

**Fig. S5 Secondary structure predictions for AflR from *D. septosporum* NZE10 and ALP3.** Pairwise alignment predicted by HHpred. The arrow indicates the location of the N349K polymorphism in ALP3.

Q	ss_pred		CCCCccccCCCCCcCCcCCCCCCCCCCCChhhhHHhhcHHHHHHccCCCCCCCCCCCCHHHHHHCCccccccccCCCC		
Q	0_NZE10	1	MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRT	70	(479)
Q	Consensus	1	~~~~~K1R~SC~~CA~SKVrC~KeKpTcsRC~~rg~~C~Y~~srR~GR~   ++  +.+.++..... . ... ... ... ++ .++  .  .+++.+ ...+ .  +	70	(479)
T	Consensus	1	~~~~~r~~~~ac~~c~~~k~~c~~~p~~c~~~c~~~~~C~y~~~~~r~~~~~	70	(479)
T	1_ALP3	1	MPESRGSESSGSTSRRASGTQHIATPKLKDSCTACATSKVKCSKDKPTCARCTRRGLTCDYGLSKRTGRT	70	(479)
T	ss_pred		CCCCccccCCCCCCCCccccCCCCCCCCCCCCcccchhHHHHHHHHccCCCCCCCCCCCCchHHcCCCCCCCCCCCC		

Q ss_pred	CCCCCCCC <span style="color:red">Hhhcc</span> CCCCCCCCCCCC <span style="color:red">c</span> <span style="color:red">hhccc</span> CCCCCC <span style="color:red">ch</span> Hhh <span style="color:red">hcccccc</span> CCCCCCCCCCCCCCCC	
Q 0_NZE10	141 AGLDQ <span style="color:blue">WNSDL</span> WSTM <span style="color:blue">FAPNEPSSNNTPANTMQ</span> THGGNGND <span style="color:blue">IDHL</span> FNDL <span style="color:blue">TSYMLGEPTDTAMSNQH</span> THTFS	210 (479)
Q Consensus	141 ~~~d~~~~~s~~~~~s~~~~~s~~~~~l~~~~~s~~~~~s~~~~~ +++ + . ++. +++++++.+.++.++ ++  .++ ++ +++.++ ++++++ +	210 (479)
T Consensus	141 ~~~~~~s~~~~~s~~~~~s~~~~~s~~~~~s~~~~~	210 (479)
T 1_ALP3	141 AGLDQ <span style="color:blue">WNSDL</span> WSTM <span style="color:blue">FAPNEPSSNNTPANTMQ</span> THGGNGND <span style="color:blue">IDHL</span> FNDL <span style="color:blue">TSYMLGEPTDTAMSNQH</span> THTFS	210 (479)
T ss_pred	CChHHccchHHhcCCCCCCCCCCCC <span style="color:red">ch</span> HhcccCCCCC <span style="color:red">ch</span> HhHHhcCChHcCCCCCCCCCCCCCCCC	

Q ss\_pred ccCCCCccccCCCCccccCCCCCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHhhC  
Q 0\_NZE10 421 SSGSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS 479 (479)  
Q Consensus 421 ~~~~~p~s~~l~qle~dLr~rLr~ls~~ii~~Lr~~  
T Consensus 421 ~~~~~p~s~~l~qle~dLr~rLr~ls~~ii~~Lr~~ 479 (479)  
T 1\_ALP3 421 SSGSSSSLESIGEDSVVGVSLSATAGSPLSSPTFDQLEADLRKRLRAVSFETIDVLRRS 479 (479)  
T ss\_pred cCCccccchhcCCCCccccCCCCCCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHhhC