Table S5. Maize carbon and nitrogen metabolism related priori candidates and the annotations

MapMan annotation (16) (http://mapman.gabipd.org/web/guest;jsessionid=6F668C7FEAD5974C806D217A3560ED

Gene ID	Chr	Physical position (AGPv1) start	Physical position (AGPv1) end	Bincode	Category
GRMZM2G062044	3	176635252	176635809	'1.1.1.2'	'PS.lightreaction.photosystem II.PSII polypeptide subunits'
GRMZM2G108467	10	90230853	90233028	'1.1.1.2'	'PS.lightreaction.photosystem II.PSII polypeptide subunits'
GRMZM2G117572	2	197154929	197157201	'1.1.1.2'	'PS.lightreaction.photosystem II.PSII polypeptide subunits'
GRMZM2G125575	4	62093645	62095382	'1.1.1.2'	'PS.lightreaction.photosystem II.PSII polypeptide subunits'
GRMZM2G134130	6	6262633	6263643	'1.1.1.2'	'PS.lightreaction.photosystem II.PSII polypeptide subunits'
GRMZM2G433927	2	106512153	106522147	'1.1.1.2'	'PS.lightreaction.photosystem II.PSII polypeptide subunits'

GRMZM2G059083	3	143463610	143469794	'1.1.5.3'	'PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase'
GRMZM2G059191	8	156141696	156145324	'1.1.5.3'	'PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase'
GRMZM2G168143	9	26960159	26962547	'1.1.5.3'	'PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase'
GRMZM2G320305	10	2176056	2180138	'1.1.5.3'	'PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase'
GRMZM2G395728	1	277938263	277941932	'1.1.5.3'	'PS.lightreaction.other electron carrier (ox/red).ferredoxin reductase'
GRMZM2G057171	4	155848284	155849738	'1.3.1'	'PS.calvin cycle.rubisco large subunit'
GRMZM2G083364	1	206925826	206926402	'1.3.1'	'PS.calvin cycle.rubisco large subunit'
GRMZM2G122563	6	124162799	124163522	'1.3.1'	'PS.calvin cycle.rubisco large subunit'

GRMZM2G308907	9	32423081	32423998	'1.3.1'	'PS.calvin cycle.rubisco large subunit'
GRMZM2G360821	6	160909590	160911677	'1.3.1'	'PS.calvin cycle.rubisco large subunit'
GRMZM2G385635	2	197200874	197205149	'1.3.1'	'PS.calvin cycle.rubisco large subunit'
GRMZM2G448344	1	203364152	203369630	'1.3.1'	'PS.calvin cycle.rubisco large subunit'
GRMZM2G026807	1	14563890	14579039	'1.3.11'	'PS.calvin cycle.RPE'
GRMZM2G178960	9	146967883	146971758	'1.3.11'	'PS.calvin cycle.RPE'
GRMZM2G026024	4	158046630	158049548	'1.3.12'	'PS.calvin cycle.PRK'
GRMZM2G162529	5	198744538	198746868	'1.3.12'	'PS.calvin cycle.PRK'
GRMZM2G463280	2	12798094	12800411	'1.3.12'	'PS.calvin cycle.PRK'

GRMZM2G098520	4	195758576	195761059	'1.3.2'	'PS.calvin cycle.rubisco small subunit'
GRMZM2G113033	2	140014260	140015449	'1.3.2'	'PS.calvin cycle.rubisco small subunit'
GRMZM2G003724	1	236749045	236778245	'1.3.3'	'PS.calvin cycle.phosphoglycerate kinase'
GRMZM2G047028	3	186579101	186585753	'1.3.3'	'PS.calvin cycle.phosphoglycerate kinase'
GRMZM2G083016	8	119381025	119386023	'1.3.3'	'PS.calvin cycle.phosphoglycerate kinase'
GRMZM2G089136	6	156407963	156411398	'1.3.3'	'PS.calvin cycle.phosphoglycerate kinase'
GRMZM2G382914	5	84109752	84113884	'1.3.3'	'PS.calvin cycle.phosphoglycerate kinase'
GRMZM2G035268	4	91417249	91422437	'1.3.4'	'PS.calvin cycle.GAP'
GRMZM2G039723	10	122103120	122104940	'1.3.4'	'PS.calvin cycle.GAP'

GRMZM2G162845	10	122233671	122235459	'1.3.4'	'PS.calvin cycle.GAP'
GRMZM2G337113	2	42721869	42724242	'1.3.4'	'PS.calvin cycle.GAP'
GRMZM2G002807	2	193007843	193011720	'1.3.5'	'PS.calvin cycle.TPI'
GRMZM2G046284	10	9746263	9748211	'1.3.6'	'PS.calvin cycle.aldolase'
GRMZM2G069195	8	9996842	10000671	'1.3.6'	'PS.calvin cycle.aldolase'
GRMZM2G089365	3	27037073	27040771	'1.3.6'	'PS.calvin cycle.aldolase'
GRMZM2G155253	4	210234914	210235873	'1.3.6'	'PS.calvin cycle.aldolase'
GRMZM2G407406	5	144273766	144276560	'1.3.6'	'PS.calvin cycle.aldolase'
GRMZM2G306732	1	38917806	38919996	'1.3.7'	'PS.calvin cycle.FBPase'

GRMZM2G322953	8	99674462	99678513	'1.3.7'	'PS.calvin cycle.FBPase'
GRMZM2G010494	3	154398189	154401921	'1.3.8'	'PS.calvin cycle.transketolase'
GRMZM2G033208	9	22732320	22736794	'1.3.8'	'PS.calvin cycle.transketolase'
AC147602.5_FG004	3	177072769	177074234	'1.3.9'	'PS.calvin cycle.seduheptulose bisphosphatase'
GRMZM2G069542	5	144071877	144079476	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G074122	4	232871577	232882863	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G082780	3	28691520	28694162	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G083841	9	59744275	59750163	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G085019	3	7081671	7087021	'1.5.1'	'PS.carbon concentrating mechanism.C4'

GRMZM2G085747	5	23759991	23766893	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G097457	8	105705465	105716361	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G110714	8	172460967	172473888	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G118770	8	173788781	173793322	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G121878	3	213888899	213896251	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G122479	6	139450513	139456198	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G159724	3	199885864	199890948	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G348512	3	213847057	213859958	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G406672	7	144685470	144695685	'1.5.1'	'PS.carbon concentrating mechanism.C4'

GRMZM2G461332	1	282407461	282409312	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G473001	7	75484741	75490481	'1.5.1'	'PS.carbon concentrating mechanism.C4'
AC226723.2_FG001	6	102225242	102229211	'1.5.1'	'PS.carbon concentrating mechanism.C4'
GRMZM2G008507	4	10453240	10459179	'2.1.1.1'	'major CHO metabolism.synthesis.sucrose.SPS'
GRMZM2G049076	9	91391649	91410418	'2.1.1.1'	'major CHO metabolism.synthesis.sucrose.SPS'
GRMZM2G055331	4	72587772	72606368	'2.1.1.1'	'major CHO metabolism.synthesis.sucrose.SPS'
GRMZM2G140107	3	159990666	159996657	'2.1.1.1'	'major CHO metabolism.synthesis.sucrose.SPS'
GRMZM2G462613	5	95633621	95641316	'2.1.1.1'	'major CHO metabolism.synthesis.sucrose.SPS'
GRMZM2G471083	6	97099643	97110587	'2.1.1.1'	'major CHO metabolism.synthesis.sucrose.SPS'

GRMZM2G055489	8	114949111	114955366	'2.1.1.2'	'major CHO metabolism.synthesis.sucrose.SPP'
GRMZM2G097641	10	89333835	89336960	'2.1.1.2'	'major CHO metabolism.synthesis.sucrose.SPP'
GRMZM2G027955	6	166682879	166688486	'2.1.2.1'	'major CHO metabolism.synthesis.starch.AGPase'
GRMZM2G068506	4	66286716	66292876	'2.1.2.1'	'major CHO metabolism.synthesis.starch.AGPase'
GRMZM2G106213	2	170508555	170519479	'2.1.2.1'	'major CHO metabolism.synthesis.starch.AGPase'
GRMZM2G144002	7	25987944	25998905	'2.1.2.1'	'major CHO metabolism.synthesis.starch.AGPase'
GRMZM2G163437	1	221043882	221048475	'2.1.2.1'	'major CHO metabolism.synthesis.starch.AGPase'
GRMZM2G391936	1	272463080	272467914	'2.1.2.1'	'major CHO metabolism.synthesis.starch.AGPase'

GRMZM2G429899	3	214837669	214847033	'2.1.2.1'	'major CHO metabolism.synthesis.starch.AGPase'
GRMZM2G008263	7	37074030	37081289	'2.1.2.2'	'major CHO metabolism.synthesis.starch.starch synthase'
GRMZM2G024993	9	23213761	23217689	'2.1.2.2'	'major CHO metabolism.synthesis.starch.starch synthase'
GRMZM2G044744	8	123924441	123932986	'2.1.2.2'	'major CHO metabolism.synthesis.starch.starch synthase'
GRMZM2G105791	5	205769894	205774893	'2.1.2.2'	'major CHO metabolism.synthesis.starch.starch synthase'
GRMZM2G121612	10	142647341	142656379	'2.1.2.2'	'major CHO metabolism.synthesis.starch.starch synthase'
GRMZM2G126988	5	32364622	32366243	'2.1.2.2'	'major CHO metabolism.synthesis.starch.starch synthase'
GRMZM2G129451	9	17537935	17547474	'2.1.2.2'	'major CHO metabolism.synthesis.starch.starch synthase'
GRMZM2G130043	4	171780270	171788690	'2.1.2.2'	'major CHO metabolism.synthesis.starch.starch synthase'

GRMZM2G141399	10	43570189	43581767	'2.1.2.2'	'major CHO metabolism.synthesis.starch.starch synthase'
GRMZM2G348551	6	113380769	113385825	'2.1.2.2'	'major CHO metabolism.synthesis.starch.starch synthase'
GRMZM2G005298	8	140600201	140604859	'2.1.2.3'	'major CHO metabolism.synthesis.starch.starch branching'
GRMZM2G032628	5	167879647	167890099	'2.1.2.3'	'major CHO metabolism.synthesis.starch.starch branching'
GRMZM2G073054	2	58470011	58473640	'2.1.2.3'	'major CHO metabolism.synthesis.starch.starch branching'
GRMZM2G088753	5	62617689	62624618	'2.1.2.3'	'major CHO metabolism.synthesis.starch.starch branching'
GRMZM2G090905	6	144743201	144745581	'2.1.2.4'	'major CHO metabolism.synthesis.starch.debranching'
GRMZM2G138060	4	41189018	41197566	'2.1.2.4'	'major CHO metabolism.synthesis.starch.debranching'
GRMZM2G150796	7	123353332	123364923	'2.1.2.4'	'major CHO metabolism.synthesis.starch.debranching'
GRMZM2G051677	6	3575322	3578436	'2.2.1.1'	'major CHO metabolism.degradation.sucrose.fructokinase'
GRMZM2G007277	4	210346826	210351596	'2.2.1.3.1'	'major CHO metabolism.degradation.sucrose.invertases.neutral'

GRMZM2G022782	8	39924160	39928400	'2.2.1.3.1'	'major CHO metabolism.degradation.sucrose.invertases.neutral'
GRMZM2G040843	10	11196483	11206942	'2.2.1.3.1'	'major CHO metabolism.degradation.sucrose.invertases.neutral'
GRMZM2G084694	3	60524343	60528210	'2.2.1.3.1'	'major CHO metabolism.degradation.sucrose.invertases.neutral'
GRMZM2G084940	1	51434476	51440869	'2.2.1.3.1'	'major CHO metabolism.degradation.sucrose.invertases.neutral'
GRMZM2G115451	2	132976276	132980088	'2.2.1.3.1'	'major CHO metabolism.degradation.sucrose.invertases.neutral'
GRMZM2G118737	5	170573207	170577262	'2.2.1.3.1'	'major CHO metabolism.degradation.sucrose.invertases.neutral'
GRMZM2G136139	4	162536638	162539641	'2.2.1.3.1'	'major CHO metabolism.degradation.sucrose.invertases.neutral'
GRMZM2G170842	4	113503323	113508452	'2.2.1.3.1'	'major CHO metabolism.degradation.sucrose.invertases.neutral'
GRMZM2G018692	2	3216441	3218852	'2.2.1.3.2'	'major CHO metabolism.degradation.sucrose.invertases.cell wall'
GRMZM2G018716	2	3212064	3214698	'2.2.1.3.2'	'major CHO metabolism.degradation.sucrose.invertases.cell wall'
GRMZM2G089836	5	66808614	66811912	'2.2.1.3.2'	'major CHO metabolism.degradation.sucrose.invertases.cell wall'

GRMZM2G095725	10	114035376	114038496	'2.2.1.3.2'	'major CHO metabolism.degradation.sucrose.invertases.cell wall'
GRMZM2G119689	2	56770929	56774210	'2.2.1.3.2'	'major CHO metabolism.degradation.sucrose.invertases.cell wall'
GRMZM2G119941	2	3172894	3176745	'2.2.1.3.2'	'major CHO metabolism.degradation.sucrose.invertases.cell wall'
GRMZM2G123633	10	114087307	114089699	'2.2.1.3.2'	'major CHO metabolism.degradation.sucrose.invertases.cell wall'
GRMZM2G139300	5	168866600	168869757	'2.2.1.3.2'	'major CHO metabolism.degradation.sucrose.invertases.cell wall'
GRMZM2G139300	5	168866600	168869757	'2.2.1.3.2'	'major CHO metabolism.degradation.sucrose.invertases.cell wall'
GRMZM2G174249	3	141917008	141920442	'2.2.1.3.2'	'major CHO metabolism.degradation.sucrose.invertases.cell wall'
GRMZM2G394450	2	22804880	22809451	'2.2.1.3.3'	'major CHO metabolism.degradation.sucrose.invertases.vacuolar'
GRMZM2G463871	4	246068493	246071007	'2.2.1.3.3'	'major CHO metabolism.degradation.sucrose.invertases.vacuolar'

GRMZM2G046686	6	136141269	136146446	'2.2.1.4'	'major CHO metabolism.degradation.sucrose.hexokinase'
GRMZM2G051806	6	130242638	130245550	'2.2.1.4'	'major CHO metabolism.degradation.sucrose.hexokinase'
GRMZM2G058745	8	123268317	123273802	'2.2.1.4'	'major CHO metabolism.degradation.sucrose.hexokinase'
GRMZM2G068913	3	148353395	148359880	'2.2.1.4'	'major CHO metabolism.degradation.sucrose.hexokinase'
GRMZM2G104081	3	6884810	6888596	'2.2.1.4'	'major CHO metabolism.degradation.sucrose.hexokinase'
GRMZM2G171373	3	200000374	200010416	'2.2.1.4'	'major CHO metabolism.degradation.sucrose.hexokinase'
GRMZM2G432801	6	160359759	160367017	'2.2.1.4'	'major CHO metabolism.degradation.sucrose.hexokinase'
GRMZM2G467069	8	157900762	157910330	'2.2.1.4'	'major CHO metabolism.degradation.sucrose.hexokinase'
GRMZM2G045171	4	167833903	167837431	'2.2.1.5'	'major CHO metabolism.degradation.sucrose.Susy'
GRMZM2G060659	5	64068518	64072884	'2.2.1.5'	'major CHO metabolism.degradation.sucrose.Susy'
GRMZM2G089713	9	11336707	11343468	'2.2.1.5'	'major CHO metabolism.degradation.sucrose.Susy'

GRMZM2G152908	9	117891216	117897889	'2.2.1.5'	'major CHO metabolism.degradation.sucrose.Susy'
GRMZM2G311182	1	56855835	56859646	'2.2.1.5'	'major CHO metabolism.degradation.sucrose.Susy'
GRMZM2G318780	1	56884526	56891725	'2.2.1.5'	'major CHO metabolism.degradation.sucrose.Susy'
GRMZM2G007939	1	89607428	89611067	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G025833	5	30088994	30091412	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G033339	10	117515762	117516625	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G034575	9	142109937	142116442	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G035749	9	110627095	110629975	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G058310	7	149715593	149718793	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G070172	1	199483190	199485177	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'

GRMZM2G074781	7	99763091	99765189	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G077202	8	28053020	28058030	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G081502	7	99772979	99774377	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G082034	1	60153179	60155186	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G103055	5	209097206	209099282	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G138468	2	183356996	183358858	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G163129	1	27199395	27203624	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G175218	3	1532910	1537185	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G181284	7	166151874	166154217	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G422938	2	60640846	60644732	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'

GRMZM2G450125	1	9028311	9031292	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G462258	2	19172527	19174657	'2.2.2.1'	'major CHO metabolism.degradation.starch.starch cleavage'
GRMZM2G069486	4	244703206	244713618	'2.2.2.1.2'	'major CHO metabolism.degradation.starch.starch cleavage.beta amylase'
GRMZM2G446515	4	57630497	57635616	'2.2.2.1.2'	'major CHO metabolism.degradation.starch.starch cleavage.beta amylase'
GRMZM2G074158	1	277192650	277201655	'2.2.2.2'	'major CHO metabolism.degradation.starch.starch phosphorylase'
GRMZM2G085577	3	177229789	177233918	'2.2.2.2'	'major CHO metabolism.degradation.starch.starch phosphorylase'
GRMZM2G013811	7	161509616	161521099	'2.2.2.4'	'major CHO metabolism.degradation.starch.D enzyme'
GRMZM2G057823	3	164152594	164155205	'4.1.10'	'glycolysis.cytosolic branch.aldolase'
GRMZM2G066024	8	162011029	162013742	'4.1.10'	'glycolysis.cytosolic branch.aldolase'
GRMZM2G003385	3	184119847	184124557	'4.1.12'	'glycolysis.cytosolic branch.phosphoglycerate mutase'

GRMZM2G050077	1	54636161	54639002	'4.1.12'	'glycolysis.cytosolic branch.phosphoglycerate mutase'
GRMZM2G054250	10	25554015	25557109	'4.1.12'	'glycolysis.cytosolic branch.phosphoglycerate mutase'
GRMZM2G146778	6	123886106	123902055	'4.1.12'	'glycolysis.cytosolic branch.phosphoglycerate mutase'
GRMZM2G334628	3	14968978	14978926	'4.1.12'	'glycolysis.cytosolic branch.phosphoglycerate mutase'
GRMZM2G048371	1	123934984	123941924	'4.1.13'	'glycolysis.cytosolic branch.enolase'
GRMZM2G064302	9	22038338	22043026	'4.1.13'	'glycolysis.cytosolic branch.enolase'
GRMZM2G131539	9	136058804	136064699	'4.1.13'	'glycolysis.cytosolic branch.enolase'
GRMZM2G446253	6	67052370	67056221	'4.1.13'	'glycolysis.cytosolic branch.enolase'
GRMZM2G481529	1	38690909	38694855	'4.1.13'	'glycolysis.cytosolic branch.enolase'
GRMZM2G003883	3	43867751	43873291	'4.1.14'	'glycolysis.cytosolic branch.pyruvate kinase (PK)'

GRMZM2G004534	10	4219852	4224759	'4.1.14'	'glycolysis.cytosolic branch.pyruvate kinase (PK)'
GRMZM2G008714	10	147754740	147759198	'4.1.14'	'glycolysis.cytosolic branch.pyruvate kinase (PK)'
GRMZM2G119175	4	193590090	193596038	'4.1.14'	'glycolysis.cytosolic branch.pyruvate kinase (PK)'
GRMZM2G124593	4	12914620	12923769	'4.1.14'	'glycolysis.cytosolic branch.pyruvate kinase (PK)'
GRMZM2G150098	2	1611586	1615673	'4.1.14'	'glycolysis.cytosolic branch.pyruvate kinase (PK)'
GRMZM2G023289	1	266953595	266960373	'4.1.2'	'glycolysis.cytosolic branch.phosphoglucomutase (PGM)'
GRMZM2G109383	5	10810133	10816262	'4.1.2'	'glycolysis.cytosolic branch.phosphoglucomutase (PGM)'
GRMZM2G162078	5	54710484	54716463	'4.1.3'	'glycolysis.cytosolic branch.glucose-6-phosphate isomerase'
GRMZM2G042502	4	161166295	161172650	'4.1.5'	'glycolysis.cytosolic branch.pyrophosphate-fructose-6-P phosphotransferase'

GRMZM2G059151	6	115343210	115349610	'4.1.5'	'glycolysis.cytosolic branch.pyrophosphate-fructose-6-P phosphotransferase'
GRMZM2G123371	5	201709349	201716521	'4.1.5'	'glycolysis.cytosolic branch.pyrophosphate-fructose-6-P phosphotransferase'
GRMZM2G143862	9	1630555	1635350	'4.1.5'	'glycolysis.cytosolic branch.pyrophosphate-fructose-6-P phosphotransferase'
GRMZM2G314094	9	45350151	45353197	'4.1.5'	'glycolysis.cytosolic branch.pyrophosphate-fructose-6-P phosphotransferase'
GRMZM2G402211	8	20572092	20575740	'4.1.5'	'glycolysis.cytosolic branch.pyrophosphate-fructose-6-P phosphotransferase'
GRMZM2G409131	7	71389323	71394350	'4.1.5'	'glycolysis.cytosolic branch.pyrophosphate-fructose-6-P phosphotransferase'
GRMZM2G413226	4	98552125	98560428	'4.1.5'	'glycolysis.cytosolic branch.pyrophosphate-fructose-6-P phosphotransferase'

GRMZM2G450163	1	221135223	221139412	'4.1.5'	'glycolysis.cytosolic branch.pyrophosphate-fructose-6-P phosphotransferase'
AC194439.3_FG002	8	84211227	84214198	'4.1.5'	'glycolysis.cytosolic branch.pyrophosphate-fructose-6-P phosphotransferase'
AC205100.3_FG001	1	35192911	35198202	'4.1.5'	'glycolysis.cytosolic branch.pyrophosphate-fructose-6-P phosphotransferase'
GRMZM2G018177	8	14444342	14448528	'4.1.7'	'glycolysis.cytosolic branch.triosephosphate isomerase (TPI)'
GRMZM2G026182	3	40809281	40838367	'4.1.7'	'glycolysis.cytosolic branch.triosephosphate isomerase (TPI)'
GRMZM2G030784	3	17551351	17555632	'4.1.7'	'glycolysis.cytosolic branch.triosephosphate isomerase (TPI)'
GRMZM2G146206	8	167524351	167528553	'4.1.7'	'glycolysis.cytosolic branch.triosephosphate isomerase (TPI)'
GRMZM2G346168	7	12287819	12313803	'4.1.7'	'glycolysis.cytosolic branch.triosephosphate isomerase (TPI)'

GRMZM2G370275	1	289976562	289978656	'4.1.7'	'glycolysis.cytosolic branch.triosephosphate isomerase (TPI)'
GRMZM2G419024	1	201233828	201238537	'4.1.7'	'glycolysis.cytosolic branch.triosephosphate isomerase (TPI)'
GRMZM2G435244	1	109959671	109963800	'4.1.7'	'glycolysis.cytosolic branch.triosephosphate isomerase (TPI)'
GRMZM2G439389	8	81412518	81428064	'4.1.7'	'glycolysis.cytosolic branch.triosephosphate isomerase (TPI)'
GRMZM2G046804	4	36717001	36721786	'4.1.8'	'glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)'
GRMZM2G051004	4	241695151	241700161	'4.1.8'	'glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)'
GRMZM2G071630	4	132040520	132043909	'4.1.8'	'glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)'
GRMZM2G104632	5	84543365	84545918	'4.1.8'	'glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)'

GRMZM2G176307	5	180736286	180741078	'4.1.8'	'glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)'
GRMZM2G180625	6	6902668	6907126	'4.1.8'	'glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)'
GRMZM2G435438	5	125000366	125006459	'4.1.8'	'glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)'
GRMZM2G462894	5	151742477	151747309	'4.1.8'	'glycolysis.cytosolic branch.glyceraldehyde 3-phosphate dehydrogenase (GAP-DH)'
GRMZM2G033526	1	96541061	96546702	'4.2.14'	'glycolysis.plastid branch.pyruvate kinase (PK)'
GRMZM2G066290	7	10401302	10405630	'4.2.14'	'glycolysis.plastid branch.pyruvate kinase (PK)'
GRMZM2G078200	1	286836678	286841037	'4.2.14'	'glycolysis.plastid branch.pyruvate kinase (PK)'
GRMZM2G144730	9	109959812	109965235	'4.2.14'	'glycolysis.plastid branch.pyruvate kinase (PK)'
GRMZM2G152686	3	210418332	210428410	'4.2.14'	'glycolysis.plastid branch.pyruvate kinase (PK)'

GRMZM2G177947	1	256542998	256548128	'4.2.14'	'glycolysis.plastid branch.pyruvate kinase (PK)'
GRMZM2G067908	7	67848870	67851654	'4.2.2'	'glycolysis.plastid branch.phosphoglucomutase (PGM)'
GRMZM2G009591	1	242185184	242190138	'4.2.4'	'glycolysis.plastid branch.phosphofructokinase (PFK)'
GRMZM2G080375	8	20732784	20736537	'4.2.4'	'glycolysis.plastid branch.phosphofructokinase (PFK)'
GRMZM2G139360	1	211900859	211905604	'4.2.4'	'glycolysis.plastid branch.phosphofructokinase (PFK)'
GRMZM2G168716	3	108475025	108479334	'4.2.4'	'glycolysis.plastid branch.phosphofructokinase (PFK)'
GRMZM2G032003	7	140914419	140921311	'4.3.1'	'glycolysis.unclear/dually targeted.UGPase'
GRMZM2G098370	5	69388731	69393204	'4.3.1'	'glycolysis.unclear/dually targeted.UGPase'
GRMZM2G025854	3	216693836	216702168	'4.3.2'	'glycolysis.unclear/dually targeted.phosphoglucomutase (PGM)'
GRMZM2G069676	7	43936183	43948640	'4.3.2'	'glycolysis.unclear/dually targeted.phosphoglucomutase (PGM)'
GRMZM2G173668	5	149061676	149062897	'4.3.2'	'glycolysis.unclear/dually targeted.phosphoglucomutase (PGM)'

GRMZM2G076075	2	184506321	184510607	'4.3.3'	'glycolysis.unclear/dually targeted.glucose-6-phosphate isomerase'
GRMZM2G140614	7	122111018	122115881	'4.3.3'	'glycolysis.unclear/dually targeted.glucose-6-phosphate isomerase'
GRMZM2G004932	6	160156143	160161758	'4.3.4'	'glycolysis.unclear/dually targeted.phosphofructokinase (PFK)'
GRMZM2G031613	7	125310846	125320697	'4.3.4'	'glycolysis.unclear/dually targeted.phosphofructokinase (PFK)'
GRMZM2G127717	2	178209545	178219000	'4.3.4'	'glycolysis.unclear/dually targeted.phosphofructokinase (PFK)'
GRMZM2G132069	3	6597988	6601927	'4.3.4'	'glycolysis.unclear/dually targeted.phosphofructokinase (PFK)'
GRMZM2G401970	6	132995615	132997967	'4.3.4'	'glycolysis.unclear/dually targeted.phosphofructokinase (PFK)'
GRMZM2G443985	9	19058790	19067919	'4.3.4'	'glycolysis.unclear/dually targeted.phosphofructokinase (PFK)'
GRMZM2G171796	6	46686689	46693962	'4.3.5'	'glycolysis.unclear/dually targeted.pyrophosphate-fructose-6-P phosphotransferase'

GRMZM2G128929	5	66703588	66705465	'5.1'	'fermentation.LDH'
GRMZM2G173192	5	66773309	66774626	'5.1'	'fermentation.LDH'
GRMZM2G038821	8	15590953	15594513	'5.2'	'fermentation.PDC'
GRMZM2G434792	7	168978040	168980265	'5.2'	'fermentation.PDC'
AC197705.4_FG001	8	116734266	116736402	'5.2'	'fermentation.PDC'
GRMZM2G098346	4	13359813	13363215	'5.3'	'fermentation.ADH'
GRMZM2G442658	1	272983401	272987295	'5.3'	'fermentation.ADH'
GRMZM2G135588	5	148710633	148715364	'6.1'	'gluconeogenese/ glyoxylate cycle.citrate synthase'
GRMZM2G072744	1	281559306	281562946	'6.3'	'gluconeogenesis.Malate DH'
GRMZM2G077415	3	103804489	103807790	'6.3'	'gluconeogenesis.Malate DH'

GRMZM2G141289	7	161914039	161916233	'6.3'	'gluconeogenesis.Malate DH'
GRMZM2G154595	6	165724751	165729511	'6.3'	'gluconeogenesis.Malate DH'
GRMZM2G161245	1	212502588	212505163	'6.3'	'gluconeogenesis.Malate DH'
GRMZM2G466833	3	212343118	212351804	'6.3'	'gluconeogenesis.Malate DH'
GRMZM2G074454	6	117984172	117989535	'7.1.3'	'OPP.oxidative PP.6-phosphogluconate dehydrogenase'
GRMZM2G083102	7	130977753	130982022	'7.2.3'	'OPP.non-reductive PP.ribulose-phosphate 3-epimerase'
GRMZM2G035599	2	142093445	142094877	'7.2.4'	'OPP.non-reductive PP.ribose 5-phosphate isomerase'
GRMZM2G104070	1	152550931	152557103	'7.2.4'	'OPP.non-reductive PP.ribose 5-phosphate isomerase'
GRMZM2G011858	7	5100934	5106501	'7.3'	'OPP.electron transfer'
GRMZM2G058760	1	284055864	284059465	'7.3'	'OPP.electron transfer'

GRMZM2G027627	9	1439993	1444635	'8.1.1.1'	'TCA / org. transformation.TCA.pyruvate DH.E1'
GRMZM2G033894	2	107216992	107220910	'8.1.1.1'	'TCA / org. transformation.TCA.pyruvate DH.E1'
GRMZM2G088565	1	174182364	174186545	'8.1.1.1'	'TCA / org. transformation.TCA.pyruvate DH.E1'
GRMZM2G097226	2	189650493	189656923	'8.1.1.1'	'TCA / org. transformation.TCA.pyruvate DH.E1'
GRMZM2G127546	1	251244344	251247178	'8.1.1.1'	'TCA / org. transformation.TCA.pyruvate DH.E1'
GRMZM2G361693	4	181808924	181813688	'8.1.1.1'	'TCA / org. transformation.TCA.pyruvate DH.E1'
GRMZM2G015132	5	154884698	154892092	'8.1.1.2'	'TCA / org. transformation.TCA.pyruvate DH.E2'
GRMZM2G036534	10	11822338	11828913	'8.1.1.2'	'TCA / org. transformation.TCA.pyruvate DH.E2'
GRMZM2G058702	1	214124644	214128934	'8.1.1.2'	'TCA / org. transformation.TCA.pyruvate DH.E2'

GRMZM2G082664	1	289228427	289231485	'8.1.1.2'	'TCA / org. transformation.TCA.pyruvate DH.E2'
GRMZM2G117786	4	89319561	89323556	'8.1.1.2'	'TCA / org. transformation.TCA.pyruvate DH.E2'
GRMZM2G121200	7	104631012	104634016	'8.1.1.2'	'TCA / org. transformation.TCA.pyruvate DH.E2'
GRMZM2G161969	4	235775165	235779518	'8.1.1.2'	'TCA / org. transformation.TCA.pyruvate DH.E2'
GRMZM2G165176	3	135511496	135517750	'8.1.1.2'	'TCA / org. transformation.TCA.pyruvate DH.E2'
GRMZM2G073774	8	78130845	78138150	'8.1.1.3'	'TCA / org. transformation.TCA.pyruvate DH.E3'
GRMZM2G145595	8	42283338	42291699	'8.1.1.3'	'TCA / org. transformation.TCA.pyruvate DH.E3'
GRMZM2G152958	8	78033895	78041028	'8.1.1.3'	'TCA / org. transformation.TCA.pyruvate DH.E3'
GRMZM2G063851	5	122930790	122937429	'8.1.2'	'TCA / org. transformation.TCA.CS'

GRMZM2G064023	4	239429877	239437026	'8.1.2'	'TCA / org. transformation.TCA.CS'
GRMZM2G009808	9	147424502	147432777	'8.1.3'	'TCA / org. transformation.TCA.aconitase'
GRMZM2G010044	4	244491906	244495878	'8.1.3'	'TCA / org. transformation.TCA.aconitase'
GRMZM2G020801	4	27965455	27972006	'8.1.3'	'TCA / org. transformation.TCA.aconitase'
GRMZM2G176397	1	8098618	8110507	'8.1.3'	'TCA / org. transformation.TCA.aconitase'
GRMZM2G364988	5	90717637	90722216	'8.1.3'	'TCA / org. transformation.TCA.aconitase'
GRMZM2G467338	2	111210985	111218286	'8.1.3'	'TCA / org. transformation.TCA.aconitase'
GRMZM2G025366	10	124999525	125003414	'8.1.4'	'TCA / org. transformation.TCA.IDH'
GRMZM2G116872	5	179738721	179739482	'8.1.4'	'TCA / org. transformation.TCA.IDH'

GRMZM2G142863	2	69207580	69214144	'8.1.5'	'TCA / org. transformation.TCA.2-oxoglutarate dehydrogenase'
GRMZM2G151041	10	109627692	109634086	'8.1.5'	'TCA / org. transformation.TCA.2-oxoglutarate dehydrogenase'
AC194977.2_FG004	7	154331843	154338113	'8.1.5'	'TCA / org. transformation.TCA.2-oxoglutarate dehydrogenase'
GRMZM2G039251	2	204104585	204110782	'8.1.6'	'TCA / org. transformation.TCA.succinyl-CoA ligase'
GRMZM2G064695	5	185263651	185276024	'8.1.6'	'TCA / org. transformation.TCA.succinyl-CoA ligase'
GRMZM2G072054	7	154540091	154546033	'8.1.6'	'TCA / org. transformation.TCA.succinyl-CoA ligase'
GRMZM2G064799	7	4240127	4244957	'8.1.7'	'TCA / org. transformation.TCA.succinate dehydrogenase'
GRMZM2G079888	2	233616254	233621560	'8.1.7'	'TCA / org. transformation.TCA.succinate dehydrogenase'
GRMZM2G010823	1	56845959	56852028	'8.1.8'	'TCA / org. transformation.TCA.fumarase'
GRMZM2G348729	4	3757415	3761592	'8.1.8'	'TCA / org. transformation.TCA.fumarase'

GRMZM2G002416	8	37410801	37414982	'8.2.11'	'TCA / org. transformation.other organic acid transformaitons.atp-citrate lyase'
GRMZM2G018566	3	43636005	43641308	'8.2.4'	'TCA / org. transformation.other organic acid transformaitons.IDH'
GRMZM2G120857	8	2302889	2310491	'8.2.4'	'TCA / org. transformation.other organic acid transformaitons.IDH'
GRMZM2G173251	1	44690227	44691933	'8.2.4'	'TCA / org. transformation.other organic acid transformaitons.IDH'
GRMZM2G404855	9	11196570	11198734	'8.2.4'	'TCA / org. transformation.other organic acid transformaitons.IDH'
GRMZM2G101290	2	19834359	19836146	'8.2.9'	'TCA / org. transformation.other organic acid transformaitons.cyt MDH'
GRMZM2G129513	1	202617705	202621864	'8.2.9'	'TCA / org. transformation.other organic acid transformaitons.cyt MDH'
GRMZM2G415359	1	230672384	230678149	'8.2.9'	'TCA / org. transformation.other organic acid transformaitons.cyt MDH'
GRMZM2G080044	9	7545549	7556197	'9.2.3'	'mitochondrial electron transport / ATP synthesis.NADH-DH.type II.mitochondrial'

GRMZM2G178254	9	143057589	143062772	'10.1'	'cell wall.precursor synthesis'
GRMZM2G116586	5	56087766	56099160	'10.1.1.20'	'cell wall.precursor synthesis.NDP sugar pyrophosphorylase.multiple NDP-Sugars'
GRMZM2G161493	6	85653771	85664177	'10.1.1.20'	'cell wall.precursor synthesis.NDP sugar pyrophosphorylase.multiple NDP-Sugars'
GRMZM2G396565	5	9701265	9705076	'10.1.1.20'	'cell wall.precursor synthesis.NDP sugar pyrophosphorylase.multiple NDP-Sugars'
GRMZM2G481027	5	213333375	213338806	'10.5.5'	'cell wall.cell wall proteins.RGP'
AC197578.4_FG001	3	191000002	191005208	'10.6.1'	'cell wall.degradation.cellulases and beta -1,4-glucanases'
GRMZM2G052844	8	143141758	143145571	'10.6.3'	'cell wall.degradation.pectate lyases and polygalacturonases'
GRMZM2G012328	2	42828109	42830223	'10.8.1'	'cell wall.pectin*esterases.PME'
GRMZM2G017555	8	5283282	5285722	'10.8.1'	'cell wall.pectin*esterases.PME'
GRMZM2G125356	10	121933301	121935490	'10.8.1'	'cell wall.pectin*esterases.PME'

GRMZM2G085547	4	169312670	169319688	'11.1.13'	'lipid metabolism.FA synthesis and FA elongation.acyl-CoA binding protein'
GRMZM2G043602	5	162570326	162575805	'11.1.4'	'lipid metabolism.FA synthesis and FA elongation.ACP oxoacyl reductase'
GRMZM2G099696	10	107949730	107957536	'11.1.4'	'lipid metabolism.FA synthesis and FA elongation.ACP oxoacyl reductase'
GRMZM2G141256	9	93250026	93253044	'11.1.4'	'lipid metabolism.FA synthesis and FA elongation.ACP oxoacyl reductase'
GRMZM2G351023	2	76461448	76483084	'11.1.4'	'lipid metabolism.FA synthesis and FA elongation.ACP oxoacyl reductase'
GRMZM2G013783	1	48808709	48813764	'11.1.8'	'lipid metabolism.FA synthesis and FA elongation.acyl coa ligase'
GRMZM2G076723	1	198591257	198596276	'12.1.1'	'N-metabolism.nitrate metabolism.NR'
GRMZM2G428027	4	176742163	176746013	'12.1.1'	'N-metabolism.nitrate metabolism.NR'
GRMZM2G079381	4	177668483	177672038	'12.1.2'	'N-metabolism.nitrate metabolism.nitrite reductase'
GRMZM2G102959	5	209105303	209108217	'12.1.2'	'N-metabolism.nitrate metabolism.nitrite reductase'

GRMZM2G036609	7	165246599	165265413	'12.2.1'	'N-metabolism.ammonia metabolism.glutamate synthase'
GRMZM2G077054	8	149895033	149906176	'12.2.1'	'N-metabolism.ammonia metabolism.glutamate synthase'
GRMZM2G085078	3	206749335	206761045	'12.2.1'	'N-metabolism.ammonia metabolism.glutamate synthase'
GRMZM2G375064	6	163302506	163314279	'12.2.1'	'N-metabolism.ammonia metabolism.glutamate synthase'
GRMZM2G024104	1	266960337	266963719	'12.2.2'	'N-metabolism.ammonia metabolism.glutamine synthase'
GRMZM2G036464	4	166172187	166175518	'12.2.2'	'N-metabolism.ammonia metabolism.glutamine synthase'
GRMZM2G046601	9	141641504	141649813	'12.2.2'	'N-metabolism.ammonia metabolism.glutamine synthase'
GRMZM2G050514	1	28082680	28086336	'12.2.2'	'N-metabolism.ammonia metabolism.glutamine synthase'
GRMZM2G098290	10	146022264	146030957	'12.2.2'	'N-metabolism.ammonia metabolism.glutamine synthase'
GRMZM2G115646	1	234991282	235014998	'12.2.2'	'N-metabolism.ammonia metabolism.glutamine synthase'

GRMZM2G178415	1	286266329	286273468	'12.3.1'	'N-metabolism.N-degradation.glutamate dehydrogenase'
GRMZM2G427097	10	133674688	133679141	'12.3.1'	'N-metabolism.N-degradation.glutamate dehydrogenase'
GRMZM2G017110	1	198083275	198087087	'13.1.1.1.1'	'amino acid metabolism.synthesis.central amino acid metabolism.GABA.Glutamate decarboxylase'
GRMZM2G098875	9	139876568	139879623	'13.1.1.1.1'	'amino acid metabolism.synthesis.central amino acid metabolism.GABA.Glutamate decarboxylase'
GRMZM2G101069	2	45433750	45436676	'13.1.1.1.1'	'amino acid metabolism.synthesis.central amino acid metabolism.GABA.Glutamate decarboxylase'
GRMZM2G355906	2	45162982	45165149	'13.1.1.1.1'	'amino acid metabolism.synthesis.central amino acid metabolism.GABA.Glutamate decarboxylase'
GRMZM2G143357	4	104159711	104161990	'13.1.4.1'	'amino acid metabolism.synthesis.branched chain group.common'
GRMZM2G175171	8	18702662	18706896	'13.1.4.1'	'amino acid metabolism.synthesis.branched chain group.common'
GRMZM2G331723	3	202075944	202078089	'13.1.4.1'	'amino acid metabolism.synthesis.branched chain group.common'

GRMZM2G104613	10	148484783	148488498	'13.1.4.4'	'amino acid metabolism.synthesis.branched chain group.leucine specific'
GRMZM2G011743	10	148060726	148064779	'13.2.3.1.1'	'amino acid metabolism.degradation.aspartate family.asparagine.L-asparaginase'
GRMZM2G105644	5	205809564	205812104	'16.1.1'	'secondary metabolism.isoprenoids.non-mevalonate pathway'
GRMZM2G419111	3	39732168	39734430	'16.1.1'	'secondary metabolism.isoprenoids.non-mevalonate pathway'
GRMZM2G137151	6	146544132	146548400	'16.1.1.1'	'secondary metabolism.isoprenoids.non-mevalonate pathway.DXS'
GRMZM2G118345	2	27970073	27973176	'16.2.1.1'	'secondary metabolism.phenylpropanoids.lignin biosynthesis.PAL'
GRMZM2G407181	1	174393878	174396786	'17.1.1.1.10'	'hormone metabolism.abscisic acid.synthesis-degradation.synthesis.9-cis-epoxycarotenoid dioxygenase'
GRMZM2G054361	1	270810521	270813011	'17.5.1.1'	'hormone metabolism.ethylene.synthesis-degradation.1-aminocyclopropane-1-carboxylate synthase'
GRMZM2G043453	5	3115494	3123220	'19.10'	'tetrapyrrole synthesis.magnesium chelatase'

GRMZM2G323024	10	147484237	147490411	'19.10'	'tetrapyrrole synthesis.magnesium chelatase'
GRMZM2G419806	10	8770449	8774928	'19.10'	'tetrapyrrole synthesis.magnesium chelatase'
GRMZM2G161673	6	64366398	64368037	'19.11'	'tetrapyrrole synthesis.magnesium protoporphyrin IX methyltransferase'
GRMZM2G043109	3	44799542	44801097	'19.12'	'tetrapyrrole synthesis.magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase'
GRMZM2G063048	1	59928668	59930266	'19.13'	'tetrapyrrole synthesis.divinyl chlorophyllide-a 8-vinyl-reductase'
GRMZM2G036455	1	226851885	226854973	'19.14'	'tetrapyrrole synthesis.protochlorophyllide reductase'
GRMZM2G073351	5	24724429	24727749	'19.14'	'tetrapyrrole synthesis.protochlorophyllide reductase'
GRMZM2G084958	2	1448799	1450386	'19.14'	'tetrapyrrole synthesis.protochlorophyllide reductase'
GRMZM2G162672	6	140474382	140479585	'19.15'	'tetrapyrrole synthesis.chlorophyll synthase'
GRMZM2G004222	9	117272696	117279058	'19.21'	'tetrapyrrole synthesis.heme oxygenase'

GRMZM2G093900	4	26739699	26747729	'19.3'	'tetrapyrrole synthesis.GSA'
GRMZM2G108125	10	141877963	141889878	'19.3'	'tetrapyrrole synthesis.GSA'
GRMZM2G116258	6	155741745	155746073	'19.3'	'tetrapyrrole synthesis.GSA'
GRMZM2G024738	8	143565684	143569182	'19.7'	'tetrapyrrole synthesis.uroporphyrinogen decarboxylase'
GRMZM2G025031	8	143570080	143573296	'19.7'	'tetrapyrrole synthesis.uroporphyrinogen decarboxylase'
GRMZM2G044074	1	56657696	56662275	'19.7'	'tetrapyrrole synthesis.uroporphyrinogen decarboxylase'
GRMZM2G046468	2	201408364	201415873	'19.7'	'tetrapyrrole synthesis.uroporphyrinogen decarboxylase'
GRMZM2G377609	3	216229977	216239524	'19.7'	'tetrapyrrole synthesis.uroporphyrinogen decarboxylase'
GRMZM2G032282	10	141554119	141563642	'19.8'	'tetrapyrrole synthesis.coproporphyrinogen III oxidase'
GRMZM2G105436	1	4695505	4698085	'19.8'	'tetrapyrrole synthesis.coproporphyrinogen III oxidase'

GRMZM2G039396	8	861425	867691	'19.9'	'tetrapyrrole synthesis.protoporphyrin IX oxidase'
GRMZM2G364901	2	35143649	35152206	'19.9'	'tetrapyrrole synthesis.protoporphyrin IX oxidase'
GRMZM2G103197	1	203879703	203880944	'19.99'	'tetrapyrrole synthesis.unspecified'
GRMZM2G127421	1	239119056	239120717	'19.99'	'tetrapyrrole synthesis.unspecified'
GRMZM2G170734	4	57460774	57462104	'19.99'	'tetrapyrrole synthesis.unspecified'
GRMZM2G077068	1	220631422	220636996	'20.1'	'stress.biotic'
GRMZM2G433184	1	123330659	123331725	'20.1'	'stress.biotic'
GRMZM2G458824	1	139905315	139907664	'20.1'	'stress.biotic'
GRMZM2G079668	1	262282335	262288193	'20.2.1'	'stress.abiotic.heat'
GRMZM2G158093	4	160462329	160467875	'20.2.1'	'stress.abiotic.heat'

GRMZM2G310431	8	167668008	167671371	'20.2.1'	'stress.abiotic.heat'
GRMZM2G136522	7	165140669	165145636	'21.1'	'redox.thioredoxin'
GRMZM2G084881	2	162770371	162775456	'21.2'	'redox.ascorbate and glutathione'
GRMZM2G134708	4	60429214	60433877	'21.2'	'redox.ascorbate and glutathione'
GRMZM2G020429	1	193471647	193475242	'23.3.1.3'	'nucleotide metabolism.salvage.phosphoribosyltransferases.upp'
GRMZM2G034143	5	65331499	65341592	'23.3.1.3'	'nucleotide metabolism.salvage.phosphoribosyltransferases.upp'
GRMZM2G169462	4	246689335	246695416	'23.3.1.3'	'nucleotide metabolism.salvage.phosphoribosyltransferases.upp'
GRMZM2G089767	2	28059009	28062983	'23.3.2.1'	'nucleotide metabolism.salvage.nucleoside kinases.adenosine kinase'
GRMZM2G135132	4	142189739	142194687	'23.3.2.1'	'nucleotide metabolism.salvage.nucleoside kinases.adenosine kinase'
GRMZM2G003648	10	104676885	104678043	'23.3.2.2'	'nucleotide metabolism.salvage.nucleoside kinases.uridine kinase'

GRMZM2G147430	5	200604317	200610357	'23.3.2.2'	'nucleotide metabolism.salvage.nucleoside kinases.uridine kinase'
GRMZM2G473385	10	104680615	104716008	'23.3.2.2'	'nucleotide metabolism.salvage.nucleoside kinases.uridine kinase'
GRMZM2G179981	5	129940462	129948912	'26.11.1'	'misc.alcohol dehydrogenases'
GRMZM2G129155	3	159135120	159146145	'26.17'	'misc.dynamin'
GRMZM2G180335	8	160441022	160450478	'26.17'	'misc.dynamin'
GRMZM2G005107	2	10282188	10285900	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G006119	7	163518840	163521166	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G025243	10	141814622	141825756	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G025885	7	166020180	166021426	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G041694	6	162588738	162594260	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G047800	4	22649232	22655449	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'

GRMZM2G050915	3	4081527	4084178	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G053958	7	83579815	83584363	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G059361	9	25811715	25812405	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G065171	2	43265679	43266780	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G065194	5	15537955	15543482	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G069523	2	76900319	76901709	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G070279	10	127263881	127267465	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G076981	7	156739143	156740465	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G087323	4	131586967	131590428	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G108338	2	68514771	68516412	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G109743	7	34831938	34840416	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G115442	1	188223477	188234787	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'

GRMZM2G128146	5	172979201	172981795	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G128577	9	114489103	114492669	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G135277	2	33443786	33447532	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G156739	1	294320452	294321554	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G162527	3	16934820	16938395	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G332976	5	3141403	3143154	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G374313	4	134129563	134132816	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G403313	3	102469345	102470428	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G455809	1	46809894	46811315	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G464885	1	86363554	86366081	'26.22'	'misc.short chain dehydrogenase/reductase (SDR)'
GRMZM2G049730	6	95876557	95878287	'26.24'	'misc.GCN5-related N-acetyltransferase'
GRMZM2G169326	5	198125731	198126989	'26.24'	'misc.GCN5-related N-acetyltransferase'
GRMZM2G126468	3	158812058	158825112	'26.3'	'misc.gluco-, galacto- and mannosidases'

GRMZM2G428518	6	90528036	90532012	'26.3.1'	'misc.gluco-, galacto- and mannosidases.alpha-galactosidase'
GRMZM2G000052	2	8944359	8949614	'26.7'	'misc.oxidases - copper, flavone etc.'
GRMZM2G030529	1	80794090	80803612	'26.7'	'misc.oxidases - copper, flavone etc.'
GRMZM2G035994	3	202104286	202106004	'26.7'	'misc.oxidases - copper, flavone etc.'
GRMZM2G106588	7	1791536	1792869	'26.7'	'misc.oxidases - copper, flavone etc.'
GRMZM2G108637	7	1561015	1562929	'26.7'	'misc.oxidases - copper, flavone etc.'
GRMZM2G148605	7	1631013	1632729	'26.7'	'misc.oxidases - copper, flavone etc.'
GRMZM2G162222	7	1571640	1573598	'26.7'	'misc.oxidases - copper, flavone etc.'
GRMZM2G396856	10	142513450	142518700	'26.7'	'misc.oxidases - copper, flavone etc.'
GRMZM2G479068	7	120716731	120722461	'26.7'	'misc.oxidases - copper, flavone etc.'
GRMZM2G000586	4	140232	141202	'26.8'	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'

GRMZM2G002304	8	158608078	158610066	'26.8'	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
GRMZM2G097981	4	3246182	3249022	'26.8'	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
GRMZM2G141799	1	39282381	39283480	'26.8'	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
GRMZM2G152258	2	227406058	227407744	'26.8'	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
GRMZM2G370988	4	3171258	3172772	'26.8'	'misc.nitrilases, *nitrile lyases, berberine bridge enzymes, reticuline oxidases, troponine reductases'
GRMZM2G008356	7	152003328	152004614	'27.3.1'	'RNA.regulation of transcription.ABI3/VP1-related B3-domain-containing transcription factor family'
GRMZM2G050939	6	18733868	18737683	'27.3.11'	'RNA.regulation of transcription.C2H2 zinc finger family'
AC235534.1_FG007	10	136522908	136529482	'27.3.22'	'RNA.regulation of transcription.HB,Homeobox transcription factor family'

GRMZM2G088114	5	68612020	68622493	'27.3.23'	'RNA.regulation of transcription.HSF,Heat-shock transcription factor family'
GRMZM2G097636	10	139828920	139830373	'27.3.25'	'RNA.regulation of transcription.MYB domain transcription factor family'
GRMZM2G097638	10	139831962	139833454	'27.3.25'	'RNA.regulation of transcription.MYB domain transcription factor family'
GRMZM2G091490	6	64902485	64904929	'27.3.27'	'RNA.regulation of transcription.NAC domain transcription factor family'
GRMZM2G160990	8	148619605	148622182	'27.3.30'	'RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family'
GRMZM2G024898	2	12699966	12704308	'27.3.32'	'RNA.regulation of transcription.WRKY domain transcription factor family'
GRMZM2G150327	1	111239368	111241402	'27.3.6'	'RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family'
GRMZM2G164835	6	91501036	91507779	'27.3.67'	'RNA.regulation of transcription.putative transcription regulator'
GRMZM2G128992	5	202842308	202844301	'27.3.99'	'RNA.regulation of transcription.unclassified'
GRMZM2G141036	4	163053052	163054833	'27.3.99'	'RNA.regulation of transcription.unclassified'
GRMZM2G071589	5	31972843	31982874	'27.4'	'RNA.RNA binding'
GRMZM2G076597	1	237084901	237093023	'27.4'	'RNA.RNA binding'

GRMZM2G163658	8	116210469	116228488	'28.1'	'DNA.synthesis/chromatin structure'
GRMZM2G534116	6	108099461	108114688	'28.1'	'DNA.synthesis/chromatin structure'
AC213050.3_FG001	6	95029863	95032085	'28.1'	'DNA.synthesis/chromatin structure'
GRMZM2G353125	6	94447091	94452045	'28.2'	'DNA.repair'
AC197555.3_FG008	3	225920322	225921245	'28.2'	'DNA.repair'
GRMZM2G337905	6	3439887	3462130	'28.99'	'DNA.unspecified'
GRMZM2G459828	4	39828519	39834124	'29.2.1.2.1.10'	'protein.synthesis.ribosomal protein.eukaryotic.40S subunit.S10'
GRMZM2G018484	5	212480742	212482922	'29.3.3'	'protein.targeting.chloroplast'
GRMZM2G038487	8	155903623	155907742	'29.3.3'	'protein.targeting.chloroplast'

GRMZM2G171390	3	142782835	142785709	'29.3.3'	'protein.targeting.chloroplast'
GRMZM2G054634	9	109909155	109913885	'29.4'	'protein.postranslational modification'
GRMZM2G169080	1	96685018	96690137	'29.4'	'protein.postranslational modification'
GRMZM2G086132	6	163919419	163927005	'29.5.11.20'	'protein.degradation.ubiquitin.proteasom'
GRMZM2G361100	2	49121099	49123057	'29.5.11.4.2'	'protein.degradation.ubiquitin.E3.RING'
GRMZM2G171713	1	150964241	150966527	'29.5.3'	'protein.degradation.cysteine protease'
GRMZM2G384762	4	35092723	35097996	'29.5.3'	'protein.degradation.cysteine protease'
GRMZM2G100889	3	17661589	17667021	'29.5.5'	'protein.degradation.serine protease'
GRMZM2G368388	3	38105805	38107975	'30.2.99'	'signalling.receptor kinases.misc'
GRMZM2G048205	5	39108198	39112618	'30.3'	'signalling.calcium'
GRMZM2G082836	1	66315589	66318972	'30.5'	'signalling.G-proteins'
GRMZM2G305211	7	154236259	154245505	'30.7'	'signalling.14-3-3 proteins'

GRMZM2G017257	9	7118375	7142045	'31.1'	'cell.organisation'
GRMZM2G026800	5	23129120	23129834	'31.1'	'cell.organisation'
GRMZM2G177224	10	148434353	148438309	'31.2'	'cell.division'
GRMZM2G050933	7	150979155	150981604	'31.3'	'cell.cycle'
GRMZM2G339563	1	10065048	10069386	'31.5.1'	'cell.cell death.plants'
GRMZM2G018251	4	245659689	245663836	'33.99'	'development.unspecified'
GRMZM2G037229	3	172143899	172146939	'34.10'	'transport.nucleotides'
GRMZM2G097421	8	100463752	100467370	'34.10'	'transport.nucleotides'
GRMZM2G366919	2	167975302	167981054	'34.12'	'transport.metal'
GRMZM2G099382	3	214325917	214328710	'34.14'	'transport.unspecified cations'
GRMZM2G333183	10	80347453	80353583	'34.16'	'transport.ABC transporters and multidrug resistance systems'
GRMZM2G432480	5	52926316	52928552	'34.16'	'transport.ABC transporters and multidrug resistance systems'

GRMZM2G062156	2	204707235	204709413	'34.2'	'transport.sugars'
GRMZM2G127591	2	26208479	26211066	'34.8'	'transport.metabolite transporters at the envelope membrane'
GRMZM2G014934	1	259776005	259778713	'35.2'	'not assigned.unknown'
GRMZM2G016586	3	123151371	123152804	'35.2'	'not assigned.unknown'
GRMZM2G019050	1	196548636	196556019	'35.2'	'not assigned.unknown'
GRMZM2G023528	4	244760047	244763636	'35.2'	'not assigned.unknown'
GRMZM2G026922	4	151524358	151533923	'35.2'	'not assigned.unknown'
GRMZM2G043336	3	128451762	128453285	'35.2'	'not assigned.unknown'
GRMZM2G046911	3	186560535	186562222	'35.2'	'not assigned.unknown'
GRMZM2G140101	3	127976340	127977840	'35.2'	'not assigned.unknown'
GRMZM2G149383	1	70171404	70176057	'35.2'	'not assigned.unknown'
GRMZM2G166145	4	243106156	243109791	'35.2'	'not assigned.unknown'
GRMZM2G324705	3	194296064	194297742	'35.2'	'not assigned.unknown'
GRMZM2G375015	6	28576111	28582357	'35.2'	'not assigned.unknown'
GRMZM2G377168	5	177312298	177313349	'35.2'	'not assigned.unknown'

GRMZM2G380414	8	16486555	16487318	'35.2'	'not assigned.unknown'
GRMZM2G426688	9	27629256	27631752	'35.2'	'not assigned.unknown'
GRMZM2G427503	6	108743849	108744462	'35.2'	'not assigned.unknown'
GRMZM2G431708	6	117957036	117976912	'35.2'	'not assigned.unknown'
GRMZM2G438299	8	170335491	170336771	'35.2'	'not assigned.unknown'
GRMZM2G472852	7	166966590	166967300	'35.2'	'not assigned.unknown'
GRMZM2G487136	8	144223076	144232743	'35.2'	'not assigned.unknown'
AC177946.2_FG004	1	19035272	19035748	'35.2'	'not assigned.unknown'
AC190623.3_FG001	3	190263687	190264151	'35.2'	'not assigned.unknown'
AC234201.1_FG003	10	149261979	149263926	'35.2'	'not assigned.unknown'
GRMZM2G054227	8	94350707	94357372	'35.2'	'not assigned.unknown'
GRMZM2G056762	5	191377937	191379331	'35.2'	'not assigned.unknown'
GRMZM2G095519	1	273521470	273523502	'35.2'	'not assigned.unknown'
GRMZM2G113775	1	19629897	19634322	'35.2'	'not assigned.unknown'
GRMZM2G119273	3	177958138	177960261	'35.2'	'not assigned.unknown'
GRMZM2G140917	6	85627983	85636336	'35.2'	'not assigned.unknown'
GRMZM2G386337	6	69663122	69672416	'35.2'	'not assigned.unknown'

F2.ajp13_mapman_gabipd_org) was used to assign genes to functional categories.

Description
'weakly similar to (166) ATCG00580 | Symbols: PSBE | PSII cytochrome b559. There have been many speculations about the function of Cyt b559, but the most favored at present is that it plays a protective role by acting as an electron acceptor or electron donor under conditions when electron flow through PSII is not optimized. | chrC:64071-64322 REVERSEweakly similar to (168) PSBE_WHEAT Cytochrome b559 alpha subunit (PSII reaction center subunit V) - Triticum aestivum (Wheat)weakly similar to (170) loc_osp1g00520 11562.m00043 protein cytochrome b559 alpha chain seq=cds; coord=3:178389274..178389831:-1; parent_gene=GRMZM2G062044'
'weakly similar to (166) ATCG00580 | Symbols: PSBE | PSII cytochrome b559. There have been many speculations about the function of Cyt b559, but the most favored at present is that it plays a protective role by acting as an electron acceptor or electron donor under conditions when electron flow through PSII is not optimized. | chrC:64071-64322 REVERSEweakly similar to (168) PSBE_WHEAT Cytochrome b559 alpha subunit (PSII reaction center subunit V) - Triticum aestivum (Wheat)weakly similar to (170) loc_osp1g00520 11562.m00043 protein cytochrome b559 alpha chain seq=cds; coord=10:90314158..90316333:-1; parent_gene=GRMZM2G108467'
'weakly similar to (166) ATCG00580 | Symbols: PSBE | PSII cytochrome b559. There have been many speculations about the function of Cyt b559, but the most favored at present is that it plays a protective role by acting as an electron acceptor or electron donor under conditions when electron flow through PSII is not optimized. | chrC:64071-64322 REVERSEweakly similar to (168) PSBE_WHEAT Cytochrome b559 alpha subunit (PSII reaction center subunit V) - Triticum aestivum (Wheat)weakly similar to (170) loc_osp1g00520 11562.m00043 protein cytochrome b559 alpha chain seq=cds; coord=2:200093026..200095298:1; parent_gene=GRMZM2G117572'
'weakly similar to (161) ATCG00580 | Symbols: PSBE | PSII cytochrome b559. There have been many speculations about the function of Cyt b559, but the most favored at present is that it plays a protective role by acting as an electron acceptor or electron donor under conditions when electron flow through PSII is not optimized. | chrC:64071-64322 REVERSEweakly similar to (164) PSBE_WHEAT Cytochrome b559 alpha subunit (PSII reaction center subunit V) - Triticum aestivum (Wheat)weakly similar to (166) loc_osp1g00520 11562.m00043 protein cytochrome b559 alpha chain seq=cds; coord=4:54746363..54748100:-1; parent_gene=GRMZM2G125575'
'very weakly similar to (82.8) AT1G67740 | Symbols: PSBY, YCF32 | PSBY | chr1:25394429-25394998 REVERSEvery weakly similar to (87.0) PSBY_SPIOL Photosystem II core complex proteins psbY, chloroplast precursor (L-arginine-metabolizing enzyme) (L-AME) [Contains: Photosystem II protein psbY-1 (psbY-A1); Photosystem II protein psbY-2 (psbY-A2)] - Spinacia oleracea (Spinach)very weakly similar to (96.3) loc_os08g02630 12008.m61984 protein photosystem II core complex proteins psbY, chloroplast precursor, putative, expressed seq=cds; coord=6:6258660..6259670:-1; parent_gene=GRMZM2G134130'
'weakly similar to (120) ATCG00580 | Symbols: PSBE | PSII cytochrome b559. There have been many speculations about the function of Cyt b559, but the most favored at present is that it plays a protective role by acting as an electron acceptor or electron donor under conditions when electron flow through PSII is not optimized. | chrC:64071-64322 REVERSEweakly similar to (120) PSBE_SOLTU Cytochrome b559 alpha subunit (PSII reaction center subunit V) - Solanum tuberosum (Potato)weakly similar to (120) loc_osp1g00520 11562.m00043 protein cytochrome b559 alpha chain seq=cds; coord=2:110191812..110201806:-1; parent_gene=GRMZM2G433927'

'highly similar to (517) AT5G66190 | Symbols: ATLFNR1 | FNR1 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within the noncyclic electron transp | chr5:26451203-26452616 REVERSEhighly similar to (525) FENR1_ORYSA Ferredoxin--NADP reductase, leaf isozyme, chloroplast precursor (EC 1.18.1.2) (FNR) - Oryza sativa (Rice)highly similar to (535) loc_os02g01340 12002.m05484 protein ferredoxin--NADP reductase, leaf isozyme, chloroplast precursor, putative, expressed seq=cds; coord=3:147290518..147292751:-1; parent_gene=GRMZM2G059083'

'highly similar to (528) AT5G66190 | Symbols: ATLFNR1 | FNR1 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within the noncyclic electron transp | chr5:26451203-26452616 REVERSEhighly similar to (545) FENR1_ORYSA Ferredoxin--NADP reductase, leaf isozyme, chloroplast precursor (EC 1.18.1.2) (FNR) - Oryza sativa (Rice)highly similar to (545) loc_os06g01850 12006.m04921 protein ferredoxin--NADP reductase, leaf isozyme, chloroplast precursor, putative, expressed seq=cds; coord=8:157455159..157458787:-1; parent_gene=GRMZM2G059191'

'highly similar to (514) AT5G66190 | Symbols: ATLFNR1 | FNR1 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within the noncyclic electron transp | chr5:26451203-26452616 REVERSEhighly similar to (530) FENR1_ORYSA Ferredoxin--NADP reductase, leaf isozyme, chloroplast precursor (EC 1.18.1.2) (FNR) - Oryza sativa (Rice)highly similar to (530) loc_os06g01850 12006.m04921 protein ferredoxin--NADP reductase, leaf isozyme, chloroplast precursor, putative, expressed seq=cds; coord=9:27014628..27017016:1; parent_gene=GRMZM2G168143'

'weakly similar to (157) AT5G66190 | Symbols: ATLFNR1 | FNR1 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within the noncyclic electron transp | chr5:26451203-26452616 REVERSEweakly similar to (156) FENR1_ORYSA Ferredoxin--NADP reductase, leaf isozyme, chloroplast precursor (EC 1.18.1.2) (FNR) - Oryza sativa (Rice)weakly similar to (159) loc_os02g01340 12002.m05484 protein ferredoxin--NADP reductase, leaf isozyme, chloroplast precursor, putative, expressed seq=cds; coord=10:2690434..2694516:-1; parent_gene=GRMZM2G320305'

'moderately similar to (260) AT5G66190 | Symbols: ATLFNR1 | FNR1 (FERREDOXIN-NADP(+)-OXIDOREDUCTASE 1); NADPH dehydrogenase/ electron transporter, transferring electrons within the cyclic electron transport pathway of photosynthesis/ electron transporter, transferring electrons within the noncyclic electron transp | chr5:26451203-26452616 REVERSEmoderately similar to (266) FENR_MESCR Ferredoxin--NADP reductase, chloroplast precursor (EC 1.18.1.2) (FNR) - Mesembryanthemum crystallinum (Common ice plant)moderately similar to (265) loc_os06g01850 12006.m04921 protein ferredoxin--NADP reductase, leaf isozyme, chloroplast precursor, putative, expressed seq=cds; coord=1:278929534..278933203:1; parent_gene=GRMZM2G395728'

'moderately similar to (289) ATCG00490 | Symbols: RBCL | large subunit of RUBISCO. Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds. | chrC:54958-56397 FORWARDmoderately similar to (306) RBL_MAIZE Ribulose bisphosphate carboxylase large chain precursor (EC 4.1.1.39) (RuBisCO large subunit) - Zea mays (Maize)moderately similar to (307) loc_os01g58020 12001.m11949 protein ribulose bisphosphate carboxylase large chain precursor, putative seq=cds; coord=4:156719448..156720902:-1; parent_gene=GRMZM2G057171'

'moderately similar to (270) ATCG00490 | Symbols: RBCL | large subunit of RUBISCO. Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds. | chrC:54958-56397 FORWARDmoderately similar to (288) RBL_MAIZE Ribulose bisphosphate carboxylase large chain precursor (EC 4.1.1.39) (RuBisCO large subunit) - Zea mays (Maize)moderately similar to (270) loc_os01g58020 12001.m11949 protein ribulose bisphosphate carboxylase large chain precursor, putative seq=cds; coord=1:207515449..207516025:-1; parent_gene=GRMZM2G083364'

'moderately similar to (238) ATCG00490 | Symbols: RBCL | large subunit of RUBISCO. Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds. | chrC:54958-56397 FORWARDmoderately similar to (257) RBL_SACOF Ribulose bisphosphate carboxylase large chain precursor (EC 4.1.1.39) (RuBisCO large subunit) - Saccharum officinarum (Sugarcane)moderately similar to (252) loc_os01g58020 12001.m11949 protein ribulose bisphosphate carboxylase large chain precursor, putative seq=cds; coord=6:123912807..123913530:1; parent_gene=GRMZM2G122563' 'highly similar to (502) ATCG00490 | Symbols: RBCL | large subunit of RUBISCO. Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds. | chrC:54958-56397 FORWARDhighly similar to (545) RBL_MAIZE Ribulose bisphosphate carboxylase large chain precursor (EC 4.1.1.39) (RuBisCO large subunit) - Zea mays (Maize)highly similar to (514) loc_osp1g00420 11562.m00031 protein ribulose 1,5-bisphosphate carboxylase/oxygenase large chain seq=cds; coord=9:32379686..32380603:1; parent_gene=GRMZM2G308907'

'highly similar to (877) ATCG00490 | Symbols: RBCL | large subunit of RUBISCO. Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds. | chrC:54958-56397 FORWARDhighly similar to (944) RBL_MAIZE Ribulose bisphosphate carboxylase large chain precursor (EC 4.1.1.39) (RuBisCO large subunit) - Zea mays (Maize)highly similar to (896) loc_osp1g00420 11562.m00031 protein ribulose 1,5-bisphosphate carboxylase/oxygenase large chain seq=cds; coord=6:160783975..160786062:1; parent_gene=GRMZM2G360821'

'highly similar to (877) ATCG00490 | Symbols: RBCL | large subunit of RUBISCO. Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds. | chrC:54958-56397 FORWARDhighly similar to (944) RBL_MAIZE Ribulose bisphosphate carboxylase large chain precursor (EC 4.1.1.39) (RuBisCO large subunit) - Zea mays (Maize)highly similar to (896) loc_osp1g00420 11562.m00031 protein ribulose 1,5-bisphosphate carboxylase/oxygenase large chain seq=cds; coord=2:200096578..200100853:-1; parent_gene=GRMZM2G385635'

'highly similar to (877) ATCG00490 | Symbols: RBCL | large subunit of RUBISCO. Protein is tyrosine-phosphorylated and its phosphorylation state is modulated in response to ABA in Arabidopsis thaliana seeds. | chrC:54958-56397 FORWARDhighly similar to (944) RBL_MAIZE Ribulose bisphosphate carboxylase large chain precursor (EC 4.1.1.39) (RuBisCO large subunit) - Zea mays (Maize)highly similar to (896) loc_osp1g00420 11562.m00031 protein ribulose 1,5-bisphosphate carboxylase/oxygenase large chain seq=cds; coord=1:203925927..203931405:-1; parent_gene=GRMZM2G448344'

'moderately similar to (411) AT5G61410 | Symbols: RPE | RPE; catalytic/ ribulose-phosphate 3-epimerase | chr5:24684085-24685836 REVERSEmoderately similar to (449) RPE_ORYSA Ribulose-phosphate 3-epimerase, chloroplast precursor (EC 5.1.3.1) (Pentose-5-phosphate 3-epimerase) (PPE) (RPE) (R5P3E) - Oryza sativa (Rice)moderately similar to (449) loc_os03g07300 12003.m101203 protein ribulose-phosphate 3-epimerase, chloroplast precursor, putative, expressed seq=cds; coord=1:14624231..14639380:1; parent_gene=GRMZM2G026807'

'moderately similar to (432) AT5G61410 | Symbols: RPE | RPE; catalytic/ ribulose-phosphate 3-epimerase | chr5:24684085-24685836 REVERSEmoderately similar to (470) RPE_ORYSA Ribulose-phosphate 3-epimerase, chloroplast precursor (EC 5.1.3.1) (Pentose-5-phosphate 3-epimerase) (PPE) (RPE) (R5P3E) - Oryza sativa (Rice)moderately similar to (470) loc_os03g07300 12003.m101203 protein ribulose-phosphate 3-epimerase, chloroplast precursor, putative, expressed seq=cds; coord=9:151316118..151319993:-1; parent_gene=GRMZM2G178960'

'highly similar to (629) AT1G32060 | Symbols: PRK | PRK (PHOSPHORIBULOKINASE); ATP binding / phosphoribulokinase/ protein binding | chr1:11532668-11534406 FORWARDhighly similar to (692) KPPR_WHEAT Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19) (Phosphopentokinase) (PRKase) (PRK) - Triticum aestivum (Wheat)highly similar to (702) loc_os02g47020 12002.m09738 protein phosphoribulokinase, chloroplast precursor, putative, expressed seq=cds; coord=4:158993661..158996579:-1; parent_gene=GRMZM2G026024'

'highly similar to (639) AT1G32060 | Symbols: PRK | PRK (PHOSPHORIBULOKINASE); ATP binding / phosphoribulokinase/ protein binding | chr1:11532668-11534406 FORWARDhighly similar to (733) KPPR_WHEAT Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19) (Phosphopentokinase) (PRKase) (PRK) - Triticum aestivum (Wheat)highly similar to (735) loc_os02g47020 12002.m09738 protein phosphoribulokinase, chloroplast precursor, putative, expressed seq=cds; coord=5:199592727..199595057:1; parent_gene=GRMZM2G162529'

'moderately similar to (307) AT1G32060 | Symbols: PRK | PRK (PHOSPHORIBULOKINASE); ATP binding / phosphoribulokinase/ protein binding | chr1:11532668-11534406 FORWARDmoderately similar to (315) KPPR_MESCR Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19) (Phosphopentokinase) (PRKase) (PRK) - Mesembryanthemum crystallinum (Common ice plant)moderately similar to (319) loc_os02g47020 12002.m09738 protein phosphoribulokinase, chloroplast precursor, putative, expressed seq=cds; coord=2:12897470..12899787:1; parent_gene=GRMZM2G463280' 'moderately similar to (228) AT1G67090 | Symbols: RBCS1A | RBCS1A (RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A); copper ion binding / ribulose-bisphosphate carboxylase | chr1:25048590-25049249 REVERSEmoderately similar to (357) RBS_MAIZE Ribulose bisphosphate carboxylase small chain, chloroplast precursor (EC 4.1.1.39) (RuBisCO small subunit) - Zea mays (Maize)moderately similar to (281) loc_os12g19381 12012.m27010 protein ribulose bisphosphate carboxylase small chain C, chloroplast precursor, putative, expressed seq=cds; coord=4:190051325..190053766:-1; parent_gene=GRMZM2G098520'

'moderately similar to (228) AT1G67090 | Symbols: RBCS1A | RBCS1A (RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A); copper ion binding / ribulose-bisphosphate carboxylase | chr1:25048590-25049249 REVERSEmoderately similar to (344) RBS_MAIZE Ribulose bisphosphate carboxylase small chain, chloroplast precursor (EC 4.1.1.39) (RuBisCO small subunit) - Zea mays (Maize)moderately similar to (283) loc_os12g19381 12012.m27010 protein ribulose bisphosphate carboxylase small chain C, chloroplast precursor, putative, expressed seq=cds; coord=2:142794871..142796060:1; parent_gene=GRMZM2G113033'

'weakly similar to (137) AT3G12780 | Symbols: PGK1 | PGK1 (PHOSPHOGLYCERATE KINASE 1); phosphoglycerate kinase | chr3:4061127-4063140 REVERSEweakly similar to (137) PGKH_SPIOL Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) (Fragment) - Spinacia oleracea (Spinach)highly similar to (739) loc_os10g30550 12010.m05915 protein phosphoglycerate kinase, chloroplast precursor, putative, expressed seq=cds; coord=1:237458102..237487302:1; parent_gene=GRMZM2G003724'

'moderately similar to (376) AT1G56190 | Symbols: | phosphoglycerate kinase, putative | chr1:21028622-21030454 FORWARDmoderately similar to (385) PGKH_TOBAC Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) - Nicotiana tabacum (Common tobacco)moderately similar to (397) loc_os05g41640 12005.m08338 protein phosphoglycerate kinase, chloroplast precursor, putative, expressed seq=cds; coord=3:188318910..188325562:-1; parent_gene=GRMZM2G047028'

'highly similar to (715) AT1G56190 | Symbols: | phosphoglycerate kinase, putative | chr1:21028622-21030454 FORWARDhighly similar to (752) PGKH_WHEAT Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) - Triticum aestivum (Wheat)highly similar to (765) loc_os05g41640 12005.m08338 protein phosphoglycerate kinase, chloroplast precursor, putative, expressed seq=cds; coord=8:120773908..120778906:-1; parent_gene=GRMZM2G083016'

'highly similar to (718) AT1G56190 | Symbols: | phosphoglycerate kinase, putative | chr1:21028622-21030454 FORWARDhighly similar to (761) PGKH_WHEAT Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) - Triticum aestivum (Wheat)highly similar to (778) loc_os05g41640 12005.m08338 protein phosphoglycerate kinase, chloroplast precursor, putative, expressed seq=cds; coord=6:156256123..156258890:-1; parent_gene=GRMZM2G089136'

'highly similar to (656) AT1G79550 | Symbols: PGK | PGK (PHOSPHOGLYCERATE KINASE); phosphoglycerate kinase | chr1:29924347-29926295 REVERSEhighly similar to (694) PGKY_WHEAT Phosphoglycerate kinase, cytosolic (EC 2.7.2.3) - Triticum aestivum (Wheat)highly similar to (707) loc_os02g07260 12002.m33575 protein phosphoglycerate kinase, cytosolic, putative, expressed seq=cds; coord=5:84822215..84825942:1; parent_gene=GRMZM2G382914'

'highly similar to (895) AT2G24270 | Symbols: ALDH11A3 | ALDH11A3; 3-chloroallyl aldehyde dehydrogenase/ glyceraldehyde-3-phosphate dehydrogenase (NADP+) | chr2:10327325-10329601 REVERSEhighly similar to (979) GAPN_MAIZE NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.9) (Non-phosphorylating glyceraldehyde 3-phosphate dehydrogenase) (Glyceraldehyde-3-phosphate dehydrogenase [NADP+]) (Triosephosphate dehydrogenase) - Zea mays (Maize)highly similar to (959) loc_os08g34210 12008.m26702 protein NADP-dependent glyceraldehyde-3-phosphate dehydrogenase, putative, expressed seq=cds; coord=4:84106470..84111628:-1; parent_gene=GRMZM2G035268'

'highly similar to (575) AT3G26650 | Symbols: GAPA, GAPA-1 | GAPA (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase/ protein binding | chr3:9795226-9796848 FORWARDhighly similar to (670) G3PA_MAIZE Glyceraldehyde-3-phosphate dehydrogenase A, chloroplast precursor (EC 1.2.1.13) (NADP-dependent glyceraldehydephosphate dehydrogenase subunit A) - Zea mays (Maize)highly similar to (648) loc_os04g38600 12004.m35146 protein glyceraldehyde-3-phosphate dehydrogenase A, chloroplast precursor, putative, expressed seq=cds; coord=10:122379626..122381446:1; parent_gene=GRMZM2G039723' 'highly similar to (582) AT3G26650 | Symbols: GAPA, GAPA-1 | GAPA (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT); glyceraldehyde-3-phosphate dehydrogenase/ protein binding | chr3:9795226-9796848 FORWARDhighly similar to (680) G3PA_MAIZE Glyceraldehyde-3-phosphate dehydrogenase A, chloroplast precursor (EC 1.2.1.13) (NADP-dependent glyceraldehydephosphate dehydrogenase subunit A) - Zea mays (Maize)highly similar to (658) loc_os04g38600 12004.m35146 protein glyceraldehyde-3-phosphate dehydrogenase A, chloroplast precursor, putative, expressed seq=cds; coord=10:122532025..122533813:1; parent_gene=GRMZM2G162845'

'moderately similar to (371) AT1G12900 | Symbols: GAPA-2 | GAPA-2 (GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A SUBUNIT 2); NAI or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr1:4392634-4393850 REVERSEmoderately similar to (473) G3PA_MAIZE Glyceraldehyde-3-phosphate dehydrogenase A, chloroplast precursor (EC 1.2.1.13) (NADP-dependent glyceraldehydephosphate dehydrogenase subunit A) - Zea mays (Maize)moderately similar to (456) loc_os04g38600 12004.m35146 protein glyceraldehyde-3-phosphate dehydrogenase A, chloroplast precursor, putative, expressed seq=cds; coord=2:42258081..42259297:-1; parent_gene=GRMZM2G337113'

'moderately similar to (439) AT2G21170 | Symbols: TIM | TIM (TRIOSEPHOSPHATE ISOMERASE); catalytic/ triose-phosphate isomerase | chr2:9071047-9073106 REVERSEmoderately similar to (478) TPIC_SECCE Triosephosphate isomerase, chloroplast precursor (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Secale cereale (Rye)highly similar to (523) loc_os09g36450 12009.m060049 protein triosephosphate isomerase, chloroplast precursor, putative, expressed seq=cds; coord=2:195920737..195924614:-1; parent_gene=GRMZM2G002807'

'highly similar to (629) AT4G38970 | Symbols: | fructose-bisphosphate aldolase, putative | chr4:18163769-18165659 REVERSEhighly similar to (710) ALFC_ORYSA Fructose-bisphosphate aldolase, chloroplast precursor (EC 4.1.2.13) (ALDP) - Oryza sativa (Rice)highly similar to (710) loc_os11g07020 12011.m28744 protein fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed seq=cds; coord=10:10194502..10196450:-1; parent_gene=GRMZM2G046284'

'highly similar to (607) AT2G01140 | Symbols: | fructose-bisphosphate aldolase, putative | chr2:95006-96491 REVERSEhighly similar to (561) ALFC_PEA Fructose-bisphosphate aldolase 1, chloroplast precursor (EC 4.1.2.13) (Fragment) - Pisum sativum (Garden pea)highly similar to (672) loc_os01g02880 12001.m06927 protein fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed seq=cds; coord=8:9901033..9904862:-1; parent_gene=GRMZM2G069195'

'highly similar to (630) AT2G01140 | Symbols: | fructose-bisphosphate aldolase, putative | chr2:95006-96491 REVERSEhighly similar to (582) ALFC_PEA Fructose-bisphosphate aldolase 1, chloroplast precursor (EC 4.1.2.13) (Fragment) - Pisum sativum (Garden pea)highly similar to (710) loc_os01g02880 12001.m06927 protein fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed seq=cds; coord=3:27391353..27395051:1; parent_gene=GRMZM2G089365'

'highly similar to (624) AT4G38970 | Symbols: | fructose-bisphosphate aldolase, putative | chr4:18163769-18165659 REVERSEhighly similar to (665) ALFC_ORYSA Fructose-bisphosphate aldolase, chloroplast precursor (EC 4.1.2.13) (ALDP) - Oryza sativa (Rice)highly similar to (665) loc_os11g07020 12011.m28744 protein fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed seq=cds; coord=4:204599067..204601053:-1; parent_gene=GRMZM2G155253'

'weakly similar to (160) AT2G01140 | Symbols: | fructose-bisphosphate aldolase, putative | chr2:95006-96491 REVERSEweakly similar to (143) ALFD_PEA Fructose-bisphosphate aldolase 2, chloroplast (EC 4.1.2.13) - Pisum sativum (Garden pea)weakly similar to (170) loc_os01g02880 12001.m06927 protein fructose-bisphosphate aldolase, chloroplast precursor, putative, expressed seq=cds; coord=5:145007924..145010718:-1; parent_gene=GRMZM2G407406'

'highly similar to (585) AT3G54050 | Symbols: | fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative | chr3:20016951-20018527 FORWARDhighly similar to (647) F16P1_ORYSA Fructose-1,6-bisphosphatase, chloroplast precursor (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) - Oryza sativa (Rice)highly similar to (647) loc_os03g16050 12003.m07042 protein fructose-1,6-bisphosphatase, chloroplast precursor, putative, expressed seq=cds; coord=1:38848595..38850785:-1; parent_gene=GRMZM2G306732' 'weakly similar to (164) AT1G43670 | Symbols: | fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative | chr1:16468184-16470347 FORWARDweakly similar to (166) F16P2_SACHY Fructose-1,6-bisphosphatase, cytosolic (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) - Saccharum hybrid (Sugarcane)weakly similar to (171) loc_os05g36270 12005.m083730 protein fructose-1,6-bisphosphatase, cytosolic, putative, expressed seq=cds; coord=8:100871386..100872445:-1; parent_gene=GRMZM2G322953'

'nearly identical (1041) AT2G45290 | Symbols: | transketolase, putative | chr2:18672737-18675589 FORWARDnearly identical (1063) TKTC_SOLTU Transketolase, chloroplast precursor (EC 2.2.1.1) (TK) - Solanum tuberosum (Potato)nearly identical (1149) loc_os04g19740 12004.m07133 protein transketolase, chloroplast precursor, putative, expressed seq=cds; coord=2:86650928..86654660:1; parent_gene=GRMZM2G010494'

'nearly identical (1148) AT3G60750 | Symbols: | transketolase, putative | chr3:22454004-22456824 FORWARDnearly identical (1289) TKTC_MAIZE Transketolase, chloroplast (EC 2.2.1.1) (TK) - Zea mays (Maize)nearly identical (1204) loc_os06g04270 12006.m05156 protein transketolase, chloroplast precursor, putative, expressed seq=cds; coord=9:22779373..22783918:1; parent_gene=GRMZM2G033208'

'weakly similar to (181) AT3G55800 | Symbols: SBPASE | SBPASE (sedoheptulose-bisphosphatase); phosphoric ester hydrolase/ sedoheptulose-bisphosphatase | chr3:20709640-20711421 FORWARDmoderately similar to (253) S17P_WHEAT Sedoheptulose-1,7-bisphosphatase, chloroplast precursor (EC 3.1.3.37) (Sedoheptulose-bisphosphatase) (SBPase) (SED(1,7)P2ase) - Triticum aestivum (Wheat)moderately similar to (263) loc_os04g16680 12004.m06845 protein sedoheptulose-1,7-bisphosphatase, chloroplast precursor, putative, expressed seq=cds; coord=3:178846540..178848005:-1; parent_gene=AC147602.5_FG004'

'nearly identical (1584) AT3G14940 | Symbols: ATPPC3 | ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpyruvate carboxylase | chr3:5025584-5029476 FORWARDnearly identical (1845) CAPP1_SORBI Phosphoenolpyruvate carboxylase 1 (EC 4.1.1.31) (PEPCase 1) (PEPC 1) (CP21) - Sorghum bicolor (Sorghum) (Sorghum vulgare)nearly identical (1788) loc_os02g14770 12002.m100156 protein phosphoenolpyruvate carboxylase 1, putative, expressed seq=cds; coord=5:144808460..144816059:-1; parent_gene=GRMZM2G069542'

'nearly identical (1590) AT1G53310 | Symbols: ATPPC1 | ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1); catalytic/ phosphoenolpyruvate carboxylase | chr1:19884261-19888070 REVERSEnearly identical (1848) CAPP1_SORBI Phosphoenolpyruvate carboxylase 1 (EC 4.1.1.31) (PEPCase 1) (PEPC 1) (CP21) - Sorghum bicolor (Sorghum) (Sorghum vulgare)nearly identical (1797) loc_os02g14770 12002.m100156 protein phosphoenolpyruvate carboxylase 1, putative, expressed seq=cds; coord=4:227269225..227280511:-1; parent_gene=GRMZM2G074122'

'nearly identical (1378) AT1G68750 | Symbols: ATPPC4 | ATPPC4; phosphoenolpyruvate carboxylase | chr1:25822942-25828104 REVERSEhighly similar to (618) CAPP2_CHLRE Phosphoenolpyruvate carboxylase 2 (EC 4.1.1.31) (PEP carboxylase 2) (PEPCase 2) (PEPC 2) - Chlamydomonas reinhardtiinearly identical (1632) loc_os01g02050 12001.m06847 protein phosphoenolpyruvate carboxylase 4, putative, expressed seq=cds; coord=3:29055457..29063476:-1; parent_gene=GRMZM2G082780'

'nearly identical (1508) AT2G42600 | Symbols: ATPPC2 | ATPPC2 (PHOSPHOENOLPYRUVATE CARBOXYLASE 2); catalytic/ phosphoenolpyruvate carboxylase | chr2:17734541-17738679 REVERSEnearly identical (1912) CAPP1_MAIZE Phosphoenolpyruvate carboxylase 1 (EC 4.1.1.31) (PEPCase 1) (PEPC 1) - Zea mays (Maize)nearly identical (1566) loc_os02g14770 12002.m100156 protein phosphoenolpyruvate carboxylase 1, putative, expressed seq=cds; coord=9:61296279..61301686:1; parent_gene=GRMZM2G083841'

'highly similar to (842) AT1G79750 | Symbols: ATNADP-ME4 | ATNADP-ME4 (NADP-malic enzyme 4); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor | chr1:30007655-30011179 REVERSEnearly identical (1136) MAOC_MAIZE NADP-dependent malic enzyme, chloroplast precursor (EC 1.1.1.40) (NADP-ME) - Zea mays (Maize)highly similar to (947) loc_os01g09320 12001.m07557 protein NADP-dependent malic enzyme, chloroplast precursor, putative, expressed seq=cds; coord=3:7275169..7280519:1; parent_gene=GRMZM2G085019' 'highly similar to (784) AT4G00570 | Symbols: | malate oxidoreductase, putative | chr4:242817-246522 REVERSEhighly similar to (797) MAON_SOLTU NAD-dependent malic enzyme 59 kDa isoform, mitochondrial precursor (EC 1.1.1.39) (NAD-ME) - Solanum tuberosum (Potato)highly similar to (968) loc_os10g35960 12010.m50425 protein NAD-dependent malic enzyme 59 kDa isoform, mitochondrial precursor, putative, expressed seq=cds; coord=5:23896374..23903276:-1; parent_gene=GRMZM2G085747'

'nearly identical (1434) AT4G15530 | Symbols: PPDK | PPDK (pyruvate orthophosphate dikinase); kinase/ pyruvate, phosphate dikinase | chr4:8864828-8870748 REVERSEnearly identical (1684) PPDK_MAIZE Pyruvate, phosphate dikinase, chloroplast precursor (EC 2.7.9.1) (Pyruvate, orthophosphate dikinase) - Zea mays (Maize)nearly identical (1625) loc_os05g33570 12005.m083718 protein pyruvate, phosphate dikinase, chloroplast precursor, putative, expressed seq=cds; coord=8:107003965..107014830:1; parent_gene=GRMZM2G097457'

'nearly identical (1637) AT3G14940 | Symbols: ATPPC3 | ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpyruvate carboxylase | chr3:5025584-5029476 FORWARDnearly identical (1880) CAPP1_SACHY Phosphoenolpyruvate carboxylase, housekeeping isozyme (EC 4.1.1.31) (PEPCase) (PEPC) - Saccharum hybrid (Sugarcane)nearly identical (1692) loc_os01g55350 12001.m11694 protein phosphoenolpyruvate carboxylase, housekeeping isozyme, putative, expressed seq=cds; coord=8:173702854..173715423:1; parent_gene=GRMZM2G110714'

'highly similar to (875) AT2G19900 | Symbols: ATNADP-ME1 | ATNADP-ME1 (NADP-malic enzyme 1); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor | chr2:8592106-8595403 REVERSEhighly similar to (895) MAOX_VITVI NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) - Vitis vinifera (Grape)nearly identical (1007) loc_os01g54030 12001.m11567 protein NADP-dependent malic enzyme, putative, expressed seq=cds; coord=8:175058638..175063179:-1; parent_gene=GRMZM2G118770'

'moderately similar to (245) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (340) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (340) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215466579..215473931:-1; parent_gene=GRMZM2G121878'

'highly similar to (838) AT1G79750 | Symbols: ATNADP-ME4 | ATNADP-ME4 (NADP-malic enzyme 4); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor | chr1:30007655-30011179 REVERSEhighly similar to (944) MAOC_ORYSA NADP-dependent malic enzyme, chloroplast precursor (EC 1.1.1.40) (NADP-ME) - Oryza sativa (Rice)highly similar to (944) loc_os01g09320 12001.m07557 protein NADP-dependent malic enzyme, chloroplast precursor, putative, expressed seq=cds; coord=6:139275339..139281024:1; parent_gene=GRMZM2G122479'

'highly similar to (940) AT5G11670 | Symbols: ATNADP-ME2 | ATNADP-ME2 (NADP-malic enzyme 2); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor | chr5:3754456-3758040 FORWARDhighly similar to (977) MAOX_VITVI NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) - Vitis vinifera (Grape)nearly identical (1080) loc_os01g52500 12001.m42715 protein NADP-dependent malic enzyme, putative, expressed seq=cds; coord=3:201684716..201689628:-1; parent_gene=GRMZM2G159724'

'moderately similar to (260) AT5G14740 | Symbols: CA2, CA18, BETA CA2 | CA2 (CARBONIC ANHYDRASE 2); carbonate dehydratase/ zinc ion binding | chr5:4758257-4762315 FORWARDmoderately similar to (338) CAHC_HORVU Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) - Hordeum vulgare (Barley)moderately similar to (331) loc_os01g45274 12001.m150428 protein carbonic anhydrase, chloroplast precursor, putative, expressed seq=cds; coord=3:215424737..215427767:-1; parent_gene=GRMZM2G348512'

'highly similar to (884) AT2G13560 | Symbols: | malate oxidoreductase, putative | chr2:5650089-5655103 FORWARDhighly similar to (884) MAOM_SOLTU NAD-dependent malic enzyme 62 kDa isoform, mitochondrial precursor (EC 1.1.1.39) (NAD-ME) - Solanum tuberosum (Potato)nearly identical (1017) loc_os07g31380 12007.m07407 protein NAD-dependent malic enzyme 62 kDa isoform, mitochondrial precursor, putative, expressed seq=cds; coord=7:150290285..150300500:-1; parent_gene=GRMZM2G406672' 'moderately similar to (322) AT5G11670 | Symbols: ATNADP-ME2 | ATNADP-ME2 (NADP-malic enzyme 2); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor | chr5:3754456-3758040 FORWARDmoderately similar to (322) MAOX_PHAVU NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) - Phaseolus vulgaris (Kidney bean) (French bean)moderately similar to (342) loc_os01g52500 12001.m42715 protein NADP-dependent malic enzyme, putative, expressed seq=cds; coord=1:283454836..283456687:-1; parent_gene=GRMZM2G461332'

'nearly identical (1636) AT1G53310 | Symbols: ATPPC1 | ATPPC1 (PHOSPHOENOLPYRUVATE CARBOXYLASE 1); catalytic/ phosphoenolpyruvate carboxylase | chr1:19884261-19888070 REVERSEnearly identical (1864) CAPP2_MAIZE Phosphoenolpyruvate carboxylase 2 (EC 4.1.1.31) (PEPCase 2) (PEPC 2) - Zea mays (Maize)nearly identical (1765) loc_os09g14670 12009.m04730 protein phosphoenolpyruvate carboxylase 2, putative, expressed seq=cds; coord=7:86433388..86439128:-1; parent_gene=GRMZM2G473001'

'very weakly similar to (90.9) AT5G11670 | Symbols: ATNADP-ME2 | ATNADP-ME2 (NADP-malic enzyme 2); malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)/ malic enzyme/ oxidoreductase, acting on NADH or NADPH, NAD or NADP as acceptor | chr5:3754456-3758040 FORWARDvery weakly similar to (95.1) MAOX_MESCR NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) - Mesembryanthemum crystallinum (Common ice plant)very weakly similar to (91.7) loc_os01g54030 12001.m11567 protein NADP-dependent malic enzyme, putative, expressed seq=cds; coord=6:102073554..102077523:1; parent_gene=AC226723.2_FG001'

'nearly identical (1037) AT4G10120 | Symbols: ATSPS4F | ATSPS4F; transferase, transferring glycosyl groups | chr4:6315033-6319785 FORWARDhighly similar to (944) SPS_MAIZE Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase) - Zea mays (Maize)nearly identical (1494) loc_os11g12810 12011.m05473 protein sucrose-phosphate synthase, putative, expressed seq=cds; coord=4:10479235..10485174:-1; parent_gene=GRMZM2G008507'

'highly similar to (839) AT5G20280 | Symbols: ATSPS1F | ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase, transferring glycosyl groups | chr5:6844994-6849997 REVERSEhighly similar to (845) SPS_SOLTU Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase) - Solanum tuberosum (Potato)nearly identical (1611) loc_os06g43630 12006.m08893 protein sucrose-phosphate synthase 1, putative, expressed seq=cds; coord=9:94333500..94352269:1; parent_gene=GRMZM2G049076'

'nearly identical (1327) AT5G20280 | Symbols: ATSPS1F | ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase, transferring glycosyl groups | chr5:6844994-6849997 REVERSEnearly identical (1343) SPS_SOLTU Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase) - Solanum tuberosum (Potato)nearly identical (1766) loc_os08g20660 12008.m26651 protein sucrose-phosphate synthase 1, putative, expressed seq=cds; coord=4:65261557..65280118:-1; parent_gene=GRMZM2G055331'

'nearly identical (1379) AT1G04920 | Symbols: ATSPS3F | ATSPS3F (sucrose phosphate synthase 3F); sucrose-phosphate synthase/ transferase, transferring glycosyl groups | chr1:1391674-1395756 REVERSEnearly identical (1933) SPS_MAIZE Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase) - Zea mays (Maize)nearly identical (1724) loc_os01g69030 12001.m150823 protein sucrose-phosphate synthase, putative, expressed seq=cds; coord=3:161252718..161258340:1; parent_gene=GRMZM2G140107'

'nearly identical (1061) AT5G20280 | Symbols: ATSPS1F | ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase, transferring glycosyl groups | chr5:6844994-6849997 REVERSEnearly identical (1081) SPS_SPIOL Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase) - Spinacia oleracea (Spinach)nearly identical (1757) loc_os02g09170 12002.m100124 protein sucrose-phosphate synthase 1, putative, expressed seq=cds; coord=5:96354714..96362409:1; parent_gene=GRMZM2G462613'

'highly similar to (588) AT5G20280 | Symbols: ATSPS1F | ATSPS1F (sucrose phosphate synthase 1F); sucrose-phosphate synthase/ transferase, transferring glycosyl groups | chr5:6844994-6849997 REVERSEhighly similar to (598) SPS_SOLTU Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-phosphate glucosyltransferase) - Solanum tuberosum (Potato)nearly identical (1242) loc_os06g43630 12006.m08893 protein sucrose-phosphate synthase 1, putative, expressed seq=cds; coord=6:96905196..96916140:1; parent_gene=GRMZM2G471083' 'highly similar to (537) AT2G35840 | Symbols: | sucrose-phosphatase 1 (SPP1) | chr2:15053952-15055776 FORWARDhighly similar to (758) loc_os01g27880 12001.m43018 protein sucrose phosphate synthase, putative, expressed seq=cds; coord=8:116304892..116311147:-1; parent_gene=GRMZM2G055489'

'moderately similar to (442) AT2G35840 | Symbols: | sucrose-phosphatase 1 (SPP1) | chr2:15053952-15055776 FORWARDhighly similar to (620) loc_os05g05270 12005.m05054 protein sucrose phosphate synthase, putative, expressed seq=cds; coord=10:89417140..89420265:1; parent_gene=GRMZM2G097641'

'highly similar to (639) AT1G27680 | Symbols: APL2 | APL2 (ADPGLC-PPASE LARGE SUBUNIT); glucose-1-phosphate adenylyltransferase | chr1:9631630-9634450 FORWARDhighly similar to (957) GLGL2_MAIZE Glucose-1-phosphate adenylyltransferase large subunit 2, chloroplast precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPase S) (Alpha-D-glucose-1-phosphate adenyl transferase) - Zea mays (Maize)highly similar to (947) loc_os05g50380 12005.m083822 protein glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor, putative, expressed seq=cds; coord=6:166587013..166592611:1; parent_gene=GRMZM2G027955'

'highly similar to (804) AT5G48300 | Symbols: ADG1, APS1 | ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE 1); glucose-1-phosphate adenylyltransferase | chr5:19570326-19572557 FORWARDhighly similar to (833) GLGS_WHEAT Glucose-1-phosphate adenylyltransferase small subunit, chloroplast precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPase B) (Alpha-D-glucose-1-phosphate adenyl transferase) Triticum aestivum (Wheat)highly similar to (838) loc_os08g25734 12008.m06589 protein glucose-1-phosphate adenylyltransferase small subunit, chloroplast precursor, putative, expressed seq=cds; coord=4:58954361..58960521:-1; parent_gene=GRMZM2G068506'

'highly similar to (821) AT5G48300 | Symbols: ADG1, APS1 | ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE 1); glucose-1-phosphate adenylyltransferase | chr5:19570326-19572557 FORWARDhighly similar to (828) GLGS_HORVU Glucose-1-phosphate adenylyltransferase small subunit, chloroplast precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPase B) (Alpha-D-glucose-1-phosphate adenyl transferase) Hordeum vulgare (Barley)highly similar to (870) loc_os09g12660 12009.m21978 protein glucose-1-phosphate adenylyltransferase small subunit, chloroplast precursor, putative, expressed seq=cds; coord=2:173380725..173391388:-1; parent_gene=GRMZM2G106213'

'highly similar to (640) AT1G27680 | Symbols: APL2 | APL2 (ADPGLC-PPASE LARGE SUBUNIT); glucose-1-phosphate adenylyltransferase | chr1:9631630-9634450 FORWARDhighly similar to (617) GLGL1_BETVU Glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPase S) (Alpha-D-glucose-1-phosphate adenyl transferase) - Beta vulgaris (Sugar beet)highly similar to (791) loc_os07g13980 12007.m05843 protein glucose-1-phosphate adenylyltransferase large subunit, chloroplast precursor, putative, expressed seq=cds; coord=7:23756173..23767134:-1; parent_gene=GRMZM2G144002'

'highly similar to (845) AT5G48300 | Symbols: ADG1, APS1 | ADG1 (ADP GLUCOSE PYROPHOSPHORYLASE 1); glucose-1-phosphate adenylyltransferase | chr5:19570326-19572557 FORWARDhighly similar to (914) GLGS_HORVU Glucose-1-phosphate adenylyltransferase small subunit, chloroplast precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPase B) (Alpha-D-glucose-1-phosphate adenyl transferase) Hordeum vulgare (Barley)highly similar to (905) loc_os08g25734 12008.m06589 protein glucose-1-phosphate adenylyltransferase small subunit, chloroplast precursor, putative, expressed seq=cds; coord=1:221648603..221653196:1; parent_gene=GRMZM2G163437'

'moderately similar to (441) AT5G19220 | Symbols: ADG2, APL1 | APL1 (ADP GLUCOSE PYROPHOSPHORYLASE LARGE SUBUNIT 1); glucose-1-phosphate adenylyltransferase | chr5:6463931-6466775 REVERSEmoderately similar to (445) GLGL1_WHEAT Glucose-1-phosphate adenylyltransferase large subunit (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPase S) (Alpha-D-glucose-1-phosphate adenyl transferase) (Fragment) - Triticum aestivum (Wheat)moderately similar to (492) loc_os03g52460 12003.m10222 protein glucose-1-phosphate adenylyltransferase large subunit 3, chloroplast precursor, putative, expressed seq=cds; coord=1:273447466..273451914:-1; parent_gene=GRMZM2G391936' 'highly similar to (570) AT1G27680 | Symbols: APL2 | APL2 (ADPGLC-PPASE LARGE SUBUNIT); glucose-1-phosphate adenylyltransferase | chr1:9631630-9634450 FORWARDnearly identical (1011) GLGL1_MAIZE Glucose-1-phosphate adenylyltransferase large subunit 1, chloroplast precursor (EC 2.7.7.27) (ADP-glucose synthase) (ADP-glucose pyrophosphorylase) (AGPase S) (Alpha-D-glucose-1-phosphate adenyl transferase) (Shrunken-2) - Zea mays (Mahighly similar to (798) loc_os01g44220 12001.m150665 protein glucose-1-phosphate adenylyltransferase large subunit 1, chloroplast precursor, putative, expressed seq=cds; coord=3:216414684..216424048:-1; parent_gene=GRMZM2G429899'

'highly similar to (771) AT1G32900 | Symbols: | starch synthase, putative | chr1:11920582-11923506 REVERSEhighly similar to (966) SSG1B_HORVU Granule-bound starch synthase 1b, chloroplast precursor (EC 2.4.1.242) (Granule-bound starch synthase Ib) (Fragment) - Hordeum vulgare (Barley)nearly identical (1030) loc_os07g22930 12007.m29139 protein granule-bound starch synthase 1b, chloroplast precursor, putative, expressed seq=cds; coord=7:34872714..34879973:-1; parent_gene=GRMZM2G008263'

'highly similar to (716) AT1G32900 | Symbols: | starch synthase, putative | chr1:11920582-11923506 REVERSEnearly identical (1076) SSG1_MAIZE Granule-bound starch synthase 1, chloroplast precursor (EC 2.4.1.242) (Granule-bound starch synthase I) (GBSS-I) - Zea mays (Maize)highly similar to (933) loc_os06g04200 12006.m31969 protein granule-bound starch synthase 1, chloroplast precursor, putative, expressed seq=cds; coord=9:23256308..23260236:-1; parent_gene=GRMZM2G024993'

'highly similar to (990) AT4G18240 | Symbols: ATSS4, SSIV, SS4 | ATSS4; transferase, transferring glycosyl groups | chr4:10082221-10087044 FORWARDmoderately similar to (368) SSY3_SOLTU Soluble starch synthase 3, chloroplast precursor (EC 2.4.1.21) (SS III) (Soluble starch synthase III) - Solanum tuberosum (Potato)nearly identical (1358) loc_os05g45720 12005.m083787 protein glycogen synthase, putative, expressed seq=cds; coord=8:125308562..125317107:1; parent_gene=GRMZM2G044744'

'highly similar to (821) AT3G01180 | Symbols: AtSS2 | AtSS2 (starch synthase 2); transferase, transferring glycosyl groups | chr3:62456-65678 REVERSEhighly similar to (962) SSY22_ORYSA Soluble starch synthase 2-2, chloroplast precursor (EC 2.4.1.21) (Soluble starch synthase II-2) - Oryza sativa (Rice)highly similar to (962) loc_os02g51070 12002.m10141 protein soluble starch synthase 2-2, chloroplast precursor, putative, expressed seq=cds; coord=5:206850855..206855627:-1; parent_gene=GRMZM2G105791'

'nearly identical (1130) AT1G11720 | Symbols: ATSS3 | ATSS3 (starch synthase 3); starch synthase/ transferase, transferring glycosyl groups | chr1:3952511-3956840 FORWARDnearly identical (1201) SSY3_SOLTU Soluble starch synthase 3, chloroplast precursor (EC 2.4.1.21) (SS III) (Soluble starch synthase III) - Solanum tuberosum (Potato)nearly identical (1712) loc_os04g53310 12004.m10222 protein soluble starch synthase 3, chloroplast precursor, putative, expressed seq=cds; coord=10:142920487..142929525:1; parent_gene=GRMZM2G121612'

'highly similar to (818) AT3G01180 | Symbols: AtSS2 | AtSS2 (starch synthase 2); transferase, transferring glycosyl groups | chr3:62456-65678 REVERSEnearly identical (1017) SSY21_ORYSA Soluble starch synthase 2-1, chloroplast precursor (EC 2.4.1.21) (Soluble starch synthase II-1) - Oryza sativa (Rice)nearly identical (1017) loc_os10g30156 12010.m05878 protein soluble starch synthase 2-1, chloroplast precursor, putative, expressed seq=cds; coord=5:33050572..33066028:-1; parent_gene=GRMZM2G126988'

'very weakly similar to (82.0) AT5G24300 | Symbols: SSI1, SSI, ATSS1 | SSI1 (SUPPRESSOR OF SALICYLIC ACID INSENSITIVITY 1); starch synthase/ transferase, transferring glycosyl groups | chr5:8266934-8270860 FORWARDweakly similar to (102) SSY1_WHEAT Starch synthase 1, chloroplast precursor (EC 2.4.1.21) (SS I) (Starch synthase I-2) (SS I-2) - Triticum aestivum (Wheat)weakly similar to (104) loc_os06g06560 12006.m05381 protein soluble starch synthase 1, chloroplast precursor, putative, expressed seq=cds; coord=9:17643701..17644469:1; parent_gene=GRMZM2G129451'

'moderately similar to (400) AT5G65685 | Symbols: | soluble glycogen synthase-related | chr5:26273252-26275864 REVERSEweakly similar to (189) SSY3_SOLTU Soluble starch synthase 3, chloroplast precursor (EC 2.4.1.21) (SS III) (Soluble starch synthase III) - Solanum tuberosum (Potato)highly similar to (907) loc_os02g56320 12002.m10655 protein glycogen synthase 2, putative, expressed seq=cds; coord=4:172606253..172677186:-1; parent_gene=GRMZM2G130043' 'nearly identical (1127) AT1G11720 | Symbols: ATSS3 | ATSS3 (starch synthase 3); starch synthase/ transferase, transferring glycosyl groups | chr1:3952511-3956840 FORWARDnearly identical (1156) SSY3_SOLTU Soluble starch synthase 3, chloroplast precursor (EC 2.4.1.21) (SS III) (Soluble starch synthase III) - Solanum tuberosum (Potato)nearly identical (1490) loc_os08g09230 12008.m05058 protein starch synthase III, putative, expressed seq=cds; coord=10:59506710..59518288:1; parent_gene=GRMZM2G141399'

'highly similar to (571) AT3G01180 | Symbols: AtSS2 | AtSS2 (starch synthase 2); transferase, transferring glycosyl groups | chr3:62456-65678 REVERSEhighly similar to (692) SSY22_ORYSA Soluble starch synthase 2-2, chloroplast precursor (EC 2.4.1.21) (Soluble starch synthase II-2) - Oryza sativa (Rice)highly similar to (692) loc_os02g51070 12002.m10141 protein soluble starch synthase 2-2, chloroplast precursor, putative, expressed seq=cds; coord=6:113233723..113238779:1; parent_gene=GRMZM2G348551'

'nearly identical (1184) AT3G20440 | Symbols: EMB2729, BE1 | alpha-amylase/ catalytic/ cation binding | chr3:7123603-7130364 REVERSEmoderately similar to (455) GLGB_SOLTU 1,4-alpha-glucan branching enzyme (EC 2.4.1.18) (Starch branching enzyme) (Q-enzyme) - Solanum tuberosum (Potato)nearly identical (1504) loc_os06g26234 12006.m32257 protein 1,4-alpha-glucan branching enzyme, putative, expressed seq=cds; coord=8:141990059..141994717:1; parent_gene=GRMZM2G005298'

'nearly identical (1214) AT5G03650 | Symbols: SBE2.2 | SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme | chr5:931924-937470 FORWARDnearly identical (1638) GLGB_MAIZE 1,4-alpha-glucan branching enzyme IIB, chloroplast precursor (EC 2.4.1.18) (Starch branching enzyme IIB) (Q-enzyme) - Zea mays (Maize)nearly identical (1366) loc_os02g32660 12002.m33706 protein 1,4-alpha-glucan branching enzyme IIB, chloroplast precursor, putative, expressed seq=cds; coord=5:168451664..168468750:-1; parent_gene=GRMZM2G032628'

'nearly identical (1269) AT5G03650 | Symbols: SBE2.2 | SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme | chr5:931924-937470 FORWARDnearly identical (1303) GLGB_MAIZE 1,4-alpha-glucan branching enzyme IIB, chloroplast precursor (EC 2.4.1.18) (Starch branching enzyme IIB) (Q-enzyme) - Zea mays (Maize)nearly identical (1313) loc_os02g32660 12002.m33706 protein 1,4-alpha-glucan branching enzyme IIB, chloroplast precursor, putative, expressed seq=cds; coord=2:58586007..58596234:1; parent_gene=GRMZM2G073054'

'highly similar to (797) AT5G03650 | Symbols: SBE2.2 | SBE2.2 (starch branching enzyme 2.2); 1,4-alpha-glucan branching enzyme | chr5:931924-937470 FORWARDnearly identical (1352) GLGB_ORYSA 1,4-alpha-glucan branching enzyme, chloroplast precursor (EC 2.4.1.18) (Starch branching enzyme) (Q-enzyme) - Oryza sativa (Rice)nearly identical (1352) loc_os06g51084 12006.m091801 protein 1,4-alpha-glucan branching enzyme, chloroplast precursor, putative, expressed seq=cds; coord=5:63317874..63324803:-1; parent_gene=GRMZM2G088753'

'highly similar to (671) AT1G03310 | Symbols: ATISA2, ISA2, DBE1, BE2 | isoamylase, putative / starch debranching enzyme, putative | chr1:813975-816623 FORWARDnearly identical (1034) loc_os05g32710 12005.m07504 protein isoamylase-type starch debranching enzyme ISO2, putative, expressed seq=cds; coord=6:144564725..144567105:1; parent_gene=GRMZM2G090905'

'nearly identical (1117) AT2G39930 | Symbols: ISA1, ATISA1 | ISA1 (ISOAMYLASE 1); alpha-amylase/ isoamylase | chr2:16666078-16672183 FORWARDnearly identical (1368) loc_os08g40930 12008.m08072 protein isoamylase, putative, expressed seq=cds; coord=4:41369510..41378299:1; parent_gene=GRMZM2G138060'

'nearly identical (1095) AT4G09020 | Symbols: ATISA3, ISA3 | ISA3 (ISOAMYLASE 3); alpha-amylase/ isoamylase | chr4:5784099-5788839 FORWARDhighly similar to (750) loc_os09g29404 12009.m06091 protein glycogen operon protein glgX, putative, expressed seq=cds; coord=7:129101505..129113096:-1; parent_gene=GRMZM2G150796'

'moderately similar to (462) AT4G10260 | Symbols: | pfkB-type carbohydrate kinase family protein | chr4:6371486-6372770 REVERSEhighly similar to (632) SCRK2_MAIZE Fructokinase-2 (EC 2.7.1.4) (ZmFRK2) - Zea mays (Maize)highly similar to (582) loc_os08g02120 12008.m04358 protein fructokinase-2, putative, expressed seq=cds; coord=6:3570233..3573134:1; parent_gene=GRMZM2G051677'

'highly similar to (847) AT4G09510 | Symbols: CINV2 | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr4:6021679-6023310 REVERSEnearly identical (1081) loc_os11g07440 12011.m28745 protein neutral/alkaline invertase, putative, expressed seq=cds; coord=4:204712664..204717434:-1; parent_gene=GRMZM2G007277' 'highly similar to (830) AT1G56560 | Symbols: | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr1:21192593-21194948 FORWARDnearly identical (1028) loc_os01g22900 12001.m42995 protein beta-fructofuranosidase, putative, expressed seq=cds; coord=8:39922110..39926350:1; parent_gene=GRMZM2G022782'

'highly similar to (848) AT5G22510 | Symbols: | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr5:7474974-7477479 REVERSEnearly identical (1092) loc_os02g32730 12002.m08366 protein alkaline/neutral invertase, putative, expressed seq=cds; coord=10:300426..310885:-1; parent_gene=GRMZM2G040843'

'highly similar to (803) AT1G56560 | Symbols: | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr1:21192593-21194948 FORWARDnearly identical (1019) loc_os01g22900 12001.m42995 protein beta-fructofuranosidase, putative, expressed seq=cds; coord=3:60778016..60781883:1; parent_gene=GRMZM2G084694'

'highly similar to (691) AT1G56560 | Symbols: | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr1:21192593-21194948 FORWARDhighly similar to (795) loc_os03g20020 12003.m07415 protein beta-fructofuranosidase, putative, expressed seq=cds; coord=1:51318993..51329214:-1; parent_gene=GRMZM2G084940'

'highly similar to (848) AT4G09510 | Symbols: CINV2 | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr4:6021679-6023310 REVERSEnearly identical (1083) loc_os11g07440 12011.m28745 protein neutral/alkaline invertase, putative, expressed seq=cds; coord=2:135722104..135725916:1; parent_gene=GRMZM2G115451'

'highly similar to (925) AT4G09510 | Symbols: CINV2 | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr4:6021679-6023310 REVERSEnearly identical (1079) loc_os02g34560 12002.m33716 protein neutral/alkaline invertase, putative, expressed seq=cds; coord=5:171276249..171280304:-1; parent_gene=GRMZM2G118737'

'highly similar to (888) AT4G09510 | Symbols: CINV2 | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr4:6021679-6023310 REVERSEnearly identical (1004) loc_os04g35280 12004.m35316 protein neutral/alkaline invertase, putative, expressed seq=cds; coord=4:163445823..163448826:1; parent_gene=GRMZM2G136139'

'highly similar to (924) AT4G09510 | Symbols: CINV2 | beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative | chr4:6021679-6023310 REVERSEnearly identical (1079) loc_os02g34560 12002.m33716 protein neutral/alkaline invertase, putative, expressed seq=cds; coord=4:114693388..114698517:-1; parent_gene=GRMZM2G170842'

'highly similar to (540) AT1G55120 | Symbols: ATFRUCT5 | ATFRUCT5 (BETA-FRUCTOFURANOSIDASE 5); hydrolase, hydrolyzing O-glycosyl compounds / levanase | chr1:20566983-20569165 FORWARDhighly similar to (897) INV6_ORYSA Beta-fructofuranosidase, insoluble isoenzyme 6 precursor (EC 3.2.1.26) (Sucrose hydrolase 6) (Invertase 6) (Cell wall beta-fructosidase 6) (OsCIN6) - Oryza sativa (Rice)highly similar to (897) loc_os04g56920 12004.m10579 protein beta-fructofuranosidase, insoluble isoenzyme 6 precursor, putative, expressed seq=cds; coord=2:3229044..3231455:1; parent_gene=GRMZM2G018692'

'moderately similar to (494) AT1G55120 | Symbols: ATFRUCT5 | ATFRUCT5 (BETA-FRUCTOFURANOSIDASE 5); hydrolase, hydrolyzing O-glycosyl compounds / levanase | chr1:20566983-20569165 FORWARDhighly similar to (704) INV7_ORYSA Beta-fructofuranosidase, insoluble isoenzyme 7 precursor (EC 3.2.1.26) (Sucrose hydrolase 7) (Invertase 7) (Cell wall beta-fructosidase 7) (OsCIN7) - Oryza sativa (Rice)highly similar to (704) loc_os09g08072 12009.m04076 protein beta-fructofuranosidase, insoluble isoenzyme 7 precursor, putative, expressed seq=cds; coord=2:3224667..3227301:1; parent_gene=GRMZM2G018716'

'weakly similar to (119) loc_os02g01590 12002.m100068 protein beta-fructofuranosidase 1 precursor, putative, expressed seq=cds; coord=5:67508656..67509581:1; parent_gene=GRMZM2G089836' 'moderately similar to (442) AT3G52600 | Symbols: AtcwINV2 | AtcwINV2 (Arabidopsis thaliana cell wall invertase 2); hydrolase, hydrolyzing O-glycosyl compounds | chr3:19507080-19508833 REVERSEhighly similar to (702) INV2_ORYSA Beta-fructofuranosidase, insoluble isoenzyme 2 precursor (EC 3.2.1.26) (Sucrose hydrolase 2) (Invertase 2) (Cell wall beta-fructosidase 2) (OsCIN2) - Oryza sativa (Rice)highly similar to (702) loc_os04g33740 12004.m08469 protein beta-fructofuranosidase, insoluble isoenzyme 2 precursor, putative, expressed seq=cds; coord=10:114236242..114239362:-1; parent_gene=GRMZM2G095725'

'highly similar to (601) AT3G52600 | Symbols: AtcwINV2 | AtcwINV2 (Arabidopsis thaliana cell wall invertase 2); hydrolase, hydrolyzing O-glycosyl compounds | chr3:19507080-19508833 REVERSEhighly similar to (908) INV2_ORYSA Beta-fructofuranosidase, insoluble isoenzyme 2 precursor (EC 3.2.1.26) (Sucrose hydrolase 2) (Invertase 2) (Cell wall beta-fructosidase 2) (OsCIN2) - Oryza sativa (Rice)highly similar to (908) loc_os04g33740 12004.m08469 protein beta-fructofuranosidase, insoluble isoenzyme 2 precursor, putative, expressed seq=cds; coord=2:56806976..56810257:1; parent_gene=GRMZM2G119689'

'highly similar to (503) AT1G55120 | Symbols: ATFRUCT5 | ATFRUCT5 (BETA-FRUCTOFURANOSIDASE 5); hydrolase, hydrolyzing O-glycosyl compounds / levanase | chr1:20566983-20569165 FORWARDhighly similar to (833) INV7_ORYSA Beta-fructofuranosidase, insoluble isoenzyme 7 precursor (EC 3.2.1.26) (Sucrose hydrolase 7) (Invertase 7) (Cell wall beta-fructosidase 7) (OsCIN7) - Oryza sativa (Rice)highly similar to (833) loc_os09g08072 12009.m04076 protein beta-fructofuranosidase, insoluble isoenzyme 7 precursor, putative, expressed seq=cds; coord=2:3185602..3188957:1; parent_gene=GRMZM2G119941'

'highly similar to (622) AT3G52600 | Symbols: AtcwINV2 | AtcwINV2 (Arabidopsis thaliana cell wall invertase 2); hydrolase, hydrolyzing O-glycosyl compounds | chr3:19507080-19508833 REVERSEhighly similar to (960) INV3_ORYSA Beta-fructofuranosidase, insoluble isoenzyme 3 precursor (EC 3.2.1.26) (Sucrose hydrolase 3) (Invertase 3) (Cell wall beta-fructosidase 3) (OsCIN3) - Oryza sativa (Rice)highly similar to (960) loc_os04g33720 12004.m08467 protein beta-fructofuranosidase, insoluble isoenzyme 3 precursor, putative, expressed seq=cds; coord=10:114288173..114290565:1; parent_gene=GRMZM2G123633'

'highly similar to (642) AT3G52600 | Symbols: AtcwINV2 | AtcwINV2 (Arabidopsis thaliana cell wall invertase 2); hydrolase, hydrolyzing O-glycosyl compounds | chr3:19507080-19508833 REVERSEnearly identical (1174) INVA_MAIZE Beta-fructofuranosidase, cell wall isozyme precursor (EC 3.2.1.26) (Sucrose hydrolase) (Invertase) - Zea mays (Maize)highly similar to (927) loc_os02g33110 12002.m100224 protein beta-fructofuranosidase, insoluble isoenzyme 1 precursor, putative, expressed seq=cds; coord=5:169454598..169459090:1; parent_gene=GRMZM2G139300'

'highly similar to (642) AT3G52600 | Symbols: AtcwINV2 | AtcwINV2 (Arabidopsis thaliana cell wall invertase 2); hydrolase, hydrolyzing O-glycosyl compounds | chr3:19507080-19508833 REVERSEnearly identical (1174) INVA_MAIZE Beta-fructofuranosidase, cell wall isozyme precursor (EC 3.2.1.26) (Sucrose hydrolase) (Invertase) - Zea mays (Maize)highly similar to (927) loc_os02g33110 12002.m100224 protein beta-fructofuranosidase, insoluble isoenzyme 1 precursor, putative, expressed seq=cds; coord=5:169454598..169459090:1; parent_gene=GRMZM2G139300'

'highly similar to (552) AT1G55120 | Symbols: ATFRUCT5 | ATFRUCT5 (BETA-FRUCTOFURANOSIDASE 5); hydrolase, hydrolyzing O-glycosyl compounds / levanase | chr1:20566983-20569165 FORWARDhighly similar to (958) INV4_ORYSA Beta-fructofuranosidase, insoluble isoenzyme 4 precursor (EC 3.2.1.26) (Sucrose hydrolase 4) (Invertase 4) (Cell wall beta-fructosidase 4) (OsCIN4) - Oryza sativa (Rice)highly similar to (958) loc_os01g73580 12001.m13385 protein beta-fructofuranosidase, insoluble isoenzyme 4 precursor, putative, expressed seq=cds; coord=3:145729813..145733247:-1; parent_gene=GRMZM2G174249'

'highly similar to (716) AT1G62660 | Symbols: | beta-fructosidase (BFRUCT3) / beta-fructofuranosidase / invertase, vacuolar | chr1:23199949-23203515 FORWARDnearly identical (1191) INV1_MAIZE Beta-fructofuranosidase 1 precursor (EC 3.2.1.26) (Sucrose 1) (Invertase 1) - Zea mays (Maize)highly similar to (956) loc_os04g45290 12004.m35180 protein beta-fructofuranosidase 1 precursor, putative, expressed seq=cds; coord=2:22880766..22885337:-1; parent_gene=GRMZM2G394450'

'highly similar to (507) AT1G12240 | Symbols: ATBETAFRUCT4, VAC-INV | ATBETAFRUCT4; beta-fructofuranosidase/ hydrolase, hydrolyzing O-glycosyl compounds | chr1:4153699-4157457 FORWARDhighly similar to (569) INV1_MAIZE Beta-fructofuranosidase 1 precursor (EC 3.2.1.26) (Sucrose 1) (Invertase 1) - Zea mays (Maize)highly similar to (739) loc_os02g01590 12002.m100068 protein beta-fructofuranosidase 1 precursor, putative, expressed seq=cds; coord=4:240446489..240449003:-1; parent_gene=GRMZM2G463871' 'moderately similar to (427) AT1G50460 | Symbols: HKL1 | HKL1 (HEXOKINASE-LIKE 1); ATP binding / fructokinase/ glucokinase/ hexokinase | chr1:18694031-18697429 FORWARDhighly similar to (649) HXK10_ORYSA Hexokinase-10 (EC 2.7.1.1) (Hexokinase-7) - Oryza sativa (Rice)highly similar to (649) loc_os05g31110 12005.m07345 protein hexokinase-1, putative, expressed seq=cds; coord=6:135959554..135964731:1; parent_gene=GRMZM2G046686'

'moderately similar to (481) AT2G19860 | Symbols: ATHXK2, HXK2 | HXK2 (HEXOKINASE 2); ATP binding / fructokinase/ glucokinase/ hexokinase | chr2:8571949-8573762 FORWARDhighly similar to (627) HXK7_ORYSA Hexokinase-7 (EC 2.7.1.1) (Hexokinase-6) - Oryza sativa (Rice)highly similar to (627) loc_os05g09500 12005.m27732 protein hexokinase-1, putative, expressed seq=cds; coord=6:129979107..129982019:1; parent_gene=GRMZM2G051806'

'highly similar to (589) AT4G29130 | Symbols: ATHXK1, GIN2, HXK1 | HXK1 (HEXOKINASE 1); ATP binding / fructokinase/ glucokinase/ hexokinase | chr4:14352338-14354865 REVERSEhighly similar to (761) HXK5_ORYSA Hexokinase-5 (EC 2.7.1.1) (Hexokinase I) - Oryza sativa (Rice)highly similar to (761) loc_os05g44760 12005.m08601 protein hexokinase-2, putative, expressed seq=cds; coord=8:124652438..124657923:1; parent_gene=GRMZM2G058745'

'highly similar to (535) AT1G50460 | Symbols: HKL1 | HKL1 (HEXOKINASE-LIKE 1); ATP binding / fructokinase/ glucokinase/ hexokinase | chr1:18694031-18697429 FORWARDhighly similar to (735) HXK3_ORYSA Hexokinase-3 (EC 2.7.1.1) (Hexokinase-8) - Oryza sativa (Rice)highly similar to (735) loc_os01g71320 12001.m13175 protein hexokinase-1, putative, expressed seq=cds; coord=3:152175317..152181802:1; parent_gene=GRMZM2G068913'

'highly similar to (506) AT4G29130 | Symbols: ATHXK1, GIN2, HXK1 | HXK1 (HEXOKINASE 1); ATP binding / fructokinase/ glucokinase/ hexokinase | chr4:14352338-14354865 REVERSEhighly similar to (672) HXK8_ORYSA Hexokinase-8 (EC 2.7.1.1) (Hexokinase-4) - Oryza sativa (Rice)highly similar to (672) loc_os01g09460 12001.m07571 protein hexokinase-1, putative, expressed seq=cds; coord=3:7078308..7082094:1; parent_gene=GRMZM2G104081'

'highly similar to (582) AT4G29130 | Symbols: ATHXK1, GIN2, HXK1 | HXK1 (HEXOKINASE 1); ATP binding / fructokinase/ glucokinase/ hexokinase | chr4:14352338-14354865 REVERSEhighly similar to (657) HXK9_ORYSA Hexokinase-9 (EC 2.7.1.1) (Hexokinase-5) - Oryza sativa (Rice)highly similar to (657) loc_os01g52450 12001.m11419 protein hexokinase-2, putative, expressed seq=cds; coord=3:201789514..201799556:-1; parent_gene=GRMZM2G171373'

'highly similar to (613) AT4G29130 | Symbols: ATHXK1, GIN2, HXK1 | HXK1 (HEXOKINASE 1); ATP binding / fructokinase/ glucokinase/ hexokinase | chr4:14352338-14354865 REVERSEhighly similar to (799) HXK5_ORYSA Hexokinase-5 (EC 2.7.1.1) (Hexokinase I) - Oryza sativa (Rice)highly similar to (799) loc_os05g44760 12005.m08601 protein hexokinase-2, putative, expressed seq=cds; coord=6:160237817..160245075:-1; parent_gene=GRMZM2G432801'

'highly similar to (535) AT1G50460 | Symbols: HKL1 | HKL1 (HEXOKINASE-LIKE 1); ATP binding / fructokinase/ glucokinase/ hexokinase | chr1:18694031-18697429 FORWARDhighly similar to (753) HXK3_ORYSA Hexokinase-3 (EC 2.7.1.1) (Hexokinase-8) - Oryza sativa (Rice)highly similar to (753) loc_os01g71320 12001.m13175 protein hexokinase-1, putative, expressed seq=cds; coord=8:159186574..159193136:1; parent_gene=GRMZM2G467069'

'nearly identical (1001) AT1G73370 | Symbols: SUS6, ATSUS6 | SUS6 (SUCROSE SYNTHASE 6); UDP-glycosyltransferase/ sucrose synthase | chr1:27584533-27588326 REVERSEhighly similar to (816) SUS2_PEA Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 2) - Pisum sativum (Garden pea)nearly identical (1244) loc_os02g58480 12002.m10869 protein sucrose synthase 2, putative, expressed seq=cds; coord=4:168743488..168746616:-1; parent_gene=GRMZM2G045171'

'nearly identical (1146) AT1G73370 | Symbols: SUS6, ATSUS6 | SUS6 (SUCROSE SYNTHASE 6); UDP-glycosyltransferase/ sucrose synthase | chr1:27584533-27588326 REVERSEhighly similar to (934) SUS2_PEA Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 2) - Pisum sativum (Garden pea)nearly identical (1536) loc_os04g24430 12004.m07574 protein sucrose synthase 2, putative, expressed seq=cds; coord=5:64769600..64773966:-1; parent_gene=GRMZM2G060659'

'nearly identical (1215) AT3G43190 | Symbols: SUS4, ATSUS4 | SUS4; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups | chr3:15179204-15182577 REVERSEnearly identical (1559) SUS1_MAIZE Sucrose synthase 1 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 1) (Shrunken-1) - Zea mays (Maize)nearly identical (1492) loc_os06g09450 12006.m091637 protein sucrose synthase 1, putative, expressed seq=cds; coord=9:11496011..11502772:1; parent_gene=GRMZM2G089713' 'nearly identical (1233) AT3G43190 | Symbols: SUS4, ATSUS4 | SUS4; UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups | chr3:15179204-15182577 REVERSEnearly identical (1661) SUS2_MAIZE Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 2) - Zea mays (Maize)nearly identical (1587) loc_os03g28330 12003.m34880 protein sucrose synthase 2, putative, expressed seq=cds; coord=9:122220190..122226863:-1; parent_gene=GRMZM2G152908'

'highly similar to (677) AT4G02280 | Symbols: SUS3, ATSUS3 | SUS3 (sucrose synthase 3); UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups | chr4:995166-998719 FORWARDhighly similar to (669) SUS2_PEA Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 2) - Pisum sativum (Garden pea)highly similar to (741) loc_os03g22120 12003.m34861 protein sucrose synthase 2, putative, expressed seq=cds; coord=1:56756360..56761192:-1; parent_gene=GRMZM2G311182'

'highly similar to (733) AT4G02280 | Symbols: SUS3, ATSUS3 | SUS3 (sucrose synthase 3); UDP-glycosyltransferase/ sucrose synthase/ transferase, transferring glycosyl groups | chr4:995166-998719 FORWARDhighly similar to (726) SUS2_PEA Sucrose synthase 2 (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase 2) - Pisum sativum (Garden pea)highly similar to (809) loc_os03g22120 12003.m34861 protein sucrose synthase 2, putative, expressed seq=cds; coord=1:56785051..56787917:-1; parent_gene=GRMZM2G318780'

'highly similar to (694) AT4G17090 | Symbols: CT-BMY, BAM3, BMY8 | CT-BMY (CHLOROPLAST BETA-AMYLASE); beta-amylase | chr4:9605266-9607250 REVERSEmoderately similar to (473) AMYB_MEDSA Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) - Medicago sativa (Alfalfa)highly similar to (814) loc_os10g41550 12010.m06918 protein beta-amylase, putative, expressed seq=cds; coord=1:95188932..95192571:-1; parent_gene=GRMZM2G007939'

'highly similar to (650) AT3G23920 | Symbols: BAM1, BMY7, TR-BAMY | BAM1 (BETA-AMYLASE 1); beta-amylase | chr3:8641722-8644199 FORWARDmoderately similar to (421) AMYB_HORVU Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) - Hordeum vulgare (Barley)highly similar to (826) loc_os10g32810 12010.m06117 protein beta-amylase, putative, expressed seq=cds; coord=5:30775043..30777461:-1; parent_gene=GRMZM2G025833'

'weakly similar to (101) AT5G18670 | Symbols: BMY3, BAM9 | BMY3; beta-amylase/ catalytic/ cation binding | chr5:6226138-6227999 FORWARDweakly similar to (169) loc_os03g22790 12003.m07677 protein beta-amylase, putative, expressed seq=cds; coord=10:117709760..117710623:-1; parent_gene=GRMZM2G033339'

'nearly identical (1223) AT5G63840 | Symbols: RSW3 | RSW3 (RADIAL SWELLING 3); glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds | chr5:25545056-25548922 FORWARDmoderately similar to (341) AGLU_BETVU Alpha-glucosidase precursor (EC 3.2.1.20) (Maltase) - Beta vulgaris (Sugar beet)nearly identical (1631) loc_os03g11720 12003.m06624 protein neutral alpha-glucosidase AB precursor, putative, expressed seq=cds; coord=9:146533570..146540061:-1; parent_gene=GRMZM2G034575'

'highly similar to (692) AT4G17090 | Symbols: CT-BMY, BAM3, BMY8 | CT-BMY (CHLOROPLAST BETA-AMYLASE); beta-amylase | chr4:9605266-9607250 REVERSEmoderately similar to (467) AMYB_MEDSA Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) - Medicago sativa (Alfalfa)highly similar to (785) loc_os10g41550 12010.m06918 protein beta-amylase, putative, expressed seq=cds; coord=9:114176716..114179596:1; parent_gene=GRMZM2G035749'

'highly similar to (655) AT4G15210 | Symbols: ATBETA-AMY, AT-BETA-AMY, RAM1 | BAM5 (BETA-AMYLASE 5); beta-amylase | chr4:8666852-8669357 REVERSEnearly identical (1011) AMYB_MAIZE Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) - Zea mays (Maize)highly similar to (894) loc_os07g35940 12007.m07847 protein beta-amylase, putative seq=cds; coord=7:155357370..155360570:1; parent_gene=GRMZM2G058310'

'moderately similar to (463) AT4G25000 | Symbols: ATAMY1, AMY1 | AMY1 (ALPHA-AMYLASE-LIKE); alpha-amylase | chr4:12852109-12853825 REVERSEhighly similar to (748) AMY3D_ORYSA Alpha-amylase isozyme 3D precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) - Oryza sativa (Rice)highly similar to (748) loc_os08g36910 12008.m26515 protein alpha-amylase isozyme 3D precursor, putative, expressed seq=cds; coord=1:199630232..199632219:1; parent_gene=GRMZM2G070172' 'highly similar to (509) AT4G25000 | Symbols: ATAMY1, AMY1 | AMY1 (ALPHA-AMYLASE-LIKE); alpha-amylase | chr4:12852109-12853825 REVERSEhighly similar to (756) AMY1_HORVU Alpha-amylase type A isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (AMY1) (Low pI alpha-amylase) - Hordeum vulgare (Barley)highly similar to (743) loc_os06g49970 12006.m31931 protein alpha-amylase isozyme C2 precursor, putative, expressed seq=cds; coord=7:105219462..105221560:-1; parent_gene=GRMZM2G074781'

'moderately similar to (407) AT4G17090 | Symbols: CT-BMY, BAM3, BMY8 | CT-BMY (CHLOROPLAST BETA-AMYLASE); beta-amylase | chr4:9605266-9607250 REVERSEmoderately similar to (302) AMYB_VIGUN Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) - Vigna unguiculata (Cowpea)highly similar to (778) loc_os01g13550 12001.m07964 protein beta-amylase, putative, expressed seq=cds; coord=8:29211106..29216116:-1; parent_gene=GRMZM2G077202'

'moderately similar to (237) AT4G25000 | Symbols: ATAMY1, AMY1 | AMY1 (ALPHA-AMYLASE-LIKE); alpha-amylase | chr4:12852109-12853825 REVERSEmoderately similar to (360) AMY1_HORVU Alpha-amylase type A isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (AMY1) (Low pI alpha-amylase) - Hordeum vulgare (Barley)moderately similar to (355) loc_os06g49970 12006.m31931 protein alpha-amylase isozyme C2 precursor, putative, expressed seq=cds; coord=7:105210274..105211672:1; parent_gene=GRMZM2G081502'

'moderately similar to (330) AT5G18670 | Symbols: BMY3, BAM9 | BMY3; beta-amylase/ catalytic/ cation binding | chr5:6226138-6227999 FORWARDweakly similar to (182) AMYB_MAIZE Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) - Zea mays (Maize)highly similar to (600) loc_os03g22790 12003.m07677 protein beta-amylase, putative, expressed seq=cds; coord=1:60087923..60089930:1; parent_gene=GRMZM2G082034'

'highly similar to (513) AT4G25000 | Symbols: ATAMY1, AMY1 | AMY1 (ALPHA-AMYLASE-LIKE); alpha-amylase | chr4:12852109-12853825 REVERSEhighly similar to (747) AMY1_ORYSA Alpha-amylase precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (Isozyme 1B) - Oryza sativa (Rice)highly similar to (748) loc_os02g52700 12002.m10300 protein alpha-amylase precursor, putative, expressed seq=cds; coord=5:209898977..209901053:-1; parent_gene=GRMZM2G103055'

'highly similar to (509) AT4G25000 | Symbols: ATAMY1, AMY1 | AMY1 (ALPHA-AMYLASE-LIKE); alpha-amylase | chr4:12852109-12853825 REVERSEhighly similar to (808) AMY3B_ORYSA Alpha-amylase isozyme 3B precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) - Oryza sativa (Rice)highly similar to (808) loc_os09g28420 12009.m05993 protein alpha-amylase isozyme 3B precursor, putative, expressed seq=cds; coord=2:186265525..186267387:1; parent_gene=GRMZM2G138468'

'nearly identical (1237) AT5G63840 | Symbols: RSW3 | RSW3 (RADIAL SWELLING 3); glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds | chr5:25545056-25548922 FORWARDmoderately similar to (336) AGLU_ORYSA Probable alpha-glucosidase Os06g0675700 precursor (EC 3.2.1.20) (Maltase) - Oryza sativa (Rice)nearly identical (1646) loc_os03g11720 12003.m06624 protein neutral alpha-glucosidase AB precursor, putative, expressed seq=cds; coord=1:27094498..27098727:1; parent_gene=GRMZM2G163129'

'moderately similar to (410) AT3G23920 | Symbols: BAM1, BMY7, TR-BAMY | BAM1 (BETA-AMYLASE 1); beta-amylase | chr3:8641722-8644199 FORWARDmoderately similar to (305) AMYB_VIGUN Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) - Vigna unguiculata (Cowpea)highly similar to (770) loc_os01g13550 12001.m07964 protein beta-amylase, putative, expressed seq=cds; coord=3:1536020..1540295:1; parent_gene=GRMZM2G175218'

'moderately similar to (377) AT5G18670 | Symbols: BMY3, BAM9 | BMY3; beta-amylase/ catalytic/ cation binding | chr5:6226138-6227999 FORWARDmoderately similar to (257) AMYB_WHEAT Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) - Triticum aestivum (Wheat)highly similar to (728) loc_os07g47120 12007.m08929 protein beta-amylase, putative, expressed seq=cds; coord=7:171860442..171862785:-1; parent_gene=GRMZM2G181284'

'highly similar to (629) AT1G76130 | Symbols: ATAMY2, AMY2 | AMY2 (ALPHA-AMYLASE-LIKE 2); alpha-amylase/ calcium ion binding / catalytic/ cation binding | chr1:28561647-28563914 FORWARDmoderately similar to (392) AMY2_HORVU Alpha-amylase type B isozyme precursor (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase) (AMY2-2) (High pI alpha-amylase) - Hordeum vulgare (Barley)highly similar to (793) loc_os04g33040 12004.m08400 protein alpha-amylase type B isozyme precursor, putative, expressed seq=cds; coord=2:60765875..60770124:-1; parent_gene=GRMZM2G422938' 'highly similar to (678) AT3G23920 | Symbols: BAM1, BMY7, TR-BAMY | BAM1 (BETA-AMYLASE 1); beta-amylase | chr3:8641722-8644199 FORWARDmoderately similar to (434) AMYB_SOYBN Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) - Glycine max (Soybean)highly similar to (850) loc_os03g04770 12003.m06004 protein beta-amylase, putative, expressed seq=cds; coord=1:9057041..9060022:1; parent_gene=GRMZM2G450125'

'weakly similar to (117) AT5G18670 | Symbols: BMY3, BAM9 | BMY3; beta-amylase/ catalytic/ cation binding | chr5:6226138-6227999 FORWARDweakly similar to (186) loc_os03g22790 12003.m07677 protein beta-amylase, putative, expressed seq=cds; coord=2:19253013..19255143:-1; parent_gene=GRMZM2G462258'

'highly similar to (664) AT5G45300 | Symbols: BMY2, BAM8 | BMY2 (BETA-AMYLASE 2); beta-amylase/ catalytic/ cation binding | chr5:18353636-18356696 FORWARDmoderately similar to (368) AMYB_SOYBN Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) - Glycine max (Soybean)highly similar to (956) loc_os02g03690 12002.m05719 protein beta-amylase, putative, expressed seq=cds; coord=4:239081202..239093194:1; parent_gene=GRMZM2G069486'

'highly similar to (726) AT4G00490 | Symbols: BAM2, BMY9 | BAM2 (BETA-AMYLASE 2); beta-amylase | chr4:222422-224862 FORWARDmoderately similar to (461) AMYB_SOYBN Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) - Glycine max (Soybean)highly similar to (879) loc_os09g39570 12009.m06895 protein beta-amylase, putative, expressed seq=cds; coord=7:62301852..62305837:1; parent_gene=GRMZM2G446515'

'nearly identical (1326) AT3G29320 | Symbols: | glucan phosphorylase, putative | chr3:11252871-11257587 FORWARDnearly identical (1356) PHSL_IPOBA Alpha-1,4 glucan phosphorylase L isozyme, chloroplast precursor (EC 2.4.1.1) (Starch phosphorylase L) - Ipomoea batatas (Sweet potato) (Batate)nearly identical (1427) loc_os03g55090 12003.m10424 protein alpha-1,4 glucan phosphorylase, L isozyme, chloroplast precursor, putative, expressed seq=cds; coord=1:278183921..278192926:-1; parent_gene=GRMZM2G074158'

'nearly identical (1329) AT3G46970 | Symbols: ATPHS2, PHS2 | PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups | chr3:17301625-17306111 REVERSEnearly identical (1491) PHSH_WHEAT Alpha-glucan phosphorylase, H isozyme (EC 2.4.1.1) (Starch phosphorylase H) - Triticum aestivum (Wheat)nearly identical (1523) loc_os01g63270 12001.m43279 protein alpha-glucan phosphorylase, H isozyme, putative, expressed seq=cds; coord=3:178982016..178990918:1; parent_gene=GRMZM2G085577'

'highly similar to (743) AT5G64860 | Symbols: DPE1 | DPE1 (DISPROPORTIONATING ENZYME); 4-alpha-glucanotransferase/ catalytic/ cation binding | chr5:25925373-25928788 REVERSEhighly similar to (743) DPEP_SOLTU 4-alpha-glucanotransferase, chloroplast precursor (EC 2.4.1.25) (Amylomaltase) (Disproportionating enzyme) (D-enzyme) - Solanum tuberosum (Potato)highly similar to (944) loc_os07g43390 12007.m08567 protein 4-alpha-glucanotransferase, chloroplast precursor, putative, expressed seq=cds; coord=7:167230471..167241954:1; parent_gene=GRMZM2G013811'

'highly similar to (576) AT2G36460 | Symbols: | fructose-bisphosphate aldolase, putative | chr2:15296929-15297732 REVERSEhighly similar to (708) ALF_MAIZE Fructose-bisphosphate aldolase, cytoplasmic isozyme (EC 4.1.2.13) - Zea mays (Maize)highly similar to (669) loc_os05g33380 12005.m07570 protein fructose-bisphosphate aldolase cytoplasmic isozyme, putative, expressed seq=cds; coord=3:165722970..165725581:1; parent_gene=GRMZM2G057823'

'highly similar to (574) AT2G36460 | Symbols: | fructose-bisphosphate aldolase, putative | chr2:15296929-15297732 REVERSEhighly similar to (700) ALF_MAIZE Fructose-bisphosphate aldolase, cytoplasmic isozyme (EC 4.1.2.13) - Zea mays (Maize)highly similar to (667) loc_os05g33380 12005.m07570 protein fructose-bisphosphate aldolase cytoplasmic isozyme, putative, expressed seq=cds; coord=8:163307256..163309969:-1; parent_gene=GRMZM2G066024'

'highly similar to (955) AT3G08590 | Symbols: | 2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative | chr3:2608683-2611237 REVERSEnearly identical (1085) PMGI_MAIZE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (PGAM-I) - Zea mays (Maize)nearly identical (1033) loc_os01g60190 12001.m42741 protein 2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative, expressed seq=cds; coord=3:185834707..185839417:-1; parent_gene=GRMZM2G003385' 'highly similar to (574) AT1G09780 | Symbols: | 2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative | chr1:3165550-3167812 REVERSEhighly similar to (598) PMGI_RICCO 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (PGAM-I) - Ricinus communis (Castor bean)highly similar to (645) loc_os03g21260 12003.m07532 protein 2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative seq=cds; coord=1:54533483..54536342:1; parent_gene=GRMZM2G050077'

'highly similar to (716) AT3G30841 | Symbols: | 2,3-biphosphoglycerate-independent phosphoglycerate mutase-related / phosphoglyceromutase-related | chr3:12591595-12593401 FORWARDhighly similar to (782) loc_os12g35040 12012.m07297 protein 2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative, expressed seq=cds; coord=10:25554428..25557522:-1; parent_gene=GRMZM2G054250'

'moderately similar to (300) AT3G08590 | Symbols: | 2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative | chr3:2608683-2611237 REVERSEmoderately similar to (343) PMGI_MAIZE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (PGAM-I) - Zea mays (Maize)moderately similar to (312) loc_os01g60190 12001.m42741 protein 2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative, expressed seq=cds; coord=6:123671813..123676490:1; parent_gene=GRMZM2G146778'

'moderately similar to (412) AT3G08590 | Symbols: | 2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative | chr3:2608683-2611237 REVERSEmoderately similar to (464) PMGI_MAIZE 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) (BPG-independent PGAM) (PGAM-I) - Zea mays (Maize)moderately similar to (430) loc_os01g60190 12001.m42741 protein 2,3-bisphosphoglycerate-independent phosphoglycerate mutase, putative, expressed seq=cds; coord=3:15212255..15222203:-1; parent_gene=GRMZM2G334628'

'highly similar to (785) AT2G36530 | Symbols: LOS2 | LOS2; copper ion binding / phosphopyruvate hydratase | chr2:15321081-15323786 REVERSEhighly similar to (879) ENO2_MAIZE Enolase 2 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 2) (2-phospho-D-glycerate hydro-lyase 2) - Zea mays (Maize)highly similar to (850) loc_os10g08550 12010.m065231 protein enolase, putative, expressed seq=cds; coord=1:125074232..125080812:-1; parent_gene=GRMZM2G048371'

'highly similar to (765) AT2G36530 | Symbols: LOS2 | LOS2; copper ion binding / phosphopyruvate hydratase | chr2:15321081-15323786 REVERSEhighly similar to (882) ENO1_MAIZE Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1) - Zea mays (Maize)highly similar to (846) loc_os06g04510 12006.m05181 protein enolase 1, putative, expressed seq=cds; coord=9:22100864..22105552:1; parent_gene=GRMZM2G064302'

'highly similar to (607) AT2G29560 | Symbols: | enolase, putative | chr2:12646635-12649694 FORWARDmoderately similar to (447) ENO_CHLRE Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) (Fragment) - Chlamydomonas reinhardtiihighly similar to (806) loc_os03g15950 12003.m07032 protein enolase, putative, expressed seq=cds; coord=9:140431817..140437712:1; parent_gene=GRMZM2G131539'

'highly similar to (612) AT2G36530 | Symbols: LOS2 | LOS2; copper ion binding / phosphopyruvate hydratase | chr2:15321081-15323786 REVERSEhighly similar to (660) ENO1_MAIZE Enolase 1 (EC 4.2.1.11) (2-phosphoglycerate dehydratase 1) (2-phospho-D-glycerate hydro-lyase 1) - Zea mays (Maize)highly similar to (655) loc_os06g04510 12006.m05181 protein enolase 1, putative, expressed seq=cds; coord=6:68232049..68235900:-1; parent_gene=GRMZM2G446253'

'moderately similar to (271) AT2G29560 | Symbols: | enolase, putative | chr2:12646635-12649694 FORWARDweakly similar to (171) ENO_MESCR Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate hydro-lyase) - Mesembryanthemum crystallinum (Common ice plant)moderately similar to (353) loc_os03g15950 12003.m07032 protein enolase, putative, expressed seq=cds; coord=1:38632794..38636740:-1; parent_gene=GRMZM2G481529'

'highly similar to (798) AT5G56350 | Symbols: | pyruvate kinase, putative | chr5:22820254-22822529 REVERSEhighly similar to (815) KPYC_TOBAC Pyruvate kinase, cytosolic isozyme (EC 2.7.1.40) (PK) - Nicotiana tabacum (Common tobacco)highly similar to (909) loc_os01g16960 12001.m08292 protein pyruvate kinase, cytosolic isozyme, putative, expressed seq=cds; coord=3:44223365..44228905:-1; parent_gene=GRMZM2G003883' 'highly similar to (913) AT3G52990 | Symbols: | pyruvate kinase, putative | chr3:19649336-19652237 FORWARDmoderately similar to (376) KPYC_TOBAC Pyruvate kinase, cytosolic isozyme (EC 2.7.1.40) (PK) - Nicotiana tabacum (Common tobacco)highly similar to (988) loc_os11g05110 12011.m079911 protein pyruvate kinase, cytosolic isozyme, putative, expressed seq=cds; coord=10:4694280..4699187:-1; parent_gene=GRMZM2G004534'

'highly similar to (870) AT5G08570 | Symbols: | pyruvate kinase, putative | chr5:2778433-2780300 FORWARDhighly similar to (875) KPYC_SOYBN Pyruvate kinase, cytosolic isozyme (EC 2.7.1.40) (PK) - Glycine max (Soybean)highly similar to (961) loc_os04g58110 12004.m10693 protein pyruvate kinase, cytosolic isozyme, putative, expressed seq=cds; coord=10:148228962..148233420:1; parent_gene=GRMZM2G008714'

'highly similar to (904) AT3G52990 | Symbols: | pyruvate kinase, putative | chr3:19649336-19652237 FORWARDmoderately similar to (376) KPYC_TOBAC Pyruvate kinase, cytosolic isozyme (EC 2.7.1.40) (PK) - Nicotiana tabacum (Common tobacco)highly similar to (979) loc_os11g05110 12011.m079911 protein pyruvate kinase, cytosolic isozyme, putative, expressed seq=cds; coord=4:187884467..187890415:-1; parent_gene=GRMZM2G119175'

'highly similar to (632) AT2G36580 | Symbols: | pyruvate kinase, putative | chr2:15339253-15342781 FORWARDmoderately similar to (322) KPYC_SOLTU Pyruvate kinase, cytosolic isozyme (EC 2.7.1.40) (PK) - Solanum tuberosum (Potato)highly similar to (863) loc_os11g10980 12011.m05291 protein pyruvate kinase, cytosolic isozyme, putative, expressed seq=cds; coord=4:12974975..12984124:-1; parent_gene=GRMZM2G124593'

'highly similar to (863) AT5G08570 | Symbols: | pyruvate kinase, putative | chr5:2778433-2780300 FORWARDhighly similar to (876) KPYC_SOYBN Pyruvate kinase, cytosolic isozyme (EC 2.7.1.40) (PK) - Glycine max (Soybean)highly similar to (958) loc_os04g58110 12004.m10693 protein pyruvate kinase, cytosolic isozyme, putative, expressed seq=cds; coord=2:1624189..1628276:1; parent_gene=GRMZM2G150098'

'highly similar to (993) AT1G23190 | Symbols: | phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative | chr1:8219946-8224186 FORWARDnearly identical (1160) PGMC2_MAIZE Phosphoglucomutase, cytoplasmic 2 (EC 5.4.2.2) (Glucose phosphomutase 2) (PGM 2) - Zea mays (Maize)nearly identical (1113) loc_os03g50480 12003.m35578 protein phosphoglucomutase, cytoplasmic 2, putative, expressed seq=cds; coord=1:267887401..267893956:1; parent_gene=GRMZM2G023289'

'highly similar to (971) AT1G23190 | Symbols: | phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative | chr1:8219946-8224186 FORWARDnearly identical (1135) PGMC1_MAIZE Phosphoglucomutase, cytoplasmic 1 (EC 5.4.2.2) (Glucose phosphomutase 1) (PGM 1) - Zea mays (Maize)nearly identical (1088) loc_os03g50480 12003.m35578 protein phosphoglucomutase, cytoplasmic 2, putative, expressed seq=cds; coord=5:10855539..10861668:-1; parent_gene=GRMZM2G109383'

'weakly similar to (108) AT5G42740 | Symbols: | glucose-6-phosphate isomerase, cytosolic (PGIC) | chr5:17136080-17140622 FORWARDweakly similar to (133) G6PI_MAIZE Glucose-6-phosphate isomerase, cytosolic (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) - Zea mays (Maize)weakly similar to (125) loc_os06g14510 12006.m091669 protein glucose-6-phosphate isomerase, cytosolic B, putative, expressed seq=cds; coord=5:55400694..55403816:-1; parent_gene=GRMZM2G162078'

'nearly identical (1012) AT1G76550 | Symbols: | pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative | chr1:28722900-28726929 REVERSEnearly identical (1024) PFPA_RICCO Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Ricinus communis (Castor bean)nearly identical (1141) loc_os02g48360 12002.m100340 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit, putative, expressed seq=cds; coord=4:162075480..162081835:-1; parent_gene=GRMZM2G042502' 'highly similar to (892) AT1G12000 | Symbols: | pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative | chr1:4050159-4053727 REVERSEhighly similar to (903) PFPB_RICCO Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Ricinus communis (Castor bean)highly similar to (988) loc_os06g13810 12006.m31864 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase beta subunit, putative, expressed seq=cds; coord=6:115191842..115198242:-1; parent_gene=GRMZM2G059151'

'nearly identical (1004) AT1G76550 | Symbols: | pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative | chr1:28722900-28726929 REVERSEnearly identical (1025) PFPA_RICCO Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Ricinus communis (Castor bean)nearly identical (1138) loc_os02g48360 12002.m100340 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit, putative, expressed seq=cds; coord=5:202565079..202572251:-1; parent_gene=GRMZM2G123371'

'highly similar to (503) AT1G12000 | Symbols: | pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative | chr1:4050159-4053727 REVERSEhighly similar to (512) PFPB_RICCO Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Ricinus communis (Castor bean)highly similar to (551) loc_os06g13810 12006.m31864 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase beta subunit, putative, expressed seq=cds; coord=9:1634017..1638812:-1; parent_gene=GRMZM2G143862'

'highly similar to (528) AT1G76550 | Symbols: | pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative | chr1:28722900-28726929 REVERSEhighly similar to (545) PFPA_RICCO Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Ricinus communis (Castor bean)highly similar to (588) loc_os06g22060 12006.m091682 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit, putative, expressed seq=cds; coord=9:45354730..45357776:1; parent_gene=GRMZM2G314094'

'weakly similar to (135) AT1G20950 | Symbols: | pyrophosphate--fructose-6-phosphate 1-phosphotransferase-related / pyrophosphate-dependent 6-phosphofructose-1-kinase-related | chr1:7297467-7301336 REVERSEweakly similar to (137) PFPA_SOLTU Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Solanum tuberosum (Potato)weakly similar to (144) loc_os06g22060 12006.m091682 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit, putative, expressed seq=cds; coord=8:20537432..20541080:-1; parent_gene=GRMZM2G402211'

'highly similar to (667) AT1G76550 | Symbols: | pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative | chr1:28722900-28726929 REVERSEhighly similar to (699) PFPA_RICCO Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Ricinus communis (Castor bean)highly similar to (805) loc_os08g25720 12008.m26670 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit, putative, expressed seq=cds; coord=7:82320997..82325866:1; parent_gene=GRMZM2G409131'

'weakly similar to (101) AT1G76550 | Symbols: | pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative | chr1:28722900-28726929 REVERSEweakly similar to (101) PFPA_SOLTU Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Solanum tuberosum (Potato)weakly similar to (103) loc_os06g22060 12006.m091682 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit, putative, expressed seq=cds; coord=4:91184550..91192853:1; parent_gene=GRMZM2G413226' 'highly similar to (815) AT1G76550 | Symbols: | pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative | chr1:28722900-28726929 REVERSEhighly similar to (858) PFPA_RICCO Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Ricinus communis (Castor bean)nearly identical (1137) loc_os08g25720 12008.m26670 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit, putative, expressed seq=cds; coord=1:221739264..221743951:-1; parent_gene=GRMZM2G450163'

'very weakly similar to (84.7) loc_os06g13810 12006.m31864 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase beta subunit, putative, expressed seq=cds; coord=8:85421696..85424667:-1; parent_gene=AC194439.3_FG002'

'weakly similar to (136) AT1G76550 | Symbols: | pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative | chr1:28722900-28726929 REVERSEweakly similar to (138) PFPA_SOLTU Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Solanum tuberosum (Potato)weakly similar to (174) loc_os02g48360 12002.m100340 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit, putative, expressed seq=cds; coord=1:35141959..35147250:-1; parent_gene=AC205100.3_FG001'

'moderately similar to (378) AT3G55440 | Symbols: ATCTIMC, TPI | TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase | chr3:20553794
20556078 FORWARDmoderately similar to (442) TPIS_MAIZE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Zea mays (Maize)moderately similar to (413) loc_os01g05490 12001.m42862 protein triosephosphate isomerase, cytosolic, putative, expressed seq=cds; coord=8:14389329..14393515:-1; parent_gene=GRMZM2G018177'

'weakly similar to (131) AT3G55440 | Symbols: ATCTIMC, TPI | TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase | chr3:20553794-20556078 FORWARDweakly similar to (167) TPIS_MAIZE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Zea mays (Maize)weakly similar to (147) loc_os01g05490 12001.m42862 protein triosephosphate isomerase, cytosolic, putative, expressed seq=cds; coord=3:41139121..41168207:-1; parent_gene=GRMZM2G026182'

'moderately similar to (386) AT3G55440 | Symbols: ATCTIMC, TPI | TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase | chr3:20553794
20556078 FORWARDmoderately similar to (465) TPIS_MAIZE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Zea mays (Maize)moderately similar to (425) loc_os01g05490 12001.m42862 protein triosephosphate isomerase, cytosolic, putative, expressed seq=cds; coord=3:17824258..17828243:1; parent_gene=GRMZM2G030784'

'moderately similar to (288) AT3G55440 | Symbols: ATCTIMC, TPI | TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase | chr3:20553794
20556078 FORWARDmoderately similar to (303) TPIS_ORYSA Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Oryza sativa (Rice)moderately similar to (325) loc_os01g62420 12001.m43510 protein triosephosphate isomerase, cytosolic, putative, expressed seq=cds; coord=8:168746526..168749489:1; parent_gene=GRMZM2G146206'

'weakly similar to (180) AT1G79600 | Symbols: | ABC1 family protein | chr1:29950105-29952516 REVERSEweakly similar to (174) TPIS_ORYSA Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Oryza sativa (Rice)weakly similar to (193) loc_os10g24954 12010.m05448 protein ulp1 protease family, C-terminal catalytic domain containing protein seq=cds; coord=7:12403371..12439528:-1; parent_gene=GRMZM2G346168' 'weakly similar to (134) AT3G55440 | Symbols: ATCTIMC, TPI | TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase | chr3:20553794-20556078 FORWARDweakly similar to (171) TPIS_MAIZE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Zea mays (Maize)weakly similar to (152) loc_os01g05490 12001.m42862 protein triosephosphate isomerase, cytosolic, putative, expressed seq=cds; coord=1:291031923..291034017:1; parent_gene=GRMZM2G370275'

'weakly similar to (190) AT1G15060 | Symbols: | LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP031088, alpha/beta hydrolase, At1g15070 (InterPro:IPR016969); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G73750.1); Has 120 Blast hits to 104 proteins in 29 species: Archae - 0; Bacteria - 61; Metazoa - 1; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 11 (source: NCBI BLink). | chr1:5184053-5186856 REVERSEweakly similar to (150) TPIS_ORYSA Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Oryza sativa (Rice)moderately similar to (250) loc_os08g27050 12008.m06718 protein expressed protein seq=cds; coord=1:201403651..201409528:-1; parent_gene=GRMZM2G419024'

'weakly similar to (128) AT3G55440 | Symbols: ATCTIMC, TPI | TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase | chr3:20553794-20556078 FORWARDweakly similar to (165) TPIS_MAIZE Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Zea mays (Maize)weakly similar to (146) loc_os01g05490 12001.m42862 protein triosephosphate isomerase, cytosolic, putative, expressed seq=cds; coord=1:111127564..111131693:1; parent_gene=GRMZM2G435244'

'moderately similar to (213) AT3G55440 | Symbols: ATCTIMC, TPI | TPI (TRIOSEPHOSPHATE ISOMERASE); triose-phosphate isomerase | chr3:2055379 20556078 FORWARDmoderately similar to (227) TPIS_ORYSA Triosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Triose-phosphate isomerase) - Oryza sativa (Rice)moderately similar to (237) loc_os01g62420 12001.m43510 protein triosephosphate isomerase, cytosolic, putative, expressed seq=cds; coord=8:82623182..82640943:1; parent_gene=GRMZM2G439389'

'highly similar to (550) AT3G04120 | Symbols: GAPC, GAPC-1, GAPC1 | GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr3:1081077-1083131 FORWARDhighly similar to (638) G3PC_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 1 (EC 1.2.1.12) - Zea mays (Maize)highly similar to (596) loc_os08g03290 12008.m26460 protein glyceraldehyde-3-phosphate dehydrogenase, cytosolic, putative, expressed seq=cds; coord=4:36880092..36884475:-1; parent_gene=GRMZM2G046804'

'highly similar to (590) AT1G16300 | Symbols: GAPCP-2 | GAPCP-2; NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr1:5574433-5577406 FORWARDmoderately similar to (481) G3PC_PINSY Glyceraldehyde-3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) - Pinus sylvestris (Scots pine)highly similar to (678) loc_os02g07490 12002.m06096 protein glyceraldehyde-3-phosphate dehydrogenase, cytosolic, putative, expressed seq=cds; coord=4:236083133..236088143:-1; parent_gene=GRMZM2G051004'

'highly similar to (561) AT1G13440 | Symbols: GAPC-2, GAPC2 | GAPC2 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr1:4608465 4610494 REVERSEhighly similar to (641) G3PE_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 (EC 1.2.1.12) - Zea mays (Maize)highly similar to (602) loc_os04g40950 12004.m35161 protein glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3, putative, expressed seq=cds; coord=4:133103720..133107109:1; parent_gene=GRMZM2G071630'

'highly similar to (597) AT1G79530 | Symbols: GAPCP-1 | GAPCP-1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE OF PLASTID 1); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr1:29916232-29919088 REVERSEmoderately similar to (483) G3PC_GINBI Glyceraldehyde-3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) - Ginkgo biloba (Ginkgo)highly similar to (693) loc_os02g07490 12002.m06096 protein glyceraldehyde-3-phosphate dehydrogenase, cytosolic, putative, expressed seq=cds; coord=5:85252669..85257667:1; parent_gene=GRMZM2G104632' 'highly similar to (561) AT1G13440 | Symbols: GAPC-2, GAPC2 | GAPC2 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C2); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr1:4608465 4610494 REVERSEhighly similar to (639) G3PE_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3 (EC 1.2.1.12) - Zea mays (Maize)highly similar to (602) loc_os04g40950 12004.m35161 protein glyceraldehyde-3-phosphate dehydrogenase, cytosolic 3, putative, expressed seq=cds; coord=5:181520274..181524899:1; parent_gene=GRMZM2G176307'

'moderately similar to (484) AT3G04120 | Symbols: GAPC, GAPC-1, GAPC1 | GAPC1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE C SUBUNIT 1); glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr3:1081077-1083131 FORWARDhighly similar to (557) G3PD_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 2 (EC 1.2.1.12) - Zea mays (Maize)highly similar to (519) loc_os08g03290 12008.m26460 protein glyceraldehyde-3-phosphate dehydrogenase, cytosolic, putative, expressed seq=cds; coord=6:6898695..6903246:-1; parent_gene=GRMZM2G180625'

'weakly similar to (105) AT1G79530 | Symbols: GAPCP-1 | GAPCP-1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE OF PLASTID 1); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr1:29916232-29919088 REVERSEweakly similar to (102) G3PC_DIACA Glyceraldehyde-3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) - Dianthus caryophyllus (Carnation) (Clove pink)weakly similar to (121) loc_os02g07490 12002.m06096 protein glyceraldehyde-3-phosphate dehydrogenase, cytosolic, putative, expressed seq=cds; coord=5:125696952..125703045:-1; parent_gene=GRMZM2G435438'

'very weakly similar to (92.8) AT1G79530 | Symbols: GAPCP-1 | GAPCP-1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE OF PLASTID 1); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr1:29916232-29919088 REVERSEvery weakly similar to (89.7) G3PC_DIACA Glyceraldehyde-3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) - Dianthus caryophyllus (Carnation) (Clove pink)weakly similar to (106) loc_os02g07490 12002.m06096 protein glyceraldehyde-3-phosphate dehydrogenase, cytosolic, putative, expressed seq=cds; coord=5:152391580..152396412:1; parent_gene=GRMZM2G462894'

'highly similar to (723) AT1G32440 | Symbols: PKp3 | PKp3 (plastidial pyruvate kinase 3); pyruvate kinase | chr1:11712205-11714963 FORWARDhighly similar to (769) KPYG_TOBAC Pyruvate kinase isozyme G, chloroplast precursor (EC 2.7.1.40) - Nicotiana tabacum (Common tobacco)highly similar to (912) loc_os10g42100 12010.m06967 protein pyruvate kinase isozyme G, chloroplast precursor, putative, expressed seq=cds; coord=1:97673409..97679050:1; parent_gene=GRMZM2G033526'

'highly similar to (867) AT3G22960 | Symbols: PKP1, PKP-ALPHA | PKP-ALPHA; pyruvate kinase | chr3:8139369-8141771 FORWARDhighly similar to (885) KPYA_RICCO Pyruvate kinase isozyme A, chloroplast precursor (EC 2.7.1.40) - Ricinus communis (Castor bean)highly similar to (928) loc_os07g08340 12007.m28952 protein pyruvate kinase isozyme A, chloroplast precursor, putative, expressed seq=cds; coord=7:10513154..10517482:1; parent_gene=GRMZM2G066290'

'highly similar to (842) AT3G22960 | Symbols: PKP1, PKP-ALPHA | PKP-ALPHA; pyruvate kinase | chr3:8139369-8141771 FORWARDhighly similar to (853) KPYA_RICCO Pyruvate kinase isozyme A, chloroplast precursor (EC 2.7.1.40) - Ricinus communis (Castor bean)highly similar to (875) loc_os07g08340 12007.m28952 protein pyruvate kinase isozyme A, chloroplast precursor, putative, expressed seq=cds; coord=1:287888635..287892994:1; parent_gene=GRMZM2G078200'

'highly similar to (718) AT5G52920 | Symbols: PKP1, PKP-BETA1, PKP2 | PKP-BETA1 (PLASTIDIC PYRUVATE KINASE BETA SUBUNIT 1); pyruvate kinase | chr5:21463680-21466612 FORWARDhighly similar to (756) KPYG_TOBAC Pyruvate kinase isozyme G, chloroplast precursor (EC 2.7.1.40) - Nicotiana tabacum (Common tobacco)highly similar to (897) loc_os10g42100 12010.m06967 protein pyruvate kinase isozyme G, chloroplast precursor, putative, expressed seq=cds; coord=9:113470642..113476065:-1; parent_gene=GRMZM2G144730'

'highly similar to (860) AT5G52920 | Symbols: PKP1, PKP-BETA1, PKP2 | PKP-BETA1 (PLASTIDIC PYRUVATE KINASE BETA SUBUNIT 1); pyruvate kinase | chr5:21463680-21466612 FORWARDhighly similar to (743) KPYG_TOBAC Pyruvate kinase isozyme G, chloroplast precursor (EC 2.7.1.40) - Nicotiana tabacum (Common tobacco)nearly identical (1006) loc_os01g47080 12001.m10904 protein pyruvate kinase isozyme G, chloroplast precursor, putative, expressed seq=cds; coord=3:211977378..211987454:1; parent_gene=GRMZM2G152686' 'highly similar to (585) AT3G22960 | Symbols: PKP1, PKP-ALPHA | PKP-ALPHA; pyruvate kinase | chr3:8139369-8141771 FORWARDhighly similar to (589) KPYA_RICCO Pyruvate kinase isozyme A, chloroplast precursor (EC 2.7.1.40) - Ricinus communis (Castor bean)highly similar to (934) loc_os03g46910 12003.m09706 protein pyruvate kinase isozyme A, chloroplast precursor, putative, expressed seq=cds; coord=1:257484405..257489535:1; parent_gene=GRMZM2G177947'

'highly similar to (741) AT1G70820 | Symbols: | phosphoglucomutase, putative / glucose phosphomutase, putative | chr1:26705594-26708034 FORWARDhighly similar to (882) loc_os06g28194 12006.m71405 protein phosphoglucomutase/phosphomannomutase family protein, putative, expressed seq=cds; coord=7:78785098..78787882:1; parent_gene=GRMZM2G067908'

'moderately similar to (432) AT2G22480 | Symbols: PFK5 | PFK5 (PHOSPHOFRUCTOKINASE 5); 6-phosphofructokinase | chr2:9545670-9548414 FORWARDhighly similar to (511) loc_os10g26570 12010.m05597 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase, putative, expressed seq=cds; coord=1:242911988..242916942:1; parent_gene=GRMZM2G009591'

'moderately similar to (499) AT5G61580 | Symbols: PFK4 | PFK4 (PHOSPHOFRUCTOKINASE 4); 6-phosphofructokinase | chr5:24761150-24763827 FORWARDhighly similar to (596) loc_os01g09570 12001.m07582 protein 6-phosphofructokinase 2, putative, expressed seq=cds; coord=8:20698287..20701876:-1; parent_gene=GRMZM2G080375'

'moderately similar to (315) AT2G22480 | Symbols: PFK5 | PFK5 (PHOSPHOFRUCTOKINASE 5); 6-phosphofructokinase | chr2:9545670-9548414 FORWARDmoderately similar to (454) loc_os08g34050 12008.m07394 protein 6-phosphofructokinase 2, putative seq=cds; coord=1:212484786..212489531:1; parent_gene=GRMZM2G139360'

'weakly similar to (137) AT2G22480 | Symbols: PFK5 | PFK5 (PHOSPHOFRUCTOKINASE 5); 6-phosphofructokinase | chr2:9545670-9548414 FORWARDweakly similar to (200) loc_os10g26570 12010.m05597 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase, putative, expressed seq=cds; coord=3:86662282..86666591:1; parent_gene=GRMZM2G168716'

'highly similar to (728) AT5G17310 | Symbols: | UTP--glucose-1-phosphate uridylyltransferase, putative / UDP-glucose pyrophosphorylase, putative / UGPase, putative | chr5:5696955-5700845 REVERSEhighly similar to (796) UGPA_HORVU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase) (UDPGP) (UGPase) - Hordeum vulgare (Barley)highly similar to (805) loc_os09g38030 12009.m22190 protein UTP--glucose-1-phosphate uridylyltransferase, putative, expressed seq=cds; coord=7:146491263..146498155:-1; parent_gene=GRMZM2G032003'

'moderately similar to (475) AT5G17310 | Symbols: | UTP--glucose-1-phosphate uridylyltransferase, putative / UDP-glucose pyrophosphorylase, putative / UGPase, putative | chr5:5696955-5700845 REVERSEmoderately similar to (487) UGPA_HORVU UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase) (UDPGP) (UGPase) - Hordeum vulgare (Barley)highly similar to (540) loc_os02g02560 12002.m05605 protein UTP--glucose-1-phosphate uridylyltransferase, putative, expressed seq=cds; coord=5:70040845..70045236:-1; parent_gene=GRMZM2G098370'

'highly similar to (934) AT5G51820 | Symbols: PGM, ATPGMP, PGM1, STF1 | PGM (PHOSPHOGLUCOMUTASE); phosphoglucomutase | chr5:21063531-21067933 REVERSEhighly similar to (935) PGMP_PEA Phosphoglucomutase, chloroplast precursor (EC 5.4.2.2) (Glucose phosphomutase) (PGM) - Pisum sativum (Garden pea)nearly identical (1050) loc_os10g11140 12010.m065237 protein phosphoglucomutase, chloroplast precursor, putative, expressed seq=cds; coord=3:218264781..218273042:1; parent_gene=GRMZM2G025854'

'highly similar to (732) AT5G17530 | Symbols: | phosphoglucosamine mutase family protein | chr5:5778168-5781863 FORWARDhighly similar to (870) loc_os07g26610 12007.m06939 protein phosphoglucomutase/phosphomannomutase family protein, putative, expressed seq=cds; coord=7:41731651..41795285:-1; parent_gene=GRMZM2G069676'

'weakly similar to (123) AT5G17530 | Symbols: | phosphoglucosamine mutase family protein | chr5:5778168-5781863 FORWARDweakly similar to (155) loc_os07g26610 12007.m06939 protein phosphoglucomutase/phosphomannomutase family protein, putative, expressed seq=cds; coord=5:149809877..149811098:1; parent_gene=GRMZM2G173668' 'moderately similar to (424) AT4G24620 | Symbols: PGI1, PGI | PGI1 (PHOSPHOGLUCOSE ISOMERASE 1); glucose-6-phosphate isomerase | chr4:12709097-12712610 REVERSEvery weakly similar to (80.5) G6PI_MAIZE Glucose-6-phosphate isomerase, cytosolic (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) - Zea mays (Maize)highly similar to (508) loc_os09g29070 12009.m22122 protein glucose-6-phosphate isomerase, putative, expressed seq=cds; coord=2:187379328..187383441:1; parent_gene=GRMZM2G076075'

'highly similar to (887) AT4G24620 | Symbols: PGI1, PGI | PGI1 (PHOSPHOGLUCOSE ISOMERASE 1); glucose-6-phosphate isomerase | chr4:12709097-12712610 REVERSEweakly similar to (124) G6PI_SPIOL Glucose-6-phosphate isomerase, cytosolic (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) - Spinacia oleracea (Spinach)nearly identical (1023) loc_os09g29070 12009.m22122 protein glucose-6-phosphate isomerase, putative, expressed seq=cds; coord=7:127859191..127864034:-1; parent_gene=GRMZM2G140614'

'highly similar to (708) AT4G26270 | Symbols: PFK3 | PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase | chr4:13301094-13304030 REVERSEvery weakly similar to (80.1) PFPB_RICCO Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Ricinus communis (Castor bean)highly similar to (983) loc_os05g44922 12005.m28064 protein 6-phosphofructokinase, putative, expressed seq=cds; coord=6:160034201..160039816:-1; parent_gene=GRMZM2G004932'

'very weakly similar to (88.6) loc_os09g30240 12009.m06175 protein 6-phosphofructokinase, putative, expressed seq=cds; coord=7:131031531..131041187:1; parent_gene=GRMZM2G031613'

'highly similar to (724) AT2G22480 | Symbols: PFK5 | PFK5 (PHOSPHOFRUCTOKINASE 5); 6-phosphofructokinase | chr2:9545670-9548414 FORWARDhighly similar to (948) loc_os09g24910 12009.m05645 protein 6-phosphofructokinase 2, putative, expressed seq=cds; coord=2:181110668..181120123:1; parent_gene=GRMZM2G127717'

'highly similar to (734) AT4G26270 | Symbols: PFK3 | PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase | chr4:13301094-13304030 REVERSEhighly similar to (939) loc_os01g09570 12001.m07582 protein 6-phosphofructokinase 2, putative, expressed seq=cds; coord=3:6801004..6804943:-1; parent_gene=GRMZM2G132069'

'highly similar to (686) AT4G26270 | Symbols: PFK3 | PFK3 (PHOSPHOFRUCTOKINASE 3); 6-phosphofructokinase | chr4:13301094-13304030 REVERSEvery weakly similar to (80.9) PFPB_RICCO Pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Ricinus communis (Castor bean)highly similar to (833) loc_os05g10650 12005.m05536 protein 6-phosphofructokinase 2, putative, expressed seq=cds; coord=6:132794943..132797295:-1; parent_gene=GRMZM2G401970'

'highly similar to (758) AT5G56630 | Symbols: PFK7 | PFK7 (PHOSPHOFRUCTOKINASE 7); 6-phosphofructokinase | chr5:22924311-22926728 FORWARDhighly similar to (899) loc_os06g05860 12006.m05312 protein 6-phosphofructokinase, putative, expressed seq=cds; coord=9:19154953..19160236:1; parent_gene=GRMZM2G443985'

'very weakly similar to (99.8) loc_os10g26570 12010.m05597 protein pyrophosphate--fructose 6-phosphate 1-phosphotransferase, putative, expressed seq=cds; coord=6:17569537..17576810:1; parent_gene=GRMZM2G171796' 'moderately similar to (445) AT4G17260 | Symbols: | L-lactate dehydrogenase, putative | chr4:9674057-9675309 FORWARDhighly similar to (620) LDH_MAIZE L-lactate dehydrogenase (EC 1.1.1.27) (LDH) - Zea mays (Maize)highly similar to (580) loc_os02g01510 12002.m05501 protein L-lactate dehydrogenase A, putative, expressed seq=cds; coord=5:67403566..67405443:1; parent_gene=GRMZM2G128929'

'moderately similar to (422) AT4G17260 | Symbols: | L-lactate dehydrogenase, putative | chr4:9674057-9675309 FORWARDhighly similar to (528) LDH_MAIZE L-lactate dehydrogenase (EC 1.1.1.27) (LDH) - Zea mays (Maize)highly similar to (561) loc_os02g01510 12002.m05501 protein L-lactate dehydrogenase A, putative, expressed seq=cds; coord=5:67473287..67474604:1; parent_gene=GRMZM2G173192'

'highly similar to (825) AT5G54960 | Symbols: PDC2 | PDC2 (pyruvate decarboxylase-2); carboxy-lyase/ catalytic/ magnesium ion binding / pyruvate decarboxylase/ thiamin pyrophosphate binding | chr5:22310858-22312681 REVERSEhighly similar to (849) PDC1_MAIZE Pyruvate decarboxylase isozyme 1 (EC 4.1.1.1) (PDC) - Zea mays (Maize)highly similar to (943) loc_os01g06660 12001.m150484 protein pyruvate decarboxylase isozyme 1, putative, expressed seq=cds; coord=8:15548387..15551947:-1; parent_gene=GRMZM2G038821'

'highly similar to (852) AT4G33070 | Symbols: | pyruvate decarboxylase, putative | chr4:15952519-15954676 REVERSEhighly similar to (917) PDC2_ORYSA Pyruvate decarboxylase isozyme 2 (EC 4.1.1.1) (PDC) - Oryza sativa (Rice)highly similar to (917) loc_os03g18220 12003.m101116 protein pyruvate decarboxylase isozyme 2, putative, expressed seq=cds; coord=7:174746426..174748651:1; parent_gene=GRMZM2G434792'

'highly similar to (937) AT4G33070 | Symbols: | pyruvate decarboxylase, putative | chr4:15952519-15954676 REVERSEnearly identical (1157) PDC1_MAIZE Pyruvate decarboxylase isozyme 1 (EC 4.1.1.1) (PDC) - Zea mays (Maize)nearly identical (1097) loc_os05g39310 12005.m08110 protein pyruvate decarboxylase isozyme 1, putative, expressed seq=cds; coord=8:118165588..118167724:1; parent_gene=AC197705.4_FG001'

'highly similar to (627) AT1G77120 | Symbols: ADH1, ADH, ATADH, ATADH1 | ADH1 (ALCOHOL DEHYDROGENASE 1); alcohol dehydrogenase | chr1:28975509-28977216 FORWARDhighly similar to (751) ADH2_MAIZE Alcohol dehydrogenase 2 (EC 1.1.1.1) - Zea mays (Maize)highly similar to (715) loc_os11g10510 12011.m05246 protein alcohol dehydrogenase 2, putative, expressed seq=cds; coord=4:13395375..13398777:-1; parent_gene=GRMZM2G098346'

'highly similar to (580) AT1G77120 | Symbols: ADH1, ADH, ATADH, ATADH1 | ADH1 (ALCOHOL DEHYDROGENASE 1); alcohol dehydrogenase | chr1:28975509-28977216 FORWARDhighly similar to (691) ADH1_MAIZE Alcohol dehydrogenase 1 (EC 1.1.1.1) - Zea mays (Maize)highly similar to (669) loc_os11g10480 12011.m28756 protein alcohol dehydrogenase 1, putative, expressed seq=cds; coord=1:273983252..273986222:-1; parent_gene=GRMZM2G442658'

'highly similar to (796) AT3G58750 | Symbols: CSY2 | CSY2 (citrate synthase 2); citrate (SI)-synthase | chr3:21724564-21727458 REVERSEhighly similar to (795) CYSZ_CUCMA Citrate synthase, glyoxysomal precursor (EC 2.3.3.1) (GCS) - Cucurbita maxima (Pumpkin) (Winter squash)highly similar to (867) loc_os02g13840 12002.m06630 protein citrate synthase, glyoxysomal precursor, putative, expressed seq=cds; coord=5:149458858..149463589:-1; parent_gene=GRMZM2G135588'

'highly similar to (556) AT5G09660 | Symbols: PMDH2 | PMDH2 (peroxisomal NAD-malate dehydrogenase 2); malate dehydrogenase | chr5:2993691-2995551 REVERSEhighly similar to (578) MDHG_ORYSA Malate dehydrogenase, glyoxysomal precursor (EC 1.1.1.37) - Oryza sativa (Rice)highly similar to (613) loc_os03g56280 12003.m10537 protein malate dehydrogenase, glyoxysomal precursor, putative, expressed seq=cds; coord=1:282537233..282540873:-1; parent_gene=GRMZM2G072744'

'moderately similar to (390) AT5G09660 | Symbols: PMDH2 | PMDH2 (peroxisomal NAD-malate dehydrogenase 2); malate dehydrogenase | chr5:2993691-2995551 REVERSEmoderately similar to (428) MDHG_ORYSA Malate dehydrogenase, glyoxysomal precursor (EC 1.1.1.37) - Oryza sativa (Rice)moderately similar to (428) loc_os12g43630 12012.m26992 protein malate dehydrogenase, glyoxysomal precursor, putative, expressed seq=cds; coord=3:91357080..91360381:-1; parent_gene=GRMZM2G077415' 'moderately similar to (389) AT3G47520 | Symbols: MDH | MDH (MALATE DEHYDROGENASE); L-malate dehydrogenase/ binding / catalytic/ malate dehydrogenase/ oxidoreductase/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor | chr3:17513657-17514868 FORWARDmoderately similar to (322) MDHM_FRAAN Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - Fragaria ananassa (Strawberry)moderately similar to (479) loc_os07g43700 12007.m29008 protein malate dehydrogenase, glyoxysomal precursor, putative, expressed seq=cds; coord=7:167638521..167640715:-1; parent_gene=GRMZM2G141289'

'moderately similar to (450) AT1G53240 | Symbols: | malate dehydrogenase (NAD), mitochondrial | chr1:19854966-19856802 REVERSEmoderately similar to (451) MDHM_FRAAN Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - Fragaria ananassa (Strawberry)highly similar to (509) loc_os01g46070 12001.m10806 protein malate dehydrogenase, mitochondrial precursor, putative, expressed seq=cds; coord=6:165631098..165635858:-1; parent_gene=GRMZM2G154595'

'highly similar to (520) AT3G47520 | Symbols: MDH | MDH (MALATE DEHYDROGENASE); L-malate dehydrogenase/ binding / catalytic/ malate dehydrogenase/ oxidoreductase/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor | chr3:17513657-17514868 FORWARDmoderately similar to (373) MDHG_ORYSA Malate dehydrogenase, glyoxysomal precursor (EC 1.1.1.37) - Oryza sativa (Rice)highly similar to (646) loc_os08g33720 12008.m07362 protein malate dehydrogenase, mitochondrial precursor, putative, expressed seq=cds; coord=1:213097242..213099953:-1; parent_gene=GRMZM2G161245'

'highly similar to (505) AT1G53240 | Symbols: | malate dehydrogenase (NAD), mitochondrial | chr1:19854966-19856802 REVERSEhighly similar to (508) MDHM_FRAAN Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37) - Fragaria ananassa (Strawberry)highly similar to (587) loc_os01g46070 12001.m10806 protein malate dehydrogenase, mitochondrial precursor, putative, expressed seq=cds; coord=3:213896741..213905427:1; parent_gene=GRMZM2G466833'

'moderately similar to (500) AT1G18270 | Symbols: | ketose-bisphosphate aldolase class-II family protein | chr1:6283634-6293772 REVERSEhighly similar to (773) loc_os06g14740 12006.m06189 protein ketose-bisphosphate aldolases family protein, expressed seq=cds; coord=6:117850410..117855773:-1; parent_gene=GRMZM2G074454'

'moderately similar to (204) AT3G01850 | Symbols: | ribulose-phosphate 3-epimerase, cytosolic, putative / pentose-5-phosphate 3-epimerase, putative | chr3:300428-301987 REVERSEmoderately similar to (231) RPE1_ORYSA Ribulose-phosphate 3-epimerase, cytoplasmic isoform (EC 5.1.3.1) (Ribulose-5-phosphate-epimerase) (Cyt-RPEase) (RPEcyt) (Pentose-5-phosphate 3-epimerase) (PPE) - Oryza sativa (Rice)moderately similar to (231) loc_os09g32810 12009.m22157 protein ribulose-phosphate 3-epimerase, putative, expressed seq=cds; coord=7:136742676..136746945:1; parent_gene=GRMZM2G083102'

'moderately similar to (240) AT2G01290 | Symbols: | ribose-5-phosphate isomerase | chr2:149192-149989 REVERSEmoderately similar to (385) loc_os04g24140 12004.m07548 protein ribose-5-phosphate isomerase, putative, expressed seq=cds; coord=2:144880257..144881689:1; parent_gene=GRMZM2G035599'

'moderately similar to (214) AT1G71100 | Symbols: RSW10 | RSW10 (RADIAL SWELLING 10); ribose-5-phosphate isomerase | chr1:26814726-26815529 FORWARDmoderately similar to (365) loc_os04g50050 12004.m09937 protein retrotransposon protein, putative, unclassified seq=cds; coord=1:152502918..152508975:1; parent_gene=GRMZM2G104070'

'highly similar to (593) AT1G30510 | Symbols: ATRFNR2 | ATRFNR2 (ROOT FNR 2); FAD binding / NADP or NADPH binding / electron carrier/ ferredoxin-NADP+ reductase/ oxidoreductase | chr1:10807150-10808984 REVERSEhighly similar to (677) FENR3_ORYSA Ferredoxin--NADP reductase, embryo isozyme, chloroplast precursor (EC 1.18.1.2) (FNR) - Oryza sativa (Rice)highly similar to (677) loc_os07g05400 12007.m05004 protein ferredoxin--NADP reductase, embryo isozyme, chloroplast precursor, putative, expressed seq=cds; coord=7:5095194..5100761:-1; parent_gene=GRMZM2G011858'

'highly similar to (607) AT1G30510 | Symbols: ATRFNR2 | ATRFNR2 (ROOT FNR 2); FAD binding / NADP or NADPH binding / electron carrier/ ferredoxin-NADP+ reductase/ oxidoreductase | chr1:10807150-10808984 REVERSEhighly similar to (689) FENR2_ORYSA Ferredoxin--NADP reductase, root isozyme, chloroplast precursor (EC 1.18.1.2) (FNR) - Oryza sativa (Rice)highly similar to (689) loc_os03g57120 12003.m35441 protein ferredoxin--NADP reductase, root isozyme, chloroplast precursor, putative, expressed seq=cds; coord=1:285137082..285140683:-1; parent_gene=GRMZM2G058760' 'highly similar to (582) AT1G24180 | Symbols: IAR4 | IAR4; oxidoreductase, acting on the aldehyde or oxo group of donors, disulfide as acceptor / pyruvate dehydrogenase (acetyl-transferring) | chr1:8560777-8563382 REVERSEhighly similar to (582) ODPA_SOLTU Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) - Solanum tuberosum (Potato)highly similar to (672) loc_os06g13720 12006.m06087 protein pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor, putative, expressed seq=cds; coord=9:1443455..1448097:1; parent_gene=GRMZM2G027627'

'highly similar to (624) AT1G01090 | Symbols: PDH-E1 ALPHA | PDH-E1 ALPHA (PYRUVATE DEHYDROGENASE E1 ALPHA); pyruvate dehydrogenase (acetyl-transferring) | chr1:47705-49166 REVERSEmoderately similar to (240) ODPA_SOLTU Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) - Solanum tuberosum (Potato)highly similar to (725) loc_os04g02900 12004.m101452 protein pyruvate dehydrogenase E1 component alpha subunit, putative, expressed seq=cds; coord=2:110896551..110900469:-1; parent_gene=GRMZM2G033894'

'highly similar to (568) AT1G30120 | Symbols: PDH-E1 BETA | PDH-E1 BETA (PYRUVATE DEHYDROGENASE E1 BETA); pyruvate dehydrogenase (acetyl-transferring) | chr1:10584350-10586477 REVERSEmoderately similar to (403) ODPB_MESVI Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1) - Mesostigma viridehighly similar to (628) loc_os12g42230 12012.m08002 protein pyruvate dehydrogenase E1 component subunit beta, putative, expressed seq=cds; coord=1:174313373..174317518:1; parent_gene=GRMZM2G088565'

'highly similar to (602) AT5G50850 | Symbols: MAB1 | MAB1 (MACCI-BOU); catalytic/ pyruvate dehydrogenase (acetyl-transferring) | chr5:20689671-20692976 FORWARDhighly similar to (589) ODPB_PEA Pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor (EC 1.2.4.1) (PDHE1-B) - Pisum sativum (Garden pea)highly similar to (689) loc_os09g33500 12009.m22013 protein pyruvate dehydrogenase E1 component subunit beta, mitochondrial precursor, putative, expressed seq=cds; coord=2:192576240..192582957:1; parent_gene=GRMZM2G097226'

'highly similar to (569) AT1G30120 | Symbols: PDH-E1 BETA | PDH-E1 BETA (PYRUVATE DEHYDROGENASE E1 BETA); pyruvate dehydrogenase (acetyl-transferring) | chr1:10584350-10586477 REVERSEmoderately similar to (418) ODPB_MESVI Pyruvate dehydrogenase E1 component subunit beta (EC 1.2.4.1) - Mesostigma viridehighly similar to (614) loc_os03g44300 12003.m34899 protein pyruvate dehydrogenase E1 component subunit beta, putative, expressed seq=cds; coord=1:251039008..251041842:-1; parent_gene=GRMZM2G127546'

'highly similar to (625) AT1G59900 | Symbols: AT-E1 ALPHA | AT-E1 ALPHA; oxidoreductase, acting on the aldehyde or oxo group of donors, disulfide as acceptor / pyruvate dehydrogenase (acetyl-transferring) | chr1:22051368-22053660 FORWARDhighly similar to (627) ODPA_SOLTU Pyruvate dehydrogenase E1 component subunit alpha, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) - Solanum tuberosum (Potato)highly similar to (703) loc_os02g50620 12002.m10096 protein pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor, putative, expressed seq=cds; coord=4:182736035..182740799:1; parent_gene=GRMZM2G361693'

'highly similar to (627) AT3G13930 | Symbols: | dihydrolipoamide S-acetyltransferase, putative | chr3:4596240-4600143 FORWARDhighly similar to (826) loc_os07g22720 12007.m06556 protein dihydrolipoyllysine-residue acetyltransferase component of pyruvatedehydrogenase complex, mitochondrial precursor, putative, expressed seq=cds; coord=5:155530969..155538363:-1; parent_gene=GRMZM2G015132'

'moderately similar to (418) AT1G34430 | Symbols: EMB3003 | EMB3003 (embryo defective 3003); acyltransferase/ dihydrolipoyllysine-residue acetyltransferase/ protein binding | chr1:12588027-12590084 REVERSEhighly similar to (592) loc_os12g08170 12012.m04804 protein dihydrolipoyllysine-residue acetyltransferase component of pyruvatedehydrogenase complex, mitochondrial precursor, putative, expressed seq=cds; coord=10:11749519..11756094:-1; parent_gene=GRMZM2G036534'

'highly similar to (530) AT3G25860 | Symbols: LTA2, PLE2 | LTA2; dihydrolipoyllysine-residue acetyltransferase | chr3:9460632-9462585 FORWARDhighly similar to (620) loc_os08g33440 12008.m07334 protein dihydrolipoyllysine-residue acetyltransferase component of pyruvatedehydrogenase complex, putative, expressed seq=cds; coord=1:214719298..214723588:1; parent_gene=GRMZM2G058702' 'highly similar to (582) AT3G52200 | Symbols: LTA3 | LTA3; ATP binding / dihydrolipoyllysine-residue acetyltransferase | chr3:19360317-19366091 FORWARDhighly similar to (805) loc_os06g30460 12006.m091708 protein dihydrolipoyllysine-residue acetyltransferase component of pyruvatedehydrogenase complex, mitochondrial precursor, putative, expressed seq=cds; coord=1:290265297..290286811:1; parent_gene=GRMZM2G082664'

'highly similar to (522) AT3G25860 | Symbols: LTA2, PLE2 | LTA2; dihydrolipoyllysine-residue acetyltransferase | chr3:9460632-9462585 FORWARDhighly similar to (612) loc_os08g33440 12008.m07334 protein dihydrolipoyllysine-residue acetyltransferase component of pyruvatedehydrogenase complex, putative, expressed seq=cds; coord=4:82008782..82012777:-1; parent_gene=GRMZM2G117786'

'moderately similar to (429) AT3G25860 | Symbols: LTA2, PLE2 | LTA2; dihydrolipoyllysine-residue acetyltransferase | chr3:9460632-9462585 FORWARDmoderately similar to (387) loc_os08g33440 12008.m07334 protein dihydrolipoyllysine-residue acetyltransferase component of pyruvatedehydrogenase complex, putative, expressed seq=cds; coord=7:110057897..110060901:-1; parent_gene=GRMZM2G121200'

'highly similar to (522) AT3G13930 | Symbols: | dihydrolipoamide S-acetyltransferase, putative | chr3:4596240-4600143 FORWARDhighly similar to (632) loc_os07g22720 12007.m06556 protein dihydrolipoyllysine-residue acetyltransferase component of pyruvatedehydrogenase complex, mitochondrial precursor, putative, expressed seq=cds; coord=4:230189571..230193924:-1; parent_gene=GRMZM2G161969'

'highly similar to (527) AT1G34430 | Symbols: EMB3003 | EMB3003 (embryo defective 3003); acyltransferase/ dihydrolipoyllysine-residue acetyltransferase/ protein binding | chr1:12588027-12590084 REVERSEhighly similar to (592) loc_os12g08170 12012.m04804 protein dihydrolipoyllysine-residue acetyltransferase component of pyruvatedehydrogenase complex, mitochondrial precursor, putative, expressed seq=cds; coord=3:139285416..139291670:-1; parent_gene=GRMZM2G165176'

'highly similar to (803) AT3G16950 | Symbols: LPD1, ptlpd1 | LPD1 (LIPOAMIDE DEHYDROGENASE 1); dihydrolipoyl dehydrogenase | chr3:5786508-5790383 REVERSEmoderately similar to (235) DLDH_PEA Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase) (Pyruvate dehydrogenase complex E3 subunit) (PDC-E3) (E3) (Glycine cleavage system L protein) - Pisum sativum (Garden pea)highly similar to (917) loc_os05g06460 12005.m05173 protein dihydrolipoyl dehydrogenase, putative, expressed seq=cds; coord=8:79300397..79307702:1; parent_gene=GRMZM2G073774'

'highly similar to (808) AT3G16950 | Symbols: LPD1, ptlpd1 | LPD1 (LIPOAMIDE DEHYDROGENASE 1); dihydrolipoyl dehydrogenase | chr3:5786508-5790383 REVERSEmoderately similar to (238) DLDH_PEA Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase) (Pyruvate dehydrogenase complex E3 subunit) (PDC-E3) (E3) (Glycine cleavage system L protein) - Pisum sativum (Garden pea)highly similar to (893) loc_os01g23610 12001.m42997 protein dihydrolipoyl dehydrogenase, putative, expressed seq=cds; coord=8:42281387..42289748:-1; parent_gene=GRMZM2G145595'

'highly similar to (803) AT3G16950 | Symbols: LPD1, ptlpd1 | LPD1 (LIPOAMIDE DEHYDROGENASE 1); dihydrolipoyl dehydrogenase | chr3:5786508-5790383 REVERSEmoderately similar to (235) DLDH_PEA Dihydrolipoyl dehydrogenase, mitochondrial precursor (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase) (Pyruvate dehydrogenase complex E3 subunit) (PDC-E3) (E3) (Glycine cleavage system L protein) - Pisum sativum (Garden pea)highly similar to (917) loc_os05g06460 12005.m05173 protein dihydrolipoyl dehydrogenase, putative, expressed seq=cds; coord=8:79203447..79210580:1; parent_gene=GRMZM2G152958'

'highly similar to (769) AT2G44350 | Symbols: ATCS, CSY4 | ATCS; ATP binding / ATP citrate synthase/ citrate (SI)-synthase | chr2:18316673-18320524 FORWARDhighly similar to (754) CISY_DAUCA Citrate synthase, mitochondrial precursor (EC 2.3.3.1) - Daucus carota (Carrot)highly similar to (870) loc_os11g33240 12011.m080018 protein citrate synthase 4, mitochondrial precursor, putative, expressed seq=cds; coord=5:123629674..123636311:1; parent_gene=GRMZM2G063851' 'highly similar to (774) AT2G44350 | Symbols: ATCS, CSY4 | ATCS; ATP binding / ATP citrate synthase/ citrate (SI)-synthase | chr2:18316673-18320524 FORWARDhighly similar to (754) CISY_DAUCA Citrate synthase, mitochondrial precursor (EC 2.3.3.1) - Daucus carota (Carrot)highly similar to (879) loc_os11g33240 12011.m080018 protein citrate synthase 4, mitochondrial precursor, putative, expressed seq=cds; coord=4:233821047..233828196:1; parent_gene=GRMZM2G064023'

'nearly identical (1164) AT2G05710 | Symbols: | aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative | chr2:2141591-2146350 FORWARDnearly identical (1180) ACOC_ORYSA Putative aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) - Oryza sativa (Rice)nearly identical (1290) loc_os03g04410 12003.m05971 protein aconitate hydratase, cytoplasmic, putative, expressed seq=cds; coord=9:151763726..151772001:-1; parent_gene=GRMZM2G009808'

'highly similar to (798) AT4G13430 | Symbols: IIL1 | IIL1 (ISOPROPYL MALATE ISOMERASE LARGE SUBUNIT 1); 4 iron, 4 sulfur cluster binding / hydro-lyase/ lyase | chr4:7804194-7807789 REVERSEvery weakly similar to (81.6) ACOC_CUCMA Aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) - Cucurbita maxima (Pumpkin) (Winter squash)highly similar to (891) loc_os02g03260 12002.m33530 protein 3-isopropylmalate dehydratase large subunit 2, putative, expressed seq=cds; coord=4:238877216..238881188:1; parent_gene=GRMZM2G010044'

'nearly identical (1422) AT2G05710 | Symbols: | aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative | chr2:2141591-2146350 FORWARDnearly identical (1497) ACOC_ORYSA Putative aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) - Oryza sativa (Rice)nearly identical (1497) loc_os08g09200 12008.m05055 protein aconitate hydratase, cytoplasmic, putative, expressed seq=cds; coord=4:28118892..28124783:1; parent_gene=GRMZM2G020801'

'nearly identical (1168) AT2G05710 | Symbols: | aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative | chr2:2141591-2146350 FORWARDnearly identical (1189) ACOC_ORYSA Putative aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) - Oryza sativa (Rice)nearly identical (1297) loc_os03g04410 12003.m05971 protein aconitate hydratase, cytoplasmic, putative, expressed seq=cds; coord=1:8135964..8147853:-1; parent_gene=GRMZM2G176397'

'weakly similar to (192) AT4G26970 | Symbols: | aconitate hydratase/ copper ion binding | chr4:13543077-13548427 FORWARDmoderately similar to (201) ACOC_ORYSA Putative aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) - Oryza sativa (Rice)moderately similar to (201) loc_os08g09200 12008.m05055 protein aconitate hydratase, cytoplasmic, putative, expressed seq=cds; coord=5:91434867..91439005:-1; parent_gene=GRMZM2G364988'

'nearly identical (1378) AT2G05710 | Symbols: | aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative | chr2:2141591-2146350 FORWARDnearly identical (1446) ACOC_ORYSA Putative aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) - Oryza sativa (Rice)nearly identical (1447) loc_os08g09200 12008.m05055 protein aconitate hydratase, cytoplasmic, putative, expressed seq=cds; coord=2:114883820..114891121:-1; parent_gene=GRMZM2G467338'

'highly similar to (577) AT4G35260 | Symbols: IDH1 | IDH1 (ISOCITRATE DEHYDROGENASE 1); isocitrate dehydrogenase (NAD+)/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor | chr4:16774494-16776233 REVERSEmoderately similar to (279) LEU3_SOLTU 3-isopropylmalate dehydrogenase, chloroplast precursor (EC 1.1.1.85) (Beta-IPM dehydrogenase) (IMDH) (3-IPM-DH) - Solanum tuberosum (Potato)highly similar to (627) loc_os02g38200 12002.m08908 protein isocitrate dehydrogenase subunit 1, mitochondrial precursor, putative, expressed seq=cds; coord=10:125331184..125335073:-1; parent_gene=GRMZM2G025366'

'moderately similar to (266) AT4G35260 | Symbols: IDH1 | IDH1 (ISOCITRATE DEHYDROGENASE 1); isocitrate dehydrogenase (NAD+)/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor | chr4:16774494-16776233 REVERSEweakly similar to (144) LEU3_SOLTU 3-isopropylmalate dehydrogenase, chloroplast precursor (EC 1.1.1.85) (Beta-IPM dehydrogenase) (IMDH) (3-IPM-DH) - Solanum tuberosum (Potato)moderately similar to (297) loc_os02g38200 12002.m08908 protein isocitrate dehydrogenase subunit 1, mitochondrial precursor, putative, expressed seq=cds; coord=5:180550035..180550796:1; parent_gene=GRMZM2G116872' 'nearly identical (1729) AT5G65750 | Symbols: | 2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative | chr5:26304212-26307947 FORWARDnearly identical (1779) loc_os04g32020 12004.m101710 protein 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor, putative, expressed seq=cds; coord=2:69290220..69296784:-1; parent_gene=GRMZM2G142863'

'nearly identical (1732) AT5G65750 | Symbols: | 2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative | chr5:26304212-26307947 FORWARDnearly identical (1779) loc_os04g32020 12004.m101710 protein 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor, putative, expressed seq=cds; coord=10:109798193..109804126:1; parent_gene=GRMZM2G151041'

'very weakly similar to (94.4) AT3G55410 | Symbols: | 2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative | chr3:20541897-20545728 FORWARDweakly similar to (102) loc_os04g32020 12004.m101710 protein 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor, putative, expressed seq=cds; coord=7:160015814..160022084:-1; parent_gene=AC194977.2_FG004'

'moderately similar to (491) AT5G23250 | Symbols: | succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative | chr5:7830460-7832265 FORWARDhighly similar to (563) SUCA_ORYSA Probable succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase subunit alpha) (SCS-alpha) - Oryza sativa (Rice)highly similar to (563) loc_os07g38970 12007.m08141 protein succinyl-CoA ligase alpha-chain 2, mitochondrial precursor, putative, expressed seq=cds; coord=2:207032350..207038547:1; parent_gene=GRMZM2G039251'

'highly similar to (638) AT2G20420 | Symbols: | succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative / SCS-beta, putative | chr2:8805574-8807858 FORWARDhighly similar to (696) SUCB_ORYSA Succinyl-CoA ligase [GDP-forming] beta-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, beta chain) (SCS-beta) - Oryza sativa (Rice)highly similar to (696) loc_os02g40830 12002.m100283 protein succinyl-CoA ligase beta-chain, mitochondrial precursor, putative, expressed seq=cds; coord=5:186081955..186094328:1; parent_gene=GRMZM2G064695'

'highly similar to (511) AT5G23250 | Symbols: | succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative | chr5:7830460-7832265 FORWARDhighly similar to (551) SUCA_ORYSA Probable succinyl-CoA ligase [GDP-forming] subunit alpha, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase subunit alpha) (SCS-alpha) - Oryza sativa (Rice)highly similar to (551) loc_os07g38970 12007.m08141 protein succinyl-CoA ligase alpha-chain 2, mitochondrial precursor, putative, expressed seq=cds; coord=7:160283320..160289262:1; parent_gene=GRMZM2G072054'

'nearly identical (1080) AT5G66760 | Symbols: SDH1-1 | SDH1-1; ATP binding / succinate dehydrogenase | chr5:26653776-26657224 FORWARDnearly identical (1108) DHSA_ORYSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (EC 1.3.5.1) (FP) (Flavoprotein subunit of complex II) - Oryza sativa (Rice)nearly identical (1108) loc_os07g04240 12007.m04893 protein succinate dehydrogenase flavoprotein subunit,mitochondrial precursor, putative, expressed seq=cds; coord=7:4234486..4239316:1; parent_gene=GRMZM2G064799'

'nearly identical (1081) AT5G66760 | Symbols: SDH1-1 | SDH1-1; ATP binding / succinate dehydrogenase | chr5:26653776-26657224 FORWARDnearly identical (1104) DHSA_ORYSA Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial precursor (EC 1.3.5.1) (FP) (Flavoprotein subunit of complex II) - Oryza sativa (Rice)nearly identical (1104) loc_os07g04240 12007.m04893 protein succinate dehydrogenase flavoprotein subunit,mitochondrial precursor, putative, expressed seq=cds; coord=2:236245150..236250456:-1; parent_gene=GRMZM2G079888'

'highly similar to (800) AT2G47510 | Symbols: FUM1 | FUM1 (FUMARASE 1); catalytic/ fumarate hydratase | chr2:19498614-19502020 FORWARDhighly similar to (860) loc_os03g21950 12003.m07599 protein fumarate hydratase 1, mitochondrial precursor, putative, expressed seq=cds; coord=1:56746484..56752553:1; parent_gene=GRMZM2G010823'

'weakly similar to (165) AT2G47510 | Symbols: FUM1 | FUM1 (FUMARASE 1); catalytic/ fumarate hydratase | chr2:19498614-19502020 FORWARDweakly similar to (172) loc_os03g21950 12003.m07599 protein fumarate hydratase 1, mitochondrial precursor, putative, expressed seq=cds; coord=4:4100301..4104478:1; parent_gene=GRMZM2G348729' 'highly similar to (773) AT3G06650 | Symbols: ACLB-1 | ACLB-1; ATP citrate synthase | chr3:2079247-2082633 REVERSEhighly similar to (799) loc_os01g19450 12001.m42644 protein ATP-citrate synthase subunit 1, putative, expressed seq=cds; coord=8:37409326..37412866:1; parent_gene=GRMZM2G002416'

'highly similar to (604) AT5G03290 | Symbols: | isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative | chr5:794043-795939 FORWARDhighly similar to (576) LEU3_SOLTU 3-isopropylmalate dehydrogenase, chloroplast precursor (EC 1.1.1.85) (Beta-IPM dehydrogenase) (IMDH) (3-IPM-DH) - Solanum tuberosum (Potato)highly similar to (694) loc_os01g16900 12001.m150554 protein 3-isopropylmalate dehydrogenase, chloroplast precursor, putative, expressed seq=cds; coord=3:43991720..43996960:1; parent_gene=GRMZM2G018566'

'highly similar to (605) AT5G03290 | Symbols: | isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative | chr5:794043-795939 FORWARDhighly similar to (572) LEU3_SOLTU 3-isopropylmalate dehydrogenase, chloroplast precursor (EC 1.1.1.85) (Beta-IPM dehydrogenase) (IMDH) (3-IPM-DH) - Solanum tuberosum (Potato)highly similar to (695) loc_os01g16900 12001.m150554 protein 3-isopropylmalate dehydrogenase, chloroplast precursor, putative, expressed seq=cds; coord=8:2312133..2319735:-1; parent_gene=GRMZM2G120857'

'moderately similar to (232) AT5G03290 | Symbols: | isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative | chr5:794043-795939 FORWARDmoderately similar to (232) LEU3_SOLTU 3-isopropylmalate dehydrogenase, chloroplast precursor (EC 1.1.1.85) (Beta-IPM dehydrogenase) (IMDH) (3-IPM-DH) - Solanum tuberosum (Potato)moderately similar to (264) loc_os01g16900 12001.m150554 protein 3-isopropylmalate dehydrogenase, chloroplast precursor, putative, expressed seq=cds; coord=1:44528827..44529892:1; parent_gene=GRMZM2G173251'

'highly similar to (564) AT5G03290 | Symbols: | isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative | chr5:794043-795939 FORWARDhighly similar to (535) LEU3_SOLTU 3-isopropylmalate dehydrogenase, chloroplast precursor (EC 1.1.1.85) (Beta-IPM dehydrogenase) (IMDH) (3-IPM-DH) - Solanum tuberosum (Potato)highly similar to (610) loc_os01g16900 12001.m150554 protein 3-isopropylmalate dehydrogenase, chloroplast precursor, putative, expressed seq=cds; coord=9:11319200..11323395:-1; parent_gene=GRMZM2G404855'

'moderately similar to (468) AT5G43330 | Symbols: | malate dehydrogenase, cytosolic, putative | chr5:17390552-17392449 FORWARDmoderately similar to (479) MDHC_ORYSA Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (PP37) - Oryza sativa (Rice)highly similar to (580) loc_os04g46560 12004.m09605 protein malate dehydrogenase, cytoplasmic, putative, expressed seq=cds; coord=2:19914845..19916501:1; parent_gene=GRMZM2G101290'

'highly similar to (625) AT5G58330 | Symbols: | malate dehydrogenase (NADP), chloroplast, putative | chr5:23580010-23582287 REVERSEhighly similar to (791) MDHP_MAIZE Malate dehydrogenase [NADP], chloroplast precursor (EC 1.1.1.82) (NADP-MDH) - Zea mays (Maize)highly similar to (697) loc_os08g44810 12008.m08453 protein malate dehydrogenase 1, chloroplast precursor, putative, expressed seq=cds; coord=1:203170067..203174226:-1; parent_gene=GRMZM2G129513'

'moderately similar to (476) AT5G43330 | Symbols: | malate dehydrogenase, cytosolic, putative | chr5:17390552-17392449 FORWARDhighly similar to (502) MDHC_MAIZE Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) - Zea mays (Maize)moderately similar to (480) loc_os10g33800 12010.m21921 protein malate dehydrogenase, cytoplasmic, putative, expressed seq=cds; coord=1:231336185..231341950:-1; parent_gene=GRMZM2G415359'

'highly similar to (604) AT5G08740 | Symbols: NDC1 | NDC1 (NAD(P)H dehydrogenase C1); NADH dehydrogenase | chr5:2848752-2851323 REVERSEhighly similar to (906) loc_os06g11140 12006.m05831 protein NADH dehydrogenase, putative, expressed seq=cds; coord=9:7619341..7624742:-1; parent_gene=GRMZM2G080044' 'highly similar to (670) AT1G74910 | Symbols: | ADP-glucose pyrophosphorylase family protein | chr1:28135770-28138456 REVERSEhighly similar to (776) loc_os03g11050 12003.m35086 protein mannose-1-phosphate guanyltransferase, putative, expressed seq=cds; coord=9:147486941..147492124:1; parent_gene=GRMZM2G178254'

'highly similar to (908) AT5G52560 | Symbols: ATUSP | ATUSP (ARABIDOPSIS THALIANA UDP-SUGAR PYROPHOSPHORYLASE); UTP-monosaccharide-1-phosphate uridylyltransferase/ UTP:arabinose-1-phosphate uridylyltransferase/ UTP:galactose-1-phosphate uridylyltransferase/ UTP:glucose 1-phosphate uridylyltransferase/ UTP:xy | chr5:21331230-21334573 FORWARDnearly identical (1054) loc_os06g48760 12006.m091778 protein UDP-sugar pyrophospharylase, putative, expressed seq=cds; coord=5:56782827..56794221:-1; parent_gene=GRMZM2G116586'

'highly similar to (934) AT5G52560 | Symbols: ATUSP | ATUSP (ARABIDOPSIS THALIANA UDP-SUGAR PYROPHOSPHORYLASE); UTP-monosaccharide-1-phosphate uridylyltransferase/ UTP:arabinose-1-phosphate uridylyltransferase/ UTP:galactose-1-phosphate uridylyltransferase/ UTP:glucose 1-phosphate uridylyltransferase/ UTP:xy | chr5:21331230-21334573 FORWARDnearly identical (1090) loc_os06g48760 12006.m091778 protein UDP-sugar pyrophospharylase, putative, expressed seq=cds; coord=6:86773351..86783757:1; parent_gene=GRMZM2G161493'

'moderately similar to (353) AT5G52560 | Symbols: ATUSP | ATUSP (ARABIDOPSIS THALIANA UDP-SUGAR PYROPHOSPHORYLASE); UTP-monosaccharide-1-phosphate uridylyltransferase/ UTP:arabinose-1-phosphate uridylyltransferase/ UTP:galactose-1-phosphate uridylyltransferase/ UTP:glucose 1-phosphate uridylyltransferase/ UTP:xy | chr5:21331230-21334573 FORWARDmoderately similar to (419) loc_os06g48760 12006.m091778 protein UDP-sugar pyrophospharylase, putative, expressed seq=cds; coord=5:9753858..9757669:1; parent_gene=GRMZM2G396565'

'weakly similar to (198) AT3G02230 | Symbols: RGP1, ATRGP1 | RGP1 (REVERSIBLY GLYCOSYLATED POLYPEPTIDE 1); cellulose synthase (UDP-forming) | chr3:415463-417304 FORWARDweakly similar to (200) UPTG_MAIZE Alpha-1,4-glucan-protein synthase [UDP-forming] (EC 2.4.1.112) (UDP-glucose:protein transglucosylase) (UPTG) (Amylogenin) (Golgi-associated protein se-wap41) - Zea mays (Maize)moderately similar to (201) loc_os07g41360 12007.m08372 protein alpha-1,4-glucan-protein synthase 1, putative, expressed seq=cds; coord=5:214137019..214142243:-1; parent_gene=GRMZM2G481027'

'highly similar to (836) AT5G20950 | Symbols: | glycosyl hydrolase family 3 protein | chr5:7107609-7110775 REVERSEnearly identical (1031) loc_os01g56510 12001.m43214 protein periplasmic beta-glucosidase precursor, putative, expressed seq=cds; coord=3:192774502..192779708:-1; parent_gene=AC197578.4_FG001'

'highly similar to (574) AT4G23820 | Symbols: | glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein | chr4:12397217-12400050 REVERSEvery weakly similar to (96.3) PGLR_ACTCH Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase) - Actinidia chinensis (Kiwi) (Yangtao)highly similar to (762) loc_os01g43160 12001.m10579 protein polygalacturonase, putative, expressed seq=cds; coord=8:144537174..144540536:1; parent_gene=GRMZM2G052844'

'moderately similar to (440) AT5G49180 | Symbols: | pectinesterase family protein | chr5:19940783-19942876 REVERSEmoderately similar to (397) PME1_CITSI Pectinesterase-1 precursor (EC 3.1.1.11) (Pectin methylesterase) (PE) - Citrus sinensis (Sweet orange)highly similar to (952) loc_os04g38560 12004.m08845 protein pectinesterase-1 precursor, putative, expressed seq=cds; coord=2:42363164..42365278:1; parent_gene=GRMZM2G012328'

'moderately similar to (460) AT3G05620 | Symbols: | pectinesterase family protein | chr3:1629658-1631766 REVERSEmoderately similar to (426) PME_PRUPE Pectinesterase PPE8B precursor (EC 3.1.1.11) (Pectin methylesterase) (PE) - Prunus persica (Peach)highly similar to (779) loc_os01g15039 12001.m08104 protein pectinesterase PPE8B precursor, putative, expressed seq=cds; coord=8:5329655..5332095:1; parent_gene=GRMZM2G017555'

'moderately similar to (438) AT5G49180 | Symbols: | pectinesterase family protein | chr5:19940783-19942876 REVERSEmoderately similar to (404) PME1_CITSI Pectinesterase-1 precursor (EC 3.1.1.11) (Pectin methylesterase) (PE) - Citrus sinensis (Sweet orange)highly similar to (942) loc_os04g38560 12004.m08845 protein pectinesterase-1 precursor, putative, expressed seq=cds; coord=10:122230413..122232602:-1; parent_gene=GRMZM2G125356' 'moderately similar to (445) AT5G04420 | Symbols: | kelch repeat-containing protein | chr5:1246867-1249455 REVERSEvery weakly similar to (82.4) DYHA_CHLRE Dynein alpha chain, flagellar outer arm (DHC alpha) - Chlamydomonas reinhardtiihighly similar to (813) loc_os02g57690 12002.m100418 protein acyl-CoA binding protein, putative, expressed seq=cds; coord=4:170221855..170228873:1; parent_gene=GRMZM2G085547'

'moderately similar to (345) AT1G24360 | Symbols: | 3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase | chr1:8640820-8643283 FORWARDmoderately similar to (370) FABG3_BRANA 3-oxoacyl-[acyl-carrier-protein] reductase 3, chloroplast precursor (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase 3) - Brassica napus (Rape)moderately similar to (412) loc_os04g30760 12004.m08180 protein 3-oxoacyl-reductase, chloroplast precursor, putative, expressed seq=cds; coord=5:163113974..163119442:-1; parent_gene=GRMZM2G043602'

'moderately similar to (374) AT1G24360 | Symbols: | 3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase | chr1:8640820-8643283 FORWARDmoderately similar to (397) FABG3_BRANA 3-oxoacyl-[acyl-carrier-protein] reductase 3, chloroplast precursor (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase 3) - Brassica napus (Rape)moderately similar to (476) loc_os04g30760 12004.m08180 protein 3-oxoacyl-reductase, chloroplast precursor, putative, expressed seq=cds; coord=10:108122298..108130104:1; parent_gene=GRMZM2G099696'

'very weakly similar to (96.3) AT1G24360 | Symbols: | 3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase | chr1:8640820-8643283 FORWARDvery weakly similar to (100) FABG3_BRANA 3-oxoacyl-[acyl-carrier-protein] reductase 3, chloroplast precursor (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase 3) - Brassica napus (Rape)weakly similar to (127) loc_os12g13930 12012.m05365 protein 3-oxoacyl-reductase, chloroplast precursor, putative, expressed seq=cds; coord=9:96194999..96198016:1; parent_gene=GRMZM2G141256'

'moderately similar to (310) AT1G24360 | Symbols: | 3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase | chr1:8640820-8643283 FORWARDmoderately similar to (327) FABG3_BRANA 3-oxoacyl-[acyl-carrier-protein] reductase 3, chloroplast precursor (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase 3) - Brassica napus (Rape)moderately similar to (371) loc_os04g30760 12004.m08180 protein 3-oxoacyl-reductase, chloroplast precursor, putative, expressed seq=cds; coord=2:76554803..76576439:1; parent_gene=GRMZM2G351023'

'highly similar to (853) AT3G16910 | Symbols: AAE7, ACN1 | AAE7 (ACYL-ACTIVATING ENZYME 7); AMP binding / acetate-CoA ligase | chr3:5773231-5775411 REVERSEweakly similar to (139) 4CL1_SOLTU 4-coumarate--CoA ligase 1 (EC 6.2.1.12) (4CL 1) (4-coumaroyl-CoA synthase 1) - Solanum tuberosum (Potato)nearly identical (1050) loc_os03g19240 12003.m07341 protein AMP-binding protein, putative, expressed seq=cds; coord=1:48684987..48690042:-1; parent_gene=GRMZM2G013783'

'nearly identical (1177) AT1G77760 | Symbols: NIA1, GNR1, NR1 | NIA1 (NITRATE REDUCTASE 1); nitrate reductase | chr1:29236005-29239367 REVERSEnearly identical (1486) NIA1_ORYSA Nitrate reductase [NADH] 1 (EC 1.7.1.1) (NR1) - Oryza sativa (Rice)nearly identical (1486) loc_os08g36480 12008.m07637 protein nitrate reductase 1, putative, expressed seq=cds; coord=1:198738739..198743220:-1; parent_gene=GRMZM2G076723'

'nearly identical (1232) AT1G77760 | Symbols: NIA1, GNR1, NR1 | NIA1 (NITRATE REDUCTASE 1); nitrate reductase | chr1:29236005-29239367 REVERSEnearly identical (1540) NIA7_HORVU Nitrate reductase [NAD(P)H] (EC 1.7.1.2) - Hordeum vulgare (Barley)nearly identical (1573) loc_os02g53130 12002.m10342 protein nitrate reductase, putative, expressed seq=cds; coord=4:177655913..177659763:1; parent_gene=GRMZM2G428027'

'highly similar to (879) AT2G15620 | Symbols: NIR1, NIR, ATHNIR | NIR1 (NITRITE REDUCTASE 1); ferredoxin-nitrate reductase/ nitrite reductase (NO-forming) | chr2:6810552-6812666 FORWARDnearly identical (1118) NIR_MAIZE Ferredoxin--nitrite reductase, chloroplast precursor (EC 1.7.7.1) (Fragment) - Zea mays (Maize)highly similar to (990) loc_os01g25484 12001.m43466 protein ferredoxin--nitrite reductase, chloroplast precursor, putative, expressed seq=cds; coord=4:178582233..178585788:1; parent_gene=GRMZM2G079381'

'highly similar to (862) AT2G15620 | Symbols: NIR1, NIR, ATHNIR | NIR1 (NITRITE REDUCTASE 1); ferredoxin-nitrate reductase/ nitrite reductase (NO-forming) | chr2:6810552-6812666 FORWARDnearly identical (1051) NIR_MAIZE Ferredoxin--nitrite reductase, chloroplast precursor (EC 1.7.7.1) (Fragment) - Zea mays (Maize)highly similar to (974) loc_os01g25484 12001.m43466 protein ferredoxin--nitrite reductase, chloroplast precursor, putative, expressed seq=cds; coord=5:209907074..209909988:-1; parent_gene=GRMZM2G102959' 'nearly identical (2554) AT5G04140 | Symbols: GLU1, GLS1, GLUS, FD-GOGAT | GLU1 (GLUTAMATE SYNTHASE 1); glutamate synthase (ferredoxin) | chr5:1130031-1138186 FORWARDnearly identical (3008) GLTB_MAIZE Ferredoxin-dependent glutamate synthase, chloroplast precursor (EC 1.4.7.1) (Fd-GOGAT) - Zea mays (Maize)nearly identical (2839) loc_os07g46460 12007.m08863 protein ferredoxin-dependent glutamate synthase, chloroplast precursor, putative, expressed seq=cds; coord=7:170961145..170979959:-1; parent_gene=GRMZM2G036609'

'nearly identical (3256) AT5G53460 | Symbols: GLT1 | GLT1; glutamate synthase (NADH) | chr5:21700518-21709629 FORWARDnearly identical (3224) GLSN_MEDSA Glutamate synthase [NADH], chloroplast precursor (EC 1.4.1.14) (NADH-GOGAT) - Medicago sativa (Alfalfa)nearly identical (3818) loc_os01g48960 12001.m11085 protein glutamate synthase, chloroplast precursor, putative, expressed seq=cds; coord=8:151204529..151215672:-1; parent_gene=GRMZM2G077054'

'nearly identical (3241) AT5G53460 | Symbols: GLT1 | GLT1; glutamate synthase (NADH) | chr5:21700518-21709629 FORWARDnearly identical (3202) GLSN_MEDSA Glutamate synthase [NADH], chloroplast precursor (EC 1.4.1.14) (NADH-GOGAT) - Medicago sativa (Alfalfa)nearly identical (3767) loc_os01g48960 12001.m11085 protein glutamate synthase, chloroplast precursor, putative, expressed seq=cds; coord=3:208332821..208344531:1; parent_gene=GRMZM2G085078'

'nearly identical (3078) AT5G53460 | Symbols: GLT1 | GLT1; glutamate synthase (NADH) | chr5:21700518-21709629 FORWARDnearly identical (3057) GLSN_MEDSA Glutamate synthase [NADH], chloroplast precursor (EC 1.4.1.14) (NADH-GOGAT) - Medicago sativa (Alfalfa)nearly identical (3311) loc_os01g48960 12001.m11085 protein glutamate synthase, chloroplast precursor, putative, expressed seq=cds; coord=6:163217461..163229234:1; parent_gene=GRMZM2G375064'

'highly similar to (609) AT5G37600 | Symbols: ATGSR1, GLN1;1, GSR 1 | ATGSR1; copper ion binding / glutamate-ammonia ligase | chr5:14933574-14935656 REVERSEhighly similar to (702) GLNA2_MAIZE Glutamine synthetase root isozyme 2 (EC 6.3.1.2) (Glutamate--ammonia ligase) - Zea mays (Maize)highly similar to (635) loc_os03g50490 12003.m10040 protein glutamine synthetase root isozyme 2, putative, expressed seq=cds; coord=1:267894143..267897525:-1; parent_gene=GRMZM2G024104'

'highly similar to (676) AT5G37600 | Symbols: ATGSR1, GLN1;1, GSR 1 | ATGSR1; copper ion binding / glutamate-ammonia ligase | chr5:14933574-14935656 REVERSEhighly similar to (733) GLNA3_MAIZE Glutamine synthetase root isozyme 3 (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS112) - Zea mays (Maize)highly similar to (714) loc_os02g50240 12002.m33860 protein glutamine synthetase root isozyme 3, putative, expressed seq=cds; coord=4:167081372..167084703:-1; parent_gene=GRMZM2G036464'

'highly similar to (501) AT5G37600 | Symbols: ATGSR1, GLN1;1, GSR 1 | ATGSR1; copper ion binding / glutamate-ammonia ligase | chr5:14933574-14935656 REVERSEhighly similar to (571) GLNA5_MAIZE Glutamine synthetase root isozyme 5 (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS117) - Zea mays (Maize)highly similar to (528) loc_os03g12290 12003.m06679 protein glutamine synthetase root isozyme 5, putative, expressed seq=cds; coord=9:146062602..146070481:1; parent_gene=GRMZM2G046601'

'highly similar to (631) AT5G37600 | Symbols: ATGSR1, GLN1;1, GSR 1 | ATGSR1; copper ion binding / glutamate-ammonia ligase | chr5:14933574-14935656 REVERSEhighly similar to (704) GLNA1_MAIZE Glutamine synthetase root isozyme 1 (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS122) - Zea mays (Maize)highly similar to (654) loc_os03g12290 12003.m06679 protein glutamine synthetase root isozyme 5, putative, expressed seq=cds; coord=1:27977783..27980656:-1; parent_gene=GRMZM2G050514'

'highly similar to (677) AT5G35630 | Symbols: GS2, GLN2, ATGSL1 | GS2 (GLUTAMINE SYNTHETASE 2); glutamate-ammonia ligase | chr5:13831220-13833239 FORWARDhighly similar to (827) GLNAC_MAIZE Glutamine synthetase, chloroplast precursor (EC 6.3.1.2) (Glutamate--ammonia ligase) (GS2) - Zea mays (Maize)highly similar to (755) loc_os04g56400 12004.m79000 protein glutamine synthetase, chloroplast precursor, putative, expressed seq=cds; coord=10:146465614..146471079:-1; parent_gene=GRMZM2G098290'

'nearly identical (1029) AT3G53180 | Symbols: | catalytic/ glutamate-ammonia ligase | chr3:19707068-19711188 FORWARDnearly identical (1409) loc_os10g31820 12010.m06033 protein protein fluG, putative, expressed seq=cds; coord=1:235645071..235668787:-1; parent_gene=GRMZM2G115646' 'highly similar to (728) AT5G18170 | Symbols: GDH1 | GDH1 (GLUTAMATE DEHYDROGENASE 1); ATP binding / glutamate dehydrogenase [NAD(P)+]/ oxidoreductase | chr5:6006172-6008248 FORWARDhighly similar to (820) DHE3_MAIZE Glutamate dehydrogenase (EC 1.4.1.3) (GDH) - Zea mays (Maize)highly similar to (794) loc_os03g58040 12003.m35454 protein glutamate dehydrogenase, putative, expressed seq=cds; coord=1:287289676..287296815:-1; parent_gene=GRMZM2G178415'

'highly similar to (702) AT5G07440 | Symbols: GDH2 | GDH2 (GLUTAMATE DEHYDROGENASE 2); ATP binding / glutamate dehydrogenase [NAD(P)+]/ glutamate dehydrogenase/ oxidoreductase | chr5:2356153-2357546 FORWARDhighly similar to (690) DHE3_VITVI Glutamate dehydrogenase (EC 1.4.1.3) (GDH) - Vitis vinifera (Grape)highly similar to (755) loc_os04g45970 12004.m09548 protein glutamate dehydrogenase 2, putative, expressed seq=cds; coord=10:134053442..134057895:1; parent_gene=GRMZM2G427097'

'highly similar to (613) AT5G17330 | Symbols: GAD, GAD1 | GAD; calmodulin binding / glutamate decarboxylase | chr5:5711141-5714839 FORWARDhighly similar to (612) DCE_PETHY Glutamate decarboxylase (EC 4.1.1.15) (GAD) - Petunia hybrida (Petunia)highly similar to (652) loc_os08g36320 12008.m080179 protein glutamate decarboxylase, putative, expressed seq=cds; coord=1:198230423..198233618:-1; parent_gene=GRMZM2G017110'

'highly similar to (830) AT5G17330 | Symbols: GAD, GAD1 | GAD; calmodulin binding / glutamate decarboxylase | chr5:5711141-5714839 FORWARDhighly similar to (815) DCE_PETHY Glutamate decarboxylase (EC 4.1.1.15) (GAD) - Petunia hybrida (Petunia)highly similar to (912) loc_os03g13300 12003.m06776 protein glutamate decarboxylase, putative, expressed seq=cds; coord=9:144297855..144300816:-1; parent_gene=GRMZM2G098875'

'highly similar to (756) AT2G02010 | Symbols: GAD4 | GAD4 (glutamate decarboxylase 4); calmodulin binding | chr2:474375-476495 REVERSEhighly similar to (764) DCE_PETHY Glutamate decarboxylase (EC 4.1.1.15) (GAD) - Petunia hybrida (Petunia)highly similar to (859) loc_os04g37460 12004.m08735 protein glutamate decarboxylase, putative, expressed seq=cds; coord=2:44991322..44994248:1; parent_gene=GRMZM2G101069'

'highly similar to (688) AT1G65960 | Symbols: GAD2 | GAD2 (GLUTAMATE DECARBOXYLASE 2); calmodulin binding / glutamate decarboxylase | chr1:24552094-24557253 FORWARDhighly similar to (689) DCE_PETHY Glutamate decarboxylase (EC 4.1.1.15) (GAD) - Petunia hybrida (Petunia)highly similar to (849) loc_os04g37500 12004.m08739 protein glutamate decarboxylase, putative, expressed seq=cds; coord=2:44720554..44722721:-1; parent_gene=GRMZM2G355906'

'highly similar to (833) AT3G48560 | Symbols: CSR1, ALS, AHAS, TZP5, IMR1 | CSR1 (CHLORSULFURON/IMIDAZOLINONE RESISTANT 1); acetolactate synthase/ pyruvate decarboxylase | chr3:18001530-18003542 REVERSEnearly identical (1083) ILV2_MAIZE Acetolactate synthase 2, chloroplast precursor (EC 2.2.1.6) (Acetohydroxy-acid synthase 2) - Zea mays (Maize)nearly identical (1009) loc_os02g30630 12002.m100215 protein acetolactate synthase III, chloroplast precursor, putative, expressed seq=cds; coord=4:96806900..96809179:-1; parent_gene=GRMZM2G143357'

'highly similar to (829) AT5G17380 | Symbols: | pyruvate decarboxylase family protein | chr5:5724920-5726720 REVERSEweakly similar to (160) ILV2_TOBAC Acetolactate synthase 2, chloroplast precursor (EC 2.2.1.6) (Acetolactate synthase II) (Acetohydroxy-acid synthase II) (ALS II) - Nicotiana tabacum (Common tobacco)nearly identical (1009) loc_os01g32080 12001.m42655 protein 2-hydroxyphytanoyl-CoA lyase, putative, expressed seq=cds; coord=8:17966967..17971201:-1; parent_gene=GRMZM2G175171'

'moderately similar to (202) AT5G17380 | Symbols: | pyruvate decarboxylase family protein | chr5:5724920-5726720 REVERSEmoderately similar to (237) loc_os01g32080 12001.m42655 protein 2-hydroxyphytanoyl-CoA lyase, putative, expressed seq=cds; coord=3:203864924..203867229:-1; parent_gene=GRMZM2G331723' 'highly similar to (598) AT1G80560 | Symbols: | 3-isopropylmalate dehydrogenase, chloroplast, putative | chr1:30287833-30290126 FORWARDhighly similar to (605) LEU3_BRANA 3-isopropylmalate dehydrogenase, chloroplast precursor (EC 1.1.1.85) (Beta-IPM dehydrogenase) (IMDH) (3-IPM-DH) - Brassica napus (Rape)highly similar to (683) loc_os03g45320 12003.m101427 protein 3-isopropylmalate dehydrogenase 2, chloroplast precursor, putative, expressed seq=cds; coord=10:148968847..148972562:1; parent_gene=GRMZM2G104613'

'moderately similar to (338) AT4G00590 | Symbols: | asparaginase 2 family protein | chr4:252835-254880 FORWARDweakly similar to (106) ASPG_LUPLU L-asparaginase precursor (EC 3.5.1.1) (L-asparagine amidohydrolase) [Contains: L-asparaginase subunit alpha; L-asparaginase subunit beta] - Lupinus luteus (European yellow lupin)highly similar to (510) loc_os04g58600 12004.m35522 protein L-asparaginase 4 precursor, putative, expressed seq=cds; coord=10:148544790..148548840:1; parent_gene=GRMZM2G011743'

'highly similar to (635) AT1G74470 | Symbols: | geranylgeranyl reductase | chr1:27991248-27992845 FORWARDhighly similar to (773) loc_os02g51080 12002.m33869 protein geranylgeranyl hydrogenase, putative, expressed seq=cds; coord=5:206890298..206892838:1; parent_gene=GRMZM2G105644'

'moderately similar to (453) AT1G74470 | Symbols: | geranylgeranyl reductase | chr1:27991248-27992845 FORWARDhighly similar to (681) loc_os01g16020 12001.m08199 protein geranylgeranyl hydrogenase, putative, expressed seq=cds; coord=3:40062008..40064270:-1; parent_gene=GRMZM2G419111'

'nearly identical (1134) AT4G15560 | Symbols: CLA1, DEF, CLA, DXS, DXPS2 | CLA1 (CLOROPLASTOS ALTERADOS 1); 1-deoxy-D-xylulose-5-phosphate synthase | chr4:8884218-8887254 FORWARDnearly identical (1289) DXS_ORYSA Probable 1-deoxy-D-xylulose-5-phosphate synthase, chloroplast precursor (EC 2.2.1.7) (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS) - Oryza sativa (Rice)nearly identical (1289) loc_os05g33840 12005.m07616 protein 1-deoxy-D-xylulose-5-phosphate synthase, chloroplast precursor, putative, expressed seq=cds; coord=6:146378412..146382661:-1; parent_gene=GRMZM2G137151'

'nearly identical (1049) AT2G37040 | Symbols: pal1, ATPAL1 | pal1 (Phe ammonia lyase 1); phenylalanine ammonia-lyase | chr2:15557602-15560237 REVERSEnearly identical (1203) PALY_WHEAT Phenylalanine ammonia-lyase (EC 4.3.1.5) - Triticum aestivum (Wheat)nearly identical (1265) loc_os04g43800 12004.m09339 protein phenylalanine ammonia-lyase, putative, expressed seq=cds; coord=2:28048958..28052061:1; parent_gene=GRMZM2G118345'

'highly similar to (603) AT3G14440 | Symbols: NCED3, ATNCED3, STO1, SIS7 | NCED3 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 3); 9-cis-epoxycarotenoid dioxygenase | chr3:4831678-4833477 REVERSEhighly similar to (735) loc_os03g44380 12003.m09477 protein 9-cis-epoxycarotenoid dioxygenase 2, putative, expressed seq=cds; coord=1:174524887..174527795:1; parent_gene=GRMZM2G407181'

'highly similar to (641) AT4G37770 | Symbols: ACS8 | ACS8; 1-aminocyclopropane-1-carboxylate synthase | chr4:17752222-17753925 FORWARDhighly similar to (788) 1A11_ORYSA 1-aminocyclopropane-1-carboxylate synthase 1 (EC 4.4.1.14) (ACC synthase 1) (S-adenosyl-L-methionine methylthioadenosine-lyase 1) - Oryza sativa (Rice)highly similar to (788) loc_os03g51740 12003.m10154 protein 1-aminocyclopropane-1-carboxylate synthase 1, putative, expressed seq=cds; coord=1:271768133..271770623:-1; parent_gene=GRMZM2G054361'

'highly similar to (984) AT1G08520 | Symbols: PDE166, CHLD | CHLD; ATP binding / magnesium chelatase/ nucleoside-triphosphatase/ nucleotide binding | chr1:2696538-2700819 FORWARDnearly identical (1006) CHLD_TOBAC Magnesium-chelatase subunit chlD, chloroplast precursor (EC 6.6.1.1) (Mg-protoporphyrin IX chelatase) (Mg-chelatase subunit D) - Nicotiana tabacum (Common tobacco)nearly identical (1081) loc_os03g59640 12003.m10861 protein magnesium-chelatase subunit chlD, chloroplast precursor, putative, expressed seq=cds; coord=5:3095645..3103371:-1; parent_gene=GRMZM2G043453' 'nearly identical (2226) AT5G13630 | Symbols: GUN5, CCH, CHLH, CCH1 | GUN5 (GENOMES UNCOUPLED 5); magnesium chelatase | chr5:4387920-4392082 REVERSEnearly identical (2452) loc_os03g20700 12003.m34853 protein Mg-chelatase subunit XANTHA-F, putative, expressed seq=cds; coord=10:147954762..147960936:1; parent_gene=GRMZM2G323024'

'highly similar to (528) AT5G45930 | Symbols: CHLI2, CHL I2, CHLI-2 | CHLI2 (MAGNESIUM CHELATASE I2); ATPase/ magnesium chelatase | chr5:18628095-18629565 FORWARDhighly similar to (545) CHLI_SOYBN Magnesium-chelatase subunit chlI, chloroplast precursor (EC 6.6.1.1) (Mg-protoporphyrin IX chelatase) - Glycine max (Soybean)highly similar to (617) loc_os03g36540 12003.m08774 protein magnesium-chelatase subunit chlI, chloroplast precursor, putative, expressed seq=cds; coord=10:9220900..9225379:-1; parent_gene=GRMZM2G419806'

'moderately similar to (314) AT4G25080 | Symbols: CHLM | CHLM (magnesium-protoporphyrin IX methyltransferase); magnesium protoporphyrin IX methyltransferase | chr4:12877216-12878128 FORWARDmoderately similar to (436) loc_os06g04150 12006.m05146 protein magnesium-protoporphyrin O-methyltransferase, putative, expressed seq=cds; coord=6:65490775..65492414:1; parent_gene=GRMZM2G161673'

'moderately similar to (451) AT3G56940 | Symbols: CRD1, CHL27, ACSF | CRD1 (COPPER RESPONSE DEFECT 1); DNA binding / magnesium-protoporphyrin IX monomethyl ester (oxidative) cyclase | chr3:21076594-21078269 FORWARDmoderately similar to (475) CRD1_HORVU Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase, chloroplast precursor (EC 1.14.13.81) (Mg-protoporphyrin IX monomethyl ester oxidative cyclase) (Protein Xantha-l) - Hordeum vulgare (Barley)moderately similar to (492) loc_os01g17170 12001.m42971 protein magnesium-protoporphyrin IX monomethyl ester cyclase,chloroplast precursor, putative, expressed seq=cds; coord=3:45201060..45202615:-1; parent_gene=GRMZM2G043109'

'moderately similar to (388) AT5G18660 | Symbols: PCB2 | PCB2 (PALE-GREEN AND CHLOROPHYLL B REDUCED 2); 3,8-divinyl protochlorophyllide a 8-vinyl reductase | chr5:6220872-6222125 REVERSEhighly similar to (518) loc_os03g22780 12003.m07676 protein PCB2, putative, expressed seq=cds; coord=1:59863427..59864863:-1; parent_gene=GRMZM2G063048'

'highly similar to (556) AT5G54190 | Symbols: PORA | PORA; oxidoreductase/ protochlorophyllide reductase | chr5:21991183-21992238 REVERSEhighly similar to (636) PORB_HORVU Protochlorophyllide reductase B, chloroplast precursor (EC 1.3.1.33) (PCR B) (NADPH-protochlorophyllide oxidoreductase B) (POR B) - Hordeum vulgare (Barley)highly similar to (639) loc_os10g35370 12010.m06361 protein protochlorophyllide reductase B, chloroplast precursor, putative, expressed seq=cds; coord=1:227507580..227510668:-1; parent_gene=GRMZM2G036455'

'highly similar to (503) AT5G54190 | Symbols: PORA | PORA; oxidoreductase/ protochlorophyllide reductase | chr5:21991183-21992238 REVERSEhighly similar to (533) PORB_HORVU Protochlorophyllide reductase B, chloroplast precursor (EC 1.3.1.33) (PCR B) (NADPH-protochlorophyllide oxidoreductase B) (POR B) - Hordeum vulgare (Barley)highly similar to (532) loc_os10g35370 12010.m06361 protein protochlorophyllide reductase B, chloroplast precursor, putative, expressed seq=cds; coord=5:24860911..24864132:-1; parent_gene=GRMZM2G073351'

'moderately similar to (446) AT5G54190 | Symbols: PORA | PORA; oxidoreductase/ protochlorophyllide reductase | chr5:21991183-21992238 REVERSEhighly similar to (501) PORA_WHEAT Protochlorophyllide reductase A, chloroplast precursor (EC 1.3.1.33) (PCR A) (NADPH-protochlorophyllide oxidoreductase A) (POR A) - Triticum aestivum (Wheat)highly similar to (522) loc_os04g58200 12004.m35518 protein protochlorophyllide reductase A, chloroplast precursor, putative, expressed seq=cds; coord=2:1461402..1462989:-1; parent_gene=GRMZM2G084958'

'weakly similar to (149) AT3G51820 | Symbols: ATG4, G4, CHLG | G4; chlorophyll synthetase | chr3:19216301-19218934 REVERSEweakly similar to (169) loc_os05g28200 12005.m083694 protein bacteriochlorophyll synthase 34 kDa chain, putative, expressed seq=cds; coord=6:140290311..140311511:1; parent_gene=GRMZM2G162672'

'moderately similar to (222) AT2G26550 | Symbols: HO2 | HO2 (HEME OXYGENASE 2); heme oxygenase (decyclizing) | chr2:11291584-11293426 REVERSEmoderately similar to (350) loc_os03g27770 12003.m35265 protein heme oxygenase 2, putative, expressed seq=cds; coord=9:121601770..121608132:-1; parent_gene=GRMZM2G004222' 'highly similar to (762) AT3G22200 | Symbols: POP2, GABA-T, HER1 | POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-aminobutyrate transaminase/ 4-aminobutyrate:pyruvate transaminase | chr3:7835286-7838863 FORWARDvery weakly similar to (94.4) GSA_CHLRE Glutamate-1-semialdehyde 2,1-aminomutase, chloroplast precursor (EC 5.4.3.8) (GSA) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT) - Chlamydomonas reinhardtiihighly similar to (904) loc_os08g10510 12008.m080107 protein aminotransferase y4uB, putative, expressed seq=cds; coord=4:26893142..26901172:1; parent_gene=GRMZM2G093900'

'highly similar to (744) AT3G22200 | Symbols: POP2, GABA-T, HER1 | POP2 (POLLEN-PISTIL INCOMPATIBILITY 2); 4-aminobutyrate transaminase/ 4-aminobutyrate:pyruvate transaminase | chr3:7835286-7838863 FORWARDvery weakly similar to (89.7) GSA_BRANA Glutamate-1-semialdehyde 2,1-aminomutase, chloroplast precursor (EC 5.4.3.8) (GSA) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT) - Brassica napus (Rape)highly similar to (899) loc_os04g52450 12004.m101652 protein aminotransferase y4uB, putative, expressed seq=cds; coord=10:142279983..142291898:1; parent_gene=GRMZM2G108125'

'highly similar to (741) AT5G63570 | Symbols: GSA1 | GSA1 (GLUTAMATE-1-SEMIALDEHYDE-2,1-AMINOMUTASE); glutamate-1-semialdehyde 2,1-aminomutase | chr5:25451957-25453620 FORWARDhighly similar to (839) GSA_ORYSA Glutamate-1-semialdehyde 2,1-aminomutase, chloroplast precursor (EC 5.4.3.8) (GSA) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT) - Oryza sativa (Rice)highly similar to (839) loc_os08g41990 12008.m08177 protein glutamate-1-semialdehyde 2,1-aminomutase, chloroplast precursor, putative, expressed seq=cds; coord=6:155589495..155593823:-1; parent_gene=GRMZM2G116258'

'very weakly similar to (97.4) AT3G14930 | Symbols: HEME1 | HEME1; uroporphyrinogen decarboxylase | chr3:5021290-5022577 FORWARDweakly similar to (103) loc_os01g43390 12001.m150657 protein uroporphyrinogen decarboxylase, chloroplast precursor, putative, expressed seq=cds; coord=8:144960649..144961374:-1; parent_gene=GRMZM2G024738'

'moderately similar to (317) AT3G14930 | Symbols: HEME1 | HEME1; uroporphyrinogen decarboxylase | chr3:5021290-5022577 FORWARDmoderately similar to (206) DCUP_TOBAC Uroporphyrinogen decarboxylase, chloroplast precursor (EC 4.1.1.37) (URO-D) (UPD) - Nicotiana tabacum (Common tobacco)moderately similar to (383) loc_os01g43390 12001.m150657 protein uroporphyrinogen decarboxylase, chloroplast precursor, putative, expressed seq=cds; coord=8:144965045..144968261:1; parent_gene=GRMZM2G025031'

'highly similar to (581) AT2G40490 | Symbols: HEME2 | HEME2; uroporphyrinogen decarboxylase | chr2:16912961-16914988 FORWARDhighly similar to (677) DCUP_MAIZE Uroporphyrinogen decarboxylase, chloroplast precursor (EC 4.1.1.37) (URO-D) (UPD) - Zea mays (Maize)highly similar to (696) loc_os03g21900 12003.m07594 protein uroporphyrinogen decarboxylase, putative, expressed seq=cds; coord=1:56558248..56562800:1; parent_gene=GRMZM2G044074'

'weakly similar to (134) AT3G14930 | Symbols: HEME1 | HEME1; uroporphyrinogen decarboxylase | chr3:5021290-5022577 FORWARDweakly similar to (123) CYSP1_MAIZE Cysteine proteinase 1 precursor (EC 3.4.22.-) - Zea mays (Maize)weakly similar to (149) loc_os01g43390 12001.m150657 protein uroporphyrinogen decarboxylase, chloroplast precursor, putative, expressed seq=cds; coord=2:204328536..204336045:1; parent_gene=GRMZM2G046468'

'moderately similar to (350) AT3G14930 | Symbols: HEME1 | HEME1; uroporphyrinogen decarboxylase | chr3:5021290-5022577 FORWARDmoderately similar to (246) DCUP_MAIZE Uroporphyrinogen decarboxylase, chloroplast precursor (EC 4.1.1.37) (URO-D) (UPD) - Zea mays (Maize)moderately similar to (421) loc_os01g43390 12001.m150657 protein uroporphyrinogen decarboxylase, chloroplast precursor, putative, expressed seq=cds; coord=3:217796555..217806102:1; parent_gene=GRMZM2G377609'

'moderately similar to (247) AT1G03475 | Symbols: LIN2, HEMF1, ATCPO-I | LIN2 (LESION INITIATION 2); coproporphyrinogen oxidase | chr1:869302-871175 REVERSEmoderately similar to (250) HEM6_HORVU Coproporphyrinogen III oxidase, chloroplast precursor (EC 1.3.3.3) (Coproporphyrinogenase) (Coprogen oxidase) - Hordeum vulgare (Barley)moderately similar to (259) loc_os04g52130 12004.m101648 protein coproporphyrinogen III oxidase, chloroplast precursor, putative, expressed seq=cds; coord=10:141915231..141924754:1; parent_gene=GRMZM2G032282'

'highly similar to (524) AT5G63290 | Symbols: | coproporphyrinogen oxidase-related | chr5:25369349-25370894 REVERSEhighly similar to (738) loc_os12g17070 12012.m073809 protein oxygen-independent coproporphyrinogen III oxidase-like protein sll1917, putative, expressed seq=cds; coord=1:4722654..4725234:-1; parent_gene=GRMZM2G105436' 'highly similar to (724) AT4G01690 | Symbols: PPOX, HEMG1, PPO1 | PPOX; protoporphyrinogen oxidase | chr4:729929-732309 FORWARDhighly similar to (720) PPOC_TOBAC Protoporphyrinogen oxidase, chloroplast precursor (EC 1.3.3.4) (PPO I) (Protoporphyrinogen IX oxidase isozyme I) (PPX I) - Nicotiana tabacum (Common tobacco)highly similar to (856) loc_os01g18320 12001.m08374 protein protoporphyrinogen oxidase, chloroplast precursor, putative, expressed seq=cds; coord=8:876212..882478:-1; parent_gene=GRMZM2G039396'

'moderately similar to (272) AT5G14220 | Symbols: HEMG2, MEE61, PPO2 | HEMG2; electron carrier/ oxidoreductase/ protoporphyrinogen oxidase | chr5:4583506-4587369 REVERSEmoderately similar to (282) PPOM_TOBAC Protoporphyrinogen oxidase, mitochondrial (EC 1.3.3.4) (PPO II) (Protoporphyrinogen IX oxidase isozyme II) (PPX II) (PX-2) - Nicotiana tabacum (Common tobacco)moderately similar to (347) loc_os04g41260 12004.m09105 protein protoporphyrinogen oxidase, mitochondrial, putative, expressed seq=cds; coord=2:34699024..34701280:1; parent_gene=GRMZM2G364901'

'moderately similar to (204) AT1G19670 | Symbols: ATCLH1, CORI1, ATHCOR1 | ATCLH1 (ARABIDOPSIS THALIANA CORONATINE-INDUCED PROTEIN 1); chlorophyllase | chr1:6803796-6804923 REVERSEweakly similar to (172) CLH1_CITSI Chlorophyllase-1, chloroplast precursor (EC 3.1.1.14) (Chlorophyll-chlorophyllido hydrolase 1) (Chlase 1) - Citrus sinensis (Sweet orange)weakly similar to (184) loc_os10g28370 12010.m05717 protein chlorophyllase-2, chloroplast precursor, putative, expressed seq=cds; coord=1:204440912..204442153:-1; parent_gene=GRMZM2G103197'

'moderately similar to (239) AT5G43860 | Symbols: ATCLH2, CLH2 | ATCLH2; chlorophyllase | chr5:17630492-17632184 FORWARDweakly similar to (168) CLH1_CITSI Chlorophyllase-1, chloroplast precursor (EC 3.1.1.14) (Chlorophyll-chlorophyllido hydrolase 1) (Chlase 1) - Citrus sinensis (Sweet orange)moderately similar to (336) loc_os10g28370 12010.m05717 protein chlorophyllase-2, chloroplast precursor, putative, expressed seq=cds; coord=1:239828646..239830307:1; parent_gene=GRMZM2G127421'

'moderately similar to (244) AT1G19670 | Symbols: ATCLH1, CORI1, ATHCOR1 | ATCLH1 (ARABIDOPSIS THALIANA CORONATINE-INDUCED PROTEIN 1); chlorophyllase | chr1:6803796-6804923 REVERSEmoderately similar to (208) CLH1_CITSI Chlorophyllase-1, chloroplast precursor (EC 3.1.1.14) (Chlorophyll-chlorophyllido hydrolase 1) (Chlase 1) - Citrus sinensis (Sweet orange)moderately similar to (201) loc_os10g28370 12010.m05717 protein chlorophyllase-2, chloroplast precursor, putative, expressed seq=cds; coord=7:62130993..62132323:1; parent_gene=GRMZM2G170734'

'moderately similar to (226) AT3G07040 | Symbols: RPM1, RPS3 | RPM1 (RESISTANCE TO P. SYRINGAE PV MACULICOLA 1); nucleotide binding / protein binding | chr3:2226244-2229024 REVERSEhighly similar to (782) loc_os02g18510 12002.m07094 protein stripe rust resistance protein Yr10, putative seq=cds; coord=1:221236143..221241717:-1; parent_gene=GRMZM2G077068'

'very weakly similar to (98.6) AT1G65870 | Symbols: | disease resistance-responsive family protein | chr1:24503624-24504193 FORWARDweakly similar to (166) loc_os11g42550 12011.m08091 protein disease resistance response protein 206, putative, expressed seq=cds; coord=1:124469547..124470613:-1; parent_gene=GRMZM2G433184'

'moderately similar to (221) AT4G37000 | Symbols: ACD2, ATRCCR | ACD2 (ACCELERATED CELL DEATH 2); red chlorophyll catabolite reductase | chr4:17442627-17443762 FORWARDmoderately similar to (313) RCCR_HORVU Red chlorophyll catabolite reductase (EC 1.-.-.-) (RCC reductase) (HvRCCR) (Fragment) - Hordeum vulgare (Barley)moderately similar to (375) loc_os10g25030 12010.m05454 protein red chlorophyll catabolite reductase, putative, expressed seq=cds; coord=1:140984467..140986816:-1; parent_gene=GRMZM2G458824'

'nearly identical (1045) AT4G24280 | Symbols: cpHsc70-1 | cpHsc70-1 (chloroplast heat shock protein 70-1); ATP binding | chr4:12590094-12593437 FORWARDnearly identical (1054) HSP7S_PEA Stromal 70 kDa heat shock-related protein, chloroplast precursor - Pisum sativum (Garden pea)nearly identical (1136) loc_os05g23740 12005.m06668 protein stromal 70 kDa heat shock-related protein, chloroplast precursor, putative, expressed seq=cds; coord=1:263143605..263149463:1; parent_gene=GRMZM2G079668'

'highly similar to (685) AT4G16660 | Symbols: | heat shock protein 70, putative / HSP70, putative | chr4:9377225-9381232 FORWARDmoderately similar to (254) HSP7C_PETHY Heat shock cognate 70 kDa protein - Petunia hybrida (Petunia)highly similar to (849) loc_os02g48110 12002.m09845 protein oxygen-regulated protein precursor, putative, expressed seq=cds; coord=4:161365940..161376882:-1; parent_gene=GRMZM2G158093' 'nearly identical (1076) AT3G12580 | Symbols: HSP70 | HSP70 (heat shock protein 70); ATP binding | chr3:3991487-3993689 REVERSEnearly identical (1087) HSP7C_PETHY Heat shock cognate 70 kDa protein - Petunia hybrida (Petunia)nearly identical (1111) loc_os01g62290 12001.m150772 protein heat shock cognate 70 kDa protein, putative, expressed seq=cds; coord=8:168955391..168958754:-1; parent_gene=GRMZM2G310431'

'highly similar to (719) AT2G41680 | Symbols: NTRC | NTRC (NADPH-DEPENDENT THIOREDOXIN REDUCTASE C); thioredoxin-disulfide reductase | chr2:17376349-17379028 REVERSEhighly similar to (809) loc_os07g46410 12007.m08858 protein bifunctional thioredoxin reductase/thioredoxin, putative, expressed seq=cds; coord=7:170855215..170860182:1; parent_gene=GRMZM2G136522'

'moderately similar to (249) AT5G03630 | Symbols: ATMDAR2 | ATMDAR2; monodehydroascorbate reductase (NADH) | chr5:922378-924616 REVERSEmoderately similar to (249) MDAR_PEA Monodehydroascorbate reductase (EC 1.6.5.4) (MDAR) (Ascorbate free radical reductase) (AFR reductase) - Pisum sativum (Garden pea)moderately similar to (298) loc_os09g39380 12009.m06876 protein monodehydroascorbate reductase, putative, expressed seq=cds; coord=2:165615333..165616565:-1; parent_gene=GRMZM2G084881'

'highly similar to (619) AT3G52880 | Symbols: ATMDAR1 | monodehydroascorbate reductase, putative | chr3:19601477-19604366 REVERSEhighly similar to (637) MDARS_CUCSA Monodehydroascorbate reductase, seedling isozyme (EC 1.6.5.4) (MDAR seedling) (Ascorbate free radical reductase seedling) (AFR reductase seedling) - Cucumis sativus (Cucumber)highly similar to (748) loc_os08g44340 12008.m08407 protein monodehydroascorbate reductase, putative, expressed seq=cds; coord=4:53078446..53083109:-1; parent_gene=GRMZM2G134708'

'moderately similar to (350) AT3G27190 | Symbols: | uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative | chr3:10039504-10042917 REVERSEmoderately similar to (373) loc_os09g32820 12009.m06368 protein uridine/cytidine kinase-like 1, putative, expressed seq=cds; coord=1:193604458..193608053:1; parent_gene=GRMZM2G020429'

'highly similar to (661) AT4G26510 | Symbols: | ATP binding / kinase/ phosphotransferase, alcohol group as acceptor / uracil phosphoribosyltransferase | chr4:13384503-13387920 FORWARDhighly similar to (852) loc_os02g17320 12002.m33637 protein uridine/cytidine kinase-like 1, putative, expressed seq=cds; coord=5:66021901..66031994:-1; parent_gene=GRMZM2G034143'

'highly similar to (680) AT4G26510 | Symbols: | ATP binding / kinase/ phosphotransferase, alcohol group as acceptor / uracil phosphoribosyltransferase | chr4:13384503-13387920 FORWARDhighly similar to (864) loc_os02g17320 12002.m33637 protein uridine/cytidine kinase-like 1, putative, expressed seq=cds; coord=4:241073345..241079426:1; parent_gene=GRMZM2G169462'

'moderately similar to (464) AT5G03300 | Symbols: ADK2 | ADK2 (ADENOSINE KINASE 2); adenosine kinase/ copper ion binding / kinase | chr5:796573-798997 FORWARDmoderately similar to (367) ADK_PHYPA Adenosine kinase (EC 2.7.1.20) (AK) (Adenosine 5'-phosphotransferase) - Physcomitrella patens (Moss)highly similar to (519) loc_os04g43750 12004.m101587 protein adenosine kinase 2, putative, expressed seq=cds; coord=2:28137894..28141868:1; parent_gene=GRMZM2G089767'

'highly similar to (577) AT5G03300 | Symbols: ADK2 | ADK2 (ADENOSINE KINASE 2); adenosine kinase/ copper ion binding / kinase | chr5:796573-798997 FORWARDmoderately similar to (474) ADK_PHYPA Adenosine kinase (EC 2.7.1.20) (AK) (Adenosine 5'-phosphotransferase) - Physcomitrella patens (Moss)highly similar to (646) loc_os02g41590 12002.m09195 protein adenosine kinase 2, putative, expressed seq=cds; coord=4:143082898..143087846:-1; parent_gene=GRMZM2G135132'

'weakly similar to (133) AT2G01460 | Symbols: | ATP binding / kinase | chr2:206136-211765 FORWARD seq=cds; coord=10:104818768..104819926:1; parent_gene=GRMZM2G003648' 'highly similar to (615) AT1G73980 | Symbols: | phosphoribulokinase/uridine kinase family protein | chr1:27820292-27823527 REVERSEhighly similar to (682) loc_os02g47860 12002.m100333 protein uridine kinase, putative, expressed seq=cds; coord=5:201458665..201464423:1; parent_gene=GRMZM2G147430'

'highly similar to (540) AT2G01460 | Symbols: | ATP binding / kinase | chr2:206136-211765 FORWARDhighly similar to (751) loc_os04g21110 12004.m07264 protein expressed protein seq=cds; coord=10:104822498..104857891:1; parent_gene=GRMZM2G473385'

'moderately similar to (495) AT5G19440 | Symbols: | cinnamyl-alcohol dehydrogenase, putative (CAD) | chr5:6556493-6558123 FORWARDmoderately similar to (219) DFRA_DIACA Dihydroflavonol-4-reductase (EC 1.1.1.219) (DFR) (Dihydrokaempferol 4-reductase) - Dianthus caryophyllus (Carnation) (Clove pink)highly similar to (567) loc_os01g34480 12001.m150871 protein dihydroflavonol-4-reductase, putative, expressed seq=cds; coord=5:130658345..130666795:1; parent_gene=GRMZM2G179981'

'highly similar to (931) AT4G33650 | Symbols: ADL2, DRP3A | DRP3A (DYNAMIN-RELATED PROTEIN 3A); GTP binding / GTPase/ phosphoinositide binding | chr4:16161073-16166587 FORWARDnearly identical (1322) loc_os01g69130 12001.m150447 protein dynamin-related protein 3A, putative, expressed seq=cds; coord=3:160397311..160408336:1; parent_gene=GRMZM2G129155'

'highly similar to (912) AT4G33650 | Symbols: ADL2, DRP3A | DRP3A (DYNAMIN-RELATED PROTEIN 3A); GTP binding / GTPase/ phosphoinositide binding | chr4:16161073-16166587 FORWARDnearly identical (1281) loc_os01g69130 12001.m150447 protein dynamin-related protein 3A, putative, expressed seq=cds; coord=8:161744495..161753951:1; parent_gene=GRMZM2G180335'

'moderately similar to (393) AT3G12800 | Symbols: SDRB, DECR | SDRB (SHORT-CHAIN DEHYDROGENASE-REDUCTASE B); binding / catalytic/ oxidoreductase | chr3:4063463-4064757 REVERSEvery weakly similar to (93.2) GRDH_ORYSA Glucose and ribitol dehydrogenase homolog (EC 1.1.1.-) - Oryza sativa (Rice)moderately similar to (491) loc_os04g52400 12004.m10134 protein peroxisomal 2,4-dienoyl-CoA reductase, putative, expressed seq=cds; coord=2:10369985..10373158:-1; parent_gene=GRMZM2G005107'

'moderately similar to (324) AT5G50700 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr5:20623259-20624995 REVERSEhighly similar to (575) loc_os12g27830 12012.m06599 protein corticosteroid 11-beta-dehydrogenase isozyme 1, putative, expressed seq=cds; coord=7:169214766..169217063:-1; parent_gene=GRMZM2G006119'

'moderately similar to (411) AT3G12800 | Symbols: SDRB, DECR | SDRB (SHORT-CHAIN DEHYDROGENASE-REDUCTASE B); binding / catalytic/ oxidoreductase | chr3:4063463-4064757 REVERSEvery weakly similar to (94.0) GRDH_DAUCA Glucose and ribitol dehydrogenase (EC 1.1.1.-) (Carrot ABA-induced in somatic embryos 5 protein) - Daucus carota (Carrot)highly similar to (509) loc_os04g52400 12004.m10134 protein peroxisomal 2,4-dienoyl-CoA reductase, putative, expressed seq=cds; coord=10:142175734..142186868:1; parent_gene=GRMZM2G025243'

'weakly similar to (116) AT3G26770 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr3:9845494-9847079 FORWARDvery weakly similar to (97.1) TS2_MAIZE Sex determination protein tasselseed-2 - Zea mays (Maize)weakly similar to (193) loc_os07g46830 12007.m08900 protein sex determination protein tasselseed-2, putative, expressed seq=cds; coord=7:171728748..171729994:1; parent_gene=GRMZM2G025885'

'moderately similar to (308) AT4G05530 | Symbols: IBR1, SDRA | IBR1 (INDOLE-3-BUTYRIC ACID RESPONSE 1); binding / catalytic/ oxidoreductase | chr4:2816462-2818074 FORWARDvery weakly similar to (99.0) GRDH_DAUCA Glucose and ribitol dehydrogenase (EC 1.1.1.-) (Carrot ABA-induced in somatic embryos 5 protein) - Daucus carota (Carrot)moderately similar to (366) loc_os09g04730 12009.m22042 protein dehydrogenase/reductase SDR family member 2, putative, expressed seq=cds; coord=6:162486424..162491946:-1; parent_gene=GRMZM2G041694'

'moderately similar to (244) AT3G26760 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr3:9843639-9844899 FORWARDweakly similar to (178) TS2_MAIZE Sex determination protein tasselseed-2 - Zea mays (Maize)moderately similar to (338) loc_os11g32030 12011.m07105 protein sex determination protein tasselseed-2, putative, expressed seq=cds; coord=4:22835928..22842145:1; parent_gene=GRMZM2G047800' 'weakly similar to (189) AT5G02540 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr5:568609-570720 FORWARDmoderately similar to (238) loc_os01g05840 12001.m42866 protein retinol dehydrogenase 11, putative, expressed seq=cds; coord=3:4133973..4135826:1; parent_gene=GRMZM2G050915'

'moderately similar to (306) AT5G15940 | Symbols: | binding / catalytic/ oxidoreductase | chr5:5202801-5204715 FORWARDmoderately similar to (435) loc_os09g17750 12009.m05033 protein dehydrogenase/reductase SDR family member on chromosome X precursor, putative, expressed seq=cds; coord=7:94515828..94520376:-1; parent_gene=GRMZM2G053958'

'moderately similar to (215) AT1G10310 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr1:3381733-3383874 REVERSEmoderately similar to (270) loc_os02g35170 12002.m08605 protein expressed protein seq=cds; coord=9:25857875..25858565:-1; parent_gene=GRMZM2G059361'

'moderately similar to (299) AT5G10050 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr5:3144254-3145643 FORWARDmoderately similar to (397) loc_os04g38420 12004.m08832 protein oxidoreductase, putative, expressed seq=cds; coord=2:42800989..42805578:1; parent_gene=GRMZM2G065171'

'moderately similar to (452) AT5G04900 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr5:1434826-1437194 FORWARDvery weakly similar to (84.7) SDR1_PICAB Short-chain type dehydrogenase/reductase (EC 1.-.-.-) - Picea abies (Norway spruce) (Picea excelsa)highly similar to (523) loc_os03g45194 12003.m09550 protein short-chain dehydrogenase/reductase SDR, putative, expressed seq=cds; coord=5:15650410..15655937:1; parent_gene=GRMZM2G065194'

'moderately similar to (207) AT1G52340 | Symbols: ABA2, SIS4, GIN1, SDR1, ISI4, SRE1, ATABA2, ATSDR1 | ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase | chr1:19489997-19491527 REVERSEmoderately similar to (204) TS2_MAIZE Sex determination protein tasselseed-2 - Zea mays (Maize)moderately similar to (345) loc_os04g33240 12004.m08419 protein sex determination protein tasselseed-2, putative, expressed seq=cds; coord=2:76993674..76995064:1; parent_gene=GRMZM2G069523'

'moderately similar to (288) AT3G59710 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr3:22055220-22057156 REVERSEmoderately similar to (409) loc_os02g39490 12002.m09037 protein carbonyl reductase 3, putative, expressed seq=cds; coord=10:127609556..127613140:-1; parent_gene=GRMZM2G070279'

'weakly similar to (154) AT4G03140 | Symbols: | binding / catalytic/ oxidoreductase | chr4:1392191-1393662 FORWARDweakly similar to (122) TS2_MAIZE Sex determination protein tasselseed-2 - Zea mays (Maize)moderately similar to (236) loc_os07g40250 12007.m08266 protein sex determination protein tasselseed-2, putative, expressed seq=cds; coord=7:162398129..162399427:1; parent_gene=GRMZM2G076981'

'moderately similar to (313) AT1G67730 | Symbols: YBR159, KCR1 | YBR159; ketoreductase/ oxidoreductase | chr1:25391676-25393365 FORWARDmoderately similar to (463) loc_os02g38440 12002.m08932 protein steroid dehydrogenase KIK-I, putative, expressed seq=cds; coord=4:132759801..132763262:-1; parent_gene=GRMZM2G087323'

'moderately similar to (317) AT5G50700 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr5:20623259-20624995 REVERSEmoderately similar to (288) loc_os04g32070 12004.m08305 protein steroleosin, putative, expressed seq=cds; coord=2:68600637..68602278:-1; parent_gene=GRMZM2G108338'

'moderately similar to (263) AT4G05530 | Symbols: IBR1, SDRA | IBR1 (INDOLE-3-BUTYRIC ACID RESPONSE 1); binding / catalytic/ oxidoreductase | chr4:2816462-2818074 FORWARDvery weakly similar to (88.6) GRDH_DAUCA Glucose and ribitol dehydrogenase (EC 1.1.1.-) (Carrot ABA-induced in somatic embryos 5 protein) - Daucus carota (Carrot)moderately similar to (317) loc_os09g04730 12009.m22042 protein dehydrogenase/reductase SDR family member 2, putative, expressed seq=cds; coord=7:32624687..32633165:-1; parent_gene=GRMZM2G109743'

'moderately similar to (254) AT3G55290 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr3:20502653-20503730 FORWARDvery weakly similar to (94.0) FABG3_BRANA 3-oxoacyl-[acyl-carrier-protein] reductase 3, chloroplast precursor (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase 3) - Brassica napus (Rape)moderately similar to (370) loc_os08g39960 12008.m26742 protein 3-oxoacyl-reductase, chloroplast precursor, putative, expressed seq=cds; coord=1:188344346..188355656:-1; parent_gene=GRMZM2G115442' 'moderately similar to (291) AT1G10310 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr1:3381733-3383874 REVERSEmoderately similar to (375) loc_os02g35170 12002.m08605 protein expressed protein seq=cds; coord=5:173685524..173688118:-1; parent_gene=GRMZM2G128146'

'moderately similar to (205) AT5G02540 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr5:568609-570720 FORWARDmoderately similar to (250) loc_os10g40030 12010.m21964 protein WW domain-containing oxidoreductase, putative, expressed seq=cds; coord=9:118060344..118063910:1; parent_gene=GRMZM2G128577'

'moderately similar to (246) AT3G59710 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr3:22055220-22057156 REVERSEmoderately similar to (380) loc_os02g39490 12002.m09037 protein carbonyl reductase 3, putative, expressed seq=cds; coord=2:33004446..33008192:1; parent_gene=GRMZM2G135277'

'moderately similar to (261) AT2G47140 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr2:19350970-19352059 REVERSEmoderately similar to (242) TS2_MAIZE Sex determination protein tasselseed-2 - Zea mays (Maize)moderately similar to (422) loc_os03g61740 12003.m11055 protein sex determination protein tasselseed-2, putative, expressed seq=cds; coord=1:295436901..295438003:-1; parent_gene=GRMZM2G156739'

'moderately similar to (367) AT5G02540 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr5:568609-570720 FORWARDmoderately similar to (466) loc_os01g05840 12001.m42866 protein retinol dehydrogenase 11, putative, expressed seq=cds; coord=3:17182875..17186450:-1; parent_gene=GRMZM2G162527'

'moderately similar to (295) AT1G52340 | Symbols: ABA2, SIS4, GIN1, SDR1, ISI4, SRE1, ATABA2, ATSDR1 | ABA2 (ABA DEFICIENT 2); alcohol dehydrogenase/ oxidoreductase/ xanthoxin dehydrogenase | chr1:19489997-19491527 REVERSEmoderately similar to (241) TS2_MAIZE Sex determination protein tasselseed-2 - Zea mays (Maize)moderately similar to (412) loc_os03g59610 12003.m10858 protein sex determination protein tasselseed-2, putative, expressed seq=cds; coord=5:3145791..3147542:-1; parent_gene=GRMZM2G332976'

'moderately similar to (263) AT3G59710 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr3:22055220-22057156 REVERSEmoderately similar to (409) loc_os02g39490 12002.m09037 protein carbonyl reductase 3, putative, expressed seq=cds; coord=4:134994992..134998245:-1; parent_gene=GRMZM2G374313'

'weakly similar to (187) AT5G10050 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr5:3144254-3145643 FORWARDmoderately similar to (268) loc_os12g43740 12012.m08147 protein expressed protein seq=cds; coord=3:92694099..92694968:-1; parent_gene=GRMZM2G403313'

'moderately similar to (290) AT3G51680 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr3:19173622-19174667 REVERSEhighly similar to (533) TS2_MAIZE Sex determination protein tasselseed-2 - Zea mays (Maize)moderately similar to (436) loc_os03g18740 12003.m07295 protein sex determination protein tasselseed-2, putative, expressed seq=cds; coord=1:46678942..46680363:1; parent_gene=GRMZM2G455809'

'moderately similar to (355) AT4G11410 | Symbols: | short-chain dehydrogenase/reductase (SDR) family protein | chr4:6945127-6947186 REVERSEweakly similar to (101) POR_AVESA Protochlorophyllide reductase (EC 1.3.1.33) (PCR) (NADPH-protochlorophyllide oxidoreductase) (POR) (Fragment) - Avena sativa (Oat)moderately similar to (436) loc_os10g40020 12010.m06775 protein WW domain-containing oxidoreductase, putative, expressed seq=cds; coord=1:87599876..87602403:-1; parent_gene=GRMZM2G464885'

'moderately similar to (203) AT4G37580 | Symbols: HLS1, COP3, UNS2 | HLS1 (HOOKLESS 1); N-acetyltransferase | chr4:17658932-17660564 FORWARDmoderately similar to (386) loc_os06g44100 12006.m08938 protein acetyltransferase, GNAT family protein, expressed seq=cds; coord=6:95712352..95714082:1; parent_gene=GRMZM2G049730'

'moderately similar to (251) AT5G16800 | Symbols: | GCN5-related N-acetyltransferase (GNAT) family protein | chr5:5524720-5526295 REVERSEmoderately similar to (322) loc_os02g46700 12002.m33825 protein N-acetyltransferase, putative, expressed seq=cds; coord=5:198971871..198973129:-1; parent_gene=GRMZM2G169326'

'highly similar to (623) AT1G67490 | Symbols: GCS1, KNF | GCS1 (GLUCOSIDASE 1); alpha-glucosidase | chr1:25280633-25286581 REVERSEhighly similar to (879) loc_os01g69210 12001.m150828 protein mannosyl-oligosaccharide glucosidase, putative, expressed seq=cds; coord=3:160074249..160087303:-1; parent_gene=GRMZM2G126468' 'highly similar to (973) AT5G11720 | Symbols: | alpha-glucosidase 1 (AGLU1) | chr5:3776840-3780025 FORWARDnearly identical (1307) AGLU_ORYSA Probable alpha-glucosidase Os06g0675700 precursor (EC 3.2.1.20) (Maltase) - Oryza sativa (Rice)nearly identical (1307) loc_os06g46284 12006.m091810 protein alpha-glucosidase precursor, putative, expressed seq=cds; coord=6:91630823..91634799:1; parent_gene=GRMZM2G428518'

'highly similar to (689) AT2G43020 | Symbols: ATPAO2 | ATPAO2 (Polyamine oxidase 2); amine oxidase/ electron carrier/ oxidoreductase | chr2:17891945-17894440 FORWARDweakly similar to (135) PAO_MAIZE Polyamine oxidase precursor (EC 1.5.3.11) - Zea mays (Maize)highly similar to (860) loc_os04g53190 12004.m35201 protein lysine-specific histone demethylase 1, putative, expressed seq=cds; coord=2:8992621..8997876:1; parent_gene=GRMZM2G000052'

'nearly identical (1134) AT4G16310 | Symbols: LDL3 | LDL3 (LSD1-LIKE3); amine oxidase/ electron carrier/ oxidoreductase | chr4:9218636-9224764 FORWARDweakly similar to (102) PAO_MAIZE Polyamine oxidase precursor (EC 1.5.3.11) - Zea mays (Maize)nearly identical (2142) loc_os10g38850 12010.m06652 protein amine oxidase, flavin-containing family protein, expressed seq=cds; coord=1:82010853..82020375:1; parent_gene=GRMZM2G030529'

'moderately similar to (361) AT4G29720 | Symbols: ATPAO5 | ATPAO5 (Polyamine oxidase 5); amine oxidase/ electron carrier/ oxidoreductase | chr4:14553456-14555057 REVERSEvery weakly similar to (84.0) PAO_MAIZE Polyamine oxidase precursor (EC 1.5.3.11) - Zea mays (Maize)highly similar to (729) loc_os01g51320 12001.m11313 protein peroxisomal N1-acetyl-spermine/spermidine oxidase, putative, expressed seq=cds; coord=3:203893426..203895144:1; parent_gene=GRMZM2G035994'

'moderately similar to (354) AT5G61290 | Symbols: | flavin-containing monooxygenase family protein / FMO family protein | chr5:24648599-24650647 FORWARDmoderately similar to (429) loc_os07g02130 12007.m04687 protein disulfide oxidoreductase/ monooxygenase/ oxidoreductase, putative seq=cds; coord=7:1787892..1789224:-1; parent_gene=GRMZM2G106588'

'moderately similar to (423) AT5G61290 | Symbols: | flavin-containing monooxygenase family protein / FMO family protein | chr5:24648599-24650647 FORWARDhighly similar to (542) loc_os01g26876 12001.m09132 protein disulfide oxidoreductase/ monooxygenase/ oxidoreductase, putative, expressed seq=cds; coord=7:1557370..1559284:1; parent_gene=GRMZM2G108637'

'moderately similar to (414) AT5G61290 | Symbols: | flavin-containing monooxygenase family protein / FMO family protein | chr5:24648599-24650647 FORWARDhighly similar to (540) loc_os07g02130 12007.m04687 protein disulfide oxidoreductase/ monooxygenase/ oxidoreductase, putative seq=cds; coord=7:1627368..1629084:1; parent_gene=GRMZM2G148605'

'moderately similar to (375) AT5G61290 | Symbols: | flavin-containing monooxygenase family protein / FMO family protein | chr5:24648599-24650647 FORWARDmoderately similar to (491) loc_os01g26876 12001.m09132 protein disulfide oxidoreductase/ monooxygenase/ oxidoreductase, putative, expressed seq=cds; coord=7:1568021..1569655:1; parent_gene=GRMZM2G162222'

'highly similar to (682) AT2G43020 | Symbols: ATPAO2 | ATPAO2 (Polyamine oxidase 2); amine oxidase/ electron carrier/ oxidoreductase | chr2:17891945-17894440 FORWARDweakly similar to (134) PAO_MAIZE Polyamine oxidase precursor (EC 1.5.3.11) - Zea mays (Maize)highly similar to (848) loc_os04g53190 12004.m35201 protein lysine-specific histone demethylase 1, putative, expressed seq=cds; coord=10:143058298..143063415:1; parent_gene=GRMZM2G396856'

'moderately similar to (268) AT1G49670 | Symbols: NQR | NQR; binding / catalytic/ oxidoreductase/ zinc ion binding | chr1:18381591-18386021 REVERSEmoderately similar to (302) loc_os09g28570 12009.m22117 protein zinc-binding alcohol dehydrogenase domain-containing protein 2, putative, expressed seq=cds; coord=7:126470209..126475939:1; parent_gene=GRMZM2G479068'

'moderately similar to (257) AT2G29150 | Symbols: | tropinone reductase, putative / tropine dehydrogenase, putative | chr2:12535715-12536964 REVERSEweakly similar to (116) SDR1_PICAB Short-chain type dehydrogenase/reductase (EC 1.-.-.-) - Picea abies (Norway spruce) (Picea excelsa)moderately similar to (293) loc_os11g43360 12011.m08171 protein tropinone reductase 2, putative seq=cds; coord=4:140232..141202:-1; parent_gene=GRMZM2G000586' 'moderately similar to (225) AT5G06060 | Symbols: | tropinone reductase, putative / tropine dehydrogenase, putative | chr5:1824066-1825833 REVERSEvery weakly similar to (99.4) SDR1_PICAB Short-chain type dehydrogenase/reductase (EC 1.-.-.-) - Picea abies (Norway spruce) (Picea excelsa)moderately similar to (295) loc_os11g43200 12011.m08155 protein tropinone reductase 2, putative seq=cds; coord=8:159899298..159901286:-1; parent_gene=GRMZM2G002304'

'moderately similar to (275) AT2G29360 | Symbols: | tropinone reductase, putative / tropine dehydrogenase, putative | chr2:12603849-12605121 FORWARDweakly similar to (127) GRDH_ORYSA Glucose and ribitol dehydrogenase homolog (EC 1.1.1.-) - Oryza sativa (Rice)moderately similar to (318) loc_os11g43200 12011.m08155 protein tropinone reductase 2, putative seq=cds; coord=4:3588667..3591754:1; parent_gene=GRMZM2G097981'

'moderately similar to (320) AT5G06060 | Symbols: | tropinone reductase, putative / tropine dehydrogenase, putative | chr5:1824066-1825833 REVERSEvery weakly similar to (96.7) GRDH_ORYSA Glucose and ribitol dehydrogenase homolog (EC 1.1.1.-) - Oryza sativa (Rice)moderately similar to (390) loc_os03g16220 12003.m101290 protein tropinone reductase, putative, expressed seq=cds; coord=1:39213217..39219522:-1; parent_gene=GRMZM2G141799'

'moderately similar to (235) AT5G06060 | Symbols: | tropinone reductase, putative / tropine dehydrogenase, putative | chr5:1824066-1825833 REVERSEvery weakly similar to (93.2) FABG4_BRANA 3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase 4) (Fragment) - Brassica napus (Rape)moderately similar to (281) loc_os11g43360 12011.m08171 protein tropinone reductase 2, putative seq=cds; coord=2:230414138..230415824:1; parent_gene=GRMZM2G152258'

'moderately similar to (271) AT1G07440 | Symbols: | tropinone reductase, putative / tropine dehydrogenase, putative | chr1:2286700-2287665 REVERSEweakly similar to (105) FABG4_BRANA 3-oxoacyl-[acyl-carrier-protein] reductase 4 (EC 1.1.1.100) (3-ketoacyl-acyl carrier protein reductase 4) (Fragment) - Brassica napus (Rape)moderately similar to (364) loc_os11g43200 12011.m08155 protein tropinone reductase 2, putative seq=cds; coord=4:3514620..3515646:1; parent_gene=GRMZM2G370988'

'moderately similar to (452) AT2G30470 | Symbols: HSI2, VAL1 | HSI2 (HIGH-LEVEL EXPRESSION OF SUGAR-INDUCIBLE GENE 2); transcription factor/ transcription repressor | chr2:12980904-12984724 REVERSEvery weakly similar to (83.2) VIV1_MAIZE Regulatory protein viviparous-1 - Zea mays (Maize)nearly identical (1250) loc_os07g37610 12007.m08011 protein HSI2, putative, expressed seq=cds; coord=7:157670367..157678433:1; parent_gene=GRMZM2G008356'

'moderately similar to (242) AT1G72050 | Symbols: TFIIIA | TFIIIA (TRANSCRIPTION FACTOR IIIA); nucleic acid binding / zinc ion binding | chr1:27115808-27117228 FORWARDmoderately similar to (371) loc_os05g03020 12005.m04836 protein transcription factor IIIA, putative, expressed seq=cds; coord=6:29282248..29286063:-1; parent_gene=GRMZM2G050939'

'highly similar to (665) AT4G00730 | Symbols: ANL2, AHDP | ANL2 (ANTHOCYANINLESS 2); transcription factor/ transcription regulator | chr4:301071-304103 REVERSEhighly similar to (881) loc_os04g48070 12004.m35428 protein homeobox protein OCL1, putative, expressed seq=cds; coord=10:136932960..136939534:1; parent_gene=AC235534.1_FG007' 'moderately similar to (494) AT1G12800 | Symbols: | S1 RNA-binding domain-containing protein | chr1:4361778-4365189 REVERSEnearly identical (1026) loc_os02g02390 12002.m05588 protein RNA binding protein, putative, expressed seq=cds; coord=5:69311998..69322471:1; parent_gene=GRMZM2G088114'

'moderately similar to (211) AT1G79180 | Symbols: ATMYB63, MYB63 | MYB63 (MYB DOMAIN PROTEIN 63); DNA binding / transcription activator/ transcription factor | chr1:29786509-29787589 FORWARDmoderately similar to (243) MYB1_MAIZE Myb-related protein Zm1 - Zea mays (Maize)moderately similar to (358) loc_os04g50770 12004.m09974 protein myb-related protein Zm1, putative, expressed seq=cds; coord=10:140190031..140191484:-1; parent_gene=GRMZM2G097636'

'moderately similar to (211) AT1G79180 | Symbols: ATMYB63, MYB63 | MYB63 (MYB DOMAIN PROTEIN 63); DNA binding / transcription activator/ transcription factor | chr1:29786509-29787589 FORWARDmoderately similar to (243) MYB1_MAIZE Myb-related protein Zm1 - Zea mays (Maize)moderately similar to (344) loc_os04g50770 12004.m09974 protein myb-related protein Zm1, putative, expressed seq=cds; coord=10:140193073..140194565:-1; parent_gene=GRMZM2G097638'

'moderately similar to (227) AT1G32770 | Symbols: ANAC012, SND1, NST3 | ANAC012 (ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 12); specific transcriptional repressor/ transcription activator/ transcription factor | chr1:11865343-11866950 REVERSEmoderately similar to (205) NAC76_ORYSA NAC domain-containing protein 76 (ONAC076) - Oryza sativa (Rice)moderately similar to (348) loc_os06g04090 12006.m05140 protein NAM protein, putative, expressed seq=cds; coord=6:66026862..66029306:1; parent_gene=GRMZM2G091490'

'very weakly similar to (96.3) AT4G28300 | Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:14015414-14016823 FORWARDmoderately similar to (479) loc_os01g48220 12001.m11014 protein expressed protein seq=cds; coord=8:149981862..149984439:-1; parent_gene=GRMZM2G160990'

'moderately similar to (217) AT2G34830 | Symbols: WRKY35, MEE24, AtWRKY35 | WRKY35 (WRKY DNA-binding protein 35); transcription factor | chr2:14693839-14696378 REVERSEhighly similar to (550) loc_os04g50920 12004.m09989 protein WRKY DNA binding domain containing protein, expressed seq=cds; coord=2:12799342..12803684:-1; parent_gene=GRMZM2G024898'

'very weakly similar to (99.4) AT2G22750 | Symbols: | basic helix-loop-helix (bHLH) family protein | chr2:9672145-9673624 FORWARDmoderately similar to (220) loc_os10g01530 12010.m03577 protein helix-loop-helix DNA-binding domain containing protein, expressed seq=cds; coord=1:112407261..112409295:-1; parent_gene=GRMZM2G150327'

'highly similar to (813) AT1G30680 | Symbols: | toprim domain-containing protein | chr1:10881665-10886060 FORWARDnearly identical (1098) loc_os06g45980 12006.m09126 protein nucleic acid binding protein, putative, expressed seq=cds; coord=6:92610561..92616400:1; parent_gene=GRMZM2G164835'

'moderately similar to (282) AT5G10770 | Symbols: | chloroplast nucleoid DNA-binding protein, putative | chr5:3403331-3405331 REVERSEmoderately similar to (497) loc_os02g48860 12002.m09920 protein aspartic proteinase nepenthesin-2 precursor, putative, expressed seq=cds; coord=5:203698818..203701217:1; parent_gene=GRMZM2G128992'

'moderately similar to (329) AT5G10770 | Symbols: | chloroplast nucleoid DNA-binding protein, putative | chr5:3403331-3405331 REVERSEhighly similar to (549) loc_os02g48860 12002.m09920 protein aspartic proteinase nepenthesin-2 precursor, putative, expressed seq=cds; coord=4:163962237..163964018:1; parent_gene=GRMZM2G141036'

'moderately similar to (438) AT5G09880 | Symbols: | RNA recognition motif (RRM)-containing protein | chr5:3081646-3085179 REVERSEhighly similar to (524) loc_os03g05830 12003.m06105 protein splicing factor, putative, expressed seq=cds; coord=5:32658760..32668791:-1; parent_gene=GRMZM2G071589'

'moderately similar to (322) AT5G09880 | Symbols: | RNA recognition motif (RRM)-containing protein | chr5:3081646-3085179 REVERSEmoderately similar to (416) loc_os10g30370 12010.m22002 protein RNA-binding region-containing protein 2, putative, expressed seq=cds; coord=1:237741444..237749566:1; parent_gene=GRMZM2G076597' 'highly similar to (806) AT3G09660 | Symbols: MCM8 | MCM8; ATP binding / DNA binding / DNA-dependent ATPase/ nucleoside-triphosphatase/ nucleotide binding | chr3:2961314-2966166 REVERSEmoderately similar to (286) MCM3_MAIZE DNA replication licensing factor MCM3 homolog (Replication origin activator) (ROA protein) (Fragment) - Zea mays (Maize)highly similar to (549) loc_os05g38850 12005.m08064 protein DNA replication licensing factor MCM8, putative, expressed seq=cds; coord=8:117615277..117633296:-1; parent_gene=GRMZM2G163658'

'weakly similar to (169) AT2G14050 | Symbols: MCM9 | MCM9; ATP binding / DNA binding / DNA-dependent ATPase/ nucleoside-triphosphatase/ nucleotide binding | chr2:5909240-5913817 FORWARDweakly similar to (174) loc_os06g11500 12006.m05867 protein minichromosome maintenance protein MCM, putative, expressed seq=cds; coord=6:111140069..111155365:1; parent_gene=GRMZM2G534116'

'moderately similar to (450) AT5G04050 | Symbols: | FUNCTIONS IN: molecular_function unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: intron maturase, type II family protein (TAIR:AT1G74350.1). | chr5:1096092-1098512 FORWARDnearly identical (1004) loc_os06g44880 12006.m09015 protein type II intron maturase family protein seq=cds; coord=6:94852018..94854240:1; parent_gene=AC213050.3_FG001'

'very weakly similar to (100) AT4G31150 | Symbols: | endonuclease V family protein | chr4:15143907-15145469 REVERSEweakly similar to (159) loc_os06g45330 12006.m09060 protein endonuclease V, putative, expressed seq=cds; coord=6:94211805..94216531:-1; parent_gene=GRMZM2G353125'

'moderately similar to (338) AT3G04880 | Symbols: DRT102 | DRT102 (DNA-DAMAGE-REPAIR/TOLERATION 2) | chr3:1346431-1347363 REVERSEmoderately similar to (490) loc_os01g36090 12001.m09906 protein DNA-damage-repair/toleration protein DRT102, putative, expressed seq=cds; coord=3:227494431..227495354:1; parent_gene=AC197555.3_FG008'

'weakly similar to (102) AT1G79530 | Symbols: GAPCP-1 | GAPCP-1 (GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE OF PLASTID 1); NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase | chr1:29916232-29919088 REVERSEweakly similar to (101) G3PD_MAIZE Glyceraldehyde-3-phosphate dehydrogenase, cytosolic 2 (EC 1.2.1.12) - Zea mays (Maize)moderately similar to (254) loc_os04g28820 12004.m07996 protein retrotransposon protein, putative, unclassified, expressed seq=cds; coord=6:3434798..3457041:-1; parent_gene=GRMZM2G337905'

'weakly similar to (114) AT5G52650 | Symbols: | 40S ribosomal protein S10 (RPS10C) | chr5:21355781-21357003 REVERSEweakly similar to (140) RS10_ORYSA 40S ribosomal protein S10 - Oryza sativa (Rice)weakly similar to (140) loc_os04g35090 12004.m08600 protein 40S ribosomal protein S10, putative, expressed seq=cds; coord=4:40010831..40016436:-1; parent_gene=GRMZM2G459828'

'highly similar to (625) AT2G24820 | Symbols: TIC55 | TIC55 (TRANSLOCON AT THE INNER ENVELOPE MEMBRANE OF CHLOROPLASTS 55); 2 iron, 2 sulfur cluster binding / electron carrier/ oxidoreductase | chr2:10575038-10576829 FORWARDweakly similar to (128) CAO_ORYSA Chlorophyllide a oxygenase, chloroplast precursor (EC 1.13.12.14) (Chlorophyll a oxygenase) (Chlorophyll b synthase) - Oryza sativa (Rice)highly similar to (783) loc_os02g54980 12002.m10525 protein pheophorbide a oxygenase, chloroplast precursor, putative, expressed seq=cds; coord=5:213279291..213281471:1; parent_gene=GRMZM2G018484'

'highly similar to (688) AT1G44446 | Symbols: CH1, ATCAO, CAO | CH1 (CHLORINA 1); chlorophyllide a oxygenase | chr1:16849132-16851152 REVERSEhighly similar to (896) CAO_ORYSA Chlorophyllide a oxygenase, chloroplast precursor (EC 1.13.12.14) (Chlorophyll a oxygenase) (Chlorophyll b synthase) - Oryza sativa (Rice)highly similar to (896) loc_os10g41780 12010.m21805 protein chlorophyllide a oxygenase, chloroplast precursor, putative, expressed seq=cds; coord=8:157169357..157173476:1; parent_gene=GRMZM2G038487' 'highly similar to (714) AT1G44446 | Symbols: CH1, ATCAO, CAO | CH1 (CHLORINA 1); chlorophyllide a oxygenase | chr1:16849132-16851152 REVERSEhighly similar to (876) CAO_ORYSA Chlorophyllide a oxygenase, chloroplast precursor (EC 1.13.12.14) (Chlorophyll a oxygenase) (Chlorophyll b synthase) - Oryza sativa (Rice)highly similar to (876) loc_os10g41780 12010.m21805 protein chlorophyllide a oxygenase, chloroplast precursor, putative, expressed seq=cds; coord=3:146605798..146608649:1; parent_gene=GRMZM2G171390'

'highly similar to (764) AT5G46570 | Symbols: BSK2 | BSK2 (BR-SIGNALING KINASE 2); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase | chr5:18894687-18897198 FORWARDweakly similar to (124) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (884) loc_os10g42110 12010.m06968 protein ATP binding protein, putative, expressed seq=cds; coord=9:113419985..113424715:-1; parent_gene=GRMZM2G054634'

'highly similar to (769) AT5G46570 | Symbols: BSK2 | BSK2 (BR-SIGNALING KINASE 2); ATP binding / binding / kinase/ protein kinase/ protein tyrosine kinase | chr5:18894687-18897198 FORWARDweakly similar to (120) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)highly similar to (883) loc_os10g42110 12010.m06968 protein ATP binding protein, putative, expressed seq=cds; coord=1:97817366..97822485:1; parent_gene=GRMZM2G169080'

'moderately similar to (379) AT3G15180 | Symbols: | proteasome-related | chr3:5111952-5115803 FORWARDhighly similar to (710) loc_os05g48340 12005.m27964 protein expressed protein seq=cds; coord=6:163821880..163829466:1; parent_gene=GRMZM2G086132'

'very weakly similar to (95.9) AT3G19380 | Symbols: PUB25 | PUB25 (PLANT U-BOX 25); binding / ubiquitin-protein ligase | chr3:6714602-6715867 REVERSEvery weakly similar to (94.0) SPL11_ORYSA Spotted leaf protein 11 (Spotted leaf11) (Cell death-related protein SPL11) - Oryza sativa (Rice)moderately similar to (360) loc_os04g35680 12004.m08657 protein U-box domain containing protein, expressed seq=cds; coord=2:48738351..48740309:-1; parent_gene=GRMZM2G361100'

'moderately similar to (259) loc_os07g23900 12007.m06668 protein F-box domain containing protein, expressed seq=cds; coord=1:150897326..150899612:1; parent_gene=GRMZM2G171713'

'weakly similar to (181) AT3G52390 | Symbols: | tatD-related deoxyribonuclease family protein | chr3:19423105-19425183 REVERSEweakly similar to (120) CYSP1_MAIZE Cysteine proteinase 1 precursor (EC 3.4.22.-) - Zea mays (Maize)moderately similar to (204) loc_os07g06440 12007.m05105 protein deoxyribonuclease tatD, putative, expressed seq=cds; coord=4:35255836..35264898:-1; parent_gene=GRMZM2G384762'

'moderately similar to (339) AT2G29050 | Symbols: ATRBL1 | ATRBL1 (Arabidopsis thaliana Rhomboid-like 1) | chr2:12478245-12479653 FORWARDmoderately similar to (327) loc_os11g47840 12011.m08581 protein membrane protein, putative, expressed seq=cds; coord=3:17930459..17939430:-1; parent_gene=GRMZM2G100889'

'weakly similar to (155) AT1G28390 | Symbols: | protein kinase family protein | chr1:9966814-9968226 REVERSEweakly similar to (138) CRI4_MAIZE Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.11.1) - Zea mays (Maize)moderately similar to (304) loc_os01g16230 12001.m08220 protein protein kinase APK1A, chloroplast precursor, putative seq=cds; coord=3:38438156..38439898:-1; parent_gene=GRMZM2G368388'

'highly similar to (544) AT5G54130 | Symbols: | calcium-binding EF hand family protein | chr5:21962900-21964841 FORWARDhighly similar to (762) loc_os10g13550 12010.m21844 protein calcium ion binding protein, putative, expressed seq=cds; coord=5:39798255..39802675:1; parent_gene=GRMZM2G048205'

'moderately similar to (284) AT5G52210 | Symbols: ATARLB1, ATGB1 | ATGB1 (ARABIDOPSIS THALIANA GTP-BINDING PROTEIN 1); GTP binding | chr5:21205567-21206840 FORWARDweakly similar to (122) ARF1_SOLTU ADP-ribosylation factor 1 - Solanum tuberosum (Potato)moderately similar to (343) loc_os03g27450 12003.m101362 protein ARF-related protein, putative, expressed seq=cds; coord=1:68107606..68110989:1; parent_gene=GRMZM2G082836'

'weakly similar to (200) AT3G02520 | Symbols: GRF7, GF14 NU | GRF7 (GENERAL REGULATORY FACTOR 7); protein binding / protein phosphorylated amino acid binding | chr3:526800-527915 REVERSEmoderately similar to (228) 14334_ORYSA 14-3-3-like protein GF14-D (G-box factor 14-3-3 homolog D) - Oryza sativa (Rice)moderately similar to (228) loc_os11g34450 12011.m07303 protein 14-3-3-like protein, putative, expressed seq=cds; coord=7:159919660..159920834:-1; parent_gene=GRMZM2G305211' 'nearly identical (1504) AT5G65460 | Symbols: | kinesin motor protein-related | chr5:26161831-26169001 REVERSEweakly similar to (138) FLA10_CHLRE Kinesin-like protein FLA10 (Protein KHP1) - Chlamydomonas reinhardtiihighly similar to (894) loc_os06g11380 12006.m05855 protein ATP binding protein, putative, expressed seq=cds; coord=9:7186959..7210629:-1; parent_gene=GRMZM2G017257'

'weakly similar to (188) AT2G46910 | Symbols: | plastid-lipid associated protein PAP / fibrillin family protein | chr2:19272427-19273856 FORWARD seq=cds; coord=5:23255313..23259490:-1; parent_gene=GRMZM2G026800'

'highly similar to (541) AT2G36250 | Symbols: FTSZ2-1, ATFTSZ2-1 | FTSZ2-1; protein binding / structural molecule | chr2:15197661-15199932 REVERSEhighly similar to (643) loc_os03g44420 12003.m09481 protein cell division protein ftsZ, putative, expressed seq=cds; coord=10:148918417..148922373:1; parent_gene=GRMZM2G177224'

'weakly similar to (113) AT4G03270 | Symbols: CYCD6;1 | CYCD6;1 (Cyclin D6;1); cyclin-dependent protein kinase | chr4:1432375-1433691 REVERSEmoderately similar to (340) loc_os07g37010 12007.m29223 protein CYCD6, putative, expressed seq=cds; coord=7:156667098..156669547:-1; parent_gene=GRMZM2G050933'

'highly similar to (738) AT3G44880 | Symbols: ACD1, LLS1, PAO | ACD1 (ACCELERATED CELL DEATH 1); iron-sulfur cluster binding / pheophorbide a oxygenase | chr3:16383858-16386204 FORWARDvery weakly similar to (85.5) CAO_ORYSA Chlorophyllide a oxygenase, chloroplast precursor (EC 1.13.12.14) (Chlorophyll a oxygenase) (Chlorophyll b synthase) - Oryza sativa (Rice)highly similar to (921) loc_os03g05310 12003.m06055 protein pheophorbide a oxygenase, chloroplast precursor, putative, expressed seq=cds; coord=1:10092334..10096672:1; parent_gene=GRMZM2G339563'

'moderately similar to (327) AT4G27760 | Symbols: FEY, FEY3 | FEY (FOREVER YOUNG); binding / catalytic/ oxidoreductase | chr4:13844151-13846563 FORWARDmoderately similar to (434) loc_os02g02470 12002.m05596 protein WW domain-containing oxidoreductase, putative, expressed seq=cds; coord=4:240037685..240041832:-1; parent_gene=GRMZM2G018251'

'moderately similar to (209) AT4G38730 | Symbols: | unknown protein | chr4:18080484-18082305 REVERSEmoderately similar to (247) loc_os01g65310 12001.m12644 protein non-imprinted in Prader-Willi/Angelman syndrome region protein 1homolog, putative, expressed seq=cds; coord=3:173795427..173798467:1; parent_gene=GRMZM2G037229'

'moderately similar to (402) AT2G21120 | Symbols: | unknown protein | chr2:9052103-9054266 REVERSEhighly similar to (581) loc_os05g35570 12005.m07787 protein non-imprinted in Prader-Willi/Angelman syndrome region protein 1, putative, expressed seq=cds; coord=8:101676586..101680204:-1; parent_gene=GRMZM2G097421'

'moderately similar to (474) AT1G15960 | Symbols: NRAMP6, ATNRAMP6 | NRAMP6; inorganic anion transmembrane transporter/ metal ion transmembrane transporter | chr1:5482202-5485066 REVERSEhighly similar to (672) loc_os07g15460 12007.m05990 protein metal transporter Nramp6, putative, expressed seq=cds; coord=2:170852138..170857890:1; parent_gene=GRMZM2G366919'

'highly similar to (638) AT5G47560 | Symbols: ATTDT, ATSDAT, TDT | TDT (TONOPLAST DICARBOXYLATE TRANSPORTER); malate transmembrane transporter/ sodium:dicarboxylate symporter | chr5:19287895-19290347 REVERSEhighly similar to (820) loc_os08g39370 12008.m07918 protein tonoplast dicarboxylate transporter, putative, expressed seq=cds; coord=3:215902932..215905725:1; parent_gene=GRMZM2G099382'

'highly similar to (920) AT2G36910 | Symbols: ATPGP1, PGP1, ABCB1 | ABCB1 (ATP BINDING CASSETTE SUBFAMILY B1); ATPase, coupled to transmembrane movement of substances / auxin efflux transmembrane transporter/ calmodulin binding | chr2:15502162-15507050 FORWARDhighly similar to (813) MDR_ORYSA Putative multidrug resistance protein (P-glycoprotein) - Oryza sativa (Rice)nearly identical (2029) loc_os08g05690 12008.m04712 protein multidrug resistance protein 11, putative seq=cds; coord=10:80571279..80577409:-1; parent_gene=GRMZM2G333183'

'moderately similar to (320) AT1G67940 | Symbols: ATNAP3 | ATNAP3; transporter | chr1:25477805-25478667 FORWARDweakly similar to (124) MDR_ORYSA Putative multidrug resistance protein (P-glycoprotein) - Oryza sativa (Rice)moderately similar to (420) loc_os06g48060 12006.m09332 protein phosphate import ATP-binding protein pstB 1, putative, expressed seq=cds; coord=5:53614005..53616345:-1; parent_gene=GRMZM2G432480' 'moderately similar to (483) AT3G18830 | Symbols: ATPLT5 | ATPLT5 (POLYOL TRANSPORTER 5); D-ribose transmembrane transporter/ D-xylose transmembrane transporter/ carbohydrate transmembrane transporter/ galactose transmembrane transporter/ glucose transmembrane transporter/ glycerol transmembrane transporter/ mann | chr3:6489000-6491209 REVERSEweakly similar to (138) STC_RICCO Sugar carrier protein C - Ricinus communis (Castor bean)highly similar to (613) loc_os07g39350 12007.m08177 protein proton myo-inositol cotransporter, putative, expressed seq=cds; coord=2:207635000..207637178:1; parent_gene=GRMZM2G062156'

'highly similar to (551) AT1G77610 | Symbols: | glucose-6-phosphate/phosphate translocator-related | chr1:29165489-29167486 FORWARDweakly similar to (105) TPT_MAIZE Triose phosphate/phosphate translocator, chloroplast precursor (cTPT) - Zea mays (Maize)highly similar to (613) loc_os04g59550 12004.m101707 protein organic anion transporter, putative, expressed seq=cds; coord=2:26289852..26292439:1; parent_gene=GRMZM2G127591'

'seq=cds; coord=1:260656556..260659264:1; parent_gene=GRMZM2G014934'

'seq=cds; coord=3:126981163..126982596:-1; parent_gene=GRMZM2G016586'

'weakly similar to (132) AT5G53620 | Symbols: | unknown protein | chr5:21781217-21785061 FORWARDmoderately similar to (308) loc_os08g43060 12008.m080226 protein expressed protein seq=cds; coord=1:196696007..196698701:-1; parent_gene=GRMZM2G019050'

'moderately similar to (328) AT5G60540 | Symbols: EMB2407, ATPDX2, PDX2 | PDX2 (PYRIDOXINE BIOSYNTHESIS 2); glutaminase/ glutaminyl-tRNA synthase (glutamine-hydrolyzing)/ protein heterodimerization | chr5:24336874-24338647 REVERSEmoderately similar to (432) loc_os02g03740 12002.m05723 protein glutamine amidotransferase subunit pdxT, putative, expressed seq=cds; coord=4:239138043..239141632:-1; parent_gene=GRMZM2G023528'

'very weakly similar to (98.6) AT4G25170 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP012943 (InterPro:IPR016606); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61490.1). | chr4:12909740-12911389 FORWARDmoderately similar to (322) loc_os02g44010 12002.m100296 protein expressed protein seq=cds; coord=4:152396996..152406561:-1; parent_gene=GRMZM2G026922'

'moderately similar to (245) loc_os04g24340 12004.m07566 protein phytase, putative seq=cds; coord=3:132154770..132156278:1; parent_gene=GRMZM2G043336'

'moderately similar to (281) AT5G44860 | Symbols: | unknown protein | chr5:18110688-18111653 REVERSEmoderately similar to (432) loc_os01g58620 12001.m12004 protein expressed protein seq=cds; coord=3:188300344..188302031:1; parent_gene=GRMZM2G046911'

'moderately similar to (267) loc_os04g24340 12004.m07566 protein phytase, putative seq=cds; coord=3:131702644..131704144:-1; parent_gene=GRMZM2G140101'

'moderately similar to (207) AT1G72640 | Symbols: | binding / catalytic | chr1:27346409-27348147 REVERSEmoderately similar to (313) loc_os03g29730 12003.m101371 protein expressed protein seq=cds; coord=1:71332736..71337389:-1; parent_gene=GRMZM2G149383'

'moderately similar to (430) AT3G44190 | Symbols: | pyridine nucleotide-disulphide oxidoreductase family protein | chr3:15902004-15903402 REVERSEhighly similar to (585) loc_os02g05680 12002.m05916 protein disulfide oxidoreductase/ electron carrier/ oxidoreductase, putative, expressed seq=cds; coord=4:237494138..237497773:-1; parent_gene=GRMZM2G166145'

'moderately similar to (491) AT1G29980 | Symbols: | INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane, anchored to membrane; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF642 (InterPro:IPR006946), Galactose-binding like (InterPro:IPR008979); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G34510.1); Has 180 Blast hits to 163 proteins in 15 species: Archae - 0; Bacteria - 10; Metazoa - 0; Fungi - 0; Plants - 170; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:10503411-10505994 REVERSEhighly similar to (672) loc_os01g55190 12001.m11679 protein expressed protein seq=cds; coord=3:196094333..196096899:-1; parent_gene=GRMZM2G324705'

'seq=cds; coord=6:13097849..13098393:-1; parent_gene=GRMZM2G375015'

'seq=cds; coord=5:178086882..178087933:1; parent_gene=GRMZM2G377168' 'seq=cds; coord=8:16443989..16444752:-1; parent_gene=GRMZM2G380414'

'weakly similar to (124) AT3G52950 | Symbols: | CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein | chr3:19634866-19636536 FORWARDweakly similar to (162) loc_os11g06930 12011.m04890 protein CBS domain containing protein, expressed seq=cds; coord=9:27709782..27712278:-1; parent_gene=GRMZM2G426688'

'seq=cds; coord=6:106804219..106804832:-1; parent_gene=GRMZM2G427503'

'nearly identical (1159) AT1G18270 | Symbols: | ketose-bisphosphate aldolase class-II family protein | chr1:6283634-6293772 REVERSEnearly identical (1417) loc_os06g14740 12006.m06189 protein ketose-bisphosphate aldolases family protein, expressed seq=cds; coord=6:117823306..117843150:-1; parent_gene=GRMZM2G431708'

'moderately similar to (253) AT5G44860 | Symbols: | unknown protein | chr5:18110688-18111653 REVERSEmoderately similar to (384) loc_os01g58620 12001.m12004 protein expressed protein seq=cds; coord=8:171597448..171598728:1; parent_gene=GRMZM2G438299'

'seq=cds; coord=7:172675158..172675868:-1; parent_gene=GRMZM2G472852'

'weakly similar to (167) AT5G13560 | Symbols: | unknown protein | chr5:4361579-4366318 REVERSEweakly similar to (136) PFPA_SOLTU Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPi-PFK) - Solanum tuberosum (Potato)moderately similar to (238) loc_os03g17270 12003.m35165 protein expressed protein seq=cds; coord=8:145658003..145667670:-1; parent_gene=GRMZM2G487136'

'seq=cds; coord=1:19104324..19104800:1; parent_gene=AC177946.2_FG004'

'very weakly similar to (81.3) loc_os01g56680 12001.m11825 protein photosystem II reaction center W protein, chloroplast precursor, putative, expressed seq=cds; coord=3:192033354..192034113:1; parent_gene=AC190623.3_FG001'

'moderately similar to (422) AT5G63910 | Symbols: FCLY | FCLY (FARNESYLCYSTEINE LYASE); prenylcysteine oxidase | chr5:25572053-25574077 REVERSEweakly similar to (160) loc_os04g59630 12004.m10838 protein prenylcysteine oxidase precursor, putative, expressed seq=cds; coord=10:149747387..149749334:-1; parent_gene=AC234201.1_FG003'

'weakly similar to (125) AT5G02060 | Symbols: | integral membrane protein, putative | chr5:404908-405774 FORWARDweakly similar to (131) loc_os01g62850 12001.m12405 protein expressed protein seq=cds; coord=8:95579124..95580800:-1; parent_gene=GRMZM2G054227'

'weakly similar to (102) AT4G25170 | Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Uncharacterised conserved protein UCP012943 (InterPro:IPR016606); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G61490.1). | chr4:12909740-12911389 FORWARDmoderately similar to (279) loc_os02g44010 12002.m100296 protein expressed protein seq=cds; coord=5:191901867..191905412:-1; parent_gene=GRMZM2G056762'

'seq=cds; coord=1:274521321..274523353:-1; parent_gene=GRMZM2G095519'

'highly similar to (563) AT1G34630 | Symbols: | unknown protein | chr1:12685317-12687107 FORWARDhighly similar to (661) loc_os03g09090 12003.m06415 protein expressed protein seq=cds; coord=1:19698949..19703374:-1; parent_gene=GRMZM2G113775'

'very weakly similar to (91.7) AT5G02060 | Symbols: | integral membrane protein, putative | chr5:404908-405774 FORWARDweakly similar to (114) loc_os05g38250 12005.m08004 protein expressed protein seq=cds; coord=3:179723501..179725522:1; parent_gene=GRMZM2G119273'

'nearly identical (1201) AT5G24810 | Symbols: | ABC1 family protein | chr5:8516902-8522616 REVERSEnearly identical (1518) loc_os06g48770 12006.m32168 protein retrotransposon protein, putative, SINE subclass, expressed seq=cds; coord=6:86747563..86755916:1; parent_gene=GRMZM2G140917'

'moderately similar to (268) loc_os11g36920 12011.m07541 protein hypothetical protein seq=cds; coord=6:70837501..70846423:1; parent_gene=GRMZM2G386337'