

Rickettsia RNA metabolism loci	Putative Arabidopsis homologue	%ID	Target
RnhB ribonuclease HII	At2g25100	34%	-
rpoB DNA-directed RNA polymerase Beta chain	rpoB	41%	in cp
	At4g21710	40%	-
	At3g18090	35%	-
	At3g23780	33%	mt
	At2g36990	31%	-
rpoH RNA polymerase Sigma-32 factor	At1g08540		cp
	At3g53920		cp
	At1g64860		cp
	At5g24120		mt
	At2g36990	31%	-
rpoC DNA-directed RNA polymerase Beta chain	rpoC1	51%	in cp
	rpoC2	33%	in cp
	At4g35800	28%	-
	At3g57660	36%	-
	At5g60040	32%	-
	At2g40030	21%	-
	At3g48830	30%	-
	At1g28090	28%	-
pcnB poly(A) polymerase	At5g23690	28%	m
	At1g22660	30%	cp/mt
	At2g17580	41%	-
	n.		
	At3g03710	44%	-
Pnp polyribonucleotide nucleotidyltransferase	At5g14580	38%	mt
	At3g03300	41%	-
rrn ribonuclease III	At5g20320	40%	-
	At1g01040	39%	-

nusBN utilization substance protein B	n.		
NusG transcription antitermination protein nusg	At3g09210 unknown	32%	mt
Rnd ribonuclease D	n.		
rho transcription termination factor	n.		
rne ribonuclease E	At2g04270	32%	-
	At3g02930	22%	cp/m*
nusA N utilization substance protein A	n.		
rpoA DNA-directed RNA polymerase alpha chain	rpoA	31%	in Cp
rnhA ribonuclease H	At3g01410	31%	mt*
	At5g51080		mt
greA transcription elongation factor greA	n.		
rph ribonuclease PH	At3g61620 RRP4	26%	-
rpoD RNA polymerase Sigma factor	At2g36990	38%	-
	At1g08540 (SIG1)	39%	cp
	At5g13730	35%	cp
	At3g53920 SIGC	30%	cp
rhIE putative ATP-dependent RNA helicase	At5g63120	39%	-
	At3g22310	40%	mt
	At1g55150	42%	-
	At3g01540 DRH1	43%	-
	At3g22330	37%	mt
	+48 other RNA helicases		
n.) could not be identified, Localization: cp) chloroplast, mt) mitochondria, -) no targeting signal, ?) has a signal sequence, unknown targeting, *) ambiguous targeting value			