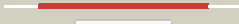


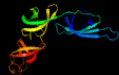
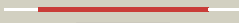






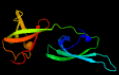

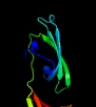

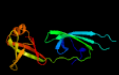






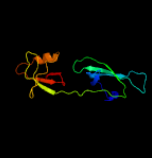

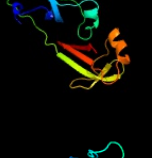

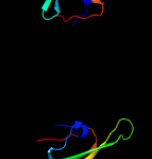
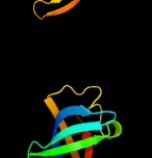
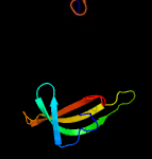

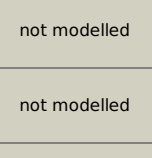


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2534c_(efp)_2858737_2859300
Date	Wed Aug 7 12:50:17 BST 2019
Unique Job ID	dd173f7f3c5263d8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3oyyA_</a>	 Alignment		100.0	34	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor p; <b>PDBTitle:</b> structure of pseudomonas aeruginosa elongation factor p
2	<a href="#">c1uebB_</a>	 Alignment		100.0	44	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> elongation factor p; <b>PDBTitle:</b> crystal structure of translation elongation factor p from2 thermus thermophilus hb8
3	<a href="#">c5j3bB_</a>	 Alignment		100.0	43	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> elongation factor p; <b>PDBTitle:</b> structure of translation elongation factor p from acinetobacter2 baumannii
4	<a href="#">c1ybyB_</a>	 Alignment		100.0	51	<b>PDB header:</b> translation <b>Chain:</b> B; <b>PDB Molecule:</b> translation elongation factor p; <b>PDBTitle:</b> conserved hypothetical protein cth-95 from clostridium thermocellum
5	<a href="#">c3a5zD_</a>	 Alignment		100.0	43	<b>PDB header:</b> ligase <b>Chain:</b> D; <b>PDB Molecule:</b> elongation factor p; <b>PDBTitle:</b> crystal structure of escherichia coli genx in complex with elongation2 factor p
6	<a href="#">c3treA_</a>	 Alignment		100.0	38	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> elongation factor p; <b>PDBTitle:</b> structure of a translation elongation factor p (efp) from coxiella2 burnetii
7	<a href="#">c1iz6B_</a>	 Alignment		100.0	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B; <b>PDB Molecule:</b> initiation factor 5a; <b>PDBTitle:</b> crystal structure of translation initiation factor 5a from pyrococcus2 horikoshii
8	<a href="#">c1bkbA_</a>	 Alignment		100.0	23	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> translation initiation factor 5a; <b>PDBTitle:</b> initiation factor 5a from archebacterium pyrobaculum2 aerophilum
9	<a href="#">c2eifA_</a>	 Alignment		100.0	26	<b>PDB header:</b> gene regulation <b>Chain:</b> A; <b>PDB Molecule:</b> protein (eukaryotic translation initiation factor 5a); <b>PDBTitle:</b> eukaryotic translation initiation factor 5a from methanococcus2 jannaschii
10	<a href="#">c3hksB_</a>	 Alignment		100.0	17	<b>PDB header:</b> translation, rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5a-2; <b>PDBTitle:</b> crystal structure of eukaryotic translation initiation2 factor eif-5a2 from arabidopsis thaliana
11	<a href="#">c3er0A_</a>	 Alignment		100.0	20	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5a-2; <b>PDBTitle:</b> crystal structure of the full length eif5a from2 saccharomyces cerevisiae

12	<a href="#">c5hy6A</a>	Alignment		100.0	16	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5a; <b>PDBTitle:</b> spodoptera frugiperda eukaryotic translation initiation factor eif5a
13	<a href="#">c1xtdA</a>	Alignment		99.9	21	<b>PDB header:</b> translation <b>Chain:</b> A; <b>PDB Molecule:</b> eukaryotic initiation factor 5a; <b>PDBTitle:</b> structural analysis of leishmania mexicana eukaryotic initiation2 factor 5a
14	<a href="#">c3cpfB</a>	Alignment		99.9	16	<b>PDB header:</b> cell cycle <b>Chain:</b> B; <b>PDB Molecule:</b> eukaryotic translation initiation factor 5a-1; <b>PDBTitle:</b> crystal structure of human eukaryotic translation initiation factor2 eif5a
15	<a href="#">d1ueba3</a>	Alignment		99.9	56	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
16	<a href="#">d1ueba1</a>	Alignment		99.9	38	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
17	<a href="#">c5wxkB</a>	Alignment		99.9	25	<b>PDB header:</b> transferase <b>Chain:</b> B; <b>PDB Molecule:</b> elongation factor p; <b>PDBTitle:</b> earp bound with domain i of ef-p
18	<a href="#">d1ueba2</a>	Alignment		99.9	38	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
19	<a href="#">c3a5zF</a>	Alignment		99.8	40	<b>PDB header:</b> ligase <b>Chain:</b> F; <b>PDB Molecule:</b> elongation factor p; <b>PDBTitle:</b> crystal structure of escherichia coli genx in complex with elongation2 factor p
20	<a href="#">c1khiA</a>	Alignment		99.3	12	<b>PDB header:</b> structural protein <b>Chain:</b> A; <b>PDB Molecule:</b> hex1; <b>PDBTitle:</b> crystal structure of hex1
21	<a href="#">d1bkba1</a>	Alignment	not modelled	99.0	26	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
22	<a href="#">d1iz6a1</a>	Alignment	not modelled	99.0	25	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
23	<a href="#">d2eifa1</a>	Alignment	not modelled	99.0	24	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
24	<a href="#">d1x6oa1</a>	Alignment	not modelled	98.6	15	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
25	<a href="#">d1khia1</a>	Alignment	not modelled	97.9	8	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
26	<a href="#">d1bkba2</a>	Alignment	not modelled	97.7	21	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
27	<a href="#">d1iz6a2</a>	Alignment	not modelled	97.5	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
28	<a href="#">d2eifa2</a>	Alignment	not modelled	97.1	31	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
29	<a href="#">d1yiva1</a>	Alignment	not modelled	66.7	14	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins

						<b>Family:</b> Fatty acid binding protein-like
30	<a href="#">d1slqa_</a>	Alignment	not modelled	62.3	22	<b>Fold:</b> VP4 membrane interaction domain <b>Superfamily:</b> VP4 membrane interaction domain <b>Family:</b> VP4 membrane interaction domain
31	<a href="#">d2hnxa1</a>	Alignment	not modelled	57.8	20	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
32	<a href="#">d1ogya1</a>	Alignment	not modelled	56.9	32	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
33	<a href="#">c3fp9E_</a>	Alignment	not modelled	52.8	36	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> proteasome-associated atpase; <b>PDBTitle:</b> crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
34	<a href="#">d1pmpa_</a>	Alignment	not modelled	51.9	14	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
35	<a href="#">d1mdca_</a>	Alignment	not modelled	50.4	17	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
36	<a href="#">d1g7na_</a>	Alignment	not modelled	49.7	23	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
37	<a href="#">d1eua1</a>	Alignment	not modelled	48.0	33	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
38	<a href="#">d1ftpa_</a>	Alignment	not modelled	48.0	18	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
39	<a href="#">d1vlfm1</a>	Alignment	not modelled	48.0	24	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
40	<a href="#">d1g8ka1</a>	Alignment	not modelled	47.5	29	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
41	<a href="#">d1bwya_</a>	Alignment	not modelled	46.8	22	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
42	<a href="#">d1dmra1</a>	Alignment	not modelled	46.2	33	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
43	<a href="#">d2iv2x1</a>	Alignment	not modelled	44.9	29	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
44	<a href="#">d1kqfa1</a>	Alignment	not modelled	42.5	33	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
45	<a href="#">d1hmsa_</a>	Alignment	not modelled	38.5	25	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
46	<a href="#">c3iyuY_</a>	Alignment	not modelled	38.5	19	<b>PDB header:</b> virus <b>Chain:</b> Y: <b>PDB Molecule:</b> outer capsid protein vp4; <b>PDBTitle:</b> atomic model of an infectious rotavirus particle
47	<a href="#">d2jioa1</a>	Alignment	not modelled	37.9	24	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
48	<a href="#">c3rswA_</a>	Alignment	not modelled	37.9	25	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid-binding protein, heart; <b>PDBTitle:</b> crystal structure of heart fatty acid binding protein (fabp3)
49	<a href="#">c5t5iL_</a>	Alignment	not modelled	37.5	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase subunit fwdd; <b>PDBTitle:</b> tungsten-containing formylmethanofuran dehydrogenase from2 methanothermobacter wolfeii, orthorhombic form at 1.9 a
50	<a href="#">d1tmoa1</a>	Alignment	not modelled	37.4	29	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
51	<a href="#">d1y5ia1</a>	Alignment	not modelled	37.3	24	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
52	<a href="#">c2q9sA_</a>	Alignment	not modelled	36.5	22	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid-binding protein; <b>PDBTitle:</b> linoleic acid bound to fatty acid binding protein 4
53	<a href="#">c1tmoA_</a>	Alignment	not modelled	35.8	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trimethylamine n-oxide reductase; <b>PDBTitle:</b> trimethylamine n-oxide reductase from shewanella massilia
54	<a href="#">c2ki8A_</a>	Alignment	not modelled	35.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tungsten formylmethanofuran dehydrogenase, <b>PDBTitle:</b> solution nmr structure of tungsten formylmethanofuran2 dehydrogenase subunit d from archaeoglobus fulgidus,3 northeast structural genomics consortium target att7
						<b>Fold:</b> Lipocalins

55	<a href="#">d1fdqa_</a>	Alignment	not modelled	35.6	17	<b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
56	<a href="#">c2z14A_</a>	Alignment	not modelled	34.5	24	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> ef-hand domain-containing family member c2; <b>PDBTitle:</b> crystal structure of the n-terminal duf1126 in human ef-2 hand domain containing 2 protein
57	<a href="#">d1h0ha1</a>	Alignment	not modelled	34.1	29	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Formate dehydrogenase/DMSO reductase, C-terminal domain
58	<a href="#">d2cqaa1</a>	Alignment	not modelled	33.0	29	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> TIP49 domain
59	<a href="#">c2kxjA_</a>	Alignment	not modelled	30.4	14	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> ubx domain-containing protein 4; <b>PDBTitle:</b> solution structure of ubx domain of human ubxd2 protein
60	<a href="#">d1b56a_</a>	Alignment	not modelled	30.2	17	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
61	<a href="#">d2pu9b1</a>	Alignment	not modelled	29.7	46	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain
62	<a href="#">c5ch7E_</a>	Alignment	not modelled	29.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> dms0 reductase family type ii enzyme, molybdopterin <b>PDBTitle:</b> crystal structure of the perchlorate reductase pcrab - phe164 gate2 switch intermediate - from azospira suillum ps
63	<a href="#">c1h0hA_</a>	Alignment	not modelled	28.6	29	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> formate dehydrogenase subunit alpha; <b>PDBTitle:</b> tungsten containing formate dehydrogenase from desulfovibrio gigas
64	<a href="#">c2kcmA_</a>	Alignment	not modelled	28.4	24	<b>PDB header:</b> nucleic acid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cold shock domain family protein; <b>PDBTitle:</b> solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a.
65	<a href="#">c1h5nC_</a>	Alignment	not modelled	28.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dms0 reductase; <b>PDBTitle:</b> dms0 reductase modified by the presence of dms and air
66	<a href="#">c5ounA_</a>	Alignment	not modelled	27.9	29	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ruvb-like protein 2; <b>PDBTitle:</b> nmr solution structure of the external dii domain of rvb2 from2 saccharomyces cerevisiae
67	<a href="#">d1ifca_</a>	Alignment	not modelled	27.0	20	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
68	<a href="#">c5ggeA_</a>	Alignment	not modelled	25.7	14	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid bindin protein, isoform b; <b>PDBTitle:</b> fatty acid-binding protein in brain tissue of drosophila melanogaster
69	<a href="#">c1ogyA_</a>	Alignment	not modelled	25.4	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic nitrate reductase; <b>PDBTitle:</b> crystal structure of the heterodimeric nitrate reductase2 from rhodobacter sphaeroides
70	<a href="#">c1eu1A_</a>	Alignment	not modelled	24.5	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethyl sulfoxide reductase; <b>PDBTitle:</b> the crystal structure of rhodobacter sphaeroides dimethylsulfoxide2 reductase reveals two distinct molybdenum coordination environments.
71	<a href="#">d2cr5a1</a>	Alignment	not modelled	24.4	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> UBX domain
72	<a href="#">c1g8jC_</a>	Alignment	not modelled	24.1	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> arsenite oxidase; <b>PDBTitle:</b> crystal structure analysis of arsenite oxidase from2 alcaligenes faecalis
73	<a href="#">c3hslX_</a>	Alignment	not modelled	24.0	18	<b>PDB header:</b> replication <b>Chain:</b> X: <b>PDB Molecule:</b> orf59; <b>PDBTitle:</b> the crystal structure of pf-8, the dna polymerase accessory subunit2 from kaposi's sarcoma-associated herpesvirus
74	<a href="#">d1sa8a_</a>	Alignment	not modelled	23.8	20	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
75	<a href="#">c3m9bK_</a>	Alignment	not modelled	23.6	35	<b>PDB header:</b> chaperone <b>Chain:</b> K: <b>PDB Molecule:</b> proteasome-associated atpase; <b>PDBTitle:</b> crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
76	<a href="#">d1opaa_</a>	Alignment	not modelled	23.2	25	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
77	<a href="#">c1vlfQ_</a>	Alignment	not modelled	21.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> Q: <b>PDB Molecule:</b> pyrogallol hydroxytransferase large subunit; <b>PDBTitle:</b> crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici complexed with inhibitor 1,2,4,5-3 tetrahydroxy-benzene
78	<a href="#">c5bvtA_</a>	Alignment	not modelled	20.4	22	<b>PDB header:</b> lipid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> epidermal fatty acid-binding protein; <b>PDBTitle:</b> palmitate-bound pfabp5
79	<a href="#">d2a0aa1</a>	Alignment	not modelled	20.1	11	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like <b>PDB header:</b> oxidoreductase

80	<a href="#">c2ivfA_</a>	Alignment	not modelled	20.0	24	<b>Chain:</b> A; <b>PDB Molecule:</b> ethylbenzene dehydrogenase alpha-subunit; <b>PDBTitle:</b> ethylbenzene dehydrogenase from aromatoleum aromaticum
81	<a href="#">d1i42a_</a>	Alignment	not modelled	19.7	9	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> UBX domain
82	<a href="#">d2gp4a1</a>	Alignment	not modelled	19.7	31	<b>Fold:</b> The "swivelling" beta/beta/alpha domain <b>Superfamily:</b> LeuD/IlvD-like <b>Family:</b> IlvD/EDD C-terminal domain-like
83	<a href="#">d2piea1</a>	Alignment	not modelled	19.0	15	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
84	<a href="#">d1ed7a_</a>	Alignment	not modelled	18.9	13	<b>Fold:</b> WW domain-like <b>Superfamily:</b> Carbohydrate binding domain <b>Family:</b> Carbohydrate binding domain
85	<a href="#">c4aayE_</a>	Alignment	not modelled	18.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E; <b>PDB Molecule:</b> aroa; <b>PDBTitle:</b> crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
86	<a href="#">c1kqgA_</a>	Alignment	not modelled	17.9	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> formate dehydrogenase, nitrate-inducible, major subunit; <b>PDBTitle:</b> formate dehydrogenase n from e. coli
87	<a href="#">d2f9ha1</a>	Alignment	not modelled	17.7	30	<b>Fold:</b> PTSIIA/GutA-like <b>Superfamily:</b> PTSIIA/GutA-like <b>Family:</b> PTSIIA/GutA-like
88	<a href="#">c1y5iA_</a>	Alignment	not modelled	17.2	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> respiratory nitrate reductase 1 alpha chain; <b>PDBTitle:</b> the crystal structure of the narghi mutant nari-k86a
89	<a href="#">d1p6pa_</a>	Alignment	not modelled	16.9	7	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
90	<a href="#">c5yyxA_</a>	Alignment	not modelled	16.5	7	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> meiosis-specific serine/threonine-protein kinase mek1; <b>PDBTitle:</b> crystal structure of the mek1 fha domain
91	<a href="#">d1uhta_</a>	Alignment	not modelled	16.3	13	<b>Fold:</b> SMAD/FHA domain <b>Superfamily:</b> SMAD/FHA domain <b>Family:</b> FHA domain
92	<a href="#">c2wkdA_</a>	Alignment	not modelled	15.6	44	<b>PDB header:</b> dna binding protein <b>Chain:</b> A; <b>PDB Molecule:</b> orf34p2; <b>PDBTitle:</b> crystal structure of a double ile-to-met mutant of protein orf34 from2 lactococcus phage p2
93	<a href="#">d2as0a1</a>	Alignment	not modelled	15.4	32	<b>Fold:</b> PUA domain-like <b>Superfamily:</b> PUA domain-like <b>Family:</b> Hypothetical RNA methyltransferase domain (HRMD)
94	<a href="#">d1vyfa_</a>	Alignment	not modelled	15.4	15	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
95	<a href="#">c2iv2X_</a>	Alignment	not modelled	15.3	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X; <b>PDB Molecule:</b> formate dehydrogenase h; <b>PDBTitle:</b> reinterpretation of reduced form of formate dehydrogenase h from e.2 coli
96	<a href="#">d2ftba1</a>	Alignment	not modelled	15.1	10	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Fatty acid binding protein-like
97	<a href="#">c3zv0D_</a>	Alignment	not modelled	15.0	15	<b>PDB header:</b> cell cycle <b>Chain:</b> D; <b>PDB Molecule:</b> h/aca ribonucleoprotein complex subunit 4; <b>PDBTitle:</b> structure of the shq1p-cbf5p complex
98	<a href="#">c6a8wA_</a>	Alignment	not modelled	15.0	11	<b>PDB header:</b> protein binding <b>Chain:</b> A; <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 64; <b>PDBTitle:</b> crystal structure of the fha domain of far9
99	<a href="#">c4ytiB_</a>	Alignment	not modelled	14.7	10	<b>PDB header:</b> transcription <b>Chain:</b> B; <b>PDB Molecule:</b> transcription elongation factor spt5; <b>PDBTitle:</b> structure of the kow2-kow3 domain of transcription elongation factor2 spt5.