Protein Identifier: *Q6NTF7*

>sp|Q6NTF7|ABC3H_HUMAN DNA dC->dU-editing enzyme APOBEC-3H OS=Homo sapiens GN=APOBEC3H PE=1 SV=3

MALLTAETFRLQFNNKRRLRRPYYPRKALLCYQLTPQNGSTPTRGYFENKKKCHAEICFINEIKSMGLDETQCYQVTCYLTWSPCSSCAWELVDFIKAHDH
LNLGIFASRLYYHWCKPQQKGLRLLCGSQVPVEVMGFPKFADCWENFVDHEKPLSFNPYKMLEELDKNSRAIKRRLERIKIPGVRAQGRYMDILCDAEV

Intro

Q6NTF7 is **DNA dC->dU-editing enzyme APOBEC-3H** a product of the APOBEC3H gene found on human chromosome 22. It is a member of the cytidine and deoxycytidylate deaminase family, which take part in catalytic reactions of cytidine and use Zn^{2+} as a cofactor. It's got 4 recorded isoforms on the UniProt database.

The A3H-var/haplotype 2 exhibits antiviral activity against vif-deficient HIV-1.

After the penetration of retroviral nucleocapsids into target cells of infection and the initiation of reverse transcription, it can induce the conversion of cytosine to uracil in the minus-sense single-strand viral DNA, leading to G-to-A hypermutations in the subsequent plus-strand viral DNA. Selectively targets single-stranded DNA and does not deaminate double-stranded DNA or single- or double-stranded RNA.

Exhibits antiviral activity also against T-cell leukemia virus type 1 (HTLV-1) and may inhibit the mobility of LTR and non-LTR retrotransposons

Antiviral activity is neutralized by the HIV-1 virion infectivity factor (VIF), that prevents its incorporation into progeny virions by both inhibiting its translation and/or by inducing its ubiquitination and subsequent degradation by the 26S proteasome.

Edit and Resubmit | Save Search Strategies | ▹Formatting options | ▹Download | How to read this page | Blast report description

PSI Blast Iteration 1

Job title: sp|Q6NTF7|ABC3H_HUMAN DNA dC->dU-editing

RID CFZX9NTD01N (Expires on 03-15 22:35 pm)

Query ID lcl|Query_77549
Description sp|Q6NTF7|ABC3H_HUMAN DNA dC->dU-editing enzyme APOBEC-3H OS=Homo sapiens GN=APOBEC3H PE=1 SV=3
Molecule type amino acid
Query Length 200

Database Name pdb
Description PDB protein database
Program BLASTP 2.6.1+ ▹Citation

Other reports: ▹Search Summary [Taxonomy reports] [Distance tree of results] [Multiple alignment] [MSA viewer]

New Analyze your query with SmartBLAST

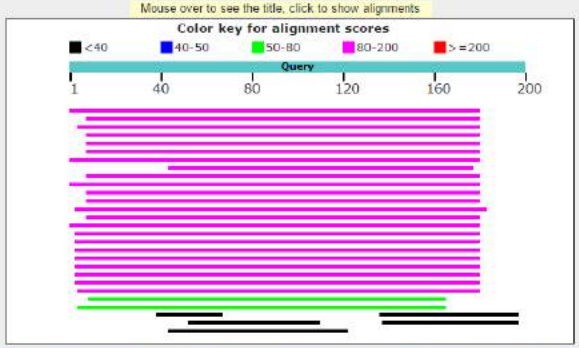
Graphic Summary

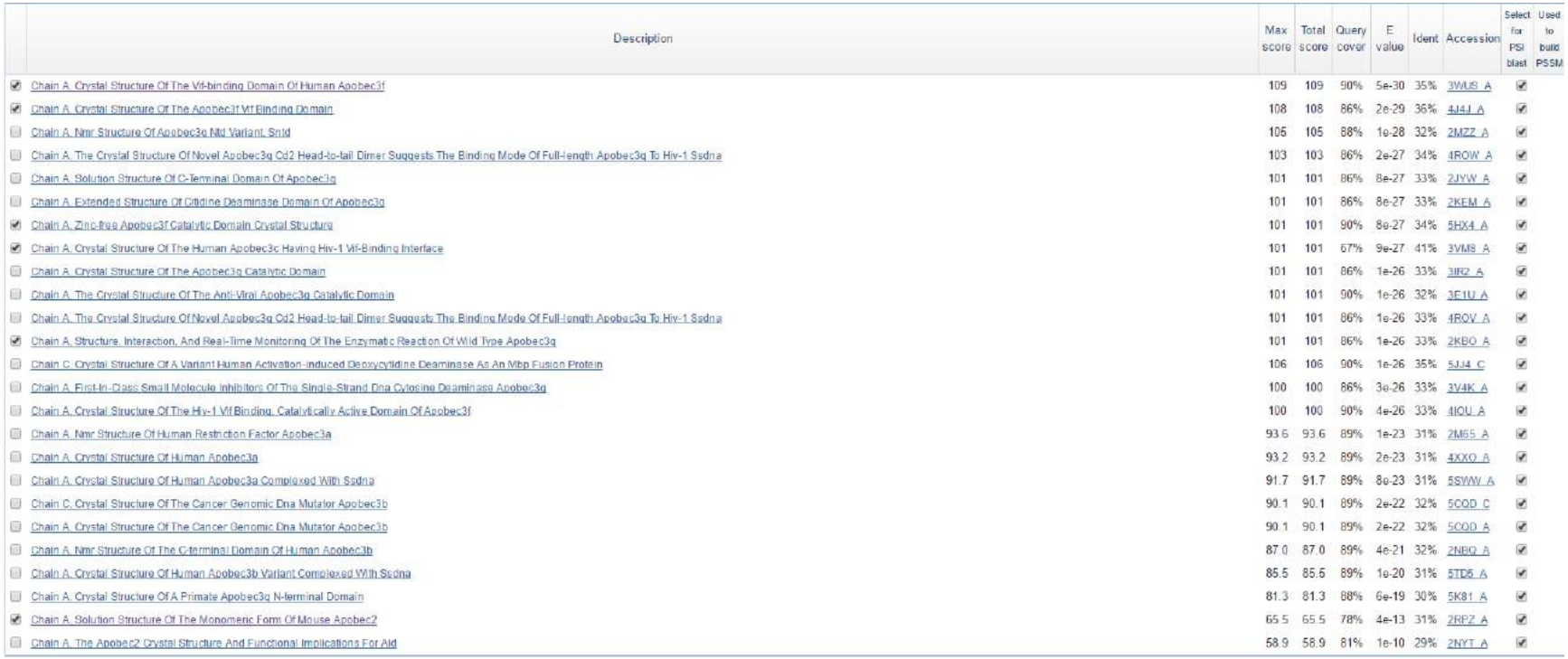
Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.

Distribution of the top 30 Blast Hits on 30 subject sequences

Mouse over to see the title, click to show alignments





Description	Max score	Total score	Query cover	E value	Ident	Accession	Select for PSI blast	Used to build PSSM
Chain A, Crystal Structure Of The Vif-binding Domain Of Human Apobec3f	109	109	90%	5e-30	35%	3WUS_A	☑	
Chain A, Crystal Structure Of The Apobec3f Vif Binding Domain	108	108	86%	2e-29	36%	4J4J_A	☑	
Chain A, Nmr Structure Of Apobec3g Ntd Variant, Sntd	105	105	88%	1e-28	32%	2MZZ_A	☑	
Chain A, The Crystal Structure Of Novel Apobec3g Cd2 Head-to-tail Dimer Suggests The Binding Mode Of Full-length Apobec3g To Hiv-1 Ssdna	103	103	86%	2e-27	34%	4ROW_A	☑	
Chain A, Solution Structure Of C-Terminal Domain Of Apobec3g	101	101	86%	8e-27	33%	2JYW_A	☑	
Chain A, Extended Structure Of Cytidine Deaminase Domain Of Apobec3g	101	101	86%	8e-27	33%	2KEM_A	☑	
Chain A, Zinc-free Apobec3f Catalytic Domain Crystal Structure	101	101	90%	8e-27	34%	5HX4_A	☑	
Chain A, Crystal Structure Of The Human Apobec3c Having Hiv-1 Vif-Binding Interface	101	101	67%	9e-27	41%	3VM8_A	☑	
Chain A, Crystal Structure Of The Apobec3g Catalytic Domain	101	101	86%	1e-26	33%	3IR2_A	☑	
Chain A, The Crystal Structure Of The Anti-Viral Apobec3g Catalytic Domain	101	101	90%	1e-26	32%	3E1U_A	☑	
Chain A, The Crystal Structure Of Novel Apobec3g Cd2 Head-to-tail Dimer Suggests The Binding Mode Of Full-length Apobec3g To Hiv-1 Ssdna	101	101	86%	1e-26	33%	4ROV_A	☑	
Chain A, Structure, Interaction, And Real-Time Monitoring Of The Enzymatic Reaction Of Wild Type Apobec3g	101	101	86%	1e-26	33%	2KBO_A	☑	
Chain C, Crystal Structure Of A Variant Human Activation-induced Deoxycytidine Deaminase As An Mbp Fusion Protein	106	106	90%	1e-26	35%	5JJ4_C	☑	
Chain A, First-In-Class Small Molecule Inhibitors Of The Single-Strand Dna Cytosine Deaminase Apobec3g	100	100	86%	3e-26	33%	3V4K_A	☑	
Chain A, Crystal Structure Of The Hiv-1 Vif Binding, Catalytically Active Domain Of Apobec3f	100	100	90%	4e-26	33%	4IOU_A	☑	
Chain A, Nmr Structure Of Human Restriction Factor Apobec3a	93.6	93.6	89%	1e-23	31%	2M65_A	☑	
Chain A, Crystal Structure Of Human Apobec3a	93.2	93.2	89%	2e-23	31%	4XXO_A	☑	
Chain A, Crystal Structure Of Human Apobec3a Complexed With Ssdna	91.7	91.7	89%	8e-23	31%	5SWW_A	☑	
Chain C, Crystal Structure Of The Cancer Genomic Dna Mutator Apobec3b	90.1	90.1	89%	2e-22	32%	5COD_C	☑	
Chain A, Crystal Structure Of The Cancer Genomic Dna Mutator Apobec3b	90.1	90.1	89%	2e-22	32%	5COD_A	☑	
Chain A, Nmr Structure Of The C-terminal Domain Of Human Apobec3b	87.0	87.0	89%	4e-21	32%	2NBQ_A	☑	
Chain A, Crystal Structure Of Human Apobec3b Variant Complexed With Ssdna	85.5	85.5	89%	1e-20	31%	5TD5_A	☑	
Chain A, Crystal Structure Of A Primate Apobec3g N-terminal Domain	81.3	81.3	88%	6e-19	30%	5K81_A	☑	
Chain A, Solution Structure Of The Monomeric Form Of Mouse Apobec2	65.5	65.5	78%	4e-13	31%	2RPZ_A	☑	
Chain A, The Apobec2 Crystal Structure And Functional Implications For Aid	58.9	58.9	81%	1e-10	29%	2NYT_A	☑	

>pdb|3WUS|A Chain A, Crystal Structure Of The Vif-binding Domain Of Human Apobec3f

MEAMYPHIFYFHFKNLRKAYGRNESWLCFTMEVVKHHSPVSWKRGVFRNQVDPETHCHAERCFLSWFCDDILSPNTNYEV

TWYTSWSPCPECAGEVAEFLARHSNVNLTIFTARLYYFWDTDYQEGLRSLSQEGASVEIMGYKDFKYCWENFVYNDDEPF

KPWKGLKYNFLFLDSKLQEI [highest score, e-value]

>pdb|4J4J|A Chain A, Crystal Structure Of The Apobec3f Vif Binding Domain

TFTFNFNNEPWVRGRHETYLCFTMEVVKHHSPVSWKRGVFRNQVDPETHCHAERCFLSWFCDDILSPNTNYEVTWYTSWS

PCPECAGEVAEFLARHSNVNLTIFTARLYYFWDTDYQEGLRSLSQEGASVEIMGYKDFKYCWENFVYNDDEPFKPWKGLK

YNFLFLDSKLQEI   [seond highest score, most identical,

>pdb|5HX4|A Chain A, Zinc-free Apobec3f Catalytic Domain Crystal Structure

MEAMDPHIFYFHFKNLRKAYGRNESWLCFTMEVVKHHSPVSWKRGVFRNQVDPETGRHAERCFLSWFADDILSPNTNYEV

TWYTSWSPCPECAGEVAEFLARHSNVNLTIKTARLYYFDDTDYQEGLRSLSQEGASVEIMGYKDFKYCWENFVYNDDEPF

KPWDGLDYNFLDLDSKLQEI

>pdb|3VM8|A Chain A, Crystal Structure Of The Human Apobec3c Having Hiv-1 Vif-Binding Interface

RNQVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCAGEVAEFLARHSNVNLTIFTARLYYFQYPCYQEGL

RSLSQEGVAVEIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRL

>pdb|2KBO|A Chain A, Structure, Interaction, And Real-Time Monitoring Of The Enzymatic Reaction Of Wild Type Apobec3g

TFTFNFNNEPWVRGRHETYLCYEVERMHNDTWVLLNQRRGFLCNQAPHKHGFLEGRHAELCFLDVIPFWKLDLDQDYRVT

CFTSWSPCFSCAQEMAKFISKNKHVSLCIFTARIYDDQGRCQEGLRTLAEAGAKISIMTYSEFKHCWDTFVDHQGCPFQP

WDGLDEHSQDLSGRLRAI

>pdb|2RPZ|A Chain A, Solution Structure Of The Monomeric Form Of Mouse Apobec2

FKFQFRNVEYSSGRNKTFLCYVVEVQSKGGQAQATQGYLEDEHAGAHAEEAFFNTILPAFDPALKYNVTWYVSSSPCAAC

ADRILKTLSKTKNLRLLILVSRLFMWEEPEVQAALKKLKEAGCKLRIMKPQDFEYIWQNFVEQEEGESKAFEPWEDIQE

M-Coffee alignment result

MSA

The multiple sequence alignment result as produced by T-coffee.

```
T-COFFEE, Version_11.00.d625267 (2016-01-11 15:25:41 - Revision d625267 - Build 507)
Cedric Notredame
SCORE=916
*
 BAD AVG GOOD
*
sp|Q6NTF7|ABC3H    :  89
pdb|3WUS|A         :  90
pdb|4J4J|A         :  90
pdb|5HX4|A         :  90
pdb|3VM8|A         :  93
pdb|2KBO|A         :  83
pdb|2RPZ|A         :  90
cons               :  91

sp|Q6NTF7|ABC3H    MALLTAETFRLQFNNKRRLRRPYYPRKALLCYQLTPQNGSTP-----TRGYFENK--------
pdb|3WUS|A         MEAMYPHIFYFHFKNLRK---AYGRNESWLCFTMEVVKHHSPVSW--KRGVFRNQVDPE----
pdb|4J4J|A         -------TFTFNFNNEPW---VRGRHETYLCFTMEVVKHHSPVSW--KRGVFRNQVDPE----
pdb|5HX4|A         MEAMDPHIFYFHFKNLRK---AYGRNESWLCFTMEVVKHHSPVSW--KRGVFRNQVDPE----
pdb|3VM8|A         ----------------------------------------------------RNQVDSE----
pdb|2KBO|A         -------TFTFNFNNEPW---VRGRHETYLCYEVERMHNDTWVLLNQRRGFLCNQAPHKHGFL
pdb|2RPZ|A         --------FKFQFRNVEY---SSGRNKTFLCYVVEVQSKGGQAQA--TQGYLEDEH-------

cons               

sp|Q6NTF7|ABC3H    KKCHAEICFINEIKSMGLDETQCYQVTCYLTWSPCSSCAWELVDFIKAHDHLNLGIFASRLYY
pdb|3WUS|A         THCHAERCFLSWFCDDILSPNTNYEVTWYTSWSPCPECAGEVAEFLARHSNVNLTIFTARLYY
pdb|4J4J|A         THCHAERCFLSWFCDDILSPNTNYEVTWYTSWSPCPECAGEVAEFLARHSNVNLTIFTARLYY
pdb|5HX4|A         TGRHAERCFLSWFADDILSPNTNYEVTWYTSWSPCPECAGEVAEFLARHSNVNLTIKTARLYY
pdb|3VM8|A         THCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCAGEVAEFLARHSNVNLTIFTARLYY
pdb|2KBO|A         EGRHAELCFLDVIPFWKLDLDQDYRVTCFTSWSPCFSCAQEMAKFISKNKHVSLCIFTARIYD
pdb|2RPZ|A         AGAHAEEAFFNTI-LPAFDPALKYNVTWYVSSSPCAACADRILKTLSKTKNLRLLILVSRLFM

cons                  *** .*:. :    :.    *.** : : ***  ** .: . :   .:: * * .:*::

sp|Q6NTF7|ABC3H    HWCKPQQKGLRLLCGSQVPVEVMGFPKFADCWENFVDHEKPLSFNPYKMLEELDKNSRAIKRR
pdb|3WUS|A         FWDTDYQEGLRSLSQEGASVEIMGYKDFKYCWENFVYNDD----EPFKPWKGLKYNFLFLDSK
pdb|4J4J|A         FWDTDYQEGLRSLSQEGASVEIMGYKDFKYCWENFVYNDD----EPFKPWKGLKYNFLFLDSK
pdb|5HX4|A         FDDTDYQEGLRSLSQEGASVEIMGYKDFKYCWENFVYNDD----EPFKPWDGLDYNFLDLDSK
pdb|3VM8|A         FQYPCYQEGLRSLSQEGVAVEIMDYEDFKYCWENFVYNDN----EPFKPWKGLKTNFRLLKRR
pdb|2KBO|A         D-QGRCQEGLRTLAEAGAKISIMTYSEFKHCWDTFVDHQG----CPFQPWDGLDEHSQDLSGR
pdb|2RPZ|A         WEEPEVQAALKKLKEAGCKLRIMKPQDFEYIWQNFVEQEEGES-KAFEPWEDIQE--------

cons                  * .*: *      : :*   .*   *:.** ::  .::  . :.

sp|Q6NTF7|ABC3H    LERIKIPGVRAQGRYMDILCDAEV
pdb|3WUS|A         LQE--------------------I
pdb|4J4J|A         LQE--------------------I
pdb|5HX4|A         LQE--------------------I
pdb|3VM8|A         L-----------------------
pdb|2KBO|A         LRA--------------------I
pdb|2RPZ|A         -----------------------

cons               
```

Expresso alignment result

MSA

The multiple sequence alignment result as produced by T-coffee.

```
T-COFFEE, Version_11.00.d625267 (2016-01-11 15:25:41 - Revision d625267 - Build 507)
Cedric Notredame
SCORE=95
*
 BAD AVG GOOD
*
sp|Q6NTF7|ABC3H    :  95
pdb|3WUS|A         :  95
pdb|4J4J|A         :  96
pdb|5HX4|A         :  96
pdb|3VM8|A         :  93
pdb|2KBO|A         :  97
pdb|2RPZ|A         :  95
cons               :   9

sp|Q6NTF7|ABC3H    MALLTAETFRLQFNNKR--RLRRPYYPRKALLCYQLTPQNGSTPT-----RGYFENK------
pdb|3WUS|A         MEAMYPHIFYFHFKNLRKAYGRNESW-----LCFTMEVVKHHSPV--SWKRGVFRNQVDPE--
pdb|4J4J|A         -------TFTFNFNNEPWVRGRHETY-----LCFTMEVVKHHSPV--SWKRGVFRNQVDPE--
pdb|5HX4|A         MEAMDPHIFYFHFKNLRKAYGRNESW-----LCFTMEVVKHHSPV--SWKRGVFRNQVDPE--
pdb|3VM8|A         ------------------------------------------------RNQVDSE--
pdb|2KBO|A         -------TFTFNFNNEPWVRGRHETY-----LCYEVERMHNDTWVLLNQRRGFLCNQ---APH
pdb|2RPZ|A         --------FKFQFRNVEYSSGRNKTF-----LCYVVEVQSKGGQA--QATQGYLEDE---H--

cons               

sp|Q6NTF7|ABC3H    -----KKCHAEICFIN----EIKSMGLDETQCYQVTCYLTWSPCSSCAWELVDFIKAHDHLNL
pdb|3WUS|A         -----THCHAERCFLSWFCDDILS---PNTN-YEVTWYTSWSPCPECAGEVAEFLARHSNVNL
pdb|4J4J|A         -----THCHAERCFLSWFCDDILS---PNTN-YEVTWYTSWSPCPECAGEVAEFLARHSNVNL
pdb|5HX4|A         -----TGRHAERCFLSWFADDILS---PNTN-YEVTWYTSWSPCPECAGEVAEFLARHSNVNL
pdb|3VM8|A         -----THCHAERCFLSWFCDDILS---PNTK-YQVTWYTSWSPCPDCAGEVAEFLARHSNVNL
pdb|2KBO|A         KHGFLEGRHAELCFLDVIPFWKLD---LDQD-YRVTCFTSWSPCFSCAQEMAKFISKNKHVSL
pdb|2RPZ|A         -----AGAHAEEAFFNTILPA-FD---PALK-YNVTWYVSSSPCAACADRILKTLSKTKNLRL

cons                    *** .*:.    .    . *.** : : ***  ** .: . :   .:: *

sp|Q6NTF7|ABC3H    GIFASRLYYHWCKPQQKGLRLLCGSQ--VPVEVMGFPKFADCWENFVD--HEKPLSFNPYKML
pdb|3WUS|A         TIFTARLYYFWDTDYQEGLRSL--SQEGASVEIMGYKDFKYCWENFVYNDDE---PFKPWK--
pdb|4J4J|A         TIFTARLYYFWDTDYQEGLRSL--SQEGASVEIMGYKDFKYCWENFVYNDDE---PFKPWK--
pdb|5HX4|A         TIKTARLYYFDDTDYQEGLRSL--SQEGASVEIMGYKDFKYCWENFVYNDDE---PFKPWD--
pdb|3VM8|A         TIFTARLYYFQYPCYQEGLRSL--SQEGVAVEIMDYEDFKYCWENFVYNDNE---PFKPWK--
pdb|2KBO|A         CIFTARIY-DDQGRCQEGLRTL--AEAGAKISIMTYSEFKHCWDTFVDHQGC---PFQPWD--
pdb|2RPZ|A         LILVSRLFMWEEPEVQAALKKL--KEAGCKLRIMKPQDFEYIWQNFVEQEEGESKAFEPWE--

cons               * .:*::      * .*: *   :    : :*   .*   *:.**    .*:*:.

sp|Q6NTF7|ABC3H    EELDKNSRAIKRRLERIKIPGVRAQGRYMDILCDAE---V
pdb|3WUS|A         --------------------GLK----YNFLFLDSKLQEI
pdb|4J4J|A         --------------------GLK----YNFLFLDSKLQEI
pdb|5HX4|A         --------------------GLD----YNFLDLDSKLQEI
pdb|3VM8|A         --------------------GLK----TNFRLLKRR---L
pdb|2KBO|A         --------------------GLD----EHSQDLSGRLRAI
pdb|2RPZ|A         --------------------DIQE----------------

cons                                  .:     
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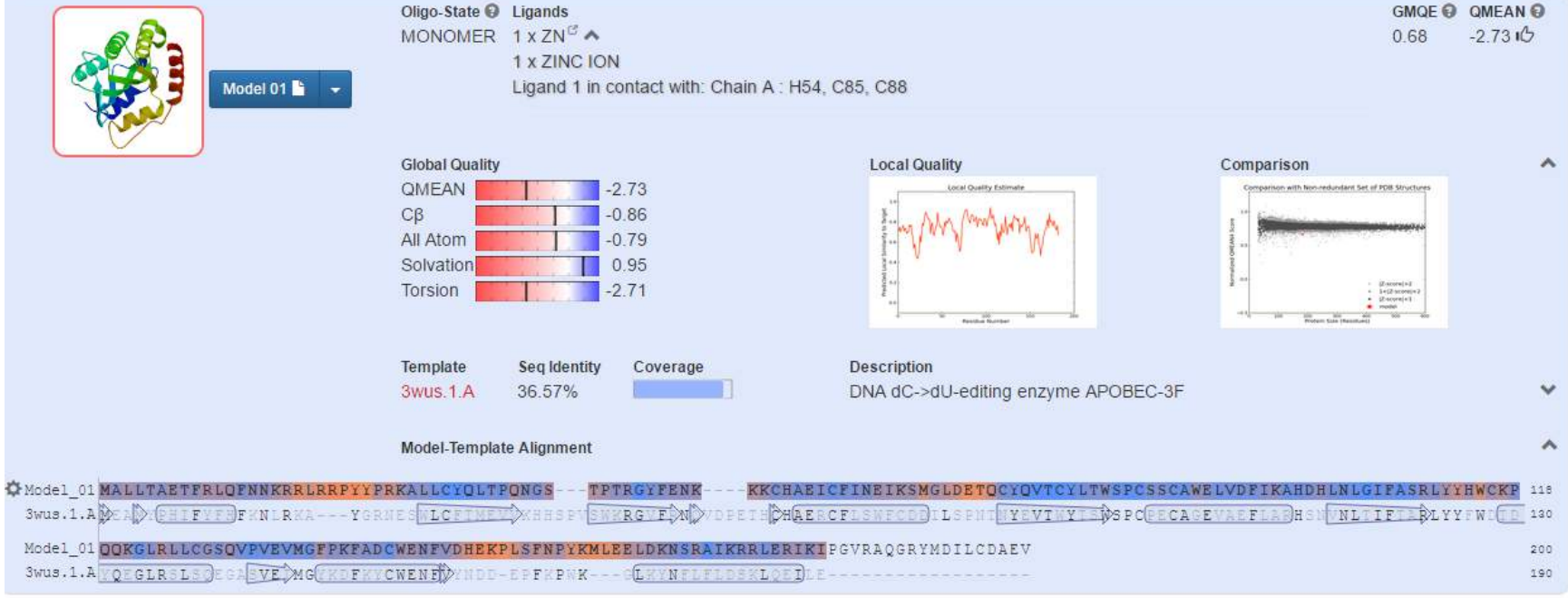
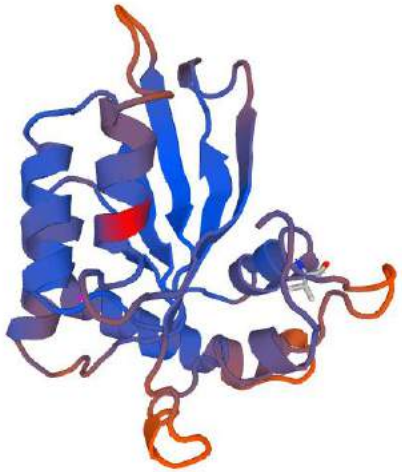
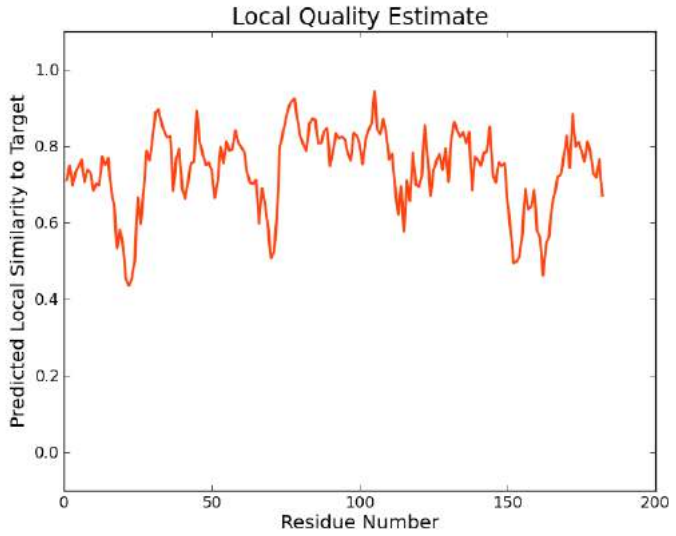
SWISS MODEL https://swissmodel.expasy.org/interactive/BrHg6c/models/



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Predicted Local Similarity to Target
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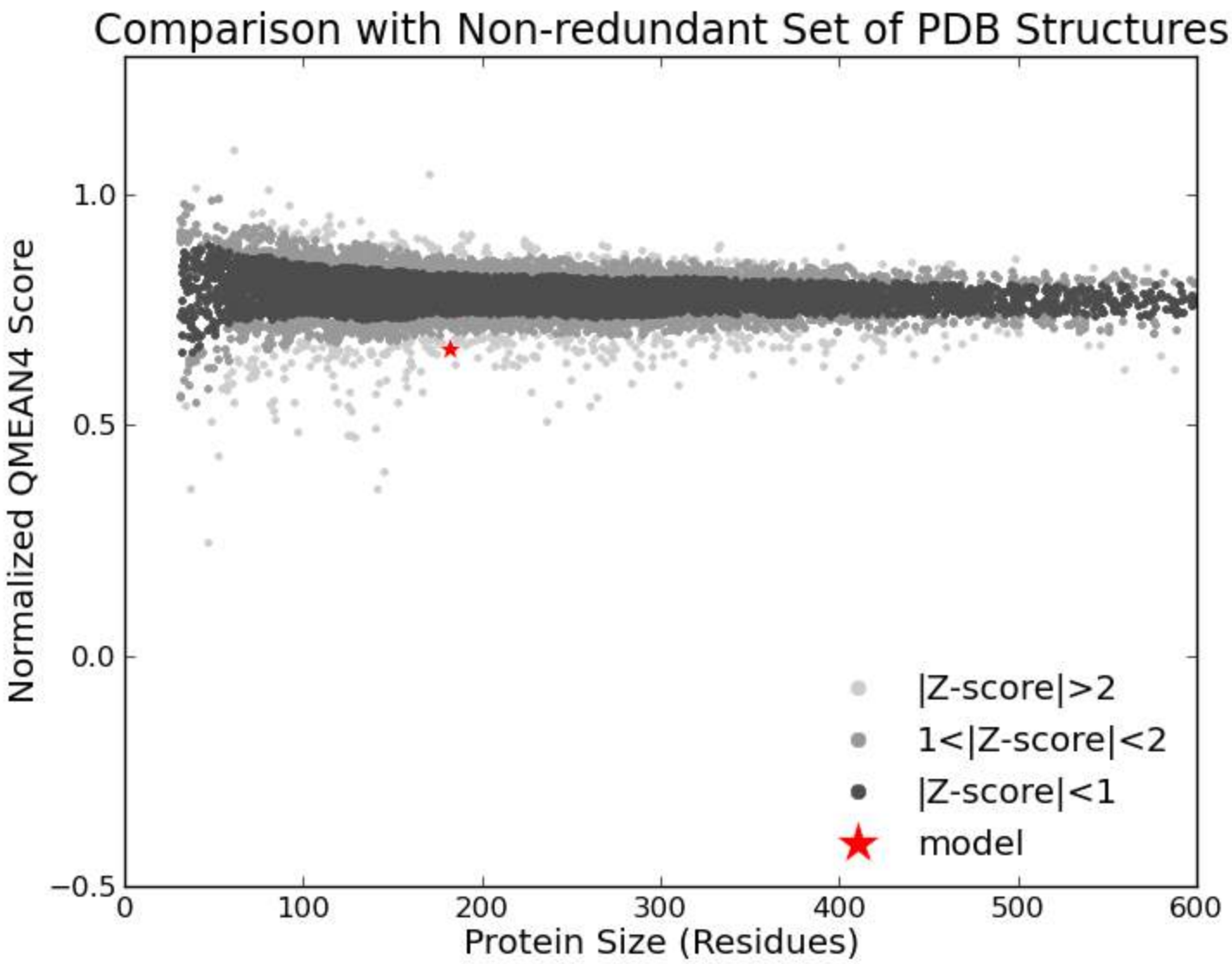
Comparison with Non-redundant Set of PDB Structures
Normalized QMEAN4 Score
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−0.5
0
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300
400
500
600
Protein Size (Residues)
|Z-score|>2
1<|Z-score|<2
|Z-score|<1
model

	Name	Title	Coverage	Identity	Method	Oligo State	Ligands
	5jj4.1.A	Maltose-binding periplasmic protein,Single-stranded DNA cytosine deaminase		40.14	X-ray, 2.8Å	monomer	1 x ZN, 1 x CA, 1 x MTT
	4j4j.2.A	DNA dC->dU-editing enzyme APOBEC-3F		39.46	X-ray, 3.1Å	monomer	1 x ZN
	4j4j.1.A	DNA dC->dU-editing enzyme APOBEC-3F		39.46	X-ray, 3.1Å	monomer	1 x ZN
	3wus.1.A	DNA dC->dU-editing enzyme APOBEC-3F		39.46	X-ray, 2.5Å	monomer	1 x ZN
	4j4j.1.A	DNA dC->dU-editing enzyme APOBEC-3F		38.93	X-ray, 3.1Å	monomer	1 x ZN
	4j4j.2.A	DNA dC->dU-editing enzyme APOBEC-3F		38.93	X-ray, 3.1Å	monomer	1 x ZN
	3vow.2.A	Probable DNA dC->dU-editing enzyme APOBEC-3C		37.71	X-ray, 2.1Å	monomer	1 x ZN
	3vow.1.A	Probable DNA dC->dU-editing enzyme APOBEC-3C		37.71	X-ray, 2.1Å	monomer	1 x ZN
	3vm8.2.A	Probable DNA dC->dU-editing enzyme APOBEC-3C		37.71	X-ray, 3.0Å	monomer	1 x ZN
	3vm8.1.A	Probable DNA dC->dU-editing enzyme APOBEC-3C		37.71	X-ray, 3.0Å	monomer	1 x ZN
	2m65.1.A	Probable DNA dC->dU-editing enzyme APOBEC-3A		36.99	NMR	monomer	1 x ZN
✓	3wus.1.A	DNA dC->dU-editing enzyme APOBEC-3F		36.57	X-ray, 2.5Å	monomer	1 x ZN
	5sww.1.A	DNA dC->dU-editing enzyme APOBEC-3A		36.30	X-ray, 3.2Å	monomer	1 x ZN
	4xxo.1.A	DNA dC->dU-editing enzyme APOBEC-3A		36.30	X-ray, 2.8Å	homo-dimer	7 x ZN
	5sww.3.A	DNA dC->dU-editing enzyme APOBEC-3A		36.30	X-ray, 3.2Å	monomer	1 x ZN

Analysis of the Results

Critical evaluation of the model and of the alignments

Discuss a possible function for the protein