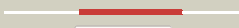




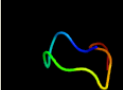



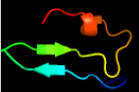
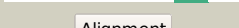
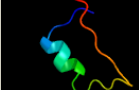
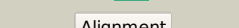

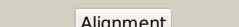

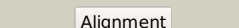
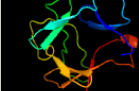
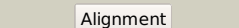
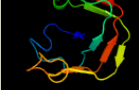


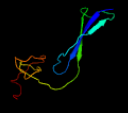


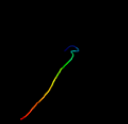

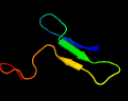

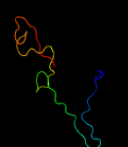
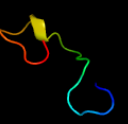


Phyre2

Email fngalenjume@gmail.com
 Description OvGM2AP_intensive_modelling
 Date Sat Mar 9 11:18:16 GMT 2019
 Unique Job ID a9c4ebca4c81f6e5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ag4a1	 Alignment		90.0	18	Fold: Ganglioside M2 (gm2) activator Superfamily: Ganglioside M2 (gm2) activator Family: Ganglioside M2 (gm2) activator
2	c3e2uF_	 Alignment		54.6	36	PDB header: protein binding Chain: F: PDB Molecule: cap-gly domain-containing linker protein 1; PDBTitle: crystal structure of the zink-knuckle 2 domain of human clip-170 in2 complex with cap-gly domain of human dynactin-1 (p150-glued)
3	c3e2uE_	 Alignment		54.6	36	PDB header: protein binding Chain: E: PDB Molecule: cap-gly domain-containing linker protein 1; PDBTitle: crystal structure of the zink-knuckle 2 domain of human clip-170 in2 complex with cap-gly domain of human dynactin-1 (p150-glued)
4	c2hqhE_	 Alignment		54.6	36	PDB header: structural protein, protein binding Chain: E: PDB Molecule: restin; PDBTitle: crystal structure of p150glued and clip-170
5	d1m1ha1	 Alignment		48.3	35	Fold: N-utilization substance G protein NusG, insert domain Superfamily: N-utilization substance G protein NusG, insert domain Family: N-utilization substance G protein NusG, insert domain
6	c5b7iA_	 Alignment		46.3	30	PDB header: hydrolase/unknown function Chain: A: PDB Molecule: crispr-associated nuclease/helicase cas3 subtype i-f/ypest; PDBTitle: cas3-acrf3 complex
7	c3e2uH_	 Alignment		41.3	44	PDB header: protein binding Chain: H: PDB Molecule: cap-gly domain-containing linker protein 1; PDBTitle: crystal structure of the zink-knuckle 2 domain of human clip-170 in2 complex with cap-gly domain of human dynactin-1 (p150-glued)
8	c3jb4A_	 Alignment		36.7	31	PDB header: virus Chain: A: PDB Molecule: vp1; PDBTitle: structure of ljunjan virus: insight into picornavirus packaging
9	d1ce7b2	 Alignment		34.1	14	Fold: beta-Trefoil Superfamily: Ricin B-like lectins Family: Ricin B-like
10	c4hspA_	 Alignment		24.2	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf3299 family protein (pa4066) from2 pseudomonas aeruginosa pao1 at 2.45 a resolution
11	d2a6aa2	 Alignment		22.7	30	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: YeaZ-like

12	c2bw2A_	Alignment		21.6	16	PDB header: signaling protein Chain: A; PDB Molecule: bypass of forespore c; PDBTitle: bofc from bacillus subtilis
13	c4qn1A_	Alignment		19.5	50	PDB header: hydrolase Chain: A; PDB Molecule: tail fiber protein; PDBTitle: crystal structure of tail fiber protein gp63.1 from e. coli phage g7c
14	d1uoza_	Alignment		18.3	12	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
15	d1njha_	Alignment		17.6	47	Fold: Hypothetical protein YojF Superfamily: Hypothetical protein YojF Family: Hypothetical protein YojF
16	c4adoA_	Alignment		17.1	32	PDB header: antibiotic resistance Chain: A; PDB Molecule: far1; PDBTitle: fusidic acid resistance protein fusb
17	d1a9xb2	Alignment		16.4	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
18	d1w7ca2	Alignment		16.0	40	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
19	d1beta_	Alignment		15.2	33	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Neurotrophin
20	d1vcoa1	Alignment		15.2	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
21	c6ak0A_	Alignment	not modelled	14.8	62	PDB header: unknown function Chain: A; PDB Molecule: cys-leu-gly-val-gly-ser-cys-val-asp-phe-ala-gly-cys-gly- PDBTitle: solution nmr structure of a new lasso peptide specialicin
22	c5tuuB_	Alignment	not modelled	14.8	52	PDB header: transcription Chain: B; PDB Molecule: transcription factor e2f4; PDBTitle: crystal structure of the e2f4-dp1 coiled coil and marked-box domains
23	c5yniB_	Alignment	not modelled	14.7	45	PDB header: transferase Chain: B; PDB Molecule: nsp10 protein; PDBTitle: crystal structure of mers-cov nsp16/nsp10 complex bound to sam and2 m7gpppg
24	c1jrxA_	Alignment	not modelled	14.7	38	PDB header: oxidoreductase Chain: A; PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
25	d1b8mb_	Alignment	not modelled	14.7	30	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Neurotrophin
26	c6efeA_	Alignment	not modelled	14.7	59	PDB header: toxin Chain: A; PDB Molecule: kappa-conotoxin vil14a; PDBTitle: nmr solution structure of vil14a
27	c1qo8A_	Alignment	not modelled	14.5	25	PDB header: oxidoreductase Chain: A; PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
28	d2d8va1	Alignment	not modelled	13.2	42	Fold: B-box zinc-binding domain Superfamily: B-box zinc-binding domain Family: B-box zinc-binding domain
						PDB header: transcription

29	c5tuvB_	Alignment	not modelled	12.9	46	Chain: B: PDB Molecule: transcription factor e2f5; PDBTitle: crystal structure of the e2f5-dp1-p107 ternary complex
30	c3wv9D_	Alignment	not modelled	11.9	43	PDB header: transferase Chain: D: PDB Molecule: hmd co-occurring protein hcge; PDBTitle: guanylylpyridinol (gp)- and atp-bound hcge from methanothermobacter2 marburgensis
31	c5fu4B_	Alignment	not modelled	11.8	32	PDB header: sugar binding protein Chain: B: PDB Molecule: cbm74-rfgh5; PDBTitle: the complexity of the ruminococcus flavefaciens cellulosome reflects2 an expansion in glycan recognition
32	c2d8vA_	Alignment	not modelled	11.3	42	PDB header: metal binding protein Chain: A: PDB Molecule: zinc finger fyve domain-containing protein 19; PDBTitle: solution structure of the b-box domain of the zinc finger2 fyve domain-containing protein 19 from mus musculus
33	c3fptC_	Alignment	not modelled	11.0	43	PDB header: immune system Chain: C: PDB Molecule: evasin-1; PDBTitle: the crystal structure of the complex between evasin-1 and2 ccl3
34	c3ij2B_	Alignment	not modelled	11.0	28	PDB header: hormone/protein binding Chain: B: PDB Molecule: beta-nerve growth factor; PDBTitle: ligand-receptor structure
35	d2bodx1	Alignment	not modelled	10.9	17	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
36	d2aaib2	Alignment	not modelled	10.7	13	Fold: beta-Trefoil Superfamily: Ricin B-like lectins Family: Ricin B-like
37	c1keeH_	Alignment	not modelled	10.5	15	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
38	c2g9tT_	Alignment	not modelled	10.5	39	PDB header: viral protein Chain: T: PDB Molecule: PDBTitle: crystal structure of the sars coronavirus nsp10 at 2.1a
39	c6faoA_	Alignment	not modelled	10.5	24	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase family 6; PDBTitle: discovery and characterization of a thermostable gh6 endoglucanase2 from a compost metagenome
40	c4d7aA_	Alignment	not modelled	10.4	86	PDB header: ligase Chain: A: PDB Molecule: trna threonylcarbamoyladenine dehydratase; PDBTitle: crystal structure of e. coli trna n6-threonylcarbamoyladenine2 dehydratase, tcda, in complex with amp at 1.801 angstrom3 resolution
41	c1rpbA_	Alignment	not modelled	10.4	71	PDB header: replication inhibitor Chain: A: PDB Molecule: tricyclic peptide rp 71955; PDBTitle: solution structure of rp 71955, a new 21 amino acid tricyclic peptide2 active against hiv-1 virus
42	d1xjha_	Alignment	not modelled	10.4	17	Fold: HSP33 redox switch-like Superfamily: HSP33 redox switch-like Family: HSP33 redox switch-like
43	d2fyga1	Alignment	not modelled	10.3	39	Fold: Coronavirus NSP10-like Superfamily: Coronavirus NSP10-like Family: Coronavirus NSP10-like
44	d1vzya2	Alignment	not modelled	10.1	30	Fold: HSP33 redox switch-like Superfamily: HSP33 redox switch-like Family: HSP33 redox switch-like
45	c1rpcA_	Alignment	not modelled	9.9	71	PDB header: replication inhibitor Chain: A: PDB Molecule: tricyclic peptide rp 71955; PDBTitle: solution structure of rp 71955, a new 21 amino acid tricyclic peptide2 active against hiv-1 virus
46	d1vm8a_	Alignment	not modelled	9.7	24	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
47	c2ro1A_	Alignment	not modelled	9.5	20	PDB header: transcription Chain: A: PDB Molecule: transcription intermediary factor 1-beta; PDBTitle: nmr solution structures of human kap1 phd finger-bromodomain
48	c2mekA_	Alignment	not modelled	9.3	21	PDB header: metal binding protein Chain: A: PDB Molecule: n-terminal domain of bilbo1; PDBTitle: n-terminal domain of bilbo1 from trypanosoma brucei
49	d1hcfa_	Alignment	not modelled	9.1	33	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Neurotrophin
50	c3p1mG_	Alignment	not modelled	9.0	33	PDB header: electron transport Chain: G: PDB Molecule: adrenodoxin, mitochondrial; PDBTitle: crystal structure of human ferredoxin-1 (fdx1) in complex with iron-2 sulfur cluster
51	c2vxoB_	Alignment	not modelled	8.8	30	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
52	c4pwuC_	Alignment	not modelled	8.8	40	PDB header: signaling protein Chain: C: PDB Molecule: modulator protein mzra; PDBTitle: crystal structure of a modulator protein mzra (kpn_03524) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 2.45 a3 resolution
53	c3higB_	Alignment	not modelled	8.8	38	PDB header: oxidoreductase Chain: B: PDB Molecule: amiloride-sensitive amine oxidase; PDBTitle: crystal structure of human diamine oxidase in complex with the2 inhibitor berenil
54	c3uowB_	Alignment	not modelled	8.8	26	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from

						plasmodium2 falciparum
55	c3gucB	Alignment	not modelled	8.6	86	PDB header: transferase Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: human ubiquitin-activating enzyme 5 in complex with amppnp
56	c3lxfC	Alignment	not modelled	8.6	50	PDB header: metal binding protein Chain: C: PDB Molecule: ferredoxin; PDBTitle: crystal structure of [2Fe-2S] ferredoxin arx from novosphingobium2 aromaticivorans
57	c4lu2A	Alignment	not modelled	8.5	33	PDB header: odorant-binding protein Chain: A: PDB Molecule: 10.7 kda salivary protein; PDBTitle: structure of ljm19
58	c3cnfT	Alignment	not modelled	8.5	47	PDB header: virus Chain: T: PDB Molecule: vp3; PDBTitle: 3.88 angstrom structure of cytoplasmic polyhedrosis virus2 by cryo-electron microscopy
59	c6h77B	Alignment	not modelled	8.5	39	PDB header: signaling protein Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: e1 enzyme for ubiquitin like protein activation in complex with ubl
60	d1bkba1	Alignment	not modelled	8.5	29	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: eIF5a N-terminal domain-like
61	d2i1sa1	Alignment	not modelled	8.4	17	Fold: MM3350-like Superfamily: MM3350-like Family: MM3350-like
62	d1e9ma	Alignment	not modelled	8.4	32	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
63	d1y88a1	Alignment	not modelled	8.3	45	Fold: SAM domain-like Superfamily: Rad51 N-terminal domain-like Family: Hypothetical protein AF1548, C-terminal domain
64	c4hceA	Alignment	not modelled	8.2	55	PDB header: cell cycle Chain: A: PDB Molecule: cell division control protein 13; PDBTitle: crystal structure of the telomeric saccharomyces cerevisiae cdc13 ob22 domain
65	c5fu7D	Alignment	not modelled	8.2	50	PDB header: gene regulation Chain: D: PDB Molecule: nanos, isoform b; PDBTitle: drosophila nanos nbr peptide bound to the not module2 of the human ccr4-not complex
66	c1h32A	Alignment	not modelled	8.2	11	PDB header: electron transfer Chain: A: PDB Molecule: diheme cytochrome c; PDBTitle: reduced soxax complex from rhodovulum sulfidophilum
67	c4owlA	Alignment	not modelled	8.1	15	PDB header: toxin Chain: A: PDB Molecule: cytolysin; PDBTitle: crystal structure of the vibrio vulnificus hemolysin/cytolysin beta-2 trefoil lectin with n-acetyl-d-lactosamine bound
68	c1gpmD	Alignment	not modelled	8.1	22	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
69	c2ywjA	Alignment	not modelled	8.0	36	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
70	c1zfnA	Alignment	not modelled	7.9	57	PDB header: transferase Chain: A: PDB Molecule: adenylyltransferase thif; PDBTitle: structural analysis of escherichia coli thif
71	c5vj7B	Alignment	not modelled	7.9	23	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin-nadp(+) reductase subunit alpha; PDBTitle: ferredoxin nadp oxidoreductase (xfn)
72	c5cl2A	Alignment	not modelled	7.9	17	PDB header: protein binding Chain: A: PDB Molecule: sporulation-control protein spo0m; PDBTitle: crystal structure of spo0m, sporulation control protein, from bacillus2 subtilis.
73	c5ts4A	Alignment	not modelled	7.8	29	PDB header: de novo protein Chain: A: PDB Molecule: denovo ntf2; PDBTitle: crystal structure of a de novo designed protein with curved beta-sheet
74	c1x4iA	Alignment	not modelled	7.8	53	PDB header: cell adhesion Chain: A: PDB Molecule: inhibitor of growth protein 3; PDBTitle: solution structure of phd domain in inhibitor of growth2 protein 3 (ing3)
75	c3mw3A	Alignment	not modelled	7.7	12	PDB header: cell adhesion Chain: A: PDB Molecule: neurexin-2-beta; PDBTitle: crystal structure of beta-neurexin 2 with the splice insert 4
76	c4bmaB	Alignment	not modelled	7.6	29	PDB header: transferase Chain: B: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: structural of aspergillus fumigatus udp-n-acetylglucosamine2 pyrophosphorylase
77	c3tqiB	Alignment	not modelled	7.6	22	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
78	c3a9fA	Alignment	not modelled	7.5	22	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c; PDBTitle: crystal structure of the c-terminal domain of cytochrome cz from2 chlorobium tepidum
79	c1w7cA	Alignment	not modelled	7.4	31	PDB header: oxidoreductase Chain: A: PDB Molecule: lysyl oxidase; PDBTitle: pplo at 1.23 angstroms

80	c3u6gB_	Alignment	not modelled	7.4	31	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein duf4425; PDBTitle: crystal structure of a domain of unknown function, duf4425 (bv_u_3708)2 from bacteroides vulgatus atcc 8482 at 1.35 a resolution
81	c4divH_	Alignment	not modelled	7.2	22	PDB header: viral protein Chain: H: PDB Molecule: orf48; PDBTitle: the structure of a 1.8 mda viral genome injection device suggests2 alternative infection mechanisms
82	d1qja_	Alignment	not modelled	7.2	16	Fold: EF Hand-like Superfamily: EF-hand Family: Eps15 homology domain (EH domain)
83	c1lf6A_	Alignment	not modelled	7.2	33	PDB header: hydrolase Chain: A: PDB Molecule: glucoamylase; PDBTitle: crystal structure of bacterial glucoamylase
84	c3h9gA_	Alignment	not modelled	7.1	67	PDB header: transferase/antibiotic Chain: A: PDB Molecule: mccb protein; PDBTitle: crystal structure of e. coli mccb + mcca-n7isoasn
85	d1b9ra_	Alignment	not modelled	7.1	37	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin-related
86	c1n9eA_	Alignment	not modelled	7.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: lysyl oxidase; PDBTitle: crystal structure of pichia pastoris lysyl oxidase pplo
87	d1jv1a_	Alignment	not modelled	7.0	24	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
88	c1vzyA_	Alignment	not modelled	7.0	30	PDB header: chaperone Chain: A: PDB Molecule: 33 kda chaperonin; PDBTitle: crystal structure of the bacillus subtilis hsp33
89	d1s16a1	Alignment	not modelled	6.9	32	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: DNA gyrase/MutL, second domain
90	c4tuB_	Alignment	not modelled	6.9	26	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin; PDBTitle: crystal structure of ferredoxin from rhodospseudomonas palustris haa2
91	c5zwoW_	Alignment	not modelled	6.8	50	PDB header: splicing Chain: W: PDB Molecule: 23 kda u4/u6.u5 small nuclear ribonucleoprotein component; PDBTitle: cryo-em structure of the yeast b complex at average resolution of 3.92 angstrom
92	c2n99A_	Alignment	not modelled	6.8	38	PDB header: neuropeptide Chain: A: PDB Molecule: ly-6/neurotoxin-like protein 1; PDBTitle: solution structure of the slurp-2, a secreted isoform of lynx1
93	c3jtcD_	Alignment	not modelled	6.7	41	PDB header: blood clotting Chain: D: PDB Molecule: vitamin k-dependent protein c; PDBTitle: importance of mg2+ in the ca2+-dependent folding of the gamma-2 carboxyglutamic acid domains of vitamin k-dependent clotting and3 anticlotting proteins
94	c6az5A_	Alignment	not modelled	6.7	42	PDB header: sugar binding protein Chain: A: PDB Molecule: alpha-amylase; PDBTitle: crystal structure of cbmd (family cbm41) from eubacterium rectale2 amy13k
95	c5o9zN_	Alignment	not modelled	6.6	50	PDB header: splicing Chain: N: PDB Molecule: zinc finger matr-in-type protein 2; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for2 activation (b complex)
96	c2ywcC_	Alignment	not modelled	6.6	38	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
97	d1xx6a2	Alignment	not modelled	6.5	19	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Type II thymidine kinase zinc finger
98	c3jtcC_	Alignment	not modelled	6.5	41	PDB header: blood clotting Chain: C: PDB Molecule: vitamin k-dependent protein c; PDBTitle: importance of mg2+ in the ca2+-dependent folding of the gamma-2 carboxyglutamic acid domains of vitamin k-dependent clotting and3 anticlotting proteins
99	c1qvD_	Alignment	not modelled	6.5	41	PDB header: blood clotting Chain: D: PDB Molecule: vitamin-k dependent protein c; PDBTitle: crystal structure of the endothelial protein c receptor with2 phospholipid in the groove in complex with gla domain of protein c.