

**Protein sequences:**

>P53\_HUMAN Cellular tumor antigen p53 - Healthy Tissue  
 MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSPLPSQAM~~DL~~M~~LD~~LSPDDIEQWFTE~~D~~PGP  
 DEAP~~R~~MPEAAPPVAPAPAAPTPAAPAPAPAPSWPLSSSVPSQKTYQGSYGFRLGFLHSGTAK  
 SVTCTYSPALNKMFCQLAKT~~C~~PVQLWVDSTPPP~~G~~TRVRAMAIYKQSQHMTEVVRRC~~P~~HHE  
 RCS~~S~~SDGLAPPQH~~L~~IRVEGNLRVEYLDDRNTF~~R~~H~~S~~VVVPYEPPEVGS~~D~~CTTIHYN~~M~~CNS  
 SCMGGMNRRPILTIITILE~~D~~SSGNLLGRNSFEV~~R~~VCAC~~P~~GRDRRTEENLRKKGE~~P~~HHELP  
 PGSTKRALPNNTSSSPQKKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG  
 GSRAHSSHLKSKKGQSTSRHKKLMFKTEGPDS~~D~~

>P53\_HUMAN Cellular tumor antigen p53 - Tumor Tissue  
 MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLS~~S~~PLPSQAM~~L~~DLMLSPDDIEQWFTE~~D~~PGP  
 DEAP~~W~~MPEAAPPVAPAPAAPTPAAPAPAPAPSWPLSSSVPSQKTYQGSYGFRLGFLHSGTAK  
 SVTCTYSPALNKMFCQLAKT~~C~~PVQLWVDSTPPP~~G~~TRVRAMAIYKQSQHMTEVVRRC~~P~~HHE  
 RCS~~S~~SDGLAPPQH~~L~~IRVEGNLRVEYLDDRNTF~~V~~H~~S~~VVVPYE~~P~~PEVGS~~D~~CTTIHYN~~M~~CNS  
 SCMGGMNRRPILTIITILE~~V~~

**Patient HLA typing results:**

HLA-A\*02:01           9  
 HLA-A\*68:01           9  
 HLA-B\*07:02           9  
 HLA-B\*35:01           9

**Step 1: Regions identified**

>Reg 1  
 SPLPSQAM~~L~~DLMLSPDD  
 >Reg 2  
 DPGPDEAP~~W~~MPEAAPPV  
 >Reg 3  
 YLDDRNTF~~V~~H~~S~~VVVPYE  
 >Reg 4  
 ILTIITILE~~V~~

**Step 2: HLA binding predictions, Step**

allele	seq_num	start	end	peptide	method	Percentile rank
HLA-A*02:01	3	1	9	YLDDRNTFV	Consensus (ann/comblib_sidney2008/smm)	0.2
HLA-B*35:01	3	8	16	FVHSVVPY	Consensus (ann/comblib_sidney2008/smm)	0.2
HLA-B*07:02	1	1	9	SPLPSQAML	Consensus (ann/comblib_sidney2008/smm)	0.4
HLA-A*02:01	2	9	17	WMPEAAPPV	Consensus (ann/comblib_sidney2008/smm)	0.4
HLA-B*07:02	1	3	11	LPSQAMLDL	Consensus (ann/comblib_sidney2008/smm)	0.5
HLA-A*02:01	4	1	9	ILTIITILEV	Consensus (ann/comblib_sidney2008/smm)	0.7
HLA-B*07:02	2	7	15	APWMPEAAP	Consensus (ann/comblib_sidney2008/smm)	1.1
HLA-A*68:01	3	8	16	FVHSVVPY	Consensus (ann/smm)	2.1

#### Step 4, wild type peptides

allele	seq_num	start	Mut peptide	Percentile rank	Wt peptide	WT Percentile Rank
HLA-A*02:01	3	1	YLDDRNTFV	0.2	YLDDRNTFR	2.4
HLA-B*35:01	3	8	FVHSVVPY	0.2	FRHSVVPY	2.3
HLA-B*07:02	1	1	SPLPSQAML	0.4	SPLPSQAMD	16
HLA-A*68:01	3	8	FVHSVVPY	2.1	FRHSVVPY	53

#### Step 5, are the mutated peptides encoded in other human proteins?

>1

YLDDRNTFV

>2

FVHSVVPY

>3

FVHSVVPY

→ All three have top hit in p53 sequence of the human proteome with 8/9 residues matching

**Step 6:** Probably FVHSVVPY, Better yet YLDDRNTFVHSVVPYE