

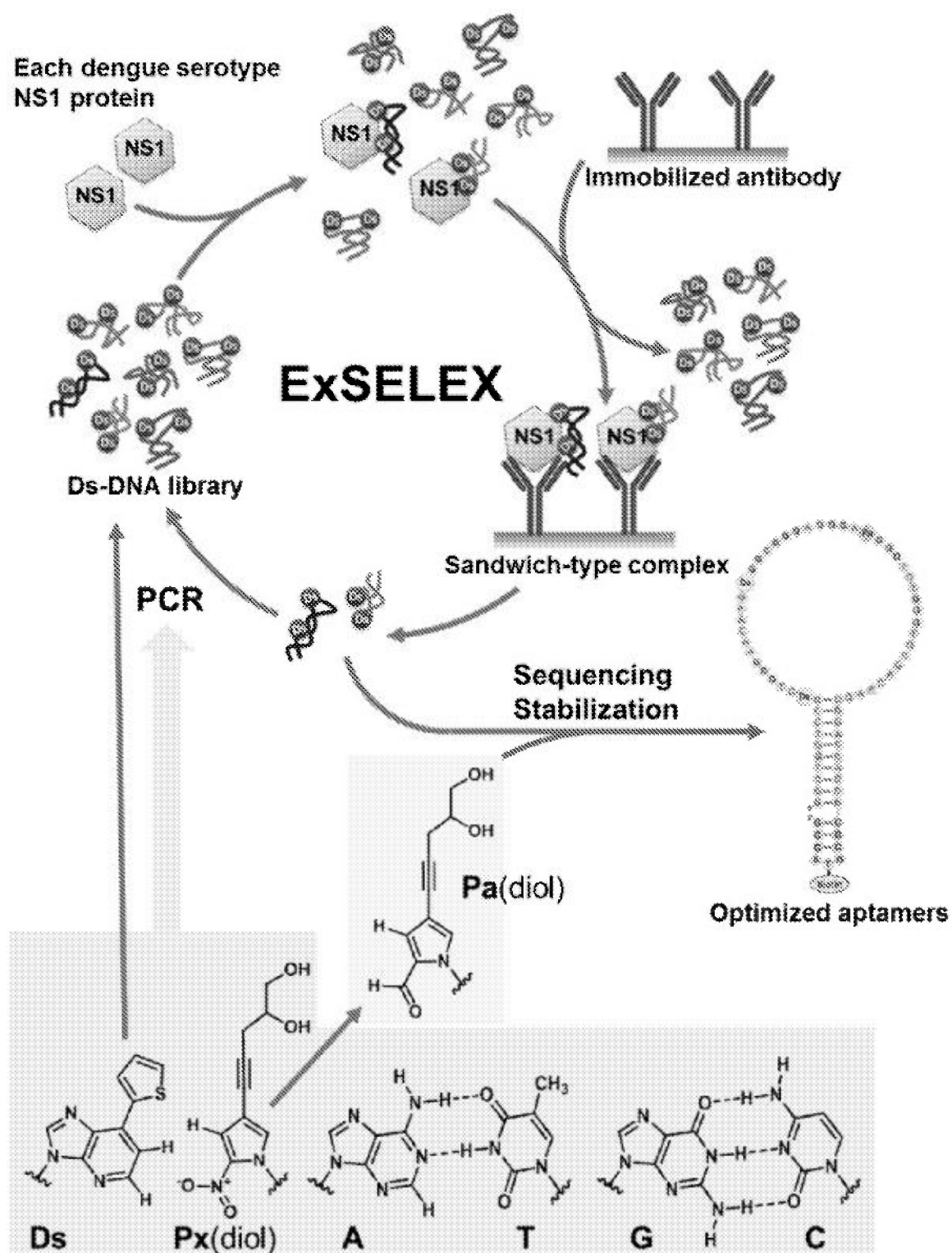


FIG. 1

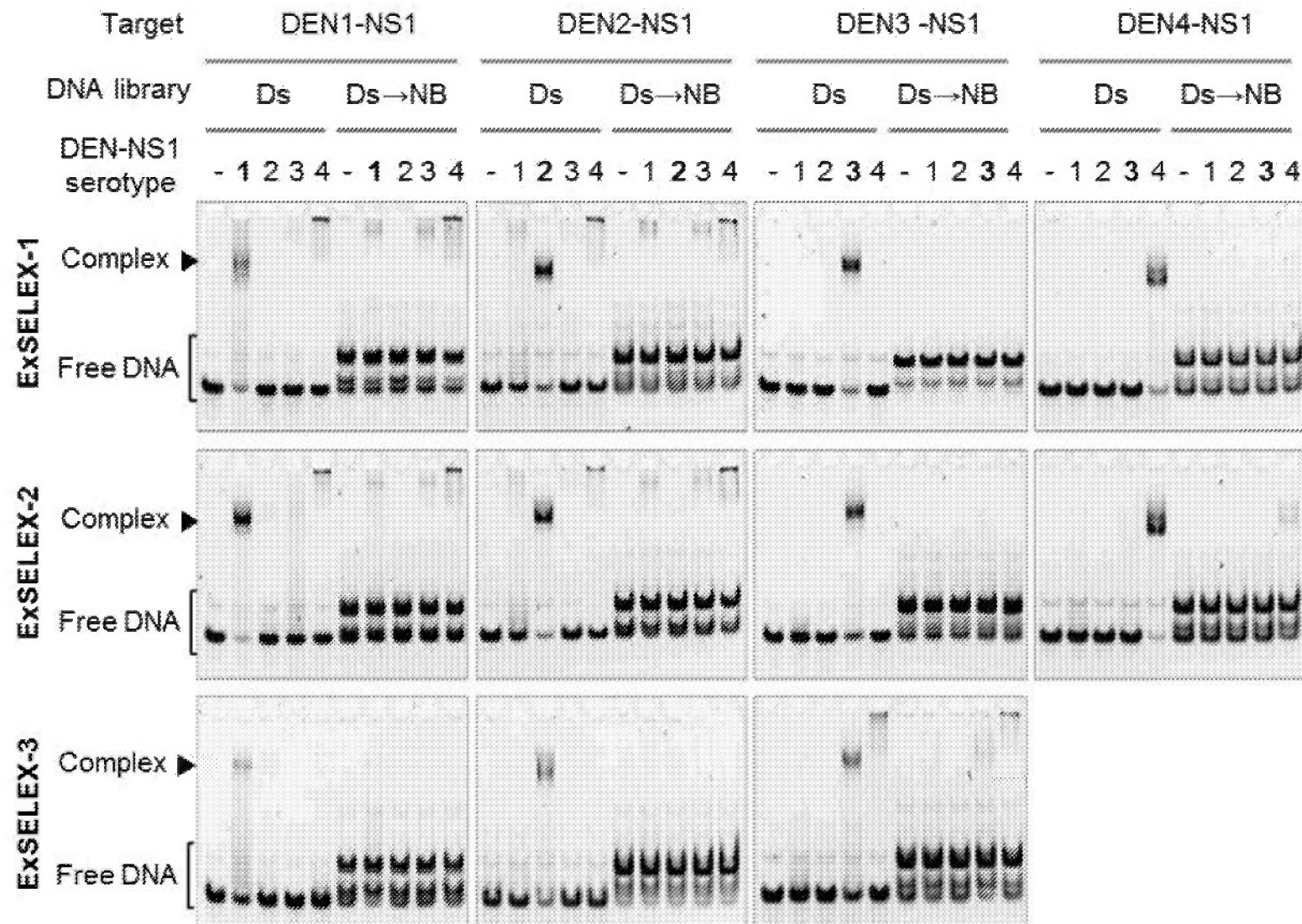


FIG. 2

			TTTCGCACTCCATGATATGGTCTACTG - [N ₄₂] - GACAAGCGGAGTAGTTAGACCGTCAAA
			Random region
ExSELEX-Target	Family	Ratio (%)	
ExSELEX-1-D1	D1-1	10.01	TGTGAxGTCCTACAATGGACTGGTGTxCTCGGxATGGCCATT
ExSELEX-1-D1		8.79	GCAGCTATGCTCAAGATCCCTGGTGTxCTCGGxATGGGACTT
ExSELEX-1-D1		7.39	TCCGCTTAGGCxAGCTGCCTGGTGTxCTCGGxATGGTCTGTGC
ExSELEX-1-D1		2.63	CCGTAACGTCxGGTTCGCTGGTGTxCTCGGxATGCTGATCCC
ExSELEX-1-D1		2.52	CACTGGTGTxCTCGGxATGGGAGTGACCATATTTCACTGGA
ExSELEX-1-D1		3.75	TACTGTCCGCATGTCxGTGCTGGTGTxCTCGGxATGCTACGT
ExSELEX-1-D1		1.68	GAGAGxATGCGCTGGTGTxCTCGGxATGCGCTCACTTCATTA
ExSELEX-1-D1	D1-2	10.62	AGGAGCGCATGTCGAGATACCAACCxCCATCCAATCxTTCTT
ExSELEX-1-D1		2.79	CAGCATGTCACTGCGxCCAATCxACAGCCAAACAAAGCAAGT
ExSELEX-1-D1		2.46	GCTTGTGCTGCGCGCCAATCxCCTATCCAACCxTCGTGTAGG
ExSELEX-2-D1	D1-3	54.58	ACGCCGGGGCCCGTAXTCAGACGTATACxATCAGGGGCACAT
ExSELEX-2-D1	D1-4	22.71	CCTGCACTGCCTCTGxAGCCCAACCxCCCATCCAATCGCTCA
ExSELEX-2-D1		11.73	TCTAAxGTCATGAGCCCAACCxCCCATCCAATCGCGATTATA
ExSELEX-2-D1		2.14	GCCGGxAGTCGCTACCAATCTAC-CCAACCATGCGxCATGCAC
ExSELEX-2-D1		1.75	CTGCTTTGTACAGGAGx-CAATCTAG-CCAACCGTCCGCACTG
ExSELEX-2-D1		1.34	ATTGTCCATAxTCGGTGGCAxTGGCAAGGTTxAGGTTATCCG
ExSELEX-2-D1			CAGCTAAGTCCAAACCACGCCAATCxAAGCGGCTGCxATGTA
ExSELEX-3-D1	D1-5	8.23	GCGACxGCGCGTCGATTGxCCAATCTTAGCCAAACCAAAATT
ExSELEX-3-D1		7.88	ACGAGCTTAGGACCTxGTACCAACCCCTCCAATCxAATTAGG
ExSELEX-3-D1		6.10	GACGGTTGTTAACGAxGTCCAACCAAGTCCCAATCxAACAAGTT
ExSELEX-3-D1		5.89	GGTAGCGCGGGAGGCxGTCCAACCTAT-CCAATCxACAGTCCG
ExSELEX-3-D1		4.11	GTCCATFGAACTGAAxACCCAATCACTCCAAACxGTTGAAG
ExSELEX-3-D1		3.31	TCCGTxAAGGTTGTGCACCCAACCAAGCTCCAATCSTxGCACA
ExSELEX-3-D1		3.22	ATACGxATTGACAAGGCCxCCAACCAAA-CCAATCCACGGCCG
ExSELEX-3-D1	D1-6	3.20	CTCTGTTTGTxAGGAGAGCCAACCAAGT-CCAATCCTCACAAC
ExSELEX-3-D1		2.75	CTACGGTTGGCGGATxTTACCAACCTCCTCCAATCxtAGTGC

FIG. 3

			TTTCGCACTCCATGATATGGTCTACTG - [N ₄₂] - GACAAGCGGAGTAGTTAGACCGTCAAA
			Random region
ExSELEX-Target	Family	Ratio (%)	
ExSELEX-1-D2	D2-1	34.41	GTCCGxCTGGGAACAAGxGGCGGGAGGGAxGGGT-GTGGGTGC
ExSELEX-1-D2		7.66	AGGGAGTAGxGAGGACCAAGxG-C-GGA-GGAxGGCG-GCGGGTGG
ExSELEX-1-D2		1.88	ATTATGGCTCxAGTCAAGxGGCAGTTGGGAxGGGTGTGGGT
ExSELEX-1-D2		17.36	TGGGAAGTCAxGGGGGCxTGGTGTAGTCGGxAGACGGGAGTT
ExSELEX-1-D2		1.13	ACGTCxAGGTTGGAAAGGxACGGCCGTxAATACATGCACAAG
ExSELEX-1-D2		20.75	CTCTAACCAACAGAGGCCAGxCCAATCTTA-CCAACCxCCCTG
ExSELEX-1-D2		2.85	AGTGTGACGGGGAGxCCAATCCGC-CCAACCxCCCTCCCCTA
ExSELEX-1-D2		3.54	CTACGTGAAGxTCCAATCTCTACCAACCTGTxTCACGAxAGT
ExSELEX-1-D2		2.79	ATAGCCTGTCCGCTTxxGTCGCCCAACCCGTGxTCCAATCCAA
ExSELEX-1-D2		1.40	AAAGGCGCGTxxGTAAGTGTCCAATCCGCGxTCCAACCACAGA
ExSELEX-2-D2	D2-2	23.26	GAATAACAAGTCCGTGCxGTCCCAATCCGTGxTCCAACCCC
ExSELEX-2-D2	D2-3	21.67	GTCTACAxGCAACGCTTTTCGxCCAACCCGTGxTCCAATCCCA
ExSELEX-2-D2	D2-4	11.97	CTTCACGAGTCAAGGxCTCCAATCCGTGxTCCAACCAGTTTT
ExSELEX-2-D2		6.97	ACCGCGAAAGTAGGCxTCAACCCGTGxTCCAATCCGCGCCGA
ExSELEX-2-D2		10.59	GCGCTCGGCTCGCGCxTCAATCCGTGxTCCAACCCCGCGCGA
ExSELEX-2-D2	D2-5	11.63	TGGCTGGGCCAxGCGTGTCTCAACCTTACCAATCTGxCACGCG
ExSELEX-2-D2	D2-6	8.27	TAGATxTTGTGAGAGxGCACCAACCAACCAATCTGxCTTGA
ExSELEX-2-D2		4.16	ACCCGTCGACCTCTCACCCAACCATCCCAATCxAGCATAAGA
ExSELEX-3-D2	D2-1	65.94	GTCCGxCTGGGAACAAGxGGCGGGAGGGAxGGGTGTGGGTGC
ExSELEX-3-D2	D2-2	1.53	GAATAACAAGTCCGTGCAGTCCCAATCCGTGxTCCAACCCC
ExSELEX-3-D2		7.99	AGACGCGCAGGACTAxGACCAATCTTACCAACCAxCTCAAGG
ExSELEX-3-D2		2.96	CCCGAxTTGCCTGCCCCxCCAACCCAGCCCAATCCATGGGGCG
ExSELEX-3-D2		2.84	CCTTGxTATGTCTTCTACCAACCAACCAATCTAxGAAGACA
ExSELEX-3-D2		2.65	CTGGCxGGGGCGAGGGCCAAACAGACCAATCCCxCGAGACCA
ExSELEX-3-D2		1.76	CACGCGAGTCxGGAAAGxCCAACCCCTACCAATCATCTTACCT
ExSELEX-3-D2		1.56	TATTCAGCxTTGTACCGxCCAATCACCAACCAACAGAGGTA

FIG. 4

			TTTCGCACTCCATGATATGGTCTACTG - [N ₄₂] - GACAAGCGGAGTAGTTAGACCGTCAAA
ExSELEX-Target	Family	Ratio (%)	Random region
ExSELEX-1-D3	D3-1	89.07	ATAGTACTCCxGTTTAACTCTGAxACTTGACGTCCATTTCATA
ExSELEX-1-D3		3.09	CTGAAGCTCCGTGCGxCCCCC-GCGGTTTGTTAAAxCCCTTTA
ExSELEX-1-D3		2.64	CTTGCxCCCCCGCGGTTTGTTTAAATGGxAGAATTCTGTAA
ExSELEX-1-D3		2.00	GTCGCTTTGCxCCCCGTCCGGTGACTGAAAATAxCACGTCAG
ExSELEX-2-D3	D3-2	81.23	AAGTGTGTCATCTAxCCTGGCCxTGTGGTACTGTAACGGCT
ExSELEX-2-D3	D3-3	15.56	GGGCTxGGTCTTCCGTxTGCAGATTAACTTFCGTGCCAGTAA
ExSELEX-3-D3	D3-1	34.13	ATAGTACTCCxGTTTAACTCTGAxACTTGACGTCCATTTCATA
ExSELEX-3-D3		27.21	TACCACTTGCAATGGACGCGxCGTATGGTGGxTCGGGGAATG
ExSELEX-3-D3		8.17	GTGTAATCCGGTTGTGAGACGGCGGAATGxATTTGGAAAGGC
ExSELEX-3-D3		8.07	CGCGCTTGGGxGACGAATTTGTACAGCGTATATCCAxCAGACG
ExSELEX-3-D3		4.85	CTCTGTGCCGTCGAGxGACCCTTAGGTTTCxGAGCTGCTAACC
ExSELEX-3-D3		2.83	CGTGGTCGAGxGGGCGTGTTTAAACGCATCACAGCCGTAGCC
ExSELEX-3-D3		3.14	ACACCGTCTxTGTATGTCGCATTCTGACTCTAxCCCCGACA
ExSELEX-3-D3		1.45	CTCTGCGCGTGGTGCxAAACTCGGGCXTTGTAATCAACTTTT

FIG. 5

			TTTCGCACTCCATGATATGGTCTACTG - [N ₄₂] - GACAAGCGGAGTAGTTAGACCGTCAAA	
ExSELEX-Target	Family	Ratio (%)	Random region	
ExSELEX-1-D4	D4-1	39.19	TCTCAACGGTTGTCAAACGGxTATCACGGCxACACACCTGCG	
ExSELEX-1-D4		13.74	ACTTTGCGCGAAAACAGCTTTATCATATAAACGCxTATCACG	
ExSELEX-1-D4		2.38	CGGTAxCGCTAAAGGACGGxTATCAAATTAAAACACCTCCTT	
ExSELEX-1-D4		9.18	TAAGAACAGCGCTGTGAACGCxTATCAAATCxAACAGCTTC	
ExSELEX-1-D4	D4-2	2.88	TCCTCTAAAGCTGTCCGCGCxTATCAAAGGAxAAACAGCCGA	
ExSELEX-1-D4		23.92	TCACAxATCGCCGTAAAGxCGAAGAGCTGCGGAATCTAAGGT	
ExSELEX-1-D4		4.40	TGGGGxGCGTGAGCTTGGCAAGGGxTTGGxTAGGGCTGGCAA	
ExSELEX-1-D4		1.29	GTCCCTCGTCCAACCGTGCCxACTCTCACTxGAGACCCAATC	
ExSELEX-2-D4	D4-3	21.96	GAGGAGACGTAACGCxTATCAAATCxAACAGCTTAGGGTCC	
ExSELEX-2-D4		17.04	TGGCGCGAGGGAATCxACGCxTATCAAATAxAACAGCTAAT	
ExSELEX-2-D4		8.60	TCGCACGTTAAACGCxACGGxTATCAAATCxAACACCTGAG	
ExSELEX-2-D4		1.43	GGCACCCATTGTCTCAACGCxTATCAAATCxAACAGCTGA	
ExSELEX-2-D4	D4-4	23.35	TATAATCCGCxTTCGTCTATGTGGxTTGGATCTGGGTCTGGCA	
ExSELEX-2-D4		7.29	CATAGCGGCAxCGGTCGGTGGGxTTGGCxGTGGGGCTGGCAC	
ExSELEX-2-D4	D4-5	3.50	CCCAAxCTTGTCTGTAAGGGxTTGGxTAGGGCTGGCAAAAAA	
ExSELEX-2-D4		2.09	GTCTGTGGGGxCTTGAAGGGxTTGGxTAGGGCTGGCAAAACAA	
ExSELEX-2-D4		1.51	GTTTTxGGTTAGTTCTTTGGGxTTGGCAxCGGGCCTGGCGTG	
ExSELEX-2-D4		1.00	CGACGGCTTAxACGTCAATGGGxTTGGCTGGGGGTCTGGCCT	

FIG. 6

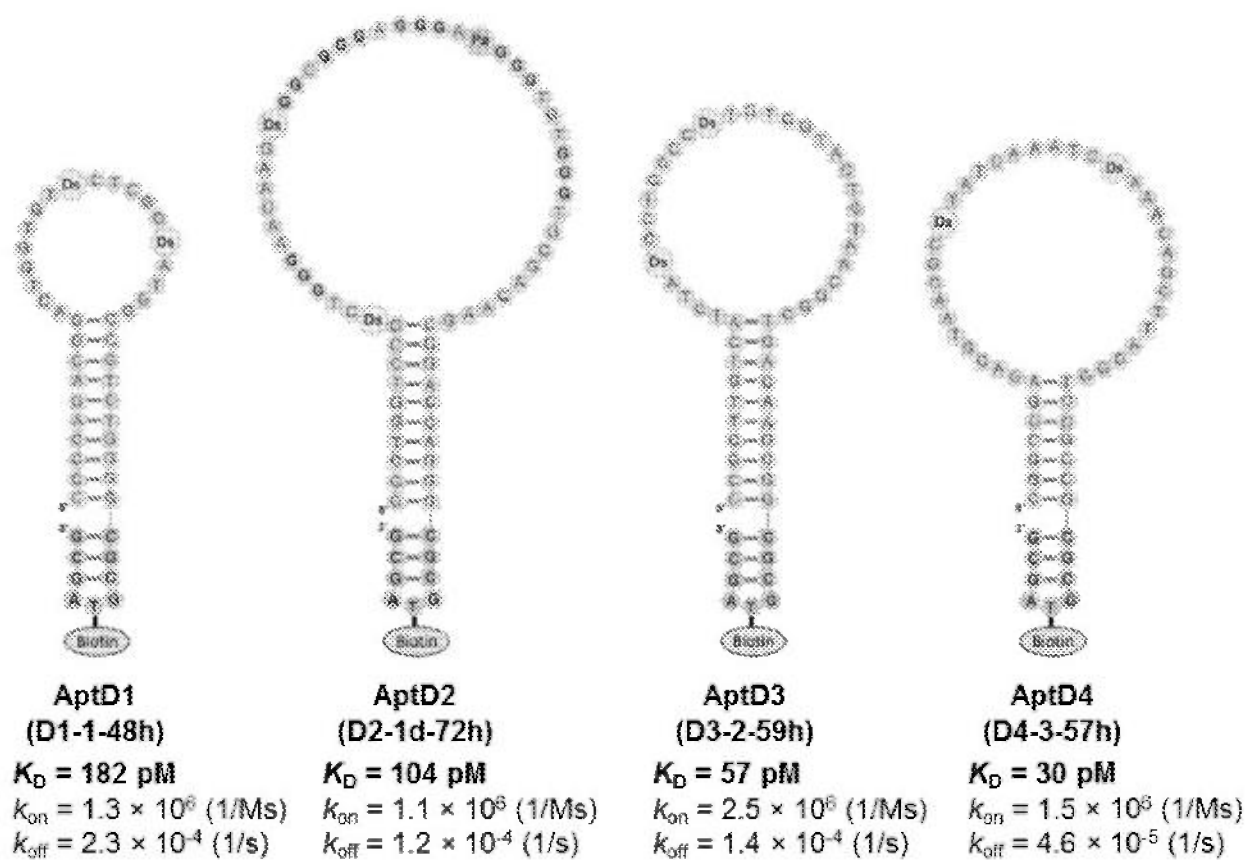
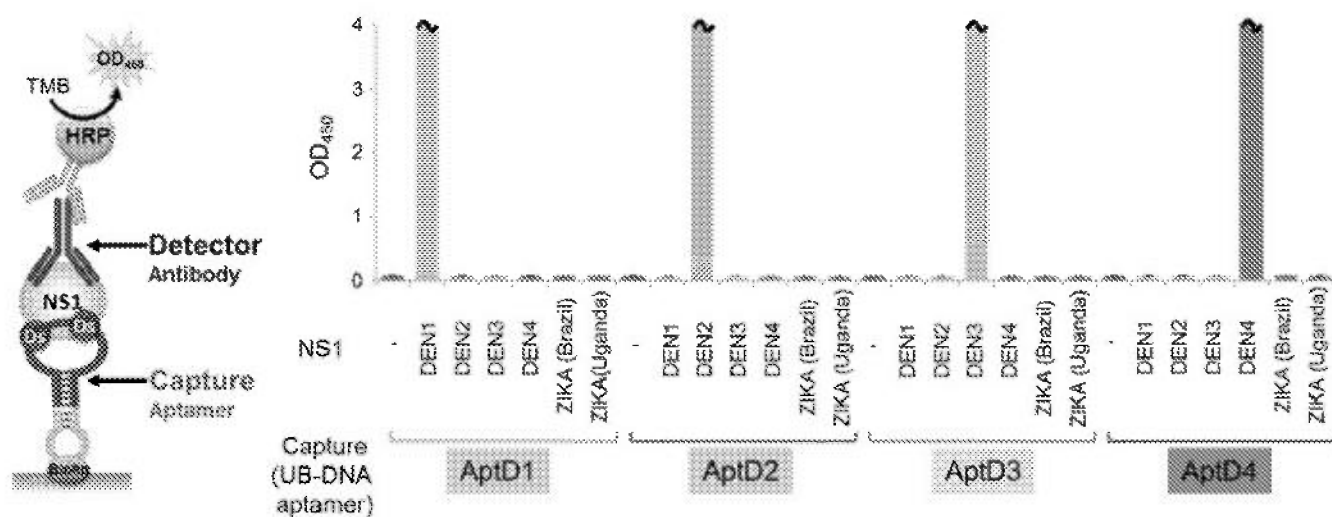
a**b**

FIG. 7

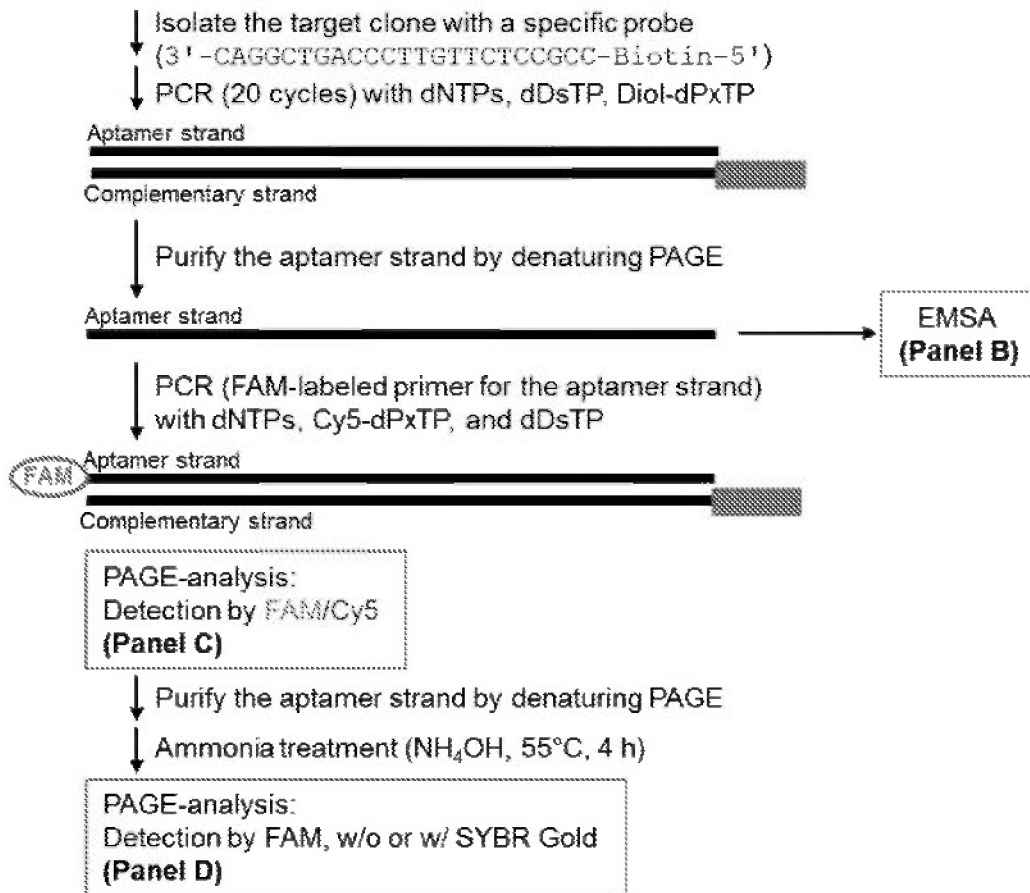
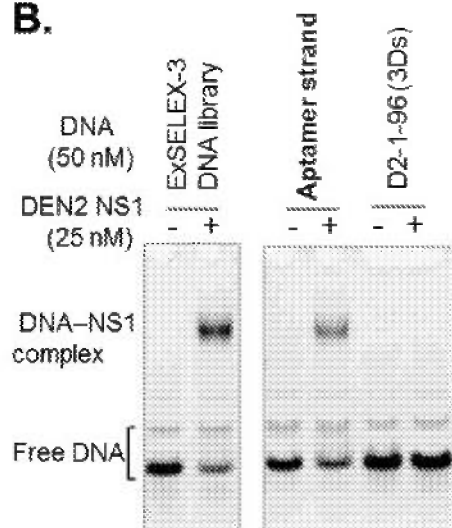
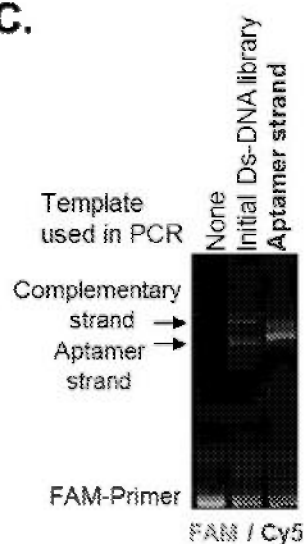
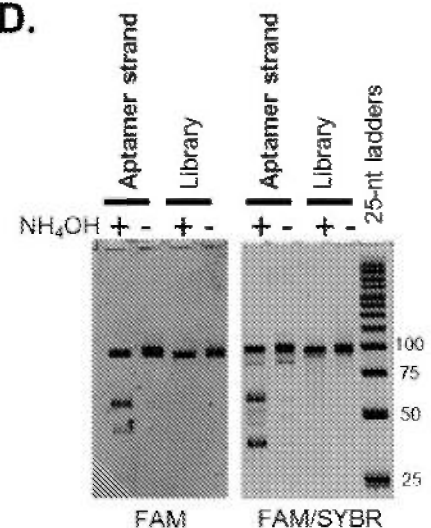
A.**Enriched DNA libraries targeting DEN-2 NS1 through ExSELEX (Round 7 in ExSELEX-3)****B.****C.****D.**

FIG. 8

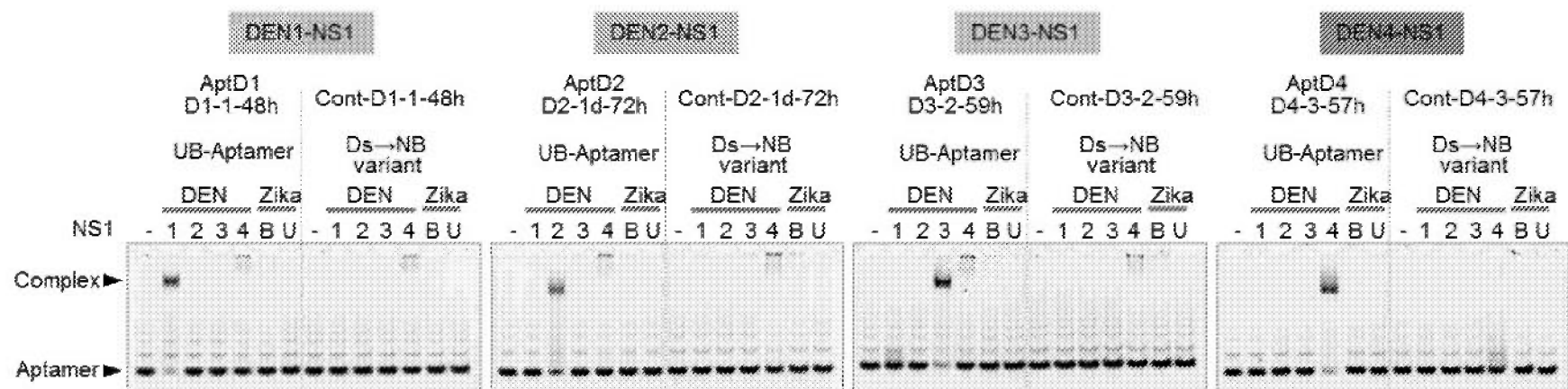


FIG. 9

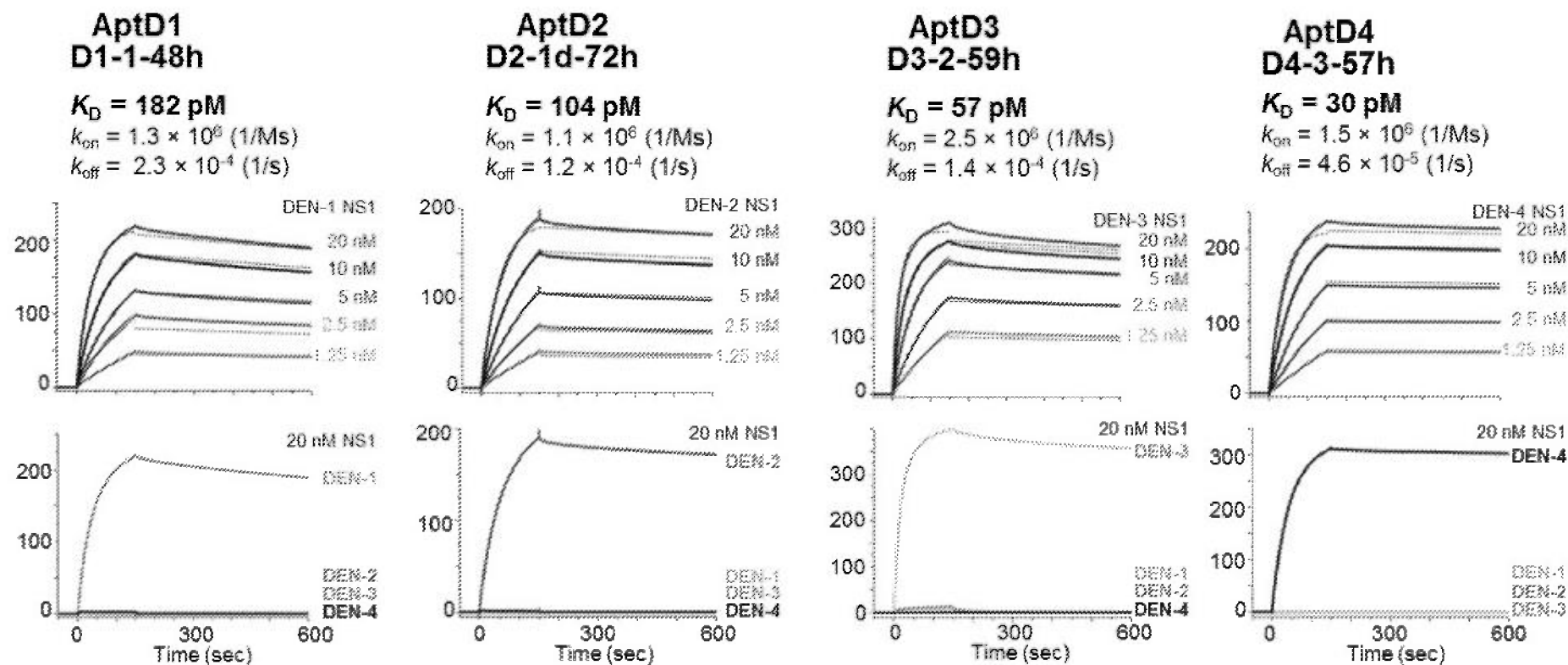


FIG. 10

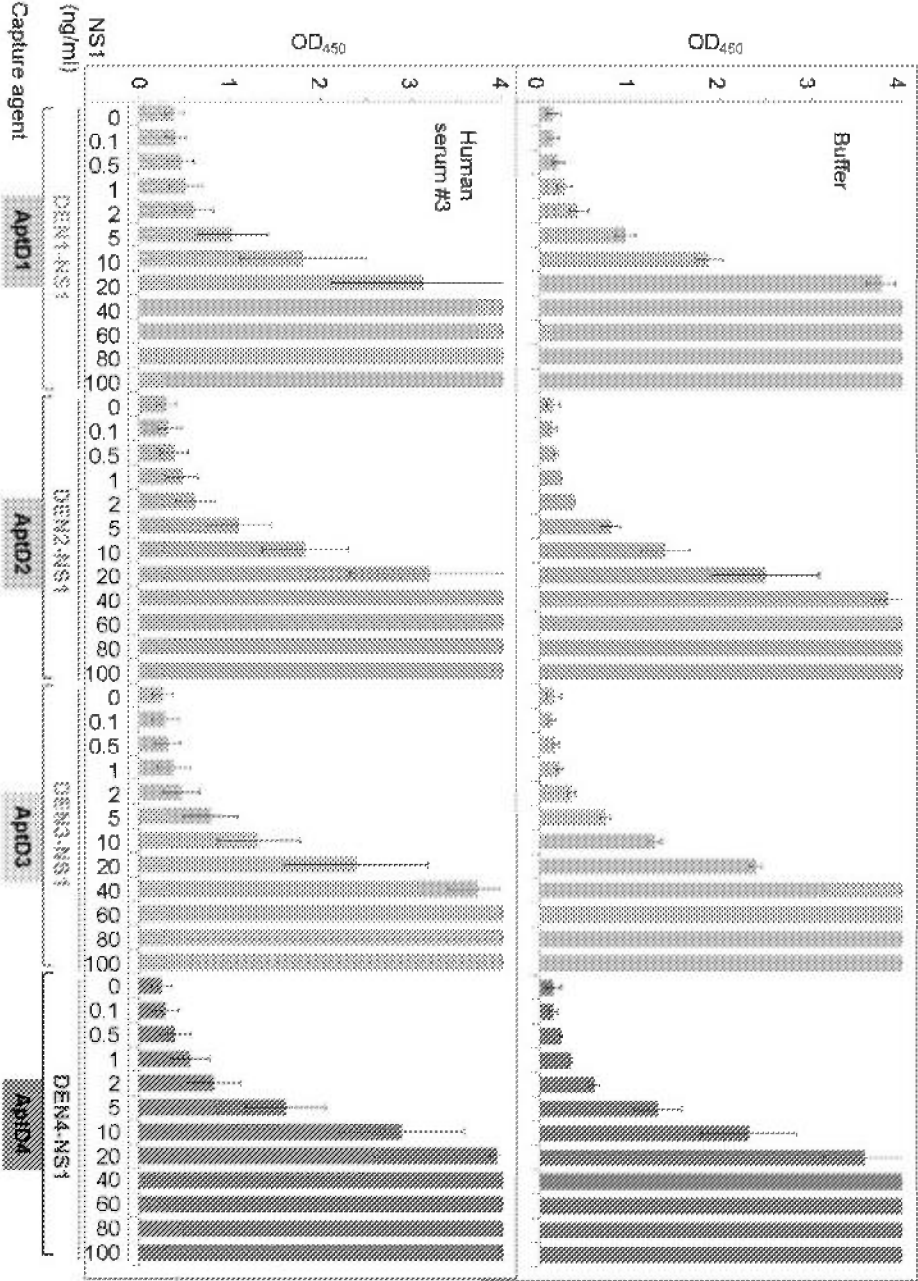


FIG. 11

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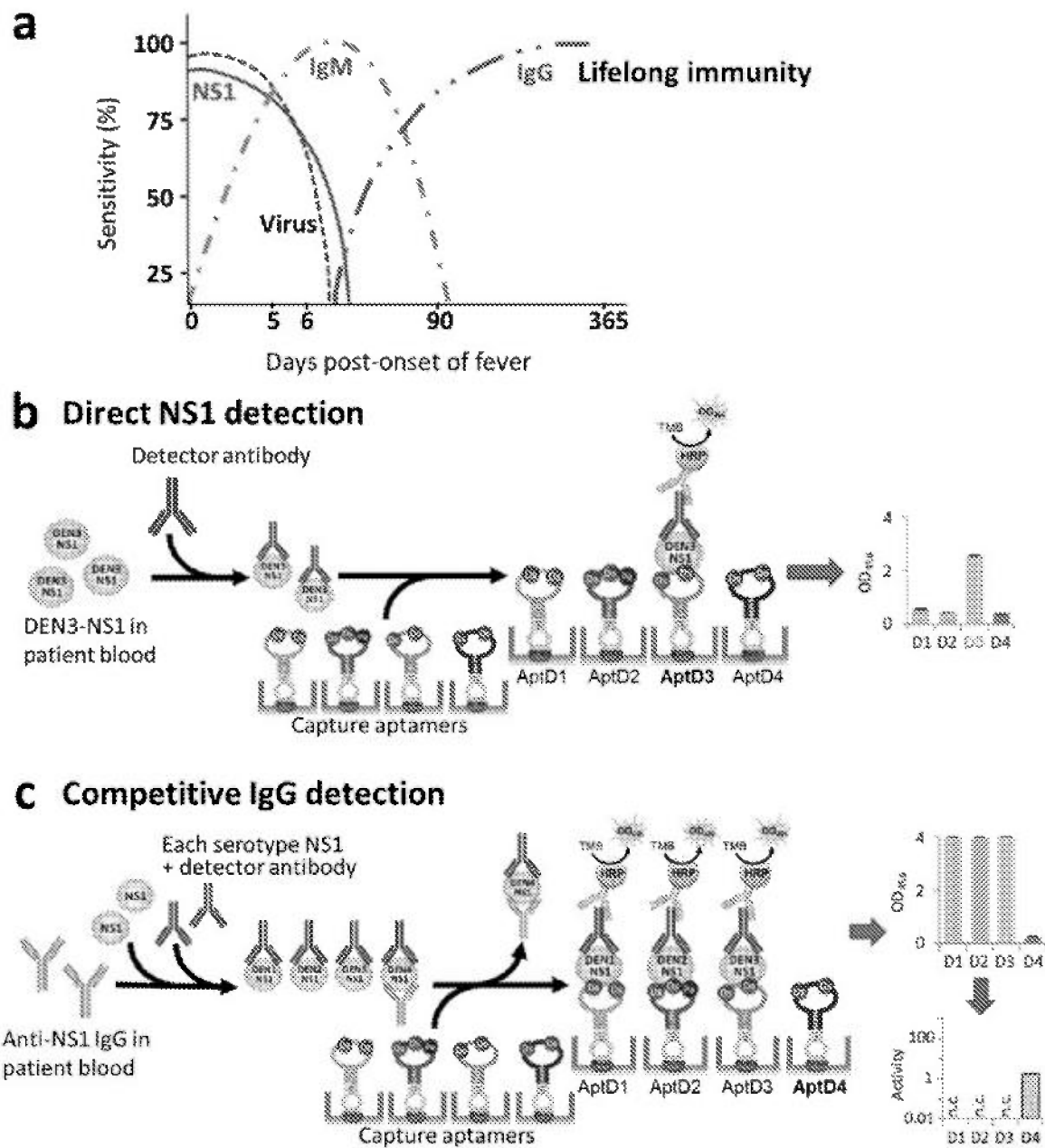


FIG. 12

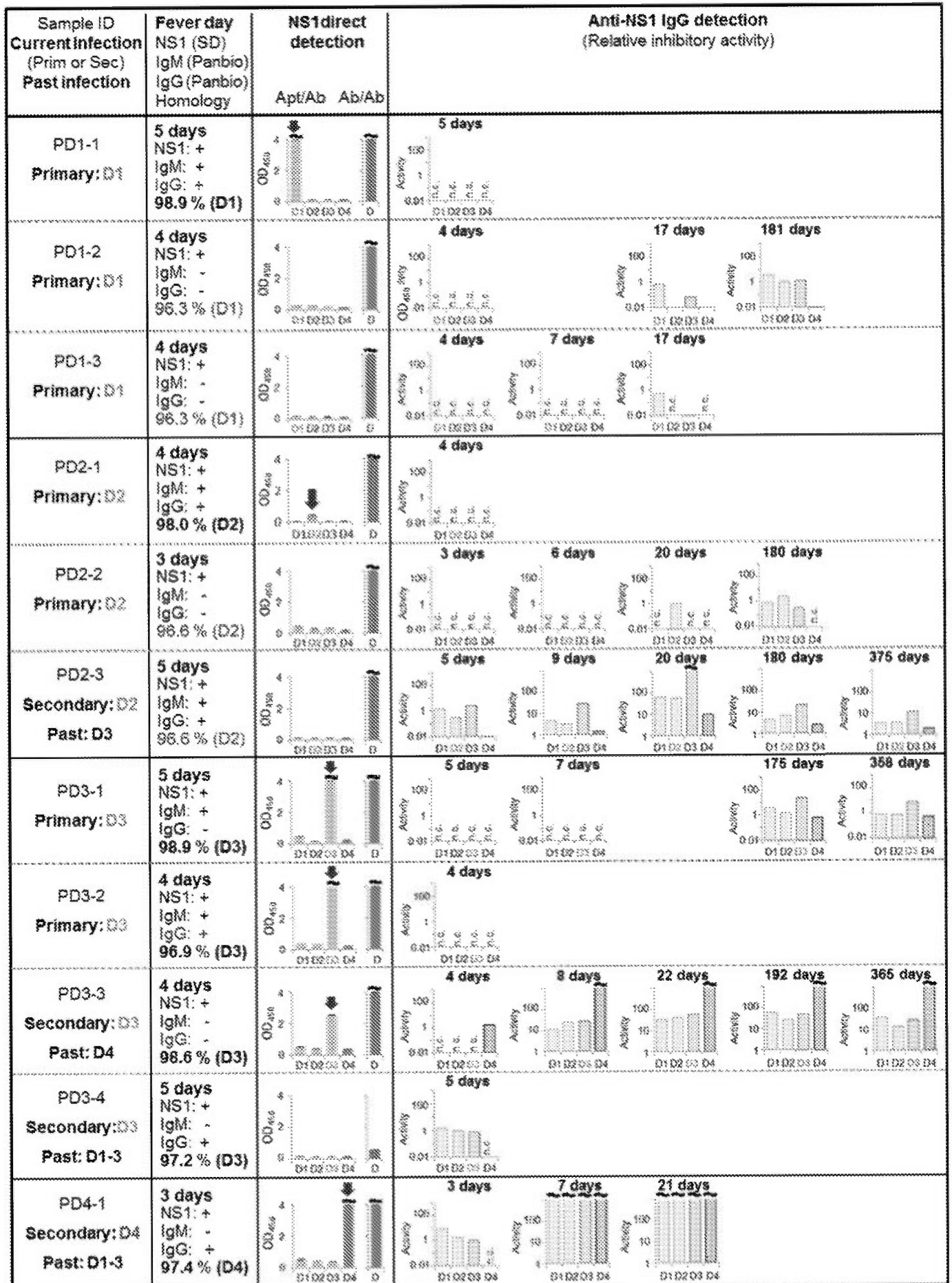


FIG. 13

A CLUSTAL O(1.2.4) multiple sequence alignment
The quality of sequencing in the gray part of PD3-4 is low.

D1 target	DSGGVINWAGRELKCGSGIFVYNEVHTWTE	QYNFQADSPNRLSAAIGHANEGVGGIRSA	TRLENIMWQISNELNHLLENDSFTVVV	90
PD1-1	*S*VIN*AG*.....VTNE*.....	*K*AD*KR*SA*GR*WEE*V*.....	*L*IN*..SN*..RI*..L*NDK*F*VVV	90
PD1-2/PD1-3	*S*VIN*AG*.....VTNE*.....	*K*AD*KR*SA*GR*WEE*V*.....	*L*IN*..SN*..RI*..L*NDK*F*VVV	90
D2 target	*S*VVS*KN*.....ITDN*.....	*K*PE*SK*AS*GR*WEE*I*.....	*L*LN*..TP*..HI*..S*NEVK*IMT	90
PD2-1	*S*VVS*KN*.....ITDN*.....	*K*PE*SK*AS*GR*WEE*I*.....	*L*LN*..TP*..HI*..S*NEVK*IMT	90
PD2-2/PD2-3	*S*VVS*KN*.....ITDN*.....	*K*PE*SK*AS*GR*WEE*I*.....	*L*LN*..TP*..HI*..S*NEVK*IMT	90
D3 target	*M*VIN*KG*.....VTNE*.....	*K*AD*KR*AT*AG*WEN*V*.....	*M*LL*..AN*..YI*..W*NNIK*L*VVV	90
PD3-1	*M*VIN*KG*.....VTNE*.....	*K*AD*KR*AT*AG*WEN*V*.....	*M*LL*..AN*..YI*..W*NNIK*L*VVV	90
PD3-2	*M*VIN*KG*.....VTNE*.....	*K*AD*KR*AT*AG*WEN*V*.....	*M*LL*..AN*..YI*..W*NNIK*L*VVV	90
PD3-3	*M*VIN*KG*.....VTNE*.....	*K*AD*KR*AT*AG*WEN*V*.....	*M*LL*..AN*..YI*..W*NNIK*L*VVV	90
PD3-4	*M*VIN*KG*.....VTNE*.....	*K*AD*KR*AT*AG*WEN*V*.....	*M*LL*..AN*..YI*..W*NNIK*L*VVV	90
D4 target	*M*VAS*EG*.....VVDN*.....	*K*PE*AR*AS*LN*WED*V*.....	*L*VN*..TN*..TV*..Q*GHLL*VVA	90
PD4-1	*M*VAS*EG*.....VVDN*.....	*K*PE*AR*AS*LN*WED*V*.....	*L*VN*..TN*..TV*..Q*GHLL*VVA	90
D1 target	GDVSGILAQGKNNIRPQPMENKYSWKSQK	AKIIGADVQNTTFIIDGPNTEPCPNQRAW	MIWSEVEDYGFPIFTNIIWLALRDSYTVQCD	180
SD1-1	*I*ILAQ*EMIR*QPMER*.....S*..	*I*IGADV*QT*..I*..D*F*..D*Q*..	*I*W*..V*..I*..L*..L*PSY*TCV*	180
PD1-2/PD1-3	*I*ILAQ*EMIR*QPMER*.....S*..	*I*IGADV*QT*..I*..D*F*..D*Q*..	*I*W*..V*..I*..L*..L*PSY*TCV*	180
D2 target	*I*IMQA*RAIR*QPTAL*.....T*..	*K*ISTESH*QT*..L*..E*..A*..NTN*..	*S*..V*..V*..L*..L*AKK*QCV*	180
PD2-1	*I*IMQA*RAIR*QPTAL*.....T*..	*K*ISTESH*QT*..L*..E*..A*..NTN*..	*S*..V*..V*..L*..L*AKK*QCV*	180
PD2-2/PD2-3	*I*IMQA*RAIR*QPTAL*.....T*..	*K*ISTESH*QT*..L*..E*..A*..NTN*..	*S*..V*..V*..L*..L*AKK*QCV*	180
D3 target	*I*VLEQ*RTLT*QPMEL*.....T*..	*K*IVTAEQ*SS*..I*..N*P*..SAS*..	*VW*..V*..V*..L*..L*REV*YTQ*	180
PD3-1	*I*VLEQ*RTLT*QPMEL*.....T*..	*K*IVTAEQ*SS*..I*..N*P*..SAS*..	*VW*..V*..V*..L*..L*REV*YTQ*	180
PD3-2	*I*VLEQ*RTLT*QPMEL*.....T*..	*K*IVTAEQ*SS*..I*..N*P*..SAS*..	*VW*..V*..V*..L*..L*REV*YTQ*	180
PD3-3	*I*VLEQ*RTLT*QPMEL*.....T*..	*K*IVTAEQ*SS*..I*..N*P*..SAS*..	*VW*..V*..V*..L*..L*REV*YTQ*	180
PD3-4	*I*VLEQ*RTLT*QPMEL*.....T*..	*K*IVTAEQ*SS*..I*..N*P*..SAS*..	*VW*..V*..V*..L*..L*REV*YTQ*	180
D4 target	*I*VLEQ*RTLT*QPMEL*.....T*..	*K*IVTAEQ*SS*..I*..N*P*..SAS*..	*VW*..V*..V*..L*..L*REV*YTQ*	180
PD4-1	*I*VLEQ*RTLT*QPMEL*.....T*..	*K*IVTAEQ*SS*..I*..N*P*..SAS*..	*VW*..V*..V*..L*..L*REV*YTQ*	180
D1 target	MRIMSAIINDSHAVHAINNYWIESSEKNTW	KLARASFIEVTPCINYSKMLWSKWLSEK	MIIPKIEGGPIQHNRPFGFTQTGAPWGL	270
PD1-1	*H*..I*..SK*.....EK*ET*	*K*..F*..P*..I*..S*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
PD1-2/PD1-3	*H*..I*..SK*.....EK*ET*	*K*..F*..P*..I*..S*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
D2 target	*K*..I*..NR*.....AL*DT*	*K*..F*..N*..H*..P*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
PD2-1	*K*..I*..NR*.....AL*DT*	*K*..F*..N*..H*..P*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
PD2-2/PD2-3	*K*..I*..NR*.....AL*DT*	*K*..F*..N*..H*..P*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
D3 target	*H*..V*..ER*.....QK*GS*	*K*..L*..T*..T*..P*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
PD3-1	*H*..V*..ER*.....QK*GS*	*K*..L*..T*..T*..P*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
PD3-2	*H*..V*..ER*.....QK*GS*	*K*..L*..T*..T*..P*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
PD3-3	*H*..V*..ER*.....QK*GS*	*K*..L*..T*..T*..P*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
PD3-4	*H*..V*..ER*.....QK*GS*	*K*..L*..T*..T*..P*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
D4 target	*H*..V*..ER*.....QK*GS*	*K*..L*..T*..T*..P*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
PD4-1	*H*..V*..ER*.....QK*GS*	*K*..L*..T*..T*..P*..S*..S*..E*	*I*..K*..I*..Y*..P*..P*..TA*..	270
D1 target	QKLELDLPCBQYTVVDHNGGNRPSKRY	PTVTKNTIHEWCHRSYLPPLRPKCHDKIN	YKCHIRPVHKKSENLAKSKVSA	352
SD1-1	*K*..L*..DL*..E*..V*..D*..H*..G*..	*P*..T*..V*..K*..N*..T*..I*..H*..E*..	*Y*..K*..C*..H*..I*..R*..P*..V*..H*..	352
PD1-2/PD1-3	*K*..L*..DL*..E*..V*..D*..H*..G*..	*P*..T*..V*..K*..N*..T*..I*..H*..E*..	*Y*..K*..C*..H*..I*..R*..P*..V*..H*..	352
D2 target	*K*..M*..DF*..D*..V*..V*..D*..G*..	*A*..S*..L*..I*..T*..E*..L*..Y*..R*..	*I*..S*..L*..I*..T*..E*..L*..Y*..R*..	352
PD2-1	*K*..M*..DF*..D*..V*..V*..D*..G*..	*A*..S*..L*..I*..T*..E*..L*..Y*..R*..	*I*..S*..L*..I*..T*..E*..L*..Y*..R*..	352
PD2-2/PD2-3	*K*..M*..DF*..D*..V*..V*..D*..G*..	*A*..S*..L*..I*..T*..E*..L*..Y*..R*..	*I*..S*..L*..I*..T*..E*..L*..Y*..R*..	352
D3 target	*K*..L*..NY*..E*..V*..I*..S*..G*..T*..	*V*..S*..L*..I*..T*..E*..L*..Y*..R*..	*I*..S*..L*..I*..T*..E*..L*..Y*..R*..	352
PD3-1	*K*..L*..NY*..E*..V*..I*..S*..G*..T*..	*V*..S*..L*..I*..T*..E*..L*..Y*..R*..	*I*..S*..L*..I*..T*..E*..L*..Y*..R*..	352
PD3-2	*K*..L*..NY*..E*..V*..I*..S*..G*..T*..	*V*..S*..L*..I*..T*..E*..L*..Y*..R*..	*I*..S*..L*..I*..T*..E*..L*..Y*..R*..	352
PD3-3	*K*..L*..NY*..E*..V*..I*..S*..G*..T*..	*V*..S*..L*..I*..T*..E*..L*..Y*..R*..	*I*..S*..L*..I*..T*..E*..L*..Y*..R*..	352
PD3-4	*K*..L*..NY*..E*..V*..I*..S*..G*..T*..	*V*..S*..L*..I*..T*..E*..L*..Y*..R*..	*I*..S*..L*..I*..T*..E*..L*..Y*..R*..	352
D4 target	*K*..I*..GE*..P*..D*..D*..D*..D*..	*A*..S*..L*..I*..T*..E*..L*..Y*..R*..	*I*..S*..L*..I*..T*..E*..L*..Y*..R*..	352
PD4-1	*K*..I*..GE*..P*..D*..D*..D*..D*..	*A*..S*..L*..I*..T*..E*..L*..Y*..R*..	*I*..S*..L*..I*..T*..E*..L*..Y*..R*..	352

B Mutated Amino Acids
(in 352 Amino Acids)

Mutated Amino Acids (in 352 Amino Acids)	4	13	7	12	4	11	6	10	9				
	D1 target	PD1-1	PD1-2 PD1-3	D2 target	PD2-1	PD2-2 PD2-3	D3 target	PD3-1	PD3-2	PD3-3	PD3-4	D4 target	PD4-1
D1_target	100.0	98.9	98.3	72.7	72.2	73.3	79.8	80.1	79.8	79.8	78.7	69.3	68.8
D2_target	72.7	73.0	72.7	100.0	98.0	96.6	73.6	74.4	73.9	73.6	73.6	72.7	72.2
D3_target	79.8	79.8	79.9	73.6	73.3	73.6	100.0	98.9	98.9	98.8	97.2	73.9	73.3
D4_target	69.3	69.3	68.8	72.7	73.0	72.4	73.9	74.2	73.0	73.9	73.9	100.0	97.4

FIG. 14

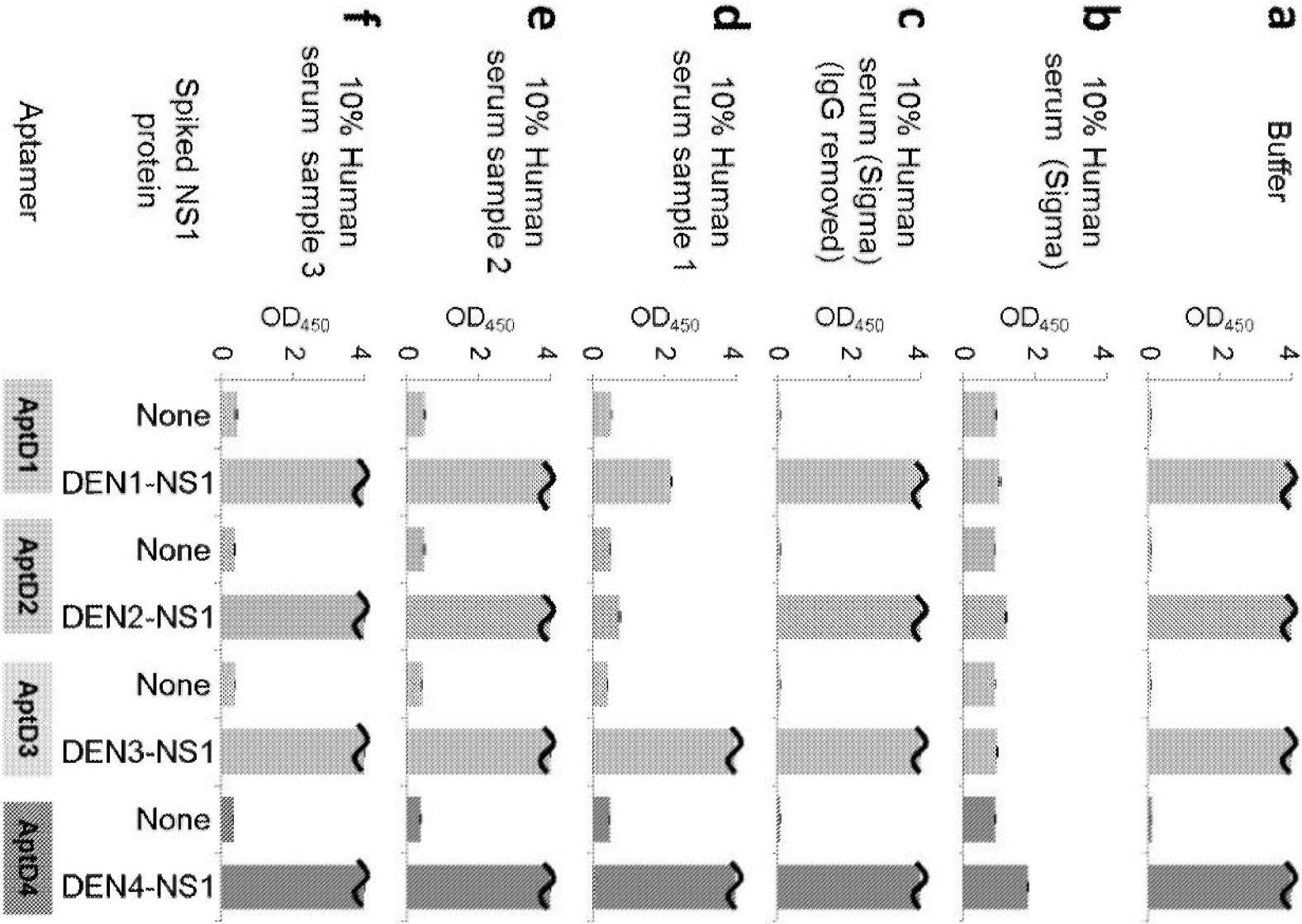


FIG. 15

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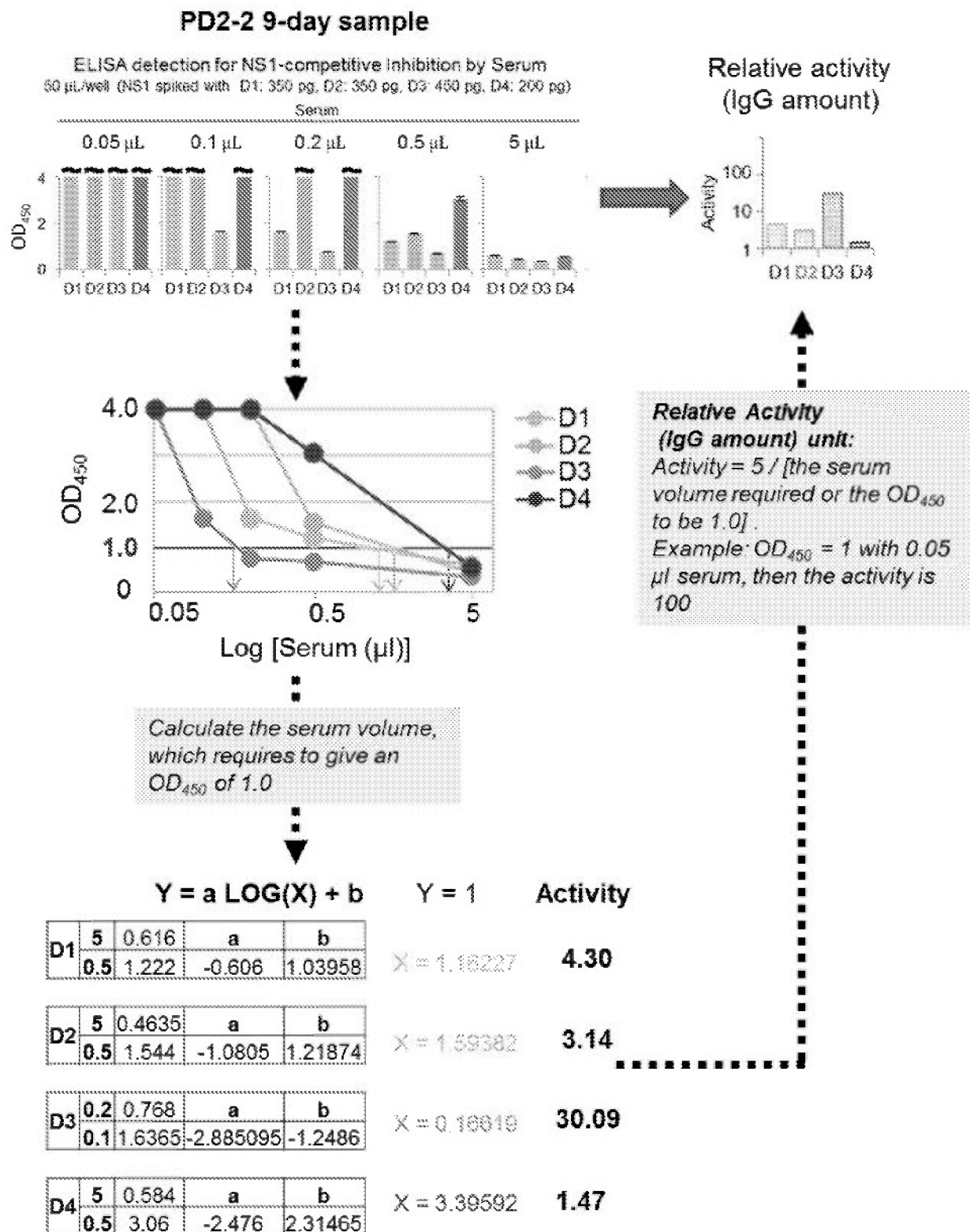


FIG. 16

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PD2-2

Fever day 5

Antibody/Antibody

Aptamer/Antibody

Fever day 9

Antibody/Antibody

Aptamer/Antibody

Fever day 20

Antibody/Antibody

Aptamer/Antibody

Fever day 180

Antibody/Antibody

Aptamer/Antibody

Fever day 375

Antibody/Antibody

Aptamer/Antibody

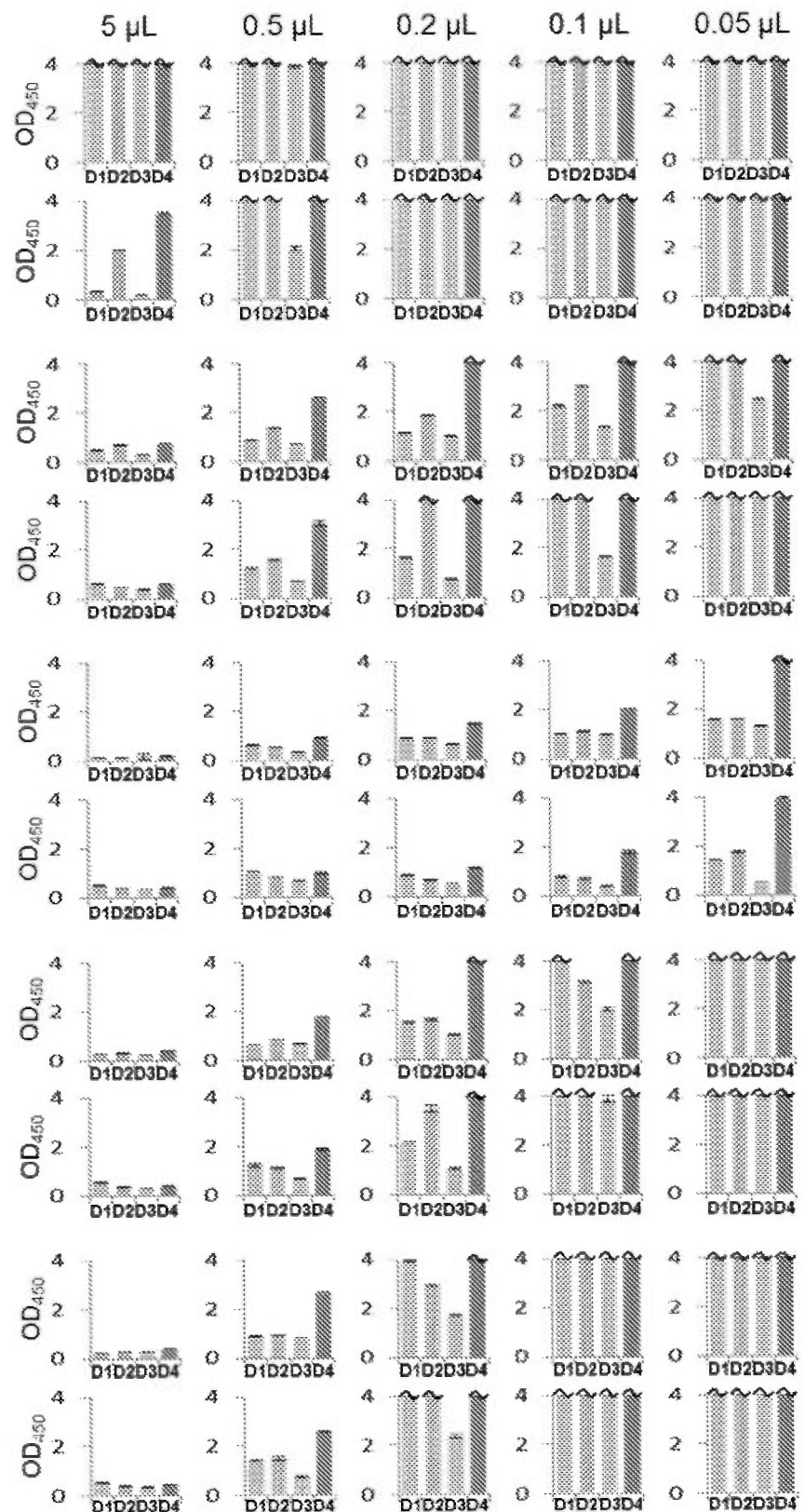


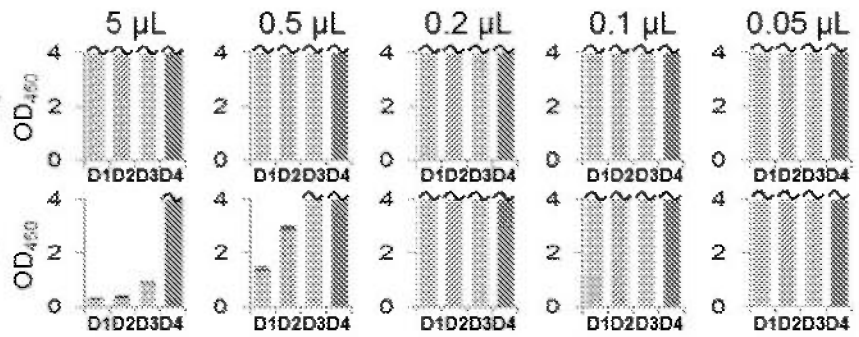
FIG. 17

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PD4-1

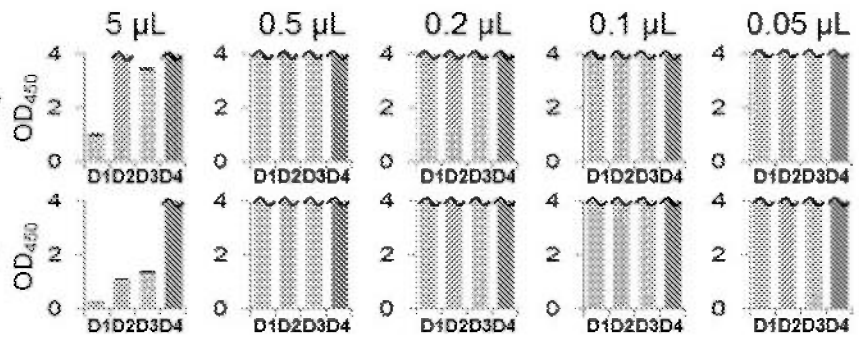
Fever day 3

Antibody/Antibody

**PD3-4**

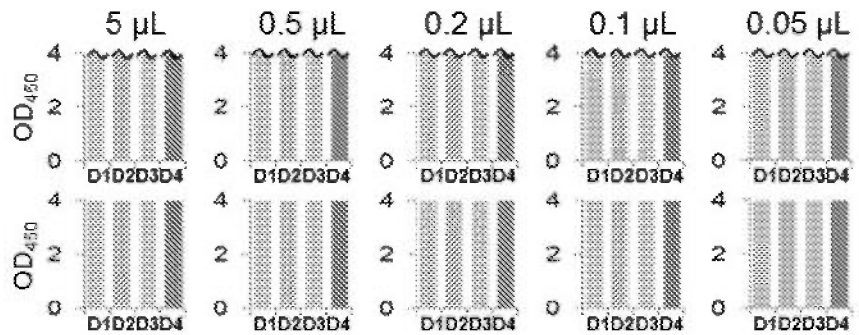
Fever day 5

Antibody/Antibody

**PD2-1**

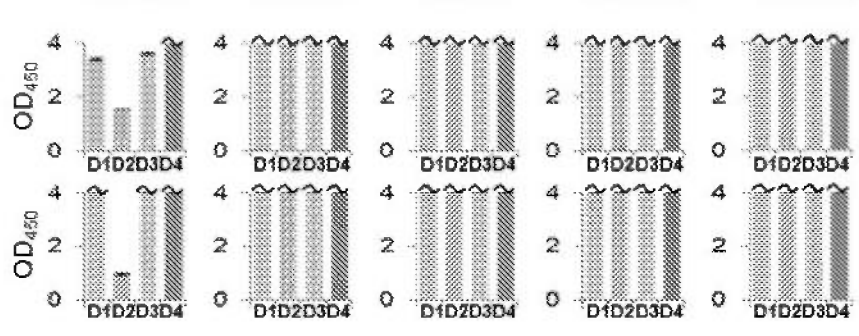
Fever day 6

Antibody/Antibody



Fever day 20

Antibody/Antibody



Fever day 180

Antibody/Antibody

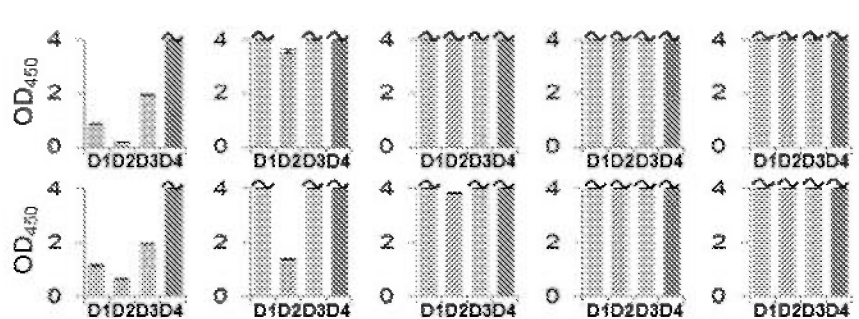


FIG. 18

D1 target	DSCVIMNIGREKCGSGTPTVNEVHTWE	QITPQADSFWLSAIGWHEGVCIESA	TULEMILNQTSNEHILLXEMTPVV	GVCSGLAQGMIRPOEHHNSKSWK	120
PDI-1	S·VIN·AG·····VTNE·····	K·AD·KR·SA·CK·KE·V·····A	L·IM···SN···HI·L·NMKT·VVV	V·V·ILAQ·PAIR·OMEH·····S	120
PDI-2/PDI-3	S·VIN·KG·····VTNE·····	K·AD·KR·SA·CK·KE·V·····A	L·IM···CN···HI·L·NMKT·VVV	N·I·IQ·PAIR·OMEH·····S	120
OD target	S·VVS·GN·····ITIN·····	K·EE·SK·AS·CK·KE·I·····V	L·LM···TE···HI·S·NEWLT·INT	K·IK·IMA·BSLR·QTEL·····T	120
PDI-1	S·VVS·KN·····ITIN·····	K·EE·SK·AS·CK·QE·I·····V	L·IM···TE···HI·S·NEWLT·INT	K·IK·IMA·BSLR·QTEL·····T	120
PDI-2/PDI-3	S·VVS·KN·····ITIN·····	K·EE·SK·AS·CK·KE·I·····V	L·IM···TE···HI·S·NEWLT·INT	K·IK·IMA·BSLR·QTEL·····T	120
D1 target	AALICADQTTI·I···R·F·EDQ··	IN·····I·····L·ARDSTQV··	HR·····I·EK·····EX·ET··	KLAR·F·····T·I·PKS·····S	240
PDI-1	AALICADQTTI·I···R·F·EDQ··	IN·····I·····L·ARDSTQV··	HR·····I·EK·····EX·ET··	KLAR·F·····T·I·PKS·····S	240
PDI-2/PDI-3	AALICADQTTI·I···R·F·EDQ··	IN·····I·····L·ARDSTQV··	HR·····I·EK·····EX·ET··	KLAR·F·····T·I·PKS·····S	240
D2 target	FMLSTEHTQT·L···S·A·NTIN··	SL·····V·····L·INEKQVF··	SK·····I·NR·····AL·DT··	KIEK·Z·····N·H·PKS·····S	240
PDI-1	FMLSTEHTQT·L···S·A·NTIN··	SL·····V·····L·INEKQVF··	SK·····I·NR·····AL·DT··	KIEK·Z·····N·H·PKS·····S	240
PDI-2/PDI-3	FMLSTEHTQT·L···S·A·NTIN··	SL·····V·····L·INEKQVF··	SK·····I·NR·····AL·DT··	KIEK·Z·····N·H·PKS·····S	240
D1 target	MIRPKISGPISQNHAPCTPTACPMNL	GKULIBDLCGTGTVVDHCNGHPSLAT	FTVTCNIHBCSCSTLPFLATKPCDCN	YGHMIFRPVKENLVKWSA	352
PDI-1	I·KING·I·····Y·E·F·TA·····	K·L·DL·E···VVD·H·GN·····	V·T·TIME·····L·EP·····	·····VK·····L·K·MS··	352
PDI-2/PDI-3	I·KING·I·····Y·E·F·TA·····	K·L·DL·E···VVD·H·GN·····	V·T·TIME·····L·EP·····	·····VK·····L·K·MS··	352
D2 target	I·KNLA·V·····Y·P·H·JT·····	K·K·DP·D···VVT·D·GN·····	AS·LITE·····L·····IN··	·····LK·····I·N·LT··	352
PDI-1	I·KNLA·V·····Y·E·H·IN·····	K·K·DP·D···VVT·P·GS·····	AS·LITE·····L·····VR··	·····LK·····I·N·LT··	352
PDI-2/PDI-3	I·KNLA·V·····Y·P·H·JT·····	K·K·DP·D···VVT·P·GN·····	AS·LITE·····L·····IR··	·····LK·····I·N·LT··	352

FIG. 19A

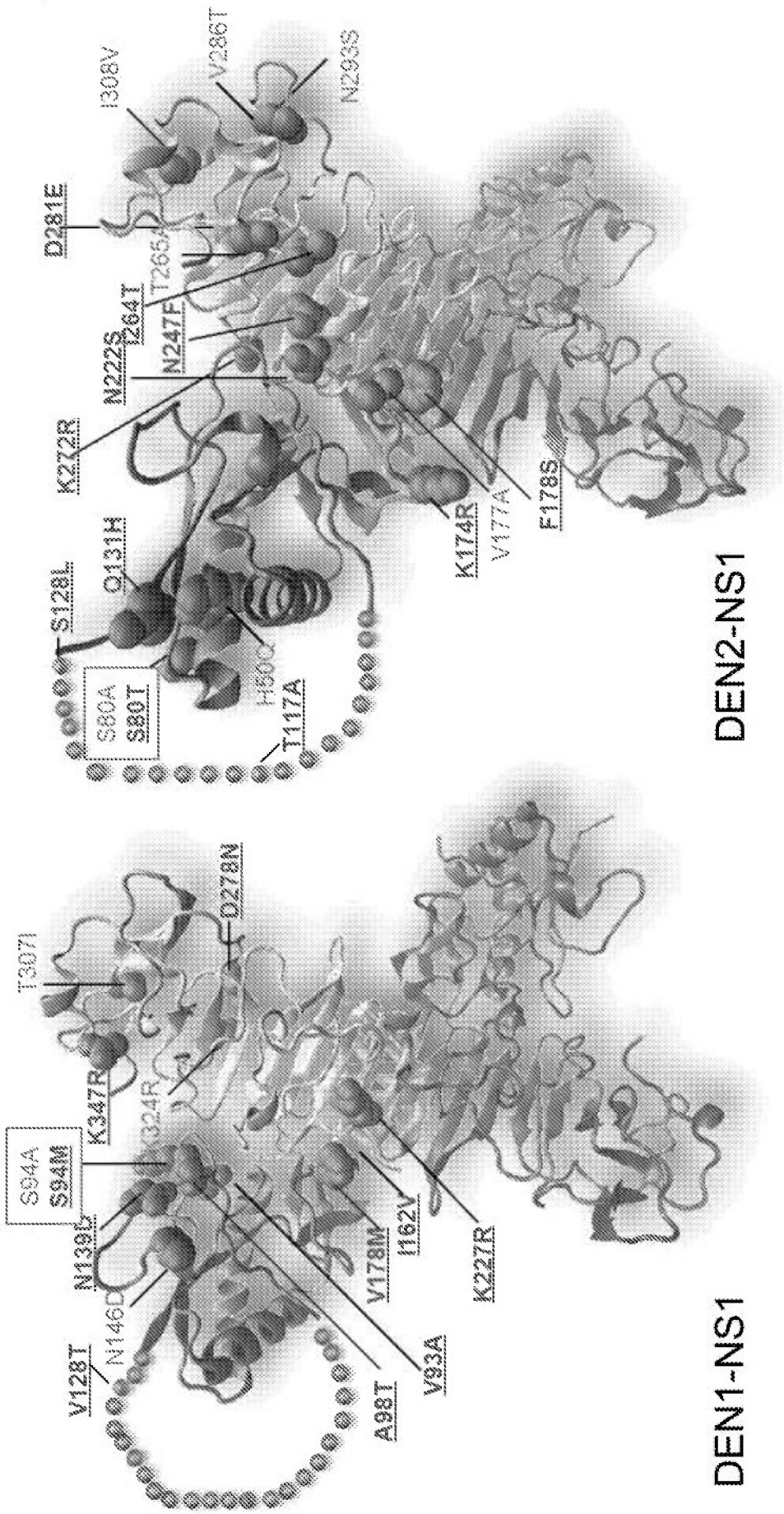


FIG. 19B

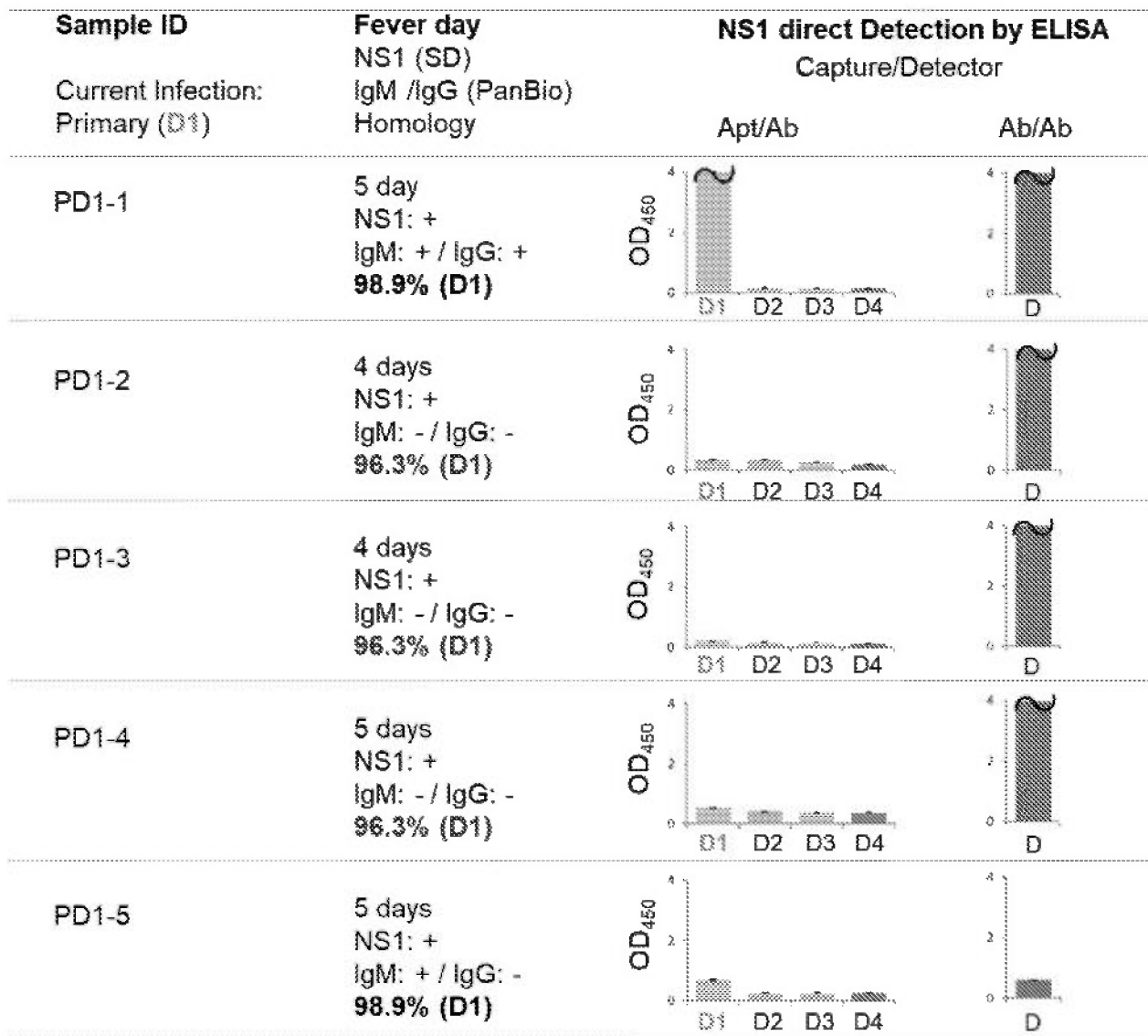


FIG. 20

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A	NA DEN1-NS1	DSGCVINWKGRELKCGSGIFVTNEVHTWTEQYKFQADSPKRLSAAIGKAWEEGVCGIRSA	60
	PD1-1/1-5	DSGCVINWKGRELKCGSGIFVTNEVHTWTEQYKFQADSPKRLSAAIGKAWEEGVCGIRSA	
	PD1-2/1-3/1-4	DSGCVINWKGRELKCGSGIFVTNEVHTWTEQYKFQADSPKRLSAAIGKAWEEGVCGIRSA	
	NA DEN1-NS1	TRLENIMWKQISNELNHILLENDMKFTVVVGDVSGILAQQGKKMIRPQPMEHKYSWKSWGK	120
	PD1-1/1-5	TRLENIMWKQISNELNHILLENDMKFTVVVGDVAGILAQQGKKMIRPQPMEHKYSWKSWGK	
	PD1-2/1-3/1-4	TRLENIMWKQISNELNHILLENDMKFTVVVGDAANGILTQGGKKMIRPQPMEHKYSWKSWGK	
	NA DEN1-NS1	AKIIGADVQNTTFIIDGPNTPCEPDNQRAWNIWEVEDYGGFIETTNIWLKLRDSYTVQCD	180
	PD1-1/1-5	AKIIGADVQNTTFIIDGPNTPCEPDNQRAWNIWEVEDYGGFIETTNIWLKLRDSYTVQCD	
	PD1-2/1-3/1-4	AKIIGADVQNTTFIIDGPNTPCEPDNQRAWNIWEVEDYGGFVETTNIWLKLRDSYTVQCD	
	NA DEN1-NS1	HRLMSAAIKDSKAVHADMGYWI ESEKNETWKLARASFI EVKTCIWFPSHTLWNGVLESE	240
	PD1-1/1-5	HRLMSAAIKDSKAVHADMGYWI ESEKNETWKLARASFI EVKTCIWFPSHTLWNGVLESE	
	PD1-2/1-3/1-4	HRLMSAAIKDSKAVHADMGYWI ESEKNETWKLARASFI EVKTCIWFPSHTLWNGVLESE	
	NA DEN1-NS1	MIIPKIYGGPISQHNYPGYFTQTAGPWHLGKLELDFDLCEGTTVVVDEHCGNRGPSLRT	300
	PD1-1/1-5	MIIPKIYGGPISQHNYPGYFTQTAGPWHLGKLELDFDLCEGTTVVVDEHCGNRGPSLRT	
	PD1-2/1-3/1-4	MIIPKIYGGPISQHNYPGYFTQTAGPWHLGKLELDFNLCEGTTVVVDEHCGNRGPSLRT	
	NA DEN1-NS1	TTVTGKTIHEWCCRSCITLPLRFRKGEDGCWYGMEIRPVKEKEENLVKSMVSA	352
	PD1-1/1-5	TTVTGKTIHEWCCRSCITLPLRFRKGEDGCWYGMEIRPVKEKEENLVKSMVSA	
	PD1-2/1-3/1-4	TTVTGKTIHEWCCRSCITLPLRFRKGEDGCWYGMEIRPVKEKEENLVKSMVSA	

B

Identity %	Native antigen D1	PD1-1 PD1-5	PD1-2 PD1-3 PD1-4
Native antigen D1	100		
PD1-1 PD1-5	98.9	100	
PD1-2 PD1-3 PD1-4	96.3	97.2	100

C

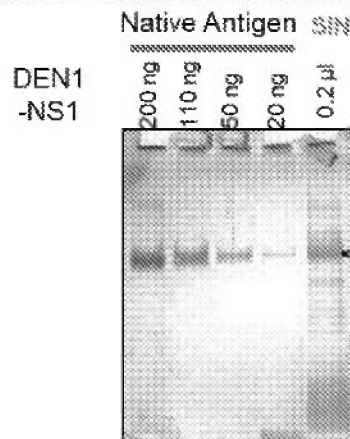


FIG. 21

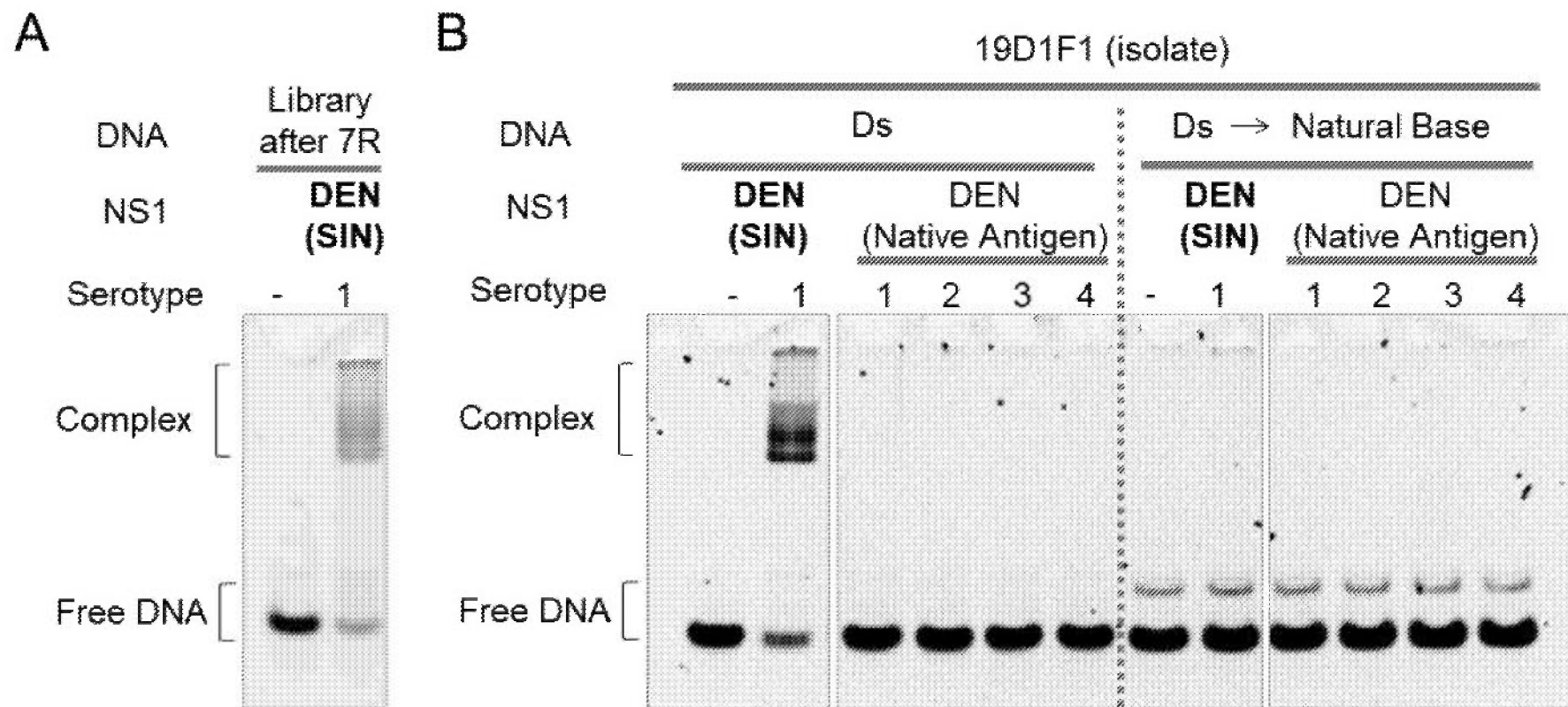


FIG. 22

A

TTTCGCACTCCATGATATGGTCTACTG - [N₄₂] - GACAAGCGGAGTAGTTAGACCGTCAAA

Random region

Family1	40,282 (93%)	AGCGAGACGATGCTGCTAAAXTACGCCGTGGT X ACGAAGACA
	34,541 (80%)	AGC N AG N CGATGCTGCTAAAXTACGCCGTGGT X ACGAAGACA
19D1F1	24,890	AGC G AG A CGATGCTGCTAAAXTACGCCGTGGT X ACGAAGACA
	5,699	AGC A AG A CGATGCTGCTAAAXTACGCCGTGGT X ACGAAGACA
	2,589	AGC A AG T CGATGCTGCTAAAXTACGCCGTGGT X ACGAAGACA
	800	AGC T AG A CGATGCTGCTAAAXTACGCCGTGGT X ACGAAGACA
	418	AGC G AG T CGATGCTGCTAAAXTACGCCGTGGT X ACGAAGACA

B

DNA	Preparation	ELISA detection			SPR	Sequence (5'-to-3') : l = Biotin, L = Biotin-dT, x = dDs, y = Diol1-dPx, N = natural bases)
		Abs450 for NS1			K _D	
		None	SIN	NA	SIN	
		DEN1-NS1	DEN1-NS1	DEN1-NS1	DEN1-NS1	
19D1F1(isolate)	PCR	0.117	>4.000	0.116	9.1 pM	1TTTCGCACTCCATGATA7GGTCTACTGAGCGAGACGATGCTGCTAAAYTACGCCGTGGTyACGAAGACAGACAGCGGAGTAGTTAGACCCGTGAAA
19D1F1 Ds→NB		0.105	0.391	0.101	N.D.	1TTTCGCACTCCATGATA7GGTCTACTGAGCGAGACGATGCTGCTAAANTACGCCGTGGTyACGAAGACAGACAGCGGAGTAGTTAGACCCGTGAAA
19D1F1-1	Chemical synthesis	0.104	0.119	0.099	N.A.	CGGCGGATGCTGCTAAAXTACGCCGTGGTxACGAAGACAGACAGCGGAGTAGTTAGACCGCGCGGCGLAGCG
19D1F1-2		0.102	0.101	0.096	N.A.	CGGCGGATGCTGCTAAAXTACGCCGTGGTxACGAAGACAGACAGCGGAGTAGTTAGACCGCGCGGCGLAGCG
19D1F1-3		0.078	3.592	0.078	27 pM	GCACTCCATGATA7GGTCTACTGAGCGAGACGATGCTGCTAAAXTACGCCGTGGTxACGAAGACAGACAGCGGAGT GT CGGCGLAGCG
19D1F1-4		0.079	0.080	0.079	N.A.	GCACTCC GTCTACTGAGCGAGACGATGCTGCTAAAXTACGCCGTGGTxACGAAGAC CGAGT GT CGGCGLAGCG
19D1F1-5		0.079	0.083	0.078	N.A.	GCACTCC G CTACTGAGCGAGACGATGCTGCTAAAXTACGCCGTGGTxACGAAGACAG CGAGT GT CGGCGLAGCG

FIG. 23

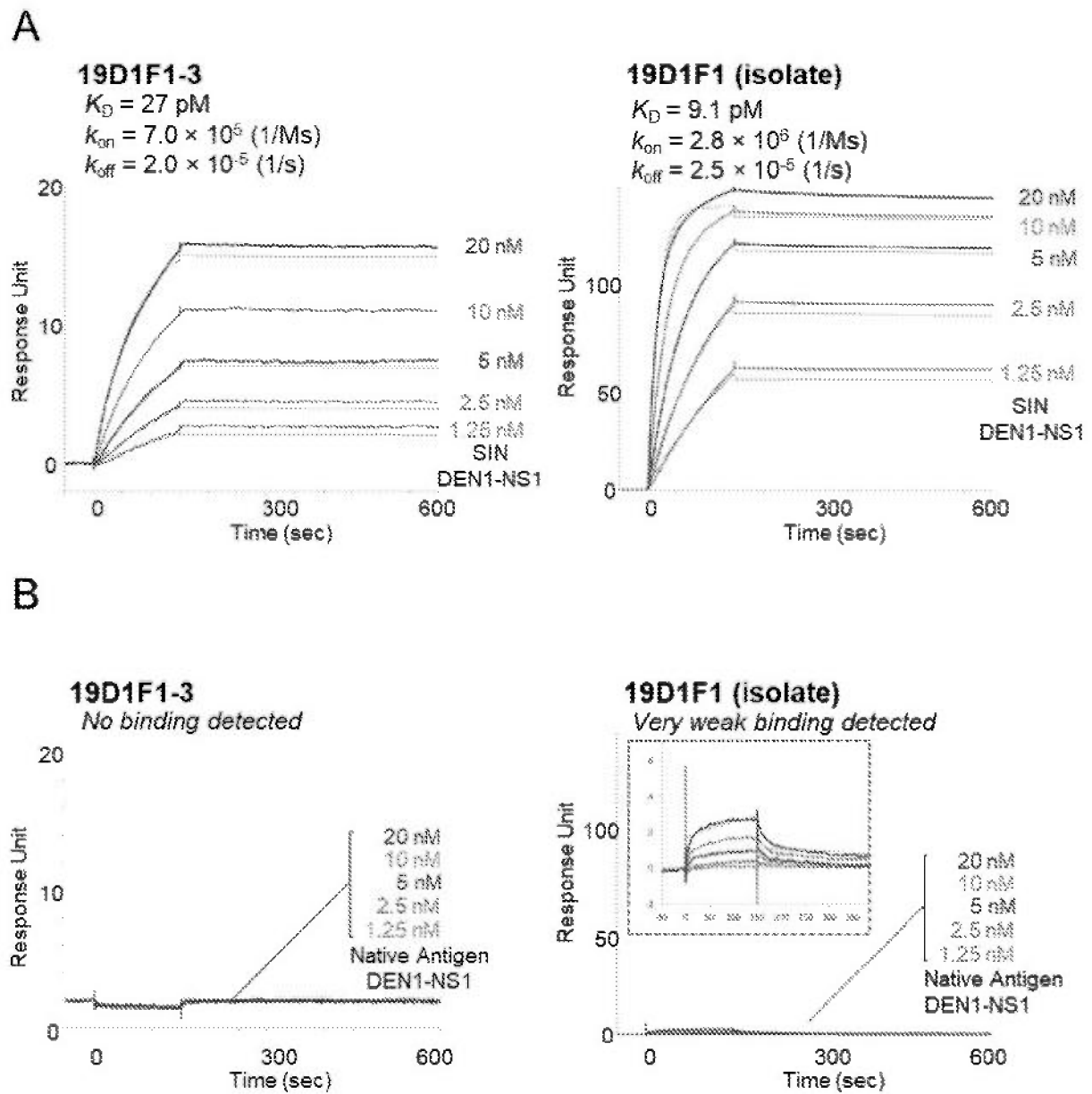
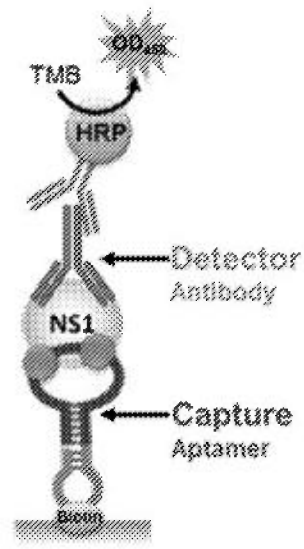
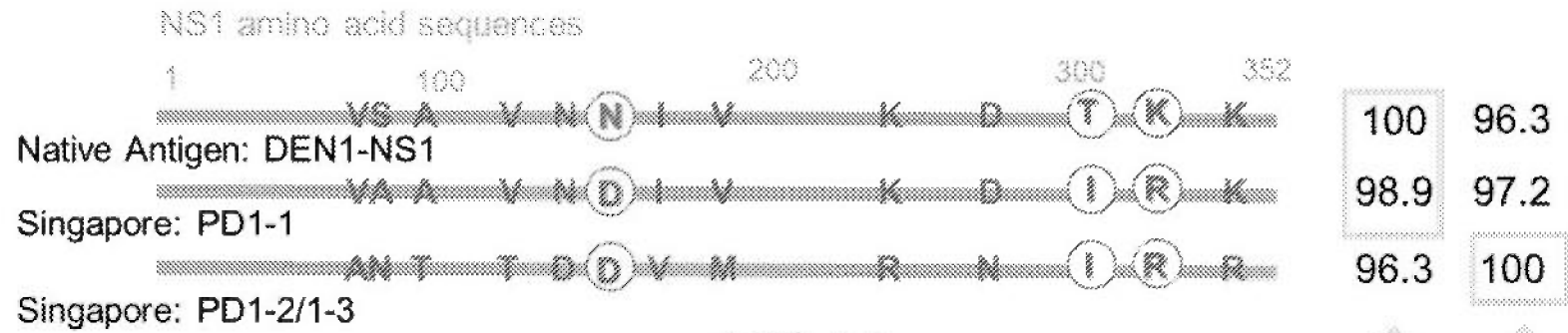
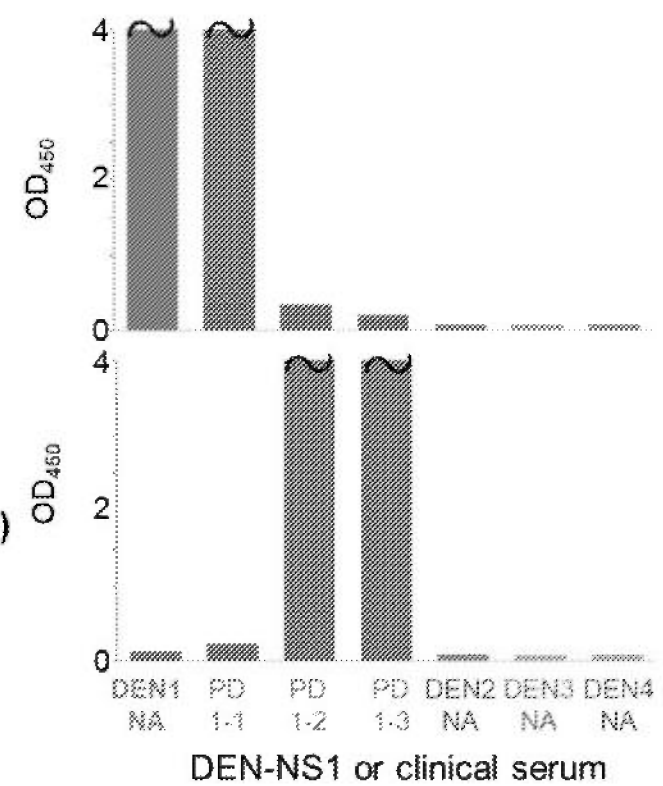


FIG. 24



**AptD1
(D1-1-48h)**

**New AptD1b
(19D1F1 isolate)**



100	96.3
98.9	97.2
96.3	100

FIG. 25

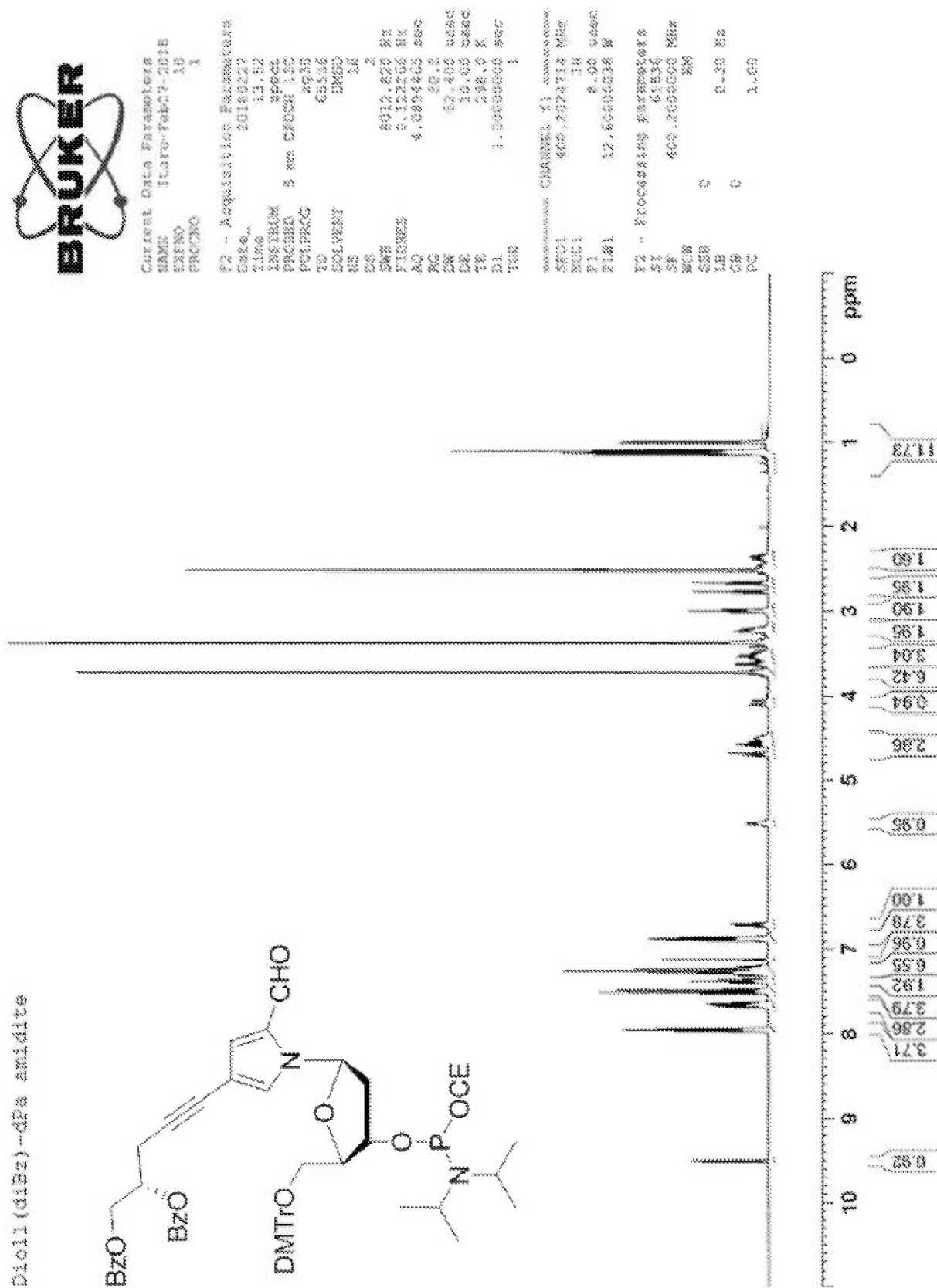


FIG. 26

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```

Current Data Parameters
NAME      11-10-2018
EXPNO     4
PROCNO    1

F2 - Acquisition Parameters
Date_     20180314
Time      20.47
INSTRUM    spect
PROBHD     5 mm PABBO BB-
PULPROG    zgpg
TD          65536
FIDRES     0.334236 Hz
SOLVENT    DMSO
NS          1024
DS          4
SWH         49019.609 Hz
FIDRES     1.495960 Hz
AQ          0.334236 sec
RG          398.24
DM          10.200 usec
DE          6.50 usec
TE          301.0 K
D1          3.0000000 sec
TD0         1

===== CHANNEL f1 =====
NUC1       13C
P1         13.23 usec
PL1        0.00 dB
===== CHANNEL f2 =====
NUC2       1H
P2         13.23 usec
PL2        0.00 dB

F3 - Processing parameters
SI          32768
SF          400.146 MHz
WDW         EM
SSB          0
LB           3.00 Hz
GB           0
PC          1.40
  
```

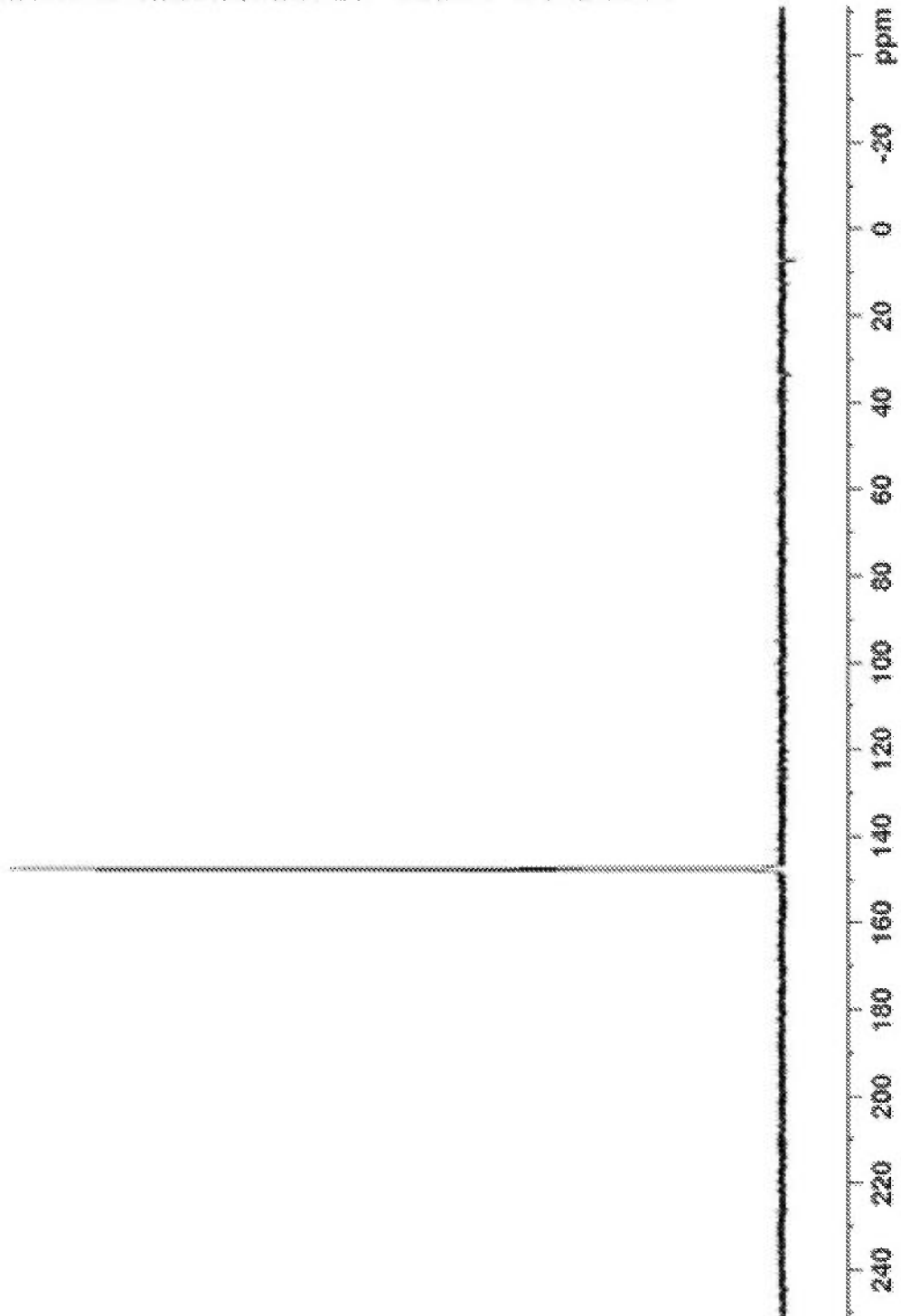


FIG. 27

A

x:Ds, d:Diol-Pa, L:Biotin-T

D2-1d-72h GGCTGGTCCGxCTGGGAACAAGxGGCGGGAGGGAAGGGTGTGGGTGCGACAAGCGGACCAGCCCCGGLAGCG
 D2-1d-72h-b GGCTGGTCCGACTGGGAACAAGxGGCGGGAGGGAAGGGTGTGGGTGCGACAAGCGGACCAGCCCCGGLAGCG
 D2-1d-72h-c GGCTGGTCCGxCTGGGAACAAGAGGGCGGGAGGGAAGGGTGTGGGTGCGACAAGCGGACCAGCCCCGGLAGCG
 D2-1d-72h-d GGCTGGTCCGxCTGGGAACAAGxGGCGGGAGGGAAGGGTGTGGGTGCGACAAGCGGACCAGCCCCGGLAGCG
 Cont-D2-1d-72h-e GGCTGGTCCGACTGGGAACAAGAGGGCGGGAGGGAAGGGTGTGGGTGCGACAAGCGGACCAGCCCCGGLAGCG

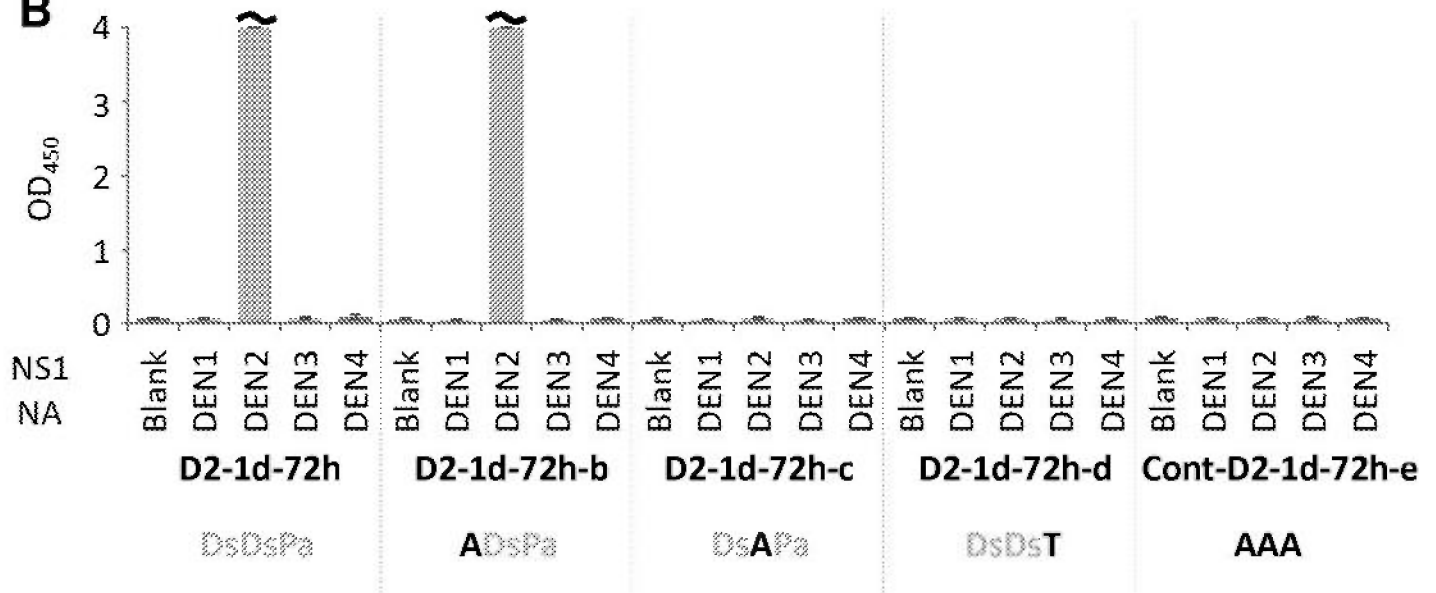
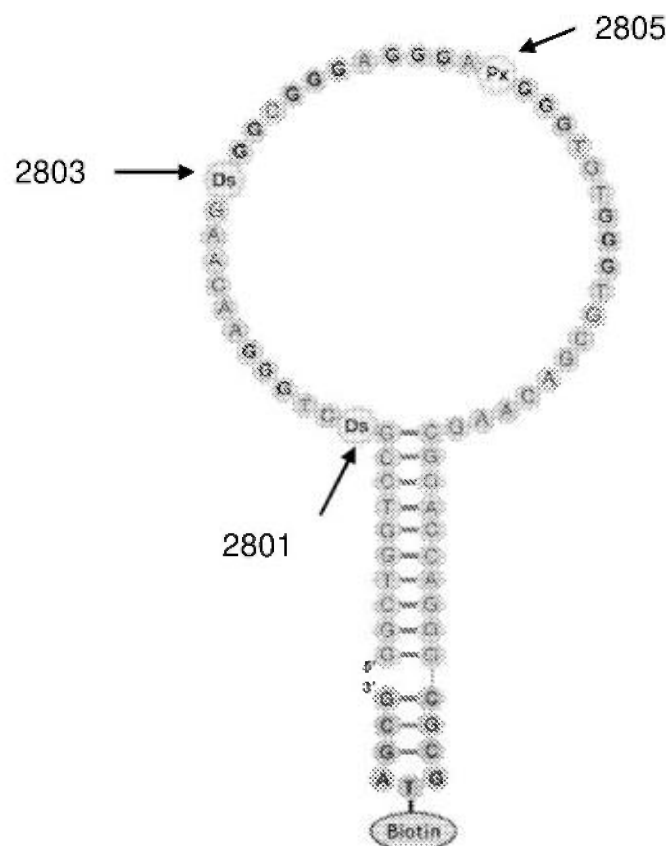
B**C**

FIG. 28