

EDCMET Scientific Results

WP1 In silico methods to identify endocrine disrupting effects of chemicals







WP1 Aim



WP1 will develop and validate novel screening approaches that can be used stand-alone or in a linked, hybrid approach.

These approaches will follow a traditional AOP paradigm, identifying MIEs and predicting the emergent adverse biological phenotype















Deliverable	Title
D1.1	A validated molecular modelling approach to identify interactions between proteins and EDs
D1.2	Preliminary list of proteins most likely to interact with EDs
D1.3	A list of proteins most likely to interact with EDs
D1.4	A binding energy interaction map to explore the quantitative interaction of EDs with proteins, as part of the overall risk assessment model
D1.5	A validated classification system linking ED exposure to adverse outcome
D1.6	Preliminary list of potential biomarkers of exposure and effect for EDs
D1.7	A list of potential biomarkers of exposure and effect for EDs
D1.8	A systems toxicology tool to predict emergent metabolic phenotype from ED exposure







D1.1: A validated molecular modelling approach to identify

interactions between proteins and EDs

1N liga

4X

4X liga

5A liga

NR	PDB ID	Resolution (Å)	Docking score	RMSD
PXR	4X1F	1.44	-10.77	0.45
CAR	1XVP	2.60	-11.46	0.85
FXR	6HL1	1.60	-5.42	0.69
LXRα	3IPQ	2.00	-17.90	0.42
LXRβ	2P54	2.30	-14.07	1.46
PPARα	4XLD	1.79	-12.50	0.80
PPARy	4XLD	2.45	-8.93	0.21
ΤRβ	1XZX	2.50	-10.72	1.10
VDR	3CS4	2.00	-12.83	1.09
AR	2AM9	1.64	-11.85	0.06
ER	1GWR	2.4	-11.22	0.40
GR	1M2Z	2.5	-12.44	0.20

	PXR									
	PDB ID	1NRL	4XF1	4XHD	5A86					
	Resolution(Å)	2.0	1.55	2.40	2.25					
RL- and	Docking Score	-7.04	-6.86	-6.91	-7.491					
	RMSD	1.30	0.18	1.96	0.02					
F1- and	Docking Score	-6.89	-10.77	-7.11	-7.93					
	RMSD	1.2	0.05	0.20	0.02					
HD- and	Docking Score	-9.63	-8.00	-10.06	-8.71					
	RMSD	0.03	0.02	1.30	1.7					
86- and	Docking Score	-7.97	-8.83	-8.99	-8.05					
	RMSD	0.38	0.02	1.70	1.30					

Molecular Initiating Event

- Receptor/ligand interaction
- DNA binding
- Protein oxidation









D1.4: A binding energy interaction map to explore the quantitative interaction of EDs with proteins



ED	Compound	CAS
1	Atrazine	1912-24-9
2	Bis(2-ethylhexyl) phthalate (DEHP)	117-81-7
3	Bisphenol A (BPA)	80-05-7
4	Carbofuran	1563-66-2
5	3OH-Carbofuran	16655-82-6
6	Cypermethrin	52315-07-8
7	Dichlorodiphenyldichloroethylene (DDE)	72-55-9
8	Diethylstilbestrol (DES)	56-53-1
9	Mono-(2-ethylhexyl) phthalate (MEHP)	4376-20-9
10	PCB 118	31508-00-6
11	PCB 153	35065-27-1
12	Perfluorooctanoic acid (PFOA)	335-67-1
13	Perfluorooctanesulfonic acid (PFOS)	1763-23-1
14	Propieonazole	60207-90-1
15	Tributyltin chloride (TBT)	1461-22-9
16	Triphenyl phosphate (TPP/TPHP)	115-86-6
17	Tris(1,3-dichloro-2-propyl) phosphate (TDCPP)	13674-87-8

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100		17	16	14	13	11	10	9	8	7	6	5	4	3	2	al 1	cryst	cc
			44	39	100	40	44			45		71			35	80	59	PXR-
		42	39			34	39			47	74	65	66		26		13	CAR1-
- 80				47										51	20		24	CAR2-
		43	41	54			36							48	32	79	53	CAR3-
			36							47		65	70	56	23	74	15	FXR-
- 60		49	45	51		38	42						66			77	29	LXRa-
		44	30	50		37	41				28	58	59	60	22	83	85	LXRb-
		54	47	43		52	50					51	65	60	32	74	36	PPARA-
40	- F	56		61		52	53	73		56		71					37	PPARG-
												57	52	52	15		20	TR-
20												73	76	73		85	0	VDR-
20										35		68	71	56		79	36	AR-
				51				73	55	41		72	71	59	28		52	ER-
0				50				61	50	43		63	47	54	27		26	GR-







Molecular

Initiating Event

 Receptor/ligand interaction
DNA binding

· Protein oxidation











D1.5: A validated classification system linking ED exposure to adverse outcome



Sakhteman et al (2021) Env. Int.. 156: 106751.



D1.5: A validated classification system linking ED exposure to adverse outcome

	Test Set 1		Test Set 2		Test Set 3		
	Average	Harmonic S	Average	Harmonic S	Average	Harmonic S	
EDC score > 0.6	113	125	165	177	48	48	
EDC score < 0.6	26	14	27	15	4	4	
Tot. EDCs	139	139	192	192	52	52	
Accuracy	81%	89%	86%	92%	92%	92%	

Sakhteman et al (2021) Env. Int.. 156: 106751.



Classification of EDC/+AO .vs EDC/-AO





D1.8: A systems toxicology tool to predict emergent metabolic phenotype from ED exposure



Hepatonet 1 Exchange rxns Internal rxns SF DMEM external pool Transport limited by CORE rates

AR; CAR FXR; GR; LXR; PPARα; PPARγ; PXR; SHP

Direct Target Genes	166
Single NR	117 (70%)
Multiple NRs	49 (30%)
Reactions regulated	306 (12%)



Simulation of lipid loading (OA/PA) (red line), predicting increased TAG production

Maldonado et al. 2018, npj Systems Biology & Applications 4:33

Wu et al. 2016, npj Systems Biology & Applications 6:16032





D1.8: A systems toxicology tool to predict emergent metabolic phenotype from ED exposure









0 0.3 1 3 10 30 100 30

S26948 (nM)

30μΜ ΡΡΑRα-ΡΡΑRγ-ΡΧR

0.3

\$26948 (nM)



300μΜ ΡΡΑRα-ΡΡΑRγ-ΡΧR





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Thank you!

www.uef.fi/edcmet



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