
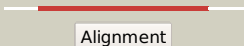

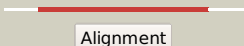







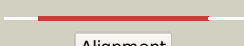

















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0522_(gabP)_613041_614345
Date	Fri Jul 26 01:50:07 BST 2019
Unique Job ID	67d5d176e74e47d6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4djiA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> probable glutamate/gamma-aminobutyrate antiporter; <b>PDBTitle:</b> structure of glutamate-gaba antiporter gadc
2	<a href="#">c6f2wA_</a>	 Alignment		100.0	17	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative amino acid/polyamine transport protein; <b>PDBTitle:</b> bacterial asc transporter crystal structure in open to in conformation
3	<a href="#">c5oqtA_</a>	 Alignment		100.0	18	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> amino acid transporter; <b>PDBTitle:</b> crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
4	<a href="#">c6irtB_</a>	 Alignment		100.0	15	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> large neutral amino acids transporter small subunit 1; <b>PDBTitle:</b> human lat1-4f2hc complex bound with bch
5	<a href="#">c3giaA_</a>	 Alignment		100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein mj0609; <b>PDBTitle:</b> crystal structure of apct transporter
6	<a href="#">c3lrcC_</a>	 Alignment		100.0	19	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> arginine/agmatine antiporter; <b>PDBTitle:</b> structure of e. coli adic (p1)
7	<a href="#">c6jmqA_</a>	 Alignment		100.0	17	<b>PDB header:</b> membrane protein/immune system <b>Chain:</b> A; <b>PDB Molecule:</b> large neutral amino acids transporter small subunit 1; <b>PDBTitle:</b> lat1-cd98hc complex bound to mem-108 fab
8	<a href="#">c6csfC_</a>	 Alignment		100.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> C; <b>PDB Molecule:</b> sodium/alanine symporter agcs; <b>PDBTitle:</b> crystal structure of sodium/alanine symporter agcs with d-alanine2 bound
9	<a href="#">c2jlnA_</a>	 Alignment		100.0	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
10	<a href="#">c6c08F_</a>	 Alignment		99.7	11	<b>PDB header:</b> membrane protein <b>Chain:</b> F; <b>PDB Molecule:</b> sodium-coupled neutral amino acid transporter 9; <b>PDBTitle:</b> zebrafish slc38a9 with arginine bound in the cytosol open state
11	<a href="#">c5nvaA_</a>	 Alignment		99.5	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> putative sodium:solute symporter; <b>PDBTitle:</b> substrate-bound outward-open state of a na+-coupled sialic acid2 symporter reveals a novel na+-site

12	<a href="#">c6c08C_</a>	Alignment		99.2	11	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> sodium-coupled neutral amino acid transporter 9; <b>PDBTitle:</b> zebrafish slc38a9 with arginine bound in the cytosol open state
13	<a href="#">c2xq2A_</a>	Alignment		99.2	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> structure of the k294a mutant of vsgl
14	<a href="#">c4wqwA_</a>	Alignment		99.0	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> divalent metal cation transporter mnth; <b>PDBTitle:</b> staphylococcus capitis divalent metal ion transporter (dmt) in complex2 with manganese
15	<a href="#">c4wgvC_</a>	Alignment		99.0	8	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> divalent metal cation transporter mnth; <b>PDBTitle:</b> crystal structure of staphylococcus capitis divalent metal ion2 transporter (dmt) in complex with nanobody
16	<a href="#">c3dh4A_</a>	Alignment		99.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
17	<a href="#">c5m87A_</a>	Alignment		98.2	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> divalent metal cation transporter mnth; <b>PDBTitle:</b> crystal structure of eremococcus coleocola manganese transporter
18	<a href="#">c5i6xA_</a>	Alignment		97.0	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium-dependent serotonin transporter; <b>PDBTitle:</b> x-ray structure of the ts3 human serotonin transporter complexed with2 paroxetine at the central site
19	<a href="#">d2a65a1</a>	Alignment		96.4	12	<b>Fold:</b> SNF-like <b>Superfamily:</b> SNF-like <b>Family:</b> SNF-like
20	<a href="#">c4ainB_</a>	Alignment		96.2	9	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of betp with asymmetric protomers.
21	<a href="#">c4m48A_</a>	Alignment	not modelled	96.2	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> transporter; <b>PDBTitle:</b> x-ray structure of dopamine transporter elucidates antidepressant2 mechanism
22	<a href="#">c2w8aC_</a>	Alignment	not modelled	93.6	9	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
23	<a href="#">c4us3A_</a>	Alignment	not modelled	93.6	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> transporter; <b>PDBTitle:</b> crystal structure of the bacterial nss member mhst in an2 occluded inward-facing state
24	<a href="#">c5kteA_</a>	Alignment	not modelled	89.6	11	<b>PDB header:</b> transport protein/immune system <b>Chain:</b> A: <b>PDB Molecule:</b> divalent metal cation transporter mnth; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans mnth, an nramp-family2 transition metal transporter
25	<a href="#">c3hfxA_</a>	Alignment	not modelled	85.5	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-carnitine/gamma-butyrobetaine antiporter; <b>PDBTitle:</b> crystal structure of carnitine transporter
26	<a href="#">c6adqP_</a>	Alignment	not modelled	36.5	14	<b>PDB header:</b> electron transport <b>Chain:</b> P: <b>PDB Molecule:</b> prokaryotic respiratory supercomplex associate factor 1 <b>PDBTitle:</b> respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
27	<a href="#">c6nbxG_</a>	Alignment	not modelled	34.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> t.elongatus ndh (data-set 2)
28	<a href="#">c3rkoF_</a>	Alignment	not modelled	22.3	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j; <b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution

29	<a href="#">d1fftb2</a>	Alignment	not modelled	19.7	8	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
30	<a href="#">c3b8eC</a>	Alignment	not modelled	18.1	11	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> sodium/potassium-transporting atpase subunit <b>PDBTitle:</b> crystal structure of the sodium-potassium pump
31	<a href="#">c5khnB</a>	Alignment	not modelled	15.4	12	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> rnd transporter; <b>PDBTitle:</b> crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn
32	<a href="#">c2m67A</a>	Alignment	not modelled	13.3	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> merf; <b>PDBTitle:</b> full-length mercury transporter protein merf in lipid bilayer2 membranes
33	<a href="#">c5do7B</a>	Alignment	not modelled	12.2	9	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp-binding cassette sub-family g member 8; <b>PDBTitle:</b> crystal structure of the human sterol transporter abcg5/abcg8
34	<a href="#">c5zlgA</a>	Alignment	not modelled	12.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome b reductase 1; <b>PDBTitle:</b> human duodenal cytochrome b (dcytb) in zinc ion and ascorbate bound2 form
35	<a href="#">c1m57H</a>	Alignment	not modelled	11.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant))
36	<a href="#">c6c14A</a>	Alignment	not modelled	11.2	10	<b>PDB header:</b> membrane protein, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> protocadherin-15; <b>PDBTitle:</b> cryoem structure of mouse pcdh15-1ec-lhfp15 complex
37	<a href="#">c4j72A</a>	Alignment	not modelled	11.1	5	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phospho-n-acetylmuramoyl-pentapeptide-transferase; <b>PDBTitle:</b> crystal structure of polyprenyl-phosphate n-acetyl hexosamine 1-2 phosphate transferase
38	<a href="#">c2na6B</a>	Alignment	not modelled	11.0	8	<b>PDB header:</b> apoptosis <b>Chain:</b> B: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
39	<a href="#">c2na6C</a>	Alignment	not modelled	11.0	8	<b>PDB header:</b> apoptosis <b>Chain:</b> C: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
40	<a href="#">c2na6A</a>	Alignment	not modelled	11.0	8	<b>PDB header:</b> apoptosis <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 6; <b>PDBTitle:</b> transmembrane domain of mouse fas/cd95 death receptor
41	<a href="#">c2lowA</a>	Alignment	not modelled	10.6	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> apelin receptor; <b>PDBTitle:</b> solution structure of ar55 in 50% hfip
42	<a href="#">d1eysh2</a>	Alignment	not modelled	10.2	10	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Photosystem II reaction centre subunit H, transmembrane region <b>Family:</b> Photosystem II reaction centre subunit H, transmembrane region
43	<a href="#">c4x5mB</a>	Alignment	not modelled	10.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of semisweet in the inward-open conformation
44	<a href="#">c6gcs6</a>	Alignment	not modelled	9.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> 6: <b>PDB Molecule:</b> nd6 subunit (nu6m); <b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica
45	<a href="#">c3j1zP</a>	Alignment	not modelled	9.8	8	<b>PDB header:</b> metal transport <b>Chain:</b> P: <b>PDB Molecule:</b> cation efflux family protein; <b>PDBTitle:</b> inward-facing conformation of the zinc transporter yiiip revealed by2 cryo-electron microscopy
46	<a href="#">c2k1aA</a>	Alignment	not modelled	9.7	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iib; <b>PDBTitle:</b> bicelle-embedded integrin alpha(iib) transmembrane segment
47	<a href="#">c6hwhL</a>	Alignment	not modelled	9.6	14	<b>PDB header:</b> electron transport <b>Chain:</b> L: <b>PDB Molecule:</b> cytochrome c oxidase subunit 2; <b>PDBTitle:</b> structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
48	<a href="#">c2bbjB</a>	Alignment	not modelled	9.4	10	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein; <b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
49	<a href="#">d3ehbb2</a>	Alignment	not modelled	9.3	17	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
50	<a href="#">c1qleB</a>	Alignment	not modelled	9.1	17	<b>PDB header:</b> oxidoreductase/immune system <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide ii; <b>PDBTitle:</b> cryo-structure of the paracoccus denitrificans four-subunit cytochrome2 c oxidase in the completely oxidized state complexed with an antibody3 fv fragment
51	<a href="#">c1ar1B</a>	Alignment	not modelled	9.1	17	<b>PDB header:</b> complex (oxidoreductase/antibody) <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase; <b>PDBTitle:</b> structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
52	<a href="#">c2yevB</a>	Alignment	not modelled	9.0	17	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase subunit 2; <b>PDBTitle:</b> structure of caa3-type cytochrome oxidase

53	<a href="#">c4n7wA</a>	Alignment	not modelled	8.9	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> transporter, sodium/bile acid symporter family; <b>PDBTitle:</b> crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
54	<a href="#">c2kncA</a>	Alignment	not modelled	8.6	9	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
55	<a href="#">d3dtub2</a>	Alignment	not modelled	8.4	16	<b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
56	<a href="#">c3ukxC</a>	Alignment	not modelled	8.1	50	<b>PDB header:</b> protein transport/inhibitor <b>Chain:</b> C: <b>PDB Molecule:</b> bimax2 peptide; <b>PDBTitle:</b> mouse importin alpha: bimax2 peptide complex
57	<a href="#">c1cl4A</a>	Alignment	not modelled	8.1	25	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (gag polyprotein); <b>PDBTitle:</b> nucleocapsid protein from mason-pfizer monkey virus (mpmv)
58	<a href="#">c4k1cB</a>	Alignment	not modelled	8.0	13	<b>PDB header:</b> membrane protein/metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar calcium ion transporter; <b>PDBTitle:</b> vcx1 calcium/proton exchanger
59	<a href="#">c5kzoA</a>	Alignment	not modelled	7.4	22	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> neurogenic locus notch homolog protein 1; <b>PDBTitle:</b> notch1 transmembrane and associated juxtamembrane segment
60	<a href="#">d1dsva</a>	Alignment	not modelled	7.4	25	<b>Fold:</b> Retrovirus zinc finger-like domains <b>Superfamily:</b> Retrovirus zinc finger-like domains <b>Family:</b> Retrovirus zinc finger-like domains
61	<a href="#">c4m5bA</a>	Alignment	not modelled	7.3	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cobalamin biosynthesis protein cbim; <b>PDBTitle:</b> crystal structure of an truncated transition metal transporter
62	<a href="#">c4m5cA</a>	Alignment	not modelled	7.3	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> cobalamin biosynthesis protein cbim; <b>PDBTitle:</b> crystal structure of an truncated transition metal transporter
63	<a href="#">c5v2sA</a>	Alignment	not modelled	7.0	19	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> envelope glycoprotein b; <b>PDBTitle:</b> crystal structure of glycoprotein b from herpes simplex virus type i
64	<a href="#">c2micA</a>	Alignment	not modelled	7.0	12	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 16; <b>PDBTitle:</b> nmr structure of p75 transmembrane domain in dpc micelles
65	<a href="#">c2micB</a>	Alignment	not modelled	7.0	12	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> tumor necrosis factor receptor superfamily member 16; <b>PDBTitle:</b> nmr structure of p75 transmembrane domain in dpc micelles
66	<a href="#">c2d5nB</a>	Alignment	not modelled	6.6	18	<b>PDB header:</b> hydrolase, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> riboflavin biosynthesis protein ribd; <b>PDBTitle:</b> crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis
67	<a href="#">c2ndjA</a>	Alignment	not modelled	6.3	10	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e member 3; <b>PDBTitle:</b> structural basis for kcne3 and estrogen modulation of the kcnq12 channel
68	<a href="#">c2m7eA</a>	Alignment	not modelled	6.2	18	<b>PDB header:</b> calmodulin-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> calcium-transporting atpase 2, plasma membrane-type; <b>PDBTitle:</b> solution structure of the calmodulin-binding domain of plant calcium-2 atpase aca2
69	<a href="#">c3wg7T</a>	Alignment	not modelled	6.1	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> T: <b>PDB Molecule:</b> cytochrome c oxidase subunit 6a2, mitochondrial; <b>PDBTitle:</b> a 1.9 angstrom radiation damage free x-ray structure of large (420kda)2 protein by femtosecond crystallography
70	<a href="#">d1v54g</a>	Alignment	not modelled	6.1	27	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Mitochondrial cytochrome c oxidase subunit VIa <b>Family:</b> Mitochondrial cytochrome c oxidase subunit VIa
71	<a href="#">c6f0gC</a>	Alignment	not modelled	6.1	23	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> ip3; <b>PDBTitle:</b> crystal structure asf1-ip3
72	<a href="#">c6f0gD</a>	Alignment	not modelled	6.1	23	<b>PDB header:</b> chaperone <b>Chain:</b> D: <b>PDB Molecule:</b> ip3; <b>PDBTitle:</b> crystal structure asf1-ip3
73	<a href="#">c4uy87</a>	Alignment	not modelled	6.0	75	<b>PDB header:</b> ribosome <b>Chain:</b> 7: <b>PDB Molecule:</b> tryptophanase; <b>PDB Fragment:</b> residues 7-85; <b>PDBTitle:</b> molecular basis for the ribosome functioning as a l-tryptophan sensor2 - cryo-em structure of a tnac stalled e.coli ribosome
74	<a href="#">c6csxA</a>	Alignment	not modelled	5.9	8	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug efflux pump subunit acrb; <b>PDBTitle:</b> single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom
75	<a href="#">c5z62G</a>	Alignment	not modelled	5.8	36	<b>PDB header:</b> electron transport <b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome c oxidase subunit 6a1, mitochondrial; <b>PDBTitle:</b> structure of human cytochrome c oxidase
76	<a href="#">c6eznH</a>	Alignment	not modelled	5.8	12	<b>PDB header:</b> membrane protein <b>Chain:</b> H: <b>PDB Molecule:</b> dolichyl-diphosphooligosaccharide--protein <b>PDBTitle:</b> cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
77	<a href="#">c2l0vA</a>	Alignment	not modelled	5.8	13	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbB-3;

77	<a href="#">c2l9uA_</a>	Alignment	not modelled	5.8	13	<b>PDBTitle:</b> spatial structure of dimeric erbb3 transmembrane domain
78	<a href="#">c2l9uB_</a>	Alignment	not modelled	5.8	13	<b>PDB header:</b> membrane protein <b>Chain:</b> B; <b>PDB Molecule:</b> receptor tyrosine-protein kinase erbb-3; <b>PDBTitle:</b> spatial structure of dimeric erbb3 transmembrane domain
79	<a href="#">c4k1cA_</a>	Alignment	not modelled	5.7	13	<b>PDB header:</b> membrane protein/metal transport <b>Chain:</b> A; <b>PDB Molecule:</b> vacuolar calcium ion transporter; <b>PDBTitle:</b> vcx1 calcium/proton exchanger
80	<a href="#">c2zxeA_</a>	Alignment	not modelled	5.6	16	<b>PDB header:</b> hydrolase/transport protein <b>Chain:</b> A; <b>PDB Molecule:</b> na, k-atpase alpha subunit; <b>PDBTitle:</b> crystal structure of the sodium - potassium pump in the e2.2k+.pi2 state
81	<a href="#">c5levA_</a>	Alignment	not modelled	5.5	11	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylglucosamine--dolichyl-phosphate n- <b>PDBTitle:</b> crystal structure of human udp-n-acetylglucosamine-dolichyl-phosphate2 n-acetylglucosaminephosphotransferase (dpagt1) (v264g mutant)
82	<a href="#">c4heaJ_</a>	Alignment	not modelled	5.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J; <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit 10; <b>PDBTitle:</b> crystal structure of the entire respiratory complex i from thermus2 thermophilus
83	<a href="#">c3fh6F_</a>	Alignment	not modelled	5.4	12	<b>PDB header:</b> transport protein <b>Chain:</b> F; <b>PDB Molecule:</b> maltose transport system permease protein malf; <b>PDBTitle:</b> crystal structure of the resting state maltose transporter from e.2 coli
84	<a href="#">d1co4a_</a>	Alignment	not modelled	5.2	50	<b>Fold:</b> Zinc domain conserved in yeast copper-regulated transcription factors <b>Superfamily:</b> Zinc domain conserved in yeast copper-regulated transcription factors <b>Family:</b> Zinc domain conserved in yeast copper-regulated transcription factors
85	<a href="#">c5i20E_</a>	Alignment	not modelled	5.2	6	<b>PDB header:</b> membrane protein <b>Chain:</b> E; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of protein
86	<a href="#">c6an7C_</a>	Alignment	not modelled	5.1	9	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> transport permease protein; <b>PDBTitle:</b> crystal structure of o-antigen polysaccharide abc-transporter
87	<a href="#">c3ux4C_</a>	Alignment	not modelled	5.1	12	<b>PDB header:</b> transport protein <b>Chain:</b> C; <b>PDB Molecule:</b> acid-activated urea channel; <b>PDBTitle:</b> crystal structure of the urea channel from the human gastric pathogen2 helicobacter pylori