

WebMCOT web-service for prediction of co-occurred DNA motifs in ChIP-seq data

(<https://webmcot.sysbio.cytogen.ru>)

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The WebMCOT application discovers motifs co-occurrence with a spacer and with an overlap in a single ChIP-seq dataset

I

Upload or Enter DNA sequences in FASTA format ?

Upload file Enter sequences

Browse... spi1_ridinger_2012_m150p150_mm9.seq

III

One or Many Partner motif(s) will be tested ?

One partner Many partners

Advanced options ?

II

Upload or Enter Anchor motif ?

Upload file Enter motif Choose motif

Browse... spi1.motif

IV

Upload or Enter Partner motif ?

Select Organism to set thresholds of recognition models
Mouse

Upload file Enter motif Choose motif

Browse... irf8.motif

V

RUN

Your task is allocated with this URL: <http://localhost:8080/app?q=67bdf340-7de1-4070-885f-110702128eb5>

EXAMPLE ?

WebMCOT interface for application of MCOT pipeline

WebMCOT Results (The Anchor SPI1 and Partner IRF8 motifs)

# Motif	Motif Name	Significance of co-occurrence Anchor/Partner, -Log10[P-value]					Asymmetry Anchor vs. Partner, [Observed - Expected], per mille	Significance of asymmetry to Anchor*/Partner, -, -Log10[P-value]			Distribution Location/Orientations vs. Fraction of peaks	Full overlap	Partial overlap	Overlap	Spacer	Any
		Full overlap	Partial overlap	Overlap	Spacer	Any		Full overlap	Overlap	Any						
Anchor		0	100.49	89.1	36.94	49.96	n/a	n/a	n/a	n/a						
Partner 1		300	68.91	300	0	300	1.26	0	0	-23.11						

The summary for the significances of various structural types of predicted CEs

