Table S1: Similarity between domains within insect Dof homologs and vertebrate BCAP homologs

		N-term	***DBB***	***AR***	***Middle***	***Coiled Coil***	***C-term***
Dof	Drosophila : Anopheles	42	**54**	**62**	22	**64**	26
BCAP	chick : Fugu	28*	**44**	**78**	27	**63**	
	mouse : Fugu	33*	**46**	**81**	25	**63**	
	chick : mouse	51	**73**	**93**	64	**88**	64

Percentages of identical amino acids in pairwise comparisons of domains of Drosophila and Anopheles Dof (acc.# O96757 and Q8T5J9) and chick, mouse and Fugu BCAP (acc.# Q9DDT2, Q9EQ32, and Ensembl:SINFRUP00000078060, respectively.). The first ten amino acids of mouse and chick BCAP are missing in the predicted Fugu gene and were ignored for the comparison of the N-terminal domain. The Fugu C-terminal domain is also incomplete, so comparisons were not made for this part. The regions of Dof were defined in the Drosophila protein as amino acids 1-215 (N-term), 216-353 (DBB), 372-440 (Ank), 441-665 (middle) 666-754 (coiled coil) and 755-1012 (C-term); the regions of BCAP were defined in the mouse protein as 1-181 (N-term), 182-317 (DBB), 335-403 (Ank), 404-590 (middle), 591-682 (coiled coil) and 683-811 (C-term). CLUSTALW was used to align the anopheles sequence to Dof and the Fugu and chicken sequence to the mouse sequence. The highest values in each comparison are highlighted in bold print.