


TRANSFAC® Matrix Report Overview

BIOBASE Matrix Report
V\$GATA5_Q4 - GATA-5

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Matrix Overview what is this? 1

Consensus sequence logo



Nucleotide position frequency

A	C	G	T	Consensus
4	0	0	13	T
17	0	0	0	A
0	0	0	17	T
0	16	0	1	C
4	2	0	11	T
4	4	5	4	N

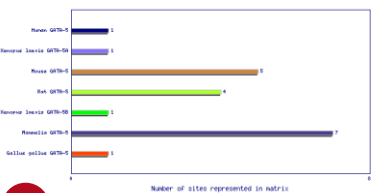


Nucleotide position frequency

A	C	G	T	Consensus
11	0	2	4	A
1	0	16	0	G
17	0	0	0	A
0	0	0	17	T
13	0	0	4	A

Experimental basis for positional weight matrix construction what is this? 2

Transcription factors



Aligned sites (17) 3

Sequence	Transcription factors	Bound Gene	Experimental evidence	Experimental source	References
AATCTC	GATA-5(m), GATA-5(r)	Trenc1(m) [details]	ChIP-seq, EMSA, Reporter, etc.	rec(mouse-NH3T3) [more...]	11, 13, 18, 19, 20
AATCTT	GATA-5(m.s.)	NOX1(h) [details]	ChIP-seq, EMSA, Reporter, etc.	Caco-2 [more...]	3
AATCTT	GATA-5(r)	Smarc2(m) [details]	ChIP-seq, EMSA, Reporter, etc.	P-19 [more...]	2
AATCTT	GATA-5(m.s.)	NOX1(h) [details]	ChIP-seq, EMSA, Reporter, etc.	Caco-2 [more...]	3
TATCAA	GATA-5(m.s.)	NOX1(h) [details]	ChIP-seq, EMSA, Reporter, etc.	Caco-2 [more...]	3
TATCAa	GATA-5(m.s.)	LCT(h) [details]	ChIP-seq, EMSA, Reporter, etc.	rec(mammalian-in vitro)	5
TATCAa	GATA-5(m)	Nppa(r) [details]	ChIP-seq, EMSA, Reporter, etc.	heart, neonatal - ET-1 [more...]	4, 8, 9, 11, 12
TATCAAT	GATA-5(m)	Gnfh1(r) [details]	ChIP-seq, EMSA, Reporter, etc.	GT1-7	1
TATCOCC	GATA-5(m)	Slc9a3(r) [details]	ChIP-seq, EMSA, Reporter, etc.	Caco-2 [more...]	7
TATCOCC	GATA-5(m), GATA-5(r)	Bmyo(r) [details]	ChIP-seq, EMSA, Reporter, etc.	neonatal cardiac myocytes [more...]	13, 17

Matrix type: factor-specific matrix 4


Matrix Category: matrix compiled from individual genomic sites



Matrix classification: ZFGATA [Find all matrices in this class](#)

Application details: compiled and aligned by BIOBASE; sites quality 4 or better

Number of sequences used: 17

Related matrices what is this? 5

Related family matrices	Consensus binding sequence derived from Positional Weight Matrix	Category method
	V\$GATA_Q6	matrix compiled from individual genomic sites

Related factor-specific matrices	Consensus binding sequence derived from Positional Weight Matrix	Category method
	V\$GATA5_Q4	universal protein binding microarrays (PBM)
	V\$GATA5_Q3	universal protein binding microarrays (PBM)

Identifiers what is this? 6

BIOBASE accession: M02006

References (22)

SI.No	PMID	Citation
1	10259093	Leclerc, G. M., Bose, S. K., Bockfor, F. R., Specific GATA-binding elements in the GnRH promoter are required for gene expression pulse activity: role of GATA-4 and GATA-5 in this intermittent process. <i>Neuroendocrinology</i> 88 (1) 1-16 (2008). Show abstract
2	18082132	Differentiation-specific expression of chromatin remodeling factor BIRM. <i>Book</i> 366 827-833 (2008). Show abstract
3	18005670	Valente, A. J., Zhou, Q., Lu, Z., He, W., Qiang, M., Ma, W., Li, G., Wang, L., Banfi, B., Steger, K., Krause, K. H., Clark, R. A., Li, S., Regulation of NOX1 expression by GATA, HNF-1alpha, and Cdx transcription factors. <i>Free Radic Biol Med</i> 44 (3) 430-43 (2008). Show abstract
4	15574300	Interleukin-18 is a pro-hypertrophic cytokine that acts through a phosphatidylinositol 3-kinase-phosphoinositide-dependent kinase-1-Akt-GATA4 signaling pathway in cardiomyocytes. <i>Book</i> 280 4553-4567 (2005). Show abstract
5	15178553	van Weering, H. M., Bosse, T., Musters, A., de Jong, E., de Jong, N., Hogen Esch, C. E., Boudreau, F., Swain, G. P., Dowling, L. H., Montgomery, R. K., Grand, R. J., Kraiskal, S. D., Complex regulation of the lactase-phlorizin hydrolase promoter by GATA-4. <i>Am J Physiol Gastrointest Liver Physiol</i> 287 (4) G999-909 (2004). Show abstract

M02006: V\$GATA5_Q4



1 The original and reverse complement nucleotide position frequency and sequence logo are both presented, making it easy to compare binding sites regardless of strand orientation.

2 The new bar graph makes it easy to see at-a-glance how many binding sites each transcription factor contributed to the compiled matrix.

3 The updated site alignment table provides (when applicable) detailed information for each of the binding sites used to compile the matrix including the binding factor, the bound gene, the experimental method and system used to determine binding, plus links to the reference(s) from which the site was taken.

4 5 The new matrix category classification system (4) and related factor-specific and family matrices (5) allows you to easily identify how a matrix was constructed and to compare it to other matrices within TRANSFAC and public domain offerings.

6 The reference section lists the complete set of supporting references.