

## Use of Computational modeling and Continuous-Flow Solid-Phase Peptide Synthesis for the design and synthesis of peptide ligands targeting HLA and Hsp90

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# Therapeutic peptides: Where are we standing?



# The Nobel Prize in Chemistry 2024



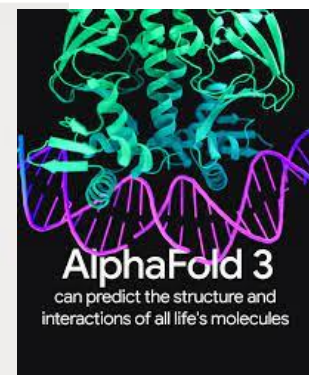
Ill. Niklas Elmehed © Nobel Prize  
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David Baker



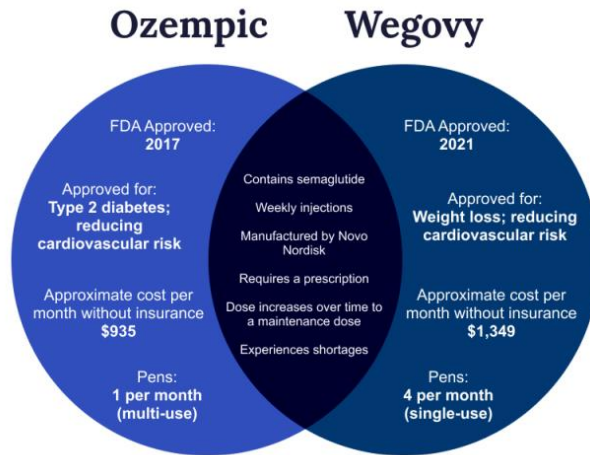
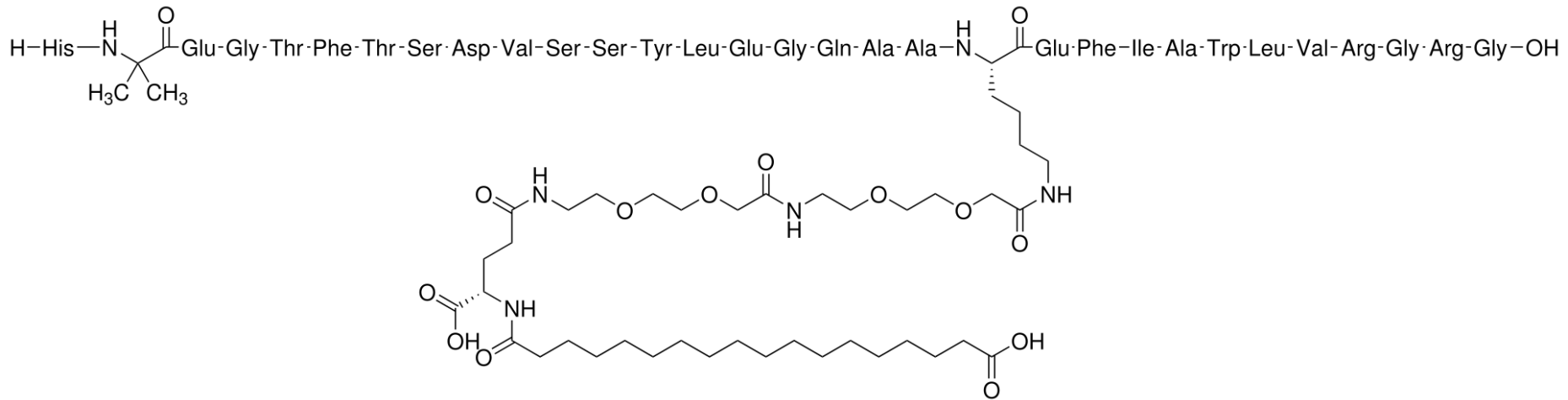
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Demis Hassabis



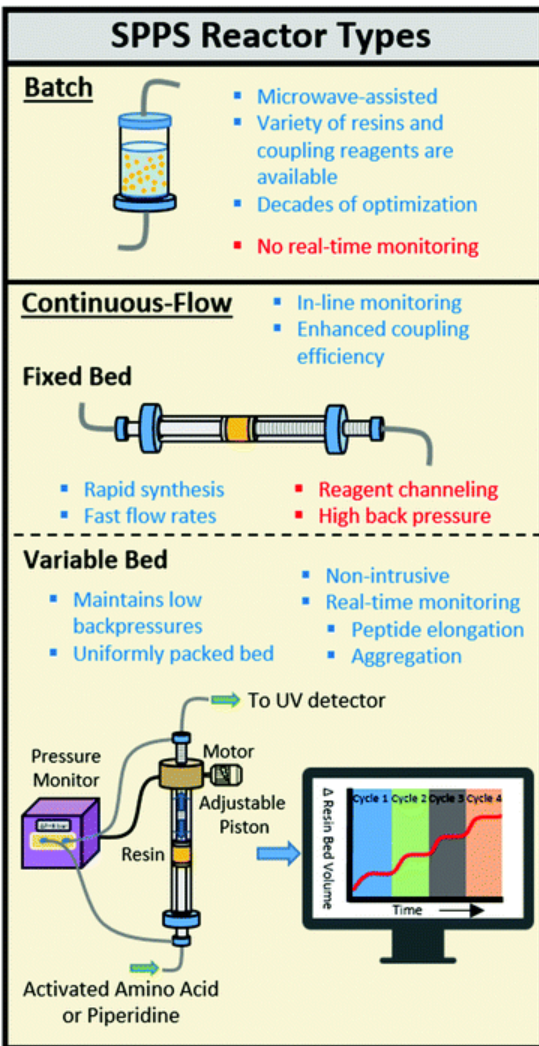
Ill. Niklas Elmehed © Nobel Prize  
Outreach  
John Jumper



Target name	Peptide name	First approval	Approved indication(s)
GLP-1 receptor	Exenatide <sup>462</sup>	2005	Indicated for Type 2 Diabetes Mellitus
	Liraglutide <sup>463</sup>	2009	
	Lixisenatide <sup>464</sup>	2013	
	Albiglutide <sup>465</sup>	2014	
	Dulaglutide <sup>466</sup>	2014	
	Semaglutide <sup>467</sup>	2017	



# Batch vs Continuous Flow SPPS



Problems with conventional batch mode SPPS:

- Atom economy (Use of huge excess of starting materials to avoid inefficient couplings)
- Use of DMF or DCM as a solvents with high waste production.
- Aggregation when peptide chain gets over 70 a.a.

ORGANIC PROCESS RESEARCH & DEVELOPMENT

**OPR&D**

pubs.acs.org/OPRD

Article

## Continuous-Flow Solid-Phase Peptide Synthesis to Enable Rapid, Multigram Deliveries of Peptides

Kyle E. Ruhl,\* Michael J. Di Maso,\* Harrison B. Rose, Danielle M. Schultz, François Lévesque, Shane T. Grosser, Steven M. Silverman, Shasha Li, Nunzio Sciammetta, and Umar Faruk Mansoor

 Cite This: *Org. Process Res. Dev.* 2024, 28, 2896–2905

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Sletten, E. T.; Nuño, M.; Guthrie, D.; Seeberger, P. H. Real-Time Monitoring of Solid-Phase Peptide Synthesis Using a Variable Bed Flow Reactor. *Chem. Commun.* **2019**, 55 (97), 14598–14601. / Ruhl, K. E.; Schultz, D. M.; Lévesque, F.; Grosser, S. T.; Mansoor, U. F. Continuous-Flow Solid-Phase Peptide Synthesis to Enable Rapid, Multigram Deliveries of Peptides. *Org. Process Res. Dev.* **2024**.

CPPC  
2024

# In Silico peptide-drug design



Contents lists available at ScienceDirect

Journal of Pharmaceutical Analysis

journal homepage: [www.elsevier.com/locate/jpa](http://www.elsevier.com/locate/jpa)



Original article

## Dock-able linear and homodetic di, tri, tetra and pentapeptide library from canonical amino acids: SARS-CoV-2 Mpro as a case study

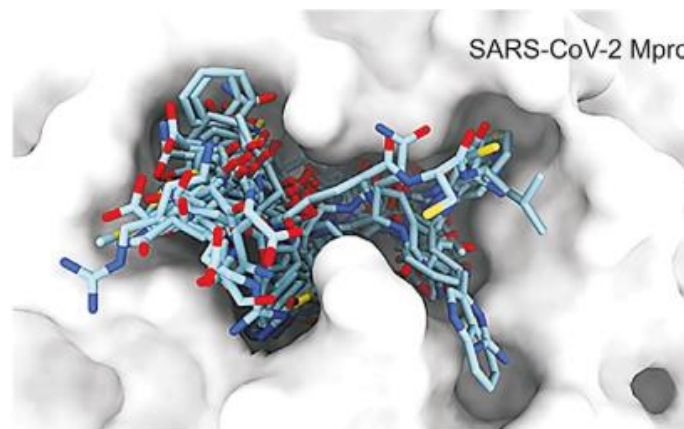


Sarfraz Ahmad <sup>a,b</sup>, Muhammad Usman Mirza <sup>a,b,\*</sup>, John F. Trant <sup>a,b,\*\*</sup>

<sup>a</sup> Department of Chemistry and Biochemistry, University of Windsor, Windsor N9B 3P4, Ontario, Canada

<sup>b</sup> Binarsu City Research Center, LaCelle MDI 3YS, Ontario, Canada

Form	Dipeptide	Tripeptide	Tetrapeptide	Pentapeptide	Total
Linear	400	8,000	160,000	3,200,000	3,368,400
Linear filtered	(400)	(8,000)	(160,000)	(1,169,013)	(1,337,413)
Cyclic	210	2,680	40,110	640,016	683,016
Total	610	10,680	200,110	3,840,016 (1,809,029 filtered)	4,051,416 (2,020,429 filtered)



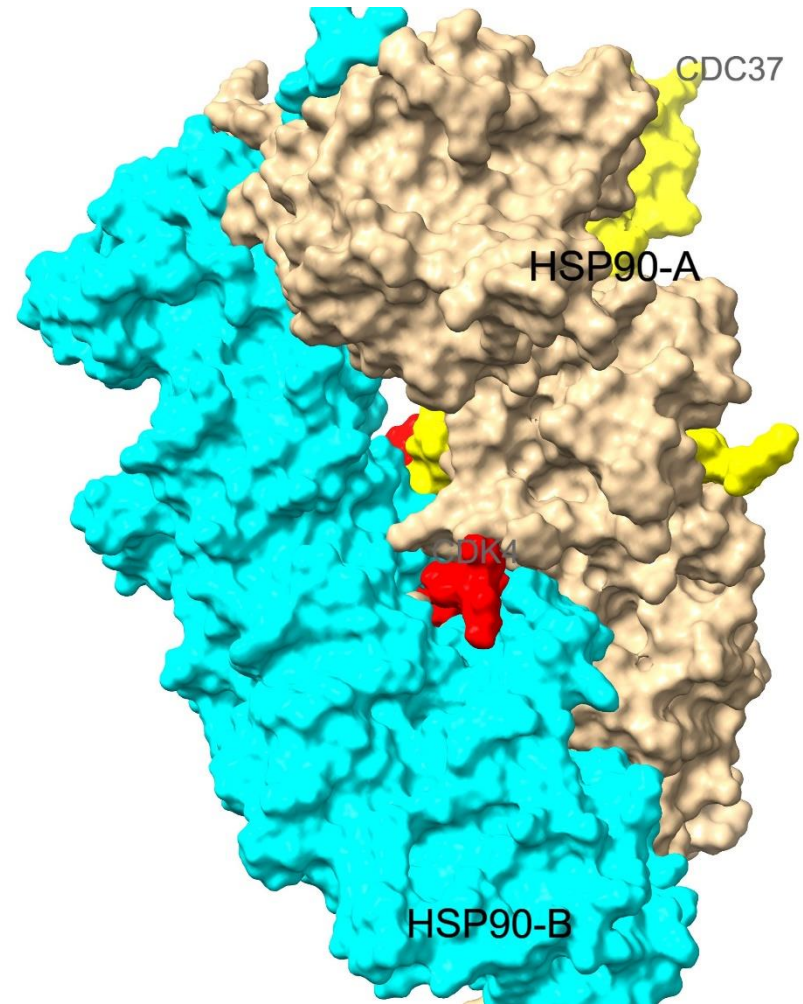
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2024

Ahmad, S., Mirza, M. U., & Trant, J. F. Dock-able linear and homodetic di, tri, tetra and pentapeptide library from canonical amino acids: SARS-CoV-2 Mpro as a case study. *Journal of Pharmaceutical Analysis*, 2023, 13(5), 523–534.

# Hsp90

Heat Shock Proteins are a set of conserved proteins classified depending upon their molecular weights (Hsp100, Hsp90, Hsp70, Hsp60 and small Hsps).

- Most Hsp are molecular chaperons that are in charge of ***proper folding*** of polypeptides or ***misfolded*** proteins, ***degrade mutant proteins*** and ***repair DNA***.
- The most abundant Hsp is Hsp90, which interacts with more than 400 substrate proteins, half of which are believed to be involved in ***cancer***.



# HLA-DR4

The Human Leukocyte Antigen DR4 was first associated with a higher risk of developing Rheumatoid Arthritis in the late 70's.

This type of Major Histocompatibility II complexes work as surface receptors whose function is to bound to pathogen antigens and present them as recognizable structures to T-cells, thus initiating the immune response to a potential infection.

From time to time, upregulation caused by extra coding information, can lead to the recognition of self peptides (like the ones present in the connective tissue of the joints) which can lead to an “auto” attack from the immune system.

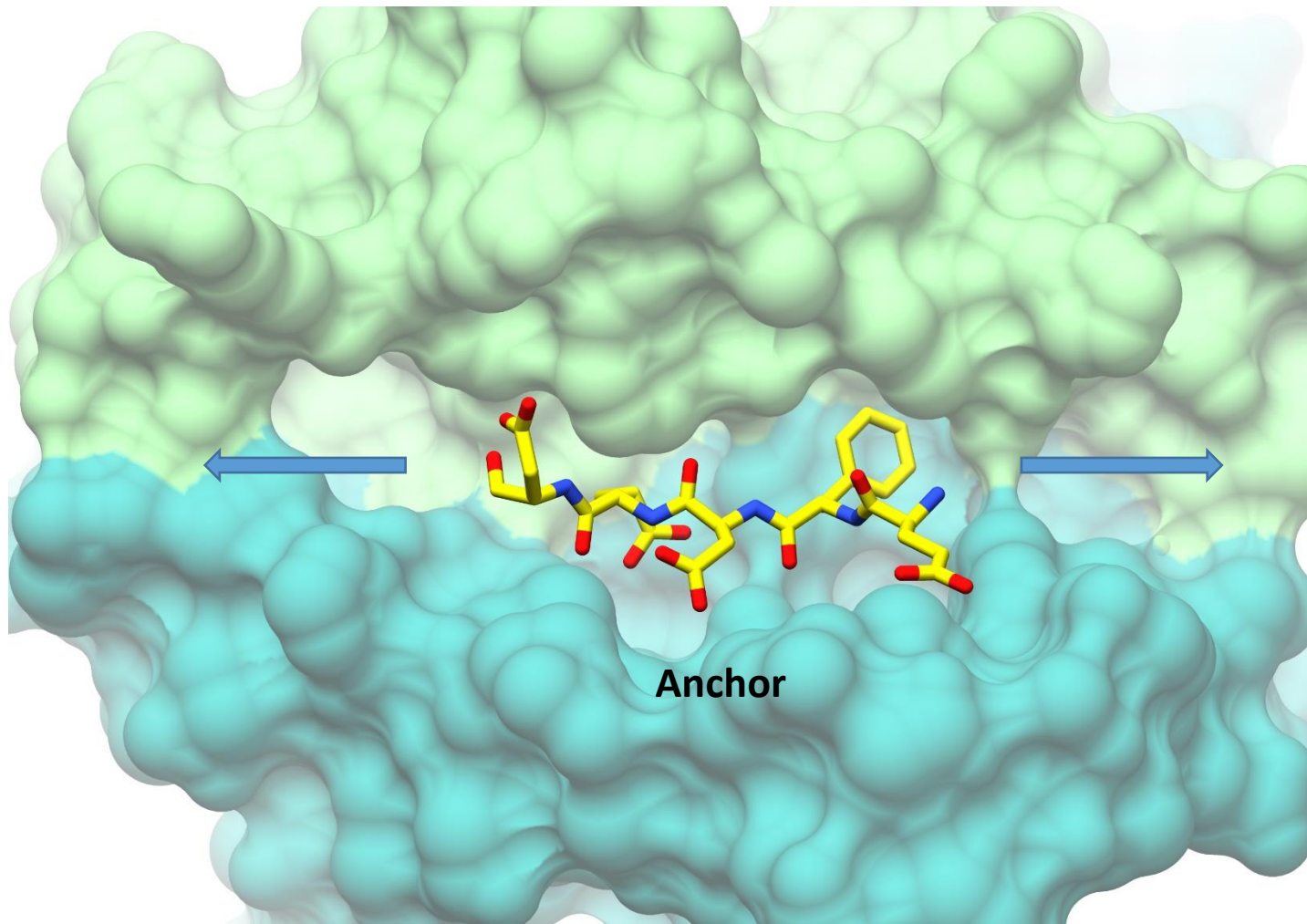


Stastny, P.; Ball, E. J.; Khan, M. A.; Olsen, N. J.; Pincus, T.; Gao, X. Hla-Dr4 and Other Genetic Markers in Rheumatoid Arthritis. *Rheumatol.* **1988**, *27* (suppl II), 132–138. Fugger, L.; Svejgaard, A. Association of MHC and Rheumatoid Arthritis HLA-DR4

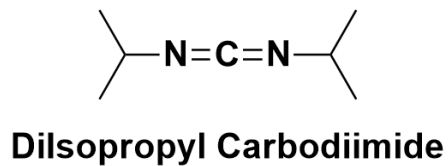
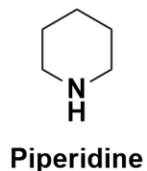
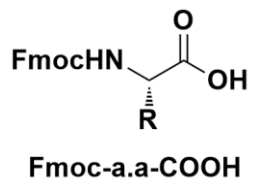
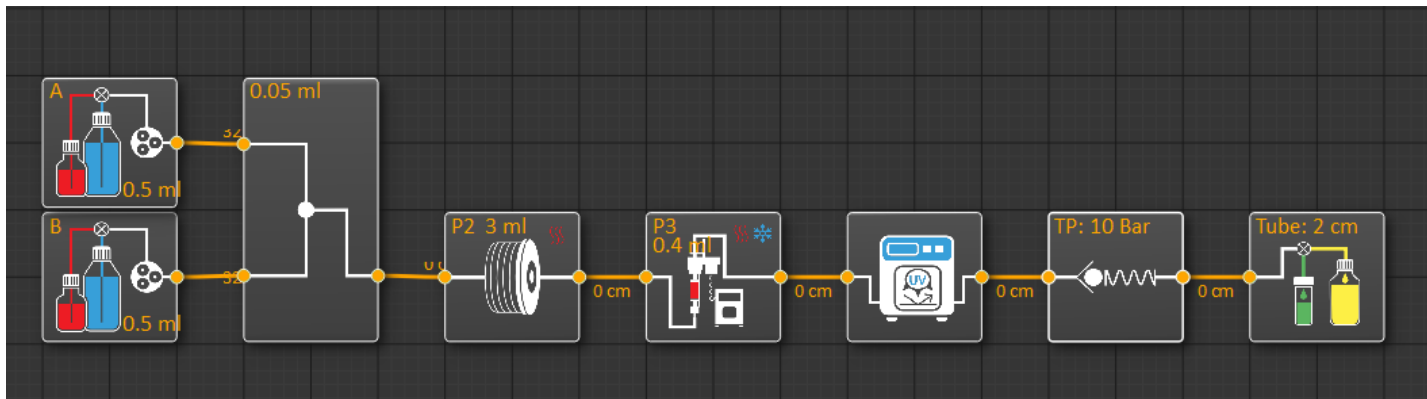
Rheumatoid Arthritis: Studies in Mice and Men. *Arthritis Res.* **2000**, *2* (3), 208–211.



# HLA blocker design:



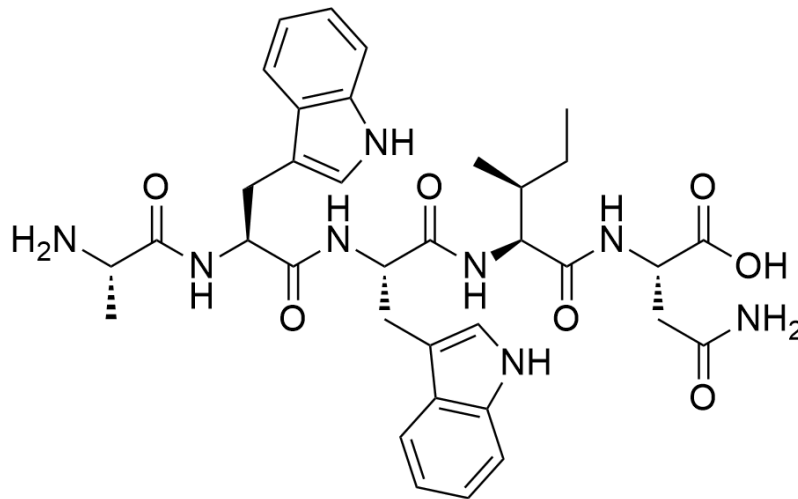
# VBFR CF-SPPS



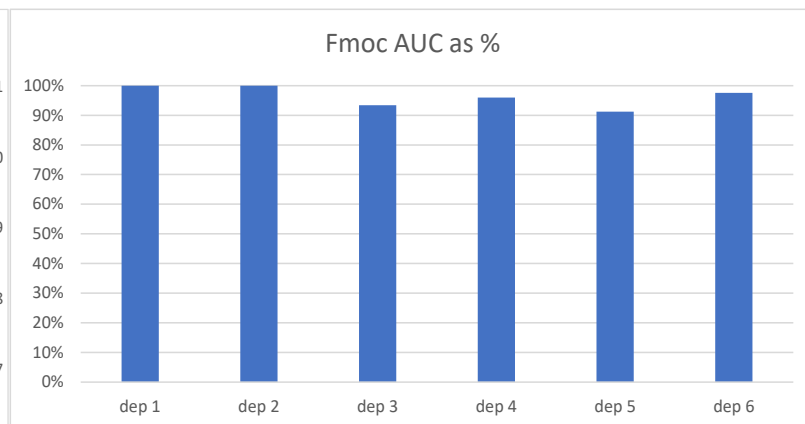
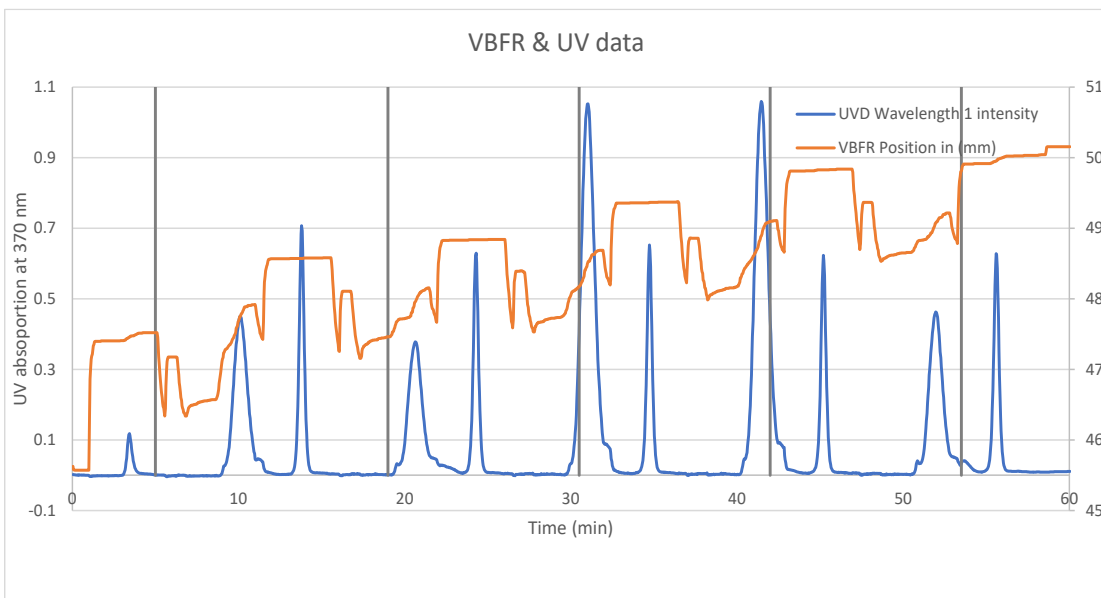
# Hsp90 ligands:

TrantTeam_ID	Sequence	M.W.	LC 214nm	LC 250nm	LR-MS
TTSA-0001	AWWIN	688.7840	83.1%	82.3%	687.8
TTSA-0002	WQWWE	833.9014	100.0%	100.0%	646.9
TTSA-0003	WWWQY	867.9619	81.7%	75.4%	867.1
TTSA-0004	WYWCY	819.9386	81.9%	73.9%	819.0
TTSA-0005	SWRYY	773.8463	88.2%	84.4%	1550
TTSA-0006	WYWWS	826.9093	91.5%	91.6%	826.1
TTSA-0007	QWMPY	723.8506	55.4%	56.7%	723.1
TTSA-0008	CWWDN	722.7791	75.9%	82.0%	722.0
TTSA-0009	FTWWG	695.7755	67.5%	76.1%	696.0
TTSA-0010	WRWRY	865.9930	69.6%	81.2%	865.3
TTSA-0011	WFYGW	757.8464	84.7%	80.8%	758.0
TTSA-0012	NTWWW	791.8641	71.5%	75.8%	792.4
TTSA-0013	WWNWI	803.9185	72.9%	70.0%	804.5
TTSA-0014	AWWYW	810.9099	76.2%	71.8%	811.4
TTSA-0015	FWCWN	754.8671	85.4%	87.3%	755.2
TTSA-0016	QWYWQ	809.8793	42.1/57.9%	44.4/55.6%	
TTSA-0017	WWQWW	890.9992	77.8%	71.9%	891.6
TTSA-0018	IYWWE	795.8928	75.9%	72.7%	796.4
TTSA-0019	WSWQD	720.7394	84.10%	84.98%	721.1
TTSA-0020	WMWWTG	866.0108	43.7%	37.4%	867.5

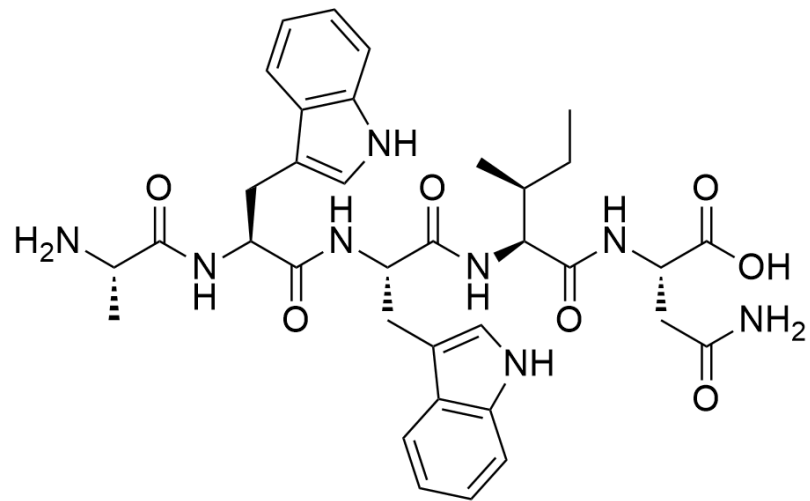
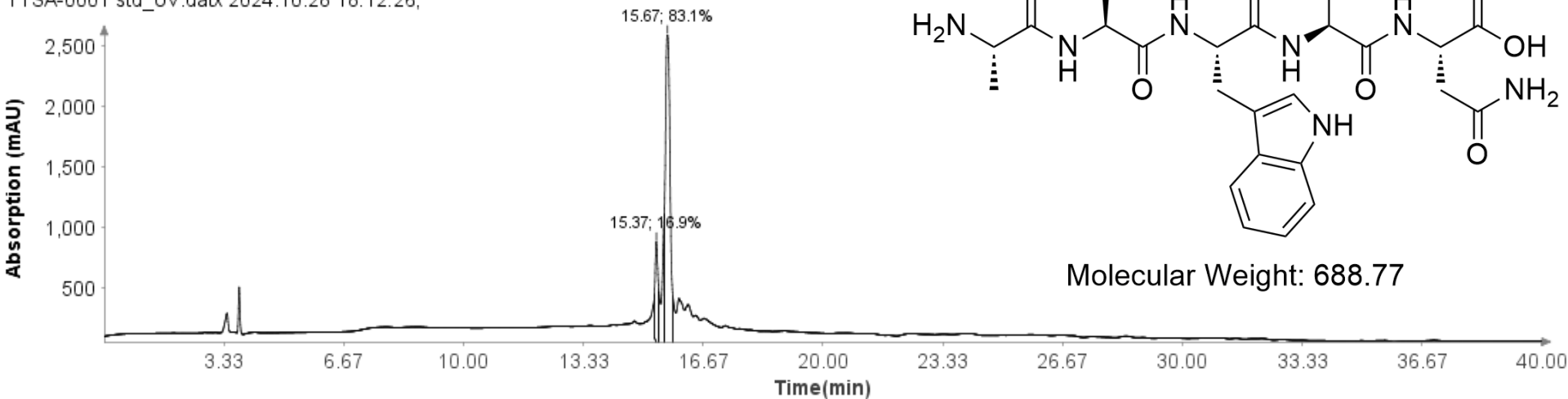
# TTSA-0001



Molecular Weight: 688.77

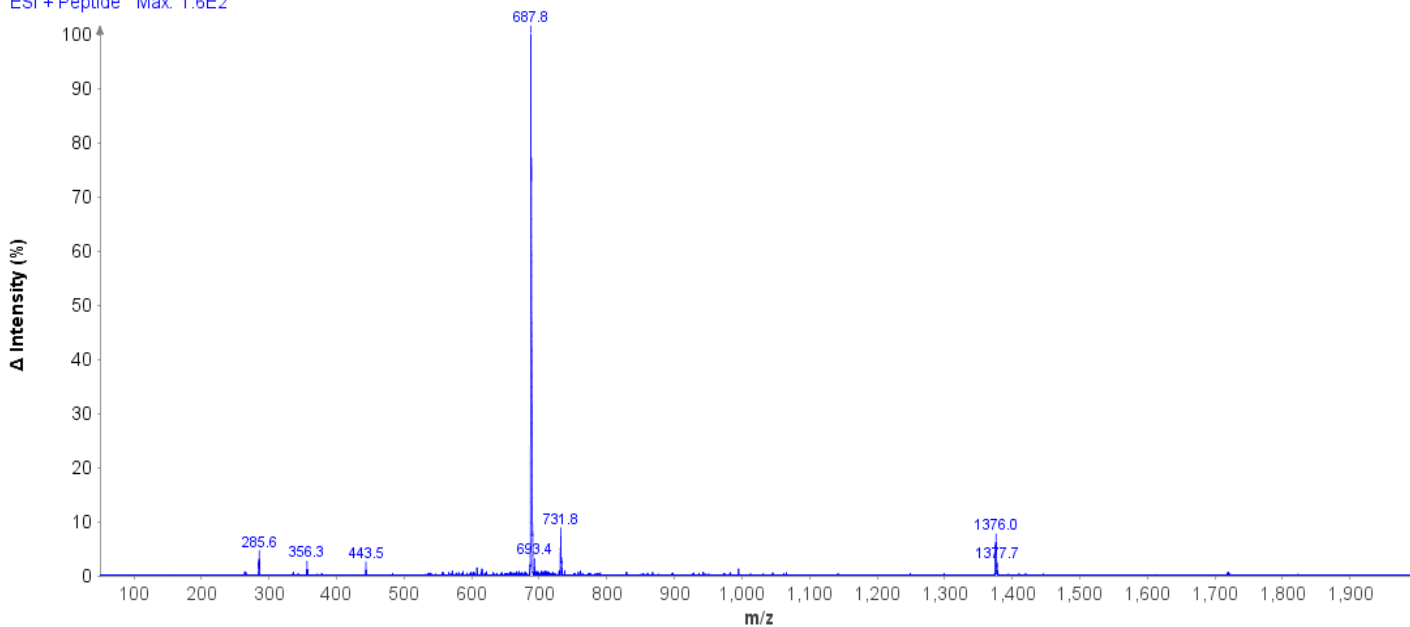


DAD: Signal B, 214 nm/Bw:4 nm  
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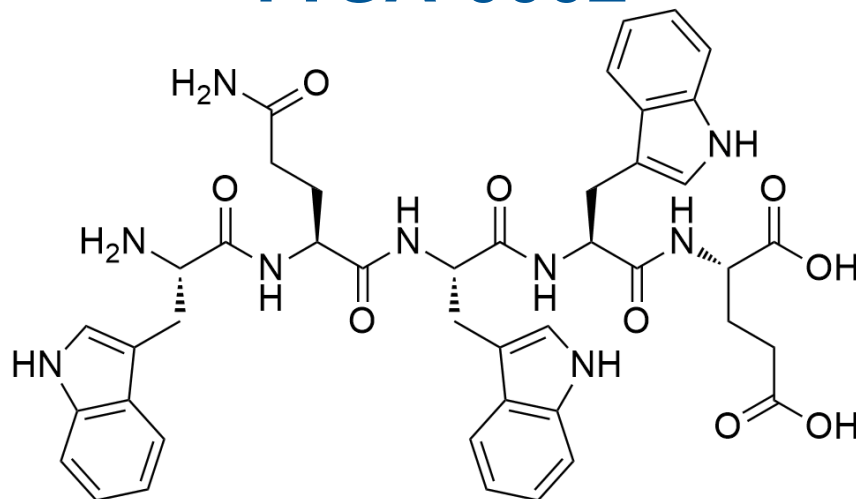


Molecular Weight: 688.77

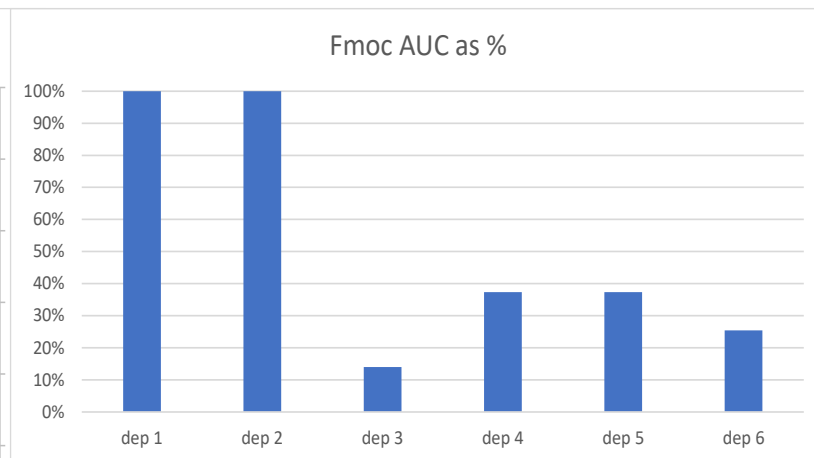
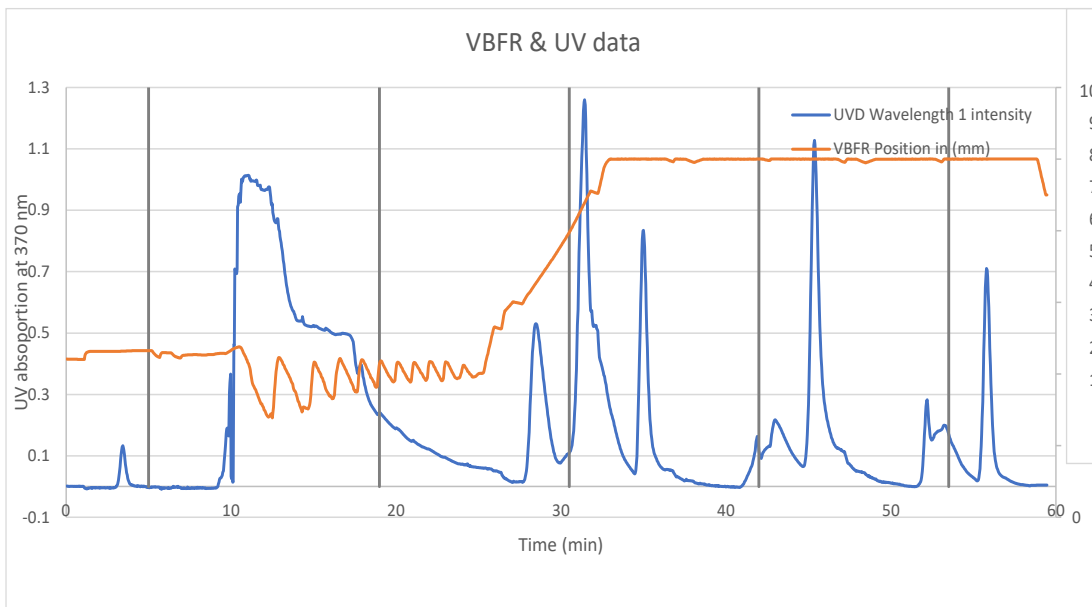
$\Delta S$  15.76 - 16.08 (33 scans)  
TTSA-0001 std.datx;  
ESI + Peptide Max: 1.6E2



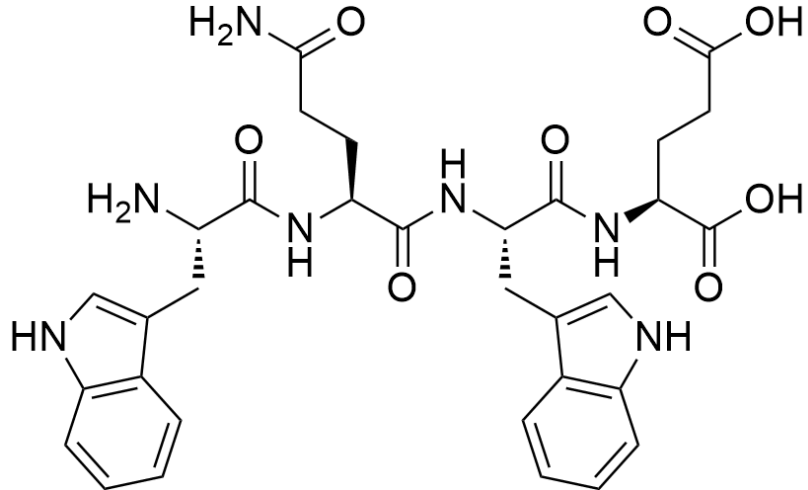
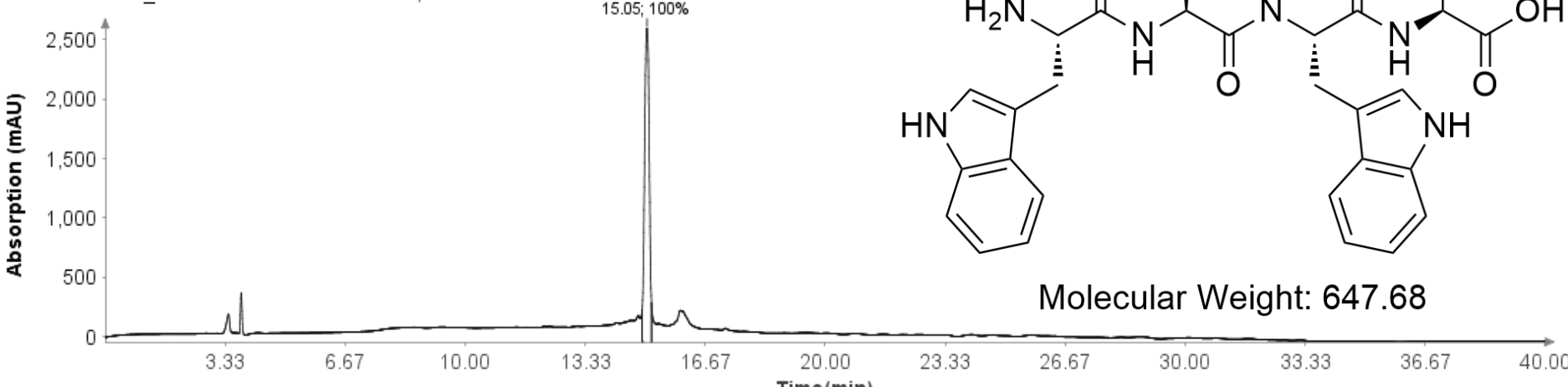
# TTSA-0002



Molecular Weight: 833.89

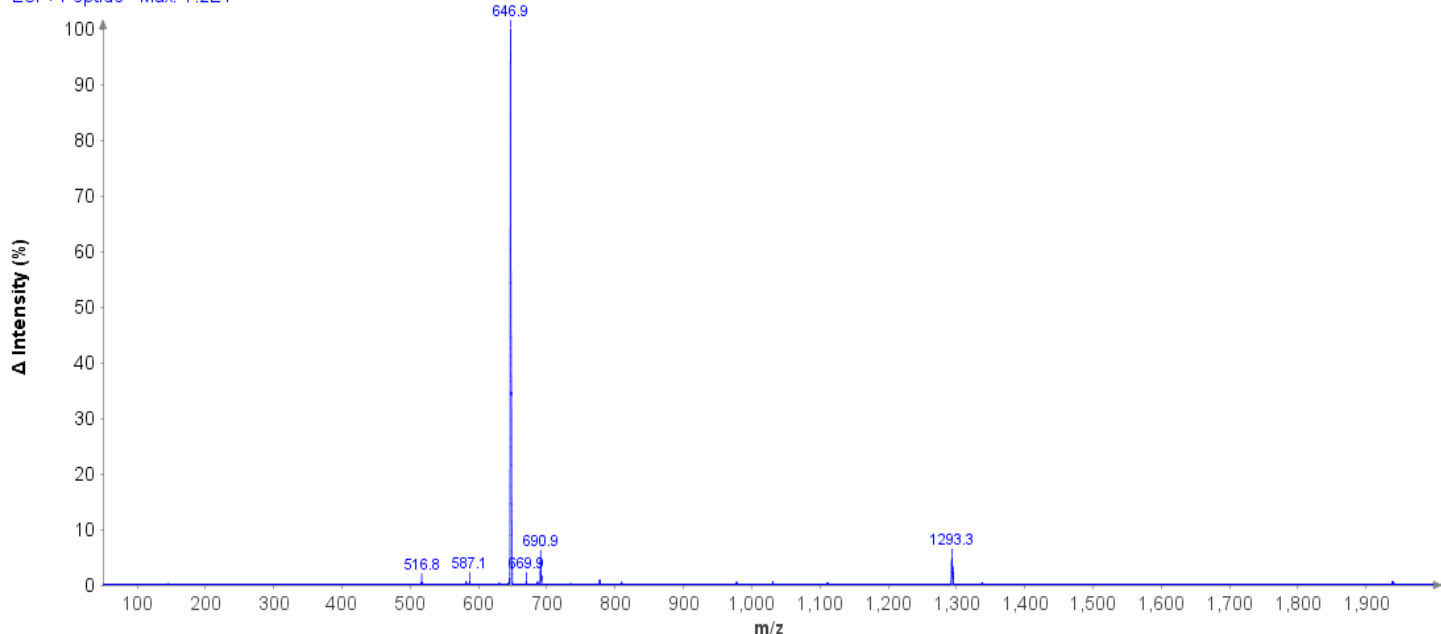


DAD: Signal B, 214 nm/Bw:4 nm  
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Molecular Weight: 647.68

ΔS 15.10 - 15.45 (36 scans)  
TTSA-0002 std.datx;  
ESI + Peptide Max: 7.2E1

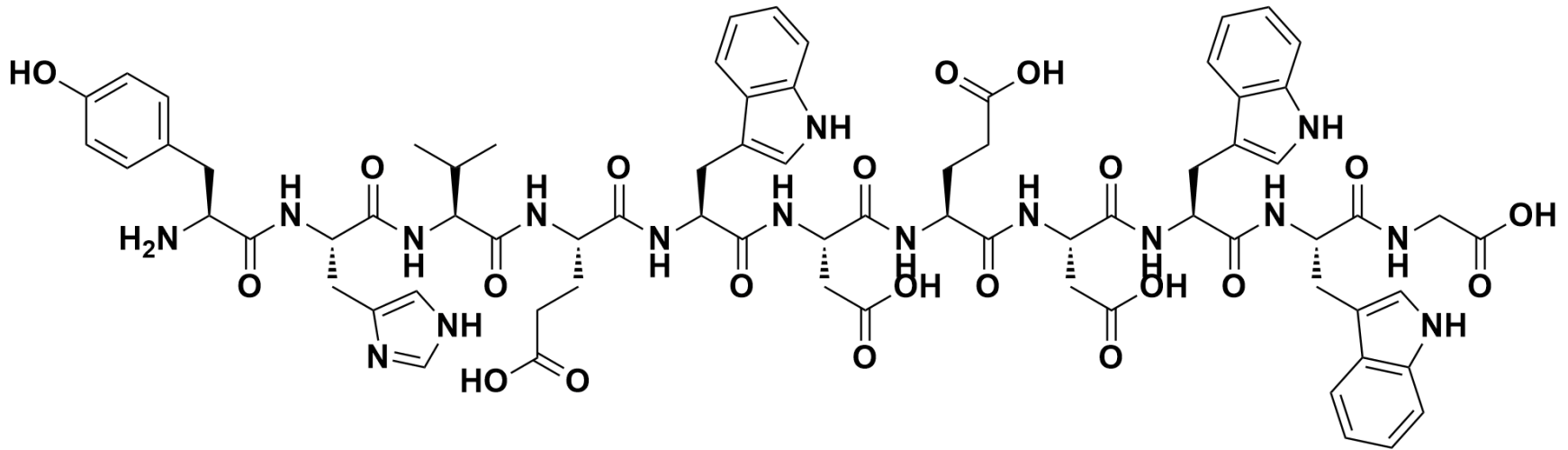


# HLA blockers:

TrantTeam_IDs	Sequence	M.W.	LC 214nm	LC 250nm	LR-MS
TTM006	WIAEWDEELRG	1403.5143	64.5%	71.3%	1404.3
TTM017	YWVEWDYEFRG	1549.6622	54.1%	53.2%	1550.1
TTM041	YHVEWDEDWWG	1521.5651	32.7%	39.7%	1522.1
TTM069	WFVDWDEDHQQ	1433.4562	84.7%	100.0%	1434.0
TTM089	YHVEFDEDFKG	1385.4525	63.3%	68.7%	1386.2
TTM108	WYVEYDEDWRG	1517.5742	53.2%	63.2%	1518.5
TTM175	WYVEFDEDFKG	1434.5247	64.2%	66.5%	1435.8
TTM314	YFVEFDEDFQG	1395.4445	100.0%	100.0%	1397.7
TTM405	YFVDWDEDHQQ	1410.4189	100.0%	100.0%	1413.1
TTM667	YIAEWDYELRG	1414.5374	51.6%	59.3%	1416.2

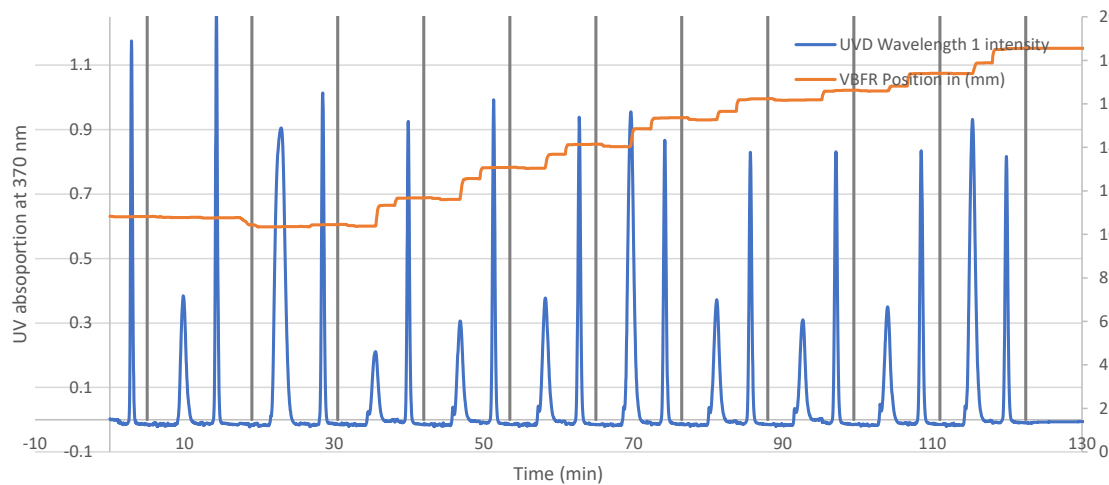


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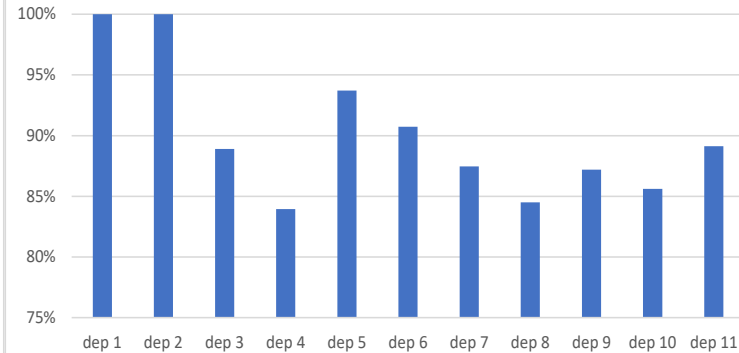


Molecular Weight: 1521.54

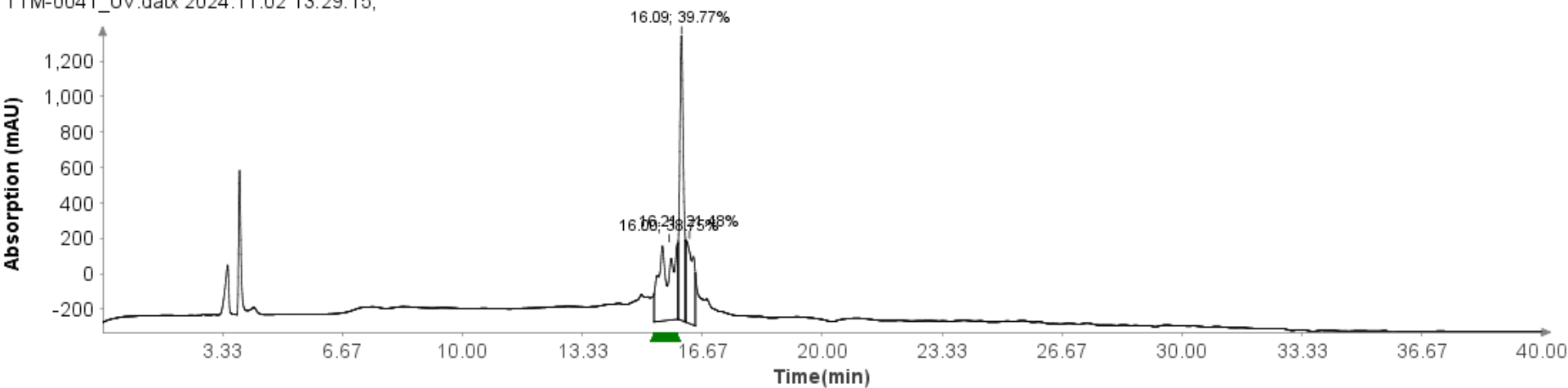
VBFR & UV data



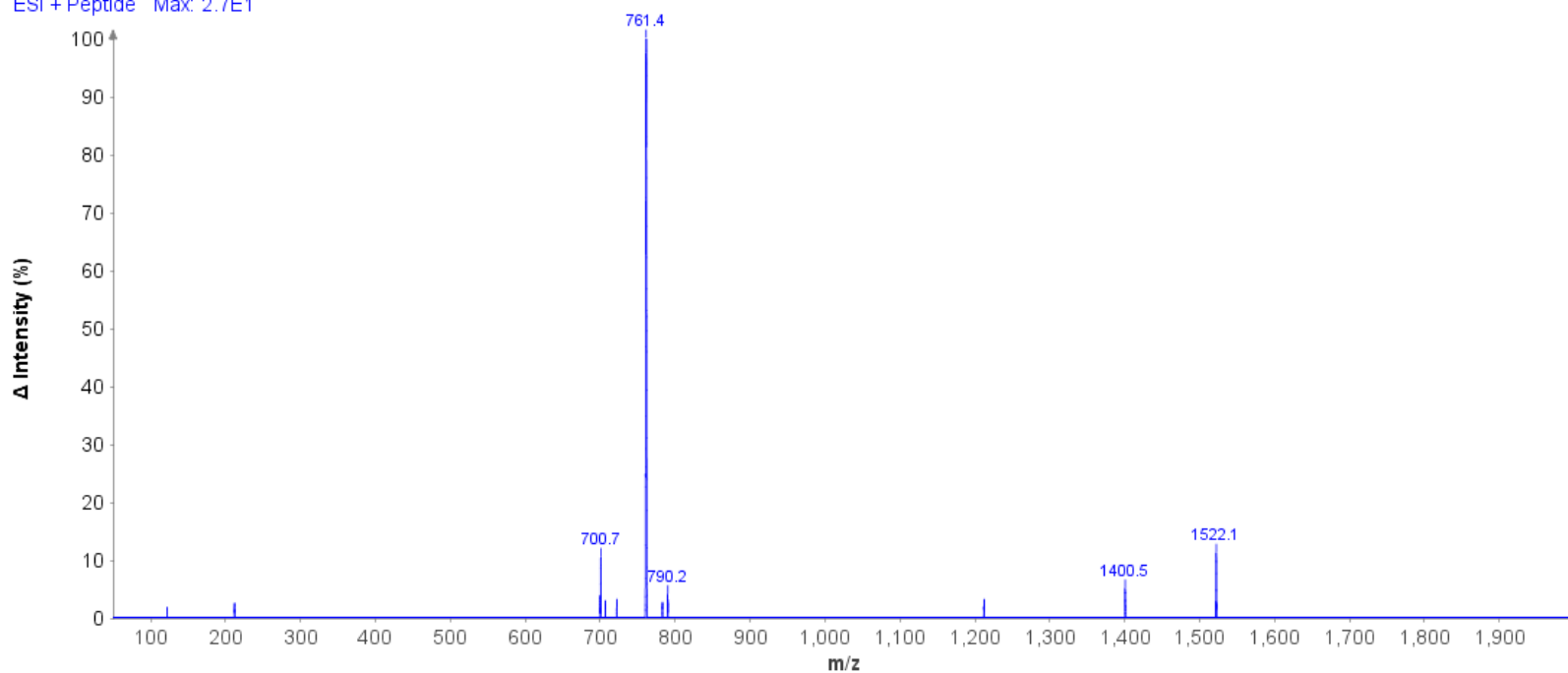
Fmoc AUC as %

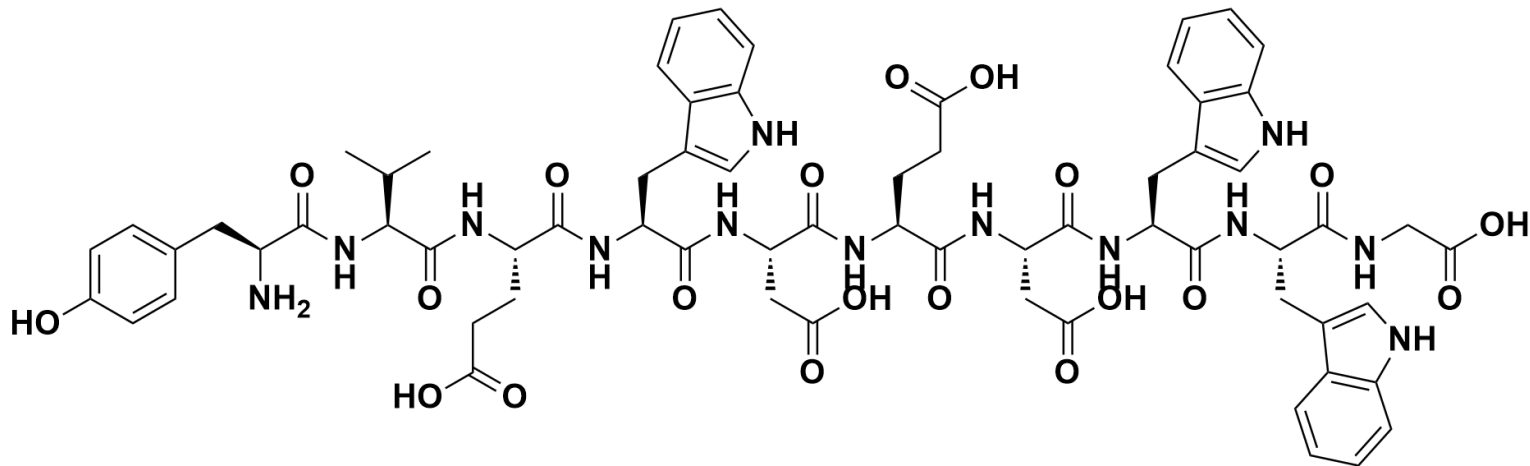


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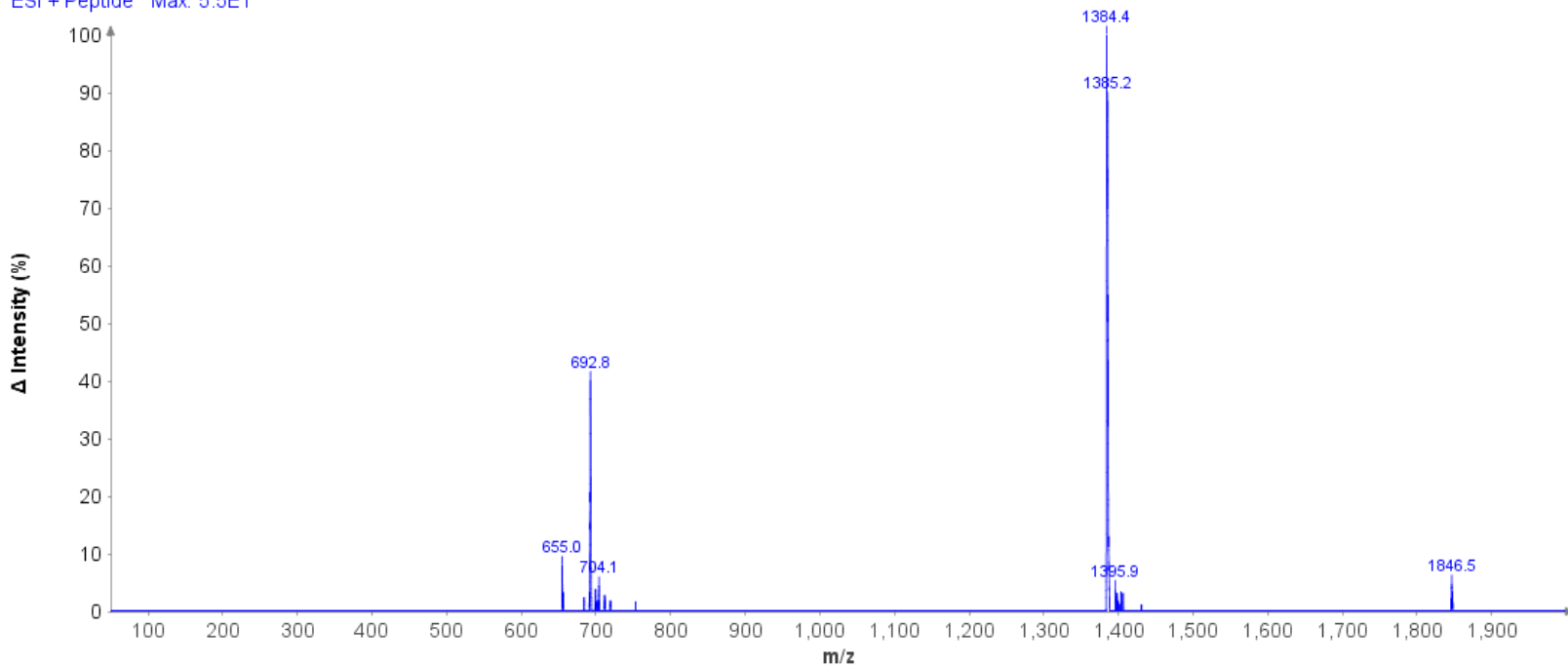
$\Delta S$  15.84 - 15.98 (15 scans)  
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ESI + Peptide Max: 2.7E1



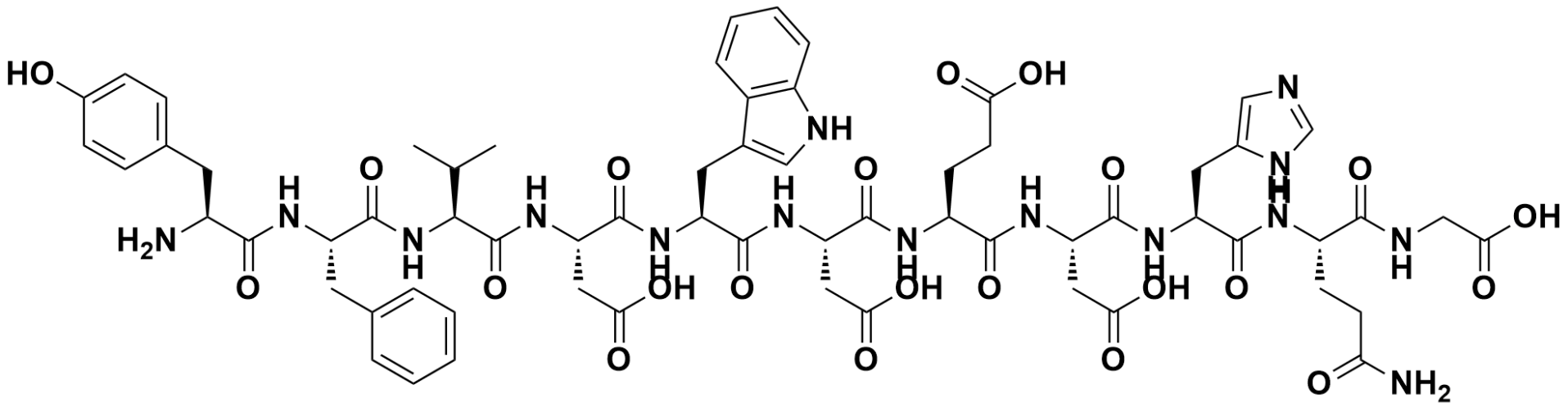


Molecular Weight: 1384.40

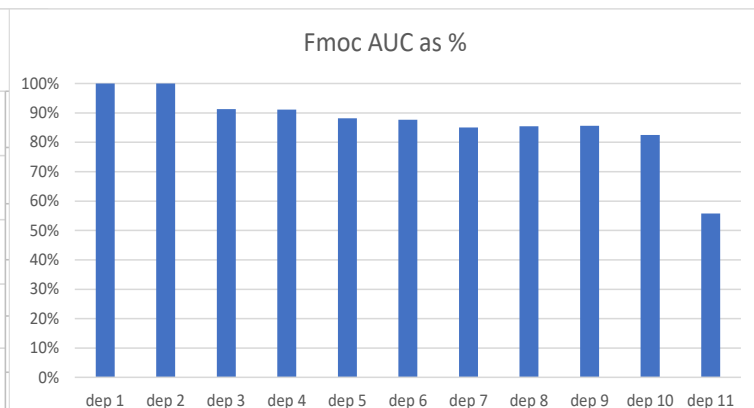
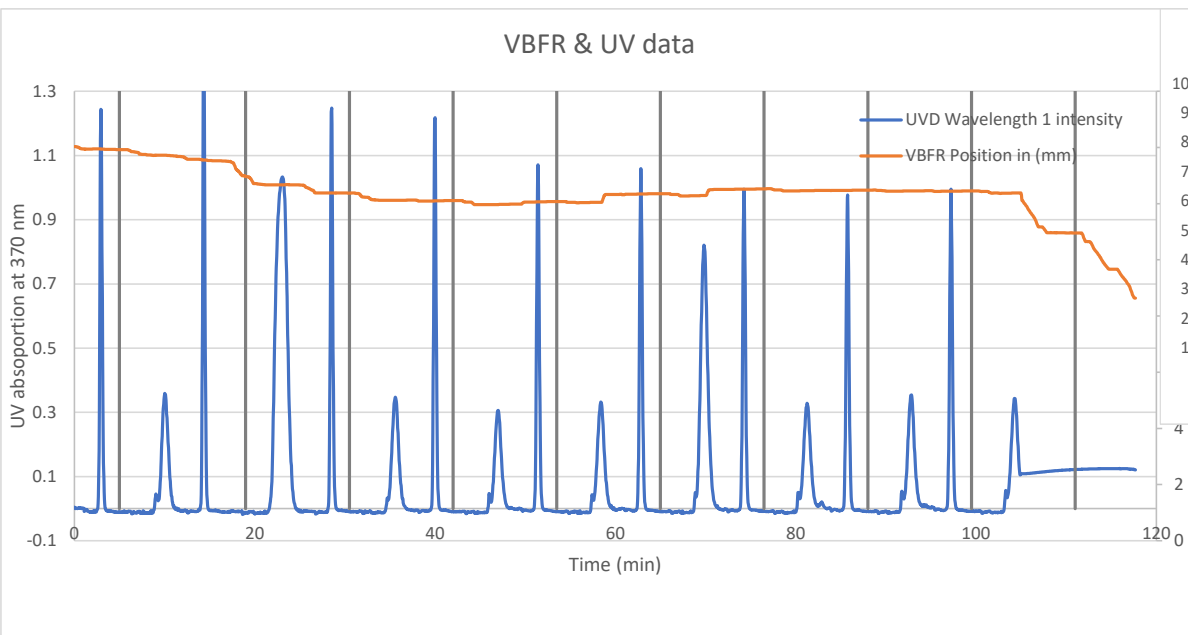
ΔS 16.15 - 16.28 {14 scans}  
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 ESI + Peptide Max: 5.5E1



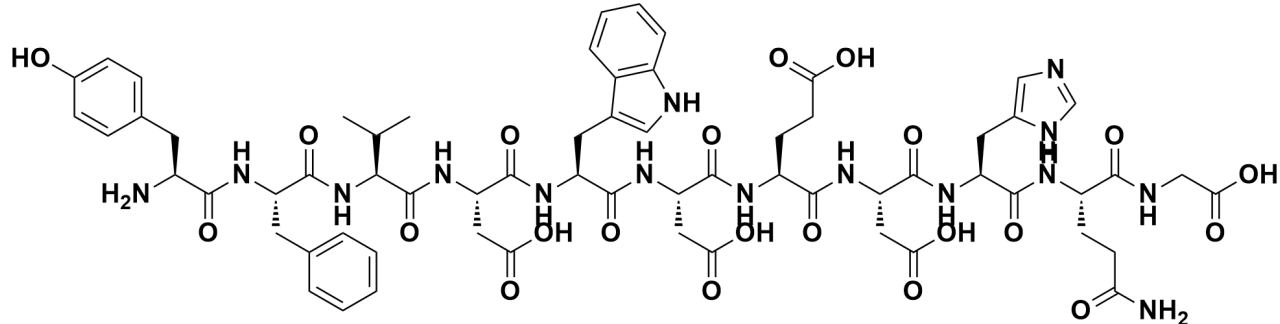
# TTM-0405



Molecular Weight: 1410.40

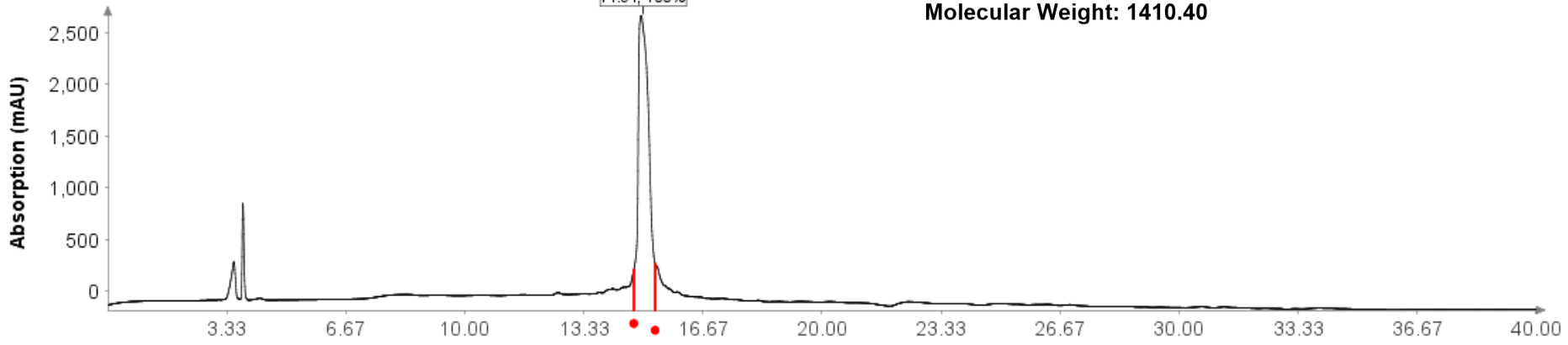


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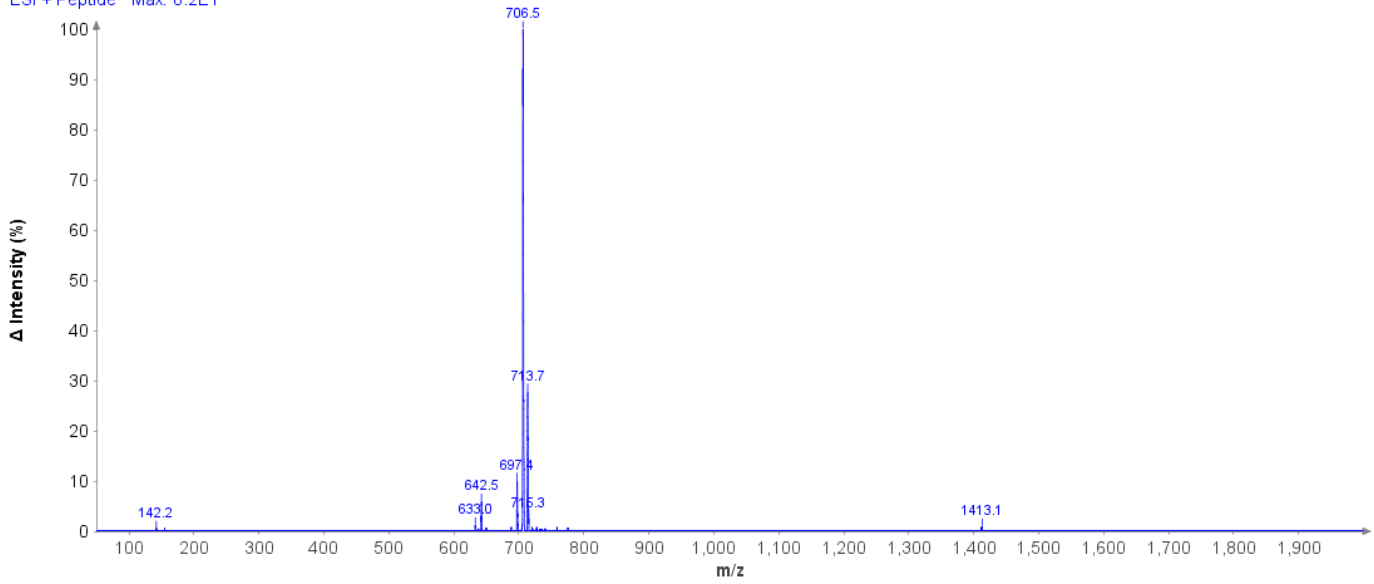


Molecular Weight: 1410.40

DAD: Signal B, 214 nm/Bw:4 nm  
TTM-0405\_UV.datx 2024.11.04 11:14:40;



ΔS 14.99 - 15.28 (30 scans)  
TTM-0405.datx;  
ESI + Peptide Max: 8.2E1



## Conclusions:

- We have created a library of di, tri, tetra and pentapeptides that is ready to use for computational purposes (docking)
- This library was used to create two different lists of candidates to target HLA-DR4 and Hsp90.
- 30 of these candidates were synthesized in a robust, efficient and quick fashion using CF-SPPS

# Acknowledgments

