











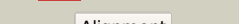

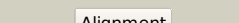

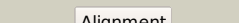



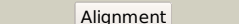



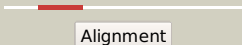

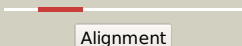


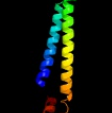
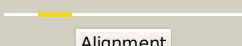
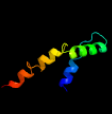
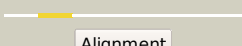

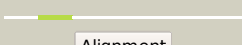

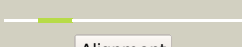



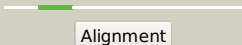
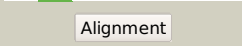
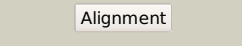

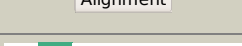
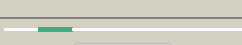
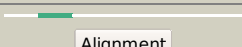



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yk0A_	 Alignment		100.0	17	PDB header: membrane protein Chain: A: PDB Molecule: erythrocyte membrane protein 1; PDBTitle: structure of the n-terminal nts-dbl1-alpha and cidr-gamma double2 domain of the pfemp1 protein from plasmodium falciparum varo3 strain.
2	c2xu0A_	 Alignment		100.0	21	PDB header: membrane protein Chain: A: PDB Molecule: erythrocyte membrane protein 1; PDBTitle: crystal structure of the nts-dbl1(alpha-1) domain of the plasmodium2 falciparum membrane protein 1 (pfemp1) from the varo strain.
3	c4gf2A_	 Alignment		100.0	21	PDB header: cell adhesion, cell invasion Chain: A: PDB Molecule: erythrocyte binding antigen 140; PDBTitle: crystal structure of plasmodium falciparum erythrocyte binding antigen2 140 (pfeba-140/baeb1)
4	c1zroB_	 Alignment		100.0	24	PDB header: cell invasion Chain: B: PDB Molecule: erythrocyte binding antigen region ii; PDBTitle: crystal structure of eba-175 region ii (rii) crystallized2 in the presence of (alpha)2,3-sialyllactose
5	dlzroa2	 Alignment		100.0	30	Fold: Duffy binding domain-like Superfamily: Duffy binding domain-like Family: Duffy binding domain
6	c3rrcA_	 Alignment		100.0	24	PDB header: cell invasion Chain: A: PDB Molecule: duffy receptor; PDBTitle: crystal structure of region ii from plasmodium vivax duffy binding2 protein
7	c3vuua_	 Alignment		100.0	23	PDB header: cell adhesion Chain: A: PDB Molecule: erythrocyte membrane protein, putative; PDBTitle: crystal structure of the merozoite surface protein mspdbl2 from p.2 falciparum
8	c3vuvA_	 Alignment		100.0	21	PDB header: cell adhesion Chain: A: PDB Molecule: erythrocyte membrane protein, putative; PDBTitle: crystal structure of the merozoite surface protein mspdbl2 from p.2 falciparum bound to zinc
9	dlzroa1	 Alignment		100.0	22	Fold: Duffy binding domain-like Superfamily: Duffy binding domain-like Family: Duffy binding domain
10	c2y8dA_	 Alignment		100.0	28	PDB header: membrane protein Chain: A: PDB Molecule: erythrocyte membrane protein 1; PDBTitle: structure of dbl6 epsilon domain from var2csa strain fcr3
11	c3cpzA_	 Alignment		100.0	26	PDB header: membrane protein Chain: A: PDB Molecule: erythrocyte membrane protein 1; PDBTitle: crystal structure of var2csa dbl3x domain in the presence of2 dodecasaccharide of csa

12	d2c6ja1	 Alignment		100.0	23	Fold: Duffy binding domain-like Superfamily: Duffy binding domain-like Family: Duffy binding domain
13	c2c6jA	 Alignment		100.0	23	PDB header: receptor Chain: A: PDB Molecule: duffy receptor, alpha form; PDBTitle: structure of p. knowlesi dbl domain capable of binding2 human duffy antigen
14	c2wauA	 Alignment		100.0	23	PDB header: membrane protein Chain: A: PDB Molecule: erythrocyte membrane protein 1 (pfemp1); PDBTitle: structure of dbl6 epsilon domain from var2csa
15	c3c64A	 Alignment		97.2	25	PDB header: cd36-binding protein,cell adhesion Chain: A: PDB Molecule: pfemp1 variant 2 of strain mc; PDBTitle: the mc179 portion of the cysteine-rich interdomain region2 (cldr) of a plasmodium falciparum erythrocyte membrane3 protein-1 (pfemp1)
16	c3j0xL	 Alignment		72.0	24	PDB header: ribosome Chain: J: PDB Molecule: 30s ribosomal protein s7; PDBTitle: structural characterization of mrna-trna translocation intermediates2 (30s ribosome of class 4b of the six classes)
17	c3j6vG	 Alignment		71.8	27	PDB header: ribosome Chain: G: PDB Molecule: 28s ribosomal protein s7, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome
18	d2qalg1	 Alignment		67.0	23	Fold: Ribosomal protein S7 Superfamily: Ribosomal protein S7 Family: Ribosomal protein S7
19	c3gtyS	 Alignment		66.4	22	PDB header: chaperone/ribosomal protein Chain: S: PDB Molecule: 30s ribosomal protein s7; PDBTitle: promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone
20	c2kp7A	 Alignment		63.0	38	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
21	d1l8qa1	 Alignment	not modelled	57.4	29	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV
22	c3bbnG	 Alignment	not modelled	53.4	24	PDB header: ribosome Chain: G: PDB Molecule: ribosomal protein s7; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome.
23	c2fyoA	 Alignment	not modelled	51.7	22	PDB header: transferase Chain: A: PDB Molecule: carnitine o-palmitoyltransferase ii, PDBTitle: crystal structure of rat carnitine palmitoyltransferase 22 in space group p43212
24	c2gboB	 Alignment	not modelled	45.0	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: upf0358 protein ef2458; PDBTitle: protein of unknown function ef2458 from enterococcus faecalis
25	d2gboa1	 Alignment	not modelled	45.0	19	Fold: Open three-helical up-and-down bundle Superfamily: EF2458-like Family: EF2458-like
26	d1qaza	 Alignment	not modelled	42.0	18	Fold: alpha/alpha toroid Superfamily: Chondroitin AC/alginate lyase Family: Alginate lyase A1-III
27	d1p3qq	 Alignment	not modelled	41.3	33	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain
28	d2nv0a1	 Alignment	not modelled	41.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
						Fold: Four-helical up-and-down bundle

29	d2ccya_	Alignment	not modelled	40.6	8	Superfamily: Cytochromes Family: Cytochrome c'-like
30	c2khdA_	Alignment	not modelled	40.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein vc_a0919; PDBTitle: solution nmr structure of vc_a0919 from vibrio cholerae.2 northeast structural genomics consortium target vcr52
31	c2h4tB_	Alignment	not modelled	39.3	24	PDB header: transferase Chain: B: PDB Molecule: carnitine o-palmitoyltransferase ii, PDBTitle: crystal structure of rat carnitine palmitoyltransferase ii
32	c1j0yD_	Alignment	not modelled	35.7	13	PDB header: hydrolase Chain: D: PDB Molecule: beta-amylase; PDBTitle: beta-amylase from bacillus cereus var. mycoides in complex2 with glucose
33	d1j1va_	Alignment	not modelled	35.4	24	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: Chromosomal replication initiation factor DnaA C-terminal domain IV
34	c3pvpA_	Alignment	not modelled	32.2	16	PDB header: dna binding protein/dna Chain: A: PDB Molecule: chromosomal replication initiator protein dnaa; PDBTitle: structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
35	c3pt3A_	Alignment	not modelled	31.9	16	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase ubr5; PDBTitle: crystal structure of the c-terminal lobe of the human ubr5 hect domain
36	c1m6bB_	Alignment	not modelled	31.8	8	PDB header: signaling protein, transferase Chain: B: PDB Molecule: receptor protein-tyrosine kinase erbb-3; PDBTitle: structure of the her3 (erbb3) extracellular domain
37	d1j09a2_	Alignment	not modelled	30.4	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
38	d1nza_	Alignment	not modelled	30.3	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
39	c3fayA_	Alignment	not modelled	30.1	10	PDB header: membrane protein Chain: A: PDB Molecule: ras gtpase-activating-like protein iqgap1; PDBTitle: crystal structure of the gap-related domain of iqgap1
40	c1m1zB_	Alignment	not modelled	29.6	18	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
41	c3s8vX_	Alignment	not modelled	29.5	22	PDB header: signaling protein Chain: X: PDB Molecule: dickkopf-related protein 1; PDBTitle: crystal structure of lrp6-dkk1 complex
42	c1m6bA_	Alignment	not modelled	29.3	8	PDB header: signaling protein, transferase Chain: A: PDB Molecule: receptor protein-tyrosine kinase erbb-3; PDBTitle: structure of the her3 (erbb3) extracellular domain
43	c3p11A_	Alignment	not modelled	28.9	8	PDB header: immune system Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-3; PDBTitle: anti-egfr/her3 fab d11 in complex with domains i-iii of the her32 extracellular region
44	c3l0aA_	Alignment	not modelled	28.4	10	PDB header: hydrolase Chain: A: PDB Molecule: putative exonuclease; PDBTitle: crystal structure of putative exonuclease (rer070207002219) from2 eubacterium rectale at 2.19 a resolution
45	d1u8xx2_	Alignment	not modelled	28.3	5	Fold: LDH C-terminal domain-like Superfamily: LDH C-terminal domain-like Family: AglA-like glucosidase
46	c2xfIB_	Alignment	not modelled	27.8	16	PDB header: hydrolase Chain: B: PDB Molecule: dyne7; PDBTitle: induced-fit and allosteric effects upon polyene binding2 revealed by crystal structures of the dynemicin3 thioesterase
47	c3be1A_	Alignment	not modelled	27.5	25	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: dual specific bh1 fab in complex with the extracellular domain of2 her2/erbb-2
48	c1q15A_	Alignment	not modelled	27.1	14	PDB header: biosynthetic protein Chain: A: PDB Molecule: cara; PDBTitle: carbapenam synthetase
49	c3vocA_	Alignment	not modelled	26.9	26	PDB header: hydrolase Chain: A: PDB Molecule: beta/alpha-amylase; PDBTitle: crystal structure of the catalytic domain of beta-amylase from2 paenibacillus polymyxa
50	d1ndba2_	Alignment	not modelled	26.9	13	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
51	d1jgta2_	Alignment	not modelled	26.5	18	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
52	c3sqiA_	Alignment	not modelled	25.7	10	PDB header: dna binding protein/dna Chain: A: PDB Molecule: kila0e03807p; PDBTitle: dna binding domain of ndc10
53	c3t79A_	Alignment	not modelled	25.7	10	PDB header: dna binding protein/dna Chain: A: PDB Molecule: kila0e03807p; PDBTitle: ndc10: a platform for inner kinetochore assembly in budding yeast
54	c3ndhA_	Alignment	not modelled	25.2	24	PDB header: hydrolase/dna Chain: A: PDB Molecule: restriction endonuclease thai; PDBTitle: restriction endonuclease in complex with substrate dna
55	d1mylB_	Alignment	not modelled	25.0	50	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors

56	c3q4nA	Alignment	not modelled	24.8	23	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein mj0754; PDBTitle: crystal structure of hypothetical protein mj0754 from methanococcus2 jannaschii dsm 2661
57	c1fokA	Alignment	not modelled	24.8	17	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein (foki restriction endonucleas); PDBTitle: structure of restriction endonuclease foki bound to dna
58	d1s05a	Alignment	not modelled	24.3	11	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
59	c3tqoA	Alignment	not modelled	24.3	9	PDB header: ligase Chain: A: PDB Molecule: cysteinyI-trna synthetase; PDBTitle: structure of the cysteinyI-trna synthetase (cyss) from coxiella2 burnetii.
60	d2o4ta1	Alignment	not modelled	24.3	26	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
61	d1bbha	Alignment	not modelled	24.2	18	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
62	d1p3qr	Alignment	not modelled	24.1	27	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain
63	c3i2tA	Alignment	not modelled	24.0	17	PDB header: transferase Chain: A: PDB Molecule: epidermal growth factor receptor, isoform a; PDBTitle: crystal structure of the unliganded drosophila epidermal growth factor2 receptor ectodomain
64	d1gqaa	Alignment	not modelled	23.6	3	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
65	c3focB	Alignment	not modelled	23.5	15	PDB header: ligase Chain: B: PDB Molecule: tryptophanyl-trna synthetase; PDBTitle: tryptophanyl-trna synthetase from giardia lamblia
66	c2ahxB	Alignment	not modelled	23.4	25	PDB header: cell cycle,signaling protein Chain: B: PDB Molecule: receptor tyrosine-protein kinase erbb-4; PDBTitle: crystal structure of erbb4/her4 extracellular domain
67	d1myla	Alignment	not modelled	23.3	50	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
68	d1b28a	Alignment	not modelled	22.6	50	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
69	d1bdta	Alignment	not modelled	22.2	50	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: Arc/Mnt-like phage repressors
70	c1nqlA	Alignment	not modelled	21.9	17	PDB header: hormone/growth factor receptor Chain: A: PDB Molecule: epidermal growth factor receptor; PDBTitle: structure of the extracellular domain of human epidermal growth factor2 (egf) receptor in an inactive (low ph) complex with egf.
71	c2k3iA	Alignment	not modelled	21.4	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yiis; PDBTitle: solution nmr structure of protein yiis from shigella flexneri.2 northeast structural genomics consortium target sfr90
72	c2nx7A	Alignment	not modelled	21.1	27	PDB header: structural protein Chain: A: PDB Molecule: nematocyst outer wall antigen; PDBTitle: structure of nowa cysteine rich domain 8
73	c1vs5G	Alignment	not modelled	20.7	22	PDB header: ribosome Chain: G: PDB Molecule: 30s ribosomal protein s7; PDBTitle: crystal structure of the bacterial ribosome from2 escherichia coli in complex with the antibiotic kasugamycin3 at 3.5a resolution. this file contains the 30s subunit of4 one 70s ribosome. the entire crystal structure contains5 two 70s ribosomes and is described in remark 400.
74	c1n0zA	Alignment	not modelled	20.5	28	PDB header: transcription Chain: A: PDB Molecule: znf265; PDBTitle: solution structure of the first zinc-finger domain from2 znf265
75	c3gocB	Alignment	not modelled	19.7	12	PDB header: hydrolase Chain: B: PDB Molecule: endonuclease v; PDBTitle: crystal structure of the endonuclease v (sav1684) from streptomyces2 avermitilis. northeast structural genomics consortium target svr196
76	d1husa	Alignment	not modelled	19.7	23	Fold: Ribosomal protein S7 Superfamily: Ribosomal protein S7 Family: Ribosomal protein S7
77	c3qwqA	Alignment	not modelled	19.5	17	PDB header: protein binding/signaling protein Chain: A: PDB Molecule: epidermal growth factor receptor; PDBTitle: crystal structure of the extracellular domain of the epidermal growth2 factor receptor in complex with an adnectin
78	d1q15a2	Alignment	not modelled	19.2	20	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
79	c4o9tH	Alignment	not modelled	19.1	33	PDB header: membrane protein Chain: H: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer
80	d1v53a1	Alignment	not modelled	18.9	8	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
						PDB header: oxidoreductase

81	c1x0lB_	Alignment	not modelled	18.5	33	Chain: B: PDB Molecule: homoisocitrate dehydrogenase; PDBTitle: crystal structure of tetrameric homoisocitrate dehydrogenase from an2 extreme thermophile, thermus thermophilus
82	c2xgja_	Alignment	not modelled	18.5	22	PDB header: hydrolase/rna Chain: A: PDB Molecule: atp-dependent rna helicase dob1; PDBTitle: structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance
83	c3u1hA_	Alignment	not modelled	18.5	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-isopropylmalate dehydrogenase; PDBTitle: crystal structure of ipmdh from the last common ancestor of bacillus
84	d1jmsa1	Alignment	not modelled	18.5	17	Fold: SAM domain-like Superfamily: DNA polymerase beta, N-terminal domain-like Family: DNA polymerase beta, N-terminal domain-like
85	d1nm8a2	Alignment	not modelled	18.1	14	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
86	d1mqva_	Alignment	not modelled	18.0	9	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
87	d1juqa_	Alignment	not modelled	17.9	8	Fold: alpha-alpha superhelix Superfamily: ENTH/VHS domain Family: VHS domain
88	d2j8wa1	Alignment	not modelled	17.8	11	Fold: Four-helical up-and-down bundle Superfamily: Cytochromes Family: Cytochrome c'-like
89	c3ga2A_	Alignment	not modelled	17.8	24	PDB header: hydrolase Chain: A: PDB Molecule: endonuclease v; PDBTitle: crystal structure of the endonuclease_v (bsu36170) from2 bacillus subtilis, northeast structural genomics3 consortium target sr624
90	c2w36B_	Alignment	not modelled	17.7	15	PDB header: hydrolase Chain: B: PDB Molecule: endonuclease v; PDBTitle: structures of endonuclease v with dna reveal initiation of2 deaminated adenine repair
91	d2zjrh1	Alignment	not modelled	17.3	25	Fold: Ribosomal protein L14 Superfamily: Ribosomal protein L14 Family: Ribosomal protein L14
92	c1q6xA_	Alignment	not modelled	17.3	35	PDB header: transferase Chain: A: PDB Molecule: choline o-acetyltransferase; PDBTitle: crystal structure of rat choline acetyltransferase
93	d1tlua2	Alignment	not modelled	17.2	38	Fold: CoA-dependent acyltransferases Superfamily: CoA-dependent acyltransferases Family: Choline/Carnitine O-acyltransferase
94	c2a91A_	Alignment	not modelled	16.9	25	PDB header: signaling protein,transferase,membrane p Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: crystal structure of erbb2 domains 1-3
95	c2h7vD_	Alignment	not modelled	16.7	18	PDB header: signaling protein Chain: D: PDB Molecule: protein kinase ypka; PDBTitle: co-crystal structure of ypka-rac1
96	d1w0da_	Alignment	not modelled	16.6	33	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Dimeric isocitrate & isopropylmalate dehydrogenases
97	c2voiB_	Alignment	not modelled	16.5	33	PDB header: apoptosis Chain: B: PDB Molecule: bh3-interacting domain death agonist p13; PDBTitle: structure of mouse a1 bound to the bid bh3-domain
98	d1neja_	Alignment	not modelled	16.2	11	Fold: Hypothetical protein YoaG Superfamily: Hypothetical protein YoaG Family: Hypothetical protein YoaG
99	c2g77A_	Alignment	not modelled	16.2	11	PDB header: hydrolase activator/protein transport Chain: A: PDB Molecule: gtpase-activating protein gyp1; PDBTitle: crystal structure of gyp1 tbc domain in complex with rab332 gtpase bound to gdp and alf3