

## Supplementary Material

### *Enhancing ubiquitin crystallization through surface entropy reduction*

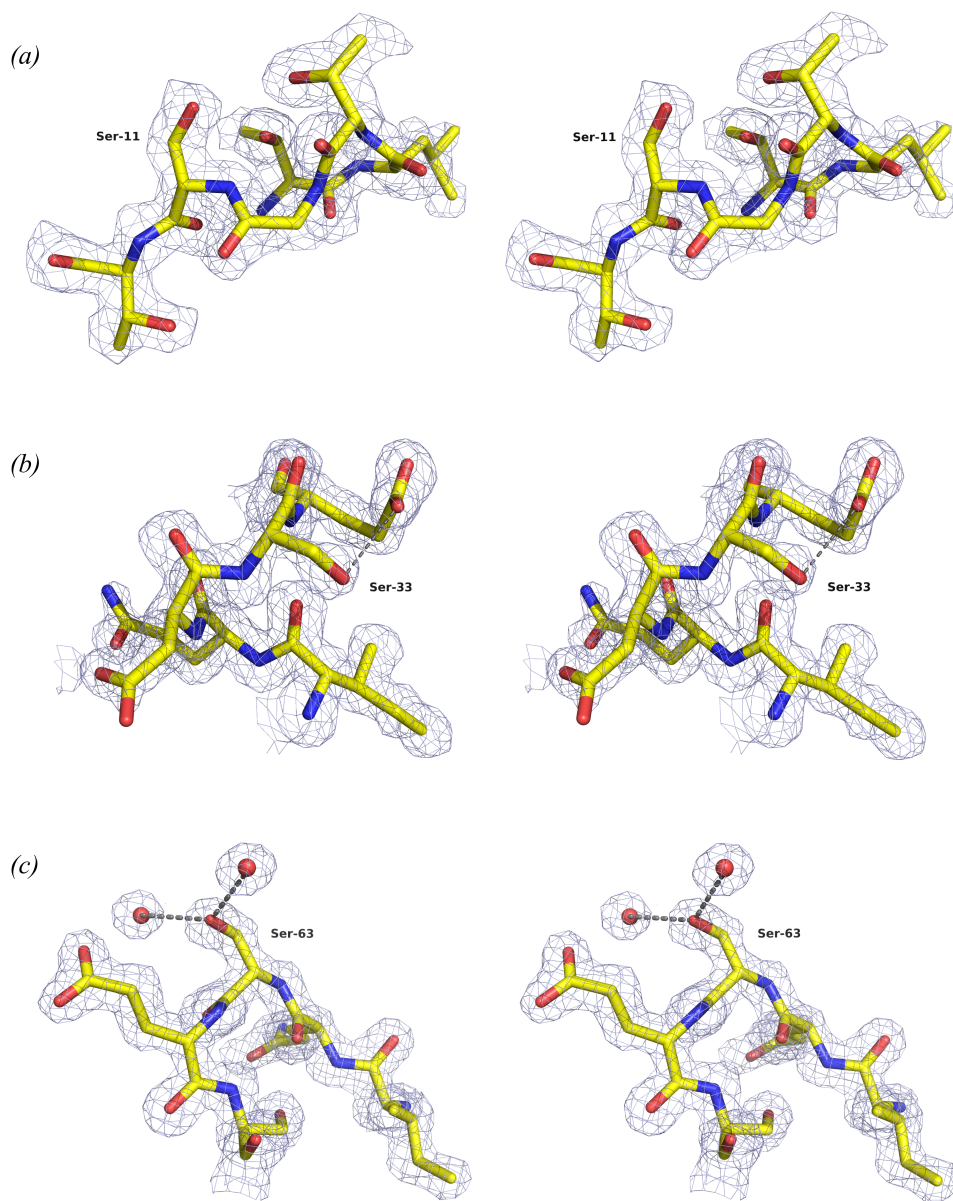
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**Table S1.** Details of hit rates for different ubiquitin variants.

	wt	K6S	K11S	K27S	K29S	K33S	K48S	K63S	K11S/K63S double mutant
Classics I	7	3	23	2	1	10	2	9	16
Classics II	4	1	27	1	0	11	2	9	18
PEGs I	0	0	18	0	0	4	2	0	---
PEGs II	1	0	12	0	0	3	1	6	---
Overall total	12	4	80	3	1	28	7	24	

**Table S2.** PDB entries used to calculate average wild-type ubiquitin structure

PDB entry	No. of independent chains in asymmetric unit
1UBI	1
1UBQ	1
1YIW	3
2ZCC	3
3ONS	1



**Figure S1.** Representative 2Fo-Fc electron density for the structures described in this paper. Stereo views are shown for maps contoured at  $1\sigma$ . Each map shows the vicinity of one of the mutant residues. (a) K11S mutant; (b) K33S mutant (B chain); a hydrogen bond is shown between the Ser-33 and Glu-34 side chains; (c) K11S/K63S double mutant; the Ser-63 side chain forms hydrogen bonds to two water molecules that bridge to an adjacent protein molecule in the lattice (adjacent molecule not shown).