

FIGURE 1

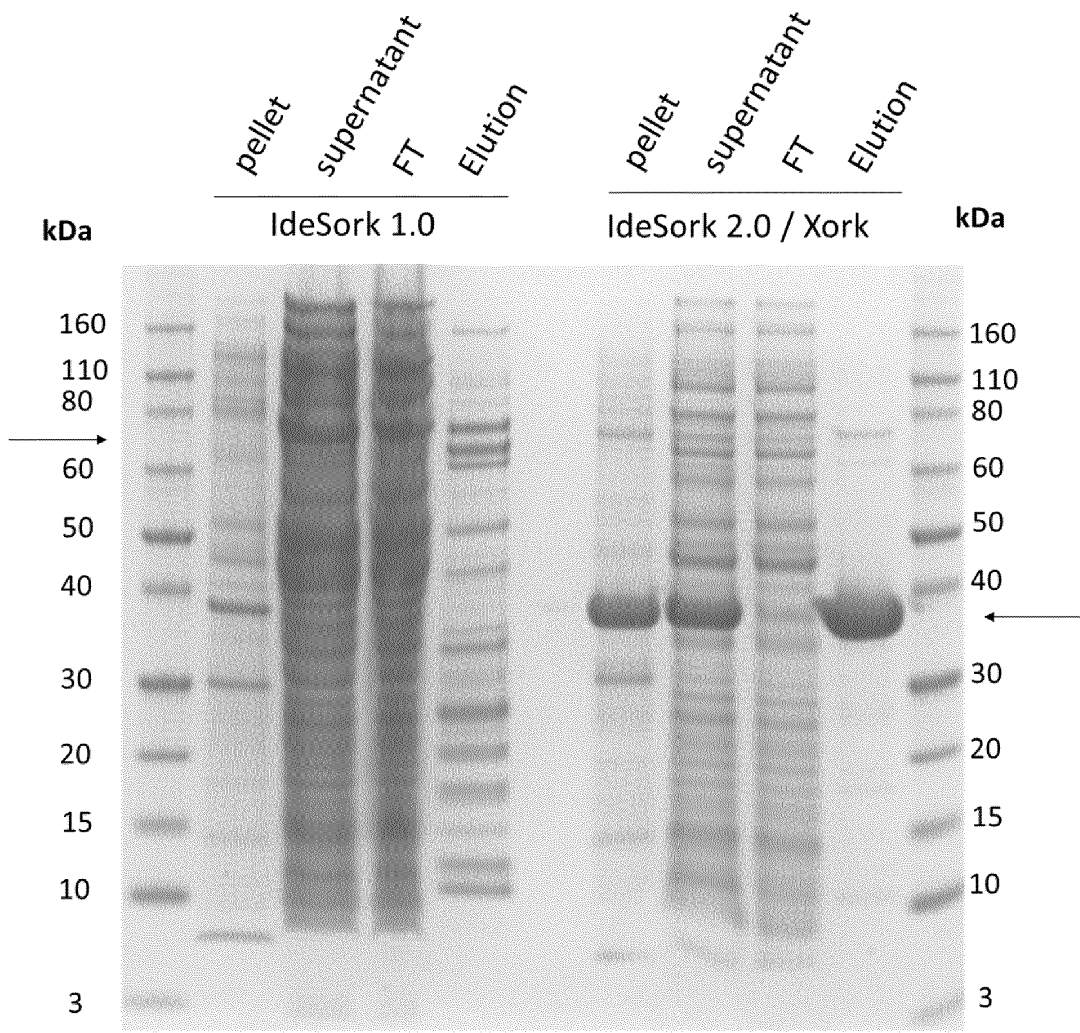


FIGURE 2

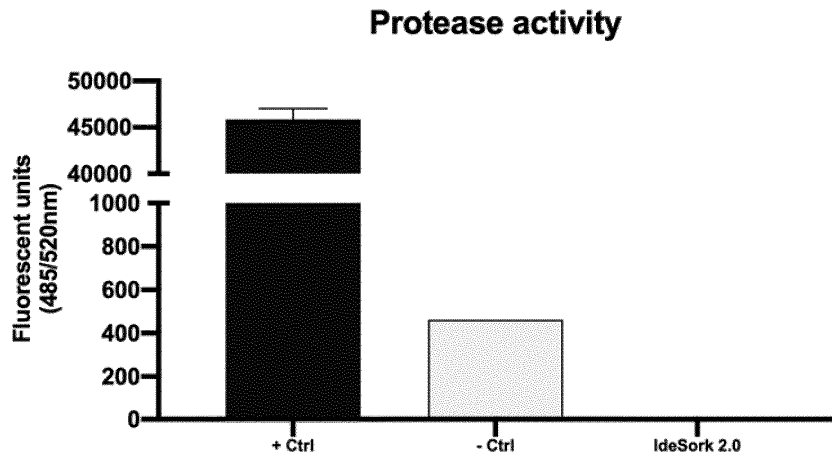


FIGURE 3

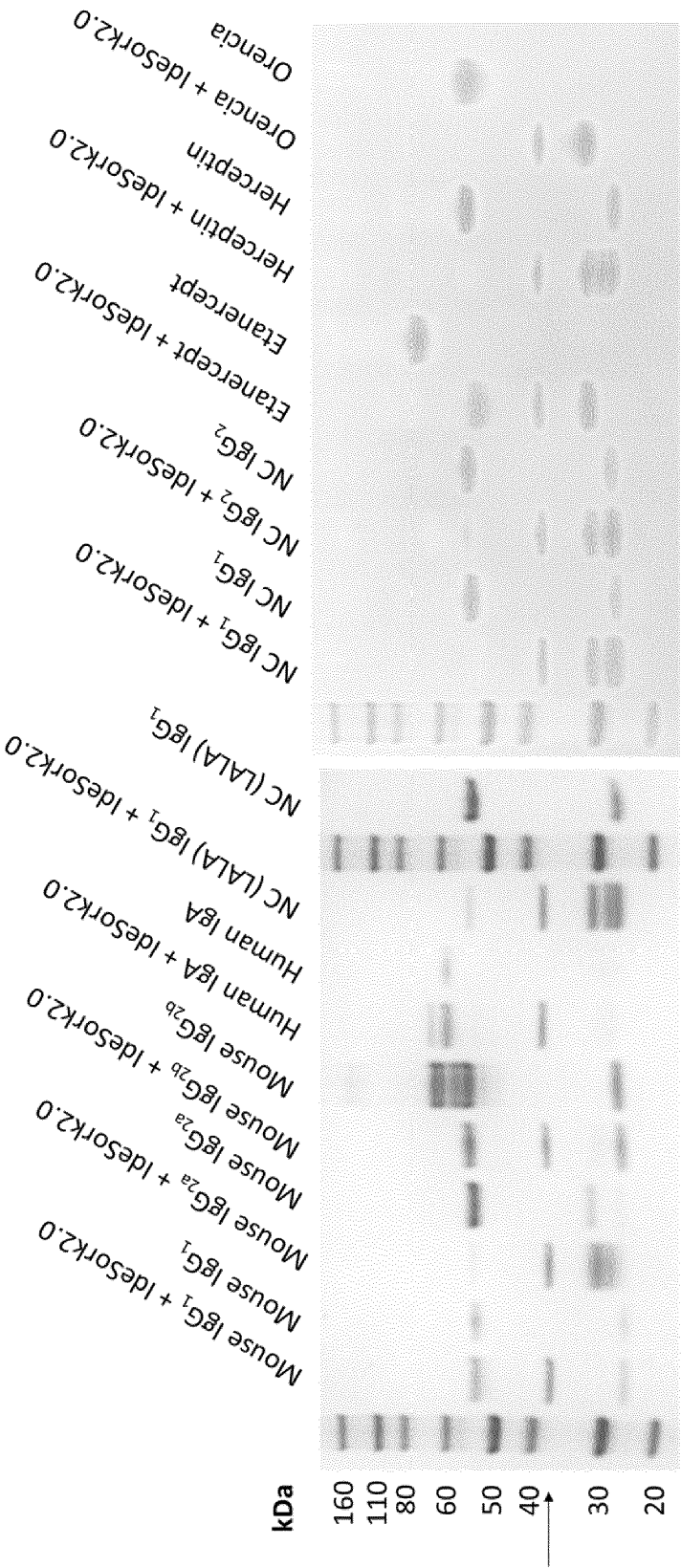


FIGURE 3 continued

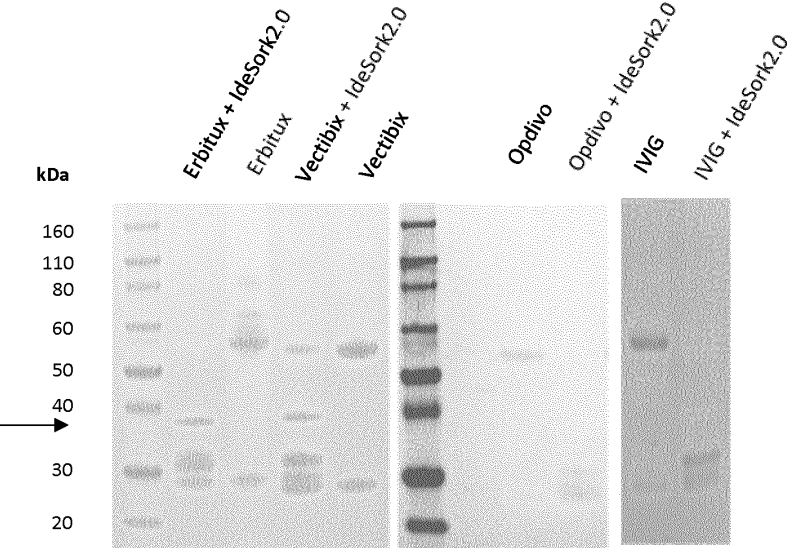


FIGURE 4

Inhibitor	Specificity	Inhibition
AEBSF	serine	++
ALLN	cysteine	++
Antipain	serine	++
Aprotinin	serine	-
Bestatin	exopeptidas	+
Chymostatin	chymotrypsin	++
E-64	cysteine	++
EDTA	Metalloprotease	-
Leupeptin	serine/cysteine	++
Pepstatin	Aspartic protease	-
Phosphoramidon	Metalloendoproteinase	++
PMSF	serine/cysteine	++

FIGURE 5

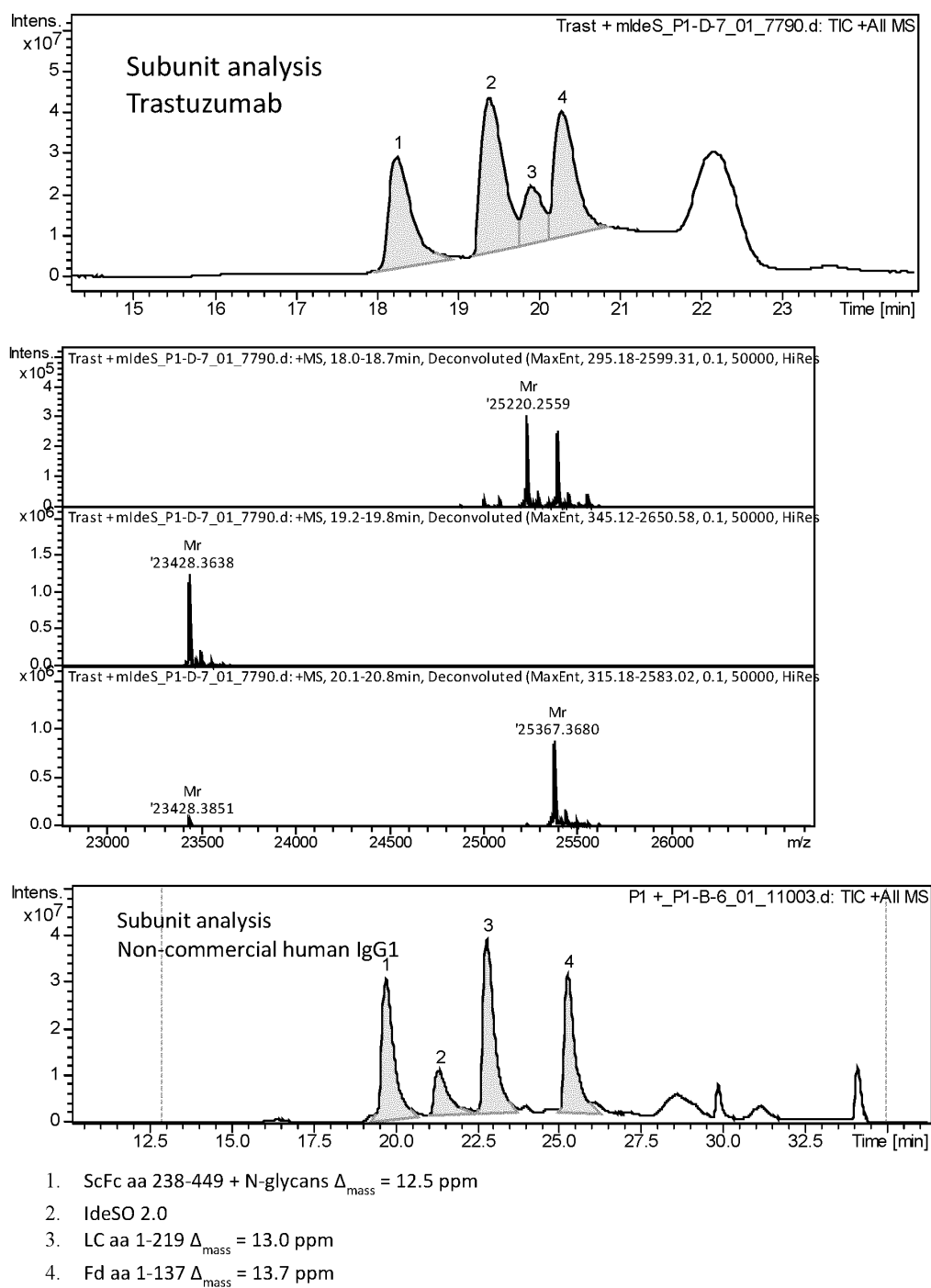


FIGURE 6

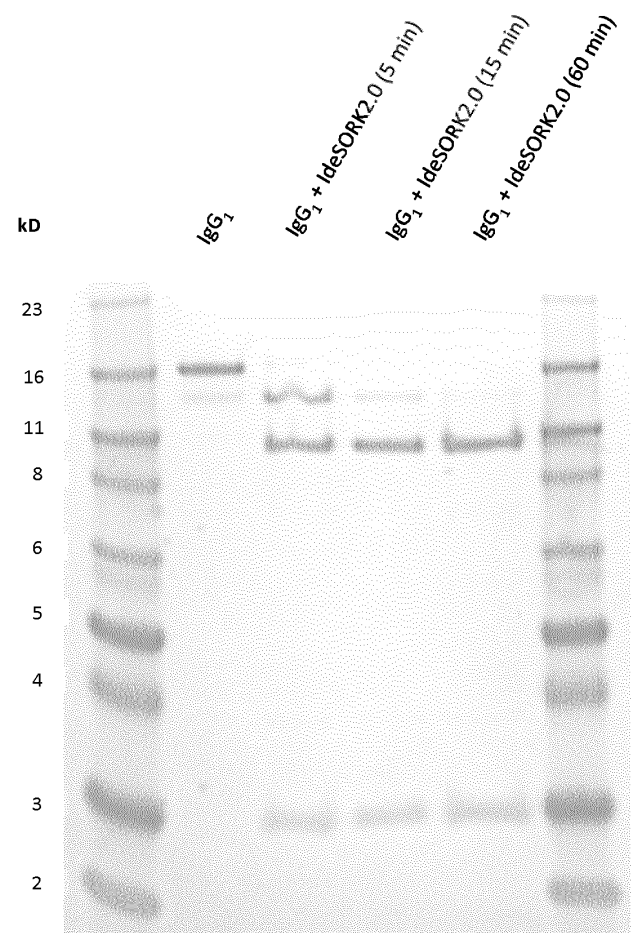


FIGURE 7A

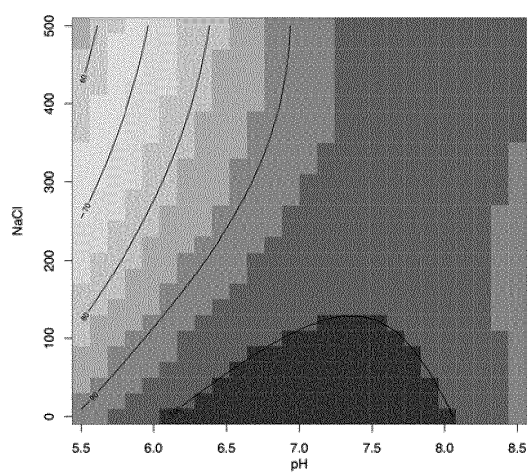
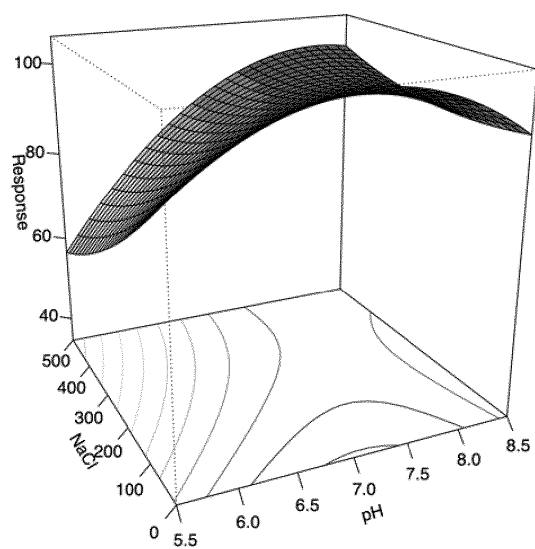


FIGURE 7B

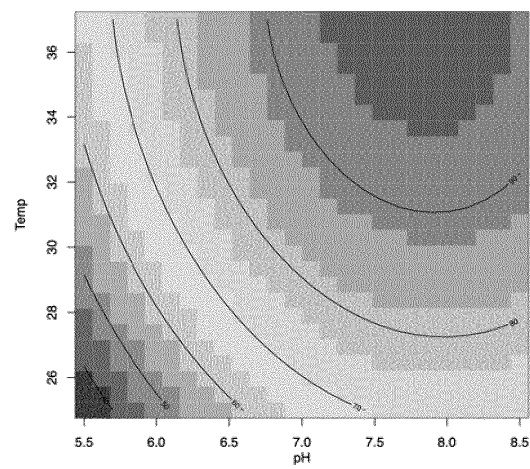
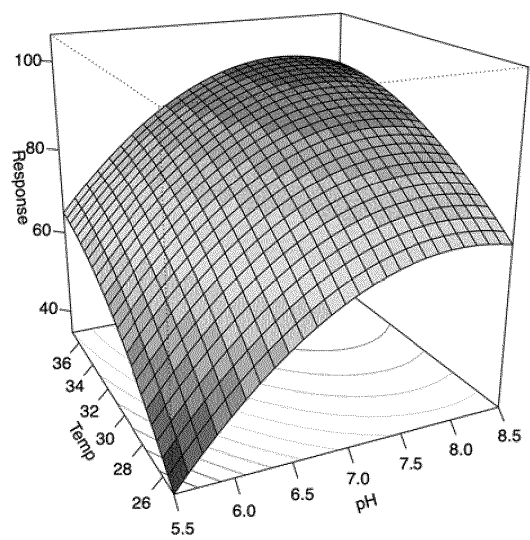


FIGURE 7C

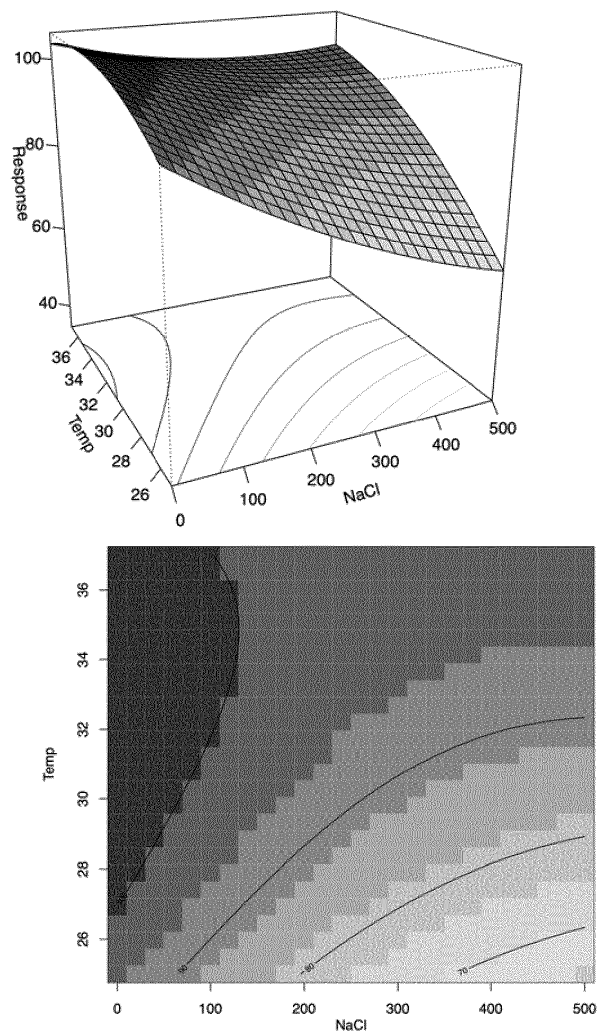


FIGURE 8A

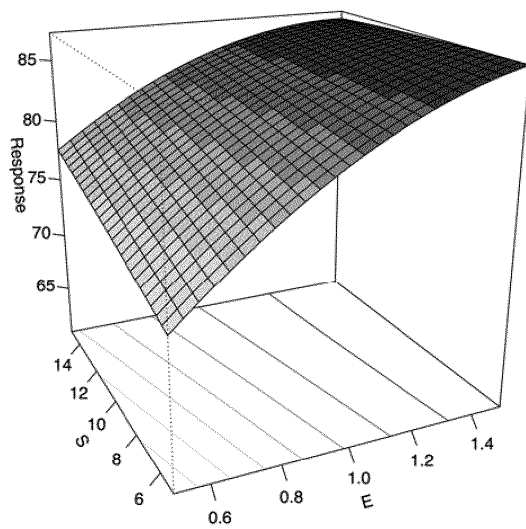


FIGURE 8B

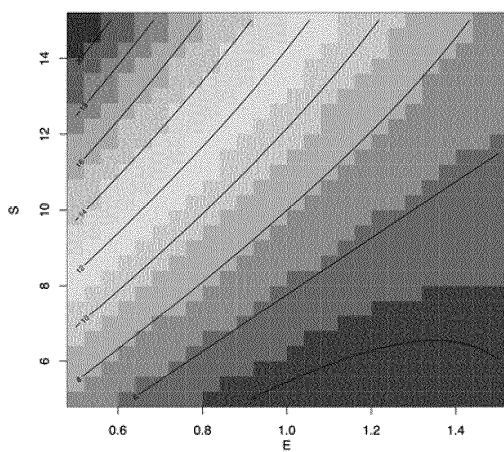
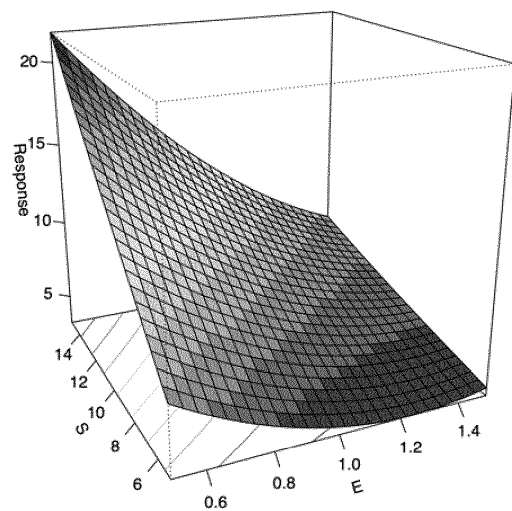
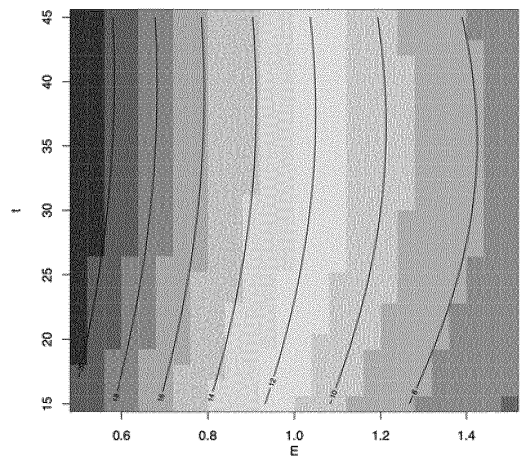
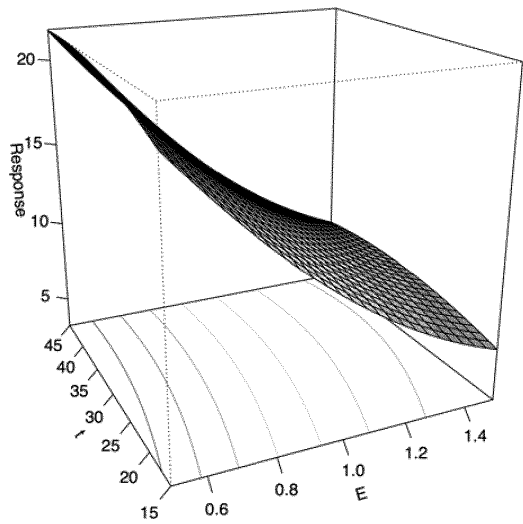


FIGURE 8C



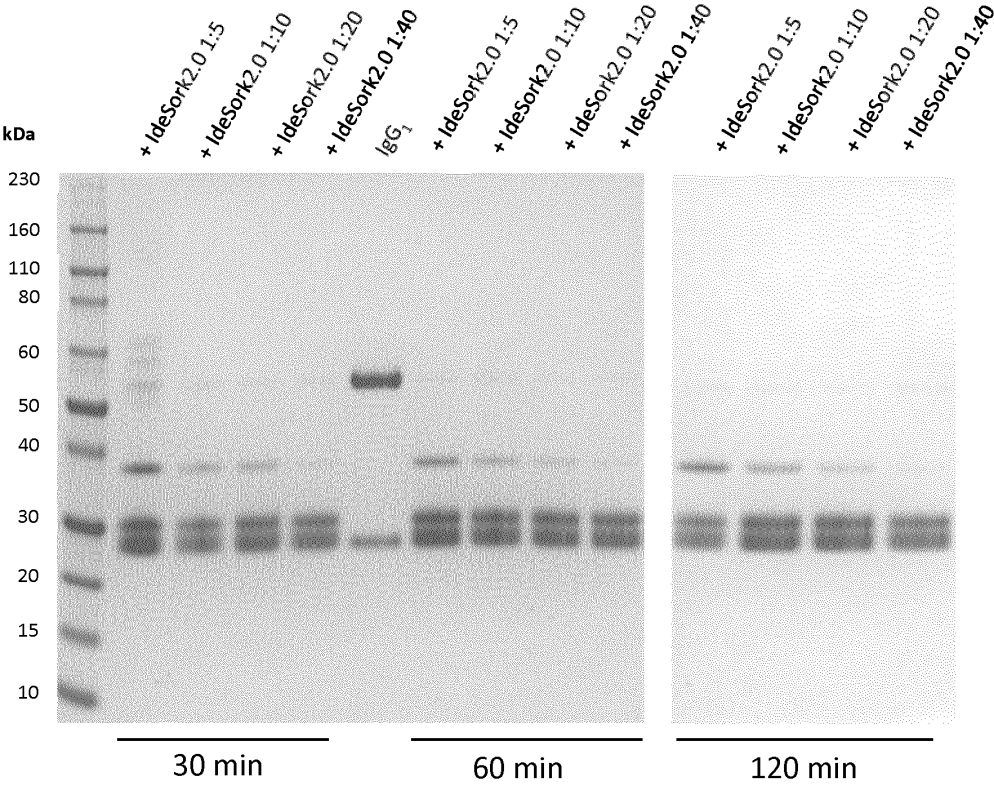


FIGURE 9

FIGURE 10

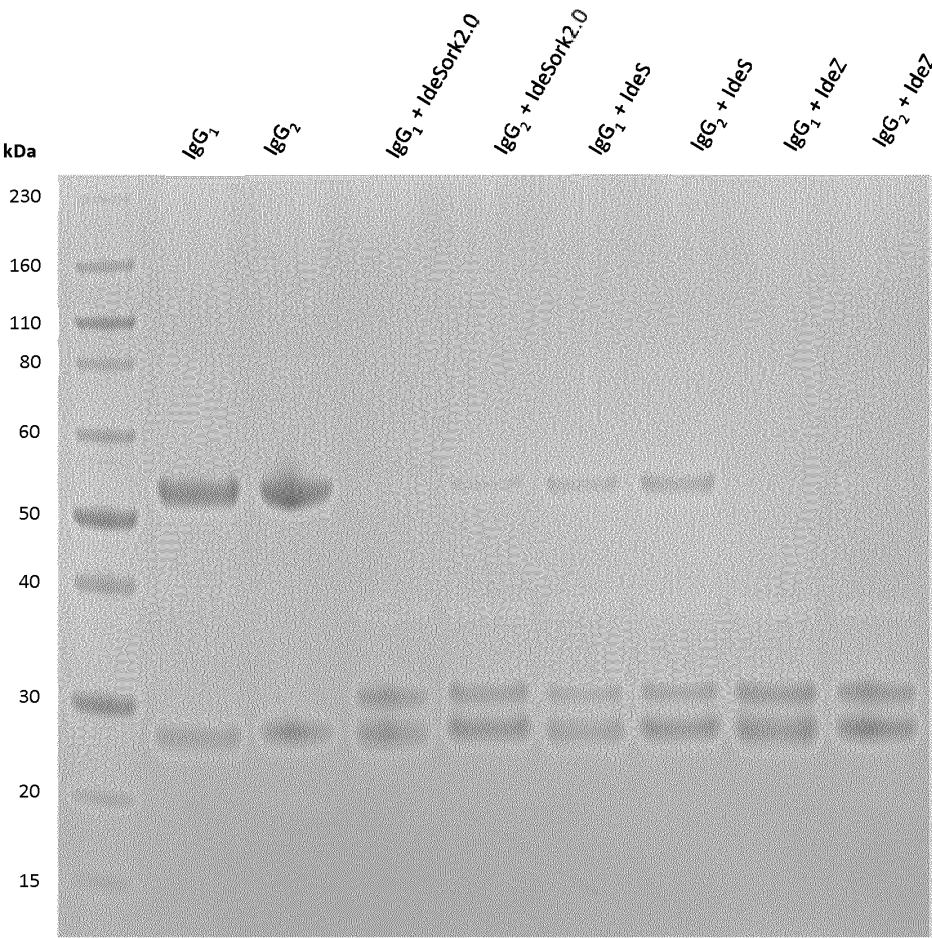


FIGURE 11

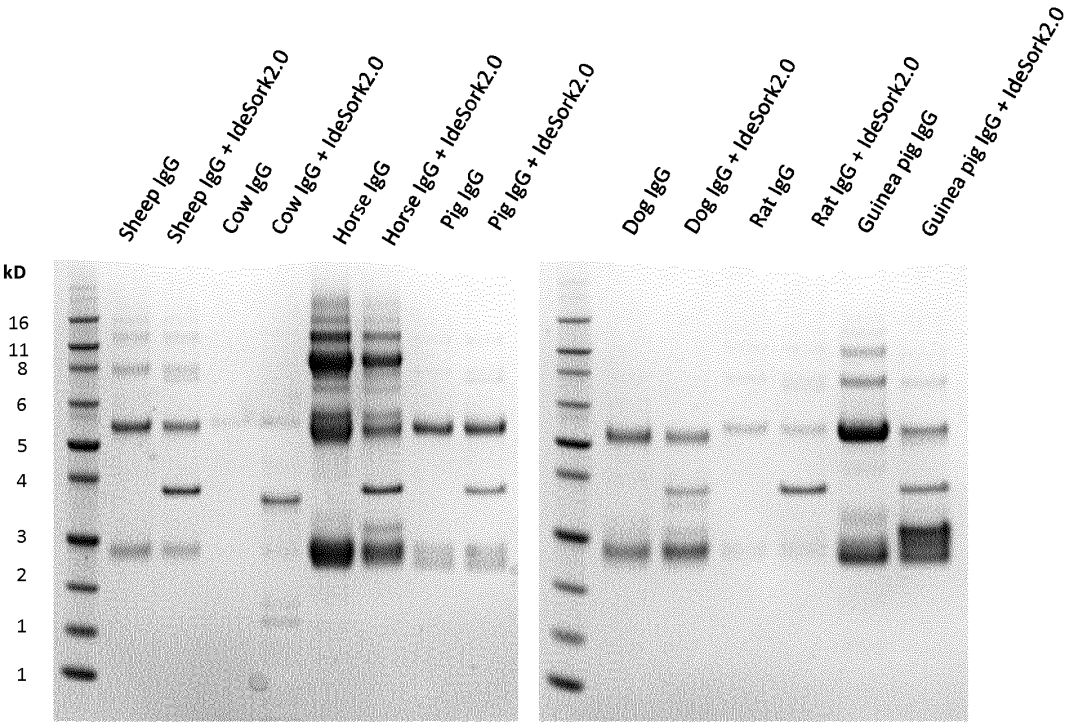
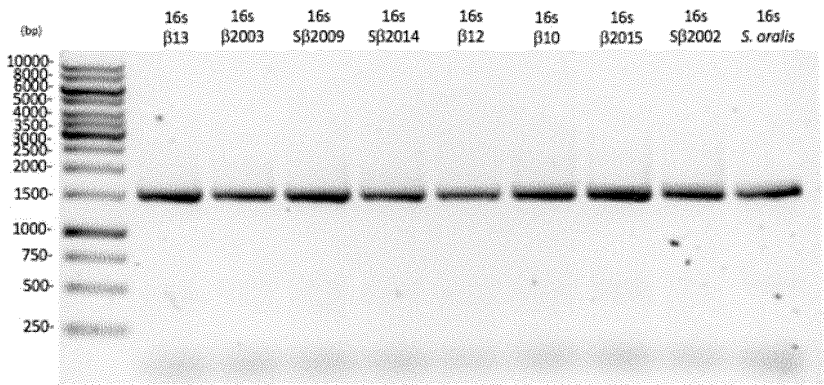


FIGURE 12

(A)



(B)

Bacterial strain	Most similar species	Similarity (%)
β12	<i>Streptococcus danieliae</i>	97.99
β13	<i>Streptococcus porcorum</i>	95.72
β2003	<i>Streptococcus porcorum</i>	95.71
β2015	<i>Streptococcus porcorum</i>	91.61
β10	<i>Streptococcus porcorum</i>	89.49
Sβ2002	<i>Staphylococcus rostri</i>	96.54
Sβ2009	<i>Staphylococcus argenteus</i>	94.08
Sβ2014	<i>Staphylococcus epidermidis</i>	96.01

Bacterial strains β13, β2003, β2015, β10, β12, Sβ2002, Sβ2009 and Sβ2014 compared to known bacterial species using EZbiocloud. The most similar species is shown in the second column and the similarity in percentages is shown in the third column.

(C)

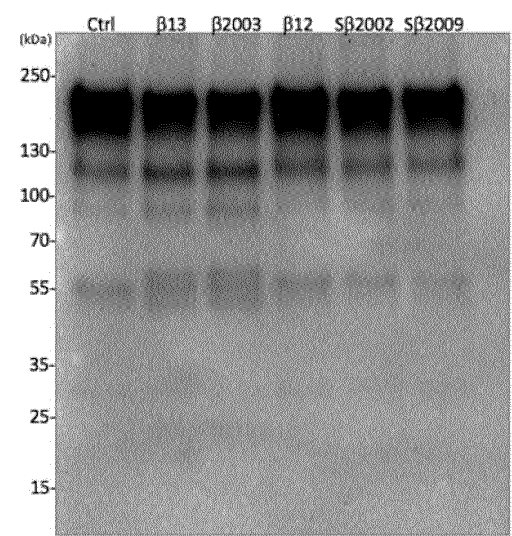
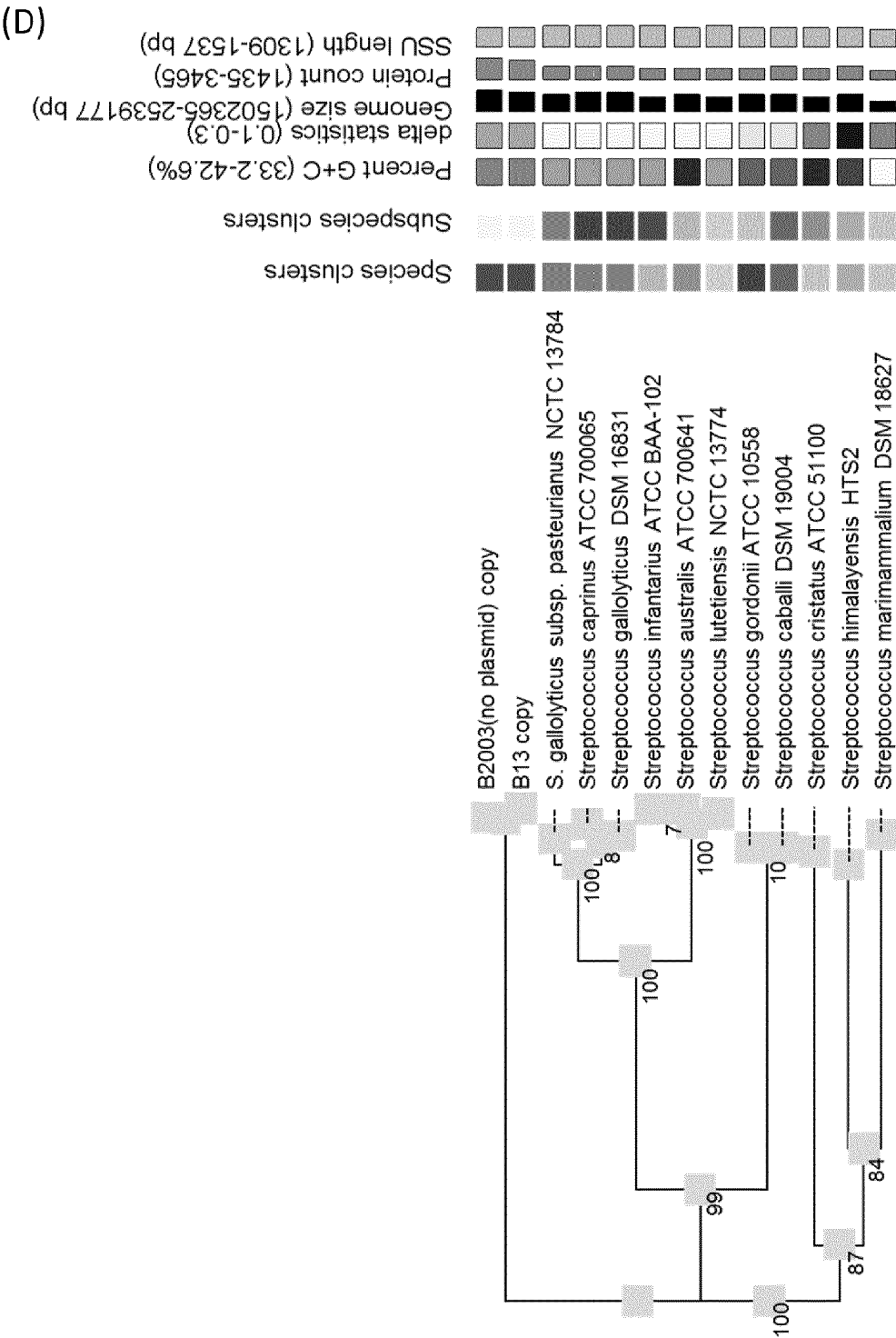


FIGURE 12 continued



CLUSTAL O(1.2.4) multiple sequence alignment

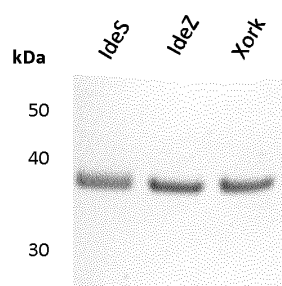
IdeSork1.0	-----MSKRKLLKKI EKKDT--SSVLTKQKKQTKLWADGVQQVDDKDFKPSTENFGTN	50
IdeSork2.0	-----MSKRKLLKKI EKKDT--SSVLTKQKKQTKLWADGVQQVDDKDFKPSTENFGTN	50
IdeS	MASMTGGQQMGRDPLADSFSAHQEI RYSEVT PYHVT SVWTGKVTPPAN-----FTQGED	54
IdeZ	-----MDDYQRNAAEVYAKEVPHQITSVWTKGVTPLTPEQ-----FRYNNED	42
	. . . : : : *.* ** :	
IdeSork1.0	YLAAEYIGIKGYDINKKFDDTDDLCSGVVAANQLHWLDRNKDYIEKYRQOSKDNGV	109
IdeSork2.0	YLAAEYIGIKGYDINKKFDDTDDLCSGVVAANQLHWLDRNKDYIEKYRQOSKDNGV	109
IdeS	VFHAPYVANQGWDYITKTFNKGDDLLCGAATAGNMLHWWFDQNKDQIKRYLEEHPEKQKI	114
IdeZ	VI HAPYLAHQGYDI TKVF DGKDNLLCGAATAGNMLHWWFDQNKTEIEAYLSKHPEKQKI	102
	: * *: *:*.* *:*. *.**.* ** *: * : :	
IdeSork1.0	TIGNTDIFELNKLHDED---QSNNFFDFIK-KSFG----NKFLQPERLLNMINGYGYL	159
IdeSork2.0	TIGNTDIFELNKLHDED---QSNNFFDFIK-KSFG----NKFLQPERLLNMINGYGYL	159
IdeS	NFNGEQMFVDKEAI DTKNHQLDSKLFEPFEKAFFPYLSTKHLGVFPDPHVIMDFINGYRLS	174
IdeZ	IFNQELFDLKAAIDTKNSQSLNFNYFRDKAFPNLSARQLGVMPSDLVDMFINGYYLN	162
	:. . :*: : * :*: *: : *: : : * : : : : *	
IdeSork1.0	TSQDKAKT----SQSPSKLNFFQKVKFN---LLTDKPTPI--NDIDEFSQTKNALQN	209
IdeSork2.0	TSQDKAKT----SQSPSKLNFFQKVKFN---LLTDKPTPI--NDIDEFSQTKNALQN	209
IdeS	LTNHGPTPVK--EGSKDPRGFI FDAVTRGDQSKLLTSRHDFKEKNLKEISDLIKELTE	232
IdeZ	VFKTQSTDVNRPYQDKDKRGFI FDAVTRGDQTLLTARHDLKNKGLNDISTIKQELTE	222
	: . . : : *: *:. . *** : : :.:*: * : *	
IdeSork1.0	HKVLAVSFASIKNRGLGHVVTVWGADFDENGKVVALYVTSDDRSKNI GNAKLGMMKLRI	269
IdeSork2.0	HKVLAVSFASIKNRGLGHVVTVWGADFDENGKVVALYVTSDDRSKNI GNAKLGMMKLRI	269
IdeS	GKALGLSH-TYANVRINHVINLWGADFDSNGNLKAI YVTSDDS-----NASIGMKKYFV	285
IdeZ	GRALALSH-TYANVISI SHVINLWGADFAENGLEAIS VVTSDSA-----NASIGMKKYFV	275
	:.*.*. : * :.***.:***** :*: *.***** **:**** :	
IdeSork1.0	EVSAQDSSTIKLTGFEDKNSGGSLRHLYSLSSTGEQIWKKYFEETEKERIRLEEADKAKL	329
IdeSork2.0	EVSAQDSSTIKLTGFEDKNSGGSLRHLYSLSSTGEQIWKKYFEETHHHHHH-----	319
IdeS	GVNSAGVAISAKEIKEDNIGAQVGLGFLTSTGQDSWNQNTSLHHHHHH-----	335
IdeZ	GINAHGHVAISAKKIEGENIGAQVGLGFLTSTSGKDIWQKLSHHHHHH-----	322
	:. . : *.* : : *.* : : *.* : : *	
IdeSork1.0	EQDRIQKEAEKLALEKA EKERIRLEEADKAKLEQDRIQKEAEKLALEKA EKERIRLE	389
IdeSork2.0	-----	319
IdeS	-----	335
IdeZ	-----	322
IdeSork1.0	EEADKAKLEQDRIQKEAEKLALEKA EKERIRLEEADKAKLEQDRIQKEAEKLALEKA	449
IdeSork2.0	-----	319
IdeS	-----	335
IdeZ	-----	322
IdeSork1.0	EKERIRLEEAAA KALEQE KQI ATAPQDPKKQENTT SEQEKPA TELPPLVNKADETETP	509
IdeSork2.0	-----	319
IdeS	-----	335
IdeZ	-----	322
IdeSork1.0	RETAPDQTPSATNTFRKILPKMNNAV SQFFSQLMGTI QIVFAFILKIFKSGSHHHHHH	566
IdeSork2.0	-----	319
IdeS	-----	335
IdeZ	-----	322

FIGURE 13B

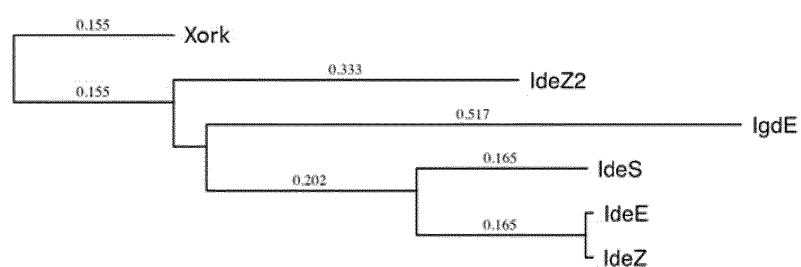
IdeSORK 2.0												IdeSORK 1.0			
Position	-14	-9	-5	0	+5	+10	+20	+50	+100	+150	+245				
Yield	<2 mg/L	<2 mg/L	12 mg/L	64 mg/L	38 mg/L	49 mg/L	44 mg/L	45 mg/L	31 mg/L	42 mg/L	10 mg/L				
Activity	13%	14%	1%	92%	93%	90%	95%	93%	82%	75%	<50%				

FIGURE 14

(A)



(B)



(C)

<i>identity</i>						
	Xork	IdeE	IdeZ	IgdE	IdeS	IdeZ2
Xork	100	26,3	26	7,4	25,1	31,3
IdeE	43,6	100	98,7	5,4	61,7	21,7
IdeZ	43,3	99,1	100	5,4	62	22
IgdE	15	14	13,9	100	6,9	7,3
IdeS	42,4	73,7	73,7	14,9	100	23,5
IdeZ2	47	36,8	37,1	15,7	39	100
<i>similarity</i>						

(D)

(E)

Xork		1 MSKRRLKKIEKDKTSSVLTQKK-QTKTLWADGVQQDDKFDPSTENFGNTYLAEEYGIG	59
IdeZ	1	MDDYQRNAAEVYAKEVPHQITSVTVTKGVTPL--TPEQFRYYNN-EDVIHAPYLAH	51
		* * . * *	*
Xork		60 KGYDINKFKFDGDDDLCSGVVAAQNQLHWLDRNKDYIEKYRQQSKDN-VTIIGNTDIFE	118
IdeZ	52	QGWDITKVDFDGNDLLCGAATAGNMLHFWFQDKTEI EAYLSKHPEKQKIIFNNQLFLD	111
		. * * *. * * * * * * * * * * * * * * * * * *	.
Xork		119 LNLKHDEDSNFDFDIKKSFG-----NKFLQFERLLNMINGYGYLTSQDKAKTS	168
IdeZ	112	LKAADIETKDSQTNSQLFNFYFTRDAKP NLSARQLGMVFDLVDLMFINGYLVNVFTQSTDV	171
		* * * * * * * * * * * * * * * * * *	.
Xork		169 QP---SPSKLNFFQVKVFN----NLLIDKTPI ND--IDEFSSQTKNALQH NKVLAVSFA	218
IdeZ	172	NRPYQDKDKRGGI F DAVFTRGDTLL TARHDLKNGKLNDISTIIKQELTEGRALASHT	231
		. * * * * * * * * * * * * * * * * * *	.
Xork		219 SIKNRGLGHVTVT VWGA DFENGKVVALYTSDSRKNIGNAKLGMKKLRIVESAQSST	278
IdeZ	232	YANVS-ISHVILWGADFNAE G NL EAI Y V T DS DAN-----ASI GMKYFVGIN AGHHVA	284
		* .. **..***** * . ***** **	.
Xork		279 IKLTGFEDKNSGGSLRHLYSLSTGEQIWKKYFEET	313
IdeZ	285	ISAKKIEGENIGAQVLGLEPTLSSGKD I WQKLS	316
		* * * * * * * * * * * * *	.

FIGURE 15

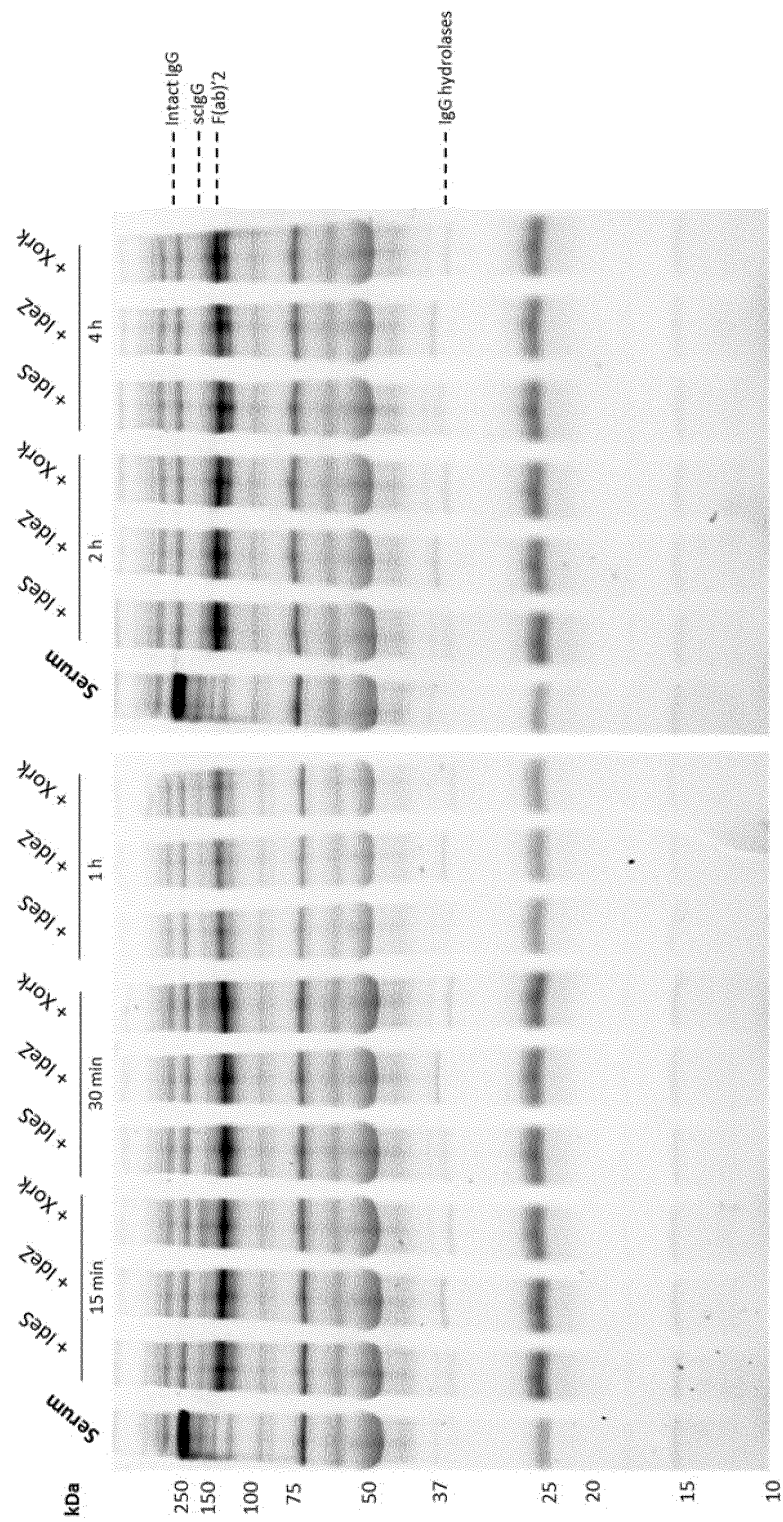


FIGURE 16

	IdeS	IdeZ	Xork
hIgG1	+++	+++	+++
hIgG2	++(+)	++(+)	+(+)
hIgG3	+++	+++	+++
hIgG4	++(+)	++(+)	++
hIgG1 LALA	+	+	+
hIgG1 Fc-fusion	+++	+++	+++
hIVIG	+++	+++	++
Equine	(+)	(+)	-
Simian	++	++	++
Canine	+	+	(+)
Leporine	+++	+++	++
Porcine	-	-	-
Bovine	-	-	-
Caprine	-	-	-
Ovine	++	++	-
Mouse IgG1	-	-	-
Mouse IgG2a	+	++	+
Mouse IgG2b	-	-	-

FIGURE 17

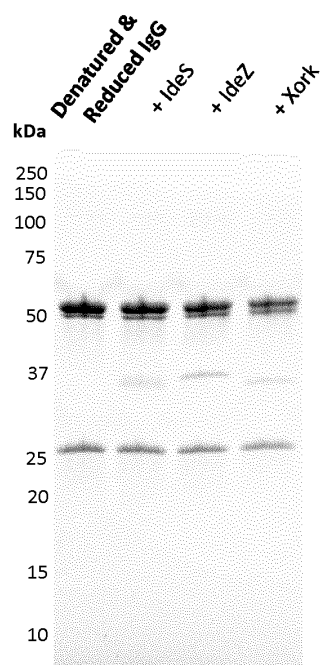
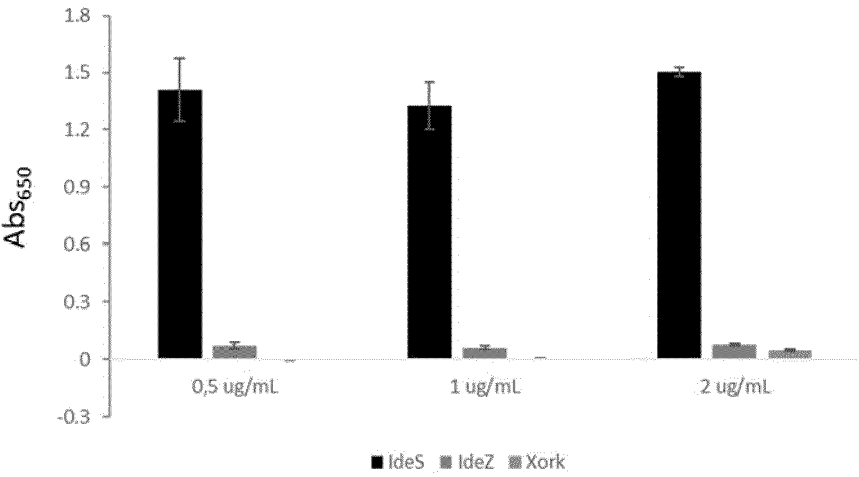


FIGURE 18

(A)



(B)

