ANNEX

PhD Thesis Marta Vilà Rico

Table A-1. Transthyretin Amyloidoses (Saraiva 2001)

Mutation	Codon change		Predominant clinical features	Origin	Reference
Cys10Arg	TGT	CGT	PN, AN, Eye	Hungary	Uemichi et al. [1992]
Leu 12Pro	CTG	CCG	LM, PN, AN	UK	Brett et al. [1999]
Asp18Glu	GAT	GAG	PN, AN	Columbia	Booth et al. [1996]
Asp18Gly	GAT	GGT	LM	Hungary	Vidal et al. [1996]
Val20Ile	GTC	ATC	Heart	Germany	Jenne et al. [1996]
Ser23Asn	AGT	AAT	Heart	Portugal	Connors et al. [1999]
Pro24Ser	CCT	TCT	Heart, CTS, PN	USA	Uemichi et al. [1995]
Val28Met	GTG	ATG	PN, AN	Portugal	Carvalho et al. [2000]
Val30Met	GTG	ATG	PN, AN, Eye	Several	Several
Val30Ala	GTG	GCG	Heart, AN	Germany	Jones et al. [1992]
Val30Leu	GTG	CTG	PN, AN	Japan	Nakazato et al. [1992]
Val30Gly	GTG	GGG	LM, Eye	France	Petersen et al. [1997]
Phe33Ile	TTC	ATC	PN, Eye	Poland	Nakazato et al. [1984]
Phe33Leu	TTC	CTC	PN, AN	Poland	Li et al. [1991]
Phe33Val	TTC	GTC	PN, AN	UK	Booth et al. [1996]
Arg34Thr	AGA	ACA	PN, Heart	Italy	Patrosso et al. [1998]
Lys35Asn	AAG	AAC	PN, AN, Heart	France	Reilly et al. [1995]
Ala36Pro	GCT	CCT	PN, Eye	Greece	Jones et al. [1991]
Asp38Ala	GAT	GCT	PN, Heart	Japan	Kishikawa et al. [1999]
Glu42Gly	GAG	GGG	PN, AN	Japan	Ueno et al. [1990]
Glu42Asp	GAG	GAT	Heart	France	Dupuy et al. [1998]
Phe44Ser	TTT	TCT	PN, AN, Heart	Ireland	Klein et al. [1998]
Ala 45Asp	GCC	GAC	Heart	Italy	Jacobson et al. [1993]
Ala45Ser	GCC	UCC	Heart	Sweden	Janunger et al. [2000]
Ala45Thr	GCC	ACC	Heart	Italy	Saraiva et al. [1992]
Gly47Arg	GGG	CGG	PN, AN	Japan	Murakami et al. [1992]
Gly47Ala	GGG	GCG	Heart, PN, AN	Italy	Ferlini et al. [1994]
Gly47Val	GGG	GTG	PN, AN, Heart	Sri Lanka	Booth et al. [1993]
Gly47Glu	GGG	GAG	PN	Germany	Altland [1999]
Thr49Ala	ACC	GCC	Heart, PN	Italy	Almeida et al. [1992]
Thr49Ile	ACC	ATC	PN, Heart	Japan	Nakamura et al. [1999]
Ser50Arg	AGT	AGG	PN, AN	Japan	Ueno et al. [1990]
Ser50Ile	AGT	ATT	Heart, PN, AN	Japan	Saeki et al. [1992]
Glu51Gly	GAG	GGG	Heart	USA	Jacobson et al. [1999]
Ser52Pro	TCT	CCT	PN, AN, Heart	UK	Booth et al. [1993]
Gly53Glu	GGA	GAA	LM, Heart	France	Camou et al. [1999]
Glu54Gly	GAG	GGG	PN, AN	UK	Reilly et al. [1995]
Glu54Lys	GAG	GAA	PN, AN, Heart	Japan	Togashi et al. [1999]
Leu55Arg	CTG	CGG	LM, PN	Germany	Altland [1999]
Leu55Pro	CTG	CCG	PN, Heart, AN	Taiwan	Jacobson et al. [1992]
His56Arg	CAT	CGT	Heart	USA	Jacobson et al. [1999]
Leu58His	CTC	CAC	CTS, Heart	Germany	Nichols et al. [1989]
Leu58Arg	CTC	CGC	CTS, AN, Eye	Japan	Saeki et al. [1991]
Thr59Lys	ACA	AAA	Heart, PN	Italy	Booth et al. [1995]
Thr60Ala	ACT	GCT	Heart, CTS	Ireland	Wallace et al. [1986]
Glu61Lys	GAG	AAG	PN	Japan	Shiomi et al. [1993]
Phe64Leu	TTT	CTT	PN, CTS, Heart	Italy	Li et at. [1991]
Phe64Ser	TTT	TCT	LM, PN, Eye	Italy	Uemichi et al. [1999]
Ile68Leu	ATA	TTA	Heart	Germany	Almeida et al. [1991]
Tyr69His	TAC	CAC	Eye	Scotland	Zeldenrust et al. [1994]
Lys70Asn	AAA	AAC	CTS, PN, Eye	Germany	Izumoto et al. [1992]
Val71Ala	GTG	GCG	PN, Eye	Spain	Almeida et al. [1993]
Ile73Val	ATA	GTA	PN, AN	Bangladesh	Booth et al. [1998]
Ser77Phe	TCT	TTT	PN	France	Planté-Bordeneuve et al. [1998]
Ser77Tyr	TCT	TAT	PN	Germany	Wallace et al. [1998]
Ile84Ser	ATC	AGC	Heart, CTS, Eye	Switzerland	Dwulet and Benson [1986]
Ile84Asn	ATC	AAC	Eye, Heart	Italy	Skinner et al. [1992]
Ile84Thr	ATC	ACC	Heart, PN, AN	Germany	Stangou et al. [1998]
Glu89Gln	GAG	CAG	PN, Heart	Italy	Almeida et al. [1992]
Gku89Lys	GAG	AAG	PN, Heart	USA	Nakamura et al. [2000]
Ala91Ser	GCA	TCA	PN, CTS, Heart	France	Misrahi et al. [1998]
Ala97Gly	GCC	GGC	Heart, PN	Japan	Yasuda et al. [1994]
Ala97Ser	GCC	TCC	PN, Heart	France	Lachmann et al. [2000]
Ile107Val	ATT	GTT	Heart, CTS, PN	Germany	Jacobson [1994]
Ile107Met	ATT	ATG	PN, Heart	Germany	Altand [1999]
Ala109Ser	GCC	TCC	PN	Japan	Date et al. [1997]
Leu111Met	CTG	ATG	Heart	Denmark	Nordlie et al. [1988]
Ser112Ile	AGC	ATC	PN, Heart	Italy	De Lucia et al. [1993]
Tyr114Cys	TAC	TGC	PN, AN, Eye	Japan	Ueno et al. [1990a]
Tyr114His	TAC	CAC	CTS	Japan	Murakami et al. [1994]
Tyr116Ser	TAT	TCT	PN, CTS	France	Misrahi et al. [1998]
Ala120Ser	GCT	TCT	Heart, PN, AN	Africa	Gillmore et al. [1999]
Val122Ile	GTC	ATC	Heart	Africa	Saraiva et al. [1990]
Val122del	GTC	Loss	Heart, PN, CTS	Equador/Spain	Uemichi et al. [1995] Munar Qués et al. [2000]
Val122Ala	GTC	GCC	Heart, Eye, PN	UK	Theberge et al. [1999]

AN, autonomic neuropathy; CTS, carpal tunnel syndrome; Eye, vitreous deposition; PN, peripheral neuropathy; LM, leptomeningeal amyloid; Heart, cardiomyopathy.

Table A-2. Non-amyloid TTR mutations and compound heterozygotes (Saraiva 2001)

Mutation	Codon change		Frequency[a]	Reference
Gly6Ser	GGT	AGT	33/558	Jacobson et al. [1995]
Met13Ile	ATG	ATC	ND	Altland [1999]
Asp74His	GAC	CAC	ND	Uemichi et al. [1994]
His90Asn	CAT	AAT	16/12,400	Saraiva et al. [1991]
Gly101Ser	GGC	AGC	ND	Kishikawa et al. [1998]
Pro102Arg	CCC	CGC	1/8,000	Almeida et al. [1991a]
Arg104Cys	CGC	TGC	ND	Saraiva et al. [1999]
Arg104His	CGC	CAC	ND	Terazaki et al. [1999]
Ala108Ala[b]	GCC	GCT	ND	Palha et al. [1997]
Ala109Thr	GCC	ACC	1/10,000	Alves et al. [1997]
Ala109Val	GCC	GTC	ND	Izumoto et al. [1993]
Thr119Met	ACG	ATG	35/10,000	Alves et al. [1997]
Pro125Ser	CCC	TCC	ND	Ferlini et al. [1996]
Compound heterozygotes				
Gly6Ser/Val30Met			7/160	Alves et al. [1996]
Gly6Ser Phe33Ile[c]			ND	Jacobson and Buxbaum [1994]
Gly6Ser/Ala45Asp			ND	Jacobson et al. [1993]
Gly6Ser/Ser77Tyr			ND	Planté-Bordeneuve et al. [1999]
Gly6Ser/Tyr114Cys			ND	Connors et al. [1999a]
Gly6Ser/Thr119Met			ND	Saraiva (personal communication)
Gly6Ser/Val122/Ala			ND	Theberge et al. [1999]
His90Asn/Val30Met			ND	Saraiva et al. [1991]
His90Asn Glu42Gly[c]			ND	Skare et al. [1994]
His90Asn/Thr119Met			ND	Alves et al. [1993]
Arg104His/Val30Met			ND	Terazaki et al. [1999]
Thr119Met/Val30Met			ND	Alves et al. [1996a]

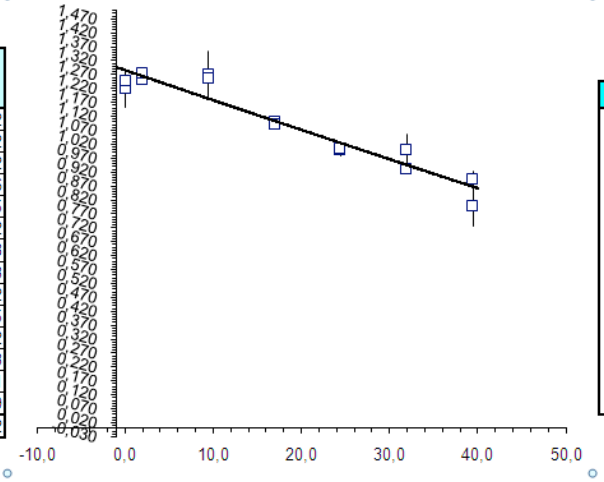
[a]Refers to mutant allele frequency.
[b]Silent mutation.
[c]Mutations on the same allele.

Bellow, all the results from the analysis of the different inhibitors (tables and adjustments) by the Kinetic Turbidimetric Assay are shown.

numero inhibidor = 4 | Referencia llista: 855

MVR_24

	[854]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,221	0,08	0,258	1,18	0,604	1,10	0,346	0,0042
	1,88	1,2514	0,08	0,292	1,12	0,784	1,033	0,492	0,0002
	9,38	1,2696	0,08	0,296	1,50	0,786	1,417	0,49	0,0072
	16,88	1,1026	0,08	0,298	1,50	0,753	1,417	0,455	4E-06
	24,38	1,0029	0,08	0,311	1,50	0,833	1,417	0,522	0,0005
	31,88	0,9338	0,08	0,327	1,50	0,823	1,417	0,496	0,0002
	39,38	0,897	0,08	0,340	1,50	0,781	1,417	0,441	0,0008
Serie 2	0,00	1,2504	0,08	0,271	1,17	0,624	1,083	0,353	0,0013
	1,88	1,2781	0,08	0,285	1,12	0,813	1,033	0,528	0,0002
	9,38	1,2558	0,08	0,293	1,50	0,783	1,417	0,49	0,005
	16,88	1,092	0,08	0,293	1,50	0,707	1,417	0,414	0,0002
	24,38	1,007	0,08	0,284	1,50	0,872	1,417	0,588	0,0003
	31,88	1,0018	0,12	0,369	1,50	0,876	1,383	0,507	0,0031
	39,38	0,7987	0,10	0,334	1,50	0,732	1,4	0,398	0,0049
							Error a	**0,001**	0,0712



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☐ corretgir per [TTR] a 4 mg/mL

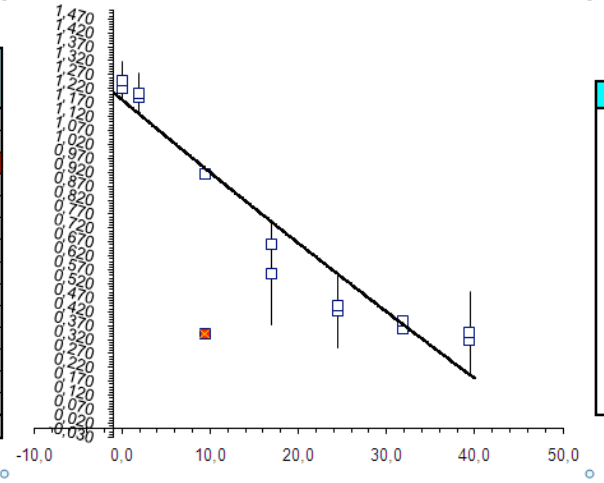
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-7,883	127,185	9,169	#####	0,001	0,017	0,011	1,2859	61,448	25,214	713,0

Punts a ignorar

numero inhibidor = 5 | Referencia llista: 856

MVR_24

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,221	0,08	0,258	1,18	0,604	1,10	0,346	0,0018
	1,88	1,1898	0,08	0,272	1,12	0,691	1,033	0,419	0,0037
	9,38	0,3411	0,08	0,243	1,50	0,655	1,417	0,412	0
	16,89	0,6632	0,13	0,254	1,50	0,604	1,367	0,35	0,0063
	24,40	0,4245	0,08	0,226	1,50	0,580	1,417	0,354	0,0171
	31,91	0,3582	0,12	0,240	1,10	0,566	0,983	0,326	0,0002
	39,41	0,3178	0,13	0,225	1,50	0,478	1,367	0,253	0,0155
Serie 2	0,00	1,2504	0,08	0,271	1,17	0,624	1,083	0,353	0,0052
	1,88	1,204	0,10	0,290	1,12	0,752	1,017	0,462	0,0056
	9,38	0,9162	0,15	0,403	1,50	0,816	1,35	0,413	0,0003
	16,89	0,558	0,25	0,568	1,50	0,862	1,25	0,294	0,034
	24,40	0,4428	0,07	0,220	1,50	0,583	1,433	0,363	0,0127
	31,91	0,3865	0,12	0,227	1,10	0,572	0,983	0,345	0,0002
	39,41	0,3445	0,13	0,225	1,50	0,497	1,367	0,272	0,0229
							Error a	**0,001**	0,0713



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0,074914204
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0,112641344
0,014089956
0,15117596

☐ corretgir per [TTR] a 4 mg/mL

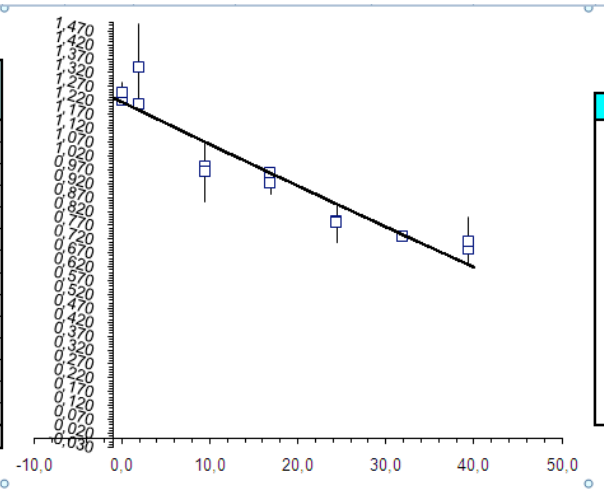
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-7,936	48,020	9,114	#####	0,003	0,016	0,026	1,1786	23,027	9,369	773,3

Punts a ignorar
7

numero inhibidor = 6 | Referencia llista: 858

MVR_24

	[855]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,221	0,08	0,258	1,18	0,604	1,10	0,346	5E-05
	1,87	1,209	0,08	0,277	1,12	0,689	1,033	0,412	0,0006
	9,37	0,9837	0,12	0,303	1,50	0,705	1,383	0,402	0,0076
	16,86	0,9221	0,13	0,339	1,50	0,740	1,367	0,401	0,0013
	24,35	0,7866	0,08	0,339	1,50	0,827	1,417	0,488	0,0036
	31,85	0,732	0,08	0,364	1,10	0,816	1,017	0,452	2E-05
	39,34	0,687	0,08	0,396	1,50	0,790	1,417	0,394	0,0035
Serie 2	0,00	1,2504	0,08	0,271	1,17	0,624	1,083	0,353	0,0013
	1,87	1,3411	0,08	0,285	1,12	0,786	1,033	0,501	0,0242
	9,37	0,9634	0,10	0,282	1,50	0,736	1,4	0,454	0,0116
	16,86	0,9616	0,13	0,338	1,50	0,754	1,367	0,416	1E-05
	24,35	0,7796	0,08	0,340	1,50	0,830	1,417	0,49	0,0045
	31,85	0,73	0,08	0,360	1,10	0,810	1,017	0,45	5E-05
	39,34	0,7144	0,13	0,414	1,50	0,803	1,367	0,389	0,0074
							Error a	**0,001**	0,0712



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☐ corretgir per [TTR] a 4 mg/mL

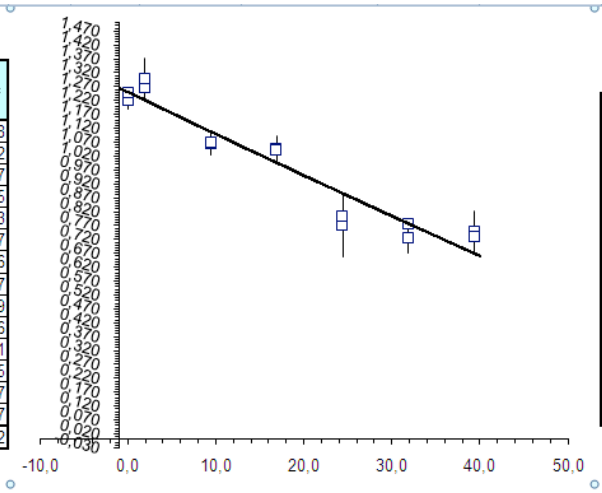
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-7,918	96,438	9,132	#####	0,002	0,018	0,015	1,2142	40,811	18,785	752,1

Punts a ignorar

numero inhibidor = 7 | Referencia llista: 859

MVR_24

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,221	0,08	0,258	1,18	0,604	1,10	0,346	0,0008
	1,87	1,2679	0,08	0,278	1,12	0,754	1,033	0,476	0,0022
	9,37	1,0668	0,12	0,324	1,50	0,763	1,383	0,439	0,0017
	16,86	1,0462	0,08	0,314	1,50	0,774	1,417	0,46	0,0025
	24,35	0,7723	0,08	0,341	1,50	0,848	1,417	0,507	0,013
	31,84	0,7258	0,15	0,393	1,10	0,768	0,95	0,375	0,0027
	39,34	0,7469	0,12	0,413	1,50	0,828	1,383	0,415	0,006
Serie 2	0,00	1,2504	0,08	0,271	1,17	0,624	1,083	0,353	2E-07
	1,87	1,298	0,08	0,271	1,12	0,763	1,033	0,492	0,0059
	9,37	1,0687	0,12	0,319	1,50	0,795	1,383	0,476	0,0016
	16,86	1,0428	0,08	0,308	1,50	0,768	1,417	0,46	0,0021
	24,35	0,8055	0,08	0,347	1,50	0,880	1,417	0,533	0,0065
	31,84	0,7764	0,20	0,459	1,10	0,856	0,9	0,397	8E-07
	39,34	0,7305	0,12	0,409	1,50	0,852	1,383	0,443	0,0037
							Error a	**0,001**	0,0712



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corretgir per [TTR] a 4 mg/mL

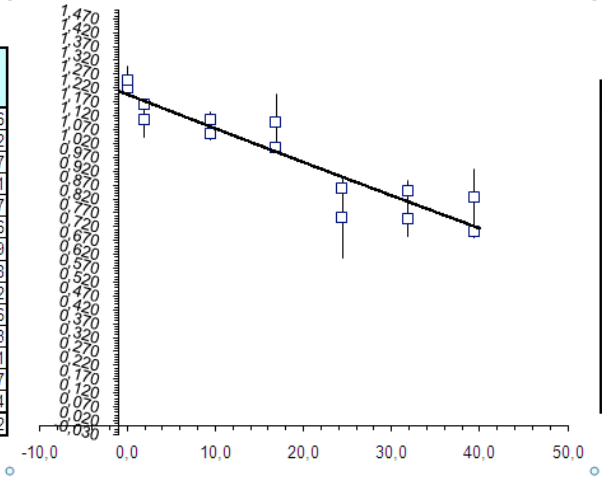
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-7,900	84,866	9,150	#####	0,002	0,016	0,015	1,2499	42,480	16,718	732,1

Punts a ignorar

numero inhibidor = 8 | Referencia llista: 860

MVR_24

		[856]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,221	0,08	0,258	1,18	0,604	1,10	0,346	0,0006
	1,87	1,1605	0,08	0,279	1,12	0,704	1,033	0,425	0,0002
	9,36	1,1085	0,08	0,276	1,50	0,755	1,417	0,479	0,0007
	16,86	1,0955	0,08	0,269	1,50	0,690	1,417	0,421	0,011
	24,35	0,8587	0,08	0,250	1,50	0,732	1,417	0,482	0,0017
	31,84	0,8508	0,08	0,240	1,10	0,668	1,017	0,428	0,0016
	39,33	0,8264	0,08	0,232	1,50	0,619	1,417	0,387	0,0109
Serie 2	0,00	1,2504	0,08	0,271	1,17	0,624	1,083	0,353	0,0028
	1,87	1,1089	0,08	0,236	1,12	0,545	1,033	0,309	0,0042
	9,36	1,0576	0,08	0,249	1,50	0,592	1,417	0,343	0,0006
	16,86	1,0076	0,07	0,226	1,50	0,550	1,433	0,324	0,0003
	24,35	0,755	0,03	0,198	1,50	0,568	1,467	0,37	0,021
	31,84	0,7493	0,05	0,201	1,10	0,537	1,05	0,336	0,0037
	39,33	0,7015	0,08	0,213	1,50	0,482	1,417	0,269	0,0004
							Error a	**0,001**	0,0712



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corretgir per [TTR] a 4 mg/mL

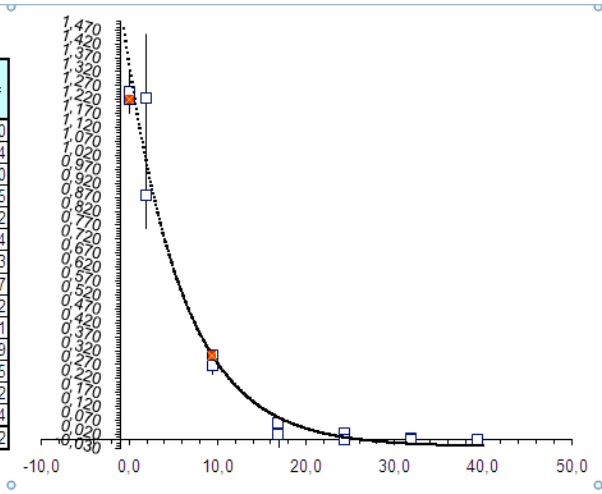
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-7,926	141,226	9,124	#####	0,001	0,022	0,012	1,1972	49,889	27,261	762,1

Punts a ignorar

numero inhibidor = 9 | Referencia llista: 200

MVR_24

		1,204	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,221	0,08	0,258	1,18	0,604	1,10	0,346	0
	1,87	1,2241	0,08	0,263	1,12	0,683	1,033	0,42	0,0544
	9,37	0,3033	0,18	0,244	1,50	0,402	1,317	0,158	0
	16,87	0,0593	0,48	0,228	1,50	0,283	1,017	0,055	0,0005
	24,37	0,024	0,08	0,212	1,50	0,230	1,417	0,018	0,0002
	31,87	0,0077	0,40	0,208	1,50	0,217	1,1	0,009	0,0004
	39,37	-0,0033	0,08	0,209	1,50	0,210	1,417	0,001	0,0003
Serie 2	0,00	1,2504	0,08	0,271	1,17	0,624	1,083	0,353	0,0057
	1,87	0,8761	0,08	0,233	1,12	0,538	1,033	0,305	0,0132
	9,37	0,2685	0,17	0,226	1,50	0,336	1,333	0,11	0,0011
	16,87	0,0186	0,47	0,197	1,50	0,211	1,033	0,014	0,0039
	24,37	0,0013	0,03	0,192	1,50	0,191	1,467	-0,001	8E-05
	31,87	0,0003	0,05	0,194	1,50	0,195	1,45	0,001	0,0002
	39,37	0,0016	0,08	0,188	1,50	0,195	1,417	0,007	0,0004
							Error a	**0,001**	0,0712



error Y
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0
0,021454211
0,01353977
0,019677781
0,015840049
0,07529208
0,114771103
0,032471765
0,062154211
0,00916023
0,012277781
0,020740049

corretgir per [TTR] a 4 mg/mL

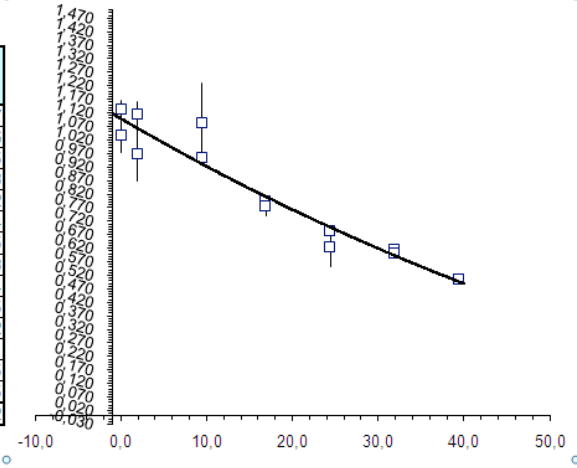
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,022	0,044	1,348	0,079	0,152	0,030	0,205	1,3257	4,443	0,333	101,7

Punts a ignorar
7
5

numero inhibidor = 1 | Referencia llista! 850

MVR_25

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,0037
	1,87	1,1144	0,10	0,265	1,12	0,624	1,017	0,359	0,0026
	9,37	1,0825	0,10	0,306	1,50	0,657	1,4	0,351	0,0225
	16,86	0,7947	0,13	0,395	1,50	0,699	1,367	0,304	0,0003
	24,35	0,6837	0,13	0,456	1,50	0,813	1,367	0,357	0,0002
	31,84	0,6149	0,13	0,529	1,50	0,858	1,367	0,329	0,0004
	39,33	0,5044	0,13	0,611	1,50	0,954	1,367	0,343	5E-05
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	0,0013
	1,87	0,9671	0,10	0,329	1,12	0,654	1,017	0,325	0,0094
	9,37	0,9544	0,10	0,345	1,50	0,682	1,4	0,337	0,0005
	16,86	0,7766	0,13	0,447	1,50	0,756	1,367	0,309	0,0012
	24,35	0,6267	0,13	0,482	1,50	0,770	1,367	0,288	0,0051
	31,84	0,6017	0,13	0,541	1,50	0,800	1,367	0,259	6E-05
	39,33	0,5044	0,12	0,601	1,50	0,862	1,383	0,261	5E-05
							Error a	**0,001**	0,0712



error Y
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0,015952378
0,01430522
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0,096774715
0,022034345
0,034052378
0,07130522
0,007951132
0,007141688

corretgir per [TTR] a 4 mg/mL

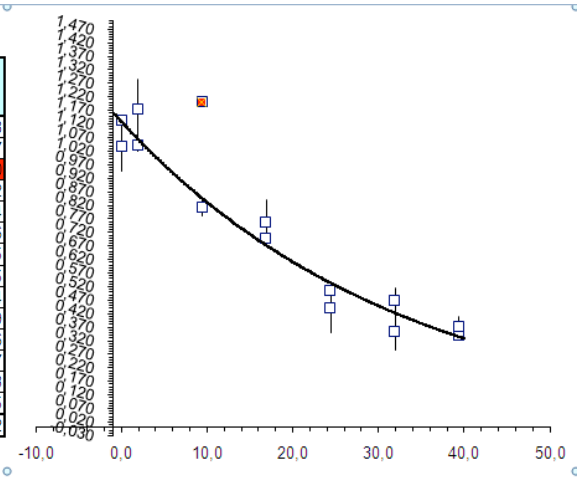
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-0,702	2,213	1,800	2,195	0,010	0,015	0,019	1,0984	35,230	3,284	163,9

Punts a ignorar

numero inhibidor = 2 | Referencia llista! 854

MVR_25

		[854]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,0078
	1,87	1,1766	0,10	0,230	1,12	0,565	1,017	0,335	0,0127
	9,37	1,201	0,15	0,269	1,50	0,570	1,35	0,301	0
	16,86	0,7573	0,15	0,301	1,50	0,613	1,35	0,312	0,0072
	24,35	0,4422	0,15	0,324	1,50	0,657	1,35	0,333	0,0084
	31,85	0,356	0,20	0,339	1,50	0,630	1,3	0,291	0,0046
	39,34	0,3431	0,18	0,360	1,50	0,633	1,317	0,273	6E-05
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	6E-05
	1,87	1,0436	0,08	0,279	1,12	0,676	1,033	0,397	0,0004
	9,37	0,8155	0,08	0,252	1,50	0,561	1,417	0,309	0,0009
	16,86	0,6976	0,10	0,296	1,50	0,618	1,4	0,322	0,0006
	24,35	0,5076	0,08	0,312	1,50	0,643	1,417	0,331	0,0007
	31,85	0,4716	0,08	0,328	1,50	0,614	1,417	0,286	0,0023
	39,34	0,3747	0,10	0,357	1,50	0,602	1,4	0,245	0,0015
							Error a	**0,001**	0,0712



error Y
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0,067670979
0,007433733
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0,02010103
0,030521151
0,025155057
0,026436652
0,047929021
0,039033733

corretgir per [TTR] a 4 mg/mL

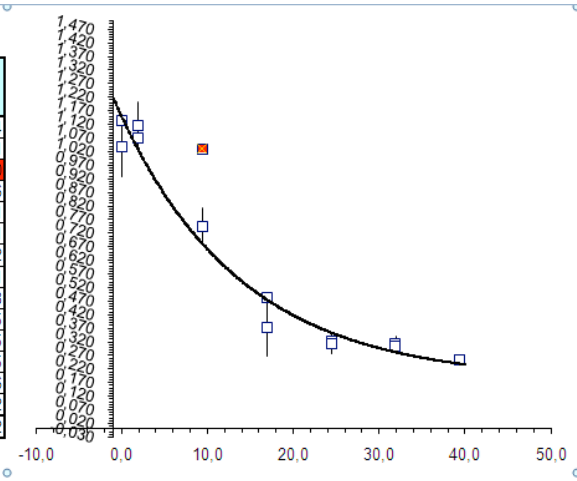
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-0,011	0,304	1,137	0,292	0,030	0,014	0,034	1,1263	22,631	1,211	100,9

Punts a ignorar
7

numero inhibidor = 3 | Referencia llista! 856

MVR_25

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,0114
	1,88	1,1153	0,10	0,231	1,12	0,635	1,017	0,404	0,0081
	9,38	1,0309	0,13	0,217	1,50	0,497	1,367	0,28	0
	16,89	0,372	0,17	0,213	1,50	0,500	1,333	0,287	0,0106
	24,40	0,3221	0,15	0,209	1,50	0,474	1,35	0,265	0,001
	31,91	0,3136	0,18	0,212	1,50	0,432	1,317	0,220	0,001
	39,41	0,2531	0,18	0,207	1,17	0,448	0,983	0,241	0,0002
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	0,0001
	1,88	1,0682	0,10	0,282	1,12	0,603	1,017	0,321	0,0018
	9,38	0,7467	0,08	0,231	1,50	0,540	1,417	0,309	0,0045
	16,89	0,4845	0,13	0,229	1,50	0,493	1,367	0,264	9E-05
	24,40	0,3157	0,08	0,207	1,50	0,482	1,417	0,275	0,0015
	31,91	0,3064	0,13	0,217	1,50	0,448	1,367	0,231	0,0006
	39,41	0,2553	0,13	0,203	1,50	0,397	1,367	0,194	0,0002
							Error a	**0,001**	0,0712



error Y
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0,103198042
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0,042658711
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0,009301958
0,03855771
0,023661772
0,014855657

corretgir per [TTR] a 4 mg/mL

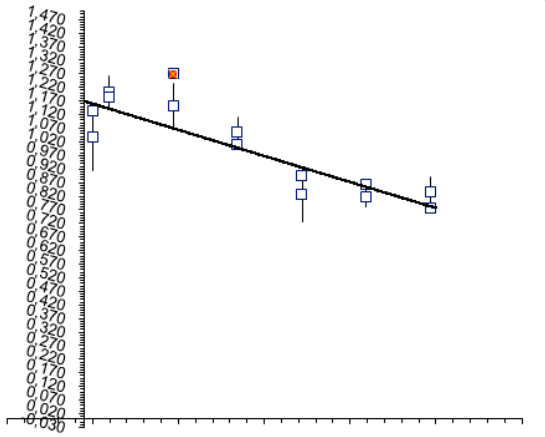
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,179	0,068	0,965	0,068	0,070	0,015	0,068	1,1443	12,841	0,513	84,3

Punts a ignorar
7

numero inhibidor = 4 | Referencia llista! 860

MVR_25

	[856]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,0151
	1,87	1,204	0,10	0,230	1,12	0,575	1,017	0,345	0,0038
	9,36	1,2696	0,10	0,233	1,50	0,590	1,4	0,357	0
	16,86	1,0559	0,12	0,226	1,50	0,598	1,383	0,372	0,0033
	24,35	0,8966	0,12	0,212	1,50	0,572	1,383	0,36	0,0009
	31,84	0,8639	0,12	0,209	1,50	0,578	1,383	0,369	8E-05
	39,33	0,838	0,15	0,215	1,17	0,495	1,017	0,28	0,003
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	0,0007
	1,87	1,1849	0,07	0,255	1,12	0,662	1,05	0,407	0,0018
	9,36	1,1543	0,07	0,247	1,50	0,618	1,433	0,371	0,0071
	16,86	1,0119	0,07	0,227	1,50	0,578	1,433	0,351	0,0002
	24,35	0,8265	0,08	0,236	1,50	0,637	1,417	0,401	0,01
	31,84	0,8192	0,08	0,223	1,50	0,587	1,417	0,364	0,0013
	39,33	0,7745	0,10	0,214	1,50	0,505	1,4	0,291	8E-05
							Error a	**0,001**	0,0712



error Y
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0,013704287
0,099859683
0,035535138
0,008821454

corretgir per [TTR] a 4 mg/mL

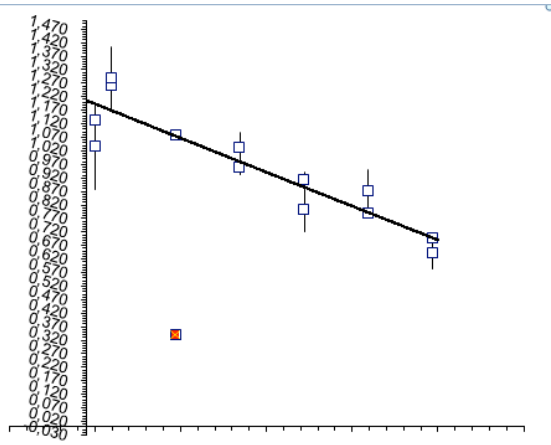
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-23,403	1599,476	24,563	#####	0,000	0,026	0,010	1,1606	60,749	######	2116,4

Punts a ignorar
7

numero inhibidor = 5 | Referencia llista! 861

MVR_25

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,0244
	1,87	1,2616	0,08	0,227	1,12	0,648	1,033	0,421	0,0084
	9,37	0,3411	0,08	0,243	1,50	0,645	1,417	0,402	0
	16,86	1,0353	0,13	0,296	1,50	0,679	1,367	0,383	0,003
	24,35	0,8053	0,10	0,254	1,50	0,676	1,4	0,422	0,0066
	31,84	0,7902	0,12	0,312	1,50	0,676	1,383	0,364	6E-06
	39,34	0,6995	0,13	0,296	1,17	0,620	1,033	0,324	2E-07
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	0,0036
	1,87	1,2885	0,05	0,241	1,12	0,656	1,067	0,415	0,014
	9,37	1,0788	0,07	0,254	1,50	0,635	1,433	0,381	1E-05
	16,86	0,9584	0,07	0,263	1,50	0,659	1,433	0,396	0,0005
	24,35	0,9148	0,05	0,261	1,50	0,709	1,45	0,448	0,0008
	31,84	0,8737	0,10	0,309	1,50	0,695	1,4	0,386	0,0066
	39,34	0,6422	0,10	0,287	1,50	0,629	1,4	0,342	0,0032
							Error a	**0,001**	0,0712



error Y
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0,003651213
0,022188943
0,028405361
0,08113554
0,056897001

corretgir per [TTR] a 4 mg/mL

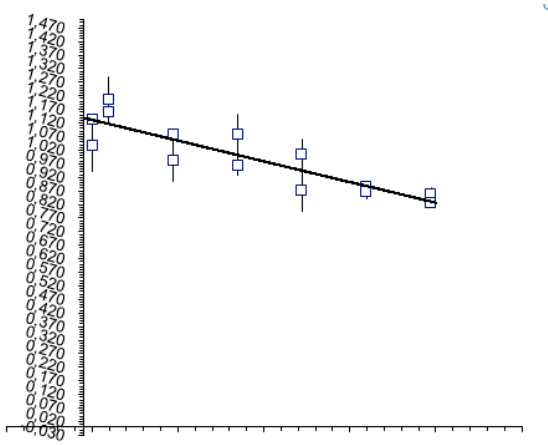
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-23,386	1137,096	24,580	#####	0,001	0,024	0,013	1,1939	47,559	76,527	2058,9

Punts a ignorar
7

numero inhibidor = 6 | Referencia llista! 862

MVR_25

	[860]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,0089
	1,88	1,1606	0,08	0,223	1,12	0,606	1,033	0,383	0,0018
	9,38	0,9837	0,10	0,268	1,50	0,623	1,4	0,355	0,0059
	16,88	1,0785	0,13	0,311	1,50	0,678	1,367	0,367	0,0057
	24,38	1,0047	0,10	0,303	1,50	0,695	1,4	0,392	0,0035
	31,88	0,8862	0,10	0,322	1,50	0,678	1,4	0,356	6E-06
	39,38	0,857	0,12	0,348	1,17	0,683	1,05	0,335	0,0006
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	4E-06
	1,88	1,2055	0,08	0,287	1,12	0,666	1,033	0,379	0,0077
	9,38	1,0804	0,07	0,265	1,50	0,630	1,433	0,365	0,0004
	16,88	0,9657	0,13	0,385	1,50	0,692	1,367	0,307	0,0014
	24,38	0,8709	0,08	0,340	1,50	0,740	1,417	0,4	0,0056
	31,88	0,8665	0,08	0,360	1,50	0,757	1,417	0,397	0,0005
	39,38	0,827	0,10	0,382	1,50	0,720	1,4	0,338	2E-05
							Error a	**0,001**	0,0712



error Y
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0,037257756
0,074851918
0,02218009
0,004741957

corretgir per [TTR] a 4 mg/mL

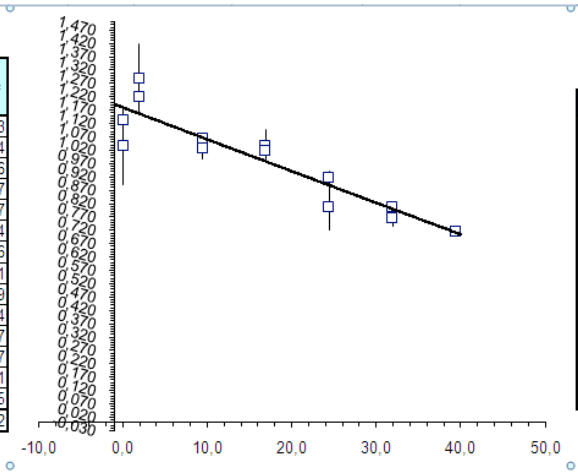
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-23,417	2230,823	24,549	#####	0,000	0,029	0,008	1,1322	74,620	######	2168,3

Punts a ignorar

numero inhibidor = 7 | Referencia llista: 863

MVR_25

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,0203
	1,87	1,2895	0,08	0,236	1,12	0,605	1,033	0,369	0,0174
	9,37	1,0668	0,12	0,325	1,50	0,694	1,383	0,369	1E-06
	16,87	1,0395	0,10	0,358	1,50	0,743	1,4	0,385	0,0037
	24,37	0,9168	0,10	0,415	1,50	0,840	1,4	0,425	0,0007
	31,87	0,8107	0,15	0,497	1,50	0,858	1,35	0,361	1E-04
	39,37	0,715	0,12	0,540	1,17	0,942	1,05	0,402	7E-06
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	0,0021
	1,87	1,2202	0,08	0,289	1,12	0,627	1,033	0,338	0,0039
	9,37	1,03	0,08	0,344	1,50	0,738	1,417	0,394	0,0014
	16,87	1,0197	0,08	0,393	1,50	0,783	1,417	0,39	0,0017
	24,37	0,8074	0,08	0,445	1,50	0,834	1,417	0,389	0,0067
	31,87	0,7684	0,08	0,479	1,50	0,863	1,417	0,384	0,001
	39,37	0,7177	0,10	0,567	1,50	0,950	1,4	0,383	3E-05
							Error a	**0,001**	0,0712



error Y
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0,002644207
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0,062556959
0,037932358
0,041150512
0,082093232
0,032362397
0,005344207

corretgir per [TTR] a 4 mg/mL

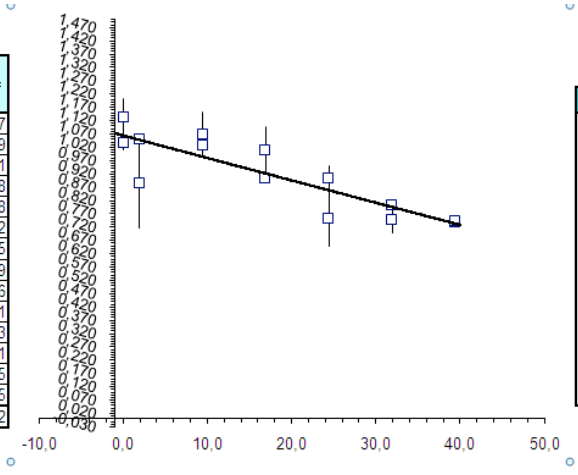
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-23,393	1086,745	24,573	#####	0,000	0,022	0,012	1,1801	49,793	72,800	2082,3

Punts a ignorar

numero inhibidor = 9 | Referencia llista: 865

MVR_25

	1,2885	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,0007
	1,87	0,8846	0,17	0,252	1,12	0,488	0,95	0,236	0,0269
	9,37	1,0697	0,15	0,281	1,50	0,624	1,35	0,343	0,0071
	16,86	1,0117	0,17	0,290	1,50	0,587	1,333	0,297	0,008
	24,36	0,7553	0,17	0,291	1,50	0,636	1,333	0,345	0,0108
	31,85	0,7495	0,18	0,300	1,50	0,593	1,317	0,293	0,0022
	39,34	0,7379	0,15	0,288	1,17	0,572	1,017	0,284	1E-05
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	0,0049
	1,87	1,0515	0,08	0,245	1,12	0,590	1,033	0,345	8E-06
	9,37	1,0307	0,08	0,254	1,50	0,606	1,417	0,352	0,0021
	16,86	0,9059	0,08	0,248	1,50	0,593	1,417	0,345	0,0003
	24,36	0,9052	0,08	0,250	1,50	0,523	1,417	0,273	0,0021
	31,85	0,8051	0,12	0,298	1,50	0,593	1,383	0,295	7E-05
	39,34	0,7427	0,08	0,282	1,50	0,593	1,417	0,311	7E-05
							Error a	**0,001**	0,0712



error Y
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0,045800224
0,008442538
0,00862292

corretgir per [TTR] a 4 mg/mL

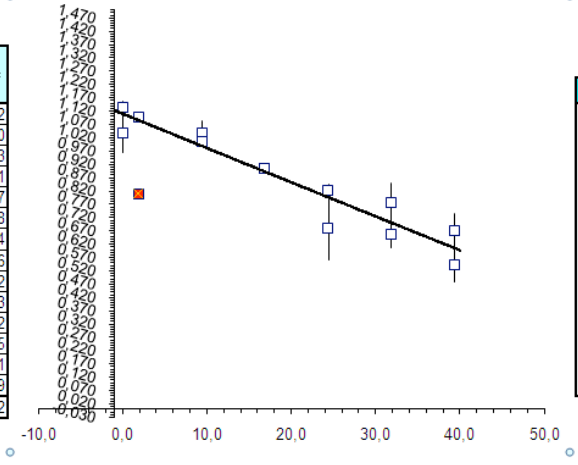
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-23,451	2288,148	24,515	#####	0,000	0,032	0,008	1,0644	63,650	######	2303,1

Punts a ignorar

numero inhibidor = 10 | Referencia llista: 866

MVR_25

	1,8754525216	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,0052
	1,87	0,8096	0,17	0,242	1,12	0,516	0,95	0,274	0
	9,36	1,0376	0,15	0,241	1,50	0,572	1,35	0,331	0,0023
	16,85	0,9048	0,17	0,256	1,50	0,579	1,333	0,323	0,0001
	24,34	0,8228	0,18	0,261	1,50	0,590	1,317	0,329	0,0007
	31,83	0,7773	0,12	0,214	1,50	0,606	1,383	0,392	0,0058
	39,32	0,6722	0,18	0,245	1,17	0,547	0,983	0,302	0,0044
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	0,0006
	1,87	1,0986	0,08	0,252	1,12	0,651	1,033	0,399	0,0002
	9,36	1,0073	0,08	0,232	1,50	0,627	1,417	0,395	0,0003
	16,85	0,9063	0,12	0,254	1,50	0,566	1,383	0,312	0,0002
	24,34	0,6807	0,12	0,248	1,50	0,624	1,383	0,376	0,0135
	31,83	0,6554	0,10	0,235	1,50	0,643	1,4	0,408	0,0021
	39,32	0,5437	0,13	0,235	1,50	0,577	1,367	0,342	0,0039
							Error a	**0,001**	0,0712



error Y
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0,116137276
0,045840841
0,062321651

corretgir per [TTR] a 4 mg/mL

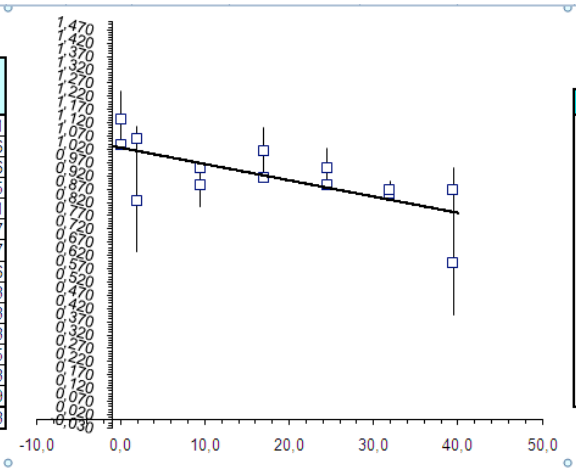
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-23,428	809,647	24,538	#####	0,001	0,018	0,013	1,1101	43,341	53,058	2210,3

Punts a ignorar
6

numero inhibidor = 11 | Referencia llista! 868

MVR_25

	1,2055	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,0001
	1,88	0,8253	0,15	0,235	1,12	0,548	0,967	0,313	0,036
	9,38	0,8877	0,15	0,253	1,50	0,564	1,35	0,311	0,0066
	16,89	0,915	0,15	0,266	1,50	0,607	1,35	0,341	6E-05
	24,40	0,8877	0,13	0,243	1,50	0,613	1,367	0,37	0,0001
	31,91	0,8566	0,10	0,241	1,50	0,620	1,4	0,379	0,0007
	39,42	0,8682	0,12	0,265	1,17	0,637	1,05	0,372	0,007
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	0,0116
	1,88	1,0627	0,07	0,226	1,12	0,586	1,05	0,360	0,0023
	9,38	0,951	0,08	0,251	1,50	0,633	1,417	0,382	0,0003
	16,89	1,0137	0,08	0,245	1,50	0,586	1,417	0,341	0,0083
	24,40	0,951	0,08	0,246	1,50	0,628	1,417	0,382	0,0055
	31,91	0,8666	0,07	0,254	1,50	0,650	1,433	0,396	0,0013
	39,42	0,5926	0,20	0,407	1,50	0,676	1,3	0,269	0,0369
							Error a	**0,001**	0,0713



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0,017744527
0,09107956
0,074416595
0,035966742
0,192169835

corretgir per [TTR] a 4 mg/mL

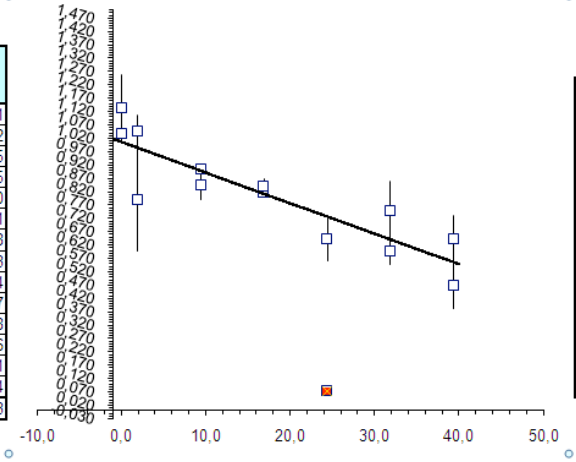
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-23,470	5726,912	24,496	#####	0,000	0,059	0,006	1,0265	84,156	######	2386,3

Punts a ignorar

numero inhibidor = 12 | Referencia llista! 870

MVR_25

	[illegible]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,001
	1,87	0,7918	0,17	0,236	1,12	0,481	0,95	0,245	0,0372
	9,36	0,9042	0,15	0,237	1,50	0,578	1,35	0,341	3E-05
	16,86	0,8161	0,15	0,224	1,50	0,559	1,35	0,335	1E-05
	24,35	0,0733	0,10	0,162	1,50	0,202	1,4	0,04	0
	31,84	0,7513	0,17	0,227	1,50	0,522	1,333	0,295	0,0121
	39,33	0,6445	0,17	0,237	1,17	0,565	1	0,328	0,0078
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	0,0163
	1,87	1,0479	0,07	0,230	1,12	0,601	1,05	0,371	0,004
	9,36	0,8465	0,10	0,233	1,50	0,548	1,4	0,315	0,0027
	16,86	0,8411	0,08	0,217	1,50	0,537	1,417	0,32	0,0008
	24,35	0,6456	0,08	0,213	1,50	0,547	1,417	0,334	0,0066
	31,84	0,5956	0,10	0,225	1,50	0,604	1,4	0,379	0,0021
	39,33	0,4701	0,13	0,236	1,50	0,554	1,367	0,318	0,0074
							Error a	**0,001**	0,0713



error Y
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0,045803105
0,086227334

corretgir per [TTR] a 4 mg/mL

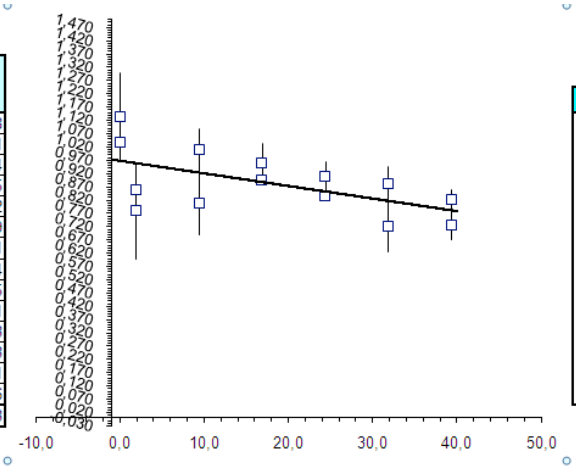
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-23,480	1651,642	24,486	#####	0,000	0,032	0,012	1,0063	44,026	######	2433,2

Punts a ignorar
9

numero inhibidor = 13 | Referencia llista! 871

MVR_25

	1,2202	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,0377	0,08	0,197	1,18	0,507	1,10	0,310	0,0048
	1,87	0,8596	0,13	0,217	1,12	0,518	0,983	0,301	0,01
	9,36	0,8086	0,15	0,224	1,50	0,525	1,35	0,301	0,0134
	16,86	0,8968	0,15	0,238	1,50	0,577	1,35	0,339	7E-05
	24,35	0,838	0,10	0,214	1,50	0,632	1,4	0,418	0,0002
	31,84	0,7229	0,15	0,242	1,50	0,591	1,35	0,349	0,009
	39,33	0,7269	0,18	0,286	1,17	0,630	0,983	0,344	0,0031
Serie 2	0,00	1,1341	0,08	0,271	1,17	0,630	1,083	0,359	0,0274
	1,87	0,7794	0,10	0,220	1,12	0,512	1,017	0,292	0,0325
	9,36	1,0085	0,10	0,253	1,50	0,580	1,4	0,327	0,0071
	16,86	0,9615	0,10	0,242	1,50	0,572	1,4	0,33	0,0053
	24,35	0,911	0,08	0,240	1,50	0,636	1,417	0,396	0,0033
	31,84	0,8821	0,10	0,250	1,50	0,611	1,4	0,361	0,0041
	39,33	0,8218	0,12	0,259	1,50	0,584	1,383	0,325	0,0016
							Error a	**0,001**	0,0713



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0,057832301
0,064357586
0,039431337

corretgir per [TTR] a 4 mg/mL

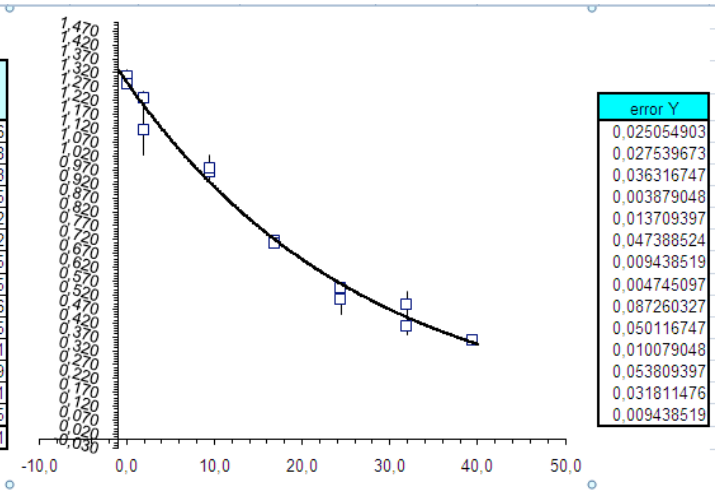
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-23,499	9854,972	24,467	#####	0,000	0,079	0,005	0,9687	102,890	######	2525,9

Punts a ignorar

numero inhibidor = 1 | Referencia llista: 930

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3087	0,08	0,273	1,18	0,629	1,10	0,356	0,0006
	1,87	1,2298	0,07	0,271	1,12	0,629	1,05	0,358	0,0008
	9,37	0,9639	0,08	0,262	1,50	0,591	1,417	0,329	0,0013
	16,87	0,7154	0,08	0,252	1,50	0,592	1,417	0,34	2E-05
	24,37	0,5476	0,08	0,242	1,25	0,571	1,167	0,329	0,0002
	31,86	0,4889	0,08	0,243	1,08	0,530	1	0,287	0,0022
	39,36	0,3601	0,08	0,233	1,50	0,488	1,417	0,255	9E-05
Serie 2	0,00	1,2789	0,08	0,210	1,17	0,558	1,083	0,348	2E-05
	1,87	1,115	0,08	0,230	1,12	0,596	1,033	0,366	0,0076
	9,37	0,9777	0,08	0,213	1,50	0,597	1,417	0,384	0,0025
	16,87	0,7092	0,12	0,234	1,50	0,531	1,383	0,297	0,0001
	24,37	0,5075	0,15	0,218	1,50	0,417	1,35	0,199	0,0029
	31,86	0,4097	0,13	0,227	1,47	0,481	1,333	0,254	0,001
	39,36	0,3601	0,12	0,215	1,50	0,467	1,383	0,252	9E-05
							Error a	**0,001**	0,0711



error Y
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☐ corretgir per [TTR] a 4 mg/mL

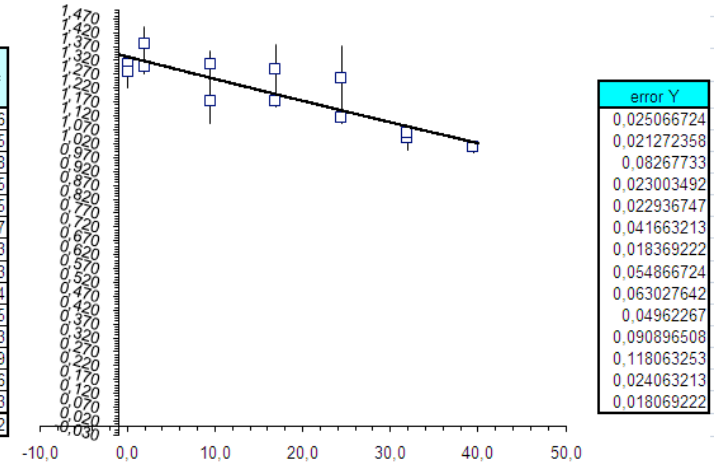
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,066	0,123	1,218	0,116	0,037	0,007	0,045	1,2836	20,287	0,533	94,9

Punts a ignorar

numero inhibidor = 2 | Referencia llista: 931

NPC-052

	[931]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3087	0,08	0,273	1,18	0,629	1,10	0,356	0,0006
	1,87	1,2973	0,08	0,293	1,12	0,653	1,033	0,36	0,0005
	9,37	1,1757	0,07	0,271	1,50	0,698	1,433	0,427	0,0068
	16,87	1,1761	0,08	0,292	1,50	0,702	1,417	0,41	0,0005
	24,37	1,1178	0,08	0,279	1,25	0,691	1,167	0,412	0,0005
	31,87	1,0416	0,10	0,295	1,08	0,703	0,983	0,408	0,0017
	39,37	1,0083	0,10	0,276	1,50	0,670	1,4	0,394	0,0003
Serie 2	0,00	1,2789	0,08	0,210	1,17	0,558	1,083	0,348	0,003
	1,87	1,3816	0,10	0,234	1,12	0,631	1,017	0,397	0,004
	9,37	1,308	0,12	0,241	1,50	0,638	1,383	0,397	0,0025
	16,87	1,29	0,10	0,229	1,50	0,648	1,4	0,419	0,0083
	24,37	1,2588	0,10	0,229	1,50	0,666	1,4	0,437	0,0139
	31,87	1,0592	0,12	0,223	1,47	0,664	1,35	0,441	0,0006
	39,37	1,0086	0,10	0,196	1,50	0,587	1,4	0,391	0,0003
							Error a	**0,001**	0,0712



error Y
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☐ corretgir per [TTR] a 4 mg/mL

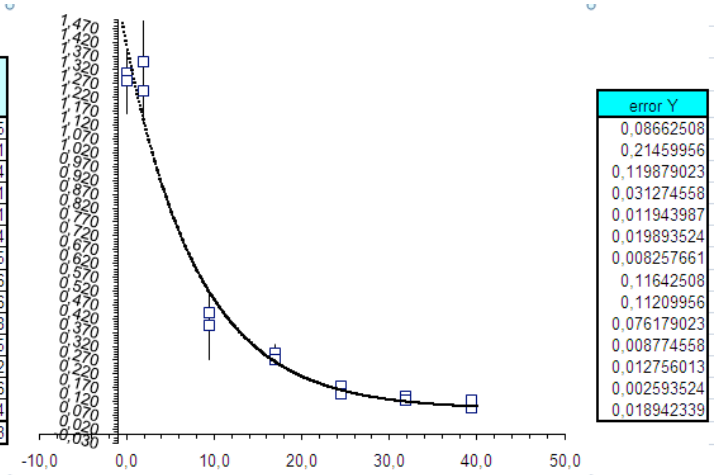
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-2,615	52,673	3,949	#####	0,002	0,029	0,008	1,3338	89,958	28,558	296,1

Punts a ignorar

numero inhibidor = 3 | Referencia llista: 932

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3087	0,08	0,273	1,18	0,629	1,10	0,356	0,0075
	1,88	1,3475	0,05	0,250	1,12	0,611	1,067	0,361	0,0461
	9,39	0,3959	0,08	0,250	1,50	0,489	1,417	0,239	0,0144
	16,89	0,2962	0,12	0,264	1,50	0,473	1,383	0,209	0,001
	24,40	0,1749	0,12	0,284	1,25	0,459	1,133	0,175	0,0001
	31,91	0,1414	0,12	0,300	1,08	0,419	0,967	0,119	0,0004
	39,42	0,0964	0,23	0,313	1,50	0,420	1,267	0,107	7E-05
Serie 2	0,00	1,2789	0,08	0,210	1,17	0,558	1,083	0,348	0,0136
	1,88	1,245	0,08	0,229	1,12	0,613	1,033	0,384	0,0126
	9,39	0,4396	0,13	0,234	1,50	0,432	1,367	0,198	0,0058
	16,89	0,2737	0,13	0,255	1,50	0,457	1,367	0,202	8E-05
	24,40	0,1502	0,12	0,275	1,50	0,461	1,383	0,186	0,0002
	31,91	0,1241	0,12	0,286	1,47	0,441	1,35	0,155	7E-06
	39,42	0,1236	0,42	0,318	1,50	0,434	1,083	0,116	0,0004
							Error a	**0,001**	0,0713



error Y
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0,11209956
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0,002593524
0,018942339

☐ corretgir per [TTR] a 4 mg/mL

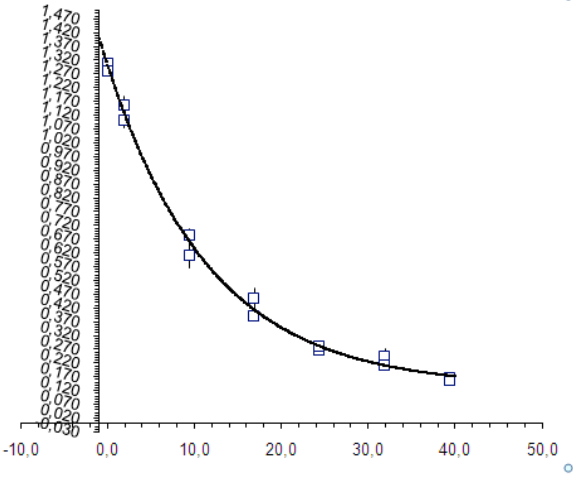
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,093	0,052	1,302	0,070	0,120	0,020	0,156	1,3953	6,400	0,343	93,3

Punts a ignorar

numero inhibidor = 4 | Referencia llista! 933

NPC-052

	[932]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3087	0,08	0,273	1,18	0,629	1,10	0,356	0,0002
	1,87	1,1576	0,08	0,281	1,12	0,625	1,033	0,344	0,0011
	9,37	0,6131	0,08	0,244	1,50	0,592	1,417	0,348	0,0022
	16,87	0,454	0,08	0,229	1,50	0,513	1,417	0,284	0,0017
	24,36	0,2693	0,08	0,209	1,25	0,431	1,167	0,222	0,0002
	31,86	0,2425	0,08	0,209	1,08	0,395	1	0,186	0,0009
	39,35	0,1687	0,08	0,204	1,27	0,379	1,183	0,175	5E-05
Serie 2	0,00	1,2789	0,08	0,210	1,17	0,558	1,083	0,348	0,0003
	1,87	1,1008	0,12	0,244	1,12	0,614	1	0,370	0,0006
	9,37	0,686	0,13	0,231	1,50	0,583	1,367	0,352	0,0007
	16,87	0,3933	0,17	0,218	1,50	0,474	1,333	0,256	0,0004
	24,36	0,2821	0,12	0,212	1,50	0,400	1,383	0,188	6E-09
	31,86	0,2143	0,08	0,199	1,10	0,402	1,017	0,203	3E-06
	39,35	0,1578	0,25	0,209	1,35	0,369	1,1	0,16	0,0003
							Error a	**0,001**	0,0711



error Y
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0,020054639
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0,001816186
0,017656657

☐ corretgir per [TTR] a 4 mg/mL

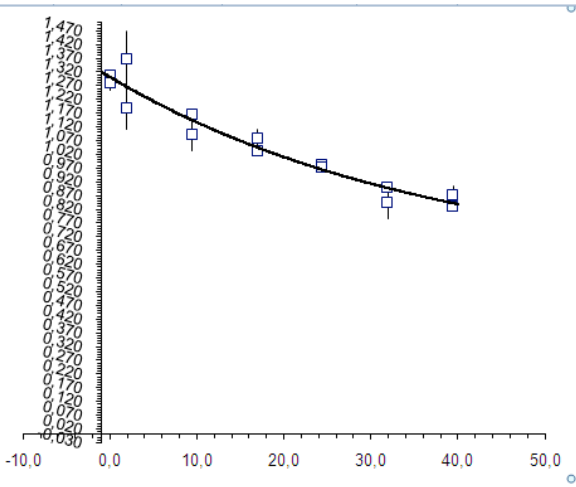
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,133	0,022	1,161	0,023	0,084	0,005	0,098	1,2948	9,663	0,138	89,7

Punts a ignorar

numero inhibidor = 5 | Referencia llista! 934

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3087	0,08	0,273	1,18	0,629	1,10	0,356	6E-05
	1,88	1,3694	0,08	0,324	1,12	0,690	1,033	0,366	0,0106
	9,38	1,0914	0,08	0,384	1,50	0,809	1,417	0,425	0,0029
	16,89	1,0351	0,08	0,455	1,50	0,901	1,417	0,446	0,0001
	24,39	0,9833	0,08	0,506	1,25	0,936	1,167	0,43	0,0004
	31,90	0,8438	0,08	0,591	1,08	1,082	1	0,491	0,0029
	39,41	0,8334	0,08	0,675	1,27	1,138	1,183	0,463	1E-04
Serie 2	0,00	1,2789	0,08	0,210	1,17	0,558	1,083	0,348	0,0005
	1,88	1,1905	0,12	0,281	1,12	0,718	1	0,437	0,0058
	9,38	1,1649	0,12	0,325	1,50	0,768	1,383	0,443	0,0004
	16,89	1,0793	0,10	0,359	1,50	0,778	1,4	0,419	0,0011
	24,39	0,9754	0,12	0,461	1,50	0,962	1,383	0,501	0,0001
	31,90	0,9003	0,08	0,484	1,10	1,051	1,017	0,567	6E-06
	39,41	0,8743	0,12	0,592	1,35	1,067	1,233	0,475	0,001
							Error a	**0,001**	0,0712



error Y
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0,033374418
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0,002347053
0,030917279

☐ corretgir per [TTR] a 4 mg/mL

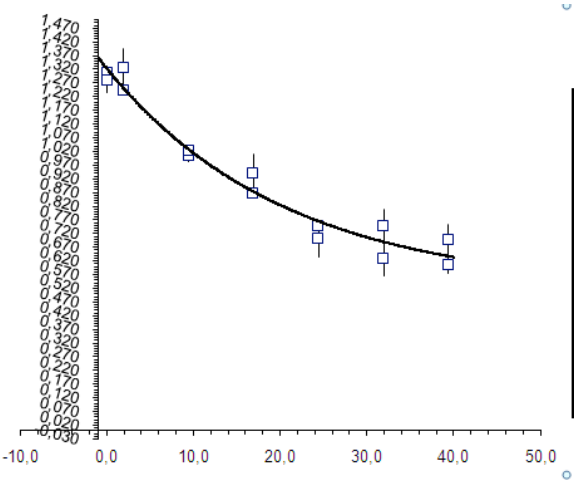
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,596	0,259	0,704	0,249	0,027	0,016	0,019	1,3008	96,565	21,126	54,2

Punts a ignorar

numero inhibidor = 6 | Referencia llista! 935

NPC-052

	[933]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3087	0,08	0,273	1,18	0,629	1,10	0,356	0,0001
	1,87	1,2446	0,08	0,290	1,12	0,620	1,033	0,33	4E-05
	9,37	1,0069	0,08	0,323	1,50	0,740	1,417	0,417	0,0005
	16,86	0,8687	0,10	0,354	1,50	0,758	1,4	0,404	2E-05
	24,35	0,7511	0,08	0,397	1,25	0,792	1,167	0,395	0,0002
	31,85	0,7499	0,08	0,443	1,08	0,841	1	0,398	0,0035
	39,34	0,6979	0,10	0,523	1,27	0,874	1,167	0,351	0,0035
Serie 2	0,00	1,2789	0,08	0,210	1,17	0,558	1,083	0,348	0,0017
	1,87	1,3245	0,12	0,278	1,12	0,665	1	0,387	0,0054
	9,37	1,0234	0,12	0,284	1,50	0,687	1,383	0,403	2E-05
	16,86	0,9424	0,13	0,333	1,50	0,717	1,367	0,384	0,0048
	24,35	0,7016	0,10	0,376	1,50	0,752	1,4	0,376	0,0041
	31,85	0,6299	0,12	0,428	1,10	0,807	0,983	0,379	0,0037
	39,34	0,6069	0,10	0,477	1,35	0,829	1,25	0,352	0,001
							Error a	**0,001**	0,0712



error Y
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0,064086235
0,060795448
0,031609446

☐ corretgir per [TTR] a 4 mg/mL

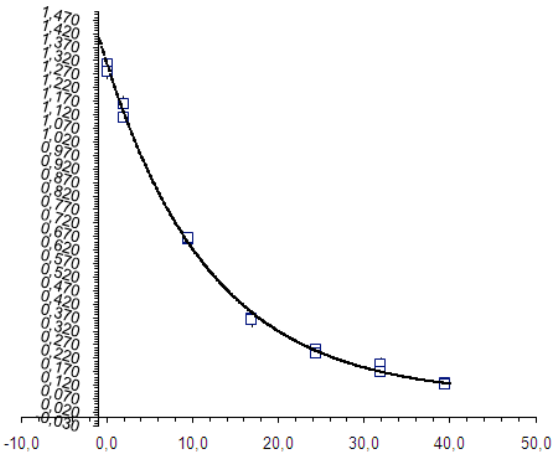
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,519	0,092	0,801	0,086	0,048	0,012	0,039	1,3202	35,904	2,227	60,7

Punts a ignorar

numero inhibidor = 7 | Referencia llista: 936

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3087	0,08	0,273	1,18	0,629	1,10	0,356	5E-05
	1,87	1,1606	0,08	0,275	1,12	0,579	1,033	0,304	0,001
	9,37	0,6628	0,10	0,324	1,50	0,649	1,4	0,325	0,0002
	16,86	0,3676	0,12	0,367	1,50	0,612	1,383	0,245	0,0005
	24,35	0,2546	0,10	0,420	1,25	0,611	1,15	0,191	4E-05
	31,84	0,197	0,12	0,486	1,08	0,627	0,967	0,141	0,0006
	39,34	0,1296	0,12	0,570	1,47	0,730	1,35	0,16	1E-07
Serie 2	0,00	1,2789	0,08	0,210	1,17	0,558	1,083	0,348	0,0005
	1,87	1,1126	0,10	0,236	1,12	0,590	1,017	0,354	0,0003
	9,37	0,6645	0,13	0,300	1,50	0,596	1,367	0,296	0,0002
	16,86	0,3651	0,12	0,353	1,50	0,613	1,383	0,26	0,0006
	24,35	0,2424	0,08	0,406	1,50	0,581	1,417	0,175	3E-05
	31,84	0,1718	0,10	0,468	1,23	0,647	1,133	0,179	6E-08
	39,34	0,1234	0,08	0,535	1,35	0,653	1,267	0,118	4E-05
							Error a	**0,001**	0,071



error Y
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0,014770778
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0,000237589
0,006512528

☐ corretgir per [TTR] a 4 mg/mL

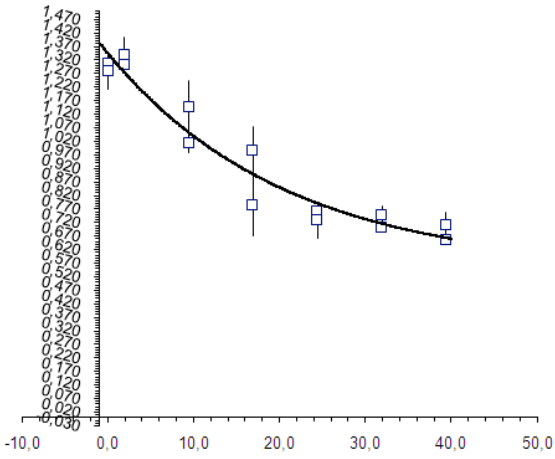
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,080	0,016	1,221	0,017	0,082	0,003	0,100	1,3019	9,340	0,089	93,8

Punts a ignorar

numero inhibidor = 8 | Referencia llista: 937

NPC-052

		[934]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3087	0,08	0,273	1,18	0,629	1,10	0,356	0,0012
	1,87	1,3397	0,08	0,298	1,12	0,605	1,033	0,307	0,0043
	9,37	1,0167	0,08	0,264	1,50	0,591	1,417	0,327	0,0013
	16,87	0,7852	0,10	0,271	1,50	0,640	1,4	0,369	0,013
	24,36	0,7627	0,10	0,266	1,25	0,624	1,15	0,358	0,0009
	31,86	0,7508	0,10	0,254	1,08	0,623	0,983	0,369	0,0011
	39,36	0,6561	0,10	0,230	1,47	0,550	1,367	0,32	8E-05
Serie 2	0,00	1,2789	0,08	0,210	1,17	0,558	1,083	0,348	0,0041
	1,87	1,306	0,10	0,242	1,12	0,625	1,017	0,383	0,001
	9,37	1,1497	0,12	0,242	1,50	0,594	1,383	0,352	0,0093
	16,87	0,9884	0,12	0,240	1,50	0,550	1,383	0,31	0,008
	24,36	0,729	0,10	0,219	1,50	0,620	1,4	0,401	0,004
	31,86	0,7019	0,12	0,217	1,23	0,582	1,117	0,365	0,0002
	39,36	0,7123	0,12	0,213	1,35	0,551	1,233	0,338	0,0022
							Error a	**0,001**	0,0712



error Y
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☐ corretgir per [TTR] a 4 mg/mL

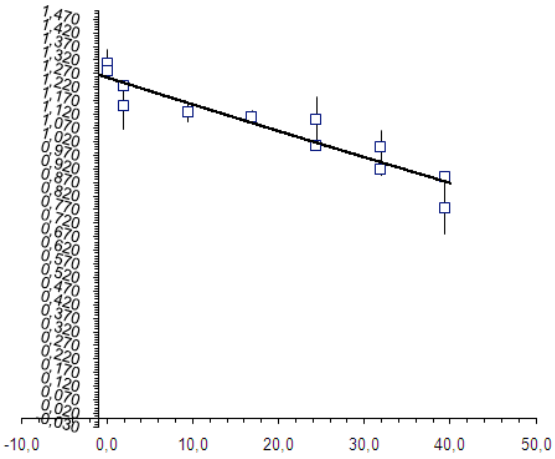
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,545	0,124	0,798	0,116	0,048	0,016	0,038	1,3427	38,276	3,467	59,4

Punts a ignorar

numero inhibidor = 9 | Referencia llista: 938

NPC-052

		1,1905	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3087	0,08	0,273	1,18	0,629	1,10	0,356	0,0028
	1,87	1,2274	0,10	0,317	1,12	0,687	1,017	0,37	1E-04
	9,37	1,1319	0,10	0,299	1,50	0,676	1,4	0,377	0,001
	16,87	1,1102	0,10	0,294	1,50	0,659	1,4	0,365	0,0004
	24,36	1,1013	0,12	0,332	1,25	0,662	1,133	0,33	0,0072
	31,86	0,921	0,10	0,295	1,08	0,689	0,983	0,394	0,0006
	39,36	0,7775	0,08	0,311	1,47	0,738	1,383	0,427	0,0093
Serie 2	0,00	1,2789	0,08	0,210	1,17	0,558	1,083	0,348	0,0005
	1,87	1,1522	0,10	0,225	1,12	0,647	1,017	0,422	0,0073
	9,37	1,1294	0,12	0,244	1,50	0,642	1,383	0,398	0,0011
	16,87	1,1135	0,12	0,246	1,50	0,653	1,383	0,407	0,0006
	24,36	1,0065	0,10	0,236	1,50	0,725	1,4	0,489	0,0001
	31,86	1,0032	0,10	0,260	1,23	0,639	1,133	0,379	0,0034
	39,36	0,8903	0,12	0,269	1,35	0,680	1,233	0,411	0,0003
							Error a	**0,001**	0,0712



error Y
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☐ corretgir per [TTR] a 4 mg/mL

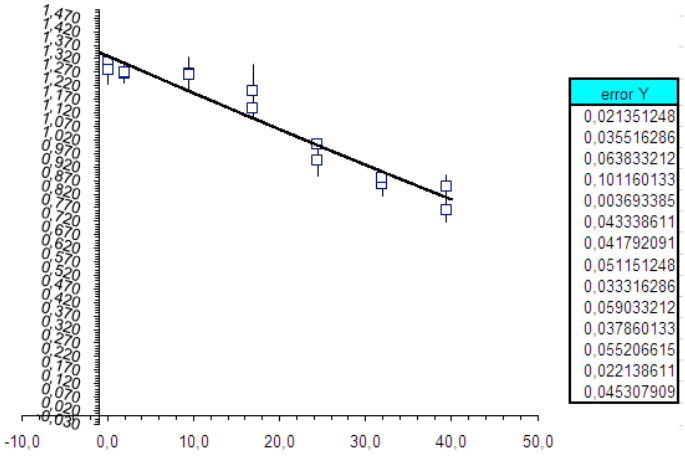
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-4,850	73,562	6,106	#####	0,002	0,020	0,010	1,2561	66,108	22,783	486,1

Punts a ignorar

numero inhibidor = 10 | Referencia llista 939

NPC-052

	1,823427833	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3087	0,08	0,273	1,18	0,629	1,10	0,356	0,0005
	1,87	1,2686	0,08	0,263	1,12	0,633	1,033	0,37	0,0013
	9,37	1,2653	0,08	0,246	1,50	0,620	1,417	0,374	0,0041
	16,87	1,2017	0,08	0,249	1,50	0,619	1,417	0,37	0,0102
	24,37	1,005	0,10	0,268	1,25	0,672	1,15	0,404	1E-05
	31,86	0,8604	0,10	0,260	1,08	0,674	0,983	0,414	0,0019
	39,36	0,8496	0,08	0,235	1,47	0,620	1,383	0,385	0,0017
Serie 2	0,00	1,2789	0,08	0,210	1,17	0,558	1,083	0,348	0,0026
	1,87	1,2708	0,10	0,215	1,12	0,608	1,017	0,393	0,0011
	9,37	1,2605	0,10	0,210	1,50	0,594	1,4	0,384	0,0035
	16,87	1,1384	0,12	0,227	1,50	0,600	1,383	0,373	0,0014
	24,37	0,9461	0,12	0,227	1,50	0,627	1,383	0,4	0,003
	31,86	0,8816	0,12	0,229	1,23	0,644	1,117	0,415	0,0005
	39,36	0,7625	0,12	0,210	1,35	0,553	1,233	0,343	0,0021
							Error a	**0,001**	0,0712



error Y
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0,059033212
0,037860133
0,055206615
0,022138611
0,045307909

☐ corretgir per [TTR] a 4 mg/mL

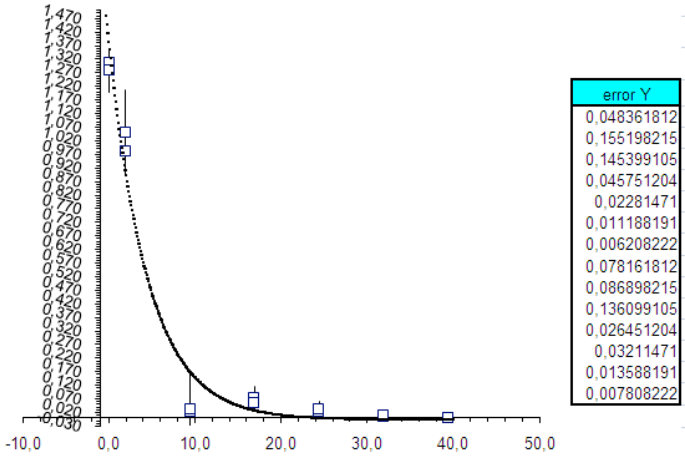
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-4,813	38,582	6,143	#####	0,002	0,015	0,014	1,3301	50,758	12,317	461,9

Punts a ignorar

numero inhibidor = 11 | Referencia llista 200

NPC-052

	1,3245	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3087	0,08	0,273	1,18	0,629	1,10	0,356	0,0023
	1,87	1,0534	0,08	0,253	1,12	0,610	1,033	0,357	0,0241
	9,37	0,0241	0,15	0,222	1,50	0,424	1,35	0,202	0,0211
	16,87	0,0743	0,33	0,196	1,50	0,274	1,167	0,078	0,0021
	24,37	0,0241	0,53	0,181	1,50	0,202	0,967	0,021	0,0005
	31,87	0,0072	0,47	0,193	1,50	0,192	1,033	-0,001	0,0001
	39,37	0,0012	0,08	0,204	1,50	0,205	1,417	0,001	4E-05
Serie 2	0,00	1,2789	0,08	0,210	1,17	0,558	1,083	0,348	0,0061
	1,87	0,9851	0,12	0,218	1,12	0,480	1	0,262	0,0076
	9,37	0,0334	0,23	0,217	1,50	0,334	1,267	0,117	0,0185
	16,87	0,055	0,40	0,190	1,42	0,237	1,017	0,047	0,0007
	24,37	0,0334	0,43	0,186	1,50	0,211	1,067	0,025	0,001
	31,87	0,0096	0,38	0,203	1,50	0,209	1,117	0,006	0,0002
	39,37	0,0028	0,12	0,205	1,50	0,208	1,383	0,003	6E-05
							Error a	**0,001**	0,0713



error Y
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0,011188191
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0,078161812
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0,136099105
0,026451204
0,03211471
0,013588191
0,007808222

☐ corretgir per [TTR] a 4 mg/mL

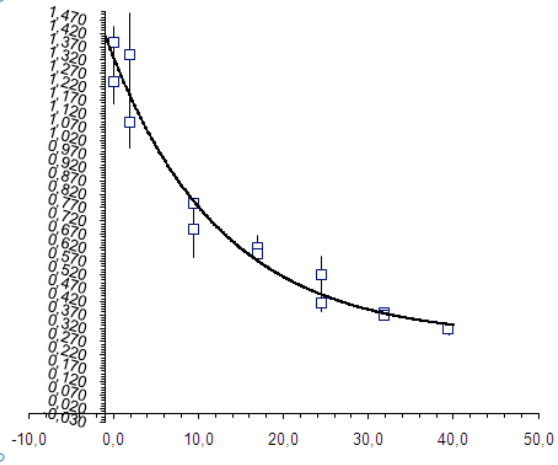
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-0,005	0,033	1,362	0,063	0,219	0,034	0,298	1,3571	3,146	0,263	100,4

Punts a ignorar

numero inhibidor = 1 | Referencia llista! 856

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3857	0,08	0,242	1,18	0,617	1,10	0,375	0,0038
	1,88	1,3415	0,07	0,234	1,12	0,579	1,05	0,345	0,0243
	9,38	0,7867	0,08	0,205	1,50	0,454	1,417	0,249	5E-05
	16,89	0,6208	0,08	0,220	1,50	0,491	1,417	0,271	0,0024
	24,40	0,4162	0,08	0,205	1,50	0,445	1,417	0,24	0,0009
	31,91	0,3795	0,08	0,213	1,50	0,442	1,417	0,229	1E-05
	39,41	0,3175	0,08	0,209	1,50	0,427	1,417	0,218	0,0003
Serie 2	0,00	1,2406	0,08	0,216	1,17	0,571	1,083	0,355	0,0069
	1,88	1,089	0,08	0,213	1,12	0,573	1,033	0,360	0,0093
	9,38	0,6892	0,08	0,209	1,50	0,481	1,417	0,272	0,0109
	16,89	0,5963	0,12	0,224	1,42	0,474	1,3	0,25	0,0006
	24,40	0,5196	0,15	0,233	1,50	0,438	1,35	0,205	0,0053
	31,91	0,3679	0,13	0,219	1,50	0,448	1,367	0,229	7E-05
	39,41	0,3175	0,12	0,223	1,50	0,474	1,383	0,251	0,0003
							Error a	**0,001**	0,0712



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0,072768754
0,008101578
0,018456092

corretgir per [TTR] a 4 mg/mL

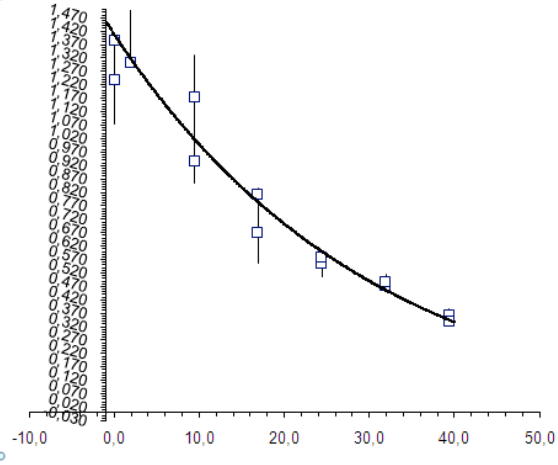
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,284	0,069	1,040	0,071	0,076	0,015	0,079	1,3238	13,321	0,582	78,6

Punts a ignorar

numero inhibidor = 2 | Referencia llista! 930

NPC-052

	[930]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3857	0,08	0,242	1,18	0,617	1,10	0,375	0,0004
	1,87	1,5278	0,08	0,236	1,12	0,612	1,033	0,376	0,0441
	9,37	1,1757	0,12	0,228	1,50	0,505	1,383	0,277	0,0249
	16,87	0,8119	0,12	0,242	1,50	0,477	1,383	0,235	0,0008
	24,37	0,5555	0,12	0,241	1,50	0,405	1,383	0,164	0,002
	31,86	0,4731	0,12	0,232	1,50	0,398	1,383	0,166	0,0003
	39,36	0,366	0,12	0,237	1,50	0,367	1,383	0,13	0,0004
Serie 2	0,00	1,2406	0,08	0,216	1,17	0,571	1,083	0,355	0,027
	1,87	1,3051	0,12	0,244	1,12	0,594	1	0,350	0,0002
	9,37	0,9366	0,12	0,226	1,50	0,498	1,383	0,272	0,0066
	16,87	0,6701	0,12	0,227	1,42	0,433	1,3	0,206	0,0129
	24,37	0,5795	0,10	0,237	1,50	0,433	1,4	0,196	0,0004
	31,86	0,4873	0,12	0,236	1,50	0,430	1,383	0,194	0,0009
	39,36	0,339	0,10	0,226	1,50	0,359	1,4	0,133	4E-05
							Error a	**0,001**	0,0713



error Y
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0,164251762
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0,020939122
0,030134333
0,006135985

corretgir per [TTR] a 4 mg/mL

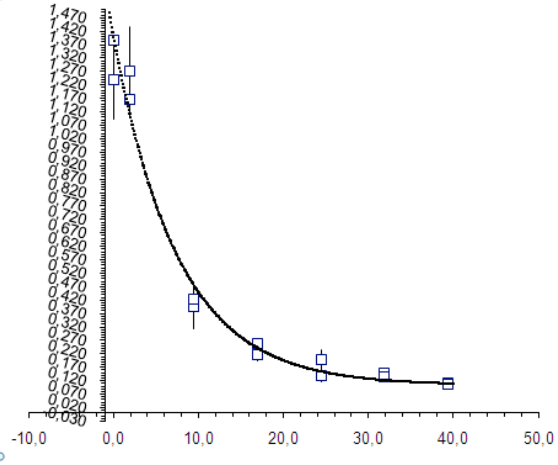
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,057	0,379	1,461	0,360	0,033	0,015	0,048	1,4049	19,968	1,244	104,0

Punts a ignorar

numero inhibidor = 3 | Referencia llista! 932

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3857	0,08	0,242	1,18	0,617	1,10	0,375	3E-06
	1,88	1,2715	0,05	0,218	1,12	0,545	1,067	0,327	0,0283
	9,39	0,3959	0,08	0,248	1,50	0,554	1,417	0,306	0,0063
	16,89	0,259	0,12	0,251	1,50	0,444	1,383	0,193	0,0003
	24,40	0,1978	0,12	0,279	1,25	0,497	1,133	0,218	0,0018
	31,91	0,1463	0,12	0,293	1,08	0,426	0,967	0,133	0,0005
	39,42	0,1111	0,28	0,315	1,50	0,439	1,217	0,124	1E-07
Serie 2	0,00	1,2406	0,08	0,216	1,17	0,571	1,083	0,355	0,0205
	1,88	1,1646	0,08	0,229	1,12	0,588	1,033	0,359	0,0038
	9,39	0,4224	0,13	0,234	1,50	0,421	1,367	0,187	0,0028
	16,89	0,2183	0,13	0,251	1,42	0,414	1,283	0,163	0,0006
	24,40	0,138	0,12	0,255	1,50	0,431	1,383	0,176	0,0003
	31,91	0,1325	0,12	0,288	1,50	0,452	1,383	0,164	8E-05
	39,42	0,1072	0,40	0,333	1,50	0,445	1,1	0,112	2E-05
							Error a	**0,001**	0,0712



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0,009059283
0,00428116

corretgir per [TTR] a 4 mg/mL

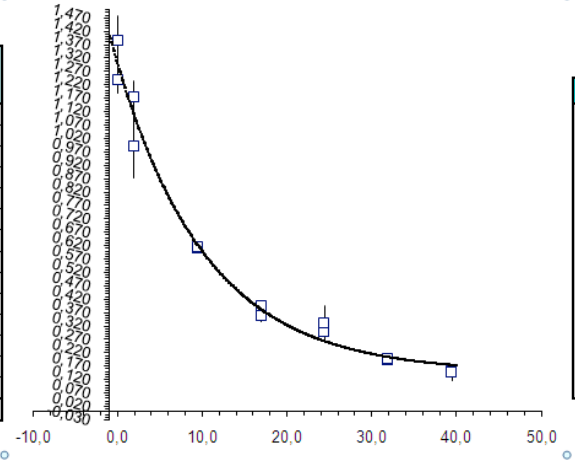
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,104	0,038	1,279	0,055	0,132	0,018	0,169	1,3838	5,902	0,275	92,5

Punts a ignorar

numero inhibidor = 4 | Referencia llista! 933

NPC-052

	[932]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3857	0,08	0,242	1,18	0,617	1,10	0,375	0,0088
	1,88	1,1732	0,10	0,230	1,12	0,542	1,017	0,312	0,0043
	9,38	0,6131	0,12	0,243	1,50	0,591	1,383	0,348	9E-05
	16,88	0,3951	0,12	0,216	1,50	0,445	1,383	0,229	0,0002
	24,39	0,3001	0,12	0,219	1,25	0,467	1,133	0,248	0,0013
	31,89	0,1955	0,12	0,207	1,08	0,355	0,967	0,148	9E-05
	39,40	0,1518	0,12	0,208	1,27	0,366	1,15	0,158	0,0006
Serie 2	0,00	1,2406	0,08	0,216	1,17	0,571	1,083	0,355	0,0026
	1,88	0,9917	0,12	0,231	1,12	0,563	1	0,332	0,0134
	9,38	0,6154	0,13	0,229	1,50	0,534	1,367	0,305	5E-05
	16,88	0,3605	0,17	0,214	1,42	0,444	1,25	0,23	0,0005
	24,39	0,3311	0,12	0,217	1,50	0,438	1,383	0,221	0,0045
	31,89	0,1994	0,08	0,205	1,10	0,388	1,017	0,183	3E-05
	39,40	0,1467	0,25	0,239	1,35	0,391	1,1	0,152	0,0009
							Error a	**0,001**	0,0712



error Y
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0,00577071
0,029362452

☐ corretgir per [TTR] a 4 mg/mL

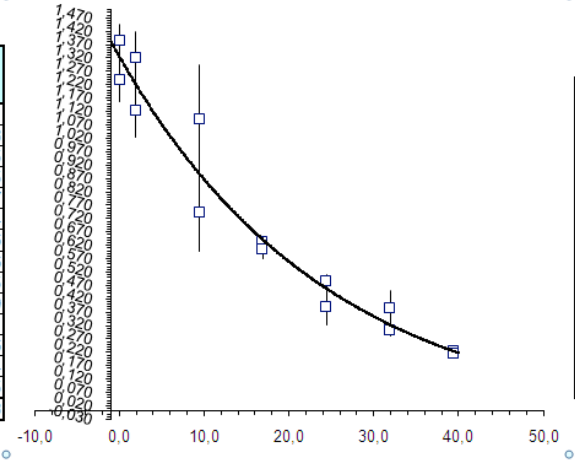
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,148	0,040	1,144	0,046	0,094	0,012	0,107	1,2919	8,870	0,277	88,6

Punts a ignorar

numero inhibidor = 5 | Referencia llista! 936

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3857	0,08	0,242	1,18	0,617	1,10	0,375	0,0041
	1,87	1,32	0,08	0,237	1,12	0,570	1,033	0,333	0,0098
	9,37	1,0914	0,12	0,285	1,50	0,610	1,383	0,325	0,0415
	16,86	0,6348	0,12	0,314	1,50	0,550	1,383	0,236	4E-05
	24,35	0,4855	0,12	0,337	1,25	0,520	1,133	0,183	0,0007
	31,84	0,3044	0,10	0,379	1,08	0,523	0,983	0,144	0,0004
	39,34	0,2269	0,12	0,406	1,27	0,513	1,15	0,107	4E-06
Serie 2	0,00	1,2406	0,08	0,216	1,17	0,571	1,083	0,355	0,0066
	1,87	1,1239	0,12	0,250	1,12	0,637	1	0,387	0,0095
	9,37	0,743	0,12	0,270	1,50	0,532	1,383	0,262	0,0209
	16,86	0,6075	0,12	0,284	1,42	0,500	1,3	0,216	0,0011
	24,35	0,3913	0,12	0,328	1,50	0,504	1,383	0,176	0,0046
	31,84	0,3879	0,12	0,370	1,10	0,566	0,983	0,196	0,004
	39,34	0,2171	0,12	0,411	1,35	0,511	1,233	0,1	6E-05
							Error a	**0,001**	0,0713



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☐ corretgir per [TTR] a 4 mg/mL

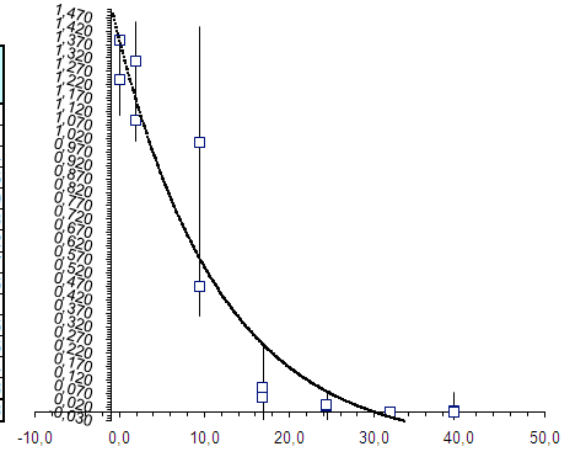
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-0,057	0,241	1,379	0,226	0,040	0,014	0,056	1,3216	16,174	0,850	104,3

Punts a ignorar

numero inhibidor = 6 | Referencia llista! 200

NPC-052

	[933]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3857	0,08	0,242	1,18	0,617	1,10	0,375	0,0001
	1,87	1,3103	0,08	0,230	1,12	0,555	1,033	0,325	0,0221
	9,37	1,0069	0,13	0,230	1,50	0,441	1,367	0,211	0,1884
	16,87	0,0915	0,32	0,201	1,50	0,301	1,183	0,1	0,026
	24,37	0,0247	0,47	0,195	1,50	0,220	1,033	0,025	0,0029
	31,87	0,0006	0,10	0,196	1,50	0,199	1,4	0,003	0,0003
	39,37	0,004	0,12	0,189	1,50	0,196	1,383	0,007	0,0052
Serie 2	0,00	1,2406	0,08	0,216	1,17	0,571	1,083	0,355	0,0177
	1,87	1,0867	0,12	0,234	1,12	0,539	1	0,305	0,0056
	9,37	0,4678	0,12	0,225	1,50	0,404	1,383	0,179	0,011
	16,87	0,0588	0,33	0,196	1,50	0,256	1,167	0,06	0,0376
	24,37	0,0271	0,25	0,197	1,50	0,222	1,25	0,025	0,0026
	31,87	0,0034	0,35	0,199	1,50	0,198	1,15	-0,001	0,0004
	39,37	0,0016	0,27	0,215	1,50	0,203	1,233	-0,012	0,0048
							Error a	**0,001**	0,0713



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☐ corretgir per [TTR] a 4 mg/mL

AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-0,129	0,141	1,503	0,150	0,081	0,024	0,122	1,3737	7,519	0,568	109,4

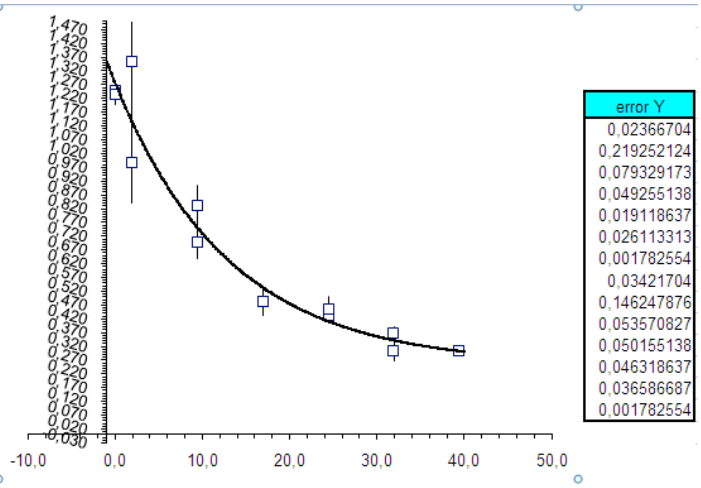
Punts a ignorar

numero inhibidor = 1 | Referencia llista! 856

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,24655	0,08	0,225	1,18	0,571	1,10	0,346	0,0006
	1,88	1,3537	0,08	0,244	1,12	0,583	1,033	0,339	0,0481
	9,38	0,8294	0,12	0,214	1,50	0,463	1,383	0,249	0,0063
	16,89	0,4842	0,12	0,216	1,50	0,417	1,383	0,201	0,0024
	24,40	0,4305	0,08	0,206	1,50	0,465	1,417	0,259	0,0004
	31,91	0,3687	0,08	0,211	1,50	0,434	1,417	0,223	0,0007
	39,41	0,3056	0,08	0,199	1,50	0,413	1,417	0,214	3E-06
Serie 2	0,00	1,236	0,08	0,226	1,17	0,584	1,083	0,358	0,0012
	1,88	0,9882	0,12	0,232	1,12	0,542	1	0,310	0,0214
	9,38	0,6965	0,12	0,215	1,50	0,488	1,383	0,273	0,0029
	16,89	0,4833	0,12	0,205	1,50	0,406	1,383	0,201	0,0025
	24,40	0,4577	0,15	0,225	1,50	0,408	1,35	0,183	0,0021
	31,91	0,306	0,13	0,205	1,50	0,401	1,367	0,196	0,0013
	39,41	0,3056	0,12	0,215	1,50	0,460	1,383	0,245	3E-06
							Error a	**0,001**	0,0713

corretgir per [TTR] a 4 mg/mL



error Y
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0,026113313
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0,03421704
0,146247876
0,053570827
0,050155138
0,046318637
0,036586687
0,001782554

AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,254	0,080	1,016	0,083	0,076	0,018	0,078	1,2702	12,833	0,662	80,0

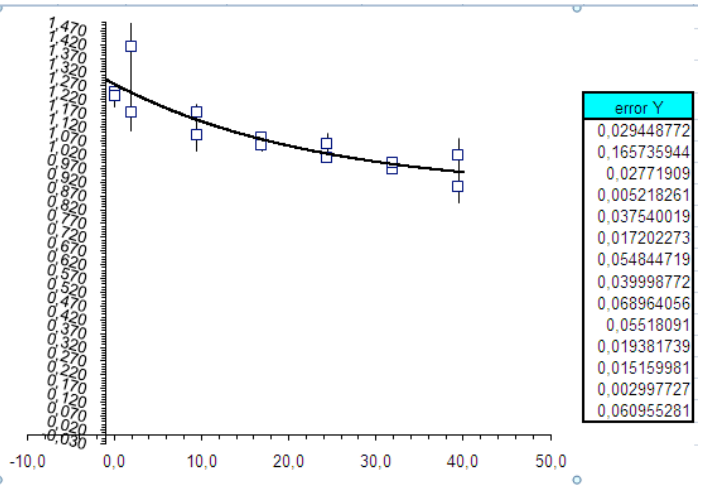
Punts a ignorar

numero inhibidor = 2 | Referencia llista! 864

NPC-052

		[864]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,24655	0,08	0,225	1,18	0,571	1,10	0,346	0,0009
	1,87	1,4119	0,08	0,246	1,12	0,676	1,033	0,43	0,0275
	9,37	1,1757	0,08	0,262	1,50	0,621	1,417	0,359	0,0008
	16,87	1,0818	0,12	0,324	1,50	0,657	1,383	0,333	3E-05
	24,37	1,0622	0,08	0,351	1,50	0,754	1,417	0,403	0,0014
	31,87	0,9697	0,12	0,384	1,50	0,715	1,383	0,331	0,0003
	39,37	0,9046	0,12	0,415	1,50	0,733	1,383	0,318	0,003
Serie 2	0,00	1,236	0,08	0,226	1,17	0,584	1,083	0,358	0,0016
	1,87	1,1772	0,12	0,245	1,12	0,563	1	0,318	0,0048
	9,37	1,0928	0,12	0,266	1,50	0,602	1,383	0,336	0,003
	16,87	1,0572	0,12	0,313	1,50	0,649	1,383	0,336	0,0004
	24,37	1,0095	0,10	0,349	1,50	0,687	1,4	0,338	0,0002
	31,87	0,9899	0,12	0,408	1,50	0,828	1,383	0,42	9E-06
	39,37	1,0204	0,10	0,433	1,50	0,842	1,4	0,409	0,0037
							Error a	**0,001**	0,0712

corretgir per [TTR] a 4 mg/mL



error Y
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0,005218261
0,037540019
0,017202273
0,054844719
0,039998772
0,068964056
0,05518091
0,019381739
0,015159981
0,002997727
0,060955281

AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,886	0,149	0,390	0,139	0,042	0,033	0,017	1,2760	#¡NUM!	#¡NUM!	30,5

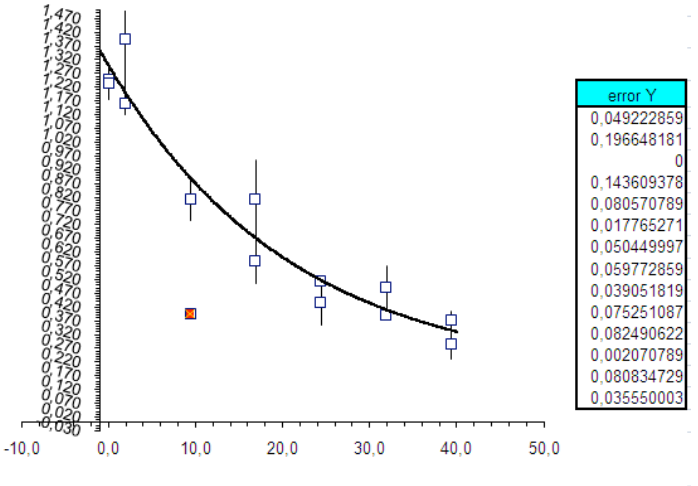
Punts a ignorar

numero inhibidor = 3 | Referencia llista! 930

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,24655	0,08	0,225	1,18	0,571	1,10	0,346	0,0024
	1,87	1,396	0,08	0,233	1,12	0,611	1,033	0,378	0,0387
	9,37	0,3959	0,10	0,230	1,50	0,537	1,4	0,307	0
	16,87	0,8147	0,12	0,224	1,50	0,606	1,383	0,382	0,0206
	24,37	0,4378	0,12	0,220	1,50	0,507	1,383	0,287	0,0065
	31,86	0,3935	0,12	0,225	1,50	0,527	1,383	0,302	0,0003
	39,36	0,2857	0,28	0,254	1,50	0,465	1,217	0,211	0,0025
Serie 2	0,00	1,236	0,08	0,226	1,17	0,584	1,083	0,358	0,0036
	1,87	1,1603	0,08	0,225	1,12	0,585	1,033	0,360	0,0015
	9,37	0,8136	0,13	0,232	1,50	0,535	1,367	0,303	0,0057
	16,87	0,5886	0,13	0,225	1,50	0,499	1,367	0,274	0,0068
	24,37	0,5163	0,12	0,225	1,50	0,552	1,383	0,327	4E-06
	31,86	0,4921	0,12	0,241	1,50	0,527	1,383	0,286	0,0065
	39,36	0,3717	0,12	0,241	1,50	0,504	1,383	0,263	0,0013
							Error a	**0,001**	0,0713

corretgir per [TTR] a 4 mg/mL



error Y
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0,143609378
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0,082490622
0,002070789
0,080834729
0,035550003

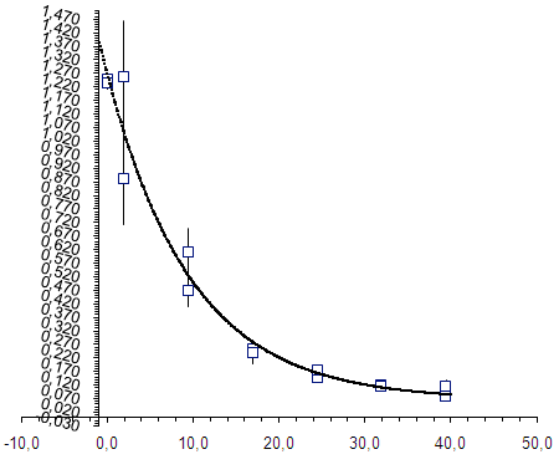
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,160	0,195	1,136	0,185	0,047	0,018	0,054	1,2958	17,850	1,077	87,7

Punts a ignorar
7

numero inhibidor = 4 | Referencia llista! 932

NPC-052

	[930]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,24655	0,08	0,225	1,18	0,571	1,10	0,346	0,0001
	1,88	1,2598	0,10	0,253	1,12	0,594	1,017	0,341	0,0436
	9,39	0,6131	0,12	0,254	1,50	0,531	1,383	0,277	0,0078
	16,89	0,2534	0,12	0,243	1,50	0,393	1,383	0,15	0,0007
	24,40	0,1501	0,12	0,254	1,50	0,377	1,383	0,123	0,0002
	31,91	0,1198	0,12	0,278	1,50	0,366	1,383	0,088	5E-05
	39,42	0,0814	0,12	0,277	1,27	0,368	1,15	0,091	4E-05
Serie 2	0,00	1,236	0,08	0,226	1,17	0,584	1,083	0,358	0,0005
	1,88	0,8827	0,12	0,228	1,12	0,523	1	0,295	0,0284
	9,39	0,4689	0,13	0,239	1,50	0,482	1,367	0,243	0,0031
	16,89	0,2416	0,17	0,249	1,50	0,406	1,333	0,157	0,0015
	24,40	0,1746	0,12	0,269	1,50	0,392	1,383	0,123	8E-05
	31,91	0,1174	0,08	0,270	1,10	0,379	1,017	0,109	2E-05
	39,42	0,1156	0,25	0,307	1,35	0,425	1,1	0,118	0,0008
							Error a	**0,001**	0,0713



error Y
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0,022497383
0,168400782
0,05592238
0,038203765
0,00886917
0,004777929
0,02770369

corretgir per [TTR] a 4 mg/mL

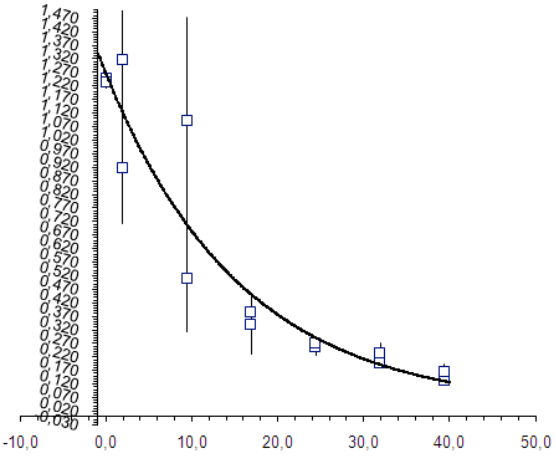
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,066	0,056	1,192	0,068	0,102	0,018	0,121	1,2585	7,370	0,355	94,7

Punts a ignorar

numero inhibidor = 5 | Referencia llista! 933

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,24655	0,08	0,225	1,18	0,571	1,10	0,346	0,0002
	1,87	1,3163	0,08	0,233	1,12	0,584	1,033	0,351	0,038
	9,37	1,0914	0,12	0,221	1,50	0,483	1,383	0,262	0,1473
	16,87	0,3429	0,12	0,201	1,50	0,327	1,383	0,126	0,0117
	24,36	0,2593	0,12	0,203	1,50	0,295	1,383	0,092	0,0011
	31,86	0,1967	0,12	0,205	1,50	0,302	1,383	0,097	1E-05
	39,35	0,1331	0,12	0,201	1,27	0,264	1,15	0,063	2E-06
Serie 2	0,00	1,236	0,08	0,226	1,17	0,584	1,083	0,358	0,0006
	1,87	0,919	0,12	0,220	1,12	0,547	1	0,327	0,0409
	9,37	0,5126	0,12	0,205	1,50	0,388	1,383	0,183	0,038
	16,87	0,3872	0,12	0,209	1,50	0,355	1,383	0,146	0,0041
	24,36	0,272	0,12	0,208	1,50	0,335	1,383	0,127	0,0004
	31,86	0,2336	0,12	0,214	1,10	0,342	0,983	0,128	0,0016
	39,35	0,1648	0,12	0,211	1,35	0,293	1,233	0,082	0,0011
							Error a	**0,001**	0,0713



error Y
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0,194950898
0,063711341
0,019726501
0,040610473
0,033053679

corretgir per [TTR] a 4 mg/mL

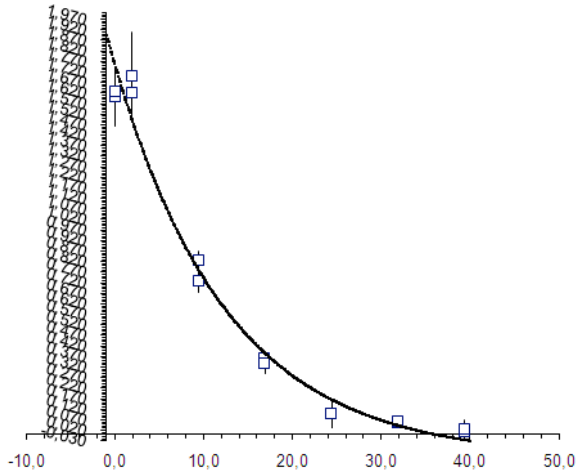
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,032	0,186	1,228	0,180	0,064	0,026	0,078	1,2595	11,290	0,894	97,5

Punts a ignorar

numero inhibidor = 4 | Referencia llista! 200

NPC-052

	#¡VALOR!	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,6047	0,08	0,224	1,18	0,631	1,10	0,407	0,0195
	1,87	1,6194	0,08	0,229	1,12	0,642	1,033	0,413	0,0164
	9,37	0,7294	0,12	0,238	1,50	0,522	1,383	0,284	0,0026
	16,87	0,3647	0,20	0,228	1,40	0,397	1,2	0,169	0,0004
	24,37	0,0994	0,47	0,201	1,08	0,258	0,617	0,057	0,0044
	31,87	0,0595	0,50	0,186	1,12	0,219	0,617	0,033	0,0003
	39,37	0,0141	0,50	0,170	1,43	0,183	0,933	0,013	0,0015
Serie 2	0,00	1,62595	0,10	0,253	1,17	0,629	1,067	0,376	0,0141
	1,87	1,7007	0,07	0,219	1,12	0,644	1,05	0,425	0,0438
	9,37	0,8271	0,13	0,229	1,50	0,510	1,367	0,281	0,0022
	16,87	0,3376	0,22	0,223	1,25	0,359	1,033	0,136	0,0023
	24,37	0,1013	0,27	0,190	1,50	0,251	1,233	0,061	0,0041
	31,87	0,0639	0,48	0,191	1,28	0,241	0,8	0,05	0,0004
	39,37	0,0248	0,13	0,184	1,33	0,200	1,2	0,016	0,0024
							Error a	**0,001**	0,0713



error Y
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0,209246613
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0,064275712
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0,04938901

corretgir per [TTR] a 4 mg/mL

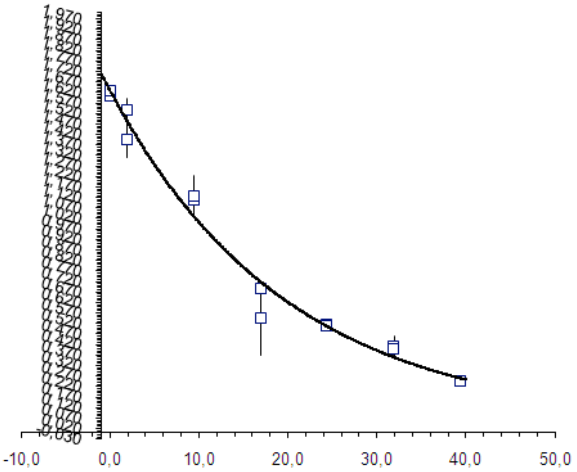
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-0,110	0,088	1,854	0,092	0,078	0,011	0,145	1,7445	8,121	0,311	106,3

Punts a ignorar

numero inhibidor = 1 | Referencia llista: 415

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,6047	0,08	0,224	1,18	0,631	1,10	0,407	0,0004
	1,88	1,3977	0,10	0,256	1,12	0,690	1,017	0,434	0,007
	9,38	1,106	0,12	0,246	1,50	0,598	1,383	0,352	0,0059
	16,88	0,6856	0,13	0,243	1,40	0,584	1,267	0,341	0,0011
	24,38	0,5137	0,17	0,245	1,08	0,490	0,917	0,245	6E-05
	31,88	0,4111	0,18	0,251	1,12	0,431	0,933	0,180	0,0026
	39,38	0,2437	0,23	0,240	1,43	0,430	1,2	0,19	0,0003
Serie 2	0,00	1,62595	0,10	0,253	1,17	0,629	1,067	0,376	5E-06
	1,88	1,5392	0,10	0,252	1,12	0,699	1,017	0,447	0,0034
	9,38	1,1298	0,10	0,241	1,50	0,581	1,4	0,34	0,0102
	16,88	0,5449	0,12	0,220	1,25	0,493	1,133	0,273	0,0302
	24,38	0,51	0,13	0,237	1,50	0,465	1,367	0,228	2E-05
	31,88	0,4	0,17	0,252	1,28	0,439	1,117	0,187	0,0016
	39,38	0,2437	0,13	0,240	1,33	0,413	1,2	0,173	0,0003
							Error a	**0,001**	0,0712



error Y
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0,016022643

corretgir per [TTR] a 4 mg/mL

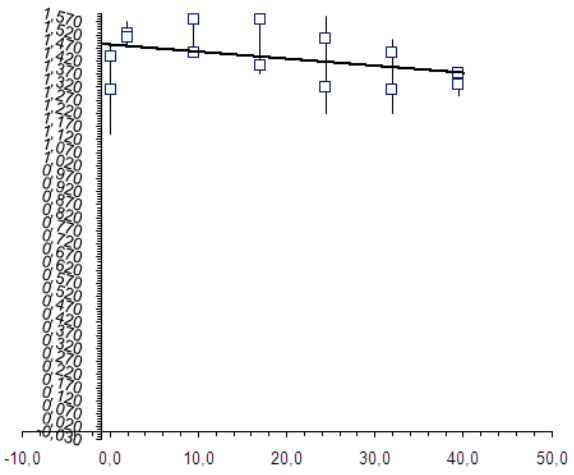
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,041	0,128	1,583	0,120	0,050	0,009	0,080	1,6236	14,316	0,483	97,5

Punts a ignorar

numero inhibidor = 2 | Referencia llista: 941

NPC-052

	[941]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,43885	0,10	0,211	1,18	0,636	1,08	0,425	0,0021
	1,88	1,5263	0,10	0,231	1,12	0,723	1,017	0,492	0,0022
	9,38	1,5812	0,12	0,233	1,50	0,712	1,383	0,479	0,0149
	16,88	1,5808	0,12	0,240	1,50	0,722	1,383	0,482	0,0202
	24,38	1,5069	0,12	0,226	1,50	0,703	1,383	0,477	0,0078
	31,88	1,4531	0,10	0,199	1,50	0,675	1,4	0,476	0,003
	39,39	1,3769	0,12	0,210	1,50	0,697	1,383	0,487	2E-06
Serie 2	0,00	1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,0292
	1,88	1,5112	0,07	0,216	1,12	0,689	1,05	0,473	0,001
	9,38	1,4541	0,07	0,217	1,50	0,724	1,433	0,507	2E-05
	16,88	1,4062	0,07	0,219	1,50	0,726	1,433	0,507	0,0011
	24,38	1,3207	0,07	0,210	1,50	0,725	1,433	0,515	0,0096
	31,88	1,3107	0,07	0,201	1,50	0,729	1,433	0,528	0,0077
	39,39	1,3336	0,07	0,200	1,50	0,694	1,433	0,494	0,002
							Error a	**0,001**	0,0713



error Y
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0,142031431
0,088294401
0,054602482
0,001544176
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0,031940228
0,004886576
0,032568569
0,097905599
0,087797518
0,044844176

corretgir per [TTR] a 4 mg/mL

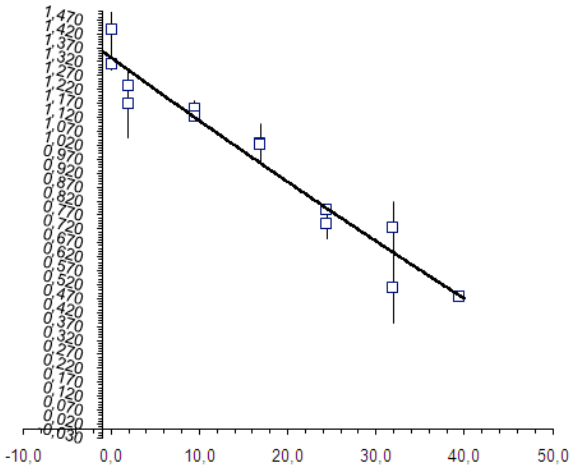
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-5,968	2556,871	7,452	#####	0,000	0,126	0,003	1,4843	288,699	######	502,1

Punts a ignorar

numero inhibidor = 1 | Referencia llista! 940

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,43885	0,10	0,211	1,18	0,636	1,08	0,425	0,0112
	1,87	1,1693	0,12	0,270	1,12	0,723	1	0,453	0,0146
	9,37	1,1507	0,13	0,329	1,50	0,789	1,367	0,46	0,0009
	16,87	1,028	0,13	0,392	1,50	0,780	1,367	0,388	0,0052
	24,37	0,7417	0,12	0,465	1,50	0,952	1,383	0,487	0,0027
	31,87	0,5095	0,12	0,498	1,50	0,851	1,383	0,353	0,0161
	39,36	0,4796	0,12	0,589	1,50	0,974	1,383	0,385	7E-06
Serie 2	0,00	1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,0004
	1,87	1,2348	0,12	0,305	1,12	0,697	1	0,392	0,0031
	9,37	1,1261	0,12	0,322	1,50	0,727	1,383	0,405	3E-05
	16,87	1,0252	0,12	0,402	1,50	0,790	1,383	0,388	0,0048
	24,37	0,789	0,12	0,454	1,50	0,828	1,383	0,374	3E-05
	31,87	0,7283	0,12	0,523	1,50	0,911	1,383	0,388	0,0085
	39,36	0,4796	0,12	0,598	1,50	0,960	1,383	0,362	7E-06
							Error a	**0,001**	0,0712



error Y
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0,126818618
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0,019843908
0,05545912
0,005095619
0,069544196
0,005123239
0,091981382
0,002555906

corretgir per [TTR] a 4 mg/mL

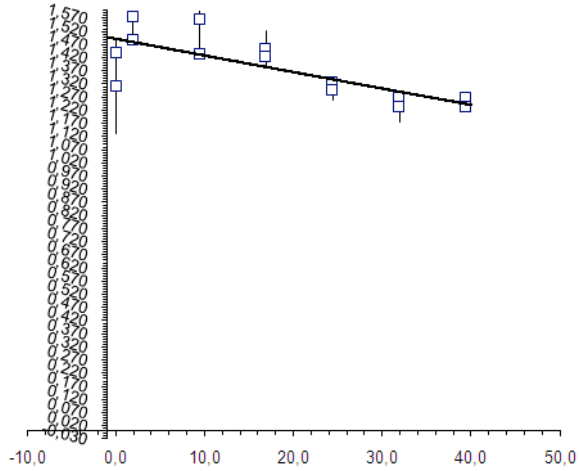
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-6,044	28,658	7,377	#####	0,003	0,013	0,023	1,3332	30,414	7,507	553,3

Punts a ignorar

numero inhibidor = 3 | Referencia llista! 942

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,43885	0,10	0,211	1,18	0,636	1,08	0,425	0,0029
	1,87	1,5781	0,12	0,257	1,12	0,744	1	0,487	0,0095
	9,37	1,5683	0,12	0,240	1,50	0,742	1,383	0,502	0,0184
	16,87	1,4562	0,13	0,253	1,50	0,691	1,367	0,438	0,005
	24,37	1,3276	0,12	0,219	1,50	0,706	1,383	0,487	0,0001
	31,87	1,2676	0,12	0,214	1,50	0,697	1,383	0,483	0,0006
	39,37	1,2664	0,12	0,204	1,50	0,669	1,383	0,465	0,0004
Serie 2	0,00	1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,0321
	1,87	1,4897	0,10	0,268	1,12	0,728	1,017	0,460	9E-05
	9,37	1,4332	0,10	0,248	1,50	0,672	1,4	0,424	2E-07
	16,87	1,425	0,10	0,247	1,50	0,735	1,4	0,488	0,0016
	24,37	1,2991	0,10	0,243	1,50	0,707	1,4	0,464	0,0015
	31,87	1,2343	0,10	0,239	1,50	0,716	1,4	0,477	0,0033
	39,37	1,2353	0,10	0,231	1,50	0,691	1,4	0,46	1E-04
							Error a	**0,001**	0,0712



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0,039536033
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0,05740567
0,009976015

corretgir per [TTR] a 4 mg/mL

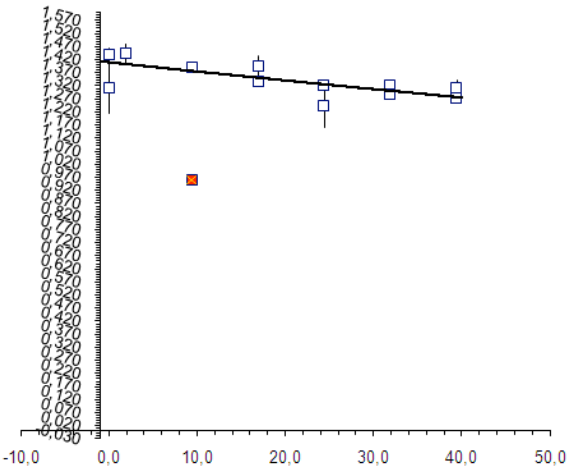
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-5,964	399,419	7,456	#####	0,001	0,047	0,006	1,4924	123,178	######	499,6

Punts a ignorar

numero inhibidor = 7 | Referencia llista 946

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,43885	0,10	0,211	1,18	0,636	1,08	0,425	0,0008
	1,88	1,4433	0,12	0,252	1,12	0,723	1	0,471	0,0015
	9,38	0,9601	0,12	0,233	1,50	0,689	1,383	0,456	0
	16,88	1,3938	0,12	0,235	1,50	0,704	1,383	0,469	0,0018
	24,38	1,2446	0,12	0,247	1,12	0,768	1	0,521	0,0067
	31,88	1,3237	0,12	0,234	1,30	0,744	1,183	0,510	0,0005
	39,38	1,3105	0,13	0,257	1,50	0,708	1,367	0,451	0,0011
Serie 2	0,00	1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,0095
	1,88	1,4437	0,07	0,216	1,12	0,698	1,05	0,482	0,0016
	9,38	1,3906	0,08	0,234	1,50	0,698	1,417	0,464	0,0002
	16,88	1,3358	0,08	0,239	1,50	0,710	1,417	0,471	0,0003
	24,38	1,3244	0,08	0,252	1,08	0,712	1	0,46	5E-06
	31,88	1,286	0,07	0,223	1,50	0,752	1,433	0,529	0,0003
	39,38	1,2758	0,08	0,239	1,50	0,726	1,417	0,487	5E-06
							Error a	**0,001**	0,0712



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0,002147733
0,015972977
0,002219714

corretgir per [TTR] a 4 mg/mL

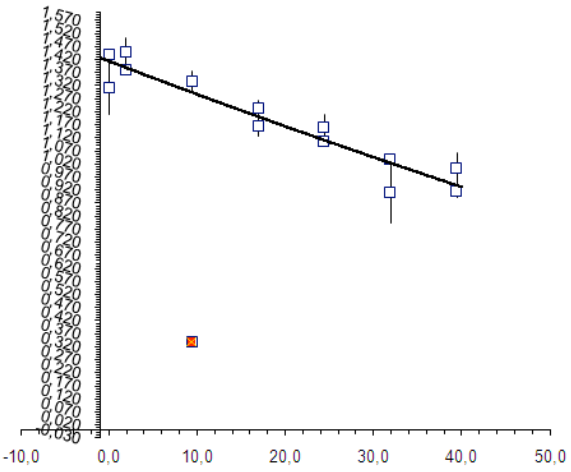
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,355	15,248	1,056	#####	0,003	0,053	0,004	1,4109	322,915	######	74,9

Punts a ignorar
7

numero inhibidor = 8 | Referencia llista 947

NPC-052

		[944]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,43885	0,10	0,211	1,18	0,636	1,08	0,425	0,0006
	1,88	1,381	0,12	0,287	1,12	0,741	1	0,454	8E-05
	9,38	0,3393	0,12	0,352	1,50	0,760	1,383	0,408	0
	16,88	1,1653	0,12	0,431	1,50	0,906	1,383	0,475	0,0013
	24,38	1,1623	0,12	0,508	1,12	0,998	1	0,49	0,0025
	31,88	1,0405	0,12	0,587	1,30	1,079	1,183	0,492	0,0003
	39,38	1,0035	0,12	0,654	1,50	1,132	1,383	0,478	0,0041
Serie 2	0,00	1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,0101
	1,88	1,4488	0,08	0,266	1,12	0,687	1,033	0,421	0,0035
	9,38	1,3364	0,08	0,348	1,50	0,794	1,417	0,446	0,0018
	16,88	1,2338	0,08	0,428	1,50	0,884	1,417	0,456	0,001
	24,38	1,1053	0,08	0,507	1,08	1,011	1	0,504	4E-05
	31,88	0,9103	0,08	0,588	1,50	1,110	1,417	0,522	0,013
	39,38	0,9162	0,10	0,678	1,50	1,170	1,4	0,492	0,0005
							Error a	**0,001**	0,0712



error Y
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0,031859293
0,006602299
0,11404857
0,023010954

corretgir per [TTR] a 4 mg/mL

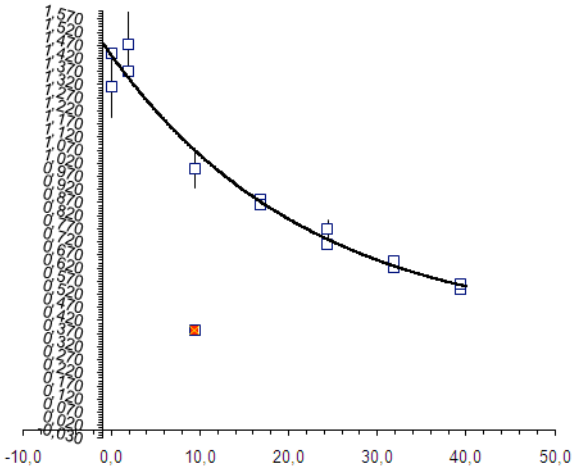
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-2,061	16,256	3,475	#####	0,004	0,019	0,013	1,4140	60,968	10,991	245,7

Punts a ignorar
7

numero inhibidor = 10 | Referencia llista 949

NPC-052

		[illegible]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00		1,43885	0,10	0,211	1,18	0,636	1,08	0,425	9E-05
	1,87		1,4762	0,12	0,226	1,12	0,690	1	0,464	0,0173
	9,37		0,3834	0,13	0,217	1,50	0,590	1,367	0,373	0
	16,87		0,8801	0,13	0,212	1,50	0,598	1,367	0,386	8E-05
	24,37		0,7677	0,12	0,205	1,12	0,556	1	0,351	0,0014
	31,86		0,6229	0,12	0,209	1,30	0,595	1,183	0,386	3E-05
	39,36		0,5397	0,12	0,201	1,50	0,542	1,383	0,341	0,0003
Serie 2	0,00		1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,0135
	1,87		1,372	0,10	0,234	1,12	0,652	1,017	0,418	0,0007
	9,37		0,9986	0,10	0,210	1,50	0,636	1,4	0,426	0,0049
	16,87		0,8612	0,12	0,218	1,50	0,584	1,383	0,366	0,0001
	24,37		0,7114	0,12	0,217	1,08	0,605	0,967	0,388	0,0003
	31,86		0,647	0,12	0,215	1,50	0,554	1,383	0,339	0,0003
	39,36		0,5593	0,12	0,210	1,50	0,530	1,383	0,32	1E-05
								Error a	**0,001**	0,0712



error Y
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0,018500637
0,003396731

corretgir per [TTR] a 4 mg/mL

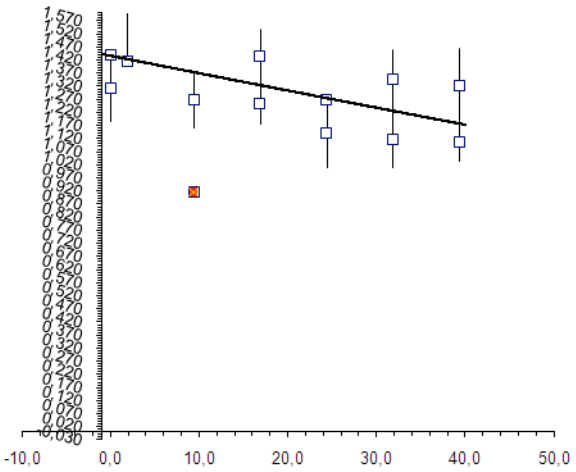
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,373	0,138	1,057	0,130	0,045	0,012	0,047	1,4293	25,341	1,184	73,9

Punts a ignorar
7

numero inhibidor = 4 | Referencia llista: 943

NPC-052

	[942]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,43885	0,10	0,211	1,18	0,636	1,08	0,425	4E-06
	1,87	1,6775	0,12	0,257	1,12	0,745	1	0,488	0,0641
	9,36	0,9157	0,12	0,228	1,50	0,684	1,383	0,456	0
	16,86	1,4333	0,13	0,236	1,50	0,689	1,367	0,453	0,0118
	24,35	1,2709	0,12	0,218	1,50	0,719	1,383	0,501	2E-05
	31,84	1,3444	0,12	0,219	1,50	0,725	1,383	0,506	0,0139
	39,33	1,3232	0,17	0,260	1,50	0,650	1,333	0,39	0,0211
Serie 2	0,00	1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,0152
	1,87	1,413	0,10	0,256	1,12	0,688	1,017	0,432	0,0001
	9,36	1,269	0,10	0,247	1,50	0,697	1,4	0,45	0,0111
	16,86	1,2514	0,10	0,232	1,50	0,653	1,4	0,421	0,0054
	24,35	1,1432	0,10	0,233	1,50	0,729	1,4	0,496	0,0175
	31,84	1,1192	0,10	0,235	1,50	0,716	1,4	0,481	0,0115
	39,33	1,1081	0,10	0,218	1,50	0,677	1,4	0,459	0,0049
							Error a	**0,001**	0,0713



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corretgir per [TTR] a 4 mg/mL

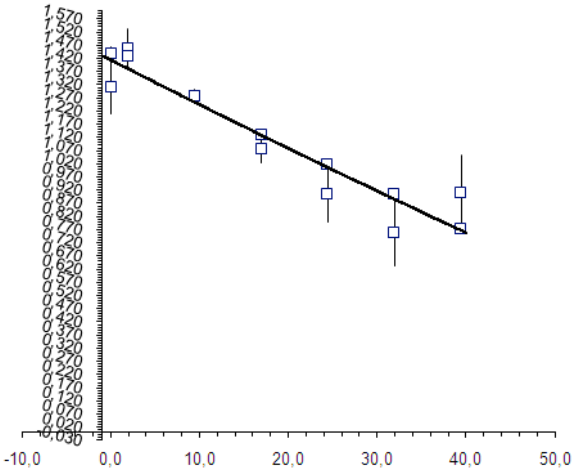
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-5,992	589,697	7,429	#####	0,001	0,073	0,007	1,4368	112,776	######	517,0

Punts a ignorar
7

numero inhibidor = 5 | Referencia llista: 944

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,43885	0,10	0,211	1,18	0,636	1,08	0,425	0,0006
	1,88	1,4572	0,12	0,247	1,12	0,696	1	0,449	0,0057
	9,38	1,2803	0,12	0,227	1,50	0,662	1,383	0,435	0,0007
	16,88	1,1308	0,15	0,257	1,50	0,645	1,35	0,388	2E-06
	24,39	0,9049	0,12	0,245	1,50	0,669	1,383	0,424	0,0104
	31,89	0,7596	0,12	0,262	1,50	0,677	1,383	0,415	0,016
	39,39	0,9116	0,12	0,256	1,50	0,679	1,383	0,423	0,0207
Serie 2	0,00	1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,01
	1,88	1,4292	0,08	0,240	1,12	0,696	1,033	0,456	0,0023
	9,38	1,2783	0,08	0,233	1,50	0,689	1,417	0,456	0,0006
	16,88	1,0774	0,12	0,254	1,50	0,629	1,383	0,375	0,0027
	24,39	1,0178	0,08	0,250	1,50	0,629	1,417	0,379	0,0001
	31,89	0,9072	0,12	0,271	1,50	0,607	1,383	0,336	0,0004
	39,39	0,7732	0,12	0,274	1,50	0,607	1,383	0,333	3E-05
							Error a	**0,001**	0,0712



error Y
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corretgir per [TTR] a 4 mg/mL

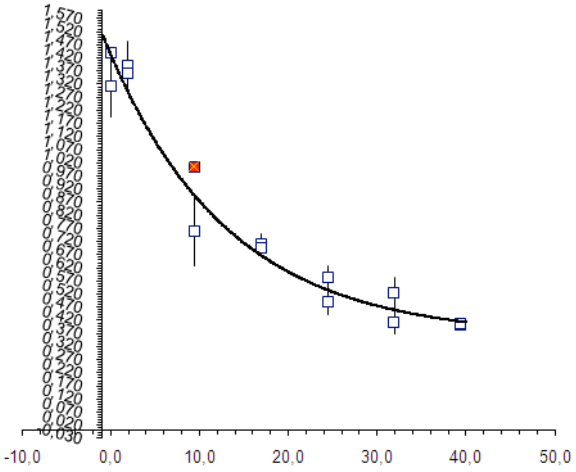
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-6,003	52,892	7,417	#####	0,002	0,017	0,017	1,4135	43,305	14,092	524,7

Punts a ignorar

numero inhibidor = 6 | Referencia llista: 945

NPC-052

	[943]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,43885	0,10	0,211	1,18	0,636	1,08	0,425	0,0001
	1,88	1,3886	0,12	0,239	1,12	0,688	1	0,449	0,0098
	9,38	0,7615	0,13	0,217	1,50	0,601	1,367	0,384	0,0178
	16,89	0,7094	0,17	0,210	1,50	0,565	1,333	0,355	0,0018
	24,40	0,4906	0,12	0,202	1,12	0,553	1	0,351	0,0021
	31,91	0,4145	0,12	0,207	1,30	0,538	1,183	0,331	0,0021
	39,41	0,4037	0,15	0,210	1,50	0,551	1,35	0,341	0,0002
Serie 2	0,00	1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,0129
	1,88	1,3601	0,12	0,268	1,12	0,647	1	0,379	0,005
	9,38	1,0055	0,12	0,224	1,50	0,604	1,383	0,38	0
	16,89	0,6966	0,15	0,216	1,50	0,549	1,35	0,333	0,0008
	24,40	0,5822	0,12	0,213	1,08	0,525	0,967	0,312	0,0021
	31,91	0,5241	0,15	0,228	1,50	0,525	1,35	0,297	0,0041
	39,41	0,4062	0,12	0,207	1,50	0,460	1,383	0,253	0,0001
							Error a	**0,001**	0,0712



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0,06368154
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corretgir per [TTR] a 4 mg/mL

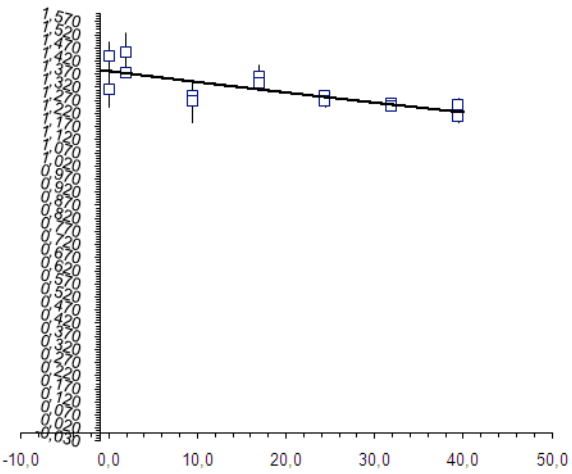
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,357	0,077	1,070	0,077	0,073	0,016	0,078	1,4270	15,006	0,709	75,0

Punts a ignorar
14

numero inhibidor = 11 | Referencia llista! 950

NPC-052

	1,3601	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,43885	0,10	0,211	1,18	0,636	1,08	0,425	0,0032
	1,87	1,4535	0,12	0,221	1,12	0,681	1	0,46	0,0062
	9,37	1,2892	0,12	0,219	1,50	0,674	1,383	0,455	0,0029
	16,87	1,3615	0,12	0,218	1,50	0,716	1,383	0,498	0,0023
	24,37	1,2892	0,12	0,213	1,12	0,747	1	0,534	3E-05
	31,87	1,2602	0,12	0,232	1,30	0,775	1,183	0,543	2E-05
	39,37	1,2548	0,12	0,225	1,50	0,708	1,383	0,483	0,0007
Serie 2	0,00	1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,0048
	1,87	1,376	0,10	0,241	1,12	0,664	1,017	0,423	2E-06
	9,37	1,2663	0,10	0,236	1,50	0,649	1,4	0,413	0,006
	16,87	1,3361	0,10	0,235	1,50	0,665	1,4	0,43	0,0005
	24,37	1,2663	0,10	0,229	1,08	0,700	0,983	0,471	0,0003
	31,87	1,249	0,10	0,246	1,50	0,729	1,4	0,483	4E-05
	39,37	1,2076	0,10	0,241	1,50	0,708	1,4	0,467	0,0004
							Error a	**0,001**	0,0712



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corretgir per [TTR] a 4 mg/mL

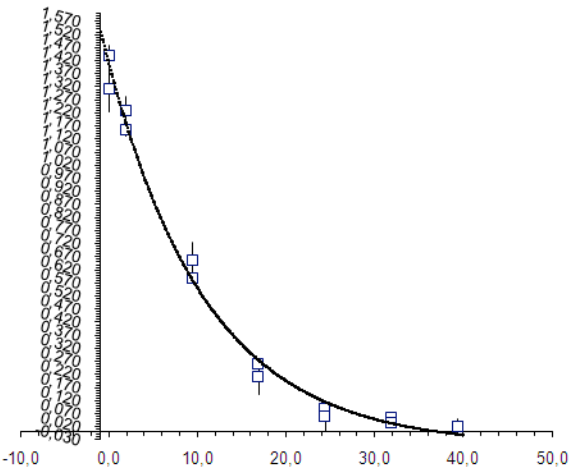
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,351	10,410	1,032	#####	0,004	0,045	0,004	1,3826	268,543	79,719	74,6

Punts a ignorar

numero inhibidor = 12 | Referencia llista! 200

NPC-052

	1,0254855394	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,43885	0,10	0,211	1,18	0,636	1,08	0,425	0,0017
	1,87	1,2314	0,12	0,222	1,12	0,656	1	0,434	0,0031
	9,37	0,5908	0,17	0,230	1,50	0,559	1,333	0,329	0,0001
	16,87	0,2613	0,28	0,215	1,50	0,396	1,217	0,181	0,0002
	24,37	0,0898	0,12	0,203	1,12	0,279	1	0,076	0,0007
	31,87	0,0547	0,28	0,202	1,30	0,251	1,017	0,049	0,0004
	39,37	0,0191	0,38	0,190	1,50	0,208	1,117	0,018	0,0007
Serie 2	0,00	1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,0071
	1,87	1,1552	0,10	0,232	1,12	0,642	1,017	0,410	0,0004
	9,37	0,655	0,12	0,225	1,50	0,460	1,383	0,235	0,0056
	16,87	0,211	0,12	0,217	1,50	0,336	1,383	0,119	0,0039
	24,37	0,0599	0,12	0,217	1,08	0,273	0,967	0,056	0,0031
	31,87	0,0354	0,53	0,220	1,50	0,255	0,967	0,035	2E-06
	39,37	0,0229	0,20	0,220	1,50	0,246	1,3	0,026	0,001
							Error a	**0,001**	0,0712



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corretgir per [TTR] a 4 mg/mL

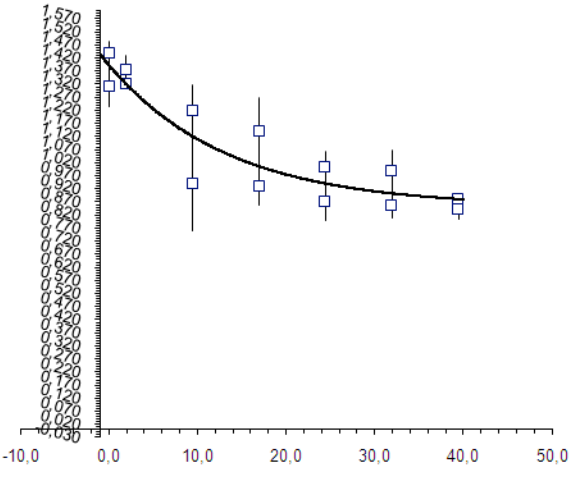
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,053	0,037	1,450	0,041	0,088	0,008	0,128	1,3976	7,435	0,170	103,8

Punts a ignorar

numero inhibidor = 9 | Referencia llista! 948

NPC-052

	1,4292	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,43885	0,10	0,211	1,18	0,636	1,08	0,425	0,0024
	1,88	1,3223	0,10	0,216	1,12	0,635	1,017	0,419	4E-06
	9,38	0,9409	0,13	0,231	1,50	0,590	1,367	0,359	0,0325
	16,88	0,9326	0,13	0,221	1,50	0,546	1,367	0,325	0,0055
	24,38	0,8721	0,13	0,220	1,12	0,547	0,983	0,327	0,0048
	31,88	0,8563	0,13	0,224	1,30	0,532	1,167	0,308	0,0022
	39,38	0,8813	0,13	0,222	1,50	0,552	1,367	0,33	7E-07
Serie 2	0,00	1,31335	0,08	0,222	1,17	0,528	1,083	0,306	0,0059
	1,88	1,377	0,10	0,245	1,12	0,694	1,017	0,449	0,0032
	9,38	1,221	0,10	0,229	1,50	0,634	1,4	0,405	0,01
	16,88	1,1398	0,10	0,219	1,50	0,613	1,4	0,394	0,0177
	24,38	1,0026	0,12	0,232	1,08	0,659	0,967	0,427	0,0038
	31,88	0,9882	0,13	0,239	1,50	0,616	1,367	0,377	0,0071
	39,38	0,845	0,12	0,229	1,50	0,588	1,383	0,359	0,0014
							Error a	**0,001**	0,0713



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0,061241848
0,084478277
0,037122727

corretgir per [TTR] a 4 mg/mL

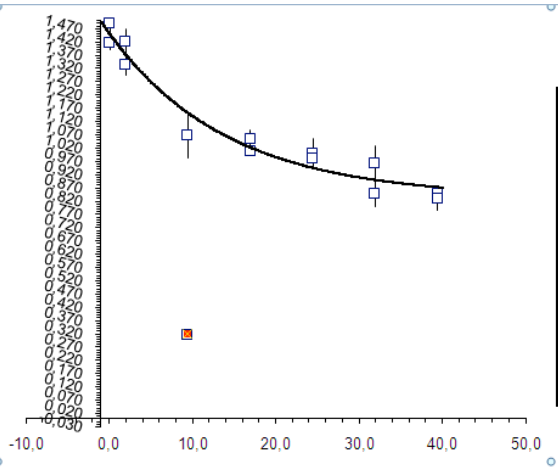
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,853	0,087	0,537	0,089	0,074	0,035	0,040	1,3899	#¡NUM!	#¡NUM!	38,6

Punts a ignorar

numero inhibidor = 5 | Referencia llista! 948

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,4207	0,08	0,242	1,18	0,614	1,10	0,372	0,0009
	1,88	1,4233	0,08	0,243	1,12	0,629	1,033	0,386	0,0024
	9,38	0,3198	0,08	0,234	1,50	0,630	1,417	0,396	0
	16,88	1,056	0,08	0,214	1,23	0,607	1,15	0,393	0,0011
	24,38	1,0025	0,08	0,214	1,32	0,612	1,233	0,398	0,0031
	31,88	0,8522	0,10	0,215	1,50	0,543	1,4	0,328	0,0024
	39,38	0,8495	0,12	0,222	1,50	0,552	1,383	0,33	0,0006
Serie 2	0,00	1,4935	0,07	0,209	1,17	0,629	1,1	0,42	0,0019
	1,88	1,3364	0,08	0,237	1,12	0,691	1,033	0,454	0,0014
	9,38	1,0696	0,08	0,215	1,50	0,585	1,417	0,37	0,0071
	16,88	1,0104	0,12	0,229	1,50	0,578	1,383	0,349	0,0002
	24,38	0,9822	0,10	0,217	1,50	0,549	1,4	0,332	0,0013
	31,88	0,9657	0,12	0,221	1,50	0,512	1,383	0,291	0,0042
	39,38	0,831	0,13	0,226	1,50	0,501	1,367	0,275	0,0019
							Error a	**0,001**	0,0712



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☐ corretgir per [TTR] a 4 mg/mL

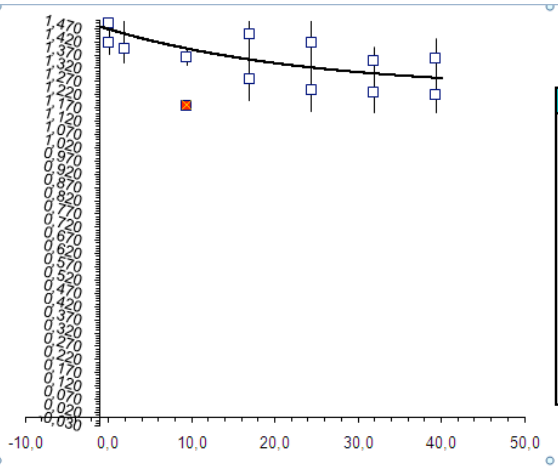
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,836	0,056	0,615	0,056	0,070	0,019	0,043	1,4502	#¡NUM!	#####	42,4

Punts a ignorar
7

numero inhibidor = 4 | Referencia llista! 943

NPC-052

		#¡VALOR!	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00		1,4207	0,08	0,242	1,18	0,614	1,10	0,372	0,0023
	1,87		1,5429	0,05	0,223	1,12	0,676	1,067	0,453	0,0084
	9,36		1,1812	0,05	0,228	1,50	0,641	1,45	0,413	0
	16,86		1,4505	0,07	0,235	1,23	0,716	1,167	0,481	0,0092
	24,35		1,4173	0,05	0,205	1,32	0,603	1,267	0,398	0,0087
	31,84		1,3517	0,05	0,220	1,50	0,741	1,45	0,521	0,0025
	39,33		1,3604	0,07	0,221	1,50	0,669	1,433	0,448	0,0056
Serie 2	0,00		1,4935	0,07	0,209	1,17	0,629	1,1	0,42	0,0006
	1,87		1,3973	0,10	0,283	1,12	0,673	1,017	0,390	0,0029
	9,36		1,3644	0,07	0,238	1,50	0,738	1,433	0,5	0,001
	16,86		1,2787	0,10	0,256	1,50	0,630	1,4	0,374	0,0057
	24,35		1,2409	0,08	0,256	1,50	0,771	1,417	0,515	0,0069
	31,84		1,2283	0,10	0,264	1,50	0,708	1,4	0,444	0,0054
	39,33		1,2206	0,10	0,252	1,50	0,628	1,4	0,376	0,0042
								Error a	**0,001**	0,0712



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☐ corretgir per [TTR] a 4 mg/mL

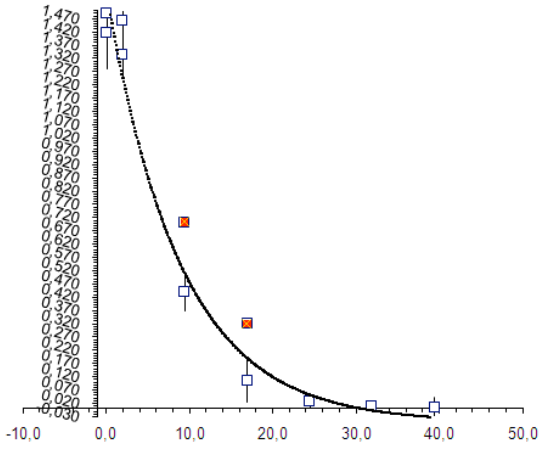
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	1,239	0,204	0,229	0,194	0,041	0,072	0,009	1,4684	#¡NUM!	#####	15,6

Punts a ignorar
7

numero inhibidor = 6 | Referencia llista! 200

NPC-052

		[943]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00		1,4207	0,08	0,242	1,18	0,614	1,10	0,372	0,0186
	1,87		1,4625	0,08	0,240	1,12	0,656	1,033	0,416	0,0445
	9,37		0,4414	0,12	0,225	1,50	0,484	1,383	0,259	0,0047
	16,87		0,1077	0,18	0,212	1,23	0,323	1,05	0,111	0,0069
	24,37		0,0299	0,30	0,234	1,32	0,257	1,017	0,023	0,0005
	31,87		0,0095	0,23	0,224	1,50	0,231	1,267	0,007	0,0002
	39,37		0,0062	0,12	0,218	1,50	0,219	1,383	0,001	0,0014
Serie 2	0,00		1,4935	0,07	0,209	1,17	0,629	1,1	0,42	0,004
	1,87		1,3337	0,12	0,222	1,12	0,603	1	0,381	0,0068
	9,37		0,704	0,17	0,230	1,50	0,508	1,333	0,278	0
	16,87		0,3205	0,28	0,215	1,50	0,359	1,217	0,144	0
	24,37		0,0291	0,20	0,203	1,50	0,211	1,3	0,008	0,0006
	31,87		0,0102	0,00	0,214	1,50	0,222	1,5	0,008	0,0003
	39,37		0,0059	0,25	0,198	1,50	0,199	1,25	0,001	0,0014
								Error a	**0,001**	0,0713



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☐ corretgir per [TTR] a 4 mg/mL

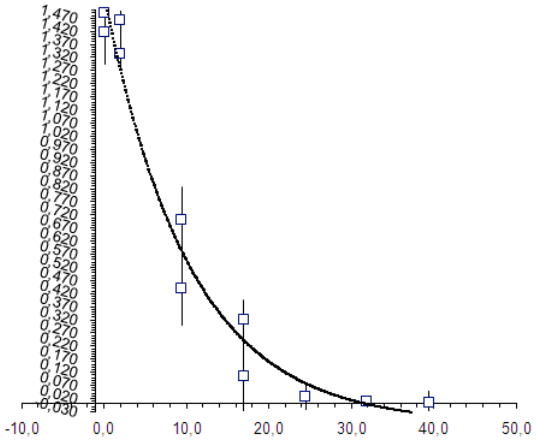
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,050	0,059	1,607	0,074	0,112	0,020	0,181	1,5571	5,888	0,310	103,2

Punts a ignorar
14
15

numero inhibidor = 6 | Referencia llista! 200

NPC-052

	[943]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,4207	0,08	0,242	1,18	0,614	1,10	0,372	0,0156
	1,87	1,4625	0,08	0,240	1,12	0,656	1,033	0,416	0,0343
	9,37	0,4414	0,12	0,225	1,50	0,484	1,383	0,259	0,0195
	16,87	0,1077	0,18	0,212	1,23	0,323	1,05	0,111	0,0183
	24,37	0,0299	0,30	0,234	1,32	0,257	1,017	0,023	0,0024
	31,87	0,0095	0,23	0,224	1,50	0,231	1,267	0,007	9E-05
	39,37	0,0062	0,12	0,218	1,50	0,219	1,383	0,001	0,002
Serie 2	0,00	1,4935	0,07	0,209	1,17	0,629	1,1	0,42	0,0027
	1,87	1,3337	0,12	0,222	1,12	0,603	1	0,381	0,0032
	9,37	0,704	0,17	0,230	1,50	0,508	1,333	0,278	0,0151
	16,87	0,3205	0,28	0,215	1,50	0,359	1,217	0,144	0,006
	24,37	0,0291	0,20	0,203	1,50	0,211	1,3	0,008	0,0025
	31,87	0,0102	0,00	0,214	1,50	0,222	1,5	0,008	0,0001
	39,37	0,0059	0,25	0,198	1,50	0,199	1,25	0,001	0,002
							Error a	**0,001**	0,0713



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0,052022383
0,056317863
0,123048078
0,077351015
0,050197932
0,010377894
0,044627583

corretgir per [TTR] a 4 mg/mL

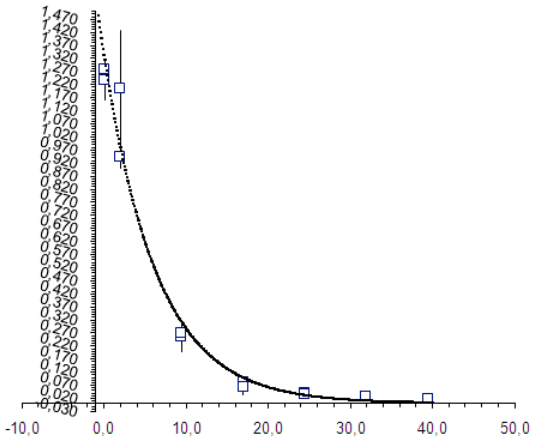
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,075	0,071	1,621	0,083	0,096	0,015	0,156	1,5455	6,714	0,308	104,9

Punts a ignorar

numero inhibidor = 12 | Referencia llista! 200

NPC-052

	1,872925482	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	0,0012
	1,87	1,2068	0,08	0,225	1,12	0,574	1,033	0,349	0,0489
	9,37	0,2568	0,08	0,213	1,50	0,334	1,417	0,121	0,0031
	16,87	0,0838	0,10	0,222	1,23	0,271	1,133	0,049	0,0003
	24,37	0,0419	0,08	0,220	1,32	0,263	1,233	0,043	6E-05
	31,87	0,0282	0,15	0,241	1,47	0,276	1,317	0,035	0,0002
	39,37	0,0207	0,15	0,243	1,43	0,270	1,283	0,027	0,0002
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,0056
	1,87	0,9442	0,08	0,215	1,12	0,489	1,033	0,274	0,0017
	9,37	0,2742	0,08	0,212	1,50	0,359	1,417	0,147	0,0015
	16,87	0,0672	0,07	0,205	1,50	0,253	1,433	0,048	0,0011
	24,37	0,0377	0,08	0,214	1,50	0,250	1,417	0,036	1E-05
	31,87	0,0302	0,08	0,221	1,50	0,265	1,417	0,044	0,0003
	39,37	0,0208	0,08	0,227	1,50	0,256	1,417	0,029	0,0002
							Error a	**0,001**	0,0712



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0,014482919

corretgir per [TTR] a 4 mg/mL

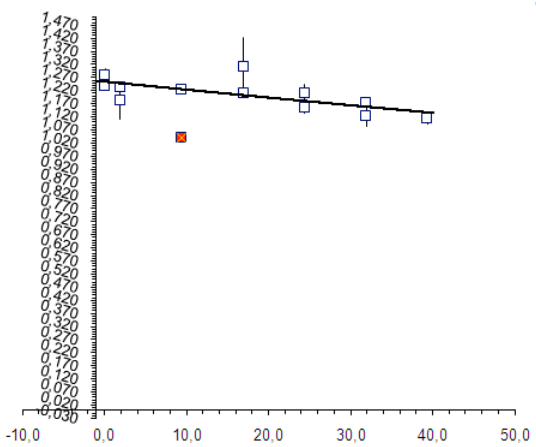
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,003	0,034	1,312	0,054	0,154	0,020	0,202	1,3151	4,510	0,238	99,7

Punts a ignorar

numero inhibidor = 1 | Referencia llista! 872

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	0,0006
	1,87	1,237	0,08	0,242	1,12	0,543	1,033	0,301	0,0002
	9,36	1,2266	0,08	0,223	1,50	0,611	1,417	0,388	8E-09
	16,85	1,2143	0,08	0,234	1,23	0,598	1,15	0,364	0,0001
	24,35	1,2133	0,08	0,231	1,32	0,555	1,233	0,324	0,001
	31,84	1,1773	0,08	0,232	1,47	0,583	1,383	0,351	0,0003
	39,33	1,1175	0,08	0,224	1,43	0,578	1,35	0,354	0,0004
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,0002
	1,87	1,1825	0,07	0,233	1,12	0,534	1,05	0,301	0,0045
	9,36	1,0411	0,08	0,222	1,50	0,555	1,417	0,333	0
	16,85	1,314	0,08	0,243	1,50	0,639	1,417	0,396	0,0121
	24,35	1,1592	0,08	0,236	1,50	0,623	1,417	0,387	0,0005
	31,84	1,1237	0,08	0,234	1,50	0,608	1,417	0,374	0,0013
	39,33	1,1175	0,08	0,224	1,50	0,604	1,417	0,38	0,0004
							Error a	**0,001**	0,0712



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0,022354449
0,036008596
0,020772858

corretgir per [TTR] a 4 mg/mL

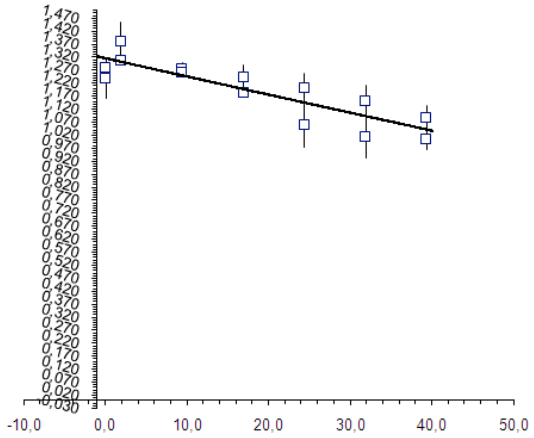
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,018	26,393	1,238	#####	0,003	0,057	0,003	1,2555	279,729	90,869	98,6

Punts a ignorar
14

numero inhibidor = 3 | Referencia llista! 874

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	0,0013
	1,87	1,3812	0,08	0,241	1,12	0,621	1,033	0,38	0,0061
	9,37	1,277	0,08	0,239	1,50	0,609	1,417	0,37	0,0007
	16,86	1,2444	0,08	0,236	1,23	0,632	1,15	0,396	0,0021
	24,35	1,2024	0,08	0,239	1,32	0,601	1,233	0,362	0,0032
	31,84	1,1548	0,08	0,238	1,47	0,548	1,383	0,310	0,0037
	39,33	1,0886	0,08	0,242	1,43	0,567	1,35	0,325	0,0021
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,0058
	1,87	1,3093	0,08	0,245	1,12	0,605	1,033	0,360	4E-05
	9,37	1,2626	0,08	0,251	1,50	0,656	1,417	0,405	0,0001
	16,86	1,1846	0,08	0,235	1,50	0,618	1,417	0,383	0,0002
	24,35	1,0601	0,08	0,239	1,50	0,643	1,417	0,404	0,0074
	31,84	1,0139	0,08	0,245	1,50	0,663	1,417	0,418	0,0065
	39,33	1,0039	0,08	0,240	1,50	0,619	1,417	0,379	0,0015
							Error a	**0,001**	0,0712



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0,085978633
0,080356556
0,038825119

corretgir per [TTR] a 4 mg/mL

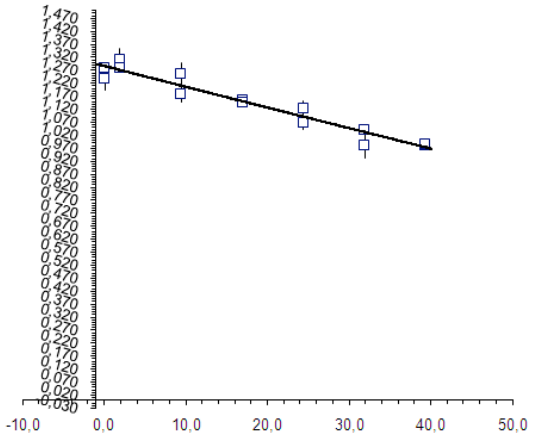
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS					
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)	
Serie 1+2	-8,094	381,653	9,411	#####	0,001	0,031	0,007	1,3165	96,604	74,054	714,8	

Punts a ignorar

numero inhibidor = 4 | Referencia llista! 875

NPC-052

	[874]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	5E-05
	1,87	1,3133	0,08	0,231	1,12	0,590	1,033	0,359	0,0017
	9,36	1,1812	0,08	0,235	1,50	0,597	1,417	0,362	0,0009
	16,86	1,1565	0,08	0,237	1,23	0,618	1,15	0,381	2E-05
	24,35	1,1242	0,08	0,238	1,32	0,608	1,233	0,37	0,001
	31,84	0,9844	0,08	0,237	1,47	0,620	1,383	0,383	0,0024
	39,33	0,9834	0,08	0,236	1,43	0,635	1,35	0,399	8E-05
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,0022
	1,87	1,2813	0,08	0,243	1,12	0,614	1,033	0,371	9E-05
	9,36	1,2564	0,08	0,244	1,50	0,624	1,417	0,38	0,002
	16,86	1,1461	0,08	0,240	1,50	0,625	1,417	0,385	3E-05
	24,35	1,0696	0,08	0,239	1,50	0,629	1,417	0,39	0,0005
	31,84	1,041	0,08	0,238	1,50	0,617	1,417	0,379	6E-05
	39,33	0,9886	0,08	0,234	1,50	0,576	1,417	0,342	0,0002
							Error a	**0,001**	0,0711



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0,044604739
0,005835659
0,022860497
0,007632692
0,013946363

corretgir per [TTR] a 4 mg/mL

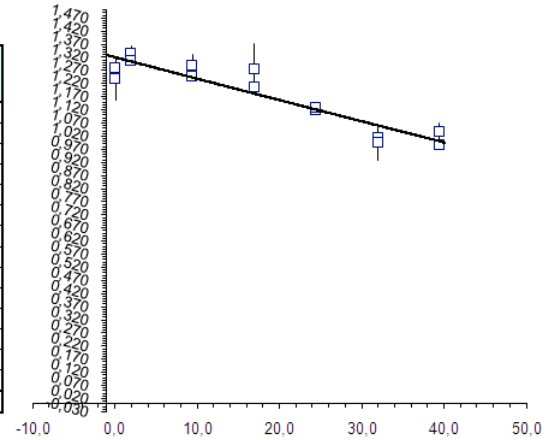
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS					
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)	
Serie 1+2	-8,109	152,978	9,396	#####	0,001	0,014	0,008	1,2872	82,505	29,440	730,0	

Punts a ignorar

numero inhibidor = 2 | Referencia llista! 873

NPC-052

	[873]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	0,0017
	1,88	1,3352	0,08	0,237	1,12	0,624	1,033	0,387	0,0009
	9,38	1,249	0,08	0,234	1,50	0,640	1,417	0,406	3E-05
	16,89	1,2088	0,08	0,247	1,23	0,602	1,15	0,355	0,0007
	24,39	1,1193	0,08	0,265	1,32	0,611	1,233	0,346	7E-06
	31,90	1,0172	0,08	0,262	1,47	0,643	1,383	0,381	0,002
	39,40	1,0364	0,08	0,249	1,43	0,610	1,35	0,361	0,0012
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,0065
	1,88	1,3107	0,08	0,240	1,12	0,601	1,033	0,361	3E-05
	9,38	1,2896	0,08	0,238	1,50	0,629	1,417	0,391	0,0021
	16,89	1,278	0,08	0,252	1,50	0,621	1,417	0,369	0,0091
	24,39	1,128	0,08	0,256	1,50	0,629	1,417	0,373	4E-05
	31,90	0,9963	0,08	0,279	1,50	0,656	1,417	0,377	0,0043
	39,40	0,9866	0,08	0,261	1,50	0,624	1,417	0,363	0,0002
							Error a	**0,001**	0,0712



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corretgir per [TTR] a 4 mg/mL

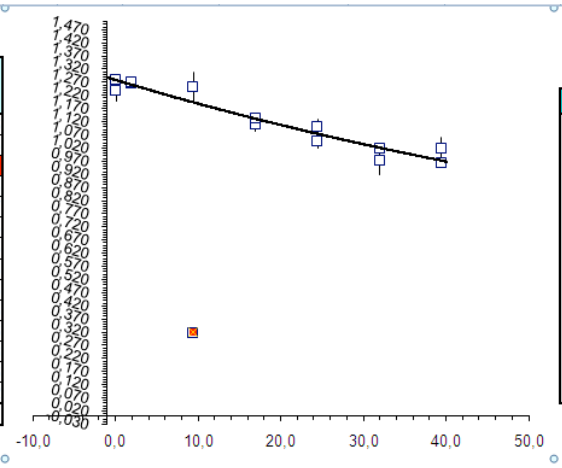
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS					
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)	
Serie 1+2	-8,092	234,386	9,413	#####	0,001	0,022	0,008	1,3209	83,055	45,602	712,6	

Punts a ignorar

numero inhibidor = 5 | Referencia llista! 876

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	1E-06
	1,88	1,2654	0,08	0,240	1,12	0,625	1,033	0,385	2E-05
	9,38	0,3198	0,08	0,232	1,50	0,613	1,417	0,381	0
	16,88	1,1091	0,08	0,243	1,23	0,625	1,15	0,382	0,0005
	24,39	1,049	0,08	0,270	1,32	0,608	1,233	0,338	0,0007
	31,89	0,9721	0,08	0,271	1,47	0,652	1,383	0,381	0,0025
	39,39	0,9643	0,08	0,251	1,43	0,625	1,35	0,374	8E-05
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,0015
	1,88	1,27	0,08	0,243	1,12	0,614	1,033	0,371	7E-05
	9,38	1,2536	0,08	0,239	1,50	0,640	1,417	0,401	0,0035
	16,88	1,1352	0,08	0,244	1,50	0,643	1,417	0,399	9E-06
	24,39	1,1034	0,08	0,255	1,50	0,622	1,417	0,367	0,0008
	31,89	1,0191	0,08	0,296	1,50	0,655	1,417	0,359	9E-06
	39,39	1,0175	0,08	0,257	1,50	0,610	1,417	0,353	0,002
							Error a	0,001	0,0711



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corretgir per [TTR] a 4 mg/mL

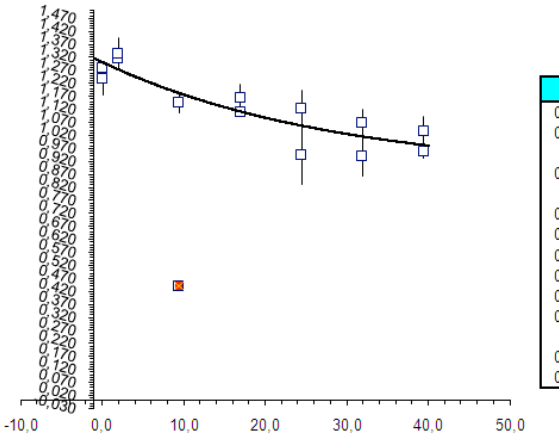
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,382	1,127	0,897	1,119	0,011	0,016	0,009	1,2790	117,957	11,870	70,1

Punts a ignorar
7

numero inhibidor = 6 | Referencia llista! 877

NPC-052

	[875]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	0,0005
	1,87	1,3195	0,08	0,240	1,12	0,600	1,033	0,36	0,002
	9,37	0,4414	0,08	0,250	1,50	0,633	1,417	0,383	0
	16,87	1,1654	0,08	0,252	1,23	0,636	1,15	0,384	0,0028
	24,37	1,1271	0,08	0,274	1,32	0,634	1,233	0,36	0,0047
	31,87	1,0686	0,08	0,295	1,47	0,702	1,383	0,407	0,0027
	39,37	1,0398	0,08	0,291	1,43	0,682	1,35	0,391	0,0031
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,0037
	1,87	1,3365	0,08	0,245	1,12	0,593	1,033	0,348	0,0038
	9,37	1,1469	0,08	0,248	1,50	0,635	1,417	0,387	0,0013
	16,87	1,1109	0,08	0,256	1,50	0,646	1,417	0,39	4E-06
	24,37	0,9454	0,08	0,275	1,50	0,715	1,417	0,44	0,0128
	31,87	0,9411	0,08	0,289	1,50	0,716	1,417	0,427	0,0057
	39,37	0,9589	0,08	0,291	1,50	0,672	1,417	0,381	0,0007
							Error a	0,001	0,0712



error Y
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corretgir per [TTR] a 4 mg/mL

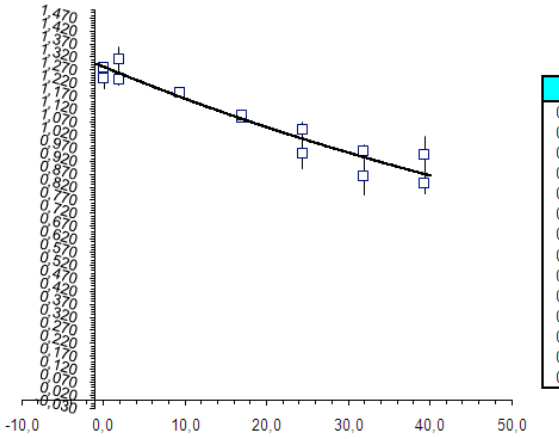
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,876	0,226	0,426	0,216	0,035	0,033	0,015	1,3015	#¡NUM!	#####	32,7

Punts a ignorar
7

numero inhibidor = 7 | Referencia llista! 878

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	6E-06
	1,87	1,3108	0,08	0,237	1,12	0,601	1,033	0,364	0,0027
	9,36	1,1856	0,08	0,238	1,50	0,580	1,417	0,342	0,0003
	16,86	1,088	0,08	0,252	1,23	0,611	1,15	0,359	2E-05
	24,35	1,0404	0,08	0,267	1,32	0,605	1,233	0,338	0,0011
	31,84	0,9601	0,08	0,271	1,47	0,627	1,383	0,356	0,0006
	39,33	0,9443	0,10	0,290	1,43	0,586	1,333	0,296	0,0054
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,0018
	1,87	1,2359	0,08	0,242	1,12	0,603	1,033	0,361	0,0005
	9,36	1,1826	0,08	0,243	1,50	0,585	1,417	0,342	0,0002
	16,86	1,0961	0,08	0,251	1,50	0,600	1,417	0,349	0,0002
	24,35	0,9496	0,08	0,259	1,50	0,633	1,417	0,374	0,0033
	31,84	0,8644	0,08	0,266	1,50	0,660	1,417	0,394	0,0051
	39,33	0,8349	0,08	0,273	1,50	0,612	1,417	0,339	0,0013
							Error a	0,001	0,0712



error Y
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0,022777613
0,015035744
0,012283057
0,057240168
0,071686567
0,036153029

corretgir per [TTR] a 4 mg/mL

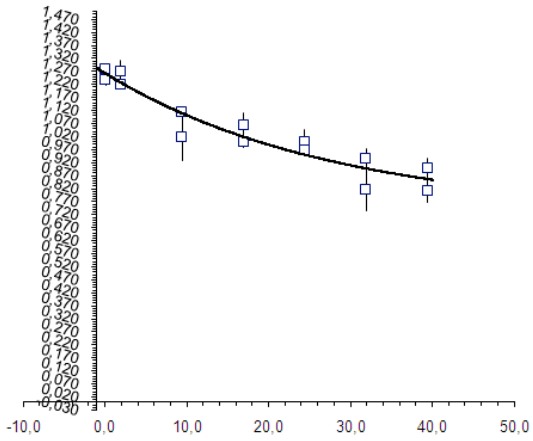
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,132	1,292	1,151	1,280	0,011	0,016	0,013	1,2827	72,397	5,800	89,7

Punts a ignorar

numero inhibidor = 8 | Referencia llista! 879

NPC-052

	[876]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	0,0003
	1,87	1,2206	0,08	0,243	1,12	0,553	1,033	0,31	5E-05
	9,37	1,0212	0,08	0,241	1,50	0,595	1,417	0,354	0,0079
	16,86	1,0014	0,08	0,246	1,23	0,598	1,15	0,352	0,0003
	24,35	1,0013	0,08	0,247	1,32	0,598	1,233	0,351	0,0025
	31,84	0,9372	0,08	0,251	1,47	0,608	1,383	0,357	0,0015
	39,34	0,8993	0,08	0,248	1,43	0,590	1,35	0,342	0,0017
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,0005
	1,87	1,2716	0,08	0,252	1,12	0,564	1,033	0,312	0,0019
	9,37	1,1155	0,08	0,244	1,50	0,569	1,417	0,325	3E-05
	16,86	1,0672	0,08	0,244	1,50	0,558	1,417	0,314	0,0022
	24,35	0,9689	0,08	0,246	1,50	0,603	1,417	0,357	0,0003
	31,84	0,817	0,08	0,250	1,50	0,624	1,417	0,374	0,0066
	39,34	0,8144	0,08	0,241	1,50	0,580	1,417	0,339	0,0019
							Error a	**0,001**	0,0712



error Y
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0,017769298
0,081467704
0,043795194

corretgir per [TTR] a 4 mg/mL

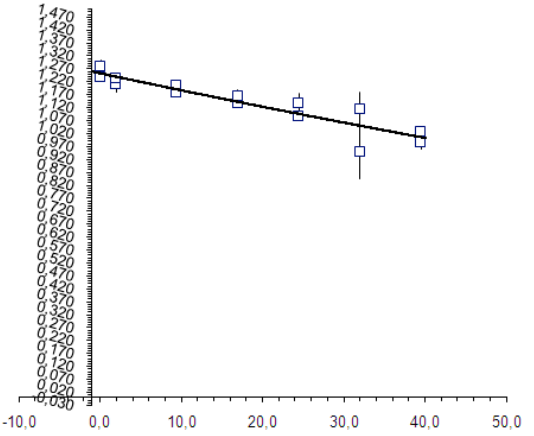
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,727	0,155	0,535	0,146	0,036	0,019	0,019	1,2625	#¡NUM!	#####	42,4

Punts a ignorar

numero inhibidor = 9 | Referencia llista! 880

NPC-052

	1,27	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	0,0007
	1,88	1,2105	0,07	0,213	1,12	0,589	1,05	0,376	0,0009
	9,38	1,178	0,08	0,235	1,50	0,612	1,417	0,377	0,0002
	16,89	1,14	0,08	0,236	1,23	0,619	1,15	0,383	1E-05
	24,40	1,0877	0,08	0,241	1,32	0,655	1,233	0,414	8E-05
	31,91	0,9503	0,08	0,243	1,47	0,587	1,383	0,344	0,0102
	39,41	1,0289	0,08	0,260	1,43	0,693	1,35	0,433	0,0005
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,0002
	1,88	1,235	0,08	0,226	1,12	0,567	1,033	0,341	3E-05
	9,38	1,2057	0,08	0,235	1,50	0,607	1,417	0,372	0,0002
	16,89	1,1676	0,08	0,243	1,50	0,616	1,417	0,373	0,0006
	24,40	1,138	0,08	0,246	1,50	0,623	1,417	0,377	0,0017
	31,91	1,117	0,08	0,242	1,50	0,614	1,417	0,372	0,0043
	39,41	0,9857	0,08	0,250	1,50	0,621	1,417	0,371	0,0005
							Error a	**0,001**	0,0711



error Y
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0,024111452
0,041218066
0,065668419
0,021403701

corretgir per [TTR] a 4 mg/mL

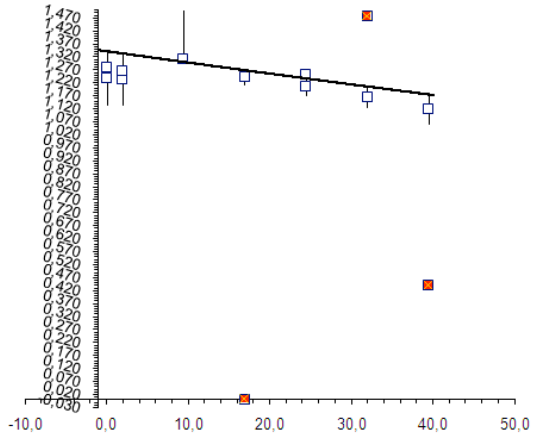
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-0,593	11,459	1,846	#####	0,004	0,024	0,007	1,2534	114,164	17,726	147,3

Punts a ignorar

numero inhibidor = 10 | Referencia llista! 881

NPC-052

	1,874961341	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	0,0039
	1,88	1,2361	0,08	0,220	1,12	0,638	1,033	0,418	0,0097
	9,38	1,3114	0,08	0,228	1,50	0,599	1,417	0,371	9E-05
	16,89	1,2429	0,08	0,233	1,23	0,621	1,15	0,388	0,0007
	24,40	1,2054	0,08	0,241	1,32	0,694	1,233	0,453	0,0011
	31,91	1,4779	0,08	0,257	1,47	0,771	1,383	0,514	0
	39,41	0,4412	0,08	0,236	1,43	0,387	1,35	0,151	0
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,0104
	1,88	1,2654	0,08	0,226	1,12	0,572	1,033	0,346	0,0048
	9,38	1,7616	0,08	0,246	1,50	0,704	1,417	0,458	0,2115
	16,89	0,0034	0,08	0,183	1,50	0,190	1,417	0,007	0
	24,40	1,2556	0,08	0,248	1,50	0,628	1,417	0,38	0,0003
	31,91	1,1676	0,08	0,260	1,50	0,678	1,417	0,418	0,0015
	39,41	1,1192	0,08	0,300	1,50	0,678	1,417	0,378	0,0033
							Error a	**0,001**	0,0713



error Y
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0,01762967
0,03935358
0,05727537

corretgir per [TTR] a 4 mg/mL

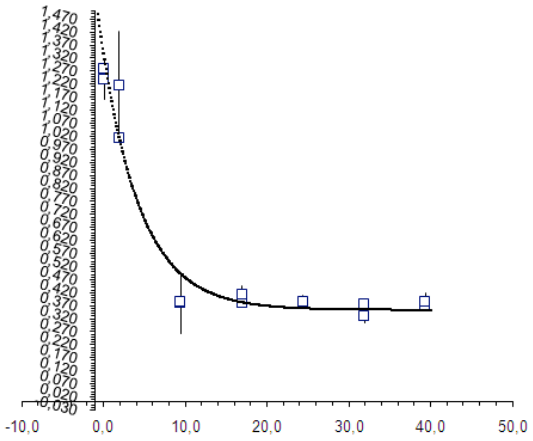
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-0,548	137,563	1,891	#####	0,002	0,177	0,004	1,3426	187,943	#####	140,8

Punts a ignorar
15
11
10

numero inhibidor = 11 Referencia llista! 882

NPC-052

	1,3365	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2802	0,07	0,217	1,18	0,538	1,12	0,321	0,0014
	1,87	1,2165	0,08	0,219	1,12	0,567	1,033	0,348	0,0434
	9,36	0,3801	0,13	0,226	1,50	0,355	1,367	0,129	0,0128
	16,85	0,3815	0,08	0,210	1,23	0,331	1,15	0,121	8E-06
	24,35	0,3801	0,08	0,203	1,32	0,475	1,233	0,272	0,0004
	31,84	0,3759	0,08	0,227	1,47	0,497	1,383	0,270	0,0004
	39,33	0,3746	0,08	0,236	1,43	0,508	1,35	0,272	0,0004
Serie 2	0,00	1,24055	0,07	0,212	1,17	0,510	1,1	0,298	0,006
	1,87	1,0144	0,08	0,213	1,12	0,458	1,033	0,245	4E-05
	9,36	0,3866	0,15	0,228	1,50	0,432	1,35	0,204	0,0114
	16,85	0,4163	0,15	0,222	1,50	0,411	1,35	0,189	0,001
	24,35	0,3866	0,15	0,217	1,50	0,410	1,35	0,193	0,0006
	31,84	0,3314	0,15	0,231	1,50	0,432	1,35	0,201	0,0006
	39,33	0,3889	0,08	0,225	1,50	0,435	1,417	0,21	0,0011
							Error a	**0,001**	0,0712



error Y
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0,106580895
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0,025276314
0,025059212
0,03346915

corretgir per [TTR] a 4 mg/mL

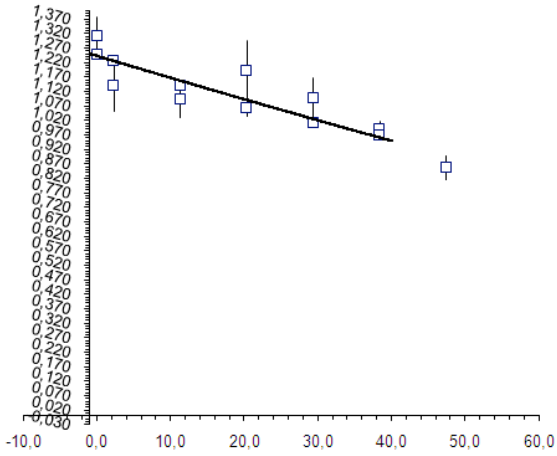
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,355	0,033	0,963	0,061	0,207	0,043	0,200	1,3180	5,560	0,561	73,1

Punts a ignorar

numero inhibidor = 1 Referencia llista! 883

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	0,0047
	2,26	1,1393	0,07	0,259	1,12	0,590	1,05	0,331	0,0074
	11,29	1,095	0,07	0,247	1,50	0,606	1,433	0,359	0,0039
	20,32	1,0628	0,07	0,270	1,50	0,649	1,433	0,379	0,0008
	29,35	1,0141	0,07	0,267	1,12	0,627	1,05	0,36	0,0001
	38,38	0,9893	0,07	0,279	1,22	0,643	1,15	0,364	0,0008
	47,41	0,857	0,08	0,297	1,50	0,639	1,417	0,342	0,0017
Serie 2	0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	2E-05
	2,26	1,2247	0,07	0,257	1,12	0,574	1,05	0,317	5E-07
	11,29	1,142	0,07	0,246	1,50	0,594	1,433	0,348	0,0002
	20,32	1,1942	0,07	0,278	1,50	0,534	1,433	0,256	0,0107
	29,35	1,0967	0,07	0,260	1,50	0,604	1,433	0,344	0,0051
	38,38	0,9692	0,07	0,267	1,50	0,614	1,433	0,347	7E-05
	47,41	0,857	0,07	0,270	1,50	0,596	1,433	0,326	0,0017
							Error a	**0,001**	0,0712



error Y
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0,000680243
0,015405979
0,103511189
0,071494509
0,008266801
0,04084954

corretgir per [TTR] a 4 mg/mL

AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-2,450	33,230	3,693	#####	0,002	0,019	0,008	1,2426	89,114	18,781	297,2

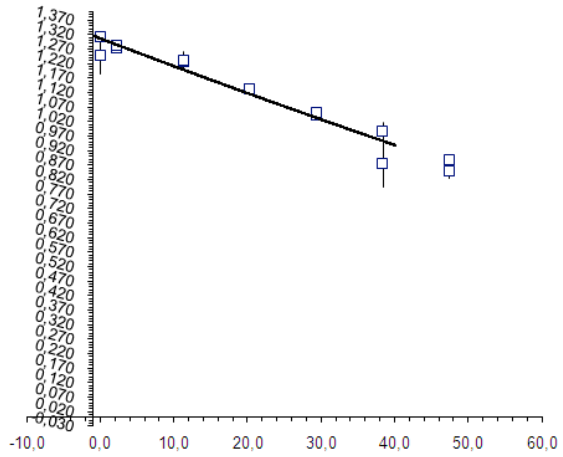
Punts a ignorar

numero inhibidor = 3 | Referencia llista! 885

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	3E-05
	2,26	1,2735	0,08	0,269	1,12	0,583	1,033	0,314	0,0001
	11,28	1,2255	0,07	0,261	1,50	0,613	1,433	0,352	0,0007
	20,30	1,1343	0,07	0,254	1,50	0,577	1,433	0,323	0,0004
	29,33	1,0438	0,07	0,263	1,12	0,563	1,05	0,3	0,0001
	38,35	0,987	0,07	0,270	1,22	0,584	1,15	0,314	0,0011
	47,37	0,8887	0,07	0,285	1,50	0,528	1,433	0,243	0,0002
Serie 2	0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	0,0035
	2,26	1,2829	0,07	0,240	1,12	0,569	1,05	0,329	1E-06
	11,28	1,2298	0,07	0,250	1,50	0,601	1,433	0,351	0,001
	20,30	1,1312	0,07	0,236	1,50	0,545	1,433	0,309	0,0003
	29,33	1,0495	0,07	0,239	1,50	0,523	1,433	0,284	0,0003
	38,35	0,8755	0,07	0,239	1,50	0,539	1,433	0,3	0,0061
	47,37	0,8506	0,07	0,239	1,50	0,498	1,433	0,259	0,0006
							Error a	**0,001**	0,0711

corretgir per [TTR] a 4 mg/mL



error Y
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0,077954451
0,024940417

AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-2,419	13,173	3,724	#####	0,003	0,010	0,010	1,3057	74,393	7,654	285,2

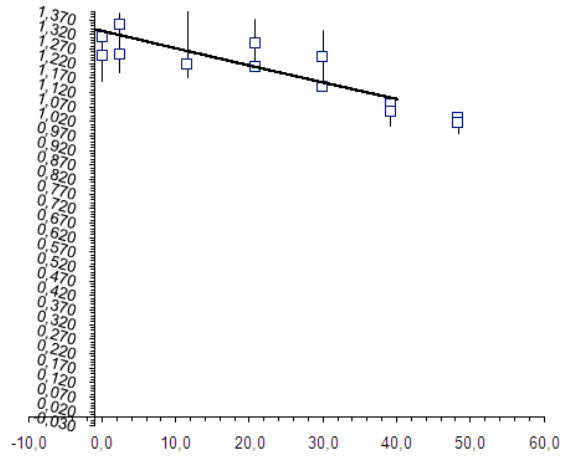
Punts a ignorar

numero inhibidor = 2 | Referencia llista! 884

NPC-052

		[884]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	0,0005
	2,30	1,3568	0,05	0,228	1,12	0,575	1,067	0,347	0,0015
	11,50	1,4038	0,05	0,233	1,50	0,643	1,45	0,41	0,0197
	20,71	1,2926	0,07	0,254	1,50	0,605	1,433	0,351	0,007
	29,91	1,245	0,07	0,249	1,12	0,586	1,05	0,337	0,008
	39,11	1,0827	0,07	0,240	1,22	0,604	1,15	0,364	0,0004
	48,31	1,0337	0,07	0,250	1,50	0,630	1,433	0,38	0,0003
Serie 2	0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	0,0074
	2,30	1,2537	0,07	0,243	1,12	0,604	1,05	0,361	0,0042
	11,50	1,2178	0,07	0,243	1,50	0,625	1,433	0,382	0,0021
	20,71	1,2114	0,07	0,249	1,50	0,586	1,433	0,337	5E-06
	29,91	1,1402	0,07	0,232	1,50	0,585	1,433	0,353	0,0002
	39,11	1,0549	0,07	0,234	1,50	0,607	1,433	0,373	0,0023
	48,31	1,0153	0,07	0,251	1,50	0,590	1,433	0,339	0,0013
							Error a	**0,001**	0,0712

corretgir per [TTR] a 4 mg/mL



error Y
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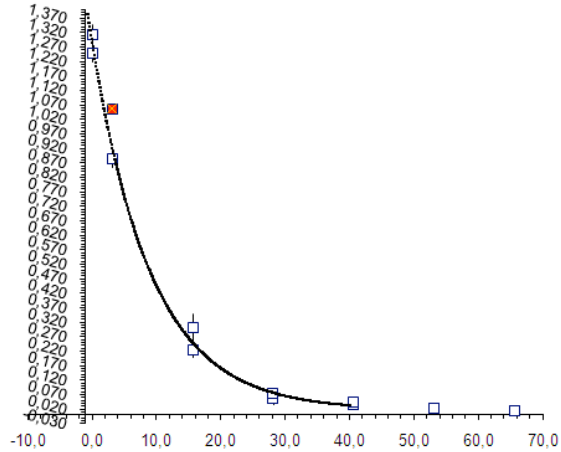
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-2,405	62,925	3,738	#####	0,002	0,028	0,006	1,3326	120,984	36,534	280,5

Punts a ignorar

numero inhibidor = 12 | Referencia llista! 200

NPC-052

	[illegible]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1		0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	0,0016
		3,12	1,0567	0,08	0,243	1,12	0,503	1,033	0,26	0
		15,62	0,2251	0,08	0,218	1,50	0,296	1,417	0,078	0,0005
		28,12	0,0578	0,08	0,218	1,50	0,250	1,417	0,032	0,0004
		40,62	0,0349	0,08	0,220	1,12	0,260	1,033	0,04	3E-06
		53,11	0,0236	0,08	0,236	1,22	0,260	1,133	0,024	2E-06
		65,61	0,0141	0,13	0,243	1,50	0,258	1,367	0,015	3E-05
Serie 2		0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	0,0006
		3,12	0,8838	0,07	0,210	1,12	0,431	1,05	0,221	0,0007
		15,62	0,2995	0,07	0,210	1,50	0,353	1,433	0,143	0,0027
		28,12	0,0737	0,07	0,207	1,50	0,246	1,433	0,039	1E-05
		40,62	0,0441	0,12	0,217	1,50	0,275	1,383	0,058	0,0001
		53,11	0,0218	0,22	0,217	1,50	0,237	1,283	0,02	6E-08
		65,61	0,0161	0,28	0,232	1,50	0,251	1,217	0,019	9E-06
								Error a	**0,001**	0,0711



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corretgir per [TTR] a 4 mg/mL

AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,018	0,011	1,253	0,019	0,109	0,005	0,136	1,2716	6,511	0,088	98,6

Punts a ignorar
6

numero inhibidor = 4 | Referencia llista! 886

NPC-052

	[885]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	0,0013
	2,75	1,236	0,07	0,263	1,12	0,639	1,05	0,376	2E-05
	13,77	1,1419	0,08	0,320	1,50	0,643	1,417	0,323	0,0013
	24,78	1,0602	0,08	0,374	1,50	0,674	1,417	0,3	0,0061
	35,79	0,8449	0,07	0,434	1,12	0,782	1,05	0,348	0,0005
	46,81	0,7936	0,08	0,512	1,22	0,852	1,133	0,340	0,001
	57,82	0,6185	0,12	0,604	1,50	0,927	1,383	0,323	0,0022
Serie 2	0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	0,0008
	2,75	1,2267	0,07	0,248	1,12	0,582	1,05	0,334	0,0002
	13,77	1,0841	0,07	0,300	1,50	0,672	1,433	0,372	0,0005
	24,78	0,916	0,08	0,372	1,50	0,719	1,417	0,347	0,0044
	35,79	0,883	0,10	0,418	1,50	0,763	1,4	0,345	0,0002
	46,81	0,7206	0,12	0,495	1,50	0,862	1,383	0,367	0,0018
	57,82	0,7186	0,12	0,560	1,50	0,858	1,383	0,298	0,0028
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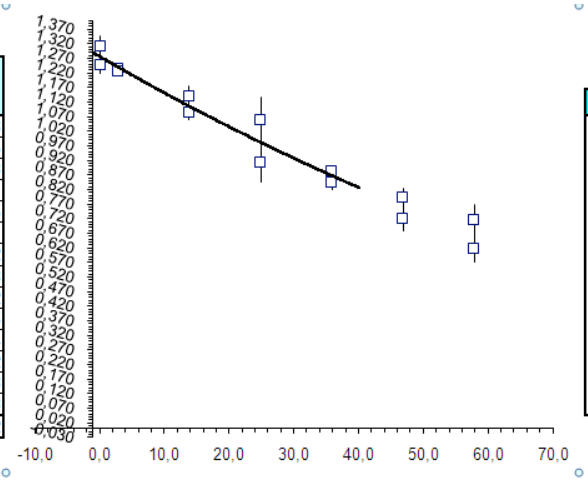

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corretgir per [TTR] a 4 mg/mL

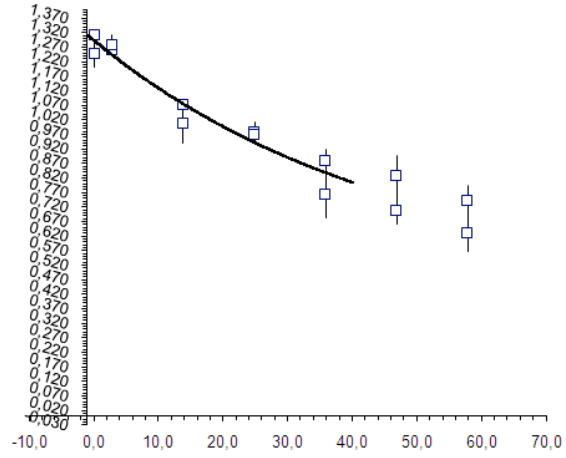
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,504	1,449	1,779	1,437	0,007	0,007	0,013	1,2753	61,125	2,552	139,5

Punts a ignorar

numero inhibidor = 5 | Referencia llista! 887

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	0,0004
	2,75	1,2616	0,07	0,271	1,12	0,636	1,05	0,365	0,0003
	13,77	1,0089	0,07	0,306	1,50	0,689	1,433	0,383	0,0043
	24,78	0,9782	0,07	0,374	1,50	0,725	1,433	0,351	0,0013
	35,79	0,8796	0,10	0,434	1,12	0,743	1,017	0,309	0,0017
	46,81	0,8286	0,10	0,502	1,22	0,816	1,117	0,314	0,0051
	57,82	0,7441	0,13	0,621	1,50	0,882	1,367	0,261	0,0026
Serie 2	0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	0,0021
	2,75	1,2784	0,07	0,251	1,12	0,577	1,05	0,326	0,0012
	13,77	1,0737	0,07	0,295	1,50	0,660	1,433	0,365	1E-06
	24,78	0,9699	0,08	0,365	1,50	0,679	1,417	0,314	0,0007
	35,79	0,762	0,10	0,436	1,50	0,777	1,4	0,341	0,0059
	46,81	0,7094	0,10	0,475	1,50	0,853	1,4	0,378	0,0023
	57,82	0,6307	0,10	0,539	1,50	0,924	1,4	0,385	0,0039
							Error a	**0,001**	0,0712



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corretgir per [TTR] a 4 mg/mL

AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,459	0,201	0,833	0,191	0,022	0,009	0,018	1,2922	67,998	3,271	64,5

Punts a ignorar

numero inhibidor = 6 | Referencia llista! 888

NPC-052

	[886]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	0,0003
	2,94	1,3049	0,07	0,258	1,12	0,638	1,05	0,38	0,0012
	14,69	0,5518	0,07	0,249	1,50	0,581	1,433	0,332	0
	26,44	1,1676	0,07	0,260	1,50	0,613	1,433	0,353	0,0059
	38,20	0,9978	0,10	0,299	1,12	0,636	1,017	0,337	0,0002
	49,95	0,9408	0,07	0,300	1,22	0,668	1,15	0,368	3E-05
	61,70	0,8877	0,12	0,336	1,50	0,622	1,383	0,286	0,0005
Serie 2	0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	0,0023
	2,94	1,2773	0,07	0,240	1,12	0,588	1,05	0,348	5E-05
	14,69	1,1419	0,08	0,255	1,50	0,597	1,417	0,342	0,0013
	26,44	1,0684	0,07	0,248	1,50	0,576	1,433	0,328	0,0005
	38,20	1,0009	0,07	0,260	1,50	0,580	1,433	0,32	9E-05
	49,95	0,9057	0,07	0,281	1,50	0,613	1,433	0,332	0,0009
	61,70	0,8599	0,10	0,303	1,50	0,627	1,4	0,324	3E-05
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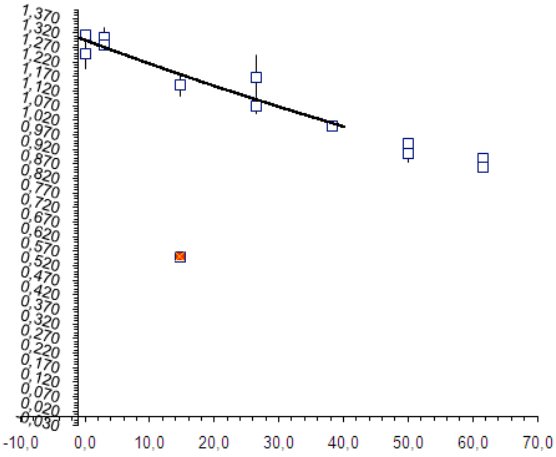

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corretgir per [TTR] a 4 mg/mL

AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h-1)	± SE	B (uA · h-1)	± SE	C (μM-1)	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-0,070	1,457	1,365	1,448	0,006	0,008	0,008	1,2948	105,168	4,352	105,4

Punts a ignorar
7

numero inhibidor = 7 | Referencia llista! 889

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	3E-05
	3,10	1,3335	0,07	0,245	1,12	0,570	1,05	0,325	0,0047
	15,48	1,0838	0,08	0,253	1,50	0,589	1,417	0,336	0,0014
	27,86	1,0038	0,08	0,257	1,50	0,581	1,417	0,324	2E-06
	40,24	0,96	0,08	0,264	1,12	0,558	1,033	0,294	0,0024
	52,63	0,9006	0,07	0,252	1,22	0,534	1,15	0,282	0,0042
	65,01	0,7474	0,10	0,288	1,50	0,576	1,4	0,288	0,0007
Serie 2	0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	0,0035
	3,10	1,3117	0,07	0,230	1,12	0,588	1,05	0,358	0,0022
	15,48	1,0494	0,07	0,227	1,50	0,525	1,433	0,298	0,0051
	27,86	1,0048	0,07	0,237	1,50	0,548	1,433	0,311	8E-08
	40,24	0,9006	0,07	0,240	1,50	0,555	1,433	0,315	0,0001
	52,63	0,8426	0,07	0,239	1,50	0,573	1,433	0,334	5E-05
	65,01	0,7383	0,08	0,256	1,50	0,548	1,417	0,292	0,0013
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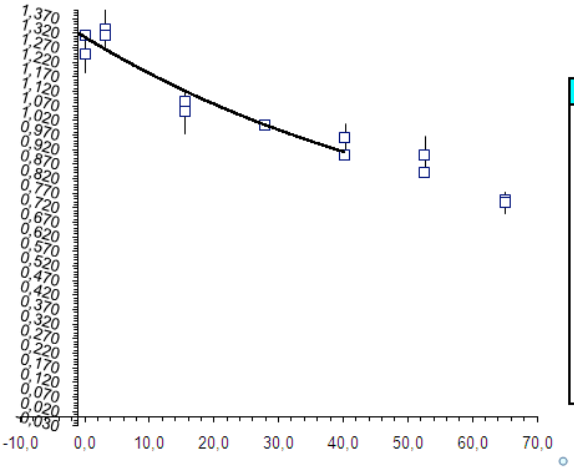

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corretgir per [TTR] a 4 mg/mL

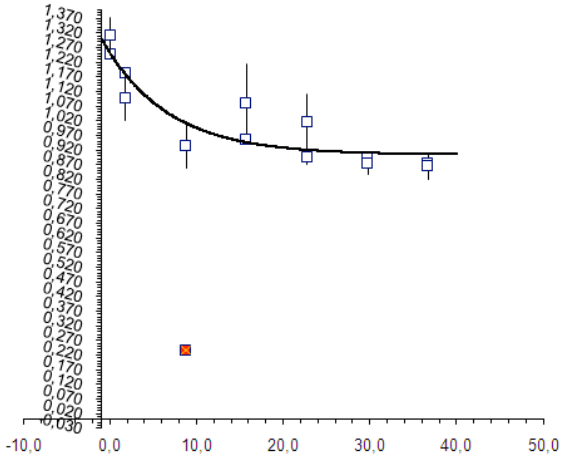
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h-1)	± SE	B (uA · h-1)	± SE	C (μM-1)	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,515	0,230	0,790	0,220	0,017	0,008	0,014	1,3056	101,823	5,577	60,5

Punts a ignorar

numero inhibidor = 8 | Referencia llista! 890

NPC-052

	[887]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	0,0039
	1,75	1,1835	0,07	0,251	1,12	0,562	1,05	0,311	4E-05
	8,73	0,2376	0,07	0,255	1,50	0,575	1,433	0,32	0
	15,72	1,0825	0,07	0,238	1,50	0,553	1,433	0,315	0,0183
	22,70	1,0165	0,07	0,235	1,12	0,582	1,05	0,347	0,009
	29,69	0,8916	0,07	0,229	1,22	0,562	1,15	0,333	0,0004
	36,67	0,8764	0,07	0,218	1,50	0,541	1,433	0,323	0,001
Serie 2	0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	4E-06
	1,75	1,0994	0,07	0,217	1,12	0,498	1,05	0,281	0,006
	8,73	0,9359	0,07	0,242	1,50	0,597	1,433	0,355	0,0058
	15,72	0,9571	0,07	0,232	1,50	0,599	1,433	0,367	0,0001
	22,70	0,898	0,07	0,217	1,50	0,605	1,433	0,388	0,0006
	29,69	0,8752	0,07	0,216	1,50	0,587	1,433	0,371	0,0013
	36,67	0,8658	0,07	0,203	1,50	0,538	1,433	0,335	0,0018
							Error a	0,001	0,0712



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corretgir per [TTR] a 4 mg/mL

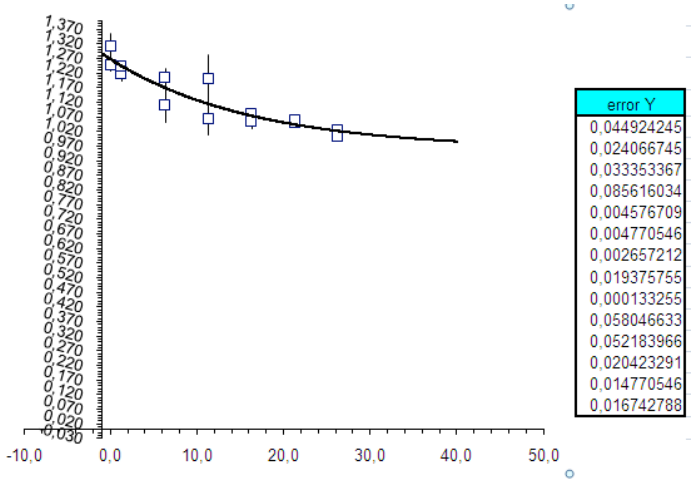
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h-1)	± SE	B (uA · h-1)	± SE	C (μM-1)	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,905	0,037	0,343	0,050	0,134	0,071	0,046	1,2487	#¡NUM!	#¡NUM!	27,5

Punts a ignorar
7

numero inhibidor = 9 | Referencia llista! 891

NPC-052

	1,2784	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	0,002
	1,25	1,2198	0,07	0,233	1,12	0,587	1,05	0,354	0,0006
	6,24	1,2031	0,07	0,235	1,50	0,607	1,433	0,372	0,0011
	11,24	1,2006	0,07	0,226	1,50	0,557	1,433	0,331	0,0073
	16,23	1,0791	0,07	0,227	1,12	0,613	1,05	0,386	2E-05
	21,23	1,0494	0,07	0,222	1,22	0,575	1,15	0,353	2E-05
	26,23	1,0252	0,07	0,226	1,50	0,588	1,433	0,362	7E-06
Serie 2	0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	0,0004
	1,25	1,244	0,07	0,220	1,12	0,537	1,05	0,317	2E-08
	6,24	1,1117	0,07	0,220	1,50	0,585	1,433	0,365	0,0034
	11,24	1,0628	0,07	0,215	1,50	0,598	1,433	0,383	0,0027
	16,23	1,0541	0,07	0,220	1,50	0,616	1,433	0,396	0,0004
	21,23	1,0594	0,08	0,228	1,50	0,595	1,417	0,367	0,0002
	26,23	1,0058	0,07	0,219	1,50	0,563	1,433	0,344	0,0003
							Error a	**0,001**	0,0711



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corretgir per [TTR] a 4 mg/mL

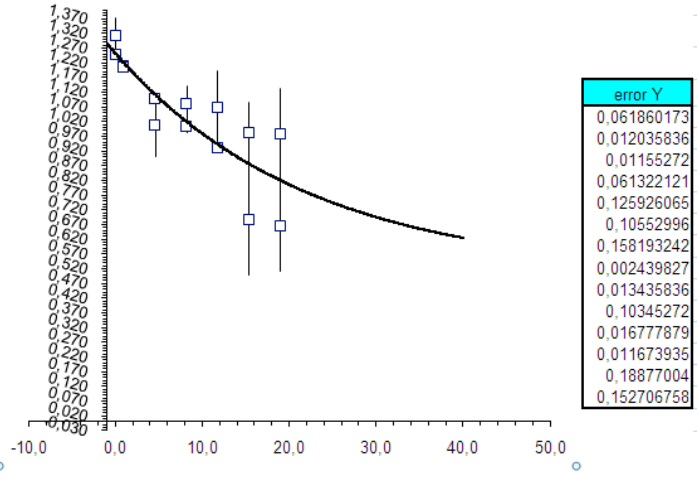
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,960	0,102	0,306	0,095	0,061	0,039	0,019	1,2662	#¡NUM!	#¡NUM!	24,2

Punts a ignorar

numero inhibidor = 10 | Referencia llista! 892

NPC-052

	2,888888888	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	0,0038
	0,90	1,2074	0,07	0,231	1,12	0,602	1,05	0,371	0,0001
	4,51	1,1001	0,07	0,229	1,50	0,618	1,433	0,389	0,0001
	8,12	1,0814	0,07	0,237	1,50	0,617	1,433	0,38	0,0038
	11,73	1,0682	0,07	0,249	1,12	0,639	1,05	0,39	0,0159
	15,35	0,9817	0,07	0,260	1,22	0,668	1,15	0,408	0,0111
	18,96	0,9782	0,07	0,261	1,50	0,636	1,433	0,375	0,025
Serie 2	0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	6E-06
	0,90	1,206	0,07	0,216	1,12	0,573	1,05	0,357	0,0002
	4,51	1,0082	0,07	0,204	1,50	0,518	1,433	0,314	0,0107
	8,12	1,0033	0,07	0,223	1,50	0,595	1,433	0,372	0,0003
	11,73	0,9306	0,08	0,226	1,50	0,542	1,417	0,316	0,0001
	15,35	0,6874	0,07	0,248	1,50	0,563	1,433	0,315	0,0356
	18,96	0,6673	0,07	0,255	1,50	0,558	1,433	0,303	0,0233
							Error a	**0,001**	0,0713



error Y
0,061860173
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0,002439827
0,013435836
0,10345272
0,016777879
0,011673935
0,18877004
0,152706758

corretgir per [TTR] a 4 mg/mL

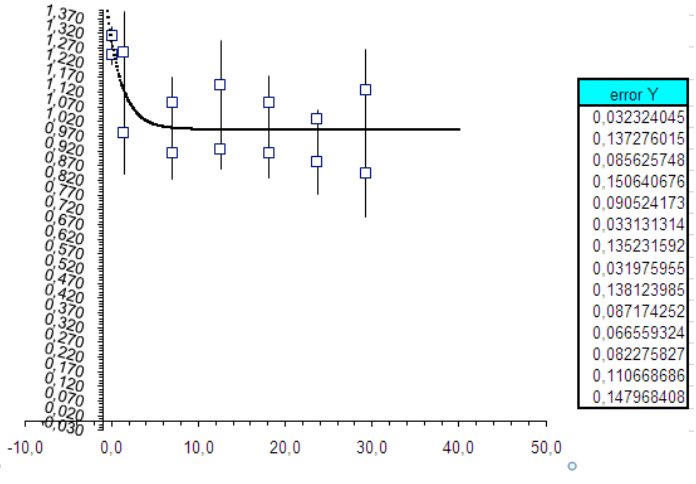
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,503	0,857	0,747	0,832	0,045	0,076	0,034	1,2492	40,147	23,570	59,8

Punts a ignorar

numero inhibidor = 11 | Referencia llista! 893

NPC-052

	1,2773	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,3111	0,08	0,259	1,18	0,536	1,10	0,277	0,001
	1,39	1,2583	0,07	0,242	1,12	0,624	1,05	0,382	0,0188
	6,96	1,0855	0,07	0,231	1,50	0,542	1,433	0,311	0,0073
	12,53	1,1458	0,07	0,230	1,50	0,596	1,433	0,366	0,0227
	18,09	1,0855	0,07	0,228	1,12	0,626	1,05	0,398	0,0082
	23,66	1,0281	0,07	0,243	1,22	0,654	1,15	0,411	0,0011
	29,23	1,1302	0,07	0,256	1,50	0,654	1,433	0,398	0,0183
Serie 2	0,00	1,2468	0,10	0,242	1,17	0,524	1,067	0,282	0,001
	1,39	0,9829	0,07	0,220	1,12	0,473	1,05	0,253	0,0191
	6,96	0,9127	0,07	0,232	1,50	0,511	1,433	0,279	0,0076
	12,53	0,9286	0,07	0,231	1,50	0,556	1,433	0,325	0,0044
	18,09	0,9127	0,07	0,227	1,50	0,558	1,433	0,331	0,0068
	23,66	0,8843	0,07	0,250	1,50	0,623	1,433	0,373	0,0122
	29,23	0,847	0,07	0,256	1,50	0,574	1,433	0,318	0,0219
							Error a	**0,001**	0,0713



error Y
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0,135231592
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0,138123985
0,087174252
0,066559324
0,082275827
0,110668686
0,147968408

corretgir per [TTR] a 4 mg/mL

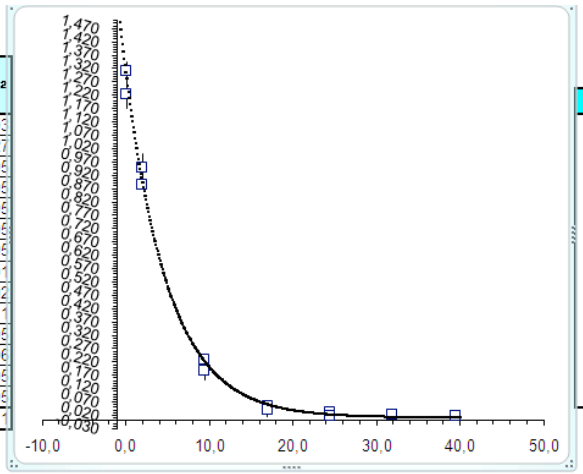
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,995	0,038	0,284	0,090	0,583	0,532	0,165	1,2788	#¡NUM!	#¡NUM!	22,2

Punts a ignorar

numero inhibidor = 1 | Referencia llista: 200

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2279	0,07	0,212	1,18	0,510	1,12	0,298	0,003
	1,87	0,9503	0,03	0,259	1,50	0,532	1,467	0,273	0,0027
	9,37	0,2313	0,05	0,219	1,47	0,317	1,417	0,098	9E-05
	16,87	0,0561	0,08	0,229	1,50	0,264	1,417	0,035	4E-05
	24,37	0,0338	0,35	0,226	1,13	0,251	0,783	0,025	8E-05
	31,87	0,0254	0,00	0,231	1,33	0,251	1,333	0,020	9E-05
	39,37	0,0187	0,33	0,219	1,33	0,236	1	0,017	2E-05
Serie 2	0,00	1,3149	0,07	0,217	1,17	0,521	1,1	0,304	0,001
	1,87	0,8856	0,07	0,268	1,12	0,481	1,05	0,213	0,0002
	9,37	0,1883	0,08	0,232	1,50	0,299	1,417	0,067	0,0011
	16,87	0,0407	0,08	0,220	1,38	0,247	1,3	0,027	0,0005
	24,37	0,0222	0,05	0,222	1,50	0,240	1,45	0,018	7E-06
	31,87	0,0254	0,07	0,225	1,50	0,248	1,433	0,023	9E-05
	39,37	0,0187	0,53	0,220	1,50	0,232	0,967	0,012	2E-05
							Error a	**0,001**	0,0711



error Y
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0,032010858
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0,021693764
0,002617414
0,009440943
0,004829237

corretgir per [TTR] a 4 mg/mL

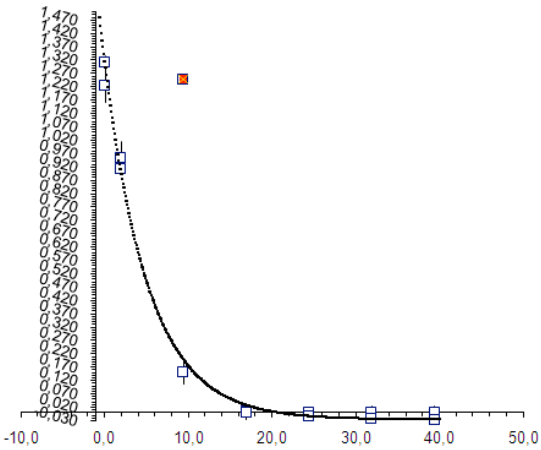
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,013	0,011	1,270	0,020	0,193	0,010	0,245	1,2829	3,651	0,092	99,0

Punts a ignorar

numero inhibidor = 2 | Referencia llista: 488

NPC-052

	[488]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2279	0,07	0,212	1,18	0,510	1,12	0,298	0,0042
	1,87	0,9568	0,03	0,256	1,50	0,530	1,467	0,274	0,0035
	9,37	1,249	0,03	0,228	1,47	0,283	1,433	0,055	0
	16,87	0,0062	0,42	0,249	1,50	0,254	1,083	0,005	0,0005
	24,37	0,0025	0,27	0,262	1,50	0,262	1,233	0	0,0002
	31,87	0,0018	0,37	0,272	1,50	0,270	1,133	-0,002	0,0005
	39,37	0,0005	0,28	0,286	1,32	0,284	1,033	-0,002	0,0006
Serie 2	0,00	1,3149	0,07	0,217	1,17	0,521	1,1	0,304	0,0005
	1,87	0,9119	0,08	0,313	1,12	0,562	1,033	0,249	0,0002
	9,37	0,1542	0,08	0,224	1,50	0,269	1,417	0,045	0,0019
	16,87	0,0036	0,08	0,243	1,38	0,242	1,3	-0,001	0,0006
	24,37	-0,0124	0,08	0,259	1,50	0,256	1,417	-0,003	7E-07
	31,87	-0,0209	0,08	0,279	1,50	0,270	1,417	-0,009	2E-07
	39,37	-0,0239	0,08	0,283	1,50	0,275	1,417	-0,008	7E-08
							Error a	**0,001**	0,0711



error Y
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0,043272764
0,025390828
0,000860484
0,000389575
0,000264931

corretgir per [TTR] a 4 mg/mL

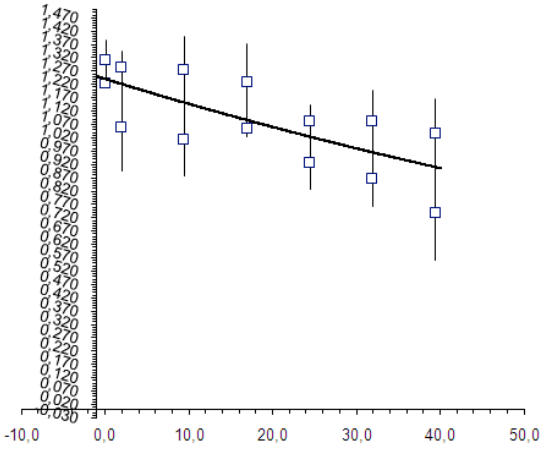
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,024	0,014	1,317	0,026	0,190	0,014	0,250	1,2924	3,552	0,117	101,9

Punts a ignorar
7

numero inhibidor = 3 | Referencia llista: 484

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2279	0,07	0,212	1,18	0,510	1,12	0,298	0,0002
	1,88	1,2852	0,07	0,363	1,50	0,675	1,433	0,312	0,0039
	9,38	1,277	0,07	0,387	1,47	0,707	1,4	0,32	0,0154
	16,88	1,2314	0,07	0,391	1,50	0,747	1,433	0,356	0,0208
	24,38	1,0849	0,07	0,417	1,50	0,802	1,433	0,385	0,0036
	31,88	1,0836	0,07	0,429	1,50	0,797	1,433	0,368	0,0137
	39,39	1,0392	0,07	0,412	1,32	0,782	1,25	0,37	0,0164
Serie 2	0,00	1,3149	0,07	0,217	1,17	0,521	1,1	0,304	0,0055
	1,88	1,0603	0,08	0,348	1,12	0,647	1,033	0,299	0,0264
	9,38	1,0153	0,08	0,375	1,50	0,701	1,417	0,326	0,0189
	16,88	1,0571	0,08	0,409	1,38	0,756	1,3	0,347	0,0009
	24,38	0,9276	0,08	0,429	1,50	0,796	1,417	0,367	0,0095
	31,88	0,8662	0,08	0,431	1,50	0,807	1,417	0,376	0,01
	39,39	0,7384	0,08	0,423	1,50	0,719	1,417	0,296	0,0299
							Error a	**0,001**	0,0713



error Y
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0,097404192
0,100241512
0,172809631

corretgir per [TTR] a 4 mg/mL

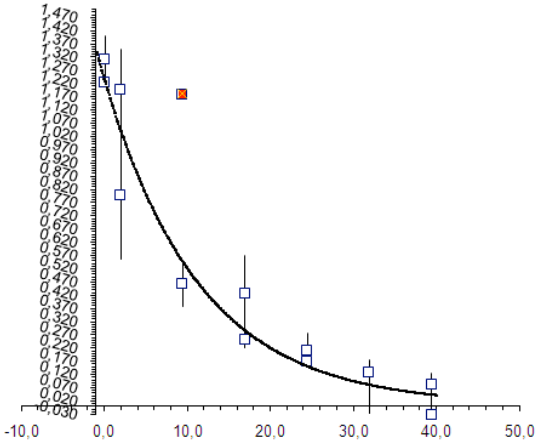
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,005	7,403	1,246	7,369	0,008	0,054	0,010	1,2408	88,328	25,163	100,4

Punts a ignorar

numero inhibidor = 4 | Referencia llista! 482

NPC-052

	[484]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2279	0,07	0,212	1,18	0,510	1,12	0,298	2E-06
	1,88	1,198	0,07	0,324	1,50	0,577	1,433	0,253	0,0234
	9,38	1,1812	0,08	0,302	1,47	0,497	1,383	0,195	0
	16,88	0,4301	0,12	0,316	1,50	0,451	1,383	0,135	0,0203
	24,38	0,2147	0,08	0,347	1,50	0,484	1,417	0,137	0,0039
	31,88	-0,0332	0,32	0,239	1,50	0,197	1,183	-0,042	0,0133
	39,38	-0,0298	0,32	0,235	1,50	0,190	1,183	-0,045	0,0057
Serie 2	0,00	1,3149	0,07	0,217	1,17	0,521	1,1	0,304	0,0073
	1,88	0,8008	0,08	0,300	1,12	0,533	1,033	0,233	0,0596
	9,38	0,4635	0,08	0,291	1,50	0,432	1,417	0,141	0,0069
	16,88	0,256	0,08	0,315	1,38	0,398	1,3	0,083	0,001
	24,38	0,1719	0,08	0,344	1,50	0,407	1,417	0,063	0,0004
	31,88	0,13	0,08	0,384	1,50	0,434	1,417	0,05	0,0023
	39,38	0,0863	0,03	0,392	1,50	0,423	1,467	0,031	0,0017
							Error a	**0,001**	0,0713



error Y
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0,031508091
0,019393167
0,047770769
0,040655179

☐ corretgir per [TTR] a 4 mg/mL

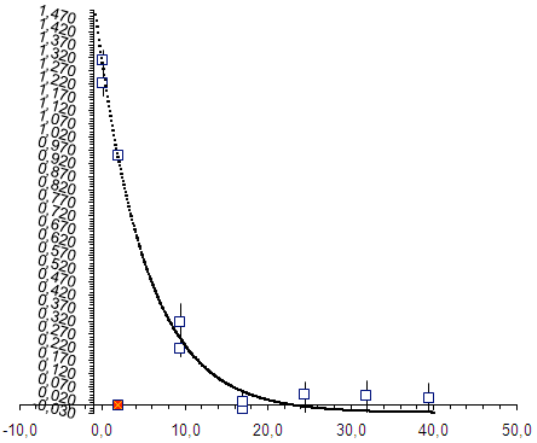
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,006	0,096	1,223	0,103	0,087	0,024	0,106	1,2292	8,021	0,530	99,5

Punts a ignorar
7

numero inhibidor = 5 | Referencia llista! 480

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2279	0,07	0,212	1,18	0,510	1,12	0,298	0,0026
	1,87	0,0023	0,00	0,164	1,50	0,169	1,5	0,005	0
	9,37	0,3198	0,28	0,186	1,47	0,178	1,183	-0,008	0,0047
	16,87	-0,0119	0,23	0,214	1,50	0,199	1,267	-0,015	0,0044
	24,37	0,0435	0,08	0,248	1,50	0,271	1,417	0,023	0,0022
	31,87	0,0368	0,35	0,323	1,50	0,362	1,15	0,039	0,0032
	39,37	0,0299	0,37	0,318	1,50	0,348	1,133	0,03	0,003
Serie 2	0,00	1,3149	0,07	0,217	1,17	0,521	1,1	0,304	0,0013
	1,87	0,9515	0,08	0,325	1,12	0,604	1,033	0,279	0,0004
	9,37	0,2186	0,08	0,277	1,50	0,344	1,417	0,067	0,0011
	16,87	0,0137	0,08	0,307	1,38	0,312	1,3	0,005	0,0016
	24,37	-0,0357	0,08	0,328	1,50	0,315	1,417	-0,013	0,0011
	31,87	-0,0351	0,08	0,336	1,50	0,324	1,417	-0,012	0,0002
	39,37	-0,0672	0,08	0,349	1,50	0,328	1,417	-0,021	0,0018
							Error a	**0,001**	0,0712



error Y
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☐ corretgir per [TTR] a 4 mg/mL

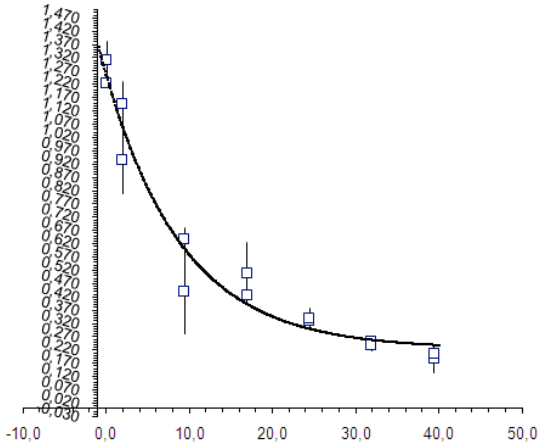
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,027	0,023	1,306	0,039	0,165	0,016	0,215	1,2793	4,080	0,165	102,1

Punts a ignorar
6

numero inhibidor = 6 | Referencia llista! 415

NPC-052

	[482]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2279	0,07	0,212	1,18	0,510	1,12	0,298	0,0004
	1,88	1,1483	0,08	0,343	1,50	0,620	1,417	0,277	0,0075
	9,38	0,4414	0,07	0,257	1,47	0,517	1,4	0,26	0,0253
	16,88	0,5115	0,07	0,230	1,50	0,390	1,433	0,16	0,0139
	24,38	0,3333	0,08	0,245	1,50	0,398	1,417	0,153	0,001
	31,88	0,2541	0,08	0,245	1,50	0,339	1,417	0,094	3E-05
	39,38	0,1888	0,08	0,246	1,50	0,314	1,417	0,068	0,0027
Serie 2	0,00	1,3149	0,07	0,217	1,17	0,521	1,1	0,304	0,0045
	1,88	0,936	0,08	0,292	1,12	0,533	1,033	0,241	0,0158
	9,38	0,6412	0,08	0,250	1,50	0,460	1,417	0,21	0,0017
	16,88	0,4265	0,08	0,233	1,38	0,379	1,3	0,146	0,0011
	24,38	0,3396	0,08	0,242	1,50	0,381	1,417	0,139	0,0015
	31,88	0,2389	0,07	0,240	1,50	0,344	1,433	0,104	0,0004
	39,38	0,2077	0,08	0,231	1,50	0,310	1,417	0,079	0,0011
							Error a	**0,001**	0,0712



error Y
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0,038539722
0,020611492
0,033186787

☐ corretgir per [TTR] a 4 mg/mL

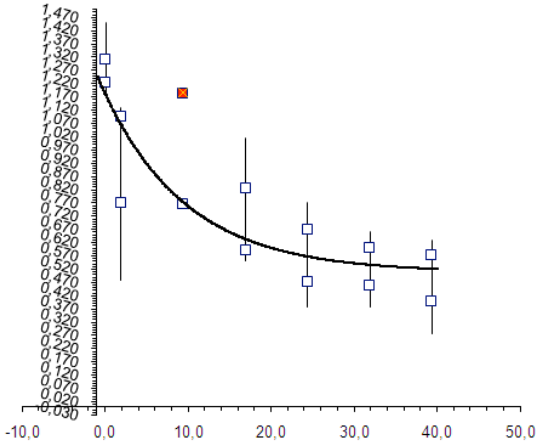
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,226	0,050	1,022	0,063	0,107	0,020	0,109	1,2475	8,814	0,460	81,9

Punts a ignorar

numero inhibidor = 7 | Referencia llista! 882

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,2279	0,07	0,212	1,18	0,510	1,12	0,298	0,0026
	1,87	1,0981	0,08	0,322	1,50	0,606	1,417	0,284	0,0012
	9,36	1,1856	0,08	0,290	1,47	0,559	1,383	0,269	0
	16,85	0,8263	0,08	0,273	1,50	0,523	1,417	0,25	0,0368
	24,35	0,6719	0,08	0,255	1,50	0,474	1,417	0,219	0,0106
	31,84	0,6004	0,08	0,246	1,50	0,465	1,417	0,219	0,0039
	39,33	0,5765	0,10	0,228	1,50	0,416	1,4	0,188	0,0029
Serie 2	0,00	1,3149	0,07	0,217	1,17	0,521	1,1	0,304	0,019
	1,87	0,7717	0,08	0,274	1,12	0,497	1,033	0,223	0,0852
	9,36	0,7675	0,08	0,261	1,50	0,484	1,417	0,223	3E-05
	16,85	0,5948	0,08	0,239	1,38	0,428	1,3	0,189	0,0016
	24,35	0,4735	0,08	0,228	1,50	0,416	1,417	0,188	0,0091
	31,84	0,4591	0,08	0,225	1,50	0,435	1,417	0,21	0,0062
	39,33	0,4	0,08	0,217	1,50	0,381	1,417	0,164	0,0151
							Error a	**0,001**	0,0713



error Y
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0,005184191
0,03973551
0,095441512
0,078697004
0,123009365

corretgir per [TTR] a 4 mg/mL

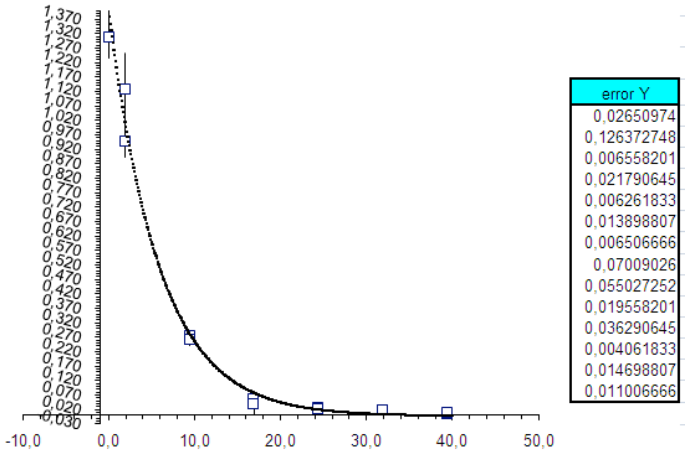
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,510	0,094	0,667	0,110	0,099	0,056	0,066	1,1770	21,477	5,231	56,7

Punts a ignorar
7

numero inhibidor = 12 | Referencia llista! 200

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	0,0007
	1,87	1,1294	0,08	0,236	1,12	0,509	1,033	0,273	0,016
	9,37	0,2744	0,08	0,216	1,50	0,347	1,417	0,131	4E-05
	16,87	0,0562	0,08	0,209	1,50	0,246	1,417	0,037	0,0005
	24,37	0,0272	0,33	0,206	1,50	0,235	1,167	0,029	4E-05
	31,87	0,0188	0,43	0,211	1,50	0,229	1,067	0,018	0,0002
	39,37	0,0069	0,37	0,227	1,50	0,234	1,133	0,007	4E-05
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0049
	1,87	0,948	0,08	0,197	1,12	0,484	1,033	0,287	0,003
	9,37	0,2614	0,10	0,201	1,50	0,318	1,4	0,117	0,0004
	16,87	0,0417	0,08	0,198	1,50	0,219	1,417	0,021	0,0013
	24,37	0,025	0,07	0,204	1,50	0,229	1,433	0,025	2E-05
	31,87	0,0196	0,43	0,212	1,50	0,233	1,067	0,021	0,0002
	39,37	0,0114	0,38	0,206	1,50	0,217	1,117	0,011	0,0001
							Error a	**0,001**	0,0712



error Y
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0,013898807
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0,019558201
0,036290645
0,004061833
0,014698807
0,011006666

corretgir per [TTR] a 4 mg/mL

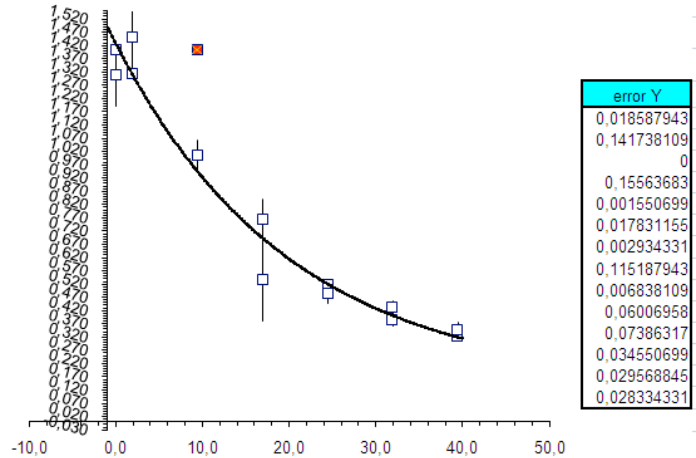
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,001	0,021	1,379	0,035	0,169	0,014	0,233	1,3780	4,090	0,148	100,1

Punts a ignorar

numero inhibidor = 2 | Referencia llista! 952

NPC-052

		[952]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	0,0003
	1,88	1,4503	0,05	0,218	1,12	0,563	1,067	0,345	0,0201
	9,38	1,4038	0,07	0,210	1,50	0,469	1,433	0,259	0
	16,89	0,5373	0,08	0,201	1,50	0,346	1,417	0,145	0,0242
	24,40	0,5188	0,12	0,214	1,50	0,360	1,383	0,146	2E-06
	31,91	0,3838	0,07	0,187	1,50	0,315	1,433	0,128	0,0003
	39,41	0,3229	0,07	0,190	1,50	0,311	1,433	0,121	9E-06
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0133
	1,88	1,3154	0,08	0,219	1,12	0,579	1,033	0,360	5E-05
	9,38	1,0039	0,12	0,213	1,50	0,527	1,383	0,314	0,0036
	16,89	0,7668	0,13	0,213	1,50	0,437	1,367	0,224	0,0055
	24,40	0,4858	0,12	0,193	1,50	0,420	1,383	0,227	0,0012
	31,91	0,4312	0,12	0,192	1,50	0,470	1,383	0,278	0,0009
	39,41	0,3483	0,12	0,190	1,50	0,438	1,383	0,248	0,0008
							Error a	**0,001**	0,0712



error Y
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0,06006958
0,07386317
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0,029568845
0,028334331

corretgir per [TTR] a 4 mg/mL

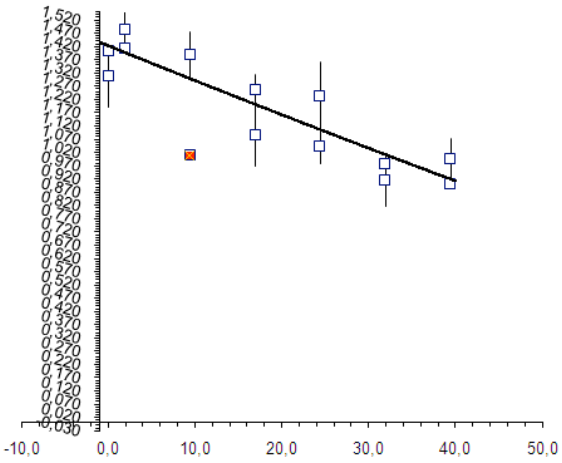
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,140	0,152	1,283	0,144	0,050	0,013	0,064	1,4231	16,226	0,748	90,2

Punts a ignorar
7

numero inhibidor = 5 | Referencia llista! 955

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	0,0003
	1,88	1,4851	0,07	0,250	1,12	0,632	1,05	0,382	0,0076
	9,38	1,0089	0,07	0,235	1,50	0,598	1,433	0,363	0
	16,88	1,0865	0,07	0,237	1,50	0,617	1,433	0,38	0,0134
	24,38	1,0438	0,07	0,238	1,50	0,596	1,433	0,358	0,0039
	31,88	0,9798	0,07	0,252	1,50	0,600	1,433	0,348	0,0011
	39,39	0,9041	0,07	0,250	1,50	0,579	1,433	0,329	0,0002
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0131
	1,88	1,4131	0,07	0,214	1,12	0,572	1,05	0,358	0,0002
	9,38	1,3878	0,07	0,216	1,50	0,687	1,433	0,471	0,0079
	16,88	1,2584	0,08	0,230	1,50	0,589	1,417	0,359	0,0032
	24,38	1,2358	0,10	0,239	1,50	0,674	1,4	0,435	0,0167
	31,88	0,9151	0,10	0,239	1,50	0,622	1,4	0,383	0,0095
	39,39	0,9982	0,10	0,247	1,50	0,640	1,4	0,393	0,0062
							Error a	0,001	0,0713



error Y
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0,129267712
0,097318531
0,078461098

corretgir per [TTR] a 4 mg/mL

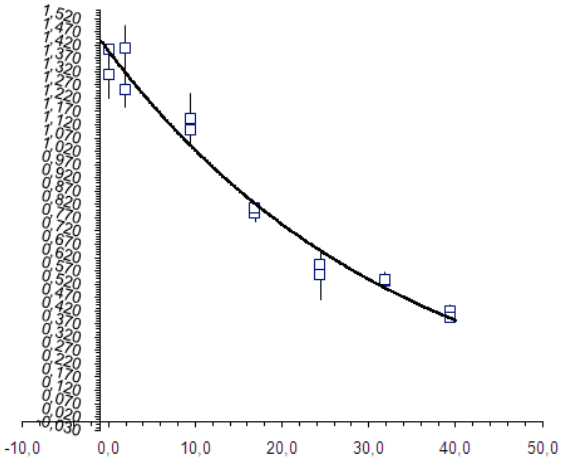
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-5,070	78,626	6,492	#####	0,002	0,026	0,013	1,4226	56,694	24,406	456,4

Punts a ignorar
7

numero inhibidor = 4 | Referencia llista! 954

NPC-052

	[953]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	0,0001
	1,87	1,4067	0,05	0,234	1,12	0,569	1,067	0,335	0,0082
	9,36	1,1419	0,05	0,301	1,50	0,591	1,45	0,29	0,0099
	16,85	0,7898	0,07	0,393	1,50	0,650	1,433	0,257	0,0011
	24,34	0,5563	0,07	0,449	1,50	0,720	1,433	0,271	0,0082
	31,83	0,533	0,08	0,540	1,50	0,788	1,417	0,248	0,0007
	39,32	0,4178	0,07	0,610	1,50	0,833	1,433	0,223	0,0006
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0075
	1,87	1,2522	0,07	0,227	1,12	0,655	1,05	0,428	0,0041
	9,36	1,1021	0,10	0,309	1,50	0,661	1,4	0,352	0,0036
	16,85	0,805	0,13	0,384	1,50	0,651	1,367	0,267	0,0003
	24,34	0,5921	0,10	0,453	1,50	0,647	1,4	0,194	0,003
	31,83	0,5364	0,10	0,532	1,50	0,713	1,4	0,181	0,0009
	39,32	0,3958	0,10	0,595	1,50	0,743	1,4	0,148	9E-06
							Error a	0,001	0,0712



error Y
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0,054743132
0,030548249
0,002961062

corretgir per [TTR] a 4 mg/mL

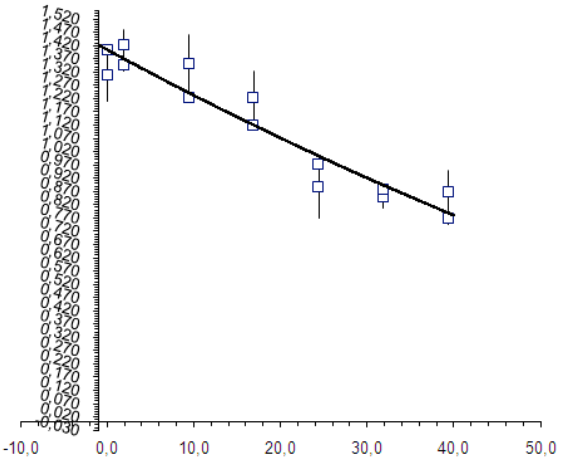
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-0,064	0,292	1,458	0,279	0,030	0,010	0,043	1,3944	22,024	0,937	104,6

Punts a ignorar

numero inhibidor = 3 | Referencia llista! 953

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	6E-07
	1,87	1,4254	0,05	0,220	1,12	0,559	1,067	0,339	0,003
	9,37	1,2255	0,05	0,253	1,50	0,648	1,45	0,395	0,0003
	16,86	1,1194	0,07	0,273	1,50	0,622	1,433	0,349	6E-07
	24,35	0,8886	0,07	0,289	1,50	0,541	1,433	0,252	0,0134
	31,84	0,8516	0,07	0,323	1,50	0,695	1,433	0,372	0,0018
	39,33	0,7691	0,08	0,345	1,50	0,560	1,417	0,215	0,0004
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0092
	1,87	1,3472	0,07	0,215	1,12	0,534	1,05	0,319	0,0005
	9,37	1,3522	0,08	0,248	1,50	0,688	1,417	0,44	0,0121
	16,86	1,2232	0,10	0,266	1,50	0,661	1,4	0,395	0,0106
	24,35	0,9734	0,07	0,282	1,50	0,660	1,433	0,378	0,001
	31,84	0,8794	0,17	0,340	1,50	0,714	1,333	0,374	0,0002
	39,33	0,8702	0,18	0,367	1,50	0,713	1,317	0,346	0,0065
							Error a	**0,001**	0,0712



error Y
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0,030834342
0,014663523
0,08081624

☐ corretgir per [TTR] a 4 mg/mL

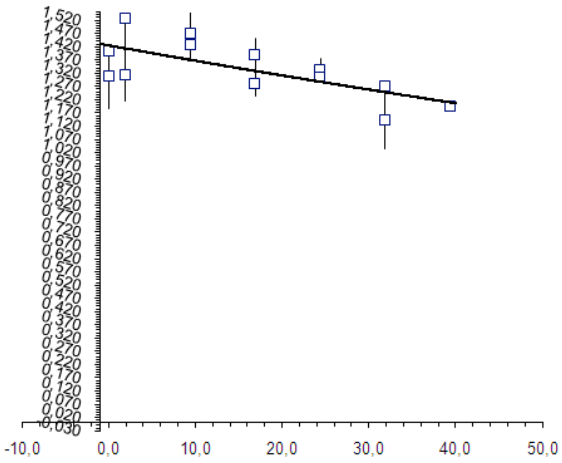
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-1,206	5,625	2,610	5,605	0,007	0,017	0,018	1,4038	45,903	5,777	185,9

Punts a ignorar

numero inhibidor = 1 | Referencia llista! 951

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	0,0004
	1,87	1,5264	0,05	0,229	1,12	0,565	1,067	0,336	0,0126
	9,37	1,4727	0,05	0,222	1,50	0,638	1,45	0,416	0,0103
	16,86	1,3916	0,05	0,226	1,50	0,641	1,45	0,415	0,0039
	24,35	1,3336	0,05	0,217	1,50	0,659	1,45	0,442	0,002
	31,84	1,1441	0,05	0,199	1,50	0,575	1,45	0,376	0,011
	39,33	1,1952	0,05	0,192	1,50	0,564	1,45	0,372	0,0002
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0138
	1,87	1,3145	0,08	0,233	1,12	0,619	1,033	0,386	0,01
	9,37	1,4257	0,07	0,205	1,50	0,693	1,433	0,488	0,003
	16,86	1,283	0,07	0,201	1,50	0,589	1,433	0,388	0,0021
	24,35	1,3061	0,07	0,204	1,50	0,688	1,433	0,484	0,0003
	31,84	1,2706	0,07	0,198	1,50	0,633	1,433	0,435	0,0005
	39,33	1,1952	0,08	0,198	1,50	0,585	1,417	0,387	0,0002
							Error a	**0,001**	0,0712



error Y
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0,017674003
0,021643621
0,015466394

☐ corretgir per [TTR] a 4 mg/mL

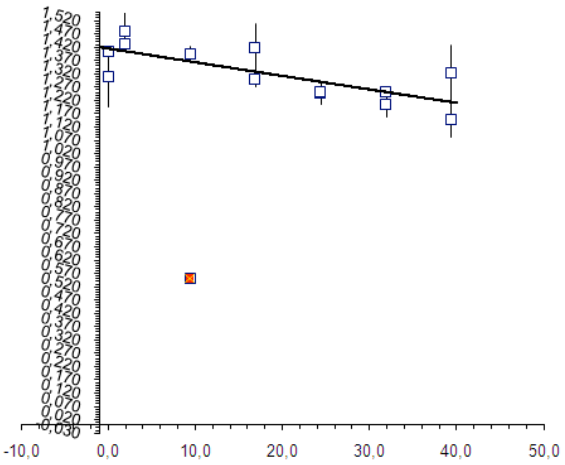
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-0,032	17,347	1,457	#####	0,004	0,052	0,006	1,4253	165,755	51,237	102,3

Punts a ignorar

numero inhibidor = 6 | Referencia llista! 956

NPC-052

	[954]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	0,0001
	1,87	1,4811	0,07	0,244	1,12	0,649	1,05	0,405	0,0057
	9,37	0,5518	0,07	0,246	1,50	0,636	1,433	0,39	0
	16,87	1,4193	0,07	0,237	1,50	0,650	1,433	0,413	0,0082
	24,37	1,2486	0,07	0,230	1,50	0,607	1,433	0,377	0,0017
	31,87	1,2074	0,07	0,226	1,50	0,618	1,433	0,392	0,002
	39,36	1,1489	0,07	0,206	1,50	0,532	1,433	0,326	0,0043
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0116
	1,87	1,4337	0,07	0,211	1,12	0,603	1,05	0,392	0,0008
	9,37	1,396	0,08	0,213	1,50	0,682	1,417	0,469	0,0008
	16,87	1,3016	0,07	0,186	1,50	0,598	1,433	0,412	0,0007
	24,37	1,2549	0,07	0,199	1,50	0,705	1,433	0,506	0,0013
	31,87	1,2546	0,07	0,209	1,50	0,683	1,433	0,474	5E-06
	39,36	1,3235	0,10	0,209	1,50	0,631	1,4	0,422	0,0119
							Error a	**0,001**	0,0712



error Y
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0,028839569
0,027056834
0,035483434
0,002261145
0,108978272

☐ corretgir per [TTR] a 4 mg/mL

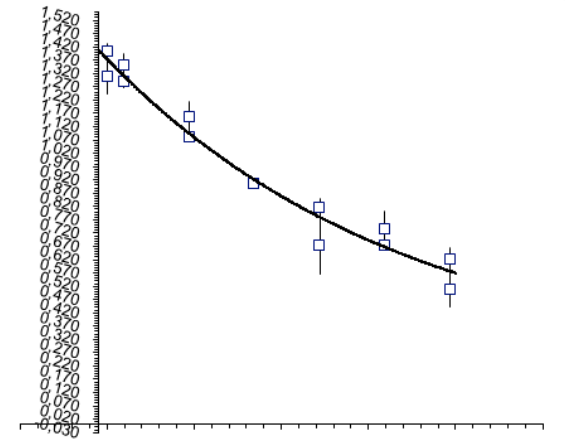
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-5,073	394,719	6,489	#####	0,001	0,049	0,005	1,4156	144,425	######	458,4

Punts a ignorar
7

numero inhibidor = 7 | Referencia llista! 957

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	0,001
	1,87	1,3529	0,07	0,223	1,12	0,569	1,05	0,346	0,0018
	9,36	1,0838	0,07	0,251	1,50	0,575	1,433	0,324	0,0001
	16,86	0,9079	0,10	0,288	1,50	0,594	1,4	0,306	0,0002
	24,35	0,6749	0,08	0,303	1,50	0,533	1,417	0,23	0,0111
	31,84	0,6762	0,07	0,330	1,50	0,561	1,433	0,231	7E-05
	39,33	0,5101	0,08	0,358	1,50	0,557	1,417	0,199	0,0045
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0041
	1,87	1,2898	0,08	0,233	1,12	0,551	1,033	0,318	0,0004
	9,36	1,1561	0,08	0,254	1,50	0,595	1,417	0,341	0,0038
	16,86	0,9054	0,10	0,279	1,50	0,564	1,4	0,285	0,0002
	24,35	0,816	0,07	0,306	1,50	0,611	1,433	0,305	0,0013
	31,84	0,7365	0,07	0,333	1,50	0,628	1,433	0,295	0,0047
	39,33	0,6233	0,08	0,377	1,50	0,613	1,417	0,236	0,0022
							Error a	**0,001**	0,0712



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0,068846089
0,046392645

☐ corretgir per [TTR] a 4 mg/mL

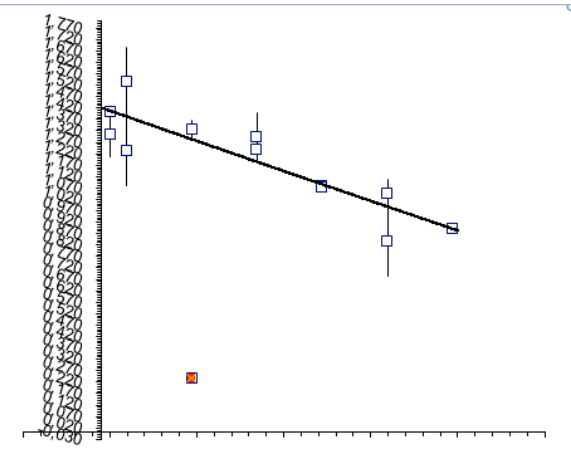
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,202	0,260	1,170	0,248	0,029	0,011	0,034	1,3723	30,492	1,375	85,3

Punts a ignorar

numero inhibidor = 8 | Referencia llista! 958

NPC-052

	[955]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	2E-05
	1,87	1,5357	0,07	0,243	1,12	0,643	1,05	0,4	0,0231
	9,37	0,2376	0,07	0,259	1,50	0,638	1,433	0,379	0
	16,86	1,2933	0,07	0,276	1,50	0,625	1,433	0,349	0,0116
	24,36	1,0798	0,07	0,300	1,50	0,672	1,433	0,372	5E-05
	31,85	1,0488	0,07	0,320	1,50	0,668	1,433	0,348	0,0035
	39,35	0,8929	0,07	0,330	1,50	0,624	1,433	0,294	3E-07
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0101
	1,87	1,2321	0,07	0,216	1,12	0,535	1,05	0,319	0,023
	9,37	1,3278	0,07	0,252	1,50	0,709	1,433	0,457	0,0019
	16,86	1,24	0,08	0,285	1,50	0,694	1,417	0,409	0,003
	24,36	1,075	0,08	0,299	1,50	0,682	1,417	0,383	0,0001
	31,85	0,8393	0,08	0,312	1,50	0,576	1,417	0,264	0,0226
	39,35	0,8948	0,10	0,339	1,50	0,667	1,4	0,328	6E-06
							Error a	**0,001**	0,0713



error Y
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0,012150667
0,15018355
0,00240668

☐ corretgir per [TTR] a 4 mg/mL

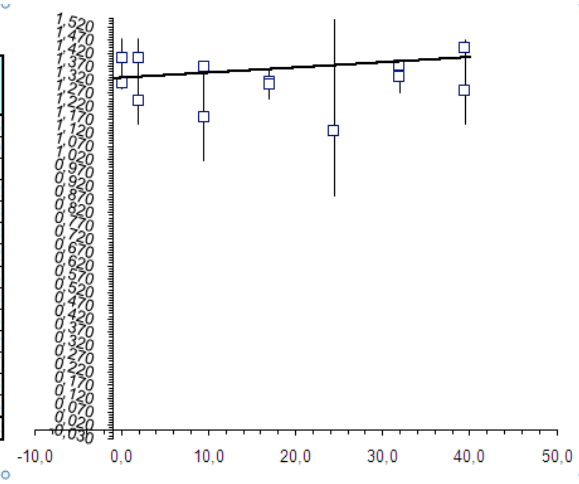
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	-15,448	574,145	16,857	#####	0,001	0,027	0,013	1,4086	53,995	61,657	1196,7

Punts a ignorar
7

numero inhibidor = 9 | Referencia llista! 959

NPC-052

	1,4131	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	0,0056
	1,88	1,2446	0,08	0,201	1,12	0,519	1,033	0,318	0,0079
	9,38	1,1831	0,08	0,211	1,50	0,532	1,417	0,321	0,0271
	16,88	1,3151	0,08	0,223	1,50	0,559	1,417	0,336	0,0022
	24,38	1,9995	0,08	0,302	1,50	0,983	1,417	0,681	0,3878
	31,88	1,3745	0,12	0,262	1,50	0,668	1,383	0,406	0,0003
	39,38	1,4406	0,08	0,246	1,50	0,698	1,417	0,452	0,0012
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0005
	1,88	1,4063	0,07	0,209	1,12	0,564	1,05	0,355	0,0053
	9,38	1,3703	0,07	0,221	1,50	0,707	1,433	0,486	0,0005
	16,88	1,306	0,07	0,222	1,50	0,682	1,433	0,46	0,0032
	24,38	1,1304	0,07	0,228	1,50	0,636	1,433	0,408	0,0607
	31,88	1,3338	0,08	0,251	1,50	0,705	1,417	0,454	0,0033
	39,38	1,2797	0,07	0,252	1,50	0,680	1,433	0,428	0,016
							Error a	**0,001**	0,0714



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0,057663637
0,126598313

corretgir per [TTR] a 4 mg/mL

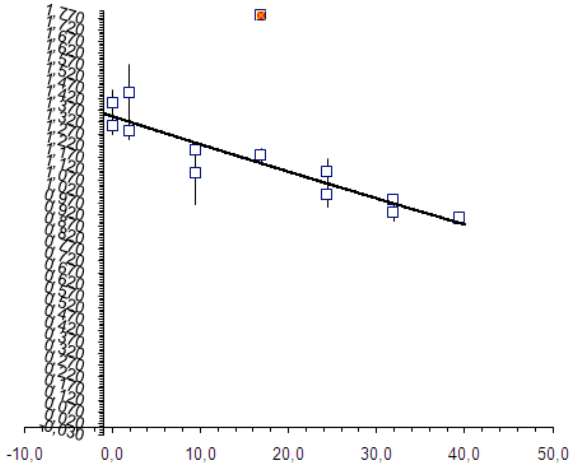
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,095	437,432	1,425	#####	-0,001	0,396	-0,002	1,3300	######	######	107,2

Punts a ignorar

numero inhibidor = 10 | Referencia llista! 960

NPC-052

	1,8745004	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	0,0034
	1,87	1,2845	0,08	0,213	1,12	0,598	1,033	0,385	0,0015
	9,37	1,1001	0,10	0,255	1,50	0,595	1,4	0,34	0,0175
	16,86	1,7823	0,08	0,374	1,50	0,971	1,417	0,597	0
	24,35	1,0071	0,10	0,336	1,50	0,654	1,4	0,318	0,0024
	31,85	0,9323	0,12	0,392	1,50	0,707	1,383	0,315	0,0014
	39,34	0,9028	0,10	0,387	1,50	0,694	1,4	0,307	0,0003
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0014
	1,87	1,4489	0,08	0,222	1,12	0,644	1,033	0,422	0,0159
	9,37	1,2037	0,08	0,247	1,50	0,605	1,417	0,358	0,0008
	16,86	1,1778	0,10	0,296	1,50	0,690	1,4	0,394	0,0012
	24,35	1,1102	0,12	0,336	1,50	0,683	1,383	0,347	0,0029
	31,85	0,9844	0,10	0,372	1,50	0,758	1,4	0,386	0,0002
	39,34	0,9071	0,07	0,405	1,50	0,782	1,433	0,377	0,0004
							Error a	**0,001**	0,0712



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0,014026687
0,02106859

corretgir per [TTR] a 4 mg/mL

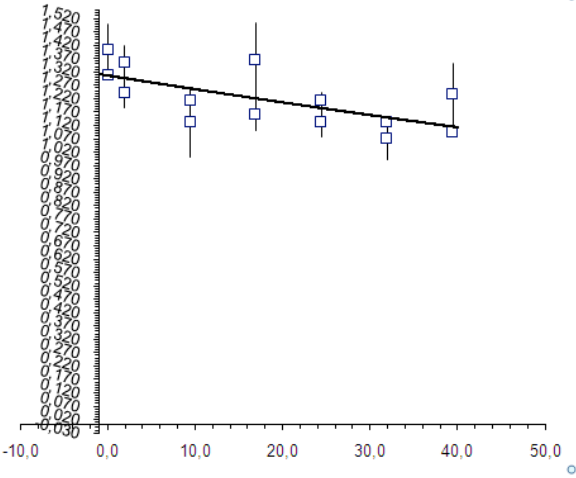
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-3,874	48,450	5,220	#####	0,002	0,023	0,012	1,3458	58,883	18,847	387,8

Punts a ignorar
8

numero inhibidor = 11 | Referencia llista! 961

NPC-052

	1,4337	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	0,0095
	1,87	1,358	0,08	0,224	1,12	0,602	1,033	0,378	0,0037
	9,37	1,1318	0,07	0,204	1,50	0,542	1,433	0,338	0,0162
	16,87	1,1626	0,08	0,231	1,50	0,588	1,417	0,357	0,0035
	24,37	1,1318	0,08	0,243	1,50	0,556	1,417	0,313	0,0029
	31,87	1,0724	0,08	0,250	1,50	0,590	1,417	0,340	0,0061
	39,37	1,0982	0,08	0,255	1,50	0,655	1,417	0,4	0,0003
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	4E-07
	1,87	1,2442	0,08	0,207	1,12	0,549	1,033	0,342	0,0028
	9,37	1,2166	0,08	0,226	1,50	0,597	1,417	0,371	0,0018
	16,87	1,3642	0,08	0,231	1,50	0,678	1,417	0,447	0,0203
	24,37	1,2166	0,08	0,223	1,50	0,633	1,417	0,41	0,001
	31,87	1,1325	0,08	0,247	1,50	0,642	1,417	0,395	0,0003
	39,37	1,2367	0,08	0,259	1,50	0,713	1,417	0,454	0,0144
							Error a	**0,001**	0,0713



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0,030903627
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corretgir per [TTR] a 4 mg/mL

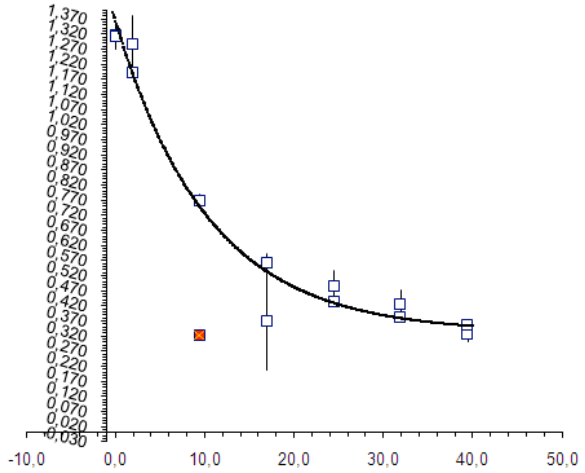
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,017	18,669	1,290	#####	0,004	0,063	0,005	1,3073	173,897	63,039	98,7

Punts a ignorar

numero inhibidor = 2 | Referencia llista: 952

NPC-052

	[952]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,31645	0,07	0,239	1,18	0,567	1,12	0,328	0,0014
	1,88	1,1938	0,07	0,239	1,12	0,575	1,05	0,336	7E-05
	9,38	0,3233	0,07	0,229	1,50	0,489	1,433	0,26	0
	16,89	0,3718	0,07	0,227	1,50	0,378	1,433	0,151	0,0263
	24,40	0,4324	0,07	0,222	1,50	0,463	1,433	0,241	4E-06
	31,91	0,3808	0,07	0,214	1,50	0,380	1,433	0,166	7E-07
	39,41	0,329	0,07	0,211	1,50	0,354	1,433	0,143	0,0007
Serie 2	0,00	1,3119	0,07	0,255	1,17	0,605	1,1	0,35	0,0018
	1,88	1,2851	0,07	0,242	1,12	0,554	1,05	0,312	0,0099
	9,38	0,77	0,07	0,217	1,50	0,492	1,433	0,275	0,0005
	16,89	0,5646	0,07	0,221	1,50	0,411	1,433	0,19	0,0009
	24,40	0,4854	0,07	0,225	1,17	0,411	1,1	0,186	0,003
	31,91	0,4266	0,07	0,223	1,50	0,434	1,433	0,211	0,0022
	39,41	0,359	0,07	0,215	1,50	0,390	1,433	0,175	1E-05
							Error a	**0,001**	0,0712



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corretgir per [TTR] a 4 mg/mL

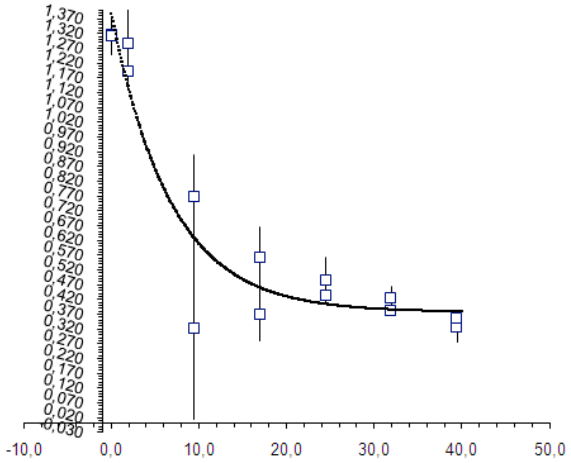
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,332	0,048	1,022	0,055	0,096	0,017	0,098	1,3543	11,310	0,509	75,5

Punts a ignorar
7

numero inhibidor = 2 | Referencia llista: 952

NPC-052

	[952]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,31645	0,07	0,239	1,18	0,567	1,12	0,328	0,0034
	1,88	1,1938	0,07	0,239	1,12	0,575	1,05	0,336	0,0035
	9,38	0,3233	0,07	0,229	1,50	0,489	1,433	0,26	0,0935
	16,89	0,3718	0,07	0,227	1,50	0,378	1,433	0,151	0,008
	24,40	0,4324	0,07	0,222	1,50	0,463	1,433	0,241	0,0007
	31,91	0,3808	0,07	0,214	1,50	0,380	1,433	0,166	4E-05
	39,41	0,329	0,07	0,211	1,50	0,354	1,433	0,143	0,0027
Serie 2	0,00	1,3119	0,07	0,255	1,17	0,605	1,1	0,35	0,004
	1,88	1,2851	0,07	0,242	1,12	0,554	1,05	0,312	0,0226
	9,38	0,77	0,07	0,217	1,50	0,492	1,433	0,275	0,0198
	16,89	0,5646	0,07	0,221	1,50	0,411	1,433	0,19	0,0106
	24,40	0,4854	0,07	0,225	1,17	0,411	1,1	0,186	0,0063
	31,91	0,4266	0,07	0,223	1,50	0,434	1,433	0,211	0,0015
	39,41	0,359	0,07	0,215	1,50	0,390	1,433	0,175	0,0005
							Error a	**0,001**	0,0713



error Y
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corretgir per [TTR] a 4 mg/mL

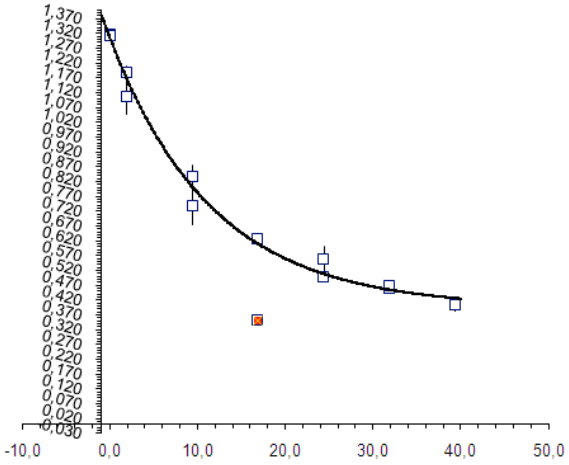
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,378	0,059	0,997	0,090	0,147	0,042	0,147	1,3750	7,961	0,852	72,5

Punts a ignorar

numero inhibidor = 1 | Referencia llista! 954

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,31645	0,07	0,239	1,18	0,567	1,12	0,328	0,0003
	1,87	1,1077	0,07	0,272	1,12	0,609	1,05	0,337	0,0033
	9,36	0,739	0,07	0,327	1,50	0,631	1,433	0,304	0,0039
	16,85	0,3508	0,07	0,408	1,50	0,520	1,433	0,112	0
	24,34	0,4997	0,07	0,486	1,50	0,761	1,433	0,275	8E-05
	31,83	0,4581	0,07	0,559	1,50	0,781	1,433	0,222	6E-06
	39,32	0,4055	0,07	0,652	1,50	0,869	1,433	0,217	0,0005
Serie 2	0,00	1,3119	0,07	0,255	1,17	0,605	1,1	0,35	0,0002
	1,87	1,1894	0,07	0,261	1,12	0,628	1,05	0,367	0,0006
	9,36	0,8387	0,07	0,334	1,50	0,648	1,433	0,314	0,0014
	16,85	0,627	0,07	0,408	1,50	0,608	1,433	0,2	0,0003
	24,34	0,557	0,07	0,482	1,17	0,696	1,1	0,214	0,0023
	31,83	0,4686	0,07	0,575	1,50	0,801	1,433	0,226	0,0002
	39,32	0,4055	0,07	0,669	1,50	0,810	1,433	0,141	0,0005
							Error a	**0,001**	0,0711



error Y
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corretgir per [TTR] a 4 mg/mL

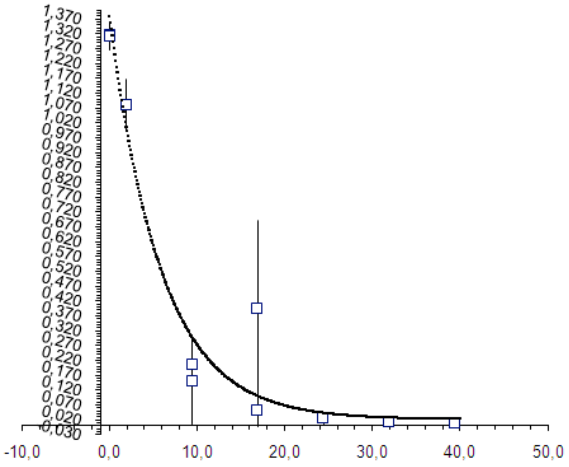
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,396	0,028	0,902	0,031	0,086	0,009	0,077	1,2986	14,867	0,393	69,5

Punts a ignorar
8

numero inhibidor = 6 | Referencia llista! 200

NPC-052

	[415]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,31645	0,07	0,239	1,18	0,567	1,12	0,328	0,0018
	1,87	1,0792	0,07	0,249	1,12	0,568	1,05	0,319	0,0068
	9,37	0,1535	0,07	0,220	1,50	0,364	1,433	0,144	0,0209
	16,87	0,051	0,07	0,222	1,50	0,255	1,433	0,033	0,0025
	24,37	0,0262	0,17	0,239	1,50	0,272	1,333	0,033	0,0004
	31,87	0,0146	0,07	0,229	1,50	0,253	1,433	0,024	0,0002
	39,37	0,0103	0,07	0,220	1,50	0,234	1,433	0,014	0,0002
Serie 2	0,00	1,3119	0,07	0,255	1,17	0,605	1,1	0,35	0,0022
	1,87	1,083	0,07	0,232	1,12	0,565	1,05	0,333	0,0075
	9,37	0,2077	0,07	0,219	1,50	0,348	1,433	0,129	0,0081
	16,87	0,3966	0,07	0,294	1,50	0,481	1,433	0,187	0,0876
	24,37	0,029	0,07	0,216	1,17	0,256	1,1	0,04	0,0003
	31,87	0,0138	0,18	0,237	1,50	0,251	1,317	0,014	0,0002
	39,37	0,0121	0,40	0,230	1,50	0,244	1,1	0,014	0,0002
							Error a	**0,001**	0,0713



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corretgir per [TTR] a 4 mg/mL

AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A ($uA \cdot h^{-1}$)	± SE	B ($uA \cdot h^{-1}$)	± SE	C (μM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (μM)	± SE	RA(%)
Serie 1+2	0,023	0,048	1,335	0,080	0,169	0,033	0,225	1,3585	4,214	0,349	98,3

Punts a ignorar

numero inhibidor = 3 | Referencia llista! 482

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,31645	0,07	0,239	1,18	0,567	1,12	0,328	0,002
	1,88	1,1877	0,07	0,260	1,12	0,591	1,05	0,331	0,0174
	9,38	0,2501	0,13	0,326	1,50	0,532	1,367	0,206	0,0327
	16,88	0,2754	0,13	0,327	1,50	0,475	1,367	0,148	0,0017
	24,38	0,2131	0,13	0,412	1,50	0,521	1,367	0,109	0,0017
	31,88	0,149	0,13	0,409	1,50	0,523	1,367	0,114	8E-06
	39,38	0,1155	0,13	0,439	1,50	0,500	1,367	0,061	0,0009
Serie 2	0,00	1,3119	0,07	0,255	1,17	0,605	1,1	0,35	0,0024
	1,88	1,0917	0,07	0,249	1,12	0,514	1,05	0,265	0,0013
	9,38	0,4433	0,07	0,281	1,50	0,442	1,433	0,161	0,0002
	16,88	0,272	0,07	0,317	1,50	0,466	1,433	0,149	0,0015
	24,38	0,2047	0,07	0,345	1,17	0,487	1,1	0,142	0,0011
	31,88	0,1556	0,07	0,389	1,50	0,484	1,433	0,095	1E-05
	39,38	0,1144	0,07	0,444	1,50	0,526	1,433	0,082	0,001
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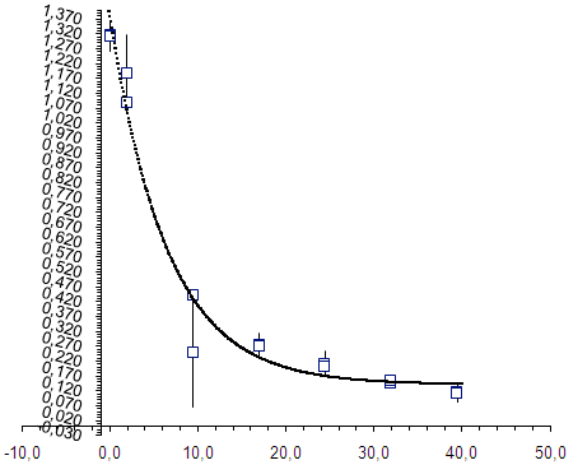

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corretgir per [TTR] a 4 mg/mL

AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,143	0,034	1,218	0,054	0,154	0,022	0,187	1,3609	5,321	0,288	89,5

Punts a ignorar

numero inhibidor = 4 | Referencia llista! 415

NPC-052

	[482]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,31645	0,07	0,239	1,18	0,567	1,12	0,328	0,0003
	1,88	1,2363	0,07	0,250	1,12	0,617	1,05	0,367	0,0046
	9,38	0,9572	0,07	0,253	1,50	0,535	1,433	0,282	0
	16,88	0,4951	0,07	0,242	1,50	0,425	1,433	0,183	0,0009
	24,38	0,3497	0,07	0,241	1,50	0,455	1,433	0,214	0,0003
	31,88	0,2487	0,13	0,256	1,50	0,417	1,367	0,161	0,0002
	39,38	0,1958	0,07	0,249	1,50	0,416	1,433	0,167	0,0008
Serie 2	0,00	1,3119	0,07	0,255	1,17	0,605	1,1	0,35	0,0005
	1,88	1,1666	0,07	0,235	1,12	0,520	1,05	0,285	3E-06
	9,38	0,6635	0,07	0,230	1,50	0,480	1,433	0,25	0,0023
	16,88	0,4451	0,07	0,231	1,50	0,415	1,433	0,184	0,0004
	24,38	0,3337	0,07	0,237	1,17	0,426	1,1	0,189	5E-08
	31,88	0,2953	0,07	0,247	1,50	0,381	1,433	0,134	0,0011
	39,38	0,2293	0,07	0,255	1,50	0,392	1,433	0,137	2E-05
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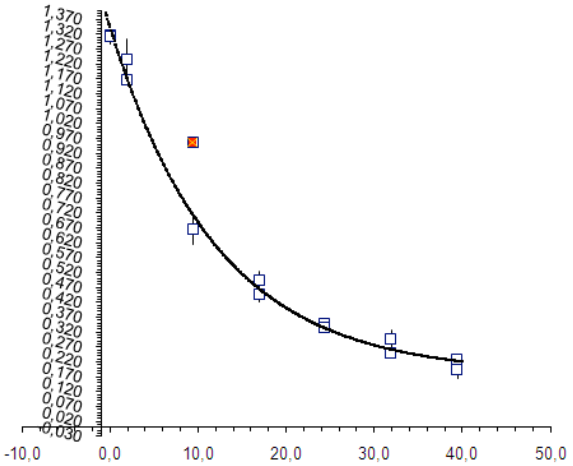

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corretgir per [TTR] a 4 mg/mL

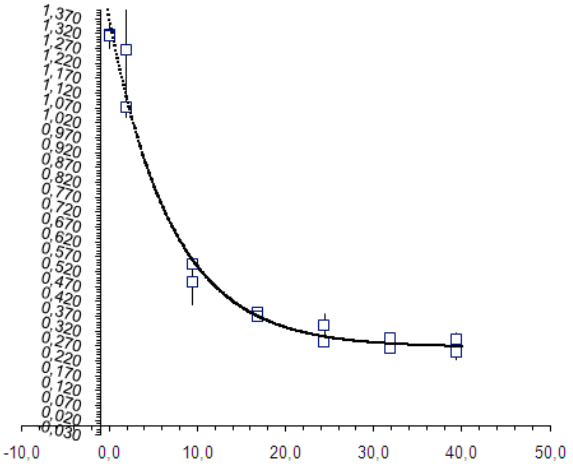
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,180	0,029	1,154	0,030	0,083	0,007	0,095	1,3341	10,426	0,195	86,5

Punts a ignorar
7

numero inhibidor = 5 | Referencia llista! 882

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,31645	0,07	0,239	1,18	0,567	1,12	0,328	0,0014
	1,87	1,2645	0,07	0,263	1,12	0,640	1,05	0,377	0,0261
	9,36	0,5451	0,07	0,228	1,50	0,477	1,433	0,249	0,0002
	16,85	0,3824	0,07	0,225	1,50	0,390	1,433	0,165	0,0002
	24,35	0,3414	0,07	0,229	1,50	0,406	1,433	0,177	0,0015
	31,84	0,2986	0,07	0,223	1,50	0,379	1,433	0,156	0,0004
	39,33	0,2501	0,07	0,219	1,50	0,372	1,433	0,153	0,0005
Serie 2	0,00	1,3119	0,07	0,255	1,17	0,605	1,1	0,35	0,0017
	1,87	1,0716	0,07	0,232	1,12	0,558	1,05	0,326	0,001
	9,36	0,4854	0,07	0,222	1,50	0,442	1,433	0,22	0,0056
	16,85	0,3695	0,07	0,223	1,50	0,376	1,433	0,153	7E-08
	24,35	0,2858	0,12	0,236	1,17	0,381	1,05	0,145	0,0003
	31,84	0,264	0,07	0,224	1,50	0,368	1,433	0,144	0,0002
	39,33	0,2936	0,07	0,229	1,50	0,364	1,433	0,135	0,0005
							Error a	**0,001**	0,0712



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corretgir per [TTR] a 4 mg/mL

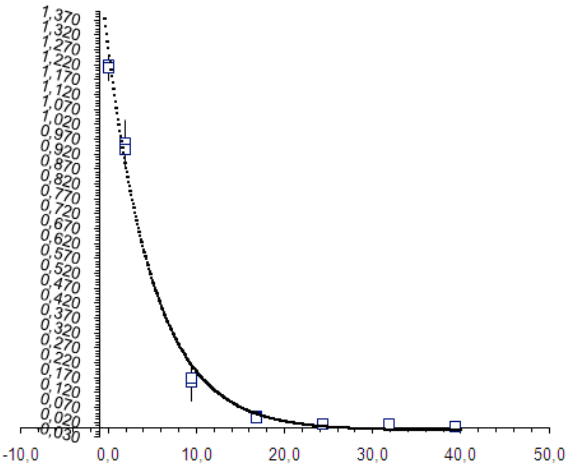
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,267	0,029	1,086	0,043	0,140	0,017	0,152	1,3533	6,969	0,300	80,3

Punts a ignorar

numero inhibidor = 7 | Referencia llista: 200

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,21815	0,07	0,206	1,18	0,454	1,12	0,248	0,0011
	1,87	0,9584	0,07	0,210	1,12	0,487	1,05	0,277	0,0061
	9,37	0,1543	0,07	0,207	1,50	0,284	1,433	0,077	0,0034
	16,87	0,0393	0,07	0,215	1,50	0,249	1,433	0,034	8E-05
	24,37	0,0146	0,07	0,216	1,50	0,230	1,433	0,014	4E-05
	31,87	0,0105	0,07	0,214	1,50	0,233	1,433	0,019	0,0002
	39,37	0,0077	0,22	0,202	1,50	0,209	1,283	0,007	0,0001
Serie 2	0,00	1,21025	0,07	0,221	1,17	0,498	1,1	0,277	0,0017
	1,87	0,9336	0,08	0,215	1,12	0,473	1,033	0,258	0,0029
	9,37	0,1706	0,08	0,203	1,50	0,286	1,417	0,083	0,0018
	16,87	0,0355	0,07	0,204	1,50	0,255	1,433	0,051	0,0002
	24,37	0,0161	0,07	0,213	1,50	0,240	1,433	0,027	7E-05
	31,87	0,0132	0,25	0,219	1,50	0,233	1,25	0,014	0,0002
	39,37	0,0069	0,10	0,216	1,50	0,223	1,4	0,007	0,0001
							Error a	**0,001**	0,0711



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☐ corretgir per [TTR] a 4 mg/mL

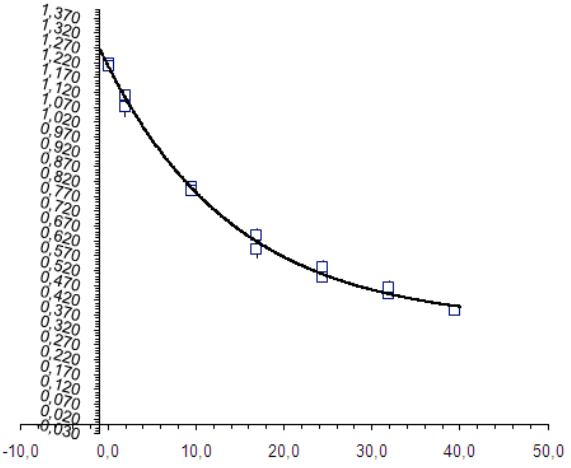
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,005	0,016	1,257	0,029	0,187	0,014	0,235	1,2514	3,689	0,129	100,4

Punts a ignorar

numero inhibidor = 1 | Referencia llista: 949

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,21815	0,07	0,206	1,18	0,454	1,12	0,248	0,0002
	1,87	1,0705	0,07	0,223	1,12	0,512	1,05	0,289	0,001
	9,37	0,8033	0,07	0,206	1,50	0,507	1,433	0,301	1E-05
	16,87	0,641	0,07	0,211	1,50	0,472	1,433	0,261	0,0005
	24,37	0,533	0,07	0,204	1,50	0,440	1,433	0,236	0,0006
	31,86	0,4431	0,07	0,203	1,50	0,394	1,433	0,191	1E-06
	39,36	0,388	0,07	0,194	1,50	0,375	1,433	0,181	0,0002
Serie 2	0,00	1,21025	0,07	0,221	1,17	0,498	1,1	0,277	3E-05
	1,87	1,112	0,07	0,213	1,12	0,512	1,05	0,299	0,0001
	9,37	0,788	0,07	0,208	1,50	0,454	1,433	0,246	0,0001
	16,87	0,5916	0,07	0,201	1,50	0,373	1,433	0,172	0,0007
	24,37	0,4996	0,07	0,203	1,50	0,372	1,433	0,169	7E-05
	31,86	0,4654	0,07	0,202	1,50	0,394	1,433	0,192	0,0005
	39,36	0,388	0,07	0,201	1,50	0,329	1,433	0,128	0,0002
							Error a	**0,001**	0,071



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☐ corretgir per [TTR] a 4 mg/mL

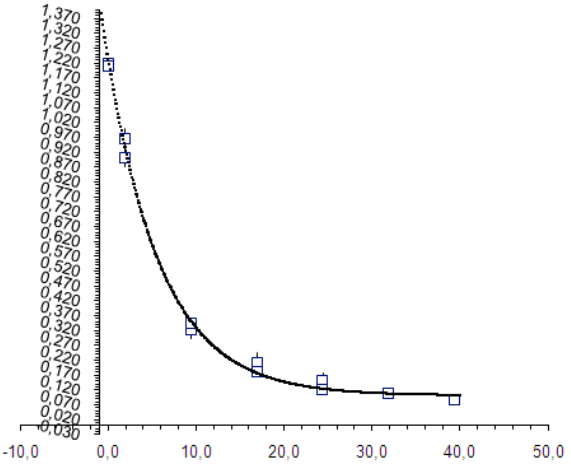
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,342	0,021	0,862	0,021	0,068	0,005	0,058	1,2044	17,718	0,246	71,6

Punts a ignorar

numero inhibidor = 2 | Referencia llista: 482

NPC-052

		[482]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,21815	0,07	0,206	1,18	0,454	1,12	0,248	5E-06
	1,88	0,9634	0,07	0,229	1,12	0,489	1,05	0,26	0,0013
	9,38	0,3233	0,07	0,274	1,50	0,380	1,433	0,106	0,0007
	16,88	0,2128	0,07	0,310	1,50	0,387	1,433	0,077	0,0013
	24,38	0,1533	0,07	0,339	1,50	0,398	1,433	0,059	0,0008
	31,88	0,107	0,07	0,371	1,50	0,416	1,433	0,045	6E-06
	39,38	0,0875	0,07	0,401	1,50	0,441	1,433	0,04	0,0003
Serie 2	0,00	1,21025	0,07	0,221	1,17	0,498	1,1	0,277	3E-05
	1,88	0,9012	0,07	0,226	1,12	0,482	1,05	0,256	0,0007
	9,38	0,3464	0,07	0,261	1,50	0,370	1,433	0,109	2E-05
	16,88	0,18	0,07	0,307	1,50	0,366	1,433	0,059	7E-06
	24,38	0,1208	0,07	0,339	1,50	0,386	1,433	0,047	2E-05
	31,88	0,1076	0,07	0,376	1,50	0,427	1,433	0,051	3E-06
	39,38	0,0888	0,07	0,413	1,50	0,458	1,433	0,045	0,0003
							Error a	**0,001**	0,0711



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0,005712217
0,025956288
0,00427992
0,002735533
0,004297681
0,001804883
0,015884181

☐ corretgir per [TTR] a 4 mg/mL

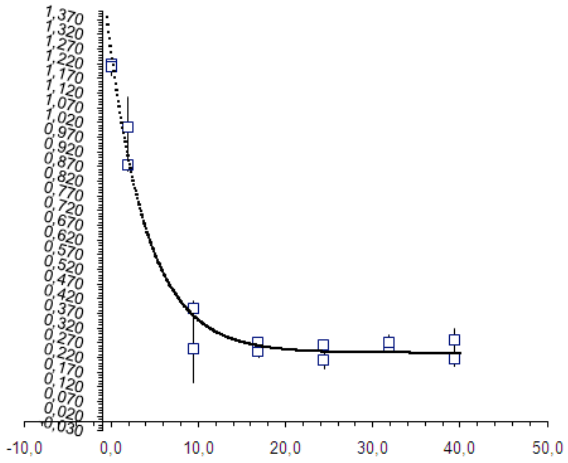
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,103	0,010	1,113	0,016	0,160	0,007	0,178	1,2160	4,933	0,087	91,6

Punts a ignorar

numero inhibidor = 3 | Referencia llista! 882

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,21815	0,07	0,206	1,18	0,454	1,12	0,248	0,0003
	1,87	1,0028	0,07	0,221	1,12	0,490	1,05	0,269	0,0112
	9,36	0,2501	0,07	0,220	1,50	0,352	1,433	0,132	0,0127
	16,85	0,2425	0,07	0,209	1,50	0,304	1,433	0,095	0,0004
	24,35	0,2131	0,07	0,217	1,50	0,296	1,433	0,079	0,0008
	31,84	0,2533	0,07	0,224	1,50	0,375	1,433	0,151	0,0002
	39,33	0,214	0,07	0,208	1,50	0,374	1,433	0,166	0,0006
Serie 2	0,00	1,21025	0,07	0,221	1,17	0,498	1,1	0,277	0,0007
	1,87	0,8769	0,08	0,219	1,12	0,478	1,033	0,259	0,0004
	9,36	0,3881	0,10	0,221	1,50	0,347	1,4	0,126	0,0006
	16,85	0,2731	0,10	0,215	1,50	0,353	1,4	0,138	0,0001
	24,35	0,2619	0,10	0,208	1,50	0,350	1,4	0,142	0,0004
	31,84	0,2697	0,10	0,224	1,50	0,390	1,4	0,166	0,001
	39,33	0,2802	0,10	0,232	1,50	0,372	1,4	0,14	0,0018
							Error a	0,001	0,0712



error Y
0,018629286
0,105608825
0,112819556
0,01898508
0,029127173
0,014729049
0,023876797
0,026529286
0,020291175
0,025180444
0,01161492
0,019672827
0,031129049
0,042323203

corretgir per [TTR] a 4 mg/mL

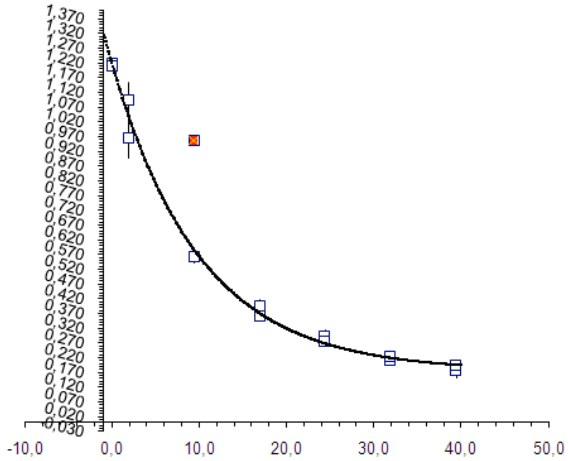
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h-1)	± SE	B (uA · h-1)	± SE	C (µM-1)	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,238	0,020	0,999	0,039	0,222	0,028	0,222	1,2368	4,350	0,276	80,8

Punts a ignorar

numero inhibidor = 4 | Referencia llista! 415

NPC-052

		[882]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,21815	0,07	0,206	1,18	0,454	1,12	0,248	8E-05
	1,88	1,0942	0,07	0,224	1,12	0,518	1,05	0,294	0,0036
	9,38	0,9572	0,07	0,226	1,50	0,467	1,433	0,241	0
	16,88	0,394	0,07	0,225	1,50	0,391	1,433	0,166	0,0005
	24,38	0,292	0,07	0,227	1,50	0,406	1,433	0,179	0,0005
	31,88	0,2115	0,07	0,230	1,50	0,384	1,433	0,154	7E-05
	39,38	0,1752	0,07	0,235	1,50	0,363	1,433	0,128	0,0005
Serie 2	0,00	1,21025	0,07	0,221	1,17	0,498	1,1	0,277	1E-06
	1,88	0,9669	0,07	0,210	1,12	0,432	1,05	0,222	0,0046
	9,38	0,5636	0,07	0,214	1,50	0,422	1,433	0,208	0,0005
	16,88	0,3624	0,07	0,218	1,50	0,362	1,433	0,144	7E-05
	24,38	0,2772	0,07	0,225	1,50	0,382	1,433	0,157	7E-05
	31,88	0,2237	0,07	0,238	1,50	0,343	1,433	0,105	1E-05
	39,38	0,1965	0,07	0,246	1,50	0,366	1,433	0,12	2E-07
							Error a	0,001	0,0711



error Y
0,008940845
0,059763981
0
0,023160932
0,023237975
0,008613544
0,021728363
0,001040845
0,067536019
0,02142299
0,008439068
0,008437975
0,003586456
0,000428363

corretgir per [TTR] a 4 mg/mL

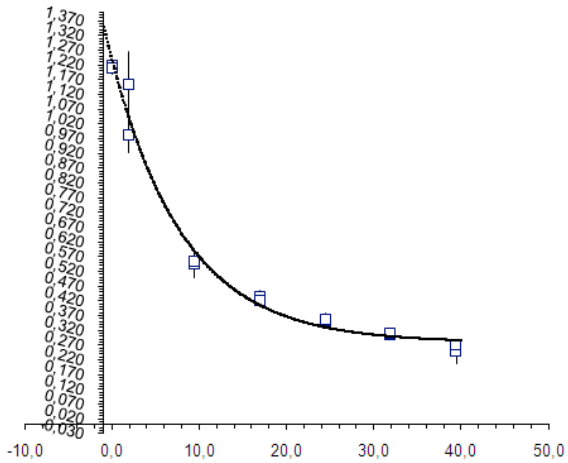
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h-1)	± SE	B (uA · h-1)	± SE	C (µM-1)	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,176	0,022	1,033	0,025	0,099	0,008	0,102	1,2092	8,904	0,183	85,5

Punts a ignorar
7

numero inhibidor = 5 | Referencia llista! 952

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,21815	0,07	0,206	1,18	0,454	1,12	0,248	0,0001
	1,88	1,1526	0,07	0,225	1,12	0,537	1,05	0,312	0,0131
	9,38	0,5451	0,07	0,208	1,50	0,458	1,433	0,25	0,0019
	16,89	0,4326	0,07	0,210	1,50	0,382	1,433	0,172	0,0007
	24,40	0,3521	0,07	0,200	1,50	0,369	1,433	0,169	0,0004
	31,91	0,3076	0,07	0,206	1,50	0,380	1,433	0,174	5E-05
	39,41	0,2482	0,07	0,197	1,50	0,314	1,433	0,117	0,0016
Serie 2	0,00	1,21025	0,07	0,221	1,17	0,498	1,1	0,277	0,0003
	1,88	0,9819	0,08	0,218	1,12	0,495	1,033	0,277	0,0032
	9,38	0,556	0,08	0,207	1,50	0,447	1,417	0,24	0,0011
	16,89	0,4222	0,08	0,208	1,50	0,366	1,417	0,158	0,0003
	24,40	0,3567	0,07	0,200	1,50	0,362	1,433	0,162	0,0007
	31,91	0,31	0,07	0,201	1,50	0,355	1,433	0,154	9E-05
	39,41	0,2709	0,08	0,208	1,50	0,337	1,417	0,129	0,0003
							Error a	0,001	0,0712



error Y
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0,044054321
0,026684307
0,020948442
0,006953341
0,040000198
0,01857902
0,056351936
0,033154321
0,016284307
0,025548442
0,009353341
0,017300198

corretgir per [TTR] a 4 mg/mL

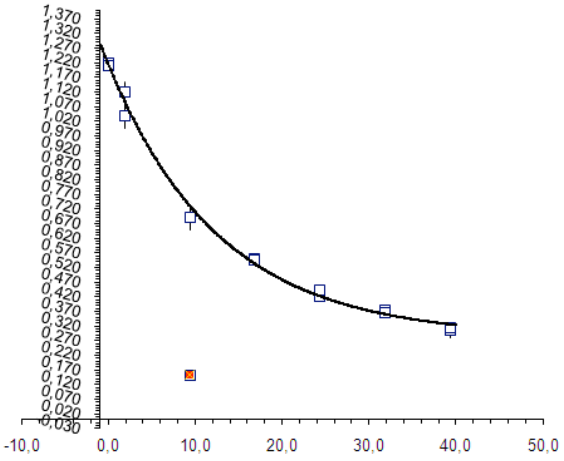
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h-1)	± SE	B (uA · h-1)	± SE	C (µM-1)	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,280	0,025	0,949	0,034	0,119	0,013	0,113	1,2288	8,727	0,292	77,2

Punts a ignorar

numero inhibidor = 6 | Referencia llista! 954

NPC-052

	[415]	V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,21815	0,07	0,206	1,18	0,454	1,12	0,248	0,0001
	1,87	1,1184	0,07	0,245	1,12	0,544	1,05	0,299	0,0013
	9,36	0,1535	0,07	0,315	1,50	0,539	1,433	0,224	0
	16,85	0,5489	0,07	0,387	1,50	0,610	1,433	0,223	0,0003
	24,34	0,4211	0,07	0,479	1,50	0,741	1,433	0,262	1E-06
	31,83	0,3754	0,07	0,548	1,50	0,746	1,433	0,198	0,0002
	39,32	0,3055	0,07	0,634	1,50	0,805	1,433	0,171	0,0005
Serie 2	0,00	1,21025	0,07	0,221	1,17	0,498	1,1	0,277	7E-06
	1,87	1,0403	0,08	0,242	1,12	0,525	1,033	0,283	0,0017
	9,36	0,6898	0,08	0,314	1,50	0,574	1,417	0,26	0,0015
	16,85	0,5445	0,08	0,393	1,50	0,599	1,417	0,206	0,0002
	24,34	0,4417	0,08	0,463	1,50	0,699	1,417	0,236	0,0004
	31,83	0,3644	0,08	0,550	1,50	0,777	1,417	0,227	1E-05
	39,32	0,3146	0,08	0,651	1,50	0,854	1,417	0,203	0,0002
							Error a	**0,001**	0,0711



error Y
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0
0,016940231
0,001134914
0,014316571
0,021502691
0,002556709
0,041805757
0,039040414
0,012540231
0,019465086
0,003316571
0,012402691

☐ corretgir per [TTR] a 4 mg/mL

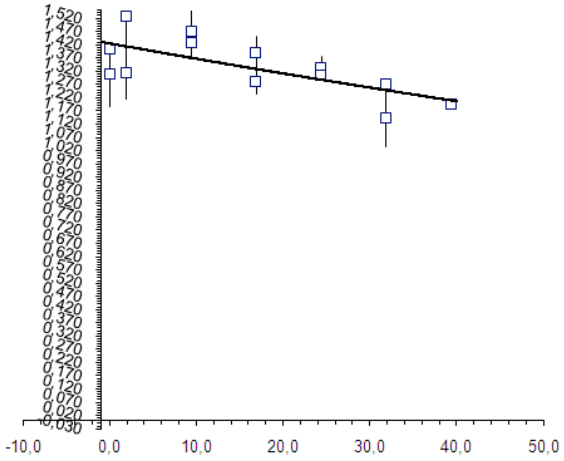
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	0,284	0,023	0,924	0,024	0,078	0,006	0,072	1,2077	13,590	0,230	76,5

Punts a ignorar
7

numero inhibidor = 1 | Referencia llista! 951

NPC-052

		V_0 (uA/h-1)	t_0 (h)	Abs_0	t_f (h)	Abs_f	Δt (h)	ΔAbs	Error Y^2
Serie 1	0,00	1,40455	0,05	0,213	1,18	0,551	1,13	0,338	0,0004
	1,87	1,5264	0,05	0,229	1,12	0,565	1,067	0,336	0,0126
	9,37	1,4727	0,05	0,222	1,50	0,638	1,45	0,416	0,0103
	16,86	1,3916	0,05	0,226	1,50	0,641	1,45	0,415	0,0039
	24,35	1,3336	0,05	0,217	1,50	0,659	1,45	0,442	0,002
	31,84	1,1441	0,05	0,199	1,50	0,575	1,45	0,376	0,011
	39,33	1,1952	0,05	0,192	1,50	0,564	1,45	0,372	0,0002
Serie 2	0,00	1,30795	0,07	0,187	1,17	0,455	1,1	0,268	0,0138
	1,87	1,3145	0,08	0,233	1,12	0,619	1,033	0,386	0,01
	9,37	1,4257	0,07	0,205	1,50	0,693	1,433	0,488	0,003
	16,86	1,283	0,07	0,201	1,50	0,589	1,433	0,388	0,0021
	24,35	1,3061	0,07	0,204	1,50	0,688	1,433	0,484	0,0003
	31,84	1,2706	0,07	0,198	1,50	0,633	1,433	0,435	0,0005
	39,33	1,1952	0,08	0,198	1,50	0,585	1,417	0,387	0,0002
							Error a	**0,001**	0,0712



error Y
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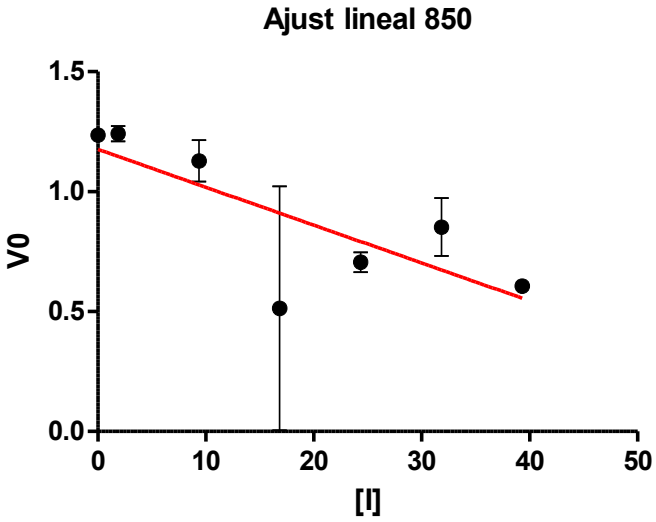
0,101649379
0,062488409
0,045174003
0,104856379
0,015466394
0,117345996
0,099781704
0,054649379
0,046111591
0,017674003
0,021643621
0,015466394

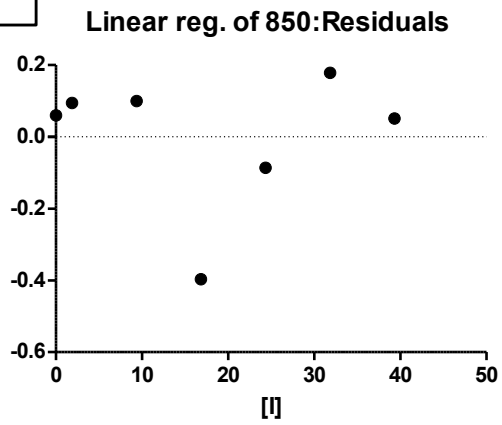
☐ corretgir per [TTR] a 4 mg/mL

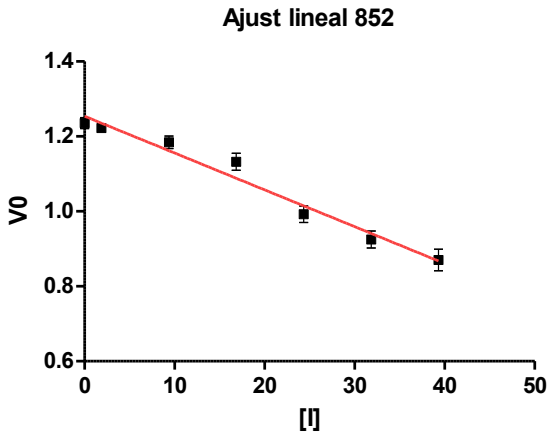
AJUST	VALORES AJUSTE ECUACIÓN Y=A+B*exp(-C*x)						PARÁMETROS				
	A (uA · h^{-1})	± SE	B (uA · h^{-1})	± SE	C (µM^{-1})	± SE	B*C	v_0 a x=0	IC_{50} (µM)	± SE	RA(%)
Serie 1+2	-0,032	17,347	1,457	#####	0,004	0,052	0,006	1,4253	165,755	51,237	102,3

Punts a ignorar

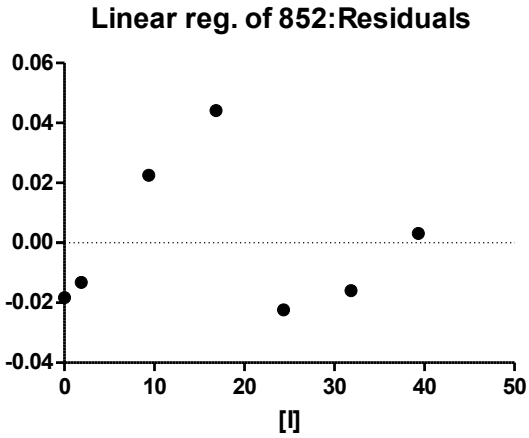


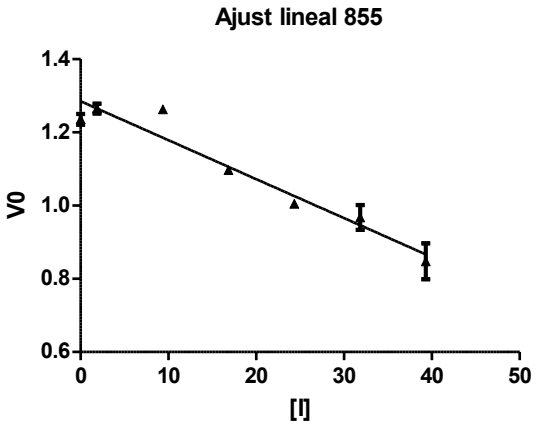
Best-fit values	
Slope	-0.01579 ± 0.005593
Y-intercept when X=0.0	1.176 ± 0.1256
X-intercept when Y=0.0	74.50
1/slope	-63.34
95% Confidence Intervals	
Slope	-0.02797 to -0.003601
Y-intercept when X=0.0	0.9025 to 1.450
X-intercept when Y=0.0	48.44 to 268.2
Goodness of Fit	
R square	0.3990
Sy.x	0.2902
Is slope significantly non-zero?	
F	7.968
DFn, DFd	1.000, 12.00
P value	0.0154
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



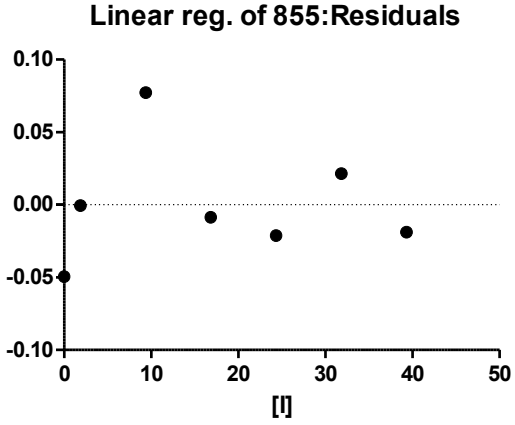


Best-fit values	
Slope	-0.009825 ± 0.0006374
Y-intercept when X=0.0	1.254 ± 0.01431
X-intercept when Y=0.0	127.6
1/slope	-101.8
95% Confidence Intervals	
Slope	-0.01121 to -0.008436
Y-intercept when X=0.0	1.223 to 1.285
X-intercept when Y=0.0	113.9 to 145.9
Goodness of Fit	
R square	0.9519
Sy.x	0.03307
Is slope significantly non-zero?	
F	237.6
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0

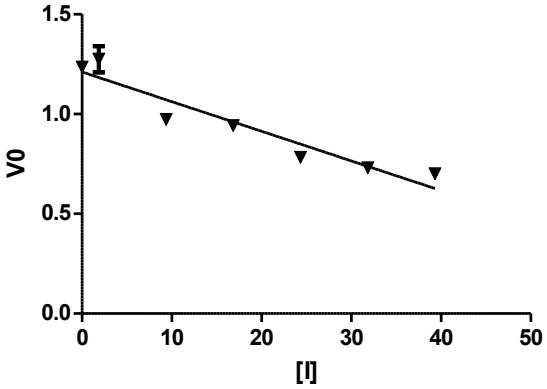




Best-fit values	
Slope	-0.01064 ± 0.0009240
Y-intercept when X=0.0	1.285 ± 0.02075
X-intercept when Y=0.0	120.8
1/slope	-94.00
95% Confidence Intervals	
Slope	-0.01265 to -0.008625
Y-intercept when X=0.0	1.240 to 1.330
X-intercept when Y=0.0	104.2 to 145.1
Goodness of Fit	
R square	0.9170
Sy.x	0.04794
Is slope significantly non-zero?	
F	132.6
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0

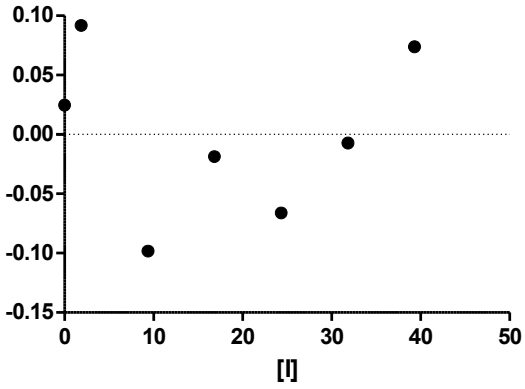


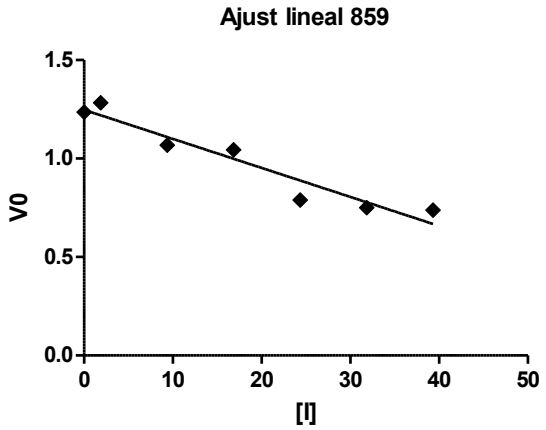
Ajust lineal 858



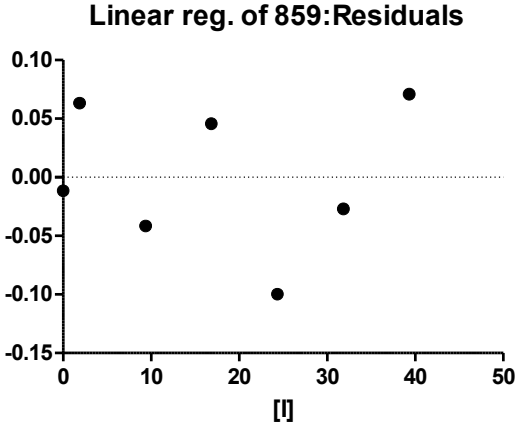
Best-fit values	
Slope	-0.01485 ± 0.001455
Y-intercept when X=0.0	1.211 ± 0.03268
X-intercept when Y=0.0	81.54
1/slope	-67.33
95% Confidence Intervals	
Slope	-0.01802 to -0.01168
Y-intercept when X=0.0	1.140 to 1.282
X-intercept when Y=0.0	69.98 to 99.20
Goodness of Fit	
R square	0.8967
Sy.x	0.07552
Is slope significantly non-zero?	
F	104.1
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0

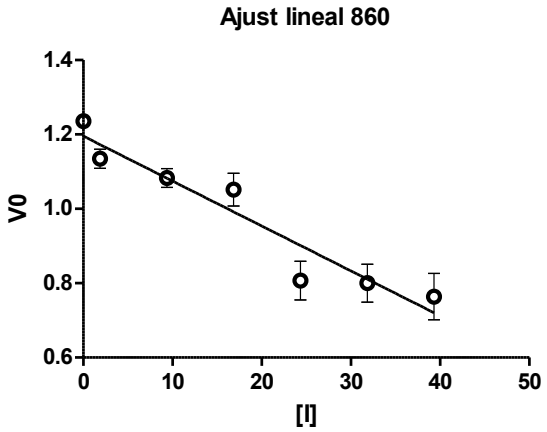
Linear reg. of 858:Residuals



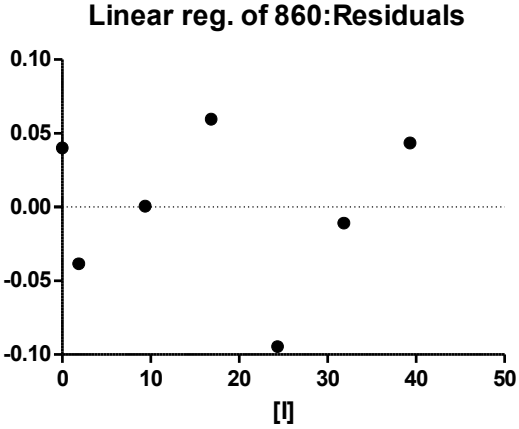


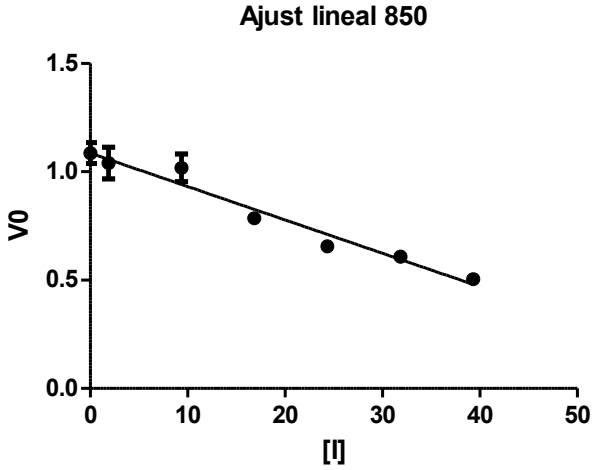
Best-fit values	
Slope	-0.01473 ± 0.001245
Y-intercept when X=0.0	1.247 ± 0.02796
X-intercept when Y=0.0	84.65
1/slope	-67.87
95% Confidence Intervals	
Slope	-0.01745 to -0.01202
Y-intercept when X=0.0	1.186 to 1.308
X-intercept when Y=0.0	73.97 to 100.0
Goodness of Fit	
R square	0.9211
Sy.x	0.06461
Is slope significantly non-zero?	
F	140.0
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



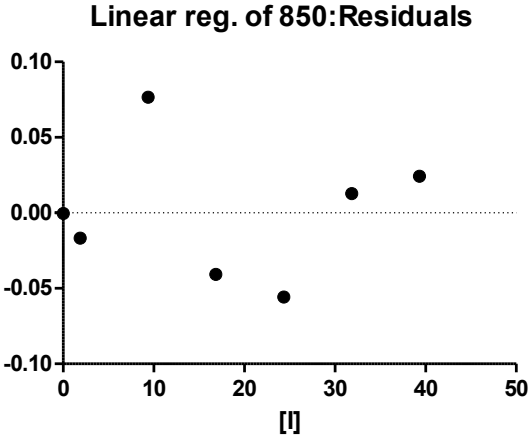


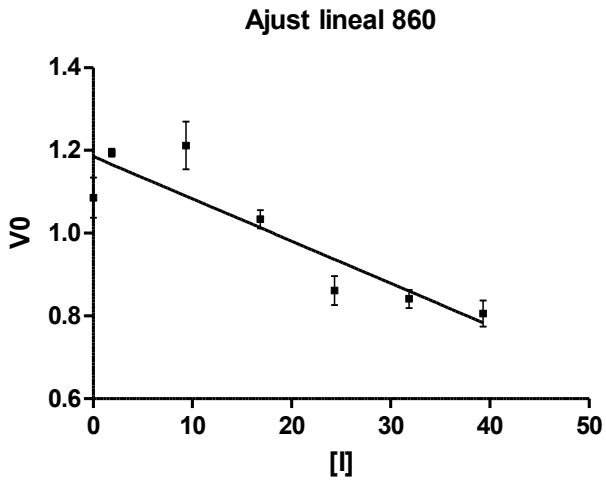
Best-fit values	
Slope	-0.01208 ± 0.001368
Y-intercept when X=0.0	1.196 ± 0.03071
X-intercept when Y=0.0	98.96
1/slope	-82.77
95% Confidence Intervals	
Slope	-0.01506 to -0.009102
Y-intercept when X=0.0	1.129 to 1.263
X-intercept when Y=0.0	82.59 to 125.9
Goodness of Fit	
R square	0.8667
Sy.x	0.07096
Is slope significantly non-zero?	
F	78.03
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



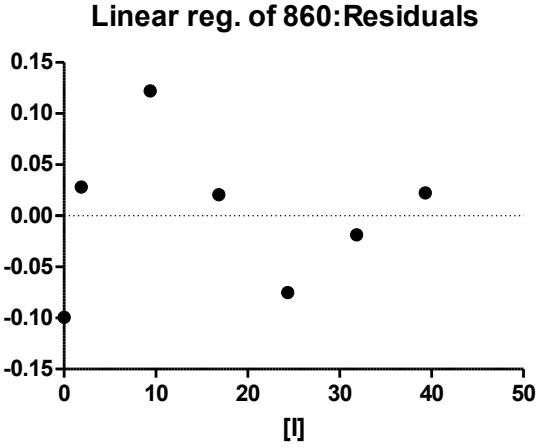


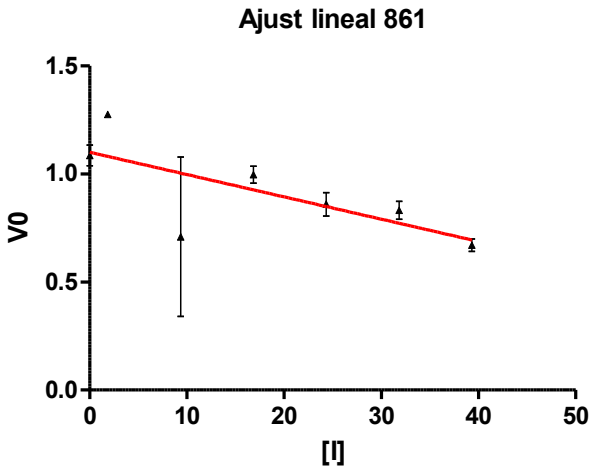
Best-fit values	
Slope	-0.01541 ± 0.001231
Y-intercept when X=0.0	1.086 ± 0.02763
X-intercept when Y=0.0	70.49
1/slope	-64.89
95% Confidence Intervals	
Slope	-0.01809 to -0.01273
Y-intercept when X=0.0	1.026 to 1.146
X-intercept when Y=0.0	62.35 to 81.93
Goodness of Fit	
R square	0.9289
Sy.x	0.06385
Is slope significantly non-zero?	
F	156.8
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



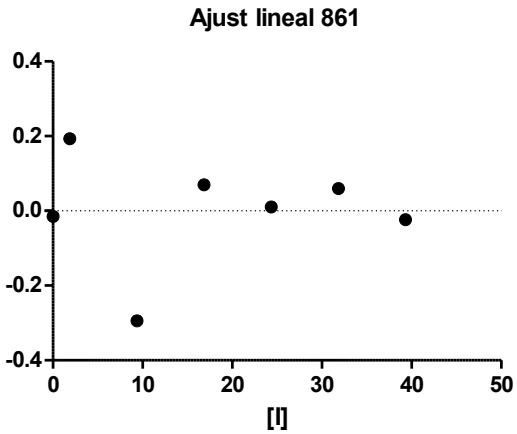


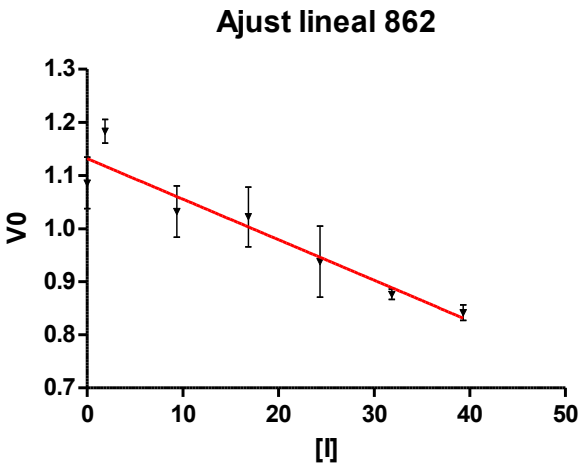
Best-fit values	
Slope	-0.01021 ± 0.001603
Y-intercept when X=0.0	1.185 ± 0.03600
X-intercept when Y=0.0	116.1
1/slope	-97.94
95% Confidence Intervals	
Slope	-0.01370 to -0.006717
Y-intercept when X=0.0	1.107 to 1.264
X-intercept when Y=0.0	90.67 to 167.6
Goodness of Fit	
R square	0.7716
Sy.x	0.08319
Is slope significantly non-zero?	
F	40.55
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



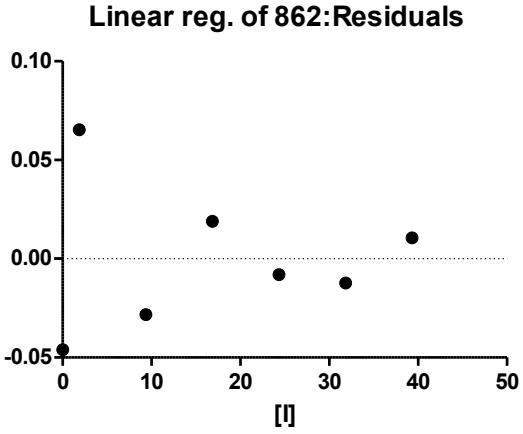


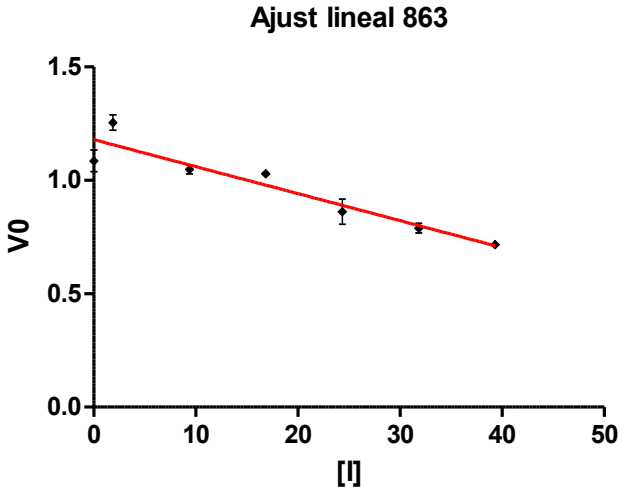
Best-fit values	
Slope	-0.01033 ± 0.004156
Y-intercept when X=0.0	1.101 ± 0.09331
X-intercept when Y=0.0	106.6
1/slope	-96.80
95% Confidence Intervals	
Slope	-0.01939 to -0.001275
Y-intercept when X=0.0	0.8978 to 1.304
X-intercept when Y=0.0	64.10 to 739.2
Goodness of Fit	
R square	0.3399
Sy.x	0.2156
Is slope significantly non-zero?	
F	6.179
DFn, DFd	1.000, 12.00
P value	0.0287
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



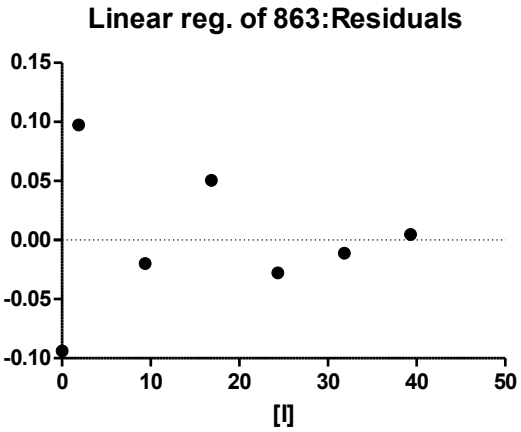


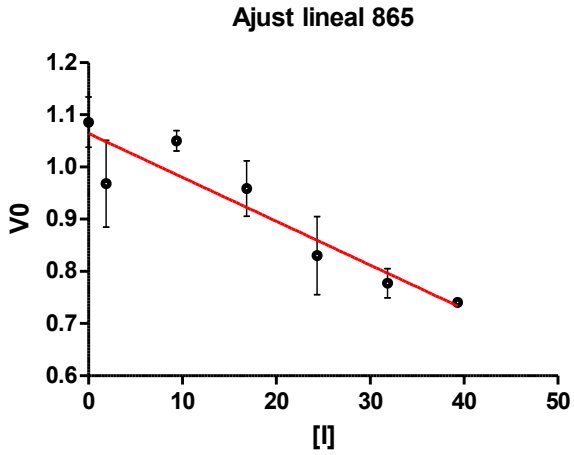
Best-fit values	
Slope	-0.007641 ± 0.001141
Y-intercept when X=0.0	1.132 ± 0.02562
X-intercept when Y=0.0	148.2
1/slope	-130.9
95% Confidence Intervals	
Slope	-0.01013 to -0.005154
Y-intercept when X=0.0	1.076 to 1.188
X-intercept when Y=0.0	115.9 to 211.3
Goodness of Fit	
R square	0.7889
Sy.x	0.05920
Is slope significantly non-zero?	
F	44.84
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



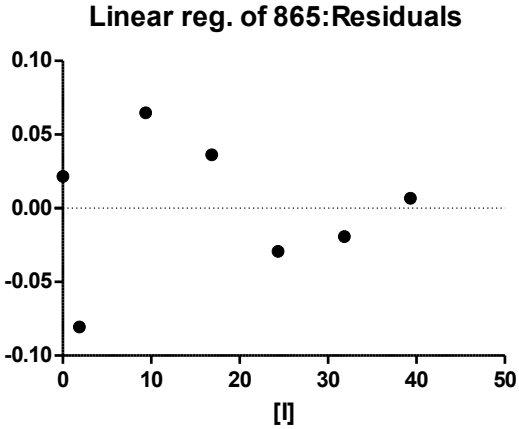


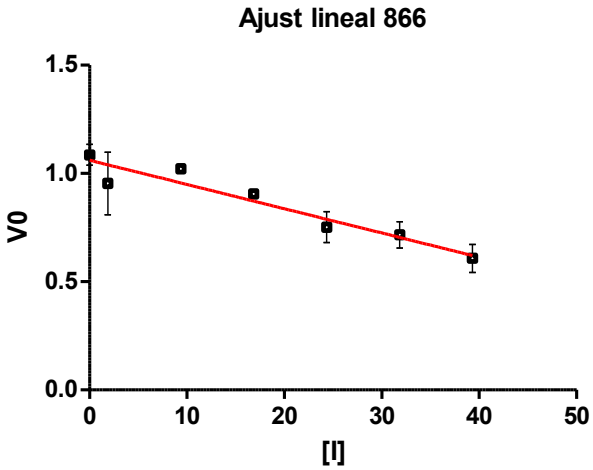
Best-fit values	
Slope	-0.01190 ± 0.001353
Y-intercept when X=0.0	1.180 ± 0.03037
X-intercept when Y=0.0	99.12
1/slope	-84.02
95% Confidence Intervals	
Slope	-0.01485 to -0.008954
Y-intercept when X=0.0	1.114 to 1.246
X-intercept when Y=0.0	82.66 to 126.2
Goodness of Fit	
R square	0.8658
Sy.x	0.07019
Is slope significantly non-zero?	
F	77.41
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



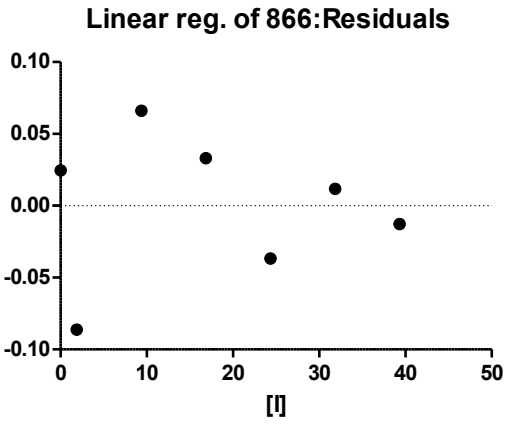


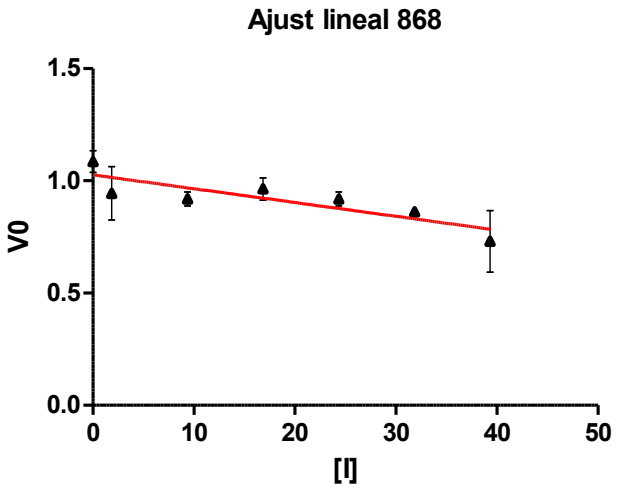
Best-fit values	
Slope	-0.008408 ± 0.001420
Y-intercept when X=0.0	1.064 ± 0.03189
X-intercept when Y=0.0	126.6
1/slope	-118.9
95% Confidence Intervals	
Slope	-0.01150 to -0.005313
Y-intercept when X=0.0	0.9948 to 1.134
X-intercept when Y=0.0	96.95 to 190.4
Goodness of Fit	
R square	0.7449
Sy.x	0.07370
Is slope significantly non-zero?	
F	35.04
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



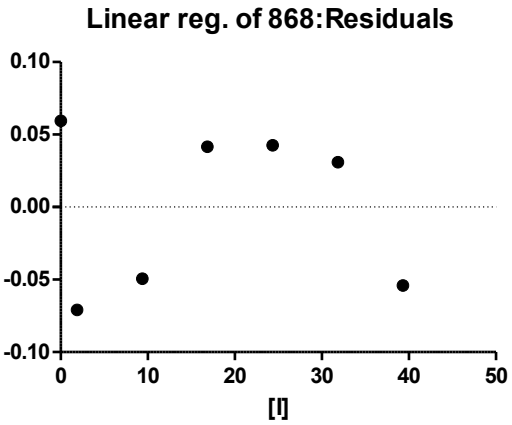


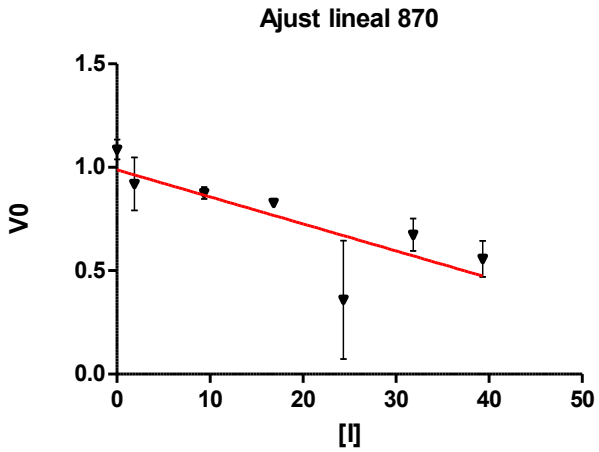
Best-fit values	
Slope	-0.01120 ± 0.001785
Y-intercept when X=0.0	1.061 ± 0.04009
X-intercept when Y=0.0	94.72
1/slope	-89.25
95% Confidence Intervals	
Slope	-0.01510 to -0.007314
Y-intercept when X=0.0	0.9740 to 1.149
X-intercept when Y=0.0	74.43 to 136.1
Goodness of Fit	
R square	0.7665
Sy.x	0.09264
Is slope significantly non-zero?	
F	39.38
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



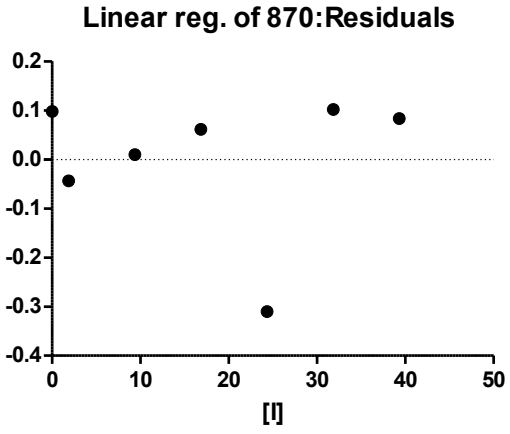


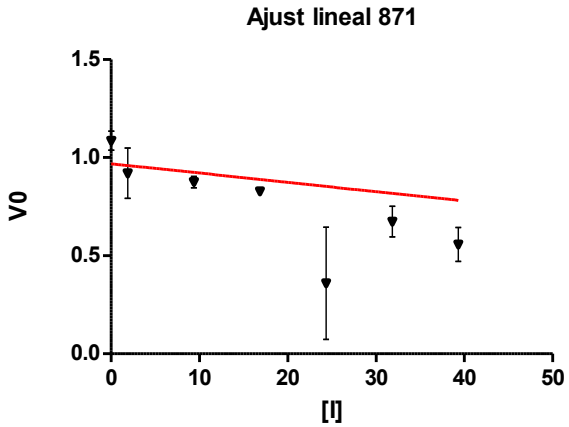
Best-fit values	
Slope	-0.006152 ± 0.001900
Y-intercept when X=0.0	1.026 ± 0.04267
X-intercept when Y=0.0	166.9
1/slope	-162.6
95% Confidence Intervals	
Slope	-0.01029 to -0.002011
Y-intercept when X=0.0	0.9335 to 1.119
X-intercept when Y=0.0	106.4 to 474.5
Goodness of Fit	
R square	0.4662
Sy.x	0.09859
Is slope significantly non-zero?	
F	10.48
DFn, DFd	1.000, 12.00
P value	0.0071
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



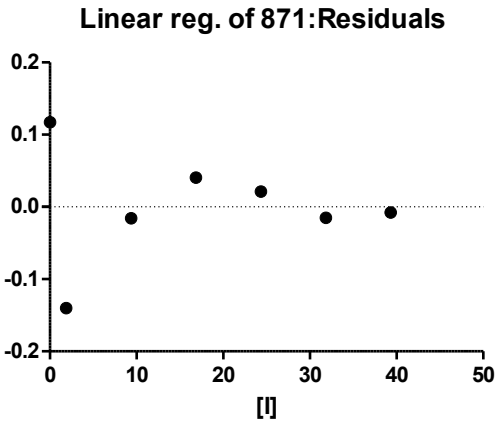


Best-fit values	
Slope	-0.01307 ± 0.003888
Y-intercept when X=0.0	0.9879 ± 0.08729
X-intercept when Y=0.0	75.60
1/slope	-76.52
95% Confidence Intervals	
Slope	-0.02154 to -0.004597
Y-intercept when X=0.0	0.7977 to 1.178
X-intercept when Y=0.0	51.74 to 183.4
Goodness of Fit	
R square	0.4850
Sy.x	0.2017
Is slope significantly non-zero?	
F	11.30
DFn, DFd	1.000, 12.00
P value	0.0057
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0

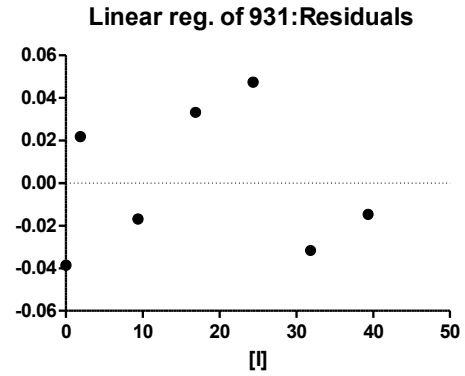


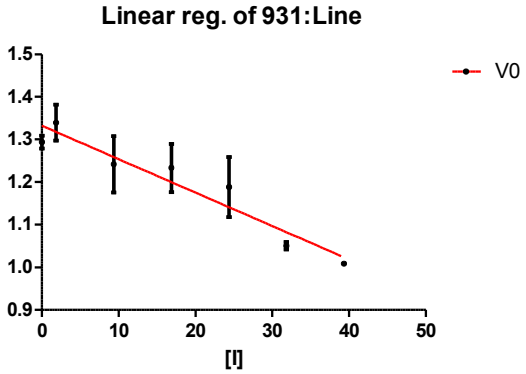


Best-fit values	
Slope	-0.004742 ± 0.001942
Y-intercept when X=0.0	0.9687 ± 0.04361
X-intercept when Y=0.0	204.3
1/slope	-210.9
95% Confidence Intervals	
Slope	-0.008974 to -0.0005090
Y-intercept when X=0.0	0.8736 to 1.064
X-intercept when Y=0.0	115.8 to 1757
Goodness of Fit	
R square	0.3318
Sy.x	0.1008
Is slope significantly non-zero?	
F	5.959
DFn, DFd	1.000, 12.00
P value	0.0311
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0

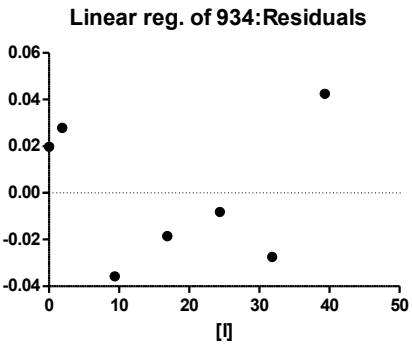


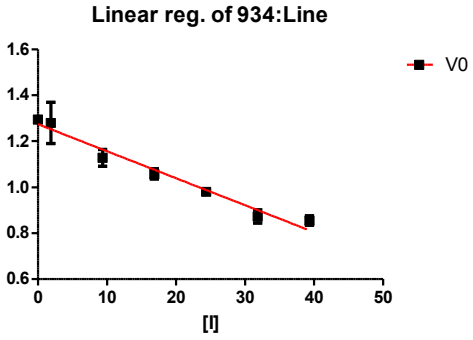
Best-fit values	
Slope	-0.007856 ± 0.001152
Y-intercept when X=0.0	1.332 ± 0.02589
X-intercept when Y=0.0	169.6
1/slope	-127.3
95% Confidence Intervals	
Slope	-0.01037 to -0.005345
Y-intercept when X=0.0	1.276 to 1.389
X-intercept when Y=0.0	132.6 to 241.2
Goodness of Fit	
R square	0.7948
Sy.x	0.05983
Is slope significantly non-zero?	
F	46.48
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



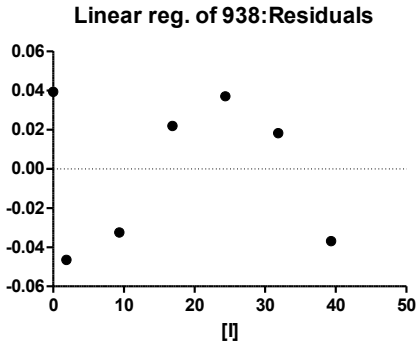


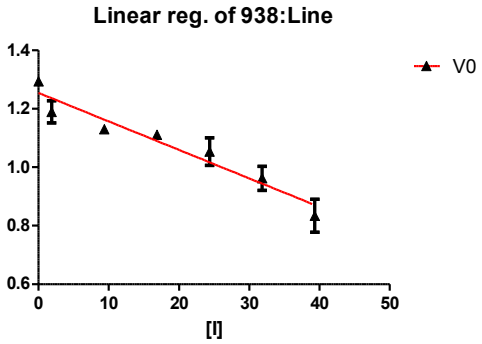
Best-fit values	
Slope	-0.01176 ± 0.001016
Y-intercept when X=0.0	1.274 ± 0.02284
X-intercept when Y=0.0	108.4
1/slope	-85.06
95% Confidence Intervals	
Slope	-0.01397 to -0.009542
Y-intercept when X=0.0	1.224 to 1.324
X-intercept when Y=0.0	93.80 to 129.6
Goodness of Fit	
R square	0.9177
Sy.x	0.05278
Is slope significantly non-zero?	
F	133.8
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



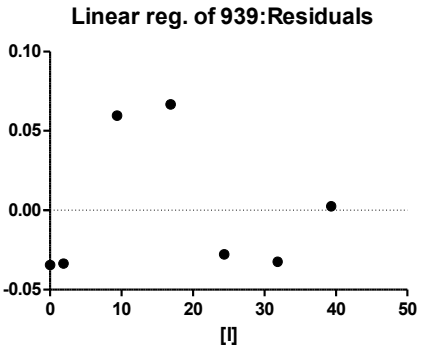


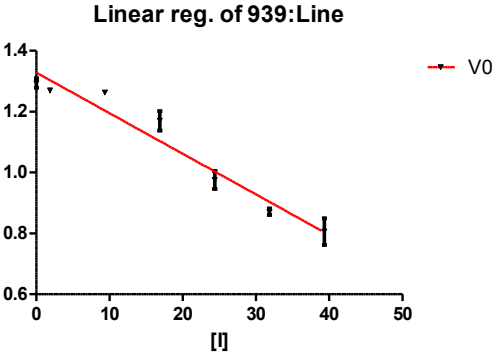
Best-fit values	
Slope	-0.009750 ± 0.001027
Y-intercept when X=0.0	1.255 ± 0.02307
X-intercept when Y=0.0	128.7
1/slope	-102.6
95% Confidence Intervals	
Slope	-0.01199 to -0.007513
Y-intercept when X=0.0	1.204 to 1.305
X-intercept when Y=0.0	107.8 to 161.9
Goodness of Fit	
R square	0.8826
Sy.x	0.05331
Is slope significantly non-zero?	
F	90.19
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



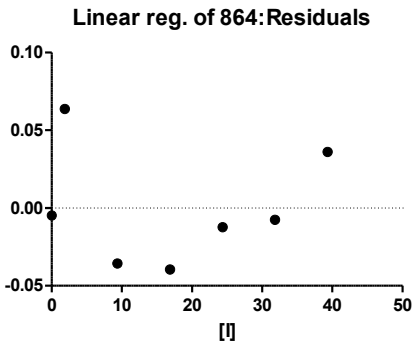


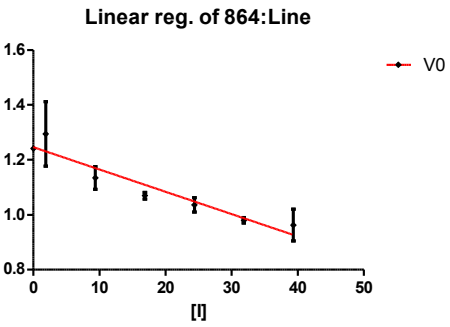
Best-fit values	
Slope	-0.01333 ± 0.001002
Y-intercept when X=0.0	1.328 ± 0.02253
X-intercept when Y=0.0	99.63
1/slope	-75.01
95% Confidence Intervals	
Slope	-0.01552 to -0.01115
Y-intercept when X=0.0	1.279 to 1.377
X-intercept when Y=0.0	87.90 to 115.9
Goodness of Fit	
R square	0.9365
Sy.x	0.05205
Is slope significantly non-zero?	
F	176.9
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



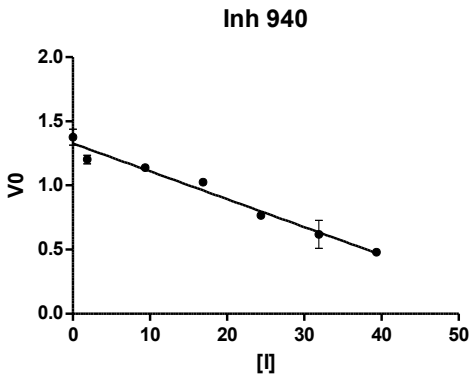


Best-fit values	
Slope	-0.006852 ± 0.0008045
Y-intercept when X=0.0	1.208 ± 0.01875
X-intercept when Y=0.0	176.3
1/slope	-145.9
95% Confidence Intervals	
Slope	-0.008622 to -0.005081
Y-intercept when X=0.0	1.167 to 1.249
X-intercept when Y=0.0	143.8 to 231.3
Goodness of Fit	
R square	0.8683
Sy.x	0.03964
Is slope significantly non-zero?	
F	72.53
DFn, DFd	1.000, 11.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	13
Number of missing values	1

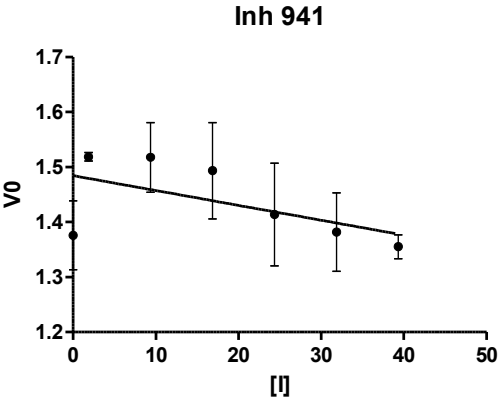




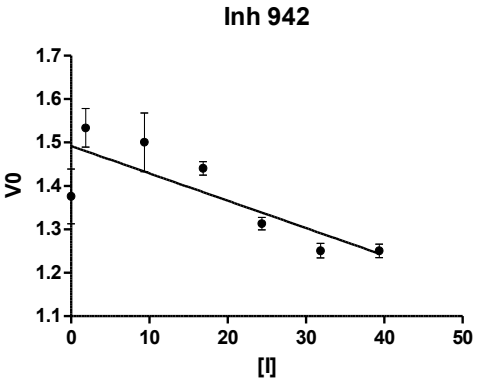
Best-fit values	
Slope	-0.02171 ± 0.001431
Y-intercept when X=0.0	1.328 ± 0.03216
X-intercept when Y=0.0	61.14
1/slope	-46.05
95% Confidence Intervals	
Slope	-0.02483 to -0.01859
Y-intercept when X=0.0	1.258 to 1.398
X-intercept when Y=0.0	55.37 to 68.74
Goodness of Fit	
R square	0.9504
Sy.x	0.07432
Is slope significantly non-zero?	
F	230.2
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



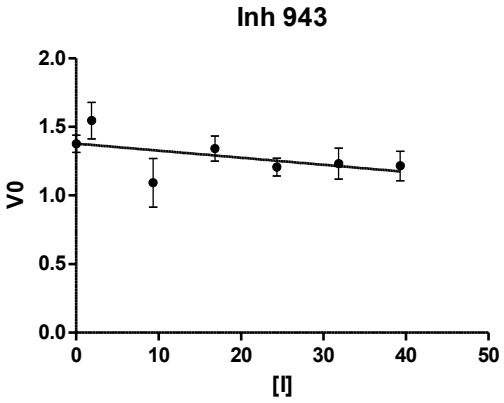
Best-fit values	
Slope	-0.002700 ± 0.001764
Y-intercept when X=0.0	1.484 ± 0.03965
X-intercept when Y=0.0	549.7
1/slope	-370.3
95% Confidence Intervals	
Slope	-0.006545 to 0.001144
Y-intercept when X=0.0	1.398 to 1.571
X-intercept when Y=0.0	236.9 to +infinity
Goodness of Fit	
R square	0.1633
Sy.x	0.09163
Is slope significantly non-zero?	
F	2.342
DFn, DFd	1.000, 12.00
P value	0.1518
Deviation from zero?	Not Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



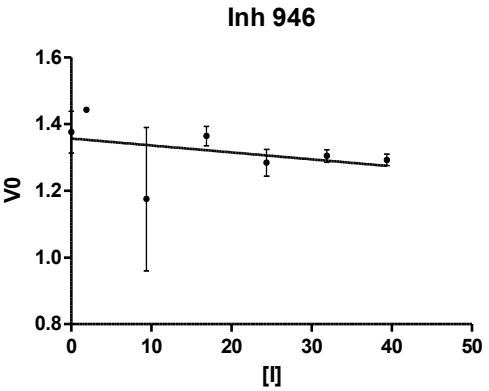
Best-fit values	
Slope	-0.006298 ± 0.001525
Y-intercept when X=0.0	1.492 ± 0.03427
X-intercept when Y=0.0	236.9
1/slope	-158.8
95% Confidence Intervals	
Slope	-0.009621 to -0.002975
Y-intercept when X=0.0	1.418 to 1.567
X-intercept when Y=0.0	161.0 to 482.0
Goodness of Fit	
R square	0.5870
Sy.x	0.07920
Is slope significantly non-zero?	
F	17.06
DFn, DFd	1.000, 12.00
P value	0.0014
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



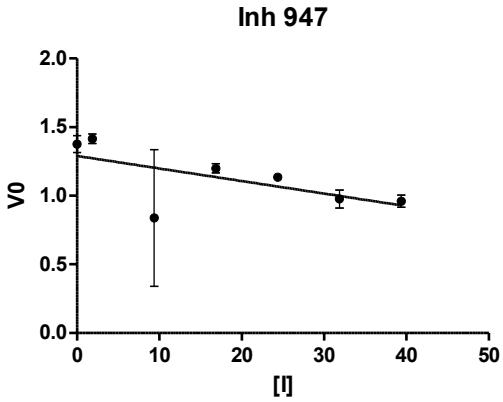
Best-fit values	
Slope	-0.005158 ± 0.003371
Y-intercept when X=0.0	1.378 ± 0.07568
X-intercept when Y=0.0	267.2
1/slope	-193.9
95% Confidence Intervals	
Slope	-0.01250 to 0.002186
Y-intercept when X=0.0	1.213 to 1.543
X-intercept when Y=0.0	120.1 to +infinity
Goodness of Fit	
R square	0.1633
Sy.x	0.1749
Is slope significantly non-zero?	
F	2.342
DFn, DFd	1.000, 12.00
P value	0.1519
Deviation from zero?	Not Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



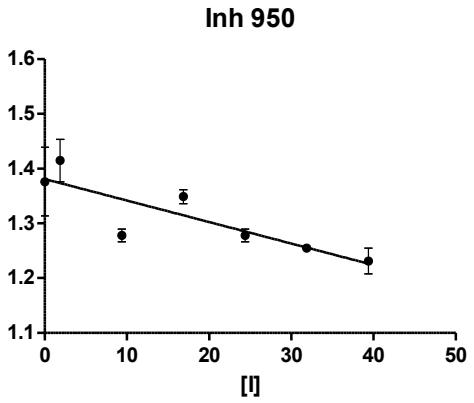
Best-fit values	
Slope	-0.002086 ± 0.002371
Y-intercept when X=0.0	1.357 ± 0.05331
X-intercept when Y=0.0	650.7
1/slope	-479.4
95% Confidence Intervals	
Slope	-0.007253 to 0.003081
Y-intercept when X=0.0	1.241 to 1.473
X-intercept when Y=0.0	199.4 to +infinity
Goodness of Fit	
R square	0.06057
Sy.x	0.1232
Is slope significantly non-zero?	
F	0.7737
DFn, DFd	1.000, 12.00
P value	0.3963
Deviation from zero?	Not Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



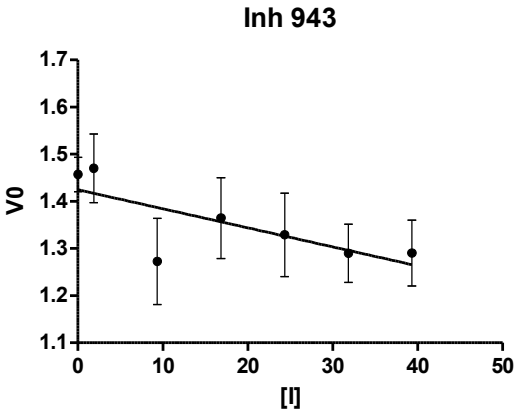
Best-fit values	
Slope	-0.009150 ± 0.005175
Y-intercept when X=0.0	1.290 ± 0.1163
X-intercept when Y=0.0	141.0
1/slope	-109.3
95% Confidence Intervals	
Slope	-0.02043 to 0.002126
Y-intercept when X=0.0	1.037 to 1.544
X-intercept when Y=0.0	71.95 to +infinity
Goodness of Fit	
R square	0.2067
Sy.x	0.2688
Is slope significantly non-zero?	
F	3.127
DFn, DFd	1.000, 12.00
P value	0.1024
Deviation from zero?	Not Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



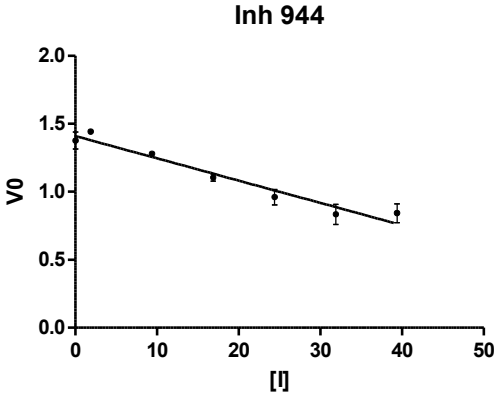
Best-fit values	
Slope	-0.003929 ± 0.0009241
Y-intercept when X=0.0	1.381 ± 0.02077
X-intercept when Y=0.0	351.5
1/slope	-254.5
95% Confidence Intervals	
Slope	-0.005942 to -0.001915
Y-intercept when X=0.0	1.336 to 1.426
X-intercept when Y=0.0	238.2 to 702.6
Goodness of Fit	
R square	0.6010
Sy.x	0.04799
Is slope significantly non-zero?	
F	18.08
DFn, DFd	1.000, 12.00
P value	0.0011
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



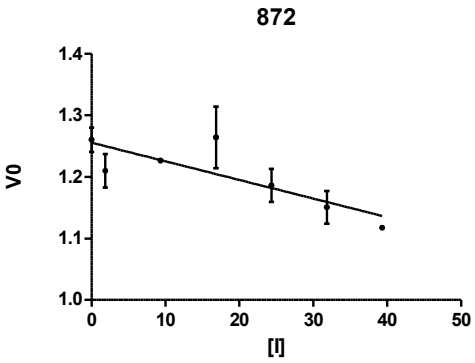
Best-fit values	
Slope	-0.004040 ± 0.001869
Y-intercept when X=0.0	1.425 ± 0.04197
X-intercept when Y=0.0	352.7
1/slope	-247.5
95% Confidence Intervals	
Slope	-0.008114 to 3.336e-005
Y-intercept when X=0.0	1.333 to 1.516
X-intercept when Y=0.0	184.2 to +infinity
Goodness of Fit	
R square	0.2802
Sy.x	0.09700
Is slope significantly non-zero?	
F	4.671
DFn, DFd	1.000, 12.00
P value	0.0516
Deviation from zero?	Not Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



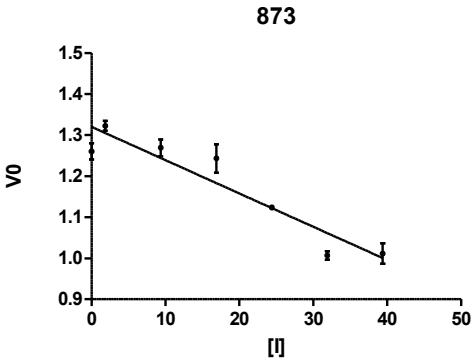
Best-fit values	
Slope	-0.01638 ± 0.001497
Y-intercept when X=0.0	1.410 ± 0.03365
X-intercept when Y=0.0	86.08
1/slope	-61.07
95% Confidence Intervals	
Slope	-0.01964 to -0.01311
Y-intercept when X=0.0	1.336 to 1.483
X-intercept when Y=0.0	74.44 to 103.4
Goodness of Fit	
R square	0.9089
Sy.x	0.07776
Is slope significantly non-zero?	
F	119.7
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



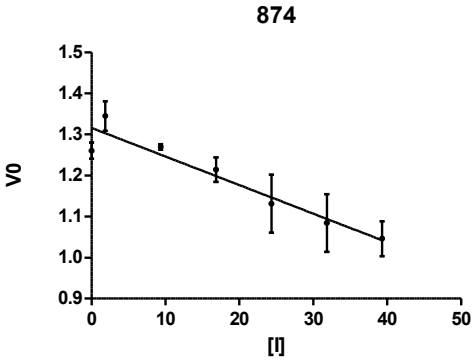
Best-fit values	
Slope	-0.003029 ± 0.0008625
Y-intercept when X=0.0	1.256 ± 0.01997
X-intercept when Y=0.0	414.5
1/slope	-330.1
95% Confidence Intervals	
Slope	-0.004928 to -0.001131
Y-intercept when X=0.0	1.212 to 1.300
X-intercept when Y=0.0	261.7 to 1080
Goodness of Fit	
R square	0.5286
Sy.x	0.04413
Is slope significantly non-zero?	
F	12.33
DFn, DFd	1.000, 11.00
P value	0.0049
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	13
Number of missing values	1



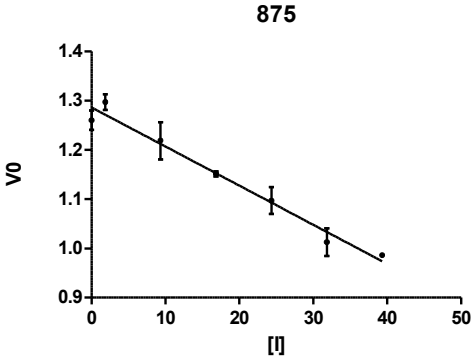
Best-fit values	
Slope	-0.008123 ± 0.0009357
Y-intercept when X=0.0	1.321 ± 0.02103
X-intercept when Y=0.0	162.6
1/slope	-123.1
95% Confidence Intervals	
Slope	-0.01016 to -0.006086
Y-intercept when X=0.0	1.275 to 1.366
X-intercept when Y=0.0	133.3 to 211.2
Goodness of Fit	
R square	0.8628
Sy.x	0.04860
Is slope significantly non-zero?	
F	75.46
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



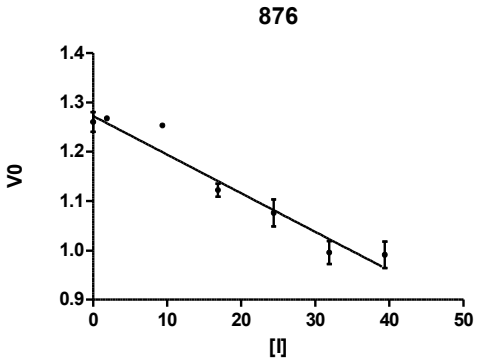
Best-fit values	
Slope	-0.006970 ± 0.001121
Y-intercept when X=0.0	1.316 ± 0.02517
X-intercept when Y=0.0	188.8
1/slope	-143.5
95% Confidence Intervals	
Slope	-0.009413 to -0.004528
Y-intercept when X=0.0	1.261 to 1.371
X-intercept when Y=0.0	144.2 to 281.4
Goodness of Fit	
R square	0.7632
Sy.x	0.05816
Is slope significantly non-zero?	
F	38.67
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



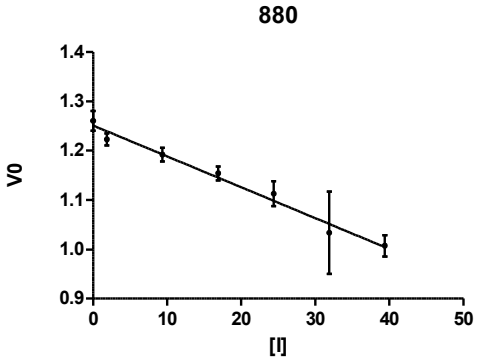
Best-fit values	
Slope	-0.007951 ± 0.0005899
Y-intercept when X=0.0	1.287 ± 0.01325
X-intercept when Y=0.0	161.8
1/slope	-125.8
95% Confidence Intervals	
Slope	-0.009236 to -0.006666
Y-intercept when X=0.0	1.258 to 1.315
X-intercept when Y=0.0	141.6 to 189.7
Goodness of Fit	
R square	0.9380
Sy.x	0.03061
Is slope significantly non-zero?	
F	181.7
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



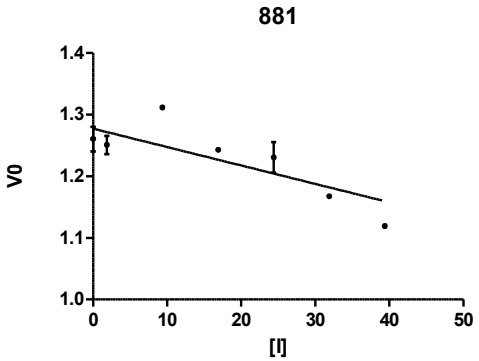
Best-fit values	
Slope	-0.007826 ± 0.0006509
Y-intercept when X=0.0	1.273 ± 0.01510
X-intercept when Y=0.0	162.6
1/slope	-127.8
95% Confidence Intervals	
Slope	-0.009259 to -0.006393
Y-intercept when X=0.0	1.239 to 1.306
X-intercept when Y=0.0	140.2 to 195.1
Goodness of Fit	
R square	0.9293
Sy.x	0.03336
Is slope significantly non-zero?	
F	144.5
DFn, DFd	1.000, 11.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	13
Number of missing values	1



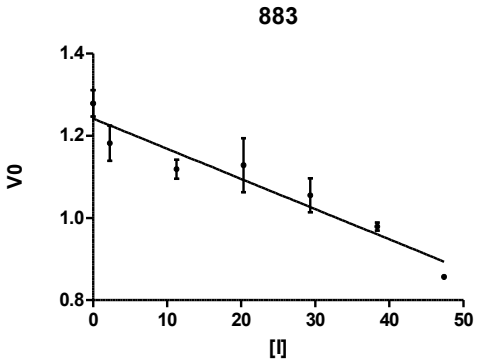
Best-fit values	
Slope	-0.006257 ± 0.0007827
Y-intercept when X=0.0	1.251 ± 0.01761
X-intercept when Y=0.0	200.0
1/slope	-159.8
95% Confidence Intervals	
Slope	-0.007962 to -0.004551
Y-intercept when X=0.0	1.213 to 1.289
X-intercept when Y=0.0	160.8 to 268.4
Goodness of Fit	
R square	0.8419
Sy.x	0.04069
Is slope significantly non-zero?	
F	63.90
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



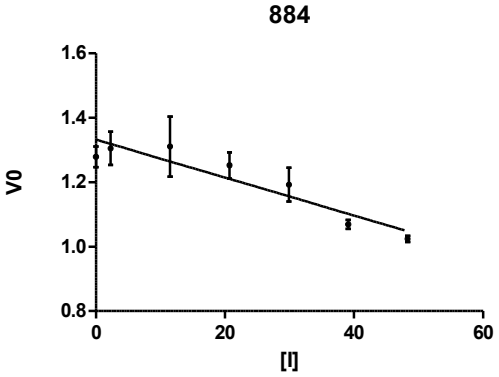
Best-fit values	
Slope	-0.002987 ± 0.0008626
Y-intercept when X=0.0	1.277 ± 0.01756
X-intercept when Y=0.0	427.6
1/slope	-334.8
95% Confidence Intervals	
Slope	-0.004976 to -0.000997
Y-intercept when X=0.0	1.237 to 1.318
X-intercept when Y=0.0	262.5 to 1250
Goodness of Fit	
R square	0.5998
Sy.x	0.03748
Is slope significantly non-zero?	
F	11.99
DFn, DFd	1.000, 8.000
P value	0.0085
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	10
Number of missing values	4



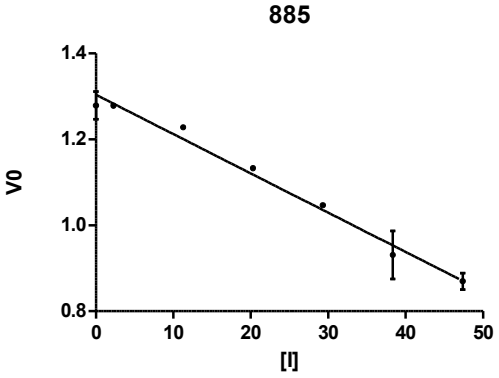
Best-fit values	
Slope	-0.007340 ± 0.0008822
Y-intercept when X=0.0	1.242 ± 0.02388
X-intercept when Y=0.0	169.2
1/slope	-136.2
95% Confidence Intervals	
Slope	-0.009262 to -0.005417
Y-intercept when X=0.0	1.190 to 1.294
X-intercept when Y=0.0	138.3 to 221.9
Goodness of Fit	
R square	0.8522
Sy.x	0.05517
Is slope significantly non-zero?	
F	69.22
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



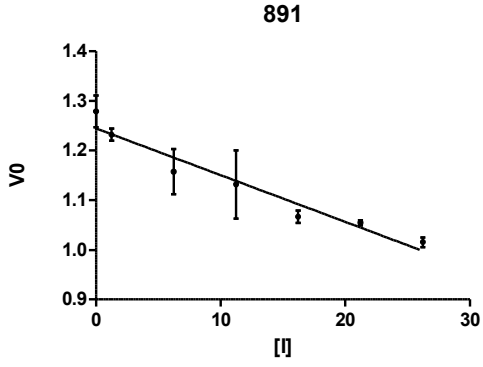
Best-fit values	
Slope	-0.005885 ± 0.001050
Y-intercept when X=0.0	1.332 ± 0.02897
X-intercept when Y=0.0	226.4
1/slope	-169.9
95% Confidence Intervals	
Slope	-0.008174 to -0.003596
Y-intercept when X=0.0	1.269 to 1.395
X-intercept when Y=0.0	168.8 to 357.0
Goodness of Fit	
R square	0.7235
Sy.x	0.06694
Is slope significantly non-zero?	
F	31.39
DFn, DFd	1.000, 12.00
P value	0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



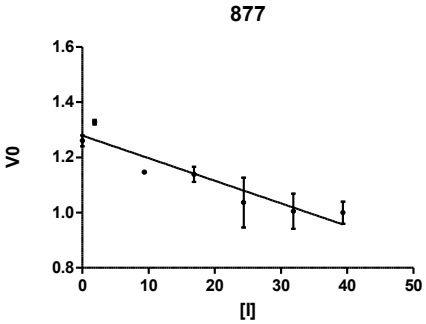
Best-fit values	
Slope	-0.009130 ± 0.0005358
Y-intercept when X=0.0	1.303 ± 0.01449
X-intercept when Y=0.0	142.8
1/slope	-109.5
95% Confidence Intervals	
Slope	-0.01030 to -0.007962
Y-intercept when X=0.0	1.272 to 1.335
X-intercept when Y=0.0	128.9 to 160.7
Goodness of Fit	
R square	0.9603
Sy.x	0.03348
Is slope significantly non-zero?	
F	290.3
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



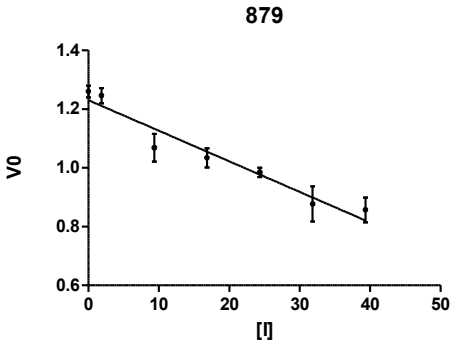
Best-fit values	
Slope	-0.009408 ± 0.001259
Y-intercept when X=0.0	1.245 ± 0.01884
X-intercept when Y=0.0	132.3
1/slope	-106.3
95% Confidence Intervals	
Slope	-0.01215 to -0.006666
Y-intercept when X=0.0	1.203 to 1.286
X-intercept when Y=0.0	105.0 to 182.0
Goodness of Fit	
R square	0.8232
Sy.x	0.04355
Is slope significantly non-zero?	
F	55.87
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



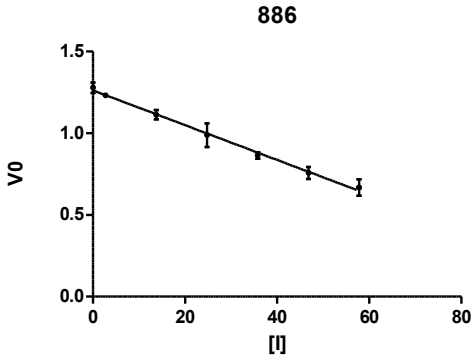
Best-fit values	
Slope	-0.008193 ± 0.001318
Y-intercept when X=0.0	1.279 ± 0.03054
X-intercept when Y=0.0	156.2
1/slope	-122.1
95% Confidence Intervals	
Slope	-0.01109 to -0.005293
Y-intercept when X=0.0	1.212 to 1.347
X-intercept when Y=0.0	119.9 to 231.9
Goodness of Fit	
R square	0.7785
Sy.x	0.06749
Is slope significantly non-zero?	
F	38.66
DFn, DFd	1.000, 11.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	13
Number of missing values	1



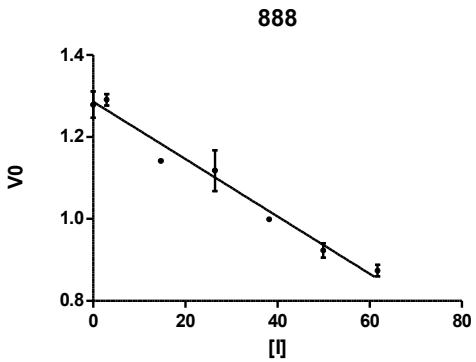
Best-fit values	
Slope	-0.01042 ± 0.001072
Y-intercept when X=0.0	1.231 ± 0.02408
X-intercept when Y=0.0	118.2
1/slope	-96.00
95% Confidence Intervals	
Slope	-0.01275 to -0.008079
Y-intercept when X=0.0	1.178 to 1.283
X-intercept when Y=0.0	99.54 to 147.5
Goodness of Fit	
R square	0.8871
Sy.x	0.05565
Is slope significantly non-zero?	
F	94.33
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0

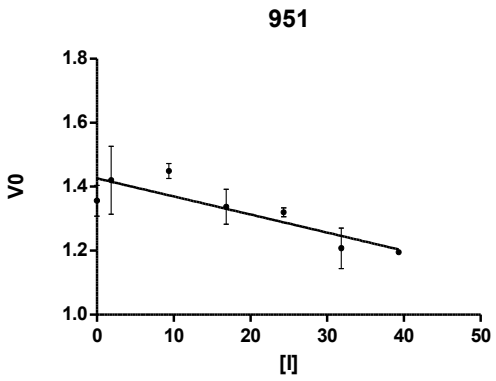


Best-fit values	
Slope	-0.01063 ± 0.0005986
Y-intercept when X=0.0	1.262 ± 0.01976
X-intercept when Y=0.0	118.7
1/slope	-94.03
95% Confidence Intervals	
Slope	-0.01194 to -0.009330
Y-intercept when X=0.0	1.219 to 1.305
X-intercept when Y=0.0	108.3 to 131.9
Goodness of Fit	
R square	0.9634
Sy.x	0.04566
Is slope significantly non-zero?	
F	315.7
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0

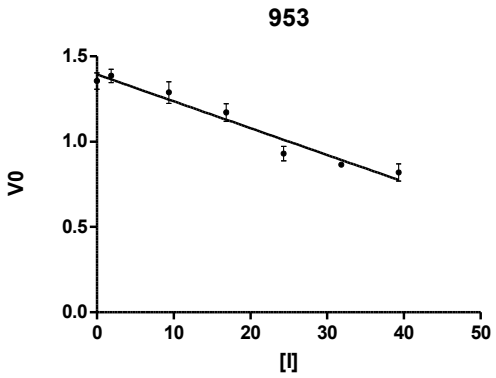


Best-fit values	
Slope	-0.007006 ± 0.0004435
Y-intercept when X=0.0	1.287 ± 0.01611
X-intercept when Y=0.0	183.6
1/slope	-142.7
95% Confidence Intervals	
Slope	-0.007982 to -0.006030
Y-intercept when X=0.0	1.251 to 1.322
X-intercept when Y=0.0	164.5 to 208.9
Goodness of Fit	
R square	0.9578
Sy.x	0.03560
Is slope significantly non-zero?	
F	249.6
DFn, DFd	1.000, 11.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	13
Number of missing values	1

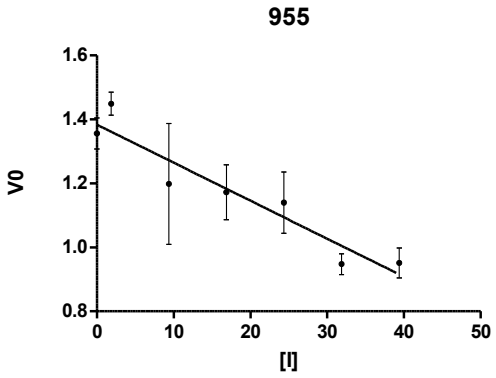




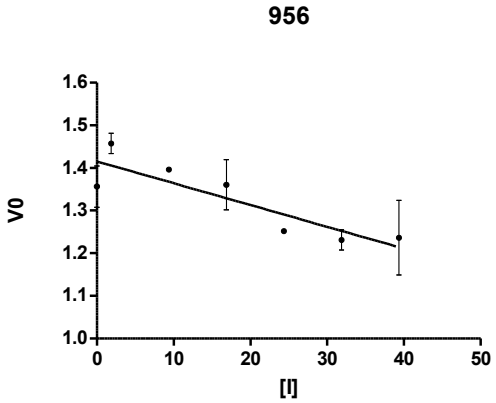
Best-fit values	
Slope	-0.005657 ± 0.001462
Y-intercept when X=0.0	1.426 ± 0.03284
X-intercept when Y=0.0	252.2
1/slope	-176.8
95% Confidence Intervals	
Slope	-0.008843 to -0.002470
Y-intercept when X=0.0	1.355 to 1.498
X-intercept when Y=0.0	167.4 to 554.9
Goodness of Fit	
R square	0.5549
Sy.x	0.07587
Is slope significantly non-zero?	
F	14.96
DFn, DFd	1.000, 12.00
P value	0.0022
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



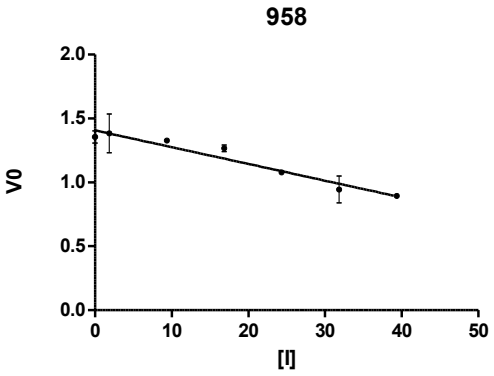
Best-fit values	
Slope	-0.01575 ± 0.001357
Y-intercept when X=0.0	1.395 ± 0.03046
X-intercept when Y=0.0	88.58
1/slope	-63.49
95% Confidence Intervals	
Slope	-0.01871 to -0.01279
Y-intercept when X=0.0	1.329 to 1.461
X-intercept when Y=0.0	77.12 to 105.2
Goodness of Fit	
R square	0.9183
Sy.x	0.07038
Is slope significantly non-zero?	
F	134.8
DFn, DFd	1.000, 12.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



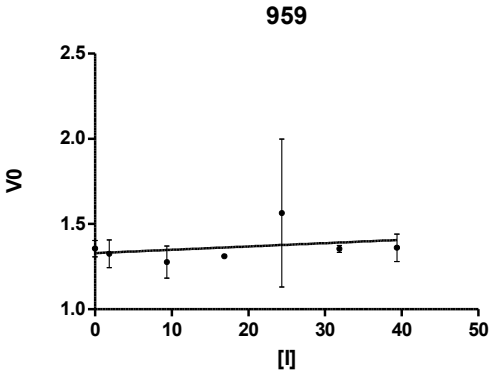
Best-fit values	
Slope	-0.01190 ± 0.002223
Y-intercept when X=0.0	1.384 ± 0.04999
X-intercept when Y=0.0	116.3
1/slope	-84.07
95% Confidence Intervals	
Slope	-0.01674 to -0.007050
Y-intercept when X=0.0	1.275 to 1.493
X-intercept when Y=0.0	87.39 to 184.5
Goodness of Fit	
R square	0.7046
Sy.x	0.1155
Is slope significantly non-zero?	
F	28.62
DFn, DFd	1.000, 12.00
P value	0.0002
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



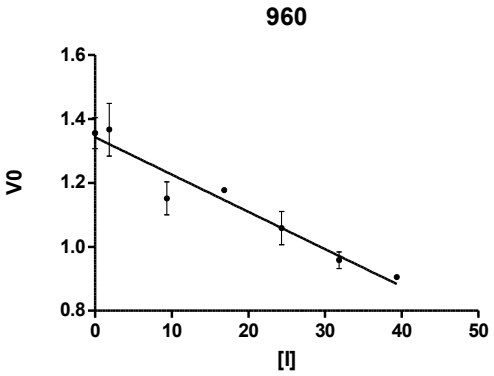
Best-fit values	
Slope	-0.005113 ± 0.001305
Y-intercept when X=0.0	1.415 ± 0.03024
X-intercept when Y=0.0	276.8
1/slope	-195.6
95% Confidence Intervals	
Slope	-0.007985 to -0.002241
Y-intercept when X=0.0	1.349 to 1.482
X-intercept when Y=0.0	183.6 to 608.2
Goodness of Fit	
R square	0.5826
Sy.x	0.06682
Is slope significantly non-zero?	
F	15.36
DFn, DFd	1.000, 11.00
P value	0.0024
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	13
Number of missing values	1



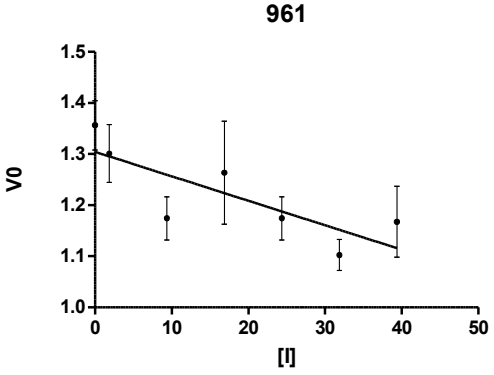
Best-fit values	
Slope	-0.01313 ± 0.001849
Y-intercept when X=0.0	1.407 ± 0.04283
X-intercept when Y=0.0	107.2
1/slope	-76.17
95% Confidence Intervals	
Slope	-0.01720 to -0.009059
Y-intercept when X=0.0	1.313 to 1.502
X-intercept when Y=0.0	85.81 to 147.5
Goodness of Fit	
R square	0.8209
Sy.x	0.09466
Is slope significantly non-zero?	
F	50.42
DFn, DFd	1.000, 11.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	13
Number of missing values	1



Best-fit values	
Slope	0.001954 ± 0.004013
Y-intercept when X=0.0	1.329 ± 0.09022
X-intercept when Y=0.0	-680.4
1/slope	511.7
95% Confidence Intervals	
Slope	-0.006790 to 0.01070
Y-intercept when X=0.0	1.133 to 1.526
X-intercept when Y=0.0	-infinity to -109.2
Goodness of Fit	
R square	0.01938
Sy.x	0.2085
Is slope significantly non-zero?	
F	0.2371
DFn, DFd	1.000, 12.00
P value	0.6351
Deviation from zero?	Not Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0



Best-fit values	
Slope	-0.01168 ± 0.001303
Y-intercept when X=0.0	1.343 ± 0.02976
X-intercept when Y=0.0	115.0
1/slope	-85.60
95% Confidence Intervals	
Slope	-0.01455 to -0.008814
Y-intercept when X=0.0	1.278 to 1.409
X-intercept when Y=0.0	95.55 to 146.9
Goodness of Fit	
R square	0.8796
Sy.x	0.06763
Is slope significantly non-zero?	
F	80.35
DFn, DFd	1.000, 11.00
P value	< 0.0001
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	13
Number of missing values	1



Best-fit values	
Slope	-0.004789 ± 0.001609
Y-intercept when X=0.0	1.305 ± 0.03615
X-intercept when Y=0.0	272.4
1/slope	-208.8
95% Confidence Intervals	
Slope	-0.008295 to -0.001284
Y-intercept when X=0.0	1.226 to 1.383
X-intercept when Y=0.0	164.5 to 968.0
Goodness of Fit	
R square	0.4248
Sy.x	0.08355
Is slope significantly non-zero?	
F	8.864
DFn, DFd	1.000, 12.00
P value	0.0115
Deviation from zero?	Significant
Data	
Number of X values	7
Maximum number of Y replicates	2
Total number of values	14
Number of missing values	0

Table A-3. Summary of top-down MS characterization of wild type (wt) and V30M TTR Cys-10 PTM isoforms

PTM	TTR	Fragmentation	Ion	Observed m	Theoretical m	Δm[a]	ppm
Free Cys	wt		983.94	13753.0116	13752.8800	-	9.57
		ECD	**pScore**	**pDE[b]**	**# fragments**	**# c-ions**	**# z-ions**
			0.991	6.61	2	0	2
		CID	**pScore**	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			0.991	6.61	10	0	10
S-Sulfo	wt		989.64	13832.8896	13832.8450	79.957	3.22
		ECD	**pScore**	**pDE[b]**	**# fragments**	**# c-ions**	**# z-ions**
			7.13E-04	97.50	3	0	3
		CID	**pScore**	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			0.069	3.55	9	6	3
S-Cys	wt		992.35	13871.9020	13871.8924	119	0.7
		ECD	**pScore**	**pDE[b]**	**# fragments**	**# c-ions**	**# z-ions**
			5.11E-11	73.20	12	5	7
		CID	**pScore**	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			2.94E-19	72.60	25	17	8
S-CysGly	wt		996.5	13928.8962	13928.9200	176.026	1.7
		ECD	**pScore**	**pDE[b]**	**# fragments**	**# c-ions**	**# z-ions**
			2.35E-34	39.40	97	53	44
		CID	**pScore**	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			1.16E-05	50.50	19	15	4
S-GSH	wt		1005.72	14057.1816	14057.9560	305.068	55[c]
		ECD	**pScore**	**pDE[b]**	**# fragments**	**# c-ions**	**# z-ions**
			1.29E-05	48.70	9	3	6
Free Cys	V30M		986.22	13784.8913	13784.8603	-	2.25
		CID	**pScore**	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			7.53E-01	4.41	6	1	5
S-Sulfo	V30M		991.93	13863.9136	13864.8173	79.957	65.18[d]
		CID	**pScore**	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			7.96E-01	3.62	4	0	4
S-Cys	V30M		994.71	13903.4582	13903.8644	119.004	0.73
		CID	**pScore**	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			1.77E-11	74.60	28	17	11
S-CysGly	V30M		998.79	13961.9241	13960.8863	176.026	74.3[c]
		CID	**pScore**	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			8.47E-05	16.70	11	3	8
S-GSH	V30M		1008.07	14089.9257	14089.9283	305.068	0.18
		CID	**pScore**	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			1.22E-04	35.10	7	5	2

[a] Mass difference compared to Free Cys form

[b] McLuckey score

[c] Isoform detected as a minor species. The monoisotopic mass could not be accurately measured due to bad ion statistics

[d] Deconvolution algorithm errors due to overlapping forms could account for the low accuracy determination of the monoisotopic mass of this form

Table A-4. Top-down MS identification of Free Cys wt TTR. ECD fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
ECD	Free Cys	wt	983.94	13753.0116	13752.8800	-	9.57
			pScore	**pDE[b]**	**# fragments**	**# c-ions**	**# z-ions**
			0.991	6.61	2	0	2

[a] Mass difference compared to Free Cys form

[b] McLuckey score

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
22	Z16	1726.8230	1726.8200	0.0055	3.2076
24	Z51	5624.8185	5624.8100	0.0055	0.9751

Figure A-1. Top-down deconvoluted MS/MS spectra of Free Cys wt TTR. ECD fragmentation

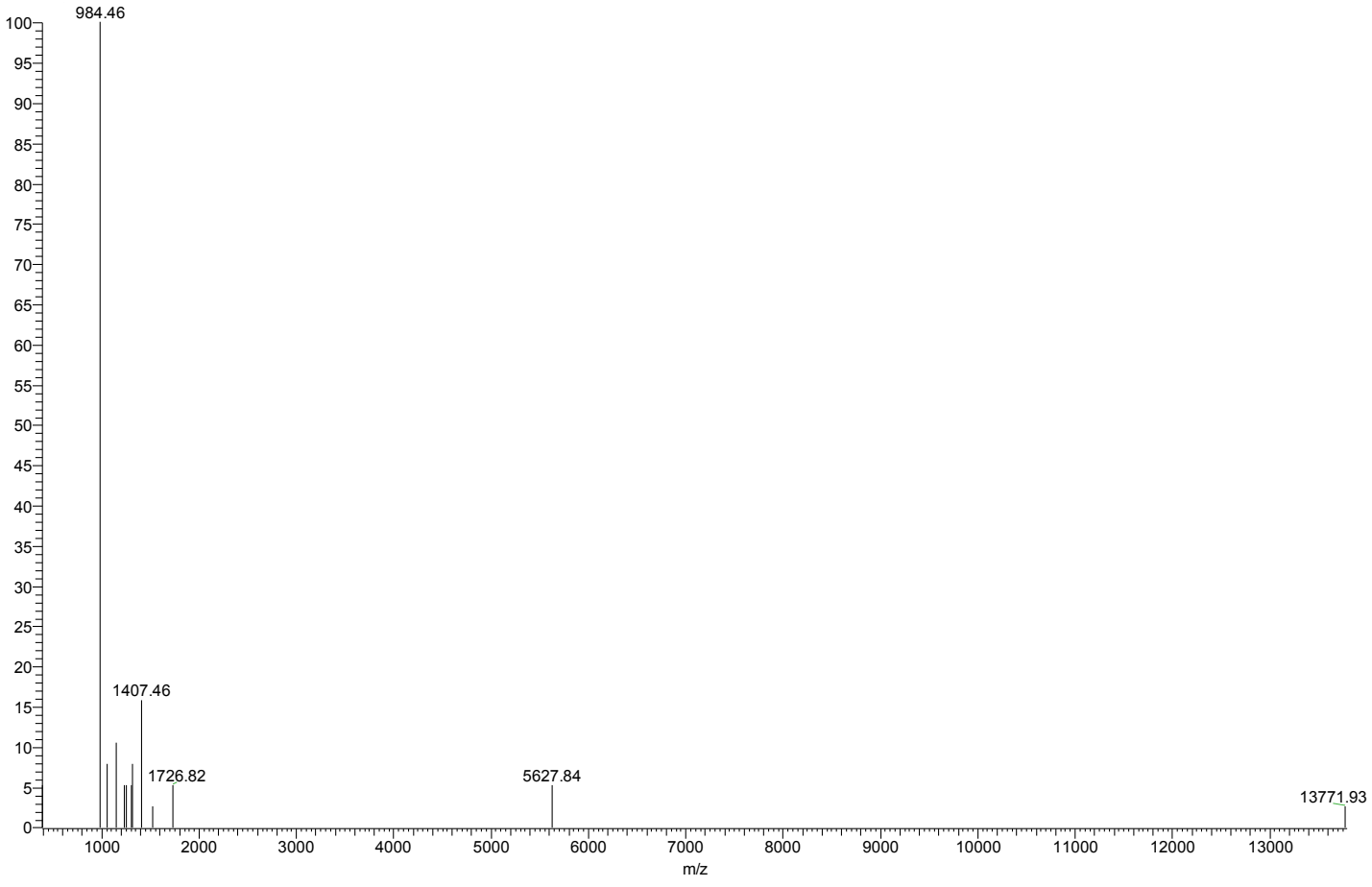


Table A-5. Top-down MS identification of Free Cys wt TTR. CID fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
CID	Free Cys	wt	983.94	13753.0116	13752.8800	-	9.57
			pScore	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			0.991	6.61	10	0	10

[a] Mass difference compared to Free Cys form

[b] McLuckey score

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
19	Y4	486.2438	486.2460	-0.0020	-4.0618
47	Y6	686.3600	686.3620	-0.0019	-2.7493
76	Y7	785.4279	785.4300	-0.0024	-3.0035
97	Y8	856.4654	856.4670	-0.0020	-2.3025
154	Y9	957.5131	957.5150	-0.0020	-2.1336
262	Y10	1058.5592	1058.5600	-0.0036	-3.3971
383	Y11	1145.5954	1145.5900	0.0006	0.5124
545	Y12	1308.6516	1308.6600	-0.0065	-4.9585
756	Y28	3041.5945	3041.5800	0.0103	3.3841
761	Y30	3270.6514	3270.6500	-0.0026	-0.7891

Figure A-2. Top-down deconvoluted MS/MS spectra of Free Cys wt TTR. CID fragmentation

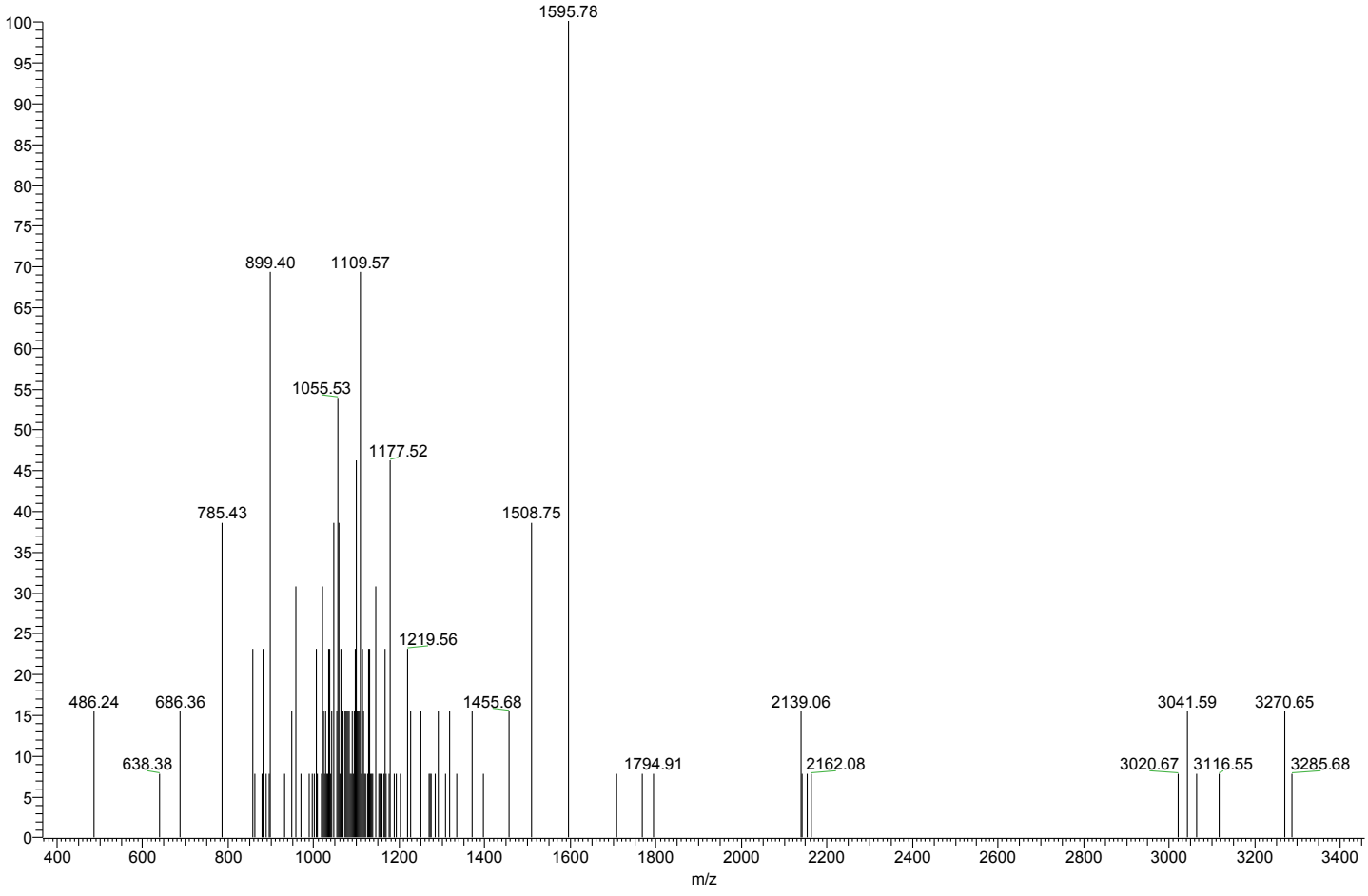


Table A-6. Top-down MS identification of S-Sulfo wt TTR. ECD fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
ECD	S-Sulfo	wt	989.64	13832.8896	13832.8450	79.957	3.22
			pScore	**pDE[b]**	**# fragments**	**# c-ions**	**# z-ions**
			7.13E-04	97.50	3	0	3

[a] Mass difference compared to Free Cys form

[b] McLuckey score

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
8	Z12	1292.6399	1292.6400	0.0025	1.8961
12	Z16	1726.8225	1726.8200	0.0050	2.9192
14	Z51	5624.8284	5624.8100	0.0154	2.7457

Figure A-3. Top-down deconvoluted MS/MS spectra of S-Sulfo wt TTR. ECD fragmentation

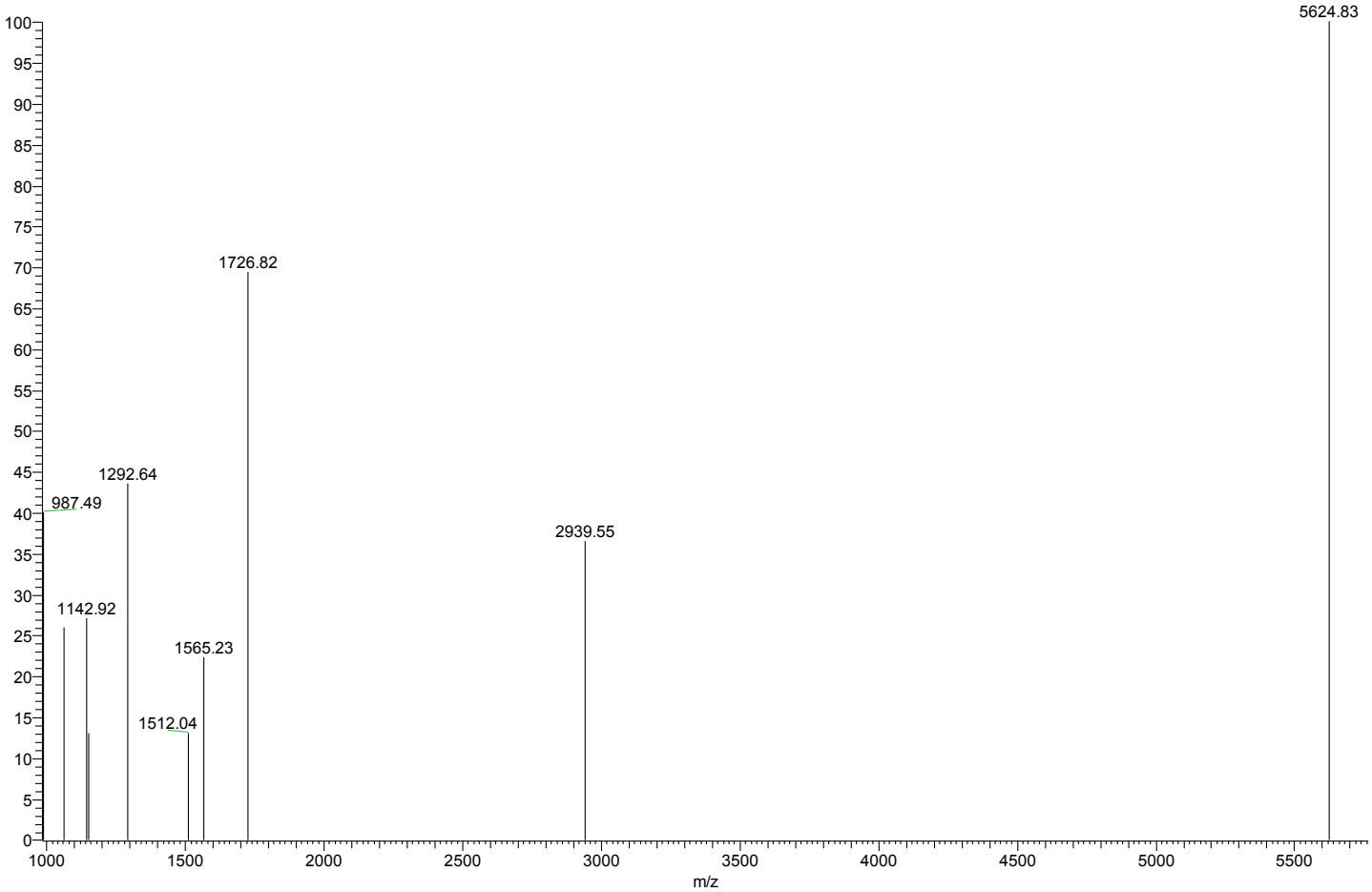


Table A-7. Top-down MS identification of S-Sulfo wt TTR. CID fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
CID*	S-Sulfo	wt	989.64	13832.8896	13832.8450	79.957	3.22
			pScore	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			0.069	3.55	9	6	3

[a] Mass difference compared to Free Cys form

[b] McLuckey score

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
376	B111	12090.1370	12090.0000	0.0837	6.9217
46	B112	12177.0699	12177.0000	0.0284	2.3347
380	B112	12177.1728	12177.0000	0.0874	7.1794
390	B115	12524.3532	12524.2000	0.1198	9.5649
53	B121	13146.5101	13146.5000	0.0243	1.8446
55	B122	13245.5937	13245.6000	0.0394	2.9783
69	Y7	785.4298	785.4300	-0.0005	-0.6162
70	Y8	856.4677	856.4670	0.0003	0.3129
53	Y119	13146.5101	13146.6000	-0.0503	-3.8299

* The fragments reported in the table are combination of CID+SID

Figure A-4. Top-down deconvoluted MS/MS spectra of S-Sulfo wt TTR. CID+SID fragmentation

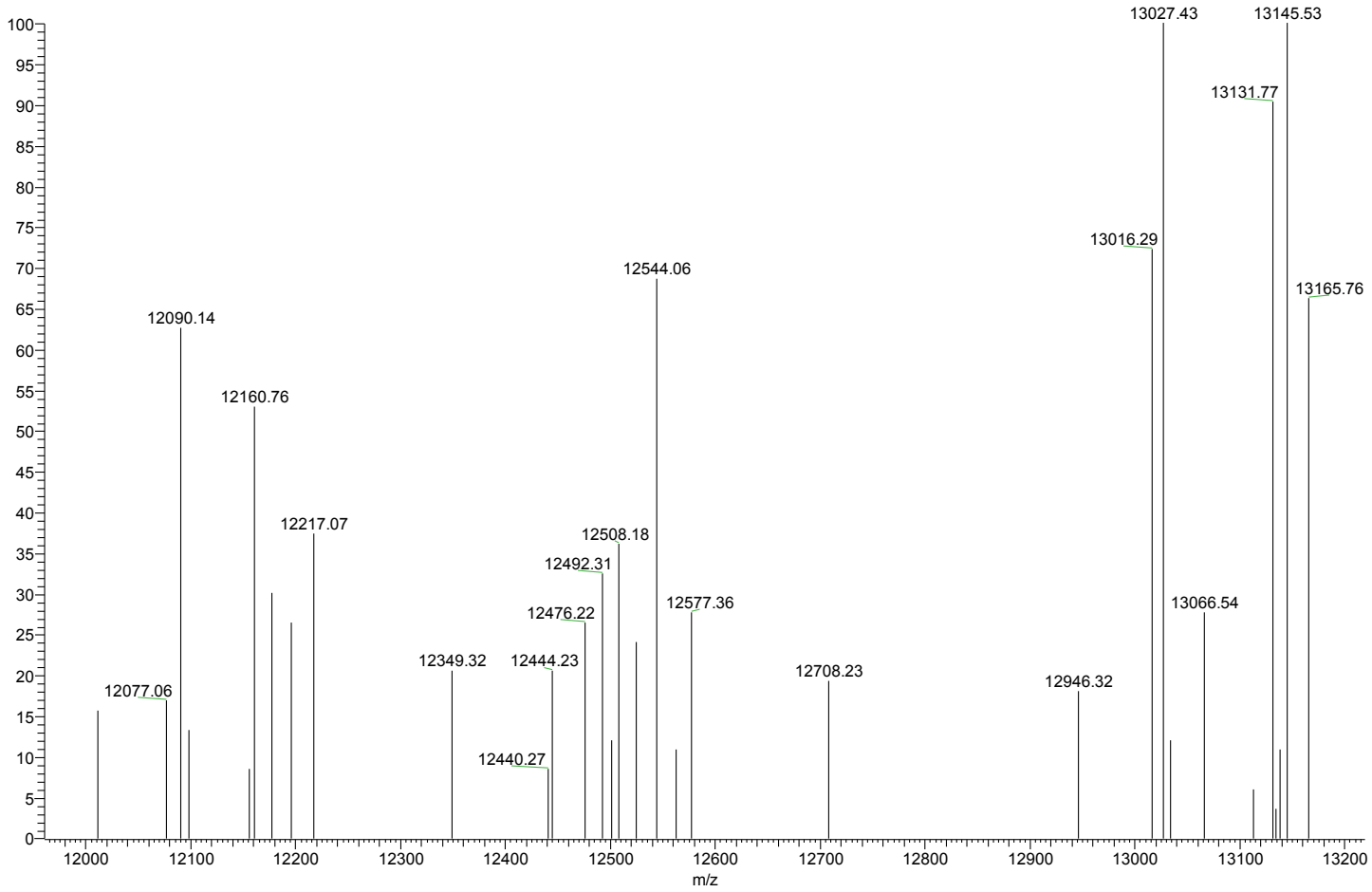


Figure A-5. Top-down deconvoluted MS/MS spectra of S-Sulfo wt TTR. CID fragmentation

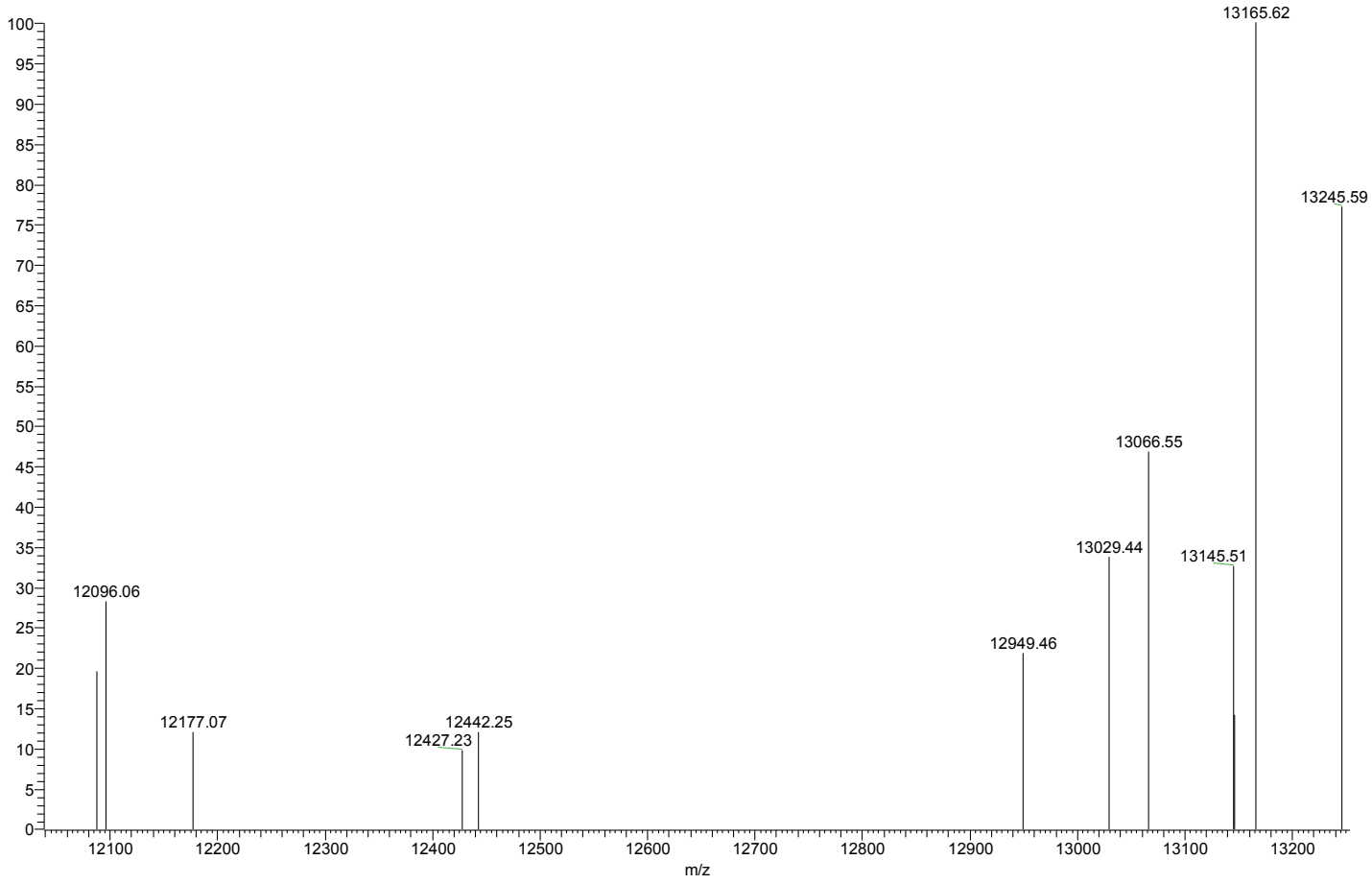


Table A-8. Top-down MS identification of S-Cys wt TTR. ECD fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
ECD	S-Cys	wt	992.35	13871.9020	13871.8924	119.0004	0.7
			pScore	**pDE[b]**	**# fragments**	**# c-ions**	**# z-ions**
			5.11E-11	73.20	12	5	7

[a] Mass difference compared to Free Cys form

[b] McLuckey score

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
58	C17	1833.9194	1833.9200	0.0043	2.3567
59	C20	2119.0478	2119.0500	0.0003	0.1529
60	C22	2332.1802	2332.1700	0.0101	4.3449
63	C27	2814.4239	2814.4200	0.0049	1.7432
65	C38	4008.0906	4008.0900	0.0048	1.1869
32	Z12	1292.6456	1292.6400	0.0082	6.3807
40	Z13	1379.6762	1379.6700	0.0068	4.9533
55	Z16	1726.8212	1726.8200	0.0037	2.1149
62	Z24	2628.3661	2628.3600	0.0100	3.7883
67	Z51	5624.8474	5624.8100	0.0344	6.1202
68	Z54	5969.0093	5968.9800	0.0267	4.4679
70	Z56	6211.1259	6211.1100	0.0165	2.6646

Figure A-6. Top-down deconvoluted MS/MS spectra of S-Cys wt TTR. ECD fragmentation

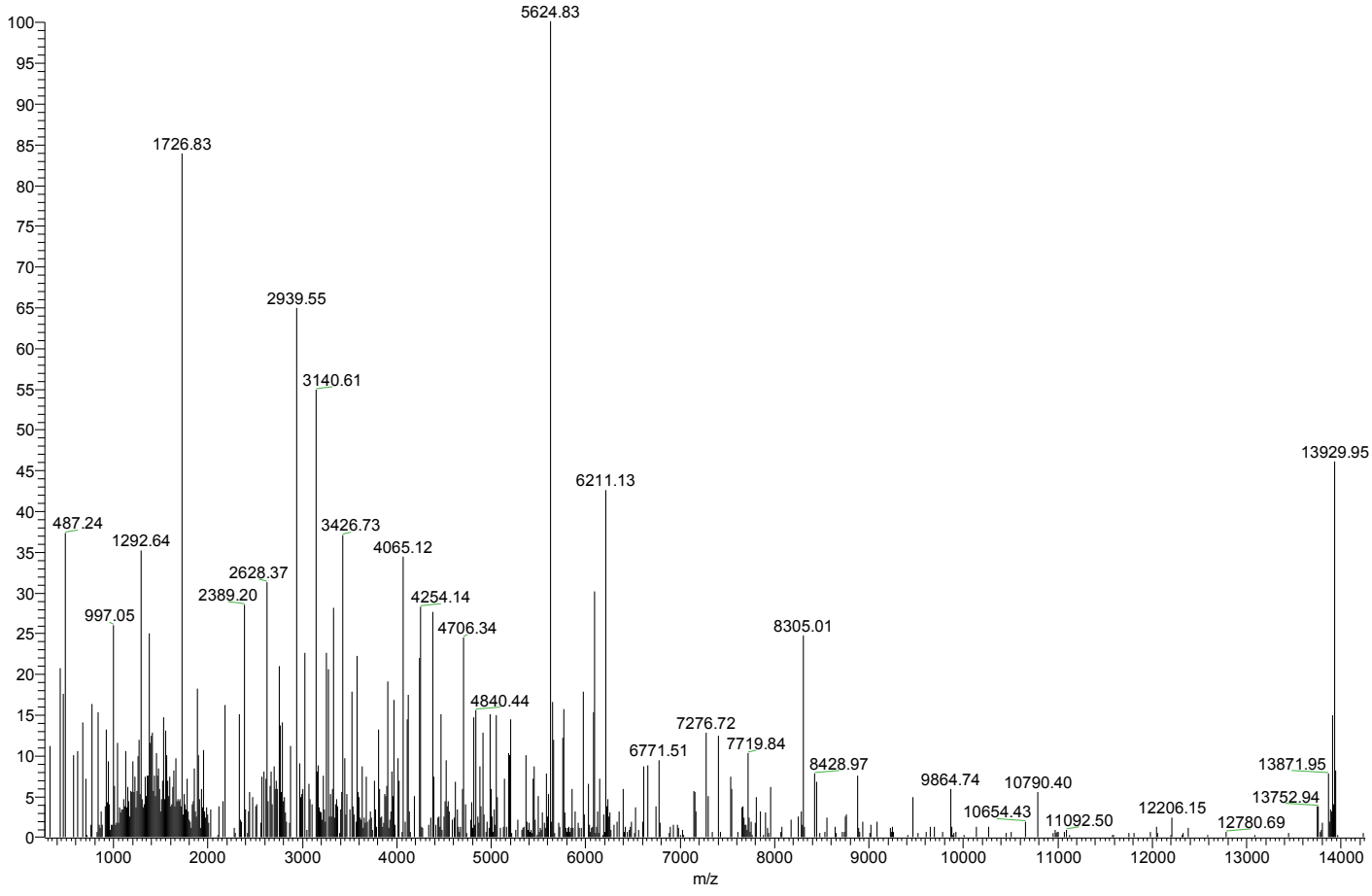


Table A-9. Top-down MS identification of S-Cys wt TTR. CID fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
CID	S-Cys	wt	992.35	13871.9020	13871.8924	119.0004	0.7
			pScore	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			2.94E-19	72.60	25	17	8

[a] Mass difference compared to Free Cys form

[b] McLuckey score

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
144	B18	1931.9222	1931.9200	0.0065	3.3480
153	B42	4522.2621	4522.2600	0.0061	1.3460
154	B54	5699.7908	5699.7800	0.0096	1.6764
156	B99	10830.3068	10830.3000	-0.0037	-0.3463
162	B111	12129.0718	12129.1000	0.0153	1.2614
165	B112	12216.1346	12216.1000	0.0461	3.7745
167	B114	12476.1938	12476.2000	-0.0108	-0.8624
170	B115	12563.2501	12563.2000	0.0135	1.0730
172	B116	12726.4016	12726.3000	0.1017	7.9920
174	B117	12813.3443	12813.3000	0.0124	0.9693
179	B119	13015.4056	13015.4000	-0.0217	-1.6650
185	B120	13086.5185	13086.5000	0.0541	4.1348
191	B121	13185.5981	13185.5000	0.0653	4.9516
196	B122	13284.6394	13284.6000	0.0382	2.8755
203	B123	13385.6850	13385.6000	0.0361	2.6962
209	B124	13499.6878	13499.7000	-0.0040	-0.2948
219	B126	13724.8604	13724.8000	0.0208	1.5177
2	Y6	686.3612	686.3620	-0.0007	-1.0199
3	Y7	785.4292	785.4300	-0.0011	-1.3470
4	Y8	856.4674	856.4670	-0.0000	-0.0432
6	Y9	957.5153	957.5150	0.0002	0.2099
62	Y10	1058.5619	1058.5600	-0.0009	-0.8719
137	Y11	1145.5946	1145.5900	-0.0002	-0.2008
191	Y119	13185.5981	13185.6000	-0.0093	-0.7061
222	Y126	13814.8963	13814.9000	0.0231	1.6714

Figure A-7. Top-down deconvoluted MS/MS spectra of S-Cys wt TTR. CID fragmentation

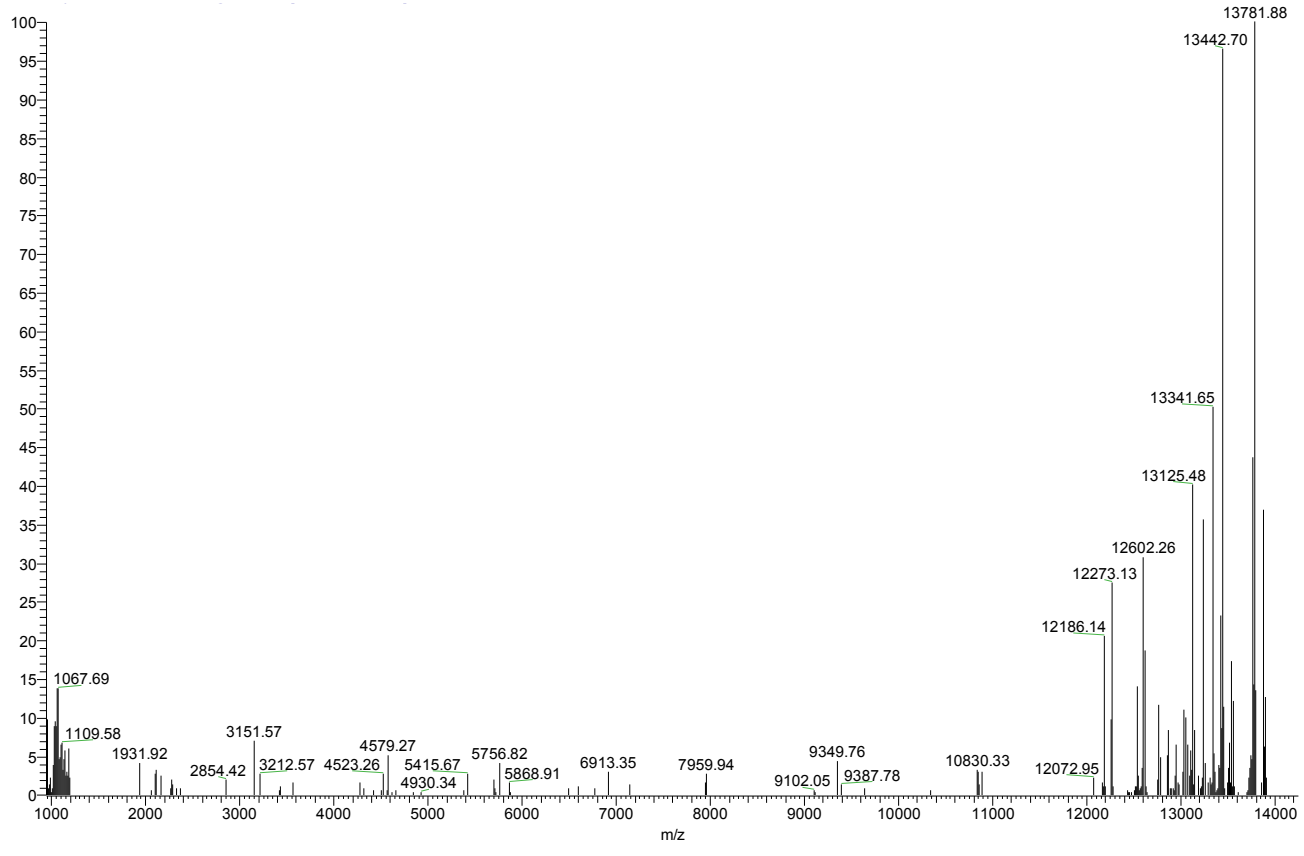


Figure A-8. Top-down deconvoluted MS/MS spectra (zoom in 2000–11000 Da) of S-Cys wt TTR. CID fragmentation

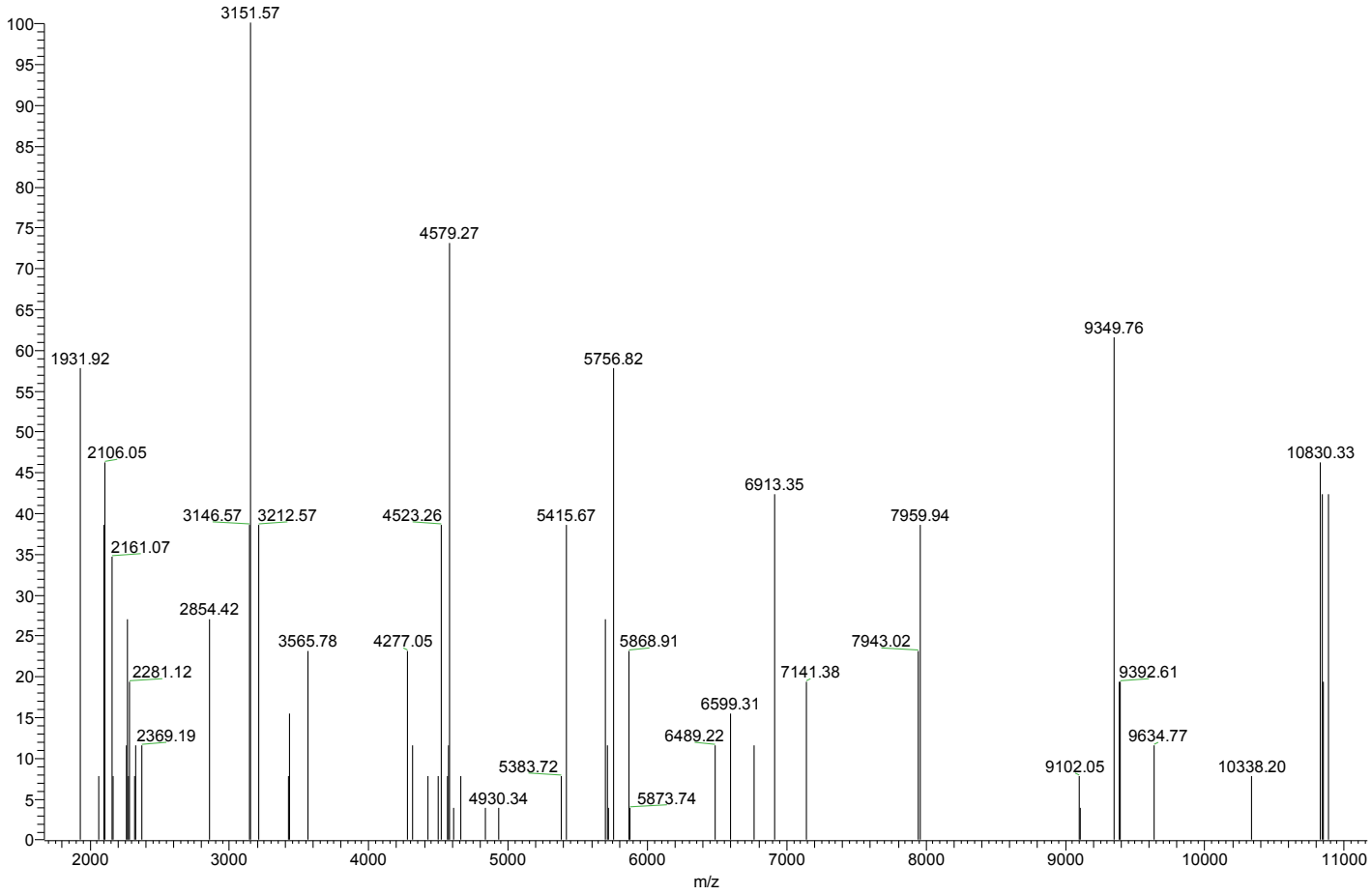


Figure A-9. Top-down deconvoluted MS/MS spectra (zoom in 12000–14200 Da) of S-Cys wt TTR. CID fragmentation

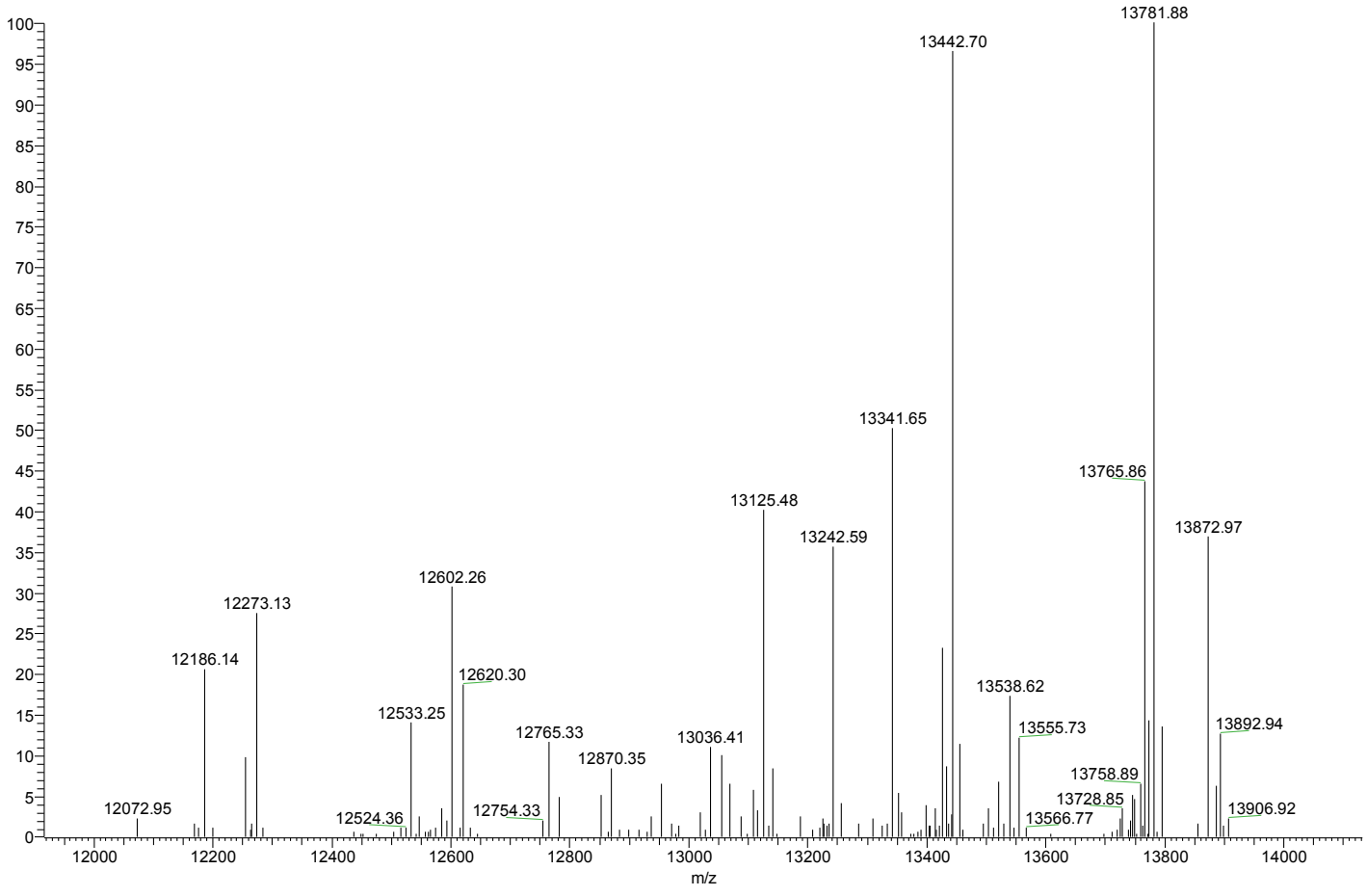


Table A-10. Top-down MS identification of S-CysGly wt TTR. ECD fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
ECD	S-CysGly	wt	996.5	13928.8962	13928.9200	176.026	1.7
			pScore	**pDE[b]**	**# fragments**	**# c-ions**	**# z-ions**
			2.35E-34	39.40	97	53	44

[a] Mass difference compared to Free Cys form

[b] McLuckey score

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
2	C3	272.1486	272.1480	0.0003	1.1942
3	C4	329.1702	329.1700	0.0004	1.1028
5	C5	430.2181	430.2180	0.0006	1.4853
7	C6	487.2397	487.2390	0.0007	1.4654
11	C7	616.2828	616.2820	0.0012	1.9520
15	C8	703.3151	703.3140	0.0015	2.0773
278	C11	1207.5016	1207.5000	0.0050	4.1524
663	C13	1451.6301	1451.6200	0.0089	6.1297
821	C14	1550.6919	1550.6900	0.0023	1.4742
970	C15	1678.7845	1678.7800	-0.0001	-0.0554
1109	C17	1890.9423	1890.9400	0.0052	2.7515
1183	C20	2176.0777	2176.0700	0.0082	3.7885
1188	C21	2332.1792	2332.1700	0.0086	3.6777
1193	C22	2389.2026	2389.1900	0.0105	4.4010
1210	C24	2573.2814	2573.2800	0.0045	1.7499
1229	C26	2757.4065	2757.4000	0.0084	3.0333
1244	C28	2970.5009	2970.5100	-0.0085	-2.8470
1257	C29	3041.5614	3041.5500	0.0149	4.8942
1266	C30	3140.6144	3140.6100	-0.0005	-0.1608
1281	C31	3277.6848	3277.6700	0.0110	3.3557
1306	C33	3523.8274	3523.8100	0.0168	4.7673
1333	C34	3679.8565	3679.9100	-0.0366	-9.9510
1353	C35	3808.0052	3808.0100	-0.0015	-0.4068
1388	C37	3950.0977	3950.0800	0.0168	4.2455
1401	C38	4065.1211	4065.1100	0.0133	3.2712
1410	C39	4180.1477	4180.1300	0.0130	3.0999
1431	C41	4467.2417	4467.2600	-0.0200	-4.4806
1460	C43	4693.3845	4693.3600	0.0274	5.8323
1472	C44	4840.4438	4840.4300	0.0183	3.7852
1479	C45	4911.4392	4911.4600	-0.0234	-4.7611
1489	C46	4998.5051	4998.4900	0.0105	2.0992
1495	C47	5055.5251	5055.5200	0.0090	1.7719
1505	C48	5183.5879	5183.6100	-0.0232	-4.4733
1513	C49	5284.6738	5284.6600	0.0150	2.8412
1546	C51	5500.7404	5500.7300	0.0070	1.2806
1557	C52	5587.7700	5587.7700	0.0046	0.8318
1565	C53	5644.7784	5644.7900	-0.0085	-1.4987
1576	C54	5773.8578	5773.8300	0.0283	4.8991
1588	C55	5886.9575	5886.9100	0.0439	7.4650
1605	C57	6081.0245	6080.9900	0.0305	5.0103
1619	C58	6194.1226	6194.0800	0.0445	7.1795
1647	C60	6396.1766	6396.1700	0.0031	0.4840
1659	C61	6525.2151	6525.2200	-0.0010	-0.1497
1660	C61	6525.2351	6525.2200	0.0190	2.9147
1661	C61	6525.2375	6525.2200	0.0214	3.2756
1667	C62	6654.2956	6654.2600	0.0369	5.5459
1723	C71	7718.8377	7718.8100	0.0247	3.2013
1735	C72	7847.8801	7847.8600	0.0245	3.1185
1736	C72	7847.8932	7847.8600	0.0376	4.7879
1748	C75	8177.0886	8177.0100	0.0743	9.0875
1753	C76	8305.0102	8305.1100	-0.0805	-9.6925
1790	C88	9691.7426	9691.8200	-0.0752	-7.7547
1791	C88	9691.7426	9691.8200	-0.0752	-7.7547

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
6	Z4	470.2257	470.2250	0.0006	1.2292
12	Z6	670.3426	670.3410	0.0014	2.1511
18	Z7	769.4114	769.4100	0.0018	2.3836
23	Z8	840.4484	840.4470	0.0017	2.0001
43	Z9	941.4985	941.4940	0.0041	4.3240
105	Z10	1042.5458	1042.5400	0.0037	3.5903
187	Z11	1129.5851	1129.5700	0.0110	9.7558
422	Z12	1292.6427	1292.6400	0.0053	4.1102
560	Z13	1379.6710	1379.6700	0.0016	1.1742
804	Z14	1542.7214	1542.7300	-0.0113	-7.3319
1008	Z16	1726.8251	1726.8200	0.0076	4.3953
1081	Z17	1839.9122	1839.9000	0.0106	5.7568
1146	Z18	1952.9954	1952.9900	0.0097	4.9534
1178	Z19	2024.0288	2024.0200	0.0060	2.9767
1200	Z23	2472.2768	2472.2500	0.0218	8.8170
1215	Z24	2628.3709	2628.3600	0.0148	5.6491
1256	Z28	3025.5928	3025.5600	0.0293	9.6771
1266	Z29	3140.6144	3140.5900	0.0240	7.6402
1280	Z30	3254.6522	3254.6300	0.0189	5.8181
1287	Z31	3325.6823	3325.6700	0.0119	3.5824
1300	Z32	3426.7313	3426.7200	0.0132	3.8643
1311	Z33	3573.8056	3573.7900	0.0191	5.3419
1393	Z37	3972.0215	3972.0000	0.0185	4.6460
1405	Z38	4109.0802	4109.0600	0.0183	4.4570
1412	Z39	4238.1166	4238.1000	0.0121	2.8664
1420	Z40	4375.1780	4375.1600	0.0146	3.3482
1439	Z41	4522.2397	4522.2300	0.0079	1.7374
1461	Z43	4706.3390	4706.3200	0.0224	4.7663
1469	Z44	4819.4149	4819.4000	0.0142	2.9506
1477	Z45	4876.4699	4876.4200	0.0477	9.7872
1496	Z47	5060.5569	5060.5400	0.0135	2.6655
1506	Z48	5188.6633	5188.6400	0.0249	4.7895
1562	Z51	5624.8312	5624.8100	0.0182	3.2410
1562	Z51	5624.8312	5624.8100	0.0182	3.2410
1592	Z54	5969.0053	5968.9800	0.0227	3.8010
1623	Z56	6211.1326	6211.1100	0.0233	3.7576
1675	Z62	6900.4370	6900.4800	-0.0472	-6.8404
1694	Z66	7404.6474	7404.7100	-0.0588	-7.9343
1696	Z67	7533.8042	7533.7500	0.0554	7.3578
1767	Z79	8746.3489	8746.3100	0.0377	4.3046
1772	Z80	8874.3849	8874.4100	-0.0213	-2.3999
1786	Z86	9462.6101	9462.6600	-0.0505	-5.3387
1789	Z87	9648.8337	9648.7400	0.0938	9.7171
1795	Z89	9864.7369	9864.8100	-0.0776	-7.8701
1810	Z96	10652.2983	10652.2000	0.0498	4.6779

Deconvoluted MS/MS spectra is shown in Chapter 2, Fig. C2-7

Table A-11. Top-down MS identification of S-CysGly wt TTR. CID fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
CID	S-CysGly	wt	996.5	13928.8962	13928.9200	176.026	1.7
			pScore	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			1.16E-05	50.50	19	15	4

[a] Mass difference compared to Free Cys form

[b] McLuckey score

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
362	B27	2854.4207	2854.4100	0.0060	2.1174
521	B42	4579.2720	4579.2800	-0.0060	-1.3124
498	B54	5756.8196	5756.8000	0.0164	2.8531
454	B64	6913.3478	6913.3400	0.0044	0.6404
277	B66	7141.3814	7141.4500	-0.0544	-7.6228
387	B110	12072.9517	12073.0000	-0.0427	-3.5360
571	B111	12186.1357	12186.1000	0.0573	4.6980
573	B112	12273.1291	12273.1000	0.0186	1.5139
567	B114	12533.2501	12533.2000	0.0235	1.8750
570	B115	12620.3038	12620.3000	0.0452	3.5831
548	B117	12870.3547	12870.4000	0.0008	0.0653
575	B121	13242.5889	13242.6000	0.0341	2.5720
579	B122	13341.6518	13341.6000	0.0286	2.1414
580	B123	13442.6972	13442.7000	0.0263	1.9557
581	B126	13781.8775	13781.9000	0.0159	1.1559
554	Y9	957.5157	957.5150	0.0006	0.6214
529	Y11	1145.5717	1145.5900	-0.0045	-3.9520
325	Y111	12168.0257	12168.1000	-0.0643	-5.2868
575	Y119	13242.5889	13242.6000	-0.0405	-3.0613

Figure A-10. Top-down deconvoluted MS/MS spectra of S-CysGly wt TTR. CID fragmentation

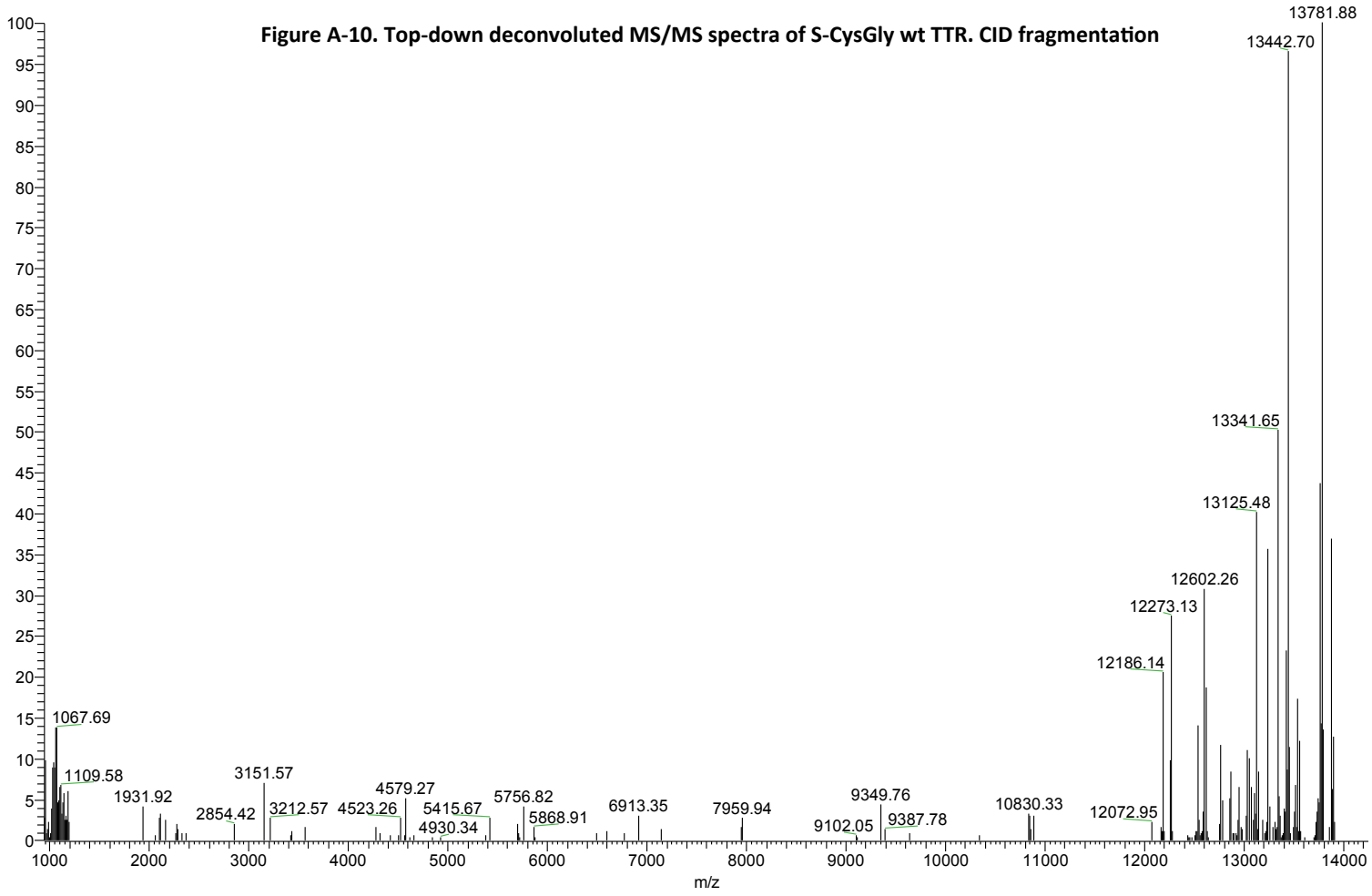


Figure A-11. Top-down deconvoluted MS/MS spectra (zoom in 200-11000 Da) of S-CysGly wt TTR. CID fragmentation

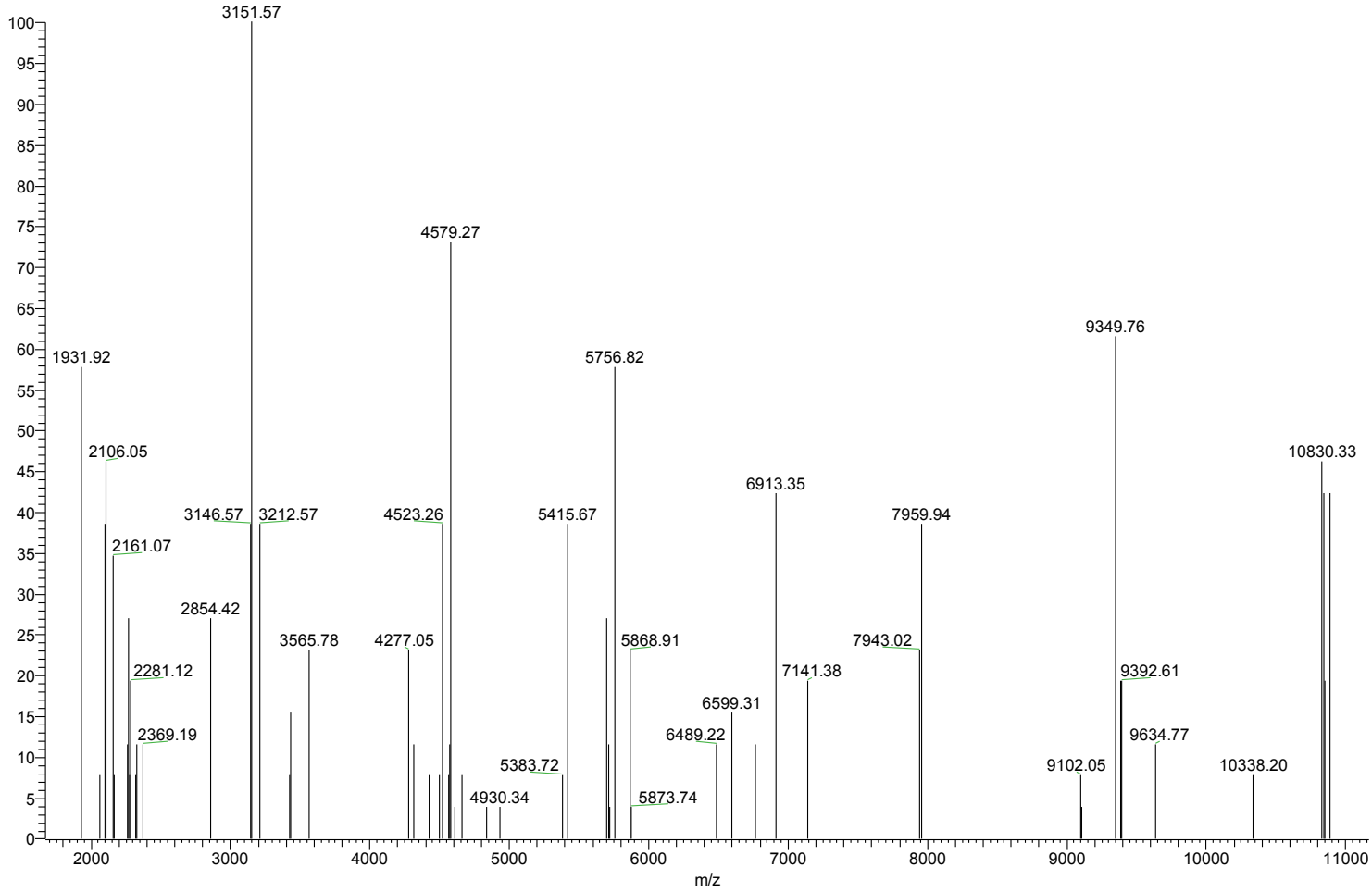


Figure A-12. Top-down deconvoluted MS/MS spectra (zoom in 12000-14200 Da) of S-CysGly wt TTR. CID fragmentation

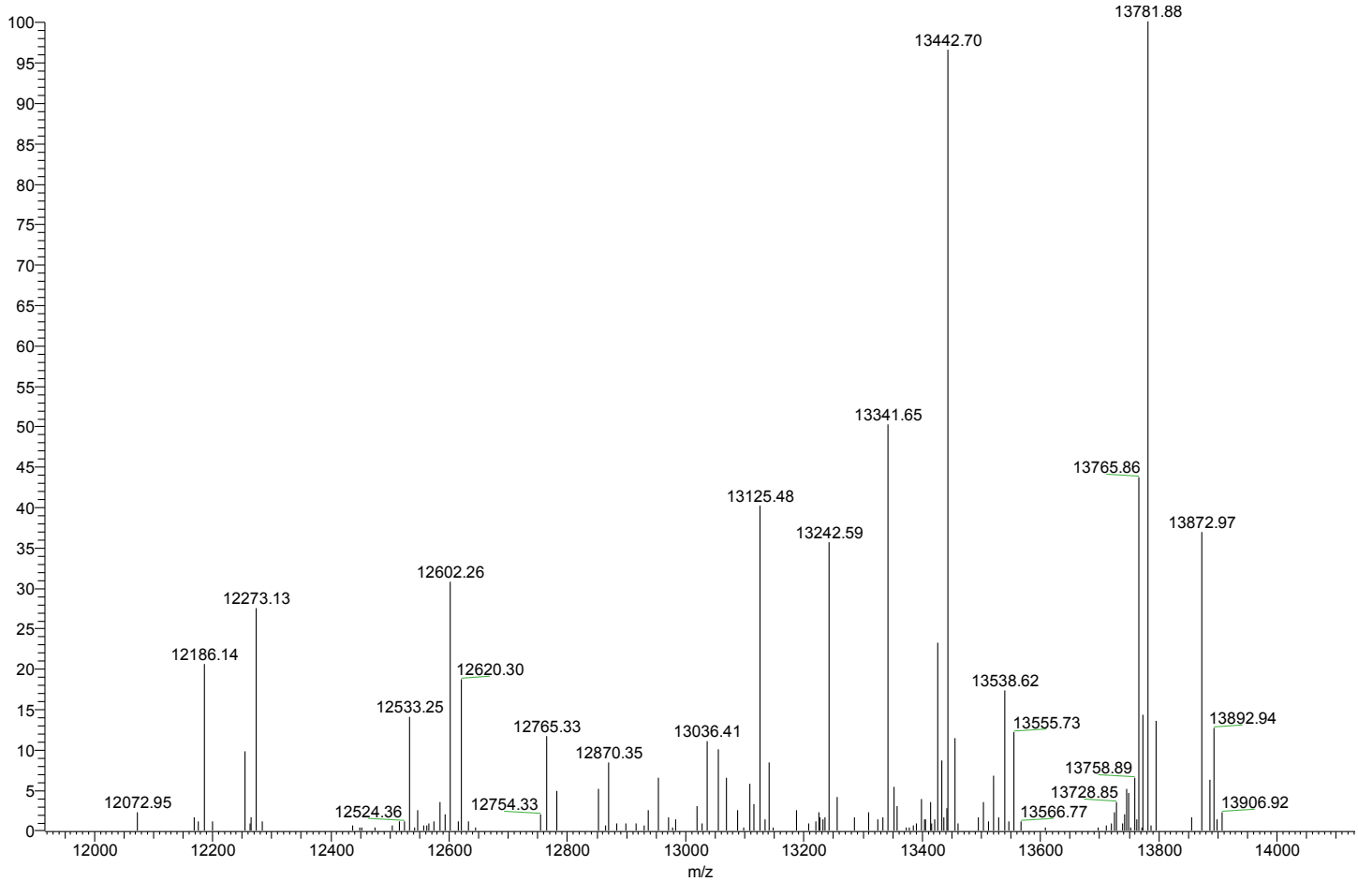


Table A-12. Top-down MS identification of S-GSH wt TTR. ECD fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
ECD	S-GSH	wt	1005.72	14057.1816	14057.9560	305.068	55[c]
			pScore	**pDE[b]**	**# fragments**	**# c-ions**	**# z-ions**
			1.29E-05	48.70	9	3	6

[a] Mass difference compared to Free Cys form

[b] McLuckey score

[c] Isoform detected as a minor species. The monoisotopic mass could not be accurately measured due to bad ion statistics

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
1	C6	487.2397	487.2390	0.0007	1.4818
89	C17	2019.9824	2019.9800	0.0033	1.6376
94	C38	4194.1513	4194.1500	0.0015	0.3657
35	Z12	1292.6422	1292.6400	0.0048	3.7009
51	Z13	1379.6706	1379.6700	0.0012	0.8901
87	Z16	1726.8261	1726.8200	0.0086	5.0034
92	Z33	3573.7833	3573.7900	-0.0032	-0.8923
93	Z33	3573.8197	3573.7900	0.0332	9.2803
95	Z51	5624.8254	5624.8100	0.0124	2.2068

Figure A-13. Top-down deconvoluted MS/MS spectra of S-GSH wt TTR. ECD fragmentation.

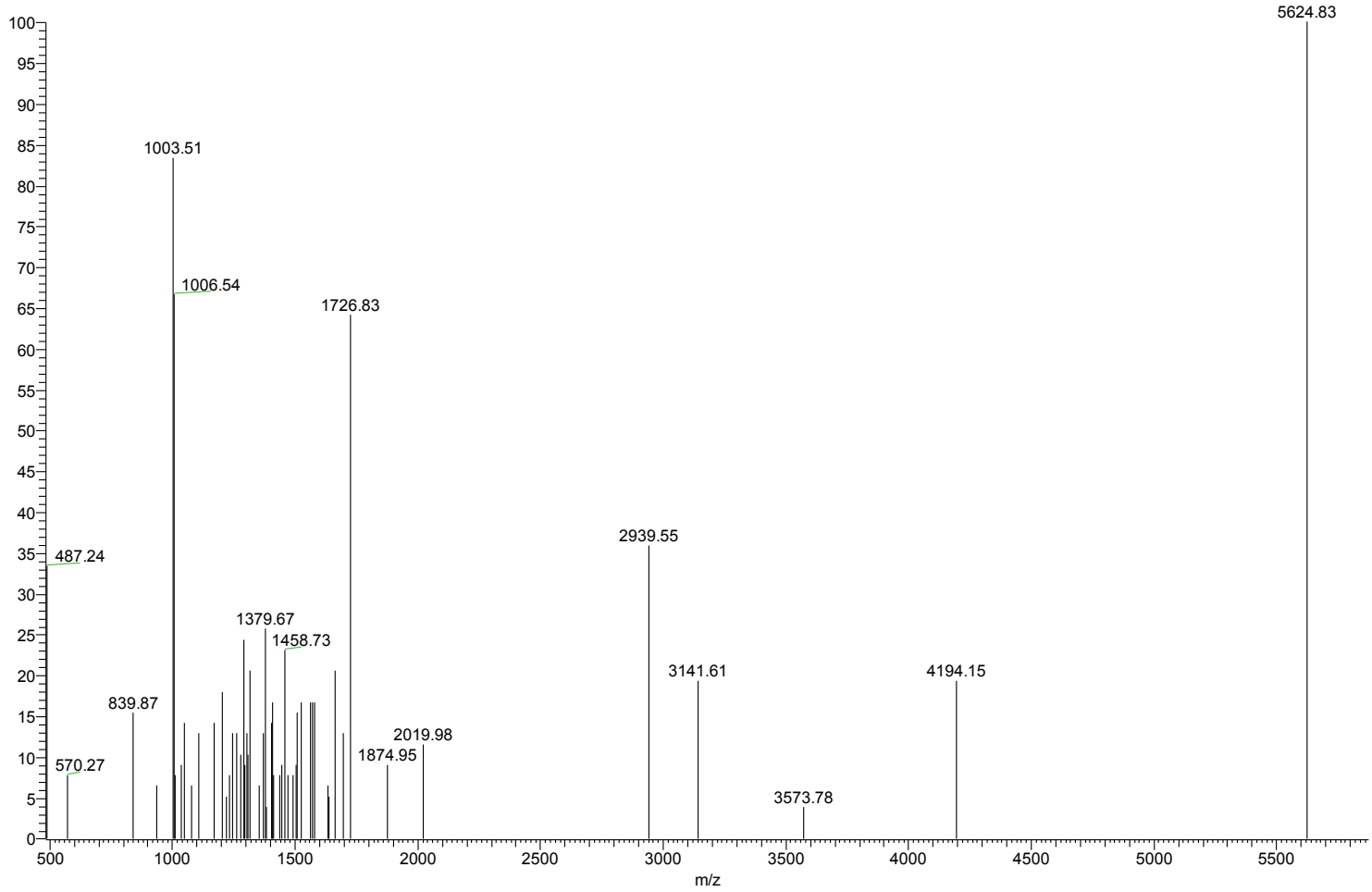


Table A-13. Top-down MS identification of Free Cys V30M TTR. CID fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
CID	Free Cys	V30M	986.22	13784.8913	13784.8603	-	2.25
			pScore	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			7.53E-01	4.41	6	1	5

[a] Mass difference compared to Free Cys form

[b] McLuckey score

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
613	B18	1812.9145	1812.9100	0.0028	1.5219
32	Y5	587.2927	587.2930	-0.0008	-1.3469
56	Y6	686.3608	686.3620	-0.0011	-1.6405
92	Y7	785.4288	785.4300	-0.0015	-1.9263
112	Y8	856.4664	856.4670	-0.0010	-1.1326
141	Y9	957.5154	957.5150	0.0003	0.2653

Figure A-14. Top-down deconvoluted MS/MS spectra of Free Cys V30M TTR. CID fragmentation

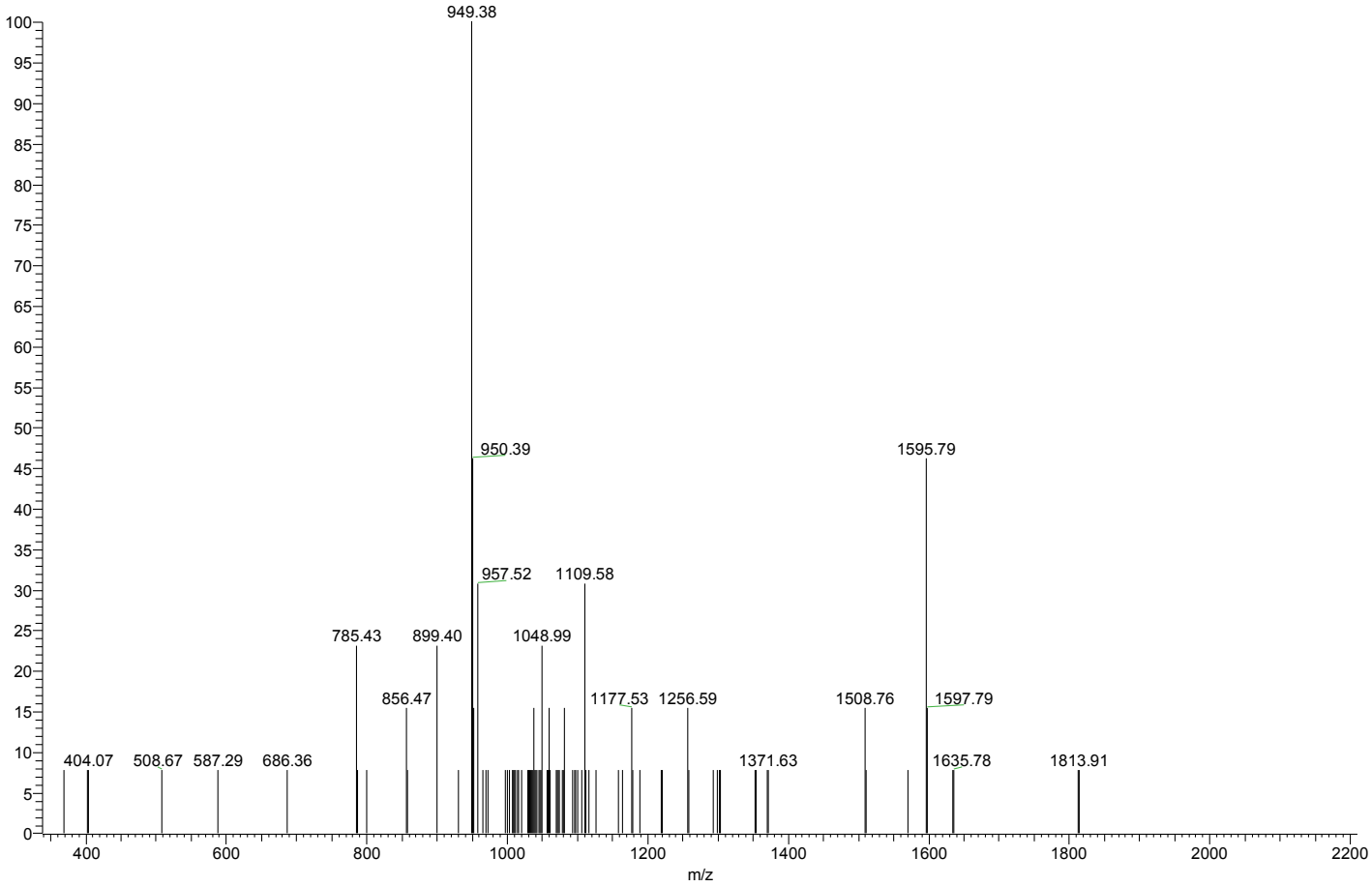


Table A-14. Top-down MS identification of S-Sulfo V30M TTR. CID fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
CID	S-Sulfo	V30M	991.93	13863.9136	13864.8173	79.957	65.18[c]
			pScore	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			7.96E-01	3.62	4	0	4

[a] Mass difference compared to Free Cys form

[b] McLuckey score

[c] Deconvolution algorithm errors due to overlapping forms could account for the low accuracy determination of the monoisotopic mass of this form

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
86	Y8	856.4663	856.4670	-0.0011	-1.2376
117	Y9	957.5155	957.5150	0.0004	0.4700
180	Y10	1058.5613	1058.5600	-0.0015	-1.4406
244	Y11	1145.5928	1145.5900	-0.0020	-1.7598

Figure A-15. Top-down deconvoluted MS/MS spectra of S-Sulfo V30M TTR. CID fragmentation

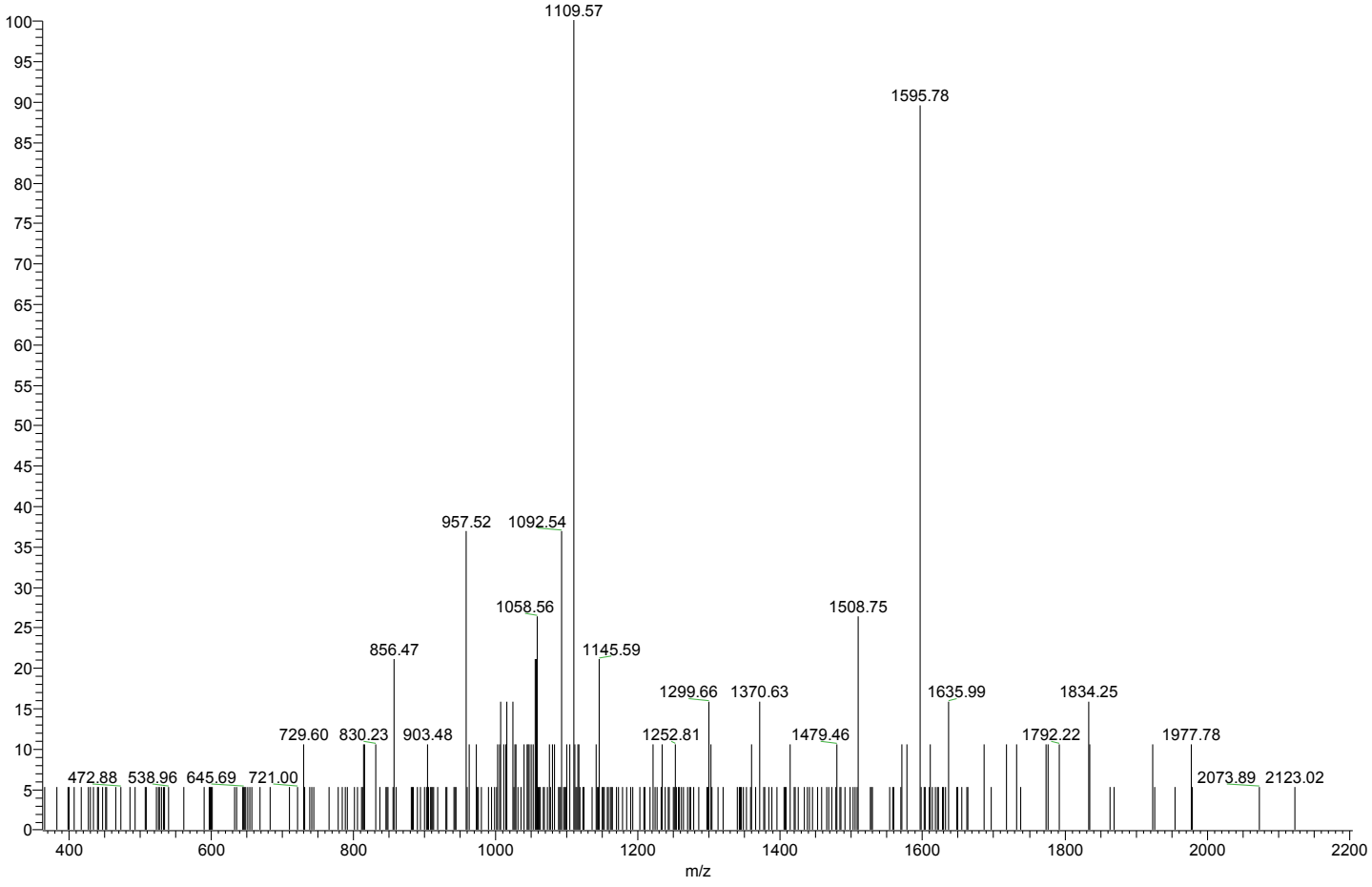


Table A-15. Top-down MS identification of S-Cys V30M TTR. CID fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
CID	S-Cys	V30M	994.71	13903.4582	13903.8644	119.004	0.73
			pScore	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			1.77E-11	74.60	28	17	11

[a] Mass difference compared to Free Cys form

[b] McLuckey score

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
238	B13	1377.5755	1377.5700	0.0026	1.8859
239	B13	1377.5755	1377.5700	0.0026	1.8859
249	B18	1931.9137	1931.9200	-0.0020	-1.0606
252	B27	2797.3843	2797.3900	-0.0084	-3.0082
272	B42	4554.2247	4554.2300	-0.0034	-0.7468
278	B54	5731.7489	5731.7500	-0.0044	-0.7725
285	B63	6741.2022	6741.2300	-0.0229	-3.3960
290	B67	7173.4043	7173.4300	-0.0217	-3.0316
300	B111	12161.0622	12161.0000	0.0336	2.7596
303	B112	12248.0677	12248.1000	0.0071	0.5772
307	B114	12508.1883	12508.2000	0.0116	0.9242
314	B115	12595.1316	12595.2000	-0.0771	-6.1198
320	B117	12845.3000	12845.3000	-0.0040	-0.3130
334	B120	13118.4376	13118.4000	0.0011	0.0839
339	B121	13217.5197	13217.5000	0.0148	1.1167
344	B122	13316.6208	13316.6000	0.0475	3.5685
353	B123	13417.6853	13417.6000	0.0643	4.7885
373	B126	13756.8289	13756.8000	0.0172	1.2525
1	Y5	587.2917	587.2930	-0.0018	-3.0768
3	Y6	686.3597	686.3620	-0.0022	-3.1441
5	Y7	785.4278	785.4300	-0.0025	-3.1728
7	Y8	856.4650	856.4670	-0.0024	-2.7894
13	Y9	957.5129	957.5150	-0.0022	-2.2767
166	Y11	1145.5891	1145.5900	-0.0057	-4.9861
167	Y11	1145.5891	1145.5900	-0.0057	-4.9861
227	Y12	1308.6569	1308.6600	-0.0012	-0.9269
259	Y33	3589.8122	3589.8100	0.0050	1.3873
276	Y45	4892.4055	4892.4400	-0.0374	-7.6492
292	Y85	9349.6309	9349.6400	-0.0078	-0.8348
339	Y119	13217.5197	13217.6000	-0.0598	-4.5273

Figure A-16. Top-down deconvoluted MS/MS spectra of S-Cys V30M TTR. CID fragmentation

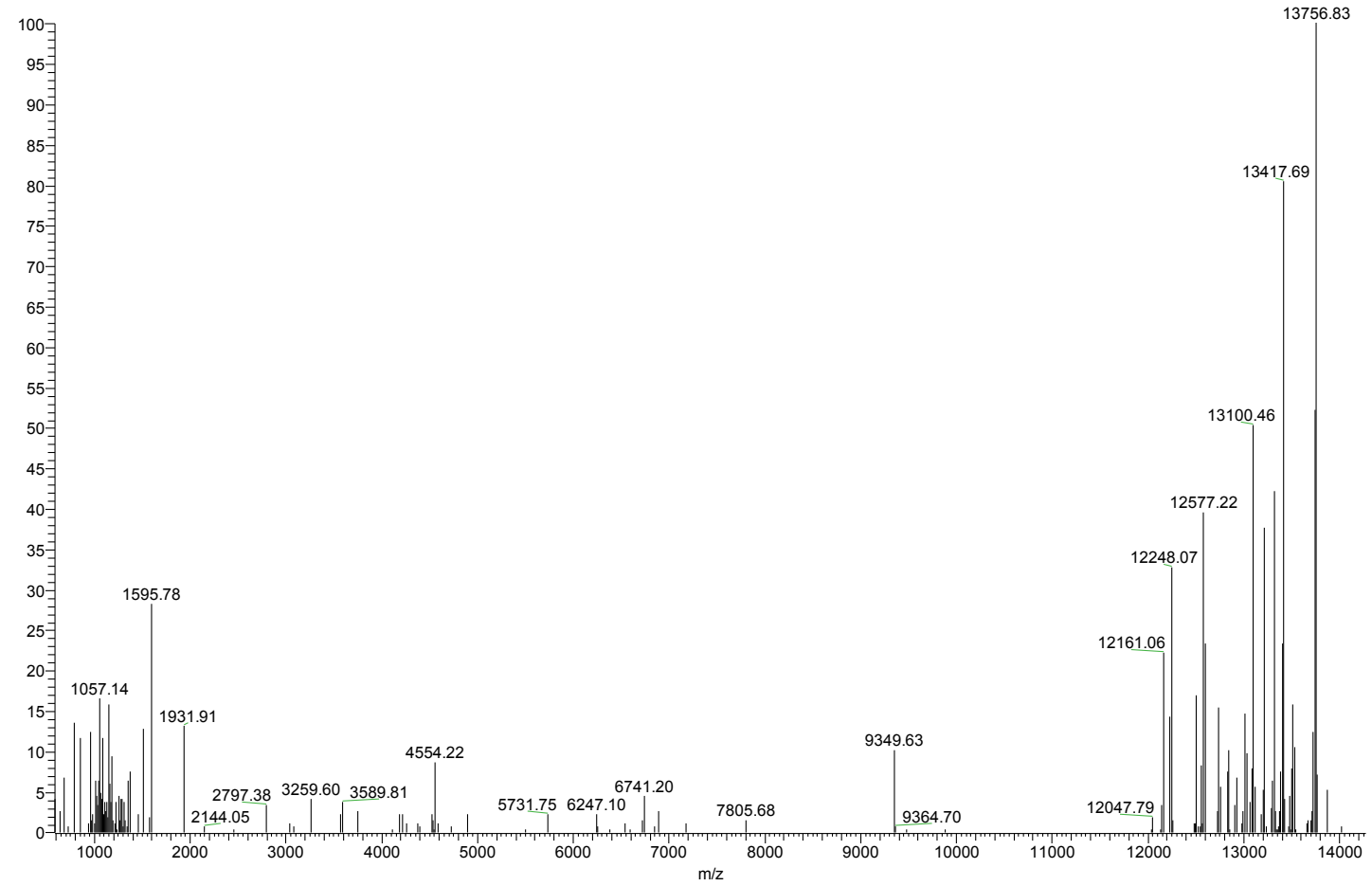


Figure A-17. Top-down deconvoluted MS/MS spectra (zoom in 12000-14200 Da) of S-Cys V30M TTR. CID fragmentation

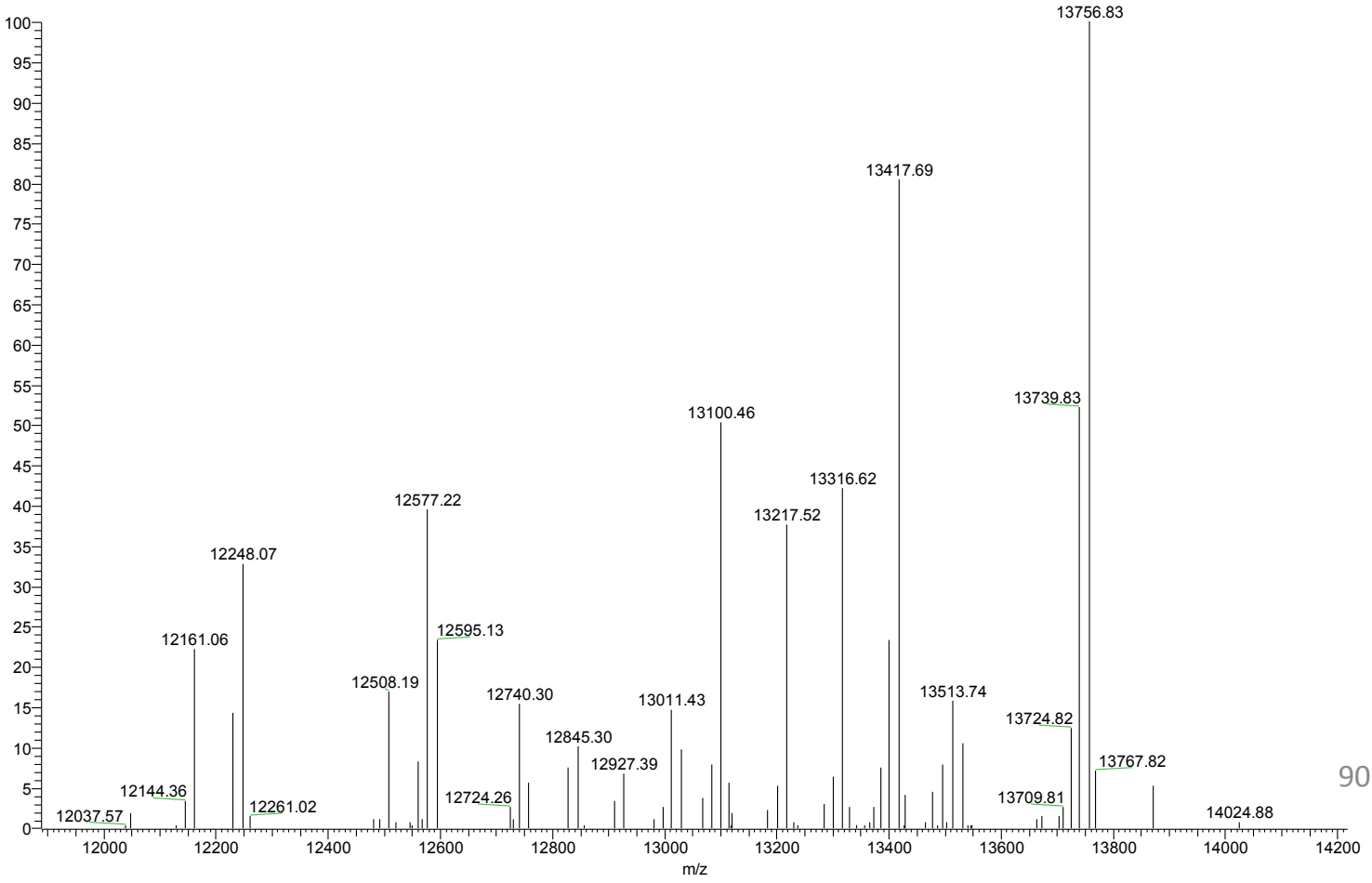


Table A-16. Top-down MS identification of S-CysGly V30M TTR. CID fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
CID	S-CysGly	V30M	998.79	13961.9241	13960.8863	176.026	74.3[c]
			pScore	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			8.47E-05	16.70	11	3	8

[a] Mass difference compared to Free Cys form

[b] McLuckey score

[c] Isoform detected as a minor species. The monoisotopic mass could not be accurately measured due to bad ion statistics

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
150	B120	13175.4482	13175.5000	-0.0104	-0.7856
246	B123	13474.6833	13474.6000	0.0403	2.9945
255	B126	13813.8644	13813.8000	0.0307	2.2210
214	Y4	486.2444	486.2460	-0.0014	-2.9471
1	Y5	587.2922	587.2930	-0.0013	-2.2544
215	Y6	686.3607	686.3620	-0.0012	-1.7658
216	Y7	785.4294	785.4300	-0.0009	-1.1140
166	Y8	856.4652	856.4670	-0.0022	-2.5243
220	Y10	1058.5651	1058.5600	0.0023	2.1973
200	Y11	1145.5957	1145.5900	0.0009	0.8223
165	Y126	13903.8871	13903.9000	0.0198	1.4233

Figure A-18. Top-down deconvoluted MS/MS spectra of S-CysGly V30M TTR. CID fragmentation

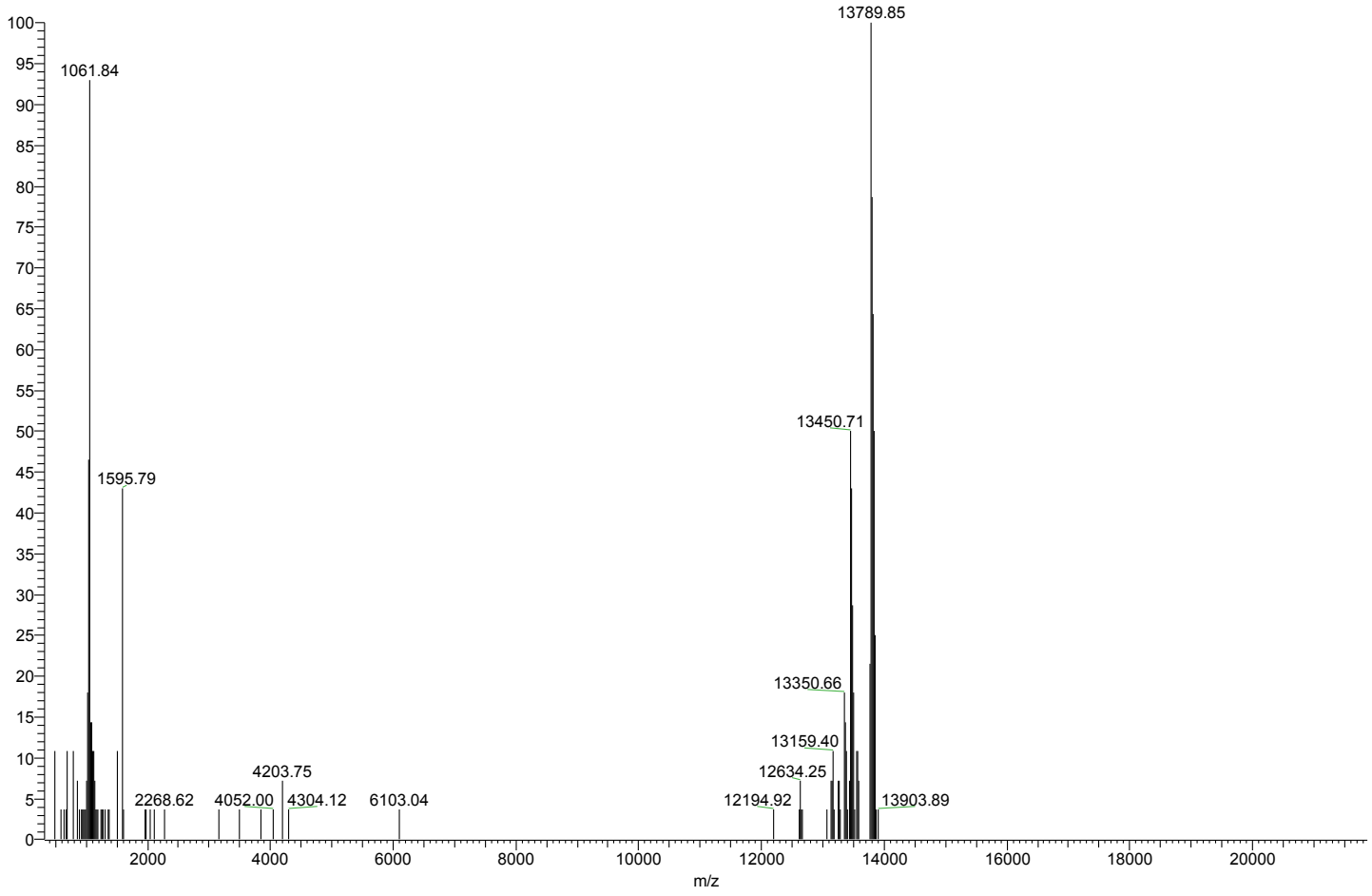


Figure A-19. Top-down deconvoluted MS/MS spectra (zoom in 400-1400 Da) of S-CysGly V30M TTR. CID fragmentation

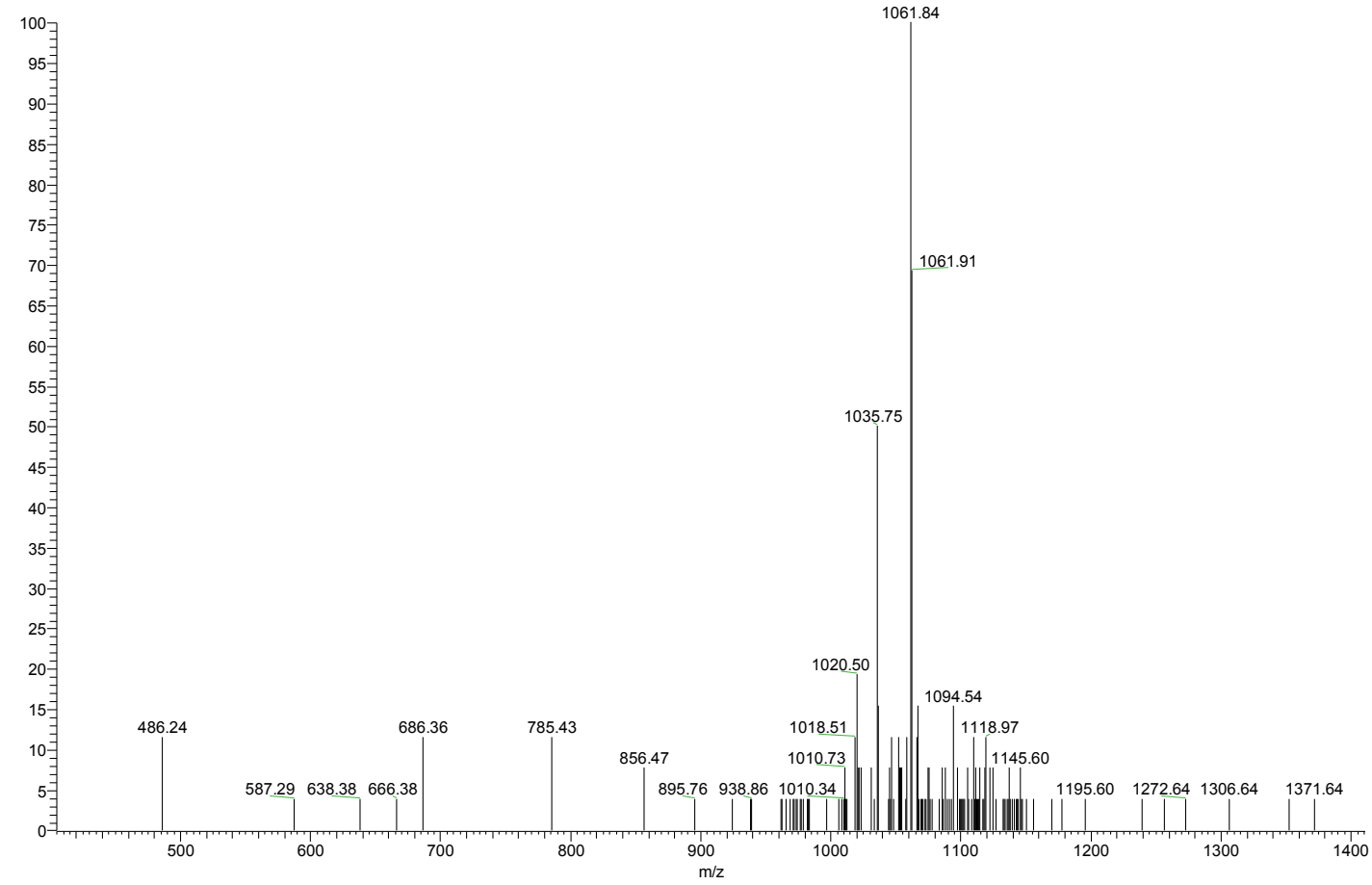


Figure A-20. Top-down deconvoluted MS/MS spectra (zoom in 12800-14000 Da) of S-CysGly V30M TTR. CID fragmentation

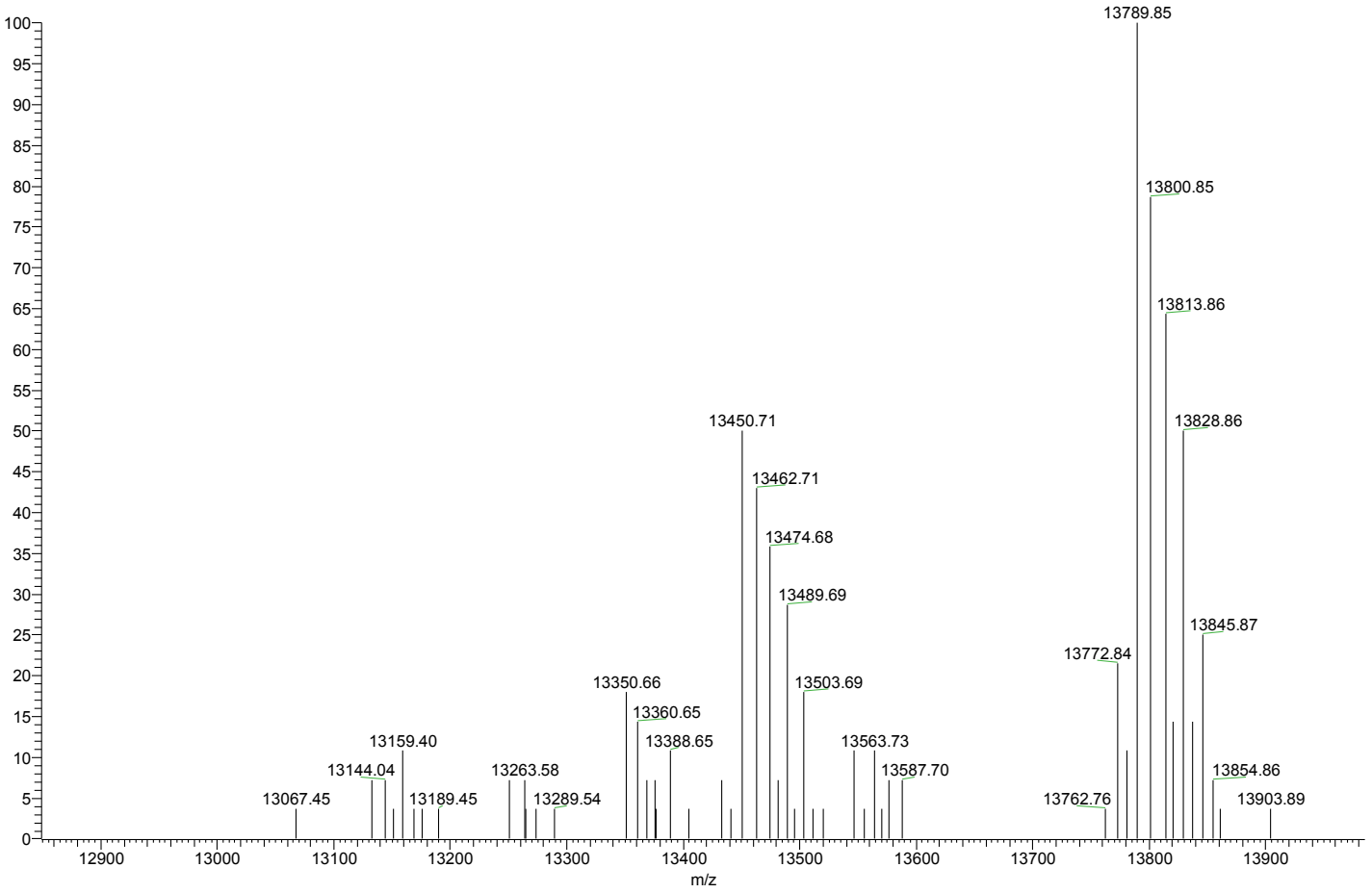


Table A-17. Top-down MS identification of S-GSH V30M TTR. CID fragmentation

Fragmentation	PTM	TTR	Ion	Observed m	Theoretical m	Δm[a]	ppm
CID	S-GSH	V30M	1008.07	14089.9257	14089.9283	305.068	0.18
			pScore	**pDE[b]**	**# fragments**	**# b-ions**	**# y-ions**
			1.22E-04	35.10	7	5	2

[a] Mass difference compared to Free Cys form

[b] McLuckey score

ID	Name	Mass Monoisotopic	Theoretical Mass	Error (Da)	Error (ppm)
77	B18	2117.9753	2117.9800	-0.0044	-2.0784
88	B121	13403.5680	13403.6000	-0.0009	-0.0649
90	B122	13502.6147	13502.6000	-0.0226	-1.6715
95	B123	13603.7156	13603.7000	0.0306	2.2464
106	B126	13942.8779	13942.9000	0.0022	0.1585
40	Y10	1058.5614	1058.5600	-0.0014	-1.3348
88	Y119	13403.5680	13403.6000	-0.0755	-5.6306

Figure A-21. Top-down deconvoluted MS/MS spectra of S-GSH V30M TTR. CID fragmentation

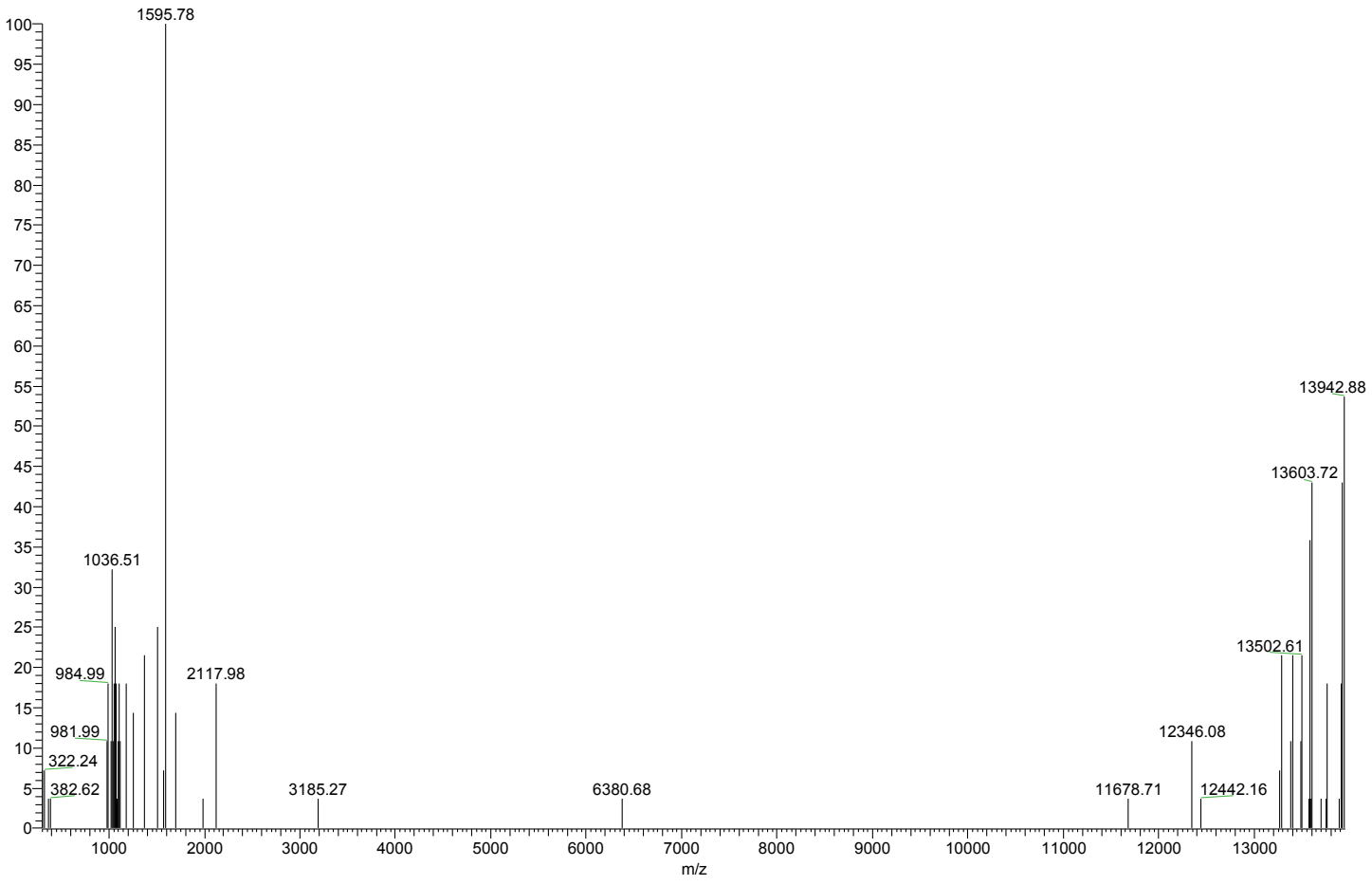


Figure A-22. Top-down deconvoluted MS/MS spectra (zoom in 800-2400 Da) of S-GSH V30M TTR. CID fragmentation

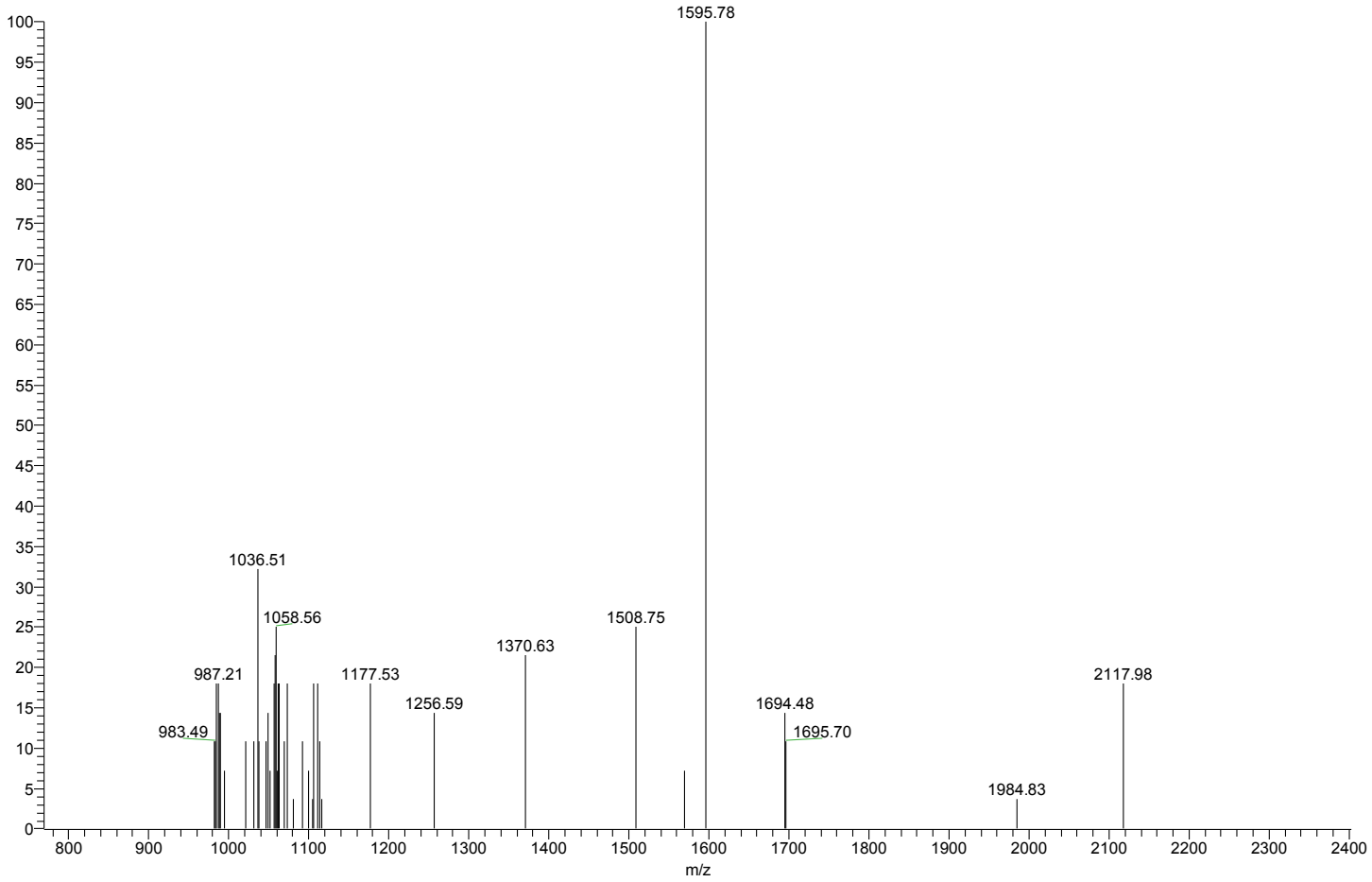


Figure A-23. Top-down deconvoluted MS/MS spectra (zoom in 13250-13950 Da) of S-GSH V30M TTR. CID fragmentation

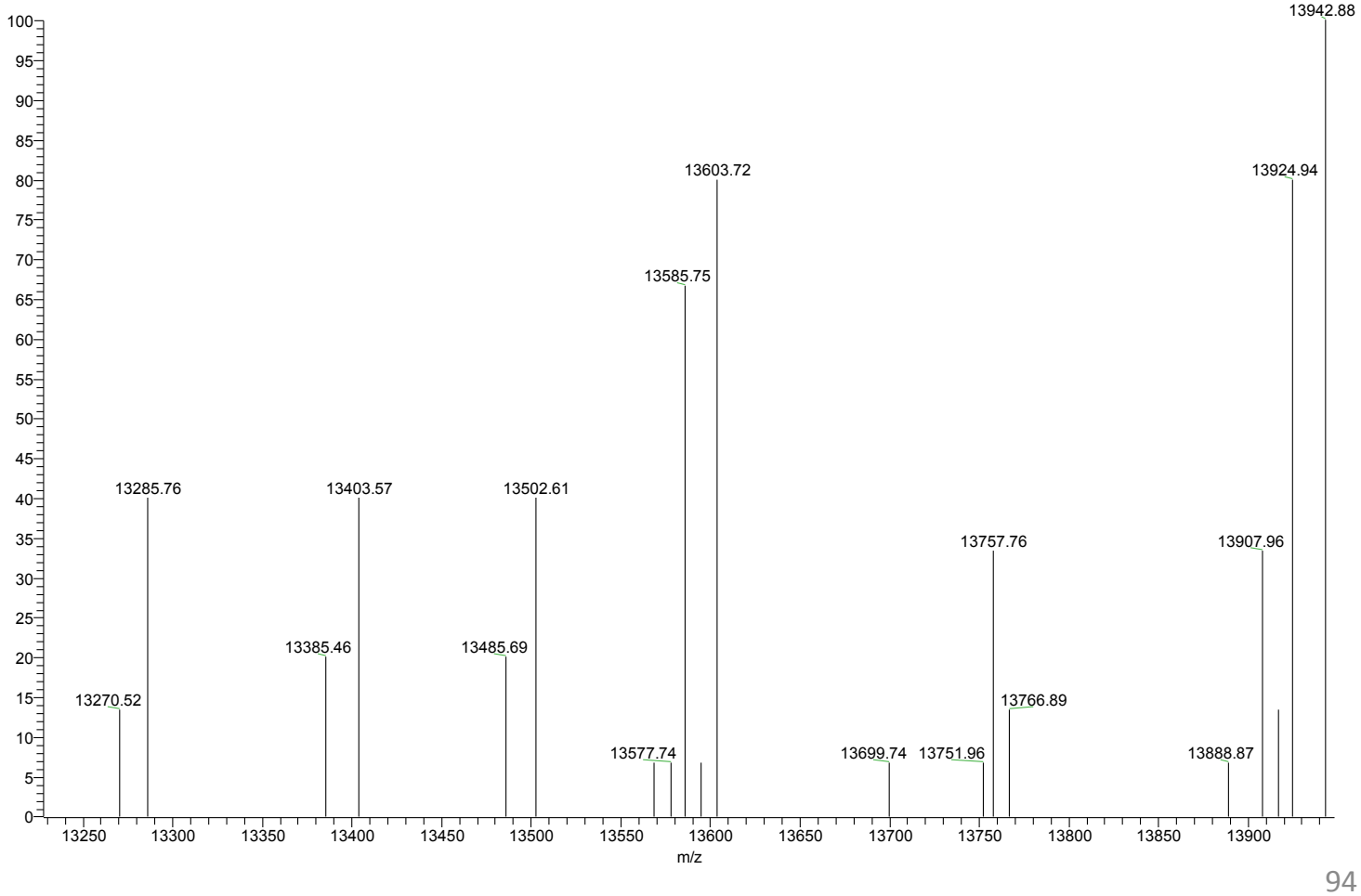


Table A-18. Absolute quantification of Cys-10 PTMs in TTR by HR-XIC

	% Each form					ng/µL Each form				
Sample[a]	**Free Cys**	**S-Cys**	**S-CysGly**	**S-GSH**	**S-Sulfo**	**Free Cys**	**S-Cys**	**S-CysGly**	**S-GSH**	**S-Sulfo**
Sample 1	13.72	67.27	0.86	0.19	17.96	7.20	35.30	0.45	0.10	9.42
Sample 2	2.57	76.19	0.86	0.25	20.14	1.60	47.47	0.54	0.15	12.55
Sample 3	3.31	78.35	1.06	0.27	17.01	3.94	93.18	1.26	0.32	20.23
Sample 4	3.24	71.47	0.77	0.2	24.32	1.68	37.01	0.40	0.10	12.60
Sample 5	1.77	80.98	0.54	0.08	16.64	0.43	19.81	0.13	0.02	4.07
Sample 6	3.19	74.84	1.11	0.26	20.6	4.34	101.61	1.50	0.35	27.98
Sample 7	2.21	75.48	1.08	0.16	21.07	2.39	81.85	1.17	0.18	22.84
Sample 8	1.91	72.38	0.83	0.2	24.68	1.50	56.96	0.65	0.16	19.42
Sample 9	2.1	76	0.6	0.22	21.09	1.64	59.64	0.47	0.17	16.55
Sample 10	2.22	72.29	1.04	0.33	24.12	2.37	77.37	1.11	0.35	25.81

[a] Samples 1-5 correspond to wt individual human samples and samples 6-10 to V30M individual human samples

Table A-19. Relative abundances of Cys-10 PTMs in TTR by intact protein

Sample[a]	Free Thiol			S-Cys			S-CysGly			S-GSH		
	% in wt	% in V30M	% in total TTR	% in wt	% in V30M	% in total TTR	% in wt	% in V30M	% in total TTR	% in wt	% in V30M	% in total TTR
Sample 1	56.04	-	-	30.10	-	-	9.53	-	-	4.33	-	-
Sample 2	57.07	-	-	30.38	-	-	8.23	-	-	4.32	-	-
Sample 3	52.42	-	-	33.70	-	-	9.99	-	-	3.89	-	-
Sample 4	51.33	-	-	35.05	-	-	9.50	-	-	4.11	-	-
Sample 5	18.32	-	-	64.43	-	-	13.27	-	-	3.98	-	-
Sample 6	24.45	21.72	23.13	51.56	53.41	52.45	16.00	16.29	16.14	7.99	8.58	8.28
Sample 7	23.44	19.99	21.81	49.14	54.04	51.45	18.87	16.25	17.63	8.55	9.72	9.10
Sample 8	28.50	27.32	27.94	46.02	47.94	46.93	17.16	15.81	16.52	8.31	8.93	8.61
Sample 9	27.59	17.38	22.56	42.95	54.27	48.53	20.09	18.67	19.39	9.37	9.68	9.52
Sample 10	20.54	30.38	24.82	50.29	31.05	41.92	18.57	23.42	20.68	10.60	15.16	12.58

[a] Samples 1-5 correspond to wt individual human samples and samples 6-10 to V30M individual human samples

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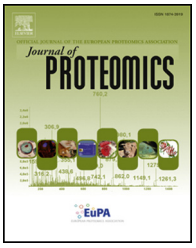

Quantitative analysis of post-translational modifications in human serum transthyretin associated with familial amyloidotic polyneuropathy by targeted LC–MS and intact protein MS☆

Marta Vilà-Rico[a], *Núria Colomé-Calls*[b], *Luna Martín-Castel*[b], *Marina Gay*[c], *Sebastián Azorín*[d], *Marta Vilaseca*[c], *Antoni Planas*[a,*], *Francesc Canals*[b,**]

[a]*Laboratory of Biochemistry, Institut Químic de Sarrià, Universitat Ramon Llull, Barcelona, Spain*
[b]*Proteomics Laboratory, Vall d'Hebron Institut d'Oncologia, Barcelona, Spain*
[c]*Institute for Research in Biomedicine (IRB Barcelona), Barcelona, Spain*
[d]*Nephrology and Transplant Unit, Hospital Clínic de Barcelona, IDIBAPS, Barcelona, Spain*

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ABSTRACT

Transthyretin (TTR) is an amyloidogenic tetrameric protein, present in human plasma, associated with several familial amyloidoses. Variability of TTR is not only due to point mutations in the encoding gene but also to post-translational modifications (PTMs) at Cys10, being the most common PTMs the S-sulfonation, S-glycinylcysteinylation, S-cysteinylation and S-glutathionylation. It is thought that PTMs at Cys10 may play an important biological role in the onset and pathological process of the amyloidosis. We report here the development of a methodology for quantification of PTMs in serum samples, as well as for the determination of serum TTR levels, from healthy (wt) and TTR-amyloidotic (V30M mutation) individuals. It involves an enrichment step by immunoprecipitation followed by mass spectrometry analysis of (i) the intact TTR protein and (ii) targeted LC–MS analysis of peptides carrying the PTMs of interest. Analysis of serum samples by the combination of the two methods affords complementary information on the relative and absolute amounts of the selected TTR PTM forms. It is shown that methods based on intact protein are biased for specific PTMs since they assume constant response factors, whereas the novel targeted LC–MS method provides absolute quantification of PTMs and total TTR variants.

Biological significance
The study of TTR has a high clinical relevance since it is responsible for diverse familial polyneuropathies. In particular, more than 80 point mutations have been described through genetic studies. However, genetic heterogeneity alone fails to explain the diverse onset and

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* *Correspondence to:* A. Planas, Institut Químic de Sarrià, Via Augusta 390, 08017 Barcelona, Spain.
** *Correspondence to:* F. Canals, Vall d'Hebron Institut d'Oncologia, Psg. Vall d'Hebron 119-129, 08035 Barcelona, Spain.
E-mail addresses: antoni.planas@iqs.edu (A. Planas), fcanals@vhio.net (F. Canals).

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pathological process of the TTR related amyloidosis. The use of proteomic characterization is required to gather information about the PTMs variants present in serum, which have been suggested to be relevant for the amyloidotic pathology. This article is part of a Special Issue entitled: HUPO 2014.

1. Introduction

Human transthyretin (hTTR; MIM#176300) is a homotetrameric protein that functions as the backup transporter for thyroxine hormone (T4) in plasma and it is its main transporter across the blood brain barrier. TTR is also the main carrier of retinol by forming a 1:1 complex with the retinol-binding protein (RBP) [1,2]. It is synthesized in the liver and the choroid plexus of the brain [3], the liver being the main responsible for plasmatic TTR production. Whereas TTR transports nearly all the circulating RBP in serum and it is the main thyroxin transporter in cerebrospinal fluid (CSF), it only transports around the 15% of the serum circulating thyroxin [4]. hTTR is an amyloidogenic protein associated with senile systemic amyloidosis (SSA), caused by wild-type (wt) TTR [5], affecting up to 25% of the population that is more than 80 years old. It is also related to several hereditary amyloidosis classified as rare diseases [6,7]: familial amyloidotic polyneuropathy (FAP), produced by single point mutants like V30M or L55P, where the pathology can develop at an early age; familial amyloidotic cardiomyopathy (FAC), mainly associated with V122I and T60A variants; and central nervous system selective amyloidosis (CNSA), the main representative being the A25T and D18G TTR variants [8].

Amyloid fibril formation is initiated by TTR tetramer dissociation into dimers and monomers that evolve to a misfolded or non-native monomer intermediate that starts an intermolecular aggregation process involving a number of states through soluble oligomers and leading to mature fibrils [9–13]. Several studies have shown that TTR intermediates (protofibrils and soluble oligomers), rather than mature fibrils, are the toxic species in cell cultures and that they may play a role in pathogenesis [14,15].

TTR is a highly abundant protein in plasma with concentrations around 0.2–0.4 μg/μL in healthy individuals. However, lower TTR levels have been described for TTR-amyloidotic patients [16,17]. It occurs as a very heterogeneous protein where variability is not only due to point mutations in the encoding gene but also to post-translational modifications (PTMs) at Cys-10, the single Cys residue in the protein sequence [18,19]. Only around 10–15% of the circulating TTR in plasma remains unmodified at this residue and the most common PTMs at Cys-10 are the S-sulfonation (S-Sulfo), S-glycinylcysteinylation (S-CysGly), S-cysteinylation (S-Cys) and S-glutathionylation (S-GSH) [20]. It is thought that PTMs may play an important biological role in the onset and pathological process of the TTR-related amyloidosis, although clinical implications are still badly understood [21–27].

Prior studies based on mass spectrometry have addressed the detection and identification of TTR variants in plasma, serum or CSF. In all cases, a common starting step involves the enrichment of TTR by the use of polyclonal antibodies or by SDS-PAGE. Analysis of the immunoprecipitated protein is then performed by MALDI-MS [28,29], MALDI-FTICR-MS [30,31] or LC–MS [20,32–36] techniques. In most cases, the study of TTR heterogeneity is based on the analysis of the intact protein, where the different TTR variants are assigned on the basis of the mass shift observed in the spectra. An additional digestion step by a combination of different enzymes (trypsin, Arg-C, Asp-N, Glu-C or Lys-C) is often performed to further confirm or determine the location of the modification [28–31,35,36]. Few studies are designed to quantify the total amount of TTR and the different TTR variants. These works are based on the study of the intact protein [29,34] or by mass fingerprinting [30,31] with the assumption that all Cys-10 forms or point mutation variants present the same response factor. However, the presence of a modification or mutation may affect the ionization of the protein resulting in different signal responses.

We here report the development of an analytical mass spectrometry methodology with the aim of quantifying the absolute concentration of the 5 most common TTR Cys-10 PTMs in serum and plasma samples. Additionally, the same methodology will allow the determination of the total amount of TTR in serum and plasma of healthy and FAP individuals bearing V30M mutation, as well as the mutant:wild type (V30M:wt) protein level ratios, which could also play a role in the development of amyloidosis. The strategy is based on targeted LC–MS high resolution analysis (HR-XIC) of a mixture of peptides coming from the digestion of the immunoprecipitated TTR in an Ultra High Resolution-QTOF instrument. For the quantification of wt TTR, V30M TTR, and their PTMs at Cys-10 (free Cys, S-Cys, S-CysGly, S-GSH and S-Sulfo) a set of 7 unique labeled TTR peptides containing the sequence of interest and their modifications were synthesized and added to the samples at known concentrations. In this way, possible changes in response factor due to the presence or absence of modifications are taken into account to determine the percentages of each modification as well as the wt:V30M ratio. In parallel, we used an ESI-MS strategy based on the analysis of the intact protein as described in the bibliography [20], where the immunoprecipitated TTR was directly infused in an Ultra High Resolution-QTOF instrument, and the relative abundance of each TTR variant was calculated based on the intensity of its corresponding signals in the MS spectra.

2. Materials and methods

2.1. Samples

Human serum samples were kindly provided by the Department of Nephrology and Urology at the Hospital Clínic de Barcelona and had the corresponding informed consent agreement.

Human blood samples were collected and allowed to clot for 30 min at room temperature and subsequently centrifuged at 1300 ×*g* for 15 min (BD Vacutainer® SST™ Tubes). Serum specimen was extracted from the tube avoiding the fraction closer to the separating gel. Aliquots of 250 μL were then prepared and immediately frozen at −80 °C until analyzed.

2.2. Characterization of TTR digestion with different proteases

Recombinant wt TTR (wt rhTTR), obtained as described in [37], was digested with trypsin (Trypsin Gold Mass Spectrometry Grade, Promega), chymotrypsin (Sigma), Asp-N (Sigma), Glu-C (Sigma) and arginine-C (Arg-C, Sigma). 100 μg of protein was digested in each protease test in 1 M urea–50 mM ammonium bicarbonate (AB) buffer, at 1:10 (trypsin), 1:50 (chymotrypsin, Arg-C, Glu-C) and 1:100 (Asp-N) enzyme:protein ratios, ON at 37 °C. Samples of each of the different digests (500 ng) were analyzed on a Maxis Impact Q-TOF spectrometer (Bruker, Bremen), coupled to a nano-HPLC system (Proxeon, Denmark). The samples, dissolved in 5% ACN–0.1% formic acid in water, were first concentrated on a 100 μm ID, 2 cm Proxeon nanotrapping column and then loaded onto a 75 μm ID, 25 cm Acclaim PepMap nanoseparation column (Dionex). Chromatography was run using a 0.1% formic acid–ACN gradient (5–35% in 20 min; flow rate 300 nL/min). The column was coupled to the mass spectrometer inlet through a Captive Spray (Bruker) ionization source. MS acquisition was set to cycles of MS (2 Hz), followed by 3 second cycles of MS/MS (4–16 Hz, intensity depending) of a variable number of the most intense precursor ions, with an intensity threshold for fragmentation of 2000 counts, and using a dynamic exclusion time of 2 min, with an automated precursor re-selection when a 3 fold increase in intensity was observed. All spectra were acquired on the range 150–2200 Da. LC–MS/MS data was analyzed using the Data Analysis 4.0 software (Bruker). Peptides were identified using Mascot (Matrix Science, London UK) by search on a database constructed with TTR sequences (wt and V30M). MS/MS spectra were searched with a precursor mass tolerance of 10 ppm, fragment tolerance of 0.05 Da, protease specificity with a maximum of 2 missed cleavages, cysteine modifications (S-Cys, S-Sulfo, S-CysGly and S-GSH) set as variable modifications and methionine oxidation also set as variable modification. Significance threshold for the identifications was set to $p < 0.01$, minimum Ions score of 20.

2.3. Targeted LC–MS analysis by high resolution-extracted ion chromatograms (HR-XIC)

2.3.1. Immunoprecipitation with hydrazide-immobilized antibody (IP Ab-ULH)

Polyclonal rabbit anti-human TTR antibody (Dako) was coupled to UltraLink® Hydrazide Resin (Thermo Scientific) following the resin manufacturer's protocol. 225 μg of immobilized antibody (Ab-ULH) was incubated with 25 μL of human serum for 1 h and 40 min at room temperature with soft agitation. After TTR binding to the Ab-ULH, 5 washes with 500 μL PBS were performed. TTR was eluted with 100 mM triethylamine (TEA, Fluka) pH = 11.5 solution. Elution was performed in 3 steps by addition of 400 μL TEA followed by 2 min of sonication on a ultrasonic bath, and the total eluted volume was concentrated to 50 μL after 8 M urea-50 mM AB buffer exchange, by diafiltration in an Amicon® Ultra-0.5 mL centrifugal Filter, Ultracel®-3 K cut off membrane (Millipore).

2.3.2. Enzymatic digestion of transthyretin

After immunoprecipitation, determination of the total protein amount for each sample was performed using Bio-Rad DC™ Protein Assay Kit (Bio-Rad). Based on the amount of protein quantified, a fraction of the immunoprecipitated TTR (10 μg) was digested with Arginine-C (Endoproteinase Arg-C Sequencing Grade, Roche) during 6 h, 37 °C at a 1:23 ratio enzyme:protein. Another fraction (10 μg) of the immunoprecipitated protein was digested with trypsin (Trypsin Gold Mass Spectrometry Grade, Promega) ON, 37 °C at a 1:10 ratio enzyme:protein.

2.3.3. Standard labeled peptides

Labeled (5C13,N15 proline) peptides for the quantification of the 5 Cys-10 forms (>98% purity and quantified by AAA) were purchased from Peptide Synthetics (United Kingdom). The different peptides for the quantification of Cys-10 modifications (Table 1) will be referred as N-term heavy peptides. Labeled (6C13,4N15 arginine) peptides for the total TTR determination (99% purity and quantified by AAA) were purchased from AQUA Peptide Sigma-Aldrich. The two different peptides (Table 1) used for the total amount of protein determination will be referred as GSPAIN peptides (wt and V30M, for the wt TTR form and the mutant V30M TTR form, respectively). Labeled (6C13,4N15 arginine) GSPAIN V30M peptide carrying methionine-sulfoxide (>95% purity and quantified by AAA) was obtained from Centro Nacional de Biotecnología, Madrid, Spain.

2.3.4. LC–MS measurement with UHR-QTOF

TTR from human samples was purified and digested with Arg-C and trypsin as described above. Standard labeled N-term peptides were spiked into Arg-C digested samples after digestion and prior to LC–MS measurement. The same procedure was followed for the standard labeled GSPAIN peptides and the trypsin digested samples. The amount of heavy peptides in column was of 50 fmols for each GSPAIN peptide and of 50, 12.5, 7.5, 200 and 200 fmols for the Free Cys, S-CysGly, S-GSH, S-Cys and S-Sulfo N-term peptides, respectively. The samples were analyzed on a UHR-QTOF mass spectrometer (Bruker Impact), coupled to a Proxeon Easy nano-LC (Bruker). Samples of the TTR digests (50 ng) spiked with the standard peptides were first loaded into a 100 μm ID, 2 cm Proxeon nanotrapping column and then separated with a 10 min 0.1% formic acid–ACN gradient (5–35% in 10 min; flow rate 300 nL/min) on a Acclaim PepMap 75 μm × 25 cm, 3 μm particle size reverse phase nanoseparation column (Dionex) coupled to the mass spectrometer inlet through a Captive Spray (Bruker) ionization source. For quantification, MS acquisition was set to cycles of MS (0.5 Hz). All spectra were acquired on the range 150–2200 Da.

2.3.5. Data analysis

LC–MS data was first processed using Data Analysis 4.1 (Bruker) and then quantified using Skyline Software (MacCoss Lab) to filter and integrate precursor signals of target peptides. Using a HR-XIC Skyline template, extracted ion chromatograms for the

Table 1 – Summary of the signals monitored and its calculated LOD and LOQ.

Peptide	Charge	Label	m/z heavy	m/z light	LOD (fmol)	LOQ (fmol)
GP*TGTGESKCP*LMVKVLDAVR	4	P 5C13,N15	543.296	540.289	1.38	4.59
GP*TGTGESKC(C)P*LMVKVLDAVR[a]	4	P 5C13,N15	573.047	570.041	2.49	8.28
GP*TGTGESKC(GSH)P*LMVKVLDAVR[b]	4	P 5C13,N15	619.563	616.557	0.09	0.29
GP*TGTGESKC(CG)P*LMVKVLDAVR[c]	4	P 5C13,N15	587.303	584.296	0.44	1.47
GP*TGTGESKC(S03H)P*LMVKVLDAVR[d]	3	P 5C13,N15	750.712	746.702	23.0	31.6
GSPAINVAVHVFR*	2	R 6C13,4N15	688.887	683.883	61.7	61.7
GSPAINVAMHVFR*	2	R 6C13,4N15	704.873	699.869	43.0	44.1

[a] C(C):S-cysteinylation (S-Cys), cysteine on the side chain of cysteine by disulfide bond.
[b] C(GSH):S-glutathionylation (S-GSH), glutathione on the side chain of cysteine by disulfide bond.
[c] C(CG): S-glycinylcysteinylation (S-CysGly), H-cysteinyl-glycine-OH on the side chain of cysteine by disulfide bond.
[d] C(SO3H):S-sulfonation (S-Sulfo).

m/z corresponding to the main isotope and charge state signal for each target peptide were used for quantification.

2.3.6. Determination of response factor for methionine oxidized GSPAIN peptide

Pure recombinant hTTR protein was quantified based on absorbance at 280 nm [37] and 10 μg of protein was spiked into a 70 μg/μL BSA solution, which was then immunoprecipitated and digested with trypsin according to the above described protocol. The resulting digested protein was used to prepare solutions at 25, 50, 100 and 150 ng/μL of digested rhTTR. A known amount of total V30M GSPAIN peptide, containing both oxidized and non-oxidized forms at unknown proportions, was added to each solution (total final concentrations of 25, 50, 100 and 150 fmol/μL, respectively). Samples were then analyzed by the described LC–MS strategy. From the results, and taking into account the known concentrations of rhTTR and total GSPAIN peptide, the response factors for the non-oxidized and oxidized forms of the V30M GSPAIN peptide were calculated.

Additionally, a standard curve for the labeled V30M GSPAIN oxidized peptide was performed in triplicate analyzing serial dilutions of the standard labeled peptide in the presence of trypsin digest of TTR as a matrix. The results were used to calculate the response factor for the oxidized form of the peptide.

2.4. Intact protein analysis

2.4.1. In solution immunoprecipitation

For TTR immunoprecipitation, 225 μg of the polyclonal rabbit anti-human TTR antibody (Dako) was incubated with 25 μL of human serum over night at 4 °C. After incubation, centrifugation at 9000 ×*g*, 10 min and 4 °C allowed the precipitation of the TTR-Ab complex. The pellet obtained was washed 3 times with 0.1 M AB buffer and finally resuspended in 50% methanol–1% formic acid [20] at approximately 4 pmol TTR/μL, according to the reported TTR concentrations in serum.

2.4.2. Intact protein measurement with UHR-QTOF

TTR immunoprecipitated as described below was analyzed on a UHR-QTOF mass spectrometer (Bruker Impact). The sample was directly infused with a syringe pump at 3 μL/min into an ESI source (Bruker). The MS acquisition method was set up to acquire only MS data during 5 min, with MS cycles of 0.5 Hz in the mass range from 50 m/z to 1500 m/z. MS data was analyzed using Data Analysis 4.1 software (Bruker).

Lock mass calibration was performed prior to averaging the spectra. All measurements were done in charge envelope +14, taking into account the intensity of the 5 most intense isotope peaks for each modification. Peak inspection was performed manually and the sum of these 5 isotopes was considered as the total intensity for a given modification. From the total intensity of each form, the percent of each modification with respect to the sum of all forms was calculated, for both wt and V30M TTR.

2.5. Top-down MS analysis

Top-down MS experiments were performed on a 7 T LTQ-FT Ultra mass spectrometer (Thermo Scientific). Purified TTR was reconstituted with ESI solution (MeOH, 1% FA (1:1, v/v)) and infused by automated nanoelectrospray using a Triversa Nanomate (Advion BioSciences) as the interface. Full MS spectra (m/z 200–2000) were acquired at 100,000 resolution (m/Δm 50% at 400 m/z) and, after full scan analysis, individual charge state ions of the multiply protonated proteoforms were selected for isolation in the LTQ using isolation widths of 5–10 m/z. Isolated ions were then fragmented by either CID or ECD. CID fragmentation was performed in the trap whereas isolated ions were guided to the FTICR cell for ECD fragmentation. Fragment detection was done in the FTICR cell for both types of fragmentation at 100,000 resolution (m/Δm 50% at 400 m/z) and averaging 200–1000 scans. For CID experiments precursor ions were activated using 30% to 40% normalized collision energy at the default activation q-value of 0.25. For ECD experiments the following settings were used: 3–5 energy (arbitrary units) corresponding to a cathode voltage of 1.5 V to 3.5 V, 127 ms delay (with 0 ms additional delay) and 15–75 ms duration. Fragmentation efficiency was optimized to maximize product ion signal intensity for both CID and ECD. The analyzer charge capacity was set to a target value of 500,000 and 1000,000 counts for CID and ECD MS/MS experiments respectively. Protein masses and zero charged fragments masses were determined by deconvolution using Xtract algorithm integrated in Xcalibur software vs 2.07 (Thermo Scientific). Data validation was done using ProSight PC 2.0 software (Thermo Scientific) in a single protein mode using a sequence gazer option.

3. Results and discussion

3.1. Immunoprecipitation of TTR from serum

The first step of both methodologies consists of immunoprecipitation of serum TTR using a polyclonal antibody. Polyclonal antibodies present several advantages, such as the lack of specificity for a certain modification or the lack of sensitivity in front of point mutations, allowing the use of the same procedure for a wide variety of samples. In addition, they can form precipitating immune complexes with homogeneous monomeric protein antigens, since each antibody can interact with a different epitope on the antigen. In the particular case of TTR, and given its tetrameric nature in plasma, they are able to form precipitating immune complexes without the need of adding immobilized protein A or G. We chose to use this immunoprecipitation "in solution" for minimal manipulation of the sample for intact protein analysis. However, in the case of the LC–MS HR-XIC strategy the antibody was first immobilized, used to capture TTR from plasma, and then treated with triethylamine, to release antibody-free TTR in order to improve the yield of the enzymatic digestion of the protein.

3.1.1. Immunoprecipitation of TTR with hydrazide-immobilized antibody and TTR recovery

Conditions for the immunoprecipitation with immobilized antibodies (Ab-ULH, see the Materials and methods section) were set up using solutions of known concentration of recombinant human TTR (rhTTR). rhTTR was prepared either in PBS buffer alone or in the presence of BSA at concentrations similar to plasma, to mimic plasmatic conditions, in case the complexity of the sample could affect the yield of the IP. The recovery from TTR solutions in the concentration range reported for plasma TTR was practically quantitative (Supplementary material, Fig. S1A). In order to further check that the amount of Ab used is enough to rescue all the plasmatic TTR, solutions ranging from 0.1 to 0.6 μg/μL of rhTTR in PBS or PBS plus 70 μg/μL BSA were immunoprecipitated (Fig. 1A). The amount of TTR in the IP fraction was quantified using the standard curve prepared from known amounts of rhTTR in a SDS-PAGE gel (Fig. 1B). The results confirmed that recovery was practically quantitative and linear in all the range of concentrations assayed. In addition, two negative controls were performed (Fig. 1A, IP BSA and IP PBS). Applying the immunoprecipitation protocol to a solution of BSA or PBS showed no bands interfering with TTR, but some background of BSA, even after extensive washing, or leaking Ab was

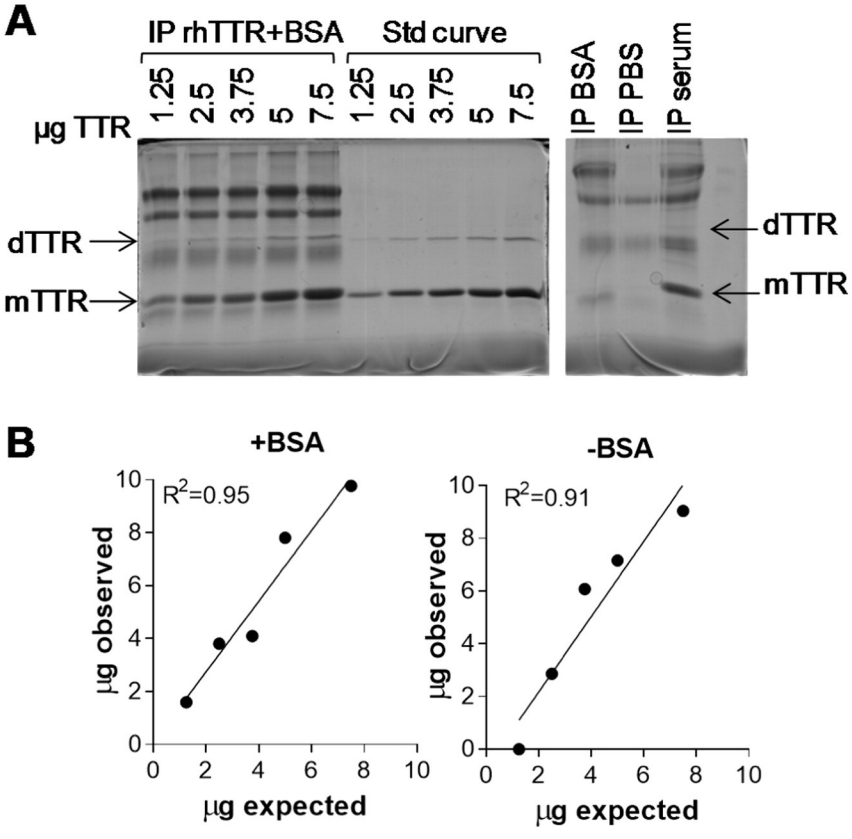


Fig. 1 – Optimization of TTR immunoprecipitation with immobilized (Ab-ULH). (A) Left: Ab-ULH IPs from solutions with increasing amounts of rhTTR, as indicated, in the presence of BSA (70 μg/μL) and rhTTR standard calibration curve. Right: control IPs from a BSA solution and PBS, and IP from serum sample. Half of each IP was loaded in the gel; (B) recovery determination for experiment in panel A and for the same experiment in the absence of BSA. Gels were stained with Coomassie Blue, scanned with LabScan and quantified using ImageQuant software (GE Healthcare). Bands corresponding to monomer and dimer of TTR are indicated with arrows as mTTR and dTTR, respectively.

observed. Finally, immunoprecipitation from human serum samples according to the established protocol was tested (Fig. 1A, IP serum), confirming quantitative recovery of serum TTR.

3.1.2. TTR recovery upon immunoprecipitation in solution

In a similar way, we checked the conditions for total recovery of TTR by immunoprecipitation with the antibody in solution, performed essentially as in [20]. Immunoprecipitation from 25 μL solutions containing rhTTR concentrations ranging from 0.2 to 0.6 μg/μL was quantitative, confirming total TTR rescue from the solution after immunoprecipitation (Supplementary material, Fig. S1B).

3.2. Strategy 1: targeted LC–MS method

3.2.1. Selection of target peptides and digestion optimization

Digestion of purified rhTTR with different enzymes was performed to test the coverage of the TTR sequence by LC–MS/MS analysis (Fig. 2). Since we are interested in the study of TTR Cys-10 modifications, digestion with trypsin does not provide a suitable peptide, due to the presence of two Lys residues too close in the sequence (Lys9 and Lys15), which would result in a peptide too short for LC–MS analysis, and with the cleavage site contiguous to the modified residue, which could affect the cleavage efficiency. Suitable peptides were observed in both the Asp-N and Arg-C digests, the later being the one giving the strongest MS signal. Thus, Arg-C digestion was selected for the analysis of the N-term peptides carrying the different modifications at Cys-10. The same digestion produces also the GSPAINVAVHVFR peptide (and its V30M mutant version) that can be used for the quantification of the total TTR amount.

Since the GSPAIN peptides are also tryptic peptides, they allowed a direct comparison between the efficiency of trypsin and Arg-C digestion of TTR. Experiments to assess the digestion performance were carried out on serum samples having both wt and V30M TTR. After immunoprecipitation with ULH immobilized antibody, the amount of the different peptides obtained was quantified using standard peptides, as detailed below. Different conditions for Arg-C digestion were tested attempting to optimize the yield, as monitored by the GSPAIN peptide quantification in comparison to a parallel trypsin digestion of the same sample. Conditions assayed included: different enzyme:protein ratios (1:15 to 1:100), presence of different denaturing agents (10% ACN, 10% trifluoroethanol, 2 M urea, 8 M urea), addition of 10 mM $CaCl_2$, different incubation times (4–16 h), different protein concentrations during the digestion, and 3 successive additions of the enzyme, at 2 h intervals. It was found (Fig. 3A and B) that the yields of the GSPAIN peptides upon Arg-C digestion were 4 to 10-fold lower than the obtained for trypsin digestion. A decrease in the amount of GSPAIN peptide measured at long digestion times was also apparent (Fig. 3B). LC–MS/MS analysis of the Arg-C digests showed the presence of some non tryptic peptides, in particular N-terminal truncated forms derived from the GSPAIN peptides (Supplementary material, Fig. S2), pointing to the presence of some minor proteolytic activity that could explain the observed decrease in the measured amount of GSPAIN peptides. Similar results were obtained when using other Arg-C enzymes available from different vendors.

Since improving the Arg-C digestion yield was not really possible, and the Arg-C N-term peptide being the best-suited for the study of Cys-10 modifications, we devised an analysis strategy based on two parallel digestions. After immunoprecipitation of serum TTR, an aliquot of the recovered protein was digested with trypsin for the quantification of the total TTR amount in serum through the GSPAIN peptides. A second aliquot was digested with Arg-C for the quantification of the different N-term peptides. Since Arg-C digestion cannot be completed, we checked that the relative amounts of each of the Cys-10 modified forms were constant along the progression of the digestion. As shown in Fig. 3C and 3D, the proportion of the different forms is constant within experimental error up to 10 h of digestion. We chose a digestion time of 6 h under these conditions to measure the relative amounts of each Cys-10 form. From those, the absolute amounts of each TTR form were calculated based on the total TTR amount determined from the analysis of the trypsin-digested protein.

3.2.2. Labeled peptide standard curves for quantification

Table 1 shows the peptide ions used in the quantification for the HR-XIC strategy, as well as the limits of detection (LOD, S/N = 3) and the limits of quantification (LOQ, S/N = 10) for the different peptides, derived from their corresponding standard curves (Supplementary material, Fig. S3). Standard curves for

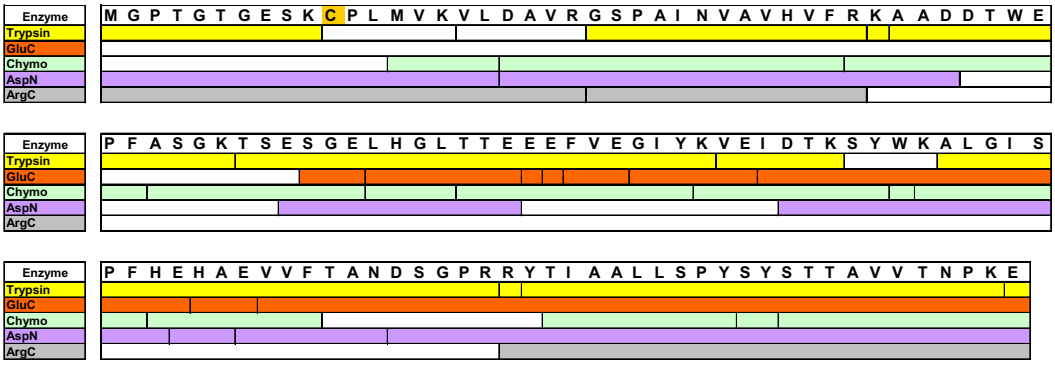


Fig. 2 – Schematic representation of the peptides resulting from rhTTR digestion with several proteases. The different boxes indicate the peptides obtained in a theoretical digestion; colored boxes indicate the peptides detected by MS/MS.

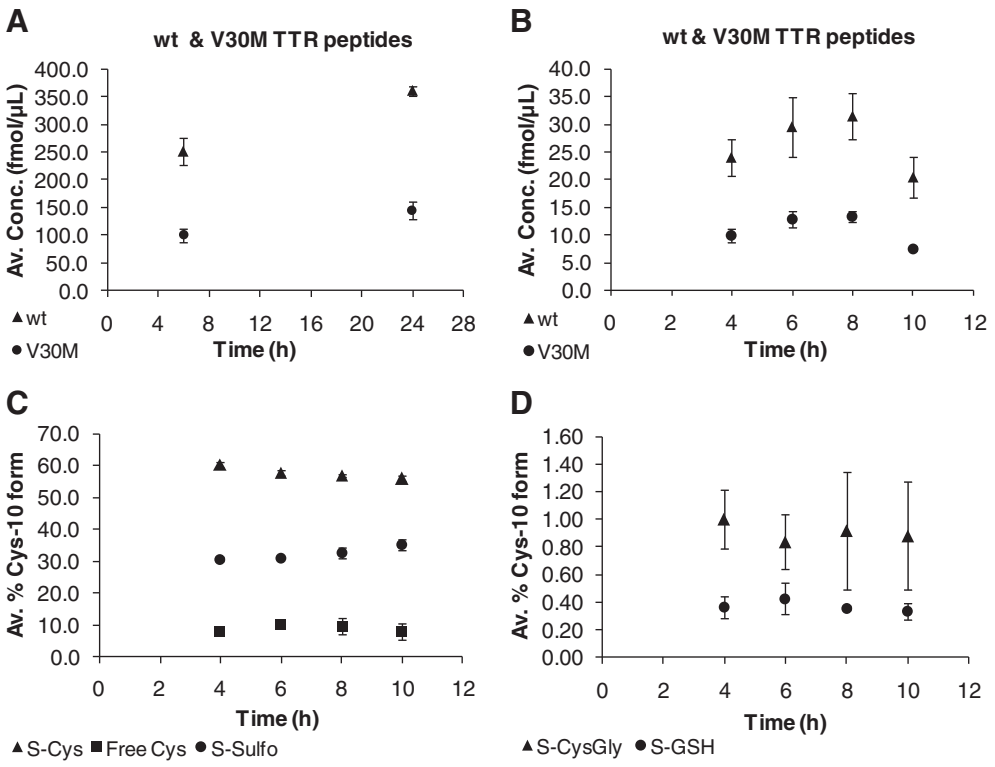


Fig. 3 – Time course of the digestions of immunoprecipitated TTR with trypsin and ArgC. (A) Trypsin digestion. Measured concentrations of GSPAINVAVHVFR (wt) and GSPAINVAMHVFR (V30M), respectively, as quantified by HR-XIC. (B) Arg-C digestion measured concentrations of GSPAIN wt and V30M TTR peptides, as in panel A. (C and D) N-term peptides measured along Arg-C digestion. The percent of each modified N-term peptide, GPTGTGESKC*PLMVKVLDAVR, was quantified by HR-XIC. In all cases, the average values measured at each time point for three replicate digestions are shown. Error bars correspond to the standard deviation. Note that the sample used for digestion was a pool of different serum samples and thus the wt:V30M ratio measured is not representative of a real sample.

each of the labeled peptides used for quantification were performed by serial dilution of Arg-C (N-term peptides) or trypsin (GSPAIN peptides) in the presence of digested immunoprecipitated TTR as matrix. The average heavy/light (H/L) ratio of the three replicates analyzed was represented against the concentration (fmol/µL) of heavy peptide injected. All the peptides presented linear standard curves in the concentration range studied, with R^2 values between 0.957 and 0.998. The charge state and isotopic species giving the strongest signal for each heavy labeled form were used for quantification.

3.2.3. Methionine oxidized peptides

The presence of methionine residues in the peptides used for quantification is normally avoided when designing peptide targeted analysis methods. In this study, however, both the N-terminal peptides used for Cys-10 modifications and the GSPAIN peptides used for total protein quantification have methionine residues. In the first case, methionine 13 is close to the modification site, and cannot be excluded from the targeted peptide by any suitable digestion procedure. In the case of the GSPAIN peptide, methionine is the site of the mutant of interest, and quantifying wt and V30M forms of TTR is one of the goals of the method. Thus, we had to take into account methionine oxidation of the peptides of interest. The signals for the ions corresponding to all possible methionine oxidized forms, both from the endogenous and the labeled peptides, were monitored in the HR-XIC LC–MS analysis.

We found that the signals for the oxidized forms for all the N-term peptides were negligible compared to the non-oxidized forms, and thus they were not further considered in the quantification. However, the standard peptide GSPAINVAMHVFR, used for quantification of total V30M TTR was found particularly prone to oxidation. The standard heavy peptide, of known total concentration derived from the amino acid analysis provided by the manufacturer, contained in fact both oxidized and non-oxidized forms at unknown proportions. Since attempts to convert the standard peptide quantitatively to the reduced or oxidized form were not successful, we devised an indirect strategy to obtain an estimation of the response factors of the oxidized and non-oxidized heavy peptide forms, and their proportions in the standard, based in the use of a rigorously quantified solution of a non-oxidized rhTTR V30M as a reference. The recombinant protein was quantified based on absorbance at 280 nm [37] and was used to prepare a solution of known concentration of rhTTR V30M spiked into a 70 µg/µL BSA solution, which was then immunoprecipitated and digested with trypsin according to the established protocol. The resulting digested protein was used to prepare solutions at various

known concentrations of digested rhTTR, to which different amounts of total V30M GSPAIN peptide, containing both oxidized and non-oxidized forms at unknown proportions, were added. Analysis of these samples by the described LC–MS strategy was used to derive response factors (signal area/fmol peptide) for the non-oxidized and oxidized forms of the V30M GSPAIN, based on the known concentrations of rhTTR and total GSPAIN peptide. A response factor significantly higher (13.63 fold) for the oxidized peptide was found.

We further confirmed the response factor for the oxidized V30M GSPAIN peptide by an independent, more accurate, measurement using a synthetic labeled standard peptide carrying a Met-sulfoxide. The standard curve for this peptide was determined as in Section 3.2.2, and is shown in Supplementary Fig. S3. Together with the results measured using the mixture of non-oxidized and oxidized forms of V30M GSPAIN, we calculated the ratio of response factors to be 11.11 (oxidized:non-oxidized V30M).

The measured response factors were used to quantify the total V30M TTR in samples, as the sum of non-oxidized and oxidized forms. In all serum samples analyzed, the proportion of the Met-30 oxidized form was found to be below 7%.

3.2.4. *Intra- and inter-assay precision for the targeted LC–MS strategy*

In order to determine intra- and inter-assay precision, a pool of serum from healthy individuals was used. From this pool, the complete sample preparation procedure, including immunoprecipitation and trypsin and Arg-C digestions, was performed in triplicate. Each of the digests was then analyzed by HR-XIC LC–MS in triplicate. The results obtained for total protein determination (trypsin digestion) and Cys-10 modified forms (Arg-C digestion) are shown in table 2. The reproducibility of the assay was very good, with coefficients of variation ≤2% for the determination of the total amount of protein and variations ≤8% for the quantification of the different Cys-10 forms, both intra- (triplicate sample processing) and inter-assay (triplicate LC–MS analysis). The only exception was for the Free Cys quantification, which presented an inter-assay coefficient of variation of 19%. It is likely that the higher variability observed for the Free Cys form reflects its susceptibility to oxidation during the manipulation of the sample. We have not explored preanalytical issues at this point of the development of the methods, but this is clearly a point to take into account, given the nature of the modifications of interest and in the light of previous reports [20].

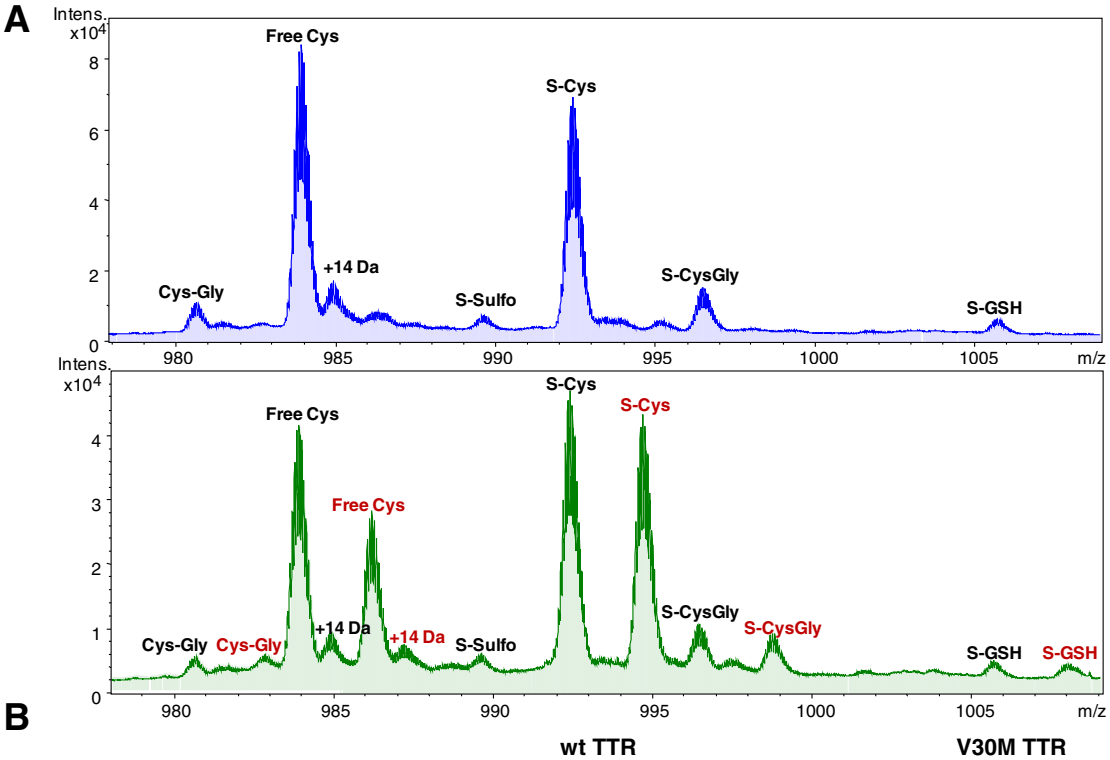
Table 2 – Determination of the intra- and inter-assay precision for the N-term Cys10 PTMs quantification and for the determination of the total TTR amount.

		Free Cys			S-Cys			S-CysGly			S-GSH			S-Sulfo			Total TTR		
		IP1	IP2	IP3	IP1	IP2	IP1	IP1	IP2	IP3	IP1	IP2	IP3	IP1	IP2	IP3	IP1	IP2	IP3
Intra-assay	STDV	0.085	0.264	0.083	0.329	0.062	0.354	0.073	0.068	0.044	0.008	0.006	0.007	0.354	0.275	0.179	0.950	0.450	0.107
	Mean (% of PTM or ng TTR/μL serum)	4.95	4.13	3.18	70.55	70.80	22.02	2.01	1.85	2.18	0.48	0.46	0.54	22.02	22.76	20.47	55.11	54.99	56.26
	CV (%)	1.71	6.4	2.61	0.47	0.09	1.61	3.65	3.68	2.04	1.66	1.31	1.29	1.61	1.21	0.87	1.72	0.82	0.19
	Av CV (%)	3.57			0.28			3.12			1.42			1.23			0.91		
Inter-assay	STDV		0.779			1.495			0.153			0.039			1.042			0.701		
	Mean (% of PTM or ng TTR/μL serum)		4.09			71.66			2.01			0.49			21.75			55.45		
	CV (%)		19.06			2.09			7.61			7.88			4.79			1.26		

3.3. *Strategy 2: intact protein MS analysis*

3.3.1. *Relative quantification by intact protein analysis*

Analysis of intact immunoprecipitated TTR from serum by direct infusion to the electrospray source on a HR-QTOF instrument (Bruker Impact) allowed us to detect signals of m/z values compatible with the main Cys-10 modified forms of wt and V30M TTR, in charge states ranging from z = 9 to z = 19. Fig. 4A shows an example of the spectra obtained for 2 different serum samples, one containing only wt TTR and the other wt and V30M TTR. All the modifications of interest are shown, plus an unknown modification corresponding to a mass shift of +14 Da. As shown in Fig. 4B, a good agreement



B

	wt TTR m/z (z=+14)			V30M TTR m/z (z=+14)		
Modification	**Observed**	**Calculated**	**Δ ppm**	**Observed**	**Calculated**	**Δ ppm**
Cys→Gly	980.6508	980.6430	7.95	982.9345	982.9267	7.94
Free Thiol	983.9357	983.9278	8.03	986.2201	986.2116	8.62
wt+14 (unknown)	984.9378	-	-	987.2216	-	-
S-Sulfo (Sulfonate)	989.6472	989.6390	8.29	-	-	-
S-Cys (Cysteinyl)	992.4357	992.4281	7.66	994.7197	994.7119	7.84
S-CysGly (CysteinylGlycine)	996.5076	996.5011	6.52	998.7926	998.7848	7.81
S-GSH (Glutathione)	1005.7259	1005.7184	7.46	1008.0107	1008.0021	8.53

Fig. 4 – TTR spectra obtained by intact protein. (A) wt TTR spectra (blue) and V30M spectra (green) obtained by intact protein strategy in Impact (Bruker); (B) table of m/z values for the different modifications monitored in the charge state +14.

between the calculated and observed m/z values was obtained. To further confirm the identity of each of the assigned ions, a top-down analysis of each of the TTR forms (Fig. 5) was performed on a 7T LTQ-FT Ultra mass spectrometer confirming in all cases the structure assigned in Fig. 4 (Supplementary material, Tables S1–S15).

By this methodology it was not possible however to quantify the relative amount of the S-Sulfo form in V30M TTR, since its whole peak is overlapped with part of the S-Cys peak in wt TTR. For comparison purposes, the relative amounts of PTMs determined by this methodology were calculated without taking into account S-Sulfo forms (neither wt, nor V30M).

3.3.2. Intra- and inter-assay precision for the intact protein strategy

To determine the intra-assay precision we performed four different immunoprecipitations from a pool of human serum, and analyzed them according to the protocol described in the Materials and methods section. A second pool was immunoprecipitated and analyzed in 4 different days to assess inter-assay precision. The results are shown in Table 3. The procedure showed to be highly robust, giving an intra-assay coefficient of variation <8% for the total intensities measured, and <6% for the calculated % of the different PTMs measured. Results of the assay of a sample on different days, after cycles of freezing and thawing, showed a higher variation (<20%) for the total intensities, but even in this case the values for percent of PTMs showed a coefficient of variation ≤4%. The ratio of total wt:V30M TTR was calculated as the ratio of the signals resulting from totalling the peaks corresponding to the modified forms for wt and V30M TTR, respectively. Determination of the ratio total wt:V30M TTR gave also coefficients of variation <0.5% for both intra- and inter-assay.

3.4. Comparison between targeted LC–MS and intact protein strategies

In order to compare the results obtained by the two different analytical strategies, a group of 10 human serum samples, five carrying only wt TTR and five carrying both wt and V30M TTR, was analyzed by the two methodologies. The results obtained by the targeted LC–MS strategy for the absolute quantity of TTR are shown in Table 4. For V30M samples, in the case of the intact protein strategy, it was also possible to calculate the

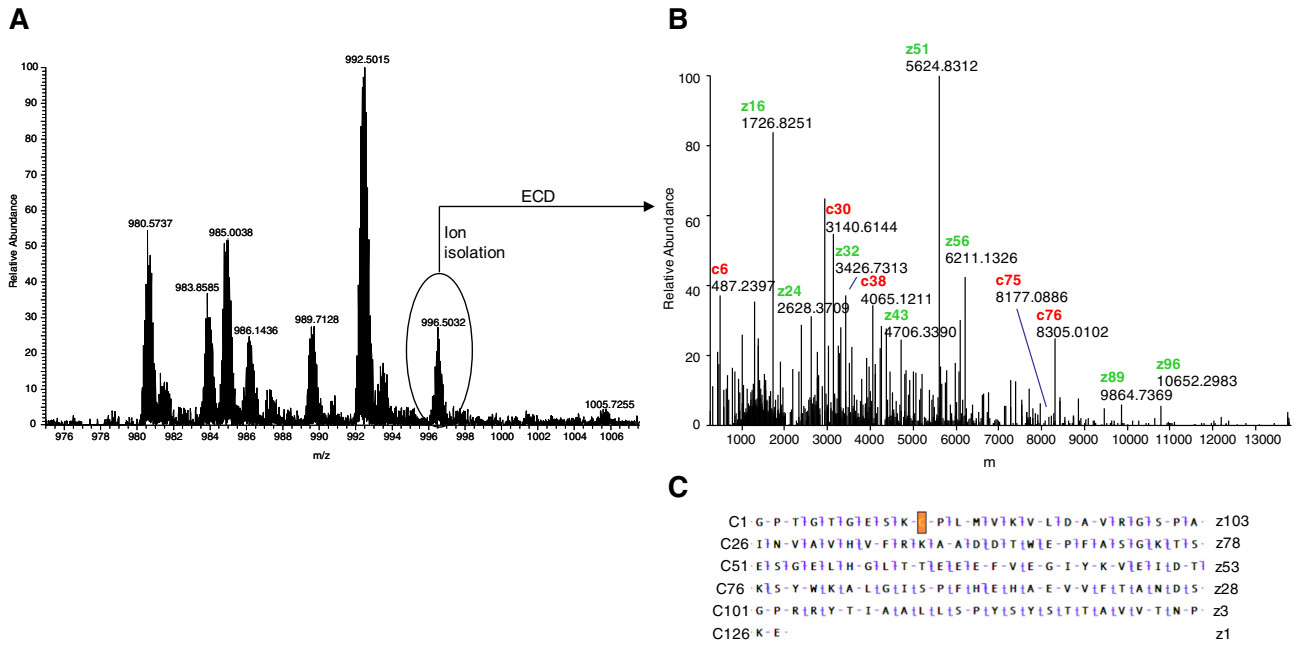


Fig. 5 – Mapping PTM sites in TTR by top-down MS. S-CysGly proteoform characterization. (A) Enlarged FT-ICR spectrum of TTR, Z = +14; (B) ion deconvoluted ECD spectrum of isolated ion m/z 996.50; (C) ECD fragmentation map showing S-CysGly PTM at Cys10, explained by fragments from C3 to C88 (total of 49 fragments).

ratio wt:V30M, by comparing the global intensity for each TTR form (Table 4, right).

Fig. 6A shows the comparison of the distribution pattern of the different Cys-10 forms, as determined by the two methods (Supplementary material, Tables S16 and S17). For this comparison, the S-Sulfo form was not considered since as it has been already mentioned, it cannot be properly quantified by the intact protein procedure. As it is clear from the figure, the observed pattern was quite different between both methodologies. By intact protein measurements, free Cys, S-CysGly and S-GSH fractions appear more abundant than they really are, according to the levels obtained from the absolute quantification. Conversely, the observed proportion for the S-Cys form appears to be much lower by intact protein measurement.

We also compared the % of total V30M and wt TTR in the serum samples, calculated by both strategies (Fig. 6B). We observed that both variants appear to be at approximately the same concentration, when looking at the intact protein level. However, absolute quantification shows that wt TTR was less abundant than V30M TTR, with a ratio around 40:60.

Comparison of the results from both techniques demonstrates that indeed, the response factor of the different TTR variants, when analyzed as intact protein, is not the same. Although relative quantification can be a good tool to compare protein forms among different samples, it is not suitable to establish which of those forms are really more abundant in a sample. The results shown here demonstrate the need for absolute quantification using labeled peptide standards to

Table 3 – Determination of the intra- and inter-assay precision for the total intensity, % of PTMs in wt and V30M TTR, and total % V30M determination by intact protein.

	Intra-assay								Inter-assay							
	In wt TTR				In V30M TTR				In wt TTR				In V30M TTR			
	TI	% PTM			TI	% PTM			TI	% PTM			TI	% PTM		
	CV (%)	Mean	STDV	CV (%)	CV (%)	Mean	STDV	CV (%)	CV (%)	Mean	STDV	CV (%)	CV (%)	Mean	STDV	CV (%)
Free Cys	5.59	15.73	0.425	2.70	4.97	22.64	0.599	2.65	17.69	13.63	0.122	0.90	18.48	19.15	0.119	0.62
S-Cys	2.06	55.17	0.911	1.65	1.50	54.90	1.182	2.15	19.00	57.89	0.686	1.19	18.79	54.89	0.477	0.87
S-CysGly	4.29	20.21	0.475	2.35	4.30	13.85	0.250	1.80	16.96	19.83	0.297	1.50	16.84	17.49	0.275	1.57
S-GSH	7.08	8.89	0.415	4.67	6.69	8.60	0.412	4.79	14.92	8.65	0.339	3.92	15.00	8.47	0.296	3.49
						Mean	STDV	CV (%)						Mean	STDV	CV (%)
% V30M TTR						46.70	0.053	0.11						48.25	0.037	0.08

Table 4 – Absolute quantification of TTR by HR-XIC and relative abundances of wt and V30M TTR by intact protein.

Sample [a]	HR-XIC					Intact protein	
	ng TTR/μL plasma						
	wt TTR	V30M TTR	Total TTR	% wt	% V30M	% wt	% V30M
Sample 1	52.41	0.08	52.49	100	–	100	–
Sample 2	62.14	0.18	62.31	100	–	100	–
Sample 3	118.79	0.16	118.95	100	–	100	–
Sample 4	51.43	0.38	51.81	100	–	100	–
Sample 5	24.42	0.06	24.47	100	–	100	–
Sample 6	51.24	84.54	135.78	37.74	62.26	51.69	48.31
Sample 7	42.73	65.71	108.44	39.4	60.6	52.76	47.24
Sample 8	25.7	52.99	78.69	32.66	67.34	52.58	47.42
Sample 9	28.09	50.44	78.48	35.73	64.27	50.71	49.29
Sample 10	38.08	68.95	107.03	35.58	64.42	56.53	43.47

[a] Samples 1–5 correspond to wt individual human samples and samples 6–10 to V30M individual human samples.

measure the absolute amounts of the different forms and thus have a real evaluation of their distribution in serum. The differences observed between the intact protein analysis and the LC–MS method would result from different response factors of the different proteoforms, which would be a consequence of their different ionization capability upon electrospray ionization. In the LC–MS method, the response of the measurement of each form is corrected by the corresponding internal standard, and therefore the proportions of the different forms measured should be closer to the real composition of the sample.

However, it should also be noted that the intact protein analysis method affords information on the relative amounts of the Cys-10 PTM forms of wt and V30M TTR proteins separately, whereas in the targeted LC–MS method the N-term peptides used for PTM quantification measure the total amounts of those PTM forms. On the other hand, as seen in Fig. 6A, due to the greater response factor for some of the minor PTM forms (S-CysGly, S-GSH), the intact protein method presents a somehow higher sensitivity for their relative quantification.

The most common technique to determine the total amount of TTR in serum samples is the ELISA method. In an attempt to compare the results here obtained for absolute quantification by the targeted LC–MS method, a set of serum samples were analyzed in parallel by both methods (see Supplementary material, Fig. S27). We observed a reasonable correlation between both techniques up to 50 ng TTR/μL serum, but the ELISA response was saturated at higher concentrations even though the measured absorbances in the ELISA were in the linear range of the standard curve. It suggests that some interference caused by serum components is affecting the ELISA method here tested. On the other hand, the total TTR concentration values measured by our LC–MS method were significantly lower than the established normal range (150–360 ng/μL) [38], suggesting a systematic bias. Incomplete recovery of the immunoprecipitated TTR, or incomplete digestion of the protein, could potentially account for this discrepancy. In the described experiments to control the immunoprecipitation procedure we found the recovery of

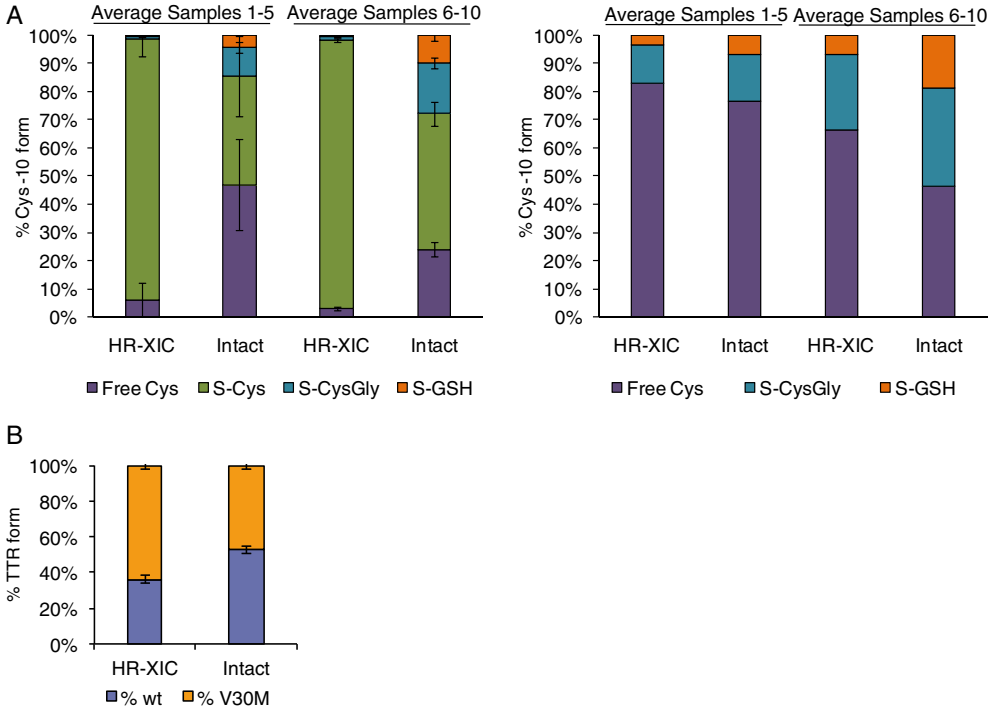


Fig. 6 – HR-XIC and intact protein measurement comparison. (A) On the left, distribution of Cys-10 modified TTR forms by both methodologies, error bars show standard deviation between the average of two groups of samples, 1–5 wt TTR, 6–10 V30M TTR; on the right, distribution of Cys-10 modified forms excluding S-Cys. (B) Percent proportion of total wt and V30M TTR measured by both methodologies for samples 6–10.

rhTTR to be practically quantitative (Fig. 1). TTR capture from plasma samples appeared to be also complete. However, it cannot be completely ruled out that elution from the antibody resin was less efficient from plasma samples. We also looked at the time-course of tryptic digestion. Although the amount of measured TTR by the LC–MS method showed no further increase after 24 h of digestion, this again does not rule out that TTR digestion is in fact incomplete. Other factors that could potentially result in the observed discrepancy could be the presence of modified TTR forms not prone to trypsin digestion, such as glycation or carbonylation derivatives. Troubleshooting of the ELISA procedure assayed, or checking alternative ELISA assays available to clarify these discrepancies is beyond the purpose of this work. Our results show that the LC–MS method developed can be at least as sensitive and robust as the usual immunological methods used, and give a further insight into the detailed composition of different TTR Cys-10 modified forms.

4. Conclusion

Two complementary MS based methods for the quantification of the most common Cys-10 PTM isoforms of TTR in plasma or serum have been set up. The targeted LC–MS method developed here, unlike previously described methods, allows the absolute quantification of the levels of each of the Cys-10 modifications, as well as the absolute concentrations of wt TTR and the amyloidotic V30M isoform. Intact protein analysis, on the other hand, provides additional valuable information of the relative distribution of the Cys-10 PTMs for wt and V30M proteins. It is shown that the intact protein ions of the different isoforms display large differences in response factors, which makes the targeted LC-S analysis, using standard peptides, mandatory for absolute quantification of their levels in serum. Overall, the combined analysis by the two developed strategies constitutes a robust method for the characterization of the PTM forms of TTR in serum, which, when applied to the appropriate clinical samples, can shed light into the relevance of these isoforms on TTR amyloidosis.

Conflict of interest

The authors declare no conflicts of interest.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.jprot.2015.04.016.

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