Phyre^2

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Description	RVBD0286_(PPE4)_349935_351476
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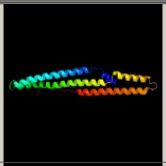
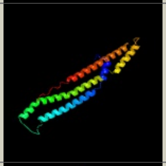
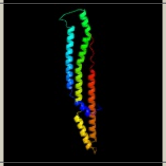
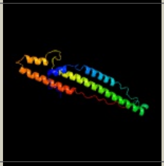
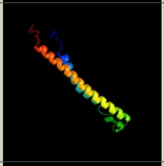
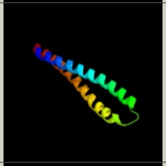
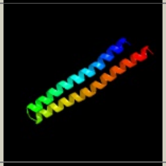
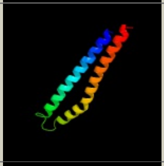
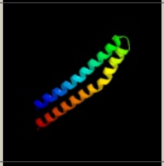
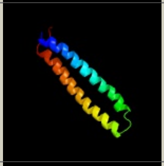
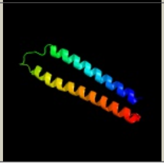
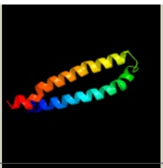
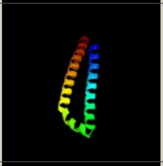
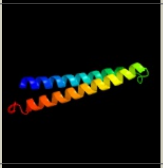
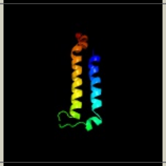
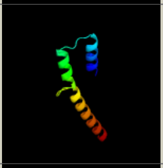
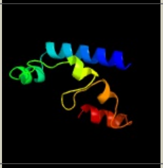
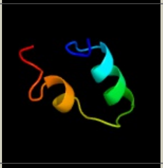
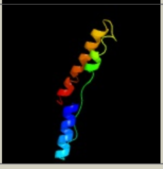
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	Alignment		100.0	43	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**ppe family protein ppe15; **PDBTitle:** crystal structure of pe8-ppe15 in complex with espg5 from m.2 tuberculosis
2	d2g38b1	Alignment		100.0	30	**Fold:**Ferritin-like **Superfamily:**PE/PPE dimer-like **Family:**PPE
3	c2g38B_	Alignment		100.0	30	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ppe family protein; **PDBTitle:** a pe/ppe protein complex from mycobacterium tuberculosis
4	c4xy3A_	Alignment		100.0	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**esx-1 secretion-associated protein espb; **PDBTitle:** structure of esx-1 secreted protein espb
5	c4wj2A_	Alignment		98.1	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**antigen mtb48; **PDBTitle:** mycobacterial protein
6	c2vs0B_	Alignment		97.7	14	**PDB header:**cell invasion **Chain:** B: **PDB Molecule:**virulence factor esxa; **PDBTitle:** structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c4iogD_	Alignment		97.5	15	**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
8	c3gvmA_	Alignment		97.5	14	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**putative uncharacterized protein sag1039; **PDBTitle:** structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	c3zbhC_	Alignment		97.1	16	**PDB header:**unknown function **Chain:** C: **PDB Molecule:**esxa; **PDBTitle:** geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	Alignment		96.6	14	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
11	c4lwsB_	Alignment		94.0	19	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	d1wa8b1	Alignment		93.6	22	**Fold:**Ferritin-like **Superfamily:**EsxAB dimer-like **Family:**ESAT-6 like
13	c4lwsA_	Alignment		92.8	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** esxa : esxb (semet) hetero-dimer from thermomonospora curvata
14	c4i0xA_	Alignment		91.7	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**esat-6-like protein mab_3112; **PDBTitle:** crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex
15	c2kg7B_	Alignment		86.2	20	**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
16	c4i0xJ_	Alignment		68.1	28	**PDB header:**structural genomics, unknown function **Chain:** J: **PDB Molecule:**esat-6-like protein mab_3113; **PDBTitle:** crystal structure of the mycobacterum abscessus esxef (mab_3112-2 mab_3113) complex
17	d1ui5a2	Alignment		38.2	19	**Fold:**Tetracyclin repressor-like, C-terminal domain **Superfamily:**Tetracyclin repressor-like, C-terminal domain **Family:**Tetracyclin repressor-like, C-terminal domain
18	d1zeea1	Alignment		24.1	33	**Fold:**Indolic compounds 2,3-dioxygenase-like **Superfamily:**Indolic compounds 2,3-dioxygenase-like **Family:**Indoleamine 2,3-dioxygenase-like
19	d1dlpa1	Alignment		14.9	18	**Fold:**beta-Prism II **Superfamily:**alpha-D-mannose-specific plant lectins **Family:**alpha-D-mannose-specific plant lectins
20	c3zfsA_	Alignment		13.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**f420-reducing hydrogenase, subunit alpha; **PDBTitle:** cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
21	c6et5j_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** J: **PDB Molecule:** **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
22	c6et5R_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** R: **PDB Molecule:**light-harvesting protein b-1015 gamma chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
23	c6et5m_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** M: **PDB Molecule:**reaction center protein m chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
24	c6et5y_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** Y: **PDB Molecule:**light-harvesting protein b-1015 alpha chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
25	c6et5I_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** I: **PDB Molecule:**light-harvesting protein b-1015 gamma chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
26	c6et5g_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** G: **PDB Molecule:**light-harvesting protein b-1015 beta chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
27	c6et5s_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** S: **PDB Molecule:**light-harvesting protein b-1015 alpha chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
28	c6et5d_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:** **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
						PDB header:photosynthesis

29	c6et55_	Alignment	not modelled	12.6	44	**Chain:** 5: **PDB Molecule:**light-harvesting protein b-1015 gamma chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
30	c6et5v_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** V: **PDB Molecule:**light-harvesting protein b-1015 alpha chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
31	c6et5U_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** U: **PDB Molecule:**light-harvesting protein b-1015 gamma chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
32	c6et5O_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** O: **PDB Molecule:**light-harvesting protein b-1015 gamma chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
33	c6et5X_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** X: **PDB Molecule:**light-harvesting protein b-1015 gamma chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
34	c6et52_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** 2: **PDB Molecule:**light-harvesting protein b-1015 gamma chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
35	c6et5a_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:** **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
36	c6et5p_	Alignment	not modelled	12.6	44	**PDB header:**photosynthesis **Chain:** P: **PDB Molecule:**light-harvesting protein b-1015 alpha chain; **PDBTitle:** reaction centre light harvesting complex 1 from blc. virids
37	c4xb6D_	Alignment	not modelled	12.5	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; **PDBTitle:** structure of the e. coli c-p lyase core complex
38	c1bkvA_	Alignment	not modelled	10.9	44	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**t3-785; **PDBTitle:** collagen
39	c1bkvB_	Alignment	not modelled	10.5	44	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**t3-785; **PDBTitle:** collagen
40	c1bkvC_	Alignment	not modelled	10.5	44	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**t3-785; **PDBTitle:** collagen
41	d1fcda3	Alignment	not modelled	10.0	23	**Fold:**CO dehydrogenase flavoprotein C-domain-like **Superfamily:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain **Family:**FAD/NAD-linked reductases, dimerisation (C-terminal) domain
42	d1vlfn1	Alignment	not modelled	8.1	100	**Fold:**Prealbumin-like **Superfamily:**Cna protein B-type domain **Family:**Cna protein B-type domain
43	c5bv9A_	Alignment	not modelled	8.0	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cellulose 1,4-beta-cellobiosidase; **PDBTitle:** the structure of bacillus pumilus gh48 in complex with cellobiose
44	c6aokA_	Alignment	not modelled	7.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ceg4; **PDBTitle:** crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
45	c1bzgA_	Alignment	not modelled	7.0	29	**PDB header:**hormone **Chain:** A: **PDB Molecule:**parathyroid hormone-related protein; **PDBTitle:** the solution structure of human parathyroid hormone-related2 protein (1-34) in near-physiological solution, nmr, 303 structures
46	c2kg7A_	Alignment	not modelled	7.0	47	**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
47	c3sjrB_	Alignment	not modelled	7.0	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved unkown function protein cv_1783 from2 chromobacterium violaceum atcc 12472
48	c2nvjA_	Alignment	not modelled	6.7	40	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**25mer peptide from vacuolar atp synthase subunit **PDBTitle:** nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
49	c6cgjA_	Alignment	not modelled	6.6	38	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**effector protein lem4 (lpg1101); **PDBTitle:** structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
50	c2iu1A_	Alignment	not modelled	6.6	28	**PDB header:**transcription **Chain:** A: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** crystal structure of eif5 c-terminal domain
51	c5l85B_	Alignment	not modelled	6.5	36	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**nuclear fragile x mental retardation-interacting protein 1; **PDBTitle:** solution structure of the complex between human znhit3 and nufip12 proteins
52	c6nbiP_	Alignment	not modelled	6.5	60	**PDB header:**signaling protein **Chain:** P: **PDB Molecule:**long-acting parathyroid hormone analog; **PDBTitle:** cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein
53	c1vytF_	Alignment	not modelled	6.5	63	**PDB header:**transport protein **Chain:** F: **PDB Molecule:**voltage-dependent l-type calcium channel **PDBTitle:** beta3 subunit complexed with aid

54	c2lkqA_	Alignment	not modelled	5.8	33	**PDB header:**immune system **Chain:** A: **PDB Molecule:**immunoglobulin lambda-like polypeptide 1; **PDBTitle:** nmr structure of the lambda 5 22-45 peptide
55	c2fulE_	Alignment	not modelled	5.6	28	**PDB header:**translation **Chain:** E: **PDB Molecule:**eukaryotic translation initiation factor 5; **PDBTitle:** crystal structure of the c-terminal domain of s. cerevisiae eif5
56	d1nkta4	Alignment	not modelled	5.2	67	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
57	d1dmua_	Alignment	not modelled	5.1	56	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Restriction endonuclease BglI
58	c1vytE_	Alignment	not modelled	5.1	63	**PDB header:**transport protein **Chain:** E: **PDB Molecule:**voltage-dependent l-type calcium channel **PDBTitle:** beta3 subunit complexed with aid
59	c3qi7A_	Alignment	not modelled	5.1	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**putative transcriptional regulator; **PDBTitle:** crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
60	c2lyyB_	Alignment	not modelled	5.0	26	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** nmr structure of the protein nb7890a from shewanella sp