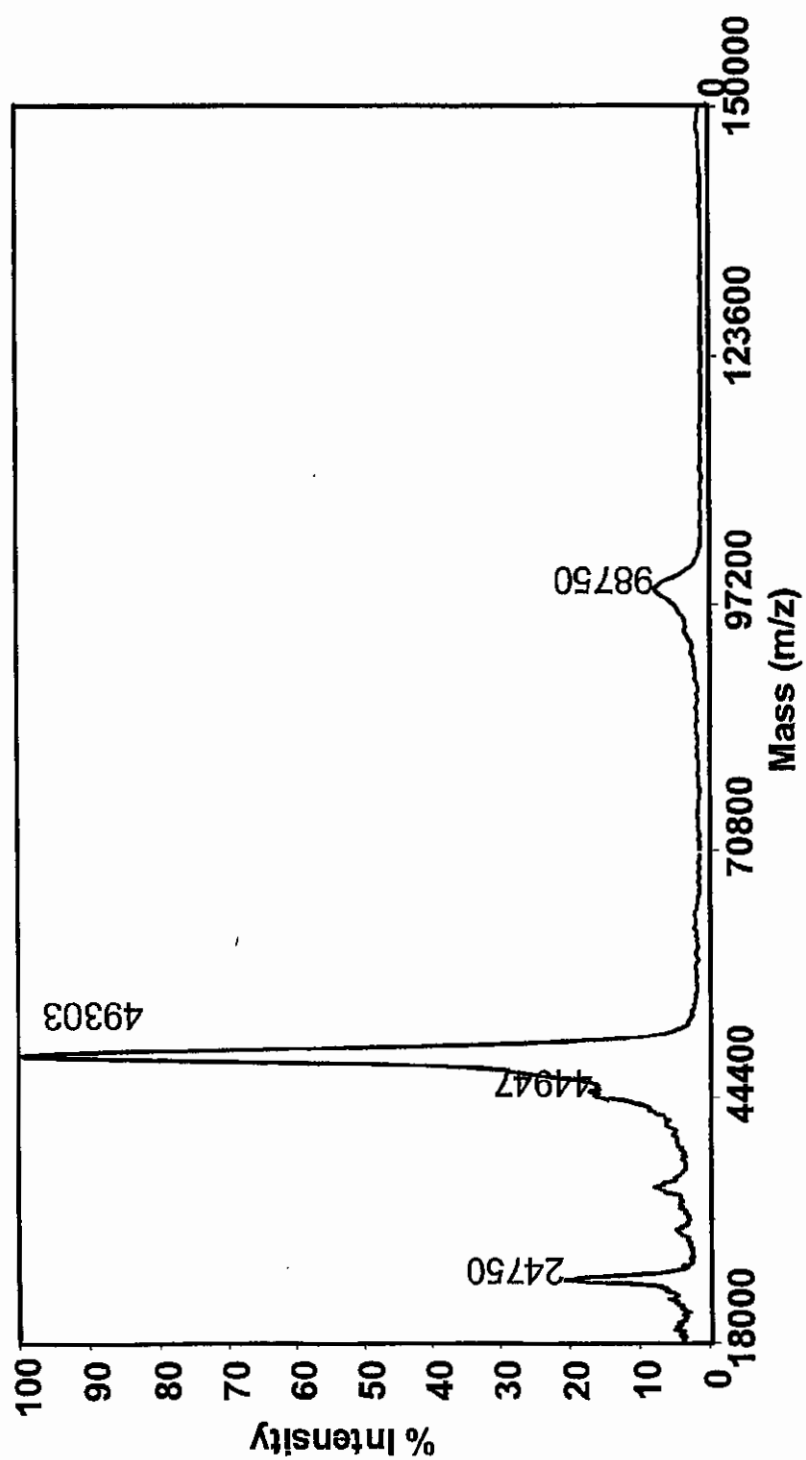


FIG. 117

337/345

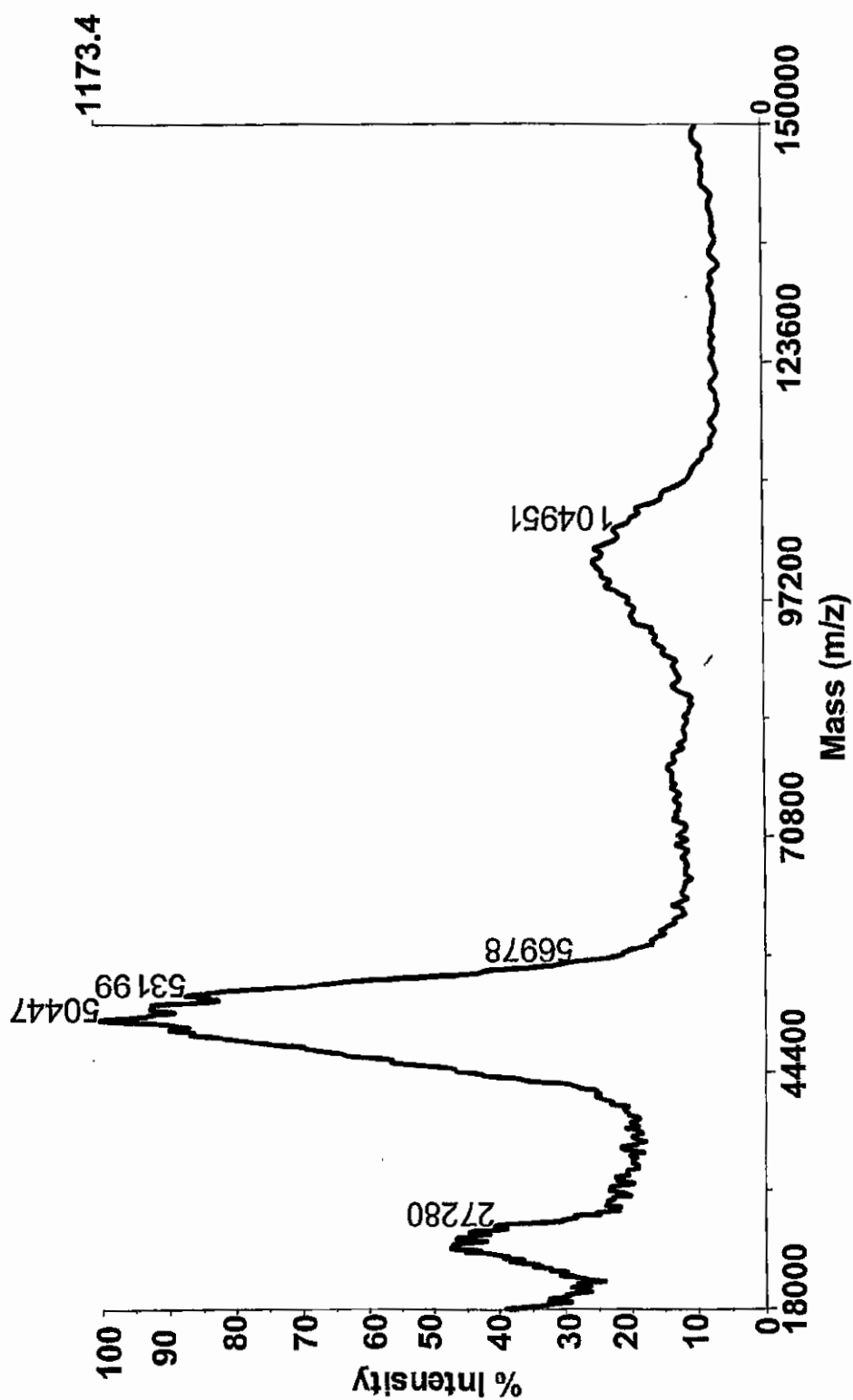


FIG. 118

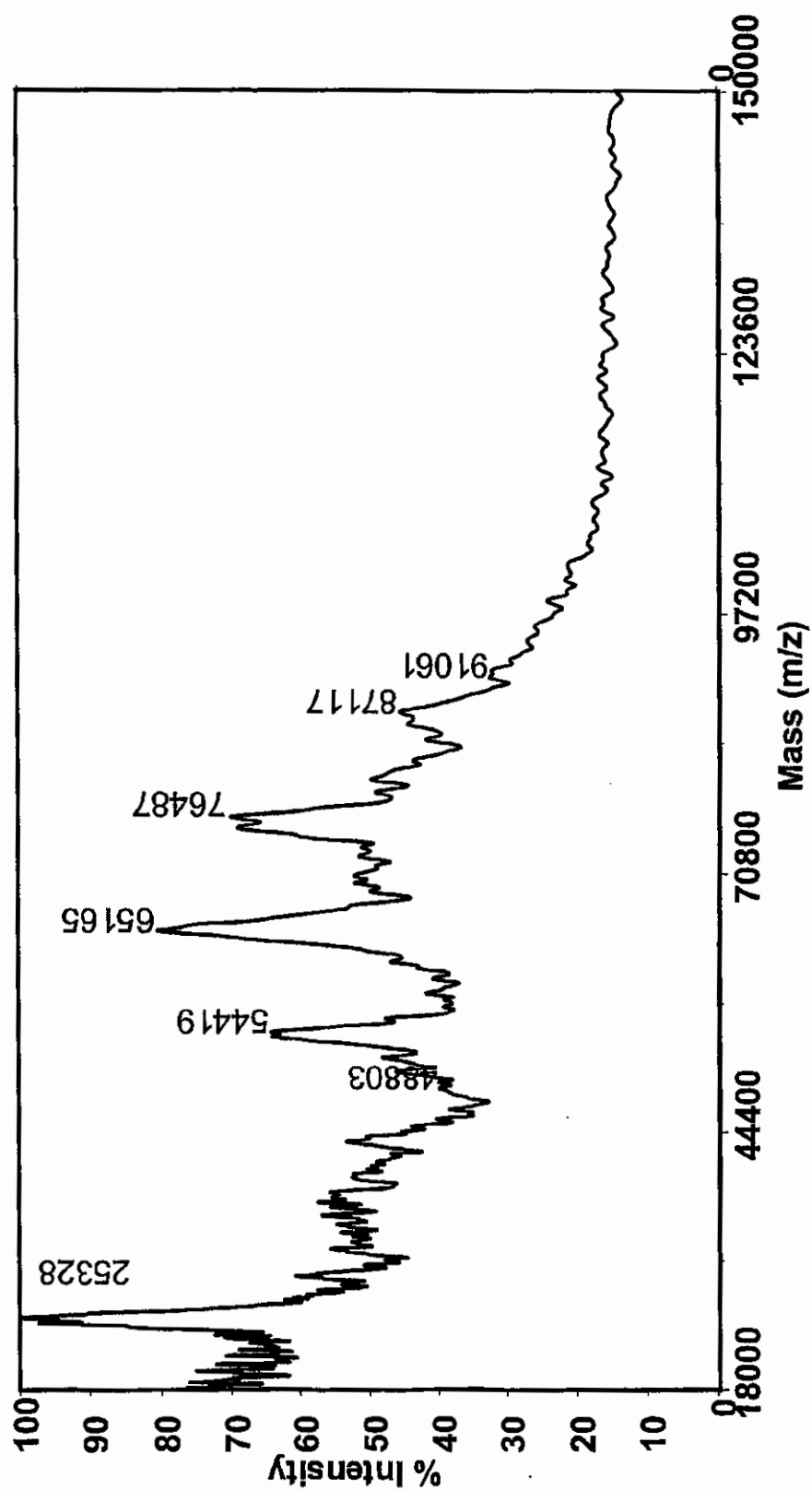


FIG. 119

339/345

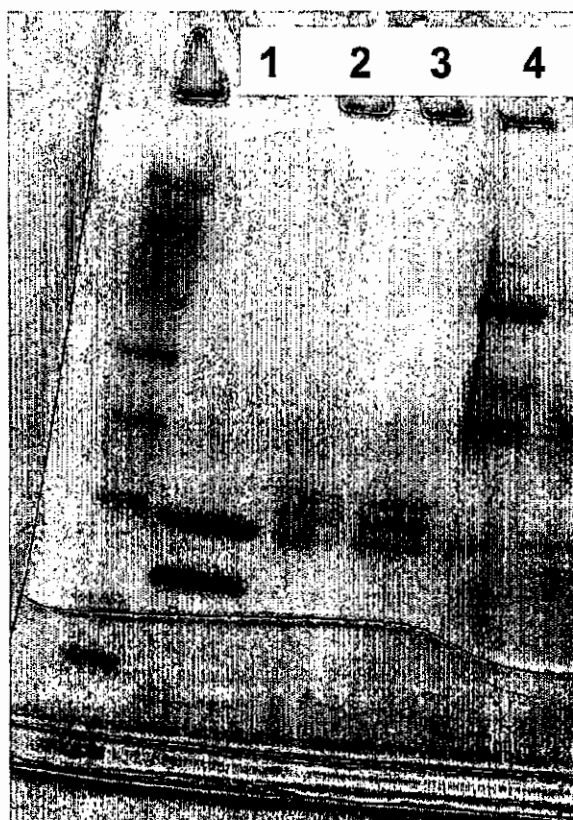


FIG. 120

340/345



FIG. 121

341/345

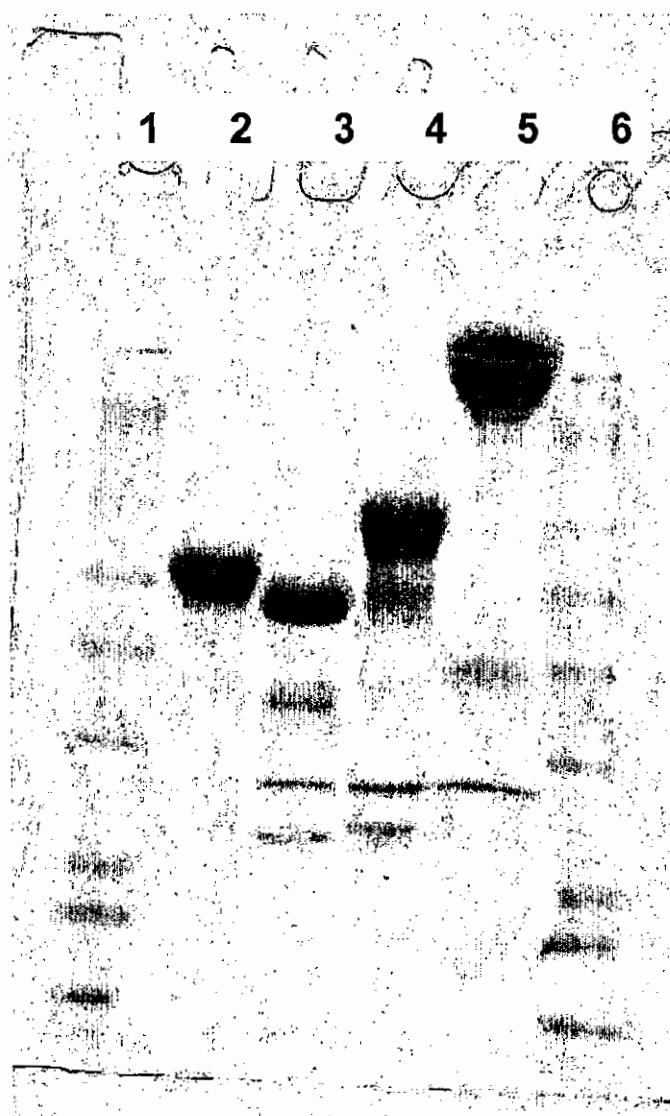


FIG. 122

342/345

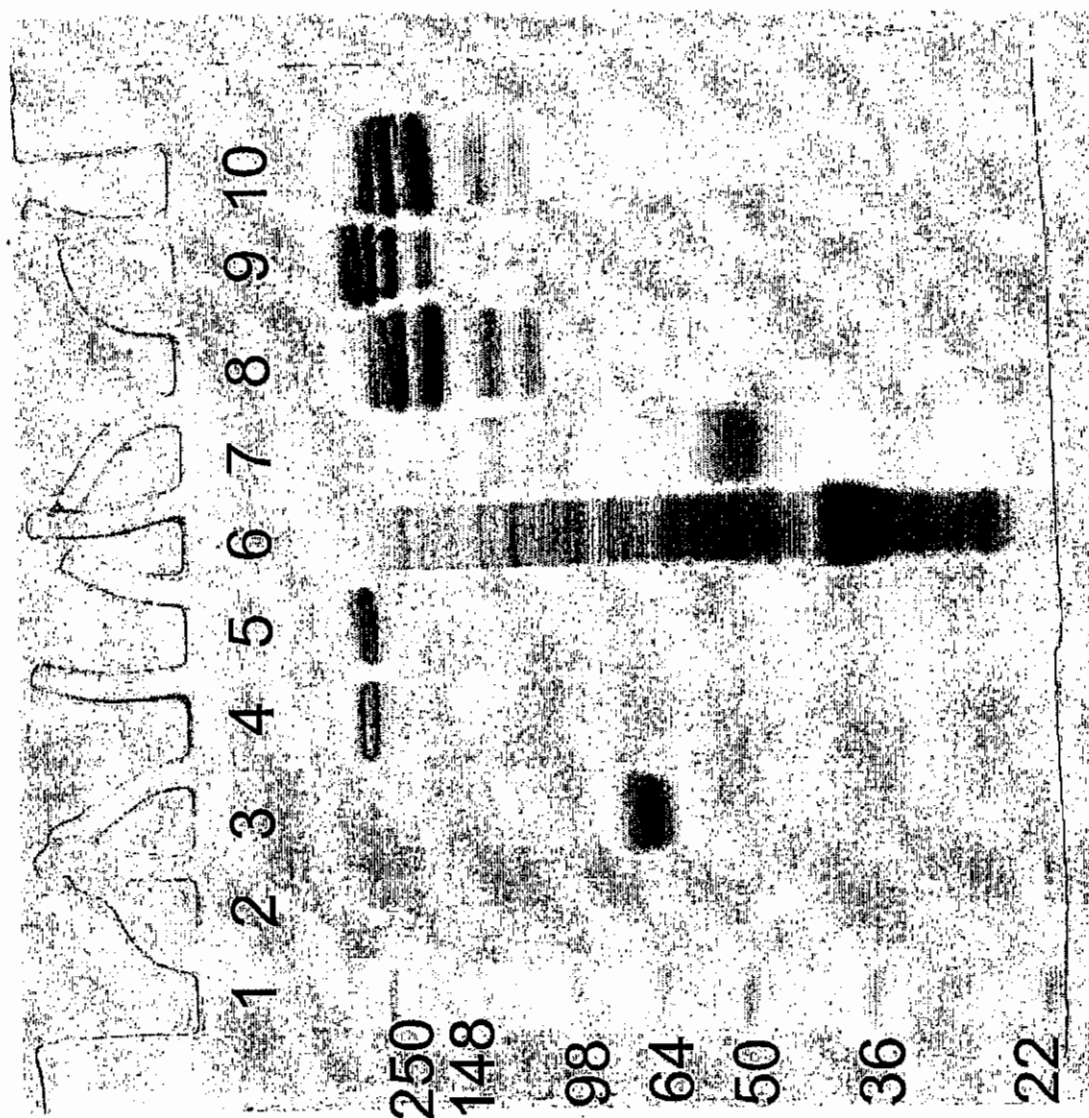


FIG. 123

343/345

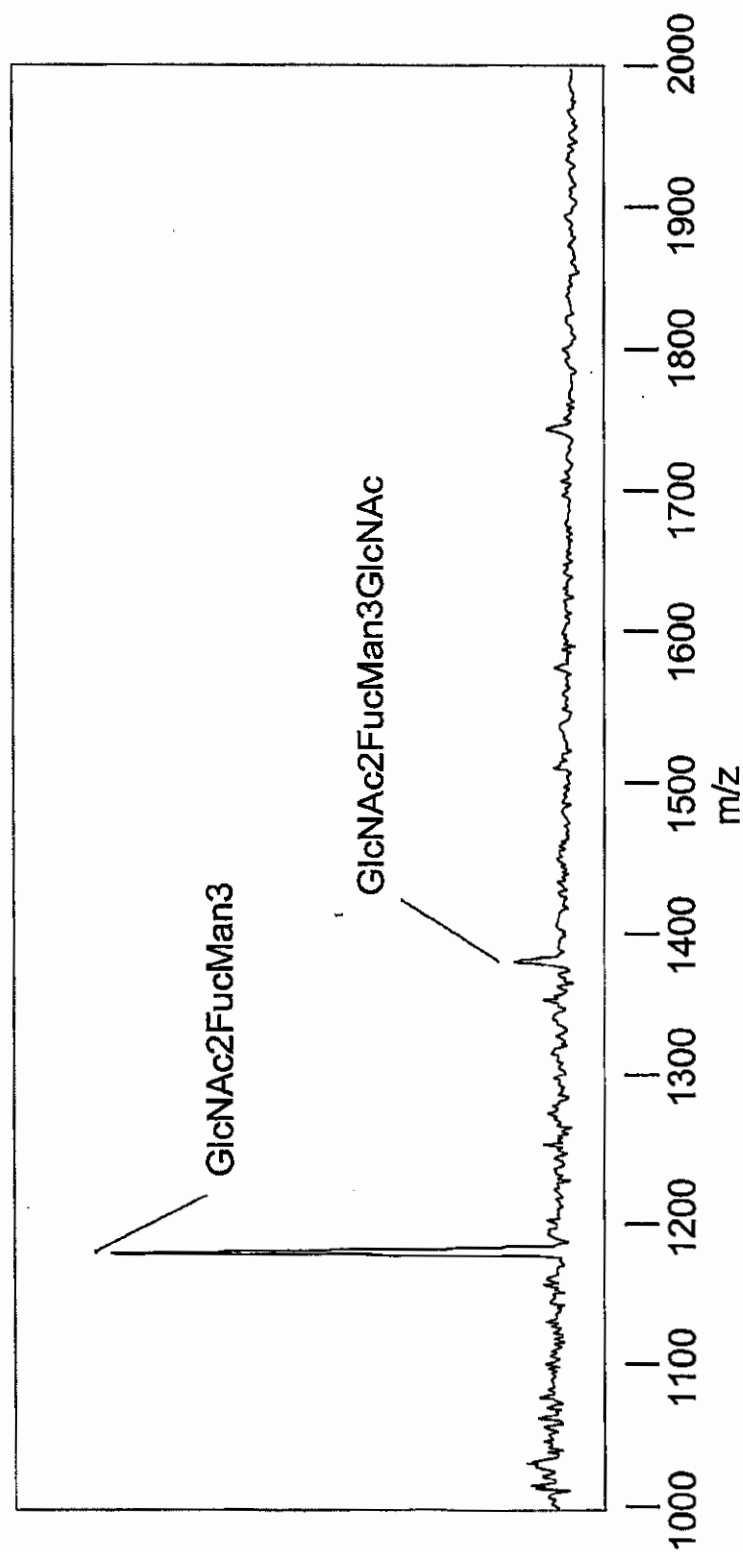


FIG. 124

344/345

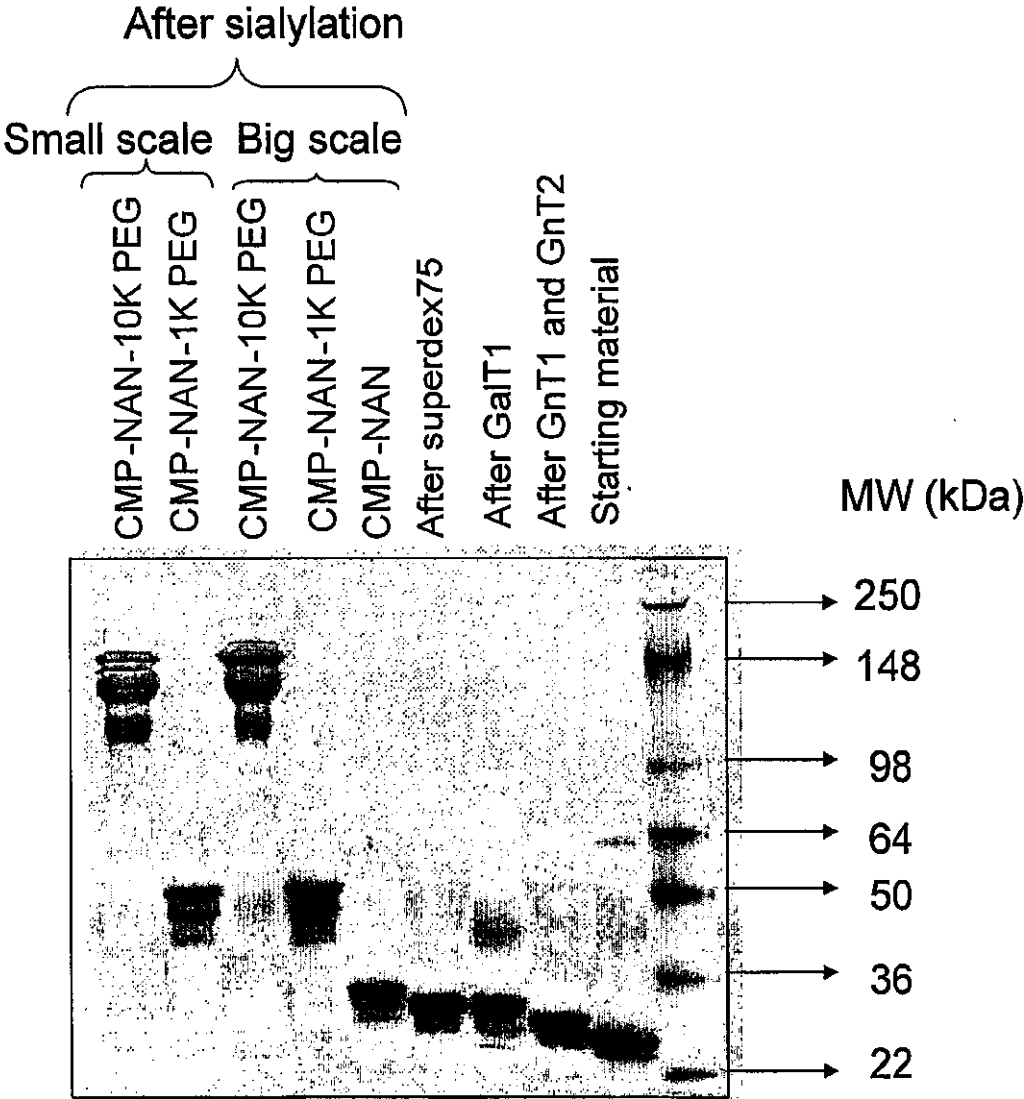


FIG. 125

345/345

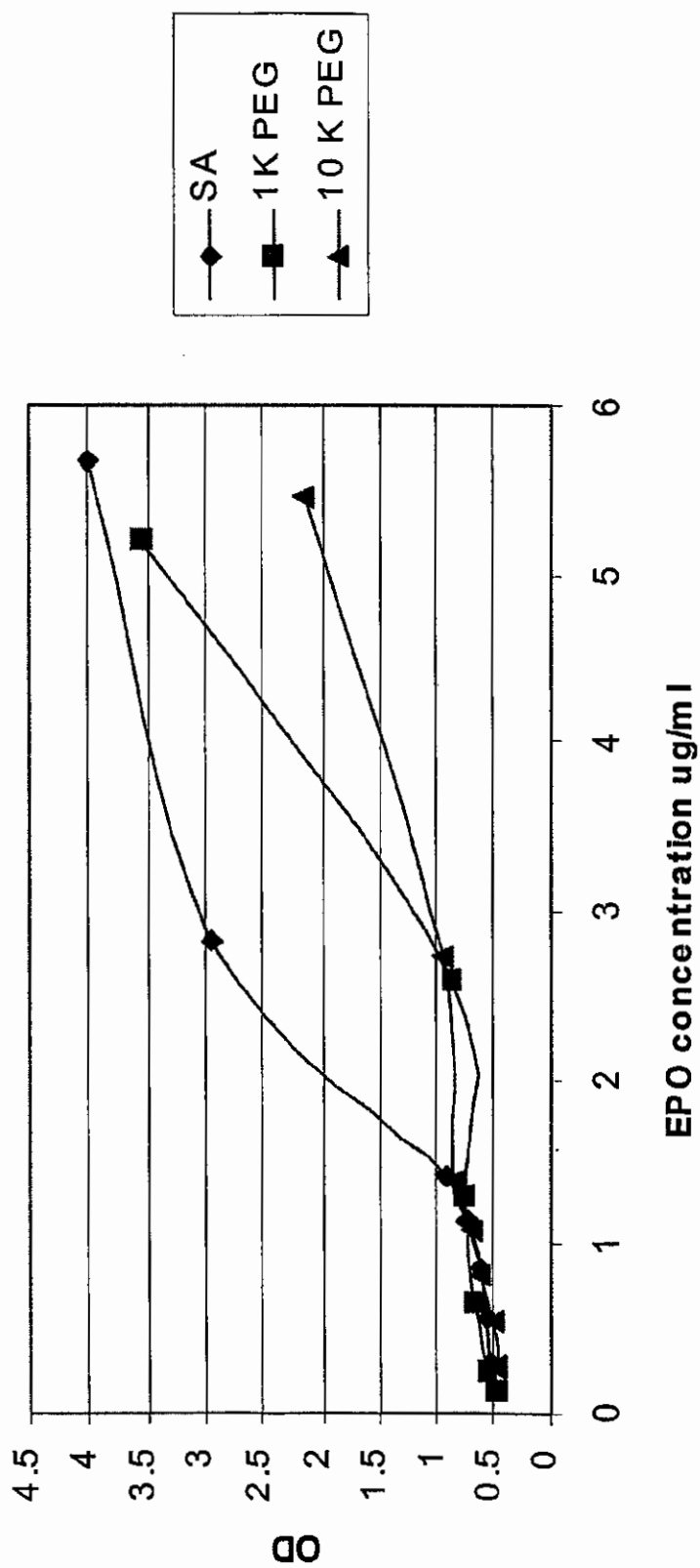


FIG. 126

WO 03/031464

PCT/US02/32263

SEQUENCE LISTING

<110> Neose Technologies, Inc.

DeFrees, Shawn

Zopf, David

Bayer, Robert

Bowe, Caryn

Hakes, David

Chen, Xi

<120> REMODELING AND GLYCOCONJUGATION OF PEPTIDES

<130> 040853-01-5050WO

<150> US 60/328,523

<151> 2001-10-10

<150> US 60/344,692

<151> 2001-10-19

<150> US 60/334,233

<151> 2001-11-08

<150> US 60/334,301

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<151> 2002-06-07

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<151> 2002-07-17

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<150> US 60/407,527

<151> 2002-08-28

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WO 03/031464

PCT/US02/32263

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Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
          20           25           30

```

```

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
35           40           45

```

```

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
50           55           60

```

```

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65           70           75           80

```

```

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
85           90           95

```

```

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
100           105           110

```

```

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
115           120           125

```

```

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
130           135           140

```

```

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe

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WO 03/031464

PCT/US02/32263

145

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WO 03/031464

PCT/US02/32263

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ctgattacag aataactggg acacttcatt tgtccatcaa tattatatcc aagatataag 1560
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aacaataaca attctgctct cttgtgtatt tgatttttgt atgaaaaaaa ctaaaaatgg 1680
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```

```

Lys Ser Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu
          20          25          30

```

```

Gly Ser Arg Arg Thr Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser
          35          40          45

```

```

Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly Phe Pro Gln Glu
          50          55          60

```

```

Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile Pro Val Leu His
65           70           75          80

```

```

Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser
          85          90          95

```

```

Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr
          100         105         110

```

```

Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val
          115         120         125

```

```

Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys
          130         135         140

```

WO 03/031464

PCT/US02/32263

Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro
 145 150 155 160

Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu
 165 170 175

Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
 180 185

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 aatgagacta ttgttgagaa cctcctggct aatgtctatc atcagataaa ccatctgaag 360
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 cttacagggt acctccgaaa ctgaagatct cctagcctgt cctctctggga ctggacaatt 600
 gcttcaagca ttcttcaacc agcagatgct gtttaagtga ctgatggcta atgtactgca 660
 aatgaaagga cactagaaga ttttgaaatt tttattaaat tatgagttat ttttatttat 720
 ttaaatttta ttttggaaaa taaattattt ttggtgc 757

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 1 5 10 15

WO 03/031464

PCT/US02/32263

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 20 25 30

Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
 35 40 45

Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
 50 55 60

Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
 65 70 75 80

Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
 85 90 95

Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
 100 105 110

Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
 115 120 125

Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
 130 135 140

Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
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His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
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 gcagtcttcg taaccagga ggaagccac ggcgtcctgc accggcgccg gcgcgccaac 120
 gcgttcctgg aggagctgcg gccgggctcc ctggagaggg agtgcaagga ggagcagtgc 180
 tccttcgagg aggcccgga gatcttcaag gacgcggaga ggacgaagct gttctggatt 240

WO 03/031464

PCT/US02/32263

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tcttacagtg atggggacca gtgtgcctca agtccatgcc agaatggggg ctcttgcaag   300
gaccagctcc agtcctatat ctgottctgc ctccctgcct tcgagggccg gaactgtgag   360
acgcacaagg atgaccagct gatctgtgtg aacgagaacg gcggtgtga gcagtactgc   420
agtgaccaca cgggcaccaa gcgtcctgt cggtgccacg aggggtactc tctgctggca   480
gacggggtgt cctgcacacc cacagttgaa tatccatgtg gaaaaatacc tattctagaa   540
aaaagaaatg ccagcaaacc ccaaggccga attgtggggg gcaagggtgtg ccccaaaggg   600
gagtgtccat ggcaggctct gttgttggtg aatggagctc agttgtgtgg ggggacctg   660
atcaacacca tctgggtggt ctccgcggcc cactgtttcg acaaaatcaa gaactggagg   720
aacctgatcg cggtgctggg cgagcacgac ctacagcagc acgacgggga tgagcagagc   780
cggcggtggt cgcaggctcat catcccagc acgtactcc cgggcaccac caaccacgac   840
atcgcgctgc tcgcctgca ccagccctg gtctcactg accatgtggt gcccctctgc   900
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atcacggagt acatgttctg tgccggctac tcggatggca gcaaggactc ctgcaagggg  1140
gacagtggag gccacatgc caccactac cggggcacgt ggtacctgac gggcatcgtc  1200
agctggggcc agggctgcgc aaccgtgggc cactttgggg tgtacaccag ggtctccag  1260
tacatcgagt ggctgcaaaa gctcatgcgc tcagagccac gccaggagt cctcctgcga  1320
gcccatttc cc                                     1332

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<210> 8
 <211> 444
 <212> PRT
 <213> Homo sapiens

<400> 8

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln
 1 5 10 15

Gly Cys Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val
 20 25 30

Leu His Arg Arg Arg Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro
 35 40 45

WO 03/031464

PCT/US02/32263

Gly Ser Leu Glu Arg Glu Cys Lys Glu Glu Gln Cys Ser Phe Glu Glu
 50 55 60

Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg Thr Lys Leu Phe Trp Ile
 65 70 75 80

Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys Gln Asn Gly
 85 90 95

Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro
 100 105 110

Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile
 115 120 125

Cys Val Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr
 130 135 140

Gly Thr Lys Arg Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala
 145 150 155 160

Asp Gly Val Ser Cys Thr Pro Thr Val Glu Tyr Pro Cys Gly Lys Ile
 165 170 175

Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys Pro Gln Gly Arg Ile Val
 180 185 190

Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln Val Leu Leu
 195 200 205

Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile
 210 215 220

Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg
 225 230 235 240

Asn Leu Ile Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly
 245 250 255

Asp Glu Gln Ser Arg Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr
 260 265 270

WO 03/031464

PCT/US02/32263

Val Pro Gly Thr Thr Asn His Asp Ile Ala Leu Leu Arg Leu His Gln
 275 280 285

Pro Val Val Leu Thr Asp His Val Val Pro Leu Cys Leu Pro Glu Arg
 290 295 300

Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser Leu Val Ser
 305 310 315 320

Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu Met
 325 330 335

Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser
 340 345 350

Arg Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala
 355 360 365

Gly Tyr Ser Asp Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly
 370 375 380

Pro His Ala Thr His Tyr Arg Gly Thr Trp Tyr Leu Thr Gly Ile Val
 385 390 395 400

Ser Trp Gly Gln Gly Cys Ala Thr Val Gly His Phe Gly Val Tyr Thr
 405 410 415

Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met Arg Ser Glu
 420 425 430

Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro
 435 440

<210> 9
 <211> 1437
 <212> DNA
 <213> Homo sapiens

<400> 9
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 ggatatctac tcagtgtctga atgtacagtt tttcttgatc atgaaaacgc caacaaaatt 120
 ctgaatcggc caaagaggta taattcaggt aaattggaag agtttggtca agggaacctt 180

WO 03/031464

PCT/US02/32263

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gagagagaat gtatggaaga aaagtgtagt tttgaagaac cacgagaagt ttttgaaaac   240
actgaaaaga caactgaatt ttggaagcag tatgttgatg gagatcagtg tgagtccaat   300
ccatgtttta atggcggcag ttgcaaggat gacattaatt cctatgaatg ttggtgtccc   360
tttggatttg aaggaaagaa ctgtgaatta gatgtaacat gtaacattaa gaatggcaga   420
tgcgagcagt tttgtaaaaa tagtgctgat aacaagggtg tttgctcctg tactgagggg   480
tatcgacttg cagaaaacca gaagtcctgt gaaccagcag tgccatttcc atgtggaaga   540
gtttctgttt cacaaacttc taagctcacc cgtgctgagg ctgtttttcc tgatgtggac   600
tatgtaaatc ctactgaagc tgaaccatt ttggataaca tcaactcaagg cacccaatca   660
tttaatgact tcaactcgggt tgttggtgga gaagatgcca aaccagggtca attcccttgg   720
cagggtgttt tgaatggtaa agttgatgca ttctgtggag gctctatcgt taatgaaaaa   780
tggattgtaa ctgctgcccc ctgtgttgaa actgggtgta aaattacagt tgtcgcaggt   840
gaacataata ttgaggagac agaacataca gagcaaaagc gaaatgtgat tgcagcaatt   900
attcctcacc acaactacaa tgcagctatt aataagtaca accatgacat tgcccttctg   960
gaactggacg aacccttagt gctaaacagc tacgttacac ctatttgcac tgctgacaag  1020
gaatacacga acatcttctc caaatttggg tctggctatg taagtggctg ggcaagagtc  1080
ttccacaaag ggagatcagc tttagttctt cagtacctta gagttccact tgttgaccga  1140
gccacatgtc ttogatctac aaagttcacc atctataaca acatgttctg tgctggcttc  1200
catgaaggag gtagagattc atgtcaagga gatagtgggg gaccccatgt tactgaagtg  1260
gaagggacca gtttcttaac tggaattatt agctggggtg aagagtgtgc aatgaaaggc  1320
aaatatggaa tatataccaa ggtatcccg tatgtcaact ggattaagga aaaaacaaag  1380
ctcacttaat gaaagatgga ttccaaggt taattcattg gaattgaaaa ttaacag   1437

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<210> 10
<211> 462
<212> PRT
<213> Homo sapiens

```

```

<400> 10

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```

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr
1           5           10          15

```

```

Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu
20          25          30

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WO 03/031464

PCT/US02/32263

```

Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn
    35                                40                                45

Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys
    50                                55                                60

Met Glu Glu Lys Cys Ser Phe Glu Glu Pro Arg Glu Val Phe Glu Asn
    65                                70                                75                                80

Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln
    85                                90                                95

Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile
    100                                105                                110

Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys
    115                                120                                125

Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe
    130                                135                                140

Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly
    145                                150                                155                                160

Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe
    165                                170                                175

Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala
    180                                185                                190

Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Pro Thr Glu Ala Glu
    195                                200                                205

Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser Phe Asn Asp Phe
    210                                215                                220

Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp
    225                                230                                235                                240

Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile
    245                                250                                255

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WO 03/031464

PCT/US02/32263

Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly
 260 265 270

Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu
 275 280 285

His Thr Glu Gln Lys Arg Asn Val Ile Arg Ala Ile Ile Pro His His
 290 295 300

Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu
 305 310 315 320

Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys
 325 330 335

Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly
 340 345 350

Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu
 355 360 365

Val Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu
 370 375 380

Arg Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe
 385 390 395 400

His Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His
 405 410 415

Val Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp
 420 425 430

Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val
 435 440 445

Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr
 450 455 460

<210> 11
 <211> 603
 <212> DNA
 <213> Homo sapiens

WO 03/031464

PCT/US02/32263

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<400> 11
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ttcttctccc agccgggtgc cccaatactt cagtgcattg gctgctgctt ctctagagca      180
tatcccactc cactaagggt caagaagacg atgttggtcc aaaagaacgt cacctcagag      240
tccacttgct gtgtagctaa atcatataac agggtcacag taatgggggg tttcaaagtg      300
gagaaccaca cggcgtgcca ctgcagtact tgttattatc acaaatttta aatgttttac      360
caagtgtgtg cttgatgact gctgattttc tggaatggaa aattaagttg tttagtgttt      420
atggctttgt gagataaaac tctccttttc cttaccatac cactttgaca cgcttcaagg      480
atatactgca gctttactgc cttcctcctt atcctacagt acaatcagca gtctagttct      540
tttcatttgg aatgaatata gcattaagct tgttccactg caaataaagc cttttaaatc      600
atc                                          603

```

```

<210> 12
<211> 116
<212> PRT
<213> Homo sapiens

```

```

<400> 12

```

```

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser
1          5          10          15

```

```

Val Phe Leu His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro
          20          25          30

```

```

Glu Cys Thr Leu Gln Glu Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro
          35          40          45

```

```

Ile Leu Gln Cys Met Gly Cys Cys Phe Ser Arg Ala Tyr Pro Thr Pro
          50          55          60

```

```

Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn Val Thr Ser Glu
65          70          75          80

```

```

Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met Gly
          85          90          95

```

```

Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr
          100          105          110

```

WO 03/031464

PCT/US02/32263

Tyr His Lys Ser
115

<210> 13
<211> 390
<212> DNA
<213> Homo sapiens

<400> 13
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tgtgagctga ccaacatcac cattgcaata gagaaagaag aatgtogttt ctgcataagc 120
atcaacacca cttggtgtgc tggctactgc tacaccaggg atctggtgta taaggaccca 180
gccaggccca aaatccagaa aacatgtacc ttcaaggaac tggatatatga aacagtgaga 240
gtgcccggct gtgctcacca tgcagattcc ttgtatacat acccagtggc caccagtgt 300
cactgtggca agtgtgacag cgacagcact gattgtactg tgcgaggcct ggggcccagc 360
tactgtcctt ttggtgaaat gaaagaataa 390

<210> 14
<211> 129
<212> PRT
<213> Homo sapiens

<400> 14

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile
1 5 10 15

Cys Cys Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys
20 25 30

Glu Glu Cys Arg Phe Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly
35 40 45

Tyr Cys Tyr Thr Arg Asp Leu Val Tyr Lys Asp Pro Ala Arg Pro Lys
50 55 60

Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val Tyr Glu Thr Val Arg
65 70 75 80

Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr Pro Val
85 90 95

WO 03/031464

PCT/US02/32263

Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys
 100 105 110

Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys
 115 120 125

Glu

<210> 15
 <211> 1342
 <212> DNA
 <213> Homo sapiens

<400> 15
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 ccgccctctc ctccaggccc gtggggctgg ccctgcaccg ccgagcttcc cgggatgagg 120
 gcccccggtg tggtcacccg gcgcgccccca ggtcgctgag ggaccccggc caggcgcgga 180
 gatgggggtg cacgaatgtc ctgcctggct gtggcttctc ctgtccctgc tgtcgctccc 240
 tctgggcctc ccagtcctgg gcgccccacc acgcctcacc tgtgacagcc gagtcctgga 300
 gaggtacctc ttggaggcca aggaggccga gaatatcacc acgggctgtg ctgaacactg 360
 cagcttgaat gagaatatca ctgtcccaga caccaaagtt aatttctatg cctggaagag 420
 gatggaggtc gggcagcagg ccgtagaagt ctggcagggc ctggccctgc tgtcggaaagc 480
 tgtcctgcgg ggccaggccc tgttggtcaa ctcttcccag ccgtgggagc ccctgcagct 540
 gcatgtggat aaagccgtca gtggccttcg cagcctcacc actctgcttc gggctctgcg 600
 agcccagaag gaagccatct cccctccaga tggggcctca gctgctccac tccgaacaat 660
 cactgtgac actttccgca aactcttcg agtctaactc aatttctctc ggggaaagct 720
 gaagctgtac acaggggagg cctgcaggac aggggacaga tgaccagggtg tgtccacctg 780
 ggcatatcca ccacctccct caccaacatt gcttgtgcca caccctcccc cgccactcct 840
 gaaccccgtc gaggggctct cagctcagcg ccagcctgtc ccatggacac tccagtgcc 900
 gcaatgacat ctacggggcc agaggaactg tccagagagc aactctgaga tctaaggatg 960
 tcacagggcc aacttgaggg ccagagcag gaagcattca gagagcagct ttaaactcag 1020
 ggacagagcc atgctgggaa gacgcctgag ctactcggc accctgcaaa atttgatgcc 1080
 aggacacgct ttggaggcga ttacctgtt ttgcaccta ccatcaggga caggatgacc 1140

WO 03/031464

PCT/US02/32263

```

tggagaactt aggtggcaag ctgtgacttc tccaggtctc acgggcatgg gcactccctt 1200
ggtggcaaga gcccccttga caccggggtg gtgggaacca tgaagacagg atgggggctg 1260
gcctctggct ctcatggggg ccaagttttg tgtattcttc aacctcattg acaagaactg 1320
aaaccaccaa aaaaaaaaaa aa 1342

```

```

<210> 16
<211> 193
<212> PRT
<213> Homo sapiens

```

```

<400> 16

```

```

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1          5          10          15

```

```

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu
          20          25          30

```

```

Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
          35          40          45

```

```

Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
          50          55          60

```

```

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
65          70          75          80

```

```

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
          85          90          95

```

```

Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
          100          105          110

```

```

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
          115          120          125

```

```

Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu
          130          135          140

```

```

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
145          150          155          160

```

```

Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu

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WO 03/031464

PCT/US02/32263

165

170

175

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
 180 185 190

Arg

<210> 17
 <211> 435
 <212> DNA
 <213> Homo sapiens

<400> 17
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 cgctcgccca gccccagcac gcagccctgg gagcatgtga atgccatcca ggaggcccg 120
 cgtctcctga acctgagtag agacactgct gctgagatga atgaaacagt agaagtcac 180
 tcagaaatgt ttgacctcca ggagccgacc tgcctacaga cccgcctgga gctgtacaag 240
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 tacaagcagc actgccctcc aaccccgga acttctgtg caaccagat taccacctt 360
 gaaagtttca aagagaacct gaaggacttt ctgcttgtca tcccctttga ctgctgggag 420
 ccagtccagg agtga 435

<210> 18
 <211> 144
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile
 1 5 10 15

Ser Ala Pro Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His
 20 25 30

Val Asn Ala Ile Gln Glu Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp
 35 40 45

Thr Ala Ala Glu Met Asn Glu Thr Val Glu Val Ile Ser Glu Met Phe
 50 55 60

WO 03/031464

PCT/US02/32263

Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg Leu Glu Leu Tyr Lys
65 70 75 80

Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro Leu Thr Met
85 90 95

Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser
100 105 110

Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys
115 120 125

Asp Phe Leu Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu
130 135 140

<210> 19
<211> 501
<212> DNA
<213> Homo sapiens

<400> 19
atgaaatata caagttatat cttggctttt cagctctgca tcgttttggg ttctcttggc 60
tggtactgcc aggaccata tgtaaaagaa gcagaaaacc ttaagaaata ttttaatgca 120
ggtcattcag atgtagcgga taatggaact cttttcttag gcattttgaa gaattggaaa 180
gaggagagt acagaaaaat aatgcagagc caaattgtct ctttttactt caaacttttt 240
aaaaacttta aagatgacca gagcatccaa aagagtgtgg agaccatcaa ggaagacatg 300
aatgtcaagt ttttcaatag caacaaaaag aaacgagatg acttcgaaaa gctgactaat 360
tattcggtaa ctgacttgaa tgtccaacgc aaagcaatac atgaactcat ccaagtgatg 420
gctgaactgt cgccagcagc taaaacaggg aagcgaaaaa ggagtcagat gctgtttcga 480
ggtcgaagag catcccagta a 501

<210> 20
<211> 166
<212> PRT
<213> Homo sapiens

<400> 20

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu

WO 03/031464

PCT/US02/32263

20	25	30
Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn 35 40 45		
Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp 50 55 60		
Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe 65 70 75 80		
Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile 85 90 95		
Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg 100 105 110		
Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val 115 120 125		
Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser 130 135 140		
Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg 145 150 155 160		
Gly Arg Arg Ala Ser Gln 165		

<210> 21

<211> 1352

<212> DNA

<213> Homo sapiens

<400> 21

ctgggacagt gaatcgacaa tgcggtcttc tgtctcgtgg ggcatacctcc tgctggcagg	60
cctgtgctgc ctggtccctg tctccctggc tgaggatccc caggagatg ctgccagaa	120
gacagatata tcccaccatg atcaggatca cccaaccttc aacaagatca cccccaacct	180
ggctgagttc gccttcagcc tataccgcc gctggcacac cagtccaaca gcaccaatat	240
cttcttctcc ccagtgaaga tcgtacagc ctttgcaatg ctctccctgg ggaccaaggc	300
tgacactcac gatgaaatcc tggagggcct gaatttcaac' ctacaggaga ttccggaggc	360

WO 03/031464

PCT/US02/32263

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tcagatccat gaaggcttcc aggaactcct ccgtaccctc aaccagccag acagccagct 420
ccagctgacc accggcaatg gcctgttccct cagcgagggc ctgaagctag tggataagtt 480
tttggaggat gttaaaaagt tgtaccactc agaagccttc actgtcaact tcggggacac 540
cgaagaggcc aagaaacaga tcaacgatta cgtggagaag ggtactcaag ggaaaattgt 600
ggatttggtc aaggagcttg acagagacac agtttttgcct ctggtgaatt acatcttctt 660
taaaggcaaa tgggagagac cctttgaagt caaggacacc gaggaagagg acttccacgt 720
ggaccaggtg accaccgtga aggtgcctat gatgaagcgt ttaggcatgt ttaacatcca 780
gcactgtaag aagctgtcca gctgggtgct gctgatgaaa tacctgggca atgccaccgc 840
catcttcttc ctgcctgatg aggggaaact acagcacctg gaaaatgaac tcaccacga 900
tatcatcacc aagttccttg aaaatgaaga cagaaggtct gccagcttac atttacccaa 960
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<210> 22
<211> 418
<212> PRT
<213> Homo sapiens

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<400> 22

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Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys
1           5           10           15

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Cys Leu Val Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala
20           25           30

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Gln Lys Thr Asp Thr Ser His His Asp Gln Asp His Pro Thr Phe Asn
35           40           45

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Lys Ile Thr Pro Asn Leu Ala Glu Phe Ala Phe Ser Leu Tyr Arg Gln
50           55           60

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WO 03/031464

PCT/US02/32263

Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe Ser Pro Val Ser
65 70 75 80

Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp Thr
85 90 95

His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro
100 105 110

Glu Ala Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn
115 120 125

Gln Pro Asp Ser Gln Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu
130 135 140

Ser Glu Gly Leu Lys Leu Val Asp Lys Phe Leu Glu Asp Val Lys Lys
145 150 155 160

Leu Tyr His Ser Glu Ala Phe Thr Val Asn Phe Gly Asp Thr Glu Glu
165 170 175

Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys Gly Thr Gln Gly Lys
180 185 190

Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val Phe Ala Leu
195 200 205

Val Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val
210 215 220

Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val
225 230 235 240

Lys Val Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys
245 250 255

Lys Lys Leu Ser Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala
260 265 270

Thr Ala Ile Phe Phe Leu Pro Asp Glu Gly Lys Leu Gln His Leu Glu
275 280 285

WO 03/031464

PCT/US02/32263

Asn Glu Leu Thr His Asp Ile Ile Thr Lys Phe Leu Glu Asn Glu Asp
 290 295 300

Arg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile Thr Gly Thr
 305 310 315 320

Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe
 325 330 335

Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys
 340 345 350

Leu Ser Lys Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly
 355 360 365

Thr Glu Ala Ala Gly Ala Met Phe Leu Glu Ala Ile Pro Met Ser Ile
 370 375 380

Pro Pro Glu Val Lys Phe Asn Lys Pro Phe Val Phe Leu Met Ile Glu
 385 390 395 400

Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val Val Asn Pro Thr
 405 410 415

Gln Lys

<210> 23
 <211> 2004
 <212> DNA
 <213> Homo sapiens

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WO 03/031464

PCT/US02/32263

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<210> 24
<211> 536
<212> PRT

WO 03/031464

PCT/US02/32263

<213> Homo sapiens

<400> 24

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser
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Arg Val Ser Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln
 20 25 30

Ala Val Ser Trp Ala Ser Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe
 35 40 45

Gly Tyr Ser Ser Val Val Cys Val Cys Asn Ala Thr Tyr Cys Asp Ser
 50 55 60

Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr Phe Ser Arg Tyr Glu
 65 70 75 80

Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly Pro Ile Gln
 85 90 95

Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln
 100 105 110

Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala
 115 120 125

Ala Leu Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu
 130 135 140

Lys Ser Tyr Phe Ser Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val
 145 150 155 160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175

Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190

Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205

Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu

WO 03/031464

PCT/US02/32263

210	215	220
Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro		
225	230	235 240
Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu		
	245	250 255
Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu		
	260	265 270
Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu		
	275	280 285
Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly		
	290	295 300
Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu		
	310	315 320
Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr		
	325	330 335
Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr		
	340	345 350
Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg		
	355	360 365
Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser		
	370	375 380
Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met		
	385	390 395 400
Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly		
	405	410 415
Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp		
	420	425 430
Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr Lys Asp		
	435	440 445

WO 03/031464

PCT/US02/32263

Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460

Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
 465 470 475 480

Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495

Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
 500 505 510

Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile
 515 520 525

His Thr Tyr Leu Trp His Arg Gln
 530 535

<210> 25
 <211> 1726
 <212> DNA
 <213> Homo sapiens

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WO 03/031464

PCT/US02/32263

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gacacttacg acaatgacat tgcgctgctg cagctgaaat cggattcgtc ccgctgtgcc     1260
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gatgtcccg gtgtgtacac caagggtacc aactacctag actggattcg tgacaacatg     1680
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<210> 26
 <211> 562
 <212> PRT
 <213> Homo sapiens

<400> 26

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Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1           5           10          15

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Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
          20           25           30

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Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
          35           40           45

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Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
          50           55           60

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WO 03/031464

PCT/US02/32263

Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
65 70 75 80

Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr
85 90 95

Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu
100 105 110

Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr
115 120 125

Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser
130 135 140

Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro
145 150 155 160

Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His
165 170 175

Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val
180 185 190

Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys
195 200 205

Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg
210 215 220

Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn
225 230 235 240

Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala
245 250 255

Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly
260 265 270

Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp
275 280 285

Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr

WO 03/031464

PCT/US02/32263

290	295	300
Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala		
305	310	315 320
Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro		
	325	330 335
Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile		
	340	345 350
Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu		
	355	360 365
Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu		
	370	375 380
Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp		
	385	390 395 400
Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser		
	405	410 415
Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro		
	420	425 430
Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly		
	435	440 445
Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys		
	450	455 460
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His		
	465	470 475 480
Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr		
	485	490 495
Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp		
	500	505 510
Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val		
	515	520 525

WO 03/031464

PCT/US02/32263

Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
 530 535 540

Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
 545 550 555 560

Arg Pro

<210> 27
 <211> 825
 <212> DNA
 <213> Homo sapiens

<400> 27
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 ttttaataaat ttgataaata taaaaaaaaa aaacaaaaaa aaaaa 825

<210> 28
 <211> 156
 <212> PRT
 <213> Homo sapiens

<400> 28

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu

WO 03/031464

PCT/US02/32263

1	5	10	15
Val Thr Asn Ser Ala Pro Thr Ser Ser Thr Lys Lys Thr Lys Lys	20	25	30
Thr Gln Leu Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu	35	40	45
Asn Gly Ile Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr	50	55	60
Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys Gln Leu Gln	65	70	75
Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala	85	90	95
Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile	100	105	110
Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys	115	120	125
Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp	130	135	140
Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr	145	150	155

<210> 29

<211> 7931

<212> DNA

<213> Homo sapiens

<400> 29

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acctcagtcg tgtacaaaaa gactctgttt gtagaattca cggatcacct tttcaacatc 240

gctaagccaa ggccaccctg gatgggtctg ctaggctcta ccatccaggc tgagggttat 300

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WO 03/031464

PCT/US02/32263

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WO 03/031464

PCT/US02/32263

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WO 03/031464

PCT/US02/32263

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WO 03/031464

PCT/US02/32263

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WO 03/031464

PCT/US02/32263

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<212> PRT
<213> Homo sapiens

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<400> 30

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```

Cys Phe Ser Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser
20           25           30

```

```

Trp Asp Tyr Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg
35           40           45

```

```

Phe Pro Pro Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val
50           55           60

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```

Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His Leu Phe Asn Ile
65           70           75           80

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Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln
85           90           95

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WO 03/031464

PCT/US02/32263

Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser
 100 105 110

His Pro Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser
 115 120 125

Glu Gly Ala Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp
 130 135 140

Asp Lys Val Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu
 145 150 155 160

Lys Glu Asn Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser
 165 170 175

Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile
 180 185 190

Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr
 195 200 205

Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly
 210 215 220

Lys Ser Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp
 225 230 235 240

Ala Ala Ser Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr
 245 250 255

Val Asn Arg Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val
 260 265 270

Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile
 275 280 285

Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser
 290 295 300

Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met
 305 310 315 320

WO 03/031464

PCT/US02/32263

Asp Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His
 325 330 335

Asp Gly Met Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro
 340 345 350

Gln Leu Arg Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp
 355 360 365

Leu Thr Asp Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser
 370 375 380

Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr
 385 390 395 400

Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro
 405 410 415

Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn
 420 425 430

Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met
 435 440 445

Ala Tyr Thr Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu
 450 455 460

Ser Gly Ile Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu
 465 470 475 480

Leu Ile Ile Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro
 485 490 495

His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys
 500 505 510

Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe
 515 520 525

Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp
 530 535 540

Pro Arg Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg

WO 03/031464

PCT/US02/32263

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Asp Leu Ala Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu						
		565		570		575
Ser Val Asp Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val						
		580		585		590
Ile Leu Phe Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu						
		595		600		605
Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp						
		610		615		620
Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val						
		625		630		635
						640
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp						
		645		650		655
Tyr Ile Leu Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe						
		660		665		670
Ser Gly Tyr Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr						
		675		680		685
Leu Phe Pro Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro						
		690		695		700
Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly						
		705		710		715
						720
Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp						
		725		730		735
Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys						
		740		745		750
Asn Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg						
		755		760		765
Ser Thr Arg Gln Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp						
		770		775		780

WO 03/031464

PCT/US02/32263

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Ile Glu Lys Thr Asp Pro Trp Phe Ala His Arg Thr Pro Met Pro Lys
785                      790                      795                      800

Ile Gln Asn Val Ser Ser Ser Asp Leu Leu Met Leu Leu Arg Gln Ser
                        805                      810                      815

Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu Ala Lys Tyr
                        820                      825                      830

Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn
                        835                      840                      845

Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly
850                      855                      860

Asp Met Val Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu
865                      870                      875                      880

Lys Leu Gly Thr Thr Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys
                        885                      890                      895

Val Ser Ser Thr Ser Asn Asn Leu Ile Ser Thr Ile Pro Ser Asp Asn
900                      905                      910

Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu Gly Pro Pro Ser Met
915                      920                      925

Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly Lys Lys
930                      935                      940

Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu
945                      950                      955                      960

Asn Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu
965                      970                      975

Ser Ser Trp Gly Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe
980                      985                      990

Lys Gly Lys Arg Ala His Gly Pro Ala Leu Leu Thr Lys Asp Asn Ala
995                      1000                      1005

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WO 03/031464

PCT/US02/32263

Leu Phe Lys Val Ser Ile Ser Leu Leu Lys Thr Asn Lys Thr Ser
1010 1015 1020

Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp Gly Pro Ser
1025 1030 1035

Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu
1040 1045 1050

Ser Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg
1055 1060 1065

Met Leu Met Asp Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met
1070 1075 1080

Ser Asn Lys Thr Thr Ser Ser Lys Asn Met Glu Met Val Gln Gln
1085 1090 1095

Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala Gln Asn Pro Asp Met
1100 1105 1110

Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg Trp Ile
1115 1120 1125

Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro
1130 1135 1140

Ser Pro Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu
1145 1150 1155

Gly Gln Asn Phe Leu Ser Glu Lys Asn Lys Val Val Val Gly Lys
1160 1165 1170

Gly Glu Phe Thr Lys Asp Val Gly Leu Lys Glu Met Val Phe Pro
1175 1180 1185

Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp Asn Leu His Glu
1190 1195 1200

Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile Glu
1205 1210 1215

WO 03/031464

PCT/US02/32263

Lys	Lys	Glu	Thr	Leu	Ile	Gln	Glu	Asn	Val	Val	Leu	Pro	Gln	Ile
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His	Thr	Val	Thr	Gly	Thr	Lys	Asn	Phe	Met	Lys	Asn	Leu	Phe	Leu
1235						1240					1245			
Leu	Ser	Thr	Arg	Gln	Asn	Val	Glu	Gly	Ser	Tyr	Asp	Gly	Ala	Tyr
1250						1255					1260			
Ala	Pro	Val	Leu	Gln	Asp	Phe	Arg	Ser	Leu	Asn	Asp	Ser	Thr	Asn
1265						1270					1275			
Arg	Thr	Lys	Lys	His	Thr	Ala	His	Phe	Ser	Lys	Lys	Gly	Glu	Glu
1280						1285					1290			
Glu	Asn	Leu	Glu	Gly	Leu	Gly	Asn	Gln	Thr	Lys	Gln	Ile	Val	Glu
1295						1300					1305			
Lys	Tyr	Ala	Cys	Thr	Thr	Arg	Ile	Ser	Pro	Asn	Thr	Ser	Gln	Gln
1310						1315					1320			
Asn	Phe	Val	Thr	Gln	Arg	Ser	Lys	Arg	Ala	Leu	Lys	Gln	Phe	Arg
1325						1330					1335			
Leu	Pro	Leu	Glu	Glu	Thr	Glu	Leu	Glu	Lys	Arg	Ile	Ile	Val	Asp
1340						1345					1350			
Asp	Thr	Ser	Thr	Gln	Trp	Ser	Lys	Asn	Met	Lys	His	Leu	Thr	Pro
1355						1360					1365			
Ser	Thr	Leu	Thr	Gln	Ile	Asp	Tyr	Asn	Glu	Lys	Glu	Lys	Gly	Ala
1370						1375					1380			
Ile	Thr	Gln	Ser	Pro	Leu	Ser	Asp	Cys	Leu	Thr	Arg	Ser	His	Ser
1385						1390					1395			
Ile	Pro	Gln	Ala	Asn	Arg	Ser	Pro	Leu	Pro	Ile	Ala	Lys	Val	Ser
1400						1405					1410			
Ser	Phe	Pro	Ser	Ile	Arg	Pro	Ile	Tyr	Leu	Thr	Arg	Val	Leu	Phe
1415						1420					1425			
Gln	Asp	Asn	Ser	Ser	His	Leu	Pro	Ala	Ala	Ser	Tyr	Arg	Lys	Lys

WO 03/031464

PCT/US02/32263

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Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu Gln Gly Ala Lys				
1445		1450		1455
Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr Gly				
1460		1465		1470
Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser				
1475		1480		1485
Val Thr Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp				
1490		1495		1500
Leu Pro Lys Thr Ser Gly Lys Val Glu Leu Leu Pro Lys Val His				
1505		1510		1515
Ile Tyr Gln Lys Asp Leu Phe Pro Thr Glu Thr Ser Asn Gly Ser				
1520		1525		1530
Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu Leu Gln Gly Thr				
1535		1540		1545
Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys Val				
1550		1555		1560
Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser				
1565		1570		1575
Lys Leu Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln				
1580		1585		1590
Ile Pro Lys Glu Glu Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys				
1595		1600		1605
Thr Ala Phe Lys Lys Lys Asp Thr Ile Leu Ser Leu Asn Ala Cys				
1610		1615		1620
Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly Gln Asn Lys				
1625		1630		1635
Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg				
1640		1645		1650

WO 03/031464

PCT/US02/32263

Leu Cys	Ser Gln Asn Pro	Pro Val Leu Lys Arg His	Gln Arg Glu
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Ile Thr	Arg Thr Thr Leu Gln	Ser Asp Gln Glu Glu	Ile Asp Tyr
1670		1675	1680
Asp Asp	Thr Ile Ser Val Glu	Met Lys Lys Glu Asp	Phe Asp Ile
1685		1690	1695
Tyr Asp	Glu Asp Glu Asn Gln	Ser Pro Arg Ser Phe	Gln Lys Lys
1700		1705	1710
Thr Arg	His Tyr Phe Ile Ala	Ala Val Glu Arg Leu	Trp Asp Tyr
1715		1720	1725
Gly Met	Ser Ser Ser Pro His	Val Leu Arg Asn Arg	Ala Gln Ser
1730		1735	1740
Gly Ser	Val Pro Gln Phe Lys	Lys Val Val Phe Gln	Glu Phe Thr
1745		1750	1755
Asp Gly	Ser Phe Thr Gln Pro	Leu Tyr Arg Gly Glu	Leu Asn Glu
1760		1765	1770
His Leu	Gly Leu Leu Gly Pro	Tyr Ile Arg Ala Glu	Val Glu Asp
1775		1780	1785
Asn Ile	Met Val Thr Phe Arg	Asn Gln Ala Ser Arg	Pro Tyr Ser
1790		1795	1800
Phe Tyr	Ser Ser Leu Ile Ser	Tyr Glu Glu Asp Gln	Arg Gln Gly
1805		1810	1815
Ala Glu	Pro Arg Lys Asn Phe	Val Lys Pro Asn Glu	Thr Lys Thr
1820		1825	1830
Tyr Phe	Trp Lys Val Gln His	His Met Ala Pro Thr	Lys Asp Glu
1835		1840	1845
Phe Asp	Cys Lys Ala Trp Ala	Tyr Phe Ser Asp Val	Asp Leu Glu
1850		1855	1860

WO 03/031464

PCT/US02/32263

Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu Leu Val Cys His
 1865 1870 1875

Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln
 1880 1885 1890

Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp
 1895 1900 1905

Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn
 1910 1915 1920

Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe His
 1925 1930 1935

Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met
 1940 1945 1950

Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser
 1955 1960 1965

Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr
 1970 1975 1980

Val Arg Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr
 1985 1990 1995

Pro Gly Val Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly
 2000 2005 2010

Ile Trp Arg Val Glu Cys Leu Ile Gly Glu His Leu His Ala Gly
 2015 2020 2025

Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro
 2030 2035 2040

Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala
 2045 2050 2055

Ser Gly Gln Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His
 2060 2065 2070

WO 03/031464

PCT/US02/32263

Tyr	Ser	Gly	Ser	Ile	Asn	Ala	Trp	Ser	Thr	Lys	Glu	Pro	Phe	Ser
2075						2080					2085			
Trp	Ile	Lys	Val	Asp	Leu	Leu	Ala	Pro	Met	Ile	Ile	His	Gly	Ile
2090						2095					2100			
Lys	Thr	Gln	Gly	Ala	Arg	Gln	Lys	Phe	Ser	Ser	Leu	Tyr	Ile	Ser
2105						2110					2115			
Gln	Phe	Ile	Ile	Met	Tyr	Ser	Leu	Asp	Gly	Lys	Lys	Trp	Gln	Thr
2120						2125					2130			
Tyr	Arg	Gly	Asn	Ser	Thr	Gly	Thr	Leu	Met	Val	Phe	Phe	Gly	Asn
2135						2140					2145			
Val	Asp	Ser	Ser	Gly	Ile	Lys	His	Asn	Ile	Phe	Asn	Pro	Pro	Ile
2150						2155					2160			
Ile	Ala	Arg	Tyr	Ile	Arg	Leu	His	Pro	Thr	His	Tyr	Ser	Ile	Arg
2165						2170					2175			
Ser	Thr	Leu	Arg	Met	Glu	Leu	Met	Gly	Cys	Asp	Leu	Asn	Ser	Cys
2180						2185					2190			
Ser	Met	Pro	Leu	Gly	Met	Glu	Ser	Lys	Ala	Ile	Ser	Asp	Ala	Gln
2195						2200					2205			
Ile	Thr	Ala	Ser	Ser	Tyr	Phe	Thr	Asn	Met	Phe	Ala	Thr	Trp	Ser
2210						2215					2220			
Pro	Ser	Lys	Ala	Arg	Leu	His	Leu	Gln	Gly	Arg	Ser	Asn	Ala	Trp
2225						2230					2235			
Arg	Pro	Gln	Val	Asn	Asn	Pro	Lys	Glu	Trp	Leu	Gln	Val	Asp	Phe
2240						2245					2250			
Gln	Lys	Thr	Met	Lys	Val	Thr	Gly	Val	Thr	Thr	Gln	Gly	Val	Lys
2255						2260					2265			
Ser	Leu	Leu	Thr	Ser	Met	Tyr	Val	Lys	Glu	Phe	Leu	Ile	Ser	Ser
2270						2275					2280			
Ser	Gln	Asp	Gly	His	Gln	Trp	Thr	Leu	Phe	Phe	Gln	Asn	Gly	Lys

WO 03/031464

PCT/US02/32263

2285		2290		2295
Val Lys	Val Phe Gln Gly	Asn Gln Asp Ser Phe Thr	Pro Val Val	
2300		2305	2310	
Asn Ser	Leu Asp Pro Pro	Leu Leu Thr Arg Tyr	Leu Arg Ile His	
2315		2320	2325	
Pro Gln	Ser Trp Val His	Gln Ile Ala Leu Arg Met	Glu Val Leu	
2330		2335	2340	
Gly Cys	Glu Ala Gln Asp	Leu Tyr		
2345		2350		

<210> 31
 <211> 1471
 <212> DNA
 <213> Homo sapiens

<400> 31
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 cggctcagag aatactatga ccagacagct cagatgtgct gcagcaaagt ctcgccgggc 180
 caacatgcaa aagtcttctg taccaagacc tcggacaccg tgtgtgactc ctgtgaggac 240
 agcacataca ccagctctg gaactgggtt cccgagtgtc tgagctgtgg ctcccgtgt 300
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 aggcccggt ggtactgcgc gctgagcaag caggaggggt gccggtgtg cgcgcgctg 420
 cgcaagtgcc gcccggtt cggcgtggcc agaccaggaa ctgaaacatc agacgtggtg 480
 tgcaagccct gtgccccggg gacgttctcc aacacgactt catccacgga tatttgcagg 540
 cccaccaga tctgtaacgt ggtggccatc cctgggaatg caagcatgga tgcagtctgc 600
 acgtccacgt cccccaccg gagtatggcc ccaggggcag tacacttacc ccagccagt 660
 tccacacgat cccaacacac gcagccaact ccagaacca gcaactgtcc aagcacctcc 720
 ttctgtctcc caatgggccc cagccccca gctgaaggga gcaactggcg cttcgtctt 780
 ccagttggac tgattgtggg tgtgacagcc ttgggtctac taataatagg agtgggtgac 840
 tgtgtcatca tgaccaggt gaaaaagaag cccttgtgcc tgcagagaga agccaagggt 900
 cctcacttgc ctgccgataa ggcccggtt acacagggcc ccgagcagca gcacctgtg 960

WO 03/031464

PCT/US02/32263

```

atcacagcgc cgagctccag cagcagctcc ctggagagct cggccagtgc gttggacaga 1020
agggcgccca ctcggaacca gccacaggca ccaggcgtgg aggccagtgg ggccggggag 1080
gcccgggcca gcaccgggag ctcagattct tcccctggtg gccatgggac ccagggtcaat 1140
gtcacctgca tcgtgaacgt ctgtagcagc tctgaccaca gctcacagtg ctctcccaa 1200
gccagctcca caatgggaga cacagattcc agcccctcgg agtccccgaa ggacgagcag 1260
gtcccccttct ccaaggagga atgtgccttt cggtcacagc tggagacgcc agagaccctg 1320
ctggggagca ccgaagagaa gccctgccc cttggagtgc ctgatgctgg gatgaagccc 1380
agttaaccag gccggtgtgg gctgtgtcgt agccaagggtg ggctgagccc tggcaggatg 1440
accctgcgaa ggggccctgg tccttcagg c 1471

```

```

<210> 32
<211> 461
<212> PRT
<213> Homo sapiens

```

```

<400> 32

```

```

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu
1           5           10           15

```

```

Trp Ala Ala Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr
          20           25           30

```

```

Ala Pro Glu Pro Gly Ser Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln
          35           40           45

```

```

Thr Ala Gln Met Cys Cys Ser Lys Cys Ser Pro Gly Gln His Ala Lys
50           55           60

```

```

Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys Asp Ser Cys Glu Asp
65           70           75           80

```

```

Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys Leu Ser Cys
          85           90           95

```

```

Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg
          100          105          110

```

```

Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu
          115          120          125

```

WO 03/031464

PCT/US02/32263

Ser Lys Gln Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg
 130 135 140

Pro Gly Phe Gly Val Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val
 145 150 155 160

Cys Lys Pro Cys Ala Pro Gly Thr Phe Ser Asn Thr Thr Ser Ser Thr
 165 170 175

Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val Val Ala Ile Pro Gly
 180 185 190

Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr Arg Ser
 195 200 205

Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser
 210 215 220

Gln His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser
 225 230 235 240

Phe Leu Leu Pro Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly
 245 250 255

Asp Phe Ala Leu Pro Val Gly Leu Ile Val Gly Val Thr Ala Leu Gly
 260 265 270

Leu Leu Ile Ile Gly Val Val Asn Cys Val Ile Met Thr Gln Val Lys
 275 280 285

Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro His Leu Pro
 290 295 300

Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu
 305 310 315 320

Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser
 325 330 335

Ala Leu Asp Arg Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly
 340 345 350

WO 03/031464

PCT/US02/32263

Val Glu Ala Ser Gly Ala Gly Glu Ala Arg Ala Ser Thr Gly Ser Ser
 355 360 365

Asp Ser Ser Pro Gly Gly His Gly Thr Gln Val Asn Val Thr Cys Ile
 370 375 380

Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys Ser Ser Gln
 385 390 395 400

Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro
 405 410 415

Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser
 420 425 430

Gln Leu Glu Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro
 435 440 445

Leu Pro Leu Gly Val Pro Asp Ala Gly Met Lys Pro Ser
 450 455 460

<210> 33
 <211> 1475
 <212> DNA
 <213> Homo sapiens

<400> 33
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 agcgccccga cctcgccacc atgagagccc tgctggcgcg cctgcttctc tgcgtcctgg 120
 tcgtgagcga ctccaaaggc agcaatgaac ttcatacaagt tccatcgaac tgtgactgtc 180
 taaatggagg aacatgtgtg tccaacaagt acttctccaa cattcactgg tgcaactgcc 240
 caaagaaatt cggagggcag cactgtgaaa tagataagtc aaaaacctgc tatgagggga 300
 atggtcactt ttaccgagga aaggccagca ctgacaccat gggcgggcc tgccctgcct 360
 ggaactctgc cactgtcctt cagcaaactg accatgccc aagatctgat gctcttcagc 420
 tgggcctggg gaaacataat tactgcagga accagacaa ccggaggcga cctggtgct 480
 atgtgcaggt gggcctaaag ccgcttgtcc aagagtgcac ggtgcatgac tgccgagatg 540
 gaaaaaagcc ctctctctct ccagaagaat taaaatttca gtgtggccaa aagactctga 600
 ggccccgctt taagattatt gggggagaat tcaccaccat cgagaaccag ccctggtttg 660
 cggccatcta caggaggcac cgggggggct ctgtcaccta cgtgtgtgga ggcagcctca 720

WO 03/031464

PCT/US02/32263

```

tcagcccttg ctgggtgatc agcgccacac actgcttcat tgattacca aagaaggagg      780
actacatcgt ctacctgggt cgctcaaggc ttaactccaa cacgcaaggg gagatgaagt      840
ttgaggtgga aaacctcatc ctacacaagg actacagcgc tgacacgctt gctcaccaca      900
acgacattgc cttgctgaag atccgttcca aggagggcag gtgtgcgcag ccatcccgga      960
ctatacagac catctgcctg ccctcgatgt ataacgatcc ccagtttggc acaagctgtg    1020
agatcactgg ctttggaaaa gagaattcta ccgactatct ctatccggag cagctgaaga    1080
tgactgttgt gaagctgatt tcccaccggg agtgtcagca gcccactac tacggctctg    1140
aagtcaccac caaaatgctg tgtgctgctg acccacagtg gaaaacagat tcttgccagg    1200
gagactcagg gggacccctc gtctgttccc tccaaggccg catgactttg actggaattg    1260
tgagctgggg ccgtggatgt gccctgaagg acaagccagg cgtctacacg agagtctcac    1320
acttcttacc ctggatccgc agtcacacca aggaagagaa tggcctggcc ctctgagggt    1380
ccccagggag gaaacgggca ccaccgctt tcttgctggt tgtcattttt gcagtagagt    1440
catctccatc agctgtaaga agagactggg aagat                                1475

```

```

<210> 34
<211> 431
<212> PRT
<213> Homo sapiens

```

```

<400> 34

```

```

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1           5           10           15

```

```

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
          20           25           30

```

```

Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
          35           40           45

```

```

His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
          50           55           60

```

```

Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65           70           75           80

```

```

Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
          85           90           95

```


WO 03/031464

PCT/US02/32263

Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
100 105 110

Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
115 120 125

Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
130 135 140

Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
145 150 155 160

Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
165 170 175

Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
180 185 190

Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
195 200 205

Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
210 215 220

Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
225 230 235 240

Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
245 250 255

Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
260 265 270

His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
275 280 285

Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
290 295 300

Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
305 310 315 320

WO 03/031464

PCT/US02/32263

Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val
 325 330 335

Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly
 340 345 350

Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys
 355 360 365

Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu
 370 375 380

Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys
 385 390 395 400

Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu
 405 410 415

Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu
 420 425 430

<210> 35

<211> 107

<212> PRT

<213> Mus musculus

<400> 35

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala
 20 25 30

Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Ser Ala Ser Phe Leu Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro Pro

WO 03/031464

PCT/US02/32263

85

90

95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 36
 <211> 120
 <212> PRT
 <213> Mus musculus

<400> 36

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr
 20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

Ala Arg Ile Tyr Pro Thr Asn Gly Tyr Thr Arg Tyr Ala Asp Ser Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys Asn Thr Ala Tyr
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Leu Val Thr Val Ser Ser
 115 120

<210> 37
 <211> 120
 <212> PRT
 <213> Mus musculus

<400> 37

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln
 1 5 10 15

WO 03/031464

PCT/US02/32263

Thr Leu Thr Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser
 20 25 30

Gly Met Ser Val Gly Trp Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu
 35 40 45

Trp Leu Ala Asp Ile Trp Trp Asp Asp Lys Lys Asp Tyr Asn Pro Ser
 50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Asn Gln Val
 65 70 75 80

Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr Tyr Tyr
 85 90 95

Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser
 115 120

<210> 38
 <211> 106
 <212> PRT
 <213> Mus musculus

<400> 38

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr
 35 40 45

Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Asp
 65 70 75 80

Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe Thr
 85 90 95

WO 03/031464

PCT/US02/32263

Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 39
 <211> 1039
 <212> DNA
 <213> Homo sapiens

<400> 39
 tcctgcacag gcagtgcctt gaagtgcttc ttcagagacc tttcttcata gactactttt 60
 ttttctttaa gcagcaaaag gagaaaattg tcatcaaagg atattccaga ttcttgacag 120
 cattctogtc atctctgagg acatcaccat catctcagga tgaggggcat gaagctgctg 180
 ggggcgctgc tggcaactggc ggccctactg cagggggccg tgtccctgaa gatcgagcc 240
 ttcaacatcc agacatttgg ggagaccaag atgtccaatg ccaccctcgt cagctacatt 300
 gtgcagatcc tgagccgcta tgacatcgcc ctggtccagg aggtcagaga cagccacctg 360
 actgccgtgg ggaagctgct ggacaacctc aatcaggatg caccagacac ctatcactac 420
 gtggtcagtg agccactggg acggaacagc tataaggagc gctacctgtt cgtgtacagg 480
 cctgaccagg tgtctgcggt ggacagctac tactacgatg atggctgcga gccctgcggg 540
 aacgacaact tcaaccgaga gccagccatt gtcaggttct tctcccggtt cacagaggtc 600
 agggagtttg ccattgttcc cctgcatgcg gccccggggg acgcagtagc cgagatcgac 660
 gctctctatg acgtctacct ggatgtccaa gagaaatggg gcttgaggga cgtcatgttg 720
 atgggcgact tcaatgcggg ctgcagctat gtgagaccct cccagtggtc atccatccgc 780
 ctgtggacaa gccccacctt ccagtggctg atccccgaca gcgctgacac cacagctaca 840
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 gttcccgact cggctcttcc ctttaacttc caggctgcct atggcctgag tgaccaactg 960
 gcccaagcca tcagtgacca ctatccagtg gaggtgatgc tgaagtgagc agcccctccc 1020
 cacaccagtt gaactgcag 1039

<210> 40
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 40

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu

WO 03/031464

PCT/US02/32263

```

1           5           10           15

Leu Gln Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr
      20           25           30

Phe Gly Glu Thr Lys Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val
      35           40           45

Gln Ile Leu Ser Arg Tyr Asp Ile Ala Leu Val Gln Glu Val Arg Asp
      50           55           60

Ser His Leu Thr Ala Val Gly Lys Leu Leu Asp Asn Leu Asn Gln Asp
      65           70           75           80

Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro Leu Gly Arg Asn
      85           90           95

Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln Val Ser
      100          105          110

Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn
      115          120          125

Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe
      130          135          140

Thr Glu Val Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly
      145          150          155          160

Asp Ala Val Ala Glu Ile Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val
      165          170          175

Gln Glu Lys Trp Gly Leu Glu Asp Val Met Leu Met Gly Asp Phe Asn
      180          185          190

Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln Trp Ser Ser Ile Arg Leu
      195          200          205

Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser Ala Asp Thr
      210          215          220

Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly
      225          230          235          240

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WO 03/031464

PCT/US02/32263

```

                20                25                30

Ile His Trp Tyr Gln Gln Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile
      35                      40                      45

Lys Tyr Ala Ser Glu Ser Met Ser Gly Ile Pro Ser Arg Phe Ser Gly
      50                      55                      60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn Thr Val Glu Ser
65                      70                      75                      80

Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro Phe
      85                      90                      95

Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu
      100                      105                      110

Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser
      115                      120                      125

Cys Val Ala Ser Gly Phe Ile Phe Ser Asn His Trp Met Asn Trp Val
      130                      135                      140

Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg Ser
145                      150                      155                      160

Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu Ser Val Lys Gly Arg
      165                      170                      175

Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr Leu Gln Met
      180                      185                      190

Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg Asn
      195                      200                      205

Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr
      210                      215                      220

Val Ser
225

<210> 43
<211> 450

```


WO 03/031464

PCT/US02/32263

<212> DNA

<213> Homo sapiens

<400> 43

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gctgcatcag aagaggccat caagcacatc actgtccttc tgccatggcc ctgtggatgc      60
gcctcctgcc cctgtctggcg ctgctggccc tctggggacc tgaccagacc gcagcctttg    120
tgaaccaaca cctgtgcggc tcacacctgg tggaagctct ctacctagtg tgcggggaac    180
gaggcttctt ctacacaccc aagaccgcc gggaggcaga ggacctgcag gtggggcagg    240
tggagctggg cgggggccct ggtgcaggca gcctgcagcc cttggccctg gaggggtccc    300
tgcagaagcg tggcattgtg gaacaatgct gtaccagcat ctgctccctc taccagctgg    360
agaactactg caactagacg cagcccgag gcagcccccc acccgccgcc tctgcaccg      420
agagagatgg aataaagccc ttgaaccagc                                450

```

<210> 44

<211> 110

<212> PRT

<213> Homo sapiens

<400> 44

```

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu
1           5           10           15

Trp Gly Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly
          20           25           30

Ser His Leu Val Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe
          35           40           45

Phe Tyr Thr Pro Lys Thr Arg Arg Glu Ala Glu Asp Leu Gln Val Gly
          50           55           60

Gln Val Glu Leu Gly Gly Gly Pro Gly Ala Gly Ser Leu Gln Pro Leu
65           70           75           80

Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile Val Glu Gln Cys Cys
          85           90           95

Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn
          100          105          110

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<210> 45

WO 03/031464

PCT/US02/32263

<211> 1203

<212> DNA

<213> Hepatitis B virus

<400> 45

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atgggaggtt ggtcttccaa acctcgacaa ggcattggga cgaatcttcc tgttcccaat    60
cctctgggat tctttcccca tcaccagttg gaccctgogt tcggagccaa ctcaaacaat    120
ccagattggg acttcaaccc caacaaggat cactggccag aggcaatcaa ggtaggagcg    180
ggagacttcg ggccagggtt caccacacca cagggcggtc ttttggggtg gagccctcag    240
gctcagggca tattgacaac agtgccagca gcgcctcttc ctgtttccac caatcggcag    300
tcaggaagac agcctactcc catctctcca cctctaagag acagtcattc tcaggccatg    360
cagtggaaat ccacaacatt ccaccaagct ctgctagatc ccagagttag gggcctatat    420
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<210> 46

<211> 400

<212> PRT

<213> Hepatitis B virus

<400> 46

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Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
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WO 03/031464

PCT/US02/32263

Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
 20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
 35 40 45

Lys Asp His Trp Pro Glu Ala Ile Lys Val Gly Ala Gly Asp Phe Gly
 50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Trp Ser Pro Gln
 65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Val Ser
 85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
 100 105 110

Arg Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His
 115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
 130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Val Ser Pro
 145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
 165 170 175

Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
 180 185 190

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
 195 200 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
 210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
 225 230 235 240

WO 03/031464

PCT/US02/32263

Pro Ile Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe Ile Ile
 245 250 255

Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
 260 265 270

Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Leu Pro Gly Thr Ser
 275 280 285

Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly
 290 295 300

Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn
 305 310 315 320

Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu
 325 330 335

Trp Glu Trp Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro
 340 345 350

Phe Val Gln Trp Phe Ala Gly Leu Ser Pro Thr Val Trp Leu Ser Val
 355 360 365

Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser
 370 375 380

Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val Tyr Ile
 385 390 395 400

<210> 47

<211> 799

<212> DNA

<213> Homo sapiens

<400> 47

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cccaaccatt cccttatcca ggcccttttga caacgctatg ctccgcgccc atcgtctgca 180

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WO 03/031464

PCT/US02/32263

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```

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<210> 48
<211> 217
<212> PRT
<213> Homo sapiens

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<400> 48

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Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1          5          10          15

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Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu
20          25          30

```

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Ser Arg Pro Phe Asp Asn Ala Met Leu Arg Ala His Arg Leu His Gln
35          40          45

```

```

Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala Tyr Ile Pro Lys
50          55          60

```

```

Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln Thr Ser Leu Cys Phe
65          70          75          80

```

```

Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr Gln Gln Lys
85          90          95

```

```

Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp
100         105         110

```

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Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val
115         120         125

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WO 03/031464

PCT/US02/32263

Tyr Gly Ala Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu
 130 135 140

Glu Gly Ile Gln Thr Leu Met Gly Arg Leu Glu Asp Gly Ser Pro Arg
 145 150 155 160

Thr Gly Gln Ile Phe Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser
 165 170 175

His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe
 180 185 190

Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys
 195 200 205

Arg Ser Val Glu Gly Ser Cys Gly Phe
 210 215

<210> 49
 <211> 963
 <212> DNA
 <213> Homo sapiens

<400> 49
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WO 03/031464

PCT/US02/32263

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 tga 963

<210> 50
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 50

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg
 20 25 30

Asp Ala Pro Ala Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu
 35 40 45

Leu Val Arg His Cys Val Ala Cys Gly Leu Leu Arg Thr Pro Arg Pro
 50 55 60

Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro Arg Thr Ala Leu Gln Pro
 65 70 75 80

Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val Asp Lys Thr
 85 90 95

His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser
 100 105 110

Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg
 115 120 125

Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro
 130 135 140

Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala
 145 150 155 160

Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val

WO 03/031464

PCT/US02/32263

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                165                170                175
Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr
      180                185                190

Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr
      195                200                205

Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu
      210                215                220

Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys
      225                230                235                240

Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser
      245                250                255

Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp
      260                265                270

Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser
      275                280                285

Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala
      290                295                300

Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
      305                310                315                320

<210> 51
<211> 107
<212> PRT
<213> Homo sapiens

<400> 51
Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
1                5                10                15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
      20                25                30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
      35                40                45

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WO 03/031464

PCT/US02/32263

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys
100 105

<210> 52
<211> 107
<212> PRT
<213> Mus musculus

<400> 52

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Ile Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 53
<211> 119
<212> PRT
<213> Homo sapiens

WO 03/031464

PCT/US02/32263

<400> 53

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

Thr Leu Val Thr Val Ser Ser
 115

<210> 54

<211> 119

<212> PRT

<213> Mus musculus

<400> 54

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr
 1 5 10 15

Ser Val Arg Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

WO 03/031464

PCT/US02/32263

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Thr Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys
85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ala
115

<210> 55
<211> 214
<212> PRT
<213> Homo sapiens

<400> 55

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Thr Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala
100 105 110

Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly
115 120 125

Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala
130 135 140

WO 03/031464

PCT/US02/32263

Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln
 145 150 155 160

Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser
 165 170 175

Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys Val Tyr
 180 185 190

Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys Ser
 195 200 205

Phe Asn Arg Gly Glu Cys
 210

<210> 56
 <211> 448
 <212> PRT
 <213> Homo sapiens

<400> 56

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr
 20 25 30

Leu Ile Glu Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
 35 40 45

Gly Val Ile Tyr Pro Gly Ser Gly Gly Thr Asn Tyr Asn Glu Lys Phe
 50 55 60

Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser Thr Asn Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe Cys
 85 90 95

Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly
 100 105 110

WO 03/031464

PCT/US02/32263

Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 115 120 125

Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu
 130 135 140

Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp
 145 150 155 160

Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu
 165 170 175

Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser
 180 185 190

Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 195 200 205

Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys
 210 215 220

Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro
 225 230 235 240

Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser
 245 250 255

Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp
 260 265 270

Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn
 275 280 285

Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val
 290 295 300

Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu
 305 310 315 320

Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys
 325 330 335

Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr

WO 03/031464

PCT/US02/32263

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WO 03/031464

PCT/US02/32263

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WO 03/031464

PCT/US02/32263

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WO 03/031464

PCT/US02/32263

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WO 03/031464

PCT/US02/32263

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WO 03/031464

PCT/US02/32263

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WO 03/031464

PCT/US02/32263

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WO 03/031464

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WO 03/031464

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WO 03/031464

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WO 03/031464

PCT/US02/32263

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Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
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Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
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Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile

WO 03/031464

PCT/US02/32263

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Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
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Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
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Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
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WO 03/031464

PCT/US02/32263

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
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Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
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Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala
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