SUPPLEMENTARY MATERIAL

Figure S1. Histogram showing the change in free energy of stabilization ($\Delta\Delta G$) for single and multiple mutants in T4 lysozyme. (a) Change in stability for 298 single-site mutants. (b) Change in stability for a total of 200 non-single-site mutants that include multiple mutants, insertion and deletion mutants and mutations that introduce disulfide bridges. The data plotted are for essentially the same mutants as in Figure 3a and 3b of the main manuscript, although the numbers of entries are slightly different because there are a few constructs for which ΔT_m or $\Delta\Delta G$ was not reported.

Table S1. Summary of the thermodynamic, crystallographic and other key information for T4 lysozyme, its mutants and complexes

Protein[a]	PDB code[b]	Activity[c] (%)	Thermodynamic data[d]			Crystallographic data[e]		Comment[f]	References
			ΔT_m (°C)	$\Delta\Delta G$ (kcal/mol)	pH	Space group	Resolution (A)		
WT	2LZM	100	67.2[g]		5.3	$P3_221$	1.7	Wild-type	1,2
WT (100K)	3FA0					$P3_221$	0.98	High resolution WT	103,111
WT*	1L63	103	65.8[g]		5.3	$P3_221$	1.8	Pseudo wild-type	3-5
WT* (100K)	1LW9					$P3_221$	1.45	Low temperature data set	87
WT* (8 bar Xe)[h]	1C6T					$P3_221$	2.0	Noble gas binding[h]	88,110,113
WT* (SeMet)			1.0	0.2	5.42			SelenoMet	83,87
Circular permutant "PERM1"[h]	1P5C		-8.8	-3.30	5.1	$P2_1$	2.5	Circular permutation	70
Extension mutant "PERMEXT"[h]	1P56		-1.9	-0.70	5.1	$P3_221$	1.8	Permutation/extension	70
I3A		~WT	-1.8	-0.7	6.5			Hydrophobic replacement	6,7,19,28
I3C (S-H)		90	-3.7	-1.2	6.5			Hydrophobic replacement	6-8
I3C (S-S)	172L	96	3.3	1.2	6.5	$P2_12_12_1$	1.9	S-S bridge to Cys 97	6-8,28
I3C/I9C/T21C/C54T/ T142C/L164C red.		43	-8.5		2.0			Triple S-S bridge	9
I3C/I9C/T21C/C54T/ T142C/L164C ox.	152L	0	23.4		2.0	$P2_12_12_1$	2.0	Triple S-S bridge	9,63
I3C/I9C/C54T/L164C	167L					$P2_12_12_1$	2.2	Cys3-Cys97; Cys9-Cys164	28
I3D		~WT	-8.5	-3.2	6.5			Hydrophobic replacement	6,7
I3E		~WT	-5.7	-2.0	6.5			Hydrophobic replacement	6,7
I3F		~WT	-3.0	-1.1	6.5			Hydrophobic replacement	6,7,19

I3G		~WT	-5.8	-2.1	6.5			Hydrophobic replacement	6,7,19
I3L	149L	100	0.9	0.4	6.5	$P2_12_12_1$	2.5	Hydrophobic replacement	6,7,64
I3L/S38D/A41V/ A82P/V131A/N144D		30	6.91	2.87	5.42			Cumulative stabilization	64
I3L/S38D/A41V/A82P/ N116D/V131A/N144D	189L	2	8.32	3.57	5.42	$P2_12_12_1$	2.6	Cumulative stabilization	64
I3L/S38D/A82P/ V131A/N144D		20	6.06	2.57	5.42			Cumulative stabilization	64
I3L/S38D/A82P/ N144D		40	5.38	2.32	5.42			Cumulative stabilization	64
I3M		~WT	-2.3	-0.9	6.5			Hydrophobic replacement	6,7
I3P	1L96	~WT	-7.3	-2.8	3.01	$P3_221$	2.0	Proline replacement	10
I3P	1L97	~WT				$P2_12_12$	2.0	Non-isomorphous hinge-bending	10
I3S		~WT	-4.6	-1.7	6.5			Hydrophobic replacement	6,7
I3T		~WT	-6.0	-2.3	6.5			Hydrophobic replacement	6,7
I3V	1L17	~WT	-1.2	-0.4	6.5	$P3_221$	1.7	Hydrophobic replacement	6,7,19
I3W		~WT	-8.0	-2.8	6.5			Hydrophobic replacement	6,7
I3Y	1L18	~WT	-5.9	-2.3	6.5	$P3_221$	1.7	Hydrophobic replacement	6,7
F4-[A]/WT*			-8.4	-3.1	5.4			Insertion	72
M6A/WT*	245L		-5.7	-1.9	3.0	$P3_221$	1.8	Solvent in cavity	73,81
M6I	256L	100	-3.4	-1.4	6.0	$P3_221$	1.8	Isomorphous form of M6I	11
M6I	150L	100	-3.4	-1.4	6.0	$P2_12_12_1$	2.2	Non-isomorphous "hinge-bending" mutant	11,44
M6L/WT*	230L	94	-10.6	-2.8	3.0	$P3_221$	1.9	Stabilization by Met_Leu	77
L7A/WT*			-4.5	-2.3	5.4			Core truncation	73,81
R8-[A]/WT*			-19.1	-5.6	5.4			Insertion	72

R8Δ/WT*			-19.4	-5.4	5.4				72
I9C/L164C/WT* red.		99	-6.5	-1.5	2.0			Stabilizing S-S bridge	8
I9C/L164C/WT* ox.	1L35	106	6.4	1.5	2.0	$P3_221$	1.8	Stabilizing S-S bridge	4
E11A		<0.01	2.6	1.1	5.42			Stability *versus* activity	62
E11D/WT*		0.02							67
E11F		<0.01	4.3	1.7	5.42			Stability *versus* activity	62
E11H/WT*	1QT6	<0.01	0.1	0.1	5.42	$P3_221$	1.9	Stability *versus* activity	62,67,78
E11M		<0.01	4.1	1.6	5.42			Stability *versus* activity	62
E11N/WT*	1QT7	<0.01	-0.6	-0.1	5.42	$P3_221$	1.8	Stability *versus* activity	62,67,78
R14A/K16A/I17A/ K19A/T21A/E22A/WT*	1T8F		-8	-3	3.02	$P6_222$	2.15	Ala-scan of β-sheet	105
R14K/WT*		106	-0.08	-0.03	5.4			Random st mutant	43
K16E	1L42	142	1.1	0.5	5.3	$P3_221$	1.8	Cumulative charge-change	12
K16E/R119E		88	0.9	0.4	5.3			Cumulative charge-change	12
K16E/R119E/K135E/ K147E	173L	40	-2.5	-1.0	5.3	$P6_5$	1.7	Cumulative charge-change	12,28
K16E/K135E		132	-1.6	-0.7	5.3			Cumulative charge-change	12
K16E/K135E/K147E		93	-4.0	-1.7	5.3			Cumulative charge-change	12
K16E/R154E		175	-1.9	-0.8	5.3			Cumulative charge-change	12
I17A/WT*	239L		-8.4	-2.7	3.0	$P3_221$	1.8	Cavity creating mutant	73,76,81
I17A/K19S/T21S/E22R/Y24I/ Y25P/WT* (“R1")[(i)]			-9	-3.2	5.42			T4L/P22L hybrid	76
I17A...(“R1R2")[(i)]			-9	-3.1	5.42			T4L/P22L hybrid	76
I17A...(“R1R3")[(i)]			-3	-3.2	5.42			T4L/P22L hybrid	76
I17A...(“R123")[(i)]			-24	--	5.42			T4L/P22L hybrid	76

I17M/WT*			-5.9	-2.2	5.4			Kinetics of folding	81
I17M/I27M/L33M/WT*			-9.3	-3.3	5.42			Kinetics of folding	87
Y18D/T26Q/WT*		13	-4.0		5.31			Second-site revertant	13
Y18H/T26Q/WT*		4.7	-3.4		5.31			Second-site revertant	13
K19S/WT*			-3.4	-1.3	5.42			T4L/P22L hybrid	76
D20A/WT*	253L	--	-0.8	-0.3	5.42	$P3_221$	2.0	Stability *versus* activity	62,67
D20C/WT*	1QTZ	+++	--	--	--	$P3_221$	2.0	Re-engineer active site	67,78
D20E/WT*	1QT5	++	--	--	--	$P3_221$	1.8	Re-engineer active site	67,78
D20N/WT*	255L	0	3.1	1.3	5.42	$P3_221$	1.8	Stability *versus* activity	62,67
D20S/WT*	254L	+	1.6	0.7	5.42	$P3_221$	1.9	Stability *versus* activity	62,67
D20T/WT*		+	2.2	0.9	5.42			Stability *versus* activity	62,67
T21C/S38D/L99A/ M102E/E108V/S117V/ T142C/N114D (“L99A/M102E/St”)	3GUI		-8.8	-3.2	5.3	$P4_12_12$	1.45	Buried charge in cavity	112
T21C...“L99A/M102E/ St” + benzene[(h)]	3GUJ					$P4_12_12$	1.6	Buried charge in cavity[(h)]	112
T21C...“L99A/M102E/ St” + toluene[(h)]	3GUK					$P4_3$	1.85	Buried charge in cavity[(h)]	112
T21C/K124C/WT*	1B6I				3.05	$P3_221$	1.8	Mechanical unfolding	86
T21C/T142C/WT* red.		68	-2.7	-0.7	2.0			Active site S-S bridge	3,8,14
T21C/T142C/WT* ox.	1KNI	0	11	2.8	2.0	$P3_221$	1.7	Active site S-S bridge	3,8,14
T21H/Q141H/T142H/ WT*	1EPY					$P3_221$	1.8	Three ligands plus Co^{2+}	85
T21H/T142H/WT*	257L		2.0	0.7	7.4	$P3_221$	1.9	Metal-binding mutant (Apo)	85
T21H/T142H/WT* + Zn^{2+}	258L		[2.7]		7.4	$P3_221$	1.8	Metal-binding mutant	85

T21H/T142H/WT* + Ni^{2+}	260L		[3.5]		7.4	$P3_221$	1.8	Metal-binding mutant	85
T21H/T142H/WT* + Co^{2+}	259L		[2.3]		7.4	$P3_221$	1.92	Metal-binding mutant	85
T21S/WT*			0.3	0.0	5.42			T4L/P22L hybrid	76
E22K/WT*		40	1.37	0.57	5.4			Random st mutant	43
E22R/WT*			2.7	1.0	5.42			T4L/P22L hybrid	76
Y24A/Y25A/T26A/ I27A/WT*	1SSW		-17	-5.5	3.02	$P3_221$	2.1	Ala scan of β-sheet	105
Y24I/WT*			-2.6	-1.0	5.42			T4L/P22L hybrid	76
Y25P/WT*			-6.3	-2.3	5.42			T4L/P22L hybrid	76
T26D/WT*	1QT3	+				$P3_221$	1.85	Re-engineer active site	67,78
T26E/WT*	1QTV	0				$P3_221$	2.3	T26E, Apo	78
T26E/WT*	148L	0				$P2_12_12$	1.9	Covalent adduct	51
T26E/WT*	180L	0				$P2_1$	1.9	Noncovalent adduct	28
T26H/WT*	1QT8	++				$P3_221$	1.9	Transglycosidase	67,78
T26Q/WT*	1QT4	0	-0.9		5.31	$P3_221$	2.1	Low activity, random selection	13,67,78
T26S/WT*	131L	75	1.35	0.57	5.4	$P3_221$	1.7	Random st mutant	43,57
I27A/WT*	240L		-10.1	-3.1	3.0	$P3_221$	1.75	Cavity creating mutant	73
I27A/I29A/WT*	248L		--			$P3_221$	1.9	Double truncation	73
I27A/I58A/WT*	249L		--			$P3_221$	1.9	Double truncation	73
I27M/WT*	1D2W		-10.1	-3.1	5.4	$P3_221$	1.9	Kinetics of folding	81,82
I27M/L33M/WT*			-10.3	-3.1	5.4			Kinetics of folding	81
I27M/L33M/WT*			-10.4	-3.0	5.42			Kinetics of folding	87
I27-[GIGHLL]/WT*	3JR6		-8.0	~-3	5.4	$P2_1$	3.0	β-sheet insertion	99

("L31d")									
G28A/I29A/G30A/WT*	1SSY		-16	-5.5	3.02	C2	2.4	Ala scan of β-sheet	105
I29A/WT*	241L		-8.2	-2.7	3.0	$P3_221$	1.7	Collapsed cavity	73
I29A/I58A/WT*	250L		--			$P3_221$	1.8	Double truncation	73
I29V/WT*			-0.2	-0.1	5.42			T4L/P22L hybrid	76
G30-[YTIGIG]/WT* ("L30c")	2B7X		-10.0	-3.7	5.4	$P2_12_12_1$	3.0	β-sheet insertion	99
G30F		<0.01	-4.9	-1.5	5.42			Stability *versus* activity	62
L32A/L33A/T34A/ E108V/WT*	1T8G		-8	-3	3.02	I422	1.8	Ala scan of β-sheet	105
L32T/WT*			-0.8	-0.3	5.42			T4L/P22L hybrid	76
L32T/T34K/K35V/ S36D/P37G/S38N/ L39S/WT* (R2)	176L		-4.9	-1.8	5.42	$P2_1$	2.2	T4/P22 hybrid	28
L32T...(R2R3)			-12	-3.0	5.42				76
L33A/WT*			-8.8	-2.9	5.4			Core truncation	73,81
L33G/WT*			-10.0	-2.9	5.42			T4L/P22L hybrid	76
L33M/WT*			-5.3	-2.0	5.4			Kinetics of folding	81
T34A/K35A/S36A/P37A	151L		-1.6	-0.7	3.0	R3	2.2	Polyalanine analysis	63,92
T34A/K35A/S36A/P37A/ S38A/N40A/S44A/E45A/ D47A/K48A/WT* ("J001A")			-10	--	3.0			Polyalanine mutagenesis	92
T34A/K35A/S36A/ P37A/S38D/N40A/ S44A/E45A/D47A/ K48A/WT* ("J002A")	174L		-3.8	--	3.0	$P6_3$	2.3	Polyalanine analysis	28,92
T34A/K35D/S36A/P37A/ S38A/N40A/S44A/E45A/ D47A/K48A/WT*			-9.2	--	3.0			Polyalanine mutagenesis	92

("J003A")									
T34A/K35D/S36D/P37A/ S38A/N40A/S44A/E45A/ D47A/K48A/WT* ("J004A")			-8.5	--	3.0			Polyalanine mutagenesis	92
T34A/K35D/S36A/P37D/ S38A/N40A/S44A/E45A/ D47A/K48A/WT* ("J005A")			-7.4	--	3.0			Polyalanine mutagenesis	92
T34A/K35D/S36A/P37A/ S38A/N40D/S44A/E45A/ D47A/K48A/WT* ("J006A")			-9.7	--	3.0			Polyalanine mutagenesis	92
T34A/K35A/S36A/P37A/ E128A/V131A/N132A ("7003A")			0.5	0.2	3.0			Polyalanine mutagenesis	92
T34K/WT*			-2.6	-1.0	5.42			T4L/P22L hybrid	76
K35V/WT*			-2.9	-1.1	5.42			T4L/P22L hybrid	76
S36D/WT*	.		-0.3	-0.1	5.42			T4L/P22L hybrid	76
P37G/WT*			0.6	0.2	5.42			T4L/P22L hybrid	76
S38D	1L19	80	1.6	0.6	6.7	$P3_221$	1.7	Helix dipole interaction	15,16,64,92
S38D/A82P/N144D		50	3.75	1.59	5.42			Cumulative stabilization	64
S38D/N144D		80	3.7	1.4	5.0			Two helix-dipole interactions	15,64
S38N/WT*	1L61	--	-0.1	0.0	6.7	$P3_221$	1.8	Helix dipole interaction	16,76
L39A/WT*		~WT	-2.5	-0.9	5.45			Insertion control	52
L39I-[NAAKSELNKAI]/ WT* ("L20", Crystal form I)	261L	50	-4.1	-1.6	5.4	$P3_221$	2.5	Tandem repeat	79
L39I-[NAAKSELNKAI]/ WT* ("L20", Crystal form II)	262L	50	-4.1	-1.6	5.4	$P2_1$	2.5	Tandem repeat	79

L39I-[NAAKSELNKAI]/ R52G/N53G/T54G/ N55G/WT* ("L20 pg")	1OYU					$P4_12_12$	2.5	Long-distance conformational change	95
L39I-[NAAKSELNKAI]/ R63A/WT* ("L20/R63A")	1T97		-10.2		5.4	$P2_1$	2.7	Ligand-triggered translocation	97
L39I..."L20/R63A" + guanidinium	1T8A		[1.7]		5.4	$P3_221$	2.0	Ligand-triggered translocation	97
L39I..."L20/R63A" + methylguanidinium, 100K[h]	2F47		[2.2]		5.4	$P3_221$	1.7	Ligand-triggered translocation[h]	98
L39S/WT*			-3.6	-1.4	5.42			T4L/P22L hybrid	76
N40A/WT*		~WT	1.2	0.43	3.0			Polyalanine helix 40-49	17
N40A/S44A/E45A/ D47A/K48A/WT*			3.1	1.1	3.0			Polyalanine mutagenesis	92
N40A/S44A/E45A/ D47A/K48A/D127A/ E128A/V131A/N132A/ WT* ("I001A")	192L		5.2	1.75	3.0	$P3_221$	1.9	Polyalanine analysis	70,92
N40-[A]/WT*	102L	~WT	-7.8	-2.8	5.45	$P3_221$	1.74	Insertion	52,56
N40-[AA]/WT*		~WT	-2.9	-1.1	5.45			Insertion	52,56
N40-[AAA]/WT*		~WT	-4.7	-1.7	5.45			Insertion	52,56
N40-[AA]/K48-[LP]/WT*	~WT	-9.8	-3.3	5.45		Insertion control		52	
N40-[AAAA]/WT*		~WT	-6.4	-2.2	5.45			Insertion	52
N40A/S44A/E45A/ D47A/K48A/WT*		~WT	3.09	1.06	3.0			Polyalanine helix 40-49	17
N40A/K43A/S44A/ E45A/L46A/D47A/ K48A/WT*	1L64	~WT	-8.47	-2.11	3.0	$P3_221$	1.9	Polyalanine helix 40-49	17,92
N40-[ES]/WT*		~WT	-1.6	-0.7	5.45			Insertion "recovery"	52,56
N40-[SLD]/WT*	103L	~WT	-1.9	-0.7	5.45	$P3_221$	1.9	Insertion "recovery"	52,56

N40-[SLD]/L46A/WT*		~WT	-8.1	-2.8	5.45			Insertion control	52
N40D/WT*		124	1.14	0.44	5.4			Random st mutant	43
N40L-[A]/WT*		~WT	-3.8	-1.3	5.45			Insertion	52,56
N40L/K43A/S44-[A]/WT*		~WT	-5.4	-1.8	5.45			Insertion control	52
A41D/WT*		105	0.71	0.29	5.4			Random st mutant	43
A41S/WT*	120L	~WT	-1.77	-0.6	3.0	$P3_221$	1.8	Add hydroxyl	54
A41V		90	1.33	0.45?	2.8			Entropic stabilization	18,64
A41V/V131A		90	1.81	0.6	2.8			Entropic stabilization	18,64
A42F/WT*			-11.2	-3.6	3.0			Introduction of strain	84
A42I/WT*			-8.9	-3.1	3.0			Introduction of strain	84
A42K/WT*		~WT	-11.0	-3.7	5.45			Insertion control	52
A42L/WT*			-10.1	-3.4	3.0			Introduction of strain	84
A42S/WT*	206L	~WT	-7.49	-2.3	3.0	$P3_221$	1.75	Add hydroxyl	54
A42V/WT*	1QTB		-7.5	-2.7	3.0	$P3_221$	1.9	Introduction of strain	84
K43A/WT*	1L66	~WT	-2.95	-0.96	3.0	$P3_221$	1.7	Polyalanine helix 40-49	17
S44A/WT*	1L68	~WT	1.2	0.44	3.0	$P3_221$	1.7	Polyalanine helix 40-49	17
S44-[A]/WT*		~WT	-11.7	-3.8	5.45			Insertion	52,56
S44-[AA]/WT*	104L	~WT	-9.9	-3.4	5.45	R32	2.8	Insertion	52,56
S44-[AAA]/WT*	205L	~WT	-6.0	-2.2	5.45	$P3_221$	2.1	Insertion	52,56
S44-[AAA]/L46A/WT*		~WT	-11.2	-3.7	5.45			Insertion control	52
S44-[AAAA]/WT*		~WT	-7.3	-2.5	5.45			Insertion	52
S44A-[AA]/WT*		~WT	-4.4	-1.7	5.45			Insertion	52,56
S44C/WT*		~WT	-0.35	-0.11	3.0			Helix propensity analysis	49,50
S44D/WT*		~WT	-0.32	-0.11	3.0			Helix propensity analysis	49,50

S44E/WT*	217L	~WT	0.00	0.00	3.0	$P3_221$	1.7	Helix propensity analysis	49,50
S44E/WT*		~WT	0.00	0.00	3.0	P2	1.9	Helix propensity analysis	28,49,50
S44F/WT*	137L	~WT	0.18	0.06	3.0	$P2_1$	1.85	Helix propensity analysis	49,50
S44G/WT*	107L		-1.55	-0.53	3.0	$P3_221$	1.8	Helix propensity analysis	49,50
S44H/WT*		~WT	0.12	0.04	3.0			Helix propensity analysis	49,50
S44I/WT*	108L	~WT	0.91	0.31	3.0	$P3_221$	1.8	Helix propensity analysis	49,50
S44K/WT*	109L	~WT	0.57	0.20	3.0	$P3_221$	1.85	Helix propensity analysis	49,50
S44L/WT*	110L	~WT	1.09	0.39	3.0	$P3_221$	1.7	Helix propensity analysis	49,50
S44M/WT*		~WT	0.92	0.33	3.0			Helix propensity analysis	49,50
S44N/WT*	111L	~WT	-0.40	-0.14	3.0	$P3_221$	1.8	Helix propensity analysis	49,50
S44P/WT*	112L		-10.3	-3.03	3.0	$P3_221$	1.8	Helix propensity analysis	49,50
S44Q/WT*		~WT	0.75	0.27	3.0			Helix propensity analysis	49,50
S44R/WT*	113L	~WT	0.68	0.24	3.0	$P3_221$	1.8	Helix propensity analysis	49,50
S44T/WT*	114L	~WT	0.03	0.01	3.0	$P3_221$	1.8	Helix propensity analysis	49,50
S44V/WT*	115L	~WT	0.29	0.10	3.0	$P3_221$	1.8	Helix propensity analysis	49,50
S44W/WT*	216L	~WT	0.15	0.05	3.0	C2	2.1	Helix propensity analysis	28,49,50
S44Y/WT*		~WT	0.54	0.19	3.0			Helix propensity analysis	49,50
S44Δ/WT*			-7.1	-2.8	5.4			Deletion	72
E45A/WT*	171L	~WT	1.47	0.55	3.0	$P2_12_12$	2.5	Polyalanine helix 40-49	17,28
E45A/K48A/WT*		~WT	1.04	0.38	3.0			Polyalanine helix 40-49	17
L46A/WT*	1L67	~WT	-8.39	-2.62	3.0	$P3_221$	1.9	Polyalanine helix 40-49	17,20
D47A/WT*	1L65	~WT	-0.81	-0.28	3.0	$P3_221$	1.7	Polyalanine helix 40-49	17
K48A/WT*		~WT	-0.93	-0.32	3.0			Polyalanine helix 40-49	17
K48-[A]/WT*		~WT	-11.2	-3.7	5.45			Insertion	52,56

K48-[AA]/WT*		~WT	-10.3	-3.5	5.45			Insertion	52,56
K48-[AAA]/WT*		~WT	-13.7	-4.2	5.45			Insertion	52,56
K48-[AAAA]/WT*		~WT	-12.5	-4.0	5.45			Insertion	52
K48-[HP]/WT*	201L	~WT	-7.0	-2.4	5.45	$P2_1$	2.0	Insertion "recovery"	52,56
K48-[LP]/WT*		~WT	-7.3	-2.5	5.45			Insertion "recovery"	52
A49S/WT*	221L	~WT	-1.53	-0.5	3.0	$P3_221$	1.7	Add hydroxyl	54
I50A/WT*	242L		-5.8	-2.0	3.0	$P3_221$	1.8	Crevice	73,81
I50M/WT*	1D2Y		-0.6	-0.4	5.4	$P3_221$	2.06	Kinetics of folding	81,82
R52A/N53A/T54A/ N55A/G56A/V57A/ I58A ("7004A")			-16.4	~-4	3.0			Polyalanine mutagenesis	92
R52V/WT*			-7.1	-2.5	5.42			T4L/P22L hybrid	76
R52V/N53A/T54S/N55G/ V57T/WT* (R3)		-9.5	-3.1	5.42			T4L/P22L hybrid		76
N53A/WT*			0.0	0.0	5.42			T4L/P22L hybrid	76
N53A/T54A/N55A/ G56A/V57A/I58A ("6005A")			-15.8	~-4	3.0			Polyalanine mutagenesis	92
N53A/T54A/N55A/ G56A/V57A/I58A/ E62A ("7005A")			-16.4	~-4	3.0			Polyalanine mutagenesis	92
N53A/N55A/V57A	190L		-4.0	-1.5	3.0	$P3_221$	2.0	Polyalanine analysis	92
N53A/N55A/V57A/ E128A/V131A/N132A ("6003A")	191L		-2.0	-0.8	3.0	$P3_221$	1.95	Polyalanine analysis	92
C54S/C97A			-1.5	-0.6	5.42			T4L/P22L hybrid	76
C54T/C97A								See WT*	
N55G	1L21	110	-1.6	-0.6	6.5	$P3_221$	1.85	"Left-handed helical" residue	21,76

G56M/WT*			-4.8	-1.8	5.42			T4L/P22L hybrid	76
V57T/WT*			-0.3	-0.2	5.42			T4L/P22L hybrid	76
I58A/WT*	243L		-10.4	-3.2	3.0	$P3_221$	1.7	Cavity	73
I58M/WT*	1D3F		--	--	--	$P3_221$	2.05	Use of SeMet	82
I58T/WT*	1G1V		-10.1	-3.4	5.4	$P3_221$	1.9	Solvent perturbation	89
T59A/WT*	1LYJ	~WT	-4.0	-1.5	6.5	$P3_221$	1.8	Replace helix cap, Thr 59	22
T59D/WT*	1LYI	~WT	-3.1	-1.2	6.5	$P3_221$	2.0	Replace helix cap, Thr 59	22
T59G/WT*	1LYH	~WT	-4.1	-1.6	6.5	$P3_221$	1.7	Replace helix cap, Thr 59	22
T59N/WT*	1LYG	~WT	-2.8	-1.1	6.5	$P3_221$	1.8	Replace helix cap, Thr 59	22
T59S/WT*	1LYF	~WT	-0.4	-0.2	6.5	$P3_221$	1.8	Replace helix cap, Thr 59	22
T59V/WT*	1LYE	~WT	-4.0	-1.5	6.5	$P3_221$	1.8	Replace helix cap, Thr 59	22
K60H		--	-0.4	-0.2	6.5			Salt bridge control	23
K60H/L13D/WT*		115	-7.1	-2.8	6.5			Salt bridge	23
K60P	1L56		-0.1	0.0	6.5	$P3_221$	1.8	Entropic stabilization	24
E64-[A]/WT*			-10.5	-3.7	5.4			Insertion	72
L66A/WT*			-10.1	-3.3	5.4			Core truncation	73,81
L66M/WT*	1D3J		-2.7	-1.0	5.4	$P3_221$	1.97	Kinetics of folding	81,82
F67A/WT*	246L		-5.7	-1.9	3.0	$P3_221$	1.8	Crevice	73
N68-[A]/WT*			-13.1	-4.4	5.4			Insertion	72
N68C/A93C/WT*	139L	0				$P3_221$	1.7	Crosslinked dimer	60
Q69P/WT*		88	-7.6	-2.9	6.5			Proline disruption	25
V71A/WT*			-4.7	-1.5	3.0			Core truncation	73
D72A	3F9L					$P3_221$	1.19	Site 96 survey	103
D72A/R96H	3FAD					$P3_221$	1.20	Site 96 survey	103

D72A/R96H + Rb^{+}	1SX7					$P3_221$	1.06	Phasing by direct methods	111
D72P/WT*	1L76	57	-7.1	-2.7	6.5	$P3_221$	1.9	Proline disruption	25
A73-[A]/WT*			-12.5	-4.2	5.4			Insertion	72
A73-[AA]/WT*			-18.0	-5.7	5.4			Insertion	72
A73-[AAA]/WT*	209L		-15.9	-5.0	5.4	$P6_222$	2.7	Insertion	72
A73-[L]/WT*			-9.0	-3.1	5.4			Insertion	72
A73-[V]/WT*			-5.2	-1.7	5.4			Insertion	72
A73S/WT*	122L	~WT	-1.27	-0.4	3.0	$P3_221$	1.8	Add hydroxyl	54
A73Δ/WT*	210L		-11.4	-3.9	5.4	$P3_221$	1.9	Deletion	72
A74P		66	-12.1	-4.6	6.5			Proline disruption	25
V75-[A]/WT*			-7.8	-2.7	5.4				72
V75T/WT*	127L	~WT	-3.70	-1.3	3.0	$P3_221$	1.85	Substitute hydroxyl	54
G77A	1L23	~WT	0.9	0.4	6.5	$P3_221$	1.7	Entropic stabilization	26
I78A/WT*	1CTW		-3.5	-1.2	5.4	$P3_221$	2.1	Core truncation	73,81
I78M/WT*	1CU0	70	-3.7	-1.5	5.42	$P3_221$	2.2	Single Met, kinetics	75,81,82
I78M/L84M/L91M/ L99M/I100M/V103M/ L118M/L121M/L133M/ WT* ("9b-M")			-24.9	-7.0	5.42			Multiple Met	87

I78M/L84M/L91M/ L99M/I100M/V103M/ L118M/L121M/L133M/ WT*, SeMet ("9b-sM")			-19.2	-7.2	5.42			SeMet	75,87
I78M/L84M/L91M/ L99M/L118M/L121M/ L133M/WT* ("7c-M")			-17.6	-5.5	5.42			Multiple Met	87
I78V/WT*	1P2R		-2.1	-0.8	5.35	$P3_221$	1.58	Core repacking	94
I78V/V87M/L118I/ M120Y/L133F/V149I/ T152V/WT* ("Core 7")	--		-9.8	-3.5	5.35			Core repacking	94
I78V/V87M/M120Y/ L133F/V149I/T152V/ WT* ("I118L/Core 7")	1PQI		-9.5	-3.3	5.35	$P3_221$	1.56	Core repacking	94
I78V/L118I/M120Y/ L133F/V149I/T152V/ WT* ("M87V/Core 7")	1PQK		-5.0	-3.0	5.35	C2	2.0	Core repacking	94
R80K/WT*		44	-0.43	-0.17	5.4			Random st mutant	43
R80K/R119H/WT*		104	-1.20	-0.47	5.4			Random st mutant	43
A82P	1L24	80	2.1	0.8	6.5	$P3_221$	1.7	Entropic stabilization	26,19,64
A82S/WT*	123L	~WT	-0.99	-0.3	3.0	$P3_221$	1.8	Add hydroxyl	54
K83H/WT*			-1.0	-0.4	6.5			Salt bridge control	23
K83H/A112D/WT*	1L41	110	-3.9	-1.5	6.5	$P3_221$	1.75	Salt bridge	23
K83M/T115E			0.1	0.04	6.5			Salt bridge	23
L84A/WT*	247L		-13.4	-3.8	3.0	$P3_221$	1.75	Large declivity	73,81
L84M/WT*	1CU2	104	-4.9	-1.9	5.42	$P3_221$	1.85	Single Met, kinetics	75,81,82
L84M/V87M/L91M/ L99M/I100M/V103M/ G110R/V111M/L118M/ L121M/L133M/WT* ("10a-M")			-23.4	-7.0	5.42			Multiple methionines	87

L84M/V87M/L91M/ L99M/I100M/V103M/ G110R/V111M/L118M/ L121M/L133M/WT*, SeMet ("10a-sM")	1LPY	-17.2	-5.2	5.42	$P3_221$	1.7	SeMet	87
L84M/V87M/L91M/ L99M/G110R/V111M/ L118M/L121M/L133M/ F153M/WT* ("9a-M")		-17.7	-5.4	5.42			Multiple methionines	83,87
L84M/V87M/L91M/ L99M/G110R/V111M/ L118M/L121M/L133M/ F153M/WT*, SeMet ("9a-sM")	1LWK	-10.3	-3.5	5.42	$P3_221$	2.1	Use of SeMet	83,87
L84M/V87M/L91M/ L99M/L111M/L118M/ L121M/L133M/WT* ("8a-M")	1LWG	-15.2	-4.9	5.42	$P3_221$	1.7	Multiple methionines	87
L84M/L91M/L99M/ WT* ("3-M")	1KW5	-8.8	-3.1	5.42	$P3_221$	1.75	Multiple methionines	83,87
L84M/L91M/L99M/ WT*, SeMet ("3-sM")		-6.6	-2.4	5.42			Use of SeMet	83,87
L84M/L91M/L99M/ I100M/V103M/L118M/ L121M/L133M/WT* ("8b-M")		-21.2	-6.5	5.42			Multiple methionines	87
L84M/L91M/L99M/ V111M/L118M/L121M/ L133M/WT* ("7b-M")	1L0K	-11.9	-4.3	5.42	$P3_221$	2.00	Multiple methionines	83,87
L84M/L91M/L99M/ V111M/L118M/L121M/ L133M/WT*, SeMet ("7b-sM")		-7.5	-2.6	5.42			Use of SeMet	83,87
L84M/L91M/L99M/ L118M/L121M/WT* ("5-M")	1D3M	-12.1	-4.3	5.42	$P3_221$	2.12	Multiple methionines	82,83,87
L84M/L91M/L99M/	1D3N	-8.5	-3.0	5.42	$P3_221$	2.00	Use of SeMet	82,83,87

L118M/L121M/WT*, SeMet ("5-sM")									
L84M/L91M/L99M/ L118M/L121M/L133M/ WT* ("6b-M")	1KY1		-13.2	-4.7	5.42	$P3_221$	2.05	Multiple methionines	87
L84M/L91M/L99M/ L118M/L121M/L133M/ V149M/I150M/F153M/ WT* ("9a-M")			-24.4	-7.0	5.42			Multiple methionines	87
L84M/L91M/L99M/ L118M/L121M/L133M/ F153M/WT* ("7a-M")	1CX7	43	-14.5	-5.0	5.42	$P3_221$	1.94	Multiple methionines	75,83,87
L84M/L91M/L99M/ L118M/L121M/L133M/ F153M/WT*, SeMet ("7a-sM")	1CX6		-8.8	-3.0	5.42	$P3_221$	2.0	SeMet	82,83,87
L84M/L91M/L99M/ L118M/L121M/F153M/ WT* ("6a-M")	1L0J		-13.3	-4.7	5.42	$P3_221$	1.98	Multiple methionines	87
L84M/L91M/L99M/ L133M/WT* ("4b-M")	1KW7		-9.6	-3.5	5.42	$P3_221$	1.89	Multiple methionines	87
L84M/L91M/L99M/ F153M/WT* ("4a-M")	1KY0		-10.5	-3.8	5.42	$P3_221$	1.97	Multiple methionines	87
K85A	3C81		-1.0	-0.6	5.35	$P3_221$	1.85	Site 96 survey	104
K85A/R96H	3C82		-9.8	-3.6	5.35	$P3_221$	1.68	Site 96 survey	104
P86A	1L25	50	-2		2.0	$P3_221$	1.8	Proline within helix	27,19
P86C	1L26	70	-1		2.0	$P3_221$	1.7	Proline within helix	27
P86D	1L27	110	0		2.0	$P3_221$	1.8	Proline within helix	27
P86G	1L28	70	-2		2.0	$P3_221$	1.9	Proline within helix	27
P86H	1L29	70	-2		2.0	$P3_221$	1.7	Proline within helix	27
P86I		70	-2		2.0			Proline within helix	27

P86L	1L30	50	-2		2.0	$P3_221$	1.7	Proline within helix	27
P86R	1L31	20	-2		2.0	$P3_221$	1.8	Proline within helix	27
P86S	1L32	70	-1		2.0	$P3_221$	1.7	Proline within helix	27
P86T		80	-1		2.0			Proline within helix	27
V87A/WT*	236L		-4.9	-1.7	3.0	$P3_221$	1.9	Cavity	73,81
V87I/WT*	1P2L		-0.8	-0.3	5.35	$P3_221$	1.58	Core repacking	94
V87I/I100V/M102L/ V103I/M106I/V111A/ M120Y/L133F/V149I/ T152V/WT* ("Core 10")	1PQD		-6.4	-2.4	5.35	$P3_221$	1.65	Core repacking	94
V87I/I100V/M102L/ M106I/V111A/M120Y/ L133F/V149I/T152V/ WT* ("I103V/Core 10")	1P3N		-4.0	-1.6	5.35	$P3_221$	1.55	Core repacking	94
V87I/I100V/M102L/ V103I/M106I/M120Y/ L133F/V149I/T152V/ WT* ("A111V/Core 10")	1PQJ		-4.8	-1.8	5.35	$P3_221$	1.90	Core repacking	94
V87I/I100V/V103I/ M106I/V111A/M120Y/ L133F/V149I/T152V/ WT* ("L102M/Core 10")	1P37		-7.2	-2.6	5.35	$P3_221$	1.57	Core repacking	94
V87M/WT*	1CU3		-6.3	-2.3	5.4	$P3_221$	2.1	Kinetics of folding	81,82
V87T/WT*	128L	~WT	-4.55	-1.6	3.0	$P3_221$	1.7	Substitute hydroxyl	54
Y88-[A]/WT*			-11.3	-3.9	5.4			Insertion	72
D89A	3C83		-1.3	-0.5	5.35	$P3_221$	1.84	Site 96 survey	104
D89A/R96H	3C7Z		-10.2	-3.8	5.35	$P3_221$	1.67	Site 96 survey	104
S90C/Q122C/WT* red.		102	-5.8	-1.4	2.0			Destabilizing S-S bridge	8
S90C/Q122C/WT* ox.		58	-0.5	-0.1	2.0			Destabilizing S-S bridge	8
S90H/WT*			-2.9	-1.1	6.5			Salt bridge control	23

S90H/Q122D/WT*		100	-5.7	-2.2	6.5			Salt bridge	23
L91A/WT*	1CU6		-7.4	-2.6	5.4	$P3_221$	2.1	Core truncation	73,81
L91M/WT*	1CU5	96	-2.0	-0.8	5.42	$P3_221$	2.05	Single Met, kinetics	75,81,82
D92N/WT*	1L55		-3.7	-1.4	6.7	$P3_221$	1.9	Helix dipole interaction	16
A93C/WT*	138L	~WT				$P3_221$	1.7	Dimer control	60
A93P			0.2	0.1	6.5			Entropic stabilization	24
A93S/WT*	224L	~WT	-0.52	-0.2	3.0	$P3_221$	1.85	Add hydroxyl	54
A93T/WT*	129L	105	0.13	0.06	5.4	$P3_221$	1.7	Random st mutant	43,57
V94A/WT*			-5.0	-1.8	3.0			Surface indentation	73
R95A/WT*			-19.8	~-6	6.7			Sidechain truncation	74
R95A/WT* (+Gua)	229L		[-18.3]		6.7	$P3_221$	1.8	Sidechain compensation	74
R96-[A]/WT*			-28.8	-6.6	5.4			Insertion	72
R96A	3C7Y		-5.11	-2.0	5.35	$P3_221$	1.95	Site 96 survey	104
R96A/WT*	175L		-7.9		6.7	C2	2.1	Multiple crystal forms	28
R96C			-7.7	-2.9	5.35			Site 96 survey	104
R96D	3C8Q		-9.5	-3.5	5.35	$P3_221$	1.63	Site 96 survey	104
R96E	3C8S		-7.0	-2.5	5.35	$P3_221$	1.68	Site 96 survey	104
R96F			-11.5	-4.2	5.35			Site 96 survey	104
R96G	3C8R		-7.1	-2.6	5.35	$P3_221$	1.8	Site 96 survey	104
R96H	1L34	100	-8.7	-3.2	3.0	$P3_221$	1.9	Random ts mutant	29-31
R96H (100K)	3F8V		-8.3	-3.1	5.35	$P3_221$	1.08	Site 96 survey	103,104
R96I			-7.9	-2.9	5.35			Site 96 survey	103,104
R96K	3C7W		-0.2	0.0	5.35	$P3_221$	1.77	Site 96 survey	103,104
R96L			-8.6	-3.2	5.35			Site 96 survey	103,104

R96M	3CDV		-7.1	-2.7	5.35	$P3_221$	1.73	Site 96 survey	103,104
R96N	3CDT		-8.0	-3.0	5.35	$P3_221$	1.63	Site 96 survey	103,104
R96P			-15.5	-5.5	5.35			Site 96 survey	103,104
R96Q	3CDR		-1.4	-0.3	5.35	$P3_221$	1.7	Site 96 survey	103,104
R96S	3CDQ		-7.0	-2.6	5.35	$P3_221$	1.68	Site 96 survey	103,104
R96T			-7.6	-2.8	5.35			Site 96 survey	103,104
R96V	3CDO		-6.4	-2.4	5.35	$P2_12_12_1$	1.87	Site 96 survey	103,104
R96W	3FI5		-12.8	-4.5	5.35	$P2_1$	1.53	Site 96 survey	103,104
R96Y	3C80		-13.2	-4.7	5.35	$P3_221$	2.0	Site 96 survey	103,104
A98C/WT*	1QSB		-2.6	-1.0	3.0	$P3_221$	1.8	Introduction of strain	84
A98F/WT*			-20.4	-5.9	3.0			Introduction of strain	84
A98I/WT*			-16.1	-4.9	3.0			Introduction of strain	84
A98L/WT*	1QS5		-13.9	-4.3	3.0	$P3_221$	2.5	Introduction of strain	84,102
A98M/WT*	1QTH		-9.3	-3.2	3.0	$P3_1$	1.9	Introduction of strain	84
A98S/WT*	125L	~WT	-7.47	-2.5	3.0	$P3_221$	1.85	Add hydroxyl	54
A98V	1L48	80	-14.8	-4.9	3.0	$P3_221$	1.7	Helix-packing ts mutant	32
A98V/WT*	1QS9		-9.2	-3.2	3.0	$P3_221$	1.85	Introduction of strain	84
A98V/V149C/T152S	1L50	75	-12.1	-4.4	3.0	$P3_221$	1.85	Helix packing analysis	32
A98V/V149I/T152S	1L51		-12.0	-4.4	3.0	$P3_221$	1.9	Helix packing analysis	32
A98V/T152S	1L49	72	-13.9	-4.8	3.0	$P3_221$	1.8	Helix packing analysis	32
A98W/WT*			-19.3	-5.7	3.0			Introduction of strain	84
L99A/WT*	1L90		-15.65	-5.0	3.01	$P3_221$	1.75	Cavity-creating mutant	20,71,81,102, 107
L99A/WT* (200 MPa)[(h)]	2B6T					$P3_221$	2.1	Lysozyme under pressure[(h)]	108,109

L99A/WT*+Bz	1L83	[6.0]	--	3.0	$P3_221$	1.7	Cavity plus benzene	33,65,66
L99A/WT*+benzofuran[(h)]	182L	[3.0]		3.0	$P3_221$	1.8	Ligand in cavity[(h)]	65,66
L99A/WT*+ethylBz[(h)]	1NHB	[3.8]		3.0	$P3_221$	1.8	Ligand in cavity[(h)]	65,66
L99A/WT* (100K)[(h)]	3DMV				$P3_221$	1.65	Halogenated benzene binding[(h)]	101
L99A/WT* + C_6F_5I[(h)]	3DN3				$P3_221$	1.8	Halogenated benzene binding[(h)]	101

L99A/WT* + C_6H_5I[(h)]	3DN4					$P3_221$	1.8	Halogenated benzene binding[(h)]	101
L99A/WT* (SeMet) + C_6F_5I[(h)]	3DN8					$P3_221$	1.7	Halogenated benzene binding[(h)]	101
L99A/WT* (SeMet) + C_6H_5I[(h)]	3DNA					$P3_221$	1.7	Halogenated benzene binding[(h)]	101
L99A/WT* (8 bar Xe)[(h)]	1C6K					$P3_221$	1.9	Noble gas binding[(h)]	88,110
L99A/M102Q/WT*[(h)]	1LGU				5.4	$P3_221$	1.9	Model binding site[(h)]	93
L99A/M102Q/WT* + 3-chlorophenol[(h)]	1LI3		[2.7]		5.4	$P3_221$	1.85	Model binding site[(h)]	93
L99A/M102L/WT*, SeMet, 100K	3DKE					$P3_221$	1.25	Cavity mutant, experimental phases	100
L99A/M102Q/WT* + 2-allyl phenol[(h)]	1OV5[(h)]		[5.4]		3.0	$P3_221$	2.1	Flexible-receptor docking	96
L99A/M102Q/WT* + 4-fluoro-phenethyl alcohol[(h)]	1OWZ		[2.4]		3.0	$P3_221$	1.9	Flexible-receptor docking[(h)]	96
L99A/E108V/WT*	1QUO	70	-8.6	-3.1	5.4	$P3_221$	1.9	Second site revertant	80
L99A/F153A/WT*	1L89		-41.8	-8.3	3.01	$P3_221$	1.9	Cavity-creating	20
L99A/F153A/WT*+Bz	1L84		[3.0]	--	4.46	$P3_221$	1.9	Cavity plus benzene	33
L99A/F153A/WT* (8 bar Xe)[(h)]	1C6N					$P3_221$	2.2	Noble gas binding[(h)]	88,110
L99F/WT*	1L91		-1.1	-0.4	3.01	$P3_221$	1.8	Hydrophobic replacement	5
L99F/M102L/WT*		104	-2.34	-0.71	3.01			Designed core repacking	34
L99F/M102L/V111I/ WT*	1L80	47	-4.02	-1.15	3.01	$P3_221$	1.8	Designed core repacking	34
L99F/M102L/V111I/ F153L/WT*	1L82	87	-1.82	-0.54	3.01	$P3_221$	2.1	Designed core repacking	34
L99F/M102L/F153L/ WT*	1L81	81	-0.68	-0.21	3.01	$P3_221$	2.0	Designed core repacking	34

L99F/V111I/WT*	1L79	85	-2.7	-0.82	3.01	$P3_221$	1.9	Designed core repacking	34
L99F/F153L/WT*		66	0.09	0.03	3.01			Designed core repacking	34
L99G/WT*	1QUD	72	-20.3	-6.3	5.4	$P3_221$	1.75	Cavity/second site revertant	80
L99G/E108V/WT*	1QUH	63	-16.3	-5.6	5.4	$P3_221$	1.85	Second site revertant	80,102
L99I/WT*	1L92		-4.0	-1.4	3.01	$P3_221$	1.7	Hydrophobic replacement	5
L99M/WT*	1L93		-2.0	-0.7	3.01	$P3_221$	1.8	Hydrophobic replacement	5,81,82
L99V/WT*	1L94		-6.6	-2.3	3.01	$P3_221$	1.8	Hydrophobic replacement	5
I100A/WT*	244L		-10.7	-3.4	3.0	$P3_221$	1.7	Cavity	73,81
I100M/WT*	1CUP	105	-4.5	-1.6	5.42	$P3_221$	1.9	Single Met, kinetics	75,81,82
I100V/WT*	1P36		-1.1	-0.4	5.35	$P3_221$	1.45	Core repacking	94
N101A/WT*	1I6S		-3.7	-1.5	5.4	$P3_221$	1.9	Solvent perturbation	89
M102A/WT*	222L		-8.2	-2.9	5.4	$P3_221$	1.9	Sidechain truncation, kinetics	73,74,81
M102A/WT*+Bz	220L		[2.9]		3.0	$P3_221$	1.85	Ligand binding	74
M102A/M106A/WT*	252L		-10.8	-3.7	5.4	$P3_221$	2.1	Double truncation	74,81
M102K/WT*	1L54	35	-20.3	-6.9	5.3	$P3_221$	1.9	Buried lysine	35,77
M102L/WT*	1L77	77	-2.54	-0.74	3.01	$P3_221$	2.05	Alternative core packing	34,77,94
M102L/V111F/WT*		42	-5.49	-1.51	3.01			Alternative core packing	34
M102V		60	-12.7		3.0			Random ts mutant	36-38
V103A/WT*	238L		-6.6	-2.2	3.0	$P3_221$	1.9	Cavity	73,81
V103I/WT*	1P7S		-1.5	-0.5	5.35	$P2_12_12_1$	1.5	Core repacking	94
V103M/WT*	1CUQ	70	-3.1	-1.2	5.42	$P3_221$	2.05	Single Met, kinetics	75,81,82
F104A/WT*	228L		-7.9	-2.7	5.4	$P3_221$	1.9	Crevice	73,74,81
F104A/WT*+Bz	227L		[2.6]		3.0	$P3_221$	2.0	Ligand binding	74

F104M/WT*	1CV0		-0.8	-0.4	5.4	$P3_221$	2.1	Kinetics of folding	81,82
Q105A	1L00	33	-1.6	-0.6	5.8	$P3_221$	1.9	Perturb Trp 138	58
Q105E	1L98	19	-3.0	-1.1	5.8	$P3_221$	1.8	Perturb Trp 138	58
Q105G	1L99	18	-3.9	-1.5	5.8	$P3_221$	1.95	Perturb Trp 138	58
Q105M/WT*	1G1W		-2.7	-1.2	5.4	$P3_221$	1.8	Solvent perturbation	89
M106A/WT*	1QSQ		-5.2	-1.9	5.4	$P3_221$	1.9	Surface indentation, kinetics	73,81
M106I/WT*	1P46		0.6	0.2	5.35	$P3_221$	1.67	Core repacking	94
M106K/WT*	231L	4	-10.5	-3.4	3.0	$P3_221$	2.5	Control for Met_Leu	77
M106L/WT*	234L	103	1.7	0.5	3.0	$P3_221$	1.9	Stabilization by Met_Leu	77
E108-[A]/WT*	211L		-7.1	-2.7	5.4	$P3_221$	1.7	Insertion	72
E108V/WT*	1QUG	87	2.4	0.7	5.4	$P3_221$	1.9	Second site revertant (L99G)	80
T109D/WT*	1L62		1.5	0.6	6.7	$P3_221$	1.7	Helix dipole interaction	16
T109N/WT*	1L59		0.3	0.1	6.7	$P3_221$	1.75	Helix dipole interaction	16
G110R/V111M/WT*	1CV1		-2.0	-0.7	5.42	$P3_221$	1.9	Kinetics of folding	81,82,87
V111A/WT*	235L		-3.7	-1.3	3.0	$P3_221$	1.9	Cavity	73,81,94
V111F/WT*		86	-4.77	-1.43	3.01			Alternative core packing	34
V111F/F153L/WT*		55	-3.52	-1.09	3.01			Alternative core packing	34
V111I/WT*	2L78	87	-2.32	-0.69	3.01	$P3_221$	2.0	Alternative core packing	34
G113A	1L60		0.8	0.3	6.5	$P3_221$	1.65	Entropic stabilization	24
G113E/WT*		165	0.79	0.30	5.4			Random st mutant	43
T115-[A]/WT*	215L		-4.7	-1.8	5.4	$P3_221$	1.9	Insertion	72
T115A/WT*	166L		-0.43	-0.14	3.01	$P3_221$	1.75	Polyalanine helix 115-123	61
T115A/N116A/S117A/ R119A/M120A/Q122A/ Q123A/WT*	157L		3.19	1.00	3.01	$P3_221$	1.85	Polyalanine helix 115-123	61

T115A/S117A/WT*	155L		2.84	0.95	3.01	$P3_221$	1.85	Polyalanine helix 115-123	61
T115A/R119A/WT*	156L		-0.52	-0.17	3.01	$P3_221$	1.8	Polyalanine helix 115-123	61
T115E	1L37	370	0.7	0.3	6.5	$P3_221$	1.85	Helix dipole/salt bridge	16,23
N116A/WT*	161L		0.49	0.17	3.01	$P3_221$	1.7	Polyalanine helix 115-123	61
N116D	1L57	10	1.6	0.6	5.7	$P3_221$	1.85	Helix dipole interaction	16,64
N116D/R119M			1.6	0.6	5.7			Helix dipole control	16
S117A/WT*	165L		3.64	1.27	3.01	$P3_221$	1.75	Polyalanine helix 115-123	61
S117A/R119A/WT*	158L		3.37	1.16	3.01	$P3_221$	1.8	Polyalanine helix 115-123	61
S117A/N132I/WT*		20	5.3	2.0	5.42			Stability *versus* activity	62
S117A/N132M		30	4.7	1.8	5.42			Stability *versus* activity	62
S117F/WT*	1TLA	10	2.8	1.1	3.0	$P3_221$	2.0	Stable repacking mutant	53
S117I		0.5	4.2	1.7	5.42			Stability *versus* activity	62
S117I/N132I		3	3.6	1.4	5.42			Stability *versus* activity	62
S117I/N132M/WT*		2	5.5	2.0	5.42			Stability *versus* activity	62
S117V		5	5.1	2.0	5.42			Stability *versus* activity	62
L118A/WT*	1CVK		-12.2	-3.5	3.01	$P3_221$	1.8	Cavity-creating mutant	20,73,81
L118I/WT*	1PQO		-3.1	-1.2	5.35	$P3_221$	1.65	Core repacking	94
L118M/WT*	1CV4	98	-1.8	-0.7	5.42	$P3_221$	1.9	Single Met, kinetics	75,81,82
L118M/L121M/WT* ("2-M")	1KS3		-5.3	-1.9	5.42	$P3_221$	2.16	Multiple methionines	87
R119-[A]/WT*	214L		-6.6	-2.6	5.4	$P6_5$	1.9	Insertion	72
R119A/WT*	164L		-0.53	-0.18	3.01	$P3_221$	1.8	Polyalanine helix 115-123	61
R119A/Q123A/WT*	159L		-0.51	-0.17	3.01	$P3_221$	1.8	Polyalanine helix 115-123	61
R119E	1L44	169	-0.1	-0.04	5.3	$P3_221$	1.7	Cumulative charge-change	35

R119E/K135E		72	-2.6	-1.1	5.3			Cumulative charge-change	35
R119E/K135E/K147E		68	-3.8	-1.6	5.3			Cumulative charge-change	35
R119H/WT*		105	-0.74	-0.29	5.4			Random st mutant	43
R119M			0.3	0.1	5.7			Helix dipole control	16
R119Δ/WT*			-10.1	-3.6	5.4			Deletion	72
M120A/WT*	160L		-0.58	-0.20	3.01	$P3_221$	1.8	Polyalanine helix 115-123	61
M120K/WT*	232L	74	-4.8	-1.6	3.0	$P3_221$	1.7	Control for Met_Leu	77
M120L/WT*	233L	104	1.7	0.5	3.0	$P3_221$	1.9	Stabilization by Met_Leu	77
M120Y/WT*	1P6Y		-0.1	-0.1	5.35	$P3_221$	1.54	Core repacking	94
L121A/WT*	200L		-9.2	-2.7	3.01	$P3_221$	2.0	Cavity-creating mutant	20,73,81
L121A/WT* (8 bar Xe)[(h)]	1C65					$P3_221$	2.0	Noble gas binding[(h)]	88
L121A/A129L/WT*	198L		-2.8	-1.1	5.4	$P3_221$	2.0	Size-switch mutant	71
L121A/A129M/WT*	199L		-2.7	-1.0	5.4	$P3_221$	1.85	Size-switch mutant	71
L121A/A129M/V149I/ WT*	141L	~WT		-1.4	3.0	$P3_221$	2.0	Core repacking	55
L121A/A129M/F153L/ WT*	140L	~WT		-1.1	3.0	$P3_221$	2.1	Core repacking	55
L121A/A129V/L133A/ F153L/WT*	142L	~WT		-3.5	3.0	$P3_221$	2.0	Core repacking	55
L121A/A129V/L133M/ F153L/WT*	143L	~WT		-2.3	3.0	$P3_221$	2.0	Core repacking	55
L121A/L133A/WT*	251L					$P3_221$	2.6	Double truncation	73
L121A/L133A/WT* (8 bar Xe)[(h)]	1C68					$P3_221$	2.5	Noble gas binding[(h)]	88
L121I/A129L/L133M/ F153W/WT*	144L	~WT		-1.3	3.0	$P3_221$	2.1	Core repacking	55
L121I/A129W/L133M/	145L	~WT		-1.4	3.0	$P3_221$	2.0	Core repacking	55

WT*									
L121M/WT*	1CV3	87	-2.1	-0.8	5.42	$P3_221$	1.8	Single Met, kinetics	75,81,82
L121M/A129L/L133M/V149I/F153W/WT*	146L	~WT		-1.3	3.0	$P3_221$	1.85	Core repacking	55
L121M/L133V/F153L/WT*	147L	~WT		-2.5	3.0	$P3_221$	2.1	Core repacking	55
Q122A/WT*	162L		-0.71	-0.24	3.01	$P3_221$	1.8	Polyalanine helix 115-123	61
Q123A/WT*	163L		-0.64	-0.22	3.01	$P3_221$	1.8	Polyalanine helix 115-123	61
Q123E	1L38	280	1.2	0.4	6.5	$P3_221$	1.8	Salt bridge	23
K124G	1L22	140	-0.2	-0.1	6.5	$P3_221$	1.7	"Left-handed helical" residue	21
W126Y			-2.7		2.0			Amber supressor	59
W126Y/W138Y/W158Y			-7.2		2.0			Amber supressor	59
D127A/E128A/V131A/N132A	1L73		3.8	1.0	2.0	$P3_221$	1.85	Polyalanine helix 126-134	39,92
D127A/E128A/V131A/N132A/L133A	1L75		-9.4	-2.3	2.0	$P3_221$	1.9	Polyalanine helix 126-134	39,92
D127-[A]/WT*			-10.1	-3.5	5.4			Insertion	72
D127A/E128A	1L72		0.8	0.2	2.0	$P3_221$	1.9	Polyalanine helix 126-134	39
D127A/E128A/V131A/N132A/K135A/S136A ("7002A")			-0.9	-0.5	3.0			Polyalanine mutagenesis	92
D127A/E128A/V131A/N132A/K135A/S136A/R137A/Y139A/N140A/Q141A ("10A01")			-0.8	-0.5	3.0			Polyalanine mutagenesis	92
D127C/R154C/WT* red.	177L	79	-5.4	-1.3	2.0	$P4_222$	2.2	Destabilizing S-S bridge (intermolecular bridge)	8
D127C/R154C/WT* ox.		52	-2.4	-0.5	2.0			Destabilizing S-S bridge	8,28,106

D127C/R154C/WT*	178L					$P42_12$	2.7	Intramolecular S-S bridge	28
D127Δ/WT*			-8.4	-3.1	5.4				72
E128A		70	0.6	0.16	2.0			Polyalanine helix 126-134	40
E128A/V131A	1L71	70	1.5	0.41	2.0	$P3_221$	1.9	Polyalanine helix 126-134	39,40
E128A/V131A/N132A	1L36	70	3.4	0.94	2.0	$P3_221$	1.7	Polyalanine helix 126-134	39,40,92
E128A/V131A/N132A/ K135A/S136A/R137A ("6004A")	168L		-1.0	-0.5	3.0	$P2_12_12$	2.9	Polyalanine analysis	28,92
E128A/V131A/N132A/ K135A/S136A/R137A/ Y139A/N140A/Q141A ("9001A")	169L		-0.9	-0.5	3.0	$P2_1$	3.0	Polyalanine analysis	28,92
E128K		4	-5.3		3.0	$P3_221$	2.4	Low activity	37,41
E128A/V131A/N132A/ L133A	1L74		-10.3	-2.6	2.0	$P3_221$	1.7	Polyalanine helix 126-134	39,92
A129F/WT*	1QTC		-2.3	-1.2	3.0	$P3_221$	2.5	Introduction of strain	84
A129L/WT*	195L		-3.2	-1.3	5.4	$P3_221$	1.9	Size-switch mutant	71,84
A129M/WT*	196L		-5.2	-1.9	5.4	$P3_221$	2.3	Size-switch mutant, kinetics	71,81,82,84
A129M/F153A/WT*	197L		-12.7	-4.3	5.4	$P3_221$	2.1	Size-switch mutant	71
A129V			-1.9	-0.7	2.85			Cavity-filling	42
A129W/WT*	1QTD		-5.1	-2.2	3.0	$P3_221$	2.5	Introduction of strain	84
A130S/WT*	118L	~WT	-2.89	-1.0	3.0	$P3_221$	1.8	Add hydroxyl	54
V131-[A]/WT*	218L		-7.9	-2.9	5.4	$P2_12_12_1$	2.1	Insertion	72
V131A	1L33	90	0.66	0.26	3.0	$P3_221$	1.7	Helix propensity analysis	18,49,50
V131A/N132A	1L70		2.3	0.62	2.0	$P3_221$	1.9	Polyalanine helix 126-134	39,40
V131D	1DYA	~WT	0.22	0.08	3.0	$P3_221$	1.9	Helix propensity analysis	49,50,64
V131E	1DYG	~WT	0.52	0.20	3.0	$P3_221$	2.1	Helix propensity analysis	49,50

V131G	1DYB	~WT	-1.80	-0.68	3.0	$P3_221$	1.75	Helix propensity analysis	49,50
V131I	1DYC	~WT	0.41	0.16	3.0	$P3_221$	2.1	Helix propensity analysis	49,50
V131L	1DYD	~WT	0.23	0.09	3.0	$P3_221$	1.9	Helix propensity analysis	49,50
V131M	1DYF	~WT	0.32	0.12	3.0	$P3_221$	1.9	Helix propensity analysis	49,50
V131S	1DYE	~WT	-0.12	-0.05	3.0	$P3_221$	1.8	Helix propensity analysis	49,50
V131T			-0.33	-0.12	3.0			Helix propensity analysis	18
N132F		40	3.3	1.3	5.42			Stability *versus* activity	62
N132I		20	3.0	1.2	5.42			Stability *versus* activity	62
N132M		40	3.6	1.5	5.42			Stability *versus* activity	62
L133A	1L69		-10.55	-3.6	3.01	$P3_221$	1.9	Cavity-creating, polyala.	20,39
L133A/WT* (8 bar Xe)[(h)]	1C6B					$P3_221$	2.2	Noble gas binding[(h)]	88
L133D/WT*		4	-17.9	-5.7	6.5			Buried aspartate	35
L133F			-0.8	-0.3	2.85			Cavity-filling	42
L133F/WT*	1P64		-0.7	-0.3	5.35	$P3_221$	1.62	Core repacking	94
L133G	226L		-11.7	-3.1	3.01	$P3_221$	1.8	Sidechain removal	74
L133G (+Bz)[(h)]	223L		[2.6]		3.01	$P3_221$	1.9	Benzene binding[(h)]	74
L133M/WT*	1CV5	106	-1.2	-0.4	5.42	$P3_221$		Single Met	75,82,87
A134S/WT*	119L	~WT	-0.44	-0.1	3.0	$P3_221$	1.65	Add hydroxyl	54
K135E	1L45	104	-2.3	-1.0	5.3	$P3_221$	1.7	Cumulative charge-change	12
K135E/K147E		128	-3.7	-1.5	5.3			Cumulative charge-change	12
N140-[A]/WT*	213L		-5.6	-2.1	5.4	$P3_221$	2.0	Insertion	72
N144-[A]/WT*			-2.0	-0.7	5.4			Insertion	72
N144D	1L20	60	1.4	0.5	6.9	$P3_221$	1.9	Helix dipole interaction	15,16,64
N144E/WT*	1L39	115	1.5	0.5	6.5	$P3_221$	1.85	Salt bridge	23

N144E/K147M			1.2	0.4	6.5			Salt bridge	23
N144H/WT*			0.7	0.3	6.7			Helix dipole control	16
A146C/C54S/C97S	170L					$P4_12_12$	2.6	Buried cysteine	28
A146T		55	-9.4		3.0			Random ts mutant	36-38
K147-[A]/WT*			-5.9	-2.1	5.4				72
K147E	1L46	120	-1.6	-0.7	5.3	$P3_221$	1.7	Cumulative charge-change	12
R148-[A]/WT*			-13.7	-4.6	5.4			Insertion	72
R148-[AA]/WT*			-17.5	-5.4	5.4			Insertion	72
R148-[AAA]/WT*			-15.9	-5.0	5.4			Insertion	72
R148-[AAAA]/WT*			-23.2	-5.6	5.4			Insertion	72
R148-[D]/WT*			-14.7	-4.8	5.4			Insertion	72
R148-[DS]/WT*			-19.0	-5.6	5.4			Insertion	72
R148-[S]/WT*			-15.7	-5.0	5.4			Insertion	72
R148-[TT]/WT*			-20.5	-5.9	5.4			Insertion	72
R148-[VP]/WT*			-22.0	-6.3	5.4			Insertion	72
V149A/WT*	237L		-11.0	-3.2	3.0	$P3_221$	1.7	Internal solvent	73,81
V149C	1L53	67	-5.1	-2.2	3.0	$P3_221$	1.85	Helix packing analysis	32
V149C/WT*	1G07		-5.5	-2.0	5.4	$P3_221$	1.7	Solvent binding	89
V149G/WT*	1G0P		-15.3	-4.9	5.4	$P3_221$	1.8	Solvent binding	89,102
V149I/WT*	1G0Q		-0.05	-0.1	5.4	$P3_221$	1.8	Solvent perturbation	89,94
V149I/T152V/WT*	1PQM				5.35	$P3_221$	1.52	Core repacking	94
V149M/WT*	1CV6		-7.8	-2.8	5.4	$P3_221$	1.9	Kinetics of folding	81,82
V149S/WT*	1G06		-13.2	-4.4	5.4	$P3_221$	1.85	Solvent binding	89
V149T/WT*	126L	~WT	-10.08	-2.8	3.0	$P3_221$	1.8	Substitute hydroxyl	54,89

I150-[A]/WT*			-24.3	-6.0	5.4				72
T151S/WT*	130L	86	0.93	0.39	5.4	$P3_221$	1.7	Random st mutant	43,57
T152A/WT*	1G0G		-4.0	-1.5	5.4	$P3_221$	1.9	Solvent perturbation	89
T152C/WT*	1G0K		-1.4	-0.5	5.4	$P3_221$	1.85	Solvent perturbation	89
T152I/WT*	1G0M		-1.0	-0.4	5.4	$P3_221$	1.7	Solvent perturbation	89
T152S	1L52	94	-6.6	-2.6	3.0	$P3_221$	1.7	Helix packing analysis	32
T152S/WT*	1G0J		-5.5	-2.0	5.4	$P3_221$	1.8	Solvent perturbation	89
T152V/WT*	1G0L		0.8	0.2	5.4	$P3_221$	1.8	Solvent perturbation	89,94
F153A/WT*	1L85		-12.3	-3.5	3.01	$P3_221$	2.0	Cavity-creating	20,73,81
F153A/WT* (8 bar Xe)[(h)]	1C62					$P3_221$	2.3	Noble gas binding[(h)]	88,110
F153I/WT*	1L86		-1.5	-0.5	3.01	$P3_221$	1.8	Hydrophobic replacement	5
F153L/WT*	1L87		0.6	0.2	3.01	$P3_221$	1.8	Hydrophobic replacement	5
F153M/WT*	1L88		-2.4	-0.8	3.01	$P3_221$	1.85	Hydrophobic replacement	5,81,82
F153V/WT*	1L95		-6.1	-1.8	3.01	$P3_221$	2.0	Hydrophobic replacement	5
R154E	1L47	90	-2.6	-1.1	5.3	$P3_221$	1.7	Cumulative charge-change	12
T155A/T157I	1L01					$P3_221$	1.7	H-bond, incidental	45
G156D	1L16	50	-6.1	-2.3	6.5	$P3_221$	1.7	Random ts mutant	46
T157A	1L02	~WT	-5.4	-1.4	2.0	$P3_221$	1.7	H-bond analysis	45
T157C	1L03	~WT	-4.9	-1.3	2.0	$P3_221$	1.7	H-bond analysis	45
T157D	1L04	~WT	-4.2	-1.1	2.0	$P3_221$	1.7	H-bond analysis	45
T157E	1L06	~WT	-5.8	-1.5	2.0	$P3_221$	1.7	H-bond analysis	45
T157F	1L07	~WT	-9.2	-2.4	2.0	$P3_221$	1.7	H-bond analysis	45
T157G	1L08	~WT	-4.2	-1.1	2.0	$P3_221$	1.7	H-bond analysis	45
T157H	1L09	~WT	-7.9	-2.1	2.0	$P3_221$	1.7	H-bond analysis	45

T157I	1L10	90	-11.0	-3.1	2.0	$P3_221$	1.7	Ts mutant	47
T157I/WT*	1LLH		-5.7	-2.05	5.42	$P3_221$	1.8	Rules for helix capping	90
T157I/W158L/WT*	--		-10.3	-3.55	5.42			Rules for helix capping	90
T157L	1L11	~WT	-5.0	-1.3	2.0	$P3_221$	1.7	H-bond analysis	45
T157N	1L12	~WT	-1.7	-0.45	2.0	$P3_221$	1.7	H-bond analysis	45
T157R	1L13	~WT	-5.1	-1.3	2.0	$P3_221$	1.7	H-bond analysis	45
T157S	1L14	~WT	-2.5	-0.66	2.0	$P3_221$	1.7	H-bond analysis	45
T157V	1L15	~WT	-6.0	-1.6	2.0	$P3_221$	1.7	H-bond analysis	45
W158L/WT*	1JQU		-4.6	-1.75	5.42	$P2_12_12_1$	2.6	Rules for helix capping	90
N163D/WT*		193	-0.50	-0.21	5.4			Random st mutant	43
L164-[AAAA]/WT*[h]	219L		0.6	0.2	5.4	$P3_221$	1.7	C-terminal extension[h]	72
L164-[ETYYTIGIGH LLTK]/WT*	1JTM					$P3_221$	1.9	C-terminal extension	91
L164-[ETYYTIGIGH LLTK/WT* (Crystal form II)	1JTN					$P2_1$	2.3	C-terminal extension	91

FOOTNOTES

[a]The table includes mutant lysozymes for which the protein was purified, characterized at least to some degree, and described in the literature. "WT" is wild-type T4 lysozyme. Unless otherwise indicated the mutants were made in this background. "WT*" is a pseudo-wildtype lysozyme in which the two naturally-occurring cysteines have been replaced by the two mutations C54T/C97A (Ref. 3). A mutant made in this background, such as L99A, is indicated L99A/WT*.

[b]Where the structure has been determined the coordinate identification in the Protein Data Bank is given.

[c]Activities were determined by several different assays. They are expressed as percent of the activity of the reference protein (WT or WT*) determined using that same assay. Activity indicated as "~WT" means that the mutant lysozyme appeared to have activity roughly the same as wild-type, but was not measured explicitly. Use of the symbols, +, ++ and +++ refer to the halo assay as defined in Refs. 67, 78.

[d]The thermodynamic data are for a representative value of pH, as quoted. ΔT_m is the change in melting temperature of the mutant protein relative to WT or WT*, whichever is the appropriate reference protein. $\Delta\Delta G$ is the change in the free energy of unfolding of the mutant protein relative to WT or WT*, a positive value corresponding to a mutant that is more stable than wild-type. Values of T_m given in square parentheses indicate the change in T_m due to the presence of the indicated ligand.

[e]Under "Crystallographic data" the space group and resolution of the data are given. Lack of an entry could mean either that crystallization was not attempted or was attempted but not successful.

[f]The "Comment" explains why the mutant was made, or other pertinent information.

[g]The numbers quoted are not ΔT_m but the T_m of WT or WT* under the stated conditions.

[h]See the references quoted for related complexes or structures. For mutant T157D see PDB entries 1L04 and 1L05.

[i]See the references quoted for a full description of this construct.

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Table S2. Crystal forms of WT and mutant T4 lysozymes

Mutant	PDB code	Space group	Cell dimensions *a* (Å) α (°)	*b* (Å) β (°)	*c* (Å) γ (°)	Mol. per asymmetric unit	V_M (Å³/Dalton)	Solvent content (%)	Resolution (Å)	R (%)	Ref.[1]
WT[2]	3FA0	$P3_221$	60.37	60.37	96.57 120	1	2.8	56	0.98	16.4	103,111
Circular permutant, "PERM1"	1P5C	$P2_1$	53.8	67.8 92.6	94.1	4	2.3	47	2.5	24.8	70
I3C (S-S)	172L	$P2_12_12_1$	32.2	50.4	97.1	1	2.1	41	1.9	19.0	6-8,28
I3C/I9C/T21C/C54T/ T142C/L164C	152L	$P2_12_12_1$	63.2	51.0	48.2	1	2.1	41	2.0	16.8	9,63
I3C/I9C/C54T/L164C	167L	$P2_12_12_1$	141.0	51.1	48.0	2	2.3	47	2.2	17.7	28
I3L[3]	149L	$P2_12_12_1$	35.8	56.6	94.2	1	2.7	54	2.6	19.2	6,7,64
I3L/S38D/A41V/A82P/ N116D/V131A/N144D[3]	189L	$P2_12_12_1$	34.6	56.8	94.4	1	2.5	50	2.6	20.0	64
I3P	1L97	$P2_12_12$	86.5	96.6	39.2	2	2.2	44	2.0	16.7	10
M6I	150L	$P2_12_12_1$	72.2	73.8	150.5	4	2.7	54	2.2	21.0	11,44
R14A/K16A/I17A/K19A/ T21A/E22A/WT*	1T8F	$P6_222$	120.5	120.5	50.3 120	1	2.8	56	2.15	22.4	105
K16E/R119E/K135E/ K147E	173L	$P6_5$	75.1	75.1	54.7 120	1	2.4	48	1.7	18.3	12,28

T21C..."L99A/M102E/St"	3GUI	$P4_12_12$	48.8	48.8	128.5	1	2.1	41	1.45	18.5	112
T21C..."L99A/M102E/St" + toluene	3GUK	$P4_3$	49.5	49.5	129.5	1	2.1	41	1.85	22.5	112
T26E/WT*	148L	$P2_12_12$	50.9	67.3	49.6	1	2.2	44	1.9	16.3	51
T26E/WT*	180L	$P2_1$	52.3	57.7 104.4	57.6	2	2.3	47	1.75	17.8	28
I27-[GIGHLL]/WT*	3JR6	$P2_1$	59.2	75.9 94.1	81.6	4	2.4	4.8	3.0	26.1	99
G28A/I29A/G30A/WT*	1SSY	C2	123.0	53.7 102.3	60.5	2	2.6	53	2.4	17.5	105
G30-[YTIGIG]/WT*	2B7X	$P2_12_12_1$	61.4	78.1	143.4	4	2.4	49	3.0	26.1	99
L32A/L33A/T34A/ E108V/WT*	1T8G	I422	96.0	96.0	77.3	1	2.4	49	1.8	18.4	105
L32T..."R2"	176L	$P2_1$	49.6	127.1 98.4	29.1	2	2.5	51	2.2	18.3	28
T34A/K35A/S36A/P37A	151L	R3	100.5	100.5	40.8 120	1	2.1	41	2.2	18.7	63,92
T34A..."J002A"	174L	$P6_3$	89.3	89.3	87.1 120	2	2.7	54	2.3	19.8	28,92
L39I..."L20"	262L	$P2_1$	57.7	55.8 111.0	65.2	2	2.7	54	2.5	22.7	79
L39I..."L20pg"	1OYU	$P4_12_12$	60.4	60.4	213.9	2	2.5	51	2.5	21.9	95
L39I..."L20/R63A"[4]	1T97	$P2_1$	54.0	54.2	58.0	2	2.2	44	2.7	23.5	97

				103.9							
S44-[AA]/WT*	104L	R32	172.1	172.1	80.0 120	2	3.2	62	2.8	17.5	52,56
S44E/WT*	-	P2	58.1	35.1 102	46.8	1	2.5	51	1.9	18.9	28,49,50
S44F/WT*[(4)]	137L	$P2_1$	54.1	55.9 103.6	59.9	2	2.3	47	1.85	15.0	49,50
S44W/WT*	216L	C2	116.5	54.4 102.3	59.5	2	2.5	51	2.1	19.4	28,49,50
E45A/WT*	171L	$P2_12_12$	29.3	129.3	48.9	1	2.6	53	2.5	21.7	17,28
K48-[HP]/WT*[(4)]	201L	$P2_1$	55.2	54.2 103.5	59.1	2	2.3	46	2.0	18.2	52,56
A73-[AAA]/WT*	209L	$P6_222$	95.9	95.9	117.9 120	1	4.3	71	2.7	17.9	72
I78V...“M87V/Core 7”	1PQK	C2	156.2	67.3 112.4	61.7	3	2.7	54	2.0	18.0	94
R96A/WT* (cf. S44W/WT*)	175L	C2	115.7	54.8 103.4	59.1	2	2.5	50	2.1	17.5	28
R96V	3CDO	$P2_12_12_1$	57.8	99.3	123.0	4	2.4	49	1.87	18.7	103,104
R96W	3FI5	$P2_1$	73.8	56.1 106.5	85.2	4	2.3	47	1.53	19.6	103,104

A98M/WT*	1QTH	$P3_1$	53.6	53.6	101.9 120	2	2.3	47	1.9	18.9	84
V103I/WT*	1P7S	$P2_12_12_1$	30.8	54.9	88.4	1	2.0	38	1.5	19.3	94
R119-[A]/WT*	214L	$P6_5$	84.7	84.7	48.0 120	1	2.7	54	1.9	18.5	72
D127C/R154C/WT*	177L	$P4_222$	72.6	72.6	82.2	1	2.9	58	2.5	22.8	8
D127C/R154C/WT*	178L	$P42_12$	118.9	118.9	39.0	1	3.7	67	2.7	19.2	28
E128A...“6004A”	168L	$P2_12_12$	157.2	177.9	40.5	5	3.1	60	2.9	19.9	28,92
E128A...“9001A”	169L	$P2_1$	40.4	112.3 91.7	135.2	5	3.4	64	3.0	16.1	28,92
V131-[A]/WT*	218L	$P2_12_12_1$	36.6	61.1	88.7	1	2.7	54	2.1	19.2	72
A146C/C54S/C97S	170L	$P4_12_12$	53.6	53.6	165.2	1	3.3	63	2.6	22.3	28
W158L	1JQU	$P2_12_12_1$	74.3	77.2	138.2	4	2.7	54	2.6	24.1	90
L164-[ETYYTIGIGH LLTK]/WT*	1JTN	$P2_1$	60.1	32.3 102.6	85.9	2	2.0	38	2.3	23.2	91

[(1)]References are given under Table S1.

[(2)]WT* and many other mutants are isomorphous with WT (see Table S1).

[(3)]I3L and I3L/S38D/A41V/A82P/N116D/V131A/N144D are isomorphous.

[(4)]S44F/WT*, K48-[HP]/WT* and L39I...“L20/R63A” are isomorphous, the last with a different origin of coordinates.