

Phaeodactylum tricornutum										Thalassiosira pseudonana														
Enzyme	Name	Pathway	Protein ID	NCBI Accession	Number of iso	genomic Coordinates	Best Blast hit	organism	% identity	accession no.	Localisation	SP	other	Loc	RC	TPIen	Signal peptide assigned	Loca Name	Protein ID	Number of iso	genomic Coordinates			
2-phosphoglycerate PGP	Photorespirat	48026	1	Pha2/chr_13	PREDICTED: Rattus norvegicus 25	XP_213235	0.761	0.249	0.028	M	3	28					mitochondria/PGP	25544			Thaps3/chr_19c_29-134214-137101			
6-Phosphogluconate 6P6GDH	Calvin cycle	45333	2	Pha2/chr_6	6-phosphogluconate Phycophthora i 68	AA176320	0.027	0.973	0.068	S	1	18	LES-IQT	ER/ppp?										
6-Phosphogluconate 6P6GDH	Calvin cycle	26934	2	Pha2/chr_6	6-phosphogluconate Phycophthora i 68	AA176320	0.200	0.174	0.538	-	4	-												
AcetylCoA syn ACS1	Glycolysis/glu	22974	2	Pha2/chr_20	acetyl-CoA syn Dicyostelium i 47	Pha2_48293	0.074	0.057	0.934	-	1	-					cytosol	ACS1	34187	1 of 2		Thaps3/chr_5:1434158-1436335		
AcetylCoA syn ACS2	Glycolysis/glu	645	2	Pha2_16tbla	AMP-depende Magnetococcus 52	ZP_00607585	0.064	0.908	0.068	S	1	16	AVA-TTH	plastid, Signal	ACS2	270246				2 of 2		Thaps3/chr_4:1493546-1498038		
Adenylate kina ADK	Purine metabo	20093	1	Pha2/chr_7	putative adeny Onyza sativa (j 52	XP_479721	0.069	0.850	0.049	S	2	22	LLA-FAP	plastid										
alanine/glyoxyl SGAT	Photorespirat	40344	1	Pha2/chr_23	serine-pyruvat Burkholderia c 47	ZP_00458764	0.933	0.019	0.068	M	1	37					mitochondria		22208	1		Thaps3/chr_4:861901-863613		
Aldolase	Aldolase	31147	1	Pha2/chr_29	haloacid dehal Arabidopsis th 34	AT5G53850	0.297	0.039	0.791	-	3	-					cytosol							
alpha carbonic CA1	Carbon metab	35370	7	Pha2/chr_7	carbonic anhy Arabidopsis th 11	NP_172287	0.21	0.814	0.06	S	2	18	VRC-RSW	putatively secr	CA1	22391							Thaps3/chr_4:1704676-1706645	
alpha carbonic CA2	Carbon metab	44526	7	Pha2/chr_4	Carbonic anhy Ories aries 8	P08060	0.022	0.956	0.075	S	2	18	TTA-GTG	putatively secr	CA2	22257							Thaps3/chr_4:1065978-1057638	
alpha carbonic CA3	Carbon metab	55029	7	Pha2/chr_21	Carbonic anhy Nostoc sp. PC 30	P94170	0.149	0.814	0.034	S	2	26	GLG-LNK	putatively secr	CA3	262006							Thaps3/chr_4:90470-90111	
alpha carbonic CA6	Carbon metab	54251	7	Pha2/chr_4	carbonic anhy Rattus norvegicus 16	291819	0.072	0.858	0.134	S	2	26	ATA-OEG	putatively secr	CA4	262009								Thaps3/chr_4:11394-113810
alpha carbonic CA7	Carbon metab	42574	7	Pha2/chr_14	Carbonic anhy Ories aries 5	P08060	0.024	0.906	0.217	S	2	16	AEA-DLF	putatively secr										
ATPase gamr AtpC	ATP synthesis	20627	1	Pha2/chr_97	ATP synthase Odontella sine 80	Q06998	0.231	0.761	0.045	S	3	15	ASA-FTT	plastid [1,3,4]										
beta carbonic CA4	Carbon metab	51305	7	Pha2/chr_14	carbonic anhy Aspergillus cla 47	XP_001273480	0.118	0.795	0.08	S	2	19	VEA-FNA	plastid [7]										
beta carbonic CA5	Carbon metab	45443	7	Pha2/chr_7	carbonic anhy Aspergillus cla 46	XP_001273480	0.084	0.845	0.082	S	2	19	VDA-LNV	putatively secr										
Beta-glucan synthesis-associ	Chrysolaminar	50238	3	Pha2/chr_28	hypothetical pr Ustilago mayd 28	XP_051820	0.128	0.836	0.021	S	2	27	TDA-SNV	ER-Golgi (secreted?)							3105	1 of 3	Thaps3/chr_3:130440-132823	
Beta-glucan synthesis-associ	Chrysolaminar	56509	3	Pha2/chr_27	hypothetical pr Ustilago mayd 28	XP_759188	0.143	0.922	0.017	S	2	30	AAS-NWI	ER-Golgi (secr TPS_138072)	4956	2 of 3							Thaps3/chr_4:2393022-2394416	
Beta-glucan synthesis-associ	Chrysolaminar	48300	3	Pha2/chr_17	hypothetical pr Ustilago mayd 30	XP_761956	0.023	0.906	0.153	S	2	23	TIS-VSI	ER-Golgi (secreted?)	9237	3 of 3							Thaps3/chr_12:940118-942696	
Beta-glucosidase (glycosyl	Hy Chrysolaminar	50351	1	Pha2/chr_29	TonB-like prot Lentsphaera s 52	ZP_01873221	SignalP HMM: 0.723	Signal Peptide not recognised by TargetP															Thaps3/chr_5:1900338-1902076	
Beta-glucosidase (glycosyl	Hy Chrysolaminar	49793	2	Pha2/chr_24	putative therm uncultured me 4	YP_684568	0.13	0.093	0.835	-	2	-												
Beta-glucosidase (glycosyl	Hy Chrysolaminar	45128	2	Pha2/chr_6	beta-glucosidase, Pedobacter sp 35	ZP_01885707	0.269	0.043	0.812	-	3	-												
bicarbonate tr SLV4_1	Carbon metab	45656	3	Pha2/chr_7	hypothetical pr Nitrococcus m 34	ZP_01128816	0.248	0.817	0.022	S	3	24	SAF-FHT	plastid	SLV4_1	270240							Thaps3/chr_1:1419165-1419927	
bicarbonate tr SLV4_2	Carbon metab	42359	3	Pha2/chr_12	probable Naa+ Cyanidioschyz 48	CMR090C	0.133	0.579	0.199	S	4	33	GSA-FTS	plastid	SLV4_2	267979								Thaps3/chr_1:974609-977268
bicarbonate tr SLV4_3	Carbon metab	54405	3	Pha2/chr_7	solute carrier F Bos taurus 32	NP_851379	0.044	0.162	0.955	-	2	-					membrane pro SLV4_3	13887					Thaps3/chr_8:159912-161745	
citrate synthas C1S7	Citrate cycle	130145	1	Pha2/chr_21	Citrate synthas Daucus carota 58	Q06433	0.891	0.035	0.115	M	2	33					mitochondria	CSN1	11411	1		Thaps3/chr_20:29093-31078		
citrate synthas ACL	Citrate cycle	134477	1	Pha2/chr_83	PREDICTED: Canis lupus fa 61	XP_860188	0.427	0.037	0.648	S	2	21					cytosol	SCS2	411	1		Thaps3/chr_4:1672995-1689910		
dihydroipoami pLDH1	Energy produc	30113	1	Pha2/chr_20	Ost5g015670 Onyza sativa (j 58	NP_001054680	0.045	0.827	0.129	S	2	21	TLA-FAP	plastid	DLDH2	24399							Thaps3/chr_11b:19098-21311	
dihydroipoami DLDH1	Glycolysis / G	26432	1	Pha2/chr_5	dihydroipoami Arabidopsis th 60	AT1G48030	0.919	0.095	0.057	M	1	32					mitochondria	LPD	36716	1		Thaps3/chr_11a:734324-735897		
Endo-1,3-beta Phatr1_44408	Chrysolaminar	54681	2	Pha2/chr_10	glycoside hydr Flavobacterium 31	YP_001196500	0.053	0.888	0.05	S	1	20	ATA-QTC	Vacuolar via ER-Golgi? (secr 35711									Thaps3/chr_7:53891-539648	
Endo-1,3-beta Phatr1_49780	Chrysolaminar	54973	2	Pha2/chr_20	endo-1,3-beta-Xanthomonas 36	NP_638562	0.044	0.899	0.051	S	1	21	VAA-QTP	Vacuolar via ER-Golgi? (secreted?)									Thaps3/chr_1:1823548-1827535	
Endo-1,3-beta-glucosidase (g	Chrysolaminar	46676	1	Pha2/chr_12	beta-glucan-bi Medicago trun 25	AB669781	0.142	0.025	0.906	-	2	-					Cytosolic type II transmembr 1554						Thaps3/chr_2:1219499-1221471	
Exo-1,3-beta-glucanase	Chrysolaminar	49294	4	Pha2/chr_21	putative exo-1 Phycophthora i 48	AA118483	0.061	0.937	0.028	S	1	32	AEA-DNT	Vacuolar via ER-Golgi? (secr 13556									Thaps3/chr_2:1219499-1221471	
Exo-1,3-beta-g Phatr1_46154	Chrysolaminar	56510	4	Pha2/chr_7	hypothetical pr Coprinopsis ci 29	EAL85291	0.082	0.818	0.093	S	2	22	VSE-REY	ER-Golgi resident, contains retention signal "REEL"										
Exo-1,3-beta-g Phatr1_48127	Chrysolaminar	56506	4	Pha2/chr_10	hypothetical pr Ustilago mayd 28	XP_761697	SignalP HMM: 0.758	Signal Peptide not recognised by TargetP																
Exo-1,3-beta-g Phatr1_50463	Chrysolaminar	49610	4	Pha2/chr_23	hypothetical pr Ustilago mayd 28	XP_761697	0.07	0.100	0.925	-	1	-					unclear							
Ferredoxin th FrB	Electron trans	50907	1	Pha2/chr_7	ferredoxin-thio Spinacia olera 65	CAA52867	0.07	0.946	0.02	S	1	18	TQA-FMP	plastid	FrB	26405								Thaps3/chr_13:610874-611571
fructose-bisph F6b3	Glycolysis	29014	5	Pha2/chr_14	fructose-bisph Cryptococcus 61	XP_568771	0.133	0.095	0.837	-	2	-					cytosol							
Fructose-1,6-bi FBP2	Calvin cycle	42347	5	Pha2/chr_22	fructose-1,6-bi Onyza sativa (j 48	NP_315561	0.043	0.104	0.953	S	1	104					cytosol							
Fructose-1,6-bi FBP3	Calvin cycle	42886	5	Pha2/chr_11	fructose-1,6 bi Bigelwella nc 39	AA279192	0.022	0.939	0.076	S	1	30	TNS-FOT	plastid										
Fructose-1,6-bi FBP2C	Calvin cycle	42456	5	Pha2/chr_11	fructose-bisph Triticum aestiv 50	CAA37908	SignalP HMM: 0.989	Signal Peptide not recognised by TargetP																
Fructose-1,6-bi FBP3C	Calvin cycle	31451	5	Pha2/chr_11	fructose-1,6-bi chloroplast Ga 45	CAC82800	0.105	0.914	0.013	S	1	25	ARA-NSI	plastid? (cleavage site might be mispredicted, "VVA-FTA" motif contained)										
Fructose-1,6-bi FBP4C	Calvin cycle	54279	5	Pha2/chr_4	fructose-1,6-bi Cyanidioschyz 42	CMO245C	0.03	0.966	0.025	S	1	28	IGA-WIP	plastid [2]										
Fructose-1,6-bi FbaC1	Calvin cycle	825	5	Pha2_16tbla	fructose-1,6-bi Odontella sine 82	AA667652	0.081	0.875	0.06	S	2	16	VVA-FAP	plastid [2,3,4,5]										
Fructose-1,6-bi FbaC2	Calvin cycle	22993	5	Pha2/chr_20	plastid C1 clas Heterocapsa t 63	AAV71135	0.171	0.815	0.077	S	2	16	CGA-FAP	plastid										
Fructose-6-Ph FSA	Calvin cycle	20779	1	Pha2/chr_10	Putative fructo Synecococcus 29	ZP_01084071	0.587	0.759	0.006	S	5	28	VWG-WTP	plastid [2]										
Fructose-bisph Fba4	Glycolysis	42447	5	Pha2/chr_1	Fructose-bisph Oceanococcus 63	Q8EL12	0.088	0.194	0.751	-	1	-					cytosol							
fructose-bisph Fba5C	Calvin cycle	51299	5	Pha2/chr_30	fructose-1,6-bi Galdieria sulps 53	AAF27641	0.228	0.833	0.011	S	2	22	AAA-FSA	plastid										
Glucokinase	Glucokinase	Glycolysis/chr	48774	1	Pha2/chr_19	Glucokinase Crocospheera 34	ZP_00516463	0.288	0.148	0.428	-	5	-										Thaps3/chr_2:758305-758252	
Glucokinase	Glucokinase	Glycolysis/chr	56514	1	Pha2/chr_19	Glucokinase Crocospheera 34	ZP_00516463	0.022	0.934	0.107	S	1	27	TNS-RMS	Vacuolar via ER-Golgi?									
Glucose-6-ph Phatr1_29709	Pentose phos	30040	2	Pha2/chr_20	Glucose-6-ph Solanum tuba 41	P27830	SignalP HMM: 0.406	TargetP predicts signal peptide, probably mispredicted																
Glucose-6-ph G6PDH6PGD	Calvin cycle	54663	2	Pha2/chr_11	6-phosphoglu Phycophthora i 63	AA176320	0.152	0.188	0.594	-	3	-					cytosol							
Glucose-6-ph G6PDH6PGD	Calvin cycle	54663	2	Pha2/chr_11	cytoplasmic gi Mesembryantif 51	AA11426	0.152	0.188	0.594	-	3	-					cytosol							
Glucose-6-ph G6P	Calvin cycle/G	53924	3	Pha2/chr_28	glucose-6-ph Vibrio cholerae 65	AAF93547	0.106	0.050	0.918															

NAD malic enz ME1	Carbon metab	56501	2	Phat2/chr 2:2	malic enzyme	Dictyostelium	46	XP_645111	0.913	0.012	0.146	M	2	16	mitochondria	MAO1	34030		Thaps3/chr 5.366187-368021
NADP malic er Probably NADP Malic enzym	27477	2	Phat2/chr 8:8	NADP-depend Phaeosulf vult	52	P12628	0.569	0.496	0.028	M	5	32	mitochondria						
oxoglutarate/r OMT1	Carbon metab	8990	2	Phat2/chr 1:1	Hypothetical pCaenorhabditis	34	AAB37890	0.447	0.147	0.375	M	5	63	mitochondria	OMT1	20731		Thaps3/chr 1.1029873-1031344	
oxoglutarate/r OMT2	Carbon metab	16785	2	Phat2/chr 2:8	oxoglutarate/r Plasmodium	38	NP_704315	0.197	0.066	0.775	-	3	-	unclear	OMT2	26386		Thaps3/chr 10.794360-795713	
Phosphoglycer PGK	Glycolysis	29197	3	Phat2/chr 1:5	phosphoglycer	Cyanidioschyz	66	CM4395C	0.303	0.775	0.023	S	3	20	plastid				
Phosphoglycer PGK	Glycolysis	51126	3	Phat2/chr 1:8	phosphoglycer	Kryptoperidini	55	AAW79329	0.361	0.06	0.685	-	4	-	cytosol				
Phosphoglycer PGK	Glycolysis	48983	3	Phat2/chr 2:0	Phosphoglycer	Synechococcus	62	ZP_01078384	0.959	0.014	0.068	M	1	42	mitochondria				
phosphoenol/PEPCK	Pyruvate meta	23074	1	Phat2/chr 2:1	phosphoenol/	Campylobacte	58	ZP_00370942	0.946	0.021	0.068	M	1	18	mitochondria	PEPCK	5186		Thaps3/chr 5.566357-568410
phosphoenol/PEPC1	Glycolysis	56026	2	Phat2/chr 17:7	Phosphoenol/	Chlamydomon	31	QGR2V6	0.04	0.519	0.043	S	1	20	SSA-SPL	ER/periplastid/PEPC	257092		Thaps3/chr 3.1899863-1902862
phosphoenol/PEPC2	Pyruvate meta	20853	2	Phat2/chr 10:10	Phosphoenol/	Alkallimnicola	41	ZP_00866642	0.947	0.013	0.105	M	1	17	mitochondria	PEPC2	268546		
Phosphofructo PFK	Glycolysis	47690	4	Phat2/chr 14:4	pyrophosphate	Cyanidioschyz	50	CM1196C	0.018	0.957	0.067	S	1	26	AAA-TYT				
Phosphofructo PFK	Glycolysis	55126	4	Phat2/chr 2:5	Pyrophosphat	Propionibacter	51	P29495	0.268	0.06	0.635	-	4	-	cytosol				
Phosphofructo PFK	Glycolysis	50424	4	Phat2/chr 2:9	pyrophosphate	Cyanidioschyz	47	CM1196C	0.051	0.075	0.954	-	1	-	cytosol				
Phosphofructo PFK	Glycolysis	56524	4	Phat2/chr 2:9	pyrophosphate	Cyanidioschyz	47	CM1196C	0.824	0.03	0.217	M	2	15	mitochondria				
Phosphogluco PGM	Glycolysis	48819	4	Phat2/chr 19:19	putative phosph	Oryza sativa	30	BA035745	0.364	0.75	0.017	S	4	26	AFA-WSP				
Phosphogluco PGM	Glycolysis	50718	4	Phat2/chr 2:6	putative cytos	Bromus inermi	44	AAF04862	0.179	0.690	0.094	S	3	22	TEA-FAH				
Phosphogluco PGM	Glycolysis	51225	4	Phat2/chr 2:3	phosphogluco/	Aedes aegypti	31	AA447077	0.073	0.074	0.931	-	1	-	cytosol				
Phosphogluco PGM	Glycolysis	50119	4	Phat2/chr 2:7	phosphogluco/	Xenopus tropi	37	NP_00101670	0.442	0.039	0.565	-	5	-	cytosol				
Phosphogluco PGL	Calvin cycle	31882	2	Phat2/chr 1:1	6-phosphogluco/	Cryptococcus	35	CNE04030	0.125	0.111	0.807	-	2	-	cytosol				
Phosphogluco PGL	Calvin cycle	38631	2	Phat2/chr 16:16	PREDICTED: R	rattus norvegi	77	XP_214236	0.088	0.945	0.026	S	1	25	CHG-FVP		PGL	10378	Thaps3/chr 16a.182262-183170
Phosphoglycer PGAM	Glycolysis	43253	7	Phat2/chr 1:2	phosphoglycer	Chlorobium	1e5	AAW71645	0.87	0.065	0.12	M	2	39	mitochondria				
Phosphoglycer PGAM	Glycolysis	43812	7	Phat2/chr 3:5	phosphoglycer	Corynebacteri	44	CA138093	0.346	0.917	0.005	S	3	30	SLA-WRT				
Phosphoglycer PGAM	Glycolysis	51298	7	Phat2/chr 3:1	2,3-bisphosph	Chlorobaculum	60	Q8KF08	0.453	0.836	0.005	S	4	17	ASP-FTH				
Phosphoglycer PGAM	Glycolysis	33839	7	Phat2/chr 4:4	Phosphoglycer	Chlorobium	ph 55	ZP_00531074	0.935	0.032	0.066	M	1	21	mitochondria				
Phosphoglycer PGAM	Glycolysis	26201	7	Phat2/chr 4:2	2,3-bisphosph	Bdellovibrio	ba 49	Q6M1P3	0.702	0.058	0.275	M	3	22	mitochondria				
Phosphoglycer PGAM	Glycolysis	35164	7	Phat2/chr 7:2	phosphoglycer	Geobacter	me 34	ABB31884	0.811	0.017	0.349	M	3	28	mitochondria				
Phosphoglycer PGAM	Glycolysis	42857	7	Phat2/chr 1:1	Phosphoglycer	Thermoanaer	52	NP_428413	0.046	0.893	0.038	S	1	24	CEA-LLV				
phosphopyruv/Enolase	Pyruvate meta	56468	1	Phat2/chr 3:1	enolase 2	Heterocapsa	1e68	AAU20794	0.287	0.777	0.016	S	3	20	TLA-FAP				
phosphopyruv/Enolase	Glycolysis	1972	2	Phat2/chr 2:3	enolase 2	Heterocapsa	1e 64	AAU20794	0.949	0.013	0.096	M	1	19	mitochondria				
phosphopyruv/Enolase? (app	Glycolysis	1974	2	Phat2/chr 2:3	enolase 2	Heterocapsa	1e 64	AAU20794	1.949	0.013	0.096	M	1	19	mitochondria?				(apparently unfunctional gene copy)
Phosphoribulo Pk	Pyruvate meta	50773	1	Phat2/chr 3:1	phosphoribulo/	Odentella	sine 81	CAA69902	0.399	0.451	0.083	S	5	15	AAA-FAP				
pyruvate carb/PCYC1	Pyruvate meta	30519	2	Phat2/chr 2:3	Hypothetical pCaenorhabditis	54	CA080272	0.882	0.011	0.226	M	2	11	mitochondria	PYC	11075		Thaps3/chr 19a.19.55337-59769	
pyruvate carb/PCYC2	Pyruvate meta	49339	2	Phat2/chr 2:1	GA13539-PA	Drosophila	psc 50	EAL26409	SignalP HMM: 1.000	Signal Peptide not recognised by TargetP	19			AAA-FAP					
pyruvate dehyd/PDHA1	Pyruvate meta	55035	1	Phat2/chr 2:1	pyruvate dehyd	Cyanidioschyz	54	CMT256C	0.926	0.031	0.083	M	1	41	mitochondria	PDHA1	268374		Thaps3/chr 2.2164413-2165762
pyruvate dehyd/DHLTA	Pyruvate meta	17401	1	Phat2/chr 1:7	putative dihyd	Oryza sativa	j 34	XP_550447	0.963	0.012	0.066	M	1	46	mitochondria	LAT2	268280	1	Thaps3/chr 2.1227397-1229212
pyruvate dehyd/DHLTA	Pyruvate meta	23850	2	Phat2/chr 2:7	dihydroipoam	Synechocystis	39	NP_441936	0.312	0.653	0.033	S	4	21	VDA-FRV				Thaps3/chr 6.1514855-1516363
pyruvate kinas PK1	Glycolysis	22404	7	Phat2/chr 17:7	pyruvate kinas	Magnetospirill	49	CAM77898	SignalP HMM: 1.000	Signal Peptide not recognised by TargetP	15			GHA-FVP					
pyruvate kinas PK2	Glycolysis	49098	7	Phat2/chr 20:20	pyruvate kinas	Achlya bisexu	58	AAU81896	0.156	0.054	0.841	-	2	-	cytosol				
pyruvate kinas PK3	Glycolysis	56445	7	Phat2/chr 20:20	pyruvate kinas	Achlya bisexu	55	AAU81896	0.096	0.278	0.565	-	4	-	cytosol				
pyruvate kinas PK4a	Glycolysis	45987	7	Phat2/chr 8:5	pyruvate kinas	Achlya bisexu	55	AAU81896	0.074	0.146	0.848	-	2	-	cytosol				
pyruvate kinas PK4b	Glycolysis	27502	7	Phat2/chr 8:5	pyruvate kinas	Achlya bisexu	55	AAU81896	0.074	0.146	0.848	-	2	-	cytosol				
pyruvate kinas PK5	Glycolysis	49009	7	Phat2/chr 2:9	pyruvate kinas	Achlya bisexu	45	AAU81896	0.939	0.013	0.111	M	1	21	mitochondria				
pyruvate kinas PK6	Glycolysis	56172	7	Phat2/chr 2:3	pyruvate kinas	Achlya bisexu	44	AAU81896	0.958	0.012	0.08	M	1	40	mitochondria	PK	22345		Thaps3/chr 4.1500482-1502190
pyruvate ortho PPDK	Pyruvate meta	21988	1	Phat2/chr 1:5	pyruvate ortho	Eleocharis	vi 46	BA21653	SignalP HMM: 0.989	Signal Peptide not recognised by TargetP	24			IFS-FVT				Thaps3/chr 8.848811-851865	
Ribosephosph RPI	Calvin cycle	60995	1	Phat2/chr 1:1	chloroplast rib	Heterocapsa	t 78	AAW79354	SignalP HMM: 0.999	Signal Peptide not recognised by TargetP	17			AHA-FTN					
Ribulosephosph RPE	Calvin cycle	17204	2	Phat2/chr 1:1	ribulose-phosph	Oceanobacter	74	ZP_01306515	0.284	0.823	0.026	S	3	17	ASA-FAP				
Ribulosephosph RPE2	Calvin cycle	20015	2	Phat2/chr 7:5	ribulose-phosph	Arabidopsis	th 54	NP_850495	0.023	0.770	0.405	S	4	23	cytosol (signal peptide mispredicted?)				
Sedoheptulose SBP	Calvin cycle	56467	1	Phat2/chr 1:1	sedoheptulose	Ostreococcus	73	CAL53197	0.088	0.079	0.909	-	1	-	cytosol				
serine hydroxy SHMT	Serine synthet	18665	3	Phat2/chr 3:8	serine hydroxy	Leishmania	me 62	CAJ03206	0.067	0.067	0.934	-	1	-	cytosol				
serine hydroxy SHMT	Serine synthet	54015	3	Phat2/chr 1:1	Serine hydroxy	Solanum tuber	68	P50433	0.78	0.061	0.174	M	2	20	mitochondria	TPS_106357	26031	1	Thaps3/chr 14.846637-848543
serine hydroxy SHMT	Serine synthet	17456	3	Phat2/chr 1:5	SHM4 (SERIN)	Arabidopsis	th 54	NP_193129	0.029	0.963	0.025	S	1	28	mitochondria	TPS_111009	269942	1	Thaps3/chr 18.322361-324155
tarttrionate sem Phat2/23256	glyoxylate met	45141	1	Phat2/chr 6:3	PREDICTED: T	ribulium casti	34	XP_974950	0.951	0.043	0.06	M	1	10	VRA-FSL				Thaps3/chr 4.513000-518856
thioredoxin f Trx-f	Redox regulati	46280	9	Phat2/chr 8:8	similar to Thion	Cyanidioschyz	52	CMN279C	0.212	0.553	0.123	S	4	33	ATA-FAP				Thaps3/chr 2.1827595-1828706
thioredoxin h Trx-h1	Redox regulati	56471	9	Phat2/chr 9:5	Hypothetical p	Xenopus laevi	61	NP_00109138	0.031	0.125	0.954	-	1	-	cytosol	TrxH	41697		Thaps3/chr 9.423656-424174
thioredoxin h Trx-h2	Redox regulati	48539	9	Phat2/chr 18:18	thioredoxin H	Halococcus	sp 53	AAU93947	0.067	0.901	0.055	S	1	21	GDA-VQG				Thaps3/chr 5.1356627-1357434
thioredoxin h, Trx H	Redox regulati	48141	9	Phat2/chr 16:16	thioredoxin (T	Oryctolagus	ca 39	P08628	0.011	0.963	0.129	S	1	31	GLY-KSI				
thioredoxin h, Trx H	Redox regulati	56521	9	Phat2/chr 16:16	thioredoxin (T	Oryctolagus	ca 39	P08628	0.133	0.697	0.141	S	3	20	VLT-NKI				
thioredoxin m Trx-m	Redox regulati	51357	9	Phat2/chr 1:6	thioredoxin-1	Synechococcus	47	P12243	0.517	0.745	0.009	S	4	29	CSA-FCS				
thioredoxin o Trx-o	Redox regulati	31720	9	Phat2/chr 1:7	thioredoxin	Flavobacteri	46	ZP_01105321	0.918	0.037	0.07	M	1	28	mitochondria	TrxO	4792		Thaps3/chr 4.1936070-1936450
thioredoxin r NADPH-FTR	Redox regulati	56519	1	Phat2/chr 14:14	thioredoxin rec	Acidiphilium	cr 45	YP_00123555	SignalP HMM: 1.000	Signal Peptide not recognised by TargetP	24			VHA-RPV					
thioredoxin y Trx Y	Redox regulati	43384	9	Phat2/chr 2:3	thioredoxin	Acarochloris	136	YP_00151688	0.015	0.986	0.034	S	1	25	IEG-FYR				
thioredoxin y Trx-y	Redox regulati	33356	9	Phat2/chr 3:6	thioredoxin y	Chlamydomon	34	AAO22057	0.433	0.683	0.02	S	4	17	AEA-FVH				Thaps3/chr 14.135157-136034
threonine-amm TDH	Amino acid me	49047																	

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