Table 1: Maximal numbers of transcription factors from each super-family in a single organism, and the organism in which the maximum is observed.

	Super-family	Maximal # TFs	Kingdom	organism	P	S	O	H	# sequences
1	lambda repressor-like DNA-binding domains	77	A,B,E	*Photorhabdus luminescens*	3	1	2	1	64
2	C-terminal effector domain	88	A,B,E	*Streptomyces avermitilis*	-	-	-	-	-
3	srf-like	122	E	*Arabidopsis thaliana*	-	-	-	-	-
4	helix-loop-helix DNA-binding domain	186	E	*Arabidopsis thaliana*	2	1	1	2	128
5	DNA-binding domain	194	B,E	*Oryza sativa*	-	-	-	-	-
6	Zn2/Cys6 DNA-binding domain	246	E	*Fusarium graminearum*	3	13	3	1	1,248
7	winged helix DNA-binding domain	299	A,B,E	*Bordetella bronchiseptica*	6	1	1	1	2,048
8	glucocorticoid receptor-like DNA-binding domain	376	A,B,E	*C.elegans*	2	9	3	2	3,456
9	homeodomain-like	417	A,B,E	*Danio rerio*	6	1	1	2	$8.4*10^6$
10	multi-domain C2H2 zinc fingers	1308	E	*Mus musculus*	6–30	1	1	1	-

The kingdom in which each super-family is observed is abbreviated as A – Archea, B – Bacteria, E – Eukaryotes. Estimates for the number of possible sequences are shown (see methods). P – number of variable positions in each half-site, S – number of possible spacing between half-sites, O – number of possible orientations, H – homo-dimers (1) or hetero-dimers (2). The number of sequences is $4^{P}*H*O*S/2$.