

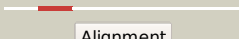

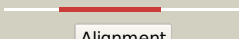














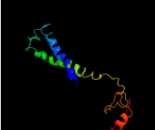

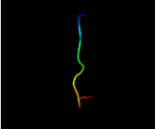
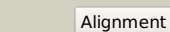





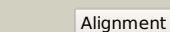
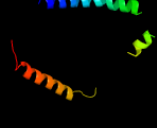


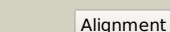

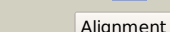





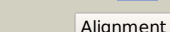
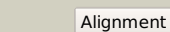
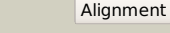

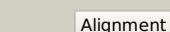
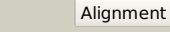
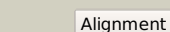
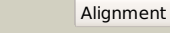
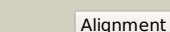


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3794_(embA)_4243411_4246695
 Date Fri Aug 9 18:20:50 BST 2019
 Unique Job ID e8cb4f68b0d6eafb





















Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ptyA_	 Alignment		100.0	45	PDB header: transferase Chain: A; PDB Molecule: arabinosyltransferase c; PDBTitle: crystal structure of the c-terminal extracellular domain of2 mycobacterium tuberculosis embc
2	c3bywB_	 Alignment		100.0	31	PDB header: transferase Chain: B; PDB Molecule: putative arabinofuranosyltransferase; PDBTitle: crystal structure of the c-terminal extracellular domain of2 arabinofuranosyltransferase from corynebacterium diphtheriae
3	c5f15A_	 Alignment		99.1	14	PDB header: transferase Chain: A; PDB Molecule: 4-amino-4-deoxy-l-arabinose (l-ara4n) transferase; PDBTitle: crystal structure of arnt from cupriavidus metallidurans bound to2 undecaprenyl phosphate
4	c3rceA_	 Alignment		98.5	13	PDB header: transferase/peptide Chain: A; PDB Molecule: oligosaccharide transferase to n-glycosylate proteins; PDBTitle: bacterial oligosaccharyltransferase pglb
5	c3wajA_	 Alignment		96.0	14	PDB header: transferase Chain: A; PDB Molecule: transmembrane oligosaccharyl transferase; PDBTitle: crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate
6	c6p2rB_	 Alignment		94.4	10	PDB header: transferase Chain: B; PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 2; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor
7	c6p25A_	 Alignment		91.7	13	PDB header: transferase Chain: A; PDB Molecule: dolichyl-phosphate-mannose--protein mannosyltransferase 1; PDBTitle: structure of s. cerevisiae protein o-mannosyltransferase pmt1-pmt22 complex bound to the sugar donor and a peptide acceptor
8	c6btmD_	 Alignment		75.3	20	PDB header: membrane protein Chain: D; PDB Molecule: alternative complex iii subunit d; PDBTitle: structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)
9	c6eznF_	 Alignment		52.9	12	PDB header: membrane protein Chain: F; PDB Molecule: dolichyl-diphosphooligosaccharide--protein PDBTitle: cryo-em structure of the yeast oligosaccharyltransferase (ost) complex
10	c6f0kD_	 Alignment		51.1	21	PDB header: membrane protein Chain: D; PDB Molecule: actd; PDBTitle: alternative complex iii
11	c4rrfD_	 Alignment		37.6	45	PDB header: ligase Chain: D; PDB Molecule: threonine--trna ligase; PDBTitle: editing domain of threonyl-trna synthetase from methanococcus2 jannaschii with l-ser3aa

12	c2hl2A_	 Alignment		35.8	45	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
13	c2lopA_	 Alignment		35.4	13	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane protein 14a; PDBTitle: backbone structure of human membrane protein tmem14a
14	d1iyjb3	 Alignment		34.2	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
15	c3jd8A_	 Alignment		31.8	19	PDB header: membrane protein Chain: A: PDB Molecule: niemann-pick c1 protein; PDBTitle: cryo-em structure of the full-length human npc1 at 4.4 angstrom
16	c4rlrA_	 Alignment		31.4	34	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c, 1 heme-binding site; PDBTitle: structure of monoheme cytochrome pcch from geobacter sulfurreducens
17	c4rrcA_	 Alignment		30.2	45	PDB header: ligase Chain: A: PDB Molecule: probable threonine--trna ligase 2; PDBTitle: n-terminal editing domain of threonyl-trna synthetase from aeropyrum2 pernix with l-thr3aa (snapshot 3)
18	c6ajjA_	 Alignment		28.9	14	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
19	c5x5iC_	 Alignment		28.4	26	PDB header: transcription Chain: C: PDB Molecule: hth-type transcriptional regulator rcda; PDBTitle: the x-ray crystal structure of a tetra family transcription regulator2 rcda involved in the regulation of biofilm formation in escherichia3 coli
20	c2mc7A_	 Alignment		25.6	44	PDB header: membrane protein Chain: A: PDB Molecule: regulatory peptide; PDBTitle: structure of salmonella mgrtr
21	c6iedA_	 Alignment	not modelled	23.5	13	PDB header: membrane protein Chain: A: PDB Molecule: heme a synthase; PDBTitle: crystal structure of heme a synthase from bacillus subtilis
22	c5zr1F_	 Alignment	not modelled	22.8	13	PDB header: dna binding protein/dna Chain: F: PDB Molecule: origin recognition complex subunit 6; PDBTitle: saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
23	d1gmnbl	 Alignment	not modelled	22.5	50	Fold: Hairpin loop containing domain-like Superfamily: Hairpin loop containing domain-like Family: Hairpin loop containing domain
24	c1iyjB_	 Alignment	not modelled	19.9	23	PDB header: gene regulation/antitumor protein Chain: B: PDB Molecule: breast cancer susceptibility; PDBTitle: structure of a brca2-dss1 complex
25	c3x27C_	 Alignment	not modelled	18.2	29	PDB header: lyase Chain: C: PDB Molecule: cucumopine synthase; PDBTitle: structure of mcbb in complex with tryptophan
26	c6dmoA_	 Alignment	not modelled	17.9	16	PDB header: protein binding Chain: A: PDB Molecule: protein patched homolog 1; PDBTitle: cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l
27	d1miau3	 Alignment	not modelled	17.6	26	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
28	c2losA_	 Alignment	not modelled	17.3	14	PDB header: membrane protein Chain: A: PDB Molecule: transmembrane protein 14c; PDBTitle: backbone structure of human membrane protein tmem14c
29	c5v2dA_	 Alignment	not modelled	17.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dioxygenase; PDBTitle: crystal structure of pseudomonas brassicacearum

						lignostilbene2 dioxygenase
30	c2m20B_	Alignment	not modelled	17.1	22	PDB header: signaling protein Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: egfr transmembrane - juxtamembrane (tm-jm) segment in bicelles: md2 guided nmr refined structure.
31	c2a2jA_	Alignment	not modelled	16.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
32	d1rwua_	Alignment	not modelled	16.4	22	Fold: Ferredoxin-like Superfamily: Ybed/HP0495-like Family: Ybed-like
33	c1rwuA_	Alignment	not modelled	16.4	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0250 protein ybed; PDBTitle: solution structure of conserved protein ybed from e. coli
34	c4xesA_	Alignment	not modelled	15.5	9	PDB header: signaling protein, hydrolase Chain: A: PDB Molecule: neurotensin receptor type 1, endolysin chimera; PDBTitle: structure of active-like neurotensin receptor
35	c1mjeA_	Alignment	not modelled	15.3	26	PDB header: gene regulation/antitumor protein/dna Chain: A: PDB Molecule: breast cancer 2; PDBTitle: structure of a brca2-dss1-ssdna complex
36	c3b9yA_	Alignment	not modelled	15.0	19	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
37	d1rc2a_	Alignment	not modelled	14.9	15	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
38	d1osna_	Alignment	not modelled	14.8	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
39	c5j54A_	Alignment	not modelled	14.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: carotenoid oxygenase; PDBTitle: the structure and mechanism of nov1, a resveratrol-cleaving2 dioxygenase
40	c1emzA_	Alignment	not modelled	14.1	44	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein e1; PDBTitle: solution structure of fragment (350-370) of the2 transmembrane domain of hepatitis c envelope glycoprotein3 e1
41	c1hymB_	Alignment	not modelled	13.8	26	PDB header: hydrolase (serine proteinase) Chain: B: PDB Molecule: hydrolyzed cucurbita maxima trypsin inhibitor v; PDBTitle: hydrolyzed trypsin inhibitor (cmti-v, minimized average nmr structure)
42	c2zopA_	Alignment	not modelled	13.7	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative uncharacterized protein tthb164; PDBTitle: x-ray crystal structure of a crispr-associated cmr5 family2 protein from thermus thermophilus hb8
43	c5u90A_	Alignment	not modelled	13.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: carotenoid oxygenase 1; PDBTitle: crystal structure of co-cao1 in complex with resveratrol
44	c2y0nE_	Alignment	not modelled	13.7	50	PDB header: transcription Chain: E: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and msl3
45	c6ithA_	Alignment	not modelled	13.4	29	PDB header: membrane protein Chain: A: PDB Molecule: syndecan-2; PDBTitle: structure of the transmembrane domain of syndecan 2 in micelles
46	c2y0nG_	Alignment	not modelled	13.3	56	PDB header: transcription Chain: G: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and msl3
47	c2y0nH_	Alignment	not modelled	13.3	56	PDB header: transcription Chain: H: PDB Molecule: male-specific lethal 1 homolog; PDBTitle: crystal structure of the complex between dosage2 compensation factors msl1 and msl3
48	c2h9aA_	Alignment	not modelled	13.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoid/iron-sulfur PDBTitle: corrinoid iron-sulfur protein
49	c2pptA_	Alignment	not modelled	12.9	26	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2
50	c4djeE_	Alignment	not modelled	12.8	10	PDB header: transferase/vitamin-binding protein Chain: E: PDB Molecule: corrinoid/iron-sulfur protein large subunit; PDBTitle: crystal structure of folate-bound corrinoid iron-sulfur protein2 (cfesp) in complex with its methyltransferase (metr), co-crystallized3 with folate
51	c3zqiB_	Alignment	not modelled	12.6	17	PDB header: transcription Chain: B: PDB Molecule: tetracycline repressor protein class b from transposon PDBTitle: structure of tetracycline repressor in complex with inducer peptide-2 tip2
52	c4huqS_	Alignment	not modelled	12.6	17	PDB header: hydrolase Chain: S: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a transporter
53	c2yclA_	Alignment	not modelled	11.7	17	PDB header: transferase Chain: A: PDB Molecule: carbon monoxide dehydrogenase corrinoid/iron-sulfur PDBTitle: complete structure of the corrinoid,iron-sulfur protein including2 the n-terminal domain with a 4fe-4s cluster
54	c4z9cA_	Alignment	not modelled	11.7	23	PDB header: transferase Chain: A: PDB Molecule: pertussis toxin-like subunit arta; PDBTitle: ecpltab oxidized
						PDB header: transcription

55	c2hxoB_	Alignment	not modelled	11.4	8	Chain: B: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: structure of the transcriptional regulator sco7222, a tetr from2 streptomyces coelicolor
56	c1t0jA_	Alignment	not modelled	11.4	4	PDB header: signaling protein Chain: A: PDB Molecule: voltage-gated calcium channel subunit beta2a; PDBTitle: crystal structure of a complex between voltage-gated calcium channel2 beta2a subunit and a peptide of the alpha1c subunit
57	c1miuA_	Alignment	not modelled	11.1	21	PDB header: gene regulation/antitumor protein Chain: A: PDB Molecule: breast cancer type 2 susceptibility protein; PDBTitle: structure of a brca2-dss1 complex
58	d1bdsa_	Alignment	not modelled	11.1	36	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
59	c1bdsA_	Alignment	not modelled	11.1	36	PDB header: anti-hypertensive, anti-viral protein Chain: A: PDB Molecule: bds-i; PDBTitle: determination of the three-dimensional solution structure of the2 antihypertensive and antiviral protein bds-i from the sea anemone3 anemone sulcata. a study using nuclear magnetic resonance and hybrid4 distance geometry-dynamical simulated annealing
60	c4ruvA_	Alignment	not modelled	11.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin 2 from staphylococcus aureus nctc8325
61	d2a2ja1	Alignment	not modelled	11.0	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
62	c5wcoC_	Alignment	not modelled	11.0	57	PDB header: viral protein Chain: C: PDB Molecule: ns2; PDBTitle: matrix protein (m1) of infectious salmon anaemia virus
63	c2q24A_	Alignment	not modelled	11.0	24	PDB header: transcription Chain: A: PDB Molecule: putative tetr family transcriptional regulator; PDBTitle: crystal structure of tetr transcriptional regulator sco0520 from2 streptomyces coelicolor
64	c3fsnA_	Alignment	not modelled	10.8	43	PDB header: isomerase Chain: A: PDB Molecule: retinal pigment epithelium-specific 65 kda protein; PDBTitle: crystal structure of rpe65 at 2.14 angstrom resolution
65	c5j7dG_	Alignment	not modelled	10.7	9	PDB header: de novo protein Chain: G: PDB Molecule: designed thioredoxin df106; PDBTitle: computationally designed thioredoxin df106
66	c4gkfA_	Alignment	not modelled	10.7	25	PDB header: unknown function Chain: A: PDB Molecule: crispr system cmr subunit cmr5; PDBTitle: crystal structure and characterization of cmr5 protein from pyrococcus2 furiosus
67	c4s21B_	Alignment	not modelled	10.5	20	PDB header: signaling protein Chain: B: PDB Molecule: bacteriophytochrome (light-regulated signal transduction PDBTitle: crystal structure of the photosensory core module of2 bacteriophytochrome rpa3015 from r. palustris
68	d1fx8a_	Alignment	not modelled	9.9	16	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
69	c1ldaA_	Alignment	not modelled	9.9	16	PDB header: transport protein Chain: A: PDB Molecule: glycerol uptake facilitator protein; PDBTitle: crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
70	c5d7tC_	Alignment	not modelled	9.9	20	PDB header: transport protein Chain: C: PDB Molecule: s-component for folate; PDBTitle: folate ecf transporter: apo state
71	c6fhtB_	Alignment	not modelled	9.8	21	PDB header: lyase Chain: B: PDB Molecule: bacteriophytochrome,adenylate cyclase; PDBTitle: crystal structure of an artificial phytochrome regulated2 adenylate/guanylate cyclase in its dark adapted pr form
72	c5v7pA_	Alignment	not modelled	9.5	24	PDB header: transferase Chain: A: PDB Molecule: protein-s-isoprenylcysteine o-methyltransferase; PDBTitle: atomic structure of the eukaryotic intramembrane ras methyltransferase2 icmt (isoprenylcysteine carboxyl methyltransferase), in complex with3 a monobody
73	d1fpoa1	Alignment	not modelled	9.5	25	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
74	c2n2aA_	Alignment	not modelled	9.5	22	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbB-2; PDBTitle: spatial structure of her2/erbB2 dimeric transmembrane domain in the2 presence of cytoplasmic juxtamembrane domains
75	c2i9hA_	Alignment	not modelled	9.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin i; PDBTitle: nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1)
76	c6ir8A_	Alignment	not modelled	9.3	19	PDB header: transcription/dna Chain: A: PDB Molecule: oswrky45; PDBTitle: rice wrky/dna complex
77	c4wkkA_	Alignment	not modelled	9.2	24	PDB header: signaling protein Chain: A: PDB Molecule: bacteriophytochrome protein; PDBTitle: the photosensory module (pas-gaf-phy) of the bacterial phytochrome2 agp1 (atbph1) in the pr form, chromophore modelled with an exocyclic3 double bond at pyrrole ring a.
78	c4gicB_	Alignment	not modelled	9.2	23	PDB header: oxidoreductase Chain: B: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus

79	c6g9oA	 Alignment	not modelled	9.2	21	PDB header: membrane protein Chain: A: PDB Molecule: volume-regulated anion channel subunit lrrc8a; PDBTitle: structure of full-length homomeric mlrrc8a volume-regulated anion2 channel at 4.25 a resolution
80	c2rekA	 Alignment	not modelled	9.2	17	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family transcriptional regulator; PDBTitle: crystal structure of tetr-family transcriptional regulator
81	c4anjA	 Alignment	not modelled	9.1	10	PDB header: motor protein/metal-bindng protein Chain: A: PDB Molecule: unconventional myosin-vi, green fluorescent protein; PDBTitle: myosin vi (mdinsert2-gfp fusion) pre-powerstroke state (mg.adp.alf4)
82	d2oeba1	 Alignment	not modelled	9.1	19	Fold: ATPD N-terminal domain-like Superfamily: AF1862-like Family: Cas Cmr5-like
83	d1y0ja1	 Alignment	not modelled	9.1	23	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Erythroid transcription factor GATA-1
84	c2biwC	 Alignment	not modelled	9.1	37	PDB header: oxidoreductase Chain: C: PDB Molecule: apocarotenoid-cleaving oxygenase; PDBTitle: crystal structure of apocarotenoid cleavage oxygenase from2 synechocystis, native enzyme
85	c5dynA	 Alignment	not modelled	9.1	33	PDB header: hydrolase Chain: A: PDB Molecule: putative peptidase; PDBTitle: b. fragilis cysteine protease
86	c2an1D	 Alignment	not modelled	9.0	13	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
87	c2cdpC	 Alignment	not modelled	8.9	16	PDB header: hydrolase Chain: C: PDB Molecule: beta-agarase 1; PDBTitle: structure of a cbm6 in complex with neoagarohexaose
88	c6d6vE	 Alignment	not modelled	8.9	33	PDB header: replication Chain: E: PDB Molecule: telomerase holoenzyme teb2 subunit; PDBTitle: cryoem structure of tetrahymena telomerase with telomeric dna at 4.82 angstrom resolution
89	c2bqpA	 Alignment	not modelled	8.8	9	PDB header: carbohydrate binding protein Chain: A: PDB Molecule: endo-b1,4-mannanase 5c; PDBTitle: mannan binding module from man5c in bound conformation
90	c2k58B	 Alignment	not modelled	8.8	24	PDB header: transport protein Chain: B: PDB Molecule: neuronal acetylcholine receptor subunit beta-2; PDBTitle: nmr structures of the first transmembrane domain of the2 neuronal acetylcholine receptor beta 2 subunit
91	c4rfuB	 Alignment	not modelled	8.6	23	PDB header: viral protein Chain: B: PDB Molecule: coat protein; PDBTitle: crystal structure of truncated p-domain from grouper nervous necrosis2 virus capsid protein at 1.2a
92	c2wvrC	 Alignment	not modelled	8.5	14	PDB header: replication Chain: C: PDB Molecule: dna replication factor cdt1; PDBTitle: human cdt1:geminin complex
93	c2mn8A	 Alignment	not modelled	8.4	35	PDB header: antimicrobial protein Chain: A: PDB Molecule: maculatin g15; PDBTitle: nmr structure of a peptoid analogue of maculatin g15 containing cis-2 nleu at position 13
94	c2mn9A	 Alignment	not modelled	8.4	35	PDB header: antimicrobial protein Chain: A: PDB Molecule: maculatin g15; PDBTitle: peptoid analogue of maculatin g15 - peptoid trans-nleu at position 13
95	c6ojrA	 Alignment	not modelled	8.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: lignostilbene-alpha,beta-dioxygenase isozyme i; PDBTitle: crystal structure of sphingomonas paucimobilis tmy1009 apo-lsda
96	d1p6xa	 Alignment	not modelled	8.3	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
97	c2lx0A	 Alignment	not modelled	8.3	25	PDB header: membrane protein Chain: A: PDB Molecule: membrane fusion protein p14; PDBTitle: arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
98	d1oedc	 Alignment	not modelled	8.3	23	Fold: Neurotransmitter-gated ion-channel transmembrane pore Superfamily: Neurotransmitter-gated ion-channel transmembrane pore Family: Neurotransmitter-gated ion-channel transmembrane pore
99	c3npeA	 Alignment	not modelled	8.3	32	PDB header: oxidoreductase Chain: A: PDB Molecule: 9-cis-epoxycarotenoid dioxygenase 1, chloroplastic; PDBTitle: structure of vp14 in complex with oxygen