

conservation	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	80								
SCPP9'DR	ATGAAGA	AAC	TTTG	TTCA	ATT	CTTT	ATGG	TACT	AAG	CATT	ACT	GCTC	ATGCC	ACTT	CAGC	TAAGA	AAGCTT	CTTG	TGGT	CA	80			
SCPP9' LW	ATGAAGA	AAC	TTTG	TTTG	TTC	ATCT	TTT	ATGG	TACT	GCC	ATA	ATGG	CTG	ATAT	CAC	CTCAG	CAAG	CTGC	ACTT	ATTT	TTAG	80		
SCPP9' PP	ATGAAGA	AAC	TTTG	TTGT	CAT	CTTT	ATGG	TACT	GCC	ATA	ATGG	CTG	ATAT	CAC	CAG	CTCA	AGA	AAG	CTG	CGT	CTGAT	CA	80	
SCPP9- CI	ATGAAGA	AAC	TTTG	TTTT	CGT	CTTT	ATGG	TTCT	GACC	CATA	AAT	TGCT	GAT	ATC	AG	CTCAG	CTCA	AGA	AAG	CTG	CGT	CTGAT	CA	80
SCPP9- C1' CC	AAG	TACT	TTAT	CAT	CTTT	ATGG	TTCT	GACT	GTA	ATT	TGCT	GAT	ATC	AC	CTCAG	CTCA	AGA	AAG	CTG	CGACT	TAT	CAG	74
SCPP9- C2' CC	ATGAAGA	AAC	TTTG	TTATA	ACC	ATT	ATGG	CTCT	GAC	CGTAA	TTG	CTG	ATAT	CAC	CTCAG	CTCA	AGA	AAG	CTG	CGT	CTGAT	CA	80	
SCPP9- C1' SG	ATGAAGA	AA	TTTG	TTATA	AAT	CTTT	ATGG	TTCT	GAC	CGTAA	TTG	CTG	ATAT	CAC	CTCAG	CTCA	AGA	AAG	CTT	CAT	CTGAT	CA	80	
SCPP9- C2' SG	ATGAAGA	AAC	TTTG	TTAT	GAC	CA	TTT	ATGG	TTCT	GAC	CGTAA	TTG	CTG	ATAT	TAC	CTCAG	CTCA	AGA	AAG	CTG	CGT	CTGAT	TAA	77
SCPP9- C1' SA	ATGAAGA	AA	TTTG	TTATA	AAT	CTTT	ATGG	TTCT	GACT	GTA	ATT	TGCT	GAT	ATC	AC	CTCAG	CTCA	AGA	AAG	CTG	CA	TCTGAT	CA	80
SCPP9- C2' SA	CTGAT	CA	8
SCPP9- C1' SR	ATGAAGA	AA	TTTG	TTATA	AAT	CTTT	ATGG	TTCT	GAC	CGTAA	TTG	CTG	ATAT	CAC	CTCAG	CTCA	AGA	AAG	CTG	CGT	CTGAT	CA	80	
SCPP9- C2' SR	ATGAAGA	AAC	TTTG	TTAT	GAC	CA	TTT	ATGG	TTCT	GAC	CGTAA	TTG	CTG	ATAT	CAC	CTCAG	CTCA	AGA	AAG	CTG	CGT	CTGAT	CA	80

conservation

	85	90	95	100	105	110		115	120	125	130	135	140	145	150	
SCPP9'DR	*	!	*	!	*	!	*	!	*	!	*	!	*	!	*	!
SCPP9'LR	C	G	G	T	C	T	G	A	A	T	G	G	A	T	G	A
SCPP9'PW	A	A	C	T	G	C	G	T	C	T	G	A	A	T	G	A
SCPP9'PP	C	G	G	T	C	T	G	A	A	T	G	G	A	T	G	A
SCPP9-CI	C	G	G	T	C	T	G	A	A	T	G	G	A	T	G	A
SCPP9-C1'CC	C	G	G	T	C	T	G	A	A	T	G	G	A	T	G	A
SCPP9-C2'CC	C	G	G	T	C	T	G	A	A	T	G	G	A	T	G	A
SCPP9-C1'SG	C	G	G	T	C	T	G	A	A	T	G	G	A	T	G	A
SCPP9-C2'SG	C	G	G	T	C	T	G	A	A	T	G	G	A	T	G	A
SCPP9-C1'SA	C	G	G	T	C	T	G	A	A	T	G	G	A	T	G	A
SCPP9-C2'SA	T	G	G	T	C	T	G	A	A	T	G	G	A	T	G	A
SCPP9-C1'SR	C	G	G	T	C	T	G	A	A	T	G	G	A	T	G	A
SCPP9-C2'SR	C	G	G	T	C	T	G	A	A	T	G	G	A	T	G	A

conservation

SCPP9'DR	T	G	G	T	G	C	T	G	G	A	G	G	T	G	C	T	G	T	T	A	A	G	G	A	C	A	G	C	C	T	C	A	T	T	C	A	C	A	G	T	T	T	C	T	T	C	T	C	C	A	T	A	T		231							
SCPP9'LP	T	G	T	T	T	C	T	G	T	G	G	T	G	T	G	C	T	G	T	T	A	A	G	A	C	A	G	C	C	T	C	G	T	T	T	A	C	A	C	A	A	T	T	T	C	T	T	C	C	A	T	A	T		237							
SCPP9'PP	T	A	T	T	T	C	T	G	T	G	G	T	G	C	T	G	C	T	G	T	T	A	A	G	A	C	A	G	C	C	T	C	G	T	T	A	C	A	C	A	A	T	T	T	C	T	T	C	C	A	T	A	T		231							
SCPP9-CI	T	T	C	T	T	C	T	G	T	G	G	T	G	C	T	G	C	T	G	T	T	A	A	G	A	C	A	G	C	C	T	C	A	T	T	A	A	C	A	C	A	G	T	T	T	C	T	T	C	C	A	T	A	T		231						
SCPP9-C1'CC	T	G	C	T	T	C	T	G	T	G	G	T	C	A	G	C	T	G	T	T	A	T	T	G	G	A	C	A	G	C	C	T	C	G	T	T	A	G	C	G	A	C	A	A	A	T	A	C	T	T	C	T	T	T	C	C	A	T	A	T		228
SCPP9-C2'CC	T	G	C	T	C	T	G	T	G	G	T	C	T	G	T	G	T	T	A	T	A	G	A	C	A	G	C	C	T	C	A	T	T	A	G	C	A	C	A	G	A	T	T	T	C	T	T	C	C	A	T	A	T		231							
SCPP9-C1'SG	T	G	C	T	C	T	G	T	G	G	T	C	T	G	T	G	T	T	A	T	T	G	G	A	C	A	G	C	C	T	C	A	T	T	A	G	C	A	C	A	G	A	T	T	T	C	T	T	C	C	C	A	T	A	T		231					
SCPP9-C2'SG	T	G	C	T	T	C	T	G	T	G	G	T	C	T	G	C	T	G	T	T	A	T	A	G	A	C	A	G	C	T	T	C	A	T	T	A	G	C	A	T	A	G	A	T	T	T	C	T	T	C	C	T	C	A	T	T		228				
SCPP9-C1'SA	T	G	C	T	T	C	T	G	T	G	G	T	C	T	G	T	T	A	T	T	G	G	A	C	A	G	C	C	T	C	A	T	T	A	G	C	A	C	A	G	A	T	T	T	C	T	T	C	C	C	A	T	A	T		231						
SCPP9-C2'SA	T	G	C	T	T	C	T	G	T	G	G	T	C	T	G	C	T	G	T	T	A	T	A	G	A	C	A	G	C	C	T	C	A	T	T	A	G	C	A	C	A	G	A	T	T	T	C	T	T	C	C	C	A	T	T		147					
SCPP9-C1'SR	T	G	C	T	T	C	T	G	T	G	G	T	C	T	G	T	T	A	T	T	G	G	A	C	A	G	C	C	T	C	A	T	T	A	G	C	A	C	A	G	A	T	T	T	C	T	T	C	C	C	A	T	A	T		231						
SCPP9-C2'SR	T	G	C	T	T	C	T	G	T	G	G	T	C	T	G	C	T	G	T	T	A	T	A	G	A	C	A	G	C	C	T	C	A	T	T	A	G	C	A	C	A	G	A	T	T	T	C	T	T	C	C	C	A	T	T		231					

	235	240	245	250	255	260	265	270	275	280	285	290	295	300	305				
conservation			*	*	*		*	*	*	*	*	*	*	*	*				
SCPP9 ^{DR}	GTGCTTCAG	...	CCTCCA	GTGGC	AC	CAGCT	CCCCT	TCGGC	CTT	CCTAAC	GCCT	GGAGCT	...	CTGCCTTA	CCCC	TTCCCT	CC	305	
SCPP9 ^{LP}	GTGCTTCAGCA	GCC	ACCT	GTGGCC	G	CAGT	TCCCT	ACGCT	CCACC	CAACAT	TGGACCT	CAGT	TGGCTT	AT	CCTTT	CGCT	CC	317	
SCPP9 ^{PP}	GTGCTTCAGCA	GCC	ACCT	GTGGCC	G	CAGT	TCCCT	ACGCT	CCACC	CAACAT	TGGACCT	CAGT	TGGCTT	AT	CCTTT	CGCT	CC	311	
SCPP9 ^{CI}	GTGCTTCAGCA	GCC	ACCT	GTGGCC	G	CAGT	TCCCT	ACGCT	CCACC	CAACAT	TGGACCT	CAGT	TGGCTT	AT	CCTTT	CGCT	CC	311	
SCPP9-C1 ^{CC}	GTGCTTCAGCA	GCC	ACCA	CCAGT	TCCCT	TCAGT	CCCC	CTCAAC	ATCGGACCT	CAGT	TGGCTT	AC	CCCTTT	TGTT	TC	302		
SCPP9-C2 ^{CC}	AT	ACTTCAGCA	GCC	ACCT	GTGGCC	G	CAGT	TCCCT	ATGGT	CCCC	CAATTT	TGGACCT	CAGT	TGGCTT	AC	CCCTTT	CGCT	TC	311
SCPP9-C1 ^{SG}	GTGCTTCAGCA	GCC	ACCA	GTTCCCT	TCGGT	CCCC	CCCAAC	ATCGGACCT	CAGT	TGGCTT	AC	CCCTTT	CGGT	TC	302			
SCPP9-C2 ^{SG}	GTGCTTCAGCA	CCC	ACCT	GTGGCC	G	CAGT	TCCCT	ATGGT	CCCC	CAACAT	TGGACCT	CAGT	TGGCTT	AC	CCCTTT	CGCT	TC	308	
SCPP9-C1 ^{SA}	GTGCTTCAGCA	GCC	ACCA	GTTCCCT	TCGGT	CCCC	CCCAAC	ATCGGACCT	CAGT	TGGCTT	AC	CCCTTT	CGGT	TC	302			
SCPP9-C2 ^{SA}	GTGCTTCAGCA	CCC	ACCT	GTGGCC	G	CAGT	TCCCT	ATGGT	CCCC	CAACAT	TGGACCT	CAGT	TGGCTT	AC	CCCTTT	CGCT	TC	227	
SCPP9-C1 ^{SR}	GTGCTTCAGCA	GCC	ACCA	GTTCCCT	TCGGT	CCCC	CCCAAC	ATCGGACCT	CAGT	TGGCTT	AC	CCCTTT	CGGT	TC	302			
SCPP9-C2 ^{SR}	GTGCTTCAGCA	CCC	ACCT	GTGGCC	G	CAGT	TCCCT	ATGGT	CCCC	CAACAT	TGGAAGCT	TGGCTT	ACTT	AC	CCCTTT	CGCT	TC	311	

		310	315	320	325	330	335	340	345	350	355	360	365	370	375	380	385	
conservation	*	!	!	!	!	!	!	!	!	!	!	!	!	!	!	!	!	
SCPP9 ^{DR}	CG	CTAA	TGGGGG	CT	TG	CCGTATT	TG	TGGCTGGA	CTT	CCTAATCAACCT	GCG	TAAT	TCCCTC	CT	CAGCAACAAGTT	TGCGG	385	
SCPP9 ^{LW}	CT	CTAAC	GGGGG	GC	TG	CCGTATTACATTGGTGG	G	CCCCAGAATCAACCAG	GGT	TATTCCTC	CT	CAGCAGCAAGTT	TGCGG				397	
SCPP9 ^{PP}	CT	CTAAC	GGGGG	GC	TG	CCGTATTACATTGGTGG	G	CCCCAGAATCAACCAG	GGAT	TATTCCTC	CT	CAGCAGCAAGTT	TGCGG				391	
SCPP9- <i>CI</i>	CT	CTAAC	GGGGG	GC	TG	CCGTATTACATTGGTGG	G	CCCCAGAATCAACCAG	G	CAAT	TATTCCTC	CT	CAGCAACAAGTT	TGCGG			391	
SCPP9- <i>C1</i> ^{CC}	A	TCTAAT	TGGGGG	GT	TG	CTGTATTACATTGGTGG	A	CCCCAGAATCAACCAG	CCAT	GATCCCTC	CG	AACAACAAGCT	TGCGA				382	
SCPP9- <i>C2</i> ^{CC}	A	CTAAT	TGGGGG	TT	TG	CAATTACATTGGTGG	G	CCCCAGAATCAACCAG	CCAT	TAATGCTCT	CG	...CAGCAAGTT	TATGG				388	
SCPP9- <i>C1</i> ^{SG}	A	CTAAT	TGGGGG	AC	TG	CCGTATTACATTGGTGG	A	CCCCAGAATCAACCAG	CCAT	GATCCCTC	CG	CAGCAACAAGTT	TGCGG				382	
SCPP9- <i>C2</i> ^{SG}	A	CTAAT	TGGGGG	TT	TG	CCGTATTACATTGGTGG	G	CCCCAGAATCAACCAG	CCAT	TAATGCTCT	CG	CAGCAACAAGTT	TGCGG				388	
SCPP9- <i>C1</i> ^{SA}	A	CTAAT	TGGGGG	AC	TG	CCGTATTACATTGGTGG	A	CCCCAGAATCAACCAG	CCAT	GATCCCTC	CG	CAGCAACAAGTT	TGCGG				382	
SCPP9- <i>C2</i> ^{SA}	A	CTAAT	TGGGGG	TT	TG	CCGTATTACATTGGTGG	G	CCCCAGAATCAACCAG	CCAT	TAATGCTCT	CG	CAGCAACAAGTT	TGCGG				307	
SCPP9- <i>C1</i> ^{SR}	A	CTAAT	TGGGGG	AC	TG	CCGTATTACATT	AGTGG	A	CCCCAGAATCAACCAG	CCAT	GATCCCTC	CG	CAGCAACAAGTT	TGCGG			382	
SCPP9- <i>C2</i> ^{SR}	A	CTAAT	TGGGGG	TT	TG	CCGTATTACATTGGTGG	G	CCCCAGAATCAACCAG	CCAT	TAATGCTCT	CG	CAGCAACAAGTT	TGCGG				391	

conservation

	390	395	400	405	410	415	420	425	430		435	440	445	450				
	!	!	!	!	!	!	!	!	!	!	!	!	!	!	!			
SCPP9 ^{DR}	CTGGACAAGG	ACCTG	CTGGA	AAT	TAAT	CAAGC	CGTTGGG	...	T	TGCCA	CAA	GGCTCACT	GGA	AGATT	TAAAG	453	
SCPP9 ^{LP}	CTGGACAAGGCC	CT	TTGGA	AAC	CAAT	CAAGCT	GCAGGCC	TAA	T	ACCAC	CA	GGTTCAC	T	GACT	AGATT	TAAAG	468
SCPP9 ^{PP}	CTGGACAAGGCC	CT	TTGGA	AAC	CAAT	CAAGCT	GCAGGCC	TAA	T	ACCAC	CA	GGTTCAC	T	GACT	AGATT	TAAAG	462
SCPP9 ^{CI}	CTGGACAAGGCC	CT	TTGGA	AAT	TAAC	CAAGCT	GT	ACCAC	CA	GGCTCACT	T	GACT	AGATT	TAAAG	453	
SCPP9 ^{C1'CC}	CTGGACAAGGCC	CT	TTGGA	AAC	CAAT	CAAGCT	GT	ACCAC	CA	GGCTCACT	T	GAAT	AGATT	TAAAG	444	
SCPP9 ^{C2'CC}	CTGGACAAGGCC	CT	TTGGA	AAT	TAAT	CAAGCT	GT	ACCAC	CA	GGCTCACT	T	AACT	AGATT	TAAAG	450	
SCPP9 ^{C1'SG}	TTGGACAAGGC	ACT	CTGGA	AAT	TAAC	CAAGCT	GT	ACCAC	CA	GGCTCACT	T	GACT	AGATT	TAAAG	444	
SCPP9 ^{C2'SG}	CTGGACAAGGCC	CT	TTGGA	TAT	TAAT	CAAGCT	GT	ACCAC	CA	TTTGATGAA	GCAATTACT	TGGC	AAA	ACC	ATT	459	
SCPP9 ^{C1'SA}	CTGGACAAGGCC	CT	TTGGA	AAT	TAAT	CAAGCT	GT	ACCAC	CA	GGCTCACT	T	GACT	AGATT	TAAAG	444	
SCPP9 ^{C2'SA}	CTGGACAAGGCC	CT	TTGGA	AAT	TAAT	CAAGCT	GT	ACCAC	CA	GGCTCACT	T	AACT	AGATT	TAAAG	369	
SCPP9 ^{C1'SR}	CTGGACAAGGCC	CT	TTGGA	AAT	TAAT	CAAGCT	GT	ACCAC	CA	GGCTCACT	T	GACT	AGATT	TAAAG	444	
SCPP9 ^{C2'SR}	CTGGACAAGGCC	CT	TTGGA	TAT	TAAT	CAAGCT	GT	ACCAC	CA	GGCTCACT	T	AACT	AGATT	TAAAG	453	

	455	460	465	470	475	480	485	490	495	500	505	510	515	520	525	530	
conservation	!!!!*	!!!!*	!!!!	!!!!	!!!!	!!!!	!!!!	!!!!	!!!!	!!!!	!!!!	!!!!	!!!!	!!!!	!!!!	!!!!	
SCPP9'DR	CGATC	ATT	TAT	TCAGA	AGGACCAC	AGCA	AGACCA	CCTGTCT	CAG	TCACC	CAGAT	GCCT	GCT	CAGCT	CAGCCCT	ACTGTGTC	533
SCPP9'LV	CGCTC	CTT	CCTCAGA	AGGACCACA	...	AGACCA	CCTGTCT	CC	ATCAC	CCAGAT	CC	CAGCT	CAGGT	CAGCCCA	ACTGTGTC		545
SCPP9'PP	CGCTC	CTT	CCTCAGA	AGGACCACA	...	AGACCA	CCTGTCT	CAG	TCACC	CAGAT	CC	CAGCT	CAGGT	CAGCCCA	ACTGTGTC		539
SCPP9-CI	CGCTC	CTT	CCTCAGA	AGGA	ACACT	GC	GAGACCA	CCTGTCT	CAAT	CACC	CAGAT	GCC	AGCT	CAGCT	CAGCCCT	ACTGTGTC	533
SCPP9-C1'CC	CGCTC	CTT	CCTCAGA	AGGACCAC	AGCA	AGACCA	CCTGT	TAAT	AATT	ATTTT	AT	GCC	AGCT	CAAGT	CAACCCT	TGCTGTGTC	524
SCPP9-C2'CC	CGCTC	TTT	CTCAGA	AGGACCAC	TGCA	AGA	CCA	CCTGTCT	TAAT	CACC	CAGAT	GCC	AGCT	CAGGT	CAACCCT	TGCTGTGTC	530
SCPP9-C1'SG	CGCTC	CTT	CCTCAGA	AGGACCAC	AGCA	AGA	...	CCTGTCT	CAAT	CACC	CAGAT	GCC	AGT	TCAGAT	CAACCCT	TGCTGTGCC	521
SCPP9-C2'SG	CGCTC	CTT	CCTCAGA	AGGACCAC	TGCA	AGA	CCA	CCTGTCT	CAAT	CACC	CAGAT	GCC	AGCC	CAGGT	CAACCCT	TGCTGTGTC	539
SCPP9-C1'SA	CGCTC	CTT	CCTCAGA	AGGACCAC	AGCA	AGA	...	CCTGTCT	CAAT	CACC	CAGAT	GCC	AGCT	TCAGAT	CAACCCT	TGCTGTGCC	521
SCPP9-C2'SA	CGCTC	CTT	CCTCAGA	AGGACCAC	TGCA	AGA	CCA	CCTGTCT	CAAT	CACC	CAGAT	GCC	AGCC	CAGGT	CAACCCT	TGCAGTGTC	449
SCPP9-C1'SR	CGCTC	CTT	CCTCAGA	AGGACCAC	AGCA	AGA	...	CCTGTCT	CAAT	CAC	ACAGAT	GCC	AGCT	TCAGAT	CAACCCT	TGCTGTGCC	521
SCPP9-C2'SR	CGCTC	CTT	CCTCAGA	AGGACCAC	TGCA	AGA	CCA	CCTGTCT	CAAT	CACC	CAGAT	GCC	AGCC	CAGGT	CAACCCT	TGCTGTGTC	533

	535	540	545	550	
conservation	!!!!!	!*	*****	*****	
SCPP9'DR	TGGAAAT	A	CTGTTGG	CTAA	552
SCPP9'LV	TGGAAAT			552
SCPP9'PP	TGGAAAT			546
SCPP9-CI	TGGAAAT	T	CTGT	GGGTAA	552
SCPP9-C1'CC	TGGAAAC	CCTGTT	GGGTAA		543
SCPP9-C2'CC	TGGAAAT	CCTGTT	GGGTAA		549
SCPP9-C1'SG	TGGAAAT	CCTGTT	GGGTAA		540
SCPP9-C2'SG	TGGAAAT	CCTGTT	GGGTAA		558
SCPP9-C1'SA	TGGAAAT	CCTGTT	GGGTAA		540
SCPP9-C2'SA	TGGAAAT	CCTGTT	GGGTAA		468
SCPP9-C1'SR	TGGAAAT	CCTGTT	GGGTAA		540
SCPP9-C2'SR	TGGAAAT	CCTGTT	GGGTAA		552

- ⓧ

non conserved
- ⓧ

≥ 55% conserved
- ⓧ

≥ 85% conserved