Superpatwhay ID	Organism taxid	Superpathway name	Step	Location	UniProt accession number
PLSP210	10029_rodents	Metabolic intermediate biosynthesis ; mevalonic acid biosynthesis ; (R)-mevalonic acid from acetyl-CoA	step 2/3	cytoplasm	P13704
PLSP210	10029_rodents	Metabolic intermediate biosynthesis ; mevalonic acid biosynthesis ; (R)-mevalonic acid from acetyl-CoA	step 3/3	endoplasmic reticulum	P00347
PLSP14	10090_rodents	Amine and polyamine degradation ; betaine degradation ; sarcosine from betaine	step 1/2	cytoplasm	O35490
PLSP14	10090_rodents	Amine and polyamine degradation ; betaine degradation ; sarcosine from betaine	step 2/2	mitochondria	Q9DBT9
PLSP23	10090_rodents	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 1/2	cytoplasm	Q91WT9
PLSP23	10090_rodents	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 1/2	nucleus	Q91WT9
PLSP23	10090_rodents	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 2/2	cytoplasm	Q8VCN5
PLSP63	10090_rodents	Amino-acid degradation ; L-phenylalanine degradation ; acetoacetic acid and fumarate from L-phenylalanine	step 3/6	cell membrane	P49429
PLSP63	10090_rodents	Amino-acid degradation ; L-phenylalanine degradation ; acetoacetic acid and fumarate from L-phenylalanine	step 3/6	cytoplasm	P49429
PLSP63	10090_rodents	Amino-acid degradation ; L-phenylalanine degradation ; acetoacetic acid and fumarate from L-phenylalanine	step 5/6	cytoplasm	Q9WVL0
PLSP116	10090_rodents	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q91WN4
PLSP116	10090_rodents	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q9CXF0
PLSP116	10090_rodents	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q78JT3
PLSP181	10090_rodents	Isoprenoid biosynthesis ; isopentenyl-PP biosynthesis via mevalonic acid pathway ; isopentenyl-PP from (R)-mevalonic acid	step 1/3	cytoplasm	Q9R008
PLSP181	10090_rodents	Isoprenoid biosynthesis ; isopentenyl-PP biosynthesis via mevalonic acid pathway ; isopentenyl-PP from (R)-mevalonic acid	step 1/3	peroxisome	Q9R008
PLSP181	10090_rodents	Isoprenoid biosynthesis ; isopentenyl-PP biosynthesis via mevalonic acid pathway ; isopentenyl-PP from (R)-mevalonic acid	step 2/3	peroxisome	Q9D1G2
PLSP231	10090_rodents	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 1/3	mitochondria	Q61586
PLSP231	10090_rodents	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 2/3	endoplasmic reticulum	Q3UN02,Q6NVG1,Q8C0N2
PLSP231	10090_rodents	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 3/3	cytoplasm	P98191
PLSP231	10090_rodents	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 3/3	endoplasmic reticulum	P98191

PLSP231	10090_rodents	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 3/3	mitochondria	Q99L43
PLSP260	10090_rodents	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 1/2	cytoplasm	Q9JHU9
PLSP260	10090_rodents	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 2/2	cytoplasm	O55023
PLSP260	10090_rodents	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 2/2	membrane	Q80V26
PLSP318	10090_rodents	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 3/6	endoplasmic reticulum	Q9CRA4
PLSP318	10090_rodents	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 4/6	membrane	Q9R1J0
PLSP318	10090_rodents	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 5/6	cell membrane	O88736
PLSP332	10090_rodents	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 1/3	endoplasmic reticulum	P53798
PLSP332	10090_rodents	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	endoplasmic reticulum	P52019
PLSP332	10090_rodents	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	microsome	P52019
PLSP14	10116_rodents	Amine and polyamine degradation ; betaine degradation ; sarcosine from betaine	step 1/2	cytoplasm	O09171
PLSP14	10116_rodents	Amine and polyamine degradation ; betaine degradation ; sarcosine from betaine	step 2/2	mitochondria	Q63342
PLSP23	10116_rodents	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 1/2	cytoplasm	P32232
PLSP23	10116_rodents	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 1/2	nucleus	P32232
PLSP23	10116_rodents	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 2/2	cytoplasm	P18757
PLSP116	10116_rodents	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	O88867
PLSP116	10116_rodents	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	P70712
PLSP116	10116_rodents	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	P46953
PLSP231	10116_rodents	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 1/3	mitochondria	P97564
PLSP231	10116_rodents	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 2/3	endoplasmic reticulum	Q4V8J4
PLSP231	10116_rodents	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 3/3	cytoplasm	O35052

PLSP231	10116_rodents	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 3/3	endoplasmic reticulum	O35052
PLSP231	10116_rodents	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 3/3	mitochondria	Q91XU8
PLSP318	10116_rodents	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 1/6	endoplasmic reticulum	Q64654
PLSP318	10116_rodents	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 1/6	microsome	Q64654
PLSP318	10116_rodents	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 3/6	endoplasmic reticulum	O35532
PLSP318	10116_rodents	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 4/6	membrane	Q5PPL3
PLSP318	10116_rodents	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 5/6	cell membrane	Q62904
PLSP332	10116_rodents	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 1/3	endoplasmic reticulum	Q02769
PLSP332	10116_rodents	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	endoplasmic reticulum	P52020
PLSP332	10116_rodents	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	microsome	P52020
PLSP116	13684_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q0V5K1
PLSP116	13684_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q0UIN2,Q0UZK0
PLSP116	162425_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q5B2N0
PLSP116	162425_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q5B0H8,Q5BC73
PLSP116	331117_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	A1DMD5
PLSP116	331117_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	A1DGW4,A1CWY1
PLSP116	331117_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	A1DB76
PLSP116	33169_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q751I2
PLSP116	33169_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q750P5
PLSP116	33169_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q75CP6
PLSP332	33169_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 1/3	endoplasmic reticulum	Q752X9
PLSP332	33169_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	endoplasmic reticulum	Q75F69

PLSP332	33169_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	microsome	Q75F69
PLSP116	341663_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q0CRI5
PLSP116	341663_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q0CPB0,Q0CZX6
PLSP116	341663_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q0D1U6
PLSP62	3702_plants	Amino-acid degradation ; L-lysine degradation via saccharopine pathway ; glutaryl-CoA from L-lysine	step 1/6	cytoplasm	Q9SMZ4
PLSP62	3702_plants	Amino-acid degradation ; L-lysine degradation via saccharopine pathway ; glutaryl-CoA from L-lysine	step 2/6	cytoplasm	Q9SMZ4
PLSP62	3702_plants	Amino-acid degradation ; L-lysine degradation via saccharopine pathway ; glutaryl-CoA from L-lysine	step 2/6	mitochondria	Q8LGI2
PLSP210	3702_plants	Metabolic intermediate biosynthesis ; mevalonic acid biosynthesis ; (R)-mevalonic acid from acetyl-CoA	step 1/3	cytoplasm	Q8S4Y1
PLSP210	3702_plants	Metabolic intermediate biosynthesis ; mevalonic acid biosynthesis ; (R)-mevalonic acid from acetyl-CoA	step 3/3	endoplasmic reticulum	P14891,P43256
PLSP301	3702_plants	Purine metabolism ; uric acid degradation ; (S)-allantoin from uric acid	step 1/3	peroxisome	O04420
PLSP301	3702_plants	Purine metabolism ; uric acid degradation ; (S)-allantoin from uric acid	step 2/3	cell membrane	Q9LVM5
PLSP301	3702_plants	Purine metabolism ; uric acid degradation ; (S)-allantoin from uric acid	step 3/3	cell membrane	Q9LVM5
PLSP332	3702_plants	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 1/3	endoplasmic reticulum	P53799
PLSP332	3702_plants	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	membrane	O65404,O65402,O65403
PLSP116	38033_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q2GQG8
PLSP116	38033_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q2H9P7,Q2H7G2
PLSP116	38033_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q2HD63
PLSP6	4058_plants	Alkaloid biosynthesis ; vindoline biosynthesis ; vindoline from tabersonine	step 1/6	endoplasmic reticulum	P98183
PLSP6	4058_plants	Alkaloid biosynthesis ; vindoline biosynthesis ; vindoline from tabersonine	step 5/6	cytoplasm	O04847
PLSP159	4081_plants	Glycan metabolism ; pectin degradation ; 2-dehydro-3-deoxy-D-gluconic acid from pectin	step 1/5	cell wall	P14280,P09607,Q96575,Q96576,Q43143
PLSP159	4081_plants	Glycan metabolism ; pectin degradation ; 2-dehydro-3-deoxy-D-gluconic acid from pectin	step 1/5	extracellular	P14280,P09607,Q96575,Q96576,Q43143
PLSP159	4081_plants	Glycan metabolism ; pectin degradation ; 2-dehydro-3-deoxy-D-gluconic acid from pectin	step 2/5	extracellular	P24396
PLSP116	425011_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	A2Q9N7,A2QMH1,A2QPD9

PLSP116	425011_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	A2R7T0,A2QJI5
PLSP116	425011_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	A2R8S7
PLSP116	44689_invertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q54RE8
PLSP116	44689_invertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q54Q04
PLSP116	44689_invertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q54S02
PLSP116	451804_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	B0Y7C3
PLSP116	451804_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	B0XS72,B0Y6H2
PLSP116	451804_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	B0Y9Z9,B0XVP0
PLSP29	4896_fungi	Amino-acid biosynthesis ; L-isoleucine biosynthesis ; L-isoleucine from 2-oxobutanoate	step 1/4	cytoplasm	O60086
PLSP29	4896_fungi	Amino-acid biosynthesis ; L-isoleucine biosynthesis ; L-isoleucine from 2-oxobutanoate	step 1/4	mitochondria	P36620
PLSP29	4896_fungi	Amino-acid biosynthesis ; L-isoleucine biosynthesis ; L-isoleucine from 2-oxobutanoate	step 2/4	mitochondria	P78827
PLSP29	4896_fungi	Amino-acid biosynthesis ; L-isoleucine biosynthesis ; L-isoleucine from 2-oxobutanoate	step 3/4	mitochondria	Q10318
PLSP31	4896_fungi	Amino-acid biosynthesis ; L-lysine biosynthesis via AAA pathway ; L-alpha-aminoadipate from 2-oxoglutarate	step 1/4	mitochondria	Q9Y823
PLSP31	4896_fungi	Amino-acid biosynthesis ; L-lysine biosynthesis via AAA pathway ; L-alpha-aminoadipate from 2-oxoglutarate	step 2/4	mitochondria	Q9UT74
PLSP31	4896_fungi	Amino-acid biosynthesis ; L-lysine biosynthesis via AAA pathway ; L-alpha-aminoadipate from 2-oxoglutarate	step 3/4	cytoplasm	O14104
PLSP51	4896_fungi	Amino-acid biosynthesis ; L-valine biosynthesis ; L-valine from pyruvate	step 1/4	cytoplasm	O60086
PLSP51	4896_fungi	Amino-acid biosynthesis ; L-valine biosynthesis ; L-valine from pyruvate	step 1/4	mitochondria	P36620
PLSP51	4896_fungi	Amino-acid biosynthesis ; L-valine biosynthesis ; L-valine from pyruvate	step 2/4	mitochondria	P78827
PLSP51	4896_fungi	Amino-acid biosynthesis ; L-valine biosynthesis ; L-valine from pyruvate	step 3/4	mitochondria	Q10318
PLSP85	4896_fungi	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 1/5	cytoplasm	P78958,O43026
PLSP85	4896_fungi	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 2/5	cytoplasm	O60101
PLSP85	4896_fungi	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 3/5	cytoplasm	O94461,Q9UT63
PLSP85	4896_fungi	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 3/5	nucleus	O94461,Q9UT63,O94420

PLSP85	4896_fungi	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 4/5	cytoplasm	P40370,Q8NKC2
PLSP209	4896_fungi	Metabolic intermediate biosynthesis ; chorismate biosynthesis ; chorismate from D-erythrose 4-phosphate and PEP	step 1/7	cytoplasm	Q9UT09
PLSP209	4896_fungi	Metabolic intermediate biosynthesis ; chorismate biosynthesis ; chorismate from D-erythrose 4-phosphate and PEP	step 1/7	nucleus	Q9UT09
PLSP209	4896_fungi	Metabolic intermediate biosynthesis ; chorismate biosynthesis ; chorismate from D-erythrose 4-phosphate and PEP	step 2/7	cytoplasm	Q9P7R0
PLSP209	4896_fungi	Metabolic intermediate biosynthesis ; chorismate biosynthesis ; chorismate from D-erythrose 4-phosphate and PEP	step 3/7	cytoplasm	Q9P7R0
PLSP209	4896_fungi	Metabolic intermediate biosynthesis ; chorismate biosynthesis ; chorismate from D-erythrose 4-phosphate and PEP	step 4/7	cytoplasm	Q9P7R0
PLSP209	4896_fungi	Metabolic intermediate biosynthesis ; chorismate biosynthesis ; chorismate from D-erythrose 4-phosphate and PEP	step 5/7	cytoplasm	Q9P7R0
PLSP209	4896_fungi	Metabolic intermediate biosynthesis ; chorismate biosynthesis ; chorismate from D-erythrose 4-phosphate and PEP	step 6/7	cytoplasm	Q9P7R0
PLSP210	4896_fungi	Metabolic intermediate biosynthesis ; mevalonic acid biosynthesis ; (R)-mevalonic acid from acetyl-CoA	step 1/3	cytoplasm	Q9UQW6
PLSP210	4896_fungi	Metabolic intermediate biosynthesis ; mevalonic acid biosynthesis ; (R)-mevalonic acid from acetyl-CoA	step 3/3	endoplasmic reticulum	Q10283
PLSP318	4896_fungi	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 1/6	endoplasmic reticulum	Q09736
PLSP318	4896_fungi	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 2/6	membrane	Q09195
PLSP318	4896_fungi	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 3/6	endoplasmic reticulum	Q9UUH4
PLSP318	4896_fungi	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 4/6	endoplasmic reticulum	O43050
PLSP324	4896_fungi	Steroid metabolism ; ergosterol biosynthesis ; ergosterol from zymosterol	step 2/5	endoplasmic reticulum	P87113
PLSP324	4896_fungi	Steroid metabolism ; ergosterol biosynthesis ; ergosterol from zymosterol	step 3/5	endoplasmic reticulum	O94457,O13666
PLSP324	4896_fungi	Steroid metabolism ; ergosterol biosynthesis ; ergosterol from zymosterol	step 5/5	membrane	P36209
PLSP332	4896_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 1/3	endoplasmic reticulum	P36596
PLSP332	4896_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	endoplasmic reticulum	Q9C1W3
PLSP332	4896_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	microsome	Q9C1W3
PLSP116	4924_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	A3LNF8
PLSP116	4924_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	A3LQD7
PLSP116	4924_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	A3LP72
PLSP30	4932_fungi	Amino-acid biosynthesis ; L-leucine biosynthesis ; L-leucine from 3-methyl-2-oxobutanoate	step 1/4	cytoplasm	P06208

PLSP30	4932_fungi	Amino-acid biosynthesis ; L-leucine biosynthesis ; L-leucine from 3-methyl-2-oxobutanoate	step 1/4	mitochondria	P06208,Q12166
PLSP30	4932_fungi	Amino-acid biosynthesis ; L-leucine biosynthesis ; L-leucine from 3-methyl-2-oxobutanoate	step 3/4	cytoplasm	P04173
PLSP31	4932_fungi	Amino-acid biosynthesis ; L-lysine biosynthesis via AAA pathway ; L-alpha-aminoadipate from 2-oxoglutarate	step 1/4	cytoplasm	P48570
PLSP31	4932_fungi	Amino-acid biosynthesis ; L-lysine biosynthesis via AAA pathway ; L-alpha-aminoadipate from 2-oxoglutarate	step 1/4	mitochondria	Q12122
PLSP31	4932_fungi	Amino-acid biosynthesis ; L-lysine biosynthesis via AAA pathway ; L-alpha-aminoadipate from 2-oxoglutarate	step 2/4	mitochondria	P49367
PLSP31	4932_fungi	Amino-acid biosynthesis ; L-lysine biosynthesis via AAA pathway ; L-alpha-aminoadipate from 2-oxoglutarate	step 3/4	mitochondria	P40495
PLSP85	4932_fungi	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 1/5	cytoplasm	P00360,P00358,P00359
PLSP85	4932_fungi	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 2/5	cytoplasm	P00560
PLSP85	4932_fungi	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 3/5	cytoplasm	Q12040,Q12008
PLSP85	4932_fungi	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 3/5	nucleus	Q12040
PLSP85	4932_fungi	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 4/5	cytoplasm	P00924,P00925
PLSP210	4932_fungi	Metabolic intermediate biosynthesis ; mevalonic acid biosynthesis ; (R)-mevalonic acid from acetyl-CoA	step 1/3	cytoplasm	P41338
PLSP210	4932_fungi	Metabolic intermediate biosynthesis ; mevalonic acid biosynthesis ; (R)-mevalonic acid from acetyl-CoA	step 3/3	endoplasmic reticulum	P12683,P12684
PLSP260	4932_fungi	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 1/2	cytoplasm	P11986
PLSP260	4932_fungi	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 2/2	cytoplasm	P38710
PLSP260	4932_fungi	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 2/2	nucleus	P38710
PLSP318	4932_fungi	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 1/6	membrane	P10614
PLSP318	4932_fungi	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 2/6	membrane	P32462
PLSP318	4932_fungi	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 3/6	endoplasmic reticulum	P53045
PLSP318	4932_fungi	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 4/6	endoplasmic reticulum	P53199
PLSP318	4932_fungi	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 5/6	endoplasmic reticulum	Q12452
PLSP324	4932_fungi	Steroid metabolism ; ergosterol biosynthesis ; ergosterol from zymosterol	step 2/5	endoplasmic reticulum	P32352
PLSP324	4932_fungi	Steroid metabolism ; ergosterol biosynthesis ; ergosterol from zymosterol	step 3/5	endoplasmic reticulum	P32353
PLSP324	4932_fungi	Steroid metabolism ; ergosterol biosynthesis ; ergosterol from zymosterol	step 5/5	membrane	P25340

PLSP332	4932_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 1/3	endoplasmic reticulum	P29704
PLSP332	4932_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	endoplasmic reticulum	P32476
PLSP332	4932_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	microsome	P32476
PLSP332	4932_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 3/3	endoplasmic reticulum	P38604
PLSP116	4952_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q6C9M8
PLSP116	4952_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q6CDM0
PLSP116	4952_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q6CFX1
PLSP116	4959_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q6BV21
PLSP116	4959_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q6BI19
PLSP116	5057_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	A1CT23
PLSP116	5057_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	A1C688,A1CHT0
PLSP116	5057_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	A1C408,A1C874
PLSP116	5062_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q2UPP1
PLSP116	5062_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q2U038,Q2UJE8
PLSP116	5062_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q2UHT9,Q2UB88
PLSP116	5085_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q4WN75
PLSP116	5085_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q4X1D4,Q4WPN0
PLSP116	5085_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q4WCF1,Q4WZC3
PLSP116	5141_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q7S3C9
PLSP116	5141_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q7RXY2,Q7S332
PLSP116	5141_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q7SDX3

PLSP116	5207_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q55W30
PLSP116	5207_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q5KK77
PLSP116	5207_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q5KLD9
PLSP116	5270_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q4P0N0
PLSP116	5270_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q4P2Q7
PLSP116	5476_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q5A7M3
PLSP116	5476_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q59QC4
PLSP116	5476_fungi	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q59K86
PLSP318	5476_fungi	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 1/6	membrane	P10613
PLSP318	5476_fungi	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 3/6	endoplasmic reticulum	O59933
PLSP332	5476_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 1/3	endoplasmic reticulum	P78589
PLSP332	5476_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	endoplasmic reticulum	Q92206
PLSP332	5476_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	microsome	Q92206
PLSP332	5478_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 1/3	endoplasmic reticulum	Q9HGZ6
PLSP332	5478_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	endoplasmic reticulum	O13306
PLSP332	5478_fungi	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	microsome	O13306
PLSP116	6238_invertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	A8Y432
PLSP116	6238_invertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	A8XKT0
PLSP116	6238_invertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q60W34
PLSP116	6239_invertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q21795
PLSP116	6239_invertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q18026
PLSP116	6239_invertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q19341

PLSP231	6239_invertebrates	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 1/3	mitochondria	Q22949
PLSP231	6239_invertebrates	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 2/3	membrane	Q11087,Q93841,Q22267
PLSP231	6239_invertebrates	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 3/3	membrane	P53439
PLSP260	7227_invertebrates	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 1/2	cytoplasm	O97477
PLSP260	7227_invertebrates	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 2/2	membrane	Q9VYF2
PLSP303	7227_invertebrates	Pyrimidine metabolism ; UMP biosynthesis via de novo pathway ; UMP from HCO(3)(-)	step 1/6	cytoplasm	P05990
PLSP303	7227_invertebrates	Pyrimidine metabolism ; UMP biosynthesis via de novo pathway ; UMP from HCO(3)(-)	step 2/6	cytoplasm	P05990
PLSP303	7227_invertebrates	Pyrimidine metabolism ; UMP biosynthesis via de novo pathway ; UMP from HCO(3)(-)	step 3/6	cytoplasm	P05990
PLSP303	7227_invertebrates	Pyrimidine metabolism ; UMP biosynthesis via de novo pathway ; UMP from HCO(3)(-)	step 4/6	mitochondria	P32748
PLSP116	7955_vertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q1RLY6
PLSP116	7955_vertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q5U3F8
PLSP260	8355_vertebrates	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 1/2	cytoplasm	Q7ZXY0,Q6DDT1
PLSP260	8355_vertebrates	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 2/2	cytoplasm	P29219
PLSP260	8355_vertebrates	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 2/2	membrane	Q6NTW5
PLSP116	8364_vertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	Q6DIZ8
PLSP116	8364_vertebrates	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	Q6DIZ0
PLSP23	9541_mammals	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 1/2	cytoplasm	Q58H57
PLSP23	9541_mammals	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 1/2	nucleus	Q58H57
PLSP23	9541_mammals	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 2/2	cytoplasm	Q60HG7
PLSP318	9601_mammals	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 1/6	endoplasmic reticulum	Q5RE72
PLSP318	9601_mammals	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 1/6	microsome	Q5RE72
PLSP318	9601_mammals	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 3/6	endoplasmic reticulum	Q5R574
PLSP14	9606_human	Amine and polyamine degradation ; betaine degradation ; sarcosine from betaine	step 1/2	cytoplasm	Q93088

PLSP14	9606_human	Amine and polyamine degradation ; betaine degradation ; sarcosine from betaine	step 2/2	mitochondria	Q9UI17
PLSP23	9606_human	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 1/2	cytoplasm	P35520
PLSP23	9606_human	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 1/2	nucleus	P35520
PLSP23	9606_human	Amino-acid biosynthesis ; L-cysteine biosynthesis ; L-cysteine from L-homocysteine and L-serine	step 2/2	cytoplasm	P32929
PLSP116	9606_human	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 1/3	mitochondria	O15229
PLSP116	9606_human	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 2/3	cytoplasm	Q16719
PLSP116	9606_human	Cofactor biosynthesis ; NAD(+) biosynthesis ; pyridine-2,3-dicarboxylate from L-kynurenine	step 3/3	cytoplasm	P46952
PLSP121	9606_human	Cofactor biosynthesis ; coenzyme A biosynthesis ; coenzyme A from pantothenate	step 1/5	cytoplasm	Q9BZ23,Q8TE04,Q9H999,Q9NVE7
PLSP121	9606_human	Cofactor biosynthesis ; coenzyme A biosynthesis ; coenzyme A from pantothenate	step 1/5	mitochondria	Q9BZ23
PLSP121	9606_human	Cofactor biosynthesis ; coenzyme A biosynthesis ; coenzyme A from pantothenate	step 4/5	cytoplasm	Q13057
PLSP121	9606_human	Cofactor biosynthesis ; coenzyme A biosynthesis ; coenzyme A from pantothenate	step 5/5	cytoplasm	Q13057
PLSP181	9606_human	Isoprenoid biosynthesis ; isopentenyl-PP biosynthesis via mevalonic acid pathway ; isopentenyl-PP from (R)-mevalonic acid	step 1/3	cytoplasm	Q03426
PLSP181	9606_human	Isoprenoid biosynthesis ; isopentenyl-PP biosynthesis via mevalonic acid pathway ; isopentenyl-PP from (R)-mevalonic acid	step 1/3	peroxisome	Q03426
PLSP181	9606_human	Isoprenoid biosynthesis ; isopentenyl-PP biosynthesis via mevalonic acid pathway ; isopentenyl-PP from (R)-mevalonic acid	step 2/3	peroxisome	Q15126
PLSP231	9606_human	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 1/3	mitochondria	Q9HCL2
PLSP231	9606_human	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 2/3	endoplasmic reticulum	Q6UWP7,Q643R3,Q53EU6
PLSP231	9606_human	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 3/3	cytoplasm	Q92903
PLSP231	9606_human	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 3/3	endoplasmic reticulum	Q92903
PLSP231	9606_human	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 3/3	mitochondria	O95674
PLSP260	9606_human	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 1/2	cytoplasm	Q9NPH2

PLSP260	9606_human	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 2/2	cytoplasm	P29218
PLSP260	9606_human	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 2/2	membrane	Q9NX62
PLSP303	9606_human	Pyrimidine metabolism ; UMP biosynthesis via de novo pathway ; UMP from HCO(3)(-)	step 1/6	cytoplasm	P27708
PLSP303	9606_human	Pyrimidine metabolism ; UMP biosynthesis via de novo pathway ; UMP from HCO(3)(-)	step 2/6	cytoplasm	P27708
PLSP303	9606_human	Pyrimidine metabolism ; UMP biosynthesis via de novo pathway ; UMP from HCO(3)(-)	step 3/6	cytoplasm	P27708
PLSP303	9606_human	Pyrimidine metabolism ; UMP biosynthesis via de novo pathway ; UMP from HCO(3)(-)	step 4/6	mitochondria	Q02127
PLSP318	9606_human	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 1/6	endoplasmic reticulum	Q16850
PLSP318	9606_human	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 1/6	microsome	Q16850
PLSP318	9606_human	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 3/6	endoplasmic reticulum	Q15800
PLSP318	9606_human	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 4/6	membrane	Q15738
PLSP318	9606_human	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 5/6	cell membrane	P56937
PLSP332	9606_human	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 1/3	endoplasmic reticulum	P37268
PLSP332	9606_human	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	endoplasmic reticulum	Q14534
PLSP332	9606_human	Terpene metabolism ; lanosterol biosynthesis ; lanosterol from farnesyl-PP	step 2/3	microsome	Q14534
PLSP85	9823_mammals	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 1/5	cytoplasm	P00355
PLSP85	9823_mammals	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 2/5	cytoplasm	Q7SIB7,Q6RI85
PLSP85	9823_mammals	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 4/5	cytoplasm	Q1KYT0
PLSP85	9823_mammals	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 4/5	myofibril	Q1KYT0
PLSP318	9823_mammals	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 1/6	endoplasmic reticulum	O46420
PLSP318	9823_mammals	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 1/6	microsome	O46420
PLSP318	9823_mammals	Steroid biosynthesis ; zymosterol biosynthesis ; zymosterol from lanosterol	step 3/6	endoplasmic reticulum	Q6UGB2
PLSP181	9913_mammals	Isoprenoid biosynthesis ; isopentenyl-PP biosynthesis via mevalonic acid pathway ; isopentenyl-PP from (R)-mevalonic acid	step 1/3	cytoplasm	Q5E9T8
PLSP181	9913_mammals	Isoprenoid biosynthesis ; isopentenyl-PP biosynthesis via mevalonic acid pathway ; isopentenyl-PP from (R)-mevalonic acid	step 1/3	peroxisome	Q5E9T8
PLSP181	9913_mammals	Isoprenoid biosynthesis ; isopentenyl-PP biosynthesis via mevalonic acid pathway ; isopentenyl-PP from (R)-mevalonic acid	step 2/3	peroxisome	Q2KIU2
PLSP231	9913_mammals	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 1/3	mitochondria	Q5GJ77

PLSP231	9913_mammals	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 2/3	membrane	Q95JH2,Q5E9R2,A3FPG8
PLSP231	9913_mammals	Phospholipid metabolism ; CDP-diacylglycerol biosynthesis ; CDP-diacylglycerol from sn-glycerol 3-phosphate	step 3/3	mitochondria	A0JNC1
PLSP260	9913_mammals	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 1/2	cytoplasm	Q2NL29
PLSP260	9913_mammals	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 2/2	cytoplasm	P20456
PLSP260	9913_mammals	Polyol metabolism ; myo-inositol biosynthesis ; myo-inositol from D-glucose 6-phosphate	step 2/2	membrane	Q2KJ53
PLSP85	9986_mammals	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 1/5	cytoplasm	P46406
PLSP85	9986_mammals	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 4/5	cytoplasm	P25704
PLSP85	9986_mammals	Carbohydrate degradation ; glycolysis ; pyruvate from D-glyceraldehyde 3-phosphate	step 4/5	myofibril	P25704