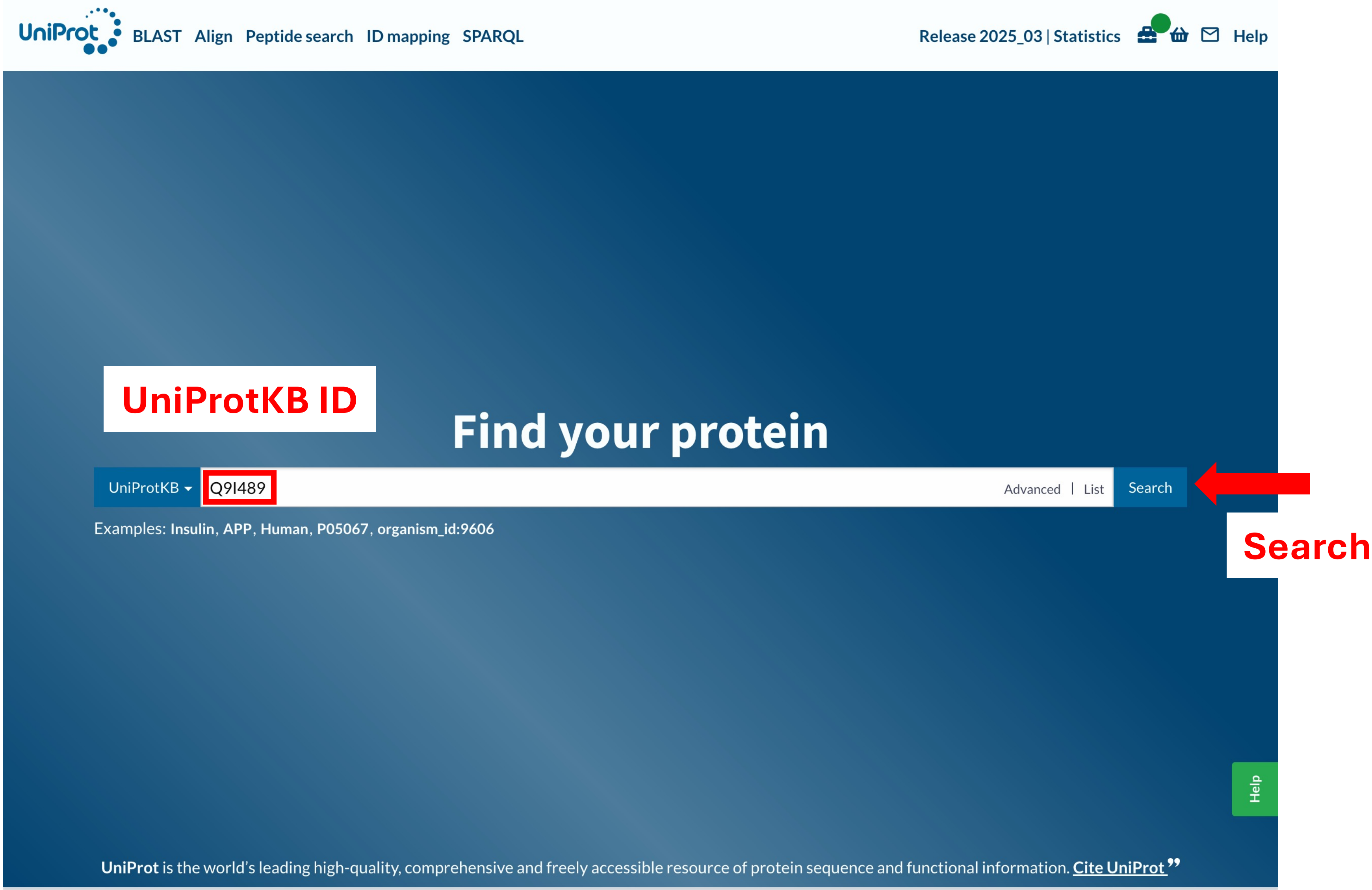
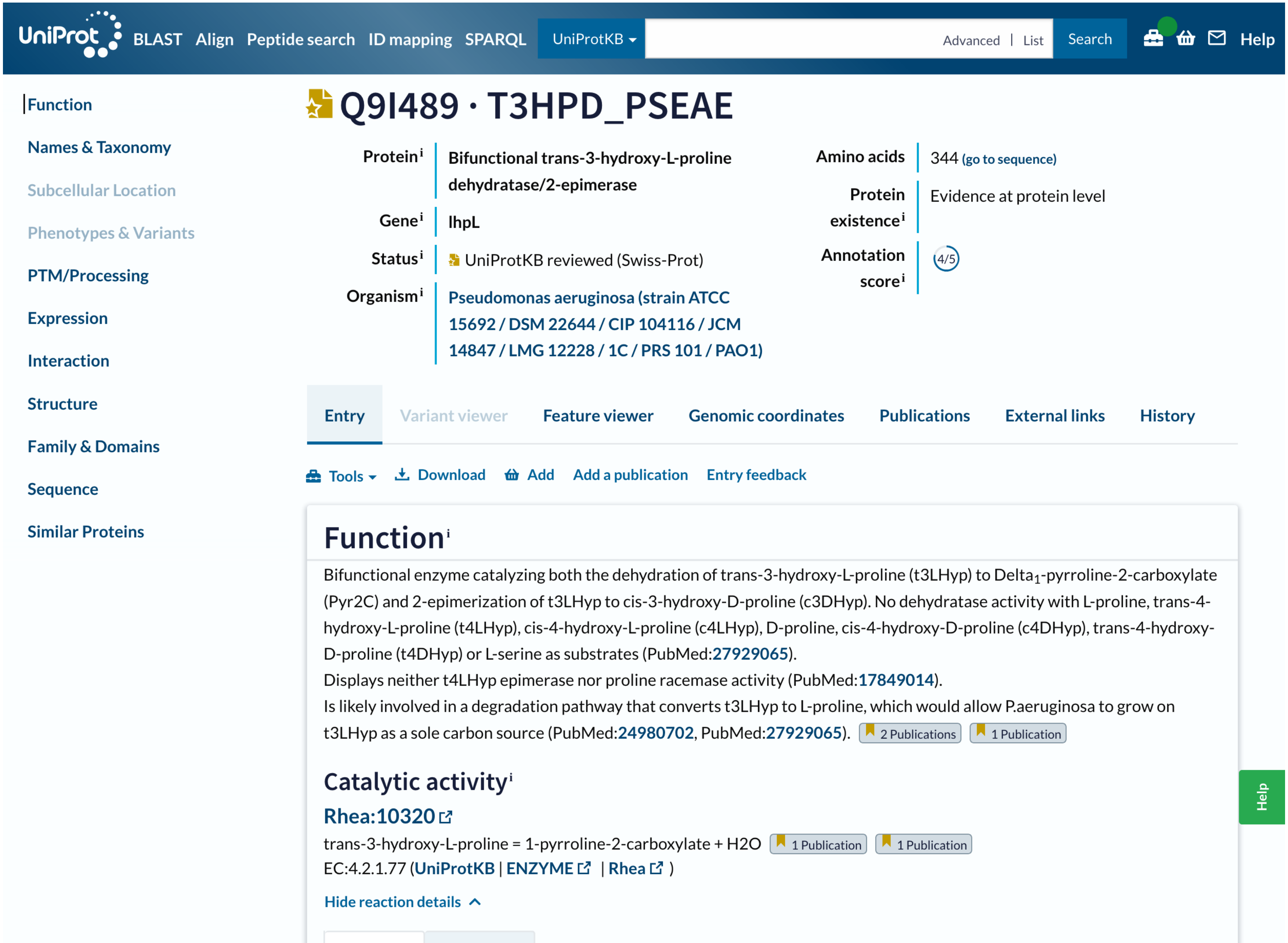
Accessing the protein and DNA sequences for an active UniProtKB ID



UniProt is the world's leading high-quality, comprehensive and freely accessible resource of protein sequence and functional information. Cite UniProt

https://www.uniprot.org/

UniProtKB annotation page



Q9I489 · T3HPD_PSEAE

Protein	Bifunctional trans-3-hydroxy-L-proline dehydratase/2-epimerase
Gene	lhpL
Status	UniProtKB reviewed (Swiss-Prot)
Organism	Pseudomonas aeruginosa (strain ATCC 15692 / DSM 22644 / CIP 104116 / JCM 14847 / LMG 12228 / 1C / PRS 101 / PAO1)
Amino acids	344 (go to sequence)
Protein existence	Evidence at protein level
Annotation score	4/5

Function

Bifunctional enzyme catalyzing both the dehydration of trans-3-hydroxy-L-proline (t3LHyp) to Delta$_1$-pyrroline-2-carboxylate (Pyr2C) and 2-epimerization of t3LHyp to cis-3-hydroxy-D-proline (c3DHyp). No dehydratase activity with L-proline, trans-4-hydroxy-L-proline (t4LHyp), cis-4-hydroxy-L-proline (c4LHyp), D-proline, cis-4-hydroxy-D-proline (c4DHyp), trans-4-hydroxy-D-proline (t4DHyp) or L-serine as substrates (PubMed:27929065).
Displays neither t4LHyp epimerase nor proline racemase activity (PubMed:17849014).
Is likely involved in a degradation pathway that converts t3LHyp to L-proline, which would allow P.aeruginosa to grow on t3LHyp as a sole carbon source (PubMed:24980702, PubMed:27929065). 2 Publications 1 Publication

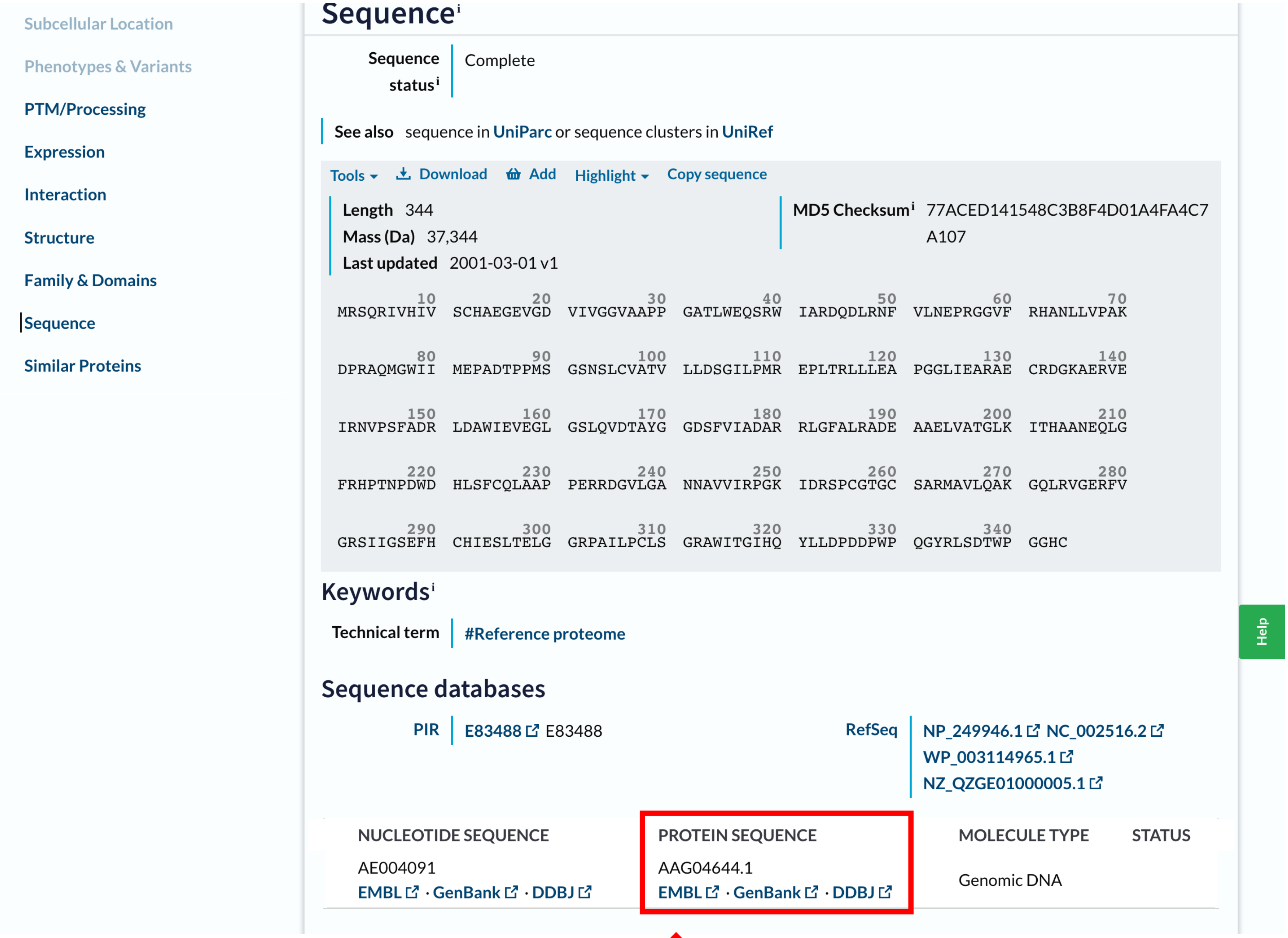
Catalytic activity

Rhea:10320

trans-3-hydroxy-L-proline = 1-pyrroline-2-carboxylate + H2O 1 Publication 1 Publication
EC:4.2.1.77 (UniProtKB | ENZYME | Rhea)

Hide reaction details

Scroll down; locate the PROTEIN SEQUENCE links



Sequence[i]

Sequence status[i]	Complete

See also sequence in UniParc or sequence clusters in UniRef

Length 344
Mass (Da) 37,344
Last updated 2001-03-01 v1

MD5 Checksum[i] 77ACED141548C3B8F4D01A4FA4C7A107

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Keywords[i]

Technical term	#Reference proteome

Sequence databases

PIR	E83488 E83488	RefSeq	NP_249946.1 NC_002516.2 WP_003114965.1 NZ_QZGE01000005.1

NUCLEOTIDE SEQUENCE	PROTEIN SEQUENCE	MOLECULE TYPE	STATUS
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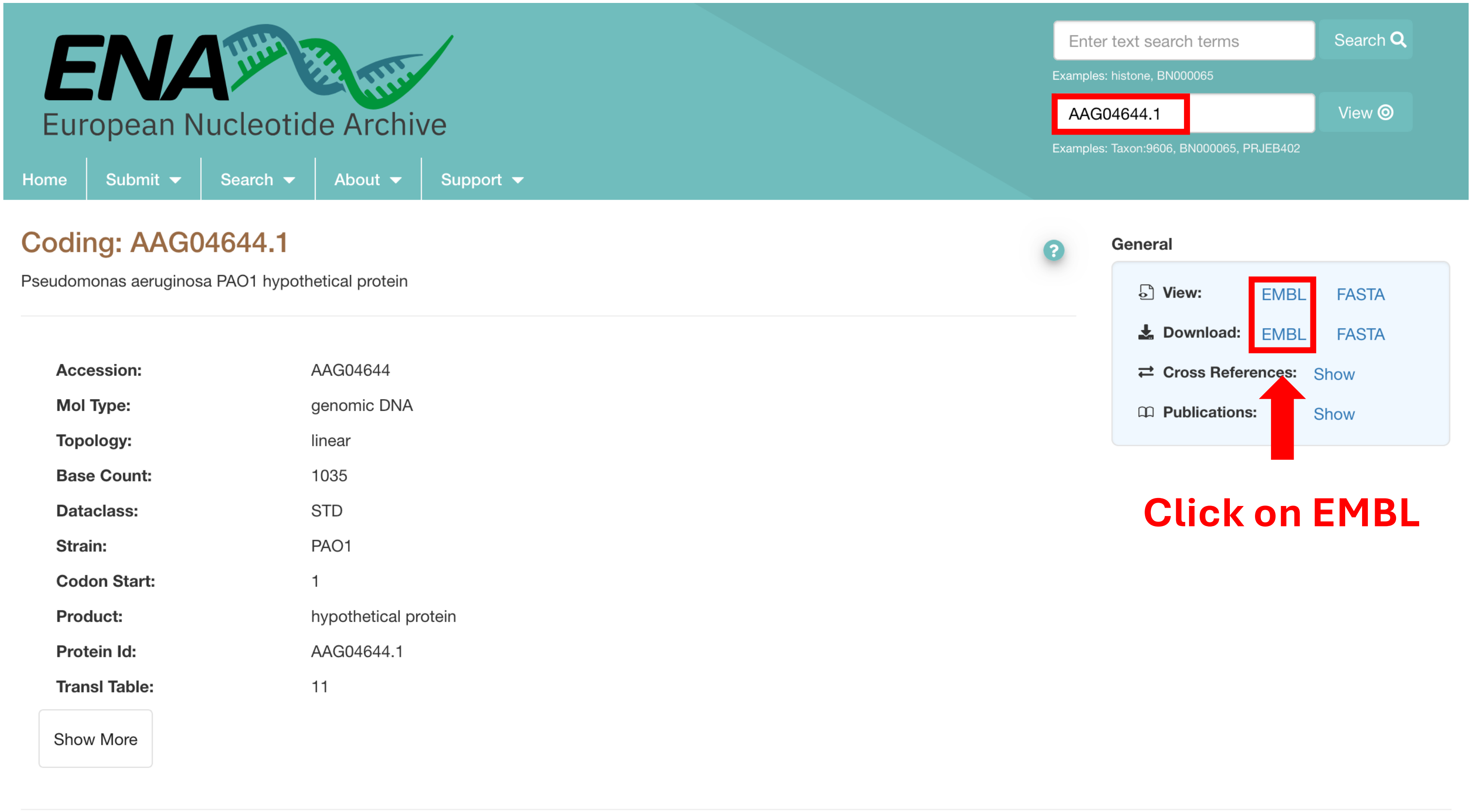
Click on EMBL

ENA page for Coding information opens



Coding: AAG04644.1

Pseudomonas aeruginosa PAO1 hypothetical protein

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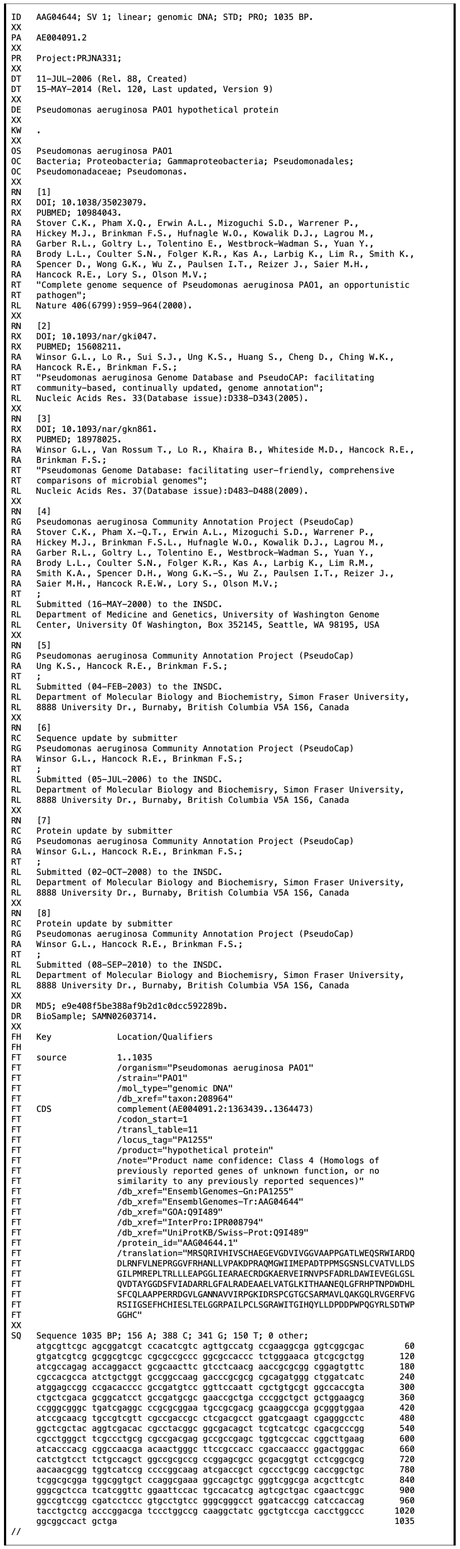
Base Count:	1035
Dataclass:	STD
Strain:	PAO1
Codon Start:	1
Product:	hypothetical protein
Protein Id:	AAG04644.1
Transl Table:	11

Click on EMBL

File with protein and DNA sequences opens



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DT   15-MAY-2014 (Rel. 120, Last updated, Version 9)
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RX   PUBMED; 10984043.
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RA   Hickey M.J., Brinkman F.S., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R., Smith K.,
RA   Spencer D., Wong G.K., Wu Z., Paulsen I.T., Reizer J., Saier M.H.,
RA   Hancock R.E., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic
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RL   Nature 406(6799):959-964(2000).
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RX   PUBMED; 15608211.
RA   Winsor G.L., Lo R., Sui S.J., Ung K.S., Huang S., Cheng D., Ching W.K.,
RA   Hancock R.E., Brinkman F.S.;
RT   "Pseudomonas aeruginosa Genome Database and PseudoCAP: facilitating
RT   community-based, continually updated, genome annotation";
RL   Nucleic Acids Res. 33(Database issue):D338-D343(2005).
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RN   [3]
RX   DOI; 10.1093/nar/gkn861.
RX   PUBMED; 18978025.
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RA   Brinkman F.S.;
RT   "Pseudomonas Genome Database: facilitating user-friendly, comprehensive
RT   comparisons of microbial genomes";
RL   Nucleic Acids Res. 37(Database issue):D483-D488(2009).
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RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J.,
RA   Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   ;
RL   Submitted (16-MAY-2000) to the INSDC.
RL   Department of Medicine and Genetics, University of Washington Genome
RL   Center, University Of Washington, Box 352145, Seattle, WA 98195, USA
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RN   [5]
RG   Pseudomonas aeruginosa Community Annotation Project (PseudoCap)
RA   Ung K.S., Hancock R.E., Brinkman F.S.;
RT   ;
RL   Submitted (04-FEB-2003) to the INSDC.
RL   Department of Molecular Biology and Biochemistry, Simon Fraser University,
RL   8888 University Dr., Burnaby, British Columbia V5A 1S6, Canada
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RN   [6]
RC   Sequence update by submitter
RG   Pseudomonas aeruginosa Community Annotation Project (PseudoCap)
RA   Winsor G.L., Hancock R.E., Brinkman F.S.;
RT   ;
RL   Submitted (05-JUL-2006) to the INSDC.
RL   Department of Molecular Biology and Biochemisry, Simon Fraser University,
RL   8888 University Dr., Burnaby, British Columbia V5A 1S6, Canada
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RG   Pseudomonas aeruginosa Community Annotation Project (PseudoCap)
RA   Winsor G.L., Hancock R.E., Brinkman F.S.;
RT   ;
RL   Submitted (02-OCT-2008) to the INSDC.
RL   Department of Molecular Biology and Biochemisry, Simon Fraser University,
RL   8888 University Dr., Burnaby, British Columbia V5A 1S6, Canada
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RN   [8]
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RG   Pseudomonas aeruginosa Community Annotation Project (PseudoCap)
RA   Winsor G.L., Hancock R.E., Brinkman F.S.;
RT   ;
RL   Submitted (08-SEP-2010) to the INSDC.
RL   Department of Molecular Biology and Biochemisry, Simon Fraser University,
RL   8888 University Dr., Burnaby, British Columbia V5A 1S6, Canada
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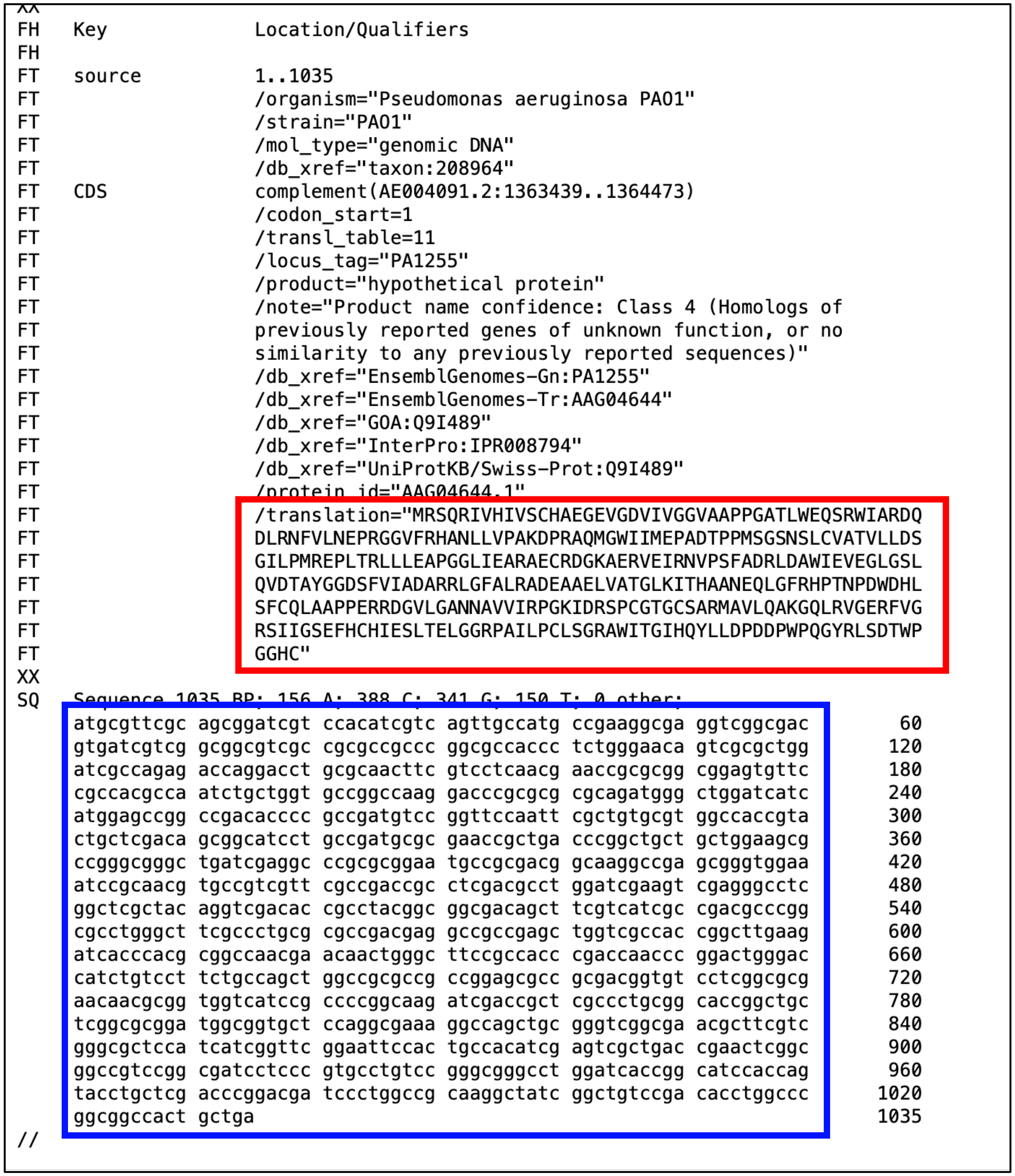

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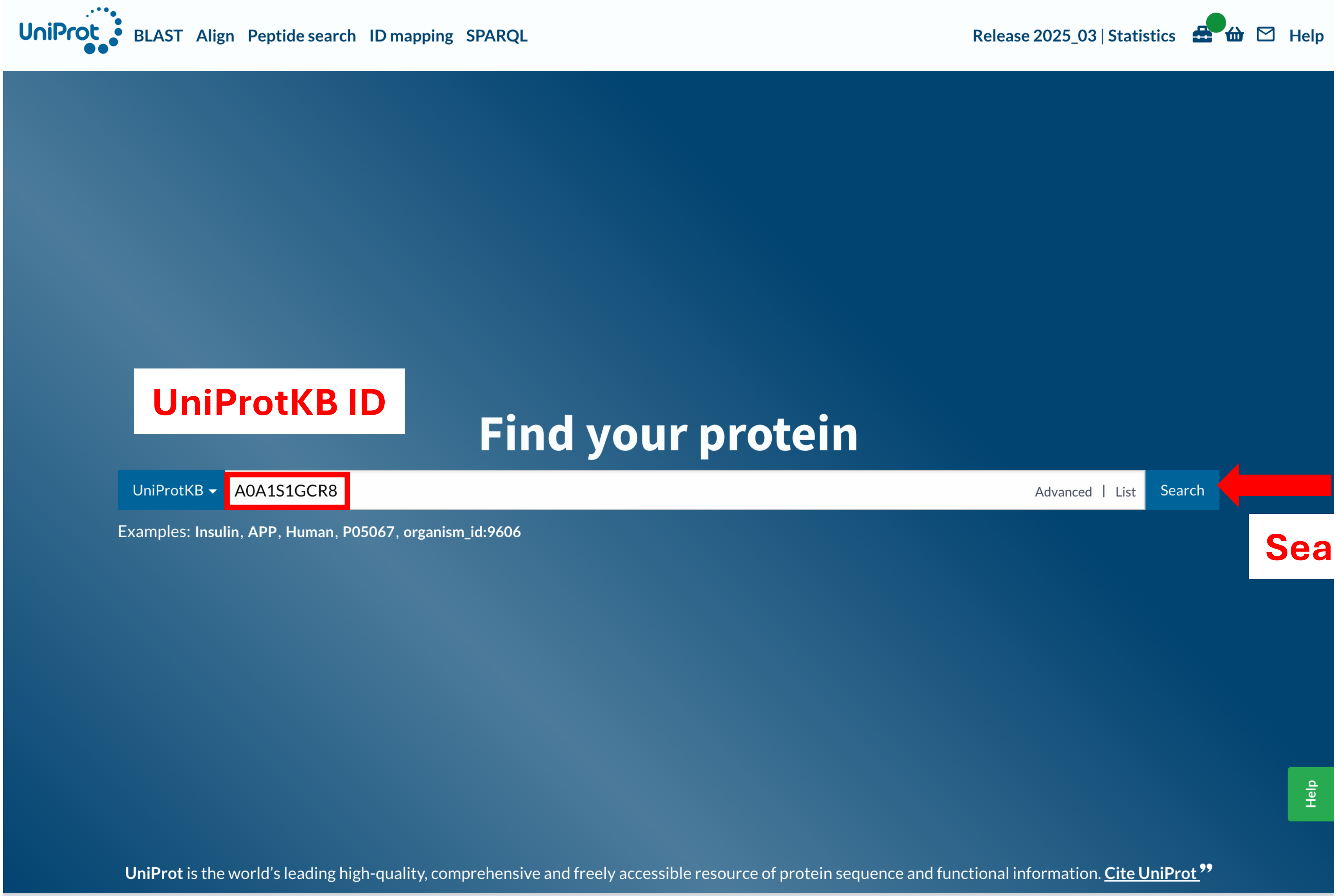
Accessing protein and DNA sequences for archived UniProtKB ID



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Examples: **Insulin**, **APP**, **Human**, **P05067**, **organism_id:9606**

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UniProtKB ID

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File with Entry history opens; click on most recent version text link

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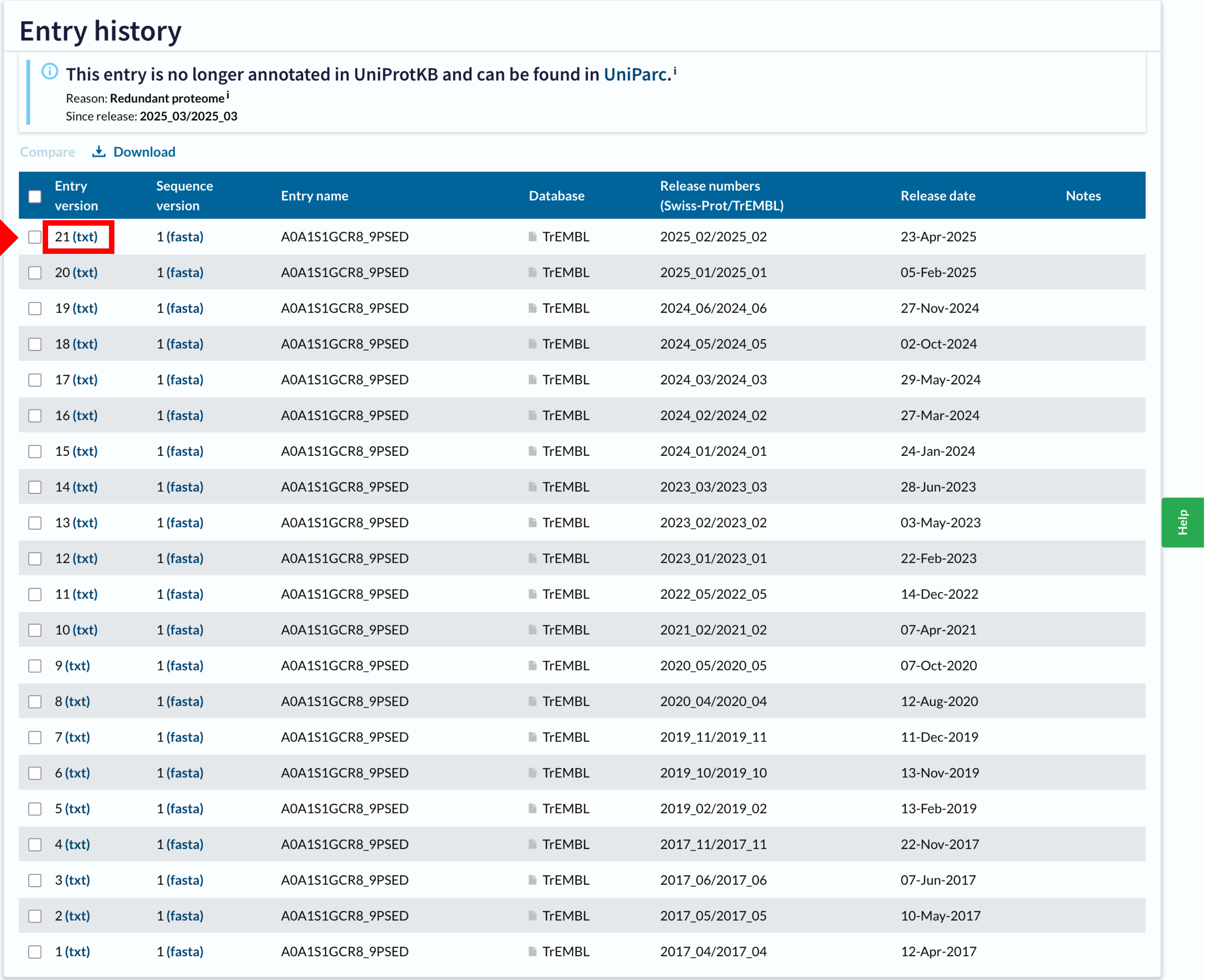

Entry history

This entry is no longer annotated in UniProtKB and can be found in UniParc.

Reason: **Redundant proteome**

Since release: **2025_03/2025_03**

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☐	Entry version	Sequence version	Entry name	Database	Release numbers (Swiss-Prot/TrEMBL)	Release date	Notes
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Entry version opens , with EMBL Protein ID and sequence

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RA   Wen L., He K., Yang H.;
RL   Submitted (FEB-2016) to the EMBL/GenBank/DDBJ databases.
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CC       {ECO:0000256|ARBA:ARBA00007529}.
CC   -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ
CC       whole genome shotgun (WGS) entry which is preliminary data.
CC       {ECO:0000313|EMBL:OHR81134.1}.
CC   ---------------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see https://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution (CC BY 4.0) License
CC   ---------------------------------------------------------------------------
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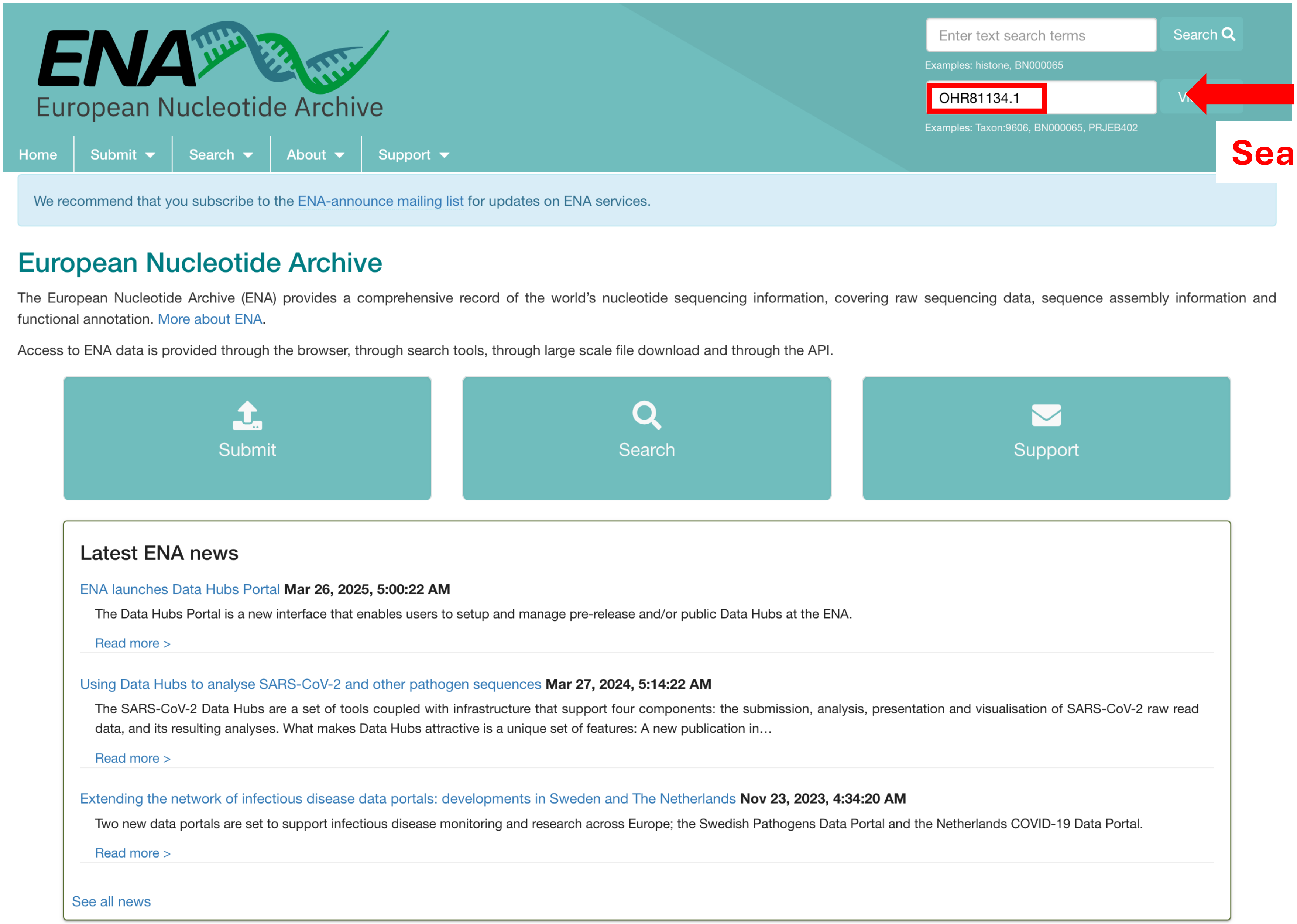
Accessing the protein and DNA sequences for an EMBL Protein ID



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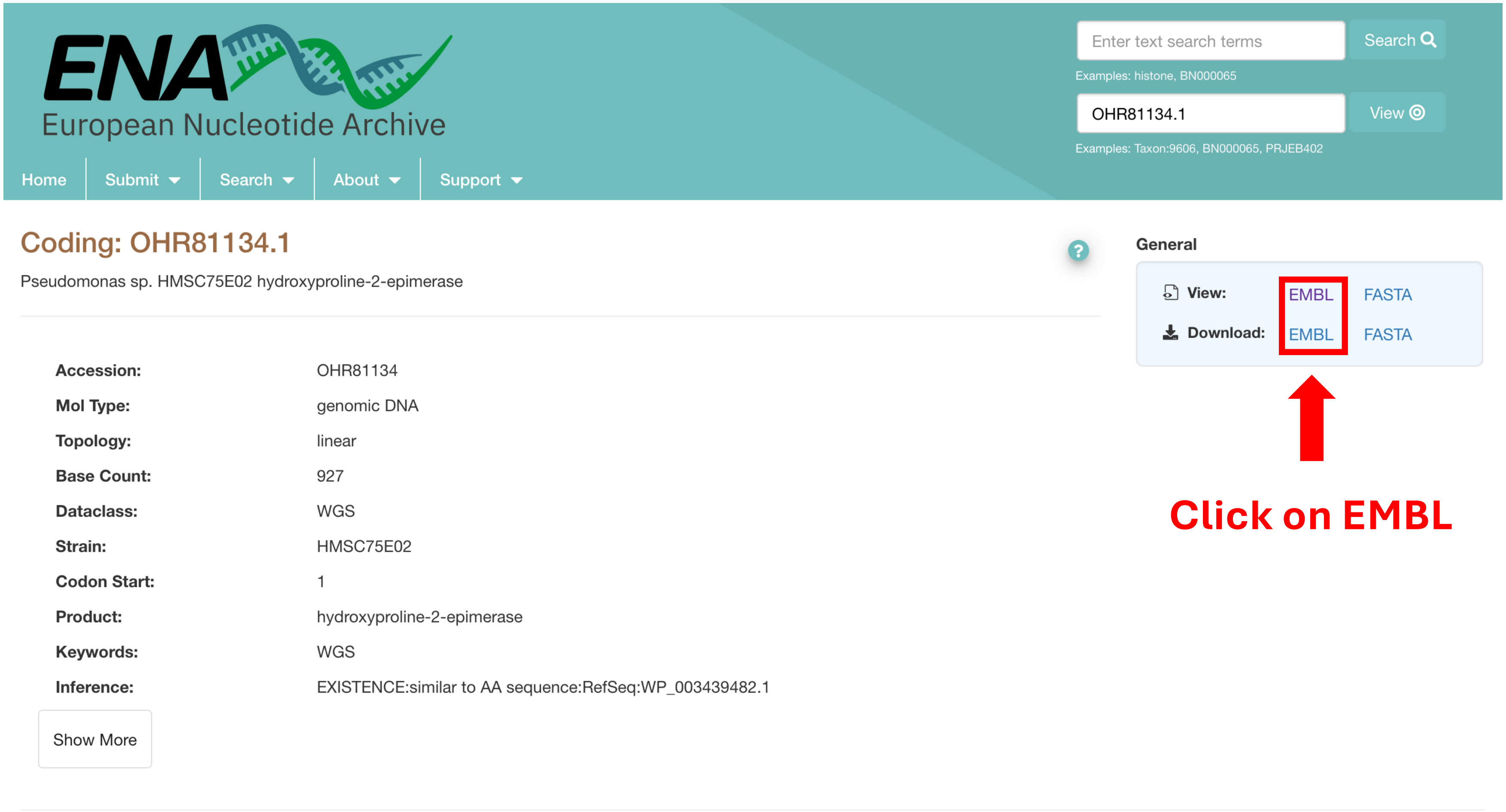
ENA page for Coding information opens



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Pseudomonas sp. HMSC75E02 hydroxyproline-2-epimerase

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Topology:	linear
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Dataclass:	WGS
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Codon Start:	1
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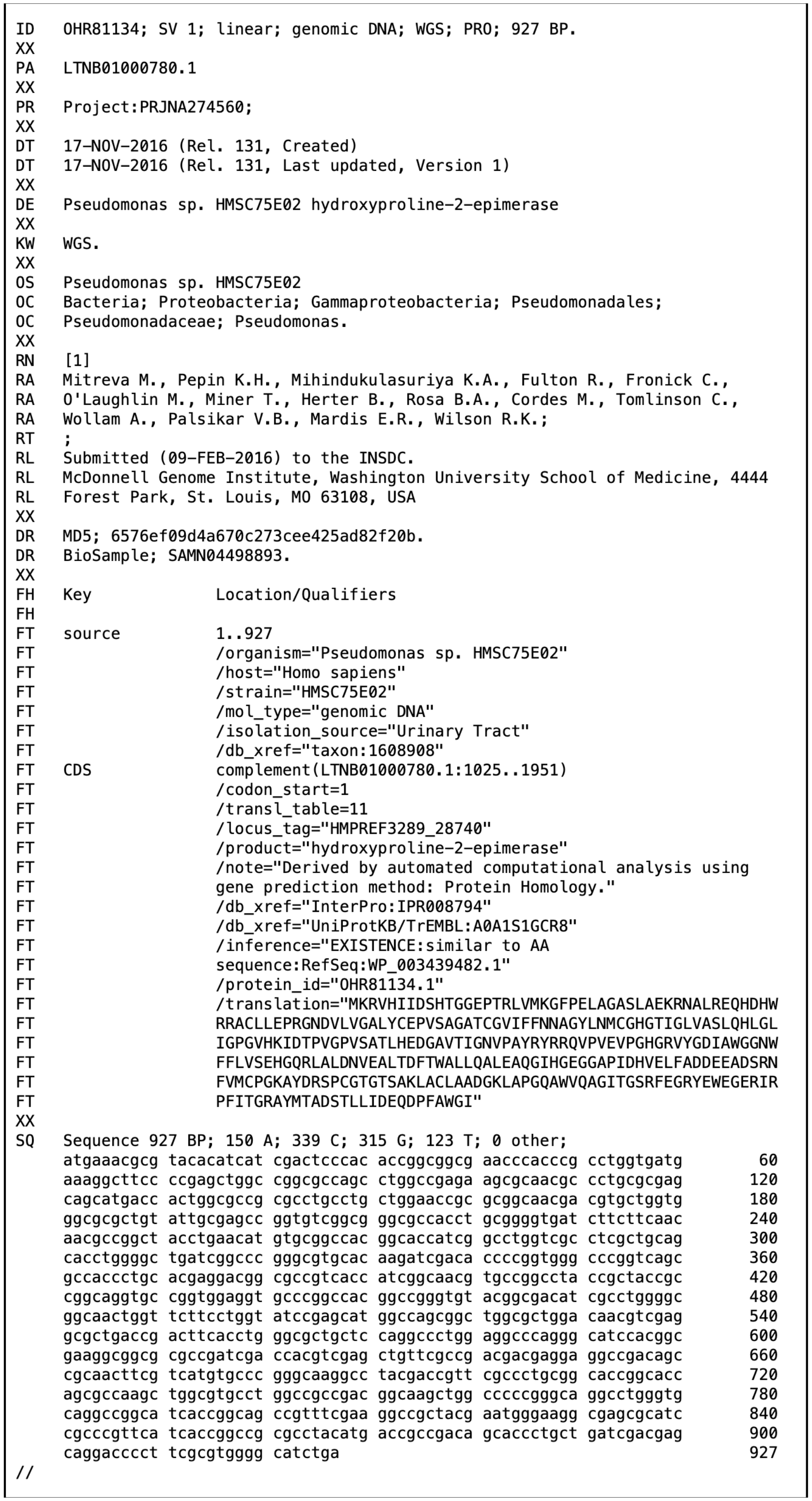
Click on EMBL

File with protein and DNA sequences opens



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RA   O'Laughlin M., Miner T., Herter B., Rosa B.A., Cordes M., Tomlinson C.,
RA   Wollam A., Palsikar V.B., Mardis E.R., Wilson R.K.;
RT   ;
RL   Submitted (09-FEB-2016) to the INSDC.
RL   McDonnell Genome Institute, Washington University School of Medicine, 4444
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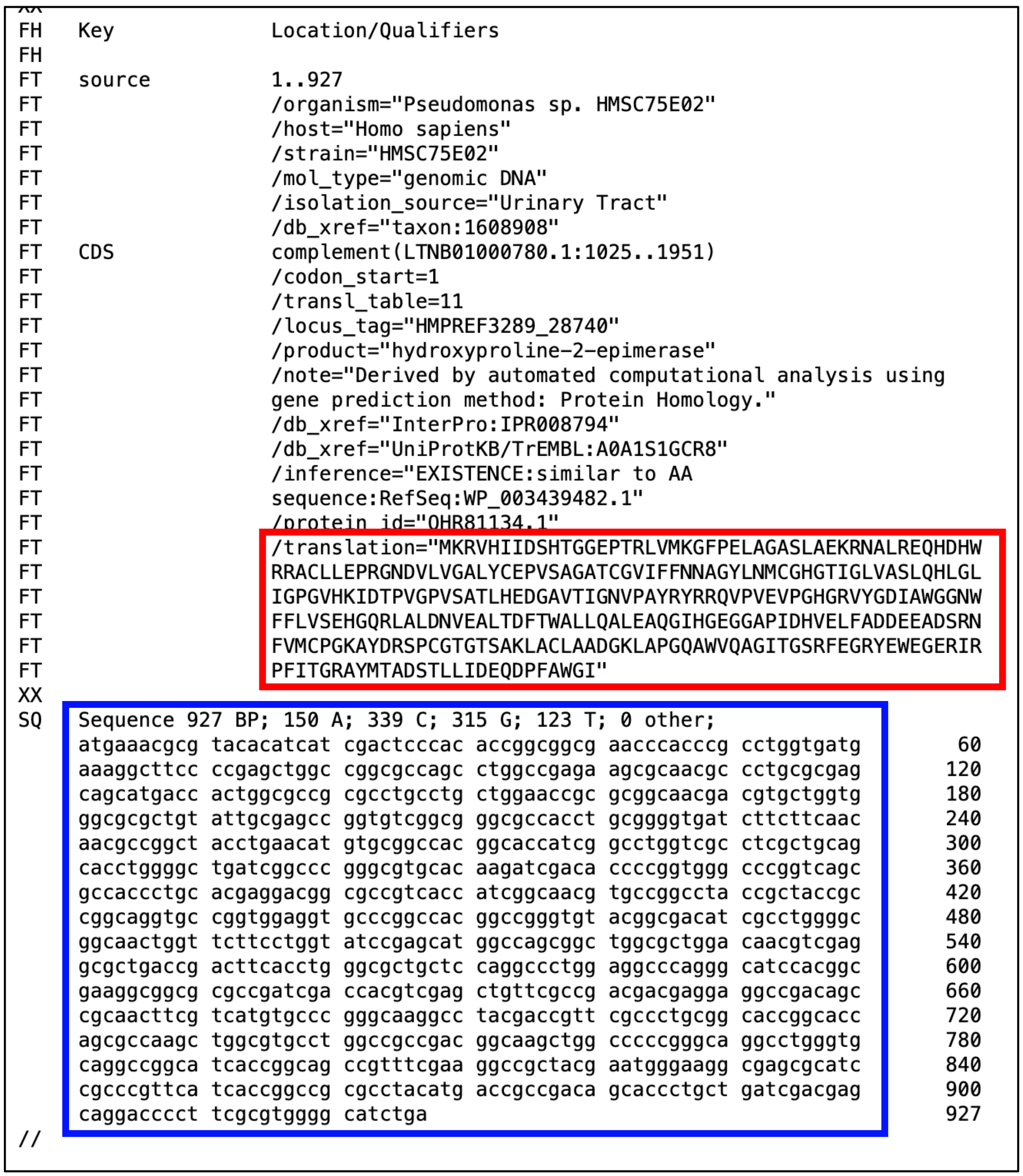

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