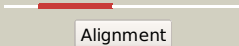
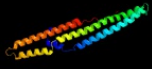


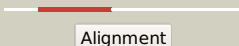



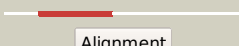
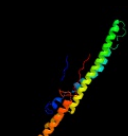
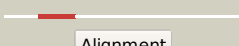

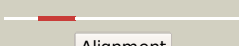
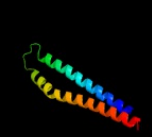
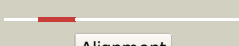
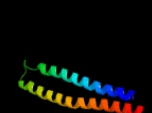



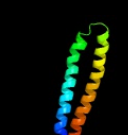




Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0442c_(PPE10)_530754_532217
 Date Tue Jul 23 14:50:51 BST 2019
 Unique Job ID 7da7ca69a847932a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	52	PDB header: protein transport Chain: B: PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	d2g38b1	 Alignment		100.0	32	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
3	c2g38B_	 Alignment		100.0	32	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
4	c4xy3A_	 Alignment		100.0	16	PDB header: protein transport Chain: A: PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		98.5	13	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c2vs0B_	 Alignment		97.9	15	PDB header: cell invasion Chain: B: PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
7	c3gvmA_	 Alignment		97.7	14	PDB header: viral protein Chain: A: PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
8	c4iogD_	 Alignment		97.7	19	PDB header: unknown function Chain: D: PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
9	c3zbhC_	 Alignment		97.6	19	PDB header: unknown function Chain: C: PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		97.1	14	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c4lwsA_	 Alignment		96.4	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata

12	c4lwsB_	Alignment		96.1	16	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		96.0	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		95.8	22	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	c2kg7B_	Alignment		92.7	18	PDB header: unknown function Chain: B; PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
16	c4i0xJ_	Alignment		67.2	16	PDB header: structural genomics, unknown function Chain: J; PDB Molecule: esat-6-like protein mab_3113; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
17	d1ui5a2	Alignment		58.7	17	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
18	d1xkna_	Alignment		26.4	16	Fold: Pentain, beta/alpha-propeller Superfamily: Pentain Family: Porphyromonas-type peptidylarginine deiminase
19	c3jywF_	Alignment		23.2	46	PDB header: ribosome Chain: F; PDB Molecule: 60s ribosomal protein l7(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution
20	c3ub0D_	Alignment		21.9	15	PDB header: replication Chain: D; PDB Molecule: non-structural protein 6, nsp6;; PDBTitle: crystal structure of the nonstructural protein 7 and 8 complex of feline coronavirus
21	c1bkvA_	Alignment	not modelled	20.6	56	PDB header: structural protein Chain: A; PDB Molecule: t3-785; PDBTitle: collagen
22	c5lzkB_	Alignment	not modelled	20.4	4	PDB header: structural genomics Chain: B; PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
23	c2ahmG_	Alignment	not modelled	20.2	19	PDB header: viral protein, replication Chain: G; PDB Molecule: replicase polyprotein 1ab, heavy chain; PDBTitle: crystal structure of sars-cov super complex of non-structural2 proteins: the hexadecamer
24	c2kg7A_	Alignment	not modelled	20.0	28	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein esxg (pe family protein); PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
25	c1bkvB_	Alignment	not modelled	19.5	56	PDB header: structural protein Chain: B; PDB Molecule: t3-785; PDBTitle: collagen
26	c1bkvC_	Alignment	not modelled	19.5	56	PDB header: structural protein Chain: C; PDB Molecule: t3-785; PDBTitle: collagen
27	c5frgA_	Alignment	not modelled	17.2	63	PDB header: protein binding Chain: A; PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
28	c2l5bA_	Alignment	not modelled	16.3	47	PDB header: apoptosis Chain: A; PDB Molecule: activator of apoptosis harakiri; PDBTitle: solution structure of the transmembrane domain of bcl-2 member2 harakiri in micelles

29	c3fy6A_	Alignment	not modelled	15.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: integron cassette protein; PDBTitle: structure from the mobile metagenome of v. cholerae. integron cassette2 protein vch_cass3
30	d1luaa2	Alignment	not modelled	13.9	29	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydromethanopterin dehydrogenase
31	c4mnpA_	Alignment	not modelled	13.6	14	PDB header: sugar binding protein Chain: A: PDB Molecule: n-acetylneuraminate-binding protein; PDBTitle: structure of the sialic acid binding protein from fusobacterium2 nucleatum subsp. nucleatum atcc 25586
32	c3zfsA_	Alignment	not modelled	13.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: f420-reducing hydrogenase, subunit alpha; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
33	c4nn3A_	Alignment	not modelled	13.3	11	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio salexigens (desal_2161), target efi-510109, with bound3 orotic acid
34	d2fgga1	Alignment	not modelled	13.1	40	Fold: dsRBD-like Superfamily: Rv2632c-like Family: Rv2632c-like
35	c2l5aA_	Alignment	not modelled	11.8	16	PDB header: nuclear protein Chain: A: PDB Molecule: histone h3-like centromeric protein cse4, protein scm3, PDBTitle: structural basis for recognition of centromere specific histone h32 variant by nonhistone scm3
36	c3qthA_	Alignment	not modelled	11.6	15	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a dinb-like protein (cps_3021) from colwellia2 psychrerythraea 34h at 2.20 a resolution
37	c4wpyA_	Alignment	not modelled	11.3	20	PDB header: de novo protein Chain: A: PDB Molecule: protein dl-rv1738; PDBTitle: racemic crystal structure of rv1738 from mycobacterium tuberculosis2 (form-ii)
38	c2ke4A_	Alignment	not modelled	11.0	63	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cjp4
39	c2iu1A_	Alignment	not modelled	10.6	28	PDB header: transcription Chain: A: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of eif5 c-terminal domain
40	c4n91A_	Alignment	not modelled	10.6	9	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 anaerococcus prevotii dsm 20548 (apre_1383), target efi-510023, with3 bound alpha/beta d-glucuronate
41	c4k8nF_	Alignment	not modelled	10.6	14	PDB header: lipid transport Chain: F: PDB Molecule: glycolipid transfer protein domain-containing protein 1; PDBTitle: crystal structure of human ceramide-1-phosphate transfer protein2 (cptp) in complex with 18:1 ceramide-1-phosphate (18:1-c1p)
42	c2fulE_	Alignment	not modelled	10.4	28	PDB header: translation Chain: E: PDB Molecule: eukaryotic translation initiation factor 5; PDBTitle: crystal structure of the c-terminal domain of s. cerevisiae eif5
43	c4ix1B_	Alignment	not modelled	10.3	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein opag_01669 from rhodococcus2 opacus pd630, target 016205
44	c2lyyB_	Alignment	not modelled	9.8	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein nb7890a from shewanella sp
45	c3b50A_	Alignment	not modelled	9.4	16	PDB header: transport protein Chain: A: PDB Molecule: sialic acid-binding periplasmic protein siap; PDBTitle: structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
46	c5vmoB_	Alignment	not modelled	9.4	50	PDB header: viral protein/apoptosis Chain: B: PDB Molecule: bcl-2 interacting mediator of cell death; PDBTitle: crystal structure of grouper iridovirus giv66:bim complex
47	c4urjA_	Alignment	not modelled	9.1	9	PDB header: unknown function Chain: A: PDB Molecule: protein fam83a; PDBTitle: crystal structure of human bj-tsa-9
48	c4c7lA_	Alignment	not modelled	9.0	30	PDB header: hydrolase Chain: A: PDB Molecule: hemagglutinin-esterase; PDBTitle: crystal structure of mouse hepatitis virus strain s2 hemagglutinin-esterase
49	c4i6jB_	Alignment	not modelled	8.9	22	PDB header: transcription Chain: B: PDB Molecule: cf-box/lrr-repeat protein 3; PDBTitle: a ubiquitin ligase-substrate complex
50	c3h8dC_	Alignment	not modelled	8.6	15	PDB header: motor protein/signaling protein Chain: C: PDB Molecule: myosin-vi; PDBTitle: crystal structure of myosin vi in complex with dab2 peptide
51	c2np3A_	Alignment	not modelled	8.4	17	PDB header: transcription Chain: A: PDB Molecule: putative tetr-family regulator; PDBTitle: crystal structure of tetr-family regulator (sco0857) from streptomyces2 coelicolor a3.
52	c4xb6D_	Alignment	not modelled	8.2	15	PDB header: transferase Chain: D: PDB Molecule: alpha-d-ribose 1-methylphosphonate 5-phosphate c-p lyase; PDBTitle: structure of the e. coli c-p lyase core complex
53	d1q42a_	Alignment	not modelled	8.2	11	Fold: Cystatin-like Superfamily: NTF2-like

						Family: NTF2-like
54	d1fcda3	Alignment	not modelled	8.2	23	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
55	c2kp7A	Alignment	not modelled	8.0	20	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
56	c5im2A	Alignment	not modelled	8.0	13	PDB header: transport protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal; PDBTitle: crystal structure of a trap solute binding protein from rhodofera x2 ferrireducens t118 (rfer_2570, target efi-510210) in complex with 3 copurified benzoate
57	c2kwuA	Alignment	not modelled	7.7	43	PDB header: protein binding/signaling protein Chain: A: PDB Molecule: dna polymerase iota; PDBTitle: solution structure of ubm2 of murine polymerase iota in complex with 2 ubiquitin
58	c3juiA	Alignment	not modelled	7.5	23	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b subunit epsilon; PDBTitle: crystal structure of the c-terminal domain of human translation2 initiation factor eif2b epsilon subunit
59	c4deyB	Alignment	not modelled	7.4	24	PDB header: transport protein Chain: B: PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: crystal structure of the voltage dependent calcium channel beta-22 subunit in complex with the cav1.2 i-ii linker.
60	c5hl8B	Alignment	not modelled	7.4	12	PDB header: protein transport Chain: B: PDB Molecule: type ii secretion system protein i; PDBTitle: 1.93 angstrom resolution crystal structure of a pullulanase-specific2 type ii secretion system integral cytoplasmic membrane protein gspI3 (c-terminal fragment; residues 309-397) from klebsiella pneumoniae4 subsp. pneumoniae ntuh-k2044
61	c3q4hB	Alignment	not modelled	7.4	20	PDB header: metal transport Chain: B: PDB Molecule: low molecular weight protein antigen 7; PDBTitle: crystal structure of the mycobacterium smegmatis esxh complex2 (msmeg_0620-msmeg_0621)
62	c1paqA	Alignment	not modelled	7.3	18	PDB header: translation Chain: A: PDB Molecule: translation initiation factor eif-2b epsilon PDBTitle: crystal structure of the catalytic fragment of eukaryotic2 initiation factor 2b epsilon
63	d1paqa	Alignment	not modelled	7.3	18	Fold: alpha-alpha superhelix Superfamily: ARM repeat Family: MIF4G domain-like
64	c3trhl	Alignment	not modelled	7.3	10	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
65	c3n6xA	Alignment	not modelled	7.2	20	PDB header: ligase Chain: A: PDB Molecule: putative glutathionylspermidine synthase; PDBTitle: crystal structure of a putative glutathionylspermidine synthase2 (mfIa_0391) from methylobacillus flagellatus kt at 2.35 a resolution
66	c5i4rA	Alignment	not modelled	7.1	43	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
67	c6o9l6	Alignment	not modelled	7.0	40	PDB header: transcription/dna Chain: 6: PDB Molecule: general transcription factor iih subunit 2; PDBTitle: human holo-pic in the closed state
68	c4gyxC	Alignment	not modelled	7.0	46	PDB header: structural protein, blood clotting Chain: C: PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
69	c3mveB	Alignment	not modelled	6.9	13	PDB header: lyase Chain: B: PDB Molecule: upf0255 protein vv1_0328; PDBTitle: crystal structure of a novel pyruvate decarboxylase
70	c4dmtA	Alignment	not modelled	6.9	55	PDB header: structural protein Chain: A: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
71	c4dmtB	Alignment	not modelled	6.9	55	PDB header: structural protein Chain: B: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
72	c4dmtC	Alignment	not modelled	6.9	55	PDB header: structural protein Chain: C: PDB Molecule: collagen iii derived peptide; PDBTitle: crystal structure of a vwf binding collagen iii derived triple helical2 peptide
73	d1rp3a1	Alignment	not modelled	6.8	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
74	d1pp7u	Alignment	not modelled	6.8	78	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: 39 kda initiator binding protein, IBP39, N-terminal domain
75	c1vytF	Alignment	not modelled	6.8	50	PDB header: transport protein Chain: F: PDB Molecule: voltage-dependent l-type calcium channel PDBTitle: beta3 subunit complexed with aid
76	d2fv7a1	Alignment	not modelled	6.8	8	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Ribokinase-like
77	c4gyxB	Alignment	not modelled	6.6	67	PDB header: structural protein, blood clotting Chain: B: PDB Molecule: type iii collagen fragment in a host peptide stabilized by

						PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
78	c4gyxA_	Alignment	not modelled	6.6	67	PDB header: structural protein, blood clotting Chain: A; PDB Molecule: type iii collagen fragment in a host peptide stabilized by PDBTitle: the von willebrand factor a3 domain binding region of type iii2 collagen stabilized by the cysteine knot
79	d1kx5a_	Alignment	not modelled	6.6	13	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
80	c3r5zB_	Alignment	not modelled	6.5	17	PDB header: unknown function Chain: B; PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
81	d1uadc_	Alignment	not modelled	6.4	18	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Other IPT/TIG domains
82	d2jbwa1	Alignment	not modelled	6.4	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: 2,6-dihydropseudooxynicotine hydrolase-like
83	c2jwbB_	Alignment	not modelled	6.3	17	PDB header: hydrolase Chain: B; PDB Molecule: 2,6-dihydroxy-pseudo-oxynicotine hydrolase; PDBTitle: crystal structure of the 2,6-dihydroxy-pseudo-oxynicotine hydrolase.
84	c3u65B_	Alignment	not modelled	6.2	6	PDB header: transport protein Chain: B; PDB Molecule: tp33 protein; PDBTitle: the crystal structure of tat-p(t) (tp0957)
85	c2nvjA_	Alignment	not modelled	6.2	50	PDB header: hydrolase Chain: A; PDB Molecule: 25mer peptide from vacuolar atp synthase subunit PDBTitle: nmr structures of transmembrane segment from subunit a from2 the yeast proton v-atpase
86	d1eqzq_	Alignment	not modelled	6.0	13	Fold: Histone-fold Superfamily: Histone-fold Family: Nucleosome core histones
87	c4grdA_	Alignment	not modelled	5.9	21	PDB header: lyase,isomerase Chain: A; PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
88	c4y9iA_	Alignment	not modelled	5.9	30	PDB header: oxidoreductase Chain: A; PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
89	c3bb9D_	Alignment	not modelled	5.9	13	PDB header: unknown function Chain: D; PDB Molecule: putative orphan protein; PDBTitle: crystal structure of a putative ketosteroid isomerase (sfri_1973) from2 shewanella frigidimarina ncimb 400 at 1.80 a resolution
90	c6epiC_	Alignment	not modelled	5.9	25	PDB header: toxin Chain: C; PDB Molecule: epsilon_1 antitoxin; PDBTitle: structure of the epsilon_1 / zeta_1 antitoxin / toxin system from2 neisseria gonorrhoeae in complex with unam-4p.
91	d1fs1a1	Alignment	not modelled	5.9	38	Fold: F-box domain Superfamily: F-box domain Family: F-box domain
92	c1fs1A_	Alignment	not modelled	5.9	38	PDB header: ligase Chain: A; PDB Molecule: cyclin a/cdk2-associated p19; PDBTitle: insights into scf ubiquitin ligases from the structure of2 the skp1-skp2 complex
93	d1szia_	Alignment	not modelled	5.8	21	Fold: Four-helical up-and-down bundle Superfamily: Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain Family: Mannose-6-phosphate receptor binding protein 1 (Tip47), C-terminal domain
94	c6aokA_	Alignment	not modelled	5.8	22	PDB header: hydrolase Chain: A; PDB Molecule: ceg4; PDBTitle: crystal structure of legionella pneumophila effector ceg4 with n-2 terminal tev protease cleavage sequence
95	c2y5tG_	Alignment	not modelled	5.7	83	PDB header: immune system Chain: G; PDB Molecule: c1; PDBTitle: crystal structure of the pathogenic autoantibody ciic1 in complex with2 the triple-helical c1 peptide
96	c6nbiP_	Alignment	not modelled	5.7	40	PDB header: signaling protein Chain: P; PDB Molecule: long-acting parathyroid hormone analog; PDBTitle: cryo-em structure of parathyroid hormone receptor type 1 in complex2 with a long-acting parathyroid hormone analog and g protein
97	c3j21Y_	Alignment	not modelled	5.6	38	PDB header: ribosome Chain: Y; PDB Molecule: 50s ribosomal protein l30p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
98	c6cgiA_	Alignment	not modelled	5.6	44	PDB header: hydrolase Chain: A; PDB Molecule: effector protein lem4 (lpg1101); PDBTitle: structure of the had domain of effector protein lem4 (lpg1101) from2 legionella pneumophila
99	c2jagA_	Alignment	not modelled	5.6	16	PDB header: membrane protein Chain: A; PDB Molecule: halorhodopsin; PDBTitle: l1-intermediate of halorhodopsin t203v