Protein sequences:

>P53_HUMAN Cellular tumor antigen p53 - Healthy Tissue
MEEPQSDPSVEPPLSQETFSDLWKLLPENNVLSPLPSQAM**D**DLMLSPDDIEQWFTEDPGP
DEAP**R**MPEAAPPVAPAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRLGFLHSGTAK
SVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHMTEVVRRCPHHE
RCSDSDGLAPPQHLIRVEGNLRVEYLDDRNTF**R**HSVVVPYEPPEVGSDCTTIHYNYMCNS
SCMGGMNRRPILTIITLE**D**SSGNLLGRNSFEVRVCACPGRDRRTEEENLRKKGEPHHELP
PGSTKRALPNNTSSSPQPKKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG
GSRAHSSHLKSKKGQSTSRHKKLMFKTEGPDSD

>P53_HUMAN Cellular tumor antigen p53 - Tumor Tissue
MEEPQSDPSVEPPLSQETFSDLWKLLPENNVL<mark>SPLPSQAM**L**DLMLSPDD</mark>IEQWFTE<mark>DPGP
DEAP**W**MPEAAPPV</mark>APAPAAPTPAAPAPAPSWPLSSSVPSQKTYQGSYGFRLGFLHSGTAK
SVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHMTEVVRRCPHHE
RCSDSDGLAPPQHLIRVEGNLRVE<mark>YLDDRNTF**V**HSVVVPYE</mark>PPEVGSDCTTIHYNYMCNS
SCMGGMNRRP<mark>ILTIITLE**V**</mark>

Patient HLA typing results:
HLA-A*02:01
HLA-A*68:01
HLA-B*07:02
HLA-B*35:01

Step 1: Mutated regions identified
>D41L
SPLPSQAMLD**L**MLSPDD
>R65W
DPGPDEAP**W**MPEAAPPV
>R213V
YLDDRNTF**V**HSVVVPYE
>D259V
ILTIITLE**V**

Step 2: HLA binding predictions on IEDB

Allele	#	Start	End	Length	Peptide	Method used	Percentile_rank
HLA-A*02:01	3	1	9	9	YLDDRNTFV	Consensus (ann/comblib_sidney2008/smm)	0.2

HLA-B*35:01	3	8	16	9	FVHSVVVPY	Consensus (ann/comblib_sidney2008/smm)	0.2
HLA-B*07:02	1	1	9	9	SPLPSQAML	Consensus (ann/comblib_sidney2008/smm)	0.4
HLA-A*02:01	2	9	17	9	WMPEAAPPV	Consensus (ann/comblib_sidney2008/smm)	0.4
HLA-B*07:02	1	3	11	9	LPSQAMLDL	Consensus (ann/comblib_sidney2008/smm)	0.5
HLA-A*02:01	4	1	9	9	ILTIITLEV	Consensus (ann/comblib_sidney2008/smm)	0.7
HLA-A*68:01	3	8	16	9	FVHSVVVPY	Consensus (ann/smm)	2.1
HLA-B*35:01	1	3	11	9	LPSQAMLDL	Consensus (ann/comblib_sidney2008/smm)	2.2
HLA-B*35:01	2	7	15	9	APWMPEAAP	Consensus (ann/comblib_sidney2008/smm)	2.2
HLA-B*07:02	2	7	15	9	APWMPEAAP	Consensus (ann/comblib_sidney2008/smm)	2.8
HLA-A*02:01	1	7	15	9	AMLDLMLSP	Consensus (ann/comblib_sidney2008/smm)	4
HLA-B*35:01	2	6	14	9	EAPWMPEAA	Consensus (ann/comblib_sidney2008/smm)	4.2
HLA-B*35:01	1	1	9	9	SPLPSQAML	Consensus (ann/comblib_sidney2008/smm)	5.2
HLA-B*35:01	2	1	9	9	DPGPDEAPW	Consensus (ann/comblib_sidney2008/smm)	5.2

Step3: BLAST identified top binding peptides to check if they are encoded in other human proteins?

Blastp Input:

```
>HLA-A0201_top_pep
YLDDRNTFV
> HLA-A6801_HLA-B3502_top_pep
FVHSVVVPY
>HLA-B0702_top_pep
SPLPSQAML
```

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

Final question: Which peptide would you choose?

Probably `FVHSVVVPY`, Better yet `YLDDRNTFVHSVVVPYE`