

Supplemental Table 1 Solvent Accessibility and Protein - Propionate Contacts

FOLD	PDB	PROTEIN	ORIGIN	solvent accessibility				propionate contacts (2.5-3.2Å)						
				area	aver.	%	aver.	Arg	His	Lys	Tyr	other		
4-helix bundle	1jgc	bacterioferritin	<i>Rhodobacter capsulatus</i>	189		22.8		1	0	0	0	0	0	
	1qpu	cyt b562	<i>Escherichia coli</i>	148	166.0	17.8	20.0	0	0	0	0	0	0	
	1bfr	bacterioferritin	<i>Escherichia coli</i>	161		19.4		0	0	0	0	0	0	
β-propeller	1qhu	hemopexin	<i>Oryctolagus cuniculus</i>	210		25.3		2	1	0	0	3	0	
CAP	1ft9	CooA	<i>Rhodospirillum rubrum</i>	233		28.1		0	0	0	0	0	1	
catalase	8cat	catalase	<i>Bos taurus</i>	3		0.4		4	1	0	0	0	0	
	1qwl	catalase	<i>Helicobacter pylori</i>	15		1.8		4	0	0	0	0	0	
	1a4e	catalase	<i>Saccharomyces cerevisiae</i>	8		1.0		4	1	0	0	0	0	
	1m7s	catalase	<i>Pseudomonas aeruginosa</i>	5	11.6	0.6	1.4	4	0	0	0	0	1	
	1m85	catalase	<i>Proteus mirabilis</i>	27		3.3		4	0	0	0	0	0	
	1dgf	catalase	<i>Homo sapiens</i>	2		0.2		3	1	0	0	0	0	
	1hbz	catalase	<i>Micrococcus</i>	30		3.6		4	0	0	0	0	1	
	1jph	catalase	<i>Escherichia coli</i>	3		0.4		2	0	0	0	0	1	
cupredoxin-like	1fft	ubiquinol oxidase	<i>Escherichia coli</i>	32		3.9		3	0	0	0	0	1	
cytochrome b5	1eue	cyt b5	<i>Rattus norvegicus</i>	219		26.4		0	0	0	0	0	2	
	1cxy	cyt b5	<i>Ectothiorhodospira v.</i>	103	184.3	12.4	22.2	0	0	2	1	2	2	
	1cyo	cyt b5	<i>Bos taurus</i>	216		26.0		0	0	0	0	0	2	
	1sox	sulfite oxidase	<i>Gallus gallus</i>	199		24.0		0	1	0	0	0	0	
dioxygenase	2d0t	indoleamine 2,3-dioxygenase	<i>Homo sapiens</i>	92		11.1		3	0	0	0	0	1	
globin-like	1q1f	neuroglobin	<i>Mus musculus</i>	132		15.9		0	0	2	2	2	0	
	1oj6	neuroglobin	<i>Homo sapiens</i>	90		10.8		0	0	2	2	2	2	
	1d8u	hemoglobin	<i>Oryza sativa</i>	102		12.3		1	0	0	0	0	1	
	1vhb	hemoglobin	<i>Vitreoscilla stercoraria</i>	169		20.4		0	0	1	0	0	0	
	1a3n	hemoglobin	<i>Homo sapiens</i>	134		16.1		0	1	1	0	0	1	
	1myt	myoglobin	<i>Thunnus albacares</i>	143	134.8	17.2	16.2	0	1	2	0	0	1	
	1spe	myoglobin	<i>Physeter catodon</i>	147		17.7		0	2	0	0	0	1	
	1lhs	myoglobin	<i>Caretta caretta</i>	171		20.6		0	1	0	0	0	1	
	1v5h/1ut0	cytoglobin	<i>Homo sapiens</i>	135		16.3		0	0	2	0	0	1	
	1cqx	flavo-hemoglobin	<i>Alcaligenes eutrophus</i>	219		26.4		0	0	1	0	0	2	
	1gvh	flavo-hemoglobin	<i>Escherichia coli</i>	39		4.7		0	1	0	0	0	2	
	1fsl	leghemoglobin	<i>Glycine max</i>	136		16.4		0	0	1	0	0	0	
	heme oxygenase	1n45	heme oxygenase	<i>Homo sapiens</i>	247		29.8		1	0	2	1	1	1
		1j77	heme oxygenase	<i>Neisseria meningitidis</i>	210		25.3		0	0	1	1	0	0
1we1		heme oxygenase	<i>Synechocystis</i>	127	184.8	15.3	22.3	4	0	1	1	1	0	
1iw0/1		heme oxygenase	<i>Corynebacterium diphtheriae</i>	155		18.7		1	0	1	1	0	0	
heme peroxidase	2cyp	cyt c peroxidase	<i>Saccharomyces cerevisiae</i>	24		2.9		0	3	1	0	0	2	
	1itk	catalase-peroxidase	<i>Haloarcula m.</i>	20		2.4		0	2	1	0	0	2	
	2gj1	lactoperoxidase	<i>Bos taurus</i>	61	72.0	7.3	8.7	3	0	0	0	0	2	
	1mwv	catalase-peroxidase	<i>Burkholderia p.</i>	30		3.6		0	2	1	0	0	2	
	1prh	prostaglandin synthase	<i>Seminal vesicl</i>	141		17.0		0	0	0	0	0	4	
	5cox	prostaglandin synthase	<i>Mus musculus</i>	156		18.8		0	0	0	0	0	4	
HemS	2j0p	HemS	<i>Yersinia enterocolitica</i>	155		18.7		4	0	1	1	1	1	
H-NOX / SONO fold	1u55	guanylate cyclase	<i>Thermoanaerobacter tengcongensis</i>	6	18.5	0.7	2.2	4	0	0	0	0	0	
	1xbn	SONO	<i>Thermoanaerobacter tengcongensis</i>	31		3.7		3	0	0	0	1	2	
immunoglobulin-like	1d7b	cellobiose dehydrogenase	<i>Phanerochaete chrysosporium</i>	179		21.6		0	0	0	2	3	3	
lipocalin	1np4	nitrophorin	<i>Rhodnius prolixus</i>	130		15.7		0	0	2	0	0	1	
meander	1dk0	hasA	<i>Serratia marcescens</i>	191		23.0		0	1	0	0	1	4	
NO	1nos	NO synthase	<i>Mus musculus</i>	159		19.2		1	0	0	0	0	0	
	3nos	NO synthase	<i>Homo sapiens</i>	122		14.7		0	0	0	0	1	0	
	1m7z	NO synthase	<i>Bacillus subtilis</i>	102	127.8	12.3	15.4	0	0	0	0	1	0	
	1qw6	NO synthase	<i>Rattus norvegicus</i>	128		15.4		0	0	0	0	2	0	
P450	2cpp	P450 mono-oxygenase	<i>Pseudomonas putida</i>	28		3.4		3	1	0	0	0	3	
	1cpt	Cytochrome P450-Terp	<i>Pseudomonas Sp.</i>	17		2.0		1	2	0	0	0	0	
	1pq2	P450 mono-oxygenase	<i>Homo sapiens</i>	17		2.0		5	2	0	0	0	2	
	1po5	P450 mono-oxygenase	<i>Oryctolagus cuniculus</i>	23		2.8		3	2	0	0	0	1	
	1dt6	P450 oxidoreductase	<i>Oryctolagus cuniculus</i>	2		0.2		4	3	0	0	0	1	
	1odo	P450 mono-oxygenase	<i>Streptomyces coelicolor</i>	16		1.9		4	2	0	0	1	0	
	1rom	P450 mono-oxygenase	<i>Fusarium oxysporium</i>	10		1.2		1	2	0	0	0	0	
	1f4t	P450 mono-oxygenase	<i>Sulfolobus solfataricus</i>	39	25.5	4.7	3.1	3	1	0	0	0	1	
	2hpd/1fah	P450 oxidoreductase	<i>Bacillus megaterium</i>	19		2.3		2	0	0	0	0	1	
	1e9x	P450 α-sterol demethylase	<i>Mycobacterium tuberculosis</i>	51		6.1		2	1	1	1	1	3	
	1n40	P450 oxidoreductase	<i>Mycobacterium tuberculosis</i>	15		1.8		4	2	0	0	0	0	
	1lfk	P450 oxidoreductase	<i>Amycolatopsis orientalis</i>	29		3.5		3	2	0	0	0	2	
	1izo	P450 oxidoreductase	<i>Bacillus Subtilis</i>	65		7.8		2	2	1	1	1	0	
PAS	1drm	FixL	<i>Bradorhizobium japonicum</i>	40	105.0	4.8	12.7	2	4	0	0	0	1	
	1v9y/z	EcDos	<i>Escherichia coli</i>	170		20.5		0	0	0	0	0	0	
serum albumin-like	1n5u	albumin	<i>Homo sapiens</i>	66		7.9		0	1	1	0	0	0	
vitamine B6 family	1jbq	cystathione beta-synthase	<i>Homo sapiens</i>	148		17.8		4	0	0	0	0	0	

Sum of contacts  
total number of contacts  
PERCENTAGE

PERCENTAGES FOLDS

	103	46	28	24	67
	103	46	28	24	67
	38.4	17.2	10.4	9.0	25.0
	propionate contacts (2.5-3.2Å)				
4-helix bundle	100.0	0.0	0.0	0.0	0.0
β-propeller	33.3	16.7	0.0	50.0	0.0
CAP	0.0	0.0	0.0	0.0	100.0
catalase	82.9	8.6	0.0	0.0	8.6
cupredoxin-like	75.0	0.0	0.0	0.0	25.0
cytochrome b5	0.0	10.0	20.0	10.0	60.0
dioxygenase	75.0	0.0	0.0	0.0	25.0
globin-like	2.9	17.1	34.3	11.4	34.3
heme oxygenase	37.5	0.0	31.3	25.0	6.3
heme peroxidase	10.3	24.1	10.3	0.0	55.2
HemS	57.1	0.0	14.3	14.3	14.3
H-NOX / SONO	70.0	0.0	0.0	10.0	20.0
immunoglobulin-like	0.0	0.0	0.0	40.0	60.0
lipocalin	0.0	0.0	66.7	0.0	33.3
meander	0.0	16.7	0.0	16.7	66.7
NO	20.0	0.0	0.0	80.0	0.0
P450	47.4	28.2	2.6	3.8	17.9
PAS	28.6	57.1	0.0	0.0	14.3
serum albumin-like	0.0	50.0	50.0	0.0	0.0
vitamin B6 family	100.0	0.0	0.0	0.0	0.0
	Arg	His	Lys	Tyr	other

