

Motif	Group Specificity	Group Specificity Rank	Site Specificity	Site Specificity Rank	Testset Sites	Average Testset Sites	StDev Testset Sites	TRANSFAC Correlation	TRANSFAC ID	Motif Finders	Sets	Repeats	Logo
1	1.10e-014	2	2.80e-014	2	7	0.41	0.51	0.66	MEIS1	AA	1, 2, 3, 4, 5	PAL	ATG:CA T T ICA
2	4.40e-012	6	6.00e-012	6	6	0.35	0.61	0.77	HSF1	AA, BP, MD, ME	3, 4, 5	PAL	T GAA A T I C A A I
3	4.80e-012	7	1.20e-011	7	9	0.53	0.72	0.88	ATF3	AA	1, 2, 4, 5	PAL	T G A C T C A C A A
4	5.50e-011	12	1.30e-010	11	7	0.41	0.51	0.60	BACH1	AA, BP, ME	1, 2, 3, 4, 5		A G A C T C T G G
5	1.70e-010	13	1.90e-010	12	5	0.29	0.59	0.62	LEF1	AA, BP, MD, ME	1, 2, 3, 4, 5		T G T C T G A A A A A I
6	7.00e-008	20	3.20e-007	22	9	0.53	0.51	0.84	MEIS1	AA, BP, MD, ME	1, 4, 5		A T G A C A I
7	7.30e-008	21	2.30e-007	20	9	0.53	0.62	0.65	NERF	AA, ME	1, 4, 5	PAL	A A C C A G A A G
8	2.30e-007	23	1.00e-006	26	15	0.88	1.50	0.66	LFA1	BP, MD, ME	1, 4, 5		G A G G G C A G G G
9	4.50e-007	24	7.40e-007	24	8	0.47	0.72	0.64	HFH3	AA	4, 5		A A G A A A I A
10	1.10e-006	29	4.40e-006	30	14	0.82	0.95	0.61	MEIS1	AA, BP, MD, ME	1, 4		G A A G G A T G C G
11	1.20e-006	30	1.90e-006	29	10	0.59	1.10	0.62	AP2GAM	AA, BP	3, 4, 5		C G G C G G G C
12	2.10e-006	32	7.80e-006	32	9	0.53	0.51	0.69	CHOP	AA, MD, ME	1, 2, 4, 5		G C T T G A
13	4.70e-006	34	1.20e-005	35	10	0.59	0.71	0.64	CACBIN	AA	3, 5		G G C T G G A A
14	4.90e-006	35	9.80e-006	34	9	0.53	0.72	0.60	NFKAPP	BP, ME	1, 4, 5	TR	A A G G G A C C G G
15	6.50e-006	36	4.90e-005	43	14	0.82	0.73	0.67	SP1_Q6	BP	1		A A G G G G G G G G A
16	1.10e-005	38	1.40e-005	36	10	0.59	1.10	0.71	AP2_Q6	AA, BP, MD, ME	1, 4, 5		G G G G C G G G G G
17	1.90e-005	41	4.50e-005	41	10	0.59	0.71	0.84	HMG1Y	AA, ME	1, 4, 5	PAL	G G A A A T T I C A
18	1.90e-005	41	2.90e-005	38	8	0.47	0.72	0.73	CEBPGA	AA, BP, ME	1, 4, 5	PAL	A A T C A A A
19	3.00e-005	44	4.50e-005	41	13	0.76	1.50	0.64	MINI19	AA	1, 2, 4, 5		G C T C T G G G G G G
20	3.00e-005	44	3.70e-005	40	8	0.47	1.00	0.61	AP2GAM	BP, ME	5	PAL,TR	T C G A G C C G G G G C
21	7.20e-005	48	2.00e-004	49	11	0.65	0.70	0.69	GKLF	AA, BP, ME	1, 2, 3, 4, 5		A A G G G G A
22	7.30e-005	49	2.10e-004	50	18	1.10	1.40	0.66	AP2_Q6	AA, MD, ME	4, 5	TR	G C G G G G G G
23	9.00e-005	50	2.00e-003	62	36	2.10	1.70	0.73	ERR1	BP, ME	1, 4, 5		T C A A G C A
24	1.10e-004	51	1.30e-004	47	8	0.47	0.87	0.66	IRF	AA	1, 2, 3, 5	PAL	A G A A A I T A
25	2.00e-004	54	1.10e-003	59	23	1.40	1.00	0.61	GF1	BP	4		G A G A T T A I
26	2.40e-004	55	1.70e-002	80	43	2.50	3.40	0.66	IRF	ME	1, 4, 5		G G G G G G G
27	2.70e-004	57	6.50e-004	56	18	1.10	1.50	0.67	SF1	BP, ME	4		G G G G A A G G T C G G
28	4.20e-004	60	1.10e-002	74	110	6.50	12.00	0.67	SPZ1	ME	1, 4, 5		G G G G T G G T T G G