

ATP consuming reactions of all models ordered by percentage (descending)

flux	reaction	percent	reaction_name	model
-33.792414859042395	biomass_C	30.96	biomass_C	iYli_2.0
-15.57395809282011	R0005	14.27	L-Glutamate:ammonia ligase (ADP-forming)	iYli_2.0
-10.23681423826108	R0779	9.38	Pyruvate:carbon-dioxide ligase (ADP-forming)	iYli_2.0
-10.0	R0371	9.16	ATP:beta-D-glucose 6-phosphotransferase	iYli_2.0
-7.8625	R0542	7.2	ATP phosphohydrolase	iYli_2.0
-7.686704555605057	R0271	7.04	ATP:L-aspartate 4-phosphotransferase	iYli_2.0
-7.489426515840258	R0280	6.86	ATP:L-homoserine O-phosphotransferase	iYli_2.0
-4.188182967656931	R0379	3.84	ATP:D-fructose-6-phosphate 1-phosphotransferase	iYli_2.0
-2.7452861239914768	R0636	2.51	ATP:UDP phosphotransferase	iYli_2.0
-2.290156884713213	R0162	2.1	Acetyl-CoA:carbon-dioxide ligase (ADP-forming)	iYli_2.0
-7.8625	xMAINTENANCE	36.19	Non-growth associated maintenance (NGAM)	iYli21
-6.527628986939356	biomass_C	30.04	biomass_C	iYli21
-2.43	R387	11.18	hexokinase (D-glucose:ATP)	iYli21
-1.5462551526753012	R636	7.12	phosphofructokinase	iYli21
-0.9624523893616116	R690	4.43	pyruvate carboxylase	iYli21
-0.5303027130543749	R603	2.44	nucleoside-diphosphate kinase (ATP:UDP)	iYli21
-0.4925877746442582	R2081	2.27	L-Glutamate:ammonia ligase (ADP-forming)	iYli21
-30.58829101581773	biomass_C	43.28	biomass_C	iYali4(cor)
-10.0	534	14.15	hexokinase (D-glucose:ATP)	iYali4(cor)
-7.8625	xMAINTENANCE	11.13	Non-growth associated maintenance (NGAM)	iYali4(cor)
-6.9318385331421934	886	9.81	phosphofructokinase	iYali4(cor)
-3.356755611746837	958	4.75	pyruvate carboxylase	iYali4(cor)
-2.484984018828337	811	3.52	nucleoside-diphosphate kinase (ATP:UDP)	iYali4(cor)
-2.308252848285325	476	3.27	glutamine synthetase	iYali4(cor)
-23.35407677100508	biomass_C	32.67	biomass_C	iMK735(cor)
-10.0	HEX1	13.99	hexokinase D glucoseATP	iMK735(cor)
-7.8625	ATPM	11.0	ATP maintenance requirement	iMK735(cor)
-7.043325083660292	ATPS	9.85	ATPase cytosolic	iMK735(cor)
-6.667043270869102	PFK	9.33	phosphofructokinase	iMK735(cor)
-3.4014752267295374	ATPCitL	4.76	ATP Citrate Lyase YL	iMK735(cor)
-1.9727489045211215	PC	2.76	pyruvate carboxylase	iMK735(cor)
-1.9509757035401971	GLNS	2.73	glutamine synthetase	iMK735(cor)
-1.89727852139327	NDPK2	2.65	nucleoside diphosphate kinase ATPUDP	iMK735(cor)
-1.6030742454091698	ACCOACr	2.24	acetyl CoA carboxylase reversible reaction	iMK735(cor)
-9.487939876306204	r1187	46.29	Biomass formation	iLC915
-2.810084	r1188	13.71	Maintenance	iLC915
-2.43	r552	11.86	ATP:alpha-D-glucose 6-phosphotransferase	iLC915
-1.7565961481520485	r557	8.57	ATP:D-fructose-6-phosphate 1-phosphotransferase	iLC915
-1.0323563955038393	r1081	5.04	Acetyl-CoA:carbon-dioxide ligase (ADP-forming)	iLC915
-0.6701226798002782	r563	3.27	ATP:adenosine 5'-phosphotransferase	iLC915

<b>-0.4502691860217551</b>	r614	2.2	ATP:UDP phosphotransferase	iLC915
<b>-40.48858725623305</b>	biomass_C	41.04	biomass_C	iNL895(cor)
<b>-13.544159437353295</b>	r_0515	13.73	glutamine synthetase	iNL895(cor)
<b>-9.975942168928624</b>	r_0573	10.11	hexokinase (D-glucose:ATP)	iNL895(cor)
<b>-6.699288284984771</b>	r_0937	6.79	pyruvate carboxylase	iNL895(cor)
<b>-5.938777145836952</b>	r_0859	6.02	phosphofructokinase	iNL895(cor)
<b>-3.8847405372029775</b>	r_0233	3.94	aspartate kinase	iNL895(cor)
<b>-3.800811150239035</b>	r_0588	3.85	homoserine kinase	iNL895(cor)
<b>-3.313714688815579</b>	r_0779	3.36	nucleoside-diphosphate kinase (ATP:UDP)	iNL895(cor)
<b>-3.006207761400651</b>	r_0163	3.05	adenylate kinase	iNL895(cor)
<b>-19.15830294844153</b>	BIOMASS_glyc	66.4	Biomass composition (g/g)- Glycerol	iMT1026v3
<b>-2.81</b>	ATPM	9.74	ATP maintenance requirement	iMT1026v3
<b>-2.43</b>	HEX1	8.42	hexokinase (D-glucose:ATP)	iMT1026v3
<b>-1.1159511329283969</b>	PFK	3.87	phosphofructokinase	iMT1026v3
<b>-0.7005929427001316</b>	PC	2.43	pyruvate carboxylase	iMT1026v3
<b>-25.10825955467242</b>	biomass_C	38.97	biomass yarrowia carbon limiting	iYLI647(cor)
<b>-10.0</b>	HEX1	15.52	hexokinase D glucoseATP	iYLI647(cor)
<b>-7.8625</b>	ATPM	12.2	ATP maintenance requirement	iYLI647(cor)
<b>-4.512953397340768</b>	PFK	7.0	phosphofructokinase	iYLI647(cor)
<b>-2.1209283811941395</b>	PC	3.29	pyruvate carboxylase	iYLI647(cor)
<b>-2.0975210306078296</b>	GLNS	3.26	glutamine synthetase	iYLI647(cor)
<b>-2.0397884176141967</b>	NDPK2	3.17	nucleoside diphosphate kinase ATPUDP	iYLI647(cor)
<b>-1.721485062375631</b>	ACCOACr	2.67	acetyl CoA carboxylase reversible reaction	iYLI647(cor)
<b>-1.4452712516273536</b>	PFK_3	2.24	phosphofructokinase s7p	iYLI647(cor)
<b>-1.3235287325042668</b>	ADK1	2.05	adenylate kinase	iYLI647(cor)

ATP producing reactions of all models ordered by percentage (descending)

flux	reaction	percent	reaction_name	model
79.0063025067278	R1088	72.37	ADP/ATP transporter, mitochondrial	iYli_2.0
19.730222424533228	R0382	18.07	ATP:pyruvate 2-O-phosphotransferase	iYli_2.0
10.368217558171834	R0369	9.5	ATP:3-phospho-D-glycerate 1-phosphotransferase	iYli_2.0
39.34925126326448	ATPtm_H	61.07	ADPATP transporter mitochondrial	iYLI647(cor)
13.119901167376176	PGK	20.36	phosphoglycerate kinase	iYLI647(cor)
11.920355780907324	PYK	18.5	pyruvate kinase	iYLI647(cor)
44.55881549830313	1110	63.05	ADP/ATP transporter	iYali4(cor)
13.613092416667156	892	19.26	phosphoglycerate kinase	iYali4(cor)
12.369149152475686	962	17.5	pyruvate kinase	iYali4(cor)
23.024770697616027	ATPtm_H	79.81	ADP/ATP transporter, mitochondrial	iMT1026v3
3.0740066765200176	PGK	10.65	phosphoglycerate kinase	iMT1026v3
2.7386098544822586	PYK	9.49	pyruvate kinase	iMT1026v3
15.218256831688263	R815	70.04	ADP/ATP transporter	iYli21
3.3734605621318963	R642	15.53	phosphoglycerate kinase	iYli21
3.1079995036750767	R694	14.3	pyruvate kinase	iYli21
44.51096607355709	ATPtm_H	62.26	ADPATP transporter mitochondrial	iMK735(cor)
14.027049479131348	PGK	19.62	phosphoglycerate kinase	iMK735(cor)
12.911483187111708	PYK	18.06	pyruvate kinase	iMK735(cor)
75.84841266285085	r_1149	76.87	ADP/ATP transporter	iNL895(cor)
11.545863993433455	r_0865	11.7	phosphoglycerate kinase	iNL895(cor)
11.10395307010465	r_0941	11.25	pyruvate kinase	iNL895(cor)
10.580953135661616	r1279	51.62	Mitochondrial pyrimidine nucleotide transporter	iLC915
3.678413929215079	r596	17.95	ATP:3-phospho-D-glycerate 1-phosphotransferase	iLC915
3.1196118259580805	r576	15.22	ATP:pyruvate 2-O-phosphotransferase	iLC915
2.3137310188442397	r1407	11.29	ADP vacuolar transport	iLC915
0.5451036331160557	r611	2.66	ATP:GDP phosphotransferase	iLC915

NADH consuming reactions of all models ordered by percentage (descending)

flux	reaction	percent	reaction_name	model
-3.555345191287369	r258	77.14	5,6,7,8-Tetrahydrofolate:NAD+ oxidoreductase	iLC915
-0.7371750402928643	r75	15.99	sn-Glycerol-3-phosphate:NAD+ 2-oxidoreductase	iLC915
-0.1418234873293574	r254	3.08	L-Proline:NADP+ 5-oxidoreductase	iLC915
-0.09361449552547	r269	2.03	NADH:ferricytochrome-b5 oxidoreductase	iLC915
-12.750974294299796	R0001	61.16	L-glutamate:NAD+ oxidoreductase (transaminating)	iYli_2.0
-7.686704555604875	R1380	36.87	L-homoserine:NAD+ oxidoreductase	iYli_2.0
-3.547602775974553	MDH	94.12	malate dehydrogenase	iMT1026v3
-10.60806912917618	163	68.8	alcohol dehydrogenase (ethanol to acetaldehyde)	iYali4(cor)
-4.53273563406716	714	29.4	malate dehydrogenase, cytoplasmic	iYali4(cor)
-15.083506390439524	NADH2_u6cm	97.11	NADH dehydrogenase cytosolicmitochondrial	iMK735(cor)
-0.3492906117875991	HSDxi	2.25	homoserine dehydrogenase NADH irreversible	iMK735(cor)
-2.983178741939755	R130	74.49	alcohol dehydrogenase (ethanol to acetaldehyde)	iYli21
-0.9624523893616064	R534	24.03	malate dehydrogenase, cytoplasmic	iYli21
-17.522462330593033	NADH2_u6cm	94.57	NADH dehydrogenase cytosolicmitochondrial	iYLI647(cor)
-0.3755270190474962	HSDxi	2.03	homoserine dehydrogenase NADH irreversible	iYLI647(cor)

NADH producing reactions of all models ordered by percentage (descending)

flux	reaction	percent	reaction_name	model
13.11990116737551	GAPD	70.81	glyceraldehyde 3 phosphate dehydrogenase	iYLI647(cor)
1.4471543049019178	IPMD	7.81	3 isopropylmalate dehydrogenase	iYLI647(cor)
1.2355994151037626	LEUDH	6.67	2-Oxoisovalerate dehydrogenase	iYLI647(cor)
1.2355994151037626	MBCOAI	6.67	isovaleryl-coa dehydrogenase	iYLI647(cor)
0.9255023064610328	PGCD	4.99	phosphoglycerate dehydrogenase	iYLI647(cor)
3.373460562131452	R344	84.24	glyceraldehyde-3-phosphate dehydrogenase	iYli21
0.2461111193645677	R2119	6.15	3-Oxopropanoate:NAD+ oxidoreductase (decarboxylating, CoA-acetylating)	iYli21
0.1942157621590909	R641	4.85	phosphoglycerate dehydrogenase	iYli21
10.368217558171908	R0367	49.73	D-glyceraldehyde-3-phosphate:NAD+ oxidoreductase (phosphorylating)	iYli_2.0
9.382490328768952	R1011	45.0	Nicotinamide adenine dinucleotide - reduced transport	iYli_2.0
13.613092416672334	486	88.29	glyceraldehyde-3-phosphate dehydrogenase	iYali4(cor)
0.9100897530585002	891	5.9	phosphoglycerate dehydrogenase	iYali4(cor)
0.3643106526983576	988	2.36	saccharopine dehydrogenase (NAD, L-lysine forming)	iYali4(cor)
14.027049479129063	GAPD	90.31	glyceraldehyde 3 phosphate dehydrogenase	iMK735(cor)
0.8606700467459832	PGCD	5.54	phosphoglycerate dehydrogenase	iMK735(cor)
3.6784139291959614	r146	79.81	D-glyceraldehyde-3-phosphate:NAD+ oxidoreductase (phosphorylating)	iLC915
0.4534384143709352	r86	9.84	3-Phospho-D-glycerate:NAD+ 2-oxidoreductase	iLC915
0.1111441055239338	r85	2.41	(1R,2S)-1-hydroxybutane-1,2,4-tricarboxylate:NAD+ oxidoreductase	iLC915
3.074006676519993	GAPD	81.56	glyceraldehyde-3-phosphate dehydrogenase	iMT1026v3
0.1992821053943454	PGCD	5.29	phosphoglycerate dehydrogenase	iMT1026v3
0.113101259442398	2OXOADOX	3.0	2-oxoadipate dehydrogenase complex	iMT1026v3
0.113101259442398	GLUTCOADHc	3.0	glutaryl-CoA dehydrogenase (citosol)	iMT1026v3
0.0754840873448916	IPMD	2.0	3-isopropylmalate dehydrogenase	iMT1026v3

NADPH consuming reactions of all models ordered by percentage (descending)

flux	reaction	percent	reaction_name	model
-6.427209323708233	471	61.55	glutamate dehydrogenase (NADP)	iYali4(cor)
-0.6085334500227906	558	5.83	hydroxymethylglutaryl CoA reductase	iYali4(cor)
-0.4574877006363648	219	4.38	aspartate-semialdehyde dehydrogenase	iYali4(cor)
-0.4574877006363648	547	4.38	homoserine dehydrogenase (NADP)	iYali4(cor)
-0.3643106526983576	678	3.49	L-aminoadipate-semialdehyde dehydrogenase (NADPH)	iYali4(cor)
-0.3643106526983576	989	3.49	saccharopine dehydrogenase (NADP, L-glutamate forming)	iYali4(cor)
-0.2733896402562333	957	2.62	pyrroline-5-carboxylate reductase	iYali4(cor)
-4.969038519641094	GLUDy	45.34	glutamate dehydrogenase NADP	iMK735(cor)
-1.3391475626706475	FAS80COA_L	12.22	fatty acyl CoA synthase n C80CoA lumped reaction	iMK735(cor)
-0.4646136295161929	HMGCOAR	4.24	Hydroxymethylglutaryl CoA reductase	iMK735(cor)
-0.4463825208902159	FAS100COA	4.07	fatty acyl CoA synthase n C100CoA	iMK735(cor)
-0.4383907521754753	FAS120COA	4.0	fatty acyl CoA synthase n C120CoA	iMK735(cor)
-0.4144154460312535	FAS140COA	3.78	fatty acyl CoA synthase n C140CoA	iMK735(cor)
-0.3744566024575505	FAS160COA	3.42	fatty acyl CoA synthase n C160CoA	iMK735(cor)
-0.3492906117875992	ASADi	3.19	aspartate semialdehyde dehydrogenase irreversible	iMK735(cor)
-0.2781501897968927	AASAD1	2.54	L aminoadipate semialdehyde dehydrogenase NADPH	iMK735(cor)
-0.2781501897968927	SACCD1	2.54	saccharopine dehydrogenase NADP L glutamate forming	iMK735(cor)
-1.3715848938689954	R330	61.82	glutamate dehydrogenase (NADP)	iYli21
-0.1298627826522493	R410	5.85	hydroxymethylglutaryl CoA reductase	iYli21
-0.0976291867465832	R164	4.4	aspartate-semialdehyde dehydrogenase	iYli21
-0.0976291867465832	R399	4.4	homoserine dehydrogenase (NADP)	iYli21
-0.0777449376159914	R505	3.5	L-aminoadipate-semialdehyde dehydrogenase (NADPH)	iYli21
-0.0777449376159914	R719	3.5	saccharopine dehydrogenase (NADP, L-glutamate forming)	iYli21
-0.0583421329273554	R689	2.63	pyrroline-5-carboxylate reductase	iYli21
-5.342303404220281	GLUDy	46.54	glutamate dehydrogenase NADP	iYLI647(cor)
-1.4384268821977964	FAS80COA_L	12.53	fatty acyl CoA synthase n C80CoA lumped reaction	iYLI647(cor)
-0.4995120712266671	HMGCOAR	4.35	Hydroxymethylglutaryl CoA reductase	iYLI647(cor)
-0.4794756273992654	FAS100COA	4.18	fatty acyl CoA synthase n C100CoA	iYLI647(cor)
-0.4709037752175204	FAS120COA	4.1	fatty acyl CoA synthase n C120CoA	iYLI647(cor)
-0.4451882186722857	FAS140COA	3.88	fatty acyl CoA synthase n C140CoA	iYLI647(cor)
-0.4023289577635612	FAS160COA	3.5	fatty acyl CoA synthase n C160CoA	iYLI647(cor)
-0.3755270190474981	ASADi	3.27	aspartate semialdehyde dehydrogenase irreversible	iYLI647(cor)
-0.2990426280842557	SACCD1	2.61	saccharopine dehydrogenase NADP L glutamate forming	iYLI647(cor)
-7.686704555604874	R0282	46.69	L-Aspartate-4-semialdehyde:NADP+ oxidoreductase (phosphorylating)	iYli_2.0
-1.935343846236368	R0125	11.76	fatty acyl-CoA synthase (n-C8:0CoA), lumped reaction	iYli_2.0
-0.6722773360610539	R0765	4.08	(R)-Mevalonate:NADP+ oxidoreductase (CoA acylating)	iYli_2.0
-0.6451146154121226	R0126	3.92	fatty acyl-CoA synthase (n-C10:0CoA)	iYli_2.0
-0.6322123231038801	R0129	3.84	fatty-acyl-CoA synthase (n-C12:0CoA)	iYli_2.0
-0.6200256865282523	R1013	3.77	Nicotinamide adenine dinucleotide phosphate - reduced transport	iYli_2.0
-0.5935054461791528	R0131	3.61	fatty-acyl-CoA synthase (n-C14:0CoA)	iYli_2.0
-0.5289939846379406	R0133	3.21	fatty-acyl-CoA synthase (n-C16:0CoA)	iYli_2.0
-0.402472197848028	R0416	2.44	N6-(L-1,3-Dicarboxypropyl)-L-lysine:NADP+ oxidoreductase	iYli_2.0
-0.402472197848028	R0422	2.44	L-2-Aminoadipate-6-semialdehyde:NADP+ 6-oxidoreductase	iYli_2.0
-1.074721072773711	r237	27.79	L-Glutamate:NADP+ oxidoreductase (deaminating)	iLC915
-0.1418234873293762	r164	3.67	L-Glutamate-5-semialdehyde:NADP+ 5-oxidoreductase (phosphorylating)	iLC915
-0.1334626774113506	r10	3.45	(3R)-3-Hydroxydecanoyl-[acyl-carrier-protein]:NADP+ oxidoreductase	iLC915

-0.1334626774113506	r201	3.45	Octanoyl-[acyl-carrier protein] reductase	iLC915
-0.1334626774113506	r23	3.45	(3R)-3-Hydroxyhexanoyl-[acyl-carrier-protein]:NADP+ oxidoreductase	iLC915
-0.1334626774113506	r210	3.45	Butyryl-[acyl-carrier protein] reductase	iLC915
-0.1334626774113506	r207	3.45	Hexadecanoyl-[acyl-carrier protein]:malonyl-CoA	iLC915
-0.1334626774113506	r205	3.45	Tetradecanoyl-[acyl-carrier protein] reductase	iLC915
-0.1334626774113506	r12	3.45	(3R)-3-Hydroxyoctanoyl-[acyl-carrier-protein]:NADP+ oxidoreductase	iLC915
-0.1334626774113506	r203	3.45	Decanoyl-[acyl-carrier protein] reductase	iLC915
-0.1334626774113506	r199	3.45	Hexanoyl-[acyl-carrier protein] reductase	iLC915
-0.1334626774113506	r197	3.45	Dodecanoyl-[acyl-carrier protein] reductase	iLC915
-0.1334626774113506	r19	3.45	(3R)-3-Hydroxydodecanoyl-[acyl-carrier-protein]:NADP+ oxidoreductase	iLC915
-0.1334626774113506	r16	3.45	(3R)-3-Hydroxytetradecanoyl-[acyl-carrier-protein]:NADP+	iLC915
-0.1334626774113506	r14	3.45	(3R)-3-Hydroxypalmitoyl-[acyl-carrier-protein]:NADP+ oxidoreductase	iLC915
-0.1334626774113506	r8	3.45	(3R)-3-Hydroxybutanoyl-[acyl-carrier protein]:NADP+ oxidoreductase	iLC915
-0.1186109043995743	r48	3.07	(R)-Mevalonate:NADP+ oxidoreductase (CoA acylating)	iLC915
-0.0981176536235076	r21	2.54	3-oxoacyl-[acyl-carrier-protein] reductase	iLC915
-0.0962965286526567	r256	2.49	5-methyltetrahydrofolate:NADP+ oxidoreductase	iLC915
-0.0936144955254601	r185	2.42	Trans-2-enoyl-CoA reductase	iLC915
-1.3579130632252334	GLUDyi	68.64	glutamate dehydrogenase (NADP)	iMT1026v3
-0.0707194760824927	ASADi	3.57	aspartate-semialdehyde dehydrogenase, irreversible	iMT1026v3
-0.0704563854932786	SACCD1	3.56	saccharopine dehydrogenase (NADP, L-glutamate forming)	iMT1026v3
-0.0680573583216777	SHK3D	3.44	shikimate dehydrogenase	iMT1026v3
-0.0395952474707705	HMGCOAR	2.0	Hydroxymethylglutaryl CoA reductase	iMT1026v3



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4.545639349993636	GND	39.6	phosphogluconate dehydrogenase	iYLI647(cor)
4.465681412374501	G6PDH2	38.9	glucose 6 phosphate dehydrogenase	iYLI647(cor)
2.091527895144857	ICDH <sub>y</sub>	18.22	isocitrate dehydrogenase NADP	iYLI647(cor)
0.3316784906535485	MTHFD	2.89	methylenetetrahydrofolate dehydrogenase NADP	iYLI647(cor)
1.357026494914588	R488	61.16	isocitrate dehydrogenase (NADP)	iYli21
0.3707923694516898	R325	16.71	glucose 6-phosphate dehydrogenase	iYli21
0.3707923694516898	R639	16.71	phosphogluconate dehydrogenase	iYli21
0.0862294417804006	R550	3.89	methylenetetrahydrofolate dehydrogenase (NADP)	iYli21
9.882162955875405	659	94.64	isocitrate dehydrogenase (NADP)	iYali4(cor)
0.4040688073092899	732	3.87	methylenetetrahydrofolate dehydrogenase (NADP)	iYali4(cor)
4.70767648460928	ICDH <sub>y</sub>	42.96	isocitrate dehydrogenase NADP	iMK735(cor)
2.9487416940213995	GND	26.91	phosphogluconate dehydrogenase	iMK735(cor)
2.874369731308157	G6PDH2	26.23	glucose 6 phosphate dehydrogenase	iMK735(cor)
0.3085054324150789	MTHFD	2.82	methylenetetrahydrofolate dehydrogenase NADP	iMK735(cor)
0.9345595716537608	G6PDH2	47.24	glucose 6-phosphate dehydrogenase	iMT1026v3
0.9345595716537608	GND	47.24	phosphogluconate dehydrogenase	iMT1026v3
0.0857248849631132	MTHFD	4.33	methylenetetrahydrofolate dehydrogenase (NADP)	iMT1026v3
7.234197192083037	R0483	43.95	6-phospho-D-gluconate:NADP+ 2-oxidoreductase (decarboxylating)	iYli_2.0
7.234197192083037	R0490	43.95	beta-D-Glucose-6-phosphate:NADP+ 1-oxoreductase	iYli_2.0
1.3834078999124015	R1461	8.4	Isocitrate:NADP+ oxidoreductase (decarboxylating)	iYli_2.0
0.3903719082830687	R0454	2.37	5,10-methylenetetrahydrofolate:NADP+ oxidoreductase	iYli_2.0
3.5550701109783134	r259	91.92	5,6,7,8-Tetrahydrofolate:NADP+ oxidoreductase	iLC915
0.267194840289408	r71	6.91	Isocitrate:NADP+ oxidoreductase (decarboxylating)	iLC915