

Supplementary files

Fig. S1: Diagrammatic representation of Structure-guided approach to design potential inhibitors of LHBs protein.

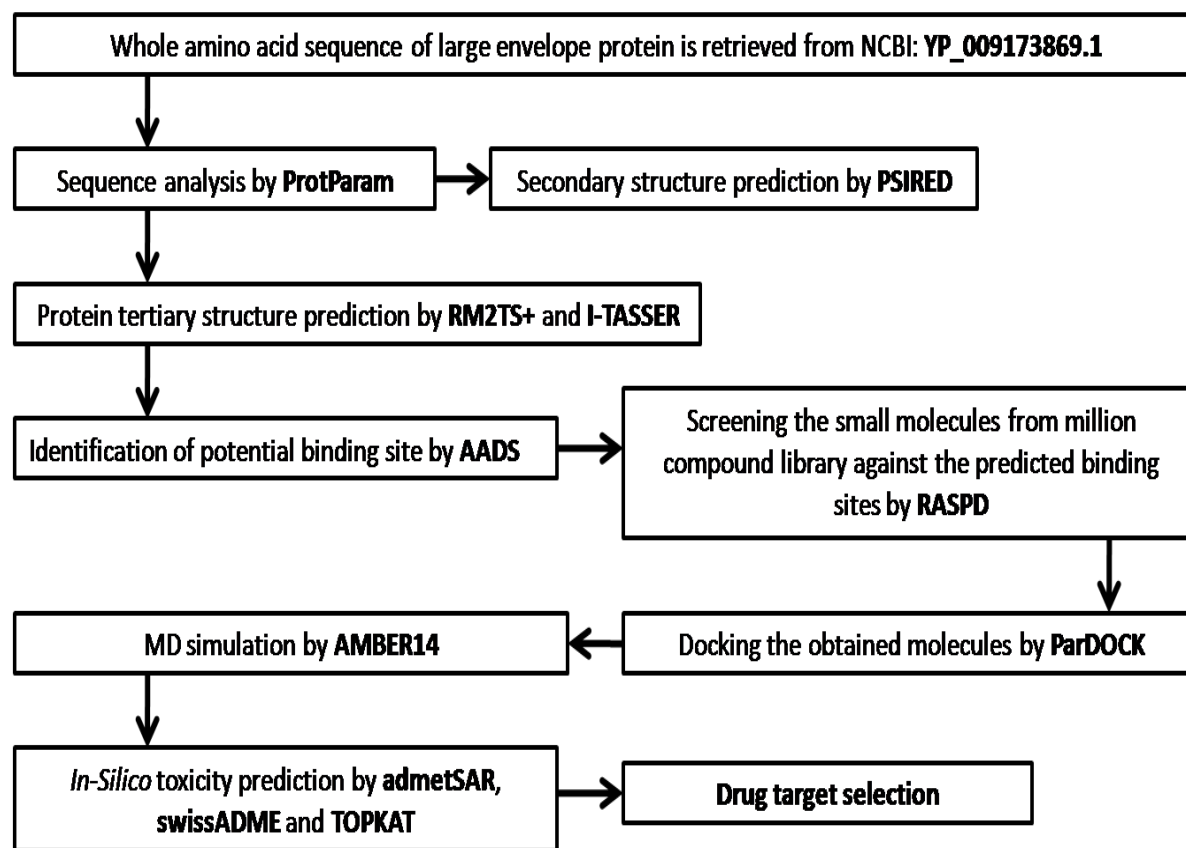
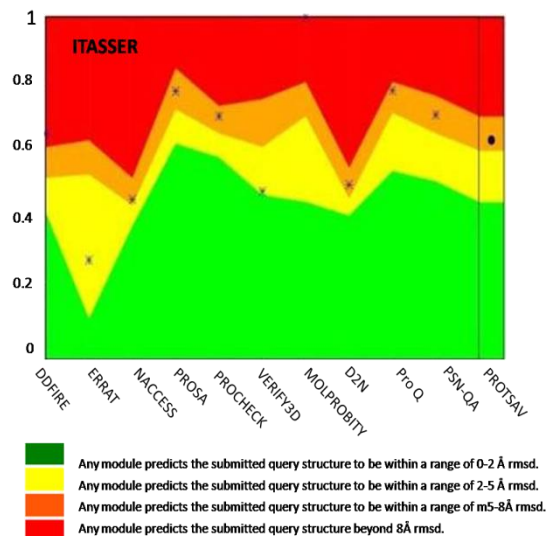
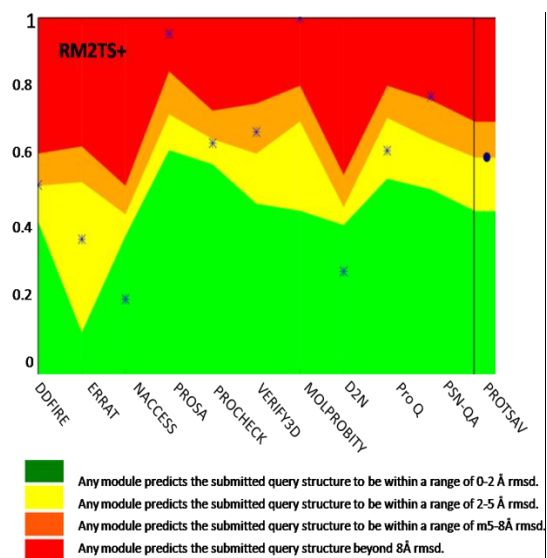


Fig. S2: Distribution of α -helix (pink), β -sheet (yellow) and coil (black) in the LHBs protein

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1 M G Q N L S T S N P L G F F P D H Q L D P A F R A N T A N P D W D F N P N K D T W P D A N K V G A G 50
51 A F G L G F T P P H G G L L G W S P Q A Q G I L Q T L P A N P P P A S T N R Q S G R Q P T P L S P P 100
101 L R N T H P Q A M Q W N S T T F H Q T L Q D P R V R G L Y F P A G G S S S G T V N P V L T T A S P L 150
151 S S I F S R I G D P A L N M E N I T S G F L G P L L V L Q A G F F L L T R I L T I P Q S L D S W W T 200
201 S L N F L G G T T V C L G Q N S Q S P T S N H S P T S C P P T C P G Y R W M C L R R F I I F L F I L 250
251 L L C L I F L L V L L D Y Q G M L P V C P L I P G S S T T S T G P C R T C M T T A Q G T S M Y P S C 300
301 C C T K P S D G N C T C I P I P S S W A F G K F L W E W A S A R F S W L S L L V P F V Q W F V G L S 350
351 P T V W L S V I W M M W Y W G P S L Y S I L S P F L P L L P I F F C L W V Y I
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Fig S3: The structures which were obtained from RM2TS+ and I-TASSER were further analyzed using various tools such as ProtSAV, Protein Structure Analysis and Validation, but for getting better structure the MD was run for 20 ns.

• **LHBs structure before MD**



• **LHBs structure after MD**

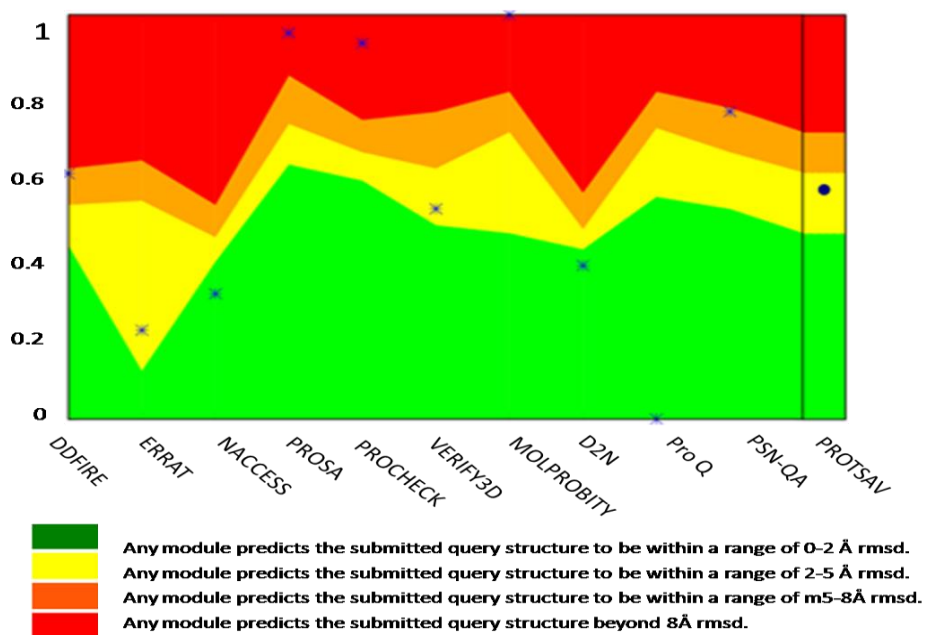


Table S1: Physiological properties of LHBs protein.

Protein	Molecular wt.(Da)	Theoretical pI	Estimated half-life	Instability index	Aliphatic index	No. of amino acid	No. of atoms	GRAVY
LHBs	42766.45	8.40	30hrs	46.08	82.24	389	5967	0.146

Table S2: 2D structure of identified ligands from ZINC database

No	ZINC ID	ParDock ID	2D Structure of Ligand
1	11882026	33625775	

2	653293	21425236	
3	19741044	72860345	
4	15000762	78876711	
5	11784805	34135187	
6	12243260	32993271	

Table S3: Comparative analysis of hydrogen bonds in LHBs and four ligands.

NO	ZINC ID	Receptor atom (LHBs)	Ligand atom	No. of H bonds	Bonding Length (Å)
1	11882026	Ala (51) [O] Trp (111) [O] Thr (104) [O]	[N] [N] [O]	3	3.33 3.08 3.32
2	653293	Pro (106) [O] Ala (108) [N]	[N] [N]	2	2.9 3.2
3	19741044	Ser (90) [N]	[O]	1	3.20
4	15000762	Ser (280) [N]	[O]	1	2.89

Table S4: Computationally predicted ADME properties of the identified compounds 1-5 by admetSAR and SwissADME. NS: (Non- Substrate); S: (Substrate); NI: (Non-Inhibitor); NT: (Non-Toxicity); NC: (Non-Carcinogen); NR: (Non-required)

Descriptor	ZINC11882026	ZINC00653293	ZINC19741044	ZINC15000762
Absorption				
Blood-Brain Barrier	BBB+	BBB+	BBB+	BBB+
Human Intestinal Absorption	HIA+	HIA+	HIA+	HIA+
GI - absorption	High	High	High	High
Caco-2 permeability	Caco2+	Caco2+	Caco2+	Caco2+
Metabolism				
CYP4502C9 Substrate	NS	NS	NS	NS
CYP4502D6 Substrate	S	NS	NS	NS
CYP4503A4 Substrate	S	S	S	S
CYP4501A2 Inhibitor	NI	NI	NI	NI

CYP4502C9 Inhibitor	NI	I	I	I
CYP4502D6 Inhibitor	NI	I	NI	NI
CYP4502C19 Inhibitor	I	I	I	NI
CYP4503A4 Inhibitor	NI	I	NI	NI
Toxicity				
AMES Toxicity	NT	NT	NT	NT
Carcinogens	NC	NC	NC	NC
Carcinogenicity (Three-class)	NR	NR	NR	NR
Number of drug likeliness rules followed*				
Lipinski	Yes	Yes	Yes	Yes
Ghose	No	No	No	Yes
Veber	Yes	Yes	Yes	Yes
Egan	Yes	Yes	Yes	Yes
Muegge	No	Yes	Yes	Yes

Table S5: TOPKAT values of the identified compounds. NM: (Non-Mutagen); NC: (Non-Carcinogen); C: (Carcinogen); NI: (Non-irritant); NS: (Non-Sensitive); S: (Sensitive)

Descriptor	ZINC11882026	ZINC00653293	ZINC19741044	ZINC15000762
Ames Mutagenicity (v3.1)	NM (0.853)	NM (0.000)	NM (0.000)	NM (0.717)
Weight of Evidence Carcinogenicity Call (v5.1)- (WOE)	NC (0.000)	NC (0.394)	C (1.000)	NC (0.003)
Rat Oral LD50 (v3.1)	2.432	3.946	4.559	2.895
Skin Irritation (v6.1)	NI (0.000)	NI (0.000)	NI (0.000)	NI (0.000)
Skin Sensitization NEG v SENS (v6.1)	NS (0.493)	NS (0.000)	NS (0.088)	NS (0.000)
Aerobic Biodegradability (v6.1)	No	Yes	No	Yes