Supplemental Table 1. GC-MS Analysis Parameters (Reproduced from Tapper et al., 2018b).

Supplemental Table 1.

Column	HP-5MS (30 m × 0.25 mm I.D. × 0.25 µm film thickness, 5% phenyl–95% methyl-polysiloxane)
Carrier gas	Helium
Column flow rate	1.2 mL/min at constant flow
Oven temperature	40°C for 1 min, 10°C/min to 200°C no hold, then 20°C/min to 310°C hold for 9 min
Injection mode	Pulsed Splitless
Injection volume	1.0µL
Inlet temp	280 °C
Inlet pressure	8.88 psi
Pulse pressure	25 psi
Purge flow	49.8 mL/min
Purge time	0.6 min
MS transfer line temp	280°C
Mass range	35-500 *m/z*
MS source temp	230°C
MS quad temp	150°C
Filament energy	70 eV
Gain factor	1.95 (1247 V)

Supplemental Table 2. Time course of CBP, DPK and CPK loss and appearance of respective alcohol metabolites CBPOH, BADPK and CPKOH in rt binding cytosols exposed for 20h (4˚C) to 20 nmole (-4 log M;100µM) or 200 nmole (-3 log M;1000µM) of each chemical per vial. Results are expressed as % of nominal for each chemical. Values represent the mean ± SD of two technical replicates from a single experiment.

Supplemental Table 2.

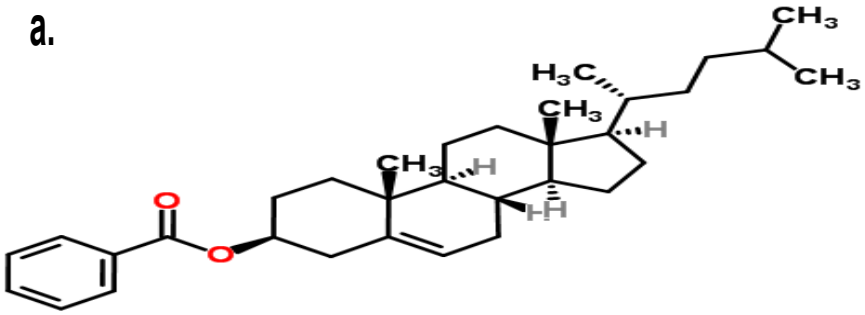
Time (h)	-4 log M (100 µM; 20 nmole nominal) (all values are % nominal)		-3 log M (1000 µM; 200 nmole nominal) (all values are % nominal)	
	DPK	BADPK	DPK	BADPK
0	103.3 ± 9.4	0.60 ± 0.1	88.6 ± 1.4	ND
4	83.9 ± 4.5	0.61 ± 0.4	103.1 ± 2.2	ND
20	93.8 ± 3.4	2.42 ± 0.2	95.0 ± 2.9	0.73 ± 0.04
	CPK	CPKOH	CPK	CPKOH
0	84.0 ± 1.4	ND	87.5 ± 2.8	ND
4	NM	NM	NM	NM
20	80.0 ± 2.1	ND	77.8 ± 1.1	ND
	CBP	CBPOH	CBP	CBPOH
0	64.4 ± 3.6	2.25 ± 0.5	69.4 ± 2.1	1.32 ± 0.4
4	45.8 ± 4.9	2.55 ± 0.3	49.3 ± 3.8	1.40 ± 0.5
20	42.2 ± 2.6	21.6 ± 0.3	60.9 ± 2.2	6.34± 0.2

ND=not detected
NM=not measured

Supplemental Figure 1. a) Structure of 26, 27-dinorergost-5-en-3-ol, benzoate (MW=476.7; CAS 58003-48-8), a potential product from the incubation of fish liver slices with CPK and CBP in presence of FBS; b) Identification match was based upon NIST library search comparison of main ions in fragmentation pattern. Top and Bottom panels are MS experimental and literature data, respectively). Match Index= 890 and Reverse Index = 880. High purity Stds were not available for structure confirmation.

Supplemental Figure 1.

a.



b.