|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Predicting 9 mer- epitope binding HLA-A\*0201 peptides (wild type and mutant)** | | | | | | | | | | | | | | | | | | |
| **Count** | | | | | **Motif** | | | | | | | | **Enzyme** | | | | | |
| 24 | | | | | Wild type | | | | | | | |  | | | | | |
| 18 | | | | | GCT | | | | | | | | AID | | | | | |
| 23 | | | | | AGC | | | | | | | | AID | | | | | |
| 22 | | | | | GTA | | | | | | | | AID | | | | | |
| 17 | | | | | GCA | | | | | | | | AID | | | | | |
| 25 | | | | | TAC | | | | | | | | AID | | | | | |
| 22 | | | | | TGC | | | | | | | | AID | | | | | |
| 22 | | | | | GA /G>C | | | | | | | | A3A/A3B | | | | | |
| 18 | | | | | GA | | | | | | | | A3A/A3B | | | | | |
| 20 | | | | | TC /C >G | | | | | | | | A3A/A3B | | | | | |
| 33 | | | | | TC | | | | | | | | A3A/A3B | | | | | |
| 23 | | | | | GAA | | | | | | | | A3A/A3B | | | | | |
| 24 | | | | | TTC | | | | | | | | A3A/A3B | | | | | |
| **Experimentally Known epitopes** | | | | | |
| **Position** | **wt Peptide** | **Affinity (nM)** | **Rank** | | |
| 154 | KTWGQYWQV | 8.46 | 0.097 | | |
| 178 | MLGTHTMEV | 7.61 | 0.082 | | |
| 870 | ITDQVPFSV | 119.5 | 1.212 | | |
| 941 | YLEPGPVTA | 81.90 | 0.940 | | |
| 619/1280 | RLMKQDFSV | 4.27 | 0.022 | | |
| 639 | RLPRIFCSC | 1673 | 5.283 | | |
| **STOP codon gain** | | | | | | | | | | | | | | | | |
| **Position** | **Sequence** | | | **Enzyme** | | | | | | | **Consist with existent mutations** | | | | | |
| 619 | RLMKQDFSV  RLMK\*DFSV | | | AID | | | | | | |  | | | | | |
| 47 | QLYPEWTEA  QLYPK\*TKA | | | A3A/A3B | | | | | | |  | | | | | |
| 399 | GMTPAEVSI  GMTPAEV\*I | | | A3A/A3B | | | | | | |  | | | | | |
| 154 | KTWGQYWQV  KTWGQY\*QV | | | AID | | | | | | |  | | | | | |
| 291 | VLQAAIPLT  VL\*AVIPLT | | | AID | | | | | | |  | | | | | |
| **Novel epitopes** | | | | | | | | | | | | | | | | |
| **mt Peptide** | **Affinity (nM)** | **Rank** | **Binding level** | | | | **wt Peptide** | **Enzyme** | | **Consist with existent mutations** | | | | | | |
| VLGGPVSG**V** | 72.2 | 0.80 | WB | | | | VLGGPVSGL | AID | |  | | | | | | |
| S**V**FTITDQV | 166.7 | 1.50 | WB | | | | SAFTITDQV | AID | |  | | | | | | |
| PLLDGT**V**TL | 194.4 1.60 | 194.4 1.60 | WB | | | | PLLDGTATL | AID | |  | | | | | | |
| VLPSP**V**CQL | 190.3 1.60 | 190.3 1.60 | WB | | | | VLPSPACQL | AID | |  | | | | | | |
| VM**D**TTLAEM | 168.4 | 1.50 | WB | | | | VMGTTLAEM | AID | | c.1157G>A p.G386D COSM4150237 Substitution - Missense | | | | | | |
| A**Q**ITTTEWV | 248.5 | 1.80 | WB | | | | AAQVTTTEWV | AID | |  | | | | | | |
| VLK**T**CLLHL | 253.9 | 1.80 | WB | | | | VLKRCLLHL | A3A/A3B | |  | | | | | | |
| FSIA**F**NFP**A** | 24.5 | 0.40 | SB | | | | FSIALNFPG | A3A/A3B | |  | | | | | | |
| **H**QVPFSVSV | 117.5 | 1.20 | WB | | | | DQVPFSVSV | A3A/A3B | |  | | | | | | |
| RLV**NT**QVPL | 93.9 | 1.00 | WB | | | | RLVKRQVPL | A3A/A3B | |  | | | | | | |
| **N**QVPFSVSV | 134.1 | 1.30 | WB | | | | DQVPFSVSV | A3A/A3B | |  | | | | | | |
| **Y**QYGSFSVT | 291.4 | 2.00 | WB | | | | DQVPFSVSV | A3A/A3B | |  | | | | | | |
| VV**F**SGTTA**V** | 30.8 | 0.40 | SB | | | | VVLSGTTAA | AID | |  | | | | | | |
| IM**S**GQEAGL | 280.6 | 2.00 | WB | | | | IMPGQEAGL | AID | |  | | | | | | |
| ALVVTH**I**YL | 207.9 | 1.70 | WB | | | | ALVVTHTYL | AID | |  | | | | | | |
| SI**I**GSLGPL | 60.1 | 0.70 | WB | | | | SITGSLGPL | AID | |  | | | | | | |
| SLGPLLDGI | 51.6 | 0.70 | WB | | | | SLGPLLDGT | AID | |  | | | | | | |
| PLLDG**I**ATL | 129.0 | 1.20 | WB | | | | PLLDGTATL | AID | |  | | | | | | |
| TLIGANA**CL** | 163.9 | 1.40 | WB | | | | TLIGANASF | A3A/A3B | |  | | | | | | |
| V**M**WVNNT**MM** | 1.80 | 1.80 | WB | | | | VIWVNNTII | A3A/A3B | |  | | | | | | |
| QLHDPSGY**V** | 247.3 | 1.80 | WB | | | | QLHDPSGYL | A3A/A3B | |  | | | | | | |
| ALVVT**D**TYL | 233.6 | 1.80 | WB | | | | ALVVTHTYL | A3A/A3B | |  | | | | | | |
| GTYCLNV**CV** | 204.1 | 1.60 | WB | | | | GTYCLNVSL | A3A/A3B | |  | | | | | | |
| **A**L**M**VG**M**LLV | 12.3 | 0.15 | SB | | | | PLIVGILLV | A3A/A3B | |  | | | | | | |
| L**M**VG**M**LLVL | 49.9 | 0.6 | WB | | | | LIVGILLVL | A3A/A3B | |  | | | | | | |
| VLKRCL**FY**L | 40.9 | 0.60 | WB | | | | VLKRCLLHL | A3A/A3B | |  | | | | | | |
| VLGGPV**F**GL | 39.3 | 0.50 | SB | | | | VLGGPVSGL | A3A/A3B | |  | | | | | | |
| YVP**F**A**YF**S**L** | 165.4 | 1.50 | WB | | | | YVPLAHSSS | A3A/A3B | |  | | | | | | |
| **F**A**YF**S**L**AFT | 281.4 | 2.00 | WB | | | | LAHSSSAFT | A3A/A3B | |  | | | | | | |
| ALVVT**Y**TYL | 208.9 | 1.70 | WB | | | | ALVVTHTYL | A3A/A3B | |  | | | | | | |
| **Y**TYLEPGPV | 155.2 | 1.40 | WB | | | | HTYLEPGPV | A3A/A3B | |  | | | | | | |
| **F**T**F**CG**FF**PV | 1.9 | 0.01 | SB | | | | LTSCGSSPV | A3A/A3B | |  | | | | | | |
| **F**VQVPTTEV | 270.7 | 1.90 | WB | | | | SVQVPTTEV | A3A/A3B | |  | | | | | | |
| S**L**IM**F**TESI | 28.0 | 0.40 | SB | | | | SSIMSTESI | A3A/A3B | |  | | | | | | |
| **F**LGPLLDGT | 101.8 | 1.10 | WB | | | | SLGPLLDGT | A3A/A3B | | c.1358C>T p.S453F COSM6574914 Substitution - Missense | | | | | | |
| G**L**GTYCLNV | 30.1 | 0.40 | SB | | | | GSGTYCLNV | A3A/A3B | |  | | | | | | |
| GTYCLNV**F**L | 109.5 | 1.10 | WB | | | | GTYCLNVSL | A3A/A3B | |  | | | | | | |
| GLGQV**S**LIV | 299.2 | 2.00 | WB | | | | GLGQVPLIV | A3A/A3B | |  | | | | | | |
| KQDF**F**VPQL | 134.0 | 1.30 | WB | | | | KQDFSVPQL | A3A/A3B | |  | | | | | | |
| LIV**D**ILLVL | 103.9 | 1.10 | WB | | | | LIVGILLVL | AID | |  | | | | | | |
| **K**SAEILQAV | 101.5 | 1.10 | WB | | | | ESAEILQAV | A3A/A3B | |  | | | | | | |
| VLKRCL**FY**L | 40.9 | 0.60 | WB | | | | VLKRCLLHL | A3A/A3B | |  | | | | | | |
| **F**LGPLLDGT | 101.8 1.10 | 101.8 1.10 | WB | | | | SLGPLLDGT | A3A/A3B | | c.1358C>T p.S453F COSM6574914 Substitution - Missense | | | | | | |
| GLGQV**S**LIV | 299.2 | 2.00 | WB | | | | GLGQVPLIV | A3A/A3B | |  | | | | | | |
| **S**LIVGILLV | 24.5 | 0.40 | SB | | | | PLIVGILLV | A3A/A3B | |  | | | | | | |
| **Increased HLA affinity** | | | | | | | | | | | | | | | | | |
| **mt Peptide** | **Affinity (nM)** | **Rank** | **Binding level** | | | **wt Peptide** | | | **Affinity (nM)** | | **Rank** | **Binding level** | | **Delta nM** | **Enzyme** | **Consist with existent mutations** | |
| GQVP**V**IVGI | 128.2 | 1.20 | WB | | | GQVPLIVGI | | | 150.7 | | 1.40 | WB | | 22.5 | AID |  | |
| GILVVLM**S**V | 59.0 | 0.70 | WB | | | GILLVLMAV | | | 75.3 | | 0.90 | WB | | 16.3 | AID |  | |
| VLM**S**VVLAS | 160.3 | 1.40 | WB | | | VLMAVVLAS | | | 201.9 | | 1.60 | WB | | 41.6 | AID |  | |
| QLYPEWTE**V** | 21.7 | 0.30 | SB | | | QLYPEWTEA | | | 180.0 | | 1.50 | WB | | 158.3 | AID |  | |
| SQVW**AA**QPV | 102.7 | 1.10 | WB | | | SQVWGGQPV | | | 129.3 | | 1.20 | WB | | 26.6 | A3A/A3B |  | |
| YL**Q**PGPVTA | 42.1 | 0.60 | WB | | | YLEPGPVTA | | | 172.7 | | 1.50 | WB | | 130.6 | A3A/A3B |  | |
| ILLV**F**MAVV | 48.9 | 0.60 | WB | | | ILLVLMAVV | | | 56.1 | | 0.70 | WB | | 7.2 | A3A/A3B |  | |
| V**F**MAVVLAS | 5.7 | 0.05 | SB | | | VLMAVVLAS | | | 201.9 | | 1.60 | WB | | 196.2 | A3A/A3B |  | |
| LLHLAVIG**V** | 39.6 0.60 | 39.6 0.60 | WB | | | LLHLAVIGA | | | 245.7 | | 1.80 | WB | | 206.1 | AID |  | |
| AVIG**V**LLAV | 9.7 | 0.12 | SB | | | AVIGALLAV | | | 9.8 | | 0.12 | SB | | 0.1 | AID |  | |
| ITDQV**S**FSV | 134.5 | 1.30 | WB | | | ITDQVPFSV | | | 211.5 | | 1.70 | WB | | 77 | AID | c.640C>T p.P214S COSM8017763 Substitution - Missense | |
| YLEPGPVT**V** | 13.3 | 0.17 | SB | | | YLEPGPVTA | | | 172.7 | | 1.50 | WB | | 159.4 | AID |  | |
| GMTP**V**EVSI | 104.3 | 1.10 | WB | | | GMTPAEVSI | | | 301.2 | | 2.00 | WB | | 196.9 | AID |  | |
| I**I**DQVPFSV | 27.7 | 0.40 | SB | | | ITDQVPFSV | | | 211.5 | | 1.70 | WB | | 183.8 | AID |  | |
| SLAD**I**NSLA | 38.2 | 0.50 | SB | | | SLADTNSLA | | | 257.7 | | 1.90 | WB | | 219.5 | AID |  | |
| RL**S**RIFCSC | 1307.1 | 4.50 | \*\*\*\*\*\*\*\* | | | RLPRIFCSC | | | 1491.6 | | 5.00 | \*\*\*\*\*\*\*\* | | 184.5 | AID |  | |
| QLY**A**EWTEA | 160.0 | 1.40 | WB | | | QLYPEWTEA | | | 180.0 | | 1.50 | WB | | 20 | A3A/A3B |  | |
| G**M**LLVLMAV | 19.8 | 0.30 | SB | | | GILLVLMAV | | | 75.3 | | 0.90 | WB | | 55.5 | A3A/A3B |  | |
| LMAVVLA**C**V | 15.7 | 0.20 | SB | | | LMAVVLASL | | | 21.0 | | 0.30 | SB | | 8.7 | A3A/A3B |  | |
| **Y**LAVIGALL | 12.3 | 0.15 | SB | | | HLAVIGALL | | | 146.6 | | 1.30 | WB | | 134.3 | A3A/A3B |  | |
| ITDQVPF**F**V | 84.9 | 0.90 | WB | | | ITDQVPFSV | | | 211.5 | | 1.70 | WB | | 126.6 | A3A/A3B |  | |
| TLI**FW**ALVV | 81.1 | 0.90 | WB | | | TLISRALVV | | | 170.3 | | 1.50 | WB | | 89.2 | A3A/A3B |  | |
| GMTPAEV**L**I | 168.9 | 1.50 | WB | | | GMTPAEVSI | | | 301.2 | | 2.00 | WB | | 132.3 | A3A/A3B |  | |
| **F**LADTNSLA | 15.4 | 0.20 | SB | | | SLADTNSLA | | | 257.7 | | 1.90 | WB | | 242.3 | A3A/A3B | c.1709C>T p.S570F COSM9165007 Substitution - Missense | |
| GQV**S**LIVGI | 103.2 | 1.10 | WB | | | GQVPLIVGI | | | 150.7 | | 1.40 | WB | | 47.5 | A3A/A3B |  | |
| LMAVVLA**F**L | 12.7 | 0.17 | SB | | | LMAVVLASL | | | 21.0 | | 0.30 | SB | | 8.3 | A3A/A3B |  | |
| RLMKQDF**F**V | 3.1 | 0.01 | SB | | | RLMKQDFSV | | | 4.9 | | 0.04 | SB | | 1.8 | A3A/A3B |  | |
| ML**D**THTMEV | 4.5 | 0.03 | SB | | | MLGTHTMEV | | | 7.5 | | 70.08 | SB | | 3 | AID |  | |
| TLISR**T**LVV | 80.0 | 0.90 | WB | | | TLISRALVV | | | 170.3 | | 1.50 | WB | | 90.3 | AID |  | |
| VLMAVVL**T**S | 178.5 | 1.50 | WB | | | VLMAVVLAS | | | 201.9 | | 1.60 | WB | | 23.4 | AID |  | |
| RLP**H**IFCSC | 779.6 | 3.50 | \*\*\*\*\*\*\*\* | | | RLPRIFCSC | | | 1491.6 | | 5.00 | \*\*\*\*\*\*\*\* | | 712 | AID | c.1925G>A p.R642H COSM300116 Substitution - Missense | |
| **Y**LAVIGALL | 12.3 | 0.15 | SB | | | HLAVIGALL | | | 146.6 | | 1.30 | WB | | 134.3 | A3A/A3B |  | |
| GQV**S**LIVGI | 103.2 | 1.10 | WB | | | GQVPLIVGI | | | 150.7 | | 1.40 | WB | | 47.5 | A3A/A3B |  | |
| **Reduced HLA affinity** | | | | | | | | | | | | | | | | | |
| **mt Peptide** | **Affinity (nM)** | **Rank** | **Binding level** | | | **wt Peptide** | | | **Affinity (nM)** | | **Rank** | **Binding level** | | **Delta nM** | **Enzyme** | **Consist with existent mutations** | |
| **S**VIGSLVSV | 9.9 | 0.12 | SB | | | AVIGALLAV | | | 9.8 | | 0.12 | SB | | -0.1 | AID |  | |
| HL**S**VIG**S**L**V** | 286.5 | 2.00 | WB | | | HLAVIGALL | | | 146.6 | | 1.30 | WB | | -139.9 | AID |  | |
| **IV**GTHTMEV | 141.4 | 1.30 | WB | | | MLGTHTMEV | | | 7.5 | | 70.08 | SB | | -133.9 | AID |  | |
| ILVVLM**S**VV | 134.0 1.30 | 134.0 1.30 | WB | | | ILLVLMAVV | | | 56.1 | | 0.70 | WB | | -77.9 | AID |  | |
| LM**S**VVLASL | 24.4 | 0.40 | SB | | | LMAVVLASL | | | 21.0 | | 0.30 | SB | | -3.4 | AID |  | |
| QLYP**QCTQ**A | 287.3 | 2.00 | WB | | | QLYPEWTEA | | | 180.0 | | 1.50 | WB | | -107.3 | A3A/A3B |  | |
| **N**TWGQYWQV | 38.0 | 0.50 | SB | | | KTWGQYWQV | | | 11.8 | | 0.15 | SB | | -26.2 | A3A/A3B |  | |
| MLGTHTM**Q**V | 9.9 | 0.12 | SB | | | MLGTHTMEV | | | 7.5 | | 0.08 | SB | | -2.4 | A3A/A3B |  | |
| GILLV**F**MAV | 142.6 | 1.30 | WB | | | GILLVLMAV | | | 75.3 | | 0.90 | WB | | -67.3 | A3A/A3B |  | |
| **T**LIKQ**H**FSV | 13.7 | 0.17 | SB | | | RLMKQDFSV | | | 4.9 | | 0.04 | SB | | -8.8 | A3A/A3B |  | |
| MLGTHTM**K**V | 19.4 | 0.30 | SB | | | MLGTHTMEV | | | 7.5 | | 70.08 | SB | | -11.9 | A3A/A3B |  | |
| **K**LIKQ**N**FSV | 6.3 | 0.06 | SB | | | RLMKQDFSV | | | 4.9 | | 0.04 | SB | | -1.4 | A3A/A3B |  | |
| HLAVIG**V**LL | 175.4 | 1.50 | WB | | | HLAVIGALL | | | 146.6 | | 1.30 | WB | | -28.8 | AID |  | |
| LMAVVL**V**SL | 35.0 | 0.50 | SB | | | LMAVVLASL | | | 21.0 | | 0.30 | SB | | -14 | AID |  | |
| **C**LPRIFCSC | 1604.3 | 5.00 | \*\*\*\*\*\*\*\* | | | RLPRIFCSC | | | 1491.6 | | 5.00 | \*\*\*\*\*\*\*\* | | -112.7 | AID |  | |
| RLMKQD**LC**V | 30.8 | 0.40 | SB | | | RLMKQDFSV | | | 4.9 | | 0.04 | SB | | -25.9 | A3A/A3B |  | |
| QLY**S**EWTEA | 207.0 | 1.70 | WB | | | QLYPEWTEA | | | 180.0 | | 1.50 | WB | | -27 | A3A/A3B |  | |
| LMAVVL**T**SL | 25.7 | 0.40 | SB | | | LMAVVLASL | | | 21.0 | | 0.30 | SB | | -4.7 | AID |  | |
| RL**I**KQDFSV | 10.2 | 0.12 | SB | | | RLMKQDFSV | | | 4.9 | | 0.04 | SB | | -5.3 | A3A/A3B |  | |
| MLGTHTM**K**V | 19.4 | 0.30 | SB | | | MLGTHTMEV | | | 7.5 | | 70.08 | SB | | -11.9 | A3A/A3B |  | |
| **Abrogated epitopes** | | | | | | | | | | | | | | | | | |
| **Position** | **wt Peptide** | **Affinity (nM)** | **Rank** | | | **Binding level** | | **Enzyme** | | **Consist with existent mutations** | | | | | | | |
| 9 | LLHLAVIGA | 245.7  3066 | 1.80  7.2 | | | WB | | AID | |
| 18 | LLAVGATKV | 117.6  4684 | 1.20  9.2 | | | WB | | AID | |  | | | | | | | |
| 47 | QLYPEWTEA | 180.0  3544 | 1.50  7.88 | | | WB | | AID | |  | | | | | | | |
| 291 | VLQAAIPLT | 400 | 2.47 | | |  | | AID | |  | | | | | | | |
| 570 | SLADTNSLA | 547 | 3.04 | | | WB | | AID | |  | | | | | | | |
| 113 | SQVWGGQPV | 129.3 | 1.20 | | | WB | | AID | |  | | | | | | | |
| 280 | YLEPGPVTA | 172.7 | 1.50 | | | WB | | AID | |  | | | | | | | |
| 576 | SLAVVSTQL | 83.7 | 0.90 | | | WB | | AID | |  | | | | | | | |
| 399 | GMTPAEVSI | 301.2 | 2.00 | | | WB | | AID | |  | | | | | | | |
| 209 | ITDQVPFSV | 211.5 | 1.70 | | | WB | | A3A/A3B | |  | | | | | | | |
| 373 | GMTPEKVPV | 261.7 | 1.90 | | | WB | | A3A/A3B | |  | | | | | | | |
| 399 | GMTPAEVSI | 301.2 | 2.00 | | | WB | | A3A/A3B | |  | | | | | | | |
| 570 | SLADTNSLA | 257.7 | 1.90 | | | WB | | A3A/A3B | |  | | | | | | | |
| 606 | LMAVVLASL | 21.0 | 0.30 | | | SB | | A3A/A3B | |  | | | | | | | |
| 373 | GMTPEKVPV | 261.7 | 1.90 | | | WB | | A3A/A3B | |  | | | | | | | |
| 399 | GMTPAEVSI | 301.2 | 2.00 | | | WB | | A3A/A3B | | c.1210G>A p.E404K  COSM9184629  Substitution - Missense | | | | | | | |
| 570 | SLADTNSLA | 257.7 | 1.90 | | | WB | | A3A/A3B | |  | | | | | | | |
| 113 | SQVWGGQPV | 129.3 | 1.20 | | | WB | | A3A/A3B | |  | | | | | | | |
| 209 | ITDQVPFSV | 211.5 | 1.70 | | | WB | | A3A/A3B | |  | | | | | | | |
| 373 | GMTPEKVPV | 261.7 | 1.90 | | | WB | | A3A/A3B | |  | | | | | | | |
| 373 | GMTPEKVPV | 261.7 | 1.90 | | | WB | | AID | |  | | | | | | | |
| 605 | VLMAVVLAS | 201.9 | 1.60 | | | WB | | AID | |  | | | | | | | |
| 9 | LLHLAVIGA | 245.7 | 1.80 | | | WB | | A3A/A3B | |  | | | | | | | |
| 11 | HLAVIGALL | 146.6 | 1.30 | | | WB | | A3A/A3B | |  | | | | | | | |
| 209 | ITDQVPFSV | 211.5 | 1.70 | | | WB | | A3A/A3B | |  | | | | | | | |
| 291 | VLQAAIPLT | 2.00 | 2.00 | | | WB | | A3A/A3B | |  | | | | | | | |
| 570 | SLADTNSLA | 257.7 | 1.90 | | | WB | | A3A/A3B | |  | | | | | | | |
| 594 | GQVPLIVGI | 150.7 | 1.40 | | | WB | | A3A/A3B | |  | | | | | | | |
| 602 | ILLVLMAVV | 56.1 | 0.70 | | | WB | | A3A/A3B | |  | | | | | | | |
| 605 | VLMAVVLAS | 201.9 | 1.60 | | | WB | | A3A/A3B | |  | | | | | | | |
| 9 | LLHLAVIGA | 245.7 | 1.80 | | | WB | | A3A/A3B | |  | | | | | | | |
| 291 | VLQAAIPLT | 2.00 | 2.00 | | | WB | | A3A/A3B | |  | | | | | | | |
| 605 | VLMAVVLAS | 201.9 | 1.60 | | | WB | | A3A/A3B | |  | | | | | | | |
| 399 | GMTPAEVSI | 301.2 | 2.00 | | | WB | | AID | |  | | | | | | | |
| 570 | SLADTNSLA | 257.7 | 1.90 | | | WB | | AID | |  | | | | | | | |
| 576 | SLAVVSTQL | 83.7 | 0.90 | | | WB | | AID | | c.1727G>A p.S576N  COSM4793733  Substitution - Missense  p.A578T COSM291075 Substitution - Missense | | | | | | | |
| 594 | GQVPLIVGI | 150.7 | 1.40 | | | WB | | AID | |  | | | | | | | |
| 601 | GILLVLMAV | 75.3 | 0.90 | | | WB | | AID | |  | | | | | | | |
| 47 | QLYPEWTEA | 180.0 | 1.50 | | | WB | | A3A/A3B | |  | | | | | | | |
| 9 | LLHLAVIGA | 245.7 | 1.80 | | | WB | | A3A/A3B | |  | | | | | | | |
| 291 | VLQAAIPLT | 283.0 | 2.00 | | | WB | | A3A/A3B | |  | | | | | | | |