# **Supplementary material**

### **Supplementary Figure 1**

		40	50	60	70	80	90	
				<u> </u>				
Helix	1-3	GSLID <mark>R</mark> SI	NWMGD <mark>IG</mark> QL <mark>N</mark> K	DLTDL <mark>R</mark> IARI	LQ <mark>Y</mark> MIA <mark>NGD</mark> DT	AAANTLAKLD	<mark>A</mark> FSKQQAY <b>L</b> AT	.'T
Helix	4-6	EADSV <mark>R</mark> L	AQYQL <mark>IS</mark> KA <mark>R</mark> Q	QLLQV <mark>R</mark> IDVH	RG <mark>Y</mark> IAE <mark>NSSAN</mark>	EQ <mark>A</mark> -ALRQLD	AALADTDNLKR	2Q
		160	170	180	190	200	210	
		100	110	120	130	140	150	
Helix	1-3	FK <mark>S</mark> PENV	KL <mark>L</mark> GELGDTIS	AYKLSL <mark>N</mark> KMF	Q <mark>G</mark> YDATRAA <mark>R</mark>	VSMDS <mark>SA</mark> IRA	DQAM <mark>DAL</mark> S <mark>Q</mark> EV	MAR
Helix	4-6	LP <mark>S</mark> ED	AR <mark>L</mark> QQFENAVL	<mark>AY</mark> RDAV <mark>R</mark> QFF	DAVANITTS <mark>R</mark>	AEMTVQGADI <sup>.</sup>	VKRS <mark>DAL</mark> YQIQ	LE <mark>R</mark>
		220	230	240	250	260	270	

Legend to Supplementary Figure 1) Alignment of the McpS-LBR sequence fragment which forms helices  $\alpha 1-\alpha 3$  (amino acids 37-158 of McpS) with the fragment that forms helices  $\alpha 4-\alpha 6$  (amino acids 160-278). The sequence alignment was done using the CLUSTALW algorithm (Thompson *et al.*, 1997, Nucleic Acids Res. 24, 4876) of the NPSA server (http://npsa-pbil.ibcp.fr/cgi-bin/npsa\_automat.pl?page=/NPSA/npsa\_clustalw.html) using a gap opening penalty of 10 and a gap extension penalty of 0.1. Arg60 and Arg183 which form direct interactions with malate and acetate, respectively, are shaded in yellow.

# **Supplementary Figure 2**

			Malate	binding										
	40	50	60	70	80	90	100	110	120	130	140	150	160	170
	10	1	00	, 0	1	1	100	110	120	130	110	130	100	1,0
pp4658	GWTSLGSLIDESNU				DTAAANTLAKT		FKSPENVK	LGELGDTISZ	VKLSLNKMRO	TYDATRAA	RVSMDSSATE		OEVMARPEAD	SVRLAOYOLTSKARO
A5W930		MGDIGOLNK	DLTDLRTAR	OYMTANGD	DTAAANTLAKL	DAFSKOOAYLATT	FKSPENVK	LIGELGDTISA	YKLSLNKMRO	3YDATRAA	RVSMDSSATE	ADOAMDALS	OEVMARPEAD	-SVRLAOYOLISKARO
BOKHR9	GWTSLGSLIDESN	MGDTGOLNK		OYMTANGD	DTAAANTOAKL	DAFSKOOAYLATT	FKSPENTK	LGELGDTISA	YKLSLNKMRO	TYDATRSA	RVTMDSSATE	ADOAMDALS	OEVMARPEAD	-SVRLAOYOLISKARO
B1J3P8	GWTSLGSLIDRSN	MGDTGKLNK		OYMTANGD	DAAAANTOAKL	DAFSKOOOYLVS	FKSPENVK	LKELGOTISE	EYEVSLNKMRA	TYKGSLAA	RDAMNVSAAF		EDVMGRPEAD	-SVRLAOYOLISKARO
O1IFB1	TGWNSLGSLIDRSN	MSDITOLNS	DLTNLRVARL	OWMLTNGD	DASAANVOAKL	DAFGNOOOHLVN	FKSPENLK	LREOGOSISE	EYRVSLEKMRO	GYKTTLAA	RDAMNOAAGE	ANEALEAIS	AAVLSNSESD	-ASRLAOYLLISKAKO
Õ4KIL8	GWTSLGSLIDRSNV	MSDITOLNS	GLTKLRVTRL	OYMLANGD	ETAAOGVONTL	DDFSAOOKKLLAS	FOSPENIK	LLOGLGATISA	YODSLNKMRN	YRSGDAA	RLAMNONAEF	RANDLINGIN	ISWVKOL-PLS	DERFTOFOAITOAKE
Õ3KID4	GWTSLGGLIDRSNV	MSDITOLNA	GLTKLRVVRL	OYMLTNGD	ETAAONVOTTL	DGFAAOOOKLISS	FKSPENVK	LLKEOAATIA	TOTSLNKMRN	YRTGNTA	RDSMATSAAT	AYGLIEALS	NRVOOM-PLS	DERFEOFOAVTAAKE
C3K1Y3	GWTSLGGLIDRSNV	MSDITOLNA	SLTKLRIVRL	OYMLANGD	EAVAONVOTSL	DAFAAOOOKLLDS	SFKSPENLK	LLNEOKGVITA	AYOOSLNKMRE	AYRNGNAS	ROVMGDKADI	ANAOIEALC	TKVOOM-PES	PERFSOFOAVTRAKE
Q888G5	GWTSMTSLINRSNV	MSDITSLNS	OLTKLRVARL	OYMVADGD	EKVAEAVOVSL	DGFKNYOOKLLAT	FKSPENVKI	MLEOLSAVIAI	VOKSLNNMRS	<b>GYKASTAA</b>	RDELTMHAGE	SIDVFELLC	DEVKKMDPAD	-ANRFEOYRIVTDAKE
048N07	GWTSMSGLINRSNV	MSDITSLNS	OLTKLRVTRL	OYMVADGD	EKVAETVÕISL	DGFKNYOOKLLTS	SFKSPENVKI	MLKÕLGVVIAI	VOKSLNNMRG	GYKASIVA	RDELSTNAGE	SIDVFELLC	AEVKKMDPAD	ANRFEOYOIVTDAKE
Õ4ZY09	GWTSMSGLINRSNV	MSDITSLNA	OLTKLRVTRL	OYMVADGD	EKVAETVÕTSL	DSFKAYOEKLRAS	FKSPENLKI	MLDÕLGIVIAI	VOKSLNNMRS	<b>GYKASTAA</b>	RDELTTHAVE	SLAVFEOLV	TEVRNMDPAD	ANRFEOYRLVTDAKD
Q48BJ3	WTSLDKLINRTD	RIGDITELSD	NLTNLRVARL	OYMLTDGD	ETAAQNMQSKL	DVFKAQQQSLLIS	FNNPLNLK	PLRELADVTRI	YEASLNSMRA	FQAGAKV	RNEMTANAM	AMRAVDSLN	DAVTQIDPAD	PARFDOAQLATAARQ
Q4ZL53	WTSLDKLIYRTD	RIGDITRLSD	NLTNLRVARL	<b>OYMLTDGD</b>	ETAAQNMQSKL	DVFKAQQQSLLVS	FNNPVNLK	PLRELADVTRI	YEASLNSMRA	VYQAGAKV	RNEMTANGTA	AMQAVESLN	NAVLQIDPAD	-PARFDLAQLANSARQ
Q87TW6	GWTSLDKLIYRTD	RIGNITELSN	INLTNLRVARL	<b>QYMLTEGD</b>	ETAAQNMQSKL	DVFRTHQQSLLTQ	OFTNPLNLKI	PLGELSDITRI	YEASLNRMRA	YQSGAKV	RGEIATHAGA	ASQTIESLN	NAVMQMDPSE	-PARFDQALLVNTARQ
A4XX26	TAWSGLGSVIQRST	MSEISQLNT	TLTNLRIARL	<b>O</b> FMLAKGD	APSSERLLTNL	DIYLQQQKKLLG	(FTNPVNVK)	LLQEQDRYNQI	YQRSLGGMRA	YAAADEA	RRKVLAEDQQ	LGELLAAMQ	RSVQLLPEYD	SSRFAQLQALTHTQA
A4VQJ2	WNGWGSLGSVIQRSGW	MTEISQLNK	TLTDLRIARL	<b>OFMLANGD</b>	AESTERLDKNL	GIYLAQQTKLLD	(FKNPINVA)	QLKEQAGYNAQ	VQNSLNDMRK	YNQANGS	RQVIDGAATE	RLSELTASVS	NHVIQLPEYD	-EDRFAQLLAISLIKE
B1J1P7	QSLISWEGMGSLVRRSEV	/VSEVSRLND	ALGDLREARL	RHAIANGA	ENEGKALQGAL	EAFQTPLAKLRG	LVKPQSLA	LIDKAEQTLRO	YAANQAQSFQ	SYQKMRAA	QKEMGALATE	RSFASIETIR	TQVRALPDAE	QRVVRSEAINQIRE
Q3KJD4	GWTGMSG <mark>II</mark> SRGD	(LGFISSLNE	LTKDLRLARL	DYEARRGE	QGPGA-VNDLL	GKLDSGLQSARGN	1IEQPSDVAI	MIDQQLAAVAH	YKRAFADMTQ	ATVQREDA	RSKLGASADN	<b>AVAKVSEVE</b>	KSLLQ	GDSVAQFNSVIELSK
С3К8Т5	TGWTGLSGVISRGD	LGYIASLND	LSKDLRIARL	DFEMRRGE	QGPAA-VNELL	GKLEGGLKTARTI	LIEQ <mark>P</mark> ADIA	LIDDQLAGVDQ	YKRAFDAMVQ	GANRENA	RSKLGDTADN	JAVLKVNEVE	KSLLQ	GDSVSQFNSVVDVSK
Q4KJM1	TGWTGLGRVIDRGDE	(LGNISVIYA	LTKDLRIARL	NYEMSRGE	HGPAA-VNDFL	KQLDDG <mark>L</mark> QDARAÇ	QLQQ <mark>P</mark> ESITI	MVDQQLDAVAH	YQKAFADMTR	ATANREAA	RSQLGATADN	JAVARVAEVE	NSLLQ	GDSVAQFNSVIDLSK
Q88D09	TGWHGMDSIIDRGDF	LGNISVIQQ	YTQELRIARQ	<b>QYD</b> RRRDD	ASLAE-LEKAL	SNLDRQVQLMLGQ	DIEQPADHQI	RLEQQREAVRI	IYQQAFNELKQ	ADQRREAS	RDVLGSSADF	AVDLIGRVQ	RSLLQ	GANINQYQHAVDVSA
A5WA54	TGWHGMDSIIDRGDF	LGNISVIQQ	YTQELRIARQ	HYDRRRDD	ASLAE-LEKAL	SNLDRQVQRMLGQ	DIEQ <mark>P</mark> ADRQI	RLEQQREAVRI	TYQQAFNELKQ	ADQRREAS	RDVLGSSADF	AVELIGRVQ	RSLLQ	GANINQYQYAVDVSA
B0KM45	AGWHGMDSIIDRGDF	CLGNISVIQQ	YTQE <mark>LRIAR</mark> Q	HYERRSDD	ASVAE-LEKAL	ANLDRQVQLMLGQ	DIEHPADRQI	RLEQQREAVRI	I <mark>Y</mark> QQAFNELKQ	AGQRREAS	RSVLGDSADK	(AAELIGRVQ	RGLLQ	GGDI <mark>NQ</mark> YQHAVEVSA
Q1I3S1	TGWMGIDSVTSRGDF	(LGNISVIHQ	YTQD <mark>LRLAR</mark> Q	DYERNRD	AAVGA-LEKA <mark>L</mark>	ANLERQVQFMLGQ	DIEL <mark>P</mark> GDRQI	RLDQQQDAIRQ	QYQQAFAELKQ	AGQRREAS	RGMLGDSADF	(AADLIGKVQ	QRLLQ	GGDIS <mark>Q</mark> YQQVVQVSA
B1J2R9	FTGWQGMDSIIDR	(LGNISVISÇ	GTQE <mark>LRIAR</mark> Q	HYQRDRNE	AAIGE-LEKA <mark>L</mark>	AGLDRQISIMLGQ	DIEQ <mark>P</mark> VDHQI	RLQQQQEAVRH	(YQQAFADLKQ	AGQRREAS	RSVLGDSADK	AAELTSRVQ	ERLLQ	-AGDITPYQSTVEVSA
Q87UY3	-SATGWFSNQALIDRGDF	RVTAIAEINE	LTLQLRINRS	RYEDLFNA	ESAAE-VRTTL	DQLDAALAYARSI	LLRSPENLQ	SLDGQIQTAR	EYRQSFADMSK	AIDVREAS	RSQMGDNADF	(AVDQANKVE	AELLK	ADNILAFNGIVGVSK
Q48PK3	-SATGWFSNQALIDRGDF	RVTAIAKINE	LTLQLRIDRT	RYEDLFNA	ESAAE-VRKTL	DQLDAALVHARNI	LLRSPE <mark>N</mark> IQ	SLDGQIQSARE	EYRQSFADVTK	AIDAREIS	RSQMGDNADF	(AVDQANKVE	AELLK	ADNILAFNGIVGVSK
Q4ZZH2	ATGWFSNQALIDRGDF	RVTAIAEVNE	LTLQLRINRM	IS <mark>Y</mark> EVLYNA	ETAAK-VRSTL	DELDAALQTARNI	LLRSPENLQ	LLDVQIQATRI	YRQSFEDMSK	AIDTREAS	RSQMGENADE	AVDQANRIE	AELLK	EDNILAFNGIVGVSK
Q1I3S0	TGWLALDGAIDRSQF	CLTQIAQLND	YSKDLRAERI	TFRVLGDD	ESRAQ-LTQTL	SQVESLLASMRPH	RYSAPEDVR	LLTDKGQIVGF	RYRSDFDKLQH	AVQTRQQR	RDALQSQTGE	ELENAISDLQ	GQLVKRLNQST	AQGEALNFIEALER-QV
Q88D08	-TISGWRALDGAIVRSQ	QLSEIGLIND	LTKDLRAERI	TYRVLNDD	ASKAR-ISNIL	DQLNSMLTTLQQF	RSNVDESRQ	LLTEKMALLQF	RLRDNFSELQR	SVASRVAL	REALQSQEHA	ALSEAIDQLQ	TQALLKMPDDS	QQSGVLGLMDTLSR-HV
A5WA55	ISGWRALDGAIVRSQ	QLSEIGLIND	LTKDLRAERI	TYRVLND	ASRAR-ISNIL	DQLNSMLTTLQQF	RSNVDESRQ	LLTEKMALLQS	SLRDTFSELQR	SVASRVAL	REALQSQEHA	ALSEAIDQLQ	TQALLKMPDNS	QQS <mark>GVLGLMDTLSR-HV</mark>
B1J2R8	-AASGWRALDDAITRSE(	QLSEIGRIND	LVKDLRAERI	TYRVLADD	ASKAQ-ITRIL	QQLDAMLTTLQQF	RSSVDESRQI	MLGQKLQLLQF	RLHENFATLOR	IVESRRGL	REAMQAQEQF	CLNGVIDELE	TQALLKMPADS	QSGLLGLMDSLTR-HV
Q87UY2	GWHGLYTMIDRSES	SLSDVSQLTS	LTKDLRADRI	TDRVEKTP	ETTAQ-VIKKL	DEMKTHLTSLHRQ	OSTEQATIT	LLNGQLQAVSE	ELEKSFAEIRSI	NRQSRNQI	RQRLDQRSEQ	ALQAVAQVE	AEVLKSVSQEQI	DSSERMEEFTNISQLRQ
Q48PK4	GWHGLYTMIDRSES	SLSDIAQLNS	LTKDLRAERI	TDRVEKTP	ESTAL-VTDKL	NEMKAQLTTLHR	SLETETIT	LLNGQFETVSF	RLEKTFADVRAI	NRQTRNQV	RTRLEQTSEQ	ALQAIALVE	SEVLKSVSQEQI	DSTERMEEFTNISQLRQ
Q4ZZH3	GWHGLYTMIDRSES	SLSDIAQ <mark>LN</mark> G	LTKDLRAERI	TDRVQKTP	ESTAL-VTEKL	NEMKAQLTLLHKQ	OSDEEATIK	LLNGQFETLNF	RIEKTFADVRDI	NRQTRNQI	RTRLEQTSEQ	ALQAIAQVE	VEVLKSVSQEQI	DSSERMEEFTNISQLRQ
Q02EU5	SNRTLTHQTALSE	QLAEVASLME	QAQQAEQS <mark>RL</mark>	AFE-AGSD	PRQAEQVRQTL	AGMLQRLQALRHS	Seldpa	ALAHQAEAIEA	AYRKAFDDLAA	ADQQRSAA	RGVLVGTAQQ	ALDSFARLE	ELMDASLAQQAC	BDPQALQRSRAVADLHQ
A3L2I2	SNRTLTHQTALSE(	QLAEVASLME	QTQQAEQG <mark>RL</mark>	AFE-AGSD	PRQAEQVRQTL	AGMLQRLQALRDS	Seldpa	ALAHQAEAIEA	AYRKAFDDLAA	ADQQRSAA	RGVLVGTAQQ	ALDSFARLE	ELMDASLAQQAC	GDPQALQRSRAVADLHQ
Q9HUB1	SNRTLTHQTALSE(	QLAEVASLME	QTQQAEQG <mark>RL</mark>	AFE-AGSD	PRQAEQVRQTL	AGMLQRLQALRDS	Seldpa	ALAHQVEAIE/	AYRKAFDDLAA	ADQQRSAA	RGVLVGTAQQ	ALDSFARLE	ELMDASLAQQAC	BDPQALQRSRAVADLHQ
B7V3G5	SNRTLTHQTALSE	QLAEVASLME	QTQQAEQG <mark>R</mark> L	AFE-AGSD	PRQAEQVRQTL	AGMLQRLQALRDS	SELDPA	ALAHQTEAIE/	AYRKAFDDLAA	ADQQRSAA	RGVLVGTAQÇ	ALDSFARLE	ELMDASLAQQAC	BDPQALQRSRAVADLHQ
A3LJ56	SNRTLTHQTALSE	QLAEVASLME	QTQQAEQG <mark>R</mark> L	AFE-AGSD	PRQAEQVRQTL	AGMLQRLQALRDS	SELDPA	ALAHQTEAIE/	AYRKAFDDLAA	ADQQRSAA	RGVLVGTAQÇ	ALDSFARLE	ELMDASLAQQAC	BDPQALQRSRAVADLHQ
A6VDJ5	SNRTLTHQTALSE	QLAEVATLME	QAQQAEQAHL	AFD-AGSD	PREAERLRRIL	TGMLERLRQLRDS	Seldpa	ALAREAEAIE	AYRGAFDDLAA	ADQQRSAA	RGVLVGSAQQ	ALDSFARLE	ELMDASLAQQAC	BDPQALQRSRAVADLHQ
A4VGE7	SLNGLLERNQF	QTRLSQVQE	ASYAVDTART	'LFE-QSGS	DAHAQQVTGKI	GEVRNHLQDIRTI	TLTAADDQRI	DIASALQYAEF	RIERSFQELKQ	ARESREQS	RGVMVSSAGE	EALKALGELE	EQIYQTLEQSAI	DDPLVVQQARALAELTR
Q4ZTX7	WTGITSLSERSE	RISDIGKLSA	LTRDVRIARL	AYSV-NYD	AERASNWLKAL	EGLENHVKYAQK	FDSPLNVP	LVNTAADALKI	DYRIHYDNLMQ	ATAAREAT	RSVFGQYADA	AGADDLQKLN	IAVARSD	-DGTPAORDAIVQAMT
Q48IU4	WTGISSLSERSER	RIADIGKLST	'L'I'RDVRIARL	AYAL-NYD	AERASNWLKAI	DSLENHVKYAQKV	FDSPLNTP	VNASAEAMKI	<b>YRVHYDNLMQ</b>	ATAAREAT	RSVFGQYADA	AADDLQKLN	IATARSD	-DGSASQRDDIIQAMT
Q882L0	WTGITSLSERSE	RIADIGKMST	LIRDVRIARL	AYWI-NYD	AERASDWLKAL	ERLEAHVKYAQE	FDSPLNIP	LVNAAAEALVI	SYRVHYDNLMR	ATAAREAT	RGAFGQYADA	AGAEDLQKLN	IAFARSD	EGSASQRDAIVQAMT
Q4ZW84	YTGKDATDTLKRRAEI	SGDIAQFSS	TARDMRIERL	VYFL-KAD	DAQASKWLEAL	ERTERQLVSISP	KFKTANN IA	LLKEAQ'I''I'MQI	LYRGFYTRSVE	TREREQL	RTLAGASGET	INGLLLKIA	EAANDE	SGNAADRQKLPALFI
Q4LBM3	-AYTGWKATEFLKDRSEI	RIGDISLFSS	JARDMRIERL	VYFL-KAD	DAOASKWMEAL	ERTELOLKAITPI	RENSAVNVA	LREADATMOR	<b>XYRSFYEOAVR</b>	TRDREKL	RIVAAASAEA	ANNLLIKIA	DSANSE	TGKFEEROKLTLLFV

	Acetate bi	inding				Ac	etate bin	ding Mala	te bind	ling					
	100	1.0.0		01.0										21.0	200
	180	190	200	210	220	230	240	) 250	26	0 27	0 280	29	0 300	310	320
pp4658		VRGVIAENS	SSANEOAALRO	ן ארזידירו ב. ז ב ברו. ז ר	ILKROLPS				LOB VENTA		L ALVOTOLER	TESTOARSI			
A20020	OLLOVETD	VRGVIAENS	SANFOAALRO		ILKROLDS	- ADTRLOOFEN		ROFRDAVANTT'	LOLUBIT V		ALYOTOLERRI	TESTOARSI		CVLAAVLTTR	
BOKHR9	OLLOVETD	VRGYTADNS	SANEOAALRO		ILKROLPA	-EDARLOOFES	SVLAYRDAN	ROFRDAVANTT'	CSRAEMTV	OGADIVKRSD	ALYOTOLORRI	TESTOARSL	OATATLLALLN	GVLAAVLTTR	OTTRPLHDTLVA
B1.T3P8	OLLOVEVD	VRGYTADNS	SAANEOAALRO		ILKROLPZ		STOAVPEAU	ROFRDAVADIT"			ALVKTOTORRI	AESAOARSI	OTTATLLALLY	CVLAAVLTTR	OTTRPLHDTLOA
01TFB1	OLVOVRLD	VRSYTADL	SDTEOTAVR	DLESALAETDS	T KROLPO	-EASRIOOFES		ROFRDATAAIG	/ARAEMTV	OGADIVKRSD	ELYKTOTERRI	DESVOARSL	OTTATLLALLY	GILAAFITTR	
04KTL8	AFOLARYE	VRGYVTTNN	JPDTEOKAVT(	DLNAATAEMDO	KSHESS	STORDALOOLET.	ALSGYRSSI	OAFKVAFTNAV	CARKEMTD	OGADIVSRSD	ALYOTOLDERI	TESAOARSL	OLISTLALIN	GVLAAVITTR	OTTRPLOETLAV
03KTD4	AFTLARYE	VRGYTATAN	JAETEOKAVG	DUDVATASLKE	NTHFAS	TOODALROLET	ALTNYRSAI	OAFKNANTDAV	DARKEMTD	OGATIVTUSE	OLYOTOLDERI	AESAOARTL	OLISTLLALIN	GTTAAFTTTR	OTTRPLOETMA
C3K1Y3	EFMLARYE	VRGYTANUS	SPDTEARAAA	DIEKAISGLKG	LSAVEGA	SEOSAL TALET.	ALGAYRTAN	ONYKAANANTV'			ELYETOLNERI	AESAOARSI	OLISTLALIN	GVTAAWVTTR	OTTRPIOETLAV
088865	NURLARYE	VRGYTTNAT	PETEOAAVAP	VI DI ATKDI DT	TKTTESS	TOADOL ROLET:	SLMAYRTTI	ONFKAATANTA	AROEMTV		AMYOLOLNERI	OESAOARTT	OTTCTLLATI	GMTAAVTTTR	OTT
048N07	NURLARYE	VRGYTTNPT	PAETEOTAVAL	RUDSATKDUDT	TKTTESC	TOADOLKOLET	SLAAYRKSI		DARKEMTV		AMYOLOLDRRI	OESAOARTT	OTTCTLLATI	GMTAAVTTTR	OTTRPLOETLAVV
047Y09	DURLARYE	VRGYTTNAT	PETEOAAVSI		KTTESC	TOADOLROLET	SLMAYRTTI	ONFKAATGTIV	DARKEMTT			OESAOARTT	OTTCTLLATI	GTTAAVTTTR	OTTRPLETLAVV
048BJ3	DLILVRYE	VRGYTSNPN	DKTETAAFO	OLDTAISHLDR	LKTTFGA	ANREOIAOFES	ALRSYRSSV	DAFKATTOTAA	SVRKDLTS	OGAAIVKLGE	ELYGIOMOMGH	DTAOARNL	OIGCVLLVMLL	GILAAIVITR	OITRPLEDTLAIV
04ZL53	DLVLVRYE	VRGYTGNPN	DKTETAAFOO	OLDSAISHLDR	RFKAAFGE	ANREOIAOFES	ALRNYRSSV	DVFKATTOTAA	SVRKDLTT		ELYGLOMOMGH	EDTAHARSL	OIGCVVLVMLL	GILAAVIITR	OITRPLEDTLAI
087TW6	DLLLVGNE	<b>VRGY</b> TAKPI	DEKTEKAVFOI	LLDTAISHLDK	LKSAFDA	GNRERITOLET.	ALRNYRASI	DAFKVTTOTAG	AVRKDLTT		ELYGIOMOLAH	ADTAKARNL	OLGCVVLVMLF	GILAAVIITR	OITRPLEDTLAI
A4XX26	ELLRLRYL	LERYESTPI	DAOTEOALAER	RIAAARASLGA	LOOAFGS	SAOODAVORISA	ALGOFEOTM	OAFKNATADIA		OOGEIVRISE	ALYKFOMERM	AIESAOARSL	OIGATLLAMLF	GVLAAWIITR	OITRPLODTLGA
A4VOJ2	DVORAOYL	LRVYMAAPO	INDAAKAIYT(	DLDAAOATLGR	RHAGALDE	DSGAAVOOIRS	/LGEYRGAI	ESLETATOAIA		OOKEIVRISD	SLYOFOLDOLI	VESAAARTR	LIVSTLLALVI	GALAAWLITR	OIVLPLRATMADVERIA
B1J1P7	NLILLRYH	VRGYTGNTN	ADTEKLMNA	DIATTVNELPG	LVARFNO	SFDAOFSTLNO	)VRAYAEAV	/EAFRGEVSKLV	CRNAMAS	~~ DINTLTGLIG	ELLDAOAVSV	SDSOFAKNL	OIFTTLLALLM	GIFAALIIAR	OISAPLOOA
O3KJD4	LLOOARYO	VRGYTYSGE	AEAEOPALD	IAAALNNLES	SLPSKLPE	OHIANLOOATE	SLKAYRAAN	/SOFRDSOVNNAL	AMARMTA	OGDILLDVSK	KLTESOTIVRI	TDAAHAKNM	~ LMIATLLALAF	GLLAAWAITR	OIIIPLEOTLKVAERV-
C3K8T5	LIÕÕARFÕ	VRGYTYSGE	VEAEOPALD	AIDNALKKIAS	SLTGOIPE	OYSTNLOOASV	SLOAYRAAN	/SOYRDSOVASA	ALKIMGV	OGDILLDRSN	KLTTSOTVVRI	ADAANAKOL	LLLATVLALIF	GLVAAWAITR	OIIIPLNOTLOVA
O4KJM1	LIÕÕARFO	VRGYTYSAF	PEAKOPALD	AIDNALNNLTS	LPSRLPE	OHVANLOOASD	SLKAYRMAN	/SAYSDAEEASA	ALKRMAA	~ O <mark>G</mark> DRLMDL <mark>S</mark> K	OLTVAOTTKRI	SDAAOAKST	LLIATLLAMLF	GLIAAWAITR	OITOPLOOTLKAA
088D09	LLOOARFO	VRGYTYSGN	JADYOOTALK	AIDOALAELRA	LPAKVPA	EHAASLDDAAT.		TOFGNAOLASE	ALORMVE	~ OGTVLLOASO	~ MMTASOTEVRI	AAAAOAKTL	LTVATVLALAL	GLLAAWAITR	OIIIPLROTLRAA
A5WA54	LLÕÕARFÕ	VRGYTYSGN	JADYOOTALK	AIDOALAELRA	LPAKVPA	EHAASLDDAAT.	AMGGYRDAN	TOFGNAOLASE	ALORMVE	OGTVLLOASO	MMTTSOTEVRI	AAAAÕAKTL	LAVATVLALAL	GLLAAWAITR	OIIIPLROTLRA
B0KM45	LLÕÕARFÕ	VRGYTYSGN	JAEFOOTALK	AIDOALAELRA	LPAKVSA	EHAAGLDDAAT.	AMGGYRDAN	TOFGNAOAASE	ALOHMAE	OGTLLLOTSO	AMTTSOTEVRI	AGAAOAKTL	LAVATVLALAL	GLLAAWAITR	OIIIPLROTLRAA
01I3S1	LLÕÕARFÕ	VRGYTYSGE	AEFOOTALN	AIDOALPVLKA	LPAKLPA	EFAASLDDAAT.	ALAAYRDAN	NOFGTAOAASE	ALORMSA	OGOVLLSTSO	DMTVSOTOVRI	OGTOOAKSM	LAGATVLALLL	GVLAAFAITR	OIIVPLROTLAAAERV-
B1J2R9	LIQQARFQ	VRGYTYSGI	DANYQOTALNA	AIDQAMTNLKA	LPAKLPA	EYAASLDDSMS.	ALAAYRDAN	/NOFGSAQSASD		QGTVLMDNSQ	KMTVSOTEVRI	AGSRKAKAL	LASATALALVI	GLLAAWAITR	OIIVPLROTLAAAE
Q87UY3	LIQQARFQ	VRGYTYSGF	RPDFEKNANQ	AIDEAVTGINT	LAGDISS	SEYLPLLQOAVV	GLKG <mark>YR</mark> AAN	/GOYRDAQAASQ	ALEKMTA	LGTTMLATSN	EMIARONKSRI	JADSDKSVLM	IAVATALALVM	SIL <mark>AAWIITR</mark>	OITTPLOETL
Q48PK3	LIQQARFQ	VRGYTYSGF	RPDFEKNANQ	AIDEAITGINT	LAGDISS	EYLPLLQOAVV	GLNG <mark>YR</mark> AAN	/GOYRDTQAASK	ALEKMTA	LGTKMLTTSD	DMIARONKSRI	ADSEKSVFM	IAVATALALVI	SILAAWVITR	QITTPLOETLE
Q4ZZH2	LIQQARFQ	VRGYTYSGF	RPDFEKDANK	AIDDAVTGINT	LAGDISS	TYSPMLQOAIA	GLNG <mark>YR</mark> AAN	/GKYRDAQAASK	ALDKMTT	LGVSMLAT <mark>S</mark> N	DLITRONKSRI	ADSAKSVQM	IIAATALAMVI	GILAAWVITR	OITTPLOETLEVV
Q1I3S0	EIASQQAS	VPAYYSEPI	QAFEQVGQN	ATRAETTLEC	LRQWLPR	VDLDSALPAPV.	ASNLGRFREQI	LSQYAQAAIIVE	LQNDMEQ	LGNQITTSSQ	ALSNHQIEQRI	EQALAARSL	MTSVALLALLI	GALAAWVISQ	QITVPLKQALRQA
Q88D08	EGANQQSL	VPAYTFVP	/EDFAKVGDN	ALNAADSSLAQ	LLEGLA	LGLPRAISEQP	GVELSK <mark>YR</mark> TSI	DOYRRAAVRVE	LQNNMEI	MGNELRTVSL	DLGKRKVEQ <mark>RI</mark>	REALAARSL	LTSVALLAMVV	GALAAWLITL	QITQPLRQTLA
A5WA55	EGANQQSL	VPAYTFAP	EDFSKVGDN	ALDAADNSLAQ	LLEGLA	LGLPRAITEQP	GVELSK <mark>Y</mark> RTSI	DOYRRAAVRVE	QLQNNMEN	MGNELRTVSL	ELGKRKVEQ <mark>RI</mark>	SEAVAARSL	LTSVALLAMVV	GALAAWLITL	QITQPLRQTLAVAARIA
B1J2R8	DGANQQSL	<b>VPAY</b> TFVPI	LEDFAKVGQA	ALDAADKSLGQ	LIQALAF	LGLSRAVMEQP	GVELGK <mark>YR</mark> ASI	LEQYRRAALSVE	QLQNDMEQI	MGNELRAVSL	ELSKRKVEQ <mark>RI</mark>	SEALAARSL	LTSVAVLALLV	GVA <mark>A</mark> GWL <mark>IT</mark> L	QITQPLRQTLA
Q87UY2	QIQVARYQ	VQA <mark>YTF</mark> TTF	(DADETAAIT)	AIDEALKEVEQ	)IAQTQAL	DPLQGLVPATE.	ALKG <mark>YR</mark> DSI	LSEFKQIQTKAE	ADQESMES	L <mark>G</mark> EKLLESVA	ALTLL <mark>Q</mark> TAQ <mark>RI</mark>	SEAANSRTM	LASVASLALLI	GLLAAWVMTR	QITVPLQQTLIAAARI-
Q48PK4	EVQIARYQ	V <mark>QAYT</mark> FTTF	RDADEAAAIV	AIDEALKEIGQ	JIGQDEDS	SESLRGLGAATT.	ALQG <mark>YR</mark> ERI	LNEFKQIQTKAE	ADQELMRS	L <mark>G</mark> DQLLDSVA	ALNRL <mark>Q</mark> TAQ <mark>RI</mark>	SEAVNSSTT	LSSVAGLALLV	GLLAAWVMTR	QITVPLQQTLLVAARIA
Q4ZZH3	QVQTA <mark>RYQ</mark>	VQTYTFTTF	RDADESAAIA	AIDEALKEIGQ	IAQDQGN	ESLQGLTPATA	ALQS <mark>YR</mark> ERI	GEFKQIQTKAE	ADQEIMEG	LGETLLDSVG	ALNHL <mark>Q</mark> TAQ <mark>RI</mark>	SEAANSSAM	LSSVAGLALLI	GLLAAWIMTR	QITVPLQQTLSAAARI-
Q02EU5	QLLMVRYQ	VRG <mark>YVF</mark> ERS	DKA <mark>EQ</mark> AAFA	AFDALRQAATI	LRGQLPG	EADAALEQAMG	SLQG <mark>YR</mark> GGI	LEQFRAGVVRTR(	AQQAMQS	STQDMARAGR	TLTEAGRQL <mark>R</mark> H	STASRDRAS	LWLIAALALAF	GCVAGWAINR	QIVR <mark>PL</mark> DEALAQAEA
A3L2I2	QLLMVRYQ	VRG <mark>YVF</mark> ERS	SDKAEQAAFA	AFDALRQAATI	LRGQLPG	EADAALEQAMG	SLQG <mark>YR</mark> GGI	LEQFRAGVIRTR(	AQQAMQS	STQDMARAGR	TLTEAGRQL <mark>R</mark> H	STASRDRAS	LWLIAALALAF	GCVAGWAINR	QIVR <mark>PL</mark> DEALAQAEA
Q9HUB1	QLLMVRYQ	VRG <mark>YVF</mark> ERS	SDKAEQAAFA	AFDALRQAATI	LRGQLPG	EADAALEQAMG	SLQG <mark>YR</mark> GGI	LEQFRAGVIRTR(	AQQAMQS	STQDMARAGR	TLTEAGRQL <mark>R</mark> H	STASRDRAS	LWLIAALALAF	GCVAGWAINR	QIVR <mark>PL</mark> DEALAQAEA
B7V3G5	QLLMVRYQ	VRG <mark>YVF</mark> ERS	SDKA <mark>EQ</mark> AAFA	AFDALRQAATI	LRGQLPG	EADAALEQAMG	S <mark>L</mark> QG <mark>YR</mark> GGI	ECTRAGVIRTR(	QAQQAMQS	STQDMARAGR	TLTEAGRQL <mark>R</mark> H	STASRDRAS	LWLIAALALAF	GCVAGWAINR	QIVR <mark>PL</mark> DEALAQAEA
A3LJ56	QLLMVRYQ	VRG <mark>YVF</mark> ERS	SDKA <mark>EQ</mark> AAFA	AFDALRQAATI	LRGQLPG	EADAALEQAMG	SLQG <mark>YR</mark> GGI	LEQFRAGVIRTR(	AQQAMQS	STQDMARAGR	TLTEAGRQL <mark>R</mark> H	STASRDRAS	LWLIAALALAF	GCVAGWAINR	QIVR <mark>PL</mark> DEALAQAEA
A6VDJ5	QLLMVRYQ	VRG <mark>YVF</mark> ERS	SDKA <mark>EQ</mark> AAFA	AFDALRQAGTA	LHGQLPE	EAGAALE <mark>Q</mark> AMR	S <mark>L</mark> QD <mark>Y</mark> RGGI	E E OFRAGVARTR	AQQAMQS	STQDMARAGQ	TLTEAGRQL <mark>R</mark> H	STASRDRAS	LWLIAALALAF	GCVAGWAINR	QIVR <mark>PL</mark> DEALALAEA
A4VGE7	RVLESRYL	<b>VRGYIF</b> QHT	reesa <mark>qla</mark> yaq	GLDRSREQADI	LRGLLPV	DQHSHLDRMTS.	ALQR <mark>YR</mark> AAI	ETFKVGMDATI	ARTALAS	EIGGLLEING	NLYRN <mark>O</mark> QTKMI	GETQQARIQ	TMLTAFASALL	GLLAAWFIAR	QIILPLRHTLAMARRIA
Q4ZTX7	LFQKM <mark>R</mark> FD	LRGYTYSLF	(AENRAP <mark>AET</mark> S	SMNTVIEFVRN	JLQGFI	GQSAIIKHLVD:	SMIS <mark>Y</mark> QNTI	LNQFTAAQARID	AQAGITK	DIGILFECAD	KLSENQVNLRV	EDVSQAKML	LSVWLIAALIM	ISAL <mark>AA</mark> WV	
Q48IU4	LFQKM <mark>R</mark> FD	L <mark>RGY</mark> TYSLF	(TENRAPAETS	SMDTVINFVKN	JLKGF – – I	SQSATIKHLVD	ALLG <mark>Y</mark> QNTI	LNQFTAAQDKID	AQAGINK	TIAILFDSAD	KLSANQVSL <mark>R</mark> I	EDVGEAKTL	LSVWLIAALIM	ISAL <mark>AAWVITR</mark>	LIVGPLLDTLK
Q882L0	LFQKM <mark>R</mark> FD	L <mark>RGY</mark> TYSLF	(AENRAP <mark>A</mark> EAS	SMSAVINFVKG	SLQGFI	SQSATIKHLVD	SMVSYQNTN	INQFTAAQASID	QAQAGITK	VIGVLFKSAD	QLSANQVSLRI	EDVDQARTL	LSVWLVAALIM	ISFL <mark>AAWVITR</mark>	LIVGPLLETLK
Q4ZW84	SVQKMRTA	.F <mark>R</mark> S <b>Y</b> TASPS	SKSGEDTVRQ	AIAQVVASIDI	LKDTS	LPRADVQALAA	GMAT <mark>Y</mark> SGQI	LETLVAAQAKVD	EAQGGITT	SIATILGITD	KMTAIQNEF <mark>R</mark> A	ASDAEKAQEK	ILLWLGLSALI	GVLAAWLITR	SIVHPL
Q4LBM3	SVQKMRTS	F <mark>R</mark> A <mark>Y</mark> TASPN	JASAEDTVRR	IGEVITQTDV	/FKNVS	STSAAIVQNLAR	/FAD <mark>Y</mark> GKQI	LEALVAVQAKVD	EAQAGITS	SITKILDI <mark>S</mark> D	KMTAIQNEF <mark>R</mark> V	/SDASDAQNK	IMLWLILSIIS	GVLAAWLITR	SIVQPLKETVAIV

Legend to Supplementary Figure 2) Sequence alignment of members of the McpS-LBR like family. The sequence of McpS-LBR (pp4658) was submitted to a BLAST search using the SwissProt/TrEMBL The database. embnet server (http://www.ch.embnet.org/software/bBLAST.html) and the blosum62 matrix were used for this search. Shown is a sequence alignment of the 47 sequences with highest sequence similarity. The sequence alignment was done using the CLUSTALW algorithm (Thompson et al., 1997, Nucleic Acids Res. 24. 4876) of **NPSA** (http://npsa-pbil.ibcp.fr/cgithe server bin/npsa automat.pl?page=/NPSA/npsa clustalw.html) using a gap opening penalty of 10 and a gap extension penalty of 0.1. The degree of sequence identity/similarity is shown in red (highly conserved residues) and green (moderately conserved residues). The secondary structure for each sequence was predicted using the consensus method of the NPSA server (http://npsapbil.ibcp.fr/cgi-bin/npsa automat.pl?page=/NPSA/npsa seccons.html) using the MLRC (Guermeur et al., 1999, Bioinformatics 15, 413-421), DSC (King & Sternberg, 1996, Protein Sci. 5:2298-310) and PhD algorithms (Rost & Sander, 1993, J. Mol. Biol. 232, 584-99). Amino acids present in αhelical sections are shaded in grey, those predicted to form β-strand are shaded in yellow and coil/turn regions are left without shading. The amino acids which interact with malate and acetate are highlighted by orange and cyan bars, respectively, in the upper part of the alignment.

### **Supplementary Figure 3**)



Legend to Supplementary Figure 3) Analysis of native and mutant McpS-LBR by far uv circular dichroism spectroscopy. Protein (0.20 mg/ml) was dialyzed against 5 mM Tris-HCl, 5 mM HEPES, 5 mM MES, pH 6.0 and spectra were recorded on a Jasco 715 spectropolarimeter (Great Dunmos, UK). Far UV spectra were recorded in quartz cells with a path length of 1 mm. Five consecutive spectra were recorded and the resulting average spectra corrected with the buffer spectrum.

### **Supplementary Figure 4**



Legend to Supplementary Figure 4) Microcalorimetric titrations of native and mutant McpS-LBR with citrate. Upper panel: (A) Raw data for the titration of 45  $\mu$ M McpS-LBR with 9.6  $\mu$ l aliquots of 1 mM citrate and (B) titration of 25  $\mu$ M McpS-LBR R254A with 12.8  $\mu$ l aliquots of 3 mM citrate. Lower panel: Integrated, concentration-normalized and dilution heat corrected raw data. Data were fitted using the "One binding site model" of the MicroCal version of ORIGIN.  $\Box$ , citrate binding to native McpS-LBR, O, citrate binding to the R254A mutant. The thermodynamic parameters derived are shown in Supplementary Table 2.

# **Supplementary Figure 5**



**Legend to Supplementary Figure 5) Electron density for acetate in the refined malate structure**. The McpS-LBD Sigma weighted 2Fo-Fc electron density map at a 1.8 level covering the acetate binding region.

### **Supplementary Figure 6)**



Legend to Supplementary Figure 6) Microcalorimetric titration of McpS-LBR and its R183A mutant with acetate. Upper panel: Raw data for the titration of 98  $\mu$ M McpS-LBR (A) and McpS-LBR R183A (B) with 50 mM acetate. In both cases protein was in 5 mM Tris-HCl, 5 mM HEPES, 5 mM MES, pH 6.0. The injection volume was in both cases 12.8  $\mu$ l. Lower panel: Integrated raw data after correction for dilution heats and normalization using ligand concentrations.  $\circ$  McpS-LBR ; $\Box$  McpS-LBR R183A. Data were fitted with the "One binding site model" of the MicroCal version of ORIGIN.

# **Supplementary Figure 7**)



Legend to Supplementary Figure 7) Microcalorimetric titration of McpS-LBR R183A with malate. Upper panel: Raw data for the titration of 35  $\mu$ M McpS-LBR with 12.8  $\mu$ l aliquots of 1 mM malate. Lower panel: Integrated, concentration-normalized and dilution heat corrected raw data. Data were fitted using the "One binding site model" of the MicroCal version of ORIGIN. The thermodynamic data derived are:  $\Delta H = -20.5 \pm 0.7$  kcal/mol and  $K_D = 9.1 \pm 0.4 \mu$ M.



Legend to Supplementary Figure 8) Effect of pH on chemotaxis of P. putida KT2440R to 50 mM acetate. Quantitative capillary assays were conducted to measure chemotaxis of P. putida KT2440R towards 20 mM HEPES, 20 mM MES buffer at pH 6.5, 7 and pH 8.2. Subsequently taxis to 50 mM acetate solutions in those 3 buffer systems was monitored (the pH of the acetate solutions was verified and small pH deviations were corrected by the addition of diluted NaOH). Experiments were conducted in triplicates and results presented are the means and standard deviation of at least three individual experiments conducted in triplicates. A modified version of the capillary assay (Adler, (1973) J Gen Microbiology 98, 77-91) was used to quantify chemotaxis. In short, mineral salt medium (MS) supplemented with 10 mM succinate was inoculated with P. putida KT2440R and grown to early stationary phase at 30°C with aeration. Cells were then diluted with MS to an OD<sub>600</sub> of 0.08 (corresponding to 10<sup>6</sup>-10<sup>7</sup> cells ml<sup>-1</sup>). Capillary tubes (Microcaps, Drummond Scientific, USA) of 1 µl capacity were sealed at one end by melting over a flame. The capillary was then warmed over the flame and the open end inserted into attractant solution (20 mM HEPES, 20 mM MES buffer at pH values of 6.5, 7 and pH 8.2 with or without 50 mM acetate). About 0.15 ml of this suspension was placed into a small chamber formed by placing a v-shaped needle on a microscope slide. The system was then closed with a glass coverslip, avoiding the formation of air bubbles. A capillary tube was immersed into the cell suspension at its open end. After incubation for 15 min at room temperature, the open end of the capillary was then rinsed and placed into a microfuge tube containing 1 ml of MS buffer. The sealed end was broken and the contents were emptied into the tube. One hundred microliters of this cellular suspension was plated onto M9 medium plates supplement with 10 mM succinate and incubated at 30°C. Colonies were counted after 48 hours growth at 30°C. Note: *P. putida* KT2440R is a rifampicilin-resistant derivative of *P. putida* KT2440. Since the *mcpS* mutant was constructed using *P. putida* KT2440R, the rifampicilin-resistant wild type strain was used for chemotaxis assays.



Legend to Supplementary Figure 9) Chemotaxis response of *Pseudomonas putida* KT2440R and KT2440R *mcpS*::Tn5 strains to buffer at different pH. Experiments were carried out as described for Supp. Fig. 8, except that the *mcpS* mutant strain was used.

### Supplementary Fig. 10)



Legend to Supplementary Figure 10) Evaluation of the influence of the presence of acetate on taxis to succinate and the presence of succinate on the presence of acetate. *P. putida* KT2440R was grown to early stationary phase at 30°C with aeration. Cells were then diluted with minimal slat medium to an  $OD_{600}$  of 0.08 (corresponding to  $10^{6}$ - $10^{7}$  cells ml<sup>-1</sup>) and acetate to a final concentration of 50 mM or succinate to a final concentration of 10 mM were added to the cellular suspension (note: the pH of the acetate and succinate mother solutions were adjusted the pH of the MS medium). Cells were then incubated at room temperature for 10 minutes. Quantitative capillary assays were conducted of acetate containing cells to acetate or to a mixture of acetate and succinate. Analogous experiments involved assays of succinate containing cells to succinate and to the mixture of acetate with succinate. The experiments were conducted as described in the legend to Supp. Figure 8. The data were corrected for background accumulation in capillaries containing buffer. Data shown are means and standard deviations from at least nine capillaries from experiments with at least three different bacterial cultures.



Legend to Supplementary Figure 11) Growth of *P. putida* KT2440R in minimal medium supplemented with different carbon sources. A) Growth curves. Cells were grown in minimal medium (M9) containing glucose, acetate, malate and succinate as carbon sources at a final concentration of 10 mM. Cells were inoculated into fresh media at an  $OD_{600}$  of 0.015 from an M9+succinate stationary-phase culture. Growth at 30°C under agitation (200 rpm) was monitored by measuring  $OD_{600}$ . B) Image of growth culture tubes at the moment growth has ceased.

Supplementary Table 1) Contacts between monomers A	A and B in the structure of McpS-LBR.
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Amino acid/atom chain A	amino acid/atom chain B	Distance (Å)
Hydrogen bonds		
Thr57/OG1	Thr57/OG1	3.73
Ser173/OG	Tyr169/OH	3.29
Ile184/O	Arg187/NH1	2.86
Ala191/O	Asn70/ND2	3.52
Glu192/OE1	Arg134/NH2	3.72
Tyr272/OH	Tyr272OH	2.80
Gln177/NE2	Ser173/O	3.80
Gln177/NE2	Gln177/OE1	3.06
Arg187/NH1	Ile184/O	2.87
Asn70/ND2	Glu192/OE1	2.72
Lys54/NZ	Asp269/OD1	3.23
Salt bridges		
Glu192/OE1	Arg134/NH2	3.72
Lys54/NZ	Asp269/OD1	3.23
Lys54/NZ	Asp269/OD2	3.01

Hydrogen bonds were defined by a donor-acceptor distance of at least 3.8 Å and a donor acceptor angle of more than 90 degrees.

Supplementary Table 2) Dissociation constants (in  $\mu$ M) determined from microcalorimetric titrations of native McpS-LBR and site-directed mutants R60A, R63A and R254A with different ligands.

	wild type	R60A	R63A	R254A
Malate	$8.5 \pm 0.7^{1}$	No binding	No binding	No binding
Fumarate	$17 \pm 2^{1}$	No binding	No binding	No binding
Oxaloacetate	$24 \pm 6^{1}$	No binding	No binding	No binding
Succinate	$82 \pm 3^{1}$	No binding	No binding	No binding
Butyrate	$92 \pm 9^1$	No binding	No binding	$107 \pm 17$
Citrate	$109 \pm 14^{1}$	$500 \pm 25$	$775 \pm 60$	$813 \pm 80$
Isocitrate	$337 \pm 42^{1}$	No binding	No binding	No binding

<sup>1</sup> Data are taken from Lacal *et al.* (2010) J. Biol. Chem. 285, 23126.

# Supplementary Table 3) Literature indicating high acetate concentrations in the natural habitat of *Pseudomonas*.

Observation	Comment and literature references
Acetogenesis under aerobic conditions	Growth on excess glucose or other highly assimilable carbon sources inhibits respiration, a behavior called the bacterial crabtree effect. As a consequence of the Crabtree effect, as much as 15% of the glucose can be excreted as acetate. As a consequence the acetate concentration in the growth medium increase to up to 10 mM – 35 mM in organisms as diverse as <i>E. coli</i> (El-Mansi and Holmes, (1989) J Gen Microbiol. 135:2875-83, Bulter et al. (2004) Proc Natl Acad Sci USA 101:2299-304), <i>Acetobacterium</i> spp. (Kim and Chang (2009) Bioresour Technol. 100:4527-30) or <i>Saccharomyces cerevisiae</i> (Aboca et al. (2012) Yeast 29:95-110).
Acetogenesis under anaerobic conditions	Under anaerobic conditions a branched TCA cycle occurs which forms succinyl-CoA by a reductive pathway and 2-ketoglutarate by an oxidative one. This branched form of the TCA cycle does not generate energy; instead it functions biosynthetically, producing precursor metabolites like acetate (Wolfe et al. (2005) Microbiol Mol Biol Rev. 69:12-50).
High abundance of acetate in sewage where it is considered as a major contaminant	Acetate is the primary product of acetogenesis in sewage (Yu et al. Water Sci Technol. (2003) 48:69-75) and the dominating volatile fatty acid in wastewater (Raunkjaer et al (1997) Water Res. 31:2727-36) and is therefore considered as a contaminant. There is large number of studies which investigate acetate degradation in sewage waters (Wang and Ford (2009) Environ Sci Technol. 43:5921–5927, Toepfer et al. (2012) FEMS Microbiol Ecol. 81:163-71)
High acetate concentrations	<i>P. putida</i> KT2440 has a saprophytic lifestyle and acetate was found to be abundantly present in plant root tissues, where it accounted for around 1 % of the total organic carbon content of roots (Rentz et al. (2004) Environ Microbiol. 6:574-83).
High acetate concentrations in plant root exudates	<i>P. putida</i> KT2440 colonizes plant roots efficiently (Molina et al. (2000) Soil Biol. Biochem. 32:315–321) and was found to use organic acids present in root exudates as the primary carbon source during rhizosphere colonization (Lugtenberg et al. (2001) Annu. Rev. Phytopathol. 39:461–490). A study of Lucas-Garcia (2001) Phytochem Anal. 12:305-11) has shown that acetate is the most abundant organic acids present in exudates of <i>Lupinu albus</i> at concentration of around 1.5 mg/g root dry weight. These results are also consistent with a NMR study, which demonstrates that acetate is by far the most abundant organic compound in wheat root exudates (Fan et al. (2001) Phytochemistry 57:209-21).

# Supplementary Table 4) Oligonucleotides used for the construction of McpS-LBR mutants.

Name	sequence	Construction of mutant
R60A	5'-TCACCGATCTAGCCATTGCGCGCCTGCA -3',	R60A
R63A	5'-TCTACGCATTGCGGCCCTGCAGTACATGA-3',	R63A
R254A	5'-ACATCACCACCTCGGCCGCCGAAATGAC-3'	R254A
R183Af1	5'-GACCGTAGCAACCATATGGGCGATATTGG-3'	R183A
R183Ar1	5'-CACATCGATGGCTACCTGCAGCAG-3`	R183A
R183Af2	5'-CCTGCAGGCTGGGATCCTGTCAGCTCTCGAT-3'	R183A
R183Ar2	5'- CTGCTGCAGGTAGCCATCGATGTG-3'	R183A

# Supplementary analysis 1)

Secondary structure prediction and three dimensional homology modeling of the ligand binding regions of 50 randomly selected cluster II chemoreceptors. The transmembrane regions of these receptors were predicted by the DAS algorithm (Cserzo et al. (1997) Prot. Eng. 10 673-676) and the sequence fragment in between both transmembrane regions, comprising the ligand binding region, were submitted to the consensus secondary structure prediction algorithm (http://npsa-pbil.ibcp.fr/cgi-bin/npsa\_automat.pl?page=/NPSA/npsa\_seccons.html). Obtained profiles were then classified as belonging to the double PDC like fold or the McpS-LBR like fold. All ligand binding regions were submitted to 3D homology modeling algorithm using CPH models (http://www.cbs.dtu.dk/services/CPHmodels/, Nielsen et al. (2010) Nucleic Acids Research 38, doi:10.1093/nar/gkq535) and in cases where modeling was possible, the resulting models are shown. The phylogenetic characteristics of the corresponding strains are indicated. At the beginning of this document the 3D structures and the secondary structure profiles of two reference proteins for double PDC and McpS-like domains are shown.

Codes for secondary structure predictions: blue bar: alpha helix, red bar: beta strand, pink bar: coil

Classification of chemoreceptors according to the size of their ligand binding region. Figure taken from Lacal et al. (2010) Env. Microbiol. 12, 2873.



Fig. 6. Classification of MCP sequences according to the size of the LBR. This study is based on the totality of MCPs that show topology Ia (2386 of bacterial origin and 50 of archaea). This topology is predominant in bacteria and archaea. The LBR of proteins of this topology is flanked by two TM regions and therefore the size of the LBR can be determined precisely.

# Reference structures and secondary structure prediction output for a double PDC domain and for the McpS-lignad binding region

1. **Double PDC domain: Crystal Structure of the extracellular domain of the putative histidine kinase from** *Methanosarcina mazei* (pdb: 3Lia, Zhang and Hendrickson, 2010, J Mol Biol. 400:335-53) and the secondary structure profile.



50	100	150	200	

## 2. Structure and secondary structure prediction for McpS-LBR of *P. putida* KT2440.





Ligand binding regions of the 50 selected chemoreceptors that match the secondary structure profile of double PDC sensor domain fold. When available, 3D homology models of these domains or fragments thereof are shown.

1) >uniprot|QOAV12|QOAV12\_SYNWW Putative methyl-accepting chemotaxis sensory transducer precursor [Syntrophomonas wolfei subsp. wolfei str. Goettingen] <u>Bacteria</u> > <u>Firmicutes</u> > <u>Clostridia</u> > <u>Clostridiales</u> > <u>Syntrophomonadaceae</u> > <u>Syntrophomonas</u>





2) >uniprot|Q9KSG7|Q9KSG7\_VIBCH Methyl-accepting chemotaxis protein [Vibrio cholerae O1 biovar El Tor str. N16961 <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Vibrionales</u> > <u>Vibrionaceae</u> > <u>Vibrio</u>





3) >uniprot|Q314Z2|Q314Z2\_DESDG Methyl-accepting chemotaxis sensory transducer [Desulfovibrio desulfuricans subsp. desulfuricans str. G20] Bacteria > Proteobacteria > Deltaproteobacteria >

Desulfovibrionales > Desulfovibrionaceae > Desulfovibrio





4) >tr|H3SL86|H3SL86\_9BACL Methyl-accepting chemotaxis protein OS=Paenibacillus dendritiformis C454 GN=PDENDC454\_21604 PE=4 SV=1 Bacteria > Firmicutes > Bacillales > Paenibacillaceae > Paenibacillus



5) >tr|A6LJU3|A6LJU3\_THEM4 Methyl-accepting chemotaxis sensory transducer OS=Thermosipho melanesiensis (strain BI429 / DSM 12029) GN=Tmel\_0322 PE=4 SV=1 Bacteria > Thermotogae > Thermotogales > Thermotogaceae >

Thermosipho



6) >tr|A5N103|A5N103\_CLOK5 Predicted methyl-accepting chemotaxis protein OS=Clostridium kluyveri (strain ATCC 8527 / DSM 555 / NCIMB 10680) GN=CKL\_2787 PE=4 SV=1 <u>Bacteria</u> > <u>Firmicutes</u> > <u>Clostridia</u> > <u>Clostridiales</u> > <u>Clostridiaceae</u> > <u>Clostridium</u>





7)>tr|E8UWG7|E8UWG7\_THEBF Chemotaxis sensory transducer OS=Thermoanaerobacter brockii subsp. finnii (strain ATCC 43586 / DSM 3389 / AKO-1) GN=Thebr\_1886 PE=4 SV=1 Bacteria > Firmicutes > Clostridia > Thermoanaerobacterales > Thermoanaerobacteriaceae > Thermoanaerobacter





8) >string|326423.RBAM\_028290|326423.RBAM\_028290 TlpB [Bacillus amyloliquefaciens FZB42]

<u>Bacteria</u> > <u>Firmicutes</u> > <u>Bacillales</u> > <u>Bacillaceae</u> > <u>Bacillus</u>





9) >uniprot|A4J3R2|A4J3R2\_9FIRM Methyl-accepting chemotaxis sensory transducer precursor [Desulfotomaculum reducens MI-1] <u>Bacteria</u> > <u>Firmicutes</u> > <u>Clostridia</u> > <u>Clostridiales</u> > Peptococcaceae > Desulfotomaculum



10) >uniprot|A6WDS8|A6WDS8\_KINRA Methyl-accepting chemotaxis sensory transducer precursor [Kineococcus radiotolerans SRS30216] Bacteria > Actinobacteria > Actinobacteridae > Actinomycetales > Kineosporiineae > Kineosporiaceae > Kineococcus



11) uniprot|Q0BGB8|Q0BGB8\_BURCM Methyl-accepting chemotaxis sensory transducer precursor [Burkholderia ambifaria AMMD] Bacteria > Proteobacteria > Betaproteobacteria > Burkholderiales > Burkholderiaceae > Burkholderia > Burkholderia cepacia complex



No 3D modelization possible

12) >uniprot|AlS1I6|AlS1I6\_SHEAM Putative methyl-accepting chemotaxis sensory transducer precursor [Shewanella amazonensis SB2B]

<u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Alteromonadales</u> > Shewanellaceae > Shewanella



### No modelling possible

13) >uniprot|A6TSC5|A6TSC5\_9CLOT Methyl-accepting chemotaxis sensory transducer precursor [Alkaliphilus metalliredigens QYMF] <u>Bacteria</u> > <u>Firmicutes</u> > <u>Clostridia</u> > <u>Clostridiales</u> > Clostridiaceae > Alkaliphilus



### No modelling possible

14) >uniprot|A3QAH0|A3QAH0\_SHELP Methyl-accepting chemotaxis sensory transducer precursor [Shewanella loihica PV-4] <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Alteromonadales</u> > Shewanellaceae > Shewanella





15) >tr|B3IZY6|B3IZY6\_BACAN Methyl-accepting chemotaxis protein OS=Bacillus anthracis Tsiankovskii-I GN=BATI\_3176 PE=4 SV=1 Bacteria > Firmicutes > Bacillales > Bacillaceae > Bacillus > Bacillus cereus group



16) >tr|B7R938|B7R938\_9THEO Methyl-accepting chemotaxis protein signaling domain protein OS=Carboxydibrachium pacificum DSM 12653 GN=CDSM653\_848 PE=4 SV=1

<u>Bacteria</u> > <u>Firmicutes</u> > <u>Clostridia</u> > <u>Thermoanaerobacterales</u> > Thermoanaerobacteriaceae > Caldanaerobacter





17) >uniprot|Q63G86|Q63G86\_BACCZ Methyl-accepting chemotaxis
protein [Bacillus cereus E33L]
Bacteria > Firmicutes > Bacillales > Bacillaceae > Bacillus >

Bacillus cereus group





18) uniprot|Q8DLC7|Q8DLC7\_SYNEL methyl-accepting chemotaxis
protein [Thermosynechococcus elongatus BP-1]
Bacteria > Cyanobacteria > Chroococcales > Thermosynechococcus



19) >uniprot|A1WD99|A1WD99\_ACISJ Methyl-accepting chemotaxis sensory transducer precursor [Acidovorax sp. JS42] Bacteria > Proteobacteria > Betaproteobacteria > Burkholderiales > Comamonadaceae > Acidovorax





20) >uniprot|Q3ADB4|Q3ADB4\_CARHZ Methyl-accepting chemotaxis protein [Carboxydothermus hydrogenoformans Z-2901] <u>Bacteria</u> > <u>Firmicutes</u> > <u>Clostridia</u> > <u>Thermoanaerobacterales</u> > Thermoanaerobacteriaceae > Carboxydothermus

50	100	150	200	



21) >tr|A6VAX7|A6VAX7\_PSEA7 Chemotactic transducer PctA OS=Pseudomonas aeruginosa (strain PA7) GN=pctA PE=4 SV=1 Bacteria > Proteobacteria > Gammaproteobacteria > Pseudomonadales > Pseudomonadaceae > Pseudomonas





22) >tr|A6EVV0|A6EVV0\_9ALTE Methyl-accepting chemotaxis protein OS=Marinobacter algicola DG893 GN=MDG893\_07065 PE=4 SV=1 <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Alteromonadales</u> > Alteromonadaceae > Marinobacter



### No modelling possible

23) >tr|E6XJV8|E6XJV8\_SHEP2 Methyl-accepting chemotaxis sensory transducer with Cache sensor OS=Shewanella putrefaciens (strain 200) GN=Sput200\_1889 PE=4 SV=1

<u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Alteromonadales</u> > <u>Shewanellaceae</u> > <u>Shewanella</u>





24)>tr|H2G1L7|H2G1L7\_OCESG Methyl-accepting chemotaxis sensory transducer OS=Oceanimonas sp. (strain GK1) GN=GU3\_04320 PE=4 SV=1 <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Aeromonadales</u> > Aeromonadaceae > Oceanimonas





25)>tr|F3BIJ7|F3BIJ7\_PSEHA Putative chemotactic transducer OS=Pseudoalteromonas haloplanktis ANT/505 GN=PH505\_ap00180 PE=4 SV=1

<u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Alteromonadales</u> > Pseudoalteromonadaceae > Pseudoalteromonas





26) >tr|A4SK06|A4SK06\_AERS4 Methyl-accepting chemotaxis protein OS=Aeromonas salmonicida (strain A449) GN=ASA\_1106 PE=4 SV=1 Bacteria > Proteobacteria > Gammaproteobacteria > Aeromonadales > Aeromonadaceae > Aeromonas





27) >tr|Q9KAL2|Q9KAL2\_BACHD Methyl-accepting chemotaxis protein OS=Bacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125) GN=BH2275 PE=4 SV=1



Ligand binding regions of the 50 selected chemoreceptors that match the secondary structure profile of the McpS-LBR. When available, 3D homology models of these domains or fragments thereof are shown.

1) uniprot|A0KGQ7|A0KGQ7\_AERHH Putative chemotaxis transducer [Aeromonas hydrophila subsp. hydrophila ATCC 7966] Bacteria > Proteobacteria > Gammaproteobacteria > Aeromonadales > Aeromonadaceae > Aeromonas



2) >tr|A7K1V8|A7K1V8\_VIBSE Methyl-accepting chemotaxis protein OS=Vibrio sp. (strain Ex25) GN=VEA\_001468 PE=4 SV=1 Bacteria > Proteobacteria > Gammaproteobacteria > Vibrionales > Vibrionaceae > Vibrio



3) uniprot|Q9RYG4|Q9RYG4\_DEIRA methyl-accepting chemotaxisrelated protein [Deinococcus radiodurans R1]

<u>Bacteria</u> > <u>Deinococcus-Thermus</u> > <u>Deinococci</u> > <u>Deinococcales</u> > <u>Deinococcaceae</u> > <u>Deinococcus</u>



4) uniprot A1U770 A1U770 MARAV Methyl-accepting chemotaxis sensory transducer [Marinobacter aquaeolei VT8]

<u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Alteromonadales</u> > <u>Alteromonadaceae</u> > <u>Marinobacter</u>



5) uniprot|Q8Y1L9|Q8Y1L9\_RALSO Putative twitching motility transmembrane protein [Ralstonia solanacearum GMI1000] <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Betaproteobacteria</u> > <u>Burkholderiales</u> > Burkholderiaceae > Ralstonia



6) uniprot|Q07HJ2|Q07HJ2\_RHOP5 Methyl-accepting chemotaxis sensory transducer precursor [Rhodopseudomonas palustris BisA53] Bacteria > Proteobacteria > Alphaproteobacteria > Rhizobiales > Bradyrhizobiaceae > Rhodopseudomonas



7) >tr|Q1IFB1|Q1IFB1\_PSEE4 Putative methyl-accepting chemotaxis transducer OS=Pseudomonas entomophila (strain L48) GN=PSEEN0717 PE=4 SV=1 Bacteria > Proteobacteria > Gammaproteobacteria > Pseudomonadales

<u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Pseudomonadare</u> > <u>Pseudomonadaceae</u> > <u>Pseudomonas</u>





8) >tr|G2L0T0|G2L0T0\_PSEAI Putative chemotaxis transducer OS=Pseudomonas aeruginosa M18 GN=PAM18\_5187 PE=4 SV=1 <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Pseudomonadales</u> > Pseudomonadaceae > Pseudomonas





9) tr|Q1QPB9|Q1QPB9\_NITHX Methyl-accepting chemotaxis sensory transducer OS=Nitrobacter hamburgensis (strain X14 / DSM 10229) GN=Nham\_1080 PE=4 SV=1

<u>Bacteria</u> > <u>Proteobacteria</u> > <u>Alphaproteobacteria</u> > <u>Rhizobiales</u> > <u>Bradyrhizobiaceae</u> > <u>Nitrobacter</u>



10) >uniprot|A5EAD2|A5EAD2\_BRASB Putative methyl-accepting chemotaxis receptor/sensory transducer [Bradyrhizobium sp. BTAi1] <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Alphaproteobacteria</u> > <u>Rhizobiales</u> > <u>Bradyrhizobiaceae</u> > <u>Bradyrhizobium</u>



11) >tr|A9W2P9|A9W2P9\_METEP Chemotaxis sensory transducer OS=Methylobacterium extorquens (strain PA1) GN=Mext\_1454 PE=4 SV=1 Bacteria > Proteobacteria > Alphaproteobacteria > Rhizobiales > Methylobacteriaceae > Methylobacterium



12) >tr|Q4KIL8|Q4KIL8\_PSEF5 Methyl-accepting chemotaxis sensory transducer OS=Pseudomonas fluorescens (strain Pf-5 / ATCC BAA-477) GN=PFL\_0778 PE=4 SV=1



13) >tr|Q2W0L7|Q2W0L7\_MAGSA Methyl-accepting chemotaxis protein OS=Magnetospirillum magneticum (strain AMB-1 / ATCC 700264) GN=amb3804 PE=4 SV=1,

<u>Bacteria</u> > <u>Proteobacteria</u> > <u>Alphaproteobacteria</u> > <u>Rhodospirillales</u> > <u>Rhodospirillaceae</u> > <u>Magnetospirillum</u>



14) >tr|D3P1U9|D3P1U9\_AZOS1 Methyl-accepting chemotaxis protein OS=Azospirillum sp. (strain B510) GN=AZL\_a10970 PE=4 SV=1 Bacteria > Proteobacteria > Alphaproteobacteria > Rhodospirillales > Rhodospirillaceae > Azospirillum



15) >tr|G2ZPS4|G2ZPS4\_9RALS Type IV pilus transmembrane protein PilJ,twitching motility, Methyl-accepting chemotaxis protein OS=blood disease bacterium R229 GN=pilJ PE=4 SV=1 <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Betaproteobacteria</u> > <u>Burkholderiales</u> > <u>Burkholderiaceae</u> > <u>Ralstonia</u>



16) >tr|B3R317|B3R317\_CUPTR TWITCHING MOTILITY TRANSMEMBRANE
PROTEIN, Methyl-accepting chemotaxis protein OS=Cupriavidus
taiwanensis (strain R1 / LMG 19424) GN=pilJ PE=4 SV=1
Bacteria > Proteobacteria > Betaproteobacteria > Burkholderiales >
Burkholderiaceae > Cupriavidus



17) >tr|D8DDK7|D8DDK7\_COMTE Methyl-accepting chemotaxis sensory transducer OS=Comamonas testosteroni S44 GN=CTS44\_24573 PE=4 SV=1 <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Betaproteobacteria</u> > <u>Burkholderiales</u> > Comamonadaceae > Comamonas



18) >tr|A7BZF5|A7BZF5\_9GAMM Methyl-accepting chemotaxis sensory transducer OS=Beggiatoa sp. PS GN=BGP\_1625 PE=4 SV=1 <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Thiotrichales</u> > Thiotrichaceae > Beggiatoa



19)>tr|D3RVN3|D3RVN3\_ALLVD Methyl-accepting chemotaxis sensory transducer OS=Allochromatium vinosum (strain ATCC 17899 / DSM 180 / NBRC 103801 / D) GN=Alvin\_0193 PE=4 SV=1 Bacteria > Proteobacteria > Gammaproteobacteria > Chromatiales > Chromatiaceae > Allochromatium



20)>tr|F7NA63|F7NA63\_XYLFA Methyl-accepting chemotaxis protein Tar OS=Xylella fastidiosa EB92.1 GN=tar PE=4 SV=1 <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Xanthomonadales</u> > Xanthomonadaceae > Xylella



21) >tr|D4SXS5|D4SXS5\_9XANT Pilus biogenesis protein OS=Xanthomonas fuscans subsp. aurantifolii str. ICPB 11122 GN=pilJ PE=4 SV=1

<u>Bacteria</u> > <u>Proteobacteria</u> > <u>Gammaproteobacteria</u> > <u>Xanthomonadales</u> > Xanthomonadaceae > Xanthomonas



22) >tr|E8TQJ1|E8TQJ1\_ALIDB Chemotaxis sensory transducer OS=Alicycliphilus denitrificans (strain JCM 14587 / BC) GN=Alide\_3630 PE=4 SV=1

<u>Bacteria</u> > <u>Proteobacteria</u> > <u>Betaproteobacteria</u> > <u>Burkholderiales</u> > Comamonadaceae > Alicycliphilus



23) >tr|Q478V7|Q478V7\_DECAR Chemotaxis sensory transducer OS=Dechloromonas aromatica (strain RCB) GN=Daro\_3896 PE=4 SV=1 <u>Bacteria</u> > <u>Proteobacteria</u> > <u>Betaproteobacteria</u> > <u>Rhodocyclales</u> > <u>Rhodocyclaceae</u> > <u>Dechloromonas</u>

