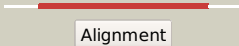



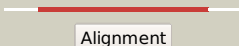

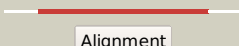
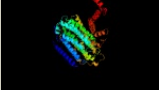
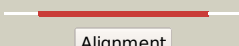

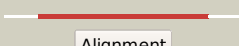

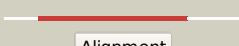


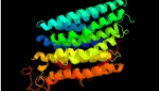

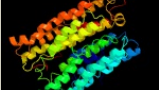




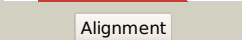

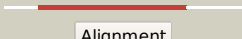

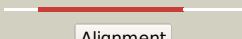












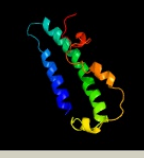
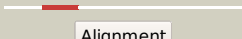
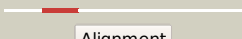

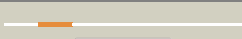

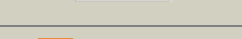
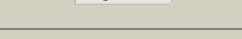
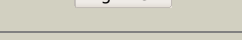


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0083 (-) _90397_92319
Date	Tue Jul 23 14:50:12 BST 2019
Unique Job ID	cae352acefff2b6f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4heaT_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: T; PDB Molecule: nadh-quinone oxidoreductase subunit 12; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
2	c3rkoL_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: L; PDB Molecule: nadh-quinone oxidoreductase subunit I; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
3	c6humF_	 Alignment		100.0	22	PDB header: proton transport Chain: F; PDB Molecule: nadh dehydrogenase subunit 5; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
4	c6gcs5_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: 5; PDB Molecule: nd5 subunit (nu5m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
5	c6g2jL_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: L; PDB Molecule: nadh-ubiquinone oxidoreductase chain 5; PDBTitle: mouse mitochondrial complex i in the active state
6	c5ldwL_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: L; PDB Molecule: nadh-ubiquinone oxidoreductase chain 5; PDBTitle: structure of mammalian respiratory complex i, class1
7	c3rkoM_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: M; PDB Molecule: nadh-quinone oxidoreductase subunit m; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
8	c6humB_	 Alignment		100.0	19	PDB header: proton transport Chain: B; PDB Molecule: nad(p)h-quinone oxidoreductase subunit 2; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
9	c6gcs4_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: 4; PDB Molecule: nd4 subunit (nu4m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
10	c6humD_	 Alignment		100.0	21	PDB header: proton transport Chain: D; PDB Molecule: nad(p)h-quinone oxidoreductase chain 4 1; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
11	c6cfwH_	 Alignment		100.0	26	PDB header: membrane protein Chain: H; PDB Molecule: monovalent cation/h+ antiporter subunit d; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase

12	c4he8M_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-quinone oxidoreductase subunit 13; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
13	c3rkoN_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-quinone oxidoreductase subunit n; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
14	c5ldwM_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4; PDBTitle: structure of mammalian respiratory complex i, class1
15	c4he8I_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: I: PDB Molecule: nadh-quinone oxidoreductase subunit 14; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
16	c6gcs2_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: 2: PDB Molecule: nd2 subunit (nu2m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
17	c5xtdi_	 Alignment		100.0	16	PDB header: oxidoreductase/electron transport Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: cryo-em structure of human respiratory complex i
18	c6g2jN_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-ubiquinone oxidoreductase chain 2; PDBTitle: mouse mitochondrial complex i in the active state
19	c5ldwN_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-ubiquinone oxidoreductase chain 2; PDBTitle: structure of mammalian respiratory complex i, class1
20	c5lc5H_	 Alignment		92.5	12	PDB header: oxidoreductase Chain: H: PDB Molecule: nadh-ubiquinone oxidoreductase chain 1; PDBTitle: structure of mammalian respiratory complex i, class2
21	c6cfwM_	 Alignment	not modelled	92.3	12	PDB header: membrane protein Chain: M: PDB Molecule: mbh13 nadh dehydrogenase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
22	c6gcs1_	 Alignment	not modelled	92.1	8	PDB header: oxidoreductase Chain: 1: PDB Molecule: nd1 subunit (nu1m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
23	c6humA_	 Alignment	not modelled	90.7	14	PDB header: proton transport Chain: A: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 1; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
24	c6humE_	 Alignment	not modelled	89.3	9	PDB header: proton transport Chain: E: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 4l; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
25	c3rkoK_	 Alignment	not modelled	86.9	16	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit k; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
26	c4heaK_	 Alignment	not modelled	86.6	17	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-quinone oxidoreductase subunit 11; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
27	c6cfwl_	 Alignment	not modelled	80.6	20	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
28	c6gcsL_	 Alignment	not modelled	79.5	16	PDB header: oxidoreductase Chain: L: PDB Molecule: nd4l subunit (nulm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia

						lipolytica
29	c6cfwG	Alignment	not modelled	78.5	15	PDB header: membrane protein Chain: G: PDB Molecule: monovalent cation/h+ antiporter subunit c; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
30	c6g2jK	Alignment	not modelled	58.6	17	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4l; PDBTitle: mouse mitochondrial complex i in the active state
31	c2l3iA	Alignment	not modelled	33.9	58	PDB header: antimicrobial protein Chain: A: PDB Molecule: aoxki4a, antimicrobial peptide in spider venom; PDBTitle: ooxki4a, spider derived antimicrobial peptide
32	d1s1qa	Alignment	not modelled	31.8	31	Fold: UBC-like Superfamily: UBC-like Family: UEV domain
33	d1a6qa1	Alignment	not modelled	31.8	17	Fold: Another 3-helical bundle Superfamily: Protein serine/threonine phosphatase 2C, C-terminal domain Family: Protein serine/threonine phosphatase 2C, C-terminal domain
34	c5lc5K	Alignment	not modelled	21.4	14	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4l; PDBTitle: structure of mammalian respiratory complex i, class2
35	c5ldwK	Alignment	not modelled	21.4	14	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4l; PDBTitle: structure of mammalian respiratory complex i, class1
36	d1o8bb1	Alignment	not modelled	21.4	13	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
37	c4x84C	Alignment	not modelled	18.7	15	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
38	c6humC	Alignment	not modelled	16.8	8	PDB header: proton transport Chain: C: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 3; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
39	c5lnkm	Alignment	not modelled	16.2	23	PDB header: oxidoreductase Chain: M: PDB Molecule: mitochondrial complex i, nd4 subunit; PDBTitle: entire ovine respiratory complex i
40	c5ldwb	Alignment	not modelled	15.3	23	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class1
41	c5o31b	Alignment	not modelled	15.3	23	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: mitochondrial complex i in the deactive state
42	c5ldxb	Alignment	not modelled	15.3	23	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class3.
43	c5lc5b	Alignment	not modelled	15.3	23	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class2
44	c2kseA	Alignment	not modelled	15.3	22	PDB header: transferase Chain: A: PDB Molecule: sensor protein qsec; PDBTitle: backbone structure of the membrane domain of e. coli histidine kinase2 receptor qsec, center for structures of membrane proteins (csm)3 target 4311c
45	c5o60M	Alignment	not modelled	15.2	45	PDB header: ribosome Chain: M: PDB Molecule: 50s ribosomal protein l15; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
46	c3fq6A	Alignment	not modelled	14.8	47	PDB header: transferase Chain: A: PDB Molecule: methyltransferase; PDBTitle: the crystal structure of a methyltransferase domain from bacteroides2 thetaiotaomicron vpi
47	c6odmK	Alignment	not modelled	14.4	33	PDB header: viral protein Chain: K: PDB Molecule: capsid vertex component 2; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
48	c4w6vA	Alignment	not modelled	13.5	8	PDB header: transport protein Chain: A: PDB Molecule: di-/tripeptide transporter; PDBTitle: crystal structure of a peptide transporter from yersinia2 enterocolitica at 3 a resolution
49	c4lnsA	Alignment	not modelled	13.0	25	PDB header: ligase Chain: A: PDB Molecule: asparagine synthetase a; PDBTitle: crystal structure of asparagine synthetase a (asna) from trypanosoma2 brucei
50	d2gf4a1	Alignment	not modelled	12.6	20	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Vng1086c-like Family: Vng1086c-like
51	d3d37a2	Alignment	not modelled	12.5	50	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: Baseplate protein-like
52	d1j4na	Alignment	not modelled	12.3	14	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
53	c5lc5A	Alignment	not modelled	12.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-ubiquinone oxidoreductase chain 3; PDBTitle: structure of mammalian respiratory complex i, class2
54	c3na2C	Alignment	not modelled	11.6	75	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function from

						mine drainage2 metagenome leptospirillum rubarum
55	c3c25A_	Alignment	not modelled	11.5	67	PDB header: hydrolase/dna Chain: A: PDB Molecule: noti restriction endonuclease; PDBTitle: crystal structure of noti restriction endonuclease bound to cognate2 dna
56	c4j15A_	Alignment	not modelled	11.5	50	PDB header: ligase Chain: A: PDB Molecule: aspartate--trna ligase, cytoplasmic; PDBTitle: crystal structure of human cytosolic aspartyl-trna synthetase, a2 component of multi-trna synthetase complex
57	d1n9wa2	Alignment	not modelled	11.4	50	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
58	c1n9wA_	Alignment	not modelled	11.3	50	PDB header: biosynthetic protein Chain: A: PDB Molecule: aspartyl-trna synthetase 2; PDBTitle: crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
59	d1bcce2	Alignment	not modelled	11.3	21	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
60	c2kwtA_	Alignment	not modelled	10.6	50	PDB header: viral protein Chain: A: PDB Molecule: protease ns2-3; PDBTitle: solution structure of ns2 [27-59]
61	c2voyK_	Alignment	not modelled	10.5	18	PDB header: hydrolase Chain: K: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
62	c4o2dB_	Alignment	not modelled	10.3	38	PDB header: ligase Chain: B: PDB Molecule: aspartate--trna ligase; PDBTitle: crystal structure of aspartyl-trna synthetase from mycobacterium2 smegmatis with bound aspartic acid
63	c3bjuB_	Alignment	not modelled	10.3	63	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna synthetase
64	c4ddpA_	Alignment	not modelled	10.1	36	PDB header: membrane protein Chain: A: PDB Molecule: beclin-1; PDBTitle: crystal structure of beclin 1 evolutionarily conserved domain(ecd)
65	c5elnC_	Alignment	not modelled	10.0	50	PDB header: ligase Chain: C: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from cryptosporidium parvum2 complexed with l-lysine
66	c3vp7A_	Alignment	not modelled	10.0	45	PDB header: protein transport Chain: A: PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: crystal structure of the beta-alpha repeated, autophagy-specific2 (bara) domain of vps30/atg6
67	c1r6rA_	Alignment	not modelled	9.9	30	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: solution structure of dengue virus capsid protein reveals a2 new fold
68	d1r6ra_	Alignment	not modelled	9.9	30	Fold: Flavivirus capsid protein C Superfamily: Flavivirus capsid protein C Family: Flavivirus capsid protein C
69	c1vw48_	Alignment	not modelled	9.9	31	PDB header: ribosome Chain: 8: PDB Molecule: 54s ribosomal protein l13, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
70	c1b8aB_	Alignment	not modelled	9.7	50	PDB header: ligase Chain: B: PDB Molecule: protein (aspartyl-trna synthetase); PDBTitle: aspartyl-trna synthetase
71	d1uzxa_	Alignment	not modelled	9.6	27	Fold: UBC-like Superfamily: UBC-like Family: UEV domain
72	c3gm1A_	Alignment	not modelled	9.5	24	PDB header: transferase Chain: A: PDB Molecule: protein tyrosine kinase 2 beta; PDBTitle: crystal structure of the focal adhesion targeting (fat)2 domain of pyk2 in complex with paxillin l4 motif-derived3 peptides
73	c6et5s_	Alignment	not modelled	9.4	10	PDB header: photosynthesis Chain: S: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
74	c6et5y_	Alignment	not modelled	9.4	10	PDB header: photosynthesis Chain: Y: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
75	c6et5d_	Alignment	not modelled	9.4	10	PDB header: photosynthesis Chain: D: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
76	c6et5g_	Alignment	not modelled	9.4	10	PDB header: photosynthesis Chain: G: PDB Molecule: light-harvesting protein b-1015 beta chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
77	c6et5l_	Alignment	not modelled	9.4	10	PDB header: photosynthesis Chain: I: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
78	c6et52_	Alignment	not modelled	9.4	10	PDB header: photosynthesis Chain: 2: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
79	c6et5v_	Alignment	not modelled	9.4	10	PDB header: photosynthesis Chain: V: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
80	c6et5o_	Alignment	not modelled	9.4	10	PDB header: photosynthesis Chain: O: PDB Molecule: light-harvesting protein b-1015 gamma

80	c6et3U	Alignment	not modelled	9.4	10	chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis PDB header: photosynthesis
81	c6et5X	Alignment	not modelled	9.4	10	Chain: X: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis PDB header: photosynthesis
82	c6et5p	Alignment	not modelled	9.4	10	Chain: P: PDB Molecule: light-harvesting protein b-1015 alpha chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis PDB header: photosynthesis
83	c6et5U	Alignment	not modelled	9.4	10	Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis PDB header: photosynthesis
84	c6et5j	Alignment	not modelled	9.4	10	Chain: J: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis PDB header: photosynthesis
85	c6et5a	Alignment	not modelled	9.4	10	Chain: A: PDB Molecule: PDBTitle: reaction centre light harvesting complex 1 from blc. viridis PDB header: photosynthesis
86	c6et55	Alignment	not modelled	9.4	10	Chain: 5: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis PDB header: photosynthesis
87	c6et5R	Alignment	not modelled	9.4	10	Chain: R: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis PDB header: photosynthesis
88	c6et5m	Alignment	not modelled	9.4	10	Chain: M: PDB Molecule: reaction center protein m chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis PDB header: photosynthesis
89	d1ppje2	Alignment	not modelled	9.3	11	Fold: Single transmembrane helix Superfamily: ISP transmembrane anchor Family: ISP transmembrane anchor
90	c1x55A	Alignment	not modelled	9.1	38	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase; PDBTitle: crystal structure of asparaginyl-trna synthetase from pyrococcus2 horikoshii complexed with asparaginyl-adenylate analogue
91	c2xgtB	Alignment	not modelled	9.1	25	PDB header: ligase Chain: B: PDB Molecule: asparaginyl-trna synthetase, cytoplasmic; PDBTitle: asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
92	c2p64B	Alignment	not modelled	9.1	18	PDB header: ligase Chain: B: PDB Molecule: f-box/wd repeat protein 1a; PDBTitle: d domain of b-trcp
93	c6ns0A	Alignment	not modelled	9.1	50	PDB header: ligase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from chlamydia trachomatis2 complexed with l-lysine and cladosporin
94	c4gj4A	Alignment	not modelled	9.1	20	PDB header: lyase Chain: A: PDB Molecule: soluble guanylyl cyclase alpha-1 subunit; PDBTitle: the crystal structure of the soluble guanylate cyclase pas alpha2 domain from manduca sexta
95	d1k04a	Alignment	not modelled	9.0	24	Fold: Four-helical up-and-down bundle Superfamily: FAT domain of focal adhesion kinase Family: FAT domain of focal adhesion kinase
96	c4doyE	Alignment	not modelled	8.9	18	PDB header: oxidoreductase Chain: E: PDB Molecule: dibenzothiophene desulfurization enzyme c; PDBTitle: crystal structure of dibenzothiophene desulfurization enzyme c
97	c2l6hA	Alignment	not modelled	8.8	24	PDB header: transferase,cell adhesion Chain: A: PDB Molecule: focal adhesion kinase 1, linker, paxillin; PDBTitle: fat domain of focal adhesion kinase tethered to ld4 motif of paxillin2 via ggs linker
98	c2p04B	Alignment	not modelled	8.7	27	PDB header: transferase Chain: B: PDB Molecule: signal transduction histidine kinase; PDBTitle: 2.1 ang structure of the dimerized pas domain of signal transduction2 histidine kinase from nostoc punctiforme pcc 73102 with homology to3 the h-noxa/h-noba domain of the soluble guanylyl cyclase
99	c5xixD	Alignment	not modelled	8.7	25	PDB header: ligase Chain: D: PDB Molecule: asparagine--trna ligase, cytoplasmic; PDBTitle: the canonical domain of human asparaginyl-trna synthetase