

# Homer *de novo* Motif Results (/rslt/)

[Known Motif Enrichment Results](#)

[Gene Ontology Enrichment Results](#)






If Homer is having trouble matching a motif to a known motif, try copy/pasting the matrix file into [STAMP](#)

More information on motif finding results: [HOMER](#) | [Description of Results](#) | [Tips](#)

Total target sequences = 10651

Total background sequences = 10152

\* - possible false positive

Rank	Motif	P-value	log P-value	% of Targets	% of Background	STD(Bg STD)	Best Match/Details	Motif File
1		1e-215	-4.951e+02	36.38%	17.26%	9.7bp (23.3bp)	LIN28A(CSD)/Homo_sapiens-RNCMPT00162-PBM/HughesRNA(0.777) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
2		1e-16	-3.869e+01	39.89%	34.23%	16.0bp (17.1bp)	STZ(C2H2)/colamp-STZ-DAP-Seq(GSE60143)/Homer(0.955) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
3		1e-15	-3.520e+01	47.35%	41.82%	16.7bp (17.1bp)	RBP1(RRM)/Drosophila_melanogaster-RNCMPT00058-PBM/HughesRNA(0.806) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
4 *		1e-9	-2.278e+01	33.56%	29.48%	15.9bp (18.2bp)	PABP(RRM)/Drosophila_melanogaster-RNCMPT00139-PBM/HughesRNA(0.968) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>
5 *		1e-8	-1.888e+01	6.68%	4.84%	14.5bp (20.2bp)	Unknown3/Arabidopsis-Promoters/Homer(0.799) <a href="#">More Information</a>   <a href="#">Similar Motifs Found</a>	<a href="#">motif file (matrix)</a>