









Phyre2

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Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5m87A_	Alignment		100.0	33	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mntH; PDBTitle: crystal structure of eremococcus coleocola manganese transporter
2	c5kteA_	Alignment		100.0	48	PDB header: transport protein/immune system Chain: A: PDB Molecule: divalent metal cation transporter mntH; PDBTitle: crystal structure of deinococcus radiodurans mntH, an nramp-family2 transition metal transporter
3	c4wgvC_	Alignment		100.0	33	PDB header: transport protein Chain: C: PDB Molecule: divalent metal cation transporter mntH; PDBTitle: crystal structure of staphylococcus capitis divalent metal ion2 transporter (dmt) in complex with nanobody
4	c4wgvA_	Alignment		100.0	33	PDB header: transport protein Chain: A: PDB Molecule: divalent metal cation transporter mntH; PDBTitle: staphylococcus capitis divalent metal ion transporter (dmt) in complex2 with manganese
5	c5nvaA_	Alignment		99.8	11	PDB header: membrane protein Chain: A: PDB Molecule: putative sodium:solute symporter; PDBTitle: substrate-bound outward-open state of a na+-coupled sialic acid2 symporter reveals a novel na+-site
6	c2xq2A_	Alignment		99.7	12	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsplt
7	c6csfC_	Alignment		99.6	12	PDB header: membrane protein Chain: C: PDB Molecule: sodium/alanine symporter agcs; PDBTitle: crystal structure of sodium/alanine symporter agcs with d-alanine2 bound
8	c3dh4A_	Alignment		99.6	13	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
9	c2jlnA_	Alignment		99.4	11	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
10	c5oqtA_	Alignment		99.1	11	PDB header: transport protein Chain: A: PDB Molecule: amino acid transporter; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
11	c6f2wA_	Alignment		98.9	11	PDB header: transport protein Chain: A: PDB Molecule: putative amino acid/polyamine transport protein; PDBTitle: bacterial asc transporter crystal structure in open to in conformation

12	c5i6xA_	Alignment		98.7	14	PDB header: membrane protein Chain: A: PDB Molecule: sodium-dependent serotonin transporter; PDBTitle: x-ray structure of the ts3 human serotonin transporter complexed with2 paroxetine at the central site
13	c6irtB_	Alignment		98.7	11	PDB header: membrane protein Chain: B: PDB Molecule: large neutral amino acids transporter small subunit 1; PDBTitle: human lat1-4f2hc complex bound with bch
14	c4us3A_	Alignment		98.6	12	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: crystal structure of the bacterial nss member mhst in an2 occluded inward-facing state
15	c6jmqA_	Alignment		98.6	9	PDB header: membrane protein/immune system Chain: A: PDB Molecule: large neutral amino acids transporter small subunit 1; PDBTitle: lat1-cd98hc complex bound to mem-108 fab
16	c3giaA_	Alignment		98.5	16	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
17	c6c08F_	Alignment		98.3	9	PDB header: membrane protein Chain: F: PDB Molecule: sodium-coupled neutral amino acid transporter 9; PDBTitle: zebrafish slc38a9 with arginine bound in the cytosol open state
18	c4djiA_	Alignment		98.1	11	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
19	d2a65a1	Alignment		98.0	15	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
20	c3lrcC_	Alignment		97.9	16	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
21	c4m48A_	Alignment	not modelled	97.8	14	PDB header: transport protein Chain: A: PDB Molecule: transporter; PDBTitle: x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
22	c6c08C_	Alignment	not modelled	97.4	12	PDB header: membrane protein Chain: C: PDB Molecule: sodium-coupled neutral amino acid transporter 9; PDBTitle: zebrafish slc38a9 with arginine bound in the cytosol open state
23	c2w8aC_	Alignment	not modelled	96.5	11	PDB header: membrane protein Chain: C: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
24	c4ainB_	Alignment	not modelled	96.1	11	PDB header: membrane protein Chain: B: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of betp with asymmetric protomers.
25	c3hfxA_	Alignment	not modelled	95.3	12	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
26	c6ajjA_	Alignment	not modelled	25.4	15	PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38
27	c2pqrD_	Alignment	not modelled	20.1	26	PDB header: apoptosis Chain: D: PDB Molecule: wd repeat protein ykr036c; PDBTitle: crystal structure of yeast fis1 complexed with a fragment of yeast2 caf4
						PDB header: protein transport

28	c5wfbB_	Alignment	not modelled	15.1	24	Chain: B: PDB Molecule: ap-4 complex accessory subunit tepsin; PDBTitle: tepsin tenth domain 1-136.
29	c2ht2B_	Alignment	not modelled	11.6	13	PDB header: membrane protein Chain: B: PDB Molecule: h(+)/cl(-) exchange transporter clca; PDBTitle: structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
30	c2pqrC_	Alignment	not modelled	10.3	37	PDB header: apoptosis Chain: C: PDB Molecule: wd repeat protein ykr036c; PDBTitle: crystal structure of yeast fis1 complexed with a fragment of yeast2 caf4
31	c6f0kF_	Alignment	not modelled	10.1	8	PDB header: membrane protein Chain: F: PDB Molecule: actf; PDBTitle: alternative complex iii
32	c1n93X_	Alignment	not modelled	10.0	32	PDB header: viral protein Chain: X: PDB Molecule: p40 nucleoprotein; PDBTitle: crystal structure of the borna disease virus nucleoprotein
33	d1n93x_	Alignment	not modelled	10.0	32	Fold: P40 nucleoprotein Superfamily: P40 nucleoprotein Family: P40 nucleoprotein
34	c3rjpA_	Alignment	not modelled	9.9	33	PDB header: transcription regulator Chain: A: PDB Molecule: curlin genes transcriptional regulator; PDBTitle: structure of a curlin genes transcriptional regulator protein from2 proteus mirabilis hi4320.
35	c3bqsB_	Alignment	not modelled	9.5	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from2 listeria monocytogenes, trigonal form
36	c2ketA_	Alignment	not modelled	8.9	25	PDB header: antibiotic Chain: A: PDB Molecule: cathelicidin-6; PDBTitle: solution structure of bmap-27
37	c2mz8A_	Alignment	not modelled	8.7	22	PDB header: transcription regulator Chain: A: PDB Molecule: sigma factor-binding protein crl; PDBTitle: solution nmr structure of salmonella typhimurium transcriptional2 regulator protein crl
38	c4lz9A_	Alignment	not modelled	8.3	15	PDB header: transport protein Chain: A: PDB Molecule: bh2163 protein; PDBTitle: structure of mate multidrug transporter dinf-bh in complex with r6g
39	d1adta1	Alignment	not modelled	8.1	22	Fold: Domain of early E2A DNA-binding protein, ADDBP Superfamily: Domain of early E2A DNA-binding protein, ADDBP Family: Domain of early E2A DNA-binding protein, ADDBP
40	c2n12A_	Alignment	not modelled	8.0	19	PDB header: motor protein,protein transport Chain: A: PDB Molecule: unconventional myosin-vi; PDBTitle: solution structure of human myosin vi isoform3 (1050-1131)
41	d2hkua2	Alignment	not modelled	7.9	41	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
42	c5n1L_	Alignment	not modelled	7.7	26	PDB header: structural protein Chain: L: PDB Molecule: invasin ipaa; PDBTitle: shigella ipaa-vbs3/tbs in complex with the talin vbs1 domain 488-512
43	c5n1G_	Alignment	not modelled	7.7	26	PDB header: structural protein Chain: G: PDB Molecule: invasin ipaa; PDBTitle: shigella ipaa-vbs3/tbs in complex with the talin vbs1 domain 488-512
44	c5a1sB_	Alignment	not modelled	7.7	11	PDB header: transport protein Chain: B: PDB Molecule: citrate-sodium symporter; PDBTitle: crystal structure of the sodium-dependent citrate symporter secits2 form salmonella enterica.
45	c5n1I_	Alignment	not modelled	7.7	26	PDB header: structural protein Chain: I: PDB Molecule: invasin ipaa; PDBTitle: shigella ipaa-vbs3/tbs in complex with the talin vbs1 domain 488-512
46	c5n1H_	Alignment	not modelled	7.7	26	PDB header: structural protein Chain: H: PDB Molecule: invasin ipaa; PDBTitle: shigella ipaa-vbs3/tbs in complex with the talin vbs1 domain 488-512
47	c5fimA_	Alignment	not modelled	7.7	13	PDB header: unknown function Chain: A: PDB Molecule: ygau; PDBTitle: the structure of kbp.k from e. coli
48	c4ev6E_	Alignment	not modelled	7.7	5	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
49	c1n6jG_	Alignment	not modelled	7.6	31	PDB header: transcription/dna Chain: G: PDB Molecule: calcineurin-binding protein cabin 1; PDBTitle: structural basis of sequence-specific recruitment of histone2 deacetylases by myocyte enhancer factor-2
50	c3rf3D_	Alignment	not modelled	7.6	26	PDB header: protein binding/toxin Chain: D: PDB Molecule: invasin ipaa; PDBTitle: shigella ipaa-vbs3 in complex with human vinculin
51	c5n1K_	Alignment	not modelled	7.5	28	PDB header: structural protein Chain: K: PDB Molecule: invasin ipaa; PDBTitle: shigella ipaa-vbs3/tbs in complex with the talin vbs1 domain 488-512
52	c6nbxG_	Alignment	not modelled	7.3	15	PDB header: oxidoreductase Chain: G: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: t.elongatus ndh (data-set 2)
53	c3gd5D_	Alignment	not modelled	7.2	33	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from gloebacter2 violaceus
54	d2yvxa3	Alignment	not modelled	7.1	20	Fold: MgtE membrane domain-like Superfamily: MgtE membrane domain-like Family: MgtE membrane domain-like

55	c5n9yB_	Alignment	not modelled	7.0	10	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
56	d1otsa_	Alignment	not modelled	6.7	14	Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel
57	c3kp9A_	Alignment	not modelled	6.7	11	PDB header: blood coagulation,oxidoreductase Chain: A: PDB Molecule: vkorc1/thioredoxin domain protein; PDBTitle: structure of a bacterial homolog of vitamin k epoxide reductase
58	c4f2gA_	Alignment	not modelled	6.7	28	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase 1; PDBTitle: the crystal structure of ornithine carbamoyltransferase from2 burkholderia thailandensis e264
59	c6cfzG_	Alignment	not modelled	6.6	21	PDB header: nuclear protein Chain: G: PDB Molecule: hsk3; PDBTitle: structure of the dash/dam1 complex shows its role at the yeast2 kinetochore-microtubule interface
60	c2voyD_	Alignment	not modelled	6.5	10	PDB header: hydrolase Chain: D: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
61	c6humG_	Alignment	not modelled	6.5	15	PDB header: proton transport Chain: G: PDB Molecule: nadh dehydrogenase subunit 6; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
62	c2dcpA_	Alignment	not modelled	6.5	12	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein (raf09-17-b18); PDBTitle: fully automated nmr structure determination of the enth-vhs2 domain at3g16270 from arabidopsis thaliana
63	c3mk7F_	Alignment	not modelled	6.5	7	PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
64	d1qbjc_	Alignment	not modelled	6.4	20	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Z-DNA binding domain
65	c5w5cE_	Alignment	not modelled	6.2	25	PDB header: exocytosis Chain: E: PDB Molecule: complexin-1; PDBTitle: crystal structure of the primed snare-complexin-synaptotagmin-1 c2ab2 complex
66	d1dxha1	Alignment	not modelled	6.1	22	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
67	c6cxhC_	Alignment	not modelled	6.1	21	PDB header: oxidoreductase Chain: C: PDB Molecule: particulate methane monooxygenase, c subunit; PDBTitle: crystal structure of particulate methane monooxygenase from2 methylomicrobium alcaliphilum 20z
68	c4j43A_	Alignment	not modelled	6.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: pyld; PDBTitle: pyld holoenzyme
69	d1otha1	Alignment	not modelled	6.0	39	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
70	c4oh7B_	Alignment	not modelled	6.0	33	PDB header: transferase Chain: B: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from brucella2 melitensis
71	c3tpfF_	Alignment	not modelled	6.0	22	PDB header: transferase Chain: F: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of anabolic ornithine carbamoyltransferase from2 campylobacter jejuni subsp. jejuni nctc 11168
72	c2h8bA_	Alignment	not modelled	6.0	25	PDB header: hormone/growth factor Chain: A: PDB Molecule: insulin-like 3; PDBTitle: solution structure of insl3
73	d1js1x1	Alignment	not modelled	6.0	28	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
74	c2ef0A_	Alignment	not modelled	6.0	33	PDB header: transferase Chain: A: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from thermus2 thermophilus
75	c1fvoB_	Alignment	not modelled	5.9	39	PDB header: transferase Chain: B: PDB Molecule: ornithine transcarbamylase; PDBTitle: crystal structure of human ornithine transcarbamylase complexed with2 carbamoyl phosphate
76	c2k6uA_	Alignment	not modelled	5.8	25	PDB header: hormone Chain: A: PDB Molecule: insulin-like 3 a chain; PDBTitle: the solution structure of a conformationally restricted2 fully active derivative of the human relaxin-like factor3 (rlf)
77	c3jcuX_	Alignment	not modelled	5.8	25	PDB header: membrane protein Chain: X: PDB Molecule: photosystem ii reaction center x protein; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
78	c3jcux_	Alignment	not modelled	5.8	25	PDB header: membrane protein Chain: X: PDB Molecule: photosystem ii reaction center x protein; PDBTitle: cryo-em structure of spinach psii-lhcii supercomplex at 3.2 angstrom2 resolution
79	c6btmC_	Alignment	not modelled	5.8	13	PDB header: membrane protein Chain: C: PDB Molecule: alternative complex iii subunit c; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
80	c2rifA_	Alignment	not modelled	5.7	10	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 3;

80	c3qj1A_	Alignment	not modelled	5.7	10	PDBTitle: structural insights into dsrna binding and rna silencing suppression2 by ns3 protein of rice hoja blanca tenuivirus PDB header: metal transport
81	c5b57B_	Alignment	not modelled	5.7	16	Chain: B; PDB Molecule: putative hemin abc transport system, membrane protein; PDBTitle: inward-facing conformation of abc heme importer bhuuv from2 burkholderia cenocepacia
82	c2kncB_	Alignment	not modelled	5.7	20	PDB header: cell adhesion Chain: B; PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaiib-beta3 transmembrane-cytoplasmic2 heterocomplex
83	c1wwpA_	Alignment	not modelled	5.7	24	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein ttha0636; PDBTitle: crystal structure of ttk003001694 from thermus thermophilus2 hb8
84	c2k6tA_	Alignment	not modelled	5.7	25	PDB header: hormone Chain: A; PDB Molecule: insulin-like 3 a chain; PDBTitle: solution structure of the relaxin-like factor
85	d1m5sa2	Alignment	not modelled	5.7	40	Fold: Ferredoxin-like Superfamily: Formylmethanofuran:tetrahydromethanopterin formyltransferase Family: Formylmethanofuran:tetrahydromethanopterin formyltransferase
86	c5mdxX_	Alignment	not modelled	5.7	13	PDB header: photosynthesis Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
87	c5mdxx_	Alignment	not modelled	5.7	13	PDB header: photosynthesis Chain: X; PDB Molecule: photosystem ii reaction center protein x; PDBTitle: cryo-em structure of the psii supercomplex from arabidopsis thaliana
88	d1pg5a1	Alignment	not modelled	5.6	28	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
89	c2m86A_	Alignment	not modelled	5.6	33	PDB header: protein binding/signaling protein Chain: A; PDB Molecule: imco-pmi; PDBTitle: solution structure of hdm2 with engineered cyclotide
90	d1wtya_	Alignment	not modelled	5.6	20	Fold: Four-helical up-and-down bundle Superfamily: Nucleotidyltransferase substrate binding subunit/domain Family: Family 1 bi-partite nucleotidyltransferase subunit
91	d2bcgg3	Alignment	not modelled	5.6	32	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: GDI-like
92	c4heaJ_	Alignment	not modelled	5.6	12	PDB header: oxidoreductase Chain: J; PDB Molecule: nadh-quinone oxidoreductase subunit 10; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
93	c2p2gD_	Alignment	not modelled	5.6	28	PDB header: transferase Chain: D; PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
94	d1pvva1	Alignment	not modelled	5.5	28	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase
95	c3a0hJ_	Alignment	not modelled	5.5	15	PDB header: electron transport Chain: J; PDB Molecule: photosystem ii reaction center protein j; PDBTitle: crystal structure of i-substituted photosystem ii complex
96	d2axtj1	Alignment	not modelled	5.5	15	Fold: Single transmembrane helix Superfamily: Photosystem II reaction center protein J, Psbj Family: Psbj-like
97	d1gr0a2	Alignment	not modelled	5.4	24	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Dihydrodipicolinate reductase-like
98	d2grrb1	Alignment	not modelled	5.4	17	Fold: alpha-alpha superhelix Superfamily: Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain Family: Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain
99	d1duvg1	Alignment	not modelled	5.4	28	Fold: ATC-like Superfamily: Aspartate/ornithine carbamoyltransferase Family: Aspartate/ornithine carbamoyltransferase