

Matrix ID	Name	Score	Relative score	Start	End	Strand	Predicted sequence
MA0024.1	E2F1	12.0993	0.98268	1821	1828	+	tttcgcg
MA0024.2	E2F1	13.6436	0.973286	430	440	-	aaggcgggagg
MA0024.2	E2F1	12.78	0.960293	611	621	+	atggcgggagc
MA0024.2	E2F1	7.61774	0.882628	698	708	-	gtggcgggatg
MA0024.2	E2F1	7.10436	0.874905	1821	1831	-	gcggcgcgaaa
MA0024.2	E2F1	6.89836	0.871806	1476	1486	-	agctcgggagg
MA0024.2	E2F1	6.71752	0.869085	511	521	+	gaggcaggagg
MA0024.2	E2F1	6.60834	0.867442	285	295	-	aaggcgggagg
MA0024.2	E2F1	6.60793	0.867436	778	788	-	caggcgtgagc
MA0024.2	E2F1	6.24431	0.861966	721	731	+	tgggcgacaga
MA0024.2	E2F1	6.24316	0.861948	1513	1523	-	agcgcggggga
MA0024.2	E2F1	6.12117	0.860113	75	85	-	cagtcgggaaa
MA0024.2	E2F1	6.06232	0.859228	946	956	+	gaggcaggaga
MA0024.2	E2F1	5.85387	0.856092	1735	1745	-	gtggcaggagc
MA0024.2	E2F1	5.65729	0.853134	1824	1834	+	cgcgccgcaag
MA0024.1	E2F1	8.32861	0.852931	1027	1034	-	tttcgctc
MA0024.1	E2F1	8.32861	0.852931	1566	1573	-	ttccgcg
MA0024.1	E2F1	8.32861	0.852931	2423	2430	+	TTACGCGC
MA0024.2	E2F1	5.40621	0.849357	965	975	+	aaccgggagg
MA0024.2	E2F1	5.00791	0.843364	1563	1573	+	ctggcgcggaa
MA0024.3	E2F1	8.73134	0.835013	1821	1832	-	tgcggcgcgaaa

MA0024. 3	E2F1	8.4027 3	0.82954 1	181 0	182 1	-	aaaggcgcgcat
MA0024. 3	E2F1	8.2834	0.82755 4	182 1	183 2	+	ttcgcgcccga
MA0024. 2	E2F1	2.9470 1	0.81235 9	102 4	103 4	+	caagagcgaaa
MA0024. 3	E2F1	7.2725 8	0.81072 5	181 0	182 1	+	atgcgcgccttt
MA0024. 3	E2F1	7.1288 3	0.80833 1	156 2	157 3	-	ttccgcgccagt
MA0024. 2	E2F1	2.5581 7	0.80650 9	165 4	166 4	+	caaggggcagc
MA0024. 2	E2F1	2.2609 2	0.80203 7	136 1	137 1	+	aacgcaccaga
MA0024. 1	E2F1	6.8135 2	0.80079 7	75	82	+	tttcccga
MA0024. 1	E2F1	6.8135 2	0.80079 7	144 5	145 2	+	tttcccga
MA0024. 2	E2F1	2.1261 7	0.80000 9	183 9	184 9	-	aaagcgccacc