

A Method for the Direct Injection and Analysis of Small Volume Human Blood Spots and Plasma Extracts Containing High Concentrations of Organic Solvents Using Revered-Phase 2D UPLC/MS

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Novelty of work:

Colour graphic

This methodology provides increased assay sensitivity and facilitates small volume biofluid analysis in high percent organic samples.

1	A Method for the Direct Injection and Analysis of Small Volume Human Blood Spots
2	and Plasma Extracts Containing High Concentrations of Organic Solvents Using
3	Revered-Phase 2D UPLC/MS
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14	Abstract
15	The emergence of micro sampling techniques holds great potential to improve
16	pharmacokinetic data quality, reduce animal usage, and save costs in safety assessment
17	studies. The analysis of these samples presents new challenges for bioanalytical
18	scientists, both in terms of sample processing and analytical sensitivity. The use of two
19	dimensional LC/MS with, at-column-dilution for the direct analysis of highly organic
20	extracts prepared from biological fluids such as dried blood spots and plasma is
21	demonstrated. This technique negated the need to dry down and reconstitute, or dilute
22	samples with water/aqueous buffer solutions, prior to injection onto a reversed-phase LC
23	system. A mixture of model drugs, including bromhexine, triprolidine, enroflexacin, and

34 24 procaine were used to test the feasibility of the method. Finally an LC/MS assay for 25 probe pharmaceutical rosuvastatin was developed from dried blood spots and protei 26 precipitated plasma. The assays showed acceptable recovery, accuracy and precisic 27 according to US FDA guidelines. The resulting analytical method showed an incres: 28 assay sensitivity of up to forty fold as compared to conventional methods by maxin 29 the amount loaded onto the system and the MS response for the probe pharmaceutic 30 rosuvastatin from small volume samples. 31 2 32 Corresponding Author: Paul_Rainville@waters.com 33 33 34 34 35 Keywords 36 At-column-dilution, dried blood spot, bioanalysis , LC/MS, 2D LC 34 39 39 39 40 41 41 42 43 43 44 41 45 45	2		
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47 Introduction

Over the last 30+ years the generation of pharmacokinetic data from pre-clinical studies and clinical trial samples has relied upon the analysis of blood-derived products in the liquid format, such as serum and plasma [1,2]. The use of a liquid format allows these samples to be easily and accurately sampled via pipetting, then the analytes isolated with techniques such as solid phase extraction, liquid-liquid extraction, or protein precipitation to remove the protein related-material [3,4]. A known quantity of the resulting liquid extract can then be quantitatively injected into the flowing stream of GC-MS or LC/MS systems. This allows the amount of sample introduced onto the system to be carefully controlled and assay sensitivity adjusted by the introduction of more or less volume [5]. Despite the benefits of liquid samples from an analytical chemistry point of view, there are several drawbacks including required sample volume, storage, handling and shipping. The collection of samples in tubes normally requires a minimum volume of 100-200 μ L of blood. Although this size of sample is not a problem for large species, such as humans, some non-human primates or dogs, it severely limits the number of samples that can be taken from rodents such as rats, mice and guinea pigs etc. As a result there has, over the last few years, been significant interest in the use of alternative "microsampling" techniques, such as volumetric absorptive microsampling (VAMS) and dried blood spot (DBS) cards for the collection, storage and shipping of blood samples. The use of these

68 formats can yield a dramatic reduction in the volume of sample required for analysis.

69 This allows serial bleeding to be performed in rodents such that a whole pharmacokinetic

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70	curve can be generated from one animal [6-13]. From a sample handling point of view,
71	many researchers have reported that the use of DBS provides sufficient sample stability
72	to allow the sample to be stored and shipped under ambient temperatures, thus
73	significantly reducing storage and transportation costs. Several recent reports have
74	estimated this saving in the region of \$0.5 million per clinical trial study [14]. Along
75	with the use of DBS, there has been interest in other forms of micro sampling
76	approaches, such a capillary tube sampling and heat disintegrated blood sampling, and
77	the aforementioned VAMS [15]. Whilst capillary sampling etc., does allow for the
78	collection and reanalysis of the blood sample they do not, unlike DBS methods, allow for
79	the shipping and storage of the sample under ambient conditions.
80	
81	Notwithstanding the advantages that DBS sample acquisition delivers in terms of
82	reduction in animal usage and reduced shipping costs, there are several analytical
83	challenges to the routine application of the technique in bioanalysis. These include
84	smaller sample volumes for analysis, additional sources of background matrix and the
85	need to change sample format prior to analysis [16]. Processing of the DBS samples
86	require the extraction of the sample from the cellulose card via punching out a fixed area
87	at the center of the spot and then soaking the spot in organo-aqueous or entirely organic
88	solvent. Most extraction solvents utilized for the extraction of compounds from DBS are
89	of high organic composition [16-24]. The result of this is that only small volumes,
90	generally less than 10 μ L of the sample, can be directly injected onto a reversed-phase
91	chromatography system without adversely affecting the chromatographic performance
92	(especially if the composition of the extraction solvent is 100 % organic) [25]. With orally

93	dosed compounds in the pre-clinical setting, a typical LC/MS system provides sufficient
94	sensitivity to quantify the samples even at the 24 hour post dose time point. However, for
95	compounds with low systemic exposure there is a need to load a greater portion of the
96	sample onto the column to provide sufficient assay sensitivity. This requires further
97	processing of the sample to reduce the proportion of organic solvent in the extracted
98	sample or reduce the overall processed sample volume, using a process such as solid
99	phase extraction or evaporation. These extra steps are not only time consuming but also
100	risk introducing errors via e.g., losses of the analyte during the process or changing the
101	sample via decomposition of thermally labile compounds etc.
102	To overcome some of the potential challenges with microsampling DBS formats,
103	analytical methodologies have been developed to directly extract the DBS via the use of
104	specialized devices such as thin layer chromatography (TLC) MS interfaces. Data from
105	these studies showed that the direct extraction of probe pharmaceuticals from cards
106	resulted in increased response for both chromatographic peak area counts and heights
107	[26]. Further approaches utilizing chip based technologies (TriVersa NanoMate [®]) have
108	been employed as well to create a liquid junction with the DBS paper and subsequent into
109	the MS [27]. Direct MS analysis of DBS has further been illustrated via paper spray MS,
110	desorption electropray ionization (DESI), and ambient sampling ionization [28-30].
111	Although these techniques do address the off line sampling issues of DBS many of these
112	techniques do not offer opportunities for sample concentration or clean up thus failing to
113	minimize matrix suppression or maximize the sensitivity of the technique.
114	Two dimensional (2D) chromatography has been used in both liquid and gas
115	chromatography to provide increased resolution and selectivity in an analysis [31,32].

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116	Over the last few years 2D chromatography has seen a resurgence in interest for both
117	comprehensive chromatography of complex samples and targeted analysis of peptide
118	therapeutics in a complex mixture [33,34]. In this LC format the analysis can be
119	performed in several different modes including trap-elute, forward flush, backward-flush
120	and heart cutting [35]. These approaches can deliver greater specificity to the analysis
121	yielding more precise and accurate results. The trapping mode of analysis offers the
122	analyst the opportunity to load a large volume of sample onto the LC system without
123	degrading the chromatographic performance. This approach is used extensively in the
124	field of nano-scale proteomics to increase the sample loading.
125	
126	The application of small trapping columns to effect the isolation of drug related
127	components from biological fluids prior to analysis by MS or LC/MS has been described
128	previously by many authors [36-38]. The complexity / sophistication of the trapping
129	process ranges from the use of a simple reversed-phase type columns, to the use of
130	restricted access media and molecular imprinted polymers. Bower et al showed that by
131	using a simple, single use, trapping cartridge plasma samples from clinical trial could be
132	quickly and efficiently analysed without the need for prior processing [36]. However, all
133	of these previous processes relied on the sample being in a solvent compatible with the
134	extraction cartridge and, as previously mentioned, this is not the case with dried blood
135	spot extracts. Thus in order to process these samples the elutropic strength of the solvent
136	must be managed prior to the first column. In the majority of the published work the first
137	dimension column was employed simply to trap the sample and remove protein related
138	material rather than provide an "analytical quality" separation.

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140 porous particles operated at greater than 6000 psi, with at-column-dilution (ACD)

141 enabling the injection of large sample volumes of organic extracts of DBS spotted with as

- 142 little as 15 µLs of blood and also plasma prepared by protein precipitation with
- 143 acetonitrile as a means to both increase bioanalytical assay sensitivity and reduce
- 144 endogenous contaminants.

2 3 4	146	Experimental
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7 8 9	148	Chemicals
10 11	149	
12 13 14	150	Methanol, acetonitrile, formic acid, and ammonium hydroxide were obtained from
15 16	151	Sigma–AldrichChemicals (St. Louis,MO,USA). Probe pharmaceuticals procaine,
17 18 10	152	brohexine, triprolidine and enrofloxacin were obtained from Sigma Aldrich (St. Louis,
20 21	153	MO. USA) . Rosuvastatin (Figure 1) and the D6 deuterated internal standard were
22 23	154	purchased from Toronto Research Chemicals (Ontario, Canada).
24 25 26	155	Human blood was purchased from Bioreclamation (Hicksville, NY) and stored
27 28	156	refrigerated prior to use (blood was used within 7 days of purchase). Human plasma was
29 30	157	also purchased from Bioreclamation and was stored at -80°C. All samples were collected
31 32 33	158	according to ethical guidelines set by the Institutional Review Board (IRB).
34 35	159	
36 37	160	Blood Spot Card Preparation
38 39 40	161	
41 42	162	The samples, calibration curves and QCs, were prepared by spiking authentic standards in
43 44 45	163	solution into fresh human blood over a concentration range of 0.1 to 100 ng/mL.
45 46 47	164	Aliquots of 15 μ L of blood were spotted onto Whatman DMPK type B cards. The centre
48 49	165	of the resulting blood spots were sampled using a 3mm diameter punch from the center of
50 51 52	166	the spot . These sample cores were suspended in 100 μL of methanol which was then
53 54 55 56	167	shaken for one hour. The resulting extract was then centrifuged for 5 minutes at 13,000

168	relative centrifugal force (rcf). The extraction solvent was removed for injection onto the
169	LC/MS system.
170	
171	Plasma Preparation
172	
173	Stock solutions for the pharmaceutical compounds used in this study were prepared in
174	methanol and diluted 1:5 in water. The samples, calibration curves and QCs, were
175	prepared by spiking the required concentrations of the authentic standards (normal and
176	deuterated) in solution into human plasma over a concentration range from 0.1 - 50
177	ng/mL. The concentration of methanol, from the stock solutions in the samples,
178	calibration curves and QCs were never greater than 5 percent organic. A 100 μ L aliquot
179	of plasma was mixed with 300 μ L of acetonitrile and then vortex mixed with the
180	resulting protein-precipitated sample centrifuged at 13,000 rcf for 5 minutes. The
181	supernatant was then removed for injection onto the LC/MS system.
182	
183	Chromatography
184	The chromatographic conditions described below were employed for procaine,
185	brohexine, triprolidine, enrofloxacin and rosuvastatin. Analysis was performed using a
186	2.1 x 30 mm direct connect XBridge TM BEH C8, 10 μ m as the trapping column and a 2.1
187	x 50 mm ACQUITY BEH C18, 1.7 μ m column as the analytical column (Waters, MA,
188	USA). The analysis was carried out on an ACQUITY Ultra Performance LC [®] system
189	with 2D technology (Waters MA, USA) equipped with a sample manager, a binary
190	solvent delivery manager for the analytical separation and a quaternary solvent delivery

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Analyst

manager to deliver the trapping column solvents. Aliquots of the samples (85 µl) were loaded onto the trapping column using the quaternary pump at a flow rate of 200 μ L/min. The samples were diluted just prior to the trapping column via a mixer carrying 100 % water at a flow rate of 800 μ L/min, thus producing a 1:5 dilution. The mixer utilized in this study is a standard Waters 50 µL mixer that contains zirconium beads. The mixer takes two fluidic pathways and combines them into a uniform single fluidic pathway. The trapping column (column 1) was maintained at 90 °C and the analytical column (column 2) at 35 °C. The elevated high column temperature of the trap column was chosen as a means to elute the analyte of interest in a minimum amount of organic mobile phase as a means to better re-focused the analytes on the analytical column. The analytes were eluted from the trapping column after the column had been washed with a mobile phase comprised of 20 % acetonitrile and 80% water (v/v). After washing, the analytes of interest were eluted from the trapping column and focused on the analytical column. The analytes were eluted from the analytical column using 95:5-45:55 % aqueous formic acid (0.1 % v/v): acetonitrile gradient over 5 minutes at 500 μ L/min. Both the trapping and analytical columns were washed using 95 % acetonitrile 5% aqueous formic acid for 0.5 min after analyte elution. The columns were returned to the starting condition for 2 min prior to the next injection.

210 1D, 2D and 2D with ACD comparisons for aqueous and organic samples

Comparisons of four different LC configurations with aqueous and organic dissolved
rosuvastatin samples were carried out on an an ACQUITY Ultra Performance LC[®]

system with 2D technology (Waters MA, USA) operating and configured in 1D, 2D, or

2D with ACD mode. The 2D method parameters that were utilized in these comparisions

were identical to the parameters previously listed with the exception of having the ACD

connected or not during the comparative experiment. The single dimension configuration

comparison employed a solvent gradient from 95 : 5 to 45 : 55 % aqueous formic acid

(0.1 % v/v): acetonitrile at 500 µL/min over 5 min. The column temperature was set at 35

°C. Mass spectrometry conditions were as described below. The rosuvastatin samples

were either dissolved in 95 : 5 aqueous formic acid (0.1 % v/v) : acetonitrile or 100 %

The column effluent was monitored by positive ion electrospray MS operating in MRM

mode on a Xevo[™] TQ-S Mass Spectrometer (Waters MS Technologies, Manchester,

UK). The collision energy was set to 32 eV, the capillary voltage to 1.0 kV and cone

transitions were monitored: Procaine $237 \Rightarrow 164$, brohexine $377 \Rightarrow 114$, triprolidine

Rosuvastatin was monitored using the transition $482 \Rightarrow 258$ and the transition $488 \Rightarrow 264$

voltage to 60 V. For procaine, brohexine, triprolidine and enrofloxacin the following MS

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methanol.

Mass Spectrometry

 $279 \Rightarrow 208$, enrofloxacin $360 \Rightarrow 316$

was employed for the D6 internal standard.

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240	Results and Discussion
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242	The sensitivity of a bioanalytical assay is dependent upon the amount material which can
243	be introduced onto the analytical measurement system. Thus with a reversed-phase
244	chromatography system a careful balance that must be made between the solution which
245	is employed to dissolve the sample, the mobile phase composition and the volume that
246	can be injected onto the system. This can result in a compromise between having the
247	optimal chromatography conditions and one that allows the maximum sample load on the
248	column.
249	The 2D ACD LC/MS system was designed to allow the loading of samples containing a
250	high percentage of organic solvent onto a reversed-phase LC system. To achieve this, the
251	highly organic extract was diluted with water directly before the trapping column via the
252	use of 50 μ L LC mixer. Employing a flow rate of 100 % water (four-fold higher than
253	that of the sample injection line flow) ensured that the 100 % organic injection
254	composition was focused onto the trapping column with no breakthrough, even though it
255	was maintained at 90 °C. The schematic in Figure 2 illustrates the set up of the
256	chromatography system. The flow of the solvents was controlled by the left hand valve,
257	which first directed the injection flow from the quaternary solvent manager onto the
258	trapping column (column 1), while the analytical column (column 2) was washed with

- solvent from the binary solvent manager with the valve in position 1. When the left hand 259

valve switches to position 2 the analytical binary solvent flows through the trapping
column eluting the analytes from the trapping column onto the analytical column. Once
the analyte of interest was eluted from the trapping column onto the analytical column the
valve was switched to the initial position of 1 whereby the analyte is eluted from the
analytical column into the mass spectrometer.

The ability of the 2D ACD LC/MS system to inject large volumes of organic solvent on to the system is illustrated in Figure 3a-3d. In this Figure, we observe the comparison of a 10 µL injection of the probe pharmaceuticals procaine, brohexine, triprolidine and enrofloxacin dissolved in 100 % water or 100 % acetonitrile onto the 2D LC system with and without the incorporation of ACD. As can be observed in Figures 3a - 3d, when samples were injected in acetonitrile without the incorporation of ACD the chromatographic peak shape suffered greatly, indeed, the majority of the analyte was not retained on the trapping column and thus no prominent peak was detected. The lack of retention for the test analytes was further determined during the method development process by placing the first column (trapping column) in line with the mass spectrometer and monitoring for the MRM transaction of the compound under evaluation with and without the at column dilution option engaged. This result was also obtained for the cholesterol lowering statin rosuvastatin where the majority (based on peak response) of the drug was unretained without the use of ACD (Figure 4).

281 The maximum volume of the 100 μ L organic extraction from the 15 μ L DBS spot that

was injected onto the 2D ACD method was determined to be $85 \ \mu$ Ls due to the minimum

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283	residual volume of the LC vials utilized in this study. This 85 μ L injection volume on the
284	2D ACD method compares with the maximum volumes of organic solvent that could be
285	directly injected onto the 1D reversed-phase LC system without prior aqueous dilution
286	before chromatographic peak fronting and break through were detected of 2 μ L or 4 μ L
287	when rosuvastatin was dissolved in acetontrile or methanol respectively. Thus, the use of
288	the ACD method resulted in an increase in assay sensitivity for the DBS assay by 20-fold
289	and 40-fold for the plasma prepared by protein precipitation with acetonitrile. With
290	greater volumes than these peak fronting and lack of retention was observed. Therefore
291	the application of 2D-LC significantly improved the mass of material that could be
292	loaded onto the system and hence of the sensitivity of the assay.
293	
294	A further advantage of the ACD configuration was that the extracted biological sample
295	can be further cleaned up by employing an organo-aqueous solvent composition from the
296	quaternary solvent delivery system that elutes the endogenous matrix components from
297	the trapping column while leaving target analytes unaffected. The analyte can then be
298	eluted from the trapping column with a mobile phase composition just sufficient to
299	remove the analyte from the trapping column while leaving the more lipophilic matrix
300	components such as phospholipids on the trapping column. Once the target analyte(s) had
301	been eluted from the trapping column and focused on the analytical column, the valve
302	was switched such that the solvent from the gradient was directed solely to the analytical
303	column. This allows the trapping column to be washed and conditioned for subsequent
304	injections while the analytical gradient is completed. The result of this is shown in
305	Figure 5. Here we observe the unoptimized and optimized 2D LC conditions whereby the

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306	residual phospholipid fraction contained in human plasma prepared by protein
307	precipitation is diverted away from the analytical column (column 2) and the mass
308	spectrometer. This provides for a means to keep the source of the mass spectrometer
309	clean therefore leading to possibly more robust methods and also removing a major
310	source of ion suppression. The use of a C_8 alkyl-bonded phase as the trapping column,
311	maintained at 90°C, and a C_{18} alkyl-bonded phase as the analytical column maintained, at
312	35°C, aids the focusing of the analytes eluted from the trapping column onto the
313	analytical column as the parameters set with the trapping column are less retentive to
314	those of the analytical column under the conditions set.
315	
316	Maximizing sensitivity is an integral method parameter and must be evaluated for any
317	bioanalytical method. Therefore the area counts of the probe pharmaceutical rosuvastatin
318	were evaluated during development of the 2D ACD LC /MS method. This evaluation
319	included both 1D and 2D LC/MS configurations as well as aqueous and organic sample
320	diluents. The data from this experiment are shown in Table 1. The same amount of
321	analyte was injected onto each system.
322	
323	The data displayed in Table 1 shows two important aspects. First, the rosuvastatin area
324	counts between the 1D, 2D and 2D ACD methods showed excellent agreement. The
325	reproducibility of each mode of operation was excellent with all %CVs being equal to or
326	less than 3%. This indicates that the incorporation of additional fittings, tubing, valves,
327	and mixer have not sequestered any of the analyte since comparison of the rosuvastatin

area counts between each configuration remains fairly constant. Second, there was a

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329	significantly higher MS response, approximately 20%, for rosuvastatin when a 100%
330	methanol solution was injected. The explanation for this result may be due to either the
331	increased solubility of rosuvastatin in methanol or perhaps a reduction in non specific
332	binding that may be present due to interaction of the analyte in the injection vial or other
333	components of the LC system. In either case, the overall sensitivity of the assay was
334	influenced positively when the sample was injected in a 100% methanol environment.
335	
336	This 2D ACD LC/MS approach was then evaluated for the analysis of rosuvastatin, in
337	dried blood spots and plasma prepared by protein precipitation. Rosuvastatin is a
338	competitive inhibitor of the enzyme HMG-CoA reductase, having a chemical structure
339	and mechanism of action similar to that of other statins (Figure 1) [39]. Its approximate
340	elimination half-life is 19 h and its time to peak plasma concentration is reached in 3–5 h
341	following oral administration. The blood spot was extracted as described in the
342	experimental section. Representative chromatograms for the lower limit of quantification
343	and blank immediately following the injection of a high concentration standard is shown
344	in Figure 6 for the blood spot analysis. From these data we can see that the blank
345	chromatogram shows no interference in the region where the peaks elutes at 4.44
346	minutes. In addition, the chromatographic peak is very symmetrical and has a peak width
347	in the order of 3 seconds at the base. The limit of detection for subsequent validation was
348	set at 0.5ng/mL with a signal to noise value of 20:1 from a 15μ L blood spot sample. This
349	compares favorably with previously published work by Sangster et-al [40] where a limit
350	of quantification of 0.1ng/mL was obtained from a much larger sample volume of 500 μ L

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of plasma processed by solid phase extraction and analysed by microbore reversed-phaseLC/MS/MS.

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The assay was validated using a 3 run protocol on 3 successive days according to the
FDA validation guidelines May 2001 [41]. The method validation data is shown in Table
2 where the inter-day precision and accuracy showed bias of 14.8% and a CV of 4.0% at
the 0.5 ng/mL level and bias of 1.4% and a CV of 1.2% at the 80 ng/mL level. An
example calibration curve and residuals plot generated from this data is shown in Figure
7.

361 While these data illustrate the quantification of a pharmaceutical compound from a DBS 362 extract using 2D ACD LC/MS, this approach could be applied to any analysis using an 363 aqueous miscible organic solvent. To illustrate this point, the assay for rosuvastatin was 364 repeated via analysis of rosuvastatin spiked into human plasma with protein precipitated 365 with acetonitrile. A representative chromatogram for the LLOQ standard and the blank 366 immediately following the 50ng/mL standard are shown in Figure 8. Here we can see 367 that the 2D system provides excellent chromatographic performance and a very clean 368 chromatogram. The plasma protein precipitation method was subjected to a one run 369 validation using a 96 well sample plate. The method was demonstrated to be linear over a range of 0.1 - 50 mg/mL with an r² value of 0.9995 obtained for the calibration line 370 371 using a linear 1/x weighting. The results obtained are displayed in Table 3. At the 0.1 372 ng/mL level the bias was -6.2% with a CV of 7.1% and at the 35ng/mL level the bias was 373 -1.0% with a CV of 1.8%. The difference in sensitivity obtained between the DBS and

2		
3 4	374	protein precipitation method can be attributed to the difference in the volume of sample
5 6 7	375	employed for each analysis. In the DBS method just $15\mu L$ of sample was sampled
8 9	376	whereas for the protein precipitation assay, 100µL of plasma was extracted.
10 11	377	
12 13 14	378	These results suggest that this approach of the 2D ACD LC/MS method can be employed
15 16	379	for the analysis of organic eluents derived from either plasma protein precipitation or
17 18 19	380	dried blood spots. This approach allows the direct injection of large volumes of organic
20 21	381	solvent, removing the need for an evaporation step for organic based solutions. This not
22 23	382	only saves time, it also eliminates the thermal energy cost involved in solvent
24 25 26	383	evaporation, eliminates any potential loss involved in re-dissolving dried extracts and
27 28	384	eliminates the potential for degradation of compounds during evaporation. Moreover this
29 30 21	385	method improves the ability to obtain low limits of quantification for small sample
32 33	386	volumes as it maximizes the amount that can be analyzed as well as reduces the potential
34 35	387	for possible matrix suppression through the use of a second dimension of
36 37 38	388	chromatographic separation.
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12 13 14	401	Conclusion
15 16	402	
17 18 19	403	The use of a 2D LC/MS approach with ACD shows great promise for the direct analysis
20 21 22	404	of organic solutions resulting from the preparation of biological fluids such as dried
23 24	405	blood spots and plasma. The implementation of ACD allowed for the highly organic
25 26 27	406	composition sample to be directly loaded and focused onto a reversed-phase trapping
28 29	407	column. Analytes of interest, such as rosuvastatin, can then be washed and selectively
30 31 32	408	eluted from the trapping column onto the analytical column. This effectively removes a
33 34	409	portion of sample matrix from being deposited onto the analytical column. With this
35 36 27	410	approach, it was possible to inject $85\mu L$ of methanolic extracts of rosuvastatin onto the
37 38 39	411	analytical system with no adverse effect on the chromatography providing between 20
40 41	412	and 40 fold increase in sensitivity compared to direct injection depending upon the
42 43 44	413	solvent used to extract the samples. Using this approach for a DBS assay, precision and
45 46	414	accuracy results for three separate batches was demonstrated to be well within the US
47 48 49	415	FDA validation guidelines for LC/MS based assays with a limit of detection for
50 51	416	rosuvastatin of 0.5 ng/ml. We further applied this approach using extracts of the same
52 53 54	417	probe pharmaceutical, prepared by protein precipitation from plasma via addition of
55 56	418	acetonitrile. Again the assay showed acceptable precision, and accuracy. Moreover the
57 58	419	method showed an increase in the MS response, possibly related to increased solubility or

420	a reduction in non-specific binding due to injection of rosuvastatin in a 100 percent
421	organic solution. This approach limits the need for evaporation and reconstitution in an
422	aqueous solvent, which could result in analyte loss due to solubility, volatility, or non
423	specific binding depending on the chemical nature of the analyte. Lastly this method
424	maximizes the amount of organic extracted biofluid samples that can be loaded onto the
425	chromatographic system making it useful for assays where sample volume may be
426	limited.

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608	Tables and Figures
609	
610	Table 1: Rosuvastatin area counts versus LC configuration and injection solvent.
611	
612	Table 2: Three day inter-day accuracy/precision dried blood spot analysis of rosuvastatin.
613	
614	Table 3: Day one intra-day accuracy/precision protein precipitation analysis of
615	rosuvastatin.
616	
617	Figure 1: Chemical structure of rosuvastatin.
618	
619	Figure 2: Schematic of 2D ACD LC/MS System.
620	
621	Figure 3: Comparison of probe pharmaceutical compounds injected dissolved in 100 %
622	aqueous and 100 % acetonitrile with ACD and without ACD. Figure 3a) brohexine
623	Figure 3b) triprolidine and Figure 3c) enrofloxacin and Figure 3d procaine.
624	
625	Figure 4: Comparison of direct injection of rosuvastatin in 100 percent methanol with and
626	without at-column-dilution.
627	
628	Figure 5: Precursors of m/z 184 indicating the presence of the residual phospholipids
629	from human plasma prepared by protein precipitation. Observed are the unoptimized (top

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3 4	630	chromatogram) and optimized (bottom chromatogram) trapping conditions whereby the
5 6 7	631	reduced signal of m/z 184 is observed.
7 8 9	632	
10 11	633	Figure 6: Chromatogram of LLOQ and blank following analysis of rosuvastatin from
12 13	634	dried blood spot at ULOQ.
14 15 16	635	
17 18	636	Figure 7: Calibration line and residuals plot for the 2D ACD LC/MS analysis of
19 20	637	rosuvastatin from dried blood spot.
21 22 23	638	
24 25	639	Figure 8: Chromatogram of LLOQ and blank following ULOQ analysis of rosuvastatin
26 27	640	in plasma following precipitation with acetonitrile.
29 30	641	
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655	Table 1					
	Area Counts					
	Injection	1D H ₂ 0	2D H ₂ 0	2D ACD H ₂	$_{2}O$ 2D ACD Me	eOH
	1	3405	3251	3374	4083	
	2	3503	3245	3350	3996	
	3	3562	3425	3591	4089	
	4	3596	3486	3603	4114	
	5	3535	3431	3507	4008	
	6	3683	3421	3494	4064	
	AVG	3547.3	3376.5	3486.5	4059.0	
	STDEV	93.1	102.3	106.1	47.1	
	%CV	2.6	3.0	3.0	1.2	
656						
657	Table 2					
		QC LLOQ	QC	Low	QC Mid	QC High
	Meen	0.5ng/mi	1.51	ig/mL	30ng/mL	80ng/mL
	wiean	0.374	1.55))/Q	29.9	01.1
	St Dov		0.02	247	0.432	1.01
	St Dev %CV	4.0	16		14	12
	St Dev %CV %Bias	4.0 14.8	1.6 3.2		1.4 -0.2	1.2 1.4
	St Dev %CV %Bias Replicates	4.0 14.8 18	1.6 3.2 18		1.4 -0.2 18	1.2 1.4 18
658 659 660 661	St Dev %CV %Bias Replicates Table 3	4.0 14.8 18	1.6 3.2 18		1.4 -0.2 18	1.2 1.4 18
658 659 660 661	St Dev %CV %Bias Replicates Table 3	4.0 14.8 18 QC LLOQ 0.100 ng/m	1.6 3.2 18 QC L 0.30	LOW)0 ng/mL	1.4 -0.2 18 QC MID 3.00 ng/mL	1.2 1.4 18 QC HIG 35.0 ng/n
658 659 660 661	St Dev %CV %Bias Replicates Table 3 Mean	4.0 14.8 18 QC LLOQ 0.100 ng/m 0.0938	1.6 3.2 18 QC L 0.30 0.30	LOW)0 ng/mL)9	1.4 -0.2 18 QC MID 3.00 ng/mL 3.17	1.2 1.4 18 QC HIG 35.0 ng/n 34.6
658 659 660 661	St Dev %CV %Bias Replicates Table 3 Mean St Dev	4.0 14.8 18 QC LLOQ 0.100 ng/m 0.0938 0.00661	1.6 3.2 18 QC L 0.30 0.30 0.01	LOW 00 ng/mL 09 173	1.4 -0.2 18 QC MID 3.00 ng/mL 3.17 0.116	1.2 1.4 18 QC HIG 35.0 ng/n 34.6 0.613
658 659 660 661	St Dev %CV %Bias Replicates Table 3 Mean St Dev % CV	4.0 14.8 18 QC LLOQ 0.100 ng/m 0.0938 0.00661 7.1%	1.6 3.2 18 QC L 0.30 0.01 5.69	LOW)0 ng/mL)9 173 %	1.4 -0.2 18 QC MID 3.00 ng/mL 3.17 0.116 3.6%	1.2 1.4 18 QC HIG 35.0 ng/n 34.6 0.613 1.8%
658 659 660 661	St Dev %CV %Bias Replicates Table 3 Mean St Dev % CV % Bias	4.0 14.8 18 QC LLOQ 0.100 ng/m 0.0938 0.00661 7.1% -6.2%	1.6 3.2 18 QC L 0.30 0.01 5.69 3.09	LOW)0 ng/mL)9 173 %	1.4 -0.2 18 QC MID 3.00 ng/mL 3.17 0.116 3.6% 5.8%	1.2 1.4 18 QC HIG 35.0 ng/m 34.6 0.613 1.8% -1.0%















