Table S1[a]: Proteins identified in MHC II complex by Nano-LC/MS/MS

Total: 41 genes

Transmembrane proteins 22 Genes

GI_ACCESSION	DAVID Gene Name
18202604	ATPASE, CA++ TRANSPORTING, UBIQUITOUS
16307541	ATPASE, NA+/K+ TRANSPORTING, ALPHA 1 POLYPEPTIDE
6671664	CALNEXIN
6680880	CD37 ANTIGEN
29789020	CD74 ANTIGEN (INVARIANT POLYPEPTIDE OF MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II ANTIGEN-ASSOCIATED)
46195798	DOLICHYL-DI-PHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
16359229	RIBOPHORIN I
31982789	HISTOCOMPATIBILITY 2, CLASS II ANTIGEN E ALPHA
6671710	CD20, MEMBRANE-SPANNING 4-DOMAINS, SUBFAMILY A, MEMBER 1
6649863	MHC CLASS II BETA
34996495	RIBOPHORIN II
37359796	RIKEN CDNA 2410014A08 GENE
14919430	SIGNAL SEQUENCE RECEPTOR, DELTA
22766917	SOLUTE CARRIER FAMILY 1 (NEUTRAL AMINO ACID TRANSPORTER), MEMBER 5
31560670	CD98, SOLUTE CARRIER FAMILY 3 (ACTIVATORS OF DIBASIC AND NEUTRAL AMINO ACID TRANSPORT), MEMBER 2
52430429	TAP BINDING PROTEIN

11596855	TRANSFERRIN RECEPTOR
13385718	TRANSMEMBRANE EMP24 PROTEIN TRANSPORT DOMAIN CONTAINING 9
40555903	TRANSMEMBRANE EMP24-LIKE TRAFFICKING PROTEIN 10 (YEAST)
7305539	TRANSPORTER 1, ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP)
549045	TRANSPORTER 2, ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP)
7305623	VESICLE-ASSOCIATED MEMBRANE PROTEIN, ASSOCIATED PROTEIN A

cellular metabolism	19 Genes
GI_ACCESSION	DAVID Gene Name
6671664	CALNEXIN
29789020	CD74 ANTIGEN (INVARIANT POLYPEPTIDE OF MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II ANTIGEN-ASSOCIATED)
6753322	CHAPERONIN SUBUNIT 4 (DELTA)
46195798	DOLICHYL-DI-PHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
54114937	ENOLASE 1, ALPHA NON-NEURON
16359229	RIBOPHORIN I
2598562	HEAT SHOCK 70KD PROTEIN 5 (GLUCOSE-REGULATED PROTEIN)
55250073	HEAT SHOCK PROTEIN 8
53600	PROLIFERATING CELL NUCLEAR ANTIGEN
31981562	PYRUVATE KINASE, MUSCLE

34996495	RIBOPHORIN II
26353478	RIBOSOMAL PROTEIN L12
12847921	RIBOSOMAL PROTEIN S3
31560670	CD98, SOLUTE CARRIER FAMILY 3 (ACTIVATORS OF DIBASIC AND NEUTRAL AMINO ACID TRANSPORT), MEMBER 2
11596855	TRANSFERRIN RECEPTOR; CD71
549045	TRANSPORTER 2, ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP)
6678469	TUBULIN, ALPHA 6
12963615	TUBULIN, BETA 3
30023842	VALOSIN CONTAINING PROTEIN

Intracellular transport	17 Genes
GI_ACCESSION	DAVID Gene Name
809561	ACTIN, GAMMA, CYTOPLASMIC 1
31980648	ATP SYNTHASE, H+ TRANSPORTING MITOCHONDRIAL F1 COMPLEX, BETA SUBUNIT
6680748	ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F1 COMPLEX, ALPHA SUBUNIT, ISOFORM 1
18202604	ATPASE, CA++ TRANSPORTING, UBIQUITOUS
16307541	ATPASE, NA+/K+ TRANSPORTING, ALPHA 1 POLYPEPTIDE
29789020	CD74 ANTIGEN (INVARIANT POLYPEPTIDE OF MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II ANTIGEN-ASSOCIATED)
6679687	PROTEIN DISULFIDE ISOMERASE ASSOCIATED 3
37359796	RIKEN CDNA 2410014A08 GENE
22766917	SOLUTE CARRIER FAMILY 1 (NEUTRAL AMINO ACID

	TRANSPORTER), MEMBER 5
11596855	TRANSFERRIN RECEPTOR
13385718	TRANSMEMBRANE EMP24 PROTEIN TRANSPORT DOMAIN CONTAINING 9
40555903	TRANSMEMBRANE EMP24-LIKE TRAFFICKING PROTEIN 10 (YEAST)
7305539	TRANSPORTER 1, ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP)
549045	TRANSPORTER 2, ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP)
6678469	TUBULIN, ALPHA 6
12963615	TUBULIN, BETA 3
30023842	VALOSIN CONTAINING PROTEIN

Endoplasmic Reticulum	16 Genes
GI_ACCESSION	DAVID Gene Name
18202604	ATPASE, CA++ TRANSPORTING, UBIQUITOUS
6671664	CALNEXIN
46195798	DOLICHYL-DI-PHOSPHOOLIGOSACCHARIDE-PROTEIN GLYCOTRANSFERASE
16359229	RIBOPHORIN I
2598562	HEAT SHOCK 70KD PROTEIN 5 (GLUCOSE-REGULATED PROTEIN)
31982789	HISTOCOMPATIBILITY 2, CLASS II ANTIGEN E ALPHA
6679687	PROTEIN DISULFIDE ISOMERASE ASSOCIATED 3
34996495	RIBOPHORIN II
37359796	RIKEN CDNA 2410014A08 GENE
14919430	SIGNAL SEQUENCE RECEPTOR, DELTA

52430429	TAP BINDING PROTEIN
13385718	TRANSMEMBRANE EMP24 PROTEIN TRANSPORT DOMAIN CONTAINING 9
40555903	TRANSMEMBRANE EMP24-LIKE TRAFFICKING PROTEIN 10 (YEAST)
7305539	TRANSPORTER 1, ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP)
549045	TRANSPORTER 2, ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP)
30023842	VALOSIN CONTAINING PROTEIN

ANTIGEN PROCESSING AND PRESENTATION	10 Genes
GI_ACCESSION	DAVID Gene Name
6671664	CALNEXIN
29789020	CD74 ANTIGEN (INVARIANT POLYPEPTIDE OF MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II ANTIGEN-ASSOCIATED)
2598562	HEAT SHOCK 70KD PROTEIN 5 (GLUCOSE-REGULATED PROTEIN)
55250073	HEAT SHOCK PROTEIN 8
31982789	HISTOCOMPATIBILITY 2, CLASS II ANTIGEN E ALPHA
6649863	MHC CLASS II BETA
6679687	PROTEIN DISULFIDE ISOMERASE ASSOCIATED 3
52430429	TAP BINDING PROTEIN
7305539	TRANSPORTER 1, ATP-BINDING CASSETTE, SUB-FAMILY B (MDR/TAP)
549045	TRANSPORTER 2, ATP-BINDING CASSETTE, SUB-FAMILY B

	(MDR/TAP)
Molecular Chaperone	5 Genes
GI_ACCESSION	DAVID Gene Name
6671664	CALNEXIN
29789020	CD74 ANTIGEN (INVARIANT POLYPEPTIDE OF MAJOR HISTOCOMPATIBILITY COMPLEX, CLASS II ANTIGEN-ASSOCIATED)
6753322	CHAPERONIN SUBUNIT 4 (DELTA)
2598562	HEAT SHOCK 70KD PROTEIN 5 (GLUCOSE-REGULATED PROTEIN)
55250073	HEAT SHOCK PROTEIN 8
uncluster	4 Genes
GI_ACCESSION	DAVID Gene Name
19527026	LEUCINE RICH REPEAT CONTAINING 59
23272960	COMPLEMENT COMPONENT 1, Q SUBCOMPONENT BINDING PROTEIN
28302158	RIKEN CDNA 2610307O08 GENE
56023216	SIMILAR TO GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (PHOSPHORYLATING)

[a] Proteins in MHC II immunoprecipitation, identified by at least two unique peptides, were functional clustered using DAVID program.

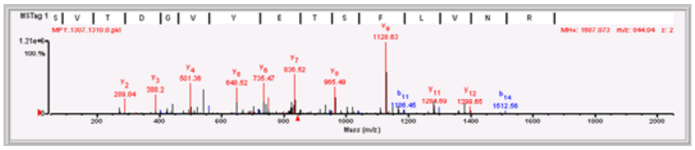
Table S2: PCR primers

Name	Sequence
MPY5	5’-GGAGTCCTGCTAGGTGTCCA-3’
MPY3	5’-CTGTTGACCTGTGTGGATGG-3’
MPYS-EGFP-For	5’CA CCG GTC TAG GAA GCA GAA TTC GCC ACC ATG CCA TAC TCC AAC CTG CAT CCA GCC-3’
MPYS-EGFP-Rev	5’G ACT AGG CTG TCC GCG GCC GCA GAT GAG GTC AG3’
HA-MPY-Rev	5'-TCA CTC GAG TCA AGC GTA GTC TGG GAC GTC GTA TGG GTA GAT GAG GTC AGT GCG GAG TGG GAG AGG-3'
GST-MPYS-For	5’CAG ACC CTG TTT GCC GGG ATC CAG GAT GCC AAA GCT GGC-3’
GST-MPYS-Rev	5’CCC AGA CAA GGC TGT CCG CGG CCG CGA TGA GGT CAG TGC G-3’
Sh5-For	5’TGGATCCGAATGTTCAATCATTCAAGAGATGATTGAACATTCGGATCCTTTTTTC
Sh5-Rev	5’TCGAGAAAAAAGGATCCGAATGTTCAATCATCTCTTGAATGATTGAACATTCGGATCCA-3’.
Sh7-For	5’TGCACATTCGTCAGGAAGAATTCAAGAGATTCTTCCTGACGAAT-3’
Sh7-Rev	5’TCGAGAAAAAAGCACATTCGTCAGGAAGAATCTCTTGAATTCTTCCTGACGAATGTGCA-3’

A

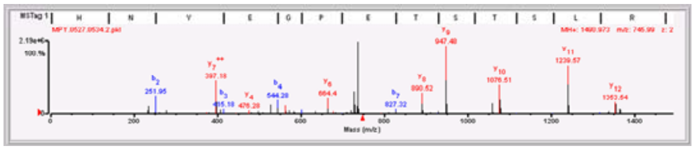
H-2 class II histocompatibility antigen alpha chain.

1	MPCSRALILG	VLALNTMLSL	CGGEDDIEAD	HVGFYGTTVY	QSPGDIGQYT	HEFDGDELFY	VDLDKKKTVW	R**LPEFGQLIL**	80
81	**FEPQGGLQNI**	**AAEKHNLGIL**	**TKRSNFTPAT**	**NEAPQATVFP**	**K**SPVLLGQPN	TLICFVDNIF	PPVINITWLR	NSK**SVTDGVY**	160
161	**ETSFLVNR**DH	SFHKLSYLTF	IPSDDDIYDC	KVEHWGLEEP	VLKHWEPEIP	APMSELTETV	VCALGLSVGL	VGIVVGTIFI	240
241	IQGLR**SGGTS**	**RHPGPL**							256



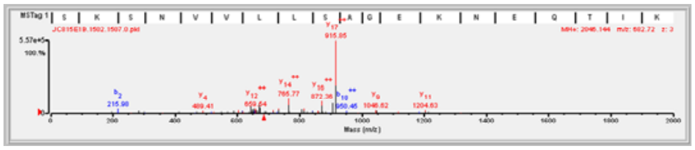
H-2 class II histocompatibility antigen, beta chain.

1	MALQIPSLLL	SAAVVVLMVL	SSPRTEGGNS	ER**HFVVQFK**G	ECYYTNGTQR	**IRLVTRYIYN**	**REEYVRYDSD**	**VGEYR**AVTEL	80
81	GRPDAEYWNS	QPEILER**TRA**	**EVDTACRHNY**	**EGPETSTSLR**	**RLEQPNVAIS**	**LSRTEALNHH**	**NTLVCSVTDF**	**YPAK**IKVRWF	160
161	R**NGQEETVGV**	**SSTQLIR**NGD	WTFQVLVMLE	MTPHQGEVYT	CHVEHPSLK**S**	**PITVEWR**AQS	ESARSKMLSG	IGGCVLGVIF	240
241	LGLGLFIRHR	SQKGPRGPPP	AGLLQ						265



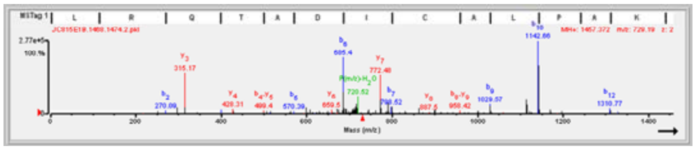
CD20

1	MSGPFPAEPT	KGPLAMQPAP	KVNLKRTSSL	VGPTQSFFMR	ESKALGAVQI	MNGLFHITLG	GLLMIPTGVF	APICLSVWYP	80
81	LWGGIMYIIS	GSLLAAAAEK	TSRKSLVKAK	VIMSSLSLFA	AISGIILSIM	DILNMTLSHF	LKMRRLELIQ	TSKPYVDIYD	160
161	CEPSNSSEKN	SPSTQYCNSI	QSVFLGILSA	MLISAFFQKL	VTAGIVENEW	KRMCTR**SKSN**	**VVLLSAGEKN**	**EQTIK**MKEEI	240
241	IELSGVSSQP	KNEEEIEIIP	VQEEEEEEAE	INFPAPPQEQ	ESLPVENEIA	P			291



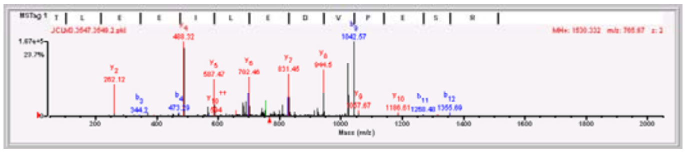
CD37

1	MSAQESCLSL	IKYFLFVFNL	FFFVLGGLIF	CFGTWILIDK	TSFVSFVGLS	FVPLQTWSKV	LAVSGVLTMA	LALLGCVGAL	80
81	KELRCLLGLY	FGMLLLLFAT	QITLGILIST	QRVRLERRVQ	ELVLRTIQSY	R**TNPDETAAE**	**ESWDYAQFQL**	**R**CCGWQSPRD	160
161	WNKAQMLKAN	ESEEPFVPCS	CYNSTATNDS	TVFDKLFFSQ	LSRLGPRAK**L**	**RQTADICALP**	**AK**AHIYREGC	AQSLQKWLHN	240
241	NIISIVGICL	GVGLLELGFM	TLSIFLCRNL	DHVYDRLARY	R				281



RIKEN cDNA 2610307O08

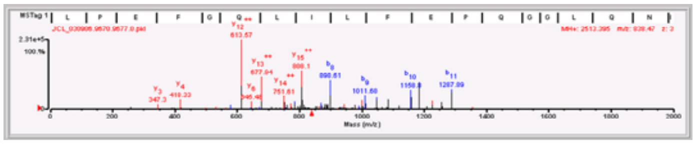
1	MPYSNLHPAI	PRPRGHRSKY	VALIFLVASL	MILWVAKDPP	NHTLKYLALH	LASHELGLLL	KNLCCLAEEL	CHVQSRYQGS	**80**
81	YWKAVRACLG	CPIHCMAMIL	LSSYFYFLQN	TADIYLSWMF	GLLVLYKSLS	MLLGLQSLTP	AEVSAVCEEK	KLNVAHGLAW	**160**
161	SYYIGYLRLI	LPGLQAR IRM	FNQLHNNMLS	GAGSRRLYIL	FPLDCGVPDN	LSVVDPNIRF	RDMLPQQNID	RAGIKNRVYS	**240**
241	NSVYEILENG	QPAGVCILEY	ATPLQTLFAM	SQDAKAGFSR	EDRLEQAKLF	CR**TLEEILED**	**VPESR**NNCR**L**	**IVYQEPTDGN**	**320**
321	**SFSLSQEVLR**	HIRQEEKEEV	TMNAPMTSVA	PPPSVLSQEP	**RLLISGMDQP**	**LPLRTDLI**			**378**



B

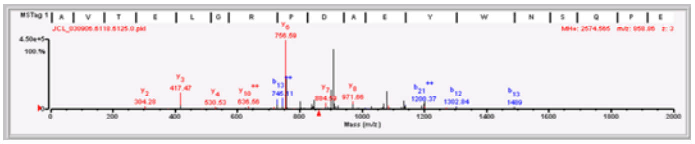
H-2 class II histocompatibility antigen alpha chain.

1	**MPCSRALILG**	**VLALNTMLSL**	**CGGEDDIEAD**	**HVGFYGTTVY**	**QSPGDIGQYT**	**HEFDGDELFY**	**VDLDKKKTVW**	**RLPEFGQLIL**	**80**
81	**FEPQGGLQNI**	**AAEKHNLGIL**	**TKRSNFTPAT**	**NEAPQATVFP**	**KSPVLLGQPN**	**TLICFVDNIF**	**PPVINITWLR**	**NSKSVTDGVY**	**160**
161	**ETSFLVNRDH**	**SFHKLSYLTF**	**IPSDDDIYDC**	**KVEHWGLEEP**	**VLKHWEPEIP**	**APMSELTETV**	**VCALGLSVGL**	**VGIVVGTIFI**	**240**
241	**IQGLRSGGTS**	**RHPGPL**							**256**



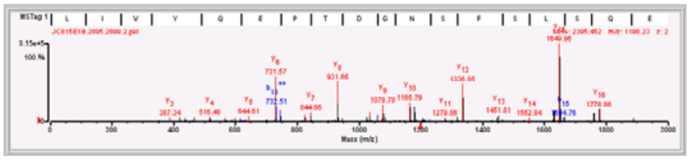
H-2 class II histocompatibility antigen, beta chain.

1	**MALQIPSLLL**	**SAAVVVLMVL**	**SSPRTEGGNS**	**ERHFVVQFKG**	**ECYYTNGTQR**	**IRLVTRYIYN**	**REEYVRYDSD**	**VGEYRAVTEL**	**80**
81	**GRPDAEYWNS**	**QPEILERTRA**	**EVDTACRHNY**	**EGPETSTSLR**	**RLEQPNVAIS**	**LSRTEALNHH**	**NTLVCSVTDF**	**YPAKIKVRWF**	**160**
161	**RNGQEETVGV**	**SSTQLIRNGD**	**WTFQVLVMLE**	**MTPHQGEVYT**	**CHVEHPSLKS**	**PITVEWRAQS**	**ESARSKMLSG**	**IGGCVLGVIF**	**240**
241	**LGLGLFIRHR**	**SQKGPRGPPP**	**AGLLQ**						**265**



MPYS (RIKEN cDNA 2610307O08)

1	**MPYSNLHPAI**	**PRPRGHRSK**Y	VALIFLVASL	MILWVAK**DPP**	**NHTLKYLALH**	**LASHELGLLL**	**K**NLCCLAEEL	CHVQSRYQGS	**80**
81	YWKAVRACLG	CPIHCMAMIL	LSSYFYFLQN	TADIYLSWMF	GLLVLYKSLS	MLLGLQSLTP	AEVSAVCEEK	KLNVAHGLAW	**160**
161	SYYIGYLR**LI**	**LPGLQARIRM**	**FNQLHNNMLS**	**GAGSRRLYIL**	**FPLDCGVPDN**	**LSVVDPNIRF**	**RDMLPQQNID**	**R**AGIKNRVYS	**240**
241	NSVYEILENG	QPAGVCILEY	ATPLQTLFAM	SQDAK**AGFSR**	**EDRLEQAK**LF	CR**TLEEILED**	**VPESRNNCRL**	**IVYQEPTDGN**	**320**
321	**SFSLSQEVLR**	HIRQEEK**EEV**	**TMNAPMTSVA**	**PPPSVLSQEP**	**RLLISGMDQP**	**LPLRTDLI**			**378**



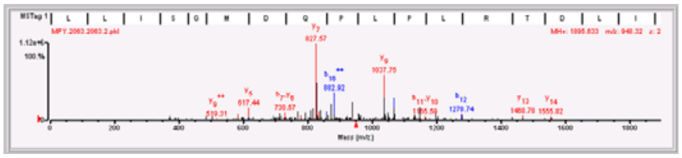


Figure S1: Spectrums of proteins identified in MHC II (A) or MPYS (B) complex by Nano-LC/MS/MS. Identified peptides is underlined.