

**PPAR β / δ interfering peptide enhanced mesenchymal stromal
cell
immunoregulatory properties**

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Table S1: Sequences of the TF65 PepScan with the corresponding signal intensities (SI)

Spot Nb	Sequences	Signal intensities
1	MDELFPLIFPAEPAQ	4,353
2	LFPLIFPAEPAQASG	65,903
3	LIFPAEPAQASGPYV	3,555
4	PAEPAQASGPYVEII	2,851
5	PAQASGPYVEIIEQP	3,862
6	ASGPYVEIIEQPKQR	22,805
7	PYVEIIEQPKQRGMR	172,781
8	EIIEQPKQRGMRFRY	126,029
9	EQPKQRGMRFRYKCE	102,462
10	KQRGMRFRYKCEGRS	149,432
11	GMRFRYKCEGRSAGS	41,231
12	FRYKCEGRSAGSIPG	31,791
13	KCEGRSAGSIPGERS	3,087
14	GRSAGSIPGERSTDT	2,736
15	AGSIPGERSTDTTKT	1,707
16	IPGERSTDTTKTHPT	14,576
17	ERSTDTTKTHPTIKI	13,651
18	TDTTKTHPTIKINGY	6,289
19	TKTHPTIKINGYTGP	41,083
20	HPTIKINGYTGPGTV	27,921
21	IKINGYTGPGTVRIS	153,746
22	NGYTGPGTVRISLVT	8,574
23	TGPGTVRISLVTKDP	19,980
24	GTVRISLVTKDPPHR	132,841
25	RISLVTKDPPHRPHP	171,742
26	LVTKDPPHRPHPHEL	45,465
27	KDPPHRPHPHELVGK	4,974
28	PHRPHPHELVGKDCR	1,439
29	PHPHELVGKDCRDGF	1,667
30	HELVGKDCRDGFYEA	2,013
31	VGKDCRDGFYEAELC	1,368
32	DCRDGFYEAELCPDR	2,362
33	DGFYEAELCPDRCIH	2,913
34	YEAELCPDRCIHSFQ	2,781
35	ELCPDRCIHSFQNLG	3,358
36	PDRCIHSFQNLGIQC	8,220
37	CIHSFQNLGIQCVKK	97,412
38	SFQNLGIQCVKKRDL	125,671
39	NLGIQCVKKRDLEQA	44,329
40	IQCCKRDLEQAISQ	41,916
41	VKKRDLEQAISQRIQ	119,520
42	RDLEQAISQRIQTNN	9,120
43	EQAISQRIQTNNNPF	2,739
44	ISQRIQTNNNPFQVP	56,351
45	RIQTNNNPFQVPIEE	2,714

46	TNNNPFQVPIEEQRG	1,902
47	NPFQVPIEEQRGDYD	3,205
48	QVPIEEQRGDYDLNA	4,210
49	IEEQRGDYDLNAVRL	8,865
50	QRGDYDLNAVRLCFQ	6,172
51	DYDLNAVRLCFQVTV	2,620
52	LNAVRLCFQVTVRDP	5,232
53	VRLCFQVTVRDPGR	25,723
54	CFQVTVRDPGRPLR	22,699
55	VTVRDPGRPLRLPP	98,511
56	RDPGRPLRLPPVLS	13,034
57	SGRPLRLPPVLSHPI	6,777
58	PLRLPPVLSHPIFDN	21,146
59	LPPVLSHPIFDNRAP	13,636
60	VLSHPIFDNRAPNTA	6,045
61	HPIFDNRAPNTAELK	3,015
62	FDNRAPNTAELKICR	21,888
63	RAPNTAELKICRVNR	105,962
64	NTAELKICRVNRNSG	37,451
65	ELKICRVNRNSGSCL	22,405
66	ICRVNRNSGSCLGGD	18,298
67	VNRNSGSCLGGDEIF	3,582
68	NSGSCLGGDEIFLLC	3,439
69	SCLGGDEIFLLCDKV	5,623
70	GGDEIFLLCDKVQKE	6,379
71	EIFLLCDKVQKEDIE	19,211
72	LLCDKVQKEDIEVYF	6,455
73	DKVQKEDIEVYFTGP	3,630
74	QKEDIEVYFTGPGWE	3,139
75	DIEVYFTGPGWEARG	3,309
76	VYFTGPGWEARGSFS	13,971
77	TGPGWEARGSFSQAD	2,549
78	GWEARGSFSQADVHR	6,064
79	ARGSFSQADVHRQVA	64,035
80	SFSQADVHRQVAIVF	5,493
81	QADVHRQVAIVFRTP	3,797
82	VHRQVAIVFRTPPYA	7,981
83	QVAIVFRTPPYADPS	4,635
84	IVFRTPPYADPSLQA	42,450
85	RTPPYADPSLQAPVR	11,722
86	PYADPSLQAPVRVSM	4,754
87	DPSLQAPVRVSMQLR	31,549
88	LQAPVRVSMQLRRPS	40,550
89	PVRVSMQLRRPSDRE	43,443
90	VSMQLRRPSDRELSE	3,108
91	QLRRPSDRELSEPME	2,219
92	RPSDRELSEPMEFQY	2,367
93	DRELSEPMEFQYLPD	2,733

94	LSEPMEFQYLPDTDD	2,280
95	PMEFQYLPDTDDRHR	3,852
96	FQYLPDTDDRHRIEE	3,901
97	LPDTDDRHRIEEKRK	4,206
98	TDDRHRIEEKRKRTY	56,552
99	RHRIEEKRKRTYETF	32,050
100	IEEKRKRTYETFKSI	48,995
101	KRKRTYETFKSIMKK	148,090
102	RTYETFKSIMKKSFP	68,598
103	ETFKSIMKKSFPSPG	85,420
104	KSIMKKSFPSPGPTD	81,525
105	MKKSFPSPGPTDPRPP	3,032
106	SPSPGPTDPRPPRR	137,061
107	SGPTDPRPPRRRIAV	88,447
108	TDPRPPRRRIAVPSR	117,857
109	RPPRRRIAVPSRSSA	84,283
110	PRRIAVPSRSSASVP	64,694
111	IAVPSRSSASVPKPA	81,654
112	PSRSSASVPKPAPQP	54,794
113	SSASVPKPAPQYPF	4,471
114	SVPKPAPQYPFTSS	6,561
115	KPAPQYPFTSSLST	59,678
116	PQYPFTSSLSTINY	30,876
117	YPFTSSLSTINYDEF	29,641
118	TSSLSTINYDEFPTM	41,159
119	LSTINYDEFPTMVFP	44,899
120	INYDEFPTMVFPSPGQ	2,707
121	DEFPTMVFPSPGQISQ	2,781
122	PTMVFPSPGQISQASA	3,956
123	VFSPGQISQASALAP	10,428
124	SGQISQASALAPAPP	3,443
125	ISQASALAPAPPQVL	2,435
126	ASALAPAPPQVLPQA	2,011
127	LAPAPPQVLPQAPAP	1,445
128	APPQVLPQAPAPAPA	1,462
129	QVLPQAPAPAPAPAM	2,902
130	PQAPAPAPAPAMVSA	2,756
131	PAPAPAPAMVSALAQ	2,777
132	APAPAMVSALAQAPA	4,802
133	PAMVSALAQAPAPVP	12,659
134	VSALAQAPAPVPVLA	5,824
135	LAQAPAPVPVLAPGP	2,657
136	APAPVPVLAPGPPQA	2,539
137	PVPVLAPGPPQAVAP	2,182
138	VLAPGPPQAVAPPAP	2,866
139	PGPPQAVAPPAPKPT	3,016
140	PQAVAPPAPKPTQAG	2,671
141	VAPPAPKPTQAGEGT	1,559

142	PAPKPTQAGEGTLSE	916
143	KPTQAGEGTLSEALL	1,205
144	QAGEGTLSEALLQLQ	1,177
145	EGTLSEALLQLQFDD	676
146	LSEALLQLQFDDIDL	492
147	ALLQLQFDDIDLGAL	384
148	QLQFDDIDLGALLGN	965
149	FDDIDLGALLGNSTD	801
150	EDLGALLGNSTDPVAV	1,449
151	GALLGNSTDPVAVFTD	1,042
152	LGNSTDPVAVFTDLAS	614
153	STDPVAVFTDLASVDN	1,054
154	PAVFTDLASVDNSEF	1,019
155	FTDLASVDNSEFQQL	1,031
156	LASVDNSEFQQLLNQ	1,528
157	VDNSEFQQLLNQGI P	1,097
158	SEFQQLLNQGI PVAP	2,355
159	QQLLNQGI PVAPHTT	1,052
160	LNQGI PVAPHTTEPM	841
161	GIPVAPHTTEPMLME	696
162	VAPHTTEPMLMEYPE	317
163	HTTEPMLMEYPEAIT	589
164	EPMLMEYPEAITRLV	952
165	LMEYPEAITRLVTGA	16,075
166	YPEAITRLVTGAQRP	31,436
167	AITRLVTGAQRPPDP	1507
168	RLVTGAQRPPDPAPA	20,988
169	TGAQRPPDPAPAPLG	641
170	QRPPDPAPAPLGAPG	1,592
171	PDPAPAPLGAPGLPN	1,789
172	APAPLGAPGLPNGLL	2,138
173	PLGAPGLPNGLLSGD	9,475
174	APGLPNGLLSGDEDF	1,127
175	LPNGLLSGDEDFSSI	908
176	GLLSGDEDFSSIADM	972
177	SGDEDFSSIADMDFS	1,095
178	EDFSSIADMDFSALL	1,079
179	SSIADMDFSALLSQI	3,301

Footnote S1: The signal intensities were measured using the macro “Protein Array Analyzer” from Image J. The measured values ranged between 174,660 and 1,368 and the threshold was set at 100,000 to determine the “binders” (highlighted in bold).

Table S2: Sequences of the length analysis of the peptide GTVRISLVTKDPPHRPHP (spot 24-25 of Table S1) with the corresponding signal intensities.

Spot	Sequences	Signal intensities
1	GTVRISLVTKDPPHRPHP	163,329
2	GTVRISLVTKDPPHRPHP	155,341
3	TVRISLVTKDPPHRPHP	176,564
4	GTVRISLVTKDPPHRPH	97,625
5	VRISLVTKDPPHRPHP	154,344
6	GTVRISLVTKDPPHRP	12,406
7	RISLVTKDPPHRPHP	80,358
8	GTVRISLVTKDPPHR	204,526
9	ISLVTKDPPHRPHP	13,386
10	GTVRISLVTKDPPH	7,567
11	SLVTKDPPHRPHP	6,839
12	GTVRISLVTKDPP	43,939
13	LVTKDPPHRPHP	6,025
14	GTVRISLVTKDP	205,800
15	VTKDPPHRPHP	6,681
16	GTVRISLVTKD	194,346
17	TKDPPHRPHP	11,797
18	GTVRISLVTK	207,007
19	KDPPHRPHP	4,225
20	GTVRISLVT	116,165
21	DPPHRPHP	5,033
22	GTVRISLV	86,789
23	PPHRPHP	33,601
24	GTVRISL	192,825
25	PHRPHP	43,456
26	GTVRIS	182,383

Footnote S2: The signal intensities were measured using the macro "Protein Array Analyzer" from Image J. The measured values ranged between 204,526 and 4,225 and the threshold was set at 100,000 to determine the "binders" (highlighted in bold).

Table S3: Sequences of the substitutional analysis of the peptide RISLVTKDPPHR (spot 8 of Table S2) with the corresponding signal intensities.

	wt	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
R	235,694	238,793	127,596	81,357	143,476	252,566	218,304	210,702	245,336	216,342	194,232	128,334	171,537	157,859	126,219	154,406	122,333	158,344	90,064	110,324	184,267
I	242,524	46,685	27,896	17,046	26,174	242,951	25,275	23,550	204,314	43,385	17,748	16,044	19,731	15,360	10,936	13,842	10,478	16,444	15,559	68,526	129,418
S	235,716	123,843	123,227	71,100	89,021	209,297	111,795	187,921	78,403	220,393	142,432	70,405	93,854	78,483	72,114	105,376	102,245	86,615	38,457	172,503	150,337
L	243,425	28,959	44,334	11,339	26,688	260,094	20,286	31,299	179,375	110,969	226,036	9,736	17,562	8,541	12,514	209,074	15,296	13,114	15,206	60,065	135,667
V	244,267	134,552	172,798	10,142	13,000	259,269	125,566	179,689	248,441	254,221	250,285	36,639	63,527	16,086	53,417	258,955	139,077	82,823	78,421	96,252	181,625
T	254,778	205,268	191,761	11,308	10,639	258,321	91,170	106,881	182,493	223,221	260,069	72,480	72,196	91,405	109,130	258,088	200,616	135,333	159,581	163,355	244,860
K	240,018	38,075	22,201	9,066	10,797	157,916	22,005	33,255	49,542	82,786	60,762	10,835	17,957	9,634	12,576	220,024	33,964	19,729	33,258	62,804	81,459
D	257,412	256,119	248,841	190,846	194,358	259,774	256,060	242,065	245,766	253,495	239,364	159,748	183,109	226,288	233,417	259,525	254,240	245,975	248,769	207,670	254,179
P	234,015	228,093	121,136	38,385	29,194	252,090	131,070	123,348	101,715	199,670	135,333	47,964	179,302	80,982	129,163	233,743	108,972	75,663	84,584	158,776	210,525
P	219,612	242,816	205,163	36,369	33,192	243,331	185,362	144,490	152,488	182,055	147,196	63,585	163,300	91,793	87,004	227,875	138,821	122,769	84,888	124,651	180,037
H	223,624	208,702	105,009	23,814	23,697	199,377	143,658	136,995	111,858	192,353	133,839	61,440	110,257	63,207	56,630	186,130	105,542	98,069	91,735	123,222	149,297
R	226,039	19,320	7,395	4,734	4,433	39,435	9,010	6,676	8,293	56,485	11,461	6,409	7,060	6,272	7,271	101,766	12,050	11,200	8,708	11,783	33,087

Footnote S3: The signal intensities were measured using the macro "Protein Array Analyzer" from Image J. The measured values ranged between 260,094 and 4,433, and the threshold was set at 80,000 to determine the "binders" (highlighted in bold). In yellow are highlighted the key amino acid positions of the peptide RISLVTKDPPHR tolerating only several replacements (not more than 5).