

Novel scaffolds for modulation of NOD2 identified by pharmacophore-based virtual screening

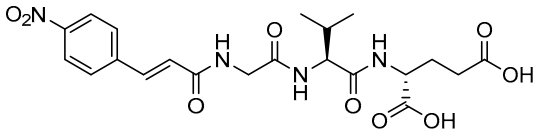
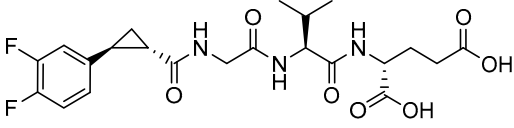
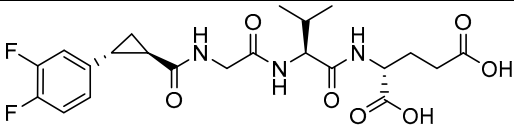
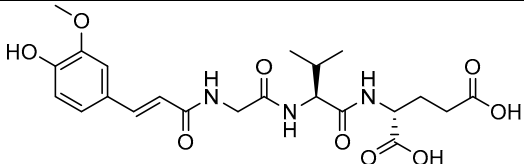
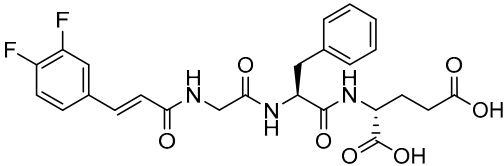
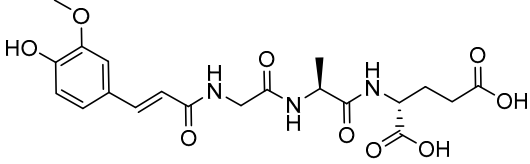
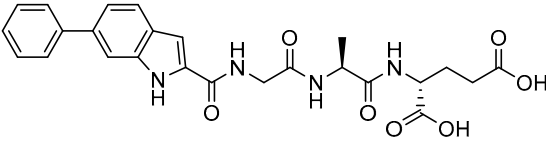
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Table S1. Structures of NOD2 agonists **S1-S12** used as a training set for ligand-based pharmacophore model generation.

Cpd.	Structure	Ref.
S1 (MDP)	<chem>O=C(CC[C@@H](NC([C@@H](NC([C@@H](C)O[C@H]1[C@H](O)[C@@H](CO)O[C@H](O)[C@@H]1NC(C)=O)=O)C)=O)C(N)=O)O</chem>	[1–3]
S2	<chem>O=C(CC[C@@H](NC([C@@H](NC([C@@H](C)O[C@H]1[C@H](O)[C@@H](CO)O[C@H](O)[C@@H]1NC(C)=O)=O)C)=O)C(O)=O)O</chem>	[3]
S3	<chem>O=C(CC[C@@H](NC([C@@H](NC([C@@H](C)O[C@H]1[C@H](O)[C@@H](CO)O[C@H](O)[C@@H]1NC(CO)=O)=O)C)=O)C(N)=O)O</chem>	[4]
S4	<chem>O=C(CC[C@@H](NC([C@@H](NC([C@@H](C)O[C@H]1[C@H](O)[C@@H](CN)O[C@H](O)[C@@H]1NC(C)=O)=O)C)=O)C(N)=O)O</chem>	[4]
S5	<chem>CC(C)[C@@H](C(N[C@@H](C(O)=O)CCC(O)=O)=O)NC(CNC/C=C/C1=CC=C(C(C)C)C=C1)=O=O</chem>	[5]

S6	 <chem>CC(C)[C@@H](C(N[C@@H](C(O)=O)CCC(O)=O)=O)NC(CNC(/C=C/C1=CC=C([N+])([O-])=O)C=C1)=O=O</chem>	[5]
S7	 <chem>CC(C)[C@@H](C(N[C@@H](C(O)=O)CCC(O)=O)=O)NC(CNC([C@@H]1[C@@H](C2=CC(F)=C(F)C=C2)C1)=O)=O</chem>	[5]
S8	 <chem>CC(C)[C@@H](C(N[C@@H](C(O)=O)CCC(O)=O)=O)NC(CNC([C@H]1[C@H](C2=CC(F)=C(F)C=C2)C1)=O)=O</chem>	[5]
S9 (SG8)	 <chem>CC(C)[C@@H](C(N[C@@H](C(O)=O)CCC(O)=O)=O)NC(CNC(/C=C/C1=CC(OC)=C(O)C=C1)=O)=O</chem>	[6]
S10	 <chem>O=C(N[C@@H](C(O)=O)CCC(O)=O)[C@H](CC1=CC=CC=C1)NC(CNC(/C=C/C2=CC(F)=C(F)C=C2)=O)=O</chem>	[6]
S11	 <chem>C[C@@H](C(N[C@@H](C(O)=O)CCC(O)=O)=O)NC(CNC(/C=C/C1=CC(OC)=C(O)C=C1)=O)=O</chem>	[6]
S12	 <chem>C[C@@H](C(N[C@@H](C(O)=O)CCC(O)=O)=O)NC(CNC(C1=CC(C=C2)=C(N1)C=C2C3=CC=CC=C3)=O)=O</chem>	[7]

Supplementary Figures

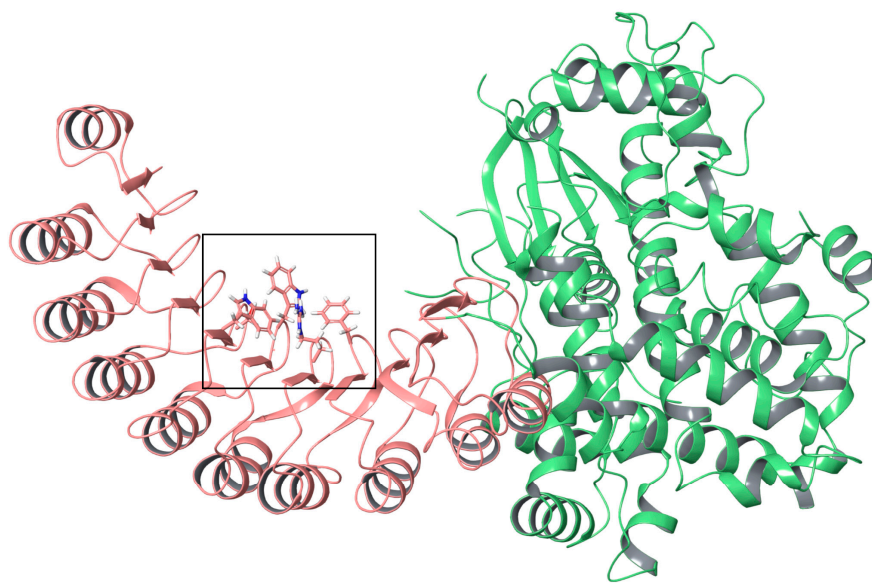


Figure S1. Structure of the homology model of human NOD2, comprised of two domains: the nucleotide-binding oligomerization domain (NOD; 215–764, green) and the leucine-rich repeat domain (LRR; 765–1040). The caspase activation and recruitment domains (CARDs; 1–214) were not modeled. The putative MDP binding site is highlighted by a rectangle.

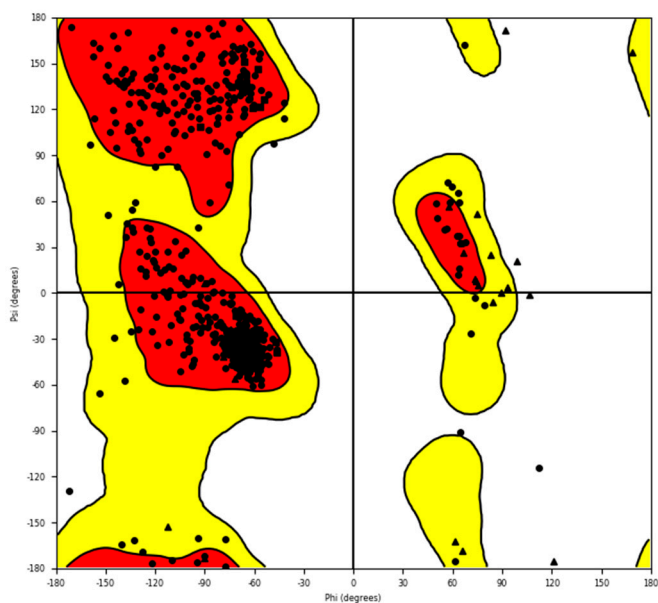


Figure S2. Ramachandran plot of the constructed homology model. Glycine is plotted as triangles, proline is plotted as squares, and all other residues are plotted as circles. The orange regions are the favored regions, the yellow regions are the allowed regions, and the white regions are the disallowed regions. 4 non-glycine residues (0.5% of 746 total residues): Ala525, Ala597, Cys632, and Ile722 are located in the disallowed region.

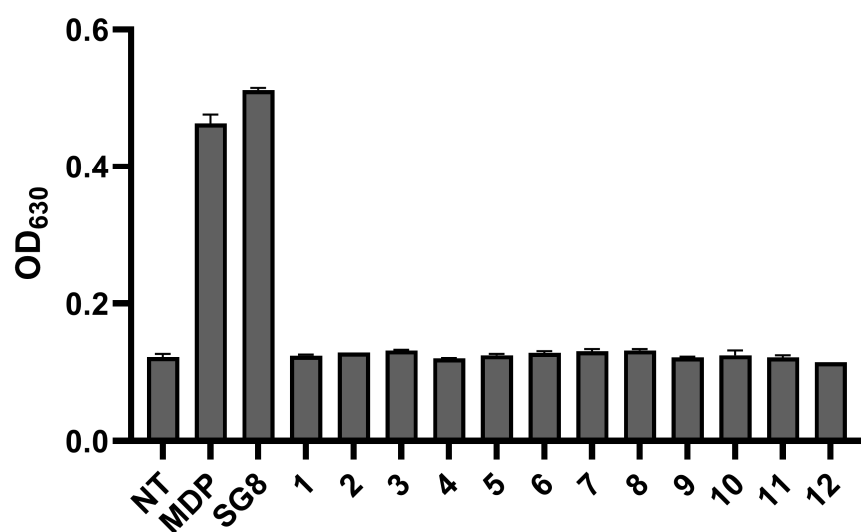


Figure S3. None of the screening hits exhibited NOD2 agonistic activity. SEAP activity in the HEK-Blue NOD2 cell supernatants was determined after 18 h treatment with the screening hits (500 μ M), MDP (1 μ M), SG8 (1 μ M), or vehicle (0.1% DMSO; NT). Data are shown as optical densities at 630 nm and are means \pm SEM of two independent experiments.

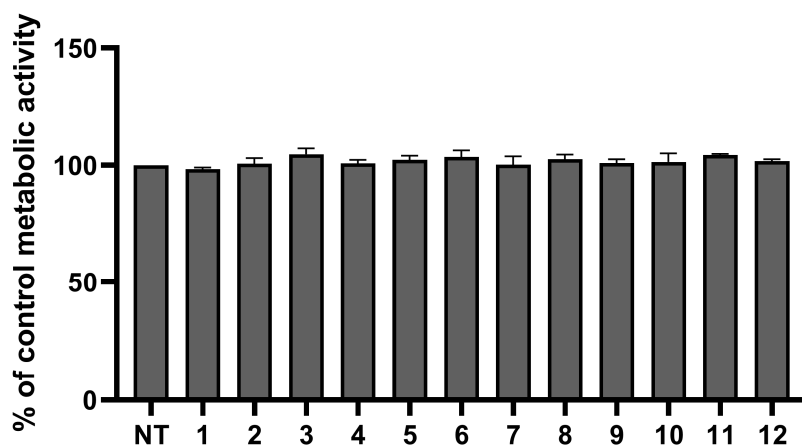
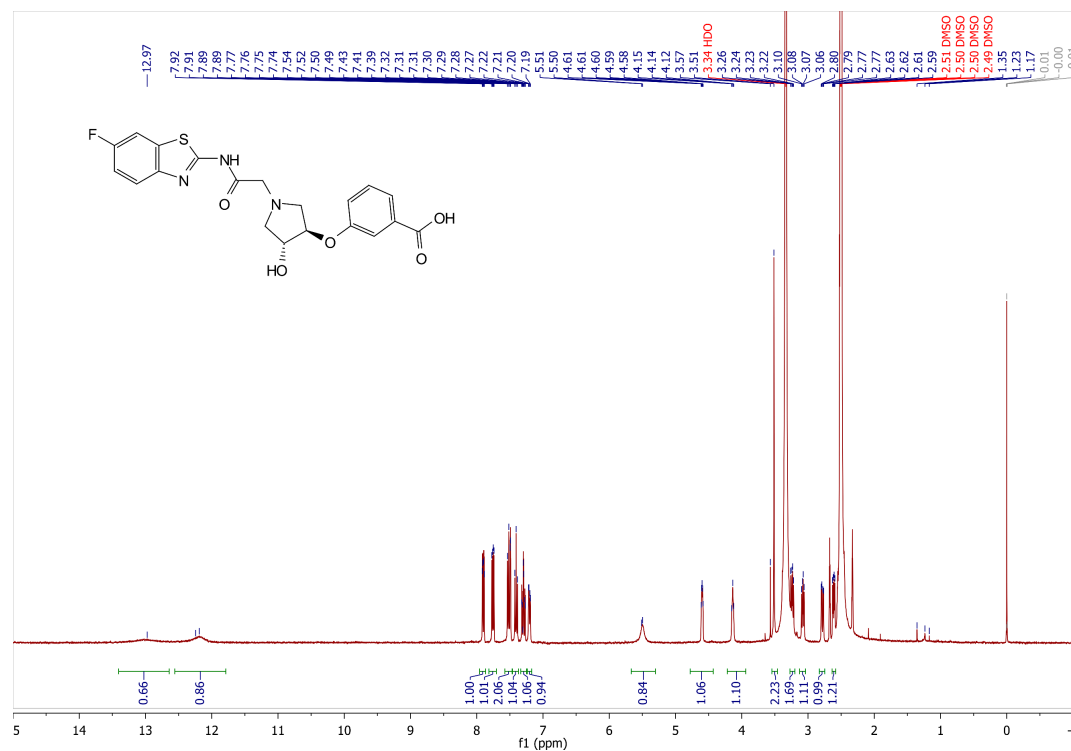


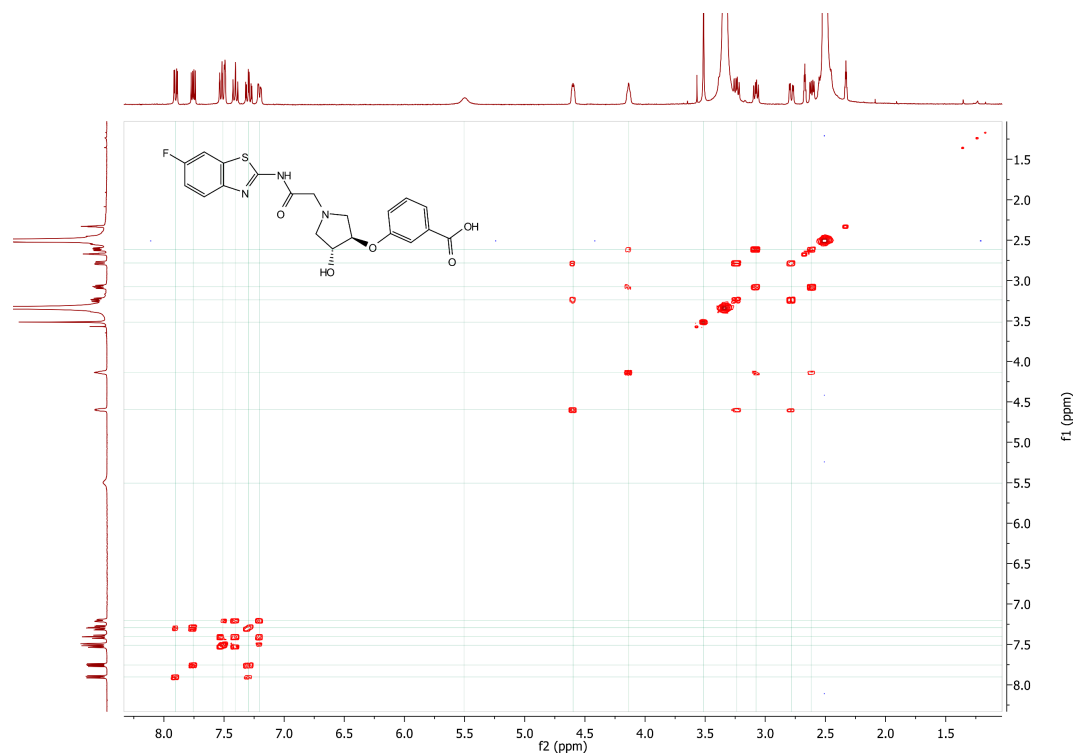
Figure S4. Metabolic activities of HEK-Blue NOD2 cells after 18 h treatment with screening hits (500 μ M). The results are shown relative to that of the untreated control (0.1% DMSO; NT). Data are means \pm SEM of two independent experiments.

NMR spectra

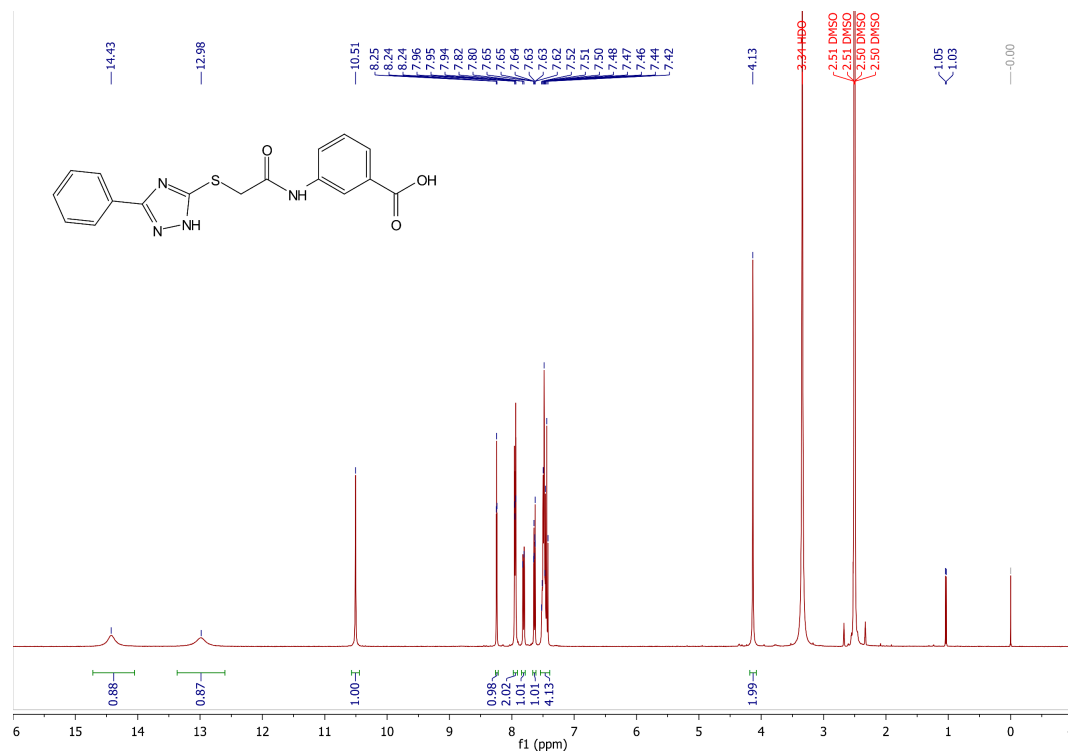
Compound 1: ^1H , 400 MHz, $\text{DMSO}-d_6$



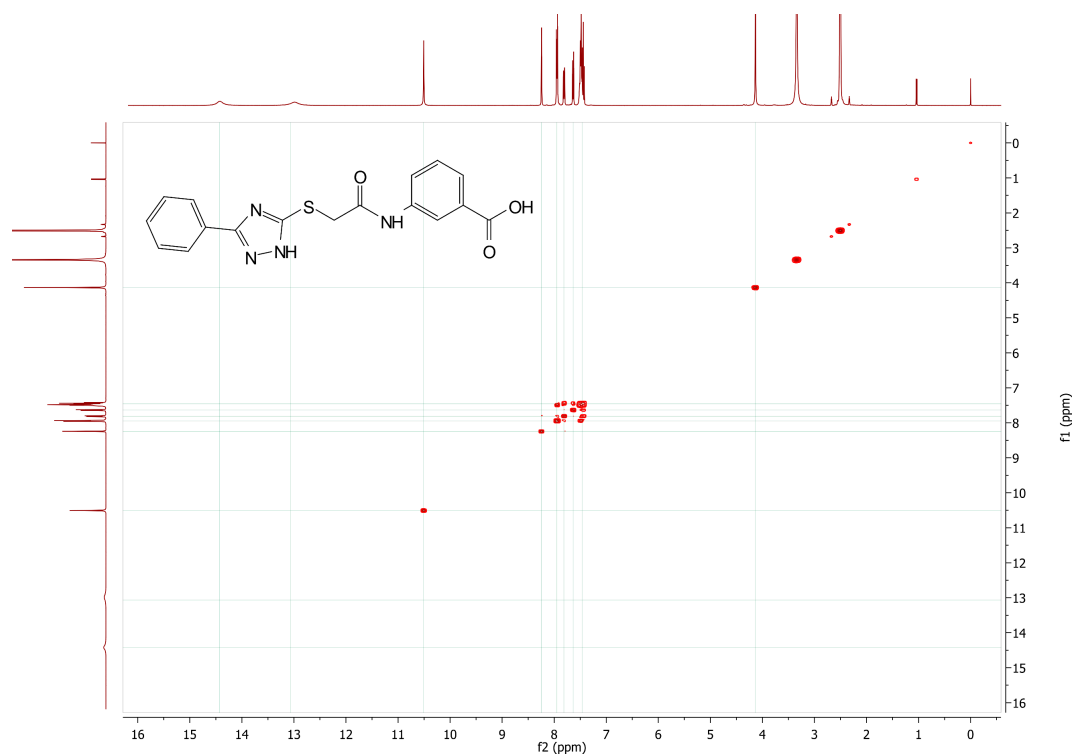
Compound 1: ^1H - ^1H COSY, 400 MHz, $\text{DMSO}-d_6$



Compound 3: ^1H , 400 MHz, $\text{DMSO}-d_6$



Compound 3: ¹H-¹H COSY, 400 MHz, DMSO-*d*₆



UHPLC traces

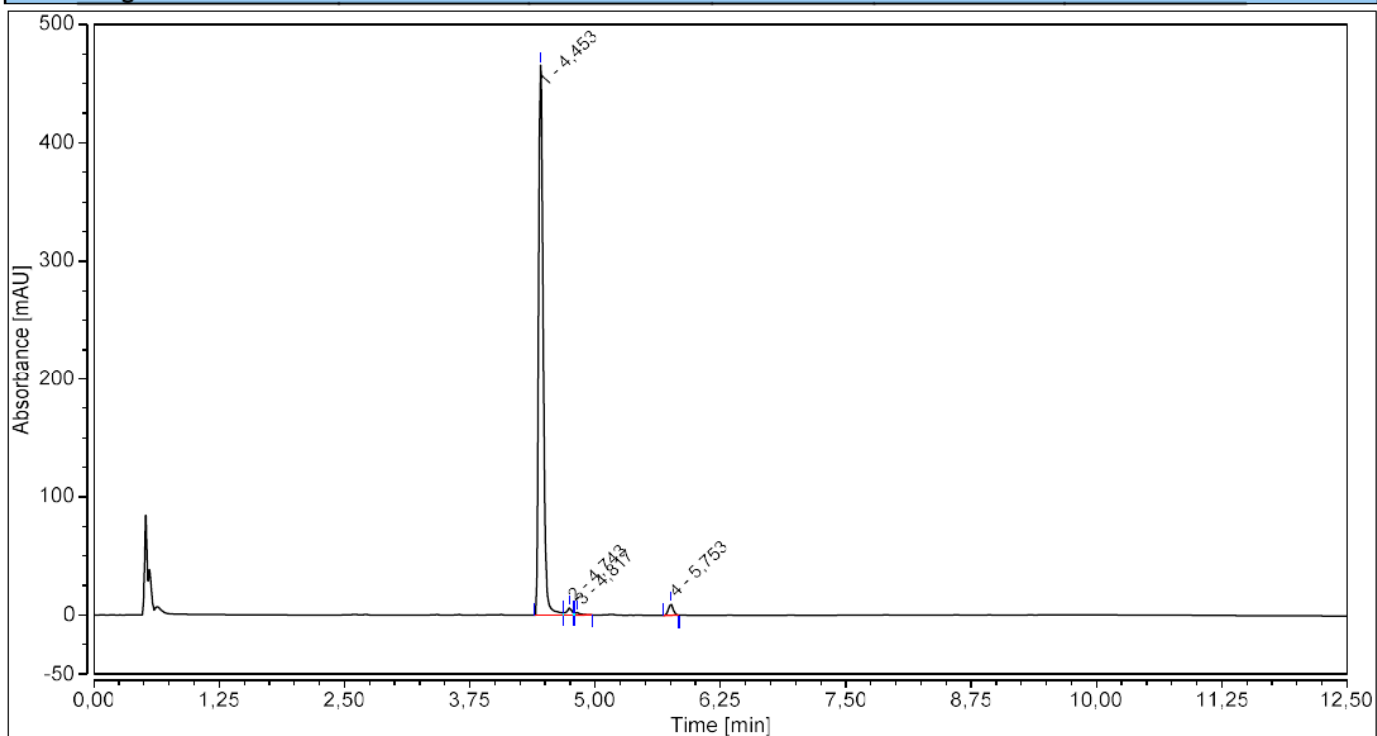
Compound 1

Chromatogram and Results

Injection Details

Injection Name:	Ax3	Run Time (min):	12,50
Processing Method:	Quantitative	Injection Volume:	5,00
Injection Date/Time:	24.feb..22 15:14	Wavelength:	254

Chromatogram



Integration Results

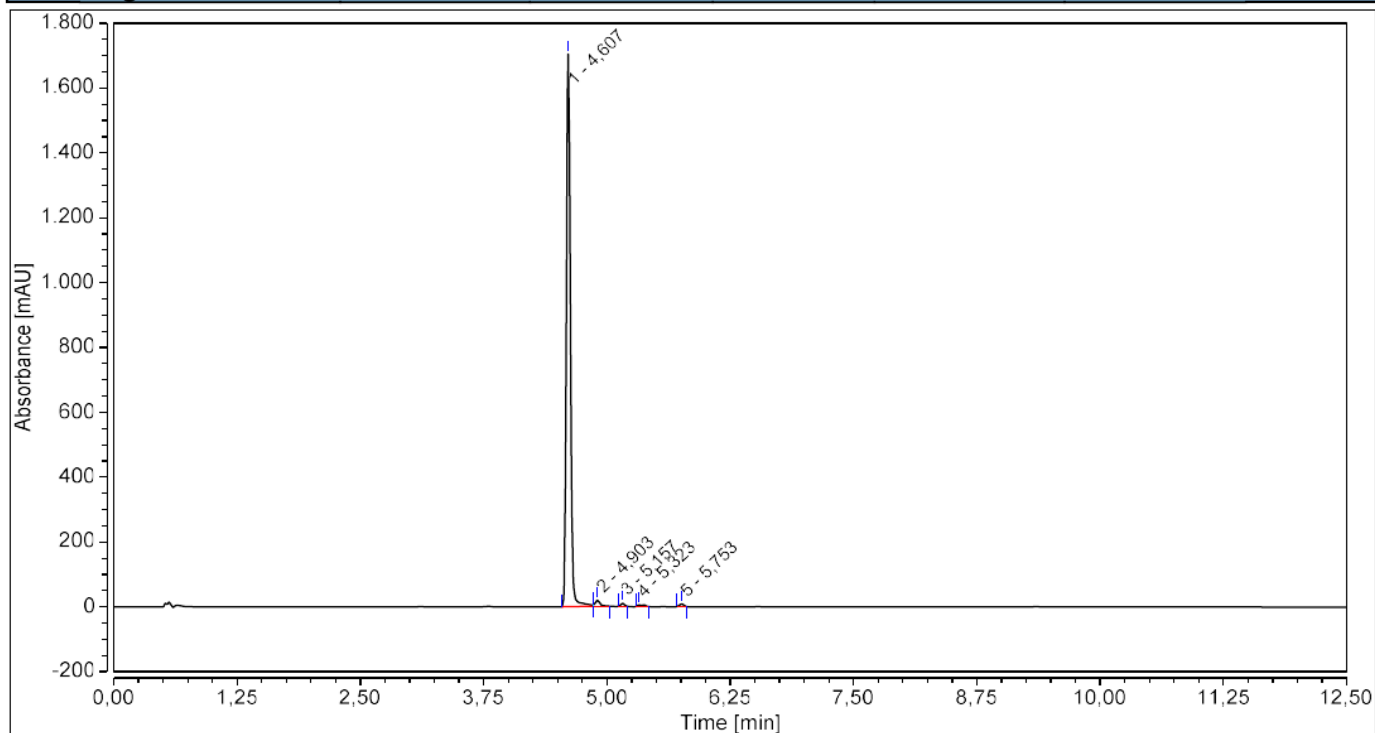
No.	Retention Time min	Area mAU*min	Height mAU	Relative Area %	Relative Height %
1	4,453	24,641	465,970	96,01	96,27
2	4,743	0,357	6,121	1,39	1,26
3	4,817	0,140	2,069	0,55	0,43
4	5,753	0,526	9,871	2,05	2,04
Total:		25,664	484,031	100,00	100,00

Chromatogram and Results

Injection Details

Injection Name:	VM2	Run Time (min):	12,50
Processing Method:	Quantitative	Injection Volume:	5,00
Injection Date/Time:	24.feb..22 15:32	Wavelength:	254

Chromatogram



Integration Results

No.	Retention Time min	Area mAU*min	Height mAU	Relative Area %	Relative Height %
1	4,607	78,789	1703,841	97,31	97,60
2	4,903	0,988	18,940	1,22	1,08
3	5,157	0,394	9,601	0,49	0,55
4	5,323	0,413	5,413	0,51	0,31
5	5,753	0,382	7,927	0,47	0,45
Total:		80,966	1745,721	100,00	100,00

References

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