

## Some of the example generated by nanoPLM

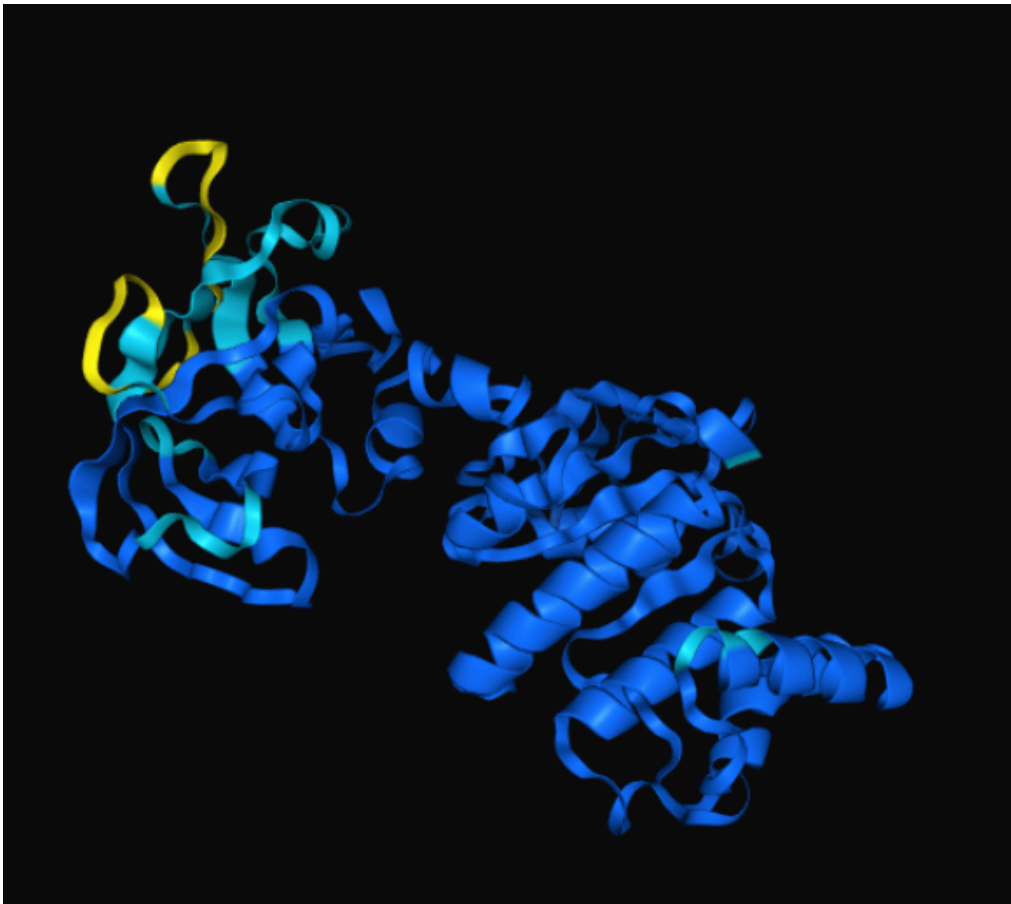
### Sequence:

MAKITLKNVNKKFGSNPVIKNIDLDIPDGQFLVLVGPSSGCGKSTLLRMVAGLETITDGDIIIIGDKRMNDVPAK  
ERGIAMVFQSYALYPHMSVYDNMAFGLKMAGVPKDEINKRVKQAAEILQLGHLLDRKPAQLSGGQRQRV  
AMGRAIVREPQVFLFDEPLSNLDAKLRVQMRTEIKRLHQRLNTTTSIYVTHDQTEAMTLGDRIAVMKDGVQLQ  
QVDTPMNMYYNNPANLFVAQFIGSPAMNLDGRIVDESGKQFVLEAGSGVRVPVPENKLAGKKGTTVTLAI  
RPEHVEISKEGGDVFSAEVSVVEPTGSDTYLYAELGGVNLVARIEARTSVTPGEKIGISFDMDKVHLFSKDT  
EEAI

pTM = 0.94

Best hit with BLASTp: `sp|Q8X8K4.1| RecName: Full=Uncharacterized ABC transporter ATP-binding protein YcjV [Escherichia coli O157:H7]`

Sequence similarity: 56.99



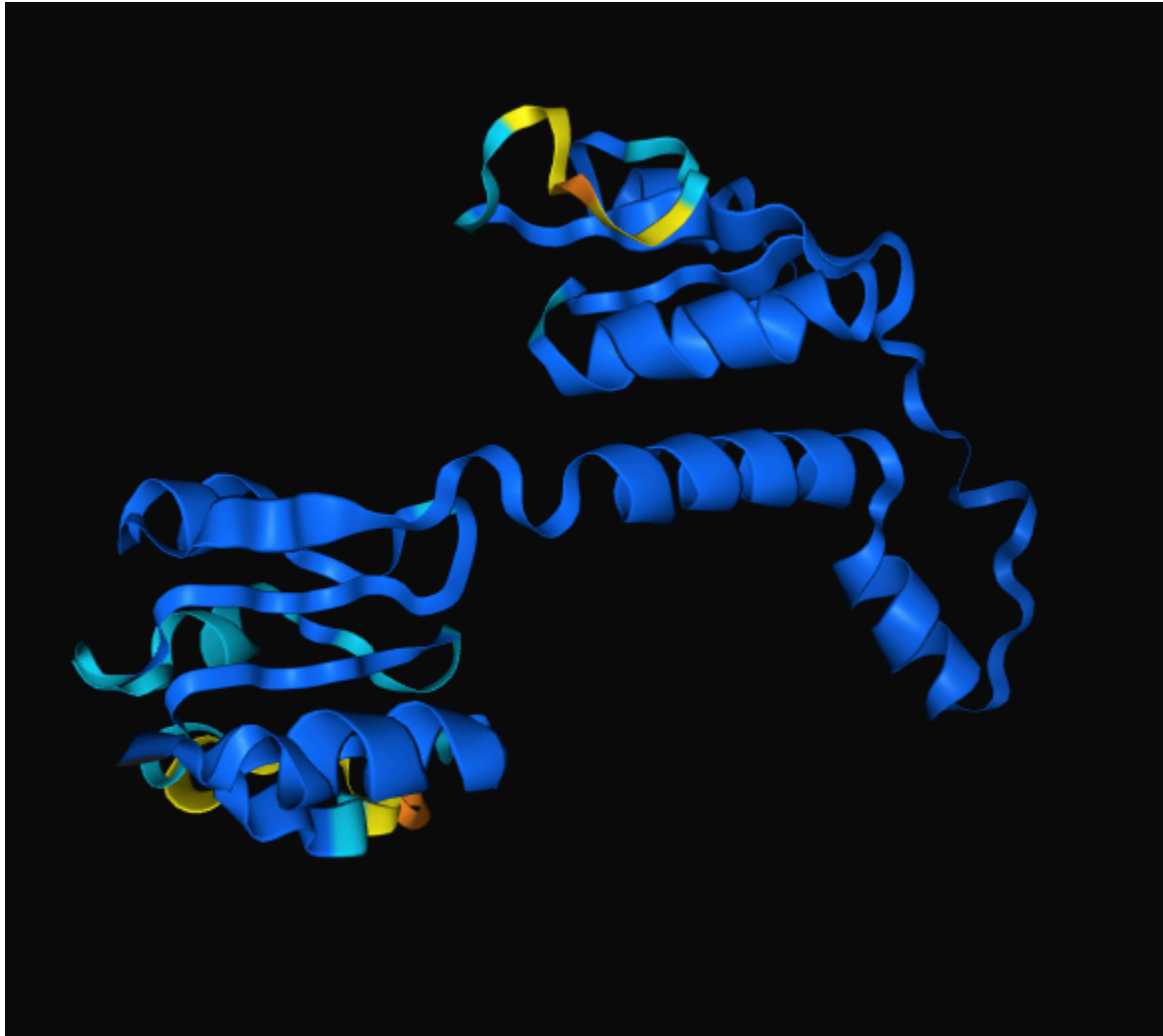
## Sequence:

MARIAVTDGMAASAIEELQARNHEVVLAHLGEEPLTESRVSAFDALVIRSATKLTSDVVASASSELKVIGRA  
GVGVDNIDLASAAEKGIAVVNAPTASTISVAELAMGHMISLLRFIPEADRGLKAGKWEKKAMKGTFLFGKT  
LGLIGSGRIGREVGVLAAQAFGMEIHAYDPYLPKPPASVAAHRVDSLADLFASVDHV

pTM = 0.79

Best hit with BLASTp: `sp|Q58424.1| RecName: Full=D-3-phosphoglycerate dehydrogenase; Short=PGDH [Methanocaldococcus jannaschii DSM 2661]`

Sequence similarity: 51.00



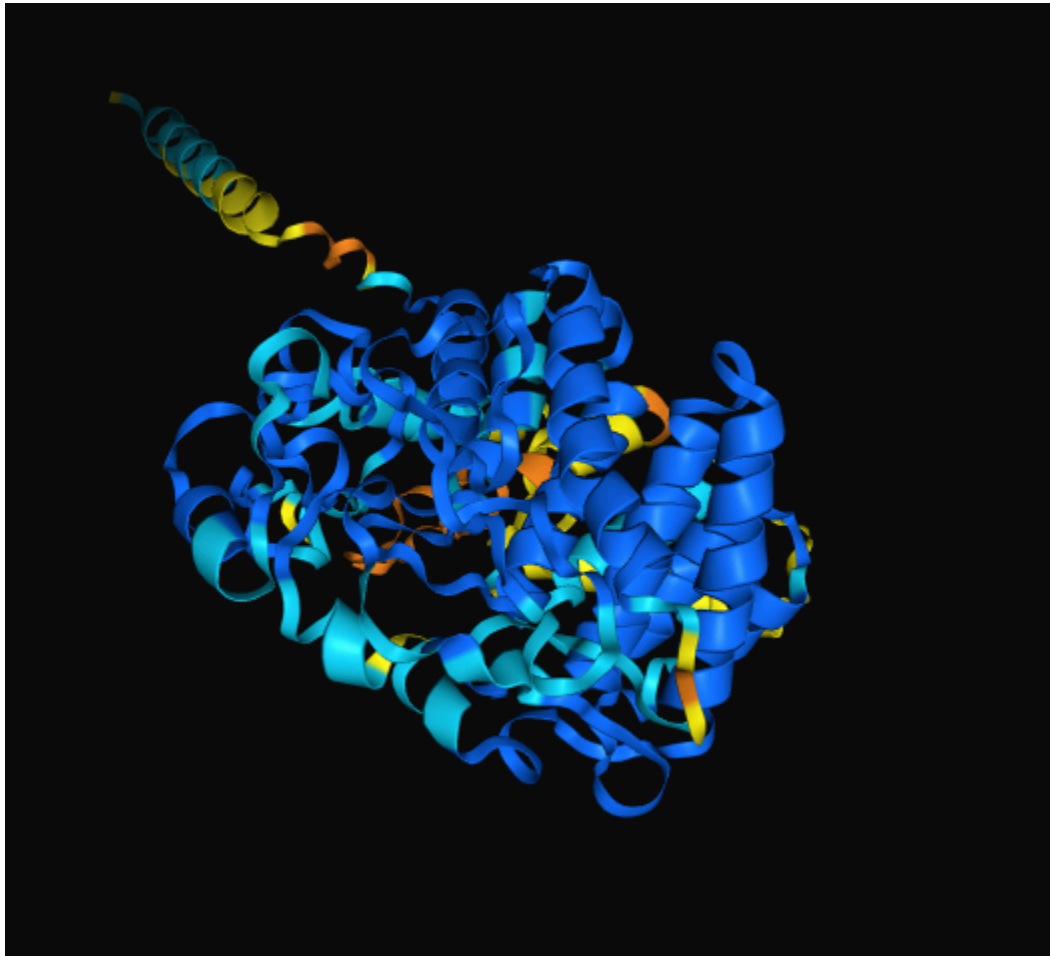
## Sequence:

MNDMAKNLILWLIIAAVLVTVMNNFSSPSESNNKLNYSFVQDVSAGRVKEVTIDGQSVTGRGFDGKTFTTT  
APNVDESLNKLISENVVVSGQPPEQQSLLGSLIIAWLIPLLLFIGVWFFFSRMQGGGGGGAFSFGKSKAR  
MMSEDQIKTTTFADVAGCDEAKEEVGELVDFLRDPSKFQKIGAKIPKGVLMVGPPGTGKTLLAKAIAAGEAKV  
PFFTISGSDFVEMFVGVGASRVDMFEQAKKSAPCIIFIDEIDAVGRQRGAGLGGGHDEREQTLNQMLVE  
MDGFEANEGIIIVIAATNRPDVLDPALLRPGRFDRQVTLGLPDVVRGREQILKVHMRRVPLGGNVDPKILARG  
TPGFSGADLANLVNEAALFAARANKRLVSMDEFELAKDKIMMGAERKSMVISEKEKRNTAYHEAGHAIVG  
HLLPKADPVFKVTIIPRGRALGVTFFLPEGDYSLSHQHLESQMASLYGGRAAEELFLGKESVSSGASNDI  
KVAT

pTM = 0.87

Best hit with BLASTp: `sp|P63343.1| RecName: Full=ATP-dependent zinc metalloprotease FtsH [Salmonella enterica subsp. enterica serovar Typhimurium str. LT2]` >`sp|P63344.1| RecName: Full=ATP-dependent zinc metalloprotease FtsH [Salmonella enterica subsp. enterica serovar Typhi]`

Sequence similarity: 76.55



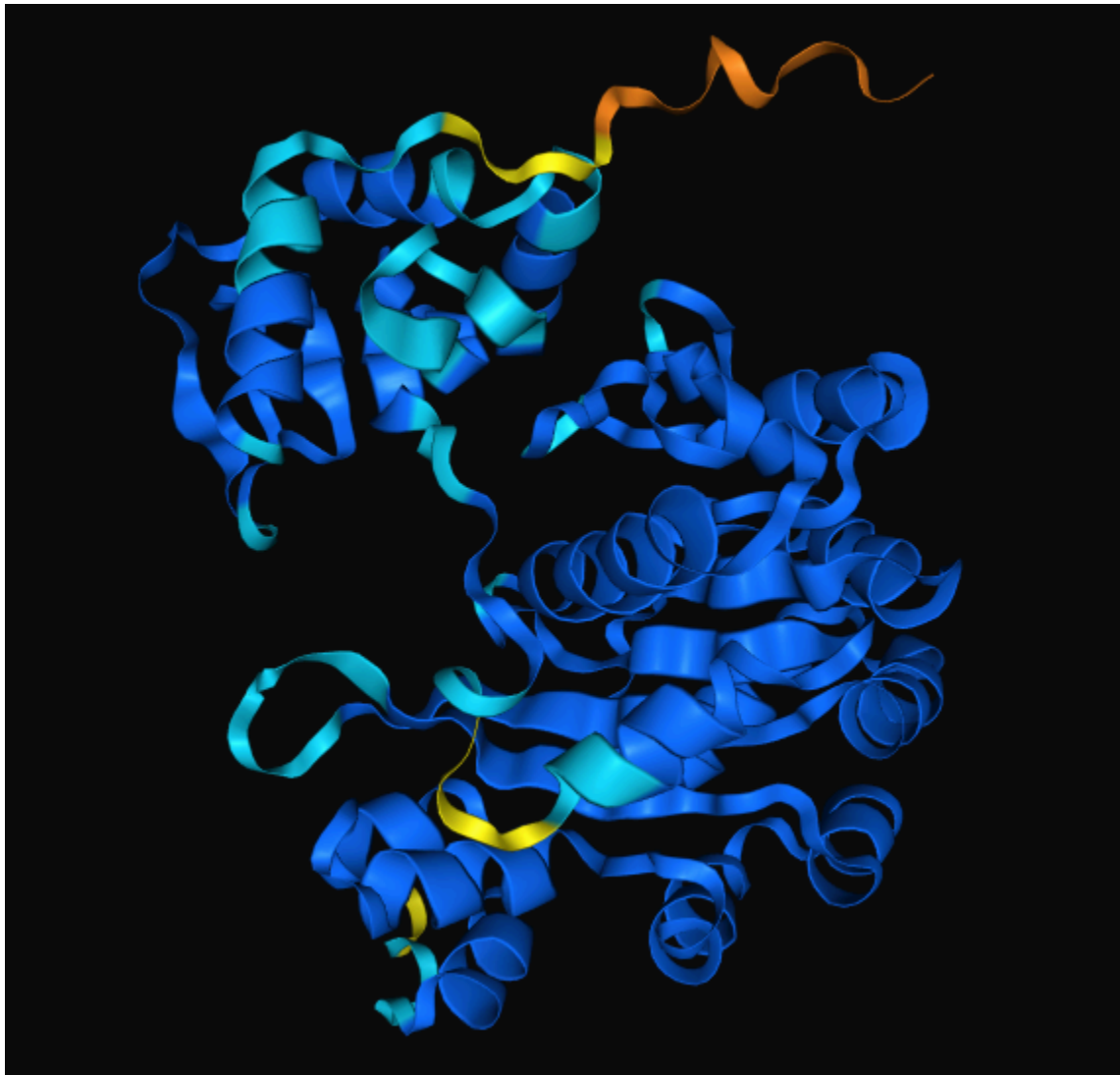
## Sequence:

MITNLDSMPSNEPLPLPPELADILDDAARRGASDVHLTVGAPPVLRIDGELTRAEAPALTADDLRAIAEALLP  
PARAEELERRLSLDVSYAIAGLARFRVNAFAQRGAVAIVFRLIPERIPSLDTLDLSGVPRALAALTQQPRGLV  
LVTGPTGSGKSTTLAAMIDLVAERRDRIITIEDPIEYLHPHRQAVVSQREIGRDTPSFAAALRSALREDPDV  
VMVGEMRDLETIRLALTAETGHLVFGTLHTSSAARTVDRVIDVFPADKEKGQVRAMVAESLRGVVAQQLIP  
KPDGSGRVAAFELLVATPAVRNLIRENKVHQLPGAMQTGAKHGMATLEEALAALLGGGALDVEAARAHAR  
DPEQLARYAGLPAAARA

pTM = 0.88

Best hit with BLASTp: `sp|P24559.1| RecName: Full=Type IV pilus  
retractation ATPase PilT [Pseudomonas aeruginosa PAO1]`

Sequence similarity: 52.16



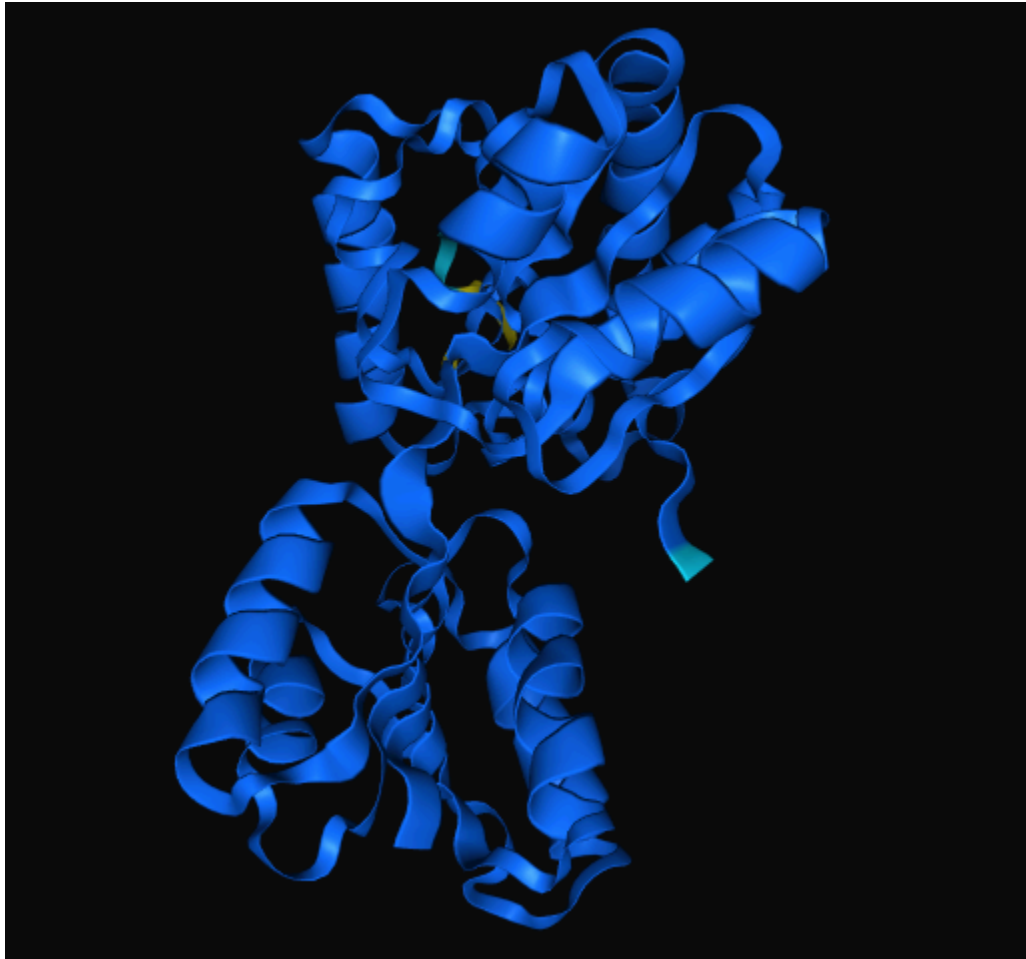
## Sequence:

VVGCIVPWNYP LLMAAWQIVPALAAGNTVVVKPSEVTPASAFALAQLAAEAGIPAGLLQVVTGLGEAAGAA  
LATHAGIAKVTFTGSTPAGRKVM EAAAGNLKRVHLELGGKSPNIVFDDADLARAVDAVAFGIFYNQGGQVCV  
AGSRLLVAESVADRLLGALAARAAALKVGDPRDAATMVGAVQHDRAAGFLERARAEGGRVACGGRAPAL  
PQAGYYVEPTLFADVDHRMRIAQEEIFGPVLTVMFPDGEAEAVRIANDTEYGLAASVWTRDIGRAHRVAS  
ELEAGTVVWNGWGESRAT

pTM = 0.93

Best hit with BLASTp: `sp|P08157.2| RecName: Full=Aldehyde  
dehydrogenase; Short=ALDDH; Short=ALDH [Aspergillus nidulans FGSC A4]`

Sequence similarity: 51.17



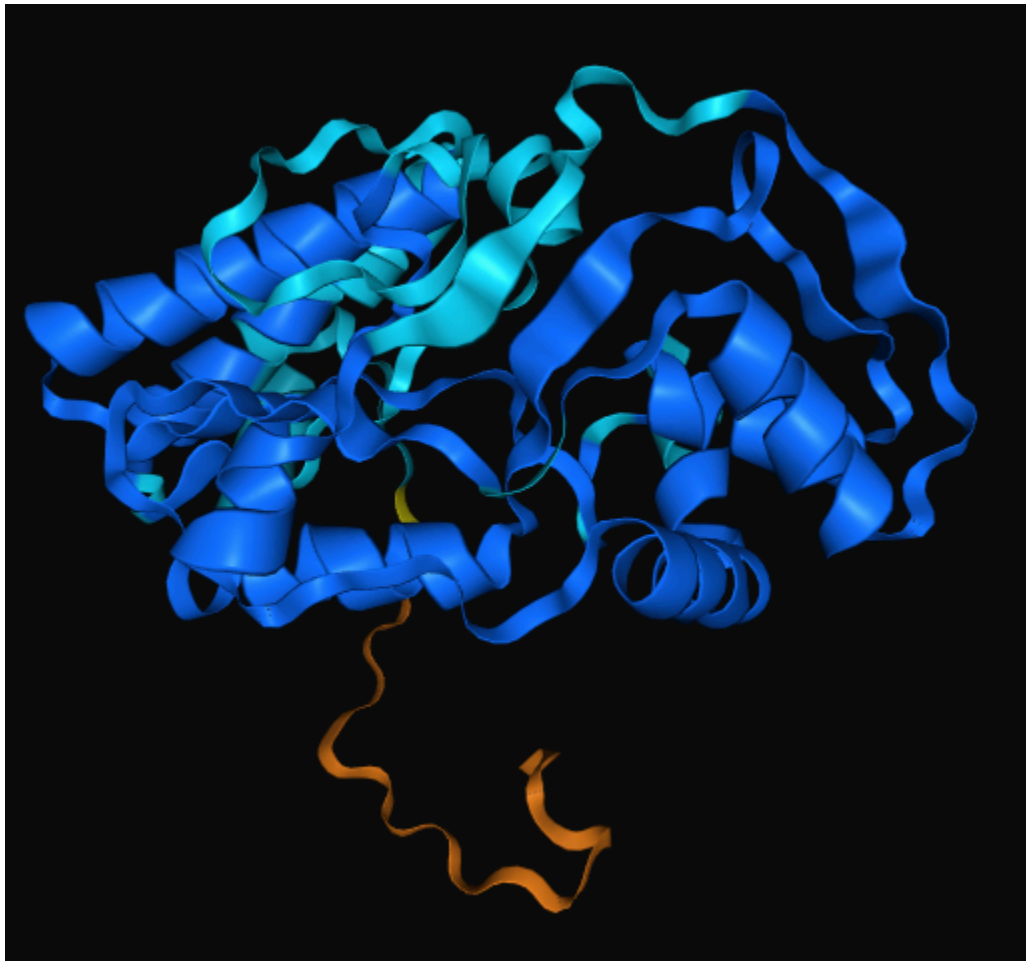
## Sequence:

KLLQRGGYKIKVLNTINFKKSVDKLEIKKIIDLINEKKPNIVFNTAADSHVEAAEKEPEKTFRLNAIGAYNVLEA  
ARENGIKRFIHISTDKVYDGQKGDYELDEEFKPVSYYGATKVYGESLVLSYNKKYNLETIIARSSNNYGPFQ  
YPEKLIPLFITNVLNNKSLPVYGDGLNVRDWIYVKDLAKALLCLENGQSSEVYNIAGSEEISNLELTKLILKI  
TGFKGKIIFDEKRPGDIRHYQADNTKIKKELGWKPKIKFKDGLKKTIDWYERNKSWWKEKINKK

pTM = 0.87

Best hit with BLASTp: `sp|Q9ZAE8.2| RecName: Full=dTDP-glucose  
4,6-dehydratase [Actinoplanes sp. SE50/110]`

Sequence similarity: 40.16



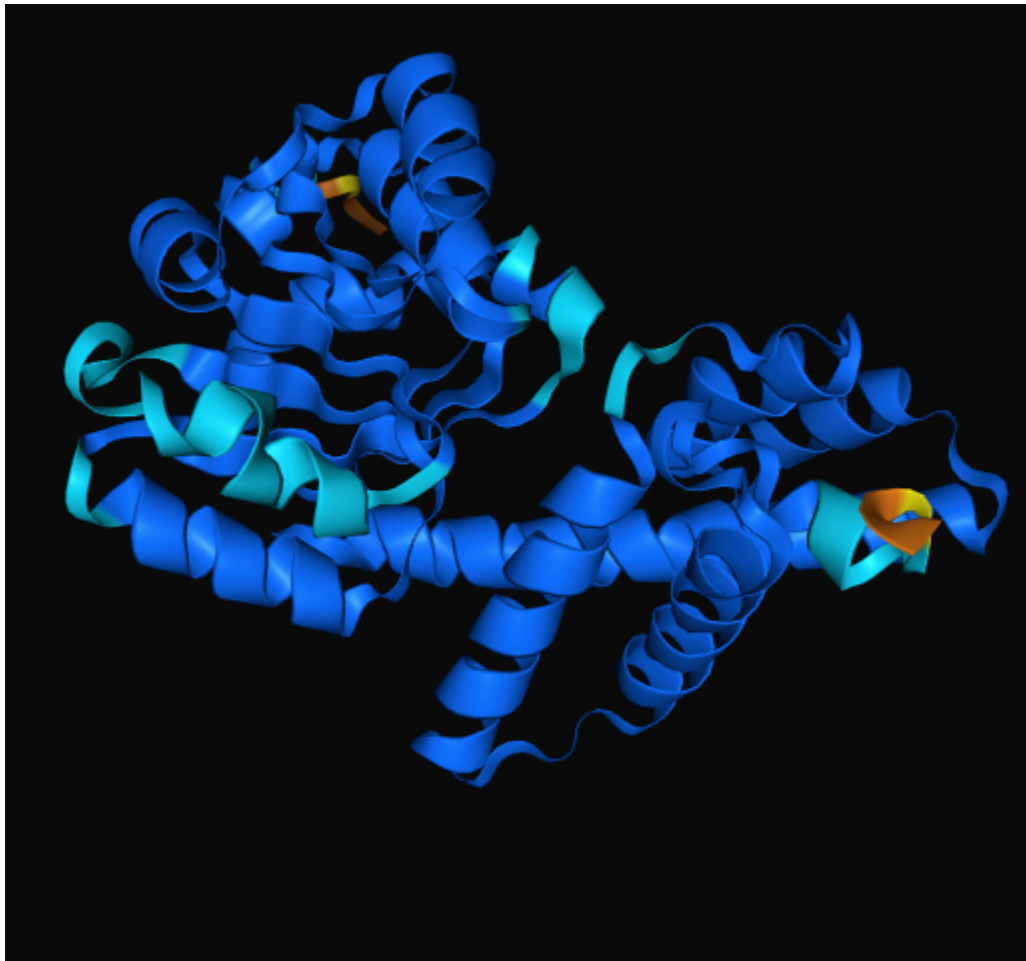
## Sequence:

MSDAARSPVTVGVVGLGTMGSGLAANLLRSGHDVVALDRSETALDRALELGTTAASSIEAAVRS AELVLA  
ALPSTALLRSTVLEAADALPGRALVTVSTGKPEVAAAAAALAAAGVRLVDAPVSGGVARAADGTLAVMV  
GGDEAALAAARPVLEAMAARVTHVGPVGAGQAVKVCNQLLVAVSIAAAAEAMLVGTSLG LDPALLYEVIRH  
AGGNSWVLENRVPHVLTDDYAPRSAVDIFVKDLGIVLDAARAADVPLPVAAAAREQYSAMVAAGLGELDT  
SAVVRVLDGAAR

pTM = 0.9

Best hit with BLASTp: `sp|Q0KBC7.1| RecName: Full=L-threonate  
dehydrogenase [Cupriavidus necator H16]`

Sequence similarity: 46.15



## Sequence:

MKIAVIGTGYVGLVSGACFAELGHDVVCVDTDEAKIAALRKGVLPIYEPGLPELIRQNLAAGRRLRFTADYQE  
SAAFAEVHFIAVGTTPPDEDGSADLQYVLAVAETIARHMTDYRVVVDKSTVPVGTAEVRRAAIAERLRAGEQ  
AEIVSNPEFLREGA AVADFMKPDRVVGAESPRAEALLRELYAPFNRNQERLMVMDVRS AELTKYAANAM  
LATRISFMNEIGNLADVLGADIEKVRRGIGSDSRIGYRFLYAGCGYGGSCFPKDVKALSRTAAEHGHDARIL  
EAVEAVNDEQKTVLLEKTRQLLGGDLAGRRAVWGLAFKPD TDDVREAPSRVLMERLWAAGADV RAYDP  
VAIEEARRVFGDQAE LALAADAYA AVEGADALVLATEWKAFRAPD

pTM = 0.94

Best hit with BLASTp: `sp|O86422.2| RecName: Full=UDP-glucose  
6-dehydrogenase; Short=UDP-Glc dehydrogenase; Short=UDP-GlcDH;  
Short=UDPGDH [Pseudomonas aeruginosa PA01]`

Sequence similarity: 57.64

