
















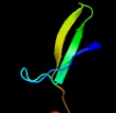

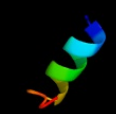




Phyre2

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Description	RVBD0459 (-) _551201_551692
Date	Tue Jul 23 14:50:54 BST 2019
Unique Job ID	d128c4792c78c808

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2apnA_	 Alignment		98.3	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hi1723; PDBTitle: hi1723 solution structure
2	d1s98a_	 Alignment		97.7	22	Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain
3	c2d2aA_	 Alignment		97.5	17	PDB header: metal transport Chain: A: PDB Molecule: sufa protein; PDBTitle: crystal structure of escherichia coli sufa involved in biosynthesis of 2 iron-sulfur clusters
4	d1nwba_	 Alignment		97.3	25	Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain
5	c1x0gA_	 Alignment		96.4	20	PDB header: metal binding protein Chain: A: PDB Molecule: isca; PDBTitle: crystal structure of isca with the [2fe-2s] cluster
6	c2k4zA_	 Alignment		95.5	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dsrr; PDBTitle: solution nmr structure of allochromatium vinosum dsrr:2 northeast structural genomics consortium target op5
7	c2qg0A_	 Alignment		89.5	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative fe-s biosynthesis protein; PDBTitle: crystal structure of a putative fe-s biosynthesis protein from 2 lactobacillus acidophilus
8	d2p2ea1	 Alignment		84.2	17	Fold: HesB-like domain Superfamily: HesB-like domain Family: HesB-like domain
9	c6imnB_	 Alignment		52.0	24	PDB header: ligase/dna Chain: B: PDB Molecule: dna ligase; PDBTitle: the crystal structure of asfvlig:ct2 complex
10	c6hqzB_	 Alignment		44.6	56	PDB header: hydrolase Chain: B: PDB Molecule: avrrpt2; PDBTitle: crystal structure of the type iii effector protein avrrpt2 from 2 erwinia amylovora, a c70 family cysteine protease
11	d1umya_	 Alignment		41.4	75	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase

12	c4cczA_			38.6	88	PDB header: transferase Chain: A; PDB Molecule: methionine synthase; PDBTitle: crystal structure of human 5-methyltetrahydrofolate-homocysteine2 methyltransferase, the homocysteine and folate binding domains
13	d3bofa2			38.6	75	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
14	d1lt7a_			36.9	75	Fold: TIM beta/alpha-barrel Superfamily: Homocysteine S-methyltransferase Family: Homocysteine S-methyltransferase
15	c3bolB_			32.9	75	PDB header: transferase Chain: B; PDB Molecule: 5-methyltetrahydrofolate s-homocysteine PDBTitle: cobalamin-dependent methionine synthase (1-566) from2 thermotoga maritima complexed with zn2+
16	c1pjca_			32.4	22	PDB header: oxidoreductase Chain: A; PDB Molecule: protein (l-alanine dehydrogenase); PDBTitle: l-alanine dehydrogenase complexed with nad
17	c2ab9A_			32.2	43	PDB header: hydrolase inhibitor Chain: A; PDB Molecule: pro-sfti-1; PDBTitle: discovery, structural determination and processing of the2 precursor protein that produces the cyclic trypsin3 inhibitor sfti-1
18	c6hpfA_			28.5	28	PDB header: hydrolase Chain: A; PDB Molecule: endo-b-mannanase; PDBTitle: structure of inactive e165q mutant of fungal non-cbm carrying gh262 endo-b-mannanase from yunnania penicillata in complex with alpha-62-3 61-di-galactosyl-mannotriose
19	c2wbrA_			27.4	50	PDB header: dna-binding protein Chain: A; PDB Molecule: gw182; PDBTitle: the rrm domain in gw182 proteins contributes to mirna-2 mediated gene silencing
20	d2ihta1			25.8	15	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
21	d2c5sa2		not modelled	21.7	22	Fold: THUMP domain Superfamily: THUMP domain-like Family: THUMP domain
22	c2brub_		not modelled	18.6	19	PDB header: oxidoreductase Chain: B; PDB Molecule: nad(p) transhydrogenase subunit alpha; PDBTitle: complex of the domain i and domain iii of escherichia coli2 transhydrogenase
23	c4dioB_		not modelled	17.6	18	PDB header: oxidoreductase Chain: B; PDB Molecule: nad(p) transhydrogenase subunit alpha part 1; PDBTitle: the crystal structure of transhydrogenase from sinorhizobium meliloti
24	d1o1ya_		not modelled	16.5	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
25	c1l7eC_		not modelled	14.4	23	PDB header: oxidoreductase Chain: C; PDB Molecule: nicotinamide nucleotide transhydrogenase, PDBTitle: crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh
26	c6hf4A_		not modelled	12.2	17	PDB header: hydrolase Chain: A; PDB Molecule: glycosyl hydrolase family 26; PDBTitle: the structure of boman26b, a gh26 beta-mannanase from bacteroides2 ovatus, complexed with g1m4
27	c2vx6A_		not modelled	12.2	30	PDB header: hydrolase Chain: A; PDB Molecule: cellvibrio japonicus mannanase cjman26c; PDBTitle: cellvibrio japonicus mannanase cjman26c gal1man4-bound form
28	c4izhA_		not modelled	11.7	19	PDB header: oxidoreductase Chain: A; PDB Molecule: nad/nadp transhydrogenase alpha subunit 1; PDBTitle: crystal structure of the alpha1 dimer of thermus

						thermophilus2 transhydrogenase in p6
29	c4i5wA_	Alignment	not modelled	11.1	23	PDB header: transferase Chain: A: PDB Molecule: 5',5'''-p-1,p-4-tetraphosphate phosphorylase 2; PDBTitle: crystal structure of yeast ap4a phosphorylase apa2 in complex with amp
30	d1pjca1	Alignment	not modelled	11.1	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
31	d2as0a1	Alignment	not modelled	11.0	17	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical RNA methyltransferase domain (HRMD)
32	c5iauD_	Alignment	not modelled	10.7	20	PDB header: hydrolase Chain: D: PDB Molecule: dipeptidase; PDBTitle: a c69-family cysteine dipeptidase from lactobacillus farcinis
33	c2oq2B_	Alignment	not modelled	10.4	8	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
34	d1rfsa_	Alignment	not modelled	10.4	26	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
35	c5z1vB_	Alignment	not modelled	10.3	26	PDB header: unknown function Chain: B: PDB Molecule: avrpib protein; PDBTitle: crystal structure of avrpib
36	d1oqka_	Alignment	not modelled	10.3	25	Fold: Rof/RNase P subunit-like Superfamily: Rof/RNase P subunit-like Family: RNase P subunit p29-like
37	c3wdrA_	Alignment	not modelled	10.1	17	PDB header: hydrolase Chain: A: PDB Molecule: beta-mannanase; PDBTitle: crystal structure of beta-mannanase from a symbiotic protist of the2 termite reticulitermes speratus complexed with gluco-manno-3 oligosaccharide
38	c5vitC_	Alignment	not modelled	9.8	39	PDB header: transferase Chain: C: PDB Molecule: mdcc; PDBTitle: crystal structure of a pseudomonas malonate decarboxylase hetero-2 tetramer in complex with malonate
39	c2n3pA_	Alignment	not modelled	9.7	78	PDB header: toxin Chain: A: PDB Molecule: asteropsin_g; PDBTitle: solution nmr structure of asteropsin g from marine sponge asteropus
40	c3d4oA_	Alignment	not modelled	9.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase subunit a; PDBTitle: crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
41	d1tj1a1	Alignment	not modelled	9.5	26	Fold: N-terminal domain of bifunctional PutA protein Superfamily: N-terminal domain of bifunctional PutA protein Family: N-terminal domain of bifunctional PutA protein
42	c5lc0B_	Alignment	not modelled	9.3	32	PDB header: hydrolase Chain: B: PDB Molecule: ns2b-ns3 protease,ns2b-ns3 protease; PDBTitle: crystal structure of zika virus ns2b-ns3 protease in complex with a2 boronate inhibitor
43	c5zr1F_	Alignment	not modelled	9.2	33	PDB header: dna binding protein/dna Chain: F: PDB Molecule: origin recognition complex subunit 6; PDBTitle: saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
44	c1p1pA_	Alignment	not modelled	9.1	75	PDB header: neurotoxin Chain: A: PDB Molecule: aa-conotoxin piva; PDBTitle: [pro7,13] aa-conotoxin piva, nmr, 12 structures
45	d1q90c_	Alignment	not modelled	9.1	23	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
46	c4narA_	Alignment	not modelled	9.1	28	PDB header: isomerase Chain: A: PDB Molecule: putative uronate isomerase; PDBTitle: crystal structure of the q9wys3 protein from thermotoga maritima.2 northeast structural genomics consortium target vr152
47	d2bvya2	Alignment	not modelled	8.9	35	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
48	d1l0wa2	Alignment	not modelled	8.8	25	Fold: DcOH-like Superfamily: GAD domain-like Family: GAD domain
49	c2imgA_	Alignment	not modelled	8.7	15	PDB header: hydrolase Chain: A: PDB Molecule: dual specificity protein phosphatase 23; PDBTitle: crystal structure of dual specificity protein phosphatase2 23 from homo sapiens in complex with ligand malate ion
50	c2v45A_	Alignment	not modelled	8.6	30	PDB header: oxidoreductase Chain: A: PDB Molecule: periplasmic nitrate reductase; PDBTitle: a new catalytic mechanism of periplasmic nitrate reductase2 from desulfovibrio desulfuricans atcc 27774 from3 crystallographic and epr data and based on detailed4 analysis of the sixth ligand
51	c4o8jB_	Alignment	not modelled	8.5	33	PDB header: ligase/rna Chain: B: PDB Molecule: rna 3'-terminal phosphate cyclase; PDBTitle: crystal structure of rtca, the rna 3'-terminal phosphate cyclase from2 pyrococcus horikoshii, in complex with racaaa3'phosphate and adenine.
52	c4uobA_	Alignment	not modelled	8.1	17	PDB header: lyase Chain: A: PDB Molecule: endonuclease iii-3; PDBTitle: crystal structure of deinococcus radiodurans endonuclease iii-3
53	d2i74a1	Alignment	not modelled	7.6	75	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Extended PAW domain

54	d2iv2x2	Alignment	not modelled	7.6	19	Fold: Formate dehydrogenase/DMSO reductase, domains 1-3 Superfamily: Formate dehydrogenase/DMSO reductase, domains 1-3 Family: Formate dehydrogenase/DMSO reductase, domains 1-3
55	d1qkia2	Alignment	not modelled	7.5	16	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Glucose 6-phosphate dehydrogenase-like
56	c3q3uA	Alignment	not modelled	7.4	59	PDB header: oxidoreductase Chain: A: PDB Molecule: lignin peroxidase; PDBTitle: trametes cervina lignin peroxidase
57	c4o1rA	Alignment	not modelled	7.4	16	PDB header: splicing Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of npudnab intein
58	c1bqfA	Alignment	not modelled	7.4	71	PDB header: hormone/growth factor Chain: A: PDB Molecule: protein (growth-blocking peptide); PDBTitle: growth-blocking peptide (gbp) from pseudaletia separata
59	c2yujA	Alignment	not modelled	7.3	24	PDB header: protein binding Chain: A: PDB Molecule: ubiquitin fusion degradation 1-like; PDBTitle: solution structure of human ubiquitin fusion degradation2 protein 1 homolog ufd1
60	d1odza	Alignment	not modelled	7.3	30	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: beta-glycanases
61	c4kr7A	Alignment	not modelled	7.3	24	PDB header: transferase/rna Chain: A: PDB Molecule: probable trna sulfurtransferase; PDBTitle: crystal structure of a 4-thiouridine synthetase - rna complex with2 bound atp
62	c4iumA	Alignment	not modelled	7.2	12	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: papain-like protease 2; PDBTitle: equine arteritis virus papain-like protease 2 (plp2) covalently bound2 to ubiquitin
63	c5u87A	Alignment	not modelled	7.0	43	PDB header: plant protein Chain: A: PDB Molecule: preproalbumin paws1; PDBTitle: nmr structure of the precursor protein paws1 comprising sfti-1 and a2 seed storage albumin
64	c4b2uA	Alignment	not modelled	7.0	67	PDB header: toxin Chain: A: PDB Molecule: s67; PDBTitle: s67, a spider venom toxin peptide from sicarius dolichocephalus
65	c5xknE	Alignment	not modelled	6.9	63	PDB header: transferase/signaling protein Chain: E: PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complex with epfl4
66	c5xknF	Alignment	not modelled	6.9	63	PDB header: transferase/signaling protein Chain: F: PDB Molecule: epidermal patterning factor-like protein 4; PDBTitle: crystal structure of plant receptor erl2 in complex with epfl4
67	c2gnnA	Alignment	not modelled	6.8	35	PDB header: hormone/growth factor Chain: A: PDB Molecule: vascular endothelial growth factor homolog; PDBTitle: crystal structure of the orf virus nz2 variant of vegf-e
68	d1b80a	Alignment	not modelled	6.7	64	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
69	c6alyA	Alignment	not modelled	6.7	30	PDB header: transcription Chain: A: PDB Molecule: mediator of rna polymerase ii transcription subunit 15; PDBTitle: solution structure of yeast med15 abd2 residues 277-368
70	c2c5sA	Alignment	not modelled	6.7	24	PDB header: rna-binding protein Chain: A: PDB Molecule: probable thiamine biosynthesis protein thii; PDBTitle: crystal structure of bacillus anthracis thii, a trna-2 modifying enzyme containing the predicted rna-binding3 thump domain
71	c2bvtB	Alignment	not modelled	6.7	35	PDB header: hydrolase Chain: B: PDB Molecule: beta-1,4-mannanase; PDBTitle: the structure of a modular endo-beta-1,4-mannanase from cellulomonas2 fimi explains the product specificity of glycoside hydrolase family3 26 mannanases.
72	d2ouwa1	Alignment	not modelled	6.7	16	Fold: AhpD-like Superfamily: AhpD-like Family: TTHA0727-like
73	d1a41a	Alignment	not modelled	6.7	25	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Eukaryotic DNA topoisomerase I, catalytic core
74	d1xkpb1	Alignment	not modelled	6.6	22	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
75	c2w23A	Alignment	not modelled	6.6	55	PDB header: oxidoreductase Chain: A: PDB Molecule: versatile peroxidase vpl2; PDBTitle: structure of mutant w169y of pleurotus eryngii versatile2 peroxidase (vp)
76	c2xv7A	Alignment	not modelled	6.5	32	PDB header: hormone Chain: A: PDB Molecule: vascular endothelial growth factor d; PDBTitle: crystal structure of vascular endothelial growth factor d
77	d1wq9a	Alignment	not modelled	6.5	29	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Platelet-derived growth factor-like
78	c2g9gA	Alignment	not modelled	6.3	75	PDB header: hydrolase Chain: A: PDB Molecule: peptide n-glycanase; PDBTitle: crystal structure of his-tagged mouse pngase c-terminal domain
79	d1pdga	Alianment	not modelled	6.3	32	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines

						Family: Platelet-derived growth factor-like
80	c2c7wB_	Alignment	not modelled	6.2	37	PDB header: growth factor Chain: B: PDB Molecule: vascular endothelial growth factor b precursor; PDBTitle: crystal structure of human vascular endothelial growth2 factor-b: identification of amino acids important for3 angiogenic activity
81	d1knya2	Alignment	not modelled	6.2	19	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Kanamycin nucleotidyltransferase (KNTase), N-terminal domain
82	c2oz5A_	Alignment	not modelled	6.2	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phosphotyrosine protein phosphatase ptpb; PDBTitle: crystal structure of mycobacterium tuberculosis protein tyrosine2 phosphatase ptpb in complex with the specific inhibitor omts
83	c3kc2A_	Alignment	not modelled	6.1	23	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
84	d2v4ja2	Alignment	not modelled	6.1	26	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
85	d2e74d1	Alignment	not modelled	6.0	25	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
86	c5cvoA_	Alignment	not modelled	6.0	36	PDB header: hydrolase/protein binding Chain: A: PDB Molecule: wd repeat-containing protein 48; PDBTitle: wdr48:usp46~ubiquitin ternary complex
87	c2yumA_	Alignment	not modelled	6.0	14	PDB header: transcription Chain: A: PDB Molecule: zinc finger zz-type-containing protein 3; PDBTitle: solution structure of the myb-like dna-binding domain of2 human zzz3 protein
88	c6f45D_	Alignment	not modelled	5.9	57	PDB header: viral protein Chain: D: PDB Molecule: receptor recognition protein; PDBTitle: crystal structure of the gp37-gp38 adhesin tip complex of the2 bacteriophage s16 long tail fiber
89	c2ak0A_	Alignment	not modelled	5.9	75	PDB header: toxin Chain: A: PDB Molecule: alpha-conotoxin mii; PDBTitle: structure of cyclic conotoxin mii-7
90	d1qpaA_	Alignment	not modelled	5.9	68	Fold: Heme-dependent peroxidases Superfamily: Heme-dependent peroxidases Family: CCP-like
91	c4yn5A_	Alignment	not modelled	5.8	24	PDB header: hydrolase Chain: A: PDB Molecule: mannan endo-1,4-beta-mannosidase; PDBTitle: catalytic domain of bacillus sp. jamb-750 gh26 endo-beta-1,4-mannanase
92	d2fhfa1	Alignment	not modelled	5.8	45	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
93	c4ynsA_	Alignment	not modelled	5.7	21	PDB header: isomerase Chain: A: PDB Molecule: lara protein; PDBTitle: a tethered niacin-derived pincer complex with a nickel-carbon bond in2 lactate racemase
94	c2gncC_	Alignment	not modelled	5.7	35	PDB header: hormone/growth factor Chain: C: PDB Molecule: vascular endothelial growth factor homolog; PDBTitle: crystal structure of the orf virus nz2 variant of vegf-e
95	c3uiwB_	Alignment	not modelled	5.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glutaredoxin 2; PDBTitle: zebrafish grx2 (apo)
96	d2dira1	Alignment	not modelled	5.4	42	Fold: THUMP domain Superfamily: THUMP domain-like Family: Minimal THUMP
97	d2gu3a1	Alignment	not modelled	5.4	29	Fold: Cystatin-like Superfamily: Cystatin/monellin Family: PepSY-like
98	c1qmiC_	Alignment	not modelled	5.4	15	PDB header: ligase Chain: C: PDB Molecule: rna 3'-terminal phosphate cyclase; PDBTitle: crystal structure of rna 3'-terminal phosphate cyclase, an2 ubiquitous enzyme with unusual topology
99	d1ywfa1	Alignment	not modelled	5.3	25	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Mycobacterial PtpB-like