

Position weight matrices (profiles) for Fnr (a), ArcA (b) and NarP (c) binding sites

Each column shows the weights of the given nucleotide in the consecutive positions of the respective binding signal.

(a)

Fnr			
A	C	G	T
-0.09	-0.09	-0.32	0.49
-0.29	0.05	-0.29	0.52
-0.26	-0.26	0.55	-0.03
0.40	-0.15	-0.37	0.12
-0.39	0.07	-0.06	0.38
-0.08	-0.01	0.02	0.07
0.07	-0.26	0.00	0.19
0.19	0.00	-0.26	0.07
0.07	0.02	-0.01	-0.08
0.38	-0.06	0.07	-0.39
0.12	-0.37	-0.15	0.40
-0.03	0.55	-0.26	-0.26
0.52	-0.29	0.05	-0.29
0.49	-0.32	-0.09	-0.09

(b)

ArcA			
A	C	G	T
-0.17	-0.17	-0.17	0.50
0.41	-0.22	-0.22	0.03
0.41	-0.22	-0.22	0.03
-0.17	0.50	-0.17	-0.17
0.50	-0.17	-0.17	-0.17
0.15	-0.31	-0.05	0.21
0.13	-0.25	-0.25	0.36
-0.04	-0.30	0.08	0.26
0.26	-0.04	-0.30	0.08
0.15	-0.31	0.21	-0.05
-0.17	-0.17	-0.17	0.50
0.03	-0.22	-0.22	0.41
0.41	0.03	-0.22	-0.22
0.50	-0.17	-0.17	-0.17
-0.17	0.50	-0.17	-0.17

(c)

NarP			
A	C	G	T
-0.25	0.06	-0.25	0.44
0.38	-0.08	-0.31	0.00
0.17	0.33	-0.17	-0.33
-0.16	0.36	-0.32	0.13
0.07	0.10	-0.40	0.23
0.07	0.30	-0.37	0.00
-0.07	0.02	-0.23	0.29
0.22	-0.18	-0.34	0.30
0.30	-0.34	-0.18	0.22
0.29	-0.23	0.02	-0.07
0.00	-0.37	0.30	0.07
0.23	-0.40	0.10	0.07
0.13	-0.32	0.36	-0.16
-0.33	-0.17	0.33	0.17
0.00	-0.31	-0.08	0.38
0.44	-0.25	0.06	-0.25