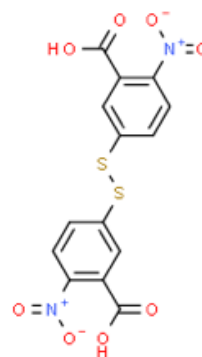
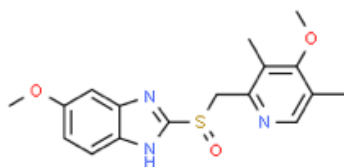


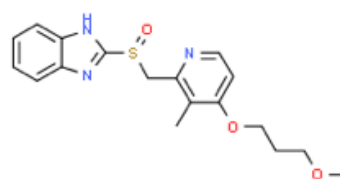
MMTS
PubChem CID: 18064



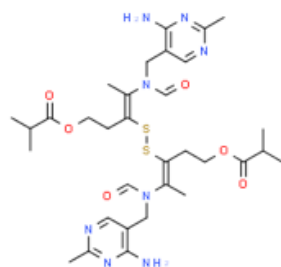
DTNB
PubChem CID: 6254



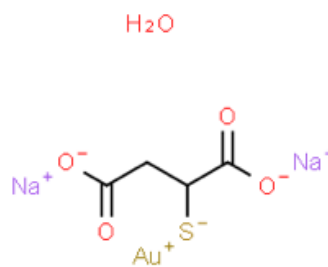
Omeprazole
PubChem CID: 4594



Rabeprazole
PubChem CID: 5029



Sulbutiamine
PubChem CID: 20055424



Aurothiomalate
PubChem CID: 134577

Figure S1. Studied molecules 2D chemical structure. The structures were obtained from Chemspider free chemical structure database (www.chemspider.com).

XP_001705755.1	MTDFSKDKEKLAQATQGGENERAEIVVVHLPQGTS-FLTSLNPEGNLLEEPICPDELRRD	59
EST48861.1	-----MQIKPQQHSEHATARTILVYEP ELAV-FVNCLHPAGSLYECPI NPESALAQ	50
WP_011027247.1	--MTSNESA VSQALGVHSEVGR LRKVLVCSPLG LAHRRLTPTNSDELLFDDVMVVENAQRD	58
WP_012482189.1	-----MRGFGVHSEVGKLR TVMVCRPSLAHQRLTPANCHDLLFDDVLVWHEAQKD	50
KFL10416.1	-----MSTEKTKLGVHSEAGKLRKVMVCSPLG LAHQRLTPSNCDELLFDDVIWVWNAQKR	54
KHL72821.1	-----MSAEKQKYGVHSEAGKLRKVMVCA PLG LAHKRLTPSNCDELLFDDVIWVDQAKRD	54
AAD55448.1	---MSVFDSKFKGIHVYSEIGELETVLVHEPGKEIDYITPARLDELLFSAILES HDARKE	57
BAQ54605.1	---MSVFDSKFKGIHVYSEIGELESVLVHEPGREIDYITPARLDELLFSAILES HDARKE	57
AGS66837.1	-----MEEEYLNPI NIFSEIGRLKKVLLHRPGEELENLTPLIMKNFLFDDIPYLKVARQE	55
NP_813907.1	-----MSHPINVFSEIGKLTVM LHRPGKELENLMPDYLERLLFDDIPFLEKAQAE	51
ARW56296.1	-----MTTPIHVYSEIGPLKTVMLKRP GRELENLTPEYLERLLFDDIPFPAVQKE	51
CAA04682.1	-----MTSPIHVNSEIGKLTVLLKRP GKEVENITPDIMYRLLFDDIPYLP TIQKE	51
	. * . : : * : * . :	

XP_001705755.1	HEGFQAVLKEKGC RVMPYDVLSEAS--P--AEREVLMDQAMASLKYELHATGARITPKM	115
EST48861.1	HRNFQKVLQSHGINVLEVECI LRSTNTDP--AQRLELEEYAAQQLTY-----IGP	98
WP_011027247.1	HAAFVGE LRRRGVEVVELHDLLAQIMALP--EARAWLLDRKITANQ-----VGIGL----	107
WP_012482189.1	HFDFVLKMQERGVEVLELHDLLGQTLANQ--QARDFLLDRRITPNV-----LGSQI----	99
KFL10416.1	HFDFVTKMRERGI DVLEMHNLTTETIQNP--EALKWILDRKITADS-----VGLGL----	103
KHL72821.1	HFDFVTKMRERGV DVLEMHNLTDIVQNK--DA LKWILDRKITPDT-----VGVLG----	103
AAD55448.1	HKEFVAELKKRGIN VVELVDLIVETYDLASKEAKEKLL EEFLDDSAP---VLSDEH----	110
BAQ54605.1	HKQFVAELKANDIN VVELIDLVAETYDLASQEA KDKLIEEFLEDSEP---VLSEEH----	110
AGS66837.1	HEVFNILKDNSVEIEYVEDLVSEVLASS-VALKNKFISQFILEAEI----KTDGV----	106
NP_813907.1	HDFAELLRSKDI EVVYLEDLAAEALINE--EVRRQFIDQFLEANI-----RSESA----	101
ARW56296.1	HDQFAETLKQQGA EVLYLEKLTAEALDDA--LVREQFIDELLTESKA----DINGA----	101
CAA04682.1	HDQFAQTLRDNGVEVLYLENLAAEAIDAG--DVKEAFLDKMLNESH I----KSPQV----	101
	* * : : . : . : . :	

XP_001705755.1	KYCVSDEYKRKVL SALST-RNLVDVILSEPV IHLAPGVRNT-----ALVTNSVEIHD	166
EST48861.1	EEYASDDYKMKV IKSLSPE-SLVKVLITAPV VYLEATTNNT-----NVITTKTEMRA	149
WP_011027247.1	-----IDAARAYLET LSP-RELAEYLVGGLATSDLPEDFRSPHLALARESTGAREYLMPP	161
WP_012482189.1	-----AEAMRPWLDEMPA-AQLAAFMIGTAISDLPEVRAKSL---MLSALPEDFVIPP	150
KFL10416.1	-----TSELRSWLESLEP-RKLAEY LIGGVAADDLPASEGADILKMYREYLGHSSFLLPP	157
KHL72821.1	-----TNEVRSWLEGLEP-RHLAEFLIGGVAGQDLPQSEGADVVKMYNDYLGHSSFILPP	157
AAD55448.1	-----RAAVKKFLQS QKSTRSLVEYMIAGITKHDLKI-----ESDLELIVDP	152
BAQ54605.1	-----KVVVRNFLKAKKTSRELVEIMMAGITKYDLGI-----EADHELIVDP	152
AGS66837.1	-----INILKDYFSNLTV-DNMVSKMISGVAREELKDCEF-SLDDWV---NGSSLFVIDP	156
NP_813907.1	-----KEKVRELMLEID DNEELIQAIAGIQKQELPKYEQEFLTDMV---EADYPFII DP	153
ARW56296.1	-----YDRLKEFLLT FDDA-DSMVEQVMGSI RKNELEREKSKSHLHELM---EDHYPFYLDP	152
CAA04682.1	-----QAALKDYLI SMAT-LDMVEKIMAGVRTNEIDIKSKALIDVSA---DDDYPFYMDP	152
	: : : :	

XP_001705755.1	SNNMVFMRDQQITTRRGIVMGQFQAPQRRREQVLALIFWKRLGARVVGD-----	215
EST48861.1	LGNIVFTRDQQIT TAKGVVIGNFSAEQRLGENALMEFVLKKIGIRPIGRIGEFYTERHIP	209
WP_011027247.1	LPNTLYTRDTT CWLYGGTLNPLYWSARHDETLLMKAIYTFHPDFK-GS--KVWW----	213
WP_012482189.1	IPNTLFQRDPSCW IYGGVTCNPMFWPARRAETLIQRAIYKFHPFIPL-GGDFQIWW----	204
KFL10416.1	LPNTQFTRDTT CWIYGGVTLNPMYWPARRQETLLTTAIYKFHPFEFA-NAEFEIYW----	211
KHL72821.1	LPNTQFTRDTT CWIYGGVTLNPMYWPARRQETLLTTAIYKFHPQFT-GADFQVWY----	211
AAD55448.1	MPNLYFTRDPFASV GNGVTIHYMRYKVRQRET LFSRFVFSNHPKLV---NTPWYY----	204
BAQ54605.1	MPNLYFTRDPFASV GNGVTIHYMRYKVRQRET LFSRFVFSNHPKLI---NTPWYY----	204
AGS66837.1	MPNVLFTRDPFAS IGNGITINKMYTKVRRRETIFA EYIFKYHSAYK--ENVPIWF----	209
NP_813907.1	MPNLYFTRDNFATM GHGISLNHMYSVTRQRETI FGQYIFDYHPRFA-GKEVPRVY----	207
ARW56296.1	MPNLYFTRDPAAA IGSLTINKMKEPARRRESLF MRYIINHHPRFK-GHEIPVWL----	206
CAA04682.1	MPNLYFTRDPAAS MGDGLTINKMTFEARQRESMFMEVIMQHHPRFA-NQGAQVWR----	206
	* : * * * : * * : .	

XP_001705755.1	----CREGGPHCMLEGGDFVPVSPGLAMMGVGLRSTYVGAQYLYMSKDLLGTR--RF-AVV	268
EST48861.1	ICGGANKLTPKATIEGGDFIALNNGIGALGVGLRSSYTAGIHLMEHDLLGTD--KF-IIV	266
WP_011027247.1	--GDPERDWGQATFEGGDIMPVGNVGVLGMGMSERTSRQAITQV-AAALFRSG--AAEHVV	268
WP_012482189.1	--GDSQDPFANASMEGGDVMPIGNGTVLIGMGERTTYQAVGQV-AQALFRSK--AAKRVI	259
KFL10416.1	--GDPDKDHGSS TLEGGDVMPIGNGVVLIGMGERTSRQAIGQV-AQSLFAKG--AAERVI	266
KHL72821.1	--GDPDKDHGNATLEGGDVMPIGKIVLIGMGERTSRQAIGQL-AQNLFAGK--AVEKVI	266
AAD55448.1	--DPA----EGLSIEGGDVFIYNNDTLVGVVSERTDLQTITLL-AKNIKANKECEFKRIV	257
BAQ54605.1	--DPS----LKLSIEGGDVFIYNNDTLVGVVSERTDLQTVTLL-AKNIVANKECEFKRIV	257
AGS66837.1	--NRW----EETSLIEGGDEFLVNLKDLLVTIGISERTEAGSVEKL-AASLFKNK-APFSTIL	261
NP_813907.1	--DRS----ESTRIEGGDELILSKEVVAIGISQRTDAASIEKI-ARNIFEQK-LGFKNIL	259
ARW56296.1	--DRD----FKFNIIEGGDELVLNEETVAIGVSERTTAQAIERL-VRNLFQRQ-SRIRRVL	258
CAA04682.1	--DRD----HIDRMEGGDELILSDKVLAIIGISQRTSAQSIEEL-AKVLFANH-SGFEEKIL	258
	: * * * . . : * . * : : :	

XP_001705755.1	KDCFDQHQRMRHLDC TFSVLHDKLVVLD DDIYI-CSGMGLRYVDEWID-VGAD--A----VK	320
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EST48861.1	KDTFDQDQDRMHLDTCTCSPLHDKLILIDEEILINPDKLRYVDEWVH-LGGY--S----DE	319
WP_011027247.1	VAGMPKLRSAAMHLDTVFTFADRDVVTLYPRIMDAV---HTFSLRPGDRAPGFDVV--DEG	323
WP_012482189.1	GCLMPKSRAAMHLDTVFSFCDDRVDVTLFAEVVDQV---RCYSMPKDDD-GTFEI--HPE	313
KFL10416.1	VAGLPKSRAAMHLDTVFSFCDDRDLVTIFPEVVKEI---VPFSLRDPSSPYGMNI--RRE	321
KHL72821.1	VAGLPKSRAAMHLDTVFSFCDDRDLVTIFPEVVKEI---VPFIIRPDESKPYGMDV--RRE	321
AAD55448.1	AINVPKWTNLMHLDTWLTMLDKDKFLYSPIANDVF---K-FWDYDLVNG--GDAPQPVND	311
BAQ54605.1	AINVPKWTNLMHLDTWLTMLDKDKFLYSPIANDVF---K-FWDYDLVNG--GAEPQPVEN	311
AGS66837.1	AFKIPKNRAYMHLDTVFTQIDYSVFTSFTS---DD---MYFSIYVLTYSNSNKNINIKKE	315
NP_813907.1	AFDIGEHRKFMHLDTVFTMIDYDKFTIHPEIEGGL---V---VYSITEKADGDIQIT-KE	312
ARW56296.1	AVEIPKSRAFMHLDTVFTMVD RDQFTIHFAIQGPE---GDMRIFVLERGKTAD E IHT-TE	314
CAA04682.1	AIKIPHKHAMMHLDTVFTMIDYDKFTIHPIGQAG---GMVDTYILEPGNN-DEIKI-TH	313
	

XP_001705755.1	KAKSSAVTCGNYVLAKAN-----VEFQQWLSENGYTIVRIPHEYQLAYGCNNL	368
EST48861.1	HKSFY-----ALNEKRTN-----IELKQYLEQSGYSIIAIPHKYQLAYGCNNL	362
WP_011027247.1	STPFVDVAKALGLPKLR--VVETGGDAYASERQQWDSGNNA--VAVEPGVVFTYDRNT-	378
WP_012482189.1	NRPMLDVVAEALDLPQLR--TVETGGNSYQAEREQWDDGNNV--VALEPGVVVAYDRNT-	368
KFL10416.1	EKTFLEVVAESLGLKKLR--VVETGGNSFAAEREQWDDGNNV--VCLEPGVVVGYDRNT-	376
KHL72821.1	NKSFIEVVGELGV-KLR--VVETGGNSFAAEREQWDDGNNV--VAVEPGVVIGYDRNT-	375
AAD55448.1	GLPLEDLKSIIGKKPTLIPIAGAGASQIDIERETHFDGTNY--LAVAPGIVIGYARNE-	368
BAQ54605.1	GLPLEGLLSIIINKPVLPIPIAGAGASQMEIERETHFDGTNY--LAIRPGVVIGYSRNE-	368
AGS66837.1	KAKLKDVLSEYLG-RKID-I IKCAGGDLIHGAREQWNDGANV--LAIAPGEVIAYS RNH-	370
NP_813907.1	KDTLDNILCKYLHLDNVQ-LIRCGAGNLTAAREQWNDGSNT--LAIAPGEVVYDRNT-	368
ARW56296.1	EHNLEPEVLKRTLGLSDVN-LIFCGGDEIASAREQWNDGSNT--LAIAPGVVVYDRNY-	370
CAA04682.1	QTDLEKVL RDALEVP E L T-LIPCGGDAVVAPREQWNDGSNT--LAIAPGVVVYDRNY-	369
	: . . : : . * *	

XP_001705755.1	NLGN----NCVLSVHQPTVDFIKADPAYISYCKSNNLPNGLDLVYVPFRGITRMYGSLHC	424
EST48861.1	HLGFTDGAHILTVHEESKLFIERHPVFKYTCQKNNIR--IVVEYVPFRSITSMYGSLHC	420
WP_011027247.1	-----LTNALLREARVEVTVIGAE LGRGRGGGHC	408
WP_012482189.1	-----YTNTLLRKAGIEVITIRGSELGRGRGGGHC	398
KFL10416.1	-----YTNTLLRKAGVEVITISASELGRGRGGGHC	406
KHL72821.1	-----YTNTLLRKAGIEVITISAGELGRGRGGGHC	405
AAD55448.1	-----KTNAALEAAGITVLPFRGNQLSLGMGNARC	398
BAQ54605.1	-----KTNAALEAAGIKVLPFHGNQLSLGMGNARC	398
AGS66837.1	-----VTNKLFEENGIKVHRI PSSELSRGRGGGPC	400
NP_813907.1	-----ITNKALEEAGVKLNYIPGSELVRGRGGGPC	398
ARW56296.1	-----ISNECLREQGIKVIEIPSGELSRGRGGGPC	400
CAA04682.1	-----VSNEENLRQYGIKVIEVPSSELSRGRGGGPC	399
	: : . : * . : *	

XP_001705755.1	ASQVYVRTPLAPAAVKA CEQEGDGI AAIYEKNGEPVDAAGKKFD CVIYIPSSVDDLIDGL	484
EST48861.1	ATQVLERDVP-TAAIDKCN S-----QVLNDEKLFDAALFIPTFF-----	458
WP_011027247.1	MTCPLVREPVD F-----	420
WP_012482189.1	MTCPIWRDPAY-----	409
KFL10416.1	MTCPIIRDPI DY-----	418
KHL72821.1	MTCPIVRDPIDY-----	417
AAD55448.1	MSMPLSRKDVK-----	409
BAQ54605.1	MSMPLSRKDVKW-----	410
AGS66837.1	MSMSLVREDI-----	410
NP_813907.1	MSMPLYREDL-----	408
ARW56296.1	MSMPLYREDVK-----	411
CAA04682.1	MSMPLVRRKT-----	409
	: : *	

XP_001705755.1	KINLRDDAAPSREI IADAYGLYQKLVSEGRVPYITWRMPSPMPVVS LKGAA---KAGSLKA	541
EST48861.1	-----ASKETIKEVYELYEKL RKEGKNVYLINKYKITELISFKNLNAKNVEGLLAE	509
WP_011027247.1	-----	420
WP_012482189.1	-----	409
KFL10416.1	-----	418
KHL72821.1	-----	417
AAD55448.1	-----	409
BAQ54605.1	-----	410
AGS66837.1	-----	410
NP_813907.1	-----	408
ARW56296.1	-----	411
CAA04682.1	-----	409

XP_001705755.1	VLDKIPQLTPFTP KAVEGAPAA YTRYLGLEQADI CVDIK	580
EST48861.1	IYGSAKKHFIQPKKQDGA VTAIER-DGLSLDDILYIF-	546

WP_011027247.1	-----	420
WP_012482189.1	-----	409
KFL10416.1	-----	418
KHL72821.1	-----	417
AAD55448.1	-----	409
BAQ54605.1	-----	410
AGS66837.1	-----	410
NP_813907.1	-----	408
ARW56296.1	-----	411
CAA04682.1	-----	409

Figure S2. Multiple sequence amino acid alignment of ADI enzyme from *G. lamblia* and different organisms. The alignment was performed in the free tool Clustal, version 1.2.4. The reference sequences used are: XP_001705755.1 Arginine deiminase [*Giardia lamblia* ATCC 50803]. EST48861.1 Arginine deiminase [*Spironucleus salmonicida*]. WP_011027247.1 Arginine deiminase [*Streptomyces coelicolor*]. WP_012482189.1 Arginine deiminase [*Rhizobium etli*]. KFL10416.1 Arginine deiminase [*Pseudomonas aeruginosa*]. KHL72821.1 Arginine deiminase [*Pseudomonas putida*]. AAD55448.1 Arginine deiminase [*Mycoplasma arthritidis*]. BAQ54605.1 Arginine deiminase [*Mycoplasma arginini*]. AGS66837.1 Arginine deiminase [*Borrelia burgdorferi* CA382]. NP_813907.1 Arginine deiminase [*Enterococcus faecalis* V583]. ARW56296.1 Arginine deiminase [*Bacillus licheniformis*]. CAA04682.1 Arginine deiminase [*Lactobacillus sakei*]. Symbols: * (asterisk) indicates positions which have a single, fully conserved residue. : (colon) indicates conservation between groups of strongly similar properties. . (period) indicates conservation between groups of weakly similar properties. – (hyphen) indicates a gap. Cysteine residues are highlighted in bold red. The C-terminal end of the protein is highlighted in bold. Residues of the catalytic site (Glu 226, His 280, and Cys 424) are highlighted in blue.