Supplementary Table 1: Comparison of NetMHCIIpan-4.0 prediction to empirical data

No	Pos	Seq	Computational (100-%Rank		Empirical (%competition)		BA vs RIPPA		EL vs RIPPA		BA+EL vs RIPPA	ELISA vs RIPPA	IC50vHA306-318	Comments
No	Pos	Seq	100-%RankB	100-%RankEL	RIPPA (Flow)	sDR4 (ELISA	RIPPA false	BA false	RIPPA false	EL false	RIPPA false Prediction false	RIPPA false ELISA false	IC50	Comments
4	22	TQLPPAYTNSFTRGVYY	77.93	81.67	61.4352688	71.8123111		1		1	1			binder
5	29	TNSFTRGVYYPDKVFRS	96.34	93.44	68.2588881	80.2509847								binder
6	36	VYYPDKVFRSSVLHSTQ	97.94	91.04	71.8359318	91.8338371								binder
8	50	STQDLFLPFFSNVTWFH	96.65	75.36	0	26.4999542		1						non-binder
9	57	PFFSNVTWFHAIHVSGT	95.27	63.91	3.6033938	34.9821379		1						non-binder
10	64	WFHAIHVSGTNGTKRFD	94.55	93.9	74.4633008	70.3993771								binder
13	85	PFNDGVYFASTEKSNII	95.54	98.94	75.3388373	67.2666483								strong binder
15	99	NIIRGWIFGTTLDSKTQ	96.11	95.52	80.624436	76.1198131								strong binder
17	113	KTQSLLIVNNATNVVIK	99.16	91.99	0	0.6938719		1		1	1		tested	non-binder
21	141	LGVYYHKNNKSWMESEF	83.4	73.47	78.8901171	72.3619126		1		1	1		tested	binder
23	155	SEFRVYSSANNCTFEYV	97.08	74.95	7.93650794	26.7289548		1						non-binder
25	169	EYVSQPFLMDLEGKQGN	77.5	92.03	63.8703408	79.5685628		1						binder
29	197	IDGYFKIYSKHTPINLV	90.51	85	0	15.6773839		1						non-binder
30	204	YSKHTPINLVRDLPQGF	86.29	94.72	51.2287105	75.4648713		1						binder
34	232	GINITRFQTLLALHRSY	98.75	92.54	58.410649	67.4344186								binder
35	239	QTLLALHRSYLTPGDSS	84.13	53.11	63.6121879	56.5951259		1		1	1			binder
40	274	TFLLKYNENGTITDAVD	86.1	90.7	27.7886652	52.0289457								weak binder/non-binder
41	281	ENGTITDAVDCALDPLS	37.79	58.56	57.8167308	25.5335715	1		1		1	1		non-binder
44	302	TLKSFTVEKGIYQTSNF	95.98	97.15	87.7169907	89.1590247								strong binder
45	309	EKGIYQTSNFRVQPTES	83.09	86.9	61.2305843	76.1312632		1		1	1			binder
46	316	SNFRVQPTESIVRFPNI	99.03	95.98	61.452514	84.986718								strong binder
50	344	ATRFASVYAWNRKRISN	91.5	74.24	0	17.149858		1						non-binder
52	358	ISNCVADYSVLYNSASF	97.12	91.96	61.169175	91.439956								strong binder
53	365	YSVLYNSASFSTFKCYG	93.06	46.52	0	35.2294586		1						non-binder
57	393	TNVYADSFVIRGDEVRQ	73.89	90.55	74.3406826	86.5828524		1						strong binder
62	428	DFTGCVIAWNSNNLDSK	93.58	92.87	0	35.6279198		1		1	1		tested	non-binder
67	463	PFERDISTEIYQAGSTP	72.19	65.58	74.8431367	62.041232		1		1	1		tested	weak binder
68	470	TEIYQAGSTPCNGVEGF	68.56	81.88	85.4190191	79.270862		1		1	1			strong binder
70	484	EGFNCYFPLQSYGFQPT	72.79	58.57	58.2807658	72.9815759		1		1	1			binder
71	491	PLQSYGFQPTNGVGYQP	91.79	98.8	90.203137	94.7787854								strong binder
74	512	VLSFELLHAPATVCGPK	93.76	80.54	63.1536595	75.6358441				1			tested	strong binder
83	575	AVRDPQTLEILDITPCS	56.5	48.44	54.9343159	60.4882294		1		1	1			weak binder
84	582	LEILDITPCSFGGVSVI	54.62	9.87	60.6553144	46.8306311		1		1	1			weak binder
88	610	VLYQDVNCTEVPVAIHA	63.52	77.88	63.6406444	53.2838692		1		1	1			weak binder
90	624	IHADQLTPTWRVYSTGS	59.82	37.46	59.2785919	29.7426033	1		1		1	1		non-binder/weak binder
91	631	PTWRVYSTGSNVFQTRA	97.64	92.63	56.3157161	67.4758341								binder
93	645	TRAGCLIGAEHVNNSYE	65.31	86.93	87.0401274	59.4899093		1		1			tested	binder
94	652	GAEHVNNSYECDIPIGA	54.09	72.2	70.6229467	0	1		1		1		tested	non-binder
96	666	IGAGICASYQTQTNSPR	58.48	49.66	56.9619623	5.4781777	1		1		1			non-binder
99	687	VASQSIIAYTMSLGAEN	94.97	87.97	89.7061174	92.5010982				1			tested	strong binder
100	694	AYTMSLGAENSVAYSNN	91.72	75.54	60.3482817	54.46877				1				binder

101	701	AENSVAYSNNSIAIPTN	92.02	95.16	81.3993624	41.0062276									1			binder
103	715	PTNFTISVTTEILPVSM	93.71	87.72	76.6549648	71.1284529				1								binder
106	736	VDCTMYICGDSTECSNL	55.33	56.64	71.3851967	31.8483682	1		1		1			1				non-binder/weak binder
108	750	SNLLLQYGSFCTQLNRA	85.97	51.66	67.1329343	2.7158325	1		1		1			1				non-binder
109	757	GSFCTQLNRALTGIAVE	94.34	50.92	85.9082099	86.2037779				1							tested	strong binder
110	764	NRALTGIAVEQDKNTQE	57.65	92.11	41.6959337	17.4085406				1							tested	non-binder
115	799	GFNFSQILPDPSKPSKR	95.51	99.08	78.9364026	79.2216853												strong binder
122	848	DLICAQKFNGLTVLPPL	94.32	73.22	3.0559766	0		1										non-binder
128	890	AGAALQIPFAMQMAYRF	92.34	31.21	44.0454506	1.2480943		1										non-binder
129	897	PFAMQMAYRFNGIGVTQ	93.09	60.87	0	0		1										non-binder
132	918	ENQKLIANQFNSAIGKI	96.2	87.79	79.1782757	41.4274271				1			1		1		tested	weak binder
133	925	NQFNSAIGKIQDSLSST	79.18	86.87	80.2636166	20.5483346		1		1			1		1		tested	weak binder
134	932	GKIQDSLSSTASALGKL	90.72	90.4	91.6756734	94.340939												strong binder
138	960	NTLVKQLSSNFGAISSV	93.35	87.99	81.5863751	75.224166				1							tested	strong binder
139	967	SSNFGAISSVLNDILSR	97.63	88.04	71.9691514	28.2048632				1			1		1		tested	weak binder
144	1002	QSLQTYVTQQLIRAAEI	97.2	91.7	81.3095383	93.1135171												strong binder
145	1009	TQQLIRAAEIRASANLA	95.94	89.62	53.1983002	51.266312				1								weak binder
146	1016	AEIRASANLAATKMSEC	99.15	94.83	81.8672874	82.624874												strong binder
150	1044	GKGYHLMSFPQSAPHGV	91.29	84.77	49.3835201	24.3055376		1										non-binder
152	1058	HGVVFLHVTYVPAQEKN	94.08	93.25	62.0561464	31.5201943									1		tested	weak binder
154	1072	EKNFTTAPAICHDGKAH	92.68	90.41	41.3924826	10.4963953		1		1			1				tested	non-binder
157	1093	GVFVSNGTHWFVTQRNF	91.54	58.47	54.5194471	38.2568025												weak binder
158	1100	THWFVTQRNFYEPQIIT	97.8	94.92	64.9437324	93.4778676												binder
160	1114	IITTDNTFVSGNCDVVI	65.75	56.61	57.2028519	10.9020905	1		1		1			1				non-binder
165	1149	KEELDKYFKNHTSPDVD	80.45	95.49	31.951954	20.2640895				1							tested	non-binder
177	1233	MLCCMTSCCSCLKGCCS	37.39	5	61.8346859	16.3854363	1		1		1			1				non-binder
180	1254	CKFDEDDSEPVLKGVKL	35.84	75.5	69.1776149	60.7199152		1		1			1					weak binder
False identification side-by-side (counts)							8	29	8	27	8	17	6	5				45 binders
False identification side-by-side (%)							4.4198895	16.0221	4.4198895	14.917	4.41989	9.392265193	3.3149171	2.762431				
Potential false positives (counts			13	5	8	0												
Potential false negatives (counts			17	23	1	7												
Potential false positives (%)			7.1823204	2.762430939	4.4198895	0												
Potential false negatives (%)			9.3922652	12.70718232	0.55248619	3.86740331												
False identification (counts)			30	28	9	7												
False identification (FDR)			16.574586	15.46961326	4.97237569	3.86740331												

This number assumes ELISA identifies the rest 113 peptides as non-binder

18 agreements (red/pink fill), 50 disagreements between prediction and yeast dsplay. The rest 113 non-binders were not evaluated by capture ELISA.
In the capture ELISA, 1 uM Bio-HA306-318 and 40 uM of a competitor peptide were used
Means of at least three independent experiments are shown