

S6 Table: Binding of D1-B2 to peptide library PepLib2

Peptide nr	Amino acid sequence	RFU	Stdev
1	MKWVTFSLLLFFSAYSRG	15	2
2	LLFSSAYSRGVFRDTHKSE	483	306
3	VFRDTHKSEIAHRFKDLGE	11	16
4	IAHFKDLGEEHFKGVLIA	40	25
5	EHFKGVLIAFSQYLQQCPF	71	13
6	FSQYLQQCPFDEHVKLVNEL	83	23
7	DEHVKLVNELTEFAKTCVAD	38	26
8	TEFAKTCVADESHAGCEKSL	38	39
9	ESHAGCEKSLHTLFGDELCK	82	11
10	HTLFGDELCKVASLRETYGD	100	11
11	VASLRETYGDMADCCEKQEP	13	8
12	MADCCEKQEPPERNECFLSHK	88	11
13	ERNECFLSHKDDSPDLPKLK	253	45
14	1DDSPDPLKLPDPNLCDEF	1288	248
15	PDPNTLCDEFKADEKKFWGK	122	38
16	KADEKKFWGKYLYEIARRHP	223	25
17	YLYEIARRHPFYAPELYYY	17	12
18	YFYAPELYYANKYNGVFQE	22	22
19	ANKYNGVFQECCQAEDKGAC	86	32
20	CCQAEDKGACLLPKIETMRE	48	8
21	LLPKIETMREKVLOSSARQR	22	46
22	KVLOSSARQRLRCASIQKFG	12411	982
23	LRCASIQKFGERALKAWSVA	1478	104
24	ERALKAWSVARLSQKFPKAE	546	32
25	RLSQKFPKAEFVEVTKLVD	26	16
26	FVEVTKLVTDLTKVHKECH	30	32
27	LTKVHKECHGDLLEADDR	136	24
28	GDLLECADDRADLAKYICDN	494	9
29	ADLAKYICDNQDTISSKLKE	67	16
30	QDTISSKLKECCDKPLLEKS	80	27
31	CSDKPLLEKSHCIAEVEKDA	4	4
32	HCIAEVEKDAIPENLPPPLTA	47	21
33	IPENLPPPLTADFAEDKDVCK	4	16
34	DFAEDKDVCKNYQEAQDAFL	17	24
35	NYQEAQDAFLGSFLYEYSRR	7	8
36	GSFLYEYSRRHPEYAVSVLL	121	81
37	HPEYAVSVLLRAKEYEATL	-4	3
38	RLAKEYEATLEECCAKDDPH	89	15
39	EECCAKDDPHACYSTVFDKL	65	14
40	ACYSTVFDKLKHLVDEPQNL	0	27
41	KHLVDEPQNLIKQNCDQFEK	63	5
42	IKQNCDQFEKLGEYGFQNAL	47	4
43	LGEYGFQNALIVRYTRKVPQ	414	25
44	IVRYTRKVPQVSTPTLVEVS	116	41
45	VSTPTLVEVSRSLGKGTRC	986	204
46	RSLGKGTRCCTKPESERMP	766	214
47	CTKPESERMPCTEDYLSLIL	36	26
48	CTEDYLSLILNRLCVLHEKT	14	4

49	NRLCVLHEKTPVSEKVTKCC	37	27
50	PVSEKVTKCCTESLVNRRPC	8074	615
51	TESLVNRRPCFSALTPDETY	41	9
52	FSALTPDETYVPKAFDEKL	-5	15
53	VPKAFDEKLFTFHADICTLP	2	11
54	TFHADICTLPDTEKQIKKQT	44	17
55	DTEKQIKKQTALVELLKHKP	27	7
56	ALVELLKHKPKATEEQLKTV	77	44
57	KATEEQLKTVMENFVAFVDK	19	19
58	MENFVAFVDKCCAADDKEAC	218	90
59	CCAADDKEACFAVEGPKLVV	104	36
60	FAVEGPKLVVSTQTALA	15	3
61	unmodified BSA (negative control)	28	
62	CML-BSA, reductive amination (positive control)	45350	
63	CML-IgG reductive amination, (positive control)	18897	
64	Peptide 1-6 (positive controls)	330	