
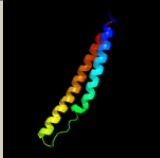
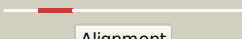

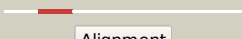
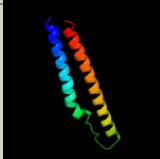







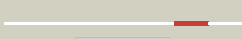


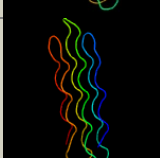

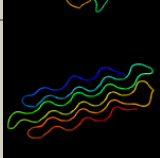
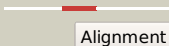
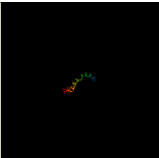
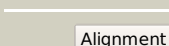


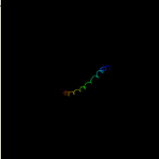

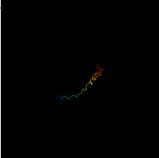

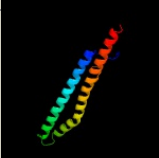

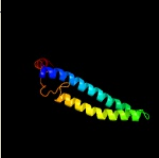



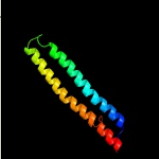

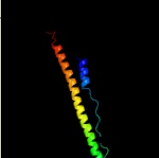
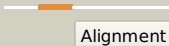


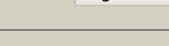
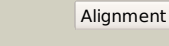
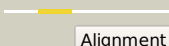
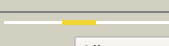



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2853_(PE_PGRS48)_3162278_3164125
 Date Wed Aug 7 12:50:52 BST 2019
 Unique Job ID 4557bd27d2db0468

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsA_	 Alignment		100.0	46	PDB header: protein transport Chain: A; PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
2	c2g38A_	 Alignment		100.0	34	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38a1	 Alignment		100.0	34	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
4	c1ygvA_	 Alignment		99.9	59	PDB header: structural protein/contractile protein Chain: A; PDB Molecule: collagen i alpha 1; PDBTitle: the structure of collagen type i. single type i collagen2 molecule: rigid refinement
5	c3hqvB_	 Alignment		99.9	29	PDB header: structural protein, contractile protein Chain: B; PDB Molecule: collagen alpha-2(i) chain; PDBTitle: low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
6	c1y0fB_	 Alignment		99.8	26	PDB header: structural protein/contractile protein Chain: B; PDB Molecule: collagen i alpha 2; PDBTitle: the structure of collagen type i. single type i collagen2 molecule
7	c3bogB_	 Alignment		97.8	39	PDB header: antifreeze protein Chain: B; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
8	c3bogA_	 Alignment		97.8	39	PDB header: antifreeze protein Chain: A; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein quasi-racemate
9	c2pneA_	 Alignment		97.6	38	PDB header: antifreeze protein Chain: A; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: crystal structure of the snow flea antifreeze protein
10	c3boiB_	 Alignment		97.6	38	PDB header: antifreeze protein Chain: B; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate
11	c3boiA_	 Alignment		97.6	38	PDB header: antifreeze protein Chain: A; PDB Molecule: 6.5 kda glycine-rich antifreeze protein; PDBTitle: snow flea antifreeze protein racemate

12	c5ctdB_	 Alignment		94.2	25	PDB header: structural protein Chain: B: PDB Molecule: collagen alpha-2(i) chain,collagen alpha-2(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
13	c1nayC_	 Alignment		93.9	25	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: gpp-foldon:x-ray structure
14	c5ctiC_	 Alignment		93.8	25	PDB header: structural protein Chain: C: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-3(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen (native form)
15	c5ctdA_	 Alignment		93.7	25	PDB header: structural protein Chain: A: PDB Molecule: collagen alpha-1(i) chain,collagen alpha-1(ix) chain; PDBTitle: crystal structure of the type ix collagen nc2 heterotrimerization2 domain with a guest fragment a2a1a1 of type i collagen
16	c3gvmA_	 Alignment		93.3	12	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
17	d1wa8a1	 Alignment		93.3	9	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
18	c4lwsA_	 Alignment		91.3	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
19	c4iogD_	 Alignment		90.8	10	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
20	c4wj2A_	 Alignment		87.9	13	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
21	c3zbhC_	 Alignment	not modelled	85.9	11	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
22	c2vs0B_	 Alignment	not modelled	83.2	12	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
23	c2kg7B_	 Alignment	not modelled	81.6	13	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
24	c2ml3A_	 Alignment	not modelled	80.9	23	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
25	c5szsC_	 Alignment	not modelled	75.2	22	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: glycan shield and epitope masking of a coronavirus spike protein2 observed by cryo-electron microscopy
26	c1k7gA_	 Alignment	not modelled	73.7	24	PDB header: hydrolase Chain: A: PDB Molecule: secreted protease c; PDBTitle: prtC from erwinia chrysanthemi: e189a mutant
27	d1wa8b1	 Alignment	not modelled	71.4	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
28	c2ml2A_	 Alignment	not modelled	70.7	16	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 6; PDBTitle: solution structure of alge6r2 subunit from the azotobacter

						vinelandii2 mannuronan c5-epimerase
29	c6nb3B_	Alignment	not modelled	68.9	22	PDB header: virus Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: mers-cov complex with human neutralizing lca60 antibody fab fragment2 (state 1)
30	c2klwA_	Alignment	not modelled	66.5	33	PDB header: de novo protein Chain: A: PDB Molecule: (pkg)10; PDBTitle: solution structure of an abc collagen heterotrimer reveals a2 single-register helix stabilized by electrostatic3 interactions
31	d1kapp1	Alignment	not modelled	65.6	24	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
32	d1k7ia1	Alignment	not modelled	65.6	25	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain
33	c5x5fC_	Alignment	not modelled	64.0	23	PDB header: viral protein Chain: C: PDB Molecule: s protein; PDBTitle: prefusion structure of mers-cov spike glycoprotein, conformation 2
34	c3ah9D_	Alignment	not modelled	62.4	41	PDB header: structural protein Chain: D: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
35	c1jiwP_	Alignment	not modelled	60.4	24	PDB header: hydrolase/hyrolase inhibitor Chain: P: PDB Molecule: alkaline metalloproteinase; PDBTitle: crystal structure of the apr-aprin complex
36	c2cuoC_	Alignment	not modelled	59.8	37	PDB header: structural protein Chain: C: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
37	c2cuoF_	Alignment	not modelled	59.8	37	PDB header: structural protein Chain: F: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
38	c2agmA_	Alignment	not modelled	59.3	21	PDB header: isomerase Chain: A: PDB Molecule: poly(beta-d-mannuronate) c5 epimerase 4; PDBTitle: solution structure of the r-module from alge4
39	c3ah9A_	Alignment	not modelled	57.9	39	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
40	c3ah9F_	Alignment	not modelled	57.9	39	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
41	c6b7nC_	Alignment	not modelled	57.3	24	PDB header: viral protein Chain: C: PDB Molecule: spike protein; PDBTitle: cryo-electron microscopy structure of porcine delta coronavirus spike2 protein in the pre-fusion state
42	c2w0cR_	Alignment	not modelled	56.3	34	PDB header: virus Chain: R: PDB Molecule: protein p3; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
43	c3ah9C_	Alignment	not modelled	55.1	39	PDB header: structural protein Chain: C: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
44	c3ah9B_	Alignment	not modelled	55.1	39	PDB header: structural protein Chain: B: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
45	c3ah9E_	Alignment	not modelled	55.1	39	PDB header: structural protein Chain: E: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)9 at 1.1 a resolution
46	c5zhyA_	Alignment	not modelled	53.9	14	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, spike glycoprotein; PDBTitle: structural characterization of the hcov-229e fusion core
47	c5i08A_	Alignment	not modelled	53.0	22	PDB header: viral protein Chain: A: PDB Molecule: spike glycoprotein, envelope glycoprotein chimera; PDBTitle: prefusion structure of a human coronavirus spike protein
48	c3a0mF_	Alignment	not modelled	52.9	39	PDB header: structural protein Chain: F: PDB Molecule: collagen-like peptide; PDBTitle: structure of (ppg)4-ovg-(ppg)4, monoclinic, twinned crystal
49	c3jclC_	Alignment	not modelled	51.7	25	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of a coronavirus spike glycoprotein2 trimer
50	c2cuoD_	Alignment	not modelled	51.6	39	PDB header: structural protein Chain: D: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
51	c2cuoB_	Alignment	not modelled	51.6	39	PDB header: structural protein Chain: B: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
52	c2cuoE_	Alignment	not modelled	51.6	39	PDB header: structural protein Chain: E: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
53	c2cuoA_	Alignment	not modelled	51.6	39	PDB header: structural protein Chain: A: PDB Molecule: collagen model peptide (pro-pro-gly)9; PDBTitle: collagen model peptide (pro-pro-gly)9
54	c6nzkB_	Alignment	not modelled	51.3	21	PDB header: viral protein Chain: B: PDB Molecule: spike surface glycoprotein; PDBTitle: structural basis for human coronavirus attachment to sialic acid2 receptors
55	c1satA_	Alignment	not modelled	48.2	19	PDB header: hydrolase (serine protease) Chain: A: PDB Molecule: serratia protease; PDBTitle: crystal structure of the 50 kda metallo protease from s.2

						marcescens
56	c5x5bB_	Alignment	not modelled	47.5	24	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: prefusion structure of sars-cov spike glycoprotein, conformation 2
57	c4z9cB_	Alignment	not modelled	47.5	31	PDB header: transferase Chain: B: PDB Molecule: subtilase cytotoxin subunit b-like protein; PDBTitle: ecpltab oxidized
58	c6cs2A_	Alignment	not modelled	46.6	20	PDB header: viral protein/hydrolase Chain: A: PDB Molecule: spike glycoprotein,fibrinin; PDBTitle: sars spike glycoprotein - human ace2 complex, stabilized variant, all2 ace2-bound particles
59	c6b3oB_	Alignment	not modelled	46.2	20	PDB header: viral protein Chain: B: PDB Molecule: spike glycoprotein; PDBTitle: tectonic conformational changes of a coronavirus spike glycoprotein2 promote membrane fusion
60	c2zj6A_	Alignment	not modelled	46.1	20	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
61	c1om8A_	Alignment	not modelled	45.3	20	PDB header: hydrolase Chain: A: PDB Molecule: serralysin; PDBTitle: crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
62	c5cx1A_	Alignment	not modelled	39.5	23	PDB header: toxin Chain: A: PDB Molecule: bifunctional hemolysin/adenylate cyclase; PDBTitle: crystal structure of rtx domain block v of adenylate cyclase toxin2 from bordetella pertussis
63	d1n7ka_	Alignment	not modelled	38.8	16	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
64	c4lwsB_	Alignment	not modelled	38.3	8	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
65	c1k6fA_	Alignment	not modelled	37.6	36	PDB header: structural protein Chain: A: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model ((pro-pro-gly)2 10j3
66	c1k6fD_	Alignment	not modelled	37.6	36	PDB header: structural protein Chain: D: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model ((pro-pro-gly)2 10j3
67	c1k6fC_	Alignment	not modelled	37.6	36	PDB header: structural protein Chain: C: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model ((pro-pro-gly)2 10j3
68	c1k6fB_	Alignment	not modelled	37.6	36	PDB header: structural protein Chain: B: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model ((pro-pro-gly)2 10j3
69	c1k6fF_	Alignment	not modelled	37.6	36	PDB header: structural protein Chain: F: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model ((pro-pro-gly)2 10j3
70	c1k6fE_	Alignment	not modelled	37.6	36	PDB header: structural protein Chain: E: PDB Molecule: collagen triple helix; PDBTitle: crystal structure of the collagen triple helix model ((pro-pro-gly)2 10j3
71	c2vsgB_	Alignment	not modelled	34.1	15	PDB header: membrane protein Chain: B: PDB Molecule: variant surface glycoprotein iltat 1.24; PDBTitle: a structural motif in the variant surface glycoproteins of trypanosoma2 brucei
72	c3v4cB_	Alignment	not modelled	33.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: aldehyde dehydrogenase (nadp+); PDBTitle: crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 melliloti 1021
73	c2d11A_	Alignment	not modelled	33.2	14	PDB header: protein binding Chain: A: PDB Molecule: metastasis suppressor protein 1; PDBTitle: structure of f-actin binding domain imd of mim (missing in metastasis)
74	c3onjA_	Alignment	not modelled	32.9	21	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
75	c5fsgA_	Alignment	not modelled	30.0	20	PDB header: viral protein Chain: A: PDB Molecule: maltose-binding periplasmic protein, hantavirus PDBTitle: structure of the hantavirus nucleoprotein provides insights2 into the mechanism of rna encapsidation and a template for3 drug design
76	c5whvF_	Alignment	not modelled	28.6	17	PDB header: toxin Chain: F: PDB Molecule: artb protein; PDBTitle: crystal structure of artb
77	c4k6lC_	Alignment	not modelled	28.1	28	PDB header: toxin Chain: C: PDB Molecule: putative pertussis-like toxin subunit; PDBTitle: structure of typhoid toxin
78	c1mg1A_	Alignment	not modelled	28.1	24	PDB header: viral protein Chain: A: PDB Molecule: protein (htlv-1 gp21 ectodomain/maltose-binding protein PDBTitle: htlv-1 gp21 ectodomain/maltose-binding protein chimera
79	c3h6pB_	Alignment	not modelled	28.0	63	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: esat-6 like protein esxs; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
80	c6cv0C_	Alignment	not modelled	27.6	22	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: cryo-electron microscopy structure of infectious bronchitis2 coronavirus spike protein
						PDB header: transport protein

81	c4kjsB_	Alignment	not modelled	25.6	23	Chain: B: PDB Molecule: cation exchanger yfke; PDBTitle: structure of native yfke
82	c4rglA_	Alignment	not modelled	24.4	23	PDB header: dna binding protein Chain: A: PDB Molecule: filamentation induced by camp protein fic; PDBTitle: crystal structure of a fic family protein (dde_2494) from <i>Desulfovibrio desulfuricans</i> g20 at 2.70 Å resolution
83	c2qubG_	Alignment	not modelled	24.2	21	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from <i>Serratia marcescens</i>
84	c5mgzA_	Alignment	not modelled	22.8	29	PDB header: transferase Chain: A: PDB Molecule: 8-demethylnovobiocic acid c(8)-methyltransferase; PDBTitle: streptomyces spheroides novo (8-demethylnovobiocic acid)2 methyltransferase) with sah
85	d2qtia1	Alignment	not modelled	22.5	25	Fold: YejL-like Superfamily: YejL-like Family: YejL-like
86	c6g7oA_	Alignment	not modelled	21.1	15	PDB header: membrane protein Chain: A: PDB Molecule: alkaline ceramidase 3,soluble cytochrome b562; PDBTitle: crystal structure of human alkaline ceramidase 3 (acer3) at 2.72 Å resolution
87	c5n7kD_	Alignment	not modelled	20.8	28	PDB header: cell adhesion Chain: D: PDB Molecule: marvel domain-containing protein 2; PDBTitle: crystal structure of the coiled-coil domain of human tricellulin
88	c5xlrC_	Alignment	not modelled	20.3	24	PDB header: viral protein Chain: C: PDB Molecule: spike glycoprotein; PDBTitle: structure of sars-cov spike glycoprotein
89	c2z8jA_	Alignment	not modelled	19.8	13	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of escherichia coli gamma-glutamyltranspeptidase in2 complex with azaserine prepared in the dark
90	c2v8sV_	Alignment	not modelled	19.4	13	PDB header: protein transport Chain: V: PDB Molecule: vesicle transport through interaction with PDBTitle: vti1b habc domain - epsinr enth domain complex
91	c4gdxA_	Alignment	not modelled	19.1	19	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase 1 heavy chain; PDBTitle: crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex
92	d1lghb_	Alignment	not modelled	19.0	27	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
93	c3w5mA_	Alignment	not modelled	18.9	19	PDB header: hydrolase Chain: A: PDB Molecule: putative rhamnosidase; PDBTitle: crystal structure of streptomyces avermitilis alpha-l-rhamnosidase
94	c4njIA_	Alignment	not modelled	18.7	16	PDB header: viral protein Chain: A: PDB Molecule: s protein; PDBTitle: crystal structure of middle east respiratory syndrome coronavirus s22 protein fusion core
95	c4c3sA_	Alignment	not modelled	18.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde dehydrogenase; PDBTitle: structure of a propionaldehyde dehydrogenase from the clostridium2 phytofermentans fucose utilisation bacterial microcompartment
96	c2kg7A_	Alignment	not modelled	18.6	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein esxg (pe family protein); PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
97	c4dbgB_	Alignment	not modelled	18.5	18	PDB header: ligase Chain: B: PDB Molecule: ring finger protein 31; PDBTitle: crystal structure of hoil-11-ubl complexed with a hoip-uba derivative
98	c3abnA_	Alignment	not modelled	18.4	38	PDB header: structural protein Chain: A: PDB Molecule: collagen-like peptide; PDBTitle: crystal structure of (pro-pro-gly)4-hyp-asp-gly-(pro-pro-gly)4 at 1.022 Å
99	c1gz3B_	Alignment	not modelled	18.2	24	PDB header: oxidoreductase Chain: B: PDB Molecule: nad-dependent malic enzyme, mitochondrial; PDBTitle: molecular mechanism for the regulation of human mitochondrial nad(p)+-2 dependent malic enzyme by atp and fumarate