**Melatonin and Related Compounds as Enzymatic Antioxidants: A Comprehensive Theoretical Study**

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|  | | | **Table S1**. Protein crystal structures Id’s and docking simulation details | | | | | |
| Enzyme | | PDB ID | | Gridbox  Center (x, y, z)  Size: Å3 | Sustrate | Negative Control | Reference  Ligand | Redocking (Å) |
| Antioxidant | SOD1 | 1CB4 | | 16.50, 71.00, 16.00  36×64×41 | O2•- | Indole | 5-Fluorouridine | N/A |
| CAT | 5ZZ1 | | -5.00, 3.50, 74.00  75×85×80 | H2O2 | Diphenyl ether | Ascorbic acid | N/A |
| GPx4 | 6ELW | | 48.40, 16.10, -19.10  38×44×38 | H2O2 | Caffeine | 102 | N/A |
| GR | 1GRE | | 21.45, 15.41, 16.99  70×60×52 | GSSG | Caffeine | GSSG | N/A |
| PRxV | 3MNG | | 8.27, 42.01, 20.50  38×40×45 | H2O2 | Diphenyl ether | 7OXC-d | N/A |
| Transcription factors | KEAP1 | 5FNR | | 14.00, 64.65, 27.20  22×22×22 | N/A | Benzoic acid | XMS | 1.89 |
| PPARγ | 2PRG | | 50.20, -38.20, 19.10  22×22×22 | Arachidonic acid | Butyric acid | Rosiglitazone | 1.64 |
| PPARα | 6LX4 | | -5.63, 3.38, 19.84  22×22×22 | Arachidonic acid | Butyric acid | Fenofibrate | 0.81 |
| IKKβ | 3RZF | | 91.94, -24.24, 54.08  22×22×22 | N/A | Benzoic acid | XNM | 2.94 |
| Prooxidant enzymes | NOX5 | 8CAK | | 36.00, -57.50, 29.00  15×15×15 | O2 | Caffeine | UF4 | 1.01 |
| p22-47phox | 1OV3 | | 67.39, 45.93, 46.54  73×40×83 | N/A | Benzoic acid | Apocynin | N/A |
| XO | 3BDJ | | 96.57, 46.75, 113.58  22×22×22 | Xanthine | Caffeine | Oxypurinol | 0.29 |
| COX2 | 5IKR | | 31.04, -21.99, -16.22  22×22×22 | Arachidonic acid | Caffeine | Mefenamic acid | 0.85 |
| LOX5 | 6NCF | | 35.42, 64.99, 38.41  22×22×22 | Arachidonic acid | Diphenylether | Zileuton | 2.84 |
| nNOS | 1FOI | | 12.97, 9.95, 34.14  22×22×22 | L-arginin | Indole | 1400W | 2.13 |
| MPO | 6WXZ | | -7.75, 14.46, -22.12  22×22×22 | H2O2 | Caffeine | AKAT7 | 0.87 |
| TRxR | 3EAN | | 62.11, -98.19, 31.85  70×95×75 | TRx | Caffeine | Ebselen | N/A |
| SOD1: Copper and zinc superoxide dismutase, CAT: catalase, GPx4: Glutathione peroxidase 4, GR: Glutathione reductase, PRxV: Peroxiredoxine V, KEAP1: Kelch-like ECH-Associated Protein 1, PPARγ: Peroxisome Proliferator Activated Receptor Gamma, PPARα: Peroxisome Proliferator Activated Receptor Alpha, IKKβ: Inhibitor of nuclear factor Kappa-B Kinase subunit Beta, NOX5: Nicotinamide adenine dinucleotide phosphate oxidase 5, p22-47phox: Proline rich region peptide, XO: Xanthine oxidase, COX2: Cliclooxygenase 2, LOX5: Lipoxygenase 5, nNOS: neuronal Nitric oxide synthase, MPO:myeloperoxidase, TRxR: Thioredoxin reductase. 102: 2-amino-3a,8a-dihydroxy-3a,8a-dihydroindeno[1,2-d]imidazol-8(3H)-one, 7OXC-d: 7-Methoxy-4-(4-methoxystyryl)-8-(piperidin-1-yl-methyl)-2H-chromen-2-one, GSSG: glutathione disulfide, XMS: (3s)-3-(4-chlorophenyl)-3-(1-methylbenzotriazol-5-yl)propanoic acid, XNM: (4-{[4-(4-chlorophenyl)pyrimidin-2-yl]amino}phenyl)[4-(2-hydroxyethyl) piperazin-1-yl]methanone, UF4: 15-(1,4-dioxa-8-azaspiro[4.5]decan-8-yl)-14-azatetracyclo[7.7.1.0^{2,7}.0^{13,17}]heptadeca-1(16),2(7),3,5,9,11,13(17),14-octaen-8-one, 1400W: N-(3-(aminomethyl)benzyl)acetamidine, AKAT7: 7-[(1R)-1,2-diphenylethyl]-3H-[1,2,3]triazolo[4,5-b]pyridin-5-amine, N/A: not applicable | | | | | | | | |

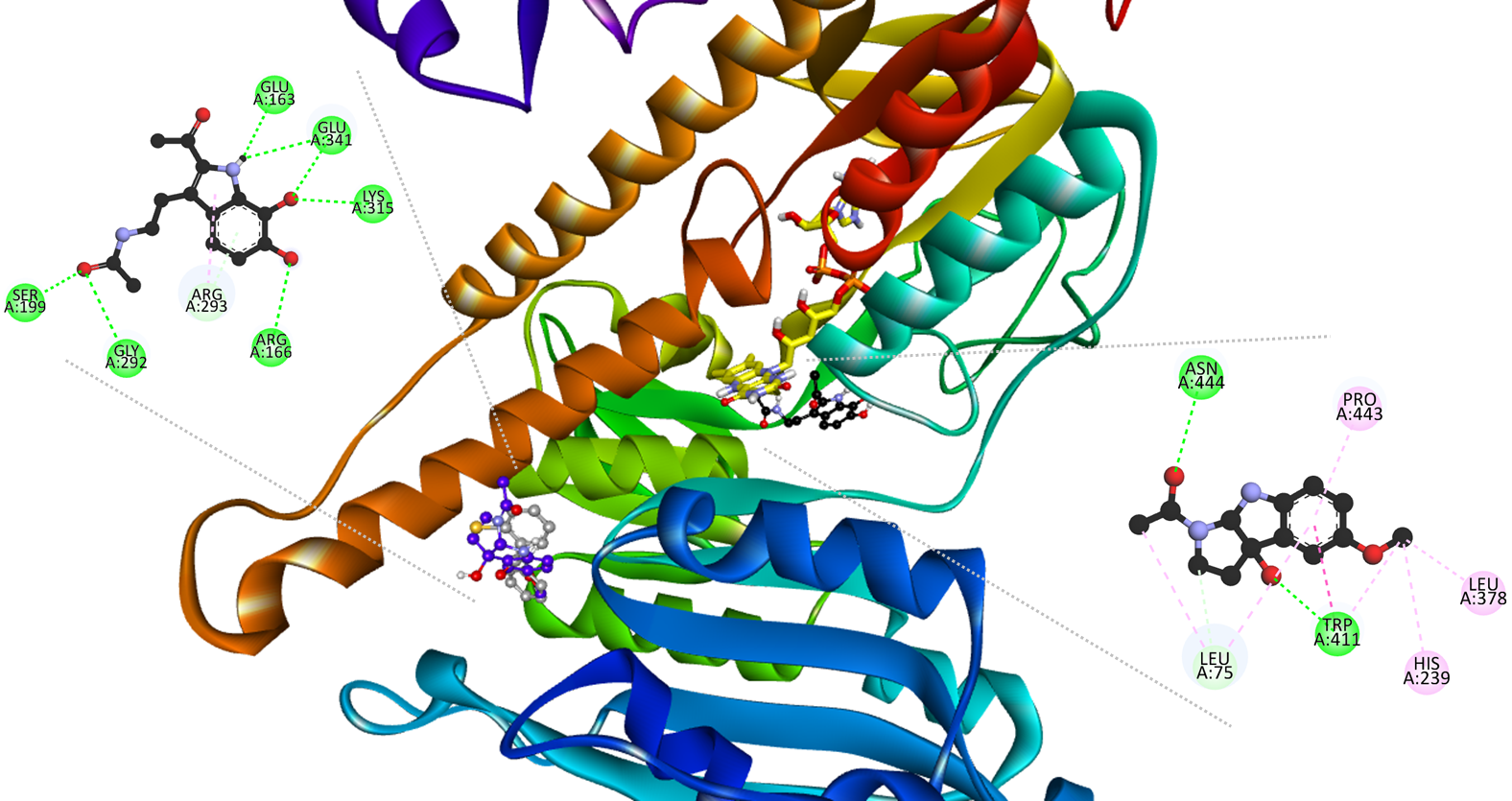
**Figure S1**. Potential energy vs. time for the KEAP1 (blue), SOD1 (orange), and p22-47phox systems during 100 ns MD under NPT conditions. After the initial equilibration, the energy remained stable without systematic drifts, consistent with the RMSD/RMSF/Rg analyses.

**Figure S2.** Radial distribution function (RDF) profiles for the ligand-residue in H-bond interactions in the SOD1 (orange, IIcD-Vall146), KEAP1 (blue, dM38-Gly603), and p22-47phox (green, 3OH-M-Ser277) complexes. The presence of defined peaks between 2.5 and 4.5 Å indicates short-range contacts and stable ligand-protein interactions.

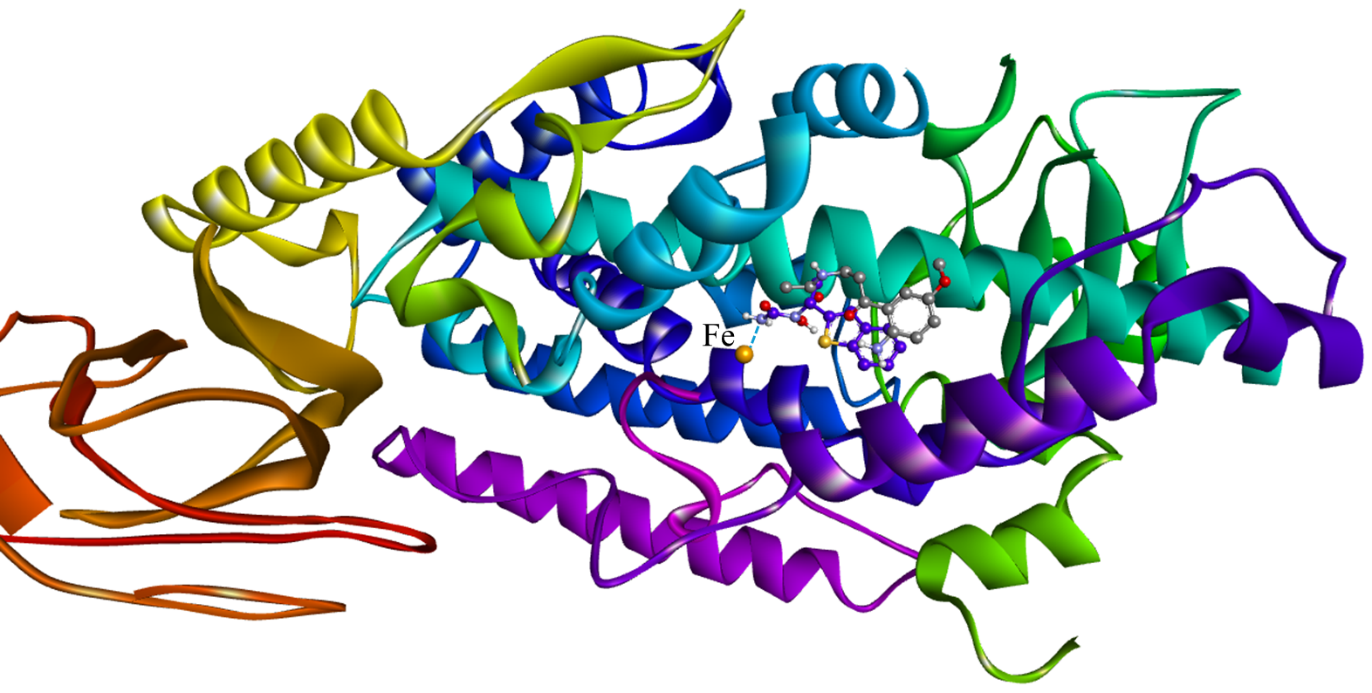
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| **Table S2.** Selected interactions of melatonin related compounds with prooxidant enzymes | | | | | | | |
| Compound | XO | COX2 | p22phox | LOX5 | NOS | MPO | TRxR |
| Melatonin | N/A | Gln178(UH), Val335(πA), Ser339(πσ), Ala502(A), Phe504(πA), Val509(A,πA,πσ), Ala513(πA), Ser516(H) | Ala252(H,πA), Glu254(πA-,UH), Lys268(πA), Asp269(H) | Phe359(πT), His360(πA), Gln363(UH), His(H), His432(πA), Arg596(H), Trp(πT), Ala603(πA) | Leu111(πσ), Ala183(UH), Arg185(πC+), Asn468(H), Ile470(πA,A), Phe475(H,UH) | N/A | His71(πA), Ala74(πA,A), Pro377(H,πA,A) |
| 3OH-M | N/A | N/A | Ser191(H), Trp193(H), Pro206(A), Tyr237(πA), Trp263(πA,UH), Pro276(A), Tyr279(H,πA) | Gln363(H), His367(H), Leu368(πσ), His372(πT,πA), Ile406(A), Ala410(πA,A) | Leu111(πS), Ala183(A), Pro184(πA,A), Ile470(πA), Ala474(A), HEM500(H) | N/A | Leu75(πA,A), His239(πA), Leu378(πA), Trp411(H,πT,πA), Pro443(πA), Asn444(H) |
| 4OH-M | N/A | N/A | Ala252(H,πA), Glu254(πA), Lys268(πA), Asp269(UH) | Gln353(H), His367(H), Leu368(πσ), Ala410(πA), His432(πA) | Pro95(A), Pro108(πA), Leu111(πσ,πA), Arg185(πC+), Asn468(UD,UH), Tyr469(H), Ile470(πA,A) | N/A | Ala74(πA), His243(UH), Pro377(H,πA), Arg416(H) |
| 6-OHM | N/A | N/A | Ala252(πA, πσ), Lys268(πC+), Ser283(H) | Thr364(UH), Leu368(πσ,A), His372(UH), Ala410(πA), His432(πA) | Leu111(πA), Pro184(πA), Arg185(πC+), Phe475(H,UH), HEM500(UH) | N/A | Ala74(πA), His243(H,πA), Pro377(H,πA), Arg416(H) |
| AFMK | N/A | N/A | Ala252(πA), Glu254(πA-), Lys268(UH), Asp269(H) | Phe359(πT), His360(πA), Gln363(H), His367(H), His432(H,πA), Pro569(UH) | Pro336(A), Val338(πA), Phe355(πA), Glu363(πA-), HEM500(H,πA,πA) | N/A | Val196(A), Ala198(H), Met219(UH), Arg221(πA,A), Ile223(UH), Arg226(H), Phe251(UH), Val252(A), Ile291(H,πσ**)** |
| AMK | N/A | N/A | Val253(H), Glu254(πA-), Asp269(H) | Phe359(πT,πA), His360(πA), Gln363(H), His367(H), His432(πA), Arg596(H), Trp599(πT), Ala603(A) | Pro336(A), Val338(πA), Phe355(πA), Glu363(πA-), HEM500(H,πT,πA) | N/A | His71(πA), leu74(A), Leu75(A), Gln78(H), Pro377(A), Arg416(H) |
| NAS | Ser876(H), Phe914(πS), Phe1009(πT), Ala1078(πA), Ala1079(πσ,πA), MTE3003(Sπ) | His75(H), Tyr371(H), Leu338(H,πA), Phe504(πT), Met508(H), Val509(A), Ser516(H), | Tyr231(H), Ala252(πA), Val253(H), Glu254(πA-), Asp269(H) | Phe359(πT), His367(H), His432(UD), Trp599(πT) | Pro336(H), Val338(πA), Glu363(H), HEM500(πT,πD,πσ,πA) | N/A | Val196(πA), Met219(H), Arg221(πA), Arg226(H), Val252(πA), Ile291(πσ,πA) |
| dM38 | N/A | N/A | Val232(πσ,πA), Gln281(H), Ser283(H,Q) | Gln363(H), Thr364(H), Leu368(A), His372(H,πS,πA), Ile406(H), Ala410(πA,A), His432(H), Leu607(πA), Ile673(H) | Gln249(H), Val338(πσ,πA), Gly358(H), Trp358(H), Tyr359(πA), Glu363(Q), Asn368(UH), HEM500(H,πC+,πD,UQ) | N/A | Phe43(H), Thr45(H), Arg164(H,πσ,πA,A,UQ), Cys296(πS,πA), Lys299(πA) FAD600(H) |
| IIcD | N/A | N/A | Val232(πσ,πA), Glu249(H), Gln281(H), Ser283(H,UH) | Gln363(H), His367(H), Leu368(πA), His372(πS), Asn407(H), Ala410(πA) | Gln249(H), Val338(σ), Asn340(H), Glu363(H), HEM500(πS,πA-) | Glu102(H), Arg239(H), Arg424(H), HEM604(πA) | Glu163(H), Arg166(H), Ser199(H), Gly292(H), Arg293(UH,πA), Lys315(H), Glu341(H) |
| NS | Arg880(H), Ser876(H),  Phe914(πS) Phe1009(πT,πA,H,UH), Thr1010(H), Ala1078(πA), Ala1079(πA)  MoM1334(UH), | His75(πA-,Q), Val345(A), Leu349(A), Leu352(A), Tyr355(πA), Trp373(πA), Phe381(πA), Tyr385(H,πA), Trp387(πA), Val523(A), Ala527(A), Ser530(H) | N/A | Phe359(πA), Leu368(A), His372(πA-), His432(πA), Pro569(πA), Trp599(πA), His600(πA), Ala603(A), Val604(A) | Gln249(H), Arg252(UQ), Tyr333(UD), Val338(πA), Trp358(H) Glu363(SB,H,Q), HEM500(Q,πA,πA-,UQ) | N/A | N/A |
| RL | Glu802(UH), Arg880(H), Ala910(πA), Phe914(πS), Phe1009(πT), Thr1010(H), Ala1078(πσ,πA), Ala1079(πσ,πA), MoM1334(Sπ,ML), MTE3003(Sπ), | Val116(A), Val349(A,πA), Leu352(πA), Tyr355(πA), Tyr385(H), Val523(πA), Ala527(A,πA), Ser530(H,UD), Leu531(A) | Glu254(πA-,UH), Asp269(H), Lys268(H) | Phe359(πT), His372(πT), Ala410(πA), Arg596(UD), Trp599(πA), His600(H), Leu607(A), Fe2701(ML) | Pro336(H,A), Val338(πA), Trp358(H), Tyr559(UH), Glu363(H), HEM500(πT,πD,πσ,πA) | Glu102(πA-), Arg239(H,πA) HEM604(H,πS,πA) | Leu75(H,πσ), Ala79(A), Leu378(σA), Trp411(H,πT), Arg416(H,πC+), Pro443(πA) |
| 3OH-M: 3-hidroxymelatonin, 4OH-M: 4-hidroxymelatonin, 6-OHM: 6-hidroxymelatonin, AFMK: N-acetyl-N-formyl-5-methoxykynurenamine, AMK: N1-acetyl-5-methoxykynuramine, NAS: N-acetylserotinin, dM38: N-(2-(6-hydroxy-7-mercapto-5-methoxy-1H-indol)ethyl)acetamide, IIcD: N-(2-(2-acetyl-6,7-dihydroxy-1H-indol-3-yl)ethyl)acetamide, NS: natural sustrate, RL: reference ligand | | | | | | | |

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| **Table S3.** Selected interactions of melatonin related compounds with antioxidant enzymes | | | |
| Compound | SOD1 | CAT | GPx4 |
| Melatonin | A: Val7(H), Val146(πA)  B: Val7(H), Gly49(UH), Cys144(UH), Val146(πσ,σA) | Arg134(H), Met211(UH), Ile216(A), Val257(πA), Trp258(UH,πS), Glu259(πA-), Phe476(πS,πA), Asn479(H) | Lys127(H), Ile129(UH), Lys135(A), Pro155(πA) |
| 3OH-M | A: Val7(H), Asn51(H), Val146(πA)  B: Val7(H), Lys9(A), Gly49(UH), Asn51(H), Val146(πσ) | Asp275(UH), Asp278(πA-), Arg551(πA), Ar551(πA) | Arg12(H), Gln123(H), Val149(H) |
| 4OH-M | A: Val7(H,σA)  B: Cys144(H), Gly145(UH) | Arg134(H), Lys253(H), Trp258(πS), Glu259(πA-), Asn479(H) | Lys127(H), Lys135(A), Ile129(πA), Pro155(πA) |
| 6-OHM | A: Asn51(H), Val146(H,πA,A)  B: Val7(πA), Lys9(πA), Val146(H) | Asp278(πA-), Arg551(πA), Val580(πA), Thr582(H), Gln594(H), Gly603(H) | Asn109(UH), Gly110(H), Lys118(H,πA), Lys121(H,πC+) |
| AFMK | A: Val7(UH,πA)  B: Cys144(A), Val146(H) | Asp275(UH), Asp278(πA-), Arg551(H,πA), Thr582(H), Gln594(H), Gly603(H) | Lys125(A), Ile129(H), Val150(UH), Lys151(πA,A), Arg152(H), Gly154(UH) |
| AMK | A: Val7(H), Cys144(H), Val146(H,πA,UD)  B: Val7(A), Asn51(H), Val146(H) | Arg134(H), Met211(UH), Ile216(A), Val257(πA), trp258(UH), Glu259(H), Phe476(πS), Asn479(H) | Lys125(A), Ile129(H), Lys151(πA,A), Arg152(H,πA), Gly154(UH) |
| NAS | A: Val7(H,πA), Val146(H)  B: Cys144(UH), Val146(πA) | Gly213(H), Lys253(UD), Leu256(H), Val257(πA), Trp258(UH), Glu259(πA-), Phe476(H,πS), Ala480(πA) | Lys127(H), Ile129(UH), Arg152(H), Pro155(πA) |
| dM38 | A: Val7(H,πA,UH), Lys9(πA), Asn51(H), Val146(H)  B: Val7(A), Gly49(H), Val146(UH) | Lys253(H), Ile538(A), Val539(H), Gly542(H) Val539(πσ,πA), Arg689(H), Asp692(H,Q) | Asp21(Q,UH), Lys31(H), Tyr32(H), Ala93(A), Lys90(UH), Val98(H), Asp101(Q,πA-), Met102(A) |
| IIcD | A: Val7(H), Gly145(UH), Val146(H)  B: Val7(H), Gly54(UH), Cys144(H), Val146(UH,H) | Lys253(H), Val539(πA,πσ), Gly542(H), Arg689(πA), Thr691(H), | Ile129(πA), Arg152(H), Gly154(H), Tyr153(UH) |
| RL | A: Val7(X), Asn51(H), Cys144(X), Gly145(UH), Val146(πA)  B: Val7(H), Lys9(H,UD), Cys144(H, UA), Gly145(UH), Val146(H) | Lys253(H), Ile538(H), Ala686(H), Thr687(H), Arg689(H,UD) | Asp21(Q,πA-), Ile22(UD), Asp23(H,Q), Val27(πA), Phe100(H), Asp101(Q,πA-), Met102(H), Phe103(πT). |
| SOD1: Copper-zinc superoxide dismutase, CAT: catalase, GPx4: Glutathione peroxidase 4. | | | |

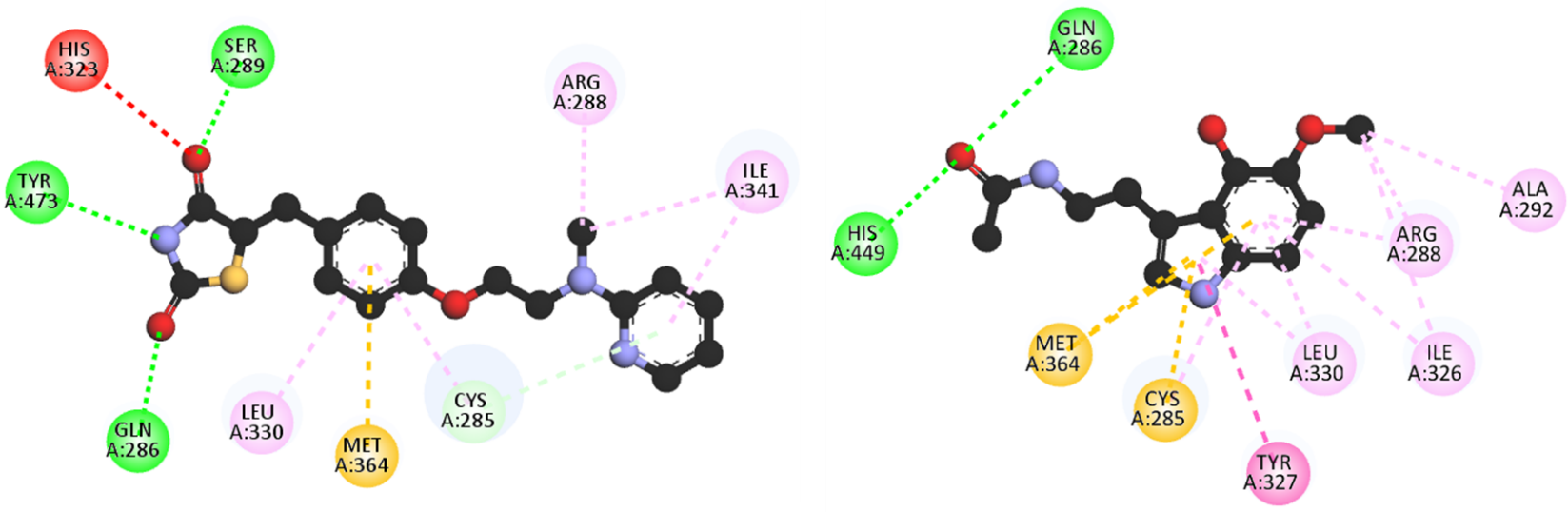
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| **Table S4.** Selected interactions of melatonin related compounds with transcriptional proteins | | | |
| Compound | PPARα | PPARγ | KEAP |
| Melatonin | Phe273(πS), Ile354(πA), Val444(πA), Ile447(πA,A), Leu456(A), His440(UH), Tyr464(UH) | Cys285(UH), Ile326(πA), Arg288(πA), Leu330(πA), Val339(A), Met364(Sπ,A), His449(H) | Leu365(H), Val512(UH), Arg415(H), Val604(H) |
| 3OH-M | Val270(A), Phe351(πA), Ile447(πA), Ala454(A), Tyr464(H) | Glu259(H,Q), Leu270(πA,A), Glu272(H), Arg280(πA), Gln283(AπS,UH), Phe287(πA) | Leu365(H), Arg415(πA), Ile416(H), Val463(H), Ala556(πA), Leu557(UH) |
| 4OH-M | Asn219(UH), Met320(H,πA,A,UH), Val324(A,UH), Tyr334(H) | Cys285(Sπ,πA), Gln286(H), Arg288(πA,A), Ala292(A), Ile326(πA,A), Tyr327(πT), Leu330(πA), Met364(Sπ), His449(H) | Leu365(H), Arg415(H),Val463(H), Val512(UH), Val604(H) |
| 6-OHM | Phe273(πA), Cys276(A), Gln277(H), Met355(πA), His440(πC+), Val444(πA) | Cys285(πA), Arg288(πA), His323(πA), Tyr327(H,πT,UH), Leu330(πA), Met364(Sπ), His449(πA), | Leu365(H), Arg415(H), Gly511(UH), Val512(UH), Ile559(H), Val604(H) |
| AFMK | Gln277(H), Hys440(H), Val444(A), Ile447(πσ), Lys448(A), Ala454(πA), Ala455(AπS), Leu456(πA,A), Tyr464(H) | Cys285(H,A), Arg288(πA), Tyr327(UH), Leu330(πσ), Val339(A), Met364(Sπ,A), | Ser363(H), Tyr334(πσ), Glhy364(UH), Leu365(UH), Asn382(H), Arg415(H,πσ), Ile416(UH), Ala556(H,πσ) |
| AMK | Ser280(H,UH), Tyr314(H), Hys440(πA,C+), Val444(πA), Ile447(A) | Cys285(πA,A), Gln286(H), Tyr327(πT), Leu330(πA,A), Met364(Sπ,A), His449(H) | Gly364(UH), Ile416(UH), Val465UH), Val604(H) |
| NAS | His440(H), Val444(πA), Ile447(πσ), Ala454(πA), Leu456(πS), Tyr464(H). | Cys285(Sπ,πA),Arg288(πA), Ile326(πA), Tyr327(πT), Leu330(πA), Met364(Sπ), His449(H), | Val465(H), Val512(H), Gly603(UH), Val604(H). |
| dM38 | Asn219(H), Met220(H), Glu286(H,Q), Leu321(πσ), Val324(πσ,πA,A), Leu331(H,πA), | Leu270(AπS,πA,A), Arg280(H), Gln283(H,AπS), Phe287(πA) | Ser363(UH), Gly364(UH), Arg415(πC+,πA), Arg483(H), Ser508(H), Ala556(πS,πA,A), Ser602(H), Gly603(UH) |
| IIcD | Asn219(H), Met220(H), Thr283(H), Ile317(H), Ty334(H,UH) | Cys285(UH), Arg288(H,πA), Leu330(πσ), Leu340(H), Met364(Sπ) | Arg415(H,πC+), Ser508(H), Tyr525(πσ), Gln530(H), Ser555(H), Ala556(πA), Ser602(H). |
| NS | Leu254(A), Val255(A), Ile272(A), Cys275(A), Cys276(A), Ser280(H), Tyr314(H), Leu321(A), Met330(A), Val332(A), Ala333(A), Ile339(A), Met355(A), Hys440(πA), Tyr464(H) | Cys285(A), Arg288(A), Hys323(UH), Leu330(A), Ile341(A), His449(πA), Tyr473(H) | N/A |
| RL | Ser280(H), Tyr314(H), Phe318(πA), Ile354(πA), His440(UH,πA), Val444(πA), Ile447(πσ), Lys448(A), Ala454(πA), Leu456(πA,A), Tyr464(H) | Cys285(πA,UH), Gln286(H), Arg288(A), Ser289(H), His323(UH), Leu330(πA), Ile341(πA,A), Met364(Sπ), Tyr473(H). | Arg415(πA), Arg483(H,Q), Ser508(H), Tyr525(πS,πA), Gln530(H), Ser555(H), Ala556(πA,A), Tyr572(πA) |

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**Figure S3.** Best docked pose for 3OH-M (blue), ebselen (gray) and IIcD in complex with TRxR. The recognized inhibitor and the metabolite are placed in the vicinity of catalytic SeC while the IIcD derivative is near to the catalytic site. 3OH-M: 3-hidroxymelatonin, IIcD: N-(2-(2-acetyl-6,7-dihydroxy-1H-indol-3-yl)ethyl)acetamide, TRxR: Thioredoxin reductase, SeC: selenocysteine.



**Figure S4.** Best docked pose for Zileuton (blue) and AMK (gray) in complex with 5-LOX. The inhibitor and the metabolite are placed in the vicinity of catalytic Fe, however, unlike AMK, Zileuton is bounded to the metallic atom. AMK: N1-acetyl-5-methoxykynuramine, 5-LOX: Lipoxygenase 5



**Figure S5.** 2D interaction map for Rosiglitazone and for 4OH-M with PPAR-γ. Intermolecular bonds are depicted in doted lines: H-bonds (green), non conventional H-bonds (light green), π-forces (yellow, pink and purple). Hydrogen atoms are omitted for clarity purposes. 4OH-M: 4-hidroxymelatonin, PPAR-γ: Peroxisome Proliferator Activated Receptor Gamma

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| **Table S5.** Synthetic conditions for IIcD retrosynthetic path. | | | | | | | | |
| Step | | Reagents | Solvent | t (h) | T (°C) | P (bar) | Special | Yav(%) |
| E | E.1 | KOH | Water | 4.0 | 30.0 | r.p | N/A | 36.0 |
| E.2 | NaNO2/HCl | Water | 1.0 | 0.0 | r.p | N/A |
| E.3 | Urea | Water | overnight | 0.0 | r.p | pH=7 |
| D | D.1 | SnCl2 | AcOEt | 4-8 | reflux | r.p | N/A | 65.0 |
| C | C.1 | MeONa | MeOH | 0.5  0.5  0.5 | reflux  15.0  -15.0 | r.p | N/A | 99.0 |
| C.2 | H2O | MeOH | 0.5 | r.t | r.p | N/A |
| B | B.1 | HNO3 | Et2O, Water | 3.0 | r.t | r.p | N/A | 97.0 |
| A | A.1 | NaHCO3 | THF, Water | overnight | r.t | r.p | N/A | 89.0 |
| A.2 | H2O | Water cooled | 0.1 | 5.0 | r.p | N/A |
| t: time, T: temperature, P: pressure, r.p: room pressure, r.t: room temperature, Yav: average yield | | | | | | | | |

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| **Table S6**. Synthetic conditions for dM38 retrosynthetic path. | | | | | | | | | |
| Step | | Reagents | Catalysts | Solvent | t (h) | T (°C) | P (bar) | Special | Yav(%) |
| F' | F'.1 | H2 | Rh(CO)2acac/ Xantphos | THF | 72.0 | 70.0 | 20.0 | N/A | 63.0 |
| F'.2 | H2SO4 | --- | THF/Water | 2.0 | reflux | r.p | N/A |
| E' | E'.1 | N/A | CH3Li | THF | 2.0 | r.t | 0.1-0.5 | N2 atmosphere | 32.0 |
| D' | D'.1 | NaI/S | CuI | DMF | 24.0 | 90.0 | r.p | N/A | 66.0 |
| D'.2 | NaBH4 | N/A | DMF | 5.0 | 5.0 | r.p | N/A |
| D'.3 | HCl | N/A | Water | 0.5 | r.t | r.p | pH 2.0-3.0 |
| C' | C'.1 | BuLi | N/A | THF/Hexane | 0.5 | -75.0 | r.p | N/A | 64.0 |
| C'.2 | (CH3O)3B | N/A | THF/Hexane | 0.1 | -75.0 | r.p | N/A |
| C'.3 | CH3COOH/H2O2 | N/A | Water | 0.5  3.0 | 0.0  r.t | r.p | N/A |
| B' | B'.1 | NaNO2/HCl | N/A | Water | 1.5 | 0.0 | r.p | N/A | 78.0 |
| B'.2 | HCl/SnCl2‧H2O | N/A | Water | 4.0 | 0.0 | r.p | N/A |
| A' | A'.1 | H2 | Pd | EtOH | 1.0 -24.0 | r.t | r.p | N/A | 97.0 |
| t: time, T: temperature, P: pressure, r.p: room pressure, r.t: room temperature, Yav: average yield, N/A: not applicable | | | | | | | | | |