Treatments	Protein function/name	Accession		
RNA regulation of transcription/RNA processing				
	GATA type zinc finger transcription factor family protein	orange1.1g029070m		
Ţ		orange1.1g029735m		
T n				
VC VI NC NI				
VC VI IVC IVI	Transducia (MID 40 report like superfersily protein	aran and 1 and 20700m		
<b>T</b>	Transducin/WD40 repeat-like superfamily protein	orange1.1g039790m		
_ + +				
VC VI NC NI				
	_   Protein targeting/Protein degradation/Protein glycosylation			
<del>-</del>	Translocon at the inner envelope membrane of	orange1.1g001818m		
Ţ	chloroplasts 110	orange1.1g003418m		
<b>→</b> -	·			
VC VI NC NI	1			
<u> </u>	Xylem bark cysteine peptidase 3	orange1.1g014761m		
<u> </u>		orange1.1g019447m		
<u> </u>				
VC VI NC NI				
	Aspartic proteinase A1	orange1.1g010466m		
		orange1.1g018226m		
		orange1.1g010486m		
		orange1.1g016523m		
		orange1.1g022584m		
VC VI NC NI		orange1.1g015145m		
т	Granulin repeat cysteine protease family protein	orange1.1g024783m		
<u>+</u>				
V6 V/ N6 NI				
VC VI NC NI	Donaleten vestisle triale A CA			
_	Regulatory particle triple-A 1A	orange1.1g014665m		
<sub>т</sub> 📥 т		orange1.1g015875m		
<u> </u>				
VC VI NC NI				
	Vacuolar processing enzyme beta	orange1.1g021650m		
<del></del>		orange1.1g023458m		
VC VI NC NI				
VC VI NC NI	Pihonhorin I	orango1 1g007127		
<del>_</del> +	Ribophorin I	orange1.1g007137m		
<u></u>				
VC VI NC NI				

	Tage	4.4.040=00
_ <u> </u>	20S proteasome alpha subunit E2	orange1.1g042723m
		orange1.1g030843m
VC VI NC NI		
	Hydroxyproline-rich glycoprotein family protein	orange1.1g016002m
		orange1.1g020409m
		orange1.1g022173m
V6 V/ N6 NI		
VC VI NC NI	Amino acid metabolism	
	Putative fumarylacetoacetase	orange1.1g018339m
<u> </u>	r diative ramai yiacetoacetase	orange1.1g019941m
T 1		orange1.1g013341m
		orange1.1g012766m
VC VI NC NI		orange1.1g014784m
	Putative chorismate synthase / 5-enolpyruvylshikimate-3-	orange1.1g022731m
<b>-</b>	phosphate phospholyase	ordinger.igozz/Jim
	phosphate phospholyase	
VC VI NC NI		
	Aspartate aminotransferase	orange1.1g012095m
		orange1.1g018665m
VC VI NC NI	Code of books to the state of t	
	S-adenosylmethionine synthetase 2	orange1.1g044843m
<b>—</b>		
VC VI NC NI		
	Stress biotic	
	Kunitz family trypsin and protease inhibitor protein	orange1.1g027419m
_		orange1.1g030834m
<u> </u>		orange1.1g048141m
		orange1.1g038462m
<u> </u>		orange1.1g028238m
		orange1.1g031474m
VC VI NC NI		orange1.1g040351m
		orange1.1g026834m
Т	Chlorophyllase	orange1.1g020188m
VC VI NC NI		
75 71 110 111	Hormone metabolism	
	NAD(P)-linked oxidoreductase superfamily protein	orange1.1g019203m
т	The control of the co	3. 3032.1203111
VC VI NC NI		i

	Lineary 2	
	Lipoxygenase 2	orange1.1g002649m
		orange1.1g002672m
		orange1.1g002644m
<u> </u>		orange1.1g002706m
<u> </u>		orange1.1g002670m
VC VI NC NI		orange1.1g007674m
Ve VI Ne Ni		orange1.1g004307m
		orange1.1g006999m
	Secondary metabolism	
т.	NAD(P)-binding Rossmann-fold superfamily protein	orange1.1g025971m
		orange1.1g020110m
VC VI NC NI		
10 11 110 111		
	1-deoxy-D-xylulose 5-phosphate reductoisomerase	orange1.1g012004m
<del> </del>		orange1.1g013846m
		0.0001.15013040111
VC VI NC NI		
	Other	
	Coproporphyrinogen III oxidase	orange1.1g016102m
1	(tetrapyrrole synthesis)	
1/2 1/1 1/2 1/1		
VC VI NC NI		1.4.04==00
	NAD(P)-linked oxidoreductase superfamily protein	orange1.1g017732m
<u> </u>	(minor CHO metabolism)	orange1.1g020098m
		orange1.1g023567m
VC VI NC NI		orange1.1g018530m
	Calreticulin 3 (signalling)	orange1.1g014968m
т.	Can eticum 3 (signaming)	orange1.1g014908m
<u> </u>		orange1.1g013000m
		Orange1.1g02002/III
VC VI NC NI		
	Glyceraldehyde-3-phosphate dehydrogenase B subunit	orange1.1g012940m
	(calvin cycle)	orange1.1g025793m
		orange1.1g015291m
		orange1.1g021979m
VC VI NC NI		4
т	Tubulin alpha-2 chain (cell organisation)	orange1.1g013066m
<del> </del>		orange1.1g014077m
		orange1.1g037616m
VC VI NC NI		
	Alcohol dehydrogenase 1 (fermentation)	orange1.1g047713m
		orange1.1g035170m
		orange1.1g017336m
		orange1.1g016933m
VC VI NC NI		orange1.1g010933111
		ni aiike1.1kn13414[]

Г	T- 1 . 6 . 11	T
_	Transducin family protein / WD-40 repeat family protein	orange1.1g010997m
+	(development)	orange1.1g016547m
		orange1.1g046899m
VC VI NC NI		orange1.1g021657m
	ATPase F1 complex, gamma subunit protein (lightreaction)	orange1.1g017613m
<u> </u>		
VC VI NC NI	Chitamata sunth and 1 (N. matakaliana)	1 1 - 000461
т	Glutamate synthase 1 (N-metabolism)	orange1.1g000461m
<b>—</b>		
VC VI NC NI		
	Miscellaneous	
	D-mannose binding lectin protein with Apple-like	orange1.1g048464m
<u></u>	carbohydrate-binding domain	orange1.1g041743m
VC VI NC NI		
	O-Glycosyl hydrolases family 17 protein	orange1.1g019362m
т —	O-Glycosyi flydrolases family 17 protein	Orange1.1g019302iii
VC VI NC NI		
	Glutathione s-transferase tau 7	orange1.1g027333m
<u> </u>		orange1.1g027498m
<u> </u>		orange1.1g043218m
VC VI NC NI		
VC VI NC NI	Alpha/beta-Hydrolases superfamily protein	orange1.1g023687m
_ <del>_</del>	Alpha/beta-riyurolases superrannily protein	orange1.1g02308711
		Ordinge1.1g051524iii
VC VI NC NI		
	Zinc-binding dehydrogenase family protein	orange1.1g037444m
		orange1.1g039200m
		orange1.1g018404m
VC VT NC NT		
10 11 110 111	Zinc-binding dehydrogenase family protein	orange1.1g019042m
_		orange1.1g042426m
		orange1.1g033914m
		orange1.1g026217m
VC VI NC NI		orange1.1g019332m
		orange1.1g019291m
	Glycosyl hydrolase family 38 protein	orange1.1g015028m
<del></del>	2., 223, 1., a. o.a.se tariii, 30 protein	orange1.1g011547m
		3-1-8-2-3
VC VI NC NI		

VC VI NC NI	Glycosyl hydrolase family 38 protein	orange1.1g002036m orange1.1g002170m orange1.1g002764m
VC VI NC NI	Pectin methylesterase inhibitor superfamily protein	orange1.1g029238m orange1.1g027094m
	Unknown	
VC VI NC NI	DC1 domain-containing protein	orange1.1g008336m orange1.1g011791m orange1.1g013684m orange1.1g021494m orange1.1g014225m orange1.1g015833m
VC VI NC NI	Class I glutamine amidotransferase-like superfamily protein	orange1.1g016237m orange1.1g029299m
VC VI NC NI	Thioredoxin family protein	orange1.1g024026m orange1.1g023026m