

	amino acid:	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
position in W-motif:	<b>consensus motif</b>																				
1st residue	<b>[PS]</b>	1	0	0	1	1	4	1	2	0	0	0	0	8	1	1	8	2	2	0	0
2d residue	<b>[SG]</b>	2	0	0	1	0	7	0	1	2	2	0	3	2	0	0	8	4	0	0	0
3d residue	<b>S</b>	0	0	0	2	0	1	1	0	1	3	1	3	2	1	0	14	3	0	0	0
4th residue	<b>T</b>	1	0	2	0	0	4	0	0	0	6	1	1	2	2	1	5	7	0	0	0
5th residue	<b>W</b>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	32	0
6th residue	<b>[GS]</b>	0	0	1	0	0	12	0	0	1	1	0	0	0	3	0	11	3	0	0	0

>dmGW182_W942	>hsTNRC6A_W1703	>nvGW182_W1167
DNENKDWSVAQPT	SDSKLTWSPGSVT	QSRLTQWKQPLLP
>dmGW182_W1024	>hsTNRC6A_W1747	>nvGW182_W1183
SLSSSTWSFNPNQ	KPPLSTWDNSPLR	TSHGETWGMPKIE
>dmGW182_W1037	>hsTNRC6A_W1758	>nvGW182_W1227
NYPSSWSDNSQQ	LRIGGGWGNSDAR	DPVSSRWGVDASL
>dmGW182_W1051	>hsTNRC6A_W1771	>nvGW182_W1309
TATSELWTSPLNK	YTPGSSWGESSSG	SIASSPWQNTPEPT
>dmGW182_W1092	>hsTNRC6A_W1872	>nvGW182_W1391
TGGANGWLQPRSG	LTPSPGWQSLGSS	SASGNSWSTQDGM
>dmGW182_W1107	>hsTNRC6A_W1919	>nvGW182_W1453
QTTNTNWTGGNTT	LHGTSLWGTPHYS	DEGISSWSTNQPI
>dmGW182_W1114	>hsTNRC6A_W1929	>nvGW182_W1574
TGGNTTWGSSWLL	HYSTSLWGPPSSS	FEQTPDWSNNPMP
	>hsTNRC6C_W1445	>nvGW182_W1589
	SDIKSTWSSGPTS	PSFGNPWSFGTVD
	>hsTNRC6C_W1487	>nvGW182_W1627
	PKPSSTWGASPLG	VPPGMQWGSSSQL
	>hsTNRC6C_W1494	>nvGW182_W1638
	GASPLGWTSSYSS	QLPAQLWGNSHPG
	>hsTNRC6C_W1504	>nvGW182_W1657
	YSSGSAWSTDTSG	SQVPSMWSFSGGA
	>hsTNRC6C_W1605	
	LPPTSSWQSSSAS	
	>hsTNRC6C_W1648	
	GSELLWGGVPQY	
	>hsTNRC6C_W1659	
	QYSSSLWGPPSAD	

**Figure S1. Consensus W-motif and the corresponding count matrix**, derived using MEME Suite (Bailey and Elkan, 1994) with a set of validated W-motifs from human TNRC6A (Q8NDV7-1) and TNRC6C (Q9HCJ0-1), *Drosophila* GW182 (Q8SY33-1) and *Nematostella* GW182 proteins. Sequences of validated W-motifs used as input in MEME motif prediction are provided below the count matrix. The numbers after W refer to the amino acid position of the corresponding W in the indicated TNRC6/GW182 proteins.