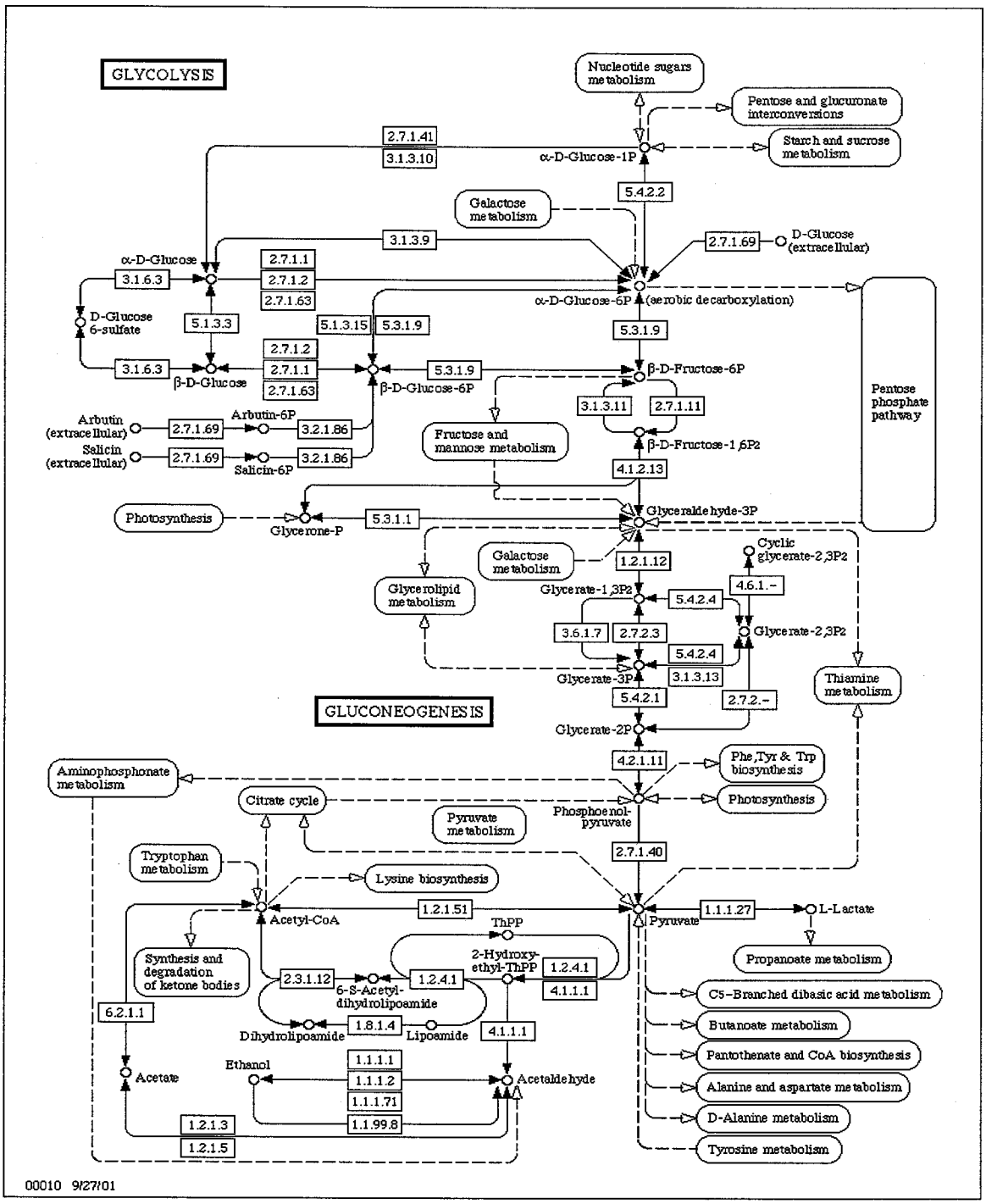

GLYCOLYSIS
Nucleotide sugars metabolism
Pentose and glucuronate interconversions
Starch and sucrose metabolism
2.7.1.41
3.1.3.10
α-D-Glucose-1P
5.4.2.2
Galactose metabolism
3.1.3.9
2.7.1.69
D-Glucose (extracellular)
α-D-Glucose
3.1.6.3
2.7.1.1
2.7.1.2
2.7.1.63
α-D-Glucose-6P
(aerobic decarboxylation)
D-Glucose 6-sulfate
5.1.3.3
5.1.3.15
5.3.1.9
5.3.1.9
3.1.6.3
β-D-Glucose
2.7.1.2
2.7.1.1
2.7.1.63
β-D-Glucose-6P
5.3.1.9
β-D-Fructose-6P
Pentose phosphate pathway
3.1.3.11
2.7.1.11
Arbutin (extracellular)
2.7.1.69
Arbutin-6P
3.2.1.86
Salicin (extracellular)
2.7.1.69
Salicin-6P
3.2.1.86
Fructose and mannose metabolism
β-D-Fructose-1,6P2
4.1.2.13
Photosynthesis
Glycerone-P
5.3.1.1
Glyceraldehyde-3P
Cyclic glycerate-2,3P2
Galactose metabolism
1.2.1.12
4.6.1.-
Glycerolipid metabolism
Glycerate-1,3P2
5.4.2.4
3.6.1.7
2.7.2.3
Glycerate-2,3P2
5.4.2.4
Glycerate-3P
3.1.3.13
Thiamine metabolism
5.4.2.1
2.7.2.-
GLUCONEOGENESIS
Glycerate-2P
4.2.1.11
Phe,Tyr & Trp biosynthesis
Aminophosphonate metabolism
Citrate cycle
Pyruvate metabolism
Phosphoenol-pyruvate
Photosynthesis
2.7.1.40
Tryptophan metabolism
Lysine biosynthesis
1.2.1.51
Acetyl-CoA
ThPP
Pyruvate
1.1.1.27
L-Lactate
2-Hydroxy-ethyl-ThPP
1.2.4.1
4.1.1.1
Synthesis and degradation of ketone bodies
2.3.1.12
6-S-Acetyl-dihydrolipoamide
1.2.4.1
Propanoate metabolism
C5-Branched dibasic acid metabolism
6.2.1.1
Butanoate metabolism
Dihydrolipoamide
1.8.1.4
Lipoamide
4.1.1.1
Pantothenate and CoA biosynthesis
Acetate
Ethanol
1.1.1.1
1.1.1.2
1.1.1.71
Acetaldehyde
Alanine and aspartate metabolism
D-Alanine metabolism
1.2.1.3
1.2.1.5
1.1.99.8
Tyrosine metabolism
00010 9/27/01

FIG 1A

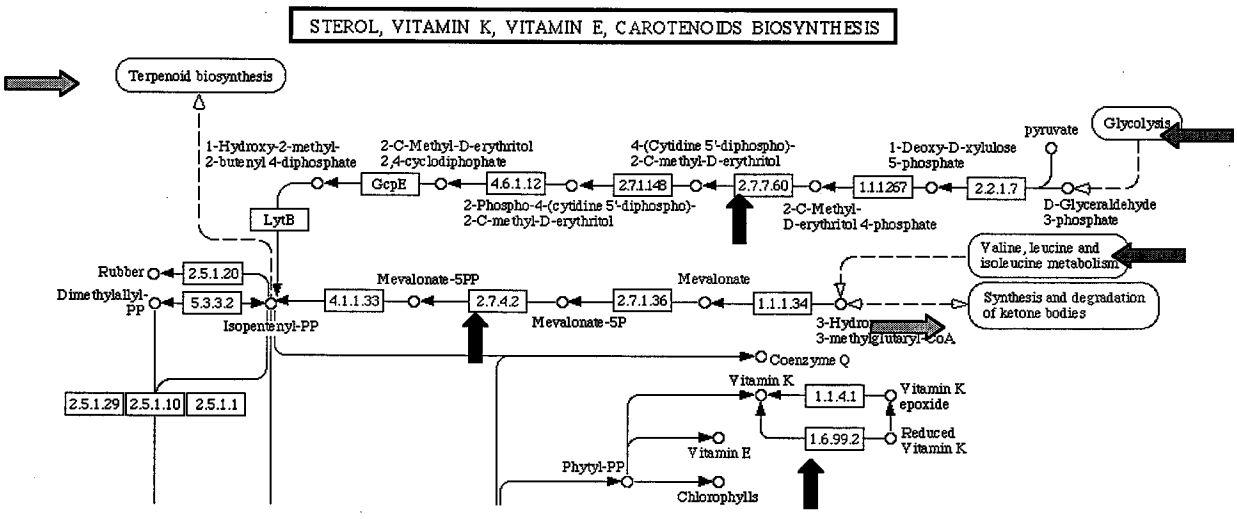

STEROL, VITAMIN K, VITAMIN E, CAROTENOIDS BIOSYNTHESIS
Terpenoid biosynthesis
1-Hydroxy-2-methyl-
2-butenyl 4-diphosphate
2-C-Methyl-D-erythritol
2,4-cyclodiphosphate
4-(Cytidine 5'-diphospho)-
2-C-methyl-D-erythritol
1-Deoxy-D-xylulose
5-phosphate
pyruvate
Glycolysis
GcpE
4.6.1.12
2.7.1.148
2.7.7.60
1.1.1.267
2.2.1.7
D-Glyceraldehyde
3-phosphate
2-Phospho-4-(cytidine 5'-diphospho)-
2-C-methyl-D-erythritol
2-C-Methyl-
D-erythritol 4-phosphate
LytB
Valine, leucine and
isoleucine metabolism
Rubber
2.5.1.20
Dimethylallyl-
PP
5.3.3.2
Isopentenyl-PP
Mevalonate-5PP
4.1.1.33
2.7.4.2
Mevalonate-5P
Mevalonate
2.7.1.36
1.1.1.34
Synthesis and degradation
of ketone bodies
3-Hydro
3-methylglutaryl-CoA
Coenzyme Q
Vitamin K
1.1.4.1
Vitamin K
epoxide
2.5.1.29
2.5.1.10
2.5.1.1
1.6.99.2
Reduced
Vitamin K
Vitamin E
Phytyl-PP
Chlorophylls

FIG 1B

```
//
ID   Q96M96      PRELIMINARY;      PRT;   766 AA.
AC   Q96M96;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-FEB-2003 (TrEMBLrel. 23, Last annotation update)
DE   Hypothetical protein FLJ32732.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=TESTIS;
RA   Ishibashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
RA   Hotuta T., Hiraoka S., Murakawa K., Takiguchi S., Kusano J.,
RA   Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
RA   Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
RA   Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA   Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA   Wagatsuma M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
RA   Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 2 PH DOMAINS.
DR   EMBL; AK057294; BAB71413.1; -.
DR   InterPro; IPR001849; PH.
DR   InterPro; IPR000219; RhoGEF.
DR   InterPro; IPR000306; Znf_FYVE.
DR   Pfam; PF01363; FYVE; 1.
DR   Pfam; PF00169; PH; 2.
DR   Pfam; PF00621; RhoGEF; 1.
DR   SMART; SM00064; FYVE; 1.
DR   SMART; SM00233; PH; 2.
DR   SMART; SM00325; RhoGEF; 1.
DR   PROSITE; PS50010; DH_2; 1.
DR   PROSITE; PS50003; PH_DOMAIN; 2.
DR   PROSITE; PS50178; ZF_FYVE; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   766 AA;  86596 MW;  125E9B0C008BAE5E CRC64;
     MEEIKPASAS CVSKEKPSKV SDLISRFEGG SSLSNYSDLK KESAVNLNAP RTPGRHGLTT
     TPQQKLLSQH LPQRQGNDAD KTQGAQTCVA NGVMAAQNQM ECEEEKAATL SSDTSIQASE
     PLLDTHIVNG ERDETATAPA SPTTDSCDGN ASDSSYRTPG IGPVLPLEER GAETETKVQE
     PENGESPLET EQLDQHHEMV ETNEQKLHKL ANELLLTERA YVNRLDLLDQ VEVCKLLEEA
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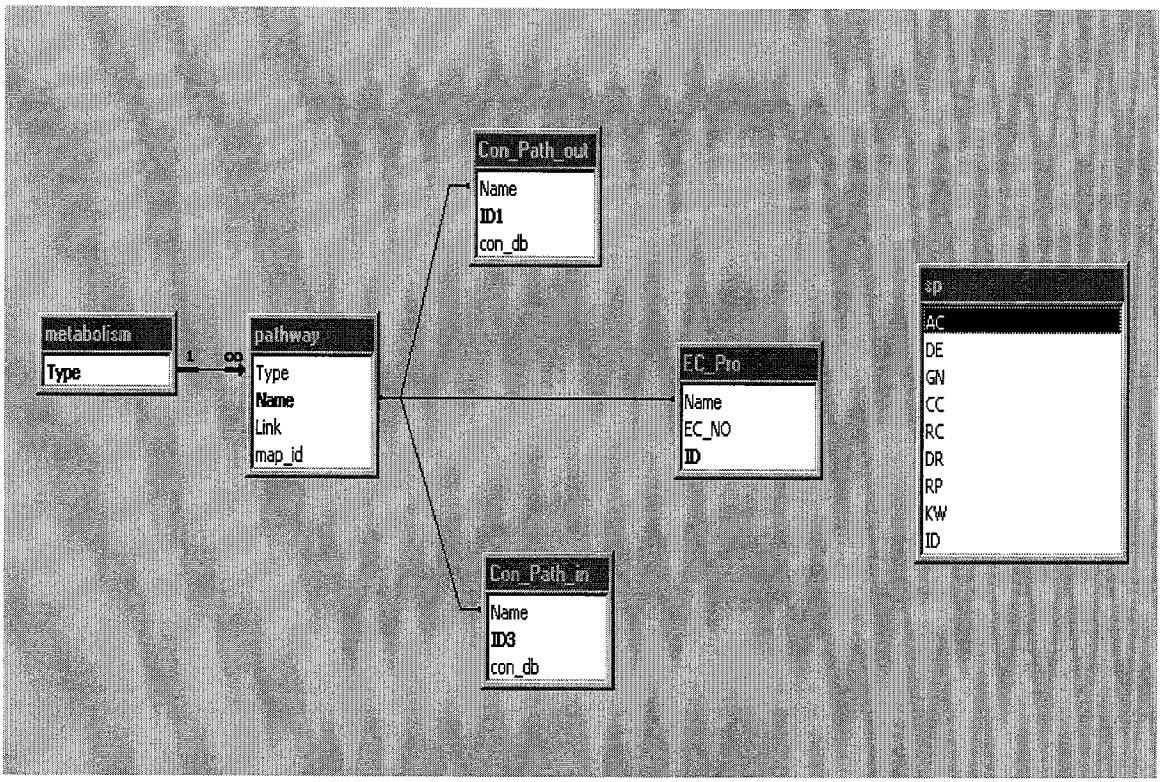

Con_Path_out
Name
ID1
con_db
metabolism
Type
1
co
pathway
Type
Name
Link
map_id
EC_Pro
Name
EC_NO
ID
Con_Path_in
Name
ID3
con_db
AC
DE
GN
CC
RC
DR
RP
KW
ID

FIG 1D

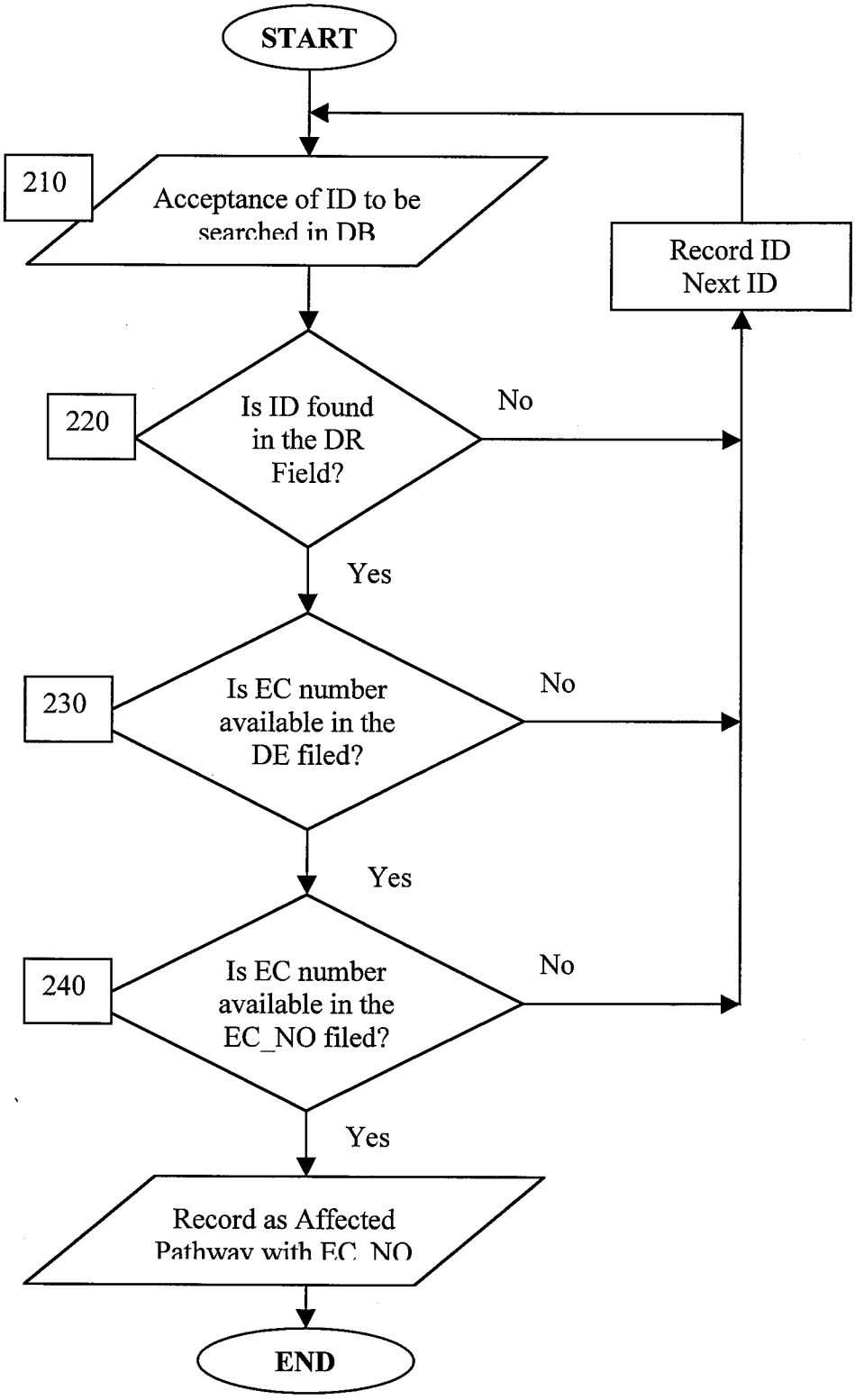
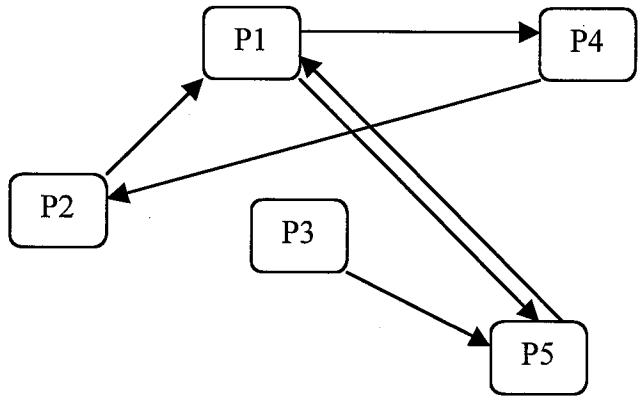

START
210
Acceptance of ID to be searched in DB
Record ID
Next ID
220
Is ID found in the DR Field?
No
Yes
230
Is EC number available in the DE filed?
No
Yes
240
Is EC number available in the EC_NO filed?
No
Yes
Record as Affected Pathway with EC_NO
END

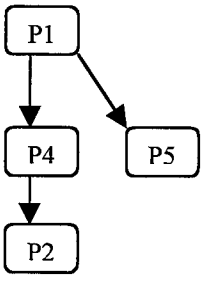
FIG 2A



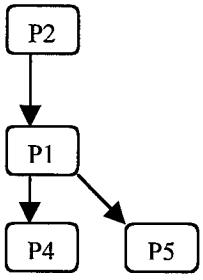
Adjacent Matrix:

	P1	P2	P3	P4	P5
P1	0	0	0	1	1
P2	1	0	0	0	0
P3	0	0	0	0	1
P4	0	1	0	0	0
P5	1	0	0	0	0

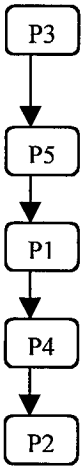
FIG 2B



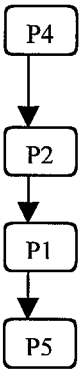
Start Node = P1
Maximum 4 nodes visited.



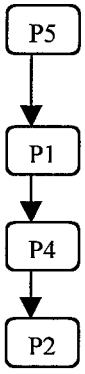
Start Node = P2
Maximum 4 nodes visited.



Start Node = P3
Maximum 5 nodes visited.



Start Node = P4
Maximum 5 nodes visited.



Start Node = P5
Maximum 5 nodes visited.

FIG 2C

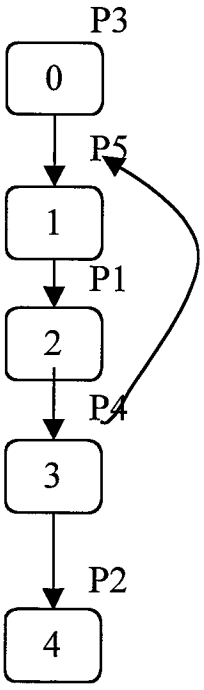


FIG 3

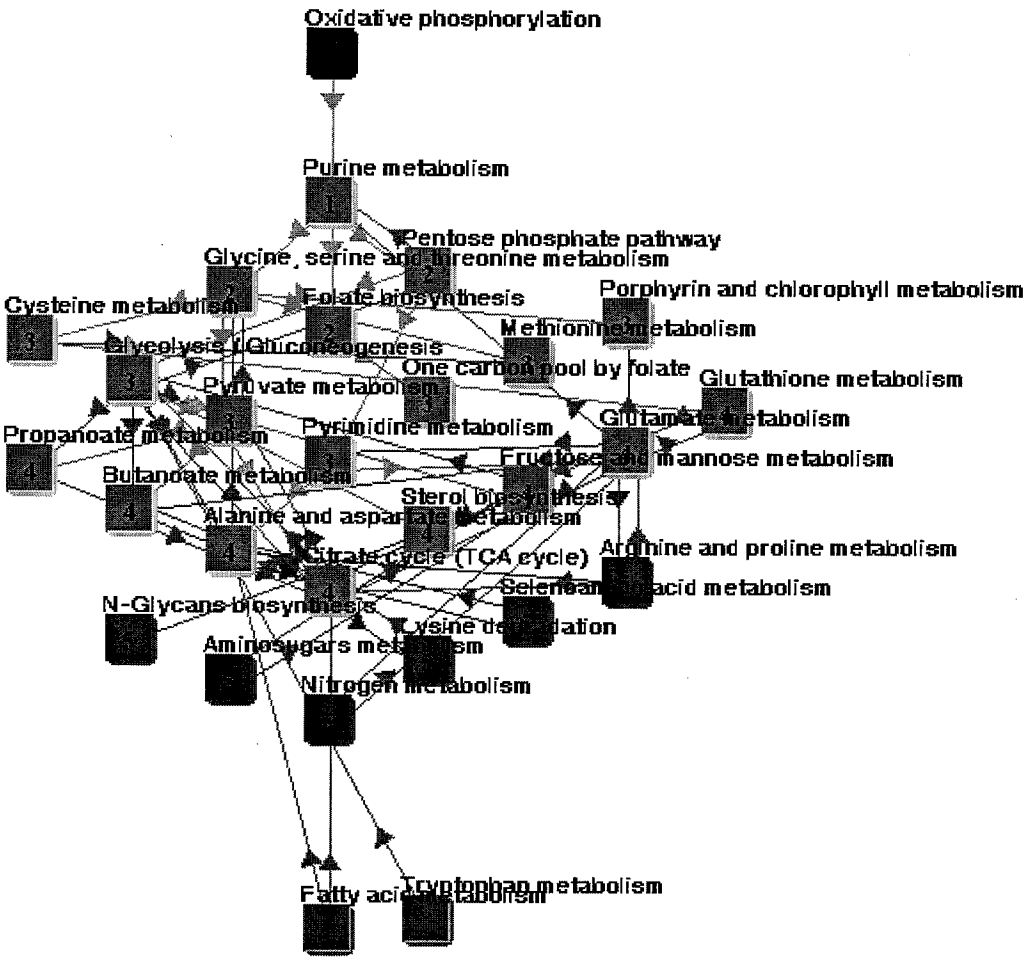

Oxidative phosphorylation
Purine metabolism
Pentose phosphate pathway
Glycine, serine and threonine metabolism
Porphyrin and chlorophyll metabolism
Cysteine metabolism
Folate biosynthesis
Methionine metabolism
Glycolysis / Gluconeogenesis
One carbon pool by folate
Glutathione metabolism
Pyruvate metabolism
Glutamate metabolism
Propanoate metabolism
Pyrimidine metabolism
Fructose and mannose metabolism
Butanoate metabolism
Sterol biosynthesis
Alanine and aspartate metabolism
Arginine and proline metabolism
Citrate cycle (TCA cycle)
Selenoamino acid metabolism
N-Glycans biosynthesis
Lysine degradation
Aminosugars metabolism
Nitrogen metabolism
Tryptophan metabolism
Fatty acid metabolism

FIG 4A

1 = Pyrimidine metabolism	17 = Alanine and aspartate metabolism
2 = Folate biosynthesis	18 = Cysteine metabolism
3 = One carbon pool by folate	19 = N-Glycans biosynthesis
4 = Pentose phosphate pathway	20 = Fructose and mannose metabolism
5 = Purine metabolism	21 = Butanoate metabolism
6 = Pyruvate metabolism	22 = Glutamate metabolism
7 = Nitrogen metabolism	23 = Oxidative phosphorylation
8 = Glycine, serine and threonine metabolism	24 = Inositol phosphate metabolism
9 = Citrate cycle (TCA cycle)	25 = Propanoate metabolism
10 = Lysine degradation	26 = Arginine and proline metabolism
11 = Aminosugars metabolism	27 = Fatty acid metabolism
12 = Sterol biosynthesis	28 = Tryptophan metabolism
13 = Methionine metabolism	29 = gamma-Hexachlorocyclohexane degradation
14 = Selenoamino acid metabolism	30 = Valine, leucine and isoleucine biosynthesis
15 = Glycolysis / Gluconeogenesis	31 = Glutathione metabolism
16 = Porphyrin and chlorophyll metabolism	32 = Tyrosine metabolism

#	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32
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FIG 4B

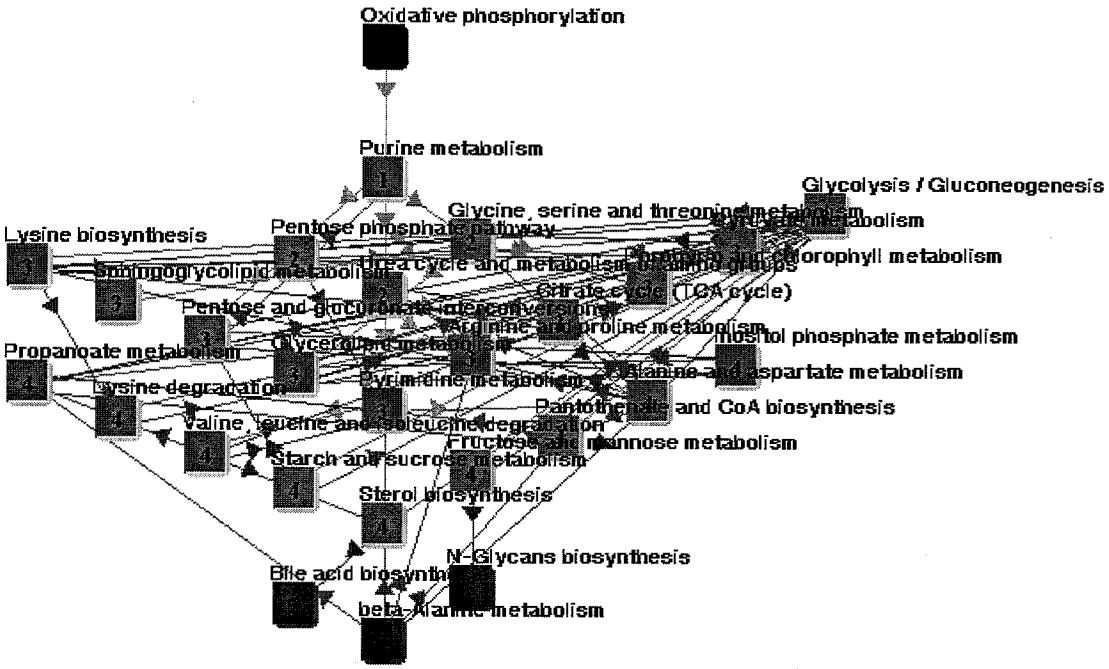

Oxidative phosphorylation
Purine metabolism
Glycolysis / Gluconeogenesis
Glycine, serine and threonine metabolism
Lysine biosynthesis
Pentose phosphate pathway
Sphingoglycolipid metabolism
Urea cycle and metabolism of amino groups
Chlorophyll metabolism
Citrate cycle (TCA cycle)
Pentose and glucuronate interconversions
Arginine and proline metabolism
Propanoate metabolism
Glycerolipid metabolism
Inositol phosphate metabolism
Pyrimidine metabolism
Alanine and aspartate metabolism
Lysine degradation
Pantothenate and CoA biosynthesis
Valine, leucine and isoleucine degradation
Fructose and mannose metabolism
Starch and sucrose metabolism
Sterol biosynthesis
N-Glycans biosynthesis
Bile acid biosynthesis
beta-Alanine metabolism

FIG 4C

1 = Purine metabolism	26 = Sphingoglycolipid metabolism
2 = Pyrimidine metabolism	27 = Ganglioside biosynthesis
3 = Sterol biosynthesis	28 = N-Glycans biosynthesis
4 = Arginine and proline metabolism	29 = Pantothenate and CoA biosynthesis
5 = Urea cycle and metabolism of amino groups	30 = Methionine metabolism
6 = beta-Alanine metabolism	31 = Selenoamino acid metabolism
7 = Glycine, serine and threonine metabolism	32 = Pyruvate metabolism
8 = Pentose phosphate pathway	33 = Fatty acid biosynthesis (path 2)
9 = Fructose and mannose metabolism	34 = Fatty acid metabolism
10 = Glycerolipid metabolism	35 = Bile acid biosynthesis
11 = Phospholipid degradation	36 = Valine, leucine and isoleucine degradation
12 = gamma-Hexachlorocyclohexane degradation	37 = Benzoate degradation via hydroxylation
13 = Oxidative phosphorylation	38 = Aminosugars metabolism
14 = Citrate cycle (TCA cycle)	39 = Alanine and aspartate metabolism
15 = Reductive carboxylate cycle (CO2 fixation)	40 = Lysine biosynthesis
16 = Glutathione metabolism	41 = Prostaglandin and leukotriene metabolism
17 = Pentose and glucuronate interconversions	42 = Glycolysis / Gluconeogenesis
18 = Starch and sucrose metabolism	43 = Lysine degradation
19 = Nucleotide sugars metabolism	44 = Inositol phosphate metabolism
20 = Tyrosine metabolism	45 = Propanoate metabolism
21 = Phenylalanine metabolism	46 = N-Glycan degradation
22 = Folate biosynthesis	47 = Fatty acid biosynthesis (path 1)
23 = Porphyrin and chlorophyll metabolism	48 = Cysteine metabolism
24 = C21-Steroid hormone metabolism	49 = Butanoate metabolism
25 = Androgen and estrogen metabolism	50 = Synthesis and degradation of ketone bodies

#	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50
1	0	0	0	0	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0
3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
4	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
5	0	1	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
6	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0
7	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	1	0	0	1	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	1	0	0
8	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
9	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0
10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0
11	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
13	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
14	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	1	1	0	1	1	0	1	0	1	0	1	0	1
15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0

FIG 4D

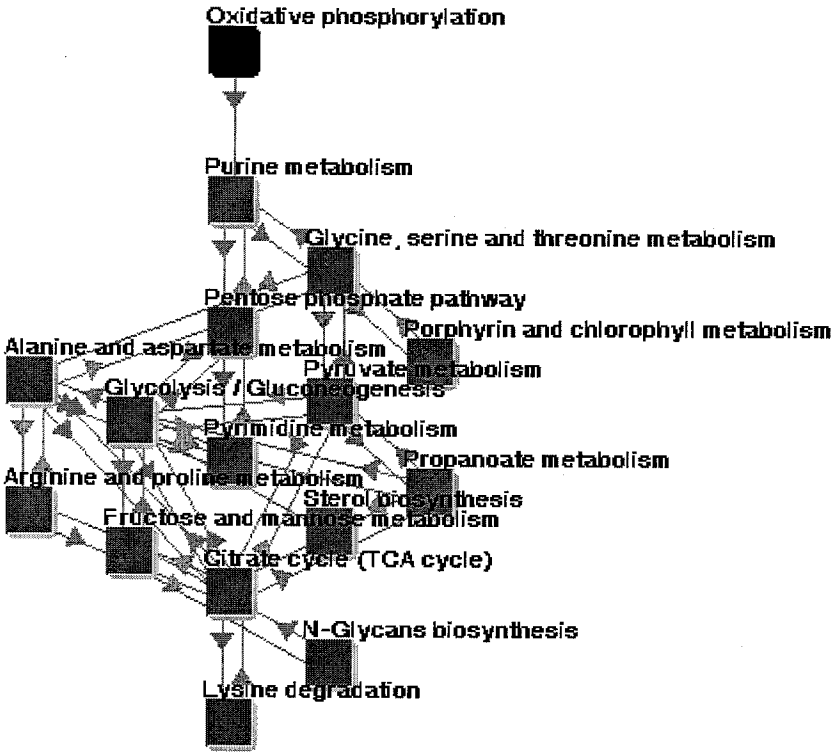

Oxidative phosphorylation
Purine metabolism
Glycine, serine and threonine metabolism
Pentose phosphate pathway
Porphyrin and chlorophyll metabolism
Alanine and aspartate metabolism
Pyruvate metabolism
Glycolysis / Gluconeogenesis
Pyrimidine metabolism
Propanoate metabolism
Arginine and proline metabolism
Sterol biosynthesis
Fructose and mannose metabolism
Citrate cycle (TCA cycle)
N-Glycans biosynthesis
Lysine degradation

FIG 4E