Table S1: Summary of Ethyl-1-cyclopropyl-2-methyl-5-[4H-1,2,4triazole-3-yl) methoxy]1-H-indole-3-carboxylate derivatives **(5a-5k).**

Aromatic aldehyde	**Compound code**	**Temp (°C)**	**Time (h)**	**Solvent**	**Yield (%)**	**Melting point (°C)**
Anisaldehyde	**5a**	25-30	22-24	Ethanol	78.90	179-181
4-clorobenzaldehyde	**5b**	25-30	22-24	Ethanol	65.78	167-169
2-hydroxy-5-nitrobenzaldehyde	**5c**	25-30	22-24	Ethanol	87.12	117-120
m-nitro benzaldehyde	**5d**	25-30	22-24	Ethanol	65.43	158-160
2,5-dimethoxybenzaldehyde	**5e**	25-30	22-24	Ethanol	88.22	180-184
2-4-dichlorobenzaldehyde	**5f**	25-30	22-24	Ethanol	59.04	187-190
6-methoxy-2-napthol aldehyde	**5g**	25-30	22-24	Ethanol	73.34	180-186
Veretraldehyde	**5h**	25-30	22-24	Ethanol	81.45	140-143
Benzaldehyde	**5i**	25-30	22-24	Ethanol	51.49	152-156
4-hydroxybenzaldehyde	**5j**	25-30	22-24	Ethanol	81	156-165
Nitrovetraldehyde	**5k**	25-30	22-24	Ethanol	58.73	190-196

Table S2: Surflex Docking score (kcal/mol) of the compounds for α-glucosidase protein in the human intestine.

Compounds	C Score [a]	Crash Score [b]	Polar Score [c]	D Score [d]	PMF Score [e]	G Score [f]	Chem Score [g]
Casuarine-Enzyme complex	8.80	-1.49	7.35	-134.360	-143.989	-307.493	-29.806
5j	7.51	-2.22	7.89	-125.230	-135.620	-250.891	-29.120
5e	6.06	-2.17	1.02	-217.788	-129.181	-241.909	-30.941
5g	4.95	-2.68	0.26	-217.877	-136.638	-257.731	-31.403
5i	3.04	-1.18	0.09	-142.781	-89.668	-140.498	-20.357
5a	2.71	-0.82	0.15	-148.895	-60.397	-168.120	-18.391
5h	2.70	-0.87	1.14	-134.452	-41.400	-141.522	-18.510
5k	2.17	-2.28	0.60	-164.709	-131.261	-171.072	-25.954
5d	2.01	-1.62	0.14	-130.224	-81.294	-143.050	-15.273

[a] CScore (Consensus Score) integrates a number of popular scoring functions for ranking the affinity of ligands bound to the active site of a receptor and reports the output of total score.

[b] Crash-score revealing the inappropriate penetration into the binding site. Crash scores close to 0 are favorable. Negative numbers indicate penetration.

[c] Polar indicating the contribution of the polar interactions to the total score. The polar score may be useful for excluding docking results that make no hydrogen bonds.

[d] D-score for charge and van der Waals interactions between the protein and the ligand.

[e] PMF-score indicating the Helmholtz free energies of interactions for protein-ligand atom pairs (Potential of Mean Force, PMF).

[f] G-score showing hydrogen bonding, complex (ligand-protein), and internal (ligand-ligand) energies.

[g] Chem-score points for H-bonding, lipophilic contact, and rotational entropy, along with an intercept term.