

N	PDB_id	Chain	RES_id	RES (WT)	RES (MUT)	$\Delta T_m_{exp}$ (°C)	$T_m_{exp}$ (WT) (°C)	$\Delta\Delta H_{m,exp}$ (kcal/mol)	$\Delta H_{m,exp}$ (WT) (kcal/mol)	$\Delta\Delta C_p,exp$ (kcal/mol K)	$\Delta C_p,exp$ (WT) (kcal/mol K)	$\Delta\Delta G_{exp}$ (kcal/mol)	Temp (°C)	$N_{res}$	R (Å)	Protein	Organism	Ref.	pH	Measure
1	1aky	A	8	VAL	ILE	-1.5	47.6	16.7	-81.3	-	-2.03	1.19	25	220	1.63	Adenylate Kinase	Saccharomyces cerevi	[1]	[7.5]	Fluorescence
2	1aky	A	48	GLN	GLU	-1.3	47.6	14.3	-81.3	-	-2.03	0.96	25	220	1.63	Adenylate Kinase	Saccharomyces cerevi	[1]	[7.7]	Fluorescence
3	1aky	A	77	THR	HIS	-1.1	47.6	31.1	-81.3	-	-2.03	2.15	25	220	1.63	Adenylate Kinase	Saccharomyces cerevi	[1]	[7.5]	Fluorescence
4	1aky	A	110	THR	HIS	-4.8	47.6	39.4	-81.3	-	-2.03	2.63	25	220	1.63	Adenylate Kinase	Saccharomyces cerevi	[1]	[7.6]	Fluorescence
5	1aky	A	169	ASN	ASP	-0.6	47.6	33.5	-81.3	-	-2.03	2.15	25	220	1.63	Adenylate Kinase	Saccharomyces cerevi	[1]	[7.5]	Fluorescence
6	1aky	A	213	ILE	PHE	-7.7	47.6	21.5	-81.3	-	-2.03	1.91	25	220	1.63	Adenylate Kinase	Saccharomyces cerevi	[1]	[7.5]	Fluorescence
7	1am7	A	31	HIS	ASP	-6.2	52.3	13.5	-113.3	-	-	1.60	25	158	2.30	Lysozyme	Lambda phage	[2]	[6.0]	Fluorescence
8	1ank	A	84	ASP	HIS	-7.2	51.8	32.0	-95.0	-	-	1.40	52	214	2.00	Adenylate Kinase	Escherichia Coli	[3]	[7.2]	DSC
9	1ank	A	85	GLY	VAL	-11.1	51.8	25.0	-95.0	-	-	2.40	52	214	2.00	Adenylate Kinase	Escherichia Coli	[3]	[7.2]	DSC
10	1ank	A	86	PHE	LEU	-2.6	51.8	-2.0	-95.0	-	-	0.80	52	214	2.00	Adenylate Kinase	Escherichia Coli	[3]	[7.2]	DSC
11	1ank	A	88	ARG	GLY	-0.8	51.8	20.0	-95.0	-	-	0.20	52	214	2.00	Adenylate Kinase	Escherichia Coli	[4]	[7.4]	DSC
12	1aqh	A	12	ASN	ARG	-0.7	44.0	21.0	-214.0	-	-	-	-	453	2.00	Alpha-amylase	Pseudoalteromonas ha	[5]	[7.2]	DSC
13	1aqh	A	64	ARG	GLU	-1.4	44.0	-0.1	-214.0	-	-	-	-	453	2.00	Alpha-amylase	Pseudoalteromonas ha	[5]	[7.2]	DSC
14	1aqh	A	150	ASN	ASP	0.8	44.0	-57.0	-214.0	-	-	-	-	453	2.00	Alpha-amylase	Pseudoalteromonas ha	[5]	[7.2]	DSC
15	1aqh	A	196	VAL	PHE	1.4	44.0	-20.0	-214.0	-	-	-	-	453	2.00	Alpha-amylase	Pseudoalteromonas ha	[5]	[7.2]	DSC
16	1aqh	A	219	LEU	ARG	-1.5	44.0	-3.0	-214.0	-	-	-	-	453	2.00	Alpha-amylase	Pseudoalteromonas ha	[5]	[7.2]	DSC
17	1aqh	A	279	GLU	TRP	-2.6	44.0	28.0	-214.0	-	-	-	-	453	2.00	Alpha-amylase	Pseudoalteromonas ha	[5]	[7.2]	DSC
18	1aqh	A	300	LYS	ARG	1.2	44.0	-9.0	-214.0	-	-	-	-	453	2.00	Alpha-amylase	Pseudoalteromonas ha	[5]	[7.2]	DSC
19	1avr	A	17	GLU	GLY	0.3	52.5	-1.0	-163.0	-	-2.46	-	-	320	2.30	Annexin V	Homo sapiens	[6]	[8.0]	DSC
20	1ayf	A	11	PHE	TRP	-5.3	50.7	-	-82.8	-	-	-	-	105	1.85	Adrenodoxin	Bos Taurus	[7]	[8.5]	CD
21	1ayf	A	43	PHE	TRP	-6.5	50.7	-	-82.8	-	-	-	-	105	1.85	Adrenodoxin	Bos Taurus	[7]	[8.5]	CD
22	1ayf	A	54	THR	ALA	-5.5	50.7	16.7	-82.8	0.17	-1.79	1.48	25	105	1.85	Adrenodoxin	Bos Taurus	[8]	[8.5]	CD
23	1ayf	A	54	THR	SER	0.3	50.7	-0.2	-82.8	-0.11	-1.79	0.12	25	105	1.85	Adrenodoxin	Bos Taurus	[8]	[8.5]	CD
24	1ayf	A	56	HIS	GLN	-4.9	50.7	25.2	-82.8	0.10	-1.79	2.17	25	105	1.85	Adrenodoxin	Bos Taurus	[8]	[8.5]	DSC
25	1ayf	A	56	HIS	ARG	-2.1	50.7	25.4	-82.8	0.77	-1.79	1.36	25	105	1.85	Adrenodoxin	Bos Taurus	[8]	[8.5]	DSC
26	1ayf	A	56	HIS	THR	-2.6	50.7	20.1	-82.8	0.38	-1.79	1.41	25	105	1.85	Adrenodoxin	Bos Taurus	[8]	[8.5]	DSC
27	1ayf	A	59	PHE	TRP	-14.6	50.7	-	-82.8	-	-1.79	-	-	105	1.85	Adrenodoxin	Bos Taurus	[7]	[8.5]	CD
28	1ayf	A	64	PHE	TRP	-3.2	50.7	-	-82.8	-	-1.79	-	-	105	1.85	Adrenodoxin	Bos Taurus	[7]	[8.5]	CD
29	1ayf	A	68	GLU	ALA	-1.1	50.7	0.7	-82.8	-	-1.79	-	-	105	1.85	Adrenodoxin	Bos Taurus	[257]	[8.5]	CD
30	1ayf	A	76	ASP	GLU	2.0	50.7	-2.0	-82.8	-0.65	-1.79	0.48	25	105	1.85	Adrenodoxin	Bos Taurus	[8]	[8.5]	DSC
31	1ayf	A	82	TYR	PHE	0.1	50.7	1.2	-82.8	-0.01	-1.79	0.10	25	105	1.85	Adrenodoxin	Bos Taurus	[8]	[8.5]	DSC
32	1ayf	A	82	TYR	LEU	-0.7	50.7	6.0	-82.8	-0.13	-1.79	0.69	25	105	1.85	Adrenodoxin	Bos Taurus	[8]	[8.5]	DSC
33	1ayf	A	82	TYR	SER	-0.8	50.7	5.0	-82.8	-0.16	-1.79	0.65	25	105	1.85	Adrenodoxin	Bos Taurus	[8]	[8.5]	DSC
34	1ayf	A	82	TYR	TRP	-0.2	50.7	-	-82.8	-	-1.79	-	-	105	1.85	Adrenodoxin	Bos Taurus	[7.8]	[8.5]	CD-DSC
35	1ayf	A	89	ARG	ALA	-11.9	50.7	41.8	-82.8	-	-1.79	-	-	105	1.85	Adrenodoxin	Bos Taurus	[257]	[8.5]	CD
36	1ayf	A	89	ARG	LYS	-17.5	50.7	48.8	-82.8	-	-1.79	-	-	105	1.85	Adrenodoxin	Bos Taurus	[257]	[8.5]	CD
37	1ayf	A	95	CYS	SER	4.4	50.7	-4.4	-82.8	0.17	-1.79	-0.93	25	105	1.85	Adrenodoxin	Bos Taurus	[8]	[8.5]	DSC
38	1azp	A	24	TRP	ALA	-9.6	90.7	11.7	-58.5	-0.01	-0.71	2.03	25	61	1.60	Sac7d	Sulfolobus acidocaldarius	[9]	[7.0]	DSC
39	1azp	A	30	VAL	ILE	5.8	90.7	-4.5	-58.5	-0.04	-0.71	-0.53	25	61	1.60	Sac7d	Sulfolobus acidocaldarius	[10]	[7.0]	DSC
40	1bni	A	8	ASP	ALA	-2.0	54.2	1.3	-141.4	-	-1.60	0.60	25	110	2.10	Barnase	Bacillus amyloliquef	[13]	[6.3]	CD
41	1bni	A	8	ASP	GLY	-3.0	54.2	3.8	-141.4	-	-1.60	1.00	25	110	2.10	Barnase	Bacillus amyloliquef	[13]	[6.3]	CD
42	1bni	A	12	ASP	GLY	-2.0	54.2	1.8	-141.4	-	-1.60	0.60	25	110	2.10	Barnase	Bacillus amyloliquef	[14]	[4.4]	DSC
43	1bni	A	14	LEU	ALA	-11.9	54.2	17.0	-141.4	-	-1.60	4.20	25	110	2.10	Barnase	Bacillus amyloliquef	[15]	[6.3]	Fluorescence
44	1bni	A	16	THR	ARG	1.3	54.2	-1.2	-141.4	-	-1.60	-0.38	25	110	2.10	Barnase	Bacillus amyloliquef	[14]	[4.4]	DSC
45	1bni	A	17	THR	ALA	-5.1	54.2	8.3	-141.4	-	-1.60	1.90	25	110	2.10	Barnase	Bacillus amyloliquef	[13]	[6.3]	CD
46	1bni	A	22	ASP	MET	-1.6	54.2	-3.7	-141.4	-	-1.60	0.09	25	110	2.10	Barnase	Bacillus amyloliquef	[14]	[4.4]	DSC
47	1bni	A	26	THR	GLY	-4.1	54.2	13.2	-141.4	-	-1.60	1.90	25	110	2.10	Barnase	Bacillus amyloliquef	[14]	[4.4]	DSC
48	1bni	A	51	ILE	VAL	-4.5	54.2	11.0	-141.4	-	-1.60	1.86	25	110	2.10	Barnase	Bacillus amyloliquef	[14]	[4.4]	DSC
49	1bni	A	52	GLY	ALA	-13.3	54.2	-	-141.4	-	-1.60	5.30	54	110	2.10	Barnase	Bacillus amyloliquef	[16]	[6.3]	DSC
50	1bni	A	53	GLY	ALA	-8.6	54.2	-	-141.4	-	-1.60	3.40	54	110	2.10	Barnase	Bacillus amyloliquef	[16]	[6.3]	DSC
51	1bni	A	53	GLY	VAL	-19.6	54.2	-	-141.4	-	-1.60	7.80	54	110	2.10	Barnase	Bacillus amyloliquef	[16]	[6.3]	DSC
52	1bni	A	54	ASP	ASN	-7.3	54.2	9.3	-141.4	-	-1.60	2.38	25	110	2.10	Barnase	Bacillus amyloliquef	[14]	[4.4]	DSC
53	1bni	A	69	ARG	MET	-5.8	54.2	19.4	-141.4	-	-1.60	2.68	25	110	2.10	Barnase	Bacillus amyloliquef	[14]	[4.4]	DSC
54	1bni	A	83	ARG	GLN	-3.3	54.2	8.5	-141.4	-	-1.60	1.40	25	110	2.10	Barnase	Bacillus amyloliquef	[14]	[4.4]	DSC
55	1bni	A	88	ILE	ALA	-11.2	54.2	19.0	-141.4	-	-1.60	4.20	25	110	2.10	Barnase	Bacillus amyloliquef	[15]	[6.3]	Fluorescence
56	1bni	A	88	ILE	VAL	-2.9	54.2	8.0	-141.4	-	-1.60	1.40	25	110	2.10	Barnase	Bacillus amyloliquef	[15]	[6.3]	Fluorescence
57	1bni	A	91	SER	ALA	-4.8	54.2	1.4	-141.4	-	-1.60	1.38	25	110	2.10	Barnase	Bacillus amyloliquef	[14]	[4.4]	DSC
58	1bni	A	92	SER	ALA	-7.2	54.2	14.2	-141.4	-	-1.60	2.65	25	110	2.10	Barnase	Bacillus amyloliquef	[14]	[4.4]	DSC
59	1bni	A	96	ILE	ALA	-9.0	54.2	13.0	-141.4	-	-1.60	3.30	25	110	2.10	Barnase	Bacillus amyloliquef	[15]	[6.3]	Fluorescence
60	1bni	A	96	ILE	VAL	-2.4	54.2	4.0	-141.4	-	-1.60	0.90	25	110	2.10	Barnase	Bacillus amyloliquef	[15]	[6.3]	Fluorescence
61	1bni_1302a	A	12	ASP	ALA	-1.0	52.2	-15.6	-137.2	-	-	-1.10	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
62	1bni_1302a	A	12	ASP	GLY	-2.3	52.2	8.5	-137.2	-	-	1.20	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
63	1bni_1302a	A	13	TYR	GLY	-15.6	52.2	44.5	-137.2	-	-	6.40	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
64	1bni_1302a	A	15	GLN	ALA	-0.9	52.2	0.5	-137.2	-	-	0.20	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
65	1bni_1302a	A	15	GLN	GLY	-2.0	52.2	14.2	-137.2	-	-	1.40	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
66	1bni_1302a	A	17	TYR	GLY	-10.3	52.2	19.8	-137.2	-	-	4.90	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
67	1bni_1302a	A	55	ILE	GLY	-5.3	52.2	25.5	-137.2	-	-	3.10	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
68	1bni_1302a	A	72	ARG	GLY	-5.7	52.2	14.4	-137.2	-	-	2.50	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
69	1bni_1302a	A	73	GLU	GLY	-12.7	52.2	36.6	-137.2	-	-	5.40	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
70	1bni_1302a	A	89	LEU	GLY	-8.7	52.2	78.7	-137.2	-	-	7.00	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
71	1bni_1302a	A	95	LEU	GLY	-9.1	52.2	38.7	-137.2	-	-	4.70	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
72	1bni_1302a	A	96	ILE	GLY	-15.7	52.2	26.9	-137.2	-	-	5.70	25	110	2.10	Barnase (pseudo-wt)	Bacillus amyloliquef	[13]	[6.3]	CD
73	1bni_1302a	A	97	TYR	GLY	-17.9	52.2	34.6	-137.2	-	-	6.60	25	110	2.10</					

102	1bvc	A	117	SER	ALA	-0.5	82.2	-	-186.5	-	-2.80	0.26	82	153	1.50	Myoglobin	Physeter catodon	[17]	[9.6]	CD
103	1bvc	A	129	GLY	ALA	2.0	82.2	-	-186.5	-	-2.80	-1.05	82	153	1.50	Myoglobin	Physeter catodon	[17]	[9.6]	CD
104	1bvc	A	135	LEU	ILE	-5.2	82.2	-	-186.5	-	-2.80	1.54	77	153	1.50	Myoglobin	Physeter catodon	[18]	[11.0]	DSC
105	1bvc	A	135	LEU	MET	-2.5	82.2	-	-186.5	-	-2.80	0.79	77	153	1.50	Myoglobin	Physeter catodon	[18]	[11.0]	DSC
106	1bvc	A	135	LEU	VAL	-8.3	82.2	-	-186.5	-	-2.80	2.25	77	153	1.50	Myoglobin	Physeter catodon	[18]	[11.0]	DSC
107	1bvc	A	137	LEU	ALA	-3.6	82.2	-	-186.5	-	-2.80	1.78	82	153	1.50	Myoglobin	Physeter catodon	[17]	[9.6]	CD
108	1bvc	A	142	ILE	ALA	-3.9	82.2	-	-186.5	-	-2.80	1.92	82	153	1.50	Myoglobin	Physeter catodon	[17]	[9.6]	CD
109	1bvc	A	142	ILE	LEU	1.8	82.2	-	-186.5	-	-2.80	-0.63	77	153	1.50	Myoglobin	Physeter catodon	[18]	[11.0]	DSC
110	1bvc	A	142	ILE	MET	2.6	82.2	-	-186.5	-	-2.80	-0.93	77	153	1.50	Myoglobin	Physeter catodon	[18]	[11.0]	DSC
111	1bvc	A	142	ILE	VAL	-0.3	82.2	-	-186.5	-	-2.80	0.12	77	153	1.50	Myoglobin	Physeter catodon	[18]	[11.0]	DSC
112	1bvc	A	149	LEU	ALA	-3.2	82.2	-	-186.5	-	-2.80	1.60	82	153	1.50	Myoglobin	Physeter catodon	[17]	[9.6]	CD
113	1c52	A	69	MET	ALA	4.0	94.9	-28.9	-30.4	-0.19	-0.31	-5.01	25	131	1.28	Cytochrome c-552	Thermus thermophilus	[240]	[7.0]	CD
114	1c52	A	69	MET	HIS	-2.0	94.9	2.6	-30.4	0.02	-0.31	0.71	25	131	1.28	Cytochrome c-552	Thermus thermophilus	[240]	[7.0]	CD
115	1c8c	A	24	TRP	ALA	-6.1	98.6	4.8	-64.4	-0.02	-0.69	0.75	25	64	1.45	Sso7d	Sulfolobus solfataricus	[11]	[7.0]	DSC
116	1c8c	A	30	ILE	VAL	-3.9	98.6	2.5	-64.4	0.04	-0.69	0.73	25	64	1.45	Sso7d	Sulfolobus solfataricus	[12]	[7.0]	DSC
117	1c8c	A	32	PHE	TYR	-10.4	98.6	10.5	-64.4	0.00	-0.69	2.14	25	64	1.45	Sso7d	Sulfolobus solfataricus	[11]	[7.2]	DSC
118	1c9o	A	2	GLN	LEU	4.0	76.9	0.7	-59.7	-	-	-0.55	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
119	1c9o	A	3	ARG	ALA	-12.0	76.9	7.2	-59.7	-	-	1.89	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
120	1c9o	A	3	ARG	GLU	-17.8	76.9	12.9	-59.7	-	-	2.75	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
121	1c9o	A	3	ARG	LYS	-0.8	76.9	5.0	-59.7	-	-	0.19	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
122	1c9o	A	3	ARG	LEU	-6.0	76.9	2.9	-59.7	-	-	0.93	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
123	1c9o	A	11	ASN	SER	2.3	76.9	-0.2	-59.7	-	-	-0.33	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
124	1c9o	A	12	GLU	LYS	-2.5	76.9	7.6	-59.7	-	-	0.43	75	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[20]	[7.0]	CD
125	1c9o	A	15	TYR	PHE	-0.2	76.9	1.9	-59.7	-	-	0.05	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
126	1c9o	A	21	GLU	ALA	-1.9	76.9	0.7	-59.7	-	-	0.29	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
127	1c9o	A	21	GLU	LYS	-1.5	76.9	11.0	-59.7	-	-	0.26	75	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[20]	[7.0]	CD
128	1c9o	A	23	GLY	GLN	-2.2	76.9	-1.0	-59.7	-	-	0.29	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
129	1c9o	A	24	SER	ASP	0.9	76.9	-3.1	-59.7	-	-	-0.22	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
130	1c9o	A	29	HIS	GLU	-3.4	76.9	-45.9	-59.7	-	-	0.76	75	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[20]	[7.0]	CD
131	1c9o	A	31	THR	SER	0.9	76.9	-1.2	-59.7	-	-	-0.17	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
132	1c9o	A	36	GLU	LYS	-0.9	76.9	14.3	-59.7	-	-	0.19	75	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[20]	[7.0]	CD
133	1c9o	A	46	GLU	ALA	-1.5	76.9	1.0	-59.7	-	-	0.22	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
134	1c9o	A	46	GLU	LYS	-2.9	76.9	-54.0	-59.7	-	-	0.64	75	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[20]	[7.0]	CD
135	1c9o	A	50	GLU	LYS	-3.4	76.9	16.7	-59.7	-	-	0.50	75	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[20]	[7.0]	CD
136	1c9o	A	53	GLN	GLU	-0.8	76.9	-0.2	-59.7	-	-	0.10	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
137	1c9o	A	55	ASN	LYS	0.8	76.9	4.8	-59.7	-	-	-0.10	75	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[20]	[7.0]	CD
138	1c9o	A	56	ARG	GLU	3.1	76.9	-1.0	-59.7	-	-	-0.76	75	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[20]	[7.0]	CD
139	1c9o	A	64	VAL	THR	-1.8	76.9	0.2	-59.7	-	-	0.26	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
140	1c9o	A	66	LEU	GLU	-8.0	76.9	8.4	-59.7	-	-	1.24	70	66	1.17	Cold Shock Protein	Bacillus caldoliticus	[19]	[7.0]	CD
141	1chk	A	28	TRP	PHE	-7.0	43.2	-25.9	-160.6	-	-	4.43	43	238	2.40	Chitosanase	Streptomyces N174	[235]	[7.0]	Fluorescence
142	1chk	A	101	TRP	PHE	-6.6	43.2	-39.8	-160.6	-	-	4.27	43	238	2.40	Chitosanase	Streptomyces N174	[235]	[7.0]	Fluorescence
143	1chk	A	104	ALA	LEU	-5.3	43.2	-	-160.6	-	-	-	-	238	2.40	Chitosanase	Streptomyces N174	[234]	[4.5]	Fluorescence
144	1chk	A	164	LYS	ARG	-1.0	43.2	-	-160.6	-	-	-	-	238	2.40	Chitosanase	Streptomyces N174	[234]	[4.5]	Fluorescence
145	1chk	A	227	TRP	PHE	-5.9	43.2	28.7	-160.6	-	-	2.51	43	238	2.40	Chitosanase	Streptomyces N174	[235]	[7.0]	Fluorescence
146	1csp	A	1	MET	ARG	10.4	55.3	-7.9	-46.1	-	-	-1.74	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
147	1csp	A	2	LEU	ARG	-3.1	55.3	5.5	-46.1	-	-	0.36	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
148	1csp	A	3	GLU	LYS	16.6	55.3	-2.4	-46.1	-	-	-2.75	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
149	1csp	A	3	GLU	LEU	9.3	55.3	-3.6	-46.1	-	-	-1.62	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
150	1csp	A	3	GLU	GLN	10.3	55.3	-7.4	-46.1	-	-	-1.31	55	67	2.45	Cold Shock Protein	Bacillus subtilis	[22]	[7.5]	CD
151	1csp	A	3	GLU	ARG	15.8	55.3	-6.2	-46.1	-	-	-2.65	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
152	1csp	A	3	GLU	VAL	10.2	55.3	-2.9	-46.1	-	-	-1.77	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
153	1csp	A	10	ASN	ASP	5.4	55.3	-4.1	-46.1	-	-	-0.67	55	67	2.45	Cold Shock Protein	Bacillus subtilis	[22]	[7.5]	CD
154	1csp	A	15	PHE	ALA	-15.8	55.3	-	-46.1	-	-	2.27	25	67	2.45	Cold Shock Protein	Bacillus subtilis	[23]	[7.0]	CD
155	1csp	A	17	PHE	ALA	-11.3	55.3	-	-46.1	-	-	1.53	25	67	2.45	Cold Shock Protein	Bacillus subtilis	[23]	[7.0]	CD
156	1csp	A	25	ASP	GLN	-8.1	55.3	10.0	-46.1	-	-	0.81	55	67	2.45	Cold Shock Protein	Bacillus subtilis	[22]	[7.5]	CD
157	1csp	A	27	PHE	ALA	-6.0	55.3	-	-46.1	-	-	0.84	25	67	2.45	Cold Shock Protein	Bacillus subtilis	[23]	[7.0]	CD
158	1csp	A	38	PHE	ALA	2.2	55.3	-	-46.1	-	-	-0.14	25	67	2.45	Cold Shock Protein	Bacillus subtilis	[23]	[7.0]	CD
159	1csp	A	43	GLU	SER	0.9	55.3	1.7	-46.1	-	-	-0.29	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
160	1csp	A	46	ALA	GLU	-5.2	55.3	6.5	-46.1	-	-	0.60	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
161	1csp	A	46	ALA	LYS	8.4	55.3	-5.5	-46.1	-	-	-1.41	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
162	1csp	A	46	ALA	LEU	4.1	55.3	0.7	-46.1	-	-	-0.81	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
163	1csp	A	48	SER	GLU	0.7	55.3	1.2	-46.1	-	-	-0.10	55	67	2.45	Cold Shock Protein	Bacillus subtilis	[22]	[7.5]	CD
164	1csp	A	48	SER	LYS	7.7	55.3	-0.5	-46.1	-	-	-1.41	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
165	1csp	A	48	SER	ARG	8.9	55.3	-2.2	-46.1	-	-	-1.58	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
166	1csp	A	50	GLU	GLN	-9.7	55.3	5.0	-46.1	-	-	1.22	55	67	2.45	Cold Shock Protein	Bacillus subtilis	[22]	[7.5]	CD
167	1csp	A	56	ARG	GLN	3.0	55.3	-3.3	-46.1	-	-	-0.38	55	67	2.45	Cold Shock Protein	Bacillus subtilis	[22]	[7.5]	CD
168	1csp	A	64	THR	ARG	6.1	55.3	-1.0	-46.1	-	-	-1.07	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
169	1csp	A	65	LYS	ILE	8.6	55.3	-1.9	-46.1	-	-	-1.53	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
170	1csp	A	66	GLU	LYS	12.9	55.3	-7.9	-46.1	-	-	-2.17	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
171	1csp	A	66	GLU	LEU	12.6	55.3	-7.4	-46.1	-	-	-2.10	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
172	1csp	A	66	GLU	VAL	10.6	55.3	-6.7	-46.1	-	-	-1.72	70	67	2.45	Cold Shock Protein	Bacillus subtilis	[21]	[7.0]	CD
173	1cyo	A	35	PHE	HIS	-12.5	70.8	-29.3	-86.6	-	-	3.41	71	93	1.50	Cytochrome b5	Bos Taurus	[24]	[7.0]	Abs
174	1cyo	A	35	PHE	LEU	-7.5	70.8	-20.8	-86.6	-	-	1.92	71	93	1.50	Cytochrome b5	Bos Taurus	[24]	[7.0]	Abs
175	1cyo	A	35	PHE	TYR	0.6	70.8	-9.1	-86.6	-	-	-0.12	71	93	1.50	Cytochrome b5	Bos Taurus	[24]	[7.0]	Abs
176	1cyo	A	45	VAL	GLU	-9.3	70.8	2.7	-86.6	-	-	2.37	71	93	1.50	Cytochrome b5	Bos Taurus	[25]	[7.0]	Abs
177	1cyo	A	45	VAL	HIS	-5.3	70.8	-3.1	-86.6	-	-	1.36	71	93	1.50	Cytochrome b5	Bos			

205	1ey0	A	21	ASP	LYS	7.9	53.1	-	-80.6	-	-2.18	-1.00	20	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[34]	[7.0]	Fluorescence
206	1ey0	A	21	ASP	ASN	7.2	53.1	-	-80.6	-	-2.18	-1.40	20	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[34]	[7.0]	Fluorescence
207	1ey0	A	22	THR	CYS	-2.8	53.1	9.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
208	1ey0	A	22	THR	ILE	-3.3	53.1	9.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
209	1ey0	A	22	THR	SER	-2.2	53.1	9.3	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
210	1ey0	A	22	THR	VAL	-2.7	53.1	9.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
211	1ey0	A	23	VAL	ALA	-12.5	53.1	3.3	-80.6	-	-2.18	1.72	20	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[31]	[7.0]	DSC
212	1ey0	A	23	VAL	PHE	-6.3	53.1	-	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[31]	[7.0]	DSC
213	1ey0	A	23	VAL	THR	-14.4	53.1	18.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
214	1ey0	A	24	LYS	GLY	-6.2	53.1	0.7	-80.6	-	-2.18	0.41	20	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[31]	[7.0]	DSC
215	1ey0	A	25	LEU	ALA	-11.5	53.1	17.6	-80.6	-0.30	-2.18	1.78	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[35]	[7.0]	DSC
216	1ey0	A	27	TYR	PHE	-3.0	53.1	3.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
217	1ey0	A	28	LYS	PHE	-4.2	53.1	-0.3	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
218	1ey0	A	29	GLY	CYS	-4.6	53.1	5.0	-80.6	-	-2.18	1.10	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[36]	[7.0]	Fluorescence
219	1ey0	A	29	GLY	PHE	-5.9	53.1	1.2	-80.6	-	-2.18	1.10	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32,36]	[7.0]	Fluorescence-CD
220	1ey0	A	32	MET	ILE	-2.3	53.1	1.7	-80.6	-	-2.18	0.60	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[37]	[7.0]	Fluorescence
221	1ey0	A	32	MET	LEU	-3.2	53.1	-0.3	-80.6	-	-2.18	0.80	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[37]	[7.0]	Fluorescence
222	1ey0	A	33	THR	CYS	-3.0	53.1	9.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
223	1ey0	A	33	THR	ILE	1.7	53.1	-6.3	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
224	1ey0	A	33	THR	SER	-4.8	53.1	3.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
225	1ey0	A	33	THR	VAL	1.8	53.1	-4.3	-80.6	-	-2.18	-0.40	20	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32,34]	[7.0]	Fluorescence-CD
226	1ey0	A	39	VAL	SER	-10.8	53.1	18.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
227	1ey0	A	39	VAL	THR	-6.8	53.1	11.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
228	1ey0	A	41	THR	CYS	2.1	53.1	-6.8	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
229	1ey0	A	41	THR	ILE	4.0	53.1	-14.3	-80.6	-	-2.18	-0.70	20	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32,34]	[7.0]	Fluorescence-CD
230	1ey0	A	41	THR	SER	-2.8	53.1	10.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
231	1ey0	A	41	THR	VAL	3.5	53.1	-8.3	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
232	1ey0	A	44	THR	CYS	0.1	53.1	6.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
233	1ey0	A	44	THR	ILE	-3.8	53.1	5.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
234	1ey0	A	44	THR	SER	-0.1	53.1	-2.8	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
235	1ey0	A	44	THR	VAL	0.2	53.1	-2.8	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
236	1ey0	A	46	HIS	TYR	-0.6	53.1	-7.2	-80.6	-	-2.18	0.00	40	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[33]	[5.4]	NMR
237	1ey0	A	47	PRO	PHE	-0.6	53.1	1.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
238	1ey0	A	48	LYS	PHE	0.0	53.1	-0.3	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
239	1ey0	A	49	LYS	PHE	-1.0	53.1	-2.3	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
240	1ey0	A	50	GLY	CYS	-2.6	53.1	9.0	-80.6	-	-2.18	0.80	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[36]	[7.0]	Fluorescence
241	1ey0	A	50	GLY	PHE	-2.5	53.1	14.0	-80.6	-	-2.18	0.40	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[36]	[7.0]	Fluorescence
242	1ey0	A	51	VAL	SER	0.0	53.1	-1.8	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
243	1ey0	A	51	VAL	THR	-0.3	53.1	-5.8	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
244	1ey0	A	52	GLU	PHE	-0.3	53.1	3.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
245	1ey0	A	54	TYR	PHE	-1.0	53.1	4.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
246	1ey0	A	54	TYR	LEU	-12.2	53.1	31.4	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
247	1ey0	A	57	GLU	CYS	-0.9	53.1	9.0	-80.6	-	-2.18	0.70	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[36]	[7.0]	Fluorescence
248	1ey0	A	57	GLU	GLY	-1.7	53.1	4.8	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[39]	[7.0]	Fluorescence-DSC
249	1ey0	A	57	GLU	PHE	-0.9	53.1	3.2	-80.6	-	-2.18	0.90	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32,36]	[7.0]	Fluorescence-CD
250	1ey0	A	59	SER	ALA	2.9	53.1	12.2	-80.6	-	-2.18	-0.50	20	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[34]	[7.0]	Fluorescence
251	1ey0	A	60	ALA	CYS	-3.6	53.1	12.0	-80.6	-	-2.18	1.20	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[36]	[7.0]	Fluorescence
252	1ey0	A	62	THR	ALA	-7.6	53.1	32.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
253	1ey0	A	62	THR	CYS	-4.1	53.1	14.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
254	1ey0	A	62	THR	PHE	0.0	53.1	14.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
255	1ey0	A	62	THR	GLY	-15.9	53.1	29.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
256	1ey0	A	62	THR	HIS	-8.1	53.1	12.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
257	1ey0	A	62	THR	ILE	-2.7	53.1	25.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
258	1ey0	A	62	THR	LYS	-17.9	53.1	34.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
259	1ey0	A	62	THR	LEU	-4.9	53.1	24.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
260	1ey0	A	62	THR	MET	-1.8	53.1	22.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
261	1ey0	A	62	THR	ASN	-16.3	53.1	32.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
262	1ey0	A	62	THR	GLN	-12.9	53.1	25.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
263	1ey0	A	62	THR	SER	-8.7	53.1	16.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
264	1ey0	A	62	THR	VAL	1.6	53.1	21.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
265	1ey0	A	65	MET	PHE	-5.8	53.1	12.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
266	1ey0	A	66	VAL	ALA	-11.9	53.1	18.2	-80.6	0.19	-2.18	1.72	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[38]	[7.0]	CD
267	1ey0	A	66	VAL	LEU	3.9	53.1	0.1	-80.6	0.13	-2.18	0.11	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[35]	[7.0]	DSC
268	1ey0	A	66	VAL	SER	-13.4	53.1	13.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
269	1ey0	A	66	VAL	THR	-6.0	53.1	3.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
270	1ey0	A	66	VAL	TRP	-7.8	53.1	10.5	-80.6	-0.12	-2.18	1.22	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[38]	[7.0]	CD
271	1ey0	A	69	ALA	THR	-13.6	53.1	15.3	-80.6	-	-2.18	2.08	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[31]	[7.0]	DSC
272	1ey0	A	70	LYS	CYS	-2.8	53.1	11.0	-80.6	-	-2.18	0.50	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[36]	[7.0]	Fluorescence
273	1ey0	A	70	LYS	PHE	0.0	53.1	0.0	-80.6	-	-2.18	0.00	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[36]	[7.0]	Fluorescence
274	1ey0	A	73	GLU	PHE	-4.8	53.1	2.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
275	1ey0	A	73	GLU	GLY	-15.2	53.1	18.5	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[39]	[7.0]	DSC
276	1ey0	A	74	VAL	THR															

308	1ey0	A	113	TYR	LEU	-0.1	53.1	-2.3	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
309	1ey0	A	114	VAL	SER	0.0	53.1	-0.8	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
310	1ey0	A	114	VAL	THR	-0.4	53.1	1.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
311	1ey0	A	115	TYR	PHE	0.2	53.1	1.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
312	1ey0	A	115	TYR	LEU	-0.6	53.1	-2.3	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
313	1ey0	A	116	LYS	PHE	0.4	53.1	0.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
314	1ey0	A	116	LYS	GLY	3.8	53.1	-4.3	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[40]	[7.2]	Fluorescence
315	1ey0	A	117	PRO	GLY	5.0	53.1	-9.3	-80.6	-	-2.18	-1.00	20	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[34]	[7.0]	Fluorescence
316	1ey0	A	117	PRO	THR	0.6	53.1	10.9	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[40]	[7.2]	Fluorescence
317	1ey0	A	120	THR	CYS	-5.5	53.1	17.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
318	1ey0	A	120	THR	ILE	-4.8	53.1	21.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
319	1ey0	A	120	THR	SER	-2.0	53.1	6.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
320	1ey0	A	120	THR	VAL	-5.1	53.1	16.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
321	1ey0	A	122	GLU	PHE	-0.6	53.1	0.2	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
322	1ey0	A	123	GLN	PHE	-1.3	53.1	0.3	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
323	1ey0	A	124	HIS	LEU	5.3	53.1	-18.8	-80.6	0.21	-2.18	-1.57	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[33-35,40]	[7.0]	Fluorescence-DSC
324	1ey0	A	127	LYS	PHE	-0.9	53.1	1.3	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
325	1ey0	A	128	SER	ALA	4.0	53.1	-9.8	-80.6	-	-2.18	-0.70	20	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32,34]	[7.0]	Fluorescence-CD
326	1ey0	A	128	SER	PHE	-3.6	53.1	7.7	-80.6	-	-2.18	-	-	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[32]	[7.0]	Fluorescence-CD
327	1ey0	A	134	LYS	CYS	-2.9	53.1	9.0	-80.6	-	-2.18	0.70	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[36]	[7.0]	Fluorescence
328	1ey0	A	134	LYS	PHE	-1.7	53.1	9.0	-80.6	-	-2.18	0.30	25	149	1.60	Staphylococcal Nuclease	Staphylococcus aureus	[36]	[7.0]	Fluorescence
329	1ezm	A	179	ARG	ALA	-7.0	69.0	-	-	-	-	-	-	301	1.50	Elastase	Pseudomonas aeruginosa	[244]	[7.5]	CD
330	1ezm	A	189	ASP	ALA	-4.0	69.0	-	-	-	-	-	-	301	1.50	Elastase	Pseudomonas aeruginosa	[244]	[7.5]	CD
331	1ezm	A	201	ASP	ALA	1.0	69.0	-	-	-	-	-	-	301	1.50	Elastase	Pseudomonas aeruginosa	[244]	[7.5]	CD
332	1ezm	A	205	ARG	ALA	1.0	69.0	-	-	-	-	-	-	301	1.50	Elastase	Pseudomonas aeruginosa	[244]	[7.5]	CD
333	1fr	A	32	HIS	ALA	-11.6	56.2	14.1	-64.5	-	-1.36	2.12	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
334	1fr	A	32	HIS	TYR	0.3	56.2	-26.3	-64.5	-	-1.36	-0.07	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
335	1fr	A	42	VAL	ALA	-4.5	56.2	0.2	-64.5	-	-1.36	0.93	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
336	1fr	A	42	VAL	GLY	-5.2	56.2	-4.1	-64.5	-	-1.36	1.15	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
337	1fr	A	42	VAL	ASN	-1.1	56.2	-2.6	-64.5	-	-1.36	0.24	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
338	1fr	A	54	GLN	ALA	-1.9	56.2	-3.1	-64.5	-	-1.36	0.41	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
339	1fr	A	59	ILE	TRP	-4.5	56.2	-0.5	-64.5	-	-1.36	0.93	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
340	1fr	A	103	TYR	ALA	-10.7	56.2	0.2	-64.5	-	-1.36	2.56	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
341	1fr	A	103	TYR	PRO	-1.1	56.2	2.4	-64.5	-	-1.36	0.26	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
342	1fr	A	104	TRP	TYR	-12.5	56.2	10.8	-64.5	-	-1.36	2.44	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
343	1fr	A	106	ALA	SER	-6.1	56.2	12.9	-64.5	-	-1.36	1.05	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
344	1fr	A	107	HIS	ALA	-4.1	56.2	4.1	-64.5	-	-1.36	0.79	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
345	1fr	A	107	HIS	TRP	-8.7	56.2	6.7	-64.5	-	-1.36	1.72	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
346	1fr	A	107	HIS	TYR	-1.0	56.2	1.7	-64.5	-	-1.36	0.19	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
347	1fr	A	110	LEU	GLU	-1.1	56.2	6.0	-64.5	-	-1.36	0.19	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
348	1fr	A	110	LEU	HIS	6.3	56.2	-12.9	-64.5	-	-1.36	-1.39	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
349	1fr	A	110	LEU	ARG	1.9	56.2	-12.0	-64.5	-	-1.36	-0.43	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
350	1fr	A	114	LYS	GLU	-3.2	56.2	1.7	-64.5	-	-1.36	0.65	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
351	1fr	A	114	LYS	ASN	10.7	56.2	-26.8	-64.5	-	-1.36	2.65	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
352	1fr	A	114	LYS	GLN	-2.7	56.2	-5.0	-64.5	-	-1.36	0.60	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
353	1fr	A	117	GLN	ALA	-4.1	56.2	-8.8	-64.5	-	-1.36	0.96	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
354	1fr	A	118	TRP	HIS	-3.3	56.2	8.4	-64.5	-	-1.36	0.60	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
355	1fr	A	118	TRP	TYR	-5.4	56.2	-2.6	-64.5	-	-1.36	1.17	56	124	2.30	Alpha-Lactalbumin	Bos Taurus	[49]	[7.4]	CD
356	1hl	A	58	ASP	ASN	0.7	60.9	-	-	-	-	-	-	334	2.30	Beta-1,4-galactanase	Aspergillus aculeatus	[243]	[4.5]	DSC
357	1hl	A	182	ASP	ASN	0.5	60.9	-	-	-	-	-	-	334	2.30	Beta-1,4-galactanase	Aspergillus aculeatus	[243]	[4.5]	DSC
358	1hl	A	295	TYR	PHE	0.3	60.9	-	-	-	-	-	-	334	2.30	Beta-1,4-galactanase	Aspergillus aculeatus	[243]	[4.5]	DSC
359	1hl	A	306	GLY	ALA	1.1	60.9	-	-	-	-	-	-	334	2.30	Beta-1,4-galactanase	Aspergillus aculeatus	[243]	[4.5]	DSC
360	1fna	A	7	ASP	LYS	7.0	62.0	-	-	-	-	-	-	91	1.80	Fibronectin III-10 (FNIII10)	Homo sapiens	[42]	[7.0]	CD
361	1fna	A	7	ASP	ASN	8.0	62.0	-	-	-	-	-	-	91	1.80	Fibronectin III-10 (FNIII10)	Homo sapiens	[42]	[7.0]	CD
362	1fvk	A	151	PRO	ALA	-10.9	72.6	45.3	-159.9	-0.13	-2.08	6.82	-	189	1.70	Disulfide Bond Formation	Escherichia Coli	[43]	[7.0]	DSC
363	1g5a	A	144	ASP	ALA	0.2	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
364	1g5a	A	144	ASP	GLU	-1.4	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
365	1g5a	A	144	ASP	ILE	-1.6	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
366	1g5a	A	147	TYR	ALA	-1.0	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
367	1g5a	A	147	TYR	PHE	-0.2	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
368	1g5a	A	147	TYR	ASN	-1.0	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
369	1g5a	A	147	HIS	ALA	-1.6	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
370	1g5a	A	187	HIS	CYS	-0.2	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
371	1g5a	A	187	HIS	ASP	-3.4	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
372	1g5a	A	187	HIS	PHE	-3.6	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
373	1g5a	A	187	HIS	GLY	-2.8	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
374	1g5a	A	187	HIS	ILE	-6.6	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
375	1g5a	A	187	HIS	LYS	-0.4	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
376	1g5a	A	187	HIS	LEU	-6.4	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
377	1g5a	A	187	HIS	MET	-0.2	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
378	1g5a	A	187	HIS	ASN	-1.4	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
379	1g5a	A	187	HIS	GLN	-3.0	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
380	1g5a	A	187	HIS	ARG	-5.0	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
381	1g5a	A	187	HIS	SER	-0.8	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
382	1g5a	A	187	HIS	THR	-4.0	47.8	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysacchara	[252]	[7.0]	DSC
383	1g5a	A	187	HIS	VAL	-4.0														



411	1g5a	A	446	ARG	GLU	-2.2	47.8	-	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysaccharea	[252]	[7.0]	DSC
412	1g5a	A	446	ARG	PHE	0.2	47.8	-	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysaccharea	[252]	[7.0]	DSC
413	1g5a	A	507	ASP	ALA	0.8	47.8	-	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysaccharea	[252]	[7.0]	DSC
414	1g5a	A	507	ASP	ILE	0.6	47.8	-	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysaccharea	[252]	[7.0]	DSC
415	1g5a	A	509	ARG	ALA	0.0	47.8	-	-	-	-	-	-	-	628	1.40	Amylosucrase	Neisseria polysaccharea	[252]	[7.0]	DSC
416	1gv5	A	103	VAL	ILE	7.8	39.0	-3.0	-30.3	-	-0.32	-0.72	25	52	1.58	c-Myb R2	Mus Musculus	[44]	[7.0]	CD-DSC	
417	1h7m	A	2	ASP	ALA	-2.5	93.8	-	-109.7	-	-1.27	0.53	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
418	1h7m	A	6	GLU	ALA	-8.6	93.8	-8.1	-109.7	-0.41	-1.27	0.89	25	102	1.96	Ribosomal L30e	Thermococcus celer	[45,46]	[7.4]	CD	
419	1h7m	A	8	ARG	ALA	-7.0	93.8	-	-109.7	-	-1.27	0.76	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
420	1h7m	A	9	LYS	ALA	-8.4	93.8	-15.1	-109.7	-0.55	-1.27	0.62	25	102	1.96	Ribosomal L30e	Thermococcus celer	[45,46]	[7.4]	CD	
421	1h7m	A	9	LYS	MET	-7.1	93.8	-13.6	-109.7	-0.48	-1.27	0.49	25	102	1.96	Ribosomal L30e	Thermococcus celer	[45]	[7.4]	CD	
422	1h7m	A	12	ASP	ALA	0.4	93.8	-	-109.7	-	-1.27	-0.24	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
423	1h7m	A	15	LYS	ALA	-6.1	93.8	-	-109.7	-	-1.27	0.91	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
424	1h7m	A	21	ARG	ALA	-1.4	93.8	-	-109.7	-	-1.27	-0.07	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
425	1h7m	A	22	LYS	ALA	1.0	93.8	-	-109.7	-	-1.27	-0.43	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
426	1h7m	A	28	LYS	ALA	-4.4	93.8	-	-109.7	-	-1.27	1.20	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
427	1h7m	A	33	LYS	ALA	-6.4	93.8	-	-109.7	-	-1.27	-0.12	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
428	1h7m	A	39	ARG	ALA	-4.8	93.8	-	-109.7	-	-1.27	0.07	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
429	1h7m	A	42	ARG	ALA	0.2	93.8	-	-109.7	-	-1.27	-0.33	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
430	1h7m	A	44	ASP	ALA	0.1	93.8	-	-109.7	-	-1.27	-0.05	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
431	1h7m	A	46	LYS	ALA	-7.4	93.8	-	-109.7	-	-1.27	1.09	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
432	1h7m	A	47	GLU	ALA	2.0	93.8	-	-109.7	-	-1.27	0.05	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
433	1h7m	A	48	ASP	ALA	3.2	93.8	-	-109.7	-	-1.27	-0.36	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
434	1h7m	A	50	GLU	ALA	2.3	93.8	-	-109.7	-	-1.27	-0.57	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
435	1h7m	A	54	ARG	ALA	-5.4	93.8	-	-109.7	-	-1.27	0.26	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
436	1h7m	A	62	GLU	ALA	-5.5	93.8	-	-109.7	-	-1.27	1.29	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
437	1h7m	A	64	GLU	ALA	0.4	93.8	-	-109.7	-	-1.27	0.26	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
438	1h7m	A	69	GLU	ALA	-2.0	93.8	-	-109.7	-	-1.27	0.74	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
439	1h7m	A	76	ARG	ALA	-1.5	93.8	-	-109.7	-	-1.27	-0.19	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
440	1h7m	A	78	HIS	ALA	-2.2	93.8	-	-109.7	-	-1.27	0.50	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
441	1h7m	A	87	ASP	ALA	-9.2	93.8	-	-109.7	-	-1.27	1.36	25	102	1.96	Ribosomal L30e	Thermococcus celer	[46]	[7.4]	CD	
442	1h7m	A	90	GLU	ALA	-0.8	93.8	1.7	-109.7	-0.02	-1.27	1.20	25	102	1.96	Ribosomal L30e	Thermococcus celer	[45,46]	[7.4]	CD	
443	1h7m	A	92	ARG	ALA	-3.7	93.8	-10.3	-109.7	-0.41	-1.27	0.52	25	102	1.96	Ribosomal L30e	Thermococcus celer	[45,46]	[7.4]	CD	
444	1h7m	A	92	ARG	MET	-3.1	93.8	-10.0	-109.7	-0.41	-1.27	0.79	25	102	1.96	Ribosomal L30e	Thermococcus celer	[45]	[7.4]	CD	
445	1h8v	A	7	TRP	TYR	-1.0	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
446	1h8v	A	35	ALA	SER	-4.0	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
447	1h8v	A	35	ALA	VAL	7.7	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
448	1h8v	A	39	SER	ASN	0.5	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
449	1h8v	A	41	GLY	ALA	2.5	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
450	1h8v	A	63	SER	VAL	-0.8	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
451	1h8v	A	66	ALA	ASN	0.1	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
452	1h8v	A	77	SER	GLY	0.1	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
453	1h8v	A	91	ASN	ASP	0.5	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
454	1h8v	A	143	SER	THR	0.5	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
455	1h8v	A	163	THR	SER	0.3	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
456	1h8v	A	167	ASN	SER	0.2	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
457	1h8v	A	170	GLY	CYS	2.1	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[48]	[8.0]	CD
458	1h8v	A	188	ALA	GLY	0.5	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[47]	[8.0]	CD
459	1h8v	A	201	PRO	CYS	3.9	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[48]	[8.0]	CD
460	1h8v	A	210	VAL	CYS	0.1	54.4	-	-	-	-	-	-	-	218	1.90	Endoglucanase Cel12A	Thricoderma reesei	[48]	[8.0]	CD
461	1hfy	A	38	THR	ALA	-6.8	65.9	16.3	-85.1	-	-1.80	1.60	59	123	2.30	Alpha-Lactalbumin	Capra hircus	[51]	[7.0]	CD	
462	1hfy	A	60	TRP	PHE	-3.3	65.9	-	-	-	-	-	-	-	123	2.30	Alpha-Lactalbumin	Capra hircus	[50]	[7.5]	Fluorescence-DSC
463	1hfy	A	118	TRP	PHE	1.1	65.9	-	-	-	-	-	-	-	123	2.30	Alpha-Lactalbumin	Capra hircus	[50]	[7.5]	Fluorescence-DSC
464	1i4n	A	184	ASP	ALA	-0.6	90.3	-13.5	-120.7	-	-	-	-	-	251	2.50	IGPS	Thermotoga maritima	[52]	[7.5]	CD
465	1i4n	A	241	ARG	ALA	-4.8	90.3	5.0	-120.7	-	-	-	-	-	251	2.50	IGPS	Thermotoga maritima	[52]	[7.5]	CD
466	1ihb	A	5	TRP	ARG	-3.7	41.5	-	-	-	-	-	-	-	162	1.95	p1BNK4c	Homo sapiens	[53]	[7.5]	CD
467	1ihb	A	37	PHE	HIS	0.8	41.5	-	-	-	-	1.24	23	162	1.95	p1BNK4c	Homo sapiens	[53]	[7.5]	CD	
468	1ihb	A	55	ARG	VAL	0.6	41.5	-	-	-	-	0.32	23	162	1.95	p1BNK4c	Homo sapiens	[53]	[7.5]	CD	
469	1ihb	A	71	PHE	ASN	4.4	41.5	-	-	-	-	-0.71	23	162	1.95	p1BNK4c	Homo sapiens	[53]	[7.5]	CD	
470	1ihb	A	82	PHE	GLN	-3.8	41.5	-	-	-	-	0.46	23	162	1.95	p1BNK4c	Homo sapiens	[53]	[7.5]	CD	
471	1ihb	A	85	THR	PHE	-7.6	41.5	-	-	-	-	-	-	-	162	1.95	p1BNK4c	Homo sapiens	[53]	[7.5]	CD
472	1ihb	A	92	PHE	ASN	4.3	41.5	-	-	-	-	1.08	-	-	162	1.95	p1BNK4c	Homo sapiens	[53]	[7.5]	CD
473	1ihb	A	108	HIS	LEU	-17.0	41.5	-	-	-	-	-	-	-	162	1.95	p1BNK4c	Homo sapiens	[53]	[7.5]	CD
474	1i02	A	6	ILE	ALA	-5.2	84.8	-	-137.0	-	-	2.91	50	213	2.00	Ribonuclease hii	Thermococcus kodakarensis	[55]	[9.0]	CD	
475	1i02	A	7	ASP	ASN	3.1	84.8	0.0	-137.0	-	-	-1.67	50	213	2.00	Ribonuclease hii	Thermococcus kodakarensis	[54]	[9.0]	DSC	
476	1i02	A	8	GLU	ALA	8.0	84.8	-33.9	-137.0	-	-	-2.65	50	213	2.00	Ribonuclease hii	Thermococcus kodakarensis	[54]	[9.0]	DSC	
477	1i02	A	8	GLU	GLN	0.7	84.8	-21.0	-137.0	-	-	-0.60	50	213	2.00	Ribonuclease hii	Thermococcus kodakarensis	[54]	[9.0]	DSC	
478	1i02	A	15	ILE	ALA	-2.2	84.8	-	-137.0	-	-	2.12	50	213	2.00	Ribonuclease hii	Thermococcus kodakarensis	[55]	[9.0]	CD	
479	1i02	A	20	ILE	ALA	-8.4	84.8	-	-137.0	-	-	4.42	50	213	2.00	Ribonuclease hii	Thermococcus kodakarensis	[55]	[9.0]	CD	
480	1i02	A	33	LEU	ALA	-11.9	84.8	-	-137.0	-	-	4.54	50	213	2.00	Ribonuclease hii	Thermococcus kodakarensis	[55]	[9.0]	CD	
481	1i02	A	56	ILE	ALA	-8.7	84.8	-	-137.0	-	-	3.97	50	213	2.00	Ribonuclease hii	Thermococcus kodakarensis	[55]	[9.0]	CD	
482	1i02	A	92	LEU	ALA	-5.6	84.8	-	-137.0	-	-	2.87	50	213	2.00	Ribonuclease hii	Thermococcus kodakarensis	[55]	[9.0]	CD	
483	1i02	A	102	ILE	ALA	-10.7	84.8	-	-137.0	-	-	4.04	50	213	2.00	Ribonuclease hii	Thermococcus kodakarensis	[55]	[9.0]	CD	
484	1i02	A	105	ASP	ALA	4.2	84.8	-33.0	-137.0	-	-	-1.58	50	213	2.00	Ribonuclease hii	Thermococcus kodakarensis	[54]	[9.0]	DSC	
485	1i02	A	118	LEU	ALA	-13.7	84.8	-	-137.0	-	-	5.26</									

514	1k2	A	63	VAL	ALA	0.1	61.4	9.3	-112.0	-	-1.26	2.02	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
515	1k2	A	63	VAL	GLY	-11.9	61.4	19.4	-112.0	-	-1.26	3.50	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
516	1k2	A	64	ALA	GLY	-2.2	61.4	-0.7	-112.0	-	-1.26	0.43	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
517	1k2	A	73	TYR	TRP	-2.5	61.4	-	-112.0	-	-1.26	-	-	124	1.10	Ribonuclease	Bos Taurus	[127]	[5.0]	CD
518	1k2	A	76	TYR	TRP	-6.1	61.4	-	-112.0	-	-1.26	-	-	124	1.10	Ribonuclease	Bos Taurus	[127]	[5.0]	CD
519	1k2	A	81	ILE	ALA	-10.3	61.4	14.3	-112.0	-	-1.26	2.99	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
520	1k2	A	81	ILE	GLY	-17.0	61.4	23.9	-112.0	-	-1.26	4.80	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
521	1k2	A	81	ILE	VAL	-0.7	61.4	6.0	-112.0	-	-1.26	0.43	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
522	1k2	A	92	TYR	TRP	1.1	61.4	-	-112.0	-	-1.26	-	-	124	1.10	Ribonuclease	Bos Taurus	[127]	[5.0]	CD
523	1k2	A	93	PRO	ALA	-10.7	61.4	-	-112.0	-	-1.26	-	-	124	1.10	Ribonuclease	Bos Taurus	[131]	[5.0]	Abs
524	1k2	A	97	TYR	PHE	-10.1	61.4	20.2	-112.0	-	-1.26	3.54	64	124	1.10	Ribonuclease	Bos Taurus	[135]	[5.0]	Abs
525	1k2	A	104	LYS	TRP	-10.9	61.4	-	-112.0	-	-1.26	-	-	124	1.10	Ribonuclease	Bos Taurus	[127]	[5.0]	CD
526	1k2	A	106	ILE	ALA	-14.9	61.4	32.5	-112.0	-	-1.26	4.37	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
527	1k2	A	106	ILE	LEU	-6.3	61.4	6.4	-112.0	-	-1.26	1.79	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
528	1k2	A	106	ILE	VAL	-3.0	61.4	1.4	-112.0	-	-1.26	0.80	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
529	1k2	A	107	ILE	ALA	-10.3	61.4	7.6	-112.0	-	-1.26	2.84	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
530	1k2	A	107	ILE	LEU	-8.6	61.4	0.5	-112.0	-	-1.26	2.19	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
531	1k2	A	107	ILE	VAL	0.6	61.4	3.6	-112.0	-	-1.26	0.08	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
532	1k2	A	108	VAL	ALA	-14.7	61.4	20.8	-112.0	-	-1.26	4.20	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
533	1k2	A	108	VAL	ILE	0.1	61.4	9.08	-112.0	-	-1.26	0.43	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
534	1k2	A	108	VAL	LEU	-2.4	61.4	3.6	-112.0	-	-1.26	0.70	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
535	1k2	A	109	ALA	GLY	-2.6	61.4	-4.30	-112.0	-	-1.26	0.43	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
536	1k2	A	114	PRO	ALA	-10.6	61.4	-	-112.0	-	-1.26	-	-	124	1.10	Ribonuclease	Bos Taurus	[131]	[5.0]	Abs
537	1k2	A	115	TYR	TRP	-4.4	61.4	-	-112.0	-	-1.26	-	-	124	1.10	Ribonuclease	Bos Taurus	[127]	[5.0]	CD
538	1k2	A	116	VAL	ALA	-3.2	61.4	-2.4	-112.0	-	-1.26	0.66	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
539	1k2	A	116	VAL	GLY	-4.4	61.4	-7.4	-112.0	-	-1.26	1.18	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
540	1k2	A	117	PRO	ALA	-6.7	61.4	-	-112.0	-	-1.26	-	-	124	1.10	Ribonuclease	Bos Taurus	[131]	[5.0]	Abs
541	1k2	A	118	VAL	ALA	-5.5	61.4	-4.1	-112.0	-	-1.26	1.92	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
542	1k2	A	118	VAL	GLY	-10.1	61.4	-3.3	-112.0	-	-1.26	2.77	40	124	1.10	Ribonuclease	Bos Taurus	[132]	[5.0]	Abs
543	1k2	A	124	VAL	TRP	-4.5	61.4	-	-112.0	-	-1.26	-	-	124	1.10	Ribonuclease	Bos Taurus	[127]	[5.0]	CD
544	1k3	A	46	PHE	LEU	-11.1	61.4	13.6	-112.0	-	-1.26	3.20	25	124	1.05	Ribonuclease	Bos Taurus	[130]	[6.0]	CD
545	1k3	A	46	PHE	VAL	-12.3	61.4	27.0	-112.0	-	-1.26	4.54	25	124	1.05	Ribonuclease	Bos Taurus	[129,130]	[6.0]	DSC-CD
546	1k3	A	67	ASN	ASP	-0.2	61.4	1.2	-112.0	0.14	-1.26	-0.61	25	124	1.05	Ribonuclease	Bos Taurus	[133]	[6.0]	DSC
547	1k3	A	75	SER	ALA	-7.9	61.4	3.9	-112.0	-	-1.26	2.50	-	124	1.05	Ribonuclease	Bos Taurus	[134]	[6.0]	CD
548	1k3	A	75	SER	CYS	-17.9	61.4	-32.3	-112.0	-	-1.26	-	-	124	1.05	Ribonuclease	Bos Taurus	[134]	[6.0]	CD
549	1k3	A	75	SER	THR	-8.9	61.4	1.6	-112.0	-	-1.26	2.80	25	124	1.05	Ribonuclease	Bos Taurus	[134]	[6.0]	CD
550	1k3	A	88	GLY	ARG	0.8	61.4	-	-112.0	-	-1.26	-	-	124	1.05	Ribonuclease	Bos Taurus	[137]	[6.0]	DSC
551	1k3	A	93	PRO	GLY	-6.2	61.4	-	-112.0	-	-1.26	2.20	62	124	1.05	Ribonuclease	Bos Taurus	[138]	[6.0]	DSC
552	1k3	A	114	PRO	GLY	-9.5	61.4	-	-112.0	-	-1.26	3.30	62	124	1.05	Ribonuclease	Bos Taurus	[138]	[6.0]	DSC
553	1k5	A	4	ALA	SER	-1.5	61.4	-5.0	-112.0	-	-1.26	0.51	61	124	1.15	Ribonuclease	Bos Taurus	[128]	[7.0]	CD
554	1k5	A	5	ALA	SER	-1.1	61.4	3.0	-112.0	-	-1.26	0.37	61	124	1.15	Ribonuclease	Bos Taurus	[128]	[7.0]	CD
555	1k5	A	123	SER	ALA	1.4	61.4	-6.0	-112.0	-	-1.26	-0.46	61	124	1.15	Ribonuclease	Bos Taurus	[128]	[7.0]	CD
556	1kfw	A	92	GLY	PRO	1.2	50.5	-	-	-	-	-0.50	16	435	1.74	Chitinase B	Arthrobacter sp TAD20	[60]	[7.5]	Fluorescence
557	1kfw	A	197	ASN	LYS	0.6	50.5	-	-	-	-	-0.80	16	435	1.74	Chitinase B	Arthrobacter sp TAD20	[60]	[7.5]	Fluorescence
558	1kfw	A	405	GLY	GLN	-0.6	50.5	-	-	-	-	-0.62	16	435	1.74	Chitinase B	Arthrobacter sp TAD20	[60]	[7.5]	Fluorescence-CD
559	1i63	A	6	MET	ALA	-4.5	65.1	9.0	-131.0	-	-2.50	1.22	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
560	1i63	A	6	MET	LEU	-10.6	65.1	53.0	-131.0	-	-2.50	4.98	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[63]	[3.0]	CD
561	1i63	A	7	LEU	ALA	-6.3	65.1	18.0	-131.0	-	-2.50	2.26	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
562	1i63	A	11	GLU	HIS	0.1	65.1	6.0	-131.0	-	-2.50	0.71	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[71]	[5.4]	CD
563	1i63	A	11	GLU	ASN	-0.6	65.1	12.0	-131.0	-	-2.50	1.43	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[71]	[5.4]	CD
564	1i63	A	14	ARG	LYS	-0.5	65.1	-1.0	-131.0	-	-2.50	0.03	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[73]	[6.8]	CD
565	1i63	A	17	ILE	ALA	-6.4	65.1	37.0	-131.0	-	-2.50	4.21	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
566	1i63	A	17	ILE	MET	-5.9	65.1	28.0	-131.0	-	-2.50	3.28	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
567	1i63	A	20	ASP	ALA	-0.8	65.1	4.0	-131.0	-	-2.50	0.50	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[71]	[5.4]	CD
568	1i63	A	20	ASP	ASN	3.1	65.1	-8.0	-131.0	-	-2.50	-1.11	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[71]	[5.4]	CD
569	1i63	A	20	ASP	SER	1.6	65.1	2.0	-131.0	-	-2.50	0.18	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[71]	[5.4]	CD
570	1i63	A	20	ASP	THR	2.2	65.1	-2.0	-131.0	-	-2.50	-0.58	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[71]	[5.4]	CD
571	1i63	A	22	GLU	LYS	1.6	65.1	-7.0	-131.0	-	-2.50	-0.57	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[73]	[6.8]	CD
572	1i63	A	26	THR	SER	1.4	65.1	-9.0	-131.0	-	-2.50	-0.57	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[73]	[6.8]	CD
573	1i63	A	27	ILE	ALA	-10.1	65.1	37.0	-131.0	-	-2.50	3.10	44	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[62]	[3.0]	CD
574	1i63	A	27	ILE	MET	-10.1	65.1	68.0	-131.0	-	-2.50	7.09	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
575	1i63	A	28	GLY	ALA	-5.1	65.1	19.0	-131.0	-	-2.50	2.20	52	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[74]	[3.0]	CD
576	1i63	A	29	ILE	ALA	-8.2	65.1	28.0	-131.0	-	-2.50	2.60	44	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[62]	[3.0]	CD
577	1i63	A	31	HIS	ASN	-11.0	65.1	-	-131.0	-	-2.50	-	-	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[75]	[5.0]	CD
578	1i63	A	33	LEU	ALA	-8.8	65.1	47.0	-131.0	-	-2.50	5.17	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
579	1i63	A	33	LEU	MET	-5.3	65.1	22.0	-131.0	-	-2.50	2.64	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
580	1i63	A	38	SER	ASN	-0.1	65.1	-	-131.0	-	-2.50	0.00	62	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[76]	[6.7]	CD
581	1i63	A	39	LEU	ALA	-2.5	65.1	-	-131.0	-	-2.50	0.90	53	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[237]	[5.5]	CD
582	1i63	A	40	ASN	ALA	0.9	65.1	2.0	-131.0	-	-2.50	0.17	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[78]	[6.7]	CD
583	1i63	A	40	ASN	ASP	1.3	65.1	2.0	-131.0	-	-2.50	-0.44	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[73]	[6.8]	CD
584	1i63	A	41	ALA	ASP	1.1	65.1	-4.0	-131.0	-	-2.50	-0.29	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[73]	[6.8]	CD
585	1i63	A	41	ALA	SER	-1.8	65.1	7.0	-131.0	-	-2.50	0.76	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[70]	[3.0]	CD
586	1i63	A	42	ALA	PHE	-11.2	65.1	57.0	-131.0	-	-2.50	5.18	25	164	1.75	T4 Lysozyme (p				

617	1163	A	50	ILE	ALA	-4.2	65.1	14.0	-131.0	-	-2.50	1.75	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
618	1163	A	50	ILE	MET	-0.6	65.1	10.0	-131.0	-	-2.50	1.19	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	CD
619	1163	A	55	ASN	CYS	-3.6	65.1	-	-131.0	-	-2.50	-	-	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[79]	[2.4]	CD
620	1163	A	58	ILE	ALA	-10.4	65.1	33.0	-131.0	-	-2.50	3.20	44	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[62]	[3.0]	CD
621	1163	A	58	ILE	THR	-10.1	65.1	46.0	-131.0	-	-2.50	3.40	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
622	1163	A	59	THR	ALA	-4.0	65.1	-	-131.0	-	-2.50	1.50	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[77]	[6.5]	CD
623	1163	A	59	THR	ASP	-3.1	65.1	-	-131.0	-	-2.50	1.20	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[77]	[6.5]	CD
624	1163	A	59	THR	GLY	-4.1	65.1	-	-131.0	-	-2.50	1.60	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[77]	[6.5]	CD
625	1163	A	59	THR	ASN	-2.6	65.1	-	-131.0	-	-2.50	1.10	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[77]	[6.5]	CD
626	1163	A	59	THR	SER	-0.4	65.1	-	-131.0	-	-2.50	0.20	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[77]	[6.5]	CD
627	1163	A	59	THR	VAL	-4.0	65.1	-	-131.0	-	-2.50	1.50	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[77]	[6.5]	CD
628	1163	A	60	LYS	HIS	-0.4	65.1	16.0	-131.0	-	-2.50	0.10	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[190]	[6.5]	CD
629	1163	A	66	LEU	ALA	-10.1	65.1	46.0	-131.0	-	-2.50	5.08	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
630	1163	A	66	LEU	MET	-2.7	65.1	8.0	-131.0	-	-2.50	1.03	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
631	1163	A	67	PHE	ALA	-5.7	65.1	12.0	-131.0	-	-2.50	1.90	44	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[62]	[3.0]	CD
632	1163	A	69	GLN	PRO	-7.6	65.1	-	-131.0	-	-2.50	2.90	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[80]	[6.5]	CD
633	1163	A	70	ASP	ASN	-11.0	65.1	-	-131.0	-	-2.50	-	-	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[75]	[5.5]	CD
634	1163	A	71	VAL	ALA	-4.7	65.1	5.0	-131.0	-	-2.50	1.50	44	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[62]	[3.0]	CD
635	1163	A	72	ASP	PRO	-7.1	65.1	-	-131.0	-	-2.50	2.70	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[80]	[6.5]	CD
636	1163	A	73	ALA	SER	-1.3	65.1	2.0	-131.0	-	-2.50	0.31	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[70]	[3.0]	CD
637	1163	A	74	ALA	PRO	-12.1	65.1	-	-131.0	-	-2.50	4.60	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[80]	[6.5]	CD
638	1163	A	75	VAL	THR	-3.7	65.1	0.0	-131.0	-	-2.50	0.49	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[70]	[3.0]	CD
639	1163	A	78	ILE	ALA	-3.5	65.1	3.0	-131.0	-	-2.50	0.57	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
640	1163	A	78	ILE	MET	-3.7	65.1	13.0	-131.0	-	-2.50	1.62	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
641	1163	A	78	ILE	VAL	-2.1	65.1	5.0	-131.0	-	-2.50	0.68	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[69]	[5.4]	CD
642	1163	A	79	LEU	CYS	-5.1	65.1	-	-131.0	-	-2.50	-	-	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[79]	[2.4]	CD
643	1163	A	80	ARG	LYS	-0.3	65.1	-2.0	-131.0	-	-2.50	0.17	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[73]	[6.8]	CD
644	1163	A	82	ALA	SER	-1.0	65.1	1.0	-131.0	-	-2.50	0.20	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[70]	[3.0]	CD
645	1163	A	83	LYS	HIS	-1.0	65.1	9.0	-131.0	-	-2.50	0.40	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[190]	[6.5]	CD
646	1163	A	84	LEU	ALA	-10.5	65.1	29.0	-131.0	-	-2.50	3.53	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
647	1163	A	84	LEU	MET	-4.9	65.1	20.0	-131.0	-	-2.50	2.42	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
648	1163	A	87	VAL	ALA	-4.3	65.1	3.0	-131.0	-	-2.50	0.57	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
649	1163	A	87	VAL	ILE	-0.8	65.1	3.0	-131.0	-	-2.50	0.63	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[69]	[5.4]	CD
650	1163	A	87	VAL	MET	-6.3	65.1	17.0	-131.0	-	-2.50	2.16	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
651	1163	A	87	VAL	THR	-4.6	65.1	8.0	-131.0	-	-2.50	1.17	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[70]	[3.0]	CD
652	1163	A	90	SER	HIS	-2.9	65.1	14.0	-131.0	-	-2.50	1.10	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[190]	[6.5]	CD
653	1163	A	91	LEU	ALA	-7.4	65.1	17.0	-131.0	-	-2.50	2.22	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
654	1163	A	91	LEU	MET	-2.0	65.1	5.0	-131.0	-	-2.50	0.66	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
655	1163	A	92	ASP	ASN	-3.7	65.1	-	-131.0	-	-2.50	1.40	62	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[76]	[6.7]	CD
656	1163	A	93	ALA	SER	-0.5	65.1	1.0	-131.0	-	-2.50	0.14	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[70]	[3.0]	CD
657	1163	A	93	ALA	THR	0.2	65.1	-4.0	-131.0	-	-2.50	-0.06	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[73]	[6.8]	CD
658	1163	A	94	VAL	ALA	-5.0	65.1	19.0	-131.0	-	-2.50	1.80	44	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[62]	[3.0]	CD
659	1163	A	96	ARG	CYS	-8.7	65.1	-	-131.0	-	-2.50	-	-	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[79]	[2.4]	CD
660	1163	A	98	ALA	SER	-7.5	65.1	16.0	-131.0	-	-2.50	2.08	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[70]	[3.0]	CD
661	1163	A	98	ALA	CYS	-2.6	65.1	8.0	-131.0	-	-2.50	1.06	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[81]	[3.0]	CD
662	1163	A	98	ALA	MET	-9.3	65.1	38.0	-131.0	-	-2.50	4.00	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[81]	[3.0]	CD
663	1163	A	98	ALA	VAL	-9.2	65.1	46.0	-131.0	-	-2.50	4.43	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[81]	[3.0]	CD
664	1163	A	99	LEU	ALA	-11.4	65.1	24.5	-131.0	-	-2.50	3.34	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[64.65]	[5.7]	CD
665	1163	A	99	LEU	PHE	-0.7	65.1	7.0	-131.0	-	-2.50	0.30	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[64]	[5.7]	CD
666	1163	A	99	LEU	ILE	-3.7	65.1	6.0	-131.0	-	-2.50	1.50	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[64]	[5.7]	CD
667	1163	A	99	LEU	MET	-1.5	65.1	-4.0	-131.0	-	-2.50	-0.41	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61.64]	[5.7]	CD
668	1163	A	99	LEU	VAL	-5.2	65.1	12.0	-131.0	-	-2.50	2.00	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[64]	[5.7]	CD
669	1163	A	100	ILE	ALA	-7.1	65.1	12.0	-131.0	-	-2.50	1.70	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
670	1163	A	100	ILE	MET	-4.5	65.1	5.0	-131.0	-	-2.50	0.80	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
671	1163	A	100	ILE	VAL	-1.1	65.1	4.0	-131.0	-	-2.50	0.40	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[69]	[5.4]	CD
672	1163	A	101	ASN	ALA	-3.7	65.1	17.0	-131.0	-	-2.50	1.50	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
673	1163	A	102	MET	ALA	-8.2	65.1	22.0	-131.0	-	-2.50	2.76	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
674	1163	A	102	MET	LEU	-2.3	65.1	14.0	-131.0	-	-2.50	1.71	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[69]	[5.4]	CD
675	1163	A	103	VAL	ALA	-4.4	65.1	8.0	-131.0	-	-2.50	1.11	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
676	1163	A	103	VAL	ILE	-1.5	65.1	3.0	-131.0	-	-2.50	0.26	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[69]	[5.4]	CD
677	1163	A	103	VAL	MET	-3.1	65.1	13.0	-131.0	-	-2.50	1.60	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
678	1163	A	104	PHE	ALA	-7.5	65.1	21.0	-131.0	-	-2.50	2.62	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
679	1163	A	104	PHE	MET	-0.8	65.1	9.0	-131.0	-	-2.50	1.08	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
680	1163	A	105	GLN	MET	-2.7	65.1	20.0	-131.0	-	-2.50	1.20	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
681	1163	A	106	MET	ALA	-5.2	65.1	16.0	-131.0	-	-2.50	2.00	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
682	1163	A	106	MET	ILE	0.6	65.1	0.0	-131.0	-	-2.50	-0.02	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[69]	[5.4]	CD
683	1163	A	106	MET	LYS	-10.5	65.1	24.0	-131.0	-	-2.50	3.50	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[63]	[3.0]	CD
684	1163	A	106	MET	LEU	1.7	65.1	3.0	-131.0	-	-2.50	0.00	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[63]	[3.0]	CD
685	1163	A	108	GLU	VAL	2.4	65.1	0.0	-131.0	-	-2.50	-0.26	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[65]	[5.4]	CD
686	1163	A	109	THR	ASP	1.5	65.1	-	-131.0	-	-2.50	-0.60	62	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[76]		

720	1163	A	135	LYS	CYS	-2.6	65.1	-	-131.0	-	-2.50	-	-	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[79]	[2.4]	CD
721	1163	A	142	THR	CYS	-0.5	65.1	-	-131.0	-	-2.50	-	-	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[79]	[2.4]	CD
722	1163	A	144	ASN	HIS	0.7	65.1	-	-131.0	-	-2.50	-0.30	62	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[76]	[6.7]	CD
723	1163	A	144	ASN	GLU	1.5	65.1	-5.0	-131.0	-	-2.50	-0.50	63	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[190]	[6.5]	CD
724	1163	A	146	ALA	CYS	-4.1	65.1	-	-131.0	-	-2.50	-	-	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[79]	[2.4]	CD
725	1163	A	149	VAL	ALA	-9.0	65.1	24.0	-131.0	-	-2.50	0.71	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61.67]	[5.4]	Fluorescence-CD
726	1163	A	149	VAL	CYS	-5.5	65.1	17.0	-131.0	-	-2.50	2.00	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
727	1163	A	149	VAL	GLY	-15.3	65.1	45.0	-131.0	-	-2.50	4.90	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
728	1163	A	149	VAL	ILE	-0.2	65.1	6.0	-131.0	-	-2.50	0.48	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67.69]	[5.4]	CD
729	1163	A	149	VAL	MET	-7.8	65.1	19.0	-131.0	-	-2.50	2.44	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	Fluorescence-CD
730	1163	A	149	VAL	SER	-13.2	65.1	36.0	-131.0	-	-2.50	4.40	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
731	1163	A	149	VAL	THR	-8.3	65.1	20.0	-131.0	-	-2.50	3.00	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
732	1163	A	151	THR	SER	1.0	65.1	-7.0	-131.0	-	-2.50	-0.39	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[73]	[6.8]	CD
733	1163	A	152	THR	ALA	-4.0	65.1	15.0	-131.0	-	-2.50	1.50	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
734	1163	A	152	THR	CYS	-1.4	65.1	3.0	-131.0	-	-2.50	0.50	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
735	1163	A	152	THR	ILE	-1.0	65.1	5.0	-131.0	-	-2.50	0.40	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
736	1163	A	152	THR	SER	-5.5	65.1	13.0	-131.0	-	-2.50	2.00	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
737	1163	A	152	THR	VAL	0.8	65.1	3.0	-131.0	-	-2.50	-0.20	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[67]	[5.4]	CD
738	1163	A	153	PHE	ALA	-9.3	65.1	22.0	-131.0	-	-2.50	2.84	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	CD
739	1163	A	153	PHE	ILE	-0.5	65.1	5.0	-131.0	-	-2.50	0.20	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[64]	[5.7]	CD
740	1163	A	153	PHE	LEU	0.8	65.1	-2.0	-131.0	-	-2.50	-0.30	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[64]	[5.7]	CD
741	1163	A	153	PHE	MET	-1.6	65.1	2.0	-131.0	-	-2.50	0.30	25	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[61]	[5.4]	CD
742	1163	A	153	PHE	VAL	-4.5	65.1	10.0	-131.0	-	-2.50	1.80	65	164	1.75	T4 Lysozyme (pseudowT)	Enterobacteria phage T4	[64]	[5.7]	CD
743	11hm	A	2	VAL	ALA	-7.9	49.2	16.3	-81.7	0.24	-1.67	1.80	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
744	11hm	A	23	ILE	VAL	-1.6	49.2	0.96	-81.7	-0.14	-1.67	0.37	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
745	11hm	A	56	ILE	VAL	-6.3	49.2	10.0	-81.7	0.38	-1.67	1.18	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
746	11hm	A	59	ILE	ALA	-5.8	49.2	6.0	-81.7	0.05	-1.67	1.06	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[88]	[2.7]	DSC
747	11hm	A	59	ILE	VAL	-4.4	49.2	10.5	-81.7	0.00	-1.67	1.20	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
748	11hm	A	74	VAL	ALA	-1.9	49.2	8.1	-81.7	0.14	-1.67	0.67	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
749	11hm	A	89	ILE	VAL	-2.7	49.2	3.3	-81.7	-0.17	-1.67	0.67	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
750	11hm	A	93	VAL	ALA	-4.4	49.2	5.5	-81.7	0.14	-1.67	0.79	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
751	11hm	A	99	VAL	ALA	-4.4	49.2	14.8	-81.7	0.41	-1.67	1.21	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
752	11hm	A	100	VAL	ALA	-2.6	49.2	9.6	-81.7	-0.17	-1.67	1.08	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
753	11hm	A	106	ILE	VAL	-4.7	49.2	11.5	-81.7	-0.05	-1.67	1.31	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
754	11hm	A	110	VAL	ALA	0.3	49.2	1.0	-81.7	0.17	-1.67	-0.12	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
755	11hm	A	121	VAL	ALA	-9.3	49.2	16.5	-81.7	0.31	-1.67	1.96	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
756	11hm	A	125	VAL	ALA	-7.0	49.2	3.8	-81.7	0.12	-1.67	1.06	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
757	11hm	A	130	VAL	ALA	-4.8	49.2	3.6	-81.7	-0.19	-1.67	0.93	25	130	1.80	Lysozyme (mutant C77/95A)	Homo sapiens	[87]	[2.7]	DSC
758	11ni	A	2	VAL	THR	-3.2	48.3	9.0	-93.0	-	-	0.90	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
759	11ni	A	5	THR	VAL	0.0	48.3	3.0	-93.0	-	-	0.00	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
760	11ni	A	16	THR	VAL	1.0	48.3	7.0	-93.0	-	-	-0.30	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
761	11ni	A	18	THR	VAL	-4.7	48.3	15.0	-93.0	-	-	1.40	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
762	11ni	A	25	ASP	LYS	3.0	48.3	-2.0	-93.0	-	-	-0.90	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[90]	[7.0]	CD
763	11ni	A	33	ASP	ALA	-16.0	48.3	34.0	-93.0	-	-	4.05	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
764	11ni	A	36	VAL	THR	-4.6	48.3	7.0	-93.0	-	-	1.30	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
765	11ni	A	38	GLN	ALA	3.5	48.3	-17.0	-93.0	-	-	-1.00	49	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[92]	[7.0]	DSC
766	11ni	A	39	ASN	ALA	-7.6	48.3	22.0	-93.0	-	-	2.20	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[93]	[7.0]	CD
767	11ni	A	39	ASN	ASP	-5.2	48.3	8.9	-93.0	-	-	1.50	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[93]	[7.0]	CD
768	11ni	A	39	ASN	SER	-8.0	48.3	18.9	-93.0	-	-	2.30	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[93]	[7.0]	CD
769	11ni	A	41	GLU	LYS	-2.5	48.3	2.0	-93.0	-	-	0.70	49	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[92]	[7.0]	DSC
770	11ni	A	43	VAL	THR	-1.6	48.3	2.0	-93.0	-	-	0.50	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
771	11ni	A	54	GLU	GLN	-5.9	48.3	11.0	-93.0	-	-	1.70	49	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[92]	[7.0]	DSC
772	11ni	A	56	THR	VAL	-6.3	48.3	10.0	-93.0	-	-	1.90	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
773	11ni	A	57	VAL	THR	-15.0	48.3	21.0	-93.0	-	-	4.40	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
774	11ni	A	59	THR	VAL	-5.6	48.3	14.0	-93.0	-	-	1.70	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
775	11ni	A	65	ARG	ALA	-3.9	48.3	11.0	-93.0	-	-	1.00	49	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[92]	[7.0]	DSC
776	11ni	A	67	THR	VAL	-0.1	48.3	7.0	-93.0	-	-	0.00	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
777	11ni	A	72	THR	VAL	-0.8	48.3	4.0	-93.0	-	-	0.20	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
778	11ni	A	74	GLU	LYS	3.9	48.3	-3.0	-93.0	-	-	-1.10	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[90]	[7.0]	CD
779	11ni	A	79	ASP	ALA	9.2	48.3	-3.0	-93.0	-	-	-1.47	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
780	11ni	A	79	ASP	GLU	-0.8	48.3	1.0	-93.0	-	-	-1.26	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
781	11ni	A	79	ASP	PHE	9.9	48.3	2.0	-93.0	-	-	-1.06	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
782	11ni	A	79	ASP	HIS	5.6	48.3	-5.0	-93.0	-	-	-1.21	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
783	11ni	A	79	ASP	ILE	9.6	48.3	2.0	-93.0	-	-	-1.02	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
784	11ni	A	79	ASP	LYS	7.6	48.3	3.0	-93.0	-	-	-0.73	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
785	11ni	A	79	ASP	LEU	8.7	48.3	16.0	-93.0	-	-	0.39	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
786	11ni	A	79	ASP	ASN	5.5	48.3	-5.0	-93.0	-	-	-1.21	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
787	11ni	A	79	ASP	ARG	9.0	48.3	2.0	-93.0	-	-	0.19	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
788	11ni	A	79	ASP	TRP	7.6	48.3	3.0	-93.0	-	-	-0.73	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
789	11ni	A	79	ASP	TYR	9.6	48.3	7.0	-93.0	-	-	-0.53	25	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[91]	[7.0]	CD
790	11ni	A	82	THR	VAL	-5.7	48.3	14.0	-93.0	-	-	1.70	48	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[89]	[7.0]	CD
791	11ni	A	85	HIS	GLN	0.1	48.3	2.0	-93.0	-	-	0.00	49	96	1.00	Ribonuclease sa	Streptomyces aureofaciens	[92]	[7.0]	D



823	11z1	A	32	ALA	SER	-1.0	64.9	3.3	-114.0	-0.07	-1.55	0.67	25	130	1.50	Lysozyme	Homo sapiens	[99]	[2.7]	DSC
824	11z1	A	35	GLU	LEU	-1.8	64.9	15.1	-114.0	0.53	-1.55	0.74	25	130	1.50	Lysozyme	Homo sapiens	[107]	[2.7]	DSC
825	11z1	A	36	SER	ALA	-3.5	64.9	5.3	-114.0	-0.26	-1.55	0.46	25	130	1.50	Lysozyme	Homo sapiens	[103]	[2.7]	DSC
826	11z1	A	37	GLY	ALA	-0.9	64.9	13.4	-114.0	0.05	-1.55	0.74	25	130	1.50	Lysozyme	Homo sapiens	[100]	[2.7]	DSC
827	11z1	A	37	GLY	GLN	-0.8	64.9	6.5	-114.0	0.43	-1.55	-0.18	25	130	1.50	Lysozyme	Homo sapiens	[104]	[2.7]	DSC
828	11z1	A	38	TYR	ALA	-8.9	64.9	25.2	-114.0	0.60	-1.55	2.77	25	130	1.50	Lysozyme	Homo sapiens	[102]	[2.7]	DSC
829	11z1	A	38	TYR	PHE	-0.6	64.9	0.5	-114.0	0.29	-1.55	-0.56	25	130	1.50	Lysozyme	Homo sapiens	[101]	[2.7]	DSC
830	11z1	A	38	TYR	GLY	-8.2	64.9	25.0	-114.0	0.62	-1.55	2.54	25	130	1.50	Lysozyme	Homo sapiens	[102]	[2.7]	DSC
831	11z1	A	40	THR	ALA	-4.7	64.9	3.6	-114.0	-0.14	-1.55	1.24	25	130	1.50	Lysozyme	Homo sapiens	[105]	[2.7]	DSC
832	11z1	A	40	THR	VAL	-4.2	64.9	4.3	-114.0	-0.02	-1.55	1.02	25	130	1.50	Lysozyme	Homo sapiens	[105]	[2.7]	DSC
833	11z1	A	43	THR	ALA	-1.1	64.9	5.7	-114.0	0.41	-1.55	-0.16	25	130	1.50	Lysozyme	Homo sapiens	[105]	[2.7]	DSC
834	11z1	A	43	THR	VAL	3.2	64.9	13.9	-114.0	0.41	-1.55	0.27	25	130	1.50	Lysozyme	Homo sapiens	[105]	[2.7]	DSC
835	11z1	A	45	TYR	PHE	0.2	64.9	1.9	-114.0	0.48	-1.55	-0.98	25	130	1.50	Lysozyme	Homo sapiens	[101]	[2.7]	DSC
836	11z1	A	47	ALA	PRO	0.3	64.9	0.7	-114.0	0.01	-1.55	0.02	25	130	1.50	Lysozyme	Homo sapiens	[108]	[2.8]	DSC
837	11z1	A	48	GLY	ALA	1.5	64.9	13.4	-114.0	-0.02	-1.55	1.53	25	130	1.50	Lysozyme	Homo sapiens	[100]	[2.7]	DSC
838	11z1	A	49	ASP	ASN	-2.7	64.9	-	-114.0	-	-1.55	1.00	65	130	1.50	Lysozyme	Homo sapiens	[98]	[4.0]	DSC
839	11z1	A	50	ARG	ALA	1.4	64.9	7.9	-114.0	0.07	-1.55	0.63	25	130	1.50	Lysozyme	Homo sapiens	[102]	[2.7]	DSC
840	11z1	A	50	ARG	GLY	0.9	64.9	12.3	-114.0	0.12	-1.55	1.08	25	130	1.50	Lysozyme	Homo sapiens	[102]	[2.7]	DSC
841	11z1	A	51	SER	ALA	-0.7	64.9	2.2	-114.0	0.14	-1.55	-0.01	25	130	1.50	Lysozyme	Homo sapiens	[103]	[2.7]	DSC
842	11z1	A	52	THR	ALA	-2.9	64.9	7.6	-114.0	0.74	-1.55	-0.38	25	130	1.50	Lysozyme	Homo sapiens	[105]	[2.7]	DSC
843	11z1	A	52	THR	VAL	-2.8	64.9	8.36	-114.0	0.38	-1.55	0.44	25	130	1.50	Lysozyme	Homo sapiens	[105]	[2.7]	DSC
844	11z1	A	54	TYR	PHE	-3.0	64.9	3.8	-114.0	-0.10	-1.55	0.98	25	130	1.50	Lysozyme	Homo sapiens	[101]	[2.7]	DSC
845	11z1	A	56	ILE	ALA	-12.5	64.9	8.8	-114.0	0.24	-1.55	2.32	25	130	1.50	Lysozyme	Homo sapiens	[106]	[2.7]	DSC
846	11z1	A	56	ILE	PHE	-15.0	64.9	12.4	-114.0	-0.24	-1.55	3.54	25	130	1.50	Lysozyme	Homo sapiens	[109]	[2.7]	DSC
847	11z1	A	56	ILE	GLY	-2.7	64.9	-	-114.0	-	-1.55	-	-	130	1.50	Lysozyme	Homo sapiens	[109]	[2.7]	DSC
848	11z1	A	56	ILE	LEU	-0.3	64.9	6.7	-114.0	0.17	-1.55	0.41	25	130	1.50	Lysozyme	Homo sapiens	[109]	[2.7]	DSC
849	11z1	A	56	ILE	MET	-5.8	64.9	8.1	-114.0	0.05	-1.55	1.49	25	130	1.50	Lysozyme	Homo sapiens	[109]	[2.7]	DSC
850	11z1	A	56	ILE	THR	-12.5	64.9	12.4	-114.0	0.50	-1.55	2.31	25	130	1.50	Lysozyme	Homo sapiens	[99]	[2.7]	DSC
851	11z1	A	56	ILE	VAL	-3.6	64.9	0.5	-114.0	0.24	-1.55	0.00	25	130	1.50	Lysozyme	Homo sapiens	[109]	[2.7]	DSC
852	11z1	A	58	GLN	ALA	3.1	64.9	10.6	-114.0	-0.07	-1.55	1.23	25	130	1.50	Lysozyme	Homo sapiens	[102]	[2.7]	DSC
853	11z1	A	58	GLN	GLY	5.7	64.9	-2.4	-114.0	0.24	-1.55	-1.61	25	130	1.50	Lysozyme	Homo sapiens	[102]	[2.7]	DSC
854	11z1	A	59	ILE	ALA	-5.2	64.9	-0.7	-114.0	-0.12	-1.55	0.36	25	130	1.50	Lysozyme	Homo sapiens	[106]	[2.7]	DSC
855	11z1	A	59	ILE	PHE	-2.6	64.9	6.9	-114.0	0.19	-1.55	0.67	25	130	1.50	Lysozyme	Homo sapiens	[109]	[2.7]	DSC
856	11z1	A	59	ILE	GLY	-12.7	64.9	7.9	-114.0	0.33	-1.55	2.17	25	130	1.50	Lysozyme	Homo sapiens	[106]	[2.7]	DSC
857	11z1	A	59	ILE	LEU	0.0	64.9	0.5	-114.0	0.31	-1.55	-0.70	25	130	1.50	Lysozyme	Homo sapiens	[109]	[2.7]	DSC
858	11z1	A	59	ILE	MET	-4.2	64.9	8.4	-114.0	0.31	-1.55	0.80	25	130	1.50	Lysozyme	Homo sapiens	[109]	[2.7]	DSC
859	11z1	A	59	ILE	SER	-11.8	64.9	7.2	-114.0	0.24	-1.55	2.05	25	130	1.50	Lysozyme	Homo sapiens	[99]	[2.7]	DSC
860	11z1	A	59	ILE	THR	-6.9	64.9	1.7	-114.0	0.05	-1.55	1.00	25	130	1.50	Lysozyme	Homo sapiens	[99]	[2.7]	DSC
861	11z1	A	59	ILE	VAL	-4.4	64.9	10.5	-114.0	0.00	-1.55	1.19	25	130	1.50	Lysozyme	Homo sapiens	[87]	[2.7]	DSC
862	11z1	A	59	ILE	TYR	-13.8	64.9	16.3	-114.0	0.24	-1.55	3.16	25	130	1.50	Lysozyme	Homo sapiens	[109]	[2.7]	DSC
863	11z1	A	61	SER	ALA	-4.3	64.9	5.5	-114.0	0.31	-1.55	0.50	25	130	1.50	Lysozyme	Homo sapiens	[103]	[2.7]	DSC
864	11z1	A	63	TYR	PHE	-0.7	64.9	3.3	-114.0	0.05	-1.55	0.35	25	130	1.50	Lysozyme	Homo sapiens	[101]	[2.7]	DSC
865	11z1	A	67	ASP	ASN	-6.1	64.9	-	-114.0	-	-1.55	2.25	25	130	1.50	Lysozyme	Homo sapiens	[98]	[4.0]	DSC
866	11z1	A	68	GLY	ALA	-0.4	64.9	6.5	-114.0	-0.07	-1.55	0.97	25	130	1.50	Lysozyme	Homo sapiens	[100]	[2.7]	DSC
867	11z1	A	70	THR	ALA	-4.7	64.9	6.9	-114.0	0.38	-1.55	0.58	25	130	1.50	Lysozyme	Homo sapiens	[105]	[2.7]	DSC
868	11z1	A	70	THR	VAL	-2.1	64.9	3.3	-114.0	0.00	-1.55	0.62	25	130	1.50	Lysozyme	Homo sapiens	[105]	[2.7]	DSC
869	11z1	A	71	PRO	GLY	-4.7	64.9	-0.6	-114.0	-0.01	-1.55	0.51	25	130	1.50	Lysozyme	Homo sapiens	[108]	[2.8]	DSC
870	11z1	A	72	GLY	ALA	-1.1	64.9	4.5	-114.0	0.14	-1.55	0.31	25	130	1.50	Lysozyme	Homo sapiens	[100]	[2.7]	DSC
871	11z1	A	74	VAL	ALA	-1.1	64.9	0.2	-114.0	0.10	-1.55	-0.07	25	130	1.50	Lysozyme	Homo sapiens	[96]	[2.7]	DSC
872	11z1	A	74	VAL	ASP	-1.4	64.9	7.17	-114.0	0.00	-1.55	0.98	25	130	1.50	Lysozyme	Homo sapiens	[95]	[2.7]	DSC
873	11z1	A	74	VAL	PHE	-0.9	64.9	4.3	-114.0	0.24	-1.55	0.04	25	130	1.50	Lysozyme	Homo sapiens	[96]	[2.7]	DSC
874	11z1	A	74	VAL	GLY	-0.7	64.9	0.0	-114.0	-0.07	-1.55	0.25	25	130	1.50	Lysozyme	Homo sapiens	[96]	[2.7]	DSC
875	11z1	A	74	VAL	ILE	1.7	64.9	25.6	-114.0	0.38	-1.55	1.93	25	130	1.50	Lysozyme	Homo sapiens	[96]	[2.7]	DSC
876	11z1	A	74	VAL	LEU	0.6	64.9	10.5	-114.0	0.31	-1.55	0.40	25	130	1.50	Lysozyme	Homo sapiens	[96]	[2.7]	DSC
877	11z1	A	74	VAL	MET	2.0	64.9	4.5	-114.0	0.00	-1.55	0.35	25	130	1.50	Lysozyme	Homo sapiens	[96]	[2.7]	DSC
878	11z1	A	74	VAL	ASN	-1.0	64.9	-1.4	-114.0	0.48	-1.55	-1.16	25	130	1.50	Lysozyme	Homo sapiens	[95]	[2.7]	DSC
879	11z1	A	74	VAL	ARG	-0.3	64.9	10.0	-114.0	-0.10	-1.55	1.44	25	130	1.50	Lysozyme	Homo sapiens	[95]	[2.7]	DSC
880	11z1	A	74	VAL	SER	-1.2	64.9	6.0	-114.0	0.36	-1.55	0.00	25	130	1.50	Lysozyme	Homo sapiens	[95]	[2.7]	DSC
881	11z1	A	74	VAL	TYR	-0.9	64.9	7.4	-114.0	-0.07	-1.55	1.13	25	130	1.50	Lysozyme	Homo sapiens	[95]	[2.7]	DSC
882	11z1	A	78	HIS	ALA	-0.5	64.9	11.3	-114.0	0.07	-1.55	1.20	25	130	1.50	Lysozyme	Homo sapiens	[102]	[2.7]	DSC
883	11z1	A	78	HIS	GLY	-0.5	64.9	6.0	-114.0	0.00	-1.55	0.76	25	130	1.50	Lysozyme	Homo sapiens	[102]	[2.7]	DSC
884	11z1	A	80	SER	ALA	1.4	64.9	-2.4	-114.0	0.14	-1.55	-0.82	25	130	1.50	Lysozyme	Homo sapiens	[103]	[2.7]	DSC
885	11z1	A	82	SER	ALA	1.1	64.9	-0.5	-114.0	0.31	-1.55	-0.98	25	130	1.50	Lysozyme	Homo sapiens	[103]	[2.7]	DSC
886	11z1	A	89	ILE	ALA	-8.7	64.9	4.5	-114.0	-0.07	-1.55	1.73	25	130	1.50	Lysozyme	Homo sapiens	[106]	[2.7]	DSC
887	11z1	A	89	ILE	VAL	-1.4	64.9	3.3	-114.0	-0.16	-1.55	0.67	25	130	1.50	Lysozyme	Homo sapiens	[87]	[2.7]	DSC
888	11z1	A	91	ASP	PRO	-1.1	64.9	4.7	-114.0	0.00	-1.55	0.70	25	130	1.50	Lysozyme	Homo sapiens	[108]	[2.8]	DSC
889	11z1	A	92	ALA	SER	2.6	64.9	10.3	-114.0	-0.43	-1.55	2.20	25	130	1.50	Lysozyme	Homo sapiens	[99]	[2.7]	DSC
890	11z1	A	93	VAL	ALA	-2.3	64.9	2.6	-114.0	0.05	-1.55	0.46	25	130	1.50	Lysozyme	Homo sapiens	[97]	[2.7]	DSC
891	11z1	A	93	VAL	THR	-2.3	64.9	13.4	-114.0	0.45	-1.55	0.78	25	130	1.50	Lysozyme	Homo sapiens	[99]	[2.7]	DSC
892	11z1	A	96	ALA	MET	0.1	64.9	15.3	-114.0	0.26	-1.55	1.15	25	130	1.50	Lysozyme	Homo sapiens	[107]	[2.7]	DSC
893	11z1	A	96	ALA	SER	-3.3	64.9	10.8	-114.0	0.29	-1.55	0.98	25	130	1.50	Lysozyme	Homo sapiens	[99]	[2.7]	DSC
894	11z1	A	99	VAL	ALA	-3.0	64.9	3.3	-114.0	0.0	-1.55	0.72	25	130	1.50	Lysozyme	Homo sapiens	[97]	[2.7]	DSC
895	11z1	A	99	VAL	THR	-1.6	64.9	9.6	-114.0	0.17	-1.55	0.								



1029	1ofr	A	206	CYS	SER	-5.4	68.7	-	-	-	-	-	-	224	1.20	Endoglucanase Cel12A	Humicola grisea	[48]	[8.0]	CD
1030	1ofr	A	216	CYS	SER	-5.5	68.7	-	-	-	-	-	-	224	1.20	Endoglucanase Cel12A	Humicola grisea	[48]	[8.0]	CD
1031	1ofr	A	216	CYS	VAL	0.8	68.7	-	-	-	-	-	-	224	1.20	Endoglucanase Cel12A	Humicola grisea	[48]	[8.0]	CD
1032	1onc	A	23	MET	LEU	-5.8	87.8	12.0	-126.7	-0.02	-1.43	2.22	25	104	1.70	Onconase	Rana pipiens	[111]	[7.0]	DSC
1033	1onc	A	28	PHE	ALA	-10.4	87.8	-	-126.7	-	-1.43	5.04	20	104	1.70	Onconase	Rana pipiens	[112]	[5.5]	DSC
1034	1onc	A	28	PHE	THR	-11.1	87.8	-	-126.7	-	-1.43	4.92	20	104	1.70	Onconase	Rana pipiens	[112]	[5.5]	DSC
1035	1onc	A	36	PHE	TYR	-9.3	87.8	-	-126.7	-	-1.43	3.70	20	104	1.70	Onconase	Rana pipiens	[112]	[5.5]	DSC
1036	1pga	A	2	THR	PRO	-6.6	84.3	-	-54.5	-	-	2.70	25	56	2.07	Protein G	Streptococcus sp.GX7805	[113]	[5.5]	CD
1037	1pga	A	6	ILE	ASN	-13.2	84.3	5.2	-54.5	-	-	1.53	25	56	2.07	Protein G	Streptococcus sp.GX7805	[114]	[5.2]	DSC
1038	1pga	A	6	ILE	THR	-13.6	84.3	5.5	-54.5	-	-	1.60	25	56	2.07	Protein G	Streptococcus sp.GX7805	[114]	[5.2]	DSC
1039	1pga	A	9	GLY	PRO	-17.0	84.3	-	-54.5	-	-	2.40	25	56	2.07	Protein G	Streptococcus sp.GX7805	[113]	[5.5]	CD
1040	1pga	A	10	LYS	PRO	-8.4	84.3	-	-54.5	-	-	0.20	25	56	2.07	Protein G	Streptococcus sp.GX7805	[113]	[5.5]	CD
1041	1pga	A	21	VAL	PRO	6.2	84.3	-	-54.5	-	-	-0.50	25	56	2.07	Protein G	Streptococcus sp.GX7805	[113]	[5.5]	CD
1042	1pga	A	23	ALA	PRO	-1.4	84.3	-	-54.5	-	-	0.30	25	56	2.07	Protein G	Streptococcus sp.GX7805	[113]	[5.5]	CD
1043	1pga	A	24	ALA	PRO	-4.6	84.3	-	-54.5	-	-	0.50	25	56	2.07	Protein G	Streptococcus sp.GX7805	[113]	[5.5]	CD
1044	1pga	A	48	ALA	PRO	-6.8	84.3	-	-54.5	-	-	0.70	25	56	2.07	Protein G	Streptococcus sp.GX7805	[113]	[5.5]	CD
1045	1pga	A	53	THR	PHE	1.9	84.3	-2.7	-54.5	-	-	-1.01	25	56	2.07	Protein G	Streptococcus sp.GX7805	[114]	[5.2]	DSC
1046	1pga	A	53	THR	ILE	1.3	84.3	2.0	-54.5	-	-	0.30	25	56	2.07	Protein G	Streptococcus sp.GX7805	[114]	[5.2]	DSC
1047	1pga	A	53	THR	VAL	-1.6	84.3	4.5	-54.5	-	-	0.80	25	56	2.07	Protein G	Streptococcus sp.GX7805	[114]	[5.2]	DSC
1048	1pga	A	53	THR	TYR	3.4	84.3	-2.5	-54.5	-	-	-0.50	25	56	2.07	Protein G	Streptococcus sp.GX7805	[114]	[5.2]	DSC
1049	1poh	A	49	LYS	ALA	6.6	63.4	-4.2	-75.8	-	-	-1.60	25	85	2.00	HPr	Escherichia Coli	[115]	[7.0]	CD
1050	1poh	A	49	LYS	ASP	7.4	63.4	-4.2	-75.8	-	-	-1.80	25	85	2.00	HPr	Escherichia Coli	[115]	[7.0]	CD
1051	1poh	A	49	LYS	GLU	8.7	63.4	-8.7	-75.8	-	-	-2.10	25	85	2.00	HPr	Escherichia Coli	[115]	[7.0]	CD
1052	1poh	A	49	LYS	GLY	5.0	63.4	-3.1	-75.8	-	-	-1.20	25	85	2.00	HPr	Escherichia Coli	[115]	[7.0]	CD
1053	1poh	A	49	LYS	MET	4.3	63.4	-0.8	-75.8	-	-	-1.00	25	85	2.00	HPr	Escherichia Coli	[115]	[7.0]	CD
1054	1poh	A	49	LYS	ASN	1.7	63.4	-1.6	-75.8	-	-	-0.40	25	85	2.00	HPr	Escherichia Coli	[115]	[7.0]	CD
1055	1poh	A	49	LYS	GLN	6.4	63.4	-12.0	-75.8	-	-	-1.50	25	85	2.00	HPr	Escherichia Coli	[115]	[7.0]	CD
1056	1poh	A	49	LYS	ARG	-1.1	63.4	0.5	-75.8	-	-	0.20	25	85	2.00	HPr	Escherichia Coli	[115]	[7.0]	CD
1057	1poh	A	49	LYS	SER	5.0	63.4	-1.0	-75.8	-	-	-1.20	25	85	2.00	HPr	Escherichia Coli	[115]	[7.0]	CD
1058	1qlp	A	160	TYR	ALA	-5.0	58.9	-	-	-	-	-	-	394	2.00	Alpha-1 Antitrypsin	Homo sapiens	[116]	[7.8]	Fluorescence
1059	1qlp	A	160	TYR	TRP	6.0	58.9	-	-	-	-	-	-	394	2.00	Alpha-1 Antitrypsin	Homo sapiens	[116]	[7.8]	Fluorescence
1060	1qlp	A	194	TRP	PHE	-0.5	58.9	-	-	-	-	-	-	394	2.00	Alpha-1 Antitrypsin	Homo sapiens	[117]	[7.8]	CD
1061	1qlp	A	238	TRP	PHE	-1.7	58.9	-	-	-	-	-	-	394	2.00	Alpha-1 Antitrypsin	Homo sapiens	[117]	[7.8]	CD
1062	1qlp	A	330	SER	ARG	-6.0	58.9	-	-	-	-	-	-	394	2.00	Alpha-1 Antitrypsin	Homo sapiens	[118]	[7.8]	Fluorescence
1063	1qlp	A	331	LYS	PHE	6.0	58.9	-	-	-	-	-	-	394	2.00	Alpha-1 Antitrypsin	Homo sapiens	[118]	[7.8]	Fluorescence
1064	1qlp	A	331	LYS	ILE	3.0	58.9	-	-	-	-	-	-	394	2.00	Alpha-1 Antitrypsin	Homo sapiens	[118]	[7.8]	Fluorescence
1065	1qlp	A	331	LYS	THR	-1.0	58.9	-	-	-	-	-	-	394	2.00	Alpha-1 Antitrypsin	Homo sapiens	[118]	[7.8]	Fluorescence
1066	1qlp	A	331	LYS	VAL	4.0	58.9	-	-	-	-	-	-	394	2.00	Alpha-1 Antitrypsin	Homo sapiens	[118]	[7.8]	Fluorescence
1067	1rbp	A	24	TRP	PHE	-12.0	68.9	-	-	-	-	2.52	69	182	2.00	Retinol Binding Protein	Homo sapiens	[119]	[7.4]	CD
1068	1rbp	A	24	TRP	LEU	-12.3	68.9	-	-	-	-	2.60	69	182	2.00	Retinol Binding Protein	Homo sapiens	[119]	[7.4]	CD
1069	1rbp	A	24	TRP	TYR	-11.0	68.9	-	-	-	-	2.20	69	182	2.00	Retinol Binding Protein	Homo sapiens	[119]	[7.4]	CD
1070	1rbp	A	91	TRP	HIS	-0.5	68.9	-	-	-	-	0.10	69	182	2.00	Retinol Binding Protein	Homo sapiens	[119]	[7.4]	CD
1071	1rbp	A	105	TRP	PHE	-2.2	68.9	-	-	-	-	0.44	69	182	2.00	Retinol Binding Protein	Homo sapiens	[119]	[7.4]	CD
1072	1rbp	A	139	ARG	GLN	-12.4	68.9	-	-	-	-	2.60	69	182	2.00	Retinol Binding Protein	Homo sapiens	[119]	[7.4]	CD
1073	1m1	C	16	VAL	ALA	-7.6	50.1	-	-96.6	-	-1.28	2.34	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[120]	[7.0]	CD-DSC
1074	1m1	C	16	VAL	CYS	-9.3	50.1	-	-96.6	-	-1.28	4.99	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[120]	[7.0]	CD-DSC
1075	1m1	C	16	VAL	SER	-15.1	50.1	-	-96.6	-	-1.28	4.69	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[120]	[7.0]	CD-DSC
1076	1m1	C	16	VAL	THR	-10.4	50.1	-	-96.6	-	-1.28	3.65	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[120]	[7.0]	CD-DSC
1077	1m1	C	24	TYR	TRP	1.6	50.1	-9.6	-96.6	-	-1.28	-1.24	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[121]	[6.0]	DSC
1078	1m1	C	25	GLN	LYS	3.4	50.1	-11.0	-96.6	-	-1.28	-1.40	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[123]	[6.0]	Fluorescence
1079	1m1	C	40	HIS	THR	-0.5	50.1	-3.7	-96.6	-	-1.28	0.26	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[121]	[6.0]	DSC
1080	1m1	C	42	TYR	TRP	-0.6	50.1	0.4	-96.6	-	-1.28	0.14	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[121]	[6.0]	DSC
1081	1m1	C	44	ASN	ALA	-5.2	50.1	9.8	-96.6	-	-1.28	1.60	51	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[124]	[7.0]	CD
1082	1m1	C	44	ASN	ASP	-5.5	50.1	12.4	-96.6	-	-1.28	1.60	51	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[124]	[7.0]	CD
1083	1m1	C	44	ASN	SER	-5.0	50.1	7.0	-96.6	-	-1.28	1.50	51	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[124]	[7.0]	CD
1084	1m1	C	45	TYR	TRP	-1.3	50.1	-10.3	-96.6	-	-1.28	-0.74	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[121]	[6.0]	DSC
1085	1m1	C	49	ASP	ALA	1.7	50.1	-5.0	-96.6	-	-1.28	-0.50	52	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[125]	[7.0]	DSC
1086	1m1	C	49	ASP	PHE	0.4	50.1	-7.0	-96.6	-	-1.28	0.40	52	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[125]	[7.0]	DSC
1087	1m1	C	49	ASP	HIS	3.4	50.1	-1.0	-96.6	-	-1.28	-1.10	55	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[125]	[7.0]	DSC
1088	1m1	C	49	ASP	TYR	0.1	50.1	-4.0	-96.6	-	-1.28	0.50	52	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[125]	[7.0]	DSC
1089	1m1	C	49	ASP	TRP	-1.1	50.1	0.0	-96.6	-	-1.28	0.90	52	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[125]	[7.0]	DSC
1090	1m1	C	58	GLU	ALA	-2.3	50.1	10.0	-96.6	-	-1.28	1.00	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[123]	[7.0]	Fluorescence
1091	1m1	C	59	TRP	TYR	-2.9	50.1	4.8	-96.6	-	-1.28	0.93	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[121]	[6.0]	DSC
1092	1m1	C	76	ASP	ALA	-15.2	50.1	25.5	-96.6	-	-1.28	3.80	15	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[122]	[7.0]	DSC
1093	1m1	C	76	ASP	ASN	-13.8	50.1	20.6	-96.6	0.20	-1.28	3.10	15	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[122]	[7.0]	DSC
1094	1m1	C	76	ASP	SER	-13.6	50.1	19.0	-96.6	-	-1.28	3.10	15	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[122]	[7.0]	DSC
1095	1m1	C	78	VAL	ALA	-7.9	50.1	-	-96.6	-	-1.28	4.08	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[120]	[7.0]	CD-DSC
1096	1m1	C	78	VAL	SER	-16.6	50.1	-	-96.6	-	-1.28	4.87	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[120]	[7.0]	CD-DSC
1097	1m1	C	78	VAL	THR	-9.8	50.1	-	-96.6	-	-1.28	3.59	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[120]	[7.0]	CD-DSC
1098	1m1	C	89	VAL	CYS	-4.9	50.1	-	-96.6	-	-1.28	3.54	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[120]	[7.0]	CD-DSC
1099	1m1	C	89	VAL	THR	-13.2	50.1	-	-96.6	-	-1.28	3.07	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[120]	[7.0]	CD-DSC
1100	1m1	C	92	HIS	ALA	-1.3	50.1	9.6	-96.6	-	-1.28	1.53	25	104	1.84	Ribonuclease T1 (pseudoWT)	Aspergillus oryzae	[121]	[6.0]	DSC
1101	1rro	A	21	PRO	ALA	-3.2	53.6	4.0	-76.0	-	-	0.74	54	108	1.30	Oncomodulin (Parvalbumin beta)	Rattus Rattus	[126]	[7.4]	DSC
1102	1rro	A	26	PRO	ALA	-3.2	53.6	5.0	-76.0	-	-	0.74	54	108	1.30					

1132	1shf	A	120	TRP	PHE	-4.4	80.1	7.1	-51.4	-	-0.68	0.55	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1133	1shf	A	120	TRP	LEU	-3.2	80.1	4.0	-51.4	-	-0.68	0.40	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1134	1shf	A	120	TRP	VAL	-8.3	80.1	12.7	-51.4	-	-0.68	0.99	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1135	1shf	A	122	ALA	GLY	-12.0	80.1	23.0	-51.4	-	-0.68	1.35	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1136	1shf	A	122	ALA	VAL	-0.6	80.1	0.2	-51.4	-	-0.68	-0.18	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1137	1shf	A	124	SER	ALA	-6.2	80.1	9.3	-51.4	-	-0.68	0.71	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[140]	[8.0]	CD
1138	1shf	A	124	SER	PHE	-18.7	80.1	22.5	-51.4	-	-0.68	1.90	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[140]	[8.0]	CD
1139	1shf	A	124	SER	HIS	-5.3	80.1	7.8	-51.4	-	-0.68	1.25	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[140]	[8.0]	CD
1140	1shf	A	124	SER	ILE	-6.8	80.1	9.4	-51.4	-	-0.68	1.41	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[140]	[8.0]	CD
1141	1shf	A	124	SER	LYS	5.4	80.1	-1.9	-51.4	-	-0.68	-0.11	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[140]	[8.0]	CD
1142	1shf	A	124	SER	LEU	-4.5	80.1	6.6	-51.4	-	-0.68	0.37	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[140]	[8.0]	CD
1143	1shf	A	124	SER	ASN	-2.6	80.1	10.0	-51.4	-	-0.68	0.73	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[140]	[8.0]	CD
1144	1shf	A	124	SER	ARG	2.5	80.1	0.7	-51.4	-	-0.68	0.18	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[140]	[8.0]	CD
1145	1shf	A	124	SER	THR	-14.5	80.1	17.5	-51.4	-	-0.68	1.65	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[140]	[8.0]	CD
1146	1shf	A	124	SER	VAL	-9.8	80.1	12.4	-51.4	-	-0.68	1.10	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[140]	[8.0]	CD
1147	1shf	A	124	SER	TYR	-18.7	80.1	20.8	-51.4	-	-0.68	2.27	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[140]	[8.0]	CD
1148	1shf	A	133	ILE	LEU	-4.9	80.1	11.3	-51.4	-	-0.68	0.75	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1149	1shf	A	133	ILE	VAL	-2.2	80.1	7.4	-51.4	-	-0.68	0.04	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1150	1shf	A	138	VAL	ALA	-17.1	80.1	17.0	-51.4	-	-0.68	2.13	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1151	1shf	A	138	VAL	PHE	-7.1	80.1	5.0	-51.4	-	-0.68	0.73	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1152	1shf	A	138	VAL	ILE	-0.2	80.1	-2.6	-51.4	-	-0.68	-0.17	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1153	1shf	A	138	VAL	LEU	0.9	80.1	1.6	-51.4	-	-0.68	0.12	25	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1154	1shf	A	138	VAL	SER	1.5	80.1	8.0	-51.4	-	-0.68	-	-	59	1.90	Fyn Tyrosine Kinase SH3	Homo sapiens	[139]	[8.0]	CD
1155	1shg	A	47	ASN	ALA	-3.5	58.9	2.9	-44.2	-	-0.69	0.46	59	62	1.80	Alpha spectrin SH3	Gallus gallus	[142]	[3.5]	DSC
1156	1shg	A	48	ASP	GLY	7.9	58.9	-6.2	-44.2	0.10	-0.69	-1.05	25	62	1.80	Alpha spectrin SH3	Gallus gallus	[141]	[3.5]	DSC
1157	1shg	A	56	ALA	GLY	-4.6	58.9	4.1	-44.2	-	-0.69	0.55	54	62	1.80	Alpha spectrin SH3	Gallus gallus	[142]	[3.2]	DSC
1158	1shg	A	56	ALA	GLU	-3.8	58.9	4.5	-44.2	-	-0.69	0.46	54	62	1.80	Alpha spectrin SH3	Gallus gallus	[142]	[3.2]	DSC
1159	1shg	A	56	ALA	LYS	-0.6	53.9	1.2	-44.2	-	-0.69	0.07	54	62	1.80	Alpha spectrin SH3	Gallus gallus	[142]	[3.2]	DSC
1160	1sup	A	22	THR	CYS	-2.5	58.9	-	-	-	-	-	-	275	1.60	Subtilisin BPN	Bacillus amyloliquef	[143]	[8.0]	DSC
1161	1sup	A	50	MET	PHE	1.8	58.9	-	-	-	-	-	-	275	1.60	Subtilisin BPN	Bacillus amyloliquef	[144]	[8.0]	DSC
1162	1sup	A	76	ASN	ASP	1.7	58.9	-	-	-	-	-	-	275	1.60	Subtilisin BPN	Bacillus amyloliquef	[144]	[8.0]	DSC
1163	1sup	A	87	SER	CYS	-1.7	58.9	-	-	-	-	-	-	275	1.60	Subtilisin BPN	Bacillus amyloliquef	[143]	[8.0]	DSC
1164	1sup	A	169	GLY	ALA	1.1	58.9	-	-	-	-	-	-	275	1.60	Subtilisin BPN	Bacillus amyloliquef	[144]	[8.0]	DSC
1165	1sup	A	206	GLN	CYS	4.7	58.9	-	-	-	-	-	-	275	1.60	Subtilisin BPN	Bacillus amyloliquef	[144]	[8.0]	DSC
1166	1sup	A	217	TYR	LYS	2.7	58.9	-	-	-	-	-	-	275	1.60	Subtilisin BPN	Bacillus amyloliquef	[144]	[8.0]	DSC
1167	1sup	A	218	ASN	ALA	-3.3	58.9	-	-	-	-	-	-	275	1.60	Subtilisin BPN	Bacillus amyloliquef	[145]	[8.0]	DSC
1168	1sup	A	218	ASN	SER	3.2	58.9	-	-	-	-	-	-	275	1.60	Subtilisin BPN	Bacillus amyloliquef	[144,145]	[8.0]	DSC
1169	1t69	A	153	CYS	PHE	-1.9	50.1	-	-	-	-	-	-	377	1.90	HDAC8	Homo sapiens	[239]	[7.0]	Fluorescence
1170	1t69	A	188	ALA	THR	-3.6	50.1	-	-	-	-	-	-	377	1.90	HDAC8	Homo sapiens	[239]	[7.0]	Fluorescence
1171	1t69	A	243	ILE	ASN	-9.5	50.1	-	-	-	-	-	-	377	1.90	HDAC8	Homo sapiens	[239]	[7.0]	Fluorescence
1172	1t69	A	311	THR	MET	-7.8	50.1	-	-	-	-	-	-	377	1.90	HDAC8	Homo sapiens	[239]	[7.0]	Fluorescence
1173	1t69	A	334	HIS	ARG	-7.0	50.1	-	-	-	-	-	-	377	1.90	HDAC8	Homo sapiens	[239]	[7.0]	Fluorescence
1174	1tca	A	210	VAL	ILE	0.8	57.7	-	-	-	-	-	-	317	1.55	Lipase	Pseudozyma antarctica	[146]	[7.0]	CD
1175	1tca	A	221	VAL	ASP	-2.0	57.7	-	-	-	-	-	-	317	1.55	Lipase	Pseudozyma antarctica	[146]	[7.0]	CD
1176	1tca	A	281	ALA	GLU	-6.8	57.7	-	-	-	-	-	-	317	1.55	Lipase	Pseudozyma antarctica	[146]	[7.0]	CD
1177	1tpk	A	65	VAL	ALA	-8.8	64.3	8.5	-81.0	-	-1.20	2.00	64	88	2.40	Tissue Plasminogen Activator	Homo sapiens	[147]	[4.5]	DSC
1178	1tpk	A	65	VAL	ILE	0.5	64.3	13.5	-81.0	-	-1.20	-0.30	64	88	2.40	Tissue Plasminogen Activator	Homo sapiens	[147]	[4.5]	DSC
1179	1tpk	A	65	VAL	LEU	-8.5	64.3	10.9	-81.0	-	-1.20	1.90	64	88	2.40	Tissue Plasminogen Activator	Homo sapiens	[147]	[4.5]	DSC
1180	1tpk	A	65	VAL	MET	-9.9	64.3	13.2	-81.0	-	-1.20	2.20	64	88	2.40	Tissue Plasminogen Activator	Homo sapiens	[147]	[4.5]	DSC
1181	1tpk	A	65	VAL	SER	-11.4	64.3	17.6	-81.0	-	-1.20	2.40	64	88	2.40	Tissue Plasminogen Activator	Homo sapiens	[147]	[4.5]	DSC
1182	1tpk	A	65	VAL	THR	-4.3	64.3	5.9	-81.0	-	-1.20	1.00	64	88	2.40	Tissue Plasminogen Activator	Homo sapiens	[147]	[4.5]	DSC
1183	1tpk_r	A	62	TRP	PHE	-17.1	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[260]	[7.4]	DSC
1184	1tpk_r	A	62	TRP	HIS	-19.0	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[260]	[7.4]	DSC
1185	1tpk_r	A	62	TRP	SER	-19.0	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[260]	[7.4]	DSC
1186	1tpk_r	A	62	TRP	TYR	-12.3	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[260]	[7.4]	DSC
1187	1tpk_r	A	72	TRP	PHE	-3.5	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[261]	[8.0]	DSC
1188	1tpk_r	A	72	TRP	LEU	-3.7	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[261]	[8.0]	DSC
1189	1tpk_r	A	72	TRP	SER	-1.7	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[261]	[8.0]	DSC
1190	1tpk_r	A	72	TRP	TYR	-2.4	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[261]	[8.0]	DSC
1191	1tpk_r	A	74	TYR	ALA	-11.1	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[259]	[8.0]	DSC
1192	1tpk_r	A	74	TYR	GLU	-16.1	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[259]	[8.0]	DSC
1193	1tpk_r	A	74	TYR	PHE	-8.9	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[259]	[8.0]	DSC
1194	1tpk_r	A	74	TYR	LYS	-13.9	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[259]	[8.0]	DSC
1195	1tpk_r	A	74	TYR	LEU	-10.3	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[259]	[8.0]	DSC
1196	1tpk_r	A	74	TYR	GLN	-11.3	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[259]	[8.0]	DSC
1197	1tpk_r	A	74	TYR	TRP	-10.8	75.6	-	-	-	-	-	-	81	2.40	Tissue Plasminogen Activator (Rec)	Homo sapiens	[259]	[8.0]	DSC
1198	1ttq	A	81	CYS	SER	-5.0	46.0	-	-	-	-	-	-	268	2.00	Tryptophan Synthase Alpha SU	Salmonella Typhimurium	[148]	[7.8]	Enzyme Act
1199	1ttq	A	118	CYS	SER	-5.0	46.0	-	-	-	-	-	-	268	2.00	Tryptophan Synthase Alpha SU	Salmonella Typhimurium	[148]	[7.8]	Enzyme Act
1200	1urp_085c	A	9	SER	ALA	-1.5	57.5	-	-	-	-	1.30	27	271	2.30	Ribose binding protein	Escherichia Coli	[262]	[7.0]	CD
1201	1urp_085c	A	13	ASN	ALA	0.7	57.5	-	-	-	-	1.00	27	271	2.30	Ribose binding protein	Escherichia Coli	[262]	[7.0]	CD
1202	1urp_085c	A	15	PHE	ALA	-5.0	57.5	-	-	-	-	3.10	27	271	2.30	Ribose binding protein	Escherichia Coli	[262]	[7.0]	CD
1203	1urp_085c	A	16	PHE	ALA	1.4	57.5	-	-	-	-	-	-	271	2.30	Ribose binding protein	Escherichia Coli	[262]	[7.0]	CD
1204	1urp_085c	A	64	ASN	ALA	-4.6	57.5	-	-	-	-	3.20	27	271	2.30	Ribose binding protein	Escherichia Coli	[262]	[7.0]	CD
1205	1urp_085c	A	89	ASP	ALA	0.7	57.5	-	-	-	-	-	-	271	2.30	Ribose binding protein	Escherichia Coli	[262]	[7.0]	CD
1206	1urp_085c	A	103	SER	ALA	0.3	57.5	-	-	-	-	0.08	-	271	2.30	Ribose binding protein	Escherichia Coli	[262]	[7.0]	CD
1207	1urp_085c	A	132	ILE	ALA	-0.2	57.5	-	-	-	-	0.57	-	271	2.30	Ribose binding protein	Escherichia Coli	[262]	[7.0]	CD
1208	1urp_085c	A	164																	



1235	1wq5	A	114	PHE	LEU	-3.3	59.5	-	-94.2	-	-4.80	-	-	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[149]	[7.2]	DSC
1236	1wq5	A	115	TYR	CYS	-2.3	59.5	-	-94.2	-	-4.80	-	-	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[149]	[7.2]	DSC
1237	1wq5	A	118	CYS	ALA	-4.3	59.5	12.0	-94.2	1.51	-4.80	-1.07	25	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[150]	[9.0]	DSC
1238	1wq5	A	118	CYS	SER	-8.5	59.5	18.6	-94.2	2.51	-4.80	-1.24	25	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[150]	[9.0]	DSC
1239	1wq5	A	118	CYS	VAL	-4.2	59.5	21.3	-94.2	2.39	-4.80	-1.19	25	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[150]	[9.0]	DSC
1240	1wq5	A	132	PRO	ALA	-2.6	59.5	-0.8	-94.2	-0.20	-4.80	0.01	25	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[152]	[9.0]	DSC
1241	1wq5	A	132	PRO	GLY	-2.3	59.5	3.8	-94.2	-0.50	-4.80	0.75	25	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[152]	[9.0]	DSC
1242	1wq5	A	154	CYS	ALA	-2.9	59.5	21.3	-94.2	0.69	-4.80	0.54	25	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[150]	[9.0]	DSC
1243	1wq5	A	154	CYS	SER	-8.2	59.5	47.8	-94.2	1.30	-4.80	1.40	25	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[150]	[9.0]	DSC
1244	1wq5	A	154	CYS	VAL	-3.3	59.5	22.7	-94.2	2.20	-4.80	-0.91	25	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[150]	[9.0]	DSC
1245	1wq5	A	207	PRO	ALA	-6.7	59.5	25.4	-94.2	-0.30	-4.80	1.85	25	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[152]	[9.0]	DSC
1246	1wq5	A	211	GLY	GLU	1.8	59.5	-15.2	-94.2	-0.60	-4.80	-0.53	25	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[153]	[7.8]	DSC
1247	1wq5	A	211	GLY	ARG	0.2	59.5	-17.2	-94.2	-0.70	-4.80	-0.53	25	268	2.30	Tryptophan Synthase Alpha SU	Escherichia Coli	[153]	[7.8]	DSC
1248	1ycc	A	7	ALA	LEU	0.8	58.0	-3.8	-82.5	-0.05	-1.37	-0.35	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[154]	[2.1]	CD
1249	1ycc	A	7	ALA	TYR	1.8	58.0	1.3	-82.5	0.14	-1.37	-0.27	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[154]	[2.1]	CD
1250	1ycc	A	10	PHE	ILE	-4.3	58.0	2.6	-82.5	-0.20	-1.37	0.91	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[155]	[4.6]	CD
1251	1ycc	A	10	PHE	MET	-15.2	58.0	22.4	-82.5	-0.13	-1.37	3.32	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[155]	[4.6]	CD
1252	1ycc	A	10	PHE	TRP	-5.2	58.0	6.9	-82.5	-0.23	-1.37	1.34	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[155]	[4.6]	CD
1253	1ycc	A	10	PHE	TYR	-1.9	58.0	7.0	-82.5	0.11	-1.37	0.67	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[155]	[4.6]	CD
1254	1ycc	A	20	VAL	CYS	1.1	58.0	19.0	-82.5	0.45	-1.37	1.06	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[156]	[4.6]	DSC
1255	1ycc	A	69	THR	GLU	5.2	58.0	-17.0	-82.5	-	-1.37	-1.5	57	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[161]	[6.0]	DSC
1256	1ycc	A	73	LYS	ILE	-5.0	58.0	9.6	-82.5	-0.25	-1.37	0.40	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[158]	[5.0]	CD
1257	1ycc	A	73	LYS	VAL	-3.2	58.0	5.4	-82.5	-0.10	-1.37	-0.10	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[158]	[5.0]	CD
1258	1ycc	A	73	LYS	TRP	-5.1	58.0	-6.0	-82.5	0.25	-1.37	1.60	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[158]	[5.0]	CD
1259	1ycc	A	76	PRO	GLY	-5.0	58.0	-	-82.5	-	-1.37	0.78	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[159]	[4.6]	CD
1260	1ycc	A	76	PRO	LEU	-4.9	58.0	-	-82.5	-	-1.37	3.44	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[159]	[4.6]	CD
1261	1ycc	A	76	PRO	ARG	-4.9	58.0	-	-82.5	-	-1.37	0.97	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[159]	[4.6]	CD
1262	1ycc	A	76	PRO	SER	-5.7	58.0	-	-82.5	-	-1.37	1.89	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[159]	[4.6]	CD
1263	1ycc	A	76	PRO	VAL	-5.2	58.0	-	-82.5	-	-1.37	1.07	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[159]	[4.6]	CD
1264	1ycc	A	76	PRO	TRP	-6.5	58.0	-	-82.5	-	-1.37	2.38	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[159]	[4.6]	CD
1265	1ycc	A	76	PRO	TYR	-6.8	58.0	-	-82.5	-	-1.37	2.07	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[159]	[4.6]	CD
1266	1ycc	A	82	PHE	TYR	-4.2	58.0	5.0	-82.5	-	-1.37	0.70	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[160]	[6.0]	DSC
1267	1ycc	A	85	LEU	ALA	-13.7	58.0	24.0	-82.5	-	-1.37	2.80	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[160]	[6.0]	DSC
1268	1ycc	A	94	LEU	ALA	-16.2	58.0	29.9	-82.5	-0.57	-1.37	3.82	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[155]	[4.6]	CD
1269	1ycc	A	94	LEU	ILE	1.3	58.0	-4.7	-82.5	-0.44	-1.37	0.02	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[155]	[4.6]	CD
1270	1ycc	A	94	LEU	THR	-13.9	58.0	24.7	-82.5	-0.12	-1.37	3.27	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[155]	[4.6]	CD
1271	1ycc	A	94	LEU	VAL	-4.0	58.0	0.9	-82.5	-0.17	-1.37	0.72	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[155]	[4.6]	CD
1272	1ycc	A	96	THR	ALA	4.3	58.0	-10.0	-82.5	-	-1.37	-1.0	57	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[161]	[6.0]	DSC
1273	1ycc	A	97	THR	PHE	1.0	58.0	-2.0	-82.5	-0.16	-1.37	-0.08	25	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[155]	[4.6]	CD
1274	1ycc	A	102	CYS	ALA	7.6	58.0	-10.0	-82.5	-	-1.37	-2.90	47	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[157]	[6.0]	Abs
1275	1ycc	A	102	CYS	SER	11.3	58.0	-8.0	-82.5	-	-1.37	-2.80	47	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[157]	[6.0]	Abs
1276	1ycc	A	102	CYS	THR	5.6	58.0	-14.7	-82.5	-	-1.37	-0.8	57	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[156,161]	[6.0]	DSC
1277	1ycc_c52a	A	52	ASN	ALA	4.5	63.3	-5.2	-78.8	-	-	-0.63	27	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[162]	[4.6]	DSC
1278	1ycc_c52a	A	52	ASN	HIS	-1.7	63.3	14.7	-78.8	-	-	1.27	37	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[162]	[4.6]	DSC
1279	1ycc_c52a	A	52	ASN	ILE	0.9	63.3	-1.2	-78.8	-	-	-2.02	27	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[162]	[5.0]	DSC
1280	1ycc_c52a	A	52	ASN	LEU	12.9	63.3	-19.6	-78.8	-	-	-2.56	27	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[162]	[4.6]	DSC
1281	1ycc_c52a	A	52	ASN	MET	13.4	63.3	-17.2	-78.8	-	-	-2.25	27	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[162]	[4.6]	DSC
1282	1ycc_c52a	A	52	ASN	GLN	2.0	63.3	0.1	-78.8	-	-	0.08	27	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[162]	[4.6]	DSC
1283	1ycc_c52a	A	52	ASN	SER	-10.7	63.3	23.8	-78.8	-	-	1.29	27	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[162]	[5.0]	DSC
1284	1ycc_c52a	A	52	ASN	THR	-8.0	63.3	18.4	-78.8	-	-	0.53	27	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[162]	[5.0]	DSC
1285	1ycc_c52a	A	52	ASN	VAL	8.8	63.3	-13.6	-78.8	-	-	-1.67	27	108	1.23	Cytochrome c (Iso-1)	Saccharomyces cerevisiae	[162]	[4.6]	DSC
1286	1yea	A	52	ASN	ILE	7.9	65.9	-14.8	-93.7	-	-1.58	-2.4	25	112	1.90	Cytochrome c (Iso-2)	Saccharomyces cerevisiae	[163]	[6.0]	DSC
1287	1ynr	A	25	TYR	PHE	3.3	119.8	-	-	-	-	-	80	2.00	Cytochrome c-552	Hydrogenobacter thermophilus	[219]	[7.0]	CD	
1288	1yu5	X	41	HIS	TYR	10.6	76.0	-	-	-	-1.1	25	67	1.40	Headpiece Villin Domain	Gallus gallus	[164]	[7.0]	CD	
1289	1yu5_41	X	53	MET	LEU	-8.0	70.0	-	-	-	-	-	36	1.40	Headpiece Villin Domain HP36	Gallus gallus	[165]	[7.0]	CD	
1290	1yu5_42	X	68	ASN	HIS	0.0	70.0	-	-	-	-	-	35	1.40	Headpiece Villin Domain HP35	Gallus gallus	[166]	[7.2]	CD	
1291	1zym	B	189	HIS	ALA	-1.5	56.7	7.7	-142.7	-	-2.70	0.90	25	258	2.50	Amino Terminal Enzyme I	Escherichia Coli	[167]	[7.5]	DSC-CD
1292	1zym	B	189	HIS	GLU	-3.5	56.7	9.0	-142.7	-	-2.70	1.31	25	258	2.50	Amino Terminal Enzyme I	Escherichia Coli	[167]	[7.5]	DSC-CD
1293	1zdr	A	20	LEU	MET	-4.8	66.2	-	-	-	-	-	164	2.00	Dihydrofolate Reductase	Geobacillus stearotherm	[238]	[7.0]	CD	
1294	1zdr	A	104	ALA	GLN	-3.6	66.2	-	-	-	-	-	164	2.00	Dihydrofolate Reductase	Geobacillus stearotherm	[238]	[7.0]	CD	
1295	1zdr	A	122	PRO	GLU	-0.9	66.2	-	-	-	-	-	164	2.00	Dihydrofolate Reductase	Geobacillus stearotherm	[238]	[7.0]	CD	
1296	1zdr	A	129	PRO	ASP	-1.6	66.2	-	-	-	-	-	164	2.00	Dihydrofolate Reductase	Geobacillus stearotherm	[238]	[7.0]	CD	
1297	2a01	A	18	TYR	PRO	0.0	59.5	-	-	-	-	-	243	2.40	Apolipoprotein A-I	Homo sapiens	[168]	[7.4]	CD	
1298	2a01	A	141	LEU	ARG	-2.0	59.5	-	-	-	-	0.30	25	243	2.40	Apolipoprotein A-I	Homo sapiens	[169]	[7.4]	CD
1299	2a01	A	230	LEU	PRO	-4.0	59.5	-	-	-	-	-	243	2.40	Apolipoprotein A-I	Homo sapiens	[168]	[7.4]	CD	
1300	2c12	I	27	LEU	ALA	-15.5	74.0	16.0	-67.0	-	-0.72	2.66	25	83	2.00	Chymotrypsin Inhibitor 2	Hordeum vulgare	[171]	[3.0]	DSC
1301	2c12	I	31	SER	ALA	-5.8	74.0	7.0	-67.0	-	-0.72	0.84	64	83	2.00	Chymotrypsin Inhibitor 2	Hordeum vulgare	[173]	[3.0]	DSC
1302	2c12	I	31	SER	GLY	-4.6	74.0	3.0	-67.0	-	-0.72	1.00	74	83	2.00	Chymotrypsin Inhibitor 2	Hordeum vulgare	[173]	[3.5]	DSC
1303	2c12	I	38	VAL	ALA	-2.9	74.0	2.5	-67.0	-	-0.72	0.46	25	83	2.00	Chymotrypsin Inhibitor 2	Hordeum vulgare	[171]	[3.5]	DSC
1304	2c12	I	39	ILE	VAL	-6.5	74.0	7.3	-67.0	-	-0.72	1.20	25	83	2.00	Chymotrypsin Inhibitor 2	Hordeum vulgare	[171]	[3.5]	DSC
1305	2c12	I	43	LYS	ALA	-1.3	74.0	-	-67.0	-	-0.72	0.26	74	83	2.00	Chymotrypsin Inhibitor 2	Hordeum vulgare	[172]	[4.2]	CD
1306	2c12	I	44	PRO	ALA	-9.1	74.0	-	-67.0	-	-0.72	1.82	74	83	2.00	Chymotrypsin				

1338	2lzm	A	26	THR	GLN	-0.9	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[184]	[5.3]	CD
1339	2lzm	A	30	GLY	ALA	0.1	65.1	6.0	-140.0	-	-2.49	-0.10	69	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[182]	[5.4]	CD
1340	2lzm	A	30	GLY	PHE	-4.9	65.1	41.0	-140.0	-	-2.49	1.50	69	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[182]	[5.4]	CD
1341	2lzm	A	37	PRO	ALA	-0.8	65.1	-	-140.0	-	-2.49	0.30	12	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[185]	[2.0]	CD
1342	2lzm	A	38	SER	ALA	-2.0	65.1	9.0	-140.0	-	-2.49	0.77	50	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[186]	[3.0]	CD
1343	2lzm	A	38	SER	ASP	1.5	65.1	4.0	-140.0	-	-2.49	-0.20	50	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[197]	[6.9]	CD
1344	2lzm	A	39	LEU	PRO	-5.5	65.1	-	-140.0	-	-2.49	2.80	12	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[185]	[2.0]	CD
1345	2lzm	A	41	ALA	VAL	0.7	65.1	-1.0	-140.0	-	-2.49	-0.16	25	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[187]	[5.4]	CD
1346	2lzm	A	44	SER	ALA	1.6	65.1	-	-140.0	-	-2.49	-0.44	48	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[193]	[2.5]	CD
1347	2lzm	A	54	CYS	THR	1.0	65.1	-	-140.0	-	-2.49	-0.30	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[188]	[6.5]	CD
1348	2lzm	A	54	CYS	VAL	-2.0	65.1	-	-140.0	-	-2.49	0.70	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[188]	[6.5]	CD
1349	2lzm	A	55	ASN	GLY	-1.6	65.1	-	-140.0	-	-2.49	0.60	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[189]	[6.5]	CD
1350	2lzm	A	60	LYS	PRO	-0.1	65.1	-	-140.0	-	-2.49	0.00	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[191]	[6.5]	CD
1351	2lzm	A	68	ASN	ALA	0.2	65.1	-	-140.0	-	-2.49	-0.05	48	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[193]	[2.5]	CD
1352	2lzm	A	77	GLY	ALA	0.9	65.1	4.0	-140.0	-	-2.49	-0.40	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[191]	[6.5]	CD
1353	2lzm	A	82	ALA	PRO	2.1	65.1	3.0	-140.0	-	-2.49	-0.80	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[191]	[6.5]	CD
1354	2lzm	A	86	PRO	ALA	-1.7	65.1	-	-140.0	-	-2.49	0.40	12	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[185,194]	[2.0]	CD
1355	2lzm	A	86	PRO	CYS	-1.0	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[194]	[2.0]	CD
1356	2lzm	A	86	PRO	ASP	-1.0	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[194]	[6.0]	CD
1357	2lzm	A	86	PRO	GLY	-1.0	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[194]	[4.0]	CD
1358	2lzm	A	86	PRO	HIS	-4.0	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[194]	[6.0]	CD
1359	2lzm	A	86	PRO	ILE	-2.0	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[194]	[2.0]	CD
1360	2lzm	A	86	PRO	LEU	-2.0	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[194]	[2.0]	CD
1361	2lzm	A	86	PRO	ARG	-3.0	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[194]	[6.0]	CD
1362	2lzm	A	86	PRO	SER	-1.0	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[194]	[6.0]	CD
1363	2lzm	A	86	PRO	THR	-1.0	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[194]	[2.0]	CD
1364	2lzm	A	93	ALA	PRO	0.2	65.1	8.0	-140.0	-	-2.49	-0.10	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[191]	[6.5]	CD
1365	2lzm	A	96	ARG	HIS	-7.0	65.1	-	-140.0	-	-2.49	2.80	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[188]	[6.5]	CD
1366	2lzm	A	98	ALA	VAL	-13.0	65.1	105.3	-140.0	-	-2.49	8.05	25	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[68,192]	[3.0]	CD
1367	2lzm	A	102	MET	THR	-13.0	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[187,197]	[5.7]	CD
1368	2lzm	A	102	MET	VAL	-12.7	65.1	41.5	-140.0	-0.07	-2.49	3.90	25	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[195]	[3.0]	CD
1369	2lzm	A	105	GLN	ALA	-1.6	65.1	17.0	-140.0	-	-2.49	0.60	66	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[196]	[5.8]	CD
1370	2lzm	A	105	GLN	GLU	-3.0	65.1	20.0	-140.0	-	-2.49	1.10	66	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[196]	[5.8]	CD
1371	2lzm	A	105	GLN	GLY	-3.9	65.1	8.0	-140.0	-	-2.49	1.50	66	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[196]	[5.8]	CD
1372	2lzm	A	113	GLY	ALA	0.8	65.1	9.0	-140.0	-	-2.49	-0.30	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[191]	[6.5]	CD
1373	2lzm	A	115	THR	GLU	0.7	65.1	0.0	-140.0	-	-2.49	-0.30	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[190]	[6.5]	CD
1374	2lzm	A	116	ASN	ASP	1.6	65.1	1.0	-140.0	-	-2.49	0.06	25	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[187,197]	[5.7]	CD
1375	2lzm	A	117	SER	PHE	2.8	65.1	8.0	-140.0	-	-2.49	-1.10	69	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[182]	[5.4]	CD
1376	2lzm	A	117	SER	ILE	4.2	65.1	12.0	-140.0	-	-2.49	-1.70	69	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[182]	[5.4]	CD
1377	2lzm	A	117	SER	VAL	5.1	65.1	7.0	-140.0	-	-2.49	-2.00	69	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[182]	[5.4]	CD
1378	2lzm	A	119	ARG	GLU	0.1	65.1	-	-140.0	-	-2.49	0.04	67	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[183]	[5.3]	CD
1379	2lzm	A	119	ARG	MET	0.3	65.1	-	-140.0	-	-2.49	-0.10	66	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[197]	[5.7]	CD
1380	2lzm	A	123	GLN	GLU	1.2	65.1	-7.0	-140.0	-	-2.49	-0.40	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[190]	[6.5]	CD
1381	2lzm	A	124	LYS	GLY	-0.2	65.1	-	-140.0	-	-2.49	0.10	65	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[189]	[6.5]	CD
1382	2lzm	A	128	GLU	ALA	0.6	65.1	1.0	-140.0	-	-2.49	-0.16	86	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[199]	[2.0]	CD
1383	2lzm	A	128	GLU	LYS	-5.3	65.1	11.4	-140.0	0.01	-2.49	1.33	25	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[195]	[3.0]	CD
1384	2lzm	A	129	ALA	VAL	-1.9	65.1	9.0	-140.0	-	-2.49	0.80	42	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[200]	[2.9]	CD
1385	2lzm	A	131	VAL	ALA	0.9	65.1	0.0	-140.0	-	-2.49	-0.05	25	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[187]	[5.4]	CD
1386	2lzm	A	131	VAL	ASP	0.2	65.1	4.0	-140.0	-	-2.49	-0.08	53	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[72]	[3.0]	CD
1387	2lzm	A	131	VAL	GLU	0.5	65.1	2.0	-140.0	-	-2.49	-0.20	53	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[72]	[3.0]	CD
1388	2lzm	A	131	VAL	GLY	-1.8	65.1	4.0	-140.0	-	-2.49	0.68	53	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[72]	[3.0]	CD
1389	2lzm	A	131	VAL	ILE	0.4	65.1	0.0	-140.0	-	-2.49	-0.16	53	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[72]	[3.0]	CD
1390	2lzm	A	131	VAL	LEU	0.2	65.1	6.0	-140.0	-	-2.49	-0.09	53	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[72]	[3.0]	CD
1391	2lzm	A	131	VAL	MET	0.3	65.1	1.0	-140.0	-	-2.49	-0.12	53	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[72]	[3.0]	CD
1392	2lzm	A	131	VAL	SER	-0.1	65.1	3.0	-140.0	-	-2.49	0.05	53	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[72]	[3.0]	CD
1393	2lzm	A	131	VAL	THR	-0.2	65.1	1.7	-140.0	-	-2.49	0.12	51	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[72,198]	[2.8]	CD
1394	2lzm	A	132	ASN	PHE	3.3	65.1	6.0	-140.0	-	-2.49	-1.30	69	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[182]	[5.4]	CD
1395	2lzm	A	132	ASN	ILE	3.0	65.1	0.0	-140.0	-	-2.49	-1.20	69	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[182]	[5.4]	CD
1396	2lzm	A	132	ASN	MET	3.6	65.1	6.0	-140.0	-	-2.49	-1.50	69	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[182]	[5.4]	CD
1397	2lzm	A	133	LEU	ALA	-10.6	65.1	38.5	-140.0	-	-2.49	3.60	52	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[84]	[3.0]	CD
1398	2lzm	A	133	LEU	PHE	-0.8	65.1	4.0	-140.0	-	-2.49	0.20	41	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[200]	[2.9]	CD
1399	2lzm	A	135	LYS	GLU	-2.3	65.1	-	-140.0	-	-2.49	1.00	67	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[183]	[5.3]	CD
1400	2lzm	A	138	TRP	TYR	-4.6	65.1	23.6	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[201]	[2.0]	CD
1401	2lzm	A	143	PRO	ALA	-5.0	65.1	-	-140.0	-	-2.49	1.00	12	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[185]	[2.0]	CD
1402	2lzm	A	144	ASN	ASP	1.4	65.1	-	-140.0	-	-2.49	-0.30	25	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[187]	[5.7]	CD
1403	2lzm	A	146	ALA	THR	-7.1	65.1	43.2	-140.0	-0.24	-2.49	4.07	25	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[188,195]	[6.5]	CD
1404	2lzm	A	147	LYS	GLU	-1.6	65.1	-	-140.0	-	-2.49	0.70	67	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[183]	[5.3]	CD
1405	2lzm	A	149	VAL	CYS	-5.1	65.1	21.0	-140.0	-	-2.49	2.44	25	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[68]	[3.0]	CD
1406	2lzm	A	152	THR	SER	-6.6	65.1	24.2	-140.0	-	-2.49	2.88	25	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[68]	[3.0]	CD
1407	2lzm	A	154	ARG	GLU	-2.6	65.1	-	-140.0	-	-2.49	1.10	67	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[183]	[5.3]	CD
1408	2lzm	A	156	GLY	ASP	-5.0	65.1	-	-140.0	-	-2.49	-	-	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[192]	[3.0]	CD
1409	2lzm	A	157	THR	ALA	-5.4	65.1	-	-140.0	-	-2.49	1.40	42	164	1.70	T4 Lysozyme	Enterobacteria phage T4	[202]	[2.0]	CD
1410																				

1441	2m2	A	52	ALA	LYS	-19.5	52.6	28.4	-92.2	-	-1.79	5.93	53	155	1.48	Ribonuclease H	Escherichia Coli	[206]	[3.0]	CD
1442	2m2	A	52	ALA	LEU	4.3	52.6	-3.0	-92.2	-	-1.79	-1.31	53	155	1.48	Ribonuclease H	Escherichia Coli	[206]	[3.0]	CD
1443	2m2	A	52	ALA	MET	1.6	52.6	-12.7	-92.2	-	-1.79	-0.49	53	155	1.48	Ribonuclease H	Escherichia Coli	[206]	[3.0]	CD
1444	2m2	A	52	ALA	ASN	-5.9	52.6	3.6	-92.2	-	-1.79	1.79	53	155	1.48	Ribonuclease H	Escherichia Coli	[206]	[3.0]	CD
1445	2m2	A	52	ALA	PRO	-5.4	52.6	6.2	-92.2	-	-1.79	1.64	53	155	1.48	Ribonuclease H	Escherichia Coli	[206]	[3.0]	CD
1446	2m2	A	52	ALA	GLN	-3.9	52.6	8.9	-92.2	-	-1.79	1.19	53	155	1.48	Ribonuclease H	Escherichia Coli	[206]	[3.0]	CD
1447	2m2	A	52	ALA	SER	-5.8	52.6	-18.4	-92.2	-	-1.79	1.76	53	155	1.48	Ribonuclease H	Escherichia Coli	[206]	[3.0]	CD
1448	2m2	A	52	ALA	THR	-2.7	52.6	-8.7	-92.2	-	-1.79	0.82	53	155	1.48	Ribonuclease H	Escherichia Coli	[206]	[3.0]	CD
1449	2m2	A	52	ALA	VAL	7.8	52.6	4.7	-92.2	-	-1.79	-1.67	53	155	1.48	Ribonuclease H	Escherichia Coli	[205]	[3.0-5.5]	CD
1450	2m2	A	52	ALA	TYR	-7.6	52.6	28.4	-92.2	-	-1.79	2.31	53	155	1.48	Ribonuclease H	Escherichia Coli	[206]	[3.0]	CD
1451	2m2	A	62	HIS	ALA	1.0	52.6	-	-92.2	-	-1.79	-0.55	25	155	1.48	Ribonuclease H	Escherichia Coli	[210]	[7.8]	CD
1452	2m2	A	62	HIS	ASP	-0.6	52.6	-5.6	-92.2	-	-1.79	0.17	52	155	1.48	Ribonuclease H	Escherichia Coli	[205]	[5.5]	CD
1453	2m2	A	62	HIS	PRO	4.1	52.6	-20.2	-92.2	-	-1.79	-2.21	25	155	1.48	Ribonuclease H	Escherichia Coli	[204]	[5.5]	CD
1454	2m2	A	62	HIS	ARG	1.3	52.6	-4.9	-92.2	-	-1.79	-0.36	52	155	1.48	Ribonuclease H	Escherichia Coli	[205]	[5.5]	CD
1455	2m2	A	68	SER	ALA	-1.5	52.6	9.8	-92.2	-	-1.79	0.45	52	155	1.48	Ribonuclease H	Escherichia Coli	[207]	[3.0]	CD
1456	2m2	A	68	SER	GLY	-8.0	52.6	14.1	-92.2	-	-1.79	2.40	52	155	1.48	Ribonuclease H	Escherichia Coli	[207]	[3.0]	CD
1457	2m2	A	68	SER	LEU	-1.6	52.6	14.8	-92.2	-	-1.79	0.48	52	155	1.48	Ribonuclease H	Escherichia Coli	[207]	[3.0]	CD
1458	2m2	A	68	SER	THR	-0.7	52.6	-7.4	-92.2	-	-1.79	0.20	52	155	1.48	Ribonuclease H	Escherichia Coli	[207]	[3.0]	CD
1459	2m2	A	68	SER	VAL	1.9	52.6	0.7	-92.2	-	-1.79	-0.57	52	155	1.48	Ribonuclease H	Escherichia Coli	[207]	[3.0]	CD
1460	2m2	A	70	ASP	ALA	3.8	52.6	-	-92.2	-	-1.79	-0.58	25	155	1.48	Ribonuclease H	Escherichia Coli	[203]	[9.0]	CD
1461	2m2	A	70	ASP	GLU	0.4	52.6	-	-92.2	-	-1.79	-0.06	25	155	1.48	Ribonuclease H	Escherichia Coli	[203]	[9.0]	CD
1462	2m2	A	70	ASP	ASN	5.5	52.6	-	-92.2	-	-1.79	-0.81	25	155	1.48	Ribonuclease H	Escherichia Coli	[203]	[9.0]	CD
1463	2m2	A	74	VAL	ALA	-12.7	52.6	-	-92.2	-	-1.79	3.40	52	155	1.48	Ribonuclease H	Escherichia Coli	[211]	[5.5]	CD
1464	2m2	A	74	VAL	ILE	2.1	52.6	-	-92.2	-	-1.79	-0.60	52	155	1.48	Ribonuclease H	Escherichia Coli	[211]	[5.5]	CD
1465	2m2	A	74	VAL	LEU	3.3	52.6	-9.4	-92.2	-	-1.79	-1.10	25	155	1.48	Ribonuclease H	Escherichia Coli	[205]	[5.5]	CD
1466	2m2	A	76	GLN	LEU	1.1	52.6	11.0	-92.2	-	-1.79	-	-	155	1.48	Ribonuclease H	Escherichia Coli	[205]	[5.5]	CD
1467	2m2	A	77	GLY	ALA	-2.9	52.6	-	-92.2	-	-1.79	0.90	50	155	1.48	Ribonuclease H	Escherichia Coli	[213]	[3.0]	CD
1468	2m2	A	80	GLN	LEU	0.8	52.6	-2.4	-92.2	-	-1.79	-	-	155	1.48	Ribonuclease H	Escherichia Coli	[205]	[5.5]	CD
1469	2m2	A	83	HIS	ALA	-0.2	52.6	-	-92.2	-	-1.79	0.12	25	155	1.48	Ribonuclease H	Escherichia Coli	[210]	[7.8]	CD
1470	2m2	A	91	LYS	ARG	0.1	52.6	-10.2	-92.2	-	-1.79	0.00	52	155	1.48	Ribonuclease H	Escherichia Coli	[209]	[5.5]	CD
1471	2m2	A	94	ASP	GLU	-1.6	52.6	-3.9	-92.2	-	-1.79	0.40	52	155	1.48	Ribonuclease H	Escherichia Coli	[209]	[5.5]	CD
1472	2m2	A	95	LYS	ALA	0.4	52.6	-1.4	-92.2	-	-1.79	-0.10	52	155	1.48	Ribonuclease H	Escherichia Coli	[209]	[5.5]	CD
1473	2m2	A	95	LYS	GLY	6.8	52.6	-8.6	-92.2	-	-1.79	-1.28	25	155	1.48	Ribonuclease H	Escherichia Coli	[205]	[5.5]	CD
1474	2m2	A	95	LYS	ASN	3.2	52.6	2.2	-92.2	-	-1.79	-0.88	52	155	1.48	Ribonuclease H	Escherichia Coli	[205]	[5.5]	CD
1475	2m2	A	113	GLN	PRO	-2.1	52.6	8.0	-92.2	-	-1.79	0.60	52	155	1.48	Ribonuclease H	Escherichia Coli	[208]	[5.5]	CD
1476	2m2	A	114	HIS	ALA	-7.7	52.6	-	-92.2	-	-1.79	-	-	155	1.48	Ribonuclease H	Escherichia Coli	[210]	[7.8]	CD
1477	2m2	A	117	LYS	ARG	0.1	52.6	-5.7	-92.2	-	-1.79	-0.03	52	155	1.48	Ribonuclease H	Escherichia Coli	[205]	[5.5]	CD
1478	2m2	A	119	GLU	VAL	2.7	52.6	-1.9	-92.2	-	-1.79	-0.74	52	155	1.48	Ribonuclease H	Escherichia Coli	[205]	[5.5]	CD
1479	2m2	A	124	HIS	ALA	0.1	52.6	-	-92.2	-	-1.79	-0.05	-	155	1.48	Ribonuclease H	Escherichia Coli	[210]	[7.9]	CD
1480	2m2	A	125	ALA	THR	0.0	52.6	1.0	-92.2	-	-1.79	0.00	52	155	1.48	Ribonuclease H	Escherichia Coli	[208]	[5.5]	CD
1481	2m2	A	127	HIS	ALA	0.9	52.6	-	-92.2	-	-1.79	0.31	25	155	1.48	Ribonuclease H	Escherichia Coli	[210]	[3.0]	CD
1482	2m2	A	134	ASP	ALA	6.8	52.6	-	-92.2	-	-1.79	-0.98	25	155	1.48	Ribonuclease H	Escherichia Coli	[203]	[9.0]	CD
1483	2m2	A	134	ASP	GLU	3.1	52.6	-19.1	-92.2	-	-1.79	-0.91	52	155	1.48	Ribonuclease H	Escherichia Coli	[212]	[5.5]	CD
1484	2m2	A	134	ASP	HIS	7.0	52.6	-24.8	-92.2	-	-1.79	2.97	25	155	1.48	Ribonuclease H	Escherichia Coli	[204]	[5.5]	CD
1485	2m2	A	134	ASP	ILE	4.6	52.6	-18.2	-92.2	-	-1.79	-1.37	52	155	1.48	Ribonuclease H	Escherichia Coli	[212]	[5.5]	CD
1486	2m2	A	134	ASP	LEU	5.5	52.6	-13.1	-92.2	-	-1.79	-1.54	52	155	1.48	Ribonuclease H	Escherichia Coli	[212]	[5.5]	CD
1487	2m2	A	134	ASP	ASN	3.2	52.6	-15.2	-92.2	-	-1.79	-1.64	25	155	1.48	Ribonuclease H	Escherichia Coli	[204]	[5.5]	CD
1488	2m2	A	134	ASP	GLN	4.8	52.6	-13.6	-92.2	-	-1.79	-1.33	52	155	1.48	Ribonuclease H	Escherichia Coli	[212]	[5.5]	CD
1489	2m2	A	134	ASP	SER	3.9	52.6	-22.0	-92.2	-	-1.79	-1.14	52	155	1.48	Ribonuclease H	Escherichia Coli	[212]	[5.5]	CD
1490	2m2	A	134	ASP	THR	3.9	52.6	-6.9	-92.2	-	-1.79	-1.07	52	155	1.48	Ribonuclease H	Escherichia Coli	[212]	[5.5]	CD
1491	2m2	A	134	ASP	VAL	4.1	52.6	-15.8	-92.2	-	-1.79	-1.20	52	155	1.48	Ribonuclease H	Escherichia Coli	[212]	[5.5]	CD
1492	2m2	A	135	GLU	LYS	-0.8	52.6	2.3	-92.2	-	-1.79	0.22	52	155	1.48	Ribonuclease H	Escherichia Coli	[205]	[5.5]	CD
1493	2ov0	A	45	TRP	TYR	-8.1	58.1	-	-	-	-	-	-	105	0.75	Amicyanin	Paracoccus denitrificans	[249]	[7.5]	CD
1494	2trx	A	26	ASP	ILE	11.0	85.4	-	-98.2	-	-2.47	-3.10	25	108	1.68	Thioedoxin	Escherichia Coli	[214]	[7.0]	DSC
1495	2trx	A	32	CYS	ALA	-13.0	85.4	-	-98.2	-	-2.47	3.70	25	108	1.68	Thioedoxin	Escherichia Coli	[214]	[7.0]	DSC
1496	2trx	A	35	CYS	ALA	-14.0	85.4	-	-98.2	-	-2.47	3.10	25	108	1.68	Thioedoxin	Escherichia Coli	[214]	[7.0]	DSC
1497	2trx	A	40	PRO	SER	-0.4	85.4	-4.9	-98.2	0.12	-2.47	-1.45	25	108	1.68	Thioedoxin	Escherichia Coli	[215]	[7.0]	DSC
1498	2trx	A	66	THR	LEU	-2.0	85.4	-	-98.2	-	-2.47	1.40	25	108	1.68	Thioedoxin	Escherichia Coli	[214]	[7.0]	DSC
1499	2trx	A	77	THR	VAL	-5.0	85.4	-	-98.2	-	-2.47	1.10	25	108	1.68	Thioedoxin	Escherichia Coli	[214]	[7.0]	DSC
1500	2trx	A	78	LEU	LYS	-13.7	85.4	6.8	-98.2	1.00	-2.47	3.90	85	108	1.68	Thioedoxin	Escherichia Coli	[215]	[7.0]	DSC
1501	2trx	A	78	LEU	ARG	-16.1	85.4	23.3	-98.2	0.80	-2.47	4.00	85	108	1.68	Thioedoxin	Escherichia Coli	[215]	[7.0]	DSC
1502	3d2c	A	134	MET	GLU	1.7	71.2	-	-	-	-	-3.02	25	181	2.18	Lipase 403	Bacillus subtilis	[256]	[7.2]	CD
1503	3d2c	A	137	MET	PRO	2.9	71.2	-	-	-	-	-3.34	25	181	2.18	Lipase 403	Bacillus subtilis	[256]	[7.2]	CD
1504	3d2c	A	163	SER	PRO	1.0	71.2	-	-	-	-	-2.11	25	181	2.18	Lipase 403	Bacillus subtilis	[256]	[7.2]	CD
1505	3k3s	A	170	LYS	PRO	-1.4	57.1	-	-	-	-	-	-	260	0.90	Carbonic Anhydrase II	Homo sapiens	[245]	[7.8]	DSC
1506	3k3s	A	234	GLU	PRO	0.8	57.1	-	-	-	-	-	-	260	0.90	Carbonic Anhydrase II	Homo sapiens	[245]	[7.8]	DSC
1507	3mbp	A	48	PRO	ALA	-0.5	64.6	9.0	-217.0	-0.70	-4.70	2.70	25	370	1.70	Maltodextrin binding protein	Escherichia Coli	[217]	[7.0]	DSC
1508	3mbp	A	48	PRO	SER	0.3	64.6	5.0	-217.0	-0.80	-4.70	2.55	25	370	1.70	Maltodextrin binding protein	Escherichia Coli	[217]	[7.0]	DSC
1509	3mbp	A	133	PRO	ALA	-0.6	64.6	25.0	-217.0	-2.30	-4.70	7.80	25	370	1.70	Maltodextrin binding protein	Escherichia Coli	[217]	[7.4]	DSC
1510	3mbp	A	133	PRO	SER	-3.4	64.6	2.0	-217.0	0.80	-4.70	-1.16	25	370	1.70	Maltodextrin binding protein	Escherichia Coli	[217]	[7.4]	DSC
1511	3mbp	A	159	PRO	ALA	-3.0	64.6	12.0	-217.0	0.60	-4.70	0.22	25	370	1.70	Maltodextrin binding protein	Escherichia Coli	[217]	[7.4]	DSC
1512	3mbp	A	159	PRO	SER	-3.6	64.6	23.0	-217.0	-1.20	-4.70	4.72	25	370	1.70	Maltodextrin binding protein	Escherichia Coli	[217]	[7.4]	DSC
1513	3sil	A	53	ALA	LEU	5.0	57.0	-	-	-	-	-0.81	25	379	1.05	Sialidase</				

1544	4lyz	A	55	ILE	PHE	-6.5	74.0	-	-130.0	-	-1.57	2.46	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[226]	[6.4]	Abs
1545	4lyz	A	55	ILE	LEU	-1.2	74.0	-	-130.0	-	-1.57	0.45	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[226]	[6.4]	Abs
1546	4lyz	A	55	ILE	MET	-6.0	74.0	-	-130.0	-	-1.57	2.27	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[226]	[6.4]	Abs
1547	4lyz	A	55	ILE	THR	-13.1	74.0	-	-130.0	-	-1.57	4.96	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[226]	[6.4]	Abs
1548	4lyz	A	55	ILE	VAL	-2.4	74.0	-	-130.0	-	-1.57	0.91	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[226]	[6.4]	Abs
1549	4lyz	A	67	GLY	ALA	-2.9	74.0	-1.7	-130.0	-0.17	-1.57	0.52	25	129	2.00	Hen egg white Lysozyme	Gallus gallus	[227]	[2.7]	DSC
1550	4lyz	A	68	ARG	LYS	-0.1	74.0	-	-130.0	-	-1.57	0.04	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1551	4lyz	A	71	GLY	ALA	-1.2	74.0	2.4	-130.0	-0.71	-1.57	2.12	25	129	2.00	Hen egg white Lysozyme	Gallus gallus	[227]	[2.7]	DSC
1552	4lyz	A	73	ARG	LYS	0.6	74.0	-	-130.0	-	-1.57	-0.23	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1553	4lyz	A	77	ASN	HIS	-1.0	74.0	-	-130.0	-	-1.57	0.38	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1554	4lyz	A	91	SER	ALA	-0.4	74.0	-	-130.0	-	-1.57	0.15	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[226]	[6.4]	Abs
1555	4lyz	A	91	SER	ASP	-6.1	74.0	-	-130.0	-	-1.57	2.31	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[226]	[6.4]	Abs
1556	4lyz	A	91	SER	THR	2.6	74.0	-	-130.0	-	-1.57	-1.00	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[226]	[6.4]	Abs
1557	4lyz	A	91	SER	VAL	-0.2	74.0	-	-130.0	-	-1.57	0.08	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[226]	[6.4]	Abs
1558	4lyz	A	91	SER	TYR	-8.1	74.0	-	-130.0	-	-1.57	3.07	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[226]	[6.4]	Abs
1559	4lyz	A	101	ASP	ALA	2.0	74.0	-	-130.0	-	-1.57	-0.76	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1560	4lyz	A	101	ASP	GLU	0.0	74.0	-	-130.0	-	-1.57	0.00	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1561	4lyz	A	101	ASP	PHE	1.9	74.0	-	-130.0	-	-1.57	-0.72	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1562	4lyz	A	101	ASP	GLY	1.2	74.0	-	-130.0	-	-1.57	-0.45	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1563	4lyz	A	101	ASP	LYS	0.5	74.0	-	-130.0	-	-1.57	-0.19	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1564	4lyz	A	101	ASP	ASN	0.1	74.0	-	-130.0	-	-1.57	-0.04	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1565	4lyz	A	101	ASP	GLN	-0.2	74.0	-	-130.0	-	-1.57	0.08	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1566	4lyz	A	101	ASP	ARG	0.7	74.0	-	-130.0	-	-1.57	-0.27	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1567	4lyz	A	101	ASP	SER	2.3	74.0	-	-130.0	-	-1.57	-0.87	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1568	4lyz	A	102	GLY	ALA	0.0	74.0	1.0	-130.0	-0.43	-1.57	1.20	25	129	2.00	Hen egg white Lysozyme	Gallus gallus	[227]	[2.7]	DSC
1569	4lyz	A	102	GLY	ARG	1.0	74.0	-	-130.0	-	-1.57	-0.38	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1570	4lyz	A	102	GLY	VAL	-0.1	74.0	-	-130.0	-	-1.57	0.04	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1571	4lyz	A	114	ARG	HIS	1.8	74.0	-	-130.0	-	-1.57	-0.68	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1572	4lyz	A	117	GLY	ALA	-4.6	74.0	3.3	-130.0	0.05	-1.57	0.82	25	129	2.00	Hen egg white Lysozyme	Gallus gallus	[227]	[2.7]	DSC
1573	4lyz	A	121	GLN	HIS	-1.2	74.0	-	-130.0	-	-1.57	0.45	74	129	2.00	Hen egg white Lysozyme	Gallus gallus	[224]	[6.4]	Abs
1574	4u2b	A	110	GLN	LEU	1.0	51.5	-	-	-	-	-	-	236	1.70	Dienelactone Hydrolase C1235	Pseudomonas knackmussii	[246]	[7.5]	Fluorescence
1575	4u2b	A	137	TYR	CYS	-0.7	51.5	-	-	-	-	-	-	236	1.70	Dienelactone Hydrolase C1235	Pseudomonas knackmussii	[246]	[7.5]	Fluorescence
1576	4u2b	A	154	ASN	ASP	2.9	51.5	-	-	-	-	-	-	236	1.70	Dienelactone Hydrolase C1235	Pseudomonas knackmussii	[246]	[7.5]	Fluorescence
1577	5dfr	A	39	PRO	CYS	-2.5	49.3	-	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[228]	[9.0]	Abs
1578	5dfr	A	68	THR	ASN	1.4	49.3	-	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[250]	[7.8]	DSC
1579	5dfr	A	108	GLN	ASP	1.6	49.3	-	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[250]	[7.8]	DSC
1580	5dfr	A	113	THR	VAL	3.9	49.3	-	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[250]	[7.8]	DSC
1581	5dfr	A	116	ASP	PHE	1.4	49.3	-	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[250]	[7.8]	DSC
1582	5dfr	A	120	GLU	PRO	1.2	49.3	-	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[250]	[7.8]	DSC
1583	5dfr	A	121	GLY	ALA	-2.7	49.3	11.7	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[229]	[7.0]	CD
1584	5dfr	A	121	GLY	CYS	-1.2	49.3	42.6	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[229]	[7.0]	CD
1585	5dfr	A	121	GLY	ASP	-5.5	49.3	16.5	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[229]	[7.0]	CD
1586	5dfr	A	121	GLY	HIS	-2.9	49.3	43.4	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[229]	[7.0]	CD
1587	5dfr	A	121	GLY	LEU	-5.2	49.3	16.3	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[229]	[7.0]	CD
1588	5dfr	A	121	GLY	SER	-2.4	49.3	3.3	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[229]	[7.0]	CD
1589	5dfr	A	121	GLY	VAL	-2.4	49.3	30.6	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[229]	[7.0]	CD
1590	5dfr	A	121	GLY	TYR	-5.5	49.3	5.5	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[229]	[7.0]	CD
1591	5dfr	A	138	SER	TYR	1.5	49.3	-	-93.9	-	-	-	-	159	2.30	Dihydrofolate Reductase	Escherichia Coli	[250]	[7.8]	DSC
1592	5pti	A	11	THR	ALA	-0.3	78.0	4.2	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1593	5pti	A	12	GLY	ALA	-16.1	78.0	35.4	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1594	5pti	A	13	PRO	ALA	0.0	78.0	-	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1595	5pti	A	15	LYS	ALA	-4.2	78.0	0.5	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1596	5pti	A	17	ARG	ALA	-4.7	78.0	-2.1	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1597	5pti	A	18	ILE	ALA	0.2	78.0	-	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1598	5pti	A	19	ILE	ALA	-4.8	78.0	1.3	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1599	5pti	A	20	ARG	ALA	0.0	78.0	-	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1600	5pti	A	22	PHE	ALA	-9.0	78.0	2.0	-84.3	-	-0.40	1.20	25	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[231]	[2.0]	DSC
1601	5pti	A	33	PHE	ALA	-16.5	78.0	64.4	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1602	5pti	A	34	VAL	ALA	0.0	78.0	-	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1603	5pti	A	35	TYR	ALA	-16.2	78.0	31.7	-84.3	-	-0.40	5.0	25	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1604	5pti	A	35	TYR	GLY	-18.0	78.0	18.0	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[231]	[2.0]	DSC
1605	5pti	A	36	GLY	ALA	-11.7	78.0	14.5	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1606	5pti	A	36	GLY	SER	-4.7	78.0	0.0	-84.3	-	-0.40	0.70	73	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[232]	[4.6]	CD
1607	5pti	A	37	GLY	ALA	-4.2	78.0	65.9	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1608	5pti	A	39	ARG	ALA	0.0	78.0	-0.4	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1609	5pti	A	46	LYS	ALA	0.0	78.0	-	-84.3	-	-0.40	-	-	58	1.00	Pancreatic Trypsin Inhibitor	Bos Taurus	[230]	[3.0]	CD
1610	5pti_m52l	A	15	LYS	ALA	-3.7	91.7	0.7	-71.0	-0.20	-0.35	1.46	25	58	1.00	Pancreatic Trypsin Inhibitor M52L	Bos Taurus	[233]	[2.0]	DSC
1611	5pti_m52l	A	15	LYS	ASP	-2.3	91.7	-0.2	-71.0	-0.01	-0.35	0.25	25	58	1.00	Pancreatic Trypsin Inhibitor M52L	Bos Taurus	[233]	[3.0]	DSC
1612	5pti_m52l	A	15	LYS	GLU	-6.1	91.7	-3.7	-71.0	0.02	-0.35	0.15	25	58	1.00	Pancreatic Trypsin Inhibitor M52L	Bos Taurus	[233]	[3.0]	DSC
1613	5pti_m52l	A	15	LYS	PHE	-5.9	91.7	2.2	-71.0	-0.08	-0.35	1.40	25	58	1.00	Pancreatic Trypsin Inhibitor M52L	Bos Taurus	[233]	[3.0]	DSC
1614	5pti_m52l	A	15	LYS	GLY	-1.9	91.7	0.0	-71.0	0.16	-0.35	-0.79	25	58	1.00	Pancreatic Trypsin Inhibitor M52L	Bos Taurus	[233]	[3.0]	DSC
1615	5pti_m52l	A	15	LYS	HIS	2.2	91.7	-2.2	-71.0	0.02	-0.35	-0.92	25	58	1.00	Pancreatic Trypsin Inhibitor M52L	Bos Taurus	[233]	[3.0]	DSC
1616	5pti_m52l	A	15	LYS	ILE	-6.1	91.7	2.5	-71.0	-0.08	-0.35	1.46	25	58	1.00	Pancreatic Trypsin Inhibitor M52L	Bos Taurus	[233]	[3.0]	DSC
1617	5pti_m52l	A	15	LYS	LEU	-4.7	91.7	1.5	-7											