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Designing novel oral-Insulin conjugates for the development of oral-Insulin tablet: Inulin-Insulin conjugate is an efficient form for oral-Insulin tablet

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ABSTRACT

Insulin is used medically to manage diabetes mellitus by frequent subcutaneous injections have turned into a part of life can be enormously distressing for patients. Hence, we anticipate to getting rid of the usage of subcutaneous injections completely. Virtual screening method (for selection of carriers), Toxtree tool (for toxicity evaluation of carriers) and Discovery Studio tool (for Pharmacopore designing, ADMET analysis, designing oral Insulin conjugates and Interaction studies between Insulin Receptor and oral Insulin conjugates) were used for proposed study. We have screened 14 competent drugs delivering agents (DDAs) from 7 chemical compound databases. The ADMET and Pharmacophoric properties of DDAs were analyzed by drug-informatics' tools. Consequently, the DDAs were mono, di & poly conjugated by covalent bonding with various binding sites of Monomeric and hexameric form of human insulin and insulin-lispro (Humalog®) individually; and novel oral-insulin conjugates (OICs) were generated. Its binding efficiency and biological activity with Insulin-receptor were determined. Inulin and Vitamin-B1 are considered as novel, safe and proficient carriers for oral delivery of Insulin. Insulin Lispro is the remarkable option for oral delivery than other Insulin forms.

Keywords: Oral Insulin: Diabetes; Drug delivery; Insulin tablets

Abbreviations: DDAs – Drug delivering agents; OICs – Oral Insulin Conjugates; Da - Dalton; FDA – Food & Drug Administration; IN-105 - Methoxy-poly(ethylene glycol)-insulin conjugates; HIM2 - Hexyl-insulin monoconjugate-2; KEGG - Kyoto Encyclopedia of Genes and Genomes; ChEBI - Chemical Entities of Biological Interest; log(Sw) - log Aqueous solubility (Solubility in water); logBB - log Brain-Blood; CYP2D6 - cytochrome P450 2D6; HIA - Human intestinal absorption; PSA - polar surface area; TOPKAT - Toxicity Prediction by Komputer Assisted Technology; BFGS - Broyden-Fletcher-Goldfarb-Shanno; BBB- Blood brain barrier; ADMET - Absorption, Distribution, Metabolism, Excretion and Toxicity; SASA - Solvent Accessible Solvent Area; MTD - Maximum tolerated dose; C1 - Vitamin B12 (cobalamin); C2 - Vitamin H (Biotin); C3 - Folic acid (Vitamin M / Vitamin B9); C4 - Vitamin B1 (Thiamin); C5 - L-Carnitine (Vitamin BT); C6 - Poly-N-vinylpyrrolidone; C7; Inulin; C8 - Poly Cysteine; C9 - Chitosan; C10 - Pectin; C11 - Poly(propylene glycol); C12 - Poly(propylene imine); C13 - Poly (lactic-co-glycolic acid); C14 - Deoxycholic acid.

1. INTRODUCTION

Drug delivery is an essential process which leads to innovation of novel carriers to manage oral delivery of some peculiar drugs such as proteins, hormones, enzymes, and peptides.¹ These Insulin drugs are requires efficient drug delivering agents (DDAs) for oral formulations to reach therapeutic targets against the interruption of biological barriers such as gastric digestion in stomach, proteolysis in intestinal regions, and poor bioavailability due to higher molecular weight.²,5,6 Now a day, the subcutaneous injection of insulin formulations has been the core therapy utilized for the management of type-1-diabetes as well as type-2-diabetes since insulin's discovery over 85years ago.²,3 Multiple doses of Insulin subcutaneous injections on the daily basis making patients painful and create 'fear of pain' among them.⁴ There are several disadvantages of this subcutaneous administration such as poor compliance, local discomfort, inconvenience, fright of soreness of multiple injections, hypoglycemic risk related to injections, occasional hyper-insulinemia due to overdoses, unsatisfactory metabolic regulations, allergy, harrowing, and insulin lipodystrophy at the site of injection.³,4 In addition, subcutaneously administered insulin is absorbed directly into the peripheral circulation without initial hepatic circulation, thereby exposing peripheral targets to higher insulin concentrations relative to the liver.⁴ As of 2014, no products appeared to be successful in the market because of lack of physical stability against biological barriers.⁴ For those effective reasons, we intend to screen novel DDAs to design efficient oral Insulin conjugates (OICs) against diabetes.

In our analysis, the monomeric & hexameric form of recombinant human insulin and Humulin were modified by the covalent bonding of short-chain DDAs. The modification takes place to the either or both amino-acids of PheB1 & LysB29 in recombinant human insulin, and also PheB1 & LysB28 in Humulin. Because, the conjugation of DDAs to Insulin forms ought to have no negative impact on the insulin's therapeutic activity since it has been formerly determined that these residues do not directly contribute in receptor binding. 12-14 On these perspectives, a study proven that DDA-recombinant Insulin conjugate (at LysB29) was physically more stable against acidic condition, not undergoes enzymatic degradation, less immunogenic, less antigenic, resistance to fibrillation in aqueous solution and improved stability against temperature, pH, and interfacial & shear forces¹⁵⁻¹⁸ when correlated with DDA-recombinant Insulin conjugate (at PheB1), and human native-Insulin.^{8,9,19} Moreover, the conjugation of recombinant Insulin with DDA can protect the self-aggregation (dimerization) in aqueous solutions.^{8,9} In this stance, Humulin has higher resistant capability against self-aggregation & other biological barriers than human recombinant-Insulin and native-Insulin.²⁰ The oligomeric-Insulin forms (chiefly hexamers) is not bioactive and the fraction of an amount is absorbed across the capillary endothelium into the systemic circulation in the absence of DDA. The dissociation of oligomer into dimmers and monomers is seen as the ratelimiting barrier to absorption that effectively affects the preparation's pharmacological response. 15 Meantime, the monomeric-Insulin forms of is highly bio-available but easily de-nature & de-folded in presence of biological barriers.¹⁵ In a study, the in-vivo pharmacodynamic assay reveals that there is no loss of biological activity after conjugation of carrier to the either site on the oligomeric form of insulin-B-chain.²¹ On the other hand, the attachment of long-chain DDA (2000Da) decreased the bioactivity of conjugates than sort-chain DDA (750Da). Hence, mono-disperse and short-chain DDAs (≤750Da) are preferred.8 From the earlier studies, we choose that Humulin, monomeric & hexameric of human recombinant insulin and short chain DDAs for designing OICs. We report, and analyze the structural series of novel DDAs and OICs by drug-informatics.

2. Methods

2.1. Carriers

2.1.1. Screening

For Virtual Screening²² of DDAs, PubChem Compound,²³ Zinc Database,²⁴ KEGG²⁵ ((Kyoto Encyclopedia of Genes and Genomes)), DrugBank,²⁶ ChemSpider,²⁷ ChEMBL,²⁸ and ChEBl²⁹ (Chemical Entities of Biological Interest), compound databases were used. Carrier agents were retrieved by the search terms of "Polymer" & "Biopolymer". The compounds were filtered through virtual screening & biomedical text mining using a defined criteria listed below, in part akin to the Lipinski's rule;³⁰ the DDAs should be: a) mono-disperse, b) short-chain (low-molecular weight (<2000Da)), c) biocompatible, d) lipophilic, e) physically stability against gastric acids and proteolytic enzymes, f) inert (no biological activity), g) non-toxic.

2.1.2. Analysis of Pharmacophoric features

The retrieved compounds were subjected to Pharmacophore analysis by Discovery Studio (Accelrys discovery studio 2.5).³¹ In Discovery Studio, a pharmacophore is defined as the essential features or chemical substructures and their corresponding 3D locations that are responsible for the similar biological activities of a set of compounds. Typically, pharmacophore features include hydrophobic (in light blue), hydrogen bond acceptor (HBA, in green), hydrogen bond donor (HBD, in Magenta), and active principles.

2.1.3. Analysis of Physico-chemical properties

The retrieved compounds were subjected to ADMET evaluation by Discovery Studio. ADMET Descriptors include:

- Aqueous Solubility: This model uses linear regression to predict the solubility of each compound in water at 25°C. Key to aqueous solubility is graded through Level, Value and Drug-likeness as follows: (level 0; log(Sw) < -8.0; Extremely low), (level 1; -8.0 < log(Sw) < -6.0; No, very low, but possible), (level 2; -6.0 < log(Sw) < -4.0; Yes, low), (level 3; -4.0 < log(Sw) < -2.0; Yes, good), (level 4; -2.0 < log(Sw) 0.0=""; Yes, optimal); (level 5; 0.0 < log(Sw); No, too soluble).
- Blood Brain Barrier Penetration: This model predicts blood-brain penetration (blood brain barrier, BBB) after oral administration. This model contains a quantitative linear regression model for the prediction of blood-brain penetration, as well as 95% and 99% confidence ellipses in the ADMET_PSA_2D, ADMET_AlogP98 plane (ADMET_PSA_2D means Fast polar surface area; ADMET_AlogP98 means Atombased LogP). There are four prediction levels within the 95% and 99% confidence ellipsoids and they are graded through Level, Value and Brain-Blood ratio as follows: (Level 0; Very high penetrants (logBB ≥ 0.7); Brain-Blood ratio greater than 5:1), (Level 1; High penetrants (0 ≤ logBB < 0.7); Brain-Blood ratio between 1:1 and 5:1), (Level 2; Medium penetrants (-0.52 < logBB < 0); Brain-Blood ratio between 0.3:1 and 1:1), (Level 3; Low penetrants (logBB ≤ -0.52); Brain-Blood ratio less than 0.3:1), (Level 4; Undefined; Outside 99% confidence ellipse).</p>
- CYP2D6 Binding: Predicts cytochrome P450 2D6 enzyme inhibition. The cytochrome P450 2D6 model predicts CYP2D6 enzyme inhibition using 2D chemical structure as input. The model classifies compounds as either 0 or 1 for non-inhibitor or inhibitor and provides an average-class-value estimate of confidence. Key to CYP2D6 is graded through Predicted class, value and Description as follows; (Predicted class 0; Non-inhibitor; Unlikely to inhibit CYP2D6 enzyme; ADMET_CYP2D6_Probability < 0.5), (Predicted class 1; Inhibitor; Likely to inhibit CYP2D6 enzyme; ADMET_CYP2D6_Probability > 0.5). ADMET_CYP2D6_Probability means CYP2D6 score or average class value.
- Hepatotoxicity: Predicts the occurrence of dose-dependent human hepatotoxicity. The hepatotoxicity model predicts potential organ toxicity for a wide range of structurally diverse compounds. Key to Hepatotoxicity is graded through Predicted class, value and

Description as follows; (Predicted class 0; Nontoxic; Unlikely to cause dose-dependent liver injuries. ADMET_Hepatotoxicity_Probability < 0.5), (Predicted class 1; Toxic; Likely to cause dose-dependent liver injuries. ADMET_Hepatotoxicity_Probability > 0.5). ADMET_Hepatotoxicity_Probability means Hepatotoxicity score (average-class value).

- Intestinal Absorption: This model predicts human intestinal absorption (HIA) after oral administration. Intestinal absorption is defined as a percentage absorbed rather than as a ratio of concentrations (cf. blood-brain penetration). A well-absorbed compound is one that is absorbed at-least 90% into the bloodstream in humans. The intestinal absorption model includes 95% and 99% confidence ellipses in the ADMET_PSA_2D, ADMET_AlogP98 plane. The ellipses define regions where well-absorbed compounds are expected to be found: 95% of well-absorbed compounds are expected to fall within the 95% ellipse, while 99% of well-absorbed compounds should fall within the 99% ellipse. Note that the location of any particular compound does not necessarily imply whether it will be well, moderately or poorly absorbed. In general, however, absorption tends to drop off quite rapidly outside the 95% ellipse. These levels are defined by the 95% (blue line) and 99% (magenta line) confidence ellipsoids. There are four prediction levels and they are graded through level, value and Description as follows: (Level 0; ADMET_Absorption_T2_2D < 6.1261 (inside 95%); Good absorption), (Level 1; 6.1261 ≤ ADMET_Absorption_T2_2D < 9.6026 (inside 99%); Moderate absorption), (Level 2; 9.6026 < ADMET_Absorption_T2_2D (outside 99%); Low absorption], (Level 3; ADMET_PSA_2D ≥ 150.0 or ADMET_AlogP98 ≤ -2.0 or ADMET_AlogP98 ≥ 7.0; Very low absorption). ADMET_Absorption_T2_2D is the Mahalanobis distance for the compound in the ADMET_PSA_2D, ADMET_AlogP98 plane. It is referenced from the center of the region of chemical space defined by well-absorbed compounds.
- Plasma Protein Binding: The plasma protein binding model predicts whether a compound is likely to be highly bound to carrier proteins in the blood. Key to Plasma Protein Binding is graded through level and Description as follows; (Level 0; Binding is < 90% (No markers flagged and AlogP98 < 4.0)), (Level 1; Binding is > 90% (flagged at 90% or AlogP98 > 4.0)), (Level 2; Binding is > 95% (flagged at 95% or AlogP98 > 5.0)). AlogP98 means Atom-based LogP from FastDesc.

2.1.4. Analysis of Toxicity

The retrieved compounds were subjected to Toxicity evaluation by Discovery Studio and TOXTREE (by IdeaConsult Ltd (Sofia, Bulgaria)).³² Toxtree is able to estimate toxic hazard by applying a decision tree approach. The classification result is shown in graphical form (green highlight for class I (non-toxic), yellow highlight for class II (Moderately toxic) and red highlight for class III (Toxic)), as well as in text form. In Discovery Studio; TOPKAT models have been re-trained using updated training sets from the legacy TOPKAT (Toxicity Prediction by Komputer Assisted Technology). The following models are extensible and are derived using calculable properties;

- FDA Rodent Carcinogenicity
- Ames Mutagenicity
- Rat Oral LD50
- Rat Maximum Tolerated Dose
- Skin Irritancy
- Skin Sensitization
- Aerobic Biodegradability

2.2. Designing Oral insulin conjugates & OIC – IR binding

For designing, Oral insulin conjugates & Interaction of OIC with IR were carried out through "LibDock" algorithm of Discovery Studio.³³ The LibDock docking program performs the following steps using a set of pre-generated ligand conformations and a receptor with a specified binding site:

- Remove hydrogen atoms.
- Rank ligand conformations and prune by Solvent Accessible Solvent Area (SASA).
- Find hotspots using a grid placed into the binding site and using polar and apolar probes. The numbers of hotspots are pruned by clustering to a user defined value.
- Dock ligand poses by aligning to the hotspots. This is performed by using triplets (i.e., three ligand atoms are aligned to three
 receptor hotspots). Poses which result in protein clashes are removed.
- A final Broyden-Fletcher-Goldfarb-Shanno (BFGS) pose optimization stage is performed using a simple pair-wise score (similar to Piecewise Linear Potential). The top scoring ligand poses are retained.
- Hydrogen atoms are added.

Hydrogen atoms added in the final step may result in small bumps with the protein. Therefore, minimization should be performed prior to using scoring functions that are sensitive to such bumps.

3. RESULTS & DISCUSSION

3.1. Carriers

3.1.1. Screening

In carrier screening (Flowchart 1), more than 1, 00,000 compounds were retrieved from 7 compound databases. Among those, 14 compounds were screened by using experimental text mining & filtration criteria (Table 1). According to data mining, most of the screened compounds in Table 1 are monodisperse such as Vitamin B12,³⁴ Vitamin H,⁴⁵ Folic acid,⁵¹ Poly-N-vinylpyrrolidone,^{67,68} Inulin,⁷⁶ Poly Cysteine,⁸⁸ Chitosan,⁹⁶⁻⁹⁸

Pectin, ¹⁰⁵ Poly (Propylene glycol), ^{112,113} Poly (Propylene imine), ^{128,129} Poly (lactic-co-glycolic acid), ^{133,134} Deoxycholic acid¹⁴¹ except Vitamin B1 and L-Carnitine, because of the lack of experimental data. Molecular weight of polymeric drug delivering molecules are varies based on length of chain, but in the case of Vitamins, molecular weights are measurable. Maximum carriers in the retrieved list have shown low-molecular weight due to short-chain in structure (<2000Daltons). L-Carnitine (162.113 Daltons), Poly-N-vinylpyrrolidone (11.141 Daltons), Inulin (342.297 Daltons), Poly Cysteine (121.158 Daltons), Pectin (194.139 Daltons) and Poly(propylene glycol) (76.094 Daltons) are possess low-molecular weight while compare with vitamins and other macromolecules in the list. All the listed molecules are biocompatible and biodegradable. ^{36,} ^{48,53,57,64,69,77,90,97,106,114,130,135,142}

Most of the carriers are having efficient oral bioavailability and intestinal permeability such as Vitamin B12,³⁶⁻³⁹ Vitamin H,⁴⁶⁻⁴⁸ Folic acid,^{54,55} Vitamin B1,⁵⁸ L-Carnitine,⁶¹⁻⁶⁵ Inulin,⁷⁸ Poly(propylene glycol),^{115,116} Poly(propylene imine),¹³¹ Poly (lactic-co-glycolic acid)^{138,139} and Deoxycholic acid.^{144,145} Chitosan,^{99,100,102,104} and Pectin¹⁰⁸ are graded as moderately efficient in bioavailability while Poly-N-vinylpyrrolidone^{70,71} and Poly Cysteine^{92,93} are very poor intestinal transport, because of the lack of lipophilicity. Biomedical text mining shows all the listed compounds are physically stable against gastric acids and proteolytic enzymes during drug delivery. ^{40,48,54,58,65,73,81,94,99,111,117,130,144,145} Among the retrieved carriers, Vitamin B12,⁴² Vitamin H,⁴⁹ Vitamin B1,⁵⁹ Poly-N-vinylpyrrolidone,⁷⁴ Inulin,^{82,83} Chitosan,⁹⁹ Poly(propylene glycol),¹²² Poly (lactic-co-glycolic acid)¹³⁷ and Deoxycholic acid¹⁴⁶ are chemically inert and they does not undergoes any biochemical transformation & aggregation during drug delivery. Through text-mining, we could not found whether Folic acid, L-Carnitine, Poly Cysteine, Pectin, and Poly(propylene imine) are inert or not. Based on the concept of toxicity, Vitamin B12,⁴⁴ Vitamin H,⁵⁰ Folic acid,⁵⁶ Vitamin B1,⁶⁰ L-Carnitine,⁶⁶ Inulin,⁸⁴ Poly Cysteine,⁹⁵ Chitosan,⁹⁹ Pectin,¹⁰⁹ Poly (lactic-co-glycolic acid)¹⁴⁰ are non-toxic materials and does not produce any untoward reactivity during drug-delivery mechanism. But, Poly-N-vinylpyrrolidone,⁷⁵ Poly(propylene glycol),¹²⁶ Poly(propylene imine),¹³² and Deoxycholic acid¹⁴⁶ are moderately toxic based on text-mining.

The experimental text-mining concludes Inulin, Chitosan and Poly (lactic-co-glycolic acid) are efficient, safe and primary drug delivering molecules of drugs that completely fulfill the filtration criteria. Inulin reduces the production of potentially toxic metabolites, induce important immune-mediated effects and reduce the cancer risk during drug delivery. Pat-87 Generally Inulin 19-81 and Chitosan 19-104 are participating in colontargeting drug delivery, possess very minimum exposure to gastric fluids in the stomach and enzymatic degradation in the small intestine. Folic acid, L-Carnitine and Pectin are eligible for drug delivery process, but we could not conclude whether they are inert. Vitamin B1 is an effectual and non-toxic carrier, may cause Anaphylaxis at higher doses. L-Carnitine & Vitamin B1 does not hold any literature evidence that they possess mono-disperse character or not. Vitamin B12 is inert, long-term usage may cause Vit-B12 deficiency. Vitamin H is inert, but it may inert the biological activity of the drug. Poly-N-vinylpyrrolidone, and Poly (propylene imine) are participating in nanoparticle-based drug delivery, and both are moderately toxic. Poly Cysteine is hydrophilic in nature; shows poor permeability across intestinal epithelium; 2,93 and no research confirmation whether it is inert. Poly(propylene glycol) is an efficient carrier for drug delivery, and inert, overdose may cause skin & eye irritation. In a studies, toxic symptoms appeared only after frequent doses of propylene glycol, used as a vehicle for medicines, were repetitively applied to the skin. Vaxic symptoms appeared only after frequent doses of propylene glycol, used as a vehicle for medicines, were repetitively applied to the skin. In drug delivering mechanism, it eliminates toxic degradation. In the second proposed colon tumorigenesis in both animals and humans.

3.1.2. Analysis of Pharmacophoric features

Pharmacophores are conceptual description of molecular principles or features that are essential for molecular recognition of a molecule through a biological macromolecule. Pharmacophoric features of Drug delivering molecules are illustrated and demonstrated by Discovery Studio software (Table 2; Figure 1). Pharmacophore features comprise hydrogen bond donor, hydrogen bond acceptors, hydrophobic centroids, aromatic rings, cations, and anions. Among those features, Acceptor, Donor, hydrophobic regions and the number of active principles of carrier molecules (Supplementary Figure 1) were investigated based on Lipinski's rule. 30 According to the rule of Lipinski, a molecule should not donate more than 5 hydrogen bonds and it should not accept more than 10 hydrogen bonds. Most of the carriers obey the rule and eligible for drug delivery except Inulin and Vitamin B12. Inulin posses 11 hydrogen bond acceptors (≤ 10 as per rule) may leads to accepting electrons transferred to it from another compound. Inulin may be an oxidizing molecule, by virtue of its accepting electrons, it itself reduced in the drug delivery process. Inulin may undergo permanent chemical alteration through covalent or ionic reaction chemistry, resulting in the complete and irreversible transfer of one or more electrons. But in this case, Inulin is a colon targeting molecule; subsequently it does not undergo any chemical transformation during drug delivery mechanism⁷⁹⁻⁸¹ like Chitosan.⁹⁹⁻¹⁰⁴ Vitamin B12 posses 7 hydrogen bond donors (≤5 as per rule) may leads to donate electrons to another compound. Vitamin B12 may be a reducing agent, by virtue of its donating electrons, it itself oxidized in the drug delivery process. Compare with another Drug delivering molecules, Inulin, Vitamin B12 and Deoxycholic acid contains maximum hydrophobic regions (Table 2) that is responsible for efficient intestinal transport. 36-39,78,144,145 The significant criteria, pharmacophoric active principle is more in Folic acid, Vitamin B1, Inulin, Chitosan and Pectin, But Vitamin B12 and Poly(propylene imine) does not hold any single active principle in their structure. The analysis of pharmacophoric features suggests that Vitamin B1, Inulin, Chitosan, and Pectin are possible Drug delivering molecules for Insulin.

3.1.3. Analysis of Physico-chemical properties

ADME descriptors of Drug delivering molecules were evaluated by Discovery Studio and listed in Table 3 (Supplementary Figure 2). Vitamin H, Vitamin B1, Poly Cysteine, Poly(propylene glycol), Poly (lactic-co-glycolic acid) and Deoxycholic acid are falls within 95% absorption ellipse that shows efficient absorption (level = 0) across intestinal epithelium, concurrently shows the sign of maximum bioavailability in drug delivering

mechanism. Poly-N-vinylpyrrolidone and Poly(propylene imine) are falls within 99% absorption ellipse that shows moderate absorption (level = 1); remaining compounds are falls outside 99% absorption ellipse shows poor absorption (level = 3). In the case of Aqueous solubility, Folic acid (-3.378) show extremely high Aqueous Solubility and drug-likeness. Vitamin H (-1.432), Vitamin B1 (-1.335), Poly-N-vinylpyrrolidone (-0.550) and Poly(propylene imine) (-0.097) shows optimal Aqueous Solubility and drug-likeness; others show poor drug-likeness. In the point of Blood-Brain-barrier (BBB) penetration, Deoxycholic acid (-0.154) is medium penetrant across Blood-Brain-barrier, because it is fall within 99% confidence ellipsoids (level = 2), the Brain-Blood ratio is between 0.3:1 and 1:1. Vitamin H (-1.229), Vitamin B1 (-1.253), Poly Cysteine (-1.362), Poly(propylene glycol) (-1.039), Poly (lactic-co-glycolic acid) (-1.713) are low penetrants across Blood-Brain-barrier, because it is within 99% confidence ellipsoids (level = 3), the Brain-Blood ratio is less than 0.3:1. Other carriers are poor penetrants because they are outside the 95% and 99% confidence ellipsoids (undefined level = 4). In the case of CYP-4502D6 binding, the carrier should be non-inhibitor because CYP-4502D6 is responsible for metabolism and elimination of drug molecules. All the listed drug delivering molecules are non-inhibitors because their ADMET CYP2D6 Probability is < 0.5. In the case of Hepatotoxicity, most of the selected carriers are non-toxic because, their ADMET hepatotoxicity probability is < 0.5. But Vitamin B12 (0.509) and Folic acid (0.662) are toxic because, their ADMET hepatotoxicity probability is > 0.5. Plasma Protein Binding capability should be <90%, then only the unbound molecule can easily penetrate the tissues to reach the active site and then to get eliminate. The Plasma Protein Binding character of all listed carriers is low and satisfies the standard value (< 4.0). Based on the overall results of Physico-chemical properties, Vitamin H, Vitamin B1, and Deoxycholic acid are superior drug delivering molecules according to their efficient solubility in liquid, moderate penetration across Blood Brain barrier, enhanced absorption across intestinal epithelial cells, noninhibition of CYP-4502D6 binding, unbound nature with plasma proteins and low hepatotoxicity.

3.1.4. Analysis of Toxicity

Toxic scale is the most significant prediction for carriers in drug delivery mechanism. Toxicity properties such as FDA Rodent Carcinogenicity, Mutagenicity, Rat oral LD50 (g/Kg Body weight), Rat maximum tolerated dose (g/Kg Body weight), Skin Irritant, Skin sensitization, Aerobic biodegradability and general toxicity were studied by Discovery Studio and Toxtree (Table 4 & Supplementary Figure 3 & 4). The listed carriers are Non-mutagen and are Non-carcinogen except Vitamin B1 and Poly-N-vinylpyrrolidone. The predicted skin irritancy is severe for Deoxycholic acid, while Vitamin H, Folic acid, Vitamin B1, Poly Cysteine, Pectin, and Poly (lactic-co-glycolic acid) are non-irritants and others are in the category of mild-irritant. Vitamin B1 is predicted under strong skin-sensitizer, whereas Folic acid and Deoxycholic acid are weak skinsensitizers; others fall under non-skin-sensitizer. The drug delivering molecules should be biodegradable in an aerobic environment after delivering the drug to receptors; otherwise it may leads to untoward reactivity. In this case, Folic acid, Vitamin B1 and Poly(propylene imine) are Non-Degradable, others are Degradable under aerobic condition. The TOPKAT model predicts the rat oral acute median lethal dose (LD50) in the toxicity test, and the rat maximum tolerated dose (MTD) of all drug delivering molecules. According to general toxicity prediction by Toxtree tool, Vitamin B12, Folic acid, Poly-N-vinylpyrrolidone, Chitosan, Poly(propylene glycol), Poly(propylene imine), and Deoxycholic acid may highly toxic while others are low in toxic category. Based on the analysis of toxicity studies, we concluded that Vitamin H, Inulin, Poly Cysteine, Pectin, and Poly (lactic-co-glycolic acid) are safe carriers for delivering oral insulin molecule.

3.2. Oral insulin conjugates

3.2.1. Designing

Human Insulin Monomer (PDB ID: 1HLS), human insulin hexamer (PDB ID: 1AIO), and Insulin Lispro (PDB ID: 1 LPH) were retrieved from Protein data bank and conjugated with all carriers individually. Nikhil J Kavimandan et al. (2006)⁹ and Hinds et al. (2000)⁸ suggest that, conjugation of carriers with B1Phe, B27Thr, B28Pro & B29Lys amino acids of human Insulin and B28Lys amino acid of Insulin Lispro will be the efficient conjugate against ADMET barriers in oral delivery. Based on our computational analysis (Discovery Studio - LibDock), the positive LibDock score indicating the competent oral-insulin conjugation.

Human Insulin Monomer (PDB ID: 1HLS), conjugated individually with all listed drug delivering molecules (Table 5 & Supplementary Figure 5); among those Inulin was mono-conjugated efficiently with B1Phe of Insulin Monomer, and Poly (lactic-co-glycolic acid) was di-conjugated competently with B1Phe & A11Cys of Insulin Monomer. Vitamin B12, Vitamin M, poly-N-vinylpyrrolidone, poly(propylene imine), and Deoxycholic acid did not shows any conjugation with amino acids of Insulin Monomer. Rest of the drug delivering molecules form the incompetent mono & di-conjugates with A & B chain amino acids of Insulin Monomer. Based on the Binding site (PHE B1) and LibDock score, Inulin (117.663) shows the competent oral-insulin conjugation (Figure 2c). Based on the LibDock score, Vitamin H (86.2835) and Vitamin B1 (94.1144) shows the competent oral-insulin conjugation (Figure 2a & 2b); but in the case of Poly (lactic-co-glycolic acid), the score is poor; even it conjugate at PHE B1 (Figure 2d).

Human insulin hexamer (PDB ID: 1AIO) conjugated individually with all listed drug delivering molecules (Table 6 & Supplementary Figure 6); among those Vitamin B1 and Inulin were mono-conjugated efficiently with B29Lys of Insulin hexamer and form the competent mono conjugates. Vitamin B12, poly-N-vinylpyrrolidone, and poly(propylene imine) did not shows any conjugation with amino acids of Insulin hexamer. Rest of the drug delivering molecules forms the incompetent mono & di-conjugates with A, B, C, D, E, F, G, H, I, J, K and L chain amino acids of Insulin hexamer. According to LibDock score, Vitamin M (114.324), Vitamin H (103.231) and Inulin (94.3543) show the competent oral-insulin conjugation (Figure 3a, 3b & 3c). Based on the Binding site (LYS B29), Inulin and Vitamin B1 shows the competent oral-insulin conjugation (Figure 3c & 3d).

Insulin Lispro (PDB ID: 1 LPH) conjugated individually with all listed drug delivering molecules (Table 7 & Supplementary Figure 7); among those Vitamin M was poly conjugated with A & B chain amino acids of Insulin Lispro such as A1Gly, A2lle, A3Val, A4Glu, A19Tyr, B4Gln, B5His, B27Thr, B28Lys, B30Thr. This conjugates efficiently bonding with B27Thr and B28Lys amino acids. It also made the inefficient multiple bonding

interactions with Insulin Lispro and may affect the absorption and bioavailability of Insulin Lispro. Vitamin B1 was di-conjugated reasonably with Lys B28 & Glu A4 of Insulin Lispro. Inulin was tetra-conjugated fairly with B28Lys, A1Gly, A3Val, and A4Glu of Insulin Lispro. Vitamin B12, Vitamin H, poly-N-vinylpyrrolidone, poly(propylene imine), and Deoxycholic acid did not shows any conjugation with amino acids of Insulin Lispro. Rest of the drug delivering molecules forms the incompetent mono, di, tetra & poly-conjugates with A & B chain amino acids of Insulin Lispro. According to LibDock score and Binding site (LYS B28), Vitamin M (131.57), Vitamin B1 (89.8971) and Inulin (76.2195) shows the competent oral-insulin conjugation (Figure 4a, 4b & 4c).

3.3. Interaction of Oral insulin conjugates with Insulin Receptor (IR)

Among the designed conjugates, Inulin-Insulin Monomer conjugate, Vitamin B1-Insulin Monomer conjugate, Vitamin H-Insulin Monomer conjugate, Vitamin M-Insulin hexamer conjugate, Vitamin M-Insulin hexamer conjugate, Inulin-Insulin hexamer conjugate, Vitamin M- Insulin Lispro conjugate, Vitamin B1 -Insulin Lispro conjugate, and Inulin- Insulin Lispro conjugate are selected as capable oral-insulin conjugates to interact with Insulin Receptor. In the case of Insulin Receptor, the leucine-rich repeat domain (L1, residues 1-157) and C-terminus of the α -chain (α CT, residues 704-715) are Insulin binding surface¹⁴⁷⁻¹⁵⁰ and they functions as a signaling element to activate its tyrosine kinase and predicted to influence Insulin receptor—Oral Insulin conjugate interaction. In the proposed work, none of oral Insulin conjugates shows interaction with α CT while Insulin Monomer - DDM Conjugates (Figure 5a) does not show interaction with L1 domain (Table 8 & Supplementary Figure 8). Insulin Hexamer - DDM Conjugates interacts with ARG86 and ASN34 residues of IR (Figure 5b), while Insulin Lispro – DDM Conjugates interacts with ARG86, ASN90 and ARG114 residues of IR (Figure 5c) which reflects the efficient binding affinity of Insulin Lispro – DDM Conjugates with IR.

In our analysis, fourteen drug delivering agents were screened and its characteristic features for oral delivery of Insulin were examined. Based on the toxicity and conjugation ability with various forms of Insulin, the drug delivering molecules were chosen for developmental studies. From the overall results we nominate Vitamin B1 and Inulin are suitable drug delivering agents because: 1) Vitamin B1 completely satisfy the defined criteria based on bio-text mining; it shows better pharmacophoric and efficient ADME features; ^{58,59} it is carcinogen but low toxic⁶⁰ as per drug informatics analysis; it shows efficient conjugation with Insulin monomer, Insulin hexamer and Insulin Lispro. Vitamin B1-insulin hexamer and Vitamin B1- Insulin Lispro conjugates shows efficient interaction with IR. Vitamin B1 is a highly recommended molecule for in-vitro and in-vivo studies. 2) Inulin absolutely satisfy the defined criteria based on bio-text mining; it shows superior pharmacophoric and moderate ADME features; ^{76,78-81} it is non-carcinogen, non-mutagen, low toxic⁸⁴ as per drug informatics analysis. It shows efficient conjugation with Insulin monomer, Insulin hexamer, and Insulin Lispro. Inulin-insulin hexamer and Inulin - Insulin Lispro conjugates shows efficient interaction with IR. Inulin is a highly recommended molecule for in-vitro and in-vivo studies.

Moreover, we choose Poly (propylene glycol) is a possible drug delivering agent because it is partially fulfills the defined criteria based on bio-text mining; it shows moderate pharmacophoric and moderate ADME features;^{115,116,122} it is non-carcinogen, non-mutagen, moderately toxic¹²⁶ as per drug informatics analysis. It shows reasonable conjugation with insulin monomer, insulin hexamer, and Insulin Lispro. In earlier studies, propylene glycol showed toxic symptoms after the frequent doses & repeated application when used as a vehicle in medicinal preparations.¹²⁴⁻¹²⁵ Meantime, in drug delivering mechanisms, it eliminates the toxic degradation,¹²⁶ and less toxic than the parent substance (Polyethylene glycol),¹²⁷ because PEG is a frequently used drug delivering molecule for oral insulin delivery^{3,8}. Consequently, Poly (propylene glycol) may be a possible carrier for further studies.

In another stand, while compare the binding efficiency of various Insulin forms; Insulin Lispro (LysB28) shows the competent conjugation with drug delivering molecules and the resultant conjugates shows therapeutically capable interaction with IR than Insulin Monomeric and hexameric form of conjugates.

4. CONCLUSION

The oral bioavailability of insulin is 1%. It may be enhanced by novel carriers that deliver insulin to the site of absorption. In the proposed work, based on the defined criteria 14 drug delivering molecules were filtered from 7 reputed compound databases and it's Pharmacophoric and ADMET properties were analyzed by Biomedical text mining and drug-informatic tools. The results from the conducted studies concluded that Inulin and Vitamin B1 are considered as novel, safe and proficient oral carriers for Insulin. (Polyethylene glycol) is an optional vehicle for oral delivery of Insulin. Insulin Lispro is the tremendous option for oral delivery than other Insulin forms. Clinical studies are recommended to develop our results.

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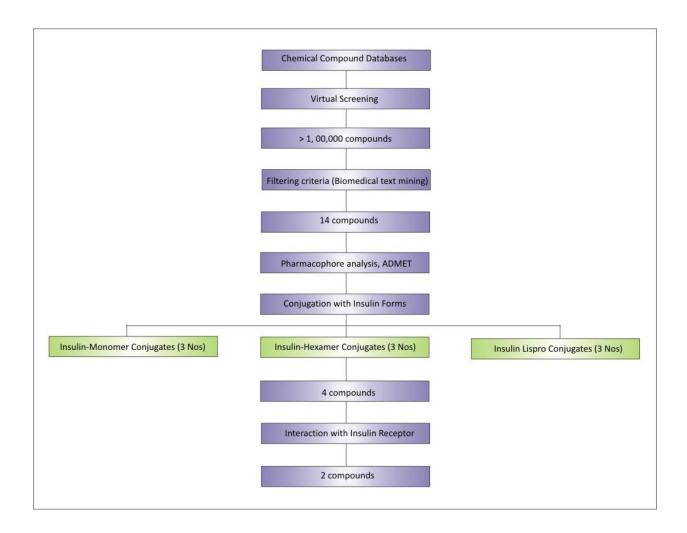
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Flowchart 1: Screening process of Drug delivering molecules

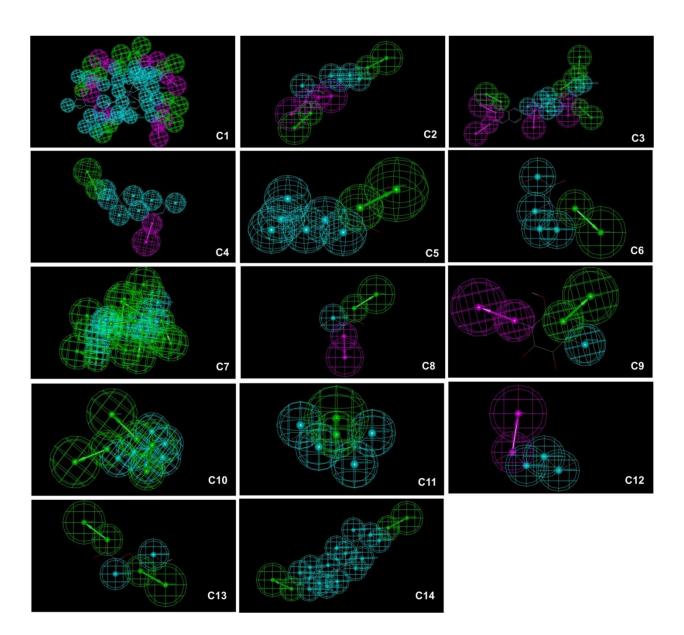


Figure 1
Pharmacophoric features of Drug delivering molecules are illustrated by Discovery Studio software. Acceptors (Green in color), Donors (Magenta in color) and Hydrophobic Regions (Blue in color) of Pharmacophoric features of all Drug delivering molecules are demonstrated and differentiated by color. C1- Vitamin B12 (cobalamin); C2- Vitamin H (Biotin); C3 - Folic acid (Vitamin M / Vitamin B9); C4 - Vitamin B1 (Thiamin); C5 - L-Carnitine (Vitamin BT); C6 - Poly-N-vinylpyrrolidone; C7; Inulin; C8 - Poly Cysteine; C9 - Chitosan; C10 - Pectin; C11 - Poly(propylene glycol); C12 - Poly(propylene imine); C13 - Poly (lactic-co-glycolic acid); C14 - Deoxycholic acid

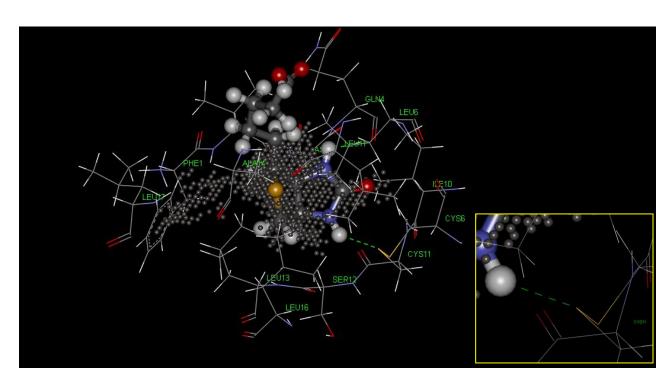


Figure 2a
Bioconjugate from Human Insulin Monomer (PDB ID: 1HLS) and Vitamin H is illustrated by Discovery Studio software. Vitamin H conjugated at CYS A11, GLN B4 and HIS B10 aminoacids of Insulin Monomer. The inner figure illustrates the CYS 11 amino acid of Insulin-A chain conjugates with Vitamin H.

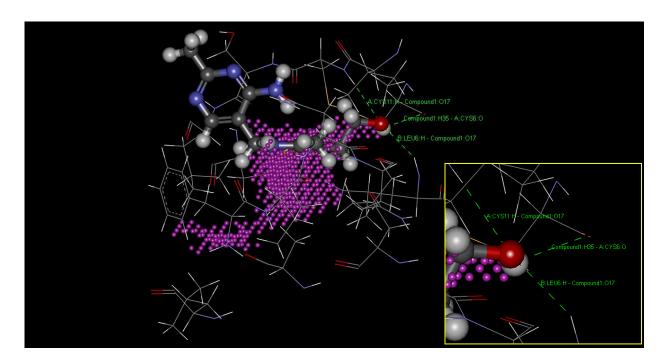


Figure 2b
Bioconjugate from Human Insulin Monomer (PDB ID: 1HLS) and Vitamin B1 is illustrated by Discovery Studio software. Vitamin B1 conjugated at CYS A6, CYS A11 and LEU B6 aminoacids of Insulin Monomer. The inner figure illustrates the CYS 6, CYS 11 amino acids of Insulin-A chain and LEU 6 amino acid of Insulin-B chain conjugates with Vitamin B1.

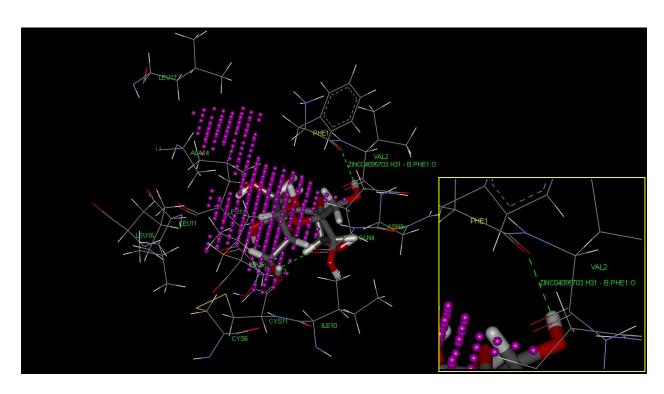


Figure 2c
Bioconjugate from Human Insulin Monomer (PDB ID: 1HLS) and Inulin is illustrated by Discovery Studio software. Inulin conjugated at PHE B1 aminoacid of Insulin Monomer. The inner figure illustrates the PHE 1 amino acid of Insulin-B chain conjugates with Inulin.

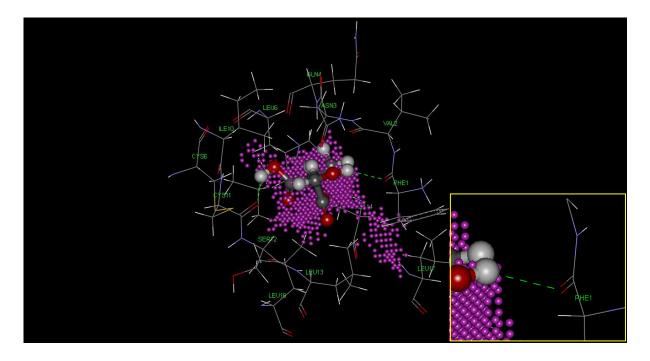


Figure 2d
Bioconjugate from Human Insulin Monomer (PDB ID: 1HLS) and Poly (lactic-co-glycolic acid) is illustrated by Discovery Studio software. Poly (lactic-co-glycolic acid) conjugated at PHE B1 and CYS A11 aminoacid of Insulin Monomer. The inner figure illustrates the PHE 1 amino acid of Insulin-B chain conjugates and with Poly (lactic-co-glycolic acid).

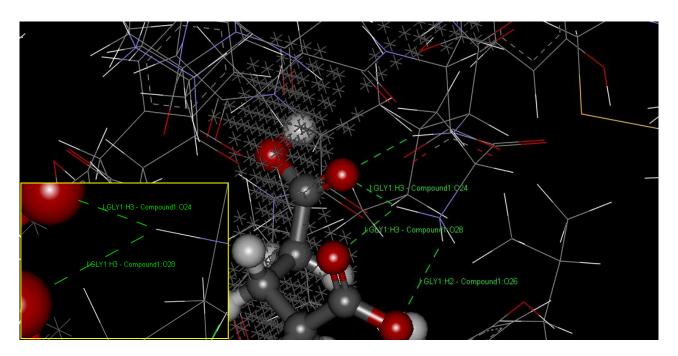
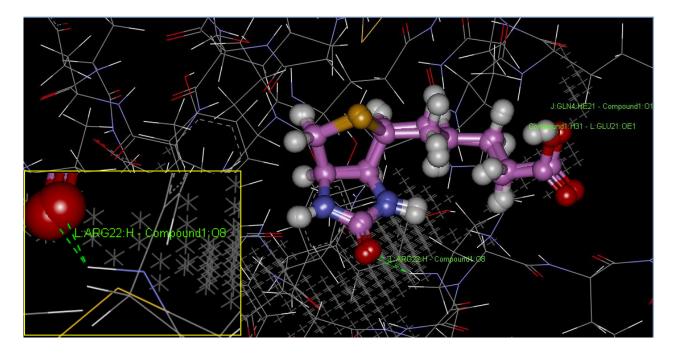


Figure 3a
Bioconjugate from Human insulin hexamer (PDB ID: 1AIO) and Vitamin M is illustrated by Discovery Studio software. Vitamin M conjugated at GLY A1 and THR B27 aminoacids of Insulin hexamer. The inner figure illustrates the GLY 1 amino acid of Insulin-A chain conjugates with Vitamin M.



Bioconjugate from Human insulin hexamer (PDB ID: 1AIO) and Vitamin H is illustrated by Discovery Studio software. Vitamin H conjugated at GLN B4 and ARG B22 aminoacids of Insulin hexamer. The inner figure illustrates the ARG 22 amino acid of Insulin-B chain conjugates with Vitamin H.

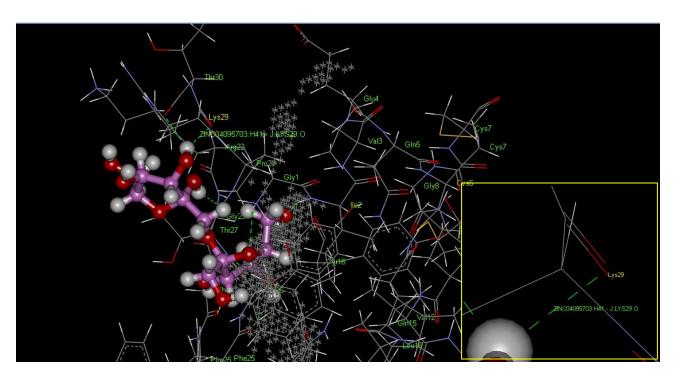


Figure 3c
Bioconjugate from Human insulin hexamer (PDB ID: 1AIO) and Inulin is illustrated by Discovery Studio software. Inulin conjugated at LYS B29 aminoacid of Insulin hexamer. The inner figure illustrates the LYS 29 amino acid of Insulin-B chain conjugates with Inulin.

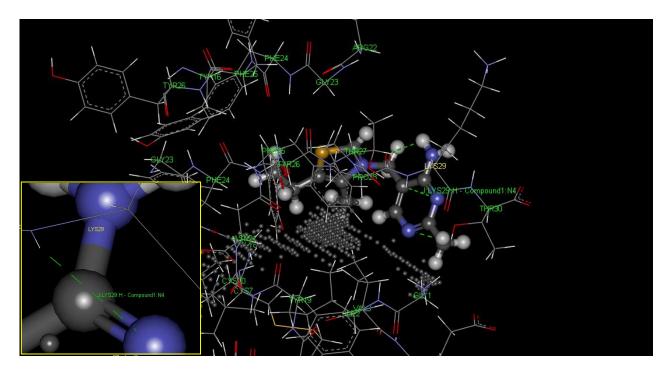


Figure 3d
Bioconjugate from Human insulin hexamer (PDB ID: 1AIO) and Vitamin B1 is illustrated by Discovery Studio software. Vitamin B1 conjugated at LYS B29 aminoacid of Insulin hexamer. The inner figure illustrates the LYS 29 amino acid of Insulin-B chain conjugates with Vitamin B1.

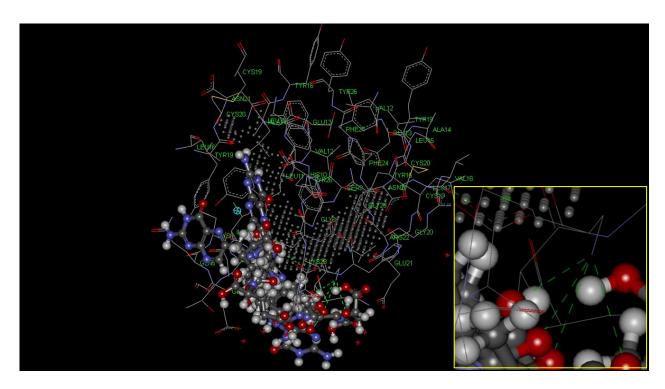


Figure 4a
Bioconjugate from Insulin Lispro (PDB ID: 1 LPH) and Vitamin M is illustrated by Discovery Studio software. Vitamin M conjugated at GLY A1, ILE
A2, VAL A3, GLU A4, TYR A19, GLN B4, HIS B5, THR B27, LYS B28 and THR B30 aminoacids of Insulin Lispro. The inner figure illustrates the LYS 28
amino acid of Insulin-B chain conjugates with Vitamin M.

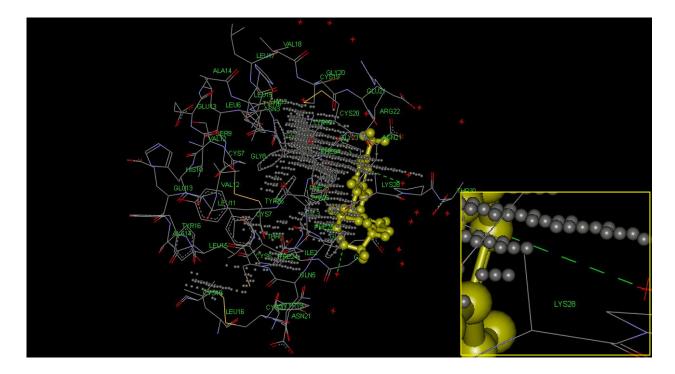


Figure 4b
Bioconjugate from Insulin Lispro (PDB ID: 1 LPH) and Vitamin B1 is illustrated by Discovery Studio software. Vitamin B1 conjugated at GLU A4 and LYS B28 aminoacids of Insulin Lispro. The inner figure illustrates the LYS 28 amino acid of Insulin-B chain conjugates with Vitamin B1.

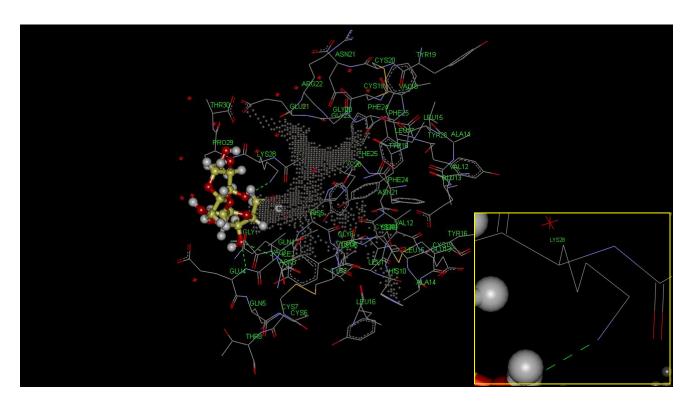


Figure 4c
Bioconjugate from Insulin Lispro (PDB ID: 1 LPH) and Inulin is illustrated by Discovery Studio software. Inulin conjugated at GLY A1, VAL A3, GLU
A4 and LYS B28 aminoacids of Insulin Lispro. The inner figure illustrates the LYS 28 amino acid of Insulin-B chain conjugates with Inulin.

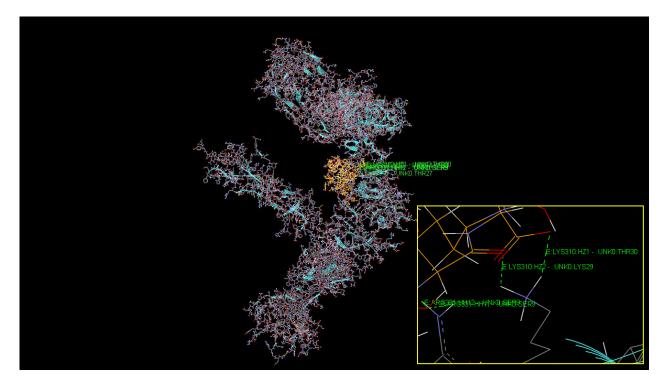


Figure 5a Interaction results of Oral insulin conjugates (Insulin Monomer (1HLS)- DDM Conjugates) with Insulin Receptor (IR). It does not show any interaction in leucine-rich repeat domain (L1, residues 1-157) and in C-terminus of the α -chain (α CT, residues 704-715). The inner figure shows the interaction in LYS310 aminoacid of IR which is not responsible for initiation of therapeutic effect.

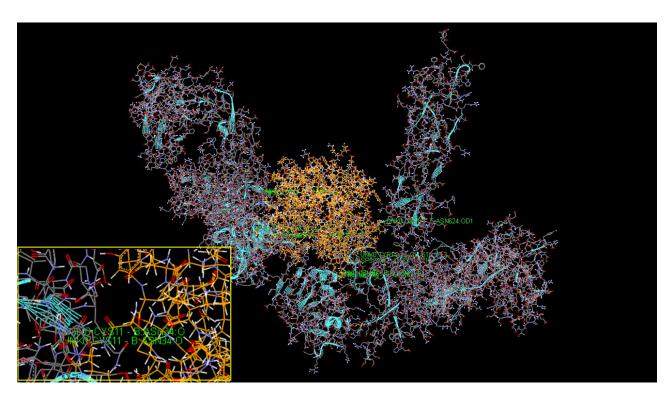


Figure 5b Interaction results of Oral insulin conjugates (Insulin Hexamer (1AIO)- DDM Conjugates)- DDM Conjugates) with Insulin Receptor (IR). It shows the interaction in ARG86, ASN34 of leucine-rich repeat domain (L1, residues 1-157) and no interaction in C-terminus of the α -chain (α CT, residues 704-715). The inner figure shows the interaction in ASN34 aminoacid of IR which is responsible for initiation of therapeutic effect.

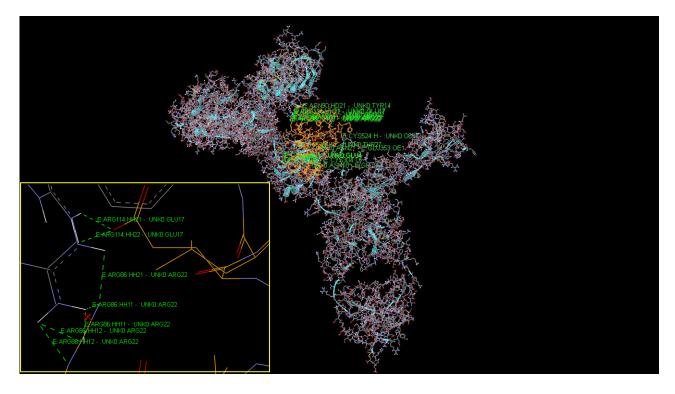


Figure 5c Interaction results of Oral insulin conjugates (Insulin Lispro (1LPH) - DDM Conjugates) with Insulin Receptor (IR). It shows the interaction in ARG86, ASN90 and ARG114 of leucine-rich repeat domain (L1, residues 1-157) and no interaction in C-terminus of the α -chain (α CT, residues 704-715). The inner figure shows the interaction in ARG86, ARG114 aminoacids of IR which is responsible for initiation of therapeutic effect.

| Filtration Criteria by experimental text mining | | | | | | | | | |
|---|---|--|--|---|---|--|--|--|---|
| S No | Carrier | Database & Identification Number | Is it Mono- disperse while participate in Drug delivering Conjugate? | Is it Short-chain (low- molecular weight (<2000Da))? (in Daltons) | Is it Biocompatible & Biodegradable? | Is it lipophilic? (Bioavailability ; Efficient intestinal transport) | Is it physically stability against gastric acids and proteolyti c enzymes? | Is it inert while participate in Drug delivering Conjugate (no biological activity)? | Is it non- toxic? |
| C1 | Vitamin B12 (cobalamin) | CHEBI ID:30411 | Mono- disperse ³⁴ | 1,357 35 | Biocompatible & Biodegradable ³⁶⁻ | Oral bioavailability is high ³⁶⁻³⁹ | Stable ^{37,38,} 40,41 | Inert ⁴² | Non-toxic & Anti mutagenic ⁴³ , |
| C2 | Vitamin H (Biotin) | CHEBI ID:15956 | Mono- disperse ⁴⁵ | 244 | Biocompatible & Biodegradable ⁴⁶⁻ | Efficient intestinal transport ⁴⁶⁻⁴⁸ | Stable ⁴⁶⁻⁴⁸ | Inert ⁴⁹ | Non –toxic ⁵⁰ |
| C3 | Folic acid (Vitamin M / Vitamin B9) | CHEBI ID:27470 | Mono- disperse ⁵¹ | 441.40 | Biocompatible & Biodegradable ^{52,5} | Oral bioavailability is high ^{54,55} | Stable ^{54,55} | No literature | Non – toxic ⁵⁴⁻⁵⁶ |
| C4 | Vitamin B1 (Thiamin) | CHEMBL ID: 1547 | No literature | 265.112 | Biocompatible & Biodegradable ⁵⁷ | Oral bioavailability is high ⁵⁸ | Stable ⁵⁸ | Inert ⁵⁹ | Non-toxic ⁶⁰ |
| C5 | L-Carnitine (Vitamin BT) | CHEMBL ID: 1149 | No literature | 162.113 | Biocompatible & Biodegradable ⁶¹⁻ | Efficient intestinal transport ⁶¹⁻⁶⁵ | Stable ⁶¹⁻⁶⁵ | No literature | Non –toxic ⁶⁶ |
| C6 | Poly-N- vinylpyrrolid one | Pubchem Compound ID: 6917 | Mono- disperse ⁶⁷⁻ | 11.141 | Biocompatible & Biodegradable ⁶⁹ | Oral bioavailability is low ^{70,71} | Stable ⁷²⁻⁷³ | Inert ⁷⁴ | Moderately toxic ⁷⁵ |
| C7 | Inulin | Zinc ID: 12358861 | Mono- disperse ⁷⁶ | 342.297 | Biocompatible & Biodegradable ⁷⁷ | Oral bioavailability is high ⁷⁸ | Stable ⁷⁹⁻⁸¹ | Inert ^{82,83} | Non – toxic ⁸⁴⁻⁸⁷ |
| C8 | Poly Cysteine | DrugBank ID: DB00151 | Mono- disperse ⁸⁸ | 121.158 89 | Biocompatible & Biodegradable ^{90,9} | Hydrophilic; poor intestinal absorption 92,93 | Stable in the presence of the peptidase α- chymotry psin, increase insulin stability against | No literature | Non –toxic ⁹⁵ |

| | | | | | | | enzymatic | | |
|-----|---------------------------------------|---------------------------|--|--|---|--|---|---------------------------------|--|
| | | | | | | | degradati on ⁹⁴ | | |
| C9 | Chitosan | ChemSpider ID: 2342878 | Mono- disperse ⁹⁶⁻ 98 | 501.482 | Biocompatible & Biodegradable ^{97,9} 9-103 | intestinal permeability is Moderate ⁹⁹⁻ | Stable ⁹⁹⁻ 102 | Inert ^{99,102} | Non – toxic ^{99,102} |
| C10 | Pectin | KEGG ID: C00714 | Mono- disperse ¹⁰⁵ | 194.139 | Biocompatible & Biodegradable (Blood Compatible) ¹⁰⁶⁻¹⁰⁹ | intestinal permeability is Moderate ¹⁰⁸ | Stable (Colon specific delivery) ¹¹ | No literature | Non – toxic ¹⁰⁹ |
| C11 | Poly(propyle ne glycol) | CHEBI ID:53262 | Mono- disperse ^{112,1} | 76.094 | Biocompatible & Biodegradable ¹¹⁴ | Oral bioavailability is high ¹¹⁵⁻¹¹⁶ | Stable (protectio n of encapsula ted substance s from degradati on) ¹¹⁷ | Inert ¹¹⁸⁻¹²² | Moderately Toxic ¹²³⁻¹²⁵ Less toxic than PEG ¹²⁶ , 127 |
| C12 | Poly(propyle ne imine) | CHEBI ID: 53266 | Mono- disperse ¹²⁸⁻ 129 | Molecular weight varies based on length of chain | Biocompatible & Biodegradable ¹³⁰ | Lipophilic ¹³¹ | Stable ¹³⁰ | No literature | Moderately Toxic ¹³² |
| C13 | Poly (lactic- co-glycolic acid) | CHEBI:53493 | Mono- disperse ^{133,1} 34 | Molecular weight varies based on length of chain | Biocompatible & Biodegradable ¹³⁵⁻ | Lipophilic ^{138,139} | Stable ¹³⁶⁻ | Inert ¹³⁷ | Non – toxic ¹⁴⁰ |
| C14 | Deoxycholic acid | DrugBank ID: DB03619 | Mono- disperse ¹⁴¹ | 392.57 | Biocompatible & Biodegradable ^{142,} | Lipophilic ^{144,145} | Stable 144,145 | Not inert ^{144,145} | Moderately Toxic ¹⁴⁶ |

| Table 2 | | | | | |
|---------|-------------------------------------|--------------------|------------------|-----------------------|-------------------------|
| Pharmac | ophoric features of carriers | | | | |
| Carrier | Carrier | Number of Acceptor | Number of Donors | Number of | Number of |
| No | | in molecule | in molecule | hydrophobic Region | Pharmacophore principle |
| C1 | Vitamin B12 (cobalamin) | 8 | 7 | 29 | Nil |
| C2 | Vitamin H (Biotin) | 2 | 2 | 5 | 6 |
| C3 | Folic acid (Vitamin M / Vitamin B9) | 4 | 4 | 7 | 10 |
| C4 | Vitamin B1 (Thiamin) | 1 | 1 | 7 | 10 |
| C5 | L-Carnitine (Vitamin BT) | 1 | 0 | 6 | 2 |
| C6 | Poly-N-vinylpyrrolidone | 1 | 0 | 4 | Nil |
| C7 | Inulin | 11 | 0 | 12 | 10 |
| C8 | Poly Cysteine | 1 | 1 | 1 | 7 |
| C9 | Chitosan | 1 | 1 | 1 | 10 |
| C10 | Pectin | 3 | 0 | 6 | 10 |
| C11 | Poly(propylene glycol) | 1 | 0 | 4 | 4 |
| C12 | Poly(propylene imine) | 0 | 1 | 3 | Nil |
| C13 | Poly (lactic-co-glycolic acid) | 2 | 0 | 2 | 8 |
| C14 | Deoxycholic acid | 2 | 0 | 14 | 7 |

Table 3
Physico-chemical properties of drug delivering molecules

| | | ADME Descriptors | | | | | | |
|-------|----------|-----------------------|---------------------------------------|--------------------|----------------|--------------------------|------------------------------|--|
| S. No | Carriers | Aqueous Solubility | Blood Brain barrier Penetration | CYP 2D6 Binding | Hepatotoxicity | Intestinal Absorption | Plasma Protein Binding | |
| 1 | C1 | -9.057 | 4.0 | 0.277 | 0.509 | 3.0 | 0.0 | |
| 2 | C2 | -1.432 | -1.229 | 0.069 | 0.264 | 0.0 | 0.0 | |
| 3 | C3 | -3.378 | 4.0 | 0.277 | 0.662 | 3.0 | 0.0 | |
| 4 | C4 | -1.335 | -1.253 | 0.336 | 0.423 | 0.0 | 0.0 | |
| 5 | C5 | 2.734 | 4.0 | 0.059 | 0.066 | 3.0 | 0.0 | |
| 6 | C6 | -0.550 | 4.0 | 0.059 | 0.324 | 1.0 | 0.0 | |
| 7 | C7 | 0.894 | 4.0 | 0.108 | 0.0139 | 3.0 | 0.0 | |
| 8 | C8 | 0.335 | -1.362 | 0.059 | 0.033 | 0.0 | 0.0 | |
| 9 | C9 | 1.736 | 4.0 | 0.029 | 0.013 | 3.0 | 0.0 | |
| 10 | C10 | 1.595 | 4.0 | 0.029 | 0.059 | 3.0 | 0.0 | |
| 11 | C11 | 0.907 | -1.039 | 0.0590 | 0.059 | 0.0 | 0.0 | |
| 12 | C12 | -0.097 | 4.0 | 0.059 | 0.324 | 1.0 | 0.0 | |
| 13 | C13 | 0.768 | -1.713 | 0.059 | 0.006 | 0.0 | 0.0 | |
| 14 | C14 | -4.409 | -0.154 | 0.485 | 0.026 | 0.0 | 1.0 | |

C1 - Vitamin B12 (cobalamin); C2 - Vitamin H (Biotin); C3 - Folic acid (Vitamin M / Vitamin B9); C4 - Vitamin B1 (Thiamin); C5 - L-Carnitine (Vitamin BT); C6 - Poly-N-vinylpyrrolidone; C7; Inulin; C8 - Poly Cysteine; C9 - Chitosan; C10 - Pectin; C11 - Poly(propylene glycol); C12 - Poly(propylene imine); C13 - Poly (lactic-co-glycolic acid); C14 - Deoxycholic acid

Table 4 Toxicity studies for Drug delivering molecules by Discovery Studio and Toxtree

| Toxi | city Predicti | on by Discovery St | udio | | | | | | Toxicity Prediction by Toxtree |
|----------|---------------|----------------------------------|-----------------|---|--|---------------------|-----------------------|-----------------------------|--------------------------------|
| S. No | Carriers | FDA Rodent Carcinogenicity | Mutagenecity | Rat oral LD50 (g/Kg Body weight) | Rat Maximum tolerated dose (g/Kg Body weight) | Skin Irritancy | Skin sensitization | Aerobic Biodegradability | Toxicity |
| 1 | C1 | Non- carcinogen | Non- mutagen | 0.093 | 0.000 | Mild- Irritant | Non- sensitizer | Degradable | High |
| 2 | C2 | Non- carcinogen | Non- mutagen | 1.109 | 0.193 | Non- Irritant | Non- sensitizer | Degradable | Low |
| 3 | C3 | Non- carcinogen | Non- mutagen | 2.819 | 1.391 | Non- Irritant | Weak- sensitizer | Non- Degradable | High |
| 4 | C4 | carcinogen | Non- mutagen | 1.308 | 0.097 | Non- Irritant | Strong- sensitizer | Non- Degradable | Low |
| 5 | C5 | Non- carcinogen | Non- mutagen | 1.101 | 0.175 | Mild- Irritant | Non- sensitizer | Degradable | Low |
| 6 | C6 | carcinogen | Non- mutagen | 1.634 | 0.181 | Mild- Irritant | Non- sensitizer | Degradable | High |
| 7 | C7 | Non- carcinogen | Non- mutagen | 20.789 | 0.000 | Mild- Irritant | Non- sensitizer | Degradable | Low |
| 8 | C8 | Non- carcinogen | Non- mutagen | 0.514 | 0.653 | Non- Irritant | Non- sensitizer | Degradable | Low |
| 9 | C9 | Non- carcinogen | Non- mutagen | 3.241 | 0.268 | Mild- Irritant | Non- sensitizer | Degradable | High |
| 10 | C10 | Non- carcinogen | Non- mutagen | 3.576 | 0.525 | Non- Irritant | Non- sensitizer | Degradable | Low |
| 11 | C11 | Non- carcinogen | Non- mutagen | 12.098 | 0.187 | Mild- Irritant | Non- sensitizer | Degradable | High |
| 12 | C12 | Non- carcinogen | Non- mutagen | 0.055 | 0.089 | Mild- Irritant | Non- sensitizer | Non- Degradable | High |
| 13 | C13 | Non- carcinogen | Non- mutagen | 2.982 | 0.427 | Non- Irritant | Non- sensitizer | Degradable | Low |
| 14 | C14 | Non- carcinogen | Non- mutagen | 6.358 | 0.190207 | Severe- Irritant | Weak- sensitizer | Degradable | High |

FDA – Food & Drug Administration;

C1 - Vitamin B12 (cobalamin); C2 - Vitamin H (Biotin); C3 - Folic acid (Vitamin M / Vitamin B9); C4 - Vitamin B1 (Thiamin); C5 - L-Carnitine (Vitamin BT); C6 - Poly-N-vinylpyrrolidone; C7; Inulin; C8 - Poly Cysteine; C9 - Chitosan; C10 - Pectin; C11 -

Poly(propylene glycol); C12 - Poly(propylene imine); C13 - Poly (lactic-co-glycolic acid); C14 - Deoxycholic acid

| Table | | | | | | | |
|-------|------------------------|--------------|-------------------|----------------------|---------------------|------------------|----------|
| Conju | gation results of Huma | | ner (PDB ID: 1HLS |), with all listed d | rug delivering mole | cules individual | ly |
| S.No | Conjugate | Binding site | LIP DOCK | Binding site | LIP DOCK | Other | LIP DOCK |
| 5.140 | Conjugate | (LYS B29) | SCORE - | (PHE B1) | SCORE - | Binding site | SCORE |
| C1 | Vitamin B12 | - | - | - | - | - | - |
| C2 | | | | | | CYS A11 | |
| | Vitamin H | - | - | - | - | HIS B10 | 86.2835 |
| | | | | | | GLN B4 | |
| C3 | Vitamin M | - | - | - | - | - | - |
| C4 | | | | | | CYS A6 | |
| | Vitamin B1 | - | - | - | - | CYS A11 | 94.1144 |
| | | | | | | LEU B6 | |
| C5 | Mitamain DT | | | | | LEU A13 | 60.0502 |
| | Vitamin BT | - | - | - | - | VAL B2 | 68.0592 |
| C6 | poly-N- | | | | | | |
| | vinylpyrrolidone | - | - | - | - | - | - |
| C7 | Inulin | - | - | PHE B1 | 117.663 | - | - |
| C8 | Poly Cysteine | - | - | - | - | GLN B4 | 53.1597 |
| C9 | | | | | | CYS A11, | |
| | Chitosan | - | - | - | - | VAL B2, | 74.4251 |
| | | | | | | ASN B3 | |
| C10 | PECTIN | - | - | - | - | CYS A11 | 63.0902 |
| C11 | POLY (PROPYLENE | | | | | VAL D2 | 76.0220 |
| | GLYCOL) | - | - | - | - | VAL B2 | 76.0238 |
| C12 | poly(propylene | | | | | | |
| | imine) | - | - | - | - | - | - |
| C13 | Poly (lactic-co- | | | DUE D4 | 60 6727 | C)(C 111 | 60 6727 |
| | glycolic acid) | - | - | PHE B1 | 68.6737 | CYS A11 | 68.6737 |
| C14 | Deoxycholic acid | - | - | - | - | - | - |

| Table | 6 gation results of Huma | n insulin hexame | er (PDR ID: 1AIO) | with all listed dru | ug delivering molec | ules individually | v. |
|-------|------------------------------------|---------------------------|---------------------|--------------------------|---------------------|-----------------------|-------------------|
| S.No | Conjugate | Binding site (LYS B29) | LIP DOCK SCORE - | Binding site (PHE B1) | LIP DOCK SCORE - | Other Binding site | LIP DOCK SCORE |
| C1 | Vit B12 | - | - | - | - | - | - |
| C2 | Vit H | - | - | - | - | GLN B4 ARG B22 | 103.231 |
| C3 | Vit M | - | - | - | - | GLY A1 THR B27 | 114.324 |
| C4 | Vit B1 | LYS B29 | 79.8834 | - | - | - | - |
| C5 | Vit BT | - | - | - | - | ARG B22 | 84.7767 |
| C6 | poly-N- vinylpyrrolidone | - | - | - | - | - | - |
| C7 | Inulin | LYS B29 | 94.3543 | - | - | - | - |
| C8 | Poly Cysteine | - | - | - | - | TYR B16 GLU B21 | 58.5629 |
| С9 | Chitosan | - | - | - | - | TYR B16 TYR B26 | 90.016 |
| C10 | PECTIN | - | - | - | - | GLN B4 | 91.0549 |
| C11 | POLY (PROPYLENE GLYCOL) | - | - | - | - | GLU B21 ARG B22 | 71.5126 |
| C12 | poly(propylene imine) | - | - | - | - | - | - |
| C13 | Poly (lactic-co- glycolic acid) | - | - | - | - | GLY B20 ARG B22 | 82.2602 |
| C14 | Deoxycholic acid | - | - | - | - | GLY A1 ILE A2 | 60.763 |

| Table Conjug | / gation results of Insuli | n Lispro (PDB ID: | 1 LPH), with all l | isted drug deliver | ing molecules indi | vidually | |
|--------------|------------------------------------|-------------------|--------------------|--------------------|--------------------|--|----------|
| S.No | Conjugate | Binding site | LIP DOCK | Binding site | LIP DOCK | Other | LIP DOCK |
| | | (LYS B28) | SCORE - | (PHE B1) | SCORE - | Binding site | SCORE |
| C1 | Vit B12 | - | - | - | - | - | - |
| C2 | Vit H | - | - | - | - | - | - |
| C3 | Vit M | LYS B28 | 131.57 | - | - | GLY A1 ILE A2, VAL A3, GLU A4, TYR A19, GLN B4 HIS B5 THR B27, THR B30 | 131.57 |
| C4 | Vit B1 | LYS B28 | 89.8971 | - | - | GLU A4 | 89.8971 |
| C5 | Vit BT | - | - | | | GLU A4, GLN B4 | 58.6757 |
| C6 | poly-N- vinylpyrrolidone | - | - | - | - | - | - |
| C7 | Inulin | LYS B28 | 76.2195 | - | - | GLY A1 VAL A3, GLU A4 | 76.2195 |
| C8 | Poly Cysteine | - | - | - | - | GLN B4 GLU A4 | 48.858 |
| C9 | Chitosan | - | - | - | - | GLY A1 ILE A2 GLU A4 THR B27 | 67.1639 |
| C10 | PECTIN | - | - | - | - | GLY A1 GLU A4 | 73.2077 |
| C11 | POLY (PROPYLENE GLYCOL) | - | - | - | - | GLY A1 | 57.6819 |
| C12 | poly(propylene imine) | - | - | - | - | - | - |
| C13 | Poly (lactic-co- glycolic acid) | - | - | - | - | GLY A1, ILE A2, GLU A4, VAL A3, THR B27, GLN 44 | 64.8442 |
| C14 | Deoxycholic acid | _ | _ | - | _ | - | - |

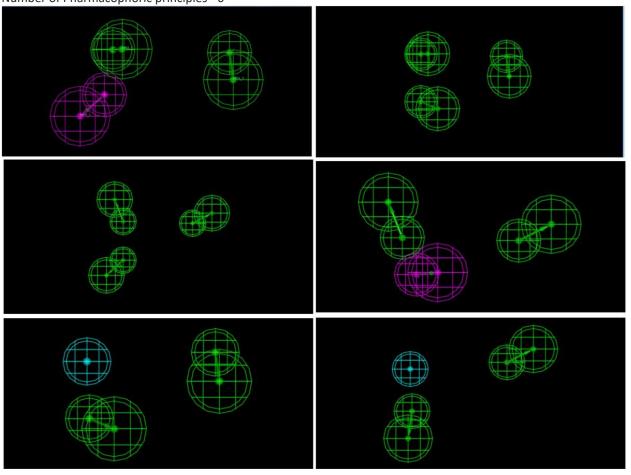
| Table 8 | | | | | | | | | |
|----------|---|--|---|--|--|--|--|--|--|
| Interact | Interaction results of Oral insulin conjugates (OIC) with Insulin Receptor (IR) | | | | | | | | |
| S. No | Conjugates | Interaction with leucine-rich repeat domain (L1, residues 1-157) | Interaction with C-terminus of the α -chain (α CT, residues 704-715) | | | | | | |
| 1 | Insulin Monomer (1HLS)- DDM Conjugates | No Interaction | No Interaction | | | | | | |
| 2 | Insulin Hexamer (1AIO)- DDM Conjugates | ARG86 ASN34 | No Interaction | | | | | | |
| 3 | Insulin Lispro (1LPH) - DDM Conjugates | ARG86 ASN90 ARG114 | No Interaction | | | | | | |

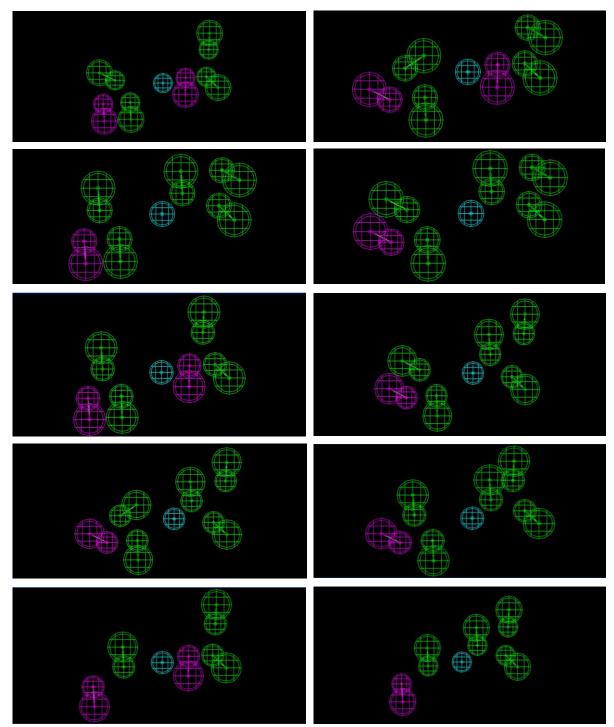
Supplementary figure 1

Pharmacophoric principles of Drug delivering molecules are illustrated by Discovery Studio software. Acceptors (Green in color), Donors (Magenta in color) of Pharmacophoric principles of all Drug delivering molecules are demonstrated and differentiated by color. C1 - Vitamin B12 (cobalamin); C2 - Vitamin H (Biotin); C3 - Folic acid (Vitamin M / Vitamin B9); C4 - Vitamin B1 (Thiamin); C5 - L-Carnitine (Vitamin BT); C6 - Poly-N-vinylpyrrolidone; C7; Inulin; C8 - Poly Cysteine; C9 - Chitosan; C10 - Pectin; C11 - Poly(propylene glycol); C12 - Poly(propylene imine); C13 - Poly (lactic-co-glycolic acid); C14 - Deoxycholic acid

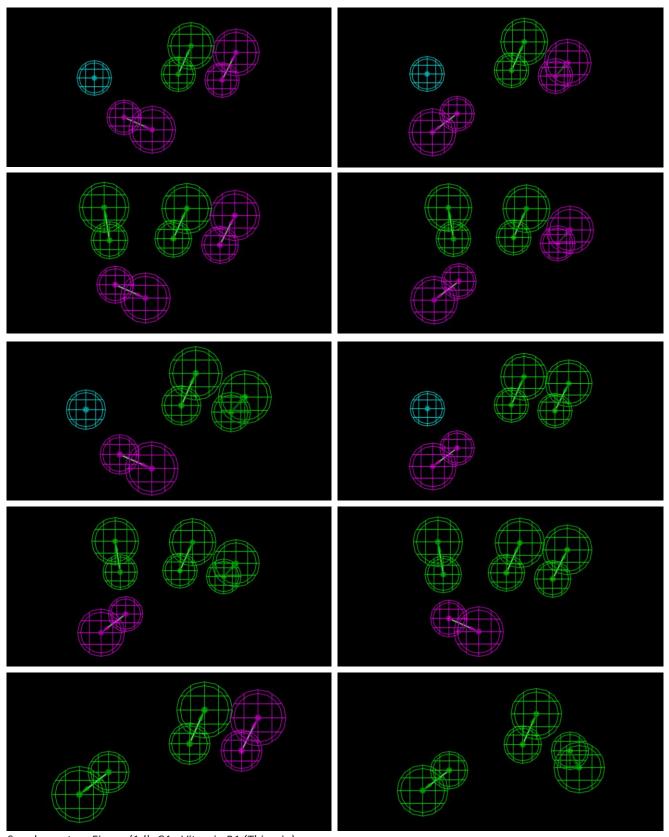
Supplementary Figure (1a): C1 - Vitamin B12 (cobalamin) Number of Pharmacophoric principles — Nil

Supplementary Figure (1b): C2 - Vitamin H (Biotin) Number of Pharmacophoric principles –6



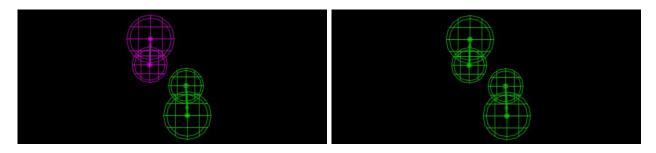


Supplementary Figure (1c): C3 - Folic acid (Vitamin M / Vitamin B9)
Number of Pharmacophoric principles –10

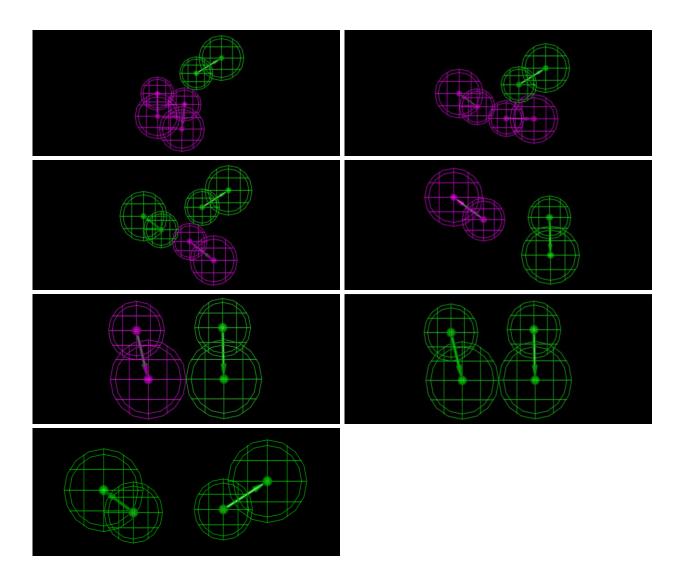


Supplementary Figure (1d): C4 - Vitamin B1 (Thiamin)
Number of Pharmacophoric principles –10

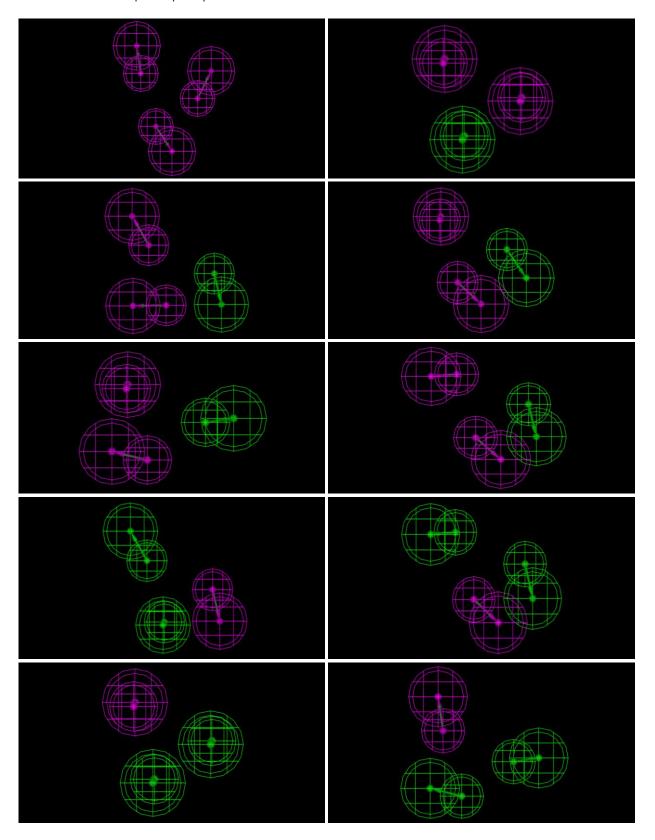
Supplementary Figure (1e): C5 - L-Carnitine (Vitamin BT) Number of Pharmacophoric principles -2

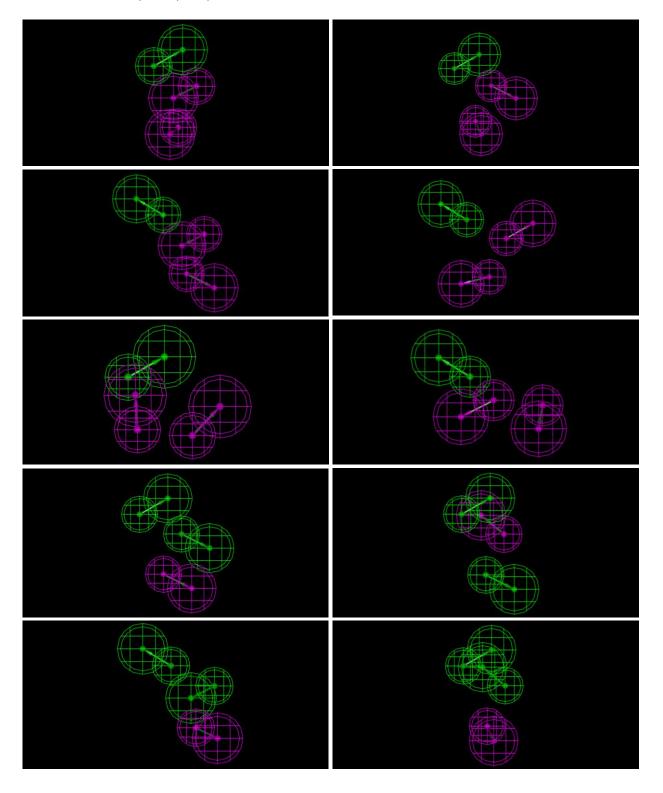


Supplementary Figure (1f): C6- Poly-N-vinylpyrrolidone Number of Pharmacophoric principles —Nil

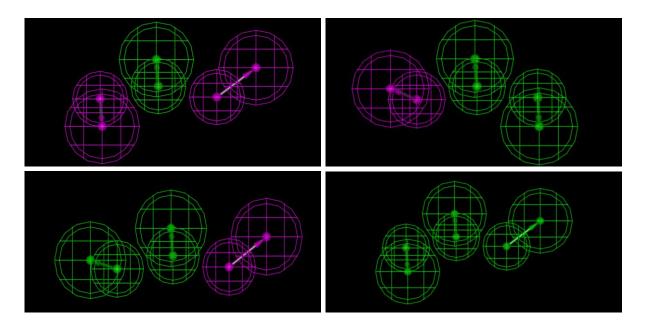


Supplementary Figure (1h): C8- Poly Cysteine Number of Pharmacophoric principles –7

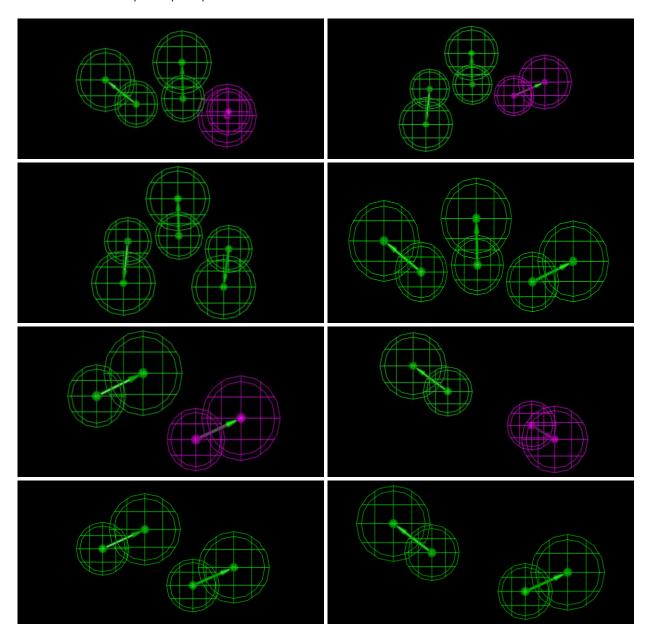


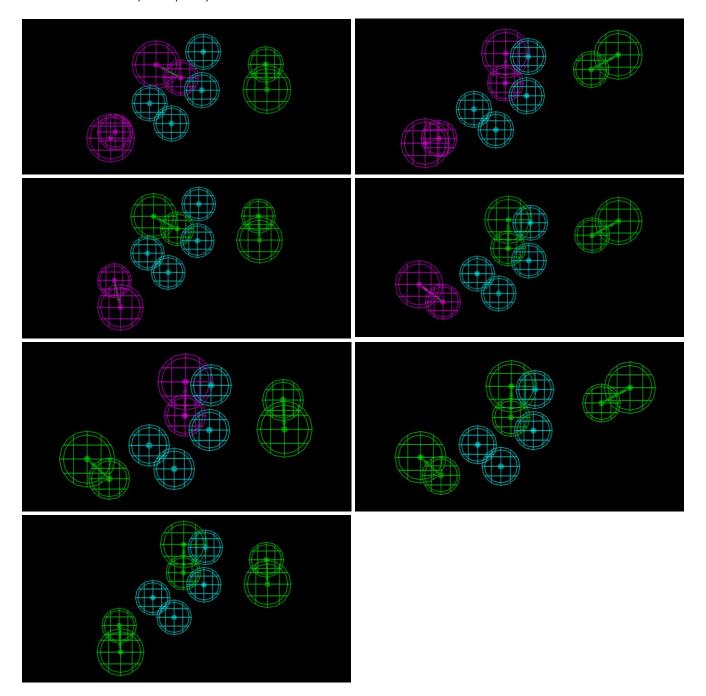


Supplementary Figure (1k): C11 – Poly(propylene glycol) Number of Pharmacophoric principles –4



Supplementary Figure (1L): C12 – Poly(propylene imine) Number of Pharmacophoric principles –Nil

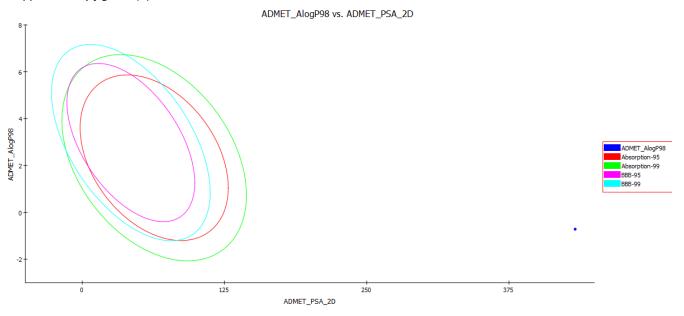




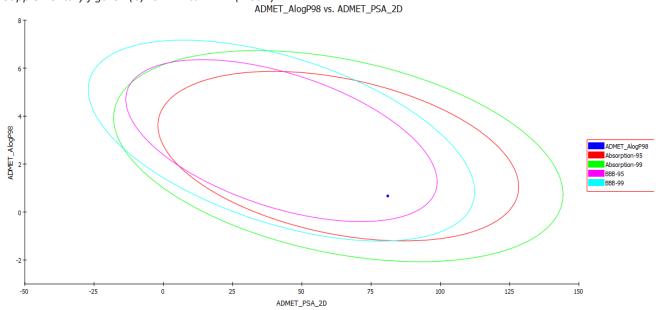
Supplementary figure 2

ADME descriptors of Drug delivering molecules by Discovery Studio; C1 - Vitamin B12 (cobalamin); C2 - Vitamin H (Biotin); C3 - Folic acid (Vitamin M / Vitamin B9); C4 - Vitamin B1 (Thiamin); C5 - L-Carnitine (Vitamin BT); C6 - Poly-N-vinylpyrrolidone; C7; Inulin; C8 - Poly Cysteine; C9 - Chitosan; C10 - Pectin; C11 - Poly(propylene glycol); C12 - Poly(propylene imine); C13 - Poly (lactic-co-glycolic acid); C14 - Deoxycholic acid

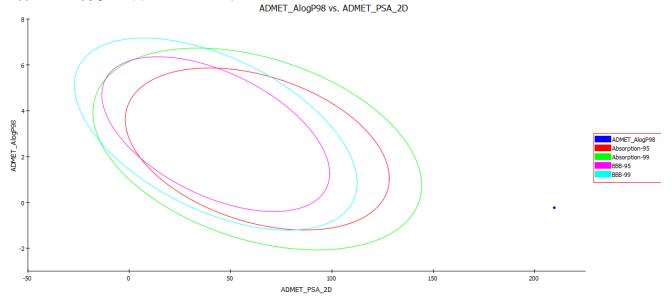
Supplementary figure 2(a)- C1 - Vitamin B12



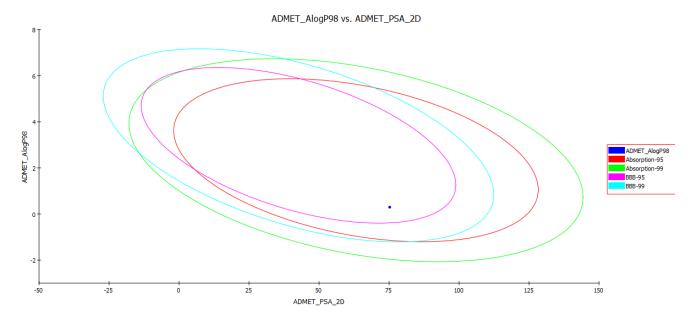
Supplementary figure 2(b)- C2 - Vitamin H (Biotin)



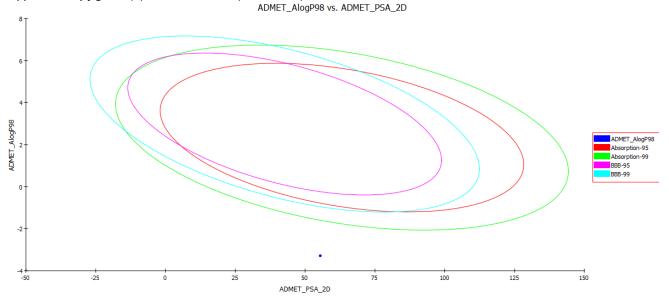
Supplementary figure 2(c)- C3 - Folic acid (Vitamin M / Vitamin B9)



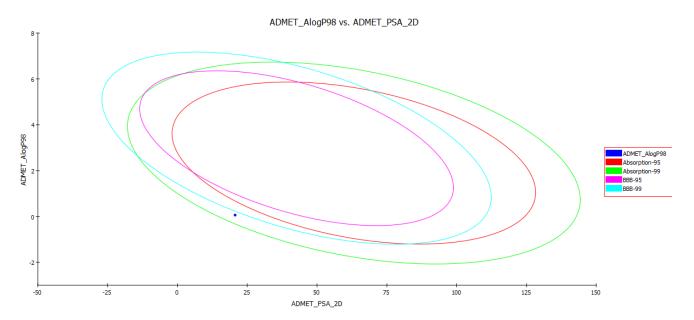
Supplementary figure 2(d)- C4 - Vitamin B1 (Thiamin)

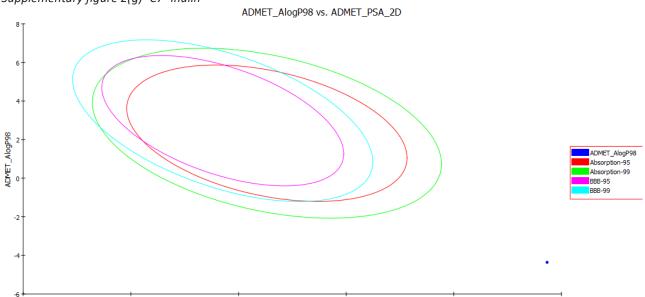


Supplementary figure 2(e)- C5 - L-Carnitine (Vitamin BT)

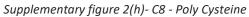


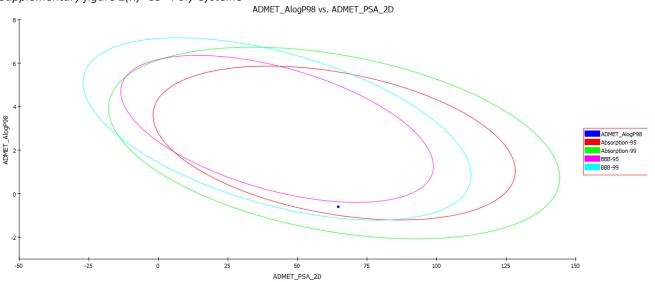
Supplementary figure 2(f)- C6 - Poly-N-vinylpyrrolidone



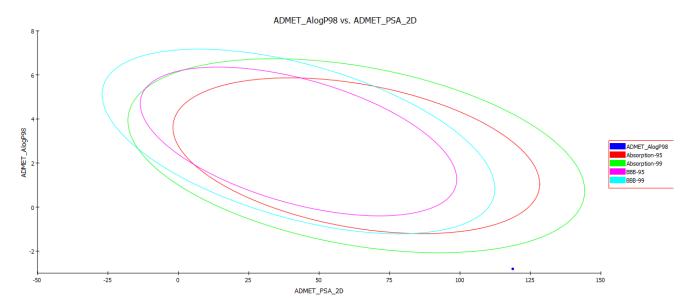


ADMET_PSA_2D

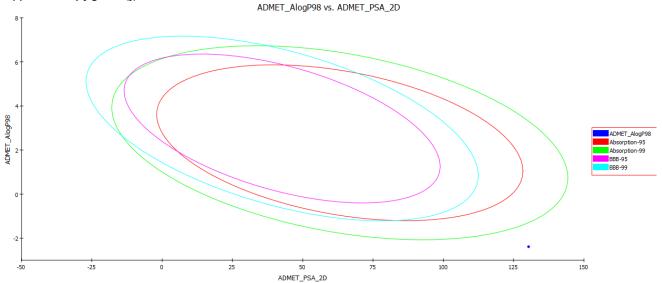




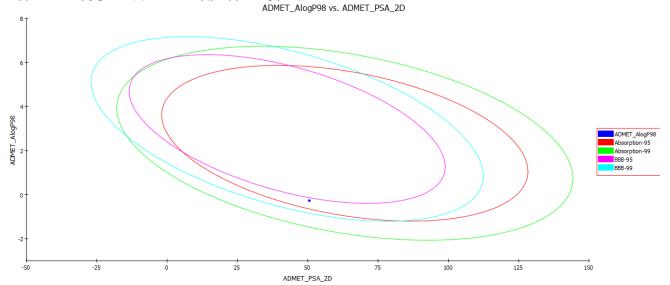
Supplementary figure 2(i)- C9 – Chitosan



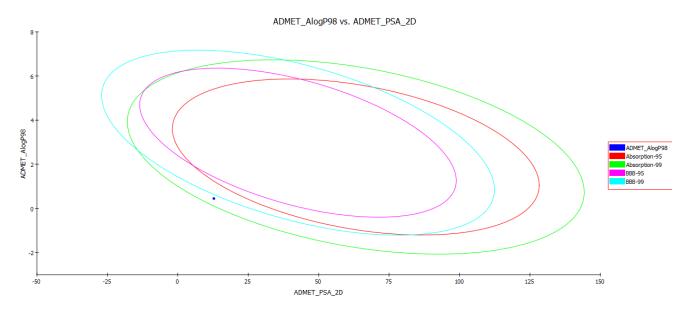




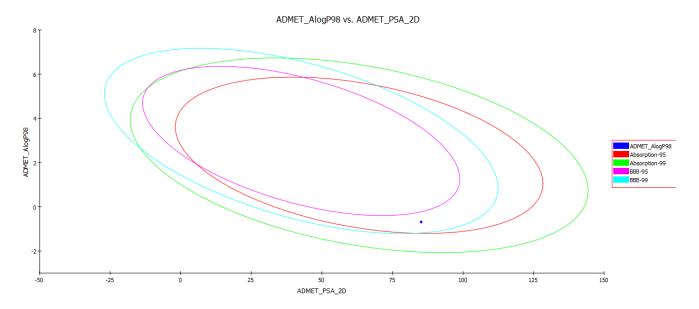
Supplementary figure 2(k)- C11 - Poly(propylene glycol)



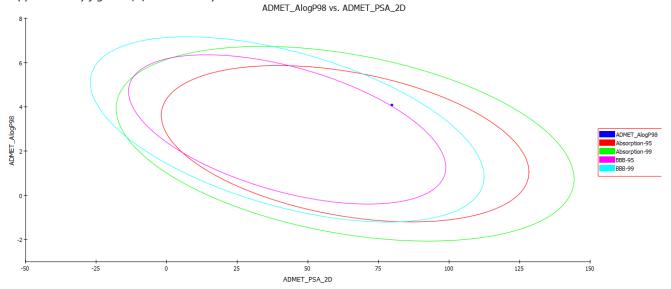
Supplementary figure 2(I)- C12 - Poly(propylene imine)



Supplementary figure 2(m)- C13 - Poly (lactic-co-glycolic acid)



Supplementary figure 2(n)- C14 - Deoxycholic acid

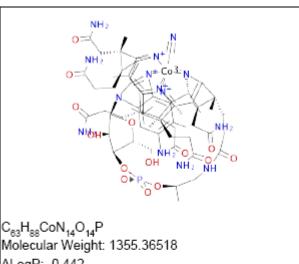


Supplementary figure 3

Toxicity studies for Drug delivering molecules by Discovery Studio; C1 - Vitamin B12 (cobalamin); C2 - Vitamin H (Biotin); C3 - Folic acid (Vitamin M / Vitamin B9); C4 - Vitamin B1 (Thiamin); C5 - L-Carnitine (Vitamin BT); C6 - Poly-N-vinylpyrrolidone; C7; Inulin; C8 -Poly Cysteine; C9 - Chitosan; C10 - Pectin; C11 - Poly(propylene glycol); C12 - Poly(propylene imine); C13 - Poly (lactic-co-glycolic acid); C14 - Deoxycholic acid

Supplementary figure 3(a)- C1 - Vitamin B12 (cobalamin)

FDA Rodent Carcinogenicity



ALogP: -0.442 Rotatable Bonds: 16 Acceptors: 16

Donors: 9

Model Prediction

Prediction: Non-Carcinogen

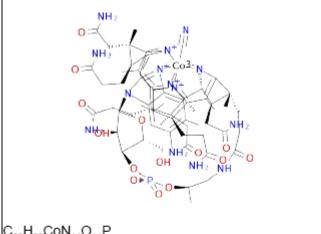
Probability: 0.230 Enrichment: 0.717 Bayesian Score: -1.075

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the category.

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Mutagenecity



C₆₃H₈₈CoN₁₄O₁₄P

Molecular Weight: 1355.36518

ALogP: -0.442 Rotatable Bonds: 16 Acceptors: 16

Donors: 9

Model Prediction

Prediction: Non-Mutagen

Probability: 0.029 Enrichment: 0.053 Bayesian Score: -21.617

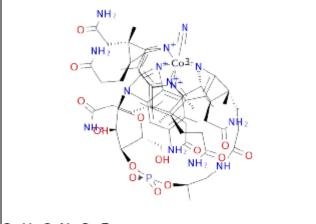
Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the category.

Enrichment: An estimate of enrichment, that is, the increased ikelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

score.

Rat oral LD50 (g/Kg Body weight)

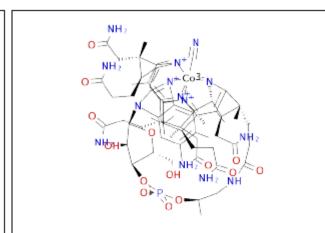


C₆₃H₈₈CoN₁₄O₁₄P

Molecular Weight: 1355.36518

ALogP: -0.442 Rotatable Bonds: 16

Acceptors: 16 Donors: 9



C₆₃H₈₈CoN₁₄O₁₄P

Molecular Weight: 1355.36518

ALogP: -0.442 Rotatable Bonds: 16

Acceptors: 16 Donors: 9

Model Prediction

Prediction: 0.093

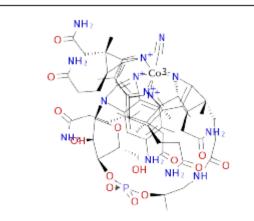
Unit: g/kg_body_weight

Model Prediction

Prediction: 0.000

Unit: g/kg_body_weight

Skin Irritancy Skin sensitization

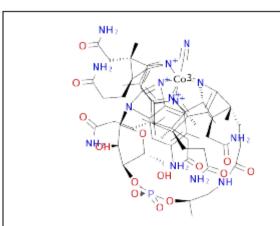


C₆₃H₈₈CoN₁₄O₁₄P

Molecular Weight: 1355.36518

ALogP: -0.442 Rotatable Bonds: 16

Acceptors: 16 Donors: 9



C₆₃H₈₈CoN₁₄O₁₄P

Molecular Weight: 1355.36518

ALogP: -0.442 Rotatable Bonds: 16 Acceptors: 16

Donors: 9

Model Prediction

Prediction: Mild Probability: 0.071 Enrichment: 0.194

Bayesian Score: -10.755

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian score.

Model Prediction

Prediction: Non-Sensitizer

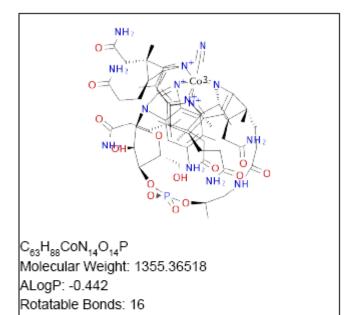
Probability: 0.502 Enrichment: 0.731 Bayesian Score: -4.826

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the category.

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian score.

Aerobic Biodegradability



Model Prediction

Prediction: Degradable

Probability: 0.634 Enrichment: 1.454 Bayesian Score: 3.091

Prediction: Positive if the Bayesian score is above the estimated

Acceptors: 16 Donors: 9

best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

score.

FDA Rodent Carcinogenicity

Mutagenecity

 $C_{10}H_{16}N_2O_3S$

Molecular Weight: 244.31064

ALogP: 0.67

Rotatable Bonds: 5 Acceptors: 4

Donors: 3

C₁₀H₁₆N₂O₃S

Molecular Weight: 244.31064

ALogP: 0.67

Rotatable Bonds: 5

Acceptors: 4 Donors: 3

Model Prediction

Prediction: Non-Carcinogen

Probability: 0.435 Enrichment: 0.845 Bayesian Score: -2.888

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

category. Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian score.

Model Prediction

Prediction: Non-Mutagen

Probability: 0.002 Enrichment: 0.004

Bayesian Score: -29.037

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the ategory.

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category.

Bayesian Score: The standard Laplacian-modified Bayesian

Rat oral LD50 (g/Kg Body weight)

C₁₀H₁₆N₂O₃S

Donors: 3

Molecular Weight: 244.31064

ALogP: 0.67 Rotatable Bonds: 5 Acceptors: 4

Molecular Weight: 244.31064

ALogP: 0.67 Rotatable Bonds: 5 Acceptors: 4 Donors: 3

Model Prediction

Prediction: 1.109 Unit: g/kg_body_weight

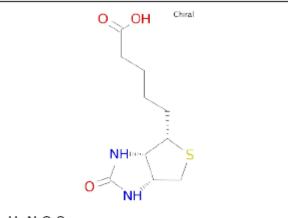
Model Prediction

Prediction: 0.193 Unit: g/kg_body_weight

 $C_{10}H_{16}N_2O_3S$

Molecular Weight: 244.31064

ALogP: 0.67 Rotatable Bonds: 5 Acceptors: 4 Donors: 3



C₁₀H₁₆N₂O₃S

Donors: 3

Molecular Weight: 244.31064

ALogP: 0.67 Rotatable Bonds: 5 Acceptors: 4

Model Prediction

Prediction: Non-Irritant Probability: 0.971 Enrichment: 1.054 Bayesian Score: -0.769

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

Prediction: Non-Sensitizer

Probability: 0.283 Enrichment: 0.412 Bayesian Score: -7.644

Prediction: Positive if the Bayesian score is above the estimated best cutoff value

best cutoff value.
Probability: The esimated probability that the sample is in the

Calegory. Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Aerobic Biodegradability

C₁₀H₁₆N₂O₃S

Molecular Weight: 244.31064

ALogP: 0.67

Rotatable Bonds: 5 Acceptors: 4

Donors: 3

Model Prediction

Prediction: Degradable

Probability: 0.759 Enrichment: 1.739 Bayesian Score: 6.104

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

category.
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category.
Bayesian Score: The standard Laplacian-modified Bayesian

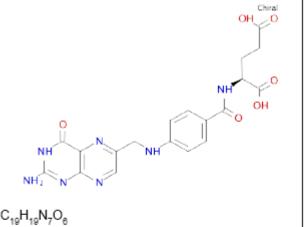
FDA Rodent Carcinogenicity

C₁₀H₁₀N₇O₈

Molecular Weight: 441.39745

ALogP: -0.232 Rotatable Bonds: 9 Acceptors: 11 Donors: 6

Mutagenecity



Molecular Weight: 441.39745

ALogP: -0.232 Rotatable Bonds: 9 Acceptors: 11 Donors: 6

Model Prediction

Prediction: Non-Carcinogen

Probability: 0.210 Enrichment: 0.655 Bayesian Score: -4.767

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian score

Model Prediction

Prediction: Non-Mutagen

Probability: 0.000 Enrichment: 0.000 Bayesian Score: -60.476

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

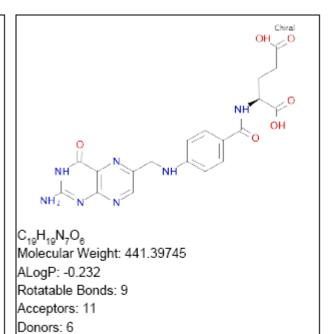
Probability: The esimated probability that the sample is in the category.

Enrichment: An estimate of enrichment, that is, the increased ikelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

C₁₉H₁₉N₇O₆

Molecular Weight: 441.39745

ALogP: -0.232 Rotatable Bonds: 9 Acceptors: 11 Donors: 6



Model Prediction

Prediction: 2.819

Unit: g/kg_body_weight

Model Prediction

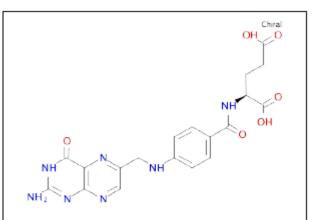
Prediction: 1.391

Unit: g/kg_body_weight

 $C_{19}H_{19}N_7O_6$

Molecular Weight: 441.39745

ALogP: -0.232 Rotatable Bonds: 9 Acceptors: 11 Donors: 6



 $C_{19}H_{19}N_7O_8$

Molecular Weight: 441.39745

ALogP: -0.232 Rotatable Bonds: 9 Acceptors: 11 Donors: 6

Model Prediction

Prediction: Non-Irritant Probability: 0.942 Enrichment: 1.023 Bayesian Score: -1.988

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

Prediction: Weak-Sensitizer

Probability: 0.802 Enrichment: 1.035 Bayesian Score: -2.527

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

category.

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Aerobic Biodegradability

Model Prediction

Prediction: Non-Degradable

Probability: 0.267 Enrichment: 0.612 Bayesian Score: -5.103

Prediction: Positive if the Bayesian score is above the estimated

Acceptors: 11 Donors: 6

best cutoff value. Probability: The esimated probability that the sample is in the

category.

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

score.

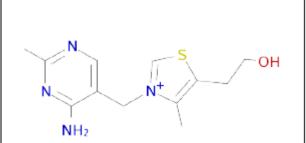
FDA Rodent Carcinogenicity

Mutagenecity

C₁₂H₁₇N₄OS

Molecular Weight: 265.35458

ALogP: 1.048 Rotatable Bonds: 4 Acceptors: 4 Donors: 2



C₁₂H₁₇N₄OS

Molecular Weight: 265.35458

ALogP: 1.048 Rotatable Bonds: 4 Acceptors: 4 Donors: 2

Model Prediction

Prediction: Carcinogen Probability: 0.239 Enrichment: 0.747 Bayesian Score: -0.319

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

category.

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

Prediction: Non-Mutagen

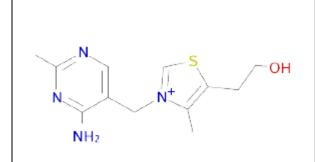
Probability: 0.274 Enrichment: 0.490 Bayesian Score: -12.406

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

best cutoff value. Probability: The esimated probability that the sample is in the

category.

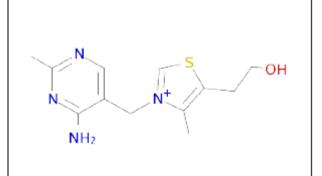
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian score.



C₁₂H₁₇N₄OS

Molecular Weight: 265.35458

ALogP: 1.048 Rotatable Bonds: 4 Acceptors: 4 Donors: 2



C₁₂H₁₇N₄OS

Molecular Weight: 265.35458

ALogP: 1.048 Rotatable Bonds: 4 Acceptors: 4 Donors: 2

Model Prediction

Prediction: 1.308

Unit: g/kg_body_weight

Model Prediction

Prediction: 0.097

Unit: g/kg_body_weight

C₁₂H₁₇N₄OS

Molecular Weight: 265.35458

ALogP: 1.048 Rotatable Bonds: 4 Acceptors: 4 Donors: 2

C₁₂H₁₇N₄OS

Molecular Weight: 265.35458

ALogP: 1.048 Rotatable Bonds: 4 Acceptors: 4 Donors: 2

Model Prediction

Prediction: Non-Irritant Probability: 0.963 Enrichment: 1.046 Bayesian Score: -1.251

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.

Probability: The esimated probability that the sample is in the

category. Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

Prediction: Strong-Sensitizer

Probability: 0.920 Enrichment: 1.187 Bayesian Score: 1.059

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

category. Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Aerobic Biodegradability

C₁₂H₁₇N₄OS

Molecular Weight: 265.35458

ALogP: 1.048 Rotatable Bonds: 4 Acceptors: 4 Donors: 2

Model Prediction

Prediction: Non-Degradable

Probability: 0.208 Enrichment: 0.478 Bayesian Score: -6.865

Prediction: Positive if the Bayesian score is above the estimated

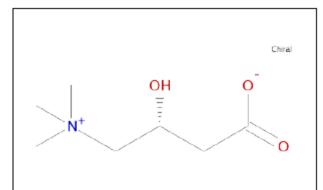
best cutoff value.

Probability: The esimated probability that the sample is in the

category.
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

FDA Rodent Carcinogenicity

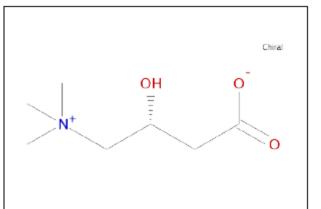
Mutagenecity



C₇H₁₅NO₃

Molecular Weight: 161.19889

ALogP: -3.29 Rotatable Bonds: 4 Acceptors: 3 Donors: 1



C₇H₁₅NO₃

Molecular Weight: 161.19889

ALogP: -3.29 Rotatable Bonds: 4 Acceptors: 3 Donors: 1

Model Prediction

Prediction: Non-Carcinogen

Probability: 0.218 Enrichment: 0.681 Bayesian Score: -2.327

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the category.

category. Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

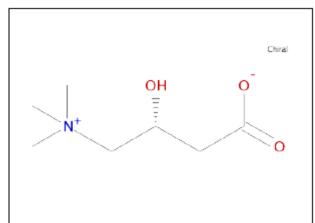
Prediction: Non-Mutagen

Probability: 0.543 Enrichment: 0.972 Bayesian Score: -6.539

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the category.

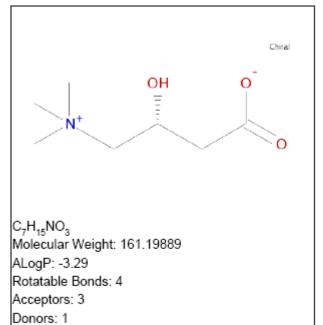
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian



C₇H₁₅NO₃

Molecular Weight: 161.19889

ALogP: -3.29 Rotatable Bonds: 4 Acceptors: 3 Donors: 1



Model Prediction

Prediction: 1.101

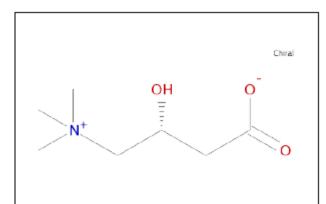
Unit: g/kg_body_weight

Model Prediction

Prediction: 0.175

Unit: g/kg_body_weight

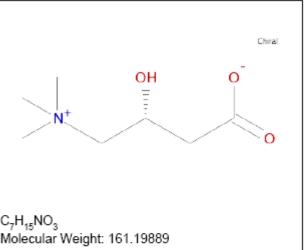
Skin Irritancy Skin sensitization



C₇H₁₅NO₃

Molecular Weight: 161.19889

ALogP: -3.29 Rotatable Bonds: 4 Acceptors: 3 Donors: 1



ALogP: -3.29 Rotatable Bonds: 4 Acceptors: 3 Donors: 1

Model Prediction

Prediction: Mild Probability: 0.170 Enrichment: 0.462 Bayesian Score: -6.587

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

Prediction: Non-Sensitizer

Probability: 0.636 Enrichment: 0.926 Bayesian Score: -2.950

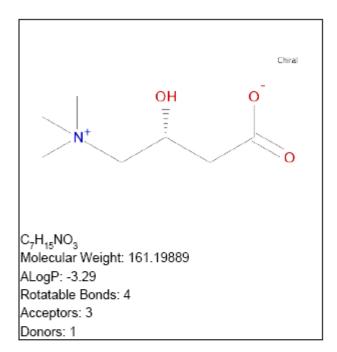
Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Aerobic Biodegradability



Model Prediction

Prediction: Degradable

Probability: 0.621 Enrichment: 1.422 Bayesian Score: 2.788

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.

Probability: The esimated probability that the sample is in the

category. Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

FDA Rodent Carcinogenicity

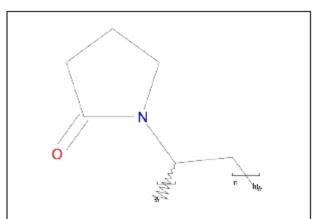
O n hu.

C₆H₉*₂NO

Molecular Weight: 111.14176

ALogP: 6.1e-002 Rotatable Bonds: 2 Acceptors: 1 Donors: 0

Mutagenecity



C₆H₉*₂NO

Molecular Weight: 111.14176

ALogP: 6.1e-002 Rotatable Bonds: 2 Acceptors: 1 Donors: 0

Model Prediction

Prediction: Carcinogen Probability: 0.256 Enrichment: 0.798 Bayesian Score: 0.693

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.

Probability: The esimated probability that the sample is in the

category.

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

Prediction: Non-Mutagen

Probability: 0.494 Enrichment: 0.885 Bayesian Score: -7.677

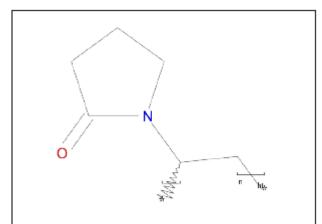
Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.

Probability: The esimated probability that the sample is in the

category.

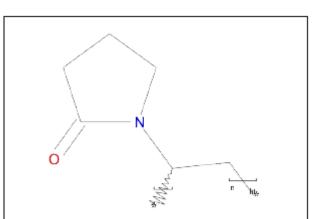
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian



C₆H₉*₂NO

Molecular Weight: 111.14176

ALogP: 6.1e-002 Rotatable Bonds: 2 Acceptors: 1 Donors: 0



C₆H₉*₂NO

Molecular Weight: 111.14176

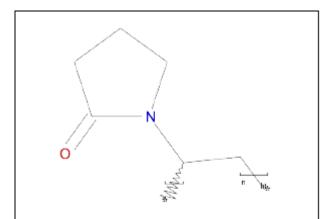
ALogP: 6.1e-002 Rotatable Bonds: 2 Acceptors: 1 Donors: 0

Model Prediction

Prediction: 1.634 Unit: g/kg_body_weight

Model Prediction

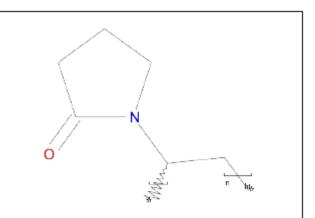
Prediction: 0.181 Unit: g/kg_body_weight Skin Irritancy Skin sensitization



C₈H₉*₂NO

Molecular Weight: 111.14176

ALogP: 6.1e-002 Rotatable Bonds: 2 Acceptors: 1 Donors: 0



C₆H₉*₂NO

Molecular Weight: 111.14176

ALogP: 6.1e-002 Rotatable Bonds: 2 Acceptors: 1 Donors: 0

Model Prediction

Prediction: Mild Probability: 0.311 Enrichment: 0.844 Bayesian Score: -2.583

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

category.
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category.
Bayesian Score: The standard Laplacian-modified Bayesian score.

Model Prediction

Prediction: Non-Sensitizer

Probability: 0.337 Enrichment: 0.492 Bayesian Score: -6.913

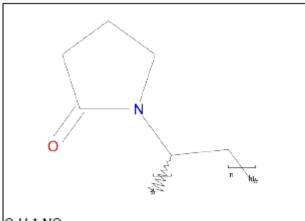
Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

category.
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category.
Bayesian Score: The standard Laplacian-modified Bayesian

score.

Aerobic Biodegradability



C₆H₉*₂NO

Donors: 0

Molecular Weight: 111.14176

ALogP: 6.1e-002 Rotatable Bonds: 2 Acceptors: 1

Model Prediction

Prediction: Degradable

Probability: 0.703 Enrichment: 1.610 Bayesian Score: 4.656

Prediction: Positive if the Bayesian score is above the estimated

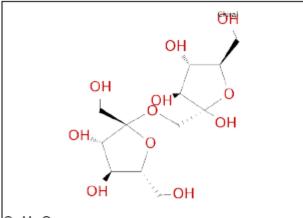
best cutoff value.

Probability: The esimated probability that the sample is in the

category.
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category.
Bayesian Score: The standard Laplacian-modified Bayesian

FDA Rodent Carcinogenicity

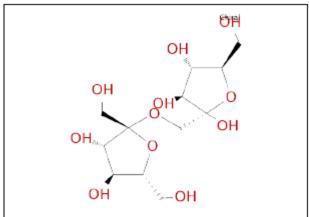
Mutagenecity



C₁₂H₂₂O₁₁

Molecular Weight: 342.29648

ALogP: -4.361 Rotatable Bonds: 6 Acceptors: 11 Donors: 8



C₁₂H₂₂O₁₁

Molecular Weight: 342.29648

ALogP: -4.361 Rotatable Bonds: 6 Acceptors: 11 Donors: 8

Model Prediction

Prediction: Non-Carcinogen

Probability: 0.216 Enrichment: 0.673 Bayesian Score: -2.679

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

Prediction: Non-Mutagen

Probability: 0.322 Enrichment: 0.577

Bayesian Score: -11.346

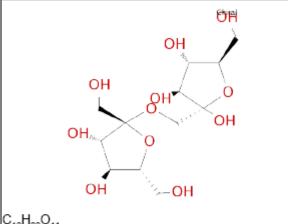
Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.

Probability: The esimated probability that the sample is in the

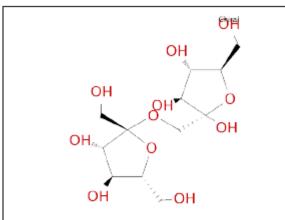
category.

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian



C₁₂H₂₂O₁₁ Molecular Weight: 342.29648

ALogP: -4.361 Rotatable Bonds: 6 Acceptors: 11 Donors: 8



C₁₂H₂₂O₁₁ Molecular Weight: 342.29648

ALogP: -4.361 Rotatable Bonds: 6 Acceptors: 11 Donors: 8

Model Prediction

Prediction: 20.789 Unit: g/kg_body_weight

Model Prediction

Prediction: 0.000

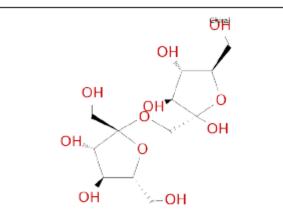
Unit: g/kg_body_weight

Skin Irritancy Skin sensitization

C₁₂H₂₂O₁₁

Molecular Weight: 342.29648

ALogP: -4.361 Rotatable Bonds: 6 Acceptors: 11 Donors: 8



C₁₂H₂₂O₁₁

Molecular Weight: 342.29648

ALogP: -4.361 Rotatable Bonds: 6 Acceptors: 11 Donors: 8

Model Prediction

Prediction: Mild Probability: 0.159 Enrichment: 0.432 Bayesian Score: -6.949

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian score.

Model Prediction

Prediction: Non-Sensitizer

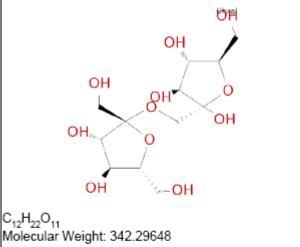
Probability: 0.670 Enrichment: 0.977 Bayesian Score: -2.394

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.
Probability: The esimated probability that the sample is in the category.

category.
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category.
Bayesian Score: The standard Laplacian-modified Bayesian

score.



ALogP: -4.361 Rotatable Bonds: 6 Acceptors: 11 Donors: 8

Model Prediction

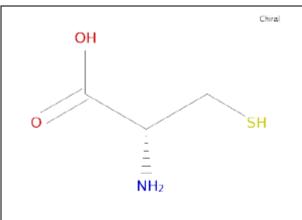
Prediction: Degradable

Probability: 0.609 Enrichment: 1.395 Bayesian Score: 2.532

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

FDA Rodent Carcinogenicity

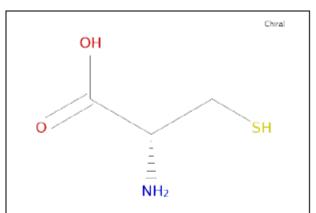


 $C_3H_7NO_2S$

Molecular Weight: 121.15818

ALogP: -3.078 Rotatable Bonds: 2 Acceptors: 4 Donors: 3

Mutagenecity



C₃H₇NO₂S

Molecular Weight: 121.15818

ALogP: -3.078 Rotatable Bonds: 2 Acceptors: 4 Donors: 3

Model Prediction

Prediction: Non-Carcinogen

Probability: 0.210 Enrichment: 0.656 Bayesian Score: -4.229

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian score.

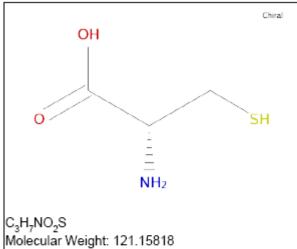
Model Prediction

Prediction: Non-Mutagen

Probability: 0.631 Enrichment: 1.130 Bayesian Score: -4.187

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

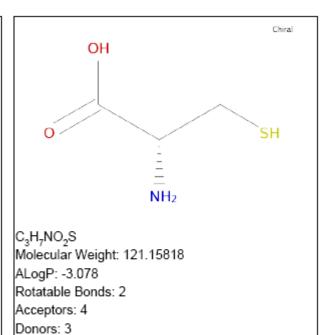


Molecular Weight: 121.15818
ALogP: -3.078
Rotatable Bonds: 2
Acceptors: 4
Donors: 3

Model Prediction

Prediction: 0.514

Unit: g/kg_body_weight

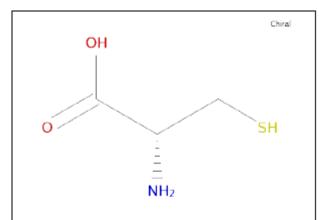


Model Prediction

Prediction: 0.653

Unit: g/kg_body_weight

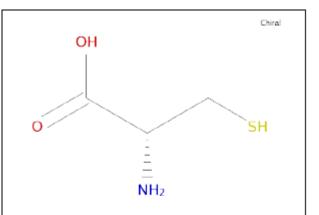
Skin Irritancy Skin sensitization



C₃H₇NO₂S

Molecular Weight: 121.15818

ALogP: -3.078 Rotatable Bonds: 2 Acceptors: 4 Donors: 3



C₃H₇NO₅S

Molecular Weight: 121.15818

ALogP: -3.078 Rotatable Bonds: 2 Acceptors: 4 Donors: 3

Model Prediction

Prediction: Non-Irritant Probability: 0.971 Enrichment: 1.055 Bayesian Score: -0.704

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.
Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian score

Model Prediction

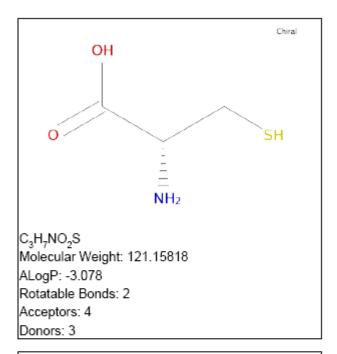
Prediction: Non-Sensitizer

Probability: 0.725 Enrichment: 1.057 Bayesian Score: -1.390

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

Aerobic Biodegradability



Model Prediction

Prediction: Degradable

Probability: 0.562 Enrichment: 1.289 Bayesian Score: 1.548

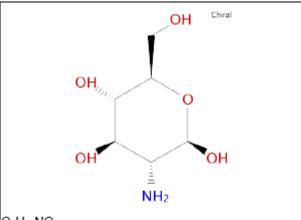
Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.

Probability: The esimated probability that the sample is in the

FDA Rodent Carcinogenicity

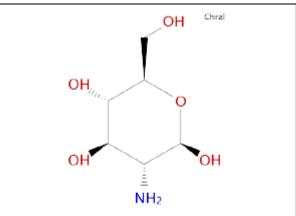
Mutagenecity



C₈H₁₃NO₅

Molecular Weight: 179.17112

ALogP: -2.804 Rotatable Bonds: 1 Acceptors: 6 Donors: 5



C₆H₁₃NO₅

Molecular Weight: 179.17112

ALogP: -2.804 Rotatable Bonds: 1 Acceptors: 6 Donors: 5

Model Prediction

Prediction: Non-Carcinogen

Probability: 0.215 Enrichment: 0.672 Bayesian Score: -2.754

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

Prediction: Non-Mutagen

Probability: 0.711 Enrichment: 1.273 Bayesian Score: -1.342

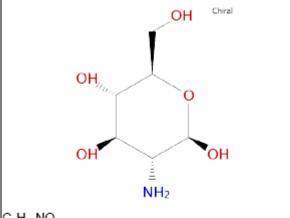
Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

category.

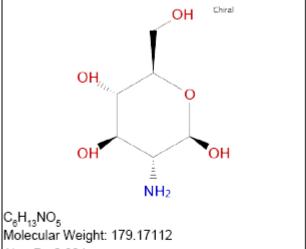
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

 $^{\mathrm{lage}}200$



C₈H₁₃NO₅ Molecular Weight: 179.17112

ALogP: -2.804 Rotatable Bonds: 1 Acceptors: 6 Donors: 5



ALogP: -2.804 Rotatable Bonds: 1 Acceptors: 6 Donors: 5

Model Prediction

Prediction: 3.241

Unit: g/kg_body_weight

Model Prediction

Prediction: 0.268

Unit: g/kg_body_weight

C₆H₁₃NO₅

Molecular Weight: 179.17112

ALogP: -2.804 Rotatable Bonds: 1 Acceptors: 6 Donors: 5

C₆H₁₃NO₅

Molecular Weight: 179.17112

ALogP: -2.804 Rotatable Bonds: 1 Acceptors: 6 Donors: 5

Model Prediction

Prediction: Mild Probability: 0.242 Enrichment: 0.659 Bayesian Score: -4.415

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

category.
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category.
Bayesian Score: The standard Laplacian-modified Bayesian score.

Model Prediction

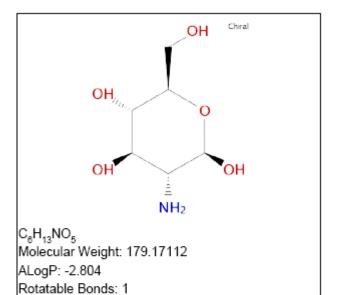
Prediction: Non-Sensitizer

Probability: 0.631 Enrichment: 0.920 Bayesian Score: -3.018

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

Aerobic Biodegradability



Donors: 5

Acceptors: 6

Model Prediction Prediction: Degradable

Probability: 0.620 Enrichment: 1.421 Bayesian Score: 2.775

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

FDA Rodent Carcinogenicity

OH ″он OH

C₆H₁₀O₇

Molecular Weight: 194.1394

ALogP: -2.386 Rotatable Bonds: 1 Acceptors: 7 Donors: 5

Model Prediction

Prediction: Non-Carcinogen

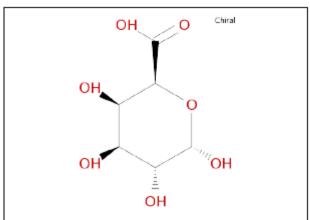
Probability: 0.213 Enrichment: 0.666 Bayesian Score: -3.131

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Mutagenecity



C₆H₁₀O₇

Donors: 5

Molecular Weight: 194.1394

ALogP: -2.386 Rotatable Bonds: 1 Acceptors: 7

Model Prediction

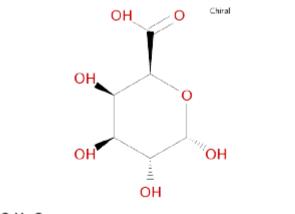
Prediction: Non-Mutagen

Probability: 0.567 Enrichment: 1.016 Bayesian Score: -5.935

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

category.



C₆H₁₀O₇

Molecular Weight: 194.1394

ALogP: -2.386 Rotatable Bonds: 1 Acceptors: 7 Donors: 5

Model Prediction

Prediction: 0.525

Unit: g/kg_body_weight

Model Prediction

Prediction: 3.576

Rotatable Bonds: 1

Acceptors: 7

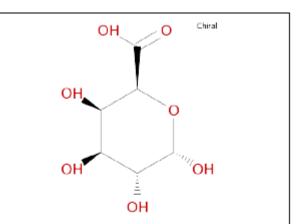
Donors: 5

Unit: g/kg_body_weight

C₆H₁₀O₇

Molecular Weight: 194.1394

ALogP: -2.386 Rotatable Bonds: 1 Acceptors: 7 Donors: 5



C₆H₁₀O₇

Molecular Weight: 194.1394

ALogP: -2.386 Rotatable Bonds: 1 Acceptors: 7 Donors: 5

Model Prediction

Prediction: Non-Irritant Probability: 0.971 Enrichment: 1.055

Bayesian Score: -0.726

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the category.

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

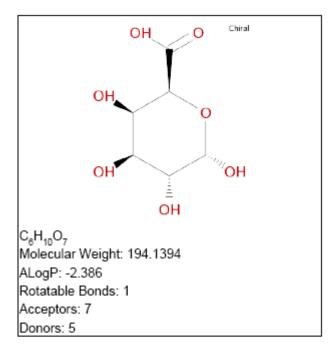
Prediction: Non-Sensitizer

Probability: 0.704 Enrichment: 1.026 Bayesian Score: -1.792

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the category.

Aerobic Biodegradability



Model Prediction

Prediction: Degradable

Probability: 0.632 Enrichment: 1.447 Bayesian Score: 3.026

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.

Probability: The esimated probability that the sample is in the

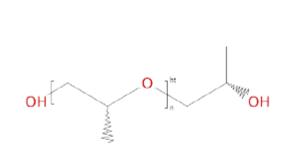
FDA Rodent Carcinogenicity

Mutagenecity

C₆H₁₄O₃

Molecular Weight: 134.17356

ALogP: -0.274 Rotatable Bonds: 4 Acceptors: 3 Donors: 2



C₆H₁₄O₃

Molecular Weight: 134.17356

ALogP: -0.274 Rotatable Bonds: 4 Acceptors: 3 Donors: 2

Model Prediction

Prediction: Non-Carcinogen

Probability: 0.222 Enrichment: 0.692 Bayesian Score: -1.865

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the category.

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian score.

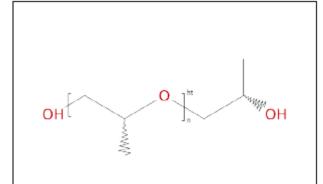
Model Prediction

Prediction: Non-Mutagen

Probability: 0.686 Enrichment: 1.229 Bayesian Score: -2.332

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

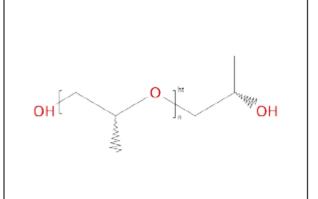
Probability: The esimated probability that the sample is in the category.



C₆H₁₄O₃

Molecular Weight: 134.17356

ALogP: -0.274 Rotatable Bonds: 4 Acceptors: 3 Donors: 2



C₆H₁₄O₃

Molecular Weight: 134.17356

ALogP: -0.274 Rotatable Bonds: 4 Acceptors: 3 Donors: 2

Model Prediction

Prediction: 12.098 Unit: g/kg_body_weight

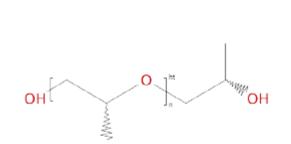
Model Prediction

Prediction: 0.187 Unit: g/kg_body_weight

C₆H₁₄O₃

Molecular Weight: 134.17356

ALogP: -0.274 Rotatable Bonds: 4 Acceptors: 3 Donors: 2



C₆H₁₄O₃

Molecular Weight: 134.17356

ALogP: -0.274 Rotatable Bonds: 4 Acceptors: 3 Donors: 2

Model Prediction

Prediction: Mild Probability: 0.244 Enrichment: 0.664 Bayesian Score: -4.358

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

category.
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category.
Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

Prediction: Non-Sensitizer

Probability: 0.513 Enrichment: 0.747 Bayesian Score: -4.681

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the category.

Aerobic Biodegradability

C₆H₁₄O₃

Molecular Weight: 134.17356

ALogP: -0.274 Rotatable Bonds: 4 Acceptors: 3 Donors: 2

Model Prediction

Prediction: Degradable

Probability: 0.711 Enrichment: 1.629 Bayesian Score: 4.861

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

FDA Rodent Carcinogenicity

Mutagenecity

Molecular Weight: 57.09438

ALogP: 0.131 Rotatable Bonds: 3 Acceptors: 1 Donors: 1

C₂H₇*₂N

Donors: 1

Molecular Weight: 57.09438

ALogP: 0.131 Rotatable Bonds: 3 Acceptors: 1

Model Prediction

Prediction: Non-Carcinogen

Probability: 0.558 Enrichment: 1.417 Bayesian Score: -0.647

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

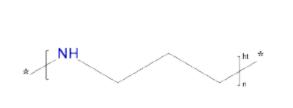
Model Prediction

Prediction: Non-Mutagen

Probability: 0.666 Enrichment: 1.192 Bayesian Score: -3.064

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the category.



C3H7*2N

Molecular Weight: 57.09438

ALogP: 0.131 Rotatable Bonds: 3 Acceptors: 1 Donors: 1



 $C_3H_7*_5N$

Molecular Weight: 57.09438

ALogP: 0.131 Rotatable Bonds: 3 Acceptors: 1 Donors: 1

Model Prediction

Prediction: 0.055

Unit: g/kg_body_weight

Model Prediction

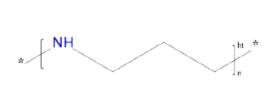
Prediction: 0.089

Unit: g/kg_body_weight

C₃H₇*₂N

Molecular Weight: 57.09438

ALogP: 0.131 Rotatable Bonds: 3 Acceptors: 1 Donors: 1



C₃H₇*₂N

Molecular Weight: 57.09438

ALogP: 0.131 Rotatable Bonds: 3 Acceptors: 1 Donors: 1

Model Prediction

Prediction: Mild Probability: 0.275 Enrichment: 0.748 Bayesian Score: -3.519

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

Prediction: Non-Sensitizer

Probability: 0.681 Enrichment: 0.993 Bayesian Score: -2.202

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

Aerobic Biodegradability

C₃H₇*₂N

Donors: 1

Molecular Weight: 57.09438

ALogP: 0.131 Rotatable Bonds: 3 Acceptors: 1

Model Prediction

Prediction: Non-Degradable

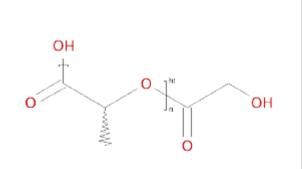
Probability: 0.514 Enrichment: 1.177 Bayesian Score: 0.529

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

FDA Rodent Carcinogenicity

Mutagenecity



Molecular Weight: 148.11402

ALogP: -0.686 Rotatable Bonds: 4 Acceptors: 5 Donors: 2

C₅H₈O₅

Molecular Weight: 148.11402

ALogP: -0.686 Rotatable Bonds: 4 Acceptors: 5 Donors: 2

Model Prediction

Prediction: Non-Carcinogen

Probability: 0.213 Enrichment: 0.664 Bayesian Score: -3.290

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian score.

Model Prediction

Prediction: Non-Mutagen

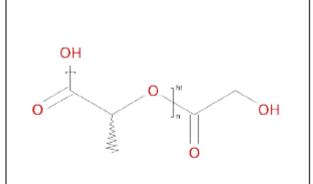
Probability: 0.543 Enrichment: 0.972 Bayesian Score: -6.541

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

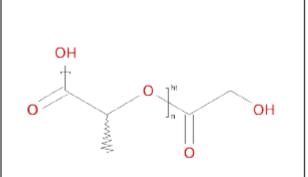
score.



C₅H₈O₅

Molecular Weight: 148.11402

ALogP: -0.686 Rotatable Bonds: 4 Acceptors: 5 Donors: 2



C₅H₈O₅

Molecular Weight: 148.11402

ALogP: -0.686 Rotatable Bonds: 4 Acceptors: 5 Donors: 2

Model Prediction

Prediction: 2.982

Unit: g/kg_body_weight

Model Prediction

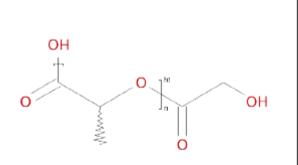
Prediction: 0.427

Unit: g/kg_body_weight

 $C_5H_8O_5$

Molecular Weight: 148.11402

ALogP: -0.686 Rotatable Bonds: 4 Acceptors: 5 Donors: 2



C₅H₈O₅

Molecular Weight: 148.11402

ALogP: -0.686 Rotatable Bonds: 4 Acceptors: 5 Donors: 2

Model Prediction

Prediction: Non-Irritant Probability: 0.972 Enrichment: 1.056 Bayesian Score: -0.615

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

category.
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category.
Bayesian Score: The standard Laplacian-modified Bayesian score.

Model Prediction

Prediction: Non-Sensitizer

Probability: 0.716 Enrichment: 1.044 Bayesian Score: -1.565

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

category. Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

score.

Aerobic Biodegradability

C₅H₈O₅

Molecular Weight: 148.11402

ALogP: -0.686 Rotatable Bonds: 4 Acceptors: 5 Donors: 2

Model Prediction

Prediction: Degradable

Probability: 0.717 Enrichment: 1.644 Bayesian Score: 5.017

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value. Probability: The esimated probability that the sample is in the

FDA Rodent Carcinogenicity

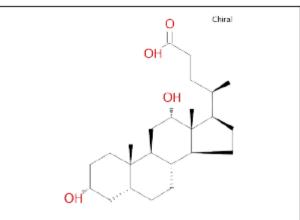
OH Chiral

 $C_{24}H_{40}O_{4}$

Molecular Weight: 392.57199

ALogP: 4.082 Rotatable Bonds: 4 Acceptors: 4 Donors: 3

Mutagenecity



C24H40O4

Molecular Weight: 392.57199

ALogP: 4.082 Rotatable Bonds: 4 Acceptors: 4 Donors: 3

Model Prediction

Prediction: Non-Carcinogen

Probability: 0.227 Enrichment: 0.707 Bayesian Score: -1.366

Prediction: Positive if the Bayesian score is above the estimated best cutoff value

best cutoff value. Probability: The esimated probability that the sample is in the

category.
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category.
Bayesian Score: The standard Laplacian-modified Bayesian score.

Model Prediction

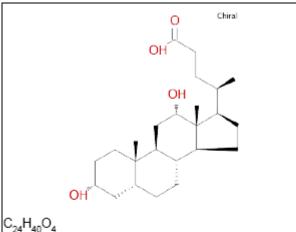
Prediction: Non-Mutagen

Probability: 0.000 Enrichment: 0.000 Bayesian Score: -64.641

Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

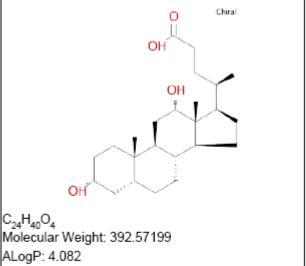
Probability: The esimated probability that the sample is in the category.

Enrichment: An estimate of enrichment, that is, the increased



Molecular Weight: 392.57199

ALogP: 4.082 Rotatable Bonds: 4 Acceptors: 4 Donors: 3



Rotatable Bonds: 4 Acceptors: 4 Donors: 3

Model Prediction

Prediction: 6.358

Unit: g/kg_body_weight

Model Prediction

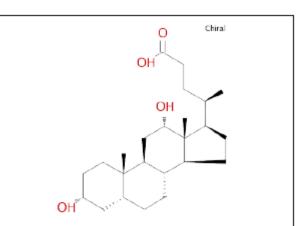
Prediction: 0.190

Unit: g/kg_body_weight

C24H40O4

Molecular Weight: 392.57199

ALogP: 4.082 Rotatable Bonds: 4 Acceptors: 4 Donors: 3



C24H40O4

Molecular Weight: 392.57199

ALogP: 4.082 Rotatable Bonds: 4 Acceptors: 4 Donors: 3

Model Prediction

Prediction: Moderate Severe

Probability: 0.472 Enrichment: 1.283 Bayesian Score: 1.758

Prediction: Positive if the Bayesian score is above the estimated

best cutoff value.

Probability: The esimated probability that the sample is in the

Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category. Bayesian Score: The standard Laplacian-modified Bayesian

Model Prediction

Prediction: Weak-Sensitizer

Probability: 0.185 Enrichment: 0.238 Bayesian Score: -8.518

Prediction: Positive if the Bayesian score is above the estimated

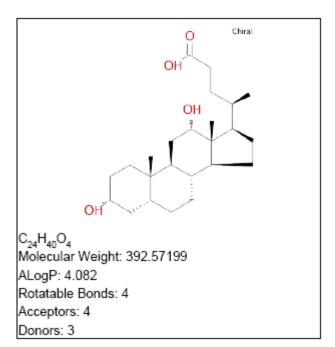
best cutoff value. Probability: The esimated probability that the sample is in the

Category.
Enrichment: An estimate of enrichment, that is, the increased likelihood (versus random) of this sample being in the category.

The standard Laplacian-modified Bayesian

Bayesian Score: The standard Laplacian-modified Bayesian

Aerobic Biodegradability



Model Prediction

Prediction: Degradable

Probability: 0.837 Enrichment: 1.919 Bayesian Score: 8.551

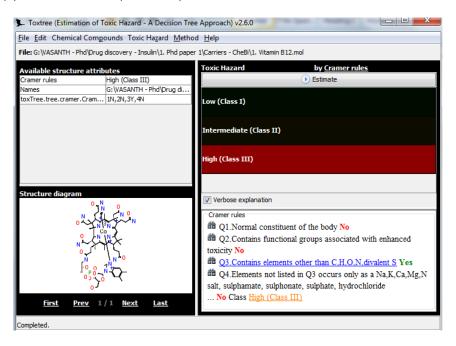
Prediction: Positive if the Bayesian score is above the estimated best cutoff value.

Probability: The esimated probability that the sample is in the category.

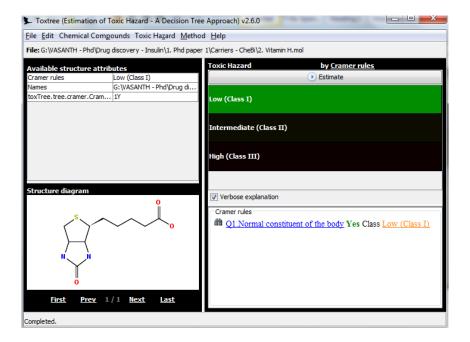
Supplementary figure 4

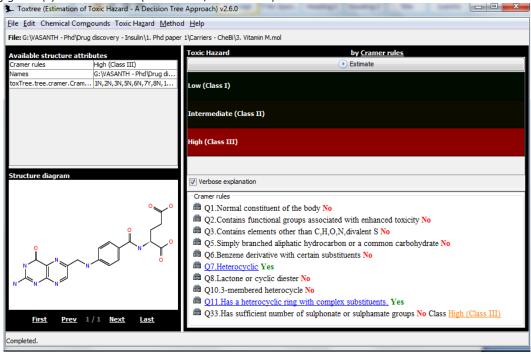
Toxicity studies for Drug delivering molecules by Toxtree; C1 - Vitamin B12 (cobalamin); C2 - Vitamin H (Biotin); C3 - Folic acid (Vitamin M / Vitamin B9); C4 - Vitamin B1 (Thiamin); C5 - L-Carnitine (Vitamin BT); C6 - Poly-N-vinylpyrrolidone; C7; Inulin; C8 - Poly Cysteine; C9 - Chitosan; C10 - Pectin; C11 - Poly(propylene glycol); C12 - Poly(propylene imine); C13 - Poly (lactic-co-glycolic acid); C14 - Deoxycholic acid

Supplementary figure 4(a)-C1 - Vitamin B12 (cobalamin)

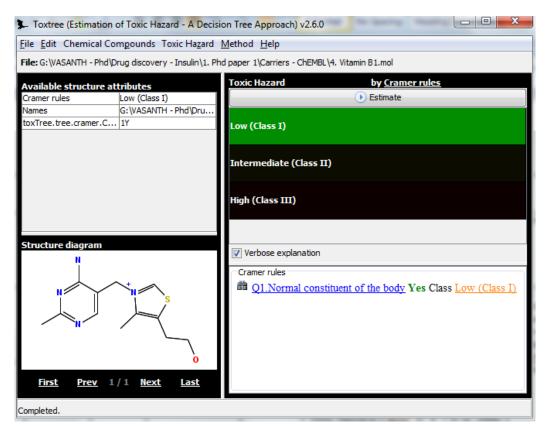


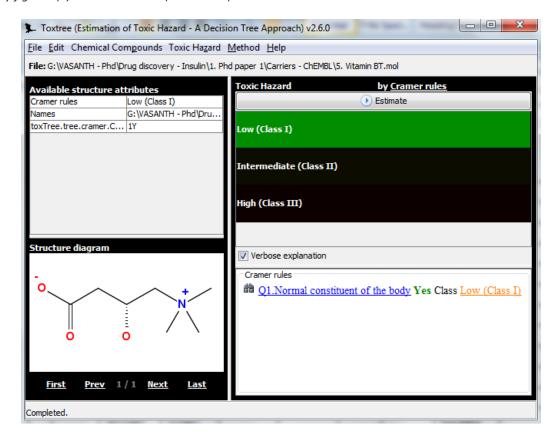
Supplementary figure 4(b)- C2 - Vitamin H (Biotin)



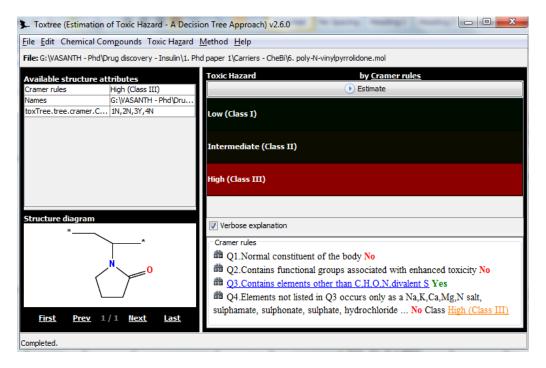


Supplementary figure 4(d)- C4 - Vitamin B1 (Thiamin)

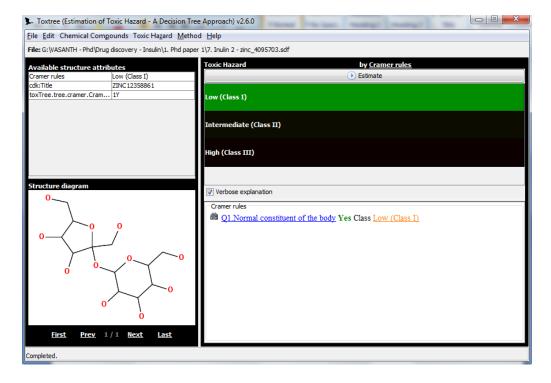




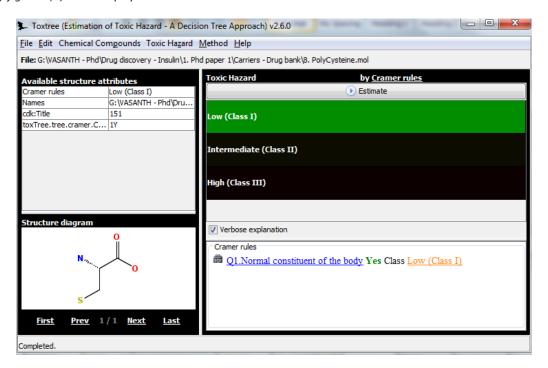
Supplementary figure 4(f)- C6 - Poly-N-vinylpyrrolidone

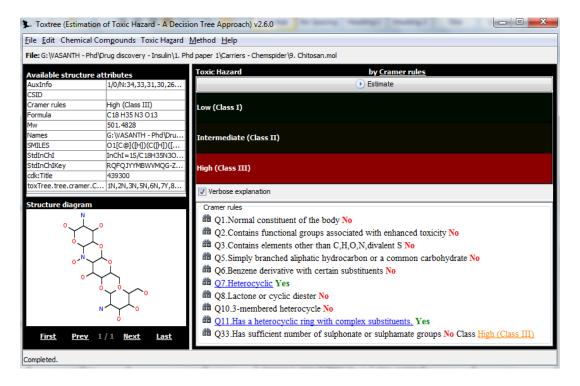


Supplementary figure 4(g)- C7; Inulin

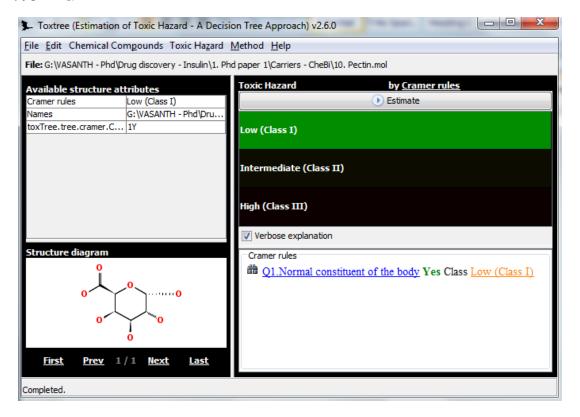


Supplementary figure 3(h)- C8 - Poly Cysteine

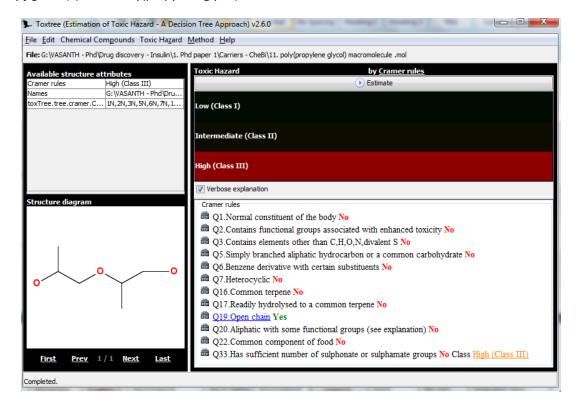




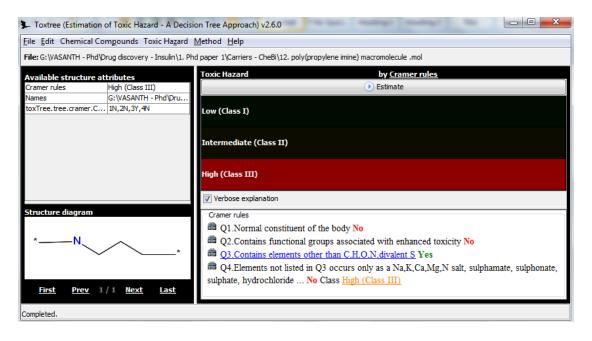
Supplementary figure 4(j)- C10 - Pectin

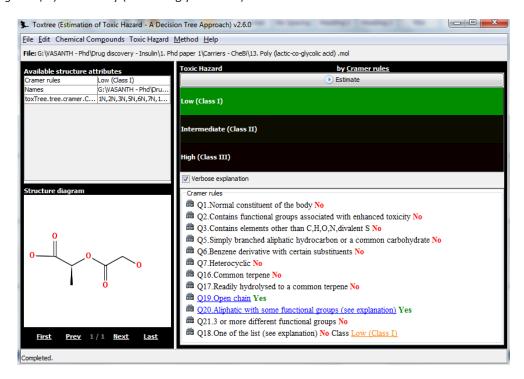


Supplementary figure 4(k)- C11 - Poly(propylene glycol)

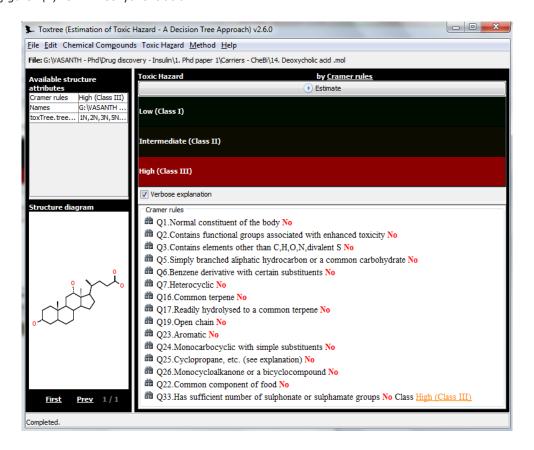


Supplementary figure 4(I)- C12 - Poly(propylene imine)



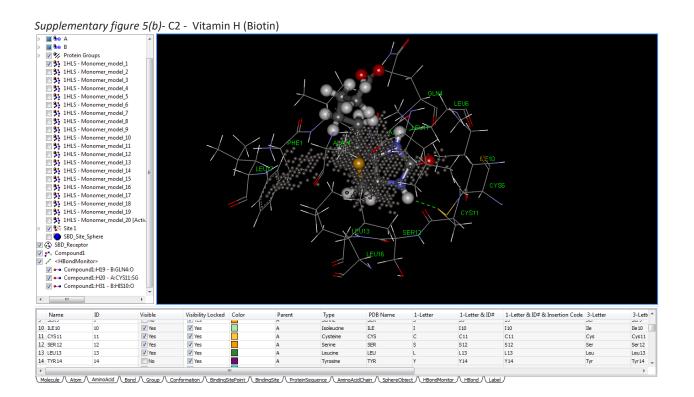


Supplementary figure 4(n)- C14 - Deoxycholic acid

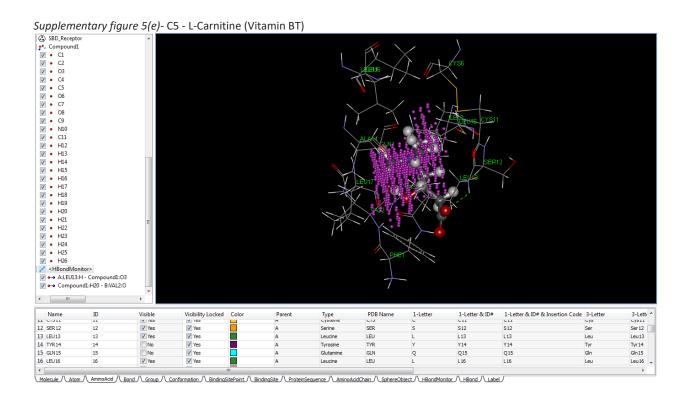


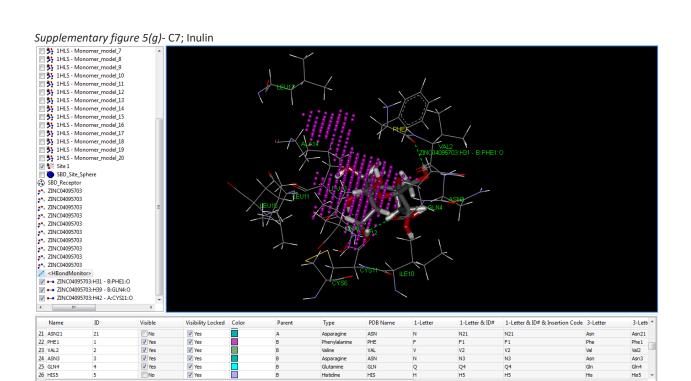
Conjugation results of Human Insulin Monomer (PDB ID: 1HLS), with all listed drug delivering molecules individually by Discovery Studio software. C1 - Vitamin B12 (cobalamin); C2 - Vitamin H (Biotin); C3 - Folic acid (Vitamin M / Vitamin B9); C4 - Vitamin B1 (Thiamin); C5 - L-Carnitine (Vitamin BT); C6 - Poly-N-vinylpyrrolidone; C7; Inulin; C8 - Poly Cysteine; C9 - Chitosan; C10 - Pectin; C11 - Poly(propylene glycol); C12 - Poly(propylene imine); C13 - Poly (lactic-co-glycolic acid); C14 - Deoxycholic acid

Supplementary figure 5(a)- C1 - Vitamin B12 (cobalamin) No Conjugation



Supplementary figure 5(c)- C3 - Folic acid (Vitamin M / Vitamin B9) No Conjugation





Asparagine

GLN

noAcidChain /\ SphereObject /\ HBondMi

Glutamine

25 GLN4 26 HIS5

✓ Yes No

cule / Atom / AminoAcid / Bond / Group / Conformation / BindingSitePoint / BindingSite / ProteinSec

N3

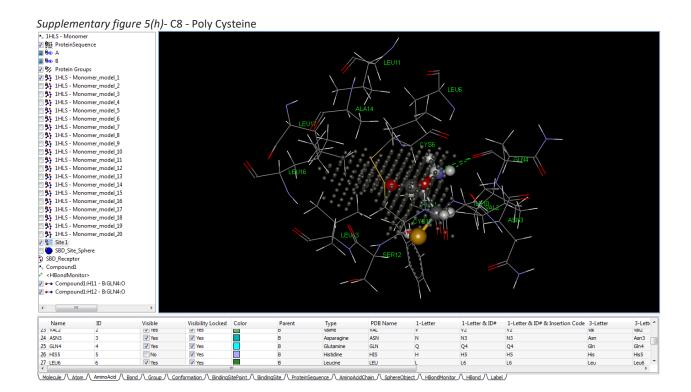
Q4 H5

Q4 H5

Asn3

Gln4 His5

Gln



Asparagine

Lifolecule / Atom / AminoAcid / Bond / Group / Conformation / BindingSitePoint / BindingSite / ProteinSequence / AminoAcidChain / SphereObject / HBondMonitor / HBond / Label

ASN

HIS

N3

N3

Asn

His

Asn3 Gln4 His5

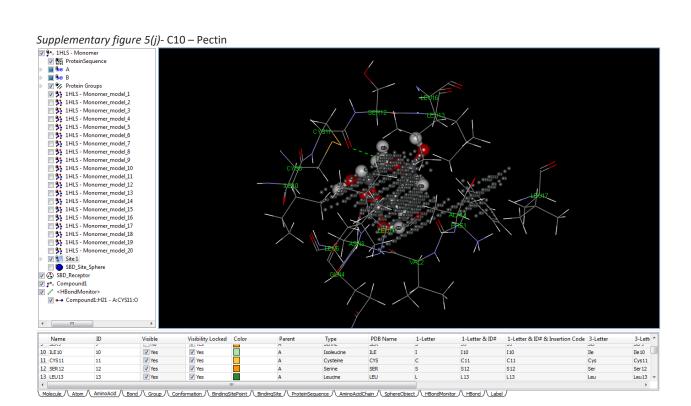
22 PHE1 23 VAL2

24 ASN3 25 GLN4 26 HIS5

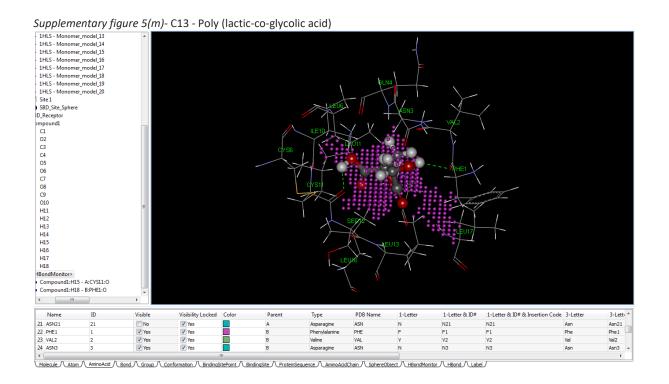
✓ Yes

✓ Yes

✓ Yes



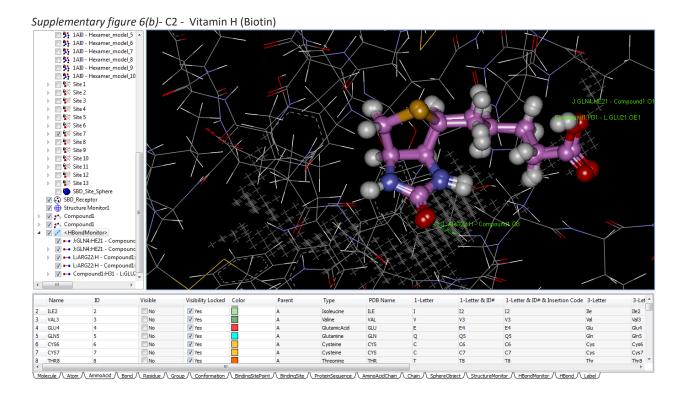
Supplementary figure 5(I)- C12 - Poly(propylene imine) No Conjugation

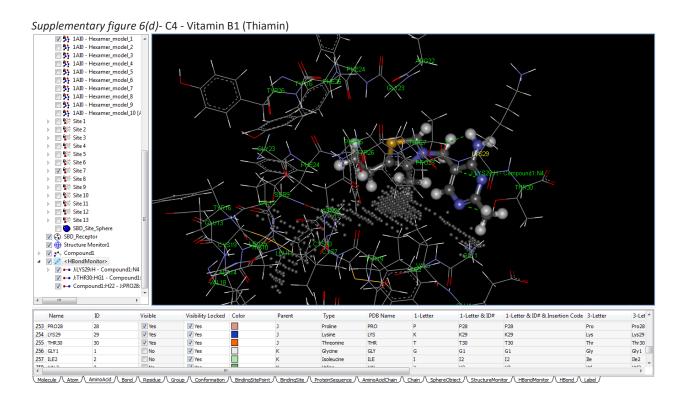


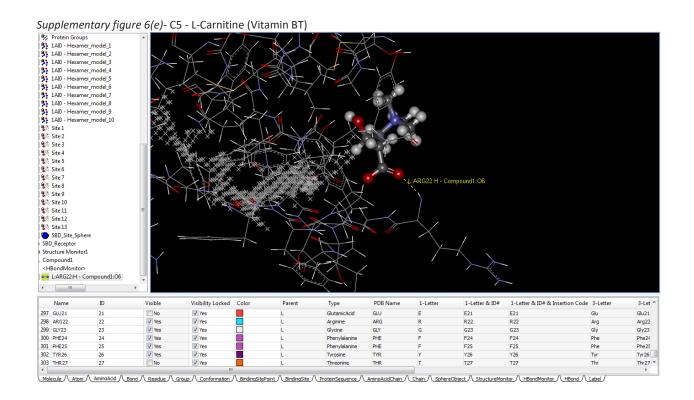
Supplementary figure 5(n)- C14 - Deoxycholic acid No Conjugation

Conjugation results of Human insulin hexamer (PDB ID: 1AIO), with all listed drug delivering molecules individually by Discovery Studio software. C1 - Vitamin B12 (cobalamin); C2 - Vitamin H (Biotin); C3 - Folic acid (Vitamin M / Vitamin B9); C4 - Vitamin B1 (Thiamin); C5 - L-Carnitine (Vitamin BT); C6 - Poly-N-vinylpyrrolidone; C7; Inulin; C8 - Poly Cysteine; C9 - Chitosan; C10 - Pectin; C11 - Poly(propylene glycol); C12 - Poly(propylene imine); C13 - Poly (lactic-co-glycolic acid); C14 - Deoxycholic acid

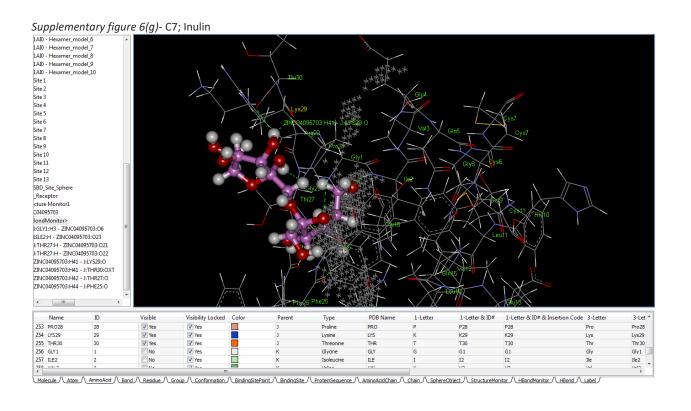
Supplementary figure 6(a)- C1 - Vitamin B12 (cobalamin) No Conjugation

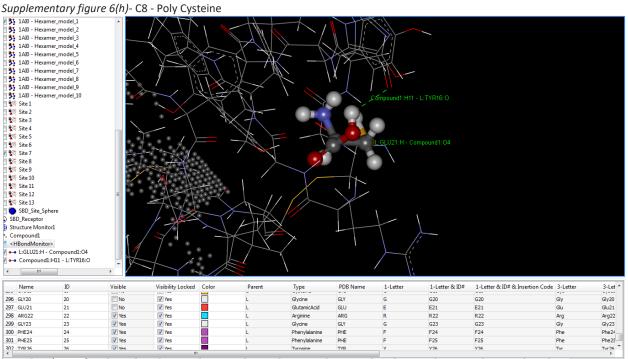




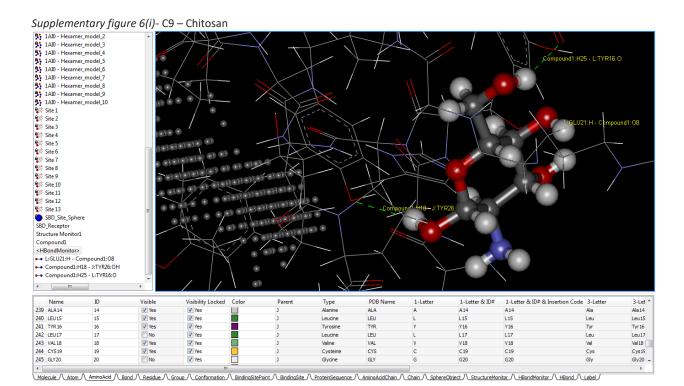


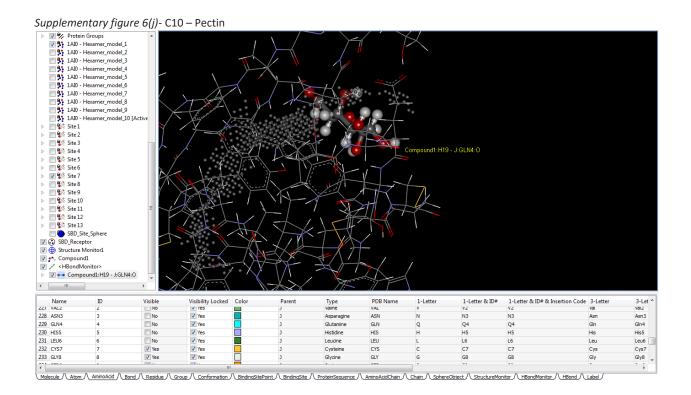
Supplementary figure 6(f)- C6 - Poly-N-vinylpyrrolidone No Conjugation

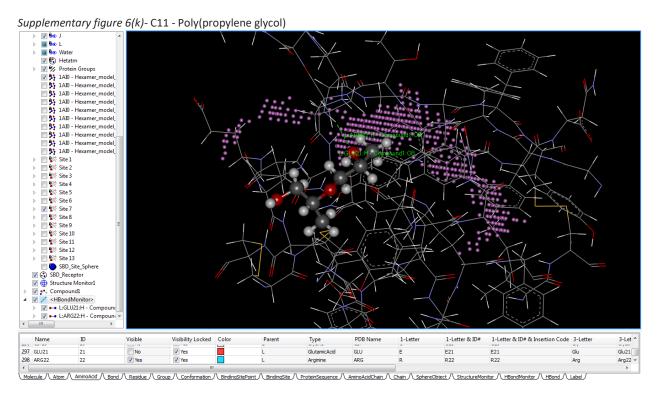




Molecule / Altom / Amino Acid / Bond / Residue / Group / Conformation / EindingSitePoint / BindingSite / ProteinSequence / Amino AcidChain / Chain / SphereObject / StructureMonitor / LeBond/Monitor / LeBond / Label /

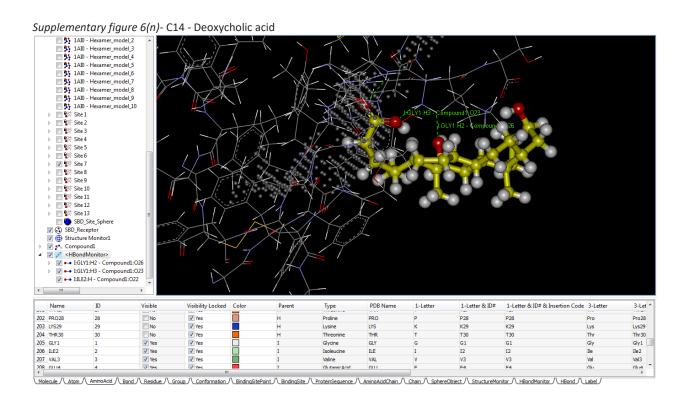






Supplementary figure 6(I)- C12 - Poly(propylene imine) No Conjugation

Molecule / Atom / AminoAcid / Bond / Residue / Group / Conformation / BindingSitePoint / BindingSite / ProteinSequence / AminoAcidChain / Chain / SphereObject / StructureMonitor / HBondMonitor / HBond / Label /



Conjugation results of Insulin Lispro (PDB ID: 1 LPH), with all listed drug delivering molecules individually by Discovery Studio software. C1 - Vitamin B12 (cobalamin); C2 - Vitamin H (Biotin); C3 - Folic acid (Vitamin M / Vitamin B9); C4 - Vitamin B1 (Thiamin); C5 - L-Carnitine (Vitamin BT); C6 - Poly-N-vinylpyrrolidone; C7; Inulin; C8 - Poly Cysteine; C9 - Chitosan; C10 - Pectin; C11 - Poly(propylene glycol); C12 - Poly(propylene imine); C13 - Poly (lactic-co-glycolic acid); C14 - Deoxycholic acid

Supplementary figure 7(a)- C1 - Vitamin B12 (cobalamin) No Conjugation

Supplementary figure 7(b)- C2 - Vitamin H (Biotin) No Conjugation

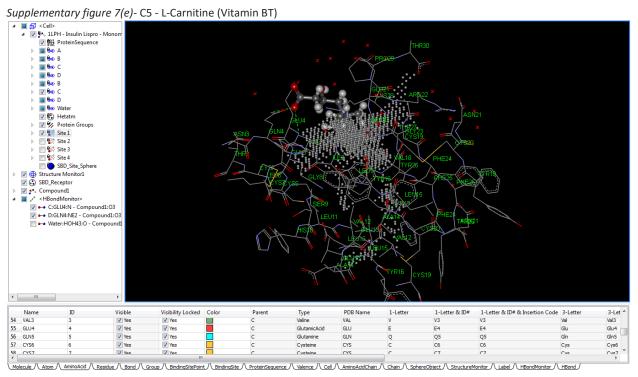
Supplementary figure 7(c)-C3 - Folic acid (Vitamin M / Vitamin B9) ■ C:GLU4:N - Compound1:N5 C:TYR19:OH - Compound1:N3

D:GLN4:N - Compound1:032

D:GLN4:NE2 - Compound1:026 → D:GLN4:NE2 - Compound1:O28 → D:GLN4:NE2 - Compound1:O26 → D:HIS5:N - Compound1:O26 □ •• D:HIS5:N - Compound1:032
 □ •• D:THR27:N - Compound1:012 ✓

✓ D:LYS28:NZ - Compound1:O22 ✓ • D:LYS28:NZ - Compound1:032 ✓ • D:LYS28:NZ - Compound1:032 D:LYS28:NZ - Compound1:022 ✓ → D:LYS28:NZ - Compound1:O12
 → D:THR30:N - Compound1:O32 ■ Water:HOH30:O - Compound1:N ─ Water:HOH30:O - Compound1:O :
 ─ Water:HOH30:O - Compound1:O ■ Water:HOH30:O - Compound1:N ■ • Water:HOH30:O - Compound1:O
 ■ • Water:HOH30:O - Compound1:N ■ Water:HOH31:O - Compound1:N Water:HOH36:0 - Compound1:0
 Water:HOH36:0 - Compound1:0 → Water:HOH36:O - Compound1:O ■ • Water:HOH36:O - Compound1:O
 ■ • Water:HOH36:O - Compound1:O ■ Water:HOH36:O - Compound1:O ■ ■ Water:HOH36:O - Compound1:O
 ■ ■ Water:HOH36:O - Compound1:O Water-HOH/IR-O - Con PDB Name 1-Letter & ID# & Insertion Code 3-Letter Visible Visibility Locked Parent 1-Letter 1-Letter & ID# 3-Let Type 98 TYR26 99 THR27 100 LYS28 101 PRO29 ✓ Yes ✓ Yes ✓ Yes V Yes V Yes V Yes Tyr26 Thr27 Lys28 Y26 T27 K28 Y26 T27 K28 Lys 29 √ Yes ✓ Yes Proline PRO P29 P29 Pro29 102 THR30 Thr Thr30

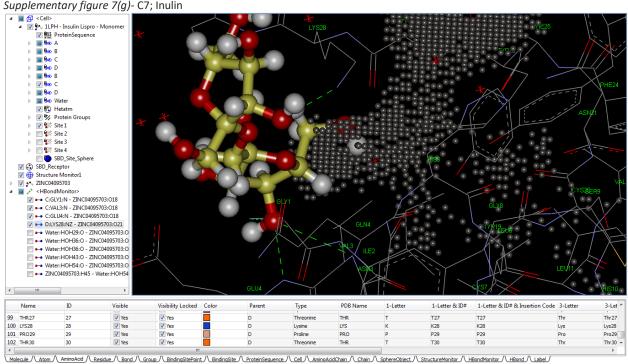
Molecule / Atom / AminoAcid / Residue / Bond / Group / BindingSitePoint / BindingSite / ProteinSequence / Velence / Cell / AminoAcidChain / Chain / SphereObject / StructureMonitor / HBondMonitor / HBond / Label /



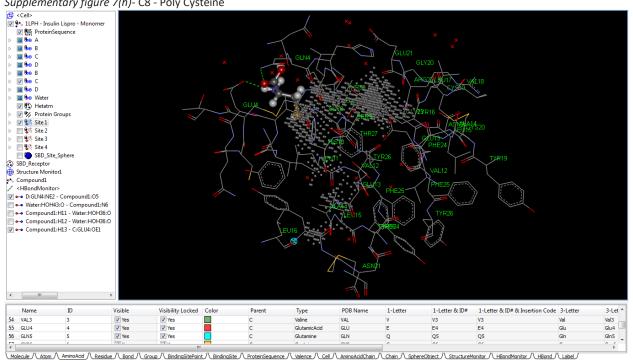
Supplementary figure 7(d)- C4 - Vitamin B1 (Thiamin)

<Cell>

§◆、1LPH - Insulin Lispro - Monomer



Supplementary figure 7(h)- C8 - Poly Cysteine



PDB Name

GLY

ILE

GLU

1-Letter

1-Letter & ID#

G1

E4

G1

E4

1-Letter & ID# & Insertion Code 3-Letter

Glv

Glu

Gly 1 Ile2 Val3

Glu4

Supplementary figure 7(j)- C10 – Pectin

Visible

✓ Yes
✓ Yes
✓ Yes
✓ Yes

Visibility Locked

✓ Yes

V Yes
V Yes
V Yes

Parent

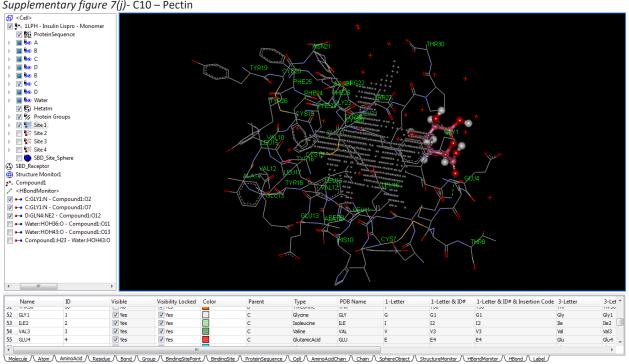
Glycine

ule 🖊 Attom 🖊 Amino Acid 🖍 Residue 🕂 Bond 🖊 Group 🖊 BindingSitePoint 🖊 BindingSite ProteinSequence 🖊 Valence 🕂 Cell 🖊 Amino AcidChain 🗍 Chain 🖊 SphereObject 🖊 StructureMonitor 🥂 HBondMonitor 🥂 HBond 🖊 Label 🗸

GlutamicAcid

Name

52 GLY1
53 ILE2
54 VAL3
55 GLU4
56 GLNS



Glycine

scule // Atom // AminoAcid // Residue // Bond // Group // BindingSitePoint // BindingSite // ProteinSequence // Cell // AminoAcidChain // Chain // SphereObiect // StructureMonitor // HBondMonitor // HBond // Label // AminoAcidChain // Chain // SphereObiect // StructureMonitor // HBondMonitor // HBond // Label // AminoAcidChain // Chain // SphereObiect // StructureMonitor // HBondMonitor // HBond // Label // AminoAcidChain // Chain // SphereObiect // StructureMonitor // HBondMonitor // HBond // Label // AminoAcidChain // Chain // SphereObiect // StructureMonitor // HBondMonitor // HBond // Label // AminoAcidChain // Chain // SphereObiect // StructureMonitor // HBondMonitor // HBond // Label // AminoAcidChain // SphereObiect // StructureMonitor // HBond // Label // SphereObiect // SphereObiect // StructureMonitor // HBond // Label // SphereObiect // StructureMonitor // HBond // Label // SphereObiect // SphereObie

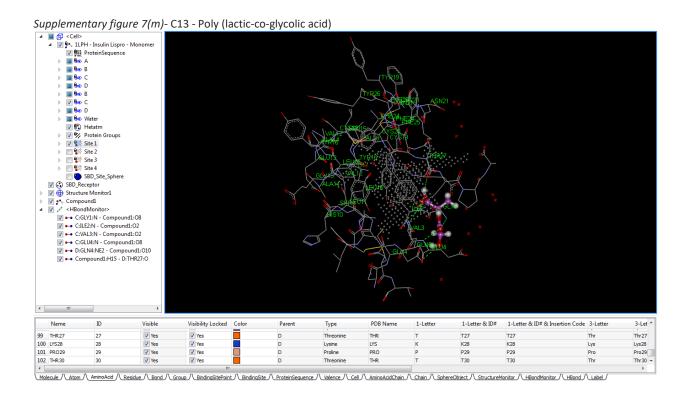
GLY

Supplementary figure 7(I)- C12 - Poly(propylene imine) No Conjugation

▼ Yes

V Yes

52 GLY1 53 ILE2 54 VAL3

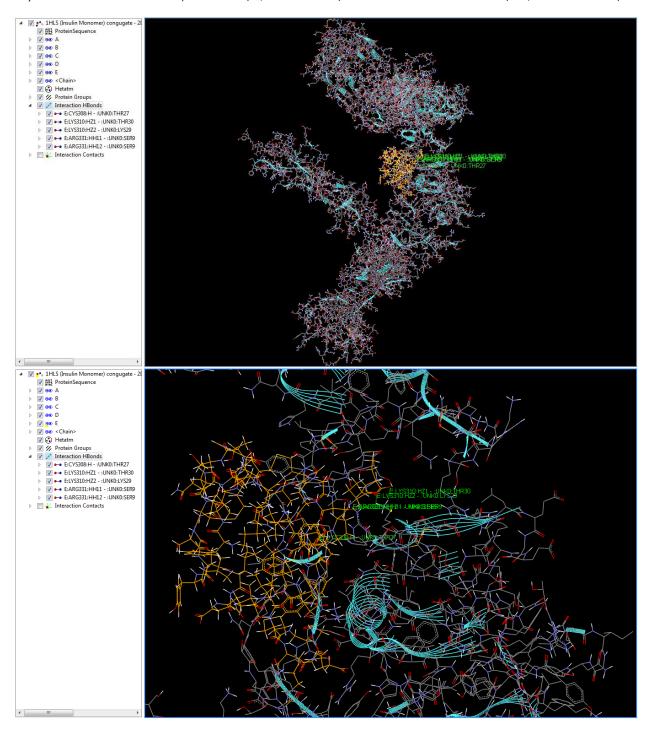


Supplementary figure 7(n)- C14 - Deoxycholic acid No Conjugation

Gly1

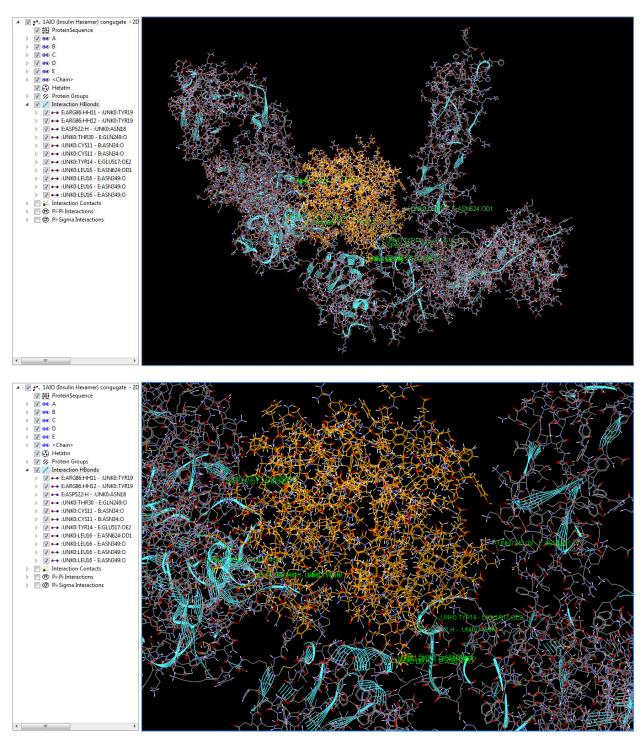
Supplementary figure 8(a)

Interaction results of Oral insulin conjugates (Insulin Monomer (1HLS)- DDM Conjugates) with Insulin Receptor (IR). It does not show any interaction in leucine-rich repeat domain (L1, residues 1-157) and in C-terminus of the α -chain (α CT, residues 704-715).



Supplementary figure 8(b)

Interaction results of Oral insulin conjugates (Insulin Hexamer (1AIO)- DDM Conjugates)- DDM Conjugates) with Insulin Receptor (IR). It shows the interaction in ARG86, ASN34 of leucine-rich repeat domain (L1, residues 1-157) and no interaction in C-terminus of the α -chain (α CT, residues 704-715).



Supplementary figure 8(c)

Interaction results of Oral insulin conjugates (Insulin Lispro (1LPH) - DDM Conjugates) with Insulin Receptor (IR). It shows the interaction in ARG86, ASN90 and ARG114 of leucine-rich repeat domain (L1, residues 1-157) and no interaction in C-terminus of the α -chain (α CT, residues 704-715).

