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(57) Abstract: The invention relates to a polypeptide, such as an Affimer polypeptide, comprising an amino acid sequence having at least 80% identity to amino acid residues 1 to 11, 13 to 15, 17 to 19, 21 to 25, 27 to 28, 35 to 37, 39, 41, 43 to 44, 46 to 47, 49 to 50, 52 to 53, 55 to 58, 63 to 64, 66, 68 to 82, 84 to 85, and 87 to 98 of SEQ ID NO: 1; characterised in that said polypeptide comprises one or more mutations relative to SEQ ID NO: 1 selected from the group consisting of: T51L, T51V, M65V, N32G, A59I, L38A, V20I, A40I, L38V, A12I, A12V, I16L, V20L, Q26E, E29M, T31K, N32D, N32H, T34V, T34R, T34D, T34P, A40V, Q42D, T45I, T45V, V48E, V48G, V48A, T51F, T51A, A59L, L67I, (V20I, L38A), (V20L, L38A), (V20I, L38V), (V20L, L38V), (E29K, K30E, E33K), (Y54D, T83D, Q86E), (A59L, G60N, D61G, N62K), (A59V, D61N, N62K), (G60N, D61G, N62K), (G60N, ΔD61, N62G), ΔD61, (A59L, G60N, ΔD61, N62G), (A59V, G60N, D61G, N62K), (A59I, G60N, D61G, N62K), (A59I, G60N, ΔD61, N62G), (A59V, G60N, ΔD61, N62G), (A59V, ΔD61), (G60P, ΔD61, N62P), (G60P, D61P, N62K), (G60P, ΔD61, N62G), (G60P, D61G, N62K), (D61N, N62K) and (T83D, Q86E). The invention also relates to various methods and nucleic acids.

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