

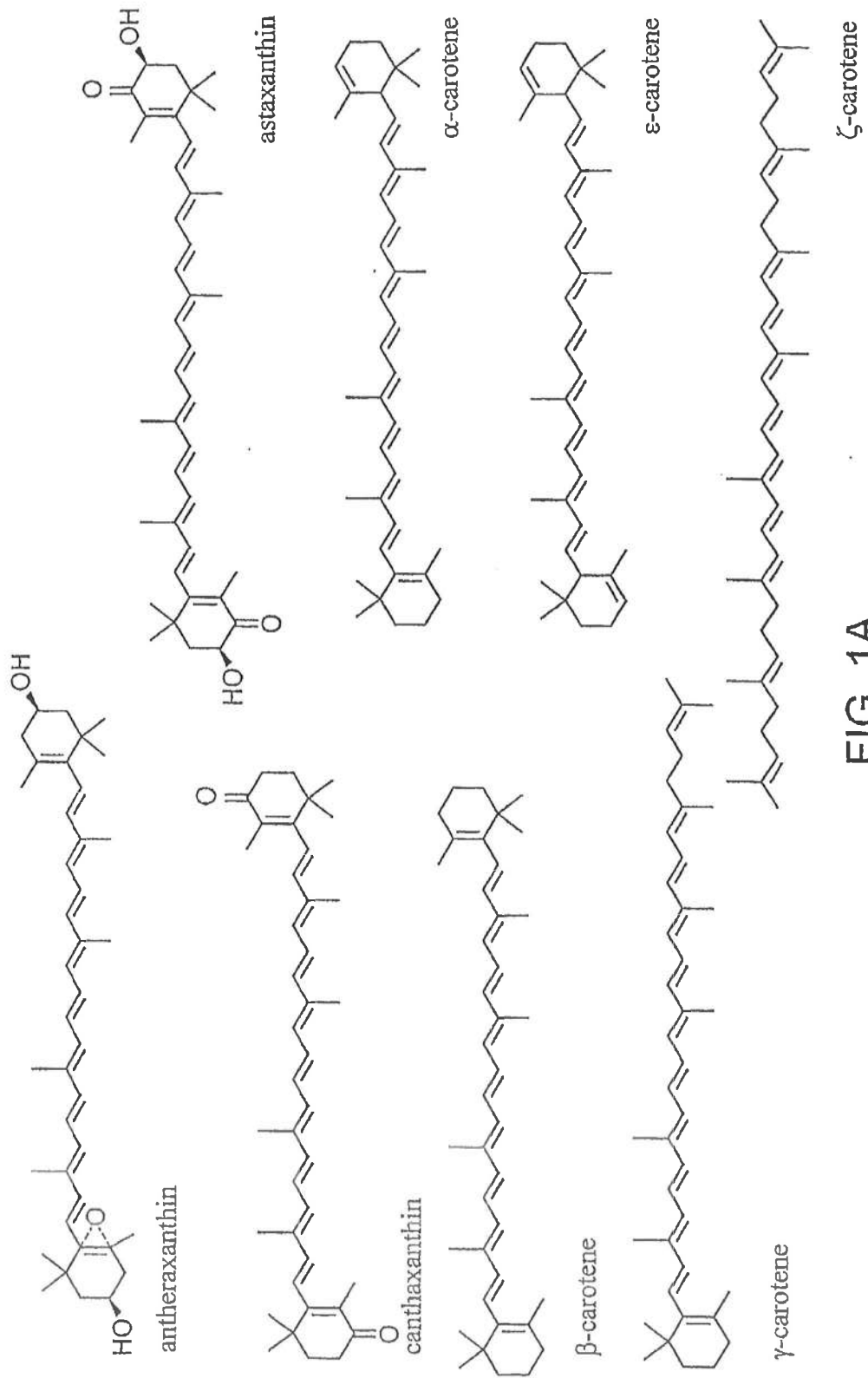


FIG. 1A

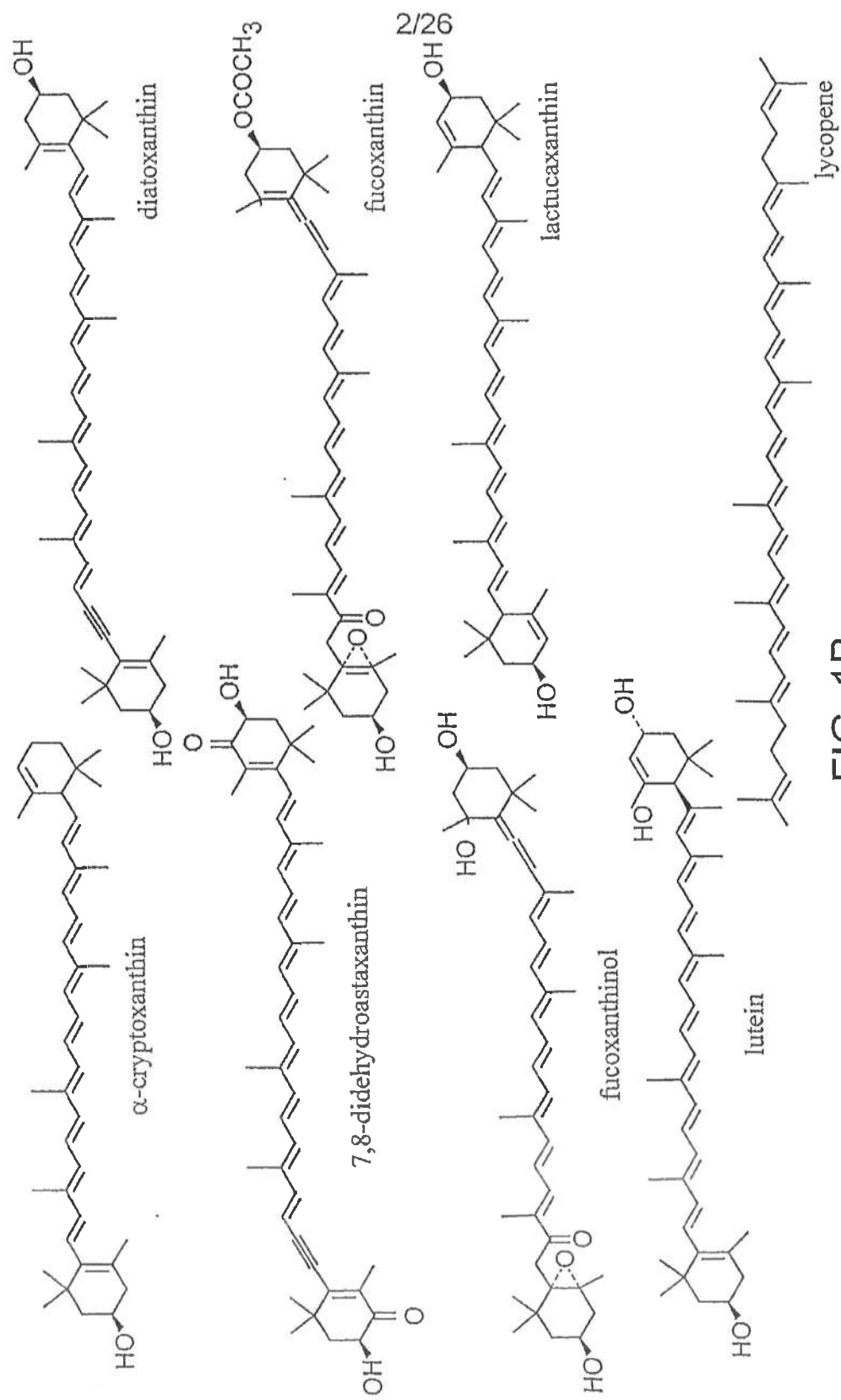


FIG. 1B

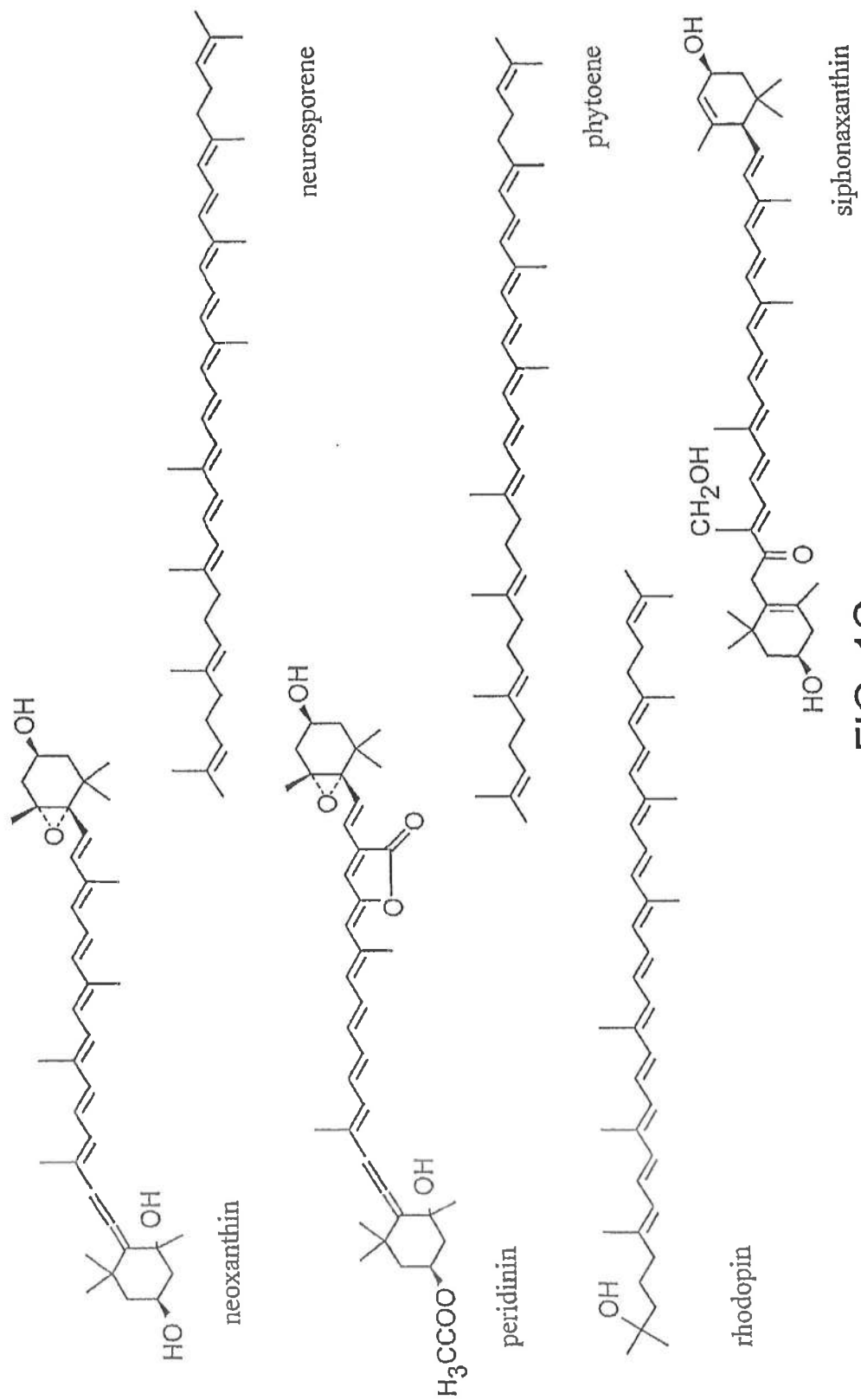


FIG. 1C

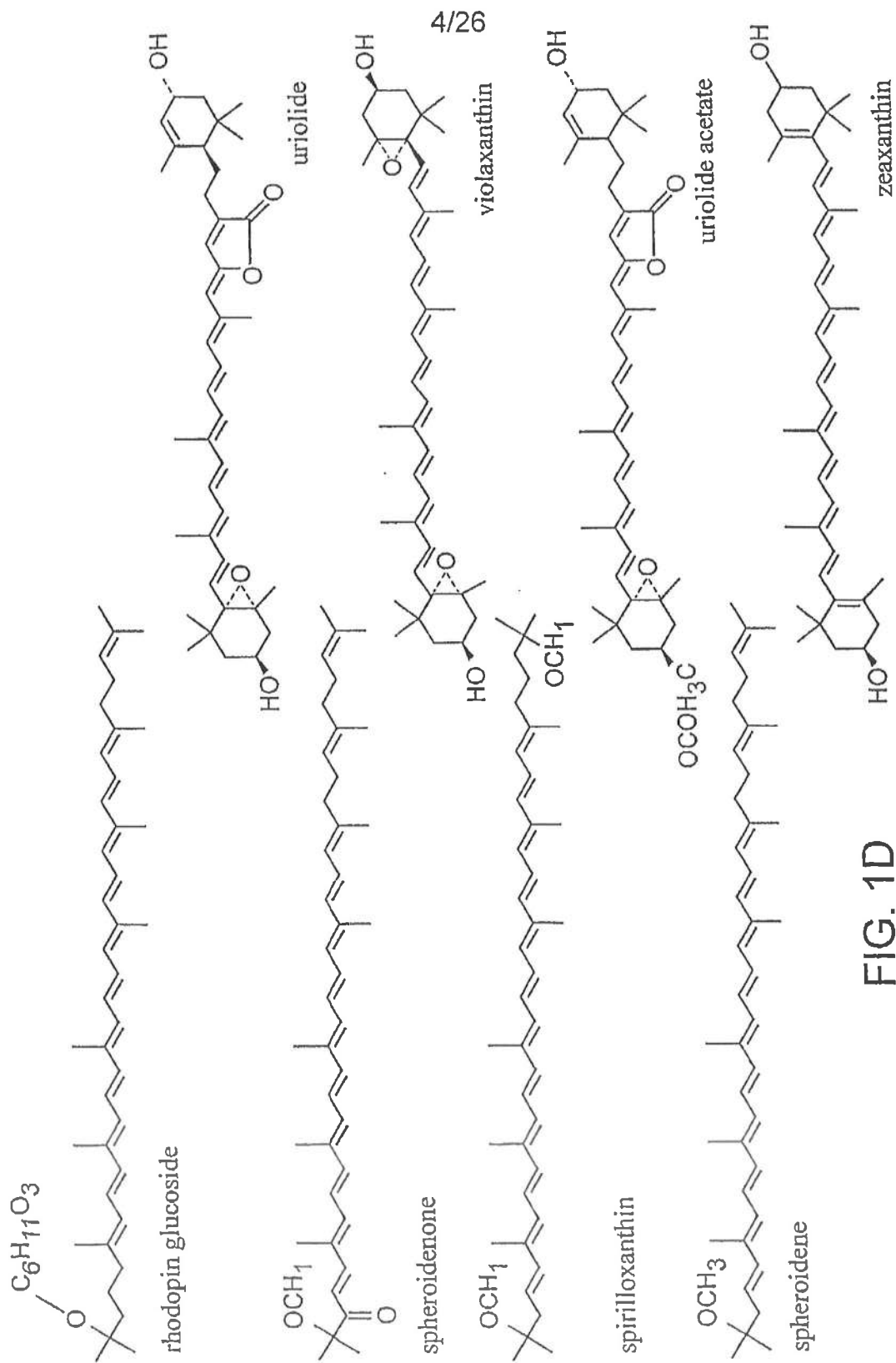


FIG. 1D

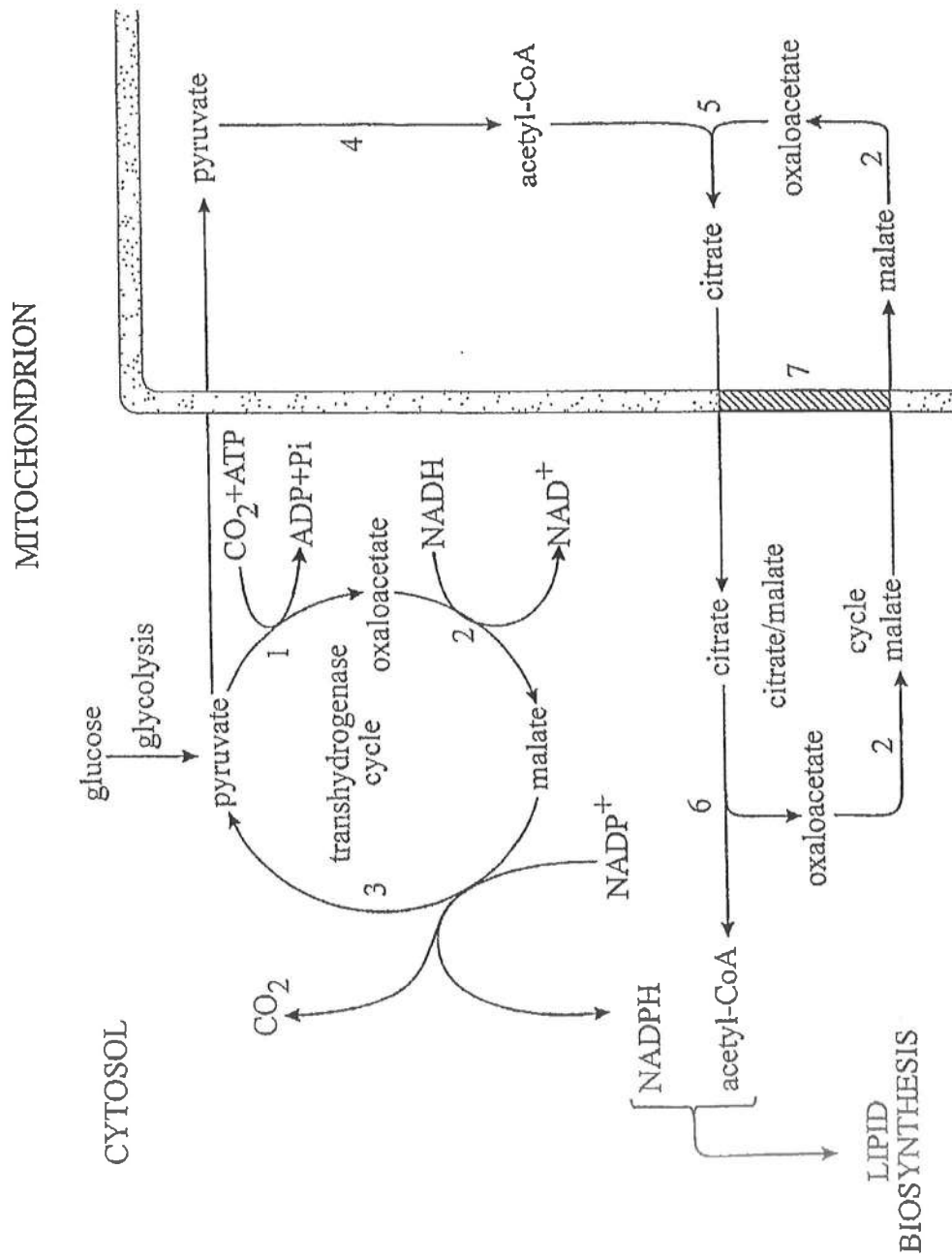


FIG. 2

MEVALONATE PATHWAY TO ISOPRENENES

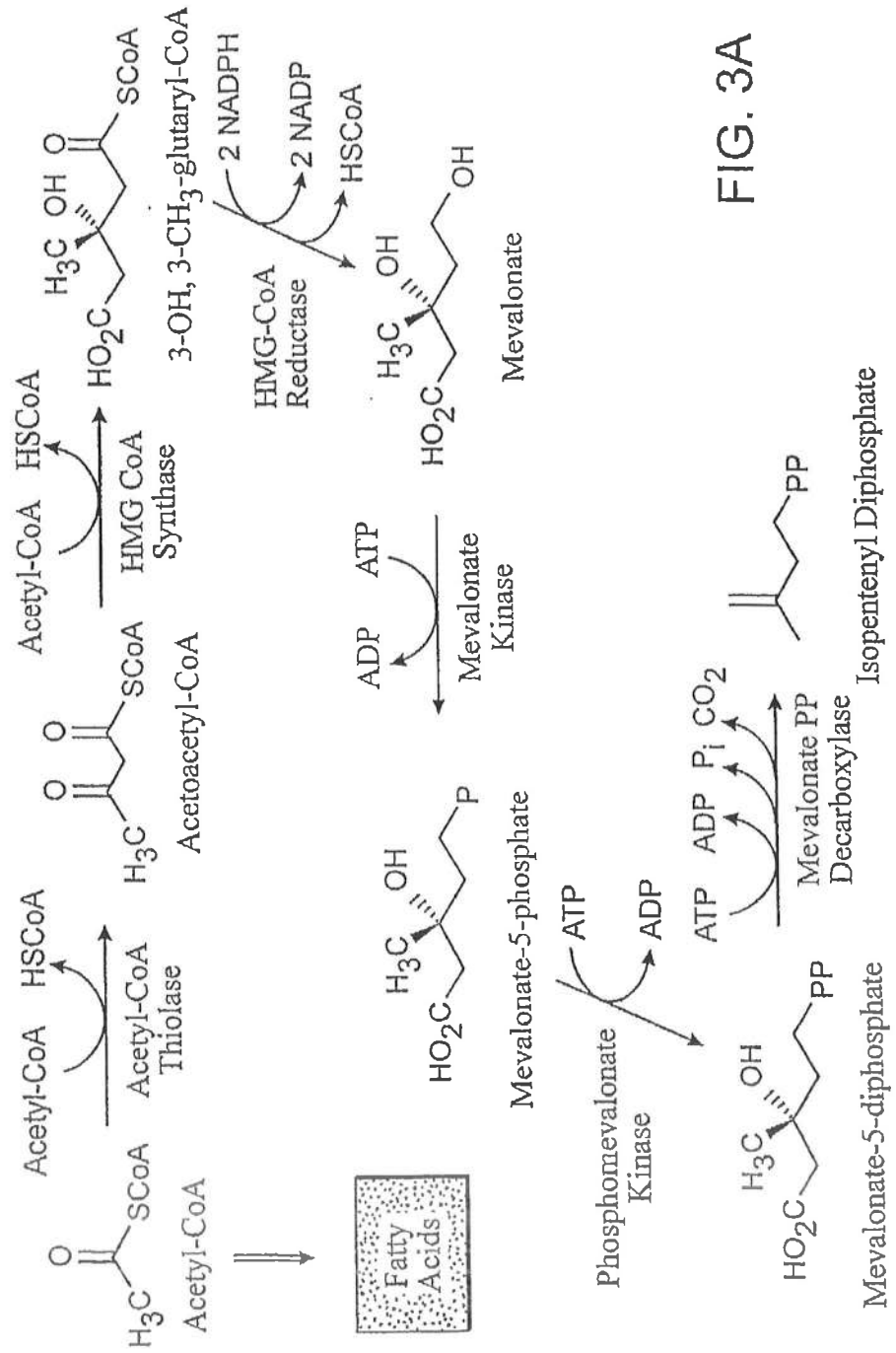


FIG. 3A

MEVALONATE PATHWAY TO ISOPRENoids

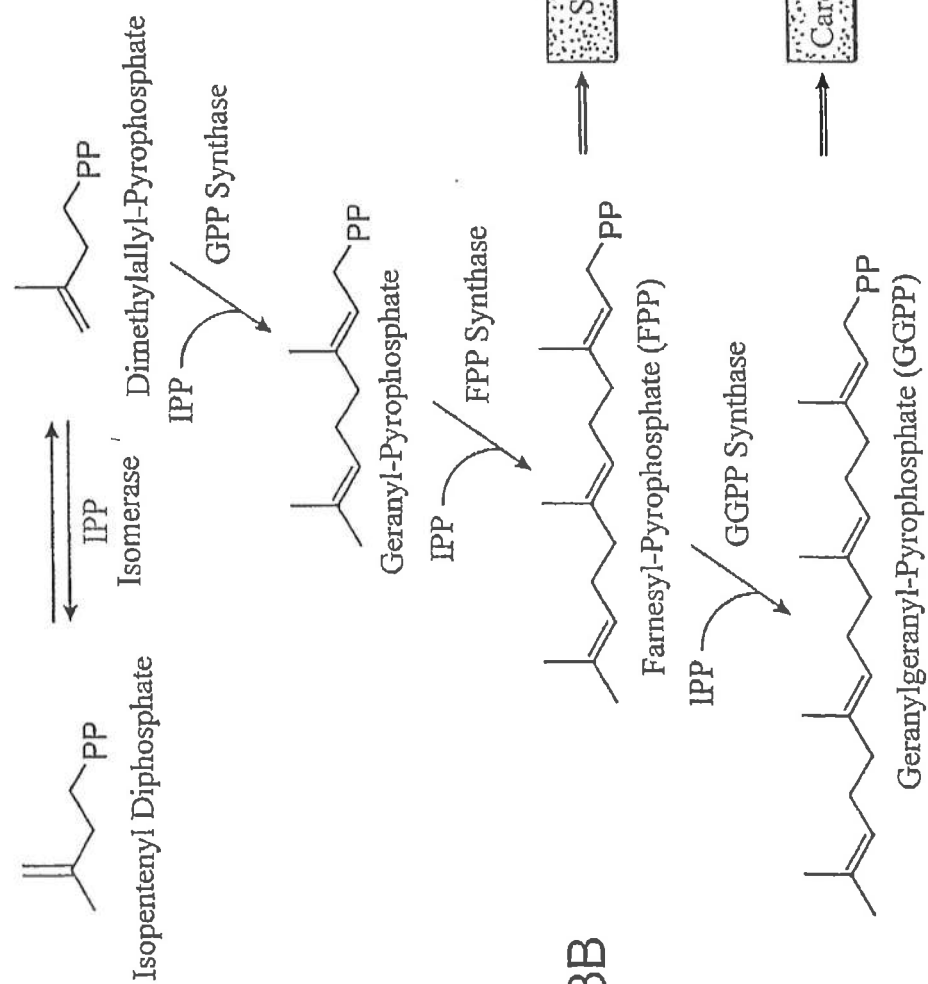


FIG. 3B

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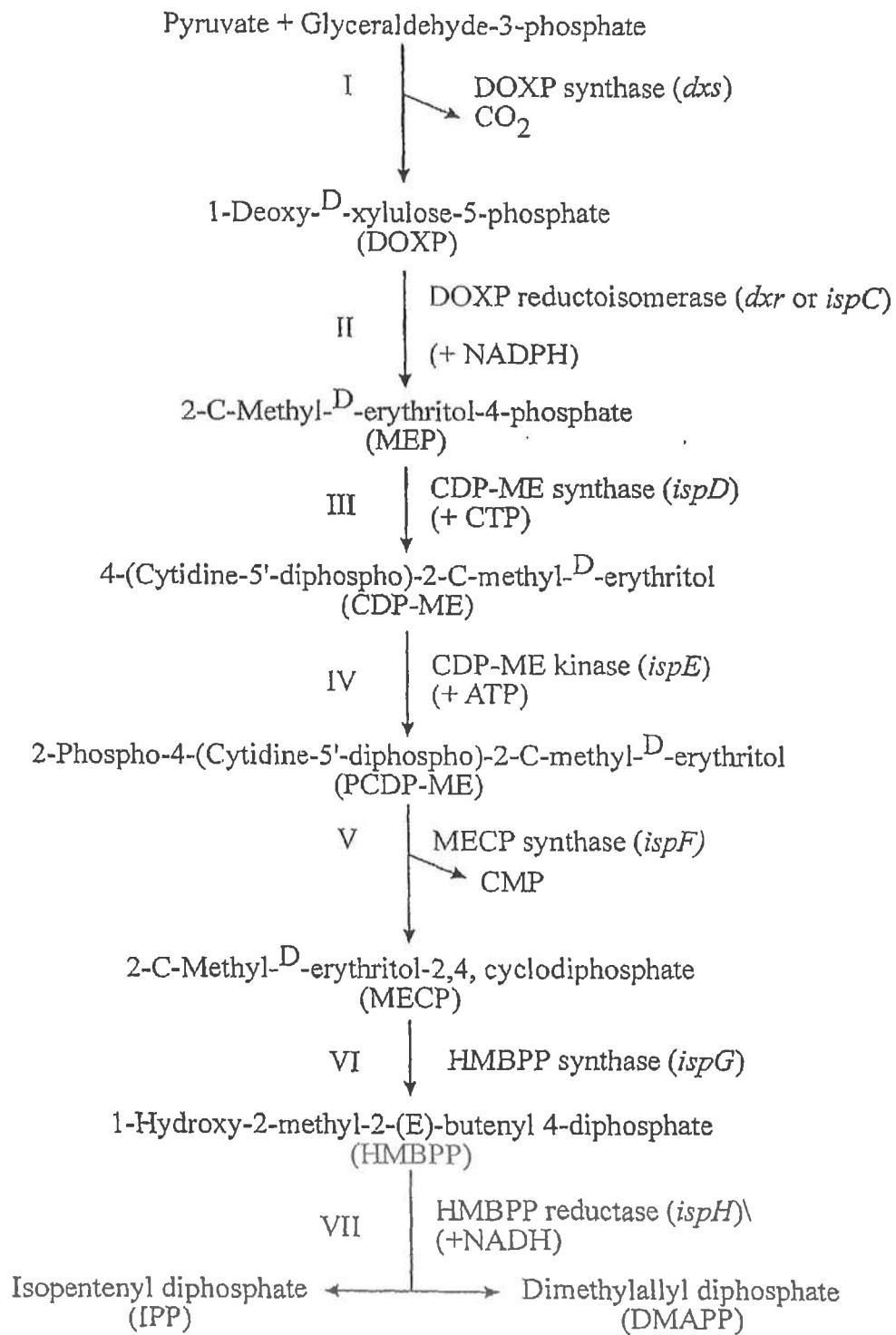


FIG. 4

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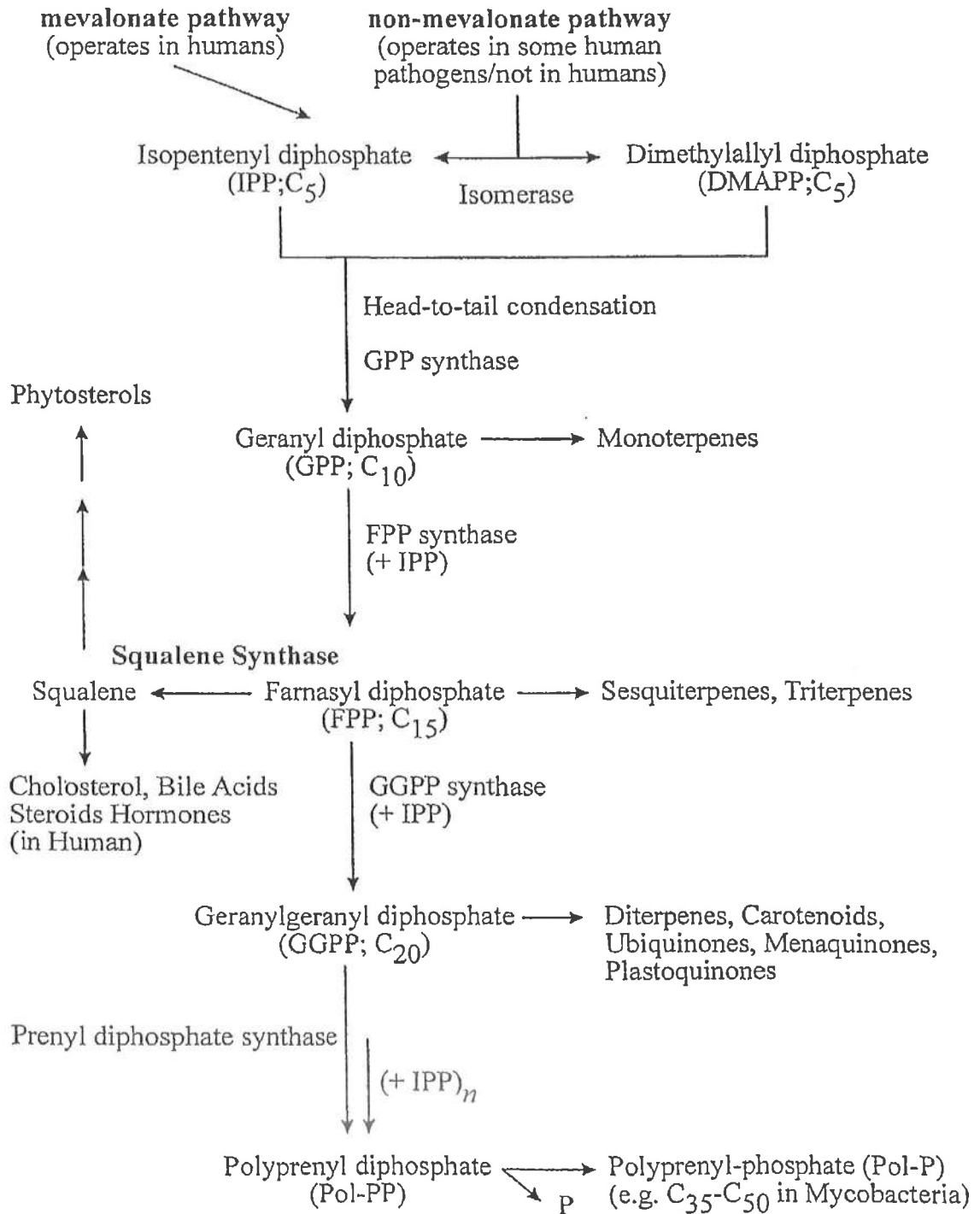


FIG. 5

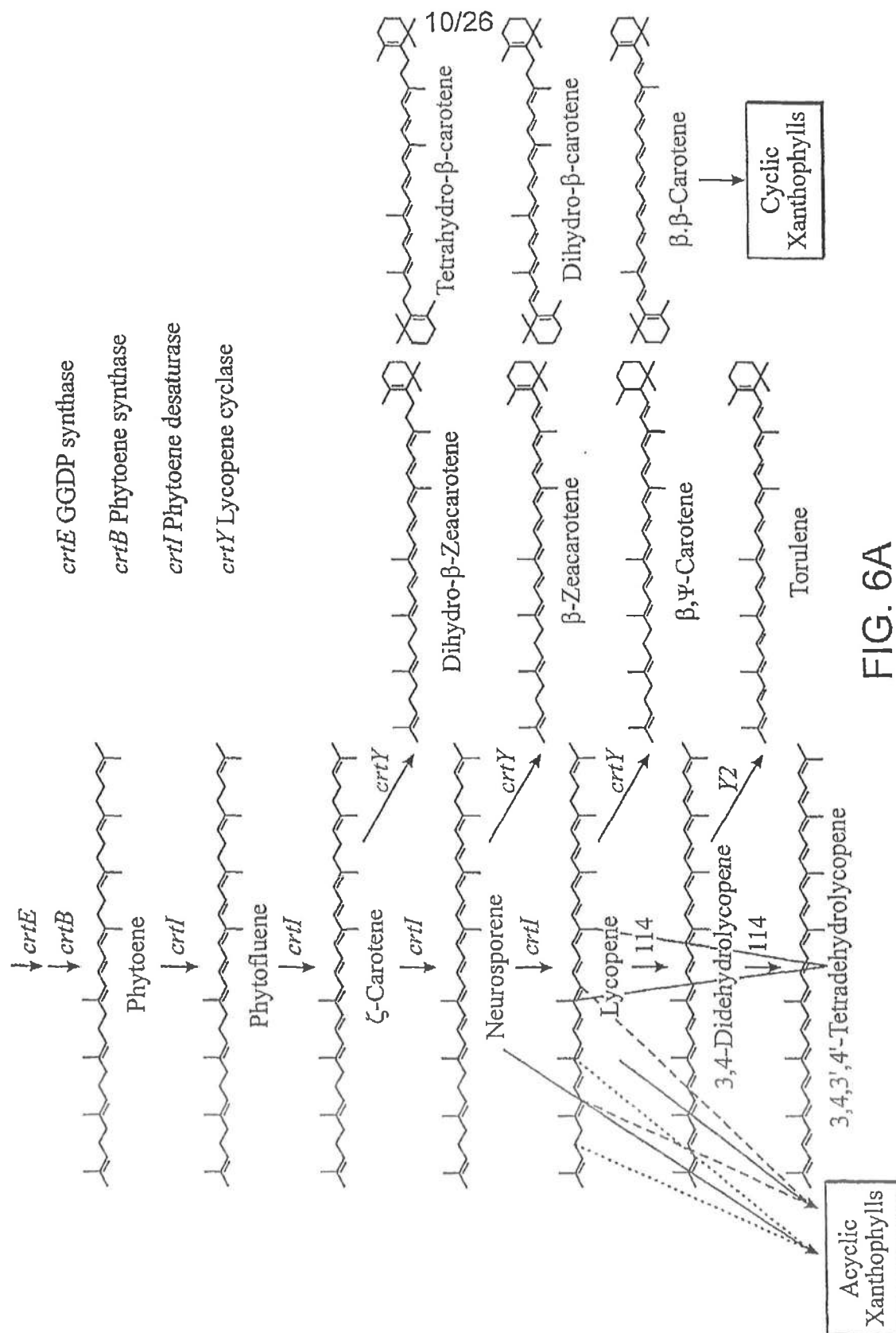


FIG. 6A

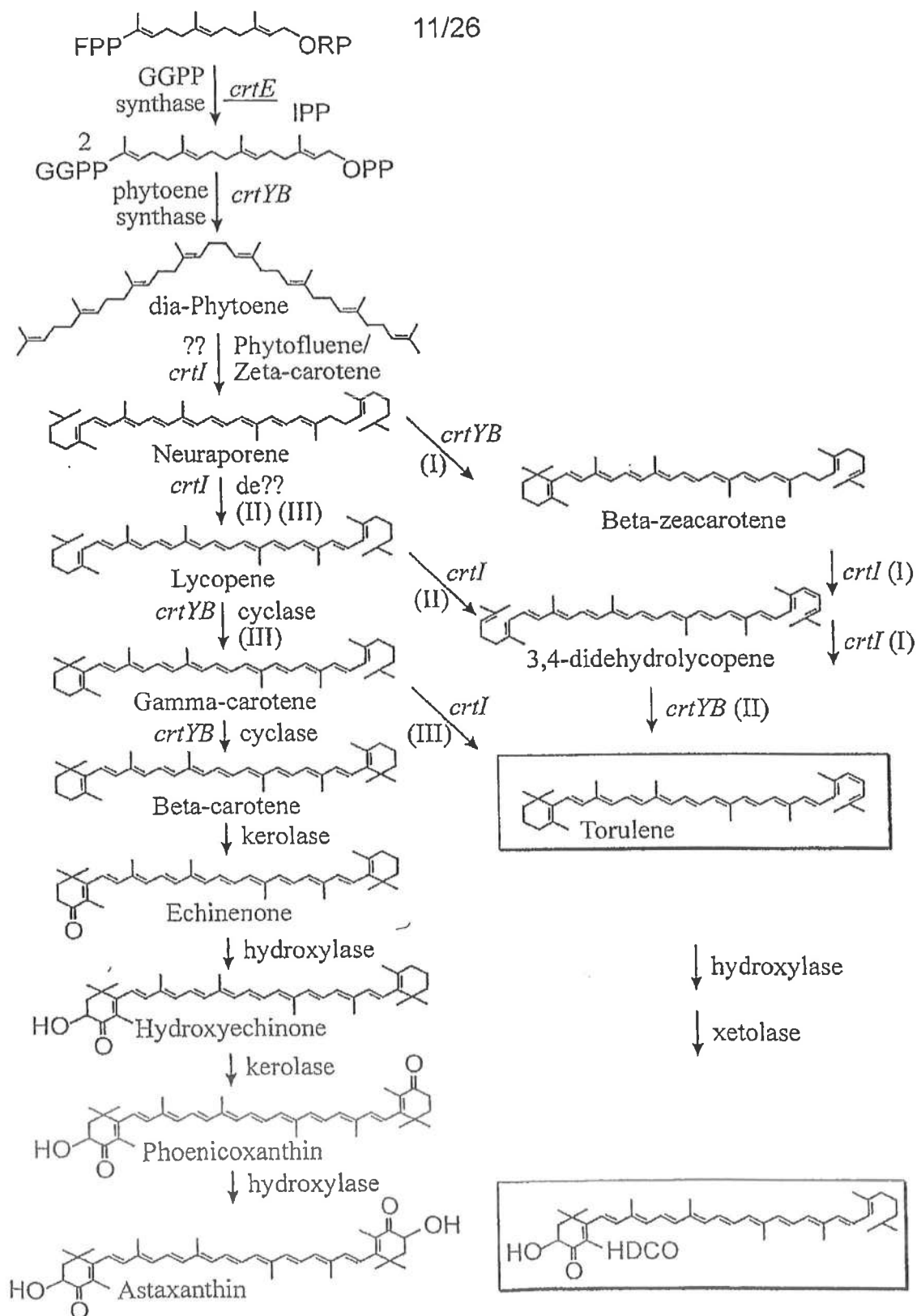


FIG. 6B

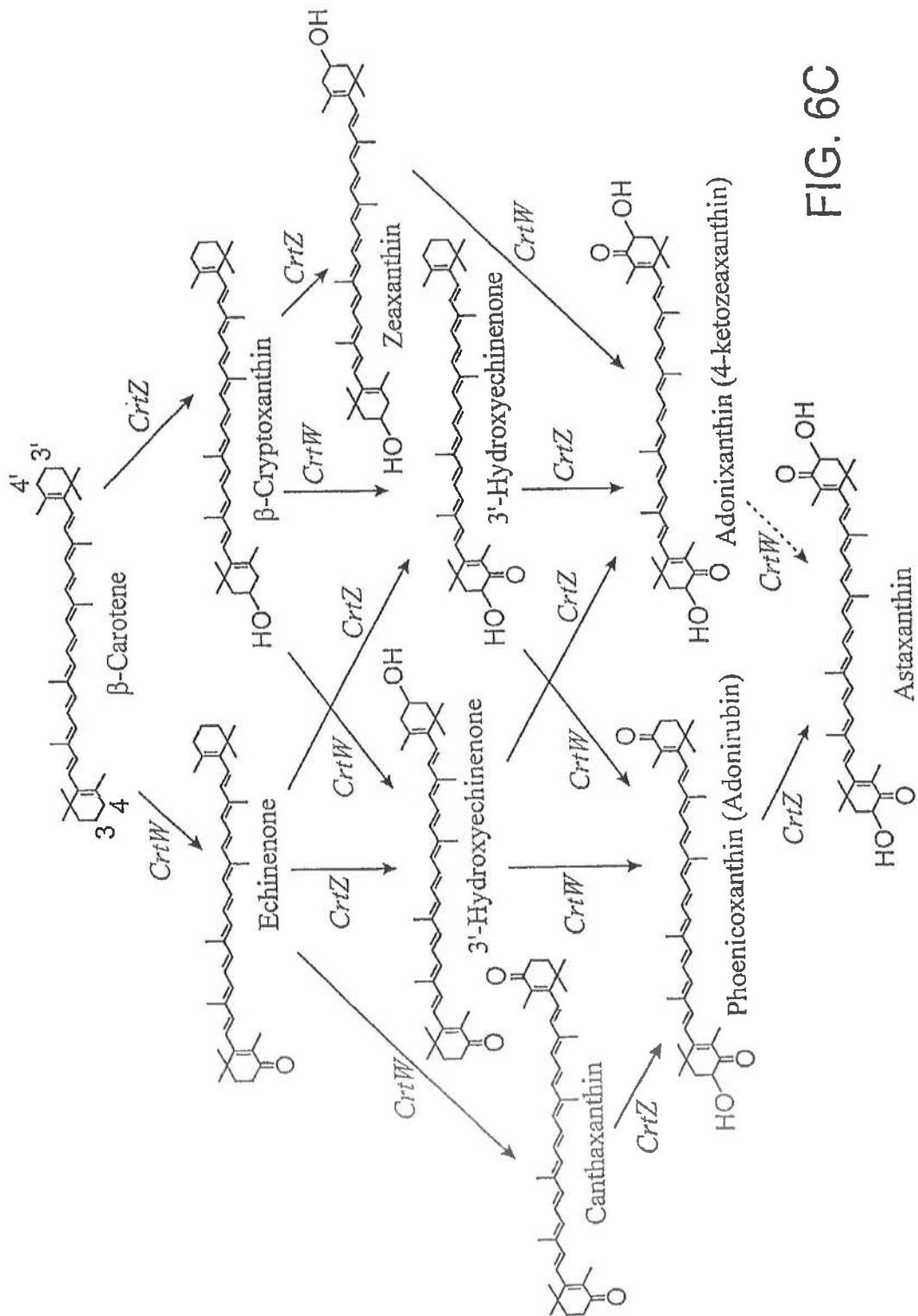


FIG. 6C

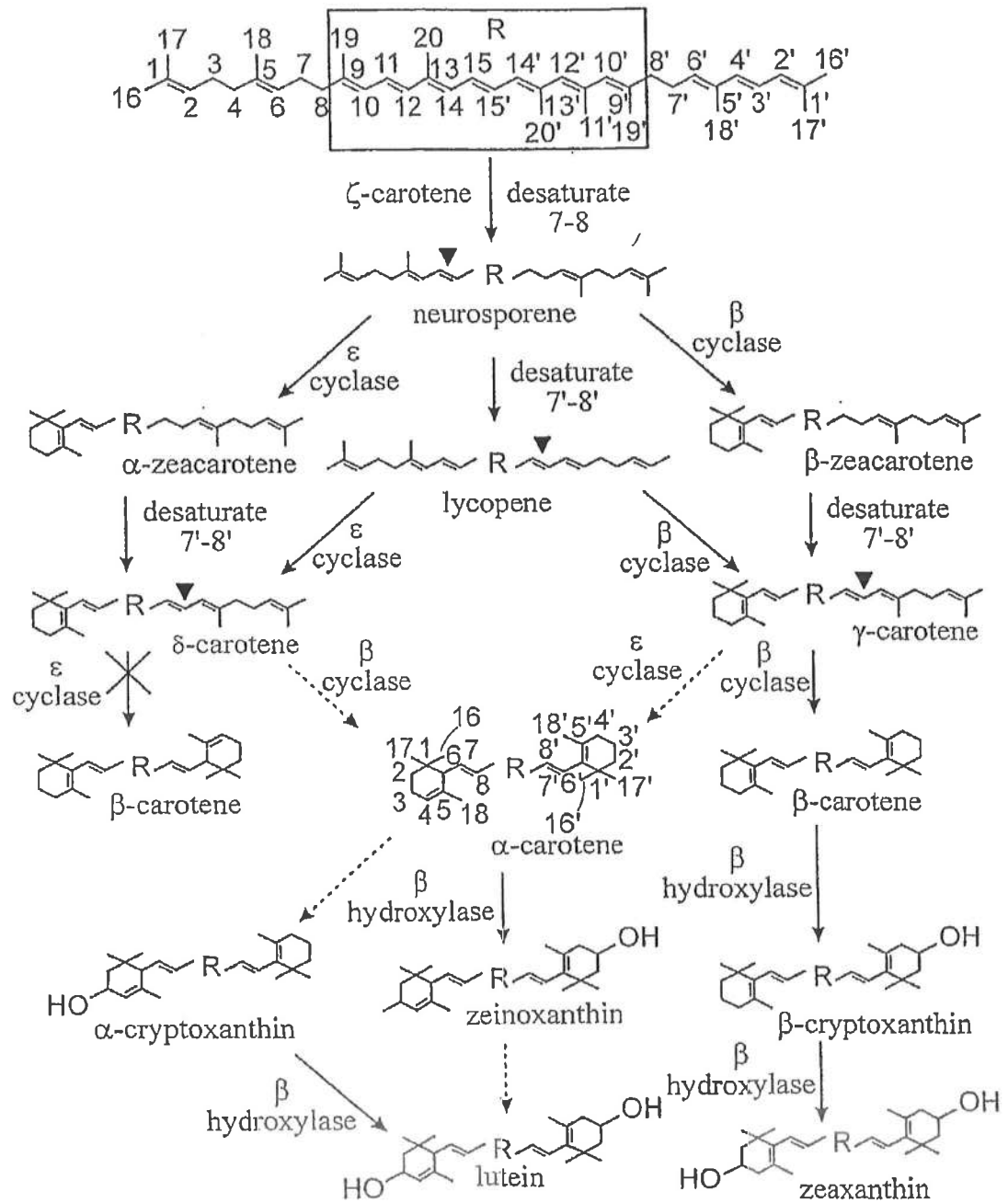


FIG. 6D

FIG. 7

Alignment of representative fungal HMG-CoA reductase polypeptides.

[illegible]

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	101		150
A. nidulans HMG	(98)	SWKQVEDSLNQDDQKVGNP	KREVDQHLALTLPDPSISKS-ASTAP
G. zeae HMG	(97)	AWNWKATEQDSIQ-----	HACADADHLALLTLVFPDTHSAESSSTAP
N. crassa HMG	(97)	EWNVQNHDP	EA-----VPANANHLALLTLVFPDTHAES--GPVVA
S. cerevisiae HMG2	(77)	YRSPVSDTWKLLS-----	SKEAADIYTPFHYLSTISFQSKDNSTILP
S. cerevisiae HMG1	(78)	YIRDSSLDGWVSIT-----	AHEASELPAPHHYLLNLNFSFNETDSIP
Y. lipolytica HMG	(65)	---WTHIAEADIP-----	SDAYRLAFAQLRVSDVQGGELAPTIP
Consensus	(101)	WRW ID I	AADA HLAL TLVFPDTQS E ASTIP
	151		200
A. nidulans HMG	(147)	AADALPVPANASAQLLPHTPNL	ESFFSHDSSLVFTLPFDQVPQFLRAVQE
G. zeae HMG	(139)	RSSHVPMPQNLSITPLPSTKNSFT	AYSQDSILAYSLPYAEG-----
N. crassa HMG	(135)	QNTVPLPSNLSITPLPSTAISFT	YSQDSALAFSLPYQAPEFLANAQE
S. cerevisiae HMG2	(121)	SLDDVIYSVDHTRYLLSEEPKIP	TELVSFNGTKWRLRNSN-----
S. cerevisiae HMG1	(122)	ELANTVFEKDNIKYLLQEDLSV	SKEISSDGTGKWLRSRDK-----
Y. lipolytica HMG	(100)	GAVASDLDHRIVM	MDYKQWAPWTASNEQIASENHIWKHSFK-----D-
Consensus	(151)	A VPVP N SI LLP T IFT	YSQDSSL FSLPYS
	201		250
A. nidulans HMG	(197)	LPDPTLEDDEGEQKR---	WIMRATRGVSGPNGTISSWLSDAWSSFVDLI
G. zeae HMG	(180)	-----	PDVVQWANNAWTEFLDLL
N. crassa HMG	(184)	IPNAVSSQETIETERGHEKKW	MIMKAARVQTRSSIVKWVQNAWVEFTDLL
S. cerevisiae HMG2	(162)	-----	FILDLNIYRNMVKQFSNKT
S. cerevisiae HMG1	(163)	-----	SLFDVKTAYSLLYDVFSENV
Y. lipolytica HMG	(142)	-----	HVAFSWIKWERWAYLRLSTLI
Consensus	(201)		DIV W NAW FSDLI

FIG. 7B

	(244)	A. nidulans HMG	KHAETIDIIIMTLGYLAMVLSFASLEFSMKQLGSKFWLATTIVLFSGMFAF	300
	(198)	G. zeae HMG	KNAETIDIVIMFLGYTAMHLTFVSLFLSMRKIGSKFWLGICTLFFSSVFAP	
	(234)	N. crassa HMG	RNAETLDIIMALGYISMHLTFVSLFLSMRMGSNFWLATSVIFSSIAP	
	(182)	S. cerevisiae HMG2	SEFDQFDLFIILAYLTIFYTLCCLENDRMKIGSKFWLSFALSNSACAL	
	(183)	S. cerevisiae HMG1	TQADPFVDLIMVTAYLMMFYTI FGLENDMRKTGSNFWLSASTVVNSASSL	
	(163)	Y. lipolytica HMG	QGADNFDAVVALGYLAMHYTFFSLFRSKRVGSHFWLASMALVSSFAP	
	(251)	Consensus	KNADTFDIIIM LGYLAMHYTF SLF SMRKLGSKFWLATS LFSSIFAF	350
			301	
	(294)	A. nidulans HMG	LFGLLVTTKFG-VPIINLLLLSEGLPEIIVTTIGFEKPITLTRAVLASITDK	
	(248)	G. zeae HMG	LFGLLVTTKLG-VPISVILLSEGLPEIIVTTIGEEKNIIVTRAVMSHAIHH	
	(284)	N. crassa HMG	LFGLLVTTKLG-VPNMNVLLSEGLPEIIVTTIGFEKNIVLTRAVLSHAIDH	
	(232)	S. cerevisiae HMG2	YLSLYTHSLLKKPASLLSLVIGLPFTVII GEKHKMRLAAFSLOKFHRI	
	(233)	S. cerevisiae HMG1	FLALYVTQCILGKEVSALTLEGLPFLVVVGKHKIKIAQYALEKFERV	
	(213)	Y. lipolytica HMG	ILAVVASSSLG-YRPSMITMSEGLPEIIVVAIGEDRKVNLADEVLTJSSSQ	
	(301)	Consensus	LLGLLVTTKLG VPISMLLLSEGLPFLVVTIGFEKKIVLTRAVALS AID	400
			351	
	(343)	A. nidulans HMG	KRQGS-----ATSTPSSIQDSIQTAIREQQFEIIRDYCIEISILIA	
	(297)	G. zeae HMG	RRQIONSKSGKSPERSMQNVIOYAVQS AIKEKGFEIMRDYAIEIVLAL	
	(333)	N. crassa HMG	RRPTE--KSGKPSKQADSASHSIQSAIQLAIKEKGFDIVKDYAIEAGIIVL	
	(282)	S. cerevisiae HMG2	S-----IDKKITVSNITTYEAMFQEGAYLIIRDYLFYISFSFIG	
	(283)	S. cerevisiae HMG1	G-----LSKRITTDIVTFESVSEGGRLIQDHLCICFAFAG	
	(262)	Y. lipolytica HMG	-----LAPMVQVITKIASKALFEYSLEVAALFA	
	(351)	Consensus	RR S SIQ AIQ AIKE GFEIRDYAIEISILIA	

FIG. 7C

FIG. 7D

		551	600
A. nidulans HMG	(524)	DPFKVAENGLD	ATYVSAKSQKLETLVTVPPIKV[K]KLEYPSTVHYAKLGS
G. zeae HMG	(488)	DPFKVASNGLD	AILAAAKSNRPILVTITPIKYELEYPSTHYALGSAIN
N. crassa HMG	(527)	DPFKVASNGLD	IIIEAARADGRETTVTITPIRYELEYPSTHYDLPQKS-
S. cerevisiae HMG2	(439)	S---	TIYSLPNFINYKDIGNLSNQVITISVLPKQVYTPLKKYHQIEDSVL-
S. cerevisiae HMG1	(440)	K---	ERVSLPDEITISNASENFKEQAVSVTPILLYKPIKSYQRIEDMVL-
Y. lipolytica HMG	(416)	TPITLSPELLHAIPASVP----	VVVTFFVPSVVVEHSQLLIQLEDALTE-
Consensus	(551)	DPFKVA NLLDAI AAKSN RETLVTVTPIKYELEYPSTHY E	S 650
A. nidulans HMG	(573)	----	QSIEIEYTDQLLDVAGGHV[L]NGVLKSIEDPVISKWIITAVLTLSIVL
G. zeae HMG	(538)	GNNAEYTD	AFHHHFQGYGVGGRMVGGILKSLIEDPVLKWIIVIALAISVAL
N. crassa HMG	(576)	----	AEVEGGDYANLGGYGGRMVGSILKSLIEDPTLSKWIIVVVALAISVAL
S. cerevisiae HMG2	(485)	----	IL-----IIDSVSNAIRDQFISKLIFFAFAVVSISI
S. cerevisiae HMG1	(486)	----	IL-----LERNVSVAIRDRFVSKLVLSALVCSAVL
Y. lipolytica HMG	(460)	----	FIACSKTIGDPVISKYIFLCIMVSTAL
Consensus	(601)	L G GG MLGSVSKSIEDPVISKWIIVIALAISIAL	700
A. nidulans HMG	(619)	NGYLFNAARWSIKEP	AAAPAKEP-----
G. zeae HMG	(588)	NGYLFNVARWGIKD	PNVPEHNIDRNELARAQQFNDTGSATLPLGEYMPPT
N. crassa HMG	(621)	NGYLFNAARWGIKD	PNVPDHPINPKELDEAQKFNDTASATLPLGEYMKPT
S. cerevisiae HMG2	(514)	NVYLLNAAKIH	TGYMNFQPQSNKTDLLVVQQKSATIEFSETRSMPLASGL
S. cerevisiae HMG1	(515)	NVYLLNAARIHTSY	TADQLVKTEVTKKSFAPVQKASTPVLTKTVISGS
Y. lipolytica HMG	(488)	NVYLLFGATREVR	TQSVKVEKHVPVIE-----K-----
Consensus	(651)	NVYLFNAARW IKDPNV EV EL Q N SA L I T	

FIG. 7E

		701		750
		(643)	-----[AKPKVYPKTDLNAGPKRSMEECEAM]LKA	
A. nidulans HMG		(638)	PMR---TEPSTPAITDDEAEGLOMTKARSDKLPNRPNEE-----LEKLI[AE	
G. zeae HMG		(671)	APSSPVAPI[TPSSTDDEND]AQAKENRAVTLAAQRATTIRSQGEL[DKMTAE	
N. crassa HMG		(564)	E----TPVTAKDIIISEEIQNN---ECVYALSSQDEPIRPLSNLVELMEK	
S. cerevisiae HMG2		(565)	K----VKSLSSAQSSSSSGPSSSSEEDDSRD[ESLDKKIRPLEE]LEALLSS	
S. cerevisiae HMG1		(518)	-----PSEKEE[ETSS]EDS[EL]TVGQPKPVTTETRS[LD]LEATMKA	
Y. lipolytica HMG		(701)	TPA TDDE S S V KI IRSLEELEALLAA	
Consensus				800
		751		
A. nidulans HMG		(671)	KRAAYLSDELL[ET]SLSGKLPGYALLKSL[ENEELMSRVD]AFLRAVKLRRA	
G. zeae HMG		(681)	KRVKE[MSDEEIVSL]MRCKIPGYALLKTLG-----DFTRAVKIRRS	
N. crassa HMG		(721)	KRTHELNDEETVHL[SLKGI]PGYALEKTLK-----DFTRAVKVRRS	
S. cerevisiae HMG2		(607)	EQLKNMNTTEVSNIVNGKLPLY[SL]EKKLE-----DTLRAVLVRRK	
S. cerevisiae HMG1		(611)	GNTKQLKNKEVAALVTHGKLPLYALEKKLG-----DTTRAVAVRRK	
Y. lipolytica HMG		(558)	GKTKLLEDHEVVKLSLEGKLPLYALEFKQLG-----DNTRAVGIRRS	
Consensus		(751)	KKTK L DEEVV LSL GKLPYALEKTLG DFTRAVKIRRS	
		801		850
A. nidulans HMG		(721)	VVSRTPATSAVTSS[LET]SKLPYKDYKDYNYALVHGACCENVIGTLPLPLGVAG	
G. zeae HMG		(722)	II[ARNRATSD]LTHSLERSKLPFEKYNW[ER]VFCACCENVIGYMPLPVGVAG	
N. crassa HMG		(762)	IIISRTKAT[TELTN]ILDRSKLPYQNVNWAQVHGACCENVIGYMPLPVGVAG	
S. cerevisiae HMG2		(648)	ALST---L-AE[SPIL]MSEKLPFRNYDYDRVFGACCENVIGYMPIPVGVIG	
S. cerevisiae HMG1		(652)	ALSI---L-AEAPVLASDRLPYKKNYDYDRVFGACCENVIGYMPLPVGVIG	
Y. lipolytica HMG		(599)	IISQ---Q-[SNTKT]LET[SKLPY]LHMDYDRVFGACCENVIGYMPLPVGVAG	
Consensus		(801)	IISR ATSALT SLESSKLPYKNYNYDRVFGACCENVIGYMPLPVGVAG	

FIG. 7F

		851	900
		PLVTDGQSYFIPMATIEGVLVASASRGAKAINAGGAVIVLTGDMTRGP	
(771)	A. nidulans HMG		
(772)	G. zeae HMG	RLVTDGQSYFIPMATTEGVLVASASRGCKAINAGGAVTLTADGMTRGP	
(812)	N. crassa HMG	PLVTDGQSFIFVPMATTEGVLVASTSRGCKAINSGGAVTLTADGMTRGP	
(694)	S. cerevisiae HMG2	PLITDGTSYHIPMATTEGCLVASAMPGCKAINAGGATTVLTKDGMTRGP	
(698)	S. cerevisiae HMG1	PLVTDGTSYHIPMATTEGCLVASAMRGCKAINAGGATTVLTKDGMIRGP	
(645)	Y. lipolytica HMG	PMNTDGKNYHIPMATTEGCLVASTMRGCKAINAGGVTTLTQDGMTRGP	
(851)	Consensus	PLVIDGQSYHIPMATTEGVLVASASRGCKAINAGGAVTLTADGMTRGP	
		901	950
(821)	A. nidulans HMG	CVGFPTIARAATAKVWLDSEEGKSVMTAAFNSTSRFARLQHIKTAAGTY	
(822)	G. zeae HMG	CVAFETIERAGAAKLWLDSEAGSDIMKKAFNSTSRFARLQSMKTALAGTN	
(862)	N. crassa HMG	CVQFETIERAGAAKLWLDSEKQSIMKKAFNSTSRFARLETMTAMAGTN	
(744)	S. cerevisiae HMG2	VVRFPITLIRSGACKIWLDSSEEGQNSIKKAFNSTSRFARLQHTQTCLAGDL	
(748)	S. cerevisiae HMG1	VVRFPITIKRSGACKIWLDSSEEGQNAIKKAFNSTSRFARLQHIQTCLAGDL	
(695)	Y. lipolytica HMG	CVSEFSLKRAGAAKIWLDSSEGLKSMRKAFNSTSRFARLQSLHSTLAGNL	
(901)	Consensus	CV FPTL RAGAAKIWLDSSEEGQ SMKKAFNSTSRFARLQHIKTAAGTTL	1000
		951	
(871)	A. nidulans HMG	LYIRFKTTTGDAMGMNMISKGVKALHVMATECGFDDMATISVSGNFCTD	
(872)	G. zeae HMG	LYIRFKTTTGDAMGMNIIISKGVHLSVMSNEAGFDDMQIVSVSGNYCTD	
(912)	N. crassa HMG	LYIRFKITTTGDAMGMNMISKGVHLSVMYNEG-FEDMNIIVSLSGNYCTD	
(794)	S. cerevisiae HMG2	LFMRFRTTTGDAMGMNMISKGV EYSLKQMV E EY GME DMEVVS VSGNYCTD	
(798)	S. cerevisiae HMG1	LFMRFRTTTSDAMGMNMISKGV EYSLKQMV E EY GME DMEVVS VSGNYCTD	
(745)	Y. lipolytica HMG	LFIRFRTTTGDAMGMNMISKGV EYSLV M V K E Y G F P L M D I V S V S G N Y C T D	
(951)	Consensus	LFIRFKTTTGDAMGMNMISKGVHLSVMV EYGFEDMEIVSVSGNYCTD	

FIG. 7G

		1001		1050
	(921)	KKAAALNWIDGRGKSVVAEATIEFGDVVRNVLKSDVDALVELNTSKNLIGS		
A. nidulans HMG	(922)	KKAAALNWIDGRGKGVVAEATIEFGDVVRNVLKSDVDALVELNISKNIIGS		
G. zeae HMG	(961)	KKAAAINVIDGRGKSVVAEATIEPADVVKNVLKTDVDTLVELNVNKNITIGS		
N. crassa HMG	(844)	KKPAAINWIEGRGKSVVAEATIEFGDVVKSVLKSDVSALVELNISKNIVGS		
S. cerevisiae HMG2	(848)	KKPAAINWIEGRGKSVVAEATIEFGDVVRKVLKSDVSALVELNIAKNLVGS		
S. cerevisiae HMG1	(795)	KKPAAINWIEGRGKSVVAEATIPAHIVKSVLKSEVDALVELNISKNLTIGS		
Y. lipolytica HMG	(1001)	KKPAAINWIDGRGKSVVAEATIPGDVVVKSVLKSDVDALVELNISKNLIGS		
Consensus		1051		1100
	(971)	AMAGSLGGFNAHASNIVTAIFLATGODPAQNVESSSCITIMKNTNCGNLQT		
A. nidulans HMG	(972)	AMAGSVGGFNAHAANIVAAIFLATGQDPAQVVESANCITLMKNLIRGALQT		
G. zeae HMG	(1011)	AMAGSMGGFNAHAANIVAAIFLATGQDPAQVVESANCITLMRNLIRGNLQI		
N. crassa HMG	(894)	AMAGSVGGFNAHAANLVTAIFLATGQDPAQNVESSSCITILMKEVDGDLRI		
S. cerevisiae HMG2	(898)	AMAGSVGGFNAHAANLVTAIFLATGQDPAQNVESSSCITILMKEVDGDLRI		
S. cerevisiae HMG1	(845)	AMAGSVGGFNAHAANLVTAIFYLATGQDPAQNVESSSCITILMSNVDGNLII		
Y. lipolytica HMG	(1051)	AMAGSVGGFNAHAANIVTAIFLATGQDPAQNVESSSCITILMKNVDGNLQI		
Consensus		1101		1150
	(1021)	AVSMPSIEVGTIGGGTILEAQGCAMIDILGVVRGSHPTNPGDNARQLARIVA		
A. nidulans HMG	(1022)	SVSMPSIEVGTILGGGTILEPQSAMIDILGVVRGSHPTNPGDNRRLARIIG		
G. zeae HMG	(1061)	SVSMPSIEVGTILGGGTILEPQSAMIDMLGVVRGPHPTNPGENARRLARIVA		
N. crassa HMG	(944)	SVSMPSIEVGTIGGGTVLEPQGAMIDILGVVRGPHPTPECANARQLARIAA		
S. cerevisiae HMG2	(948)	SVSMPSIEVGTIGGGTVLEPQGAMIDILSVVRGPHATAPGTNARQLARIVA		
S. cerevisiae HMG1	(895)	SVSMPSIEVGTIGGGTILEPQGAMLEMLGVVRGPHIETPGANAQQLARIAA		
Y. lipolytica HMG	(1101)	SVSMPSIEVGTIGGGTILEPQGAMLDLLGVVRGPHPTNPGDNARQLARIAA		
Consensus				

FIG. 7H

		1151		1200
A. nidulans HMG	(1071)	AAVLAGELSLCSALAAGHLVRAHMAHNRSAAPTRSAATPVSAAVGATRGLS		
G. zeae HMG	(1072)	ASVLAGELSLCSALAAGHLVRAHMQHNRSAAPSRSTTPAPMTPVRSFDTK		
N. crassa HMG	(1111)	AAVLAGELSLCSALAAGHLVKAHMAHNRSAAPTRTSTPAPAAAAGLTMTS		
S. cerevisiae HMG2	(994)	CAVLAGELSLCSALAAGHLVQSHMTHNRKTNKANELP----QPSNKGPPC		
S. cerevisiae HMG1	(998)	CAVLAGELSLCAALAAGHLVQSHMTHNRKPAEPTKPNLNDATDINRLKDG		
Y. lipolytica HMG	(945)	SGVLAAELSLCSALAAGHLVQSHMTHNRSAOPTPAKQSQADLQRLONGSN		
Consensus	(1151)	AAVLAGELSLCSALAAGHLVQAHMTHNRSAAPTRS TP A T		1250
		1201		
A. nidulans HMG	(1121)	MTSSR-----		
G. zeae HMG	(1122)	VRCQPNNKDIRNILLTQHPSKPTITYSKRVIKSTIHLNPLILALFDNSVQ		
N. crassa HMG	(1161)	S-----N---PNAAAVERSR-----		
S. cerevisiae HMG2	(1040)	KTSALL-----		
S. cerevisiae HMG1	(1048)	SVTCIKS-----		
Y. lipolytica HMG	(995)	TCIRS-----		
Consensus	(1201)	I S		
		1251		1289
A. nidulans HMG	(1126)	-----		
G. zeae HMG	(1172)	TRDVQLGDQVSTRGTLDAVGGPQGGGVAAGVARRVVG		
N. crassa HMG	(1174)	-----		
S. cerevisiae HMG2	(1046)	-----		
S. cerevisiae HMG1	(1055)	-----		
Y. lipolytica HMG	(1000)	-----		
Consensus	(1251)	-----		

FIG. 71

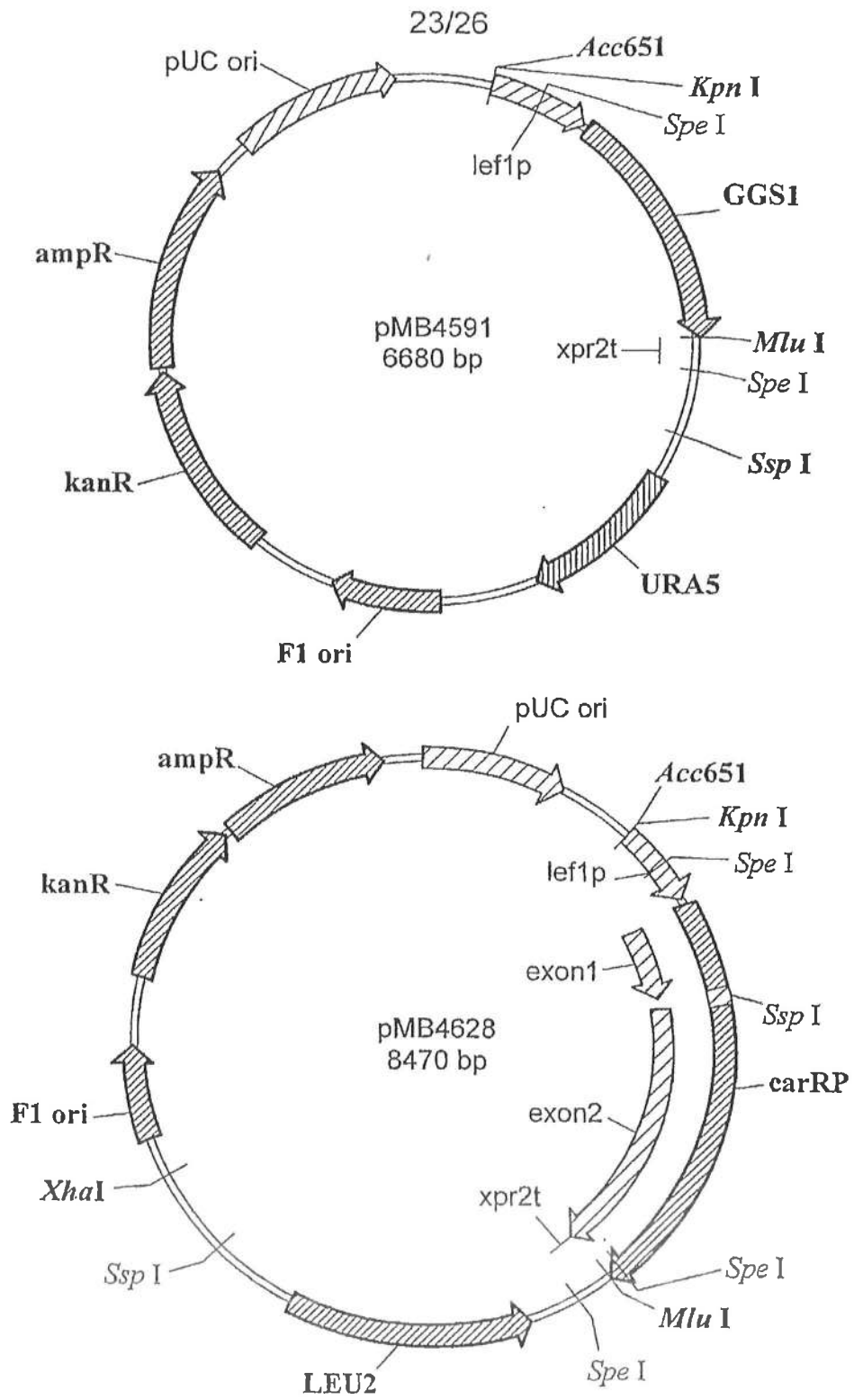


FIG. 8A

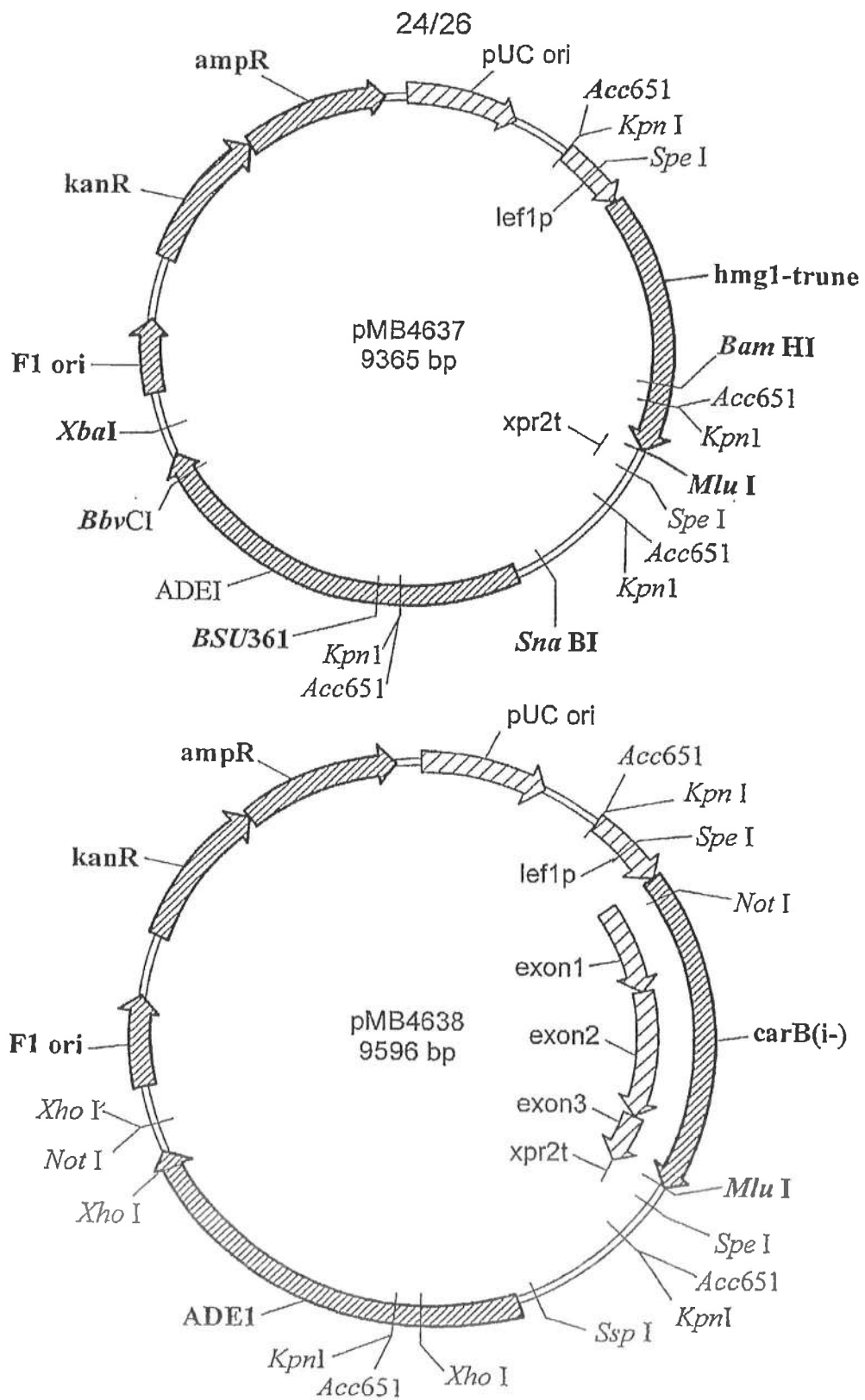


FIG. 8B

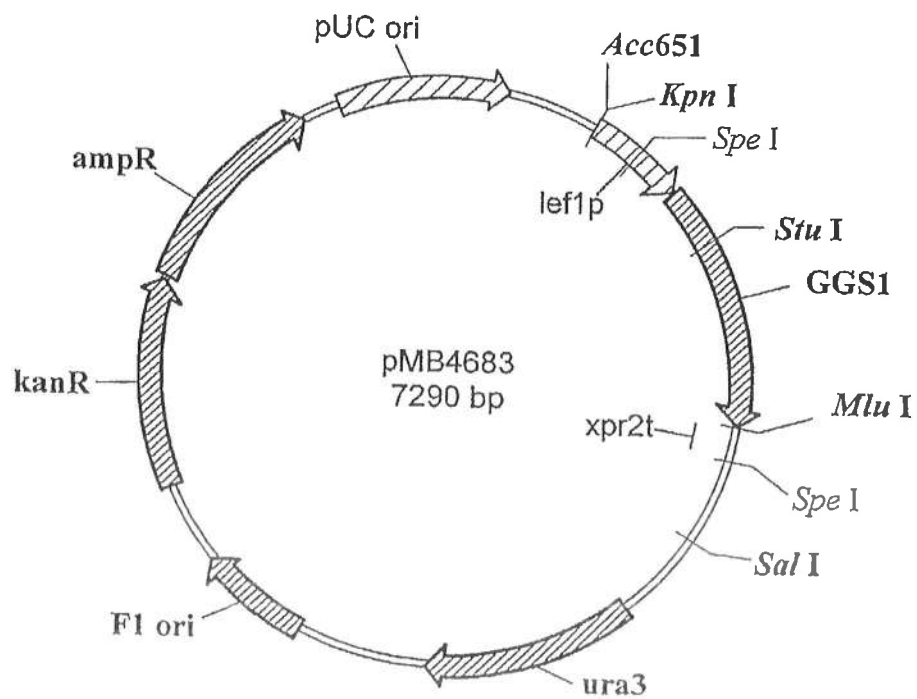
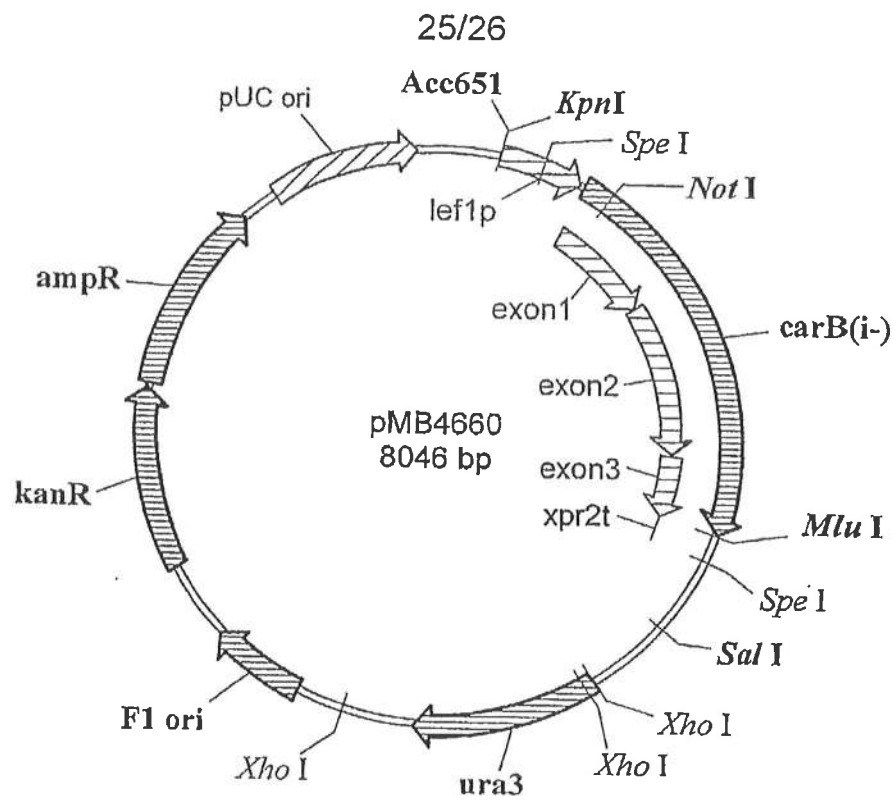


FIG. 8C

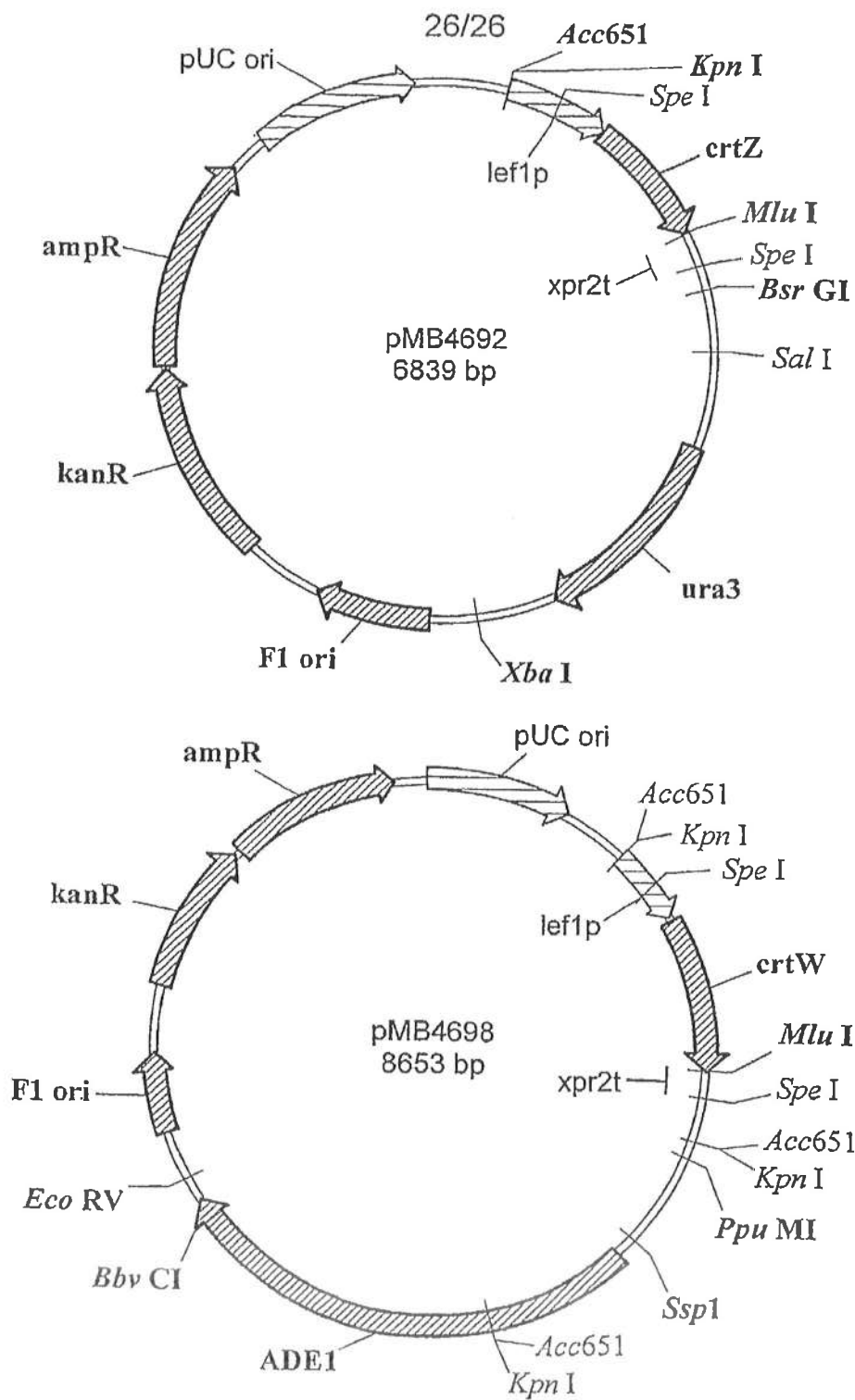


FIG. 8D