Model SEED Tutorial Part 2: Model SEED Biochemistry Database

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Presented by: Christopher Henry

August 31-September 2

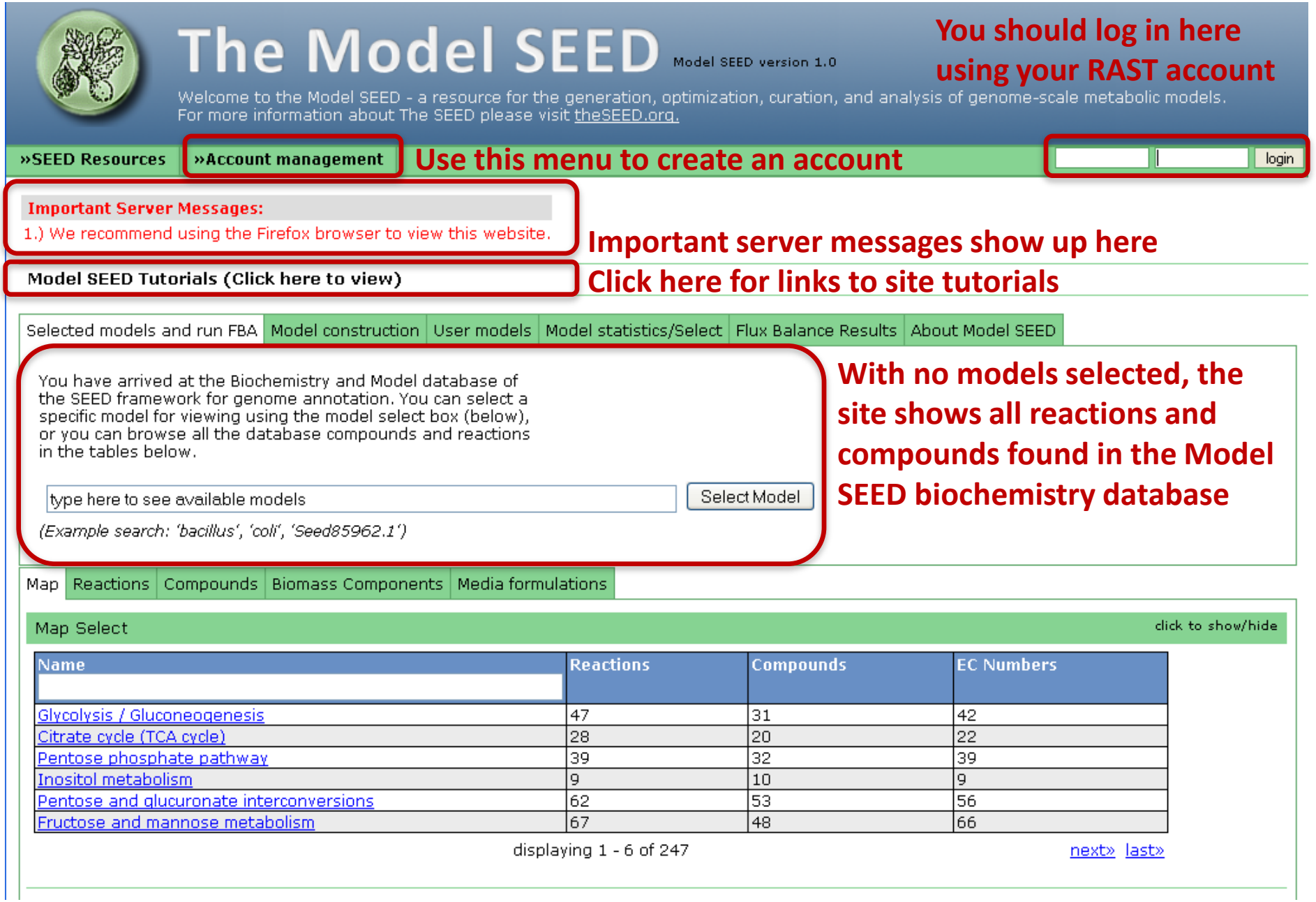
Fellowship for Interpretation of Genomes

HOPE COLLEGE

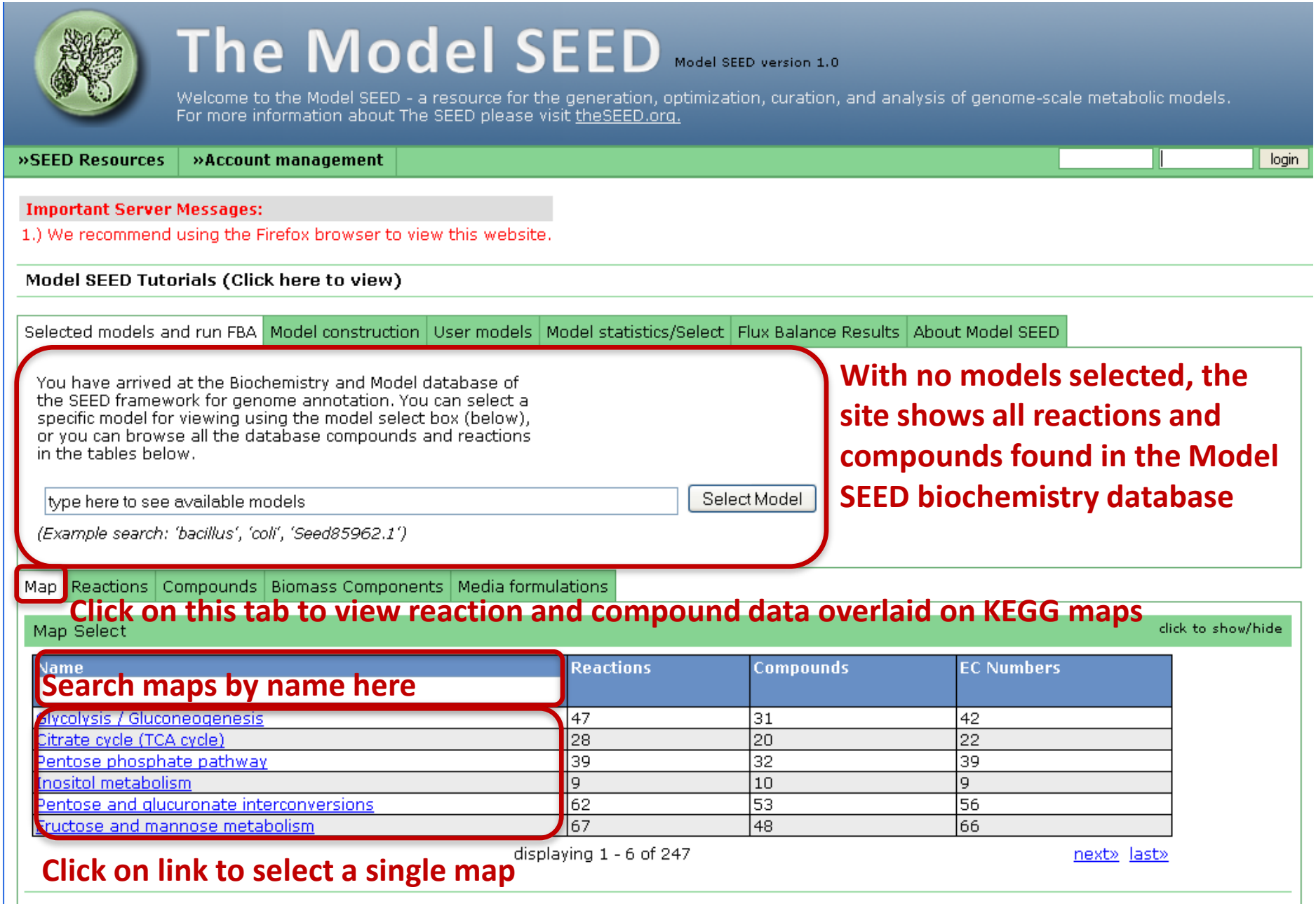
Model SEED Biochemistry Database

- Model SEED Homepage
- Viewing reactions/compound on KEGG maps
- Reactions and Compound pages
- Reaction data table
- Compound data table
- Media data table

http://www.theseed.org/models/



http://www.theseed.org/models/



Exploring the Biochemistry Database KEGG Maps

Map | Reactions | Compounds | Biomass Components | Media formulations

Map Select

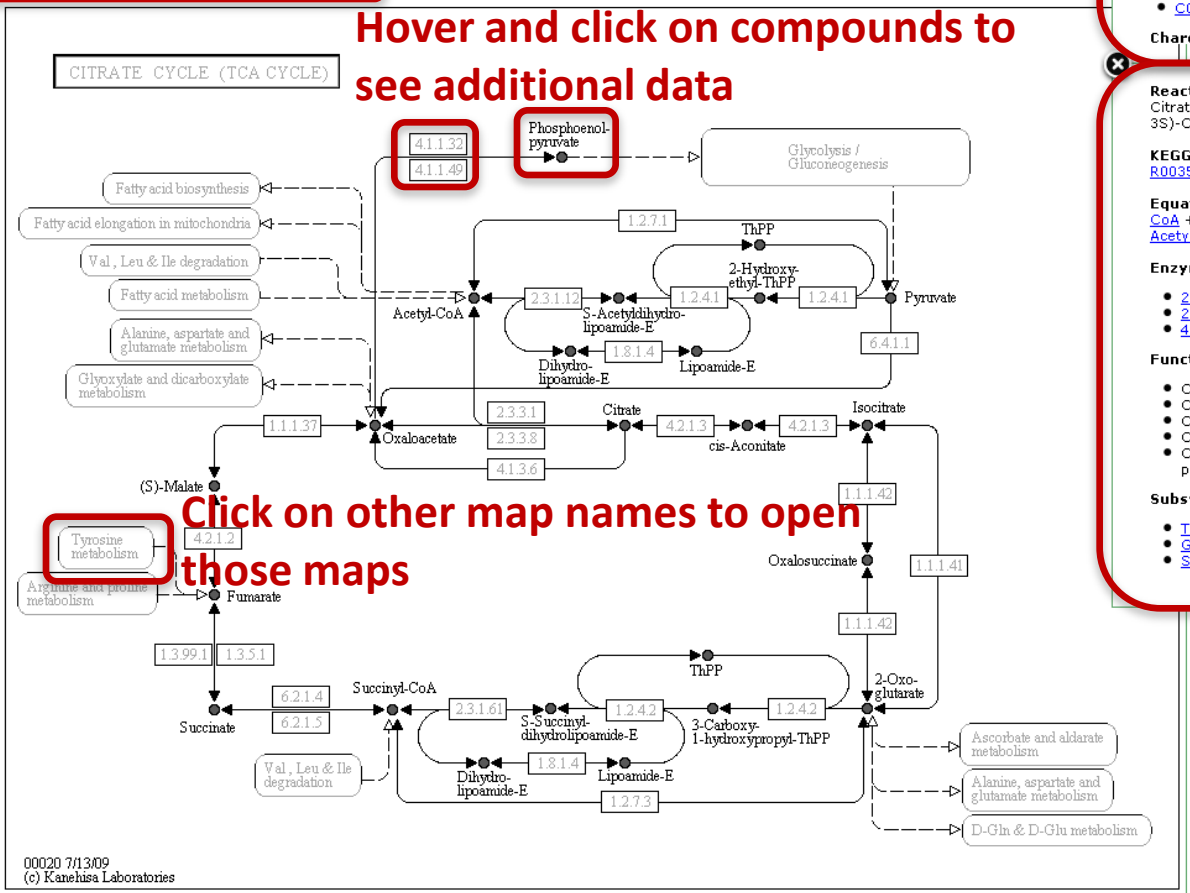
Name	Reactions	Compounds	EC Numbers
Glycolysis / Gluconeogenesis	47	31	42
Citrate cycle (TCA cycle)	28	20	22
Pentose phosphate pathway	39	32	39
Inositol metabolism	9	10	9
Pentose and glucuronate interconversions	62	53	56
Fructose and mannose metabolism	67	48	66

displaying 1 - 6 of 247 next» last»

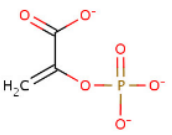
Glycolysis / Glucon... | Citrate cycle (TCA ...

Multiple maps can be opened

Hover and click on compounds to see additional data



Click on other map names to open those maps



Compound cpd00061:
Phosphoenolpyruvate
Phosphoenolpyruvic acid
PEP
phosphoenolpyruvate

C3H3O6P

KEGG ID:
- C00074

Charge: -2

Click on compound link to visit compound page

Reaction rxn00256
Citrate oxaloacetate-lyase ((pro-3S)-CH2COO- -> acetyl-CoA)

KEGG ID:
R00351

Equation:
CoA + H+ + Citrate <=> H2O + Acetyl-CoA + Oxaloacetate

Enzyme(s)
- 2.3.3.1
- 2.3.3.3
- 4.1.3.7

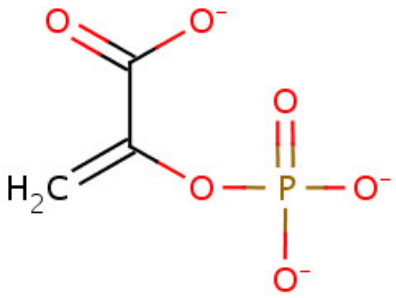
Functional Roles:
- Citrate synthase (si) (EC 2.3.3.1)
- Citrate synthase (si) (EC 2.3.3.1)
- Citrate synthase (si) (EC 2.3.3.1)
- Citrate synthase (si) (EC 2.3.3.1)
- Citrate synthase, mitochondrial precursor (EC 2.3.3.1)

Subsystems:
- TCA Cycle
- Glyoxylate bypass
- Serine-glyoxylate cycle

Hover and click on reactions to see additional reaction data

Compound Page of Model SEED Database

Viewing data for compound cpd00061

DATABASE	cpd00061
NAME	Phosphoenolpyruvate, Phosphoenolpyruvic acid, PEP, phosphoenolpyruvate
FORMULA	C3H3O6P
MASS	166
CHARGE	-2
DELTAG	-316.08
DELTAGERR	0.58973
STRUCTURAL_CUES	prim_phos:1, WdblCWW:1, WCOOn:1, WdblCH2:1, Origin:1, OCCC:1
DBLINKS	KEGG:C00074, iJR904:pep, iAO358:dll_67, iAG612:cbs_107, iAF692:pep, iSB619:pep, iAF1260:pep, iIT341:pep, iAbaylyiv4:PHOSPHO-ENOL-PYRUVATE, iND750:pep, iYO844:pep, iPS189:pep, iNJ661:pep, iJN746:pep
PKA	1:12:3, 3.55:0, 6.39:4
STRUCTURE	

Structural Cues used to calculate ΔG

Name of compound in KEGG and publicly published models

Table of reactions compound participates in.

Reactions involving compound cpd00061

display 50 items per page

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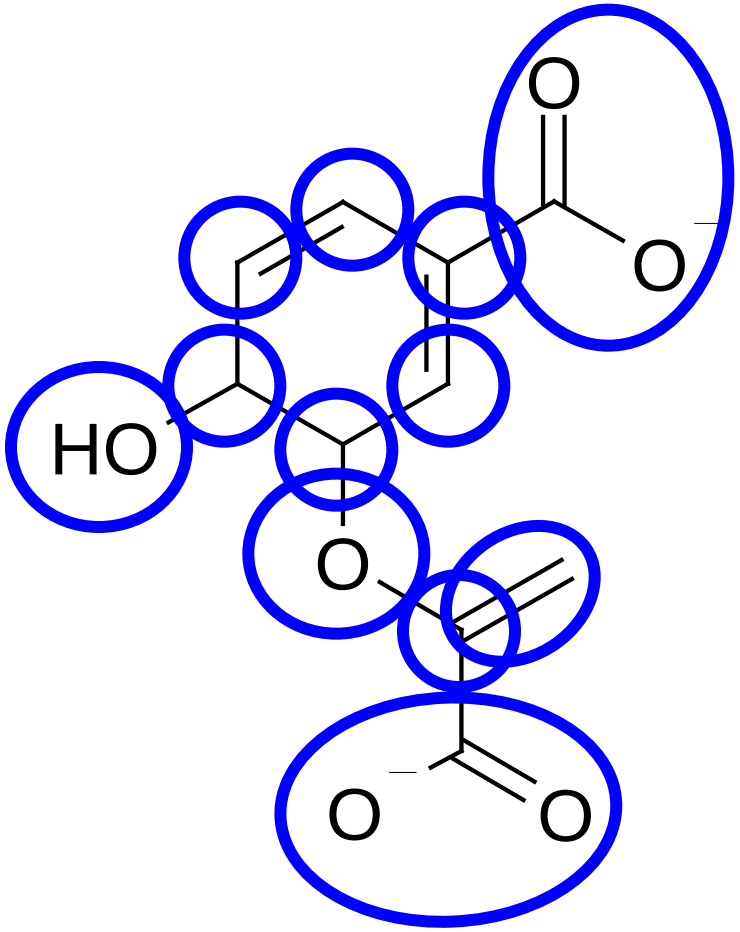
Reaction	Name	Equation	Roles	Subsystems	KEGG MAP	Enzyme	KEGG RID	...
rxn00147	ATP:pyruvate,water phosphotransferase, phosphoenolpyruvate synthase, ATP:pyruvate,water phosphotransferase, PPS, phosphoenolpyruvatesynthase, pyruvate,water dikinase	H2O + ATP + Pyruvate => Orthophosphate + AMP + Phosphoenolpyruvate + H+	Phosphoenolpyruvate synthase (EC 2.7.9.2)	Pyruvate metabolism I: anaplerotic reactions, PEP Glycolysis and Gluconeogenesis, including Archaeal enzymes	00620 00720	2.7.9.2	R00199	

Group contribution method for estimating $\Delta_f G'^{\circ}$

- In the group contribution method, the estimated $\Delta_f G'^{\circ}$ of a molecular is equal to the sum of the estimated energies for the molecular substructures that make up the molecule



Group	$\Delta_f G'^{\circ}_{group}$	Count	Uncertainty
[-COO^-]	-82.2	2	0.3
$[-OH]_{sec}$	-42.2	1	0.4
$[-CH=]_{ring}$	4.6	3	0.5
[-O-]	-24.9	1	0.9
[>C=]	14.5	1	0.7
$[>CH-]_{ring}$	5.5	2	0.6
$[-CH_2-]$	0.9	1	0.1
$[>C=]_{ring}$	9.7	1	1.0
$[=CH_2]$	4.8	1	1.1

Chorismate: -176.8 ± 2.3 kcal/mol

$$\text{Uncertainty}_{\Delta_r G'^{\circ}} = \sqrt{\sum_{i}^{\text{Number of groups}} \left(n_i \varepsilon_{\Delta_g G_i'^{\circ}} \right)^2}$$

Jankowski et al, Biophysical Journal, 2008

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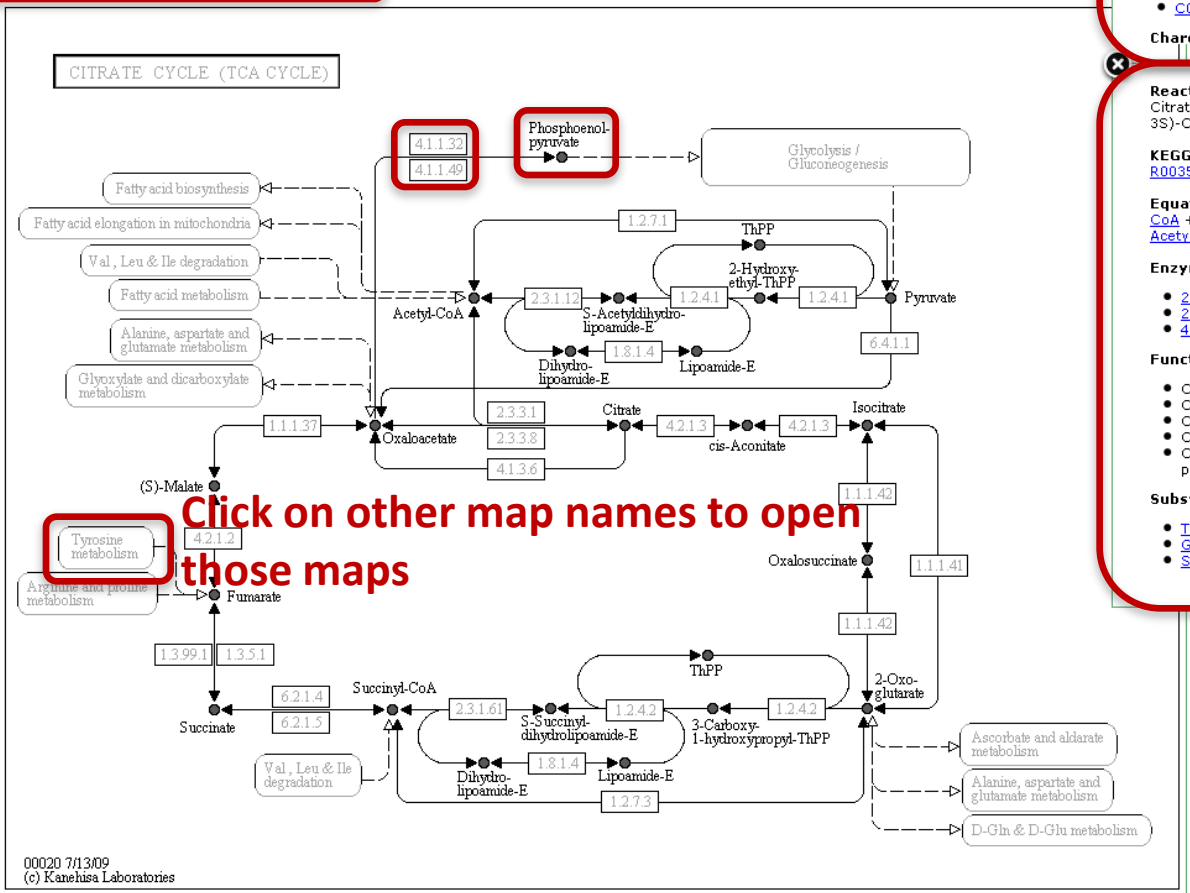
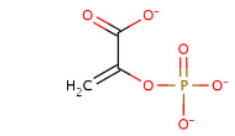
displaying 1 - 6 of 247 next» last»

Glycolysis / Glucon... | Citrate cycle (TCA ...

Multiple maps can be opened



Click on other map names to open those maps



Compound: cpd00061:
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PEP
phosphoenolpyruvate

C3H3O6P

KEGG ID:

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Click on compound link to visit compound page

Reaction: rxn00256
Citrate oxaloacetate-lyase ((pro-3S)-CH2COO- -> acetyl-CoA)

KEGG ID:
R00351

Equation:
CoA + H+ + Citrate <=> H2O + Acetyl-CoA + Oxaloacetate

Enzyme(s)

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- Citrate synthase (si) (EC 2.3.3.1)
- Citrate synthase (si) (EC 2.3.3.1)
- Citrate synthase, mitochondrial precursor (EC 2.3.3.1)

Subsystems:

- TCA Cycle
- Glyoxylate bypass
- Serine-glyoxylate cycle

Click on reaction link to visit reaction page

Reaction Page of Model SEED Database

Viewing data for reaction rxn01871

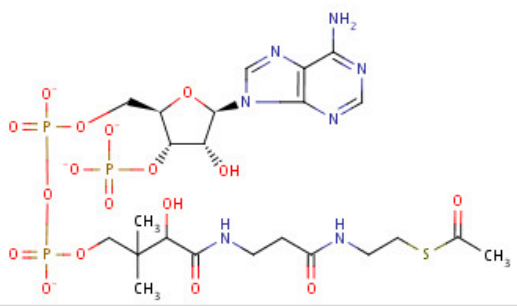
DATABASE	rxn01871
NAME	acetyl-CoA:enzyme N6-(dihydrolipoyl)lysine S-acetyltransferase, pyruvate dehydrogenase (dihydrolipoamide) reversible, dihydrolipoamide acetyltransferase component of PDH complex, dihydrolipoamide transacetylase component of PDH complex
EQUATION	Acetyl-CoA + Dihydrolipoamide <=> CoA + S-Acetyldihydrolipoamide
ENZYME	2.3.1.12
PATHWAY	Glycolysis / Gluconeogenesis, Alanine and aspartate metabolism, Pyruvate metabolism, Glycolysis, Gluconeogenesis, rn00010, rn00252, rn00620
DBLINKS	ARGONNE:rxn01871:rxn06179, KEGG:R02569, iAO358:rll_310, iNJ661:PDHbr, iJN746:PDHbr
DELTAG	0
DELTAGERR	2
THERMODYNAMIC REVERSIBILITY	
MAIN EQUATION	cpd00022 + cpd00449 <=> cpd00836

Equation contains links to compound pages

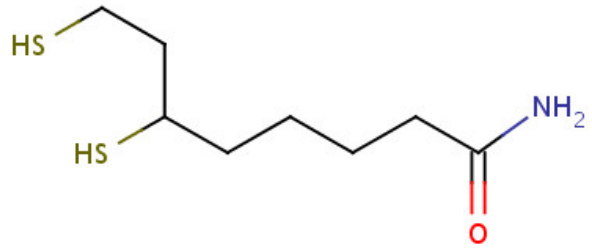
Name of reaction in KEGG and published models.

Reactants of reaction

(1) cpd00022c

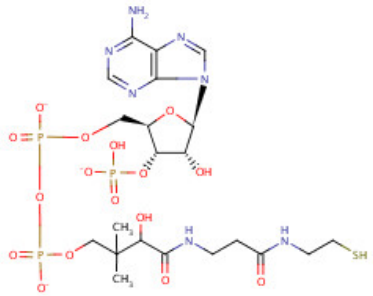


(1) cpd00449c

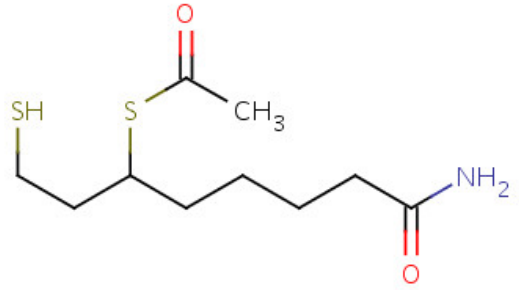


Products of reaction

(1) cpd00010c



(1) cpd00836c



Model SEED Reaction Table

Click on this tab to view a table of all reactions in the Model SEED database

Map | Reactions | Compounds | Biomass Components | Media formulations

display 50 items per page

displaying 1 - 50 of 12980

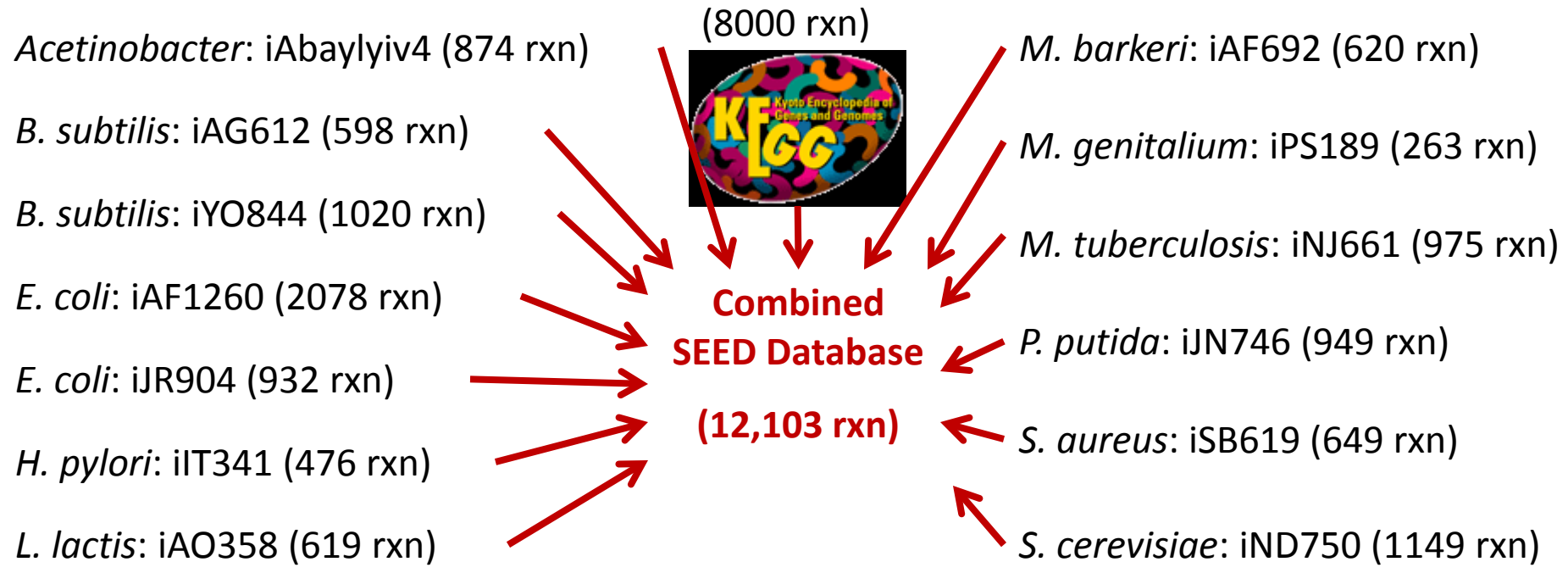
~13,000 reactions in database

next» last»

Reaction	Equation	Roles	KEGG MAP	Enzyme	KEGG RID
rxn00001	H2O + Pyrophosphate => (2) Orthophosphate + (2) H+	Inorganic pyrophosphatase (EC 3.6.1.1) Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1) Inorganic pyrophospatase PpaX		3.6.1.1	R00004
rxn00002	H2O + (3) H+ + Urea-1-carboxylate => (2) CO2 + (2) NH3	Allophanate hydrolase 2 subunit 1 (EC 3.5.1.54) Allophanate hydrolase (EC 3.5.1.54) Allophanate hydrolase 2 subunit 2 (EC 3.5.1.54)	Urea cycle and metabolism of amino groups Atrazine degradation	3.5.1.54	R00005
rxn00003	CO2 + 2-Acetolactate <= (2) Pyruvate + H+		C5-Branched dibasic acid metabolism Pantothenate and CoA biosynthesis	2.2.1.6 4.1.3.18	R00006 R00226
rxn00004	4-Hydroxy-4-methyl-2-oxoglutarate <=> (2) Pyruvate		Benzoate degradation via hydroxylation C5-Branched dibasic acid metabolism	4.1.3.17	R00008
rxn00006	(2) H2O2 => (2) H2O + Oxygen	Catalase (EC 1.11.1.6)		1.11.1.6	R00009
rxn00007	H2O + alpha,alpha-Trehalose <=> (2) D-Glucose	Trehalase (EC 3.2.1.28) Cytoplasmic trehalase (EC 3.2.1.28)	Starch and sucrose metabolism	3.2.1.28	R00010
rxn00008	(2) H2O <= H2O2 + (2) H+			1.11.1.13	R00011
rxn00009	(2) GTP <=> Pyrophosphate + P1,P4-Bis(5'-guanosyl) tetraphosphate			2.7.7.45	R00012
rxn00010	(2) Glyoxylate + H+ => CO2 + 2-Hydroxy-3-oxopropanoate	Glyoxylate carboligase (EC 4.1.1.47)	Glyoxylate and dicarboxylate metabolism	4.1.1.47	R00013
rxn00011	CO2 + 2-(alpha-Hydroxyethyl)thiamine diphosphate <= Pyruvate + Thiamin diphosphate + H+	Acetolactate synthase small subunit (EC 2.2.1.6), predicted, Archaeal type Pyruvate dehydrogenase E1 component (EC 1.2.4.1) Acetolactate synthase small subunit (EC 2.2.1.6), predicted, Archaeal type 2 Acetolactate synthase, catabolic (EC 2.2.1.6) Pyruvate decarboxylase (EC 4.1.1.1)	Glycolysis / Gluconeogenesis Citrate cycle (TCA cycle) Valine, leucine and isoleucine biosynthesis Pyruvate metabolism Butanoate metabolism	1.2.4.1 2.2.1.6 4.1.1.1	R00014

Biochemistry Database in the SEED

•A biochemistry database was constructed combining content from the **KEGG** and **13** published genome-scale models into a non-redundant set of compounds and reactions



•Reactions were then mapped to the functional roles in the SEED based on EC number, substrate names, and enzyme names:

REACTION	COMPLEX	FUNCTIONAL ROLE	GENE
$NAD^+ + NADPH \leftrightarrow NADH + NADP^+$	→ Gene complex	NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)	→ peg.100
		NAD(P) transhydrogenase alpha subunit (EC 1.6.1.2)	→ peg.101

www.theseed.org/models/

Model SEED Reaction Table

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Map | Reactions | Compounds | Biomass Components | Media formulations

display 50 items per page

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Table is paginated

next» last»

Reaction	Equation	Roles	KEGG MAP	Enzyme	KEGG RID
rxn00001	H2O + Pyrophosphate => (2) Orthophosphate + (2) H+	Inorganic pyrophosphatase (EC 3.6.1.1) Manganese-dependent inorganic pyrophosphatase (EC 3.6.1.1) Inorganic pyrophospatase PpaX		3.6.1.1	R00004
rxn00002	H2O + (3) H+ + Urea-1-carboxylate => (2) CO2 + (2) NH3	Allophanate hydrolase 2 subunit 1 (EC 3.5.1.54) Allophanate hydrolase (EC 3.5.1.54) Allophanate hydrolase 2 subunit 2 (EC 3.5.1.54)	Urea cycle and metabolism of amino groups Atrazine degradation	3.5.1.54	R00005
rxn00003	CO2 + 2-Acetolactate <= (2) Pyruvate + H+		C5-Branched dibasic acid metabolism Pantothenate and CoA biosynthesis	2.2.1.6 4.1.3.18	R00006 R00226
rxn00004	4-Hydroxy-4-methyl-2-oxoglutarate <=> (2) Pyruvate		Benzoate degradation via hydroxylation C5-Branched dibasic acid metabolism	4.1.3.17	R00008
rxn00006	(2) H2O2 => (2) H2O + Oxygen	Catalase (EC 1.11.1.6)		1.11.1.6	R00009
rxn00007	H2O + alpha,alpha-Trehalose <=> (2) D-Glucose	Trehalase (EC 3.2.1.28) Cytoplasmic trehalase (EC 3.2.1.28)	Starch and sucrose metabolism	3.2.1.28	R00010
rxn00008	(2) H2O <= H2O2 + (2) H+			1.11.1.13	R00011
rxn00009	(2) GTP <=> Pyrophosphate + P1,P4-Bis(5'-guanosyl) tetraphosphate			2.7.7.45	R00012
rxn00010	(2) Glyoxylate + H+ => CO2 + 2-Hydroxy-3-oxopropanoate	Glyoxylate carboligase (EC 4.1.1.47)	Glyoxylate and dicarboxylate metabolism	4.1.1.47	R00013
rxn00011	CO2 + 2-(alpha-Hydroxyethyl)thiamine diphosphate <= Pyruvate + Thiamin diphosphate + H+	Acetolactate synthase small subunit (EC 2.2.1.6), predicted, Archaeal type Pyruvate dehydrogenase E1 component (EC 1.2.4.1) Acetolactate synthase small subunit (EC 2.2.1.6), predicted, Archaeal type 2 Acetolactate synthase, catabolic (EC 2.2.1.6) Pyruvate decarboxylase (EC 4.1.1.1)	Glycolysis / Gluconeogenesis Citrate cycle (TCA cycle) Valine, leucine and isoleucine biosynthesis Pyruvate metabolism Butanoate metabolism	1.2.4.1 2.2.1.6 4.1.1.1	R00014

Search by compound name

Links to KEGG Map in Map tab

SEED Functional roles of reaction

Model SEED Compound Table

Click on this tab to view a table of all compounds in the Model SEED database

Map | Reactions | Compounds | Biomass Components | Media formulations

export table

Sort by Column headers e.g. largest and smallest mass

display 50 items per page

displaying 1 - 50 of 18324

next» last»

Compound	Name	Formula	Mass	KEGG MAP	KEGG CID	Model ID
cpd00001	H2O, Water, HO-, OH-, h2o	H2O	18	Oxidative phosphorylation Photosynthesis Carbon fixation in photosynthetic organisms Riboflavin metabolism Amyotrophic lateral sclerosis (ALS)	C01328 C00001	C01328 C00001 cpd00969 WATER h2o cbs_1 cbs_152 cll_9
cpd00002	ATP, Adenosine 5'-triphosphate, atp	C10H13N5O13P3	504	Oxidative phosphorylation Photosynthesis Purine metabolism Puromycin biosynthesis Zeatin biosynthesis Calcium signaling pathway Neuroactive ligand-receptor interaction Type II diabetes mellitus Parkinson's disease	C00002	C00002 ATP atp cbs_274 cbs_42 cll_0
cpd00003	NAD+, NAD, Nicotinamide adenine dinucleotide, DPN, Diphosphopyridine nucleotide, Nadide, Nicotinamideadeninedinucleotide, nad	C21H26N7O14P2	662	Oxidative phosphorylation Glutamate metabolism Nicotinate and nicotinamide metabolism	C00003	C00003 NAD nad cbs_61 cbs_35 cbs_150 cll_22 nad+
cpd00004	NADH, DPNH, Nicotinamide adenine dinucleotide - reduced, Nicotinamideadeninedinucleotide-reduced, nadh	C21H27N7O14P2	663	Oxidative phosphorylation Calcium signaling pathway	C00004	C00004 cpd15266 NADH nadh cbs_37 cll_23 cll_19
cpd00005	NADPH, TPNH, Nicotinamide adenine dinucleotide phosphate - reduced, Nicotinamideadeninedinucleotidephosphate-reduced, nadph	C21H27N7O17P3	742	Photosynthesis Glutathione metabolism	C00005	cpd15267 C00005 NADPH nadph cbs_23 cbs_63 cll_61
cpd00006	NADP+, NADP, Nicotinamide adenine dinucleotide phosphate, beta-Nicotinamide adenine dinucleotide phosphate, TPN, Triphosphopyridine nucleotide, Nicotinamide adenine dinucleotide phosphate -, Nicotinamideadeninedinucleotidephosphate, nadp	C21H26N7O17P3	741	Photosynthesis Glutathione metabolism Nicotinate and nicotinamide metabolism	C00006	C00006 NADP nadp cbs_26 cll_63 nadp+
cpd00007	Oxygen,	O2	32	Oxidative phosphorylation	C00007	C00007

Links to KEGG Maps that contain compound

Model SEED Media Table

Click on this tab to view a table of all media formulations in the Model SEED database

Map | Reactions | Compounds | Biomass Components | Media formulations

Media Formulations Currently Available in the Database

Sort and search by media name or by compound name

display 50 items per page

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Media name	Media compound names	Media compound ids
7H9	Calcium, Citrate, Chloride, Copper2, Fe3+, D-Glucose, L-Glutamate, Glycerol, Succinate, H2O, H+, Sodium, NH3, Oxygen, Orthophosphate, Sulfate, HCO3-, Potassium	cpd00063, cpd00137, cpd00099, cpd00058, cpd10516, cpd00027, cpd00023, cpd00100, cpd00036, cpd00001, cpd00067, cpd00971, cpd00013, cpd00007, cpd00009, cpd00048, cpd00242, cpd00205
ArgonneLBMedia	Hydrogen sulfide, Lipoate, Thiamin monophosphate, CMP, UMP, AMP, GMP, Guanosine, Adenosine, L-Alanine, L-Arginine, Arsenic acid, L-Aspartate, Calcium, Cadmium, chromate, L-Cystine, Deoxyadenosine, Deoxycytidine, Fe3+, Folate, D-Glucose, L-Glutamate, Glycine, H+, H2O, Hg2+, L-Histidine, Hypoxanthine, L-Isoleucine, Inosine, Potassium, L-Leucine, L-Lysine, L-Methionine, Magnesium, Sodium, Nicotinate, L-Phenylalanine, Orthophosphate, Pantothenate, L-Proline, Riboflavin, L-Serine, Sulfate, L-Threonine, Thymidine, L-Tryptophan, L-Tyrosine, Uracil, Uridine, L-Valine, Zinc, Oxygen, Chloride, Copper2, Cobalt, Manganese, Fe2+, Heme, Pyridoxal, Vitamin B12	cpd00239, cpd00541, cpd00793, cpd00046, cpd00091, cpd00018, cpd00126, cpd00311, cpd00182, cpd00035, cpd00051, cpd01048, cpd00041, cpd00063, cpd01012, cpd11595, cpd00381, cpd00438, cpd00654, cpd10516, cpd00393, cpd00027, cpd00023, cpd00033, cpd00067, cpd00001, cpd00531, cpd00119, cpd00226, cpd00322, cpd00246, cpd00205, cpd00107, cpd00039, cpd00060, cpd00254, cpd00971, cpd00218, cpd00066, cpd00009, cpd00644, cpd00129, cpd00220, cpd00054, cpd00048, cpd00161, cpd00184, cpd00065, cpd00069, cpd00092, cpd00249, cpd00156, cpd00034, cpd00007, cpd00099, cpd00058, cpd00149, cpd00030, cpd10515, cpd00028, cpd00215, cpd03424
ArgonneLBMedia_jose	CMP, Calcium, Fe3+, D-Glucose, Potassium, Magnesium, Sulfate, Zinc, Oxygen, Chloride, Copper2, Cobalt, Manganese	cpd00046, cpd00063, cpd10516, cpd00027, cpd00205, cpd00254, cpd00048, cpd00034, cpd00007, cpd00099, cpd00058, cpd00149, cpd00030
ArgonneNMSMedia	Hydrogen sulfide, L-Arginine, L-Alanine, L-Asparagine, L-Aspartate, Biotin, Citrate, Cobalt, Chloride, Copper2, L-Cysteine, Fe3+, Folate, D-Glucose, L-Glutamine, L-Glutamate, H+, H2O, L-Histidine, L-Leucine, L-Lysine, L-Methionine, Manganese, Molybdate, Nicotinate, L-Phenylalanine, Orthophosphate, L-Proline, Riboflavin, L-Serine, Thiamin, L-Threonine, L-Tryptophan, L-Tyrosine, L-Valine, Calcium, Potassium, Magnesium, Oxygen, Zinc, Fe2+, L-Isoleucine, Pyridoxal, Vitamin B12	cpd00239, cpd00051, cpd00035, cpd00132, cpd00041, cpd00104, cpd00137, cpd00149, cpd00099, cpd00058, cpd00084, cpd10516, cpd00393, cpd00027, cpd00053, cpd00023, cpd00067, cpd00001, cpd00119, cpd00107, cpd00039, cpd00060, cpd00030, cpd11574, cpd00218, cpd00066, cpd00009, cpd00129, cpd00220, cpd00054, cpd00305, cpd00161, cpd00065, cpd00069, cpd00156, cpd00063, cpd00205, cpd00254, cpd00007, cpd00034, cpd10515, cpd00322, cpd00215, cpd03424
BHI	Chorismate, Adenosine, L-Alanine, L-Arginine, Arsenic acid, L-Aspartate, Calcium, Cadmium, chromate, L-Cystine, Deoxyadenosine, Deoxycytidine, Fe3+, Folate, D-Glucose, L-Glutamate, Glycine, H+, H2O, Hg2+, L-Histidine, Hypoxanthine, L-Isoleucine, Inosine, Potassium, L-Leucine, L-Lysine, L-Methionine, Magnesium, Sodium, Nicotinate, L-Phenylalanine, Orthophosphate, Pantothenate, L-Proline, Riboflavin, L-Serine, Sulfate, L-Threonine, Thymidine, L-Tryptophan, L-Tyrosine, Uracil, Uridine, L-Valine, Zinc, Oxygen, L-Cysteine, L-Glutamine, trans-4-Hydroxy-L-proline, Ascorbate,	cpd00216, cpd00182, cpd00035, cpd00051, cpd01048, cpd00041, cpd00063, cpd01012, cpd11595, cpd00381, cpd00438, cpd00654, cpd10516, cpd00393, cpd00027, cpd00023, cpd00033, cpd00067, cpd00001, cpd00531, cpd00119, cpd00226, cpd00322, cpd00246, cpd00205, cpd00107, cpd00039, cpd00060, cpd00254, cpd00971, cpd00218, cpd00066, cpd00009, cpd00644, cpd00129, cpd00220, cpd00054, cpd00048, cpd00161, cpd00184, cpd00065, cpd00069, cpd00092, cpd00249, cpd00156, cpd00034, cpd00007, cpd00084, cpd00053, cpd00851, cpd00059, cpd00443, cpd00104, cpd00098, cpd00010, cpd00056,

Compound name and ID link to compound page

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