Modeling of Mammalian Ribonuclease Inhibitor Complex With Bacterial Ribonuclease Binase

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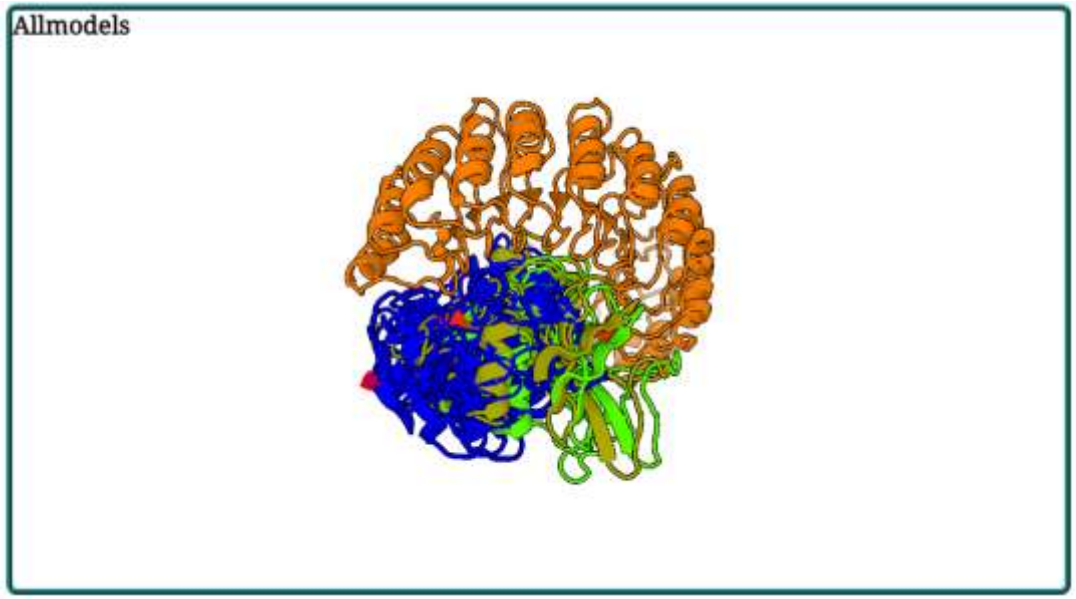
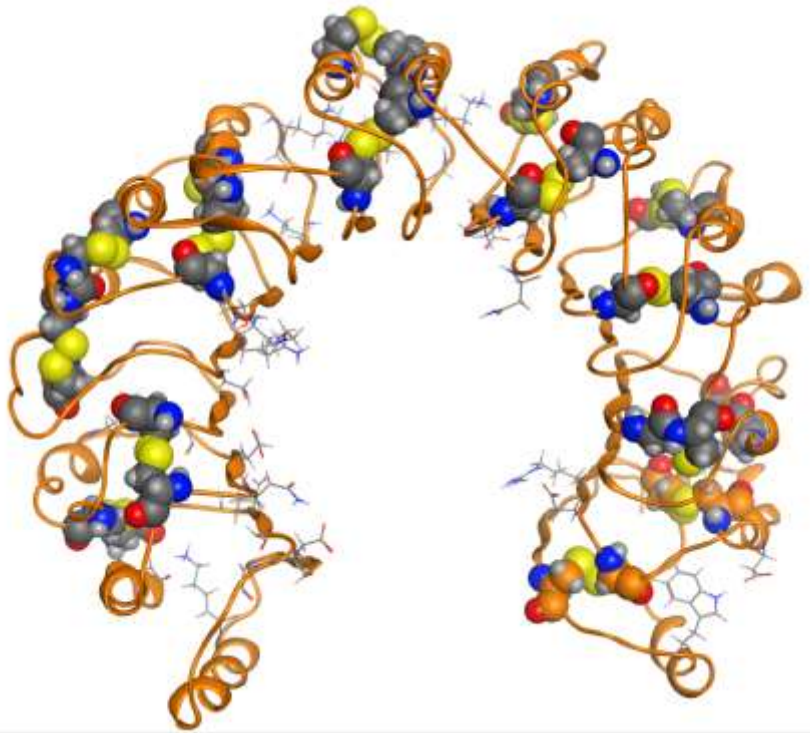
As a result of the MST experiment, we found, that the mammalian ribonuclease inhibitor (RI) creates a stable complex with the bacterial ribonuclease binase. We aimed to determine the mechanism of their interaction.

- We used programs MOE (Molecular Operating Environment) and ZDOCK. We received 11 models of the oxidized RI in complex with the binase and 11 models of the RI in complex with the binase. There was no structure of the oxidized RI in PDB (Protein Database Bank), so we modelled it.

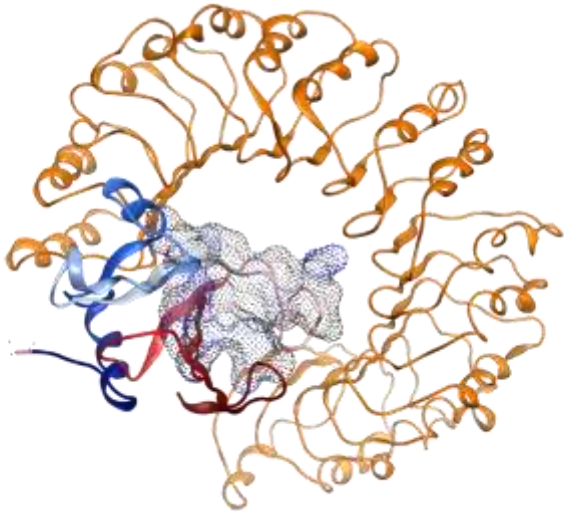


Model	S	S Atomic	RC	RC Atomic	Cluster		
complex.6	0.7690	0.9860	47	945	3	N	>
complex.3	0.7427	0.8373	38	707	1	L	>
complex.4	0.6871	0.9980	39	880	1	L	>
complex.2	0.6111	0.6483	35	543	1	L	>
complex.1	0.6082	0.8569	29	718	1	L	>
complex.5	0.5965	0.5878	39	608	2	M	>
complex.10	0.5497	0.6358	31	581	1	L	>
complex.9	0.5205	0.6115	29	500	2	M	>
complex.7	0.5117	0.3696	29	364	3	N	>
complex.8	0.4854	0.6165	26	532	1	L	>

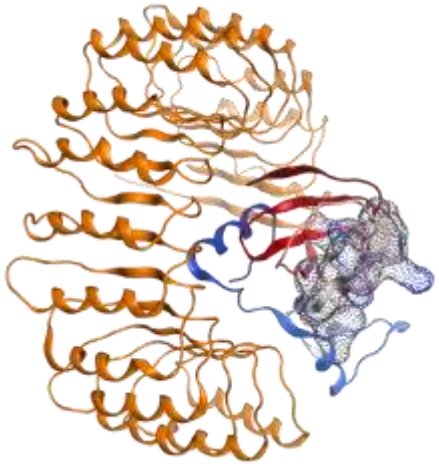
We have chosen the models, where the binase binds with the RI, but its catalytic center is opened.



The model of the oxidized RI



The model of the oxidized RI in complex with binase



The model of the RI in complex with binase

Using the computer modeling we have shown, that the RI and the binase could create a complex and its energy was predicted

	Total energy of the complex, Kcal/mol	RI energy, Kcal/mol	Binase energy. Kcal/mol	Difference, Kcal/mol
RI + binase	-10056.1	-7327.82	-2111.2	-617.08
Oxidized RI + binase	-10044	-7336.13	-2132.31	-575.56

Interaction residues in the model structures

Oxidized RI	Binase	Energy, kcal/mol
Asp403	Arg71	-2.5
Gln10	Arg68	-1.57
Trp438	Lys17	-1.55
Ile459	Trp93	-1.53
Trp263	Ser56	-1.01
Tyr434	Ser90	-0.76
Arg63	Leu62	-0.69
Asp378	Ser27	-0.41
Asn407	Gln28	-0.38
Asp435	Arg71	-0.16

RI	Binase	Energy, kcal/mol
Asp435	Arg71	-4.13
Ser460	Gln28	-3.32
Ser207	Arg107	-2.7
Asn178	Arg109	-2.37
Leu433	Gln28	-1.88
Asp35	Thr5	-1.39
Asp121	Ile108	-1.36
Trp261	Ile14	-1.36
Trp438	Gln28	-1.25
Ile459	Pro20	-1.23
Asp121	Arg109	-1.13
Arg63	Asp11	-0.67
Ile436	Gln28	-0.52
Asp36	Thr5	-0.42
Glu12	Val78	-0.41
Trp318	Lys17	-0.4

Acknowledgment

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