

SCO no.	Annotated function	Streptomyces		Actinobacteria		Other Gram +ves		E. coli	
		Distribution	% ID	Distribution	% ID	Distribution	% ID	Distribution	% ID
1480	sIHF	U	100	U	50-70	P	50	A	
3767	TerB	P	80-90	VS	50-70	A		A	
4614	YajQ	U	100	U	70	P	50-70	Present	40
2140	Putative regulator (Lrp/AsnC family)	U	80-90	P	50-60	P	40	A	
2950	HupA	U	100	P	50	P	40	A *	
5725	UF	U	80	P	50-90	VS	40	A	
1489	Putative DNA binding protein BldD	U	100	P	70	A		A	
1839	Putative transcriptional regulator	U	100	P	50-80	A		A	
5592	UF	U	100	U	70	U	40	A	
3793	YjqA	P	90	P	40	VS	40	A	
5783	UF	U	50-80	P	40	VS	30	A	
3013	Putative two-component response regulator	U	100	U	80	P	60	Present	40
4232	Putative transcriptional factor regulator	U	100	U	80	U	30-60	A	
3328	UF	U	100	U	40-80	P	40	A	
6482	UF	U	80	P	50	A		A	
2911	Uncharacterised	U	80	P	60-70	VS	30-40	Present	40
2093	Uncharacterised	U	80-90	P	40-50	VS	40	A	
4199	Lysine-rich UF	U	60-100	P	30	VS	30	A	
3571	Putative transcriptional regulator CRP	U	90	U	60	U	40	Present	30
0204	Putative regulator (luxR family)	P	80	P	60	A		A	
3375	Lsr2 protein	U	90	U	50	A		A	
5607	Putative transcriptional regulator	VS	50	VS	40	A		A	
5556	HupS	U	90	P	50	VS	40	Present *	40
1366	PadR regulator	P	90	P	40-50	P	40	Present	40
4493	Putative regulator (Lrp/AsnC family)	U	90	VS	50	A		Present	30

Figure 3.12 Phylogenetic distributions of 42 putative NAPs identified in the previous section. Distribution is classified as ubiquitous (U; green), patchy (P; blue), very sparse (VS; dark red) or absent (A; black). Typical identity (%) is given at the amino acid level.