Table S14. Sequence IDs and protein threading results from transcripts with significant internal transcriptional starts sites in MED4 under N-limitation. The sequences highlighted in bold contain internal start sites with an NicA binding site during transcription and a pyrimidine binding site for protein S1 binding during translation. The genes in this table combine for more than 90% of the gene expression during the treatment.

protein 5 minuing during dantisation. The genes in anis acute commune (or more main 90% of the gene expression during the readment. Structure Structure													
		with hest		Model	Residues	Amino Acids	Difference Between Full length		Accession Number of CDD Domain				Theoretical N-Savings
Sequenc	e ID	match	Protein	Confidence	aligned	in Sequence	and Internal Protein Length	CDD Domain Affected by Internal TSS	Affected	Result	NtcA Binding	Pyrimidine Rich	(mol N/mol protein)
PMM02		clhyuA	Alkyl hydroperoxide reductase subunit	100	301	318						. ,	(
PMM02		c1hyuA	, , , , ,	100	241	251	67	None	N/A	Protein aligns by MSA to major structural elements of PDB structure	esYes	Yes	79
PMM02		c5da0A	Sulfate transporter	100	460	554							
								Possible specific transcription of HCO3_cotransp super family					
PMM02	14 Int	c3mglA		99	110	156	398	domain	cl23746	Protein has specific structural element or subunit transcribed	Yes	Yes	474
PMM03		c2i4cA	putative cyanate ABC transporter, substrate binding protein	100	361	561							
PMM03		c2i4cA		100	365	406	155	None	N/A	Protein aligns by MSA to major structural elements of PDB structure	esYes	Yes	210
PMM10 PMM10		c2b5oA	Ferredoxin-nadp reductase	100 100	288 234	373 238	135	None	N/A	Protein aligns by MSA to major structural elements of PDB structure		Yes	179
PMM10 PMM14		c3lu0C	RNA polymerase	100	1032	238 1100	135	None	N/A	Protein aligns by MSA to major structural elements of PDB structure	es ves	Yes	1/9
r MM14	100	connoc	KNA polymerase	100	1032	1100		Possible modification of RNA polymerase beta subunit as					
PMM14	85 Int	c3lu0C		100	936	988	112	almost entire protein is single domain	cd00653	Protein aligns by MSA to major structural elements of PDB structure	s Yes	Yes	155
PMM15		cllm1A	Glutamate synthase [nadph] large chain	100	1461	1521							
PMM15	12 Int	c2vdcF		100	410	413	1108	Possible specific transcription of GXGXG superfamily domain.	cl00239	Protein has specific structural element or subunit transcribed	Yes	Yes	1501
PMM16		c4igcX	Type II alternative RNA polymerase sigma factor, sigma-70 family	100	338	339							
PMM16		c4igcX		100	176	187	111	Likely loss of Sigma-70 factor, region 1.2 domain	pfam00140	Protein lacks structural element or structure is incomplete	Yes	Yes	380
PMM000		c2vv5D	putative membrane transport protein	91	79	310							
PMM000		c4b4aA_	and the second second	89 11	19 13	205 112	105	Possible modification of the Ycf66 protein N-terminus domain	pfam07444	Protein lacks structural element or structure is incomplete	No	No	136
PMM003		c2kbcA_ c2kbcA	putative hormone protein	14	13	95	17	No domains detected	N/A	Protein lacks structural element or structure is incomplete	No	No	28
PMM016		c5kinD	tryptophan synthase beta chain	100	393	417	17	NO domains detected	N/A	Protein lacks structural element or structure is incomplete	NO	NO	20
PMM016		d1v8za1	ti yptopiian synthase beta chain	100	371	377	40	None	N/A	Protein aligns by MSA to major structural elements of PDB structures	No	No	59
PMM026		c5aexB	ammonium transporter	100	419	486							
PMM026		c5aexB		100	403	405	81	None	N/A	Protein aligns by MSA to major structural elements of PDB structures	No	No	113
PMM036		c3znul	putative lyase protein	49	73	105							
PMM036	68 Int	d1kp0a1		53	31	84	21	First 16 aas of a Domain of Unknown Function	pfam11746	Protein lacks structural element or structure is incomplete	No	Yes	29
PMM04	45	c1m56G	cytochrome c oxidase subunit I	100	512	544							
								Possible modification of cytochrome c oxidase subunit I as almost					
PMM04- PMM05-		c3aerC_	light-independent protochlorophyllide reductase subunit n	100 100	451 407	463 421	81	entire protein is single domain	TIGR02891	Protein aligns by MSA to major structural elements of PDB structures	NO	Yes	105
FWINIU34	43	CSderC	ngnt-independent protochiorophyliide reductase subunit n	100	407	421		Possible modification of light-independent protochlorophyllide					
PMM054	45 Int	c3aerC		100	256	263	158	reductase subunit n as almost entire protein is single domain	PRK02842	Protein aligns by MSA to major structural elements of PDB structures	No	Yes	210
PMM066		d1l1la	B12-dependent (class II) ribonucleotide reductase	100	653	805	150	reduction strong in as united citate protein is single domain	111102012	Trotain digits by Wast to major structural elements of 1 55 structures	140	163	210
PMM066	61 Int	d1l1la		100	599	706	99	None	N/A	Protein aligns by MSA to major structural elements of PDB structures	No	Yes	144
PMM068	84	d1smpi	putative metalloprotease inhibitor	52	23	117							
PMM068		d2v3za1		40	32	105	12	None	N/A	Protein lacks structural element or structure is incomplete	No	No	15
PMM068		c3edsA	putative ctp pyrophosphohydrolase	24	18	111							
PMM068		c3edsA_	ferritin	40 100	27 177	89 184	22	No domains detected	N/A	Protein lacks structural element or structure is incomplete	Yes	Yes	36
PMM080		c3a9qR_ c3qz3A	territin	100	160	184	18	None	N/A	Protein aligns by MSA to major structural elements of PDB structures	No	No	24
PMM08		c4a94D	putative carboxypeptidase inhibitor	73	18	82	10	No domains detected	NA	Protein aligns by Wisk to major structural elements of PDB structures	140	NO	24
PMM08		c4a94D	parative carboxypeproduce minutes	73	18	81	1	No domains detected		Protein lacks structural element or structure is incomplete	No	Yes	1
PMM09		d1qo0a	urea ABC transporter, Periplasmic binding protein-like I	100	368	439							
PMM097		d1qo0a		100	357	381	58	None	N/A	Protein aligns by MSA to major structural elements of PDB structures	No	Yes	72
PMM107	77	c4ew8A	adaptive-response sensory kinase protein divl	100	228	375							
PMM107		c4ew8A		100	207	226	149	None	N/A	Protein has specific structural element or subunit transcribed	No	Yes	211
PMM112		c4l6rA	putatuve cytochrome b562 and glucagon receptor chimera	33	30	237							
PMM112 PMM115		d1oz9a c2axtc_	photosystem ii cp43 protein	19 100	13 446	180 460	57	None	N/A	Protein lacks structural element or structure is incomplete	No	Yes	88
I MIMIT.	56	CZBAIC	photosystem ii cp43 protein	100	440	400		Possible modification of the photosystem ii cp43 protein as almost					
PMM11:	58 Int	c2axtc		100	416	416	44	entire protein is single domain	TIGR01153	Protein aligns by MSA to major structural elements of PDB structures	Yes	No	64
PMM118		3wvfA	membrane protein insertase yidc	100	183	379		,					
								Possible modification of the membrane protein insertase yidc					
PMM118		c3wvfA		100	177	288	91	protein as almost entire protein is single domain	PRK02654	Protein aligns by MSA to major structural elements of PDB structures	No	Yes	120
PMM130	01	c3n5mD	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	100	392	417							
								Possible modification of the acetylomithine aminotransferase					
PMM130		c4ysnD		100	243	245	225	protein as almost entire protein is single domain	PRK02627	Protein aligns by MSA to major structural elements of PDB structures	No	No	229
PMM13 PMM13		c5f4hF c5f4hF	nucleotide binding protein pinc	100 100	159 159	369 368	1	Possible specific transcription of (PiIT N terminus) domain	cd09877	Protein has specific structural element or subunit transcribed	No	Yes	
PMM14		c4my4A_	2,3-bisphosphoglycerate-independent phosphoglycerate	100	500	540	1	rossible specific transcription of (Firt N terminus) domain	Cu098//	Protein has specific structural element or subunit transcribed	NO	res	1
			-,		500	5-10		Possible modification of the 2,3-bisphosphoglycerate-independent					
PMM143	34 Int	c4my4A		100	449	474	66	phosphoglycerate protein as almost entire protein is single domain	cd16010	Protein aligns by MSA to major structural elements of PDB structures	No	No	89
PMM162		c3dhyC	adenosylhomocysteinase	100	463	475				- , ,			
								loss of the beginning amino acids in the homotetramer interface					
PMM162		c3n58D		100	339	339	136	on conserved domain SAHH	PRK05476	Protein aligns by MSA to major structural elements of PDB structures	No	No	178
PMM163		c5lmtX	translation initiation factor if-3	100	162	190							
PMM163		c5lmtX	and the Court His and death and an	100	107 124	119 146	71	loss of part of translation initiation factor 3 N terminal domain	pfam05198	Protein aligns by MSA to major structural elements of PDB structures	No	Yes	113
PMM164 PMM164		d2gexa1 d2gexa1	putative SnoaL-like polyketide cyclase	100	124 94	146	35	loss of the beginning amino acids in the SnoaL-like domain	pfam12680	Protein aligns by MSA to major structural elements of PDB structures	No	Yes	111
						•••	33	Segming animo delas in the shout-like dollani	phinizooo				111