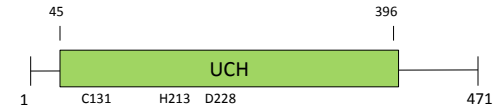
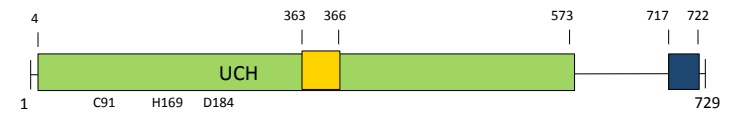


# UCH Domains

## FlyDUB: CG8445 (Calypso)



## Closest Human DUB: BAP1

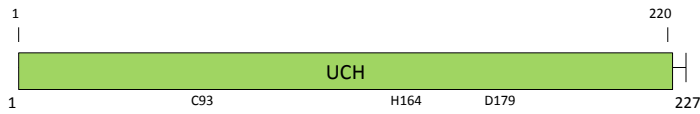


HBM-like motif

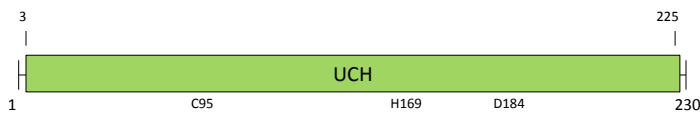
Nuclear localization signal

Coverage – 73%  
E-value – 2e-107  
Max Identity – 61%

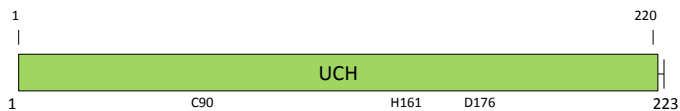
## FlyDUB: CG4265 (Uch)



## Closest Human DUB: UCHL3



## Second Closest Human DUB: UCHL1



UCHL3:

Coverage – 97%

E-value – 2e-77

Max Identity – 51%

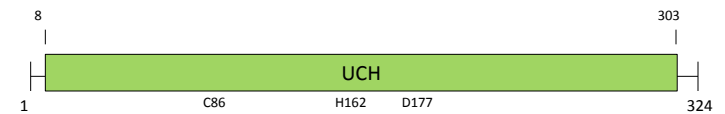
UCHL1:

Coverage – 98%

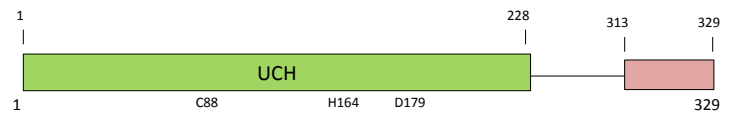
E-value – 1e-66

Max Identity – 45%

## FlyDUB: CG3431 (Uch-L3)



## Closest Human DUB: UCH-L5/UCH37

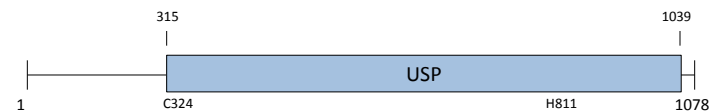


ADRM1 interacting region

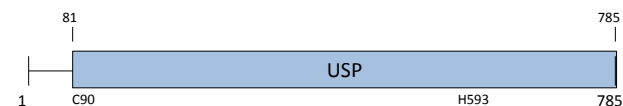
Coverage – 99%  
E-value – 2e-144  
Max Identity – 60%

# USP Domains

FlyDUB: CG15817

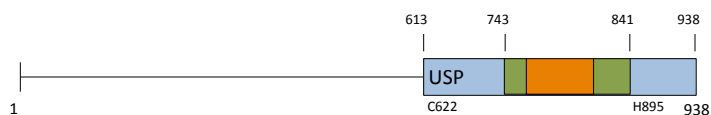


Closest Human DUB: USP1

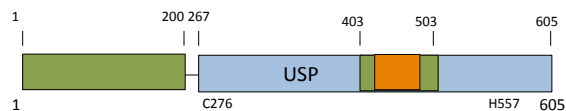


Coverage – 41%  
E-value – 4e-18  
Max Identity – 41%

FlyDUB: CG14619



Closest Human DUB: USP2

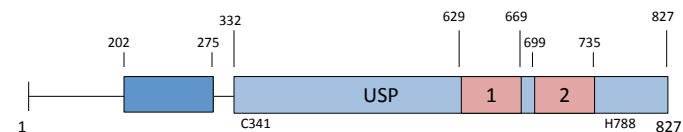


Zinc-binding residues:  
425, 428, 476, 479 in USP2  
765, 768, 814, 817 in CG14619

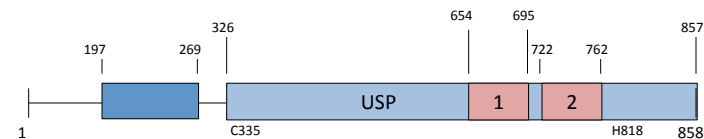
MDM4 interacting domain: E-value 2e-33, 56% identity

Coverage – 34%  
E-value – 1e-91  
Max Identity – 47%

FlyDUB: CG12082



Closest Human DUB: USP5/isopeptidase T

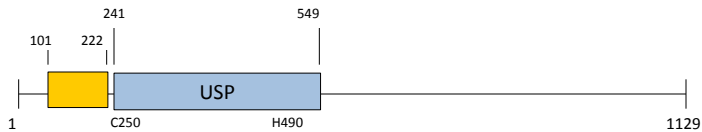


UBA domains:  
1 E-value 2e-13, 57% identity  
2 E-value 3e-10, 51% identity

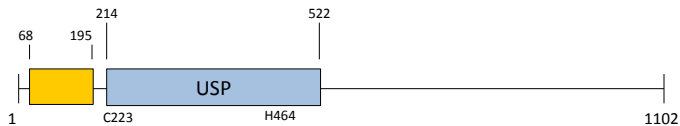
UBP-type zinc finger: E-value 3e-35, 77% identity

Coverage – 99%  
E-value – 0.0  
Max Identity – 51%

**FlyDUB: CG1490 (Usp7)**



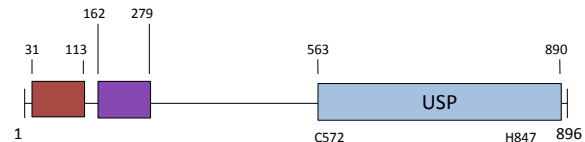
**Closest Human DUB: USP7/HAUSP**



MATH domain: E-value 2e-35, 48% identity

Coverage – 95%  
E-value – 0.0  
Max Identity – 49%

**FlyDUB: CG5798 (Ubpy)**



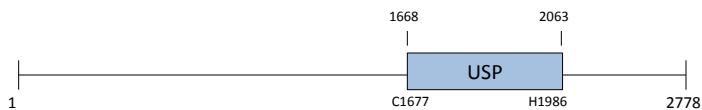
**Closest Human DUB: USP8/UBPY**



SH3 domain  
MIT domain: E-value 1e-12, 34% identity  
Rhodanese domain: E-value 2e-19, 33% identity

Coverage – 92%  
E-value – 2e-89  
Max Identity – 45%

**FlyDUB: CG1945 (faf)**



**Closest Human DUB: USP9X/FAF-X**



Coverage – 92%  
E-value – 0.0  
Max Identity – 47%

**FlyDUB: CG32479**

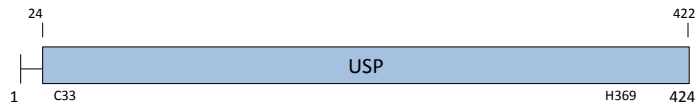


**Closest Human DUB: USP10**

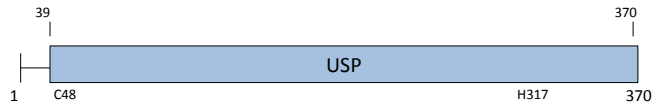


Coverage – 27%  
E-value – 4e-89  
Max Identity – 41%

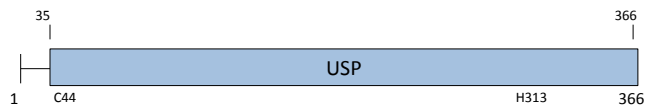
**FlyDUB: CG7023**



**Closest Human DUB: USP12**



**Second Closest Human DUB: USP46**



USP12: Coverage – 80% E-value – 2e-118 Max Identity – 77%	USP46: Coverage – 58% E-value – 1e-125 Max Identity – 77%
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**FlyDUB: CG5384**



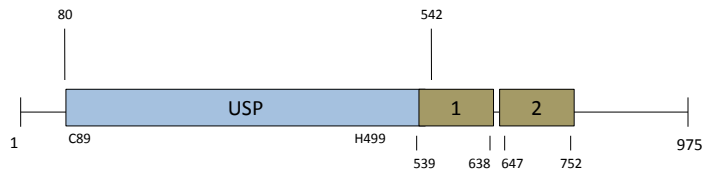
**Closest Human DUB: USP14**



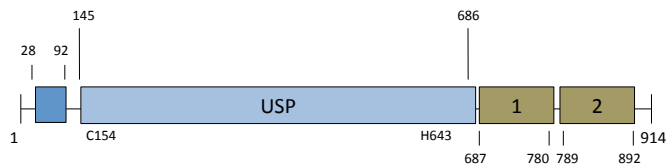
Coverage – 99% E-value – 0.0 Max Identity – 55%
---

UBL domain: E-value 8e-24, 60% identity

**FlyDUB: CG8494**



**Closest Human DUB: USP20**

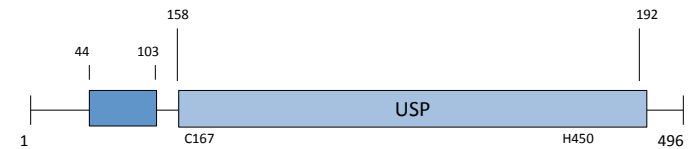


UBP-type zinc finger

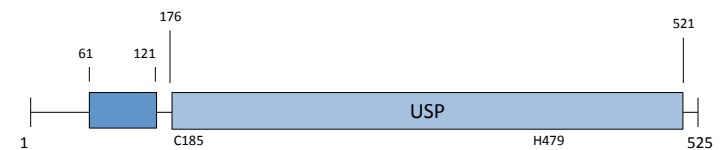
DUSP domains:  
1 E-value 8e-23, 43% identity  
2 E-value 8e-22, 38% identity

Coverage – 67% E-value – 2e-156 Max Identity – 48%
--

**FlyDUB: CG4166 (Non-stop)**



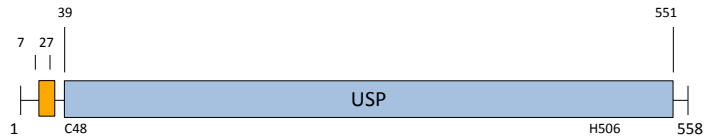
**Closest Human DUB: USP22**



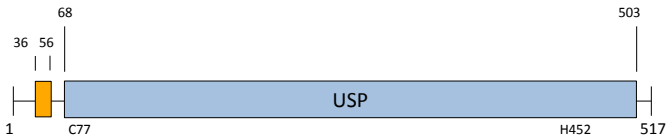
UBP-type zinc finger: E-Value 2e-108, 44% identity

Coverage – 100% E-value – 0.0 Max Identity – 51%
--

**FlyDUB: CG3016**



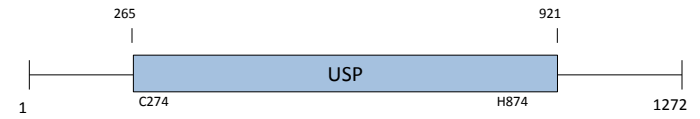
**Closest Human DUB: USP30**



Transmembrane region: E-value 0.001, 43% identity

Coverage – 72%  
E-value – 8e-42  
Max Identity – 35%

**FlyDUB: CG30421**



**Closest Human DUB: USP31**



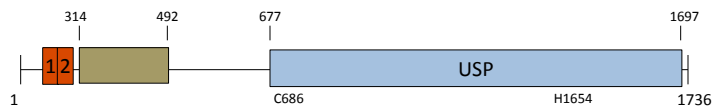
**Second Closest Human DUB: USP43**



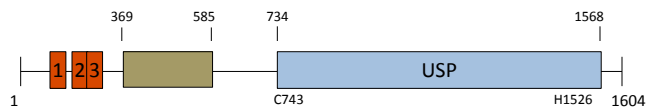
USP31:  
Coverage – 54%  
E-value – 3e-138  
Max Identity – 37%

USP43:  
Coverage – 56%  
E-value – 1e-132  
Max Identity – 37%

**FlyDUB: CG8334**



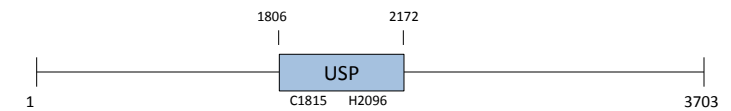
**Closest Human DUB: USP32**



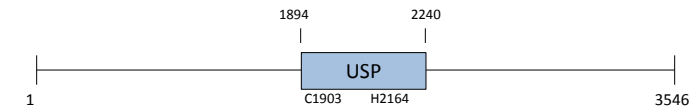
USP32  
EF-hand 1: 91-126  
EF-hand 2: 228-263  
EF-hand 3: 264-299  
CG8334  
EF-hand 1: 168-196 (E-value 1e-13, 82% identity)  
EF-hand 2: 197-232 (E-value 7e-10, 61% identity)  
DUSP domain: E-value 9e-27, 31% identity

Coverage – 78%  
E-value – 0.0  
Max Identity – 47%

**FlyDUB: CG5794**

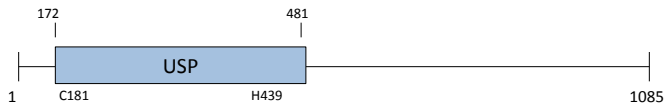


**Closest Human DUB: USP34**

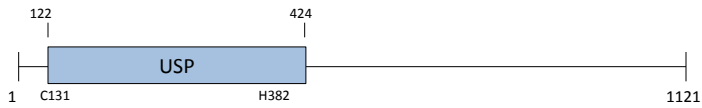


Coverage – 77%  
E-value – 0.0  
Max Identity – 53%

**FlyDUB: CG5505 (Scrawny/Usp36)**



**Closest Human DUB: USP36**

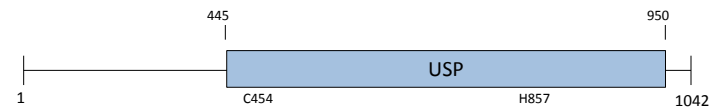


Coverage – 40%  
E-value – 3e-75  
Max Identity – 34%

**FlyDUB: CG8830**

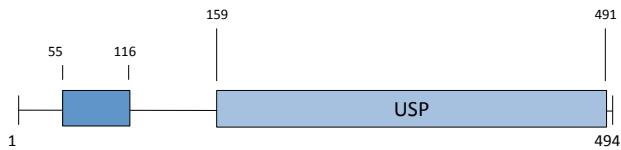


**Closest Human DUB: USP38**

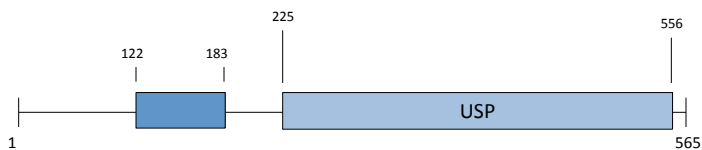


Coverage – 80%  
E-value – 2e-48  
Max Identity – 30%

**FlyDUB: CG7288**



**Closest Human DUB: U4/U6.U5 tri-snRNP-associated protein 2 (inactive USP39)**



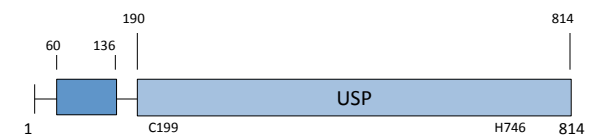
Coverage – 92%  
E-value – 0.0  
Max Identity – 65%

UBP-type zinc finger: E-Value 3e-31, 82% identity

**FlyDUB: CG4165**



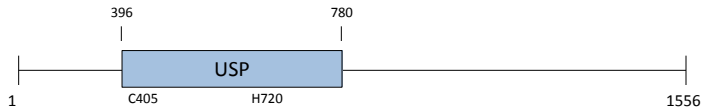
**Closest Human DUB: USP45**



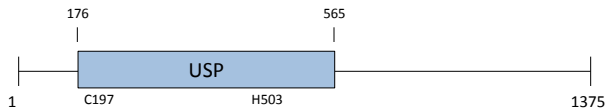
Coverage – 54%  
E-value – 1e-36  
Max Identity – 47%

UBP-type zinc finger: E-value 6e-15, 43% identity

**FlyDUB: CG5486 (Ubp64E)**

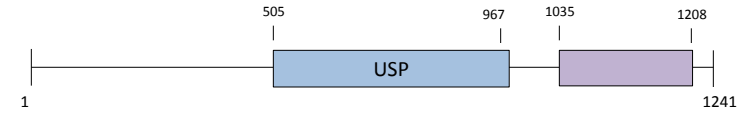


**Closest Human DUB: USP47**

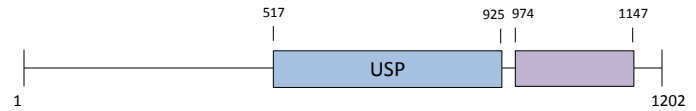


Coverage – 56%  
E-value – 2e-170  
Max Identity – 50%

**Fly DUB: CG8232**



**Closest Human DUB: PAB-dependent poly(A)-specific ribonuclease subunit 2 isoform 1 (USP52)**



Exonuclease domain: E-value 6e-76, 72% identity

Coverage – 96%  
E-value – 0.0  
Max Identity – 41%

**Fly DUB: CG2904 (Echinus)**

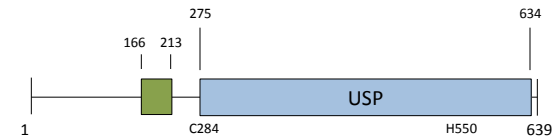


**Closest Human DUB: inactive USP54**

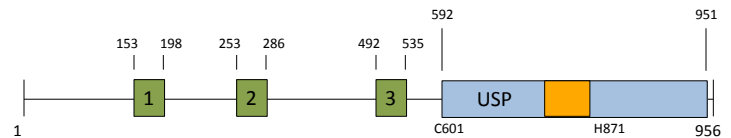


Coverage – 15%  
E-value – 7e-89  
Max Identity – 50%

**Fly DUB: CG5603 (Cylindromatosis)**



**Closest Human DUB: CYLD isoform 1**



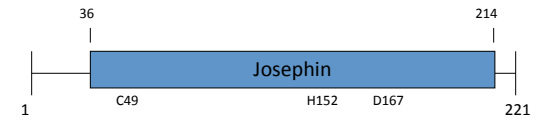
CAP-Gly domains:  
3 E-value 5e-7, 43% identity

Zinc binding residues: 788, 791, 799, 802, 817, 820, 825, 833

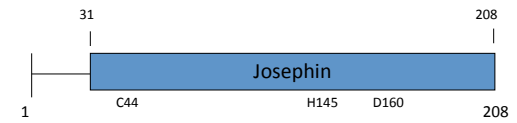
Coverage – 80%  
E-value – 7e-144  
Max Identity – 46%

# Josephin Domains

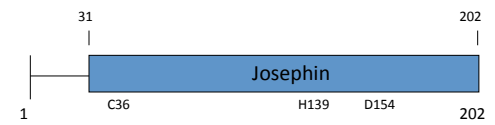
## Fly DUB: CG3781



## Closest Human DUB: JOSD2



## Second Closest Human DUB: JOSD1



### Josephin Domains:

JOSD2 E-value 3e-44, 50% identity

JOSD1 E-value 7e-43, 44% identity

### JOSD2

Coverage – 85%

E-value – 1e-53

Max Identity – 49%

### JOSD1

Coverage – 77%

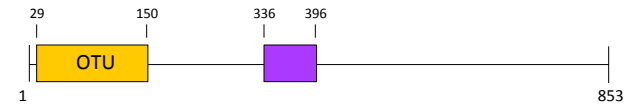
E-value – 1e-48

Max Identity – 45%



# OTU Domains

## Fly DUB: CG12743 (Otu)



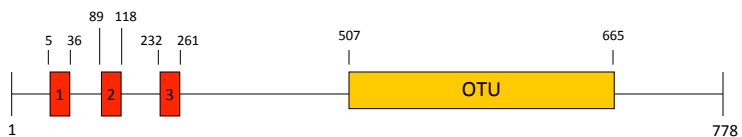
## Closest Human DUB: OTU domain-containing protein 4 (OTUD4), isoform CRA-f



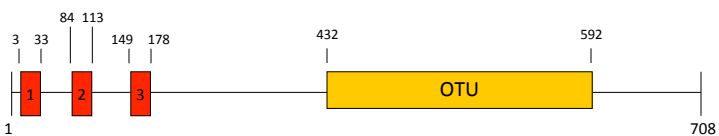
putative Tudor domain by Prosite analysis

Coverage – 56%  
E-value – 2e-42  
Max Identity – 30%

## Fly DUB: CG9448 (Trabid)



## Closest Human DUB: TRABID



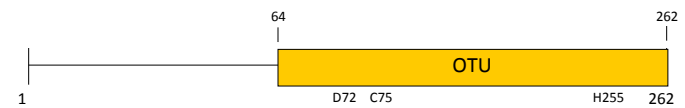
RanBP2-type zinc finger:

- 1 E-value 5e-12, 67% identity
- 2 E-value 2e-11, 57% identity
- 3 E-value 1e-10, 68% identity

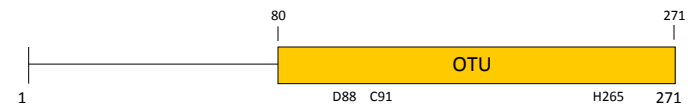
OTU Domain: E-value 2e-70, 68% identity

Coverage – 96%  
E-value – 0.0  
Max Identity – 43%

## Fly DUB: CG4968

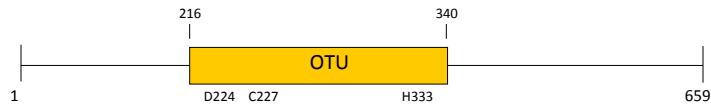


## Closest Human DUB: ubiquitin thioesterase OTUB1

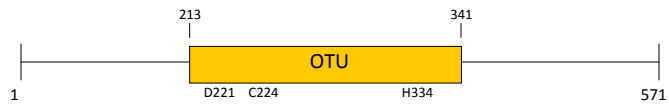


Coverage – 95%  
E-value – 8e-98  
Max Identity – 56%

**Fly DUB: CG6091**

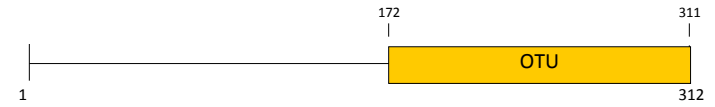


**Closest Human DUB: OTUD5 protein**

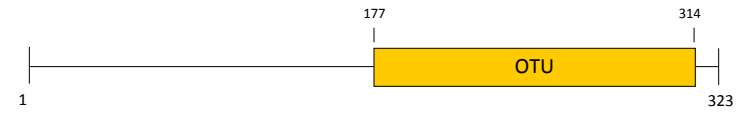


Coverage – 36%  
E-value – 1e-76  
Max Identity – 48%

**Fly DUB: CG7857**

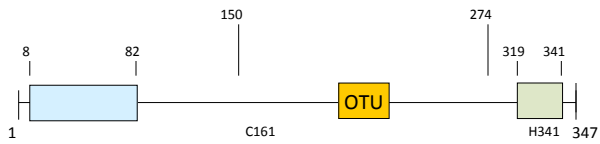


**Closest Human DUB: OTU domain-containing protein 6B, OTU6B**

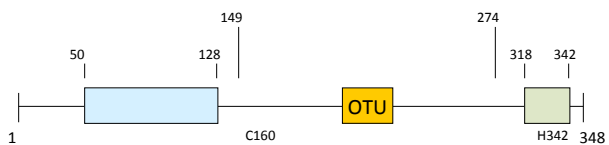


Coverage – 91%  
E-value – 8e-61  
Max Identity – 39%

**FlyDUB: CG4603**



**Closest Human DUB: OTU1/YOD1**

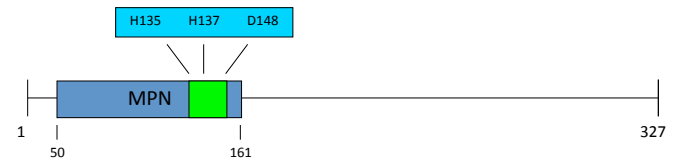


UBX-like domain: E-value 9e-11, 37% identity  
C2H2-type zinc finger: E-value 1e-8, 64% identity

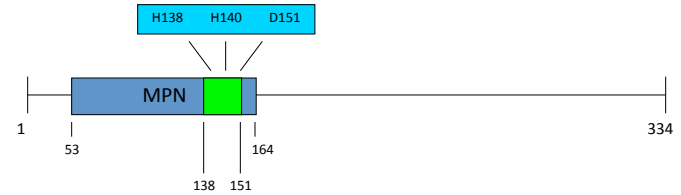
Coverage – 98%  
E-value – 5e-84  
Max Identity – 42%

# MPN Domains

**Fly DUB: CG14884 (Csn5)**



**Closest Human DUB: COP9 signalosome complex subunit 5, SCN5**



JAMM Motif  
 Zinc Coordinating Residues  
 MPN Domain: E-value 1e-55, 83% identity

Coverage – 98%  
 E-value – 0.0  
 Max Identity – 75%

**Fly DUB: CG6932 (Csn6)**



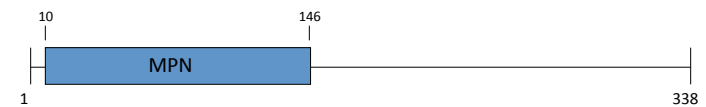
**Closest Human DUB: COP9 signalosome complex subunit 6, CSN6**



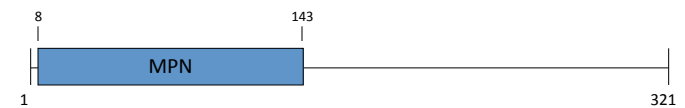
MPN Domain: E-value 2e-30, 60% identity  
 Interaction with VPR: E-value 2e-46, 64% identity

Coverage – 87%  
 E-value – 2e-146  
 Max Identity – 62%

**Fly DUB: CG3416 (Mov34)**



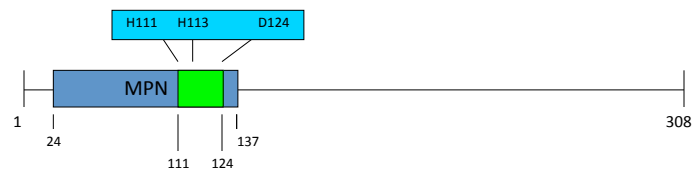
**Closest Human DUB: 26S proteasome non-ATPase regulatory subunit 7, PSMD7**



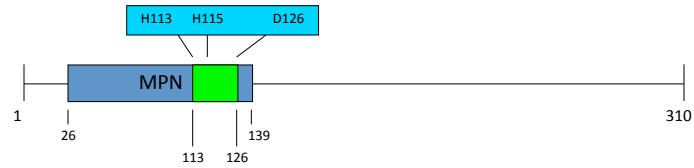
MPN Domain: E-value 6e-75, 90% identity

Coverage – 85%  
 E-value – 2e-170  
 Max Identity – 82%

**Fly DUB: CG18174 (Rpn11)**



**Closest Human DUB: 26S proteasome non-ATPase regulatory subunit 14, POH1, PSMD14**



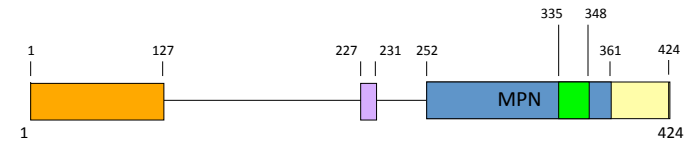
JAMM Motif  
Zinc Coordinating Residues  
MPN Domain: E-value 1e-65, 98% identity

Coverage – 94%  
E-value – 0.0  
Max Identity – 90%

**Fly DUB: CG2224**



**Closest Human DUB: STAM-binding protein, AMSH**



Interaction with CHMP3  
Interaction with STAM1  
JAMM Motif  
Catalytic Domain: E-value 1e-61, 58% identity

Coverage – 97%  
E-value – 3e-106  
Max Identity – 42%

**Fly DUB: CG9769**



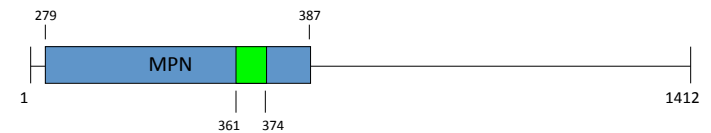
**Closest Human DUB: eukaryotic translation initiation factor 3 subunit H, EIF3H**



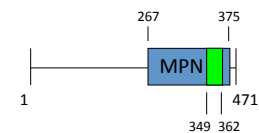
MPN Domain: E-value 1e-34, 53% identity

Coverage – 93%  
E-value – 4e-99  
Max Identity – 46%

**Fly DUB: CG4751**



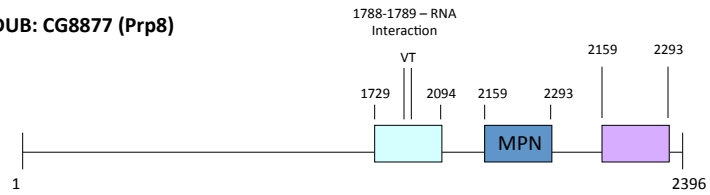
**Closest Human DUB: MPND (MPN domain-containing protein) isoform 1**



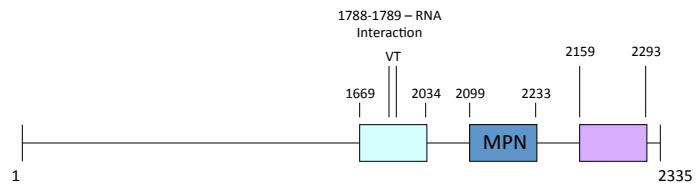
JAMM Motif  
MPN Domain: E-value 7e-32, 49% identity

Coverage – 27%  
E-value – 8e-80  
Max Identity – 37%

**Fly DUB: CG8877 (Prp8)**



**Closest Human DUB: pre-mRNA-processing-splicing factor 8, PRPF8**



MPN Domain: E-value 4e-73, 85% identity

Interacts with pre-mRNA 5' splice

EFTUb2/SNRNP200 Interaction

Coverage – 97%

E-value – 0.0

Max Identity – 91%