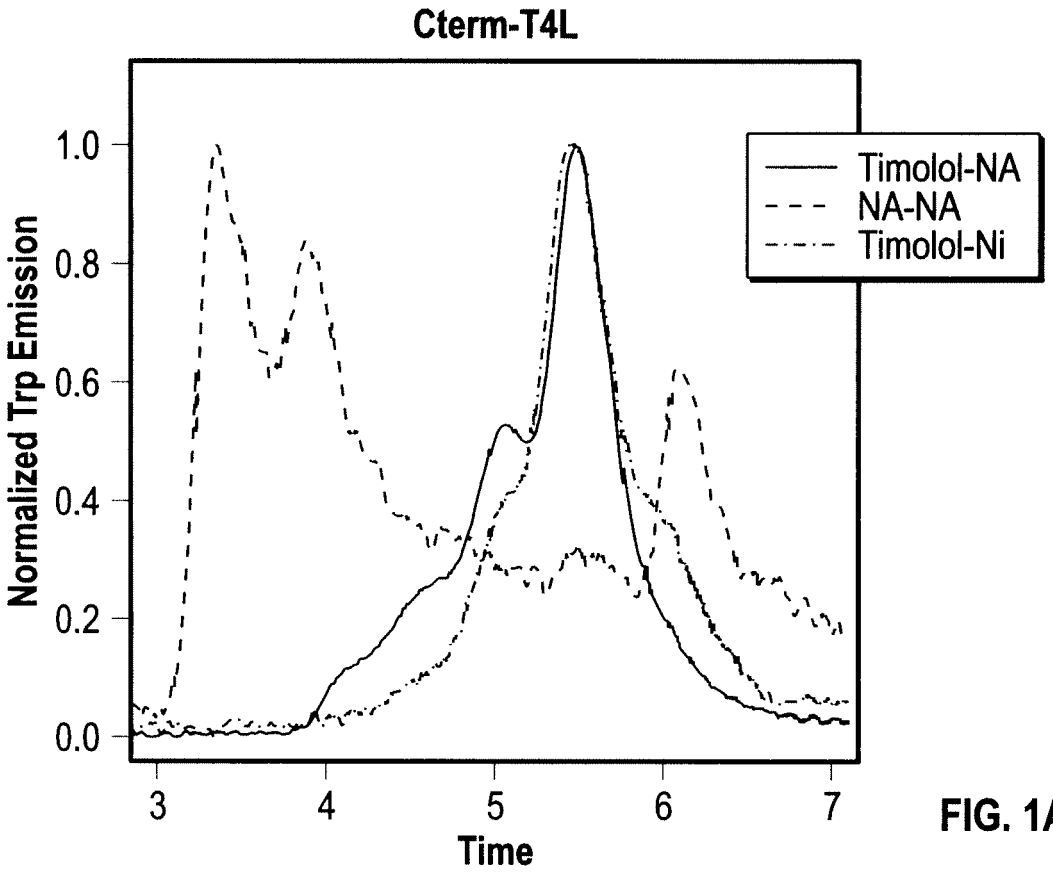

Cterm-T4L
Normalized Trp Emission
1.0
0.8
0.6
0.4
0.2
0.0
3
4
5
6
7
Time
Timolol-NA
NA-NA
Timolol-Ni

FIG. 1A

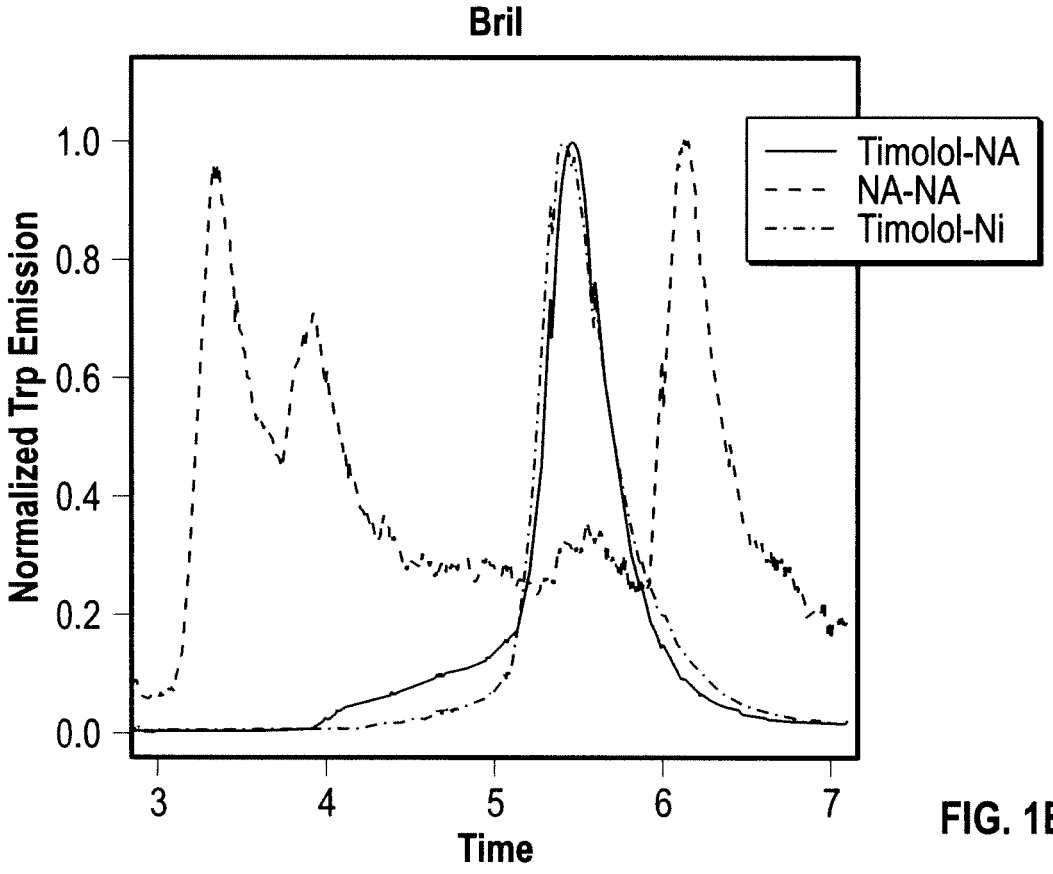

Bril
Normalized Trp Emission
1.0
0.8
0.6
0.4
0.2
0.0
3
4
5
6
7
Time
Timolol-NA
NA-NA
Timolol-Ni

FIG. 1B

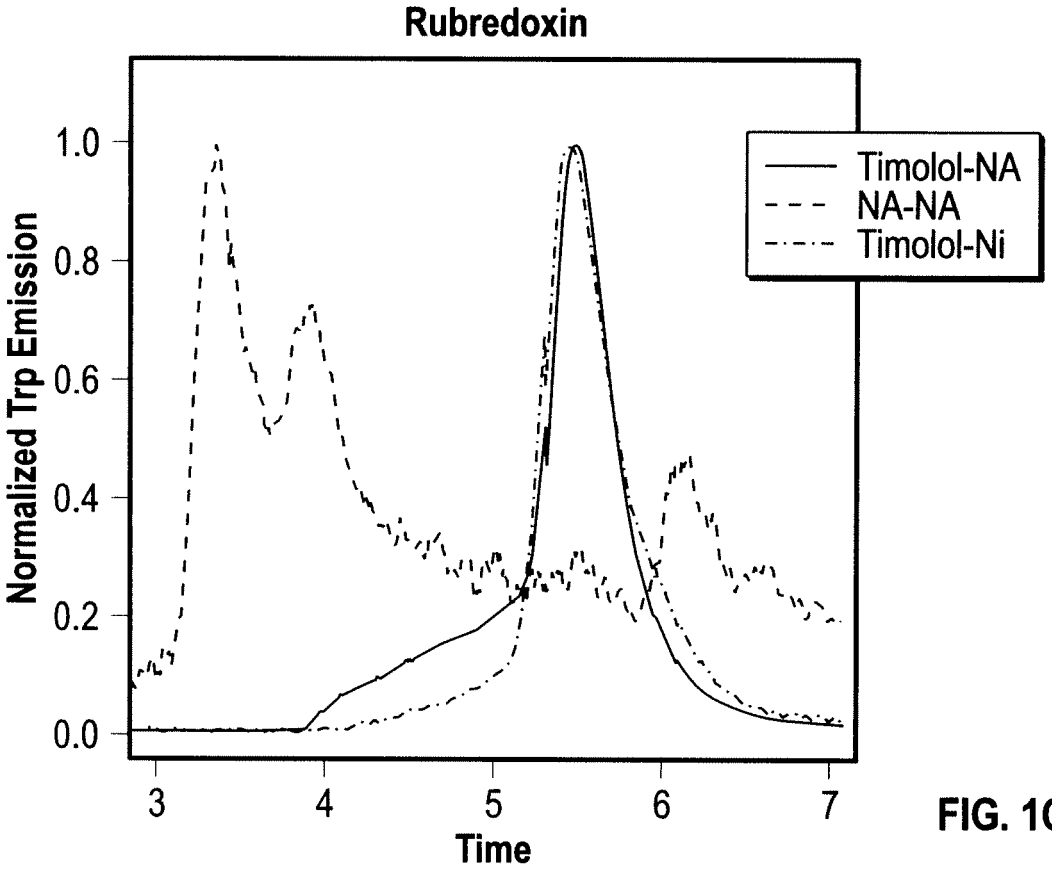

Rubredoxin
Normalized Trp Emission
1.0
0.8
0.6
0.4
0.2
0.0
3
4
5
6
7
Time
Timolol-NA
NA-NA
Timolol-Ni

FIG. 1C

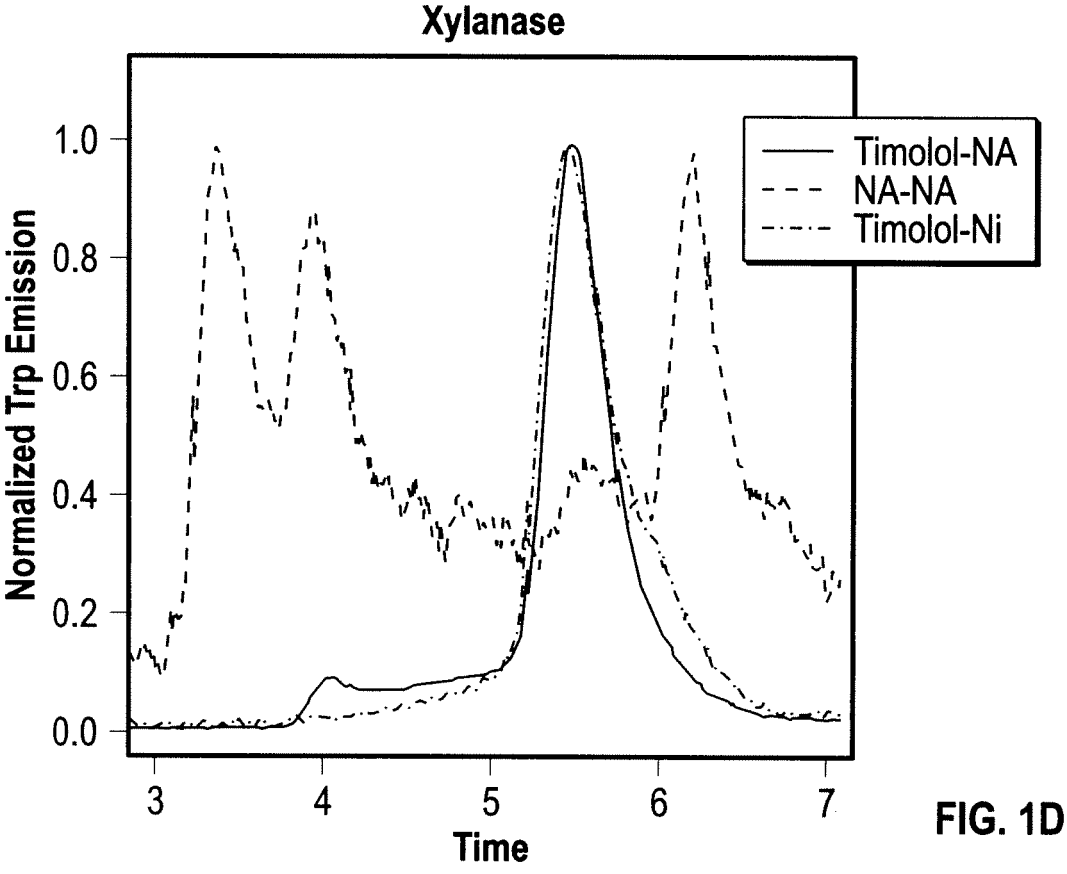

Xylanase
Normalized Trp Emission
1.0
0.8
0.6
0.4
0.2
0.0
3
4
5
6
7
Time
Timolol-NA
NA-NA
Timolol-Ni

FIG. 1D

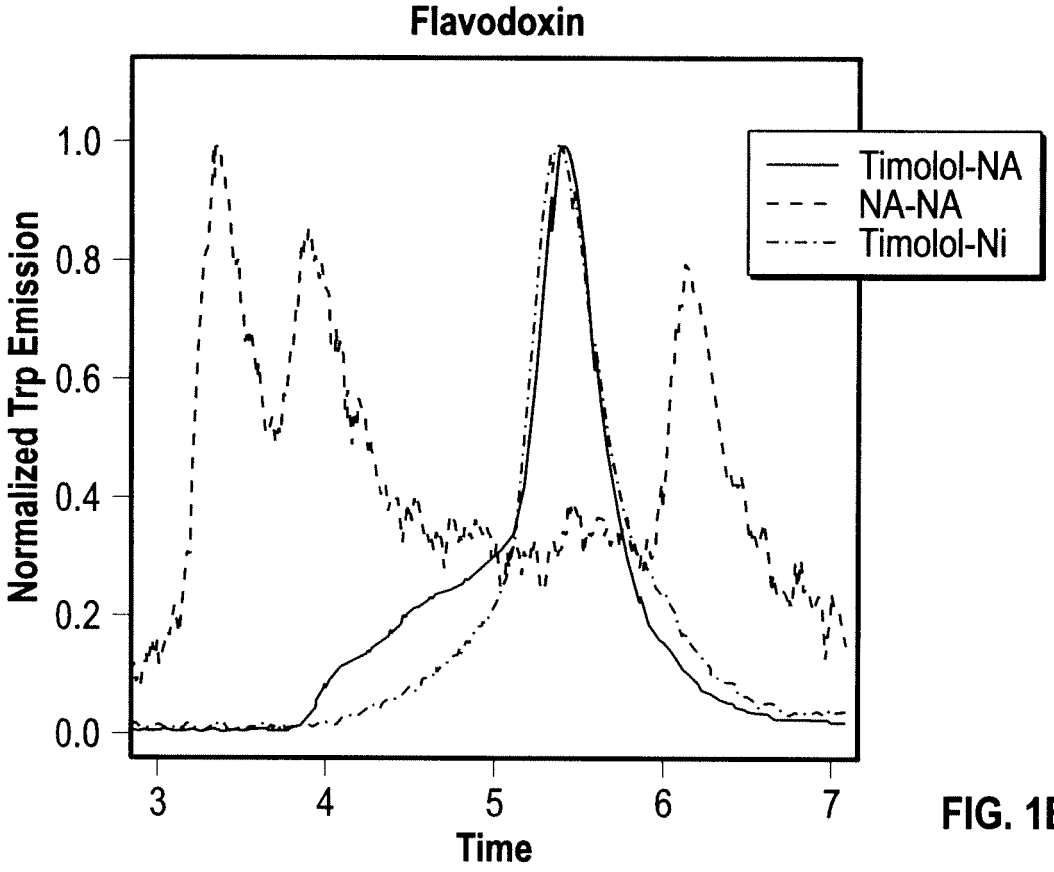

Flavodoxin
Normalized Trp Emission
1.0
0.8
0.6
0.4
0.2
0.0
3
4
5
6
7
Time
Timolol-NA
NA-NA
Timolol-Ni

FIG. 1E

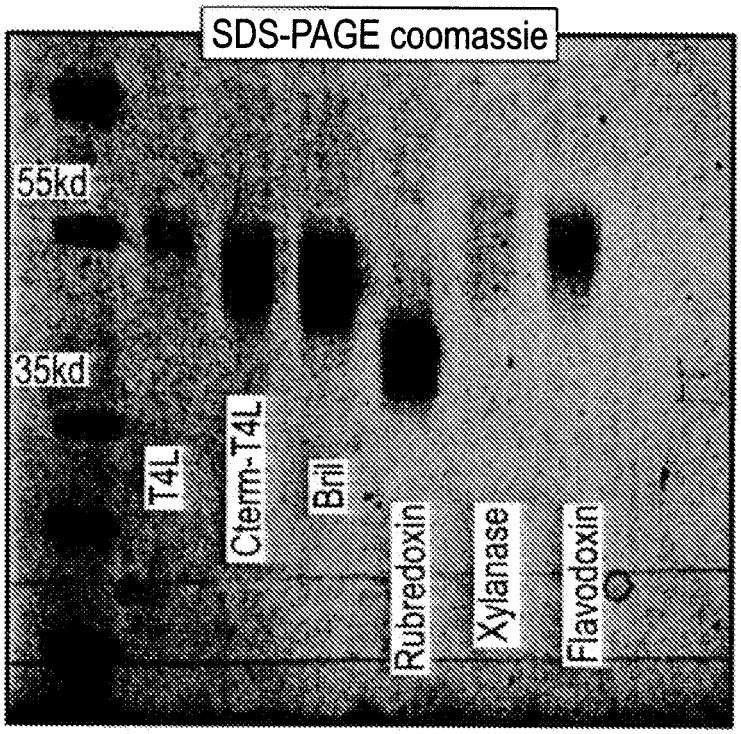

SDS-PAGE coomassie
55kd
35kd
T4L
Cterm-T4L
Bril
Rubredoxin
Xylanase
Flavodoxin

FIG. 1F

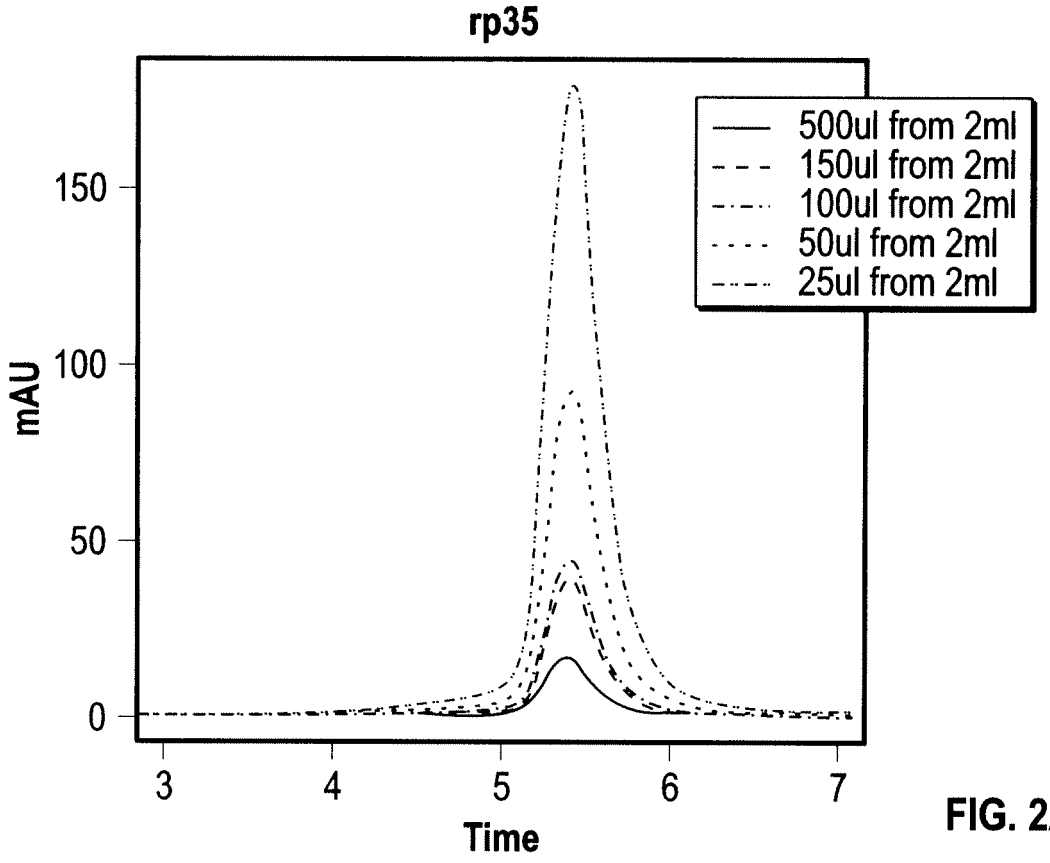

rp35
500ul from 2ml
150ul from 2ml
100ul from 2ml
50ul from 2ml
25ul from 2ml
mAU
150
100
50
0
3
4
5
6
7
Time

FIG. 2A

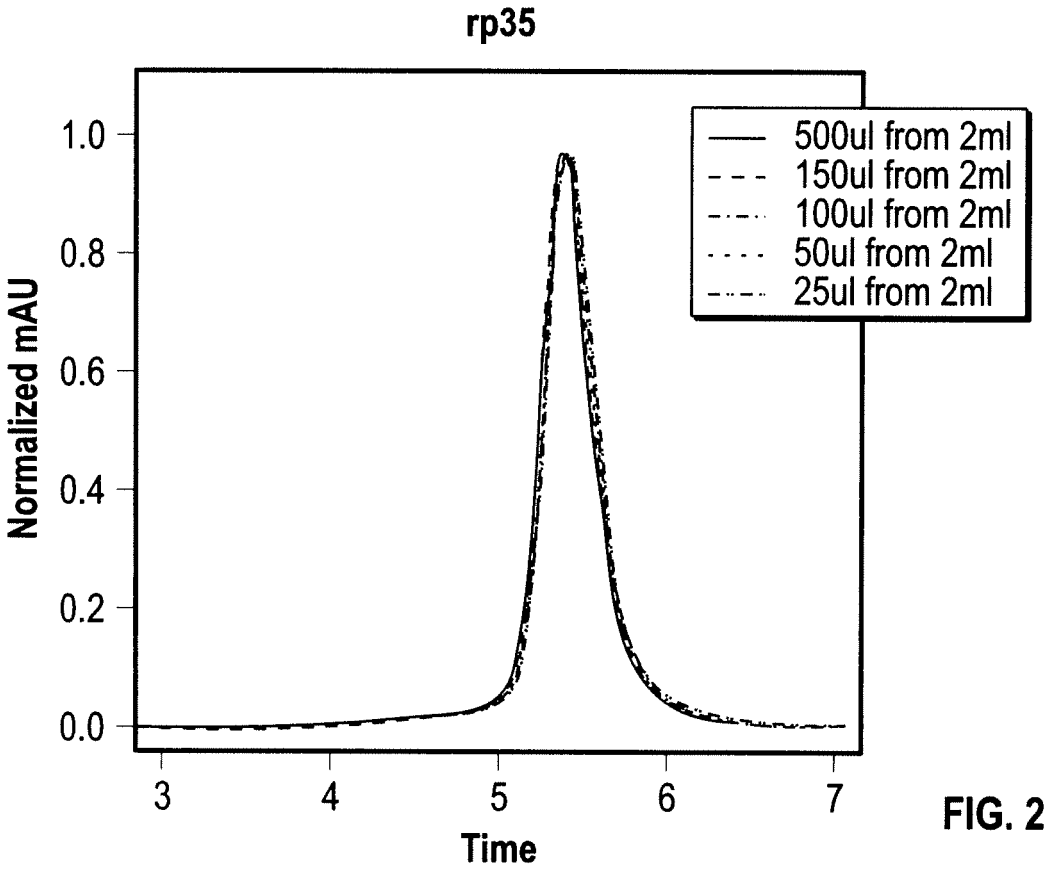

rp35
500ul from 2ml
150ul from 2ml
100ul from 2ml
50ul from 2ml
25ul from 2ml
Normalized mAU
1.0
0.8
0.6
0.4
0.2
0.0
3
4
5
6
7
Time

FIG. 2B

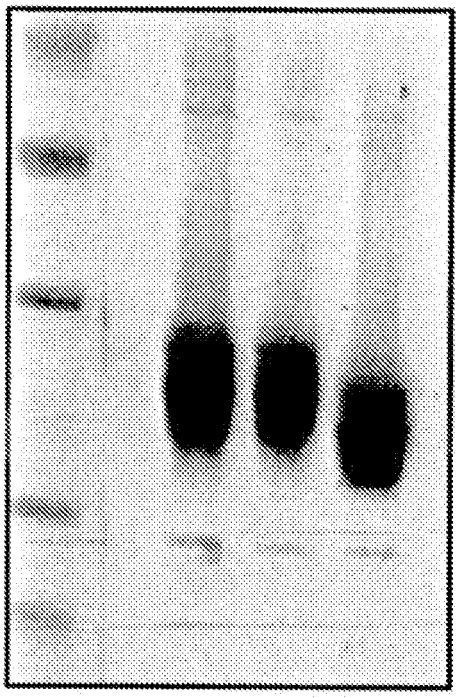


FIG. 2C

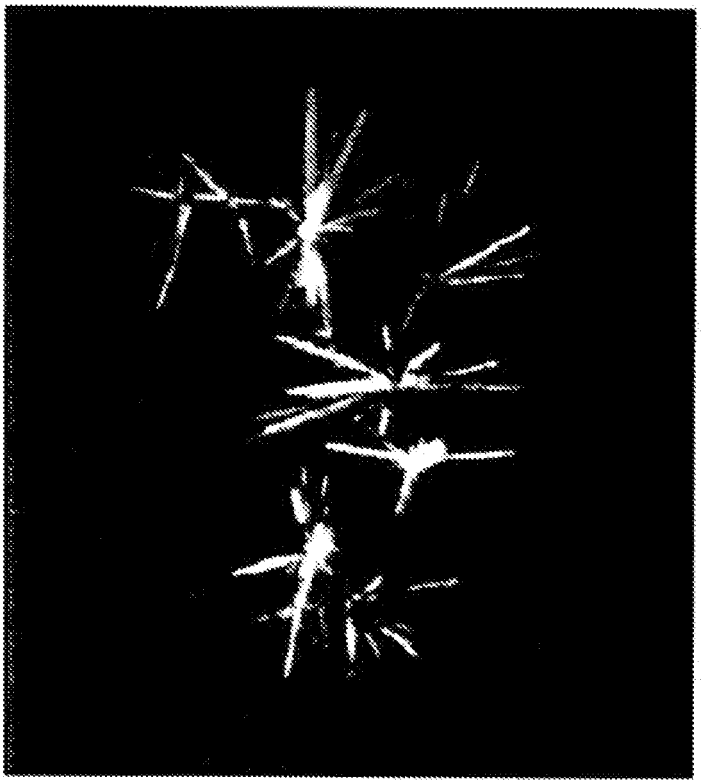


FIG. 2D

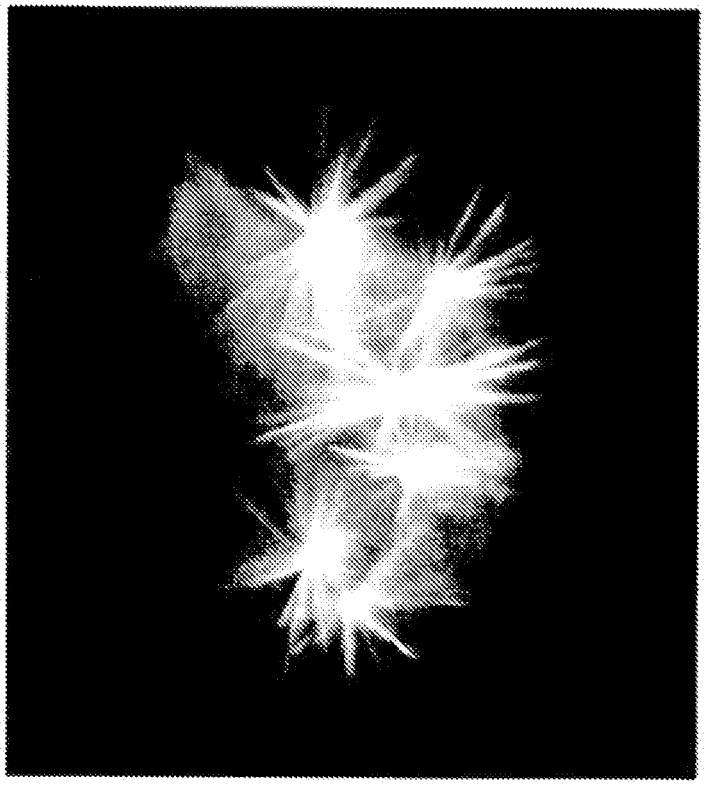


FIG. 2E

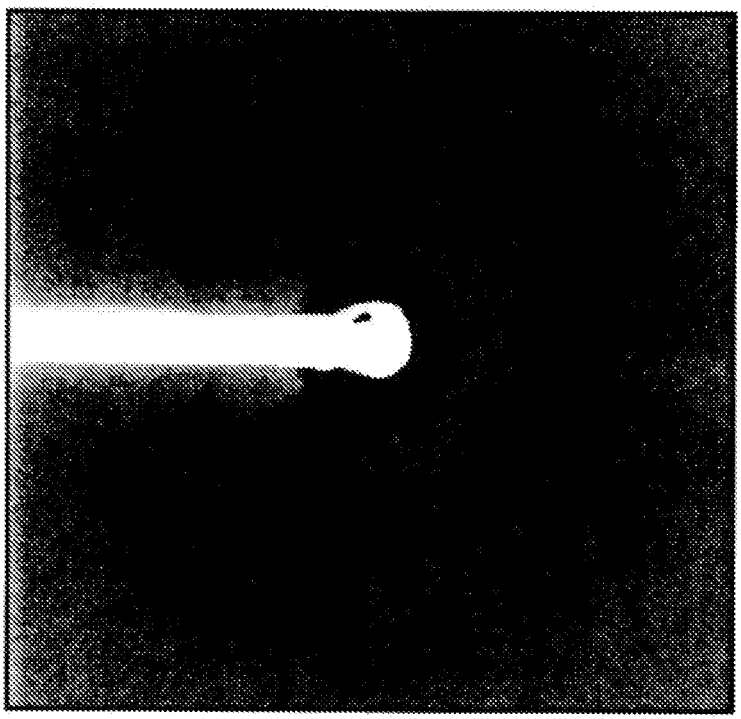


FIG. 2F

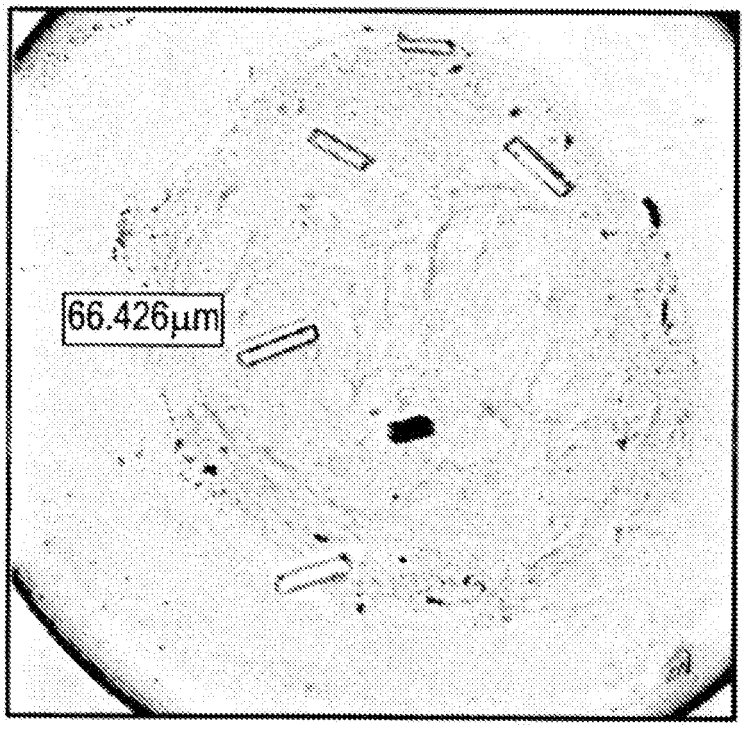


FIG. 3A

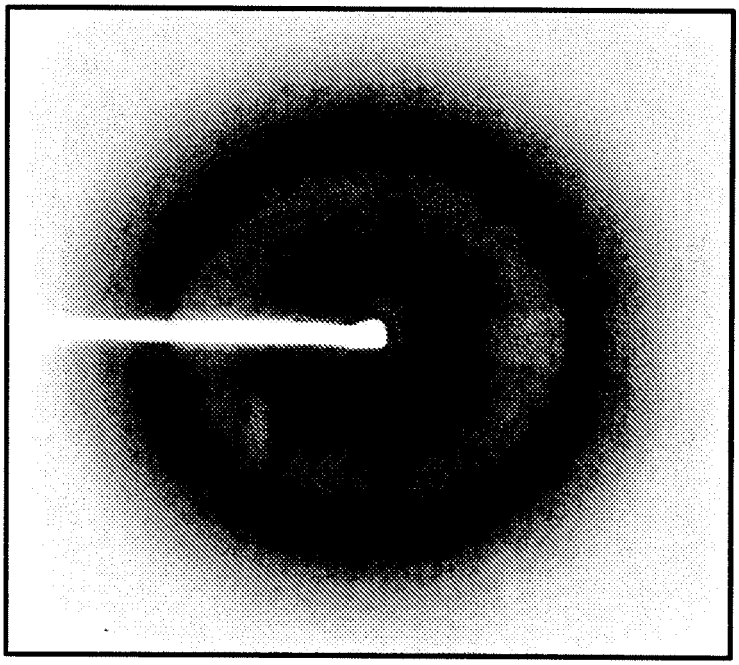


FIG. 3B

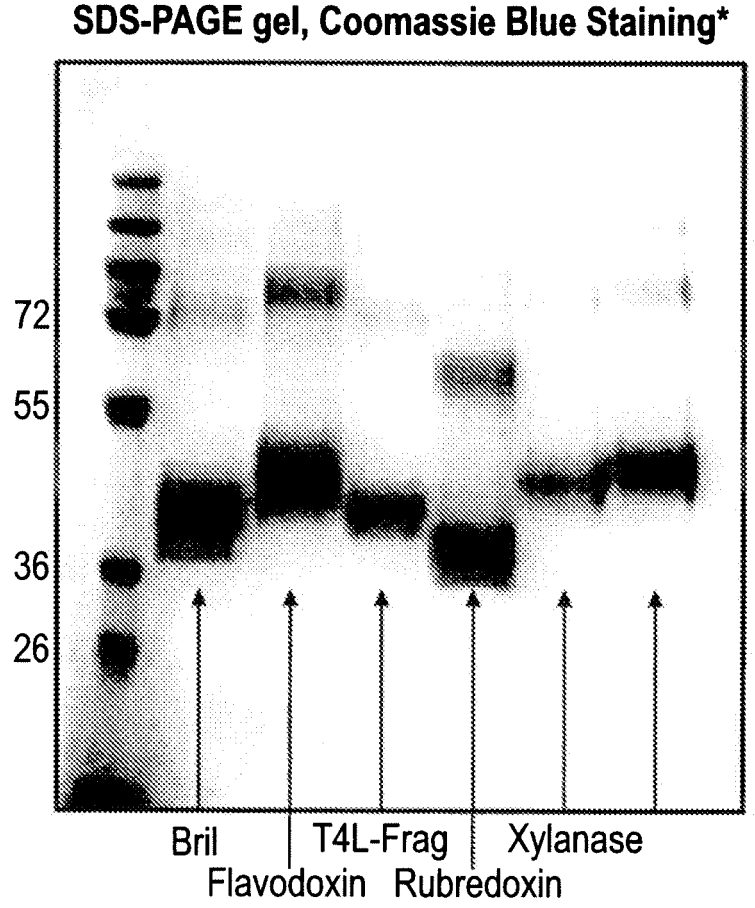

SDS-PAGE gel, Coomassie Blue Staining*
72
55
36
26
Bril
Flavodoxin
T4L-Frag
Rubredoxin
Xylanase

FIG. 4A

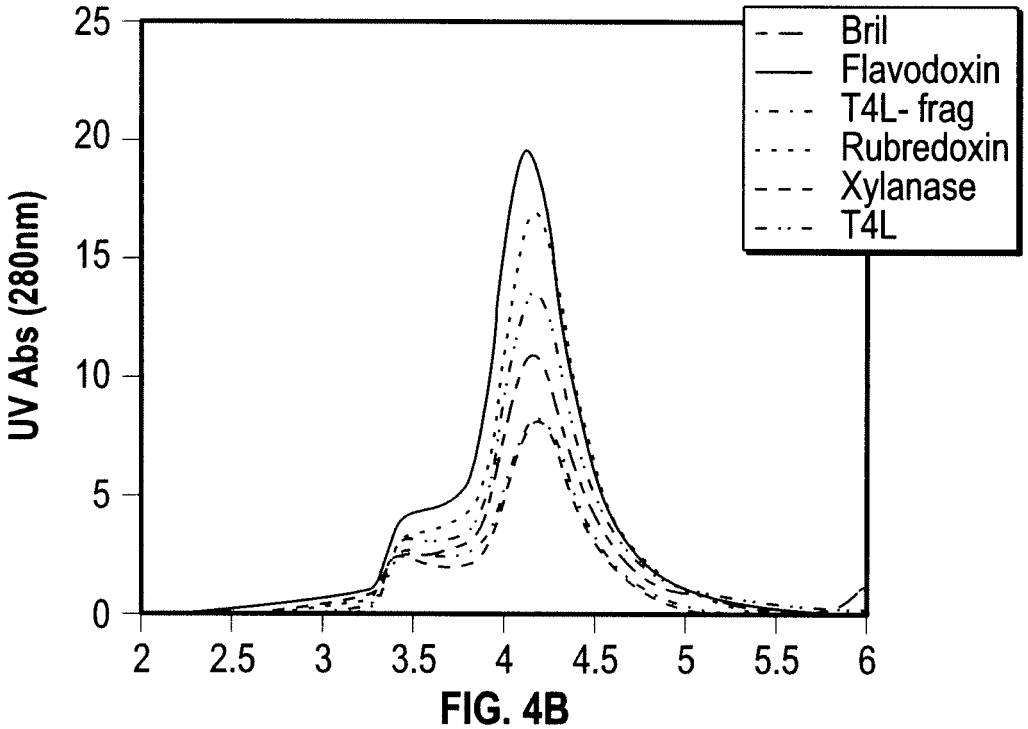
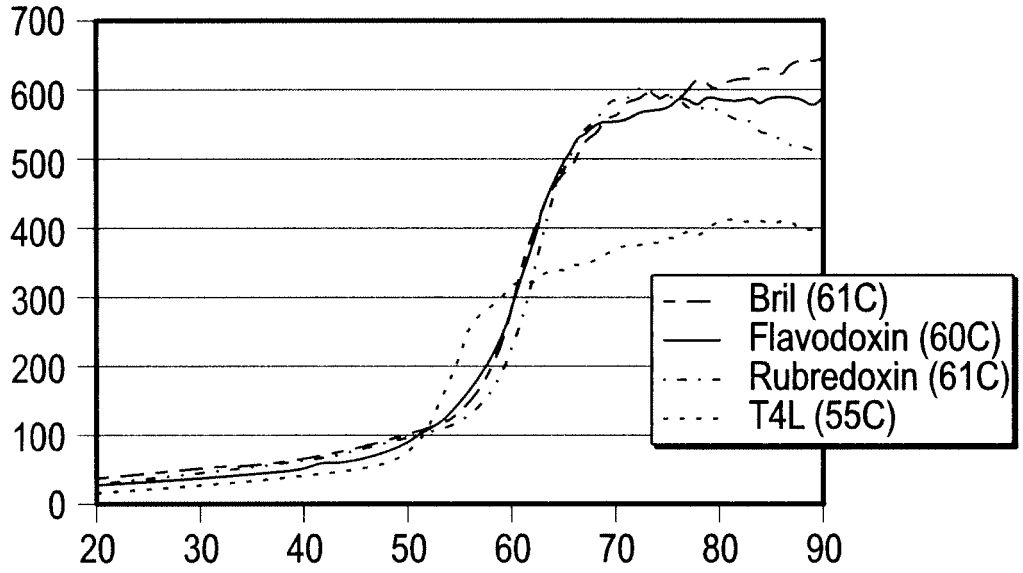
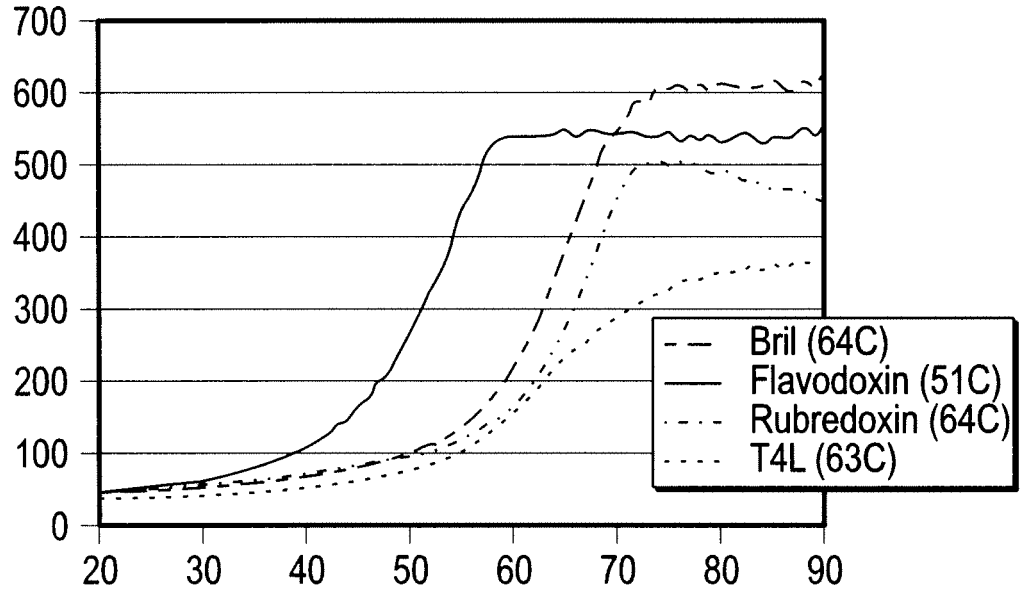

UV Abs (280nm)
25
20
15
10
5
0
2
2.5
3
3.5
4
4.5
5
5.5
6
Bril
Flavodoxin
T4L- frag
Rubredoxin
Xylanase
T4L

FIG. 4B



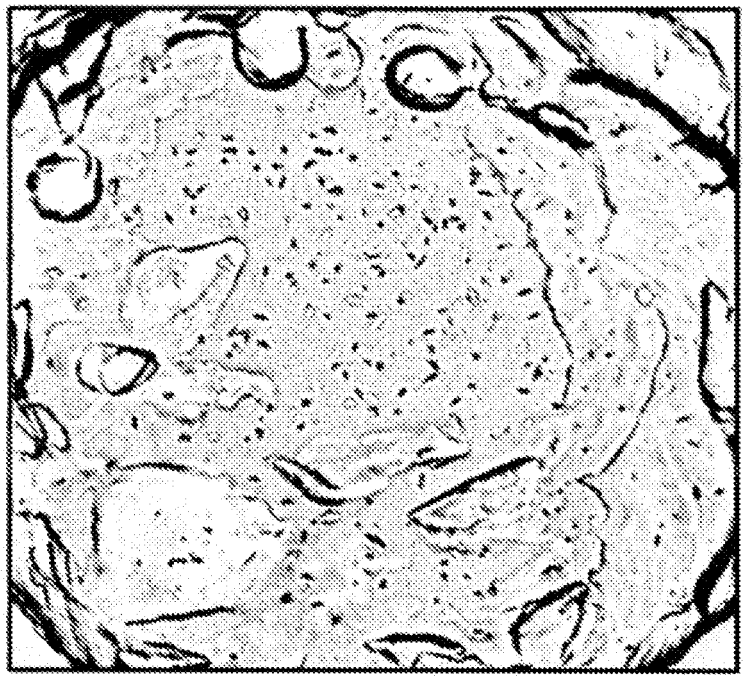
	Bril	Flavodoxin	Rubredoxin	T4L (Control)
ZM241385	61°C	60°C	61°C	55°C

FIG. 4C



	Bril	Flavodoxin	Rubredoxin	T4L (Control)
UK432097	64°C	51°C	64°C	63°C

FIG. 4D



$MgSO_4$, pH 5.0

FIG. 5

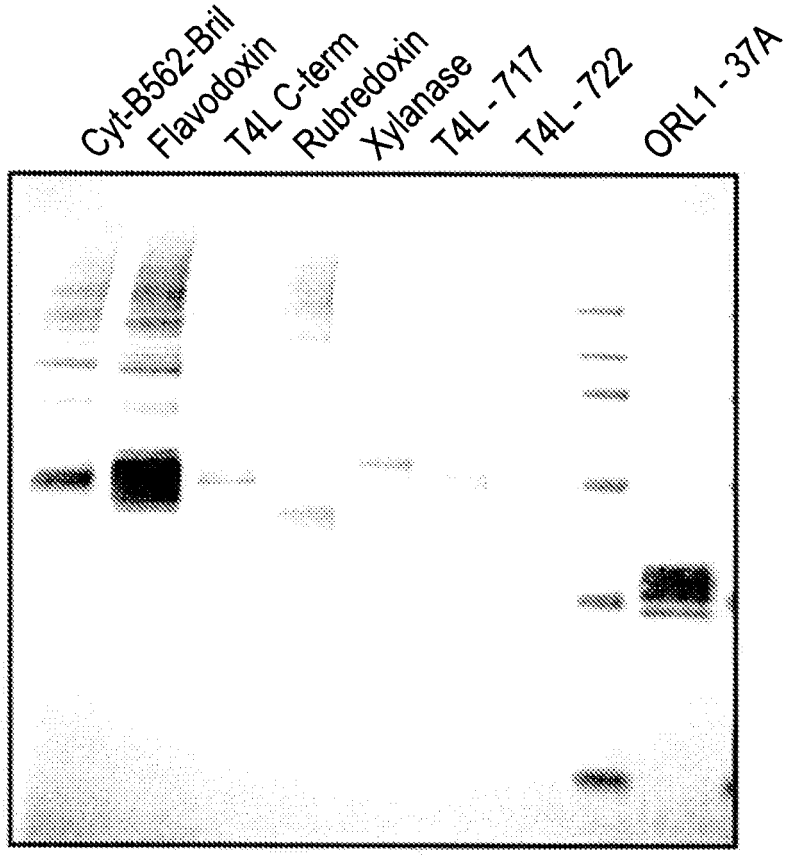


FIG. 6A

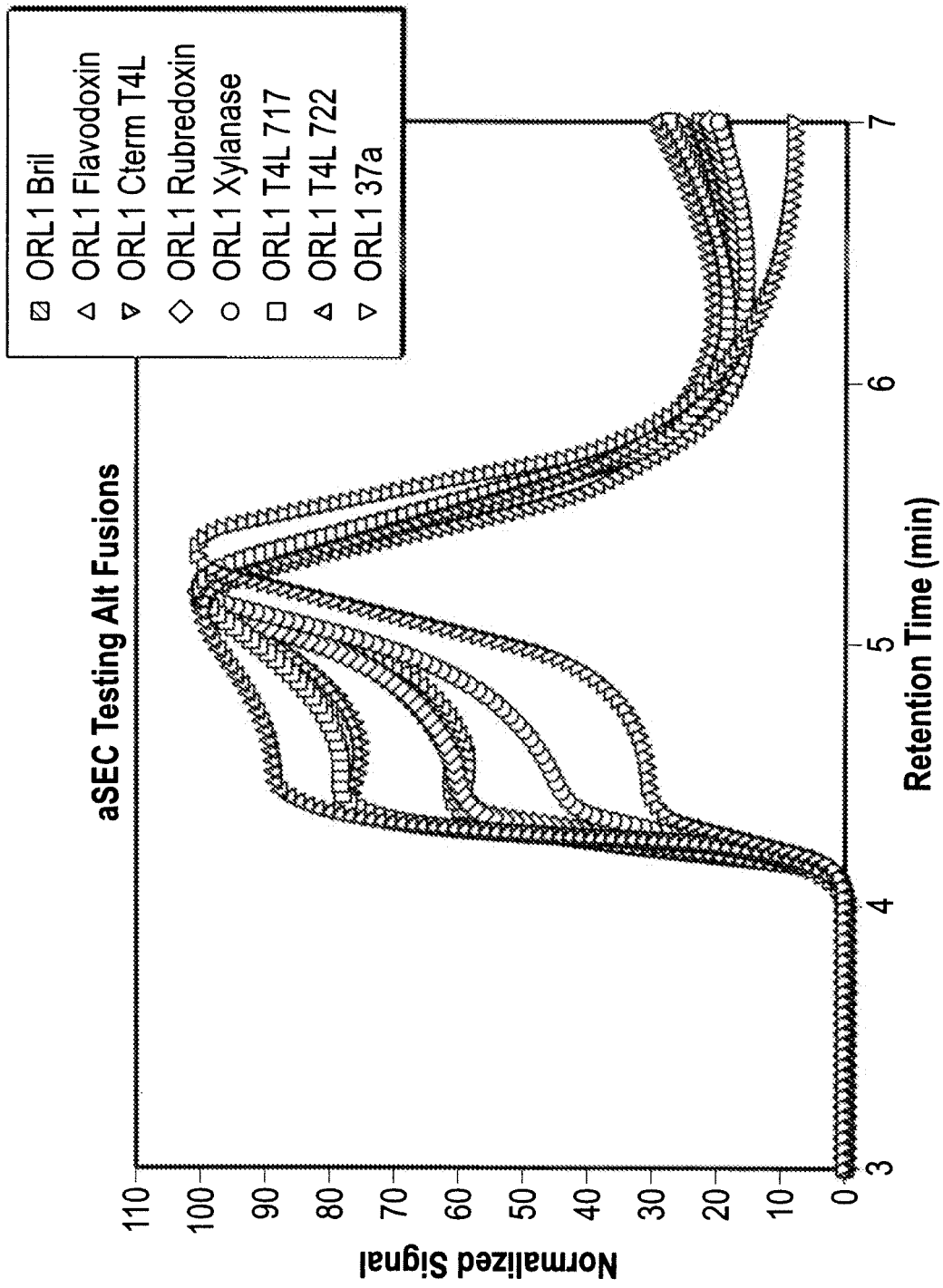

aSEC Testing Alt Fusions
ORL1 Bril
ORL1 Flavodoxin
ORL1 Cterm T4L
ORL1 Rubredoxin
ORL1 Xylanase
ORL1 T4L 717
ORL1 T4L 722
ORL1 37a
Normalized Signal
0
10
20
30
40
50
60
70
80
90
100
110
3
4
5
6
7
Retention Time (min)

FIG. 6B

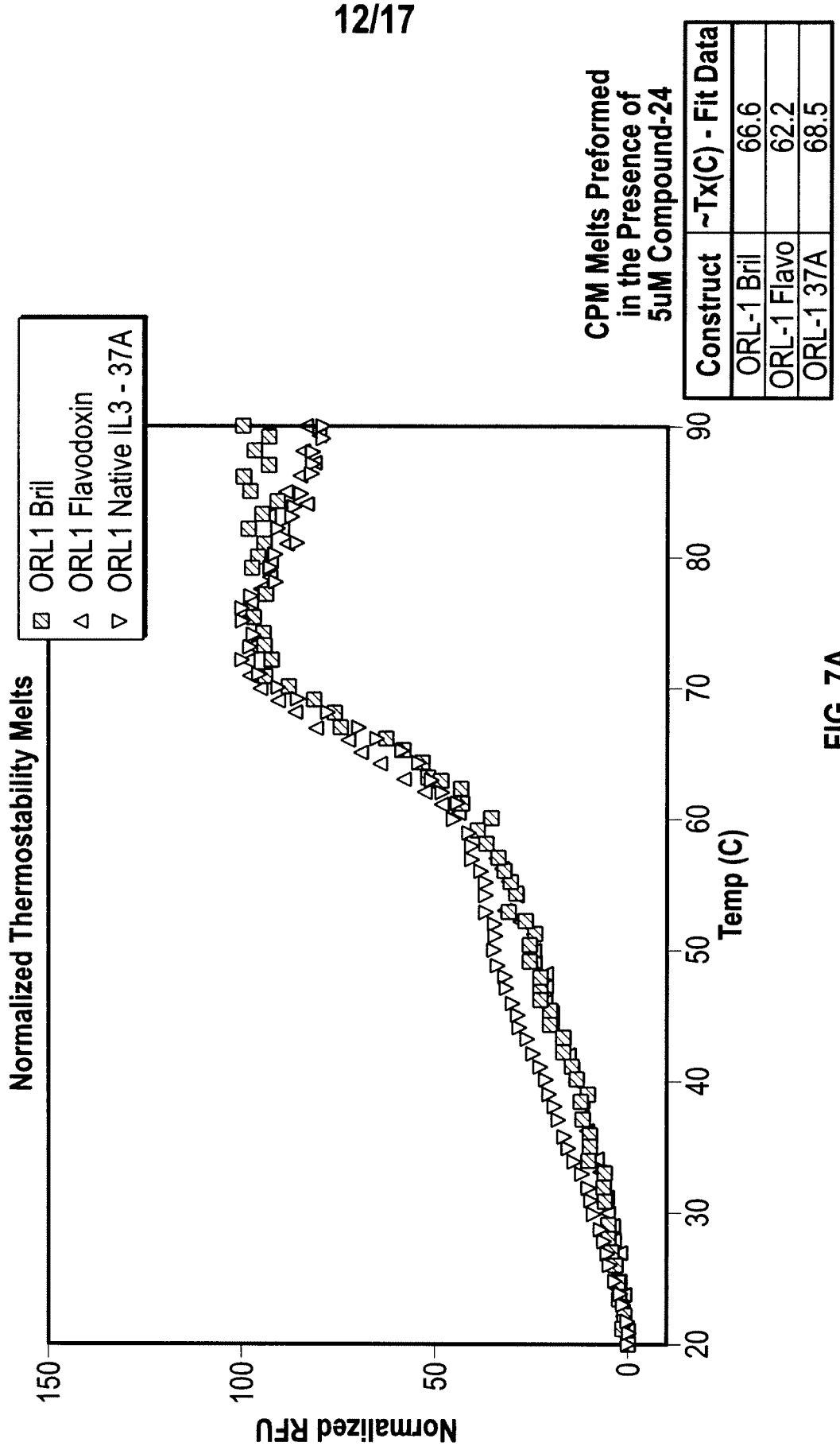
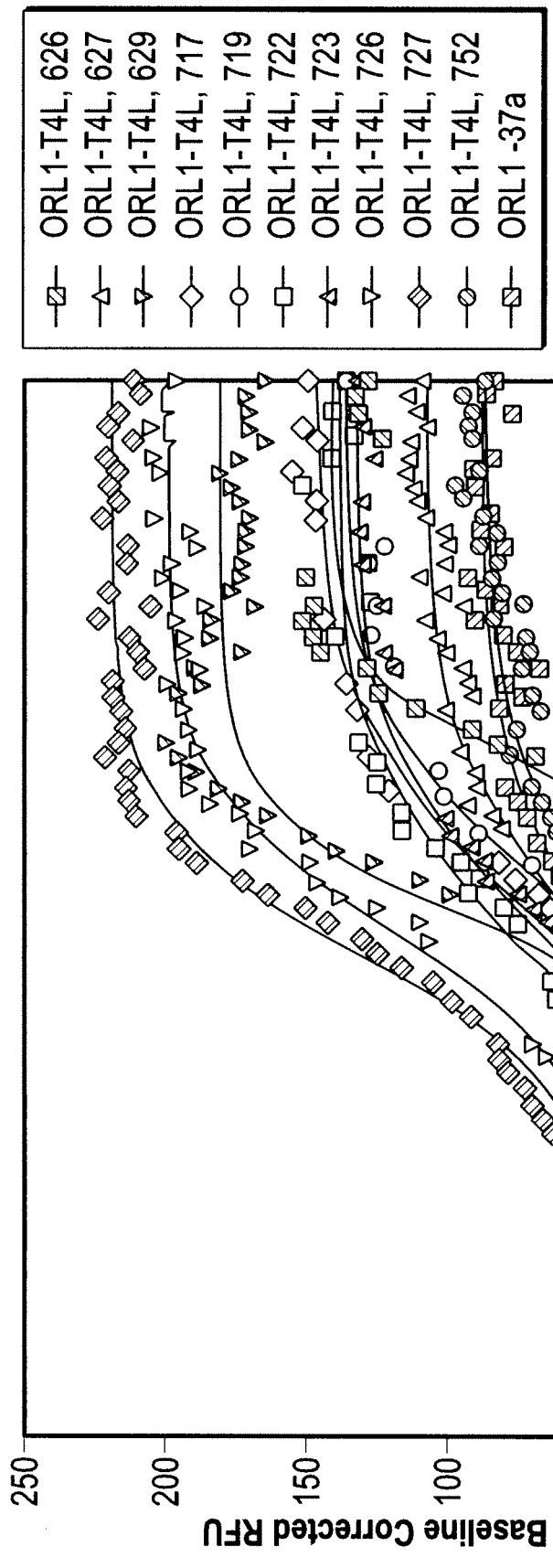

Normalized Thermostability Melts
ORL1 Bril
ORL1 Flavodoxin
ORL1 Native IL3 - 37A
CPM Melts Preformed in the Presence of 5uM Compound-24
Construct | ~Tx(C) - Fit Data
ORL-1 Bril | 66.6
ORL-1 Flavo | 62.2
ORL-1 37A | 68.5
Normalized RFU
150
100
50
0
20
30
40
50
60
70
80
90
Temp (C)

FIG. 7A



CPM Melts Preformed in the Presence of 2uM Compound-24

T4L Fusions	IMPT #	~Tm(C) - Fit Data	IMPT #	~Tm(C) - Fit Data	IMPT #	~Tm(C) - Fit Data
	626	52.3	719	57.4	727	52
	627	54.7	722	54.4	752	55.5
	629	55	723	54.7	pf37a	65
	717	56	726	53.6		

FIG. 7B

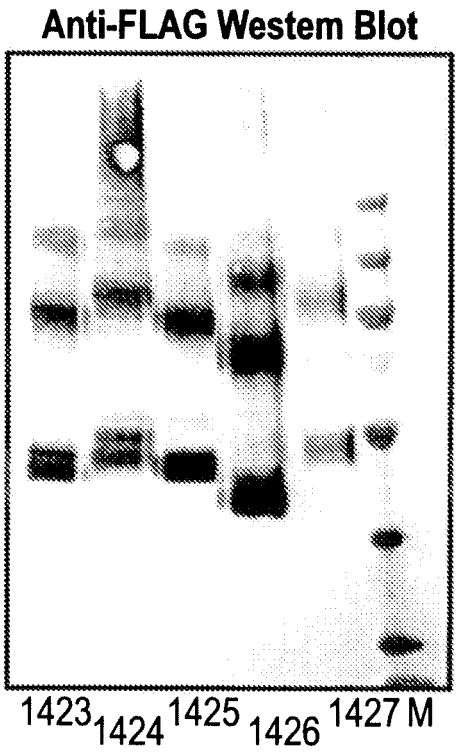

Anti-FLAG Western Blot
1423
1424
1425
1426
1427
M

FIG. 8A

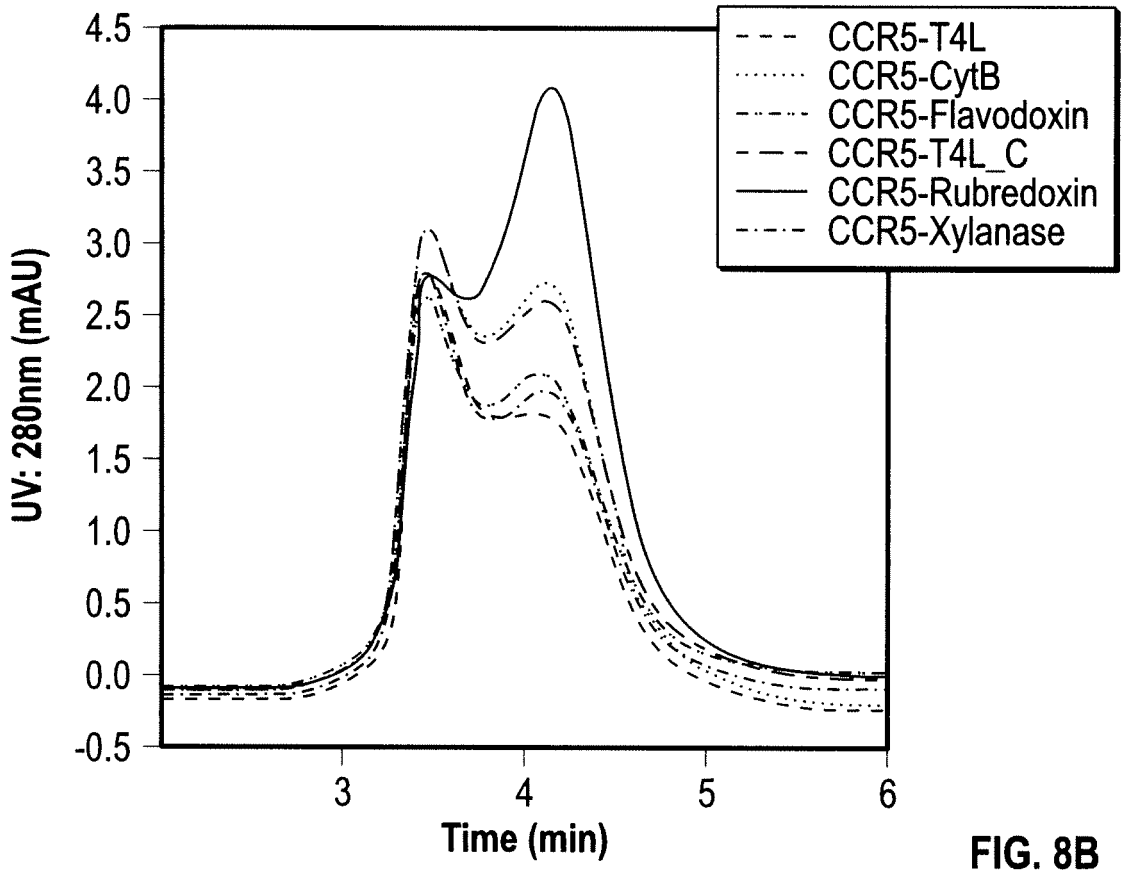

(CytB) (Flavo-)(T4L_C)(Rubre-) (Xylanase)
CCR5-T4L
CCR5-CytB
CCR5-Flavodoxin
CCR5-T4L_C
CCR5-Rubredoxin
CCR5-Xylanase
UV: 280nm (mAU)
4.5
4.0
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
-0.5
3
4
5
6
Time (min)

FIG. 8B

PDB ID	Classification	Title of Primary Citation	Source	res	Bfactor	het	swiss	Charge	Mass	N-terminus to C-terminus distance Å
2rhf	HYDROLASE	D. radiodurans RecQ HRDC domain 3	DEINOCOCCUS RADIODURANS	1.1	13.28	MSE,PO4		-4	7878	10.1
2ehs	LIPID	Crystal structure of acyl carrier protein from Aquifex aeolicus (form 1)	AQUIFEX AEOLICUS	1.3	13.95	NA,ZN	ACP_AQUAE	-14	7885	12.1
2ip6	ANTIMICROBIAL PROTEIN	Crystal structure of PedB	PEDIOCOCCUS PENTOSACEUS	1.35	13.68	SO4		-1	9202	12.9
3i7m	HYDROLASE	N-terminal domain of Xaa-Pro dipeptidase from Lactobacillus brevis.	LACTOBACILLUS BREVIS	1.46	14.1	MSE		-10	15812	11.4
1x3o	LIPID TRANSPORT	Crystal structure of the acyl carrier protein from thermus thermophilus HB8	THERMUS THERMOPHILUS	1.5	24.29		ACP_THET8	-12	8505	7.8
1u84	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	Crystal Structure of APC36109 from Bacillus stearothermophilus	GEOBACILLUS STEAROTHERMO-PHILUS	1.6	13.72	EDO,GOL		-4	8483	11.9
1h75	ELECTRON TRANSPORT	Structural basis for the thioredoxin-like activity profile of the glutaredoxin-like protein NrdH-redoxin from Escherichia coli.	ESCHERICHIA COLI	1.7	20.61		NRDH_ECOLI	1	8241	13.3
2huj	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	Crystal structure of a protein of uknown function (NP_471338.1) from Listeria innocua at 1.74 A resolution	LISTERIA INNOCUA	1.74	31.92	MSE		-3	14052	13.9
1ysq	GENE REGULATION	The crystal structure of transcriptional regulator YaiJ	ESCHERICHIA COLI	1.75	25.98	PO4	YIAJ_ECOLI	-6	18710	10.6

Figure 9

PDB ID	Classification	Title of Primary Citation	Source	res	Bfactor	het	swiss	Charge	Mass	N-terminus to C-terminus distance Å
3ls0	PHOTOSYNTHESIS	Crystal Structure of Cyanobacterial PsbQ from Synechocystis sp. PCC 6803	SYNECHOCYSTIS SP.	1.8	20.69			-1	11916	9.5
2qr3	TRANSCRIPTION	Crystal structure of the N-terminal signal receiver domain of two-component system response regulator from Bacteroides fragilis	BACTEROIDES FRAGILIS	1.8	23.95			-4	12606	13.4
1zuh	TRANSFERASE	Structural Basis for Shikimate-binding Specificity of Helicobacter pylori Shikimate Kinase	HELICOBACTER PYLORI	1.8	25.76		AROK_HELPY	-2	15792	13.0
2b8i	LIPID BINDING PROTEIN	Crystal Structure and Functional Studies Reveal that PAS Factor from Vibrio vulnificus is a Novel Member of the Saposin-Fold Family	VIBRIO VULNIFICUS	1.8	30.03			-5	7951	9.4
2cgq	PROTEIN TRANSPORT	A putative acyl carrier protein(Rv0033) from Mycobacterium tuberculosis	MYCOBACTERIUM TUBERCULOSIS	1.83	29.53			-7	7969	11.7
3fxh	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	Crystal structure from the mobile metagenome of Halifax Harbour Sewage Outfall: Integron Cassette Protein HFX_CASS2	UNCULTURED BACTERIUM	1.837	38.54	MSE		-4	12060	13.8
3nph	PHOTOSYNTHESIS	Crystal structure of the pfam00427 domain from Synechocystis sp. PCC 6803	SYNECHOCYSTIS SP.	1.849	24.75			-7	14341	13.6

Figure 9 Continued

PDB ID	Classification	Title of Primary Citation	Source	res	Bfactor	het	swiss	Charge	Mass	N-terminus to C-terminus distance Å
2o4d	UNKNOWN FUNCTION	Crystal Structure of a hypothetical protein from Pseudomonas aeruginosa	PSEUDOMONAS AERUGINOSA	1.85	28.84	MSE		-4	15273	7.4
1tmy	CHEMOTAXIS	Chey from Thermotoga Maritima (APO-I)	THERMOTOGA MARITIMA	1.9	32		CHEY_THEMA	0	11980	7.0
1vku	BIOSYNTHETIC PROTEIN	Crystal structure of Acyl carrier protein (TM0175) from Thermotoga maritima at 2.00 A resolution	THERMOTOGA MARITIMA	2	33.46	MSE		-10	9275	13.7
2es9	STRUCTURAL GENOMICS, UNKNOWN FUNCTION	Crystal structure of Q8ZRJ2 from salmonella typhimurium. NESG TARGET STR65	SALMONELLA TYPHIMURIUM	2	36.27	MSE		-4	10401	8.1

Figure 9 Continued