

[Table of Contents](#) ↓

**Matrix Overview** [what is this?](#)

Consensus sequence logo



Nucleotide position frequency

A	C	G	T	Consensus
10	20	4	6	C
6	11	17	6	N
14	12	13	1	N
0	0	0	40	T
0	1	39	0	G
40	0	0	0	A
0	32	2	6	C
0	1	39	0	G
4	9	0	27	T
14	19	3	4	M
23	4	7	6	A

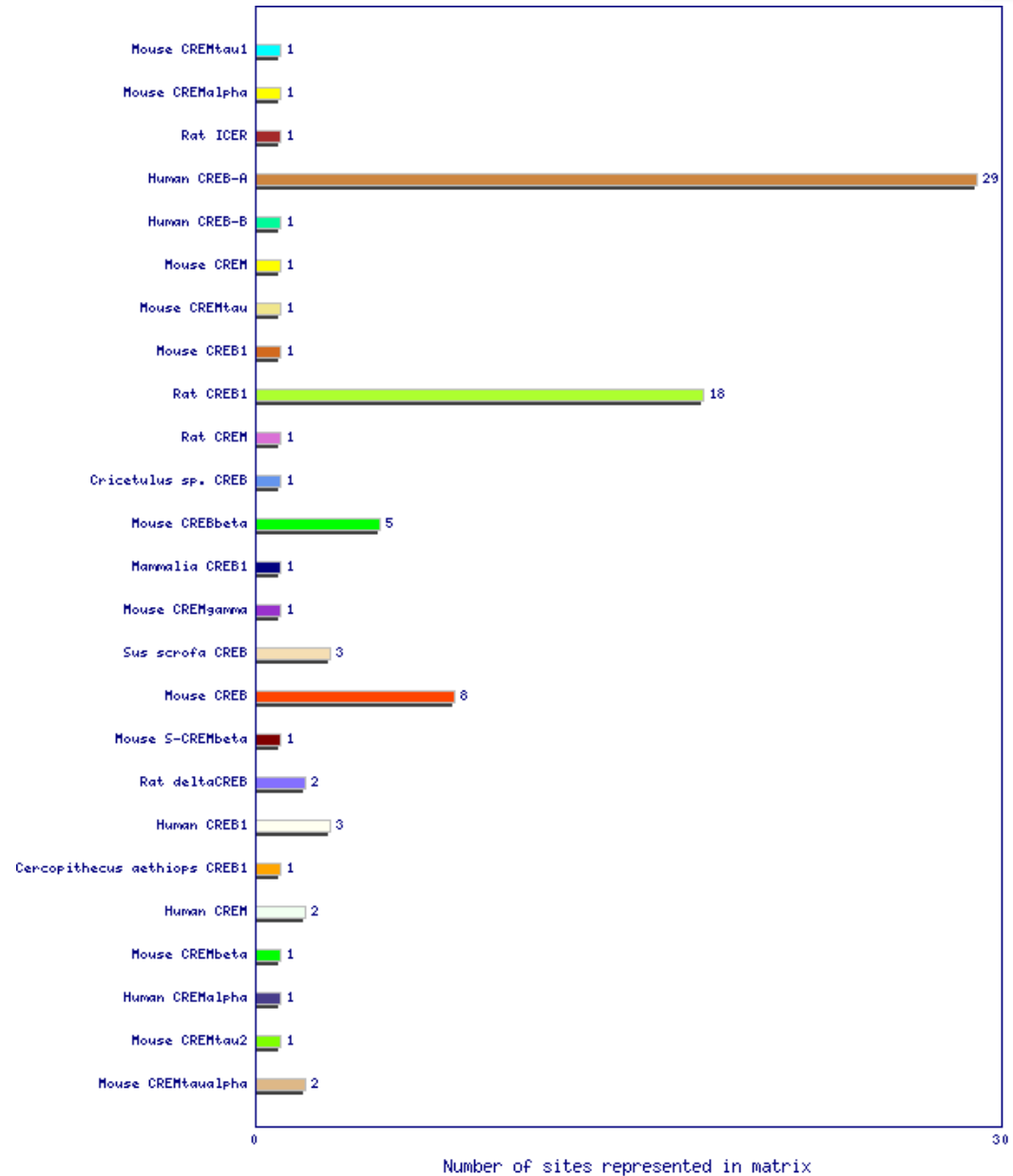
Nucleotide position frequency

A	C	G	T	Consensus
6	7	4	23	T
4	3	19	14	K
27	0	9	4	A
0	39	1	0	C
6	2	32	0	G
0	0	0	40	T
0	39	1	0	C
40	0	0	0	A
1	13	12	14	N
6	17	11	6	N
6	4	20	10	G

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

## Transcription factors

- Human CREB-A
- Human CREB1
- Human CREMalpha
- Human CREB-B
- Human CREM
- Mouse CREB1
- Mouse CREBbeta
- Mouse S-CREBbeta
- Mouse CREMbeta
- Mouse CREMtau1
- Mouse CREMalpha
- Mouse CREM
- Mouse CREMtau
- Mouse CREMgamma
- Mouse CREB
- Mouse S-CREBbeta
- Mouse CREMtau2
- Mouse CREMtaualpha
- Rat ICER
- Rat CREM
- Rat CREB1
- Rat deltaCREB
- Mammalia CREB1



## Aligned sites (40)

Show  entries Search:

Sequence	Transcription factors	Bound Gene	Experimental evidence	Experimental source	References
AAATGACGTAA	CREB-A(h)	E4(AD) [details]	CI DM FA FO GS SS IP SE OT	rec(human-E.coli) [more...]	<a href="#">54 ↗</a> , <a href="#">64 ↗</a> , <a href="#">82 ↗</a>
AAATGACGTAA	CREB-A(h)	E4(AD) [details]	CI DM FA FO GS SS IP SE OT	HeLa [more...]	<a href="#">54 ↗</a>
AAGTGACGTAA	CREB-B(h)	E4(AD) [details]	CI DM FA FO GS SS IP SE OT	HeLa [more...]	<a href="#">24 ↗</a> , <a href="#">29 ↗</a> , <a href="#">37 ↗</a> , <a href="#">44 ↗</a> , <a href="#">76 ↗</a> , <a href="#">83 ↗</a> , <a href="#">107 ↗</a>
ACGTCATGTCT			CI DM FA FO GS SS IP SE OT		
AGATGACGCAT	CREB-A(h)	HLA-DRA(h) [details]	CI DM FA FO GS SS IP SE OT	Raji [more...]	<a href="#">12 ↗</a> , <a href="#">13 ↗</a> , <a href="#">20 ↗</a> , <a href="#">68 ↗</a> , <a href="#">90 ↗</a> , <a href="#">91 ↗</a> , <a href="#">102 ↗</a> , <a href="#">110 ↗</a>

Showing 1 to 5 of 40 entries 
[First](#) [Previous](#) [1](#) [2](#) [3](#) [4](#) [5](#) [Next](#) [Last](#)

**Matrix type :** family matrix

**Matrix Category :** matrix compiled from individual genomic sites

**Matrix classification :** BZIP

**Application details :** compiled and aligned by TRANSFAC; sites quality 6 or better

**Number of sequences used :** 40







**Additional transcription factors linked to the matrix :** ICER-xbb1(h), CREB(b), CREMdeltaC-F(r), S-CREM(m), CREB1(b), CREB(mv), CREM-Ib(h), ICER-I(m), CREBomega(m), deltaCREB(m), CREM-isoform1(b), CREMtau(r), CREM-isoform2(b), ICER-IIgamma(m), CREM(b), CREMtau(m.s.), CREMdeltaC-G(r), CREM(m.s.), CREB1(s), CREM-Ia(h), ICER-II(m), CREMepsilon(m), CREM-isoform8(h), ICER-

## Profile membership [what is this?](#)

**Profiles which include this matrix :** lung-specific profile, redox-sensitive profile, cell cycle-specific profile, liver-specific profile, pancreatic beta-cell-specific profile, pituitary-specific profile, nerve system specific profile










## Related matrices [what is this?](#)

Show  entries Search:

Related family matrices 	Consensus binding sequence derived from Positional Weight Matrix 	Category method 
	V\$CREB_Q3	matrix compiled from individual genomic sites
	V\$CREB_Q2_01	matrix compiled from individual genomic sites
	V\$CREBATF_Q6	matrix compiled from individual genomic sites

Showing 1 to 3 of 3 entries

Show  entries Search:

Related factor-specific matrices 	Consensus binding sequence derived from Positional Weight Matrix 	Category method 	Recommended factor-specific matrix 
	V\$CREB1_03	ChIP-Seq	
	V\$CREB1_04	ChIP-Seq	
	V\$CREB1_05	ChIP-Seq	
	V\$CREB1_06	ChIP-Seq	
	V\$CREB1_16	ChIP-Seq	

Showing 1 to 5 of 29 entries 
[First](#)
[Previous](#)
[1](#)
[2](#)
[3](#)
[4](#)
[5](#)
[Next](#)
[Last](#)

**Identifiers** [what is this?](#)

**BIOBASE accession** : M00917

## References (115)

SI.No	PMID	Citation
1	<a href="#">20171190</a>	Thonpho, A., Sereeruk, C., Rojvirat, P., Jitrapakdee, S., Identification of the cyclic AMP responsive element (CRE) that mediates transcriptional regulation of the pyruvate carboxylase gene in HepG2 cells. <i>Biochem Biophys Res Commun</i> 393 (4) 714-9 (2010). <a href="#">Show abstract</a>
2	<a href="#">20022930</a>	Seo, H. Y., Kim, M. K., Min, A. K., Kim, H. S., Ryu, S. Y., Kim, N. K., Lee, K. M., Kim, H. J., Choi, H. S., Lee, K. U., Park, K. G., Lee, I. K., Endoplasmic reticulum stress-induced activation of activating transcription factor 6 decreases cAMP-stimulated hepatic gluconeogenesis via inhibition of CREB. <i>Endocrinology</i> 151 (2) 561-8
		CRE2 sequence. <i>Biochim Biophys Acta</i> 1769 (2) 79-91 (2007). <a href="#">Show abstract</a>
4	<a href="#">15322221</a>	Kyttaris, V. C., Juang, Y. T., Tenbrock, K., Weinstein, A., Tsokos, G. C., Cyclic adenosine 5'-monophosphate response element modulator is responsible for the decreased expression of c-fos and activator protein-1 binding in T cells from patients with systemic lupus erythematosus. <i>J Immunol</i> 173 (5) 3557-63 (2004). <a href="#">Show abstract</a>
5	<a href="#">12164863</a>	Eberhardt, W., Engels, C., Muller, R., Pfeilschifter, J., Mechanisms of dexamethasone-mediated inhibition of cAMP-induced tPA expression in rat mesangial cells. <i>Kidney Int</i> 62 (3) 809-21 (2002). <a href="#">Show abstract</a>

Showing 1 to 5 of 115 entries

[First](#) [Previous](#) [1](#) [2](#) [3](#) [4](#) [5](#) [Next](#) [Last](#)