

**Table 1. Free energy change as a function of mutation to alanine**

Approximate location	Residue	$\Delta\Delta G_{\text{Mut}}$
“Lipid-facing” residues	Ile <sup>77</sup> Ala	+0.1 ( $\pm 0.2$ )
	Phe <sup>78</sup> Ala	-0.1 ( $\pm 0.3$ )
	Met <sup>81</sup> Ala	-0.2 ( $\pm 0.1$ )
	Ile <sup>85</sup> Ala	-0.4 ( $\pm 0.1$ )
	Gly <sup>86</sup> Ala	-0.1 ( $\pm 0.2$ )
“Helix-interaction” residues	Leu <sup>75</sup> Ala	+1.3 ( $\pm 0.1$ )
	Ile <sup>76</sup> Ala	+1.8 ( $\pm 0.1$ )
	Gly <sup>79</sup> Ala	+1.7 ( $\pm 0.2$ )
	Val <sup>80</sup> Ala	+0.4 ( $\pm 0.2$ )
	Gly <sup>83</sup> Ala	+3.2 ( $\pm 0.2$ )
	Val <sup>84</sup> Ala	+1.0 ( $\pm 0.2$ )
	Thr <sup>87</sup> Ala	+0.9 ( $\pm 0.1$ )

These are the data plotted in Fig. 3.