

**Appendix table 2a. Putative *Arabidopsis* homologues for rickettsial DNA metabolism**

Rickettsia gene	Putative A.t. homologue	Function	%Identity	Targeting
	At1g50840	Unknown protein	34%	
		Putative DNA repair and replication loci		mt/cp
GyrA	At3g10690	Putative GyraseA	49%	mt
GyrB	At5g04130	Putative Gyrase B	35%	mt
	At3g10270	Putative GyraseB	39%	mt
	At5g04110	Putative Gyrase B	39%	-
rvB	At5g22330	Ruv DNA helicase like	24%	-
	At5g67630	rvB like		-
	At3g49830	rvB-like		-
holB	At4g24790	DNA polymerase III like		-
	At2g02480	STICHEL		-
recN	At2g27170	Putative chromatin associated protein	20%	-
	At5g07660			-
	At3g54670			-
	At1g65010			-
rnhB	At2g25100			
uvrB	n.			cp/mt
xthA1	At2g41460	ARP	30%	mt
	At4g36050	Putative protein	36%	cp
	At3g48425		25%	
xseB	n.			
XerD	n.			
RuvA	n.			
DNA N	n.			
DNA A	n.			
recR	n.			cp
uvrD	At4g25120	putative protein		

recJ	n.			cp
priA	At3g02060	Helicase like protein	29%	-
	At5g41880	DNA polymerase alpha		cp
	At1g70070		27%	
DNAB	n.			
recO	n.			-
RecA	At2g19490		56%	cp
	At1g79050		52%	mt
	At3g10140		41%	mt
	At3g32920		52%	mt
uvrC	n.			-
RecF	At5g07660	SMC like protein	23%	-
	At3g54670	AtSMC1	32%	mt
	At5g61460	MIM	28%	cp
mfd	At3g02060			cp
	At1g30680		33%	
xseA	n.			
himA	n.			mt
rnHA	At3g01410	RnaseH		mt
	At5g51080	RnaseH		-
	At1g24090	RnaseH		
dnaQ	At5g26940	exonuclease		
addA	At4g25120	Possibly, putative protein		
dnaE	n.			
xerC	n.			
uvrA	n.			mt/cp
DNAG	At1g30680		29%	-
	At1g30660			
dnaX	At2g02450	DNA polymIII like	34%	
	At1g14460		33%	
	At4g24790		33%	
	At5g45720		29%	mt

	At4g18820		28%	-
mutL	At4g09190	MLH1		-
	At4g02460	PMS1		-
	At4g35520			cp
MutS	At4g02070		38%	-
	At3g24495	MSH7	37%	-
	At3g18524	MSH2	31%	cp
	At4g25540		28%	
	At4g17380		37%	mt
	At3g24320	MSH1	27%	mt
topA	At4g31210	DNA topoisomerase like	38%	mt
	At5g63920	DNA topoisomerase III	23%	mt
	At2g32000	DNA topoisomerase III putative	29%	-
Mpg	At3g12040	DNA-3-Methyladenine glycosidase	42%	-
NthIII	At2g31450	Endonuclease like	26%	-
	At1g14460		33%	-
	At3g10010	DML2	27%	-
RadA	At5g50340	DNA repair protein like	42%	mt
Ssb	At4g11060	Putative protein	23%	mt
	At3g18580	Hypothetical protein	29%	cp
RecG	At3g02060	Helicase like protein	33%	-
	At2g01440	Putative RECG	31%	mt
polA	At3g20540	Putative DNA polymerase	36%	cp
	At4g32700	Putative protein	25%	?
	At1g34380	DNA polymerase typeI	27%	cp
	At3g52050	Putative protein	24%	mt*

n.) could not be identified, Localization: cp) chloroplast, mt) mitochondria, -) no targeting signal, ?) has a signal sequence, unknown targeting, \*) ambiguous targeting value