Supplemental Information

Replacement per- and polyfluoroalkyl substances (PFAS) are potent modulators of lipogenic and drug metabolizing gene expression signatures in primary human hepatocytes

Emily Marques[†], Marisa Pfohl[†], Wei Wei[†], Giuseppe Tarantola[†], Lucie Ford[¶], Ogochukwu Amaeze[§], Jessica Alesio[^], Sangwoo Ryu[^], Xuelian Jia^{α}, Hao Zhu^{$\alpha\beta$}, Geoffrey D. Bothun[^], and Angela Slitt^{**}

† Department of Biomedical and Pharmaceutical Sciences, University of Rhode Island, Kingston, RI, USA

[¶]Department of Biology and Biomedical Sciences, Salve Regina University, Newport, RI 02840, USA

[§] Department of Clinical Pharmacy & Biopharmacy, Faculty of Pharmacy, University of Lagos, Nigeria

^a The Rutgers Center for Computational and Integrative Biology, Camden, New Jersey, USA

^β Department of Chemistry, Rutgers University, Camden, New Jersey, USA

^ Department of Chemical Engineering, University of Rhode Island, Kingston, RI, USA

*Corresponding author: Dr. Angela Slitt, Email: <u>angela_slitt@uri.edu</u>

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| | Human Half- Life | Detections in | Detections in | Detections in | Detections in |
|--------------|---|---------------|---------------|-----------------------|------------------|
| DEAS | | Human | Human Liver | Environmental | Environmental |
| ITAS | | Blood/Serum | | Exposed Animal | (Soil/Water/Air) |
| | | | | Liver | |
| PFBS (C4s) | 25.8 days ¹ | 2–5 | 6 | 7,8 | 9–12 |
| PFHxS (C6s) | 8.5 years ¹³ ^{2-5,14} | | 6,14,15 | 7,8,16,17 | 7,9–12,18 |
| PFOS (C8s) | 5.4 years ¹³ | 2–5,14 | 6,14,15 | 7,8,16,17,19,20 | 7,9–12,18,21 |
| PFBA (C4) | 75 hours ²² | 3 | 6 | 7,8 | 7,9,11,21 |
| PFPeA (C5) | Unknown | 3 | 6 | 7,8 | 7,9,11,12,21 |
| PFHxA (C6) | 32 days ²³ | 3 | 6 | 7,8 | 7,9,11,12,21 |
| PFHpA (C7) | 1.5 years ²⁴ | 2–5,14 | 6,14 | 7,8 | 7,9–12,21 |
| PFOA (C8) | 3.8 years ¹³ | 2–5,14 | 6,14,15 | 7,8,16,17,19 | 7,9–12,18,21 |
| PFNA (C9) | 4.3 years ²⁴ | 2–5,14 | 6,14,15 | 7,8,16,19 | 7,9–12,18,21 |
| PFDA (C10) | 12 years ²⁴ | 2–5,14 | 14,15 | 7,8,16,17,19,20 | 7,9,11,12,18,21 |
| PFUnDA (C11) | 12 years ²⁴ | 2–5,14 | 14,15 | 7,16,17,19,20 | 7,9,12,18,21 |
| PFDoDA (C12) | Unknown | 3,5,14 | 6,14 | 7,8,16,17,19,20 | 7,9,12,18,21 |
| PFTrDA (C13) | Unknown | 5 | 6 | 7,16,17,19 | 9,12,21 |
| PFTeDA (C14) | Unknown | | | 7,16,19,20 | 9,12,21 |

Supplemental Table 1. Human and Environmental Exposure to per- and polyfluoroalkyl substances (PFAS)

| HFPO-DA (GenX, PFPrOPrA) | Unknown | 7 | 7,25 | 7,11 |
|--------------------------|---------|--------|----------|---------|
| 6:2 FTS | Unknown | 26 | 20 | 9,18 |
| FOSA | Unknown | 2–5,26 | 16,17,19 | 9,12,18 |
| MetFOSA | Unknown | | | 9,12 |
| EtFOSA | Unknown | 5 | | 9,12,18 |

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| PFAS | Chemical name | CAS # | Purity (%) | Catalog# (Lot) |
|--------------------------------|---|----------------|---------------|--------------------------|
| PFBS (C4s) | Perfluorobutane sulfonic acid | 375-73-5 | 100 | S-74451 (27461) |
| PFHxS (C6s) | Potassium perfluorohexanesulfonate | 3871-99-6 | 98 | S-17292M (21279) |
| PFOS (C8s) | Potassium perfluorooctanesulfonate | 2795-39-3 | 98 | PFOS-002N (24187) |
| PFBA (C4) | Perfluorobutanoic acid | 375-224 | 98 | S-17292K (21247) |
| PFPeA (C5) | Perfluoropentanoic acid | 2706-90-3 | 97.0 | S-17292A (21240) |
| PFHxA (C6) | Perfluorohexanoic acid | 307-24-2 | 97.0 | S-17292B (21241) |
| PFHpA (C7) | Perfluoroheptanoic acid | 375-85-9 | 99.0 | S-17292C (21242) |
| PFOA (C8) | Perfluorooctanoic acid | 335-67-1 | 100.0 | PFOA- 001N (27462) |
| PFNA (C9) | Perfluorononanoic acid | 375-95-1 | 97.0 | S-17292E (21243) |
| PFDA (C10) | Perfluorodecanoic acid | 335-76-2 | 98.0 | S-17292F (21244) |
| PFUnDA (C11) | Perfluoroundecanoic acid | 2058-94-8 | 95.0 | S-17292G (21245) |
| PFDoDA (C12) | Perfluorododecanoic acid | 307-55-1 | 95.0 | S-17292H (21246) |
| PFTrDA (C13) | Perfluorotridecanoic acid | 72629-94- 8 | 100.0 | S-27319-03 (27641-01) |
| PFTeDA (C14) | Perfluorotetradecanoic acid | 376-06-7 | 97.0 | S-27319-02 (27490-01) |
| HFPO-DA (GenX, PFPrOPrA) | Perfluoro(2-methyl-3- oxahexanoic) acid | 13252-13- 6 | 95.7 | S-17292T (28563) |
| FOSA | Perfluorooctane sulfonamide | 754-91-6 | 95.3 | S-72644-05 (27475-01) |
| MetFOSA | N-Methyl perfluoro-1- octanesulfonamide | 31506-32- 8 | 95.9 | S-72644-06 (29478) |
| EtFOSA | N-Ethyl perfluoro-1- octanesulfonamide | 4151-50-2 | 97.1 | S-72644-07 (29479) |
| 6:2 FTS | 1H, 1H, 2H, 2H-Perfluorooctane sulfonic acid (6:2) | 27619-97- 2 | 99.2 | S-72644-04 (27468-01) |

Supplemental Table 2. PFAS information used for hepatocytes treatments

Complete list of per- and polyfluoroalkyl substances (PFAS) that were purchased from AccuStandard Inc. (New Haven, CT, USA) for use in our assays.

| Endpoint | Thresholds* | Inactives | Actives | Endpoint | Thresholds* | Inactives | Actives |
|-----------------------|-------------|-----------|----------|-----------------|-------------|-----------|-----------|
| Lipid accumulation | 1.25 | 9 | 10 | FASN | 1.2 | 10 | 9 |
| NR113 | 1.45 | 10 | 9 | <u>CYP2B6**</u> | <u>1.5</u> | <u>4</u> | <u>15</u> |
| ABCA1 | 1.35 | 10 | 9 | FABP1 | 1.02 | 9 | 10 |
| CIDEA | 1 | 14 | 5 | CPT1B1 | 1 | 12 | 7 |
| SOD1 | 1.23 | 9 | 10 | SLC27A1 | 1.17 | 8 | 11 |
| GSTM3 | 1.2 | 11 | 8 | UGT1A1 | 1.2 | 10 | 9 |
| SULT2A1 | 1.5 | 7 | 12 | GSTA1 | 1.1 | 9 | 10 |
| SLCO1B1 | 1.2 | 10 | 9 | EHHADH | 1.25 | 9 | 10 |
| MT-RNR2 | 1 | 14 | 5 | HMGCS1 | 1.35 | 10 | 9 |
| BDH2 | 1.16 | 10 | 9 | ACOT2 | 1.25 | 10 | 9 |
| CYP4A11 | 1.1 | 8 | 11 | PCK2 | 1.3 | 8 | 11 |
| LPL | 1 | 8 | 11 | NR1L2 | 1.27 | 9 | 10 |
| CYP7A1 | 1.1 | 8 | 11 | SCD | 1.4 | 8 | 11 |
| <u>SAA1</u> ** | <u>1</u> | <u>15</u> | <u>4</u> | MTTP | 1.3 | 10 | 9 |
| PPAR-a | 1.17 | 9 | 10 | GPAM | 1.41 | 9 | 10 |
| NFE2L2 | 1.2 | 10 | 9 | CD36 | 1.2 | 8 | 11 |
| FABP4 | 1.2 | 11 | 8 | PPAR-γ | 1.3 | 9 | 10 |
| NQO1 | 1.23 | 9 | 10 | SREBF1 | 1.3 | 9 | 10 |

Supplemental Table 3. The details of 36 modeling sets shown by classifications and relevant thresholds.

*A PFAS was defined as "inactive" when the fold change of relevant gene expression was less than or equal to the threshold value or defined as "active" when the fold change is larger than the

threshold. The threshold value was defined 1) between 1 and 1.5 for all the endpoints and 2) to balance the two classifications of PFASs. ** For SAA1, the number of actives is less than five, for CYP2B6, the number of inactives is less than five, using the above threshold criterion. Both of these two endpoints were excluded for modeling because the minimum requirement of a classification for modeling is five.

| Endpoint | Algorithm | Descriptor | CCR | Endpoint | Algorithm | Descriptor | CCR |
|--------------------|-----------|------------|------|----------|-----------|------------|------|
| Lipid accumulation | SVM | Dragon | 0.79 | FASN | RF | Dragon | 0.68 |
| NR113 | RF | Dragon | 0.79 | CYP2B6 | - | - | - |
| ABCA1 | SVM | RDKit | 0.68 | FABP1 | SVM | RDKit | 0.69 |
| CIDEA | SVM | RDKit | 0.66 | CPT1B1 | SVM | Dragon | 0.70 |
| SOD1 | kNN | Dragon | 0.79 | SLC27A1 | RF | FCFP6 | 0.63 |
| GSTM3 | kNN | Dragon | 0.77 | UGT1A1 | SVM | Dragon | 0.84 |
| SULT2A1 | SVM | RDKit | 0.83 | GSTA1 | kNN | Dragon | 0.74 |
| SLCO1B1 | kNN | Dragon | 0.84 | EHHADH | RF | RDKit | 0.74 |
| MT-RNR2 | SVM | RDKit | 0.66 | HMGCS1 | SVM | Dragon | 0.64 |
| BDH2 | kNN | Dragon | 0.63 | ACOT2 | SVM | Dragon | 0.84 |
| CYP4A11 | SVM | Dragon | 0.91 | PCK2 | SVM | Dragon | 0.79 |
| LPL | RF | Dragon | 0.70 | NR1L2 | SVM | Dragon | 0.78 |
| CYP7A1 | SVM | RDKit | 0.83 | SCD | RF | RDKit | 0.71 |
| SAA1 | - | - | - | MTTP | SVM | Dragon | 0.84 |
| PPAR-α | RF | RDKit | 0.68 | GPAM | RF | RDKit | 0.74 |
| NFE2L2 | SVM | Dragon | 0.79 | CD36 | SVM | Dragon | 0.63 |
| FABP4 | kNN | RDKit | 0.63 | PPAR-γ | SVM | RDKit | 0.74 |
| NQO1 | SVM | Dragon | 0.73 | SREBF1 | SVM | RDKit | 0.79 |

<u>Supplemental Table 4</u>. Model performance for all endpoints using five-fold cross validation.

Supplemental Scheme 1. Map detailing relationship of measured gene targets and hepatic steatosis.



Red arrows indicate hypothesized mechanism of lipid accumulation and hepatic steatosis observed in hepatocytes, by induction of sterol regulatory element-binding protein (SREBP) and lipid synthesis and storage genes.

Supplemental Figure 1. Cell viability assay.



Human hepatocytes were treated with various PFAS (0.25-25 μ M) and 1 μ M of staurosporine (ST; positive control for cytotoxicity) in 0.1% DMSO in media for 48 hours. The CellTiter-Glo Luminescent Cell Viability Assay reagent (Promega Corporation, Madison, WI) was added to wells according to manufacturer's protocol and luminescence was evaluated on a GloMax 96 microplate luminometer (Promega Corporation, Madison, WI). Percent cell viability was calculated compared to DMSO vehicle controls. Staurosporine reduced cell viability to 68%, while all PFAS treatments, except for 0.25 μ M PFBS and 25 μ M PFUnDA, significantly increased cell viability (p<0.05). This increase in ATP is likely due to induction of peroxisomal beta-oxidation pathway through activation of peroxisome proliferator-activated receptors (PPAR) that has been observed with many of these PFAS compounds. Calculations were done using an ANOVA followed by Fisher's LSD test. All values are means \pm SEM; N = 4. "x" indicates no significant difference from DMSO controls.



Supplemental Figure 2. Relationship of lipid accumulation and gene expression trends with albumin protein binding

Protein binding association constants (K_a) of several PFAS were determined using am equilibrium dialysis experiment conducted by Allendorf et al. (2019). All trends were calculated using bivariate Pearson correlation and are reported as (Pearson correlation coefficient, and P value). (A) As molecular weight was identified the strongest predictor of activity in our descriptor analysis, K_a was plotted and correlated with molecular weight (0.7401, 0.0142*). (B) Lipid accumulation at 25 μ M plotted against K_a (-0.2962, 0.4060). Fold change of all 35 measured genes at 0.25 μ M (C; -0.5479, 0.1011), 2.5 μ M (D; -0.6200, 0.0558), and 25 μ M (E; 0.2781, 0.4366) were summed and plotted against K_a values. Similarly, fold change of key lipid synthesis gene targets, SREBF1 (F; -0.6221, 0.0548) and SCD (G; -0.6111, 0.0605), at 25 μ M were also plotted against K_a values. K_a values are means \pm SD, and all other values are means \pm SEM; N = 3-4.

Allendorf, F., Berger, U., Goss, K.U., Ulrich, N., 2019. Partition coefficients of four perfluoroalkyl acid alternatives between bovine serum albumin (BSA) and water in comparison to ten classical perfluoroalkyl acids. Environ. Sci. Process. Impacts 21, 1852– 1863. https://doi.org/10.1039/c9em00290a