Supplementary table A: Datasheets of *in silico* bindingscores of HSP70 epitopes

	Amino acid nr	**Amino acid sequence**	**Binding score**	**DR type**	**Author**
Region 38-52					
Literature	38-52	TPSYVAFTDTERLIG	N.A.	DR7	(Chicz et al. 1993)
	38-54	TPSYVAFTDTERLIGDA	N.A.	DR7	(Chicz et al. 1993)
Syfpeithi	44	FTDTERLIG	24	DR1	
	39	PSYVAFTDT	20	DR4	
	39	PSYVAFTDT	32	DR7	
	41	YVAFTDTER	27	DR11	
Rankpep	40	SYVAFTDTE	12.526	DR7	
Propred (DR4)	38	TPSYVAFTD	0.941	DR4	
	41	YVAFTDTER	0.861	DR4	
Sette Algorithm	42	VAFTDTERL	0	—	
	50	LIGDAAKNQ	0	—	
Chosen	38-52	TPSYVAFTDTERLIG			
Region 168-186					
Literature	168-184	NVLRIINEPTAAAIAYG	N.A.	DR4/DR53	(Dengjel et al. 2005)
	168-182	NVLRIINEPTAAAIA	N.A.	HLA mix	(Halder et al. 1997)
	172-186	IINEPTAAAIAYGLD	N.A.	DQ6	(Sanjeevi et al. 2002)
	167-184	LNVLRIINEPTAAAIAYG	N.A.	DRB1*0401	(Muntasell et al. 2004)
Syfpeithi	167	LNVLRIINE	27	DR1	
	170	LRIINEPTA	25	DR1	
	161	AGTIAGLNV	24	DR1	
	166	GLNVLRIIN	26	DR4	
	169	VLRIINEPT	26	DR4	
	167	LNVLRIINE	20	DR4	
	167	LNVLRIINE	24	DR7	
	178	AAAIAYGLD	22	DR7	
	167	LNVLRIINE	18	DR11	
Rankpep	172	IINEPTAAA	17.818	DRB1*0101	
	177	TAAAIAYGL	10.83	DRB1*0101	
	172	IINEPTAAA	12.862	DRB4	
Propred (DR4)	169	VLRIINEPT	1.096	DR4	
Sette Algorithm	164	IAGLNVLRI	3	DR1/4/7	
	167	LNVLRIINE	0	—	
	172	IINEPTAAA	2	DR1/4	

	173	INEPTAAAI	2	DR1/4	
Chosen	161-175	AGTIAGLNVLRIINE			
	167-181	LNVLRIINEPTAAAI			
Region 238-252					
Literature	238-252	VNHFIAEFKRKHKKD	N.A.	DR11w52	(Newcomb et al. 1993)
Syfpeithi	239	NHFIAEFKR	26	DR4	
	235	NRMVNHFIA	20	DR4	
	232	DFDNRMVNH	18	DR4	
	232	DFDNRMVNH	21	DR11	
	238	VNHFIAEFK	20	DR11	
	242	IAEFKRKHK	18	DR11	
Rankpep	234	DNRMVNHFI	9.559	DR1	
	241	FIAEFKRKH	12.262	DR4	
	234	DNRMVNHFI	11.526	DR7	
Propred (DR4)	234	DNRMVNHFI	0.891	DR4	
Sette Algorithm	233	FDNRMVNHF	0	—	
	237	MVNHFIAEF	2	DR1/4	
	238	VNHFIAEFK	0	—	
Chosen	235-249	NRMVNHFIAEFKRKH			
Region 291-304					
Literature	291-304	IDFYTSITRARFEE	N.A.	DR11w52	(Newcomb et al. 1993)
Syfpeithi	291	IDFYTSITR	25	DR1	
	285	DSLYEGIDF	24	DR1	
	285	DSLYEGIDF	22	DR4	
	291	IDFYTSITR	22	DR4	
	294	YTSITRARF	20	DR4	
	287	LYEGIDFYT	18	DR4	
	290	GIDFYTSIT	254	DR7	
	291	IDFYTSITR	22	DR7	
	294	YTSITRARF	22	DR7	
	291	IDFYTSITR	28	DR11	
	285	DSLYEGIDF	22	DR11	
Rankpep	293	FYTSITRAR	9.474	DR1	
	293	FYTSITRAR	10.215	DRB1*0401	
Propred (DR4)	300	ARFEELNAD	0.950	DR4	
Sette Algorithm	291	IDFYTSITR	0	—	
	293	FYTSITRAR	2	DR4/7	

	302	FEELNADLF	0	—	
Chosen	290-304	GIDFYTSITRARFEE			
Region 445-460					
Literature	445-457	GERAMTKDNNLLG	N.A.	DR4	(Friede et al. 1996)
	445-460	GERAMTKDNNLLGKFE	N.A.	DR4/DR53	(Dengjel et al. 2005)
Syfpeithi	440	IQVYEGERA	22	DR4	
	439	LIQVYEGER	20	DR4	
	446	ERAMTKDNN	20	DR4	
	453	NNLLGKFEL	20	DR4	
	442	VYEGERAMT	18	DR4	
Rankpep	443	YEGERAMTK	9.358	DRB1*0101	
	449	MTKDNNLLG	13.235	DRB1*0401	
	448	AMTKDNNLL	21.283	DR7	
Propred (DR4)	445	GERAMTKDN	1.003	DR4	
	442	VYEGERAMTK	0.624	DR4	
Sette Algorithm	443	YEGERAMTK	1	DR4	
	456	LGKFELTGI	0	—	
Chosen	443-457	YEGERAMTKDNNLLG			
Region 482-498					
Literature	482-498	ANGILNVSAVDKSTGKE		DR4	(Lippolis et al. 2002)
	484-497	GILNVSAVDKSTGK		DR4	(Lippolis et al. 2002)
	484-498	GILNVSAVDKSTGKE		DR4/DR53	(Dengjel et al. 2005)
Syfpeithi	482	ANGILNVSA	20	DR4	
	486	LNVSAVDKS	18	DR4	
	479	DIDANGILN	18	DR4	
	485	ILNVSAVDK	26	DR11	
Rankpep	475	EVTFDIDAN	10.491	DR4	
	484	GILNVSAVD	8.332	DRB1*0401	
	482	ANGILNVSA	13.44	DRB1*0102	
Propred (DR4)	487	NVSAVDKST	0.634	DR4	
Sette Algorithm	480	IDANGILNV	1	DR1	
	485	ILNVSAVDK	0	—	
	486	LNVSAVDKS	0	—	
Chosen	482-496	ANGILNVSAVDKSTG			

Supplementary table A. Peptide sequence selection was based upon regions of HSP70 described in literature as eluted from HLA (Chicz et al. 1993; Dengjel et al. 2005; Friede et al. 1996; Halder et al. 1997; Lippolis et al. 2002; Newcomb et al. 1993; Sanjeevi et al. 2002; Suri et al. 2005; Verreck et al. 1996). See for an overview of the literature table 2. Peptides sequences were screened for their theoretical MHC-binding motifs in the databases: Syfpeithi (http://www.syfpeithi.de/home), Rankpep (http://bio.dfci.harvard.edu/RANKPEP/), HLA-DR4Pred (http://www.imtech.res.in/raghava/propred/index), and the pan-DR binding computer algorithm of Sette (Southwood et al. 1998). Seven human HSP70-peptides were selected: H38 (38-52), H161 (161-175), H167 (167-181), H235 (235-249), H290 (290-304), H443 (443-457), H482 (482-496).