Subsystem: Terminal cytochrome oxidases

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Abbrev	Functional Role
TPC	Transport ATP-binding protein cydC
TPD	Transport ATP-binding protein cydD
CydA	Cytochrome d ubiquinol oxidase subunit I (EC 1.10.3)
CydB	Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3)
СуоА	Cytochrome O ubiquinol oxidase subunit II (EC 1.10.3)
СуоВ	Cytochrome O ubiquinol oxidase subunit I (EC 1.10.3)
CyoC	Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3)
CyoD	Cytochrome O ubiquinol oxidase subunit IV (EC 1.10.3)
AA3-6001	AA3-600 quinol oxidase subunit l
AA3-600II	AA3-600 quinol oxidase subunit II
AA3-600III	AA3-600 quinol oxidase subunit IIII
AA3-600IV	AA3-600 quinol oxidase subunit IV
TPCD	Transport ATP-binding protein cydCD
Qxtl	putative Cytochrome bd2, subunit l
Qxtll	putative Cytochrome bd2, subunit II

Subset	
cytochrome_bd2_complex	14,15
cytochrome_bd_complex_lowO2	3,4
cytochrome_bo_complex_highO2	5,6,7,8
cytochrome_caa3_complex	9,10,11,12
required_for_bd_expr	1,2,13

Olga Vassieva Fellowship for Interpretation of Genomes

- In many bacteria the electron transport is highly diversified and there is more than one terminal respiratory oxidase. Different combinations of these complexes can be present in one organism. Terminal cytochrome oxidases exchange electrons either with the quinione pool or directly with cytochromes, depending on their redox potential.
- The best-characterized terminal oxidases are those that are homologous to the aa3-type cytochrome c oxidases of mitochondria. The latter and bb3 (alternative) types of terminal oxidases are included in the Subsystem 'Terminal cytochrome c oxidases' and are excluded from from this subsystem arbitrary because of the high volume of functional roles in both subsystems. Here we include cytochrome bo, bd, its variation bd2, and caa3 complexes. The subsystem is studied and annotated in all SEED organisms. About 15 variant codes corresponding to observed combinations are defined

An operational variant of this subsystem can be asserted in 330 out of 350 included organisms

Subsystem diagram (fragment)

Part of the respiratory chain diagram illustrating the role of terminal oxidases in respiration



Subsystem Spreadsheet (a fragment)

Examples of functional variants and multiprotein complexes

Organism	Variant Code	TPC	TPD	CydA	CydB	СуоА	СуоВ	CyoC	CyoD	AA3-600I	АА3-600П	AA3-600III	AA3-600IV
Synechocystis sp. PCC 6803 [B]	1	?	?	<u>606</u>	607								
Anabaena variabilis ATCC 29413 [B]	1	?	?	<u>1553,</u> <u>3834</u> , <u>4043</u> , <u>4046</u>	<u>1555,</u> <u>4044,</u> <u>4045</u>	\			(C	aa3	
Bacillus subtilis subsp. subtilis str. 168 [B]	2	<u>3879</u>	<u>3878</u>	<u>3074</u> , <u>3881</u>	<u>3880</u>	bd				<u>3821</u>	<u>3822</u>	<u>3820</u>	3819
Mycobacterium tuberculosis CDC1551 [B]	3	<u>1703</u>	<u>1704</u>	<u>1706</u>	<u>1705</u>								
Escherichia coli CFT073 [B]	4	<u>995</u>	<u>996</u>	<u>1087</u> , 784	<u>1088</u> , 785	21	<u>520</u>	<u>519</u>	<u>518</u>	Qxt	tI QxtI		
Proteus mirabilis HI4320 [B]	11	<u>2010</u>	<u>2011</u>	<u>1168</u>	<u>1169</u>	<u>916</u> , <u>917</u>	<u>2672</u> , <u>918</u>	<u>2673</u>	<u>2674</u>	211	26, <u>2127.</u> 5 <u>816</u>		
Pseudomonas aeruginosa PAO1 [B]	15					<u>318</u>	<u>1319</u>	<u>1320</u>	<u>1321</u>	39	29 3928	bd2	
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Open questions, comments, conjectures

- Cytochrome complex bd is composed of the two main subunits CydA and CydB, but in the majority of organisms it requires additional proteins CydD and CydC for its expression.
- Function of CydC,D is not clear, although they belongs to a family of ATP-binding cassette transporters. In E.coli CydCD has been shown to transports cysteine, which is crucial for redox homeostasis in the periplasm (Pittman et al., 2002).
- In B. subtilis overexpression of cydAB alone does not lead to production of functional cytochrome bd complex even in a CydD mutant strain (Winstedt et al, 1998). Potential function of these additional subunits in Gram positive organisms remains a mystery.
- CydD, and CydC subunits are missing in some organisms, e.g. cyanobacteria. It is not clear though, if they are required for a functional bd complex in these particular organisms. The so called bd2 complex (homologous to bd) seems to not require CydC or CydD:
 - no clear homologs of known CydC,D subunits can be asserted in these organisms
 - the corresponding gene clusters do not include any putative transporters potential gene candidates for the CydD and CydC functional roles
- Can it be that all CydC,D-less bd complexes are actually bd2 ones? Is it just a matter of terminology or a meaningful difference between the bd and bd2 complexes?