Fig. 1

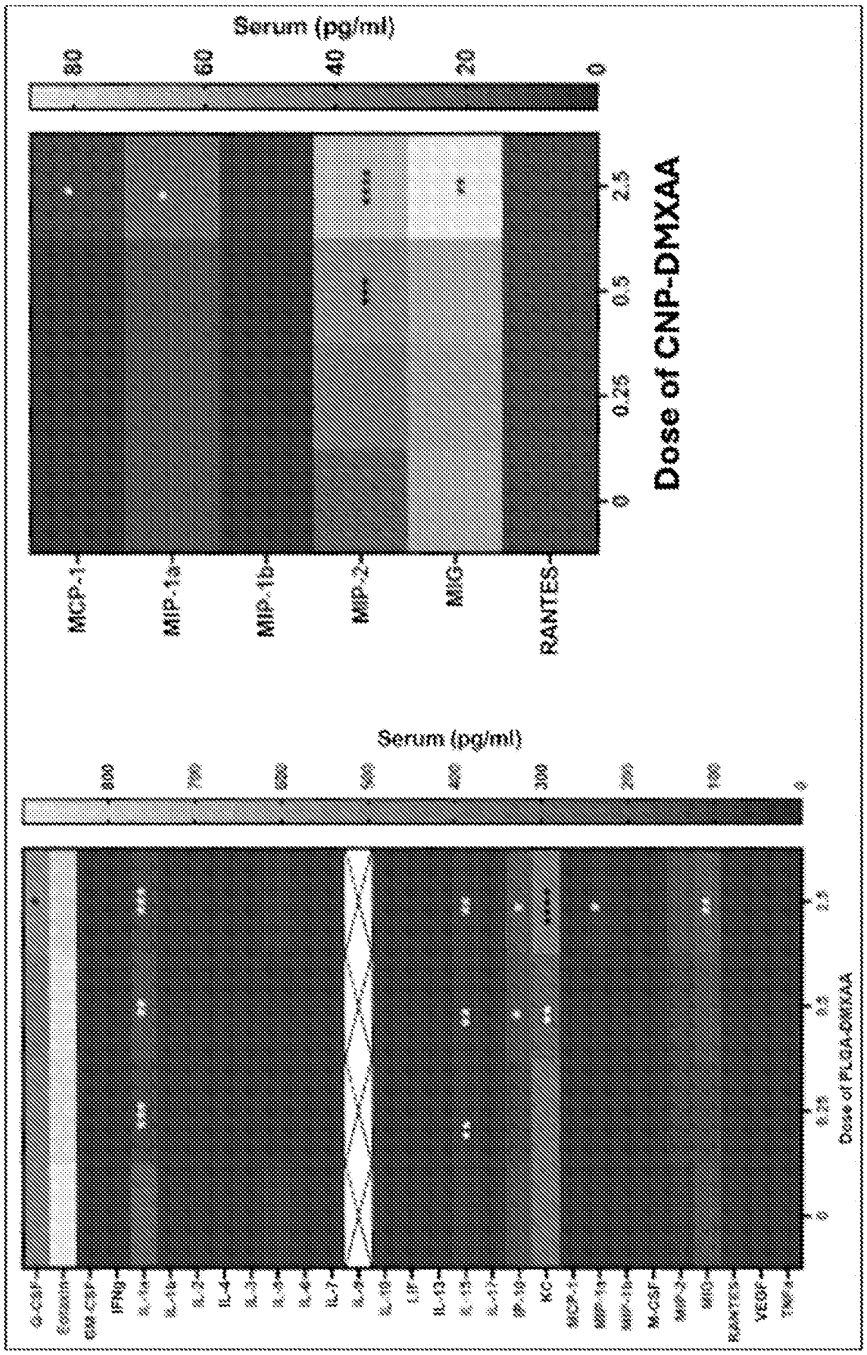

Serum (pg/ml)
80
60
40
20
0
MCP-1
MIP-1a
MIP-1b
MIP-2
MIG
RANTES
0
0.25
0.5
2.5
Dose of CNP-DMXAA
Serum (pg/ml)
800
600
400
300
200
100
0
IFNg
IL-4
IL-5
IL-6
IL-7
IL-10
IL-13
IL-15
IL-17
IP-10
KC
MCP-1
MIP-1a
MIP-1b
M-CSF
MIP-2
MIG
RANTES
VEGF
TNF-a
0.25
0.5
2.5
Dose of PLGA-DMXAA

Fig. 2

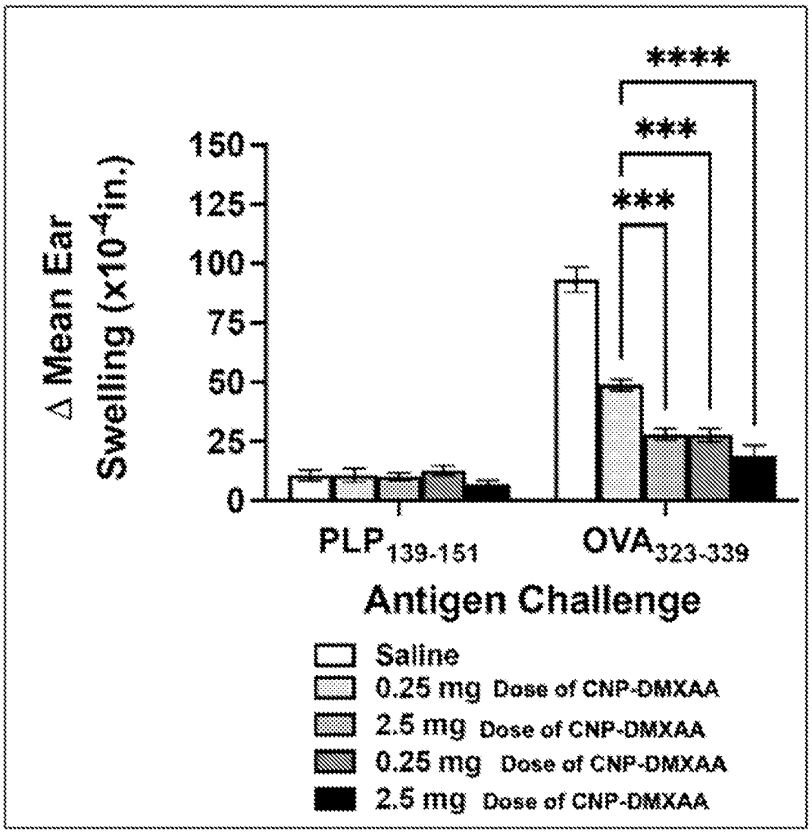

****
***
***
150
125
100
75
50
25
0
Δ Mean Ear Swelling (x10^{-4}in.)
PLP$_{139-151}$
OVA$_{323-339}$
Antigen Challenge
Saline
0.25 mg Dose of CNP-DMXAA
2.5 mg Dose of CNP-DMXAA
0.25 mg Dose of CNP-DMXAA
2.5 mg Dose of CNP-DMXAA

Fig. 3

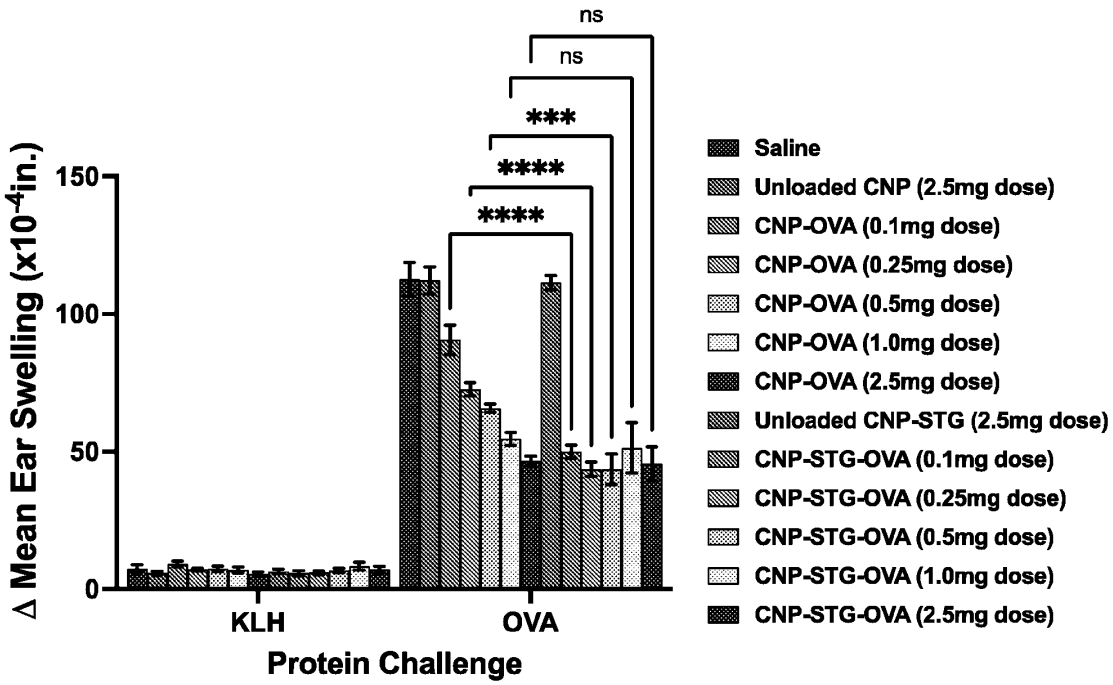

ns
ns
***
****
****
Δ Mean Ear Swelling (x10^{-4}in.)
150
100
50
0
KLH
OVA
Protein Challenge
Saline
Unloaded CNP (2.5mg dose)
CNP-OVA (0.1mg dose)
CNP-OVA (0.25mg dose)
CNP-OVA (0.5mg dose)
CNP-OVA (1.0mg dose)
CNP-OVA (2.5mg dose)
Unloaded CNP-STG (2.5mg dose)
CNP-STG-OVA (0.1mg dose)
CNP-STG-OVA (0.25mg dose)
CNP-STG-OVA (0.5mg dose)
CNP-STG-OVA (1.0mg dose)
CNP-STG-OVA (2.5mg dose)

Fig. 4

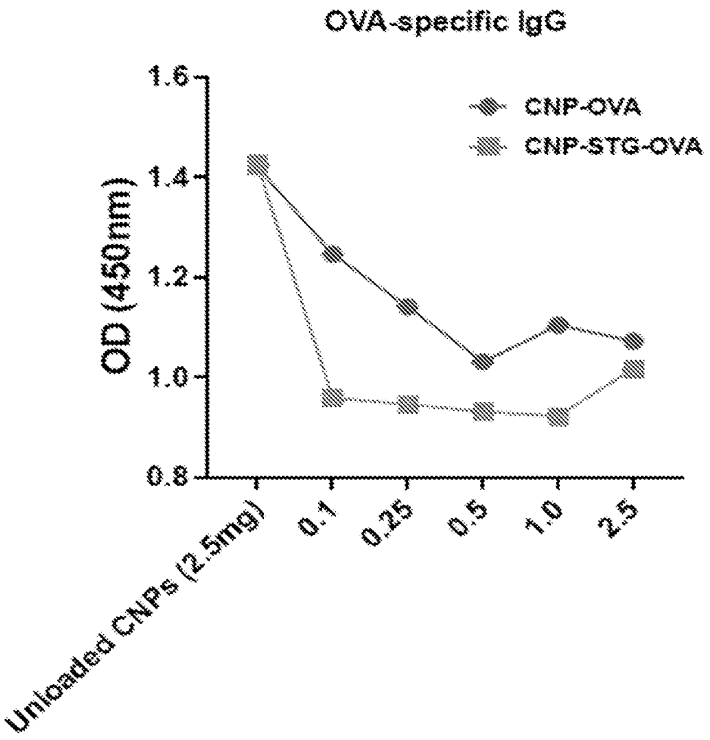

OVA-specific IgG
CNP-OVA
CNP-STG-OVA
OD (450nm)
1.6
1.4
1.2
1.0
0.8
Unloaded CNPs (2.5mg)
0.1
0.25
0.5
1.0
2.5

Fig. 5

Protein Name	Gene Name	Uniprot ID
Acetylcholine receptor subunit alpha	AChRa	E7ENE5
Acetylcholine receptor subunit alpha	AChR alpha subunit	P02708
Nicotinic cholinergic receptor alpha 1	AChRa1	Q53SH4
Acetylcholine receptor subunit epsilon	AChRe	Q04844
Acetylcholine receptor subunit delta	ACHRδ	Q07001
Acetylcholine receptor subunit beta	ACHRβ	P11230
Acetylcholine receptor subunit gamma	ACHRγ	P07510
Agrin	AGRN	O00468
Muscle, skeletal receptor tyrosine-protein kinase	MUSK	O15146
Cortactin	CTTN	Q14247
Titin	TTN	Q8WZ42
Ryanodine receptor 1	RYR1	P21817
Ryanodine receptor 2	RYR2	Q92736
Ryanodine receptor 3	RYR3	Q15413
Frizzled-9 (Fz-9) (hFz9) (FzE6) (CD antigen CD349)	FZD9 FZD3	O00144
Segment polarity protein dishevelled homolog DVL-1 (Dishevelled-1) (DSH homolog 1)	DVL1	O14640
Low-density lipoprotein receptor-related protein 4 (LRP-4) (Multiple epidermal growth factor-like domains 7)	LRP4, KIAA0816, LRP10 MEGF7	O75096
Neuronal acetylcholine receptor subunit beta-2	CHRNB2	P17787
Choline O-acetyltransferase (CHOACTase) (ChAT) (Choline acetylase) (EC 2.3.1.6)	CHAT	P28329
Neuronal acetylcholine receptor subunit alpha-5	CHRNA5 NACHRA5	P30532
Neuronal acetylcholine receptor subunit beta-4	CHRNB4	P30926
Neuronal acetylcholine receptor subunit alpha-3	CHRNA3 NACHRA3	P32297
Neuronal acetylcholine receptor subunit alpha-7	CHRNA7 NACHRA7	P36544
Neuronal acetylcholine receptor subunit alpha-4	CHRNA4 NACRA4	P43681
Neuronal acetylcholine receptor subunit beta-3	CHRNB3	Q05901
Acetylcholine receptor subunit delta	CHRND ACHRD	Q07001
Serine/threonine-protein kinase PAK 1 (EC 2.7.11.1) (Alpha-PAK) (p21-activated kinase 1) (PAK-1) (p65-PAK)	PAK1	Q13153

43 kDa receptor-associated protein of the synapse (RAPsyn) (43 kDa postsynaptic protein) (Acetylcholine receptor-associated 43 kDa protein) (RING finger protein 205)	RAPSN RNF205	Q13702
Neuronal acetylcholine receptor subunit alpha-2	CHRNA2	Q15822
Neuronal acetylcholine receptor subunit alpha-6	CHRNA6	Q15825
Protein Dok-7 (Downstream of tyrosine kinase 7)	DOK7 C4orf25	Q18PE1
Protein RIC-3 (Resistant to inhibitor of cholinesterase 3)	RIC3 UNQ720/PRO1385	Q7Z5B4
Pleckstrin homology-like domain family B member 2 (Protein LL5-beta)	PHLDB2 LL5B	Q86SQ0
AchR epsilon subunit	CHRNE	Q8N731
Neuronal acetylcholine receptor subunit alpha-10 (Nicotinic acetylcholine receptor subunit alpha-10) (NACHR alpha-10)	CHRNA10 NACHRA10	Q9GZZ6
Myelin basic protein	MBP	P02686
Proteolipid protein	PLP	P60201
Myelin-oligodendrocyte glycoprotein	MOG	Q16653
Proinsulin	INS	P01308
Islet-specific glucose-6-phosphatase catalytic subunit-related protein (IGRP)	G6PC2	Q9NQR9
Glutamic acid decarboxylase 65 (GAD65)	GAD65	Q05329
Zinc transporter 8 (ZnT8)	SLC30A8	Q8IWU4
Collagen type XI	COL11A1	P12107
Human cartilage gp39	CHI3L1	P36222
gp130-RAPS	IL6ST	P40189
Fibrillarin	FBL	P22087
Myelin associated glycoprotein	MAG	P20916
αβ-crystallin	CRYAB	P02511
RAS guanyl-releasing protein 2	RASGRP2	O95267
GDP-l-fucose synthase	TSTA3	O43716
β-synuclein	SNCB	Q16143
2',3'-cyclic nucleotide 3'-phosphodiesterase	CNP	P09543
Myelin oligodendrocyte basic protein (MOBP)	MOBP	Q13875
Oligodendrocyte-specific protein (OSP)	CLDN11	O75508
Transaldolase H	TALDO1	P37837
S100 beta	S100B	P04271
Contactin 2/TAG-1	CNTN2	Q02246
KIR4.1	KCNJ10	P78508
Anoctamin 2	ANO2	Q9NQ90
Thyroid stimulating hormone receptor	TSHR	P16473

Insulin-like growth factor 1 receptor (IGF-1R)	IGF1R	P08069
Thyroglobulin	TG	P01266
Thyroid peroxidase	TPO	P07202
Sodium-iodide symporter	SLC5A5	Q92911
Cytosolic 5'-nucleotidase 1A (cN1A)	NT5C1A	Q9BTC0
Alpha myosin heavy chain (αMyHC)	MYH6	P13533
Beta myosin heavy chain (βMyHC)	MYH7	P12883
Heat shock protein 60 (HSP60)	HSPD1	P10809
Jo-1	HARS	P12081
Proteinase 3 (PR3)	PRTN3	P24158
21-Hydroxylase (21OH)	CP21A	P08686
Ro/SSA La/SSB	SSB	P05455
17-α-hydroxylase	CYP17A1 CYP17 S17AH	P05093
Cholesterol Side-Chain Cleavage Enzyme	hrpA HI_1070	P45018
Cytochrome P450 2D6 (CYP2D6)	CYP2D6 CYP2DL1	P10635
Phospholipase A2 Receptor (PLA2R)	PLA2R1 CLEC13C	Q13018
GPIIb	ITGA2B GP2B ITGAB	P08514
GPIIIa	ITGB3 GP3A	P05106
GABA-A Receptor-associated Protein (GABARAP)	GABARAP FLC3B HT004	O95166
Gephyrin	GPHN GPH KIAA1385	Q9NQX3
Amphiphysin	AMPH AMPH1	P49418
ADAMTS13	ADAMTS13 C9orf8 UNQ6102/PRO20085	Q76LX8
Myeloperoxidase	MPO	P05164
Trichohyalin	TCHH THH THL TRHY	Q07283
Tyrosinase-related Protein 2	DCT TYRP2	P40126
Non-collagenous (NC1) domain of the α3 chain of Type IV collagen (α3(IV)NC1)	COL4A5	P29400
β2 Glycoprotein-I (β2GPI)	APOH B2G1	P02749
C1-INH	SERPING1 C1IN C1NH	P05155
Actin	ACTB	P60709
CYP11A1	CYP11A1 CYP11A	P05108
Laminin 332	CD6	P30203
β-4-integrin	ITGB4	P16144
Connexin 26	GJB2	P29033
Cell density-enhanced protein tyrosine phosphatase-1 (DEP-1/CD148)	PTPRJ DEP1	Q12913
Cardiac Myosin	MYH7 MYHCB	P12883
Collagen XVII	COL17A1 BP180 BPAG2	Q9UMD9
Extracellular Matrix Protein 1 (ECM1)	ECM1	Q16610
Peptidyl arginine deiminase-4	PADI4 PAD4 PADI5 PDI5	Q9UM07
Muscle Specific Kinase (MuSK)	MUSK	O15146

Low-density lipoprotein receptor-related protein 4	LRP1B LRPDIT	Q9NZR2
Vimentin	VIM	P08670
Glycoprotein gp70	HSPD1 HSP60	P10809
Fibrinogen alpha	FGA	P02671
Fibrinogen beta chain	FGB	P02675
Fibrinogen gamma chain	FGG PRO2061	P02679
Collagen Type II	COL2A1	P02458
α-enolase	ENO1 ENO1L1 MBPB1 MPB1	P06733
Clusterin	CLU APOJ CLI KUB1 AAG4	P10909
PAD2	PAD2	Q9Y2J8
PAD4	PAD4	Q9UM07
Pyruvate dehydrogenase dehydrolipoamide acetyltransferase (PDC-E2)	DLAT	P10515
Aquaporin 4	AQP4	P55087
Desmoglein 1	DSG1 CDHF4	Q02413
Desmoglein 3	DSG3	P32926
BP180 (BPAG2)	COL17A1 BP180 BPAG2	Q9UMD9
BP230	DST BP230 BP240 BPAG1 DMH DT KIAA0728	Q03001
Orexin-1	HCRT OX PPORX PPOX	O43612
Orexin-2	HCRTR1	O43613
Protein O-mannosyltransferase 1 (POMT1)	POMT1	Q9Y6A1
Tribbles homologue 2	TRIB2	Q92519
Tyrosinase	TYR	P14679
Melan-A (MLANA)	MLANA MART1	Q16655
Premelanosome protein (PMEL)	PMEL	P40967
α-enolase	ENO1 ENO1L1 MBPB1 MPB1	P06733
Tenascin	TNC HXB	P24821
Aggrecan	ACAN	P16112

Fig. 5 continued

Fig. 6

SEQ ID NO:	Peptide	Sequence
SEQ ID 5141	AChRα (48-67)	QIVTTNVRLKQQWVDYNLKW
SEQ ID 5142	AChRα (101-120)	AIVKFTKVLLQYTGHITWTP
SEQ ID 5143	AChRα isoform α (324-357)	STHVMPNWVRKVFIDTIPNIMFFSTMKRPSREKQ
SEQ ID 5144	AChRα (419-437)	IIGTLAVFAGRLIELNQQG
SEQ ID 5145	AChRε (116-130)	IDGQFGVAYDANVLV
SEQ ID 5146	AChRε (201-215)	ENGEWAIDFCPGVIR
SEQ ID 5147	AChRε (236-250)	IRRKPLFYVINIIVP
SEQ ID 5148	AChRε (414-435)	GAAAPEVRCCVDAVNFVAESTR
SEQ ID 5149	AChRα (125-163)	KSYCEIIVTHFPFDEQNCSMKLGTWTYDGSVVAINP ESD
SEQ ID 5150	AChRα (386-411)	MKSDQESNNAAAEWKYVAMVMDHILL
SEQ ID 5151	AChRα (256-269)	FLLVIVELIPSTSS
SEQ ID 5152	AChRα (167-183)	AIFKSYCEIIVTHFPFD
SEQ ID 5153	AChRα (43-58)	EDHRQVVEVTVGLQLI
SEQ ID 5154	AChRα (123-138)	IHIPSEKIWRPDLVLY
SEQ ID 5155	AChRα (112-127)	WNPDDYGGVKKIHIPS
SEQ ID 5156	AChRα (76-91)	LKQQWVDYNLKWNPDD
SEQ ID 5157	AChRα (66-76)	YNLKWNPDDYGGVKKIHI
SEQ ID 5158	AChRα (351-368)	IEGIKYIAETMKSDQESN
SEQ ID 5159	AChRα (68-113)	QIVTTNVRLKQQWVDYNLKWNPDDYGGVKKIHIPSE KIWRPDLVLY
SEQ ID 5160	AChRα (121-158)	AIVKFTKVLLQYTGHITWTPPAIFKSYCEIIVTHFPFD
SEQ ID 5161	AChRε (201-250)	ENGEWAIDFCPGVIRRHHGGATDGPGETDVIYSLIIR RKPLFYVINIIVP

Fig. 7

SEQ ID	Peptide	AMINO ACID SEQUENCE	Post-translational modification
SEQ ID 5162	NA1	MNPNQKIITIGSVCM	
SEQ ID 5163	NA2	QKIITIGSVCMTIGM	
SEQ ID 5164	NA3	TIGSVCMTIGMANLI	
SEQ ID 5165	NA4	VCMTIGMANLILQIG	
SEQ ID 5166	NA5	IGMANLILQIGNIIS	
SEQ ID 5167	NA6	NLILQIGNIISIWIS	
SEQ ID 5168	NA7	QIGNIISIWISHSIQ	
SEQ ID 5169	NA8	IISIWISHSIQLGNQ	
SEQ ID 5170	NA9	WISHSIQLGNQNQIE	
SEQ ID 5171	NA10	SIQLGNQNQIETCNQ	
SEQ ID 5172	NA11	GNQNQIETCNQSVIT	
SEQ ID 5173	NA12	QIETCNQSVITYENN	
SEQ ID 5174	NA13	CNQSVITYENNTWVN	
SEQ ID 5175	NA14	VITYENNTWVNQTYV	
SEQ ID 5176	NA15	ENNTWVNQTYVNISN	
SEQ ID 5177	NA16	WVNQTYVNISNTNFA	
SEQ ID 5178	NA17	TYVNISNTNFAAGQS	
SEQ ID 5179	NA18	ISNTNFAAGQSVVSV	
SEQ ID 5180	NA19	NFAAGQSVVSVKLAG	
SEQ ID 5181	NA20	GQSVVSVKLAGNSSL	
SEQ ID 5182	NA21	VSVKLAGNSSLCPVS	
SEQ ID 5183	NA22	LAGNSSLCPVSGWAI	
SEQ ID 5184	NA23	SSLCPVSGWAIYSKD	
SEQ ID 5185	NA24	PVSGWAIYSKDNSVR	
SEQ ID 5186	NA25	WAIYSKDNSVRIGSK	
SEQ ID 5187	NA26	SKDNSVRIGSKGDVF	
SEQ ID 5188	NA27	SVRIGSKGDVFVIRE	
SEQ ID 5189	NA28	GSKGDVFVIREPFIS	
SEQ ID 5190	NA29	DVFVIREPFISCSPL	
SEQ ID 5191	NA30	IREPFISCSPLECRT	
SEQ ID 5192	NA31	FISCSPLECRTFFLT	
SEQ ID 5193	NA32	SPLECRTFFLTQGAL	
SEQ ID 5194	NA33	CRTFFLTQGALLNDK	
SEQ ID 5195	NA34	FLTQGALLNDKHSNG	
SEQ ID 5196	NA35	GALLNDKHSNGTIKD	

SEQ ID 5197	NA36	NDKHSNGTIKDRSPY	
SEQ ID 5198	NA37	SNGTIKDRSPYRTLM	
SEQ ID 5199	NA38	IKDRSPYRTLMSCPI	
SEQ ID 5200	NA39	SPYRTLMSCPIGEVP	
SEQ ID 5201	NA40	TLMSCPIGEVPSPYN	
SEQ ID 5202	NA41	CPIGEVPSPYNSRFE	
SEQ ID 5203	NA42	EVPSPYNSRFESVAW	
SEQ ID 5204	NA43	PYNSRFESVAWSASA	
SEQ ID 5205	NA44	RFESVAWSASACHDG	
SEQ ID 5206	NA45	VAWSASACHDGINWL	
SEQ ID 5207	NA46	ASACHDGINWLTIGI	
SEQ ID 5208	NA47	HDGINWLTIGISGPD	
SEQ ID 5209	NA48	NWLTIGISGPDNGAV	
SEQ ID 5210	NA49	IGISGPDNGAVAVLK	
SEQ ID 5211	NA50	GPDNGAVAVLKYNGI	
SEQ ID 5212	NA51	GAVAVLKYNGIITDT	
SEQ ID 5213	NA52	VLKYNGIITDTIKSW	
SEQ ID 5214	NA53	NGIITDTIKSWRNNI	
SEQ ID 5215	NA54	TDTIKSWRNNILRTQ	
SEQ ID 5216	NA55	KSWRNNILRTQESEC	
SEQ ID 5217	NA56	NNILRTQESECACVN	
SEQ ID 5218	NA57	RTQESECACVNGSCF	
SEQ ID 5219	NA58	SECACVNGSCFTVMT	
SEQ ID 5220	NA59	CVNGSCFTVMTDGPS	
SEQ ID 5221	NA60	SCFTVMTDGPSNGQA	
SEQ ID 5222	NA61	VMTDGPSNGQASYKI	
SEQ ID 5223	NA62	GPSNGQASYKIFRIE	
SEQ ID 5224	NA63	GQASYKIFRIEKGKI	
SEQ ID 5225	NA64	YKIFRIEKGKIVKSV	
SEQ ID 5226	NA65	RIEKGKIVKSVEMNA	
SEQ ID 5227	NA66	GKIVKSVEMNAPNYH	
SEQ ID 5228	NA67	KSVEMNAPNYHYEEC	
SEQ ID 5229	NA68	MNAPNYHYEECSCYP	
SEQ ID 5230	NA69	NYHYEECSCYPDSSE	
SEQ ID 5231	NA70	EECSCYPDSSEITCV	
SEQ ID 5232	NA71	CYPDSSEITCVCRDN	
SEQ ID 5233	NA72	SSEITCVCRDNWHGS	
SEQ ID 5234	NA73	TCVCRDNWHGSNRPW	
SEQ ID 5235	NA74	RDNWHGSNRPWVSFN	

SEQ ID 5236	NA75	HGSNRPWVSFNQNLE	
SEQ ID 5237	NA76	RPWVSFNQNLEYQIG	
SEQ ID 5238	NA77	SFNQNLEYQIGYICS	
SEQ ID 5239	NA78	NLEYQIGYICSGIFG	
SEQ ID 5240	NA79	QIGYICSGIFGDNPR	
SEQ ID 5241	NA80	ICSGIFGDNPRPNDK	
SEQ ID 5242	NA81	IFGDNPRPNDKTGSC	
SEQ ID 5243	NA82	NPRPNDKTGSCGPVS	
SEQ ID 5244	NA83	NDKTGSCGPVSSNGA	
SEQ ID 5245	NA84	GSCGPVSSNGANGVK	
SEQ ID 5246	NA85	PVSSNGANGVKGFSY	
SEQ ID 5247	NA86	NGANGVKGFSYKYGN	
SEQ ID 5248	NA87	GVKGFSYKYGNGVWI	
SEQ ID 5249	NA88	FSYKYGNGVWIGRTK	
SEQ ID 5250	NA89	YGNGVWIGRTKSISS	
SEQ ID 5251	NA90	VWIGRTKSISSRNGF	
SEQ ID 5252	NA91	RTKSISSRNGFEMIW	
SEQ ID 5253	NA92	ISSRNGFEMIWDPNG	
SEQ ID 5254	NA93	NGFEMIWDPNGWTGT	
SEQ ID 5255	NA94	MIWDPNGWTGTDNNF	
SEQ ID 5256	NA95	PNGWTGTDNNFSIKQ	
SEQ ID 5257	NA96	TGTDNNFSIKQDIVG	
SEQ ID 5258	NA97	NNFSIKQDIVGINEW	
SEQ ID 5259	NA98	IKQDIVGINEWSGYS	
SEQ ID 5260	NA99	IVGINEWSGYSGSFV	
SEQ ID 5261	NA100	NEWSGYSGSFVQHPE	
SEQ ID 5262	NA101	GYSGSFVQHPELTGL	
SEQ ID 5263	NA102	SFVQHPELTGLDCIR	
SEQ ID 5264	NA103	HPELTGLDCIRPCFW	
SEQ ID 5265	NA104	TGLDCIRPCFWVELI	
SEQ ID 5266	NA105	CIRPCFWVELIRGRP	
SEQ ID 5267	NA106	CFWVELIRGRPKENT	
SEQ ID 5268	NA107	ELIRGRPKENTIWTS	
SEQ ID 5269	NA108	GRPKENTIWTSGSSI	
SEQ ID 5270	NA109	ENTIWTSGSSISFCG	
SEQ ID 5271	NA110	WTSGSSISFCGVNSD	
SEQ ID 5272	NA111	SSISFCGVNSDTVGW	
SEQ ID 5273	NA112	FCGVNSDTVGWSWPD	
SEQ ID 5274	NA113	NSDTVGWSWPDGAEL	

SEQ ID 5275	NA114	VGWSWPDGAELPFTI	
SEQ ID 5276	NA115	WPDGAELPFTIDK	
5277	NP1	MASQGTKRSYEQMET	
5278	NP2	IGGIGRFYIQMCTEL	
5279	NP3	GRFYIQMCTELKLSD	
5280	NP4	RMVLSAFDERRNKYL	
5281	NP5	SAFDERRNKYLEEHP	
5282	NP6	ERRNKYLEEHPSAGK	
5283	NP7	KYLEEHPSAGKDPKK	
5284	NP8	EHPSAGKDPKKTGGP	
5285	NP9	AGKDPKKTGGPIYRR	
5286	NP10	MIWHSNLNDATYQRT	
5287	NP11	SNLNDATYQRTRALV	
5288	NP12	DATYQRTRALVRTGM	
5289	NP13	QRTRALVRTGMDPRM	
5290	NP14	ALVRTGMDPRMCSLM	
5291	NP15	TGMDPRMCSLMQGST	
5292	NP16	PRMCSLMQGSTLPRR	
5293	NP17	SLMQGSTLPRRSGAA	
5294	NP18	GSTLPRRSGAAGAAV	
5295	NP19	PRRSGAAGAAVKGVG	
5296	NP20	IKRGINDRNFWRGEN	
5297	NP21	RMCNILKGKFQTAAQ	
5298	NP22	AMMDQVRESRNPGNA	
5299	NP23	RSALILRGSVAHKSC	
5300	NP24	ILRGSVAHKSCLPAC	
5301	NP25	RPNENPAHKSQLVWM	
5302	NP26	NPAHKSQLVWMACHS	
5303	NP27	KSQLVWMACHSAAFE	
5304	NP28	VWMACHSAAFEDLRV	
5305	NP29	LRSRYWAIRTRSGGN	
5306	NP30	YWAIRTRSGGNTNQQ	
5307	NP31	SFQGRGVFELSDEKA	
5308	NP32	PSFDMSNEGSYFFGD	
5309	NP33	MSNEGSYFFGDNAEE	
5310	NP35	GTKRSYEQMETGGER	
5311	NP36	SYEQMETGGERQDAT	

5312	NP37	METGGERQDATEIRA	
5313	NP38	GERQDATEIRASVGR	
5314	NP39	DATEIRASVGRMIGG	
5315	NP40	IRASVGRMIGGIGRF	
5316	NP41	VGRMIGGIGRFYIQM	
5317	NP42	IQMCTELKLSDYDGR	
5318	NP43	TELKLSDYDGRLIQN	
5319	NP44	LSDYDGRLIQNSITI	
5320	NP45	DGRLIQNSITIERMV	
5321	NP46	IQNSITIERMVLSAF	
5322	NP47	ITIERMVLSAFDERR	
5323	NP48	PKKTGGPIYRRVDGK	
5324	NP49	GGPIYRRVDGKWMRE	
5325	NP50	YRRVDGKWMRELILY	
5326	NP51	DGKWMRELILYDKQE	
5327	NP52	MRELILYDKQEIRRV	
5328	NP53	ILYDKQEIRRVWRLA	
5329	NP54	KQEIRRVWRLANNGE	
5330	NP55	RRVWRLANNGEDATA	
5331	NP56	RLANNGEDATAGLTH	
5332	NP57	NGEDATAGLTHIMIW	
5333	NP58	ATAGLTHIMIWHSNL	
5334	NP59	LTHIMIWHSNLNDAT	
5335	NP60	GAAGAAVKGVGTIAM	
5336	NP61	AAVKGVGTIAMELIR	
5337	NP62	GVGTIAMELIRMIKR	
5338	NP63	IAMELIRMIKRGIND	
5339	NP64	LIRMIKRGINDRNFW	
5340	NP65	INDRNFWRGENGRRT	
5341	NP66	NFWRGENGRRTRVAY	
5342	NP67	GENGRRTRVAYERMC	
5343	NP68	RRTRVAYERMCNILK	
5344	NP69	VAYERMCNILKGKFQ	
5345	NP70	ILKGKFQTAAQRAMM	
5346	NP71	KFQTAAQRAMMDQVR	
5347	NP72	AAQRAMMDQVRESRN	
5348	NP73	QVRESRNPGNAEIED	

5349	NP74	SRNPGNAEIEDLIFL	
5350	NP75	GNAEIEDLIFLARSA	
5351	NP76	IEDLIFLARSALILR	
5352	NP77	IFLARSALILRGSVA	
5353	NP78	SVAHKSCLPACVYGL	
5354	NP79	KSCLPACVYGLAVAS	
5355	NP80	PACVYGLAVASGHDF	
5356	NP81	YGLAVASGHDFEREG	
5357	NP82	VASGHDFEREGYSLV	
5358	NP83	HDFEREGYSLVGIDP	
5359	NP84	REGYSLVGIDPFKLL	
5360	NP85	SLVGIDPFKLLQNSQ	
5361	NP86	IDPFKLLQNSQVVSL	
5362	NP87	KLLQNSQVVSLMRPN	
5363	NP88	NSQVVSLMRPNENPA	
5364	NP89	VSLMRPNENPAHKSQ	
5365	NP91	CHSAAFEDLRVSSFI	
5366	NP92	AFEDLRVSSFIRGKK	
5367	NP93	LRVSSFIRGKKVIPR	
5368	NP94	SFIRGKKVIPRGKLS	
5369	NP95	GKKVIPRGKLSTRGV	
5370	NP96	IPRGKLSTRGVQIAS	
5371	NP97	KLSTRGVQIASNENV	
5372	NP98	RGVQIASNENVETMD	
5373	NP99	IASNENVETMDSNTL	
5374	NP100	ENVETMDSNTLELRS	
5375	NP101	TMDSNTLELRSRYWA	
5376	NP102	NTLELRSRYWAIRTR	
5377	NP103	RTRSGGNTNQQKASA	
5378	NP104	GGNTNQQKASAGQIS	
5379	NP105	NQQKASAGQISVQPT	
5380	NP106	ASAGQISVQPTFSVQ	
5381	NP107	QISVQPTFSVQRNLP	
5382	NP108	QPTFSVQRNLPFERA	
5383	NP109	SVQRNLPFERATVMA	
5384	NP110	NLPFERATVMAAFSG	
5385	NP111	ERATVMAAFSGNNEG	

5386	NP112	VMAAFSGNNEGRTSD	
5387	NP113	FSGNNEGRTSDMRTE	
5388	NP114	NEGRTSDMRTEVIRM	
5389	NP115	TSDMRTEVIRMMESA	
5390	NP116	RTEVIRMMESAKPED	
5391	NP117	IRMMESAKPEDLSFQ	
5392	NP118	ESAKPEDLSFQGRGV	
5393	NP119	PEDLSFQGRGVFELS	
5394	NP120	RGVFELSDEKATNPI	
5395	NP121	ELSDEKATNPIVPSF	
5396	NP122	EKATNPIVPSFDMSN	
5397	NP123	NPIVPSFDMSNEGSY	
5398	NP124	GSYFFGDNAEEYDS	
5399	NP126	DGKWMRELILYDKEE	
5400	NP128	PKKTGGPIYRRVGGK	
5401	NP129	GGPIYRRVGGKWMRE	
5402	NP130	YRRVGGKWMRELILY	
5403	NP131	GGKWMRELILYDKEE	
5404	NP132	MRELILYDKEEIRRV	
5405	NP133	ILYDKEEIRRVWRQA	
5406	NP134	KEEIRRVWRQANNGE	
5407	NP135	RRVWRQANNGEDATA	
5408	NP136	RQANNGEDATAGLTH	
5409	NP138	GTKRSYEQMETDGER	
5410	NP139	SYEQMETDGERQNAT	
5411	NP140	METDGERQNATEIRA	
5412	NP141	GERQNATEIRASVGK	
5413	NP142	NATEIRASVGKMIGG	
5414	NP143	IRASVGKMIGGIGRF	
5415	NP144	VGKMIGGIGRFYIQM	
5416	NP145	IQMCTELKLSDYEGR	
5417	NP146	TELKLSDYEGRLIQN	
5418	NP147	LSDYEGRLIQNSLTI	
5419	NP148	EGRLIQNSLTIERMV	
5420	NP149	IQNSLTIERMVLSAF	
5421	NP150	LTIERMVLSAFDERR	
5422	NP151	PKKTGGPIYRRVNGK	

5423	NP152	GGPIYRRVNGKWMRE	
5424	NP153	YRRVNGKWMRELILY	
5425	NP154	NGKWMRELILYDKEE	
5426	NP155	MRELILYDKEEIRRI	
5427	NP156	ILYDKEEIRRIWRQA	
5428	NP157	KEEIRRIWRQANNGD	
5429	NP158	RRIWRQANNGDDATA	
5430	NP159	RQANNGDDATAGLTH	
5431	NP160	NGDDATAGLTHMMIW	
5432	NP161	ATAGLTHMMIWHSNL	
5433	NP162	LTHMMIWHSNLNDAT	
5434	NP163	GAAGAAVKGVGTMVM	
5435	NP164	AAVKGVGTMVMELVR	
5436	NP165	GVGTMVMELVRMIKR	
5437	NP166	MVMELVRMIKRGIND	
5438	NP167	LVRMIKRGINDRNFW	
5439	NP168	INDRNFWRGENGRKT	
5440	NP169	NFWRGENGRKTRIAY	
5441	NP170	GENGRKTRIAYERMC	
5442	NP171	RKTRIAYERMCNILK	
5443	NP172	IAYERMCNILKGKFQ	
5444	NP173	ILKGKFQTAAQKAMM	
5445	NP174	KFQTAAQKAMMDQVR	
5446	NP175	AAQKAMMDQVRESRN	
5447	NP176	QVRESRNPGNAEFED	
5448	NP177	SRNPGNAEFEDLTFL	
5449	NP178	GNAEFEDLTFLARSA	
5450	NP179	FEDLTFLARSALILR	
5451	NP180	TFLARSALILRGSVA	
5452	NP181	SVAHKSCLPACVYGP	
5453	NP182	KSCLPACVYGPAVAS	
5454	NP183	PACVYGPAVASGYDF	
5455	NP184	YGPAVASGYDFEREG	
5456	NP185	VASGYDFEREGYSLV	
5457	NP186	YDFEREGYSLVGIDP	
5458	NP187	REGYSLVGIDPFRLL	
5459	NP188	SLVGIDPFRLLQNSQ	

5460	NP189	IDPFRLLQNSQVYSL	
5461	NP190	RLLQNSQVYSLIRPN	
5462	NP191	NSQVYSLIRPNENPA	
5463	NP192	YSLIRPNENPAHKSQ	
5464	NP193	CHSAAFEDLRVLSFI	
5465	NP194	AFEDLRVLSFIKGTK	
5466	NP195	LRVLSFIKGTKVLPR	
5467	NP196	SFIKGTKVLPRGKLS	
5468	NP197	GTKVLPRGKLSTRGV	
5469	NP198	LPRGKLSTRGVQIAS	
5470	NP199	KLSTRGVQIASNENM	
5471	NP200	RGVQIASNENMETME	
5472	NP201	IASNENMETMESSTL	
5473	NP202	ENMETMESSTLELRS	
5474	NP203	TMESSTLELRSRYWA	
5475	NP204	STLELRSRYWAIRTR	
5476	NP205	RTRSGGNTNQQRASA	
5477	NP206	GGNTNQQRASAGQIS	
5478	NP207	NQQRASAGQISIQPT	
5479	NP208	ASAGQISIQPTFSVQ	
5480	NP209	QISIQPTFSVQRNLP	
5481	NP210	QPTFSVQRNLPFDRT	
5482	NP211	SVQRNLPFDRTTIMA	
5483	NP212	NLPFDRTTIMAAFNG	
5484	NP213	DRTTIMAAFNGNTEG	
5485	NP214	IMAAFNGNTEGRTSD	
5486	NP215	FNGNTEGRTSDMRTE	
5487	NP216	TEGRTSDMRTEIIRM	
5488	NP217	TSDMRTEIIRMMESA	
5489	NP218	RTEIIRMMESARPED	
5490	NP219	IRMMESARPEDVSFQ	
5491	NP220	ESARPEDVSFQGRGV	
5492	NP221	PEDVSFQGRGVFELS	
5493	NP222	RGVFELSDEKAASPI	
5494	NP223	ELSDEKAASPIVPSF	
5495	NP224	EKAASPIVPSFDMSN	
5496	NP225	SPIVPSFDMSNEGSY	

5497	NP226	GSYFFGDNAEEYDN	
5498	NP228	SVQRNLPFDRTTVMA	
5499	NP229	NLPFDRTTVMAAFSG	
5500	NP230	DRTTVMAAFSGNTEG	
5501	NP231	VMAAFSGNTEGRTSD	
5502	NP232	FSGNTEGRTSDMRTE	
5503	NP234	AAQKAMMDQVRESRD	
5504	NP235	AMMDQVRESRDPGNA	
5505	NP236	QVRESRDPGNAEFED	
5506	NP237	SRDPGNAEFEDLTFL	
5507	NP238	LRVLSFIKGTKVVPR	
5508	NP239	SFIKGTKVVPRGKLS	
5509	NP240	GTKVVPRGKLSTRGV	
5510	NP241	VPRGKLSTRGVQIAS	
5511	NP242	NLPFDRTTVMAAFTG	
5512	NP243	DRTTVMAAFTGNTEG	
5513	NP244	VMAAFTGNTEGRTSD	
5514	NP245	FTGNTEGRTSDMRTE	
5515	NP247	LPRGKLSTRGVQITS	
5516	NP248	KLSTRGVQITSNENM	
5517	NP249	RGVQITSNENMETME	
5518	NP250	ITSNENMETMESSTL	
5519	NP251	ENMETMESSTLELGS	
5520	NP252	TMESSTLELGSRYWA	
5521	NP253	STLELGSRYWAIRTR	
5522	NP254	LGSRYWAIRTRSGGN	
5523	NP255	LPRGKLSTRGVQIAP	
5524	NP256	KLSTRGVQIAPNENM	
5525	NP257	RGVQIAPNENMETME	
5526	NP258	IAPNENMETMESSTL	
5527	NP260	KLSTRGVQIASDENM	
5528	NP261	RGVQIASDENMETME	
5529	NP262	IASDENMETMESSTL	
5530	NP264	KLSTRGVQIASNEDM	
5531	NP265	RGVQIASNEDMETME	
5532	NP266	IASNEDMETMESSTL	
5533	NP267	EDMETMESSTLELRS	

5534	NP269	KLSTRGVQIASNEHM	
5535	NP270	RGVQIASNEHMETME	
5536	NP271	IASNEHMETMESSTL	
5537	NP272	EHMETMESSTLELRS	
5538	NP274	RGVQIASNEHMGTME	
5539	NP275	IASNEHMGTMESSTL	
5540	NP276	EHMGTMESSTLELRS	
5541	NP278	INLHQRDEVLPRGKL	
5542	NP279	QRDEVLPRGKLSNRG	
5543	NP280	VLPRGKLSNRGVQIA	
5544	NP281	GKLSNRGVQIASNEH	
5545	NP282	NRGVQIASNEHMATME	

Fig. 7 continued

SEQ ID NO:	**Peptide**	**AMINO ACID SEQUENCE**	**Post-translational modification**
5546	PB1	MDVNPTLLFLKIPAQ	
5547	PB2	PTLLFLKIPAQNAIS	
5548	PB3	FLKIPAQNAISTTFP	
5549	PB4	PAQNAISTTFPYTGD	
5550	PB5	AISTTFPYTGDPPYS	
5551	PB6	TFPYTGDPPYSHGTG	
5552	PB7	TGDPPYSHGTGTGYT	
5553	PB8	PYSHGTGTGYTMDTV	
5554	PB9	GTGTGYTMDTVNRTH	
5555	PB10	GYTMDTVNRTHQYSE	
5556	PB11	DTVNRTHQYSEKGKW	
5557	PB12	RTHQYSEKGKWTTNT	
5558	PB13	YSEKGKWTTNTETGA	
5559	PB14	GKWTTNTETGAPQLN	
5560	PB15	TNTETGAPQLNPIDG	
5561	PB16	TGAPQLNPIDGPLPE	
5562	PB17	QLNPIDGPLPEDNEP	
5563	PB18	IDGPLPEDNEPSGYA	
5564	PB19	LPEDNEPSGYAQTDC	
5565	PB20	NEPSGYAQTDCVLEA	
5566	PB21	GYAQTDCVLEAMAFL	
5567	PB22	TDCVLEAMAFLEESH	
5568	PB23	LEAMAFLEESHPGIF	

5569	PB24	AFLEESHPGIFENSC	
5570	PB25	ESHPGIFENSCLETM	
5571	PB26	GIFENSCLETMEVVQ	
5572	PB27	NSCLETMEVVQQTRV	
5573	PB28	ETMEVVQQTRVDKLT	
5574	PB29	VVQQTRVDKLTQGRQ	
5575	PB30	TRVDKLTQGRQTYDW	
5576	PB31	KLTQGRQTYDWTLNR	
5577	PB32	GRQTYDWTLNRNQPA	
5578	PB33	YDWTLNRNQPAATAL	
5579	PB34	LNRNQPAATALANTI	
5580	PB35	QPAATALANTIEVFR	
5581	PB36	TALANTIEVFRSNGL	
5582	PB37	NTIEVFRSNGLTANE	
5583	PB38	VFRSNGLTANESGRL	
5584	PB39	NGLTANESGRLIDFL	
5585	PB40	ANESGRLIDFLKDVM	
5586	PB41	GRLIDFLKDVMESMN	
5587	PB42	DFLKDVMESMNKEEI	
5588	PB43	DVMESMNKEEIEITT	
5589	PB44	SMNKEEIEITTHFQR	
5590	PB45	EEIEITTHFQRKRRV	
5591	PB46	ITTHFQRKRRVRDNM	
5592	PB47	FQRKRRVRDNMTKKM	
5593	PB48	RRVRDNMTKKMVTQR	
5594	PB49	DNMTKKMVTQRTIGK	
5595	PB50	KKMVTQRTIGKKKQR	
5596	PB51	TQRTIGKKKQRLNKR	
5597	PB52	IGKKKQRLNKRGYLI	
5598	PB53	KQRLNKRGYLIRALT	
5599	PB54	NKRGYLIRALTLNTM	
5600	PB55	YLIRALTLNTMTKDA	
5601	PB56	ALTLNTMTKDAERGK	
5602	PB57	NTMTKDAERGKLKRR	
5603	PB58	KDAERGKLKRRAIAT	
5604	PB59	RGKLKRRAIATPGMQ	
5605	PB60	KRRAIATPGMQIRGF	
5606	PB61	IATPGMQIRGFVYFV	
5607	PB62	GMQIRGFVYFVETLA	

5608	PB63	RGFVYFVETLARSIC	
5609	PB64	YFVETLARSICEKLE	
5610	PB65	TLARSICEKLEQSGL	
5611	PB66	SICEKLEQSGLPVGG	
5612	PB67	KLEQSGLPVGGNEKK	
5613	PB68	SGLPVGGNEKKAKLA	
5614	PB69	VGGNEKKAKLANVVR	
5615	PB70	EKKAKLANVVRKMMT	
5616	PB71	KLANVVRKMMTNSQD	
5617	PB72	VVRKMMTNSQDTEIS	
5618	PB73	MMTNSQDTEISFTIT	
5619	PB74	SQDTEISFTITGDNT	
5620	PB75	EISFTITGDNTKWNE	
5621	PB76	TITGDNTKWNENQNP	
5622	PB77	DNTKWNENQNPRMFL	
5623	PB78	WNENQNPRMFLAMIT	
5624	PB79	QNPRMFLAMITYITR	
5625	PB80	MFLAMITYITRNQPE	
5626	PB81	MITYITRNQPEWFRN	
5627	PB82	ITRNQPEWFRNILSM	
5628	PB83	QPEWFRNILSMAPIM	
5629	PB84	FRNILSMAPIMFSNK	
5630	PB85	LSMAPIMFSNKMARL	
5631	PB86	PIMFSNKMARLGKGY	
5632	PB87	SNKMARLGKGYMFES	
5633	PB88	ARLGKGYMFESKRMK	
5634	PB89	KGYMFESKRMKIRTQ	
5635	PB90	FESKRMKIRTQIPAE	
5636	PB91	RMKIRTQIPAEMLAS	
5637	PB92	RTQIPAEMLASIDLK	
5638	PB93	PAEMLASIDLKYFNE	
5639	PB94	LASIDLKYFNESTKK	
5640	PB95	DLKYFNESTKKKIEK	
5641	PB96	FNESTKKKIEKIRPL	
5642	PB97	TKKKIEKIRPLLIDG	
5643	PB98	IEKIRPLLIDGTASL	
5644	PB99	RPLLIDGTASLSPGM	
5645	PB100	IDGTASLSPGMMMGM	
5646	PB101	ASLSPGMMMGMFNML	

5647	PB102	PGMMMGMFNMLSTVL	
5648	PB103	MGMFNMLSTVLGVSI	
5649	PB104	NMLSTVLGVSILNLG	
5650	PB105	TVLGVSILNLGQKKY	
5651	PB106	VSILNLGQKKYTKTI	
5652	PB107	NLGQKKYTKTIYWWD	
5653	PB108	KKYTKTIYWWDGLQS	
5654	PB109	KTIYWWDGLQSSDDF	
5655	PB110	WWDGLQSSDDFALIV	
5656	PB111	LQSSDDFALIVNAPN	
5657	PB112	DDFALIVNAPNHEGI	
5658	PB113	LIVNAPNHEGIQAGV	
5659	PB114	APNHEGIQAGVDRFY	
5660	PB115	EGIQAGVDRFYRTCK	
5661	PB116	AGVDRFYRTCKLVGI	
5662	PB117	RFYRTCKLVGINMSK	
5663	PB118	TCKLVGINMSKKKSY	
5664	PB119	VGINMSKKKSYINKT	
5665	PB120	MSKKKSYINKTGTFE	
5666	PB121	KSYINKTGTFEFTSF	
5667	PB122	NKTGTFEFTSFFYRY	
5668	PB123	TFEFTSFFYRYGFVA	
5669	PB124	TSFFYRYGFVANFSM	
5670	PB125	YRYGFVANFSMELPS	
5671	PB126	FVANFSMELPSFGVS	
5672	PB127	FSMELPSFGVSGVNE	
5673	PB128	LPSFGVSGVNESADM	
5674	PB129	GVSGVNESADMSIGV	
5675	PB130	VNESADMSIGVTVIK	
5676	PB131	ADMSIGVTVIKNNMI	
5677	PB132	IGVTVIKNNMINNDL	
5678	PB133	VIKNNMINNDLGPAT	
5679	PB134	NMINNDLGPATAQMA	
5680	PB135	NDLGPATAQMALQLF	
5681	PB136	PATAQMALQLFIKDY	
5682	PB137	QMALQLFIKDYRYTY	
5683	PB138	QLFIKDYRYTYRCHR	
5684	PB139	KDYRYTYRCHRGDTQ	
5685	PB140	YTYRCHRGDTQIQTR	

5686	PB141	CHRGDTQIQTRRSFE	
5687	PB142	DTQIQTRRSFELKKL	
5688	PB143	QTRRSFELKKLWDQT	
5689	PB144	SFELKKLWDQTQSKV	
5690	PB145	KKLWDQTQSKVGLLV	
5691	PB146	DQTQSKVGLLVSDGG	
5692	PB147	SKVGLLVSDGGPNLY	
5693	PB148	LLVSDGGPNLYNIRN	
5694	PB149	DGGPNLYNIRNLHIP	
5695	PB150	NLYNIRNLHIPEVCL	
5696	PB151	IRNLHIPEVCLKWEL	
5697	PB152	HIPEVCLKWELMDDD	
5698	PB153	VCLKWELMDDDYRGR	
5699	PB154	WELMDDDYRGRLCNP	
5700	PB155	DDDYRGRLCNPLNPF	
5701	PB156	RGRLCNPLNPFVSHK	
5702	PB157	CNPLNPFVSHKEIDS	
5703	PB158	NPFVSHKEIDSVNNA	
5704	PB159	SHKEIDSVNNAVVMP	
5705	PB160	IDSVNNAVVMPAHGP	
5706	PB161	NNAVVMPAHGPAKSM	
5707	PB162	VMPAHGPAKSMEYDA	
5708	PB163	HGPAKSMEYDAVATT	
5709	PB164	KSMEYDAVATTHSWI	
5710	PB165	YDAVATTHSWIPKRN	
5711	PB166	ATTHSWIPKRNRSIL	
5712	PB167	SWIPKRNRSILNTSQ	
5713	PB168	KRNRSILNTSQRGIL	
5714	PB169	SILNTSQRGILEDEQ	
5715	PB170	TSQRGILEDEQMYQK	
5716	PB171	GILEDEQMYQKCCNL	
5717	PB172	DEQMYQKCCNLFEKF	
5718	PB173	YQKCCNLFEKFFPSS	
5719	PB174	CNLFEKFFPSSSYRR	
5720	PB175	EKFFPSSSYRRPVGI	
5721	PB176	PSSSYRRPVGISSMV	
5722	PB177	YRRPVGISSMVEAMV	
5723	PB178	VGISSMVEAMVSRAR	
5724	PB179	SMVEAMVSRARIDAR	

5725	PB180	AMVSRARIDARVDFE	
5726	PB181	RARIDARVDFESGRI	
5727	PB182	DARVDFESGRIKKEE	
5728	PB183	DFESGRIKKEEFSEI	
5729	PB184	GRIKKEEFSEIMKIC	
5730	PB185	KEEFSEIMKICSTIE	
5731	PB186	SEIMKICSTIEELRR	
5732	PB187	KICSTIEELRRQK	

Fig. 7 continued

SEQ ID NO:	Peptide	AMINO ACID SEQUENCE	Post-translational modification
5733	RFX4-1	MNWAAFGGSEFFIPE	
5734	RFX4-2	AFGGSEFFIPEGIQI	
5735	RFX4-3	GSEFFIPEGIQID	
5736	RFX4-4	SEFFIPEGIQI	
5737	RFX4-5	SEFFIPEGIQIDSRC	
5738	RFX4-6	IPEGIQIDSRCPLSR	
5739	RFX4-7	IQIDSRCPLSRNITE	
5740	RFX4-8	SRCPLSRNITEWYHY	
5741	RFX4-9	LSRNITEWYHYYGIA	
5742	RFX4-10	ITEWYHYYGIAVKES	
5743	RFX4-11	YHYYGIAVKESSQYY	
5744	RFX4-12	GIAVKESSQYYDVMY	
5745	RFX4-13	KESSQYYDVMYSKKG	
5746	RFX4-14	QYYDVMYSKKGAAWV	
5747	RFX4-15	VMYSKKGAAWVSETG	
5748	RFX4-16	KKGAAWVSETGKKEV	
5749	RFX4-17	AWVSETGKKEVSKQT	
5750	RFX4-18	ETGKKEVSKQTVAYS	
5751	RFX4-19	KEVSKQTVAYSPRSK	
5752	RFX4-20	KQTVAYSPRSKLGTL	
5753	RFX4-21	AYSPRSKLGTLLPEF	
5754	RFX4-22	RSKLGTLLPEFPNVK	
5755	RFX4-23	GTLLPEFPNVKDLNL	
5756	RFX4-24	PEFPNVKDLNLPASL	
5757	RFX4-25	NVKDLNLPASLPEEK	
5758	RFX4-26	LNLPASLPEEKVSTF	
5759	RFX4-27	ASLPEEKVSTFIMMY	

5760	RFX4-28	EEKVSTFIMMYRTHC	
5761	RFX4-29	STFIMMYRTHCQRIL	
5762	RFX4-30	MMYRTHCQRILDTVI	
5763	RFX4-31	THCQRILDTVIRANF	
5764	RFX4-32	RILDTVIRANFDEVQ	
5765	RFX4-33	TVIRANFDEVQSFLL	
5766	RFX4-34	ANFDEVQSFLLHFWQ	
5767	RFX4-35	EVQSFLLHFWQGMPP	
5768	RFX4-36	FLLHFWQGMPPHMLP	
5769	RFX4-37	FWQGMPPHMLPVLGS	
5770	RFX4-38	MPPHMLPVLGSSTVV	
5771	RFX4-39	MLPVLGSSTVVNIVG	
5772	RFX4-40	LGSSTVVNIVGVCDS	
5773	RFX4-41	TVVNIVGVCDSILYK	
5774	RFX4-42	IVGVCDSILYKAISG	
5775	RFX4-43	CDSILYKAISGVLMP	
5776	RFX4-44	LYKAISGVLMPTVLQ	
5777	RFX4-45	ISGVLMPTVLQALPD	
5778	RFX4-46	LMPTVLQALPDSLTQ	
5779	RFX4-47	VLQALPDSLTQVIRK	
5780	RFX4-48	LPDSLTQVIRKFAKQ	
5781	RFX4-49	LTQVIRKFAKQLDEW	
5782	RFX4-50	IRKFAKQLDEWLKVA	
5783	RFX4-51	AKQLDEWLKVALHDL	
5784	RFX4-52	DEWLKVALHDLPENL	
5785	RFX4-53	KVALHDLPENLRNIK	
5786	RFX4-54	HDLPENLRNIKFELS	
5787	RFX4-55	ENLRNIKFELSRRFS	
5788	RFX4-56	NIKFELSRRFSQILR	
5789	RFX4-57	ELSRRFSQILRRQTS	
5790	RFX4-58	RFSQILRRQTSLNHL	
5791	RFX4-59	ILRRQTSLNHLCQAS	
5792	RFX4-60	QTSLNHLCQASRTVI	
5793	RFX4-61	NHLCQASRTVIHSAD	
5794	RFX4-62	QASRTVIHSADITFQ	
5795	RFX4-63	TVIHSADITFQMLED	
5796	RFX4-64	SADITFQMLEDWRNV	
5797	RFX4-65	TFQMLEDWRNVDLNS	
5798	RFX4-66	LEDWRNVDLNSITKQ	

5799	RFX4-67	RNVDLNSITKQTLYT	
5800	RFX4-68	LNSITKQTLYTMEDS	
5801	RFX4-69	TKQTLYTMEDSRDEH	
5802	RFX4-70	LYTMEDSRDEHRKLI	
5803	RFX4-71	EDSRDEHRKLITQLY	
5804	RFX4-72	DEHRKLITQLYQEFD	
5805	RFX4-73	KLITQLYQEFDHLLE	
5806	RFX4-74	QLYQEFDHLLEEQSP	
5807	RFX4-75	EFDHLLEEQSPIESY	
5808	RFX4-76	LLEEQSPIESYIEWL	
5809	RFX4-77	QSPIESYIEWLDTMV	
5810	RFX4-78	ESYIEWLDTMVDRCV	
5811	RFX4-79	EWLDTMVDRCVVKVA	
5812	RFX4-80	TMVDRCVVKVAAKRQ	
5813	RFX4-81	RCVVKVAAKRQGSLK	
5814	RFX4-82	KVAAKRQGSLKKVAQ	
5815	RFX4-83	KRQGSLKKVAQQFLL	
5816	RFX4-84	SLKKVAQQFLLMWSC	
5817	RFX4-85	VAQQFLLMWSCFGTR	
5818	RFX4-86	FLLMWSCFGTRVIRD	
5819	RFX4-87	WSCFGTRVIRDMTLH	
5820	RFX4-88	GTRVIRDMTLHSAPS	
5821	RFX4-89	IRDMTLHSAPSFGSF	
5822	RFX4-90	TLHSAPSFGSFHLIH	
5823	RFX4-91	APSFGSFHLIHLMFD	
5824	RFX4-92	GSFHLIHLMFDDYVL	
5825	RFX4-93	LIHLMFDDYVLYLLE	
5826	RFX4-94	MFDDYVLYLLESLHC	
5827	RFX4-95	YVLYLLESLHCQERA	
5828	RFX4-96	LLESLHCQERANELM	
5829	RFX4-97	LHCQERANELMRAMK	
5830	RFX4-98	ERANELMRAMKGEGS	
5831	RFX4-99	ELMRAMKGEGSTAEV	
5832	RFX4-100	AMKGEGSTAEVREEI	
5833	RFX4-101	EGSTAEVREEIILTE	
5834	RFX4-102	AEVREEIILTEAAAP	
5835	RFX4-103	EEIILTEAAAPTPSP	
5836	RFX4-104	LTEAAAPTPSPVPSF	
5837	RFX4-105	AAPTPSPVPSFSPAK	

5838	RFX4-106	PSPVPSFSPAKSATS	
5839	RFX4-107	PSFSPAKSATSVEVP	
5840	RFX4-108	PAKSATSVEVPPPSS	
5841	RFX4-109	ATSVEVPPPSSPVSN	
5842	RFX4-110	EVPPPSSPVSNPSPE	
5843	RFX4-111	PSSPVSNPSPEYTGL	
5844	RFX4-112	VSNPSPEYTGLSTTG	
5845	RFX4-113	SPEYTGLSTTGAMQS	
5846	RFX4-114	TGLSTTGAMQSYTWS	
5847	RFX4-115	TTGAMQSYTWSLTYT	
5848	RFX4-116	TWSLTYTVTTAAGSP	
5849	RFX4-117	TYTVTTAAGSPAENS	
5850	RFX4-118	TTAAGSPAENSQQLP	
5851	RFX4-119	GSPAENSQQLPCMRN	
5852	RFX4-120	ENSQQLPCMRNTHVP	
5853	RFX4-121	QLPCMRNTHVPSSSV	
5854	RFX4-122	MRNTHVPSSSVTHRI	
5855	RFX4-123	HVPSSSVTHRIPVYP	
5856	RFX4-124	SSVTHRIPVYPHREE	
5857	RFX4-125	HRIPVYPHREEHGYT	
5858	RFX4-126	VYPHREEHGYTGSYN	
5859	RFX4-127	REEHGYTGSYNYGSY	
5860	RFX4-128	GYTGSYNYGSYGNQH	
5861	RFX4-129	SYNYGSYGNQHPHPM	
5862	RFX4-130	GSYGNQHPHPMQSQY	
5863	RFX4-131	NQHPHPMQSQYPALP	
5864	RFX4-132	HPMQSQYPALPHDTA	
5865	RFX4-133	SQYPALPHDTAISGP	
5866	RFX4-134	ALPHDTAISGPLHYA	
5867	RFX4-135	DTAISGPLHYAPYHR	
5868	RFX4-136	SGPLHYAPYHRSSAQ	
5869	RFX4-137	HYAPYHRSSAQYPFN	
5870	RFX4-138	YHRSSAQYPFNSPTS	
5871	RFX4-139	SAQYPFNSPTSRMEP	
5872	RFX4-140	PFNSPTSRMEPCLMS	
5873	RFX4-141	PTSRMEPCLMSSTPR	
5874	RFX4-142	MEPCLMSSTPRLHPT	
5875	RFX4-143	LMSSTPRLHPTPVTP	
5876	RFX4-144	TPRLHPTPVTPRWPE	

5877	RFX4-145	HPTPVTPRWPEVPSA	
5878	RFX4-146	VTPRWPEVPSANTCY	
5879	RFX4-147	WPEVPSANTCYTSPS	
5880	RFX4-148	PSANTCYTSPSVHSA	
5881	RFX4-149	TCYTSPSVHSARYGN	
5882	RFX4-150	SPSVHSARYGNSSDM	
5883	RFX4-151	HSARYGNSSDMYTPL	
5884	RFX4-152	YGNSSDMYTPLTTRR	
5885	RFX4-153	SDMYTPLTTRRNSEY	
5886	RFX4-154	TPLTTRRNSEYEHMQ	
5887	RFX4-155	TRRNSEYEHMQHFPG	
5888	RFX4-156	SEYEHMQHFPGFAYI	
5889	RFX4-157	HMQHFPGFAYINGEA	
5890	RFX4-158	FPGFAYINGEASTGW	
5891	RFX4-159	AYINGEASTGWAK	
5892	RFX4-160	MHCGLLEEPDMDSTE	
5893	RFX4-161	LLEEPDMDSTESWIE	
5894	RFX4-162	PDMDSTESWIERCLN	
5895	RFX4-163	STESWIERCLNESEN	
5896	RFX4-164	WIERCLNESENKRYS	
5897	RFX4-165	CLNESENKRYSSHTS	
5898	RFX4-166	SENKRYSSHTSLGNV	
5899	RFX4-167	RYSSHTSLGNVSNDE	
5900	RFX4-168	HTSLGNVSNDENEEK	
5901	RFX4-169	GNVSNDENEEKENNR	
5902	RFX4-170	NDENEEKENNRASKP	
5903	RFX4-171	EEKENNRASKPHSTP	
5904	RFX4-172	NNRASKPHSTPATLQ	
5905	RFX4-173	SKPHSTPATLQWLEE	
5906	RFX4-174	STPATLQWLEENYEI	
5907	RFX4-175	TLQWLEENYEIAEGV	
5908	RFX4-176	LEENYEIAEGVCIPR	
5909	RFX4-177	YEIAEGVCIPRSALY	
5910	RFX4-178	EGVCIPRSALYMHYL	
5911	RFX4-179	IPRSALYMHYLDFCE	
5912	RFX4-180	ALYMHYLDFCEKNDT	
5913	RFX4-181	HYLDFCEKNDTQPVN	
5914	RFX4-182	FCEKNDTQPVNAASF	
5915	RFX4-183	NDTQPVNAASFGKII	

5916	RFX4-184	PVNAASFGKIIRQQF	
5917	RFX4-185	ASFGKIIRQQFPQLT	
5918	RFX4-186	KIIRQQFPQLTTRRL	
5919	RFX4-187	QQFPQLTTRRLGTRG	
5920	RFX4-188	QLTTRRLGTRGQSKY	
5921	RFX4-189	RRLGTRGQSKYHYYG	
5922	RFX4-190	TRGQSKYHYYGIAVK	
5923	RFX4-191	SKYHYYGIAVKESSQ	
5924	RFX4-192	YYGIAVKESSQYYDV	
5925	RFX4-193	MIKRRAHPGAGGDRT	
5926	RFX4-194	RAHPGAGGDRTRPRR	
5927	RFX4-195	GAGGDRTRPRRRRST	
5928	RFX4-196	DRTRPRRRRSTESWI	
5929	RFX4-197	PRRRRSTESWIERCL	
5930	RFX4-198	RSTESWIERCLNESE	
5931	RFX4-199	SWIERCLNESENKRY	
5932	RFX4-200	GLSTTGNGKSFKNFG	
5933	RFX4-201	TGNGKSFKNFG	
5934	RFX4-202	NGKSFKNFG	
5935	RFX4-203	SPEYTGLSTTGAMQA	
5936	RFX4-204	TGLSTTGAMQAYTWS	
5937	RFX4-205	TTGAMQAYTWSLTYT	
5938	RFX4-206	MQAYTWSLTYTVTTA	
5939	RFX4-207	WPEVPSANTCYTNPS	
5940	RFX4-208	PSANTCYTNPSVHSA	
5941	RFX4-209	TCYTNPSVHSARYGN	
5942	RFX4-210	NPSVHSARYGNSSDM	
5943	RFX4-211	MQSYTWSLTYTVTTA	
5944	RFX4-212	LMPTVLQALPDSLTQ	
5945	RFX4-213	VLQALPDSLTQVIRK	
5946	RFX4-214	LTQVIRKFAKQLDEW	

Fig. 7 continued

SEQ ID NO:	**Peptide**	**AMINO ACID SEQUENCE**	**Post-translational modification**
5947	HCRT1	MNLPSTKVSWAAVTL	
5948	HCRT2	STKVSWAAVTLLLLL	
5949	HCRT3	SWAAVTLLLLLLLLP	
5950	HCRT4	VTLLLLLLLLPPALL	

5951	HCRT5	LLLLLLPPALLSSGA	
5952	HCRT6	LLPPALLSSGAAAQP	
5953	HCRT7	ALLSSGAAAQPLPDC	
5954	HCRT8	SGAAAQPLPDCCRQK	
5955	HCRT9	AQPLPDCCRQKTCSC	
5956	HCRT10	AQPLPDCCRQKTCSC	Double disulfide bond
5957	HCRT11	PDCCRQKTCSCRLYE	
5958	HCRT12	PDCCRQKTCSCRLYE	Double disulfide bond
5959	HCRT13	RQKTCSCRLYELLHG	
5960	HCRT14	CSCRLYELLHGAGNH	
5961	HCRT15	LYELLHGAGNHAAGI	
5962	HCRT16	LHGAGNHAAGILTLG	
5963	HCRT17	GNHAAGILTLGKRRS	
5964	HCRT18	AGILTLGKRRSGPPG	
5965	HCRT19	TLGKRRSGPPGLQGR	
5966	HCRT20	RRSGPPGLQGRLQRL	
5967	HCRT21	PPGLQGRLQRLLQAS	
5968	HCRT22	QGRLQRLLQASGNHA	
5969	HCRT23	QRLLQASGNHAAGIL	
5970	HCRT24	QASGNHAAGILTMGR	
5971	HCRT25	NHAAGILTMGRRAGA	
5972	HCRT26	GILTMGRRAGAEPAP	
5973	HCRT27	MGRRAGAEPAPRPCL	
5974	HCRT28	AGAEPAPRPCLGRRC	
5975	HCRT29	PAPRPCLGRRCSAPA	
5976	HCRT30	PCLGRRCSAPAAASV	
5977	HCRT31	RRCSAPAAASVAPGG	
5978	HCRT32	APAAASVAPGGQSGI	
5979	HCRT33	HGAGNHAAGILTL	
5980	HCRT34	EPLPDCCRQKTCSCR	
5981	HCRT35	pEPLPDCCRQKTCSCR	(pyroglutamte N terminus)
5982	HCRT36	HGAGNHAAGILTL	
5983	HCRT37	HGAGNHAAGILTL	(C-amidated (NH2))
5984	HCRT38	DCCRQKTCSCRLYEL	
5985	HCRT39	DCCRQKTCSCRLYEL	Double disulfide bond
5986	HCRT40	ASGNHAAGILTM	
5987	HCRT41	ASGNHAAGILTM	(C-amidated (NH2))

Fig. 7 continued

Fig. 8

SEQ ID NO:	Peptide	Amino acid sequence
5988	PDC-E2$_{65-84}$	SGATPRNRLLLQLLGSPGRR
5989	PDC-E2$_{73-92}$	LLLQLLGSPGRRYYSLPPHQ
5990	PDC-E2$_{89-108}$	PPHQKVPLPSLSPTMQAGTI
5991	PDC-E2$_{97-116}$	PSLSPTMQAGTIARWEKKEG
5992	PDC-E2$_{113-132}$	KKEGDKINEGDLIAEVETDK
5993	PDC-E2$_{209-228}$	QAPGSSYPPHMQVLLPALSP
5994	PDC-E2$_{217-236}$	PHMQVLLPALSPTMTMGTVQ
5995	PDC-E2$_{241-260}$	KVGEKLSEGDLLAEIETDKA
5996	PDC-E2$_{273-292}$	AKILVPEGTRDVPLGTPLCI
5997	PDC-E2$_{321-340}$	PTPPPVAAVPPTPQPLAPTP
5998	PDC-E2$_{401-420}$	PAAVVPPTGPGMAPVPTGVF
5999	PDC-E2$_{425-444}$	ISNIRRVIAQRLMQSKQTIP
6000	PDC-E2$_{449-468}$	SIDVNMGEVLLVRKELNKFF
6001	PDC-E2$_{545-564}$	NDVVSLATKAREGKLQPHEF
6002	PDC-E2$_{617-636}$	MMSVTLSCDHRVVDGAVGAQ
6003	PDC-E2$_{625-644}$	DHRVVDGAVGAQWLAEFRKY
6004	PDC-E2$_{137-156}$	FESLEECYMAKILVAEGTRD
6005	PDC-E2$_{145-164}$	MAKILVAEGTRDVPIGAIIC
6006	PDC-E2$_{153-172}$	GTRDVPIGAIICITVGKPED
6007	PDC-E2$_{257-276}$	TDKATIGFEVQEEGYLAKIL
6008	PDC-E2$_{281-300}$	TRDVPLGTPLCIIVEKEADI
6009	PDC-E2$_{305-324}$	DYRPTEVTDLKPQVPPPTPP
6010	PDC-E2$_{155-185}$	KVGEKLSEGDLLAEIETDKATIGFEVQEEGY

Fig. 9

SEQ ID NO:	Protein name	Sequence
SEQ ID 4981	Insulin (preproinsulin (PPI))	MALWMRLLPLLALLALWGPDPAAAFVNQHL CGSHLVEALYLVCGERGFFYTPKTRREAED LQVGQVELGGGPGAGSLQPLALEGSLQKR GIVEQCCTSICSLYQLENYCN
SEQ ID 6011	Glutamic acid decarboxylase 65-kDa isoform (GAD65)	MNYAFLHATDLLPACDGERPTLAFLQDVMNI LLQYVVKSFDRSTKVIDFHYPNELLQEYNWE LADQPQNLEEILMHCQTTLKYAIKTGHPRYF NQLSTGLDMVGLAADWLTSTANTNMFTYEI APVFVLLEYVTLKKMREIIGWPGGSGDGIFS PGGAISNMYAMMIARFKMFPEVKEKGMAAL PRLIAFTSEHSHFSLKKGAAALGIGTDSVILIK CDERGKMIPSDLERRILEAKQKGFVPFLVSA TAGTTVYGAFDPLLAVADICKKYKIWMHVDA AWGGGLLMSRKHKWKLSGVERANSVTWNP HKMMGVPLQCSALLVREEGLMQNCNQMHA SYLFQQDKHYDLSYDTGDKALQCGRHVDVF KLWLMWRAKGTTGFEAHVDKCLELAEYLYN IIKNREGYEMVFDGKPQHTNVCFWYIPPSLR TLEDNEERMSRLSKVAPVIKARMMEYGTTM VSYQPLGDKVNFFRMVISNPAATHQDIDFLIE EIERLGQDL
SEQ ID 6012	Islet-specific glucose-6-phosphatase catalytic subunit-related protein (IGRP)	MDFLHRNGVLIIQHLQKDYRAYYTFLNFMSN VGDPRNIFFIYFPLCFQFNQTVGTKMIWVAVI GDWLNLIFKWILFGHRPYWWVQETQIYPNH SSPCLEQFPTTCETGPGSPSGHAMGASCV WYVMVTAALSHTVCGMDKFSITLHRLTW SFLWSVFWLIQISVCISRVFIATHFPHQVILGV IGGMLVAEAFEHTPGIQTASLGTYLKTNLFLF LFAVGFYLLLRVLNIDLLWSVPIAKKWCANPD WIHIDTTPFAGLVRNLGVLFGLGFAINSEMFL LSCRGGNNYTLSFRLLCALTSLTILQLYHFLQ IPTHEEHLFYVLSFCKSASIPLTVVAFIPYSVH MLMKQSGKKSQ
SEQ ID 2421	Zinc transporter 8 (ZnT8)	MEFLERTYLVNDKAAKMYAFTLESVELQQK PVNKDQCPRERPEELESGGMYHCHSGSKP TEKGANEYAYAKWKLCSASAICFIFMIAEVV GGHIAGSLAVVTDAAHLLIDLTSFLLSLFSLW LSSKPPSKRLTFGWHRAEILGALLSILCIWVV TGVLVYLACERLLYPDYQIQATVMIIVSSCAV AANIVLTVVLHQRCLGHNHKEVQANASVRA AFVHALGDLFQSISVLISALIIYFKPEYKIADPI CTFIFSILVLASTITILKDFSILLMEGVPKSLNY SGVKELILAVDGVLSVHSLHIWSLTMNQVILS AHVATAASRDSQVVRREIAKALSKSFTMHSL TIQ MESPVDQDPD CLFCEDPCD

SEQ ID 2028	Tyrosine phosphatase like autoantigen or insulinoma antigen-2 (IA2;ICA512,PTPRN)	MRRPRRPGGLGGSGGLRLLLCLLLLSSRPG GCSAVSAHGCLFDRRLCSHLEVCIQDGLFG QCQVGVGQARPLLQVTSPVLQRLQGVLRQL MSQGLSWHDDLTQYVISQEMERIPRLRPPE PRPRDRSGLAPKRPGPAGELLLQDIPTGSAP AAQHRLPQPPVGKGGAGASSSLSPLQAELL PPLLEHLLLPPQPPHPSLSYEPALLQPYLFH QFGSRDGSRVSEGSPGMVSVGPLPKAEAP ALFSRTASKGIFGDHPGHSYGDLPGPSPAQ LFQDSGLLYLAQELPAPSRARVPRLPEQGS SSRAEDSPEGYEKEGLGDRGEKPASPAVQP DAALQRLAAVLAGYGVELRQLTPEQLSTLLT LLQLLPKGAGRNPGGVVNVGADIKKTMEGP VEGRDTAELPARTSPMPGHPTASPTSSEVQ QVPSPVSSEPPKAARPPVTPVLLEKKSPLGQ SQPTVAGQPSARPAAEEYGYIVTDQKPLSLA AGVKLLEILAEHVHMSSGSFINISVVGPALTF RIRHNEQNLSLADVTQQAGLVKSELEAQTGL QILQTGVGQREEAAAVLPQTAHSTSPMRSV LLTLVALAGVAGLLVALAVALCVRQHARQQD KERLAALGPEGAHGDTTFEYQDLCRQHMAT KSLFNRAEGPPEPSRVSSVSSQFSDAAQAS PSSHSSTPSWCEEPAQANMDISTGHMILAY MEDHLRNRDRLAKEWQALCAYQAEPNTCA TAQGEGNIKKNRHPDFLPYDHARIKLKVESS PSRSDYINASPIIEHDPRMPAYIATQGPLSHTI ADFWQMVWESGCTVIVMLTPLVEDGVKQC DRYWPDEGASLYHVYEVNLVSEHIWCEDFL VRSFYLKNVQTQETRTLTQFHFLSWPAEGT PASTRPLLDFRRKVNKCYRGRSCPIIVHCSD GAGRTGTYILIDMVLNRMAKGVKEIDIAATLE HVRDQRPGLVRSKDQFEFALTAVAEEVNAIL KALPQ
SEQ ID 2487	IA-2β (Phogrin, PTPRN2)	MGPPLPLLLLLLLLLPPRVLPAAPSSVPRGR QLPGRLGCLLEEGLCGASEACVNDGVFGRC QKVPAMDFYRYEVSPVALQRLRVALQKLSG TGFTWQDDYTQYVMDQELADLPKTYLRRPE ASSPARPSKHSVGSERRYSREGGAALANAL RRHLPFLEALSQAPASDVLARTHTAQDRPP AEGDDRFSESILTYVAHTSALTYPPGSRTQL REDLLPRTLGQLQPDELSPKVDSGVDRHHL MAALSAYAAQRPPAPPGEGSLEPQYLLRAP SRMPRPLLAPAAPQKWPSPLGDSEDPSSTG DGARIHTLLKDLQRQPAEVRGLSGLELDGM AELMAGLMQGVDHGVARGSPGRAALGESG EQADGPKATLRGDSFPDDGVQDDDDRLYQ EVHRLSATLGGLLQDHGSRLLPGALPFARPL DMERKKSEHPESSLSSEEETAGVENVKSQT YSKDLLGQQPHSEPGAAAFGELQNQMPGP SKEEQSLPAGAQEALSDGLQLEVQPSEEEA RGYIVTDRDPLRPEEGRRLVEDVARLLQVPS

		SAFADVEVLGPAVTFKVSANVQNVTTEDVE KATVDNKDKLEETSGLKILQTGVGSKSKLKF LPPQAEQEDSTKFIALTLVSLACILGVLLASG LIYCLRHSSQHRLKEKLSGLGGDPGADATAA YQELCRQRMATRPPDRPEGPHTSRISSVSS QFSDGPIPSPSARSSASSWSEEPVQSNMDI STGHMILSYMEDHLKNKNRLEKEWEALCAY QAEPNSSFVAQREENVPKNRSLAVLTYDHS RVLLKAENSHSHSDYINASPIMDHDPRNPAY IATQGPLPATVADFWQMVWESGCVVIVMLT PLAENGVRQCYHYWPDEGSNLYHIYEVNLV SEHIWCEDFLVRSFYLKNLQTNETRTVTQFH FLSWYDRGVPSSSRSLLDFRRKVNKCYRGR SCPIIVHCSDGAGRSGTYVLIDMVLNKMAKG AKEIDIAATLEHLRDQRPGMVQTKEQFEFAL TAVAEEVNAILKALPQ
SEQ ID 6013	glutamic acid decarboxylase 67-kDa isoform (GAD67),	MASSTPSSSATSSNAGADPNTTNLRPTTYD TWCGVAHGCTRKLGLKICGFLQRTNSLEEK SRLVSAFKERQSSKNLLSCENSDRDARFRR TETDFSNLFARDLLPAKNGEEQTVQFLLEVV DILLNYVRKTFDRSTKVLDFHHPHQLLEGME GFNLELSDHPESLEQILVDCRDTLKYGVRTG HPRFFNQLSTGLDIIGLAGEWLTSTANTNMF TYEIAPVFVLMEQITLKKMREIVGWSSKDGD GIFSPGGAISNMYSIMAARYKYFPEVKTKGM AAVPKLVLFTSEQSHYSIKKAGAALGFGTDN VILIKCNERGKIIPADFEAKILEAKQKGYVPFY VNATAGTTVYGAFDPIQEIADICEKYNLWLHV DAAWGGGLLMSRKHRHKLNGIERANSVTW NPHKMMGVLLQCSAILVKEKGILQGCNQMC AGYLFQPDKQYDVSYDTGDKAIQCGRHVDI FKFWLMWKAKGTVGFENQINKCLELAEYLY AKIKNREEFEMVFNGEPEHTNVCFWYIPQSL RGVPDSPQRREKLHKVAPKIKALMMESGTT MVGYQPQGDKANFFRMVISNPAATQSDIDF LIEEIERLGQDL
SEQ ID 6014	Islet cell antigen-69 (ICA69)	MSGHKCSYPWDLQDRYAQDKSVVNKMQQ KYWETKQAFIKATGKKEDEHVVASDADLDA KLELFHSIQRTCLDLSKAIVLYQKRICFLSQEE NELGKFLRSQGFQDKTRAGKMMQATGKAL CFSSQQRLALRNPLCRFHQEVETFRHRAISD TWLTVNRMEQCRTEYRGALLWMKDVSQEL DPDLYKQMEKFRKVQTQVRLAKKNFDKLKM DVCQKVDLLGASRCNLLSHMLATYQTTLLHF WEKTSHTMAAIHESFKGYQPYEFTTLKSLQD PMKKLVEKEEKKKINQQESTDAAVQEPSQLI SLEEENQRKESSSFKTEDGKSILSALDKGST HTACSGPIDELLDMKSEEGACLGPVAGTPE PEGADKDDLLLLSEIFNASSLEEGEFSKEWA AVFGDGQVKEPVPTMALGEPDPKAQTGSG

		FLPSQLLDQNMKDLQASLQEPAKAASDLTA WFSLFADLDPLSNPDAVGKTDKEHELLNA
SEQ ID 6015	Chromogranin A	MRSAAVLALLLCAGQVTALPVNSPMNKGDT EVMKCIVEVISDTLSKPSPMPVSQECFETLR GDERILSILRHQNLLKELQDLALQGAKERAH QQKKHSGFEDELSEVLENQSSQAELKEAVE EPSSKDVMEKREDSKEAEKSGEATDGARP QALPEPMQESKAEGNNQAPGEEEEEEEEAT NTHPPASLPSQKYPGPQAEGDSEGLSQGLV DREKGLSAEPGWQAKREEEEEEEEEAEAG EEAVPEEEGPTVVLNPHPSLGYKEIRKGESR SEALAVDGAGKPGAEEAQDPEGKGEQEHS QQKEEEEEMAVVPQGLFRGGKSGELEQEE ERLSKEWEDSKRWSKMDQLAKELTAEKRLE GQEEEEDNRDSSMKLSFRARAYGFRGPGP QLRRGWRPSSREDSLEAGLPLQVRGYPEE KKEEEGSANRRPEDQELESLSAIEAELEKVA HQLQALRRG
SEQ ID 6016	Chromogranin A isoform	MRSAAVLALLLCAGQVTALPVNSPMNKGDT EVMKCIVEVISDTLSKPSPMPVSQECFETLR GDERILSILRHQNLLKELQDLALQGAKERAH QQKKHSGFEDELSEVLENQSSQAELKGRSE ALAVDGAGKPGAEEAQDPEGKGEQEHSQQ KEEEEEMAVVPQGLFRGGKSGELEQEEERL SKEWEDSKRWSKMDQLAKELTAEKRLEGQ EEEEDNRDSSMKLSFRARAYGFRGPGPQL RRGWRPSSREDSLEAGLPLQVRGYPEEKK EEEGSANRRPEDQELESLSAIEAELEKVAHQ LQALRRG
SEQ ID 6017	Peripherin	MSHHPSGLRAGFSSTSYRRTFGPPPSLSPG AFSYSSSSRFSSSRLLGSASPSSSVRLGSFR SPRAGAGALLRLPSERLDFSMAEALNQEFLA TRSNEKQELQELNDRFANFIEKVRFLEQQNA ALRGELSQARGQEPARADQLCQQELRELRR ELELLGRERDRVQVERDGLAEDLAALKQRL EEETRKREDAEHNLVLFRKDVDDATLSRLEL ERKIESLMDEIEFLKKLHEEELRDLQVSVESQ QVQQVEVEATVKPELTAALRDIRAQYESIAA KNLQEAEEWYKSKYADLSDAANRNHEALRQ AKQEMNESRRQIQSLTCEVDGLRGTNEALL RQLRELEEQFALEAGGYQAGAARLEEELRQ LKEEMARHLREYQELLNVKMALDIEIATYRKL LEGEESRISVPVHSFASLNIKTTVPEVEPPQD SHSRKTVLIKTIETRNGEVVTESQKEQRSEL DKSSAHSY
SEQ ID 6018	Peripherin-2	MALLKVKFDQKKRVKLAQGLWLMNWFSVLA GIIIFSLGLFLKIELRKRSDVMNNSESHFVPNS LIGMGVLSCVFNSLAGKICYDALDPAKYARW KPWLKPYLAICVLFNIILFLVALCCFLLRGSLE

		NTLGQGLKNGMKYYRDTDTPGRCFMKKTID MLQIEFKCCGNNGFRDWFEIQWISNRYLDF SSKEVKDRIKSNVDGRYLVDGVPFSCCNPS SPRPCIQYQITNNSAHYSYDHQTEELNLWVR GCRAALLSYYSSLMNSMGVVTLLIWLFEVTIT IGLRYLQTSLDGVSNPEESESESESEGWLLEKS VPETWKAFLESVKKLGKGNQVEAEGAGAG QAPEAG
SEQ ID 6019	Islet amyloid peptide (pplAPP),	MGILKLQVFLIVLSVALNHLKATPIESHQVEK RKCNTATCATQRLANFLVHSSNNFGAILSST NVGSNTYGKRNAVEVLKREPLNYLPL
SEQ ID 6020	carboxypeptidase H/E	MAGRGGSALLALCGALAACGWLLGAEAQE PGAPAAGMRRRRRLQQEDGISFEYHRYPEL REALVSVWLQCTAISRIYTVGRSFEGRELLVI ELSDNPGVHEPGEPEFKYIGNMHGNEAVGR ELLIFLAQYLCNEYQKGNETIVNLIHSTRIHIM PSLNPDGFEKAASQPGELKDWFVGRSNAQ GIDLNRNFPDLDRIVYVNEKEGGPNNHLLKN MKKIVDQNTKLAPETKAVIHWIMDIPFVLSAN LHGGDLVANYPYDETRSGSAHEYSSSPDDA IFQSLARAYSSFNPAMSDPNRPPCRKNDDD SSFVDGTTNGGAWYSVPGGMQDFNYLSSN CFEITVELSCEKFPPEETLKTYWEDNKNSLIS YLEQIHRGVKGFVRDLQGNPIANATISVEGID HDVTSAKDGDYWRLLIPGNYKLTASAPGYLA ITKKVAVPYSPAAGVDFELESFSERKEEEKE ELMEWWKMMSETLNF
SEQ ID 6021	Heat shock protein 60 (Hsp60),	MLRLPTVFRQMRPVSRVLAPHLTRAYAKDV KFGADARALMLQGVDLLADAVAVTMGPKGR TVIIEQSWGSPKVTKDGVTVAKSIDLKDKYK NIGAKLVQDVANNTNEEAGDGTTTATVLARS IAKEGFEKISKGANPVEIRRGVMLAVDAVIAE LKKQSKPVTTPEEIAQVATISANGDKEIGNIIS DAMKKVGRKGVITVKDGKTLNDELEIIEGMK FDRGYISPYFINTSKGQKCEFQDAYVLLSEK KISSIQSIVPALEIANAHRKPLVIIAEDVDGEAL STLVLNRLKVGLQVVAVKAPGFGDNRKNQL KDMAIATGGAVFGEEGLTLNLEDVQPHDLG KVGEVIVTKDDAMLLKGKGDKAQIEKRIQEII EQLDVTTSEYEKEKLNERLAKLSDGVAVLKV GGTSDVEVNEKKDRVTDALNATRAAVEEGI VLGGGCALLRCIPALDSLTPANEDQKIGIEIIK RTLKIPAMTIAKNAGVEGSLIVEKIMQSSSEV GYDAMAGDFVNMVEKGIIDPTKVVRTALLDA AGVASLLTTAEVVVTEIPKEEKDPGMGAMG GMGGGMGGGMF

SEQ ID 6022	Zinc transporter 8 (ZnT8), variant	MEFLERTYLVNDKAAKMYAFTLESVELQQK PVNKDQCPRERPEELESGGMYHCHSGSKP TEKGANEYAYAKWKLCSASAICFIFMIAEVV GGHIAGSLAVVTDAAHLLIDLTSFLLSLFSLW LSSKPPSKRLTFGWHRAEILGALLSILCIWVV TGVLVYLACERLLYPDYQIQATVMIIVSSCAV AANIVLTVVLHQRCLGHNHKEVQANASVRA AFVHALGDLFQSISVLISALIIYFKPEYKIADPI CTFIFSILVLASTITILKDFSILLMEGVPKSLNY SGVKELILAVDGVLSVHSLHIWSLTMNQVILS AHVATAASRDSQVVRREIAKALSKSFTMHSL TIQMESPVDQDPDCLFCEDPC
SEQ ID 6023	Hybrid insulin peptide #1	GQVELGGG-NAVEVLK
SEQ ID 6024	Hybrid insulin peptide #2	GQVELGGG-SSPETLI
SEQ ID 6025	Hybrid insulin peptide #3	GQVELGGG-GIVEQCC
SEQ ID 6026	Hybrid insulin peptide #4	GQVELGGG-TPIESHQ
SEQ ID 6027	Hybrid insulin peptide #5	GQVELGGG-NAVEVLK
SEQ ID 6028	Hybrid insulin peptide #6	VCGERGFF-EELVARSE
SEQ ID 6029	Hybrid insulin peptide #7	HLVEALYL-EELVARSE
SEQ ID 6030	Hybrid insulin peptide #8	ICSLYQLE-FVNQHLCG
SEQ ID 6031	Hybrid insulin peptide #9	SLQKRGIV-EELVARSE
SEQ ID 6032	Hybrid insulin peptide #10	CSLYQLEN-SVPHFSDE
SEQ ID 6033	Hybrid insulin peptide #11	QPLALEGS-ALSSQHQA

Fig. 9 continued