

S2 Table: BSA peptide library PepLib2

Peptide nr	20mer aa stretch	Amino acid sequence
1	1-20	MKWVTFISLLLLFSSAYSRG
2	11-30	LLFSSAYSRGVFRRDTHKSE
3	21-40	VFRRDTHKSEIAHRFKDLGE
4	31-50	IAHRFKDLGEEHFKGLVLI
5	41-60	EHFKGLVLIAFSQYLQQCPF
6	51-70	FSQYLQQCPFDEHVKLVNEL
7	61-80	DEHVKLVNELTEFAKTCVAD
8	71-90	TEFAKTCVADESHAGCEKSL
9	81-100	ESHAGCEKSLHTLFGDELCK
10	91-110	HTLFGDELCKVASLRETYGD
11	101-120	VASLRETYGDMADCCEKQEP
12	111-130	MADCCEKQEPERNECFLSHK
13	121-140	ERNECFLSHKDDSPDLPKPK
14	131-150	DDSPDLPKPKPDPNTLCDEF
15	141-160	PDPNTLCDEFKADEKKFWGK
16	151-170	KADEKKFWGKYLEIARRHP
17	161-180	YLEIARRHPYFYAPPELLYY
18	171-190	YFYAPPELLYYANKYNGVFQE
19	181-200	ANKYNGVFQECCQAEDKGAC
20	191-210	CCQAEDKGACLLPKIETMRE
21	201-220	LLPKIETMREKVLASSARQR
22	211-230	KVLASSARQLRCASIQKFG
23	221-240	LRCASIQKFGERALKAWSVA
24	231-250	ERALKAWSVARLSQKFPKAE
25	241-260	RLSQKFPKAEFVEVTKLVTD
26	251-270	FVEVTKLVTDLTKVHKECCH
27	261-280	LTKVHKECCHGDLLCADDR
28	271-290	GDLLCADDRADLAKYICDN
29	281-300	ADLAKYICDNQDTISSKLKE
30	291-310	QDTISSKLKECCDKPILLEKS
31	301-320	CCDKPILLEKSHCIAEVEKDA
32	311-330	HCIAEVEKDAIPENLPPLTA
33	321-340	IPENLPPLTADFAEDKDVCK
34	331-350	DFAEDKDVCKNYQEAKDAFL
35	341-360	NYQEAKDAFLGSFLYEYSRR
36	351-370	GSFLYEYSRRHPEYAVSVLL
37	361-380	HPEYAVSVLLRLAKEYEATL
38	371-390	RLAKEYEATLEECCAADDPH
39	381-400	EECCAADDPHACYSTVFDKL
40	391-410	ACYSTVFDKHLVDEPQNL
41	401-420	KHLVDEPQNLKQNCQDFEK
42	411-430	IKQNCQDFEKLGEYGFQNAL
43	421-440	LGEYGFQNALIVRYTRKVPQ
44	431-450	IVRYTRKVPQVSTPTLVEVS
45	441-460	VSTPTLVEVSRSLGKVGTRC
46	451-470	RSLGKVGTRCCTKPESERMP
47	461-480	CTKPESERMPCTEDYLSLIL
48	471-490	CTEDYLSLILNRLCVLHEKT

49	481-500	NRLCVLHEKTPVSEKVTKCC
50	491-510	PVSEKVTCCCTESLVNRRPC
51	501-520	TESLVNRRPCFSALTPDETY
52	511-530	FSALTPDETYVPKAFDEKLF
53	521-540	VPKAFDEKLFFHADICTLP
54	531-550	TFHADICTLPDTEKQIKKQT
55	541-560	DTEKQIKKQTALVELLKHKP
56	551-570	ALVELLKHKPKATEEQLKTV
57	561-580	KATEEQLKTMENFVAFVDK
58	571-590	MENFVAFVDKCCAADDKEAC
59	581-600	CCAADDKEACFAVEGPKLVV
60	591-607	FAVEGPKLVVSTQTALA
61		unmodified BSA (negative control)
62		CML-BSA, reductive amination (positive control)
63		CML-IgG, reductive amination (positive control)
64		Peptide 1-6 (positive controls)