

Fig. 1A

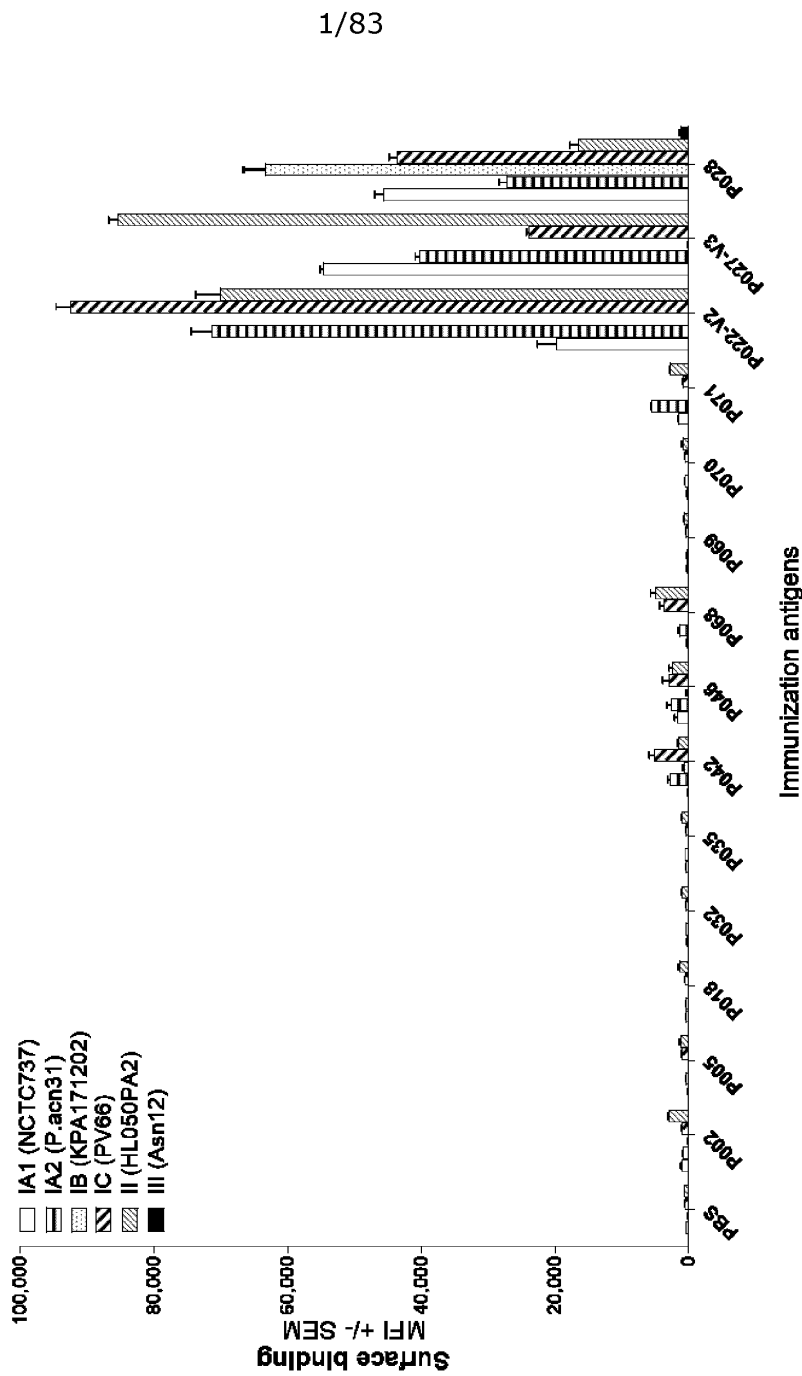


Fig. 1B

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	IA1 (NCTC737)	IA2 (P.acn31)	IB (KPA171202)	IC (pV66)	II (HL050PA2)	III (Asn12)
PBS	-	-	-	-	-	-
P002	-	-	-	-	-	-
P005	-	-	-	-	-	-
P018	-	-	-	-	-	-
P032	-	-	-	-	-	-
P035	-	-	-	-	-	-
P042	+	-	+/-	-	-	-
P046	-	-	-	+	-	-
P068	-	-	-	-	-	-
P069	-	-	-	-	-	-
P070	-	-	-	-	-	-
P071	-	-	-	-	-	-
P022-V2	+++	+++	-	+++	+++	-
P027-V3	+++	+++	-	+	++	-
P028	++	+	++	++	+	+/-

Fig. 1C

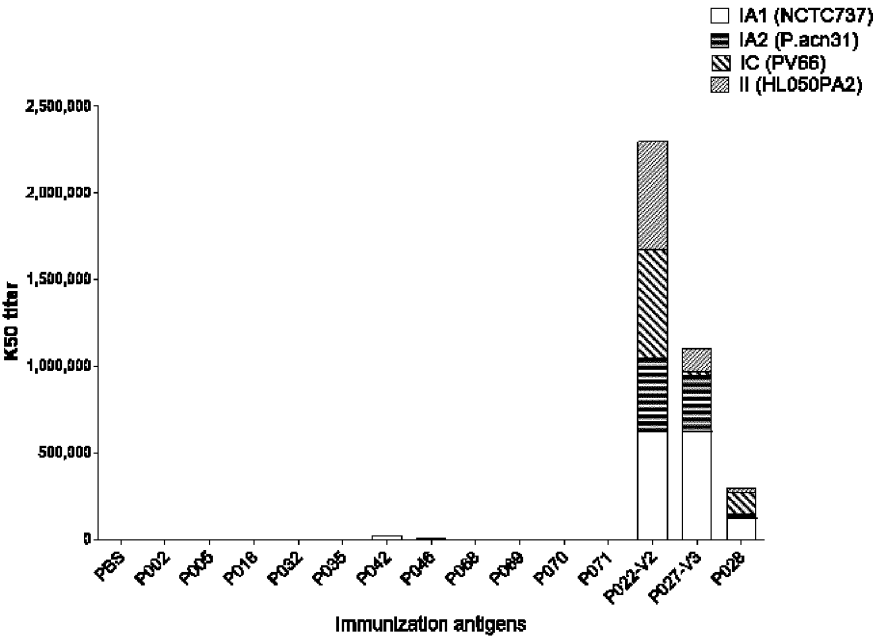
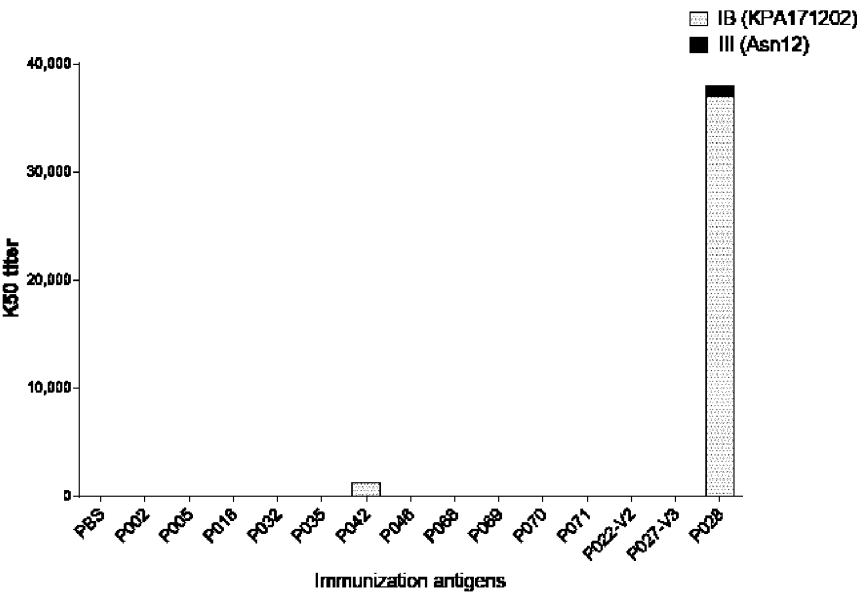


Fig. 1D



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Fig. 2

	EC50 titers	
	pre-immune	immune (final bleed)
PBS	<500	<500
P002	<250	919642
P005	<100	18750
P018	<500	45219
P032	<500	53999
P035	<500	75577
P042	<500	52277
P046	883	15280
P068	<100	5625
P069	<2500	248302
P070	<500	82930
P071	<500	213468
P022-V2	<250	348172
P027-V3	<250	220395
P028	<250	77251

Fig. 3

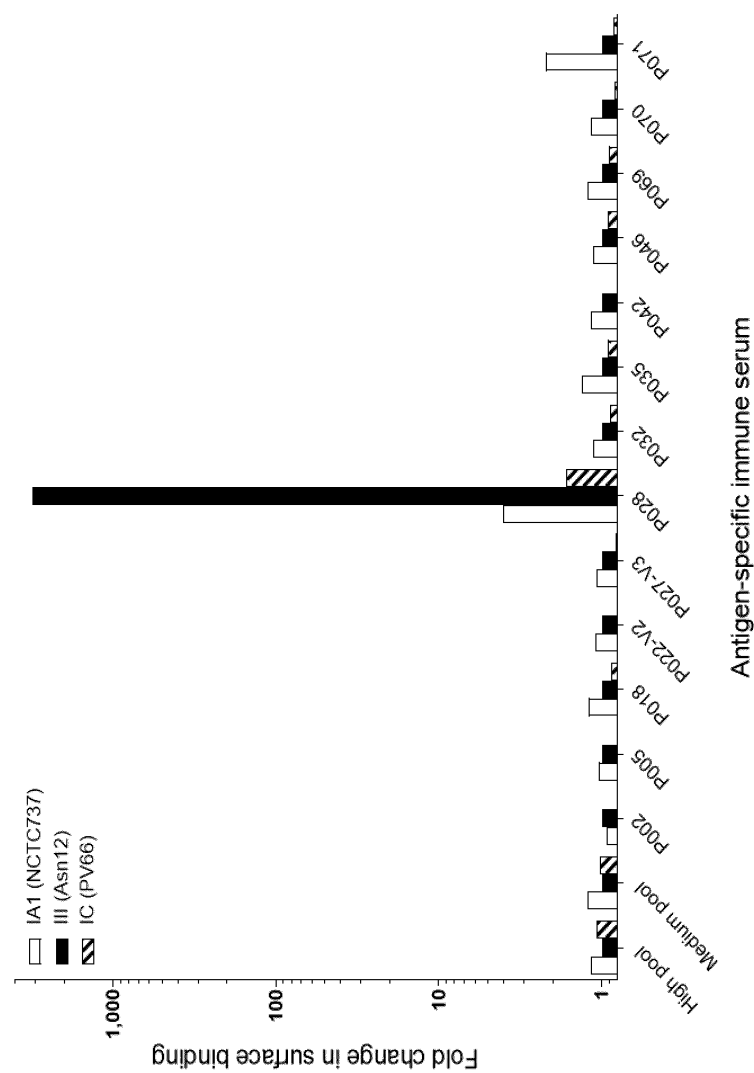


Fig. 4

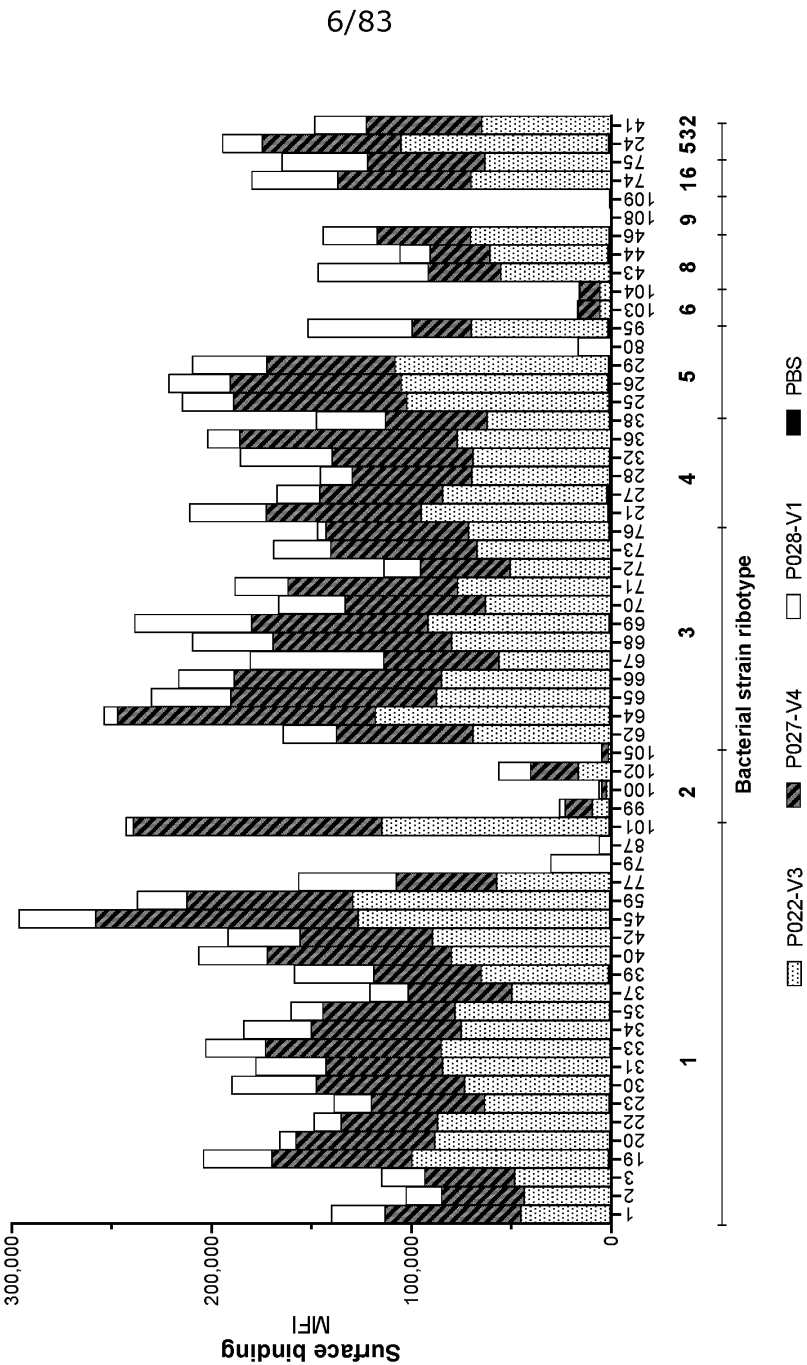


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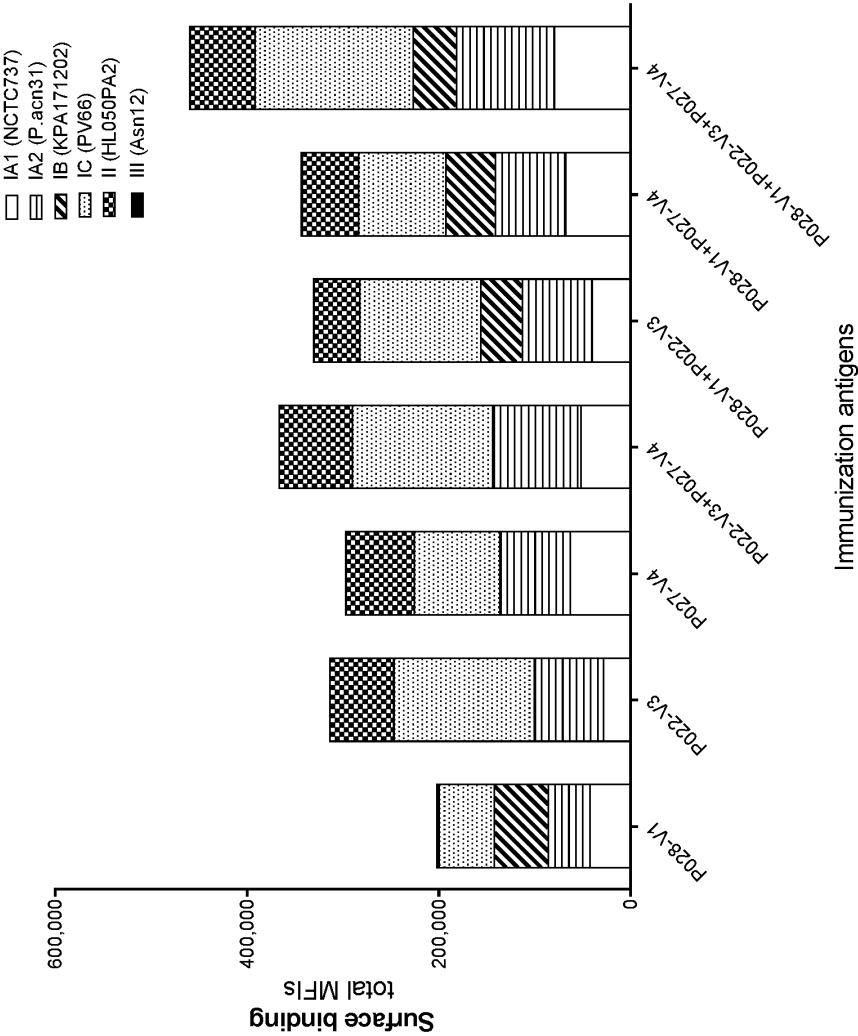
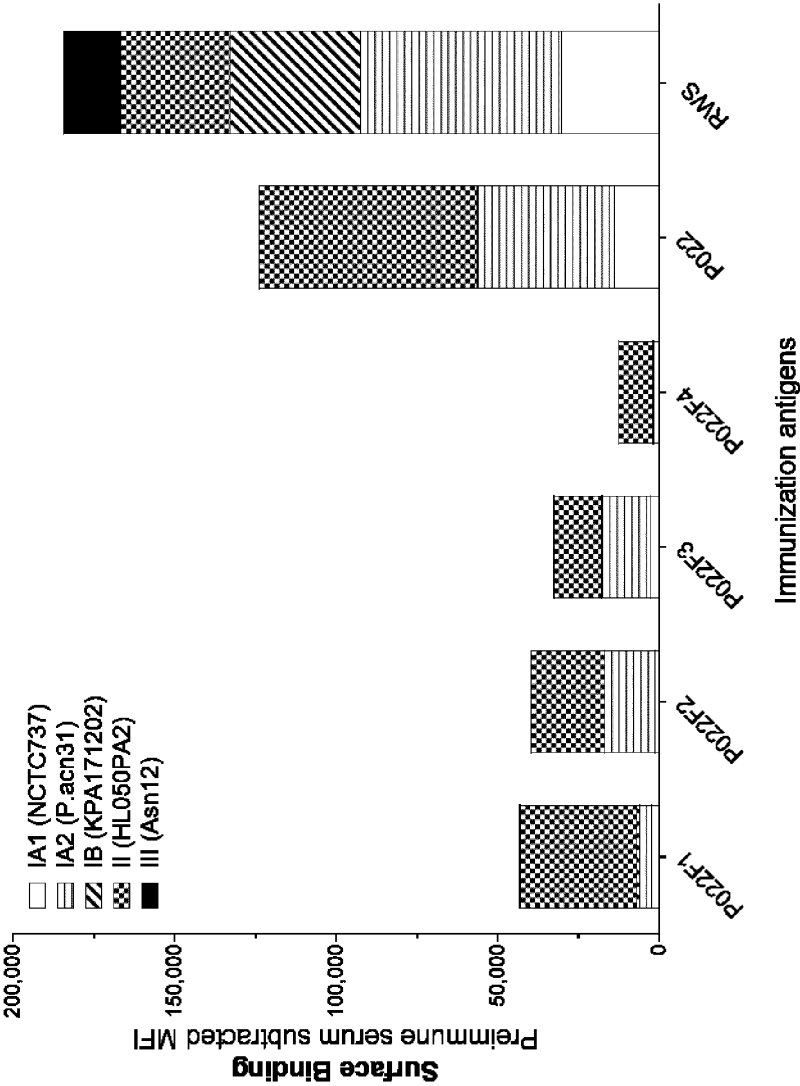


Fig. 6



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Fig. 7A

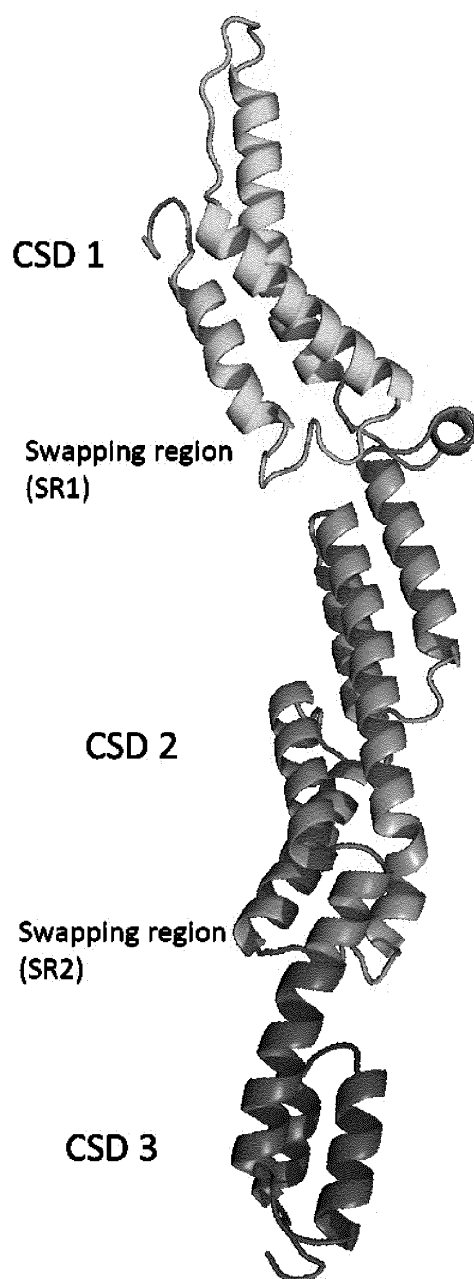


Fig. 7B

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CSD1-CDS2 junction. Swap region is shown (SR1) :

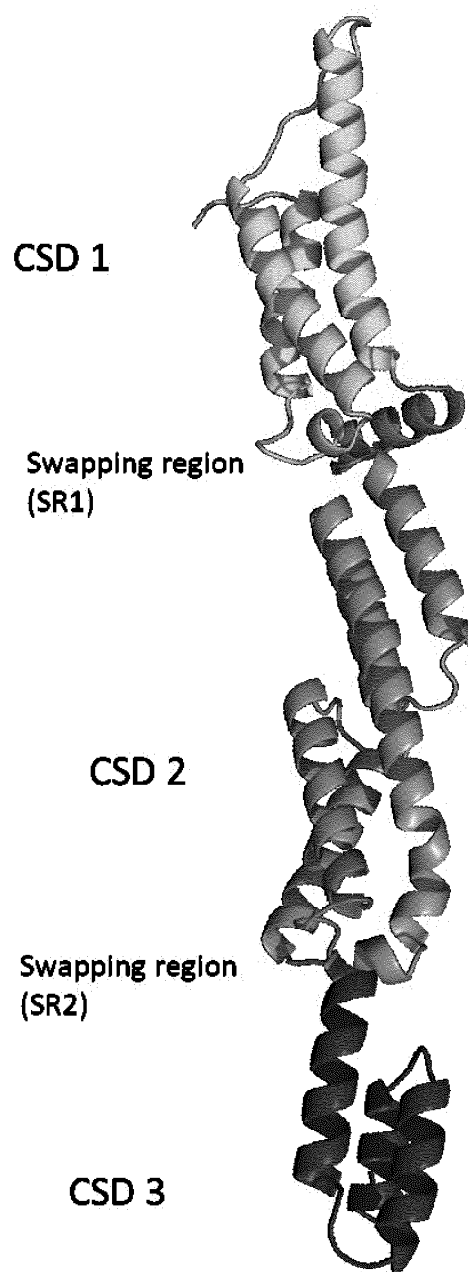
	CSD1	SR1	CSD2
P022	DAKIQRAAAAVDLG	IKATLAA	TIIIPNALHSAAFKDAVVANLVAAGVDK
P027	DAAVQHAAAAIDLS	FKAILGAS	IIPNALGSAAFKNAVIANLVAAGIDK
H4	DAKIQRAAAAVDLG	IKATLAA	TIIIPNALGSAAFKNAVIANLVAAGIDK
	** :*:****:***:** *.:***** *****:***:*****:**		

CSD2-CDS3 junction. Swap region is shown (SR2) :

	CSD2	SR2	CSD3
P022	AVQIAPRIIDRLA	KEP	LLAINTAKLMKNI
P027	AISLAPHIVKRLA	KEP	LLAFNTAKLVKD
H4	AISLAPHIVKRLA	KEP	LLAFNTAKLMKNI
	*:.:***:**.*****:***:*****:***:*****: .:*** .		

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Fig. 7C



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Fig. 7D



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Fig. 7E



Fig. 8

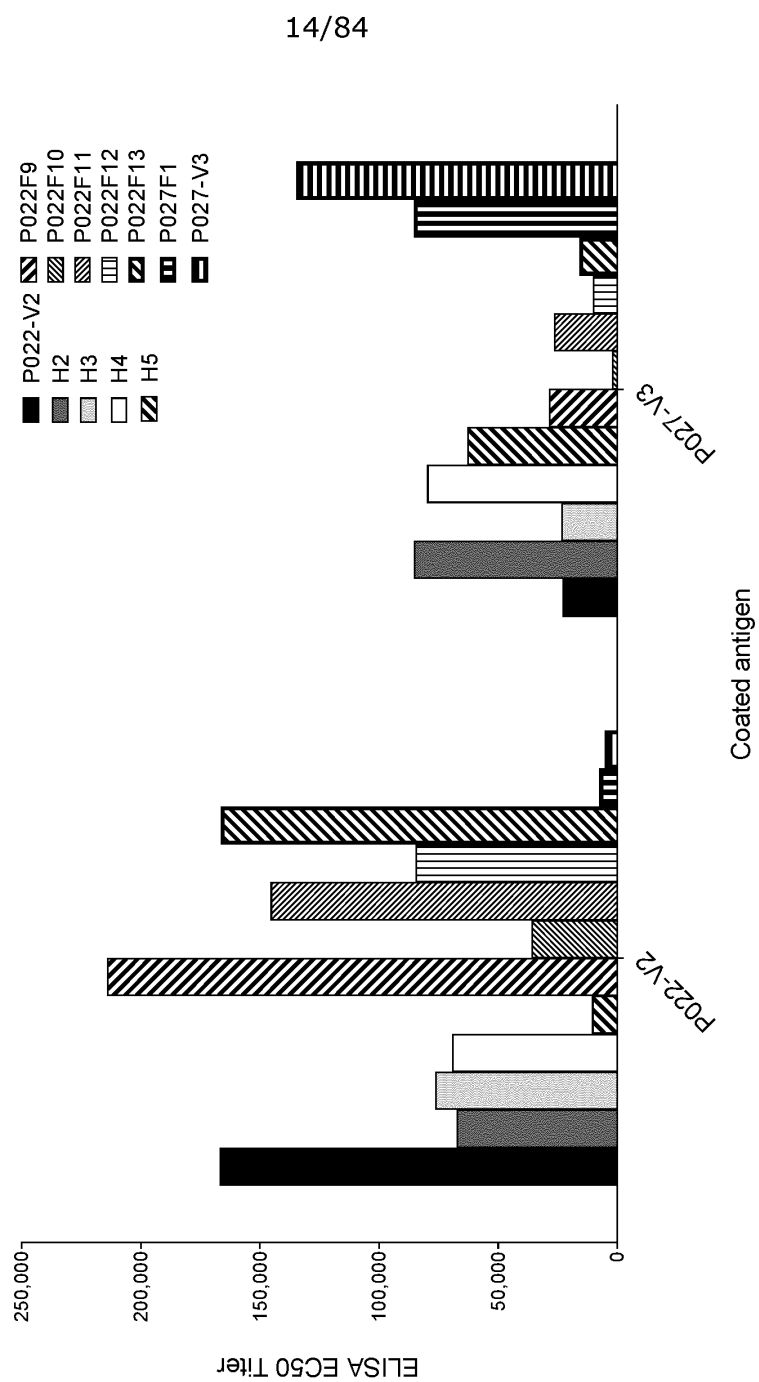


Fig. 9

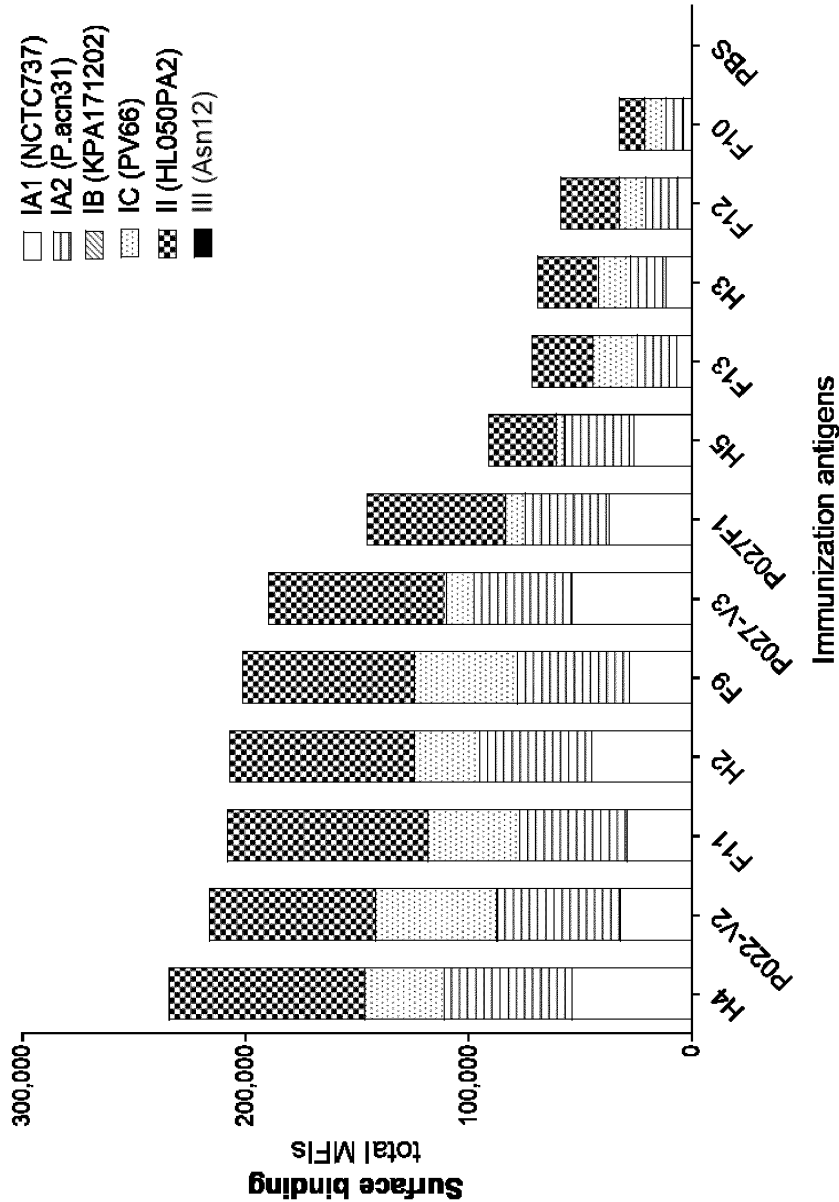


Fig. 10A

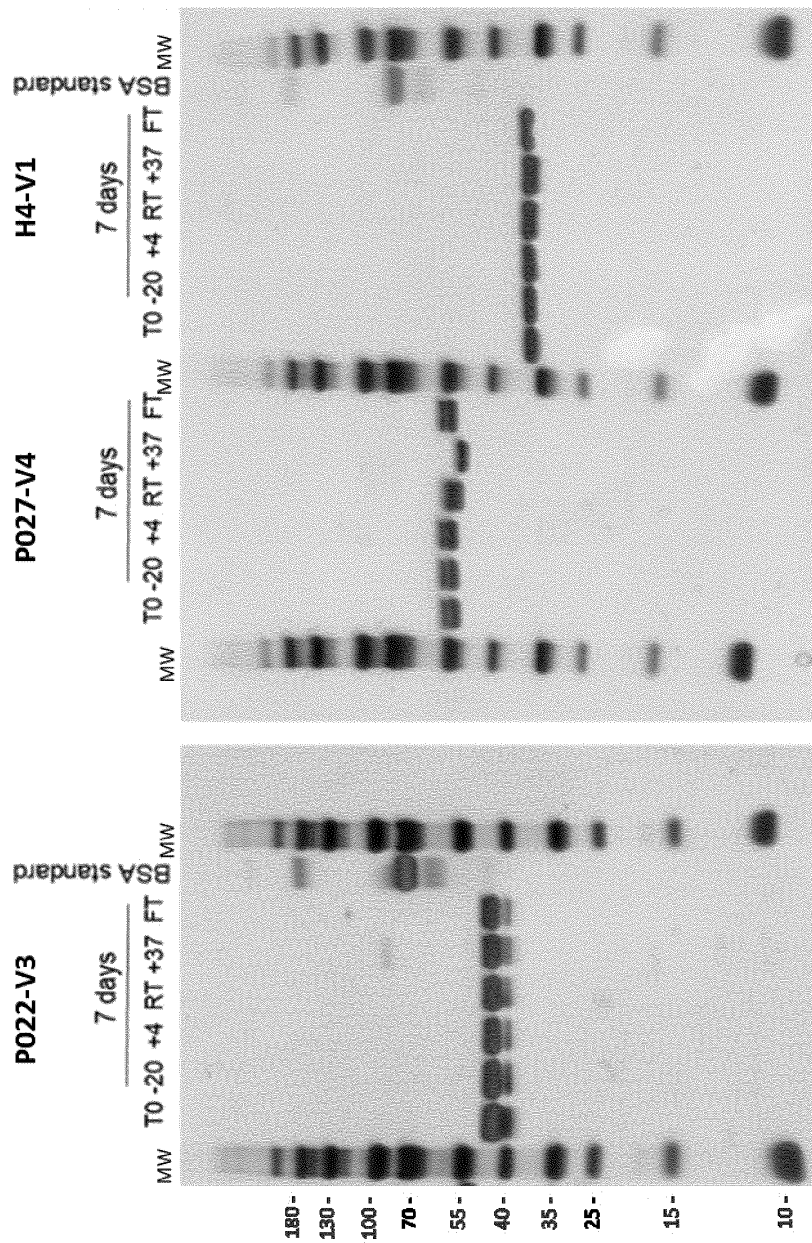


Fig. 10B

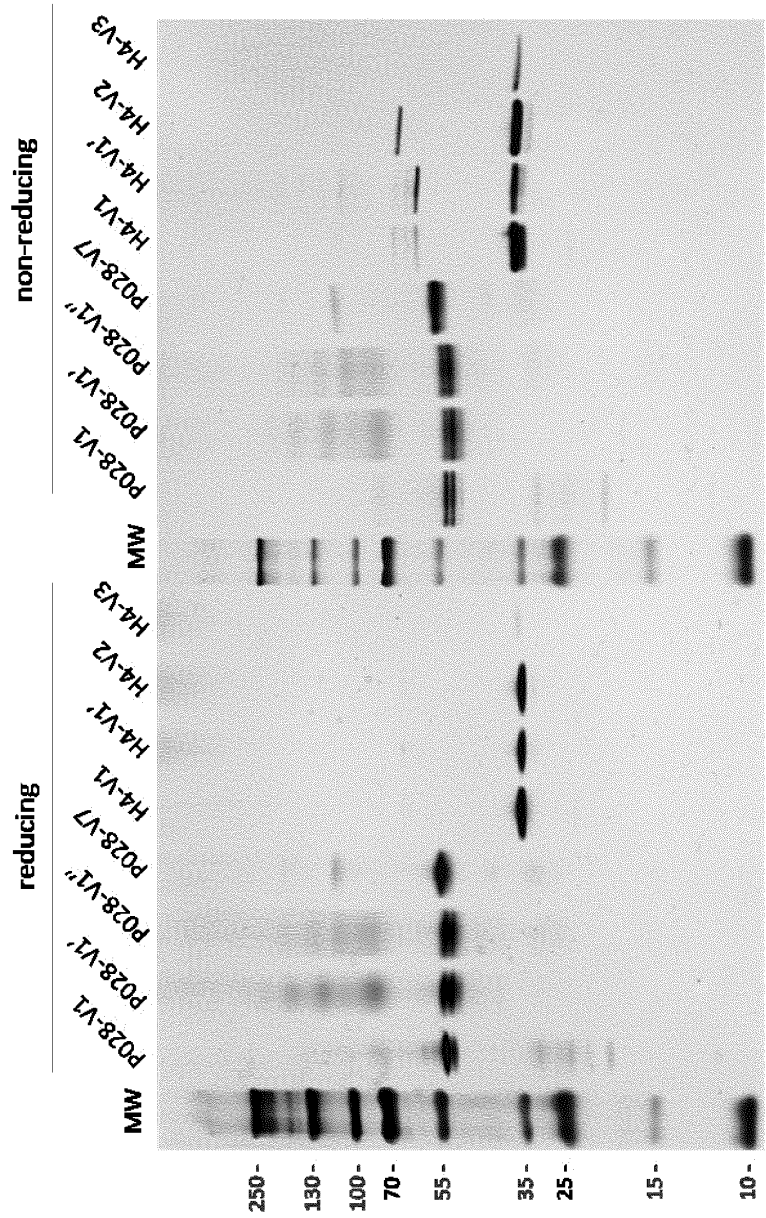
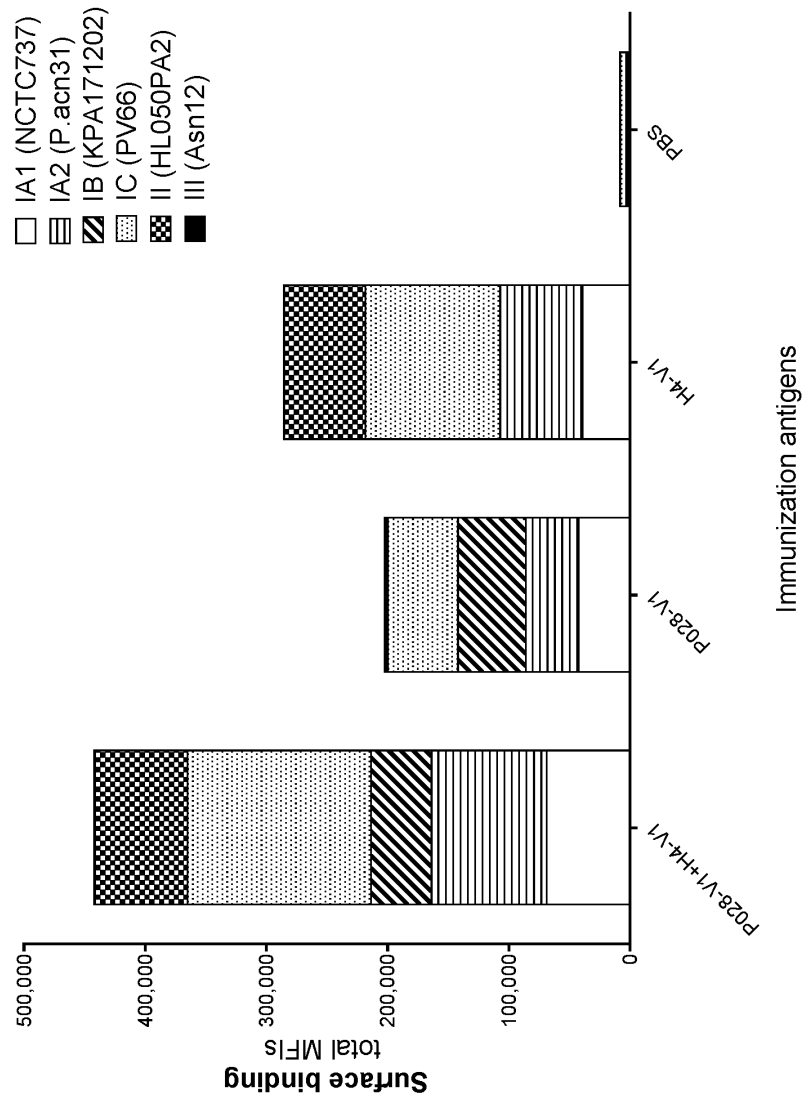


Fig. 11A



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Fig. 11B

	IA1 (NCTC737)	IA2 (P.acn31)	IB (KPA171202)	II (HL050PA2)	III (Asn12)
P028+H4	+++	+++	+	++	+/-
P028	++	++	++	++	+/-
H4	+++	+++	-	+++	-
PBS	-	-	-	-	-

Fig. 11C

	IA1 (NCTC737)	IA2 (P.acn31)	IB (KPA171202)	IC (PV66)	II (HL060PA1)	III (Asn12)
P028-V7+H4-V3	+++	+++	+	+++	+++	-
P028-V7	+++	+	+++	+	+++	+/-
H4-V3	+++	+++	-	+++	+	-
PBS	-	-	-	-	-	-

[illegible]

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Fig. 12B cont.

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Fig. 12B cont.

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Fig. 12B cont.

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EFS88206.1          PTPTPTPTPKP-----TPTPTPKPTPTPKPK
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WP_002541876.1      PTPTPTPTPTPTP-----TPTP-----T---PTPTPTPTPTPTPTPTPKPK
WP_134790435.1      PTPTPTPTPTPKPTPT-----TPTPTPKPK
AEW82361.1          PTPTPTPT---TPKPTP-----TPTPKPTPTPKPK
WP_098816751.1      PTPTPTPTPTPKPTPTPTPKPTPT-----PTPKPTPTPTPTPTPTPTPTPTPTPKPK
EGE68409.1          PTPTPTPTPTP-----TPTP-----TPTPTPTPTPKPTPTP-----TPTPTPTPKPK
PZQ65062.1          PTPTPTPTPTPTPTPTPTPTPTPTPT-----PTPT
HAF96864.1          PTPTPTPTPTPKPT-----T---PTPTPTPKPK
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WP_002542452.1 PTPAPAPTSGATSDESTSRSGGHSQGGSGTHYIHHGVAPVLTHSSDLPSTGF
WP_120363082.1 PTPAPAPTSGATSDS-----IHHGVAPVLTHSSDLPSTGF
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Fig. 12C cont.

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WP 06997199.1
WP 060633522.1
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WP 064664380.1
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WP_032506096.1 ATKSGSLKSYGSGVHMTGHHGILDMTLAEP SLQIKGSTGHLYLDVKSSSMDGKKNTNYGRVD
GAE75471.1    ATKSGSLKSYGSGVHMTGHHGILDMTLAEP SLQIKGSTGHLYLDVKSSSMDGKKNTNYGRVD
WP_002526234.1 ATKSGSLKSYGSGVHMTGHHGILDMTLAEP SLQIKGSTGHLYLDVKSSSMDGKKNTNYGRVD
WF_064661676.1 ATKSGSLKSYGSGVHMTGHHGILDMTLAEP SLQIKGSTGHLYLDVKSSSMDGKKNTNYGRVD
ESS85979.1   ATKSGSLKSYGSGVHMTGHHGILDMTLAEP SLQIKGSTGHLYLDVKSSSMDGKKNTNYGRVD
CQA9N1       ATKSGSLKSYGSGVHMTGHHGILDMTLAEP SLQIKGSTGHLYLDVKSSSMDGKKNTNYGRVD
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WP_058833371.1 ATKSGSLKSYGSGVHMTGHHGILDMTLAEP SLQIKGSTGHLYLDVKSSSMDGKKNTNYGRVD
WF_134868546.1 ATKSGSLKSYGSGVHMTGHHGILDMTLAEP SLQIKGSTGHLYLDVKSSSMDGKKNTNYGRVD
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GAE72536.1   -----MTGHHGILDMTLAEP SLQIKGSTGHLYLDVKSSSMDGKKNTNYGRVD
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TKW70951.1   -----
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GAE68623.1   -----
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Domain
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Fig. 12D cont.

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GAE75471.1 FATFGVSVSGNAAIKGSPVKLTATGAKAFAGFYSW-----
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WF_064661676.1 FATFGVSVSGNAAIKGSPVKLTATGAKAFAGFYRAGEPMNPLSTNLTLSAEKVCVHNVTVD
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Q69A91 FATFGVSVSGNAAIKGSPVKLTATGAKAFAGFYRAGEPMNPLSTNLTLSAEKVCVHNVTVD
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GAE72534.1 -----
WF_070689252.1 FATFGVSVSGNAAIKGSPVKLTATGAKAFAGFYRAGEPMNPLSTNLTLSAEKVCVHNVTVD
GAE68624.1 -----
TKW70951.1 -----
WF_070651110.1 FATFGVSVSGNAAIKGSPVKLTATGAKAFAGFYRAGEPMNPLSTNLTLSAEKVCVHNVTVD
GAE78839.1 FATFGVSVSGNAAIKGSPVKLTATGAKLLP-VFTAGEPMNPLSTNLTLSAEKVCVHNVTVD
GAE68623.1 FATFRVSVSGNTAIQGSPVKLTATGTAKAFAGFYRAGEPMNPLSTNLTLSAEKVCVHNVTVD
WF_015011468.1 FATFGVSVSGNAAIKGSPVKLTATGAKAFAGFYRAGEPMNPLSTNLTLSAEKVCVHNVTVD
WF_115864668.1 FATFGVSVSGNAAIKGSPVKLTATGAKAFAGFYRAGEPMNPLSTNLTLSAEKVCVHNVTVD
WF_032505161.1 FATFGVSVSGNAAIKGSPVKLTATGAKAFAGFYRAGEPMNPLSTNLTLSAEKVCVHNVTVD
WF_002532188.1 FATFGVSVSGNAAIKGSPVKLTATGAKAFAGFYRAGEPMNPLSTNLTLSAEKVCVHNVTVD
WF_098681135.1 FATFGVSVSGNAAIKGSPVKLTATGAKAFAGLYRAGEPMNPLSTNLTLSAEKVCVHNVTVD
WF_002547326.1 FATFGVSVSGNAAIKGSPVKLTATGAKAFAGFYRAGEPMNPLSTNLTLSAEKVCVHNVTVD
Domain XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
```


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Fig. 12D cont.

HCW43569.1	-VVCR-RY----
TKW72552.1	-VVCRRHAARI-
WP_032506096.1	-VVCR-RYAARI
GAE75471.1	-----
WP_002526234.1	-VVCR-RYAARI
WP_064661676.1	-VVCR-RYAARI
ESS85979.1	-VVCR-RYAARI
Q6A9N1	-VVCR-RYAARI
WP_002545986.1	-VVCR-RYAARI
WP_058833371.1	-VVCR-RYAARI
WP_134868546.1	-VVCR-RYAARI
PZQ74368.1	-----
GAE72536.1	-----
WP_002521827.1	-VVCR-RYAARI
HAP96815.1	-VVCR-RYAARI
WP_002544456.1	-VVCR-RYAARI
WP_024513551.1	-VVCR-RYAARI
GAE72537.1	-VVCR-RYAARI
WP_048738316.1	-VVCR-RYAARI
WP_002523757.1	-VVCR-RYAARI
WP_032502852.1	-VVCR-RYAARI
WP_002537090.1	-VVCR-RYVARI
GAE72534.1	-----
WP_070689252.1	-VVCR-RYAARI
GAE68624.1	-----
TKW70951.1	-----
WP_070651110.1	-VVCR-RYAARI
GAE78839.1	PFVERRHFARRQ
GAE68623.1	-VVCR-RYAARI
WP_015011468.1	-VVCR-RYAARI
WP_115884668.1	-VVCR-RYAARI
WP_032505161.1	-VVCR-RYAARI
WP_002532188.1	-VVCR-RYAARI
WP_098681135.1	-VVCR-RYAARI
WP_002547326.1	-VVCR-RYAARI
Domain	XXXXXXXXXX

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Fig. 13A

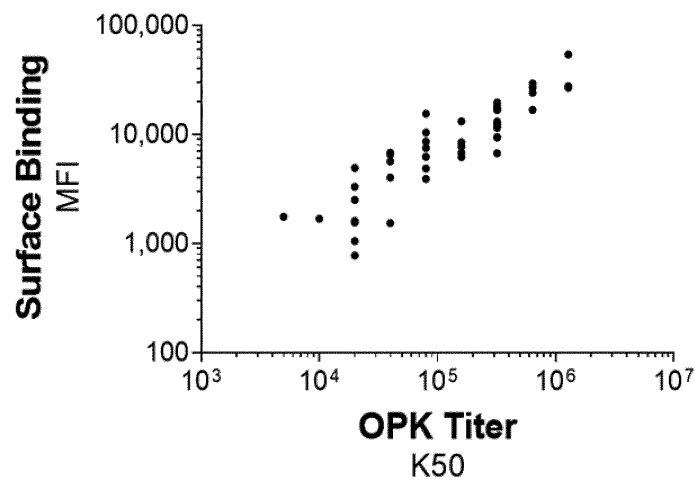


Fig. 13B

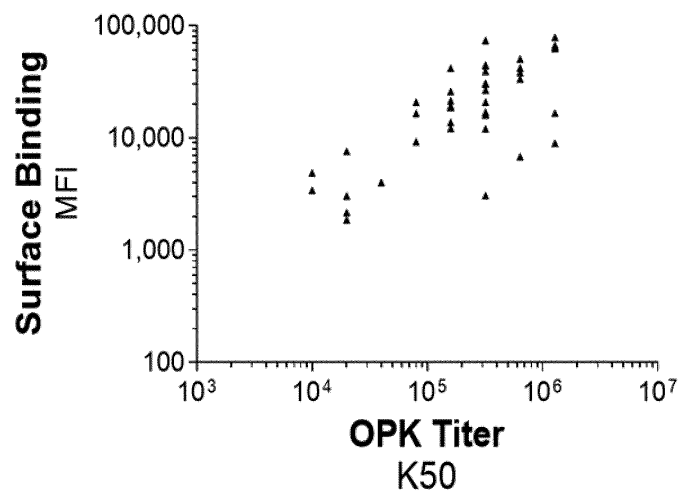


Fig. 14A

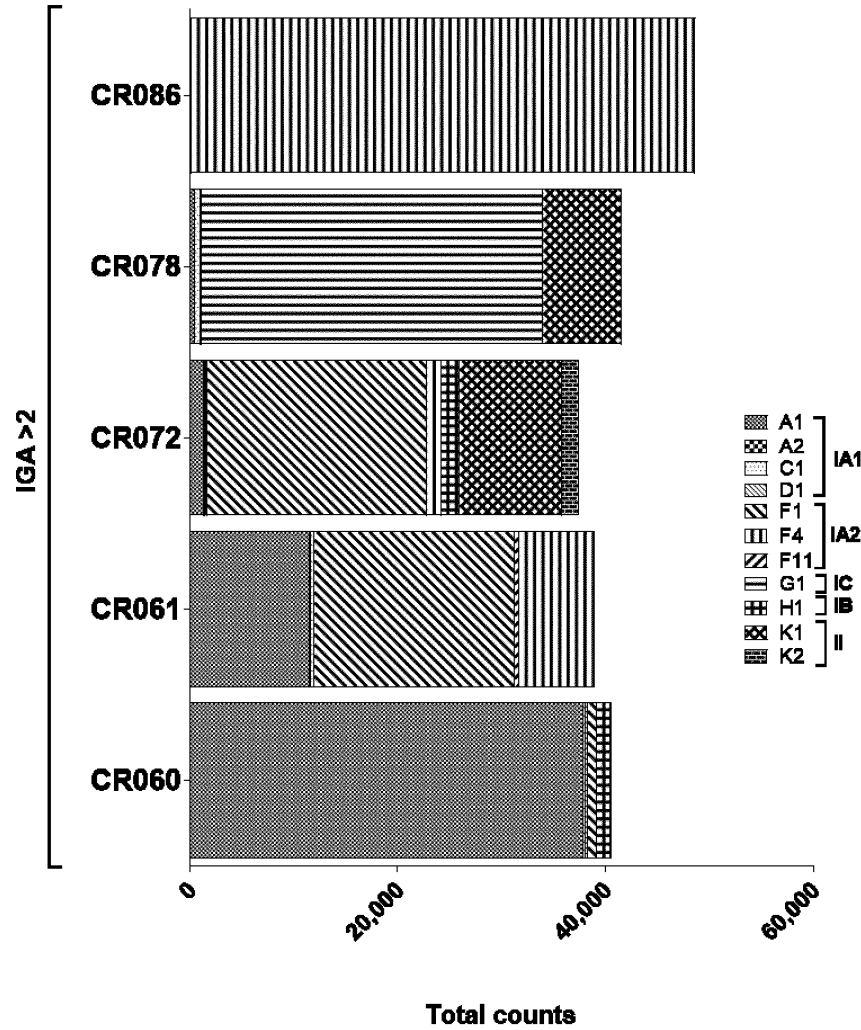


Fig. 14B

Subject	Acne Lesion		Skin Pores	
	SLST	MLST	SLST	MLST
CR086	F4	IA2	A1, F4, G1, unknown	IA1, IA2, IC, unknown
CR078	G1, K1	IC, II	A1, C1, C2, G1, K1	IA1, IC, II
CR072	A1, F1, F4, H1, K1, K2	IA1, IA2, IB, II	A1, F1, H1, K1	IA1, IA2, IB, II
CR061	A1, F1, F4	IA1, IA2	A1, A2, D1, F1	IA1, IA2
CR060	A1, H1	IA1, IB	A1, F1, H1	IA1, IA2, IB

Fig. 15

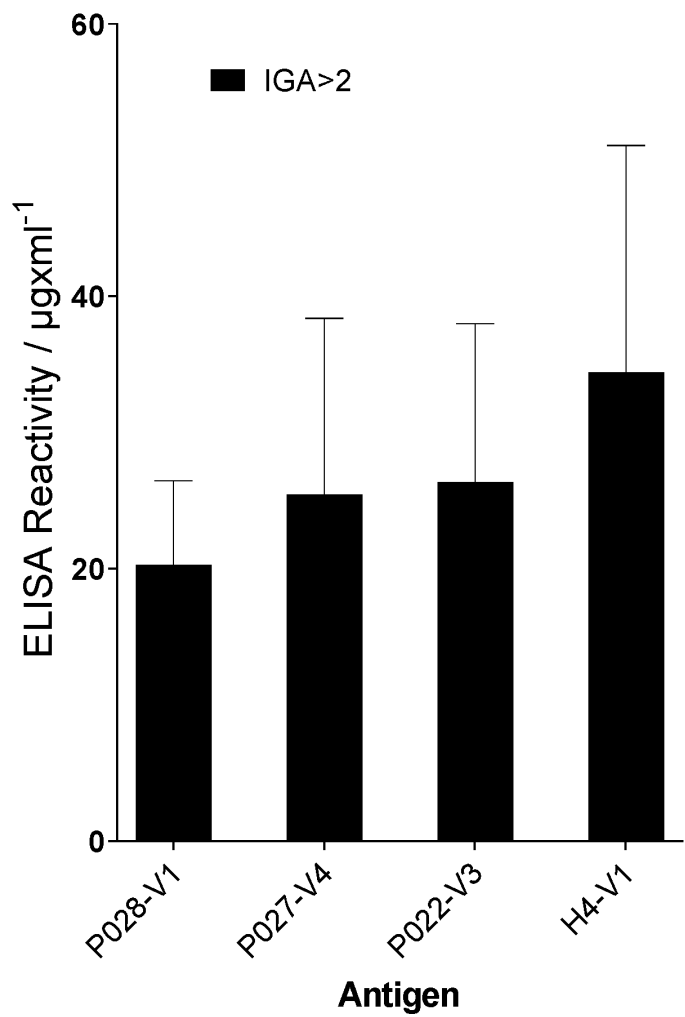


Fig. 16A

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MLST	Strain	P028-V1	P022-V3	H4-V1	P027-V4	P071	PBS
IA1	NCTC 737	26913	44805	58817	67797	2741	676
IA1	HL013PA2	29846	84763	91188	87915	7926	588
IA1	HL038PA1	15963	76898	86338	108661	613	520
IA1	HL002PA2	34415	79676	87216	91939	7044	596
IA1	IAI027	9235	85329	90277	97318	10382	595
IA1	A019-#2	67518	115188	86857	69750	9849	1945
IA1	Hung.#4	5762	70747	61918	49890	29012	1606
IA1	IAI 013	30125	82219	79753	69890	8844	796
IA1	IAI 016	14604	65230	51334	34059	6767	89
IA1	A015 SK1	25374	60752	55111	46100	15153	1303
IA1	A016P SK1	12004	85111	76582	61247	19604	1574
IA1	A016H SK2	18224	75464	67954	54345	28781	2050
IA1	SK 137	34198	98570	85477	70046	12645	1490
IA1	HL005PA3	35128	84119	75689	58338	4267	409
IC	PV66	52193	68346	53892	29547	2895	1901
IC	Hung.#2	97911	125962	88996	38392	4628	2918
II	HL060PA1	15873	16664	18789	23691	3108	192
II	HL110PA3	319	5710	6915	10945	1722	159
II	HL110PA4	358	5715	6834	10074	1750	162
II	HL082PA2	105	1660	2205	3277	597	80

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Fig. 16B

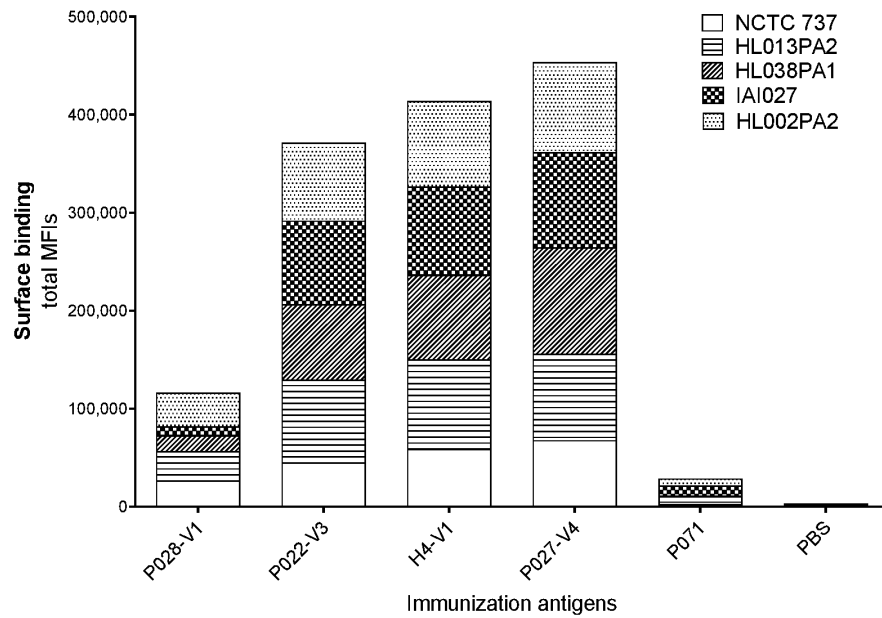
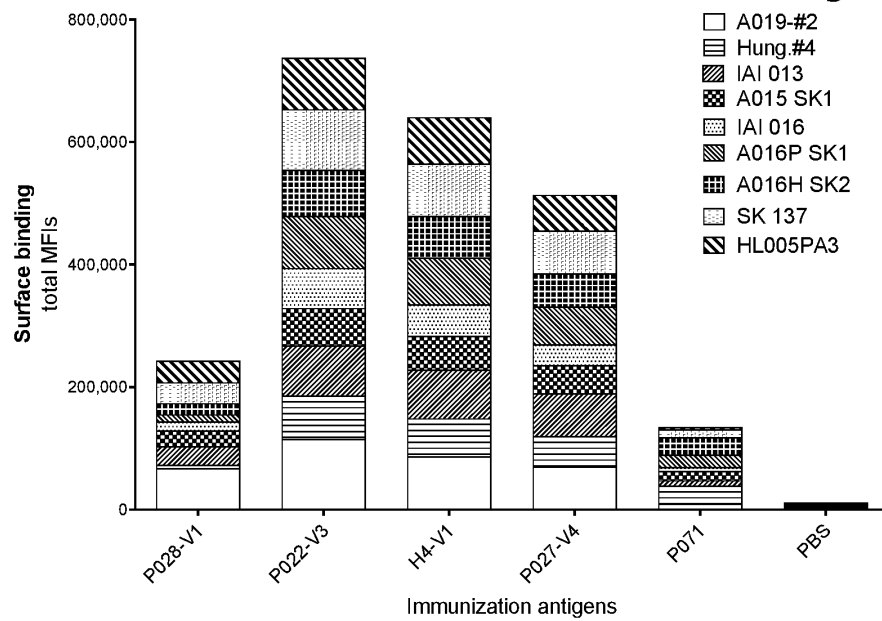


Fig. 16C



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Fig. 16D

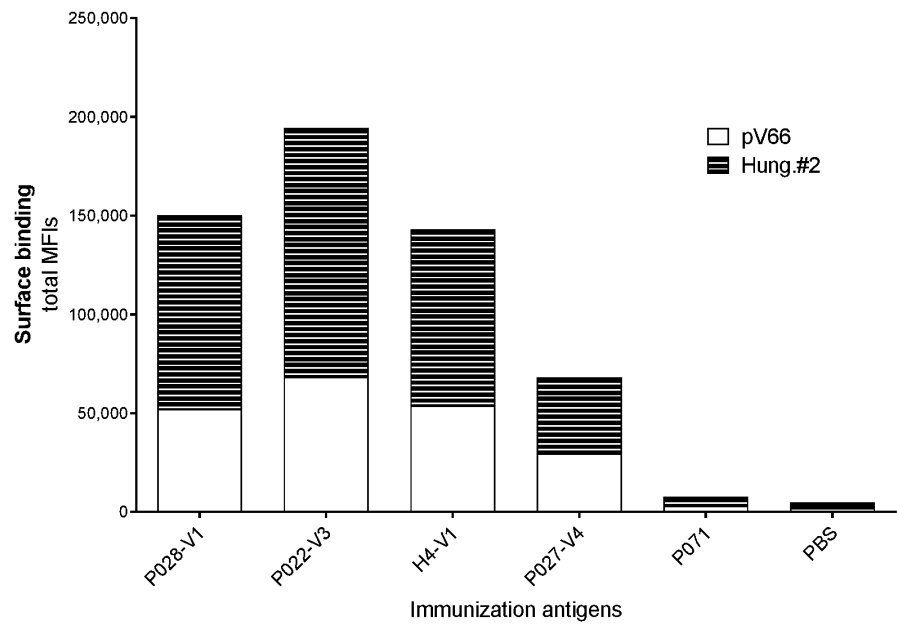


Fig. 16E

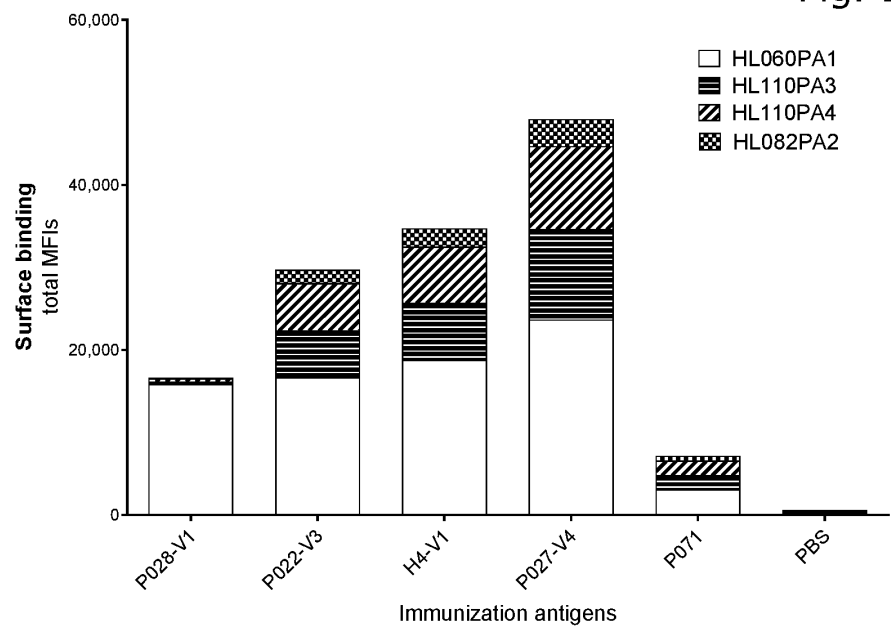


Fig. 16F

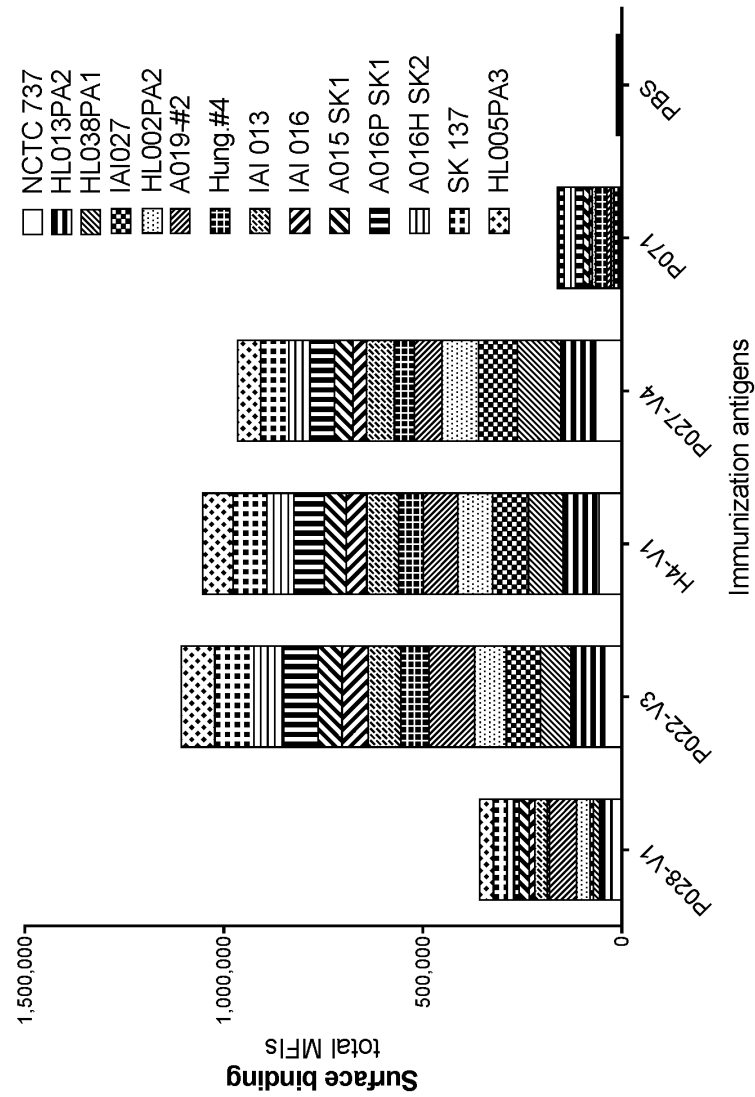


Fig. 17A

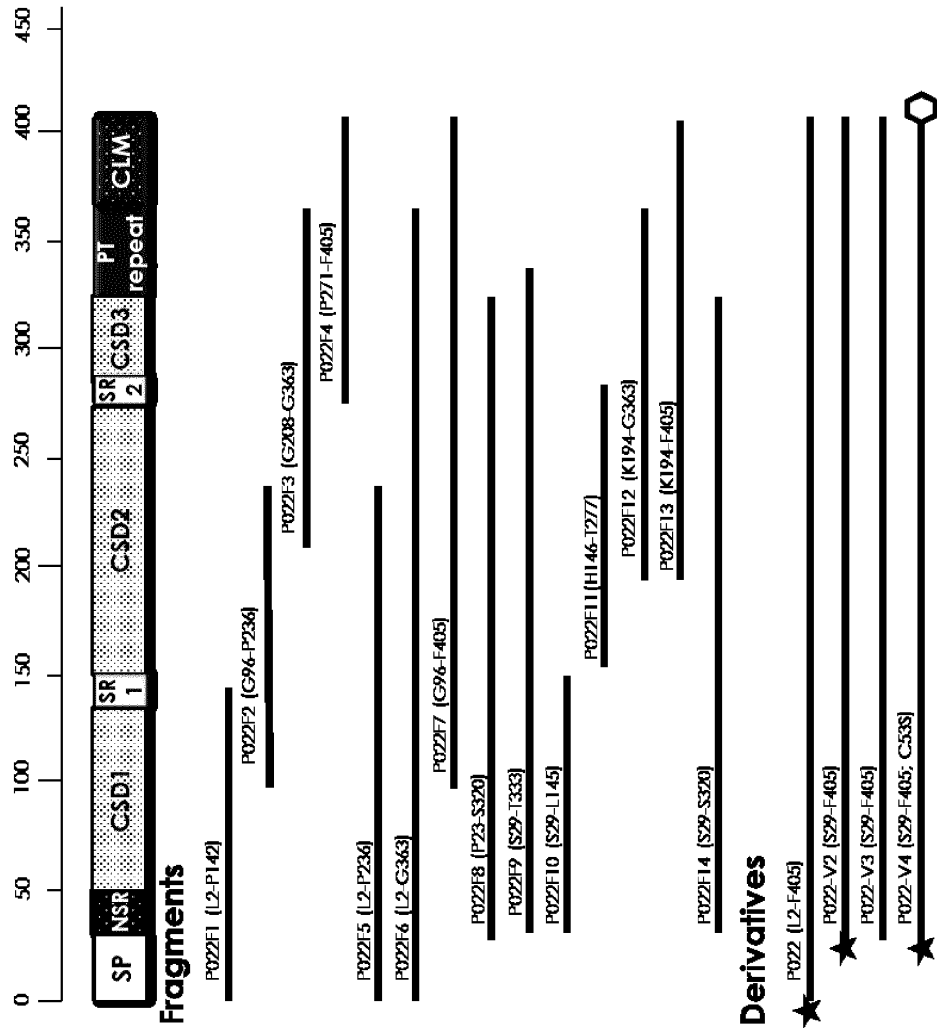


Fig. 17B

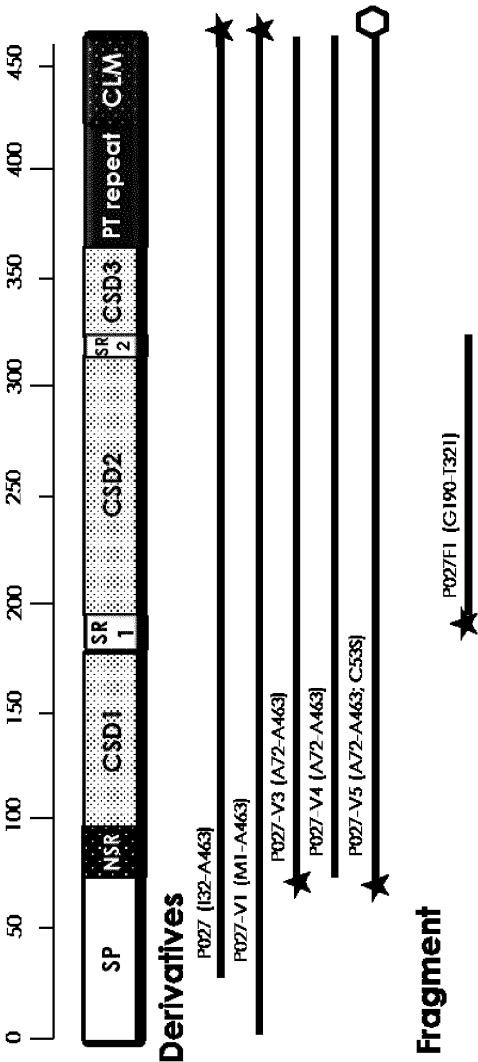


Fig. 17C

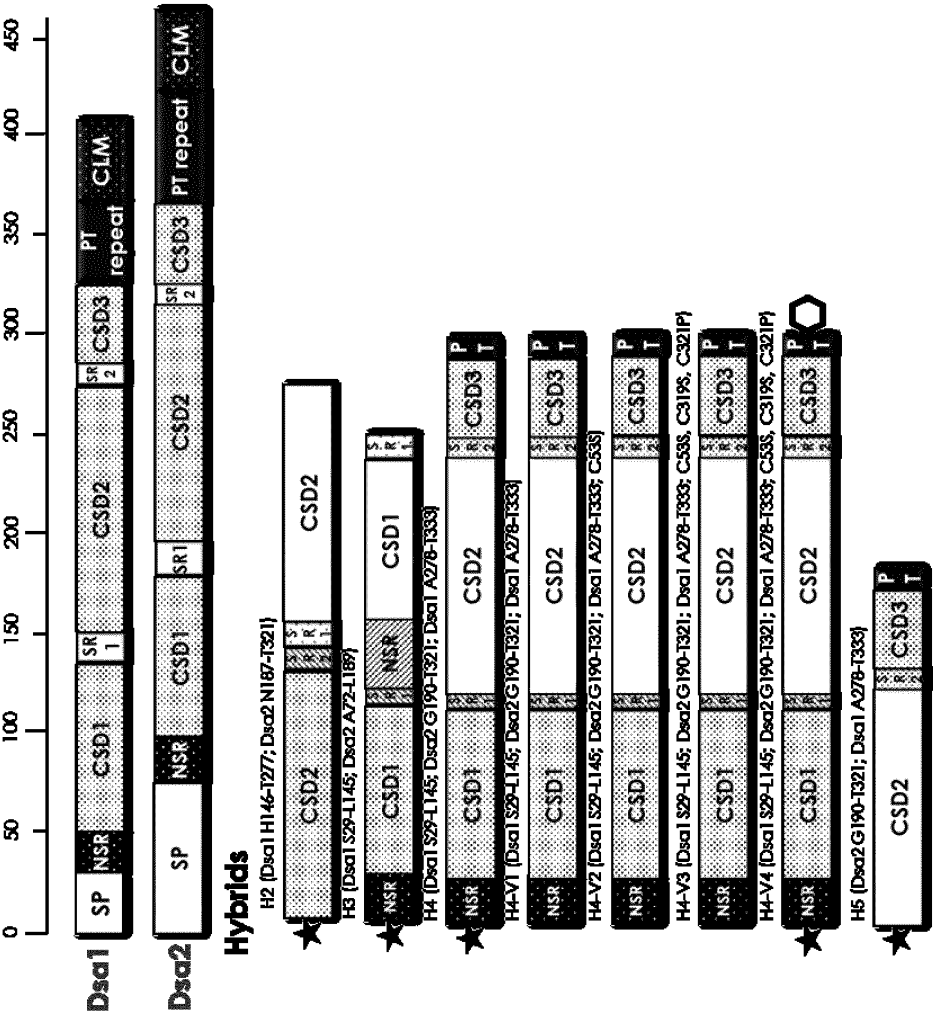


Fig. 18A

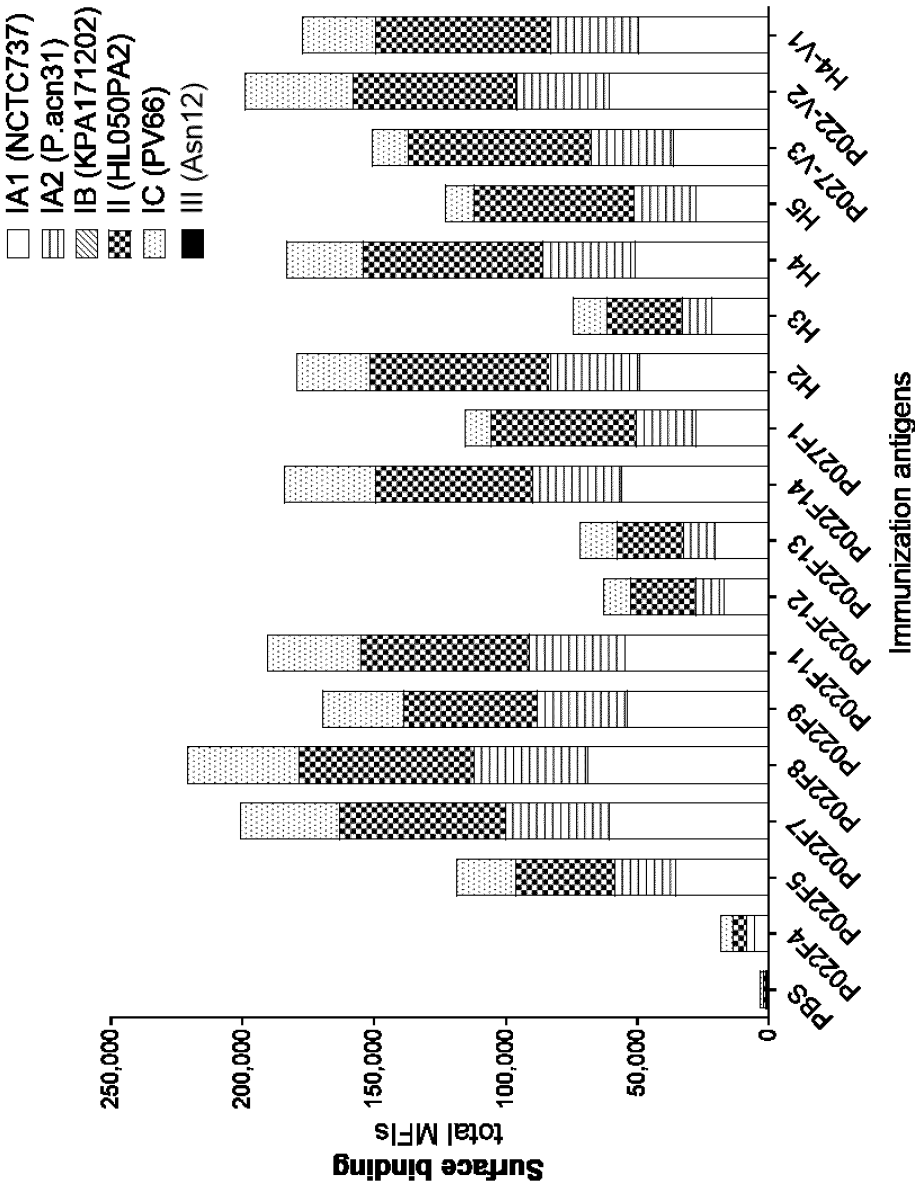


Fig. 18B

	serum dilution	P022F4	P022F7	P022F8	P022F9	P022F14	P022F11	H2	H3	H4	H5	P022-V2	P027F1	P027-V3
% killing (ctr)	10000	0	97	97	98	96	96	98	97	97	94	97	97	96
	20000	0	98	98	98	98	97	97	91	97	98	99	98	98
	40000	0	96	97	98	98	97	98	73	95	98	98	96	95
	80000	0	98	98	97	98	97	95	33	98	97	97	88	96
	160000	0	97	97	97	94	96	98	24	96	95	97	82	95
	320000	0	98	93	96	96	92	93	7	97	94	95	60	92
	640000	1	96	96	83	91	79	78	0	96	80	86	49	75
	1280000	0	80	90	52	68	47	38	0	96	36	51	38	38

Fig. 18C

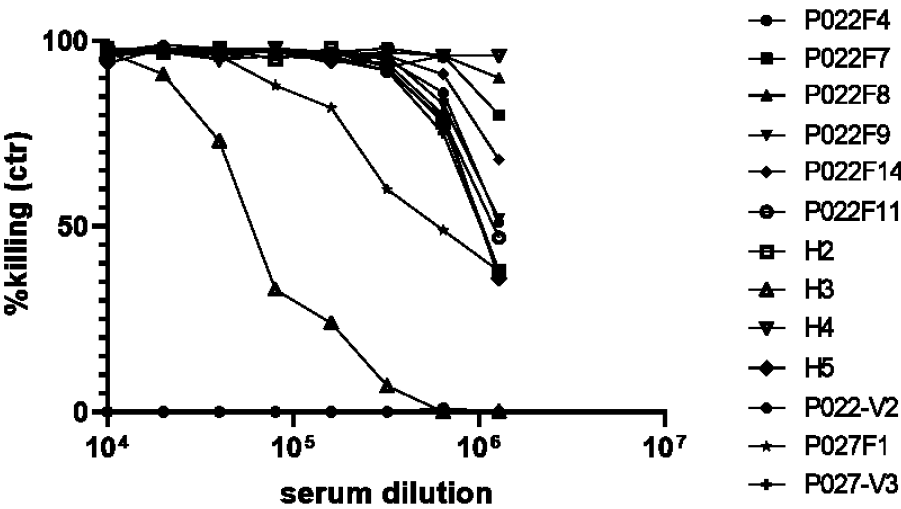


Fig. 19A

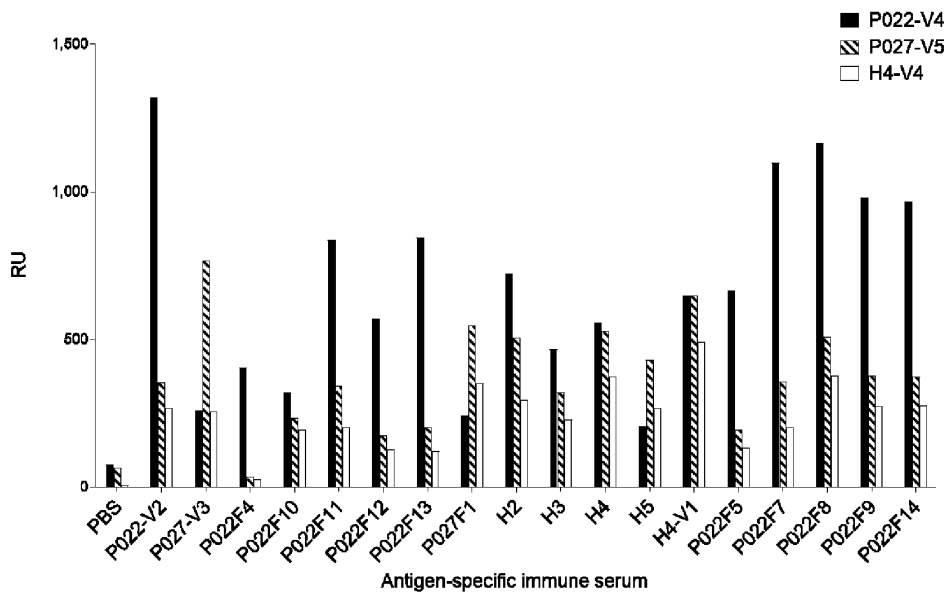


Fig. 19B

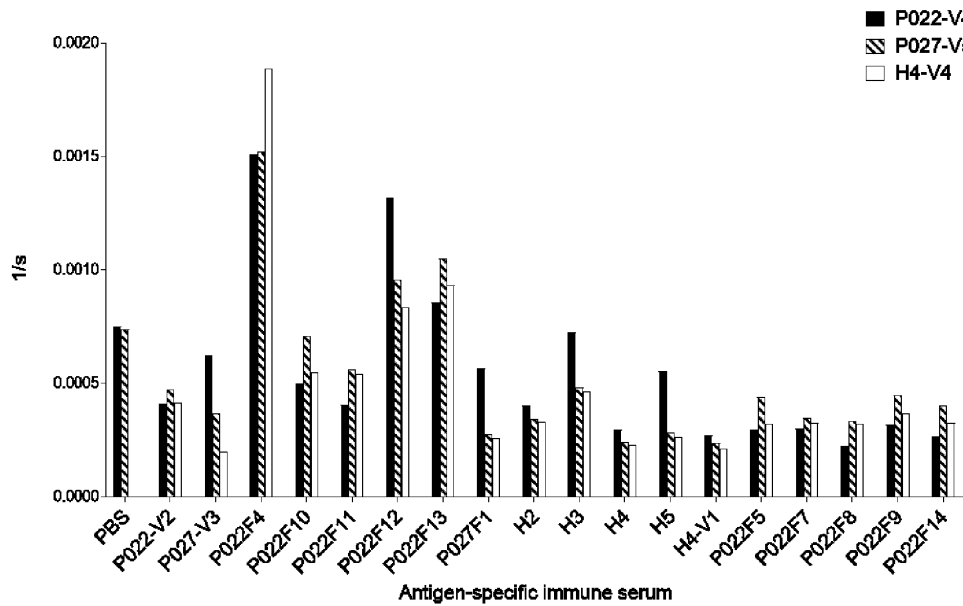
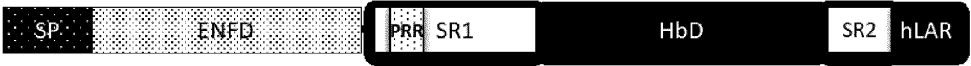


Fig. 20A



Fragments

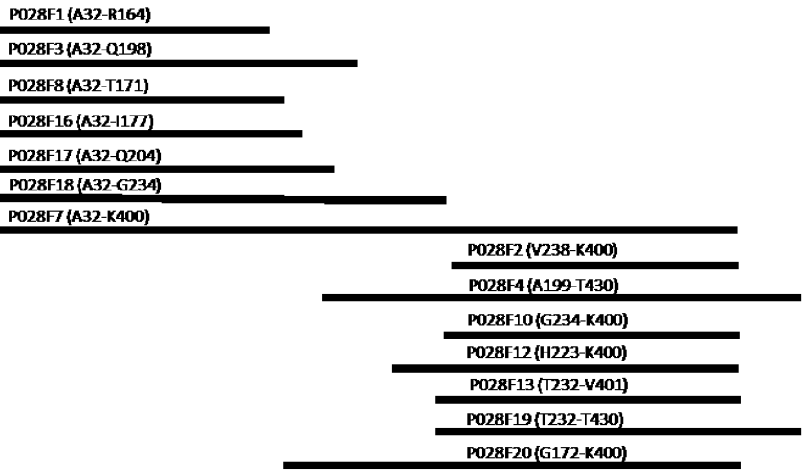


Fig. 20B

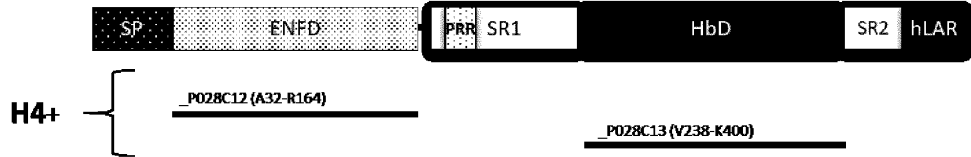


Fig. 20C

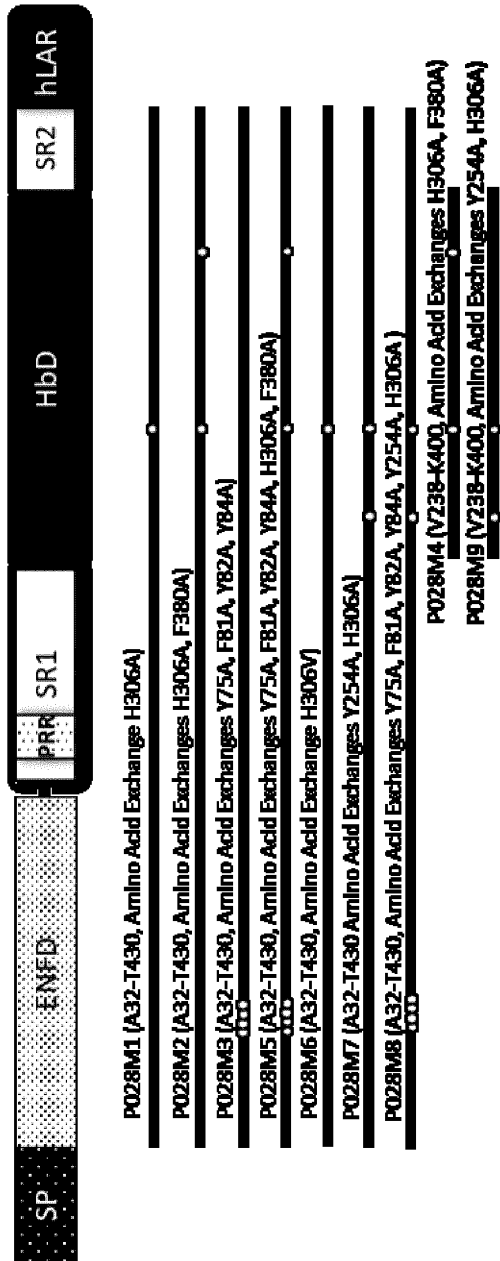


Fig. 21A

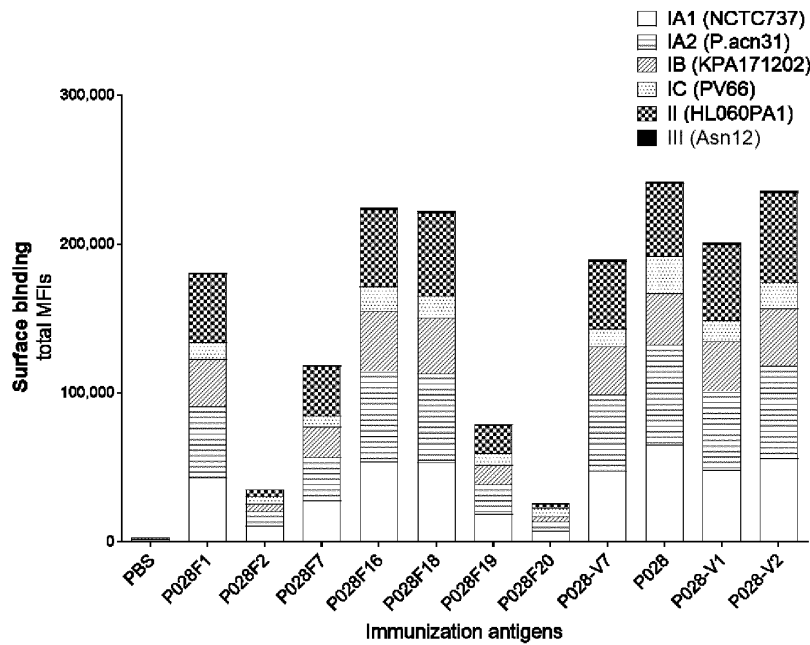
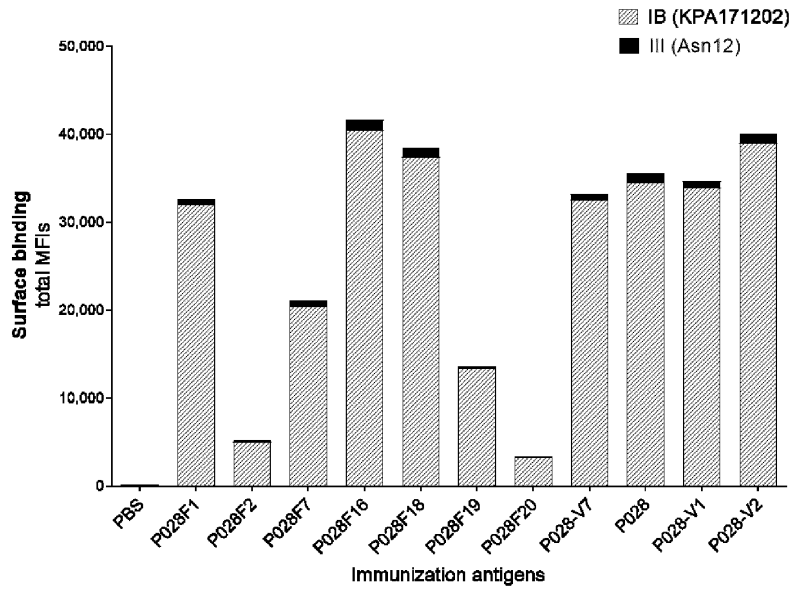


Fig. 21B



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Fig. 21C

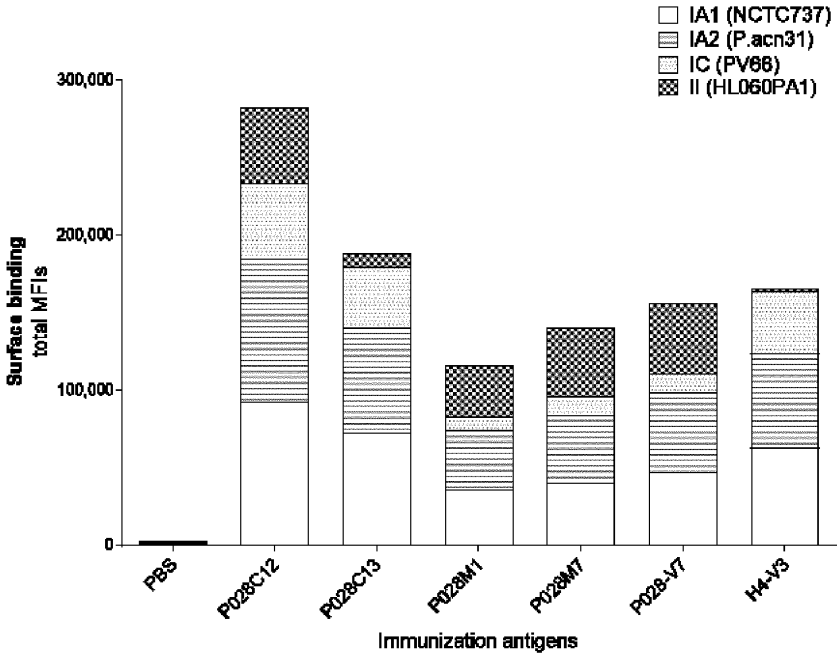
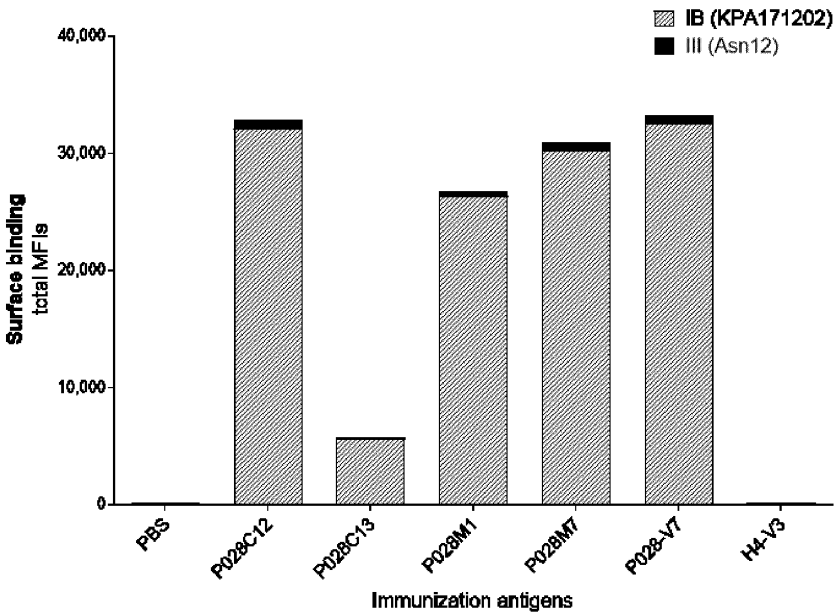


Fig. 21D



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Fig. 22C

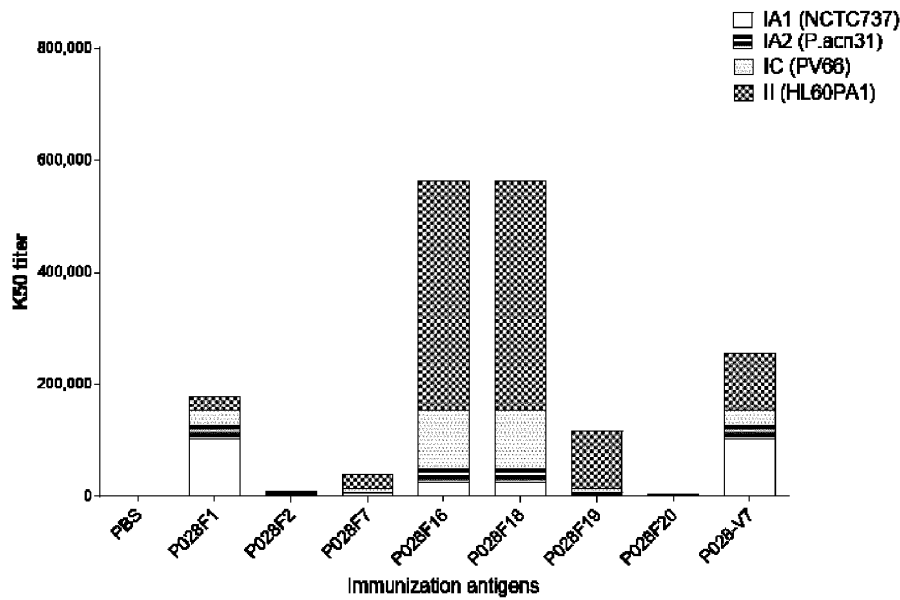
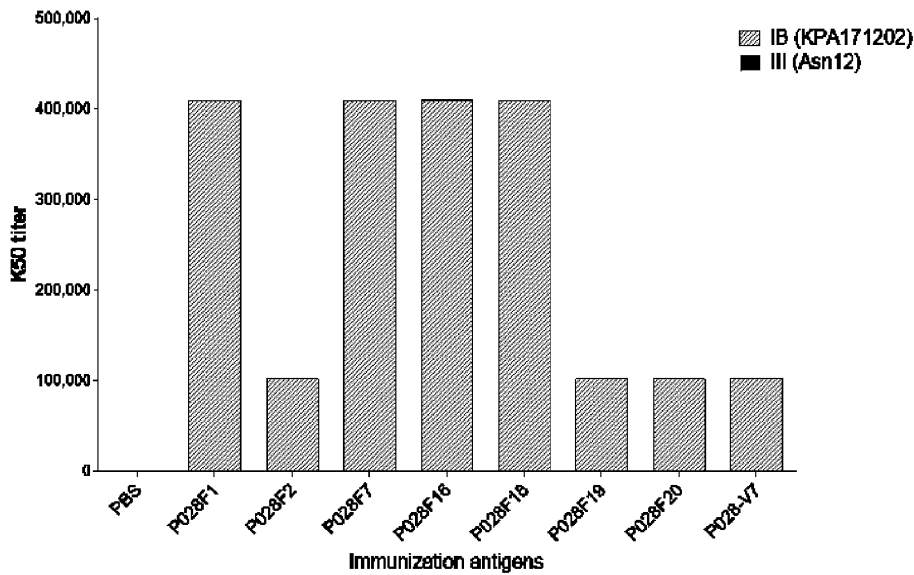


Fig. 22D



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Fig. 23A

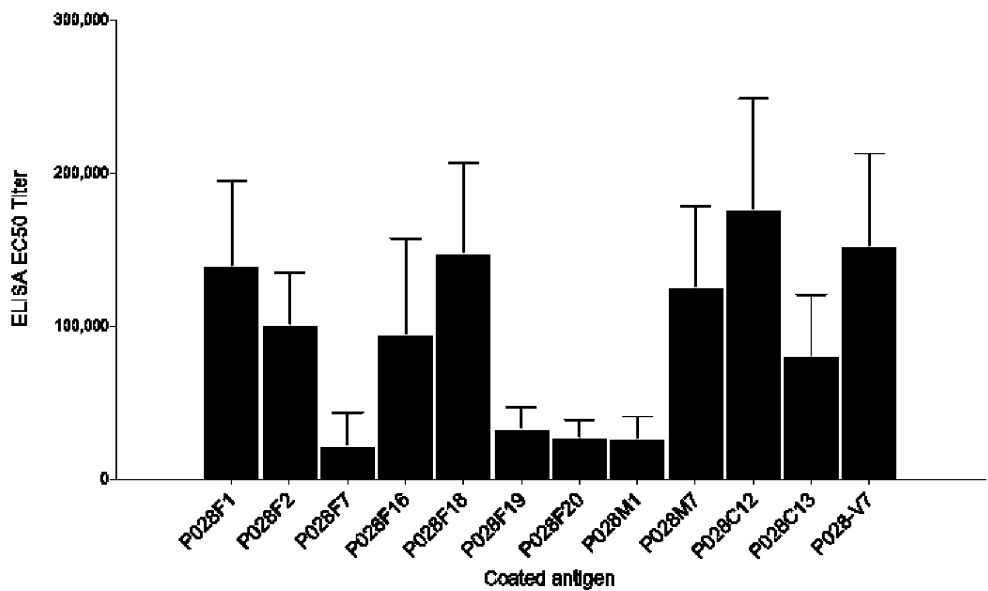


Fig. 23B

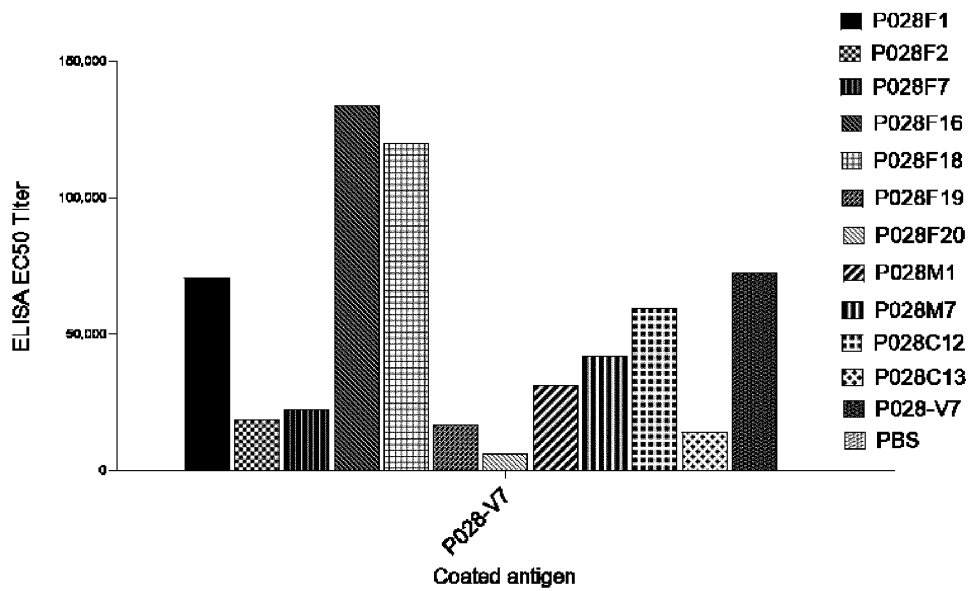


Fig. 23C

Immunization Antigen	EC50 P028-V7	EC50 Self-Antigen	SD (Self-Antigen)
P028F1	70772	139755	55339
P028F2	18773	101396	34036
P028F7	22600	23000	20711
P028F16	134072	95356	62243
P028F18	120039	148394	58969
P028F19	16886	33643	13841
P028F20	6449	27917	11393
P028M1	31470	27042	14269
P028M7	41844	126069	52767
P028C12	59794	176775	72178
P028C13	14200	80930	40028
P028-V7	72672	152658	60262
PBS	<250	n/a	n/a

Fig. 24A

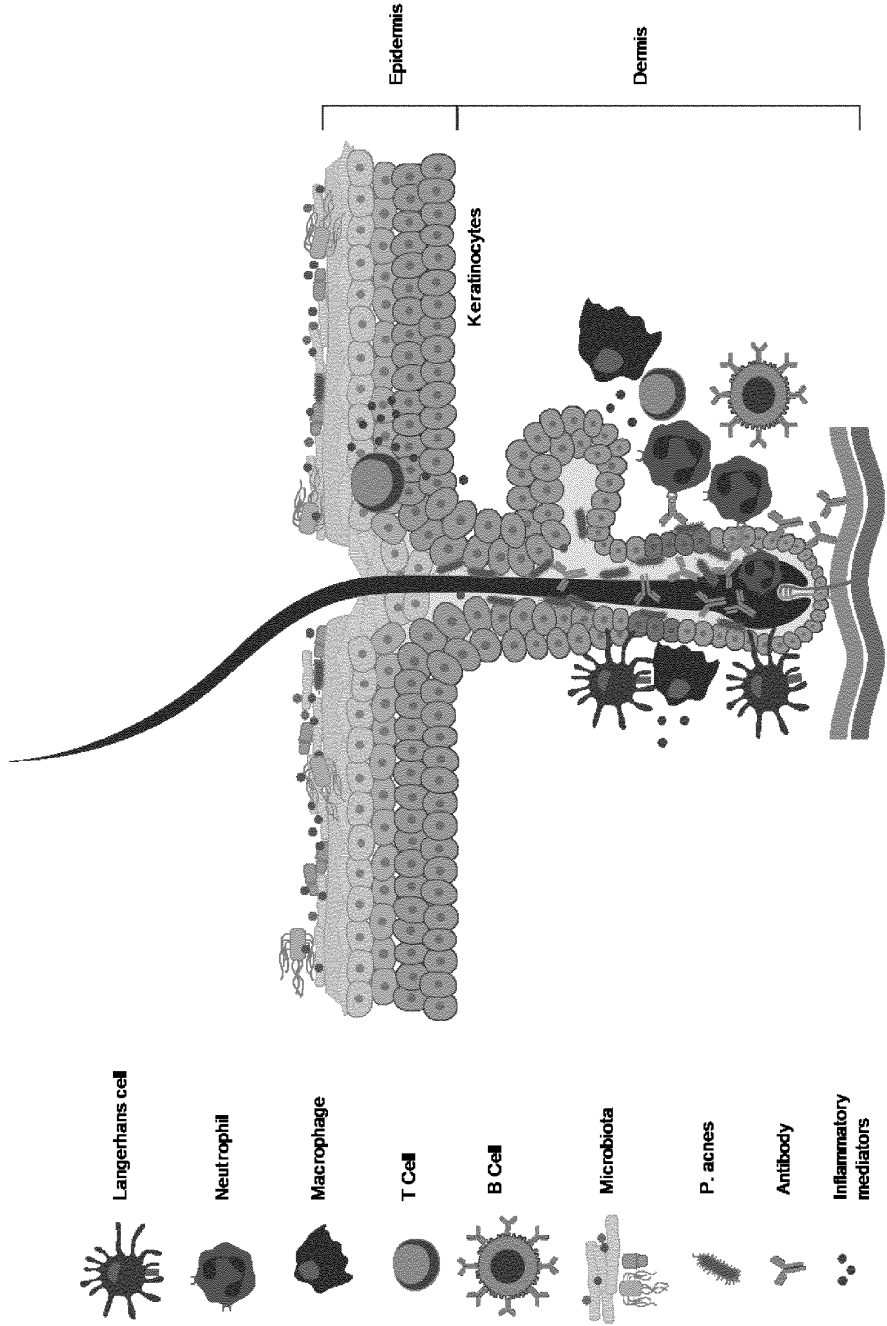


Fig. 24B

