Supplementary Table S1. BLAST analysis of oxidoreductases in *E. coli*

		BLAST (Exclude *Escherichia* (taxid:561))	Literature	Protein BLAST against known *E. coli* ALR/ADH Enyzmes*							BLAST *E. coli* genome against ALR/ADH Enyzmes found				
ECO GENE #	**Oxidoreductases**	**Domains, likely substrate preference, cofactor, etc**	**available?**	**YqhD**	**AdhP**	**EutG**	**YiaY**	**YjgB**	**FucO**	**BetA**	**DkgA**	**YahK**	**GldA**	**YbbO**	**YghA**
EG10425	HdhA	7-alpha-hydroxysteroid dehydrogenase, NAD(P)-binding, Rossman family												5.00E-08	**3.00E-22**
EG10993	Tdh	L-threonine 3-dehydrogenase	**Yes**		**5.00E-26**			7.00E-09				1.00E-12			
EG11134	YdjA	FMN Nitroreductse family, NAD(P)	**Yes**												
EG11292	YghA	Short Chain dehydrogenase/reductase family, NAD-binding, Rossman Family													
EG11309	YdbC	Aldo/Keto reductase family, aryl-alcohol dehydrogenase									2.00E-06				
EG11315	YhdH	Quinone oxidoreductase family, Zn-binding dehydrogenase/oxidoreductase, alcohol dehydrogenase		0.12	5.00E-04	0.36		0.016				2.6		0.13	
EG11581	YbiC	Malate/lactate dehydrogenase family													
EG11648	DkgB	2,5-diketo-D-gluconic acid reductase B, Aldo/Keto reductase family, methylglyoxal reductase	**Yes**								**2.00E-45**				
EG11759	YciK	Short Chain Dehydrogenase, 3-oxoacyl-[ACP] reductase, NAD(P)-binding, Rossman fold												2.00E-13	1.00E-09
EG11904	GldA	Glycerol dehydrogenase, NAD-binding	**Yes**			0.002	1.00E-04		2.00E-09						
EG12019	YohF	Short Chain/Acetoin dehydrogenase, 3-oxoacyl-[ACP] reductase, NAD(P), Rossman fold												4.00E-10	8.00E-18
EG12035	YeiP	elongation factor-P like protein													
EG12036	YeiQ	D-mannoate oxidoreductase/dehydrogenase, Rossman domain, NAD-binding													
EG12133	UcpA	Short Chain Dehydrogenase, 3-oxoacyl-[ACP] reductase, NAD(P)-binding, Rossman fold	**Yes**											4.00E-17	1.00E-16
EG12185	YqiB	dehydrogrnase/oxidoreductase													
EG12229	YhiN	NAD/FAD dehydrogenase, or pyridine nucleotide-disulfide oxidoreductase								3.5					
EG12272	GhrB	Bifunctional glyoxylate/hydroxypyruvate reductase B, 2-hydroxyacid dehydrogenase family	**Yes**												
EG12345	YdfG	Short Chain Dehydrogenase, 3-oxoacyl-[ACP] reductase, NAD(P)-binding, Rossman fold	**Yes**											2.00E-10	0.004
EG12361	KduD	2-deoxy-D-gluconate 3-dehydrogenase, NAD(P)-binding, Rossman family	**Yes**											2.00E-04	5.00E-13
EG12409	AegA	Oxidoreductase, Fe-S binding subunit, Glutamate synthase NADPH small chain	**Yes**												
EG12417	gatD	Galactitol-1-phosphate 5-dehydrogenase, Zn-binding dehydrogenase family	**Yes**		4.00E-15			1.00E-07				4.00E-10			
EG12452	RspB	dehydrogenase/oxidoreductase, Zn-binding, starvation sensing protein			**1.00E-24**			1.00E-10				6.00E-11			
EG12540	IdnO	5-keto-D-gluconate 5-reductase, gluconate 5-dehydrogenase, NAD(P)-binding, Rossman family	**Yes**											6.00E-07	3.00E-14
EG12541	IdnD	L-idonate 5-dehydrogenase, GroES-like protein			5.00E-18			9.00E-09				2.00E-07			
EG12545	YjhC	Gfo/ldh/mocA family oxidoreductase, NAD-binding, Rossman Family, KpLE2 phage-like element													
EG12590	YjjN	Soribtol/galactonate oxidoreductase, Zn-binding, Alcohol dehydrogenase, GroES domain	**Yes**		5.00E-17			3.00E-11				9.00E-12			
EG12692	YbdH	Oxidoreductase, 3-hydroquinate synthase family, glycerol/alcohol dehydrogenase, Fe-dependent													
EG12729	YgjR	Oxidoreductase/dehydrogenase, NADH-binding													
EG12729	YgjR	NAD-binding oxidoreductase, Rossman Family													
EG12809	yhcC	Radical SAM superfamily, Fe-S oxidoreductase													
EG12927	YrfF	dehydrogenase, intracellullar growth attenuator	**Yes**												
EG12944	YhhX	NAD(P)-binding, dehydrogenase/oxidoreductase													
EG12971	YgfF	NAD(P)-binding, Short Chain Dehydrogenase family, Rossman Fold												2.00E-08	
EG12976	YggP	L-sorbose 1-phosphate oxidoreductase/dehydrogenase			0.13										
EG12983	YggW	HemN Family oxidoreductase, coproporphyrinogen III oxidase													
EG13010	YghZ	Aldo/keto reductase like, L-glyceraldehyde 3-phosphate reductase	**Yes**								4.00E-05				
EG13015	DkgA	2,5-diketo-D-gluconic acid reductase A, Aldo/Keto reductase family, methylglyoxal reductase	**Yes**												
EG13061	YgfK	Selenate reductase													
EG13063	YgfM	Selenate reductase, FAD-binding													
EG13069	YgfS	Oxidoreductase, Fe-S subunit, effector protein, electron transporter													
EG13077	YqfA	Oxidoreductase, inner membrance protein, hemolysin channel protein													
EG13093	Tas	Aldo/Keto reductase family	**Yes**								1.00E-08				
EG13104	YgbJ	NAD-binding oxidoreductase/dehydrogenase, D-beta-hydroxy butyrate dehydrogenase													
EG13121	YgcN	NAD/FAD oxidoreductase, electron transfer flavoprotein-quinone oxidoreductase								3.5					
EG13128	YgcU	FAD-binding oxidoreductase/dehydrogenase, alkylglycerone-phosphate synthase													
EG13130	YgcW	Oxidoreductase, Short chain dehydrogense family, 2-deoxy-D-gluconate 3-dhydrogenase												4.00E-11	3.00E-14
EG13262	YbbO	NAD(P)-binding, Short Chain Dehydrogenase family, Rossman Fold													2.00E-09
EG13420	YdhF	Aldo/Keto oxidoreductase family													
EG13464	YphC	Alcohol Dehydrogenase, Zn-binding, NAD(P)-binding	**Yes**		**8.00E-20**			1.00E-07				2.00E-05			
EG13483	YdjG	Aldo/Keto reductase family	**Yes**								2.00E-10				
EG13486	YdjJ	Alcohol/sorbitol Dehydrogenase, Zn-binding, GroES-like protien			**8.00E-23**			3.00E-07				4.00E-10			
EG13488	YdjL	Alcohol Dehydrogenase, Zn-binding, NAD(P)-binding			9.00E-17			3.00E-09				1.00E-06			
EG13491	YeaE	aldehyde reductase, Aldo/Keto reductase family	**Yes**								**7.00E-22**				
EG13510	YeaX	Dioxygenase subunit, oxidoreductase, FAD/NAD-binding, iron-sulfer cluster													
EG13537	YbdR	Alcohol Dehydrogenase, Zn-binding, GroES-like protien			2.00E-15			3.00E-05				8.00E-05			
EG13580	YkgC	Pyridine nucleotide-disulfide oxidoreductase													
EG13582	YkgE	L-lactate dehydrogenase, dehydrogenase subunit, Fe-S oxidoreductase subunit													
EG13595	YahK	Alcohol Dehydrogenase, Zn-binding, NAD(P)-binding	**Yes**		**7.00E-30**			**2.00E-46**							
EG13611	YajO	NAD(P)-xylose reductase, Aldo/Keto reductase family, 2-carboxybenzaldehyde reductase	**Yes**												
EG13683	YbjN	Sensory transduction regulator													
EG13688	YbjS	NAD dependent epimerase/dehydratase family													
EG13689	YbjT	dTDP-glucose enzyme, epimerase/dehydratase, NAD(P)-binding, Rossman family												0.058	
EG13869	GhrA	Bifunctional glyoxylate/hydroxypyruvate reductase A, 2-hydroxyacid dehydrogenase family	**Yes**												
EG13879	YceM	Virulence Factor, oxidoreductase, NAD-binding													
EG13914	YcjQ	Alcohol Dehydrogenase, Zn-binding			2.00E-05										
EG13916	YcjS	Oxidoreductase/dehydrogenase, NADH-binding													
EG13931	YdgJ	NAD-binding, oxidoreductase, Rossman fold													
EG13956	YdhV	Aldehyde ferredoxin oxidoreductase	**Yes**												
EG14200	YfgD	Aresenate reductase													
EG14262	YciW	Oxidoreductase, amidase/aminotransferase													
EG14420	YmjC	Dehydratase/epimerase. NAD(P)-binding, Rossman Fold													
EG50010	FrmA	Class III alcohol dehydrogenase, S-(hydroxymethyl)glutathione dehydrogenase	**Yes**		**6.00E-28**			7.00E-08				6.00E-16			

*Expected activity ~E-20 or less was selected as more likely candidates

🟥 Candidates for screening