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New nitazoxanide derivatives: design, synthesis, biological evaluation, and molecular docking studies as antibacterial and antimycobacterial agents

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FIGURE S2. ¹H-NMR spectrum of compound 3a.



FIGURE S3. ¹³C-NMR spectrum of compound 3a.

FIGURE S4. ESI-mass spectrum of compound 3a.



FIGURE S5. FT-IR spectrum of compound 3b.



FIGURE S6. ¹H-NMR spectrum of compound 3b.



FIGURE S7. ¹³C-NMR spectrum of compound 3b.



FIGURE S8. ¹H-NMR spectrum of compound 5a.



FIGURE S9. ESI-mass spectrum of compound 5a.



FIGURE S10. FT-IR spectrum of compound 5b.



FIGURE S11. ¹H-NMR spectrum of compound 5b.



FIGURE S12. FT-IR spectrum of compound 5c.



FIGURE S13. ¹H-NMR spectrum of compound 5c.



FIGURE S14. ¹H- NMR spectrum of compound 5d.



FIGURE S15. ¹³C- NMR spectrum of compound 5d.



FIGURE S16. ESI-mass spectrum of compound 5d.



FIGURE S17. ¹H-NMR spectrum of compound 5e.



FIGURE S18. ¹H-NMR spectrum of compound 5f.



FIGURE S19. ¹³C-NMR spectrum of compound 5f.



FIGURE S20. ¹H-NMR spectrum of compound 5g.







FIGURE S23. ESI-mass spectrum of compound 5h.



FIGURE S24. ¹H-NMR spectrum of compound 5i.



FIGURE S25. ¹H-NMR spectrum of compound 5j.



FIGURE S26. ¹³C-NMR spectrum of compound 5j.



FIGURE S27. FT-IR spectrum of compound 5k.



FIGURE S28. ¹H-NMR spectrum of compound 5k.



FIGURE S29. ¹³C-NMR spectrum of compound 5k.



FIGURE S30. FT-IR spectrum of compound 51.





FIGURE S31. ¹H-NMR spectrum of compound 51.



FIGURE S32. FT-IR spectrum of compound 5m.



FIGURE S33. ¹H-NMR spectrum of compound 5m.



FIGURE S34. ¹³C-NMR spectrum of compound 5m.



FIGURE S35. FT-IR spectrum of compound 5n.



FIGURE S36. ¹H-NMR spectrum of compound 5n.



FIGURE S37. FT-IR spectrum of compound 50.



FIGURE S38. ¹H-NMR spectrum of compound 50.





FIGURE S39. ¹³C-NMR spectrum of compound 50.

FIGURE S40. FT-IR spectrum of compound 5p.



FIGURE S41. ¹H-NMR spectrum of compound 5p.





FIGURE S43. ESI-mass spectrum of compound 5p.



FIGURE S44. ¹H-NMR spectrum of compound 5q.



FIGURE S45. ¹³C-NMR spectrum of compound 5q.





Requester Data:

Name:Dr. Mahmoud Saleh MahmoudAuthority:Faculty of Pharmacy, Assuit University

Sample Data:

Nineteen samples had been submitted for elemental analysis.

MZ ₁	30/0			
	57.47	2.15	27.68	10.50
MZ_2	51.60	2.79	20.19	6.61
MZ ₃	50.88	3.14	19.07	6.08
MZ ₄	47.15	2.67	19.40	18.5
MZ ₅	43.23	3.01	23.45	8.97
MZ ₆	43.21	2.69	21.70	8.30
MZ ₇	53.15	3.04	20.79	7.96
MZ ₈	54.29	3.47	20.04	7.68
MZ ₉	50.60	4.52	22.95	7.42
MZ ₁₀	41.75	2.27	22.59	8.43
MZ11	44.16	2.36	17.45	5.49
MZ ₁₂	47.60	4.15	22.94	7.28
MZ ₁₃	54.78	4.50	22.39	6.41
MZ ₁₄	48.91	4.68	25.47	7.09
MZ ₁₅	52.47	3.15	19.68	6.47
MZ ₁₆	48.15	2.47	18.85	5.98
MZ ₁₇	49.78	2.43	19.51	6.33
MZ ₁₈	49.33	4.29	23.76	7.94
	41.59	2.47	24.41	9.45

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FIGURE S46. Elemental analysis of the synthesized compound 3a, 3b, 5a-q.

Compound	experimental
No.	code
3a	Mz1
3b	Mz19
5a	Mz5
5b	Mz10
5c	Mz6
5d	Mz7
5e	Mz8
5f	Mz9
5g	Mz18
5h	Mz12
5i	Mz14
5j	Mz13
5k	Mz2
51	Mz17
5m	Mz16
5n	Mz11
50	Mz15
5p	Mz3
5q	Mz4

3. Antibacterial activity

Table S1. Antibacterial activity against different bacterial test strains. MIC (in $\mu g/mL$) values
represent the average of at least two replicate experiments.

ID	Gra	Gram-negative strains Gram-		Gram-pos	itive strains	Anaerobe strain	
	E. coli ATCC 8739	P. aeruginosa ATCC 27853	K. pneumoniae ATCC 10031		S. aureus ATCC 6538	E. faecalis ATCC 19433	H. pylori ATCC 700392
TIZ	48	96	64		40	36	3
NTZ	32	128	56		32	48	4
Cipro	0.1	1.5	3		1	2	0.5
3a	1.5	>512	96		3	8	32
3b	3	32	12		4	0.75	4
5a	>512	128	32		>512	48	16
5b	2.5	4	6		32	>512	8
5c	1.5	6	2		4	>512	1.5
5d	>512	>512	16		12	8	6
5e	3	128	>512		512	32	2.5
5f	32	>512	512		4	12	0.75
5g	2.5	3	5		1.5	>512	8
5h	512	64	8		3	>512	4
5i	>512	64	4		2	>512	3
5j	6	1.5	128		256	1	16
5k	>512	8	>512		16	2	64
51	>512	4	>512		8	2.5	2
5m	256	>512	32		>512	>512	2.5
5n	12	3	2.5		0.5	5	2
50	0.75	4	2		256	3	1.5
5p	8	>512	256		48	96	5
5q	2	16	12		2	>512	8

4. Molecular docking

Table S2. Ligand-protein complex interactions of the tested compounds 5c, 5e, 5f, 5m, 5n and 5o along with NTZ within the active site of PFOR.

Compd.	Score kcal/mol	H-bond interactions (Å)	Other interactions (Å)
Co-crystallized Pyruvate	-4.45	Thr31 (2.94, 3.06) Arg114 (2.97, 2.98, 3.40)	Arg114 (2.98) Ionic interaction
NTZ	-7.39	Arg114 (3.37) Thr31 (2.77) Asn 996 (2.99)	-
5c	-8.72	Thr838 (3.51) Asn996 (3.05) Gly839 (3.44)	Arg114 (3.96) pi-H Tyr994 (4.56) pi-H Thr31 (4.74) pi-H Arg114 (3.94) pi-cation Phe869 (3.53) pi-pi
5e	-8.64	Pro29 (3.27) Asn996 (3.13) Thr997 (3.49) Thr31 (2.74)	Cys840 (3.70, 4.54) pi-H Ser841 (4.89) pi-H Asn996 (4.30) pi-H Phe869 (3.71) ni-ni
5f	-8.87	Arg 114 (3.42) Thr 31 (3.72)	Tyr 994 (4.35) pi-H Phe 969 (3.80)

5m	-7.78	Trp 965 (3.19) Tyr994 (3.24) Ser995 (3.53) Arg114 (2.91) Ser841 (2.72)	Tyr994 (3.31) pi-H Arg114 (4.20) pi-cation Ile123 (4.59) pi-H Ser995 (4.67) pi-H
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o polar o acidic o basic o greasy proximity contour	 sidechain acceptor sidechain donor backbone acceptor backbone donor ligand exposure 	o solvent residue metal complex solvent contact metal/ion contact receptor exposure	 arene-arene H arene-H + arene-cation
5n	-8.05	Thr997 (3.20) Thr838 (2.89) Met989 (3.26) Gly964 (2.78) Ser995 (2.90) Arg114 (2.85) Ser841 (2.69, 2.90)	Arg114 (4.15) pi-cation Ile123 (4.48) pi-H Glu817 (3.33) pi-H Gly962 (3.50) pi-H Asn996 (3.55, 4.54)
50	-8.37	Arg 114 (3.00) Thr 997 (3.46) Gly964 (2.78) Tyr994 (3.17) Ser995 (2.94)	Phe869 (3.59) pi-H Tyr994 (4.44) pi-H

FIGURE S47. Color scheme for the 2D representations of the interactions between the docked ligands and the active site of the enzyme.



FIGURE S48. Redocking of co-crystallized pyruvate within the active site of PFOR (2C42).



FIGURE S49. Interaction of NTZ with the active site of PFOR (2C42).



FIGURE S50. Interaction of 5c with the active site of PFOR (2C42).



FIGURE S51. Interaction of 5e with the active site of PFOR (2C42).



FIGURE S52. Interaction of 5m with the active site of PFOR (2C42).



FIGURE S53. Interaction of 5n with the active site of PFOR (2C42).



FIGURE S54. Interaction of 50 with the active site of PFOR (2C42).

Compd.	Score kcal/mol	H-bond interactions (Å)	Other interactions (Å)
		Ser303 (2.69)	
		Ser349 (2.78, 2.92)	
o-crystallized ligand		Ser347 (2.86)	
(G6P)	-6.22	Thr352 (2.51)	-
(001)		Glu488 (2.54)	
		Thr302 (3.10, 3.16, 3.19)	
		Lys485 (3.25)	
		Ser303 (2.92, 3.08)	
		Ser347 (3.10, 3.31)	
NTZ	-7.06	Gln348 (3.04)	-
		Ser401 (4.23, 3.33, 3.43)	
		Ser349 (2.76, 2.95)	
		Ala602 (3.27, 3.46)	
	-7.10	Ser401 (3.09, 3.46)	
3a		Lys485 (3.78)	-
		Ser347 (2.90, 3.27)	
		Ser349 (3.03, 3.49)	
		Thr352 (2.89)	
		Lys603 (2.93)	
		Ser347 (2.90)	
3b	-7.23	Thr352 (2.77)	-
		Cys300 (2.87)	
		Ser604 (3.37)	
		Val605 (3.06)	
		Ala602 (3.45, 3.71)	
		Lys603 (2.79)	Leu601 (3.61)
5c	-7.48	Ser401 (3.14, 3.47)	pi-H
		Lys485 (3.65)	F
		Ser347 (2.98)	
		Ser349 (3.19, 3.32)	
		Ala602 (3.41, 3.65)	
		Lys603 (2.78)	
-	F 00	Ser401 (3.10, 3.35)	Leu601 (3.64)
5n	-7.99	Thr352 (2.90)	pi-H
		Ser347 (2.97)	
		Ser349 (3.17. 3.30)	

Table S3. Ligand-protein complex interactions of the tested compounds 3, 4, 5c, 5n, 5o and 5q along with NTZ within the active site of G6PS (2J6H).

50	-8.15	Ser401 (3.49) Ser347 (2.90, 3.35) Ser349 (3.11) Thr352 (2.88)	Leu601 (3.38) pi-H Val605 (3.94, 4.48) pi-H
5q	-8.49	Thr 302 (3.06) Lys603 (2.90) Cys300 (2.88) Ser347 (2.92) Thr352 (2.81)	Leu484 (3.86) pi-H Lys487 (3.68) pi-pi



FIGURE S55. Interaction of co-crystallized ligand to the active site of G6PS (2J6H).



FIGURE S56. Interaction of NTZ with the active site of G6PS (2J6H).





raction of compound 3a with the active site of G6PS (2J6H).



FIGURE S58. Interaction of compound 3b with the active site of G6PS (2J6H).



URE S59. Interaction of compound 5c with the active site of G6PS (2J6H).

FIGURE S60. Interaction of compound 50 with the active site of G6PS(2J6H).





 Table S4. Ligand-protein complex interactions of the tested compounds 3, 4, 5b and 5e along

Co-crystallized Ligand (G7D)	-8.33	Ile94 (3.20) Asp27 (2.59, 3.04, 3.34) Arg60 (2.83, 2.87)	Arg32 (3.30, 3.41) Ionic interaction Arg60 (2.83, 2.87, 3.81, 3.42) Ionic interaction Phe 31 (4.31)
NTZ	-6.14	Arg60 (3.06) Gln 28 (3.55)	Arg60 (3.06, 3.60) Ionic interaction Gln28 (4.60) Pi-H interaction
3a	-6.35	Arg 60 (2.94, 2.99) Trp 6 (4.16)	Arg 60 (2.94, 2.99, 3.97) Ionic interaction Gln 28 (4.59) Pi-H interaction
3b	-6.68	Gln28 (3.54) Arg32 (3.40) Arg60 (2.98, 3.46) Ile20 (3.85) Thr46 (3.78)	Arg60 (3.46, 2.98, 3.79) Ionic interaction Gln 28 (4.63) Pi-H
5b	-6.65	Arg32 (3.40) Thr 46 (3.93) Ser49 (4.18) Arg60 (2.98)	Arg60 (2.98, 3.75) Ionic interaction Arg32 (3.28, 3.69) Ionic interaction Ile20 (3.55) pi-H Gln28 (4.39) pi-H Phe31 (4.19) pi-H
5e	-7.43	Gln28 (3.29) Arg60 (2.83, 4.24)	Arg60 (2.83, 3.24, 3.48, 3.98) Ionic interaction Ile20 (3.66) pi-H Gln28 (4.52) pi-H Val54 (4.87)



FIGURE S62. Interaction of co-crystallized ligand with the active site of DHFR (6DDW).



FIGURE S63. Interaction of NTZ with the active site of DHFR (6DDW).



FIGURE S64. Interaction of compound 3a with the active site of DHFR (6DDW).



FIGURE S65. Interaction of compound 5b with the active site of DHFR (6DDW).



FIGURE S66. Interaction of compound 5e with the active site of DHFR (6DDW).