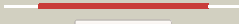



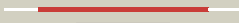







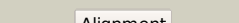


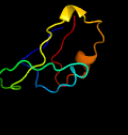





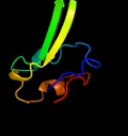

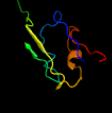

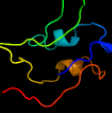
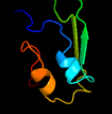

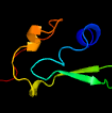

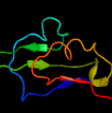


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1786 (-)_2024835_2025038
Date	Fri Aug 2 13:30:39 BST 2019
Unique Job ID	d33e1f842638145d

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4id8A_	 Alignment		99.7	33	PDB header: electron transport Chain: A; PDB Molecule: putative ferredoxin; PDBTitle: the crystal structure of a [3Fe-4S] ferredoxin associated with2 cyp194a4 from r. palustris haa2
2	d1iqza_	 Alignment		99.6	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
3	d1fxra_	 Alignment		99.6	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
4	d1sj1a_	 Alignment		99.5	30	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
5	d1vjwa_	 Alignment		99.5	31	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
6	c1dw1A_	 Alignment		99.2	22	PDB header: electron transfer Chain: A; PDB Molecule: ferredoxin i; PDBTitle: the ferredoxin-cytochrome complex using heteronuclear nmr2 and docking simulation
7	c3gyxl_	 Alignment		98.6	27	PDB header: oxidoreductase Chain: J; PDB Molecule: adenylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
8	d1xera_	 Alignment		98.5	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Archaeal ferredoxins
9	d1jnrb_	 Alignment		98.5	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
10	c5t5iG_	 Alignment		98.5	24	PDB header: oxidoreductase Chain: G; PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdg; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
11	c5odhG_	 Alignment		98.5	27	PDB header: oxidoreductase Chain: G; PDB Molecule: heterodisulfide reductase, subunit a; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus soaked with heterodisulfide3 for 3.5 minutes

12	c5c4iB_	Alignment		98.3	17	PDB header: oxidoreductase Chain: B: PDB Molecule: oxalate oxidoreductase subunit delta; PDBTitle: structure of an oxalate oxidoreductase
13	c6huml_	Alignment		98.3	19	PDB header: proton transport Chain: I: PDB Molecule: nad(p)h-quinone oxidoreductase subunit i; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
14	c1gthD_	Alignment		98.3	16	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dhd) from pig, ternary complex with 2 nadph and 5-iodouracil
15	d1gtea5	Alignment		98.3	13	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
16	d2fug91	Alignment		98.3	24	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
17	c2fugG_	Alignment		98.3	24	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase chain 9; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
18	c2gmhA_	Alignment		98.2	3	PDB header: oxidoreductase Chain: A: PDB Molecule: electron transfer flavoprotein-ubiquinone PDBTitle: structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
19	d1blua_	Alignment		98.2	16	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
20	c6cfwN_	Alignment		98.2	22	PDB header: membrane protein Chain: N: PDB Molecule: nadh-plastoquinone oxidoreductase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
21	d3c8ya3	Alignment	not modelled	98.2	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
22	c6cipD_	Alignment	not modelled	98.2	25	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with 2 acetyl-tpp bound
23	c2vpyB_	Alignment	not modelled	98.2	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nrfc protein; PDBTitle: polysulfide reductase with bound quinone inhibitor, 2 pentachlorophenol (pcp)
24	c6gcsi_	Alignment	not modelled	98.2	17	PDB header: oxidoreductase Chain: I: PDB Molecule: tyky subunit (nuim); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
25	d1fxda_	Alignment	not modelled	98.1	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Single 4Fe-4S cluster ferredoxin
26	c5t5iN_	Alignment	not modelled	98.1	12	PDB header: oxidoreductase Chain: N: PDB Molecule: tungsten formylmethanofuran dehydrogenase subunit fwdf; PDBTitle: tungsten-containing formylmethanofuran dehydrogenase from 2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
27	d1hfel2	Alignment	not modelled	98.1	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
28	d1dura_	Alignment	not modelled	98.1	15	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins

29	c5lc5l_	Alignment	not modelled	98.1	20	PDB header: oxidoreductase Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 8, PDBTitle: structure of mammalian respiratory complex i, class2
30	c4heaO_	Alignment	not modelled	98.1	25	PDB header: oxidoreductase Chain: O: PDB Molecule: nadh-quinone oxidoreductase subunit 9; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
31	d2fug34	Alignment	not modelled	98.1	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
32	c2fgoA_	Alignment	not modelled	98.0	11	PDB header: electron transport Chain: A: PDB Molecule: ferredoxin; PDBTitle: structure of the 2[4fe-4s] ferredoxin from pseudomonas2 aeruginosa
33	c1kqfB_	Alignment	not modelled	98.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: formate dehydrogenase, nitrate-inducible, iron-sulfur PDBTitle: formate dehydrogenase n from e. coli
34	d1jb0c_	Alignment	not modelled	98.0	23	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
35	d1rgva_	Alignment	not modelled	98.0	13	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
36	c1hfeL_	Alignment	not modelled	98.0	20	PDB header: hydrogenase Chain: L: PDB Molecule: protein (fe-only hydrogenase (e.c.1.18.99.1) PDBTitle: 1.6 a resolution structure of the fe-only hydrogenase from2 desulfovibrio desulfuricans
37	c2c3yA_	Alignment	not modelled	98.0	22	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus
38	c4z3zE_	Alignment	not modelled	97.9	18	PDB header: oxidoreductase Chain: E: PDB Molecule: iron-sulfur cluster-binding oxidoreductase, putative PDBTitle: active site complex bambc of benzoyl coenzyme a reductase in complex2 with zinc
39	d1kqfb1	Alignment	not modelled	97.9	17	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
40	c2zvsB_	Alignment	not modelled	97.9	14	PDB header: electron transport Chain: B: PDB Molecule: uncharacterized ferredoxin-like protein yfhI; PDBTitle: crystal structure of the 2[4fe-4s] ferredoxin from escherichia coli
41	d2fdna_	Alignment	not modelled	97.8	11	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
42	d1h98a_	Alignment	not modelled	97.8	27	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
43	c6czaB_	Alignment	not modelled	97.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: 4fe-4s ferredoxin, iron-sulfur binding domain protein; PDBTitle: the arsenate respiratory reductase (arr) complex from shewanella sp.2 ana-3 bound to phosphate
44	d1bc6a_	Alignment	not modelled	97.8	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
45	c1c4cA_	Alignment	not modelled	97.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (fe-only hydrogenase); PDBTitle: binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpl) from clostridium3 pasteurianum
46	c1gx7A_	Alignment	not modelled	97.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic [fe] hydrogenase large subunit; PDBTitle: best model of the electron transfer complex between cytochrome c3 and2 [fe]-hydrogenase
47	c1ti2F_	Alignment	not modelled	97.8	16	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici
48	d7fd1a_	Alignment	not modelled	97.7	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: 7-Fe ferredoxin
49	c5xf9F_	Alignment	not modelled	97.7	22	PDB header: oxidoreductase Chain: F: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
50	d2gmha3	Alignment	not modelled	97.6	3	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: ETF-QO domain-like
51	d1fcaa_	Alignment	not modelled	97.6	12	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
52	c2ivfB_	Alignment	not modelled	97.6	27	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
53	d1vlfn2	Alignment	not modelled	97.6	18	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins

						Family: Ferredoxin domains from multidomain proteins
54	c2v2kB	Alignment	not modelled	97.6	21	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: the crystal structure of fdxa, a 7fe ferredoxin from2 mycobacterium smegmatis
55	c5lnk3	Alignment	not modelled	97.5	19	PDB header: oxidoreductase Chain: 3: PDB Molecule: mitochondrial complex i, 75 kda subunit; PDBTitle: entire ovine respiratory complex i
56	c4yddF	Alignment	not modelled	97.5	19	PDB header: oxidoreductase Chain: F: PDB Molecule: dmsO reductase family type ii enzyme, iron-sulfur subunit; PDBTitle: crystal structure of the perchlorate reductase pcrab from azospira2 suillum ps
57	c6gcsA	Alignment	not modelled	97.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 75-kda protein (nuam); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
58	d1clfa	Alignment	not modelled	97.5	19	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Short-chain ferredoxins
59	c5lc5G	Alignment	not modelled	97.4	21	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class2
60	c6fahE	Alignment	not modelled	97.4	20	PDB header: flavoprotein Chain: E: PDB Molecule: caffeyl-coa reductase-etf complex subunit care; PDBTitle: molecular basis of the flavin-based electron-bifurcating caffeyl-coa2 reductase reaction
61	d1h0hb	Alignment	not modelled	97.3	16	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
62	c5ldxG	Alignment	not modelled	97.1	21	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class3.
63	c5ldwG	Alignment	not modelled	97.1	21	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-ubiquinone oxidoreductase 75 kda subunit, PDBTitle: structure of mammalian respiratory complex i, class1
64	c2fugC	Alignment	not modelled	97.1	21	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh-quinone oxidoreductase chain 3; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
65	d2c42a5	Alignment	not modelled	97.0	20	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
66	d1y5ib1	Alignment	not modelled	96.9	15	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
67	d3c7bb1	Alignment	not modelled	95.7	22	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
68	c2v4jA	Alignment	not modelled	95.5	31	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
69	c6f0kB	Alignment	not modelled	95.5	22	PDB header: membrane protein Chain: B: PDB Molecule: fe-s-cluster-containing hydrogenase; PDBTitle: alternative complex iii
70	c2v4jE	Alignment	not modelled	95.4	21	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
71	c3j16B	Alignment	not modelled	95.3	15	PDB header: ribosome Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
72	c3c7bE	Alignment	not modelled	95.2	25	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
73	c3c7bA	Alignment	not modelled	94.4	28	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit alpha; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
74	c3bk7A	Alignment	not modelled	92.9	25	PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abc1/rnaase-l inhibitor protein from2 pyrococcus abyssi
75	c5dqrA	Alignment	not modelled	91.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: 7-hydroxymethyl chlorophyll a reductase, chloroplastic; PDBTitle: the crystal structure of arabidopsis 7-hydroxymethyl chlorophyll a2 reductase (hcar)
76	c1nekB	Alignment	not modelled	90.8	19	PDB header: oxidoreductase/electron transport Chain: B: PDB Molecule: succinate dehydrogenase iron-sulfur protein; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
						PDB header: oxidoreductase/oxidoreductase inhibitor Chain: F: PDB Molecule: iron-sulfur subunit of succinate

77	c3vrBF_	Alignment	not modelled	89.8	19	dehydrogenase; PDBTitle: mitochondrial rho-quinol-fumarate reductase from the parasitic nematode ascaris suum with the specific inhibitor flutolanil and 3 substrate fumarate
78	c3zfsB_	Alignment	not modelled	89.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: f420-reducing hydrogenase, subunit gamma; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a 2 methanogenic archaeon with bound substrate
79	d1nekB1	Alignment	not modelled	89.1	19	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
80	c2h89B_	Alignment	not modelled	87.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit; PDBTitle: avian respiratory complex ii with malonate bound
81	d2v4jB1	Alignment	not modelled	87.4	26	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
82	c6btmB_	Alignment	not modelled	87.0	32	PDB header: membrane protein Chain: B: PDB Molecule: alternative complex iii subunit b; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
83	d1kf6B1	Alignment	not modelled	83.2	32	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
84	d2bs2B1	Alignment	not modelled	82.0	25	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
85	c3cf4A_	Alignment	not modelled	80.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: acetyl-coa decarboxylase/synthase alpha subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex
86	c5odcC_	Alignment	not modelled	79.2	19	PDB header: oxidoreductase Chain: C: PDB Molecule: heterodisulfide reductase, subunit c; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from 2 methanothermococcus thermolithotrophicus at 2.3 a resolution
87	c2bs2E_	Alignment	not modelled	76.2	25	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinnella succinogenes
88	c5xmjL_	Alignment	not modelled	74.4	22	PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
89	c4ur1A_	Alignment	not modelled	73.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: tetrachloroethene reductive dehalogenase catalytic subunit PDBTitle: crystal structure of the pce reductive dehalogenase from s.2 multivorans in complex with dibromoethene
90	c2b76N_	Alignment	not modelled	70.3	38	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
91	c4rasC_	Alignment	not modelled	68.9	17	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, nad-binding/iron-sulfur cluster-binding PDBTitle: reductive dehalogenase structure suggests a mechanism for b12-2 dependent dehalogenation
92	c5d6sB_	Alignment	not modelled	62.2	17	PDB header: oxidoreductase Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: structure of epoxyqueuosine reductase from streptococcus thermophilus.
93	c5d0bB_	Alignment	not modelled	58.8	29	PDB header: oxidoreductase/rna Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: crystal structure of epoxyqueuosine reductase with a trna-tyr2 epoxyqueuosine-modified trna stem loop
94	d2v4ja1	Alignment	not modelled	43.9	29	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
95	c2vdcL_	Alignment	not modelled	42.6	29	PDB header: oxidoreductase Chain: I: PDB Molecule: glutamate synthase [nadph] small chain; PDBTitle: the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
96	d3c7ba1	Alignment	not modelled	42.1	21	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
97	c4yifD_	Alignment	not modelled	29.8	29	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase subunit a; PDBTitle: insights into flavin-based electron bifurcation via the nadh-dependent 2 reduced ferredoxin-nadp oxidoreductase structure
98	c5jcaL_	Alignment	not modelled	24.2	29	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-dependent ferredoxin:nadp oxidoreductase (nfni) PDBTitle: nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus
99	c4p6vA_	Alignment	not modelled	22.2	17	PDB header: oxidoreductase Chain: A: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit a; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae