Supplementary Material (ESI) for Organic and Biomolecular Chemistry

Design of Substituted Tetrahydrofuran Derivatives for HIV-1 Protease Inhibitors: Synthesis, Biological Evaluation, and X-ray Structural Studies

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General Methods.

All chemicals and reagents were purchased from commercial suppliers and used without further purification unless otherwise noted. The following reaction solvents were distilled prior to use: dichloromethane from calcium hydride, diethyl ether and tetrahydrofuran from Na/benzophenone, methanol and ethanol from activated magnesium under argon. All reactions were carried out under an argon atmosphere in either flame or oven-dried (120 °C) glassware. TLC analysis was conducted using glass-backed Thin-Layer Silica Gel Chromatography Plates (60 Å, 250 µm thickness, F-254 indicator). Column chromatography was performed using 230-400 mesh, 60 Å pore diameter silica gel. ¹H and ¹³C NMR spectra were recorded at room temperature on a Bruker AV800, DRX-500 and ARX-400. Chemical shifts (δ values) are reported in parts per million, and are referenced to the deuterated residual solvent peak. NMR data is reported as: δ value (chemical shift, J-value (Hz), integration, where s = singlet, d = doublet, t = triplet, q = quartet, brs = broad singlet). Optical rotations were recorded on a Perkin Elmer 341 polarimeter. HRMS and LRMS spectra were recorded at the Purdue University Department of Chemistry Mass Spectrometry Center. HPLC analysis and purification was done an on Agilent 1100 series instrument using a YMC Pack ODS-A column of 4.6 mm ID for analysis and either 10 mm ID or 20 mm ID for purification. The purity of test compounds was determined by HRMS and HPLC analysis. All test compounds showed $\geq 90\%$ purity.

Expression and purification of protease species

Expression and purification of protease were carried out as previously described [1]. Briefly, Rosetta (DE3) pLysS strain (Novagen) was transformed with an expression vector (pET-30a), which contained the genes of wild-type HIV-1^{NL4-3}-PR (PR^{WT}) using heat-shock. The culture was grown in a shake flask containing 30 mL of Luria broth plus kanamycin and chloramphenicol (LB^{Km+/Cp+}) at 37°C overnight. In the expression of PRWT, twenty milliliter of the grown culture was added to 1 L of ZYM-10052 [1.0% N-Z amine, 0.5% yeast extract, 25 mM disodium hydrogenphosphate, 25 mM potassium dihydrogenphosphate, 50 mM ammonium chloride, 5 mM sodium sulfate, 1.0% glycerol, 0.05% glucose, 0.2% α-lactose, 2 mM magnesium sulphate] plus kanamycin and chloramphenicol (ZYM-10052^{Km+/Cp+}). The ZYM-10052^{Km+/Cp+} culture was further continued at 37°C for 20~22 hours. Then the culture was spun down for pellet collection, and thus-obtained pellets were stored at -80 °C until use. For purification of PR^{WT}, the pellet was resuspended in buffer A [20 mM Tris, 1 mM EDTA, and 1 mM DTT] and lysed with sonication. The cell lysates were separated into a supernatant fraction and an inclusion body fraction with centrifugation. PR^{WT} was confirmed to be present in the inclusion body fraction, which was washed five times with buffer A containing 2 M urea and then with buffer A without urea. The twice-washed pellet was solubilized and PRs were unfolded with 100 mM formic acid (pH 2.8). The unfolded PRs were purified using the fast protein liquid chromatography system (ÄKTA pure 25; GE Healthcare) and separated using the reverse phase chromatography column (RESOURS RPC 3 mL; GE Healthcare) using the gradient of buffer B [1.0% formic acid, 2.0% acetonitrile] and buffer C [1% formic acid, 70% acetonitrile]. The flow rate was set to 1.0 mL min⁻¹ and the column was equilibrated with 75% buffer B and 25% buffer C. Then, the amount of buffer C was increased to 75% over a 30 min period (10-time the column volume). PRWT was eluted with 35~50% buffer C. After the elution, buffer C amount was increased to 100% in 6 min and returned to the starting condition over the next 6 min. The peak fractions including PRWT were collected and three-time diluted with buffer B. The diluted PRWT solution was injected into the ÄKTA pure 25 again and the targeted PR^{WT} was purified using the same purification step as described above. The collected fractions containing PRWT were subjected to desalting (HiTrap Desalting; GE Healthcare) and the eluted solution was equilibrated using 100 mM formic acid and stored at -80 °C until use.

The unfolded PR^{WT} was refolded with the addition of a neutralizing buffer A [100 mM ammonium acetate pH 6.0, 0.005% Tween-20], making the final pH 5.0 to 5.2. The PR^{WT}-containing solution was run through Amicon Ultra-15 10K centrifugal filter units (Millipore), giving a solution containing PR (5~8 mg/ml) in 10 mM ammonium acetate pH 5.0 and 0.005% Tween-20. Occasionally, twice greater concentrations of a test compound were used for crystalization. After centrifugation, the supernatants were collected and subjected to crystallization using the hanging-drop vapor diffusion method. Nextal Tubes ProComplex Suite (QIAGEN) and Wizard Crystallization Screen Series (Emerald BioSystems) were used for the first screening to determine the optimum crystallization condition.

	PR/compound 4l (GRL-072-17A)
Space group	P2 ₁ 2 ₁ 2
Unit cell dimensions: (Å)	
a	58.57
b	85.88
с	46.31
Resolution range (Å)	50-1.32 (1.37-1.32)
Redundancy (final shell)	5.8 (4.8)
Unique reflections	51438 (3856)
Completeness (%) overall (final shell)	93.6 (71.5)
R _{merge} (%) overall (final shell)	8.9 (51.2)
$I/\sigma(I)$ overall (final shell)	17.1 (3.9)
Refinement	
R (%)	13.2
R _{free} (%)	16.4
No. of solvent atoms	232
RMS deviation from ideality	
Bonds (Å)	0.019
Angle (degree)	2.2
Average B-factors (Å ²)	
Whole chain atoms	16.4
Inhibitor	13.5
Solvent	25.4

Table S1: Crystallographic Data Collection and Refinement Statistics

Figure S1: 2Fo-Fc electron density map showing two alternative conformations of inhibitor 41. The 2Fo-Fc electron density map (gray) for inhibitor **4I** in the X-ray structure with HIV protease is contoured at a level of 1 sigma. The carbon atoms are shown in green for conformation A and in yellow for conformation B of inhibitor with relative occupancies of 0.55 and 0.45.



Geometric Criteria for Weak Interactions.

Hydrogen bond interactions are defined by standard geometrical criteria as described in [1, 2]. The geometric criteria for weak interactions are: C-H...O (distance between C and O<=3.5 Å, angle >=90°), O-H... π (distance<=4.3 Å to centroid of π system, angle >=120°), C-H... π (distance<=4.5 Å, angle >=120°) [1-3], lone pair (n)- π as C=O... π (distance is between 2.8 to 3.8 Å to center of π system, angle between two planes <=90°) [4] and π - π stacking [5].

References

(1) Manfred S. Weiss, Maria Brandl, Jürgen Sühnel, Debnath Pal and Rolf Hilgenfeld, "More hydrogen bonds for the (structural) biologist"; *Trends Biochem. Sci.* **2001**, *9*, 521-523.

(2) Baker, E.N. and Hubbard, R.E. Hydrogen bonding in globular proteins. *Prog. Biophys. Mol. Biol.* **1984**, 44, 97–179

(3) Brandl, M. et al. (2001) C–H ... π interactions in proteins. J. Mol. Biol. 2001, 307, 357–377

(4) Prakash Panwaria and Aloke Das. Understanding the $n \rightarrow \pi^*$ non-covalent interaction using different experimental and theoretical approaches. *Phys. Chem. Chem. Phys.* **2022**, *24*, 22371-22389

(5) Mutasem Sinnokrot, Charles David Sherrill, Highly Accurate Coupled Cluster Potential Energy Curves for the Benzene Dimer: Sandwich, T-Shaped, and Parallel-Displaced Configurations. J. Phys. Chem. A 2004, 108, 46, 10200–10207.

HIV-1 Protease inhibitory assay. The assay is based upon reported procedure (1). Fluorescence measurements were made using PerkinElmer LS-50B Luminescence Spectrophotometer. Ten microliters of a stock solution (0.05 mg/mL) of HIV protease were incubated with five different concentrations of substrate 2-(aminobenzoyl)-Thr-Ile-Nle-Phe(p-N0₂)-Gln-ArgNH₂ (Km = 37 at 37 °C with the increase in fluorescence monitored. A stock solution of 1 mM substrate in DMSO was diluted to 0.1 mM with assay buffer and used for the assay. All kcat and Km values were obtained employing standard data fitting techniques for a reaction obeying Michaelis-Menten kinetics. The data curves were fitted using SigmaPlot. The active enzyme concentrations were calculated from the intercept of the linear fit to the IC₅₀ versus [S] plots with the IC₅₀ axis. The K_i values were obtained from the IC₅₀ values estimated from an inhibitor dose-response curve with the spectroscopic assay using the equation $K_i = (IC_{50}-[E]/2)/(1+ [S]/Km)$, where [E] and [S] are the PR and substrate concentrations. The measurements were repeated at least three times to produce the average values given in Table 3.

Cells, viruses, and antiviral agents. The MT-2 cells were obtained from the NIH AIDS Reagent Program, NIAID, NIH, Bethesda, MD, USA (2). Human CD4⁺ MT-2 cells were grown in RPMI-1640-based culture medium supplemented with 10% fetal calf serum (FCS: JRH Biosciences, Lenexa, MD), 50 unit/mL penicillin, and 100 μ g/mL of kanamycin (3,4). Darunavir (DRV) was synthesized as previously described (5).

- (1) Toth, M. V.; Marshall, G. R. International Journal of Peptide and Protein Research. **1990**, *36*, 544–550.
- (2) Haertle, T., et al. "Metabolism and Anti-Human Immunodeficiency Virus-1 Activity of 2-Halo-2', 3'-Dideoxyadenosine Derivatives." J. Biol. Chem. **1988**, *263*, 5870-5875.
- (3) Yoshimura, K., et al. Proc. Natl. Acad. Sci. USA 1999, 96, 8675-8680.
- (4) Koh, Y., et al. Antimicrob. Agents Chemother. 2009, 53, 987-996.
- (5) Ghosh, A. K., Leshchenko, S., Noetzel, M. "Stereoselective Photochemical 1,3-Dioxolane Addition to 5-Alkoxymethyl-2(5H)-furanone: Synthesis of Bistetrahydrofuranyl Ligand for HIV Protease Inhibitor UIC-94017 (TMC-114)" J. Org. Chem. 2004, 69, 7822-7829







¹H NMR (500 MHz, CDCl₃)

ent-6

















H1 standard parameters, CDC13, GNP probe.







Hi standard parameters, CDC13, GNP probe.







Hi standard parameters, CDC13, QNP probe.









S-23







7,7,28 2,1,28 2,2,29 2,2,29 2,2,29 2,2,29 2,2,29 2,2,29 2,2,29 2,2,29 2,2,29 2,2,29 2,2,29 2,2,29 2,2,29 2,3,2,





7.25









¹H NMR (400 MHz, CDCl₃)







A B 20 A B







8.27 7.38 7.28 7.38 8.27 7.38 7.28 7.28 8.27 7.28 8.27 7.28 8.28 7.28 8.29 8.27 8.21 8.27 8.22 8.27 8.28 8.27 8.29 8.27 8.20 8.28 8.21 8.22</t


¹H NMR (400 MHz, CDCl₃) Me¹¹¹ 0 28g 0



















Construction of the second secon





H1 standard parameters, CDC13, GNP probe.



C 7.73 7.71 7.29 7.29 7.29 6.97 6.97







RIC-AS-12464_APCI+_ASH-OBC-ENT-8 #1-30 RT: 0.01-0.45 AV: 30 NL: 1.01E6 T: FTMS + p APCI corona Full ms [100.00-500.00]





RIC-AS-12472_APCI+_MeOH_ASH-OBC-ent-9 #1-30 RT: 0.00-0.44 AV: 30 NL: 3.82E5 T: FTMS + p APCI corona Full ms [100.00-500.00]











RIC-AS-12464_APCI+_ASH-OBC-Ent-11 #1-30 RT: 0.01-0.44 AV: 30 NL: 6.21E5 T: FTMS + p APCI corona Full ms [105.00-195.00]









RIC-AS-12464_APCI+_ASH-OBC-15r #1-30 RT: 0.01-0.43 AV: 30 NL: 4.57E5 T: FTMS + p APCI corona Full ms [100.00-340.00]





RIC-AS-12472_APCI+_MeOH_ASH-OBC-ent-15 #1-30 RT: 0.00-0.44 AV: 30 NL: 5.36E5 T: FTMS + p APCI corona Full ms [100.00-500.00]

RIC-AS-12464_APCI+_ASH-OBC-16 #1-30 RT: 0.01-0.44 AV: 30 NL: 3.88E5 T: FTMS + p APCI corona Full ms [160.00-500.00]



RIC-AS-12455_ESI+_ACN+H2O_DL-01-159-ENT-16 #1-34 RT: 0.01-0.49 AV: 34 NL: 1.41E5 T: FTMS + p ESI Fuil ms [100.00-800.00]



RIC-AS-12464_APCI+_ASH-OBC-17 #1-30 RT: 0.01-0.45 AV: 30 NL: 1.52E4 T: FTMS + p APCI corona Full ms [105.00-400.00]





RIC-AS-12464_APCI+_ASH-OBC-18 #1-30 RT: 0.00-0.42 AV: 30 NL: 1.43E6 T: FTMS + p APCI corona Full ms [100.00-500.00]





RIC-AS-12455_APCI+_ACN+H2O_ASH-OBC-20 #1-35 RT: 0.01-0.50 AV: 35 NL: 2.69E7









RIC-AS-12455_APCI+_ACN+H2O_ASH-OBC-23 #1-34 RT: 0.01-0.50 AV: 34 NL: 1.86E6 T: FTMS + p APCI corona Full ms [100.00-800.00]





RIC-AS-12455_ESI+_ACN+H2O_ASH-OBC-27 #1-35 RT: 0.00-0.49 AV: 35 NL: 3.51E7 T: FTMS + p ESI Full ms [100.00-800.00]







RIC-AS-12455_APCI+_ACN+H2O_DL-01-090 #1-35 RT: 0.01-0.50 AV: 35 NL: 2.30E6 T: FTMS + p APCI corona Full ms [100.00-800.00]





RIC-AS-12455_APCI+_ACN+H2O_DL-01-170 #1-35 RT: 0.00-0.49 AV: 35 NL: 5.79E7 T: FTMS + p APCI corona Full ms [100.00-800.00]



RIC-AS-12464_APCI+_ASH-OBC-28D #1-30 RT: 0.00-0.43 AV: 30 NL: 8.36E5 T: FTMS + p APCI corona Full ms [160.00-500.00]



RIC-AS-12455_APCI+_ACN+H2O_DL-03-064 #1-33 RT: 0.01-0.49 AV: 33 NL: 2.87E5 T: FTMS + p APCI corona Full ms [100.00-800.00]





RIC-AS-12464_APCI+_ASH-OBC-28G #1-30 RT: 0.01-0.43 AV: 30 NL: 8.83E6



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RIC-AS-12464_APCI+_ASH-OBC-28H #1-30_RT: 0.00-0.44_AV: 30_NL: 3.95E5 T: FTMS + p APCI corona Full ms [100.00-500.00]












RIC-AS-12639_ESI+_MeOH_ASH-OBC-4k #1-30 RT: 0.00-0.42 AV: 30 NL: 3.06E8 T: FTMS + p ESI Full ms [150.00-800.00]





RIC-AS-12639_ESI+_MeOH_ASH-OBC-4L #1-30 RT: 0.01-0.42 AV: 30 NL: 1.40E7 T: FTMS + p ESI Full ms [150.00-800.00]

S.NO	Inhibitor	HPLC Purity			
1	4a	94%			
2	4b	92%			
3	4c	92%			
4	4d	92%			
5	4e	93%			
6	4f	92%			
7	4g	92%			
8	4h	92%			
9	4i	92%			
10	4j	92%			
11	4k	92%			
12	41	93%			

HPLC purity (Table 2, SI) data of inhibitors 4a-l.

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Area Percent Report

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Dilution	:	1.0000			
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Use Multiplier	& Dilution	Factor wi	th ISTDs		

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Data File C:\Chem32\1\Data\ASH-OBC-4A-254 504.D Sample Name: ASH-OBC-4A-254 Signal 1: VWD1 B, Wavelength=254 nm Peak RetTime Type Width Area Height Area # [min] [min] [mAU*s] [mAU] % ----|-----|----|-----|------|------| 1 22.424 BB 0.6460 3347.90381 73.41902 93.7246 2 24.773 BB 0.7943 224.16246 4.02157 6.2754 Totals : 3572.06627 77.44059

*** End of Report ***

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Sample Name: ASH-OBC-4B-254-NEW-2





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Signal 1: VWD1 B, Wavelength=254 nm

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#	[min]		[min]	[mAU*s]	[mAU]	%	
1	1.545	BB	0.1477	40.19727	3.98483	0.9102	
2	16.218	BB	0.4717	4033.29370	120.75713	91.3297	
3	17.830	BB	0.5817	342.69839	8.26544	7.7600	

Totals : 4416.18937 133.00740

*** End of Report ***

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 1.0000

 Sample Amount:
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 1.00000 [ng/ul] (not used in calc.)

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Page 1 of 2

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Data File C:\Chem32\1\Data\ASH-OBC-4D-254 506.D Sample Name: ASH-OBC-4D-254





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Dilution	:	1.0000			
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Signal 1: VWD1 B, Wavelength=254 nm

Peak R	etTime	Туре	Width	Area	Height	Area
#	[min]		[min]	[mAU*s]	[mAU]	%
-						
1	5.140	VB	0.2000	39.90999	2.80452	0.5154
2	6.246	BV	0.1628	25.37671	2.33571	0.3277
3	6.561	VV	0.2155	41.59143	2.79735	0.5371
4	7.267	VV	0.2244	7063.14893	451.75095	91.2196
5	8.116	VB	0.3196	572.98694	25.55422	7.4001
Totals	:			7743.01400	485.24274	

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Data File C:\Chem32\1\Data\ASH-OBC-4E-254 507.D Sample Name: ASH-OBC-4E-254 Signal 1: VWD1 B, Wavelength=254 nm Peak RetTime Type Width Area Height Area # [min] [min] [mAU*s] [mAU] % ----|-----|----|------|-------|-------| 1 12.611 BV 0.3749 2883.74438 109.64135 92.9486 2 14.000 VB 0.4923 218.77094 6.28154 7.0514 Totals : 3102.51532 115.92289

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Sample Amount:

Page 1 of 2

1.00000 [ng/ul] (not used in calc.)

Data File C:\Chem32\1\Data\ASH-OBC-4F-254-NEW-3 532.D Sample Name: ASH-OBC-4F-254-NEW-3

Signal 1: VWD1 A, Wavelength=254 nm

Peak	RetTime	Туре	Width	Area	Height	Area
#	[min]		[min]	[mAU*s]	[mAU]	%
1	9.644	BV	0.2596	34.56042	1.94261	0.5452
2	11.681	VV	0.3583	5821.04443	229.20386	91.8309
3	12.866	VB	0.4174	483.26801	16.09259	7.6239
Total	ls :			6338.87286	247.23906	

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Sample Name: ASH-OBC-4G-254





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Data File C:\Chem32\1\Data\ASH-OBC-4G-254 511.D Sample Name: ASH-OBC-4G-254

Signal 1: VWD1 B, Wavelength=254 nm

Peak	RetTime Ty	be Width	Area	Height	Area	
#	[min]	[min]	[mAU*s]	[mAU]	%	
1	10.944 BV	0.3353	4591.29541	193.17729	92.2622	
2	12.122 VB	0.4154	385.06030	13.15954	7.7378	
Total	s :		4976.35571	206.33683		

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Dilution	:	1.0000)		
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Data File C:\Chem32\1\Data\ASH-OBC-4H-254 517.D Sample Name: ASH-OBC-4H-254 Signal 1: VWD1 B, Wavelength=254 nm Peak RetTime Type Width Area Height Area # [min] [min] [mAU*s] [mAU] % ----|------|-----|------|------|------| 1 8.438 BB 0.2235 26.27509 1.72747 0.2791 2 9.784 BV 0.3103 8653.25684 390.81973 91.9159 3 10.790 VB 0.3718 734.78949 27.67530 7.8050 Totals : 9414.32142 420.22251

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		(modified after loading)			
Method Info	:	Pump leak test method		Μ	
					[°] Ph 4 i
Sample Info	:	50% MeCN/H20			ÓMe
		1 mL/min			
		254 nm		С	Concentration = 1 mg/mL of compound in
		5 uL inj.		Ŭ	$ACN \cdot H_{2}O(1 \cdot 1)$
		1.0 mL/min			
		ymcpak-odsa			



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)ata File C:\Chem32\1\Data\ASH-OBC-4I-254 518.D
Sample Name: ASH-OBC-4I-254

Signal 1: VWD1 B, Wavelength=254 nm

Peak #	RetTime [min]	Туре	Width [min]	Area [mAU*s]	Height [mAU]	Area %	
1	7.890	VV	0.2521	5774.38965	323.73325	92.0484	
2	8.738	VB	0.3283	498.82303	21.36840	7.9516	
Total	s :			6273.21268	345.10165		

*** End of Report ***

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Sample Operator	:	SYSTEM		
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		(modified after loading)		H QH OMe
Method Info	:	Pump leak test method		
Sample Info	:	50% MeCN/H20		O Ph 4i
		1 mL/min		о́Ме
		254 nm		Concentration = 1 mg/ml of compound in
		5 uL inj.		$ACN \cdot H_{2}O(1 \cdot 1)$
		1.0 mL/min		
		ymcpak-odsa		



LC2 6/8/2024 5:07:13 PM SYSTEM

Data File C:\Chem32\1\Data\ASH-OBC-4J-254 519.D Sample Name: ASH-OBC-4J-254

Signal 1: VWD1 B, Wavelength=254 nm

Peak R	etTime	Туре	Width	Area	Height	Area
#	[min]		[min]	[mAU*s]	[mAU]	%
-						
1	7.210	VV	0.2273	1518.76587	95.61581	91.7905
2	7.999	VB	0.3058	135.83417	6.29474	8.2095
Totals	:			1654.60004	101.91054	

*** End of Report ***

Data File C:\Chem32\1\Data\ASH-OBC-4K-254-12 539.D Sample Name: ASH-OBC-4K-254-12

_____ Acq. Operator : SYSTEM Sample Operator : SYSTEM Acq. Instrument : LC2 Location : 1 Injection Date : 6/11/2024 12:20:39 PM Inj Volume : 5.000 µl Acq. Method : C:\Chem32\1\Methods\AB-02-34A.M Last changed : 6/11/2024 12:19:49 PM by SYSTEM (modified after loading) Analysis Method : C:\Chem32\1\Methods\AB-02-34A.M OMe Last changed : 6/11/2024 2:41:19 PM by SYSTEM (modified after loading) Method Info : Pump leak test method ó ò Ph 4k Sample Info : 50% MeCN/H20 1.0 mL/min Concentration = 0.8 mg/mL of compound in 254 nm ACN : H₂O (1 : 1) 5 uL inj. 1.0 mL/min ymcpak-odsa



Area Percent Report

Sorted By	:	Signal			
Multiplier	:	1.0000			
Dilution	:	1.0000			
Sample Amount:		:	1.00000	[ng/ul]	(not used in calc.
Use Multiplier	& Dilution	Factor wi	th ISTDs		

LC2 6/11/2024 2:42:05 PM SYSTEM

Data File C:\Chem32\1\Data\ASH-OBC-4K-254-12 539.D
Sample Name: ASH-OBC-4K-254-12

Signal 1: VWD1 A, Wavelength=254 nm

Peak	RetTime	Туре	Width	Area	Height	Area	
#	[min]		[min]	[mAU*s]	[mAU]	%	
1	1.781	BB	0.1468	12.47250	1.11284	0.2138	
2	2.455	BV	0.2072	4.74914	3.43689e-1	0.0814	
3	13.980	VV	0.4281	5388.28711	177.54451	92.3706	
4	15.368	VB	0.4793	427.82523	12.62603	7.3341	
Totals :			5833.33398	191.62706			

*** End of Report ***

Data File C:\Chem32\1\Data\ASH-OBC-4L-254 520.D
Sample Name: ASH-OBC-4L-254





Use Multiplier & Dilution Factor with ISTDs

Data File C:\Chem32\1\Data\ASH-OBC-4L-254 520.D Sample Name: ASH-OBC-4L-254

 Signal 1: VWD1 B, Wavelength=254 nm

 Peak RetTime Type Width Area

 # [min] [min] [mAU*s] [mAU] %

 ----|-----|-----|------|------|

 1 16.563 BV
 0.4878 7291.14063 211.69453 92.6870

 2 18.239 VB
 0.5549 575.26935 14.62415 7.3130

 Totals :
 7866.40997 226.31868

*** End of Report ***

LC2 6/8/2024 5:53:07 PM SYSTEM