Virtual screening of novel M. tuberculosis PknA/PknB dual inhibitors as anti-tuberculosis agents

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Introduction



Results

Biological prediction, docking energy and pharmacokinetic prediction of hit compounds

CHEMBL_ID	PknB		ТВ		MTB	H37Rv	H37Ra	R-MTB	R-H37R	Rv MycoCSM	Caseum FU(%)	MRTD log (mg/kg/day)	Docking (kcal/mo	
													PknA	PknB
CHEMBL12573	310 0.286	0.020	0.204	0.164		0.387			0.350	-4.559	1.296	0.067	-6.11	-8.61
CHEMBL1356	3360.199	0.034	0.233	0.130		0.352		0.030	0.043	-4.641	0.198	0.461	-6.17	-8.48
CHEMBL14037	777 0.109	0.078	0.217	0.148	0.001	0.050				-4.957	18.565	0.117	-6.93	-8.43
CHEMBL15384	43 0.115	0.072	0.357	0.046	0.154	0.500	0.039	0.121	0.237	-4.992	0.274	0.475	-6.35	-8.09

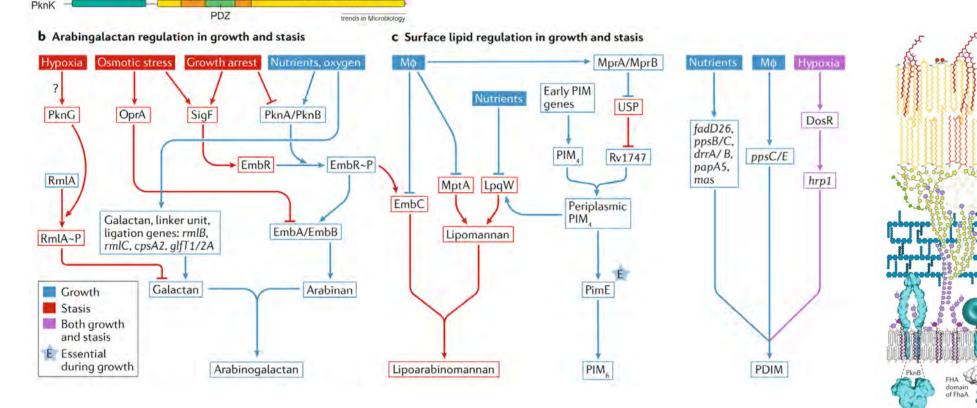
Report 2021

10 million people fell ill with TB. 1.5 million people deaths in 2020. Most TB cases were in the WHO regions of South-East Asia (43%)

> □ Ser/Thr protein kinases (STPKs) have been interested in anti-tuberculosis drug development.

□ *M. tuberculosis* STPK family contains 11 putative eukaryotic-like protein kinases

□ PknA and PknB controls the switch between peptidoglycan elongation and septum formation in bacteria.



Trends Microbiol. 2000, 8(5), 238-244. Nat Rev Microbiol. 2020, 18(1), 47-59 Tuberculosis report 2021, WHO



Absorption

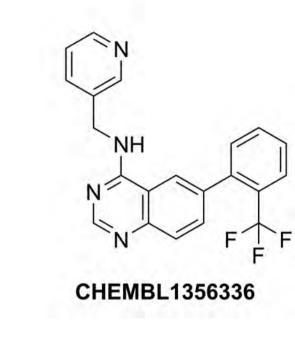
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CHEMBL ID	Water solubility	Caco2 permeability (log Papp in 10 ⁻⁶ cm/s)	Intestinal absorption (human) (% Absorbed)	Skin Permeability	P-glycoprotein substrate	P-glycoprotein I inhibitor	P-glycoprotein I inhibitor
CHEMBL1257310	-4.38	0.92	88.96	-2.91	No	No	Yes
CHEMBL1356336	6-4.54	1.46	93.65	-2.74	Yes	Yes	Yes
CHEMBL1403777	-2.96	1.20	96.83	-2.74	Yes	Yes	Yes
CHEMBL153843	-4.16	1.00	91.07	-2.77	Yes	Yes	Yes

Distribution

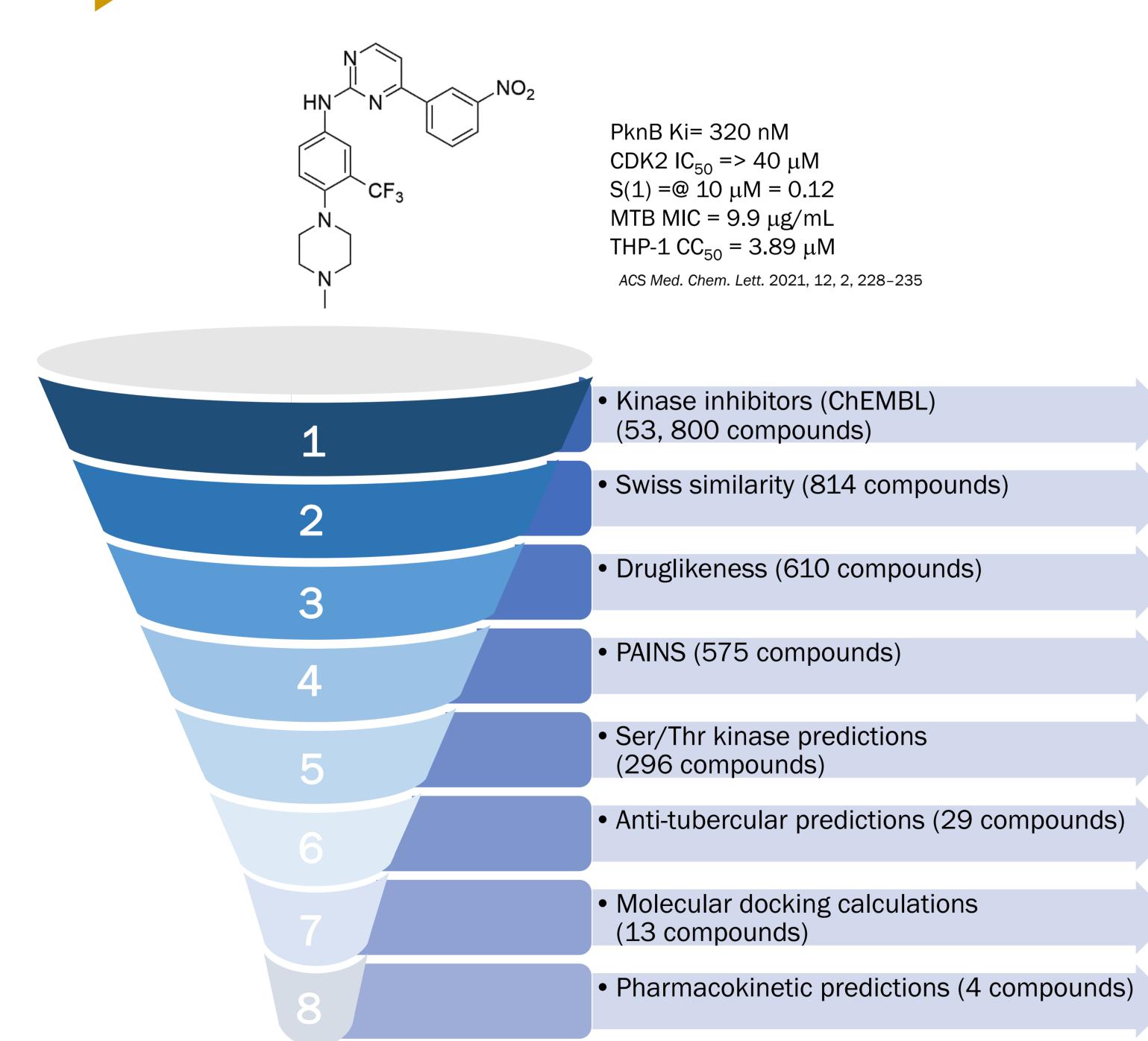
CHEMBL ID	VDss (human) (log L/kg)	Fraction unbound (human) (Fu)	BBB permeability (log BB)	CNS permeability (log PS)
CHEMBL1257310	-0.17	0.15	-0.15	-2.24
CHEMBL1356336	0.10	0.10	0.51	-1.81
CHEMBL1403777	0.46	0.14	-1.21	-3.64
CHEMBL153843	-0.08	0.07	0.07	-1.83

Metabolism & Excretion

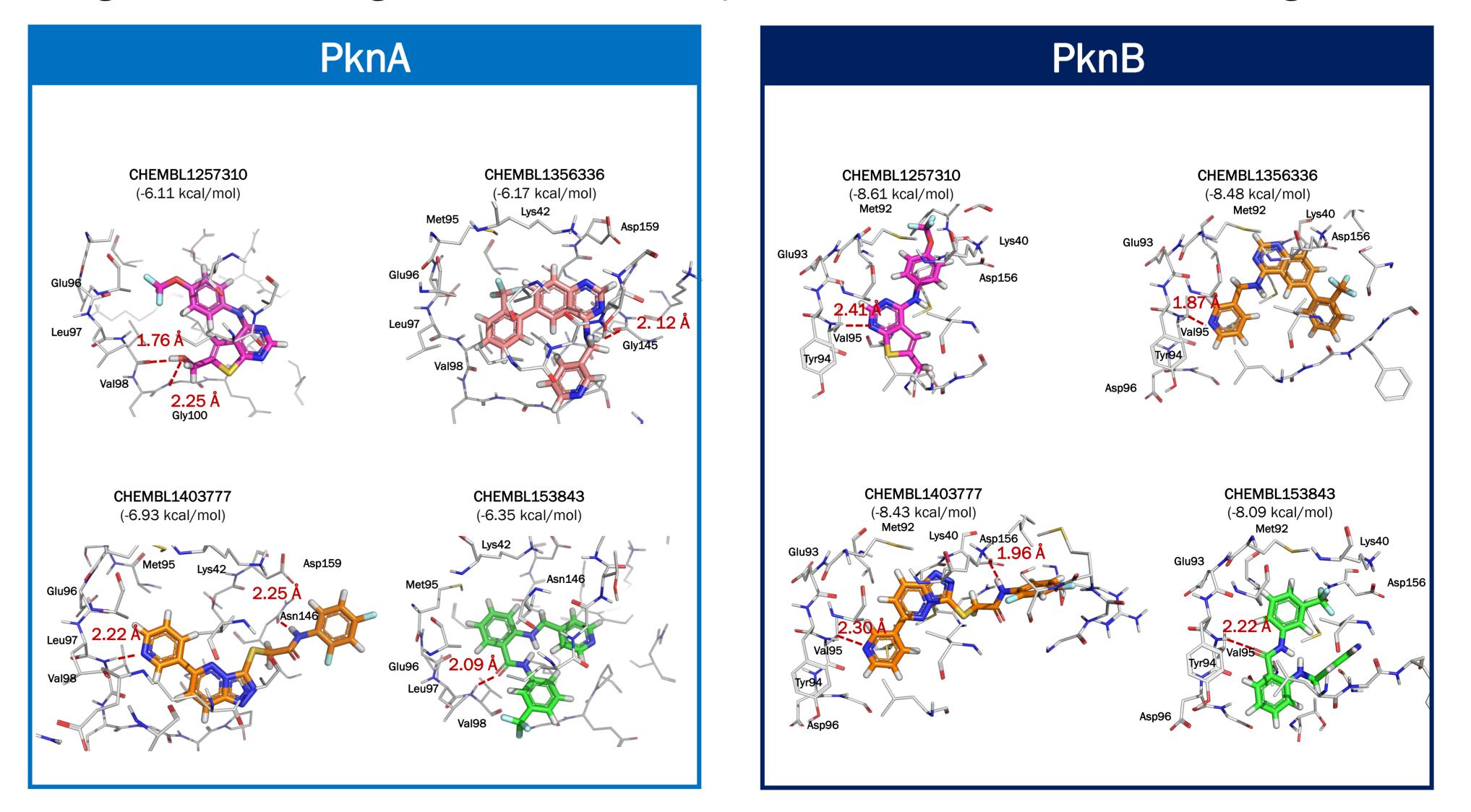
	Metabo	lism							Exc	retion		
CHEMBL ID	CYP2D6 substra	6 CYP3A4 te substrate	CYP1A2 inhibitio			YP2C9 hibitior	CYP2D inhibiti			al Clearar ; ml/min/	$\frac{1}{k\sigma}$	Renal OCT2 Substrate
CHEMBL1257310	No	Yes	Yes	Yes	Y	es	No	No	0.1	5	Ν	10
CHEMBL1356336	No	Yes	Yes	Yes	Ye	es	Yes	Yes	0.2	5	Ν	0
CHEMBL1403777	No	Yes	Yes	No	N	0	No	Yes	0.0	9	Ν	10
CHEMBL153843	Yes	Yes	Yes	Yes	Y	es	No	Yes	0.0	7	Ν	0
		MRTD (human) (log mg/kg/day)	Inflibitor	nERG II inhibit or	Oral Rat Acute Toxicity (LD ₅₀) (mol/kg	Chr Tox (LO mg, bw/	′day)		on	log u	ty	toxicity (log mM)
CHEMBL1257310	Yes	0.07	No	Yes	2.82	1.5	0	Yes	No	0.77		1.10
CHEMBL1356336	Yes	0.46	No	Yes	2.69	0.5	6	Yes	No	0.31		0.72
CHEMBL1403777	No	0.12	No	Yes	2.55	0.8		Yes	No	0.29		-0.87
CHEMBL153843	No	0.48	No	Yes	2.69	0.9	0	Yes	No	0.68		0.47







Binding mode and binding interactions of hit compounds derived from molecular docking calculations



Virtual screening workflow to identify of PknA/PknB dual inhibitors

Conclusions

- □ Four kinase inhibitors (CHEMBL1257310, CHEMBL1356336, CHEMBL1403777 and CHEMBL153843) were discovered as PknA/PknB dual inhibitors as anti-tuberculosis agents based on virtual screening and pharmacokinetic prediction.
- The predicted biological evaluation using several methods were confirmed that these finding compounds were promising structure for future validation as anti-tuberculosis agents.
- Strong binding affinity in the ATP binding site of PknA and PknB was obtained from molecular docking calculations. These hits shared hydrogen bond interaction with Val98 and Val95 backbone for PknA and PknB, respectively as the key interaction for binding.

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