Table 5. The solvent-accessible area, r_s, of putative binding motifs for GroEL interactors in *E. coli* with known three-dimensional structure (1).

Swiss-Prot ID	Protein	Start	End	r_s
TPX_ECOLI	Thiol peroxidase (EC 1.11.1.-) (Scavengase P20)	58	64	0.6207
		78	84	0.0126
		119	127	0.2670
PTGA_ECOLI	Glucose-specific phosphotransferase enzyme IIA	37	41	0.2030
	component (EC 2.7.1.-) (PTS system glucose-	57	61	0.0906
	specific EIIA component) (EIIA-Glc) (EIII-Glc)	136	142	0.0234
FABA_ECOLI	3-hydroxydecanoyl-[acyl-carrier-protein])	31	35	0.3200
	dehydratase (EC 4.2.1.60)	62	68	0.4143
	(Beta-hydroxydecanoyl thioester dehydrase	145	153	0.2864
IPYR_ECOLI	Inorganic pyrophosphatase (EC 3.6.1.1)	36	40	0.3934
	(Pyrophosphate phospho- hydrolase) (PPase)	46	52	0.3507
RRF_ECOLI	Ribosome recycling factor (Ribosome releasing factor) (RRF)	164	168	0.2254
GRPE_ECOLI	GrpE protein (HSP-70 cofactor)	84	88	0.5178
	(Heat shock protein B25.3) (HSP24)	154	158	0.3636
DEOD_ECOLI	Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine phosphorylase) (PNP)	123	127	0.4972
DEOC_ECOLI	Deoxyribose-phosphate aldolase (EC 4.1.2.4)	42	46	0.0634
	(Phosphodeoxyriboaldolase)	90	94	0.2492
	(Deoxyriboaldolase) (DERA)	171	175	0.5128
		213	217	0.2650
		238	242	0.3418
PANB_ECOLI	3-methyl-2-oxobutanoate	39	43	0.0834
	hydroxymethyltransferase (EC 2.1.2.11)	68	72	0.0902
	(Ketopantoate hydroxymethyltransferase)	77	81	0.2520
		86	92	0.2771
		116	122	0.2934

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		165	169	0.2114
		176	180	0.0816
		192	200	0.2231
		210	218	0.0500
EFTS_ECOLI	Elongation factor Ts (EF-Ts)	53	61	0.2218
		79	83	0.3506
		152	156	0.0000
		231	237	0.3609
		269	273	0.6220
BLAT_ECOLI	Beta-lactamase TEM precursor (EC 3.5.2.6) (TEM-1) (TEM-2) (TEM-3) (TEM-4) (TEM-5) (TEM-6) (TEM-8/CAZ-2) (TEM-16/CAZ-7) (TEM-24/CAZ-6) (IRT-4) (Penicillinase)	228	232	0.2102
		245	251	0.0016
		258	262	0.0994
OMPA_ECOLI	Outer membrane protein A precursor (Outer membrane protein II*)	98	102	0.3110
		120	126	0.1730
RBSB_ECOLI	D-ribose-binding periplasmic protein precursor (EC 3.6.3.17)	3	11	0.0707
		13	17	0.3356
		33	39	0.2311
		58	64	0.0890
		113	117	0.0834
		146	154	0.3617
		184	190	0.0730
		207	213	0.2364
		227	231	0.2888
SERA_ECOLI	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) (PGDH)	80	86	0.1830
		118	122	0.2486

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		140	146	0.6296
		174	178	0.2258
		232	236	0.1098
		355	363	0.3893
		377	381	0.0002
GLYA_ECOLI	Serine hydroxymethyltransferase (EC 2.1.2.1)	102	106	0.0532
	(Serine methylase) (SHMT)	167	171	0.0378
		194	198	0.2290
		206	210	0.0554
		236	240	0.0000
		253	257	0.1892
		271	275	0.0514
		316	320	0.0050
PURA_ECOLI	Adenylosuccinate synthetase (EC 6.3.4.4)	3	11	0.0052
	(IMP–aspartate ligase) (AdSS) (AMPSase)	41	47	0.3369
		70	78	0.1237
		190	194	0.2200
		198	202	0.2720
		215	219	0.1554
		287	293	0.2727
		325	329	0.0606
		358	362	0.2150
		392	396	0.2392
ODP1_ECOLI	Pyruvate dehydrogenase E1 component	134	140	0.0254
	(EC 1.2.4.1)	145	149	0.0106
		223	229	0.0503
		252	258	0.0236

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		344	348	0.1880
		355	359	0.2808
		384	390	0.0040
		494	498	0.0712
		577	585	0.0124
		594	602	0.0423
		608	612	0.2712
		660	664	0.0068
		684	690	0.0434
		846	850	0.0642
PPIC_ECOLI	Peptidyl-prolyl cis-trans isomerase C (EC 5.2.1.8) (PPIase C) (Rotamase C) (Parvulin)	3	7	0.1298
YDHD_ECOLI	Probable monothiol glutaredoxin ydhD	15	19	0.0918
		38	44	0.2640
		72	80	0.1649
MOAC_ECOLI	Molybdenum cofactor biosynthesis protein C	40	44	0.1534
		52	56	0.2728
		77	81	0.4258
		120	124	0.2174
GREA_ECOLI	Transcription elongation factor greA (Transcript cleavage factor greA)	27	31	0.3862
		84	88	0.2024
PPIB_ECOLI	Peptidyl-prolyl cis-trans isomerase B (EC 5.2.1.8) (PPIase B) (Rotamase B)	9	15	0.2296
		46	52	0.2030
		82	90	0.2172
		119	123	0.0908
MOAB_ECOLI	Molybdenum cofactor biosynthesis protein B	10	16	0.0550
		52	56	0.3266

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		61	65	0.3600
		70	76	0.0284
		87	91	0.1538
		120	124	0.1180
		130	134	0.0158
DPS_ECOLI	DNA protection during starvation protein	58	62	0.3854
		88	94	0.3410
MUG_ECOLI	G/U mismatch-specific DNA glycosylase	102	108	0.0781
	(EC 3.2.2.-) (Mismatch-specific uracil	133	139	0.0491
	DNA-glycosylase) (UDG)	161	165	0.5968
AROK_ECOLI	Shikimate kinase I (EC 2.7.1.71) (SKI)	6	12	0.0234
		74	80	0.1503
		98	102	0.0416
YFBU_ECOLI	UPF0304 protein yfbU	13	21	0.3533
SEQA_ECOLI	SeqA protein	89	93	0.1716
		117	121	0.2940
		143	149	0.1521
YCIO_ECOLI	Protein yciO	2	8	0.3276
		27	33	0.0539
		36	40	0.0036
		191	195	0.4418
ENGB_ECOLI	Probable GTP-binding protein engB	110	114	0.0786
		136	140	0.2906
GLRX2_ECOLI	Glutaredoxin 2 (Grx2)	98	102	0.1830
		211	215	0.4864
ARAD_ECOLI	L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)	37	43	0.0657
	(Phosphoribulose isomerase)	80	84	0.0562

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		146	152	0.0963
		164	170	0.1211
		172	176	0.0074
		185	189	0.1718
FABG_ECOLI	3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) (3-ketoacyl- acyl carrier protein reductase)	5	13	0.1594
		18	26	0.1103
		118	122	0.2178
		150	154	0.1188
		217	221	0.1844
		239	243	0.3798
LPXA_ECOLI	Acyl-[acyl-carrier-protein]–UDP-N-acetylglucosamine O-acyltransferase (EC 2.3.1.129) (UDP-N-acetylglucosamine acyltransferase)	10	14	0.4132
		28	36	0.2393
		46	52	0.1707
		115	119	0.1860
		131	139	0.2343
		160	166	0.1986
		182	188	0.0867
		250	256	0.3220
KDSA_ECOLI	2-dehydro-3-deoxyphosphooctonate aldolase (EC 2.5.1.55) (Phospho-2- dehydro-3-deoxyoctonate aldolase) (3-deoxy-D-manno-octulosonic acid 8- phosphate synthetase) (KDO-8-phosphate synthetase) (KDO 8-P synthase) (KDOPS)	18	24	0.0760
		115	121	0.3137
		131	135	0.1268
		194	198	0.0000
HSLO_ECOLI	33 kDa chaperonin (Heat shock protein 33) (HSP33)	10	18	0.6104
		78	84	0.1304
		112	118	0.2150

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		154	160	0.3360
		208	212	0.3302
ROB_ECOLI	Right origin-binding protein	62	66	0.0058
		99	103	0.2094
		175	179	0.1718
		194	202	0.0698
		215	221	0.3647
		222	228	0.1259
		237	241	0.2014
YADB_ECOLI	Hypothetical protein yadB	22	30	0.0521
		38	42	0.1258
		73	79	0.3731
		168	172	0.2608
		173	177	0.0244
		245	249	0.1988
YDHF_ECOLI	Hypothetical oxidoreductase ydhF (EC 1.-.-.-)	15	19	0.0210
		164	172	0.2871
		188	196	0.2738
TAS_ECOLI	Tas protein	70	76	0.3007
		271	275	0.2682
		290	294	0.0352
		299	307	0.1401
PYRC_ECOLI	Dihydroorotase (EC 3.5.2.3) (DHOase)	37	45	0.0440
		201	205	0.0740
		208	214	0.4956
		217	225	0.1123
		243	249	0.0894

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
ALF_ECOLI	Fructose-bisphosphate aldolase class II (EC 4.1.2.13) (FBP aldolase)	27	31	0.1604
		79	87	0.1559
		306	314	0.4338
		330	334	0.4690
		339	343	0.2426
OMPF_ECOLI	Outer membrane protein F precursor (Porin ompF) (Outer membrane protein 1A) (Outer membrane protein IA) (Outer membrane protein B)	81	87	0.2489
		224	230	0.2421
		255	259	0.2130
		271	275	0.2158
SERC_ECOLI	Phosphoserine aminotransferase (EC 2.6.1.52) (PSAT)	10	14	0.2954
		78	84	0.0421
		100	104	0.1850
		142	146	0.1476
		190	194	0.0020
		206	210	0.0010
		243	251	0.0782
		351	355	0.2238
ODO2_ECOLI	Dihydrolipoyllysine-residue succinyltransferase component of 2- oxoglutarate dehydrogenase complex (EC 2.3.1.61) (E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex)	197	203	0.3311
		341	345	0.0218
		365	369	0.0766
		398	402	0.5100
ISCS_ECOLI	Cysteine desulfurase (EC 2.8.1.7) (ThiI transpersulfidase) (NifS protein homolog)	104	110	0.1759
		161	169	0.2030
		214	218	0.0094
		312	316	0.3420
		335	339	0.0650

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
RHO_ECOLI	Transcription termination factor rho	32	36	0.1304
		70	76	0.2274
		129	135	0.4269
		174	182	0.1538
		193	199	0.2797
		200	204	0.3408
		225	231	0.1620
		378	382	0.3290
		401	405	0.4108
CISY_ECOLI	Citrate synthase (EC 2.3.3.1)	130	136	0.1333
		138	142	0.1724
		169	173	0.0124
		182	186	0.3882
		247	251	0.1068
		268	272	0.3944
		365	369	0.0352
		380	384	0.0542
ACCC_ECOLI	Biotin carboxylase (EC 6.3.4.14) (A subunit of acetyl-CoA carboxylase) (EC 6.4.1.2) (ACC)	11	15	0.0182
		41	45	0.2288
		74	82	0.1218
		99	107	0.2003
		118	122	0.2514
		145	149	0.1894
		220	224	0.2648
		282	286	0.2048
		369	373	0.1746
		386	392	0.0343

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		407	413	0.3461
DCEA_ECOLI	Glutamate decarboxylase alpha (EC 4.1.1.15)	92	96	0.2044
	(GAD-alpha)	127	135	0.0779
		155	161	0.0094
		185	191	0.3183
		247	251	0.0000
		256	260	0.3656
		285	289	0.0016
		297	301	0.4138
		311	315	0.3012
		322	326	0.0444
		348	352	0.2384
		376	380	0.0000
		416	420	0.3830
DNAK_ECOLI	Chaperone protein dnaK (Heat shock protein 70)	13	17	0.0772
	(Heat shock 70 kDa protein) (HSP70)	37	43	0.0777
		64	68	0.1054
		99	103	0.1648
		136	140	0.1390
		172	176	0.0310
		189	193	0.0148
SYT_ECOLI	Threonyl-tRNA synthetase (EC 6.1.1.3)	90	98	0.2036
	(Threonine–tRNA ligase) (ThrRS)	100	104	0.0872
		170	174	0.1076
		220	224	0.0902
		261	267	0.2753
		295	299	0.3336

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		511	517	0.0516
		534	538	0.0122
		541	545	0.0020
		591	597	0.0299
		604	610	0.2110
LON_ECOLI	ATP-dependent protease La (EC 3.4.21.53)	599	603	0.1176
		681	685	0.0010
GYRA_ECOLI	DNA gyrase subunit A (EC 5.99.1.3)	116	120	0.4014
		132	136	0.0996
		164	170	0.0313
		172	176	0.5412
		192	196	0.0804
		218	224	0.1036
		238	242	0.2304
		313	321	0.3496
		333	339	0.1659
		408	414	0.3897
		418	422	0.4728
		446	450	0.2276
HLPA_ECOLI	Histone-like protein HLP-1 precursor (DNA-binding 17 kDa protein)	132	138	0.6241
UBIC_ECOLI	Chorismate–pyruvate lyase (EC 4.-.-.-)	71	75	0.2770
		102	106	0.2326
		115	121	0.4140
		154	158	0.0246
CRP_ECOLI	Catabolite gene activator (cAMP receptor protein) (cAMP-regulatory protein)	338	342	0.0772
		345	349	0.1044

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		410	414	0.4234
		432	436	0.4722
		502	506	0.1158
GCH1_ECOLI	GTP cyclohydrolase I (EC 3.5.4.16) (GTP-CH-I)	11	15	0.2962
		122	126	0.0312
		157	165	0.0627
		169	173	0.1662
TRMD_ECOLI	tRNA (Guanine-N(1)-)-methyltransferase	59	67	0.1766
	(EC 2.1.1.31) (M1G- methyltransferase)	106	110	0.2532
	(tRNA [GM37] methyltransferase)	134	140	0.4661
		193	199	0.4384
YCFH_ECOLI	Putative deoxyribonuclease ycfH (EC 3.1.21.-)	88	92	0.0474
		138	142	0.1042
		206	210	0.2222
		220	224	0.0342
DAPA_ECOLI	Dihydrodipicolinate synthase (EC 4.2.1.52)	5	13	0.0061
	(DHDPS)	36	40	0.0736
		129	133	0.0660
		241	247	0.3466
END4_ECOLI	Endonuclease IV (EC 3.1.21.2)	27	33	0.0731
	(Endodeoxyribonuclease IV)	160	164	0.1242
		182	186	0.0424
		265	269	0.4302
NANA_ECOLI	N-acetylneuraminate lyase (EC 4.1.3.3)	7	11	0.0304
	(N-acetylneuraminic acid aldolase)	49	55	0.1923
	(N-acetylneuraminate pyruvate-lyase)	89	93	0.2166
	(Sialic acid lyase) (Sialate lyase)	107	111	0.3328

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
	(Sialic acid aldolase) (NALase)	133	137	0.0606
		182	190	0.2211
		196	200	0.3204
METF_ECOLI	5,10-methylenetetrahydrofolate reductase	113	121	0.2293
	(EC 1.7.99.5)	148	152	0.0548
		182	186	0.0600
		232	236	0.3174
		283	289	0.1807
ARAC_ECOLI	Arabinose operon regulatory protein	69	73	0.0176
		94	102	0.2584
		111	119	0.2913
		148	156	0.2322
HEM2_ECOLI	Delta-aminolevulinic acid dehydratase	28	32	0.1162
	(EC 4.2.1.24) (Porphobilinogen synthase)	110	116	0.2497
	(ALAD) (ALADH)	149	153	0.0640
		163	171	0.1356
		273	277	0.1852
		310	314	0.0342
DHAS_ECOLI	Aspartate-semialdehyde dehydrogenase	14	18	0.1064
	(EC 1.2.1.11) (ASA dehydrogenase) (ASADH)	91	95	0.1924
		138	142	0.0062
		145	149	0.1338
		194	198	0.6584
		317	325	0.3768
BIOF_ECOLI	8-amino-7-oxononanoate synthase (EC 2.3.1.47)	31	35	0.1600
	(AONS) (8-amino-7- ketopelargonate synthase)	100	104	0.1908
	(7-keto-8-amino-pelargonic acid synthetase)	107	115	0.1290

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
	(7-KAP synthetase)	169	173	0.1554
	(L-alanine–pimelyl CoA ligase)	198	202	0.2530
		218	222	0.1780
		227	233	0.0530
		242	248	0.0646
		279	285	0.1724
		321	325	0.0448
		341	345	0.1040
METK_ECOLI	S-adenosylmethionine synthetase (EC 2.5.1.6)	23	27	0.0086
	(Methionine adenosyltransferase)	48	56	0.2108
	(AdoMet synthetase) (MAT)	58	62	0.4596
		87	95	0.4248
		119	123	0.2922
		130	134	0.2940
		199	203	0.2262
		220	224	0.2752
		228	236	0.2496
		273	277	0.0098
		284	288	0.0914
		308	314	0.2860
PHEA_ECOLI	P-protein [Includes: Chorismate mutase (EC 5.4.99.5) (CM); Prephenate dehydratase (EC 4.2.1.51) (PDT)]	88	96	0.3646
SUFS_ECOLI	Cysteine desulfurase (EC 2.8.1.7)	23	31	0.1402
	(Selenocysteine lyase) (EC 4.4.1.16)	49	55	0.3586
	(Selenocysteine reductase)	131	135	0.3808
	(Selenocysteine beta-lyase) (SCL)	165	173	0.0412

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		234	238	0.0002
		253	257	0.3378
		333	337	0.0178
		362	366	0.2318
		367	373	0.3204
		381	387	0.0290
TYPH_ECOLI	Thymidine phosphorylase (EC 2.4.2.4)	37	41	0.2714
	(TdRPase)	94	102	0.0036
		150	156	0.0534
		207	213	0.2786
		217	221	0.1268
		235	239	0.0134
		243	249	0.0627
		276	280	0.0188
		314	320	0.1604
		335	339	0.4344
		340	344	0.3094
		360	364	0.0950
		398	402	0.0724
AMPA_ECOLI	Cytosol aminopeptidase (EC 3.4.11.1)	15	23	0.0177
	(Leucine aminopeptidase) (LAP)	58	64	0.3444
	(Leucyl aminopeptidase) (Aminopeptidase A/I)	177	183	0.0920
		199	207	0.1733
		234	240	0.0911
		264	268	0.0336
		296	304	0.0093
		355	359	0.0114

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		371	375	0.0630
		381	385	0.2440
		393	399	0.1041
		404	410	0.2083
		485	493	0.0093
DHSA_ECOLI	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	31	39	0.1131
		93	97	0.2486
		134	138	0.0628
		142	150	0.1084
		162	166	0.1598
		181	187	0.1663
		188	192	0.1702
		261	265	0.1594
		381	389	0.0542
		477	481	0.2598
		556	560	0.0610
FRDA_ECOLI	Fumarate reductase flavoprotein subunit (EC 1.3.99.1)	44	50	0.2164
		51	57	0.1064
		73	81	0.0912
		124	128	0.1318
		169	173	0.0200
		186	192	0.0743
		239	243	0.1614
		251	255	0.0438
		291	295	0.1012
		309	313	0.1852
		373	377	0.0030

TABLE 5: (continued)

Swiss-Prot ID	Protein	Start	End	r_s
		421	425	0.4710
		500	504	0.2272
		520	524	0.1200
		550	554	0.0292
CAN_ECOLI	Carbonic anhydrase 2 (EC 4.2.1.1)	10	14	0.4928
		15	19	0.4618
		35	41	0.1310
		58	62	0.2818
		92	98	0.0490
		117	121	0.3064
		177	181	0.0720

Binding regions are identified through starting and ending positions along the protein sequence.

I. REFERENCES

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