

## **Supporting Information**

# Ramachandran Plot (glycines excluded)

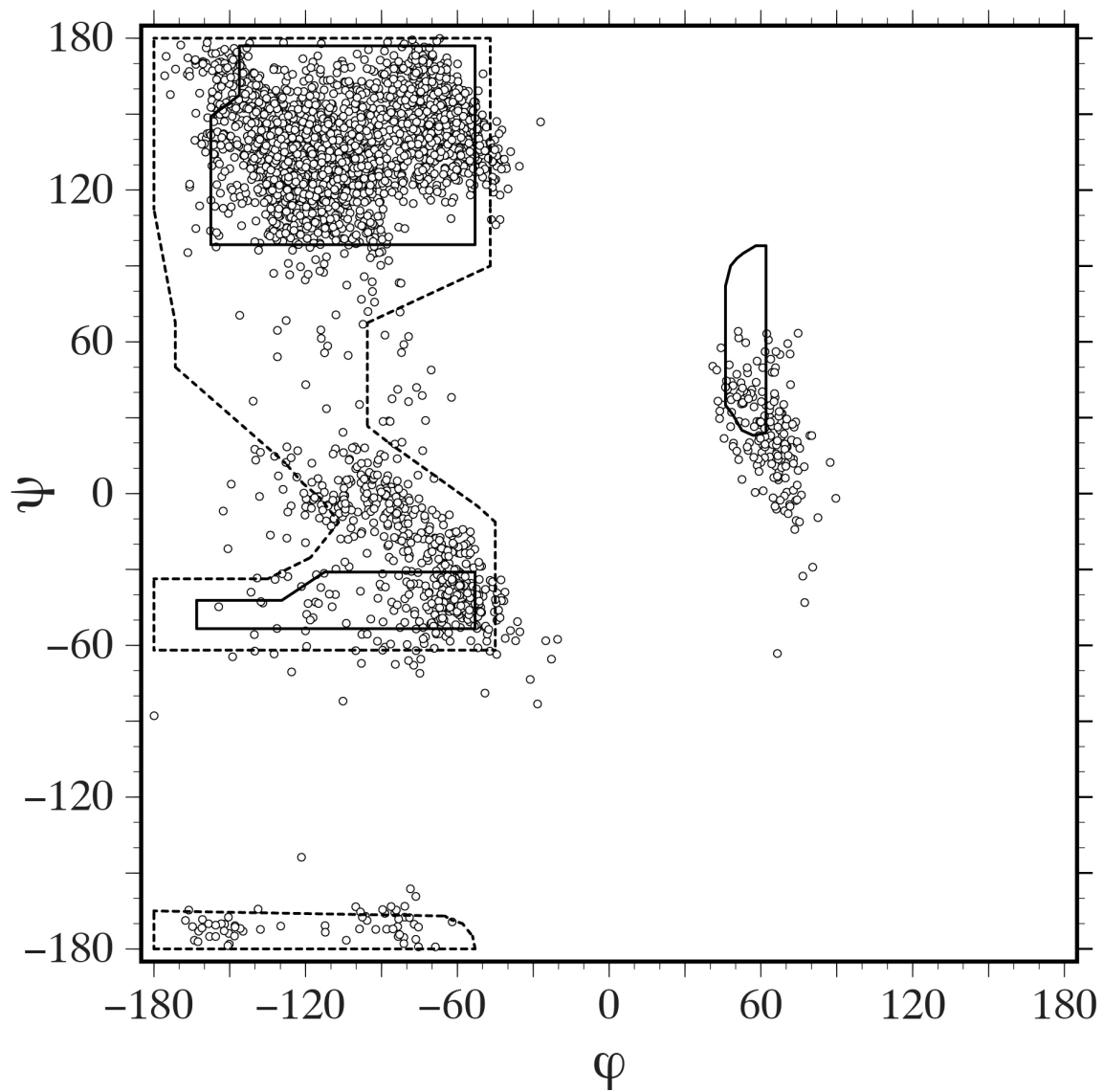


Figure S1

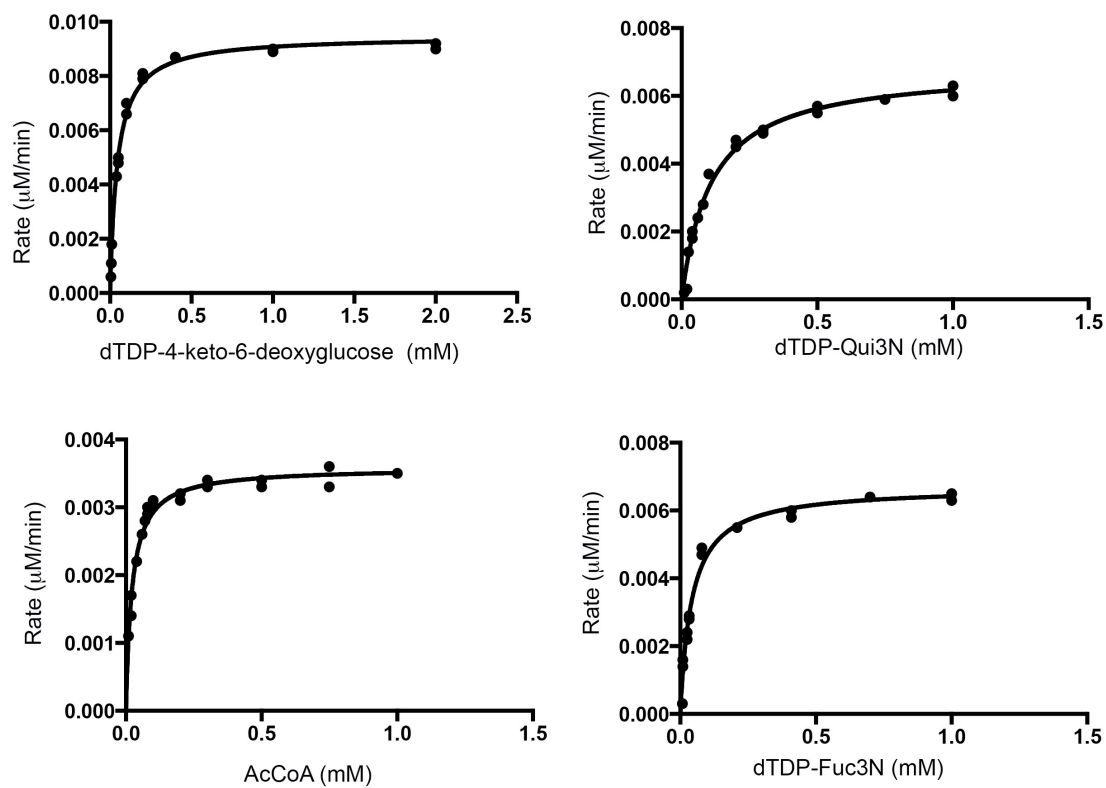


Figure S2 Substrate Saturation Curves

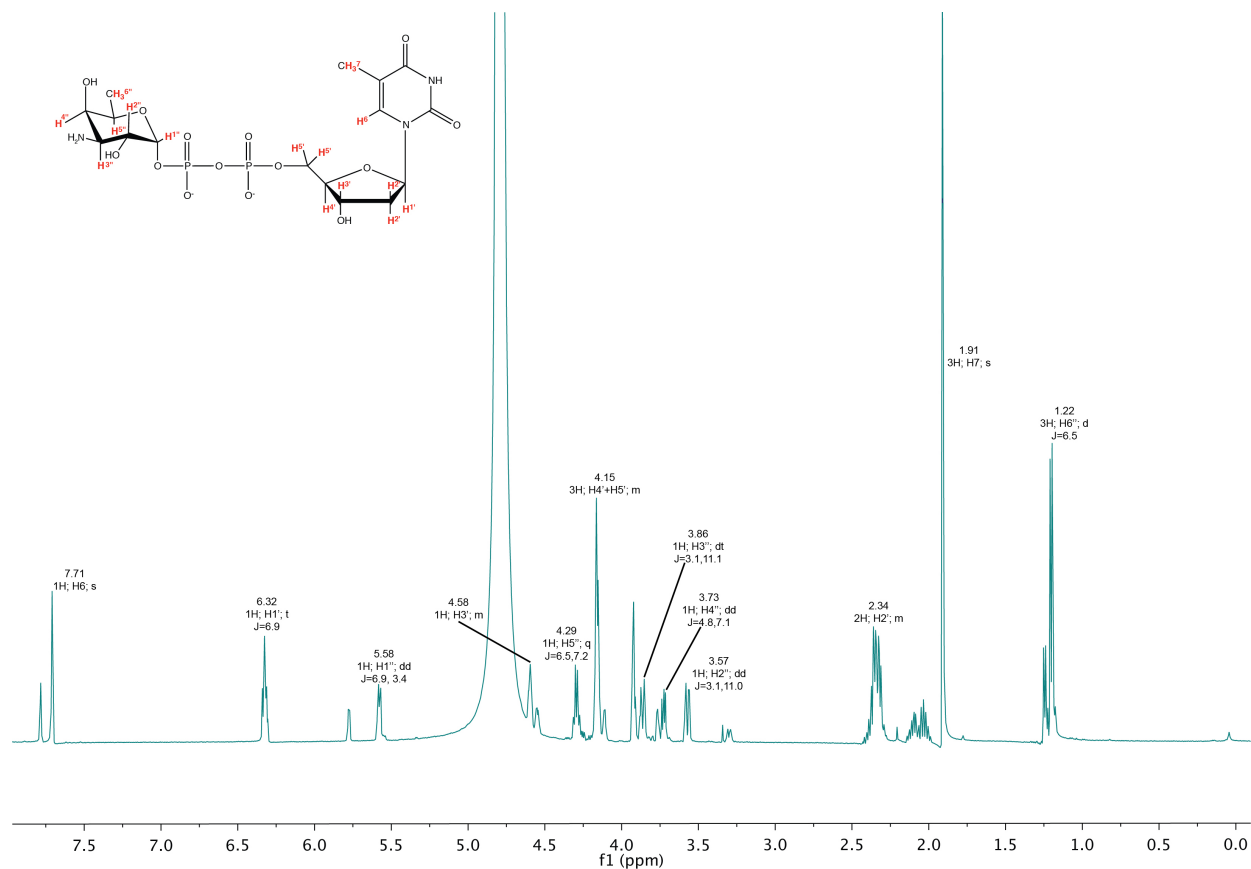


Figure S3

<sup>1</sup>H NMR spectrum of the ketoisomerase product from FtdD following transamination to generate a stable 3-amino sugar. As the sugar was purified via HPLC and lyophilized to dryness, minor breakdown products of the nucleotide-linked sugar, or minor contaminants acquired during HPLC assays, were present in the NMR spectrum. These are noted in the small, unlabeled peaks on the spectrum.

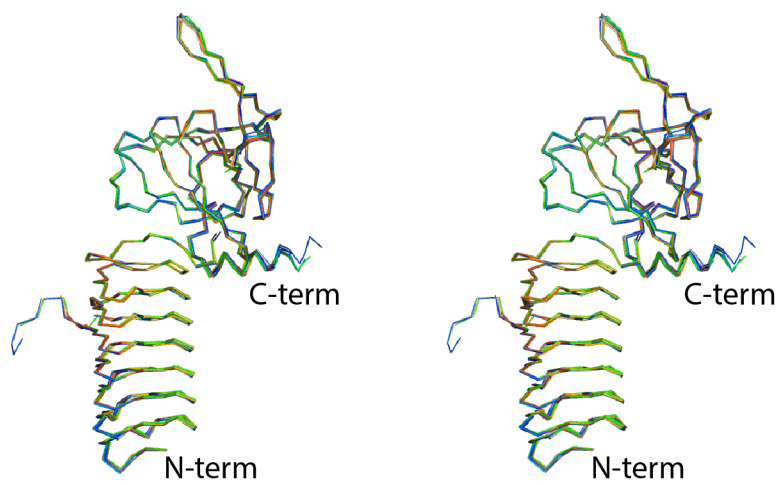


Figure S4

Shown in stereo is an overlay of all twelve subunits in the asymmetric unit.

Figure S5

Amino Acid Sequence Alignments of the Class A Bifunctional Enzymes (colored in red are the cupin domains)

<u>AFC34907</u>	1	MSLINLINFPILGDDRGSLIAIESNKTIPFEIKRVYYIFDTKKDIARGFHAKNLSQILFCVKGSCRIVLDDGFRR	76
<u>WP_005327799</u>	1	MSLIKLIDLPSLGDQRGGLVAIESNQSIQFEIKRLYYIFNTT-NQSRGFHAHIDLKQVAVCVKGS CRFILDNGHTR	75
<u>WP_005289027</u>	1	MSLKKLIDLPLDGDQRGGLVAIEANQHIFPEIKRIYYIFSASKDKPRGFHAHKDLKQLAICLHGQCRF ILDDGYSK	76
<u>WP_009512147</u>	1	MSLKKLIDLPLDGDQRGGLVAIEANQHIFDIKRIYYIFSASKNKPRGFHAHKDLKQLAICLHGQCRF ILDDGYSK	76
<u>AFC34907</u>	77	ECVTLSEPNKGILVENLVWREMHDFSDDCVLLVVLASQHYDESDYIRHYDDFLNEIHRPFMHHLSDVKCQNI GKNTRVWQY	156
<u>WP_005327799</u>	76	EEVTLNSPTQGLYIDALTWREMHDFSEDCVLLVVLASQHYDESDYIRDYQEFLEKVKHPFIHPLADVKSQKIGQKTKIWQF	155
<u>WP_005289027</u>	77	EEVLLNSPTQGLIIESMTWREMHDFSEDCVLLVVLASEHYDESDYIRSYDEFISVVNRPFHPLSDVHSPHIGQNT RVWQY	156
<u>WP_009512147</u>	77	EEVLLNSPTQGLIIESMTWREMHDFSEDCVLLVVLASEHYDESDYIRSYDEFISVVNRPFHPLSDVHSPHIGQNT RVWQY	156
<u>AFC34907</u>	157	VVIFEHAQIGENCNICSHCLIENDVIGNNVTIKSGVFLWDGIYVGDNVFIGPNATFTNDRVPRSKQYPDKFMKT VIKEG	236
<u>WP_005327799</u>	156	SVVLQNAMIGENCNICAHTLIENDVIGNNVTIKSGVYVWDGITLEDNVFIGPCVAFTNDKKPRSKQYPEKFPQTIVEMG	235
<u>WP_005289027</u>	157	SVILKNAVIGAGCNICAHTLIENDVHIGDNVTVKSGVYLWDGITLEDNVFIGPSVAFTNDKKPRSKQYPDSFAKT VVEQG	236
<u>WP_009512147</u>	157	SVILKNAVIGAGCNICAHTLIENDVHIGDNVTVKSGVYLWDGITLEDNVFIGPSVAFTNDKKPRSKQYPDSFAKT VVEQG	236
<u>AFC34907</u>	237	ASIGANATILPGITIGKNAMIGAGAVVTKDVL DNEIVIGNPARVKG----	282
<u>WP_005327799</u>	236	ASIGANATILPGIRIGQNALIGAGAVVTKDVPANAIVVGNPAIIKGYV--	283
<u>WP_005289027</u>	237	ASIGANATILPGIRIGKNALIGAGAVVTKDVPENAIMVGNPAIIKGYIeq	286
<u>WP_009512147</u>	237	ASIGANATILPGIRIGKNALIGAGAVVTKDVPENAIMVGNPAIIKGYIeq	286
<u>AFC34907</u>		<i>Pasteurella multocida</i>	
<u>WP_005327799</u>		<i>Acinetobacter</i> sp. CIP 102143	
<u>WP_005289027</u>		<i>Acinetobacter</i> sp. NIPH 3623	
<u>WP_009512147</u>		<i>Acinetobacter baumannii</i>	

Amino Acid Sequence Alignments of the Class B Bifunctional Enzymes (colored in red are the cupin domains)

<a href="#">YP 563661</a>	1	M-----IHKLADVQSQNIGDNTKVWQFCVILAGAVIGRNCNICANSLIENDVVIGDNVTIKSGVQIWDGIHIQDDVFI	73
<a href="#">YP 522503</a>	1	MSQ--pF-IHTLADVHSTTIGTGTRIWQFVVALAGAKIGQDCNVC SHCLIENDVVIGDRVTVKSGVQLWDGLRVGDDVFI	77
<a href="#">YP 001269238</a>	1	MSGnrnFFVHSHALCESENIGDTRVWAFAHILPGASLGRECNVCDNVFIENDVVIGDRVTLKCGVQIWDGITIEDDVFI	80
<a href="#">WP 006465577</a>	1	-----MKIHPSADVQTSQIGTDTTIWQYVVILAGARIGRDVNINAHCFIENDVTIGDRVTIKSGVYLWDGIRVEDDVFI	74
<a href="#">WP 007835313</a>	1	MNP--pF-IHSEADVKSTAIGDGTRIWQFSVVFEGAKIGSDCNICSHTLVESDVIIGDRVTVKSGVQLWDGLRVANDVFI	77
<a href="#">NP 790904</a>	1	MSSgkdFFVHSHALCESENIGKDSRVWAFAHILPGARLGSECNVCDNVFIENDVIGDRVTLKCGVQVWDGITIEDDVFI	80
<a href="#">WP 003365665</a>	1	MSSgkdFFVHSHALCESENIGKDSRVWAFAHILPGASLGSECNVCDNVFIENDVIGDRVTLKCGVQVWDGITIEDDVFI	80
<a href="#">WP 006890961</a>	1	MKN---YYVHPQAICESNNTNTRIWAFAHILPNAKIGEECNICDGVFVENDVVVGNRVTIKCGVQLWDGVELEDDVFI	77
<a href="#">WP 008212526</a>	1	MPQ--pVHVHALADVQTASIGAGTHIWQFVVALPGARIGNDCNICSHCFIENDVVIGDRVTIKNGVQLWDGLRVGDDVFI	78
<a href="#">WP 005793127</a>	1	MLN--eVQIHPTAEVLTENIGSGTTIWQMVVVLKGAIVIGKNVNICAQCFIEDDVVIGDRVTVKSGVYLWDGVRLGDDVFI	78
<a href="#">YP 002138423</a>	1	MKY----FVHDKALVLESSKIGNNTRVWAFAHILPGATVGSECNICDNVFIENDVVLGERVTVKCGVQLWDGVVLEDDVFI	76
<a href="#">YP 006720291</a>	1	MK-----IHPLSDVQAKQIGQGTSIWQYVVVLPGAVIGSDCNICSHCFIENAVVIGDRVTIKCGVQIWDGLRVEDDVFI	74
<a href="#">YP 005635798</a>	1	M-S---YFVHPNALCESENIGEGTRVWAFAHVLPGARLGRDCNICDGVFVESDVIIGDRVTVKCGVQLWDGVRLGDDVFI	76
<a href="#">YP 521972</a>	1	MSA---YFKHSHALVETDNIGAGTRIWAFAHILPGARIGSGCNICDGVFIESDVVVGGDDVTIKCGVQLWDGITIESGVFI	77
<a href="#">NP 636007</a>	1	M-S---HFVHPNALCESDITIGEGTRVWAFAHVLPGARLGRDCNICDGVFIESDVVVGGDRVTVKCGVQLWDGVRLGDDVFI	76
<a href="#">WP 008903201</a>	1	MNDsv--YFHPQALCESLSVGARTRIWAFAHILPEARIGADCNICDHVFVENQVTVGDRVTIKCGVQLWDGISVEDDVFI	78
<a href="#">YP 995492</a>	1	MPD-y--FVHPQALCESTAVGAGTRIWAFAHVLPGARIGADCNVCDHVF IENDVWLADRVTIKCGVQLWDGIRLESDFVFI	77
<a href="#">YP 826939</a>	1	MHS-----AIVETRSLGGGTTVGAFAHILPGAVIGVDCRIGGQTFIENDVRIGDRVTLENGQVWDGITIEDDVFI	71
<a href="#">WP 007192445</a>	1	MTEqa-YFVHPAGICESSTIGAGTRIWAFSHVLPGARVGGDCNICDHVF IENDVNLGDRVTIKSGVQLWDGIRVGDDVFI	79
<a href="#">WP 009102868</a>	1	MPS---PFIHPLSDCQSTNIGEGTRVWQFSVVLPEAKVGEDCNICSHCFIENDVVIGNRVTVKCGVQLWDGIRVEDDVFI	77
<a href="#">WP 005048231</a>	1	MTGsgdYFVHPQIGICESTKIGGGTRVWAFSHVLPGAVLGADVNVNDHVF IENDVIGDRVTLKSGVQVWDGIQLGDDVFI	80
<a href="#">YP 003806326</a>	1	MQSs-----KLCHLCAGATIAASARLGDHVVVYPGATVADDCLVAGFTQLWPGVRLERGA	57
<a href="#">YP 563661</a>	74	GNVTFFTNDKQPRSKIYPDEYLKTIIVKKGASIGANSTILPGILIGENAMVGAGAVITKNVPDNAIVIGNPGRITGYVEA-	152
<a href="#">YP 522503</a>	78	GNASFANDRFPRSKITPEKFLQTEVEKEGASIGAGATILPGITIGRNAMVAAGAVVTRSVPNAIVVGNPAKIVGYVDA-	156
<a href="#">YP 001269238</a>	81	GNATFTNDLFPFRSKVYPQTFRSRTIIRKASLGANCTILPGLTIGINAMVGAGAVVTRSIPPNAIVVGNPAKIIIGYVDAK	160
<a href="#">WP 006465577</a>	75	GNVTFFTNDKFPFRSKVYPERFVETTLERGASIGGGATILPGVHIGRGALVGAGAVVTKSVPPYAVVTGCPARITGYVDAG	154
<a href="#">WP 007835313</a>	78	GNASFANDRFPRSRKKPTKFLGSTLHEGASIGAGAVILPGIEIGRNAMVAAGAVVTRSVPANAIVVGNPAKIVGYVDA-	156
<a href="#">NP 790904</a>	81	GNATFTNDLFPFRSKVYPQTFARTIIRKASLGANCTILPGITIGINAMVGAGAVVTRSVPNAIVVGNPAKIIIGYVDAK	160
<a href="#">WP 003365665</a>	81	GNATFTNDLFPFRSKVYPQSFARTIIRKASLGANCTILPGITIGINAMVGAGAVVTRSVPNAIVVGNPAKIIIGYVDAK	160
<a href="#">WP 006890961</a>	78	GNVTFFTNDKFPFRSKVYPENFARIVISKGASIGANATLLPNITVGVNAMIGAGAVVTRSVPNAIVVGNPAKIVGYVDAK	157
<a href="#">WP 008212526</a>	79	GNVTFSTNDKFPFRSKQHLATALLTEIESGASLGAGATILPGLKIGRHAMVGAGAVVTRSVPANAIVVGNPARIVGYADA-	157

<u>WP 005793127</u>	79	GPNVTFTNDKFPFRSKQHLEALVTRVEAGASIGGGAVVLPGLIVGRGAMVAGAVVTKSVPPYAIVTGSPARIMGYVENT	158
<u>YP 002138423</u>	77	GPNATFTNDLFPFRSKKYPEQFAKTIVRQASIGANATILAGVCIGKNAMVAGAVVTKNVPNAIVVGNPARIHGYVTSK	156
<u>YP 006720291</u>	75	GPNVTFTNDLFPFRSKQHPKEFAKTVIQKGASIGANATILAGSTIGRNAMVAGAVVTKSVPPNAIVVGNPARITGYVSTI	154
<u>YP 005635798</u>	77	GPNATFTNDLFPFRSRVYPEKFLGTVVESGASIGANATILAGTTIGSGAMIGAGAVVTRSVPPNAIVVGNPARIVGYV---	153
<u>YP 521972</u>	78	GPNVTFTNDNFPRSKQYLKAPERTLVQAHSSIGANATILPGVTVAPGAMIGAGSVVTRSVPPNAIVQGNPARIVGYTNTK	157
<u>NP 636007</u>	77	GPNATFTNDLFPFRSRVYPEKFLGTVVESGASIGANATILAGTTIGSGAMIGAGAVVTRSVPPNAIVVGNPARIVGYV---	153
<u>WP 008903201</u>	79	GPNATFANDNFPRSRQRPDQYARTVIQKGASIGANATILPGIIVGPKAMVAGAVVVRDVPARAIIVVGNPARIVGYAEEA	158
<u>YP 995492</u>	78	GPNATFSNDRFPFRSRQRPPEAFARTVVRQASIGANATLLPGITVGAQAMVAGAVVTRSVPPKAIIVVGNPAKIVGYVQTP	157
<u>YP 826939</u>	72	GPNATFSNDPFPFRSRQHPAEFARTLIRRGASIGANATILPGLTIGEKAVVEAGAVVTRDIPPLAIVAGNPARISGYVGAG	151
<u>WP 007192445</u>	80	GPNATFTNDRFPFRSKRYPESFAVTTLEDGASIGANATILPGLTIGKRAMVAGAVVTRSVPPNAVAGNPAQIIGYQSAS	159
<u>WP 009102868</u>	78	GPNVTFTNDRFPFRSQYQYVDRFAQTVIKRGASIGANATLLPGITVGDAMVAGAVVTSVDPVPGAVVGNPAAVRRYAQIP	157
<u>WP 005048231</u>	81	GPNATFTNDPFPFRSKQYQYVDRFAQTVIKRGASIGANATLLPGITVGDAMVAGAVVTSVDPVPGAVVGNPAAVRRYAQIP	160
<u>YP 003806326</u>	58	GPGVTIQPPD-----EADASTVSGPNCRIGANATILRGVVRVGEAGVVEPGSVVAQSVPPHAIIVSGAPARITGYVDSR	130
<u>YP 563661</u>	153	NTGVIMPS----NNFELK---LQM-SKVKGVSLHKFHLVNDLRGNLSVGEFEKDIPTPKRYFTVFGVNPKEVRGEHAHK	224
<u>YP 522503</u>	157	DRNKGDIG----EGQAVIVGA-QE-TQVRGVSLHRMPRVIDIRGSLTVGEFDRSIPFAVKRYFMVFDVPSMETRGEHAHR	230
<u>YP 001269238</u>	161	PVSTKAEN----EVTPTYSEGAE--TSVKGVKLHTMKVTDIRGSLVGEFERSIPFKTERYFLVYDVPTAETRGEHAHR	234
<u>WP 006465577</u>	155	EQPREEDR---vEMPSEDRVVAL--DVKGVTLHRLKQVSDIRGDLVGEFEPVDIPFVPSRYFLVYNVPSEKTRGEHAHH	229
<u>WP 007835313</u>	157	S-DQODGA----APQPSRPGA-SA-TRVTGVNLHRLLRVADIRGSLTVGEFERTIPFNAKRYFMVFDVPSIETRGEHAHR	229
<u>NP 790904</u>	161	PVNANSET----RAEQKAPGVTA--TSVKNVTLHTMNEVADIRGSLVGEFERSVPPFKTERYFLVYDVPTAETRGEHAHR	234
<u>WP 003365665</u>	161	PVNASSET----RPEKAAPGVTA--TSVKNVTLHTMNEVADIRGSLVGEFERSVPPFKSERYFLVYDVPTAETRGEHAHR	234
<u>WP 006890961</u>	158	NDKIASSE----KLNHQKQKLE--TTVSGVTLHNFRAVPDMRGSLVGEFEREIPFRPLRYFLVFDVPTAETRGEHAHI	231
<u>WP 008212526</u>	158	QSGGLDK----VTEAAATGTVQS-SRVAGVSLVTLPRITDIRGSLTVGEFQRVVPEAKRYFMVFDVPSVETRGEHAHR	232
<u>WP 005793127</u>	159	ASAKPDGRpralVVPVAVANSVEQV--VGVDVALHRMKFVQDMRGNSLVGEFEKDVPPAKRYFLVFSVPSEKTRGEHAHR	236
<u>YP 002138423</u>	157	PAAASVPQ--kspSOMPEEF-----KSLTGTTLHRMPIITDMRGSLSSGELAKMLPFIPKRYFLVFDVNPKEVRGEHSHK	229
<u>YP 006720291</u>	155	PAQQ---K-hseIEVGENIGTVGQ-SAIPGVQFVRLPIIPDLRGSLVFAEFQYLPFIPKRYFLVFDVQSREVRGEHAHK	229
<u>YP 005635798</u>	154	SDKDANQP----AALPVDQGITD--TAVPGVKLYRMPFADMRGSLVSGDFDSFLPFNARRYFLVYGVPTQETRGEHAHK	227
<u>YP 521972</u>	158	AQGSTEPQ---LfkDERKPPYSdrTAARGVTVHKFPLIPDIRGSLTVGEFQHIIPFVPKRYFLVFDVPSKETRGEHAHR	233
<u>NP 636007</u>	154	SDKDATGS----APSPTGQGITD--TAVPGVKLYRMPFADMRGSLVSGDFETFLPFNAKRYFLVYGVPTQETRGEHAHK	227
<u>WP 008903201</u>	159	FQVGGGTat----QISSQEQPSVRaTGVRGVTLHKLKNVADMRGSLVMEMEDGIPFTARRSFLVYDVPSEEIRGEHAHR	234
<u>YP 995492</u>	158	---GAKTGt-----PGPRpTGVDGVTLHHLHQVQDMRGSLVSAEFGSDVPFAVRRYFLVFDVPSMQVRGEHAHH	223
<u>YP 826939</u>	152	SISADATat-----APPELGVRpTRVAGVMLHRLPQVDDLGRNLSFGEIGEQQVFAVKRYFVVYGVPSKNIRGEHAHR	224
<u>WP 007192445</u>	160	ESKQARLgTlsvLEASRLAVEGLPaLAVKGCGLVQLPVFNDLRGDLMVAQFDRHLPFSPKRVFVYHVPNDHVRGEHAHR	239
<u>WP 009102868</u>	158	SSPQAIDAs-----ASLGAELIGGCQMLELPTITDMRGKLTIAQWDQHLPSPERTFFVHHVPSSEKIRGEHAHR	226
<u>WP 005048231</u>	161	EPTAARGPvg-----DPGAAEG-----ITRLRTVSDIRGALLPIDLPGDLPTPQRVFVHGVPSKEVRGEHAHR	225
<u>YP 003806326</u>	131	SAQQVLAWrg--QAEVQETGAVVR-LDVGdVTLHRLSLVHDPRGDLVFGFARDIPFAVKRYFMVFNVPSEKVRGEHAHR	207
<u>YP 563661</u>	225	ECKQFLICVSGNCSVLVDDGENREEYVLDSIDKGIYLPMTWGVQYKYSKDAVLLVFASHYYDSDDYIRDYSTFKQMRON	304
<u>YP 522503</u>	231	VCHQFLICVRGCCAVVADDGTHRQEFLLDRPDVGIHLPMPVWGIQYKYSADAVLLVYASHYYDNADYIRNYSEFRQLVGA	310



<u>YP 001269238</u>	235	ECHQFLVAVKGSVHVVADDGINREEFVLDKPNKGIHLPMTWGIQYRYSQDAVLMVFASHYYDADDYIRNYDEFKSLINS	314
<u>WP 006465577</u>	230	KCRQFLICVKGSCSVVADDGRSRIEVLDDSPDLGIYLPPLTWGTQYKYSSDAVLLVFASDSYDAQDYIRDYESFLQTVSP	309
<u>WP 007835313</u>	230	ECHQFLICVRGSCSVVADDGFNRQEFLLDRQDLGIHIPPMIWIQYKYSQDAVLLVFASHYYNEADYIRDYSEFQKLIEM	309
<u>NP 790904</u>	235	ICHQFLVAVKGSVHVVADDGVNREEFILDKPNQGIHLPMTWGIQYRYSQDAVLLVFASHYYDAGDYIRNYEEFKSLI-A	313
<u>WP 003365665</u>	235	ICHQFLVAVKGSVHVVADDGVNREEFILDKPNQGIHLPMTWGIQYRYSQDAVLLVFASHYYDAGDYIRNYEEFKSLI-A	313
<u>WP 006890961</u>	232	KCQQFLIAVKGSVRVVDGKNREEFLLDRNNSGLYLPAMTWGIQYHYSQDAVLLVFASEYYESSDYIRNYSDFIEAAKN	311
<u>WP 008212526</u>	233	QCHQFLICVRGRVSVVADDGVHREEFLLDRPNLGLHLSPMVWGIQYKYSADAVLLVFASHYYDGADYIRDYSEFVKLTGA	312
<u>WP 005793127</u>	237	ECHQFLICVKGSCAVVDDGKSRCEVLLDDSPDLGLHLPMTWGIQYKYSADAVLLVFTSHDYDAADYIRSYAEFVALVDE	316
<u>YP 002138423</u>	230	QLHQFLVCVKGACSLLVDDSVHREEILLNSPNIGAHIPPMVWGVQYNFSPDAVLMVLASDAYDPDDYVRNYDDFLAMRGA	309
<u>YP 006720291</u>	230	ELHQFLVCVKGACSVVDDGNCREEYILNTPGAALHIPPLVWGVQYKYSQDAVLMVLASDVYKPEDYIRDYDQFIALVKK	309
<u>YP 005635798</u>	228	RCHQFLICVSGSVRVLADDGTRRIDVELNSPNQGIHLPMTWGTQYKYSKDAVLLVFASEPYDSDEYIRDYADFKSLANA	307
<u>YP 521972</u>	234	TCHQFLICIRGSCSVLADDGLNRTEVHLDSPDKGIYLPMTWGIQYKYSQDAVLLVFASHNYDAADYIRSYSEFLEEVENQ	313
<u>NP 636007</u>	228	RCHQFLICVSGSVRVLADDGTRRIDVELNSPQGIHLPMTWGTQYKYSKDAVLLVFASESYDTDEYIRDYSDFKSLANA	307
<u>WP 008903201</u>	235	RCAQFLVAVKGRHLHAVADDGARREEFVLDSPDLGLYLPMTWGVQYRYSQDAVLLVLASEHYEPHDYIRDYDEF--LQAA	312
<u>YP 995492</u>	224	QCRQFLVAVKGSVHVLADDARHSEEFILDRPALGLLPPMTWSVQYRYSQDAVLLVLASEHYDPEDYIRDYDRFVVLARA	303
<u>YP 826939</u>	225	ALHQFLICVHGRCHVVGDGVRQEFVLDRLPSLGLHIPPMVWASQYKYSQDAVLLVLASENYDPASYIRDYSEFVQLVSV	304
<u>WP 007192445</u>	240	ECAQFLVALNGALSVVDDGAERQEIRLDYPGVGLLIPPLVWGIQYRFSAVAVLAVFASHDYESNEYIRDYDEFRLRVTA	319
<u>WP 009102868</u>	227	ECQQVLVAISGHVEVVIDDGRQRQVALNDRQALHIPAGVWATQYGYSSDCVLLVVFASHNYDES DYIRDYDAFRKFRGV	306
<u>WP 005048231</u>	226	RCEQFLVCLTGSVSCIVDDGHDRREFVLDSPSMGLHMPMTWGTQYRYSADAVLVCVFASELYDDSDYIRDYEEFLALANG	305
<u>YP 003806326</u>	208	VCHQFLICAKGGCAVVVDDGATRCEVFLDDSPDLGLYLPMTWGTQYKCSGDTLLCVFTSHYYDPADYIRDYAEFLALVHK	287

<u>YP 563661</u>		-----		<i>Shewanella denitrificans</i> OS217
<u>YP 522503</u>	311	SA-----	312	<i>Rhodoferax ferrireducens</i> T118
<u>YP 001269238</u>	315	HLs-----	317	<i>Pseudomonas putida</i> F1
<u>WP 006465577</u>	310	KDeis-----	314	<i>Herbaspirillum frisingense</i>
<u>WP 007835313</u>	310	KI-----	311	<i>Variovorax</i> sp. CF313
<u>NP 790904</u>	314	NAe-----	316	<i>Pseudomonas syringae</i> pv. <i>tomato</i> str. DC3000
<u>WP 003365665</u>	314	NAe-----	316	<i>Pseudomonas syringae</i>
<u>WP 006890961</u>	312	NEpl-----	315	<i>Methylobacter tundripaludum</i>
<u>WP 008212526</u>	313	SA-----	314	<i>Rhodanobacter</i> sp. 115
<u>WP 005793127</u>	317	GAa-----	319	<i>Acidovorax delafieldii</i>
<u>YP 002138423</u>	310	V-----	310	<i>Geobacter bemidjiensis</i> Bem
<u>YP 006720291</u>		-----		<i>Geobacter metallireducens</i> GS-15
<u>YP 005635798</u>	308	AG-----	309	<i>Xanthomonas campestris</i> pv. <i>raphani</i> 756C
<u>YP 521972</u>		-----		<i>Rhodoferax ferrireducens</i> T118
<u>NP 636007</u>	308	AR-----	309	<i>Xanthomonas campestris</i> pv. <i>campestris</i> ATCC 33913
<u>WP 008903201</u>	313	VTrpt-----sp	319	<i>Acidovorax</i> sp. NO-1
<u>YP 995492</u>	304	LHrppaagidsp	315	<i>Verminophrobacter eiseniae</i> EF01-2
<u>YP 826939</u>	305	LK-----	306	<i>Candidatus Solibacter usitatus</i> Ellin6076

<a href="#">WP 007192445</a>	320	PEspt-----	324	<i>Thiocapsa marina</i>
<a href="#">WP 009102868</a>	307	EE-----	308	<i>Rhodopirellula</i> sp. SWK7
<a href="#">WP 005048231</a>	306	N-----	306	<i>Microbacterium laevaniformans</i>
<a href="#">YP 003806326</a>	288	SPnnaa-----	293	<i>Desulfarculus baarsii</i> DSM 2075

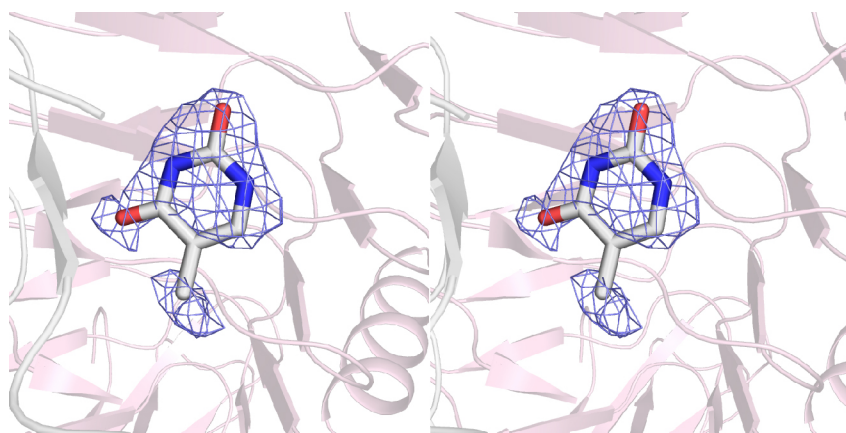


Figure S6

Electron density corresponding to a thymine molecule at low occupancy. The omit map, contoured at  $2\sigma$ , was calculated at 2.2 Å resolution with coefficients of the form  $F_o - F_c$ , where  $F_o$  was the native structure factor amplitude and  $F_c$  was the calculated structure factor amplitude (the ligand was not included in the X-ray coordinate file so it did not contribute to the phasing).