Table S4: MS quantification results for the proline-rich sequence hubs as defined in the results section (Table 2). The two experiments where the PRS was dysfunctional were used for comparison (pep. comp. and W8RY33A). N.d. relates to MS spectra where ^{12}C peptides were below noise levels while 13C peak intensities were at least >10 above noise levels. StDev was obtained by MS Quant.

protein	SwissProt ID	Mass [Da]	pulldown	band	#:peptides	#:C13	total score	% seq. coverage	quantified peptides	enrichment factor	StDev*
CA150	TCRG1_HUMAN	123882	pep comp.	14	51	51	2520	31	5	36	9
CA150	TCRG1_HUMAN	123882	W8RY33A	44	75	75	3556	42	5	46	14
NpwBP	WBP11_HUMAN	69954	pep comp.	22	40	40	2361	36	4	30	5
NpwBP	WBP11_HUMAN	69954	W8RY33A	39	45	45	2194	40	5	36	11
PSF	SFPQ_HUMAN	76102	pep comp.	21	67	67	2751	46	4	20	5
PSF	SFPQ_HUMAN	76102	W8RY33A	40	73	72	3026	50	4	13	4
SF1	SF01_HUMAN	68155	pep comp.	25	9	9	419	12	§	>10	
SF1	SF01_HUMAN	68155	W8RY33A	38	8	8	425	13	2	26	5
SF3a120	SF3A1_HUMAN	88831	pep comp.	19	48	48	2422	46	5	36	8
SF3a120	SF3A1_HUMAN	88831	W8RY33A	41	50	50	2480	45	n.d.	>10	
SF3a66	SF3A2_HUMAN	49224	pep comp.	31	18	18	704	28	n.d.	>10	
SF3a66	SF3A2_HUMAN	49224	W8RY33A	32	15	15	559	28	2	23	4
SF3b145	SF3B2_HUMAN	97596	pep comp.	16	56	56	3341	58	6	40	17
SF3b145	SF3B2_HUMAN	97596	W8RY33A	43	72	72	3673	62	4	33	7
SF3b49	SF3B4_HUMAN	44357	pep comp.	39	5	5	363	19	#	>10	
SF3b49	SF3B4_HUMAN	44357	W8RY33A	28	6	6	233	11	§	>10	
SmB'	RSMB_HUMAN	24594	pep comp.	47	1	1	59	3	#	>10	
U1-A	SNRPA_HUMAN	31128	W8RY33A	18	15	15	639	46	2	30	11
U1-C	RU1C_HUMAN	17381	pep comp.	47	4	4	170	18	§	>10	
U1-C	RU1C_HUMAN	17381	W8RY33A	15	4	4	202	18	§	>10	
ZNF207	ZN207_HUMAN	50717	pep comp.	33	7	7	504	13	§	>10	
ZNF207	ZN207_HUMAN	50717	W8RY33A	30	11	11	640	18	§	>10	