Corrections

Atomic Resolution Structures of the Core Domain of Avian Sarcoma Virus Integrase and Its D64N Mutant, by Jacek Lubkowski, Zbigniew Dauter, Fan Yang, Jerry Alexandratos, George Merkel, Anna Marie Skalka, and Alexander Wlodawer*, Volume 38, Number 41, October 12, 1999, pages 13512−13522.

Page 13514. In Table 1, the bottom three sections were misaligned with respect to the the previous sections in the table. Table 1 should appear as follows.

Table 1: Crystallization Conditions, Data Collection, and Refinement Statistics for ASV IN Structures

selected crystallization conditions	ASVIN-CIT	ASVIN-HEP	ASVIN-AS	D64N-CIT	ASVIN-TRN	D64N-TRN
buffer	0.1 M citrate	0.1 M Hepes	0.1 M Hepes	0.1 M citrate	0.1 M acetate	0.1 M Hepes
(pH)	(6.0)	(7.5)	(7.5)	(6.0)	(6.0)	(7.5)
precipitant	20% PEG4000	20% PEG4000	2 M$(NH_4)_2SO_4$	20% PEG4000	20% PEG4000	20% PEG4000
protein definition	core	core	core	core, mutant D64N	core	core, mutant D64N
			Data Collection Statistics			
total no. of reflections	357 298	250 390	1 034 785	345 764	262 703	345 283
no. of unique reflections	34 367	69 419	89 063	53 915	58 386	59 166
resolution range (Å)	13.0−1.42	15.0−1.06	20.0−1.02	20.0−1.20	15.0−1.15	15.0−1.15
completeness (overall) (%)	99.0	90.1	100.0	97.1	93.5	94.7
completeness (highest resolution shell) (%)	98.9 (1.47)	86.7 (1.08)	99.6 (1.04)	90.4 (1.22)	70.7 (1.19)	81.9 (1.19)
R_{sym}	0.046	0.034	0.056	0.060	0.037	0.046
average $I/\sigma(I)$ (overall)	39.5	32.3	43.6	28.4	35.5	44.8
average $I/\sigma(I)$ (highest resolution shell)	5.2	3.2	2.9	2.2	2.0	9.5
			Data Collection Strategy			
no. of passes	2	3	3	2	2	2
exposure time/frame (s)	5/150	12/20/120	15/30/120	60/180	20/60	20/60
maximum resolution (Å)	2.0/1.42	2.40/1.40/1.06	2.35/1.50/1.02	2.40/1.20	2.50/1.15	2.50/1.15
unit cell (a/c, Å)	66.18/78.73	65.37/80.14	65.54/80.12	66.56/78.36	66.13/78.59	65.54/80.07
			Refinement Statistics			
resolution range (Å)	10.0−1.42	10.0−1.06	10.0−1.02	10.0−1.20		
crystallographic R[a]	0.187	0.143	0.129	0.147		
rmsd bonds (Å)	0.014	0.016	0.015	0.020		
angle distances (Å)	0.029	0.031	0.030	0.029		
			Avg Coordinate Errors (Å) (No. of Atoms)[b]			
all atoms		0.020 (1034)	0.019 (1031)	0.028 (1030)		
C		0.021 (652)	0.020 (648)	0.029 (645)		
O		0.018 (184)	0.016 (189)	0.026 (197)		
N		0.021 (194)	0.020 (192)	0.028 (184)		
S		0.008 (4)	0.006 (3)	0.012 (4)		
			Average B Factor (Å^2)			
all protein non-H atoms	19.9	15.2	13.2	18.4		
main-chain atoms	17.5	13.5	11.5	16.2		
side-chain atoms	22.4	16.9	14.9	20.7		
solvent atoms	36.8	20.0	26.7	27.3		
no. of non-hydrogen protein atoms	1118	1132	1155	1114		
no. of solvent atoms	203	137	192	211		
no. of heterogen atoms[c]	19	15	27	18		

[a] Crystallographic R values are calculated on the basis of all observed intensities, which were measured within the resolution range used during the refinement. [b] The average errors of coordinates are obtained by inversion of the LSQ matrix. Only the atoms in single sites are included (disordered sites excluded; number of included atoms shown in parentheses). [c] The number shown corresponds to the nonprotein, nonsolvent atoms (citrate and glycerol molecules).

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