

Supplementary Material S4. Structural parameters of similarity between Z τ of human TOP2B (Q02880) and Z α /Z β of various proteins: human ADAR1 (P55265), human ZBP1 (Q9H171), PKZ from *Danio rerio* (Q5NE12), E3 from *Vaccinia virus* (P21605), and ORF112 from *Cyprinid herpesvirus 3* (A4FTK7), together with negative controls UFM1 (P61960) and H4 (P62805) from *Homo sapiens*. p-values lower than the 0.05 threshold are in bold.

Feature	Parameter	Units	Domain								
			Z α	Z β	Z α 1	Z α 2	Z α	Z α	Z α	n.c.	n.c.
Protein			ADAR1p150	ADAR1p150	ZBP1	ZBP1	PKZ	E3	ORF112	UFM1	H4
RMSD	structure	Å	2.4	2.7	2.6	3.2	2.5	2.6	2.9	3.4	2.8
p-value	structure	10 ⁻³	0.14	0.38	0.44	3.5	0.27	0.38	0.97	196	55
Equivalent positions	structure	no.	64	63	60	62	60	61	61	42	51
Gaps	sequence	%	30	32	34	33	34	32	34	36	7
Identity	sequence	%	7.7	7.6	3.3	5.4	2.2	4.4	6.5	9.1	7.3
Similarity	sequence	%	29	24	18	19	17	19	21	23	20