

Unlocking the molecular mechanism of glycine reuptake inhibition

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Nordic EMBL Partnership for Molecular Medicin

EMBL



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- Bitopertin, one of the most advanced GlyT1 inhibitors failed in a phase III clinical trial study







CV and CVI constructs of GlyT1



Synthetic single-domain antibodies (sybodies) for inhibitor-bound conformation of GlyT1





Markus Seeger Iwan Zimmermann



Inhibition state-specific Sybody

"960" crystallization conditions $\bigcup_{i=1}^{n}$

"1" crystallization condition











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"960" crystallization conditions

"1" crystallization condition

Serial helical line scan data collection @ EMBL P14 beamline

- $5 \times 10 \ \mu m^2$ beam size
- Flux: 1.3×10^{13} ph/sec
- 12.7 KeV

Region of interest: $60 \times 14 - 290 \times 340 \ \mu m^2$ $100 - 10,000 \ frames$







19.145, 504 	July 2019 Octob								r 2019	
JE ROD'	Loops	ROIs	Diffra patte	ction F erns	rames with >15 spots	Total min data set	ni da s	ita sets used	Frames used	
	409 514		1,365,232		30,837	229		207	3,400	
Resolution Limit (Å)	Nu Obser	mber of ved L	Reflecti Inique	ons Possible	e Completene	ess R-I	=actor served	I/Sigma	R-meas	CC(1/2) (%)
25.0	18	33	30	31	96.8%	1(0.0%	15.99	10.9%	99.3
15.0	144	45	221	222	99.5%	1'	1.8%	17.59	12.8%	99.1
10.0	459	95	670	675	99.3%	12	2.7%	16.15	13.8%	98.9
5.0	20247		3177	3211	98.9%	44.6%		5.19	48.6%	89.3
4.0	46129		7219	7283	99.1%	61.0%		4.41	66.3%	84.5
3.8	8249		1297	1311	98.9%	12	7.8%	2.16	139.1%	51.2
3.6	9726		1582	1606	98.5%	15	3.2%	1.50	167.3%	46.7
3.4	7500		1217	1227	99.2%	29	9.2%	1.00	326.4%	30.1
Total	1534	451	24071	24304	99.0%	4	1.5%	4.38	45.1%	97.5
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Roger Dawson Peter Stohler





Markus Seeger Iwan Zimmermann P14 beamline



Cryo-EM Aarhus: Thomas Boesen Andreas Bøgglid

SPC: Maria Garcia Alai Christian Guenther Ioana-Maria Nemtanu

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Why GlyT1 inhibitors have not made it as a drug, yet?

