






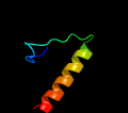

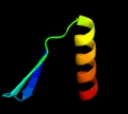



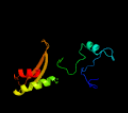

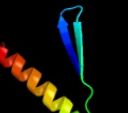
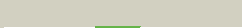


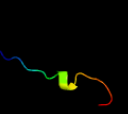

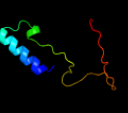


Phyre2

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 Date Thu Aug 8 16:20:16 BST 2019
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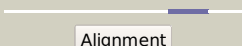
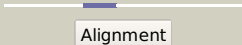
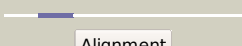
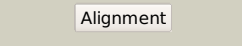
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6avhA_	 Alignment		81.4	15	PDB header: ligase, plant protein Chain: A: PDB Molecule: gh3.15 acyl acid amido synthetase; PDBTitle: gh3.15 acyl acid amido synthetase
2	c4ewvB_	 Alignment		70.6	13	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with amcpp
3	d2qmwA2	 Alignment		65.6	8	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
4	d1ddwa_	 Alignment		63.4	6	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
5	d1xoda1	 Alignment		61.0	22	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
6	c3o1lB_	 Alignment		60.6	21	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
7	c4eplA_	 Alignment		58.1	15	PDB header: ligase Chain: A: PDB Molecule: jasmonic acid-amido synthetase jar1; PDBTitle: crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile
8	d1i7aa_	 Alignment		56.3	8	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
9	c2mdaB_	 Alignment		55.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: tyrosine 3-monooxygenase; PDBTitle: the solution structure of the regulatory domain of tyrosine2 hydroxylase
10	c5l0lB_	 Alignment		47.8	35	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein lpg0439
11	c2im5C_	 Alignment		47.4	15	PDB header: transferase Chain: C: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of nicotinate phosphoribosyltransferase from2 porphyromonas gingivalis

12	c3do6B_	Alignment		41.9	14	PDB header: ligase Chain: B: PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of putative formyltetrahydrofolate synthetase2 (tm1766) from thermotoga maritima at 1.85 a resolution
13	d1evha_	Alignment		41.8	19	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
14	c1zhvA_	Alignment		40.6	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu0741; PDBTitle: x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
15	d2dfaa1	Alignment		39.3	20	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
16	c4j38A_	Alignment		36.8	26	PDB header: immune system Chain: A: PDB Molecule: outer surface protein e; PDBTitle: structure of borrelia burgdorferi outer surface protein e in complex2 with factor h domains 19-20
17	d1nh8a2	Alignment		34.4	11	Fold: Ferredoxin-like Superfamily: GlnB-like Family: ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
18	c2ivfB_	Alignment		33.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: ethylbenzene dehydrogenase beta-subunit; PDBTitle: ethylbenzene dehydrogenase from aromatoleum aromaticum
19	d1qc6a_	Alignment		33.0	17	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
20	d1pdoa_	Alignment		32.3	14	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
21	c3iprC_	Alignment	not modelled	30.6	11	PDB header: transferase Chain: C: PDB Molecule: pts system, iia component; PDBTitle: crystal structure of the enterococcus faecalis gluconate2 specific eiiA phosphotransferase system component
22	c2m3aA_	Alignment	not modelled	30.5	35	PDB header: dna binding protein Chain: A: PDB Molecule: protein knl-2; PDBTitle: nmr solution structure of a myb-like dna binding domain of knl-2 from2 c. elegans
23	c5td7A_	Alignment	not modelled	29.2	16	PDB header: hydrolase Chain: A: PDB Molecule: zgc:55652; PDBTitle: crystal structure of histone deacetylase 10
24	d1qz9a_	Alignment	not modelled	28.8	14	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
25	c4yubB_	Alignment	not modelled	28.3	19	PDB header: ligase Chain: B: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of human nicotinic acid phosphoribosyltransferase
26	d1y7pa1	Alignment	not modelled	27.9	15	Fold: Flavodoxin-like Superfamily: CheY-like Family: AF1403 C-terminal domain-like
27	c3a5vA_	Alignment	not modelled	27.3	21	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of alpha-galactosidase i from mortierella vinacea
28	c2jp2A_	Alignment	not modelled	26.1	24	PDB header: signaling protein Chain: A: PDB Molecule: sprouty-related, evh1 domain-containing protein PDBTitle: solution structure and resonance assignment of the n-2 terminal evh1 domain from the human spread2 protein3 (sprouty-related protein with evh1 domain isoform 2)

29	d1iuga_	Alignment	not modelled	26.1	17	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
30	c5a4jC_	Alignment	not modelled	25.3	23	PDB header: ligase Chain: C: PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of fthfs1 from t.acetoxydans re1
31	c3lrmB_	Alignment	not modelled	24.1	26	PDB header: hydrolase Chain: B: PDB Molecule: alpha-galactosidase 1; PDBTitle: structure of alfa-galactosidase from saccharomyces cerevisiae with2 raffinose
32	c6cxdA_	Alignment	not modelled	24.1	16	PDB header: hydrolase Chain: A: PDB Molecule: peptidase b; PDBTitle: crystal structure of peptidase b from yersinia pestis co92 at 2.75 a2 resolution
33	d1xmka1	Alignment	not modelled	23.6	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
34	d2ed6a1	Alignment	not modelled	23.2	17	Fold: WSSV envelope protein-like Superfamily: WSSV envelope protein-like Family: WSSV envelope protein-like
35	c5az0A_	Alignment	not modelled	23.2	24	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of aldo-keto reductase (akr2e5) of the silkworm,2 bombyx mori
36	d1h70a_	Alignment	not modelled	22.6	5	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Dimethylarginine dimethylaminohydrolase DDAH
37	d1m6sa_	Alignment	not modelled	22.4	10	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: AAT-like
38	c5xlmB_	Alignment	not modelled	21.9	20	PDB header: transferase Chain: B: PDB Molecule: serine/threonine-protein kinase pkn1; PDBTitle: monomer form of m.tuberculosis pkn1 sensor domain
39	d1o7fa1	Alignment	not modelled	19.1	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: DEP domain
40	d1m32a_	Alignment	not modelled	19.1	19	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
41	c3lutA_	Alignment	not modelled	18.9	33	PDB header: membrane protein Chain: A: PDB Molecule: voltage-gated potassium channel subunit beta-2; PDBTitle: a structural model for the full-length shaker potassium channel kv1.2
42	d3eaua1	Alignment	not modelled	18.9	33	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
43	c2nyiB_	Alignment	not modelled	18.7	23	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria sulphuraria
44	c3e9kA_	Alignment	not modelled	18.4	16	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase-3-hydroxyhippuric acid2 inhibitor complex
45	c4maiA_	Alignment	not modelled	17.7	28	PDB header: oxidoreductase Chain: A: PDB Molecule: aa11 lytic polysaccharide monoxygenase; PDBTitle: structure of aspergillus oryzae aa11 lytic polysaccharide2 monoxygenase with cu(i)
46	d1uasa2	Alignment	not modelled	17.4	26	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
47	c4yddF_	Alignment	not modelled	17.4	19	PDB header: oxidoreductase Chain: F: PDB Molecule: dms0 reductase family type ii enzyme, iron-sulfur subunit; PDBTitle: crystal structure of the perchlorate reductase pcrab from azospira2 suillum ps
48	c6czaB_	Alignment	not modelled	17.1	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
49	c1bplA_	Alignment	not modelled	17.0	20	PDB header: glycosyltransferase Chain: A: PDB Molecule: alpha-1,4-glucon-4-gluconohydrolase; PDBTitle: glycosyltransferase
50	c4bjuB_	Alignment	not modelled	17.0	25	PDB header: isomerase Chain: B: PDB Molecule: n-acetylglucosamine-phosphate fumigase; PDBTitle: genetic and structural validation of aspergillus fumigatus2 n-acetylphosphoglucosamine mutase as an antifungal target
51	d1a9xa4	Alignment	not modelled	16.8	11	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
52	c5xgzA_	Alignment	not modelled	16.8	21	PDB header: hydrolase Chain: A: PDB Molecule: beta-glycosidase; PDBTitle: metagenomic glucose-tolerant glycosidase
53	c2j75A_	Alignment	not modelled	16.7	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase a; PDBTitle: beta-glucosidase from thermotoga maritima in complex with2 neuromycin
54	d1ru8a_	Alignment	not modelled	16.5	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases

55	d1r46a2	Alignment	not modelled	16.5	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
56	c2csuB_	Alignment	not modelled	16.4	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: 457aa long hypothetical protein; PDBTitle: crystal structure of ph0766 from pyrococcus horikoshii ot3
57	c6fmgC_	Alignment	not modelled	16.3	11	PDB header: transferase Chain: C: PDB Molecule: pts system mannose-specific transporter subunit iiaB; PDBTitle: structure of the mannose transporter iia domain from streptococcus2 pneumoniae
58	c4b2gB_	Alignment	not modelled	16.2	21	PDB header: signaling protein Chain: B: PDB Molecule: gh3-1 auxin conjugating enzyme; PDBTitle: crystal structure of an indole-3-acetic acid amido synthase from vitis2 vinifera involved in auxin homeostasis
59	c3nx3A_	Alignment	not modelled	16.1	15	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
60	c3w7bB_	Alignment	not modelled	15.6	28	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase from thermus2 thermophilus hb8
61	c1ti2F_	Alignment	not modelled	15.2	13	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrogallol hydroxytransferase small subunit; PDBTitle: crystal structure of pyrogallol-phloroglucinol transhydroxylase from2 pelobacter acidigallici
62	c2lnaA_	Alignment	not modelled	15.0	17	PDB header: hydrolase Chain: A: PDB Molecule: afg3-like protein 2; PDBTitle: solution nmr structure of the mitochondrial inner membrane domain2 (residues 164-251), ftsH_ext, from the paraplegin-like protein afg3l23 from homo sapiens, northeast structural genomics consortium target4 hr6741a
63	c4e4jI_	Alignment	not modelled	14.9	28	PDB header: hydrolase Chain: J: PDB Molecule: arginine deiminase; PDBTitle: crystal structure of arginine deiminase from mycoplasma penetrans
64	c3hqtB_	Alignment	not modelled	14.9	3	PDB header: transferase Chain: B: PDB Molecule: cai-1 autoinducer synthase; PDBTitle: plp-dependent acyl-coa transferase cqsa
65	c4hl7A_	Alignment	not modelled	14.8	22	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of nicotinate phosphoribosyltransferase (target2 nysgr-026035) from vibrio cholerae
66	d1z7da1	Alignment	not modelled	14.6	8	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
67	c1ybeA_	Alignment	not modelled	14.5	11	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase
68	c3ke3A_	Alignment	not modelled	14.3	13	PDB header: transferase Chain: A: PDB Molecule: putative serine-pyruvate aminotransferase; PDBTitle: crystal structure of putative serine-pyruvate aminotransferase2 (yp_263484.1) from psychrobacter arcticum 273-4 at 2.20 a resolution
69	c4xi7A_	Alignment	not modelled	14.3	26	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mib1; PDBTitle: crystal structure of the mzm-rep domains of mind bomb 1 in complex2 with jagged1 n-box peptide
70	c6ierA_	Alignment	not modelled	14.1	18	PDB header: hydrolase Chain: A: PDB Molecule: beta-glucosidase 1317; PDBTitle: apo structure of a beta-glucosidase 1317
71	d1ktba2	Alignment	not modelled	13.8	17	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
72	d2ns0a1	Alignment	not modelled	13.7	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
73	c2wztA_	Alignment	not modelled	13.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase; PDBTitle: crystal structure of a mycobacterium aldo-keto reductase in its apo2 and liganded form
74	c2pfuA_	Alignment	not modelled	13.6	5	PDB header: transport protein Chain: A: PDB Molecule: biopolymer transport exbd protein; PDBTitle: nmr structure determination of the periplasmic domain of exbd from2 e.coli
75	d2b8ea1	Alignment	not modelled	13.5	11	Fold: HAD-like Superfamily: HAD-like Family: Meta-cation ATPase, catalytic domain P
76	c5yj7C_	Alignment	not modelled	13.5	21	PDB header: hydrolase Chain: C: PDB Molecule: glycoside hydrolase; PDBTitle: structural insight into the beta-gh1 glucosidase bgln1 from oleaginous2 microalgae nannochloropsis
77	c1yirA_	Alignment	not modelled	13.3	15	PDB header: transferase Chain: A: PDB Molecule: nicotinate phosphoribosyltransferase 2; PDBTitle: crystal structure of a nicotinate phosphoribosyltransferase
78	d3beda1	Alignment	not modelled	12.7	11	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
79	c2hzaA_	Alignment	not modelled	12.3	16	PDB header: hydrolase Chain: A: PDB Molecule: kynureninase; PDBTitle: crystal structure of homo sapiens kynureninase

80	c5viuB_		Alignment	not modelled	12.2	8	PDB header: transferase Chain: B: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase from2 elizabethkingia anophellis
81	c4nziA_		Alignment	not modelled	12.0	21	PDB header: hydrolase Chain: A: PDB Molecule: putative alpha-galactosidase; PDBTitle: crystal structure of a putative alpha-galactosidase (bf1418) from2 bacteroides fragilis nctc 9343 at 1.57 a resolution
82	c2ro0A_		Alignment	not modelled	11.9	42	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase esa1; PDBTitle: solution structure of the knotted tudor domain of the yeast2 histone acetyltransferase, esa1
83	c4ec1A_		Alignment	not modelled	11.7	22	PDB header: isomerase Chain: A: PDB Molecule: serine racemase; PDBTitle: crystal structure of the cytoplasmic domain of vancomycin resistance2 serine racemase vantg
84	c6eacC_		Alignment	not modelled	11.7	29	PDB header: transferase Chain: C: PDB Molecule: selo; PDBTitle: pseudomonas syringae selo
85	c1vraB_		Alignment	not modelled	11.7	21	PDB header: transferase Chain: B: PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
86	d1xw8a_		Alignment	not modelled	11.6	17	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
87	c3n0vD_		Alignment	not modelled	11.6	21	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
88	d1a1va2		Alignment	not modelled	11.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
89	c2dr1A_		Alignment	not modelled	11.4	21	PDB header: transferase Chain: A: PDB Molecule: 386aa long hypothetical serine aminotransferase; PDBTitle: crystal structure of the ph1308 protein from pyrococcus horikoshii ot3
90	c2ifsA_		Alignment	not modelled	11.4	10	PDB header: signaling protein Chain: A: PDB Molecule: wiskott-aldrich syndrome protien interacting protein and PDBTitle: structure of the n-wasp evh1 domain in complex with an extended wip2 peptide
91	c3lv2A_		Alignment	not modelled	10.9	9	PDB header: transferase Chain: A: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate aminotransferase; PDBTitle: crystal structure of mycobacterium tuberculosis 7,8-diaminopelargonic2 acid synthase in complex with substrate analog sinefungin
92	d1szna2		Alignment	not modelled	10.9	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
93	d1yksa2		Alignment	not modelled	10.5	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
94	c2nvaH_		Alignment	not modelled	10.4	16	PDB header: lyase Chain: H: PDB Molecule: arginine decarboxylase, a207r protein; PDBTitle: the x-ray crystal structure of the paramecium bursaria chlorella virus2 arginine decarboxylase bound to agmatine
95	c1z7dE_		Alignment	not modelled	10.4	10	PDB header: transferase Chain: E: PDB Molecule: ornithine aminotransferase; PDBTitle: ornithine aminotransferase py00104 from plasmodium yoelii
96	c3rmuD_		Alignment	not modelled	10.2	4	PDB header: isomerase Chain: D: PDB Molecule: methylmalonyl-coa epimerase, mitochondrial; PDBTitle: crystal structure of human methylmalonyl-coa epimerase, mcee
97	d1i2ha_		Alignment	not modelled	10.2	6	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
98	d1knwa2		Alignment	not modelled	10.2	10	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
99	d1yira1		Alignment	not modelled	10.1	19	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: Monomeric nicotinate phosphoribosyltransferase C-terminal domain