

DeFT™

De-immunization of Functional Therapeutics

Protect Your Therapeutic from Immune System Response

The FDA has suggested that protein therapeutics developers assess and manage unwanted immunogenicity. DeFT™ is cost effective and highly accurate in establishing and eliminating the immunogenic risks hidden within your protein therapeutic or biologic. Our deimmunization strategy is focused on the identification and elimination of T-cell epitopes contained within your candidate sequence.

EpiMatrix Results

Current Accession: CLASS2-BENCHMARK * Current Sequence: CLIP

Top 10% of Z-Scores | Top 5% of Z-Scores | Top 1% of Z-Scores

All Z-Scores in Top 5% are Considered "Hits"

Matrix:			DRB1*0101	DRB1*0301	DRB1*0401	DRB1*0701	DRB1*0801	DRB1*1101	DRB1*1301	DRB1*1501	Hit	Average
AA Sequence	AA Start	GRAVY	Z-Score	Z-Score	Z-Score	Z-Score	Z-Score	Z-Score	Z-Score	Z-Score	Count	Z-Score
PVSKMRMAT	1	-.19	-.21	-.05	-.79	-.75	1.91	1.55	.45	1.22	1	.42
VSKMRMATP	2	-.19	.52	.75	.27	-1.79	.36	1.12	-.48	-.68	0	.01
SKMRMATPL	3	-.23	1.46	.50	.19	1.87	.54	-.05	.81	1.90	2	.90
KMRMATPLL	4	.28	2.16	.97	1.42	.86	.94	1.45	-.14	1.09	1	1.10
MRMATPLLM	5	.92	2.81	2.80	2.54	2.46	1.65	1.62	2.76	2.95	7	2.45
RMATPLLMQ	6	.32	-.34	-.71	.74	.29	.65	.78	.11	.74	0	-.28
MATPLLMQA	7	1.02	-.84	-.28	.04	-1.29	-.11	.67	.36	1.44	0	-.00
Maximum Score			2.81	2.80	2.54	2.46	1.91	1.62	2.76	2.95	--	--
Hit Count			2.00	1.00	1.00	2.00	2.00	.00	1.00	2.00	11.00	--

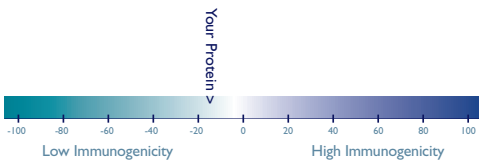
Total Assessments:	56
Total Significant Z:	25.82
Expected Z:	6.23
Deviation:	19.6
Deviation per 1000:	349.92

Deimmunization Begins with EpiMatrix

EpiMatrix defines the leading edge in computational immunology by consistently delivering accurate assessments of potential epitopes in a given candidate sequence.

Deimmunization begins with an EpiMatrix screening and is followed with a Clustimer analysis.

EpiMatrix Protein Immunogenicity Report



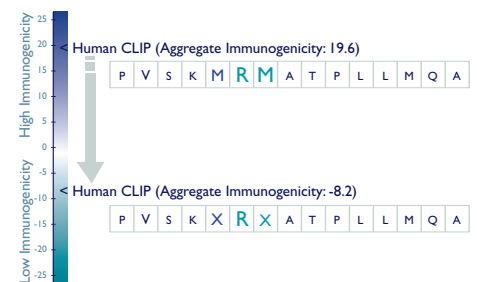
How Immunogenic Is That Sequence?

Clustimer examines a protein sequence and its epitopes and defines those areas that are most dense with epitopes in a given segment. With Clustimer, we are able to locate the most immunogenic regions and prioritize deimmunization.

When Functional Regions are Immunogenic

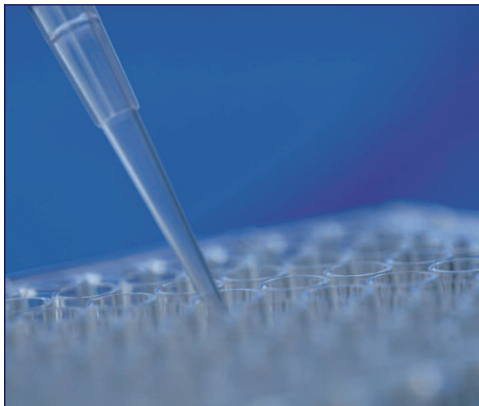
EpiMatrix and Clustimer provide critical immunogenic data about your protein therapeutic. In cases where functional sequences are also immunogenic, we identify key amino acid residues that are crucial to MHC binding. Minimal modification of a few non-functional amino acid residues may be all that is needed to protect your effective therapeutic from an immune response.

Targeted Amino Acid Modification



Fast, Cost-Effective Reengineering

Working with your protein engineers we recommend deimmunized analogs to immunogenic sequences that will have minimal effect on 3D structure and functionality.



In Vivo Confirmation

We are equipped to test your original protein and its deimmunized analog for immunogenicity in transgenic mice expressing human MHC molecules. This is an inexpensive and reliable alternative to a premature return to Phase I Trials.

Contact EpiVax Today for More Information

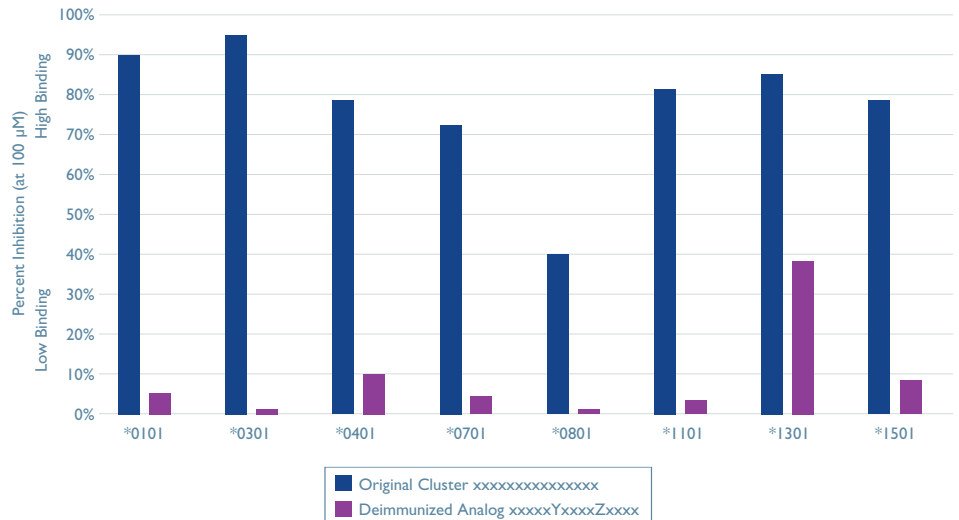
At EpiVax we understand the scientific, financial and regulatory challenges faced by developers of biological therapeutics because we are in the same business.

We have built our reputation by delivering accurate information within tight timeframes to today's industry leaders. DeFT is a proven life-saver to functional therapeutics that would otherwise never survive Clinical Trials.

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Example Data:
Binding One Cluster and its Deimmunized Analog to each of Eight MHC Class II Alleles



In Vitro Confirmation

We have developed a suite of the most sensitive and specific recombinant soluble MHC II binding assays available on the market. If exposed blood samples are available, we offer T-cell restimulation assays (ELISpot) to confirm the immunogenicity of sample sequences and the deimmunization of their sequence analogs.



Contact EpiVax today for more information on how DeFT can serve your therapeutic development goals.

