

Additional file 5: Hidden Markov model of the RWD Binding Domain (RWDBD) region

HMMER3/f [3.1b2 | February 2015]

NAME Multiple_alignment
LENG 379
ALPH amino
RF no
MM no
CONS yes
CS no
MAP yes
DATE Tue Mar 7 03:12:44 2017
NSEQ 52
EFFN 1.431396
CKSUM 2957843090
STATS LOCAL MSV -11.1835 0.69959
STATS LOCAL VITERBI -12.0138 0.69959
STATS LOCAL FORWARD -5.1609 0.69959
HMM

Table with columns for amino acid positions (A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y) and rows for sequence positions (COMPO). The table shows log-odds scores for each amino acid at each position. The first column is labeled 'COMPO' and contains numbers 1 through 18, representing sequence positions. The subsequent columns represent amino acids: A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W, Y. Each cell contains a numerical value representing the log-odds score for that amino acid at that position. For example, at position 1, the score for 'g' is -1.0, and for 'i' it is -1.0. The scores generally fluctuate between -2 and 2.

	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518	4.58477	3.61503	
374	0.02842	4.40100	4.15064	0.61958	0.77255	0.48576	0.95510														
	2.68758	3.06514	4.49881	3.89855	2.80482	3.83734	4.12221	2.36144	3.71429	2.18023	3.04386	3.94343	4.19956	3.86613	3.77094	3.14341	2.91940	2.10608	2.78722	2.14087	399 v - - -
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518	4.58477	3.61503	
	0.01857	4.39115	5.11350	0.61958	0.77255	0.50083	0.93148														
375	2.67740	3.46757	4.45202	3.85041	2.41099	3.82949	4.15508	2.09632	3.67684	1.97179	2.32326	3.92718	4.19212	3.84237	3.75272	2.69018	2.75203	2.25586	4.70516	3.52582	400 l - - -
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518	4.58477	3.61503	
	0.01857	4.39115	5.11350	0.61958	0.77255	0.50083	0.93148														
376	2.00810	5.12869	2.85360	2.14999	4.44511	3.45238	3.65993	3.91080	2.18182	3.42219	4.18239	2.69567	3.85774	2.53686	2.89886	2.37306	2.64806	3.50494	5.58075	4.18701	401 a - - -
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518	4.58477	3.61503	
	0.01857	4.39115	5.11350	0.61958	0.77255	0.50083	0.93148														
377	2.65843	4.45888	3.42159	2.85727	3.36506	2.42004	3.84957	2.41947	2.69084	2.51571	3.55940	3.07279	3.98830	3.13685	3.04316	2.59355	2.49225	2.59358	5.03139	3.78209	402 i - - -
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518	4.58477	3.61503	
	0.19460	4.39115	1.80517	0.61958	0.77255	0.50083	0.93148														
378	2.53221	4.27927	3.71778	3.34133	3.36618	3.75993	4.10052	2.33022	3.25000	1.35986	3.31412	3.65379	3.73254	3.52960	3.51848	3.05153	2.96025	2.25745	4.93819	3.73632	403 l - - -
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518	4.58477	3.61503	
	0.02211	4.21866	4.94101	0.61958	0.77255	0.48686	0.95335														
379	2.59261	5.20324	2.05933	1.91102	4.52690	3.42336	3.66622	3.85010	2.36584	3.50009	4.25665	2.89325	3.04869	2.66269	2.94103	2.38138	2.95496	3.58368	5.64636	4.23299	404 e - - -
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518	4.58477	3.61503	
	0.01329	4.32774	*	0.61958	0.77255	0.00000	*														

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