Supplementary Tables 6-9

1fxlABU1U2			1pvoAGU1C2			
Chain. R. Num	R. Type	Ps. Type	Chain R. Num	R. Type	Ps. Type	Type
A.128	Tyr	DAC	A.80	Tyr	DAC	s
A.128	Tyr	PII	A.80	Tyr	PII	s
A.155	Arg	ALI	A.58	Leu	ALI	s
A.170	Phe	PII	A.64	Phe	PII	s
A.172	Arg	DON	A.75	Gly	DON	
A.201	Lys	ALI	A.112	Ala	ALI	s
A.203	Ala	ACC	A.110	Tyr	ACC	b

Table S6: Similar Phe-Tyr binding platform. Alignment between HuD RBD (1fxl) and Rho terminating factor (1pvo) according to the similarity of dinucleotide binding sites revealed by the AND-set cluster 23. Each rows details the matched pseudocenters of two binding sites. Each three columns present the details of a specific site: (i) chain identifier and residue number; (ii) residue type; (iii) pseudocenter type, which can be donor (DON), acceptor (ACC), mixed donor/acceptor (DAC), hydrophobic aliphatic (ALI) or aromatic (PI). The last column presents the origin of the feature: backbone(b) or side-chain(s) if it is the same for all the matched pseudocenters.

1m5oCBC40A41			1sj3PRC53A54			1urnAPC10A11			1a9nBQC11A12			2a8vADC1C2			2a8vBEC1C2			
Chain. R. Num	R. Type	Ps. Type	Chain R. Num	R. Type	Ps. Type	Chain R. Num	R. Type	Ps. Type	Chain R. Num	R. Type	Ps. Type	Chain R. Num	R. Type	Ps. Type	Chain R. Num	R. Type	Ps. Type	Type
C.13	Tyr	PI	P.13	Tyr	PI	A.13	Tyr	PI	B.13	Tyr	PI	A.80	Tyr	PI	B.80	Tyr	PII	s
C.56	Phe	PI	P.56	Phe	PI	A.56	Phe	PI	B.56	Phe	PI	A.64	Phe	PI	B.64	Phe	PI	s
C.88	Lys	DON	P.88	Lys	DON	A.88	Lys	DON	B.88	Lys	DON	A.110	Tyr	DON	B.110	Tyr	DON	b
C.89	Thr	DAC	P.89	Thr	DAC	A.89	Thr	DAC	B.89	Thr	DAC	A.110	Tyr	DAC	B.110	Tyr	DAC	s
C.91	Ser	DAC	P.91	Ser	DAC	A.91	Ser	DAC	B.91	Ser	DAC	A.78	Asp	ACC	B.78	Asp	ACC	s

Table S7: Phe-Tyr binding platform of RBDs. The common physico-chemical properties revealed by the alignment of 6 dinucleotide binding sites of RRMs and Rho termination factors of the AND-set cluster 94 (see Supplementary Table S4). The columns headers are as in Table S6.

1m8xACU2G3U4			1m8xACU4A5U6			1m8xACU6A7U8			
Chain. R. Num	R. Type	Ps. Type	Chain R. Num	R. Type	Ps. Type	Chain R. Num	R. Type	Ps. Type	Type
A.1043	Asn	ACC	A.971	Asn	ACC	A.899	Asn	ACC	s
A.1044	Tyr	PI	A.972	His	PI	A.900	Tyr	PI	s
A.1047	Gln	ACC	A.975	Gln	ACC	A.903	Gln	ACC	s
A.1047	Gln	DON	A.975	Gln	DON	A.903	Gln	DON	s
A.1076	Lys	ACC	A.1004	Pro	ACC	A.932	Met	ACC	b
A.1080	Asn	DON	A.1008	Arg	DON	A.936	Arg	DON	s
A.1083	Glu	ACC	A.1011	Gln	ACC	A.939	Gln	ACC	s
A.1119	Gln	ACC	A.1040	Gln	ACC	A.968	Gln	ACC	b
A.1120	Tyr	DAC	A.1041	Tyr	DAC	A.968	Gln	ACC	s
A.1122	Asn	ACC	A.1043	Asn	ACC	A.971	Asn	ACC	s
A.1123	Tyr	DAC	A.1044	Tyr	DAC	A.972	His	DAC	s
A.1123	Tyr	PI	A.1044	Tyr	PI	A.972	His	PI	s
A.1126	Gln	ACC	A.1047	Gln	ACC	A.975	Gln	ACC	s
A.1126	Gln	DON	A.1047	Gln	DON	A.975	Gln	DON	s

Table S8: Repetitive patterns of Pumilio protein. The MultiBind alignment of the 2 consecutive repetitive dinucleotide binding sites of the Pumilio protein (PDB:1m8x, AND-set clusters 81-82). These are located on the repeats 6-8, 4-5 and 2-4, which are described by the three main table columns respectively. The sub columns headers are as in Table S5.

2anrABU12C13A14C15			2py9AFC9C10C11U12			1ec6ADU12C13A14C15			
Chain. R. Num	R. Type	Ps. Type	Chain R. Num	R. Type	Ps. Type	Chain R. Num	R. Type	Ps. Type	Type
A.14	Ser	ACC	A.22	Gly	ACC	A.14	Glu	ACC	b
A.15	Tyr	ACC	A.23	Lys	ACC	A.15	Asn	ACC	b
A.18	Gly	PI	A.26	Gly	PI	A.18	Gly	PI	b
A.18	Gly	ACC	A.26	Gly	ACC	A.18	Gly	ACC	b
A.19	Ser	DON	A.27	Ser	DON	A.19	Ala	DON	b
A.21	Ile	ALI	A.29	Ile	ALI	A.21	Leu	ALI	s
A.22	Gly	PI	A.30	Gly	PI	A.22	Gly	PI	b
A.22	Gly	ACC	A.30	Gly	ACC	A.22	Gly	ACC	b
A.23	Lys	DON	A.31	Lys	DON	A.23	Lys	DON	b
A.23	Lys	ALI	A.31	Lys	ALI	A.23	Lys	ALI	s
A.24	Gly	DON	A.32	Lys	DON	A.24	Gly	DON	b
A.24	Gly	PI	A.32	Lys	PI	A.24	Gly	PI	b
A.24	Gly	ACC	A.32	Lys	ACC	A.24	Gly	ACC	b
A.25	Gly	DON	A.33	Gly	DON	A.25	Gly	DON	b
A.28	Ile	ALI	A.36	Val	ALI	A.28	Leu	ALI	s
A.29	Val	ALI	A.37	Lys	ALI	A.29	Val	ALI	s
A.32	Gln	DON	A.40	Arg	DON	A.32	Gln	DON	s
A.39	Ile	ACC	A.47	Ile	ACC	A.39	Ile	ACC	b
A.40	Lys	DON	A.48	Asn	DON	A.40	Gln	DON	s
A.41	Leu	DON	A.49	Ile	DON	A.41	Ile	DON	b
A.41	Leu	ACC	A.49	Ile	ACC	A.41	Ile	ACC	b
A.41	Leu	ALI	A.49	Ile	ALI	A.41	Ile	ALI	s
A.54	Arg	DON	A.57	Arg	DON	A.54	Arg	DON	s
A.54	Arg	DON	A.57	Arg	DON	A.54	Arg	DON	s

Table S9: KH-motif patterns The MultiBind alignment between 3 consecutive dinucleotide binding sites of proteins with KH-motifs: (1) Nova-1 (PDB: 2anrA); (2) Poly(rC)-binding protein 2 (PDB:2py9A); (3) Neuro-oncological ventral antigen 2, Nova-2 (PDB:1ec6A), which are described by the AND-set clusters 164, 41, 42. The columns headers are as in Table S5.