

Cytisine derivatives as new anti-*Escherichia coli* agents: *in silico* and *in vitro* studies

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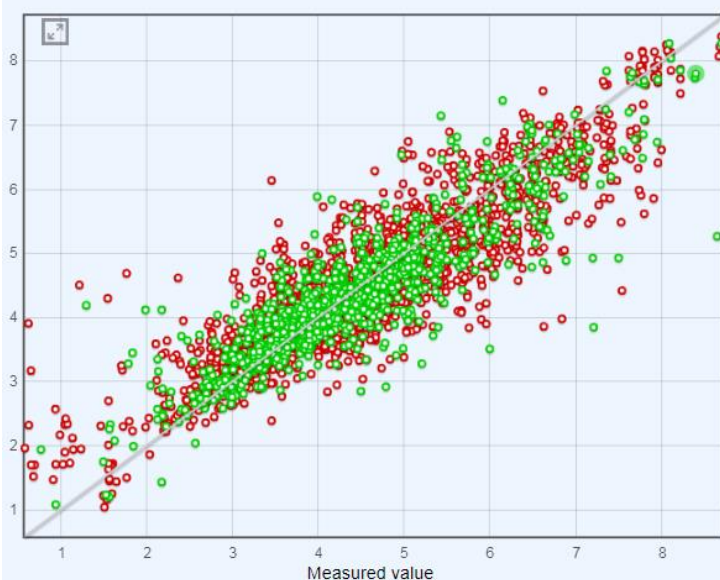
Results and discussion

Regression models from Table 1

Model name: M1_MIC_TRANSNN_10/10 - 348863 [rename] , published in Cytisine derivatives as new anti- Escherichia coli in vitro studies
Public ID is 891

Predicted property: MIC modeled in $-\log(M)$
Training method: TRANSNN

Data Set	#	R2	q2	RMSE	MAE
Training set: EColi_Set_IV (training)	3758 records	0.804 ± 0.009	0.803 ± 0.009	0.485 ± 0.01	0.326 ± 0.006
Test set: EColi_Set_IV (test) [x]	1352 records	0.8 ± 0.02	0.8 ± 0.02	0.49 ± 0.02	0.32 ± 0.01

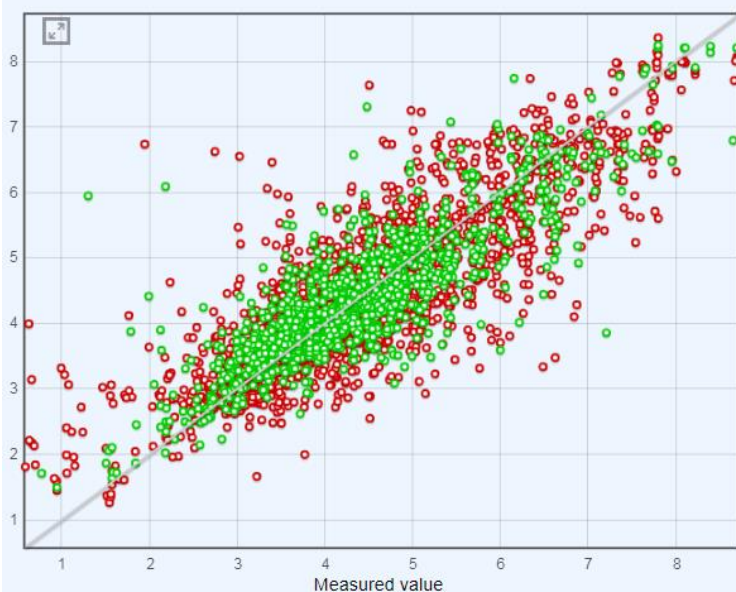


a)

Model name: M2_MIC_ASNN_[ALogPS, CDK23 (cons,topol,geom,elect,hybr), OEstate] - 438223 [rename] , published new anti- Escherichia coli agents: in silico and in vitro studies
Public ID is 892

Predicted property: MIC modeled in $-\log(M)$
Training method: ASNN

Data Set	#	R2	q2	RMSE	MAE
Training set: EColi_Set_IV (training)	3763 records	0.73 ± 0.01	0.72 ± 0.01	0.58 ± 0.01	0.392 ± 0.007
Test set: EColi_Set_IV (test) [x]	1350 records	0.74 ± 0.02	0.74 ± 0.02	0.57 ± 0.03	0.39 ± 0.01

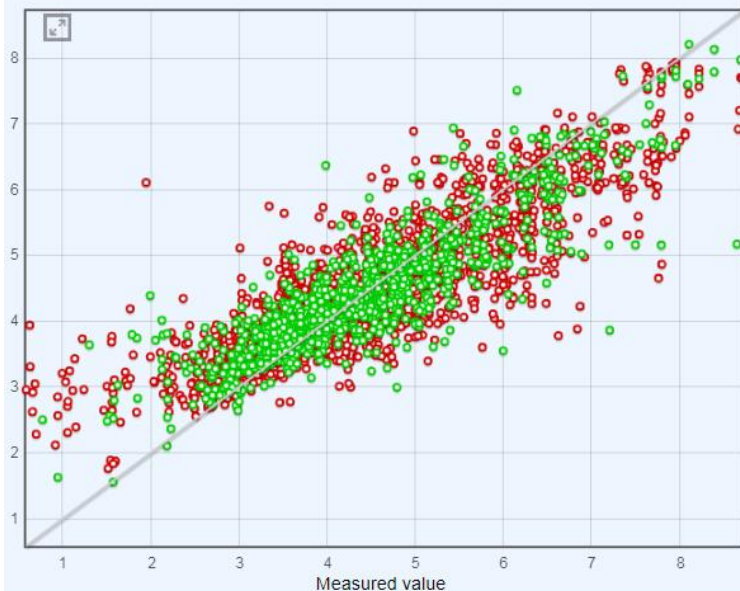


b)

Model name: M3_MIC_RFR_[A]LogPS, CDK23 (cons.topol.geom.elect.hybr), OEstate] - 438236 [rename] , published new anti- Escherichia coli agents: in silico and in vitro studies
Public ID is 893

Predicted property: MIC modeled in $-\log(M)$
Training method: RFR

Data Set	#	R2	q2	RMSE	MAE
● Training set: EColi_Set_IV (training)	3763 records	0.761 ± 0.01	0.751 ± 0.009	0.55 ± 0.01	0.377 ± 0.007
● Test set: EColi_Set_IV (test) [x]	1350 records	0.78 ± 0.02	0.77 ± 0.02	0.53 ± 0.02	0.36 ± 0.01

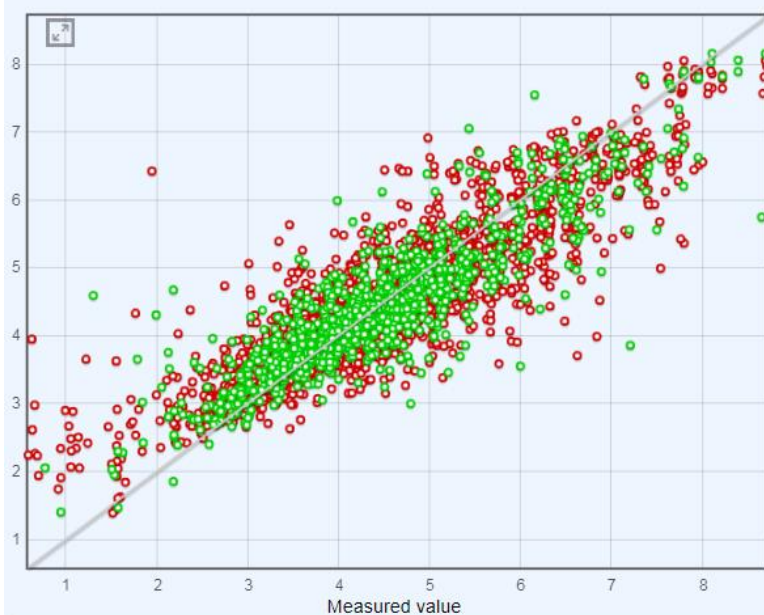


c)

Model name: M4_Consensus MIC - 438239 [rename] , published in Cytisine derivatives as new anti- Escherichia studies
Public ID is 894

Predicted property: MIC modeled in $-\log(M)$
Training method: Consensus

Data Set	#	R2	q2	RMSE	MAE
● Training set: EColi_Set_IV (training)	3775 records	0.795 ± 0.01	0.792 ± 0.009	0.5 ± 0.01	0.341 ± 0.006
● Test set: EColi_Set_IV (test) [x]	1360 records	0.8 ± 0.02	0.79 ± 0.01	0.5 ± 0.02	0.33 ± 0.01

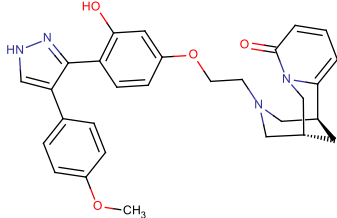
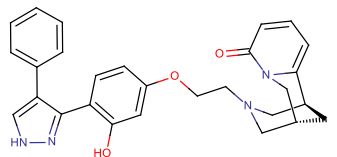
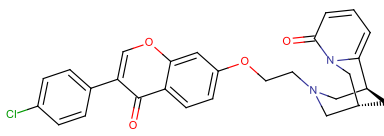
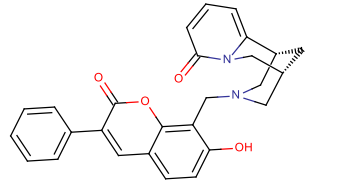
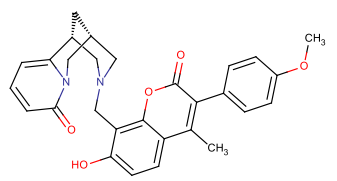
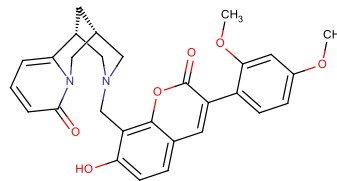
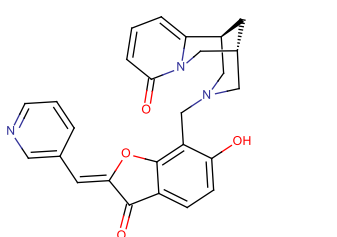


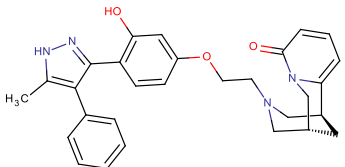
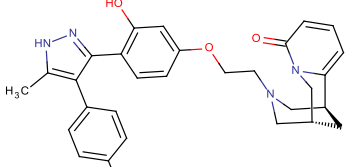
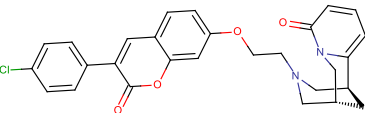
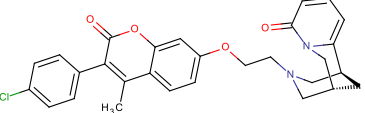
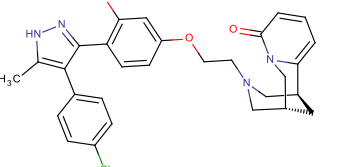
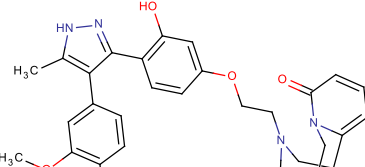
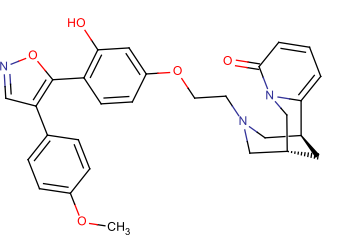
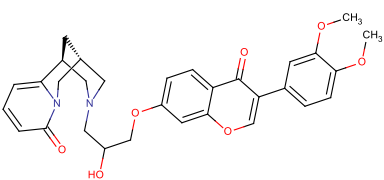
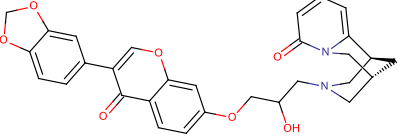
d)

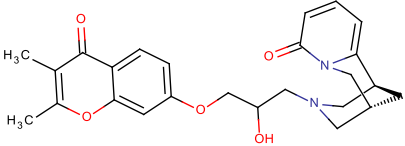
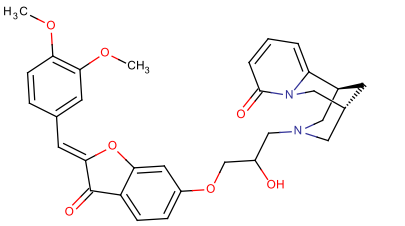
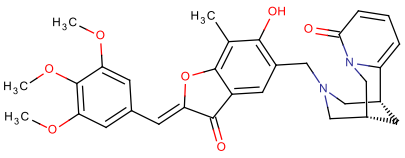
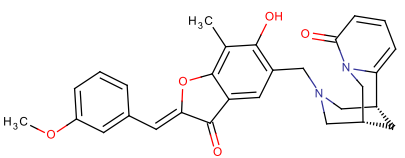
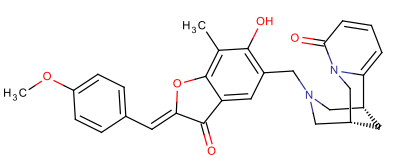
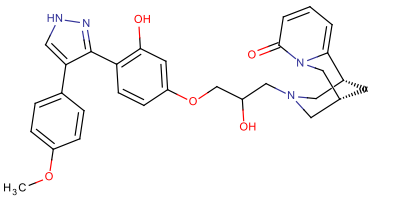
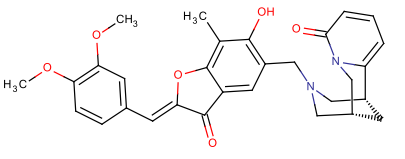
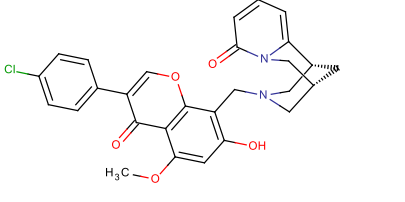
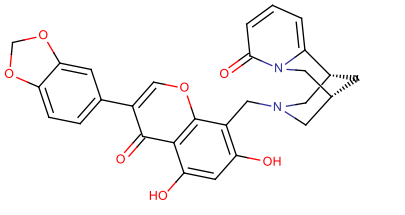
Fig. S1. Regression machine learning models built by the OCHEM server (<http://ochem.eu>). a-c) Statistical coefficients calculated for regression models by a different MLT; d) Consensus model calculated by averaging the previous three models.

Evaluation activity of new compounds

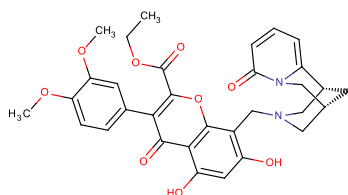
Table 2S. Anti-*Escherichia coli* activity calculated by using the consensus regression model for 26 virtual compounds

Comp. No	Chemical Structure	log(1/MIC), M	CONSENSUS STD	Estimated RMSE	AD
1		5.65	0.99	1.34	FALSE
2		5.51	1.1	1.34	FALSE
3		4.59	0.54	1.34	FALSE
4 ^b		4.64	0.28	0.61	TRUE
5 ^b		4.57	0.25	0.61	TRUE
6 ^b		4.61	0.2	0.41	TRUE
7 ^a		5.05	0.43	0.74	TRUE

8		5.46	1.12	1.34	FALSE
9		5.54	1.11	1.34	FALSE
10		4.39	0.53	1.34	FALSE
11		4.51	0.55	1.34	FALSE
12		5.52	1.01	1.34	FALSE
13 ^a		5.55	1.09	1.34	TRUE
14 ^a		4.53	0.39	0.61	TRUE
15 ^a		4.60	0.24	0.61	TRUE
16		4.67	0.51	1.34	FALSE

17 ^a		4.34	0.24	0.61	TRUE
18 ^a		4.88	0.16	0.41	TRUE
19		5.11	0.55	1.34	FALSE
20		5.22	0.66	1.34	FALSE
21		5.25	0.73	1.34	FALSE
22		5.69	1	1.34	FALSE
23		5.07	0.54	1.34	FALSE
24 ^a		4.91	0.21	0.41	TRUE
25		5.02	0.64	1.34	FALSE

26^b



4.61 0.32 0.61 TRUE

^aFinal set compounds are represented in bold. ^bCompound predicted as high toxic; MIC - minimal inhibitory concentration; CONSENSUS-STD - the standard deviation of the predictions, obtained from an ensemble of models; RMSE is the root mean square error; AD –applicability domain.