





















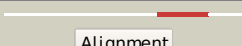
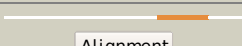

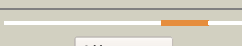
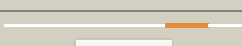

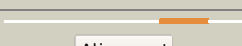


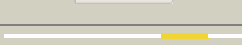


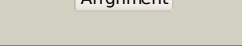
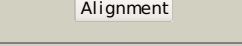
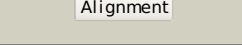
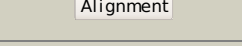
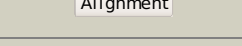
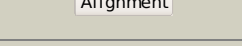
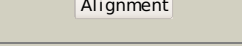
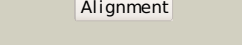
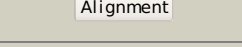
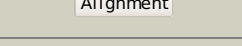
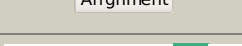
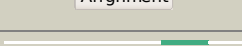
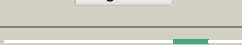
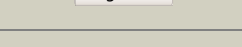


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1w25B_	 Alignment		100.0	29	PDB header: signaling protein Chain: B: PDB Molecule: stalked-cell differentiation controlling protein; PDBTitle: response regulator pled in complex with c-digmp
2	c3ezuA_	 Alignment		100.0	25	PDB header: signaling protein Chain: A: PDB Molecule: ggdef domain protein; PDBTitle: crystal structure of multidomain protein of unknown function with2 ggdef-domain (np_951600.1) from geobacter sulfurreducens at 1.95 a3 resolution
3	c3breA_	 Alignment		99.9	24	PDB header: signaling protein Chain: A: PDB Molecule: probable two-component response regulator; PDBTitle: crystal structure of p.aeruginosa pa3702
4	c3i5aA_	 Alignment		99.9	24	PDB header: signaling protein Chain: A: PDB Molecule: response regulator/ggdef domain protein; PDBTitle: crystal structure of full-length wpsr from pseudomonas syringae
5	c3i5cA_	 Alignment		99.9	28	PDB header: signaling protein Chain: A: PDB Molecule: fusion of general control protein gcn4 and wpsr response PDBTitle: crystal structure of a fusion protein containing the leucine zipper of2 gcn4 and the ggdef domain of wpsr from pseudomonas aeruginosa
6	c3i5bA_	 Alignment		99.9	29	PDB header: signaling protein Chain: A: PDB Molecule: wpsr response regulator; PDBTitle: crystal structure of the isolated ggdef domain of wpsr from2 pseudomonas aeruginosa
7	c3ignA_	 Alignment		99.9	33	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase; PDBTitle: crystal structure of the ggdef domain from marinobacter2 aquaeolei diguanylate cyclase complexed with c-di-gmp -3 northeast structural genomics consortium target mqr89a
8	d1w25a3	 Alignment		99.9	31	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: GGDEF domain
9	c3ic1A_	 Alignment		99.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: eal/ggdef domain protein; PDBTitle: x-ray structure of protein (eal/ggdef domain protein) from2 m.capsulatus, northeast structural genomics consortium3 target mcr174c
10	c3hvaA_	 Alignment		99.9	23	PDB header: transferase Chain: A: PDB Molecule: protein fimx; PDBTitle: crystal structure of fimx ggdef domain from pseudomonas2 aeruginosa
11	c3qyvB_	 Alignment		99.9	23	PDB header: signaling protein/inhibitor Chain: B: PDB Molecule: response regulator; PDBTitle: a novel interaction mode between a microbial ggdef domain and the bis-2 (3, 5)-cyclic di-gmp

12	c3mtkA_	Alignment		99.9	18	PDB header: transferase Chain: A: PDB Molecule: diguanylate cyclase/phosphodiesterase; PDBTitle: x-ray structure of diguanylate cyclase/phosphodiesterase from2 caldicellulosiruptor saccharolyticus, northeast structural genomics3 consortium target clr27c
13	c3pjwA_	Alignment		99.9	19	PDB header: lyase Chain: A: PDB Molecule: cyclic dimeric gmp binding protein; PDBTitle: structure of pseudomonas fluorescence lapd ggdef-eal dual domain, i23
14	c3hvwA_	Alignment		99.8	18	PDB header: lyase Chain: A: PDB Molecule: diguanylate-cyclase (dgc); PDBTitle: crystal structure of the ggdef domain of the pa2567 protein2 from pseudomonas aeruginosa, northeast structural genomics3 consortium target par365c
15	c3gfbB_	Alignment		98.9	14	PDB header: hydrolase, signaling protein Chain: B: PDB Molecule: klebsiella pneumoniae blrp1; PDBTitle: klebsiella pneumoniae blrp1 ph 6 manganese/cy-digmp complex
16	c3p7nB_	Alignment		97.6	10	PDB header: dna binding protein Chain: B: PDB Molecule: sensor histidine kinase; PDBTitle: crystal structure of light activated transcription factor el222 from2 erythrobacter litoralis
17	c2qv6D_	Alignment		97.3	16	PDB header: hydrolase Chain: D: PDB Molecule: gtp cyclohydrolase iii; PDBTitle: gtp cyclohydrolase iii from m. jannaschii (mj0145)2 complexed with gtp and metal ions
18	c1cjkA_	Alignment		95.3	12	PDB header: lyase/lyase/signaling protein Chain: A: PDB Molecule: adenylate cyclase, type v; PDBTitle: complex of gs-alpha with the catalytic domains of mammalian adenylyl2 cyclase: complex with adenosine 5'-(alpha thio)-triphosphate (rp),3 mg, and mn
19	dlwc1a_	Alignment		95.1	16	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
20	c1wc6B_	Alignment		95.1	15	PDB header: lyase Chain: B: PDB Molecule: adenylate cyclase; PDBTitle: soluble adenylyl cyclase cyac from s. platensis in complex2 with rp-atpalphas in presence of bicarbonate
21	c1ybuA_	Alignment	not modelled	94.5	17	PDB header: hydrolase Chain: A: PDB Molecule: lipj; PDBTitle: mycobacterium tuberculosis adenylyl cyclase rv1900c chd, in complex2 with a substrate analog.
22	c3mr7B_	Alignment	not modelled	94.1	11	PDB header: hydrolase Chain: B: PDB Molecule: adenylate/guanylate cyclase/hydrolase, alpha/beta fold PDBTitle: crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi
23	c3r5gB_	Alignment	not modelled	94.0	14	PDB header: lyase Chain: B: PDB Molecule: cyab; PDBTitle: crystal structure of the adenylyl cyclase cyab from p. aeruginosa
24	dlazsa_	Alignment	not modelled	94.0	10	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
25	dlfx2a_	Alignment	not modelled	93.2	13	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain
26	c2w01C_	Alignment	not modelled	91.6	14	PDB header: lyase Chain: C: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of the guanylyl cyclase cya2
27	c3uvjC_	Alignment	not modelled	91.0	15	PDB header: lyase Chain: C: PDB Molecule: guanylate cyclase soluble subunit alpha-3; PDBTitle: crystal structure of the catalytic domain of the heterodimeric human2 soluble guanylate cyclase 1.
28	dlfx4a_	Alignment	not modelled	90.7	17	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenylyl and guanylyl cyclase catalytic domain

29	c3et6A		Alignment	not modelled	90.0	9	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase beta; PDBTitle: the crystal structure of the catalytic domain of a eukaryotic2 guanylate cyclase
30	c1yk9A		Alignment	not modelled	89.6	12	PDB header: lyase Chain: A: PDB Molecule: adenylate cyclase; PDBTitle: crystal structure of a mutant form of the mycobacterial2 adenyl cyclase rv1625c
31	c1y10C		Alignment	not modelled	87.8	8	PDB header: lyase Chain: C: PDB Molecule: hypothetical protein rv1264/mt1302; PDBTitle: mycobacterial adenyl cyclase rv1264, holoenzyme, inhibited state
32	c2aq4A		Alignment	not modelled	82.9	17	PDB header: transferase Chain: A: PDB Molecule: dna repair protein rev1; PDBTitle: ternary complex of the catalytic core of rev1 with dna and dctp.
33	c1k1qA		Alignment	not modelled	82.7	17	PDB header: transcription Chain: A: PDB Molecule: dbh protein; PDBTitle: crystal structure of a dinb family error prone dna2 polymerase from sulfolobus solfataricus
34	c3gqcB		Alignment	not modelled	81.9	18	PDB header: transferase/dna Chain: B: PDB Molecule: dna repair protein rev1; PDBTitle: structure of human rev1-dna-dntp ternary complex
35	dlazsb		Alignment	not modelled	80.6	14	Fold: Ferredoxin-like Superfamily: Nucleotide cyclase Family: Adenyl and guanylyl cyclase catalytic domain
36	c3onqB		Alignment	not modelled	77.9	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: regulator of polyketide synthase expression; PDBTitle: crystal structure of regulator of polyketide synthase expression2 bad_0249 from bifidobacterium adolescentis
37	c1s97D		Alignment	not modelled	77.0	16	PDB header: transferase/dna Chain: D: PDB Molecule: dna polymerase iv; PDBTitle: dpo4 with gt mismatch
38	dlim4a		Alignment	not modelled	74.4	16	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
39	c3mr2A		Alignment	not modelled	63.5	26	PDB header: transferase/dna Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: human dna polymerase eta in complex with normal dna and incoming2 nucleotide (nrm)
40	c2wz1B		Alignment	not modelled	62.7	12	PDB header: lyase Chain: B: PDB Molecule: guanylate cyclase soluble subunit beta-1; PDBTitle: structure of the catalytic domain of human soluble2 guanylate cyclase 1 beta 3.
41	c2oh2B		Alignment	not modelled	62.1	18	PDB header: transferase/dna Chain: B: PDB Molecule: dna polymerase kappa; PDBTitle: ternary complex of human dna polymerase
42	c2r8kB		Alignment	not modelled	57.5	13	PDB header: replication, transferase/dna Chain: B: PDB Molecule: dna polymerase eta; PDBTitle: structure of the eukaryotic dna polymerase eta in complex with 1,2-2 d(gpg)-cisplatin containing dna
43	dlxxaa		Alignment	not modelled	57.0	14	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
44	d2o5aa1		Alignment	not modelled	54.1	17	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: lojap/YbeB-like
45	c3nrdB		Alignment	not modelled	53.8	11	PDB header: nucleotide binding protein Chain: B: PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad (hit) protein (smc02904) from2 sinorhizobium meliloti 1021 at 2.06 a resolution
46	c3oheA		Alignment	not modelled	53.4	10	PDB header: hydrolase Chain: A: PDB Molecule: histidine triad (hit) protein; PDBTitle: crystal structure of a histidine triad protein (maqu_1709) from2 marinobacter aquaeolei vt8 at 1.20 a resolution
47	c3imiB		Alignment	not modelled	51.7	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hit family protein; PDBTitle: 2.01 angstrom resolution crystal structure of a hit family protein2 from bacillus anthracis str. 'ames ancestor'
48	c1jihA		Alignment	not modelled	49.5	18	PDB header: translation Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: yeast dna polymerase eta
49	d1k1sa2		Alignment	not modelled	43.9	15	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
50	d1t94a2		Alignment	not modelled	43.7	18	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
51	d1jiha2		Alignment	not modelled	43.0	20	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
52	d1jx4a2		Alignment	not modelled	42.1	17	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
53	c3af5A		Alignment	not modelled	41.6	17	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph1404; PDBTitle: the crystal structure of an archaeal cpsf subunit, ph1404 from2 pyrococcus horikoshii
54	c3i24B		Alignment	not modelled	40.7	13	PDB header: hydrolase Chain: B: PDB Molecule: hit family hydrolase; PDBTitle: crystal structure of a hit family hydrolase protein from2 vibrio fischeri. northeast structural genomics consortium3 target id

					vfr176
55	c1xaxA_	Alignment	not modelled	40.6	10 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0054 protein hi0004; PDBTitle: nmr structure of hi0004, a putative essential gene product2 from haemophilus influenzae
56	d1gx1a_	Alignment	not modelled	39.4	17 Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
57	c3upsA_	Alignment	not modelled	39.3	15 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: iojap-like protein; PDBTitle: crystal structure of iojap-like protein from zymomonas mobilis
58	c3hf3A_	Alignment	not modelled	37.8	8 PDB header: oxidoreductase Chain: A: PDB Molecule: chromate reductase; PDBTitle: old yellow enzyme from thermus scotoductus sa-01
59	d1w55a2	Alignment	not modelled	35.4	19 Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
60	d1t0aa_	Alignment	not modelled	35.1	19 Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
61	c3v4gA_	Alignment	not modelled	34.3	10 PDB header: dna binding protein Chain: A: PDB Molecule: arginine repressor; PDBTitle: 1.60 angstrom resolution crystal structure of an arginine repressor2 from vibrio vulnificus cmcp6
62	d1b4ba_	Alignment	not modelled	33.5	15 Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
63	c3f0gA_	Alignment	not modelled	33.4	18 PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: co-crystal structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase with cmp
64	c1t3nB_	Alignment	not modelled	33.1	22 PDB header: replication/dna Chain: B: PDB Molecule: polymerase (dna directed) iota; PDBTitle: structure of the catalytic core of dna polymerase iota in2 complex with dna and dttp
65	c2pmpA_	Alignment	not modelled	32.5	15 PDB header: lyase Chain: A: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: structure of 2c-methyl-d-erythritol 2,4-cyclodiphosphate synthase from2 the isoprenoid biosynthetic pathway of arabidopsis thaliana
66	d2id1a1	Alignment	not modelled	31.6	9 Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: iojap/YbeB-like
67	d1y23a_	Alignment	not modelled	31.2	15 Fold: HIT-like Superfamily: HIT-like Family: HIT (HINT, histidine triad) family of protein kinase-interacting proteins
68	c3l7xA_	Alignment	not modelled	30.9	12 PDB header: cell cycle Chain: A: PDB Molecule: putative hit-like protein involved in cell-cycle PDBTitle: the crystal structure of smu.412c from streptococcus mutans ua159
69	d1iv3a_	Alignment	not modelled	30.8	17 Fold: Bacillus chorismate mutase-like Superfamily: lpsF-like Family: lpsF-like
70	c3l0oB_	Alignment	not modelled	30.4	22 PDB header: hydrolase Chain: B: PDB Molecule: transcription termination factor rho; PDBTitle: structure of rna-free rho transcription termination factor from2 thermotoga maritima
71	c3k30B_	Alignment	not modelled	30.2	9 PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardiodes simplex
72	d1ps9a1	Alignment	not modelled	30.1	17 Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
73	c2h90A_	Alignment	not modelled	29.9	14 PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
74	d1x6va1	Alignment	not modelled	28.6	15 Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
75	d2ox6a1	Alignment	not modelled	24.1	19 Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: YdiL-like
76	c1ps9A_	Alignment	not modelled	23.4	19 PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
77	c2filA_	Alignment	not modelled	23.1	23 PDB header: replication/dna Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: ternary complex of human dna polymerase iota with dna and dttp
78	d1wdia_	Alignment	not modelled	22.8	16 Fold: QueA-like Superfamily: QueA-like Family: QueA-like
79	c1qgeE_	Alignment	not modelled	22.2	23 PDB header: hydrolase Chain: E: PDB Molecule: protein (triacylglycerol hydrolase); PDBTitle: new crystal form of pseudomonas glumae (formerly chromobacterium2 viscosum atcc 6918) lipase
					PDB header: oxidoreductase Chain: A: PDB Molecule: nadh/flavin oxidoreductase/nadh

80	c3l5aA_	Alignment	not modelled	22.0	10	oxidase; PDBTitle: crystal structure of a probable nadh-dependent flavin oxidoreductase2 from staphylococcus aureus
81	c3p0tB_	Alignment	not modelled	21.9	7	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an hit-like protein from mycobacterium2 paratuberculosis
82	d2p5ma1	Alignment	not modelled	21.9	9	Fold: DCoH-like Superfamily: C-terminal domain of arginine repressor Family: C-terminal domain of arginine repressor
83	d2btoa1	Alignment	not modelled	21.8	12	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
84	c2kloA_	Alignment	not modelled	21.0	8	PDB header: cell cycle Chain: A: PDB Molecule: dna replication factor cdt1; PDBTitle: structure of the cdt1 c-terminal domain
85	c3qkbB_	Alignment	not modelled	21.0	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein with unknown function which belongs to2 pfam duf74 family (pepe_0654) from pediococcus pentosaceus atcc 257453 at 2.73 a resolution
86	c2zztA_	Alignment	not modelled	20.3	17	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the cytosolic domain of the cation2 diffusion facilitator family protein
87	c3cagF_	Alignment	not modelled	19.8	9	PDB header: dna binding protein Chain: F: PDB Molecule: arginine repressor; PDBTitle: crystal structure of the oligomerization domain hexamer of the2 arginine repressor protein from mycobacterium tuberculosis in complex3 with 9 arginines.
88	d1cm3a_	Alignment	not modelled	19.7	14	Fold: HPr-like Superfamily: HPr-like Family: HPr-like
89	c2btoA_	Alignment	not modelled	19.5	12	PDB header: cytoskeletal protein Chain: A: PDB Molecule: tubulin btuba; PDBTitle: structure of btuba from prosthecobacter dejongei
90	c3nx3A_	Alignment	not modelled	19.5	21	PDB header: transferase Chain: A: PDB Molecule: acetylornithine aminotransferase; PDBTitle: crystal structure of acetylornithine aminotransferase (argd) from2 campylobacter jejuni
91	c2hl2A_	Alignment	not modelled	19.4	11	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase; PDBTitle: crystal structure of the editing domain of threonyl-trna2 synthetase from pyrococcus abyssi in complex with an3 analog of seryladenylate
92	c3nuiA_	Alignment	not modelled	19.4	17	PDB header: transferase Chain: A: PDB Molecule: pyruvate transaminase; PDBTitle: crystal structure of omega-transferase from vibrio fluvialis js17
93	d3bypa1	Alignment	not modelled	19.3	19	Fold: Alpha-lytic protease prodomain-like Superfamily: Cation efflux protein cytoplasmic domain-like Family: Cation efflux protein cytoplasmic domain-like
94	c3anoA_	Alignment	not modelled	18.7	11	PDB header: transferase Chain: A: PDB Molecule: ap-4-a phosphorylase; PDBTitle: crystal structure of a novel diadenosine 5',5'''-p1,p4-tetraphosphate2 phosphorylase from mycobacterium tuberculosis h37rv
95	c2uzhB_	Alignment	not modelled	18.4	12	PDB header: lyase Chain: B: PDB Molecule: 2c-methyl-d-erythritol 2,4-cyclodiphosphate PDBTitle: mycobacterium smegmatis 2c-methyl-d-erythritol-2,4-2 cyclodiphosphate synthase (ispf)
96	d1xm5a_	Alignment	not modelled	18.3	10	Fold: Zincin-like Superfamily: Metalloproteases ("zincins"), catalytic domain Family: Predicted metal-dependent hydrolase
97	d1vr6a1	Alignment	not modelled	18.2	7	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I DAHP synthetase
98	c3l0mA_	Alignment	not modelled	18.1	15	PDB header: protein binding Chain: A: PDB Molecule: drara; PDBTitle: crystal structure of rab1-activation domain and p4m domain of2 sidm/drara from legionella
99	c3ksvA_	Alignment	not modelled	18.0	9	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: hypothetical protein from leishmania major