

Supplementary Material for “Optimization of a Series of Dipeptides with a P3 - Neopentyl asparagine residue as potent non-covalent Inhibitors of the Chymotrypsin-like activity of the Human 20S Proteasome”

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### Crystallographic data and refinement statistics

	Compound	
	20	34
PDB ID	3SDI	3SDK
Space group	P2 <sub>1</sub>	P2 <sub>1</sub>
Unit cell dimensions (Å, °)	a= 136.6 b= 299.5 c= 145.5 β= 113.2	136.1 299.4 146.2 112.9
Wavelength (Å)	0.97958	0.97958
Resolution (Å)	50 - 2.65	50 - 2.7
R <sub>sym</sub> <sup>a</sup> (%)	9.9 (37.8) <sup>b</sup>	8.3 (36.1)
Total observations	1097554	1044183
Unique reflections	297624	280182
Average redundancy	3.7	3.7
<I/σ>	9.5 (1.9)	8.9 (2.5)
Completeness (%)	95.8 (78.8)	95.3 (71.6)
Refinement resolution (Å)	50 – 2.65	50 - 2.7
Reflections (working/test)	290919/ 5996	274063/ 5652
R <sub>cryst</sub> /R <sub>free</sub> (%) <sup>c</sup>	21.9/25.3	22.3/25.8
Protein atoms	48900	49137
ligand atoms	84	86
MES atoms	24	24
Mg <sup>2+</sup> atoms	20	10

Water atoms	1	0
rmsd bond lengths (Å)	0.010	0.009
rmsd bond angles (°)	1.26	1.18
Ramachandran analysis		
most-favored (%/#)	90.9/5038	90.9/5050
additional allowable (%/#)	8.6/478	8.4/468
generously allowed (%/#)	0.3/16	0.4/21
disallowed (%/#)	0.2/12	0.3/16

<sup>a</sup> $R_{\text{sym}} = (\sum_{\text{hkl}} \sum_i |I_i(\text{hkl}) - \langle I(\text{hkl}) \rangle|) / \sum_{\text{hkl}} \sum_i I_i(\text{hkl})$  for  $n$  independent reflections and  $i$  observations of a given reflection.  $\langle I(\text{hkl}) \rangle$  is the average intensity of the  $i^{\text{th}}$  observation.

<sup>b</sup>numbers in parenthesis are for highest resolution shell.

<sup>c</sup> $R_{\text{cryst}} = \sum_h ||F_o(\mathbf{h})| - |F_c(\mathbf{h})|| / \sum_h |F_o(\mathbf{h})|$ , where  $F_o$  and  $F_c$  are the observed and calculated structure factors, respectively.