the amino acid substitution at position R356 is a substitution by an amino acid selected from the group consisting of E, S, V, Y, and L,

the amino acid substitution at position R269 is a substitution by an amino acid selected from the group consisting of E, S, P, K, and V, and

the amino acid substitution at position K350 is a substitution by an amino acid selected from the group consisting of M, E, V, G, T, and R.

35. The variant protease of claim **27**, wherein said variant protease comprises a combination of substitutions selected from the group consisting of

(i) 280S, 346E (MutB);

(ii) 280H, 269S, K350V (MutG);

(iii) 269P, 280A, 346E, 350M (MutH);

(iv) 269K, 280H, 346E, 350E (Muti);

(v) 269E, 280S, 346S, 350T (MutJ); and

(vi) 269V, 280Q, 346V, 350G (MutK).

36. The variant protease of claim **27** having the amino acid sequence of SEQ ID NO: 6 (bdSENP1), except for the substitution at position N280, optionally, if present, in combination with the additional substitutions at positions R269, R346, and/or K350.

37. The variant protease of claim **36** having the amino acid sequence of any one of SEQ ID NO: 56 to SEQ ID NO: 70.

38. A process of purifying a protein of interest, comprising the steps of

(i) providing a protein of interest to be purified wherein said protein comprises an affinity tag fused to said protein via a variant SUMO protease cleavage site (PCS);

(ii) binding the protein of step (i) to an affinity matrix via said affinity tag; and

(iii) eluting the protein from the affinity matrix using a variant protease of claim **25**;

thereby purifying the protein;

wherein said variant SUMO PCS comprises a C-terminal Gly-Gly SUMO motif, and, when fused to the N-terminus of MBP having the amino acid sequence of SEQ ID NO: 71, is cleaved more efficiently after the C-terminal Gly-Gly SUMO motif by a protease having the amino acid sequence of SEQ ID NO: 57 (MutB bdSENP1) as compared to cleavage by a protease having the amino acid sequence of SEQ ID NO: 7 (scUlp1) or SEQ ID NO: 8 (hsSENP2), when tested at the same concentration under standard conditions of 1 hour incubation at 21° C., an initial concentration of SUMO PCS-MBP fusion of 100 μM in a buffer consisting of 45 mM Tris/HCl pH 7.5, 250 mM NaCl, 2 mM $MgCl_2$, 250 mM sucrose, 10 mM DTT.

39. The process of claim **38**, wherein said variant SUMO PCS has at least 80% sequence identity over the full-length of SEQ ID NO: 3 (bdSUMO), or which is a homolog of the bdSUMO protease cleavage site shown in SEQ ID NO: 3, wherein said variant protease cleavage site, when aligned to the full-length sequence of SEQ ID NO: 3, comprises a substitution at the position corresponding to D67 of the aligned SEQ ID NO: 3, wherein the amino acid at said position is substituted by a another amino acid selected from the group consisting of K, R, N, A and H.

40. The process of claim **39**, wherein said variant SUMO PCS, when aligned to the full-length sequence of SEQ ID NO: 3, further comprises:

(a) a substitution at the position corresponding to Q75 of the aligned SEQ ID NO: 3, wherein the amino acid at said position is substituted by another amino acid selected from the group consisting of R, W, A, H, M, I, P, and F; or

(b) a substitution at the position corresponding to T60 of the aligned SEQ ID NO: 3, wherein the amino acid at said position is substituted by a another amino acid selected from the group consisting of S, N, K, P, H, R, and Q; or

(c) both of (a) and (b).

41. The process of claim **39**, wherein, wherein said variant SUMO PCS comprises a combination of substitutions selected from the group consisting of

(i) 67K, 60K, 75R (Mut1);

(ii) 67K, 60P, 75W (Mut8);

(iii) 67K, 75R (Mut10);

(iv) 67K, 60S, 75H (Mut11);

(v) 67K, 60S, 75W (Mut12);

(vi) 67K, 60S, 75A (Mut13);

(vii) 67K, 60N, 75W (Mut14); and

(viii) 67K, 60N, 75A (Mut15).

42. The process of claim **39**, wherein said variant SUMO PCS has the amino acid sequence of SEQ ID NO: 3 (bdSUMO), except for the substitution D67K.

43. The process of claim **42**, wherein said variant SUMO PCS has additional substitutions at position T60, or at position Q75, or at both positions T60 and Q75.

44. The process of claim **42**, wherein variant SUMO PCS has an amino acid sequence selected from the group consisting of SEQ ID NO: 41 to SEQ ID NO: 55.

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