MPI
Bioinformatics
Toolkit

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HHpred ?

Job ID: Madi_gp59, Parent Job ID: 7512949, Created: 8 minutes ago

Input Parameters Results Raw Output Probability Plot Query Template MSA Query MSA

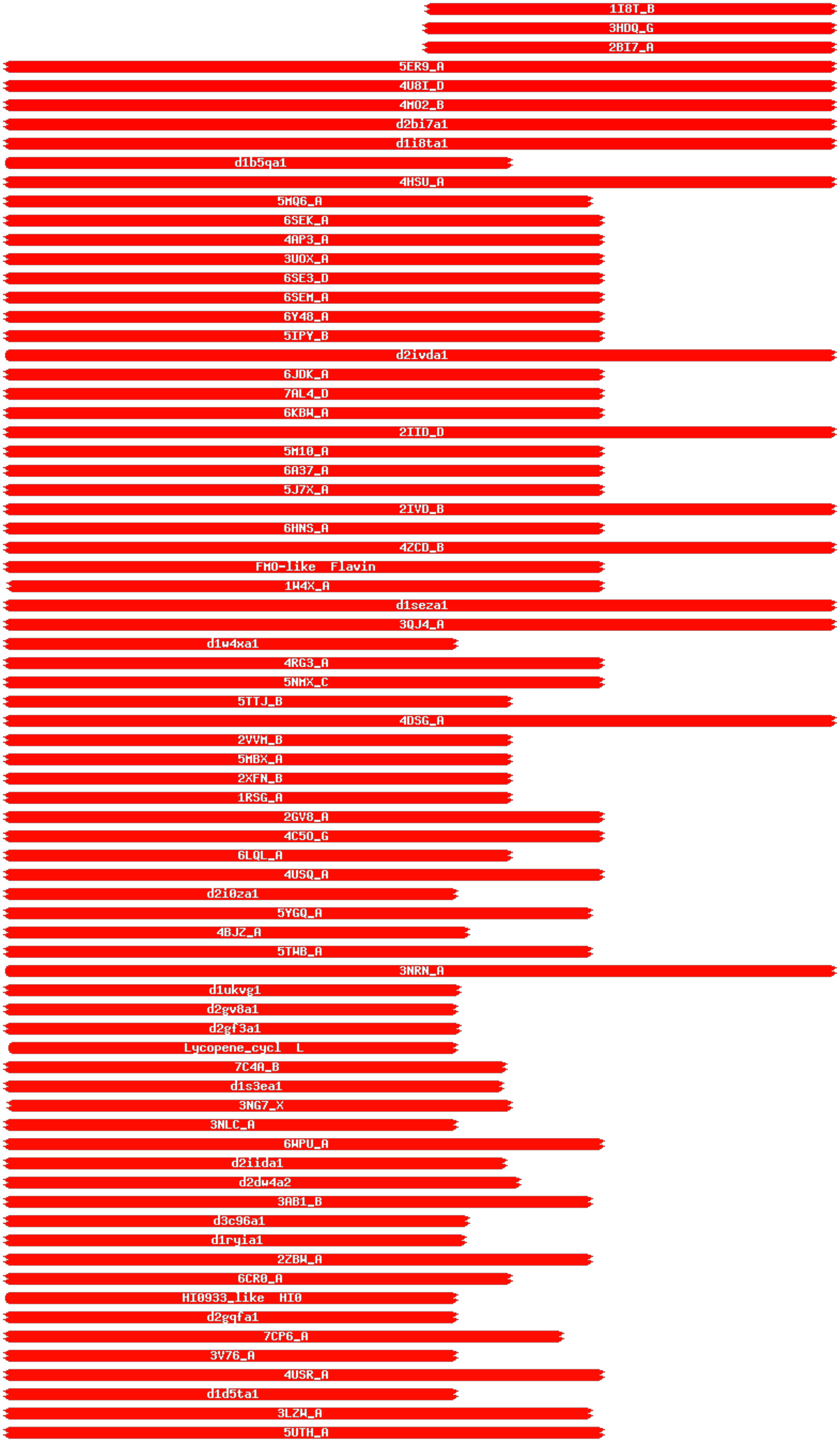
Vis Hits Aln | Select All Forward Forward Query A3M Model using selection Download HHR Color Seqs Wrap Seqs

Number of Hits: **250**
Query MSA diversity (Neff): **9.65976**

Visualization

Resubmit Section

148 290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2BI7_A
5ER9_A
4U8I_D
4M02_B
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d1i8ta1
d1b5qa1
4HSU_A
5MQ6_A
6SEK_A
4AP3_A
3UOX_A
6SE3_D
6SEM_A
6Y48_A
5IPY_B
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6JDK_A
7AL4_D
6KBW_A
2IID_D
5M10_A
6A37_A
5J7X_A
2IVD_B
6HNS_A
4ZCD_B
FMO-like Flavin
1W4X_A
d1seza1
3QJ4_A
d1w4xa1
4RG3_A
5NMX_C
5TTJ_B
4DSG_A
2VVM_B
5MBX_A
2XFN_B
1RSG_A
2GV8_A
4C50_G
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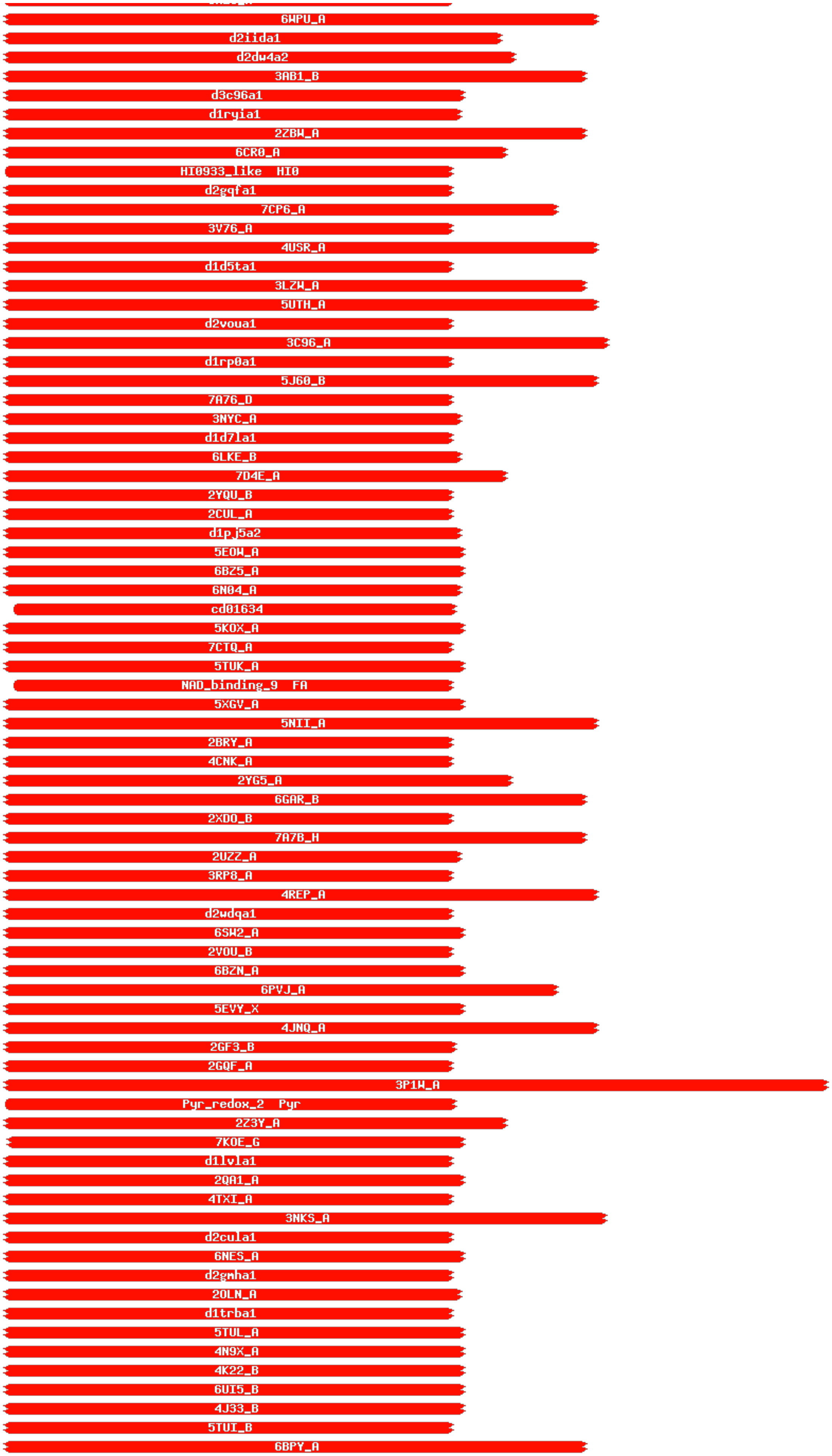
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7A76_D
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NAD_binding_9 FA
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5NII_A
2BRY_A
4CNK_A
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2XDO_B
7A7B_H
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3RP8_A
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6BZN_A
6PVJ_A
5EVY_X
4JNQ_A
2GF3_B
2GQF_A
3P1W_A
Pyr_redox_2 Pyr
2Z3Y_A
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2OLN_A
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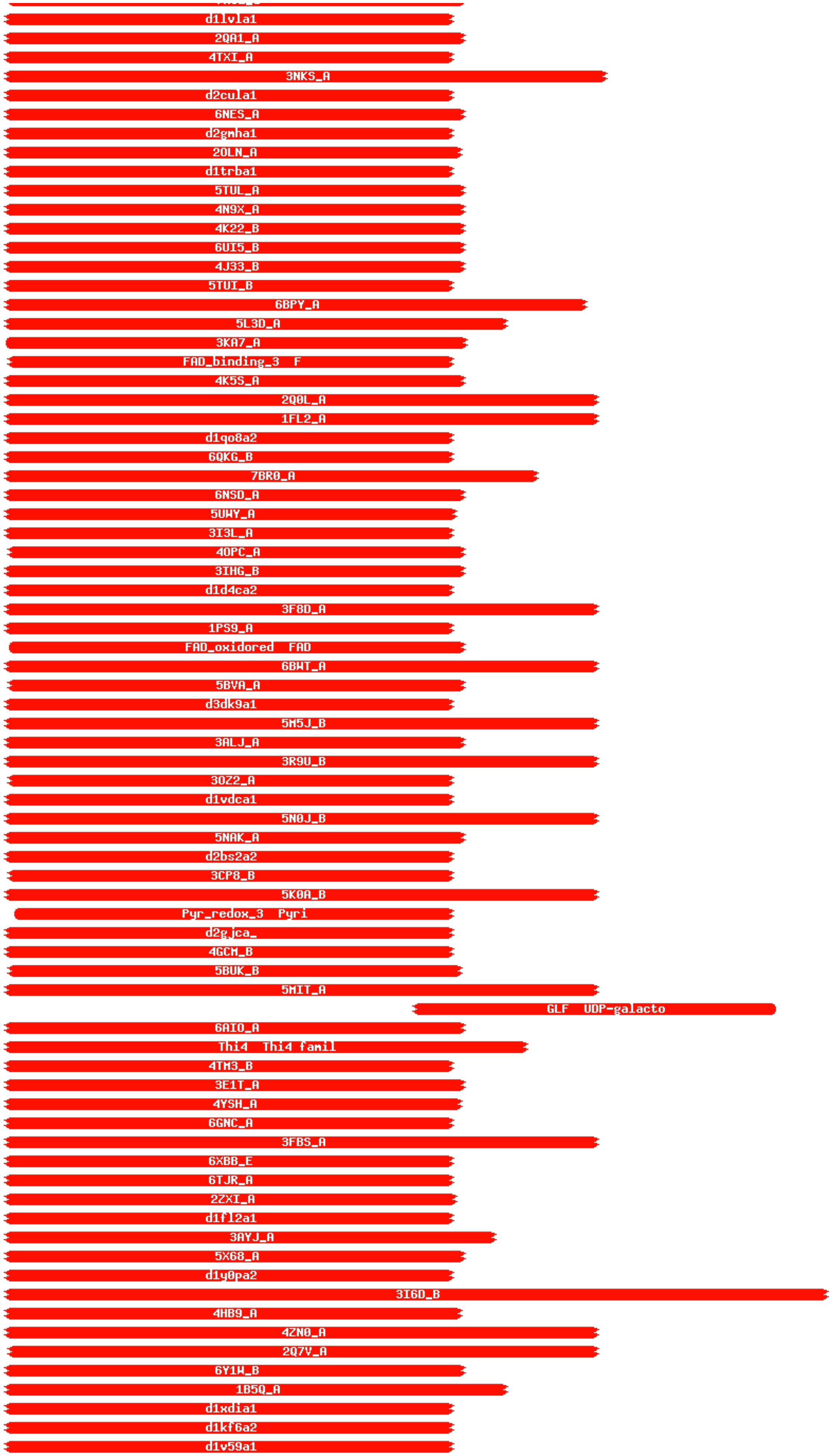
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3KA7_A
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6NSD_A
5UWY_A
3I3L_A
4OPC_A
3IHG_B
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3F8D_A
1PS9_A
FAD_oxidored FAD
6BWT_A
5BVA_A
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5K0A_B
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4GCM_B
5BUK_B
5MIT_A
GLF UDP-galacto
6AIO_A
Thi4 Thi4 famil
4TM3_B
3E1T_A
4YSH_A
6GNC_A
3FBS_A
6XBB_E
6TJR_A
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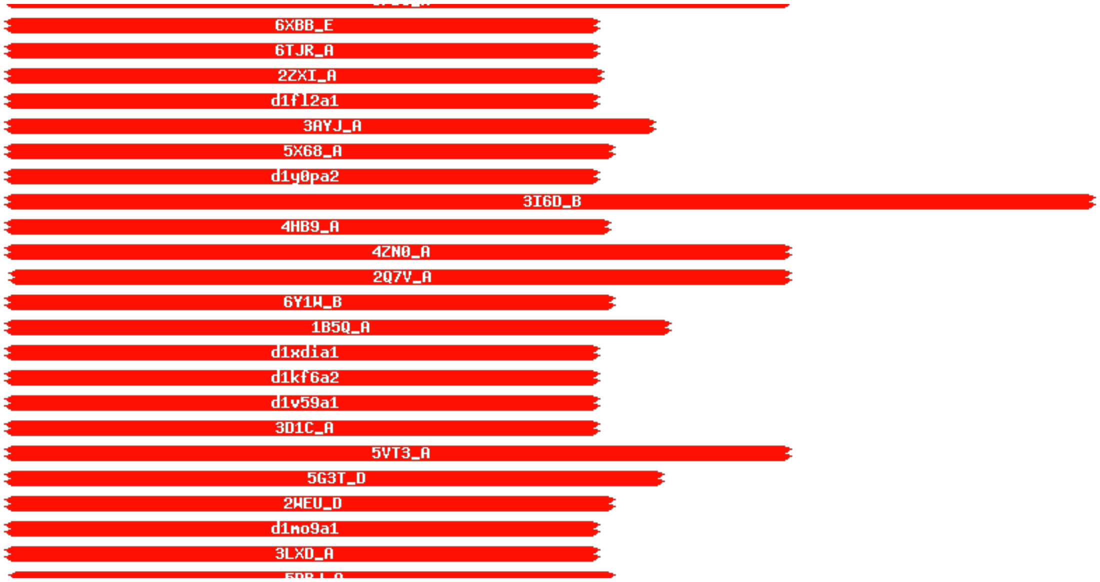

Hitlist

Show 25 Entries Search:

Nr	Hit	Name	Probability	E-value	Score	SS	Aligned cols	Target Length
☐ 1	1I8T_B	UDP-GALACTOPYRANOSE MUTASE; Rossmann Fold, FAD, UDP-galactopyranose, mutase, contractase, ISOMERASE; HET: FAD; 2.4A {Esc	99.8	8.7e-19	159.17	11.5	127	367
☐ 2	3HDQ_G	UDP-galactopyranose mutase; UDP-galactopyranose mutase, Substrate and inhibitor, ISOMERASE; HET: GDU, FAD; 2.36A {Deinoc	99.75	8.2e-18	154.56	10.2	127	397
☐ 3	2BI7_A	UDP-GALACTOPYRANOSE MUTASE; FAD, FLAVOPROTEIN, ISOMERASE, LIPOPOLYSACCHARIDE BIOSYNTHESIS; HET: FAD; 2.0A {KLEBSIELLA PN	99.72	3.6e-16	143.26	14.8	127	384
☐ 4	5ER9_A	UDP-galactopyranose mutase; galactofuranose, enzyme conformation, ISOMERASE; HET: NO3, SO4, UDP, FAD; 1.689A {Mycobacter	99.7	1.2e-16	146.9	9.2	244	400
☐ 5	4U8I_D	UDP-galactopyranose mutase; NUCLEOTIDE BINDING, MUTASE, FLAVIN ADENINE DINUCLEOTIDE BINDING, ISOMERASE; HET: EDO, SO4, F	99.65	5.5e-15	140.43	14.7	268	513
☐ 6	4MO2_B	UDP-galactopyranose mutase; UDP-N-acetylgalactopyranose mutase, UNGM, capsular polysaccharides, bifunctional, drug targe	99.56	8.5e-14	126.46	12.8	231	368
☐ 7	d2bi7a1	c.4.1.3 (A:2-247,A:317-384) UDP-galactopyranose mutase, N-terminal domain {Klebsiella pneumoniae [TaxId: 573]}	99.54	8.3e-15	130.73	3.7	212	315
☐ 8	d1i8ta1	c.4.1.3 (A:1-244,A:314-367) UDP-galactopyranose mutase, N-terminal domain {Escherichia coli [TaxId: 562]}	99.5	1e-13	122.77	7.5	181	299

Nr	Hit	Name	Probability	E-value	Score	SS	Aligned cols	Target Length
☐ 9	d1b5qa1	c.3.1.2 (A:5-293,A:406-463) Polyamine oxidase {Maize (Zea mays) [TaxId: 4577]}	99.33	5.2e-11	107.07	13.1	164	348
☐ 10	4HSU_A	Lysine-specific histone demethylase 1B; histone demethylase, OXIDOREDUCTASE; HET: FAD; 1.988A {Homo sapiens}	99.29	1.7e-10	115.87	15.7	262	776
☐ 11	5MQ6_A	Pyridine nucleotide-disulfide oxidoreductase-like protein; Flavin, monooxygenase, Baeyer-Villiger, oxygen, biocatalysis,	99.29	1.4e-10	114.27	14.6	168	655
☐ 12	6SEK_A	Ancestral Flavin-containing monooxygenase 5; Flavin, enzyme, membrane protein, Ancestral Sequence Reconstruction, OXIDOR	99.29	2.8e-10	109.43	16.2	178	533
☐ 13	4AP3_A	STEROID MONOOXYGENASE; OXIDOREDUCTASE, BAEYER-VILLIGER; HET: SO4, FAD, NAP; 2.39A {RHODOCOCCUS RHODOCHROUS}	99.28	3.5e-10	109.15	16.7	175	549
☐ 14	3UOX_A	OTEMO; Baeyer-Villiger monooxygenase, OXIDOREDUCTASE; HET: FAD; 1.956A {Pseudomonas putida}	99.28	3.2e-10	109.15	15.9	175	545
☐ 15	6SE3_D	Ancestral Flavin-containing monooxygenase (FMO) 3-6; Flavin, enzyme, membrane protein, Ancestral Sequence Reconstruction	99.27	3.6e-10	108.69	16.2	178	532
☐ 16	6SEM_A	Ancestral Flavin-containing monooxygenase (FMO) 2; Flavin, enzyme, membrane protein, Ancestral Sequence Reconstruction;	99.26	3.9e-10	108.47	15.9	178	535
☐ 17	6Y48_A	Baeyer-Villiger monooxygenase; Baeyer-Villiger monooxygenase, FLAVOPROTEIN; HET: FAD, NAP; 2.087A {Aspergillus flavus NR	99.26	2.6e-10	110.31	14.6	173	561
☐ 18	5IPY_B	Flavin-containing monooxygenase; flavin-containing monooxygenase, FLAVOPROTEIN; HET: NAP, FAD; 1.5A {Roseovarius nubinhi	99.24	5.4e-10	105.39	15.2	190	453
☐ 19	d2ivda1	c.3.1.2 (A:10-306,A:415-464) Protoporphyrinogen oxidase {Myxococcus xanthus [TaxId: 34]}	99.24	3.2e-10	102.46	13.2	216	348
☐ 20	6JDK_A	Baeyer-Villiger monooxygenase; monooxygenase, OXIDOREDUCTASE; HET: FAD; 2.495A {Parvibaculum lavamentivorans (strain DS-	99.24	3.2e-10	109.13	13.8	173	544
☐ 21	7AL4_D	Ancestral Flavin-containing monooxygenase 1 (mammalian); FMO Paired Rossman fold Xenobiotic detoxification, FLAVOPROTEIN	99.23	7e-10	106.6	15.9	178	531
☐ 22	6KBW_A	Trimethylamine monooxygenase; flavin-containing monooxygenase, FLAVOPROTEIN; HET: NAP, FAD; 1.686A {Myroides profundi}	99.23	4.9e-10	106.13	14.4	190	467
☐ 23	2IID_D	L-amino-acid oxidase; flavoenzyme, FAD binding domain, reaction mechanism, sustrate binding, OXIDOREDUCTASE; HET: PHE, N	99.23	1.5e-9	102.03	17.7	270	498
☐ 24	5M10_A	Cyclohexanone Monooxygenase from Thermocrispum municipale; Cyclohexanone monooxygenase Baeyer-Villiger monooxygenases Fl	99.21	1e-9	105.5	16	175	541

	Nr	Hit	Name	Probability	E-value	Score	SS	Aligned cols	Target Length
☐	25	6A37_A	Putative flavin-binding monooxygenase; cyclohexanone monooxygenase, FAD binding, OXIDOREDUCTASE; HET: FAD; 2.204A {Acine	99.21	1.1e-9	105.75	16	175	552

Displaying 1 to 25 of 250 hits

« ‹ 1 2 3 4 ... › »

Alignments

Template alignment | Template 3D Structure | PDBe

☐ 1. **1I8T_B UDP-GALACTOPYRANOSE MUTASE; Rossmann Fold, FAD, UDP-galactopyranose, mutase, contractase, ISOMERASE; HET: FAD; 2.4A {Escherichia coli} SCOP: c.4.1.3, d.16.1.7**

Probability: 99.8%, E-value: 8.7e-19, Score: 159.17, Aligned cols: 127, Identities: 17%, Similarity: 0.175, Template Neff: 9.8

```
Q ss_pred                 EEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCCCCCceEEEeecCcccc--
Q Q_Madi_gp59      148    SEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTSLVPWTRLSKVHGFTSI--   225 (291)
Q Consensus        148    ~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~~~~~r~~~~~~~~~~--   225 (291)
                          +.+|.||+|+|++.+.+.          ..+.++|.+..+...+.+... ..+..|+|..+.+.+|+|+++++.+...
T Consensus        222    ~~~d~vI~T~Pl~~l~~~----------~~~~l~~~~~~~~~~~~~~~~~~~-~~~~~~~~~~d~~~~~~Rv~~~~~~~~~~   290 (367)
T 1I8T_B          222    SKAHRIIYTGPIDQYFDY----------RFGALEYRSLKFETERHEFPN-FQGNAVINFTDANVPYTRIIEHKHFDYVET   290 (367)
T ss_dssp                 TTEEEEEECSCHHHHTTT----------TTCCCCEEEEEEEEEEESSSC-SSSSSEEEECCTTSSCSEEEEGGGGSCCCC
T ss_pred                 hhCCeEEEeecHHHHHhh----------ccCCCceeeEEEEEEEEcCCc-cCCCcEEEeCCCCCcceEEEEhhccCCCCC


Q ss_pred                 -------eecC------CCCCCCcceeEEecccccCCCCCCCCCCCCCEEEeccccccccCCcHHHHHHHHHHHHHhc
Q Q_Madi_gp59      226    -------EWPH------HAAQPHTQAVRVRKPLHYTPGPHQNGSPTANWLHVGRYGQFEKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus        226    -------e~~~------~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gr~g~~~~~~~~~~~~~~~~~~~~~~~~   290 (291)
                                 |+++      ...||.+.....+...+++..   ... ..||+++||+|.|+| .++|+||++++++++++
T Consensus        291    ~~~~~~~E~~~~~~~~~~~~~ypv~~~~~~~~~~~~~~~~~~~---~~~-~~nl~~~GR~g~~~y-~~m~~~i~~~~~~a~~i   363 (367)
T 1I8T_B          291    KHTVVTKEYPLEWKVGDEPYYPVNDNKNMELFKKYREL---ASR-EDKVIFGGRLAEYKY-YDMHQVISAALYQVKNI   363 (367)
T ss_dssp                 SCEEEEEEEEECCCTTSCCCEECCCHHHHHHHHHHHHH---HHH-CTTEEECSTTTTTCC-CCHHHHHHHHHHHHHHH
T ss_pred                 CcEEEEEEeeCCCCCCCCcCCccCChhhHHHHHHHHHH---Hhc-CCCEEEcccccCCCC-CCHHHHHHHHHHHHHHh
```

Template alignment | Template 3D Structure | PDBe

☐ 2. **3HDQ_G UDP-galactopyranose mutase; UDP-galactopyranose mutase, Substrate and inhibitor, ISOMERASE; HET: GDU, FAD; 2.36A {Deinococcus radiodurans}**

Probability: 99.75%, E-value: 8.2e-18, Score: 154.56, Aligned cols: 127, Identities: 16%, Similarity: 0.195, Template Neff: 9.2

```
Q ss_pred                 EEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCCCCCceEEEeecCcccc-
Q Q_Madi_gp59      147    LSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTSLVPWTRLSKVHGFTSI-   225 (291)
Q Consensus        147    ~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~~~~~r~~~~~~~~~~-   225 (291)
                          ++.+|.||+|+|++.|.+.          ..+.++|++..+..+.++.+. ..+..|+|+++++. |+|+++++|+++.
T Consensus        249    ~~~~d~visT~Pl~~l~~~----------~~~~l~~r~~~~~~~~~~~~~~~~~-~~~~~~~~~~y~~~~~-f~Ri~~~~n~~~~~   316 (397)
T 3HDQ_G          249    FIPFQHMIYTGPVDAFFDF----------CYGKLPYRSLEFRHETHDTEQ-LLPTGTVNYPNDYA-YTRVSEFKHITGQR   316 (397)
T ss_dssp                 TSCBSCEEECSCHHHHTTT----------TTCCCCEEEEEEEEEEESSSC-SSSSSEEECSSSSS-SSEEEEHHHHHCCC
T ss_pred                 hcCCCeEEEeccHHHHhhh----------hcCCCCcceEEEEEEEEchhh-cCCCeEEEccCCCC-eEEEEeHHhcCCCC


Q ss_pred                 --------eecC---CCCCCCcceeEEecccccCCCCCCCCCCCCCEEEeccccccccCCcHHHHHHHHHHHHHhc
Q Q_Madi_gp59      226    --------EWPH---HAAQPHTQAVRVRKPLHYTPGPHQNGSPTANWLHVGRYGQFEKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus        226    --------e~~~---~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gr~g~~~~~~~~~~~~~~~~~~~~~~~~   290 (291)
                                  |+++   .+.||+++.+..+....+...   ... .+||+++||+|.|+| ++||+||++|+++++++
T Consensus        317    ~~~t~l~~E~~~~~~~~~~~~p~~~~~~~~~~~~~~~~~~~~~~---~~~-~~nl~~~GR~g~~~y-~~md~~i~~~~~~a~~i   387 (397)
T 3HDQ_G          317    HHQTSVVYEYPRAEGDPYYPVPRPENAELYKKYEAL---ADA-AQDVTFVGRLATYRY-YNMDQVVAQALATFRRL   387 (397)
T ss_dssp                 CSSEEEEEEEEESSSSCCEECCSHHHHHHHHHHHHH---HHT-CTTEEECSTTTTTCC-CCHHHHHHHHHHHHHHH
T ss_pred                 CCCeEEEEEEEcCCCCCCCCCCCCHHHHHHHHHHHHH---HHH-CCCEEEeeCccCCCC-CCHHHHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDBe

☐ 3. **2BI7_A UDP-GALACTOPYRANOSE MUTASE; FAD, FLAVOPROTEIN, ISOMERASE, LIPOPOLYSACCHARIDE BIOSYNTHESIS; HET: FAD; 2.0A {KLEBSIELLA PNEUMONIAE} SCOP: d.16.1.7, c.4.1.3**

Probability: 99.72%, E-value: 3.6e-16, Score: 143.26, Aligned cols: 127, Identities: 17%, Similarity: 0.179, Template Neff: 9.2

```
Q ss_pred                 EEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCCCCCceEEEeecCcccc-
Q Q_Madi_gp59      147    LSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTSLVPWTRLSKVHGFTSI-   225 (291)
Q Consensus        147    ~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~~~~~r~~~~~~~~~~-   225 (291)
```

```
                        .+.+|.||+|+|++.|.+.          ..+.|+|+++.+..+..+.+  ..+.+|+|+++++.+|+|+++++|+++.
T Consensus       224   ~~~~d~vIsTiPl~~l~~~----------~~~~L~yr~~~~~~~~~~~~~~--~~~~~~~~~~~~~~~f~Ri~e~~n~~~~~   291 (384)
T 2BI7_A          224   RTHYDHVFYSGPLDAFYGY----------QYGRLGYRTLDFKKFTYQGD--YQGCAVMNYCSVDVPYTRITEHKYFSPWE   291 (384)
T ss_dssp              GGGSSEEEECSCHHHHTTT----------TTCCCCEEEEEEEEEEEESC--SSSSSEEEECSTTSSSSEEEEGGGGCTTS
T ss_pred              hhcCCeEEEEeeHHHHccc----------CcCCCCcceEEEEEEEeCCC--cCCCcEEEeCCCCCcceEEEeHHhCCccc


Q ss_pred              ---------eecC------CCCCCCcceeEEecccccCCCCCCCCCCCCEEEecccccccccCCcHHHHHHHHHHHHHHhc
Q Q_Madi_gp59      226   ---------EWPH------HAAQPHTQAVRVRKPLHYTPGPHQNGSPTANWLHVGRYGQFEKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus       226   ---------e~~~------~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gr~g~~~~~~~~~~~~~~~~~~~~~~~   290 (291)
                                 |++.      .+.||++..+..++++.+...   +.+ .+||+++||+|.|+| .|||+||++|+++|+++
T Consensus       292   ~~~~~~~~~e~~~~~~~~~~~~ypv~~~~~~~~~~~~~~~~~~---l~~-~~ni~~~GR~G~~~Y-~nmd~~i~~~~~~a~~i   366 (384)
T 2BI7_A          292   QHDGSVCYKEYSRACEENDIPYYPIRQMGEMALLEKYLSL---AEN-ETNITFVGRLGTYRY-LDMDVTIAEALKTAEVY   366 (384)
T ss_dssp              CCSEEEEEEEEEEECCTTCCCCEECCCHHHHHHHHHHHHH---HTT-CSSEEECHHHHTTCC-CCHHHHHHHHHHHHHHH
T ss_pred              cCCCeEEEEEeeCcccCCCcccccCChhHHHHHHHHHHHH---Hhh-cCCEEEeeCcccCcc-cCHHHHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDBe

☐ **4.** **5ER9_A UDP-galactopyranose mutase; galactofuranose, enzyme conformation, ISOMERASE; HET: NO3, SO4, UDP, FAD; 1.689A {Mycobacterium smegmatis}**

Probability: 99.7%, E-value: 1.2e-16, Score: 146.9, Aligned cols: 244, Identities: 15%, Similarity: 0.13, Template Neff: 10.1

```
Q ss_pred              CeEEEECCCHHHHHHHHHHHHc-CCeEEEECCCCCccccchhHhcCCCCC---CCcc-----------------------
Q Q_Madi_gp59      1     MTIAILGCGPTGLLAAHACTLE-GYDVAIFSRKRKSELFGSQYLHNPIPG---LTPE-----------------------   53 (291)
Q Consensus       1     ~~V~IIGaG~aGl~aA~~L~~~-g~~v~i~E~~~~~~~~G~~~~~~~~~~---~~~~-----------------------   53 (291)
                        ++|+|||||+|||+||+.|++. |++|+|+|++++   .||........+   ...+
T Consensus       5     ~~viIiGaGiaGL~aA~~L~~~~g~~v~vlE~~~~---~GG~~~s~~~~g~g~~~~d~G~h~~~~~~~~i~~ll~~~~~~   81 (400)
T 5ER9_A          5     FDLFVVGSGFFGLTIAERAATQLGKRVLVIERRPH---IGGNAYSEPEPETGIEVHKYGAHLFHTSNKRVWDYVRQFTDF   81 (400)
T ss_dssp              CSEEEECCSHHHHHHHHHHHHHHCCCEEEECSSSS---SSGGGCCEECTTTCCEECTTCCCCEEESCHHHHHHHTTTCCB
T ss_pred              ceEEEECCCHHHHHHHHHHHHHHhCCcEEEEeCCCC---CCCCceeeecCCCCcEEEecCCCceecCCHHHHHHHHHhcCC


Q ss_pred              --------------------------------------------------------------------------------
Q Q_Madi_gp59      54    --------------------------------------------------------------------------------   53 (291)
Q Consensus       54    --------------------------------------------------------------------------------   53 (291)

T Consensus       82    ~~~~~~~~~~~~G~~~~~p~~~~~~~~~~~~~~l~~~~~~~~~l~~~~~~~~~~~~~~~s~~e~l~~~~g~~~~~~~~~~~~~~   161 (400)
T 5ER9_A          82    TGYQHRVFAMHNGQAYQFPMGLGLVSQFFGRYFSPDEARALIAEQASEIDTKDAKNFEEKAISLVGRPLYEAFIKHYTAK   161 (400)
T ss_dssp              CCCCCCEEEEETTEEEEESSSHHHHHHHHTSCCCHHHHHHHHHHHHTTSCGGGCCSHHHHHHHHHCHHHCCCCCHHHHHH
T ss_pred              CCcccEEEEEECCEEEecCCCHHHHHHHHccCCCHHHHHHHHHHHHhccCCcccccHHHHHHHHHhHHHHHHHHHHHHHH


Q ss_pred              cCCCCCeeeEecCCCceechhhccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeec
Q Q_Madi_gp59      54    SDKGVPVKYVVRGTPEEYRRKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENS   133 (291)
Q Consensus       54    l~~~~~~~~~~~~~~~~~~~~~~~~y~~k~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~V~~i~~   133 (291)
                        +     +......-...+..+..............-...+...+...+++.|.+.     .+.     .....++|++|+
T Consensus       162   ~-----~g~~~~~ls~~~~~~~~~~~~~~~~~~~~~~~~~~~~p~gG~~~l~~~L~~~-----~g~----~I~l~~~V~~I~-   226 (400)
T 5ER9_A          162   Q-----WQTDPKDLPASNITRLPVRYTFDNRYFNDTYEGLPVEGYTKWLENMAAD-----ERI----EVRLDTDWFDVR-   226 (400)
T ss_dssp              H-----HTSCGGGSCGGGCSCCCCCSSSCCCSCCCSEEECBTTCHHHHHHHHTCS-----TTE----EEECSCCHHHHH-
T ss_pred              H-----hCCCHHHCChhHhcCCcccccCCcccccccceeecccCcHHHHHHHHHhC-----CCC----EEEeCCchhhch-


Q ss_pred              CCCCCeEEEEcCCEEEECE--EEECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCCCC
Q Q_Madi_gp59      134   DVGVGGYVNWDLGLSEYEL--VISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTSLV   211 (291)
Q Consensus       134   ~~~~~v~V~~~~g~~~aD~--VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~~~~~~   211 (291)
                        .   +++       +.+|.  ||+|+|++.+...          ..+.+.|.+..+..+..+.+...+ ..|+++.+.+.
T Consensus       227   ~---~v~-------~~~d~~~vI~t~p~~~l~~~----------~~~~l~~~~~~~~~~~~~~~~~~~~~~-~~~~~~~~~~~~~~   285 (400)
T 5ER9_A          227   D---DLR-------AANPDAPVVYTGPLDRYFDY----------AEGRLGWRTLDFELEVLETGDFQG-TPVMNYNDLDV   285 (400)
T ss_dssp              H---HHH-------HHSTTCCEEECSCHHHHTTT----------TTCCCCEEEEEEEEEEESSSCSSS-SSEEEECSTTS
T ss_pred              h---HHh-------hhCCCCCEEEEecHHHHcch----------hcCCCCcceEEEEEEEecCCccCC-CCEEEeCCCCC


Q ss_pred              CceEEEeecCcccc------------eecC-C-----CCCCCcceeEEecccccCCCCCCCCCCC-----CCEEEEecccc
Q Q_Madi_gp59      212   PWTRLSKVHGFTSI------------EWPH-H-----AAQPHTQAVRVRKPLHYTPGPHQNGSPT-----ANWLHVGRYG   268 (291)
Q Consensus       212   ~~~r~~~~~~~~~~~~~~------------e~~~-~-----~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-----~~~~~~~~gr~g   268 (291)
                        +++|++.++.+...            |+|+ .     ..||.+.....+...++      ...+.     ++|+++||+|
T Consensus       286   ~~~ri~~~~~~~~~~~~~~~~~~~~~~~~~~l~~e~~~~~~~~~~~~~~~~~~~P~~~~~~~~~~~~~~~~~~------~~~~~~~~~~~~~~i~~~Gr~~   359 (400)
T 5ER9_A          286   PYTRIHEFRHFHPERTYPTDKTVIMREYSRFADNDDEPYYPINTEADRAVLAAY------RARAKAETASAKVLFGGRLG   359 (400)
T ss_dssp              SCSEEEEGGGGCTTSCCCSSCEEEEEEEEEECCTTSCCCEECCCHHHHHHHHHH------HHHHHHHHHHHCEEECHHHH
T ss_pred              CceEEEEhhhCCcccCCCCCcEEEEEEeeccCCCCCCccCccCCHHHHHHHHHH------HHHHHHHhccCCEEEeeccc


Q ss_pred              ccccCCcHHHHHHHHHHHHHhc
Q Q_Madi_gp59      269   QFEKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus       269   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   290 (291)
                        .|.| .++|+||++++++++++
T Consensus       360   ~~~~-~~~~~~~i~~~~~~~a~~l   380 (400)
```

```
T 5ER9_A          360   TYQY-LDMHMAIASALSMFDNV   380 (400)
T ss_dssp               HTCC-CCHHHHHHHHHHHCCCC
T ss_pred               cCCC-CCHHHHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDBe

☐ 5. **4U8I_D UDP-galactopyranose mutase; NUCLEOTIDE BINDING, MUTASE, FLAVIN ADENINE DINUCLEOTIDE BINDING, ISOMERASE; HET: EDO, SO4, FDA; 2.05A {Aspergillus fumigatus}**

Probability: 99.65%, E-value: 5.5e-15, Score: 140.43, Aligned cols: 268, Identities: 12%, Similarity: 0.035, Template Neff: 10.1

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHc-CCeEEEECCCCCccccchhHhc-CCCCCCCcc-------------------------
Q Q_Madi_gp59     1     MTIAILGCGPTGLLAAHACTLE-GYDVAIFSRKRKSELFGSQYLH-NPIPGLTPE-------------------------   53 (291)
Q Consensus       1     ~~V~IIGaG~aGl~aA~~L~~~-g~~v~i~E~~~~~~~~G~~~~~-~~~~~~~~~-------------------------   53 (291)
                        ++|+|||||+|||+||+.|+++ |.+|+|+|++++   .||.... ....+...+
T Consensus       11    ~~vvIiGaG~aGL~aA~~L~~~~g~~V~vlE~~~~---~GG~~~s~~~~~G~~~D~G~~~~~~~~~~~~~~l~~~~~~~~   87 (513)
T 4U8I_D          11    VDVLVIGAGPTGLGAAKRLNQIDGPSWMIVDSNET---PGGLASTDVTPEGFLYDVGGHVIASHYKYFDDCLDEALPKED   87 (513)
T ss_dssp               CSEEEECCSHHHHHHHHHHHHHCCSCEEEEESSSS---CCGGGCEEECTTSCEEESSCCCCCCCBHHHHHHHHHHSCSGG
T ss_pred               ceEEEECCCHHHHHHHHHHHhcCCCcEEEEeCCCC---CCCccceeecCCCcEEeCCCCeeecCCHHHHHHHHHHCCCCc


Q ss_pred               --------------------------------------------------------------------------------
Q Q_Madi_gp59     54    --------------------------------------------------------------------------------   53 (291)
Q Consensus       54    --------------------------------------------------------------------------------   53 (291)

T Consensus       88    ~~~~~~~~~~~~~~g~~~~~p~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~l~~~~g~~~~~~~~~~~~~   167 (513)
T 4U8I_D          88    DWYTHQRISYVRCQGQWVPYPFQNNISMLPKEEQVKCIDGMIDAALEARVANTKPKTFDEWIVRMMGTGIADLFMRPYNF   167 (513)
T ss_dssp               GEEEEECCEEEEETTEEEESSGGGGGGGSCHHHHHHHHHHHHHHHHHHHTCCSCCSSHHHHHHHHHCHHHHHHTHHHHHH
T ss_pred               cceeeecceEEEECCEEEeCCcchhhhcCCHHHHHHHHHHHHHHHHHHHhcCCCCCCHHHHHHHHhCHHHHHHccccchh


Q ss_pred               ---------cCCCCCeeeEecCCceechhhcccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCccee
Q Q_Madi_gp59     54    ---------SDKGVPVKYVVRGTPEEYRRKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMV   124 (291)
Q Consensus       54    ---------l~~~~~~~~~~~~~~~~~y~~k~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~   124 (291)
                                 +...+...............................-..+...+...+.+.+.+.+......++.
T Consensus       168   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~p~~gG~~~l~~~la~~l~~~~v~~~~------   241 (513)
T 4U8I_D          168   KVWAVPTTKMQCAWLGERVAAPNLKAVTTNVILGKTAGNWGPNATFRFPARGGTGGIWIAVANTLPKEKTRFGE------   241 (513)
T ss_dssp               HHHSSCGGGBCSGGGCSSCSCCCHHHHHHHHHHTCCCCSCBTTBEEEEESSSCHHHHHHHHHTTSCGGGEEESG------
T ss_pred               hhcCCCHHHCChHHHhhcCCCCCHHHHHHHHHhccCCCCCCCcceEEecCCCChHHHHHHHHhhCCccCcEEcc------


Q ss_pred               eeceeEeecCCCCCeEEEEcCC-EEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceecccee--cCCCC
Q Q_Madi_gp59     125   ASFFKRENSDVGVGGYVNWDLG-LSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGREL--FDKDN   201 (291)
Q Consensus       125   ~~~V~~i~~~~~~~~v~V~~~~g-~~~aD~VI~t~p~~~l~~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~--~~~~~   201 (291)
                        .++|++|+..   +..|.+.+| ++.||.||+|+|++.+.  .....|.++.....+.|....+..+.+..+.  .....
T Consensus       242   ~~~V~~I~~~---~~~V~~~~g~~~~~d~VIst~P~~~l~--~~~~~~~~~~~~~~l~~~~~~~v~l~~~~~~~~~~~~~~~   316 (513)
T 4U8I_D          242   KGKVTKVNAN---NKTVTLQDGTTIGYKKLVSTMAVDFLA--EAMNDQELVGLTKQLFYSSTHVIGVGVRGSRPERIGDK   316 (513)
T ss_dssp               GGCEEEEETT---TTEEEETTSCEEECSEEEECSCHHHHH--HHTTCHHHHHHHHHTSCEEEEEEEEEEESSCCTTTTTC
T ss_pred               CCceEEEEcC---CCEEEEcCCCEEECCEEEECCCHHHHH--HhcCcHHHHHHHhhCCCceEEEEEEEEcCCCchhcCCc


Q ss_pred               EEEEecCCCCCceEEEeecCccc---------------------------------------------------------
Q Q_Madi_gp59     202   TIICDGTSLVPWTRLSKVHGFTS---------------------------------------------------------   224 (291)
Q Consensus       202   ~~~~~~~~~~~~~~~r~~~~~~~~~~~---------------------------------------------------------   224 (291)
                        .|++..+.+.++.|++.+.++..
T Consensus       317   ~~~~~~~~~~~~~~~r~~~~~~~~~~~~~~~~p~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~e~~~~~~~~~~~~~~~~~l~~~~~~~   396 (513)
T 4U8I_D          317   CWLYFPEDNCPFYRATIFSNYSPYNQPEASAALPTMQLADGSRPQSTEAKEGPYWSIMLEVSESSMKPVNQETILADCIQ   396 (513)
T ss_dssp               CEEECCSTTCSCSEEECGGGTCTTSSCCTTCCBCCCEETTSCCCSCCSCBCCCEEEEEEEEEEBTTBCCCTTTHHHHHHH
T ss_pred               eEEEecCCCCCeEEEEehhhcCcccCCCccccccccccCCCCCCCcccCCCCeeEEEEEEEEcCCCCCCCHHHHHHHHHH


Q ss_pred               -------------------ceecC-CCCCCCcceeEEecccccCCCCCCCCCCCCCEEEeccccccccC-CcHHHHHHHH
Q Q_Madi_gp59     225   -------------------IEWPH-HAAQPHTQAVRVRKPLHYTPGPHQNGSPTANWLHVGRYGQFEKG-VVVTDAFDQV   283 (291)
Q Consensus       225   -------------------~e~~~-~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gr~g~~~~~~-~~~~~~~~~~~~   283 (291)
                                           ..|+. .+.|.......+++..+.      ...  ++++++||+|.|.|. .++|.|+..+
T Consensus       397   ~L~~~~~~~~~~~~~~i~~~~~~~~~~~~~~ayp~~~~~~~~~~~~~~~~~~~~~~------l~~--~~l~~~Gr~g~~~y~~~~~d~a~~~G   468 (513)
T 4U8I_D          397   GLVNTEMLKPTDEIVSTYHRRFDHGYPTPTLEREGTLTQILPK------LQD--KDIWSRGRFGSWRYEVGNQDHSFMLG   468 (513)
T ss_dssp               HHHHTTSSCTTCEEEEEEEEEEEEEEECCBTTHHHHHHHHHHH------HHT--TTEEECSTTTTCCGGGCSHHHHHHHH
T ss_pred               HHHHCCCCCChhheEEEEEEEEeCCccCCCCccchHHHHHHHHH------HHh--CCceecCCCCcccccCCCHHHHHHHH


Q ss_pred               HHHHHhc
Q Q_Madi_gp59     284   TKKLKEM   290 (291)
Q Consensus       284   ~~~~~~~   290 (291)
                        +++++++
T Consensus       469   ~~aA~~i   475 (513)
T 4U8I_D          469   VEAVDNI   475 (513)
T ss_dssp               HHHHHHH
```

```
T ss_pred               HHHHHHH
```

Template alignment | Template 3D Structure | PDBe

☐ **6. 4MO2_B UDP-galactopyranose mutase; UDP-N-acetylgalactopyranose mutase, UNGM, capsular polysaccharides, bifunctional, drug target, FAD, ISOMERASE; HET: FAD, SO4, GOL, FDA; 2.0A {Campylobacter jejuni subsp. jejuni}**

Probability: 99.56%, E-value: 8.5e-14, Score: 126.46, Aligned cols: 231, Identities: 16%, Similarity: 0.182, Template Neff: 10.8

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCc-c--------------------------
Q Q_Madi_gp59      1    MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTP-E--------------------------   53 (291)
Q Consensus        1    ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~-~--------------------------   53 (291)
                        ++++|+|||++|+++|..|.+.|.++.++|+...   .|+.+.....++... +
T Consensus        2    ~~~~i~g~g~~gl~~a~~l~~~~~~~~~~e~~~~---~gg~~~t~~~~g~~~~d~G~~~~~~~~~~i~~~~~~~~~~~~~   78 (368)
T 4MO2_B           2    YDYLIVGSGLFGSIFAYEATEKGYTCLVVEQREH---IGGNCYTENIKNINVHKYGAHIFRTSDQNIWDYMNQFCEFNHF   78 (368)
T ss_dssp               EEEEEECCSHHHHHHHHHHHHTTCCEEEECSSSS---SSGGGCEEEETTEEEETTSCCCEEESCHHHHHHHTTTCCBCCC
T ss_pred               ceEEEECCCHHHHHHHHHHHHCCCeEEEEcCCCC---CccccceeeccCCeEEecCCCCcccCCCHHHHHHHHHhhhcCc


Q ss_pred               ----------------------------------------------------------------------cCCCCCeeeE
Q Q_Madi_gp59     54    ----------------------------------------------------------------------SDKGVPVKYV   63 (291)
Q Consensus       54    ----------------------------------------------------------------------l~~~~~~~~~   63 (291)
                                                                                              .
T Consensus       79    ~~~~~~~~~g~~~~~p~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~s~~~~~~~~~g~~~~~~~~~~---------   149 (368)
T 4MO2_B          79    INSPIAIYKDEIYNLPFNMNTFSKLWGIKTPNEARKIIEMQKQIIQHPPKNLEEQAISLVGTDVYEKLIKG---------   149 (368)
T ss_dssp               CCCCEEEETTEEEESSSSHHHHHHHHCCCSHHHHHHHHHHHHTTCCSCCSSHHHHHHHHHCHHHCCCCCHH---------
T ss_pred               ccCcEEEECCEEeecCCCHHHHHHHhcCCCHHHHHHHHHhhhccCCCCCCCHHHHHHHHHHHHHHHHHhcc---------


Q ss_pred               ecCCceechhhcccccccC------------------cccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee
Q Q_Madi_gp59     64    VRGTPEEYRRKTHGKWWDG------------------HIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA   125 (291)
Q Consensus       64    ~~~~~~~y~~k~~~~~~d~------------------~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~   125 (291)
                               |..+.|+.  +.                  ...+.....+..-+...+++.|.+.        .    +....
T Consensus      150    -------~~~~~~g~--~~~~~s~~~~~~~~~~~~~~~~~~~~~~~~~~p~gG~~~l~~~L~~~-------i----~i~~~   209 (368)
T 4MO2_B         150    -------YTEKQWGR--SCKDLPASIIRRLPVRYIYDNNYFNDPYQGIPKGGYTAIFDKMLKK-------S----KVILN   209 (368)
T ss_dssp               -------HHHHHHTS--CGGGSCGGGCCCCCCCCSSCCCSCCCSEEECBTTCSHHHHHHHTTT-------S----EEECS
T ss_pred               -------hhHHHhCC--CHHHCCHhHHhcCCccccCCCCccCCccCcccCCChHHHHHHHHhc-------C----EEEeC


Q ss_pred               eceeEeecCCCCCeEEEEcCCEEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEE
Q Q_Madi_gp59    126    SFFKRENSDVGVGGYVNWDLGLSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIIC   205 (291)
Q Consensus      126    ~~V~~i~~~~~~~v~V~~~~g~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~   205 (291)
                        ++|.+|. .+.+          +.||.||+|+|++.+...          ..+.++|.+..+....++.+.. .+..|++
T Consensus      210    ~~V~~i~-~~~~----------~~~d~VI~t~p~~~l~~~----------~~~~l~~~~~~~~~~~~~~~~~~-~~~~~~~   267 (368)
T 4MO2_B         210    TDFLKYK-DKFK----------NKAKKIVFTGCIDAYYDY----------RYGALEYRSLKFEHKILNLDNF-QGVAVVN   267 (368)
T ss_dssp               CCGGGGH-HHHH----------TTEEEEEECSCHHHHTTT----------TTCCCCEEEEEEEEEEESSSCS-SSSSEEE
T ss_pred               Cchhhch-HHhh----------hcCCEEEEcCCHHHHhcc----------ccCCCCCCeEEEEEEEeccccc-CCCcEEE


Q ss_pred               ecCCCCCceEEEeecCcccc---------eecC------CCCCCCcceeEEecccccCCCCCCCCCCCCCEEEecccccc
Q Q_Madi_gp59    206    DGTSLVPWTRLSKVHGFTSI---------EWPH------HAAQPHTQAVRVRKPLHYTPGPHQNGSPTANWLHVGRYGQF   270 (291)
Q Consensus      206    ~~~~~~~~~r~~~~~~~~~~---------e~~~------~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gr~g~~   270 (291)
                        +.+.+.+++|+++++.+...         |+++      ...||.+.....+...++    .......++++++||+|.|
T Consensus      268    ~~~~~~~~~r~~~~~~~~~~~~~~~~~~i~~e~~~~~~~~~~~~~~~p~~~~~~~~~~~~~~~~----~~~~~~~~~~l~~~Gr~~~~   343 (368)
T 4MO2_B         268    YTDKEIPYTRIIEHKHFEFGNTDTTVISEEYPLEWIKGIEPYYPINDEKNQALYEKY----KQLAKHESNVYFGGRLGEY   343 (368)
T ss_dssp               ECCTTSSCSEEEEGGGGTTCCCSCEEEEEEEEECCCTTSCCCEECCCHHHHHHHHHH----HHHHHTSTTEEECHHHHTT
T ss_pred               eCCCCCCceEEEEccccCCCCCCCeEEEEecCccccCCCcccccccChHHHHHHHHH----HHHHhhcCCEEEecCcccC


Q ss_pred               ccCCcHHHHHHHHHHHHHhc
Q Q_Madi_gp59    271    EKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus      271    ~~~~~~~~~~~~~~~~~~~~   290 (291)
                        .| ..+|+||++|+++++++
T Consensus      344    ~~-~~~~~~i~~a~~~a~~l   362 (368)
T 4MO2_B         344    RY-YDMQDVVRSALLFCKNE   362 (368)
T ss_dssp               SC-CCHHHHHHHHHHHHHHH
T ss_pred               CC-CCHHHHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDB | NCBI

☐ **7. d2bi7a1 c.4.1.3 (A:2-247,A:317-384) UDP-galactopyranose mutase, N-terminal domain {Klebsiella pneumoniae [TaxId: 573]}**

Probability: 99.54%, E-value: 8.3e-15, Score: 130.73, Aligned cols: 212, Identities: 14%, Similarity: 0.082, Template Neff: 9.8

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcc---------------------------
Q Q_Madi_gp59      1    MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPE---------------------------   53 (291)
Q Consensus        1    ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~---------------------------   53 (291)
                        ++|+|||||++|+++|+.|++.|.+|+|+|+.+.   .|+.............
```

```
T Consensus       3      ~~v~IiGaG~~Gl~~A~~l~~~g~~v~v~e~~~~---~GG~~~~~~~~~~~~~~~~~G~h~~~~~~~~v~~~~~~~~~~~   79 (315)
T d2bi7a1         3      KKILIVGAGFSGAVIGRQLAEKGHQVHIIDQRDH---IGGNSYDARDSETNVMVHVYGPHIFHTDNETVWNYVNKHAEMM   79 (315)
T ss_dssp                CEEEEECCSHHHHHHHHHHHTTTCEEEEEESSSS---SSGGGCEEECTTTCCEEETTSCCCEEESCHHHHHHHHTTSCEE
T ss_pred                cEEEEECCCHHHHHHHHHHHHCCCeEEEEeCCCC---CCCccccCccCCCCceeEecCccccCCCHHHHHHHHHHHhhhc


Q ss_pred                ----------------------------------------cCCCCCeeeEecCCceechhhcccccccCcccccccCcch
Q Q_Madi_gp59      54     ----------------------------------------SDKGVPVKYVVRGTPEEYRRKTHGKWWDGHIGQDEFEPDH   93 (291)
Q Consensus       54     ----------------------------------------l~~~~~~~~~~~~~~~~y~~k~~~~~~d~~~~~~~~~~~~   93 (291)
                                                                 +............+...|..+..+...-..+ +..+..-.
T Consensus       80     ~~~~~~~~~~~G~~~~~P~~~~~l~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~e~~~~~~G~~l~~~f-~~~y~~k~   158 (315)
T d2bi7a1         80     PYVNRVKATVNGQVFSLPINLHTINQFFSKTCSPDEARALIAEKGDSTIADPQTFEEEALRFIGKELYEAF-FKGYTIKQ   158 (315)
T ss_dssp                ECCCCEEEEETTEEEEESCCHHHHHHHTTCCCCHHHHHHHHHHHSCCSCSSCCBHHHHHHHHHCHHHHCCC-CCHHHHHH
T ss_pred                cccceEEEEECCEEEeCCCCHhhHHHHhcccCCHHHHHHHHHHhCCCCCCCCCcHHHHHHHHHHHHHHHHH-cHHHHHHH


Q ss_pred                hhccHHHHHHHHHHHhhhhcC----------------CCCCCCcceeeeceeEeecCCCCCeEEEEcCCEEEECEEEECC
Q Q_Madi_gp59      94     QAWDIRQHYDMLWRTYVGKIE----------------PYSIPTKGMVASFFKRENSDVGVGGYVNWDLGLSEYELVISTV   157 (291)
Q Consensus       94     ~~~~~~~~~~~l~~~~~~~~~----------------~~~~~~~~~~~~~V~~i~~~~~~~v~V~~~~g~~~aD~VI~t~   157 (291)
                         +...+.++-...+..++....                ++...++.+..+.+..++...+     ........+|.||+|+
T Consensus       159    wg~~~~~ls~~~~~r~~~~~~~~~~~~~~~~~~~~p~~G~~~l~~~ll~~~~i~v~l~~~-----~~~~~~~~~d~VI~T~   233 (315)
T d2bi7a1         159    WGMQPSELPASILKRLPVRFNYDDNYFNHKFQGMPKCGYTQMIKSILNHENIKVDLQRE-----FIVEERTHYDHVFYSG   233 (315)
T ss_dssp                HSSCGGGSBGGGCCSCCCCSSSCCCSCCCSEEEEETTHHHHHHHHHHCSTTEEEEESCC-----CCGGGGGGSSEEEECS
T ss_pred                hCCCHHHCChhHHhcCCccccCCCCCccccCCCCcccceeecccccHHHHHHHHhCCCCeEEEeCCc-----eeecccccCCeEEEee


Q ss_pred                CHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCCCCCceEEEeecCcccceecCCCCCCCcc
Q Q_Madi_gp59      158    PRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTSLVPWTRLSKVHGFTSIEWPHHAAQPHTQ   237 (291)
Q Consensus       158    p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~~~~~~r~~~~~~~~~~e~~~~~~~~~~~   237 (291)
                         |++.+...          ..|.++|                                                      .
T Consensus       234    pld~l~~~----------~~g~l~~------------------------------------------------------~   249 (315)
T d2bi7a1         234    PLDAFYGY----------QYGRLXR------------------------------------------------------Q   249 (315)
T ss_dssp                CHHHHTTT----------TTCCC-C------------------------------------------------------C
T ss_pred                cHHHHccC----------ccCCCcC------------------------------------------------------C


Q ss_pred                eeEEecccccCCCCCCCCCCCCCEEEeccccccccCCcHHHHHHHHHHHHHhc
Q Q_Madi_gp59      238    AVRVRKPLHYTPGPHQNGSPTANWLHVGRYGQFEKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus       238    ~~~~~~~~~~~~~~~~~~~~~~~~~~~gr~g~~~~~~~~~~~~~~~~~~~~~~   290 (291)
                         ..+.++..+|    .+.....+||+.+||.|+|+| .+||+||++|+++++++
T Consensus       250    ~~~~~~~~~y----~~~~~~~~~~~~~~Gr~~~y~y-~~m~~~i~~a~~~~~~~   297 (315)
T d2bi7a1         250    MGEMALLEKY----LSLAENETNITFVGRLGTYRY-LDMDVTIAEALKTAEVY   297 (315)
T ss_dssp                HHHHHHHHHH----HHHHTTCSSEEECHHHHTTCC-CCHHHHHHHHHHHHHHH
T ss_pred                hhHHHHHHHH----HHHHHhcCCEEEEecccccee-cCHHHHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDB | NCBI

☐ **8. d1i8ta1 c.4.1.3 (A:1-244,A:314-367) UDP-galactopyranose mutase, N-terminal domain {Escherichia coli [TaxId: 562]}**

Probability: 99.5%, E-value: 1e-13, Score: 122.77, Aligned cols: 181, Identities: 14%, Similarity: 0.158, Template Neff: 10.2

```
Q ss_pred                CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcc---------------------------
Q Q_Madi_gp59      1      MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPE---------------------------   53 (291)
Q Consensus       1      ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~~---------------------------   53 (291)
                         ++|+|||||+||+++|..|++.|.+|+|+|+.+.   .|+........+....
T Consensus       2      ~~v~IiGaG~aG~~~a~~l~~~g~~v~v~e~~~~---~gG~~~~~~~~g~~~~~~~G~h~~~~~~~~v~~~~~~~~~~~~~   78 (299)
T d1i8ta1         2      YDYIIVGSGLFGAVCANELKKLNKKVLVIEKRNH---IGGNAYTEDCEGIQIHKYGAHIFHTNDKYIWDYVNDLVEFNRF   78 (299)
T ss_dssp                EEEEEECCSHHHHHHHHHHGGGTCCEEEECSSSS---SSGGGCEEEETTEEEETTSCCCEEESCHHHHHHHHTTSCBCCC
T ss_pred                ceEEEECCCHHHHHHHHHHHHcCCeEEEEccCCC---CCccccceecCCCCceeeccccceEEcCCCHHHHHHHHHHccccCC


Q ss_pred                -----------------------------------------------------------------------cCCCCCeee
Q Q_Madi_gp59      54     -----------------------------------------------------------------------SDKGVPVKY   62 (291)
Q Consensus       54     -----------------------------------------------------------------------l~~~~~~~~   62 (291)
                                                                                                .
T Consensus       79     ~~~~~~~~~g~~~~~P~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~G~~l~~~~~~~--------   150 (299)
T d1i8ta1         79     TNSPLAIYKDKLFNLPFNMNTFHQMWGVKDPQEAQNIINAQKKKYGDKVPENLEEQAISLVGEDLYQALIKG--------   150 (299)
T ss_dssp                CCCCEEEETTEEEESSBSHHHHHHHHCCCCHHHHHHHHHHHTTTTCCCCCCSHHHHHHHHHHHHHCCCCCCH--------
T ss_pred                CCCCeEEECCEEEEcccChhHHHHHhCCCCHHHHHHHHHHHHHHhCCCCCCCHHHHHHHHHHHHHHHHHHHH--------


Q ss_pred                EecCCceechhhcccccccCcccccccCcchhhcc-------------HHHHHHHHHHHhhhhcCCCCCCCcceeeecee
Q Q_Madi_gp59      63     VVRGTPEEYRRKTHGKWWDGHIGQDEFEPDHQAWD-------------IRQHYDMLWRTYVGKIEPYSIPTKGMVASFFK   129 (291)
Q Consensus       63     ~~~~~~~~y~~k~~~~~~d~~~~~~~~~~~~~~~~-------------~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~V~   129 (291)
                                 |..++|+. .....+............            +...+..+.+.+..   +.    +....+.|.
T Consensus       151    --------~~~k~wg~-~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~G~~~l~~~l~~---gi----~v~l~~~v~   214 (299)
T d1i8ta1         151    --------YTEKQWGR-SAKELPAFIIKRIPVRFTFDNNYFSDRYQGIPVGGYTKLIEKMLE---GV----DVKLGIDFL   214 (299)
T ss_dssp                --------HHHHHHSS-CGGGSCTTSSCCCCBCSSSCCCSCCCSEEECBTTCHHHHHHHHHT---TS----EEECSCCGG
```

```
T ss_pred                 --------HhHHHhCC-ChhhCChhHHccCCCCCCCCCCccCCCcCccCCCcHHHHHHHHhC---CC----eEEcCCccc


Q ss_pred                 EeecCCCCCeEEEEcCCEEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59      130    RENSDVGVGGYVNWDLGLSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus        130    ~i~~~~~~~~~v~V~~~~g~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~   209 (291)
                          ++.           +++.+.+|.||+|+|.+.+...          ..|.++
T Consensus        215    ~~~-----------~~~~~~~d~VI~T~pid~~~~~----------~~g~L~----------------------------   245 (299)
T d1i8ta1          215    KDK-----------DSLASKAHRIIYTGPIDQYFDY----------RFGALX----------------------------   245 (299)
T ss_dssp                 GSH-----------HHHHTTEEEEEECSCHHHHTTT----------TTCCC-----------------------------
T ss_pred                 ccc-----------hhHHhhCCeEEEecChHHhcCc----------ccCCCC----------------------------


Q ss_pred                 CCCceEEEeecCcccceecCCCCCCCcceeEEecccccCCCCCCCC--CCCCCEEEeccccccccCCcHHHHHHHHHHHH
Q Q_Madi_gp59      210    LVPWTRLSKVHGFTSIEWPHHAAQPHTQAVRVRKPLHYTPGPHQNG--SPTANWLHVGRYGQFEKGVVVTDAFDQVTKKL   287 (291)
Q Consensus        210    ~~~~~r~~~~~~~~~~e~~~~~~~~~~~~~~~~~~~~~~~~~~~~~--~~~~~~~~~gr~g~~~~~~~~~~~~~~~~~~~   287 (291)
                                                  .......+..+|      ..  ...++||.+||.|+|+| .+||++|++|++..
T Consensus        246    --------------------------~~~~~~~~~~~y------~~~~~~~~~~v~~~Gr~~~y~y-~~m~~~i~~al~~~   292 (299)
T d1i8ta1          246    --------------------------NDNKNMELFKKY------RELASREDKVIFGGRLAEYKY-YDMHQVISAALYQV   292 (299)
T ss_dssp                 --------------------------CSHHHHHHHHHH------HHHHHHCTTEEECSTTTTTSC-CCHHHHHHHHHHHH
T ss_pred                 --------------------------CChhHHHHHHHH------HHHHhccCCEEEEecCcccee-cCHHHHHHHHHHHH


Q ss_pred                 Hhc
Q Q_Madi_gp59      288    KEM   290 (291)
Q Consensus        288    ~~~   290 (291)
                          +++
T Consensus        293    ~~~   295 (299)
T d1i8ta1          293    KNI   295 (299)
T ss_dssp                 HHH
T ss_pred                 HHh
```

Template alignment | Template 3D Structure | PDB | NCBI

☐ **9. d1b5qa1 c.3.1.2 (A:5-293,A:406-463) Polyamine oxidase {Maize (Zea mays) [TaxId: 4577]}**

Probability: 99.33%, E-value: 5.2e-11, Score: 107.07, Aligned cols: 164, Identities: 11%, Similarity: -0.015, Template Neff: 11.5

```
Q ss_pred                 CeEEEECCCHHHHHHHHHHHHcCC-eEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecC--Cceechhhccc
Q Q_Madi_gp59      1      MTIAILGCGPTGLLAAHACTLEGY-DVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRG--TPEEYRRKTHG   77 (291)
Q Consensus        1      ~~V~IIGaG~aGl~aA~~L~~~g~-~v~i~E~~~~~~~~~G~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~--~~~~y~~k~~~   77 (291)
                          ++|+|||||+|||+||+.|++.|+ +|+|+|++++   .|+........+...++   -.-|+....  ...........
T Consensus        1      ~~VvIVGaG~aGl~aA~~L~~~g~~~V~vlEa~~r---~GGr~~~~~~~~~~~~~d~---g~~~i~~~~~~~~~~~~~~~~~~~~~   74 (348)
T d1b5qa1          1      PRVIVVGAGMSGISAAKRLSEAGITDLLILEATDH---IGGRMHKTNFAGINVEL---GANWVEGVNGGKMNPIWPIVNS   74 (348)
T ss_dssp                 CCEEEECCBHHHHHHHHHHHHTTCCCEEEECSSSS---SBTTSCEEEETTEEEES---SCCEEEEESSSSCCTHHHCCCC
T ss_pred                 CcEEEECCCHHHHHHHHHHHHCCCCCEEEEecCCC---CCCceeEeeeCCeEEEc---ccceeccCCCCCCCChHHHHHh


Q ss_pred                 ccccCccccccc--------------------------------------------------------------------
Q Q_Madi_gp59      78     KWWDGHIGQDEF--------------------------------------------------------------------   89 (291)
Q Consensus        78     ~~~d~~~~~~~~~~~~~~--------------------------------------------------------------------   89 (291)
                          ...-.....+..
T Consensus        75     ~~~~~~~~~~~~~~~~~~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   154 (348)
T d1b5qa1          75     TLKLRNFRSDFDYLAQNVYKEDGGVYDEDYVQKRIELADSVEEMGEKLSATLHASGRDDMSILAMQRLNEHQPNGPATPV   154 (348)
T ss_dssp                 CSCCCEEECCCTTGGGCEEETTSSBCCHHHHHHHHHHHHHHHHHHHHHHHTSCTTSTTCCBHHHHHHHHHTSSSSCCSHH
T ss_pred                 hcCCccccCCchHhhccEEcCCCCccCHHHHHHHHHHHHHHHHHHHHHHHHHHHhhcCCCchHHHHHHHHHhcCCCCCCChH


Q ss_pred                 --------------------------------------CcchhhccHHHHHHHHHHHhhhhc--------CCCCCCCcce
Q Q_Madi_gp59      90     --------------------------------------EPDHQAWDIRQHYDMLWRTYVGKI--------EPYSIPTKGM   123 (291)
Q Consensus        90     --------------------------------------~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~--------~~~~~~~~~~~~~~~~~~   123 (291)
                                                          ......-+...++..+...+....        ... .+
T Consensus        155    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~g~~~l~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i-~l----   229 (348)
T d1b5qa1          155    DMVVDYYKFDYEFAEPPRVTSLQNTVPLATFSDFGDDVYFVADQRGYEAVVYYLAGQYLKTDDKSGKIVDPRL-QL----   229 (348)
T ss_dssp                 HHHHHCCCCCHHHSSCTTTBBSTTTSSCHHHHHHCSEEEEECCTTCTTHHHHHHHHTTSCBCTTTCCBCCTTE-ES----
T ss_pred                 HHHHHHHhhchhhcCCCCcCCcccccCcccchhcCCceeEEecCCcHHHHHHHHHhhhccCCCCCCCccCCce-ec----


Q ss_pred                 eeeceeEeecCCCCCeEEEEcCC-EEEECEEEECCCHHHHcCCCCcccCccchhh
Q Q_Madi_gp59      124    VASFFKRENSDVGVGGYVNWDLG-LSEYELVISTVPRDIWQLPGDEYIYSEGWAI   177 (291)
Q Consensus        124    ~~~~V~~i~~~~~~~~~v~V~~~~g-~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~   177 (291)
                           .++|++|+ .++++++|++++| ++.||.||+|+|+..+....+.|.|.||..+
T Consensus        230    -~t~V~~I~-~~~~~v~V~~~~G~~~~ad~VI~t~p~~~l~~~~i~f~p~Lp~~k   282 (348)
T d1b5qa1          230    -NKVVREIK-YSPGGVTVKTEDNSVYSADYVMVSASLGVLQSDLIQFKPKLPTWK   282 (348)
T ss_dssp                 -SCCEEEEE-ECSSCEEEEETTSCEEEESEEEECSCHHHHHTTSSEEESCCCHHH
T ss_pred                 -CCceEEEE-eCCCCeEEEeCCCCEEEcCEEEEccchHHHHccccccCCCCCHHH
```

Template alignment | Template 3D Structure | PDBe

☐ **10. 4HSU_A Lysine-specific histone demethylase 1B; histone demethylase, OXIDOREDUCTASE; HET: FAD; 1.988A {Homo sapiens}**

Probability: 99.29%, E-value: 1.7e-10, Score: 115.87, Aligned cols: 262, Identities: 13%, Similarity: 0.043, Template Neff: 9.2

```
Q ss_pred                CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCC-CCCCcccCCCCCeeeEe---------------
Q Q_Madi_gp59     1      MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPI-PGLTPESDKGVPVKYVV---------------   64 (291)
Q Consensus       1      ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~~~G~~~~~~~~~-~~~~~~~l~~~~~~~~~~~~---------------   64 (291)
                         ++|+|||||++||+||+.|++.|.+|+|+|++++   .||....... .+.....   -...+..
T Consensus       337    ~~VvIIGAGiaGLaaA~~L~~~G~~V~VlEa~~~---iGGr~~s~~~~~g~~~d~---Ga~~i~~~~~~~l~~l~~qlgl   410 (776)
T 4HSU_A          337    KSVIIIGAGPAGLAAARQLHNFGIKVTVLEAKDR---IGGRVWDDKSFKGVTVGR---GAQIVNGCINNPVALMCEQLGI   410 (776)
T ss_dssp                CEEEEECCSHHHHHHHHHHHHHTCEEEEECSSSS---SCTTCCEECCSTTCCEES---SCCEEECCTTCHHHHHHHHHTC
T ss_pred                CEEEEECCCHHHHHHHHHHHHCCCcEEEEcCCCC---CCCeeeeccCCCCcEecC---CCEEEcCCCCCHHHHHHHHhCC


Q ss_pred                --------------------------------------------------------------------------------
Q Q_Madi_gp59     65     --------------------------------------------------------------------------------   64 (291)
Q Consensus       65     --------------------------------------------------------------------------------   64 (291)

T Consensus       411    ~~~~~~~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l   490 (776)
T 4HSU_A          411    SMHKFGERCDLIQEGGRITDPTIDKRMDFHFNALLDVVSEWRKDKTQLQDVPLGEKIEEIYKAFIKESGIQFSELEGQVL   490 (776)
T ss_dssp                CCEECCSCCCEECTTSCBCCHHHHHHHHHHHHHHHHHHHHHGGGCCGGGCCBHHHHHHHHHHHHHHHSCCCCCHHHHHHH
T ss_pred                CeEecCCCcceecCCCccCChHHHHHHHHHHHHHHHHHHHHHhcccccCCCCHHHHHHHHHHHHHHHHCCCCcHHHHHHH


Q ss_pred                -----------cCCceechhhcccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeec
Q Q_Madi_gp59     65     -----------RGTPEEYRRKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENS   133 (291)
Q Consensus       65     -----------~~~~~~y~~k~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~V~~i~~   133 (291)
                                    ...........|..  ...+............+...+.+.+.+       +.    +....++|++|+
T Consensus       491    ~~~~~~l~~~~g~~l~~ls~~~~~~~--~~~~~~~~~g~~~~~~~G~~~l~~~l~~-------gv----~I~~~~~V~~I~-   556 (776)
T 4HSU_A          491    QFHLSNLEYACGSNLHQVSARSWDH--NEFFAQFAGDHTLLTPGYSVIIEKLAE-------GL----DIQLKSPVQCID-   556 (776)
T ss_dssp                HHHHHHHHHHHTSCTTTBBTTTTTG--GGGSCCCCSCEEECTTCTHHHHHHHHT-------TS----CEESSCCEEEEE-
T ss_pred                HHHHHHHHHHhCCCHHHccccccCc--chHHHHhcCCceeeCCcHHHHHHHHHC-------CC----CeecCCCEEEEE-


Q ss_pred                CCCCCeEEEEcCC-EEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCCCCC
Q Q_Madi_gp59     134    DVGVGGYVNWDLG-LSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTSLVP   212 (291)
Q Consensus       134    ~~~~~v~V~~~~g-~~~aD~VI~t~p~~~l~~~~~~~~f~p~lp~~~g~~~~~g~~~~~~~v~~~e~~~~~~~~~~~~~~~~~~~~~~~   212 (291)
                         .+++++.|.+.+| ++.||.||+|+|+..+....+.|.|.+|......  ..+--...+...-..+++..|.-...+...
T Consensus       557    ~~~~~v~V~~~~G~~i~ad~VV~a~p~~~l~~~~i~f~p~Lp~~k~~a--i~~l~~~~~~~kv~l~f~~~fW~~~~~~~~~~~   634 (776)
T 4HSU_A          557    YSGDEVQVTTTDGTGYSAQKVLVTVPLALLQKGAIQFNPPLSEKKMKA--INSLGAGIIEKIALQFPYRFWDSKVQGADF   634 (776)
T ss_dssp                CSSSSEEEEETTCCEEEESEEEECCCHHHHHHTCSEEESCCCHHHHHH--HHHEEEECCEEEEEECSSCTTHHHHTTCSE
T ss_pred                eCCCeEEEEECCCCEEEeCEEEECCCHHHHhCCCCCCCCCCCHHHHHH--HHhcCCCeeEEEEEEcCcccCCcccCCCcc


Q ss_pred                ceEEEeecCcccc--------------------------------------------------------------eecC-
Q Q_Madi_gp59     213    WTRLSKVHGFTSI--------------------------------------------------------------EWPH-   229 (291)
Q Consensus       213    ~~r~~~~~~~~~~~~~~~~--------------------------------------------------------------e~~~-   229 (291)
                         |..+.........                                                              .|..
T Consensus       635    fg~~~~~~~~r~~~~~f~~~~~~~~~~~~vl~~~i~g~~~~~~~~~~~deei~~~~~~~L~~~f~~~~~p~p~~~~v~~W~~d   714 (776)
T 4HSU_A          635    FGHVPPSASKRGLFAVFYDMDPQKKHSVLMSVIAGEAVASVRTLDDKQVLQQCMATLRELFKEQEVPDPTKYFVTRWSTD   714 (776)
T ss_dssp                EEECCSSSTTTTEEEEEEESCTTSCSCEEEEEECTHHHHHTTTSCHHHHHHHHHHHHHHHTTTSCCCCCSEEEECCGGGC
T ss_pred                cccCCCccccCCceEEEEeCCCcCCccEEEEEEehHHHHHHhcCCHHHHHHHHHHHHHHHhCCCCCCCCcEEEEeccCCC


Q ss_pred                ---CCCCCCcceeEEecccccCCCCCCCCCCCCC-EEEeccccccccCCcHHHHHHHHHHHHHhc
Q Q_Madi_gp59     230    ---HAAQPHTQAVRVRKPLHYTPGPHQNGSPTAN-WLHVGRYGQFEKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus       230    ---~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-~~~~gr~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   290 (291)
                            .-.|.+..........+.      ......+ +|++|-+-...+.-.++.|+..++..+++|
T Consensus       715    ~~~~gays~~~~g~~~~~~~~~~~------l~~~~~~~~~l~fAGe~t~~~~~~~~tv~GA~~SG~raA~~I   773 (776)
T 4HSU_A          715    PWIQMAYSFVKTGGSGEAYDI------IAEDIQGTVFFAGEATNRHFPQTVTGAYLSGVREASKI   773 (776)
T ss_dssp                TTTCCSEEEEBTTCCTHHHHH------HHCCBTTTEEECSGGGCSSSCSSHHHHHHHHHHHHHHH
T ss_pred                CCCCCCCCCccCCCChHHHHH------HhccCCCcEEECCHHhCCCCCCcHHHHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDBe

☐ **11. 5MQ6_A Pyridine nucleotide-disulfide oxidoreductase-like protein; Flavin, monooxygenase, Baeyer-Villiger, oxygen, biocatalysis, Oxidoreductase; HET: FAD, NDP; 2.0A {Myceliophthora thermophila}**

Probability: 99.29%, E-value: 1.4e-10, Score: 114.27, Aligned cols: 168, Identities: 17%, Similarity: 0.077, Template Neff: 8.7

```
Q ss_pred                CeEEEECCCHHHHHHHHHHHHcCC-----eEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhc
Q Q_Madi_gp59     1      MTIAILGCGPTGLLAAHACTLEGY-----DVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKT   75 (291)
Q Consensus       1      ~~V~IIGaG~aGl~aA~~L~~~g~-----~v~i~E~~~~~~~~~~G~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~y~~k~   75 (291)
                         .+|+|||||++|+++|..|.+.|.     +++|+|+...   .|+.|....+|+..|..   ..+.+........+...
T Consensus       79     ~~VvIIGaG~aGl~~A~~L~~~g~~~~~~~~v~iiE~~~~~---~GG~w~~n~ypg~~~d~---~~~~~~~~~~~~~~~~~~~~~~-   151 (655)
```

```
T 5MQ6_A            79    YKFIILGAGYGGLLYAVRLAEAGLASGPDDILMVDAAGG---FGGTWWWNRYPGLHCDV---ESYSYMPLLEETGYIPK-   151 (655)
T ss_dssp                 EEEEEECCSHHHHHHHHHHHHTTSCCSTTSEEEECSSSS---TTTHHHHCCCTTCBCSS---CHHHHSTTHHHHTCCCS-
T ss_pred                 eEEEEEccCHHHHHHHHHHHHCCCCCCCCcEEEEeCCCC---CCCcchhhcCCCcccCC---chhccCCcchhcCCCCh-


Q ss_pred                 ccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCCe-EEEEcCC-------
Q Q_Madi_gp59        76    HGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVGG-YVNWDLG-------   146 (291)
Q Consensus         76    ~~~~~d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~v-~V~~~~g-------   146 (291)
                                            ..+..+..+...+..........    ..+.+ ++|++++++++.+. .|.+.++
T Consensus         152   ------------------~~~~~~~ei~~yl~~~a~~~~l~----~~i~f~t~V~~~~~~~~~~~~~w~V~~~~g~~~~~~~   209 (655)
T 5MQ6_A            152   ------------------SKYAAGPELLEHAYRIATQWKLH----DKALFRSNVKTIRWDDESRLWSLEVTEGRGPGQQS   209 (655)
T ss_dssp                 ------------------BSSCBHHHHHHHHHHHHHHTTCT----TSEECSEEEEEEEEETTTTEEEEEEEECCCTTSCC
T ss_pred                 ------------------hhcCChHHHHHHHHHHHHHcCCC----ccEECcceEeeEEEeCCCCeEEEEEEcCCCCCcCc


Q ss_pred                 ---EEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceecccee------------cCCCCEEEE
Q Q_Madi_gp59        147   ---LSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGREL------------FDKDNTIIC   205 (291)
Q Consensus         147   ---~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~------------~~~~~~~~~   205 (291)
                             ++.||.||+|+        +..-.|.+|..+|...|.|..+|....+.++            ...+.|.++
T Consensus         210   ~~~~~~ad~VI~At--------G~~s~p~~P~ipG~~~f~G~~~hs~~w~~~~~~~~~~~~~~~~~~~~K~V~VI   275 (655)
T 5MQ6_A            210   RELKLQARYVLLAS--------GILTNPQVPKIPGLETFTGPVFHTARWNYDVTGGSPTDEALNRLEGKRVGII   275 (655)
T ss_dssp                 EEEEEEEEEEEECC--------CSSCSBEEECCTTGGGCCSCEEEGGGCCHHHHCSBTTBCCCGGGTTCEEEEE
T ss_pred                 cEEEEEEeEEEEec--------cCCCCCCCCCCCCcccCCCcccccccccccCCCCCCCchHHHhhCCCEEEEE
```

Template alignment | Template 3D Structure | PDBe

☐ 12. **6SEK_A Ancestral Flavin-containing monooxygenase 5; Flavin, enzyme, membrane protein, Ancestral Sequence Reconstruction, OXIDOREDUCTASE; HET: FAD, EPE, GLC, LMT, NAP; 2.7A {synthetic construct}**

Probability: 99.29%, E-value: 2.8e-10, Score: 109.43, Aligned cols: 178, Identities: 13%, Similarity: 0.094, Template Neff: 9.8

```
Q ss_pred                 CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59        1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus         1     ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~~G~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                          ++|+|||||+||+++|..|.+.|++++|+|+.+.   .|+.|.....+......                -.........
T Consensus         4     ~~v~IIGaG~sGl~aa~~l~~~g~~v~i~E~~~~---~GG~w~~~~~~~~~~~~~----------------~~~~~~~~~~   64 (533)
T 6SEK_A            4     KRIAVIGAGASGLTSIKCCLEEGLEPVCFERTDD---IGGLWRFQENPEEGRAS----------------IYKSVIINTS   64 (533)
T ss_dssp                 CEEEEECCSHHHHHHHHHHHTTTCEEEEECSSSS---SCGGGSCCSSCBTTBCC----------------CCTTCBCSSC
T ss_pred                 cEEEEECCCHHHHHHHHHHHHcCCCcEEEeCCCC---CCCCCcccCCCCCCCcc----------------cccceEEeeC


Q ss_pred                 cCcccccccCc--chhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCC----CCeEEEEcCC----EEE
Q Q_Madi_gp59        81    DGHIGQDEFEP--DHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVG----VGGYVNWDLG----LSE   149 (291)
Q Consensus         81    d~~~~~~~~~~~--~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~----~~v~V~~~~g----~~~   149 (291)
                          .....+..+.+  ....+.....+.+.++.+.......    ..+.+ ++|++++...+    +.+.|.++++    +..
T Consensus         65    ~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~yl~~~a~~~~l~----~~i~~~t~V~~v~~~~~~~~~~~~~~w~V~~~~~~~~~~~~~~~~   140 (533)
T 6SEK_A            65    KEMMCFSDYPIPDHYPNFMHNSQVLEYFRMYAKEFDLL----KYIQFKTTVCSVKKQPDFSTSGQWEVVTECEGKKEVDV   140 (533)
T ss_dssp                 HHHHSBTTBCCCTTSCSSCBHHHHHHHHHHHHHHTTCG----GGEECSCEEEEEEECTTHHHHCCEEEEEEBTTBCCEEE
T ss_pred                 CccccCCCCCCCCCCCCCCCHHHHHHHHHHHHHHcCCH----HHEEcCCEEEEEEECCCCCCCcEEEEEEeCCeEEEEEE


Q ss_pred                 ECEEEECCCHHHHcCCCCcccCccc--hhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59        150   YELVISTVPRDIWQLPGDEYIYSEG--WAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus         150   aD~VI~t~p~~~l~~~~~~f~p~lp--~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~~~   209 (291)
                          +|.||+|+        +..-.|.+|  ..+|...|.|..+|..-......+....++.-+.+
T Consensus         141   ~d~Vvvat--------G~~~~p~~p~~~~~g~~~f~g~~~hs~~~~~~~~~~~~gk~V~VVG~G   194 (533)
T 6SEK_A            141   FDGVMVCT--------GHHTNAHLPLESFPGIEKFKGQYFHSRDYKNPEGFTGKRVIIIGIG   194 (533)
T ss_dssp                 ESEEEECC--------CSSSEECCCGGGSTTTTTCCSEEEEGGGCCCSGGGTTCEEEEECCS
T ss_pred                 eCEEEEcc--------CCCCCCCCCCCCCCccccCcEEEeeeecCCccccCCCEEEEEECCC
```

Template alignment | Template 3D Structure | PDBe

☐ 13. **4AP3_A STEROID MONOOXYGENASE; OXIDOREDUCTASE, BAEYER-VILLIGER; HET: SO4, FAD, NAP; 2.39A {RHODOCOCCUS RHODOCHROUS}**

Probability: 99.28%, E-value: 3.5e-10, Score: 109.15, Aligned cols: 175, Identities: 15%, Similarity: 0.115, Template Neff: 10

```
Q ss_pred                 CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59        1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus         1     ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~~G~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                          .+|+|||||++|+++|..|.+.|.+++|+|+...   .|+.|....+++..+..   ....+.............|.
T Consensus         22    ~~v~IIGaG~aGl~~a~~l~~~g~~~~i~e~~~~---~Gg~w~~~~~~~~~~~d~---~~~~~~~~~~~~~~~~~~~~~~~~---   92 (549)
T 4AP3_A            22    YDVVVVGAGIAGLYAIHRFRSQGLTVRAFEAASG---VGGVWYWNRYPGARCDV---ESIDYSYSFSPELEQEWNWS---   92 (549)
T ss_dssp                 EEEEEECCSHHHHHHHHHHHHTTCCEEEECSSSS---SCTHHHHCCCTTCBCSS---CTTTSSCCSCHHHHHHCCCS---
T ss_pred                 eeEEEECCCHHHHHHHHHHHHCCCCEEEEcCCCC---CCCcceecCCCCCcccC---CcccccccCChhHhhcCCCc---


Q ss_pred                 cCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCC-eEEEEcCC-EEEECEEEECC
Q Q_Madi_gp59        81    DGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVG-GYVNWDLG-LSEYELVISTV   157 (291)
```

```
Q Consensus       81    d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~-v~V~~~~g-~~~aD~VI~t~   157 (291)
                                     ..+..+..+.+.+..+.....-.    ..+.+ ++|.++.++++.. +.|.++++ .+.||.||+|+
T Consensus       93    -------------~~~~~~~ei~~yl~~~~~~~~l~----~~i~~~~~V~~~~~~~~~~~w~V~~~~g~~~~a~~vI~At   155 (549)
T 4AP3_A          93    -------------EKYATQPEILAYLEHVADRFDLR----RDIRFDTRVTSAVLDEEGLRWTVRTDRGDEVSARFLVVAA   155 (549)
T ss_dssp               -------------SSSCBHHHHHHHHHHHHHHTTCG----GGEECSCCEEEEEEETTTTEEEEEETTCCEEEEEEEEECC
T ss_pred               -------------hhcCCHHHHHHHHHHHHHHhCCc----ccEEcCCEEEEEEEcCCCCEEEEEECCCCEEEEEEEEEee


Q ss_pred               CHHHHcCCCCcccCccchhhccCcccCceecceeccce-ecCCCCEEEEecCC
Q Q_Madi_gp59      158   PRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRE-LFDKDNTIICDGTS   209 (291)
Q Consensus       158   p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e-~~~~~~~~~~~~~~   209 (291)
                                +..-.|..|..+|...|.|..+|..-.+.. ..+....+..-+.+
T Consensus       156   --------G~~~~p~~p~~~g~~~f~g~~~h~~~~~~~~~~~~gk~V~ViG~G   200 (549)
T 4AP3_A          156   --------GPLSNANTPAFDGLDRFTGDIVHTARWPHDGVDFTGKRVGVIGTG   200 (549)
T ss_dssp               --------CSEEECCCCCCTTGGGCCSEEEEGGGCCTTCCCCBTCEEEEECCS
T ss_pred               --------CCCCCCCCCCCCCCCCCCCcEeEeecCCCCCCCCCCCEEEEEccC
```

Template alignment | Template 3D Structure | PDBe

☐ **14. 3UOX_A OTEMO; Baeyer-Villiger monooxygenase, OXIDOREDUCTASE; HET: FAD; 1.956A {Pseudomonas putida}**

Probability: 99.28%, E-value: 3.2e-10, Score: 109.15, Aligned cols: 175, Identities: 13%, Similarity: 0.083, Template Neff: 10.4

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59      1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus       1     ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                        .+|+|||||++|+++|..|.+.|.+++|+|+...   .|+.|....+++..+..................+...
T Consensus       10    ~~v~IIGaG~aGl~~a~~l~~~g~~v~i~e~~~~---~Gg~w~~~~~p~~~~~~~~~~~~~~~~~~~~~~~~~~~------   80 (545)
T 3UOX_A          10    LDAVVIGAGVTGIYQAFLINQAGMKVLGIEAGED---VGGTWYWNRYPGCRLDTESYAYGYFALKGIIPEWEWS------   80 (545)
T ss_dssp               EEEEEECCSHHHHHHHHHHHHTTCCEEEECSSSS---SCTHHHHCCCTTCBCSSCHHHHCHHHHTTSSTTCCCS------
T ss_pred               eeEEEECCCHHHHHHHHHHHHCCCCEEEEcCCCC---CCCCccccCCCCcccCCccccccccccccCCCcCCCc------


Q ss_pred               cCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCCe-EEEEcCC-EEEECEEEECC
Q Q_Madi_gp59      81    DGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVGG-YVNWDLG-LSEYELVISTV   157 (291)
Q Consensus       81    d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~v-~V~~~~g-~~~aD~VI~t~   157 (291)
                                     ..+..+..+...+..+.......    ..+.+ ++|+++.+.++++. .|.++++ .+.+|.||+|+
T Consensus       81    -------------~~~~~~~ei~~yl~~~a~~~~l~----~~i~~~~~V~~~~~~~~~~~w~v~~~~g~~~~~d~vI~At   143 (545)
T 3UOX_A          81    -------------ENFASQPEMLRYVNRAADAMDVR----KHYRFNTRVTAARYVENDRLWEVTLDNEEVVTCRFLISAT   143 (545)
T ss_dssp               -------------BSSCBHHHHHHHHHHHHHHHTCG----GGEECSCCEEEEEEEGGGTEEEEEETTTEEEEEEEEEECC
T ss_pred               -------------cccCCHHHHHHHHHHHHHHcCch----hhEeCCcEEEEEEEeCCCCEEEEEECCCcEEEEEEEEECC


Q ss_pred               CHHHHcCCCCcccCccchhhccCcccCceecceeccce-------ecCCCCEEEEecCC
Q Q_Madi_gp59      158   PRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRE-------LFDKDNTIICDGTS   209 (291)
Q Consensus       158   p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e-------~~~~~~~~~~~~~~   209 (291)
                                +....|.+|..+|...|.|..+|..-.+..       ..+....++.-+.+
T Consensus       144   --------G~~~~p~~p~~~g~~~f~g~~~hs~~~~~~~~~~~~~~~~~~gk~V~ViG~G   194 (545)
T 3UOX_A          144   --------GPLSASRMPDIKGIDSFKGESFHSSRWPTDAEGAPKGVDFTGKRVGVIGTG   194 (545)
T ss_dssp               --------CSCBC---CCCTTGGGCCSEEEEGGGCCBCTTSCBSCCCCBTCEEEEECCS
T ss_pred               --------CCccCCCCCCCCChhhcCCeeccccccCCCCCCCCCcccCCCCEEEEEcCC
```

Template alignment | Template 3D Structure | PDBe

☐ **15. 6SE3_D Ancestral Flavin-containing monooxygenase (FMO) 3-6; Flavin, enzyme, membrane protein, Ancestral Sequence Reconstruction; HET: FAD, OXY, NAP; 2.8A {synthetic construct}**

Probability: 99.27%, E-value: 3.6e-10, Score: 108.69, Aligned cols: 178, Identities: 13%, Similarity: 0.104, Template Neff: 9.7

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59      1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus       1     ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                        ++|+|||||+||+++|..|.+.|++++|+|+.+.   .|+.|............                ..........
T Consensus       3     ~~v~IIGaG~sGl~aa~~l~~~g~~v~i~E~~~~---~GG~w~~~~~~~~~~~~~~----------------~~~~~~~~~~   63 (532)
T 6SE3_D          3     KKVAIIGAGVSGLASIRSCLEEGLEPTCFERSDD---IGGLWKFSDHAEEGRAS----------------IYQSVFTNSS   63 (532)
T ss_dssp               CEEEEECCSHHHHHHHHHHHHTTCEEEEECSSSC---SSGGGSCCSSCCTTSCC----------------CCTTCBCSSC
T ss_pred               CEEEEECCCHHHHHHHHHHHHcCCCcEEEeCCCC---CCCCccccCCCcCCCcc----------------cccceEeccC


Q ss_pred               cCcccccccCc--chhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCC----CCeEEEEcCC----EEE
Q Q_Madi_gp59      81    DGHIGQDEFEP--DHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVG----VGGYVNWDLG----LSE   149 (291)
Q Consensus       81    d~~~~~~~~~~--~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~----~~v~V~~~~g----~~~   149 (291)
                        .....+.++.+  .+..+..+..+.+.+..+.....-.    ..+.+ ++|++++...+    +.+.|.++++    +..
T Consensus       64    ~~~~~~~~~~p~~~~~~~~~~~~~~~i~~yl~~~a~~~~l~----~~i~~~~~V~~v~~~~~~~~~~~~~~w~v~~~~~~~~~~~~~~~~   139 (532)
T 6SE3_D          64    KEMMCFPDFPYPDDFPNFMHNSKLQEYITAFAKEKNLL----KYIQFKTLVSSVNKRPDFSVTGQWDVTTEKDGKKESAV   139 (532)
T ss_dssp               GGGSSBTTBCCCTTSCSSCBHHHHHHHHHHHHHHHTCG----GGEETTCEEEEEEECTTHHHHCCEEEEEESSSCEEEEE
T ss_pred               CcccCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHCCCH----HHEEcCeEEEEEEECCCCCCCCcEEEEEecCCcEEEEE
```

```
Q ss_pred               ECEEEECCCHHHHcCCCCcccCccc--hhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59     150   YELVISTVPRDIWQLPGDEYIYSEG--WAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus       150   aD~VI~t~p~~~l~~~~~~f~p~lp--~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~   209 (291)
                        +|.||+|+        +..-.|.+|  ..+|...|.|+.+|..-......+....++.-+.+
T Consensus       140   ~d~vvvat--------G~~~~p~~p~~~~~g~~~f~g~~~Hs~~~~~~~~~~gk~V~VVG~G   193 (532)
T 6SE3_D          140   FDAVMICS--------GHHVYPNLPKESFPGLKHFKGKCFHSRDYKEPGIFKGKRVLVIGLG   193 (532)
T ss_dssp              ESEEEECC--------CSSSEECCCGGGSTTGGGCCSEEEEGGGCCCSGGGTTCEEEEECCS
T ss_pred              ECEEEEcc--------ccccCCCCCCCCCCCcccCCceeeeeeccCCccccCCCEEEEECCC
```

Template alignment | Template 3D Structure | PDBe

☐ 16. **6SEM_A Ancestral Flavin-containing monooxygenase (FMO) 2; Flavin, enzyme, membrane protein, Ancestral Sequence Reconstruction; HET: FAD; 2.8A {synthetic construct}**

Probability: 99.26%, E-value: 3.9e-10, Score: 108.47, Aligned cols: 178, Identities: 12%, Similarity: 0.089, Template Neff: 9.9

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCcccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59       1   MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus         1   ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                        ++|+|||||++|+++|..|.+.|++++|+|+.+.   .|+.|............                -.........
T Consensus         3   ~~v~IIGaG~sGl~~a~~l~~~g~~v~i~E~~~~---~GG~w~~~~~~~~~~~~----------------~~~~~~~~~~   63 (535)
T 6SEM_A           3   KKVAVIGAGVSGLISLKCCVDEGLEPTCFERTED---IGGLWRFKENVEDGRAS----------------IYQSVITNTS   63 (535)
T ss_dssp              CEEEEECCSHHHHHHHHHHHHHTCEEEEECSSSS---SCGGGSCCSSCCTTSCC----------------CCTTCBCSSC
T ss_pred              CEEEEECCCHHHHHHHHHHHHcCCCCEEEeCCCC---CCCCceeccCCCCCccc----------------cccceEEecC


Q ss_pred               cCcccccccCc--chhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCC----CCeEEEEcCC----EEE
Q Q_Madi_gp59      81   DGHIGQDEFEP--DHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVG----VGGYVNWDLG----LSE   149 (291)
Q Consensus        81   d~~~~~~~~~~--~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~----~~v~V~~~~g----~~~   149 (291)
                        .....+.++.+  ....+.....+.+.+..+.....-.    ..+.+ ++|++++...+    +.+.|.+.++    +..
T Consensus        64   ~~~~~~sd~p~~~~~~~~~~~~~~~~~~~~yL~~~a~~~~l~----~~i~~~~~V~~v~~~~~~~~~~~~~~w~V~~~~~g~~~~~~   139 (535)
T 6SEM_A          64   KEMSCFSDFPMPEHFPNFLHNSKLLEYFRIFAKKFDLL----KYIQFQTTVLSVKKCPDFSSSGQWEIVTESNGKEQSAV   139 (535)
T ss_dssp              STTTSBTTBCCCTTSCSSCBHHHHHHHHHHHHHHTTGG----GGEETTCEEEEEEECCC----CCEEEEEECSSCEEEEE
T ss_pred              ccccCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHcCCH----HHEECCcEEEEEEECCCCCCCCcEEEEEEeCCeEEEEE


Q ss_pred               ECEEEECCCHHHHcCCCCcccCccc--hhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59     150   YELVISTVPRDIWQLPGDEYIYSEG--WAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus       150   aD~VI~t~p~~~l~~~~~~f~p~lp--~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~   209 (291)
                        +|.||+|+        +..-.|.+|  ..+|...|.|..+|..-......+....++.-+.+
T Consensus       140   ~d~VVvat--------G~~~~p~~p~~~~~g~~~f~g~~~Hs~~~~~~~~~~gk~V~VVG~G   193 (535)
T 6SEM_A         140   FDAVMVCS--------GHHILPHIPLQSFPGIERFKGQYFHSRQYKHPEGFEGKRILVIGIG   193 (535)
T ss_dssp              ESEEEECC--------CSSSEECCCGGGSTTTTTCCSEEEEGGGCCCSTTCTTCEEEEESCC
T ss_pred              eCEEEECC--------CCCCCCCCCCCCCCCccccCceEEeceecCCccccCCCEEEEEcCC
```

Template alignment | Template 3D Structure | PDBe

☐ 17. **6Y48_A Baeyer-Villiger monooxygenase; Baeyer-Villiger monooxygenase, FLAVOPROTEIN; HET: FAD, NAP; 2.087A {Aspergillus flavus NRRL3357}**

Probability: 99.26%, E-value: 2.6e-10, Score: 110.31, Aligned cols: 173, Identities: 13%, Similarity: 0.066, Template Neff: 10

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCcccccchhHhcCCCCCCCcccCC-CCCeeeEecCCceechhhccccc
Q Q_Madi_gp59       1   MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDK-GVPVKYVVRGTPEEYRRKTHGKW   79 (291)
Q Consensus         1   ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~-~~~~~~~~~~~~~~~~~y~~k~~~~~   79 (291)
                        .+|+|||||++|+++|..|.+.|.+++|+|+...   .|+.|....+++..+.... ..............+...+...
T Consensus        26   ~~v~IIGaG~~Gl~~a~~l~~~g~~~~i~e~~~~---~Gg~w~~~~yp~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-   101 (561)
T 6Y48_A          26   VDVLIVGAGFGGIYSLYEMRKLGLKAVIYEAGND---IGGTWRWNCYPGAGVDSEVPEYQLSIPETWKDWTWSTNYPNY-   101 (561)
T ss_dssp              CSEEEECCSHHHHHHHHHHHHHTCCEEEECSSSS---SCTHHHHSCCTTCBCSSCTTSSSCCCHHHHTTCCCSBSSCBH-
T ss_pred              eeEEEECCCHHHHHHHHHHHHCCCCEEEEcCCCC---CCCCccccCCCCcccCCCCccccCCCchhhcCCCCccCCCCH-


Q ss_pred               ccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCCe-EEEEcCC-EEEECEEEEC
Q Q_Madi_gp59      80   WDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVGG-YVNWDLG-LSEYELVIST   156 (291)
Q Consensus        80   ~d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~~~v-~V~~~~g-~~~aD~VI~t   156 (291)
                                               .++.+.+......+++. ..+.+ ++|.++++.+.++. .|.++++ ++.||.||+|
T Consensus       102   -----------------------~ei~~yl~~~~~~~~~l~-~~i~~~~~V~~~~~~~~~~~~~~w~v~~~~g~~~~~~~~vV~A   157 (561)
T 6Y48_A         102   -----------------------EDLRKYFDHVDKVLDIK-KDCAFNSVVVGAHFHTVEGRWHIRTADGRTARAKYFIIA   157 (561)
T ss_dssp              -----------------------HHHHHHHHHHHHHHCCG-GGEESSCCEEEEEEETTTTEEEEEETTSCEEEESEEEEC
T ss_pred              -----------------------HHHHHHHHHHHHHhCCc-ccEEeceEEEEEEEeCCCCEEEEEECCCCEEEEEEEEEc


Q ss_pred               CCHHHHcCCCCcccCccchhhccCcccCceecceecc-ceecCCCCEEEEecCC
Q Q_Madi_gp59     157   VPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEG-RELFDKDNTIICDGTS   209 (291)
Q Consensus       157   ~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~-~e~~~~~~~~~~~~~~~~   209 (291)
                        +        +..-.|.+|..+|...|.|..+|....+ ....+....+..-+.+
T Consensus       158   t--------G~~~~p~~p~~~g~~~f~g~~~hs~~~~~~~~~~~~~~~gk~V~ViG~G   203 (561)
```

```
T 6Y48_A          158   A--------GFAAKRYIPEWPGIEKFKGIVHHSSFWPDEKIDVRGKRCAIIGTG   203 (561)
T ss_dssp               C--------CSCCSBCCCSCGGGGTCCSEEEEGGGCCSSCCCCBTSEEEEECCS
T ss_pred               e--------ecccCCCCCCCCCcccccceEeeccccCcccCCcCCCEEEEEeCC
```

Template alignment | Template 3D Structure | PDBe

☐ **18. 5IPY_B Flavin-containing monooxygenase; flavin-containing monooxygenase, FLAVOPROTEIN; HET: NAP, FAD; 1.5A {Roseovarius nubinhibens (strain ATCC BAA-591 / DSM 15170 / ISM)}**

Probability: 99.24%, E-value: 5.4e-10, Score: 105.39, Aligned cols: 190, Identities: 15%, Similarity: 0.057, Template Neff: 9.6

```
Q ss_pred               CeEEEECCCHHHHHHHHHH---HHcCC---eEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhh
Q Q_Madi_gp59     1     MTIAILGCGPTGLLAAHAC---TLEGY---DVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRK   74 (291)
Q Consensus       1     ~~V~IIGaG~aGl~aA~~L---~~~g~---~v~i~E~~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k   74 (291)
                        ++|+|||||+|||++|..|   .+.|.   +|+|+|+.+.   .|+.|......+.....   .......+........+
T Consensus       3     ~~V~IIGaG~aGL~aa~~l~~~~~~g~~~~~v~v~E~~~~---~GG~w~~~~~~~~~~~~~---~~~~~~~y~~l~tn~p~   76 (453)
T 5IPY_B          3     KRVAVIGAGPSGLAQLRAFQSAADQGAEIPEIVCFEKQAN---WGGLWNYTWRTGLDENG---EPVHCSMYRYLWSNGPK   76 (453)
T ss_dssp               CEEEEECCSHHHHHHHHHHHHHHHTTCCCCEEEEECSSSS---SCGGGSCCSCCSBCTTS---SBCCCCCCTTCBCSSCG
T ss_pred               cEEEEECCCHHHHHHHHHHHHHHHCCCCCCcEEEEeCCCC---CCCCCCCCCCCCCCCCC---CccccccCCcccccCCh


Q ss_pred               cccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCC-CCeEEEEcCC------
Q Q_Madi_gp59     75    THGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVG-VGGYVNWDLG------   146 (291)
Q Consensus       75    ~~~~~~d~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~-~~v~V~~~~g------   146 (291)
                        ....+.+-.+................+.+-+.+........-.+.     + ++|.+++...+ +.+.|.+.++
T Consensus       77    ~~~~f~d~~~~~~~~~~~~~~~~~~~v~~yL~~~a~~~~l~~~I~-----~~t~V~~v~~~~~~~~w~V~~~~~~~~~~~   151 (453)
T 5IPY_B          77    EGLEFADYSFEEHFGKQIASYPPRAVLFDYIEGRVHKADVRKWIR-----FNSPVRWVSYDAETAKFTVTAHNHETDSTY   151 (453)
T ss_dssp               GGTCBTTBCHHHHHTSCCCSSCBHHHHHHHHHHHHHHHTCGGGEE-----SSCCEEEEEEETTTTEEEEEEEETTTTEEE
T ss_pred               hhhcCCCCCCchhcCCCccCCCCHHHHHHHHHHHHHHhCChhhEE-----CCCeEEEEEEeCCCCeEEEEEEECCCCcEE


Q ss_pred               EEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59     147   LSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus       147   ~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~   209 (291)
                        ++.+|.||+|+        +..-.|.+|..+|...|.|..+|..-......+....++.-+.+
T Consensus       152   ~~~~D~VVvAt--------G~~s~p~~P~i~g~~~f~g~v~hs~~~~~~~~~~~~gk~VlVVG~G   206 (453)
T 5IPY_B          152   SAAFDHVICAS--------GHFSTPNVPFYEGFDTFNGRIVHAHDFRDAREFEGKDVLVMGAS   206 (453)
T ss_dssp               EEEESEEEECC--------CSSSEECCCCCTTTTTCSSEEEEGGGCCCGGGGTTCEEEEECSS
T ss_pred               EEEeCEEEEeC--------CCCCCCCCCCCCChhhCCCeEeeHHHhcCchhhCCCEEEEEcCC
```

Template alignment | Template 3D Structure | PDB | NCBI

☐ **19. d2ivda1 c.3.1.2 (A:10-306,A:415-464) Protoporphyrinogen oxidase {Myxococcus xanthus [TaxId: 34]}**

Probability: 99.24%, E-value: 3.2e-10, Score: 102.46, Aligned cols: 216, Identities: 13%, Similarity: 0.021, Template Neff: 11

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCC-----------------------
Q Q_Madi_gp59     1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKG-----------------------   57 (291)
Q Consensus       1     ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~~G~~~~~~~~~~~~~~l~~~-----------------------   57 (291)
                        ++|+|||||+|||+||+.|++.|++|+|+|++++   .|+.......++...+....
T Consensus       1     ~~v~VIGaG~aGLtaA~~L~~~g~~v~l~E~~~~---~GG~~~t~~~~~~~~d~G~~~~~~~~~~~~~~l~~~lgl~~~~~   77 (348)
T d2ivda1         1     MNVAVVGGGISGLAVAHHLRSRGTDAVLLESSAR---LGGAVGTHALAGYLVEQGPNSFLDREPATRALAAALNLEGRIR   77 (348)
T ss_dssp               CCEEEECCBHHHHHHHHHHHTTTCCEEEECSSSS---SBTTCCEEEETTEEEESSCCCEETTCHHHHHHHHHTTCGGGEE
T ss_pred               CeEEEECCCHHHHHHHHHHHHcCCCEEEEeCCCC---CCCceeEEEeCCeEEccCCCcccCCCHHHHHHHHHcCCcCeEE


Q ss_pred               ------CCeeeEecCCceechhhcccccccCccccc--------------------------------------------
Q Q_Madi_gp59     58    ------VPVKYVVRGTPEEYRRKTHGKWWDGHIGQD--------------------------------------------   87 (291)
Q Consensus       58    ------~~~~~~~~~~~~~~~y~~k~~~~~~~d~~~~~~~--------------------------------------------   87 (291)
                              ...+....+....+................
T Consensus       78    ~~~~~~~~~~~~~~~~~~~~p~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~l~~~~~~~~~~~~~~~~~~   157 (348)
T d2ivda1         78    AADPAAKRRYVYTRGRLRSVPASPPAFLASDILPLGARLRVAGELFSRRAPEGVDESLAAFGRRHLGHRATQVLLDAVQT   157 (348)
T ss_dssp               CSCSSCCCEEEEETTEEEECCCSHHHHHTCSSSCHHHHHHHHGGGGCCCCCTTCCCBHHHHHHHHTCHHHCCCCCHHHHH
T ss_pred               ECCcccCceEEEECCccccCCCCchHHhcCCCCCHHHHHHHHhhhhcCCCCCCCCCCHHHHHHHHhCHHHHHHHHHHHHHH


Q ss_pred               -----------------------------------------------------ccCcchhhccHHHHHHHHHHHhhhhcC
Q Q_Madi_gp59     88    -----------------------------------------------------EFEPDHQAWDIRQHYDMLWRTYVGKIE   114 (291)
Q Consensus       88    -----------------------------------------------------~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~   114 (291)
                                                                             ........-+...+.+.+.+.+.....
T Consensus       158   ~~~~~~~~~~s~~~~~~~~~~~~~~~~~s~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~G~~~l~~~la~~lg~~i~   237 (348)
T d2ivda1         158   GIYAGDVEQLSVAATFPMLVKMEREHRSLILGAIRAQKAQRQAALPAGTAPKLSGALSTFDGGLQVLIDALAASLGDAAH   237 (348)
T ss_dssp               HHHCCCTTTBBHHHHCHHHHHHHHHHSSHHHHHHHHHHHHTCC----CCSCCCCCCEEEETTCTHHHHHHHHHHHGGGEE
T ss_pred               chhcCCHHHHhHHHHhHHHHHHHHhcCcHHHHHHHHHHHHHHhcCCCCCCccccceeeccccHHHHHHHHHHHhccccc


Q ss_pred               CCCCCCcceeeeceeEeecCCCCCeEEEEcC----CEEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecce
Q Q_Madi_gp59     115   PYSIPTKGMVASFFKRENSDVGVGGYVNWDL----GLSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDL   190 (291)
```

```
Q Consensus      115   ~~~~~~~~~~~~~V~~i~~~~~~~v~V~~~~----g~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~   190 (291)
                       ..          ++|++|.  .+++++.|.+.+    .+++||.||+|+|+..+.+-.....+.+-......
T Consensus      238   ~~----------~~V~~I~-~~~~~~~v~~~~~~~~~~~~~~~d~VV~a~p~~~~~~ll~~~~~~~~~~~~~~----------   297 (348)
T d2ivda1        238   VG---------ARVEGLA-REDGGWRLIIEEHGRRAELSVAQVVLAAPAHATAKLLRPLDDALAALVAGI----------   297 (348)
T ss_dssp             SS---------EEEEEEE-CC--CCEEEEEETTEEEEEECSEEEECSCHHHHHHHHTTTCHHHHHHHHTC----------
T ss_pred             cC---------CeEEEEE-EeCCeEEEEEeeCCcceEEEECEEEECCCHHHHHHhccccCHHHHHHHhCC----------


Q ss_pred             eccceecCCCCEEEEecCCCCCceEEEeecCccccceecCCCCCCCcceeEEeccccCCCCCCCCCCCCCCEEEecccccc
Q Q_Madi_gp59   191   VEGRELFDKDNTIICDGTSLVPWTRLSKVHGFTSIEWPHHAAQPHTQAVRVRKPLHYTPGPHQNGSPTANWLHVGRYGQF   270 (291)
Q Consensus      191   v~~~e~~~~~~~~~~~~~~~~~~~r~~~~~~~~~~~e~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gr~g~~   270 (291)
                                                                .|.......+++....      ....| ++|.   .|.+
T Consensus      298   -----------------------------------------~~~~~~~~~~~~~~~~~~------~~~~~-~~~~---~G~~   326 (348)
T d2ivda1        298   -----------------------------------------XYNLGHLERVAAIDAA------LQRLP-GLHL---IGNA   326 (348)
T ss_dssp             -----------------------------------------CBTTHHHHHHHHHHHH------HHTST-TEEE---CSTT
T ss_pred             -----------------------------------------CCCCChHHHHHHHHHH------HHhCC-CEEE---eccC


Q ss_pred             ccCCcHHHHHHHHHHHHHHhc
Q Q_Madi_gp59   271   EKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus      271   ~~~~~~~~~~~~~~~~~~~~   290 (291)
                       .+++.++||+.+|...++++
T Consensus      327   ~~g~~~~~~i~~a~~~a~~~   346 (348)
T d2ivda1        327   YKGVGLNDCIRNAAQLADAL   346 (348)
T ss_dssp             TSCCSHHHHHHHHHHHHHHH
T ss_pred             CCCCCHHHHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDBe

☐ 20. **6JDK_A Baeyer-Villiger monooxygenase; monooxygenase, OXIDOREDUCTASE; HET: FAD; 2.495A {Parvibaculum lavamentivorans (strain DS-1 / DSM 13023 / NCIMB 13966)}**

Probability: 99.24%, E-value: 3.2e-10, Score: 109.13, Aligned cols: 173, Identities: 15%, Similarity: 0.074, Template Neff: 10.3

```
Q ss_pred             CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCC-CCCeeeEecCCceechhhccccc
Q Q_Madi_gp59     1   MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDK-GVPVKYVVRGTPEEYRRKTHGKW   79 (291)
Q Consensus        1   ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~~l~~-~~~~~~~~~~~~~~y~~k~~~~~   79 (291)
                       .+|+|||||++|+++|..|++.|++++|+|+...   .|+.|....+|+..+....  ...+..........+.......
T Consensus       18   ~~v~IIGaG~~Gl~~a~~l~~~g~~v~i~e~~~~---~Gg~w~~~~~p~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-   93 (544)
T 6JDK_A        18   FDALIVGAGFNGIYQLHRLRQEGFKVRLFEAGAD---MGGIWYWNCYPGARVDSHIPIYEFSIEELWRDWNWTERFPAW-   93 (544)
T ss_dssp             EEEEEECCSHHHHHHHHHHHHTTCCEEEEESSSS---SCTHHHHCCSTTCBCSSCTTTSSCCCHHHHTTCCCSBSSCBH-
T ss_pred             eEEEEECCCHHHHHHHHHHHHCCCCEEEEeCCCC---CCCCccccCCCCCcCCCCCcccCCCChHHHhccCCCCCCCCCH-


Q ss_pred             ccCcccccccCcchhhccHHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCCe-EEEEcCC-EEEECEEEEC
Q Q_Madi_gp59    80   WDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVGG-YVNWDLG-LSEYELVIST   156 (291)
Q Consensus       80   ~d~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~v-~V~~~~g-~~~aD~VI~t   156 (291)
                                              .++.+.+......+++. ..+.+ ++|.++++.++... .|.+++| ++.+|.||+|
T Consensus       94   -----------------------~~i~~yl~~~~~~~~l~-~~i~~~~~v~~~~~~~~~~~~w~v~~~~g~~~~~d~vI~A   149 (544)
T 6JDK_A        94   -----------------------DELRRYFHYVDKKLDLS-RDIRFGMRVSAAEFDEARDQWVIRTTDGTVVRARFFILC   149 (544)
T ss_dssp             -----------------------HHHHHHHHHHHHHHHTCG-GGEEETCCEEEEEEEGGGTEEEEEETTSCEEEEEEEEEC
T ss_pred             -----------------------HHHHHHHHHHHHHHcCCc-ccEECCcEEEEeEEECCCCEEEEEECCCcEEEEeEEEEC


Q ss_pred             CCHHHHcCCCCcccCccchhhccCcccCceecceeccce-ecCCCCEEEEecCC
Q Q_Madi_gp59   157   VPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRE-LFDKDNTIICDGTS   209 (291)
Q Consensus      157   ~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e-~~~~~~~~~~~~~~   209 (291)
                       +        +..-.|.+|..+|...|.|..+|....+.+ ..+....+..-+.+
T Consensus      150   t--------G~~s~p~~p~i~g~~~f~g~~~hs~~~~~~~~~~~gk~V~ViG~G   195 (544)
T 6JDK_A       150   T--------GFASKPYIPNYKGLESFAGESFHTGLWPQEGASFTGKRVGVVGTG   195 (544)
T ss_dssp             C--------CSCSSBCCCCCTTGGGCCSEEEEGGGCCTTCCCCTTCEEEEECCS
T ss_pred             c--------ccCCCCCCCCCCChhhcCCccccccCCCccCCCCCCEEEEECCC
```

Template alignment | Template 3D Structure | PDBe

☐ 21. **7AL4_D Ancestral Flavin-containing monooxygenase 1 (mammalian); FMO Paired Rossman fold Xenobiotic detoxification, FLAVOPROTEIN; HET: FAD, GOL, LMT, NAP; 3.0A {Felis catus}**

Probability: 99.23%, E-value: 7e-10, Score: 106.6, Aligned cols: 178, Identities: 14%, Similarity: 0.091, Template Neff: 10.1

```
Q ss_pred             CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59     1   MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus        1   ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                       ++|+|||||++|+++|..|.+.|.+++|+|+.+.   .|+.|...........                    ..........
T Consensus        3   ~~v~IIGaG~sGl~~a~~l~~~g~~v~v~E~~~~---~Gg~w~~~~~~~~~~~~----------------~~~~~~~~~~   63 (531)
T 7AL4_D         3   KRVAIVGAGVSGLASIKCCLEEGLEPTCFERSDD---LGGLWRFTEHVEEGRAS----------------LYKSVVSNSC   63 (531)
T ss_dssp             CEEEEECCBHHHHHHHHHHHHTTCEEEEECSSSS---SBGGGSCCSSCCTTSCC----------------CCTTCBCSSC
```

```
T ss_pred               cEEEEECCCHHHHHHHHHHHHcCCCcEEEeCCCC---CCCCcccccCCcCCccc----------------cccceEEeeC


Q ss_pred               cCcccccccCc--chhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCC----CCeEEEEcCC----EEE
Q Q_Madi_gp59     81    DGHIGQDEFEP--DHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVG----VGGYVNWDLG----LSE   149 (291)
Q Consensus        81    d~~~~~~~~~~--~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~----~~v~V~~~~g----~~~   149 (291)
                        .....+.++.+  ....+..+..+.+.+..+.......    ..+.+ ++|++++...+    +.+.|.+.++    +..
T Consensus        64    ~~~~~~~~~~~~~~~~~~~~~~~~~~yL~~~a~~~~l~----~~i~~~t~V~~v~~~~~~~~~~~~~~~w~v~~~~~~~~~~~~~~   139 (531)
T 7AL4_D          64    KEMSCYSDFPFPEDYPNYVPNSQFLEYLKMYANRFNLL----KHIQFKTKVCSVTKCPDFTVTGQWEVVTQHEGKQESAI   139 (531)
T ss_dssp               TTTSSCTTCCCCTTSCSSCBHHHHHHHHHHHHHHTTCG----GGEESSCEEEEEEECTTHHHHCCEEEEEEBTTBCCCCE
T ss_pred               ccccCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHcCCH----HhEecCCEEEEEEECCCCCCCCcEEEEEEcCCeEEEEE


Q ss_pred               ECEEEECCCHHHHcCCCCcccCccc--hhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59     150   YELVISTVPRDIWQLPGDEYIYSEG--WAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus        150   aD~VI~t~p~~~l~~~~~~f~p~lp--~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~~~   209 (291)
                        +|.||+|+        +..-.|.+|  ...|...|.|..+|.........+....++.-+.+
T Consensus        140   ~d~VVvAt--------G~~s~p~~p~~~~~g~~~f~g~~~Hs~~~~~~~~~~~~~k~V~VvG~G   193 (531)
T 7AL4_D          140   FDAVMVCT--------GFLTDPYLPLDSFPGINTFKGQYFHSRQYKHPDIFKDKRVLVVGMG   193 (531)
T ss_dssp               ESEEEECC--------CSSSSBCCCGGGSTTCTTCCSEEEEGGGCCCGGGGSSCEEEEESCC
T ss_pred               eCEEEEcC--------CCCCCCCCCCCCCCCcccCCceEeeeeecCChhHhCCCEEEEECCC
```

Template alignment | Template 3D Structure | PDBe

☐ **22. 6KBW_A Trimethylamine monooxygenase; flavin-containing monooxygenase, FLAVOPROTEIN; HET: NAP, FAD; 1.686A {Myroides profundi}**

Probability: 99.23%, E-value: 4.9e-10, Score: 106.13, Aligned cols: 190, Identities: 13%, Similarity: 0.038, Template Neff: 9.3

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCC------eEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhh
Q Q_Madi_gp59     1     MTIAILGCGPTGLLAAHACTLEGY------DVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRK   74 (291)
Q Consensus        1     ~~V~IIGaG~aGl~aA~~L~~~g~------~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k   74 (291)
                        ++|+|||||+|||++|..|++.+.      +|+|+|+.+.   .|+.|......+....-   .......+........+
T Consensus        4     ~~VaIIGaG~aGL~aA~~l~~~~~~~~~~~~~~~v~v~E~~~~---iGG~w~~~~~~~~~~~~~~~---~~~~~~~~y~~l~~n~p~   77 (467)
T 6KBW_A          4     LKVGIIGAGPSGLAMLRAFESEQKKGNPIPEIKCYEKQDN---WGGMWNYTWRTGVGKYG---EPIHGSMYKYLWSNGPK   77 (467)
T ss_dssp               CEEEEECCSHHHHHHHHHHHHHHTTTCCCCEEEEECSSSS---SCGGGCCCSCCSBCTTS---SBCCCCCCTTCBCSSCG
T ss_pred               cEEEEECCCHHHHHHHHHHHHHHHcCCCCCcEEEEeCCCC---CcCCcccCCCCCCCCCC---CcccCccccCcccCCCh


Q ss_pred               cccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCC-CCeEEEEcCC------
Q Q_Madi_gp59     75    THGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVG-VGGYVNWDLG------   146 (291)
Q Consensus        75    ~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~-~~v~V~~~~g------   146 (291)
                        ....+.+..+................+.+.+.+.+.+......-.+.     + ++|++++...+ +.+.|.+.++
T Consensus        78    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~yL~~~a~~~~l~~~I~-----~~~~V~~v~~~~~~~~~~~w~V~~~~~~~~~~~~~~   152 (467)
T 6KBW_A          78    ECLEFSDYTFMEHFKQPISSYPPREVLFDYIQGRIKQSNARDFIK-----FNTVARWVDYLEDKKQFRVIFDDLVKNETF   152 (467)
T ss_dssp               GGTCBTTBCHHHHHSSCCCSSCBHHHHHHHHHHHHTTTTGGGGEE-----CSEEEEEEEEETTTTEEEEEEEETTTTEEE
T ss_pred               hHhcCCCCCCchhcCCCccCCCCHHHHHHHHHHHHHHcCChhhee-----CCcEEEEEEEeCCCCeEEEEEEECCCCeEE


Q ss_pred               EEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59     147   LSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus        147   ~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~~~   209 (291)
                        +..+|.||+|+        +..-.|.+|..+|...|.|+.+|..-......+....++.-+.+
T Consensus        153   ~~~~D~VVvAt--------G~~s~p~~P~~~g~~~f~g~~~hs~~~~~~~~~~~~gk~VlVVG~G   207 (467)
T 6KBW_A          153   EEYFDYLVVGT--------GHFSTPNMPYFKGIDSFPGTVMHAHDFRGADQFIDKDILLIGSS   207 (467)
T ss_dssp               EEEESEEEECC--------CSSSEECCCCCTTGGGCCSEEEEGGGCCCGGGGTTCEEEEECCS
T ss_pred               EEEeCEEEEeC--------CCCCCCCCCCCCChhhCCCeEEEeeccCChHHhCCCeEEEECCC
```

Template alignment | Template 3D Structure | PDBe

☐ **23. 2IID_D L-amino-acid oxidase; flavoenzyme, FAD binding domain, reaction mechanism, sustrate binding, OXIDOREDUCTASE; HET: PHE, NAG, FUC, FAD; 1.8A {Calloselasma rhodostoma} SCOP: c.3.1.2, d.16.1.5**

Probability: 99.23%, E-value: 1.5e-9, Score: 102.03, Aligned cols: 270, Identities: 11%, Similarity: -0.005, Template Neff: 12

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59     1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus        1     ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                        .+|+|||||++|++||+.|++.|.+|+|+|+.+.   .|+..............+....................-....
T Consensus        34    ~dvvIIGaG~aGl~aA~~L~~~g~~v~vlE~~~~---~GG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   110 (498)
T 2IID_D          34    KHVVIVGAGMAGLSAAYVLAGAGHQVTVLEASER---PGGRVRTYRNEEAGWYANLGPMRLPEKHRIVREYIRKFDLRLN   110 (498)
T ss_dssp               CEEEEECCBHHHHHHHHHHHHTTCEEEEECSSSS---SBTTCCEEEETTTTEEEESSCCCEETTCHHHHHHHHHTTCCEE
T ss_pred               CeEEEECccHHHHHHHHHHHHCCCcEEEEEecCC---CccceEEEecCCCceeEeecCccCCCCCHHHHHHHHHcCCeec


Q ss_pred               -------------------------cCcccccccCcchh-----------------------------------------
Q Q_Madi_gp59     81    -------------------------DGHIGQDEFEPDHQ-----------------------------------------   94 (291)
Q Consensus        81    -------------------------d~~~~~~~~~~~~~~~~~~-----------------------------------------   94 (291)
                                                 ..............
```

```
T Consensus      111  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  190 (498)
T 2IID_D         111  EFSQENDNAWYFIKNIRKKVGEVKKDPGLLKYPVKPSEAGKSAGQLYEESLGKVVEELKRTNCSYILNKYDTYSTKEYLI  190 (498)
T ss_dssp             EECSCCTTSEEEETTEEEEHHHHHHCGGGGCCCCCGGGTTCCHHHHHHHHTHHHHHHHHHSCHHHHHHHHTTSBHHHHHH
T ss_pred             ccCCcCCCceEEEeCeeeceeeeecCCcccccccCHHHCCCCHHHHHHHHHHHHHHHHHhcChhHHHhhcCCCcHHHHHH


Q ss_pred             -------------------------------------------hccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEe
Q Q_Madi_gp59     95   -------------------------------------------AWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRE  131 (291)
Q Consensus      95   -------------------------------------------~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~V~~i  131 (291)
                                                                 ..........+...+....... ..     .++|++|
T Consensus      191  ~~~~~g~g~~~~~~a~~~~~~~~~v~~~~~~~~~~~~~~~~~~~~~~~~g~~~~~~~~~~~~~~~i-~~-----~~~V~~I  264 (498)
T 2IID_D         191  KEGDLSPGAVDMIGDLLNEDSGYYVSFIESLKHDDIFAYEKRFDEIVDGMDKLPTAMYRDIQDKV-HF-----NAQVIKI  264 (498)
T ss_dssp             HTSCCCHHHHHHHHHHTTCGGGTTSBHHHHHHHHHHHTTCCCEEEETTCTTHHHHHHHHHTGGGE-ES-----SCEEEEE
T ss_pred             HccCCCHHHHHHHHHHhhcccCccHHHHHHHhhcccccccccceEecCchhHHHHHHHHhcccce-eC-----CceEEEE


Q ss_pred             ecCCCCCeEEEEcC-----CEEEECEEEECCCHHHHcCCCCcccCccc----hhhccCcccCceecceeccceec-----
Q Q_Madi_gp59     132  NSDVGVGGYVNWDL-----GLSEYELVISTVPRDIWQLPGDEYIYSEG----WAIGDAPERGVFVDDLVEGRELF-----  197 (291)
Q Consensus      132  ~~~~~~~v~V~~~~-----g~~~aD~VI~t~p~~~l~~~~~~f~p~lp----~~~g~~~~~g~~~~~~v~~~e~~-----  197 (291)
                      . .++++++|.+++     ..+.||.||+|+|.....  ...+.|.++    .......+.......+..+....
T Consensus      265  ~-~~~~~v~v~~~~~~g~~~~i~ad~VV~a~g~~~~~--~l~~~~~l~~~~~~~~~~~~~~~~~~~v~~~~~~~~~~~~~~~~  341 (498)
T 2IID_D         265  Q-QNDQKVTVVYETLSKETPSVTADYVIVCTTSRAVR--LIKFNPPLLPKKAHALRSVHYRSGTKIFLTCTTKFWEDDGI  341 (498)
T ss_dssp             E-ECSSCEEEEEECSSSCCCEEEESEEEECSCHHHHT--TSEEESCCCHHHHHHHHHCCEECEEEEEEEESSCGGGGGTC
T ss_pred             E-ECCCeEEEEEEcCCCCCcEEEeCEEEEcCCHHHHh--cCCcCCCCCHHHHHHHHhCCCCCeeEEEEEECCccccccCC


Q ss_pred             -------CCCCEEEEecCCCCCceEEEeecCcccc-------------------------------------------ee
Q Q_Madi_gp59     198  -------DKDNTIICDGTSLVPWTRLSKVHGFTSI-------------------------------------------EW  227 (291)
Q Consensus      198  -------~~~~~~~~~~~~~~~~~~~r~~~~~~~~~~~~~~-------------------------------------------e~  227 (291)
                             .....++++.+...+-...+... +..-                                           .|
T Consensus      342  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~w  420 (498)
T 2IID_D         342  HGGKSTTDLPSRFIYYPNHNFTNGVGVIIA-YGIGDDANFFQALDFKDCADIVFNDLSLIHQLPKKDIQSFCYPSVIQKW  420 (498)
T ss_dssp             CSSEEEESSTTCEEECCSSCCTTSCEEEEE-EEETHHHHTTTTSCHHHHHHHHHHHHHHHHTCCHHHHHHHEEEEEEEEG
T ss_pred             cccccccCCCCceEEeeccccCCCceEEEE-EEechhHHHHHcCCHHHHHHHHHHHHHHHhCCChHhHHhhcccceeeec


Q ss_pred             cC----CCCCCCcceeEEeccccccCCCCCCCCCCCCCEEEeccccccccCCcHHHHHHHHHHHHHhc
Q Q_Madi_gp59     228  PH----HAAQPHTQAVRVRKPLHYTPGPHQNGSPTANWLHVGRYGQFEKGVVVTDAFDQVTKKLKEM  290 (291)
Q Consensus      228  ~~----~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gr~g~~~~~~~~~~~~~~~~~~~~~~~~~~  290 (291)
                      +.    ...|+...........+.      ......++|++|-+....+ -.++.|+..+...+++|
T Consensus      421  ~~~~~~~g~~~~~~p~~~~~~~~~~~~------~~~~~~~~l~~aGd~~~~~~-~~~~~A~~sG~~aA~~i  480 (498)
T 2IID_D         421  SLDKYAMGGITTFTPYQFQHFSDP------LTASQGRIYFAGEYTAQAH-GWIDSTIKSGLRAARDV  480 (498)
T ss_dssp             GGCTTTCSSEECCCTTHHHHHHHH------HHCCBTTEEECSGGGSSSS-SCHHHHHHHHHHHHHHH
T ss_pred             ccCCCCCCccCcCCCCCchhhcch------hccCCCCEEECCccccccc-CcHHHHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDBe

☐ 24. **5M10_A Cyclohexanone Monooxygenase from Thermocrispum municipale; Cyclohexanone monooxygenase Baeyer-Villiger monooxygenases Flavoenzymes, oxidoreductase; HET: FAD, GOL, NAP, TRS; 1.22A {Thermocrispum municipale}**

Probability: 99.21%, E-value: 1e-9, Score: 105.5, Aligned cols: 175, Identities: 14%, Similarity: 0.101, Template Neff: 10.5

```
Q ss_pred             CeEEEECCCHHHHHHHHHHHHc-CCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhccccc
Q Q_Madi_gp59     1    MTIAILGCGPTGLLAAHACTLE-GYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKW  79 (291)
Q Consensus      1    ~~V~IIGaG~aGl~aA~~L~~~-g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~y~~k~~~~~  79 (291)
                      .+|+|||||++|+++|..|.+. |.+++|+|++..   .|+.|....+++..+..   ....+...-.........|.
T Consensus      9    ~~v~IIGaG~~Gl~~a~~l~~~~g~~v~i~e~~~~---~Gg~w~~~~~~~~~~~~~~~---~~~~~~~~~~~~~~~~~~~~~~~--  80 (541)
T 5M10_A         9    LDAIVIGAGFGGIYMLHKLRNDLGLSVRVFEKGGG---VGGTWYWNKYPGAKSDT---EGFVYRYSFDKELLREYDWT--  80 (541)
T ss_dssp             EEEEEECCSHHHHHHHCCCCCCTCCCEEEECSSSS---SCTHHHHCCSTTCBCSS---CGGGSSCCSCHHHHHHCCCC--
T ss_pred             ceEEEECCCHHHHHHHHHHHHHcCCcEEEEeCCCC---CCCCcccCCCCCCccCC---CcccccccCCHHHHhcCCCC--


Q ss_pred             ccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCCe-EEEEcCC-EEEECEEEEC
Q Q_Madi_gp59     80   WDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVGG-YVNWDLG-LSEYELVIST  156 (291)
Q Consensus      80   ~d~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~~v-~V~~~~g-~~~aD~VI~t  156 (291)
                                    ..+..+..+...+..+.......    ..+.+ ++|.++.+.++... .|.++++ .+.+|.||+|
T Consensus      81   --------------~~~~~~~~~~i~~yl~~~~~~~~~~l~----~~i~~~~~~V~~~~~~~~~~~~~~w~v~~~~g~~~~a~~vI~A  142 (541)
T 5M10_A         81   --------------TRYLDQPDVLAYLEHVVERYDLA----RDIQLNTEVTDAIFDEETELWRVTTAGGETLTARFLVTA  142 (541)
T ss_dssp             --------------BSSCBHHHHHHHHHHHHHHTTCG----GGEETTCCEEEEEEETTTTEEEEEETTSCEEEEEEEEEC
T ss_pred             --------------ccCCCHHHHHHHHHHHHHHcCCh----hcEEcceEEEEEEEeCCCCEEEEEECCCCEEEEeEEEEC


Q ss_pred             CCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59     157  VPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS  209 (291)
Q Consensus      157  ~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~~~~~  209 (291)
                      +        +..-.|.+|..+|...|.|+.+|..-.+....+....+..-+.+
T Consensus      143  t--------G~~~~p~~p~i~g~~~f~g~~~hs~~~~~~~~~~~~~~~~~k~V~ViG~G  187 (541)
T 5M10_A         143  L--------GLLSRSNIPDIPGRDSFAGRLVHTNAWPEDLDITGKRVGVIGTG  187 (541)
```

```
T ss_dssp               C--------CTTCSBCCCCCTTGGGCCSEEEEGGGCCTTCCCTTSEEEEECCS
T ss_pred               c--------cccCCCCCCCCCCCcCCCceEeeccCCCCCcCCCCCeEEEEcCC
```

Template alignment | Template 3D Structure | PDBe

☐ 25. **6A37_A Putative flavin-binding monooxygenase; cyclohexanone monooxygenase, FAD binding, OXIDOREDUCTASE; HET: FAD; 2.204A {Acinetobacter calcoaceticus}**

Probability: 99.21%, E-value: 1.1e-9, Score: 105.75, Aligned cols: 175, Identities: 13%, Similarity: 0.042, Template Neff: 10.1

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHc-CCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhccccc
Q Q_Madi_gp59     1     MTIAILGCGPTGLLAAHACTLE-GYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKW   79 (291)
Q Consensus       1     ~~V~IIGaG~aGl~aA~~L~~~-g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~   79 (291)
                        .+|+|||||++|+++|..|.+. |.+++|+|+.+.   .|+.|....+|+..+.                 .....+..
T Consensus       27    ~~v~IIGaG~sGl~~a~~l~~~~g~~v~i~E~~~~---~Gg~w~~~~~p~~~~~-----------------~~~~~~~~-   85 (552)
T 6A37_A          27    FDAIIIGAGFGGLYSLKKLRDDFNLKVRAFDRATE---VGGTWFWNQYPGALSD-----------------SETHLYCY-   85 (552)
T ss_dssp               EEEEEECCSHHHHHHHCCCCCCTCCCEEEECSSSS---SCTHHHHCCCTTCEEE-----------------EETTTSSC-
T ss_pred               ceEEEECCCHHHHHHHHHHHHhCCCcEEEEeCCCC---CCCCCCcCCCCCccCC-----------------CCchhhcc-


Q ss_pred               ccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCC-eEEEEcCC-EEEECEEEEC
Q Q_Madi_gp59     80    WDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVG-GYVNWDLG-LSEYELVIST   156 (291)
Q Consensus       80    ~d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~-v~V~~~~g-~~~aD~VI~t   156 (291)
                         ...........+...+..+..+...+..+.......    ..+.+ ++|.++.++++.. +.|.++++ .+.||.||+|
T Consensus       86    -s~~~~~~~~~~~~~~~~~~~~i~~yl~~~~~~~~l~----~~i~~~~~V~~~~~~~~~~~w~v~~~~g~~~~a~~vI~A   160 (552)
T 6A37_A          86    -SWDKELLQEMEIKRKYISQPDVLAYLKRVADKHDLR----KDIQFETGIRSAYFDEENSFWNVTTENDEKFTARFLITA   160 (552)
T ss_dssp               -SSCHHHHHHSCCCBSEEEHHHHHHHHHHHHHHTTCG----GGEECSCCEEEEEEETTTTEEEEEETTCCEEEEEEEEEC
T ss_pred               -cCChHHHhcCCcccCCCHHHHHHHHHHHHHHHcCCh----hhEEeceEEEEEEEeCCCCEEEEEECCCcEEEEEEEEEc


Q ss_pred               CCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59     157   VPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus       157   ~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~   209 (291)
                        +        +..-.|.+|..+|...|.|..+|..-.+....+....+..-+.+
T Consensus       161   t--------G~~s~p~~p~~~g~~~f~g~~~hs~~~~~~~~~~~~~k~V~ViG~G   205 (552)
T 6A37_A          161   L--------GLLAAPNLPKIKGIETFKGELHHTSRWPKDVTFSGKRVGVIGTG   205 (552)
T ss_dssp               C--------CCCCCCCCCCCTTGGGCCSEEEEGGGCCSSCCCTTCEEEEECCS
T ss_pred               c--------cccCCCCCCCCCccccCCCceeecccCCCCCCCCCCeEEEEccC
```

Template alignment | Template 3D Structure | PDBe

☐ 26. **5J7X_A Dimethylaniline monooxygenase, putative; Baeyer-Villiger monooxygenase, oxidoreductase; HET: TAM, FAD; 1.9A {Aspergillus flavus}**

Probability: 99.2%, E-value: 6e-10, Score: 107.5, Aligned cols: 173, Identities: 15%, Similarity: 0.067, Template Neff: 10.1

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHc-CCeEEEECCCCCccccchhHhcCCCCCCCcccCC-CCCeeeEecCCceechhhcccc
Q Q_Madi_gp59     1     MTIAILGCGPTGLLAAHACTLE-GYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDK-GVPVKYVVRGTPEEYRRKTHGK   78 (291)
Q Consensus       1     ~~V~IIGaG~aGl~aA~~L~~~-g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~-~~~~~~~~~~~~~~~y~~k~~~~   78 (291)
                        .+|+|||||++|+++|..|.+. |.+++|+|+.+.   .|+.|....+++..+.... ...+..........+...+...
T Consensus       13    ~~v~IIGaG~~Gl~~a~~l~~~~g~~~~i~e~~~~---~Gg~w~~~~y~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   89 (549)
T 5J7X_A          13    LDALIIGSGFSGIYLLHKLRDELKLKVKIFEAESD---IGGTWNNNRYPGARVDCPVPFYAYSLPEVWQSWNWTELYPNQ   89 (549)
T ss_dssp               EEEEEECCSHHHHHHHCCCCCCTCCCEEEECSSSS---SSTHHHHCCCTTCBCSSCTTSSSCCCHHHHTTCCCSBSSCBH
T ss_pred               ccEEEECCCHHHHHHHHHHHHHHCCCCEEEEeCCCC---CCCCcccCCCCCccccCCCccccCCchHHHccCCccccCCCH


Q ss_pred               cccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCC-CCeEEEEcCC-EEEECEEEE
Q Q_Madi_gp59     79    WWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVG-VGGYVNWDLG-LSEYELVIS   155 (291)
Q Consensus       79    ~~d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~-~~v~V~~~~g-~~~aD~VI~   155 (291)
                                                .++.+.+......+++. ..+.+ ++|+++.++++ +.+.|.+++| .+.+|.||+
T Consensus       90    ------------------------~ei~~yl~~~~~~~~l~-~~i~~~~~V~~~~~~~~~~~w~V~~~~g~~~~ad~vI~   144 (549)
T 5J7X_A          90    ------------------------KEIKSYFDHVDRVLDVR-KDCLFHSRVNEGTFDEATGRWTVWTTDGKVATAKYLLV   144 (549)
T ss_dssp               ------------------------HHHHHHHHHHHHHHCCG-GGEESSCCEEEEEEETTTTEEEEEETTSCEEEEEEEEE
T ss_pred               ------------------------HHHHHHHHHHHHHhCCc-ccEEEEeEEEEeEEeCCCCeEEEEECCCcEEEEeEEEE


Q ss_pred               CCCHHHHcCCCCcccCccchhhccCcccCceecceeccc--eecCCCCEEEEecCC
Q Q_Madi_gp59     156   TVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGR--ELFDKDNTIICDGTS   209 (291)
Q Consensus       156   t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~--e~~~~~~~~~~~~~~   209 (291)
                        |+        +..-.|.+|..+|...|.|..+|..-.+.  ...+....+..-+.+
T Consensus       145   At--------G~~s~p~~p~~~g~~~f~G~~~hs~~~~~~~~~~~~~~gk~V~ViG~G   192 (549)
T 5J7X_A          145   AV--------GFASKSYLPDWKGLDSFKGTIYHSAHWPEAEEISVKGKKVAVIGTG   192 (549)
T ss_dssp               CC--------CCCBCCCCCCCTTGGGCSSEEEETTSCCCSSCCCCBTCEEEEECCS
T ss_pred               Cc--------cCCCCCCCCCCCcccccCCceeehhhCCcHHhcCCCCCeEEEEeCC
```

Template alignment | Template 3D Structure | PDBe

☐ 27. **2IVD_B PROTOPORPHYRINOGEN OXIDASE; PROTOPORPHYRINOGEN OXIDASE, PORPHYRIN BIOSYNTHESIS, CHLOROPHYLL BIOSYNTHESIS, OXIDOREDUCTASE, HAEM BIOSYNTHESIS, HEME BIOSYNTHESIS, FAD, PORPHYRIA, ACIFLUORFEN, FLAVOPROTEIN; HET: ACJ, GOL, FAD, TWN; 2.3A {MYXOCOCCUS XANTHUS} SCOP: c.3.1.2, d.16.1.5**

Probability: 99.2%, E-value: 2.3e-9, Score: 101.49, Aligned cols: 266, Identities: 12%, Similarity: 0.035, Template Neff: 10.6

```
Q ss_pred                 CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCC-----------------------
Q Q_Madi_gp59      1      MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKG-----------------------   57 (291)
Q Consensus        1      ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~-----------------------   57 (291)
                          ++|+|||||+|||+||+.|+++|++|+|+|++.+   .||........+..++....
T Consensus        17     ~~v~IIGgG~aGL~aA~~L~~~g~~v~vlE~~~~---~GGr~~t~~~~g~~~d~G~~~~~~~~~~~~~l~~~lgl~~~~~   93 (478)
T 2IVD_B           17     MNVAVVGGGISGLAVAHHLRSRGTDAVLLESSAR---LGGAVGTHALAGYLVEQGPNSFLDREPATRALAAALNLEGRIR   93 (478)
T ss_dssp                 CEEEEECCSHHHHHHHHHHHHTTCEEEEECSSSS---SCSSCCEEEETTEEEESSCCCEETTCHHHHHHHHHTTCGGGEE
T ss_pred                 CcEEEECCcHHHHHHHHHHHhcCCCEEEEecCCc---ccccceeeeeCCeEEccCCCeecCCCHHHHHHHHHcCCcCcEE


Q ss_pred                 ------CCeeeEecCCceechhhcccccc-----------------------cCccccccc-------------------
Q Q_Madi_gp59      58     ------VPVKYVVRGTPEEYRRKTHGKWW-----------------------DGHIGQDEF-------------------   89 (291)
Q Consensus        58     ------~~~~~~~~~~~~~~~y~~k~~~~~~~-----------------------d~~~~~~~~~-------------------   89 (291)
                                ...+....+....+.........                       ....+...+
T Consensus        94     ~~~~~~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~l~~~~~~~~~~~~~~~~~~   173 (478)
T 2IVD_B           94     AADPAAKRRYVYTRGRLRSVPASPPAFLASDILPLGARLRVAGELFSRRAPEGVDESLAAFGRRHLGHRATQVLLDAVQT   173 (478)
T ss_dssp                 ECCTTCCCCEEECSSSEEECCSSHHHHHHCSSSCHHHHHHHHGGGGCCCCCTTCCCBHHHHHHHHHCHHHCCCCCHHHHH
T ss_pred                 eCChhhcceEEEECCEEEeCCCCcHHHHhCCCCCHHHHHHHHhHhhcCCCCCCCCCCHHHHHHHHhCHHHHHHHHHHHHH


Q ss_pred                 -------------------------------------------------------CcchhhccHHHHHHHHHHHhhhhcC
Q Q_Madi_gp59      90     -------------------------------------------------------EPDHQAWDIRQHYDMLWRTYVGKIE   114 (291)
Q Consensus        90     -------------------------------------------------------~~~~~~~~~~~~~~~l~~~~~~~~~~~   114 (291)
                                                                                 ......-+...+.+.|.+.+
T Consensus        174    ~~~~~~~~~~s~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gG~~~l~~~L~~~l-----   248 (478)
T 2IVD_B           174    GIYAGDVEQLSVAATFPMLVKMEREHRSLILGAIRAQKAQRQAALPAGTAPKLSGALSTFDGGLQVLIDALAASL-----   248 (478)
T ss_dssp                 HHHCCCTTTBBHHHHCHHHHHHHHHHSSHHHHHHHHHHHHHTC--------CCCCCEEEETTCTHHHHHHHHHHH-----
T ss_pred                 chhCCCHHHHhHHHHcHHHHHHHHHcChHHHHHHHHHHHHHHhcCCCCCCccccceeccccHHHHHHHHHHHHh-----


Q ss_pred                 CCCCCCcceee-eceeEeecCCCCCeEEEEcC-C---EEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecc
Q Q_Madi_gp59      115    PYSIPTKGMVA-SFFKRENSDVGVGGYVNWDL-G---LSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDD   189 (291)
Q Consensus        115    ~~~~~~~~~~~~~-~~V~~i~~~~~~~~~v~V~~~~~-g---~~~aD~VI~t~p~~~l~~~~~~~~f~p~lp~~~g~~~~~~g~~~~~   189 (291)
                           -    ..+.. ++|++|+ ..+++++|.+.+ |   +++||.||+|+|++.+.+-.....+..........+.......
T Consensus        249    -g----~~i~~~~~V~~I~-~~~~~~v~v~~~~~g~~~~~~~ad~VI~A~p~~~l~~il~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   322 (478)
T 2IVD_B           249    -G----DAAHVGARVEGLA-REDGGWRLIIEEHGRRAELSVAQVVLAAPAHATAKLLRPLDDALAALVAGIAYAPIAVVH   322 (478)
T ss_dssp                 -G----GGEETTCEEEEEE-ECSSSEEEEEEETTEEEEEEESEEEECSCHHHHHHHHTTTCHHHHHHHHTCEEEEEEEEE
T ss_pred                 -C----ccEEcCCceEEEE-EcCCEEEEEEccCCceeEEEeCEEEEcCCHHHHHHHccccCHHHHHHHccCCCCCEEEEE


Q ss_pred                 eeccceecC--CCCEEEEecCCCCCceEEEeecCcccc------------------------------------------
Q Q_Madi_gp59      190    LVEGRELFD--KDNTIICDGTSLVPWTRLSKVHGFTSI------------------------------------------   225 (291)
Q Consensus        190    ~v~~~e~~~~--~~~~~~~~~~~~~~~~~~~~~~r~~~~~~~~~~~~~~~~~------------------------------------------   225 (291)
                          +..+.+...  ...-++.....+.+....+........
T Consensus        323    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~   402 (478)
T 2IVD_B           323    LGFDAGTLPAPDGFGFLVPAEEQRRMLGAIHASTTFPFRAEGGRVLYSCMVGGARQPGLVEQDEDALAALAREELKALAG   402 (478)
T ss_dssp                 EEECTTSSCCCCSSEEECCGGGCCSCCEEEEHHHHCGGGBCTTCEEEEEEEECTTCGGGGGSCHHHHHHHHHHHHHHHHC
T ss_pred                 EEEecccCCCCCCeeEEechhhCCceeEEEEecccCCCcCCCCcEEEEEEecCCCCcccccCCHHHHHHHHHHHHHHHhC


Q ss_pred                 -----------eecC-CCCCCCcceeEEecccccCCCCCCCCCCCCCEEEeccccccccCCcHHHHHHHHHHHHHhc
Q Q_Madi_gp59      226    -----------EWPH-HAAQPHTQAVRVRKPLHYTPGPHQNGSPTANWLHVGRYGQFEKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus        226    -----------e~~~~-~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gr~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   290 (291)
                                     .|+. ...++...........+.       .....++|.   .|.|.-+..+++|++.+...++.+
T Consensus        403    ~~~~~~~~~~~~~~w~~~~~p~~~~~g~~~~~~~~~~~~~~~~~~~-------~~~~~~~~~l~~---aGd~~~~g~~ie~a~~~sg~~aa~~i   469 (478)
T 2IVD_B           403    VTARPSFTRVFRWPLGIPQYNLGHLERVAAIDAA-------LQRLPGLHL---IGNAYKGVGLNDCIRNAAQLADAL   469 (478)
T ss_dssp                 CCSCCSEEEEEEEEEEEEECBTTHHHHHHHHHHH-------HHTSTTEEE---CSTTTSCCSHHHHHHHHHHHHHHH
T ss_pred                 CCCCCeeEEEEEcCcCCCCCCCCHHHHHHHHHHH-------HHhCCCEEE---ecCCCCCCCHHHHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDBe

☐ 28. **6HNS_A Small molecule metabolism; drug metabolism, monooxygenase, thermostability, indigo, FLAVOPROTEIN; HET: NAP, FAD; 1.84A {Nitrincola lacisaponensis}**

Probability: 99.19%, E-value: 1.7e-9, Score: 102.01, Aligned cols: 190, Identities: 16%, Similarity: 0.081, Template Neff: 10.1

```
Q ss_pred                 CeEEEECCCHHHHHHHHHH---HHcCC---eEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCCceechhh
Q Q_Madi_gp59      1      MTIAILGCGPTGLLAAHAC---TLEGY---DVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRK   74 (291)
Q Consensus        1      ~~V~IIGaG~aGl~aA~~L---~~~g~---~v~i~E~~~~~~~~~~G~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~y~~k   74 (291)
                          ++|+|||||+||+++|..|   .+.|.   +|+|+|+.+.   .|+.|......+.....   .......+........+
T Consensus        3      ~~V~IIGaG~aGl~aa~~l~~~~~~~~g~~~~~~v~v~E~~~~---~GG~w~~~~~~~~~~~~~~~~~---~~~~~~~~~~~~~l~~~~~~   76 (454)
T 6HNS_A           3      TRVAIIGAGPCGLAQLRAFQSAAAKGAAIPELVCFEKQSD---WGGMWNYTWRTGVDEHG---EPVHGSMYRYLWSNGPK   76 (454)
```

```
T ss_dssp                CEEEEECCSHHHHHHHHHHHHHHHTTCCCCEEEEECSSSS---SCGGGSCCSCCSBCTTS---SBCCCCCCTTCBCSSCH
T ss_pred                CEEEEECCCHHHHHHHHHHHHHHHCCCCCCcEEEEECCCC---CCCCCccCCCCCCCCCC---CcCCCccccCccccCCH


Q ss_pred                cccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCC-CCeEEEEcCC------
Q Q_Madi_gp59     75     THGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVG-VGGYVNWDLG------   146 (291)
Q Consensus       75     ~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~-~~v~V~~~~g------   146 (291)
                         ....+.+..+................+.+.+.+........-.+.     + ++|++++..++ +.+.|.+.++
T Consensus       77     ~~~~~~~~~~~~~~~~~~~~~~~~~~v~~yL~~~a~~~gl~~~i~-----~~~~V~~v~~~~~~~~w~V~~~~~~~~~~~   151 (454)
T 6HNS_A          77     ECLEFADYTFDEHFGRPIGSYPPREVLWDYIKGRVEKAGVRDYIR-----FNTAVRQVSYDETSGLFSVTVQDHSNNRVY   151 (454)
T ss_dssp                HHHCBTTBCHHHHHSSCCCSSCBHHHHHHHHHHHHHHHTCGGGEE-----CSEEEEEEEEETTTTEEEEEEEETTTTEEE
T ss_pred                HHhcCCCCCCChhcCCCCCCCCCHHHHHHHHHHHHHHHCChhhEE-----CCcEEEEEEEcCCCCEEEEEEEECCCCeEE


Q ss_pred                EEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59     147    LSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus       147    ~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~   209 (291)
                         ++.+|.||+|+        +..-.|.+|...|...|.|..+|..-......+....++.-+.+
T Consensus       152    ~~~~d~VVvAt--------G~~s~p~~P~i~g~~~f~g~~~hs~~~~~~~~~~~k~V~VvG~G   206 (454)
T 6HNS_A          152    TETFDYVVNAC--------GHFSTPNTPYFEGFERFGGRVLHAHDFRDALEFKDKDILVVGSS   206 (454)
T ss_dssp                EEEESEEEECC--------CSSSEECCCCCBTTTTCCSEEEEGGGCCCGGGGTTCEEEEECSS
T ss_pred                EEEeCEEEEcC--------CCCCCCCCCCCCChhhhCCeEEEeEeeCChhhcCCCeEEEEcCC
```

Template alignment | Template 3D Structure | PDBe

☐ 29. **4ZCD_B Renalase; Renalase, oxidase, flavoenzyme, OXIDOREDUCTASE; HET: NAD, FAD; 1.6605A {Pseudomonas syringae pv. phaseolicola (strain 1448A / Race 6)}**

Probability: 99.19%, E-value: 2.8e-9, Score: 95.56, Aligned cols: 269, Identities: 14%, Similarity: 0.054, Template Neff: 11.5

```
Q ss_pred                CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCC-------------
Q Q_Madi_gp59     1      MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGT-------------   67 (291)
Q Consensus       1      ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~~G~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~-------------   67 (291)
                         .+|+|||||++|+++|+.|++.|.+|+|+|+.+.   .|+.......+......   ....+.....
T Consensus       3      ~dv~IvG~G~~Gl~~A~~L~~~g~~v~l~e~~~~---~~g~~~~~~~~~~~~~~~~~---g~~~~~~~~~~~~~~~~~~~~~~~   76 (336)
T 4ZCD_B          3      VPIAIIGTGIAGLSAAQALTSAGHQVHLFDKSRG---SGGRMSSKRSDAGSLDM---GAQYFTARDRRFATAVKQWQAQG   76 (336)
T ss_dssp                CCEEEECCSHHHHHHHHHHHHTTCCEEEECSSSS---SCGGGCCBCCTTSCBCC---SCCCBCCCSHHHHHHHHHHHHTT
T ss_pred                ccEEEECCCHHHHHHHHHHHHCCCcEEEEeCCCC---CCccccccccCCCCccc---CCceeeeCCHHHHHHHHHHHHCC


Q ss_pred                ceechhhcccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCCeEEEEcCC
Q Q_Madi_gp59     68     PEEYRRKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVGGYVNWDLG   146 (291)
Q Consensus       68     ~~~y~~k~~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~~~v~V~~~~g   146 (291)
                         ........................  ..+.....+..+.+.+.....-.        . ++|+++. .+++++++...++
T Consensus       77     ~~~~~~~~~~~~~~~~~~~~~~~~~~--~~~~~~~~~~~~~~~~~~~~~~~~~i~--------~~~~v~~i~-~~~~~~~~~~~~~~~   145 (336)
T 4ZCD_B          77     HVSEWTPLLYNFHGGRLSPSPDEQ--VRWVGEPGMSAITRAMRGDLPVS--------FSCRITDVF-RGEQHWNLLDAES   145 (336)
T ss_dssp                SEEEECCCEEEEETTEEEECCCCC--CEEEESSSTTHHHHHHHTTCCEE--------CSCCEEEEE-ECSSCEEEEETTC
T ss_pred                CceeccccеEEEeCCcccCCCCCC--cceecCCCchHHHHHHhcCCCEE--------EceEEEEEE-ECCCeEEEEeCCC


Q ss_pred                --EEEECEEEECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCCCCCceEEEeecCccc
Q Q_Madi_gp59     147    --LSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTSLVPWTRLSKVHGFTS   224 (291)
Q Consensus       147    --~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~~~~~~~r~~~~~~~~~~   224 (291)
                           .++||.||+|+|...+. ......|.+........+.......+..+.....+...++.....-..........+...
T Consensus       146    ~~~~~a~~vi~a~g~~~~~-~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   224 (336)
T 4ZCD_B          146    ENHGPFSHVIIATPAPQAT-ALLAAAPKLASVVAGVKMDPTWAVALAFETPLQTPMQGCFVQDSPLDWLARNRSKPGRDD   224 (336)
T ss_dssp                CEEEEESCEEECSCHHHHG-GGCTTCHHHHHHHHTCCEEEEEEEEEEESSCCSCCCCEEEECSSSEEEEEEGGGSTTCCC
T ss_pred                CceeecCEEEECCCHHHHH-HHHHhCHHHHHHhcCCceeeeEEEEEEeCCCCCCCCCcceeeCCCccHHHhcCCCCCCCC


Q ss_pred                c------------------------------eecC--CCCCCCcceeEEecccccCCCCC----CCCCCCCCEEEecccc
Q Q_Madi_gp59     225    I------------------------------EWPH--HAAQPHTQAVRVRKPLHYTPGPH----QNGSPTANWLHVGRYG   268 (291)
Q Consensus       225    ~------------------------------e~~~--~~~~~~~~~~~~~~~~~~~~~~~~~~~~~----~~~~~~~~~~~~~~gr~g   268 (291)
                         -                              ++..  ....+.+...++.+.....|...    ......++++.   .|
T Consensus       225    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~w~~~~~~~~~~~~~~~~~~~~~l~l---~G   301 (336)
T 4ZCD_B          225    TLDSWVLHATSQWSRQNLDASREQVIEHLHGAFAELIDCAMPAPVFSLAHRWLYARPAGSHEWGALSDADLGIYV---CG   301 (336)
T ss_dssp                SSEEEEEEECHHHHHHTTTCCHHHHHHHHHHHHHHHCSSCCCCCSEEEEEEEEEEEESSCCCCCCEEETTTTEEE---CC
T ss_pred                CCceEEEEeCHHHHHHHhhcCHHHHHHHHHHHHHHHcCCCCCCCCeeeeeeehhcCCCCCCCCCccccCCCCEEE---EE


Q ss_pred                ccccCCcHHHHHHHHHHHHHhc
Q Q_Madi_gp59     269    QFEKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus       269    ~~~~~~~~~~~~~~~~~~~~~~   290 (291)
                         .|..+..+++|++++..+++++
T Consensus       302    Da~~~~gi~~a~~sg~~~a~~l   323 (336)
T 4ZCD_B          302    DWCLSGRVEGAWLSGQEAARRL   323 (336)
T ss_dssp                GGGTTSSHHHHHHHHHHHHHHH
T ss_pred                HhHhCCCHHHHHHHHHHHHHHH
```

Template alignment | CDD

☐ **30. PF00743.21 ; FMO-like ; Flavin-binding monooxygenase-like**

Probability: 99.18%,   E-value: 1.6e-9,   Score: 104.13,   Aligned cols: 178,   Identities: 13%,   Similarity: 0.093,   Template Neff: 10.1

```
Q ss_pred                  CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59      1       MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus        1       ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                           ++|+|||||++|+++|..|.+.|++++|+|+.+.   .|+.|............                ..........
T Consensus        2       ~~v~IIGaG~sGl~aa~~l~~~g~~v~v~E~~~~---~GG~w~~~~~~~~~~~~----------------~~~~~~~~~~   62 (531)
T PF00743.21       2       KRIAVIGGGVSGLSSIKCCLEEGLEPVCFERSAD---IGGLWRFQENPEEGRAS----------------IYKSVIINTS   62 (531)
T ss_pred                  CEEEEECCCHHHHHHHHHHHHcCCCcEEEeCCCC---CCCCCcccCCCCCCCcc----------------cccceEEeeC


Q ss_pred                  cCcccccccCc--chhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCC----CCeEEEEcCC----EEE
Q Q_Madi_gp59      81      DGHIGQDEFEP--DHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVG----VGGYVNWDLG----LSE   149 (291)
Q Consensus        81      d~~~~~~~~~~--~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~----~~v~V~~~~g----~~~   149 (291)
                           .....+.++.+  ....+..+..+.+.+..+.......    ..+.+ ++|++++..++    +.+.|.+.++    ...
T Consensus        63      ~~~~~f~d~~~~~~~~~~~~~~~~~v~~yl~~~a~~~~l~----~~I~~~~~V~~v~~~~~~~~~~~~~w~v~~~~~~~~~~~~   138 (531)
T PF00743.21       63      KEMMCFSDYPIPDHYPNFMHNSHVLEYFRMYAKEFGLL----KYIQFKTTVCNVKKRPDFSTSGQWEVVTEHEGKTKVDV   138 (531)
T ss_pred                  ccccCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHhCCH----HHEEcCCEEEEEEECCCCCCCcEEEEEEeCCeEEEEE


Q ss_pred                  ECEEEECCCHHHHcCCCCcccCccc--hhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59      150     YELVISTVPRDIWQLPGDEYIYSEG--WAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus        150     aD~VI~t~p~~~l~~~~~~f~p~lp--~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~   209 (291)
                           +|.||+|+        +..-.|.+|  ..+|...|.|..+|..-......+....+..-+.+
T Consensus        139     ~d~VIvat--------G~~s~p~~p~~~~~g~~~f~g~~~hs~~~~~~~~~~~~~k~VlVVG~G   192 (531)
T PF00743.21       139     FDAVMVCT--------GHHTNAHLPLESFPGIEKFKGQYFHSRDYKNPEAFTGKRVVIIGIG   192 (531)
T ss_pred                  eCEEEEcc--------CCCCCCCCCCCCCCCccccccEEeeeeccCChhHhCCCeEEEEcCC
```

Template alignment | Template 3D Structure | PDBe

☐ **31. 1W4X_A PHENYLACETONE MONOOXYGENASE; BAEYER-VILLIGER, MONOOXYGENASE, FAD, OXYGENASE; HET: FAD; 1.7A {THERMOBIFIDA FUSCA} SCOP: c.3.1.5**

Probability: 99.15%,   E-value: 3.3e-9,   Score: 102.22,   Aligned cols: 174,   Identities: 14%,   Similarity: 0.086,   Template Neff: 10.4

```
Q ss_pred                  eEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhccccccc
Q Q_Madi_gp59      2       TIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWWD   81 (291)
Q Consensus        2       ~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~~d   81 (291)
                           +|+|||||++|+++|..|.+.|.+++|+|+...   .|+.|....+|+..+..   ....+...-.........|.
T Consensus        18      ~v~IIGaG~aGl~~a~~l~~~g~~~~i~e~~~~---~Gg~w~~~~~p~~~~~~---~~~~~~~~~~~~~~~~~~~~~~----   87 (542)
T 1W4X_A           18      DVLVVGAGFSGLYALYRLRELGRSVHVIETAGD---VGGVWYWNRYPGARCDI---ESIEYCYSFSEEVLQEWNWT----   87 (542)
T ss_dssp                  EEEEECCSHHHHHHHHHHHHTTCCEEEECSSSS---SCTHHHHCCCTTCBCSS---CTTTSSCCSCHHHHHHCCCC----
T ss_pred                  EEEEECCCHHHHHHHHHHHHCCCCEEEEeCCCC---CCCchhhcCCCCccccc---CcccccccCCHHHHHhCCCC----


Q ss_pred                  CcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCC-eEEEEcCC-EEEECEEEECCC
Q Q_Madi_gp59      82      GHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVG-GYVNWDLG-LSEYELVISTVP   158 (291)
Q Consensus        82      ~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~~-v~V~~~~g-~~~aD~VI~t~p   158 (291)
                                       ..+..+.-+...+..+.......    ..+.+ +.|..+.+..+.. +.|.++++ .+++|.||+|+
T Consensus        88      ------------~~~~~~~~ei~~yl~~~~~~~~~~~~----~~i~~~~~v~~~~~~~~~~~~~~w~v~~~~g~~~~a~~vV~At-   150 (542)
T 1W4X_A           88      ------------ERYASQPEILRYINFVADKFDLR----SGITFHTTVTAAAFDEATNTWTVDTNHGDRIRARYLIMAS-   150 (542)
T ss_dssp                  ------------BSSCBHHHHHHHHHHHHHHTTGG----GGEECSCCEEEEEEETTTTEEEEEETTCCEEEEEEEEECC-
T ss_pred                  ------------ccCCCHHHHHHHHHHHHHHcCCC----CCcEEeEEEEEeEEeCCCCEEEEEECCCCEEEEEEEEECc-


Q ss_pred                  HHHHcCCCCcccCccchhhccCcccCceecceeccce-ecCCCCEEEEecCC
Q Q_Madi_gp59      159     RDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRE-LFDKDNTIICDGTS   209 (291)
Q Consensus        159     ~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e-~~~~~~~~~~~~~~   209 (291)
                                  +..-.|.+|..+|...|.|..+|..-.+.. .......+..-+.+
T Consensus        151     -------G~~~~p~~p~i~g~~~f~g~~~h~~~~~~~~~~~~~gk~V~ViG~G   195 (542)
T 1W4X_A           151     -------GQLSVPQLPNFPGLKDFAGNLYHTGNWPHEPVDFSGQRVGVIGTG   195 (542)
T ss_dssp                  -------CSCCCCCCCCTTGGGCCSEEEEGGGCCSSCCCCBTCEEEEECCS
T ss_pred                  -------cCCCCCCCCCCCCcccCCCccccccCCCCCCCCCCCCEEEEECCC
```

Template alignment | Template 3D Structure | PDB | NCBI

☐ **32. d1seza1 c.3.1.2 (A:13-329,A:442-497) Protoporphyrinogen oxidase {Tobacco (Nicotiana tabacum) [TaxId: 4097]}**

Probability: 99.14%,   E-value: 5.9e-10,   Score: 102.1,   Aligned cols: 204,   Identities: 14%,   Similarity: 0.066,   Template Neff: 10.6

```
Q ss_pred                  CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcc---------------------------
Q Q_Madi_gp59      1       MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPE---------------------------   53 (291)
Q Consensus        1       ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~---------------------------   53 (291)
```

```
                           ++|+|||||+|||+||+.|++.|++|+|+|++++   .|+........+...+
T Consensus       2        ~~v~IIGaGiaGL~aA~~L~~~g~~v~l~E~~~~---~GG~~~t~~~~g~~~d~G~~~~~~~~~~~~~l~~~lgl~~~~~   78 (374)
T d1seza1         2        KRVAVIGAGVSGLAAAYKLKIHGLNVTVFEAEGK---AGGKLRSVSQDGLIWDEGANTMTESEGDVTFLIDSLGLREKQQ   78 (374)
T ss_dssp                  CEEEEECCSHHHHHHHHHHHTTSCEEEEECSSSS---SCSSCCEEEETTEEEESSCCCBCCCSHHHHHHHHHTTCGGGEE
T ss_pred                  CeEEEECCCHHHHHHHHHHHHcCCeEEEEeCCCC---CCCceEEEEeCCeEEecCCCCcCCCchHHHHHHHHcCCccccc


Q ss_pred                  --------------------------------------------------------------------------------
Q Q_Madi_gp59      54       --------------------------------------------------------------------------------   53 (291)
Q Consensus       54       --------------------------------------------------------------------------------   53 (291)

T Consensus       79       ~~~~~~~~~~~~~g~~~~~p~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~fl~~~~g~~~~~~~~~   158 (374)
T d1seza1         79       FPLSQNKRYIARNGTPVLLPSNPIDLIKSNFLSTGSKLQMLLEPILWKNKKLSQVSDSHESVSGFFQRHFGKEVVDYLID   158 (374)
T ss_dssp                  CCSSCCCEEEESSSSEEECCSSHHHHHHSSSSCHHHHHHHHTHHHHC----------CCCBHHHHHHHHHCHHHCCCCCH
T ss_pred                  CCccCCCEEEEECCeeccCCCChHHHHhccccCHHHHHHHHHHHHHhccchhhccCCCCCccHHHHHHHHHCHHHHHHHH


Q ss_pred                  cCCCCCeeeEecCCceechhhcccccccCccc-------------------------------------------ccccC
Q Q_Madi_gp59      54       SDKGVPVKYVVRGTPEEYRRKTHGKWWDGHIG-------------------------------------------QDEFE   90 (291)
Q Consensus       54       l~~~~~~~~~~~~~~~~~y~~k~~~~~~d~~~~-------------------------------------------~~~~~   90 (291)
                           +                +....|+...+.--.                                           .....
T Consensus       159      p----------------~~~gi~~~d~~~ls~~~~~~~l~~~~~~~~s~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   222 (374)
T d1seza1         159      P----------------FVAGTCGGDPDSLSMHHSFPELWNLEKRFGSVILGAIRSKLSPKNEKKQGPPKTSANKKRQRG   222 (374)
T ss_dssp                  H----------------HHHHHHSCCGGGSBHHHHCHHHHHHHHHTSCHHHHHHHHTTC----------CCCSCCSTTCS
T ss_pred                  H----------------HhchhcCCCHHHhcHHHhhHHHHHHHHhhchHHHHHHHhhhCcccccCCCCCCCcccccCCce


Q ss_pred                  cchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeecCCC-----CCeEEEE-----cCC-EEEECEEEECCCH
Q Q_Madi_gp59      91       PDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENSDVG-----VGGYVNW-----DLG-LSEYELVISTVPR   159 (291)
Q Consensus       91       ~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~V~~i~~~~~-----~~v~V~~-----~~g-~~~aD~VI~t~p~   159 (291)
                           .+...-+...+.+.|.+.++......        .++|++|+...+     +.+.|.+     .++ .+.||.||+|+|.
T Consensus       223      ~~~~~gG~~~l~~~L~~~l~~~~i~l--------~~~V~~I~~~~~~~~~~~~~~~~~~v~~~~~~~~~~~~~~~~~ad~Vi~a~p~   294 (374)
T d1seza1         223      SFSFLGGMQTLTDAICKDLREDELRL--------NSRVLELSCSCTEDSAIDSWSIISASPHKRQSEEESFDAVIMTAPL   294 (374)
T ss_dssp                  CBEETTCTHHHHHHHHTTSCTTTEET--------TCCEEEEEEECSSSSSSCEEEEEEBCSSSSCBCCCEESEEEECSCH
T ss_pred                  eEEeccHHHHHHHHHHHhcccCceec--------CceEEEEEecCCCCCccCceEEEEecCCcccCCccccCEEEEecCH


Q ss_pred                  HHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCCCCCceEEEeecCcccceecCCCCCCCccee
Q Q_Madi_gp59      160      DIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTSLVPWTRLSKVHGFTSIEWPHHAAQPHTQAV   239 (291)
Q Consensus       160      ~~l~~~~~~~f~p~lp~~~g~~~~~~g~~~~~~~v~~~e~~~~~~~~~~~~~~~~~~~~~~~~~r~~~~~~~~~~~~~e~~~~~~~~~~~~~~~~~   239 (291)
                           ..+.  ...+.|..+.....                                              .+|. ..|.+....
T Consensus       295      ~~l~--~~~~~~~~~~~~~~~~~----------------------------------------------aip~-~~~~~~~~~~~   325 (374)
T d1seza1         295      CDVK--SMKIAKRGNPFLLN----------------------------------------------FIPE-VXYGHNYDS   325 (374)
T ss_dssp                  HHHH--TSEEESSSSBCCCT----------------------------------------------TSCC-C-CCTTHHH
T ss_pred                  HHHH--hCccccCCCeeeec----------------------------------------------cCcc-ccCCCChHH


Q ss_pred                  EEeccccCCCCCCCCCCCCCCEEEeccccccccCCcHHHHHHHHHHHHHhc
Q Q_Madi_gp59      240      RVRKPLHYTPGPHQNGSPTANWLHVGRYGQFEKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus       240      ~~~~~~~~~~~~~~~~~~~~~~~~~~~gr~g~~~~~~~~~~~~~~~~~~~~~~~~~   290 (291)
                           -++...+.       ...-+++|.   .|.|..++.+.|||+++.++++++
T Consensus       326      ~~~~~~~~-------~~~~~~l~~---~g~~~~Gv~v~~~i~~~~~~~~a~~~   366 (374)
T d1seza1         326      VLDAIDKM-------EKNLPGLFY---AGNHRGGLSVGKALSSGCNAADLV   366 (374)
T ss_dssp                  HHHHHHHH-------HHHSTTEEE---CCSSSSCSSHHHHHHHHHHHHHHH
T ss_pred                  HHHHHHHH-------HHHCCCEEE---cccccCCccHHHHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDBe

☐ 33. **3QJ4_A Renalase; FAD/NAD(P)-binding Rossmann fold Superfamily, Flavin containing amine oxidoreductase, Monoamine oxidase, NAD, extracellular, OXIDOREDUCTASE; HET: FAD, SO4; 2.5A {Homo sapiens}**

Probability: 99.14%, E-value: 5.7e-9, Score: 94.1, Aligned cols: 267, Identities: 12%, Similarity: -0.001, Template Neff: 11.2

```
Q ss_pred                  CeEEEECCCHHHHHHHHHHHHcC---CeEEEECCCCCccccchhHhcCCCCC---CCcccCCCCCeeeEecCC-------
Q Q_Madi_gp59      1        MTIAILGCGPTGLLAAHACTLEG---YDVAIFSRKRKSELFGSQYLHNPIPG---LTPESDKGVPVKYVVRGT-------   67 (291)
Q Consensus       1        ~~V~IIGaG~aGl~aA~~L~~~g---~~v~i~E~~~~~~~~~G~~~~~~~~~~~---~~~~l~~~~~~~~~~~~~~-------   67 (291)
                           ++|+|||||++|+++|+.|++.|   .+|+|+|+...   .|+.........   ....    ..........
T Consensus       2        ~~v~IiG~G~~Gl~~A~~L~~~g~~~~~v~iiE~~~~---~gg~~~~~~~~~~~~~~~~~~----~g~~~~~~~~~~~~~~~~~   74 (342)
T 3QJ4_A          2        AQVLIVGAGMTGSLCAALLRRQTSGPLYLAVWDKADD---SGGRMTTACSPHNPQCTAD----LGAQYITCTPHYAKKHQ   74 (342)
T ss_dssp                  EEEEEECCSHHHHHHHHHHHSCC-CCEEEEEECSSSS---SCGGGCEEECSSCTTCEEE----SSCCCEEECSSHHHHTH
T ss_pred                  CeEEEECCCHHHHHHHHHHHhhCCCCeEEEEEeCCCC---CccceeeeeCCCCCCceEE----cCCeeeeCChhhHHHHH


Q ss_pred                  --ceechhhcccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCCeEEEEc
Q Q_Madi_gp59      68       --PEEYRRKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVGGYVNWD   144 (291)
Q Consensus       68       --~~~y~~k~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~~v~V~~~   144 (291)
                             .......-....................+..+..+..+...+......- +.     . ++|++++ ..++++.|.++
T Consensus       75       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-i~-----~~~~v~~i~-~~~~~~~~~v~~~   147 (342)
```

```
T 3QJ4_A          75     RFYDELLAYGVLRPLSSPIEGMVMKEGDCNFVAPQGISSIIKHYLKESGAE-VY-----FRHRVTQIN-LRDDKWEVSKQ   147 (342)
T ss_dssp                HHHHHHHHTTSCEECCSCEETCCC--CCEEEECTTCTTHHHHHHHHHHTCE-EE-----SSCCEEEEE-ECSSSEEEEES
T ss_pred                HHHHHHHHCCCceeCcCcccCccccCCCcceecCccHHHHHHHHHHHCCCe-EE-----eceeEEEEE-eCCCEEEEEec


Q ss_pred                CC-EEEECEEEECCCHHHHcCCCCccc----CccchhhccCcccCceecceecccceecCCCCEEEEecCCCCCceEEEee
Q Q_Madi_gp59      145    LG-LSEYELVISTVPRDIWQLPGDEYI----YSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTSLVPWTRLSKV   219 (291)
Q Consensus        145    ~g-~~~aD~VI~t~p~~~l~~~~~~f~----p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~~~~~~r~~~~   219 (291)
                         ++ ++.+|.||+|+|...+.+-...+.    +..........+.......+..+.....+..........+....-+...
T Consensus        148    ~~~~~~~~~vi~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~v~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   227 (342)
T 3QJ4_A          148    TGSPEQFDLIVLTMPVPEILQLQGDITTLISECQRQQLEAVSYSSRYALGLFYEAGTKIDVPWAGQYITSNPCIRFVSID   227 (342)
T ss_dssp                SSCCEEESEEEECSCHHHHTTCBSTHHHHSCHHHHHHHHTCCBCCEEEEEEECSSCC--CCSCSEEECSSCSSEEEEEEH
T ss_pred                CCChhcCCEEEEcCCHHHHHhccCchHHhcCHHHHHHHhhcceeeeeeeehhccCCCCCCCCcceeecCCCCeEEEEEec


Q ss_pred                cCcccc------------------------------------------eecC-------CCCCCCcceeEEecccccCCC
Q Q_Madi_gp59      220    HGFTSI------------------------------------------EWPH-------HAAQPHTQAVRVRKPLHYTPG   250 (291)
Q Consensus        220    ~~~~~~------------------------------------------e~~~-------~~~~~~~~~~~~~~~~~~~~~   250 (291)
                         ......                                          +.|.       .-.+..+...........
T Consensus        228    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~p~~~~~~~~~~~~~w~~~~~~~~~~~~~~~~---   304 (342)
T 3QJ4_A          228    NKKRNIESSEIGPSLVIHTTVPFGVTYLEHSIEDVQELVFQQLENILPGLPQPIATKCQKWRHSQVTNAAANCPGQM---   304 (342)
T ss_dssp                HHHTTCCCC-CCCEEEEEECHHHHHHTTTSCHHHHHHHHHHHHHHHSCSCCCCSEEEEEEETTCSBSSCCSSSCSCE---
T ss_pred                CCcCCCCCCCCCCEEEEEeecccchhHhccCCHHHHHHHHHHHHHHHCCCCCCCcEEEEEecCcccccCCCCCCCcce---


Q ss_pred                CCCCCCCCCCEEEeccccccccCCcHHHHHHHHHHHHHhc
Q Q_Madi_gp59      251    PHQNGSPTANWLHVGRYGQFEKGVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus        251    ~~~~~~~~~~~~~~gr~g~~~~~~~~~~~~~~~~~~~~~~   290 (291)
                            .....++++.   .|.|..+-.++.|+..++..++++
T Consensus        305    ---~~~~~~~l~~---~Gd~~~~~~~~gA~~sg~~~a~~i   338 (342)
T 3QJ4_A          305    ---TLHHKPFLAC---GGDGFTQSNFDGCITSALCVLEAL   338 (342)
T ss_dssp                ---EEETTTEEEE---CSGGGSCSSHHHHHHHHHHHHHHH
T ss_pred                ---eecCCCcEEE---ccCCCCCCCcchHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDB | NCBI

☐ **34. d1w4xa1 c.3.1.5 (A:10-154,A:390-542) Phenylacetone monooxygenase {Thermobifida fusca [TaxId: 2021]}**

Probability: 99.13%, E-value: 3.2e-9, Score: 94.29, Aligned cols: 134, Identities: 13%, Similarity: 0.046, Template Neff: 10.6

```
Q ss_pred                CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59      1      MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus        1      ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                         ++|+|||||++|+.+|..|++.|.+|+|+|+.+.   .|+.|....+|+..+..   ....+...-.........|..
T Consensus        8      ~~vvIIG~G~~G~~~A~~l~~~g~~v~l~e~~~~---~gg~~~~~~~p~~~~~~---~~~~~~~~~~~~~~~~~~~~~~--   79 (299)
T d1w4xa1         8      VDVLVVGAGFSGLYALYRLRELGRSVHVIETAGD---VGGVWYWNRYPGARCDI---ESIEYCYSFSEEVLQEWNWTE--   79 (299)
T ss_dssp                EEEEEECCSHHHHHHHHHHHHTTCCEEEECSSSS---SCTHHHHCCCTTCBCSS---CTTTSSCCSCHHHHHHCCCCB--
T ss_pred                eEEEEECCCHHHHHHHHHHHHCCCCEEEEecCCC---CCCcccccCCCCccccc---CccceEEeCChHHHhhCCCCc--


Q ss_pred                cCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeecCCCCCeEEEEcCC-EEEECEEEECCC
Q Q_Madi_gp59      81     DGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENSDVGVGGYVNWDLG-LSEYELVISTVP   158 (291)
Q Consensus        81     d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~V~~i~~~~~~~~v~V~~~~g-~~~aD~VI~t~p   158 (291)
                                      .......+...+...+.+....-++  .......+.+++ ..++.+.|.++++ .+.||.||+|++
T Consensus        80     -------------~~~~~~~~~~~~~~~~~~~~~~~v--~~~~~~~~~~~~-~~~~~~~~v~~~~g~~~~ad~vI~atG   142 (299)
T d1w4xa1         80     -------------RYASQPEILRYINFVADKFDLRSGI--TFHTTVTAAAFD-EATNTWTVDTNHGDRIRARYLIMASG   142 (299)
T ss_dssp                -------------SSCBHHHHHHHHHHHHHHTTGGGGE--ECSCCEEEEEEE-TTTTEEEEEETTCCEEEEEEEEECCC
T ss_pred                -------------cCCCHHHHHHHHHHHHHHhCCCCCe--EeccEEEEEEEe-CCCCEEEEEECCCcEEEEeEEEEcCC
```

Template alignment | Template 3D Structure | PDBe

☐ **35. 4RG3_A Cyclohexanone monooxygenase; Baeyer-Villiger monooxygenase, Baeyer-Villiger oxidation, biocatalysis, flavoprotein, green chemistry, protein engineering, Rossmann fold, Oxidoreductase, FAD, NADPH, cyclohexanone; HET: FAD, NAP, BCN; 1.94A {Rhodococcus sp. HI-31}**

Probability: 99.12%, E-value: 3.5e-9, Score: 102.23, Aligned cols: 174, Identities: 14%, Similarity: 0.088, Template Neff: 10.3

```
Q ss_pred                CeEEEECCCHHHHHHHHHHHHc-CCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhccccc
Q Q_Madi_gp59      1      MTIAILGCGPTGLLAAHACTLE-GYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKW   79 (291)
Q Consensus        1      ~~V~IIGaG~aGl~aA~~L~~~-g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~y~~k~~~~~   79 (291)
                         .+|+|||||++|+++|..|++. |.+++|+|+...   .|+.|....+++..+..   ....+...-.........|.
T Consensus        17     ~~v~IIGaG~~Gl~~a~~l~~~~g~~~~i~e~~~~---~gg~w~~~~~~~~~~~~~~---~~~~~~~~~~~~~~~~~~~~--   88 (548)
T 4RG3_A          17     VDAVVIGAGFGGIYAVHKLHHELGLTTVGFDKADG---PGGTWYWNRYPGALSDT---ESHLYRFSFDRDLLQESTWK--   88 (548)
T ss_dssp                EEEEEECCSHHHHHHHHCCCCCTCCCEEEECSSSS---SCTHHHHCCCTTCEEEE---EGGGSSCCSCHHHHHHCCCS--
T ss_pred                eEEEEECCCHHHHHHHHHHHHHcCCCEEEEcCCCC---CCCCchhcCCCCCcCCC---cchhccccCChhHhhcCCCc--


Q ss_pred                ccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCC--eEEEEcCC-EEEECEEEE
Q Q_Madi_gp59      80     WDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVG--GYVNWDLG-LSEYELVIS   155 (291)
```

```
Q Consensus       80    ~d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~--v~V~~~~g-~~~aD~VI~   155 (291)
                                      ..+..+..+...+..+.......    ..+.+ ++|.++. ..++.  +.|.++++ .+.+|.||+
T Consensus       89    --------------~~~~~~~~i~~yl~~~a~~~~l~----~~i~~~~~V~~~~-~~~~~~~w~v~~~~g~~~~a~~vI~   149 (548)
T 4RG3_A          89    --------------TTYITQPEILEYLEDVVDRFDLR----RHFKFGTEVTSAL-YLDDENLWEVTTDHGEVYRAKYVVN   149 (548)
T ss_dssp               --------------BSEEEHHHHHHHHHHHHHHTTCG----GGEECSCCEEEEE-EETTTTEEEEEETTSCEEEEEEEEE
T ss_pred               --------------ccCCCHHHHHHHHHHHHHHhCCH----HhEECCCEEEEEE-EECCCCEEEEEECCCCEEEEEEEEE


Q ss_pred               CCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59     156    TVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus      156    t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~   209 (291)
                        |+        +..-.|.+|..+|...|.|..+|..-.+....+....+..-+.+
T Consensus      150    At--------G~~s~~~~p~i~g~~~f~g~~~hs~~~~~~~~~~gk~V~VvG~G   195 (548)
T 4RG3_A         150    AV--------GLLSAINFPNLPGLDTFEGETIHTAAWPEGKSLAGRRVGVIGTG   195 (548)
T ss_dssp               CC--------CSSCSBCCCCCTTGGGCCSEEEEGGGCCTTCCCTTSEEEEECCS
T ss_pred               Cc--------ccccccCCCCCCCCCCCCCcEEecccCCCCCCCCCCEEEEEcCC
```

Template alignment | Template 3D Structure | PDBe

☐ **36.** **5NMX_C Flavin-containing monooxygenase; pyrrolizidine alkaloid N-oxygenase, oxidoreductase, flavin-containing monooxygenase, rossmann fold, FAD, NADP, two dinucleotide binding domain flavoprotein, senecionine; HET: NAP, FAD; 1.6A {Zonocerus variegatus}**

Probability: 99.12%, E-value: 4.7e-9, Score: 97.93, Aligned cols: 185, Identities: 16%, Similarity: 0.068, Template Neff: 10.6

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCcccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59       1    MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus         1    ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                        ++|+|||||+||+++|..|++.|++|+|+|+...   .|+.|............   .............-..+....+.
T Consensus        2    ~~V~IIGaG~aGl~aA~~l~~~g~~v~v~e~~~~---~gg~~~~~~~~~~~~~~~---~~~~~~~~~~~~~~~~~~~~~~~   75 (425)
T 5NMX_C           2    RRVAVLGAGPSGLTAARYLKQAGFEVMVFERYHH---VGGTWNYTDETWMSEDG---RPVYSSMYQNLFVNLPKELMAFP   75 (425)
T ss_dssp               CEEEEECCSHHHHHHHHHHHHTTCEEEEEESSSS---SSGGGSCCSCCSBCTTS---SBCCCCCCTTCBCSSCHHHHSBT
T ss_pred               CeEEEECCCHHHHHHHHHHHHCCCeEEEEEcCCC---CCCceeeCCCcccCCCC---CccchhHhcccccCCCHHHhcCC


Q ss_pred               cCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeecCCCCCeEEEEcCC-E-----EEECEE
Q Q_Madi_gp59      81    DGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENSDVGVGGYVNWDLG-L-----SEYELV   153 (291)
Q Consensus        81    d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~-~~V~~i~~~~~~~v~V~~~~g-~-----~~aD~V   153 (291)
                        +..+....-    .......+...+...+........+.     + +.|++++ ..++++.|...+. .     +.+|.|
T Consensus       76    ~~~~~~~~~----~~~~~~~~~~~~l~~~~~~~~~~~~i~-----~~~~V~~v~-~~~~~~~v~~~~~~~~~~~~~~~d~v   145 (425)
T 5NMX_C          76    DFPFHDIEG----SYVPSKEVLKYFDNFTDAFDLRKLIK-----LQHHVENVR-PCESGWLVTVTDLTTMVEHSFEFDAV   145 (425)
T ss_dssp               TBCCCSCSC----SSCBHHHHHHHHHHHHHHTTCGGGEE-----ETEEEEEEE-EETTEEEEEEEETTTTEEEEEEESEE
T ss_pred               CCCCCCCCC----CCCCHHHHHHHHHHHHHHcChHHhee-----CcEEEEEEE-eCCCeEEEEEEECCCCEEEEEEECEE


Q ss_pred               EECCCHHHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59     154    ISTVPRDIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus      154    I~t~p~~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~   209 (291)
                        |+|+        +....|.+|...+...+.+...+.........+....+..-+.+
T Consensus      146    vva~--------G~~~~~~~p~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~v~iiG~G   193 (425)
T 5NMX_C         146    VVCT--------GQTWCPLYPDVEGRSFFRGRLTHAHEFRSPEPFRNKRVLIVGAG   193 (425)
T ss_dssp               EECC--------CSSSSBCCCCCBTGGGCCSEEEEGGGCCCSGGGTTCEEEEECCS
T ss_pred               EEeC--------CCCCCcCCCCCCCCcccccceeeeEecCCCcccCCCeEEEECCC
```

Template alignment | Template 3D Structure | PDBe

☐ **37.** **5TTJ_B Amine oxidase; nicotine degradation, flavoenzyme, monoamine oxidase family, PHBH fold, OXIDOREDUCTASE; HET: FAD; 2.2A {Pseudomonas putida (strain S16)}**

Probability: 99.09%, E-value: 2.9e-9, Score: 101.16, Aligned cols: 165, Identities: 16%, Similarity: 0.19, Template Neff: 10.6

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCcccccchhHhcCCCCCCCcc---------------------------
Q Q_Madi_gp59       1    MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPE---------------------------   53 (291)
Q Consensus         1    ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~~---------------------------   53 (291)
                        .+|+|||||+|||+||..|++.|.+|+|+|++++   .||........+...+
T Consensus       54    ~dViIIGaG~aGL~aA~~L~~~G~~V~vlEa~~~---~GGr~~t~~~~g~~~~~G~~~~~~~~~~~~~~~~~~~~gl~~~~~   130 (490)
T 5TTJ_B          54    YDVVVVGGGFAGATAARECGLQGYRTLLLEARSR---LGGRTFTSRFAGQEIEFGGAWVHWLQPHVWAEMQRYGLGVVED   130 (490)
T ss_dssp               EEEEEECCSHHHHHHHHHHHHTTCCEEEECSSSS---SCTTCCEEEETTEEEESSCCEECTTSHHHHHHHHHTTCCEEEC
T ss_pred               eeEEEECCCHHHHHHHHHHHHCCCeEEEEeCCCC---cCCcceEeeeCCeeEEecCEEecCCCHHHHHHHHHcCCCccCC


Q ss_pred               --cCCCCCeeeEecCCceec------------------------------------------------------------
Q Q_Madi_gp59      54    --SDKGVPVKYVVRGTPEEY------------------------------------------------------------   71 (291)
Q Consensus        54    --l~~~~~~~~~~~~~~~~y------------------------------------------------------------   71 (291)
                          ...+....+...+.....
T Consensus      131    ~~~~~~~~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~l~~~~~~~~~~~~   210 (490)
T 5TTJ_B         131    PLTNLDKTLIMYNDGSVESISPDEFGKNIRIAFEKLCHDAWEVFPRPHEPMFTERARELDKSSVLDRIKTLGLSRLQQAQ   210 (490)
T ss_dssp               CCCCCSEEEEECTTCCEEEECHHHHHHHHHHHHHHHTTTHHHHCSSTTSGGGSHHHHHHTTSBHHHHHTTSCCCHHHHHH
```

```
T ss_pred               CCccccceEEEEcCCeeEecCHHHHHHHHHHHHHHHhcchHhhCCCCCCcccChhHHhhccCcHHHHHHHcCCCHHHHHH


Q ss_pred               -----------------hhhcccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee-eceeEeec
Q Q_Madi_gp59      72    -----------------RRKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA-SFFKRENS   133 (291)
Q Consensus        72    -----------------~~k~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~-~~V~~i~~   133 (291)
                                         ...+.............+......+....-...+.+.+.+....- +.     . ++|++|+
T Consensus        211   ~~~~~~~~~~~~~~~~s~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gG~~~l~~~l~~~~g~~-i~-----~~~~V~~I~-   283 (490)
T 5TTJ_B          211   INSYMALYAGETTDKFGLPGVLKLFACGGWNYDAFMDTETHYRIQGGTIGLINAMLTDSGAE-VR-----MSVPVTAVE-   283 (490)
T ss_dssp               HHHHHHHHHTSCTTSBBHHHHHHHHHHTTTCHHHHHHTTSSEEETTHHHHHHHHHHHHHTCE-EE-----CSCCEEEEE-
T ss_pred               HHHHHHHHhCCCchhcCHHHHHHHHhcCCCChHHhhhhcccEEecChHHHHHHHHHhhcCCc-ee-----cCCCcEEEE-


Q ss_pred               CCCCCeEEEEcCC-EEEECEEEECCCHHHHcCCCCcccCccchhh
Q Q_Madi_gp59      134   DVGVGGYVNWDLG-LSEYELVISTVPRDIWQLPGDEYIYSEGWAI   177 (291)
Q Consensus        134   ~~~~~v~V~~~~g-~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~   177 (291)
                        .+++++.|.+++| ++.||.||+|+|+..+.  .+.|.|.+|...
T Consensus        284   ~~~~~v~V~~~~g~~~~ad~VI~a~P~~~l~--~i~~~p~l~~~~   326 (490)
T 5TTJ_B          284   QVNGGVKIKTDDDEIITAGVVVMTVPLNTYK--HIGFTPALSKGK   326 (490)
T ss_dssp               CCTTSEEEEESSCCEEEEEEEEECCCGGGGG--GSEEESCCCHHH
T ss_pred               EeCCeEEEEeCCCCEEEECEEEEcCCHHHhc--ccccCCCCCHHH
```

Template alignment | Template 3D Structure | PDBe

☐ **38. 4DSG_A UDP-galactopyranose mutase; Rossmann fold, flavin adenine dinucleotide, ISOMERASE; HET: UDP, FAD; 2.249A {Trypanosoma cruzi}**

Probability: 99.08%, E-value: 4.3e-9, Score: 99.95, Aligned cols: 270, Identities: 17%, Similarity: 0.066, Template Neff: 10.5

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCe-EEEECCCCCccccchhHhcCCC-CCCCcc-------------------------
Q Q_Madi_gp59      1     MTIAILGCGPTGLLAAHACTLEGYD-VAIFSRKRKSELFGSQYLHNPI-PGLTPE-------------------------   53 (291)
Q Consensus        1     ~~V~IIGaG~aGl~aA~~L~~~g~~-v~i~E~~~~~~~~G~~~~~~~~-~~~~~~-------------------------   53 (291)
                        ++++|||||++|+++|..|++.|.. ++|+|++.+   .||....... .+...+
T Consensus        10    ~~~~i~g~g~~g~~~a~~l~~~g~~~~~~~~e~~~~---~GGr~~t~~~~~g~~~d~G~~~~~~~~~~~~~~~~~~~~~~~   86 (484)
T 4DSG_A          10    PKIVIIGAGPTGLGAAVRLTELGYKNWHLYECNDT---PGGLSRSFLDENGFTWDLGGHVIFSHYQYFDDVMDWAVQGWN   86 (484)
T ss_dssp               CCEEEECCSHHHHHHHHHHHHTTCCSEEEEESSSS---SSGGGCEEECTTSCEEESSCCCBCCSBHHHHHHHHHHCSCEE
T ss_pred               CcEEEECCCHHHHHHHHHHHHcCCCeEEEEeCCCC---CCCcceEEEcCCCcEEecccceEecCCHHHHHHHHHHhcCCc


Q ss_pred               --------------------------------------------------------------------------------
Q Q_Madi_gp59      54    --------------------------------------------------------------------------------   53 (291)
Q Consensus        54    --------------------------------------------------------------------------------   53 (291)

T Consensus        87    ~~~~~~~~~~~g~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~l~~~~g~~~~~~~~~~~~~~~~~~   166 (484)
T 4DSG_A          87    VLQRESWVWVRGRWVPYPFQNNIHRLPEQDRKRCLDELVRSHARTYTEPPNNFEESFTRQFGEGIADIFMRPYNFKVWAV   166 (484)
T ss_dssp               EEECCCEEEETTEEEESSGGGCGGGSCHHHHHHHHHHHHHHHHCCCSSCCSSHHHHHHHHHHHHHCCCCCHHHHHHHHSS
T ss_pred               eeecceEEEECCEEecCCchhhhhcCCHHHHHHHHHHHHHHhhcccCCCCCCCHHHHHHHhhcHHHHHHhccchHHhcCC


Q ss_pred               ----cCCCCCeeeEecCCceechhhcccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeec--
Q Q_Madi_gp59      54    ----SDKGVPVKYVVRGTPEEYRRKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASF--   127 (291)
Q Consensus        54    ----l~~~~~~~~~~~~~~~~~~~~~y~~k~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~--   127 (291)
                            +...+.................................+...-+...+.+.|.+.++.....+        .++
T Consensus        167   ~~~~~s~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gG~~~l~~~l~~~l~~~~i~l--------~~~~~   238 (484)
T 4DSG_A          167   PPCLMSTEWVEERVAPVDLERIRRNIQENRDDLGWGPNATFRFPQRGGTGIIYQAIKEKLPSEKLTF--------NSGFQ   238 (484)
T ss_dssp               CGGGBCSSSCTTTSCCCCHHHHHHHHHHTCCCCCCSTTSEEEEESSSCTHHHHHHHHHHSCGGGEEE--------CGGGC
T ss_pred               CHHHCCHHHHHhhCCCCCHHHHHHHHhcCCCcCCCCCcceeecCCCCChHHHHHHHHHhCCcCCeec--------CCCcc


Q ss_pred               eeEeecCCCCCeEEEEcCC-EEEECEEEECCCHHHHcCCCCccc----CccchhhccCcccCceecceeccceec--CCC
Q Q_Madi_gp59      128   FKRENSDVGVGGYVNWDLG-LSEYELVISTVPRDIWQLPGDEYI----YSEGWAIGDAPERGVFVDDLVEGRELF--DKD   200 (291)
Q Consensus        128   V~~i~~~~~~~v~V~~~~g-~~~aD~VI~t~p~~~l~~~~~~f~----p~lp~~~g~~~~~g~~~~~~v~~~e~~--~~~   200 (291)
                        |++|+ .+++  .|.+++| .+.||.||+|+|+..+......-.    +.+........+.+.....+..+.+..  ...
T Consensus        239   V~~I~-~~~~--~V~~~~g~~~~ad~VI~t~p~~~l~~ll~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~l~~~~~~~~~~~~~~   315 (484)
T 4DSG_A          239   AIAID-ADAK--TITFSNGEVVSYDYLISTVPFDNLLRMTKGTGFKGYDEWPAIADKMVYSSTNVIGIGVKGTPPPHLKT   315 (484)
T ss_dssp               EEEEE-TTTT--EEEETTSCEEECSEEEECSCHHHHHHHEECSSCTTGGGHHHHHHHCCEEEEEEEEEEEESCCCGGGTT
T ss_pred               cEEEE-CCCC--EEEEcCCcEEECCEEEECCCHHHHHHHhcCCCCCCccchHHHHhhCceeeEEEEEEEEcCCCCCCCCC


Q ss_pred               CEEEEecCCCCCceEEEeecCcccc------------------------------------------------eecC--C
Q Q_Madi_gp59      201   NTIICDGTSLVPWTRLSKVHGFTSI------------------------------------------------EWPH--H   230 (291)
Q Consensus        201   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~r~~~~~~~~~~~~~~~~~~~~~~~~------------------------------------------------e~~~~--~   230 (291)
                        ..+++..+.+.++.|...+..+...                                                .|-.  .
T Consensus        316   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~p~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~~~~   395 (484)
T 4DSG_A          316   ACWLYFPEDTSPFYRATVFSNYSKYNVPEGHWSLMLEVSESKYKPVNHSTLIEDCIVGCLASNLLLPEDLLVSKWHYRIE   395 (484)
T ss_dssp               CCEEECCSTTCSCSEEECGGGTCGGGSCTTEEEEEEEEEEBTTBCCCTTSHHHHHHHHHHHTTSCCTTCCEEEEEEEEEE
T ss_pred               CcEEEccCCCCCceEEEehhhcCCccCCCCeeEEEEEEEcCCCCCCCHHHHHHHHHHHHHHCCCCCCHHheEEEEEEEec


Q ss_pred               CCCCCcceeEEecccccCCCCCCCCCCC-CCEEEecccccccc-CCcHHHHHHHHHHHHHHhc
```

```
Q Q_Madi_gp59      231    AAQPHTQAVRVRKPLHYTPGPHQNGSPT-ANWLHVGRYGQFEK-GVVVTDAFDQVTKKLKEM   290 (291)
Q Consensus        231    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~-~~~~~~gr~g~~~~-~~~~~~~~~~~~~~~~~~   290 (291)
                          ..||.+.........+.      ...++ +++|.+||+|.|.| .-.++.|++.+...++++
T Consensus        396    ~a~p~~~~~~~~~~~~~~~------~~~~~~~~l~~aG~~~~~~~~~~~~~~~A~~sG~~~A~~i   451 (484)
T 4DSG_A           396    KGYPTPFIGRNNLLEKA------QPELMSRCIYSRGRFGAWRYEVGNQDHSFMQGVEAIDHV   451 (484)
T ss_dssp                  EEEECCBTTHHHHHHHH------HHHHHHTTEEECSTTTTCCGGGCSHHHHHHHHHHHHHHH
T ss_pred                  CceecCCCChHHHHHHH------HHHHHhCCeEecCCCcccccccCCHHHHHHHHHHHHHHH
```

Template alignment | Template 3D Structure | PDBe

☐ 39. **2VVM_B MONOAMINE OXIDASE N; MONOAMINE OXIDASE, ASPERGILLUS NIGER, FAD, PEROXISOME, FLAVOPROTEIN, OXIDOREDUCTASE, ENANTIOSELECTIVITY, DIRECTED EVOLUTION VARIANT; HET: EDO, FAD, PRO; 1.85A {ASPERGILLUS NIGER}**

Probability: 99.08%, E-value: 2.1e-9, Score: 102.31, Aligned cols: 165, Identities: 12%, Similarity: 0.072, Template Neff: 10.5

```
Q ss_pred                 CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCC-----------------------
Q Q_Madi_gp59      1      MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKG-----------------------   57 (291)
Q Consensus        1      ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~-----------------------   57 (291)
                          .+|+|||||+|||+||+.|+++|++|+|+|++++   .||........+...++...
T Consensus        40     ~~viIIGaG~aGL~aA~~L~~~G~~v~vlEa~~r---~GGr~~t~~~~g~~~e~Ga~~i~~~~~~i~~~~~~~~~~~~~~~   116 (495)
T 2VVM_B           40     WDVIVIGGGYCGLTATRDLTVAGFKTLLLEARDR---IGGRSWSSNIDGYPYEMGGTWVHWHQSHVWREITRYKMHNALS   116 (495)
T ss_dssp                  CCEEEECCBHHHHHHHHHHHHTTCCEEEECSSSB---SBTTCCEEEETTEEEECSCCCBCTTSHHHHHHHHHTTCTTCEE
T ss_pred                  eeEEEECCCHHHHHHHHHHHHCCCcEEEEeccCC---CCCcceEeeeCCceeeecCccccCCCHHHHHHHHHhCcccccc


Q ss_pred                 ----------------------------------------CCeeeEecCCceechhhcccccccCcccccccCcchhhc-
Q Q_Madi_gp59      58     ----------------------------------------VPVKYVVRGTPEEYRRKTHGKWWDGHIGQDEFEPDHQAW-   96 (291)
Q Consensus        58     ----------------------------------------~~~~~~~~~~~~~~~y~~k~~~~~~~d~~~~~~~~~~~~~~~-   96 (291)
                                                                ..................+....-..+...++..+....
T Consensus        117    ~~~~~~~~~~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~l~~~~   196 (495)
T 2VVM_B           117    PSFNFSRGVNHFQLRTNPTTSTYMTHEAEDELLRSALHKFTNVDGTNGRTVLPFPHDMFYVPEFRKYDEMSYSERIDQIR   196 (495)
T ss_dssp                  ESCCCSSSCCEEEEESSTTCCEEECHHHHHHHHHHHHHHHHCSSSSTTTTTCSCTTSTTSSTTHHHHHTCBHHHHHHHHG
T ss_pred                  CCcccccCcccEEeecCCCceeecChHHHHHHHHHHHHHHccCCCCCcceeecCCCCccCCccHHHHhcCCHHHHHHHHH


Q ss_pred                 --------------------------------------------------------cHHHHHHHHHHHhhhhcCCCCCCC
Q Q_Madi_gp59      97     --------------------------------------------------------DIRQHYDMLWRTYVGKIEPYSIPT   120 (291)
Q Consensus        97     --------------------------------------------------------~~~~~~~~~l~~~~~~~~~~~~~~~~~~~   120 (291)
                                                                                +...+.+.+.+.+......- +.
T Consensus        197    ~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~l~~~~~~~~~~~~~~~~~~~~~~~gG~~~l~~~l~~~l~~~~~~~-I~-   274 (495)
T 2VVM_B           197    DELSLNERSSLEAFILLCSGGTLENSSFGEFLHWWAMSGYTYQGCMDCLMSYKFKDGQSAFARRFWEEAAGTGRLG-YV-   274 (495)
T ss_dssp                  GGCCHHHHHHHHHHHHHHHSSCTTTSBHHHHHHHHHHTTSSHHHHHHHHHSEEETTCHHHHHHHHHHHHHHTTCEE-EE-
T ss_pred                  hcCCHHHHHHHHHHHHHHhCCCcccCCHHHHHHHHHhcCCchHHHHHHHhheeeCCCchHHHHHHHHHHhccCCce-EE-


Q ss_pred                 cceee-eceeEeecCCCCCeEEEEcCC-EEEECEEEECCCHHHHcCCCCcccCccchhh
Q Q_Madi_gp59      121    KGMVA-SFFKRENSDVGVGGYVNWDLG-LSEYELVISTVPRDIWQLPGDEYIYSEGWAI   177 (291)
Q Consensus        121    ~~~~~~-~~V~~i~~~~~~~~~~~v~V~~~~~g-~~~aD~VI~t~p~~~l~~~~~~~~f~p~lp~~~   177 (291)
                              . ++|++|+ .++++++|++.+| +++||.||+|+|+..+.  .+.|.|.+|...
T Consensus        275    ----~~~~V~~I~-~~~~~~v~V~~~~g~~~~ad~VI~avP~~~l~--~I~f~p~L~~~~   326 (495)
T 2VVM_B           275    ----FGCPVRSVV-NERDAARVTARDGREFVAKRVVCTIPLNVLS--TIQFSPALSTER   326 (495)
T ss_dssp                  ----SSCCEEEEE-EETTEEEEEETTSCEEEESEEEECCCGGGGG--GSEEESCCCHHH
T ss_pred                  ----eCCceeEEE-ecCCeeEEEeCCCCEEEEcEEEEccCHHHhc--ccEeCCCCCHHH
```

Template alignment | Template 3D Structure | PDBe

☐ 40. **5MBX_A Peroxisomal N(1)-acetyl-spermine/spermidine oxidase; flavin amine oxidase, oxidoreductase; HET: SP5, FAD; 1.4A {Mus musculus}**

Probability: 99.07%, E-value: 3.8e-9, Score: 99.93, Aligned cols: 162, Identities: 13%, Similarity: -0.067, Template Neff: 11.5

```
Q ss_pred                 CeEEEECCCHHHHHHHHHHHHc--CCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCce---------
Q Q_Madi_gp59      1      MTIAILGCGPTGLLAAHACTLE--GYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPE---------   69 (291)
Q Consensus        1      ~~V~IIGaG~aGl~aA~~L~~~--g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~---------   69 (291)
                          ++|+|||||+|||+||+.|.+.  |.+|+|+|++++   .||........+...++   -..++.......
T Consensus        5      ~~V~IIGaG~aGL~aA~~L~~~~~~~~~~v~vlEa~~r---~GGr~~t~~~~~~~~~e~---G~~~~~~~~~~~~~~~~~~~l~~~l   78 (497)
T 5MBX_A           5      PRVLVVGSGIAGLGAAQKLCSHRAAPHLRVLEATAS---AGGRIRSERCFGGVVEL---GAHWIHGPSQDNPVFQLAAEF   78 (497)
T ss_dssp                  CEEEEECCBHHHHHHHHHHHC---CCEEEEECSSSS---SBTTCCEEEETTEEEES---SCCCBSSCSTTCHHHHHHHHT
T ss_pred                  CeEEEECCCHHHHHHHHHHHHCCCCCcEEEEecCCC---CCCcceEEEeCCeeEEc---CCeeecCCCCCCHHHHHHHHh


Q ss_pred                 --------------------------------------------------------------------------------
Q Q_Madi_gp59      70     --------------------------------------------------------------------------------   69 (291)
Q Consensus        70     --------------------------------------------------------------------------------   69 (291)

T Consensus        79     g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   158 (497)
T 5MBX_A           79     GLLGEKELSEENQLVDTGGHVALPSMIWSSSGTSVSLELMTEMARLFYGLIERTREFLNESETPMASVGEFLKKEISQQV   158 (497)
T ss_dssp                  TCCCHHHHSHHHHHC---------CEEEETTSCBCCHHHHHHHHHHHHHHHHHGGGGTTCSSCSSSBHHHHHHHHHHHHH
```

```
T ss_pred               CCCCccccChhhccccCCCCccCCceEEcCCCcccCHHHHHHHHHHHHHHHHHHHHHHhcCCCCCCcHHHHHHHHHHHHH


Q ss_pred               ------------------------------echhhcccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCC
Q Q_Madi_gp59     70    ------------------------------EYRRKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIP   119 (291)
Q Consensus       70    ------------------------------~y~~k~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~   119 (291)
                                                      .....+........+..........-+...+.+.+.+.+......+
T Consensus       159   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gG~~~l~~~l~~~l~~~~i~l---   235 (497)
T 5MBX_A          159   ASWTEDDEDTRKRKLAILNTFFNIECCVSGTHSMDLVALAPFGEYTVLPGLDCILAGGYQGLTDRILASLPKDTVAF---   235 (497)
T ss_dssp               TTCC------HHHHHHHHHHHHHHHHHHHTCSCGGGBBTTTGGGSCCCSSCCBCCTTCTHHHHHHHHHHSCTTCEES---
T ss_pred               HhCCCCCHHHHHHHHHHHHHHHHHHHHHHHhcCCChHHHhccccCceeCCCCCeeecCchHHHHHHHHHhcCCcccEec---


Q ss_pred               CcceeeeceeEeecCCCC-----------CeEEEEcCC-EEEECEEEECCCHHHHcCCC-CcccCccchhh
Q Q_Madi_gp59     120   TKGMVASFFKRENSDVGV-----------GGYVNWDLG-LSEYELVISTVPRDIWQLPG-DEYIYSEGWAI   177 (291)
Q Consensus       120   ~~~~~~~~~V~~i~~~~~~-----------~v~V~~~~g-~~~aD~VI~t~p~~~l~~~~-~~f~p~lp~~~   177 (291)
                             .+.|++|+ .+++           .++|++++| +++||.||+|+|++.+.... +.|.|.+|...
T Consensus       236   -----~~~V~~I~-~~~~~~~~~~~~~~~~~~~v~v~~~~g~~~~ad~VI~a~P~~~l~~~~~~~~~~~p~l~~~~   300 (497)
T 5MBX_A          236   -----DKPVKTIH-WNGSFQEAAFPGETFPVLVECEDGARLPAHHVIVTVPLGFLKEHQDTFFEPPLPAKK   300 (497)
T ss_dssp               -----SCCEEEEE-CSSCEECSSSSCCEESEEEEETTCCEEEESEEEECCCHHHHHHHHHHHEESCCCHHH
T ss_pred               -----CCceeEEE-cCCcccccCCCCCCCCEEEEeCCCcEEEcCEEEEcCCcchhccCCcccCCCCCCHHH
```

Template alignment | Template 3D Structure | PDBe

☐ **41. 2XFN_B Amine oxidase [flavin-containing] B; FLAVOPROTEIN, OXIDOREDUCTASE; HET: XCG, C15, FAD; 1.6A {Homo sapiens} SCOP: c.3.1.2, d.16.1.5**

Probability: 99.07%, E-value: 3.7e-9, Score: 101.01, Aligned cols: 146, Identities: 12%, Similarity: 0.013, Template Neff: 11

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcc---------------------------
Q Q_Madi_gp59     1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPE---------------------------   53 (291)
Q Consensus       1     ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~~---------------------------   53 (291)
                        ++|+|||||+|||+||+.|++.|.+|+|+|++++   .||.............
T Consensus       5     ~~ViIIGaG~aGl~aA~~L~~~g~~V~ilEa~~r---~GGr~~s~~~~~~~~~~d~g~~~~~~~~~~~~~~~l~~~lg~~~~~   81 (520)
T 2XFN_B          5     CDVVVVGGGISGMAAAKLLHDSGLNVVVLEARDR---VGGRTYTLRNQKVKYVDLGGSYVGPTQNRILRLAKELGLETYK   81 (520)
T ss_dssp               CSEEEECCBHHHHHHHHHHHHTTCCEEEEESSSS---SBTTCCEEEETTTEEEESSCCEECTTCHHHHHHHHHTTCCEEE
T ss_pred               eeEEEECCCHHHHHHHHHHHHCCCCEEEEeCCCC---CCCcccEEecCCcceEEccccccCccHHHHHHHHHHhCCceee


Q ss_pred               --------------------------------------------------------------------------------
Q Q_Madi_gp59     54    --------------------------------------------------------------------------------   53 (291)
Q Consensus       54    --------------------------------------------------------------------------------   53 (291)

T Consensus       82    ~~~~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~l~~~~~~~~~   161 (520)
T 2XFN_B          82    VNEVERLIHHVKGKSYPFRGPFPPVWNPITYLDHNNFWRTMDDMGREIPSDAPWKAPLAEEWDNMTMKELLDKLCWTESA   161 (520)
T ss_dssp               CCCSSEEEEEETTEEEEECSSSCCCCSHHHHHHHHHHHHHHHHHHTTSCTTCGGGSTTHHHHHTSBHHHHHHHHCSSHHH
T ss_pred               ecCccCeEEEECCeeceecCCCCCCCChhHHHHHHHHHHHHHHHhcCCCCCcccCCCHHHHhcCCHHHHHHHHhCCCHHH


Q ss_pred               ------------------------cCCCCCeeeEecCCceechhhcccccccCcccccccCcchhhccHHHHHHHHHHHh
Q Q_Madi_gp59     54    ------------------------SDKGVPVKYVVRGTPEEYRRKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTY   109 (291)
Q Consensus       54    ------------------------l~~~~~~~~~~~~~~~~~~~~~~~y~~k~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~   109 (291)
                                                +                .............-...........-+...+.+.+.+.+
T Consensus       162   ~~~~~~~~~~~~~~~~~~~s~~~~~----------------~~~~~~~~~~~~~~~~~~~~~~~~~gG~~~l~~~l~~~l   225 (520)
T 2XFN_B          162   KQLATLFVNLCVTAETHEVSALWFL----------------WYVKQCGGTTRIISTTNGGQERKFVGGSGQVSERIMDLL   225 (520)
T ss_dssp               HHHHHHHHHHHHSSCTTTSBHHHHH----------------HHHHTTTCHHHHHCSTTSTTSEEETTCTHHHHHHHHHHH
T ss_pred               HHHHHHHHHcccCCChHHccHHHHH----------------HHHHHcCchhHhhccCCCcceeeeecchHHHHHHHHHHH


Q ss_pred               hhhcCCCCCCCcceeeeceeEeecCCCCCeEEEEcCC-EEEECEEEECCCHHHHcCCCCcccCccchhh
Q Q_Madi_gp59     110   VGKIEPYSIPTKGMVASFFKRENSDVGVGGYVNWDLG-LSEYELVISTVPRDIWQLPGDEYIYSEGWAI   177 (291)
Q Consensus       110   ~~~~~~~~~~~~~~~~~~~~~~~~~~V~~i~~~~~~~v~V~~~~g-~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~   177 (291)
                        ......-         ++|++|+ .+++++.|.+.++ ++.||.||+|+|+..+.  .+.|.|.+|...
T Consensus       226   g~~I~l~---------~~V~~I~-~~~~~~v~v~~~~g~~~~ad~VI~A~p~~~~~~--~i~~~p~l~~~~   282 (520)
T 2XFN_B          226   GDRVKLE---------RPVIYID-QTRENVLVETLNHEMYEAKYVISAIPPTLGM--KIHFNPPLPMMR   282 (520)
T ss_dssp               GGGEEES---------CCEEEEE-CSSSSEEEEETTSCEEEESEEEECSCGGGGG--GSEEESCCCHHH
T ss_pred               CCCEecC---------CCeEEEE-ECCCcEEEEeCCCCEEEEcEEEECCCHHHhc--cceeCCCCCHHH
```

Template alignment | Template 3D Structure | PDBe

☐ **42. 1RSG_A FMS1 protein; FAD binding motif, OXIDOREDUCTASE; HET: FAD, MSE; 1.9A {Saccharomyces cerevisiae}**

Probability: 99.06%, E-value: 1.1e-9, Score: 104.28, Aligned cols: 165, Identities: 15%, Similarity: 0.1, Template Neff: 11.2

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCC-eEEEECCCCCccccchhHhcCC-CCCCCcccCCC---------------------
Q Q_Madi_gp59     1     MTIAILGCGPTGLLAAHACTLEGY-DVAIFSRKRKSELFGSQYLHNP-IPGLTPESDKG---------------------   57 (291)
Q Consensus       1     ~~V~IIGaG~aGl~aA~~L~~~g~-~v~i~E~~~~~~~~G~~~~~~~~-~~~~~~~~l~~~---------------------   57 (291)
                        ++|+|||||+|||+||+.|++.|. +|+|+|++++   .||...... ..+...++...
T Consensus       9     ~~V~IIGaG~aGL~aA~~L~~~g~~~v~vlEa~~r---~GGr~~t~~~~~g~~~d~G~~~~~~~~~~~~~~~~~~~~~~~~~   85 (516)
```

```
T 1RSG_A        9     KKVIIIGAGIAGLKAASTLHQNGIQDCLVLEARDR---VGGRLQTVTGYQGRKYDIGASWHHDTLTNPLFLEEAQLSLND   85 (516)
T ss_dssp             EEEEEECCBHHHHHHHHHHHHTTCCSEEEECSSSS---SBTTCCEEECGGGCEEESSCCEECCTTTCHHHHHHHHHHHHH
T ss_pred             CeEEEECCCHHHHHHHHHHHHCCCCcEEEEeCCCC---CccceeEEEcCCCCEEEEeceEEeCCCCCHHHHHHHcccCCC


Q ss_pred             ---------------------------------------------------------------------------CCeee
Q Q_Madi_gp59    58    ---------------------------------------------------------------------------VPVKY   62 (291)
Q Consensus     58    ---------------------------------------------------------------------------~~~~~   62 (291)
                                                                                             ..+..
T Consensus     86    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   165 (516)
T 1RSG_A        86    GRTRFVFDDDNFIYIDEERGRVDHDKELLLEIVDNEMSKFAELEFHQHLGVSDCSFFQLVMKYLLQRRQFLTNDQIRYLP   165 (516)
T ss_dssp             CCCCEECCCCCCEEEETTTEECTTCTTTCHHHHHHHHHHHHHHHC-------CCBHHHHHHHHHHHHGGGSCHHHHHHHH
T ss_pred             CCeEEEECCCCeEEEeCCCCcccCCHHHHHHHHHHHHHHHHHHHHHHHHHcCCCCccHHHHHHHHHHHhhccCCHHHHhHHH


Q ss_pred             EecCCceechhhcccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeecCCCCC-eEE
Q Q_Madi_gp59    63    VVRGTPEEYRRKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENSDVGVG-GYV   141 (291)
Q Consensus     63    ~~~~~~~~y~~k~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~V~~i~~~~~~~-v~V   141 (291)
                      ........+....+....................+...+.+.+.+.++......        .++|++|. .++++ +.|
T Consensus     166   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~g~~~l~~~la~~l~~~~v~l--------~~~V~~I~-~~~~~~v~V   236 (516)
T 1RSG_A        166   QLCRYLELWHGLDWKLLSAKDTYFGHQGRNAFALNYDSVVQRIAQSFPQNWLKL--------SCEVKSIT-REPSKNVTV   236 (516)
T ss_dssp             HHHGGGHHHHTBCTTTSBHHHHCCCCSSCCEEESCHHHHHHHHHTTSCGGGEET--------TCCEEEEE-ECTTSCEEE
T ss_pred             HHHHHHHHHcCCChhHhchhccccCcccccchhcCHHHHHHHHHhhCCcceEEe--------cceeEEEE-ecCCCCEEE


Q ss_pred             EEcCC-EEEECEEEECCCHHHHcCC---------CCcccCccchhh
Q Q_Madi_gp59    142   NWDLG-LSEYELVISTVPRDIWQLP---------GDEYIYSEGWAI   177 (291)
Q Consensus     142   ~~~~g-~~~aD~VI~t~p~~~l~~~---------~~~f~p~lp~~~   177 (291)
                      .+++| +++||.||+|+|++.+...         .+.|.|.+|...
T Consensus     237   ~~~~g~~~~ad~VI~avP~~~l~~~~~~~~~~~~~~~~i~~~p~l~~~~   282 (516)
T 1RSG_A        237   NCEDGTVYNADYVIITVPQSVLNLSVQPEKNLRGRIEFQPPLKPVI   282 (516)
T ss_dssp             EETTSCEEEEEEEEECCCHHHHHGGGSSCSCSTTCCEEESCCCHHH
T ss_pred             EeCCCCEEEeCEEEEecCHHHHccCCCCCccCCCcceecCCCCHHH
```

Template alignment | Template 3D Structure | PDBe

☐ **43. 2GV8_A monooxygenase; FMO, FAD, NADPH, cofactor complex, oxygenase, PSI, Structural Genomics, Protein Structure Initiative, New York SGX Research; HET: MSE, NDP, FAD, GOL; 2.1A {Schizosaccharomyces pombe} SCOP: c.3.1.5**

Probability: 99.05%, E-value: 1e-8, Score: 96.54, Aligned cols: 182, Identities: 13%, Similarity: 0.011, Template Neff: 10.3

```
Q ss_pred             CeEEEECCCHHHHHHHHHHHHcCC--eEEEECCCCCcccccchhHhcCCCCCCCcccCCCCCe------------------
Q Q_Madi_gp59    1     MTIAILGCGPTGLLAAHACTLEGY--DVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPV------------------   60 (291)
Q Consensus     1     ~~V~IIGaG~aGl~aA~~L~~~g~--~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~------------------   60 (291)
                      ++|+|||||+||+++|..|.+.|.  +|+|+|+...   .|+.|............     .
T Consensus     7     ~~v~IIGaG~aGl~aa~~l~~~g~~~~v~v~E~~~~---~GG~w~~~~~~~~~~~~~-----~~~~~~~~~~~~~~~~~~~   78 (447)
T 2GV8_A        7     RKIAIIGAGPSGLVTAKALLAEKAFDQVTLFERRGS---PGGVWNYTSTLSNKLPV-----PSTNPILTTEPIVGPAALP   78 (447)
T ss_dssp             CEEEEECCSHHHHHHHHHHHTTTCCSEEEEECSSSS---SSTTCSCCSCCCSCCCS-----SBCCTTCCCCCBCCSSSCC
T ss_pred             CEEEEECCCHHHHHHHHHHHHcCCCCcEEEEecCCC---CCCceecCCCCCCCCCC-----CCCCcCCCCCCCCCCCCCC


Q ss_pred             --eeEecCCceechhhcccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeecCCCCC
Q Q_Madi_gp59    61    --KYVVRGTPEEYRRKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENSDVGVG   138 (291)
Q Consensus     61    --~~~~~~~~~~~~~y~~k~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~V~~i~~~~~~~   138 (291)
                        ....+.....-..+....+.+..+.....    .......+.+-+.+......... .+     .++|++++ ..++.
T Consensus     79    ~~~~~~y~~l~~n~~~~~~~~~~~~~~~~~~~~~----~~~~~~~~v~~yL~~~a~~~~~~i-~~-----~t~V~~v~-~~~~~   147 (447)
T 2GV8_A        79    VYPSPLYRDLQTNTPIELMGYCDQSFKPQTL----QFPHRHTIQEYQRIYAQPLLPFI-KL-----ATDVLDIE-KKDGS   147 (447)
T ss_dssp             BCCCCCCTTCBCSSCHHHHSCTTCCCCTTCC----SSCBHHHHHHHHHHHHGGGGGGE-EC-----SEEEEEEE-EETTE
T ss_pred             CCCCccccCCCcCCCHHHhcCCCCCCCCCCCC----CCCCHHHHHHHHHHHHHHHHHHhcE-Ee-----cEEEEEEE-EcCCE


Q ss_pred             eEEEEcC------C-EEEECEEEECCCHHHHcCCCCcccCccchhhccCcc----cCceecceeccceecCCCCEEEEec
Q Q_Madi_gp59    139   GYVNWDL------G-LSEYELVISTVPRDIWQLPGDEYIYSEGWAIGDAPE----RGVFVDDLVEGRELFDKDNTIICDG   207 (291)
Q Consensus     139   v~V~~~~------g-~~~aD~VI~t~p~~~l~~~~~~~~f~p~lp~~~g~~~~----~g~~~~~~~v~~~e~~~~~~~~~~~~~~   207 (291)
                      +.|.+.+      . +..+|.||+|+        +..-.|.+|..+|...|    .|..+|.........+....++.-+
T Consensus     148   w~V~~~~~~~~~g~~~~~~~~~d~VVvAt--------G~~s~p~~p~~~g~~~~~~~~~~~g~~~hs~~~~~~~~~~~~~gk~VlVvG   219 (447)
T 2GV8_A        148   WVVTYKGTKAGSPISKDIFDAVSICN--------GHYEVPYIPNIKGLDEYAKAVPGSVLHSSLFREPELFVGESVLVVG   219 (447)
T ss_dssp             EEEEEEESSTTCCEEEEEESEEEECC--------CSSSSBCBCCCBTHHHHHHHSTTSEEEGGGCCCGGGGTTCCEEEEC
T ss_pred             EEEEEEECCCCCeEEEEEcCEEEEcC--------CCCCCCCCCCCCCHHHHHHHCCCcEEEcccCCChHHhCCCEEEEEC


Q ss_pred                   CC
Q Q_Madi_gp59    208   TS   209 (291)
Q Consensus     208   ~~   209 (291)
                      .+
T Consensus     220   ~g   221 (447)
T 2GV8_A        220   GA   221 (447)
T ss_dssp             SS
```

```
T ss_pred              CC
```

Template alignment | Template 3D Structure | PDBe

☐ **44. 4C5O_G FLAVIN MONOOXYGENASE; OXIDOREDUCTASE; HET: SO4, FAD; 2.6A {STENOTROPHOMONAS MALTOPHILIA}**

Probability: 99.04%, E-value: 2.1e-8, Score: 90.24, Aligned cols: 168, Identities: 13%, Similarity: -0.029, Template Neff: 12.1

```
Q ss_pred              CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59    1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus      1     ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                       .+|+|||||++|+++|..|++.|.+++|+|+...   .|+.|.........        ...........+....+..
T Consensus      4     ~~v~iiG~G~~G~~~a~~l~~~g~~v~vie~~~~---~g~~~~~~~~~~~~--------~~~~~~~~~~~~~~~~~~~~~--   70 (357)
T 4C5O_G         4     VDVVVIGGGQSGLSAGYFLRRSGLSYVILDAEAS---PGGAWQHAWHSLHL--------FSPAGWSSIPGWPMPASQG--   70 (357)
T ss_dssp              EEEEEECCSHHHHHHHHHHHHSSCCEEEECCSSS---SSGGGGGSCTTCBC--------SSCGGGSCCSSSCCCCCSS--
T ss_pred              eeEEEECCCHHHHHHHHHHHHCCCCEEEEeCCCC---CCCcccccccceEE--------ecCchhhcCCCCCCCCCCC--


Q ss_pred              cCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeecCCCCCeEEEEcCC-EEEECEEEECCCH
Q Q_Madi_gp59    81    DGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENSDVGVGGYVNWDLG-LSEYELVISTVPR  159 (291)
Q Consensus      81    d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~V~~i~~~~~~~~v~V~~~g-~~~aD~VI~t~p~  159 (291)
                                    .......+...+...+....... .+     .++|.++. ..++.+.|.+.++ .+.+|.||+|+
T Consensus      71    -------------~~~~~~~~~~~l~~~~~~~~~~~-~~-----~~~v~~i~-~~~~~~~v~~~~~~~~~~~d~vilat--  128 (357)
T 4C5O_G         71    -------------PYPARAEVLAYLAQYEQKYALPV-LR-----PIRVQRVS-HFGERLRVVARDGRQWLARAVISAT--  128 (357)
T ss_dssp              -------------SSCBHHHHHHHHHHHHHHTTCCE-EC-----SCCEEEEE-EETTEEEEEETTSCEEEEEEEEECC--
T ss_pred              -------------CCCCHHHHHHHHHHHHHHcCCCc-cc-----ceeEEEEE-ecCCeEEEEEccCCEEEEcEEEEcc--


Q ss_pred              HHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59    160   DIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS  209 (291)
Q Consensus      160   ~~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~  209 (291)
                             +..-.|..|..++...+.+..++..............++.-+.+
T Consensus      129   ------G~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vvviG~G  172 (357)
T 4C5O_G         129   ------GTWGEAYTPEYQGLESFAGIQLHSAHYSTPAPFAGMRVAIIGGG  172 (357)
T ss_dssp              ------CSTTSBCCCCTTGGGCCSEEEEGGGCCCSGGGTTCEEEEEECCS
T ss_pred              ------cCCCCCCCCCCCChhcCCeEEecccCCCCcccCCCEEEEEECCC
```

Template alignment | Template 3D Structure | PDBe

☐ **45. 6LQL_A Amine oxidase; Cyclohexylamine Oxidase, OXIDOREDUCTASE; HET: F0C, FAD; 1.8A {Erythrobacteraceae bacterium CCH12-C2}**

Probability: 99.03%, E-value: 8.9e-9, Score: 95.78, Aligned cols: 162, Identities: 12%, Similarity: -0.029, Template Neff: 12

```
Q ss_pred              CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59    1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus      1     ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                       ++|+|||||++||+||+.|+++|++|+|+|++++   .||.......+......+.+..........+..+....-....
T Consensus      7     ~~v~IIGaG~sGL~aA~~L~~~g~~v~v~E~~~~---~GGr~~s~~~~~~~~~~~~g~~~~~~~~~~~~~l~~~~~l~~~   83 (453)
T 6LQL_A         7     ADVIVIGAGPSGSYAAKLLHDQGVRVKLVEAKDR---VGGRTWSTKSDAPGGPIDFGGQWIGETHVLLPELGAELGLETV   83 (453)
T ss_dssp              CSEEEECCSHHHHHHHHHHHHTTCCEEEECSSSS---SCTTCCEESSSSTTSCEESSCCCBCTTCCHHHHHHHHTTCCEE
T ss_pred              ccEEEECCCHHHHHHHHHHHHCCCcEEEEcCCCC---CcCcccceecCCCCCeeecCCcccCCCChHHHHHHHHhCCEEE


Q ss_pred              cCccccccc-----------------------------------------------------------------------
Q Q_Madi_gp59    81    DGHIGQDEF-----------------------------------------------------------------------   89 (291)
Q Consensus      81    d~~~~~~~~-----------------------------------------------------------------------   89 (291)
                       .........
T Consensus      84    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~l~~~~~~~~~  163 (453)
T 6LQL_A         84    SSVKPGNDLFVFNGDVEVGEEDQVPSGASWAGELSRSFELLDEVGTRLGWAAPWASEHVGELDSMTVAQWLEQNVQSSEV  163 (453)
T ss_dssp              ECCCCSEEEEEETTEEEECBTTBCCTTCTTHHHHHHHHHHHHHHHHHHCSSCGGGSTTHHHHTTSBHHHHHHHHCCCHHH
T ss_pred              ccCCCCCeEEEECCEEEecCCcCCCCCcchhHHHHHHHHHHHHHHHHhCCCCCCcCCCHHHHhcCcHHHHHHHcCCCHHH


Q ss_pred              --------------------------------------------CcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceee
Q Q_Madi_gp59    90    --------------------------------------------EPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVA  125 (291)
Q Consensus      90    --------------------------------------------~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~  125 (291)
                                                                   ...+..-+...+.+.+.+.+     +.    +....
T Consensus      164   ~~~~~~~~~~~~~~~~~~~s~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gG~~~l~~~la~~l-----g~----~I~~~  234 (453)
T 6LQL_A         164   RLIHEVMVNILNGASTTEVSMAYWAYFVHQGEGIESLIGTRSGAQVAWFIGGMGQVTELIADKL-----GD----DVHLN  234 (453)
T ss_dssp              HHHHHHHHHHHSSSCTTTSBHHHHHHHHHHTTCHHHHHCSSSSSCCEEETTCTHHHHHHHHHHH-----GG----GEESS
T ss_pred              HHHHHHHHHHHhCCCHHHcCHHHHHHHHHhcCcHHHHccCCCcccceeEEechhHHHHHHHHHHH-----CC----cEEcC


Q ss_pred              eceeEeecCCCCCeEEEEcCCEEEECEEEECCCHHHHcCCCCcccCccchhh
Q Q_Madi_gp59    126   SFFKRENSDVGVGGYVNWDLGLSEYELVISTVPRDIWQLPGDEYIYSEGWAI  177 (291)
Q Consensus      126   ~~V~~i~~~~~~~~v~V~~~g~~~aD~VI~t~p~~~l~~~~~~f~p~lp~~~  177 (291)
                       ++|++|. .++++++|.++++.+.||.||+|+|+..+.  .+.|.|.+|...
T Consensus      235   ~~V~~I~-~~~~~v~v~~~~~~~~ad~VI~a~p~~~~~--~i~~~~~l~~~~  283 (453)
```

```
T 6LQL_A          235   WPVTRIE-QDPTGVTVFSGERRLRASFAILAAPPSAGS--RMIFDPPLPPKR   283 (453)
T ss_dssp               CCCCEEE-EETTEEEEEETTEEEEESEEEECSCHHHHH--TSEEESCCCHHH
T ss_pred               CCceEEE-ECCCCeEEEeCCcEEEEEEEEEeCChHHHh--cCccCCCCCHHH
```

Template alignment | Template 3D Structure | PDBe

☐ **46. 4USQ_A PYRIDINE NUCLEOTIDE-DISULFIDE OXIDOREDUCTASE; FLAVIN, FAD, NAD(P)H, OXIDOREDUCTASE; HET: FAD; 2.39A {CELLVIBRIO SP. BR}**

Probability: 99.02%, E-value: 3.6e-8, Score: 88.97, Aligned cols: 168, Identities: 15%, Similarity: 0.025, Template Neff: 12

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCcccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59      1    MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus        1    ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                        .+|+|||||++|+++|..|.+.|.+++|+|+...   .|+.|.........        ...........+....+..
T Consensus        14   ~~v~IiGaG~aGl~~a~~l~~~g~~~~vie~~~~---~g~~~~~~~~~~~~~--------~~~~~~~~~~~~~~~~~~~--   80 (361)
T 4USQ_A          14   TDIVIIGGGQAALSVAYYLRRSKYSFVMLDAEQT---PGGAWLHGWDSLRL--------FSPSTWSSLSGWQMPPTGE--   80 (361)
T ss_dssp               EEEEEECCSHHHHHHHHHHTTSSSCEEEECSSSS---SCGGGGGSCTTCBC--------SSCGGGSCCSSSCCCCCSS--
T ss_pred               CeEEEECCCHHHHHHHHHHHHCCCCEEEEeCCCC---CCCccccccCccEe--------ecCcchhccCCCCCCCCCC--


Q ss_pred               cCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeecCCCCCeEEEEcCCEEEECEEEECCCHH
Q Q_Madi_gp59      81   DGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENSDVGVGGYVNWDLGLSEYELVISTVPRD   160 (291)
Q Consensus        81   d~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~V~~i~~~~~~~~v~V~~~~g~~~aD~VI~t~p~~   160 (291)
                                     .......+.+.+........... ..     .+.|.+++ ..++.+.+..+++.+.+|.||+|+
T Consensus        81   -------------~~~~~~~~~~~~~~~~~~~~~~~~~-~~-----~~~v~~i~-~~~~~~~~v~~~~~~~~~~~~lvlAt---   137 (361)
T 4USQ_A          81   -------------TYPSRDQVVDYLRHYESRYEFPV-QR-----PVWVSAVN-NLGDRLEVVSERQQWRARVVISAT---   137 (361)
T ss_dssp               -------------SCCBHHHHHHHHHHHHHHTTCCE-EC-----SCCCCEEE-ECSSSEEEECSSCEEEEEEEEECC---
T ss_pred               -------------CCCCHHHHHHHHHHHHHHhCCCc-cC-----CeEEEEEe-eCCCeEEEeeCCeEEEEcEEEECC---


Q ss_pred               HHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEEecCC
Q Q_Madi_gp59      161  IWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIICDGTS   209 (291)
Q Consensus        161  ~l~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~~~~   209 (291)
                             +....|.+|..++...+.+..++..............+..-+.+
T Consensus        138  -----G~~~~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~v~ivG~g   181 (361)
T 4USQ_A          138  -----GTWRNPFIPAYPGADLFQGAQLHSAHYQSPAPFAGQKVLVVGGG   181 (361)
T ss_dssp               -----CSTTSBCCCCCTTTTTCCSEEEEGGGCCCSGGGTTCEEEEECCH
T ss_pred               -----CCCCCCCCCCCCCCCccCCeEeeceecCCccccCCCEEEEECCC
```

Template alignment | Template 3D Structure | PDB | NCBI

☐ **47. d2i0za1 c.3.1.8 (A:1-192,A:362-420) Flavoprotein BC4706 {Bacillus cereus [TaxId: 1396]}**

Probability: 99.02%, E-value: 3.4e-9, Score: 91.09, Aligned cols: 149, Identities: 14%, Similarity: 0.055, Template Neff: 11.4

```
Q ss_pred               CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCcccccchhHhcCCCCCCCcccCCCCCeeeEecCCceechhhcccccc
Q Q_Madi_gp59      1    MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus        1    ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                        ++|+|||||++|+++|+.|++.|++|+|+|+...   .++.+.................................+....
T Consensus        3    ~dvvIVG~G~~Gl~~A~~L~~~g~~v~vie~~~~---~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   79 (252)
T d2i0za1         3    YDVIVIGGGPSGLMAAIGAAEEGANVLLLDKGNK---LGRKLAISGGGRCNVTNRLPLDEIVKHIPGNGRFLYSAFSIFN   79 (252)
T ss_dssp               CSEEEECCSHHHHHHHHHHHHTTCCEEEECSSSS---SCHHHHHTGGGTCCCEECSCHHHHHHTCTBTGGGGHHHHHHSC
T ss_pred               eEEEEECCCHHHHHHHHHHHHCCCeEEEEeCCCC---ccccccccCCcccccCCCCCHHHHHHhCCCcHHHHHHHHhccC


Q ss_pred               cCcccccccCc------------chhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeecCCCCCeEEEEcCC-E
Q Q_Madi_gp59      81   DGHIGQDEFEP------------DHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENSDVGVGGYVNWDLG-L   147 (291)
Q Consensus        81   d~~~~~~~~~~------------~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~V~~i~~~~~~~~v~V~~~~g-~   147 (291)
                        ...........            +........+.+.+.+.+....... ..     .++|+++...++....|.++++ .
T Consensus        80   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~gv~i-~~-----~~~v~~i~~~~~~~~~~~v~~~~g~~   153 (252)
T d2i0za1         80   NEDIITFFENLGVKLKEEDHGRMFPVSNKAQSVVDALLTRLKDLGVKI-RT-----NTPVETIEYENGQTKAVILQTGEV   153 (252)
T ss_dssp               HHHHHHHHHHTTCCEEECGGGEEEETTCCHHHHHHHHHHHHHHTTCEE-EC-----SCCEEEEEEETTEEEEEEETTCCE
T ss_pred               ChhHHHHHHHhCceeeeeecCccCCCCccHHHHHHHHHHHHHHCCCeE-Ec-----CCeeEEEEEECCeEEEEEeCCCCE


Q ss_pred               EEECEEEECCC
Q Q_Madi_gp59      148  SEYELVISTVP   158 (291)
Q Consensus        148  ~~aD~VI~t~p   158 (291)
                        +.+|.||+|++
T Consensus        154  i~ad~vV~A~G   164 (252)
T d2i0za1         154  LETNHVVIAVG   164 (252)
T ss_dssp               EECSCEEECCC
T ss_pred               EEcCEEEEeCC
```

Template alignment | Template 3D Structure | PDBe

☐ 48. **5YGQ_A Ferredoxin--NADP reductase; electron transport, fad, flavoprotein, nadp, OXIDOREDUCTASE; HET: FAD; 2.4A {Rhodopseudomonas palustris (strain ATCC BAA-98 / CGA009)}**

Probability: 98.99%, E-value: 2.6e-8, Score: 89.1, Aligned cols: 153, Identities: 16%, Similarity: 0.126, Template Neff: 12.1

```
Q ss_pred                CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCCceechhhcccccc
Q Q_Madi_gp59      1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
Q Consensus        1     ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                         ++|+|||||++|+++|..|++.|++++|+|+...   .|+.+...........
T Consensus        7     ~~v~IiG~G~~G~~~a~~l~~~g~~v~l~e~~~~---~gg~~~~~~~~~~~~~--------------------------   57 (342)
T 5YGQ_A          7     TDVLIVGAGPCGLFAVFELGLLDVKAHLVDILDK---VGGQCAELYPEKPIYDI--------------------------   57 (342)
T ss_dssp               EEEEEECCSHHHHHHHHHHHTTTCCEEEECSSSS---SSHHHHHHCTTSEECCS--------------------------
T ss_pred               ccEEEECCCHHHHHHHHHHHhCCCCeEEEeCccc---cCCcccccCCCCCccCC--------------------------


Q ss_pred                cCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeecCCCCCeEEEEcCC-EEEECEEEECCCH
Q Q_Madi_gp59      81    DGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENSDVGVGGYVNWDLG-LSEYELVISTVPR   159 (291)
Q Consensus        81    d~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~V~~i~~~~~~~v~V~~~~g-~~~aD~VI~t~p~   159 (291)
                                   ..............+...+......+ ..     .+.+..+....+..+.|.++++ .+.+|.+|+|+
T Consensus        58    ----------~~~~~~~~~~~~~~~~~~~~~~~~~~~~-~~-----~~~v~~v~~~~~~~~~~v~~~~g~~~~~~~lvia~--   119 (342)
T 5YGQ_A          58    ----------PGIPMVTGHGLTEALMEQIKPFNPTF-HL-----SEMVENVEKIGDPGFRVTTNAGKVFECTVLVVAA--   119 (342)
T ss_dssp               ----------TTCSCEEHHHHHHHHHHHHTTSCCEE-EC-----SCCEEEEEEEETTEEEEEETTSCEEEEEEEEECC--
T ss_pred               ----------CCCCcCCcchHHHHHHHHHHHHCCCc-cc-----CceEEEEEEcCCCcEEEEeCCCcEEEEeEEEEee--


Q ss_pred                HHHcCCCCcccCccchhhccCcccCceecceecccceecCCCCEEEE
Q Q_Madi_gp59      160   DIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIIC   205 (291)
Q Consensus        160   ~~l~~~~~~~f~p~lp~~~g~~~~~g~~~~~~v~~~e~~~~~~~~~~~   205 (291)
                              +.....|.++...+...+.+..++..........+.+.++
T Consensus        120   -----G~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~vi   160 (342)
T 5YGQ_A          120   -----GGGSFLPKRPPVPGVEAYEGTSVHYAVRKMEDFRGKDILIV   160 (342)
T ss_dssp               -----TTCEEEECCCTTTCSCGGGTTTBCSSCSCGGGGTTCEEEEE
T ss_pred               -----CCccCCCCCCCCCCCCcccCCcceeEEeccHHHhCCCEEEEE
```

Template alignment | Template 3D Structure | PDBe

☐ 49. **4BJZ_A PROBABLE SALICYLATE MONOOXYGENASE; OXIDOREDUCTASE, GENTISATE, PHOSPHOLIPID; HET: P3A, FAD; 1.51A {RHODOCOCCUS JOSTII}**

Probability: 98.98%, E-value: 4.3e-9, Score: 98.05, Aligned cols: 153, Identities: 14%, Similarity: -0.021, Template Neff: 10.8

```
Q ss_pred                CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCC--------CCeeeEecCCCceech
Q Q_Madi_gp59      1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKG--------VPVKYVVRGTPEEYR   72 (291)
Q Consensus        1     ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~--------~~~~~~~~~~~~~~y~   72 (291)
                         .+|+|||||++|+++|..|++.|++|+|+|+.+.....|......  +.....+..-         ...............
T Consensus        7     ~~v~IiGaG~aGl~~A~~L~~~g~~v~v~E~~~~~~~~~g~~~~l--~~~~~~~l~~~g~~~~~~~~~~~~~~~~~~~~~~~   84 (424)
T 4BJZ_A          7     ARIIIAGGGIGGAANALALAQKGANVTLFERASEFGEVGAGLQVG--PHGARILDSWGVLDDVLSRAFLPKNIVFRDAIT   84 (424)
T ss_dssp               CEEEEECCSHHHHHHHHHHHHTTCEEEEEESSSSCCCCSSEEEEC--HHHHHHHHHTTCHHHHHHTSBCCSEEEEEETTT
T ss_pred               CeEEEECCCHHHHHHHHHHHHCCCeEEEEeCCCCCCCcCceeEeC--hHHHHHHHHcCChHHHHHhccCCceEEEEeCCC


Q ss_pred                hhccccccCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeecCCCCCeEEEEcCC-EEEEC
Q Q_Madi_gp59      73    RKTHGKWWDGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENSDVGVGGYVNWDLG-LSEYE   151 (291)
Q Consensus        73    ~k~~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~V~~i~~~~~~~~v~V~~~~g-~~~aD   151 (291)
                         ...............+....+...+..+.+.|.+.+....... .+     .++|+++. .+++.+.|.+++| ++++|
T Consensus        85    ~~[illegible]~~~~[illegible]~~~~[illegible]l~~~L[illegible]~gv~[illegible]~~~v[illegible]~~~~[illegible]ad   157 (424)
T 4BJZ_A          85    AEVLTKIDLGSEFRGRYGGPYFVTHRSDLHATLVDAARAAGAEL-HT-----GVTVTDVI-TEGDKAIVSTDDGRTHEAD   157 (424)
T ss_dssp               CCEEEEEECSHHHHHHHTSCCEEEEHHHHHHHHHHHHHHTTCEE-EE-----SCCEEEEE-EETTEEEEEETTSCEEEES
T ss_pred               ccEEEeeeCchhHHHhhCCCeEEecHHHHHHHHHHHHHHcCCEE-Ec-----CCceEEEE-ecCCEEEEEeCCCCEEEec


Q ss_pred                EEEECCCHHHH
Q Q_Madi_gp59      152   LVISTVPRDIW   162 (291)
Q Consensus        152   ~VI~t~p~~~l   162 (291)
                         .||.|.|..+.
T Consensus        158   ~vIgADG~~S~   168 (424)
T 4BJZ_A          158   IALGMDGLKSR   168 (424)
T ss_dssp               EEEECCCTTCS
T ss_pred               EEEECCCChHH
```

Template alignment | Template 3D Structure | PDBe

☐ 50. **5TWB_A Ferredoxin--NADP reductase; siderophore, iron, oxidoreductase, flavin adenine dinucleotide; HET: FAD; 1.822A {Staphylococcus aureus (strain USA300)}**

Probability: 98.97%, E-value: 3.4e-8, Score: 89.27, Aligned cols: 152, Identities: 12%, Similarity: 0.035, Template Neff: 11.2

```
Q ss_pred                CeEEEECCCHHHHHHHHHHHHcCCeEEEECCCCCccccchhHhcCCCCCCCcccCCCCCeeeEecCCCceechhhcccccc
Q Q_Madi_gp59      1     MTIAILGCGPTGLLAAHACTLEGYDVAIFSRKRKSELFGSQYLHNPIPGLTPESDKGVPVKYVVRGTPEEYRRKTHGKWW   80 (291)
```

```
Q Consensus       1    ~~V~IIGaG~aGl~aA~~L~~~g~~v~i~E~~~~~~~~G~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~y~~k~~~~~~   80 (291)
                       ++|+|||||+||++||..|++.|.+++|+|+...   .|+.+...                         .....|..
T Consensus       2    ~~v~IIG~G~aGl~aa~~l~~~~~~v~l~e~~~~---~gg~~~~~-------------------------~~~~~~~~--   51 (344)
T 5TWB_A          2    KDVTIIGGGPSGLYASFYAGLRDMSVRLIDVQSE---LGGKMRIY-------------------------PEKIIWDI--   51 (344)
T ss_dssp             EEEEEECCSHHHHHHHHHHHHTTCCEEEECSSSS---SCGGGGGC-------------------------TTSEECCS--
T ss_pred             eeEEEECCCHHHHHHHHHHHhCCCeEEEEECCCC---CCCeeccc-------------------------CCcccccC--


Q ss_pred             cCcccccccCcchhhccHHHHHHHHHHHhhhhcCCCCCCCcceeeeceeEeecCCCCCeEEEEcCC-EEEECEEEECCCH
Q Q_Madi_gp59     81   DGHIGQDEFEPDHQAWDIRQHYDMLWRTYVGKIEPYSIPTKGMVASFFKRENSDVGVGGYVNWDLG-LSEYELVISTVPR   159 (291)
Q Consensus       81   d~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~V~~i~~~~~~~~v~V~~~~g-~~~aD~VI~t~p~   159 (291)
                                 ...........+.............. ..     .++|.++....+..+.|.++++ .+.+|.||+|+
T Consensus       52   ----------~~~~~~~~~~~~~~~~~~~~~~~~~~~~-~~-----~~~v~~i~~~~~~~~~~~v~~~~g~~~~~~~lvlAt--   113 (344)
T 5TWB_A          52   ----------GGIAPKPCHEILKDTIKQGLYFKPEV-HL-----NERVVDIRKKAERHFEVETEAGEIYTSKAVIIAI--   113 (344)
T ss_dssp             ----------TTCCSEEHHHHHHHHHHHHTTTCCEE-EC-----SCCEEEEEEEETTEEEEEETTCCEEEEEEEEEECC--
T ss_pred             ----------CCCCCCCHHHHHHHHHHhhhcCCCeE-Ee-----CeEEEEEEECCCCeEEEEECCCcEEEEcEEEEcc--


Q ss_pred             HHHcCCCCcccCccchhhccCcccCceecceeccceecCCCCEEEE
Q Q_Madi_gp59     160  DIWQLPGDEYIYSEGWAIGDAPERGVFVDDLVEGRELFDKDNTIIC   205 (291)
Q Consensus       160  ~~l~~~~~~~f~p~lp~~~g~~~~~g~~~~~~~v~~~e~~~~~~~~~~~~~~   205 (291)
                            +...+.|..+...+...+....++......+...++++.+.
T Consensus       114  -----G~~~~~p~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~vi   154 (344)
T 5TWB_A          114  -----GAGIINPKQLDVKGVERYQLTNLHYVVQSYRRFKDKDVLIS   154 (344)
T ss_dssp             -----TTCEEEECCCSCTTCTTGGGTTEESCCSCSGGGTTCEEEEE
T ss_pred             -----cCCCCCcccCCCCCccccccccceeeecchhhcCCCEEEEE
```

If you use HHpred on our Toolkit for your research, please cite as appropriate:

> A Completely Reimplemented MPI Bioinformatics Toolkit with a New HHpred Server at its Core.
> Zimmermann L, Stephens A, Nam SZ, Rau D, Kübler J, Lozajic M, Gabler F, Söding J, Lupas AN, Alva V. J Mol Biol. 2018 Jul 20. S0022-2836(17)30587-9.
>
> Protein Sequence Analysis Using the MPI Bioinformatics Toolkit.
> Gabler F, Nam SZ, Till S, Mirdita M, Steinegger M, Söding J, Lupas AN, Alva V. Curr Protoc Bioinformatics. 2020 Dec;72(1):e108. doi: 10.1002/cpbi.108.
>
> Protein homology detection by HMM-HMM comparison.
> Söding J. Bioinformatics. 2005 Apr 1;21(7):951-60.
>
> Fast and accurate automatic structure prediction with HHpred.
> Hildebrand A, Remmert M, Biegert A, Söding J. Proteins. 2009;77 Suppl 9:128-32.
>
> Automatic Prediction of Protein 3D Structures by Probabilistic Multi-template Homology Modeling.
> Meier A, Söding J. PLoS Comput Biol. 2015 Oct 23;11(10):e1004343.