wt-SiHa

wt-SiHa + IFNγ

HLA-A

```
        10         20         30         40         50
MAVMAPRTLV LLLSGALALT QTWAGSHSMR YFSTSVSRPG RGEPRFIAVG
        60         70         80         90        100
YVDDTQFVRF DSDAASQRME PRAPWIEQEG PEYWDEETGK VKAHSQTDRE
       110        120        130        140        150
NLRIALRYYN QSEAGSHTLQ MMFGCDVGSD GRFLRGYHQY AYDGKDYIAL
       160        170        180        190        200
KEDLRSWTAA DMAAQITKRK WEAAHVAEQQ RAYLEGTCVD GLRRYLENGK
     * 210        220 *      230        240        250
ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT WQRDGEDQTQ
       260 *      270        280        290        300
DTELVETRPA GDGTFQKWAA VVVPSGEEQR YTCHVQHEGL PKPLTLRWEP
       310        320        330        340        350
SSQPTVPIVG IIAGLVLLGA VITGAVVAAV MWRRNSSDRK GGSYSQAASS
       360
DSAQGSDVSL TACKV
```

HLA-B

```
        10         20         30         40         50
MRVTAPRTLL LLLWGAVALT ETWAGSHSMR YFHTSVSRPG RGEPRFITVG
        60         70         80 *       90      * 100
YVDDTLFVRF DSDATSPRKE PRAPWIEQEG PEYWDRETQI SKTNTQTYRE
       110        120        130        140        150
SLRNLRGYYN QSEAGSHTLQ SMYGCDVGPD GRLLRGHNQY AYDGKDYIAL
       160        170        180        190        200
NEDLRSWTAA DTAAQITQRK WEAARVAEQL RAYLEGECVE WLRRYLENGK
       210        220        230  *     240        250
ETLQRADPPK THVTHHPISD HEATLRCWAL GFYPAEITLT WQRDGEDQTQ
       260 *      270        280        290        300
DTELVETRPA GDRTFQKWAA VVVPSGEEQR YTCHVQHEGL PKPLTLRWEP
       310        320        330        340        350
SSQSTVPIVG IVAGLAVLAV VVIGAVVAAV MCRRKSSGGK GGSYSQAACS
       360
DSAQGSDVSL TA
```

HLA-C

```
        10         20         30         40         50
MRVMAPRTLI LLLSGALALT ETWACSHSMR YFSTSVSRPG RGEPRFIAVG
        60         70         80         90        100
YVDDTQFVRF DSDAASPRGE PRAPWVEQEG PEYWDRETQK YKRQAQTDRV
       110        120        130        140        150
SLRNLRGYYN QSEAGSHTLQ WMFGCDLGPD GRLLRGYDQS AYDGKDYIAL
       160        170        180        190        200
NEDLRSWTAA DTAAQITQRK WEAAREAEQR RAYLEGTCVE WLRRYLENGK
       210        220        230        240        250
ETLQRAEHPK THVTHHPVSD HEATLRCWAL GFYPAEITLT WQWDGEDQTQ
       260 *      270        280        290        300
DTELVETRPA GDGTFQKWAA VVVPSGEEQR YTCHVQHEGL PEPLTLRWEP
       310        320        330        340        350
SSQPTIPIVG IVAGLAVLAV LAVLGAVVAV VMCRRKSSGG KGGSCSQAAS
       360
SNSAQGSDES LIACKA
```

Unique peptide for HLA*

IFITM1/IFITM3 null

IFITM1/IFIMT3 null + IFNγ

HLA-A

```
        10         20         30         40         50
MAVMAPRTLV LLLSGALALT QTWAGSHSMR YFSTSVSRPG RGEPRFIAVG
        60         70         80         90        100
YVDDTQFVRF DSDAASQRME PRAPWIEQEG PEYWDEETGK VKAHSQTDRE
       110        120        130        140        150
NLRIALRYYN QSEAGSHTLQ MMFGCDVGSD GRFLRGYHQY AYDGKDYIAL
       160        170        180        190        200
KEDLRSWTAA DMAAQITKRK WEAAHVAEQQ RAYLEGTCVD GLRRYLENGK
      *210        220        230  *     240        250
ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT WQRDGEDQTQ
       260        270        280        290        300
DTELVETRPA GDGTFQKWAA VVVPSGEEQR YTCHVQHEGL PKPLTLRWEP
       310        320        330        340        350
SSQPTVPIVG IIAGLVLLGA VITGAVVAAV MWRRNSSDRK GGSYSQAASS
       360
DSAQGSDVSL TACKV
```

HLA-B

```
        10         20         30         40         50
MRVTAPRTLL LLLWGAVALT ETWAGSHSMR YFHTSVSRPG RGEPRFITVG
        60         70         80         90        100
YVDDTLFVRF DSDATSPRKE PRAPWIEQEG PEYWDRETQI SKTNTQTYRE
       110        120        130        140        150
SLRNLRGYYN QSEAGSHTLQ SMYGCDVGPD GRLLRGHNQY AYDGKDYIAL
       160        170        180        190        200
NEDLRSWTAA DTAAQITQRK WEAARVAEQL RAYLEGECVE WLRRYLENGK
       210        220        230        240        250
ETLQRADPPK THVTHHPISD HEATLRCWAL GFYPAEITLT WQRDGEDQTQ
       260        270        280        290        300
DTELVETRPA GDRTFQKWAA VVVPSGEEQR YTCHVQHEGL PKPLTLRWEP
       310        320        330        340        350
SSQSTVPIVG IVAGLAVLAV VVIGAVVAAV MCRRKSSGGK GGSYSQAACS
       360
DSAQGSDVSL TA
```

HLA-C

```
        10         20         30         40         50
MRVMAPRTLI LLLSGALALT ETWACSHSMR YFSTSVSRPG RGEPRFIAVG
        60         70         80         90        100
YVDDTQFVRF DSDAASPRGE PRAPWVEQEG PEYWDRETQK YKRQAQTDRV
       110        120        130        140        150
SLRNLRGYYN QSEAGSHTLQ WMFGCDLGPD GRLLRGYDQS AYDGKDYIAL
       160        170        180        190        200
NEDLRSWTAA DTAAQITQRK WEAAREAEQR RAYLEGTCVE WLRRYLENGK
       210        220        230        240        250
ETLQRAEHPK THVTHHPVSD HEATLRCWAL GFYPAEITLT WQWDGEDQTQ
       260        270        280        290        300
DTELVETRPA GDGTFQKWAA VVVPSGEEQR YTCHVQHEGL PEPLTLRWEP
       310        320        330        340        350
SSQPTIPIVG IVAGLAVLAV LAVLGAVVAV VMCRRKSSGG KGGSCSQAAS
       360
SNSAQGSDES LIACKA
```

Unique peptide for HLA*

IFITM1 null

IFITM1 null + IFNγ

HLA-A

```
        10         20         30         40         50
MAVMAPRTLV LLLSGALALT QTWAGSHSMR YFSTSVSRPG RGEPRFIAVG
        60         70         80         90        100
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       110        120        130        140        150
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       160        170        180        190        200
KEDLRSWTAA DMAAQITKRK WEAAHVAEQQ RAYLEGTCVD GLRRYLENGK
       210        220        230  *     240        250
ETLQRTDPPK THMTHHPISD HEATLRCWAL GFYPAEITLT WQRDGEDQTQ
       260        270        280        290        300
DTELVETRPA GDGTFQKWAA VVVPSGEEQR YTCHVQHEGL PKPLTLRWEP
       310        320        330        340        350
SSQPTVPIVG IIAGLVLLGA VITGAVVAAV MWRRNSSDRK GGSYSQAASS
       360
DSAQGSDVSL TACKV
```

HLA-B

```
        10         20         30         40         50
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       110        120        130        140        150
SLRNLRGYYN QSEAGSHTLQ SMYGCDVGPD GRLLRGHNQY AYDGKDYIAL
       160        170        180        190        200
NEDLRSWTAA DTAAQITQRK WEAARVAEQL RAYLEGECVE WLRRYLENGK
       210        220        230        240        250
ETLQRADPPK THVTHHPISD HEATLRCWAL GFYPAEITLT WQRDGEDQTQ
       260        270        280        290        300
DTELVETRPA GDRTFQKWAA VVVPSGEEQR YTCHVQHEGL PKPLTLRWEP
       310        320        330        340        350
SSQSTVPIVG IVAGLAVLAV VVIGAVVAAV MCRRKSSGGK GGSYSQAACS
       360
DSAQGSDVSL TA
```

HLA-C

```
        10         20         30         40         50
MRVMAPRTLI LLLSGALALT ETWACSHSMR YFSTSVSRPG RGEPRFIAVG
        60         70         80         90        100
YVDDTQFVRF DSDAASPRGE PRAPWVEQEG PEYWDRETQK YKRQAQTDRV
       110        120        130        140        150
SLRNLRGYYN QSEAGSHTLQ WMFGCDLGPD GRLLRGYDQS AYDGKDYIAL
       160        170        180        190        200
NEDLRSWTAA DTAAQITQRK WEAAREAEQR RAYLEGTCVE WLRRYLENGK
       210        220        230        240        250
ETLQRAEHPK THVTHHPVSD HEATLRCWAL GFYPAEITLT WQWDGEDQTQ
       260        270        280        290        300
DTELVETRPA GDGTFQKWAA VVVPSGEEQR YTCHVQHEGL PEPLTLRWEP
       310        320        330        340        350
SSQPTIPIVG IVAGLAVLAV LAVLGAVVAV VMCRRKSSGG KGGSCSQAAS
       360
SNSAQGSDES LIACKA
```

Unique peptide for HLA*